wwPDB EM Validation Summary Report (i)

Jun 3, 2024 – 03:58 PM EDT

PDB ID	:	7UNG
EMDB ID	:	EMD-26624
Title	:	48-nm repeat of the human respiratory doublet microtubule
Authors	:	Gui, M.; Croft, J.T.; Zabeo, D.; Acharya, V.; Kollman, J.M.; Burgoyne, T.; Hoog, J.L.; Brown, A.
Deposited on	:	2022-04-11
Resolution	:	3.60 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

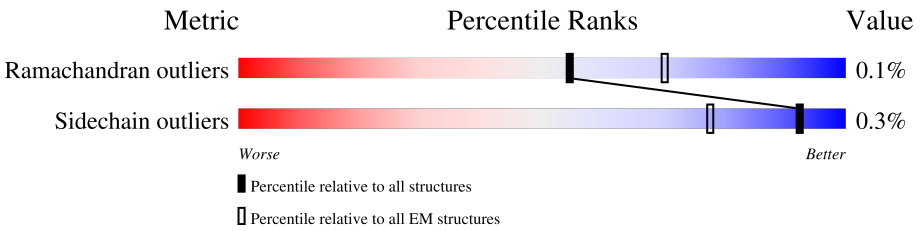
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	229	23% 77%
1	7	229	5% 64% 36%
2	1	833	33% 67%
2	2	833	53% 46%
3	3	514	58% 42%
3	4	514	42% 58%
4	5	376	99%
4	6	376	98%
5	8	194	5% 86% 13%

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Mol	Chain	Length	Quality of chain
5	9	194	25% 75%
6	A	101	50% 50%
7	A0	418	52% 47%
7	A1	418	93% 6%
7	A2	418	93% 6%
7	A3	418	80% 20%
7	A4	418	8% 92%
8	AA	451	96%
8	AC	451	97%
8	AE	451	97%
8	AG	451	97%
8	AI	451	97%
8	AK	451	97%
8	AM	451	96%
8	BA	451	95%
8	BC	451	97%
8	BE	451	95%
8	BG	451	97%
8	BI	451	95%
8	BK	451	97%
8	BM	451	96%
8	CA	451	95%
8	CC	451	97%
8	CE	451	95% 5%
8	CG	451	97%

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Mol	Chain	Length	Quality of chain
8	CI	451	96%
8	CK	451	97%
8	CM	451	95%
8	DA	451	84% 15%
8	DC	451	95% 5%
8	DE	451	95%
8	DG	451	95% 5%
8	DI	451	95% 5%
8	DK	451	95% 5%
8	DM	451	95%
8	EC	451	97%
8	EE	451	97%
8	EG	451	97%
8	EI	451	97%
8	EK	451	97%
8	EM	451	97%
8	FC	451	95%
8	FE	451	95%
8	FG	451	95% 5%
8	FI	451	95% 5%
8	FK	451	95% 5%
8	FM	451	95% 5%
8	GC	451	96%
8	GE	451	95% 5%
8	GG	451	95%

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Mol	Chain	Length	Quality of chain
8	GI	451	95% 5%
8	GK	451	95%
8	GM	451	96%
8	HC	451	95%
8	HE	451	96%
8	HG	451	95%
8	HI	451	95%
8	HK	451	95%
8	HM	451	95%
8	HO	451	86% 14%
8	IC	451	95%
8	IE	451	96%
8	IG	451	97%
8	II	451	96%
8	IK	451	97%
8	IM	451	96%
8	IO	451	95%
8	JC	451	97%
8	JE	451	95% 5%
8	JG	451	95% 5%
8	JI	451	95% 5%
8	JK	451	95%
8	JM	451	95% 5%
8	KC	451	96%
8	KE	451	95%

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Mol	Chain	Length	Quality of chain
8	KG	451	96%
8	KI	451	95% 5%
8	KK	451	95%
8	KM	451	96%
8	KO	451	95%
8	LC	451	96%
8	LE	451	97%
8	LG	451	95%
8	LI	451	96%
8	LK	451	96%
8	LM	451	95%
8	MC	451	97%
8	ME	451	95%
8	MG	451	95%
8	MI	451	96%
8	MK	451	97%
8	MM	451	98%
8	NC	451	97%
8	NE	451	96%
8	NG	451	96%
8	NI	451	97%
8	NK	451	96%
8	NM	451	96%
8	OC	451	97%
8	OE	451	97%

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Mol	Chain	Length	Quality of chain
8	OG	451	98%
8	OI	451	98%
8	OK	451	97%
8	OM	451	97%
8	OO	451	94% 6%
8	PC	451	97%
8	PE	451	97%
8	PG	451	97%
8	PI	451	97%
8	PK	451	97%
8	PM	451	97%
8	PO	451	97%
8	QC	451	97%
8	QE	451	98%
8	QG	451	97%
8	QI	451	97%
8	QK	451	97%
8	QM	451	97%
8	QO	451	98%
8	RC	451	90% 9%
8	RE	451	95% 5%
8	RG	451	96%
8	RI	451	97%
8	RK	451	97%
8	RM	451	97%

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Mol	Chain	Length	Quality of chain
8	RO	451	97%
8	SE	451	95% 5%
8	SG	451	95% 5%
8	SI	451	95%
8	SK	451	94%
8	SM	451	95%
8	SO	451	95%
8	TE	451	95% 5%
8	TG	451	95% 5%
8	TI	451	96%
8	TK	451	95% 5%
8	TM	451	95%
8	TO	451	95% 5%
8	UE	451	95%
8	UG	451	95%
8	UI	451	95%
8	UK	451	95%
8	UM	451	95%
8	UO	451	95%
8	VE	451	97%
8	VG	451	95%
8	VI	451	97%
8	VK	451	95%
8	VM	451	97%
8	VO	451	96%

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Mol	Chain	Length	Quality of chain
8	WE	451	96%
8	WG	451	95% 5%
8	WI	451	97%
8	WK	451	95% 5%
8	WM	451	96%
8	WO	451	96%
9	AB	445	98%
9	AD	445	98%
9	AF	445	97%
9	AH	445	97%
9	AJ	445	97%
9	AL	445	98%
9	BB	445	96%
9	BD	445	95%
9	BF	445	95%
9	BH	445	95%
9	BJ	445	95%
9	BL	445	96%
9	CB	445	96%
9	CD	445	96%
9	CF	445	95%
9	CH	445	96%
9	CJ	445	95%
9	CL	445	96%
9	DB	445	95%

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Mol	Chain	Length	Quality of chain
9	DD	445	95%
9	DF	445	95%
9	DH	445	96%
9	DJ	445	95%
9	DL	445	95%
9	EB	445	96%
9	ED	445	95%
9	EF	445	95%
9	EH	445	95%
9	EJ	445	95%
9	EL	445	95%
9	EN	445	96%
9	FB	445	95%
9	FD	445	96%
9	FF	445	95%
9	FH	445	95%
9	FJ	445	96%
9	FL	445	95%
9	FN	445	95%
9	GB	445	91% 8%
9	GD	445	95%
9	GF	445	95%
9	GH	445	96%
9	GJ	445	96%
9	GL	445	95%

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Mol	Chain	Length	Quality of chain
9	GN	445	95%
9	HB	445	94%
9	HD	445	95%
9	HF	445	96%
9	HH	445	95%
9	HJ	445	95%
9	HL	445	94%
9	HN	445	94%
9	IB	445	91% 9%
9	ID	445	95%
9	IF	445	96%
9	IH	445	95%
9	IJ	445	96%
9	IL	445	95%
9	IN	445	95%
9	JB	445	95%
9	JD	445	96%
9	JF	445	95%
9	JH	445	95%
9	JJ	445	95%
9	JL	445	95%
9	JN	445	95%
9	KB	445	92% 7%
9	KD	445	96%
9	KF	445	95%

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Mol	Chain	Length	Quality of chain
9	KH	445	96%
9	KJ	445	95%
9	KL	445	96%
9	KN	445	95%
9	LB	445	98%
9	LD	445	95%
9	LF	445	98%
9	LH	445	95%
9	LJ	445	99%
9	LL	445	95%
9	LN	445	98%
9	MB	445	96%
9	MD	445	96%
9	MF	445	97%
9	MH	445	96%
9	MJ	445	96%
9	ML	445	96%
9	MN	445	97%
9	NB	445	95%
9	ND	445	96%
9	NF	445	96%
9	NH	445	95%
9	NJ	445	95%
9	NL	445	95%
9	NN	445	95%

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Mol	Chain	Length	Quality of chain
9	OB	445	96%
9	OD	445	97%
9	OF	445	96%
9	OH	445	96%
9	OJ	445	97%
9	OL	445	96%
9	ON	445	96%
9	PD	445	96%
9	PF	445	96%
9	PH	445	95%
9	PJ	445	96%
9	PL	445	96%
9	PN	445	96%
9	QD	445	96%
9	QF	445	96%
9	QH	445	96%
9	QJ	445	96%
9	QL	445	96%
9	QN	445	96%
9	RD	445	95%
9	RF	445	96%
9	RH	445	95%
9	RJ	445	95%
9	RL	445	96%
9	RN	445	96%

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Mol	Chain	Length	Quality of chain
9	SD	445	95%
9	SF	445	95%
9	SH	445	95%
9	SJ	445	95%
9	SL	445	96%
9	SN	445	95%
9	TD	445	95%
9	TF	445	96%
9	TH	445	95%
9	TJ	445	95%
9	TL	445	95%
9	TN	445	95%
9	TP	445	94% 5%
9	UD	445	95%
9	UF	445	95%
9	UH	445	95%
9	UJ	445	96%
9	UL	445	94%
9	UN	445	95%
9	UP	445	96%
9	VD	445	96%
9	VF	445	95%
9	VH	445	95%
9	VJ	445	95%
9	VL	445	95%

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Mol	Chain	Length	Quality of chain
9	VN	445	95%
9	VP	445	95%
9	WD	445	95%
9	WF	445	95%
9	WH	445	96%
9	WJ	445	95%
9	WL	445	95%
9	WN	445	96%
9	WP	445	95%
10	B	495	36% 64%
10	C	495	72% 28%
11	B0	430	45% 55%
11	B1	430	91% 9%
11	B2	430	91% 9%
11	B3	430	82% 18%
11	B4	430	12% 88%
11	B5	430	12% 12% 88%
11	B6	430	79% 82% 18%
11	B7	430	84% 91% 9%
11	B8	430	86% 91% 9%
11	B9	430	43% 45% 55%
12	C0	490	7% 93%
12	C1	490	22% 68% 31%
12	C2	490	15% 79% 20%
12	C3	490	16% 80% 20%

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Mol	Chain	Length	Quality of chain
12	C4	490	9% 44% 55%
13	D	485	37% 63%
14	D0	435	61% 39%
14	D1	435	91% 9%
14	D2	435	91% 9%
14	D3	435	73% 27%
14	D5	435	72% 73% 27%
14	D6	435	87% 91% 9%
14	D7	435	88% 91% 9%
14	D8	435	61% 61% 39%
15	E	301	92% 8%
15	F	301	7% 92% 8%
16	F0	222	70% 29%
16	F1	222	72% 28%
16	F2	222	42% 70% 30%
16	F3	222	71% 29%
16	F4	222	72% 28%
16	F5	222	61% 70% 30%
16	F6	222	70% 29%
16	F7	222	71% 28%
16	F8	222	27% 70% 30%
16	G0	222	72% 28%
16	G1	222	71% 29%
16	G2	222	41% 70% 30%
16	G3	222	71% 29%

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Mol	Chain	Length	Quality of chain
16	G4	222	71% · 28%
16	G5	222	9% 70% 30%
16	G6	222	70% 29%
16	G7	222	· 72% 28%
16	G8	222	63% 70% 30%
16	H0	222	70% 29%
16	H1	222	· 72% 28%
16	H2	222	23% 70% 30%
17	G	121	11% 76% · 22%
18	H	275	· 29% 71%
18	I	275	27% 53% 47%
18	J	275	8% 53% 47%
18	K	275	22% 52% · 47%
18	L	275	8% 52% 47%
18	M	275	17% 52% 47%
18	N	275	9% 52% · 47%
19	I1	150	· 58% · 41%
20	J1	284	29% 71%
20	J2	284	79% · 20%
20	J3	284	· 79% · 20%
20	J4	284	71% · 28%
20	J5	284	23% 77%
21	K1	134	· 82% · 17%
22	L1	147	· 86% 14%
22	L2	147	· 61% · 39%

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Mol	Chain	Length	Quality of chain
23	M1	201	9% 51% 49%
23	M2	201	50% 50%
23	M3	201	50% 49%
23	M4	201	50% 49%
24	O	382	7% 93%
24	P	382	96%
24	Q	382	10% 90%
24	R	382	19% 57% 43%
24	S	382	15% 43% 57%
25	T	640	75% 24%
25	U	640	76% 24%
25	V	640	76% 24%
26	W	749	5% 81% 18%
26	X	749	6% 93% 6%
26	Y	749	5% 93% 6%
26	Z	749	5% 68% 32%
27	XA	193	96%
27	XB	193	96%
27	XC	193	96%
27	XD	193	96%
27	XE	193	95%
27	XF	193	96%
27	XG	193	96%
28	YB	257	86% 14%
28	YC	257	86% 14%

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Mol	Chain	Length	Quality of chain
28	YD	257	85% 14%
28	YE	257	86% 14%
28	YF	257	85% 14%
28	YG	257	86% 14%
29	a	551	31% 68%
29	b	551	5% 61% 39%
29	c	551	8% 51% 48%
29	d	551	39% 60%
30	e	620	98%
30	f	620	98%
30	g	620	98%
31	h	256	57% 43%
31	i	256	5% 97%
31	j	256	5% 96%
31	k	256	98%
32	l	177	66% 34%
32	m	177	66% 34%
32	n	177	66% 34%
33	o	552	72% 27%
33	o1	552	7% 93%
33	p	552	28% 71%
34	q	169	66% 34%
34	r	169	66% 34%
34	s	169	66% 34%
35	y	136	46% 54%

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Mol	Chain	Length	Quality of chain
35	z	136	82% 18%

2 Entry composition (i)

There are 38 unique types of molecules in this entry. The entry contains 1265783 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 Protein CFAP95.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	52	418	265	75	77	1	0	0
1	7	146	1197	757	206	230	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	272	2226	1407	388	424	7	0	0
2	2	446	3607	2298	629	667	13	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	297	2514	1539	476	489	10	0	0
3	4	215	1837	1120	349	358	10	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	5	371	2943	1873	506	543	21	0	0
4	6	371	2943	1873	506	543	21	0	0

- Molecule 5 is a protein called Protein CFAP107.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	8	168	1414	909	251	251	3	0	0
5	9	48	411	261	71	78	1	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	191	PHE	LEU	conflict	UNP Q8N1D5
9	191	PHE	LEU	conflict	UNP Q8N1D5

- Molecule 6 is a protein called Protein CFAP141.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A	50	423	269	75	76	3	0	0

- Molecule 7 is a protein called Tektin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A0	220	1771	1102	325	335	9	0	0
7	A1	391	3185	1978	576	619	12	0	0
7	A2	391	3185	1978	576	619	12	0	0
7	A3	333	2715	1688	485	532	10	0	0
7	A4	35	Total	C	N	O		0	0
			294	183	59	52			

- Molecule 8 is a protein called Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AA	439	3429	2170	583	654	22	0	0
8	AC	439	3429	2170	583	654	22	0	0
8	AE	439	3429	2170	583	654	22	0	0
8	AG	439	3429	2170	583	654	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AI	439	3429	2170	583	654	22	0	0
8	AK	439	3429	2170	583	654	22	0	0
8	AM	439	3429	2170	583	654	22	0	0
8	BA	432	3383	2143	575	643	22	0	0
8	BC	439	3429	2170	583	654	22	0	0
8	BE	432	3383	2143	575	643	22	0	0
8	BG	439	3429	2170	583	654	22	0	0
8	BI	432	3383	2143	575	643	22	0	0
8	BK	439	3429	2170	583	654	22	0	0
8	BM	433	3387	2145	576	644	22	0	0
8	CA	432	3385	2144	575	644	22	0	0
8	CC	439	3429	2170	583	654	22	0	0
8	CE	430	3371	2137	573	639	22	0	0
8	CG	439	3429	2170	583	654	22	0	0
8	CI	431	3377	2140	574	641	22	0	0
8	CK	439	3429	2170	583	654	22	0	0
8	CM	431	3377	2140	574	641	22	0	0
8	DA	383	2978	1887	504	567	20	0	0
8	DC	430	3371	2137	573	639	22	0	0
8	DE	431	3379	2141	574	642	22	0	0
8	DG	430	3371	2137	573	639	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	DI	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	DK	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	DM	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	EC	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	EE	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	EG	438	3423	2167	582	652	22	0	0
			Total	C	N	O	S		
8	EI	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	EK	438	3423	2167	582	652	22	0	0
			Total	C	N	O	S		
8	EM	438	3423	2167	582	652	22	0	0
			Total	C	N	O	S		
8	FC	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	FE	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	FG	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	FI	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	FK	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	FM	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	GC	435	3409	2158	579	650	22	0	0
			Total	C	N	O	S		
8	GE	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	GG	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	GI	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	GK	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	GM	434	3402	2154	578	648	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	HC	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	HE	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	HG	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	HI	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	HK	431	3377	2140	574	641	22	0	0
			Total	C	N	O	S		
8	HM	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	HO	389	3058	1935	520	582	21	0	0
			Total	C	N	O	S		
8	IC	433	3393	2148	576	647	22	0	0
			Total	C	N	O	S		
8	IE	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	IG	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	II	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	IK	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	IM	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	IO	431	3377	2140	574	641	22	0	0
			Total	C	N	O	S		
8	JC	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	JE	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	JG	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	JI	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	JK	431	3377	2140	574	641	22	0	0
			Total	C	N	O	S		
8	JM	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	KC	433	3390	2148	576	644	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	KE	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	KG	433	3390	2148	576	644	22	0	0
			Total	C	N	O	S		
8	KI	430	3373	2138	573	640	22	0	0
			Total	C	N	O	S		
8	KK	433	3390	2148	576	644	22	0	0
			Total	C	N	O	S		
8	KM	438	3423	2167	582	652	22	0	0
			Total	C	N	O	S		
8	KO	432	3383	2143	575	643	22	0	0
			Total	C	N	O	S		
8	LC	433	3389	2146	576	645	22	0	0
			Total	C	N	O	S		
8	LE	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	LG	434	3397	2150	577	648	22	0	0
			Total	C	N	O	S		
8	LI	436	3410	2158	580	650	22	0	0
			Total	C	N	O	S		
8	LK	433	3390	2148	576	644	22	0	0
			Total	C	N	O	S		
8	LM	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	MC	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	ME	432	3386	2146	575	643	22	0	0
			Total	C	N	O	S		
8	MG	432	3384	2145	575	642	22	0	0
			Total	C	N	O	S		
8	MI	433	3392	2149	576	645	22	0	0
			Total	C	N	O	S		
8	MK	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	MM	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	NC	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	NE	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	NG	439	3429	2170	583	654	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	NI	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	NK	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	NM	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	OC	441	3445	2180	585	658	22	0	0
			Total	C	N	O	S		
8	OE	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	OG	441	3445	2180	585	658	22	0	0
			Total	C	N	O	S		
8	OI	441	3445	2180	585	658	22	0	0
			Total	C	N	O	S		
8	OK	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	OM	441	3445	2180	585	658	22	0	0
			Total	C	N	O	S		
8	OO	422	3309	2092	563	632	22	0	0
			Total	C	N	O	S		
8	PC	441	3445	2180	585	658	22	0	0
			Total	C	N	O	S		
8	PE	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	PG	441	3445	2180	585	658	22	0	0
			Total	C	N	O	S		
8	PI	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	PK	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	PM	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	PO	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	QC	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	QE	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	QG	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	QI	440	3436	2175	584	655	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	QK	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	QM	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	QO	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	RC	411	3209	2029	547	612	21	0	0
			Total	C	N	O	S		
8	RE	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	RG	432	3384	2145	575	642	22	0	0
			Total	C	N	O	S		
8	RI	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	RK	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	RM	440	3436	2175	584	655	22	0	0
			Total	C	N	O	S		
8	RO	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	SE	429	3365	2134	572	637	22	0	0
			Total	C	N	O	S		
8	SG	430	3373	2138	573	640	22	0	0
			Total	C	N	O	S		
8	SI	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	SK	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	SM	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	SO	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	TE	429	3365	2134	572	637	22	0	0
			Total	C	N	O	S		
8	TG	430	3373	2138	573	640	22	0	0
			Total	C	N	O	S		
8	TI	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	TK	429	3365	2134	572	637	22	0	0
			Total	C	N	O	S		
8	TM	431	3379	2141	574	642	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	TO	429	3365	2134	572	637	22	0	0
			Total	C	N	O	S		
8	UE	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	UG	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	UI	432	3385	2144	575	644	22	0	0
			Total	C	N	O	S		
8	UK	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	UM	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	UO	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	VE	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	VG	433	3393	2148	576	647	22	0	0
			Total	C	N	O	S		
8	VI	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	VK	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	VM	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	VO	431	3379	2141	574	642	22	0	0
			Total	C	N	O	S		
8	WE	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	WG	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	WI	438	3423	2167	582	652	22	0	0
			Total	C	N	O	S		
8	WK	430	3371	2137	573	639	22	0	0
			Total	C	N	O	S		
8	WM	439	3429	2170	583	654	22	0	0
			Total	C	N	O	S		
8	WO	431	3379	2141	574	642	22	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AB	437	3433	2155	585	667	26	0	0
9	AD	437	3433	2155	585	667	26	0	0
9	AF	437	3433	2155	585	667	26	0	0
9	AH	437	3433	2155	585	667	26	0	0
9	AJ	437	3433	2155	585	667	26	0	0
9	AL	437	3433	2155	585	667	26	0	0
9	BB	427	3356	2109	575	646	26	0	0
9	BD	426	3348	2105	574	643	26	0	0
9	BF	427	3356	2109	575	646	26	0	0
9	BH	426	3348	2105	574	643	26	0	0
9	BJ	430	3373	2119	578	650	26	0	0
9	BL	426	3348	2105	574	643	26	0	0
9	CB	428	3361	2112	576	647	26	0	0
9	CD	426	3348	2105	574	643	26	0	0
9	CF	427	3356	2109	575	646	26	0	0
9	CH	426	3348	2105	574	643	26	0	0
9	CJ	427	3356	2109	575	646	26	0	0
9	CL	426	3348	2105	574	643	26	0	0
9	DB	426	3348	2105	574	643	26	0	0
9	DD	426	3348	2105	574	643	26	0	0
9	DF	426	3348	2105	574	643	26	0	0
9	DH	426	3348	2105	574	643	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	DJ	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	DL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	EB	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	ED	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	EF	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	EH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	EJ	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	EL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	EN	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	FB	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	FD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	FF	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	FH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	FJ	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	FL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	FN	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	GB	410	3208	2016	548	619	25	0	0
			Total	C	N	O	S		
9	GD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	GF	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	GH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	GJ	430	3373	2119	578	650	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	GL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	GN	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	HB	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	HD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	HF	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	HH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	HJ	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	HL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	HN	425	3339	2100	572	641	26	0	0
			Total	C	N	O	S		
9	IB	407	3197	2010	544	618	25	0	0
			Total	C	N	O	S		
9	ID	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	IF	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	IH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	IJ	429	3368	2116	577	649	26	0	0
			Total	C	N	O	S		
9	IL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	IN	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	JB	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	JD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	JF	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	JH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	JJ	426	3348	2105	574	643	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	JL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	JN	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	KB	412	3222	2021	550	625	26	0	0
			Total	C	N	O	S		
9	KD	431	3382	2124	579	653	26	0	0
			Total	C	N	O	S		
9	KF	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	KH	431	3382	2124	579	653	26	0	0
			Total	C	N	O	S		
9	KJ	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	KL	431	3382	2124	579	653	26	0	0
			Total	C	N	O	S		
9	KN	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	LB	440	3456	2168	588	674	26	0	0
			Total	C	N	O	S		
9	LD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	LF	439	3451	2165	587	673	26	0	0
			Total	C	N	O	S		
9	LH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	LJ	443	3483	2183	591	683	26	0	0
			Total	C	N	O	S		
9	LL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	LN	440	3456	2168	588	674	26	0	0
			Total	C	N	O	S		
9	MB	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	MD	432	3391	2129	580	656	26	0	0
			Total	C	N	O	S		
9	MF	431	3382	2124	579	653	26	0	0
			Total	C	N	O	S		
9	MH	432	3391	2129	580	656	26	0	0
			Total	C	N	O	S		
9	MJ	432	3391	2129	580	656	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	ML	432	3391	2129	580	656	26	0	0
			Total	C	N	O	S		
9	MN	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	NB	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	ND	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	NF	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	NH	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	NJ	429	3368	2116	577	649	26	0	0
			Total	C	N	O	S		
9	NL	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	NN	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	OB	431	3382	2124	579	653	26	0	0
			Total	C	N	O	S		
9	OD	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	OF	432	3391	2129	580	656	26	0	0
			Total	C	N	O	S		
9	OH	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	OJ	432	3391	2129	580	656	26	0	0
			Total	C	N	O	S		
9	OL	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	ON	431	3382	2124	579	653	26	0	0
			Total	C	N	O	S		
9	PD	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	PF	432	3391	2129	580	656	26	0	0
			Total	C	N	O	S		
9	PH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	PJ	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	PL	429	3368	2116	577	649	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	PN	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	QD	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	QF	430	3373	2119	578	650	26	0	0
			Total	C	N	O	S		
9	QH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	QJ	429	3368	2116	577	649	26	0	0
			Total	C	N	O	S		
9	QL	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	QN	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	RD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	RF	429	3368	2116	577	649	26	0	0
			Total	C	N	O	S		
9	RH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	RJ	428	3361	2112	576	647	26	0	0
			Total	C	N	O	S		
9	RL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	RN	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	SD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	SF	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	SH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	SJ	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	SL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	SN	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	TD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	TF	427	3356	2109	575	646	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	TH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	TJ	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	TL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	TN	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	TP	421	3302	2074	567	635	26	0	0
			Total	C	N	O	S		
9	UD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	UF	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	UH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	UJ	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	UL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	UN	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	UP	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	VD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	VF	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	VH	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	VJ	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	VL	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	VN	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	VP	427	3356	2109	575	646	26	0	0
			Total	C	N	O	S		
9	WD	426	3348	2105	574	643	26	0	0
			Total	C	N	O	S		
9	WF	426	3348	2105	574	643	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	WH	426	3348	2105	574	643	26	0	0
9	WJ	426	3348	2105	574	643	26	0	0
9	WL	426	3348	2105	574	643	26	0	0
9	WN	427	3356	2109	575	646	26	0	0
9	WP	427	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
			Total	C	N	O	S		
10	B	180	1507	921	287	289	10	0	0
10	C	356	3062	1903	551	592	16	0	0

- Molecule 11 is a protein called Tektin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	B0	193	1574	958	294	315	7	0	0
11	B1	392	3187	1956	586	630	15	0	0
11	B2	391	3180	1951	585	629	15	0	0
11	B3	354	2868	1760	521	572	15	0	0
11	B4	51	412	255	76	80	1	0	0
11	B5	51	254	152	51	51		0	0
11	B6	354	1766	1058	354	354		0	0
11	B7	391	1951	1169	391	391		0	0
11	B8	392	1956	1172	392	392		0	0
11	B9	193	962	576	193	193		0	0

- Molecule 12 is a protein called Tektin-3.

Mol	Chain	Residues	Atoms	AltConf	Trace
12	C0	33	Total C N O 285 171 54 60	0	0
12	C1	336	Total C N O S 2732 1683 495 541 13	0	0
12	C2	393	Total C N O S 3199 1968 584 632 15	0	0
12	C3	394	Total C N O S 3210 1974 588 633 15	0	0
12	C4	219	Total C N O S 1786 1111 321 341 13	0	0

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

Mol	Chain	Residues	Atoms	AltConf	Trace
13	D	179	Total C N O S 1459 919 260 271 9	0	0

- Molecule 14 is a protein called Tektin-4.

Mol	Chain	Residues	Atoms	AltConf	Trace
14	D0	266	Total C N O S 2180 1326 409 432 13	0	0
14	D1	396	Total C N O S 3256 1989 616 632 19	0	0
14	D2	398	Total C N O S 3275 2000 620 636 19	0	0
14	D3	317	Total C N O S 2603 1596 492 498 17	0	0
14	D5	317	Total C N O 1583 948 317 318	0	0
14	D6	398	Total C N O 1987 1190 398 399	0	0
14	D7	396	Total C N O 1976 1184 396 396	0	0
14	D8	266	Total C N O 1327 794 266 267	0	0

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

Mol	Chain	Residues	Atoms	AltConf	Trace
15	E	277	Total C N O S 2227 1403 397 415 12	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	F	277	2227	1403	397	415	12	0	0

- Molecule 16 is a protein called Sperm acrosome-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	F0	157	1263	788	225	240	10	0	0
16	F1	160	1289	805	231	243	10	0	0
16	F2	156	776	464	156	156		0	0
16	F3	157	1263	788	225	240	10	0	0
16	F4	160	1289	805	231	243	10	0	0
16	F5	156	776	464	156	156		0	0
16	F6	157	1263	788	225	240	10	0	0
16	F7	160	1289	805	231	243	10	0	0
16	F8	156	776	464	156	156		0	0
16	G0	159	1278	799	227	242	10	0	0
16	G1	158	1271	794	226	241	10	0	0
16	G2	156	776	464	156	156		0	0
16	G3	157	1263	788	225	240	10	0	0
16	G4	160	1289	805	231	243	10	0	0
16	G5	156	776	464	156	156		0	0
16	G6	157	1263	788	225	240	10	0	0
16	G7	160	1289	805	231	243	10	0	0
16	G8	156	776	464	156	156		0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	H0	157	1263	788	225	240	10	0	0
			Total	C	N	O	S		
16	H1	160	1289	805	231	243	10	0	0
			Total	C	N	O			
16	H2	156	776	464	156	156		0	0

- Molecule 17 is a protein called Uncharacterized protein C15orf65.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	G	94	750	478	127	139	6	0	0

- Molecule 18 is a protein called Protein FAM166B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	H	80	619	405	108	103	3	0	0
			Total	C	N	O	S		
18	I	145	1080	698	187	189	6	0	0
			Total	C	N	O	S		
18	J	146	1085	701	188	190	6	0	0
			Total	C	N	O	S		
18	K	145	1080	698	187	189	6	0	0
			Total	C	N	O	S		
18	L	145	1080	698	187	189	6	0	0
			Total	C	N	O	S		
18	M	145	1080	698	187	189	6	0	0
			Total	C	N	O	S		
18	N	146	1085	701	188	190	6	0	0

- Molecule 19 is a protein called UPF0686 protein C11orf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	I1	89	763	481	135	143	4	0	0

- Molecule 20 is a protein called Isoform 2 of Cilia- and flagella-associated protein 77.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	J1	81	704	448	135	119	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	J2	226	1849	1169	349	323	8	0	0
			Total	C	N	O	S		
20	J3	226	1849	1169	349	323	8	0	0
			Total	C	N	O	S		
20	J4	205	1674	1064	313	290	7	0	0
			Total	C	N	O	S		
20	J5	65	514	324	94	93	3	0	0

- Molecule 21 is a protein called Protein FAM183A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	K1	111	945	594	179	170	2	0	0

- Molecule 22 is a protein called Uncharacterized protein C5orf49.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	L1	127	1045	659	195	190	1	0	0
			Total	C	N	O	S		
22	L2	90	746	469	139	137	1	0	0

- Molecule 23 is a protein called Protein FAM166C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	M1	102	825	526	147	148	4	0	0
			Total	C	N	O	S		
23	M2	101	818	521	146	147	4	0	0
			Total	C	N	O	S		
23	M3	102	825	526	147	148	4	0	0
			Total	C	N	O	S		
23	M4	102	825	526	147	148	4	0	0

- Molecule 24 is a protein called RIB43A-like with coiled-coils protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	O	25	212	129	51	31	1	0	0
			Total	C	N	O	S		
24	P	368	3089	1886	608	584	11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Q	40	327	203	56	67	1	0	0
			Total	C	N	O	S		
24	R	219	1816	1105	354	348	9	0	0
			Total	C	N	O	S		
24	S	165	1387	852	269	263	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	T	484	3984	2570	666	734	14	0	0
			Total	C	N	O	S		
25	U	485	3992	2576	667	735	14	0	0
			Total	C	N	O	S		
25	V	485	3992	2576	667	735	14	0	0

- Molecule 26 is a protein called EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	W	614	5064	3269	845	926	24	0	0
			Total	C	N	O	S		
26	X	701	5797	3742	964	1063	28	0	0
			Total	C	N	O	S		
26	Y	701	5797	3742	964	1063	28	0	0
			Total	C	N	O	S		
26	Z	510	4239	2739	702	776	22	0	0

- Molecule 27 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	XA	186	1549	998	270	274	7	0	0
			Total	C	N	O	S		
27	XB	186	1549	998	270	274	7	0	0
			Total	C	N	O	S		
27	XC	186	1549	998	270	274	7	0	0
			Total	C	N	O	S		
27	XD	186	1549	998	270	274	7	0	0
			Total	C	N	O	S		
27	XE	186	1549	998	270	274	7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	XF	186	1549	998	270	274	7	0	0
27	XG	186	1549	998	270	274	7	0	0

- Molecule 28 is a protein called Parkin coregulated gene protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	YB	220	1771	1147	301	314	9	0	0
28	YC	220	1771	1147	301	314	9	0	0
28	YD	220	1771	1147	301	314	9	0	0
28	YE	220	1771	1147	301	314	9	0	0
28	YF	220	1771	1147	301	314	9	0	0
28	YG	220	1771	1147	301	314	9	0	0

- Molecule 29 is a protein called Cilia- and flagella-associated protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	a	174	1467	898	279	280	10	0	0
29	b	334	2878	1734	571	560	13	0	0
29	c	284	2419	1475	454	472	18	0	0
29	d	218	1858	1126	373	353	6	0	0

- Molecule 30 is a protein called Cilia- and flagella-associated protein 52.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	610	4717	2978	827	882	30	0	0
30	f	610	4717	2978	827	882	30	0	0
30	g	610	4717	2978	827	882	30	0	0

- Molecule 31 is a protein called Enkurin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	h	146	1210	766	213	227	4	0	0
31	i	250	2023	1290	350	373	10	0	0
31	j	248	2010	1283	348	370	9	0	0
31	k	250	2023	1290	350	373	10	0	0

- Molecule 32 is a protein called Protein Flattop.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	l	117	908	577	159	168	4	0	0
32	m	117	908	577	159	168	4	0	0
32	n	117	908	577	159	168	4	0	0

- Molecule 33 is a protein called Protein CFAP210.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	o	404	3471	2149	654	653	15	0	0
33	o1	36	301	185	60	55	1	0	0
33	p	158	1285	809	229	243	4	0	0

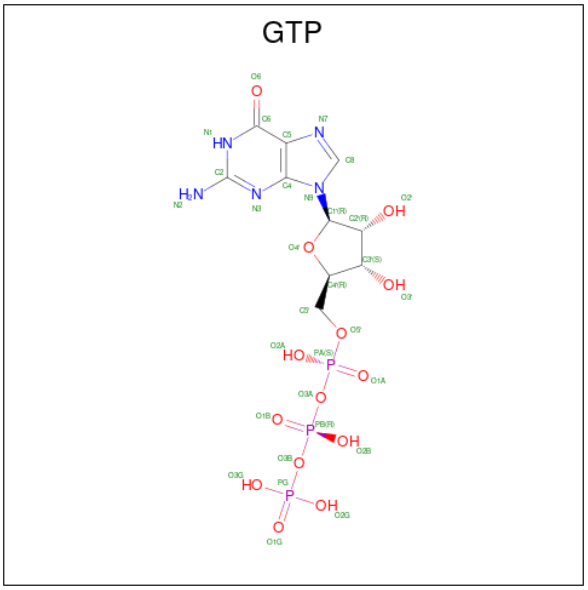
- Molecule 34 is a protein called Protein CFAP276.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	q	112	906	568	166	171	1	0	0
34	r	112	906	568	166	171	1	0	0
34	s	112	906	568	166	171	1	0	0

- Molecule 35 is a protein called UPF0691 protein C9orf116.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	y	63	498	312	88	94	4	0	0
			Total	C	N	O	S		
35	z	111	891	559	163	165	4	0	0

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	AA	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	AC	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	AE	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	AG	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	AI	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	AK	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	AM	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	BA	1	32	10	5	14	3	0
			Total	C	N	O	P	
36	BC	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	BE	1	32	10	5	14	3	0
36	BG	1	32	10	5	14	3	0
36	BI	1	32	10	5	14	3	0
36	BK	1	32	10	5	14	3	0
36	BM	1	32	10	5	14	3	0
36	CA	1	32	10	5	14	3	0
36	CC	1	32	10	5	14	3	0
36	CE	1	32	10	5	14	3	0
36	CG	1	32	10	5	14	3	0
36	CI	1	32	10	5	14	3	0
36	CK	1	32	10	5	14	3	0
36	CM	1	32	10	5	14	3	0
36	DA	1	32	10	5	14	3	0
36	DC	1	32	10	5	14	3	0
36	DE	1	32	10	5	14	3	0
36	DG	1	32	10	5	14	3	0
36	DI	1	32	10	5	14	3	0
36	DK	1	32	10	5	14	3	0
36	DM	1	32	10	5	14	3	0
36	EC	1	32	10	5	14	3	0
36	EE	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	EG	1	32	10	5	14	3	0
36	EI	1	32	10	5	14	3	0
36	EK	1	32	10	5	14	3	0
36	EM	1	32	10	5	14	3	0
36	FC	1	32	10	5	14	3	0
36	FE	1	32	10	5	14	3	0
36	FG	1	32	10	5	14	3	0
36	FI	1	32	10	5	14	3	0
36	FK	1	32	10	5	14	3	0
36	FM	1	32	10	5	14	3	0
36	GC	1	32	10	5	14	3	0
36	GE	1	32	10	5	14	3	0
36	GG	1	32	10	5	14	3	0
36	GI	1	32	10	5	14	3	0
36	GK	1	32	10	5	14	3	0
36	GM	1	32	10	5	14	3	0
36	HC	1	32	10	5	14	3	0
36	HE	1	32	10	5	14	3	0
36	HG	1	32	10	5	14	3	0
36	HI	1	32	10	5	14	3	0
36	HK	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	HM	1	32	10	5	14	3	0
36	HO	1	32	10	5	14	3	0
36	IC	1	32	10	5	14	3	0
36	IE	1	32	10	5	14	3	0
36	IG	1	32	10	5	14	3	0
36	II	1	32	10	5	14	3	0
36	IK	1	32	10	5	14	3	0
36	IM	1	32	10	5	14	3	0
36	IO	1	32	10	5	14	3	0
36	JC	1	32	10	5	14	3	0
36	JE	1	32	10	5	14	3	0
36	JG	1	32	10	5	14	3	0
36	JI	1	32	10	5	14	3	0
36	JK	1	32	10	5	14	3	0
36	JM	1	32	10	5	14	3	0
36	KC	1	32	10	5	14	3	0
36	KE	1	32	10	5	14	3	0
36	KG	1	32	10	5	14	3	0
36	KI	1	32	10	5	14	3	0
36	KK	1	32	10	5	14	3	0
36	KM	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	KO	1	32	10	5	14	3	0
36	LC	1	32	10	5	14	3	0
36	LE	1	32	10	5	14	3	0
36	LG	1	32	10	5	14	3	0
36	LI	1	32	10	5	14	3	0
36	LK	1	32	10	5	14	3	0
36	LM	1	32	10	5	14	3	0
36	MC	1	32	10	5	14	3	0
36	ME	1	32	10	5	14	3	0
36	MG	1	32	10	5	14	3	0
36	MI	1	32	10	5	14	3	0
36	MK	1	32	10	5	14	3	0
36	MM	1	32	10	5	14	3	0
36	NC	1	32	10	5	14	3	0
36	NE	1	32	10	5	14	3	0
36	NG	1	32	10	5	14	3	0
36	NI	1	32	10	5	14	3	0
36	NK	1	32	10	5	14	3	0
36	NM	1	32	10	5	14	3	0
36	OC	1	32	10	5	14	3	0
36	OE	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	OG	1	32	10	5	14	3	0
36	OI	1	32	10	5	14	3	0
36	OK	1	32	10	5	14	3	0
36	OM	1	32	10	5	14	3	0
36	OO	1	32	10	5	14	3	0
36	PC	1	32	10	5	14	3	0
36	PE	1	32	10	5	14	3	0
36	PG	1	32	10	5	14	3	0
36	PI	1	32	10	5	14	3	0
36	PK	1	32	10	5	14	3	0
36	PM	1	32	10	5	14	3	0
36	PO	1	32	10	5	14	3	0
36	QC	1	32	10	5	14	3	0
36	QE	1	32	10	5	14	3	0
36	QG	1	32	10	5	14	3	0
36	QI	1	32	10	5	14	3	0
36	QK	1	32	10	5	14	3	0
36	QM	1	32	10	5	14	3	0
36	QO	1	32	10	5	14	3	0
36	RC	1	32	10	5	14	3	0
36	RE	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	RG	1	32	10	5	14	3	0
36	RI	1	32	10	5	14	3	0
36	RK	1	32	10	5	14	3	0
36	RM	1	32	10	5	14	3	0
36	RO	1	32	10	5	14	3	0
36	SE	1	32	10	5	14	3	0
36	SG	1	32	10	5	14	3	0
36	SI	1	32	10	5	14	3	0
36	SK	1	32	10	5	14	3	0
36	SM	1	32	10	5	14	3	0
36	SO	1	32	10	5	14	3	0
36	TE	1	32	10	5	14	3	0
36	TG	1	32	10	5	14	3	0
36	TI	1	32	10	5	14	3	0
36	TK	1	32	10	5	14	3	0
36	TM	1	32	10	5	14	3	0
36	TO	1	32	10	5	14	3	0
36	UE	1	32	10	5	14	3	0
36	UG	1	32	10	5	14	3	0
36	UI	1	32	10	5	14	3	0
36	UK	1	32	10	5	14	3	0

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

- Molecule 37 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	AA	1	1	1	0
37	AC	1	1	1	0
37	AE	1	1	1	0
37	AG	1	1	1	0
37	AI	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	AK	1	1	1	0
37	AM	1	1	1	0
37	BA	1	1	1	0
37	BC	1	1	1	0
37	BE	1	1	1	0
37	BG	1	1	1	0
37	BI	1	1	1	0
37	BK	1	1	1	0
37	BM	1	1	1	0
37	CA	1	1	1	0
37	CC	1	1	1	0
37	CE	1	1	1	0
37	CG	1	1	1	0
37	CI	1	1	1	0
37	CK	1	1	1	0
37	CM	1	1	1	0
37	DA	1	1	1	0
37	DC	1	1	1	0
37	DE	1	1	1	0
37	DG	1	1	1	0
37	DI	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	DK	1	1	1	0
37	DM	1	1	1	0
37	EC	1	1	1	0
37	EE	1	1	1	0
37	EG	1	1	1	0
37	EI	1	1	1	0
37	EK	1	1	1	0
37	EM	1	1	1	0
37	FC	1	1	1	0
37	FE	1	1	1	0
37	FG	1	1	1	0
37	FI	1	1	1	0
37	FK	1	1	1	0
37	FM	1	1	1	0
37	GC	1	1	1	0
37	GE	1	1	1	0
37	GG	1	1	1	0
37	GI	1	1	1	0
37	GK	1	1	1	0
37	GM	1	1	1	0
37	HC	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	HE	1	1	1	0
37	HG	1	1	1	0
37	HI	1	1	1	0
37	HK	1	1	1	0
37	HM	1	1	1	0
37	HO	1	1	1	0
37	IC	1	1	1	0
37	IE	1	1	1	0
37	IG	1	1	1	0
37	II	1	1	1	0
37	IK	1	1	1	0
37	IM	1	1	1	0
37	IO	1	1	1	0
37	JC	1	1	1	0
37	JE	1	1	1	0
37	JG	1	1	1	0
37	JI	1	1	1	0
37	JK	1	1	1	0
37	JM	1	1	1	0
37	KC	1	1	1	0
37	KE	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	KG	1	1	1	0
37	KI	1	1	1	0
37	KK	1	1	1	0
37	KM	1	1	1	0
37	KO	1	1	1	0
37	LC	1	1	1	0
37	LE	1	1	1	0
37	LG	1	1	1	0
37	LI	1	1	1	0
37	LK	1	1	1	0
37	LM	1	1	1	0
37	MC	1	1	1	0
37	ME	1	1	1	0
37	MG	1	1	1	0
37	MI	1	1	1	0
37	MK	1	1	1	0
37	MM	1	1	1	0
37	NC	1	1	1	0
37	NE	1	1	1	0
37	NG	1	1	1	0
37	NI	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	NK	1	1	1	0
37	NM	1	1	1	0
37	OC	1	1	1	0
37	OE	1	1	1	0
37	OG	1	1	1	0
37	OI	1	1	1	0
37	OK	1	1	1	0
37	OM	1	1	1	0
37	OO	1	1	1	0
37	PC	1	1	1	0
37	PE	1	1	1	0
37	PG	1	1	1	0
37	PI	1	1	1	0
37	PK	1	1	1	0
37	PM	1	1	1	0
37	PO	1	1	1	0
37	QC	1	1	1	0
37	QE	1	1	1	0
37	QG	1	1	1	0
37	QI	1	1	1	0
37	QK	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	QM	1	1	1	0
37	QO	1	1	1	0
37	RC	1	1	1	0
37	RE	1	1	1	0
37	RG	1	1	1	0
37	RI	1	1	1	0
37	RK	1	1	1	0
37	RM	1	1	1	0
37	RO	1	1	1	0
37	SE	1	1	1	0
37	SG	1	1	1	0
37	SI	1	1	1	0
37	SK	1	1	1	0
37	SM	1	1	1	0
37	SO	1	1	1	0
37	TE	1	1	1	0
37	TG	1	1	1	0
37	TI	1	1	1	0
37	TK	1	1	1	0
37	TM	1	1	1	0
37	TO	1	1	1	0

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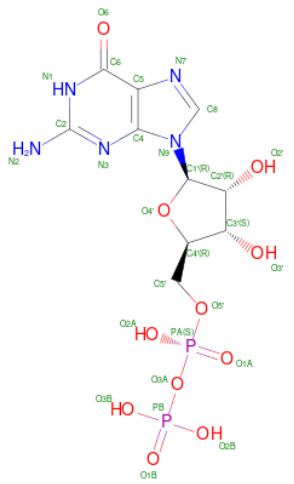
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
37	UE	1	1	1	0
37	UG	1	1	1	0
37	UI	1	1	1	0
37	UK	1	1	1	0
37	UM	1	1	1	0
37	UO	1	1	1	0
37	VE	1	1	1	0
37	VG	1	1	1	0
37	VI	1	1	1	0
37	VK	1	1	1	0
37	VM	1	1	1	0
37	VO	1	1	1	0
37	WE	1	1	1	0
37	WG	1	1	1	0
37	WI	1	1	1	0
37	WK	1	1	1	0
37	WM	1	1	1	0
37	WO	1	1	1	0

- Molecule 38 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

GDP



Mol	Chain	Residues	Atoms					AltConf
38	AB	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	AD	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	AF	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	AH	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	AJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	AL	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	BB	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	BD	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	BF	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	BH	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	BJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	BL	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	CB	1	Total	C	N	O	P	0
			28	10	5	11	2	
38	CD	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
38	CF	1	28	10	5	11	2	0
38	CH	1	28	10	5	11	2	0
38	CJ	1	28	10	5	11	2	0
38	CL	1	28	10	5	11	2	0
38	DB	1	28	10	5	11	2	0
38	DD	1	28	10	5	11	2	0
38	DF	1	28	10	5	11	2	0
38	DH	1	28	10	5	11	2	0
38	DJ	1	28	10	5	11	2	0
38	DL	1	28	10	5	11	2	0
38	EB	1	28	10	5	11	2	0
38	ED	1	28	10	5	11	2	0
38	EF	1	28	10	5	11	2	0
38	EH	1	28	10	5	11	2	0
38	EJ	1	28	10	5	11	2	0
38	EL	1	28	10	5	11	2	0
38	EN	1	28	10	5	11	2	0
38	FB	1	28	10	5	11	2	0
38	FD	1	28	10	5	11	2	0
38	FF	1	28	10	5	11	2	0
38	FH	1	28	10	5	11	2	0

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

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

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
38	LJ	1	28	10	5	11	2	0
38	LL	1	28	10	5	11	2	0
38	LN	1	28	10	5	11	2	0
38	MB	1	28	10	5	11	2	0
38	MD	1	28	10	5	11	2	0
38	MF	1	28	10	5	11	2	0
38	MH	1	28	10	5	11	2	0
38	MJ	1	28	10	5	11	2	0
38	ML	1	28	10	5	11	2	0
38	MN	1	28	10	5	11	2	0
38	NB	1	28	10	5	11	2	0
38	ND	1	28	10	5	11	2	0
38	NF	1	28	10	5	11	2	0
38	NH	1	28	10	5	11	2	0
38	NJ	1	28	10	5	11	2	0
38	NL	1	28	10	5	11	2	0
38	NN	1	28	10	5	11	2	0
38	OB	1	28	10	5	11	2	0
38	OD	1	28	10	5	11	2	0
38	OF	1	28	10	5	11	2	0
38	OH	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
38	OJ	1	28	10	5	11	2	0
38	OL	1	28	10	5	11	2	0
38	ON	1	28	10	5	11	2	0
38	PD	1	28	10	5	11	2	0
38	PF	1	28	10	5	11	2	0
38	PH	1	28	10	5	11	2	0
38	PJ	1	28	10	5	11	2	0
38	PL	1	28	10	5	11	2	0
38	PN	1	28	10	5	11	2	0
38	QD	1	28	10	5	11	2	0
38	QF	1	28	10	5	11	2	0
38	QH	1	28	10	5	11	2	0
38	QJ	1	28	10	5	11	2	0
38	QL	1	28	10	5	11	2	0
38	QN	1	28	10	5	11	2	0
38	RD	1	28	10	5	11	2	0
38	RF	1	28	10	5	11	2	0
38	RH	1	28	10	5	11	2	0
38	RJ	1	28	10	5	11	2	0
38	RL	1	28	10	5	11	2	0
38	RN	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
38	SD	1	28	10	5	11	2	0
38	SF	1	28	10	5	11	2	0
38	SH	1	28	10	5	11	2	0
38	SJ	1	28	10	5	11	2	0
38	SL	1	28	10	5	11	2	0
38	SN	1	28	10	5	11	2	0
38	TD	1	28	10	5	11	2	0
38	TF	1	28	10	5	11	2	0
38	TH	1	28	10	5	11	2	0
38	TJ	1	28	10	5	11	2	0
38	TL	1	28	10	5	11	2	0
38	TN	1	28	10	5	11	2	0
38	TP	1	28	10	5	11	2	0
38	UD	1	28	10	5	11	2	0
38	UF	1	28	10	5	11	2	0
38	UH	1	28	10	5	11	2	0
38	UJ	1	28	10	5	11	2	0
38	UL	1	28	10	5	11	2	0
38	UN	1	28	10	5	11	2	0
38	UP	1	28	10	5	11	2	0
38	VD	1	28	10	5	11	2	0

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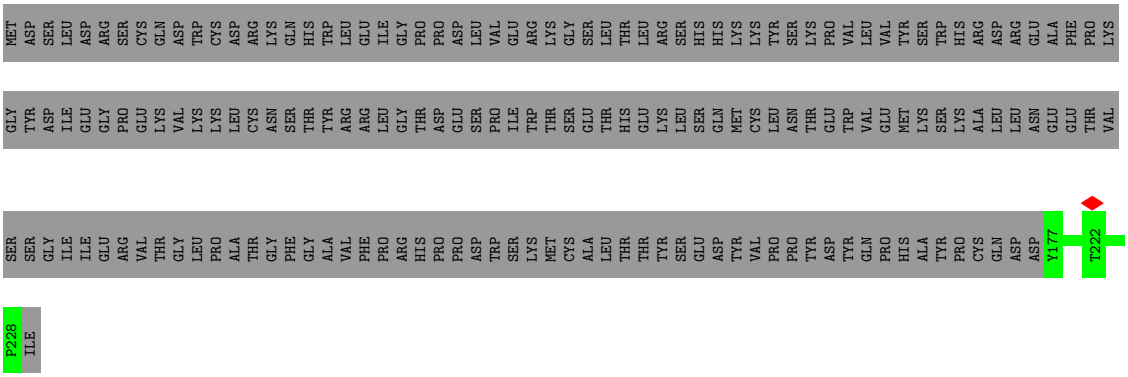
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
38	VF	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	VH	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	VJ	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	VL	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	VN	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	VP	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WD	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WF	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WH	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WJ	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WL	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WN	1	28	10	5	11	2	0
			Total	C	N	O	P	
38	WP	1	28	10	5	11	2	0

3 Residue-property plots (i)

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

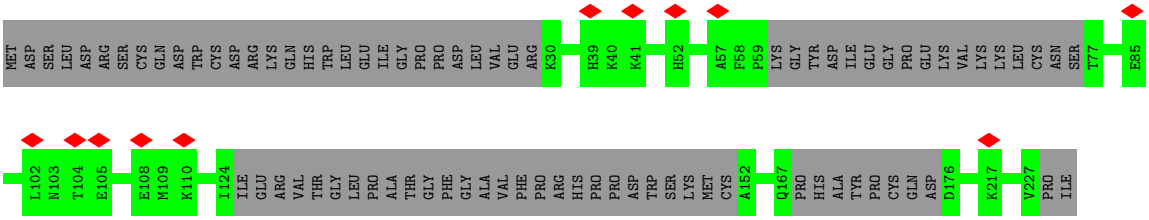
- Molecule 1: Protein CFAP95

Chain 0:



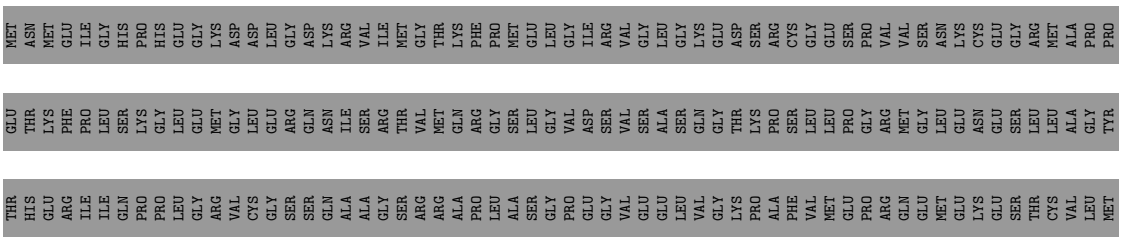
- Molecule 1: Protein CFAP95

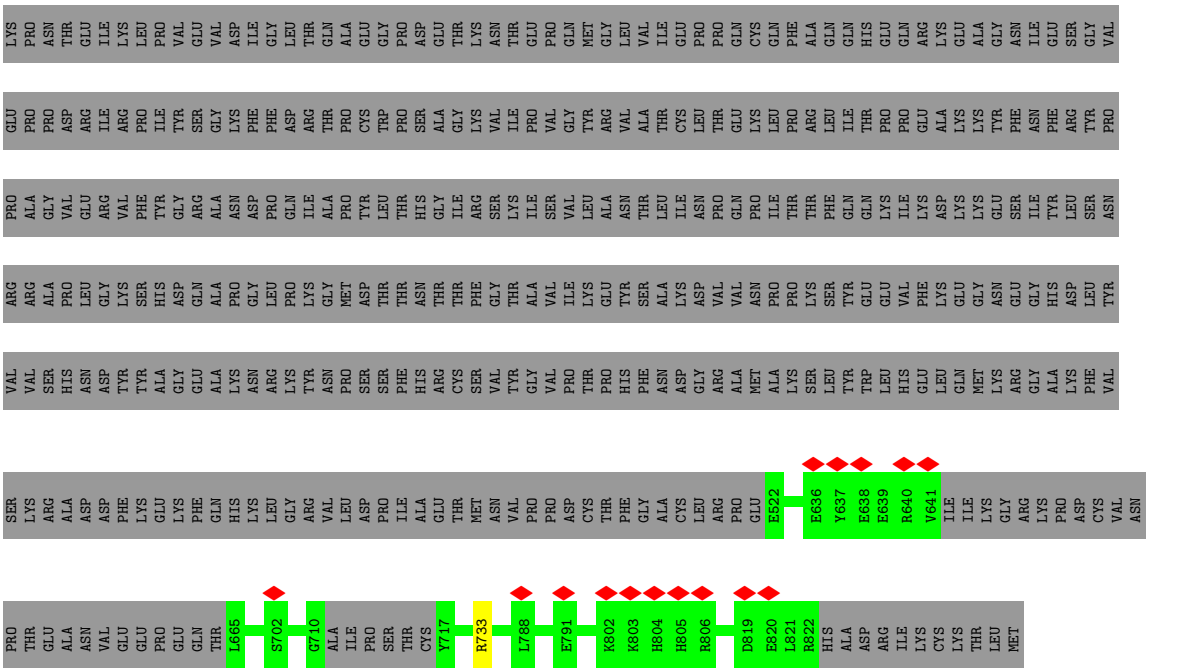
Chain 7:



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

Chain 1:



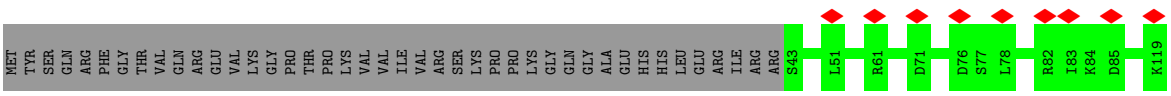


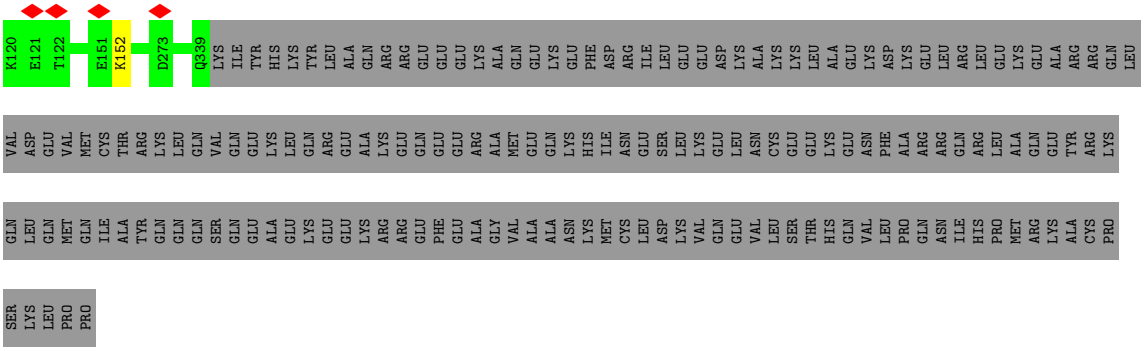
• Molecule 2: EF-hand domain-containing family member B

Chain 2:

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

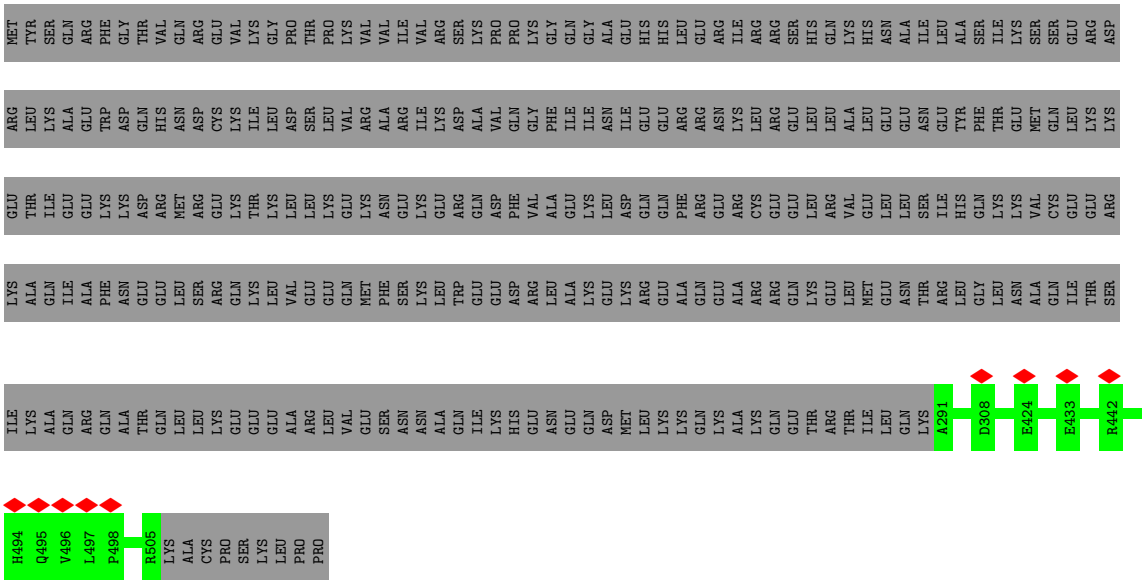
Chain 3:





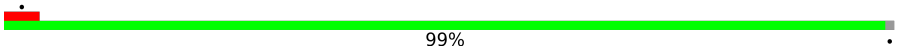
• Molecule 3: Cilia- and flagella-associated protein 53

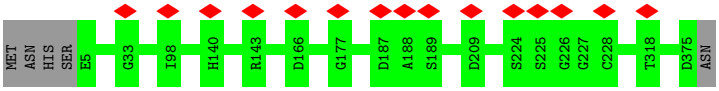
Chain 4:



• Molecule 4: Nucleoside diphosphate kinase 7

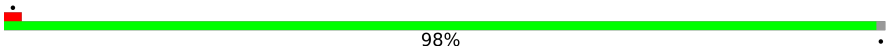
Chain 5:

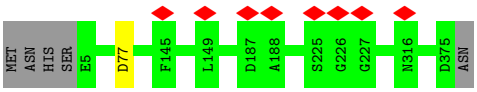




• Molecule 4: Nucleoside diphosphate kinase 7

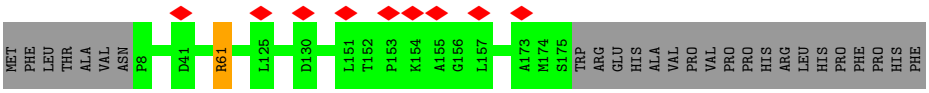
Chain 6:





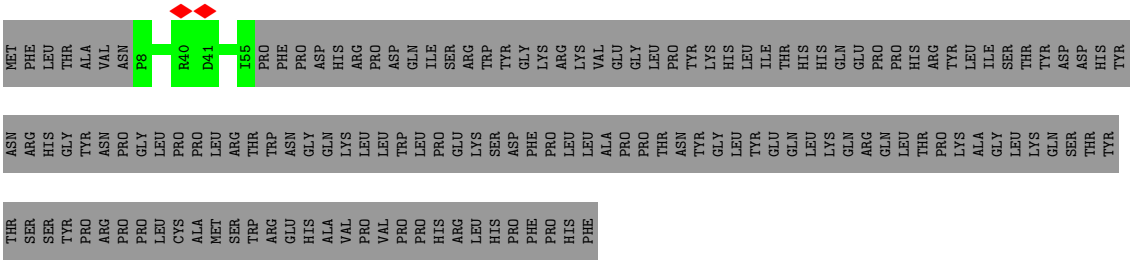
• Molecule 5: Protein CFAP107

Chain 8:



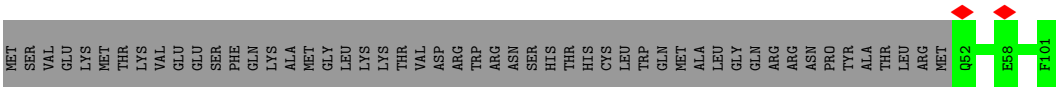
• Molecule 5: Protein CFAP107

Chain 9:



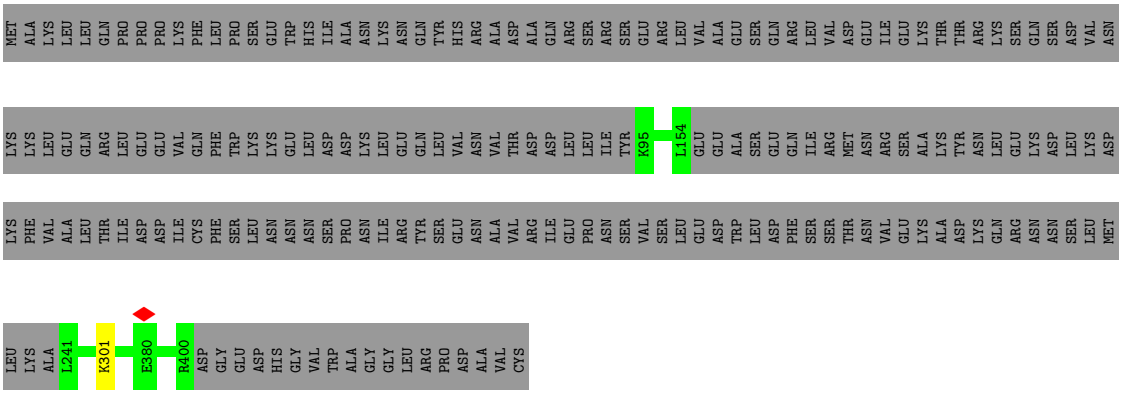
• Molecule 6: Protein CFAP141

Chain A:



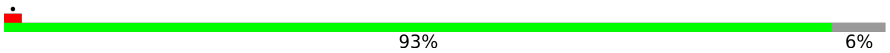
• Molecule 7: Tektin-1

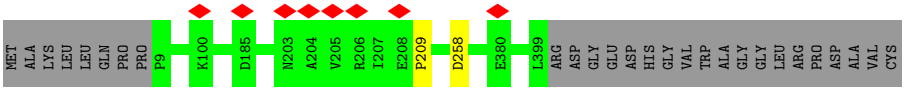
Chain A0:



• Molecule 7: Tektin-1

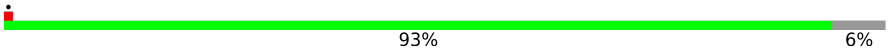
Chain A1:

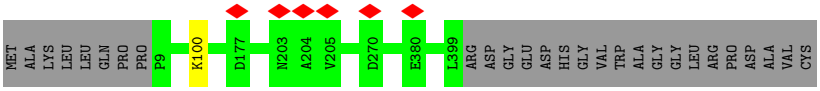




• Molecule 7: Tektin-1

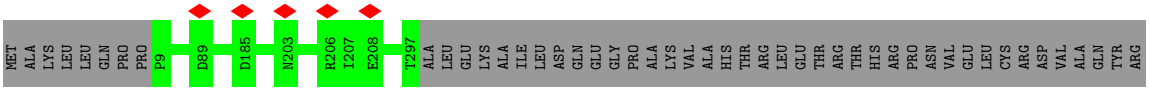
Chain A2:

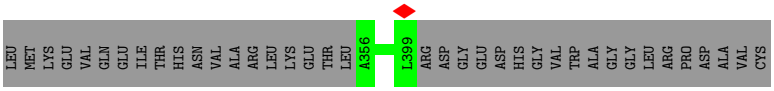




• Molecule 7: Tektin-1

Chain A3:



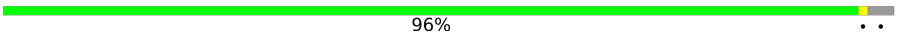


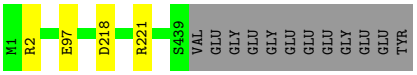
• Molecule 7: Tektin-1

Chain A4:

• Molecule 8: Tubulin alpha-1A chain

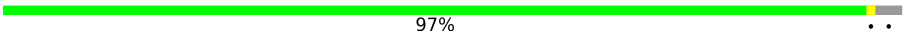
Chain AA:

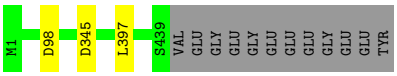




• Molecule 8: Tubulin alpha-1A chain

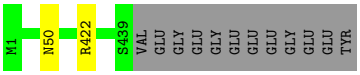
Chain AC:





- Molecule 8: Tubulin alpha-1A chain

Chain AE: 97%



- Molecule 8: Tubulin alpha-1A chain

Chain AG: 97%

- Molecule 8: Tubulin alpha-1A chain

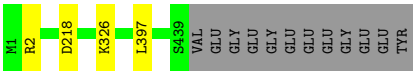
Chain AI: 97%

- Molecule 8: Tubulin alpha-1A chain

Chain AK: 97%

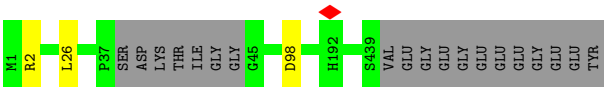
- Molecule 8: Tubulin alpha-1A chain

Chain AM: 96%



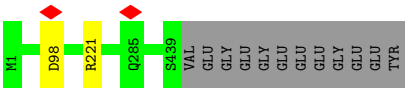
- Molecule 8: Tubulin alpha-1A chain

Chain BA: 95%



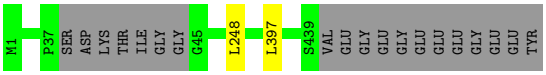
- Molecule 8: Tubulin alpha-1A chain

Chain BC: 97%



- Molecule 8: Tubulin alpha-1A chain

Chain BE: 95%

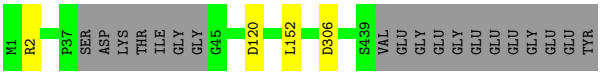


- Molecule 8: Tubulin alpha-1A chain

Chain BG: 97%

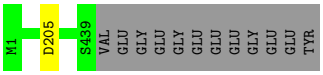
- Molecule 8: Tubulin alpha-1A chain

Chain BI: 95%



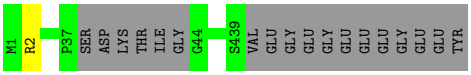
- Molecule 8: Tubulin alpha-1A chain

Chain BK: 97%



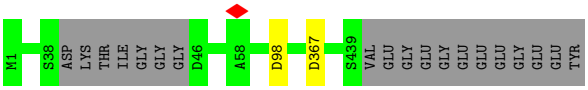
- Molecule 8: Tubulin alpha-1A chain

Chain BM: 96%



- Molecule 8: Tubulin alpha-1A chain

Chain CA: 95%

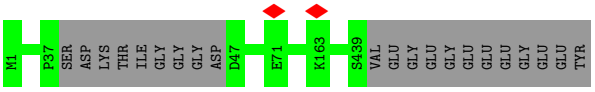


- Molecule 8: Tubulin alpha-1A chain

Chain CC: 97%

- Molecule 8: Tubulin alpha-1A chain

Chain CE: 95% 5%

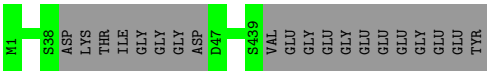


- Molecule 8: Tubulin alpha-1A chain

Chain CG: 97%

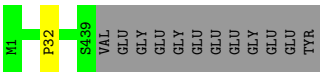
- Molecule 8: Tubulin alpha-1A chain

Chain CI: 96%



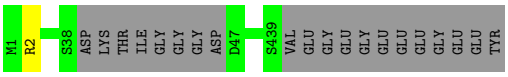
- Molecule 8: Tubulin alpha-1A chain

Chain CK: 97%



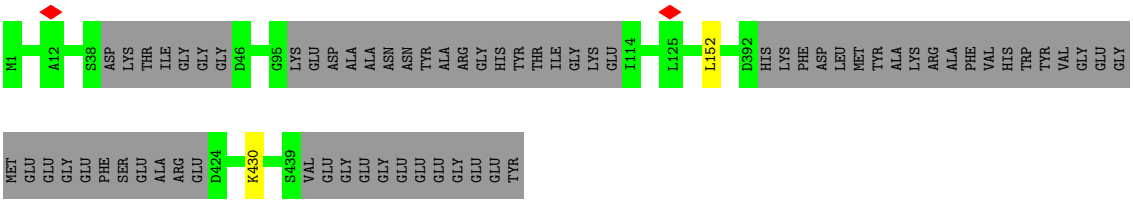
- Molecule 8: Tubulin alpha-1A chain

Chain CM: 95%



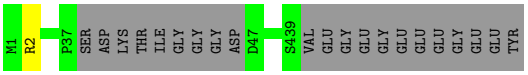
- Molecule 8: Tubulin alpha-1A chain

Chain DA: 84% 15%



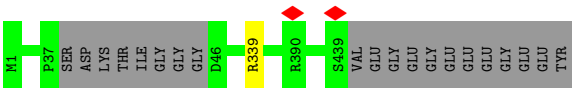
- Molecule 8: Tubulin alpha-1A chain

Chain DC: 95% 5%



• Molecule 8: Tubulin alpha-1A chain

Chain DE: 95%



• Molecule 8: Tubulin alpha-1A chain

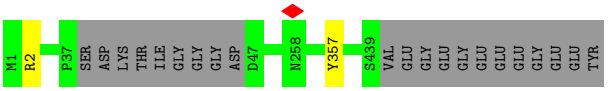
Chain DG: 95% 5%

• Molecule 8: Tubulin alpha-1A chain

Chain DI: 95% 5%

• Molecule 8: Tubulin alpha-1A chain

Chain DK: 95% 5%

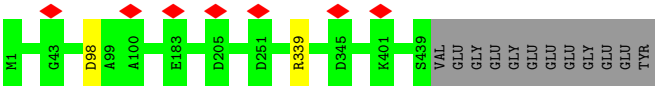


• Molecule 8: Tubulin alpha-1A chain

Chain DM: 95%

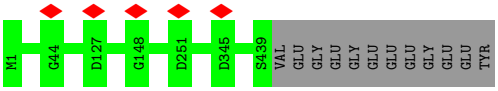
• Molecule 8: Tubulin alpha-1A chain

Chain EC: 97%



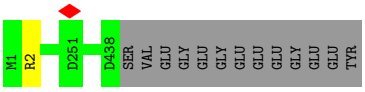
• Molecule 8: Tubulin alpha-1A chain

Chain EE: 97%



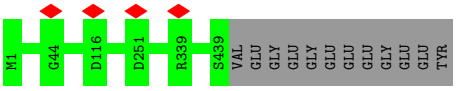
• Molecule 8: Tubulin alpha-1A chain

Chain EG: 97%



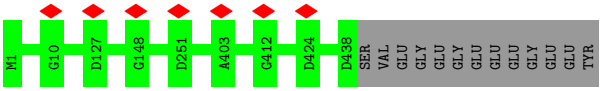
• Molecule 8: Tubulin alpha-1A chain

Chain EI: 97%



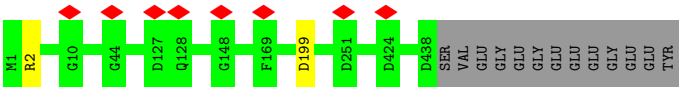
• Molecule 8: Tubulin alpha-1A chain

Chain EK: 97%



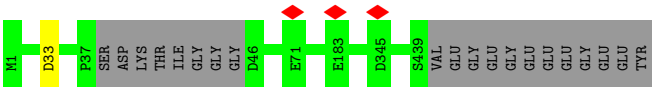
• Molecule 8: Tubulin alpha-1A chain

Chain EM: 97%



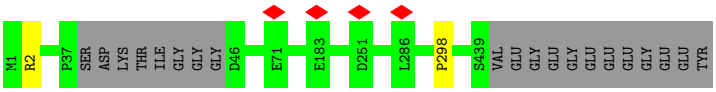
• Molecule 8: Tubulin alpha-1A chain

Chain FC: 95%



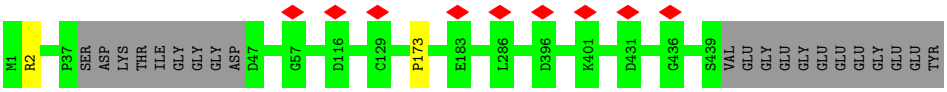
• Molecule 8: Tubulin alpha-1A chain

Chain FE: 95%



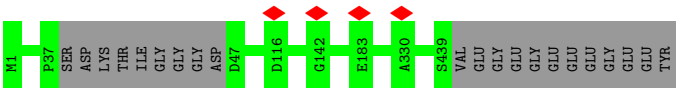
• Molecule 8: Tubulin alpha-1A chain

Chain FG: 95% 5%



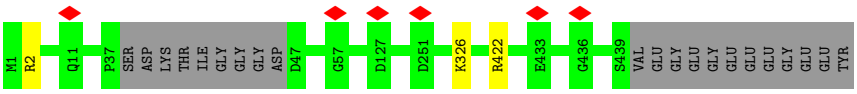
• Molecule 8: Tubulin alpha-1A chain

Chain FI: 95% 5%



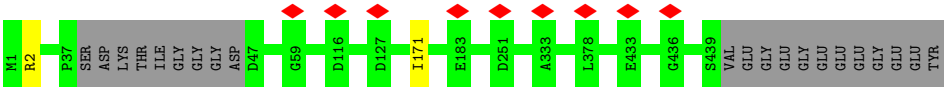
• Molecule 8: Tubulin alpha-1A chain

Chain FK: 95% 5%



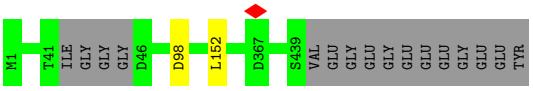
• Molecule 8: Tubulin alpha-1A chain

Chain FM: 95% 5%



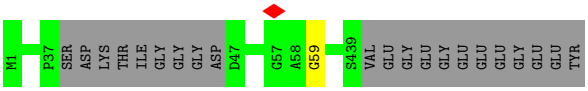
• Molecule 8: Tubulin alpha-1A chain

Chain GC: 96%



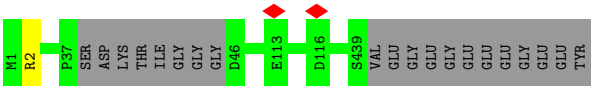
• Molecule 8: Tubulin alpha-1A chain

Chain GE: 95% 5%



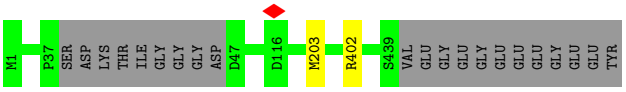
• Molecule 8: Tubulin alpha-1A chain

Chain GG: 95%



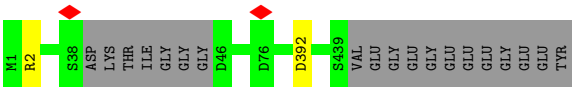
- Molecule 8: Tubulin alpha-1A chain

Chain GI: 95% 5%



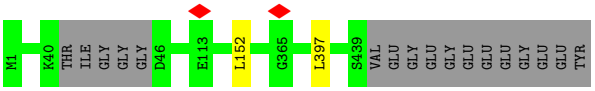
- Molecule 8: Tubulin alpha-1A chain

Chain GK: 95%



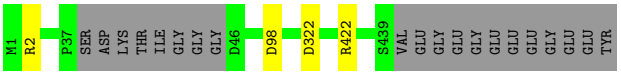
- Molecule 8: Tubulin alpha-1A chain

Chain GM: 96%



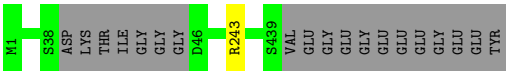
- Molecule 8: Tubulin alpha-1A chain

Chain HC: 95%



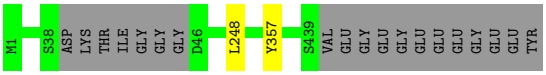
- Molecule 8: Tubulin alpha-1A chain

Chain HE: 96%



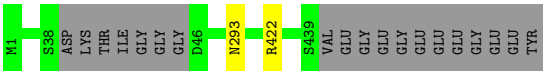
- Molecule 8: Tubulin alpha-1A chain

Chain HG: 95%



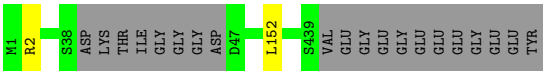
- Molecule 8: Tubulin alpha-1A chain

Chain HI: 95%



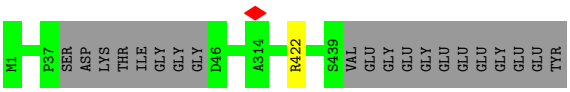
- Molecule 8: Tubulin alpha-1A chain

Chain HK: 95%



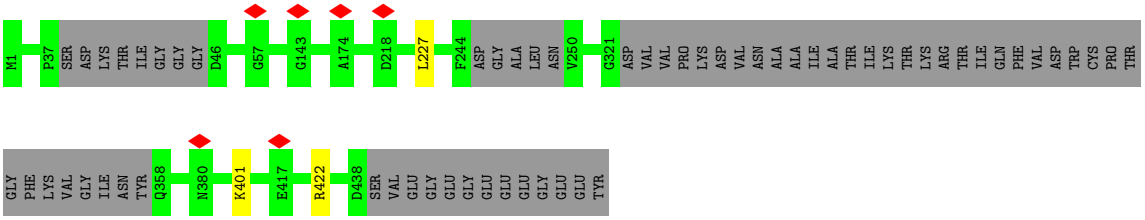
- Molecule 8: Tubulin alpha-1A chain

Chain HM: 95%



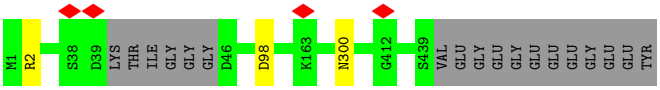
- Molecule 8: Tubulin alpha-1A chain

Chain HO: 86% 14%



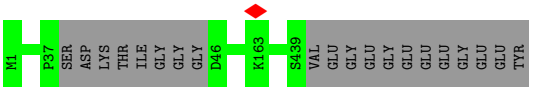
- Molecule 8: Tubulin alpha-1A chain

Chain IC: 95%



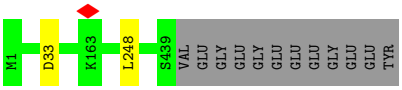
- Molecule 8: Tubulin alpha-1A chain

Chain IE: 96%



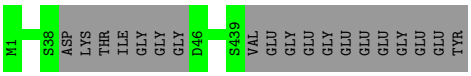
- Molecule 8: Tubulin alpha-1A chain

Chain IG: 97%



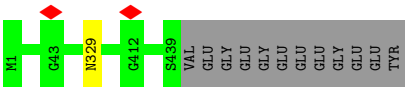
- Molecule 8: Tubulin alpha-1A chain

Chain II: 96%



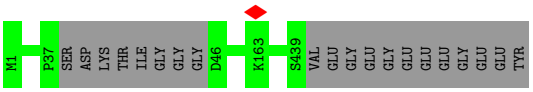
• Molecule 8: Tubulin alpha-1A chain

Chain IK: 97%



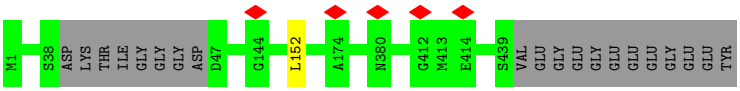
• Molecule 8: Tubulin alpha-1A chain

Chain IM: 96%



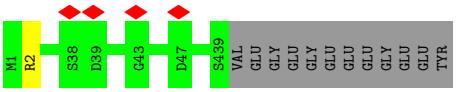
• Molecule 8: Tubulin alpha-1A chain

Chain IO: 95%



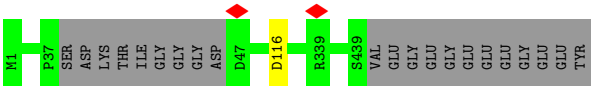
• Molecule 8: Tubulin alpha-1A chain

Chain JC: 97%



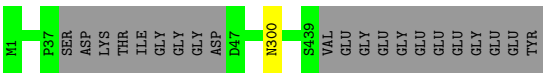
• Molecule 8: Tubulin alpha-1A chain

Chain JE: 95% 5%



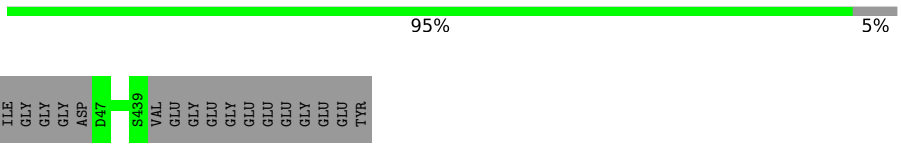
• Molecule 8: Tubulin alpha-1A chain

Chain JG: 95% 5%



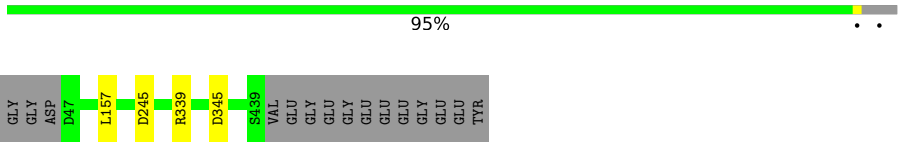
- Molecule 8: Tubulin alpha-1A chain

Chain JI:



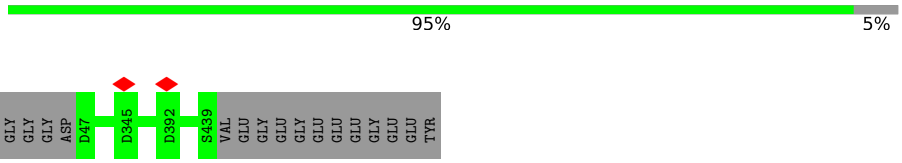
- Molecule 8: Tubulin alpha-1A chain

Chain JK:



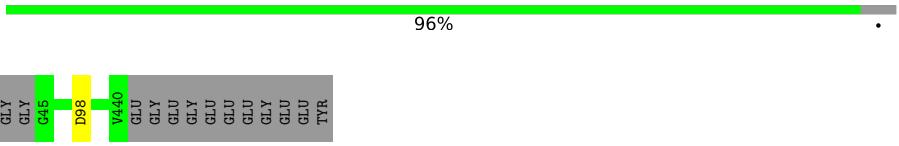
- Molecule 8: Tubulin alpha-1A chain

Chain JM:



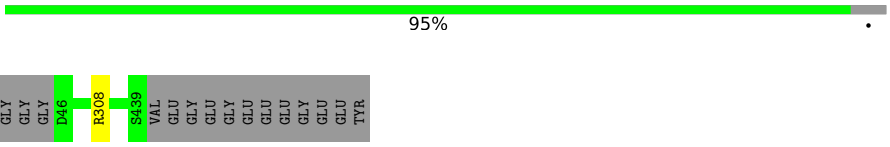
- Molecule 8: Tubulin alpha-1A chain

Chain KC:



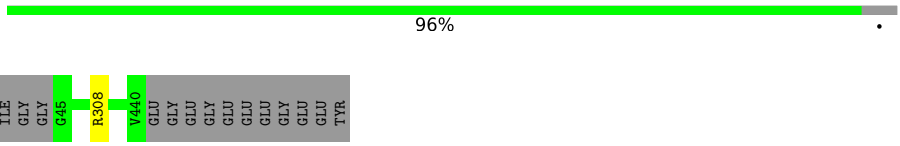
- Molecule 8: Tubulin alpha-1A chain

Chain KE:



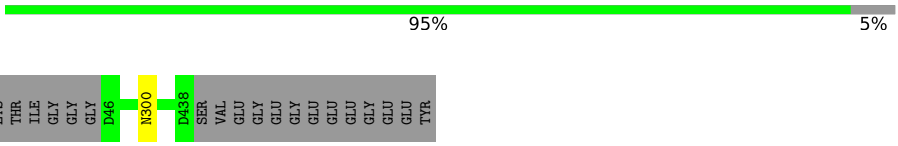
- Molecule 8: Tubulin alpha-1A chain

Chain KG:



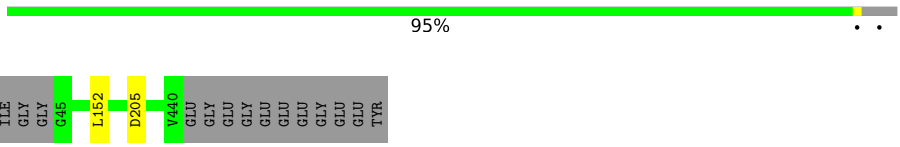
- Molecule 8: Tubulin alpha-1A chain

Chain KI:



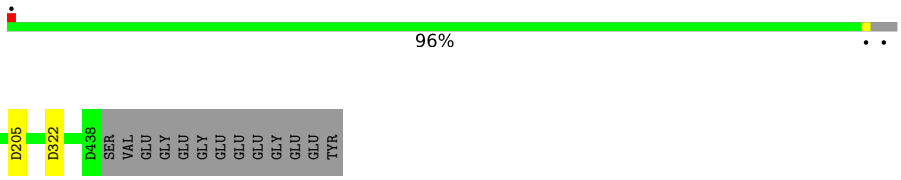
- Molecule 8: Tubulin alpha-1A chain

Chain KK:



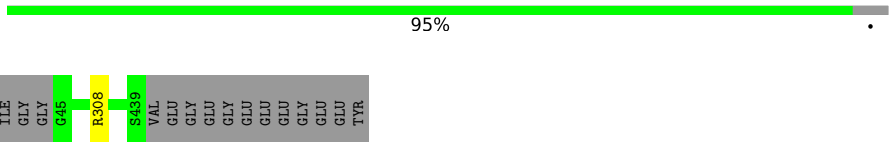
- Molecule 8: Tubulin alpha-1A chain

Chain KM:



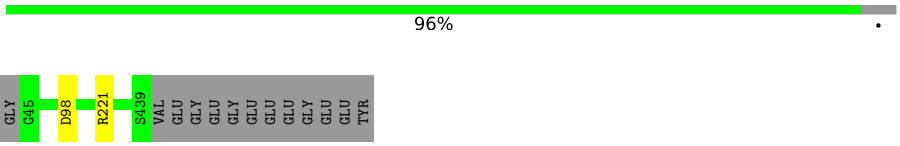
- Molecule 8: Tubulin alpha-1A chain

Chain KO:



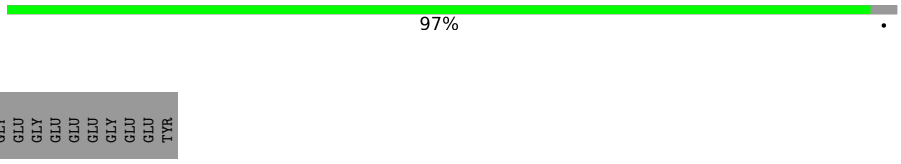
- Molecule 8: Tubulin alpha-1A chain

Chain LC:



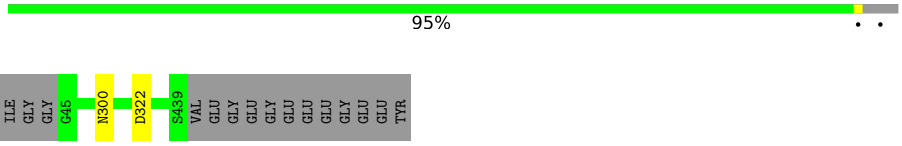
- Molecule 8: Tubulin alpha-1A chain

Chain LE:



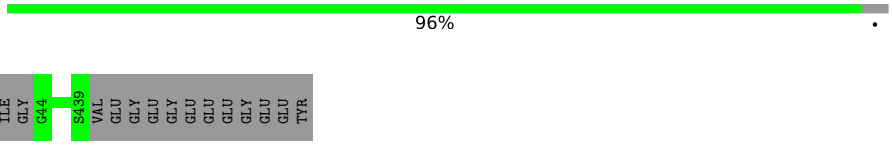
- Molecule 8: Tubulin alpha-1A chain

Chain LG:



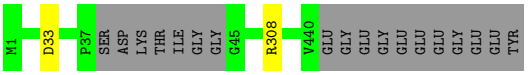
- Molecule 8: Tubulin alpha-1A chain

Chain LI:



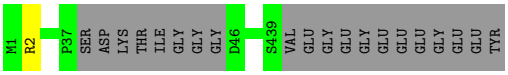
- Molecule 8: Tubulin alpha-1A chain

Chain LK: 96%



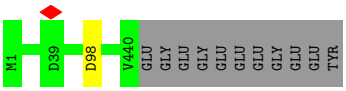
- Molecule 8: Tubulin alpha-1A chain

Chain LM: 95%



- Molecule 8: Tubulin alpha-1A chain

Chain MC: 97%

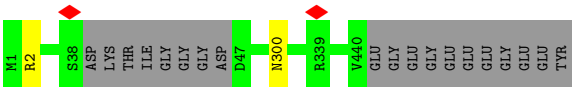


- Molecule 8: Tubulin alpha-1A chain

Chain ME: 95%

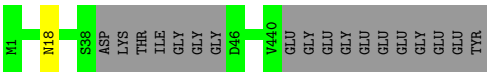
- Molecule 8: Tubulin alpha-1A chain

Chain MG: 95%



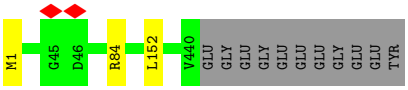
- Molecule 8: Tubulin alpha-1A chain

Chain MI: 96%



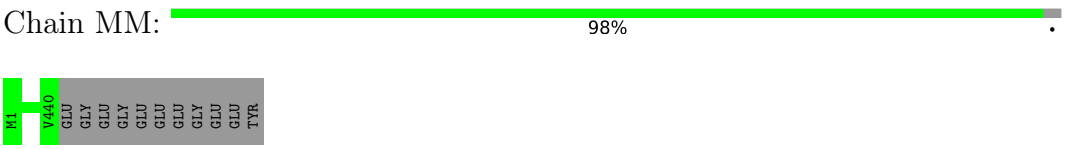
- Molecule 8: Tubulin alpha-1A chain

Chain MK: 97%



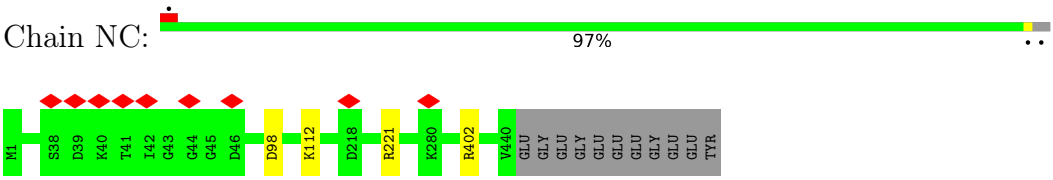
- Molecule 8: Tubulin alpha-1A chain

Chain MM:



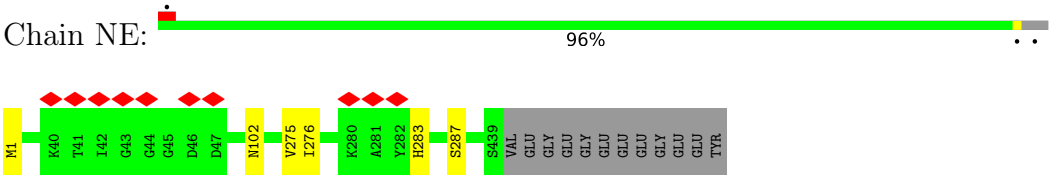
- Molecule 8: Tubulin alpha-1A chain

Chain NC:



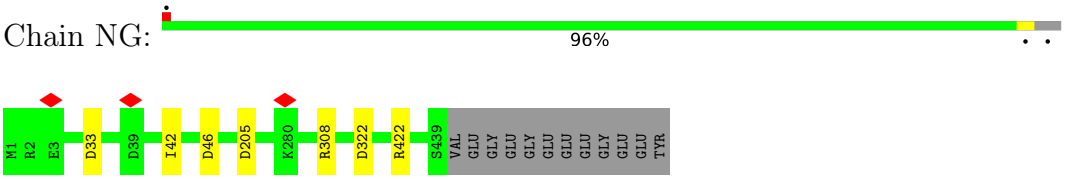
- Molecule 8: Tubulin alpha-1A chain

Chain NE:



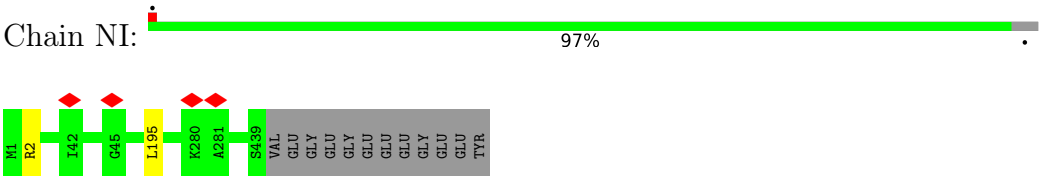
- Molecule 8: Tubulin alpha-1A chain

Chain NG:



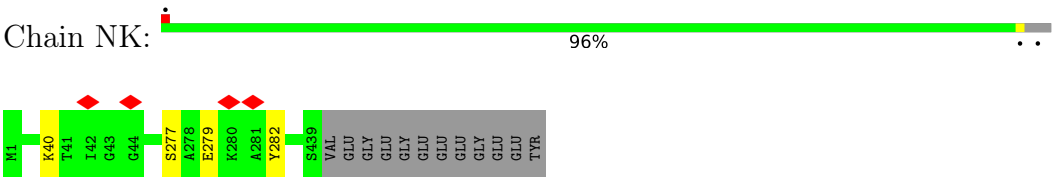
- Molecule 8: Tubulin alpha-1A chain

Chain NI:



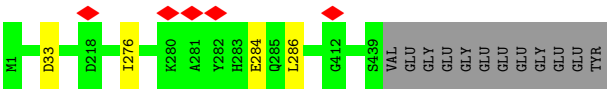
- Molecule 8: Tubulin alpha-1A chain

Chain NK:



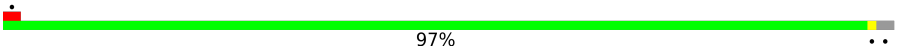
- Molecule 8: Tubulin alpha-1A chain

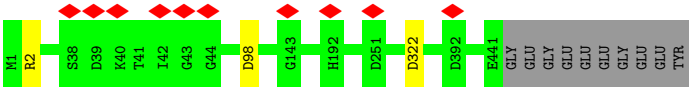
Chain NM:



• Molecule 8: Tubulin alpha-1A chain

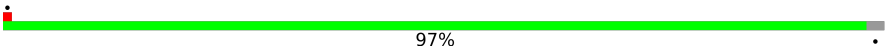
Chain OC:

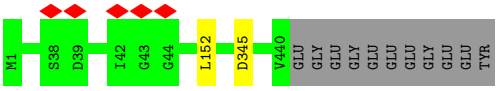




• Molecule 8: Tubulin alpha-1A chain

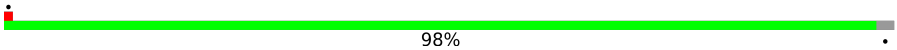
Chain OE:

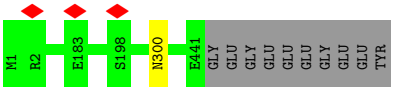




• Molecule 8: Tubulin alpha-1A chain

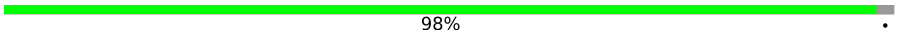
Chain OG:





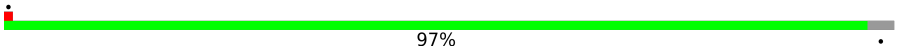
• Molecule 8: Tubulin alpha-1A chain

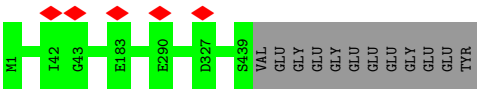
Chain OI:



• Molecule 8: Tubulin alpha-1A chain

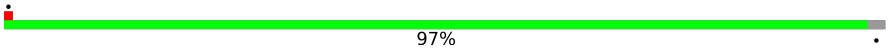
Chain OK:

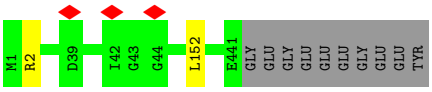




• Molecule 8: Tubulin alpha-1A chain

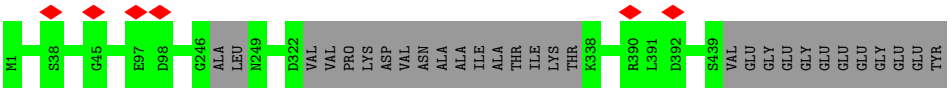
Chain OM:





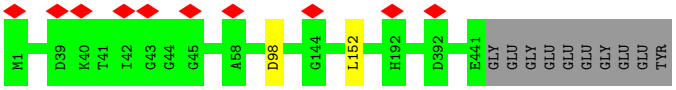
• Molecule 8: Tubulin alpha-1A chain

Chain OO: 94% 6%



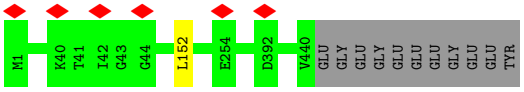
• Molecule 8: Tubulin alpha-1A chain

Chain PC: 97%



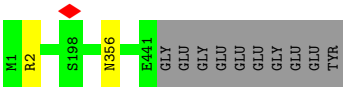
• Molecule 8: Tubulin alpha-1A chain

Chain PE: 97%



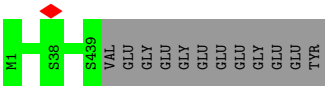
• Molecule 8: Tubulin alpha-1A chain

Chain PG: 97%



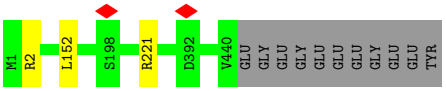
• Molecule 8: Tubulin alpha-1A chain

Chain PI: 97%



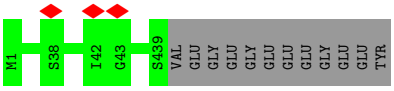
• Molecule 8: Tubulin alpha-1A chain

Chain PK: 97%



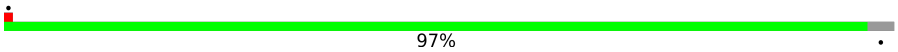
• Molecule 8: Tubulin alpha-1A chain

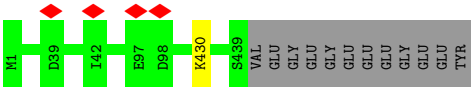
Chain PM: 97%



- Molecule 8: Tubulin alpha-1A chain

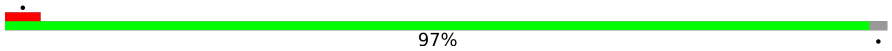
Chain PO:

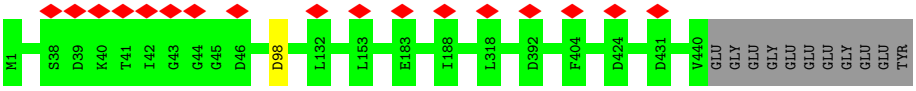




- Molecule 8: Tubulin alpha-1A chain

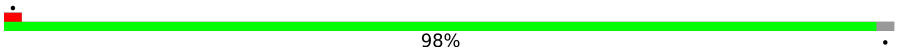
Chain QC:

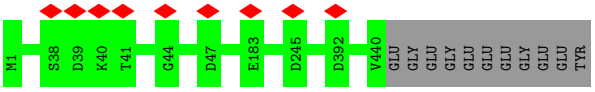




- Molecule 8: Tubulin alpha-1A chain

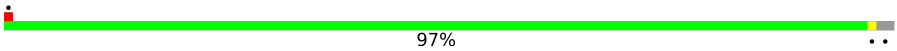
Chain QE:

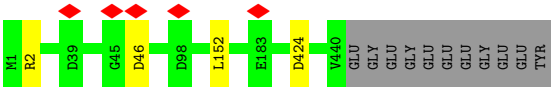




- Molecule 8: Tubulin alpha-1A chain

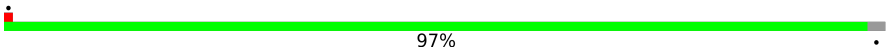
Chain QG:

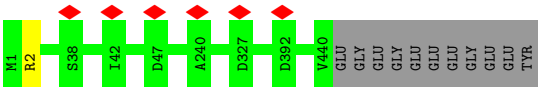




- Molecule 8: Tubulin alpha-1A chain

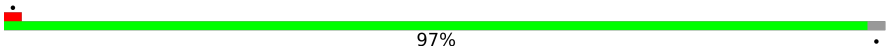
Chain QI:

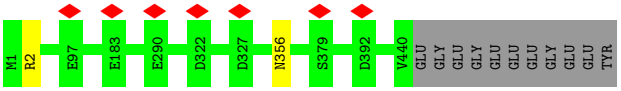




- Molecule 8: Tubulin alpha-1A chain

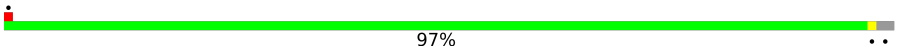
Chain QK:

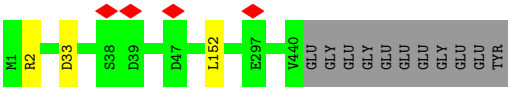




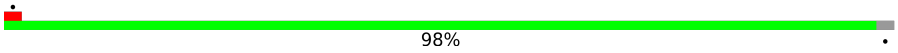
- Molecule 8: Tubulin alpha-1A chain

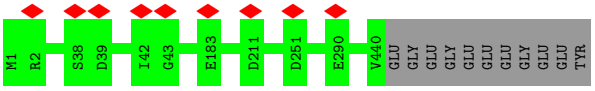
Chain QM:





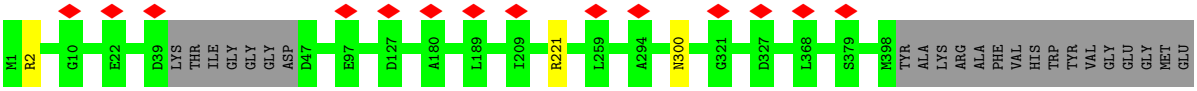
• Molecule 8: Tubulin alpha-1A chain

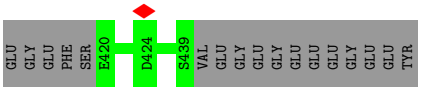
Chain QO: 



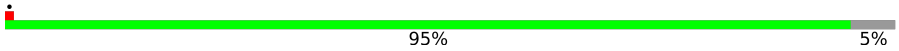
• Molecule 8: Tubulin alpha-1A chain

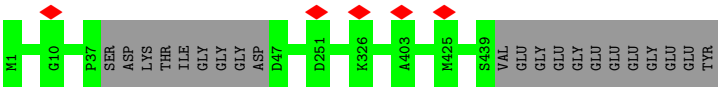
Chain RC: 



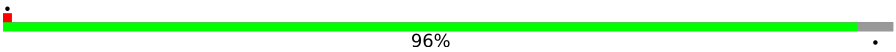


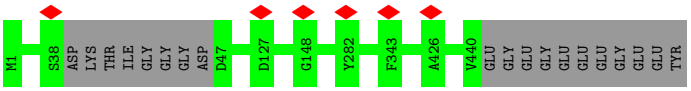
• Molecule 8: Tubulin alpha-1A chain

Chain RE: 

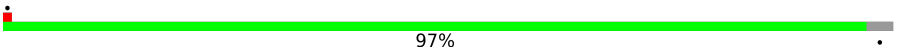


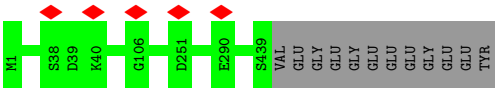
• Molecule 8: Tubulin alpha-1A chain

Chain RG: 

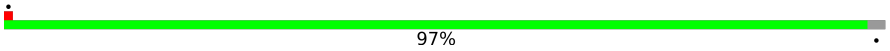


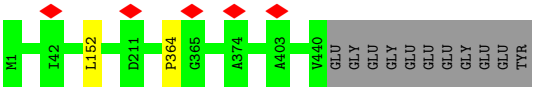
• Molecule 8: Tubulin alpha-1A chain

Chain RI: 



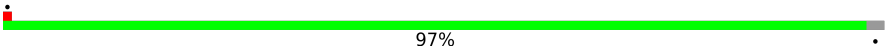
• Molecule 8: Tubulin alpha-1A chain

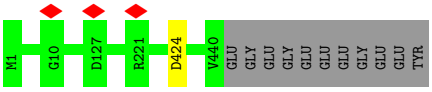
Chain RK: 



• Molecule 8: Tubulin alpha-1A chain

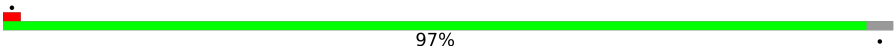
Chain RM:

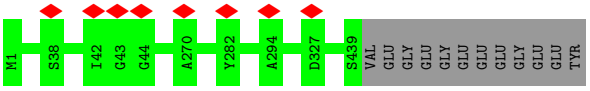




• Molecule 8: Tubulin alpha-1A chain

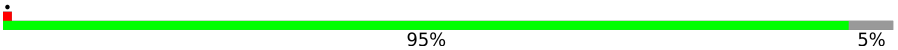
Chain RO:

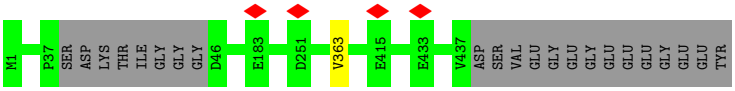




• Molecule 8: Tubulin alpha-1A chain

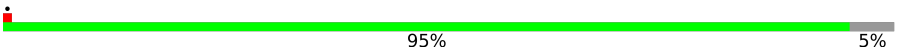
Chain SE:

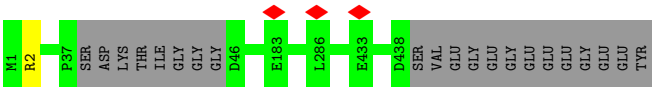




• Molecule 8: Tubulin alpha-1A chain

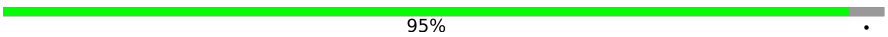
Chain SG:

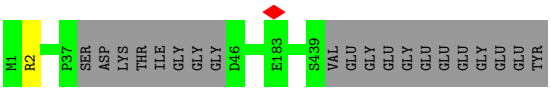




• Molecule 8: Tubulin alpha-1A chain

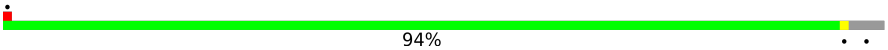
Chain SI:





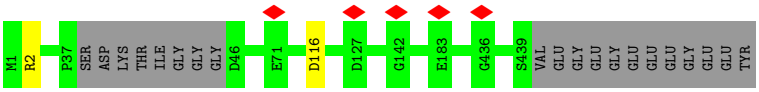
• Molecule 8: Tubulin alpha-1A chain

Chain SK:



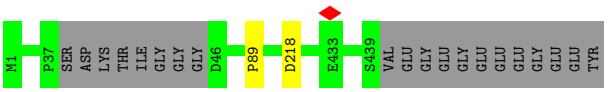
• Molecule 8: Tubulin alpha-1A chain

Chain SM: 95%



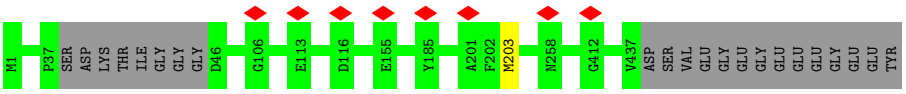
• Molecule 8: Tubulin alpha-1A chain

Chain SO: 95%



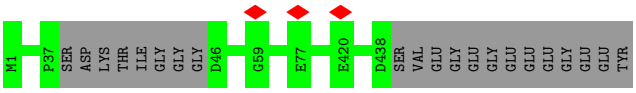
• Molecule 8: Tubulin alpha-1A chain

Chain TE: 95% 5%



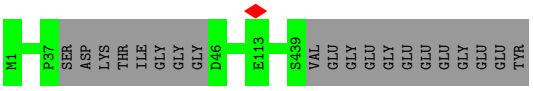
• Molecule 8: Tubulin alpha-1A chain

Chain TG: 95% 5%



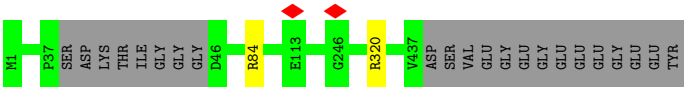
• Molecule 8: Tubulin alpha-1A chain

Chain TI: 96%



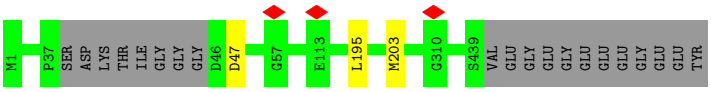
• Molecule 8: Tubulin alpha-1A chain

Chain TK: 95% 5%



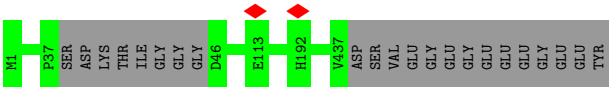
• Molecule 8: Tubulin alpha-1A chain

Chain TM: 95%



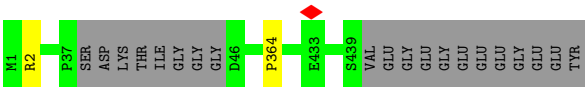
- Molecule 8: Tubulin alpha-1A chain

Chain TO: 95% 5%



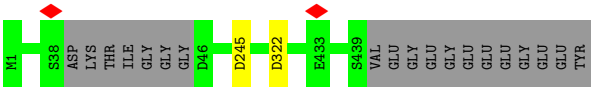
- Molecule 8: Tubulin alpha-1A chain

Chain UE: 95%



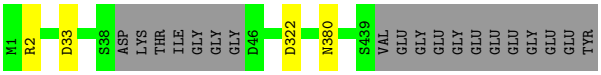
- Molecule 8: Tubulin alpha-1A chain

Chain UG: 95%



- Molecule 8: Tubulin alpha-1A chain

Chain UI: 95%

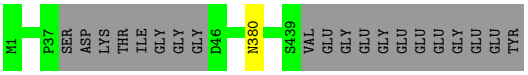


- Molecule 8: Tubulin alpha-1A chain

Chain UK: 95%

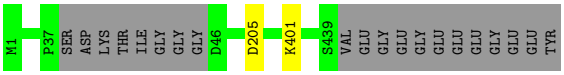
- Molecule 8: Tubulin alpha-1A chain

Chain UM: 95%



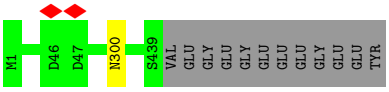
- Molecule 8: Tubulin alpha-1A chain

Chain UO: 95%



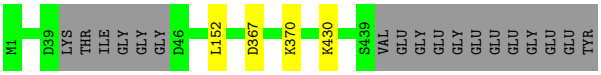
- Molecule 8: Tubulin alpha-1A chain

Chain VE: 97%



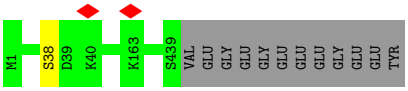
- Molecule 8: Tubulin alpha-1A chain

Chain VG: 95%



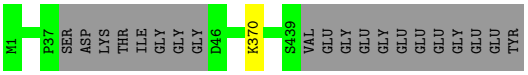
- Molecule 8: Tubulin alpha-1A chain

Chain VI: 97%



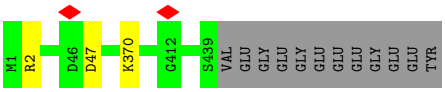
- Molecule 8: Tubulin alpha-1A chain

Chain VK: 95%



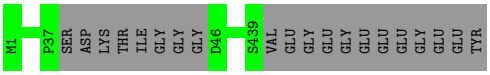
- Molecule 8: Tubulin alpha-1A chain

Chain VM: 97%



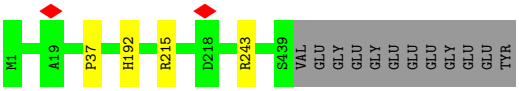
- Molecule 8: Tubulin alpha-1A chain

Chain VO: 96%



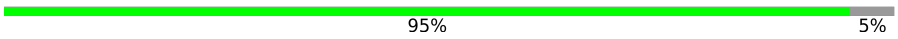
- Molecule 8: Tubulin alpha-1A chain

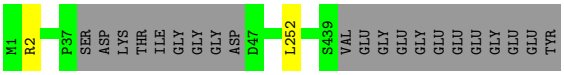
Chain WE: 96%



• Molecule 8: Tubulin alpha-1A chain

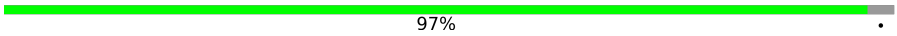
Chain WG:

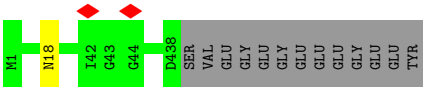




• Molecule 8: Tubulin alpha-1A chain

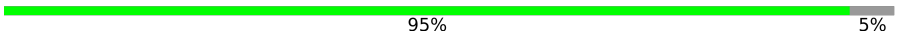
Chain WI:

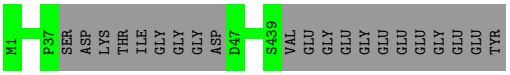




• Molecule 8: Tubulin alpha-1A chain

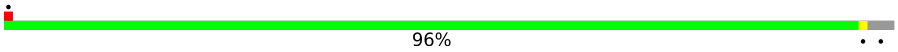
Chain WK:





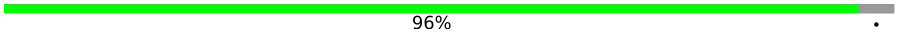
• Molecule 8: Tubulin alpha-1A chain

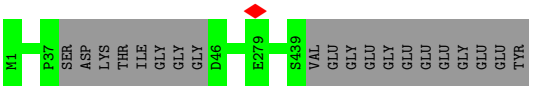
Chain WM:



• Molecule 8: Tubulin alpha-1A chain

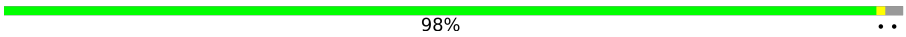
Chain WO:

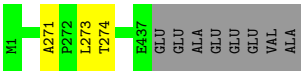




• Molecule 9: Tubulin beta-4B chain

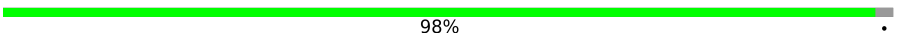
Chain AB:

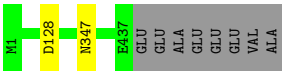




• Molecule 9: Tubulin beta-4B chain

Chain AD:





• Molecule 9: Tubulin beta-4B chain

Chain AF: 97%

• Molecule 9: Tubulin beta-4B chain

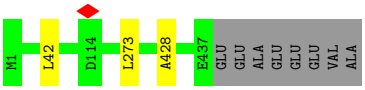
Chain AH: 97%

• Molecule 9: Tubulin beta-4B chain

Chain AJ: 97%

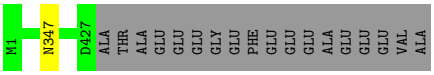
• Molecule 9: Tubulin beta-4B chain

Chain AL: 98%



• Molecule 9: Tubulin beta-4B chain

Chain BB: 96%

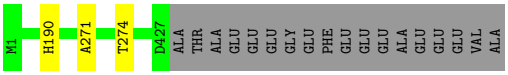


• Molecule 9: Tubulin beta-4B chain

Chain BD: 95%

• Molecule 9: Tubulin beta-4B chain

Chain BF: 95%

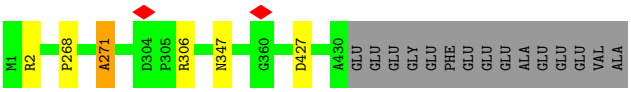


• Molecule 9: Tubulin beta-4B chain

Chain BH: 95%

• Molecule 9: Tubulin beta-4B chain

Chain BJ: 95%

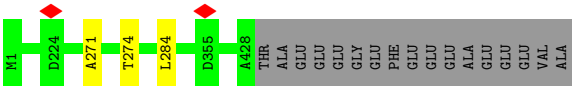


• Molecule 9: Tubulin beta-4B chain

Chain BL: 96%

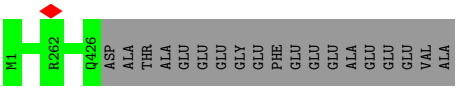
• Molecule 9: Tubulin beta-4B chain

Chain CB: 96%



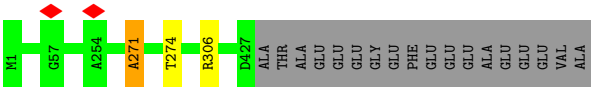
• Molecule 9: Tubulin beta-4B chain

Chain CD: 96%



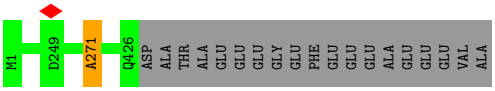
• Molecule 9: Tubulin beta-4B chain

Chain CF: 95%



• Molecule 9: Tubulin beta-4B chain

Chain CH: 96%



• Molecule 9: Tubulin beta-4B chain

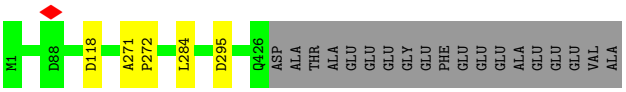
Chain CJ: 95%

• Molecule 9: Tubulin beta-4B chain

Chain CL: 96%

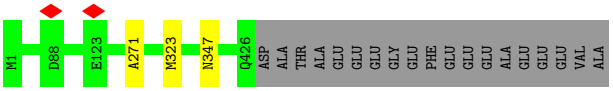
• Molecule 9: Tubulin beta-4B chain

Chain DB: 95%



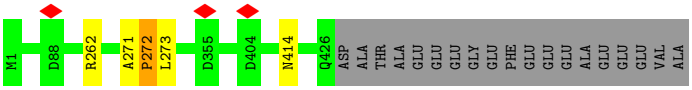
• Molecule 9: Tubulin beta-4B chain

Chain DD: 95%



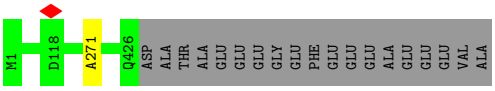
• Molecule 9: Tubulin beta-4B chain

Chain DF: 95%



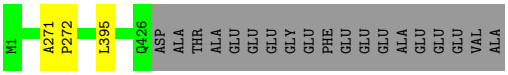
• Molecule 9: Tubulin beta-4B chain

Chain DH: 96%



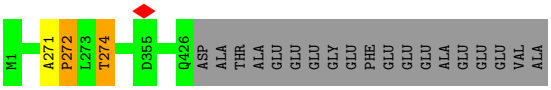
• Molecule 9: Tubulin beta-4B chain

Chain DJ: 95%



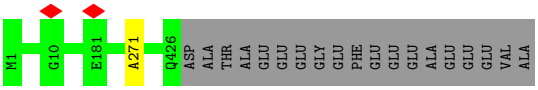
• Molecule 9: Tubulin beta-4B chain

Chain DL: 95%



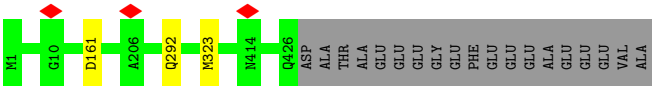
• Molecule 9: Tubulin beta-4B chain

Chain EB: 96%



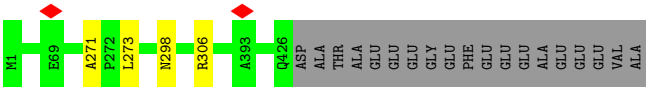
• Molecule 9: Tubulin beta-4B chain

Chain ED: 95%



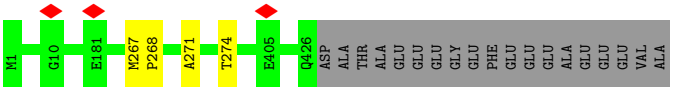
• Molecule 9: Tubulin beta-4B chain

Chain EF: 95%



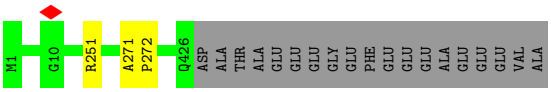
• Molecule 9: Tubulin beta-4B chain

Chain EH: 95%



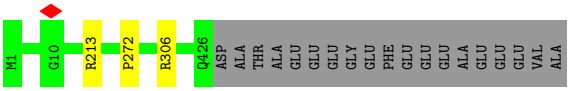
• Molecule 9: Tubulin beta-4B chain

Chain EJ: 95%



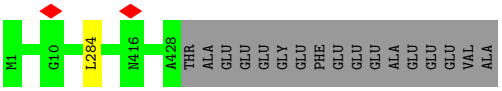
• Molecule 9: Tubulin beta-4B chain

Chain EL: 95%



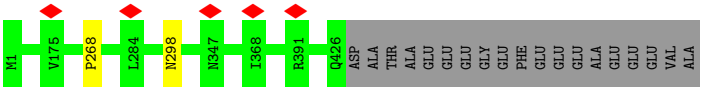
• Molecule 9: Tubulin beta-4B chain

Chain EN: 96%



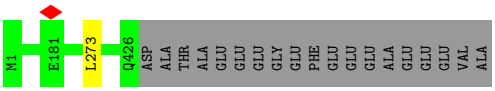
• Molecule 9: Tubulin beta-4B chain

Chain FB: 95%



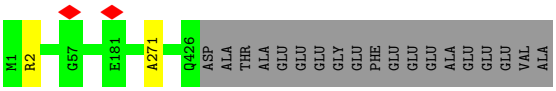
• Molecule 9: Tubulin beta-4B chain

Chain FD: 96%



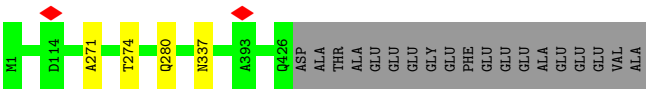
• Molecule 9: Tubulin beta-4B chain

Chain FF: 95%



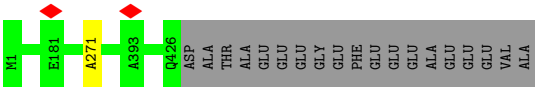
• Molecule 9: Tubulin beta-4B chain

Chain FH: 95%



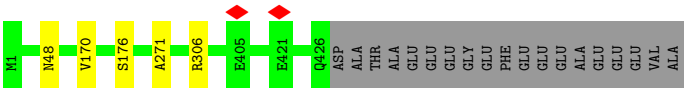
• Molecule 9: Tubulin beta-4B chain

Chain FJ: 96%



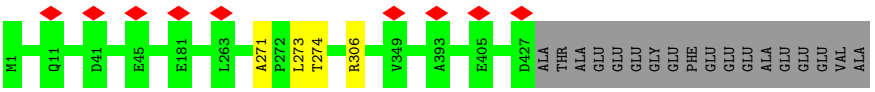
• Molecule 9: Tubulin beta-4B chain

Chain FL: 95%



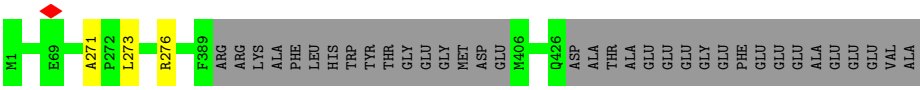
• Molecule 9: Tubulin beta-4B chain

Chain FN: 95%



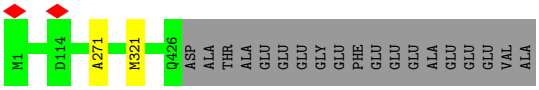
• Molecule 9: Tubulin beta-4B chain

Chain GB: 91% 8%



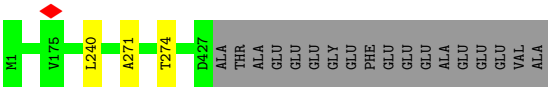
• Molecule 9: Tubulin beta-4B chain

Chain GD: 95%



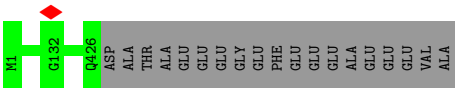
• Molecule 9: Tubulin beta-4B chain

Chain GF: 95%



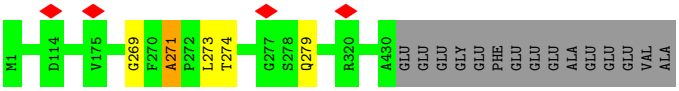
• Molecule 9: Tubulin beta-4B chain

Chain GH: 96%



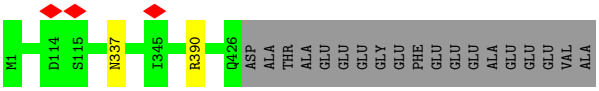
• Molecule 9: Tubulin beta-4B chain

Chain GJ: 96%



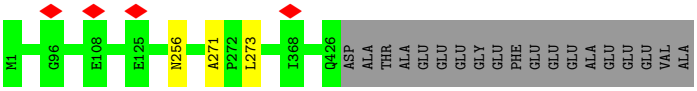
- Molecule 9: Tubulin beta-4B chain

Chain GL: 95%



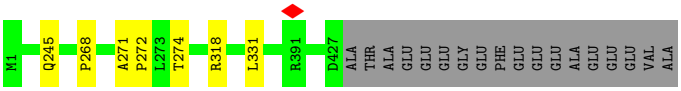
- Molecule 9: Tubulin beta-4B chain

Chain GN: 95%



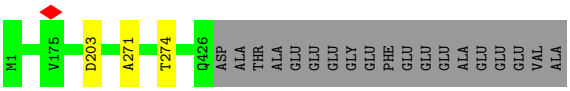
- Molecule 9: Tubulin beta-4B chain

Chain HB: 94%



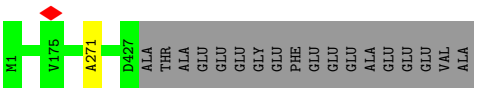
- Molecule 9: Tubulin beta-4B chain

Chain HD: 95%



- Molecule 9: Tubulin beta-4B chain

Chain HF: 96%

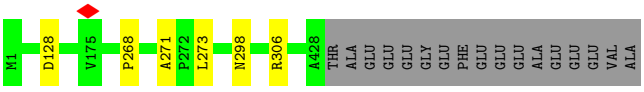


- Molecule 9: Tubulin beta-4B chain

Chain HH: 95%

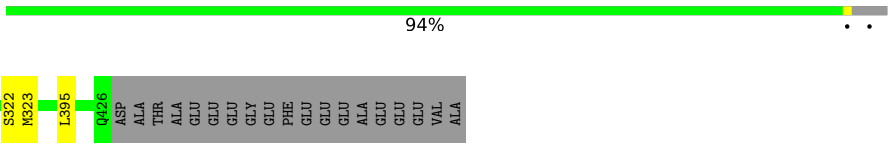
- Molecule 9: Tubulin beta-4B chain

Chain HJ: 95%



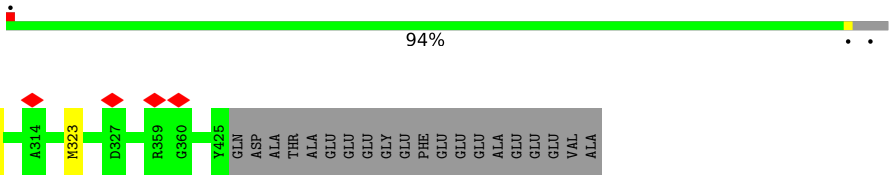
- Molecule 9: Tubulin beta-4B chain

Chain HL:



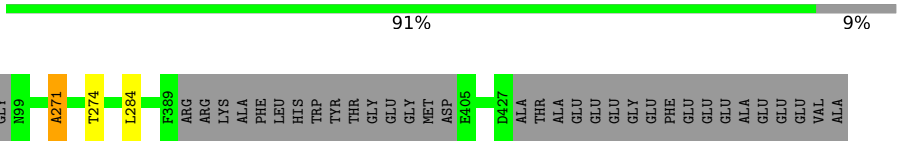
- Molecule 9: Tubulin beta-4B chain

Chain HN:



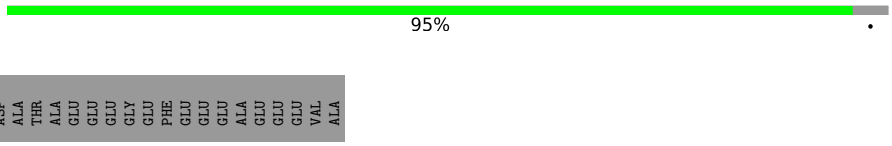
- Molecule 9: Tubulin beta-4B chain

Chain IB:



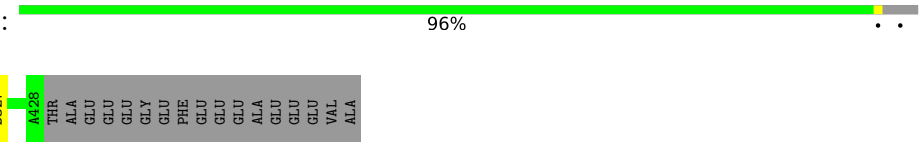
- Molecule 9: Tubulin beta-4B chain

Chain ID:



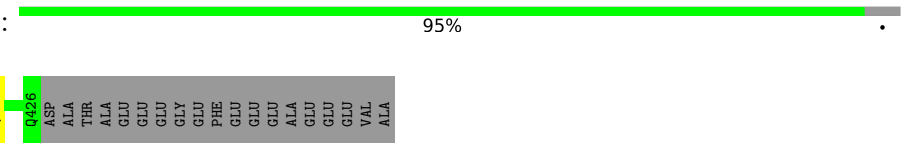
- Molecule 9: Tubulin beta-4B chain

Chain IF:



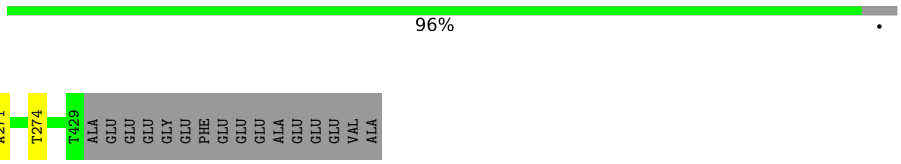
- Molecule 9: Tubulin beta-4B chain

Chain IH:



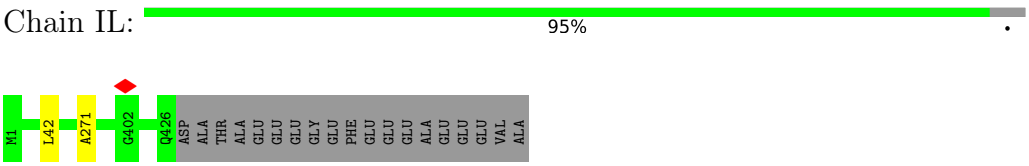
- Molecule 9: Tubulin beta-4B chain

Chain IJ:



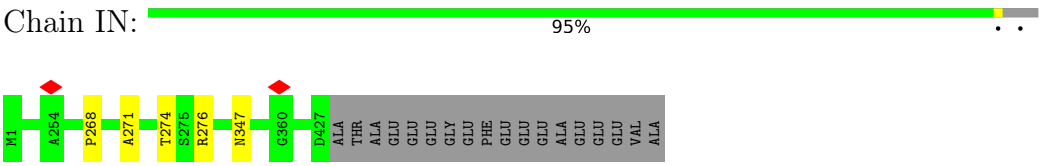
- Molecule 9: Tubulin beta-4B chain

Chain IL:



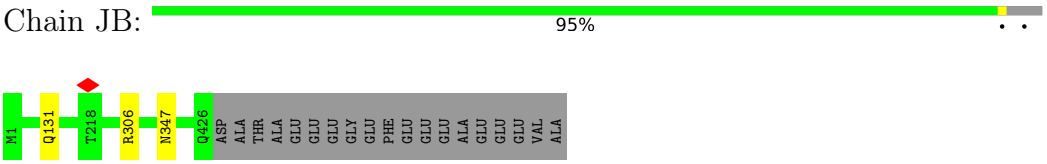
• Molecule 9: Tubulin beta-4B chain

Chain IN:



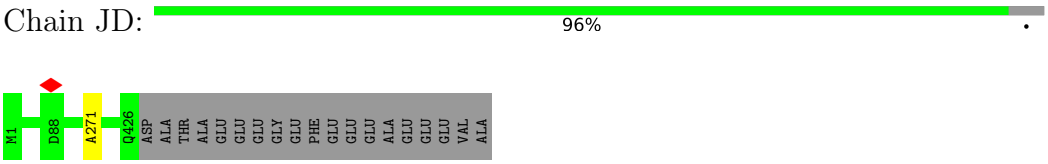
• Molecule 9: Tubulin beta-4B chain

Chain JB:



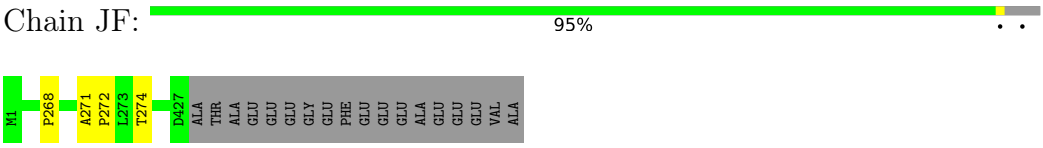
• Molecule 9: Tubulin beta-4B chain

Chain JD:



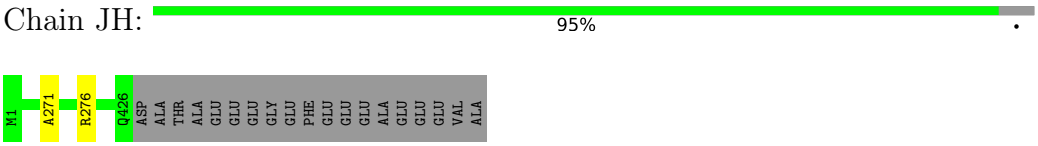
• Molecule 9: Tubulin beta-4B chain

Chain JF:



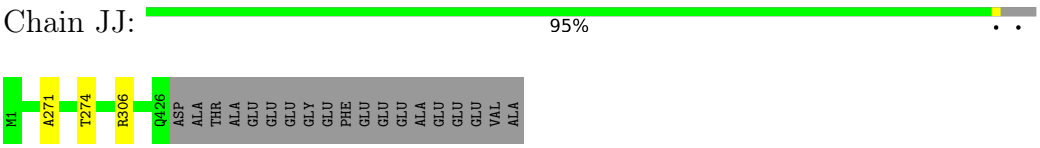
• Molecule 9: Tubulin beta-4B chain

Chain JH:



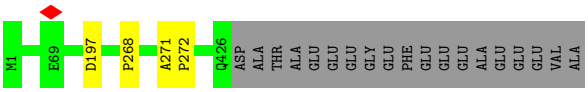
• Molecule 9: Tubulin beta-4B chain

Chain JJ:



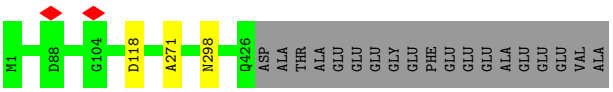
• Molecule 9: Tubulin beta-4B chain

Chain JL: 95%



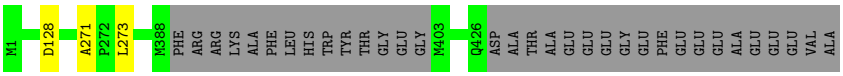
• Molecule 9: Tubulin beta-4B chain

Chain JN: 95%



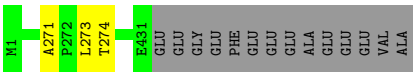
• Molecule 9: Tubulin beta-4B chain

Chain KB: 92% 7%



• Molecule 9: Tubulin beta-4B chain

Chain KD: 96%

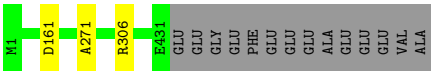


• Molecule 9: Tubulin beta-4B chain

Chain KF: 95%

• Molecule 9: Tubulin beta-4B chain

Chain KH: 96%



• Molecule 9: Tubulin beta-4B chain

Chain KJ: 95%

• Molecule 9: Tubulin beta-4B chain

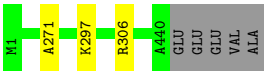
Chain KL: 96%

• Molecule 9: Tubulin beta-4B chain

Chain KN: 95%

• Molecule 9: Tubulin beta-4B chain

Chain LB: 98%

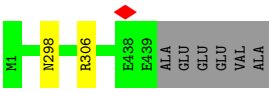


• Molecule 9: Tubulin beta-4B chain

Chain LD: 95%

• Molecule 9: Tubulin beta-4B chain

Chain LF: 98%

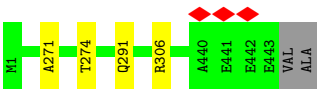


• Molecule 9: Tubulin beta-4B chain

Chain LH: 95%

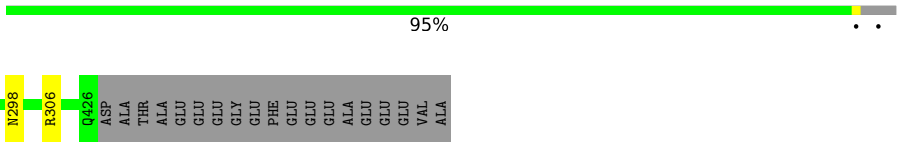
• Molecule 9: Tubulin beta-4B chain

Chain LJ: 99%



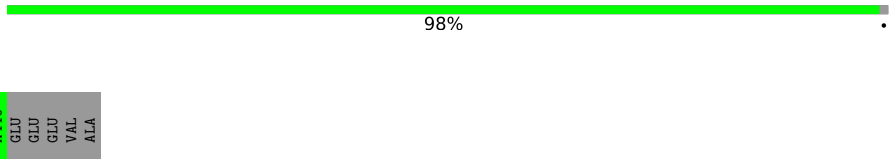
• Molecule 9: Tubulin beta-4B chain

Chain LL:



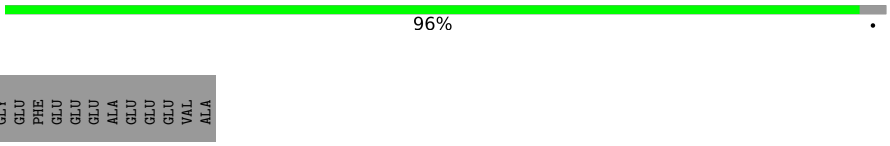
• Molecule 9: Tubulin beta-4B chain

Chain LN:



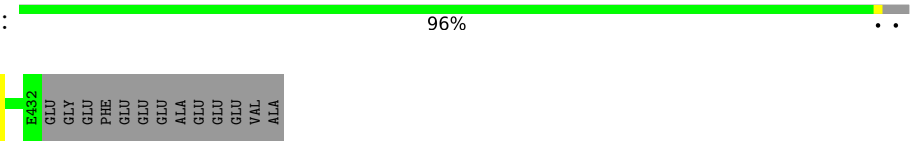
• Molecule 9: Tubulin beta-4B chain

Chain MB:



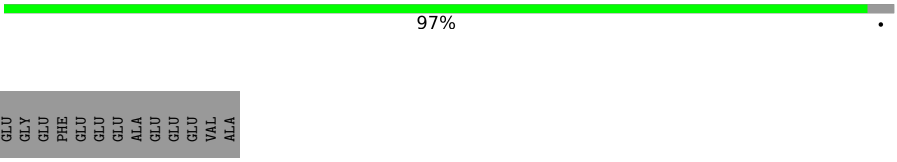
• Molecule 9: Tubulin beta-4B chain

Chain MD:



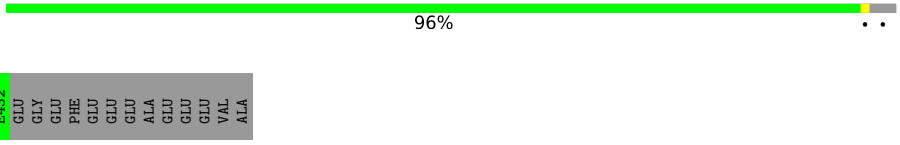
• Molecule 9: Tubulin beta-4B chain

Chain MF:



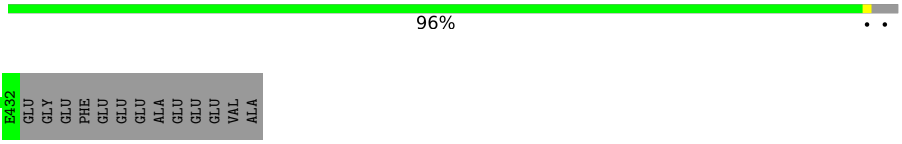
• Molecule 9: Tubulin beta-4B chain

Chain MH:



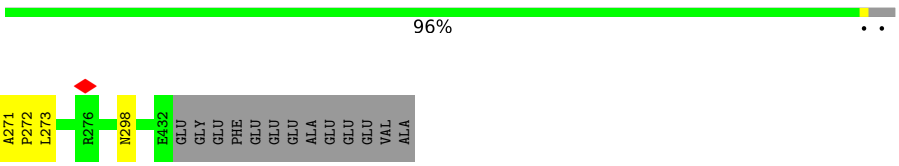
• Molecule 9: Tubulin beta-4B chain

Chain MJ:



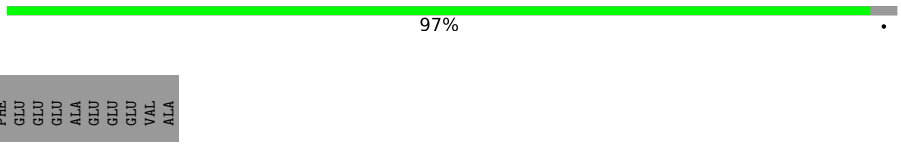
• Molecule 9: Tubulin beta-4B chain

Chain ML:



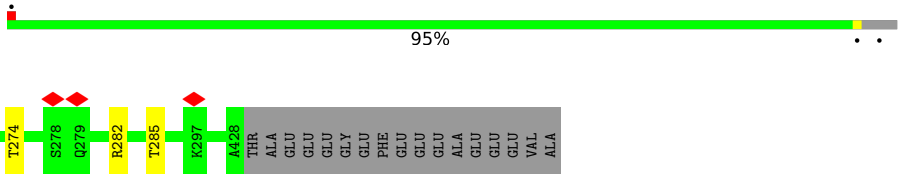
• Molecule 9: Tubulin beta-4B chain

Chain MN:



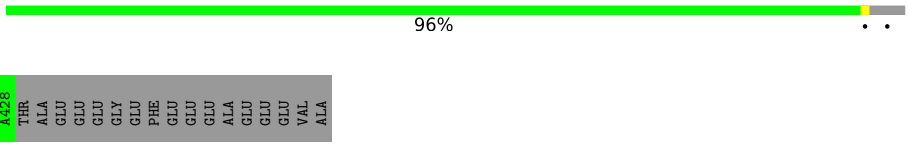
• Molecule 9: Tubulin beta-4B chain

Chain NB:



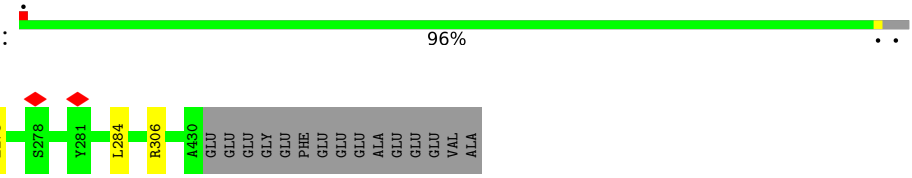
• Molecule 9: Tubulin beta-4B chain

Chain ND:



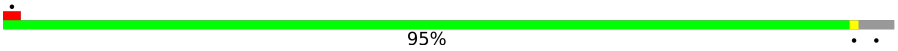
• Molecule 9: Tubulin beta-4B chain

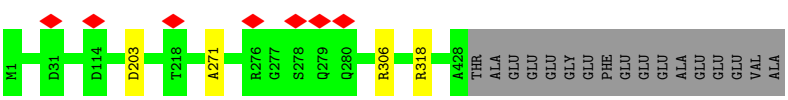
Chain NF:



• Molecule 9: Tubulin beta-4B chain

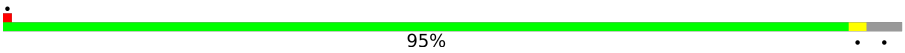
Chain NH:

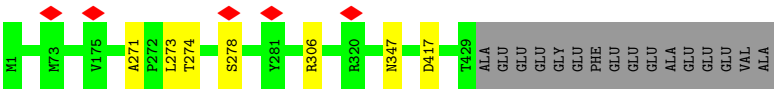




• Molecule 9: Tubulin beta-4B chain

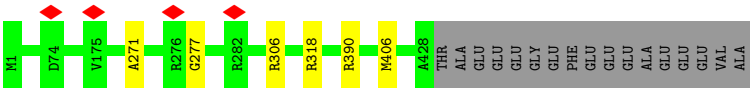
Chain NJ:





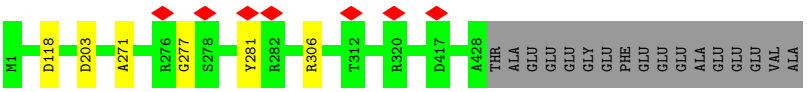
• Molecule 9: Tubulin beta-4B chain

Chain NL: 95%



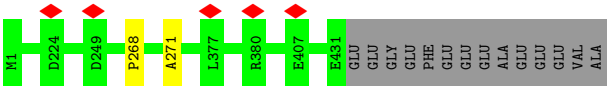
• Molecule 9: Tubulin beta-4B chain

Chain NN: 95%



• Molecule 9: Tubulin beta-4B chain

Chain OB: 96%

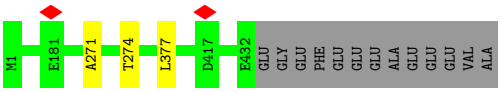


• Molecule 9: Tubulin beta-4B chain

Chain OD: 97%

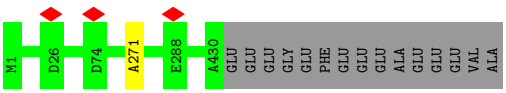
• Molecule 9: Tubulin beta-4B chain

Chain OF: 96%



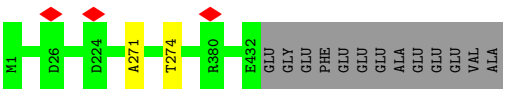
• Molecule 9: Tubulin beta-4B chain

Chain OH: 96%



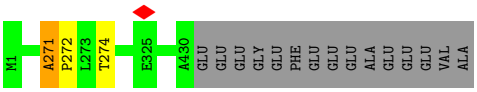
• Molecule 9: Tubulin beta-4B chain

Chain OJ: 97%



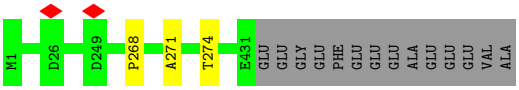
• Molecule 9: Tubulin beta-4B chain

Chain OL: 96%



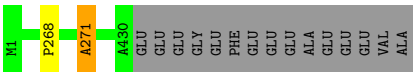
• Molecule 9: Tubulin beta-4B chain

Chain ON: 96%



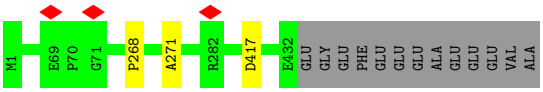
• Molecule 9: Tubulin beta-4B chain

Chain PD: 96%



• Molecule 9: Tubulin beta-4B chain

Chain PF: 96%

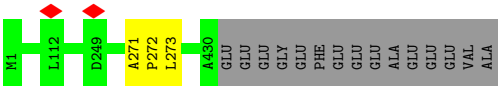


• Molecule 9: Tubulin beta-4B chain

Chain PH: 95%

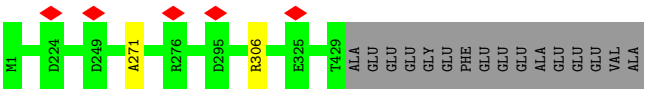
• Molecule 9: Tubulin beta-4B chain

Chain PJ: 96%



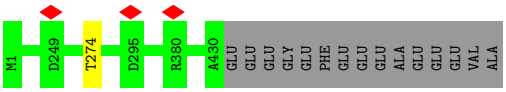
• Molecule 9: Tubulin beta-4B chain

Chain PL: 96%



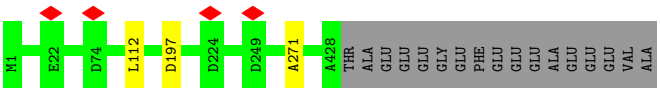
• Molecule 9: Tubulin beta-4B chain

Chain PN: 96%



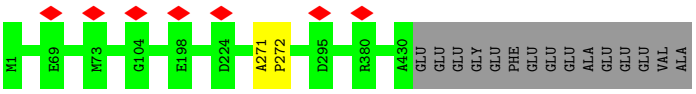
• Molecule 9: Tubulin beta-4B chain

Chain QD: 96%



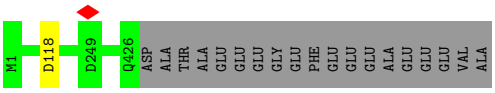
• Molecule 9: Tubulin beta-4B chain

Chain QF: 96%



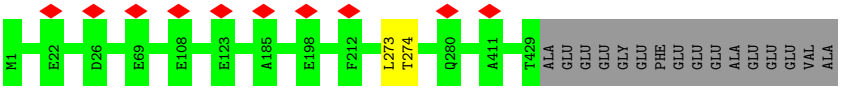
• Molecule 9: Tubulin beta-4B chain

Chain QH: 96%



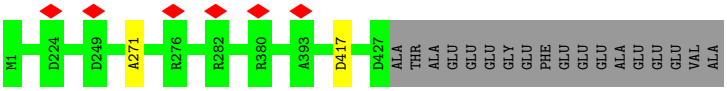
• Molecule 9: Tubulin beta-4B chain

Chain QJ: 96%



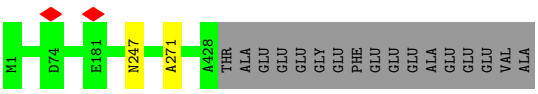
• Molecule 9: Tubulin beta-4B chain

Chain QL: 96%



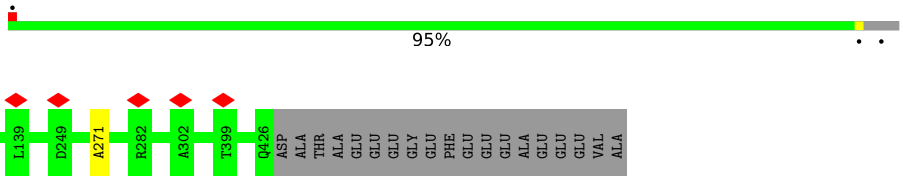
• Molecule 9: Tubulin beta-4B chain

Chain QN: 96%



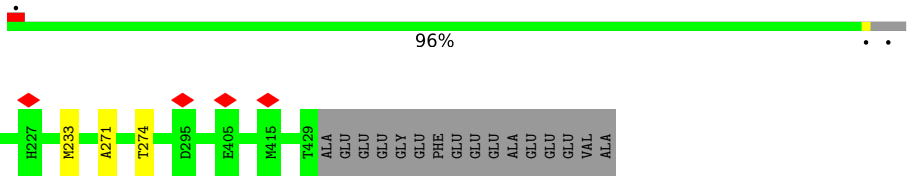
- Molecule 9: Tubulin beta-4B chain

Chain RD:



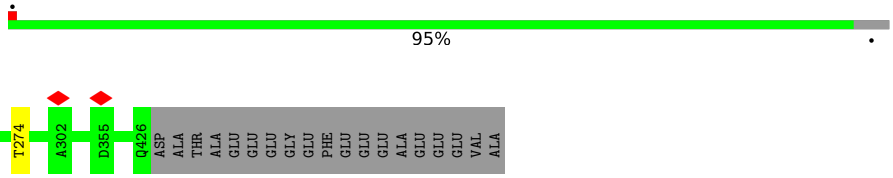
- Molecule 9: Tubulin beta-4B chain

Chain RF:



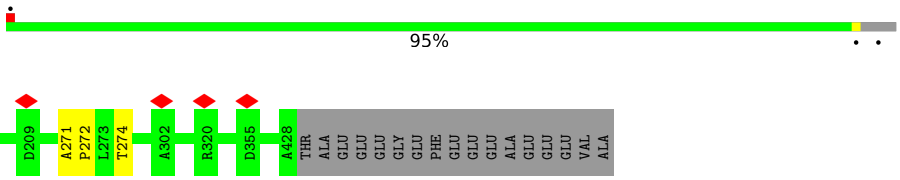
- Molecule 9: Tubulin beta-4B chain

Chain RH:



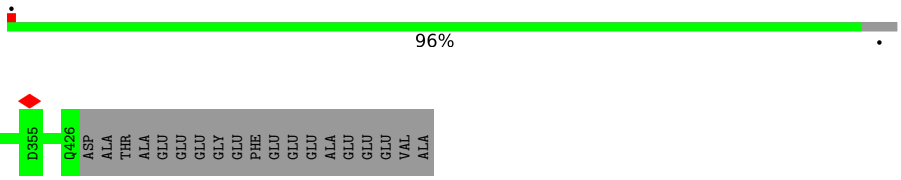
- Molecule 9: Tubulin beta-4B chain

Chain RJ:



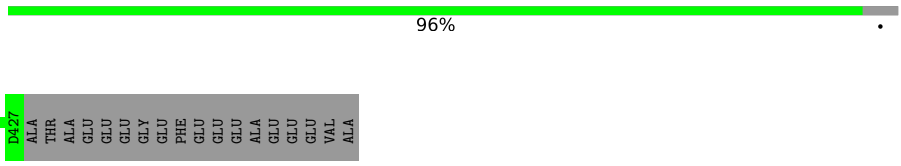
- Molecule 9: Tubulin beta-4B chain

Chain RL:



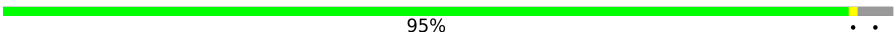
- Molecule 9: Tubulin beta-4B chain

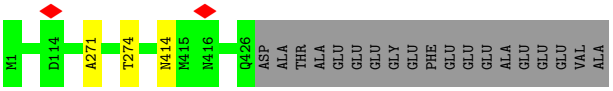
Chain RN:



- Molecule 9: Tubulin beta-4B chain

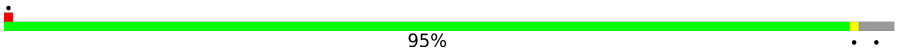
Chain SD:

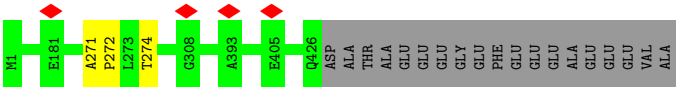




• Molecule 9: Tubulin beta-4B chain

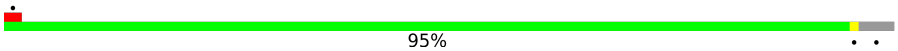
Chain SF:

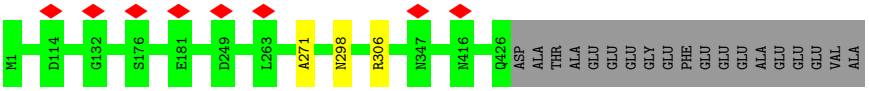




• Molecule 9: Tubulin beta-4B chain

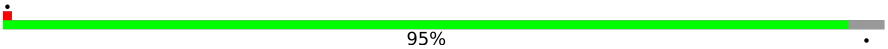
Chain SH:

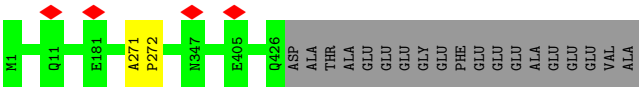




• Molecule 9: Tubulin beta-4B chain

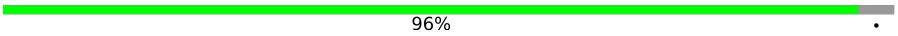
Chain SJ:

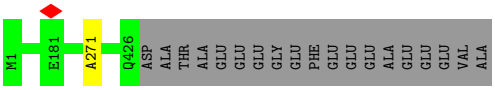




• Molecule 9: Tubulin beta-4B chain

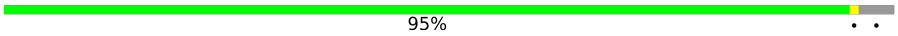
Chain SL:

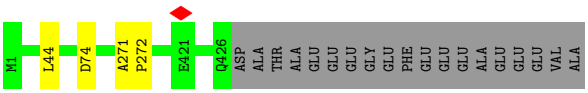




• Molecule 9: Tubulin beta-4B chain

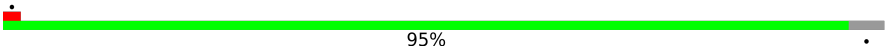
Chain SN:

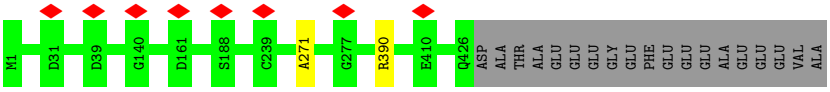




• Molecule 9: Tubulin beta-4B chain

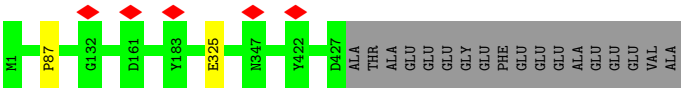
Chain TD:





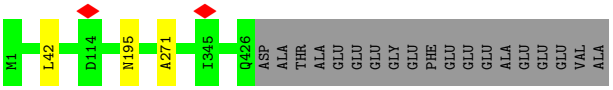
• Molecule 9: Tubulin beta-4B chain

Chain TF: 96%



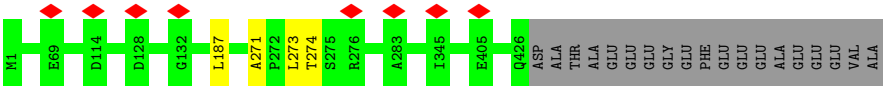
• Molecule 9: Tubulin beta-4B chain

Chain TH: 95%



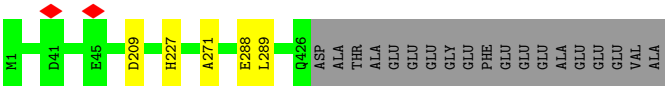
• Molecule 9: Tubulin beta-4B chain

Chain TJ: 95%



• Molecule 9: Tubulin beta-4B chain

Chain TL: 95%

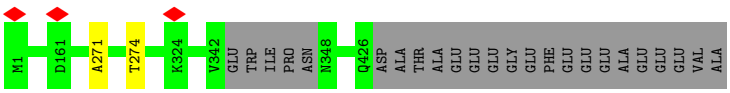


• Molecule 9: Tubulin beta-4B chain

Chain TN: 95%

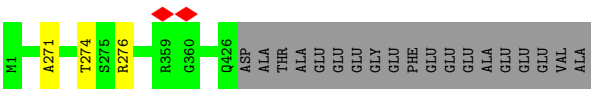
• Molecule 9: Tubulin beta-4B chain

Chain TP: 94% 5%



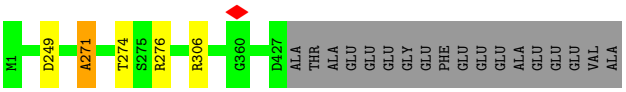
• Molecule 9: Tubulin beta-4B chain

Chain UD: 95%



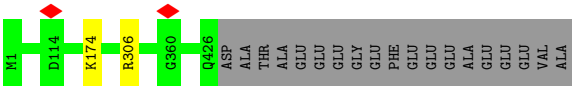
• Molecule 9: Tubulin beta-4B chain

Chain UF: 95%



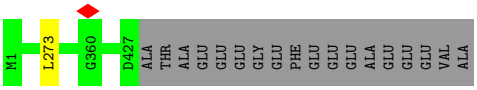
• Molecule 9: Tubulin beta-4B chain

Chain UH: 95%



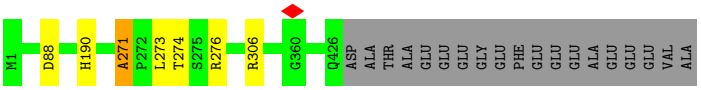
• Molecule 9: Tubulin beta-4B chain

Chain UJ: 96%



• Molecule 9: Tubulin beta-4B chain

Chain UL: 94%

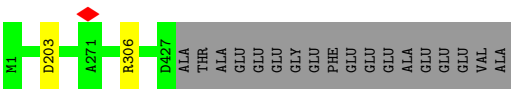


• Molecule 9: Tubulin beta-4B chain

Chain UN: 95%

• Molecule 9: Tubulin beta-4B chain

Chain UP: 96%

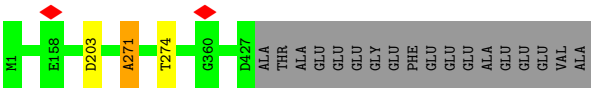


• Molecule 9: Tubulin beta-4B chain

Chain VD: 96%

• Molecule 9: Tubulin beta-4B chain

Chain VF: 95%



• Molecule 9: Tubulin beta-4B chain

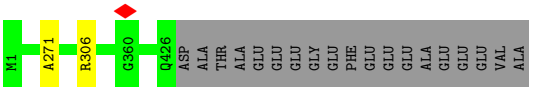
Chain VH: 95%

• Molecule 9: Tubulin beta-4B chain

Chain VJ: 95%

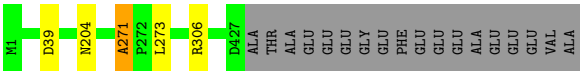
• Molecule 9: Tubulin beta-4B chain

Chain VL: 95%



• Molecule 9: Tubulin beta-4B chain

Chain VN: 95%

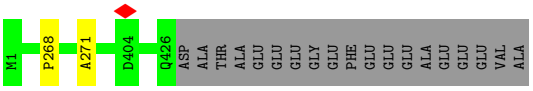


• Molecule 9: Tubulin beta-4B chain

Chain VP: 95%

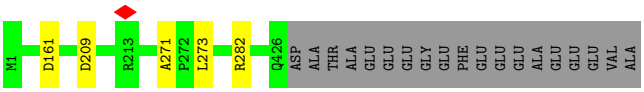
• Molecule 9: Tubulin beta-4B chain

Chain WD: 95%



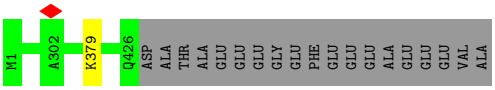
• Molecule 9: Tubulin beta-4B chain

Chain WF: 95%



• Molecule 9: Tubulin beta-4B chain

Chain WH: 96%

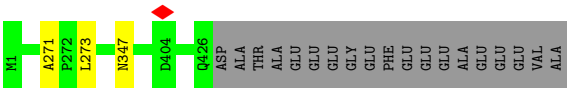


• Molecule 9: Tubulin beta-4B chain

Chain WJ: 95%

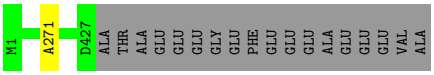
• Molecule 9: Tubulin beta-4B chain

Chain WL: 95%



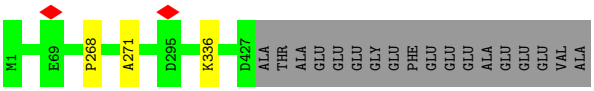
• Molecule 9: Tubulin beta-4B chain

Chain WN: 96%



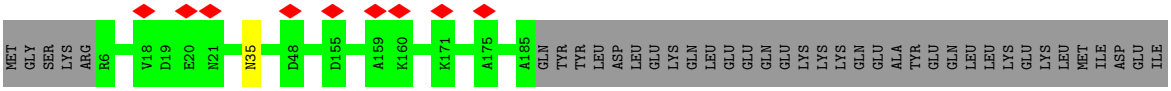
• Molecule 9: Tubulin beta-4B chain

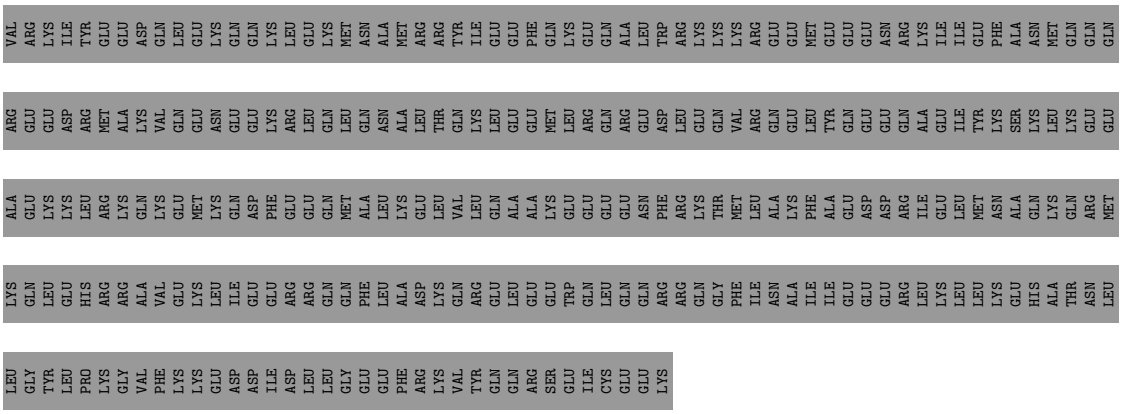
Chain WP: 95%



• Molecule 10: Meiosis-specific nuclear structural protein 1

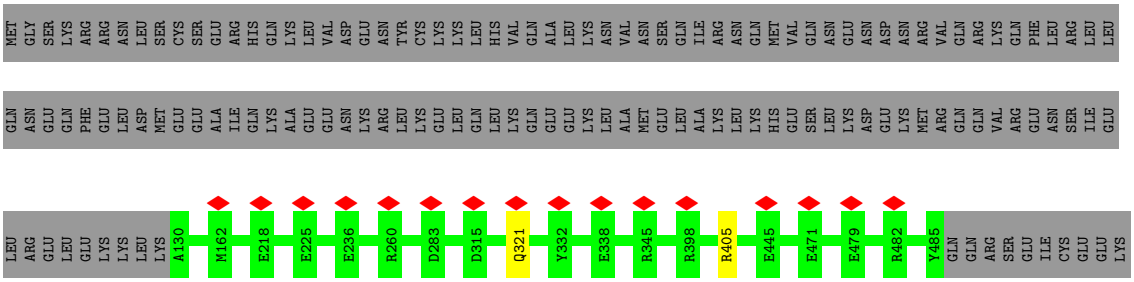
Chain B: 36% 64%





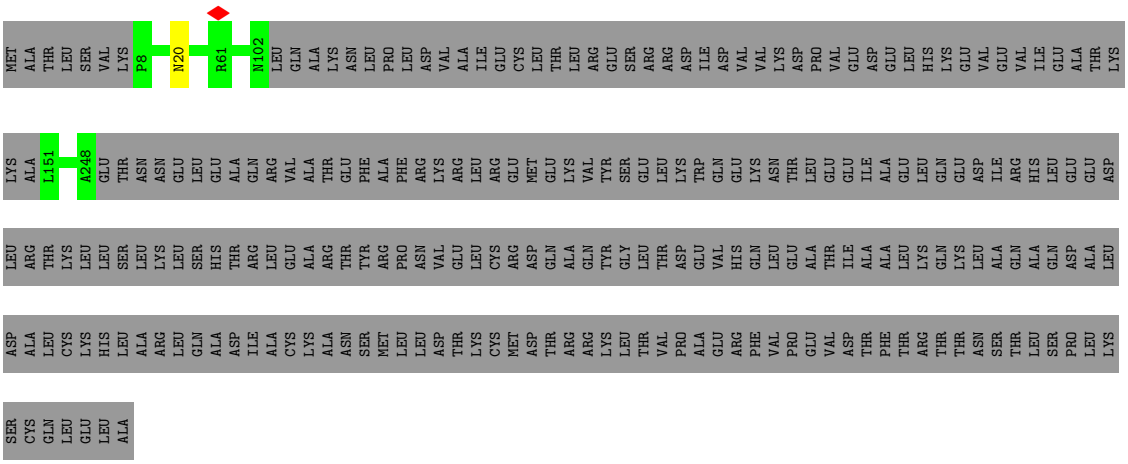
• Molecule 10: Meiosis-specific nuclear structural protein 1

Chain C:



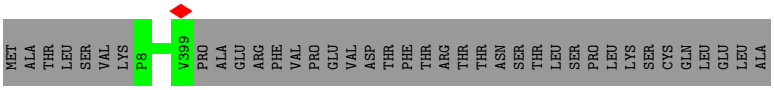
• Molecule 11: Tektin-2

Chain B0:



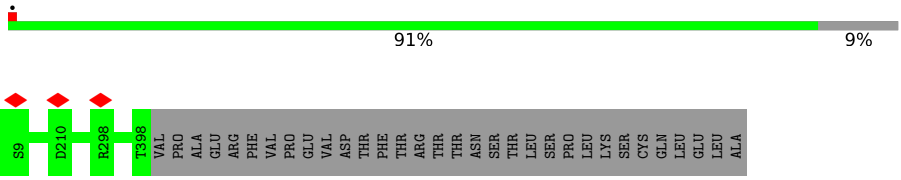
• Molecule 11: Tektin-2

Chain B1:



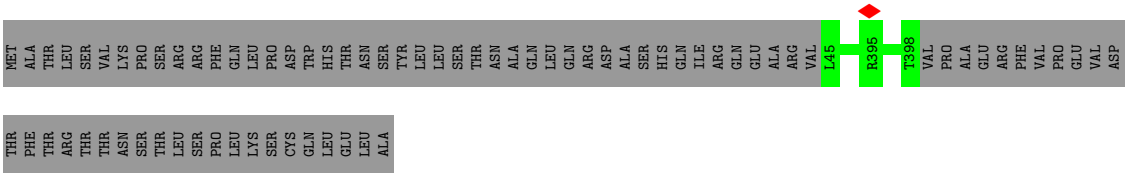
- Molecule 11: Tektin-2

Chain B2:



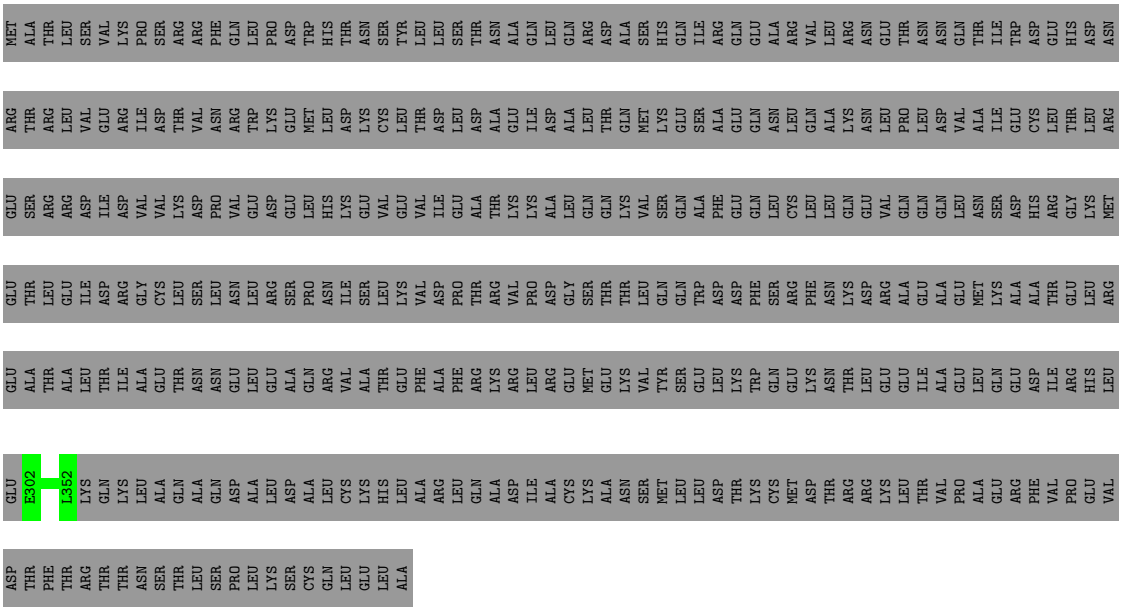
- Molecule 11: Tektin-2

Chain B3:



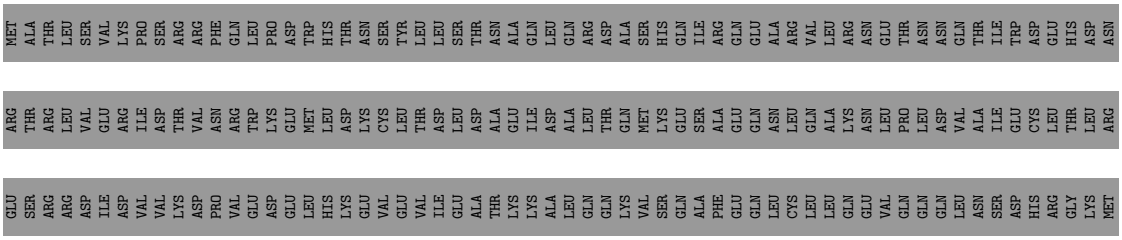
- Molecule 11: Tektin-2

Chain B4:



- Molecule 11: Tektin-2

Chain B5:



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

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

GLU E302 D303 L304 R305 T306 K307 L308 L309 S310 L311 K312 L313 S314 H315 T316 R317 L318 E319 A320 R321 T322 Y323 R324 P325 N326 V327 E328 L329 C330 R331 D332 Q333 A334 Q335 Y336 G337 L338 T339 D340 E341 V342 H343 Q344 L345 E346 A347 T348 I349 A350 A351 L352 LYS GLN LYS LEU ALA GLN ALA GLN

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

PRO LEU LYS SER CYS GLN LEU GLU LEU ALA

- Molecule 11: Tektin-2

Chain B6:

MET ALA THR LEU SER VAL LYS PRO SER ARG ARG PHE GLN LEU PRO ASP TRP HIS THR ASN SER TYR LEU LEU SER THR ASN ALA GLN LEU GLN ARG ASP ALA SER HIS GLN ILE ARG GLN GLU ALA ARG VAL L45 R46 N47 E48 T49 N50 N51 Q52 T53 I54 W55 D56 E57 H58 D59 N60

R61 T62 R63 L64 V65 E66 R67 I68 D69 T70 V71 N72 R73 W74 K75 E76 W77 L78 D79 K80 C81 L82 T83 D84 L85 D86 A87 E88 I89 D90 A91 L92 T93 Q94 M95 K96 E97 S98 A99 E100 Q101 N102 L103 Q104 A105 K106 N107 L108 P109 L110 D111 V112 A113 I114 E115 C116 L117 T118 L119 R120

E121 S122 R123 R124 D125 I126 D127 V128 V129 K130 D131 P132 V133 E134 D135 E136 L137 H138 K139 E140 V141 E142 V143 I144 E145 A146 T147 K148 K149 A150 L151 Q152 Q153 K154 V155 S156 Q157 A158 F159 E160 Q161 L162 C163 L164 L165 Q166 E167 V168 Q169 Q170 Q171 L172 N173 S174 D175 H176 R177 G178 K179 M180

E181 T182 L183 E184 I185 D186 R187 G188 C189 L190 S191 L192 N193 L194 R195 S196 P197 N198 I199 S200 L201 K202 V203 D204 P205 T206 R207 V208 P209 D210 G211 S212 T213 T214 L215 Q216 Q217 W218 D219 D220 F221 S222 R223 F224 N225 K226 D227 R228 A229 E230 A231 E232 M233 K234 A235 A236 T237 E238 L239 R240

E241 A242 T243 A244 L245 T246 I247 A248 E249 T250 N251 N252 E253 L254 E255 A256 Q257 R258 V259 A260 T261 E262 F263 A264 F265 R266 K267 R268 L269 R270 E271 M272 E273 S277 E278 L279 K280 W281 Q282 E283 K284 N285 T286 L287 E288 E289 I290 A291 E292 L293 Q294 E295 D296 I297 R298 H299 L300 E301 E302

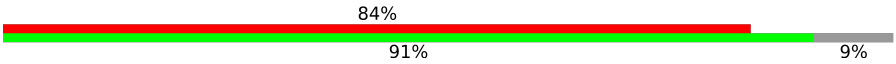
D303 L304 R305 T306 K307 L308 L309 S310 L311 K312 L313 S314 H315 T316 R317 L318 E319 A320 R321 T322 Y323 R324 P325 N326 V327 E328 L329 C330 R331 D332 Q333 A334 Q335 Y336 G337 L338 T339 D340 E341 V342 H343 Q344 L345 E346 A347 T348 I349 A350 A351 L352 K353 Q354 K355 L356 A357 Q358 A359 Q360 D361 A362

L363 D364 A365 L366 C367 K368 H369 L370 A371 R372 L373 Q374 A375 D376 I377 A378 C379 K380 A381 N382 S383 M384 L385 L386 D387 T388 K389 C390 M391 D392 T393 R394 R395 K396 L397 T398 VAL PRO ALA GLU ARG PHE VAL PRO GLU VAL ASP THR PHE THR ARG THR THR ASN SER THR LEU SER PRO LEU

LYS SER CYS GLN LEU GLU LEU ALA

- Molecule 11: Tektin-2

Chain B7:



MET ALA THR LEU SER VAL LYS P8 S9 R10 R11 F12 Q13 L14 P15 D16 W17 H18 T19 N20 S21 Y22 L23 L24 S25 T26 N27 A28 Q29 L30 Q31 R32 D33 A34 S35 H36 Q37 I38 R39 Q40 E41 A42 R43 V44 L45 R46 M47 E48 T49 N50 N51 Q52 T53 I54 W55 D56 E57 H58 D59 M60

R61 T62 R63 L64 V65 E66 R67 I68 D69 T70 V71 N72 R73 W74 K75 E76 M77 L78 D79 K80 C81 L82 T83 D84 L85 D86 A87 E88 I89 D90 A91 L92 T93 Q94 M95 K96 E97 S98 A99 E100 Q101 N102 L103 Q104 A105 K106 N107 L108 P109 L110 D111 V112 A113 I114 E115 C116 L117 T118 L119 R120

E121 S122 R123 R124 D125 I126 D127 V128 V129 K130 D131 P132 V133 E134 D135 E136 L137 H138 K139 E140 V141 E142 V143 I144 E145 A146 T147 K148 K149 A150 L151 Q152 Q153 K154 V155 S156 Q157 A158 F159 E160 Q161 L162 C163 L164 L165 Q166 E167 V168 Q169 Q170 Q171 L172 N173 S174 D175 H176 R177 G178 K179 M180

E181 T182 L183 E184 I185 D186 R187 G188 C189 L190 S191 L192 N193 L194 R195 S196 P197 N198 I199 S200 L201 K202 V203 D204 P205 T206 R207 V208 P209 D210 G211 S212 T213 T214 L215 Q216 Q217 W218 D219 D220 F221 S222 R223 F224 N225 K226 D227 R228 A229 E230 A231 E232 M233 K234 A235 A236 T237 E238 L239 R240

E241 A242 T243 A244 L245 T246 I247 A248 E249 T250 N251 N252 E253 L254 E255 A256 Q257 R258 V259 A260 T261 E262 F263 A264 F265 R266 K267 R268 E271 M272 E273 K274 V275 Y276 S277 E278 L279 K280 W281 Q282 E283 K284 N285 T286 L287 E288 E289 I290 A291 E292 L293 Q294 E295 D296 E302 D303 L304 R305

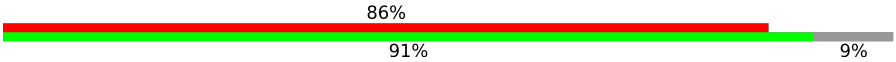
T306 K307 L308 L309 S310 L311 K312 L313 S314 H315 T316 R317 L318 E319 A320 R321 T322 Y323 R324 P325 N326 V327 E328 L329 C330 R331 D332 Q333 A334 Q335 Y336 G337 L338 T339 D340 E341 V342 H343 Q344 L345 E346 A347 T348 I349 A350 A351 L352 K353 Q354 K355 L356 A357 Q358 A359 Q360 D361 A362 L363 D364 A365

L366 C367 K368 H369 L370 A371 R372 L373 Q374 A375 D376 I377 A378 C379 N382 S383 M384 L385 L386 D387 T388 K389 C390 M391 D392 T393 R394 R395 K396 L397 T398 VAL PRO ALA GLU ARG PHE VAL PRO GLU VAL ASP THR PHE THR ARG THR THR ASN SER THR LEU SER PRO LEU LYS SER CYS GLN

LEU GLU LEU ALA

- Molecule 11: Tektin-2

Chain B8:



MET ALA THR LEU SER VAL LYS P8 S9 R10 R11 F12 Q13 L14 P15 D16 W17 H18 T19 N20 S21 Y22 L23 L24 S25 T26 N27 A28 Q29 L30 Q31 R32 D33 A34 S35 H36 Q37 I38 R39 Q40 E41 A42 R43 V44 L45 R46 M47 E48 T49 N50 N51 Q52 T53 I54 W55 D56 D59 M60 R61

T62 R63 L64 V65 E66 R67 I68 D69 T70 V71 N72 R73 W74 K75 E76 M77 L78 D79 K80 C81 L82 T83 D84 L85 D86 A87 E88 I89 D90 A91 L92 T93 Q94 M95 K96 E97 S98 A99 E100 Q101 N102 L103 Q104 A105 K106 N107 L108 P109 L110 D111 V112 A113 I114 E115 C116 L117 T118 L119 R120 E121

S122 R123 R124 D125 I126 D127 V128 V129 K130 D131 P132 V133 E134 D135 E136 L137 H138 K139 E140 V141 E142 V143 I144 E145 A146 T147 K148 K149 A150 Q153 K154 V155 S156 Q157 A158 F159 E160 Q161 L162 C163 L164 L165 Q166 E167 V168 Q169 Q170 Q171 L172 N173 S174 D175 H176 R177 G178 K179 M180 E181 T182

L183 E184 I185 D186 R187 G188 C189 L190 S191 L192 N193 L194 R195 S196 P197 N198 I199 S200 L201 K202 V203 D204 P205 T206 R207 V208 P209 D210 G211 S212 T213 T214 L215 Q216 Q217 W218 D219 D220 F221 S222 R223 F224 N225 K226 D227 R228 A229 E230 A231 E232 M233 K234 A235 A236 T237 E238 L239 R240 E241 A242

T243 A244 L245 T246 I247 A248 E249 T250 N251 N252 E253 L254 E255 A256 Q257 R258 V259 A260 T261 E262 F263 A264 F265 R266 K267 R268 L269 R270 E271 M272 E273 K274 V275 Y276 S277 E278 L279 K280 W281 Q282 E283 K284 N285 T286 L287 E288 E289 I290 A291 E292 L293 Q294 E295 D296 I297 R298 H299 L300 E301 E302

D303 L304 R305 T306 K307 L308 L309 S310 L311 K312 L313 S314 H315 T316 R317 L318 E319 A320 R321 T322 Y323 R324 P325 N326 V327 E328 L329 C330 R331 D332 Q333 A334 Q335 Y336 G337 L338 T339 D340 E341 V342 H343 Q344 L345 E346 A347 T348 I349 A350 A351 L352 K353 Q354 K355 L356 A357 Q358 A359 Q360 D361 A362

L363 D364 A365 L366 C367 K368 H369 L370 A371 R372 L373 Q374 A375 D376 I377 A378 C379 K380 A381 N382 S383 M384 L385 L386 D387 T388 K389 C390 M391 D392 T393 R394 R395 K396 L397 T398 V399 PRO ALA GLU ARG PHE VAL PRO GLU VAL ASP THR PHE THR ARG THR THR ASN SER THR LEU SER PRO LEU

LYS SER CYS GLN LEU GLU LEU ALA

- Molecule 11: Tektin-2

Chain B9:

MET ALA THR LEU SER VAL LYS P8 S9 R10 R11 F12 Q13 L14 P15 D16 W17 H18 T19 N20 S21 Y22 L23 L24 S25 T26 N27 A28 Q29 L30 Q31 R32 D33 A34 S35 H36 Q37 I38 R39 Q40 E41 A42 R43 V44 L45 R46 N47 E48 T49 N50 N51 Q52 T53 I54 W55 D56 E57 H58 D59 N60

R61 T62 R63 L64 V65 E66 R67 I68 D69 T70 V71 N72 R73 W74 K75 E76 M77 L78 D79 K80 C81 L82 T83 D84 L85 D86 A87 E88 I89 D90 A91 L92 T93 Q94 M95 K96 E97 S98 A99 E100 Q101 N102 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 LYS ASP PRO VAL GLU ASP GLU LEU HIS LYS GLU VAL GLU VAL ILE GLU ALA THR LYS LYS ALA L151 Q152 Q153 K154 V155 S156 Q157 A158 F159 E160 Q161 L162 C163 L164 L165 Q166 E167 V168 Q169 Q170 Q171 L172 N173 S174 D175 H176 R177 G178 K179 M180

E181 T182 L183 E184 I185 D186 R187 G188 C189 L190 S191 L192 N193 L194 R195 S196 P197 N198 I199 S200 L201 K202 V203 D204 P205 T206 R207 V208 P209 D210 G211 S212 T213 T214 L215 Q216 Q217 W218 D219 D220 F221 S222 R223 F224 N225 K226 D227 R228 A229 E230 A231 E232 M233 K234 A235 A236 T237 E238 L239 R240

E241 A242 T243 A244 L245 T246 I247 A248 GLU THR ASN ASN GLU LEU GLU ALA GLN ARG VAL ALA THR GLU PHE ALA PHE ARG LYS ARG LEU ARG GLU MET GLU LYS VAL TYR SER GLU LEU LYS TRP GLN GLU LYS ASN THR LEU GLU GLU ILE ALA GLU LEU GLN GLU ASP ILE ARG HIS LEU

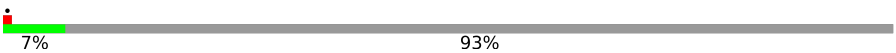
GLU GLU ASP LEU ARG THR LYS LEU LEU SER LEU LYS LEU SER HIS THR ARG LEU GLU ALA ARG THR TYR ARG PRO ASN VAL GLU LEU CYS ARG ASP GLN ALA GLN TYR GLY LEU THR ASP GLU VAL HIS GLN LEU GLU ALA THR ILE ALA ALA LEU LYS GLN LYS LEU ALA GLN ALA GLN

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

PRO LEU LYS SER CYS GLN LEU GLU LEU ALA

- Molecule 12: Tektin-3

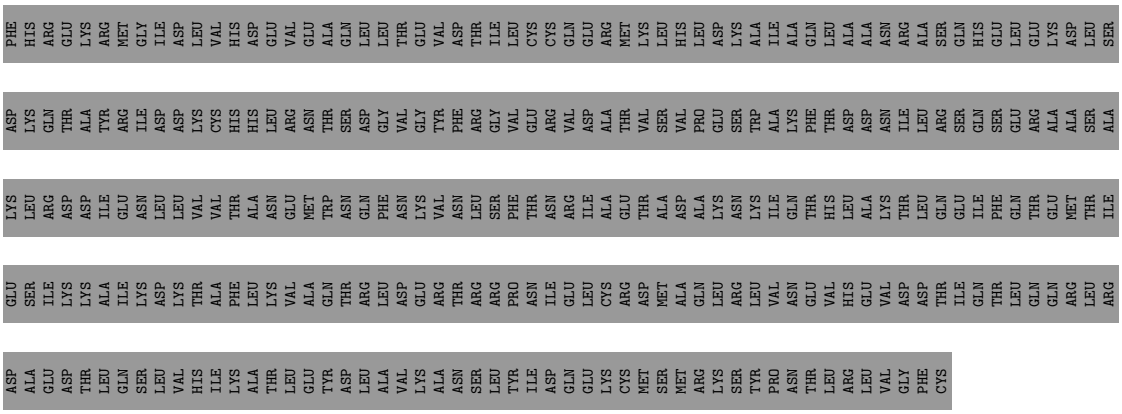
Chain C0:



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

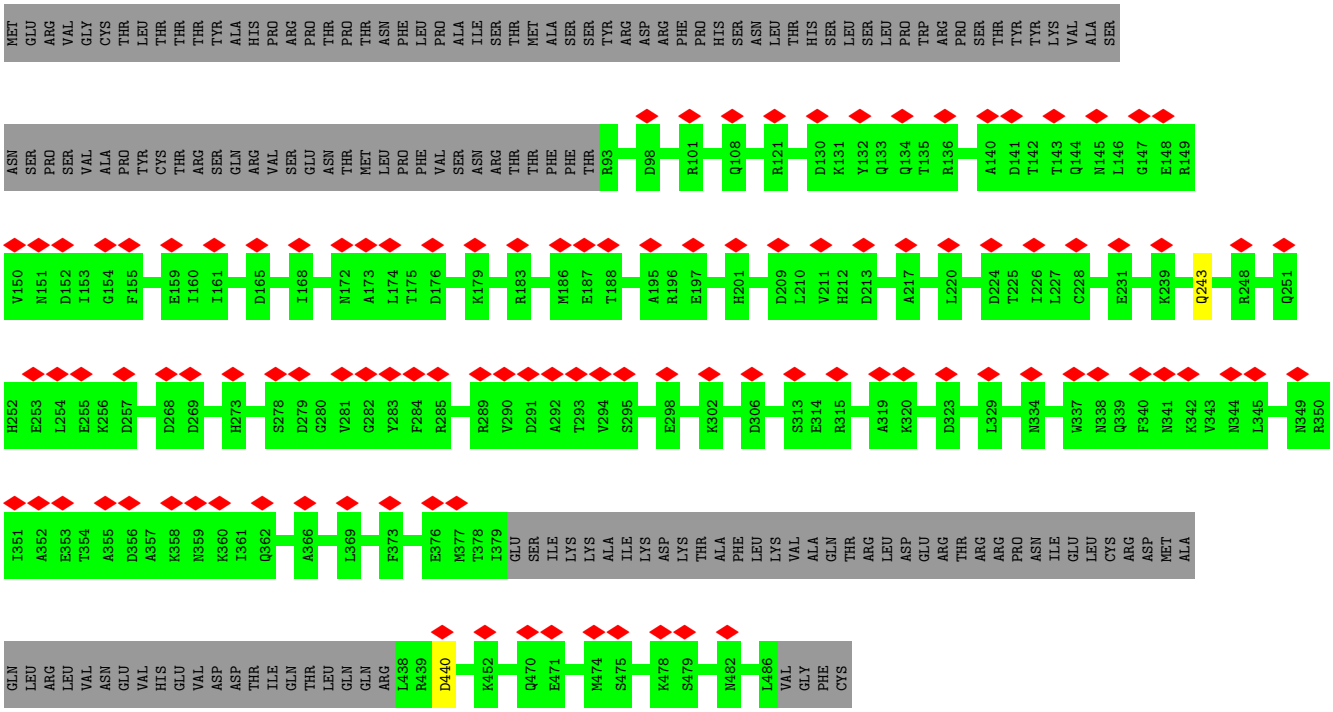
ASN SER PRO SER VAL ALA PRO TYR CYS THR ARG SER GLN ARG VAL SER GLU ASN THR MET LEU PRO PHE VAL SER ASN ARG THR THR PHE PHE T92 R93 D97 R101 T105 K119 V122 D123 T124 SER ARG LEU ILE GLN ASP LYS TYR GLN GLN THR ARG LYS THR GLN

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



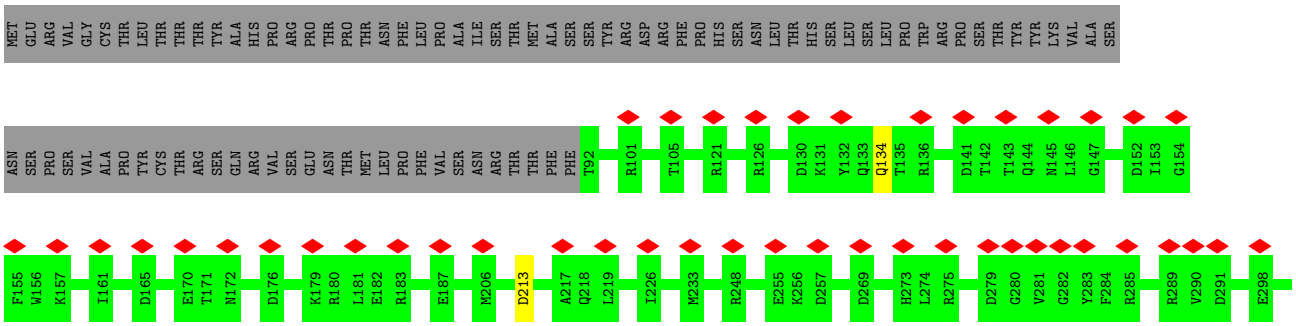
- Molecule 12: Tektin-3

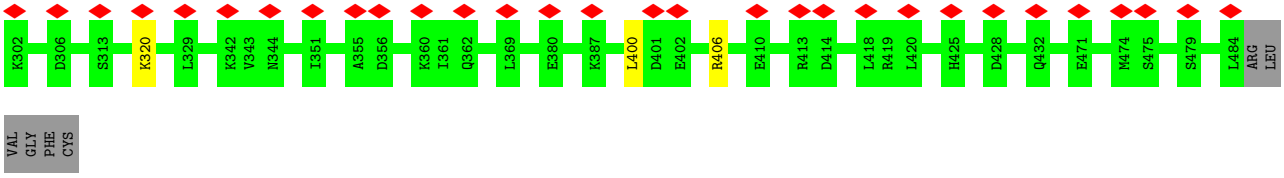
Chain C1:



- Molecule 12: Tektin-3

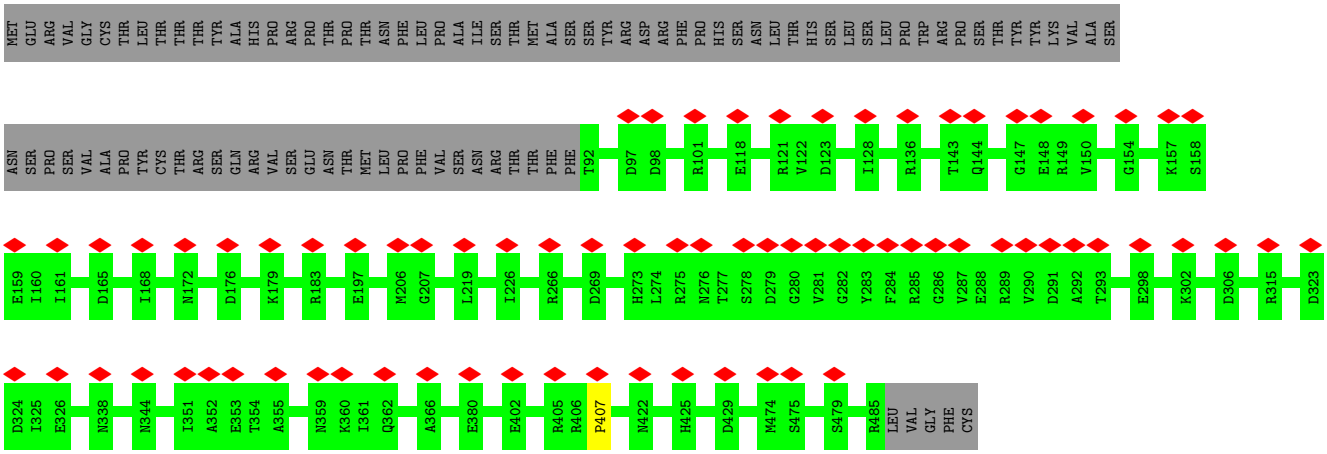
Chain C2:





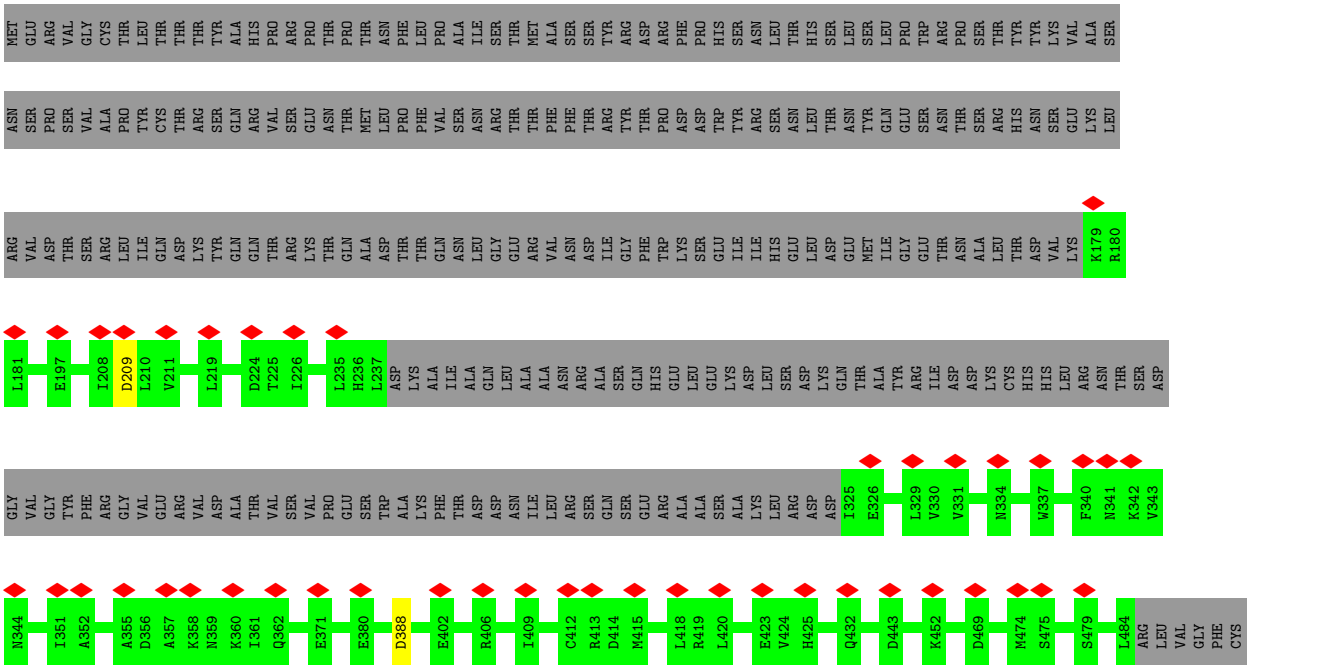
• Molecule 12: Tektin-3

Chain C3:



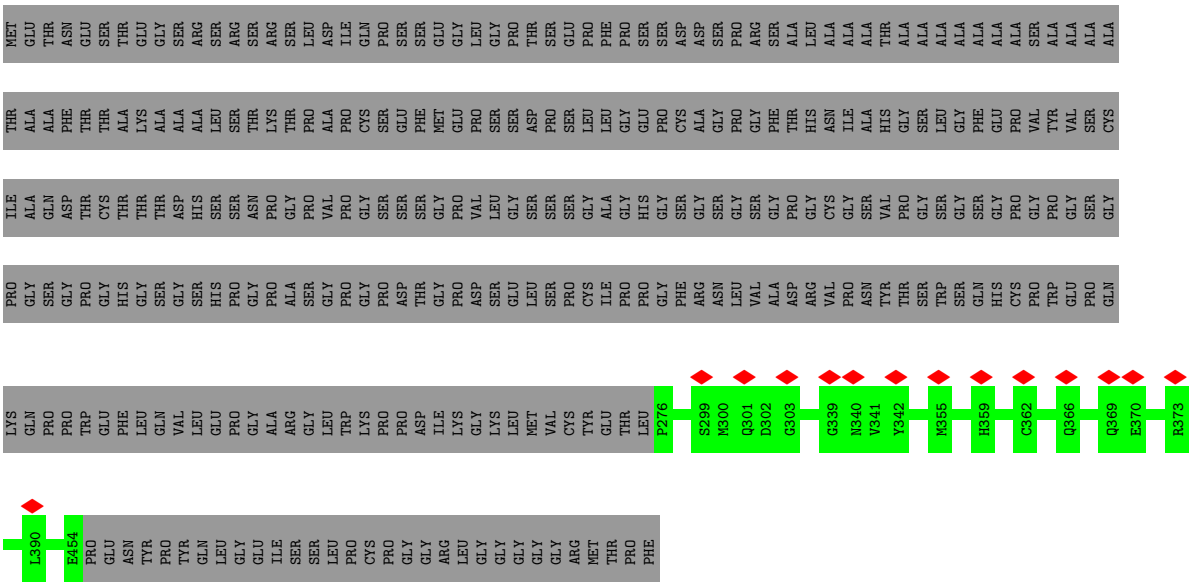
• Molecule 12: Tektin-3

Chain C4:



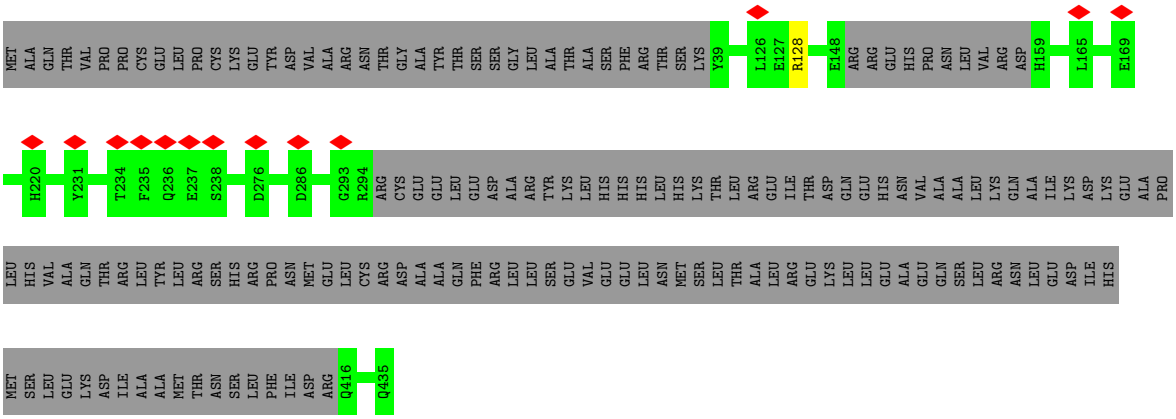
• Molecule 13: Sperm-associated antigen 8

Chain D:



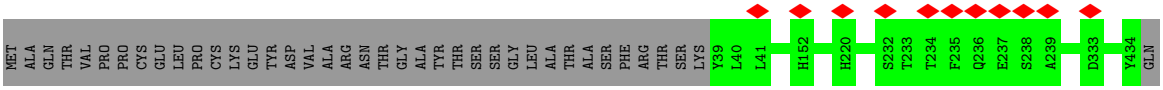
- Molecule 14: Tektin-4

Chain D0:



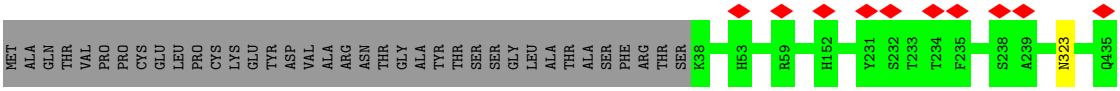
- Molecule 14: Tektin-4

Chain D1:



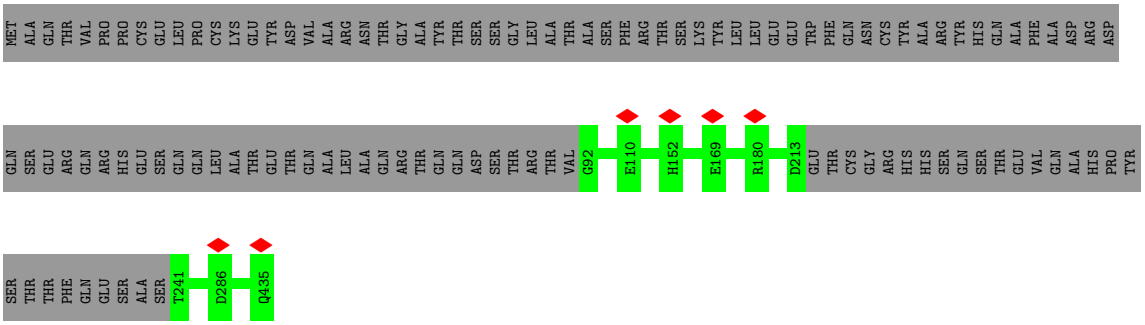
- Molecule 14: Tektin-4

Chain D2:



- Molecule 14: Tektin-4

Chain D3:

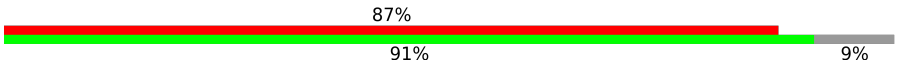


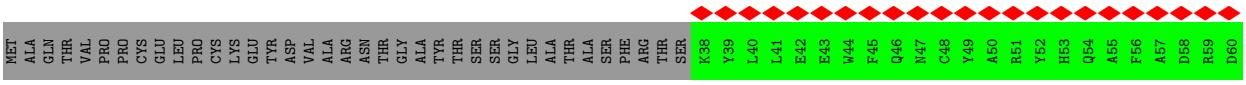
- Molecule 14: Tektin-4

Chain D5:

- Molecule 14: Tektin-4

Chain D6:





Q61 S62 E63 R64 Q65 R66 H67 E68 S69 Q70 Q71 L72 A73 T74 E75 T76 Q77 A78 L79 A80 Q81 R82 T83 Q84 Q85 D86 S87 T88 R89 T90 V91 G92 E93 R94 L95 Q96 D97 T98 H99 S100 W101 K102 S103 E104 L105 Q106 R107 E108 M109 E110 A111 L112 A113 A114 E115 T116 N117 L118 L119 L120

A121 Q122 K123 Q124 R125 L126 E127 R128 A129 L130 D131 A132 T133 E134 V135 P136 F137 S138 I139 T140 T141 D142 N143 L144 Q145 C146 R147 E148 R149 R150 E151 H152 P153 N154 L155 V156 R157 D158 H159 V160 E161 T162 E163 L164 L165 K166 E167 A168 E169 L170 I171 R172 N173 I174 Q175 E176 L177 L178 K179 R180

T181 I182 M183 Q184 A185 V186 S187 Q188 I189 R190 L191 N192 R193 E194 H195 K196 E197 T198 C199 E200 M201 D202 W203 S204 D205 K206 M207 E208 A209 Y210 N211 I212 D213 E214 T215 C216 G217 R218 H219 H220 S221 Q222 S223 T224 E225 V226 Q227 A228 H229 P230 Y231 S232 T233 T234 F235 Q236 E237 S238 A239 S240

T241 P242 E243 T244 R245 A246 K247 F248 T249 Q250 D251 N252 L253 C254 R255 A256 Q257 R258 E259 R260 L261 A262 S263 A264 N265 L266 R267 V268 L269 V270 D271 C272 I273 L274 R275 D276 T277 S278 E279 D280 L281 R282 L283 Q284 C285 D286 A287 V288 N289 L290 A291 F292 G293 R294 R295 C296 E297 E298 L299 E300

D301 A302 R303 Y304 K305 L306 H307 H308 H309 L310 H311 K312 T313 L314 R315 E316 I317 T318 D319 Q320 E321 H322 N323 V324 A325 A326 L327 K328 Q329 A330 I331 K332 D333 K334 E335 A336 P337 L338 H339 V340 A341 Q342 T343 R344 L345 Y346 S349 H350 R351 P352 N353 M354 E355 L356 C357 R358 D359 A360 A361

Q362 F363 R364 L365 L366 S367 E368 V369 E370 E371 L372 N373 M374 S375 L376 T377 A378 L379 R380 E381 K382 L383 L384 E385 A386 E387 Q388 R391 N392 L393 E394 D395 I396 H397 M398 S399 L400 E401 K402 D403 I404 A405 A406 M407 T408 N409 S410 L411 F412 I413 D414 R415 Q416 K417 C418 M419 A420 H421 R422

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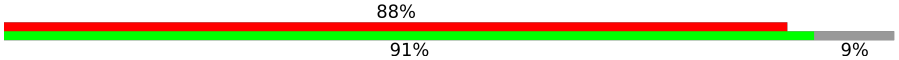
- Molecule 14: Tektin-4

Chain D7:



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Q61 S62 E63 R64 Q65 R66 H67 E68 S69 Q70 Q71 L72 A73 T74 E75 T76 Q77 A78 L79 A80 Q81 R82 T83 Q84 Q85 D86 S87 T88 R89 T90 V91 G92 E93 R94 L95 Q96 D97 T98 H99 S100 W101 K102 S103 E104 L105 Q106 R107 E108 M109 E110 A111 L112 A113 A114 E115 T116 N117 L118 L119 L120

A121 Q122 K123 Q124 R125 L126 E127 R128 A129 L130 D131 A132 T133 E134 V135 P136 F137 S138 I139 T140 T141 D142 N143 L144 Q145 C146 R147 E148 R149 R150 E151 H152 P153 N154 L155 V156 R157 D158 H159 V160 E161 T162 E163 L164 L165 K166 E167 A168 E169 L170 I171 R172 N173 I174 Q175 E176 L177 L178 K179 R180

T181 I182 M183 Q184 A185 V186 S187 Q188 I189 R190 L191 N192 R193 E194 E197 E200 M201 D202 W203 S204 D205 K206 M207 E208 A209 Y210 N211 I212 D213 E214 T215 C216 G217 R218 H219 H220 S221 Q222 S223 T224 E225 V226 Q227 A228 H229 P230 Y231 S232 T233 T234 F235 Q236 E237 S238 A239 S240 T241 P242

E243 T244 R245 A246 K247 F248 T249 Q250 D251 N252 L253 C254 R255 A256 Q257 R258 E259 R260 L261 A262 S263 A264 N265 L266 R267 V268 L269 V270 D271 C272 I273 L274 R275 D276 T277 S278 E279 D280 L281 R282 L283 Q284 C285 D286 A287 V288 N289 L290 A291 F292 G293 R294 R295 C296 E297 E298 L299 E300 D301 A302

R303 Y304 K305 L306 H307 H308 H309 L310 H311 K312 T313 L314 R315 E316 I317 T318 D319 Q320 E321 H322 N323 V324 A325 A326 L327 K328 Q329 A330 I331 K332 D333 K334 E335 A336 P337 L338 H339 V340 A341 Q342 T343 R344 L345 Y346 L347 R348 S349 H350 R351 P352 N353 M354 E355 L356 C357 R358 D359 A360 A361 Q362

F363 R364 L365 L366 S367 E368 V369 E370 E371 L372 N373 M374 S375 L376 T377 A378 L379 R380 E381 K382 L383 L384 E385 A386 E387 Q388 S389 L390 R391 N392 L393 E394 D395 I396 H397 M398 S399 L400 E401 K402 D403 I404 A405 A406 M407 T408 N409 S410 L411 F412 I413 D414 R415 Q416 K417 C418 M419 A420 H421 R422

T423 R424 Y425 P426 T427 I428 L429 Q430 L431 A432 G433 Y434 GLN

• Molecule 14: Tektin-4

Chain D8: 61% 61% 39%

MET ALA GLN THR VAL PRO PRO CYS GLU LEU PRO CYS LYS GLU TYR ASP VAL ALA ARG ASN THR GLY ALA TYR THR SER SER GLY LEU ALA THR ALA SER PHE ARG THR SER LYS Y39 L40 L41 E42 E43 W44 F45 Q46 N47 C48 Y49 A50 R51 Y52 H53 Q54 A55 F56 A57 D58 R59 D60

Q61 S62 E63 R64 Q65 R66 H67 E68 S69 Q70 Q71 L72 A73 T74 E75 T76 Q77 A78 L79 A80 Q81 R82 T83 Q84 Q85 D86 S87 T88 R89 T90 V91 G92 E93 R94 L95 Q96 D97 T98 H99 S100 W101 K102 S103 E104 L105 Q106 R107 E108 M109 E110 A111 L112 A113 A114 E115 T116 N117 L118 L119 L120

A121 Q122 K123 Q124 R125 L126 E127 R128 A129 L130 D131 A132 T133 E134 V135 P136 F137 S138 I139 T140 T141 D142 N143 L144 Q145 C146 R147 E148 ARG ARG GLU HIS PRO ASN LEU VAL ARG ASP H159 V160 E161 T162 E163 L164 L165 K166 E167 A168 E169 L170 I171 R172 N173 I174 Q175 E176 L177 L178 K179 R180

T181 I182 M183 Q184 A185 V186 S187 Q188 I189 R190 L191 N192 R193 E194 H195 K196 E197 T198 C199 E200 M201 D202 W203 S204 D205 K206 M207 E208 A209 Y210 N211 I212 D213 E214 T215 C216 G217 R218 H219 H220 S221 Q222 S223 T224 E225 V226 Q227 A228 H229 P230 Y231 S232 T233 T234 F235 Q236 E237 S238 A239 S240

T241 P242 E243 T244 R245 A246 K247 F248 T249 Q250 D251 N252 L253 C254 R255 A256 Q257 R258 E259 R260 L261 A262 S263 A264 N265 L266 R267 V268 L269 V270 D271 C272 I273 L274 R275 D276 T277 S278 E279 D280 L281 R282 L283 Q284 C285 D286 A287 V288 N289 L290 A291 F292 G293 R294 ARG CYS GLU GLU LEU GLU

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

ALA GLN PHE ARG LEU LEU SER GLU VAL GLU GLU LEU ASN MET SER LEU THR ALA LEU ARG GLU LYS LEU LEU GLU ALA GLU GLN SER LEU ARG ASN LEU GLU ASP ILE HIS MET SER LEU GLU LYS ASP ILE ALA ALA MET THR ASN SER LEU PHE ILE ASP ARG Q416 K417 C418 M419 A420

H421 R422 T423 R424 Y425 P426 T427 I428 L429 Q430 L431 A432 G433 Y434 Q435

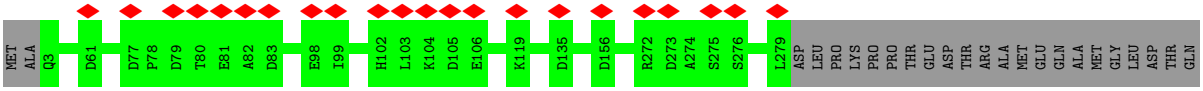
• Molecule 15: Cilia- and flagella-associated protein 161

Chain E: 92% 8%

MET ALA Q3 D61 D79 T80 E81 A82 D83 Q100 L103 K104 D105 E108 D135 D273 S276 L279 ASP LEU PRO LYS PRO PRO THR GLU ASP THR ARG ALA MET GLU GLN ALA MET GLY LEU ASP THR GLN

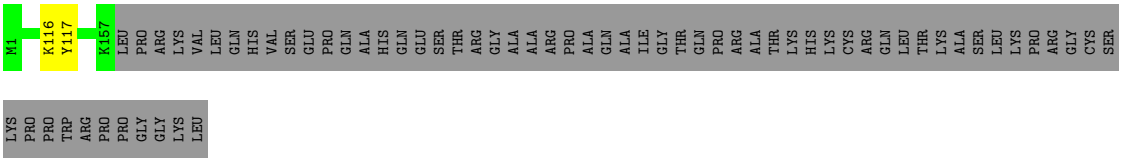
• Molecule 15: Cilia- and flagella-associated protein 161

Chain F: 7% 92% 8%



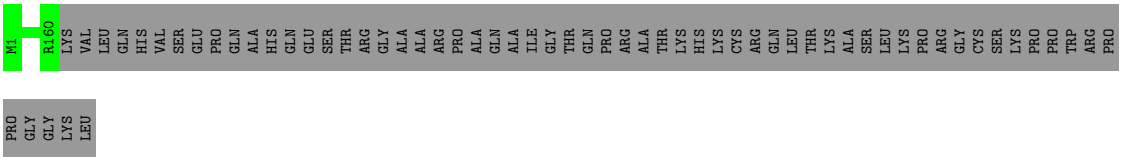
• Molecule 16: Sperm acrosome-associated protein 9

Chain F0:



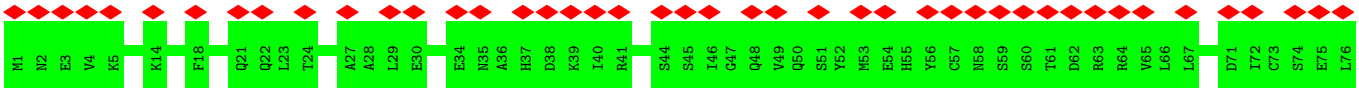
• Molecule 16: Sperm acrosome-associated protein 9

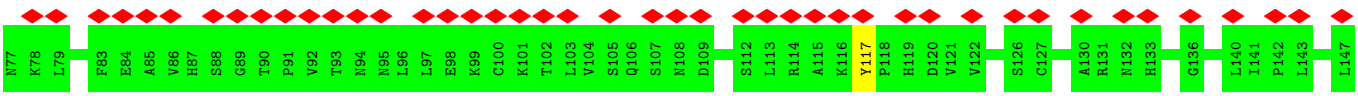
Chain F1:

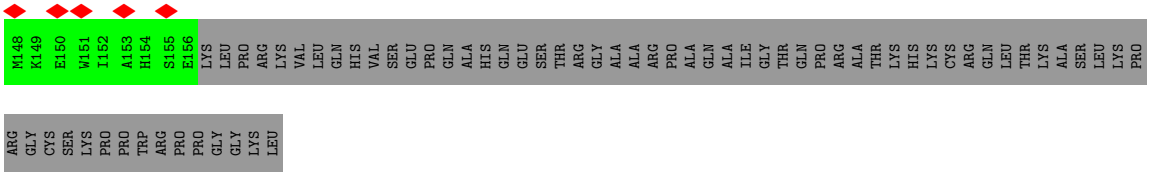


• Molecule 16: Sperm acrosome-associated protein 9

Chain F2:

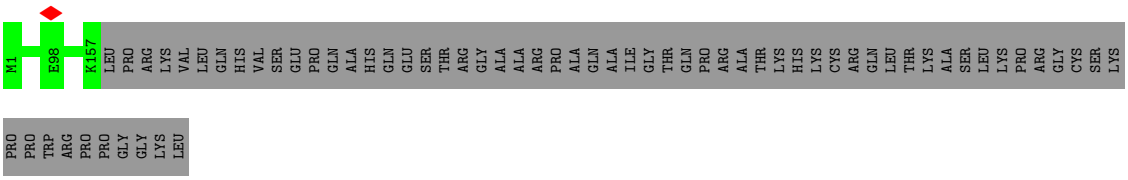






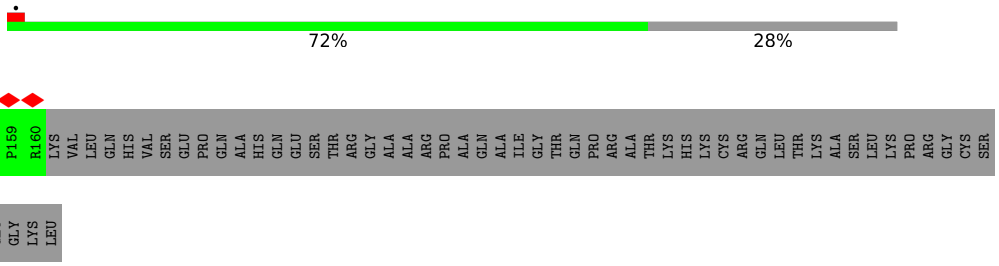
• Molecule 16: Sperm acrosome-associated protein 9

Chain F3:



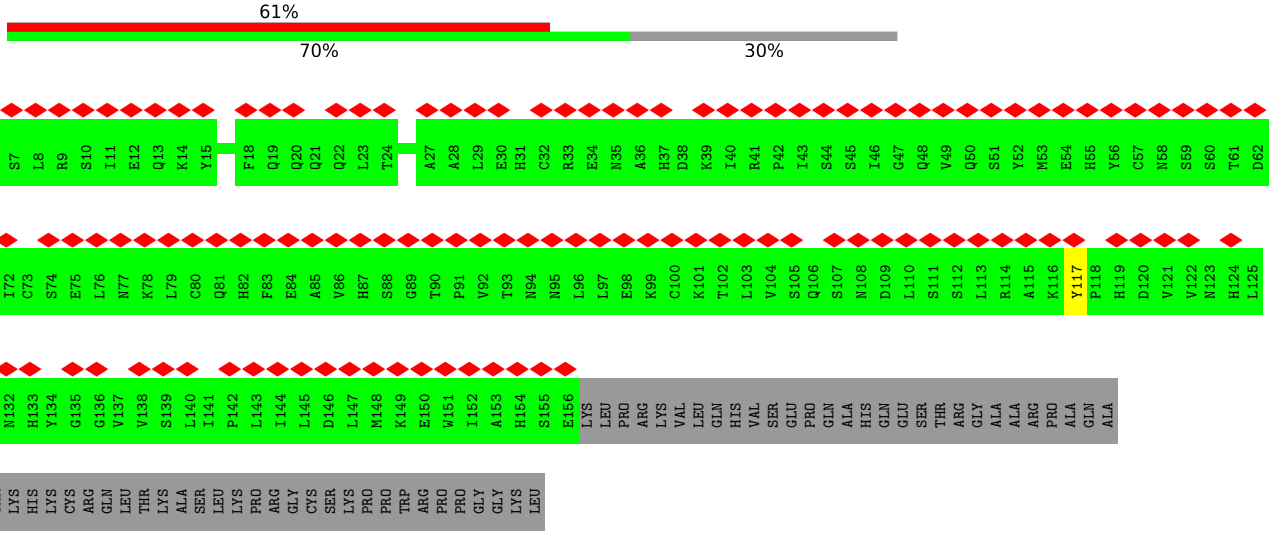
• Molecule 16: Sperm acrosome-associated protein 9

Chain F4:



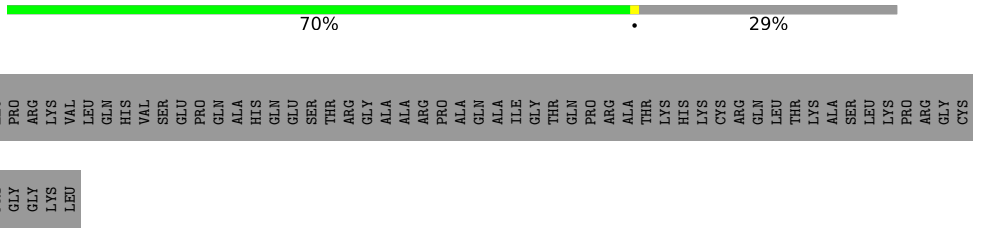
• Molecule 16: Sperm acrosome-associated protein 9

Chain F5:



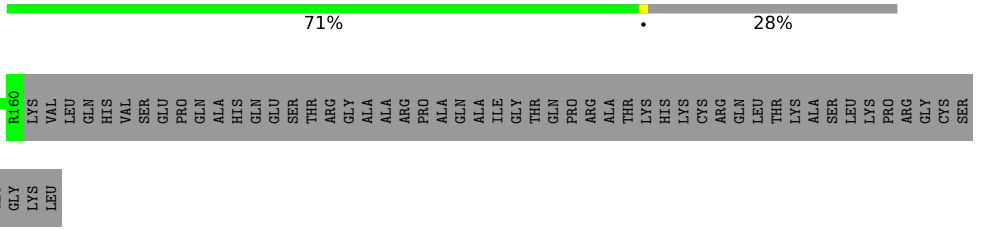
• Molecule 16: Sperm acrosome-associated protein 9

Chain F6:



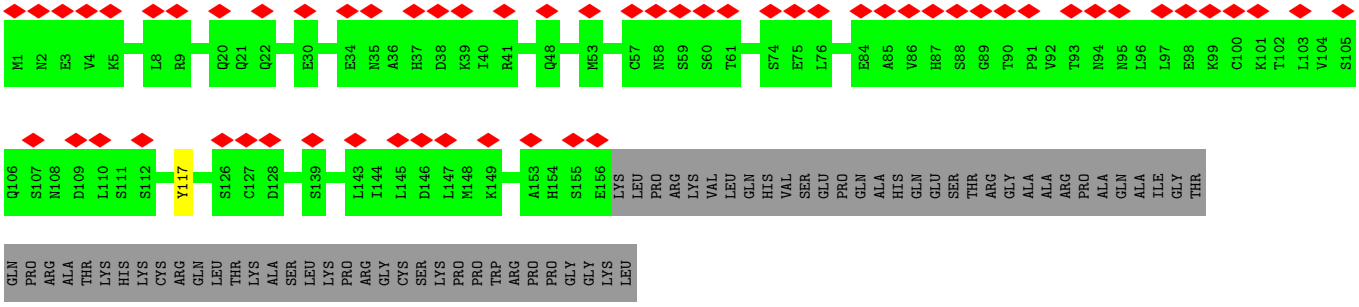
• Molecule 16: Sperm acrosome-associated protein 9

Chain F7:



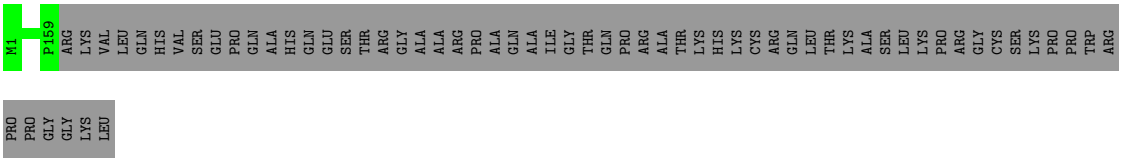
• Molecule 16: Sperm acrosome-associated protein 9

Chain F8:



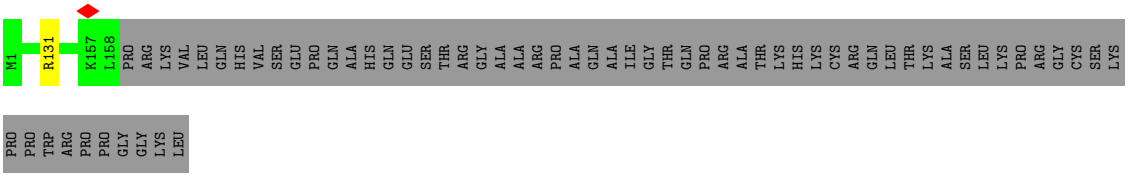
- Molecule 16: Sperm acrosome-associated protein 9

Chain G0:



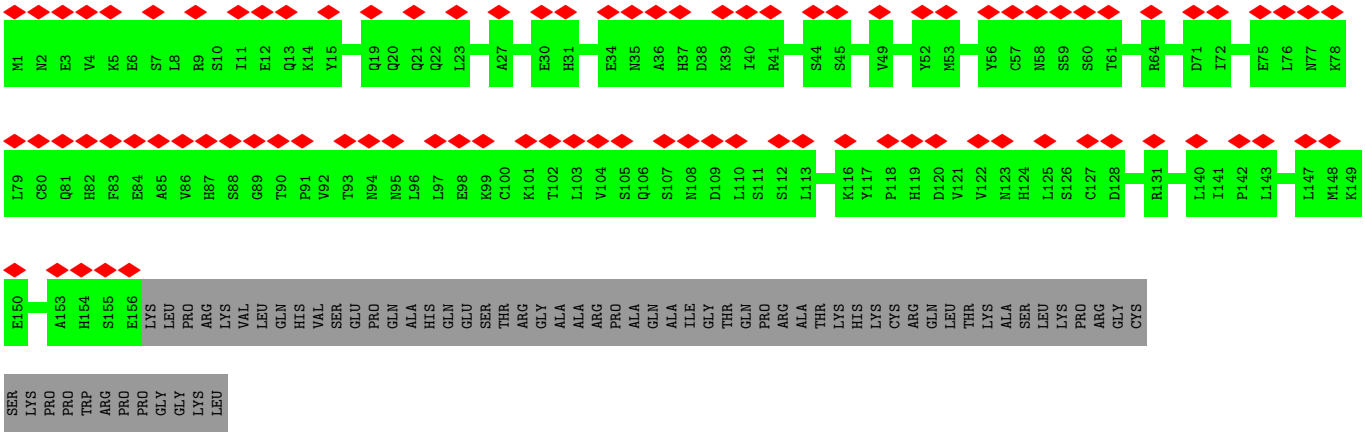
- Molecule 16: Sperm acrosome-associated protein 9

Chain G1:



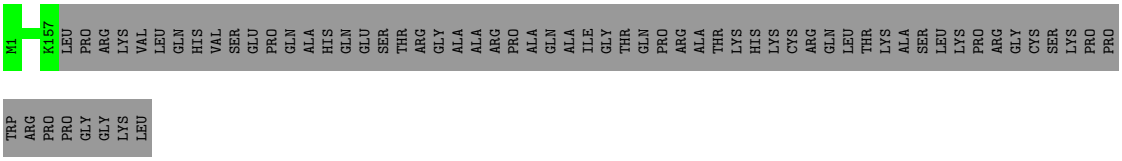
- Molecule 16: Sperm acrosome-associated protein 9

Chain G2:



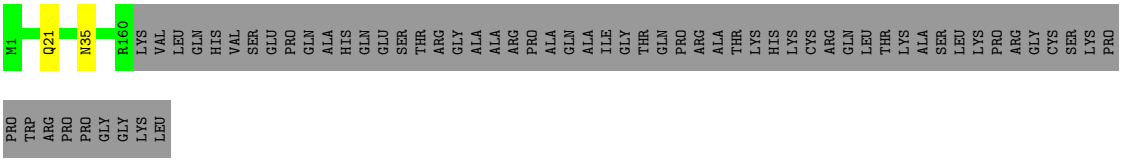
- Molecule 16: Sperm acrosome-associated protein 9

Chain G3:



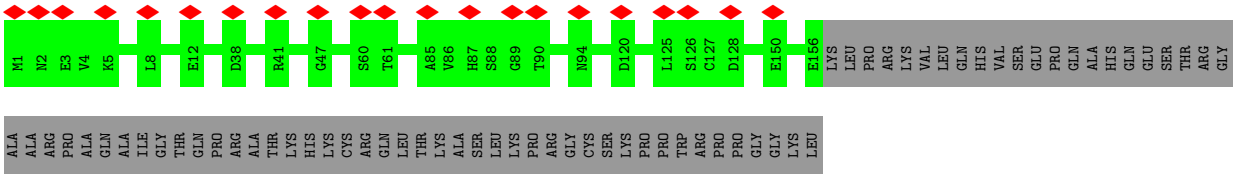
• Molecule 16: Sperm acrosome-associated protein 9

Chain G4:



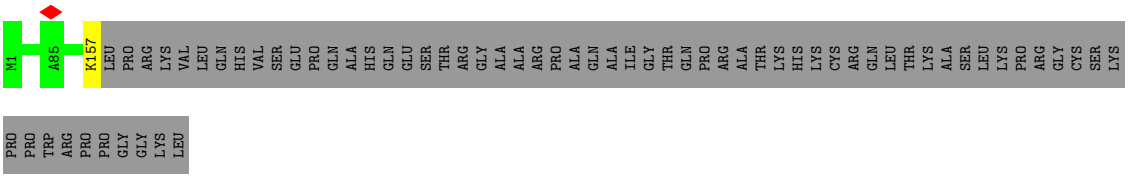
• Molecule 16: Sperm acrosome-associated protein 9

Chain G5:



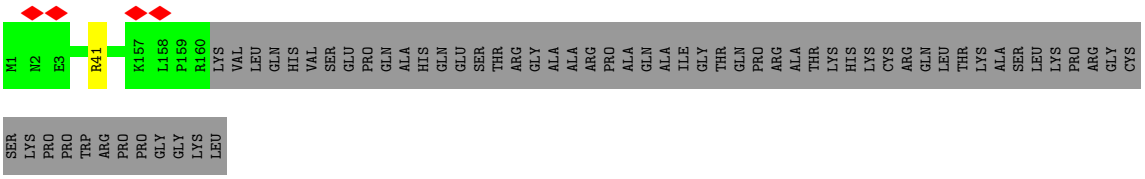
• Molecule 16: Sperm acrosome-associated protein 9

Chain G6:



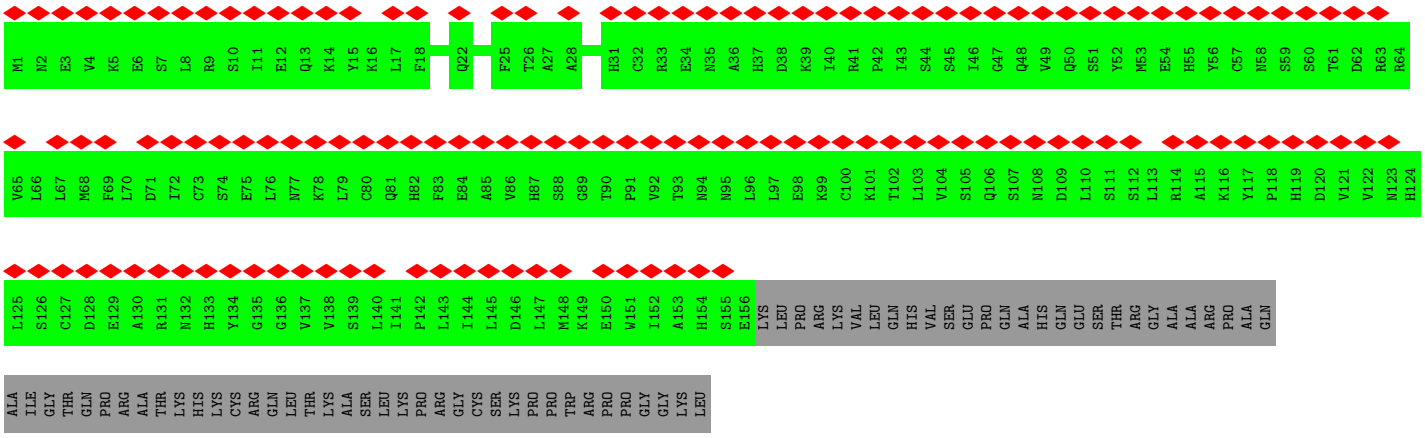
• Molecule 16: Sperm acrosome-associated protein 9

Chain G7:



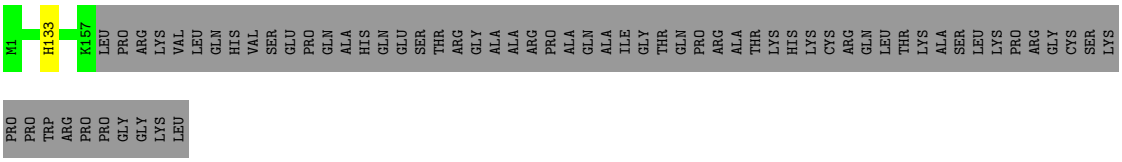
• Molecule 16: Sperm acrosome-associated protein 9

Chain G8:



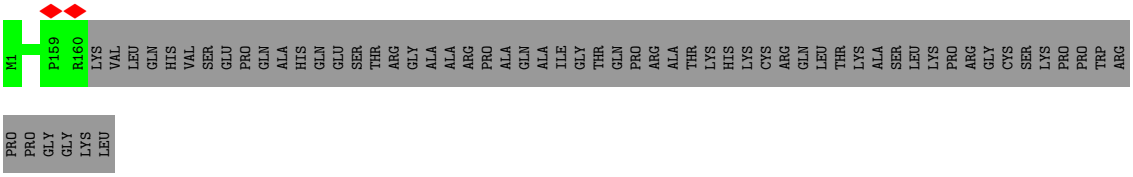
- Molecule 16: Sperm acrosome-associated protein 9

Chain H0:



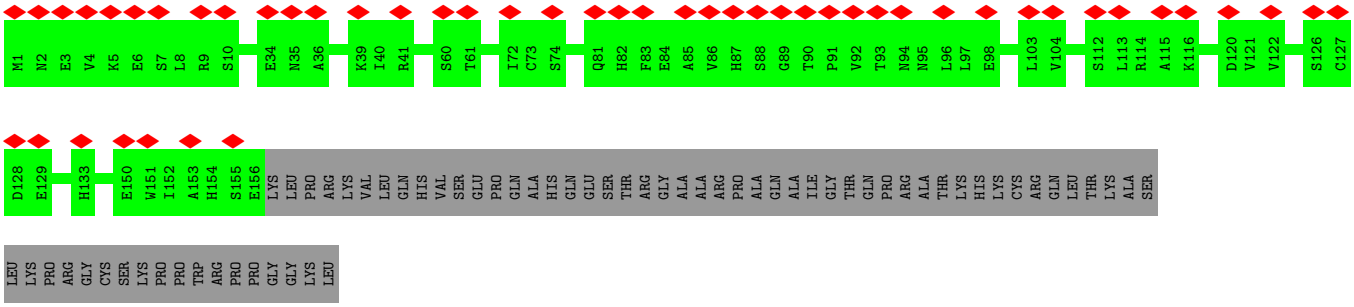
- Molecule 16: Sperm acrosome-associated protein 9

Chain H1:



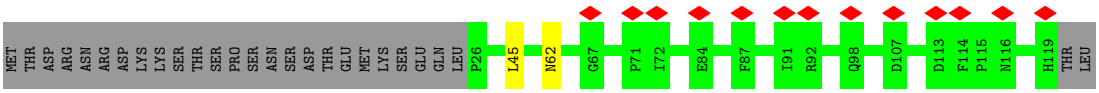
- Molecule 16: Sperm acrosome-associated protein 9

Chain H2:



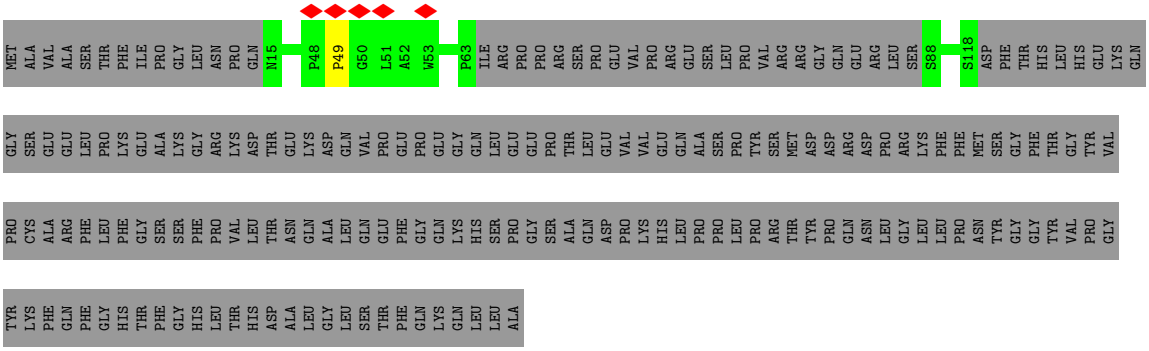
- Molecule 17: Uncharacterized protein C15orf65

Chain G:



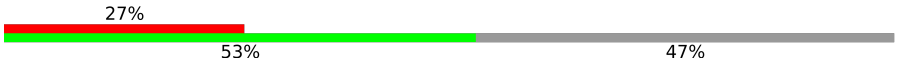
• Molecule 18: Protein FAM166B

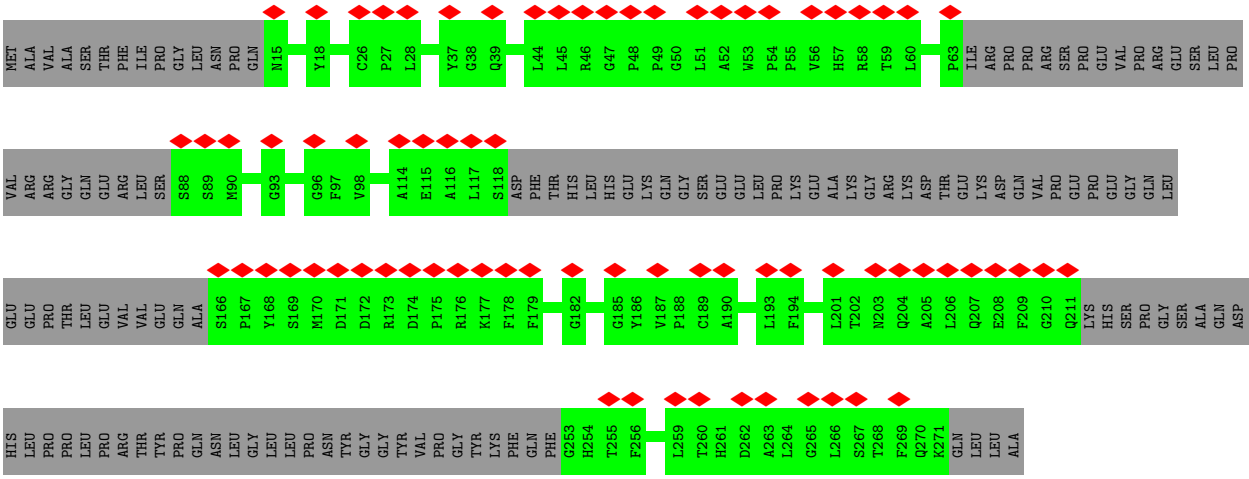
Chain H:



• Molecule 18: Protein FAM166B

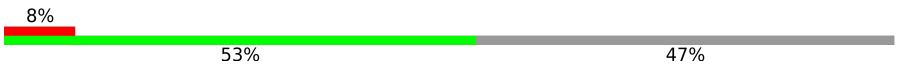
Chain I:

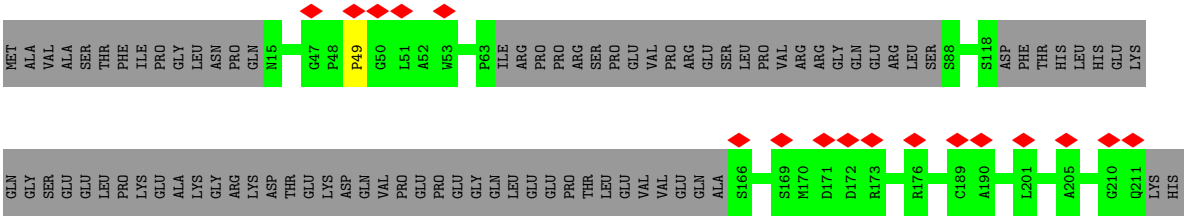


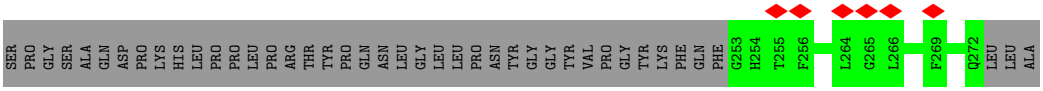


• Molecule 18: Protein FAM166B

Chain J:

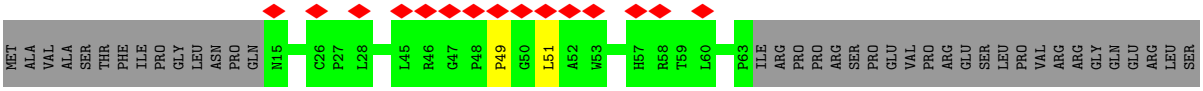


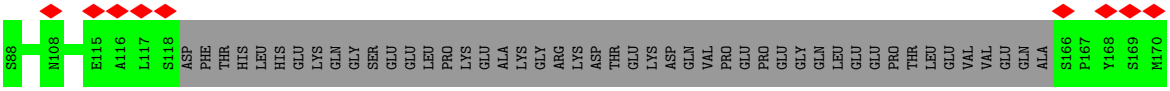


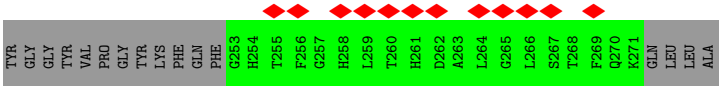


• Molecule 18: Protein FAM166B

Chain K:

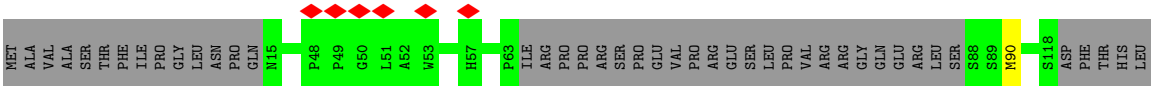


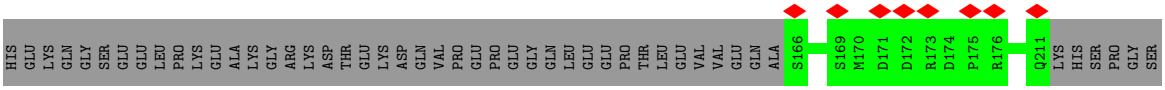


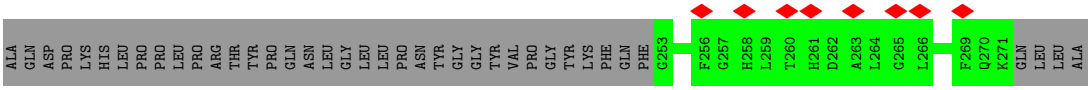


• Molecule 18: Protein FAM166B

Chain L:

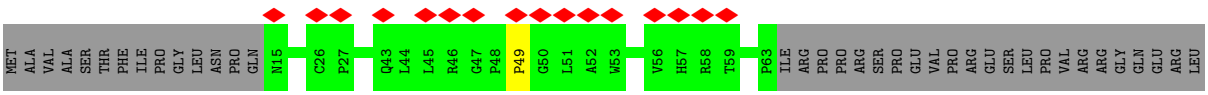


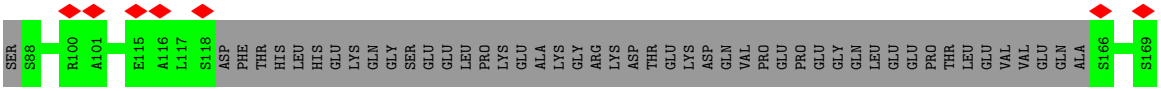


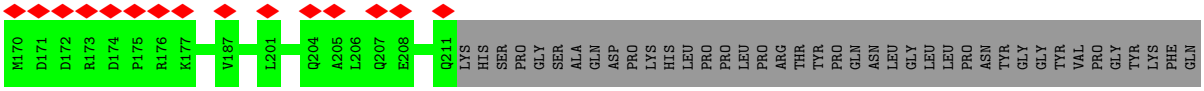


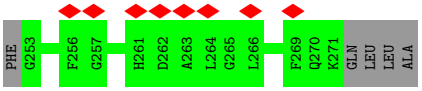
• Molecule 18: Protein FAM166B

Chain M:



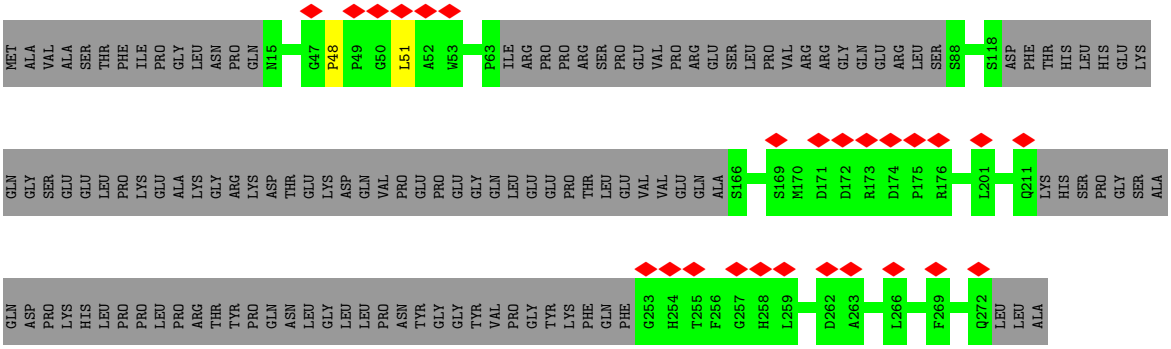






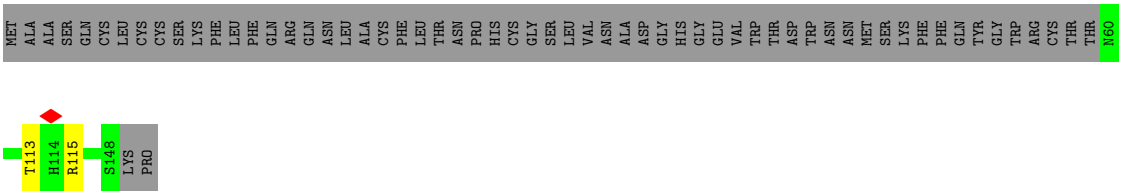
• Molecule 18: Protein FAM166B

Chain N:



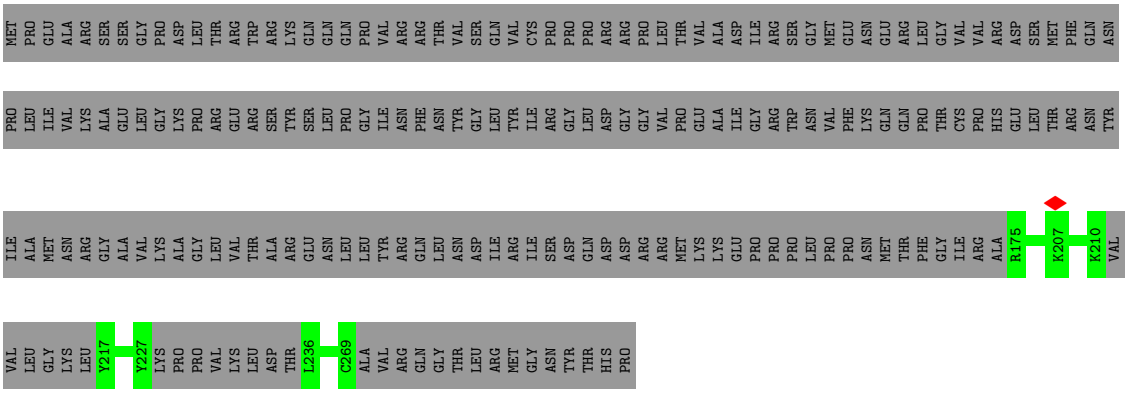
• Molecule 19: UPF0686 protein C11orf1

Chain I1:



• Molecule 20: Isoform 2 of Cilia- and flagella-associated protein 77

Chain J1:

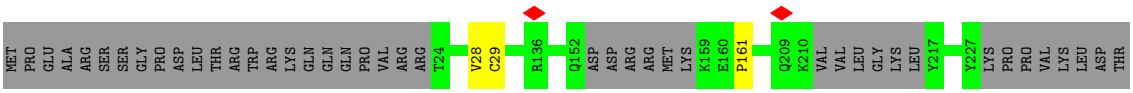


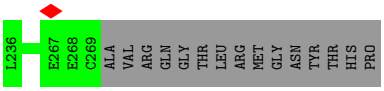
• Molecule 20: Isoform 2 of Cilia- and flagella-associated protein 77

Chain J2:

• Molecule 20: Isoform 2 of Cilia- and flagella-associated protein 77

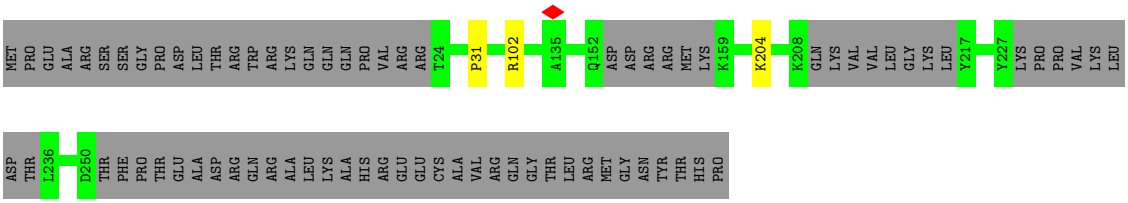
Chain J3:





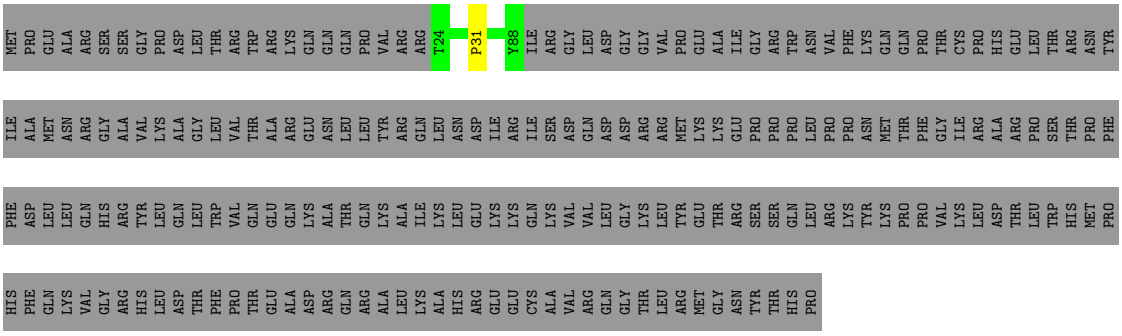
• Molecule 20: Isoform 2 of Cilia- and flagella-associated protein 77

Chain J4:



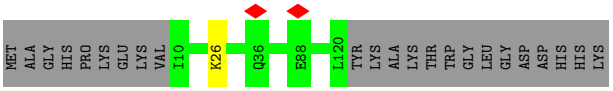
• Molecule 20: Isoform 2 of Cilia- and flagella-associated protein 77

Chain J5:



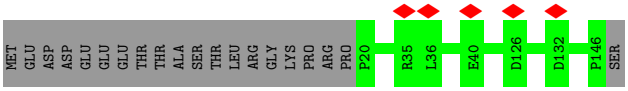
• Molecule 21: Protein FAM183A

Chain K1:



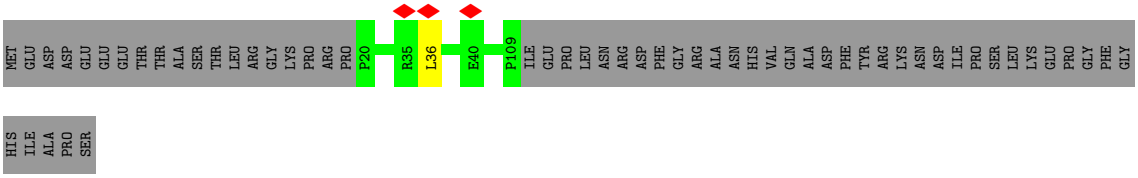
• Molecule 22: Uncharacterized protein C5orf49

Chain L1:



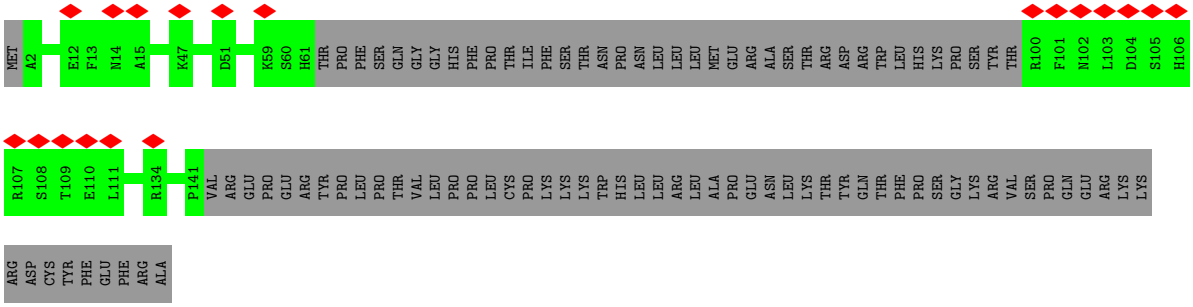
• Molecule 22: Uncharacterized protein C5orf49

Chain L2:



• Molecule 23: Protein FAM166C

Chain M1:

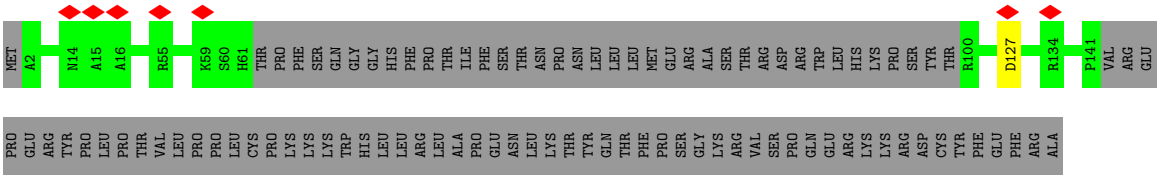


• Molecule 23: Protein FAM166C

Chain M2:

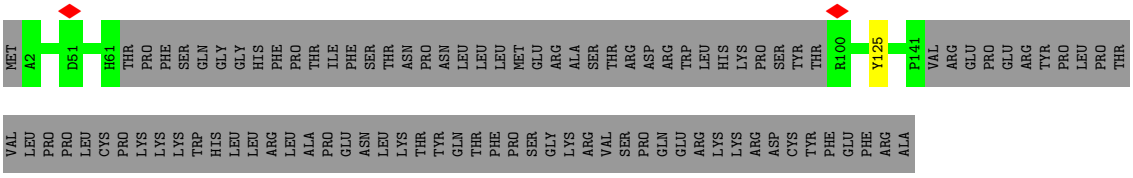
• Molecule 23: Protein FAM166C

Chain M3:



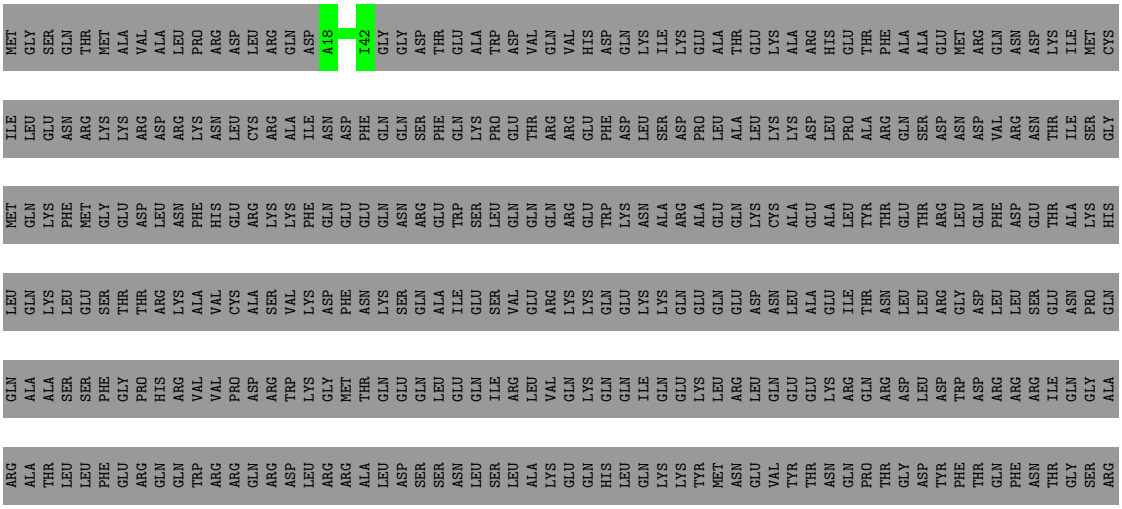
• Molecule 23: Protein FAM166C

Chain M4:



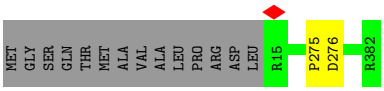
• Molecule 24: RIB43A-like with coiled-coils protein 2

Chain O: 7% 93%



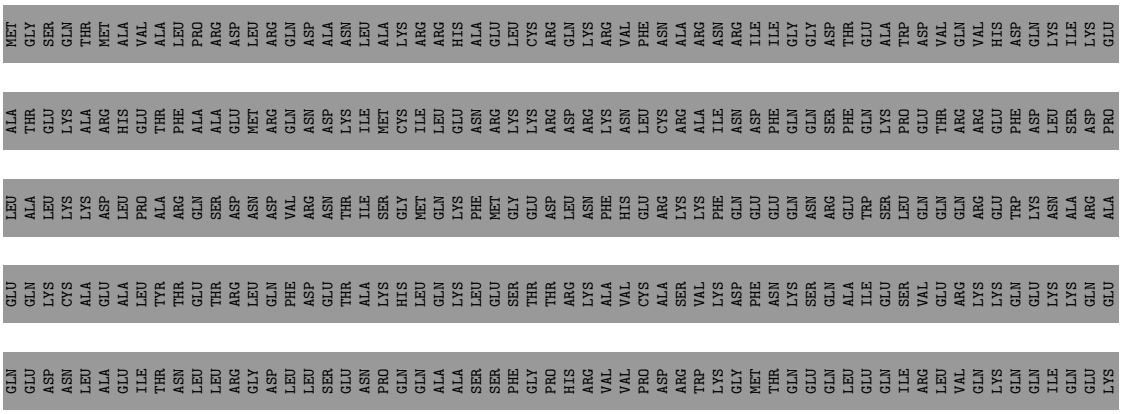
• Molecule 24: RIB43A-like with coiled-coils protein 2

Chain P: 96%



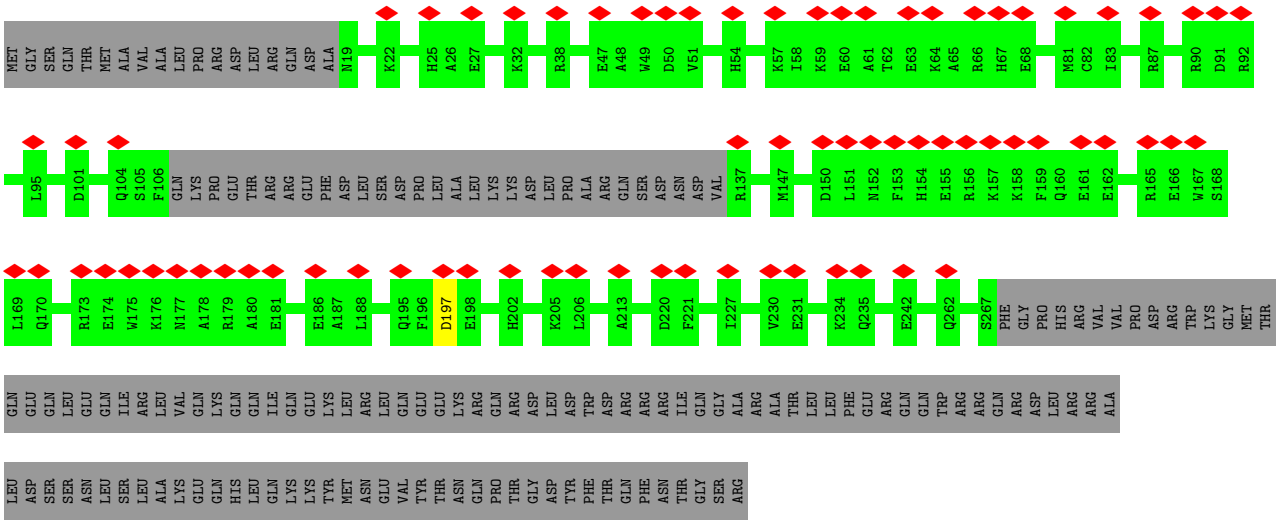
• Molecule 24: RIB43A-like with coiled-coils protein 2

Chain Q: 10% 90%



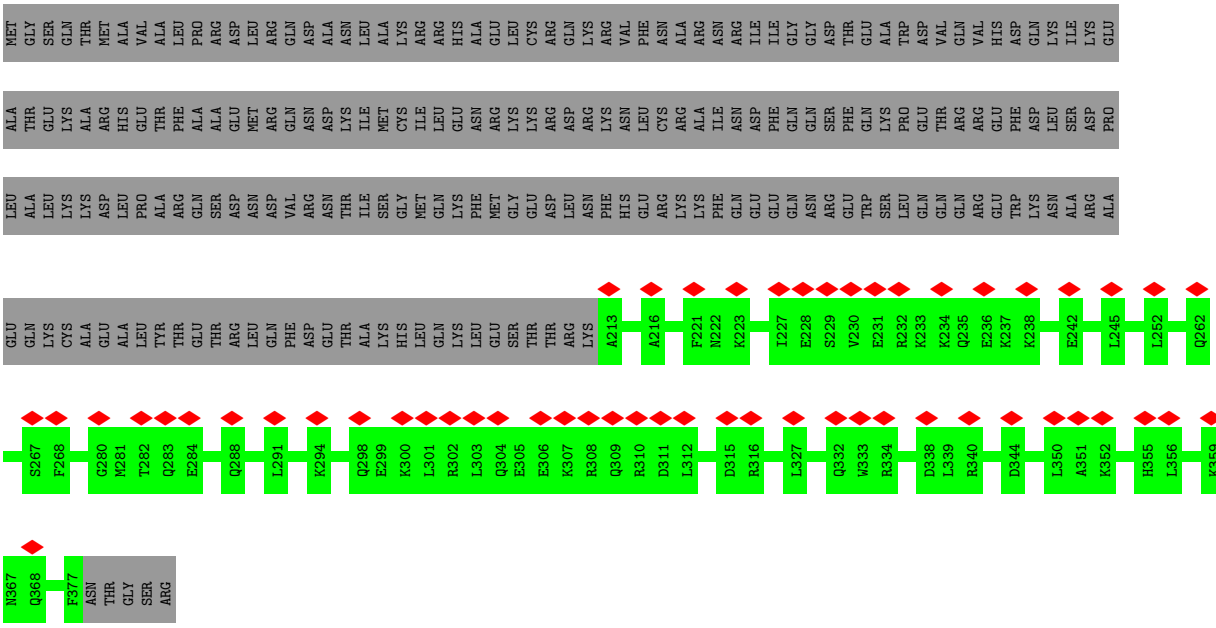
• Molecule 24: RIB43A-like with coiled-coils protein 2

Chain R:



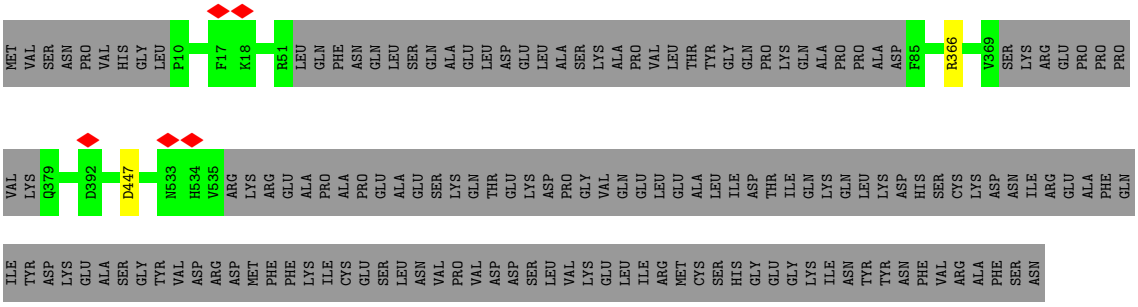
• Molecule 24: RIB43A-like with coiled-coils protein 2

Chain S:



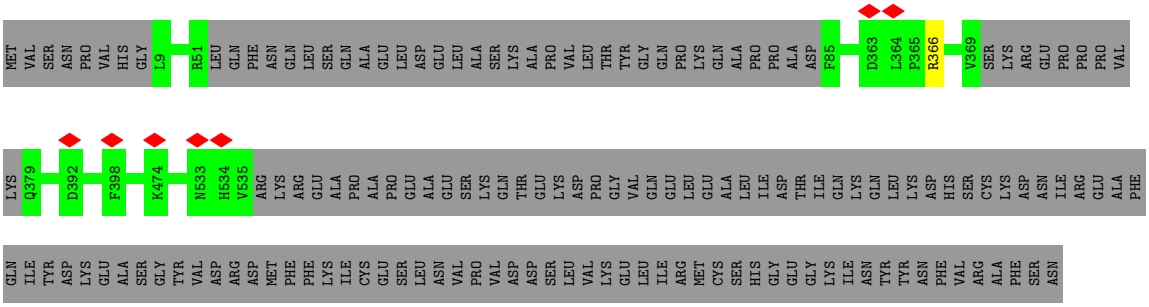
• Molecule 25: EF-hand domain-containing protein 1

Chain T:



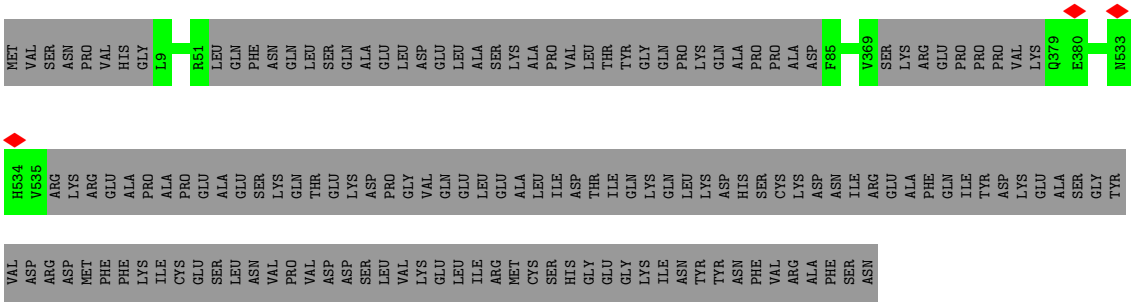
• Molecule 25: EF-hand domain-containing protein 1

Chain U:



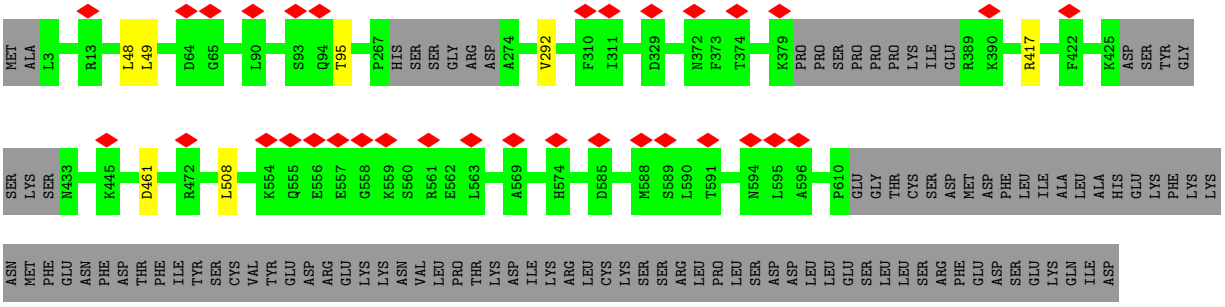
• Molecule 25: EF-hand domain-containing protein 1

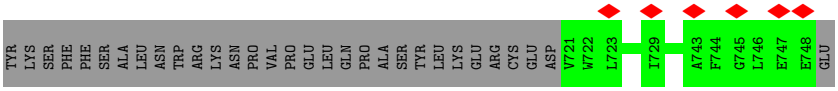
Chain V:



• Molecule 26: EF-hand domain-containing family member C2

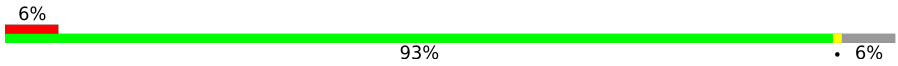
Chain W:

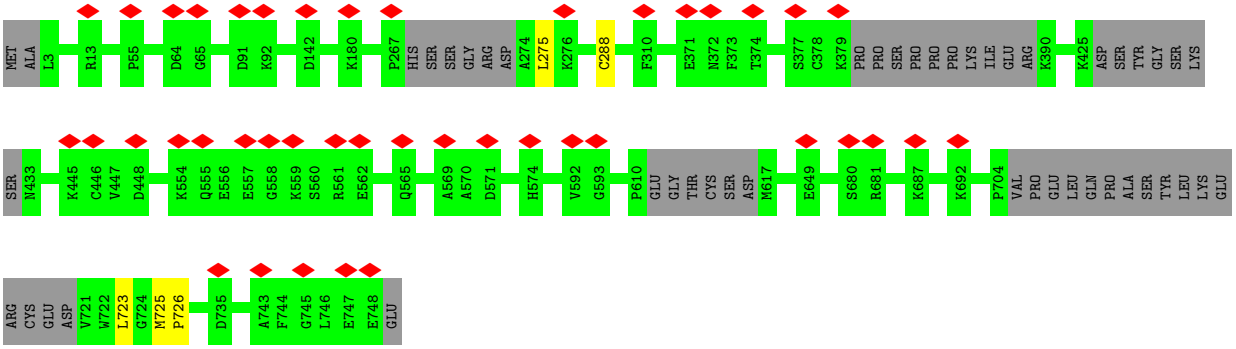




• Molecule 26: EF-hand domain-containing family member C2

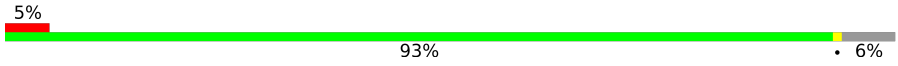
Chain X:

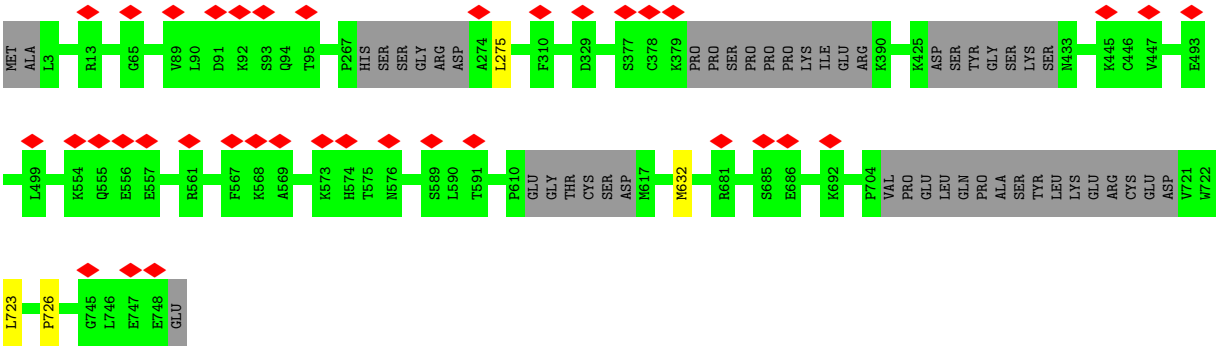




• Molecule 26: EF-hand domain-containing family member C2

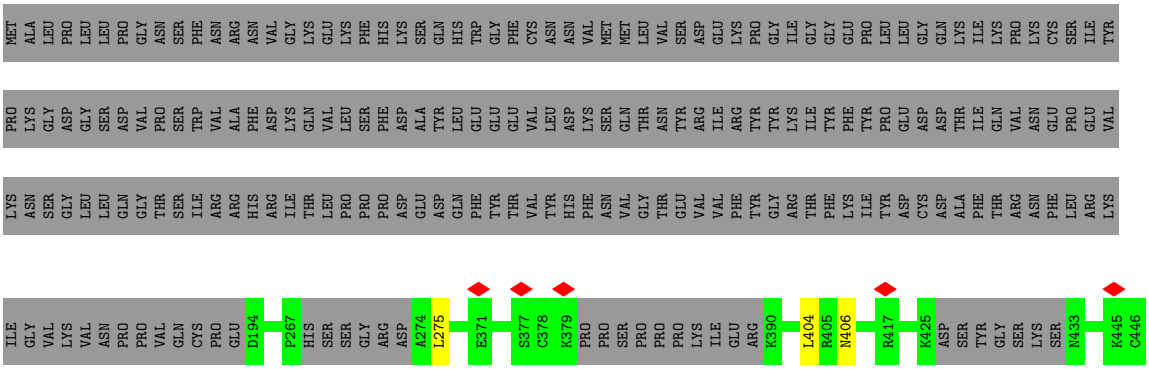
Chain Y:

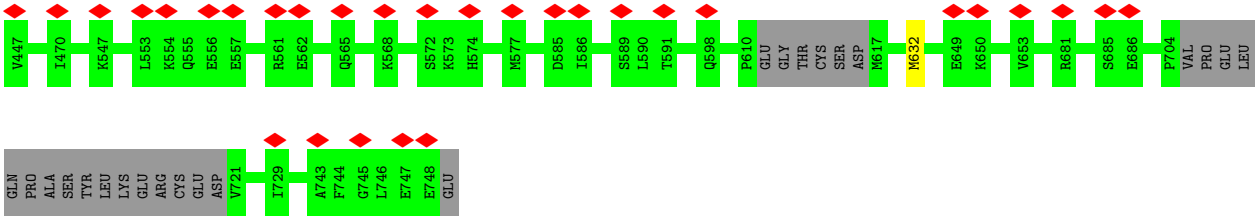




• Molecule 26: EF-hand domain-containing family member C2

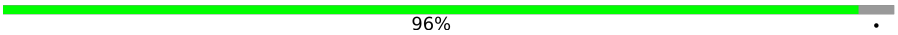
Chain Z:





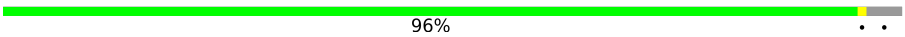
• Molecule 27: Cilia- and flagella-associated protein 20

Chain XA:



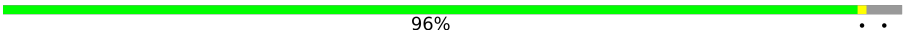
• Molecule 27: Cilia- and flagella-associated protein 20

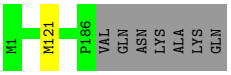
Chain XB:



• Molecule 27: Cilia- and flagella-associated protein 20

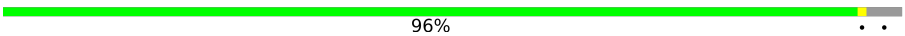
Chain XC:





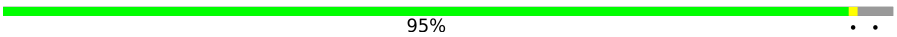
• Molecule 27: Cilia- and flagella-associated protein 20

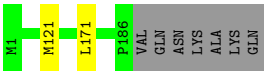
Chain XD:



• Molecule 27: Cilia- and flagella-associated protein 20

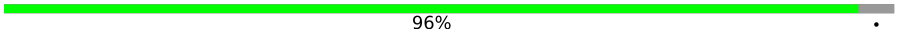
Chain XE:





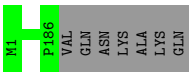
• Molecule 27: Cilia- and flagella-associated protein 20

Chain XF:



• Molecule 27: Cilia- and flagella-associated protein 20

Chain XG: 96%

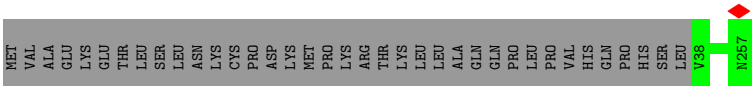


• Molecule 28: Parkin coregulated gene protein

Chain YB: 86% 14%

• Molecule 28: Parkin coregulated gene protein

Chain YC: 86% 14%

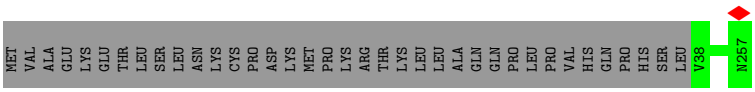


• Molecule 28: Parkin coregulated gene protein

Chain YD: 85% 14%

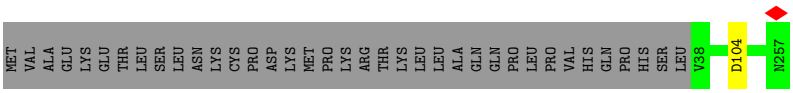
• Molecule 28: Parkin coregulated gene protein

Chain YE: 86% 14%



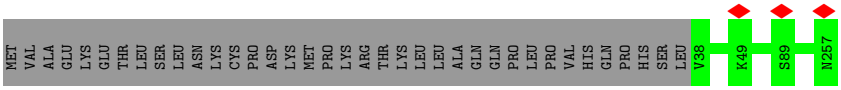
• Molecule 28: Parkin coregulated gene protein

Chain YF: 85% 14%



• Molecule 28: Parkin coregulated gene protein

Chain YG: 86% 14%



• Molecule 29: Cilia- and flagella-associated protein 45

Chain a: 31% 68%

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

HIS THR LEU GLN LYS THR LEU THR ALA LEU GLY LEU ASP ARG LYS P76 T94 GLU ASP PRO SER GLY GLU SER LEU ILE ILE S105 P106 E107 R111 W114 A115 V118 L119 T120 R121 E122 E125 A126 Q129 D140 Q151 K152 GLU MET VAL TRP ASN ASN N159 K160

K161 L162 N181 E189 M265 GLU LYS ASN GLN GLU GLU ARG SER LEU LEU ALA GLU GLN ARG GLU GLN GLU LYS GLU GLN MET LEU GLU TYR MET GLU GLN LEU GLU PHE GLU ALA GLU GLN GLU ASP LEU LYS ASP MET GLU ARG ARG GLN GLN GLN LYS LEU LYS MET GLN ALA GLU ILE LYS ARG

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

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

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

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

- Molecule 29: Cilia- and flagella-associated protein 45

Chain b: 5% 61% 39%

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

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

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

ASN LYS LEU ARG MET GLU GLN GLU GLU GLU LEU LYS ASP MET SER LYS ILE ILE LEU ASN ALA LYS CYS HIS ALA ILE ARG ASP ALA Q210 E295 E296 D297 L298 K299 R304 Q305 Q306 T318 K326 A327 E328 E333 D337 E359 R362 R371 L372 M375 Q376

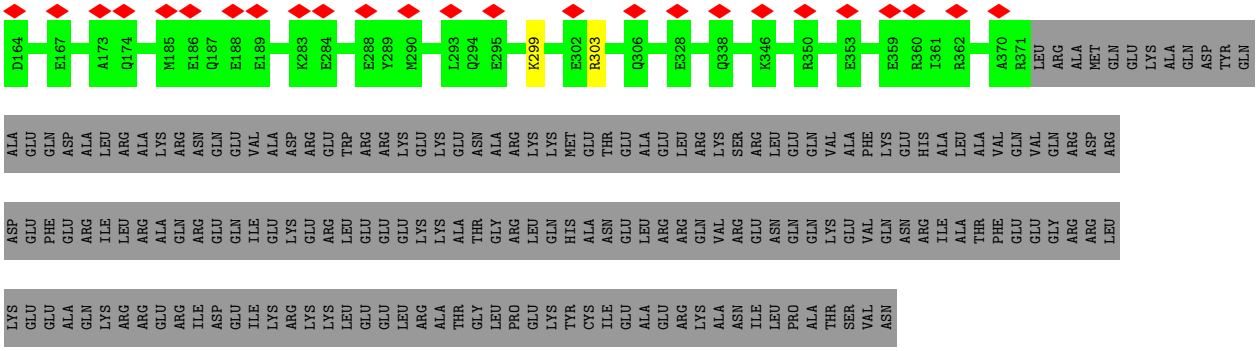
E377 K378 A379 Q380 D381 Y382 Q383 A384 D387 D442 A527 T528 G529 N543 ILE LEU PRO ALA THR SER VAL ASN

- Molecule 29: Cilia- and flagella-associated protein 45

Chain c: 8% 51% 48%

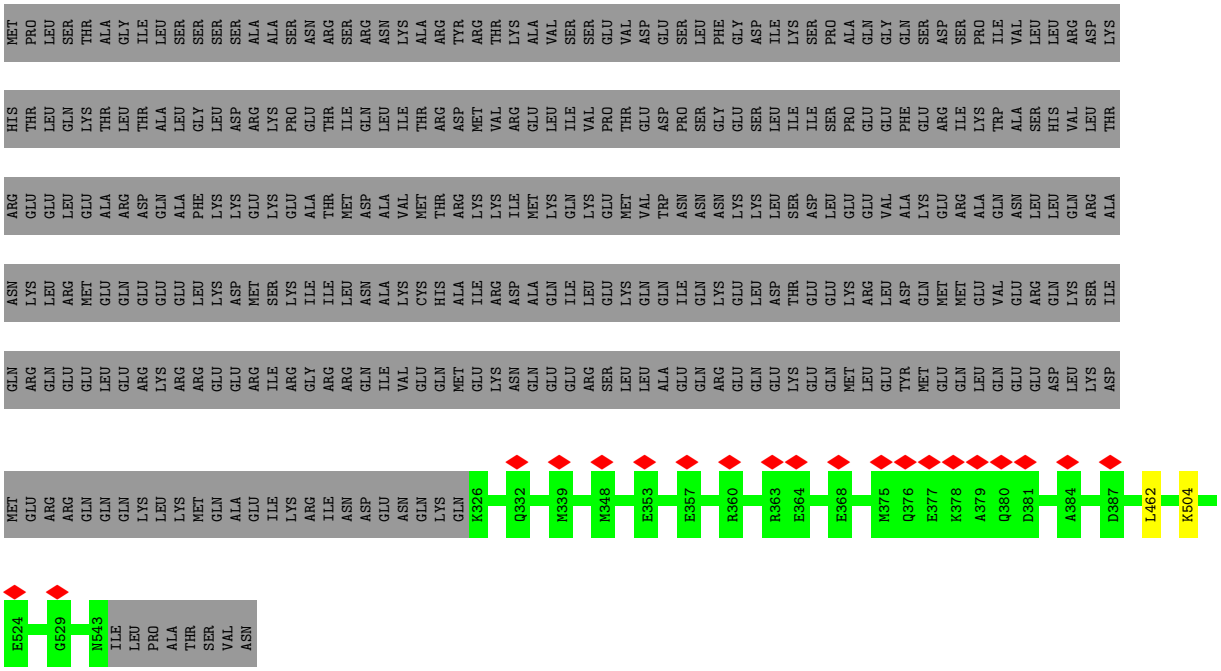
MET PRO LEU SER THR ALA GLY ILE LEU SER SER SER SER ALA ALA SER ASN ARG SER ARG ASN LYS ALA ARG TYR ARG THR LYS ALA VAL SER SER GLU VAL ASP GLU SER LEU PHE GLY ASP ILE LYS SER PRO ALA GLN GLY GLN SER ASP SER PRO ILE VAL LEU LEU ARG ASP LYS

HIS THR LEU GLN LYS THR LEU THR ALA LEU GLY LEU ASP ARG LYS PRO E77 T94 GLU ASP PRO SER GLY GLU SER LEU ILE ILE SER P106 R111 W114 A115 S116 H117 V118 L119 T120 R121 E122 E123 L124 E125 A126 R127 D128 Q129 A130 E134 D140 N159 K160 K161



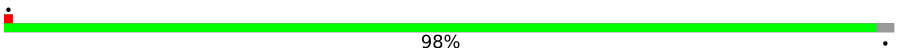
- Molecule 29: Cilia- and flagella-associated protein 45

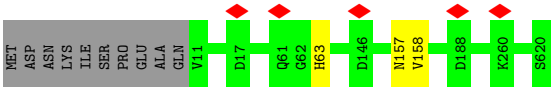
Chain d:



- Molecule 30: Cilia- and flagella-associated protein 52

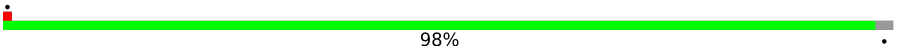
Chain e:

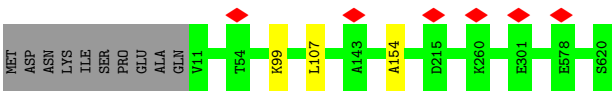




- Molecule 30: Cilia- and flagella-associated protein 52

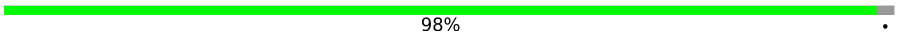
Chain f:

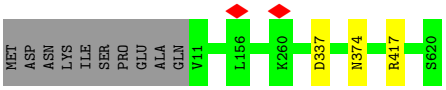




- Molecule 30: Cilia- and flagella-associated protein 52

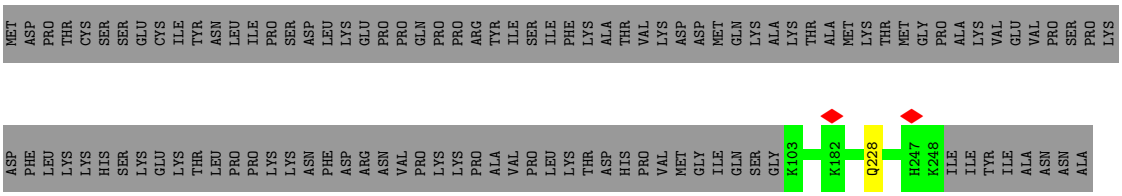
Chain g:





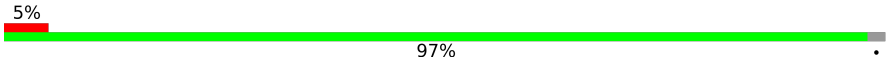
• Molecule 31: Enkurin

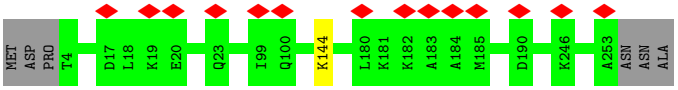
Chain h:



• Molecule 31: Enkurin

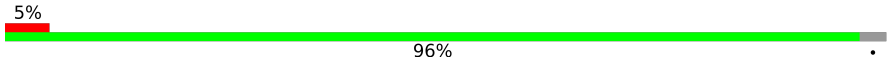
Chain i:

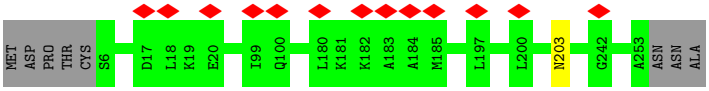




• Molecule 31: Enkurin

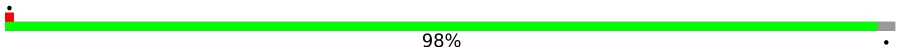
Chain j:





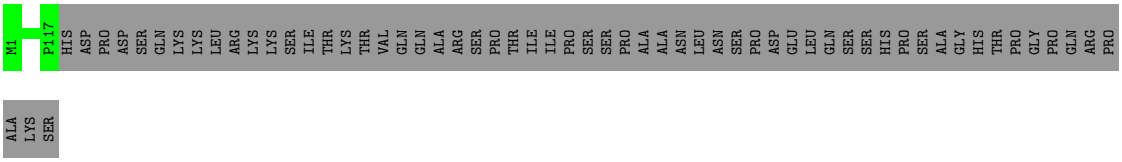
• Molecule 31: Enkurin

Chain k:



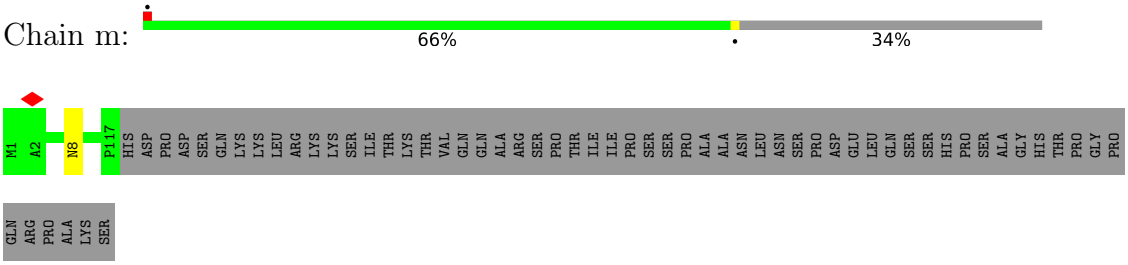
• Molecule 32: Protein Flattop

Chain l:



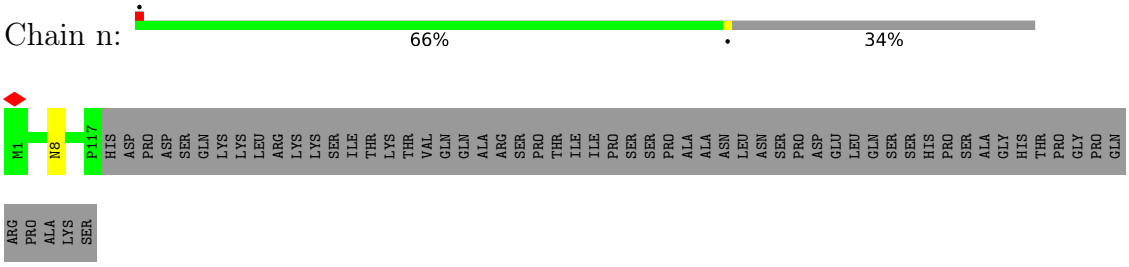
• Molecule 32: Protein Flattop

Chain m:



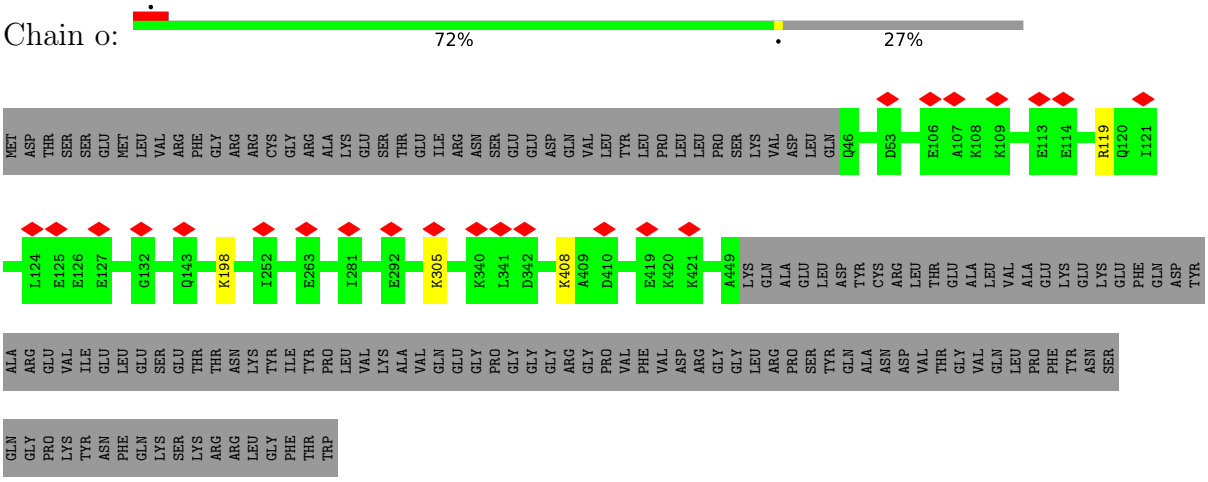
- Molecule 32: Protein Flattop

Chain n:



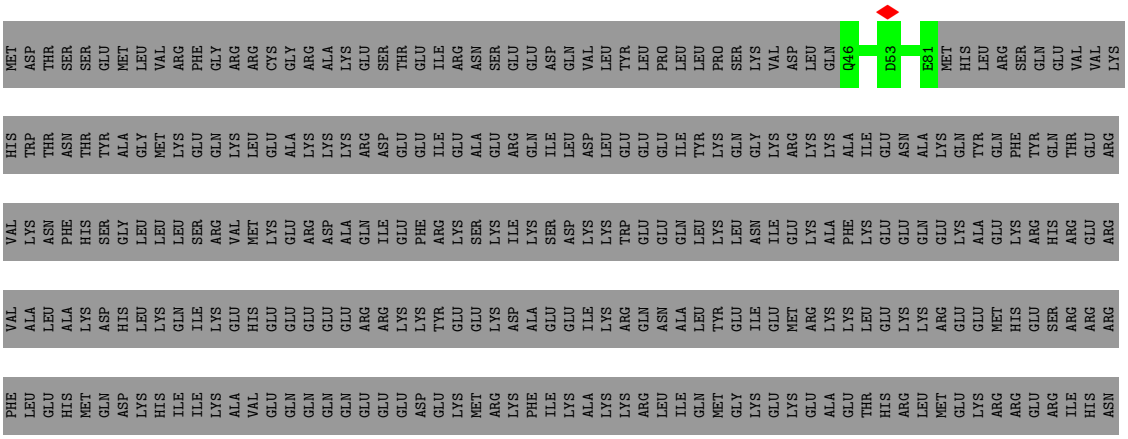
- Molecule 33: Protein CFAP210

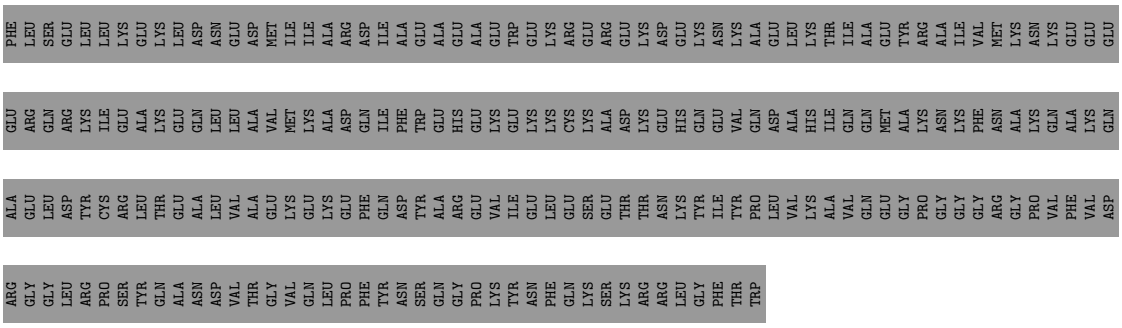
Chain o:



- Molecule 33: Protein CFAP210

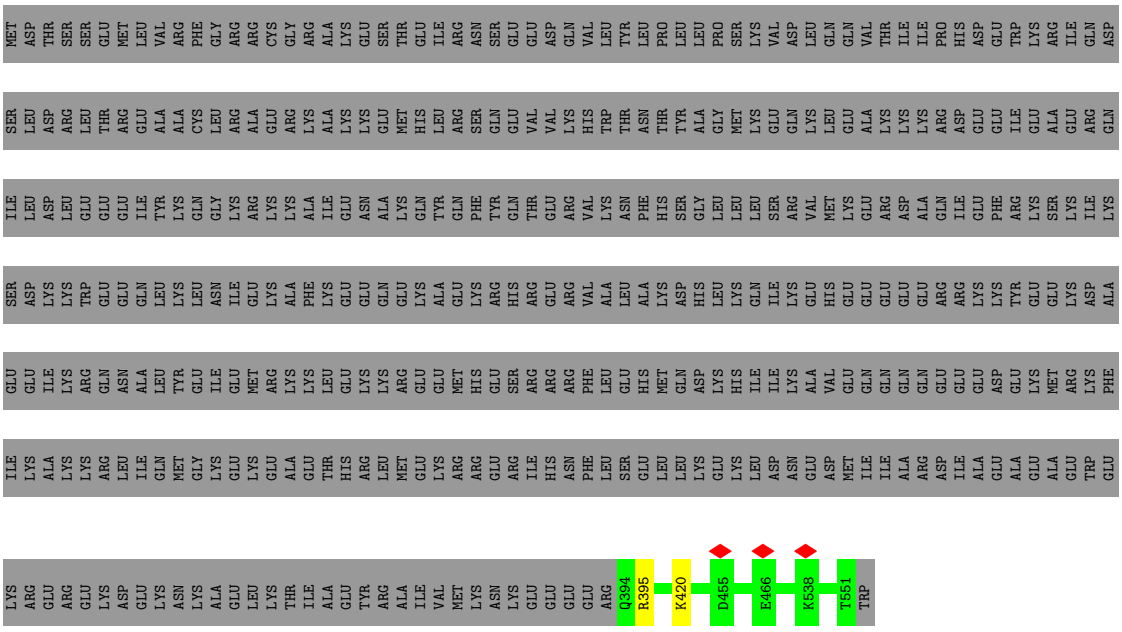
Chain o1:





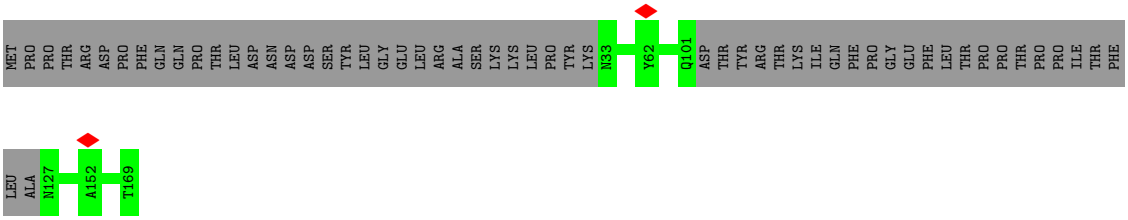
• Molecule 33: Protein CFAP210

Chain p:



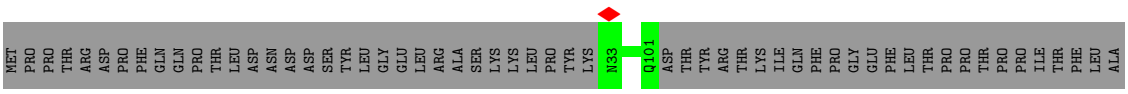
• Molecule 34: Protein CFAP276

Chain q:



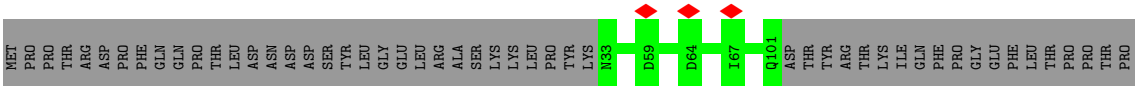
• Molecule 34: Protein CFAP276

Chain r:



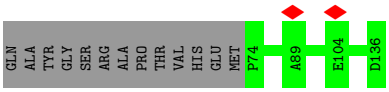
• Molecule 34: Protein CFAP276

Chain s:



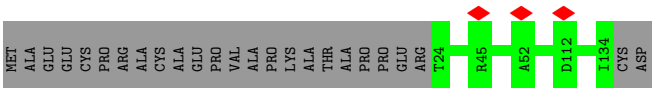
• Molecule 35: UPF0691 protein C9orf116

Chain y:



• Molecule 35: UPF0691 protein C9orf116

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	208558	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	24.733	Depositor
Minimum map value	-13.575	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	701.44, 701.44, 701.44	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	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: GTP, GDP, MG

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	0.29	0/429	0.64	0/580
1	7	0.28	0/1227	0.59	0/1659
2	1	0.27	0/2265	0.55	0/3049
2	2	0.27	0/3697	0.53	0/4999
3	3	0.33	0/2531	0.58	0/3362
3	4	0.35	0/1851	0.57	0/2456
4	5	0.27	0/3006	0.55	0/4056
4	6	0.28	0/3006	0.54	1/4056 (0.0%)
5	8	0.30	0/1467	0.61	1/1999 (0.1%)
5	9	0.27	0/422	0.57	0/570
6	A	0.29	0/429	0.45	0/571
7	A0	0.29	0/1785	0.53	0/2399
7	A1	0.32	0/3221	0.56	2/4335 (0.0%)
7	A2	0.33	0/3221	0.56	0/4335
7	A3	0.32	0/2744	0.57	0/3689
7	A4	0.31	0/303	0.66	0/410
8	AA	0.28	0/3507	0.52	1/4761 (0.0%)
8	AC	0.29	0/3507	0.55	2/4761 (0.0%)
8	AE	0.28	0/3507	0.55	0/4761
8	AG	0.29	0/3507	0.54	3/4761 (0.1%)
8	AI	0.28	0/3507	0.54	0/4761
8	AK	0.29	0/3507	0.54	0/4761
8	AM	0.28	0/3507	0.53	2/4761 (0.0%)
8	BA	0.27	0/3460	0.55	1/4697 (0.0%)
8	BC	0.26	0/3507	0.52	0/4761
8	BE	0.29	0/3460	0.57	2/4697 (0.0%)
8	BG	0.28	0/3507	0.55	2/4761 (0.0%)
8	BI	0.28	0/3460	0.56	3/4697 (0.1%)
8	BK	0.28	0/3507	0.56	1/4761 (0.0%)
8	BM	0.29	0/3464	0.54	0/4702
8	CA	0.26	0/3462	0.53	1/4700 (0.0%)
8	CC	0.27	0/3507	0.53	0/4761

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
8	CE	0.26	0/3448	0.55	0/4681
8	CG	0.27	0/3507	0.53	2/4761 (0.0%)
8	CI	0.28	0/3454	0.56	0/4689
8	CK	0.28	0/3507	0.57	2/4761 (0.0%)
8	CM	0.29	0/3454	0.55	0/4689
8	DA	0.27	0/3041	0.56	1/4133 (0.0%)
8	DC	0.26	0/3448	0.54	0/4681
8	DE	0.27	0/3456	0.54	0/4692
8	DG	0.27	0/3448	0.54	1/4681 (0.0%)
8	DI	0.27	0/3448	0.55	0/4681
8	DK	0.26	0/3448	0.55	1/4681 (0.0%)
8	DM	0.26	0/3456	0.53	1/4692 (0.0%)
8	EC	0.27	0/3507	0.57	0/4761
8	EE	0.27	0/3507	0.54	0/4761
8	EG	0.27	0/3501	0.56	0/4753
8	EI	0.27	0/3507	0.56	0/4761
8	EK	0.26	0/3501	0.54	0/4753
8	EM	0.27	0/3501	0.58	1/4753 (0.0%)
8	FC	0.26	0/3456	0.54	1/4692 (0.0%)
8	FE	0.28	0/3456	0.57	2/4692 (0.0%)
8	FG	0.28	0/3448	0.56	2/4681 (0.0%)
8	FI	0.27	0/3448	0.56	0/4681
8	FK	0.27	0/3448	0.55	0/4681
8	FM	0.26	0/3448	0.55	1/4681 (0.0%)
8	GC	0.27	0/3486	0.56	1/4732 (0.0%)
8	GE	0.27	0/3448	0.56	1/4681 (0.0%)
8	GG	0.26	0/3456	0.55	0/4692
8	GI	0.27	0/3448	0.55	0/4681
8	GK	0.27	0/3462	0.55	1/4700 (0.0%)
8	GM	0.28	0/3479	0.58	2/4722 (0.0%)
8	HC	0.26	0/3456	0.53	1/4692 (0.0%)
8	HE	0.26	0/3462	0.52	0/4700
8	HG	0.27	0/3462	0.56	2/4700 (0.0%)
8	HI	0.26	0/3462	0.52	0/4700
8	HK	0.28	0/3454	0.55	1/4689 (0.0%)
8	HM	0.28	0/3456	0.54	0/4692
8	HO	0.28	0/3126	0.57	1/4238 (0.0%)
8	IC	0.26	0/3470	0.53	0/4711
8	IE	0.28	0/3456	0.55	0/4692
8	IG	0.26	0/3507	0.54	2/4761 (0.0%)
8	II	0.27	0/3462	0.54	0/4700
8	IK	0.26	0/3507	0.51	0/4761
8	IM	0.29	0/3456	0.56	0/4692

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
8	IO	0.27	0/3454	0.56	1/4689 (0.0%)
8	JC	0.26	0/3507	0.53	0/4761
8	JE	0.27	0/3448	0.54	1/4681 (0.0%)
8	JG	0.27	0/3448	0.53	0/4681
8	JI	0.27	0/3448	0.54	0/4681
8	JK	0.29	0/3454	0.58	3/4689 (0.1%)
8	JM	0.26	0/3448	0.54	0/4681
8	KC	0.30	0/3467	0.55	0/4707
8	KE	0.28	0/3462	0.53	0/4700
8	KG	0.30	0/3467	0.55	0/4707
8	KI	0.31	0/3450	0.55	1/4684 (0.0%)
8	KK	0.29	0/3467	0.56	2/4707 (0.0%)
8	KM	0.29	0/3501	0.55	2/4753 (0.0%)
8	KO	0.29	0/3460	0.54	0/4697
8	LC	0.29	0/3466	0.54	0/4705
8	LE	0.28	0/3507	0.53	0/4761
8	LG	0.30	0/3474	0.56	2/4716 (0.0%)
8	LI	0.29	0/3487	0.54	1/4732 (0.0%)
8	LK	0.30	0/3467	0.56	1/4707 (0.0%)
8	LM	0.29	0/3456	0.52	0/4692
8	MC	0.28	0/3514	0.55	0/4771
8	ME	0.28	0/3463	0.54	1/4702 (0.0%)
8	MG	0.28	0/3461	0.54	0/4699
8	MI	0.29	0/3469	0.53	0/4710
8	MK	0.28	0/3514	0.55	1/4771 (0.0%)
8	MM	0.30	0/3514	0.54	0/4771
8	NC	0.28	0/3514	0.56	0/4771
8	NE	0.27	0/3507	0.54	0/4761
8	NG	0.27	0/3507	0.58	4/4761 (0.1%)
8	NI	0.27	0/3507	0.55	1/4761 (0.0%)
8	NK	0.26	0/3507	0.54	0/4761
8	NM	0.27	0/3507	0.54	1/4761 (0.0%)
8	OC	0.29	0/3523	0.55	1/4783 (0.0%)
8	OE	0.28	0/3514	0.56	2/4771 (0.0%)
8	OG	0.28	0/3523	0.53	0/4783
8	OI	0.29	0/3523	0.54	0/4783
8	OK	0.26	0/3507	0.52	0/4761
8	OM	0.29	0/3523	0.54	1/4783 (0.0%)
8	OO	0.29	0/3384	0.54	0/4588
8	PC	0.29	0/3523	0.55	1/4783 (0.0%)
8	PE	0.29	0/3514	0.54	1/4771 (0.0%)
8	PG	0.28	0/3523	0.54	0/4783
8	PI	0.27	0/3507	0.51	0/4761

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
8	PK	0.28	0/3514	0.55	1/4771 (0.0%)
8	PM	0.27	0/3507	0.53	0/4761
8	PO	0.27	0/3507	0.53	0/4761
8	QC	0.28	0/3514	0.55	0/4771
8	QE	0.28	0/3514	0.52	0/4771
8	QG	0.28	0/3514	0.55	2/4771 (0.0%)
8	QI	0.28	0/3514	0.54	0/4771
8	QK	0.27	0/3514	0.53	0/4771
8	QM	0.29	0/3514	0.55	2/4771 (0.0%)
8	QO	0.27	0/3514	0.55	0/4771
8	RC	0.28	0/3278	0.55	0/4451
8	RE	0.27	0/3448	0.54	0/4681
8	RG	0.27	0/3461	0.57	0/4699
8	RI	0.27	0/3507	0.55	0/4761
8	RK	0.28	0/3514	0.58	2/4771 (0.0%)
8	RM	0.28	0/3514	0.56	1/4771 (0.0%)
8	RO	0.27	0/3507	0.55	0/4761
8	SE	0.27	0/3442	0.56	0/4673
8	SG	0.27	0/3450	0.54	0/4684
8	SI	0.27	0/3456	0.55	0/4692
8	SK	0.26	0/3456	0.54	2/4692 (0.0%)
8	SM	0.27	0/3456	0.57	1/4692 (0.0%)
8	SO	0.27	0/3456	0.55	2/4692 (0.0%)
8	TE	0.27	0/3442	0.57	0/4673
8	TG	0.28	0/3450	0.58	0/4684
8	TI	0.27	0/3456	0.52	0/4692
8	TK	0.27	0/3442	0.53	0/4673
8	TM	0.27	0/3456	0.55	2/4692 (0.0%)
8	TO	0.28	0/3442	0.58	0/4673
8	UE	0.26	0/3456	0.52	1/4692 (0.0%)
8	UG	0.26	0/3462	0.56	2/4700 (0.0%)
8	UI	0.27	0/3462	0.56	2/4700 (0.0%)
8	UK	0.26	0/3456	0.53	0/4692
8	UM	0.26	0/3456	0.55	0/4692
8	UO	0.26	0/3456	0.54	1/4692 (0.0%)
8	VE	0.26	0/3507	0.54	0/4761
8	VG	0.28	0/3470	0.58	2/4711 (0.0%)
8	VI	0.27	0/3507	0.52	0/4761
8	VK	0.27	0/3456	0.54	0/4692
8	VM	0.27	0/3507	0.53	1/4761 (0.0%)
8	VO	0.26	0/3456	0.53	0/4692
8	WE	0.27	0/3507	0.55	0/4761
8	WG	0.26	0/3448	0.55	1/4681 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
8	WI	0.27	0/3501	0.55	0/4753
8	WK	0.29	0/3448	0.55	0/4681
8	WM	0.28	0/3507	0.57	2/4761 (0.0%)
8	WO	0.28	0/3456	0.55	0/4692
9	AB	0.30	0/3509	0.58	1/4754 (0.0%)
9	AD	0.30	0/3509	0.60	1/4754 (0.0%)
9	AF	0.31	0/3509	0.58	2/4754 (0.0%)
9	AH	0.30	0/3509	0.58	2/4754 (0.0%)
9	AJ	0.31	0/3509	0.58	1/4754 (0.0%)
9	AL	0.31	0/3509	0.59	1/4754 (0.0%)
9	BB	0.27	0/3431	0.55	0/4649
9	BD	0.28	0/3423	0.55	1/4638 (0.0%)
9	BF	0.28	0/3431	0.55	1/4649 (0.0%)
9	BH	0.29	0/3423	0.57	1/4638 (0.0%)
9	BJ	0.30	0/3448	0.59	2/4673 (0.0%)
9	BL	0.30	0/3423	0.57	1/4638 (0.0%)
9	CB	0.29	0/3436	0.59	2/4656 (0.0%)
9	CD	0.27	0/3423	0.56	0/4638
9	CF	0.29	0/3431	0.57	1/4649 (0.0%)
9	CH	0.28	0/3423	0.57	1/4638 (0.0%)
9	CJ	0.28	0/3431	0.56	1/4649 (0.0%)
9	CL	0.29	0/3423	0.56	0/4638
9	DB	0.27	0/3423	0.59	4/4638 (0.1%)
9	DD	0.28	0/3423	0.60	2/4638 (0.0%)
9	DF	0.29	0/3423	0.59	2/4638 (0.0%)
9	DH	0.28	0/3423	0.61	1/4638 (0.0%)
9	DJ	0.28	0/3423	0.59	2/4638 (0.0%)
9	DL	0.29	0/3423	0.60	3/4638 (0.1%)
9	EB	0.28	0/3423	0.58	1/4638 (0.0%)
9	ED	0.27	0/3423	0.57	1/4638 (0.0%)
9	EF	0.28	0/3423	0.58	1/4638 (0.0%)
9	EH	0.28	0/3423	0.59	3/4638 (0.1%)
9	EJ	0.27	0/3423	0.57	2/4638 (0.0%)
9	EL	0.27	0/3423	0.56	0/4638
9	EN	0.28	0/3436	0.60	1/4656 (0.0%)
9	FB	0.26	0/3423	0.55	0/4638
9	FD	0.27	0/3423	0.58	0/4638
9	FF	0.28	0/3423	0.59	0/4638
9	FH	0.28	0/3423	0.58	1/4638 (0.0%)
9	FJ	0.28	0/3423	0.58	1/4638 (0.0%)
9	FL	0.27	0/3423	0.58	0/4638
9	FN	0.27	0/3431	0.57	1/4649 (0.0%)
9	GB	0.28	0/3277	0.59	1/4441 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
9	GD	0.28	0/3423	0.55	1/4638 (0.0%)
9	GF	0.27	0/3431	0.58	2/4649 (0.0%)
9	GH	0.28	0/3423	0.58	0/4638
9	GJ	0.29	0/3448	0.60	2/4673 (0.0%)
9	GL	0.28	0/3423	0.58	0/4638
9	GN	0.26	0/3423	0.55	1/4638 (0.0%)
9	HB	0.27	0/3431	0.56	2/4649 (0.0%)
9	HD	0.27	0/3423	0.55	2/4638 (0.0%)
9	HF	0.27	0/3431	0.53	0/4649
9	HH	0.27	0/3423	0.55	1/4638 (0.0%)
9	HJ	0.28	0/3436	0.59	2/4656 (0.0%)
9	HL	0.28	0/3423	0.57	2/4638 (0.0%)
9	HN	0.28	0/3414	0.60	3/4626 (0.1%)
9	IB	0.28	0/3265	0.56	2/4424 (0.0%)
9	ID	0.27	0/3423	0.53	1/4638 (0.0%)
9	IF	0.28	0/3436	0.58	3/4656 (0.1%)
9	IH	0.29	0/3423	0.57	2/4638 (0.0%)
9	IJ	0.28	0/3443	0.56	1/4666 (0.0%)
9	IL	0.28	0/3423	0.56	2/4638 (0.0%)
9	IN	0.28	0/3431	0.57	1/4649 (0.0%)
9	JB	0.27	0/3423	0.55	0/4638
9	JD	0.27	0/3423	0.55	1/4638 (0.0%)
9	JF	0.27	0/3431	0.56	2/4649 (0.0%)
9	JH	0.28	0/3423	0.58	1/4638 (0.0%)
9	JJ	0.27	0/3423	0.54	1/4638 (0.0%)
9	JL	0.29	0/3423	0.60	3/4638 (0.1%)
9	JN	0.29	0/3423	0.60	2/4638 (0.0%)
9	KB	0.29	0/3290	0.56	2/4458 (0.0%)
9	KD	0.31	0/3457	0.57	1/4685 (0.0%)
9	KF	0.28	0/3423	0.55	1/4638 (0.0%)
9	KH	0.32	0/3457	0.58	2/4685 (0.0%)
9	KJ	0.28	0/3423	0.55	1/4638 (0.0%)
9	KL	0.31	0/3457	0.60	2/4685 (0.0%)
9	KN	0.29	0/3423	0.55	3/4638 (0.1%)
9	LB	0.29	0/3532	0.56	1/4785 (0.0%)
9	LD	0.29	0/3423	0.55	1/4638 (0.0%)
9	LF	0.30	0/3527	0.56	0/4778
9	LH	0.29	0/3423	0.55	1/4638 (0.0%)
9	LJ	0.30	0/3559	0.57	1/4821 (0.0%)
9	LL	0.29	0/3423	0.57	2/4638 (0.0%)
9	LN	0.30	0/3532	0.57	1/4785 (0.0%)
9	MB	0.30	0/3448	0.58	1/4673 (0.0%)
9	MD	0.29	0/3466	0.56	2/4697 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
9	MF	0.28	0/3457	0.56	0/4685
9	MH	0.30	0/3466	0.58	1/4697 (0.0%)
9	MJ	0.28	0/3466	0.56	2/4697 (0.0%)
9	ML	0.30	0/3466	0.61	2/4697 (0.0%)
9	MN	0.28	0/3448	0.56	0/4673
9	NB	0.28	0/3436	0.56	1/4656 (0.0%)
9	ND	0.29	0/3436	0.56	1/4656 (0.0%)
9	NF	0.28	0/3448	0.58	0/4673
9	NH	0.29	0/3436	0.57	1/4656 (0.0%)
9	NJ	0.28	0/3443	0.58	3/4666 (0.1%)
9	NL	0.29	0/3436	0.60	2/4656 (0.0%)
9	NN	0.28	0/3436	0.59	3/4656 (0.1%)
9	OB	0.30	0/3457	0.58	1/4685 (0.0%)
9	OD	0.29	0/3448	0.55	0/4673
9	OF	0.28	0/3466	0.56	2/4697 (0.0%)
9	OH	0.30	0/3448	0.58	1/4673 (0.0%)
9	OJ	0.29	0/3466	0.57	1/4697 (0.0%)
9	OL	0.29	0/3448	0.56	1/4673 (0.0%)
9	ON	0.30	0/3457	0.56	1/4685 (0.0%)
9	PD	0.29	0/3448	0.56	1/4673 (0.0%)
9	PF	0.29	0/3466	0.57	2/4697 (0.0%)
9	PH	0.28	0/3423	0.55	1/4638 (0.0%)
9	PJ	0.28	0/3448	0.56	1/4673 (0.0%)
9	PL	0.29	0/3443	0.56	1/4666 (0.0%)
9	PN	0.30	0/3448	0.57	0/4673
9	QD	0.30	0/3436	0.59	3/4656 (0.1%)
9	QF	0.28	0/3448	0.55	1/4673 (0.0%)
9	QH	0.27	0/3423	0.54	1/4638 (0.0%)
9	QJ	0.28	0/3443	0.55	0/4666
9	QL	0.27	0/3431	0.57	2/4649 (0.0%)
9	QN	0.29	0/3436	0.55	1/4656 (0.0%)
9	RD	0.28	0/3423	0.58	2/4638 (0.0%)
9	RF	0.28	0/3443	0.58	2/4666 (0.0%)
9	RH	0.27	0/3423	0.54	1/4638 (0.0%)
9	RJ	0.28	0/3436	0.58	2/4656 (0.0%)
9	RL	0.27	0/3423	0.56	0/4638
9	RN	0.27	0/3431	0.58	1/4649 (0.0%)
9	SD	0.27	0/3423	0.56	1/4638 (0.0%)
9	SF	0.28	0/3423	0.59	2/4638 (0.0%)
9	SH	0.27	0/3423	0.57	1/4638 (0.0%)
9	SJ	0.27	0/3423	0.57	2/4638 (0.0%)
9	SL	0.28	0/3423	0.59	1/4638 (0.0%)
9	SN	0.28	0/3423	0.58	3/4638 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
9	TD	0.27	0/3423	0.54	1/4638 (0.0%)
9	TF	0.28	0/3431	0.57	1/4649 (0.0%)
9	TH	0.27	0/3423	0.58	2/4638 (0.0%)
9	TJ	0.27	0/3423	0.57	2/4638 (0.0%)
9	TL	0.27	0/3423	0.59	2/4638 (0.0%)
9	TN	0.28	0/3423	0.58	1/4638 (0.0%)
9	TP	0.26	0/3373	0.57	1/4566 (0.0%)
9	UD	0.27	0/3423	0.54	1/4638 (0.0%)
9	UF	0.27	0/3431	0.55	2/4649 (0.0%)
9	UH	0.26	0/3423	0.54	0/4638
9	UJ	0.27	0/3431	0.54	0/4649
9	UL	0.27	0/3423	0.56	2/4638 (0.0%)
9	UN	0.27	0/3431	0.55	1/4649 (0.0%)
9	UP	0.27	0/3431	0.55	1/4649 (0.0%)
9	VD	0.27	0/3423	0.54	1/4638 (0.0%)
9	VF	0.28	0/3431	0.57	2/4649 (0.0%)
9	VH	0.28	0/3423	0.56	1/4638 (0.0%)
9	VJ	0.28	0/3431	0.56	1/4649 (0.0%)
9	VL	0.27	0/3423	0.55	0/4638
9	VN	0.28	0/3431	0.57	2/4649 (0.0%)
9	VP	0.26	0/3431	0.52	1/4649 (0.0%)
9	WD	0.28	0/3423	0.57	1/4638 (0.0%)
9	WF	0.29	0/3423	0.58	3/4638 (0.1%)
9	WH	0.27	0/3423	0.55	0/4638
9	WJ	0.28	0/3423	0.55	0/4638
9	WL	0.29	0/3423	0.57	1/4638 (0.0%)
9	WN	0.28	0/3431	0.56	1/4649 (0.0%)
9	WP	0.29	0/3431	0.57	1/4649 (0.0%)
10	B	0.32	0/1515	0.53	0/2006
10	C	0.34	0/3089	0.54	0/4093
11	B0	0.30	0/1594	0.54	0/2152
11	B1	0.31	0/3223	0.52	0/4347
11	B2	0.32	0/3216	0.52	0/4337
11	B3	0.31	0/2896	0.53	0/3903
11	B4	0.26	0/416	0.57	0/562
11	B5	0.23	0/253	0.32	0/352
11	B6	0.28	0/1765	0.32	0/2467
11	B7	0.28	0/1950	0.31	0/2726
11	B8	0.29	0/1955	0.31	0/2733
11	B9	0.27	0/960	0.29	0/1339
12	C0	0.32	0/291	0.60	0/395
12	C1	0.31	0/2768	0.56	1/3733 (0.0%)
12	C2	0.30	0/3239	0.57	1/4368 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
12	C3	0.30	0/3250	0.56	0/4382
12	C4	0.29	0/1803	0.53	2/2426 (0.1%)
13	D	0.28	0/1502	0.61	0/2038
14	D0	0.30	0/2209	0.53	0/2976
14	D1	0.31	0/3303	0.56	0/4452
14	D2	0.33	0/3322	0.56	0/4475
14	D3	0.31	0/2634	0.58	0/3542
14	D5	0.27	0/1581	0.30	0/2207
14	D6	0.28	0/1986	0.31	0/2775
14	D7	0.28	0/1975	0.32	0/2761
14	D8	0.27	0/1324	0.30	0/1845
15	E	0.26	0/2278	0.53	0/3085
15	F	0.25	0/2278	0.53	0/3085
16	F0	0.29	0/1286	0.59	1/1735 (0.1%)
16	F1	0.28	0/1313	0.55	0/1772
16	F2	0.23	0/775	0.35	0/1081
16	F3	0.29	0/1286	0.58	0/1735
16	F4	0.30	0/1313	0.58	1/1772 (0.1%)
16	F5	0.24	0/775	0.35	0/1081
16	F6	0.31	0/1286	0.66	2/1735 (0.1%)
16	F7	0.28	0/1313	0.56	2/1772 (0.1%)
16	F8	0.24	0/775	0.35	0/1081
16	G0	0.30	0/1302	0.58	0/1758
16	G1	0.31	0/1294	0.58	0/1746
16	G2	0.24	0/775	0.35	0/1081
16	G3	0.29	0/1286	0.52	0/1735
16	G4	0.30	0/1313	0.56	1/1772 (0.1%)
16	G5	0.23	0/775	0.34	0/1081
16	G6	0.29	0/1286	0.57	0/1735
16	G7	0.28	0/1313	0.54	0/1772
16	G8	0.23	0/775	0.34	0/1081
16	H0	0.30	0/1286	0.61	0/1735
16	H1	0.32	0/1313	0.58	0/1772
16	H2	0.24	0/775	0.36	0/1081
17	G	0.28	0/775	0.68	1/1058 (0.1%)
18	H	0.28	0/643	0.54	0/881
18	I	0.28	0/1115	0.55	0/1518
18	J	0.28	0/1120	0.58	0/1525
18	K	0.27	0/1115	0.61	0/1518
18	L	0.28	0/1115	0.57	0/1518
18	M	0.27	0/1115	0.53	0/1518
18	N	0.27	0/1120	0.52	0/1525
19	I1	0.28	0/791	0.50	0/1075

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
20	J1	0.28	0/721	0.58	0/964
20	J2	0.28	0/1892	0.58	0/2553
20	J3	0.32	0/1892	0.63	0/2553
20	J4	0.29	0/1714	0.59	0/2315
20	J5	0.30	0/525	0.66	0/711
21	K1	0.26	0/970	0.62	0/1317
22	L1	0.26	0/1075	0.58	0/1454
22	L2	0.27	0/766	0.63	1/1035 (0.1%)
23	M1	0.31	0/851	0.62	0/1153
23	M2	0.29	0/843	0.58	0/1141
23	M3	0.30	0/851	0.61	1/1153 (0.1%)
23	M4	0.29	0/851	0.57	0/1153
24	O	0.30	0/213	0.73	0/281
24	P	0.30	0/3132	0.54	1/4187 (0.0%)
24	Q	0.31	0/333	0.49	0/448
24	R	0.30	0/1836	0.52	1/2446 (0.0%)
24	S	0.30	0/1406	0.51	0/1883
25	T	0.28	0/4085	0.55	1/5532 (0.0%)
25	U	0.28	0/4093	0.56	0/5544
25	V	0.29	0/4093	0.56	0/5544
26	W	0.28	0/5192	0.59	4/7006 (0.1%)
26	X	0.28	0/5941	0.56	1/8009 (0.0%)
26	Y	0.28	0/5941	0.57	1/8009 (0.0%)
26	Z	0.28	0/4337	0.58	2/5833 (0.0%)
27	XA	0.27	0/1583	0.55	0/2137
27	XB	0.26	0/1583	0.55	0/2137
27	XC	0.26	0/1583	0.55	0/2137
27	XD	0.27	0/1583	0.57	1/2137 (0.0%)
27	XE	0.26	0/1583	0.56	1/2137 (0.0%)
27	XF	0.27	0/1583	0.56	0/2137
27	XG	0.27	0/1583	0.56	0/2137
28	YB	0.27	0/1814	0.53	0/2452
28	YC	0.26	0/1814	0.52	0/2452
28	YD	0.27	0/1814	0.54	1/2452 (0.0%)
28	YE	0.26	0/1814	0.50	0/2452
28	YF	0.28	0/1814	0.55	1/2452 (0.0%)
28	YG	0.28	0/1814	0.55	0/2452
29	a	0.30	0/1473	0.60	0/1951
29	b	0.34	0/2890	0.62	0/3818
29	c	0.31	0/2430	0.60	0/3216
29	d	0.33	0/1869	0.63	1/2472 (0.0%)
30	e	0.27	0/4811	0.58	1/6512 (0.0%)
30	f	0.27	0/4811	0.59	2/6512 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
30	g	0.27	0/4811	0.60	1/6512 (0.0%)
31	h	0.30	0/1230	0.60	0/1643
31	i	0.26	0/2065	0.49	0/2773
31	j	0.27	0/2052	0.52	0/2755
31	k	0.28	0/2065	0.50	0/2773
32	l	0.26	0/934	0.53	0/1271
32	m	0.28	0/934	0.51	0/1271
32	n	0.26	0/934	0.51	0/1271
33	o	0.32	0/3512	0.54	0/4648
33	o1	0.25	0/304	0.55	0/406
33	p	0.30	0/1309	0.51	0/1754
34	q	0.25	0/930	0.48	0/1259
34	r	0.26	0/930	0.55	0/1259
34	s	0.27	0/930	0.55	0/1259
35	y	0.28	0/510	0.59	0/691
35	z	0.27	0/916	0.60	0/1244
All	All	0.28	0/1283717	0.56	333/1739902 (0.0%)

There are no bond length outliers.

The worst 5 of 333 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	CK	32	PRO	CA-N-CD	-10.04	97.44	111.50
8	FG	173	PRO	CA-N-CD	-9.64	98.00	111.50
8	FE	298	PRO	CA-N-CD	-9.59	98.08	111.50
9	HN	271	ALA	C-N-CD	-9.50	99.69	120.60
9	KL	209	ASP	CB-CG-OD1	8.42	125.88	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	50/229 (22%)	44 (88%)	6 (12%)	0	100	100
1	7	138/229 (60%)	127 (92%)	11 (8%)	0	100	100
2	1	266/833 (32%)	259 (97%)	7 (3%)	0	100	100
2	2	442/833 (53%)	436 (99%)	6 (1%)	0	100	100
3	3	295/514 (57%)	292 (99%)	3 (1%)	0	100	100
3	4	213/514 (41%)	213 (100%)	0	0	100	100
4	5	369/376 (98%)	358 (97%)	11 (3%)	0	100	100
4	6	369/376 (98%)	361 (98%)	8 (2%)	0	100	100
5	8	166/194 (86%)	151 (91%)	15 (9%)	0	100	100
5	9	46/194 (24%)	41 (89%)	5 (11%)	0	100	100
6	A	48/101 (48%)	48 (100%)	0	0	100	100
7	A0	216/418 (52%)	215 (100%)	1 (0%)	0	100	100
7	A1	389/418 (93%)	383 (98%)	6 (2%)	0	100	100
7	A2	389/418 (93%)	382 (98%)	7 (2%)	0	100	100
7	A3	329/418 (79%)	324 (98%)	5 (2%)	0	100	100
7	A4	33/418 (8%)	32 (97%)	1 (3%)	0	100	100
8	AA	437/451 (97%)	428 (98%)	8 (2%)	1 (0%)	47	79
8	AC	437/451 (97%)	425 (97%)	11 (2%)	1 (0%)	47	79
8	AE	437/451 (97%)	426 (98%)	11 (2%)	0	100	100
8	AG	437/451 (97%)	425 (97%)	12 (3%)	0	100	100
8	AI	437/451 (97%)	424 (97%)	12 (3%)	1 (0%)	47	79
8	AK	437/451 (97%)	428 (98%)	9 (2%)	0	100	100
8	AM	437/451 (97%)	424 (97%)	13 (3%)	0	100	100
8	BA	428/451 (95%)	414 (97%)	13 (3%)	1 (0%)	47	79
8	BC	437/451 (97%)	425 (97%)	11 (2%)	1 (0%)	47	79

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	BE	428/451 (95%)	416 (97%)	12 (3%)	0	100	100
8	BG	437/451 (97%)	420 (96%)	17 (4%)	0	100	100
8	BI	428/451 (95%)	415 (97%)	13 (3%)	0	100	100
8	BK	437/451 (97%)	420 (96%)	17 (4%)	0	100	100
8	BM	429/451 (95%)	419 (98%)	10 (2%)	0	100	100
8	CA	428/451 (95%)	418 (98%)	9 (2%)	1 (0%)	47	79
8	CC	437/451 (97%)	423 (97%)	13 (3%)	1 (0%)	47	79
8	CE	426/451 (94%)	413 (97%)	13 (3%)	0	100	100
8	CG	437/451 (97%)	418 (96%)	19 (4%)	0	100	100
8	CI	427/451 (95%)	412 (96%)	15 (4%)	0	100	100
8	CK	437/451 (97%)	425 (97%)	12 (3%)	0	100	100
8	CM	427/451 (95%)	414 (97%)	13 (3%)	0	100	100
8	DA	375/451 (83%)	364 (97%)	11 (3%)	0	100	100
8	DC	426/451 (94%)	413 (97%)	13 (3%)	0	100	100
8	DE	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
8	DG	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
8	DI	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
8	DK	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
8	DM	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
8	EC	437/451 (97%)	423 (97%)	13 (3%)	1 (0%)	47	79
8	EE	437/451 (97%)	426 (98%)	11 (2%)	0	100	100
8	EG	436/451 (97%)	412 (94%)	24 (6%)	0	100	100
8	EI	437/451 (97%)	418 (96%)	19 (4%)	0	100	100
8	EK	436/451 (97%)	420 (96%)	16 (4%)	0	100	100
8	EM	436/451 (97%)	419 (96%)	17 (4%)	0	100	100
8	FC	427/451 (95%)	416 (97%)	11 (3%)	0	100	100
8	FE	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
8	FG	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
8	FI	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
8	FK	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
8	FM	426/451 (94%)	410 (96%)	16 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	GC	431/451 (96%)	420 (97%)	10 (2%)	1 (0%)	47	79
8	GE	426/451 (94%)	420 (99%)	6 (1%)	0	100	100
8	GG	427/451 (95%)	414 (97%)	13 (3%)	0	100	100
8	GI	426/451 (94%)	419 (98%)	7 (2%)	0	100	100
8	GK	428/451 (95%)	422 (99%)	6 (1%)	0	100	100
8	GM	430/451 (95%)	417 (97%)	13 (3%)	0	100	100
8	HC	427/451 (95%)	414 (97%)	12 (3%)	1 (0%)	47	79
8	HE	428/451 (95%)	420 (98%)	8 (2%)	0	100	100
8	HG	428/451 (95%)	414 (97%)	14 (3%)	0	100	100
8	HI	428/451 (95%)	419 (98%)	9 (2%)	0	100	100
8	HK	427/451 (95%)	416 (97%)	11 (3%)	0	100	100
8	HM	427/451 (95%)	417 (98%)	10 (2%)	0	100	100
8	HO	381/451 (84%)	369 (97%)	12 (3%)	0	100	100
8	IC	429/451 (95%)	422 (98%)	6 (1%)	1 (0%)	47	79
8	IE	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
8	IG	437/451 (97%)	423 (97%)	14 (3%)	0	100	100
8	II	428/451 (95%)	416 (97%)	12 (3%)	0	100	100
8	IK	437/451 (97%)	427 (98%)	10 (2%)	0	100	100
8	IM	427/451 (95%)	414 (97%)	13 (3%)	0	100	100
8	IO	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
8	JC	437/451 (97%)	423 (97%)	14 (3%)	0	100	100
8	JE	426/451 (94%)	412 (97%)	14 (3%)	0	100	100
8	JG	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
8	JI	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
8	JK	427/451 (95%)	411 (96%)	16 (4%)	0	100	100
8	JM	426/451 (94%)	413 (97%)	13 (3%)	0	100	100
8	KC	429/451 (95%)	418 (97%)	10 (2%)	1 (0%)	47	79
8	KE	428/451 (95%)	415 (97%)	13 (3%)	0	100	100
8	KG	429/451 (95%)	417 (97%)	12 (3%)	0	100	100
8	KI	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
8	KK	429/451 (95%)	419 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	KM	436/451 (97%)	421 (97%)	15 (3%)	0	100	100
8	KO	428/451 (95%)	413 (96%)	15 (4%)	0	100	100
8	LC	429/451 (95%)	418 (97%)	10 (2%)	1 (0%)	47	79
8	LE	437/451 (97%)	422 (97%)	15 (3%)	0	100	100
8	LG	430/451 (95%)	417 (97%)	13 (3%)	0	100	100
8	LI	432/451 (96%)	420 (97%)	12 (3%)	0	100	100
8	LK	429/451 (95%)	420 (98%)	9 (2%)	0	100	100
8	LM	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
8	MC	438/451 (97%)	426 (97%)	11 (2%)	1 (0%)	47	79
8	ME	428/451 (95%)	411 (96%)	17 (4%)	0	100	100
8	MG	428/451 (95%)	417 (97%)	11 (3%)	0	100	100
8	MI	429/451 (95%)	418 (97%)	11 (3%)	0	100	100
8	MK	438/451 (97%)	428 (98%)	10 (2%)	0	100	100
8	MM	438/451 (97%)	420 (96%)	18 (4%)	0	100	100
8	NC	438/451 (97%)	423 (97%)	14 (3%)	1 (0%)	47	79
8	NE	437/451 (97%)	424 (97%)	13 (3%)	0	100	100
8	NG	437/451 (97%)	424 (97%)	12 (3%)	1 (0%)	47	79
8	NI	437/451 (97%)	427 (98%)	10 (2%)	0	100	100
8	NK	437/451 (97%)	429 (98%)	8 (2%)	0	100	100
8	NM	437/451 (97%)	424 (97%)	13 (3%)	0	100	100
8	OC	439/451 (97%)	428 (98%)	10 (2%)	1 (0%)	47	79
8	OE	438/451 (97%)	427 (98%)	11 (2%)	0	100	100
8	OG	439/451 (97%)	424 (97%)	15 (3%)	0	100	100
8	OI	439/451 (97%)	429 (98%)	10 (2%)	0	100	100
8	OK	437/451 (97%)	428 (98%)	9 (2%)	0	100	100
8	OM	439/451 (97%)	425 (97%)	14 (3%)	0	100	100
8	OO	416/451 (92%)	402 (97%)	14 (3%)	0	100	100
8	PC	439/451 (97%)	426 (97%)	12 (3%)	1 (0%)	47	79
8	PE	438/451 (97%)	425 (97%)	13 (3%)	0	100	100
8	PG	439/451 (97%)	420 (96%)	19 (4%)	0	100	100
8	PI	437/451 (97%)	424 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	PK	438/451 (97%)	426 (97%)	12 (3%)	0	100	100
8	PM	437/451 (97%)	423 (97%)	14 (3%)	0	100	100
8	PO	437/451 (97%)	425 (97%)	12 (3%)	0	100	100
8	QC	438/451 (97%)	420 (96%)	17 (4%)	1 (0%)	47	79
8	QE	438/451 (97%)	424 (97%)	14 (3%)	0	100	100
8	QG	438/451 (97%)	420 (96%)	17 (4%)	1 (0%)	47	79
8	QI	438/451 (97%)	422 (96%)	16 (4%)	0	100	100
8	QK	438/451 (97%)	425 (97%)	13 (3%)	0	100	100
8	QM	438/451 (97%)	425 (97%)	13 (3%)	0	100	100
8	QO	438/451 (97%)	418 (95%)	20 (5%)	0	100	100
8	RC	405/451 (90%)	389 (96%)	16 (4%)	0	100	100
8	RE	426/451 (94%)	418 (98%)	8 (2%)	0	100	100
8	RG	428/451 (95%)	410 (96%)	18 (4%)	0	100	100
8	RI	437/451 (97%)	417 (95%)	20 (5%)	0	100	100
8	RK	438/451 (97%)	427 (98%)	11 (2%)	0	100	100
8	RM	438/451 (97%)	421 (96%)	17 (4%)	0	100	100
8	RO	437/451 (97%)	420 (96%)	17 (4%)	0	100	100
8	SE	425/451 (94%)	415 (98%)	10 (2%)	0	100	100
8	SG	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
8	SI	427/451 (95%)	410 (96%)	17 (4%)	0	100	100
8	SK	427/451 (95%)	417 (98%)	10 (2%)	0	100	100
8	SM	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
8	SO	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
8	TE	425/451 (94%)	414 (97%)	11 (3%)	0	100	100
8	TG	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
8	TI	427/451 (95%)	417 (98%)	10 (2%)	0	100	100
8	TK	425/451 (94%)	412 (97%)	13 (3%)	0	100	100
8	TM	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
8	TO	425/451 (94%)	413 (97%)	12 (3%)	0	100	100
8	UE	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
8	UG	428/451 (95%)	417 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	UI	428/451 (95%)	415 (97%)	13 (3%)	0	100	100
8	UK	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
8	UM	427/451 (95%)	417 (98%)	10 (2%)	0	100	100
8	UO	427/451 (95%)	416 (97%)	11 (3%)	0	100	100
8	VE	437/451 (97%)	420 (96%)	17 (4%)	0	100	100
8	VG	429/451 (95%)	413 (96%)	16 (4%)	0	100	100
8	VI	437/451 (97%)	423 (97%)	13 (3%)	1 (0%)	47	79
8	VK	427/451 (95%)	419 (98%)	8 (2%)	0	100	100
8	VM	437/451 (97%)	428 (98%)	9 (2%)	0	100	100
8	VO	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
8	WE	437/451 (97%)	423 (97%)	13 (3%)	1 (0%)	47	79
8	WG	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
8	WI	436/451 (97%)	420 (96%)	16 (4%)	0	100	100
8	WK	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
8	WM	437/451 (97%)	415 (95%)	22 (5%)	0	100	100
8	WO	427/451 (95%)	408 (96%)	19 (4%)	0	100	100
9	AB	435/445 (98%)	418 (96%)	17 (4%)	0	100	100
9	AD	435/445 (98%)	419 (96%)	16 (4%)	0	100	100
9	AF	435/445 (98%)	415 (95%)	20 (5%)	0	100	100
9	AH	435/445 (98%)	417 (96%)	17 (4%)	1 (0%)	47	79
9	AJ	435/445 (98%)	418 (96%)	16 (4%)	1 (0%)	47	79
9	AL	435/445 (98%)	410 (94%)	24 (6%)	1 (0%)	47	79
9	BB	425/445 (96%)	405 (95%)	20 (5%)	0	100	100
9	BD	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	BF	425/445 (96%)	409 (96%)	16 (4%)	0	100	100
9	BH	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
9	BJ	428/445 (96%)	413 (96%)	13 (3%)	2 (0%)	29	68
9	BL	424/445 (95%)	408 (96%)	15 (4%)	1 (0%)	47	79
9	CB	426/445 (96%)	413 (97%)	13 (3%)	0	100	100
9	CD	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	CF	425/445 (96%)	410 (96%)	14 (3%)	1 (0%)	47	79

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	CH	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	47	79
9	CJ	425/445 (96%)	407 (96%)	16 (4%)	2 (0%)	29	68
9	CL	424/445 (95%)	410 (97%)	13 (3%)	1 (0%)	47	79
9	DB	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	47	79
9	DD	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	DF	424/445 (95%)	407 (96%)	16 (4%)	1 (0%)	47	79
9	DH	424/445 (95%)	396 (93%)	28 (7%)	0	100	100
9	DJ	424/445 (95%)	403 (95%)	20 (5%)	1 (0%)	47	79
9	DL	424/445 (95%)	397 (94%)	26 (6%)	1 (0%)	47	79
9	EB	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	ED	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	EF	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	EH	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	EJ	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	EL	424/445 (95%)	411 (97%)	12 (3%)	1 (0%)	47	79
9	EN	426/445 (96%)	417 (98%)	9 (2%)	0	100	100
9	FB	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
9	FD	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	FF	424/445 (95%)	410 (97%)	13 (3%)	1 (0%)	47	79
9	FH	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
9	FJ	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
9	FL	424/445 (95%)	405 (96%)	17 (4%)	2 (0%)	29	68
9	FN	425/445 (96%)	416 (98%)	9 (2%)	0	100	100
9	GB	406/445 (91%)	396 (98%)	10 (2%)	0	100	100
9	GD	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	GF	425/445 (96%)	406 (96%)	19 (4%)	0	100	100
9	GH	424/445 (95%)	406 (96%)	18 (4%)	0	100	100
9	GJ	428/445 (96%)	408 (95%)	19 (4%)	1 (0%)	47	79
9	GL	424/445 (95%)	403 (95%)	21 (5%)	0	100	100
9	GN	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
9	HB	425/445 (96%)	408 (96%)	15 (4%)	2 (0%)	29	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	HD	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	HF	425/445 (96%)	405 (95%)	19 (4%)	1 (0%)	47	79
9	HH	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	47	79
9	HJ	426/445 (96%)	411 (96%)	14 (3%)	1 (0%)	47	79
9	HL	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	HN	423/445 (95%)	407 (96%)	16 (4%)	0	100	100
9	IB	401/445 (90%)	385 (96%)	15 (4%)	1 (0%)	47	79
9	ID	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	IF	426/445 (96%)	408 (96%)	18 (4%)	0	100	100
9	IH	424/445 (95%)	404 (95%)	19 (4%)	1 (0%)	47	79
9	IJ	427/445 (96%)	410 (96%)	17 (4%)	0	100	100
9	IL	424/445 (95%)	403 (95%)	21 (5%)	0	100	100
9	IN	425/445 (96%)	406 (96%)	18 (4%)	1 (0%)	47	79
9	JB	424/445 (95%)	406 (96%)	18 (4%)	0	100	100
9	JD	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	JF	425/445 (96%)	409 (96%)	15 (4%)	1 (0%)	47	79
9	JH	424/445 (95%)	402 (95%)	22 (5%)	0	100	100
9	JJ	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	JL	424/445 (95%)	401 (95%)	22 (5%)	1 (0%)	47	79
9	JN	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
9	KB	408/445 (92%)	392 (96%)	16 (4%)	0	100	100
9	KD	429/445 (96%)	415 (97%)	14 (3%)	0	100	100
9	KF	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
9	KH	429/445 (96%)	416 (97%)	13 (3%)	0	100	100
9	KJ	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	KL	429/445 (96%)	410 (96%)	18 (4%)	1 (0%)	47	79
9	KN	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
9	LB	438/445 (98%)	423 (97%)	15 (3%)	0	100	100
9	LD	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	LF	437/445 (98%)	418 (96%)	19 (4%)	0	100	100
9	LH	424/445 (95%)	403 (95%)	21 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	LJ	441/445 (99%)	424 (96%)	17 (4%)	0	100	100
9	LL	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	LN	438/445 (98%)	421 (96%)	17 (4%)	0	100	100
9	MB	428/445 (96%)	414 (97%)	14 (3%)	0	100	100
9	MD	430/445 (97%)	416 (97%)	13 (3%)	1 (0%)	47	79
9	MF	429/445 (96%)	414 (96%)	15 (4%)	0	100	100
9	MH	430/445 (97%)	415 (96%)	14 (3%)	1 (0%)	47	79
9	MJ	430/445 (97%)	418 (97%)	12 (3%)	0	100	100
9	ML	430/445 (97%)	414 (96%)	15 (4%)	1 (0%)	47	79
9	MN	428/445 (96%)	411 (96%)	17 (4%)	0	100	100
9	NB	426/445 (96%)	410 (96%)	15 (4%)	1 (0%)	47	79
9	ND	426/445 (96%)	411 (96%)	15 (4%)	0	100	100
9	NF	428/445 (96%)	406 (95%)	22 (5%)	0	100	100
9	NH	426/445 (96%)	404 (95%)	21 (5%)	1 (0%)	47	79
9	NJ	427/445 (96%)	409 (96%)	18 (4%)	0	100	100
9	NL	426/445 (96%)	404 (95%)	22 (5%)	0	100	100
9	NN	426/445 (96%)	404 (95%)	21 (5%)	1 (0%)	47	79
9	OB	429/445 (96%)	412 (96%)	16 (4%)	1 (0%)	47	79
9	OD	428/445 (96%)	412 (96%)	16 (4%)	0	100	100
9	OF	430/445 (97%)	413 (96%)	17 (4%)	0	100	100
9	OH	428/445 (96%)	409 (96%)	19 (4%)	0	100	100
9	OJ	430/445 (97%)	415 (96%)	15 (4%)	0	100	100
9	OL	428/445 (96%)	408 (95%)	18 (4%)	2 (0%)	29	68
9	ON	429/445 (96%)	414 (96%)	14 (3%)	1 (0%)	47	79
9	PD	428/445 (96%)	410 (96%)	16 (4%)	2 (0%)	29	68
9	PF	430/445 (97%)	411 (96%)	18 (4%)	1 (0%)	47	79
9	PH	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
9	PJ	428/445 (96%)	414 (97%)	13 (3%)	1 (0%)	47	79
9	PL	427/445 (96%)	407 (95%)	20 (5%)	0	100	100
9	PN	428/445 (96%)	404 (94%)	24 (6%)	0	100	100
9	QD	426/445 (96%)	407 (96%)	19 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	QF	428/445 (96%)	411 (96%)	16 (4%)	1 (0%)	47	79
9	QH	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	QJ	427/445 (96%)	408 (96%)	19 (4%)	0	100	100
9	QL	425/445 (96%)	414 (97%)	11 (3%)	0	100	100
9	QN	426/445 (96%)	408 (96%)	18 (4%)	0	100	100
9	RD	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	RF	427/445 (96%)	410 (96%)	17 (4%)	0	100	100
9	RH	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	47	79
9	RJ	426/445 (96%)	408 (96%)	17 (4%)	1 (0%)	47	79
9	RL	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
9	RN	425/445 (96%)	409 (96%)	16 (4%)	0	100	100
9	SD	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	SF	424/445 (95%)	406 (96%)	18 (4%)	0	100	100
9	SH	424/445 (95%)	412 (97%)	12 (3%)	0	100	100
9	SJ	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	SL	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	SN	424/445 (95%)	408 (96%)	15 (4%)	1 (0%)	47	79
9	TD	424/445 (95%)	413 (97%)	11 (3%)	0	100	100
9	TF	425/445 (96%)	403 (95%)	22 (5%)	0	100	100
9	TH	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
9	TJ	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
9	TL	424/445 (95%)	400 (94%)	24 (6%)	0	100	100
9	TN	424/445 (95%)	402 (95%)	22 (5%)	0	100	100
9	TP	417/445 (94%)	402 (96%)	15 (4%)	0	100	100
9	UD	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
9	UF	425/445 (96%)	411 (97%)	13 (3%)	1 (0%)	47	79
9	UH	424/445 (95%)	413 (97%)	11 (3%)	0	100	100
9	UJ	425/445 (96%)	407 (96%)	18 (4%)	0	100	100
9	UL	424/445 (95%)	411 (97%)	12 (3%)	1 (0%)	47	79
9	UN	425/445 (96%)	407 (96%)	17 (4%)	1 (0%)	47	79
9	UP	425/445 (96%)	412 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	VD	424/445 (95%)	411 (97%)	13 (3%)	0	100	100
9	VF	425/445 (96%)	404 (95%)	20 (5%)	1 (0%)	47	79
9	VH	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
9	VJ	425/445 (96%)	408 (96%)	16 (4%)	1 (0%)	47	79
9	VL	424/445 (95%)	408 (96%)	15 (4%)	1 (0%)	47	79
9	VN	425/445 (96%)	406 (96%)	18 (4%)	1 (0%)	47	79
9	VP	425/445 (96%)	411 (97%)	14 (3%)	0	100	100
9	WD	424/445 (95%)	412 (97%)	11 (3%)	1 (0%)	47	79
9	WF	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
9	WH	424/445 (95%)	401 (95%)	23 (5%)	0	100	100
9	WJ	424/445 (95%)	401 (95%)	23 (5%)	0	100	100
9	WL	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
9	WN	425/445 (96%)	401 (94%)	24 (6%)	0	100	100
9	WP	425/445 (96%)	405 (95%)	19 (4%)	1 (0%)	47	79
10	B	178/495 (36%)	177 (99%)	1 (1%)	0	100	100
10	C	354/495 (72%)	352 (99%)	2 (1%)	0	100	100
11	B0	189/430 (44%)	188 (100%)	1 (0%)	0	100	100
11	B1	390/430 (91%)	383 (98%)	7 (2%)	0	100	100
11	B2	389/430 (90%)	381 (98%)	8 (2%)	0	100	100
11	B3	352/430 (82%)	343 (97%)	9 (3%)	0	100	100
11	B4	49/430 (11%)	47 (96%)	2 (4%)	0	100	100
11	B5	49/430 (11%)	47 (96%)	2 (4%)	0	100	100
11	B6	352/430 (82%)	348 (99%)	4 (1%)	0	100	100
11	B7	389/430 (90%)	385 (99%)	4 (1%)	0	100	100
11	B8	390/430 (91%)	385 (99%)	5 (1%)	0	100	100
11	B9	189/430 (44%)	189 (100%)	0	0	100	100
12	C0	31/490 (6%)	30 (97%)	1 (3%)	0	100	100
12	C1	332/490 (68%)	326 (98%)	6 (2%)	0	100	100
12	C2	391/490 (80%)	385 (98%)	5 (1%)	1 (0%)	41	75
12	C3	392/490 (80%)	379 (97%)	12 (3%)	1 (0%)	41	75
12	C4	215/490 (44%)	211 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	D	177/485 (36%)	165 (93%)	12 (7%)	0	100	100
14	D0	260/435 (60%)	256 (98%)	4 (2%)	0	100	100
14	D1	394/435 (91%)	389 (99%)	5 (1%)	0	100	100
14	D2	396/435 (91%)	391 (99%)	5 (1%)	0	100	100
14	D3	313/435 (72%)	308 (98%)	5 (2%)	0	100	100
14	D5	313/435 (72%)	309 (99%)	4 (1%)	0	100	100
14	D6	396/435 (91%)	390 (98%)	6 (2%)	0	100	100
14	D7	394/435 (91%)	383 (97%)	11 (3%)	0	100	100
14	D8	260/435 (60%)	257 (99%)	3 (1%)	0	100	100
15	E	275/301 (91%)	265 (96%)	10 (4%)	0	100	100
15	F	275/301 (91%)	267 (97%)	8 (3%)	0	100	100
16	F0	155/222 (70%)	150 (97%)	4 (3%)	1 (1%)	25	64
16	F1	158/222 (71%)	152 (96%)	6 (4%)	0	100	100
16	F2	154/222 (69%)	150 (97%)	3 (2%)	1 (1%)	25	64
16	F3	155/222 (70%)	150 (97%)	5 (3%)	0	100	100
16	F4	158/222 (71%)	155 (98%)	3 (2%)	0	100	100
16	F5	154/222 (69%)	150 (97%)	3 (2%)	1 (1%)	25	64
16	F6	155/222 (70%)	148 (96%)	7 (4%)	0	100	100
16	F7	158/222 (71%)	150 (95%)	8 (5%)	0	100	100
16	F8	154/222 (69%)	150 (97%)	3 (2%)	1 (1%)	25	64
16	G0	157/222 (71%)	150 (96%)	7 (4%)	0	100	100
16	G1	156/222 (70%)	148 (95%)	8 (5%)	0	100	100
16	G2	154/222 (69%)	149 (97%)	5 (3%)	0	100	100
16	G3	155/222 (70%)	150 (97%)	5 (3%)	0	100	100
16	G4	158/222 (71%)	150 (95%)	8 (5%)	0	100	100
16	G5	154/222 (69%)	151 (98%)	3 (2%)	0	100	100
16	G6	155/222 (70%)	150 (97%)	5 (3%)	0	100	100
16	G7	158/222 (71%)	149 (94%)	9 (6%)	0	100	100
16	G8	154/222 (69%)	149 (97%)	5 (3%)	0	100	100
16	H0	155/222 (70%)	151 (97%)	3 (2%)	1 (1%)	25	64
16	H1	158/222 (71%)	153 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	H2	154/222 (69%)	149 (97%)	5 (3%)	0	100	100
17	G	92/121 (76%)	88 (96%)	4 (4%)	0	100	100
18	H	76/275 (28%)	72 (95%)	3 (4%)	1 (1%)	12	50
18	I	137/275 (50%)	131 (96%)	6 (4%)	0	100	100
18	J	138/275 (50%)	131 (95%)	6 (4%)	1 (1%)	22	61
18	K	137/275 (50%)	134 (98%)	2 (2%)	1 (1%)	22	61
18	L	137/275 (50%)	131 (96%)	6 (4%)	0	100	100
18	M	137/275 (50%)	131 (96%)	5 (4%)	1 (1%)	22	61
18	N	138/275 (50%)	130 (94%)	7 (5%)	1 (1%)	22	61
19	I1	87/150 (58%)	85 (98%)	2 (2%)	0	100	100
20	J1	75/284 (26%)	72 (96%)	3 (4%)	0	100	100
20	J2	218/284 (77%)	209 (96%)	8 (4%)	1 (0%)	29	68
20	J3	218/284 (77%)	208 (95%)	8 (4%)	2 (1%)	17	57
20	J4	197/284 (69%)	186 (94%)	10 (5%)	1 (0%)	29	68
20	J5	63/284 (22%)	58 (92%)	4 (6%)	1 (2%)	9	46
21	K1	109/134 (81%)	100 (92%)	9 (8%)	0	100	100
22	L1	125/147 (85%)	116 (93%)	9 (7%)	0	100	100
22	L2	88/147 (60%)	83 (94%)	5 (6%)	0	100	100
23	M1	98/201 (49%)	94 (96%)	4 (4%)	0	100	100
23	M2	97/201 (48%)	94 (97%)	3 (3%)	0	100	100
23	M3	98/201 (49%)	95 (97%)	3 (3%)	0	100	100
23	M4	98/201 (49%)	95 (97%)	3 (3%)	0	100	100
24	O	23/382 (6%)	23 (100%)	0	0	100	100
24	P	366/382 (96%)	359 (98%)	6 (2%)	1 (0%)	41	75
24	Q	38/382 (10%)	37 (97%)	1 (3%)	0	100	100
24	R	215/382 (56%)	215 (100%)	0	0	100	100
24	S	163/382 (43%)	161 (99%)	2 (1%)	0	100	100
25	T	478/640 (75%)	447 (94%)	31 (6%)	0	100	100
25	U	479/640 (75%)	451 (94%)	28 (6%)	0	100	100
25	V	479/640 (75%)	454 (95%)	25 (5%)	0	100	100
26	W	604/749 (81%)	571 (94%)	32 (5%)	1 (0%)	47	79

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	X	689/749 (92%)	638 (93%)	49 (7%)	2 (0%)	41	75
26	Y	689/749 (92%)	642 (93%)	46 (7%)	1 (0%)	51	83
26	Z	498/749 (66%)	468 (94%)	30 (6%)	0	100	100
27	XA	184/193 (95%)	178 (97%)	6 (3%)	0	100	100
27	XB	184/193 (95%)	177 (96%)	7 (4%)	0	100	100
27	XC	184/193 (95%)	178 (97%)	6 (3%)	0	100	100
27	XD	184/193 (95%)	178 (97%)	6 (3%)	0	100	100
27	XE	184/193 (95%)	175 (95%)	9 (5%)	0	100	100
27	XF	184/193 (95%)	174 (95%)	10 (5%)	0	100	100
27	XG	184/193 (95%)	177 (96%)	7 (4%)	0	100	100
28	YB	218/257 (85%)	212 (97%)	6 (3%)	0	100	100
28	YC	218/257 (85%)	213 (98%)	5 (2%)	0	100	100
28	YD	218/257 (85%)	210 (96%)	8 (4%)	0	100	100
28	YE	218/257 (85%)	215 (99%)	3 (1%)	0	100	100
28	YF	218/257 (85%)	215 (99%)	3 (1%)	0	100	100
28	YG	218/257 (85%)	211 (97%)	7 (3%)	0	100	100
29	a	168/551 (30%)	167 (99%)	1 (1%)	0	100	100
29	b	332/551 (60%)	332 (100%)	0	0	100	100
29	c	280/551 (51%)	277 (99%)	3 (1%)	0	100	100
29	d	216/551 (39%)	216 (100%)	0	0	100	100
30	e	608/620 (98%)	582 (96%)	24 (4%)	2 (0%)	41	75
30	f	608/620 (98%)	583 (96%)	25 (4%)	0	100	100
30	g	608/620 (98%)	582 (96%)	26 (4%)	0	100	100
31	h	144/256 (56%)	142 (99%)	2 (1%)	0	100	100
31	i	248/256 (97%)	242 (98%)	5 (2%)	1 (0%)	34	71
31	j	246/256 (96%)	244 (99%)	2 (1%)	0	100	100
31	k	248/256 (97%)	244 (98%)	4 (2%)	0	100	100
32	l	115/177 (65%)	110 (96%)	5 (4%)	0	100	100
32	m	115/177 (65%)	112 (97%)	2 (2%)	1 (1%)	17	57
32	n	115/177 (65%)	111 (96%)	3 (3%)	1 (1%)	17	57
33	o	402/552 (73%)	400 (100%)	2 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	o1	34/552 (6%)	33 (97%)	1 (3%)	0	100	100
33	p	156/552 (28%)	153 (98%)	3 (2%)	0	100	100
34	q	108/169 (64%)	102 (94%)	6 (6%)	0	100	100
34	r	108/169 (64%)	98 (91%)	10 (9%)	0	100	100
34	s	108/169 (64%)	103 (95%)	5 (5%)	0	100	100
35	y	61/136 (45%)	59 (97%)	2 (3%)	0	100	100
35	z	109/136 (80%)	104 (95%)	5 (5%)	0	100	100
All	All	159406/181357 (88%)	153891 (96%)	5408 (3%)	107 (0%)	54	83

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	AC	98	ASP
8	BC	98	ASP
12	C2	213	ASP
12	C3	407	PRO
9	DF	272	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/209 (22%)	47 (100%)	0	100	100
1	7	135/209 (65%)	135 (100%)	0	100	100
2	1	243/724 (34%)	242 (100%)	1 (0%)	91	97
2	2	392/724 (54%)	391 (100%)	1 (0%)	92	97
3	3	274/470 (58%)	273 (100%)	1 (0%)	91	97
3	4	197/470 (42%)	197 (100%)	0	100	100
4	5	315/320 (98%)	315 (100%)	0	100	100
4	6	315/320 (98%)	315 (100%)	0	100	100
5	8	157/181 (87%)	156 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	9	47/181 (26%)	47 (100%)	0	100	100
6	A	44/90 (49%)	44 (100%)	0	100	100
7	A0	195/376 (52%)	194 (100%)	1 (0%)	88	95
7	A1	356/376 (95%)	356 (100%)	0	100	100
7	A2	356/376 (95%)	355 (100%)	1 (0%)	92	97
7	A3	305/376 (81%)	305 (100%)	0	100	100
7	A4	31/376 (8%)	31 (100%)	0	100	100
8	AA	369/378 (98%)	367 (100%)	2 (0%)	88	95
8	AC	369/378 (98%)	369 (100%)	0	100	100
8	AE	369/378 (98%)	367 (100%)	2 (0%)	88	95
8	AG	369/378 (98%)	369 (100%)	0	100	100
8	AI	369/378 (98%)	367 (100%)	2 (0%)	88	95
8	AK	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	AM	369/378 (98%)	367 (100%)	2 (0%)	88	95
8	BA	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	BC	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	BE	364/378 (96%)	364 (100%)	0	100	100
8	BG	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	BI	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	BK	369/378 (98%)	369 (100%)	0	100	100
8	BM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	CA	365/378 (97%)	365 (100%)	0	100	100
8	CC	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	CE	363/378 (96%)	363 (100%)	0	100	100
8	CG	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	CI	364/378 (96%)	364 (100%)	0	100	100
8	CK	369/378 (98%)	369 (100%)	0	100	100
8	CM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	DA	327/378 (86%)	326 (100%)	1 (0%)	92	97
8	DC	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	DE	364/378 (96%)	363 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	DG	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	DI	363/378 (96%)	361 (99%)	2 (1%)	86	94
8	DK	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	DM	364/378 (96%)	364 (100%)	0	100	100
8	EC	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	EE	369/378 (98%)	369 (100%)	0	100	100
8	EG	368/378 (97%)	367 (100%)	1 (0%)	92	97
8	EI	369/378 (98%)	369 (100%)	0	100	100
8	EK	368/378 (97%)	368 (100%)	0	100	100
8	EM	368/378 (97%)	367 (100%)	1 (0%)	92	97
8	FC	364/378 (96%)	364 (100%)	0	100	100
8	FE	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	FG	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	FI	363/378 (96%)	363 (100%)	0	100	100
8	FK	363/378 (96%)	360 (99%)	3 (1%)	81	91
8	FM	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	GC	368/378 (97%)	368 (100%)	0	100	100
8	GE	363/378 (96%)	363 (100%)	0	100	100
8	GG	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	GI	363/378 (96%)	361 (99%)	2 (1%)	86	94
8	GK	365/378 (97%)	364 (100%)	1 (0%)	92	97
8	GM	367/378 (97%)	367 (100%)	0	100	100
8	HC	364/378 (96%)	362 (100%)	2 (0%)	88	95
8	HE	365/378 (97%)	364 (100%)	1 (0%)	92	97
8	HG	365/378 (97%)	365 (100%)	0	100	100
8	HI	365/378 (97%)	363 (100%)	2 (0%)	88	95
8	HK	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	HM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	HO	329/378 (87%)	327 (99%)	2 (1%)	86	94
8	IC	366/378 (97%)	364 (100%)	2 (0%)	88	95
8	IE	364/378 (96%)	364 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	IG	369/378 (98%)	369 (100%)	0	100	100
8	II	365/378 (97%)	365 (100%)	0	100	100
8	IK	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	IM	364/378 (96%)	364 (100%)	0	100	100
8	IO	364/378 (96%)	364 (100%)	0	100	100
8	JC	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	JE	363/378 (96%)	363 (100%)	0	100	100
8	JG	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	JI	363/378 (96%)	363 (100%)	0	100	100
8	JK	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	JM	363/378 (96%)	363 (100%)	0	100	100
8	KC	365/378 (97%)	365 (100%)	0	100	100
8	KE	365/378 (97%)	363 (100%)	2 (0%)	88	95
8	KG	365/378 (97%)	363 (100%)	2 (0%)	88	95
8	KI	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	KK	365/378 (97%)	364 (100%)	1 (0%)	92	97
8	KM	368/378 (97%)	367 (100%)	1 (0%)	92	97
8	KO	364/378 (96%)	362 (100%)	2 (0%)	88	95
8	LC	365/378 (97%)	364 (100%)	1 (0%)	92	97
8	LE	369/378 (98%)	369 (100%)	0	100	100
8	LG	366/378 (97%)	364 (100%)	2 (0%)	88	95
8	LI	367/378 (97%)	366 (100%)	1 (0%)	92	97
8	LK	365/378 (97%)	364 (100%)	1 (0%)	92	97
8	LM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	MC	370/378 (98%)	370 (100%)	0	100	100
8	ME	365/378 (97%)	364 (100%)	1 (0%)	92	97
8	MG	365/378 (97%)	363 (100%)	2 (0%)	88	95
8	MI	366/378 (97%)	365 (100%)	1 (0%)	92	97
8	MK	370/378 (98%)	368 (100%)	2 (0%)	88	95
8	MM	370/378 (98%)	370 (100%)	0	100	100
8	NC	370/378 (98%)	367 (99%)	3 (1%)	81	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	NE	369/378 (98%)	363 (98%)	6 (2%)	62	83
8	NG	369/378 (98%)	367 (100%)	2 (0%)	88	95
8	NI	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	NK	369/378 (98%)	365 (99%)	4 (1%)	73	88
8	NM	369/378 (98%)	366 (99%)	3 (1%)	81	91
8	OC	371/378 (98%)	370 (100%)	1 (0%)	92	97
8	OE	370/378 (98%)	370 (100%)	0	100	100
8	OG	371/378 (98%)	370 (100%)	1 (0%)	92	97
8	OI	371/378 (98%)	370 (100%)	1 (0%)	92	97
8	OK	369/378 (98%)	369 (100%)	0	100	100
8	OM	371/378 (98%)	370 (100%)	1 (0%)	92	97
8	OO	356/378 (94%)	356 (100%)	0	100	100
8	PC	371/378 (98%)	371 (100%)	0	100	100
8	PE	370/378 (98%)	370 (100%)	0	100	100
8	PG	371/378 (98%)	369 (100%)	2 (0%)	88	95
8	PI	369/378 (98%)	369 (100%)	0	100	100
8	PK	370/378 (98%)	368 (100%)	2 (0%)	88	95
8	PM	369/378 (98%)	369 (100%)	0	100	100
8	PO	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	QC	370/378 (98%)	370 (100%)	0	100	100
8	QE	370/378 (98%)	370 (100%)	0	100	100
8	QG	370/378 (98%)	369 (100%)	1 (0%)	92	97
8	QI	370/378 (98%)	369 (100%)	1 (0%)	92	97
8	QK	370/378 (98%)	368 (100%)	2 (0%)	88	95
8	QM	370/378 (98%)	369 (100%)	1 (0%)	92	97
8	QO	370/378 (98%)	370 (100%)	0	100	100
8	RC	349/378 (92%)	346 (99%)	3 (1%)	78	90
8	RE	363/378 (96%)	363 (100%)	0	100	100
8	RG	365/378 (97%)	365 (100%)	0	100	100
8	RI	369/378 (98%)	369 (100%)	0	100	100
8	RK	370/378 (98%)	370 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	RM	370/378 (98%)	370 (100%)	0	100	100
8	RO	369/378 (98%)	369 (100%)	0	100	100
8	SE	362/378 (96%)	361 (100%)	1 (0%)	92	97
8	SG	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	SI	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	SK	364/378 (96%)	361 (99%)	3 (1%)	81	91
8	SM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	SO	364/378 (96%)	364 (100%)	0	100	100
8	TE	362/378 (96%)	361 (100%)	1 (0%)	92	97
8	TG	363/378 (96%)	363 (100%)	0	100	100
8	TI	364/378 (96%)	364 (100%)	0	100	100
8	TK	362/378 (96%)	360 (99%)	2 (1%)	86	94
8	TM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	TO	362/378 (96%)	362 (100%)	0	100	100
8	UE	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	UG	365/378 (97%)	365 (100%)	0	100	100
8	UI	365/378 (97%)	363 (100%)	2 (0%)	88	95
8	UK	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	UM	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	UO	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	VE	369/378 (98%)	368 (100%)	1 (0%)	92	97
8	VG	366/378 (97%)	364 (100%)	2 (0%)	88	95
8	VI	369/378 (98%)	369 (100%)	0	100	100
8	VK	364/378 (96%)	363 (100%)	1 (0%)	92	97
8	VM	369/378 (98%)	367 (100%)	2 (0%)	88	95
8	VO	364/378 (96%)	364 (100%)	0	100	100
8	WE	369/378 (98%)	366 (99%)	3 (1%)	81	91
8	WG	363/378 (96%)	362 (100%)	1 (0%)	92	97
8	WI	368/378 (97%)	367 (100%)	1 (0%)	92	97
8	WK	363/378 (96%)	363 (100%)	0	100	100
8	WM	369/378 (98%)	367 (100%)	2 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	WO	364/378 (96%)	364 (100%)	0	100	100
9	AB	374/380 (98%)	372 (100%)	2 (0%)	88	95
9	AD	374/380 (98%)	373 (100%)	1 (0%)	92	97
9	AF	374/380 (98%)	369 (99%)	5 (1%)	69	86
9	AH	374/380 (98%)	372 (100%)	2 (0%)	88	95
9	AJ	374/380 (98%)	372 (100%)	2 (0%)	88	95
9	AL	374/380 (98%)	373 (100%)	1 (0%)	92	97
9	BB	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	BD	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	BF	367/380 (97%)	365 (100%)	2 (0%)	88	95
9	BH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	BJ	368/380 (97%)	365 (99%)	3 (1%)	81	91
9	BL	366/380 (96%)	366 (100%)	0	100	100
9	CB	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	CD	366/380 (96%)	366 (100%)	0	100	100
9	CF	367/380 (97%)	365 (100%)	2 (0%)	88	95
9	CH	366/380 (96%)	366 (100%)	0	100	100
9	CJ	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	CL	366/380 (96%)	366 (100%)	0	100	100
9	DB	366/380 (96%)	366 (100%)	0	100	100
9	DD	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	DF	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	DH	366/380 (96%)	366 (100%)	0	100	100
9	DJ	366/380 (96%)	366 (100%)	0	100	100
9	DL	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	EB	366/380 (96%)	366 (100%)	0	100	100
9	ED	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	EF	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	EH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	EJ	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	EL	366/380 (96%)	364 (100%)	2 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	EN	367/380 (97%)	367 (100%)	0	100	100
9	FB	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	FD	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	FF	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	FH	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	FJ	366/380 (96%)	366 (100%)	0	100	100
9	FL	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	FN	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	GB	353/380 (93%)	351 (99%)	2 (1%)	86	94
9	GD	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	GF	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	GH	366/380 (96%)	366 (100%)	0	100	100
9	GJ	368/380 (97%)	365 (99%)	3 (1%)	81	91
9	GL	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	GN	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	HB	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	HD	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	HF	367/380 (97%)	367 (100%)	0	100	100
9	HH	366/380 (96%)	366 (100%)	0	100	100
9	HJ	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	HL	366/380 (96%)	362 (99%)	4 (1%)	73	88
9	HN	365/380 (96%)	363 (100%)	2 (0%)	88	95
9	IB	353/380 (93%)	352 (100%)	1 (0%)	92	97
9	ID	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	IF	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	IH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	IJ	368/380 (97%)	367 (100%)	1 (0%)	92	97
9	IL	366/380 (96%)	366 (100%)	0	100	100
9	IN	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	JB	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	JD	366/380 (96%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	JF	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	JH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	JJ	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	JL	366/380 (96%)	366 (100%)	0	100	100
9	JN	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	KB	355/380 (93%)	354 (100%)	1 (0%)	92	97
9	KD	369/380 (97%)	367 (100%)	2 (0%)	88	95
9	KF	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	KH	369/380 (97%)	368 (100%)	1 (0%)	92	97
9	KJ	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	KL	369/380 (97%)	367 (100%)	2 (0%)	88	95
9	KN	366/380 (96%)	366 (100%)	0	100	100
9	LB	376/380 (99%)	374 (100%)	2 (0%)	88	95
9	LD	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	LF	376/380 (99%)	374 (100%)	2 (0%)	88	95
9	LH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	LJ	379/380 (100%)	376 (99%)	3 (1%)	81	91
9	LL	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	LN	376/380 (99%)	375 (100%)	1 (0%)	92	97
9	MB	368/380 (97%)	368 (100%)	0	100	100
9	MD	370/380 (97%)	369 (100%)	1 (0%)	92	97
9	MF	369/380 (97%)	368 (100%)	1 (0%)	92	97
9	MH	370/380 (97%)	369 (100%)	1 (0%)	92	97
9	MJ	370/380 (97%)	369 (100%)	1 (0%)	92	97
9	ML	370/380 (97%)	367 (99%)	3 (1%)	81	91
9	MN	368/380 (97%)	368 (100%)	0	100	100
9	NB	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	ND	367/380 (97%)	365 (100%)	2 (0%)	88	95
9	NF	368/380 (97%)	364 (99%)	4 (1%)	73	88
9	NH	367/380 (97%)	365 (100%)	2 (0%)	88	95
9	NJ	368/380 (97%)	364 (99%)	4 (1%)	73	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	NL	367/380 (97%)	363 (99%)	4 (1%)	73	88
9	NN	367/380 (97%)	365 (100%)	2 (0%)	88	95
9	OB	369/380 (97%)	369 (100%)	0	100	100
9	OD	368/380 (97%)	368 (100%)	0	100	100
9	OF	370/380 (97%)	369 (100%)	1 (0%)	92	97
9	OH	368/380 (97%)	368 (100%)	0	100	100
9	OJ	370/380 (97%)	369 (100%)	1 (0%)	92	97
9	OL	368/380 (97%)	367 (100%)	1 (0%)	92	97
9	ON	369/380 (97%)	368 (100%)	1 (0%)	92	97
9	PD	368/380 (97%)	368 (100%)	0	100	100
9	PF	370/380 (97%)	370 (100%)	0	100	100
9	PH	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	PJ	368/380 (97%)	367 (100%)	1 (0%)	92	97
9	PL	368/380 (97%)	367 (100%)	1 (0%)	92	97
9	PN	368/380 (97%)	367 (100%)	1 (0%)	92	97
9	QD	367/380 (97%)	367 (100%)	0	100	100
9	QF	368/380 (97%)	368 (100%)	0	100	100
9	QH	366/380 (96%)	366 (100%)	0	100	100
9	QJ	368/380 (97%)	366 (100%)	2 (0%)	88	95
9	QL	367/380 (97%)	367 (100%)	0	100	100
9	QN	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	RD	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	RF	368/380 (97%)	367 (100%)	1 (0%)	92	97
9	RH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	RJ	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	RL	366/380 (96%)	366 (100%)	0	100	100
9	RN	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	SD	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	SF	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	SH	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	SJ	366/380 (96%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	SL	366/380 (96%)	366 (100%)	0	100	100
9	SN	366/380 (96%)	366 (100%)	0	100	100
9	TD	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	TF	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	TH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	TJ	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	TL	366/380 (96%)	363 (99%)	3 (1%)	81	91
9	TN	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	TP	361/380 (95%)	360 (100%)	1 (0%)	92	97
9	UD	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	UF	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	UH	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	UJ	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	UL	366/380 (96%)	361 (99%)	5 (1%)	67	85
9	UN	367/380 (97%)	363 (99%)	4 (1%)	73	88
9	UP	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	VD	366/380 (96%)	366 (100%)	0	100	100
9	VF	367/380 (97%)	366 (100%)	1 (0%)	92	97
9	VH	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	VJ	367/380 (97%)	365 (100%)	2 (0%)	88	95
9	VL	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	VN	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	VP	367/380 (97%)	364 (99%)	3 (1%)	81	91
9	WD	366/380 (96%)	366 (100%)	0	100	100
9	WF	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	WH	366/380 (96%)	365 (100%)	1 (0%)	92	97
9	WJ	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	WL	366/380 (96%)	364 (100%)	2 (0%)	88	95
9	WN	367/380 (97%)	367 (100%)	0	100	100
9	WP	367/380 (97%)	366 (100%)	1 (0%)	92	97
10	B	163/455 (36%)	162 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	C	322/455 (71%)	320 (99%)	2 (1%)	86	94
11	B0	176/388 (45%)	175 (99%)	1 (1%)	86	94
11	B1	353/388 (91%)	353 (100%)	0	100	100
11	B2	352/388 (91%)	352 (100%)	0	100	100
11	B3	318/388 (82%)	318 (100%)	0	100	100
11	B4	45/388 (12%)	45 (100%)	0	100	100
12	C0	33/446 (7%)	33 (100%)	0	100	100
12	C1	303/446 (68%)	302 (100%)	1 (0%)	92	97
12	C2	356/446 (80%)	353 (99%)	3 (1%)	81	91
12	C3	357/446 (80%)	357 (100%)	0	100	100
12	C4	201/446 (45%)	201 (100%)	0	100	100
13	D	163/393 (42%)	163 (100%)	0	100	100
14	D0	237/387 (61%)	236 (100%)	1 (0%)	91	97
14	D1	355/387 (92%)	355 (100%)	0	100	100
14	D2	357/387 (92%)	356 (100%)	1 (0%)	92	97
14	D3	285/387 (74%)	285 (100%)	0	100	100
15	E	246/266 (92%)	246 (100%)	0	100	100
15	F	246/266 (92%)	246 (100%)	0	100	100
16	F0	146/199 (73%)	146 (100%)	0	100	100
16	F1	149/199 (75%)	149 (100%)	0	100	100
16	F3	146/199 (73%)	146 (100%)	0	100	100
16	F4	149/199 (75%)	149 (100%)	0	100	100
16	F6	146/199 (73%)	146 (100%)	0	100	100
16	F7	149/199 (75%)	148 (99%)	1 (1%)	84	93
16	G0	148/199 (74%)	148 (100%)	0	100	100
16	G1	147/199 (74%)	146 (99%)	1 (1%)	84	93
16	G3	146/199 (73%)	146 (100%)	0	100	100
16	G4	149/199 (75%)	148 (99%)	1 (1%)	84	93
16	G6	146/199 (73%)	145 (99%)	1 (1%)	84	93
16	G7	149/199 (75%)	148 (99%)	1 (1%)	84	93
16	H0	146/199 (73%)	146 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	H1	149/199 (75%)	149 (100%)	0	100	100
17	G	88/115 (76%)	87 (99%)	1 (1%)	73	88
18	H	66/235 (28%)	66 (100%)	0	100	100
18	I	106/235 (45%)	106 (100%)	0	100	100
18	J	106/235 (45%)	106 (100%)	0	100	100
18	K	106/235 (45%)	105 (99%)	1 (1%)	78	90
18	L	106/235 (45%)	105 (99%)	1 (1%)	78	90
18	M	106/235 (45%)	106 (100%)	0	100	100
18	N	106/235 (45%)	105 (99%)	1 (1%)	78	90
19	I1	86/139 (62%)	84 (98%)	2 (2%)	50	76
20	J1	75/252 (30%)	75 (100%)	0	100	100
20	J2	200/252 (79%)	199 (100%)	1 (0%)	88	95
20	J3	200/252 (79%)	199 (100%)	1 (0%)	88	95
20	J4	182/252 (72%)	180 (99%)	2 (1%)	73	88
20	J5	58/252 (23%)	58 (100%)	0	100	100
21	K1	105/123 (85%)	104 (99%)	1 (1%)	76	88
22	L1	113/131 (86%)	113 (100%)	0	100	100
22	L2	82/131 (63%)	82 (100%)	0	100	100
23	M1	87/180 (48%)	87 (100%)	0	100	100
23	M2	86/180 (48%)	86 (100%)	0	100	100
23	M3	87/180 (48%)	87 (100%)	0	100	100
23	M4	87/180 (48%)	86 (99%)	1 (1%)	73	88
24	O	21/342 (6%)	21 (100%)	0	100	100
24	P	331/342 (97%)	331 (100%)	0	100	100
24	Q	37/342 (11%)	36 (97%)	1 (3%)	44	73
24	R	194/342 (57%)	194 (100%)	0	100	100
24	S	150/342 (44%)	150 (100%)	0	100	100
25	T	439/577 (76%)	438 (100%)	1 (0%)	93	98
25	U	440/577 (76%)	439 (100%)	1 (0%)	93	98
25	V	440/577 (76%)	440 (100%)	0	100	100
26	W	561/688 (82%)	559 (100%)	2 (0%)	91	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X	645/688 (94%)	643 (100%)	2 (0%)	92	97
26	Y	645/688 (94%)	643 (100%)	2 (0%)	92	97
26	Z	471/688 (68%)	469 (100%)	2 (0%)	91	97
27	XA	174/180 (97%)	174 (100%)	0	100	100
27	XB	174/180 (97%)	173 (99%)	1 (1%)	86	94
27	XC	174/180 (97%)	173 (99%)	1 (1%)	86	94
27	XD	174/180 (97%)	174 (100%)	0	100	100
27	XE	174/180 (97%)	173 (99%)	1 (1%)	86	94
27	XF	174/180 (97%)	174 (100%)	0	100	100
27	XG	174/180 (97%)	174 (100%)	0	100	100
28	YB	192/227 (85%)	192 (100%)	0	100	100
28	YC	192/227 (85%)	192 (100%)	0	100	100
28	YD	192/227 (85%)	192 (100%)	0	100	100
28	YE	192/227 (85%)	192 (100%)	0	100	100
28	YF	192/227 (85%)	192 (100%)	0	100	100
28	YG	192/227 (85%)	192 (100%)	0	100	100
29	a	162/495 (33%)	161 (99%)	1 (1%)	86	94
29	b	302/495 (61%)	302 (100%)	0	100	100
29	c	263/495 (53%)	261 (99%)	2 (1%)	81	91
29	d	189/495 (38%)	188 (100%)	1 (0%)	88	95
30	e	514/523 (98%)	514 (100%)	0	100	100
30	f	514/523 (98%)	513 (100%)	1 (0%)	93	98
30	g	514/523 (98%)	512 (100%)	2 (0%)	91	97
31	h	133/233 (57%)	132 (99%)	1 (1%)	81	91
31	i	228/233 (98%)	228 (100%)	0	100	100
31	j	226/233 (97%)	225 (100%)	1 (0%)	91	97
31	k	228/233 (98%)	228 (100%)	0	100	100
32	l	100/153 (65%)	100 (100%)	0	100	100
32	m	100/153 (65%)	100 (100%)	0	100	100
32	n	100/153 (65%)	100 (100%)	0	100	100
33	o	366/495 (74%)	362 (99%)	4 (1%)	73	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	o1	32/495 (6%)	32 (100%)	0	100	100
33	p	134/495 (27%)	132 (98%)	2 (2%)	65	84
34	q	100/153 (65%)	100 (100%)	0	100	100
34	r	100/153 (65%)	100 (100%)	0	100	100
34	s	100/153 (65%)	100 (100%)	0	100	100
35	y	58/117 (50%)	58 (100%)	0	100	100
35	z	98/117 (84%)	98 (100%)	0	100	100
All	All	134531/150776 (89%)	134112 (100%)	419 (0%)	92	97

5 of 419 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	NB	274	THR
8	PK	221	ARG
27	XE	121	MET
9	ND	285	THR
8	NK	279	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 252 such sidechains are listed below:

Mol	Chain	Res	Type
21	K1	18	GLN
9	UP	292	GLN
9	MJ	298	ASN
8	UO	102	ASN
9	WH	204	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 451 ligands modelled in this entry, 149 are monoatomic - leaving 302 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	$\#\|Z\| > 2$
36	GTP	II	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.64	7 (21%)
38	GDP	GL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	SF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.25	4 (13%)
36	GTP	GG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	OO	501	37	26,34,34	1.19	2 (7%)	32,54,54	1.65	7 (21%)
36	GTP	BA	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
38	GDP	RH	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.31	5 (16%)
38	GDP	OD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.37	4 (13%)
36	GTP	CC	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.64	7 (21%)
38	GDP	HL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	MJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	VE	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.62	7 (21%)
36	GTP	AG	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	HE	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
38	GDP	CL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	CF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
38	GDP	ML	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
36	GTP	PE	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.56	7 (21%)
36	GTP	JI	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.67	7 (21%)
36	GTP	SO	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.49	7 (21%)
38	GDP	BF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.40	4 (13%)
38	GDP	QL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
38	GDP	AB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.41	4 (13%)
38	GDP	SJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.37	5 (16%)
36	GTP	EI	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.58	7 (21%)
36	GTP	TM	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.52	7 (21%)
38	GDP	BJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.39	4 (13%)
38	GDP	RD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.37	5 (16%)
36	GTP	PM	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.63	7 (21%)
38	GDP	QN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	HG	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.60	7 (21%)
38	GDP	RN	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	SH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	5 (16%)
38	GDP	PL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	GN	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	KJ	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	ON	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	UF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	SG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.52	7 (21%)
36	GTP	BC	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.61	7 (21%)
36	GTP	CK	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.64	7 (21%)
38	GDP	GD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	UG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.62	7 (21%)
36	GTP	EK	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	RO	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.54	7 (21%)
38	GDP	EH	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.30	4 (13%)
38	GDP	TF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
38	GDP	NB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.39	4 (13%)
36	GTP	LM	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.51	7 (21%)
36	GTP	MK	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.58	7 (21%)
36	GTP	LC	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.62	7 (21%)
38	GDP	UD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	BI	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.60	7 (21%)
36	GTP	FK	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.42	6 (18%)
38	GDP	PN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	QE	501	37	26,34,34	1.20	2 (7%)	32,54,54	1.58	7 (21%)
38	GDP	CJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.37	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
38	GDP	PJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	MC	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.55	7 (21%)
38	GDP	WJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
38	GDP	HH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	NM	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.52	7 (21%)
38	GDP	WL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	OI	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.71	6 (18%)
38	GDP	FD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	5 (16%)
38	GDP	FF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
38	GDP	HB	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.34	4 (13%)
36	GTP	QG	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.60	7 (21%)
38	GDP	WF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	IG	501	37	26,34,34	1.12	2 (7%)	32,54,54	1.63	6 (18%)
36	GTP	GM	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.57	6 (18%)
36	GTP	IC	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.56	7 (21%)
36	GTP	NC	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	SI	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.47	7 (21%)
38	GDP	LH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
38	GDP	QJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	OJ	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.33	4 (13%)
38	GDP	KF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.38	4 (13%)
36	GTP	GE	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	FG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.54	7 (21%)
38	GDP	UJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	MM	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.56	7 (21%)
36	GTP	AM	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	PC	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.59	6 (18%)
36	GTP	WM	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.53	6 (18%)
36	GTP	ME	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.54	7 (21%)
38	GDP	AH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.39	4 (13%)
38	GDP	ED	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	KH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	OK	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.53	6 (18%)
38	GDP	VF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
36	GTP	RK	501	37	26,34,34	1.20	2 (7%)	32,54,54	1.67	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
36	GTP	NE	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.58	7 (21%)
38	GDP	FN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	5 (16%)
36	GTP	DG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.63	6 (18%)
38	GDP	OB	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.42	4 (13%)
38	GDP	GH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	VD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
38	GDP	JL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	4 (13%)
36	GTP	DA	501	37	26,34,34	1.10	2 (7%)	32,54,54	1.53	6 (18%)
38	GDP	AD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.38	4 (13%)
38	GDP	JF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
38	GDP	PF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	BG	501	37	26,34,34	1.19	2 (7%)	32,54,54	1.58	7 (21%)
36	GTP	QM	501	37	26,34,34	1.19	2 (7%)	32,54,54	1.56	7 (21%)
36	GTP	TO	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	EM	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	BM	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.61	7 (21%)
36	GTP	HO	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.58	7 (21%)
36	GTP	OC	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.70	7 (21%)
36	GTP	PI	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.61	7 (21%)
36	GTP	QK	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.52	6 (18%)
38	GDP	LD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	TP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	BE	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	DI	501	37	26,34,34	1.11	2 (7%)	32,54,54	1.69	6 (18%)
38	GDP	VN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	VP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	TE	501	37	26,34,34	1.12	2 (7%)	32,54,54	1.56	6 (18%)
38	GDP	RL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.32	4 (13%)
36	GTP	LG	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.60	7 (21%)
38	GDP	TN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.32	4 (13%)
36	GTP	VM	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	WK	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.63	6 (18%)
36	GTP	OG	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	PK	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.50	7 (21%)
38	GDP	JD	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	$\#\|Z\| > 2$
36	GTP	HI	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.68	7 (21%)
36	GTP	PO	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
38	GDP	LF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	MD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
38	GDP	UN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
38	GDP	NJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	WD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	KM	501	37	26,34,34	1.20	2 (7%)	32,54,54	1.65	7 (21%)
38	GDP	QF	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	GF	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.29	4 (13%)
36	GTP	TI	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.49	7 (21%)
36	GTP	WO	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.55	6 (18%)
38	GDP	TH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
36	GTP	WG	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.69	6 (18%)
38	GDP	FH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	5 (16%)
38	GDP	WH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.32	4 (13%)
36	GTP	CA	501	37	26,34,34	1.12	2 (7%)	32,54,54	1.58	6 (18%)
38	GDP	NH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	UH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	LL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	LK	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.62	7 (21%)
36	GTP	VI	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.58	7 (21%)
38	GDP	DD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.28	4 (13%)
38	GDP	PD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	PG	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.61	7 (21%)
36	GTP	CI	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.66	6 (18%)
36	GTP	DC	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.60	6 (18%)
38	GDP	AF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.40	4 (13%)
36	GTP	BK	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	KK	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.63	7 (21%)
36	GTP	GI	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	HM	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.55	7 (21%)
36	GTP	JE	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.57	7 (21%)
36	GTP	CM	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.63	7 (21%)
38	GDP	DJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.31	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
36	GTP	HC	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.51	7 (21%)
36	GTP	QO	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.64	7 (21%)
36	GTP	VK	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.63	7 (21%)
38	GDP	MN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.38	4 (13%)
38	GDP	OF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	EL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.25	4 (13%)
36	GTP	DK	501	37	26,34,34	1.12	2 (7%)	32,54,54	1.69	6 (18%)
38	GDP	BH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.38	4 (13%)
36	GTP	OM	501	37	26,34,34	1.19	2 (7%)	32,54,54	1.58	7 (21%)
38	GDP	EF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.34	5 (16%)
38	GDP	SN	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.34	5 (16%)
38	GDP	UP	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	MH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
38	GDP	IL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	EC	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.55	7 (21%)
38	GDP	MF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.32	4 (13%)
36	GTP	DE	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.55	6 (18%)
38	GDP	DL	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.29	4 (13%)
36	GTP	QC	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.51	7 (21%)
38	GDP	DB	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.28	4 (13%)
36	GTP	KE	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.63	7 (21%)
38	GDP	DF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	NK	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.58	7 (21%)
36	GTP	EE	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.54	7 (21%)
36	GTP	RC	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.56	7 (21%)
38	GDP	ND	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	EB	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.32	4 (13%)
38	GDP	PH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	VG	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.60	7 (21%)
38	GDP	BB	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.37	4 (13%)
36	GTP	SE	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.54	7 (21%)
36	GTP	UI	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	UO	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	UK	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.61	7 (21%)
36	GTP	WE	501	37	26,34,34	1.12	2 (7%)	32,54,54	1.55	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
36	GTP	JK	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.58	7 (21%)
38	GDP	DH	502	-	24,30,30	0.98	1 (4%)	30,47,47	1.29	4 (13%)
36	GTP	IE	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.62	7 (21%)
38	GDP	EN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.32	4 (13%)
36	GTP	JG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.65	7 (21%)
36	GTP	UE	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.62	7 (21%)
38	GDP	HD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	QH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
36	GTP	NG	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.60	8 (25%)
38	GDP	VJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.37	4 (13%)
36	GTP	RI	501	37	26,34,34	1.19	2 (7%)	32,54,54	1.65	7 (21%)
36	GTP	TK	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.56	7 (21%)
38	GDP	IB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	FJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
38	GDP	LB	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.37	4 (13%)
38	GDP	ID	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	FL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	5 (16%)
38	GDP	JN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
36	GTP	FI	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.44	6 (18%)
36	GTP	RG	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.58	7 (21%)
38	GDP	HN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
38	GDP	JH	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	RJ	502	-	24,30,30	0.98	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	NF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.39	4 (13%)
38	GDP	VL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	KD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	IN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	UL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
36	GTP	UM	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.51	7 (21%)
38	GDP	LN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.38	4 (13%)
38	GDP	LJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.41	4 (13%)
36	GTP	AC	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.53	7 (21%)
38	GDP	AJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.44	4 (13%)
36	GTP	DM	501	37	26,34,34	1.10	2 (7%)	32,54,54	1.68	6 (18%)
36	GTP	SM	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.48	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
38	GDP	AL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.40	4 (13%)
36	GTP	GK	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	IO	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.63	7 (21%)
36	GTP	AK	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	CE	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.57	7 (21%)
38	GDP	NN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.39	4 (13%)
38	GDP	VH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
36	GTP	HK	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.60	7 (21%)
38	GDP	RF	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.34	5 (16%)
38	GDP	WN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	FM	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.47	7 (21%)
36	GTP	JM	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.61	7 (21%)
38	GDP	CD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	WI	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.64	6 (18%)
38	GDP	TJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
36	GTP	AA	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.53	7 (21%)
38	GDP	CB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.39	4 (13%)
38	GDP	EJ	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.26	4 (13%)
38	GDP	TD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	CG	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.62	7 (21%)
38	GDP	JJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
36	GTP	VO	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.61	7 (21%)
38	GDP	SL	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.35	5 (16%)
36	GTP	RM	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	AE	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.57	7 (21%)
38	GDP	GJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
36	GTP	IK	501	37	26,34,34	1.13	2 (7%)	32,54,54	1.63	7 (21%)
38	GDP	QD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	TG	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.61	7 (21%)
38	GDP	KB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.39	4 (13%)
38	GDP	MB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.39	4 (13%)
36	GTP	QI	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
36	GTP	JC	501	37	26,34,34	1.14	2 (7%)	32,54,54	1.60	6 (18%)
36	GTP	NI	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.56	7 (21%)
38	GDP	WP	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.32	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
38	GDP	HF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	SD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	5 (16%)
36	GTP	GC	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.49	7 (21%)
38	GDP	IF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
36	GTP	FC	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.50	7 (21%)
38	GDP	CH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.30	4 (13%)
38	GDP	HJ	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.35	4 (13%)
38	GDP	BD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	KC	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
38	GDP	GB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	IH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.37	4 (13%)
36	GTP	EG	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.57	7 (21%)
36	GTP	SK	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.46	7 (21%)
38	GDP	JB	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	IM	501	37	26,34,34	1.12	2 (7%)	32,54,54	1.63	6 (18%)
38	GDP	IJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.37	4 (13%)
36	GTP	KI	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.62	7 (21%)
38	GDP	OH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
36	GTP	AI	501	37	26,34,34	1.20	2 (7%)	32,54,54	1.53	7 (21%)
36	GTP	KO	501	37	26,34,34	1.18	2 (7%)	32,54,54	1.67	7 (21%)
36	GTP	FE	501	37	26,34,34	1.15	2 (7%)	32,54,54	1.54	7 (21%)
36	GTP	LI	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.57	7 (21%)
38	GDP	BL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.37	4 (13%)
38	GDP	NL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.38	4 (13%)
36	GTP	MI	501	37	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
36	GTP	RE	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.64	7 (21%)
38	GDP	TL	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	OE	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.58	7 (21%)
36	GTP	MG	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.57	7 (21%)
36	GTP	KG	501	-	26,34,34	1.19	2 (7%)	32,54,54	1.63	7 (21%)
38	GDP	FB	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.34	4 (13%)
38	GDP	KN	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.42	4 (13%)
38	GDP	KL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
38	GDP	OL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.35	4 (13%)
36	GTP	LE	501	37	26,34,34	1.17	2 (7%)	32,54,54	1.63	7 (21%)

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
36	GTP	II	501	37	-	4/18/38/38	0/3/3/3
38	GDP	GL	502	-	-	0/12/32/32	0/3/3/3
38	GDP	SF	502	-	-	0/12/32/32	0/3/3/3
36	GTP	GG	501	37	-	4/18/38/38	0/3/3/3
36	GTP	OO	501	37	-	7/18/38/38	0/3/3/3
36	GTP	BA	501	37	-	5/18/38/38	0/3/3/3
38	GDP	RH	502	-	-	0/12/32/32	0/3/3/3
38	GDP	OD	502	-	-	2/12/32/32	0/3/3/3
36	GTP	CC	501	37	-	8/18/38/38	0/3/3/3
38	GDP	HL	502	-	-	1/12/32/32	0/3/3/3
38	GDP	MJ	502	-	-	3/12/32/32	0/3/3/3
36	GTP	VE	501	37	-	4/18/38/38	0/3/3/3
36	GTP	AG	501	37	-	4/18/38/38	0/3/3/3
36	GTP	HE	501	37	-	4/18/38/38	0/3/3/3
38	GDP	CL	502	-	-	2/12/32/32	0/3/3/3
38	GDP	CF	502	-	-	2/12/32/32	0/3/3/3
38	GDP	ML	502	-	-	4/12/32/32	0/3/3/3
36	GTP	PE	501	37	-	5/18/38/38	0/3/3/3
36	GTP	JI	501	37	-	2/18/38/38	0/3/3/3
36	GTP	SO	501	37	-	3/18/38/38	0/3/3/3
38	GDP	BF	502	-	-	3/12/32/32	0/3/3/3
38	GDP	QL	502	-	-	3/12/32/32	0/3/3/3
38	GDP	AB	502	-	-	1/12/32/32	0/3/3/3
38	GDP	SJ	502	-	-	0/12/32/32	0/3/3/3
36	GTP	EI	501	37	-	6/18/38/38	0/3/3/3
36	GTP	TM	501	37	-	3/18/38/38	0/3/3/3
38	GDP	BJ	502	-	-	4/12/32/32	0/3/3/3
38	GDP	RD	502	-	-	1/12/32/32	0/3/3/3
36	GTP	PM	501	37	-	8/18/38/38	0/3/3/3
38	GDP	QN	502	-	-	4/12/32/32	0/3/3/3
36	GTP	HG	501	37	-	4/18/38/38	0/3/3/3
38	GDP	RN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	SH	502	-	-	4/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	GDP	PL	502	-	-	2/12/32/32	0/3/3/3
38	GDP	GN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	KJ	502	-	-	3/12/32/32	0/3/3/3
38	GDP	ON	502	-	-	3/12/32/32	0/3/3/3
38	GDP	UF	502	-	-	2/12/32/32	0/3/3/3
36	GTP	SG	501	37	-	5/18/38/38	0/3/3/3
36	GTP	BC	501	37	-	4/18/38/38	0/3/3/3
36	GTP	CK	501	37	-	10/18/38/38	0/3/3/3
38	GDP	GD	502	-	-	3/12/32/32	0/3/3/3
36	GTP	UG	501	37	-	5/18/38/38	0/3/3/3
36	GTP	EK	501	37	-	5/18/38/38	0/3/3/3
36	GTP	RO	501	37	-	5/18/38/38	0/3/3/3
38	GDP	EH	502	-	-	2/12/32/32	0/3/3/3
38	GDP	TF	502	-	-	1/12/32/32	0/3/3/3
38	GDP	NB	502	-	-	1/12/32/32	0/3/3/3
36	GTP	LM	501	-	-	5/18/38/38	0/3/3/3
36	GTP	MK	501	37	-	5/18/38/38	0/3/3/3
36	GTP	LC	501	37	-	7/18/38/38	0/3/3/3
38	GDP	UD	502	-	-	1/12/32/32	0/3/3/3
36	GTP	BI	501	37	-	4/18/38/38	0/3/3/3
36	GTP	FK	501	37	-	5/18/38/38	0/3/3/3
38	GDP	PN	502	-	-	3/12/32/32	0/3/3/3
36	GTP	QE	501	37	-	9/18/38/38	0/3/3/3
38	GDP	CJ	502	-	-	1/12/32/32	0/3/3/3
38	GDP	PJ	502	-	-	2/12/32/32	0/3/3/3
36	GTP	MC	501	37	-	5/18/38/38	0/3/3/3
38	GDP	WJ	502	-	-	2/12/32/32	0/3/3/3
38	GDP	HH	502	-	-	0/12/32/32	0/3/3/3
36	GTP	NM	501	37	-	5/18/38/38	0/3/3/3
38	GDP	WL	502	-	-	1/12/32/32	0/3/3/3
36	GTP	OI	501	-	-	3/18/38/38	0/3/3/3
38	GDP	FD	502	-	-	4/12/32/32	0/3/3/3
38	GDP	FF	502	-	-	2/12/32/32	0/3/3/3
38	GDP	HB	502	-	-	1/12/32/32	0/3/3/3
36	GTP	QG	501	37	-	6/18/38/38	0/3/3/3
38	GDP	WF	502	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GTP	IG	501	37	-	7/18/38/38	0/3/3/3
36	GTP	GM	501	37	-	5/18/38/38	0/3/3/3
36	GTP	IC	501	37	-	5/18/38/38	0/3/3/3
36	GTP	NC	501	37	-	5/18/38/38	0/3/3/3
36	GTP	SI	501	37	-	5/18/38/38	0/3/3/3
38	GDP	LH	502	-	-	4/12/32/32	0/3/3/3
38	GDP	QJ	502	-	-	2/12/32/32	0/3/3/3
38	GDP	OJ	502	-	-	2/12/32/32	0/3/3/3
38	GDP	KF	502	-	-	3/12/32/32	0/3/3/3
36	GTP	GE	501	37	-	6/18/38/38	0/3/3/3
36	GTP	FG	501	37	-	5/18/38/38	0/3/3/3
38	GDP	UJ	502	-	-	3/12/32/32	0/3/3/3
36	GTP	MM	501	37	-	5/18/38/38	0/3/3/3
36	GTP	AM	501	37	-	4/18/38/38	0/3/3/3
36	GTP	PC	501	37	-	8/18/38/38	0/3/3/3
36	GTP	WM	501	37	-	8/18/38/38	0/3/3/3
36	GTP	ME	501	37	-	5/18/38/38	0/3/3/3
38	GDP	AH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	ED	502	-	-	3/12/32/32	0/3/3/3
38	GDP	KH	502	-	-	0/12/32/32	0/3/3/3
36	GTP	OK	501	37	-	4/18/38/38	0/3/3/3
38	GDP	VF	502	-	-	1/12/32/32	0/3/3/3
36	GTP	RK	501	37	-	3/18/38/38	0/3/3/3
36	GTP	NE	501	37	-	4/18/38/38	0/3/3/3
38	GDP	FN	502	-	-	0/12/32/32	0/3/3/3
36	GTP	DG	501	37	-	8/18/38/38	0/3/3/3
38	GDP	OB	502	-	-	4/12/32/32	0/3/3/3
38	GDP	GH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	VD	502	-	-	0/12/32/32	0/3/3/3
38	GDP	JL	502	-	-	1/12/32/32	0/3/3/3
36	GTP	DA	501	37	-	9/18/38/38	0/3/3/3
38	GDP	AD	502	-	-	1/12/32/32	0/3/3/3
38	GDP	JF	502	-	-	1/12/32/32	0/3/3/3
38	GDP	PF	502	-	-	3/12/32/32	0/3/3/3
36	GTP	BG	501	37	-	5/18/38/38	0/3/3/3
36	GTP	QM	501	37	-	8/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GTP	TO	501	37	-	4/18/38/38	0/3/3/3
36	GTP	EM	501	37	-	5/18/38/38	0/3/3/3
36	GTP	BM	501	37	-	4/18/38/38	0/3/3/3
36	GTP	HO	501	37	-	9/18/38/38	0/3/3/3
36	GTP	OC	501	37	-	6/18/38/38	0/3/3/3
36	GTP	PI	501	37	-	3/18/38/38	0/3/3/3
36	GTP	QK	501	37	-	9/18/38/38	0/3/3/3
38	GDP	LD	502	-	-	4/12/32/32	0/3/3/3
38	GDP	TP	502	-	-	1/12/32/32	0/3/3/3
36	GTP	BE	501	37	-	4/18/38/38	0/3/3/3
36	GTP	DI	501	37	-	3/18/38/38	0/3/3/3
38	GDP	VN	502	-	-	3/12/32/32	0/3/3/3
38	GDP	VP	502	-	-	1/12/32/32	0/3/3/3
36	GTP	TE	501	37	-	5/18/38/38	0/3/3/3
38	GDP	RL	502	-	-	0/12/32/32	0/3/3/3
36	GTP	LG	501	37	-	5/18/38/38	0/3/3/3
38	GDP	TN	502	-	-	4/12/32/32	0/3/3/3
36	GTP	VM	501	37	-	7/18/38/38	0/3/3/3
36	GTP	WK	501	37	-	5/18/38/38	0/3/3/3
36	GTP	OG	501	37	-	5/18/38/38	0/3/3/3
36	GTP	PK	501	37	-	4/18/38/38	0/3/3/3
38	GDP	JD	502	-	-	2/12/32/32	0/3/3/3
36	GTP	HI	501	37	-	8/18/38/38	0/3/3/3
36	GTP	PO	501	37	-	4/18/38/38	0/3/3/3
38	GDP	LF	502	-	-	1/12/32/32	0/3/3/3
38	GDP	MD	502	-	-	2/12/32/32	0/3/3/3
38	GDP	UN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	NJ	502	-	-	1/12/32/32	0/3/3/3
38	GDP	WD	502	-	-	4/12/32/32	0/3/3/3
36	GTP	KM	501	37	-	5/18/38/38	0/3/3/3
38	GDP	QF	502	-	-	2/12/32/32	0/3/3/3
38	GDP	GF	502	-	-	1/12/32/32	0/3/3/3
36	GTP	TI	501	37	-	2/18/38/38	0/3/3/3
36	GTP	WO	501	37	-	3/18/38/38	0/3/3/3
38	GDP	TH	502	-	-	3/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GTP	WG	501	37	-	7/18/38/38	0/3/3/3
38	GDP	FH	502	-	-	3/12/32/32	0/3/3/3
38	GDP	WH	502	-	-	2/12/32/32	0/3/3/3
36	GTP	CA	501	37	-	4/18/38/38	0/3/3/3
38	GDP	NH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	UH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	LL	502	-	-	3/12/32/32	0/3/3/3
36	GTP	LK	501	37	-	6/18/38/38	0/3/3/3
36	GTP	VI	501	37	-	6/18/38/38	0/3/3/3
38	GDP	DD	502	-	-	1/12/32/32	0/3/3/3
38	GDP	PD	502	-	-	4/12/32/32	0/3/3/3
36	GTP	PG	501	37	-	7/18/38/38	0/3/3/3
36	GTP	CI	501	37	-	8/18/38/38	0/3/3/3
36	GTP	DC	501	37	-	5/18/38/38	0/3/3/3
38	GDP	AF	502	-	-	2/12/32/32	0/3/3/3
36	GTP	BK	501	37	-	5/18/38/38	0/3/3/3
36	GTP	KK	501	-	-	8/18/38/38	0/3/3/3
36	GTP	GI	501	37	-	4/18/38/38	0/3/3/3
36	GTP	HM	501	37	-	4/18/38/38	0/3/3/3
36	GTP	JE	501	37	-	2/18/38/38	0/3/3/3
36	GTP	CM	501	37	-	3/18/38/38	0/3/3/3
38	GDP	DJ	502	-	-	1/12/32/32	0/3/3/3
36	GTP	HC	501	37	-	4/18/38/38	0/3/3/3
36	GTP	QO	501	37	-	8/18/38/38	0/3/3/3
36	GTP	VK	501	37	-	5/18/38/38	0/3/3/3
38	GDP	MN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	OF	502	-	-	3/12/32/32	0/3/3/3
38	GDP	EL	502	-	-	2/12/32/32	0/3/3/3
36	GTP	DK	501	37	-	3/18/38/38	0/3/3/3
38	GDP	BH	502	-	-	3/12/32/32	0/3/3/3
36	GTP	OM	501	37	-	7/18/38/38	0/3/3/3
38	GDP	EF	502	-	-	0/12/32/32	0/3/3/3
38	GDP	SN	502	-	-	3/12/32/32	0/3/3/3
38	GDP	UP	502	-	-	1/12/32/32	0/3/3/3
38	GDP	MH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	IL	502	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GTP	EC	501	37	-	5/18/38/38	0/3/3/3
38	GDP	MF	502	-	-	1/12/32/32	0/3/3/3
36	GTP	DE	501	37	-	3/18/38/38	0/3/3/3
38	GDP	DL	502	-	-	1/12/32/32	0/3/3/3
36	GTP	QC	501	37	-	3/18/38/38	0/3/3/3
38	GDP	DB	502	-	-	0/12/32/32	0/3/3/3
36	GTP	KE	501	-	-	7/18/38/38	0/3/3/3
38	GDP	DF	502	-	-	1/12/32/32	0/3/3/3
36	GTP	NK	501	37	-	5/18/38/38	0/3/3/3
36	GTP	EE	501	37	-	5/18/38/38	0/3/3/3
36	GTP	RC	501	-	-	6/18/38/38	0/3/3/3
38	GDP	ND	502	-	-	0/12/32/32	0/3/3/3
38	GDP	EB	502	-	-	0/12/32/32	0/3/3/3
38	GDP	PH	502	-	-	3/12/32/32	0/3/3/3
36	GTP	VG	501	37	-	8/18/38/38	0/3/3/3
38	GDP	BB	502	-	-	1/12/32/32	0/3/3/3
36	GTP	SE	501	37	-	5/18/38/38	0/3/3/3
36	GTP	UI	501	37	-	5/18/38/38	0/3/3/3
36	GTP	UO	501	37	-	5/18/38/38	0/3/3/3
36	GTP	UK	501	37	-	3/18/38/38	0/3/3/3
36	GTP	WE	501	37	-	5/18/38/38	0/3/3/3
36	GTP	JK	501	37	-	5/18/38/38	0/3/3/3
38	GDP	DH	502	-	-	2/12/32/32	0/3/3/3
36	GTP	IE	501	37	-	4/18/38/38	0/3/3/3
38	GDP	EN	502	-	-	1/12/32/32	0/3/3/3
36	GTP	JG	501	37	-	2/18/38/38	0/3/3/3
36	GTP	UE	501	37	-	4/18/38/38	0/3/3/3
38	GDP	HD	502	-	-	1/12/32/32	0/3/3/3
38	GDP	QH	502	-	-	4/12/32/32	0/3/3/3
36	GTP	NG	501	37	-	5/18/38/38	0/3/3/3
38	GDP	VJ	502	-	-	2/12/32/32	0/3/3/3
36	GTP	RI	501	37	-	3/18/38/38	0/3/3/3
36	GTP	TK	501	37	-	5/18/38/38	0/3/3/3
38	GDP	IB	502	-	-	1/12/32/32	0/3/3/3
38	GDP	FJ	502	-	-	1/12/32/32	0/3/3/3
38	GDP	LB	502	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	GDP	ID	502	-	-	2/12/32/32	0/3/3/3
38	GDP	FL	502	-	-	3/12/32/32	0/3/3/3
38	GDP	JN	502	-	-	2/12/32/32	0/3/3/3
36	GTP	FI	501	37	-	6/18/38/38	0/3/3/3
36	GTP	RG	501	37	-	3/18/38/38	0/3/3/3
38	GDP	HN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	JH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	RJ	502	-	-	1/12/32/32	0/3/3/3
38	GDP	NF	502	-	-	1/12/32/32	0/3/3/3
38	GDP	VL	502	-	-	1/12/32/32	0/3/3/3
38	GDP	KD	502	-	-	2/12/32/32	0/3/3/3
38	GDP	IN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	UL	502	-	-	1/12/32/32	0/3/3/3
36	GTP	UM	501	37	-	8/18/38/38	0/3/3/3
38	GDP	LN	502	-	-	4/12/32/32	0/3/3/3
38	GDP	LJ	502	-	-	3/12/32/32	0/3/3/3
36	GTP	AC	501	37	-	4/18/38/38	0/3/3/3
38	GDP	AJ	502	-	-	2/12/32/32	0/3/3/3
36	GTP	DM	501	37	-	3/18/38/38	0/3/3/3
36	GTP	SM	501	37	-	5/18/38/38	0/3/3/3
38	GDP	AL	502	-	-	1/12/32/32	0/3/3/3
36	GTP	GK	501	37	-	5/18/38/38	0/3/3/3
36	GTP	IO	501	37	-	6/18/38/38	0/3/3/3
36	GTP	AK	501	37	-	4/18/38/38	0/3/3/3
36	GTP	CE	501	37	-	4/18/38/38	0/3/3/3
38	GDP	NN	502	-	-	1/12/32/32	0/3/3/3
38	GDP	VH	502	-	-	0/12/32/32	0/3/3/3
36	GTP	HK	501	37	-	4/18/38/38	0/3/3/3
38	GDP	RF	502	-	-	1/12/32/32	0/3/3/3
38	GDP	WN	502	-	-	3/12/32/32	0/3/3/3
36	GTP	FM	501	37	-	5/18/38/38	0/3/3/3
36	GTP	JM	501	37	-	4/18/38/38	0/3/3/3
38	GDP	CD	502	-	-	2/12/32/32	0/3/3/3
36	GTP	WI	501	37	-	3/18/38/38	0/3/3/3
38	GDP	TJ	502	-	-	3/12/32/32	0/3/3/3
36	GTP	AA	501	37	-	4/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	GDP	CB	502	-	-	2/12/32/32	0/3/3/3
38	GDP	EJ	502	-	-	1/12/32/32	0/3/3/3
38	GDP	TD	502	-	-	3/12/32/32	0/3/3/3
36	GTP	CG	501	37	-	6/18/38/38	0/3/3/3
38	GDP	JJ	502	-	-	1/12/32/32	0/3/3/3
36	GTP	VO	501	37	-	4/18/38/38	0/3/3/3
38	GDP	SL	502	-	-	0/12/32/32	0/3/3/3
36	GTP	RM	501	37	-	6/18/38/38	0/3/3/3
36	GTP	AE	501	37	-	3/18/38/38	0/3/3/3
38	GDP	GJ	502	-	-	4/12/32/32	0/3/3/3
36	GTP	IK	501	37	-	5/18/38/38	0/3/3/3
38	GDP	QD	502	-	-	4/12/32/32	0/3/3/3
36	GTP	TG	501	37	-	5/18/38/38	0/3/3/3
38	GDP	KB	502	-	-	3/12/32/32	0/3/3/3
38	GDP	MB	502	-	-	1/12/32/32	0/3/3/3
36	GTP	QI	501	37	-	6/18/38/38	0/3/3/3
36	GTP	JC	501	37	-	4/18/38/38	0/3/3/3
36	GTP	NI	501	37	-	4/18/38/38	0/3/3/3
38	GDP	WP	502	-	-	3/12/32/32	0/3/3/3
38	GDP	HF	502	-	-	0/12/32/32	0/3/3/3
38	GDP	SD	502	-	-	3/12/32/32	0/3/3/3
36	GTP	GC	501	37	-	5/18/38/38	0/3/3/3
38	GDP	IF	502	-	-	2/12/32/32	0/3/3/3
36	GTP	FC	501	37	-	5/18/38/38	0/3/3/3
38	GDP	CH	502	-	-	1/12/32/32	0/3/3/3
38	GDP	HJ	502	-	-	1/12/32/32	0/3/3/3
38	GDP	BD	502	-	-	1/12/32/32	0/3/3/3
36	GTP	KC	501	37	-	4/18/38/38	0/3/3/3
38	GDP	GB	502	-	-	3/12/32/32	0/3/3/3
38	GDP	IH	502	-	-	2/12/32/32	0/3/3/3
36	GTP	EG	501	37	-	5/18/38/38	0/3/3/3
36	GTP	SK	501	37	-	6/18/38/38	0/3/3/3
38	GDP	JB	502	-	-	1/12/32/32	0/3/3/3
36	GTP	IM	501	37	-	8/18/38/38	0/3/3/3
38	GDP	IJ	502	-	-	1/12/32/32	0/3/3/3
36	GTP	KI	501	-	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	GDP	OH	502	-	-	1/12/32/32	0/3/3/3
36	GTP	AI	501	37	-	4/18/38/38	0/3/3/3
36	GTP	KO	501	37	-	7/18/38/38	0/3/3/3
36	GTP	FE	501	37	-	4/18/38/38	0/3/3/3
36	GTP	LI	501	37	-	5/18/38/38	0/3/3/3
38	GDP	BL	502	-	-	2/12/32/32	0/3/3/3
38	GDP	NL	502	-	-	1/12/32/32	0/3/3/3
36	GTP	MI	501	37	-	5/18/38/38	0/3/3/3
36	GTP	RE	501	-	-	3/18/38/38	0/3/3/3
38	GDP	TL	502	-	-	4/12/32/32	0/3/3/3
36	GTP	OE	501	37	-	4/18/38/38	0/3/3/3
36	GTP	MG	501	37	-	5/18/38/38	0/3/3/3
36	GTP	KG	501	-	-	6/18/38/38	0/3/3/3
38	GDP	FB	502	-	-	1/12/32/32	0/3/3/3
38	GDP	KN	502	-	-	3/12/32/32	0/3/3/3
38	GDP	KL	502	-	-	1/12/32/32	0/3/3/3
38	GDP	OL	502	-	-	4/12/32/32	0/3/3/3
36	GTP	LE	501	37	-	9/18/38/38	0/3/3/3

The worst 5 of 451 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	RK	501	GTP	C5-C6	-4.37	1.38	1.47
36	RE	501	GTP	C5-C6	-4.34	1.38	1.47
36	QE	501	GTP	C5-C6	-4.29	1.38	1.47
36	BG	501	GTP	C5-C6	-4.28	1.38	1.47
36	RI	501	GTP	C5-C6	-4.28	1.38	1.47

The worst 5 of 1643 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
38	AB	502	GDP	PA-O3A-PB	-4.58	117.11	132.83
38	AJ	502	GDP	PA-O3A-PB	-4.56	117.17	132.83
38	OB	502	GDP	PA-O3A-PB	-4.54	117.26	132.83
36	DM	501	GTP	PB-O3B-PG	-4.49	117.42	132.83
38	AF	502	GDP	PA-O3A-PB	-4.47	117.50	132.83

There are no chirality outliers.

5 of 1035 torsion outliers are listed below:

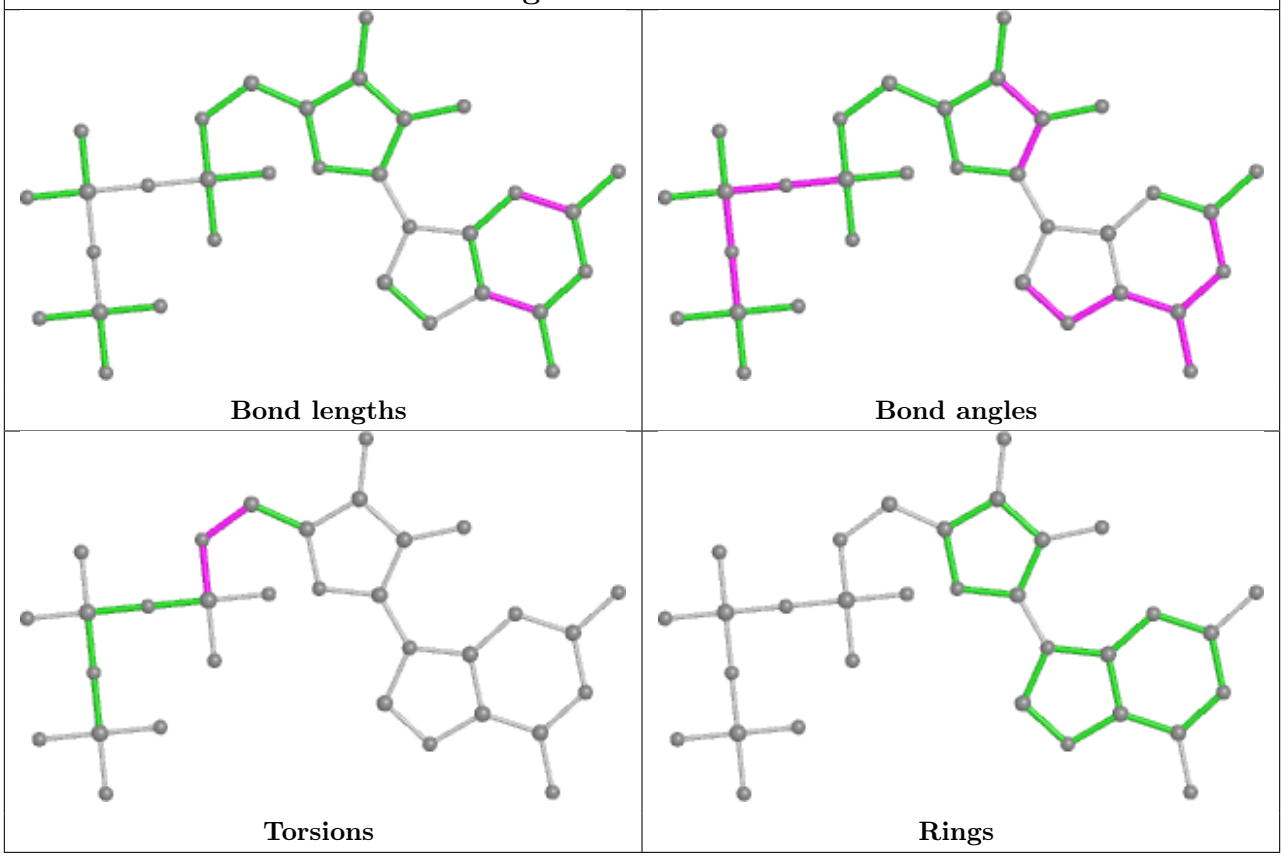
Mol	Chain	Res	Type	Atoms
36	AE	501	GTP	PB-O3A-PA-O5'
36	AG	501	GTP	C5'-O5'-PA-O1A
36	AK	501	GTP	C5'-O5'-PA-O3A
36	AK	501	GTP	C5'-O5'-PA-O1A
36	AM	501	GTP	PB-O3A-PA-O5'

There are no ring outliers.

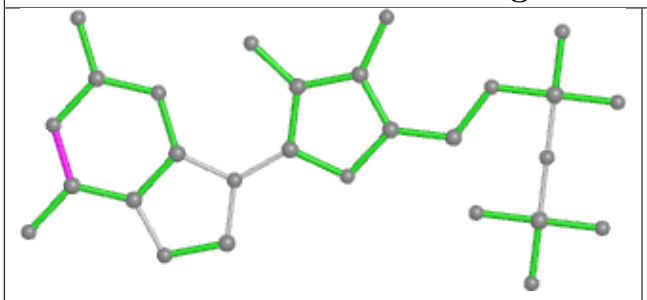
No monomer is involved in short contacts.

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.

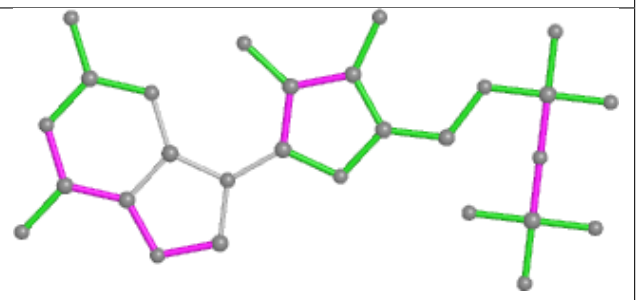
Ligand GTP II 501



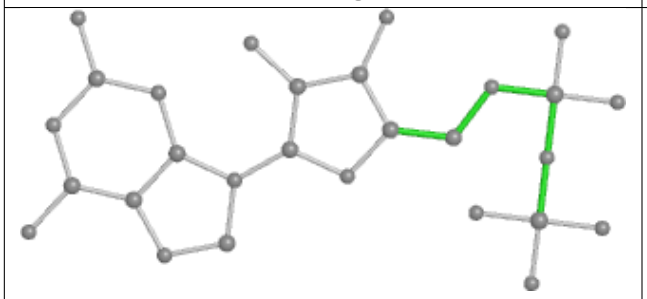
Ligand GDP GL 502



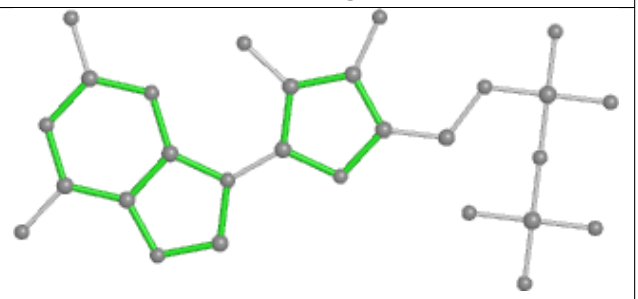
Bond lengths



Bond angles

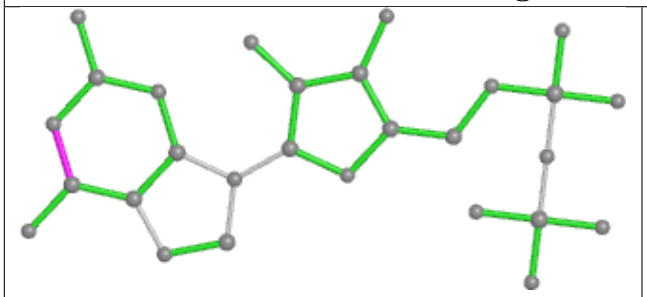


Torsions



Rings

Ligand GDP SF 502



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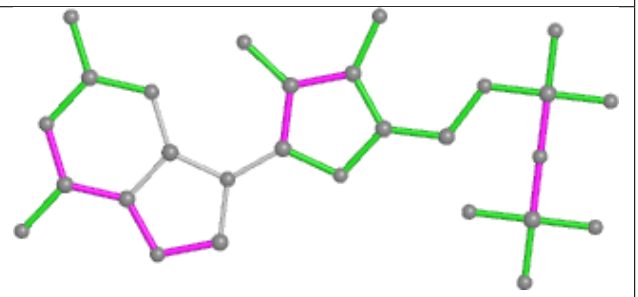

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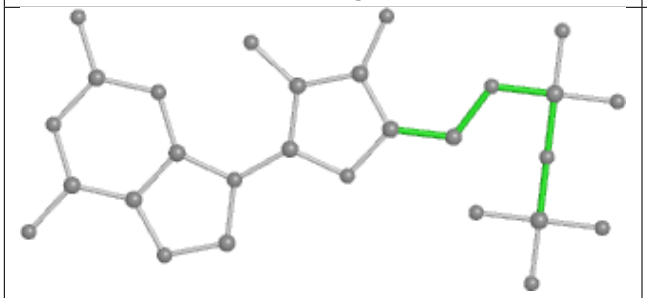

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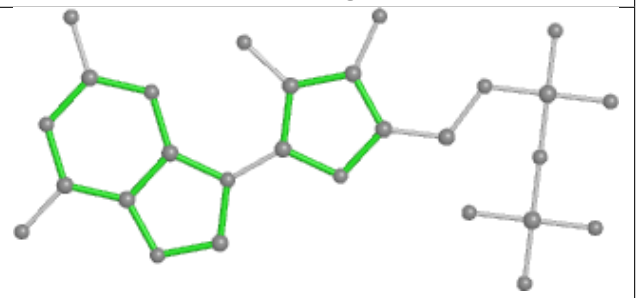
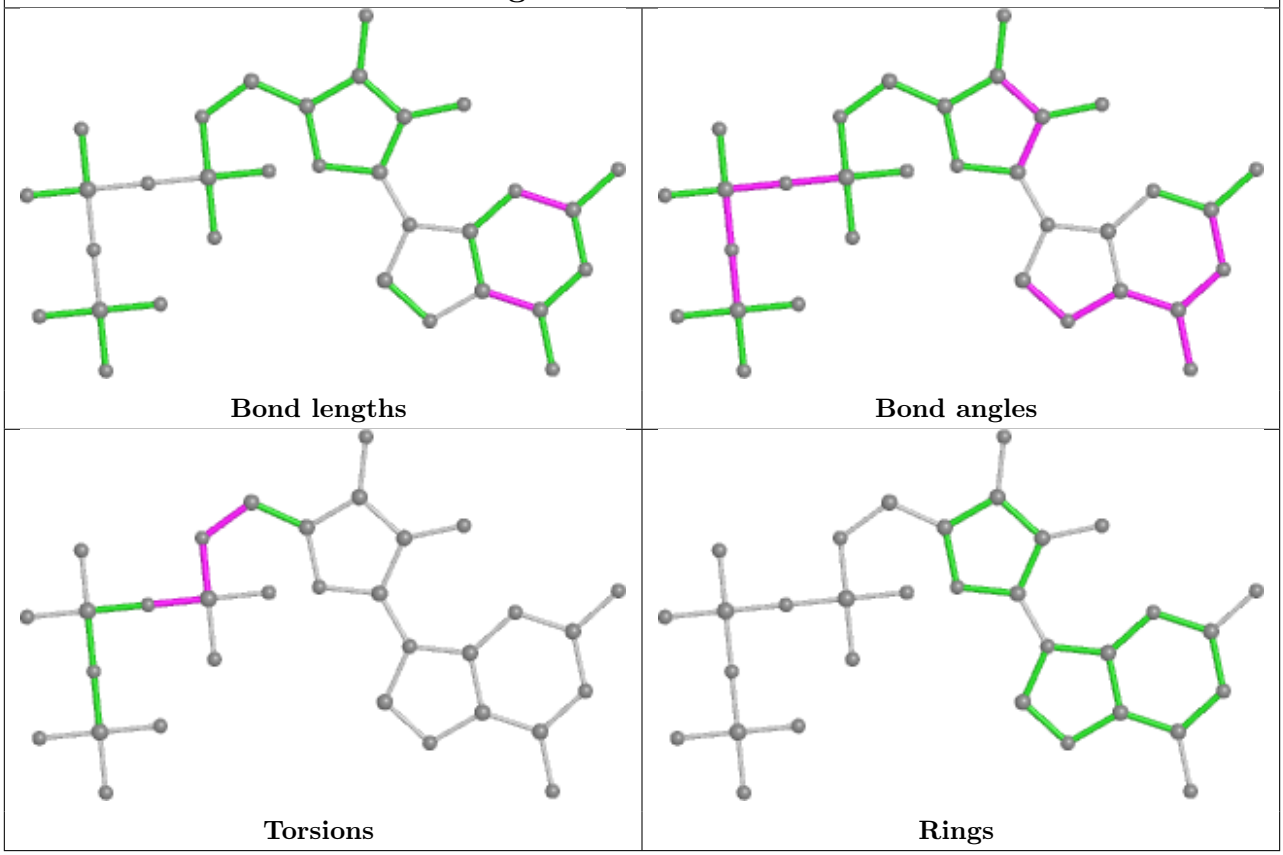


Rings

Ligand GTP GG 501



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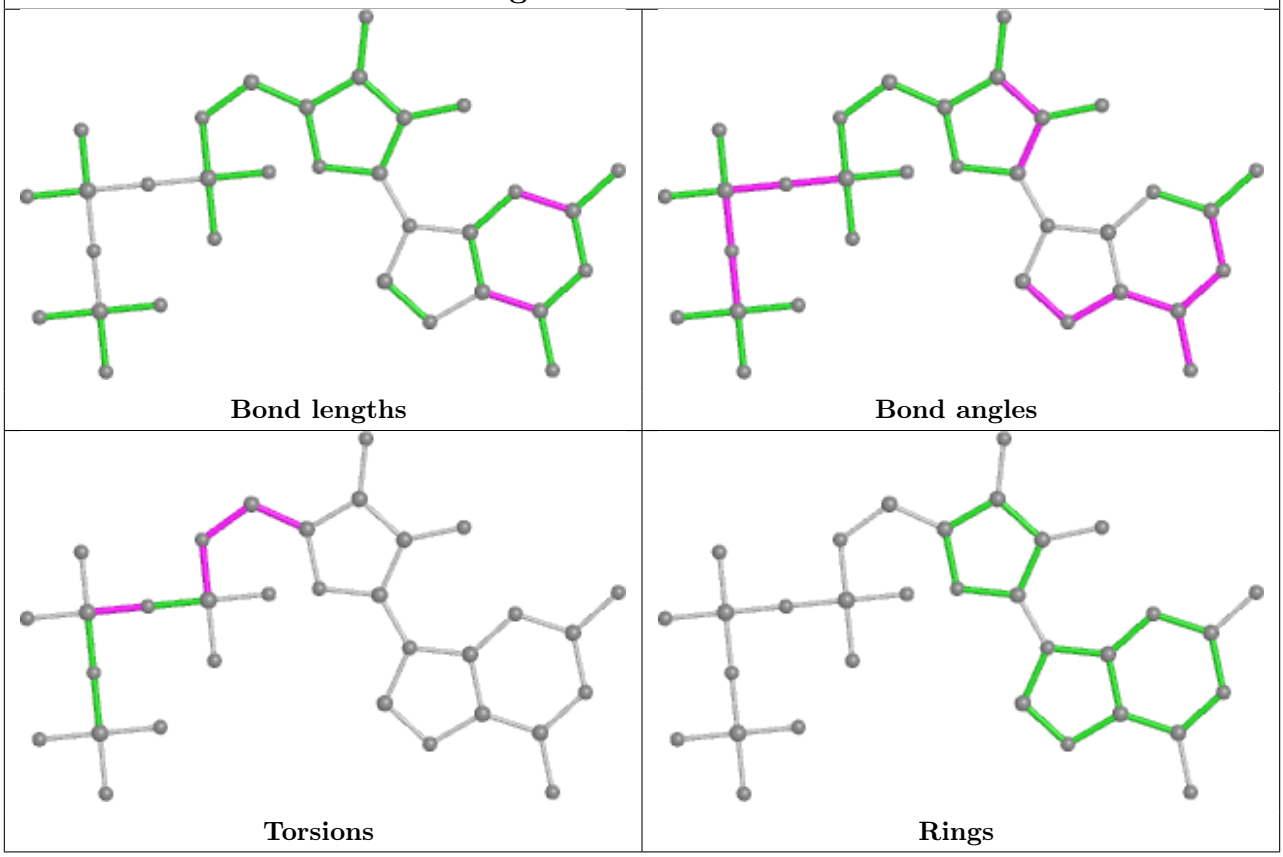

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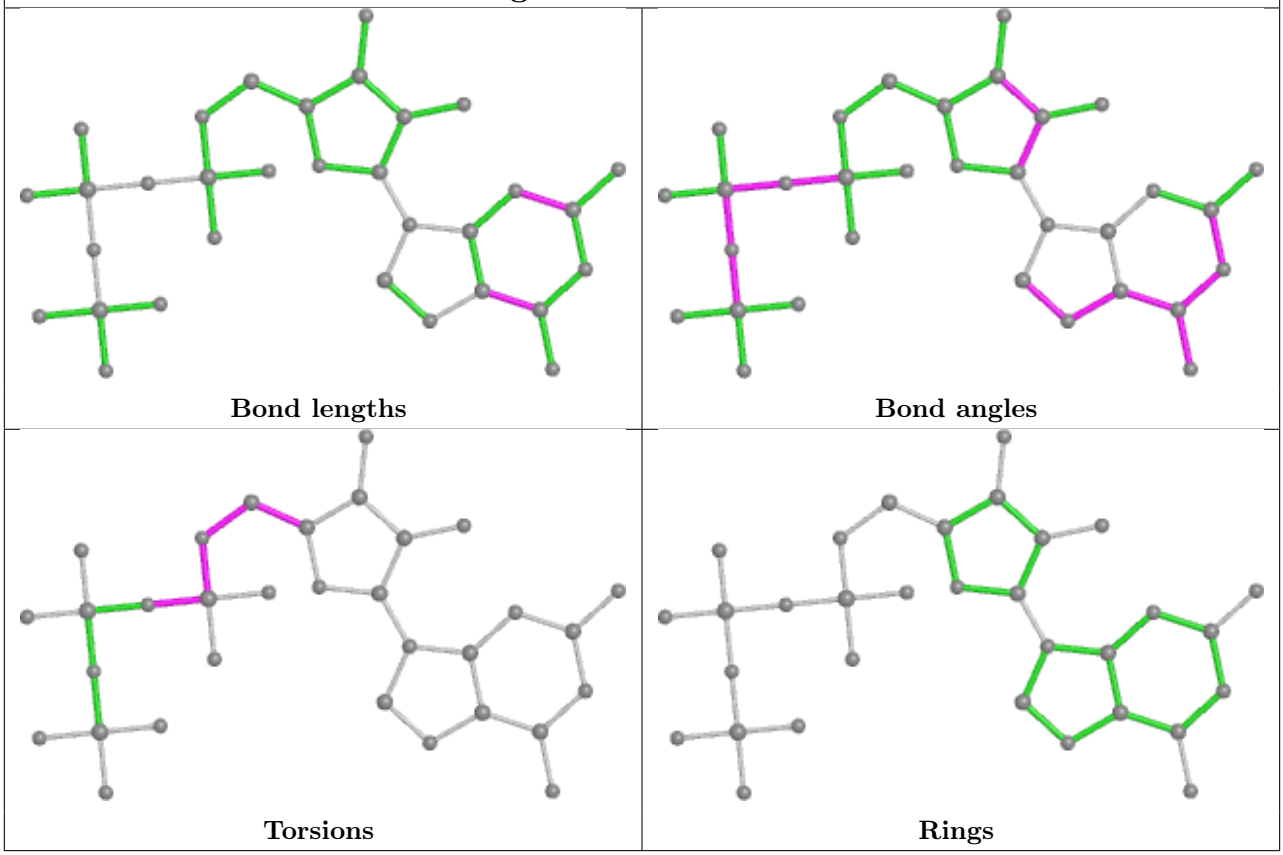

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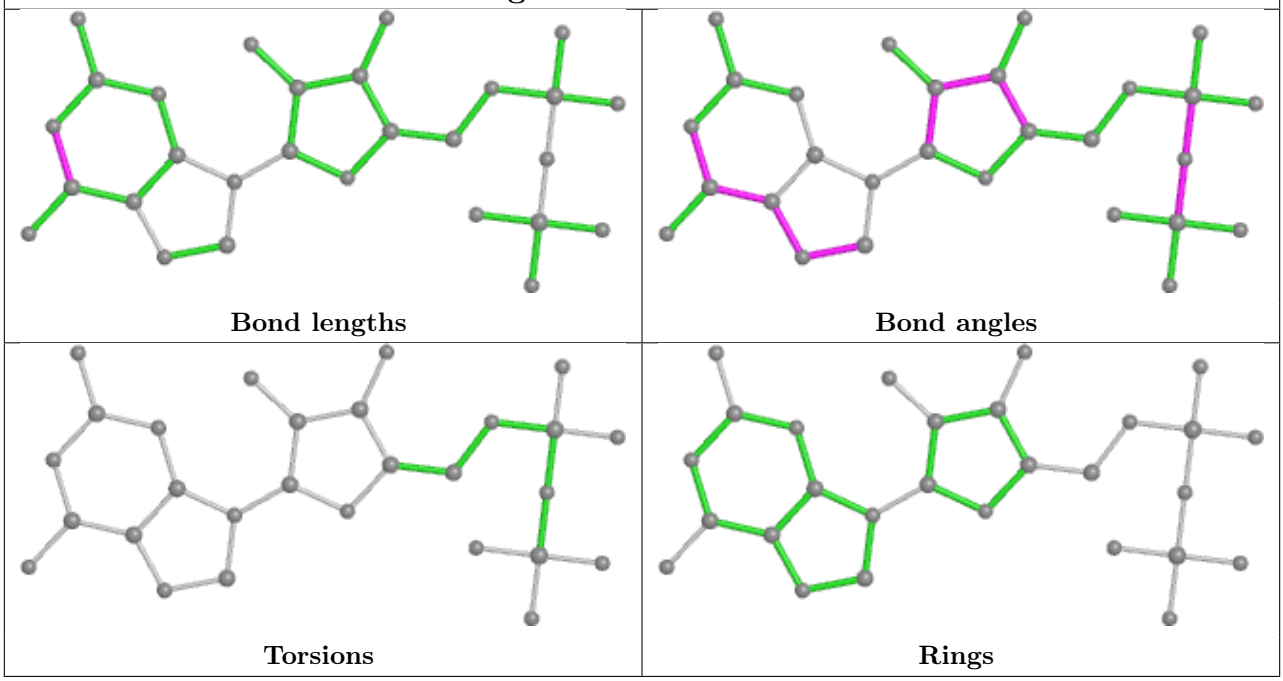

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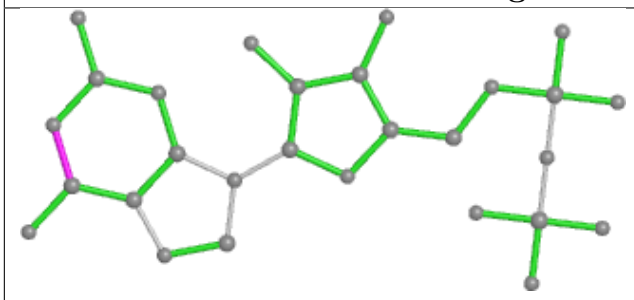

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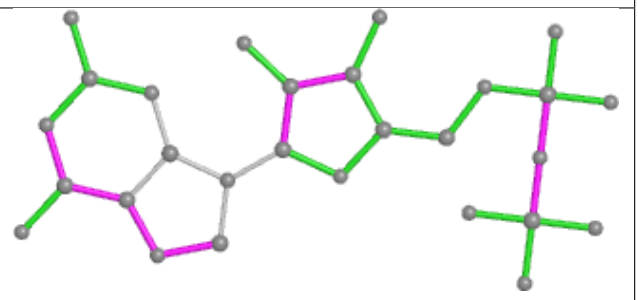
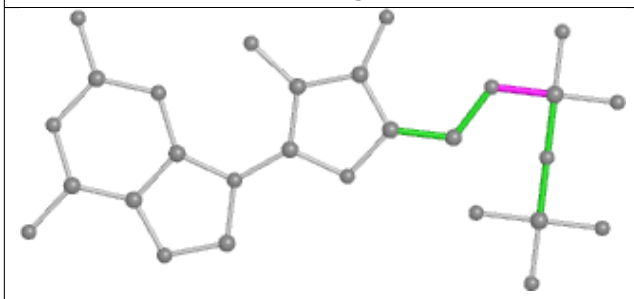


Bond angles



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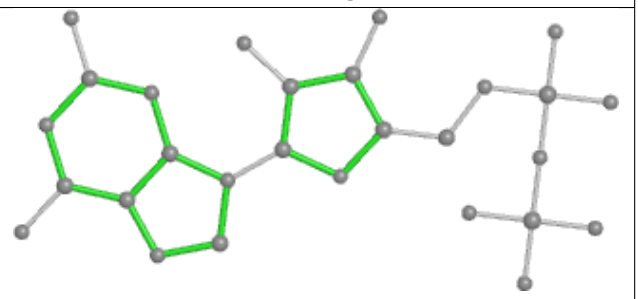
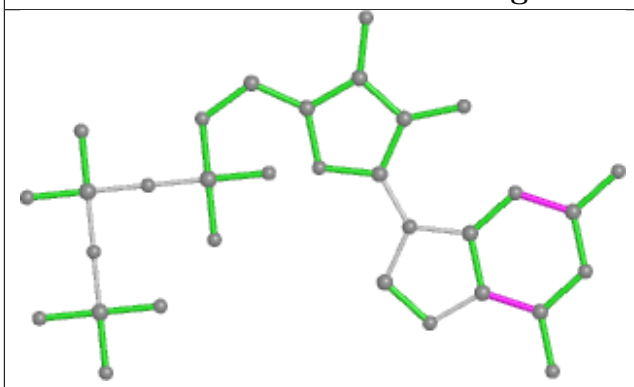


Rings

Ligand GTP CC 501



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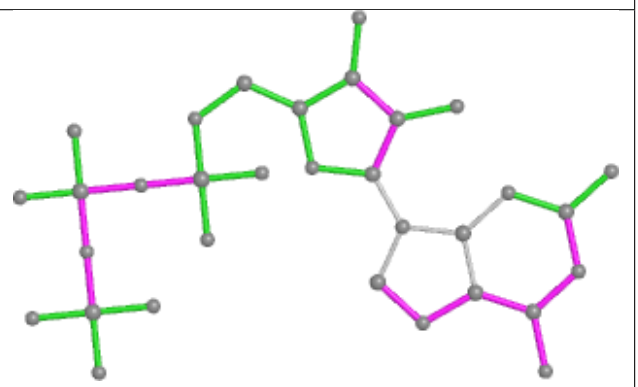

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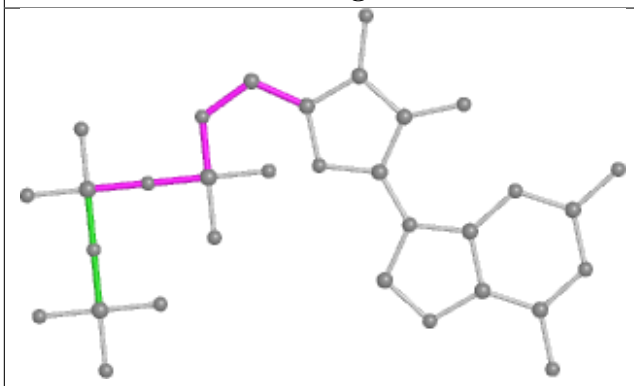

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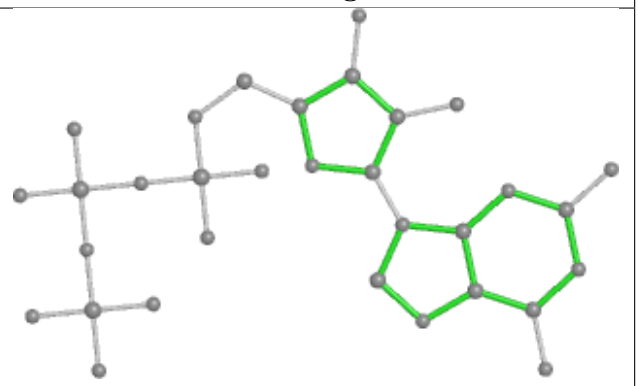
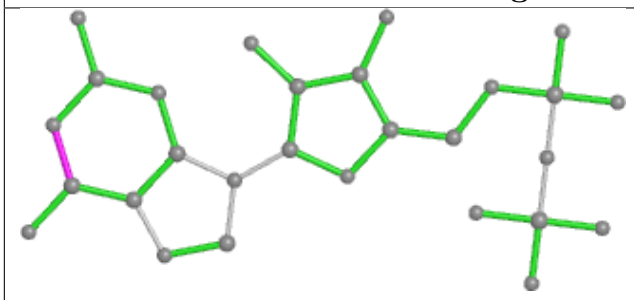


Rings

Ligand GDP HL 502



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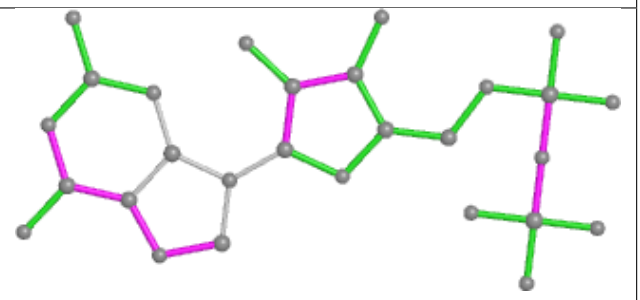

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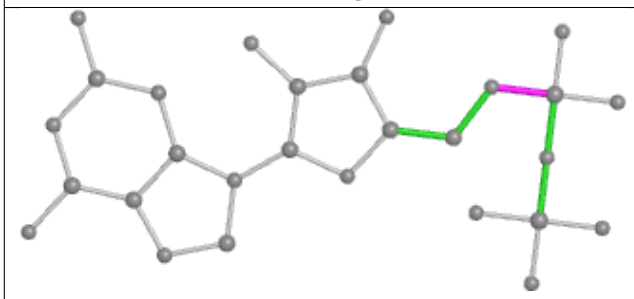

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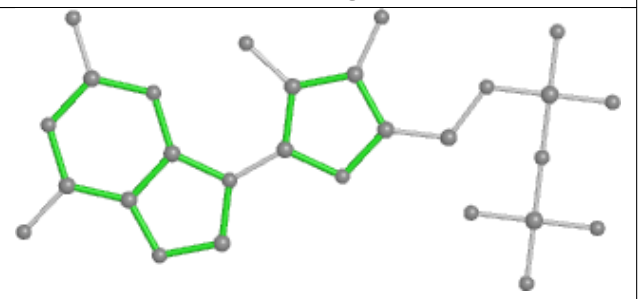
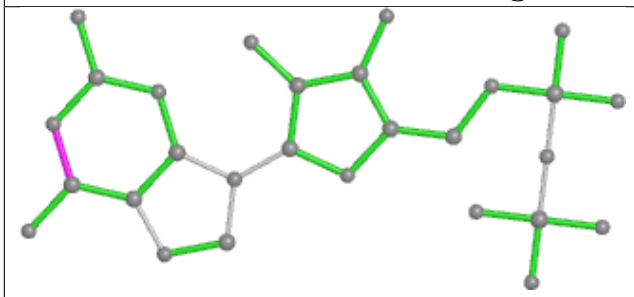


Rings

Ligand GDP MJ 502



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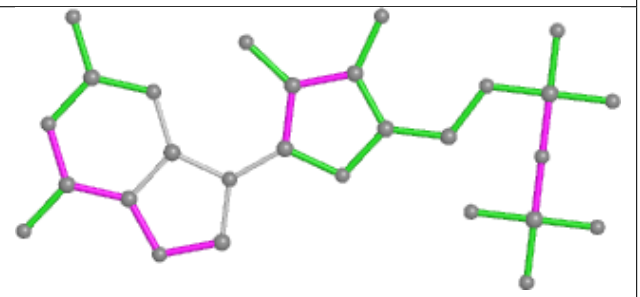

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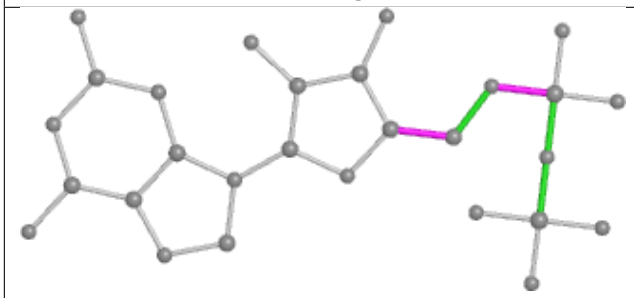

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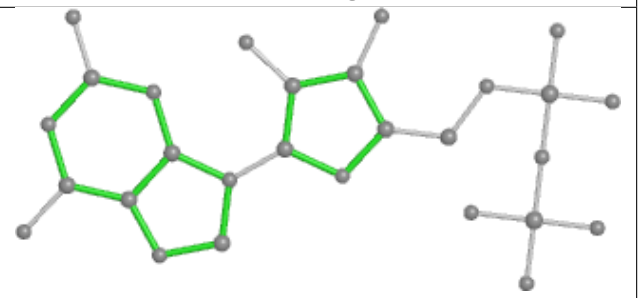
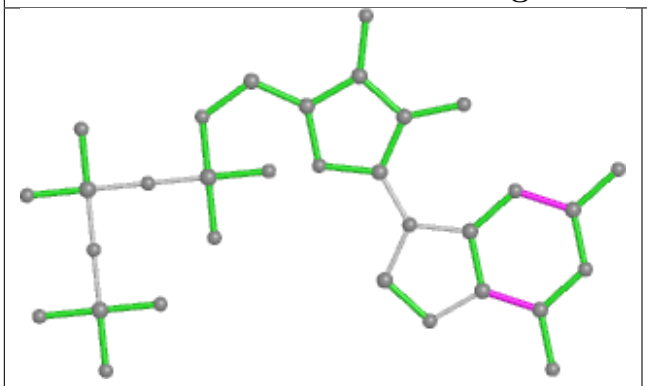


Rings

Ligand GTP VE 501



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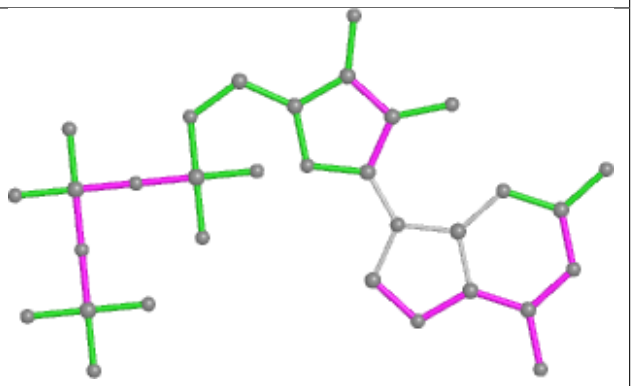

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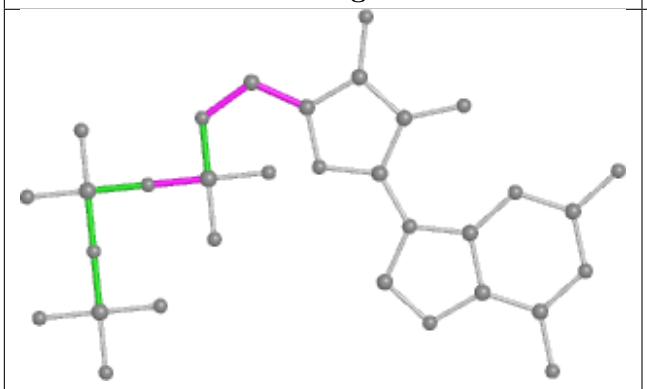

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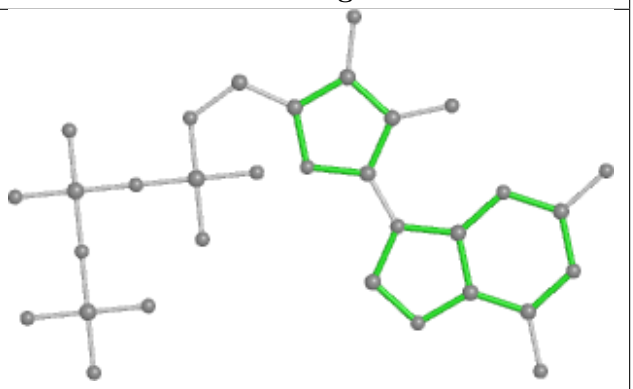
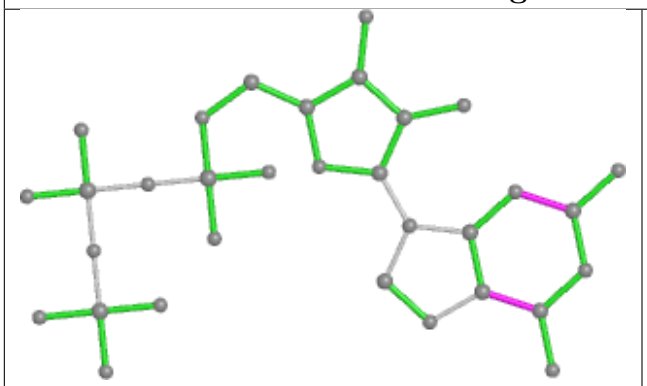


Rings

Ligand GTP AG 501



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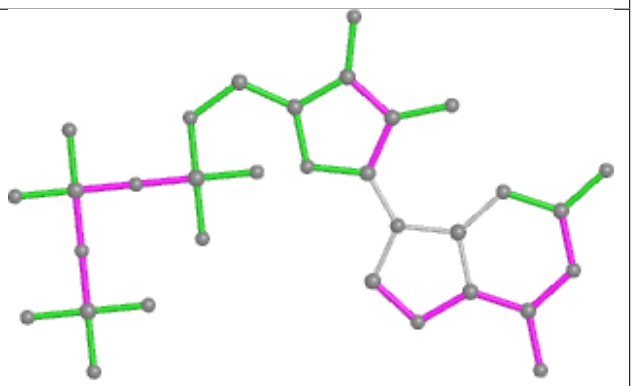

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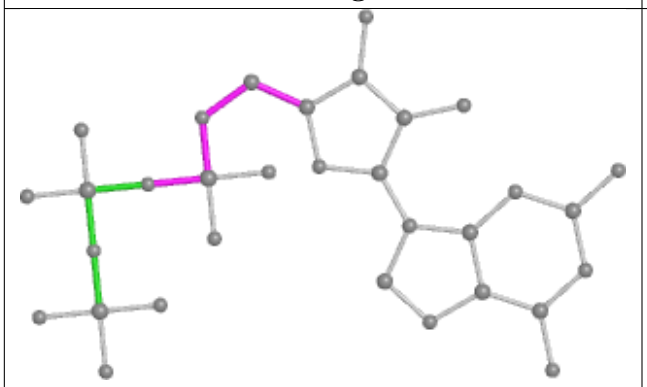

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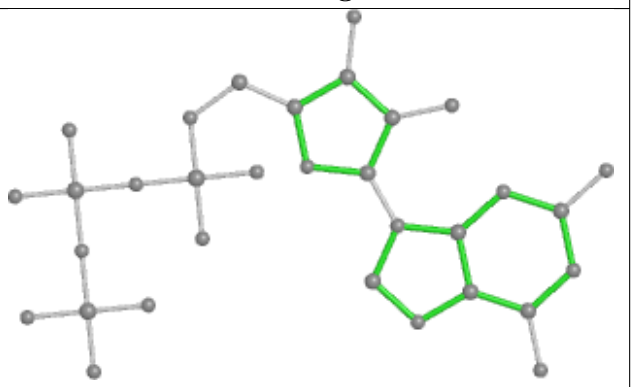

Rings

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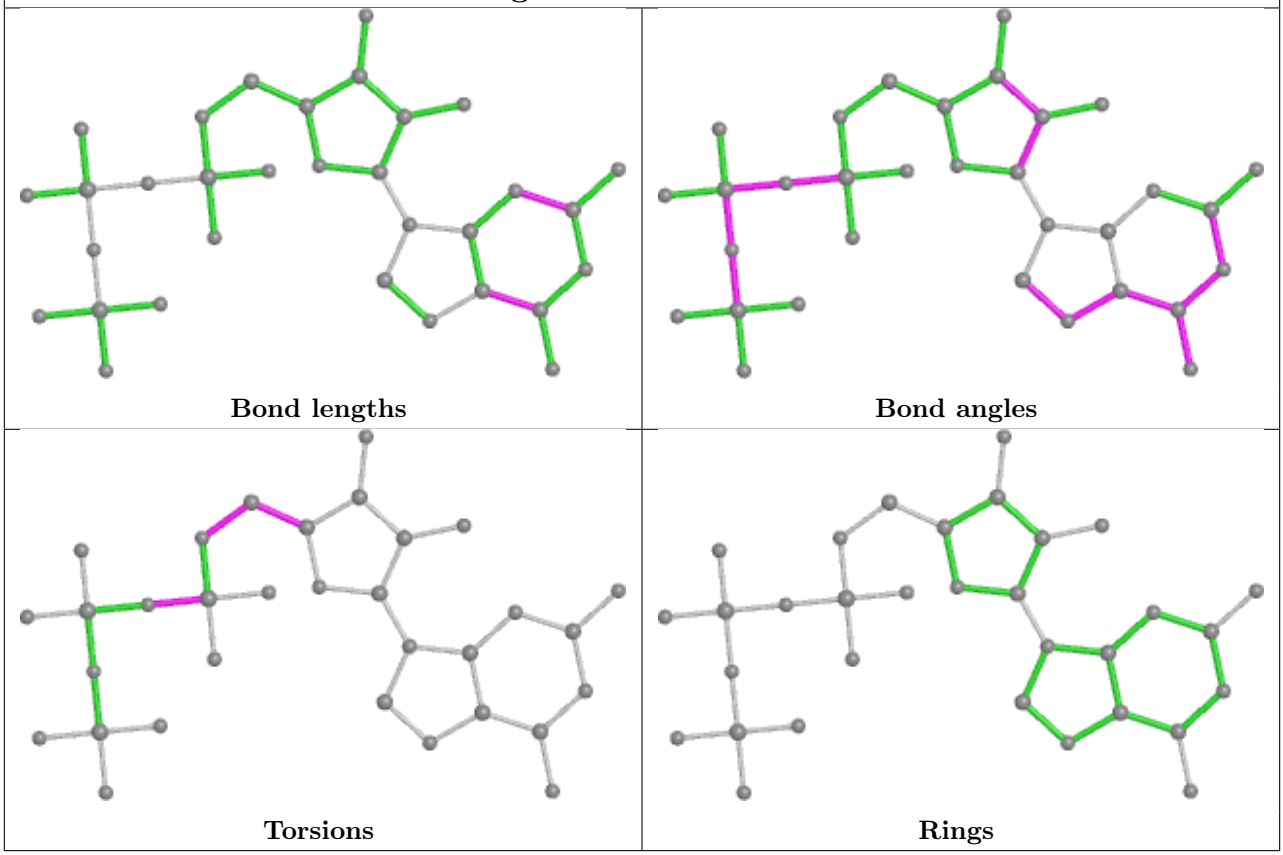

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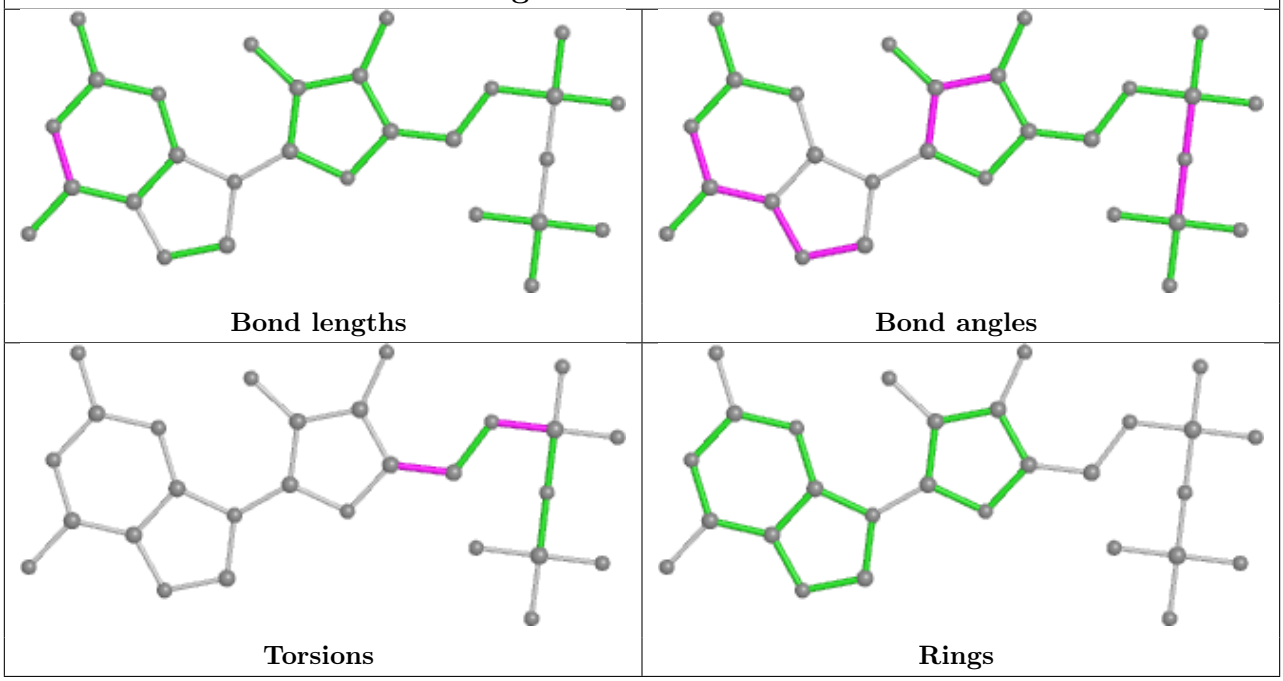

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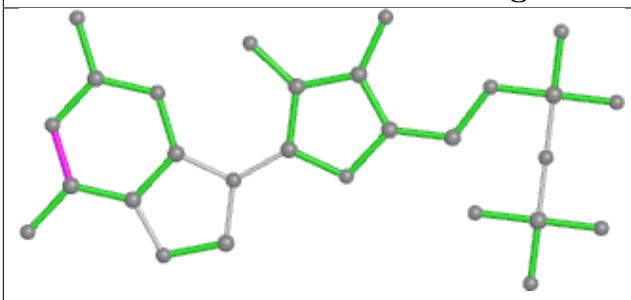

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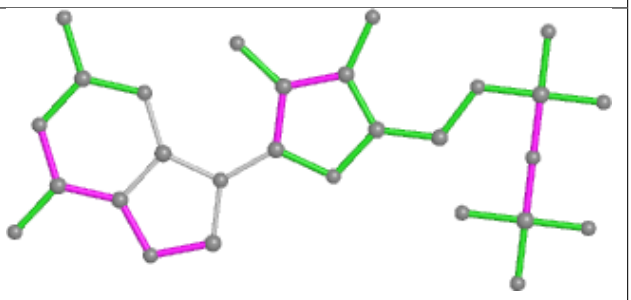
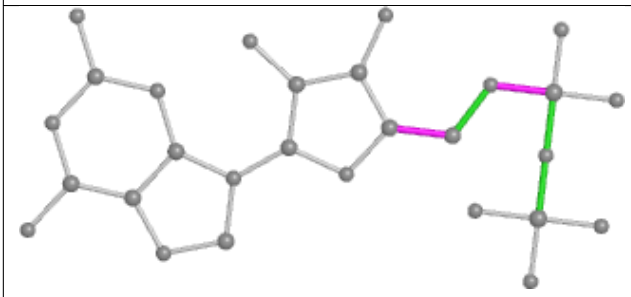


Bond angles



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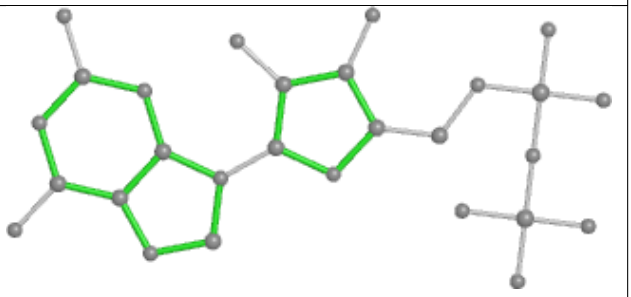

Rings

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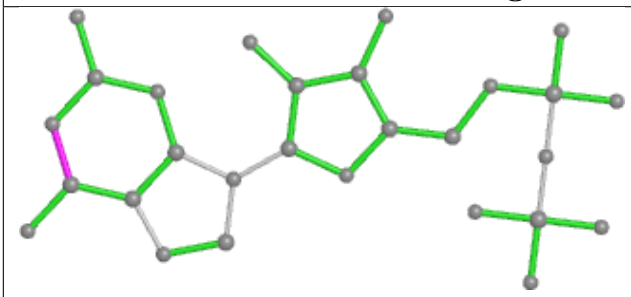

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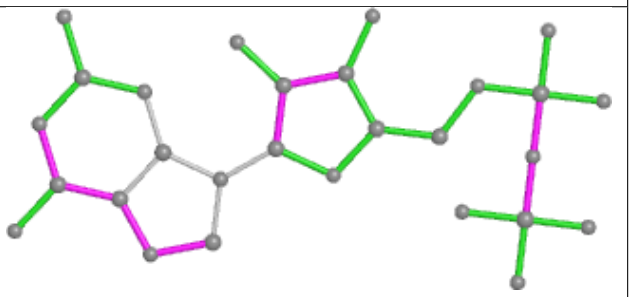

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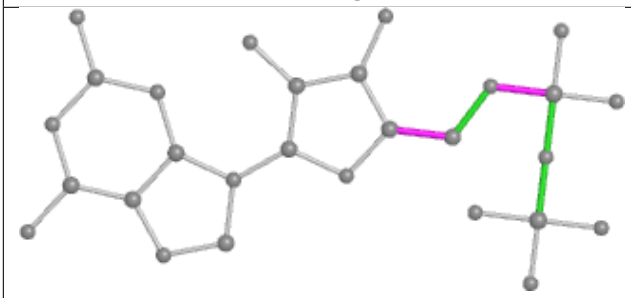

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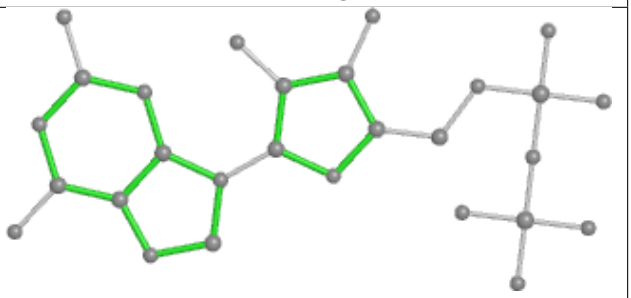

Rings

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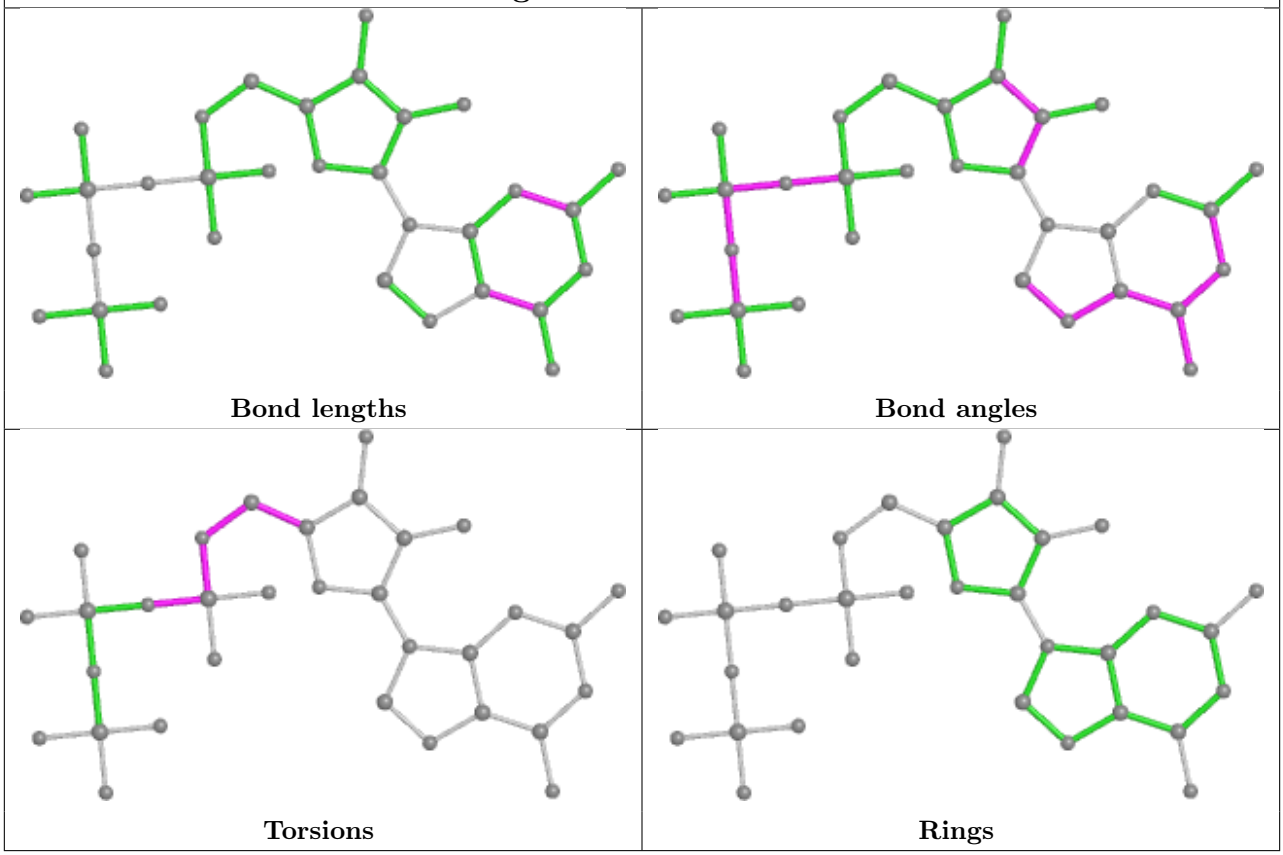

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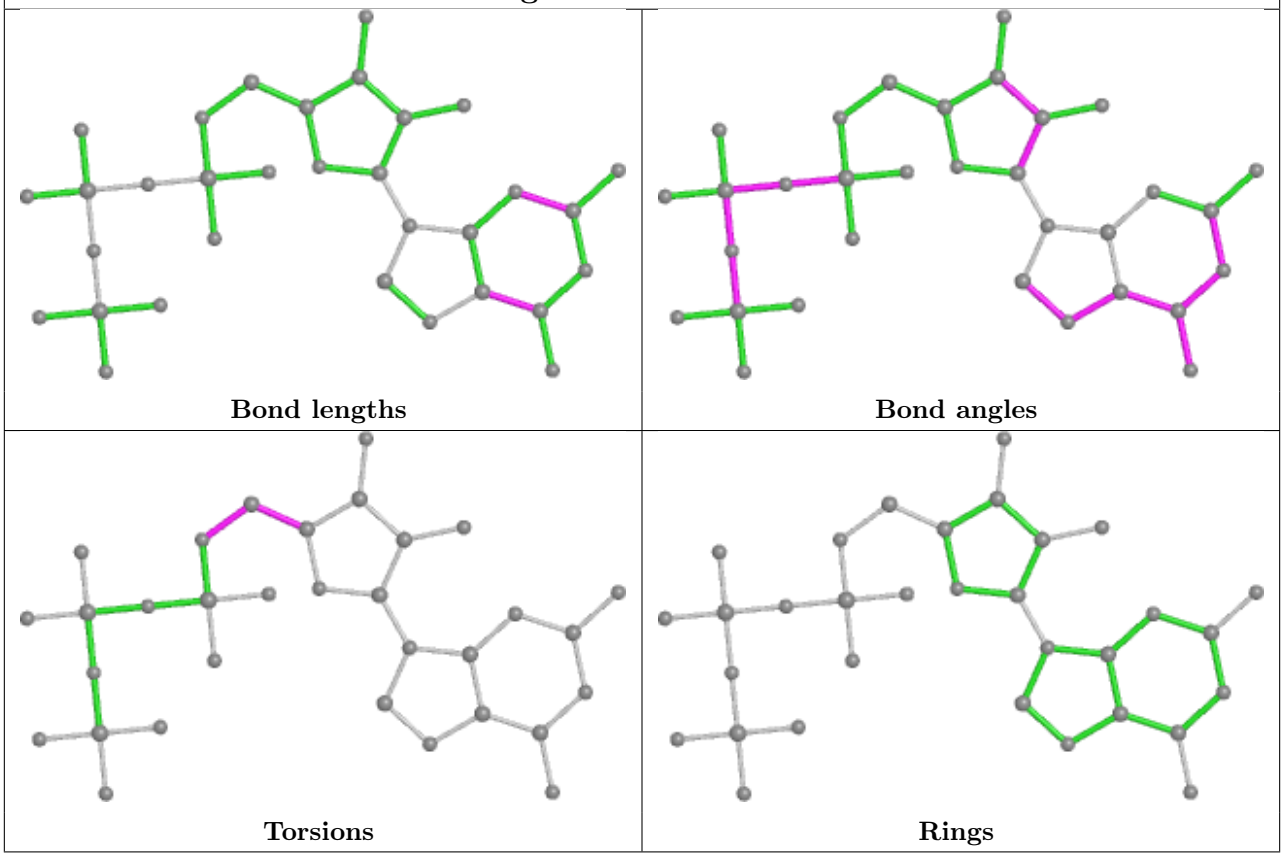

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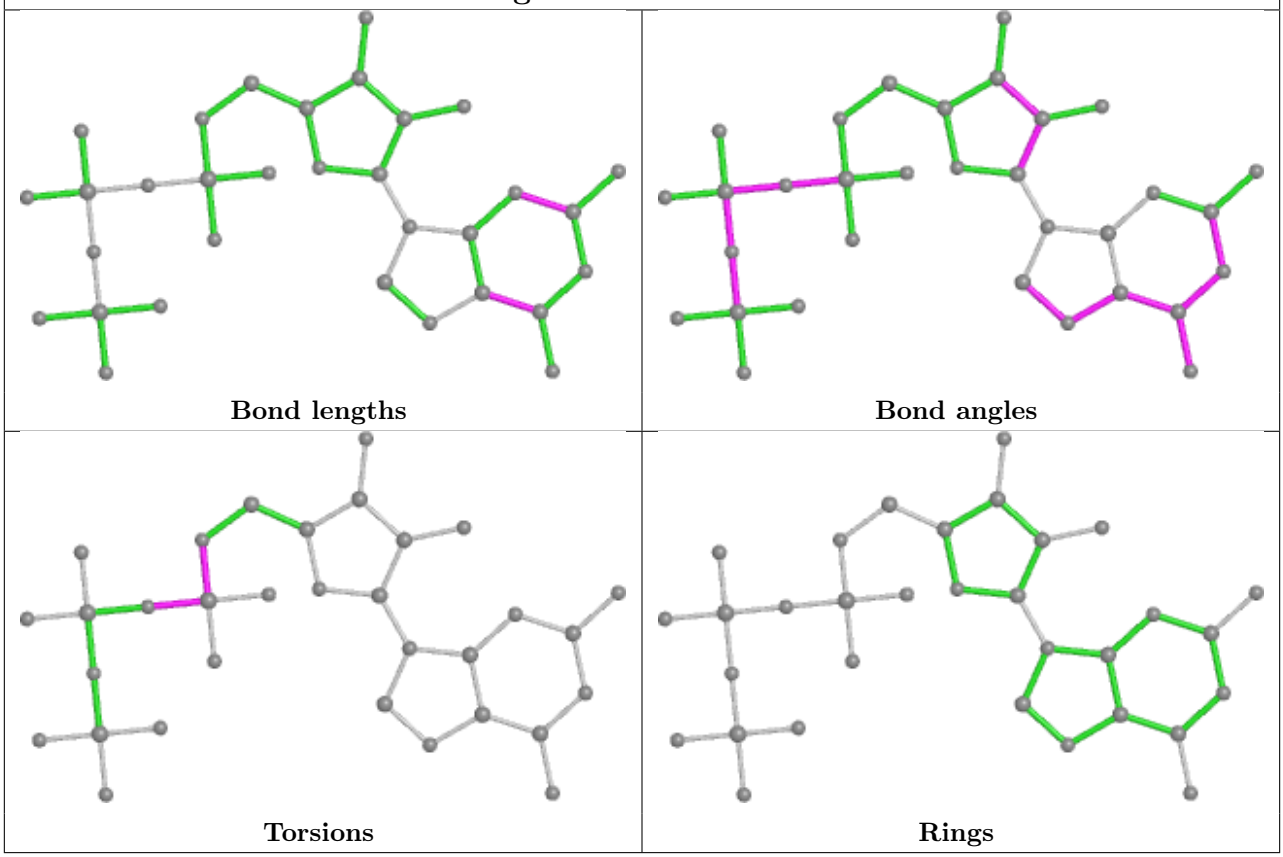

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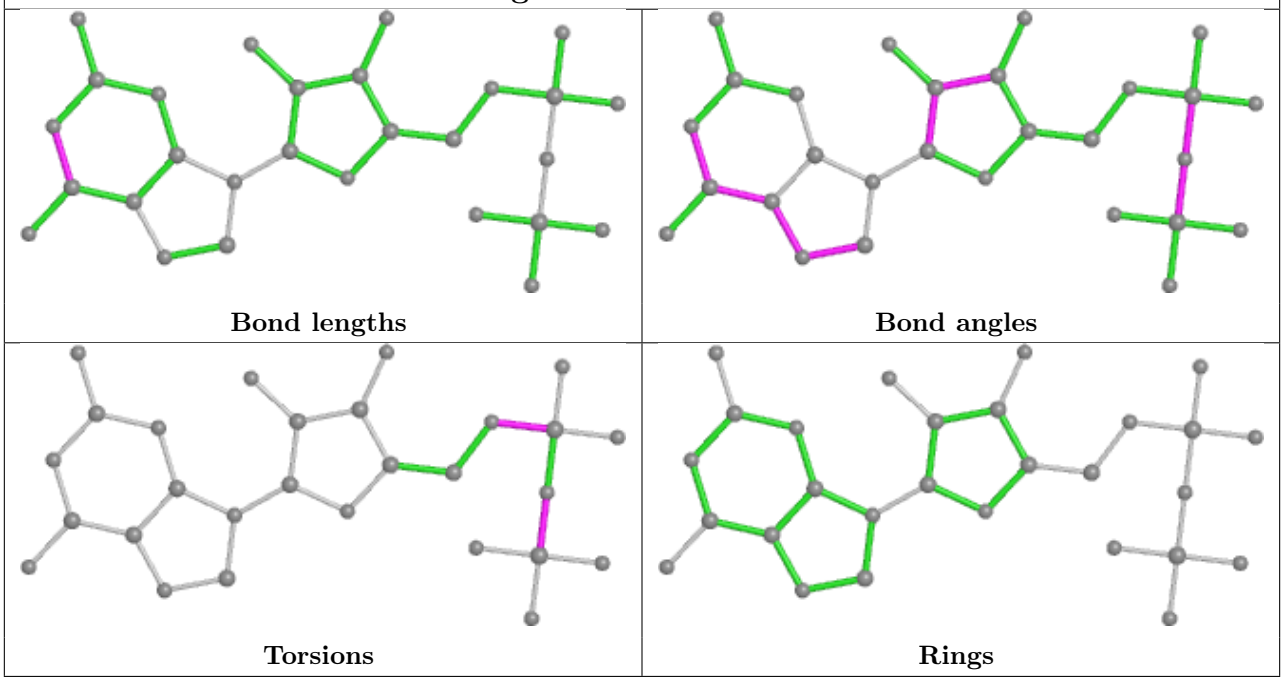

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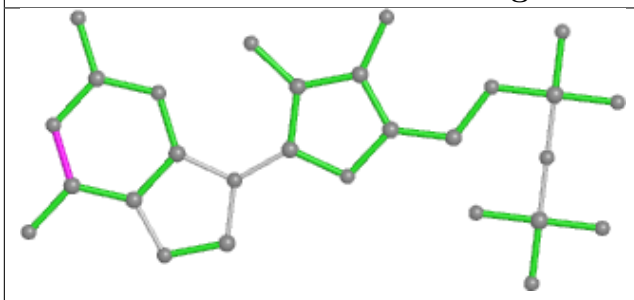
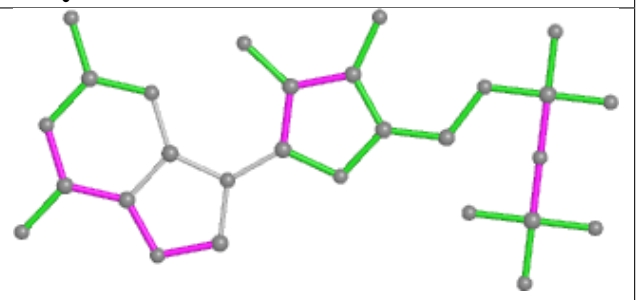
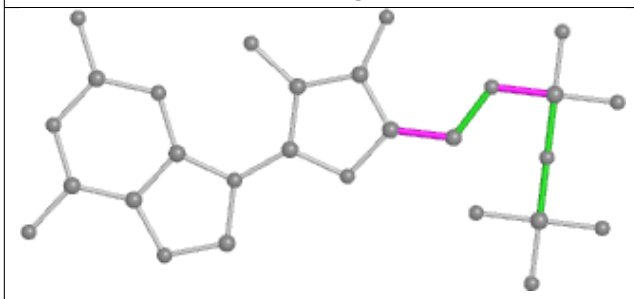


Bond lengths



Bond angles



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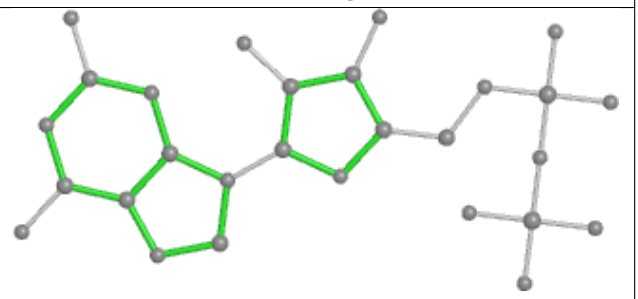
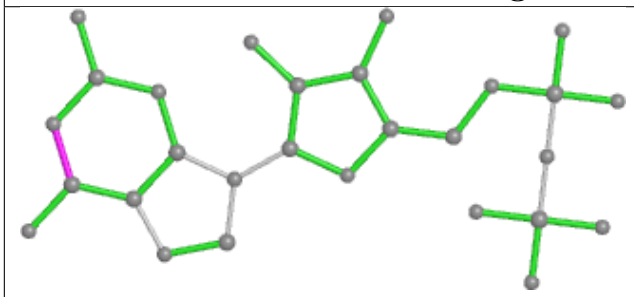


Rings

Ligand GDP AB 502



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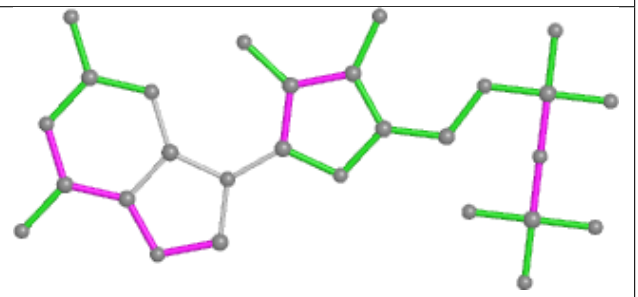

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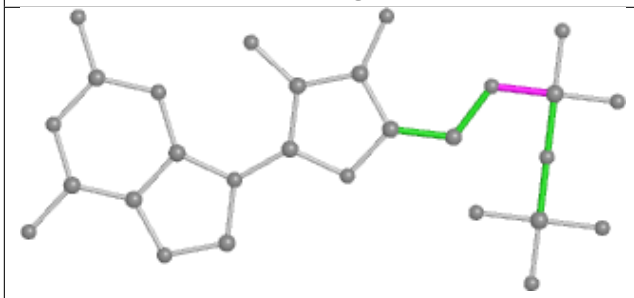

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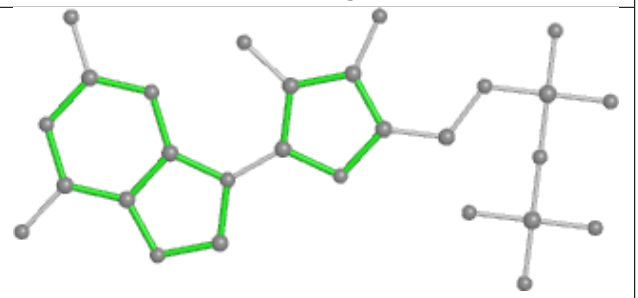
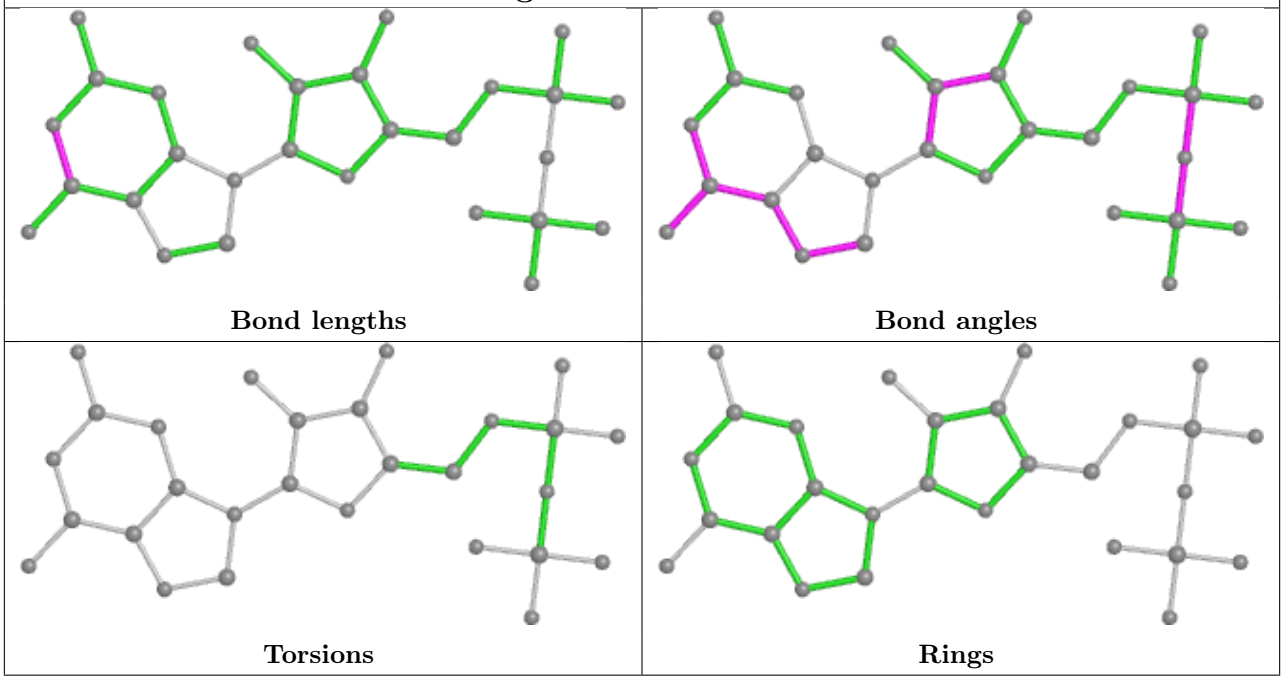
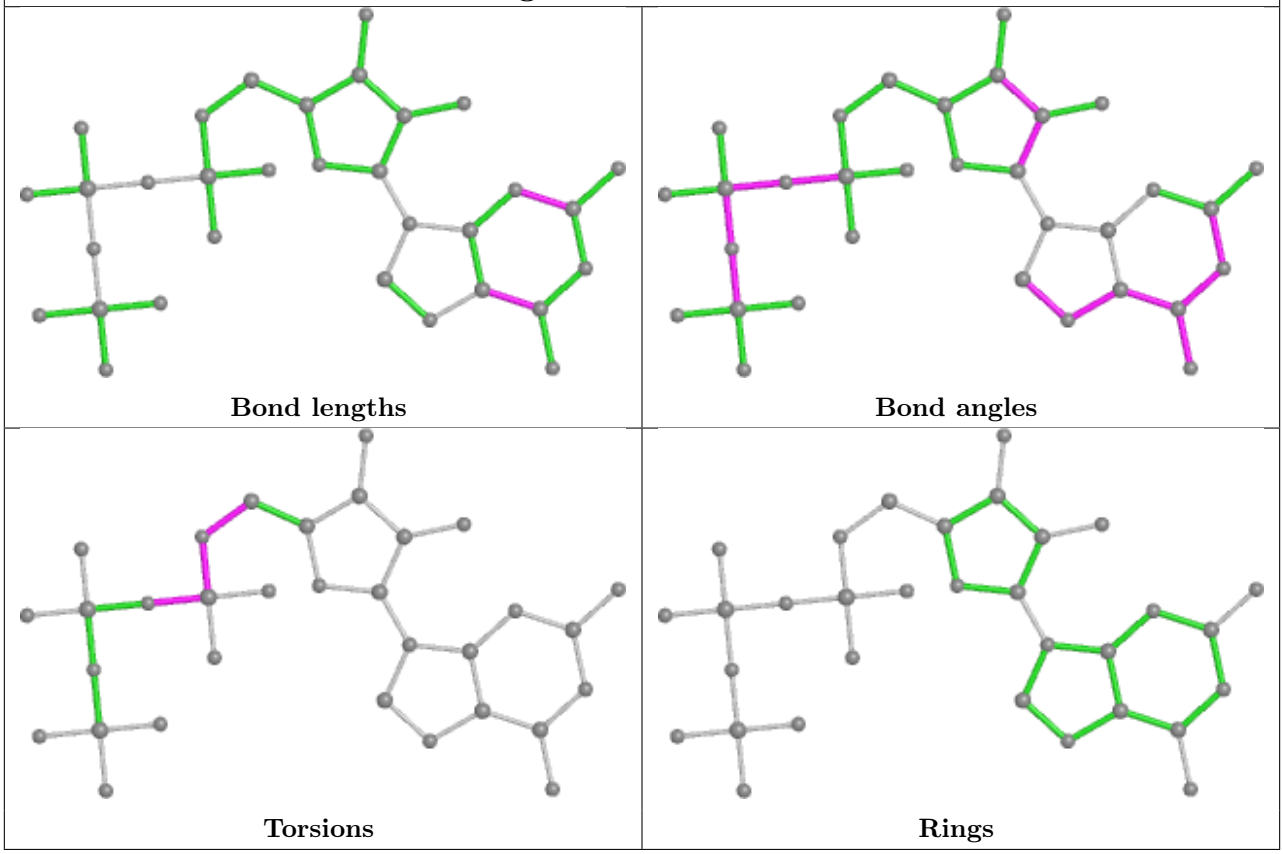


Rings

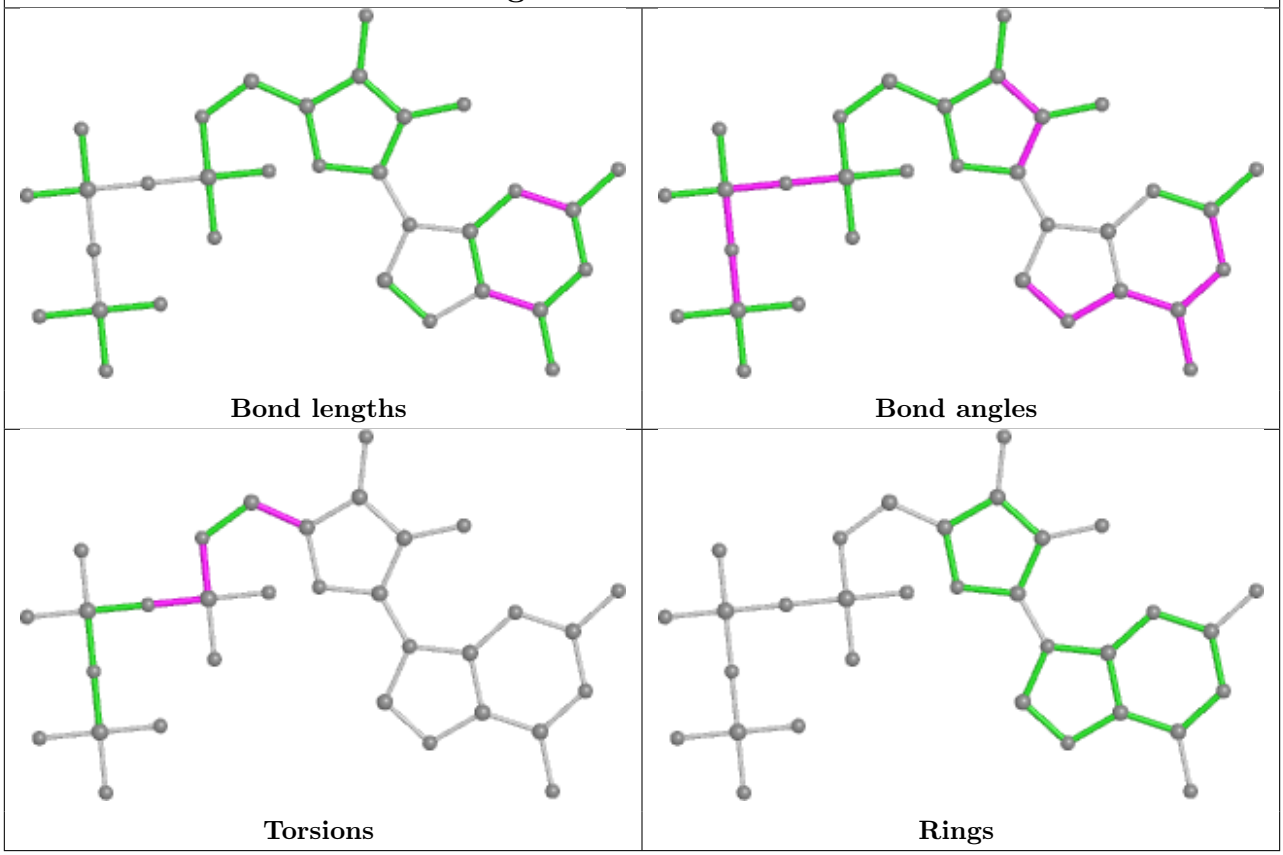
Ligand GDP SJ 502



Ligand GTP EI 501



Ligand GTP TM 501



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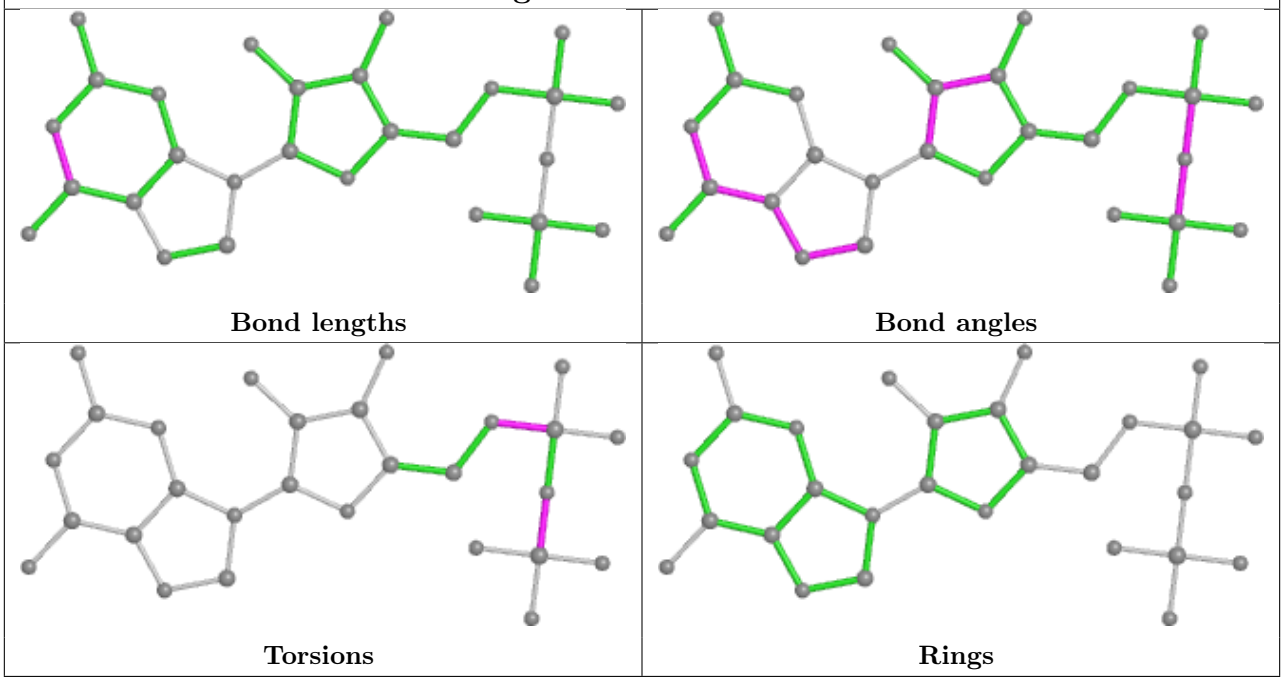

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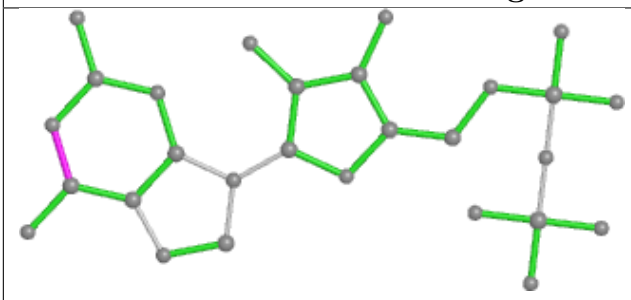

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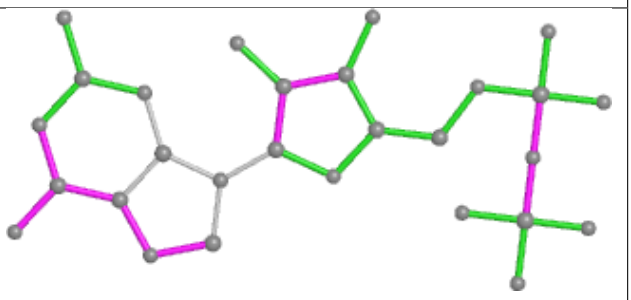
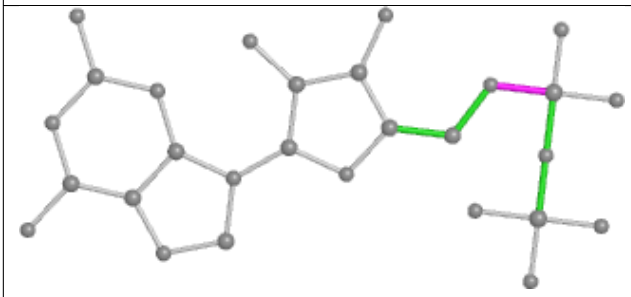
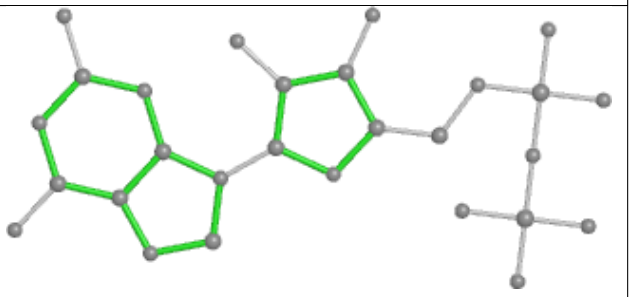


Bond angles

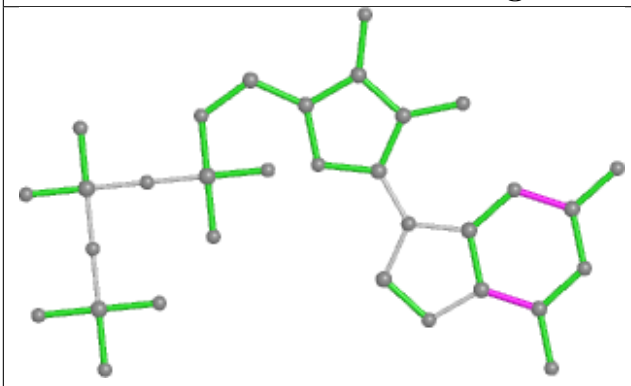


Torsions



Rings

Ligand GTP PM 501



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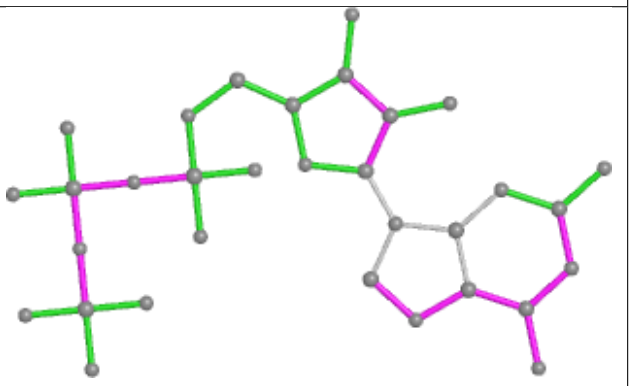

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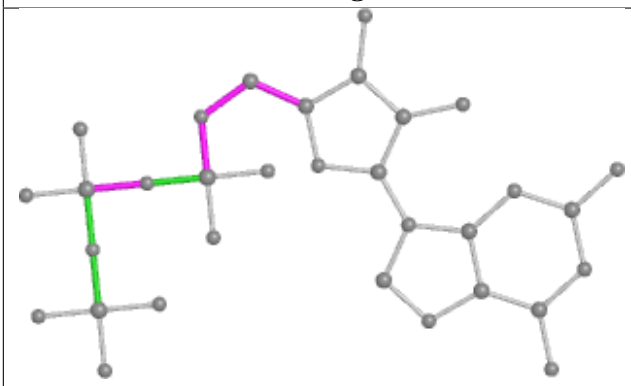

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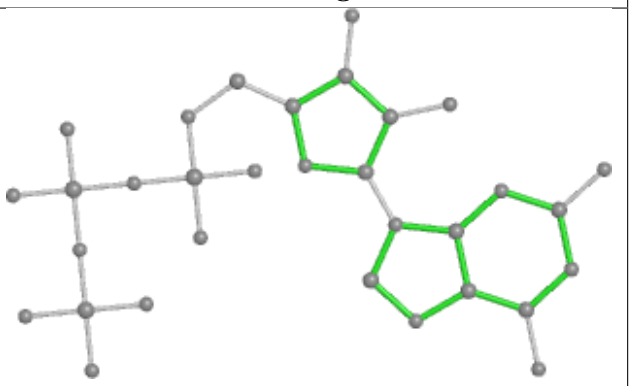
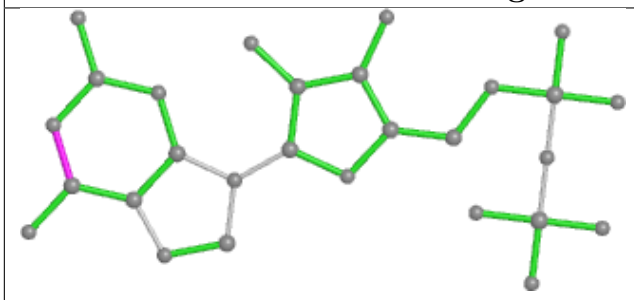


Rings

Ligand GDP QN 502



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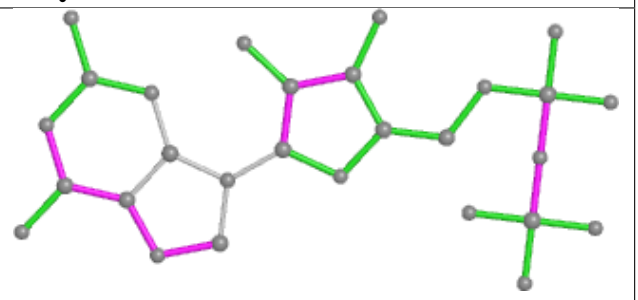

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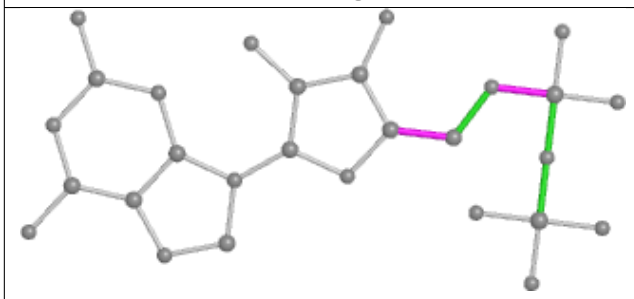

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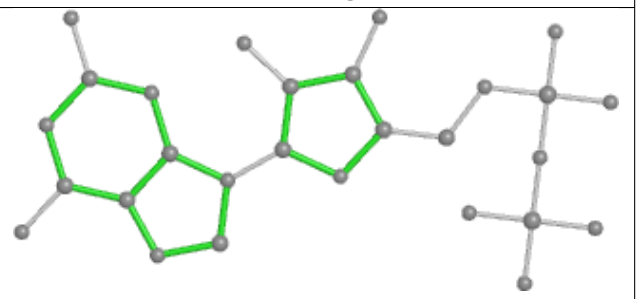

Rings

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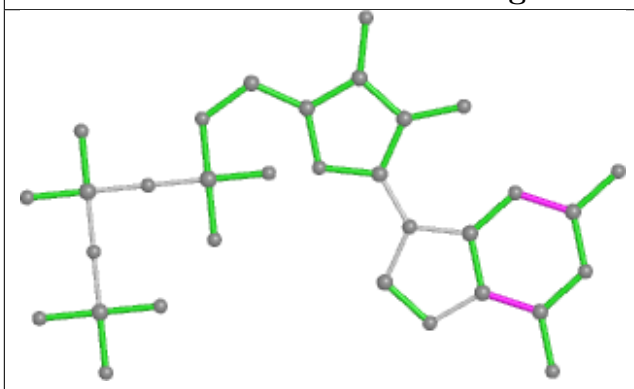

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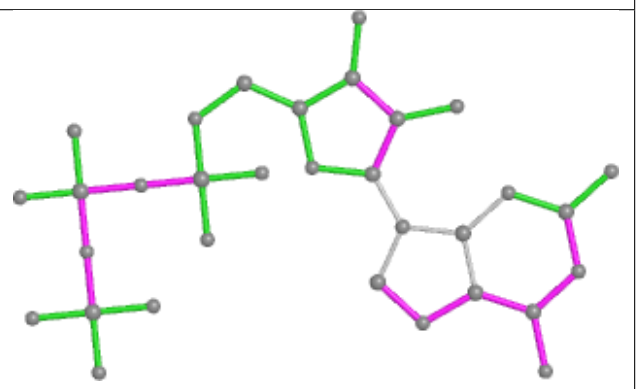

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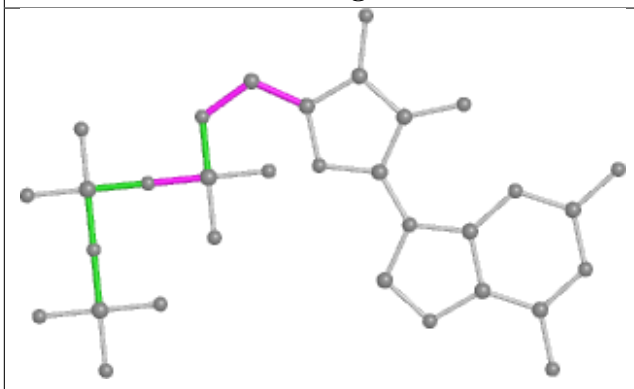

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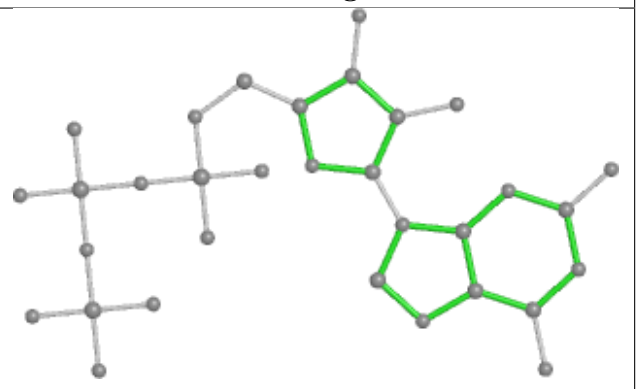
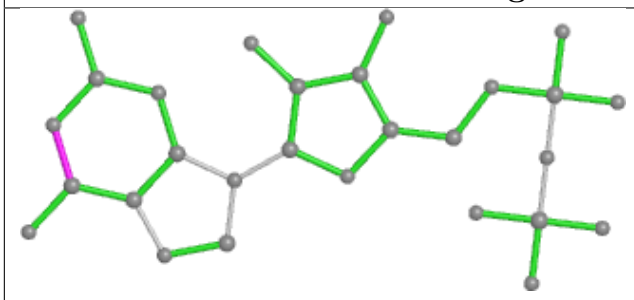


Rings

Ligand GDP RN 502



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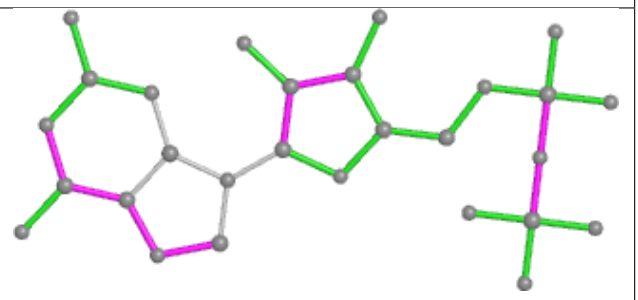

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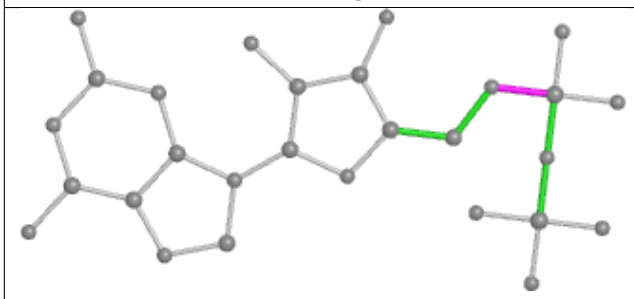

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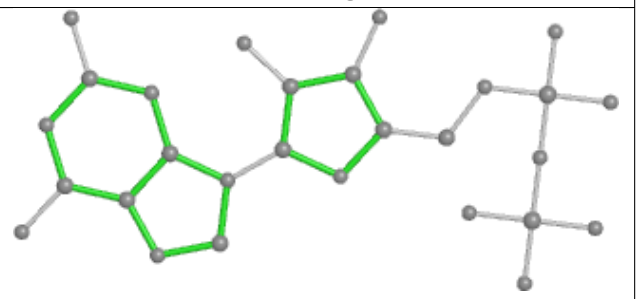
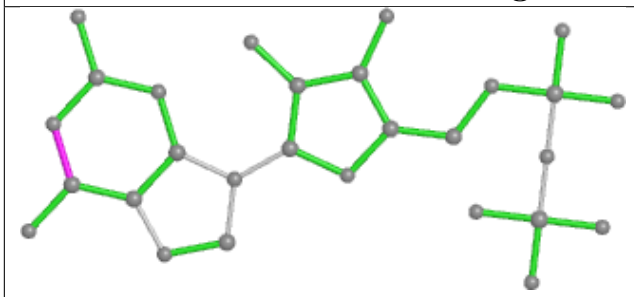


Rings

Ligand GDP SH 502



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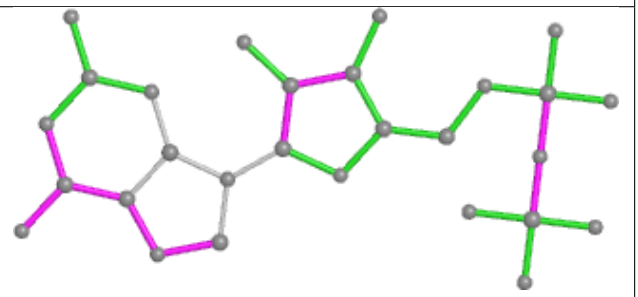

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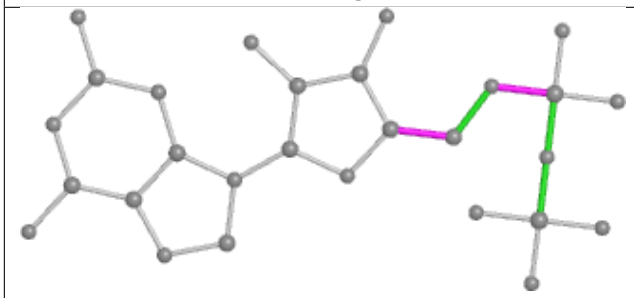

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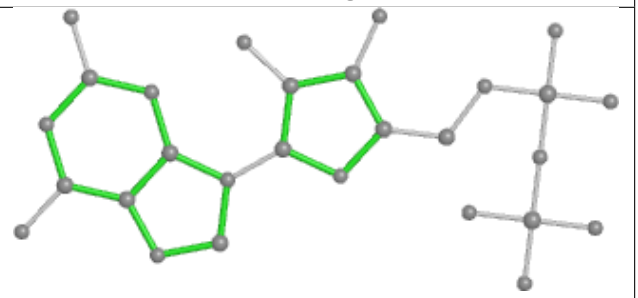
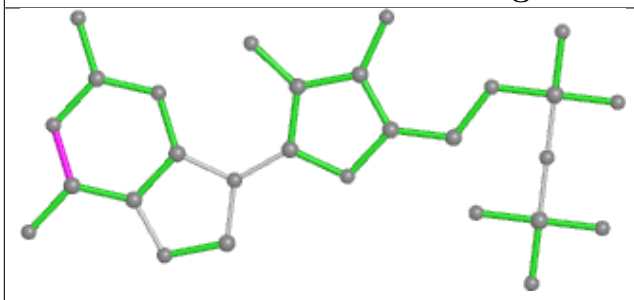


Rings

Ligand GDP PL 502



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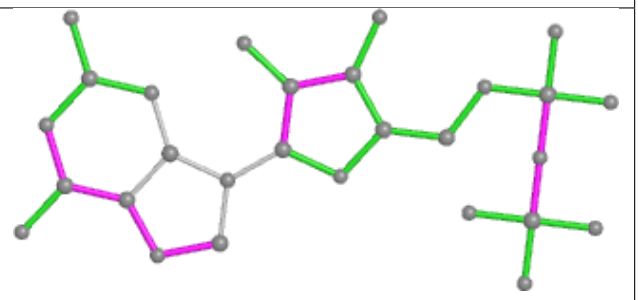

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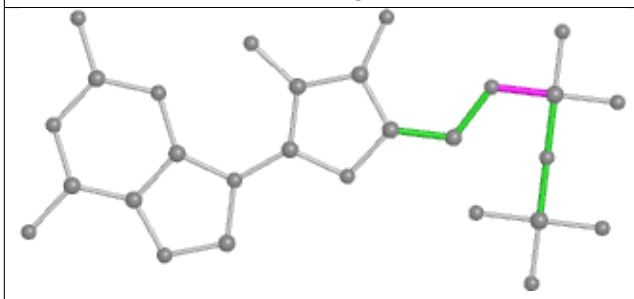

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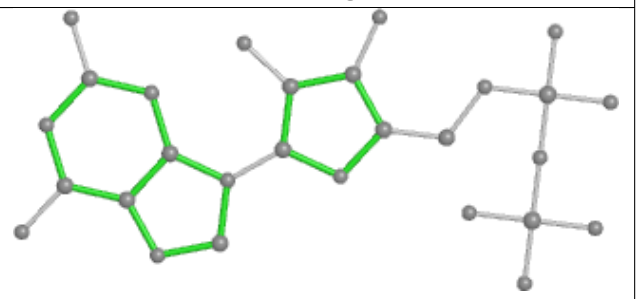
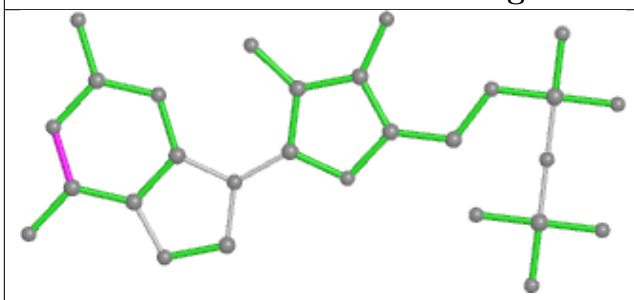


Rings

Ligand GDP GN 502



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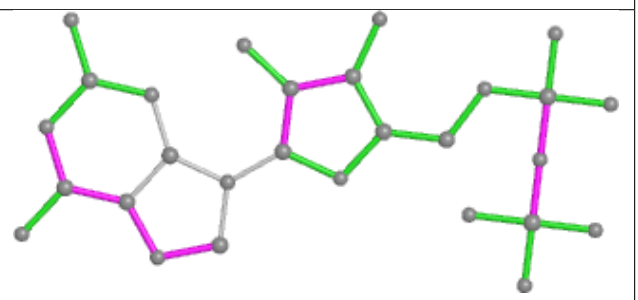

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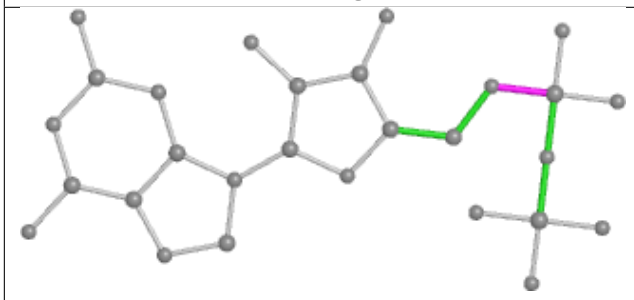

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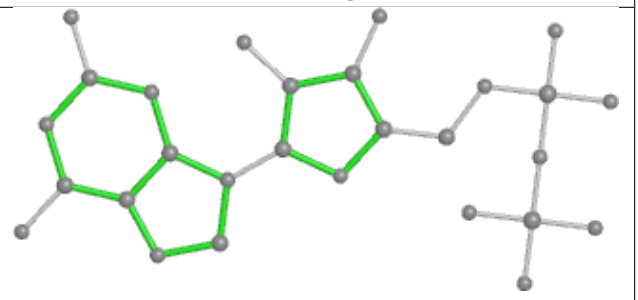

Rings

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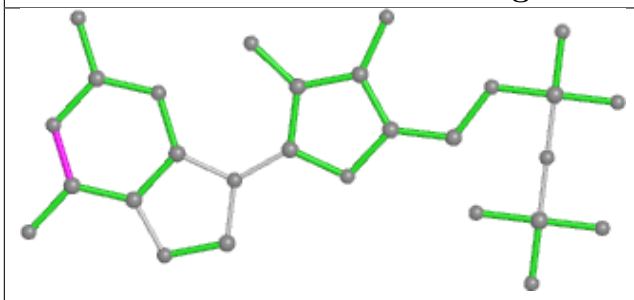

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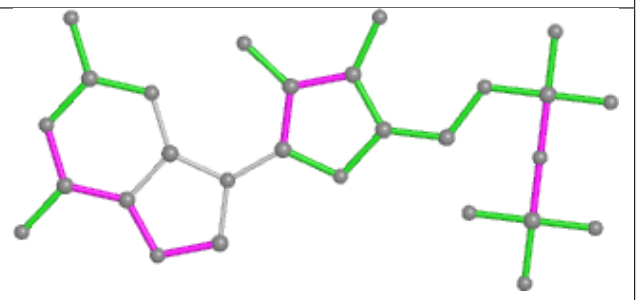
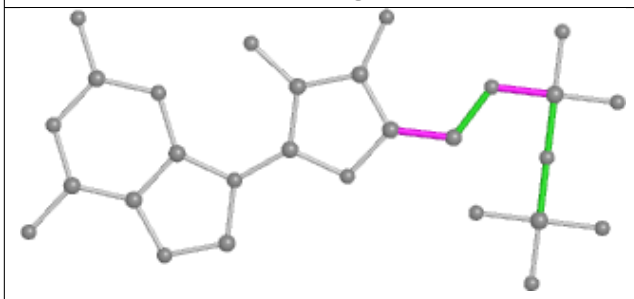


Bond angles



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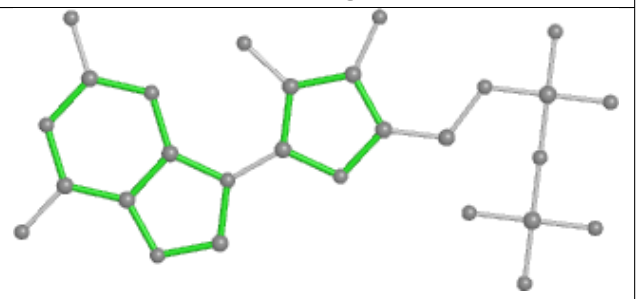
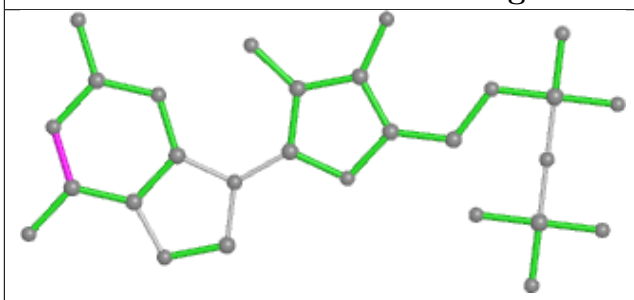


Rings

Ligand GDP ON 502



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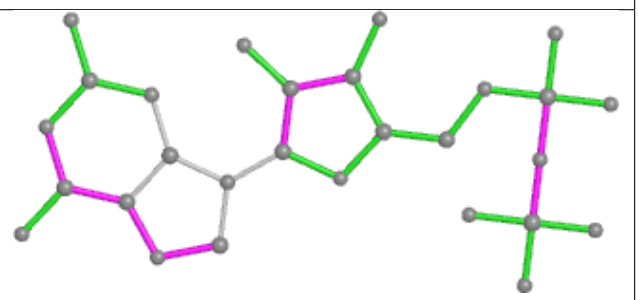

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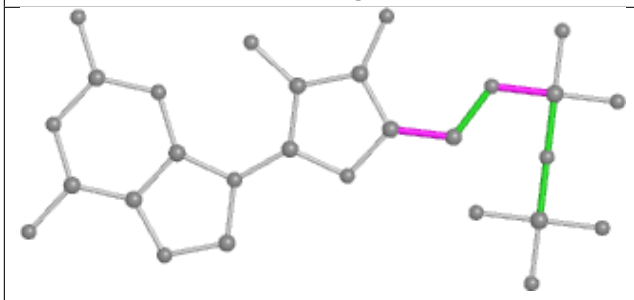

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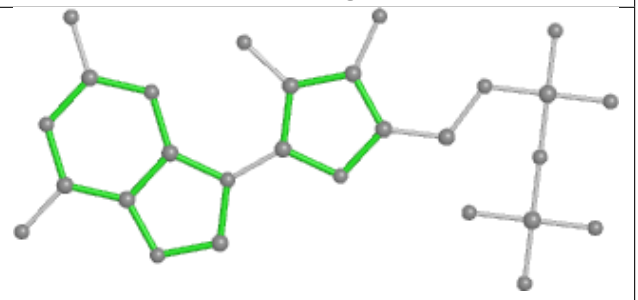
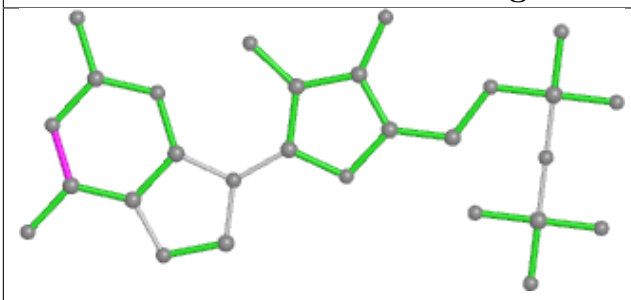


Rings

Ligand GDP UF 502



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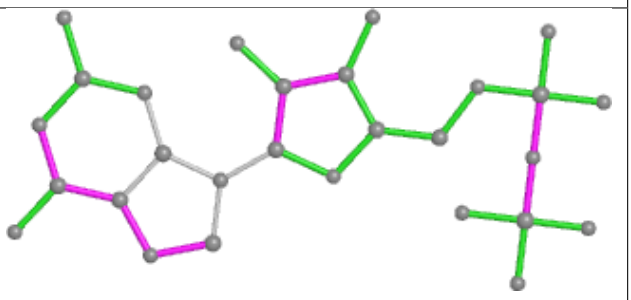
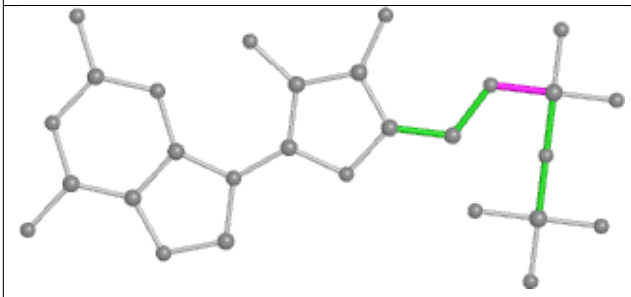


Bond angles



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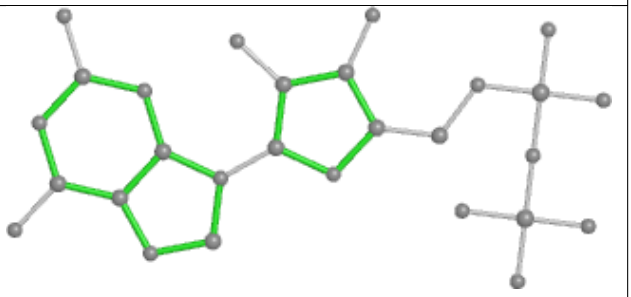
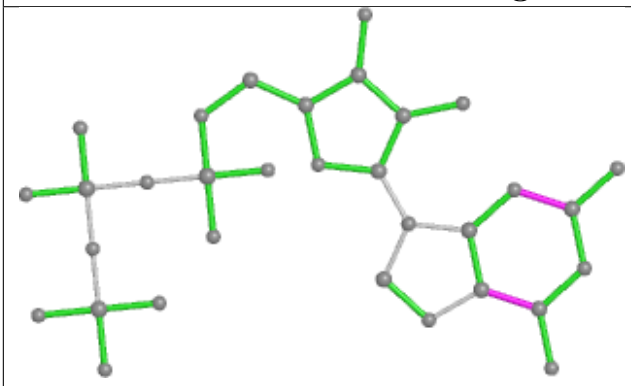


Rings

Ligand GTP SG 501



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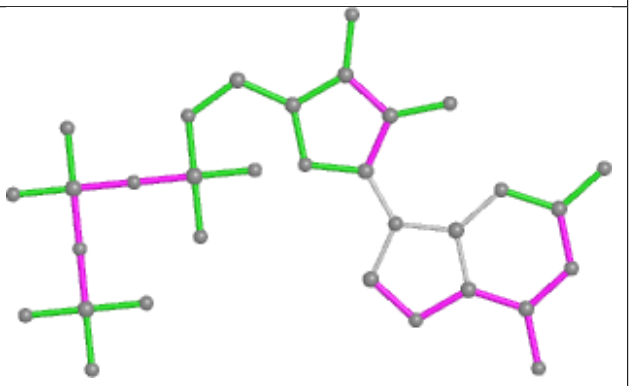

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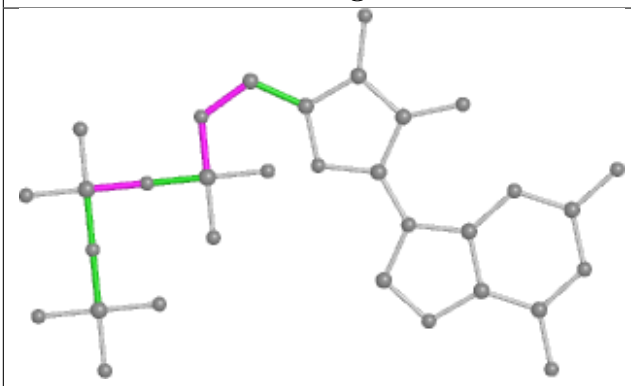

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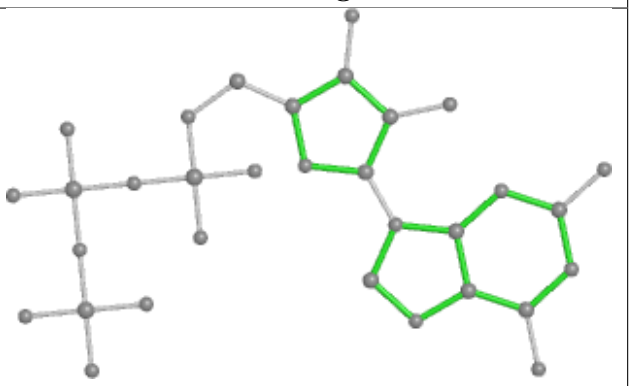
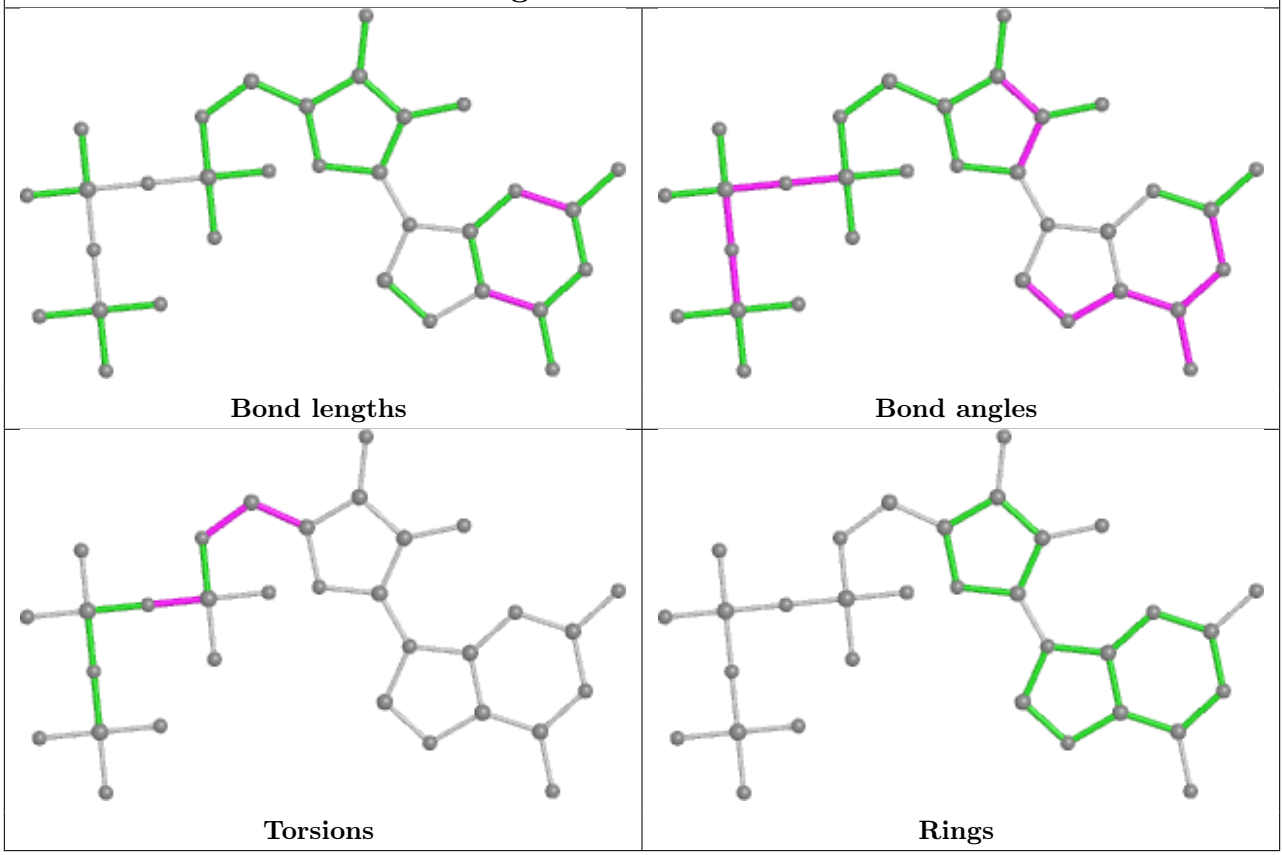


Rings

Ligand GTP BC 501



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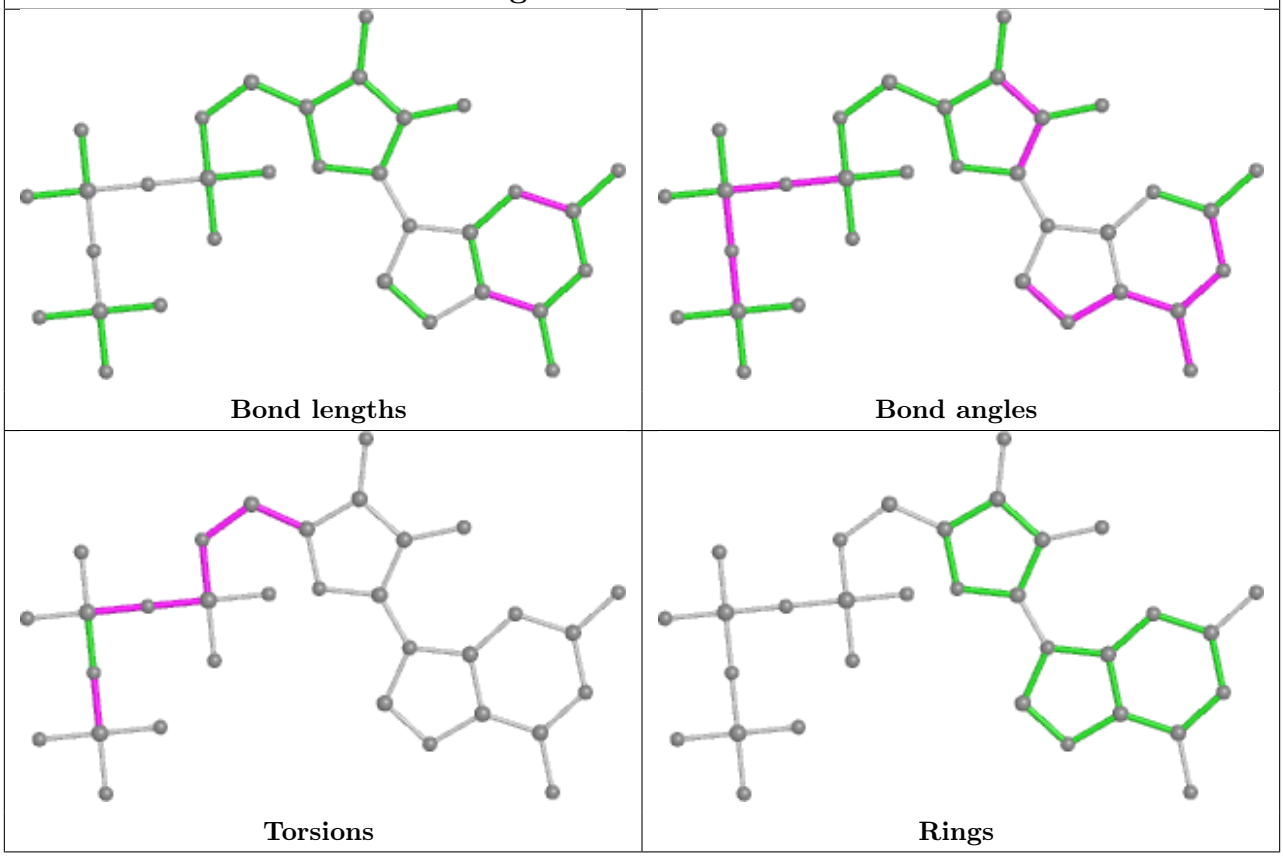

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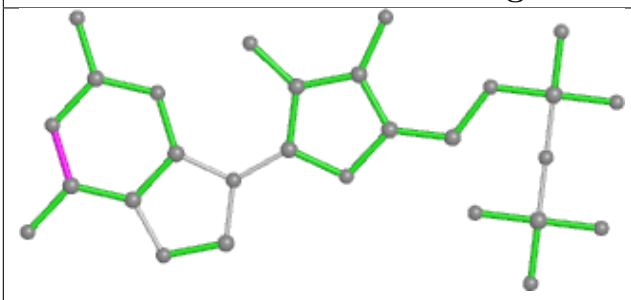

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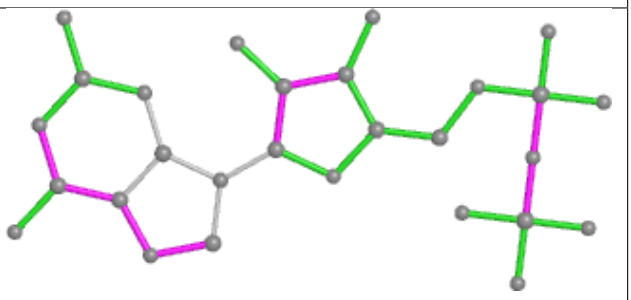
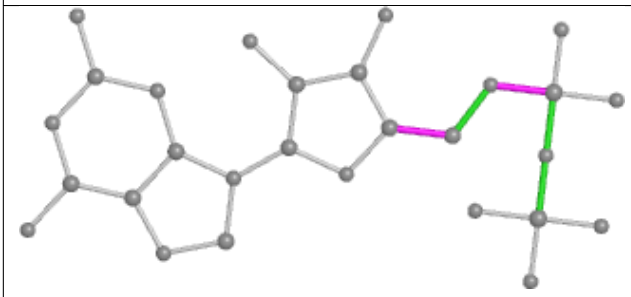


Bond angles



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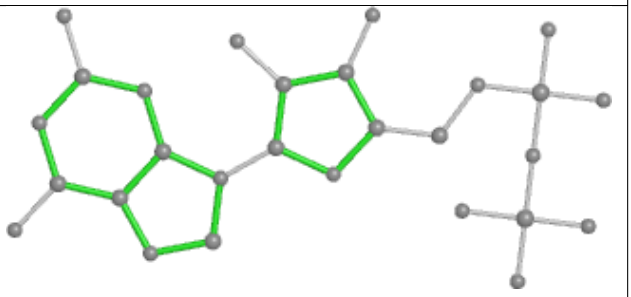

Rings

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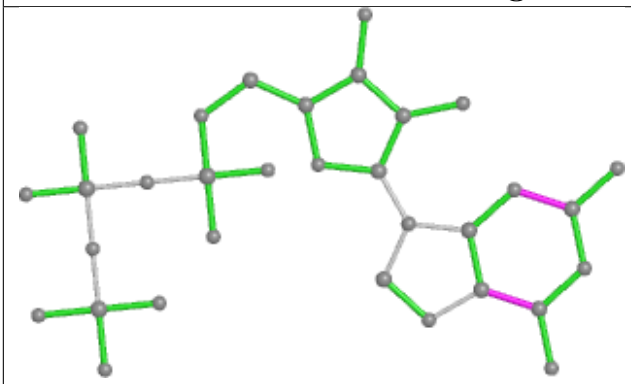

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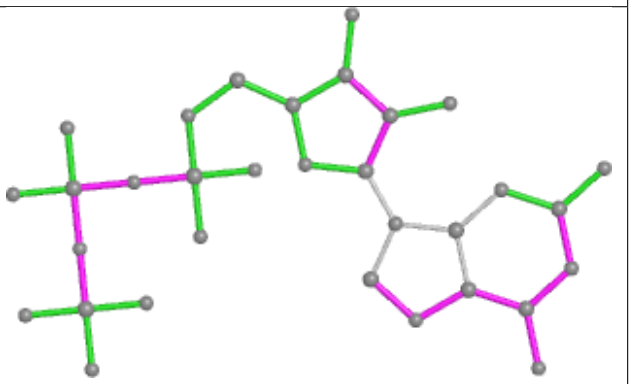
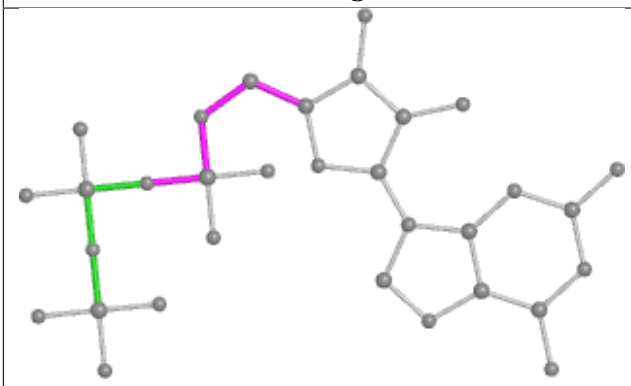
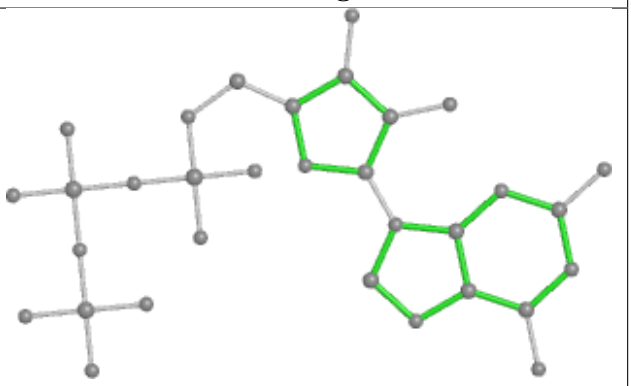


Bond angles

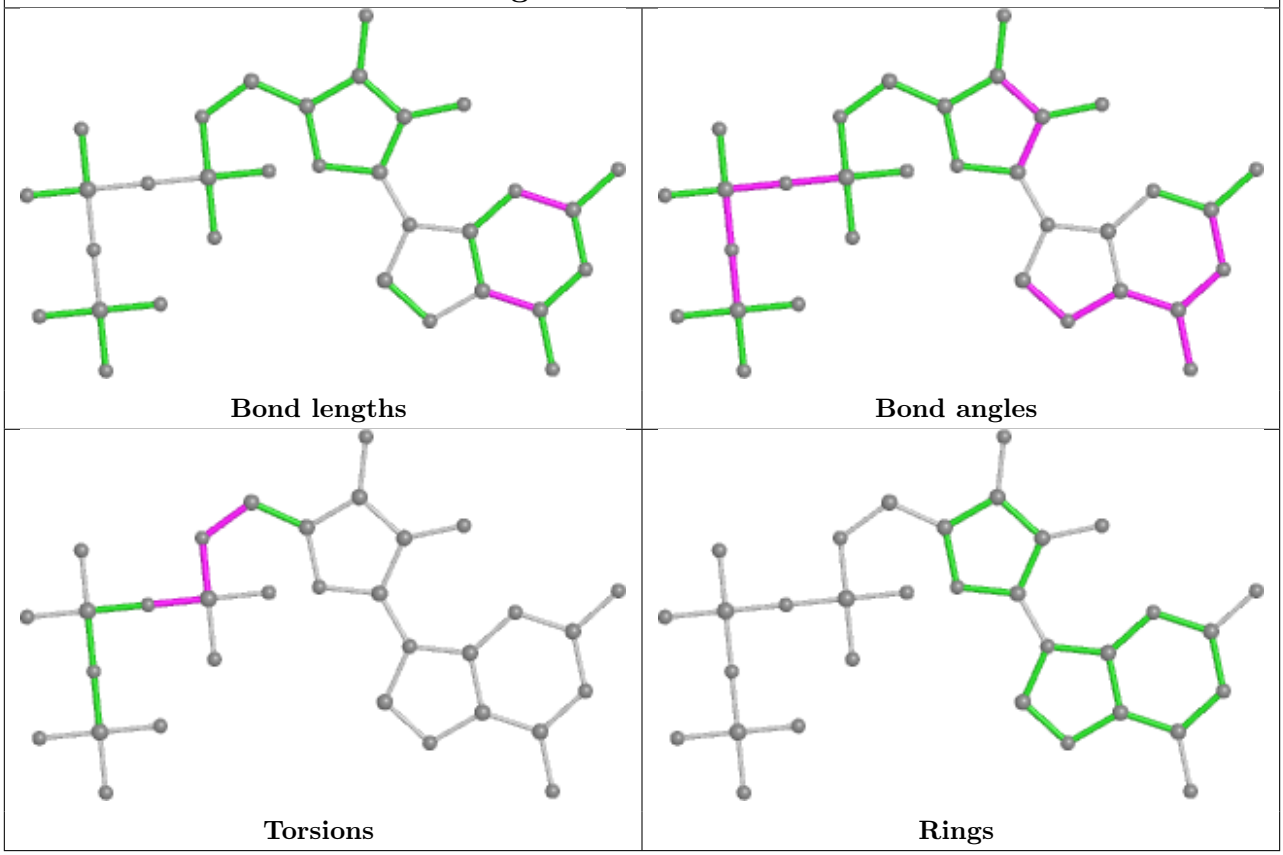


Torsions



Rings

Ligand GTP EK 501



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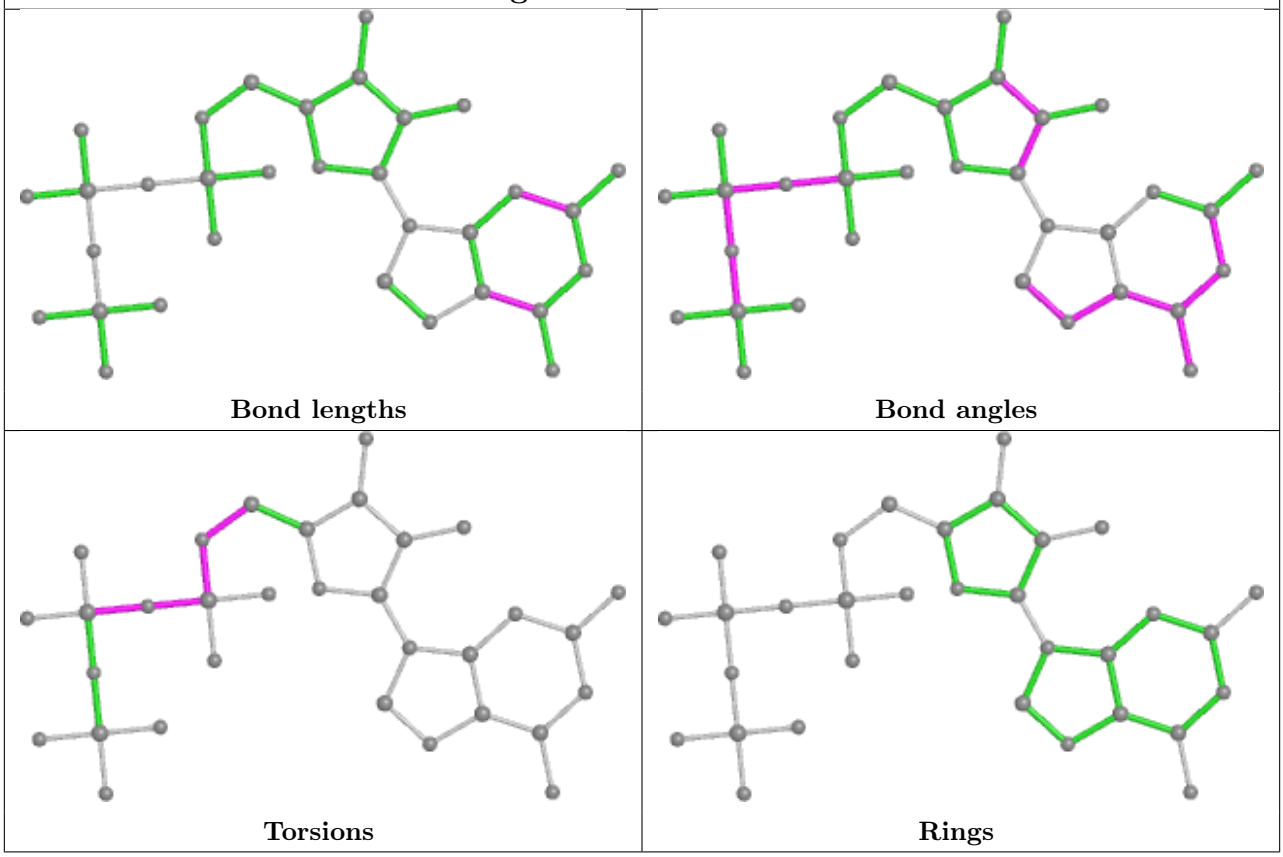
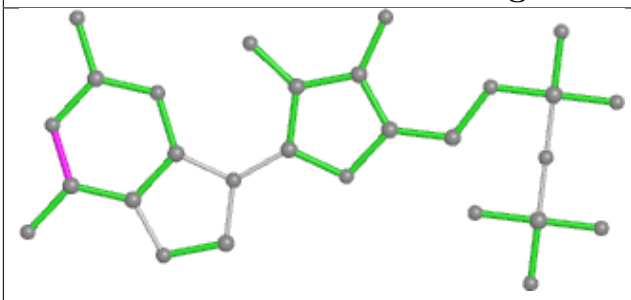


Ligand GDP EH 502



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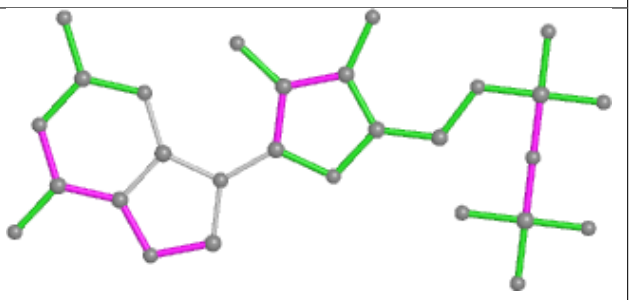
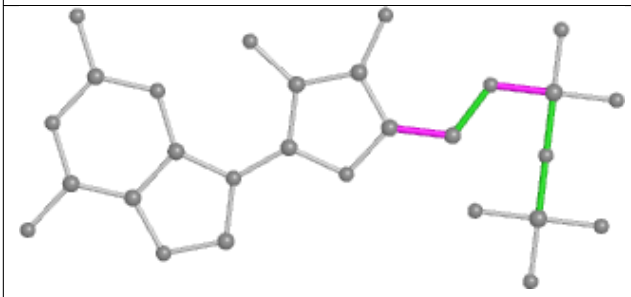


Bond angles



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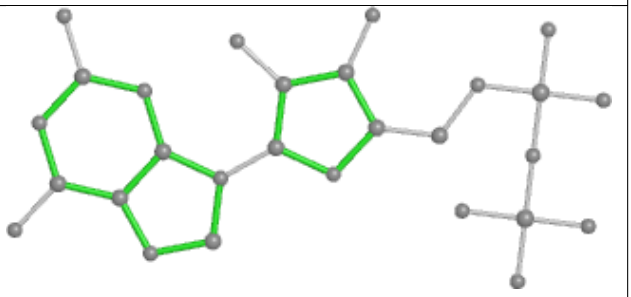
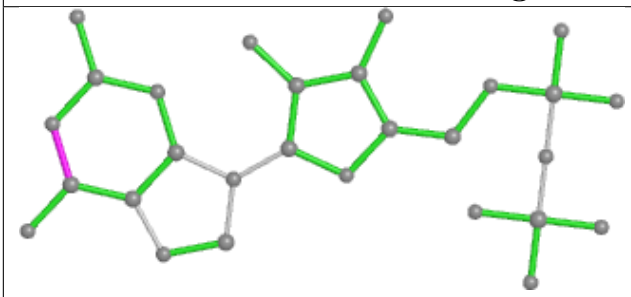


Rings

Ligand GDP TF 502



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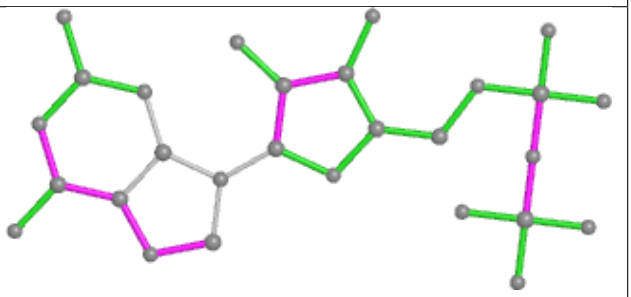
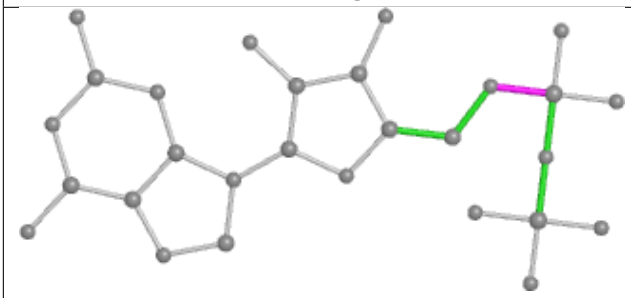


Bond angles



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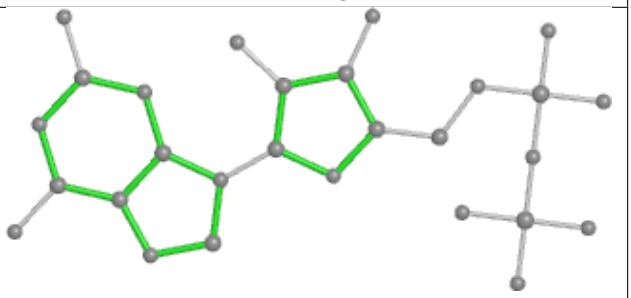

Rings

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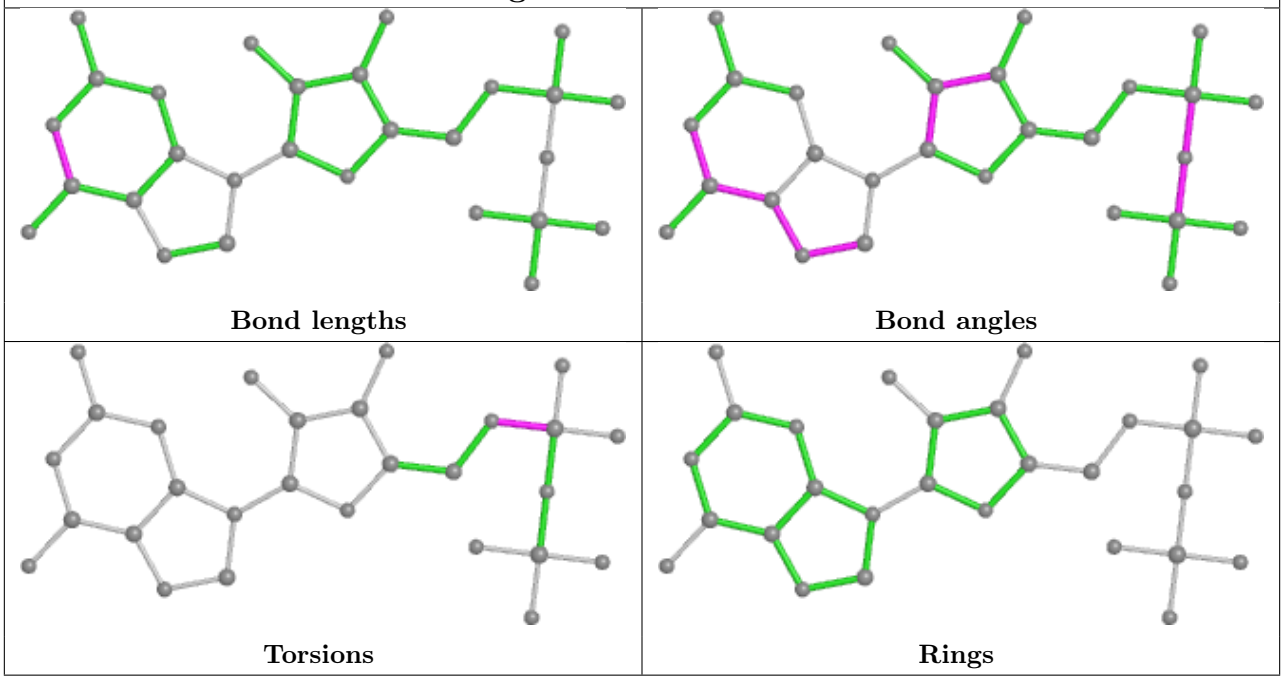

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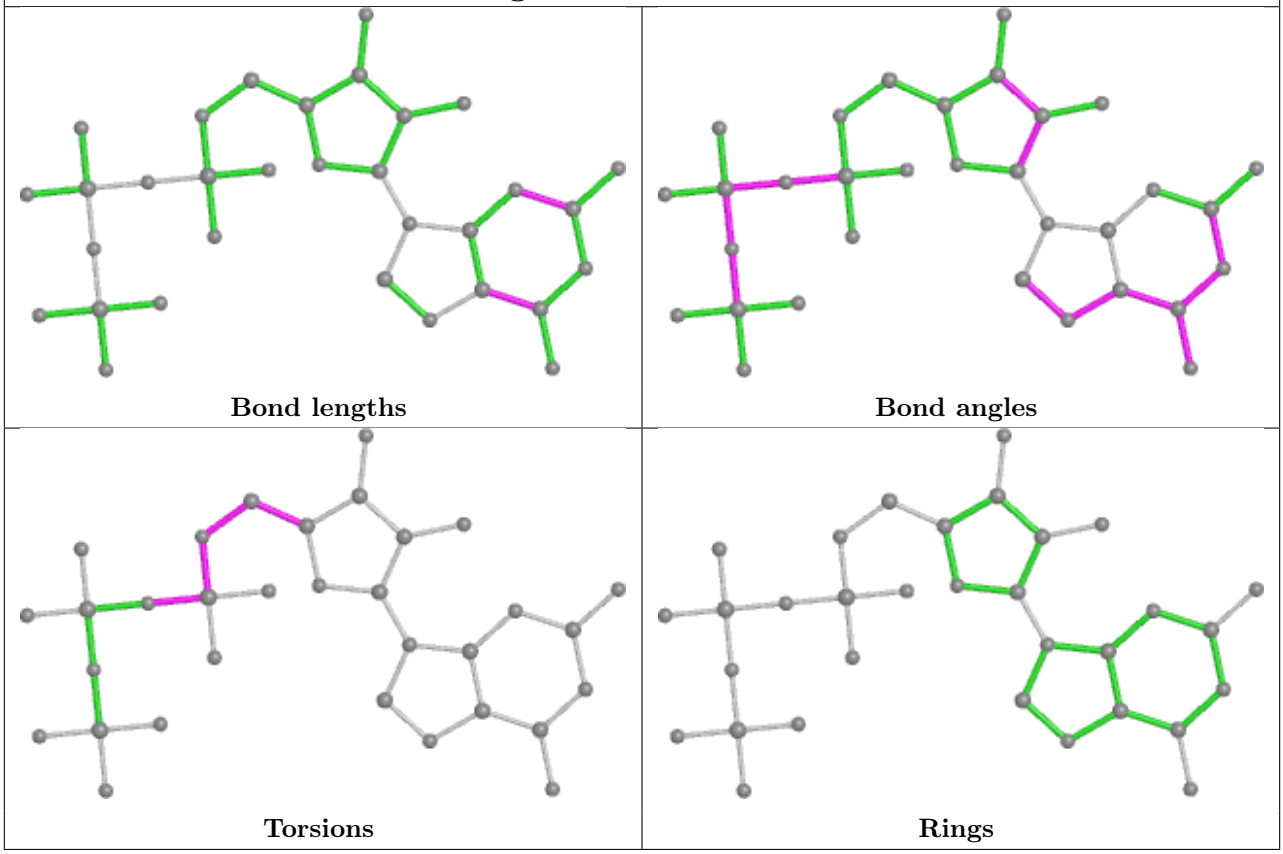

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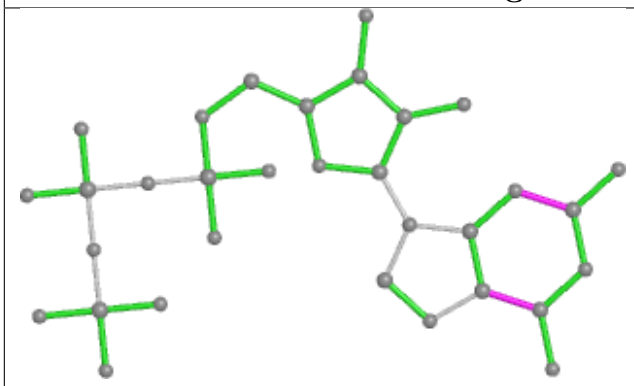

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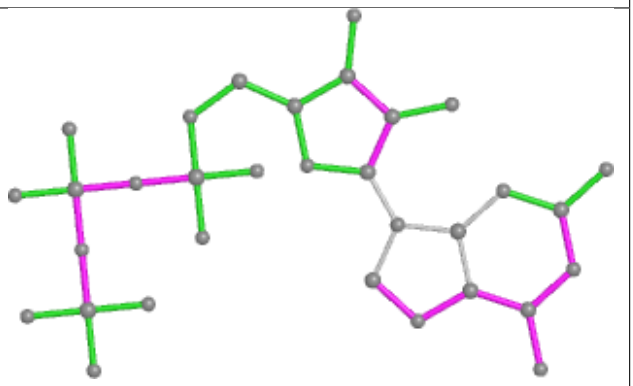
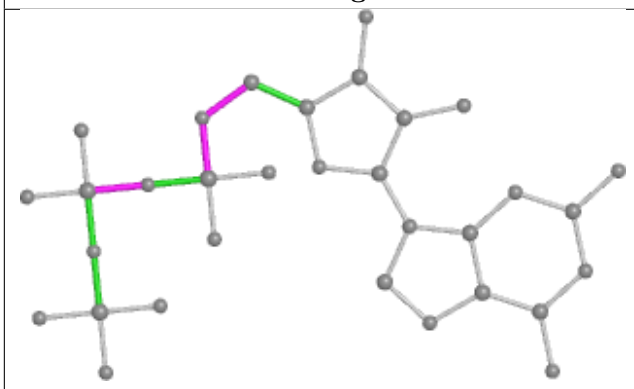


Bond angles



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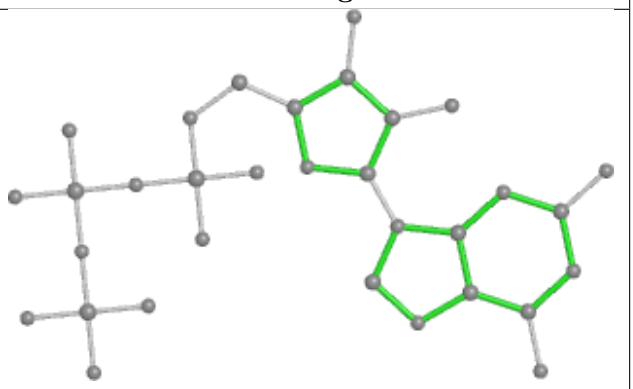
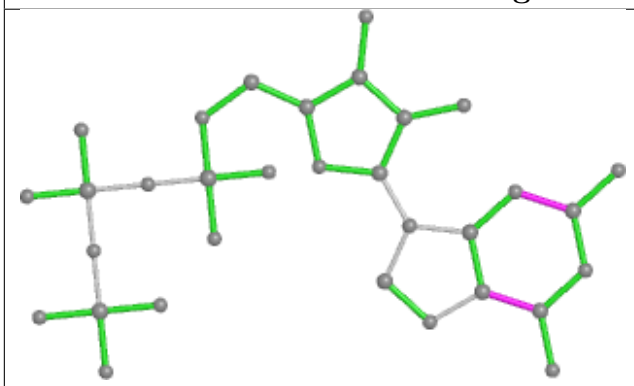


Rings

Ligand GTP LC 501



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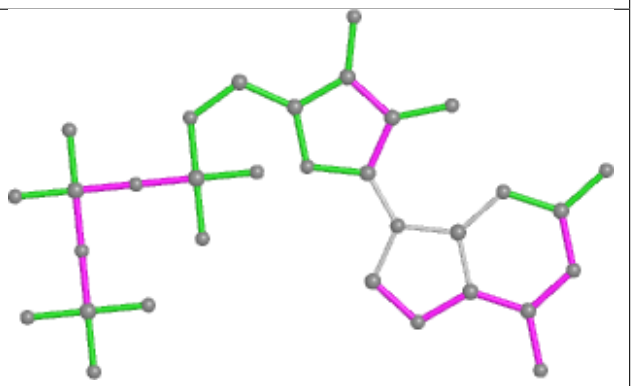

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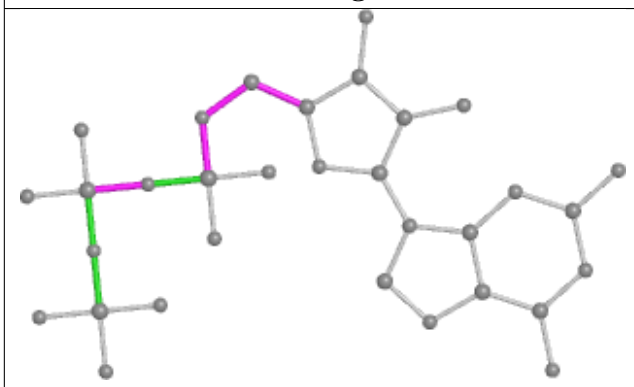

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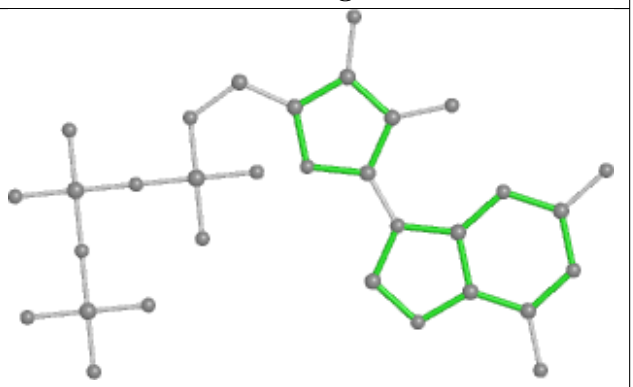

Rings

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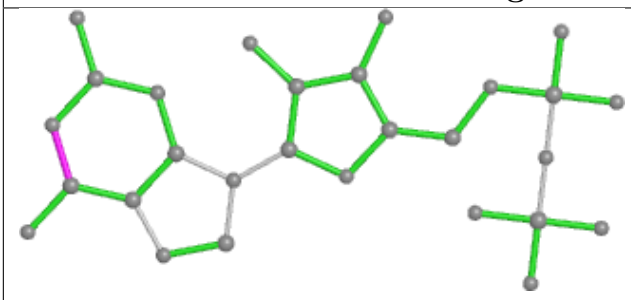

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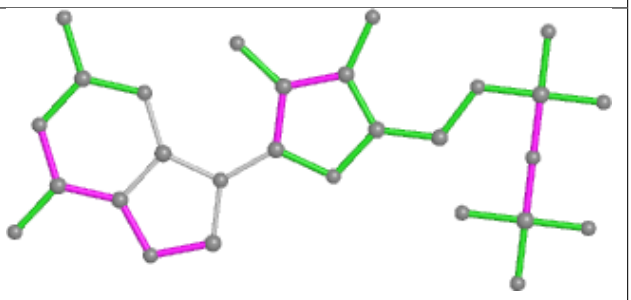

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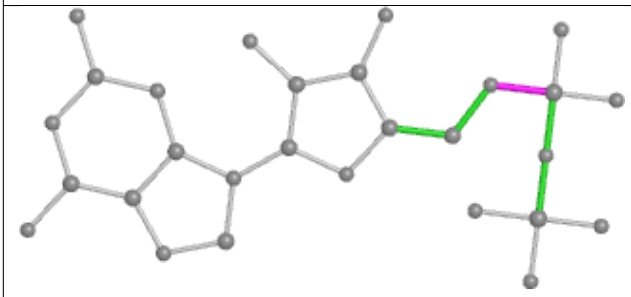

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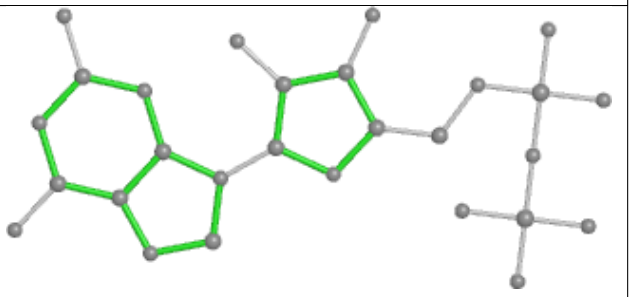
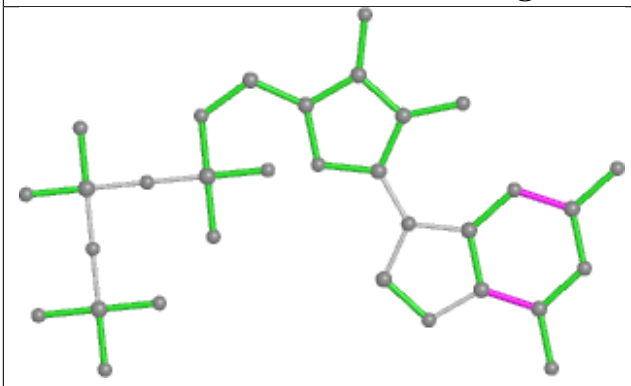


Rings

Ligand GTP BI 501



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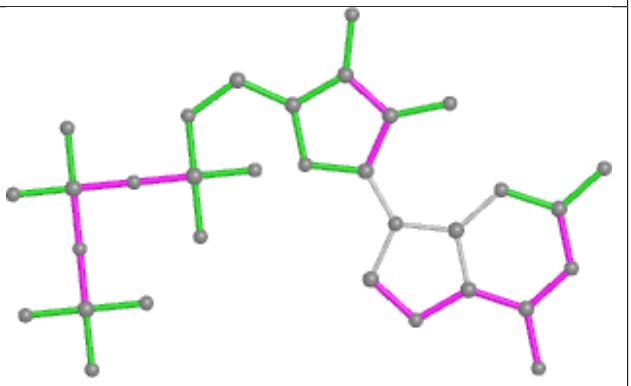

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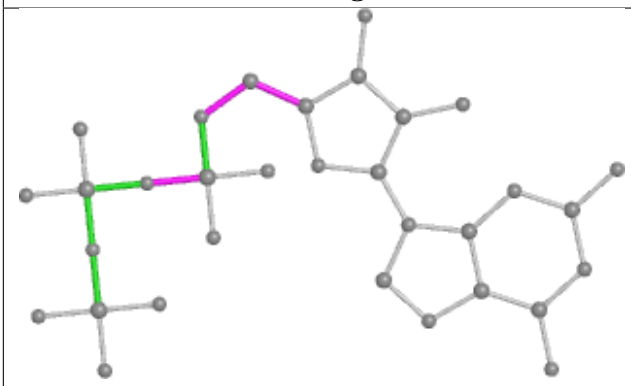

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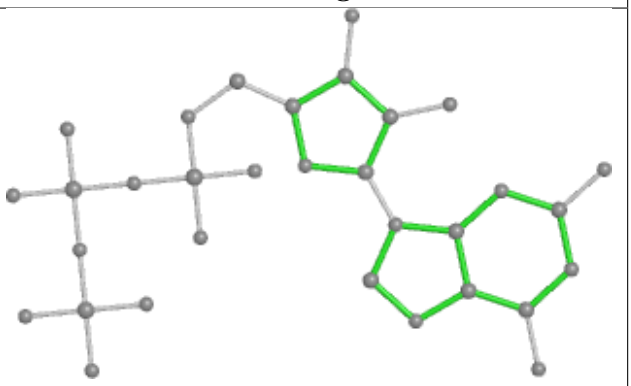

Rings

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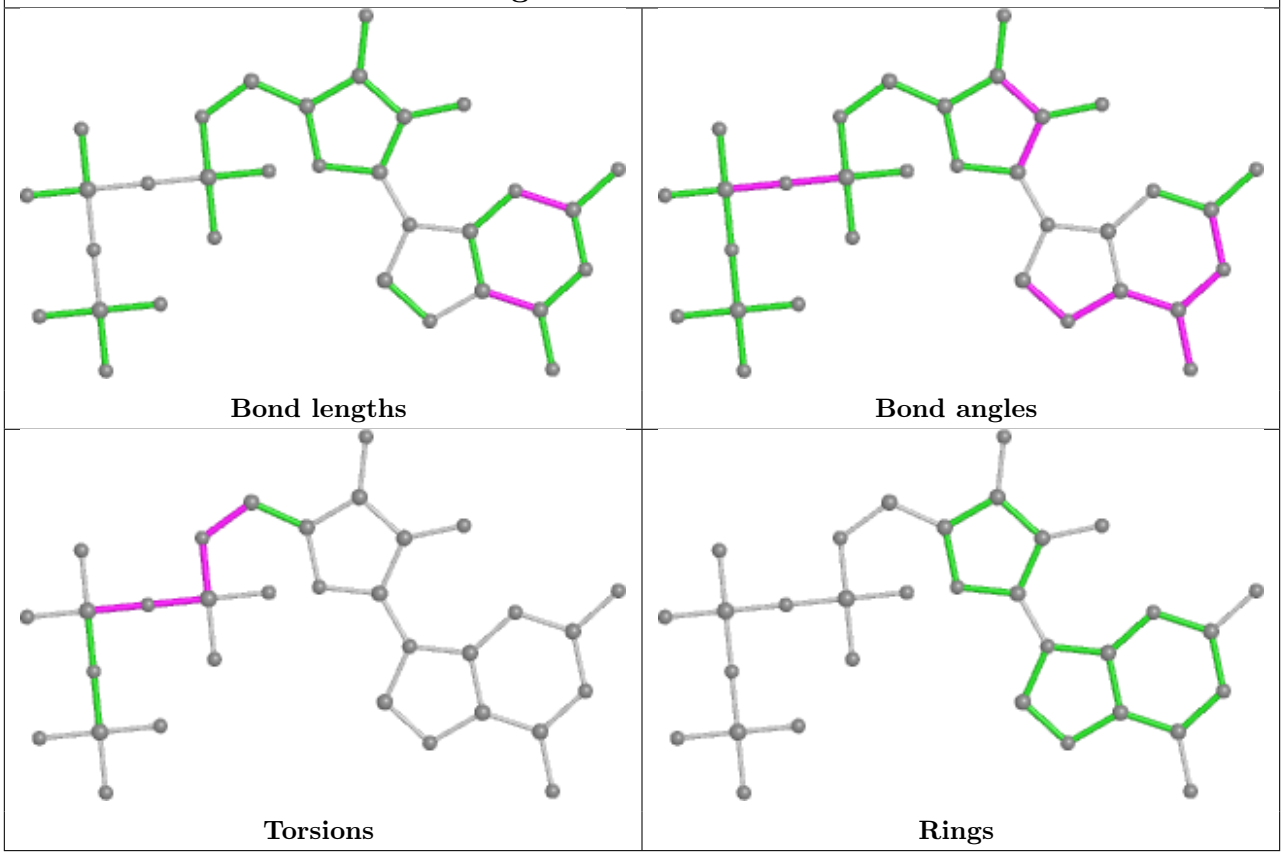

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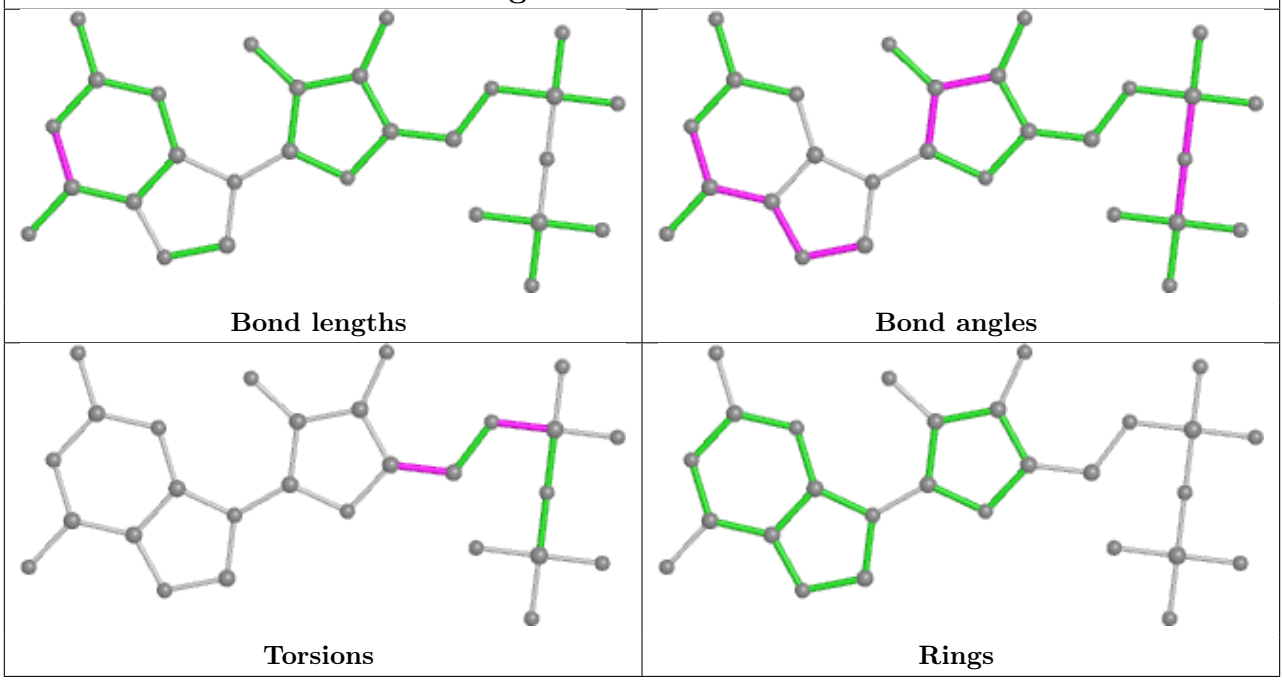

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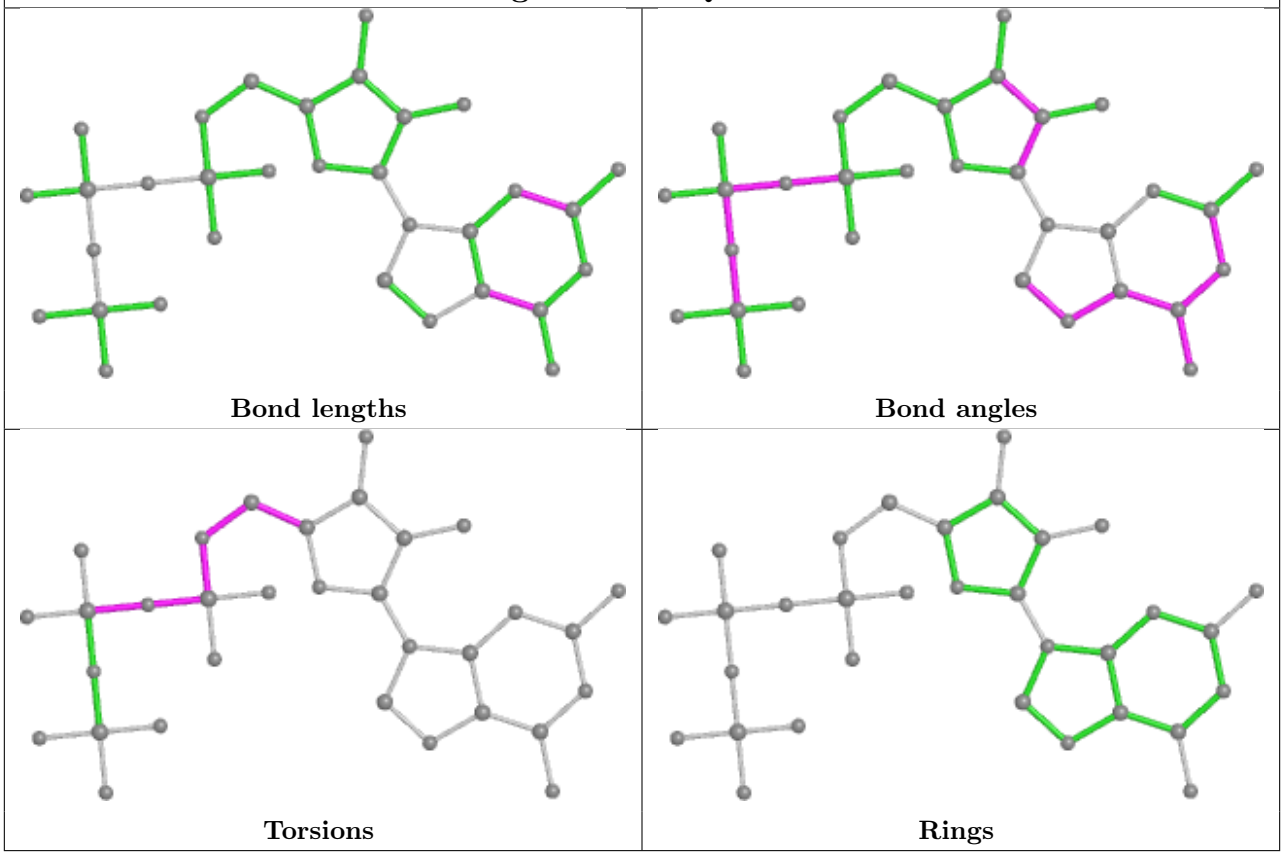

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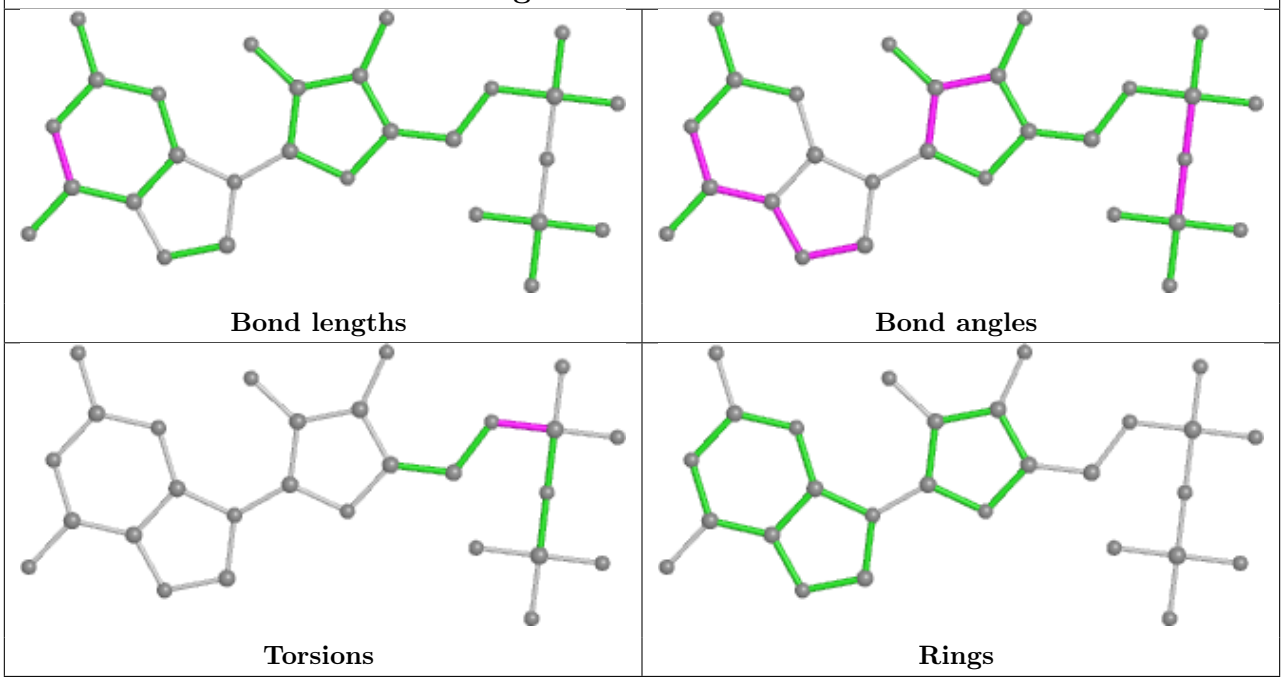

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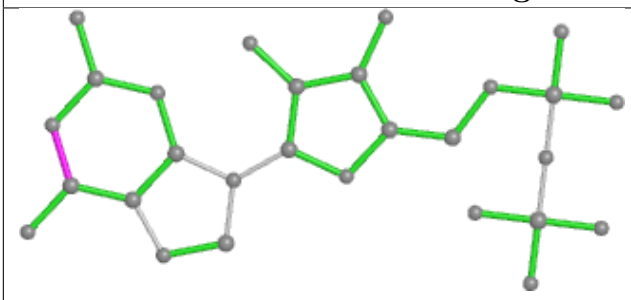

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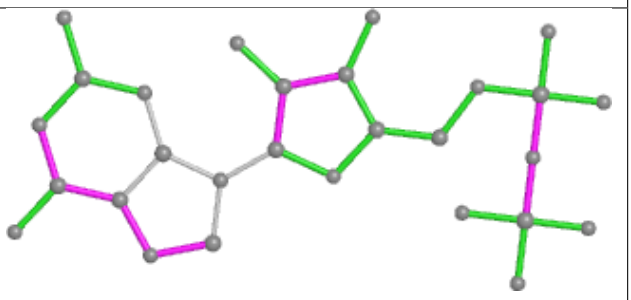
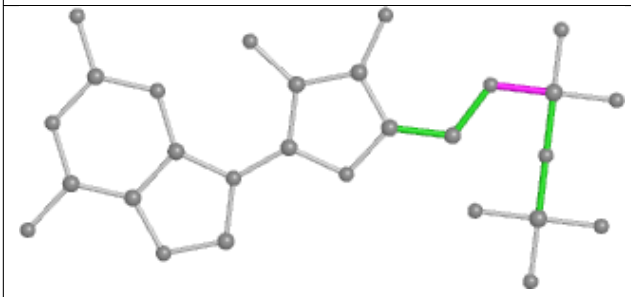
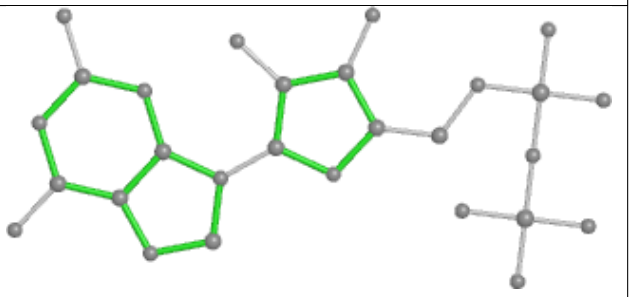


Bond angles

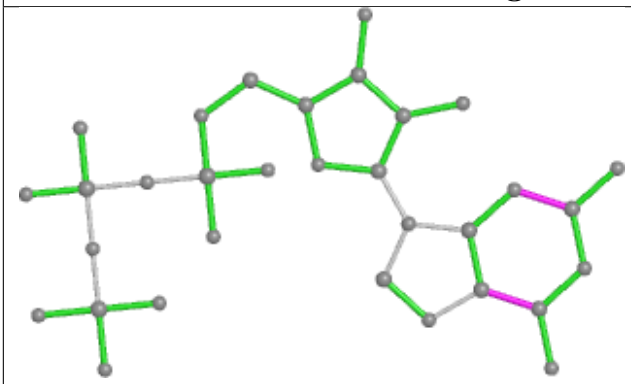


Torsions



Rings

Ligand GTP MC 501



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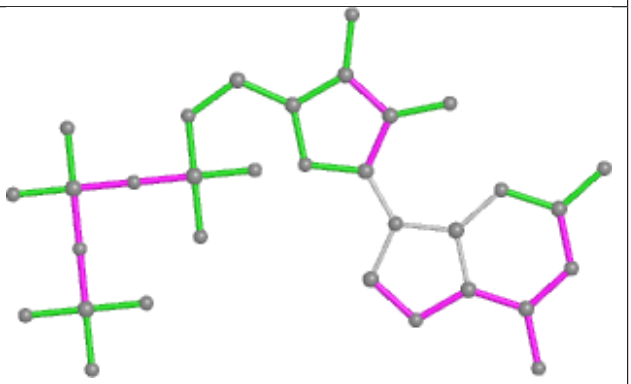

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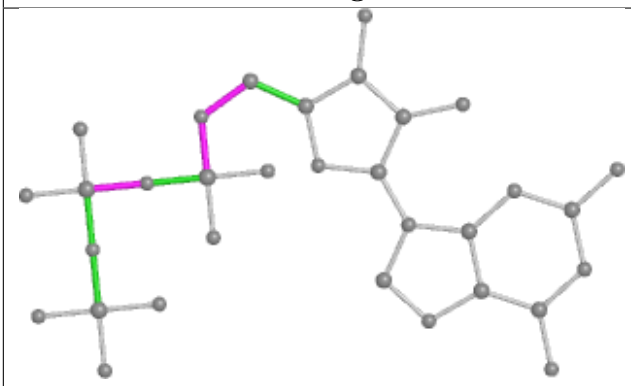

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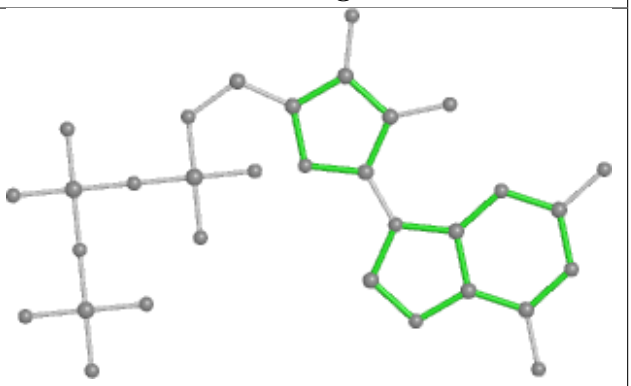
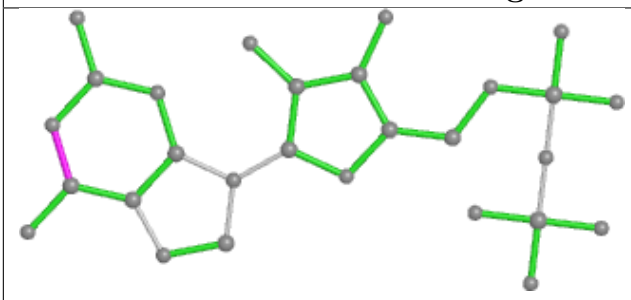


Rings

Ligand GDP WJ 502



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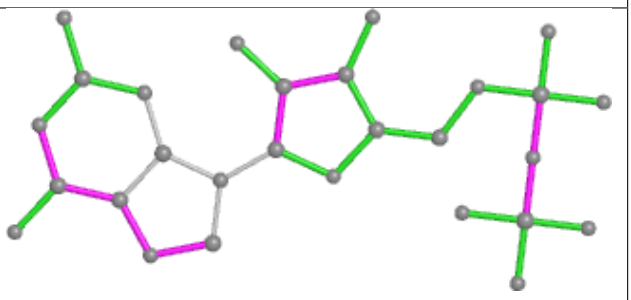

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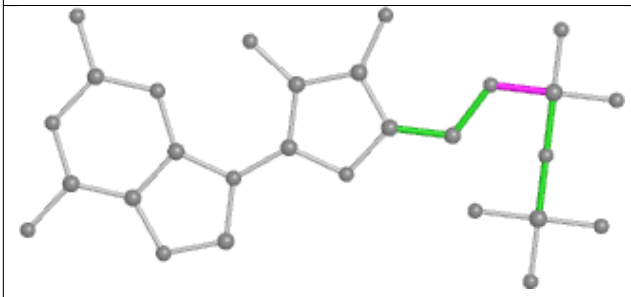

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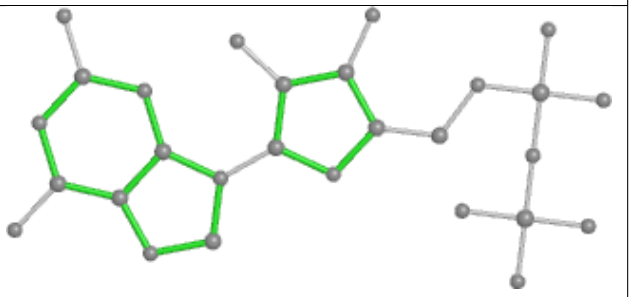
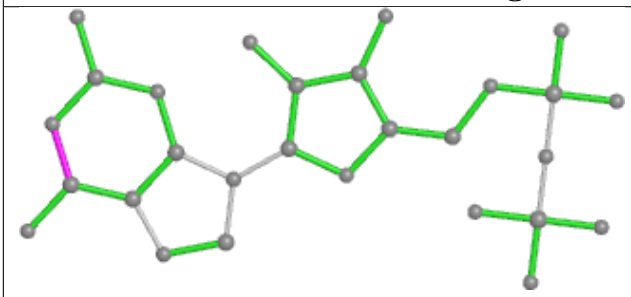


Rings

Ligand GDP HH 502



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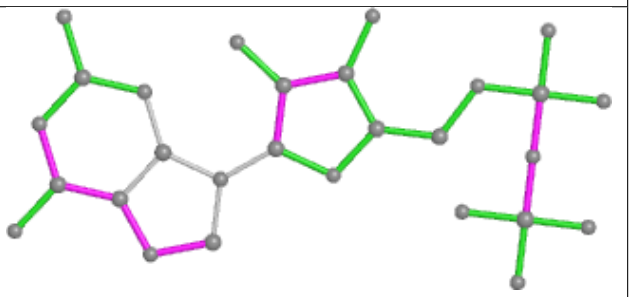

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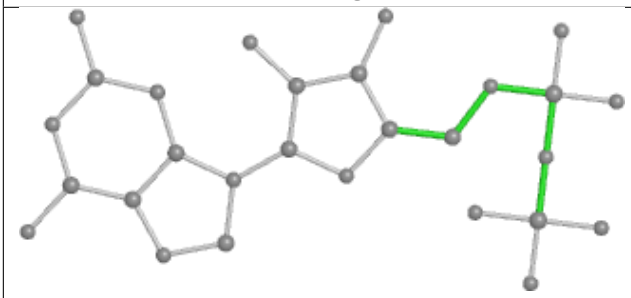

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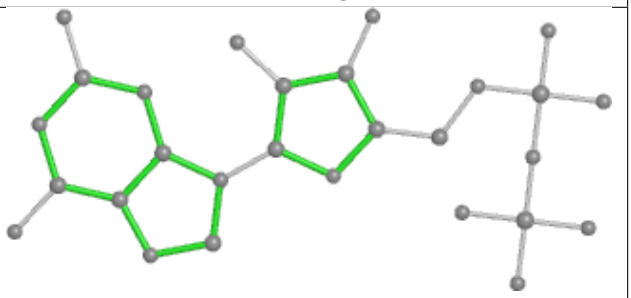

Rings

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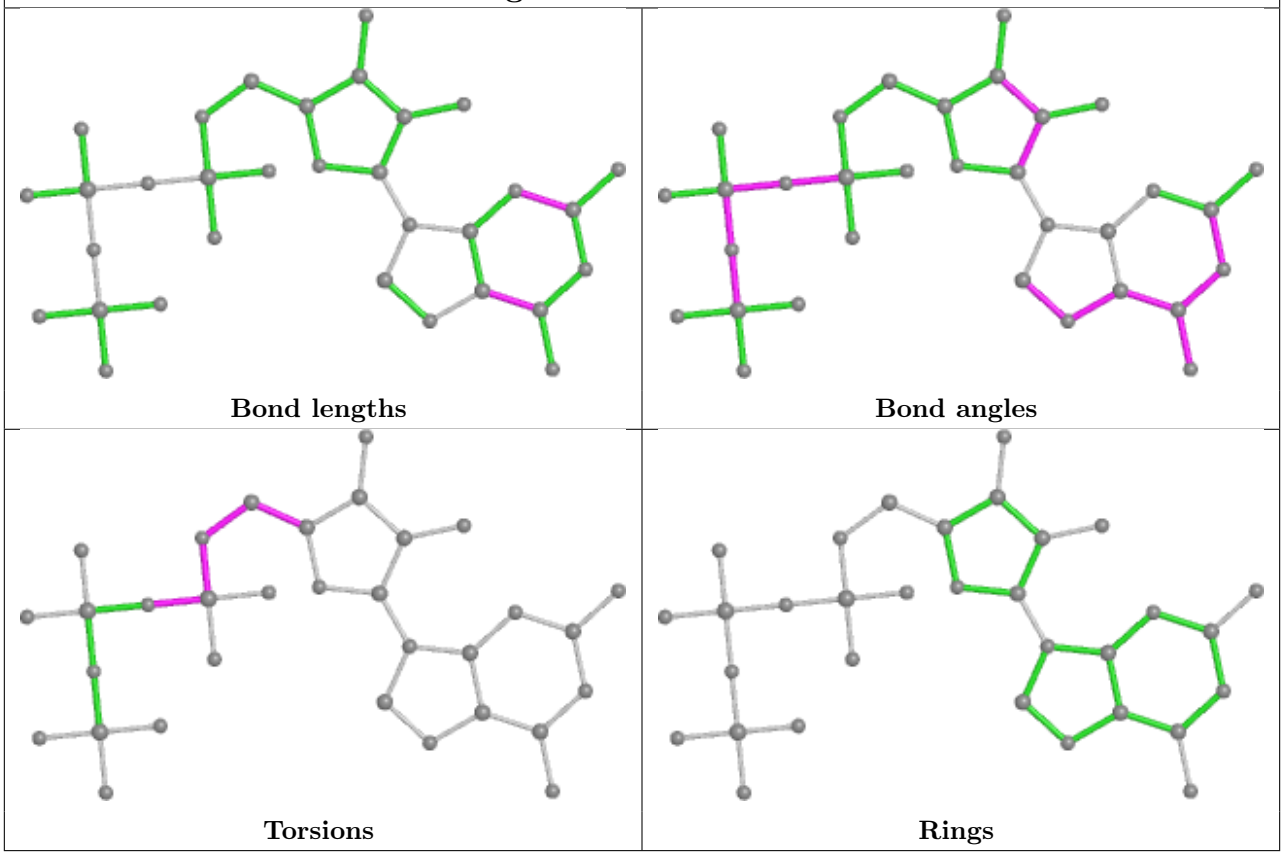

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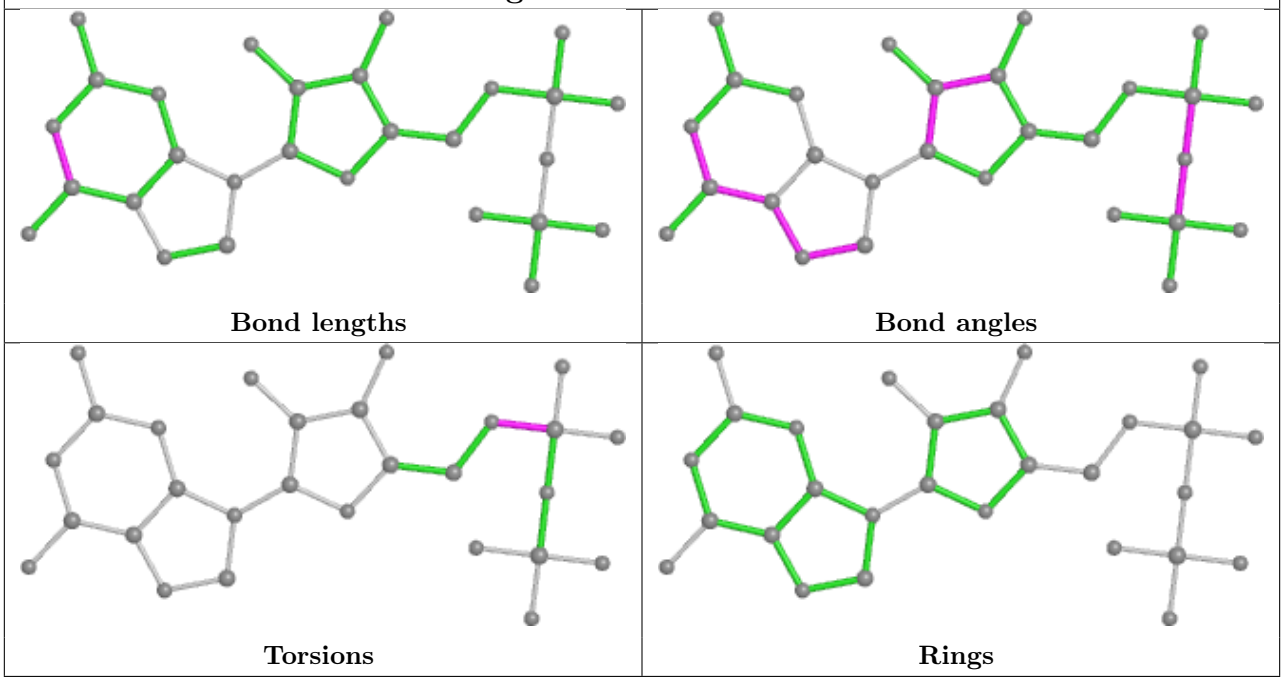

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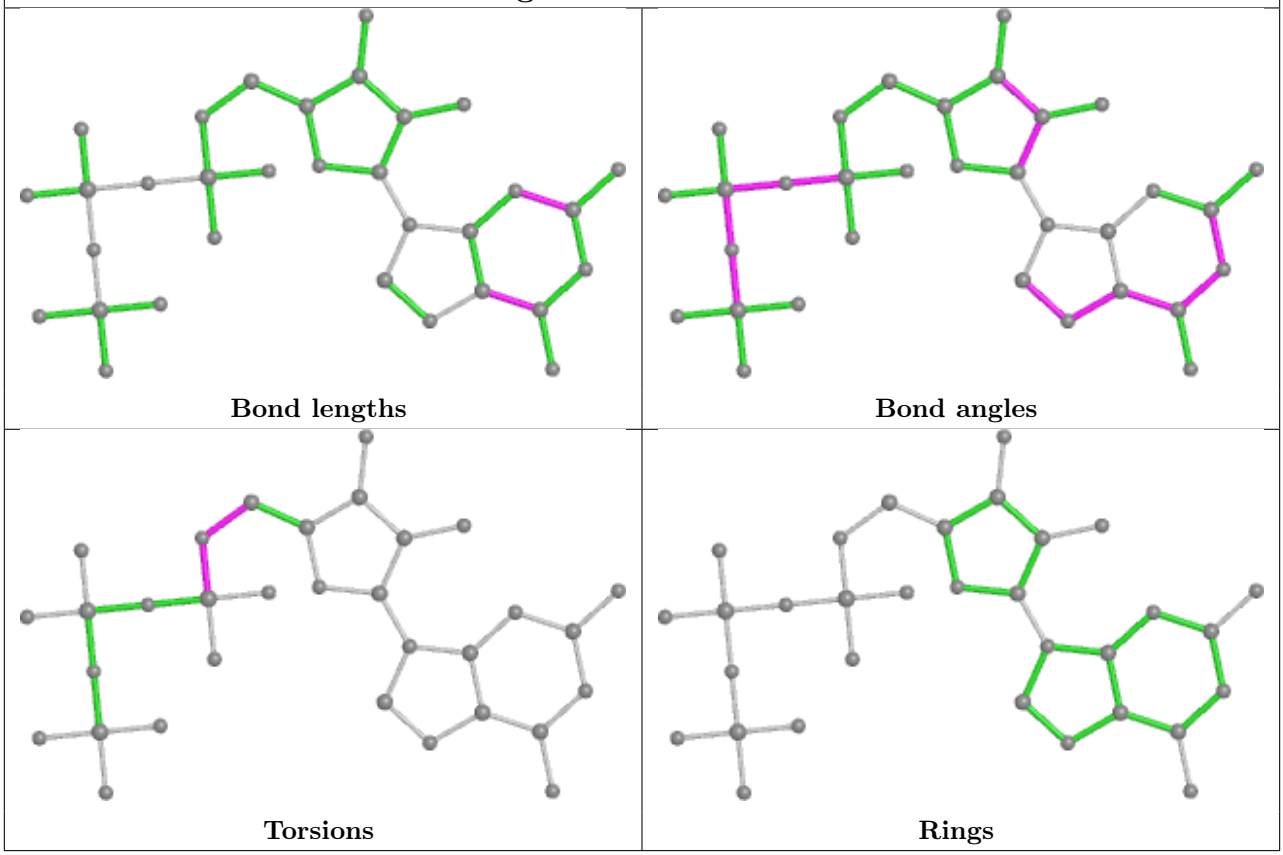

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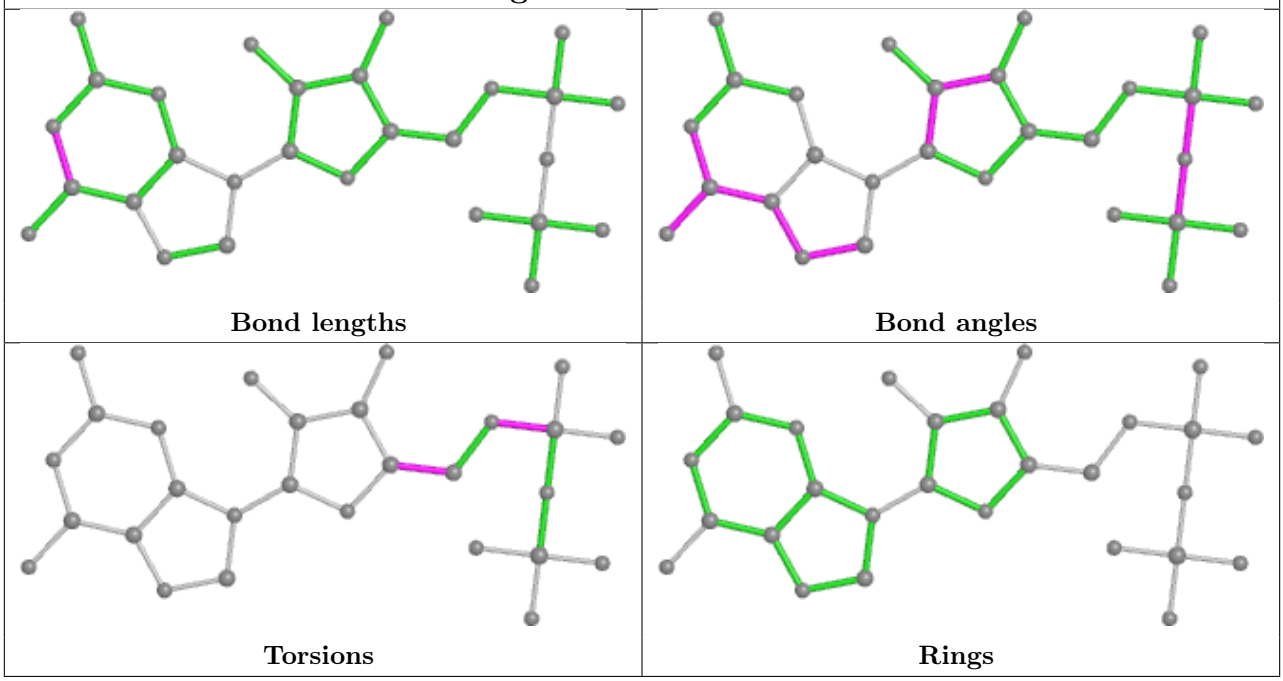

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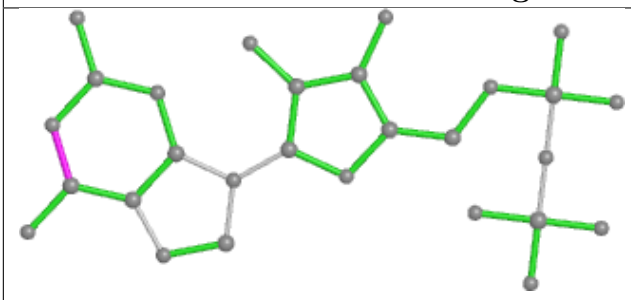
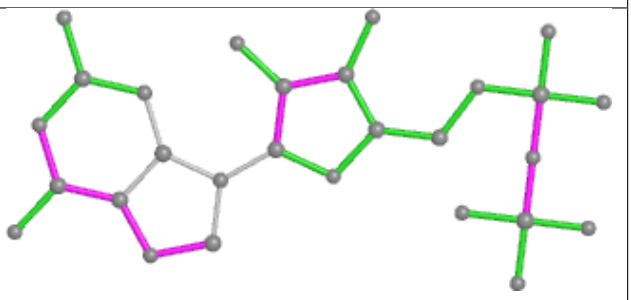
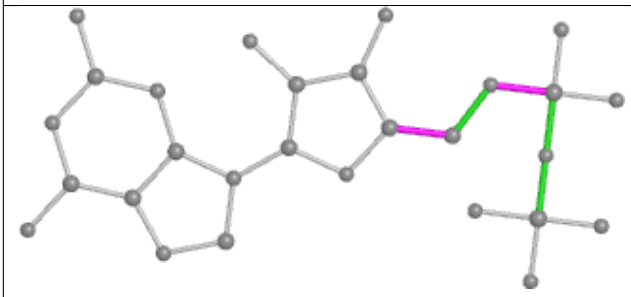


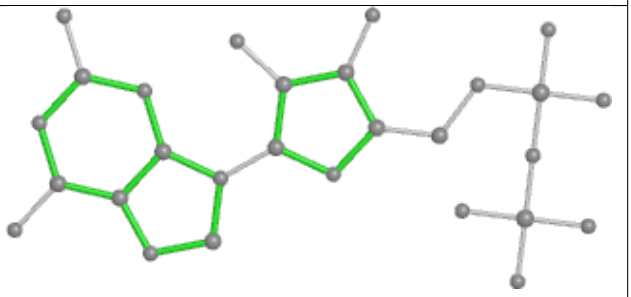
Bond lengths



Bond angles



Torsions



Rings

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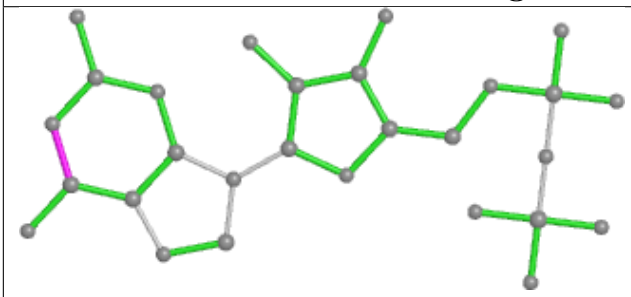

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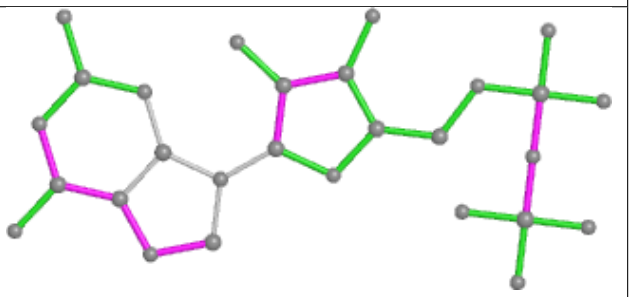
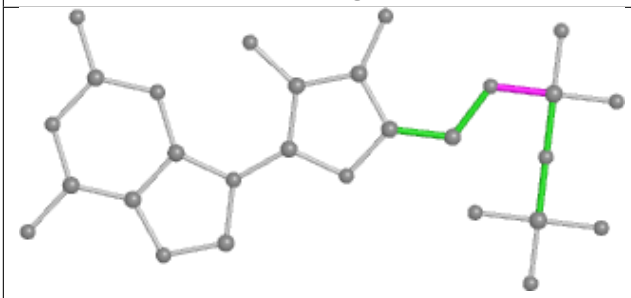
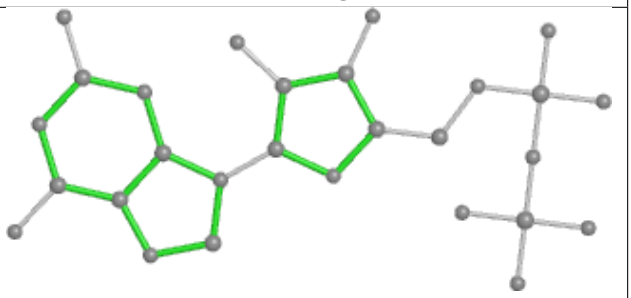


Bond angles

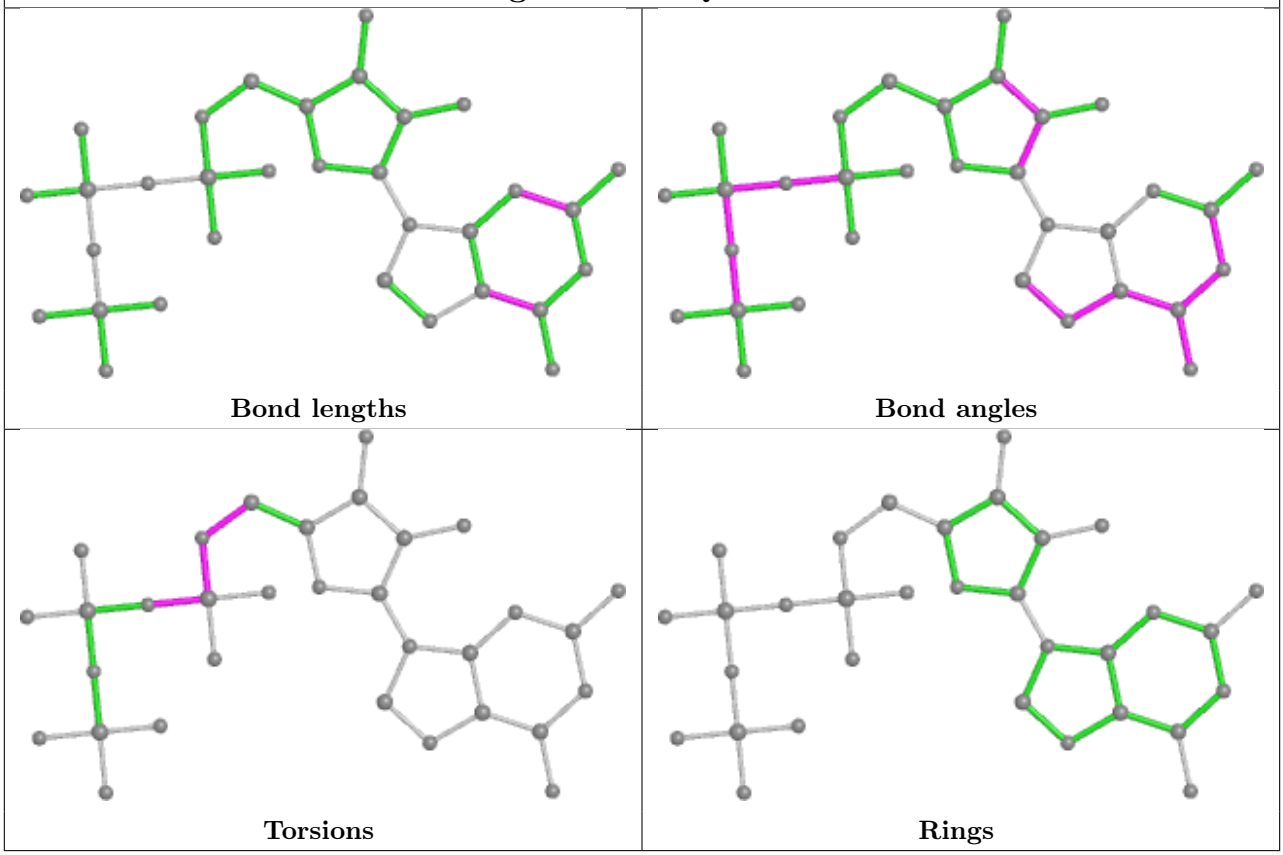


Torsions

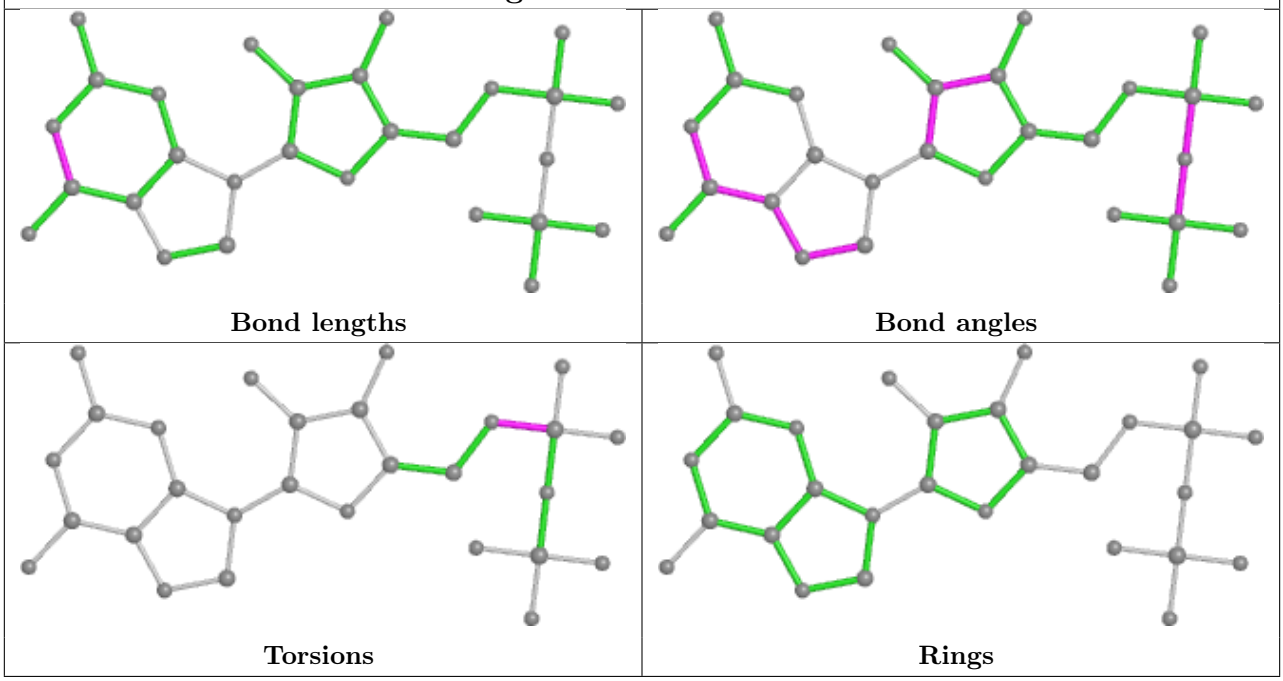


Rings

Ligand GTP QG 501



Ligand GDP WF 502



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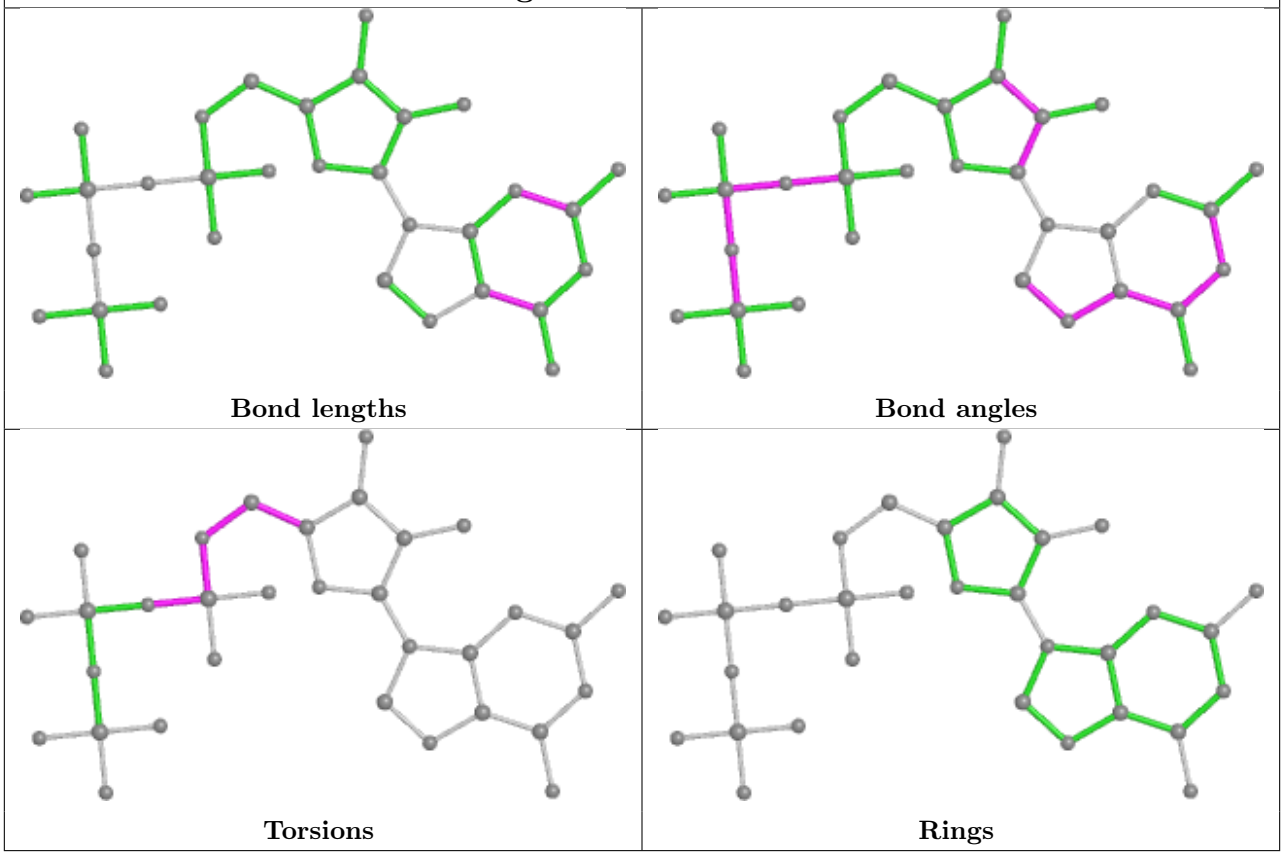

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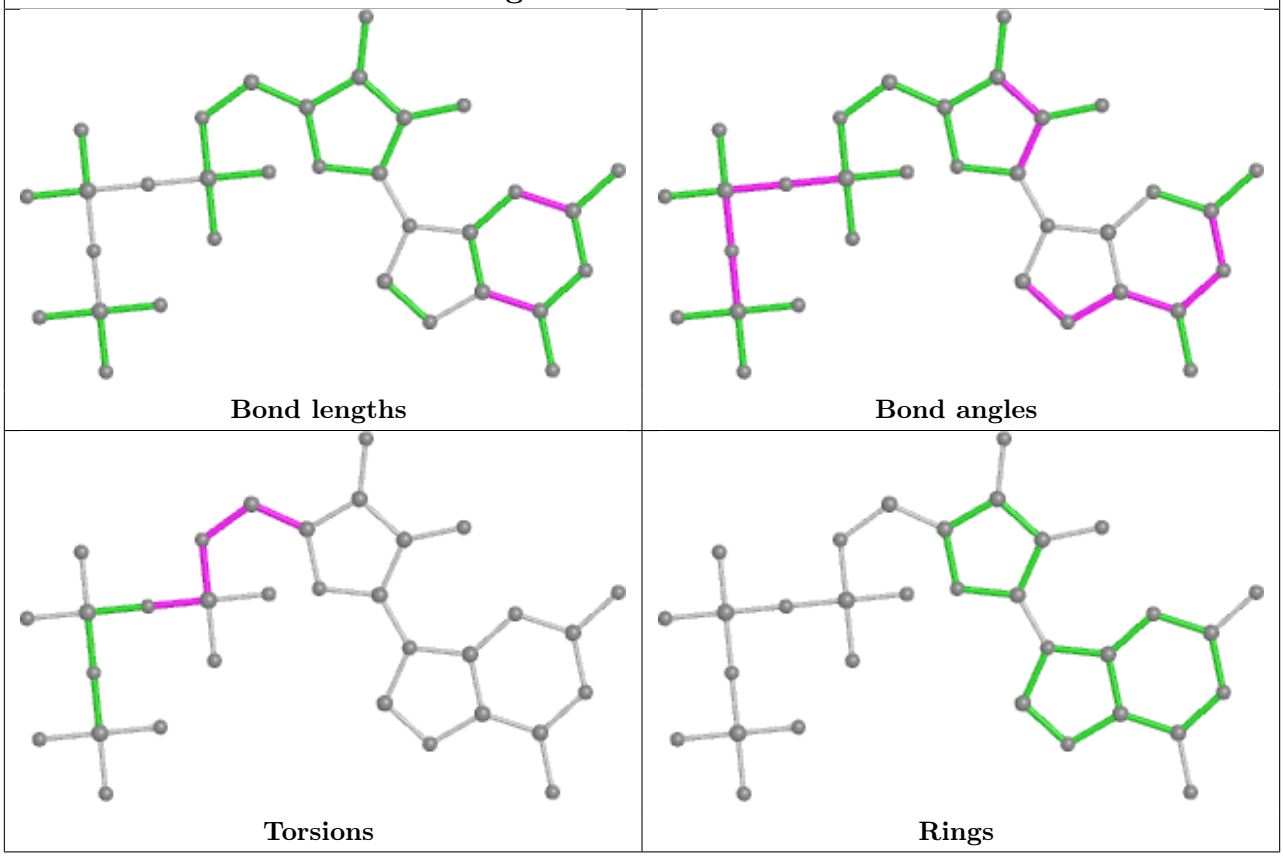

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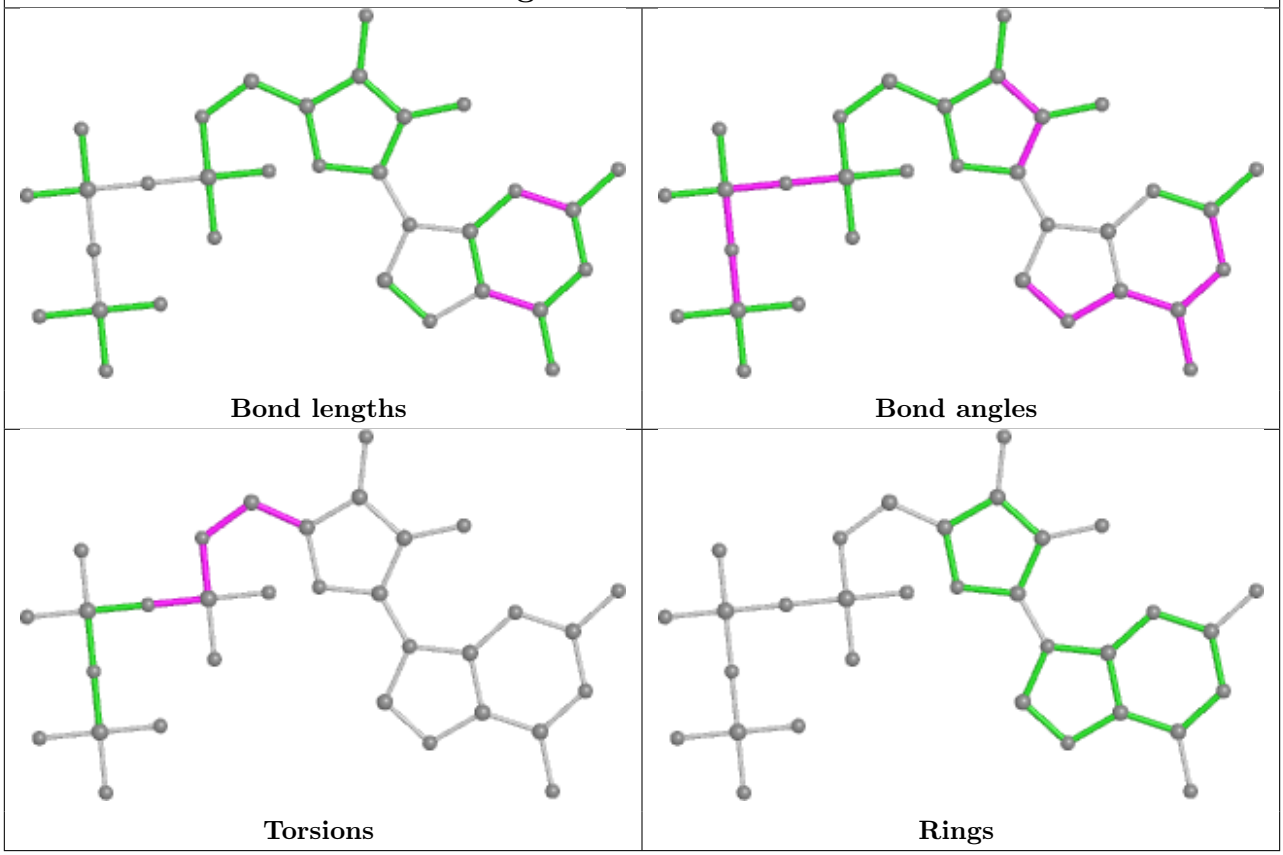

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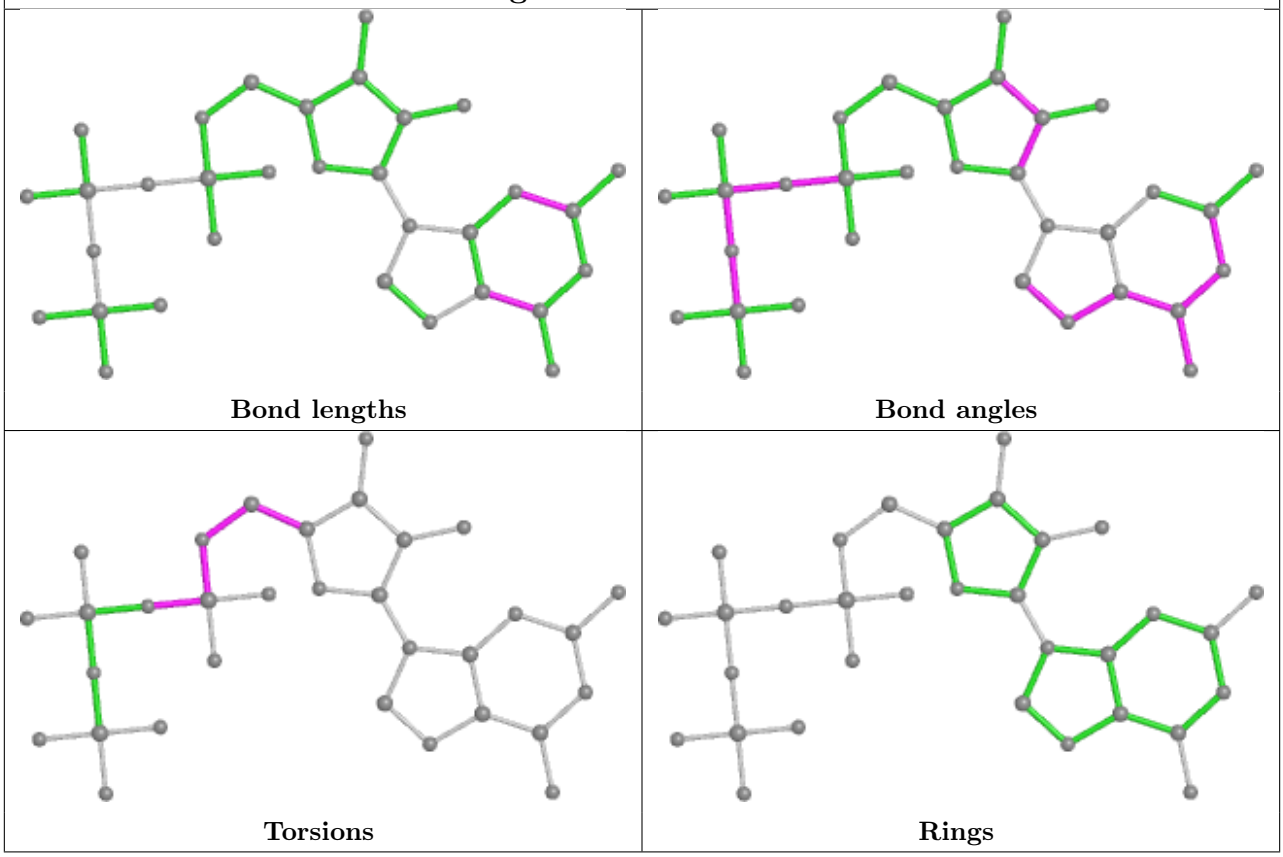

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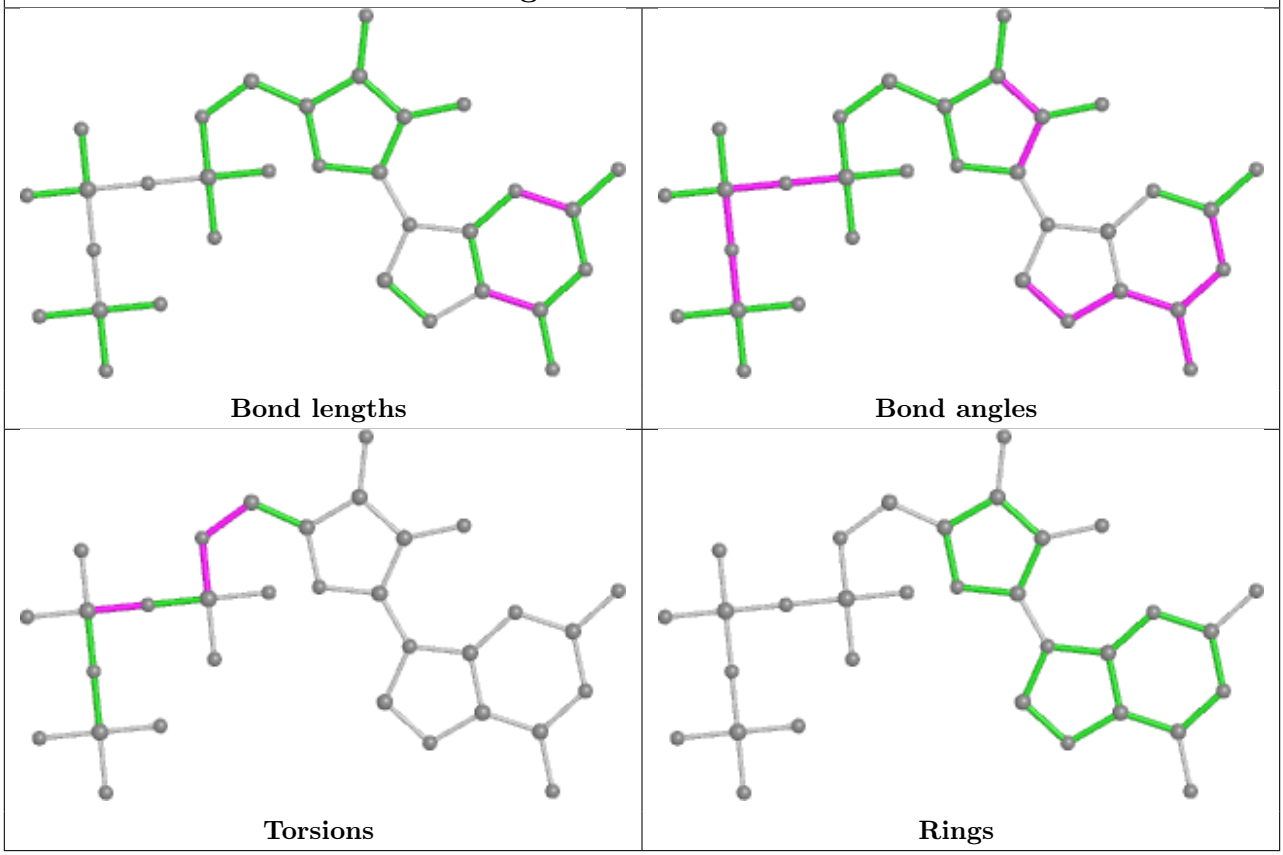
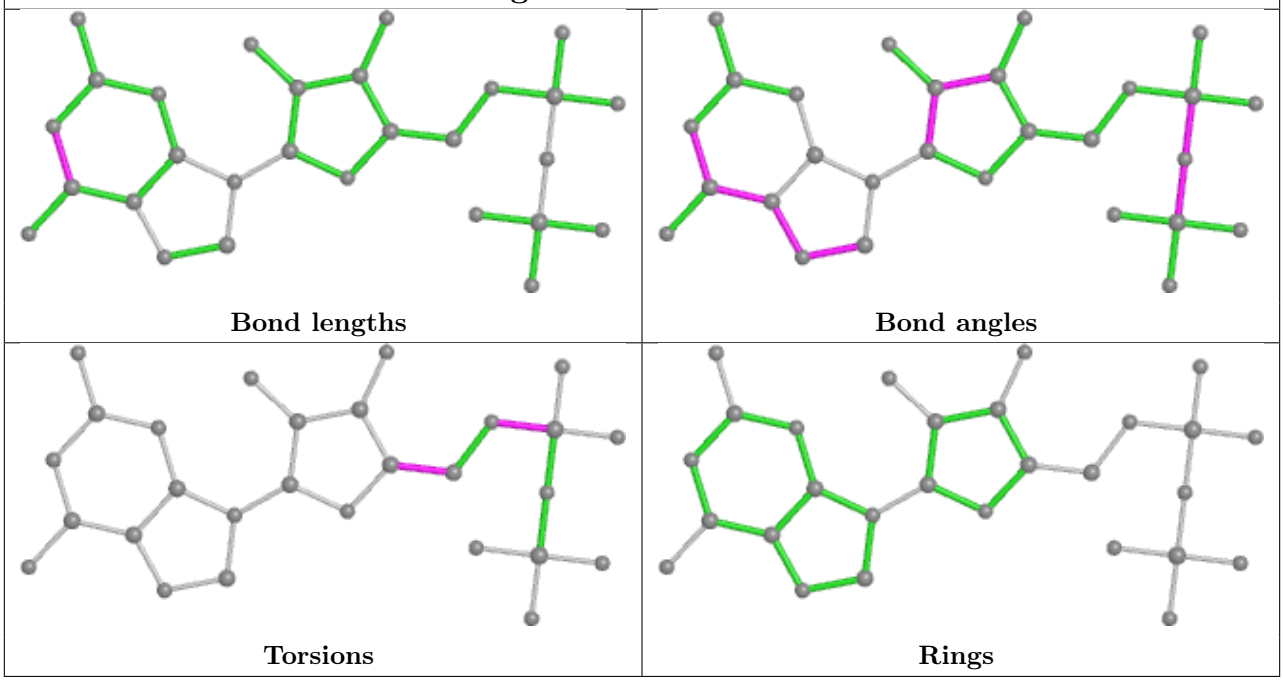
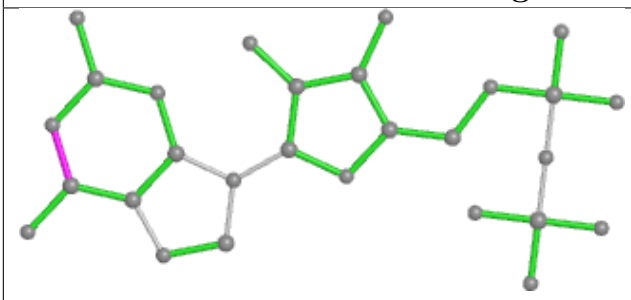
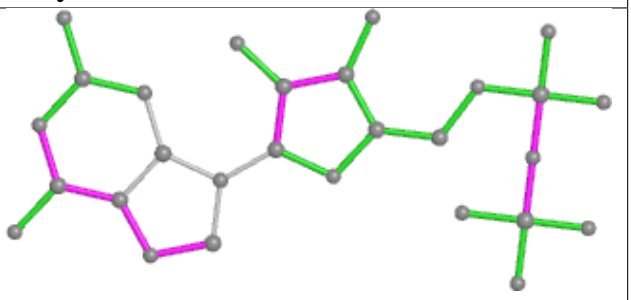
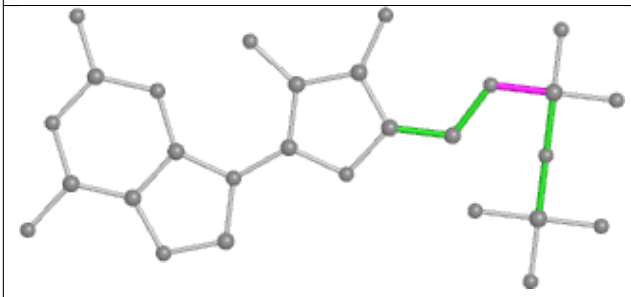
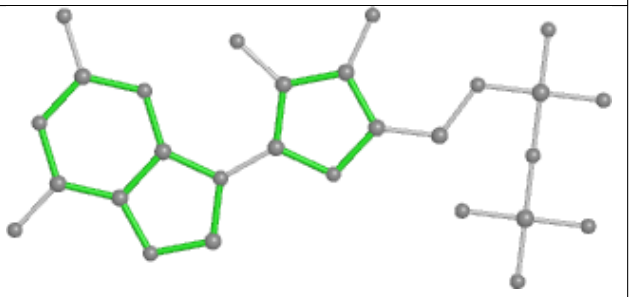
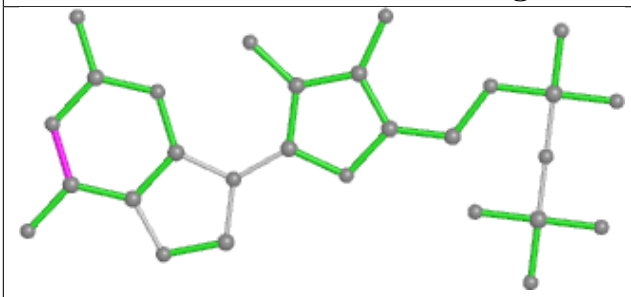
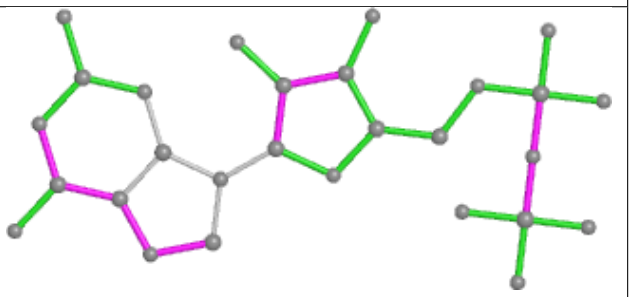
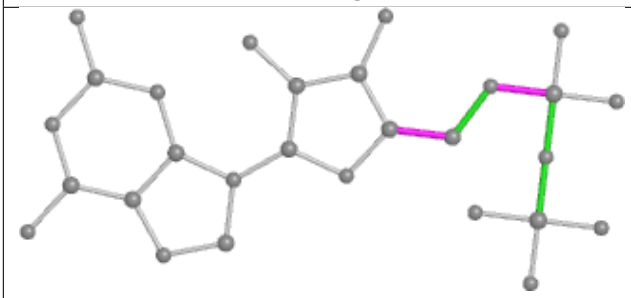
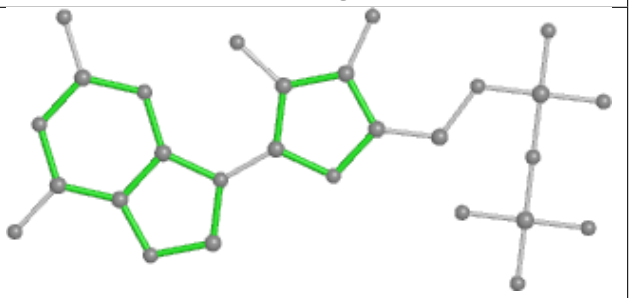


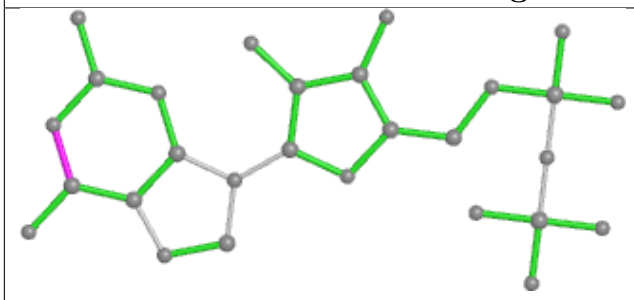
Ligand GDP LH 502



Ligand GDP QJ 502	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP OJ 502	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP KF 502



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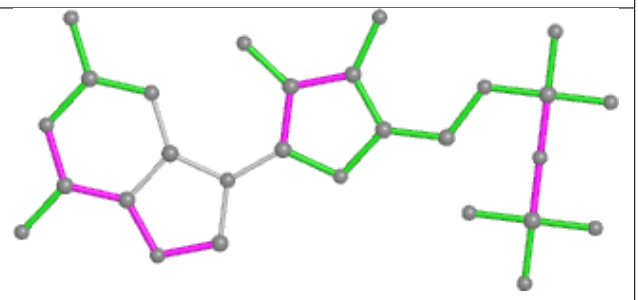
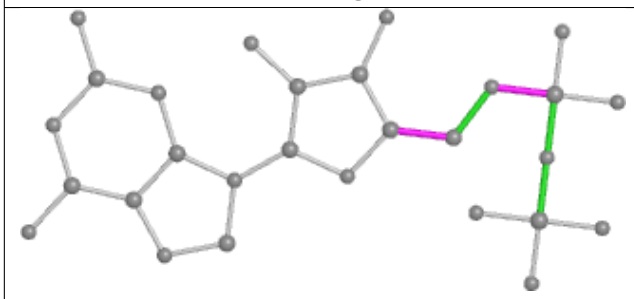


Bond angles



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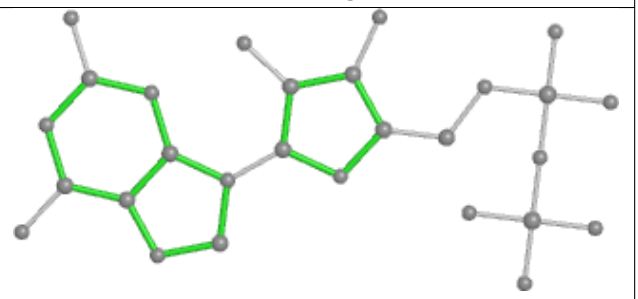
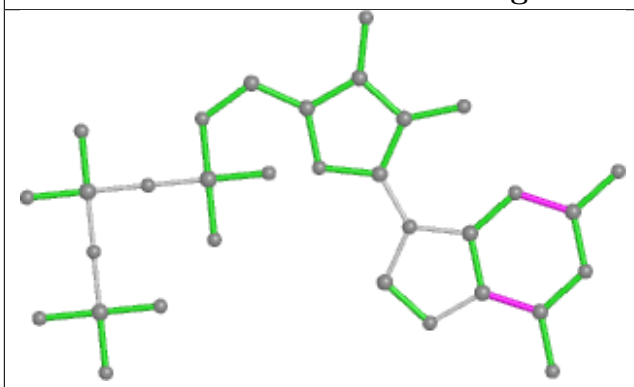


Rings

Ligand GTP GE 501



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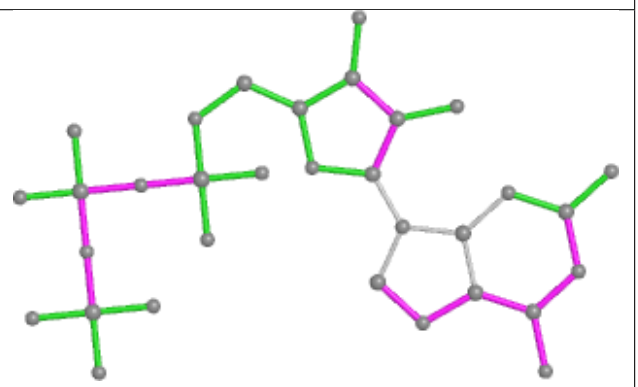

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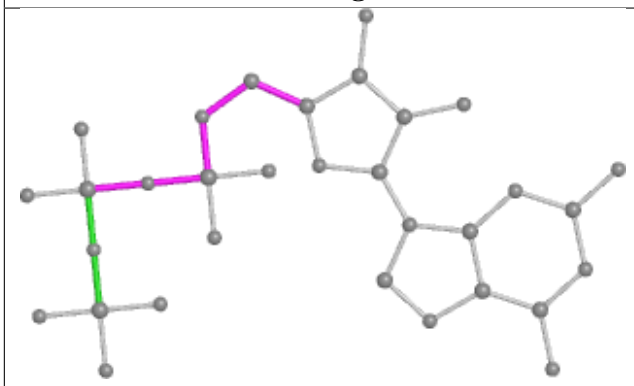

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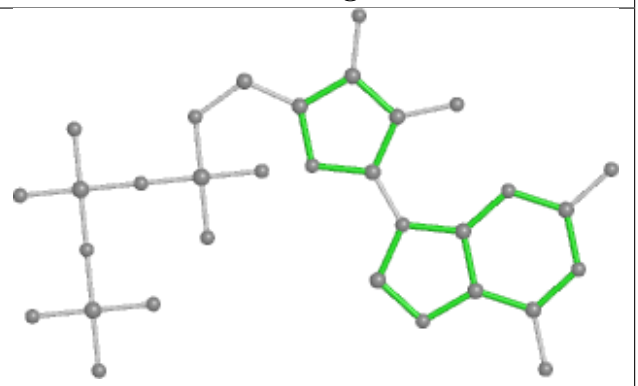
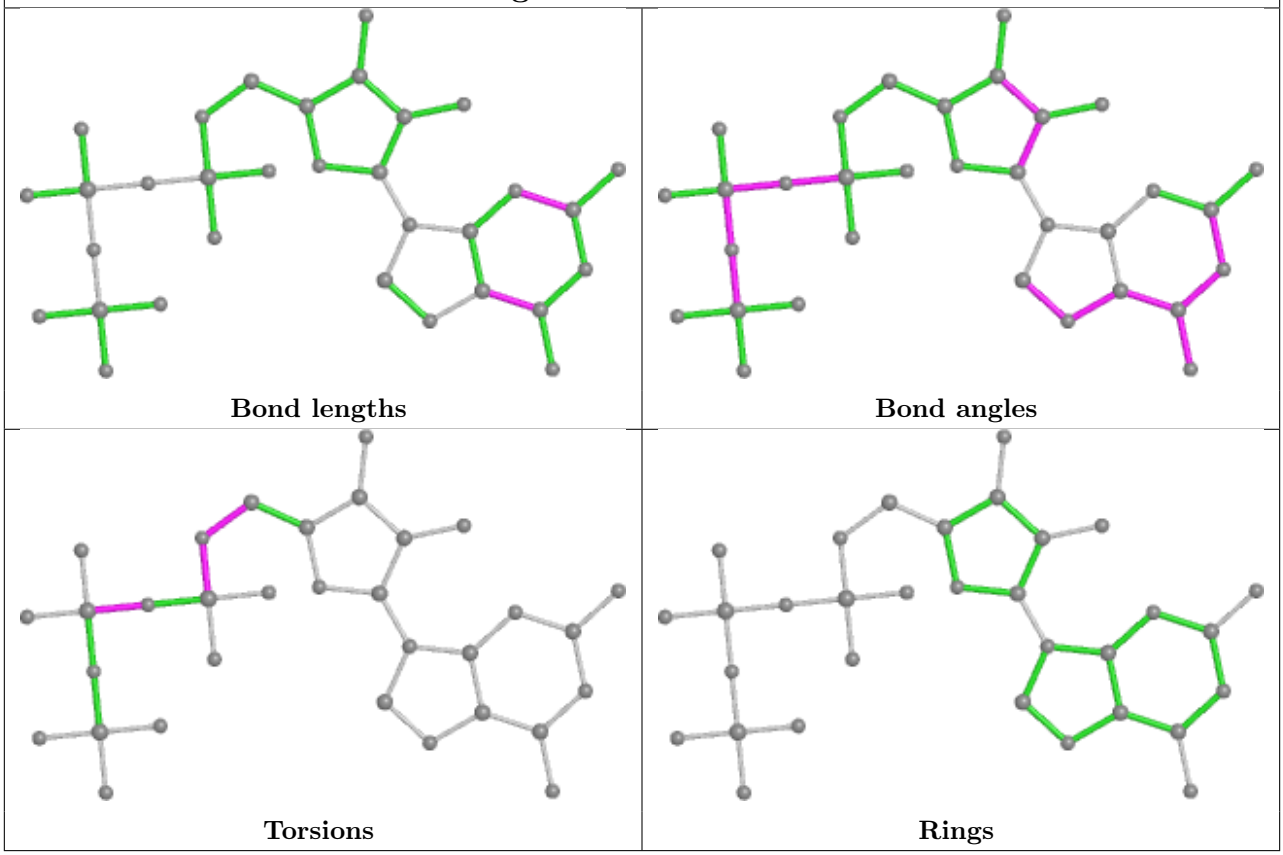
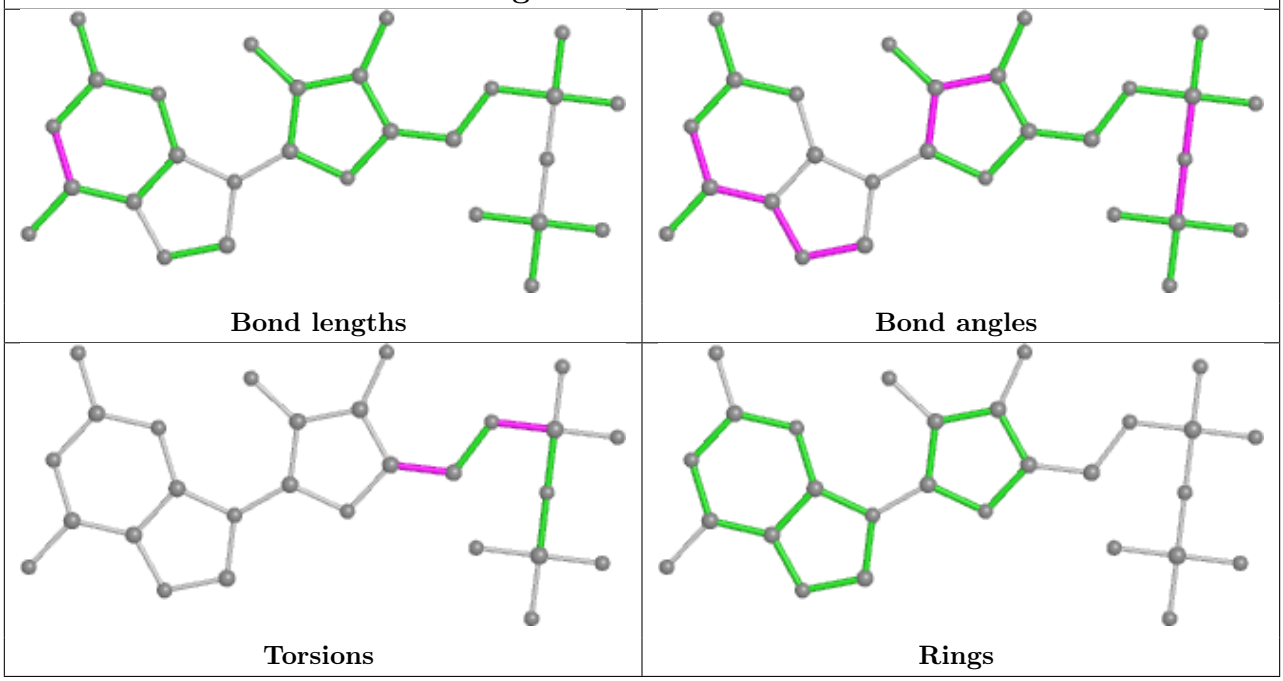


Rings

Ligand GTP FG 501



Ligand GDP UJ 502



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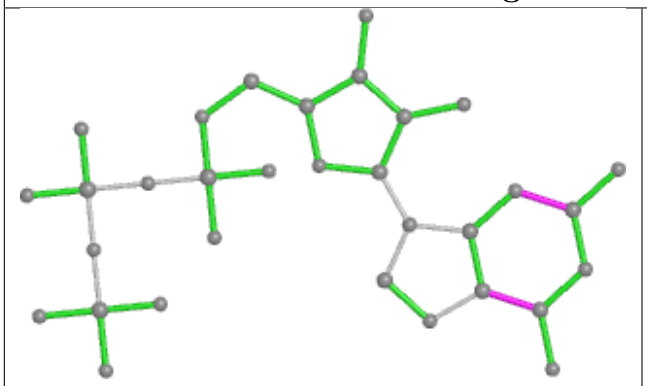

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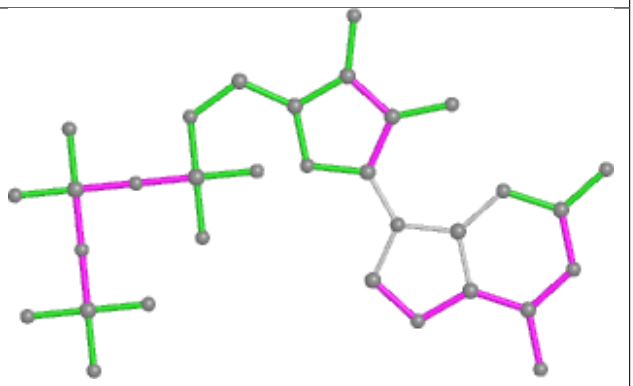

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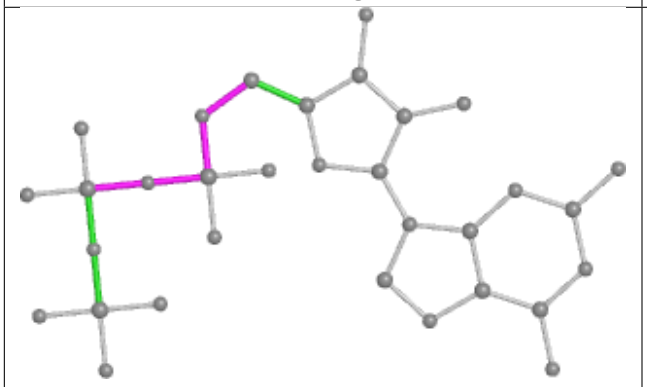

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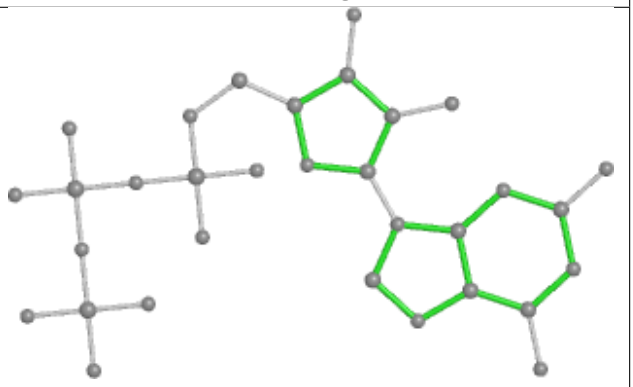
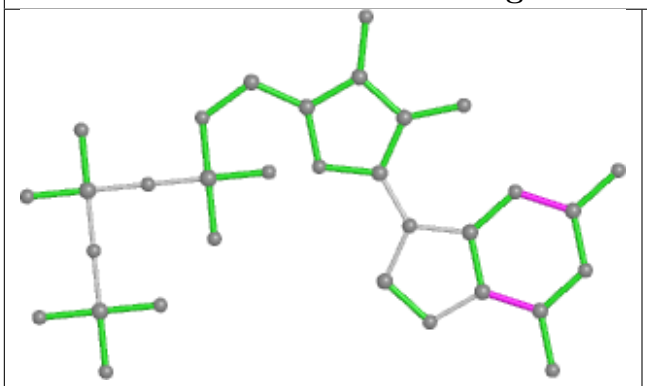


Rings

Ligand GTP AM 501



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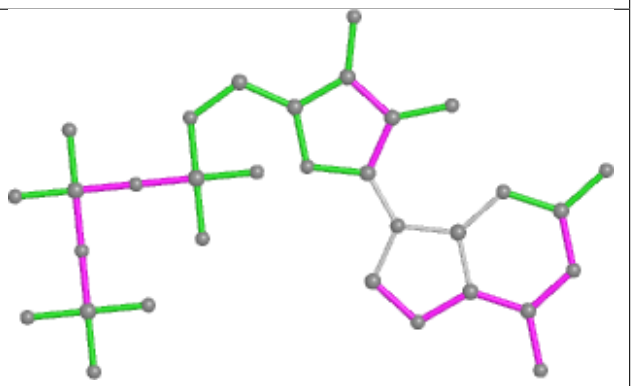

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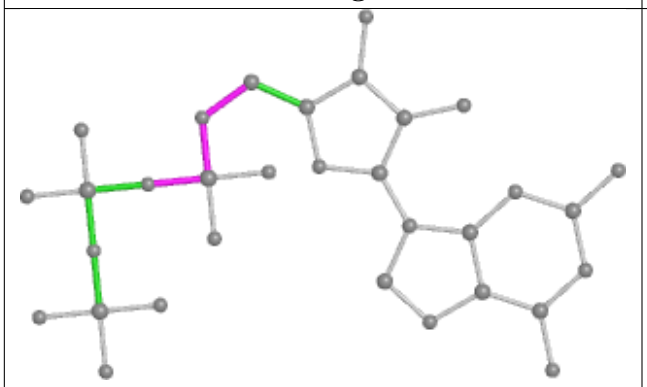

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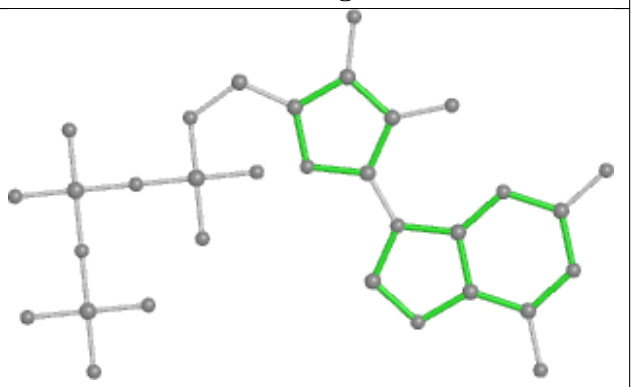
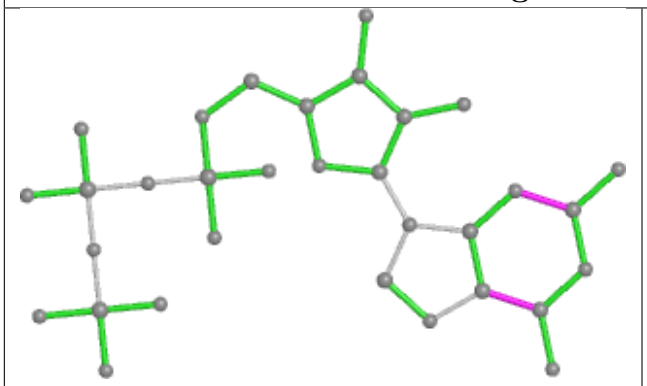


Rings

Ligand GTP PC 501



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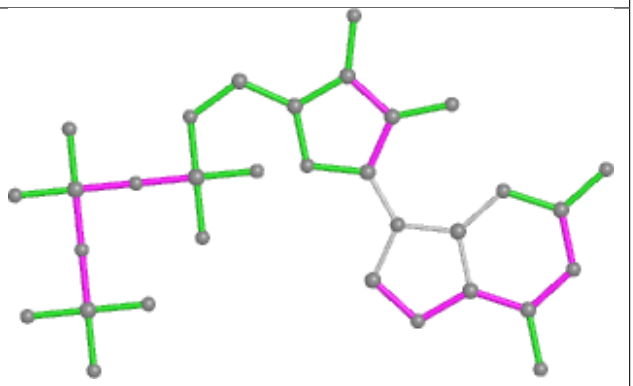
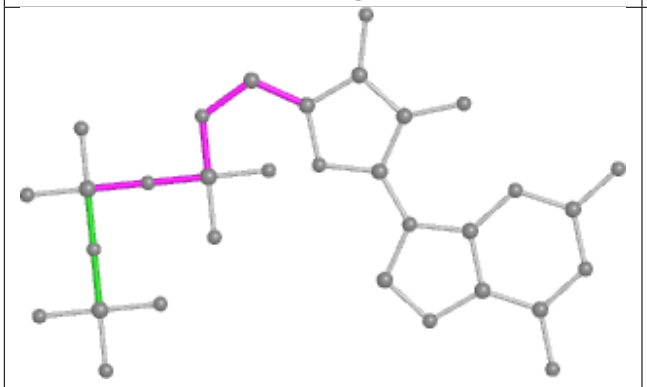


Bond angles



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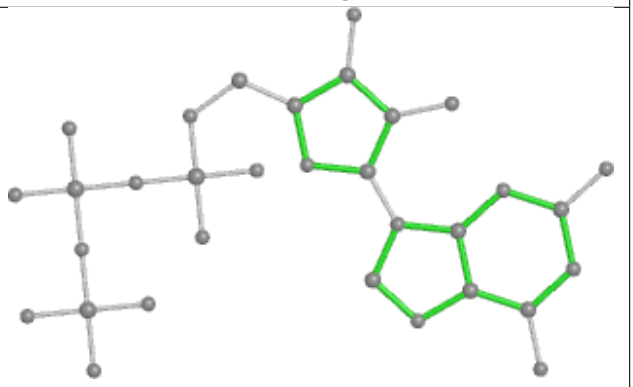
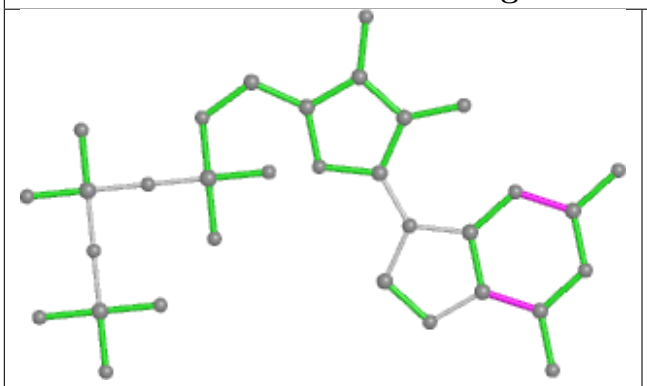


Rings

Ligand GTP WM 501



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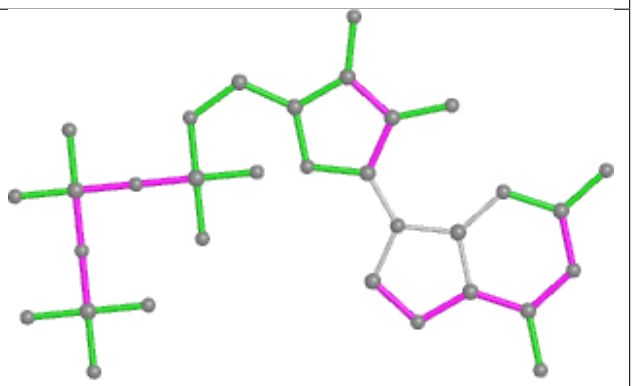

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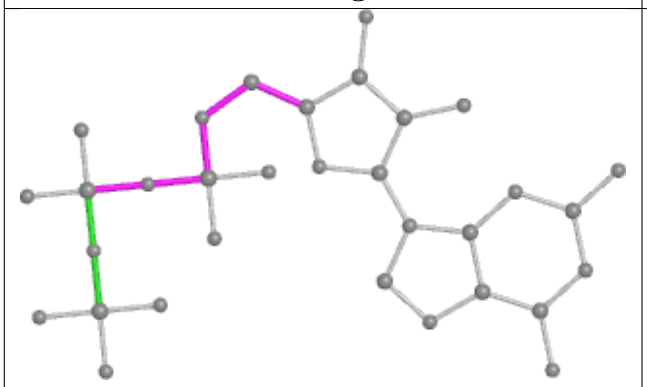

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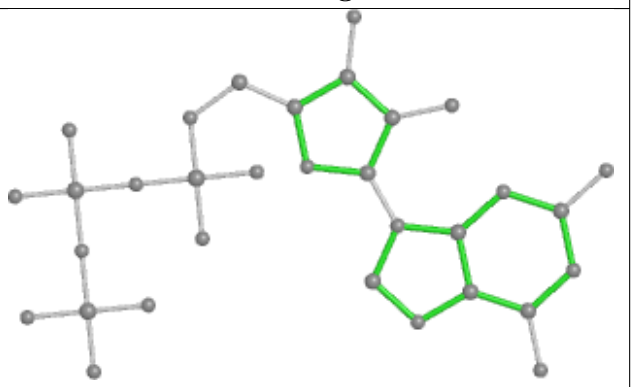
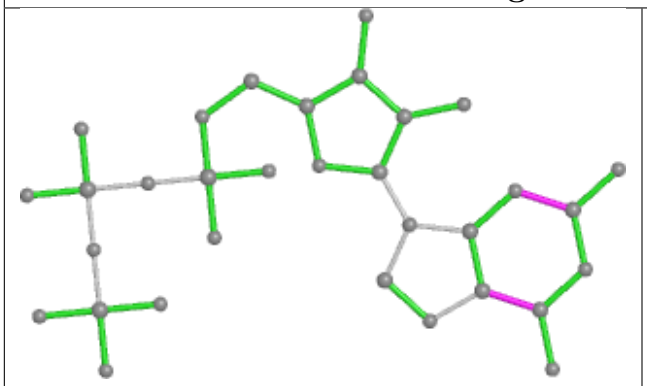


Rings

Ligand GTP ME 501



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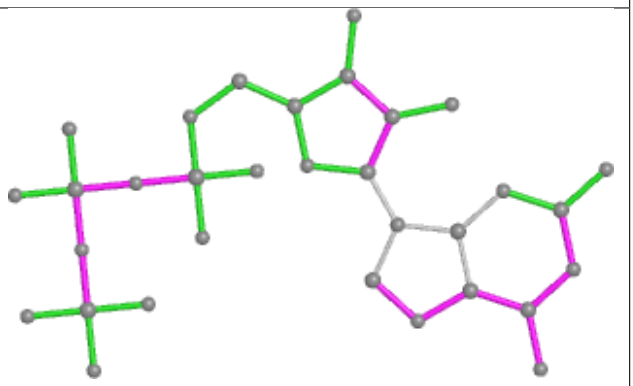
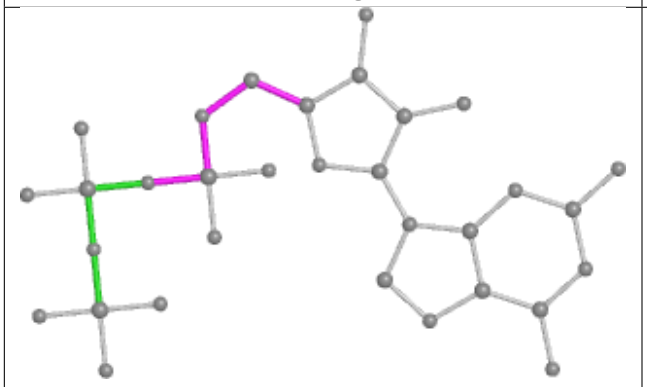


Bond angles



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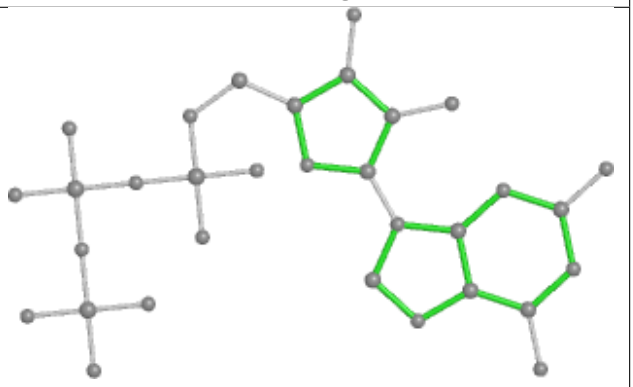
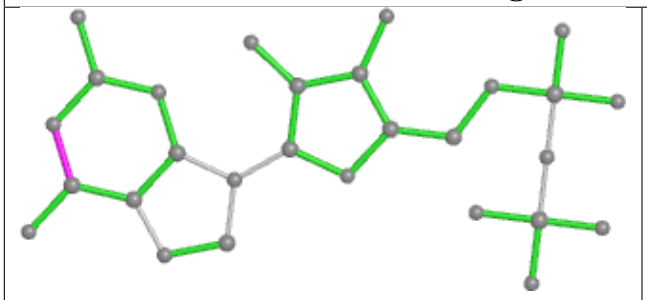


Rings

Ligand GDP AH 502



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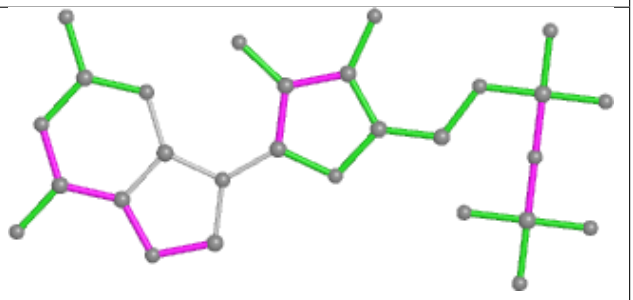

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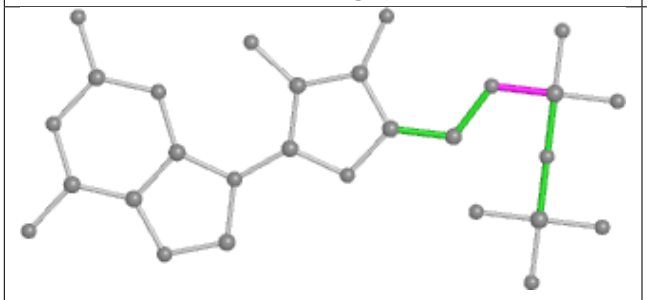

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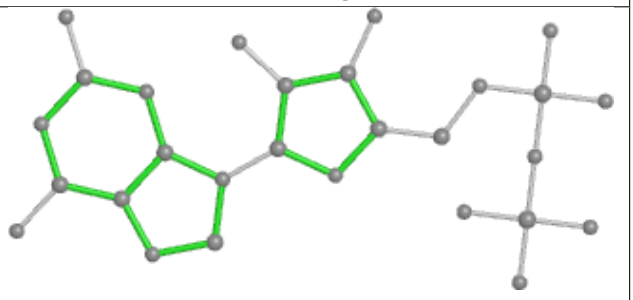
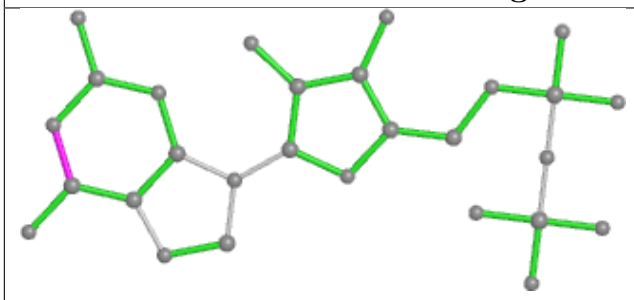


Rings

Ligand GDP ED 502



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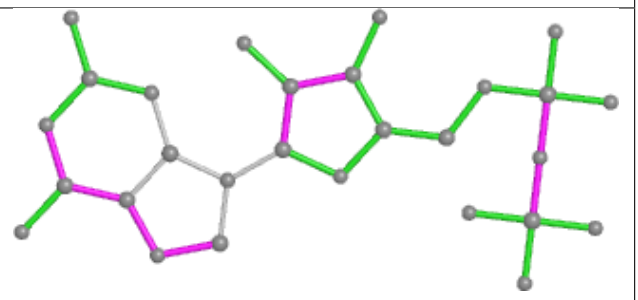
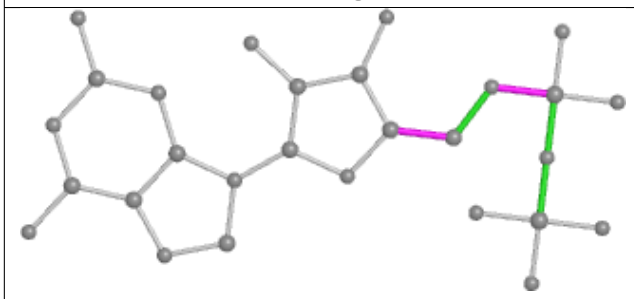


Bond angles



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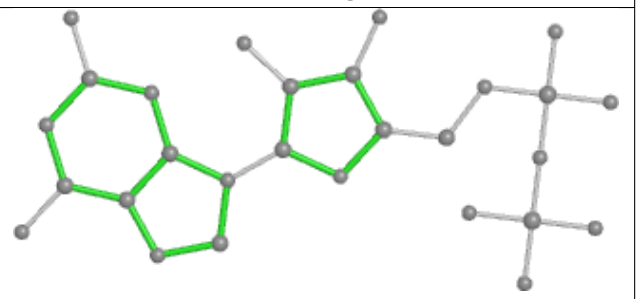
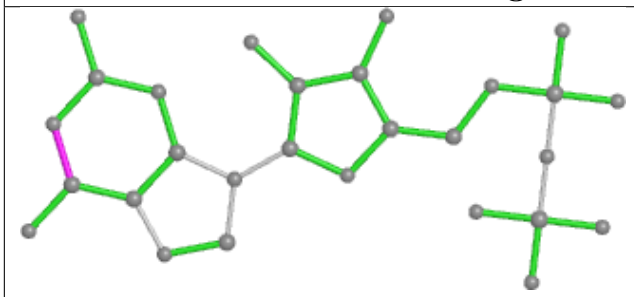


Rings

Ligand GDP KH 502



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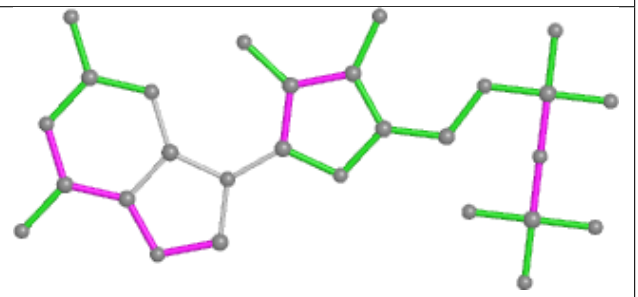

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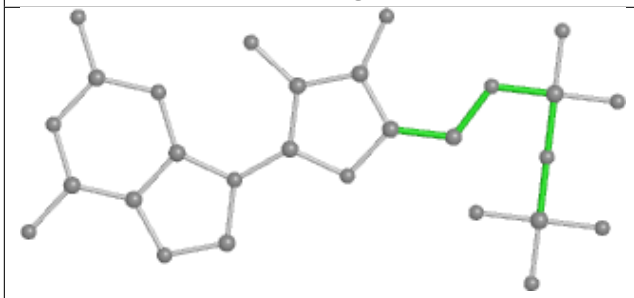
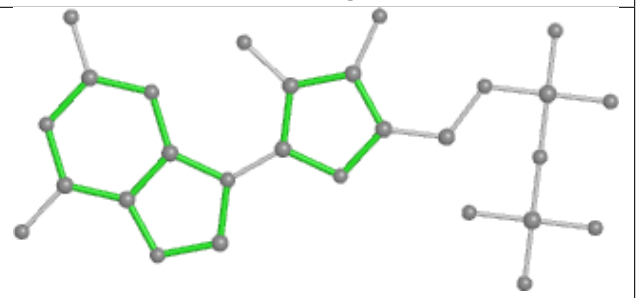
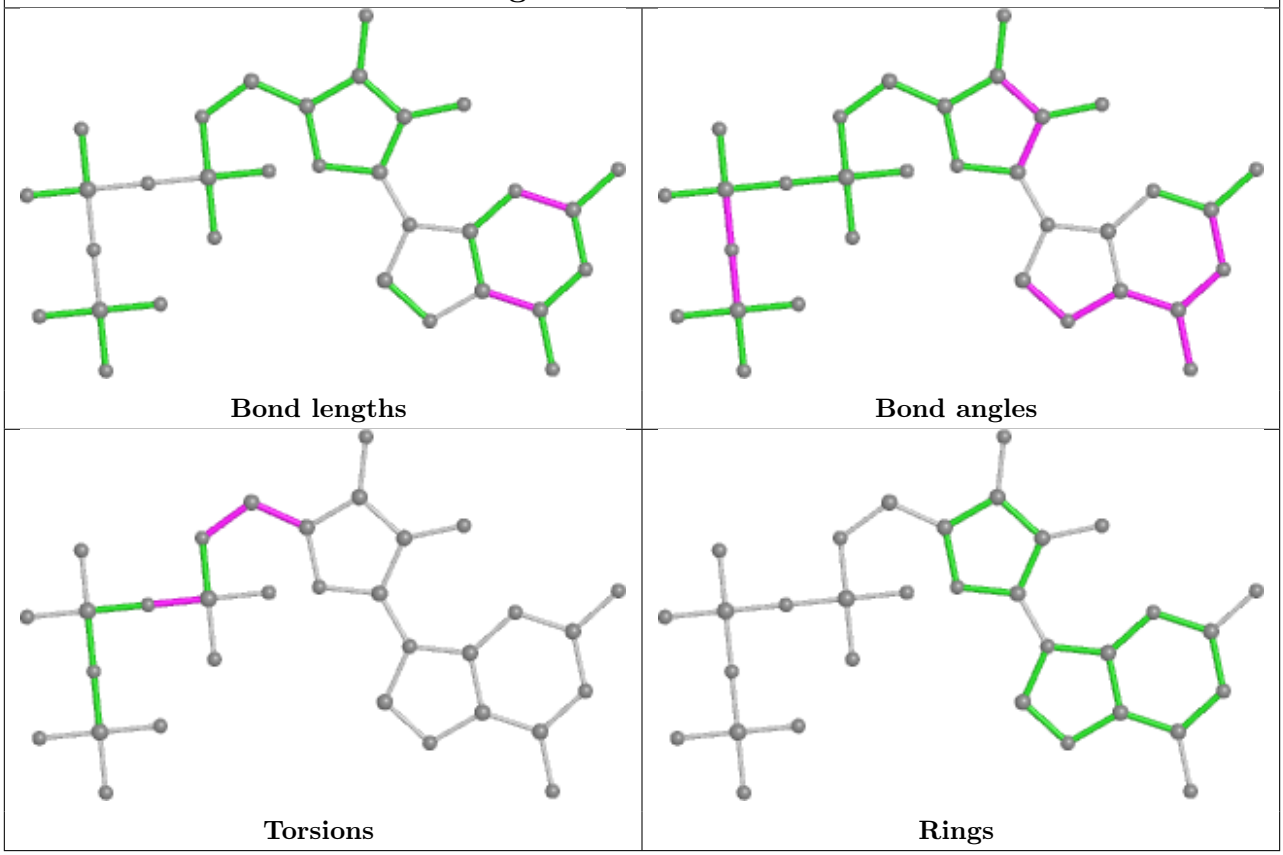


Torsions



Rings

Ligand GTP OK 501



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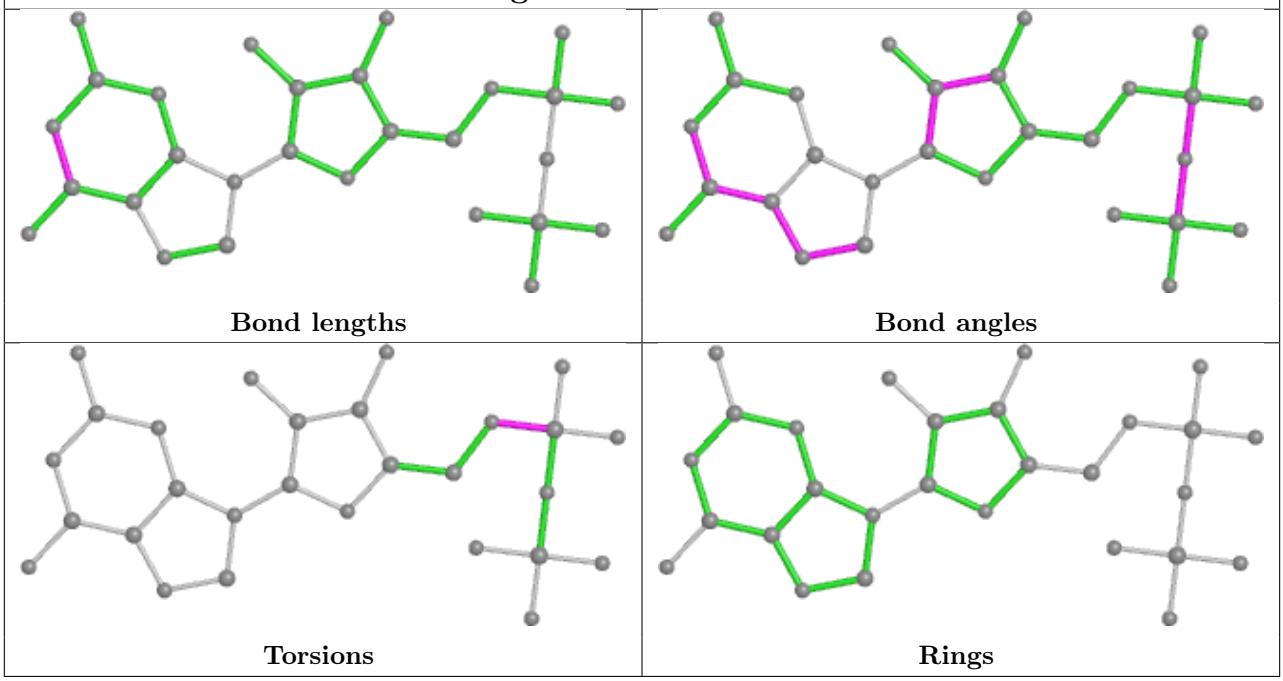

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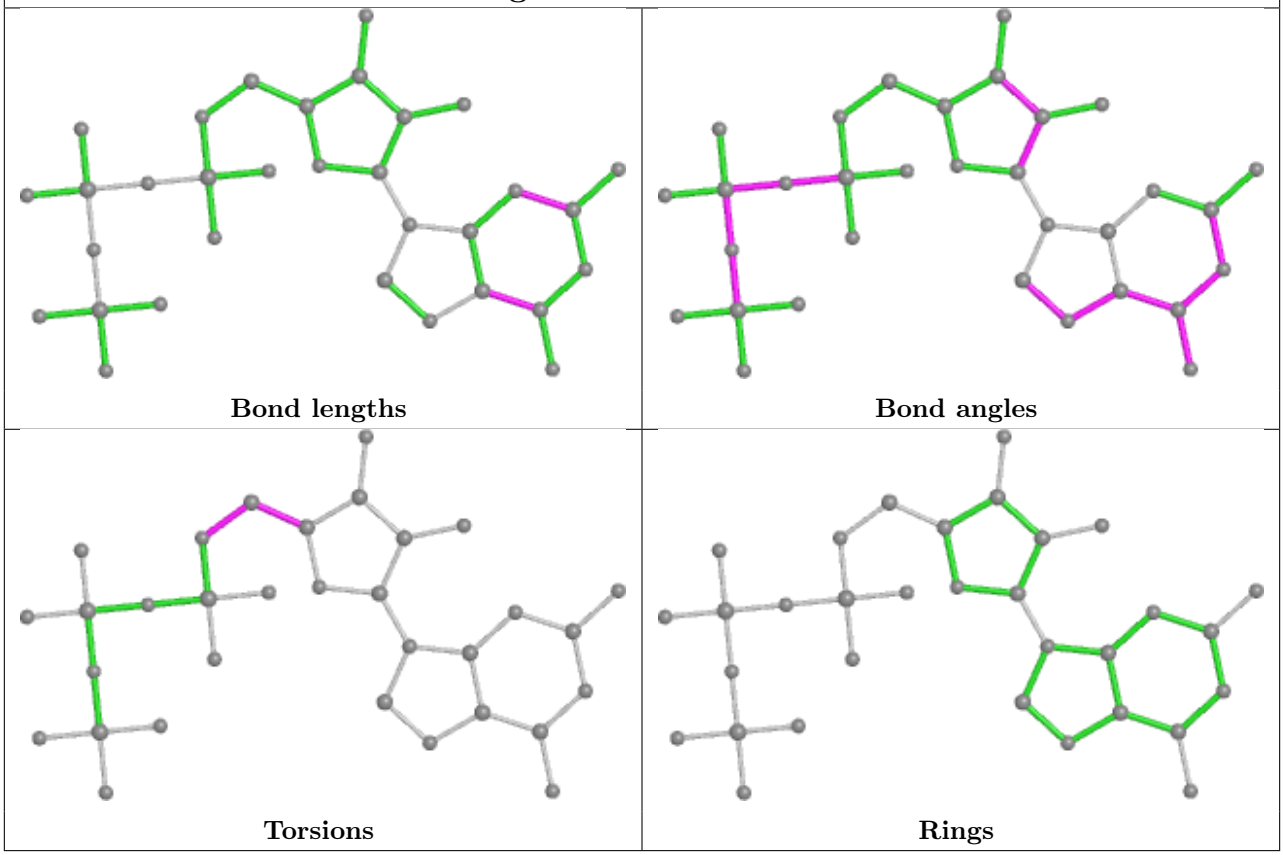

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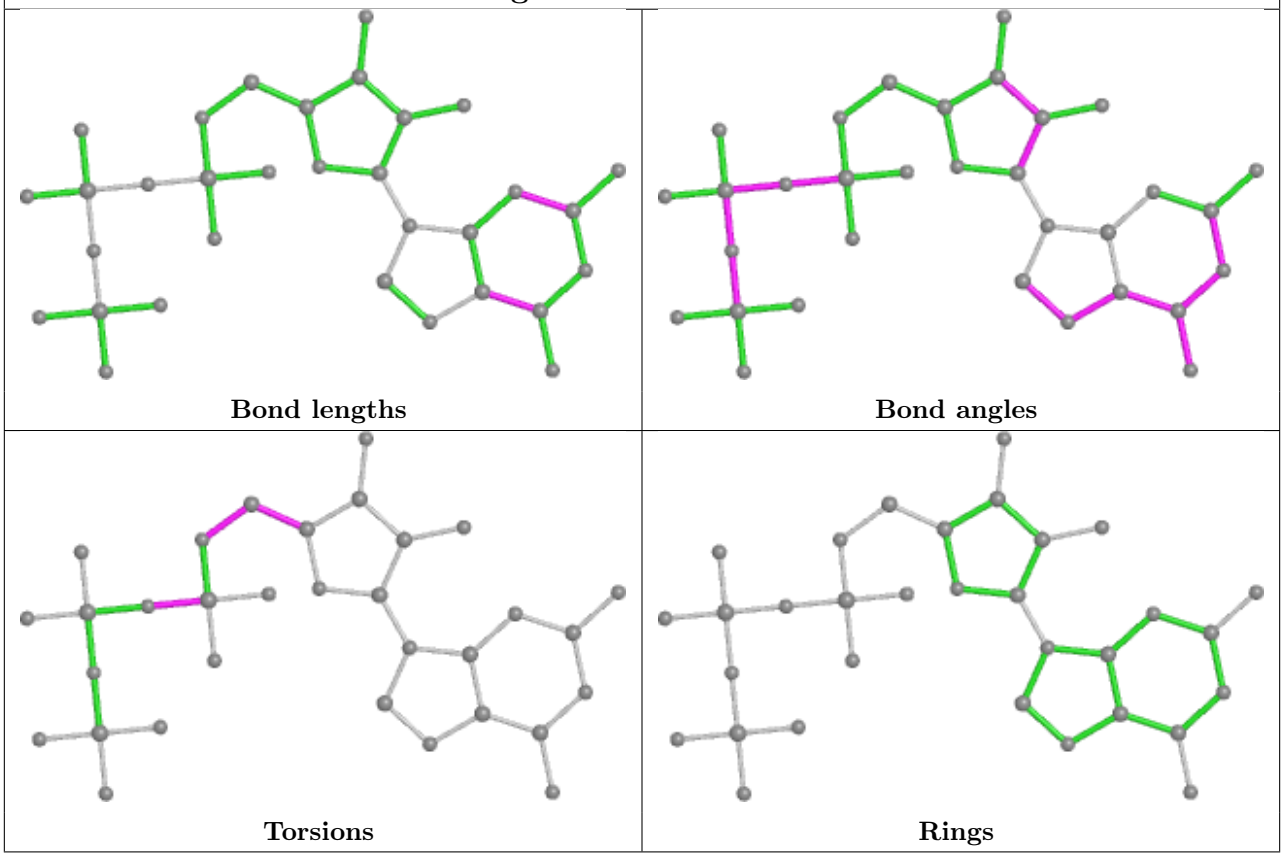

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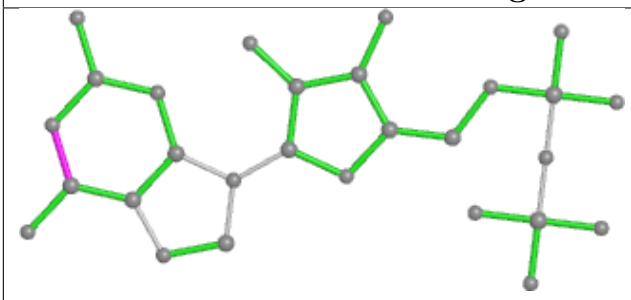

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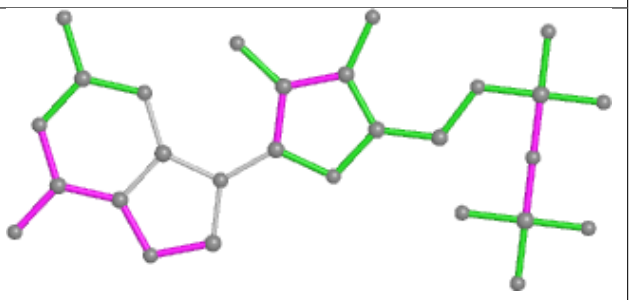

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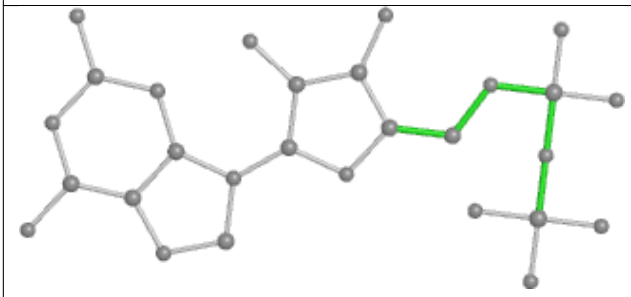
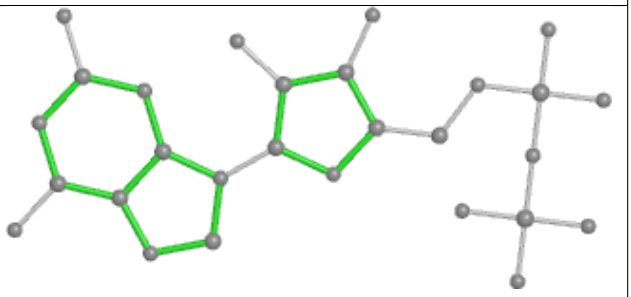
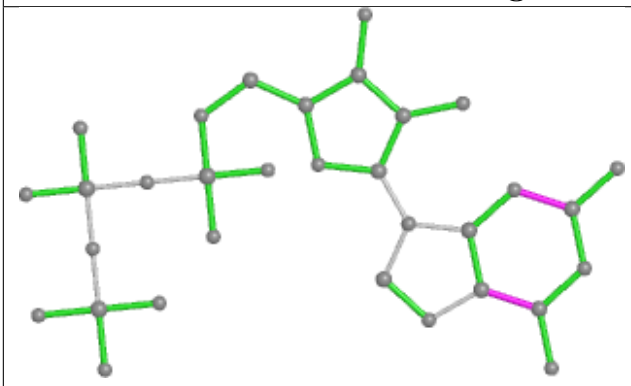


Torsions



Rings

Ligand GTP DG 501



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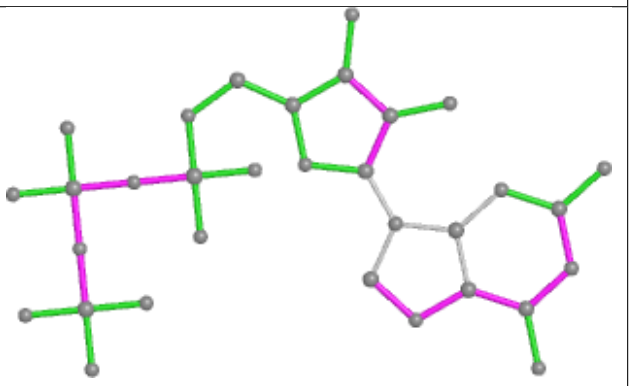

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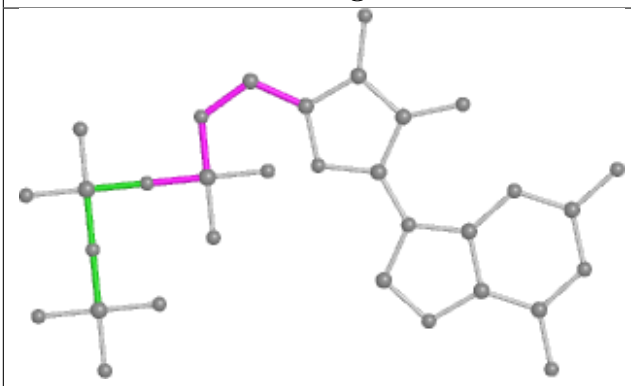

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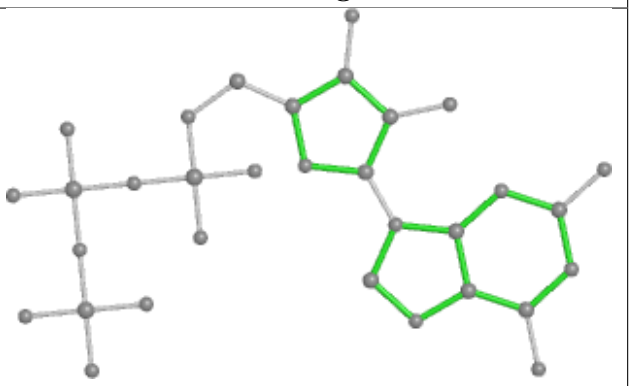
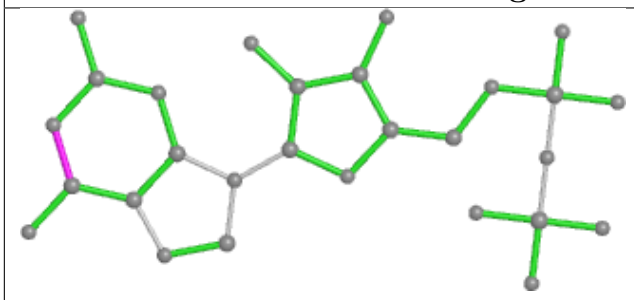


Rings

Ligand GDP OB 502



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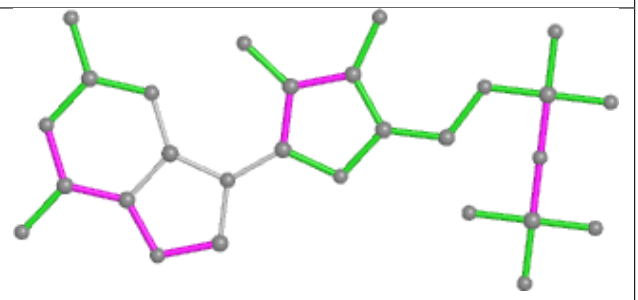

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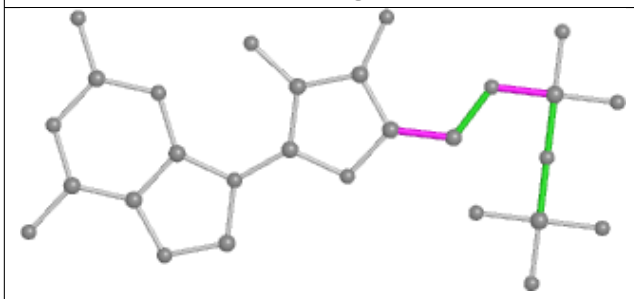

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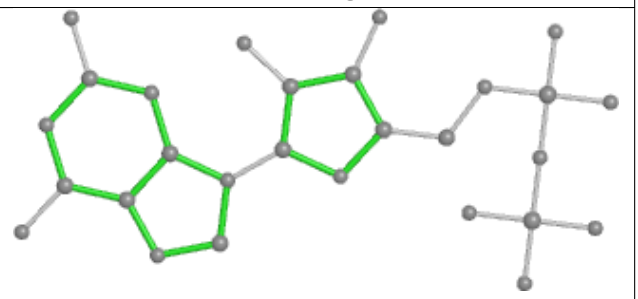
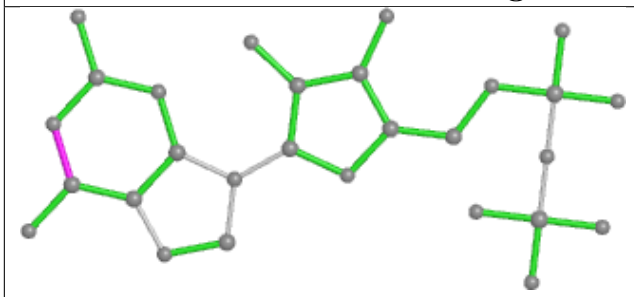


Rings

Ligand GDP GH 502



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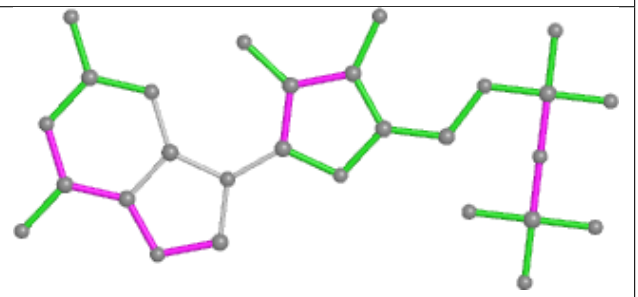

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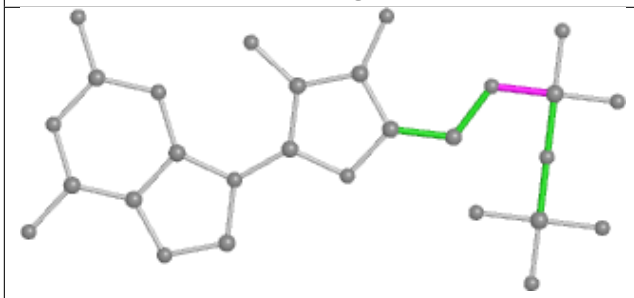

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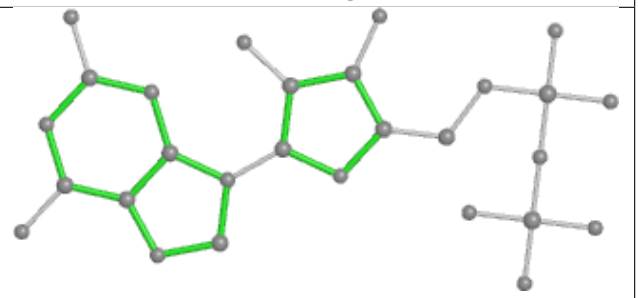

Rings

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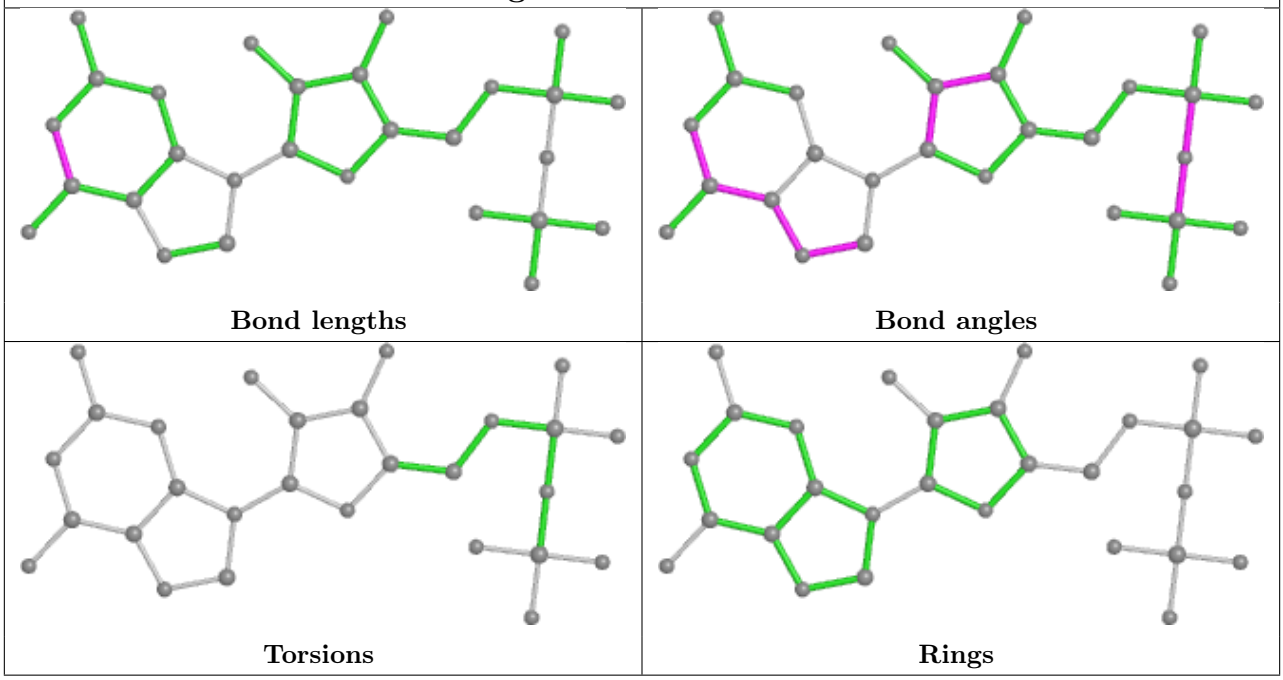

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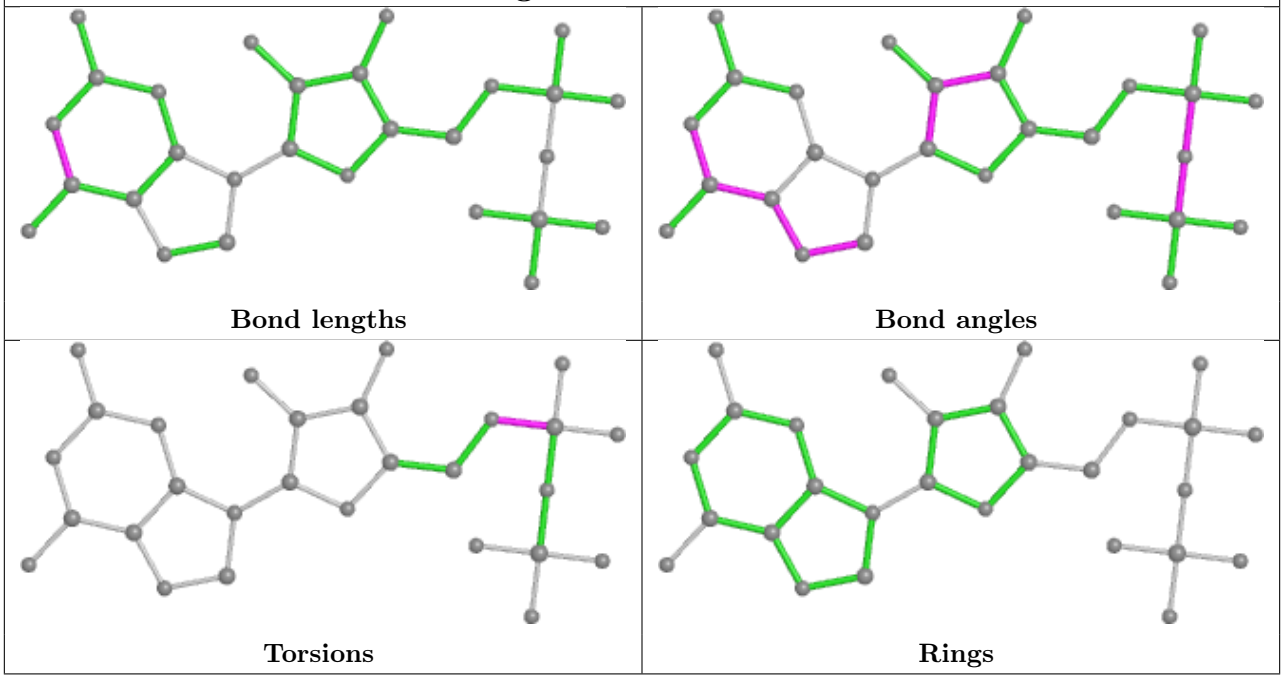

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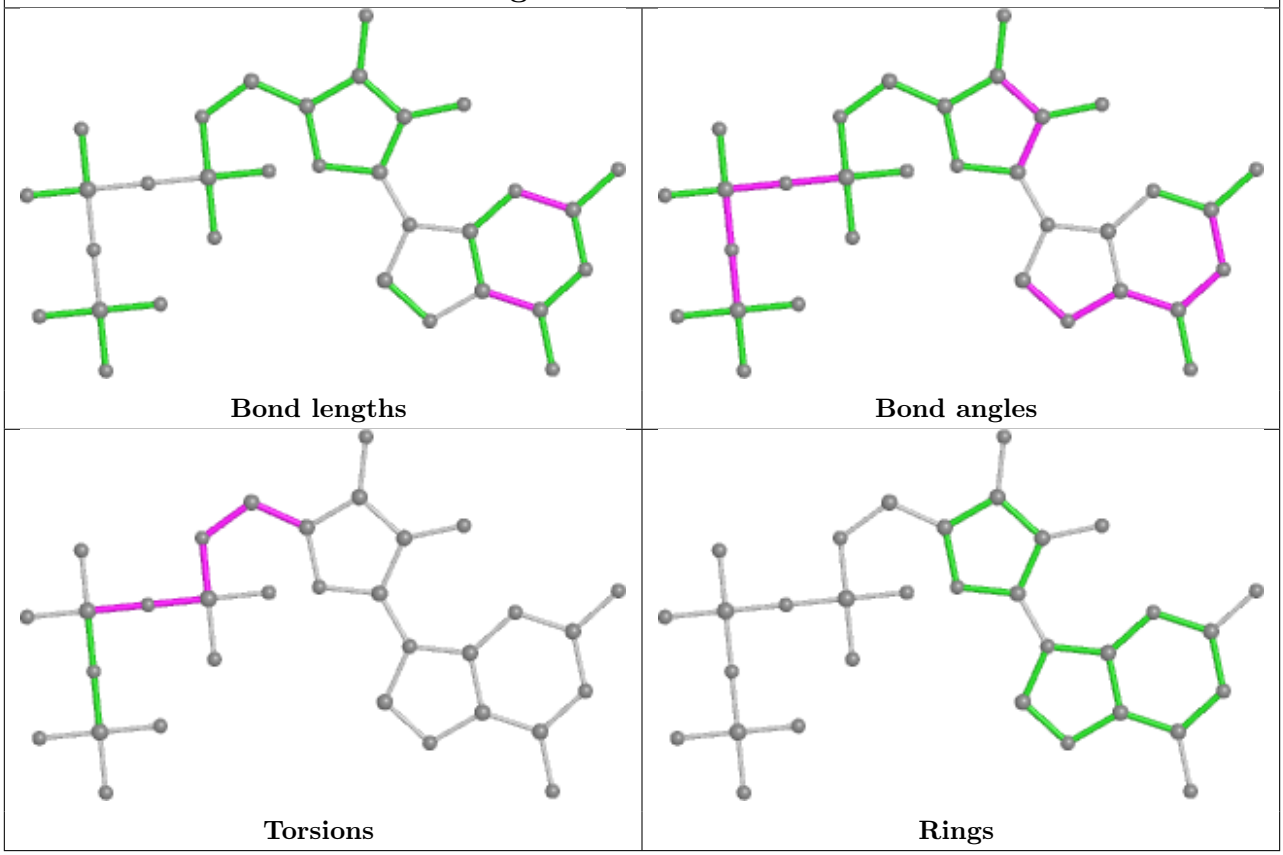

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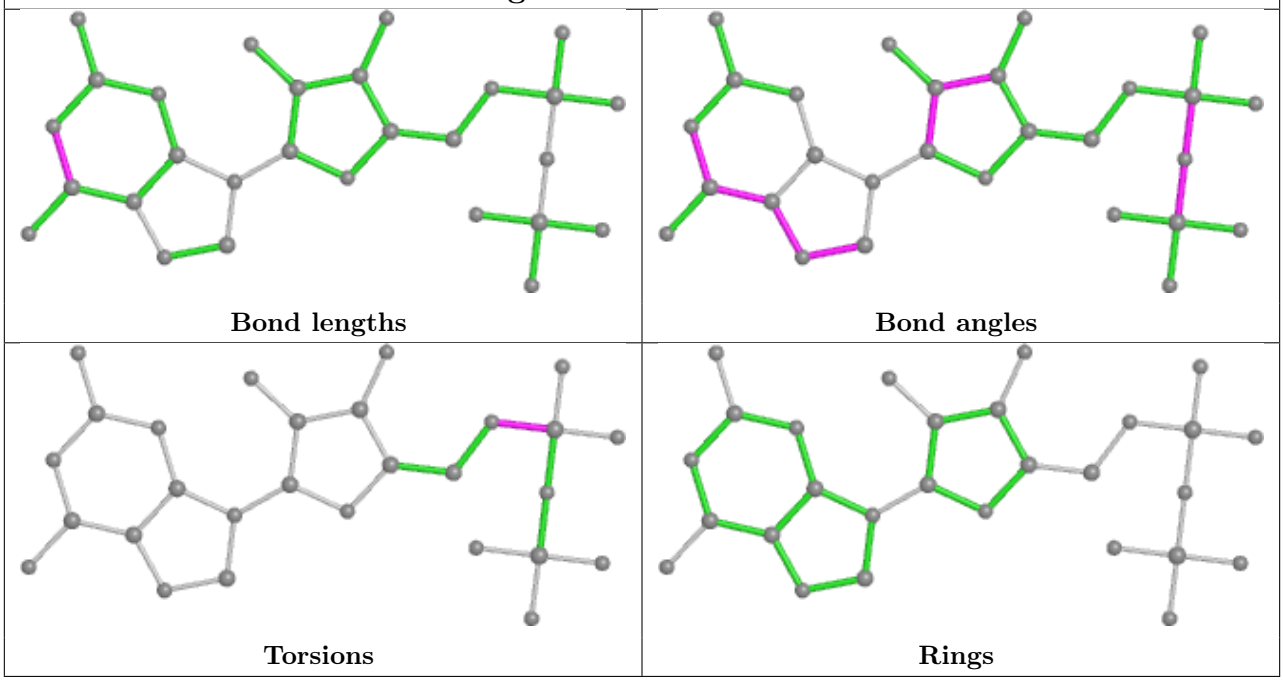

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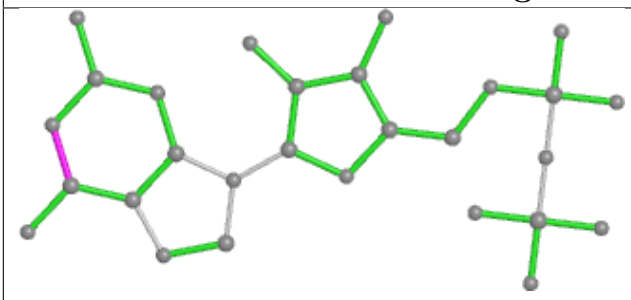

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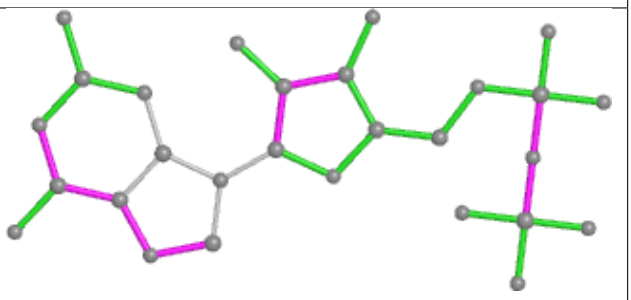
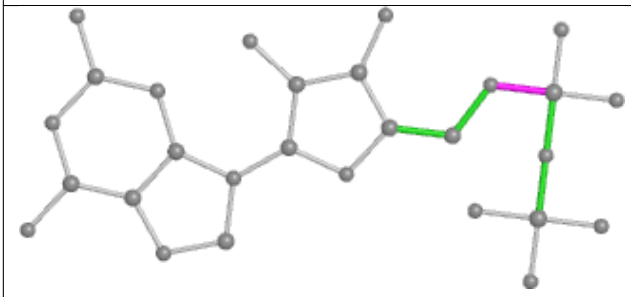


Bond angles



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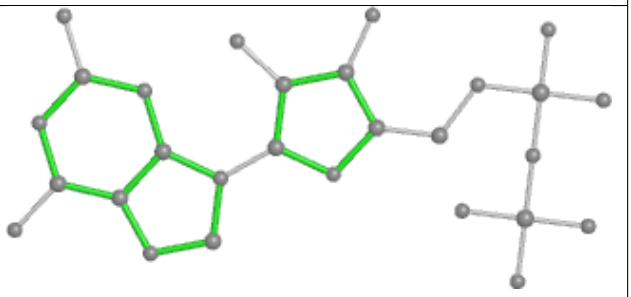
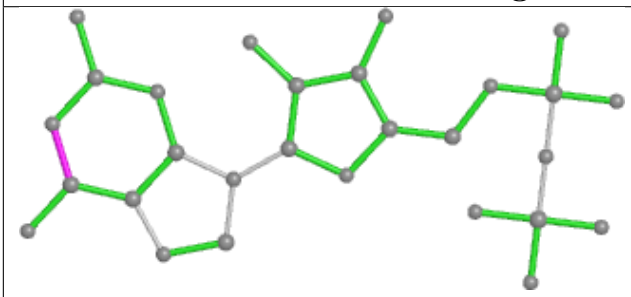


Rings

Ligand GDP PF 502



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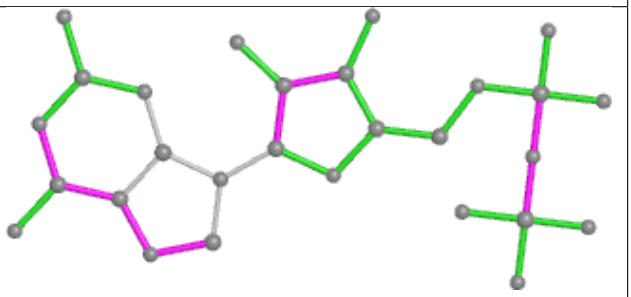

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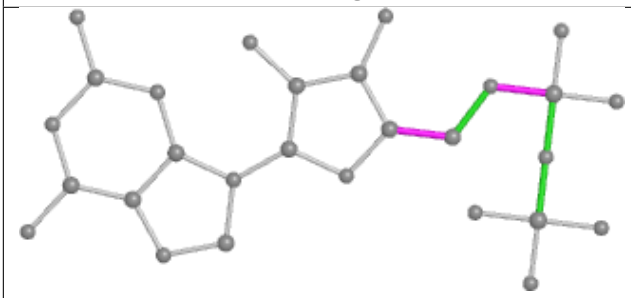

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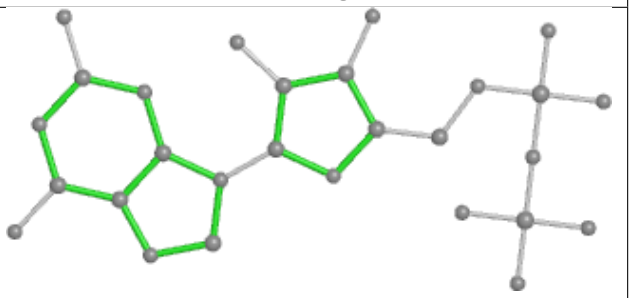

Rings

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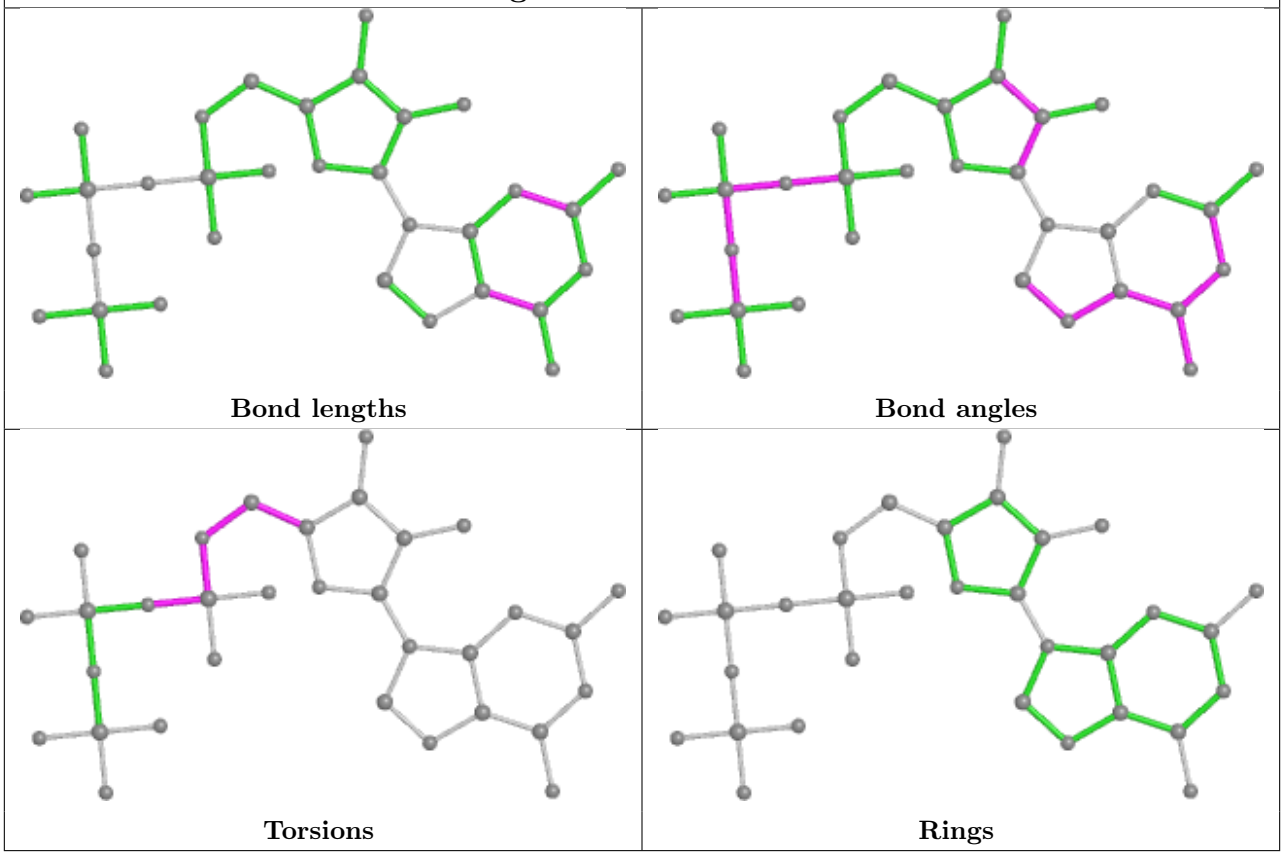

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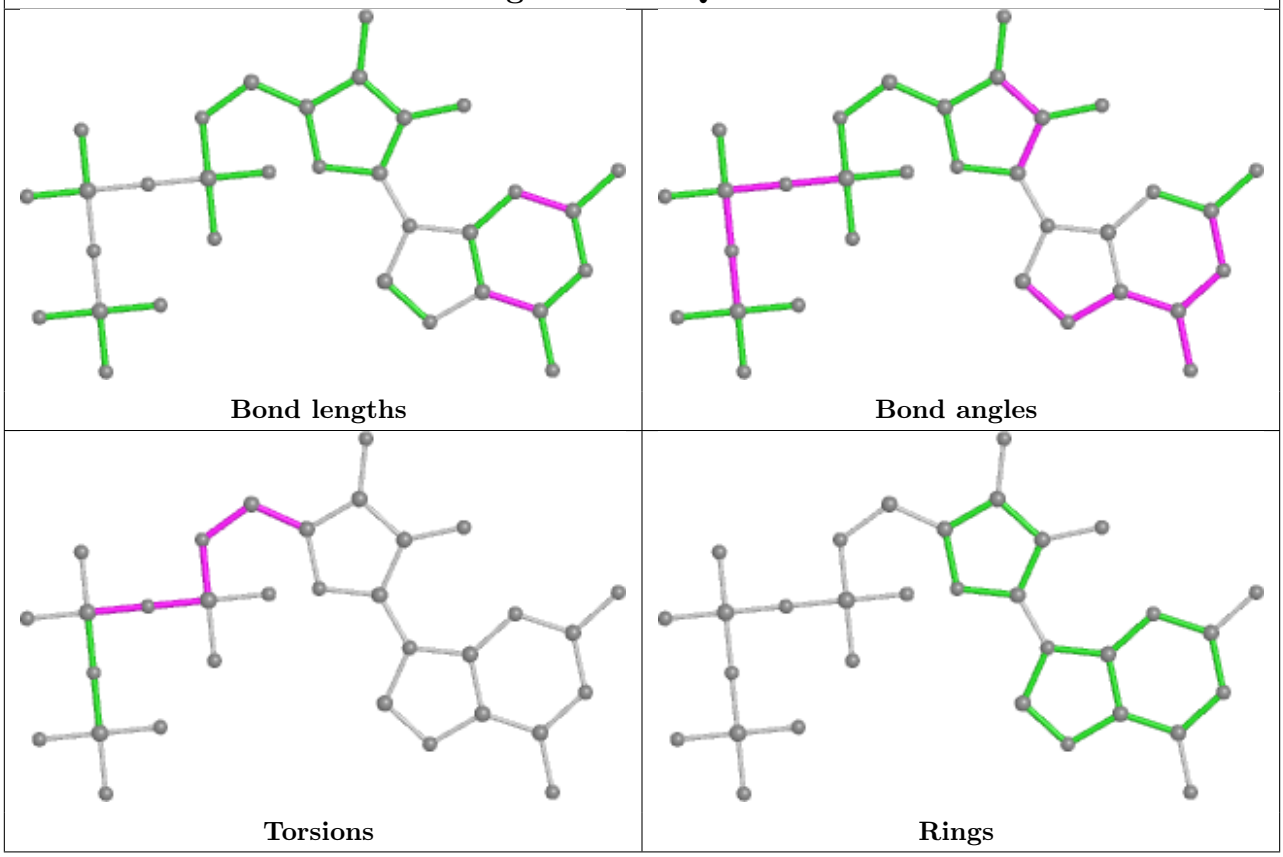

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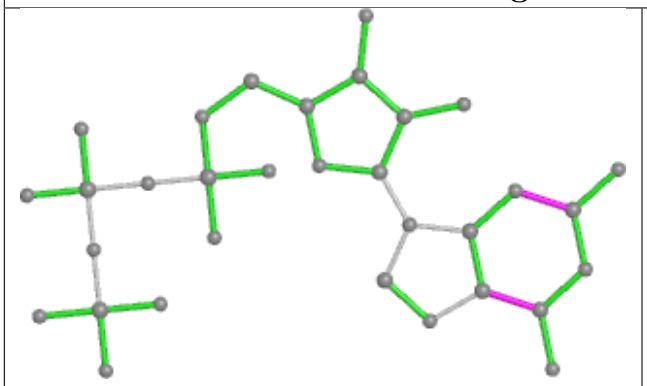

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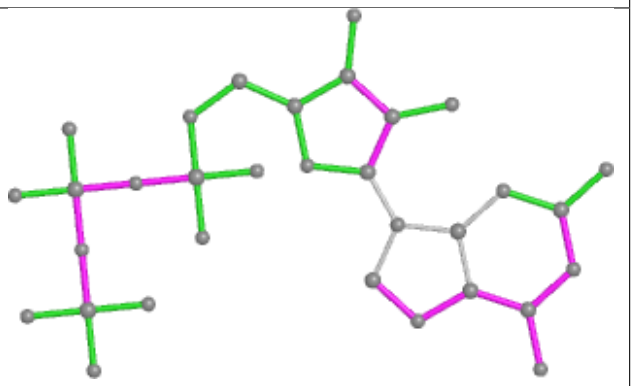

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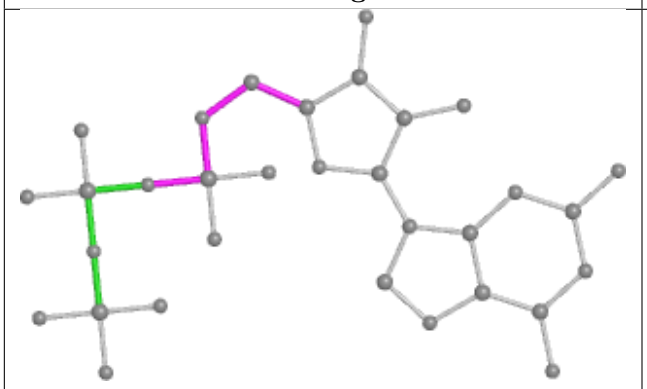
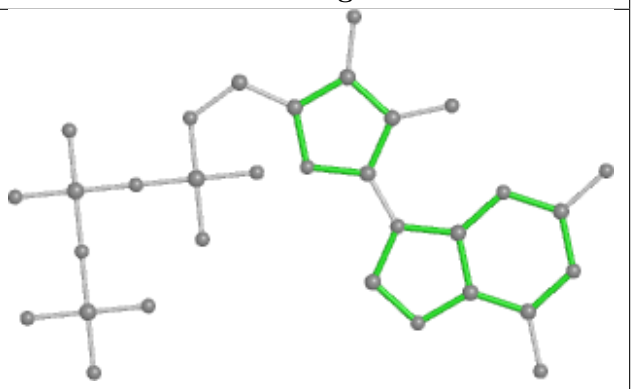


Torsions



Rings

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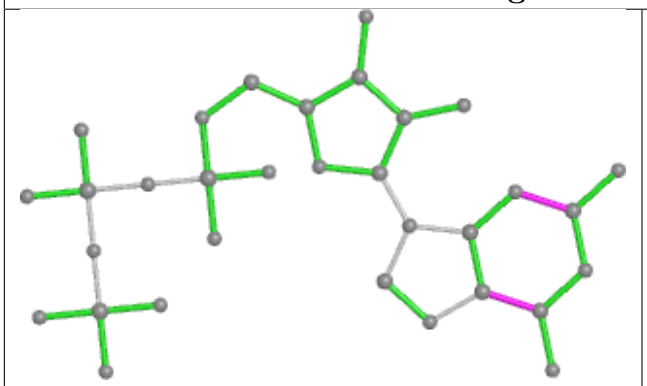

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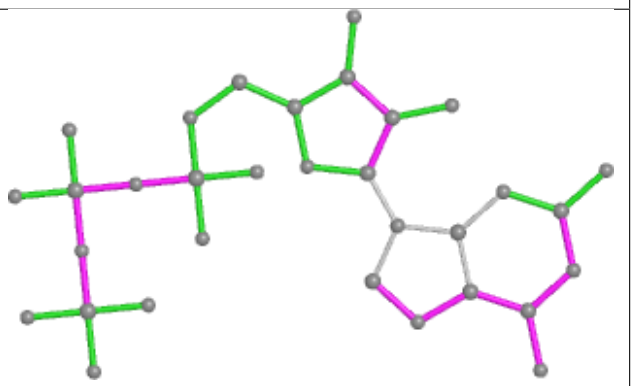
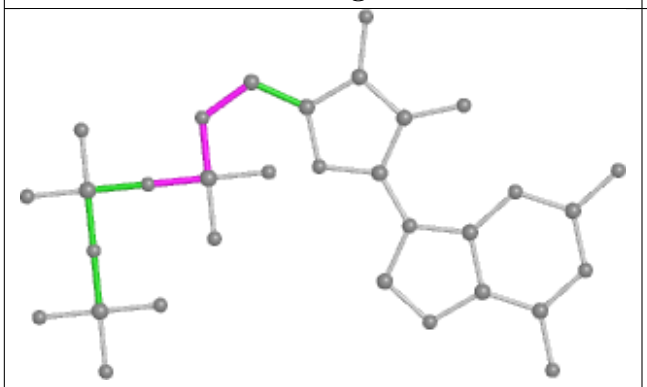
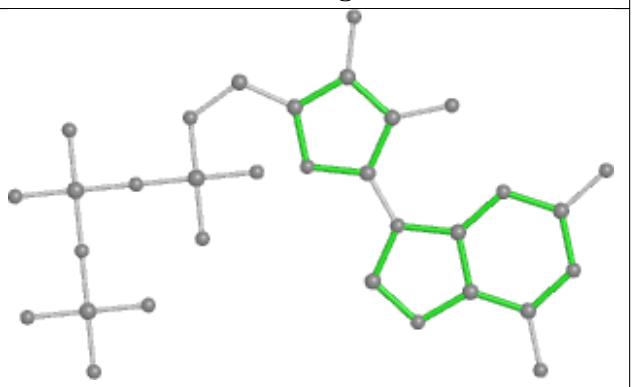


Bond angles

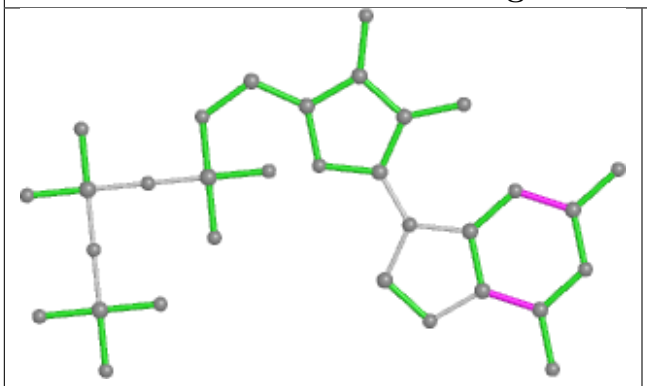


Torsions



Rings

Ligand GTP BM 501



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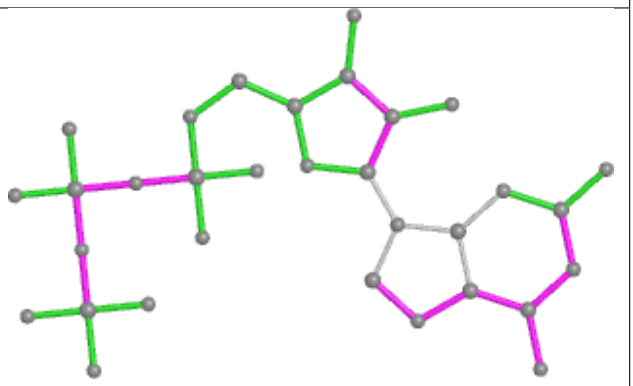

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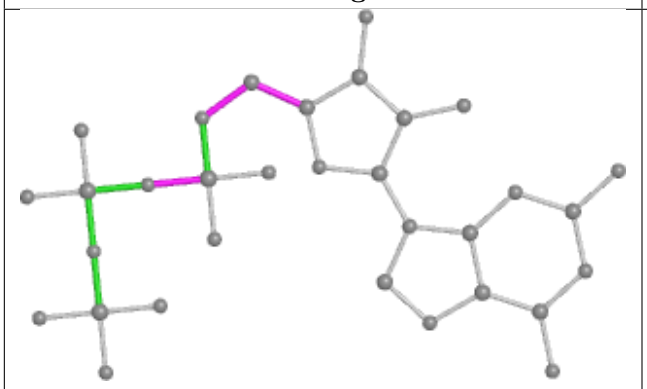

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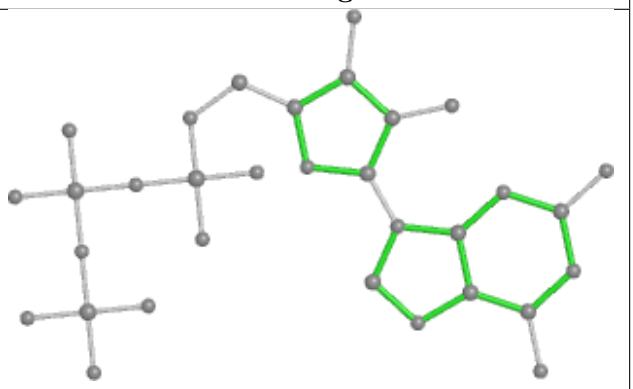
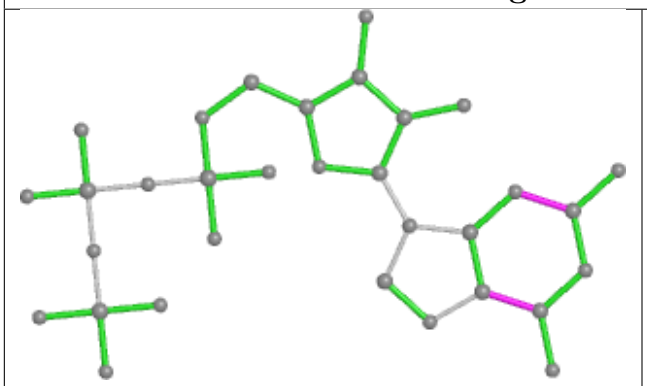


Rings

Ligand GTP HO 501



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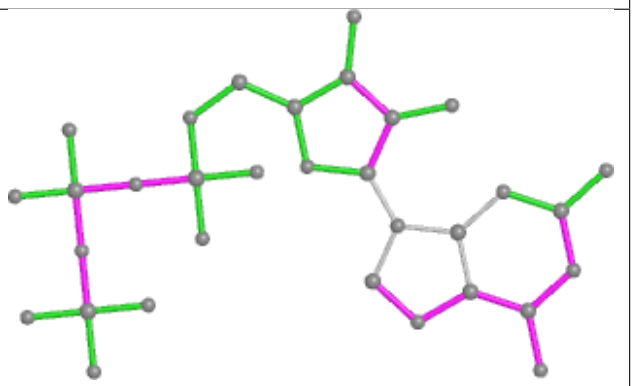

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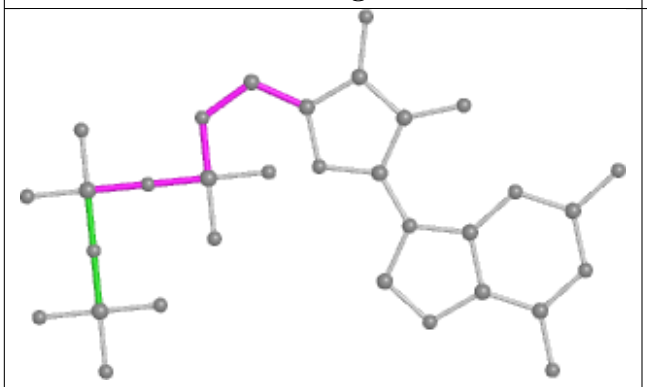
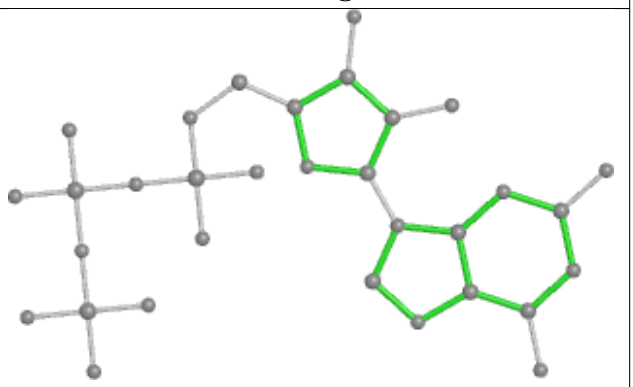


Torsions



Rings

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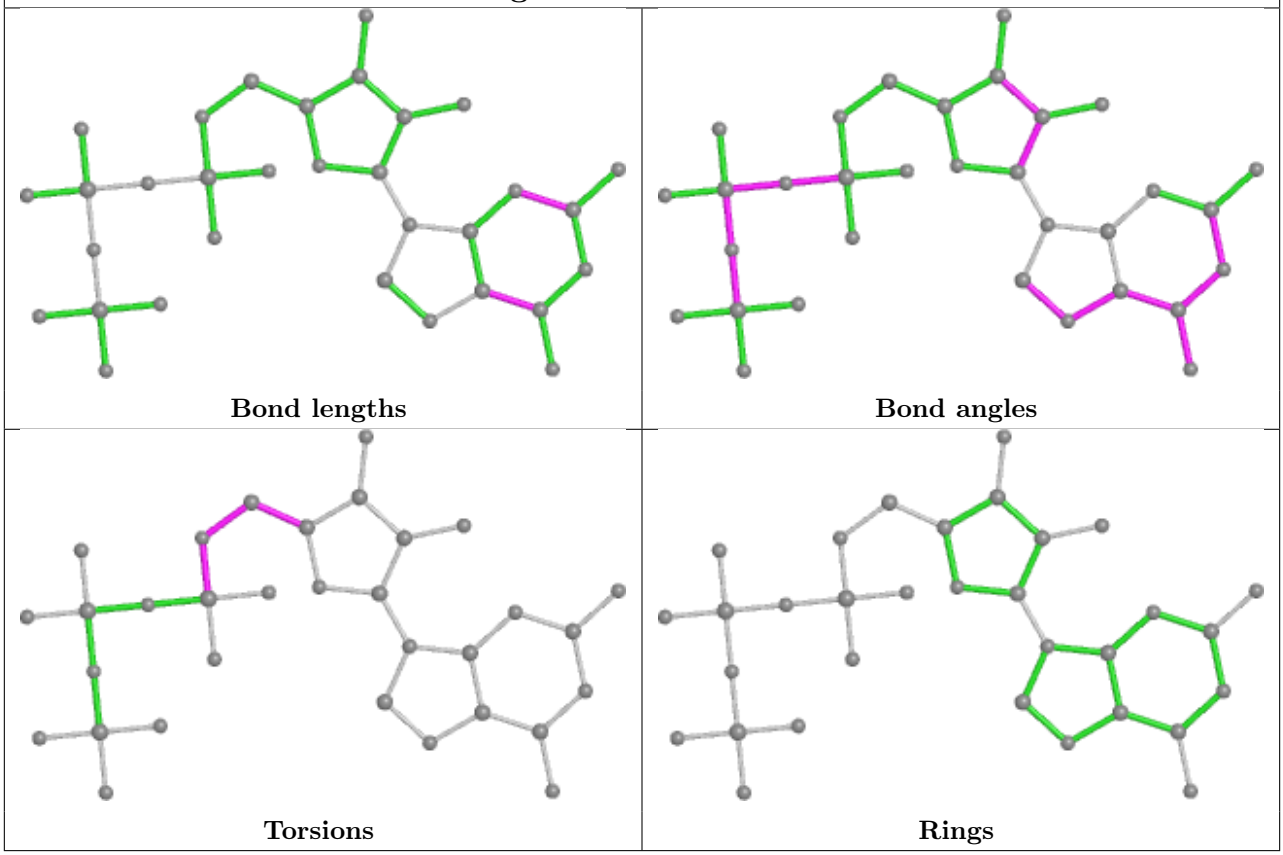
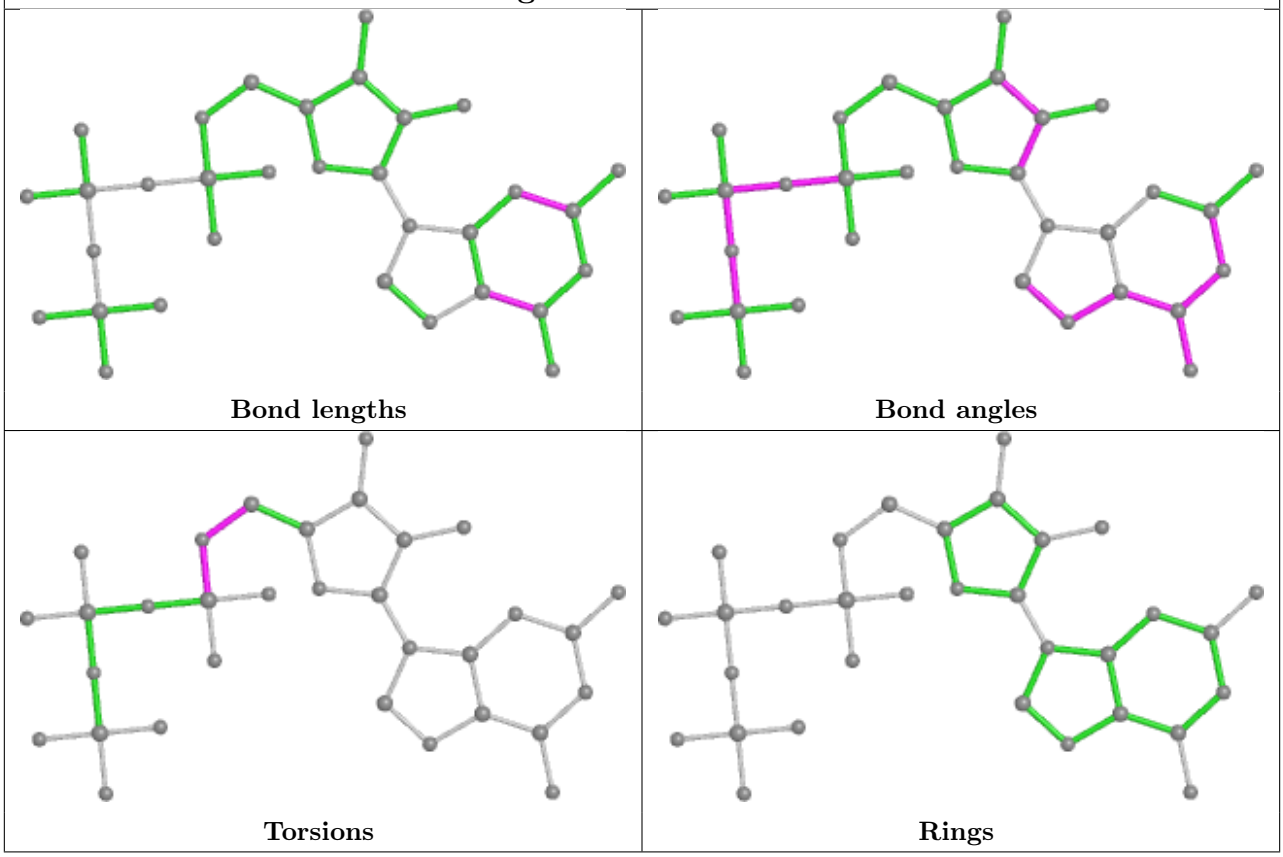


Ligand GTP PI 501



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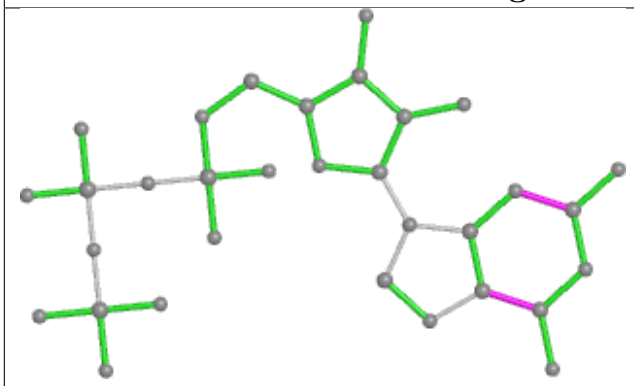

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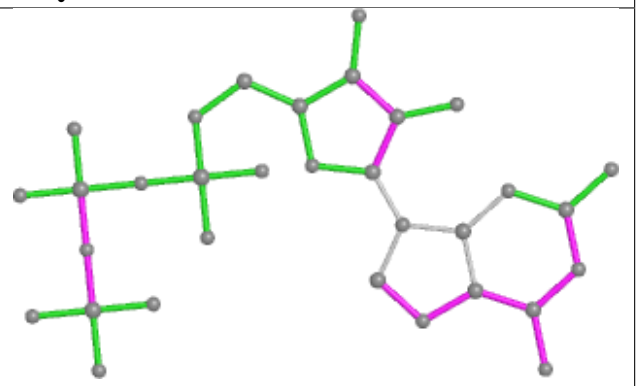
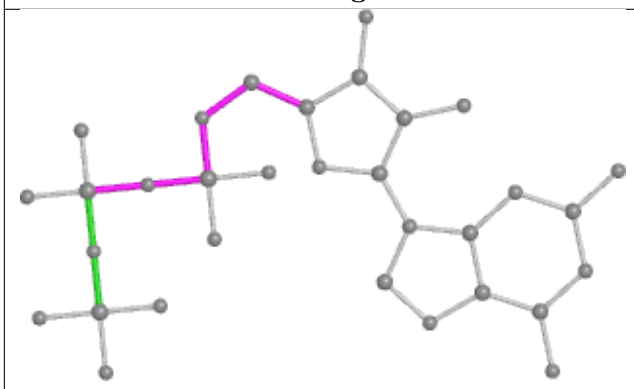


Bond angles



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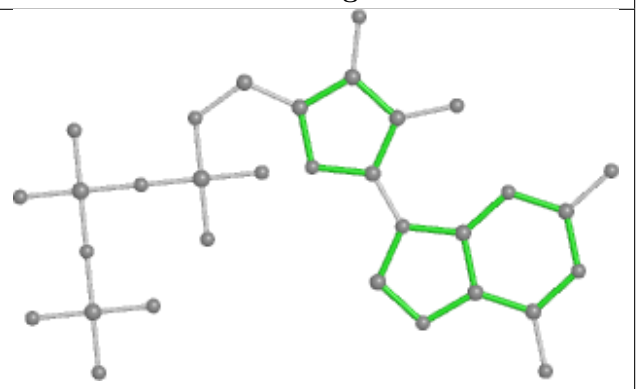

Rings

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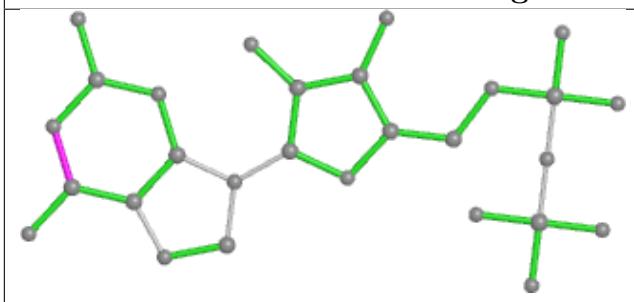

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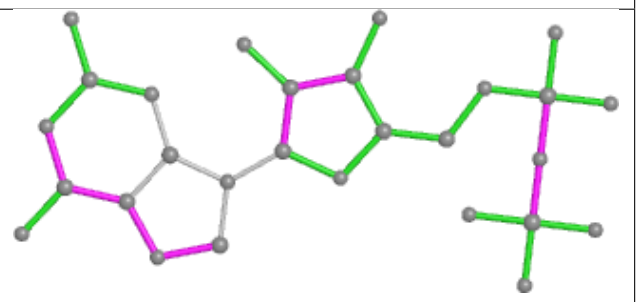

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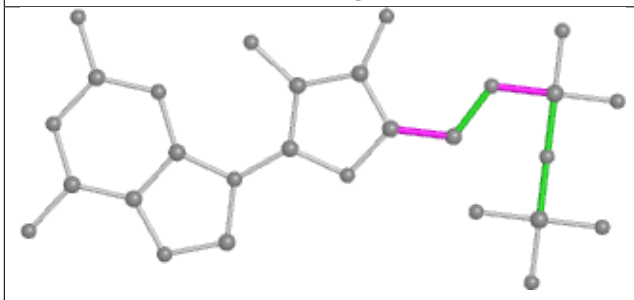
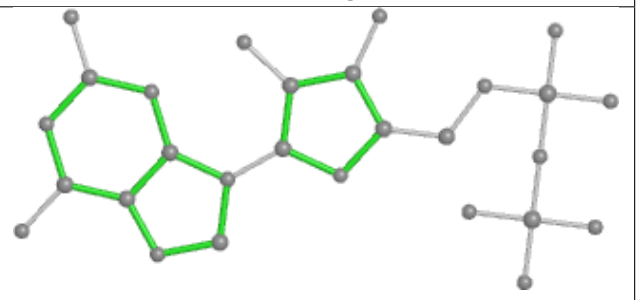
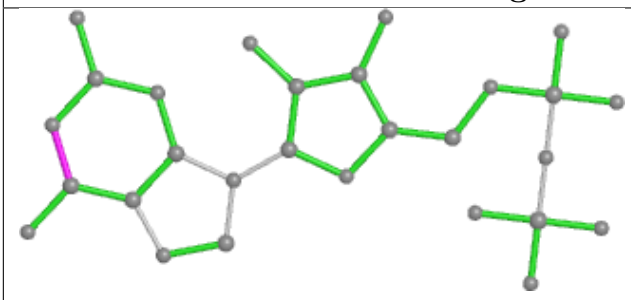


Torsions

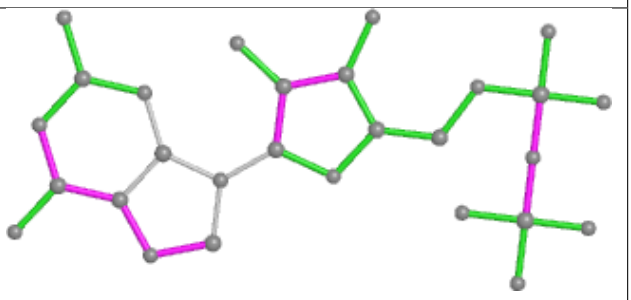


Rings

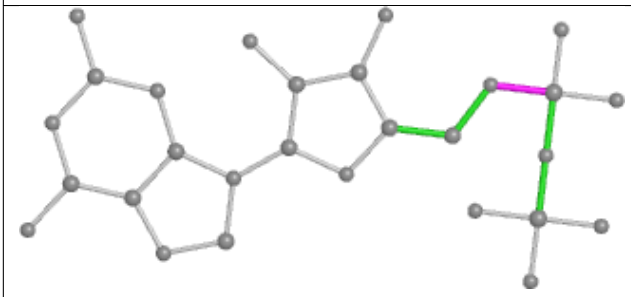
Ligand GDP TP 502



Bond lengths



Bond angles



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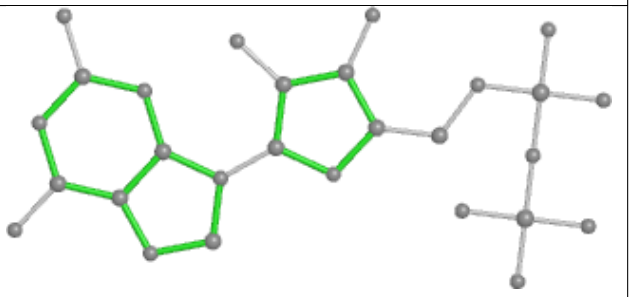
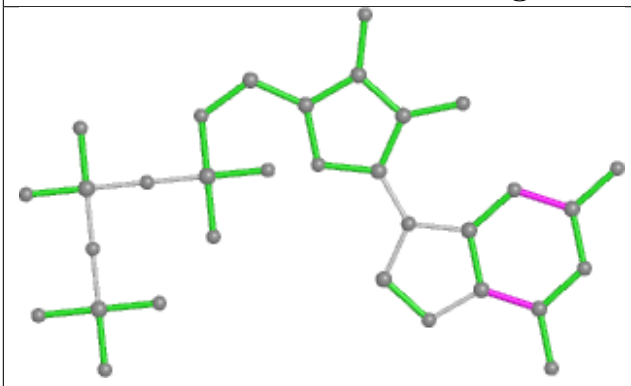


Rings

Ligand GTP BE 501



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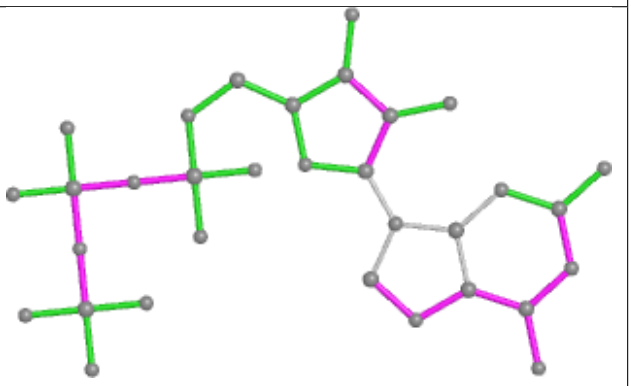

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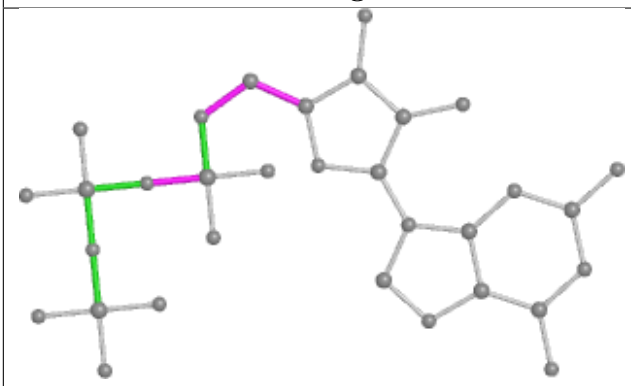

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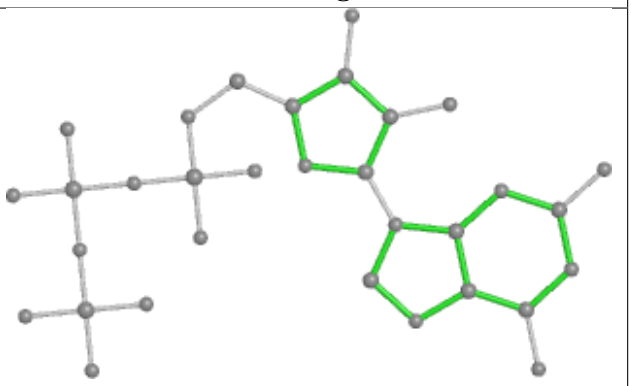
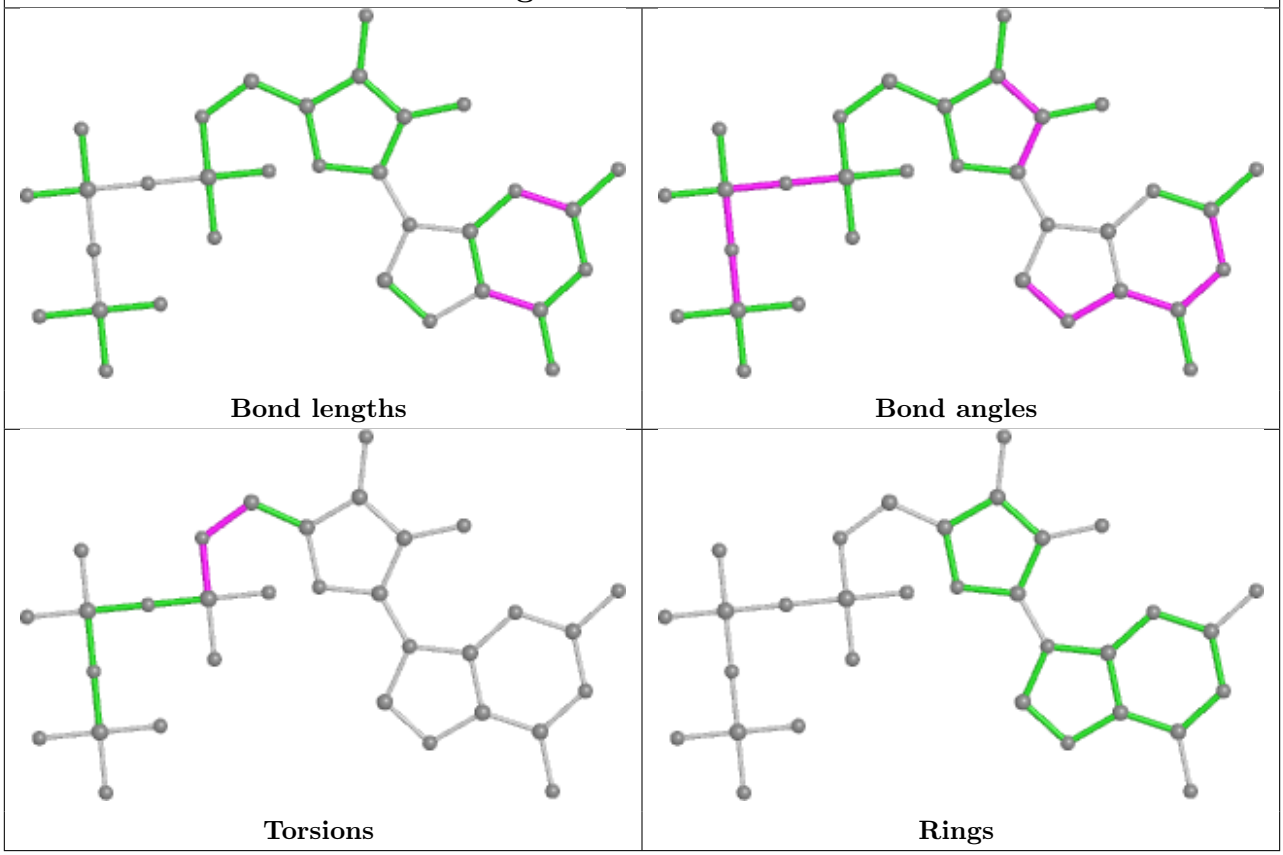
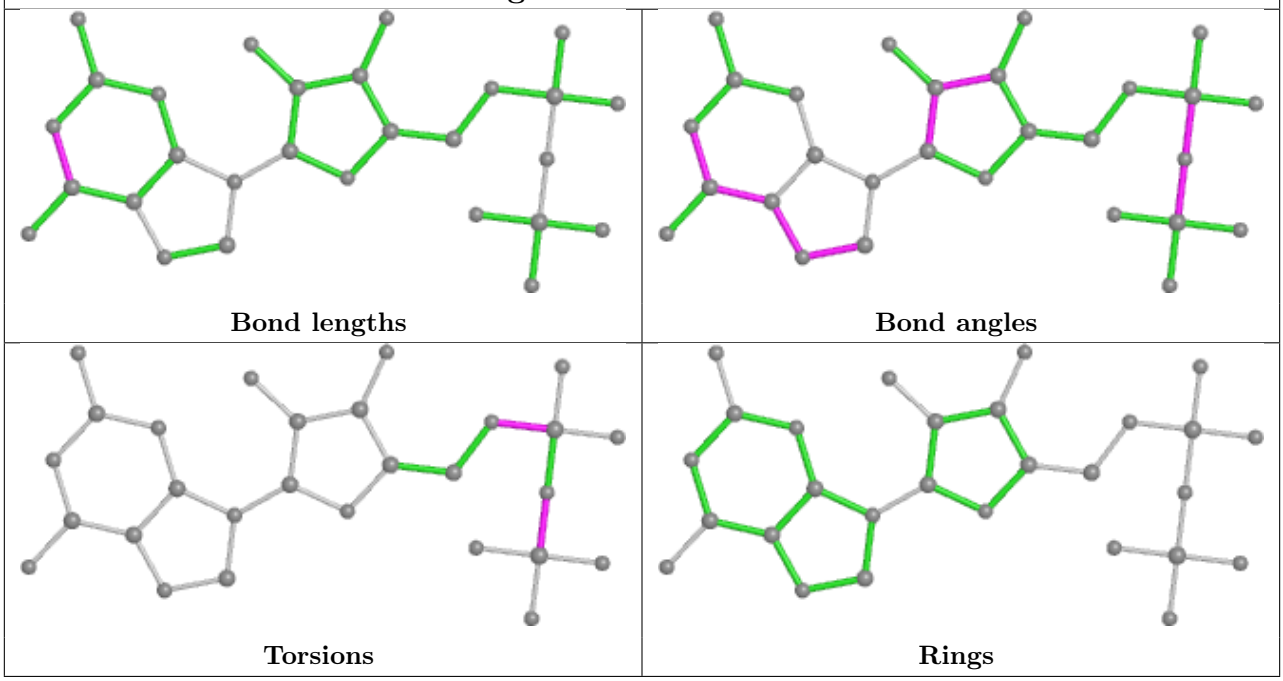


Rings

Ligand GTP DI 501



Ligand GDP VN 502



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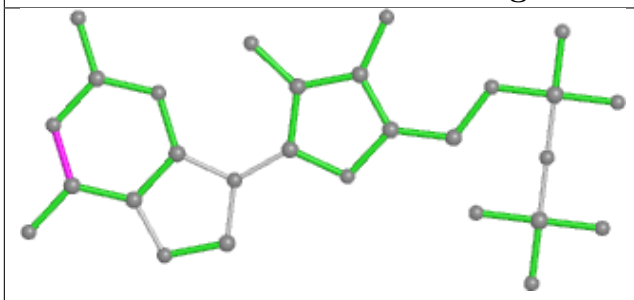

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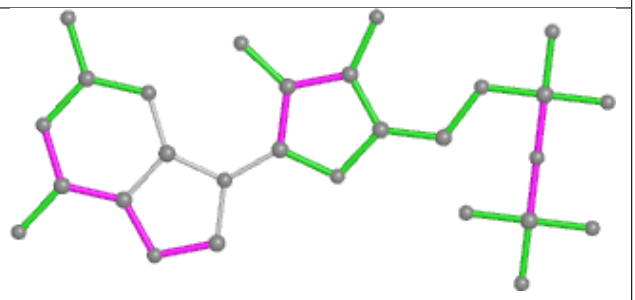
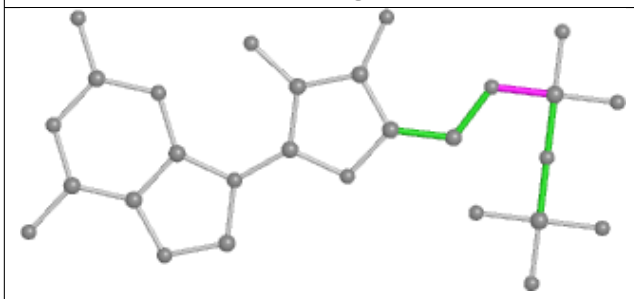


Bond angles



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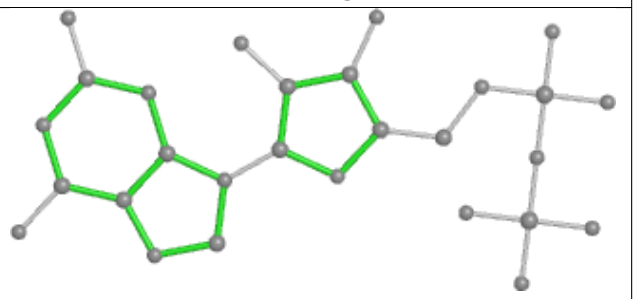
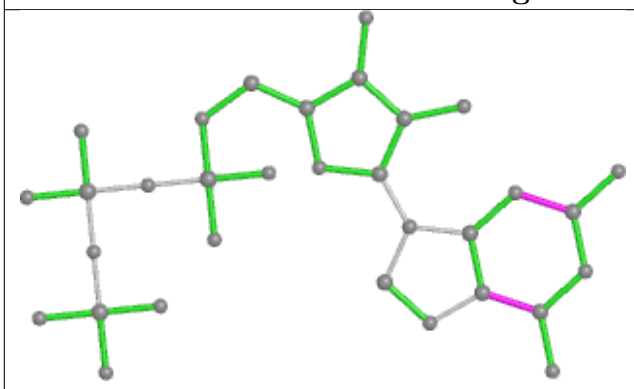
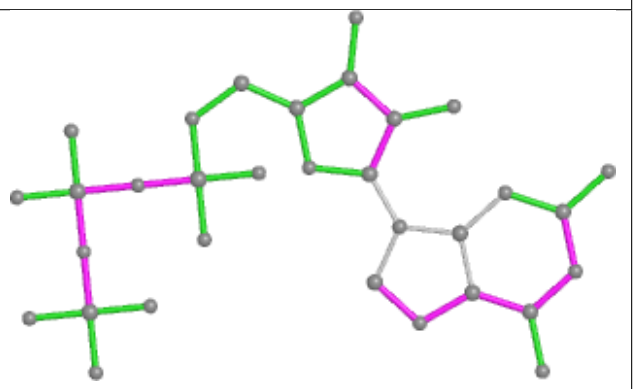


Rings

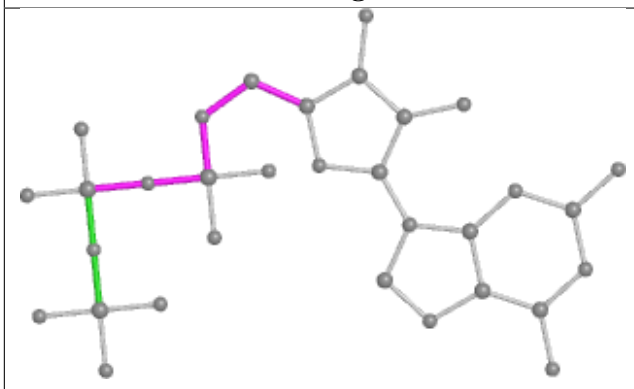
Ligand GTP TE 501



Bond lengths



Bond angles



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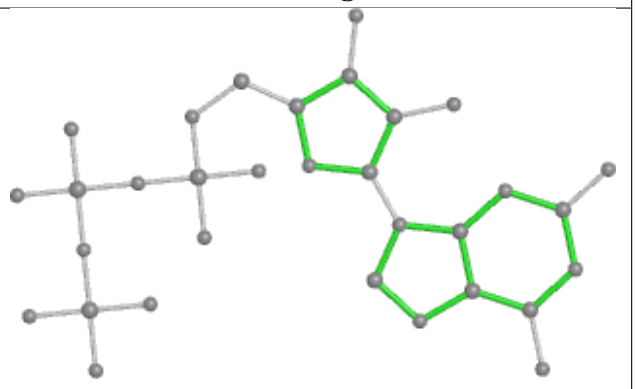
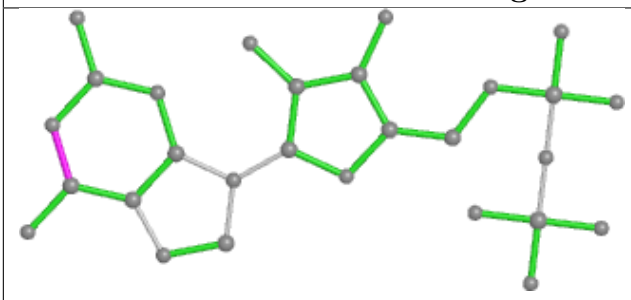


Rings

Ligand GDP RL 502



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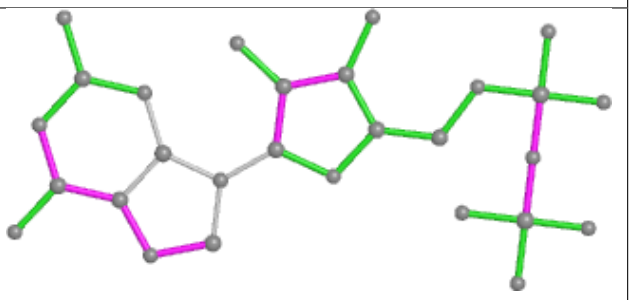

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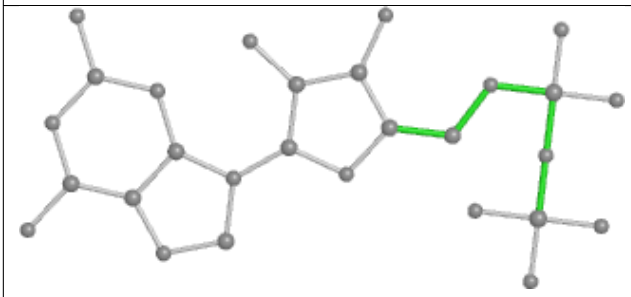

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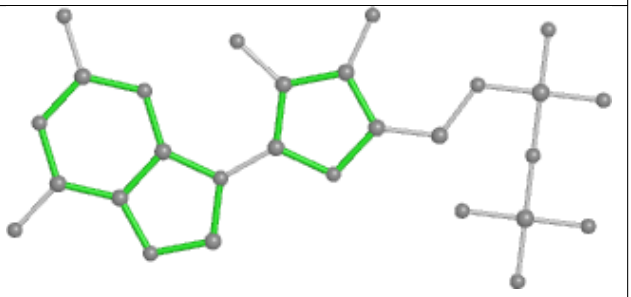
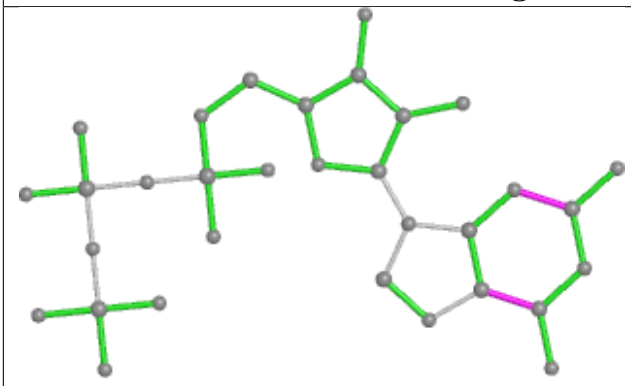


Rings

Ligand GTP LG 501



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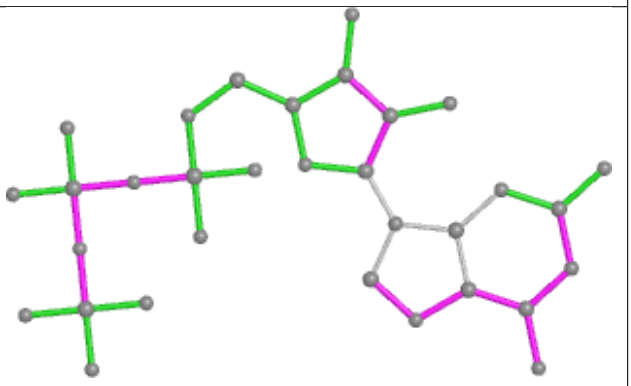

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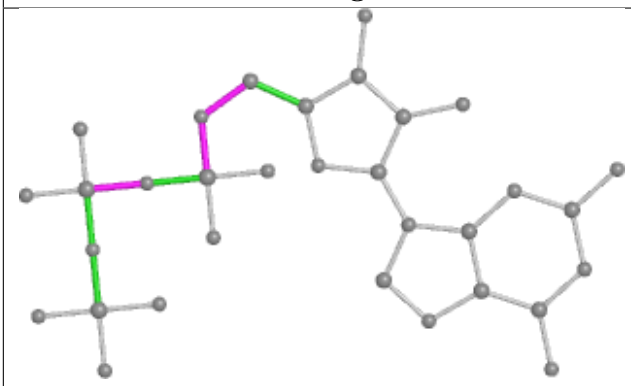

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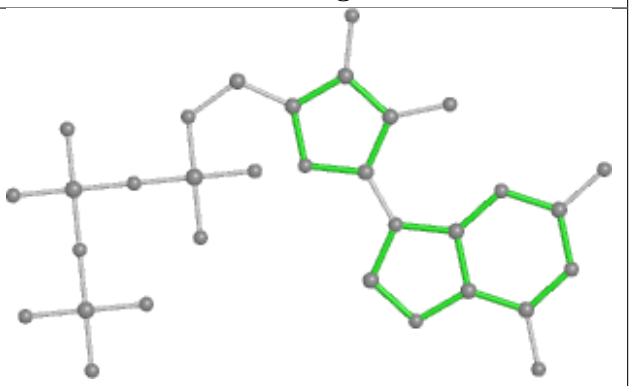
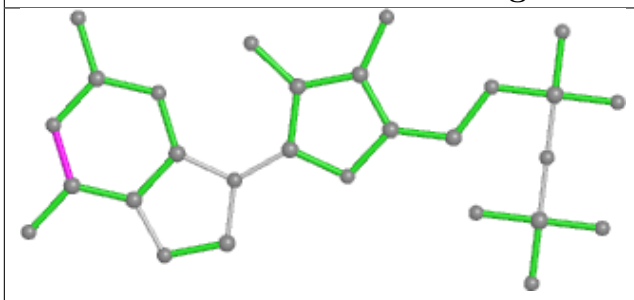


Rings

Ligand GDP TN 502



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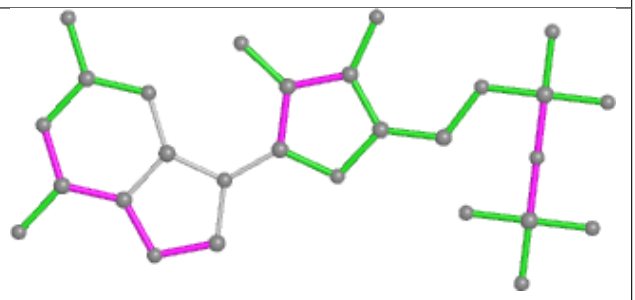

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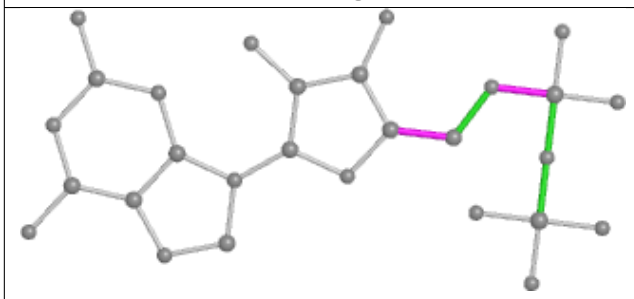

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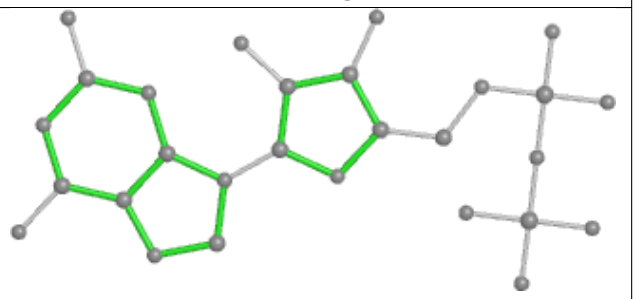
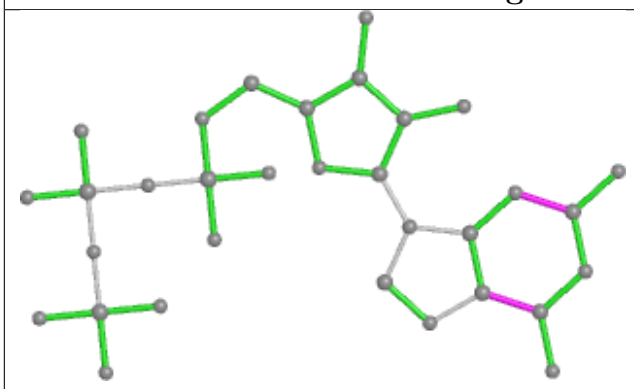


Rings

Ligand GTP VM 501



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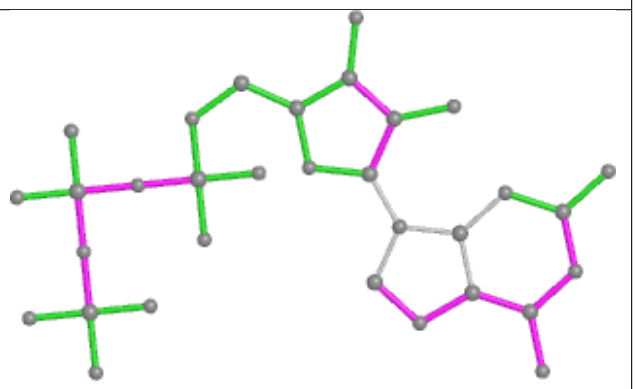

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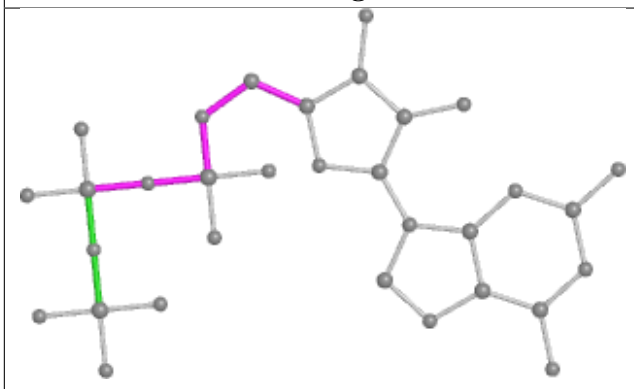

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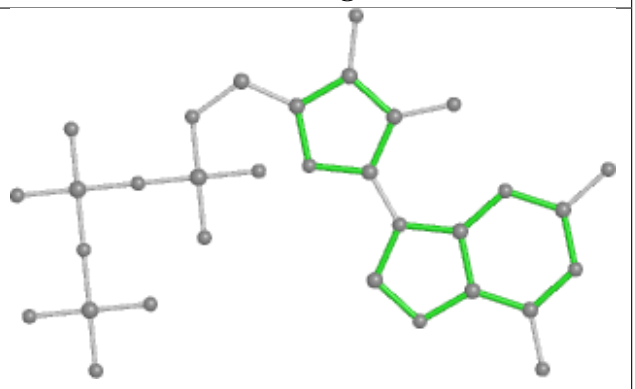
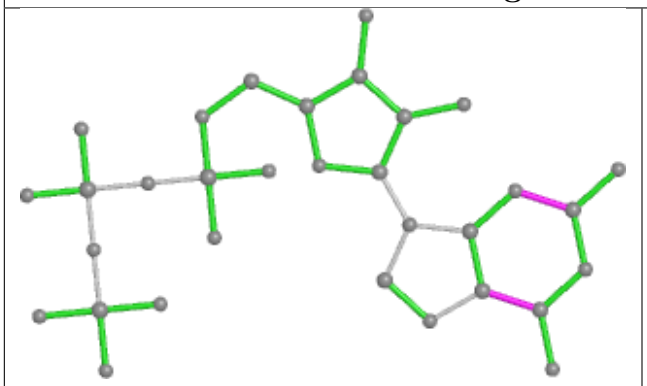


Rings

Ligand GTP WK 501



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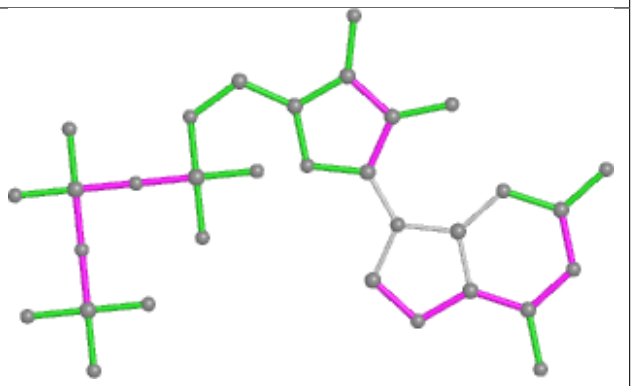

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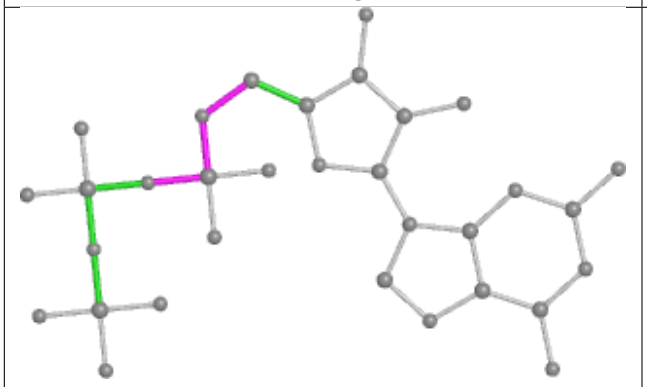

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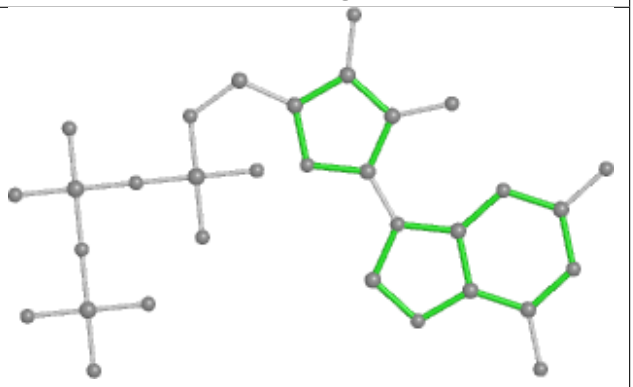
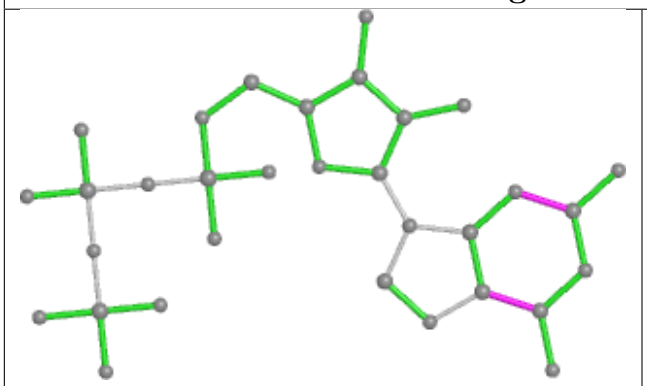


Rings

Ligand GTP OG 501



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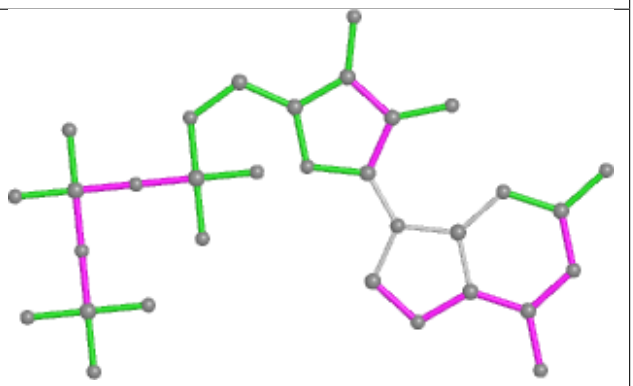

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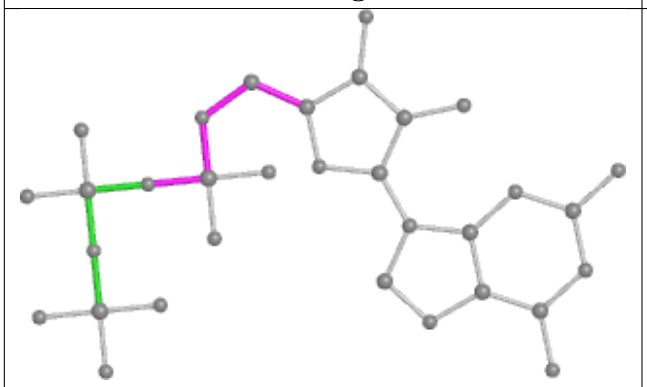

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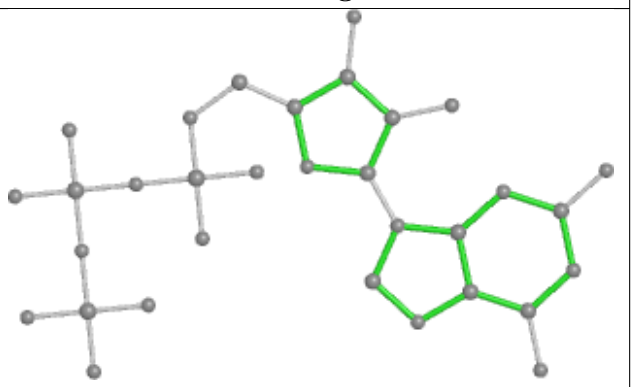
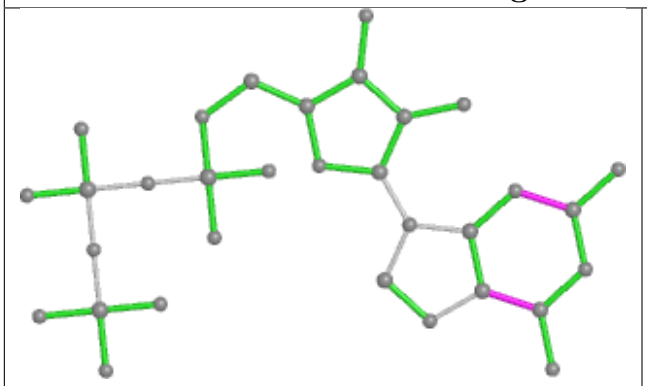


Rings

Ligand GTP PK 501



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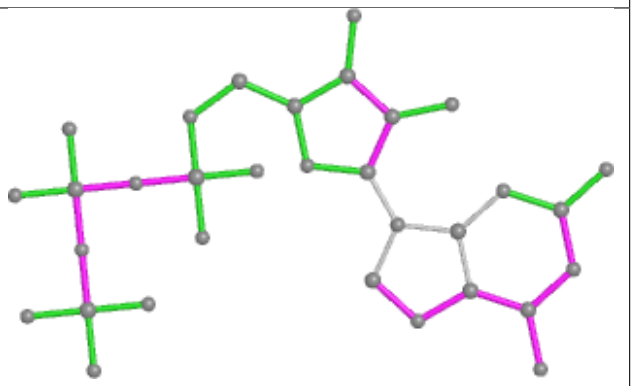

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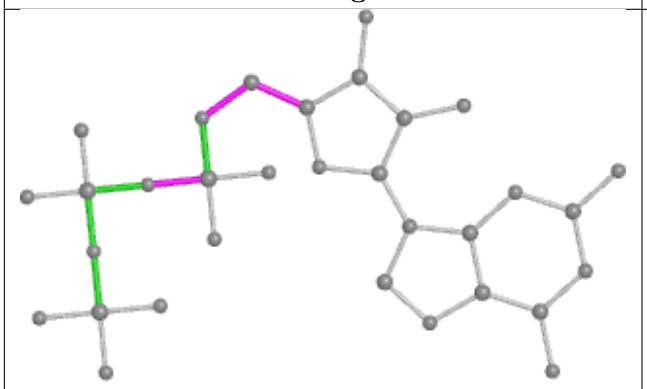

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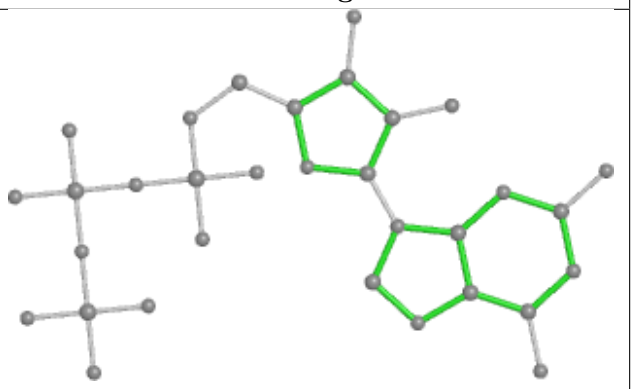
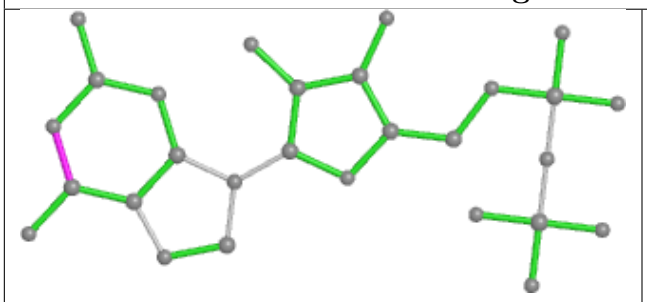


Rings

Ligand GDP JD 502



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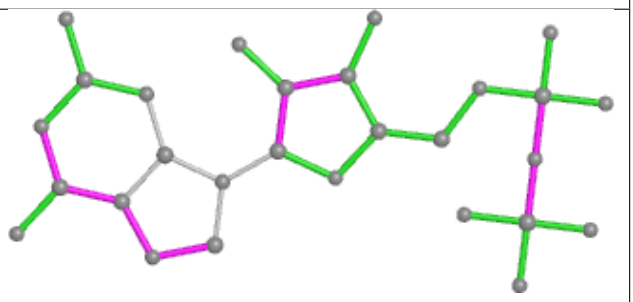

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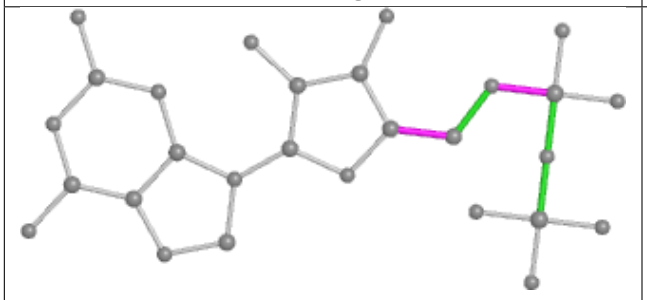

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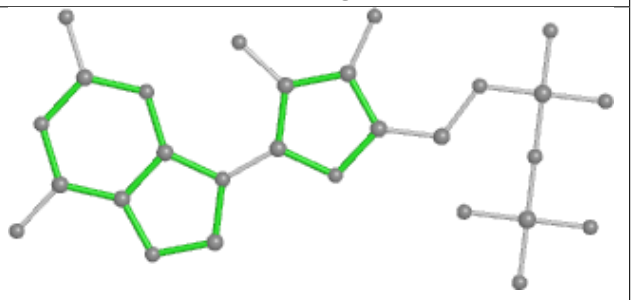
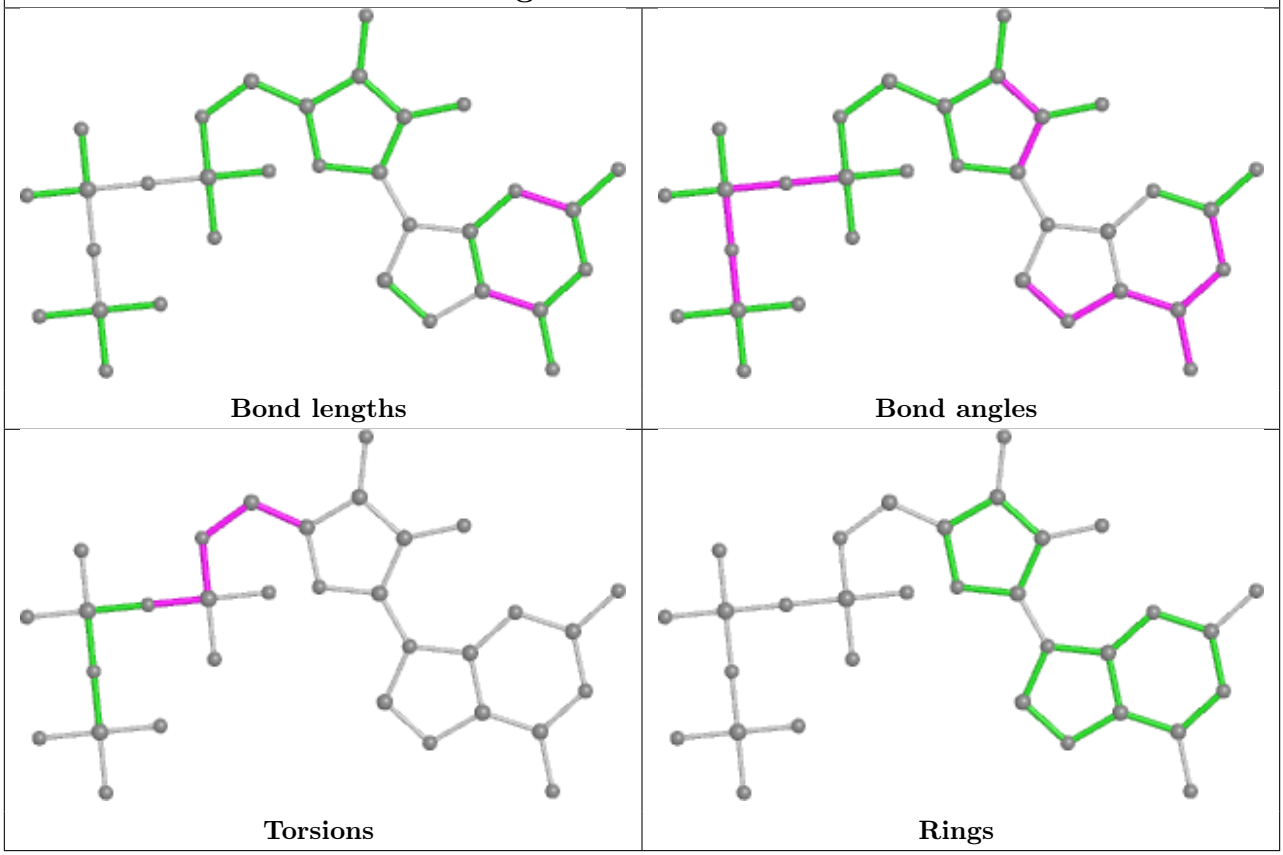
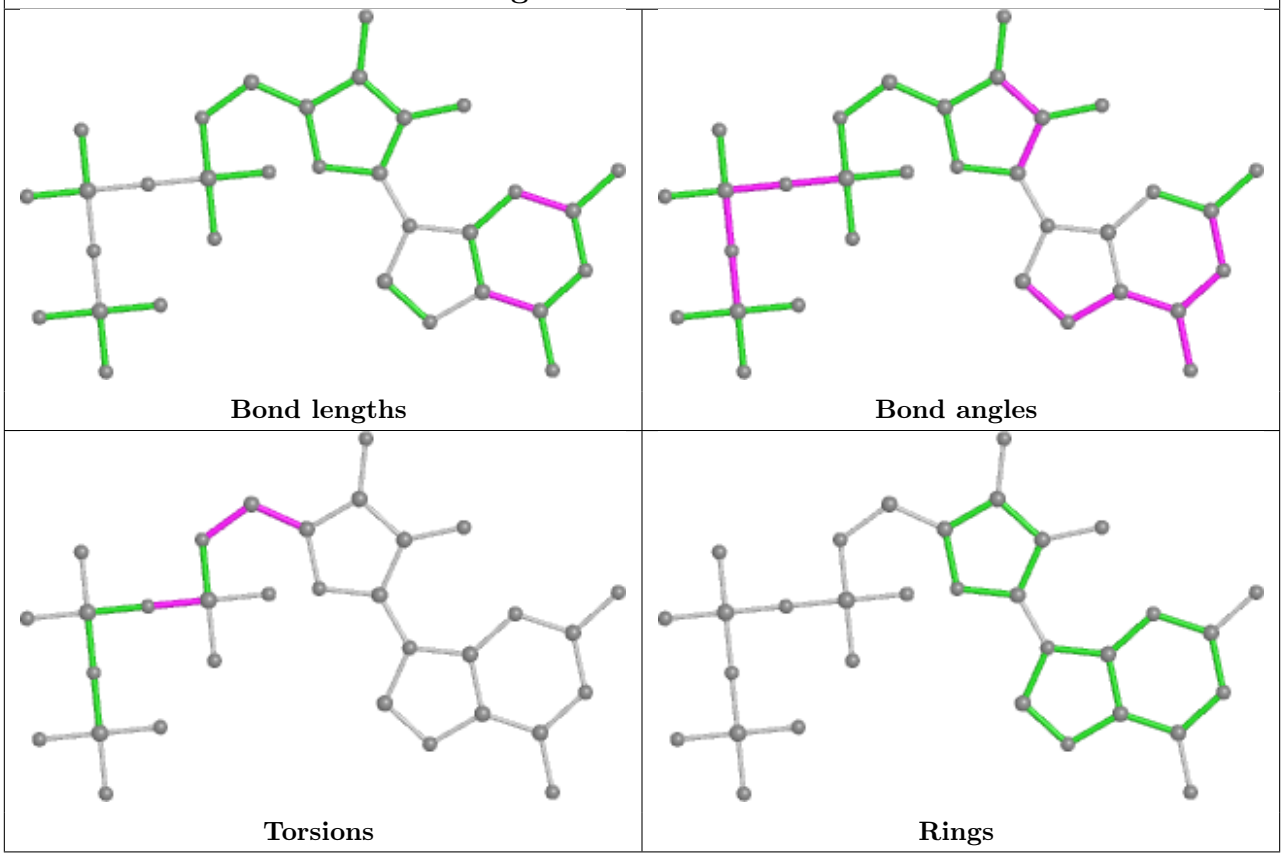


Rings

Ligand GTP HI 501



Ligand GTP PO 501



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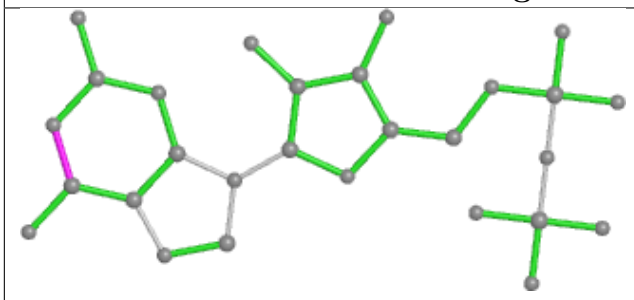

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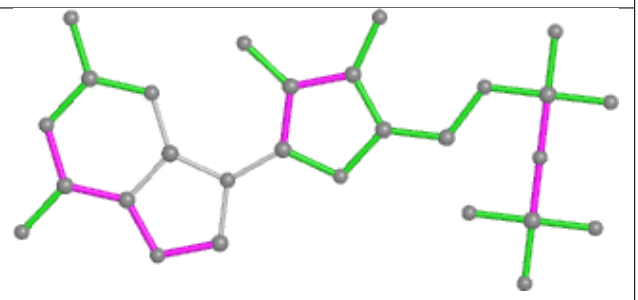
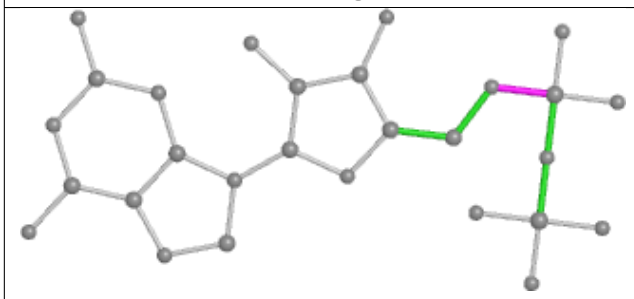


Bond angles



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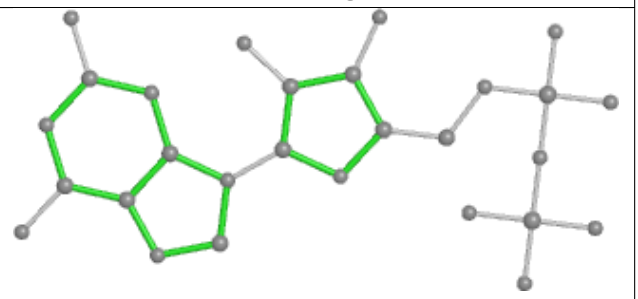
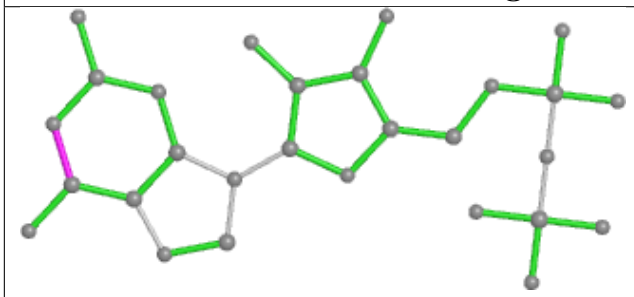


Rings

Ligand GDP MD 502



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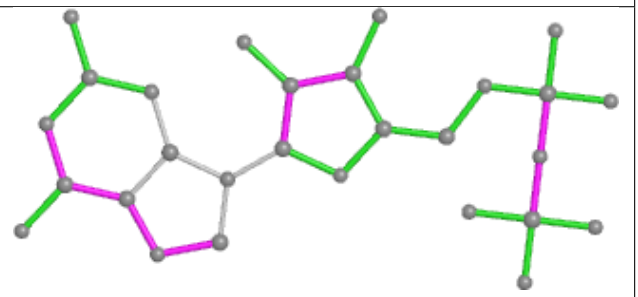
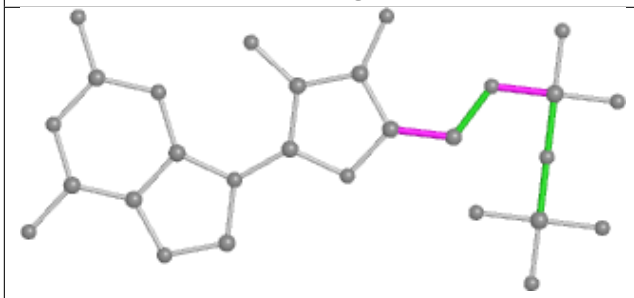
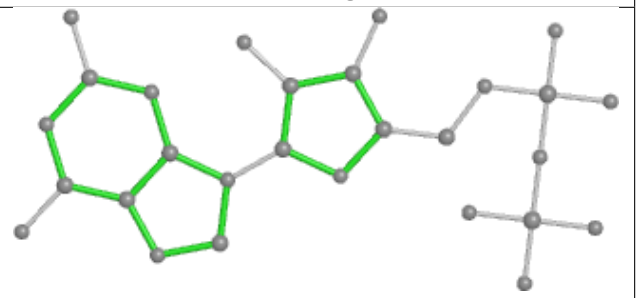


Bond angles

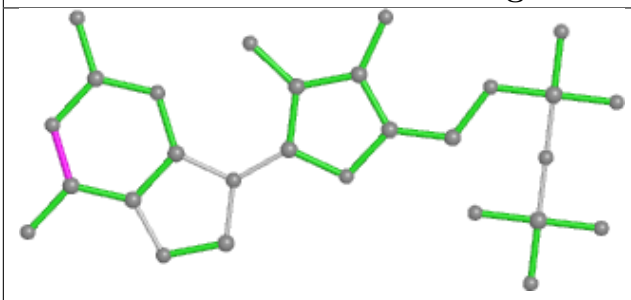


Torsions



Rings

Ligand GDP UN 502



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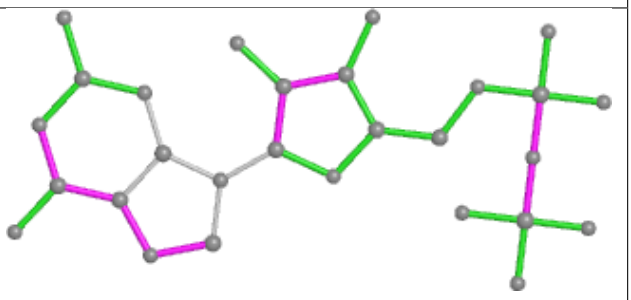

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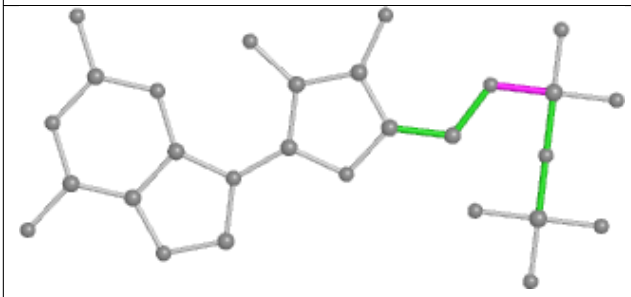

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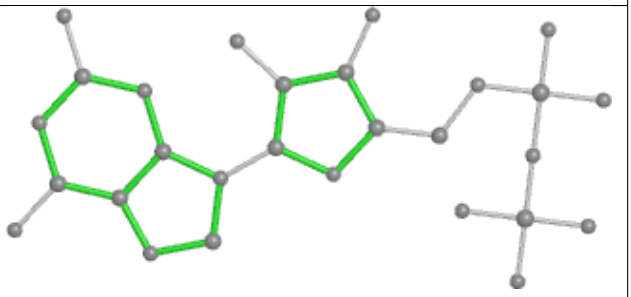
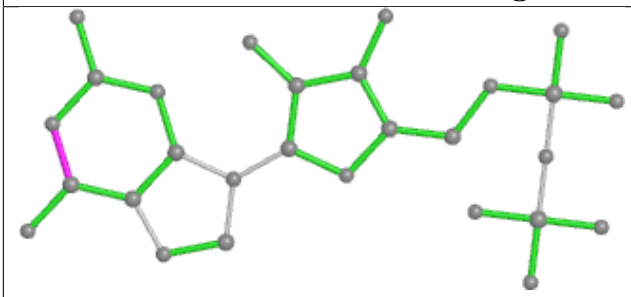


Rings

Ligand GDP NJ 502



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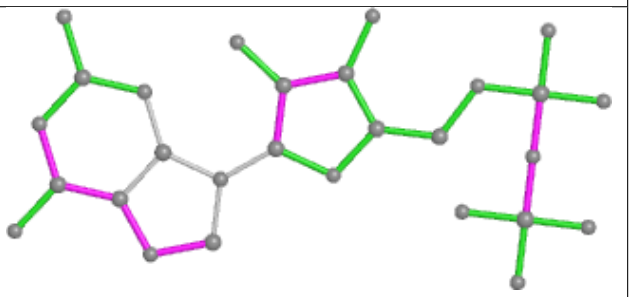

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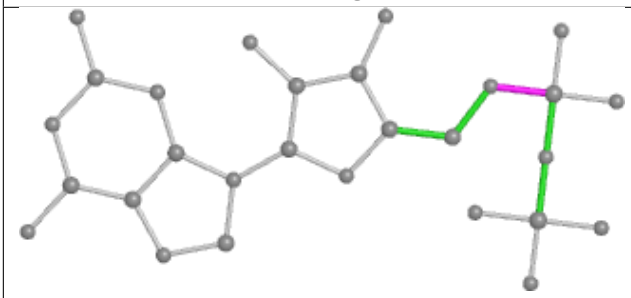

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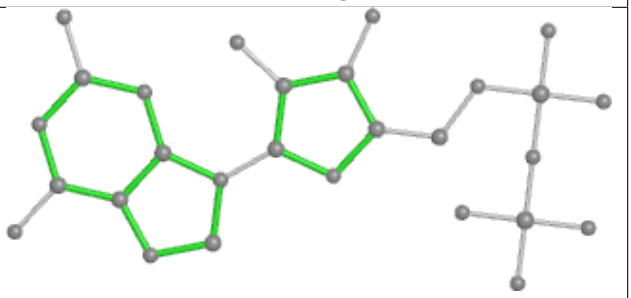
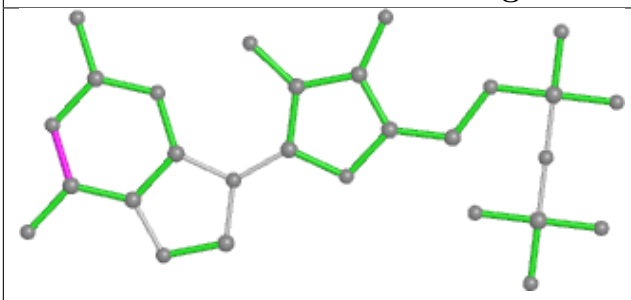


Rings

Ligand GDP WD 502



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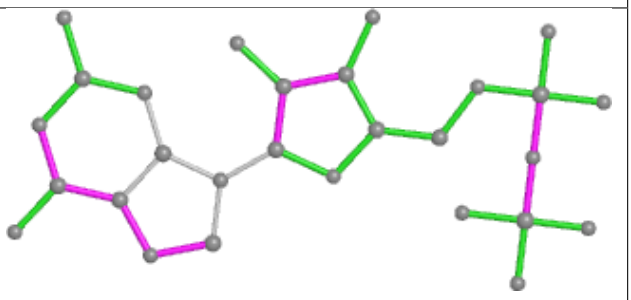

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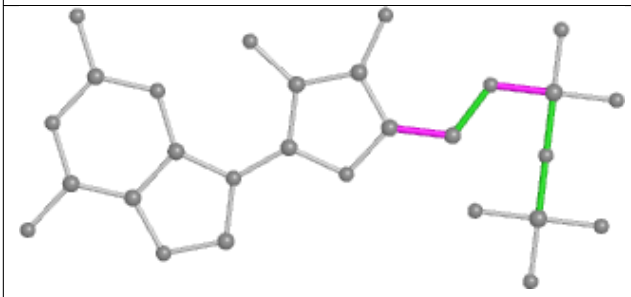

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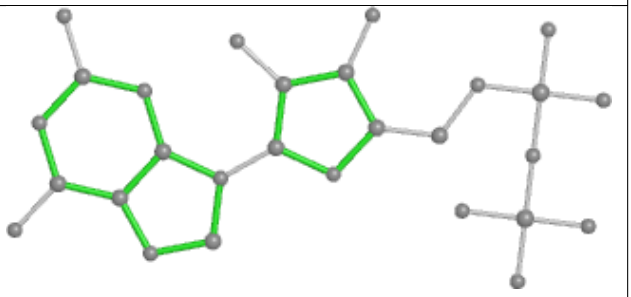
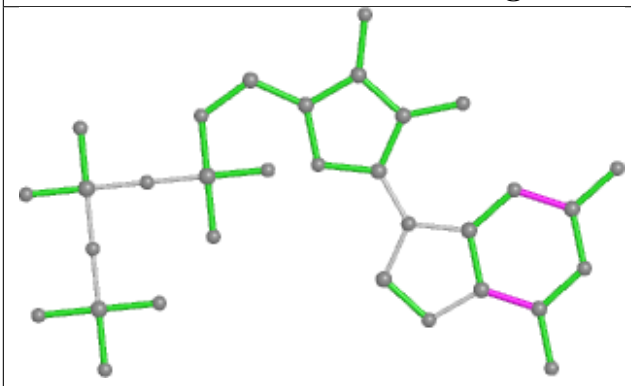


Rings

Ligand GTP KM 501



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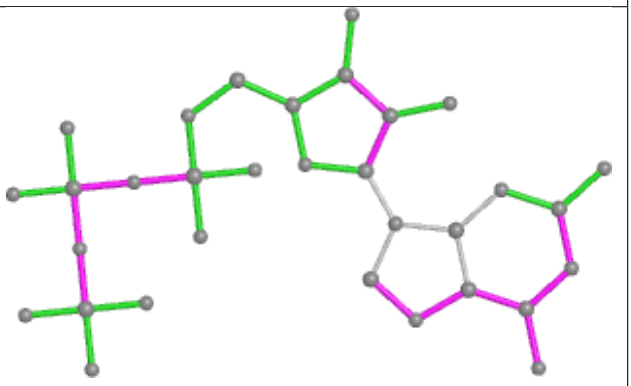

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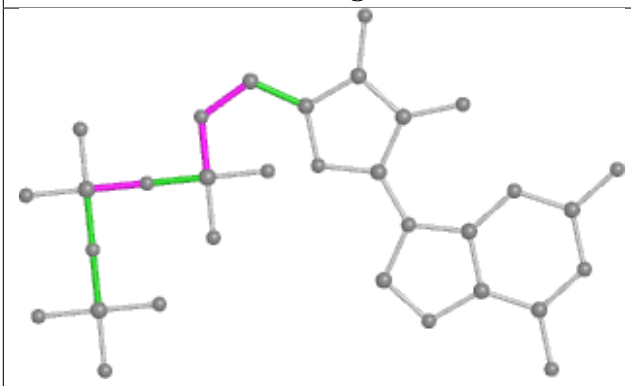

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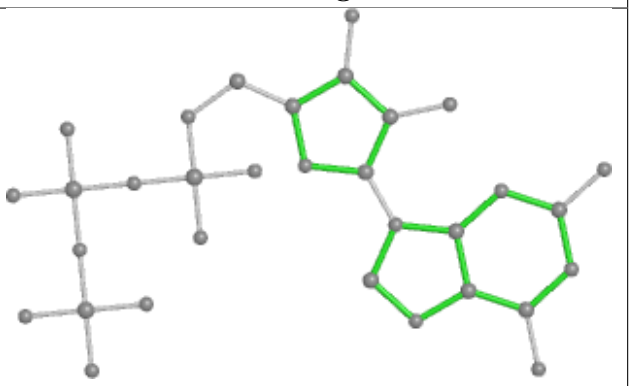
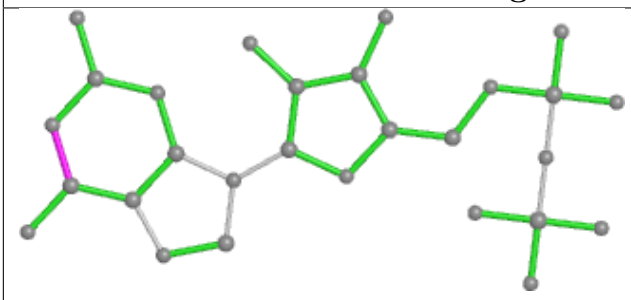


Rings

Ligand GDP QF 502



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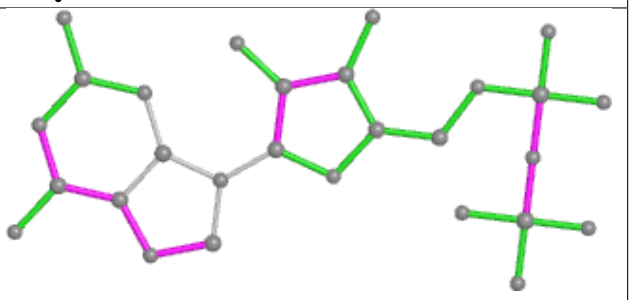

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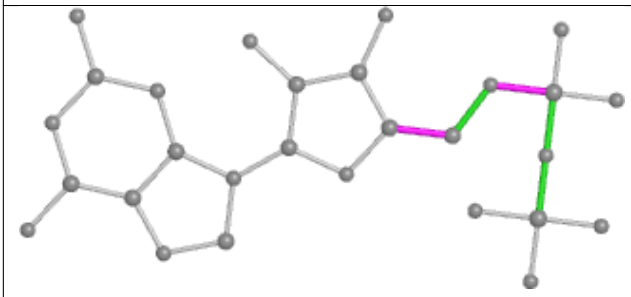

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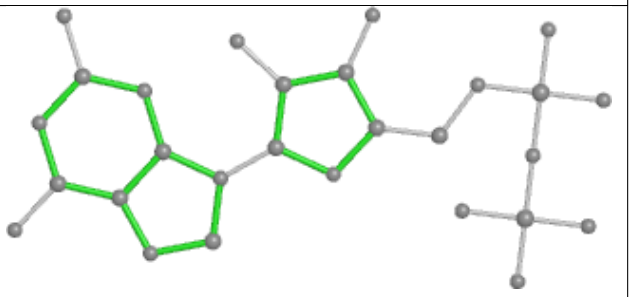
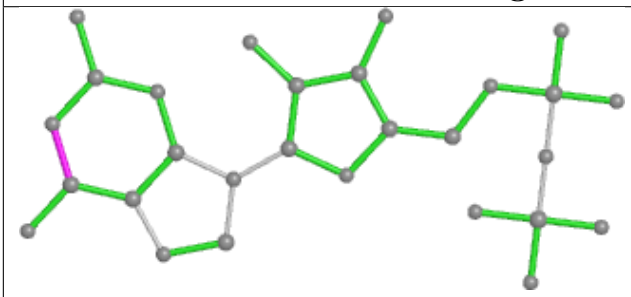


Rings

Ligand GDP GF 502



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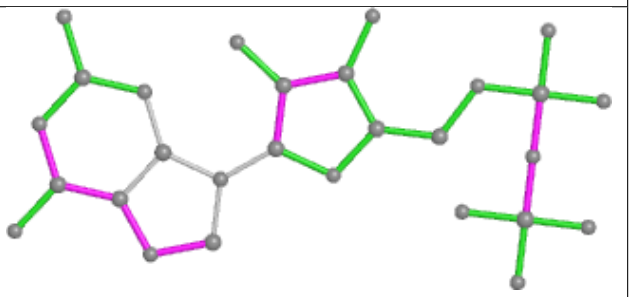

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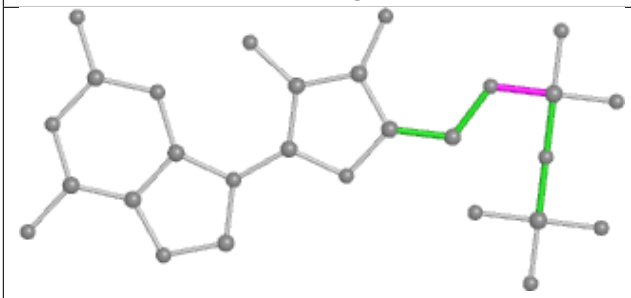

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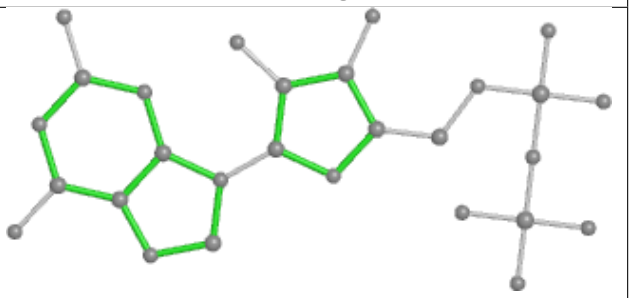
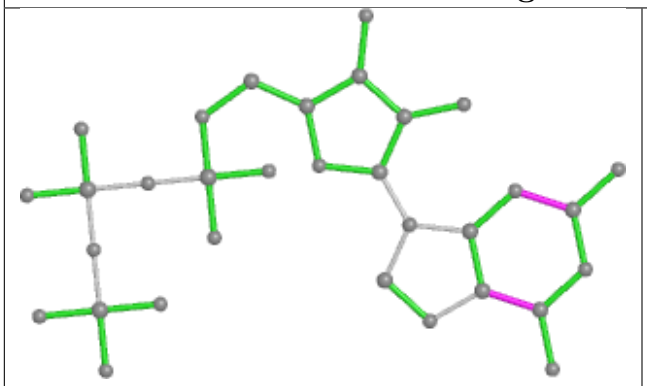


Rings

Ligand GTP TI 501



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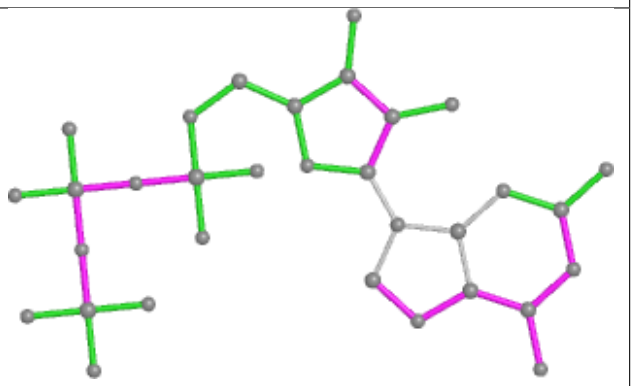

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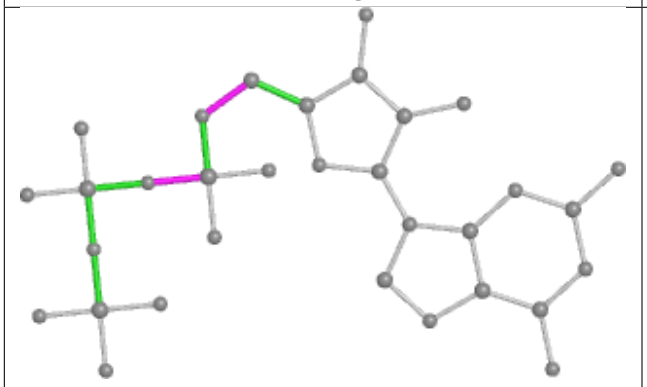

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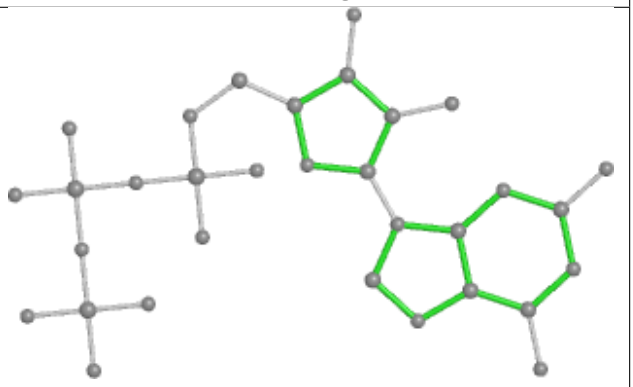
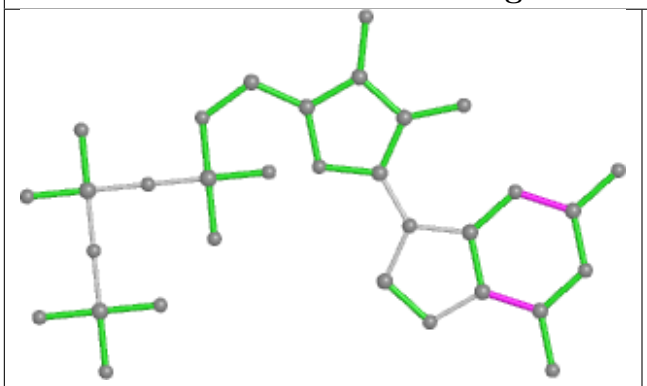


Rings

Ligand GTP WO 501



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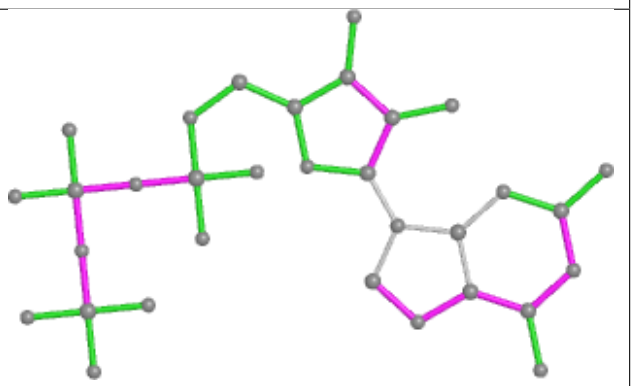

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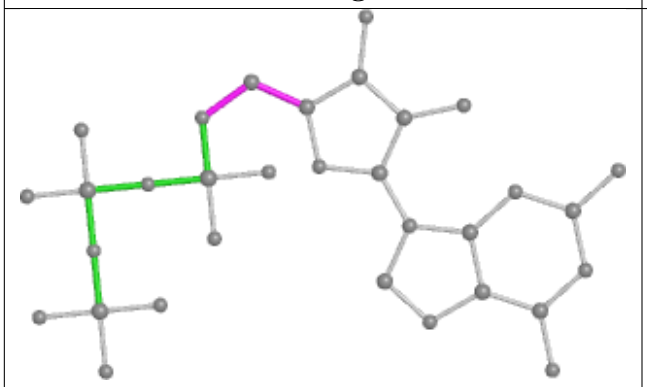

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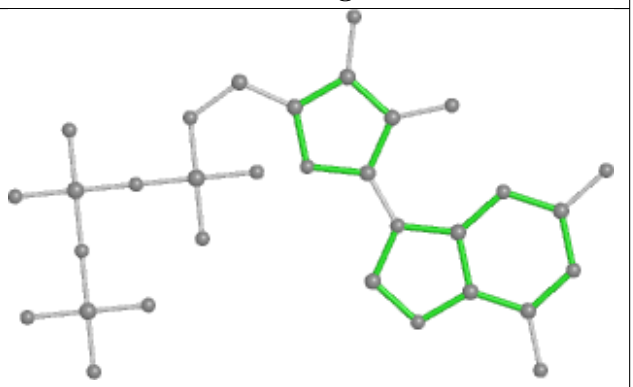
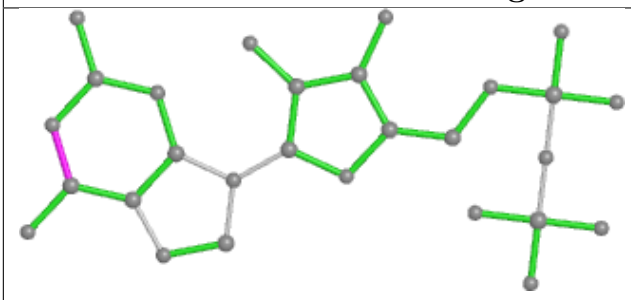


Rings

Ligand GDP TH 502



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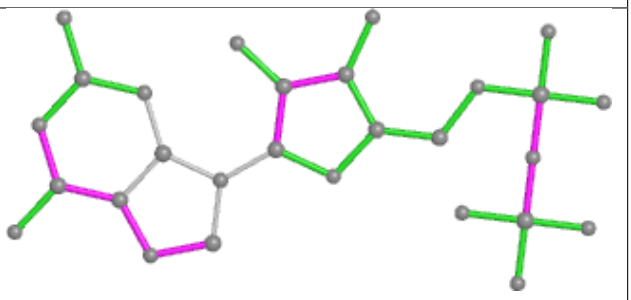
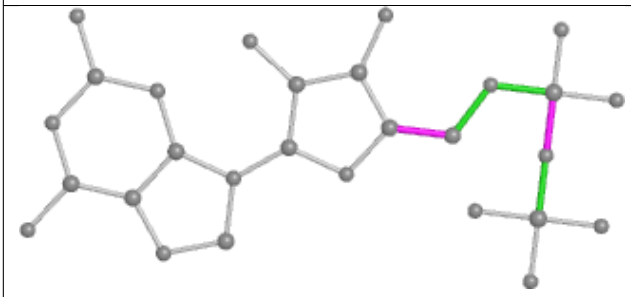


Bond angles



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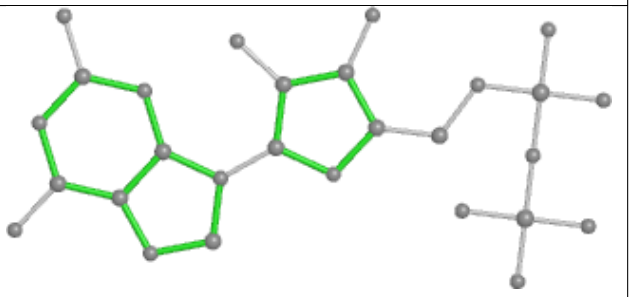
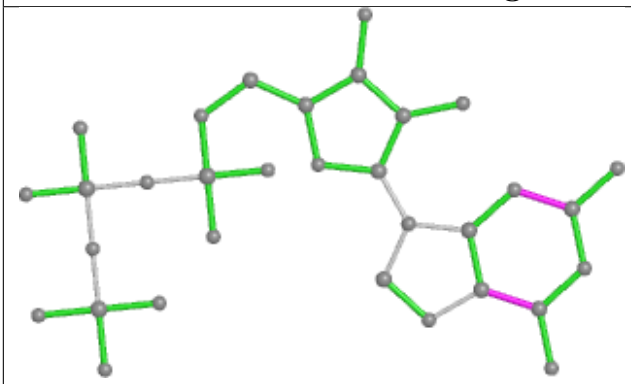


Rings

Ligand GTP WG 501



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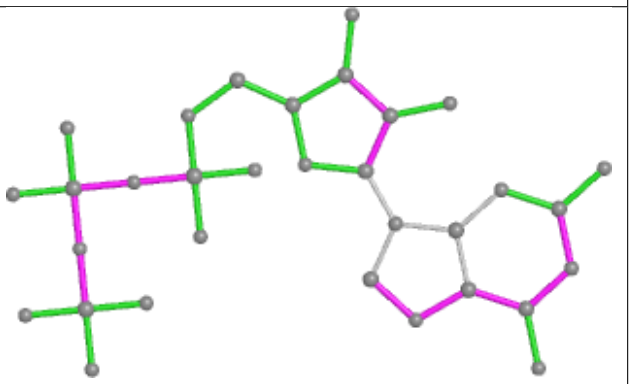

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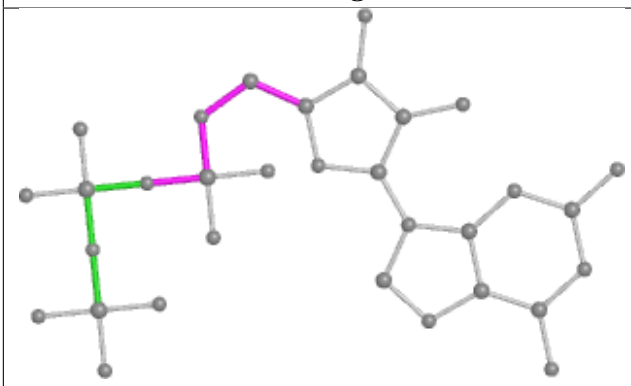

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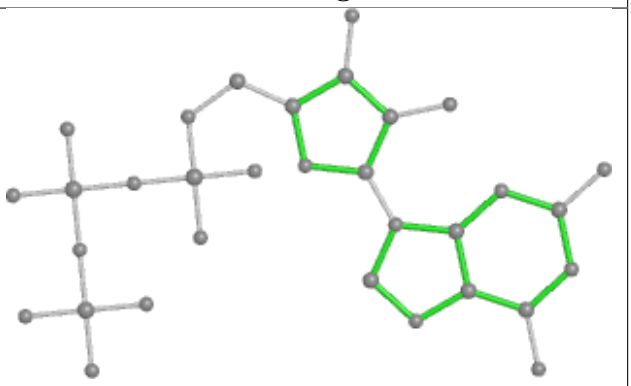
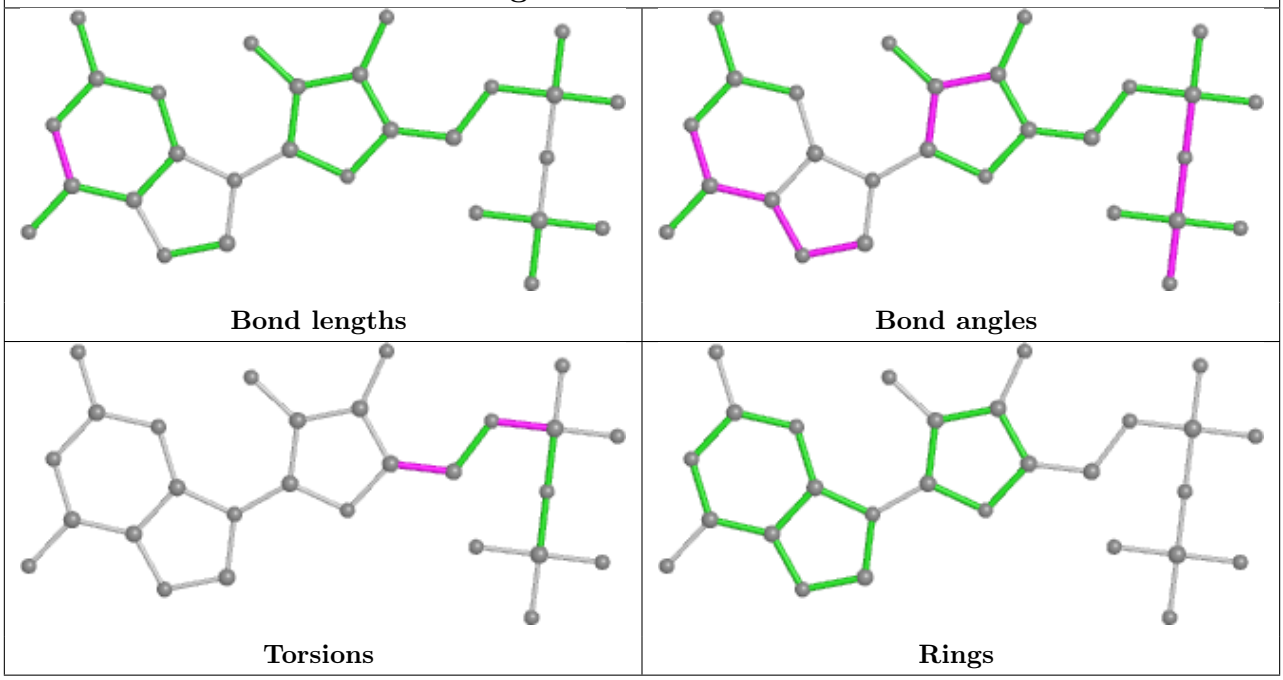
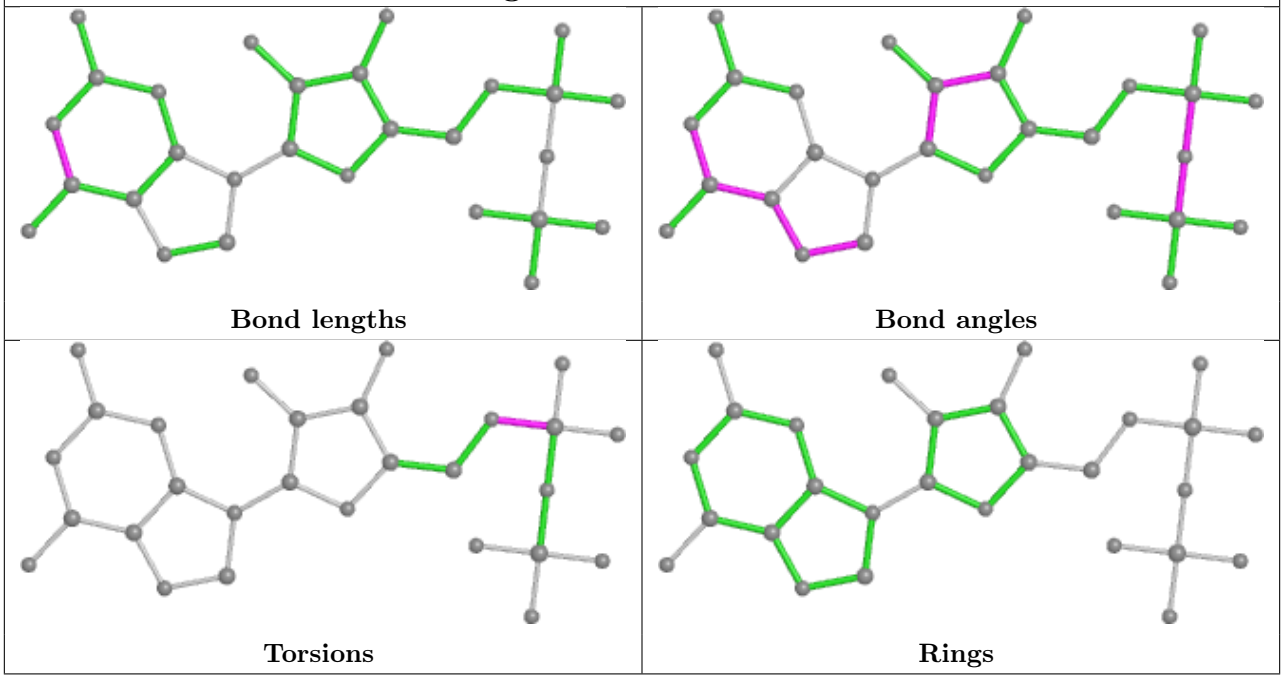


Rings

Ligand GDP FH 502



Ligand GDP WH 502



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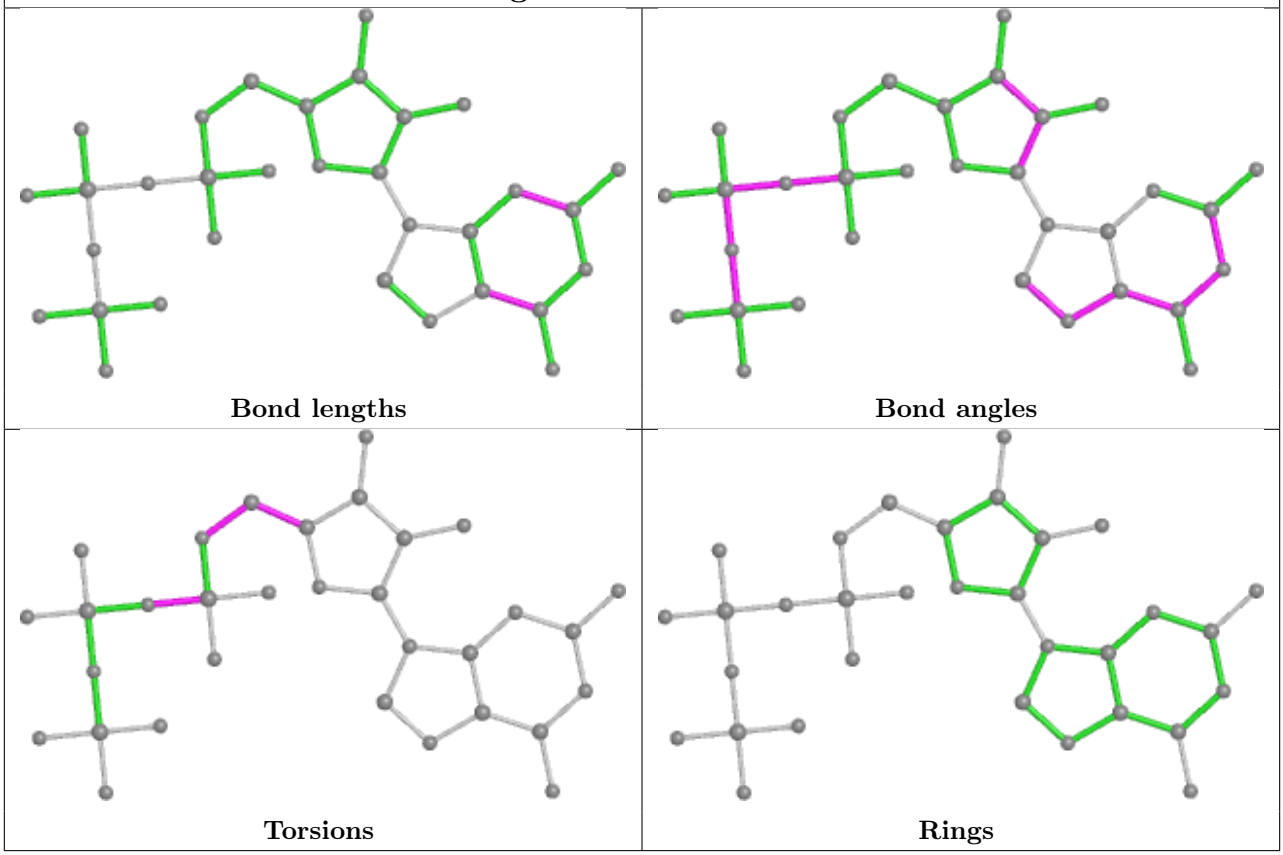

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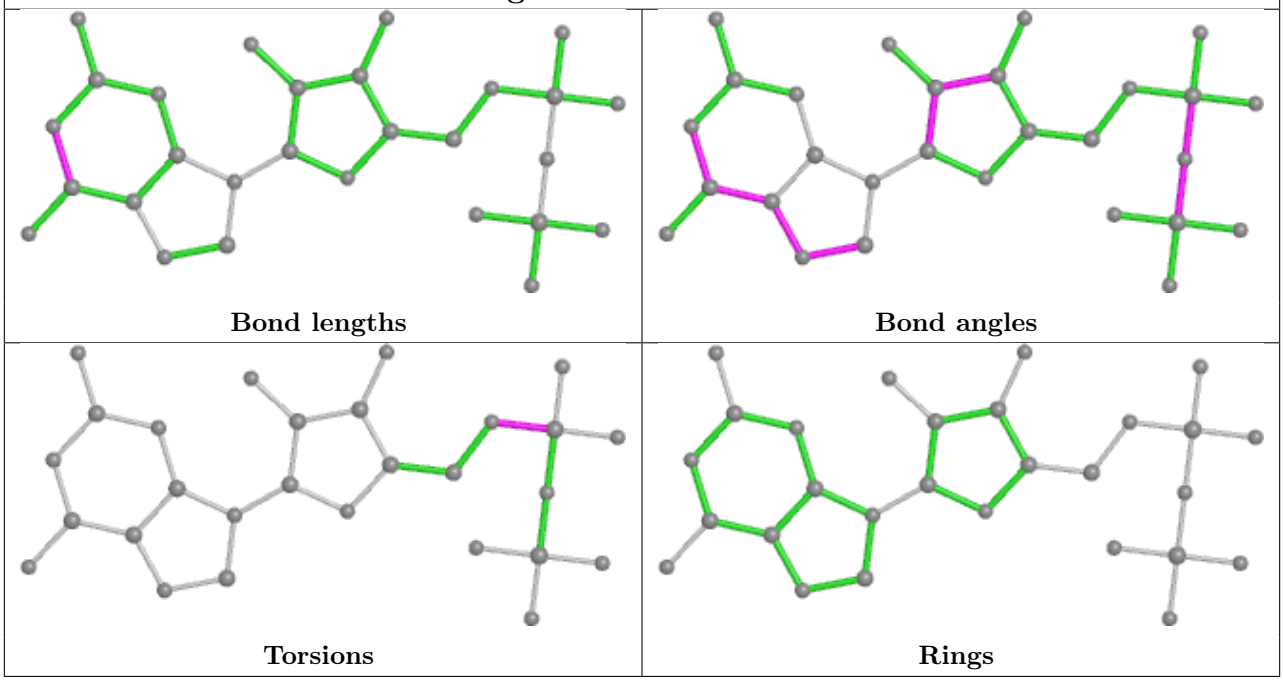

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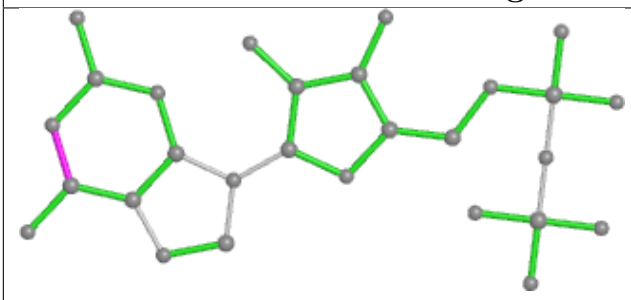
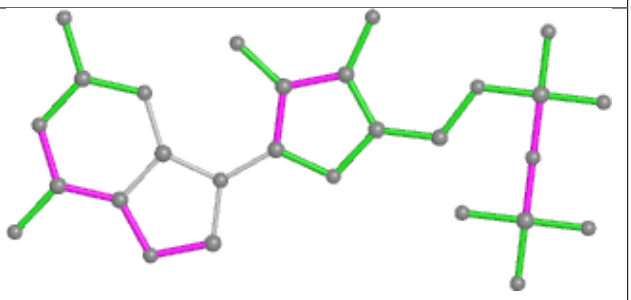
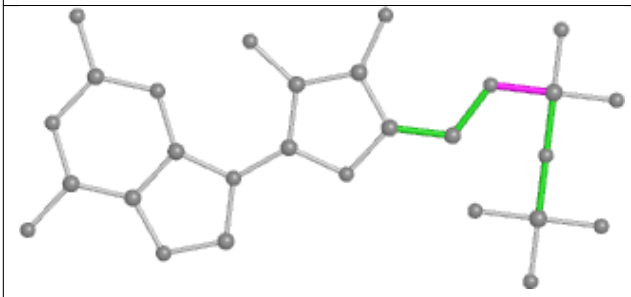


Bond lengths



Bond angles



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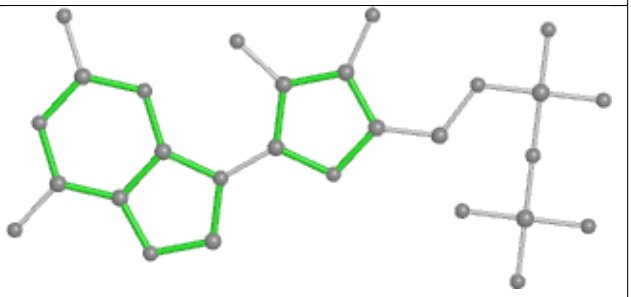
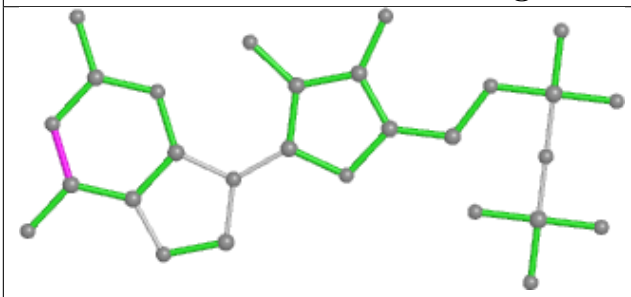


Rings

Ligand GDP LL 502



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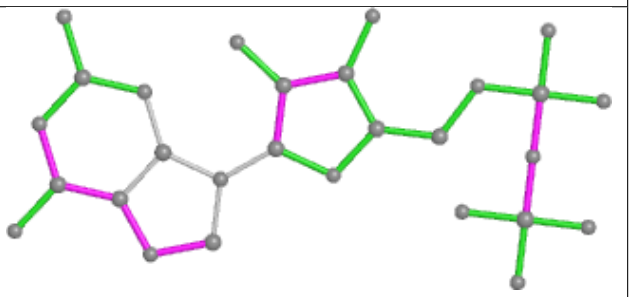

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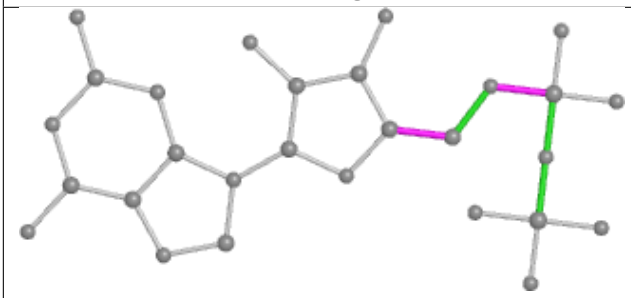

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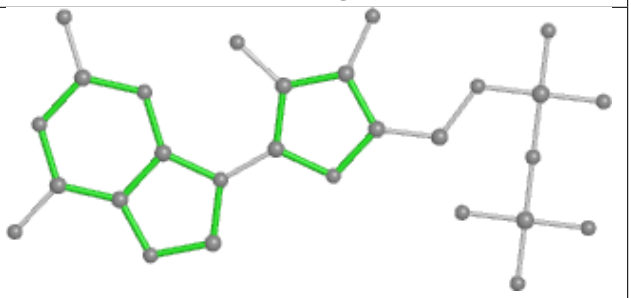
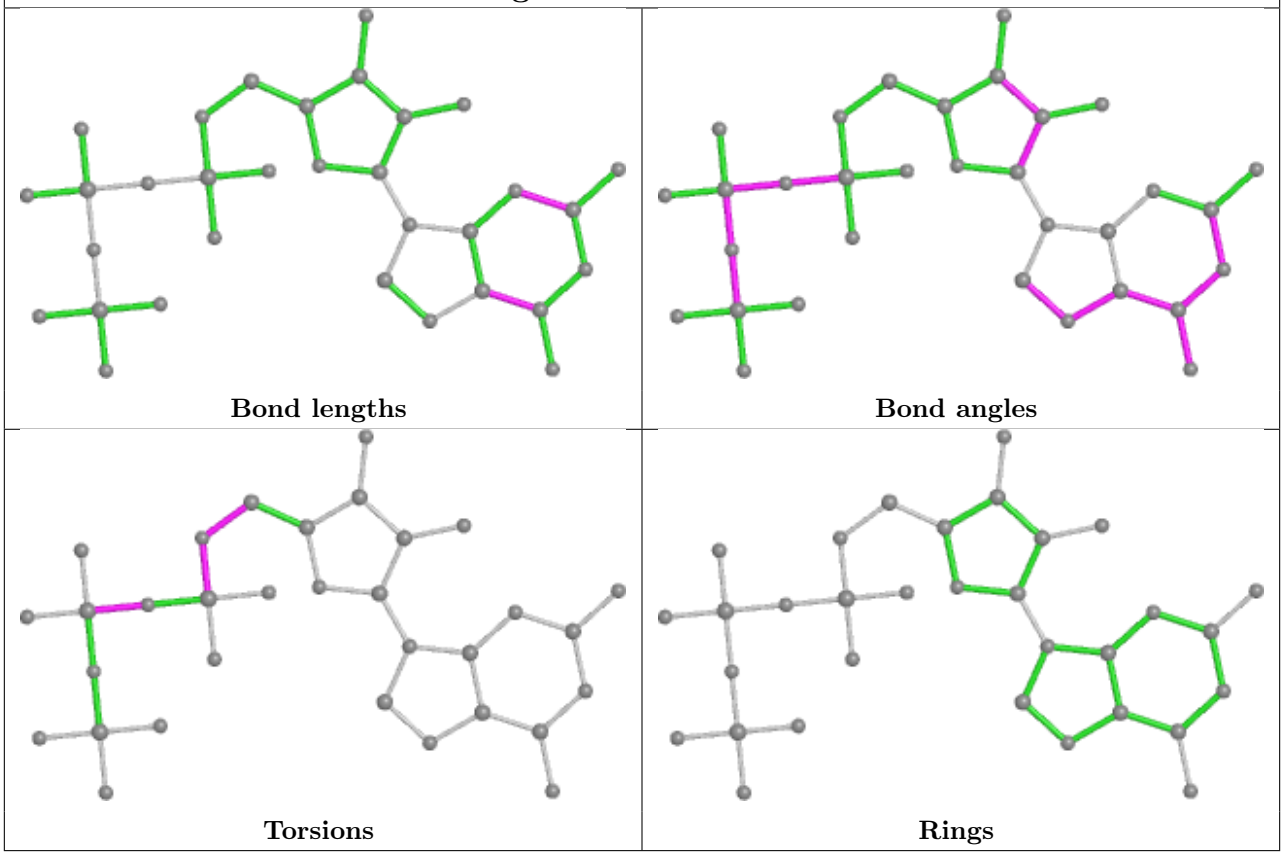
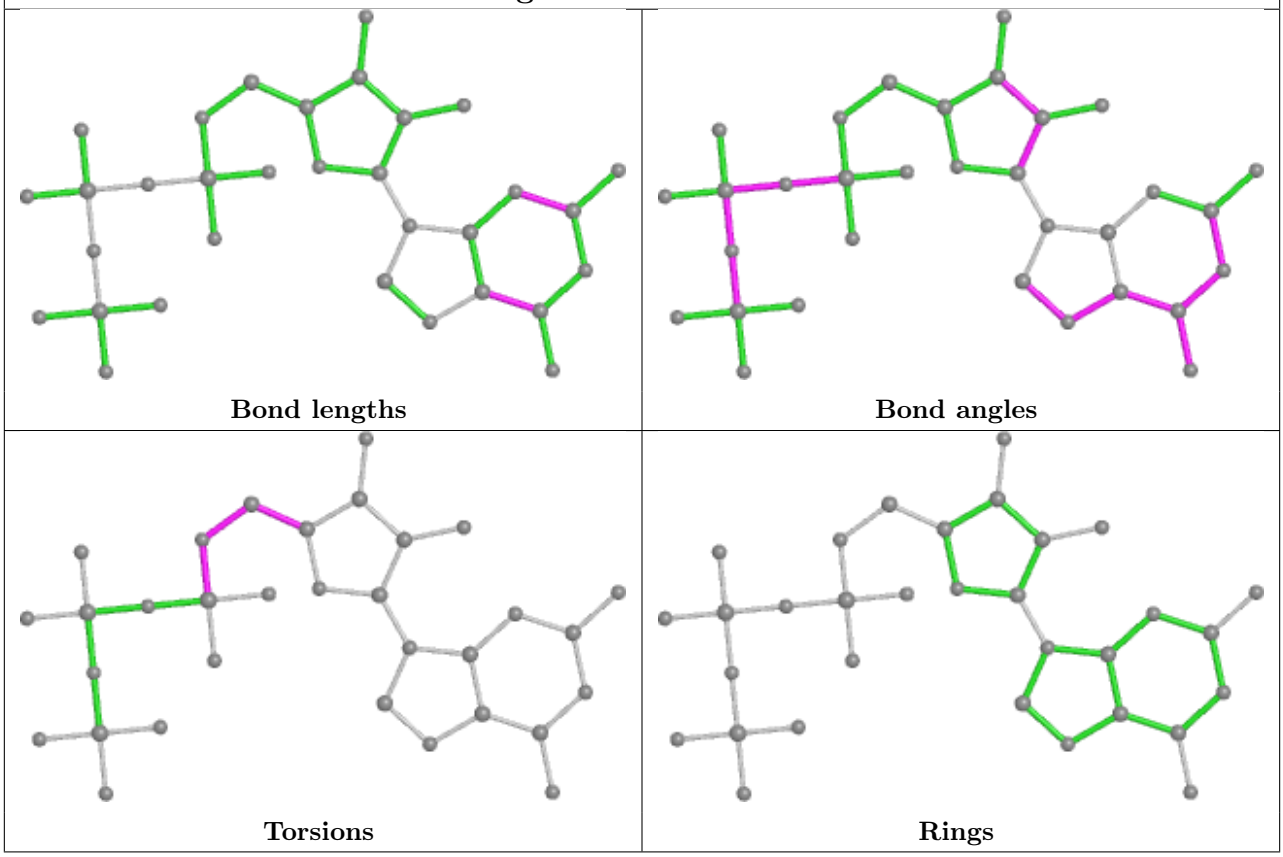


Rings

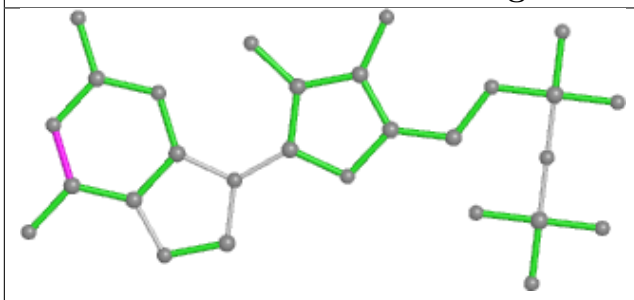
Ligand GTP LK 501



Ligand GTP VI 501



Ligand GDP DD 502



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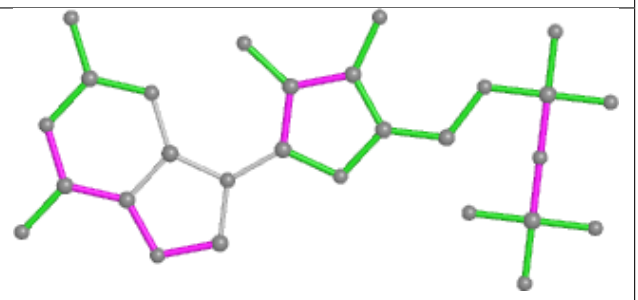

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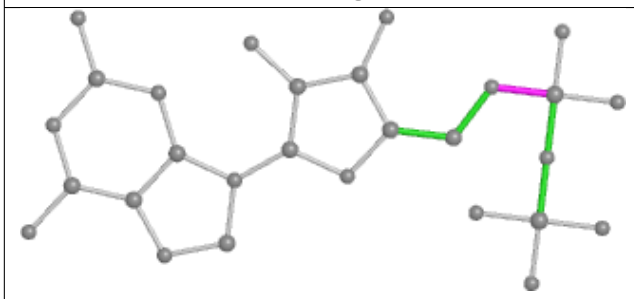

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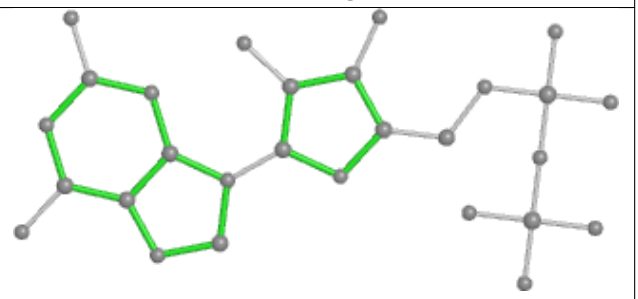
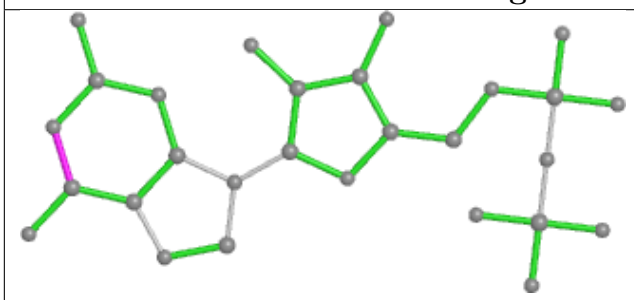
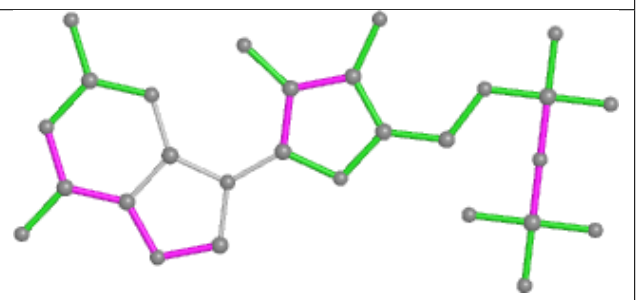


Rings

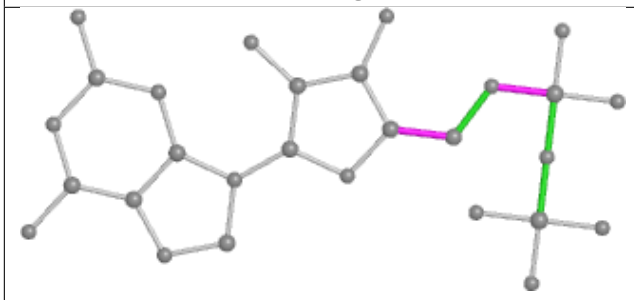
Ligand GDP PD 502



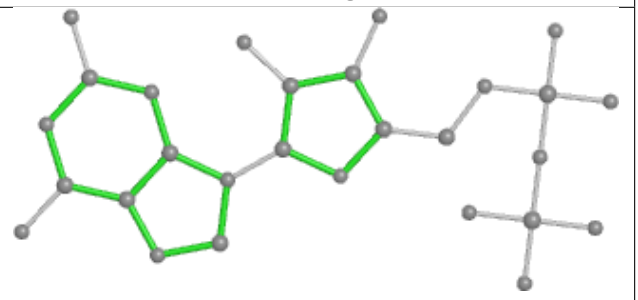
Bond lengths



Bond angles

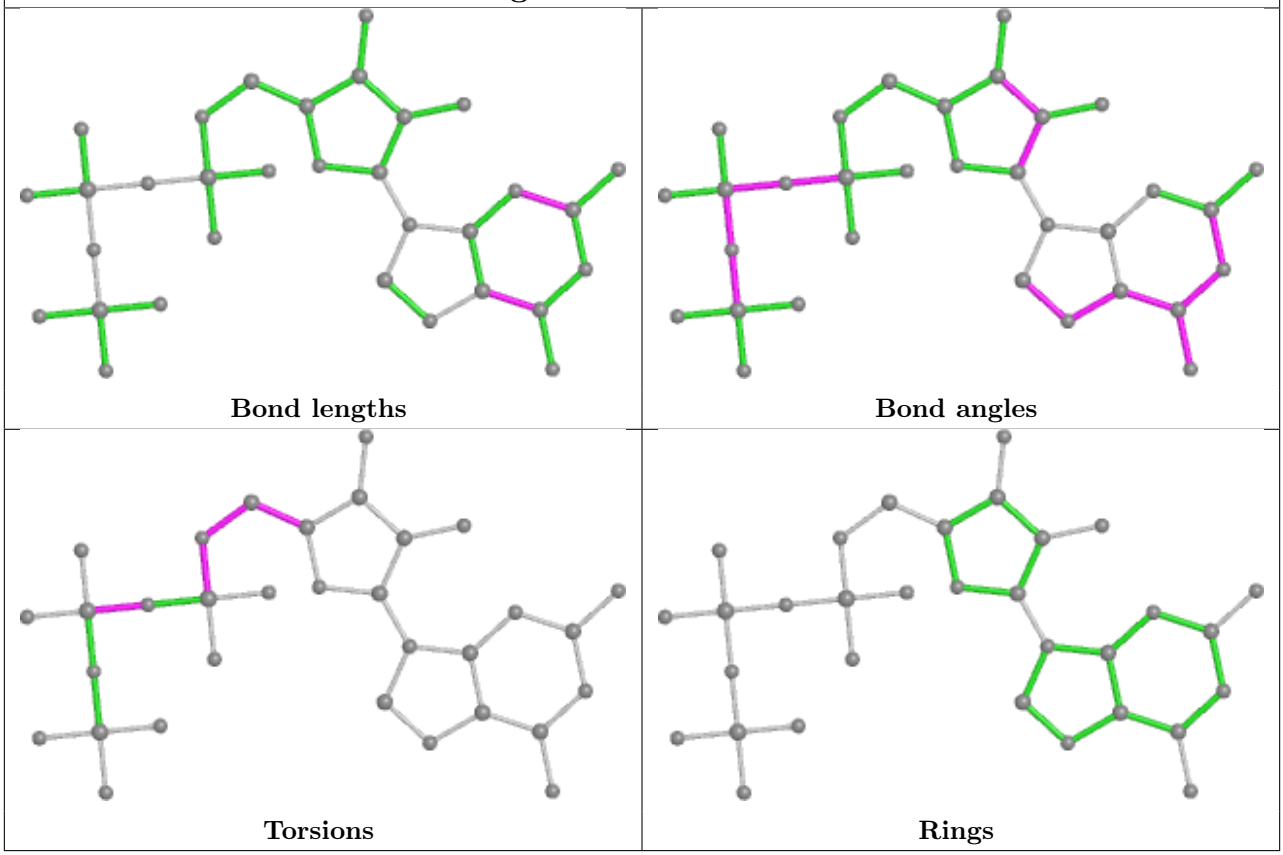


Torsions

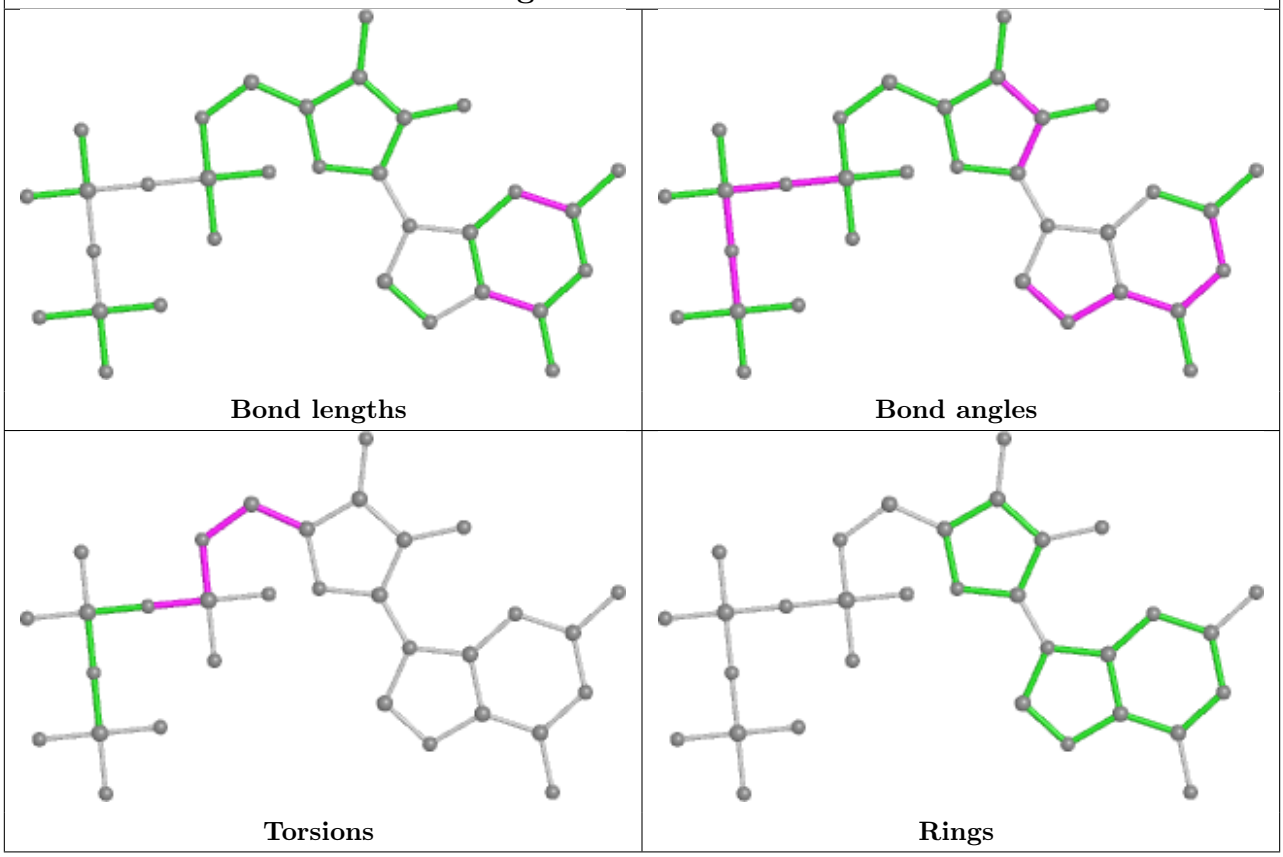


Rings

Ligand GTP PG 501



Ligand GTP CI 501



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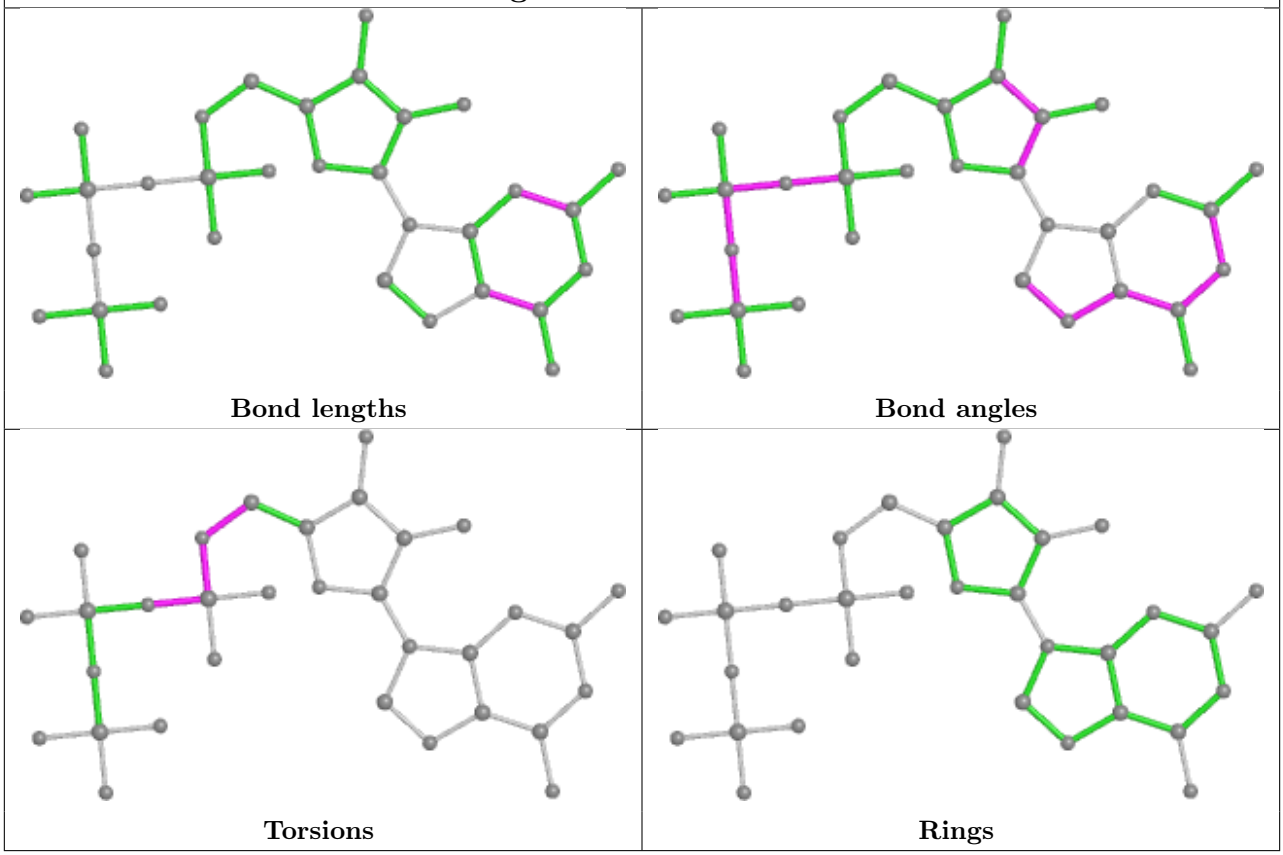

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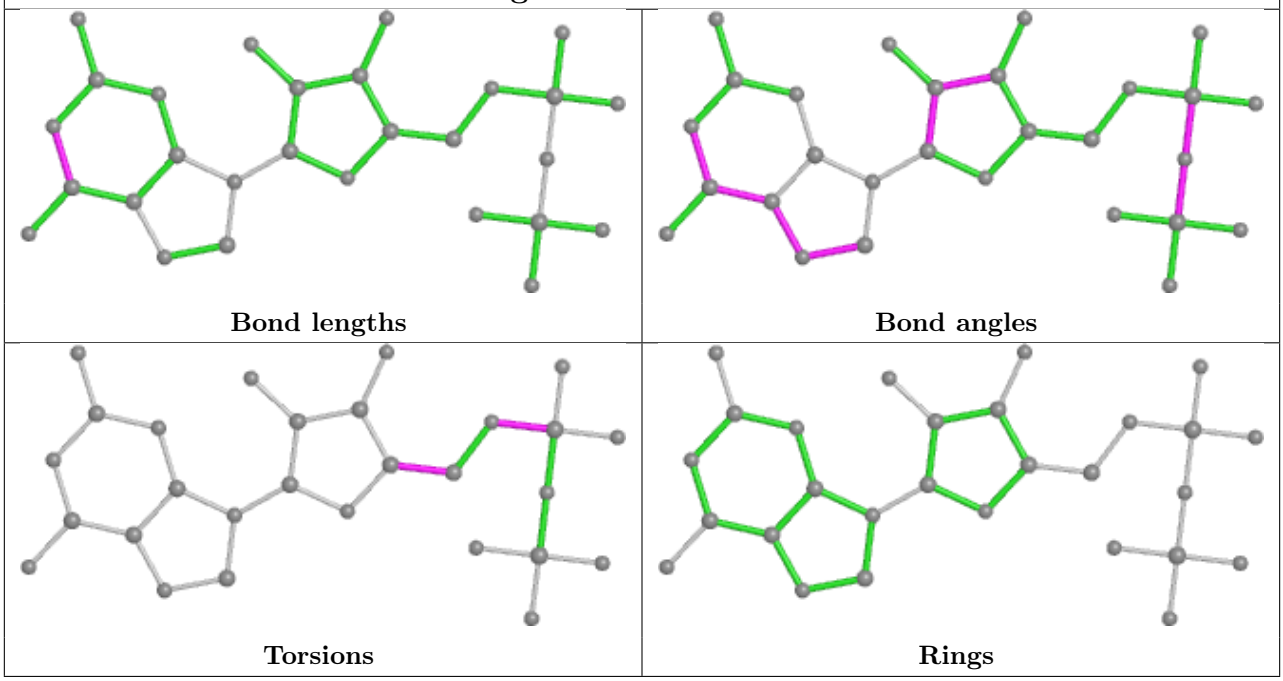

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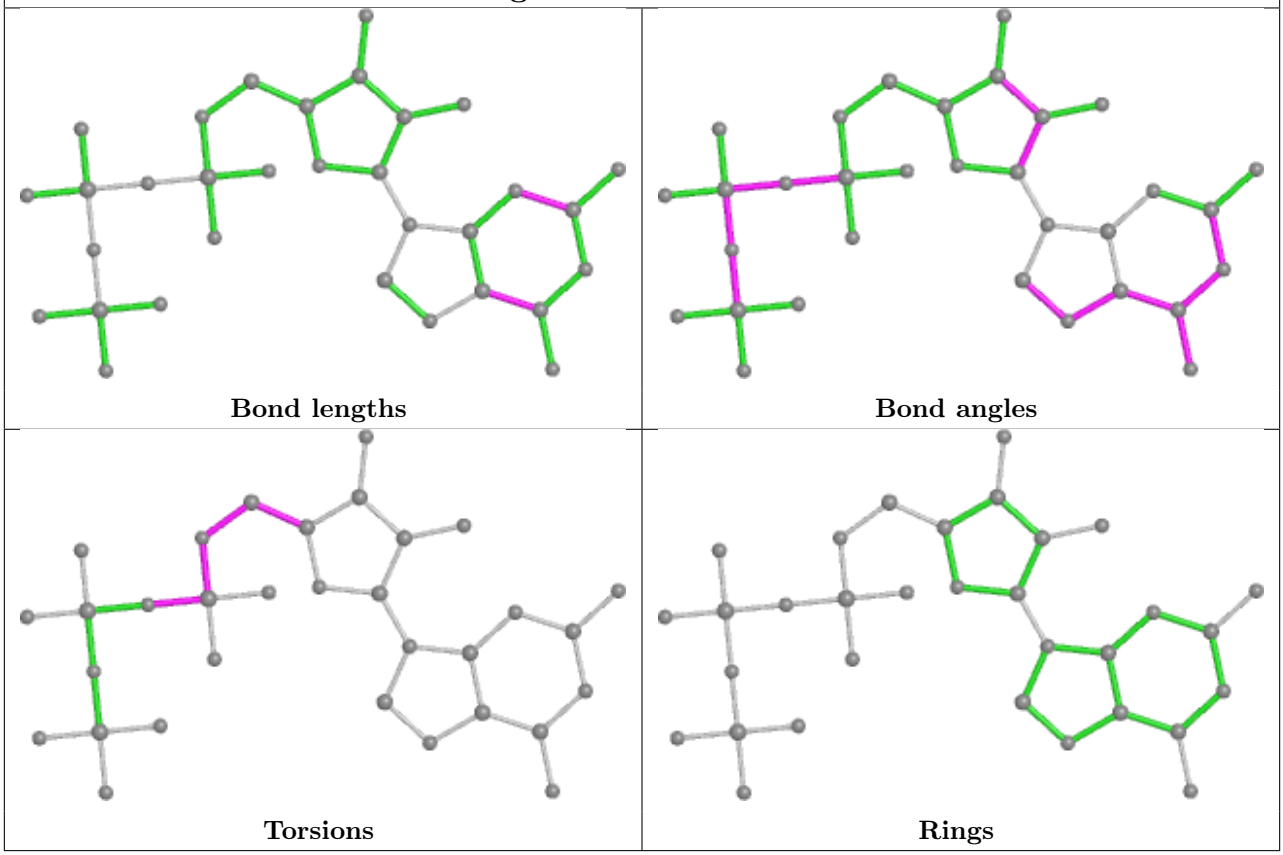

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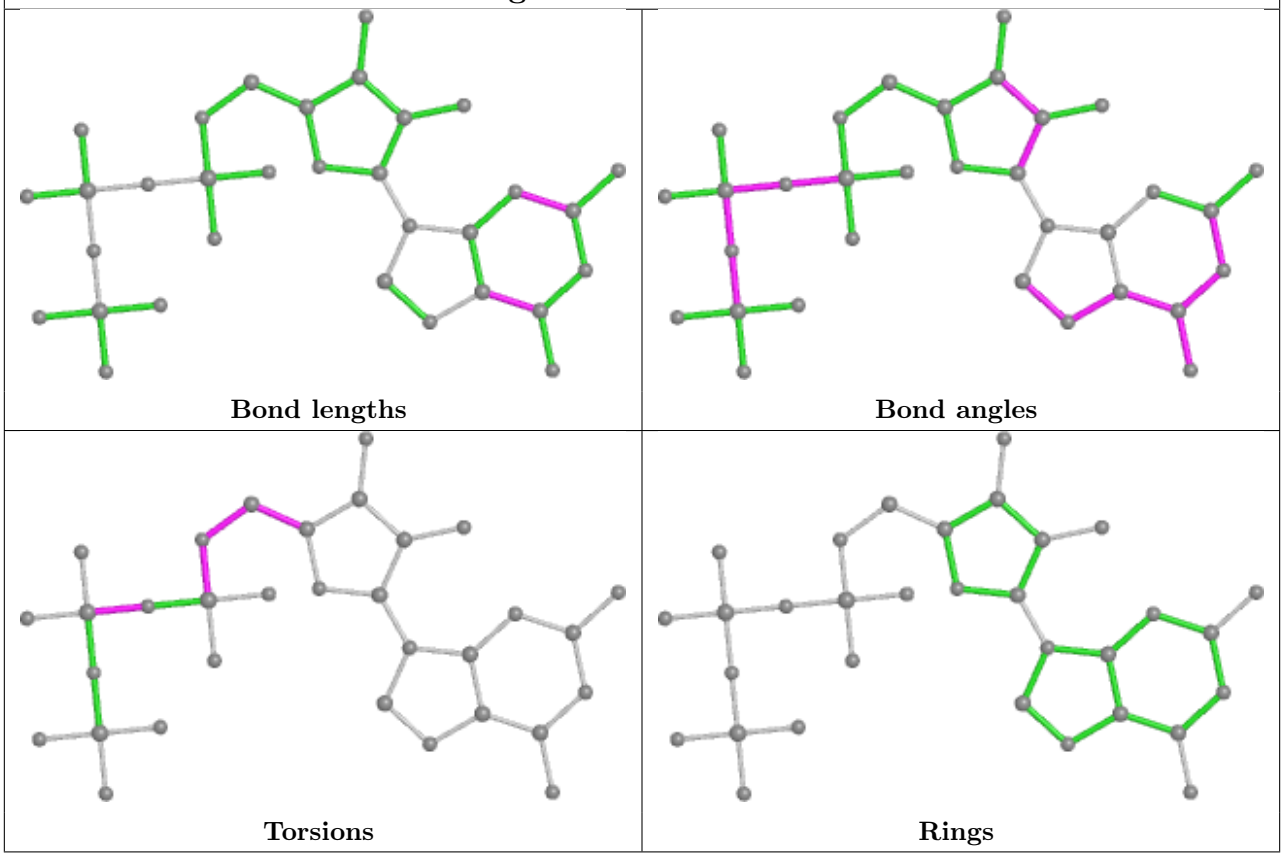

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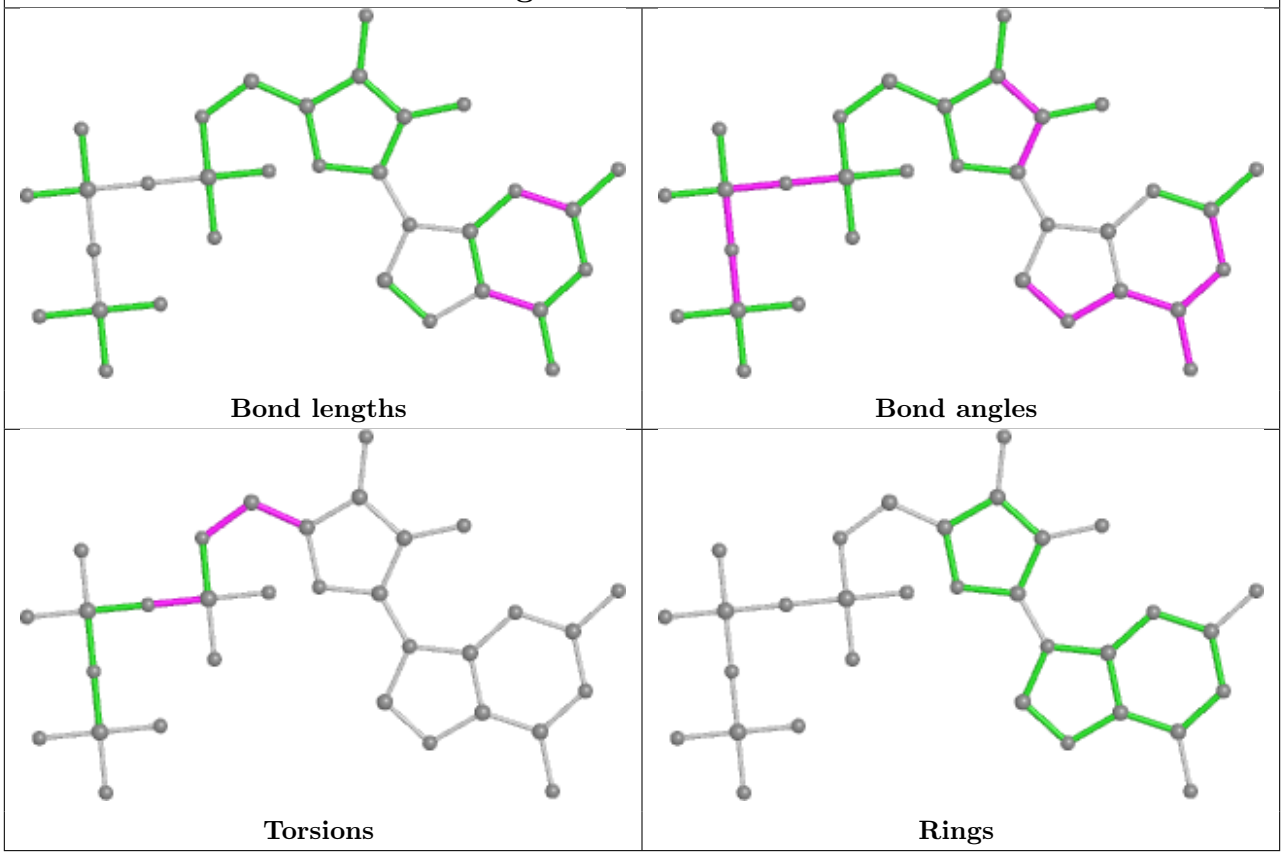

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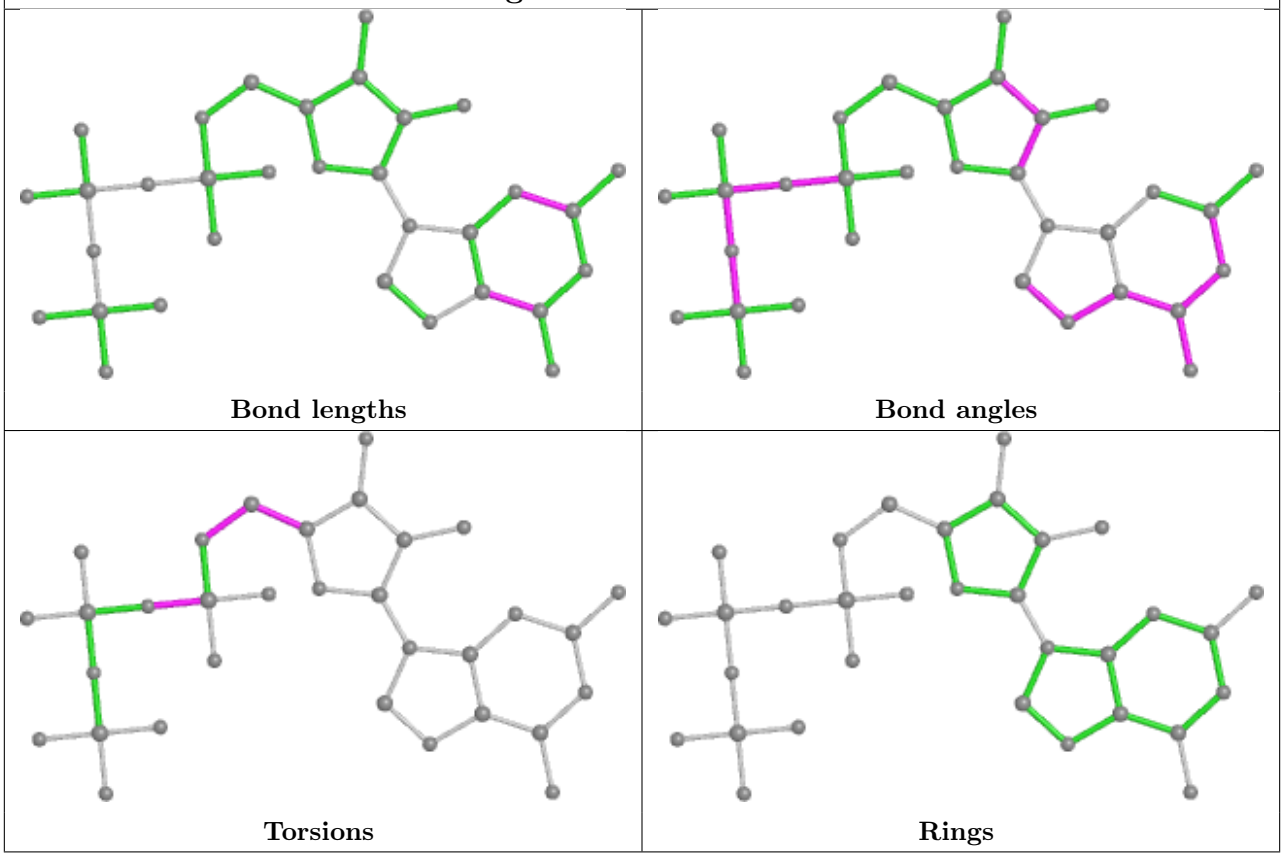

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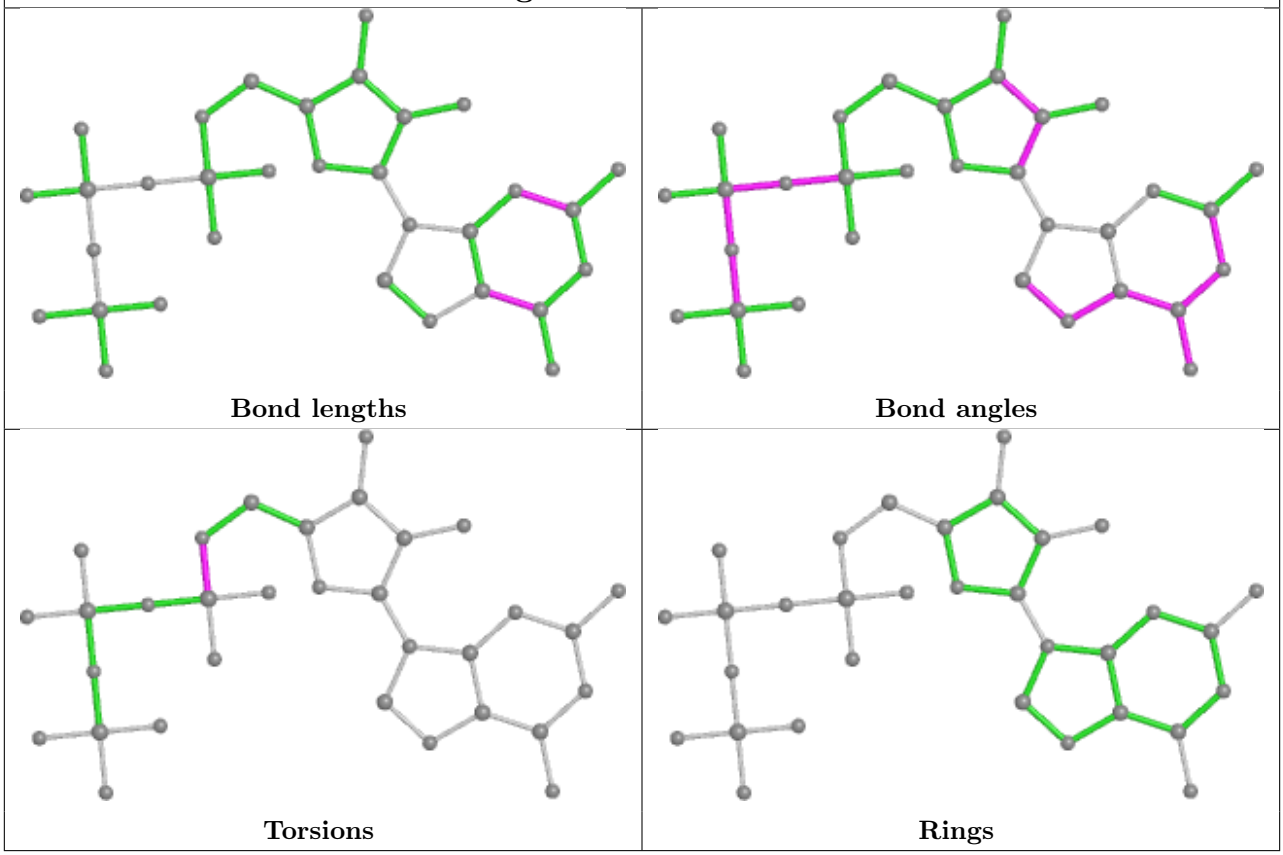
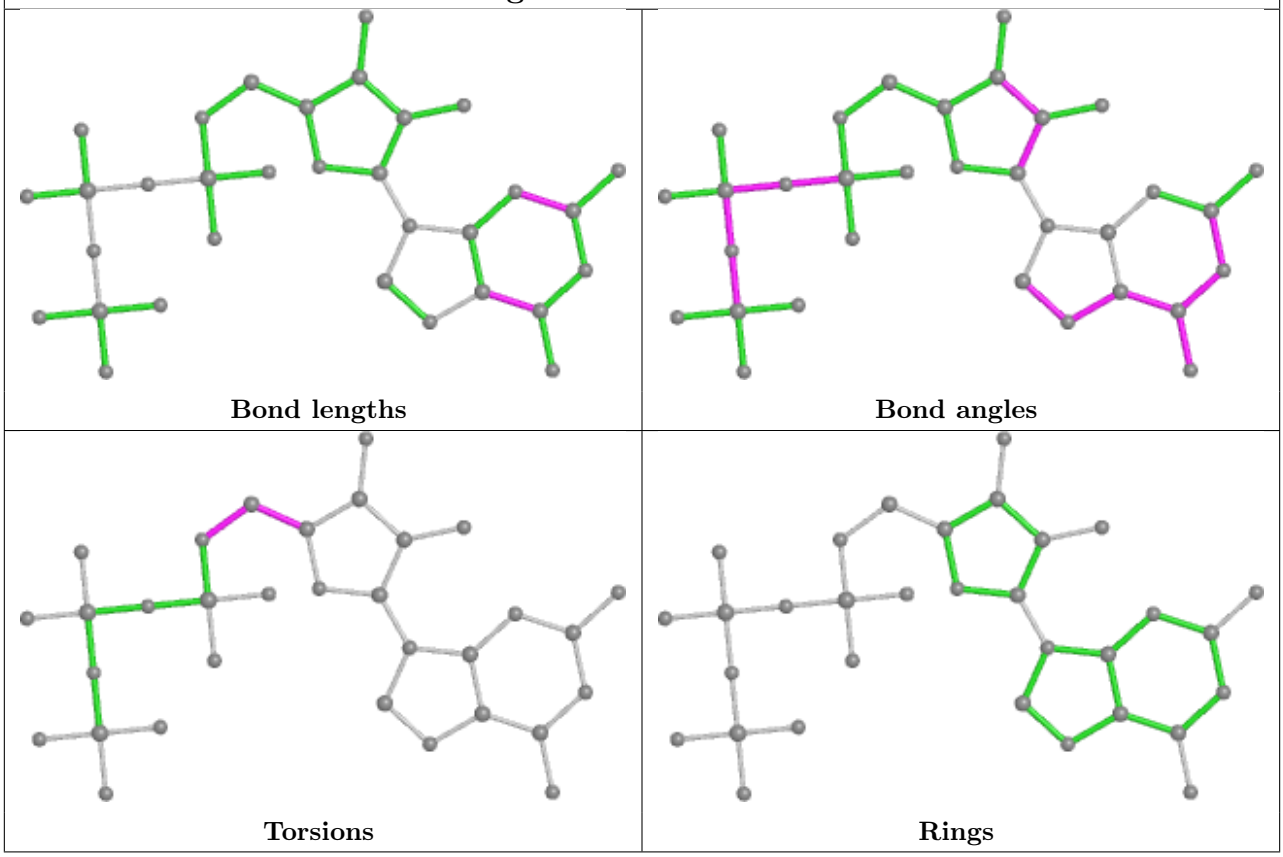
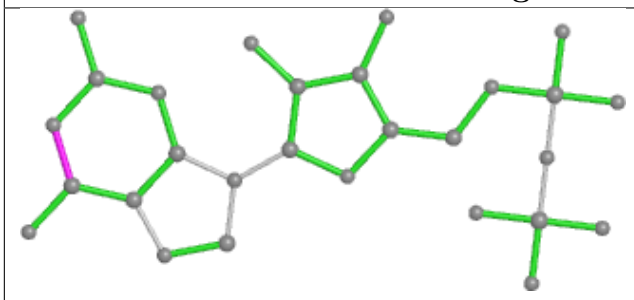


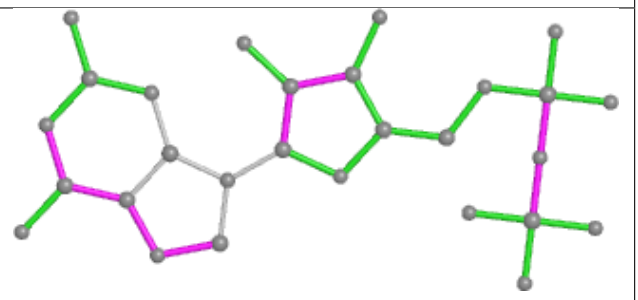
Ligand GTP CM 501



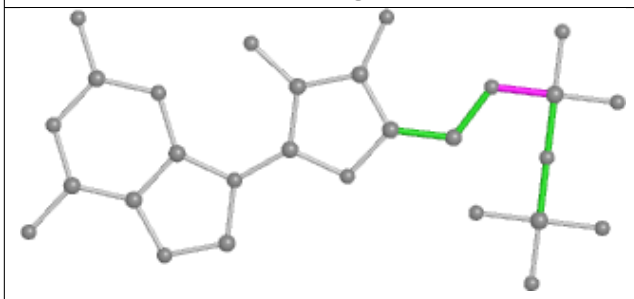
Ligand GDP DJ 502



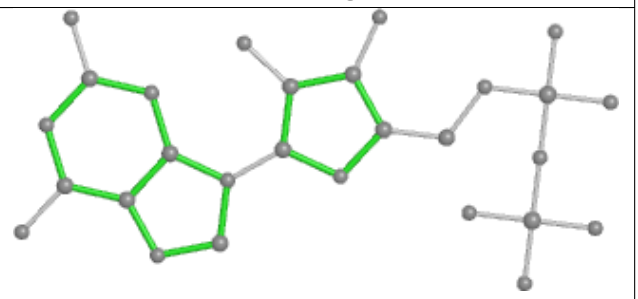
Bond lengths



Bond angles

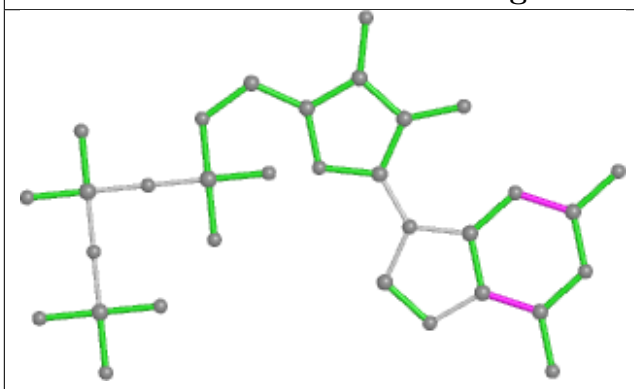


Torsions



Rings

Ligand GTP HC 501



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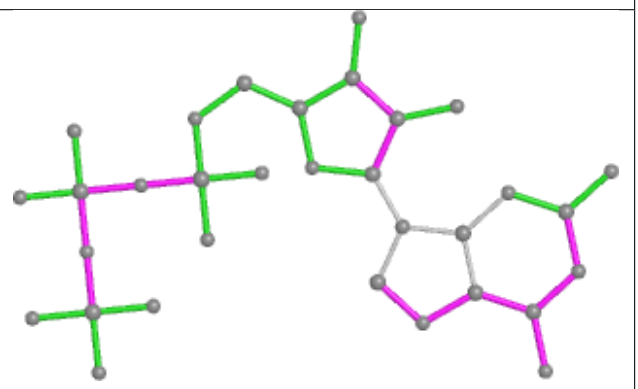
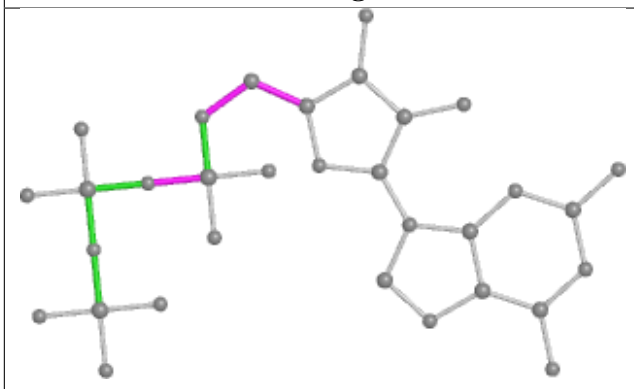


Bond angles



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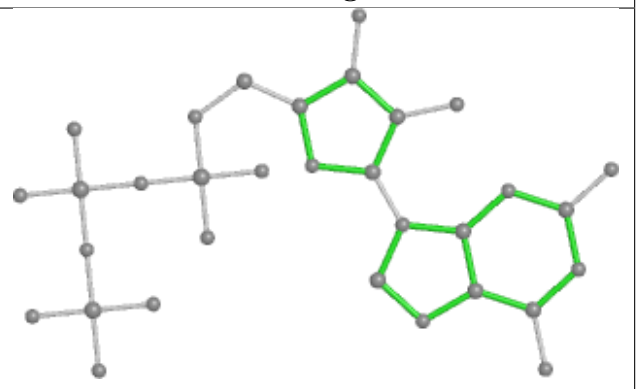
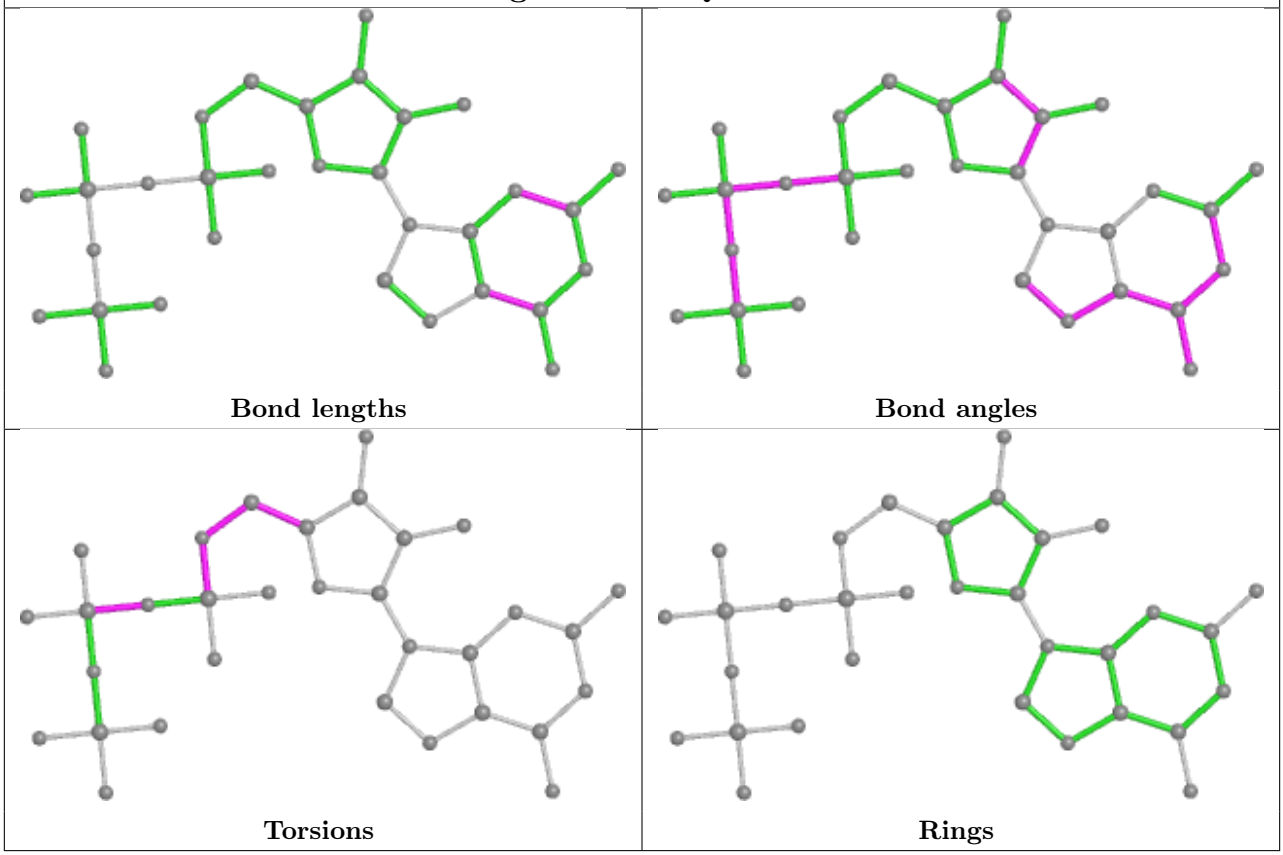


Rings

Ligand GTP QO 501



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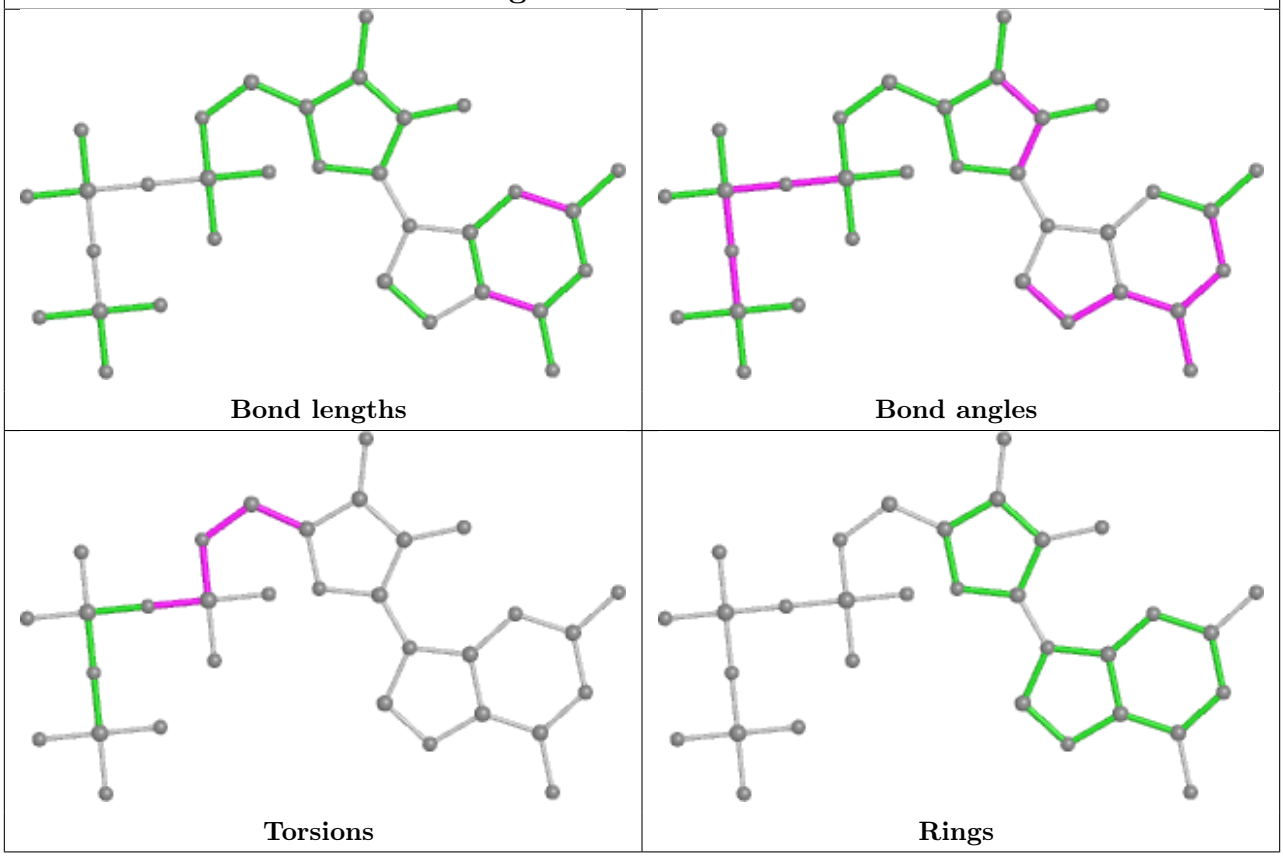

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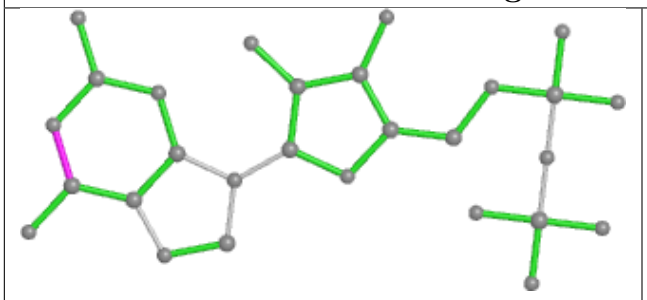

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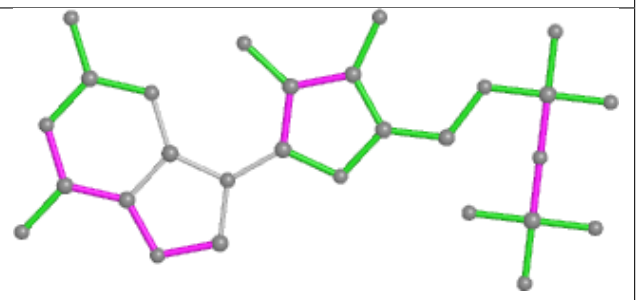
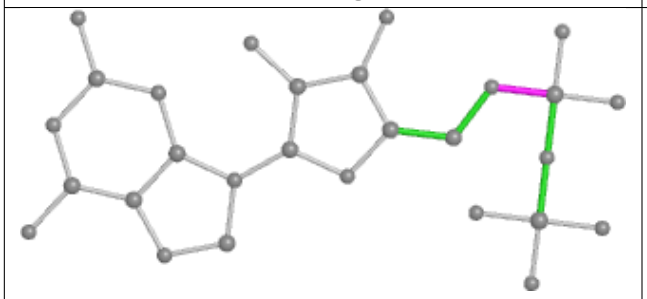


Bond angles



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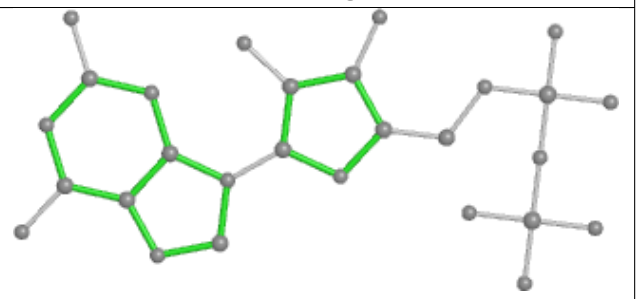
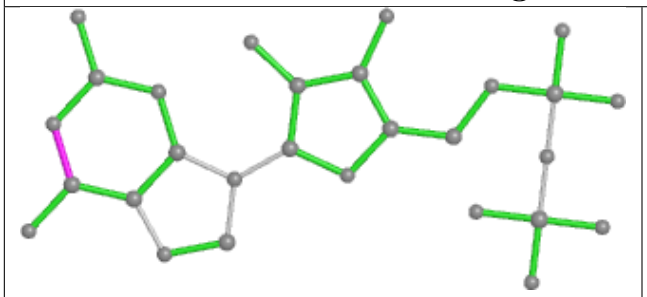


Rings

Ligand GDP OF 502



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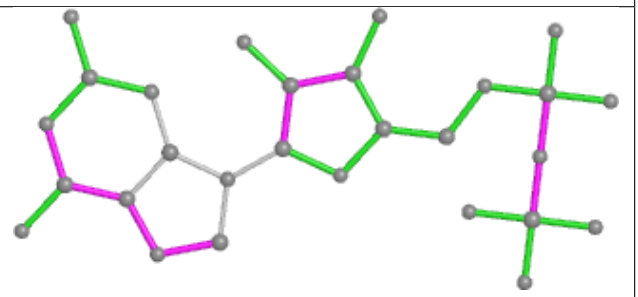
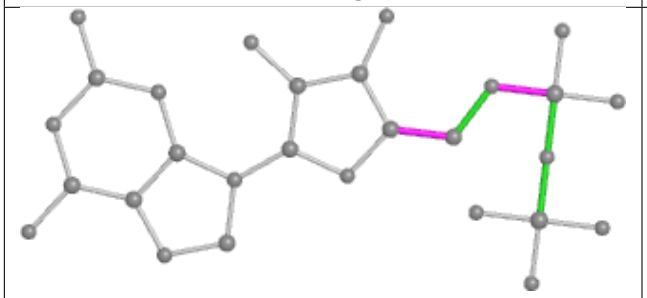


Bond angles



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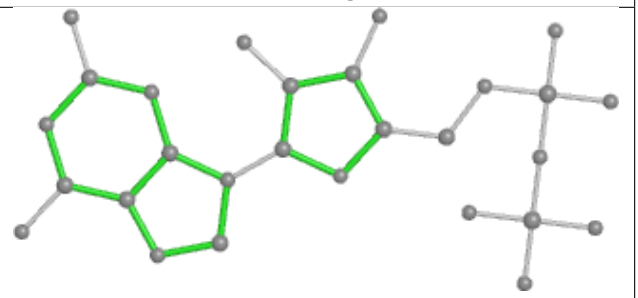
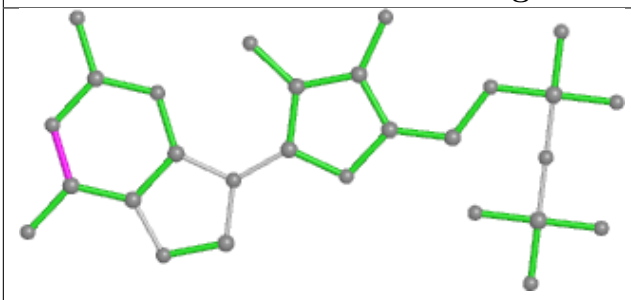


Rings

Ligand GDP EL 502



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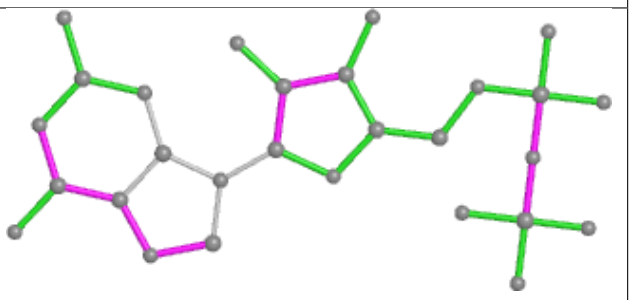
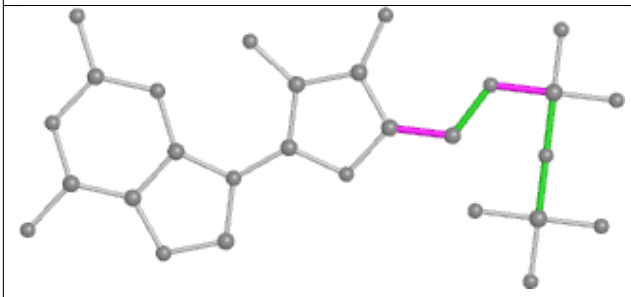


Bond angles



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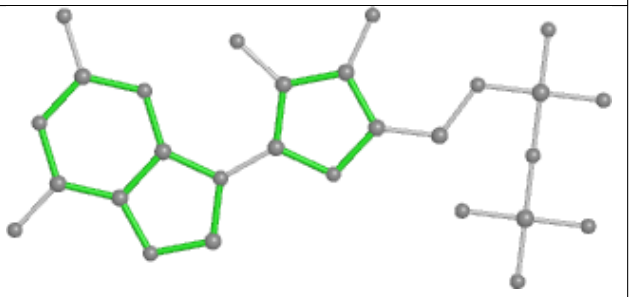
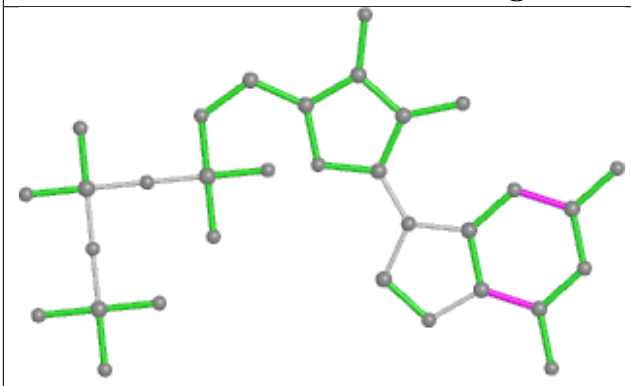


Rings

Ligand GTP DK 501



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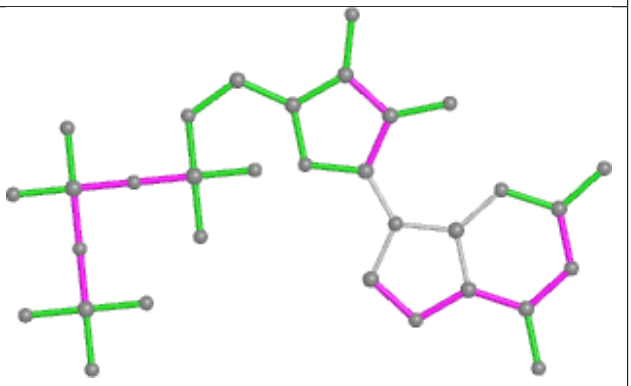
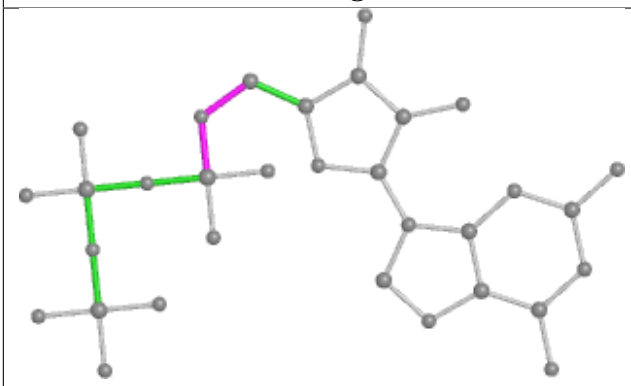


Bond angles



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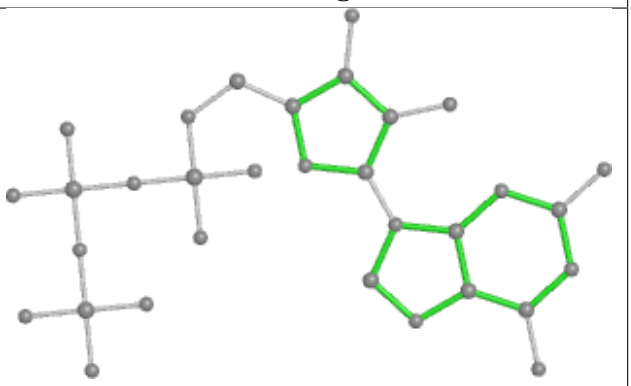
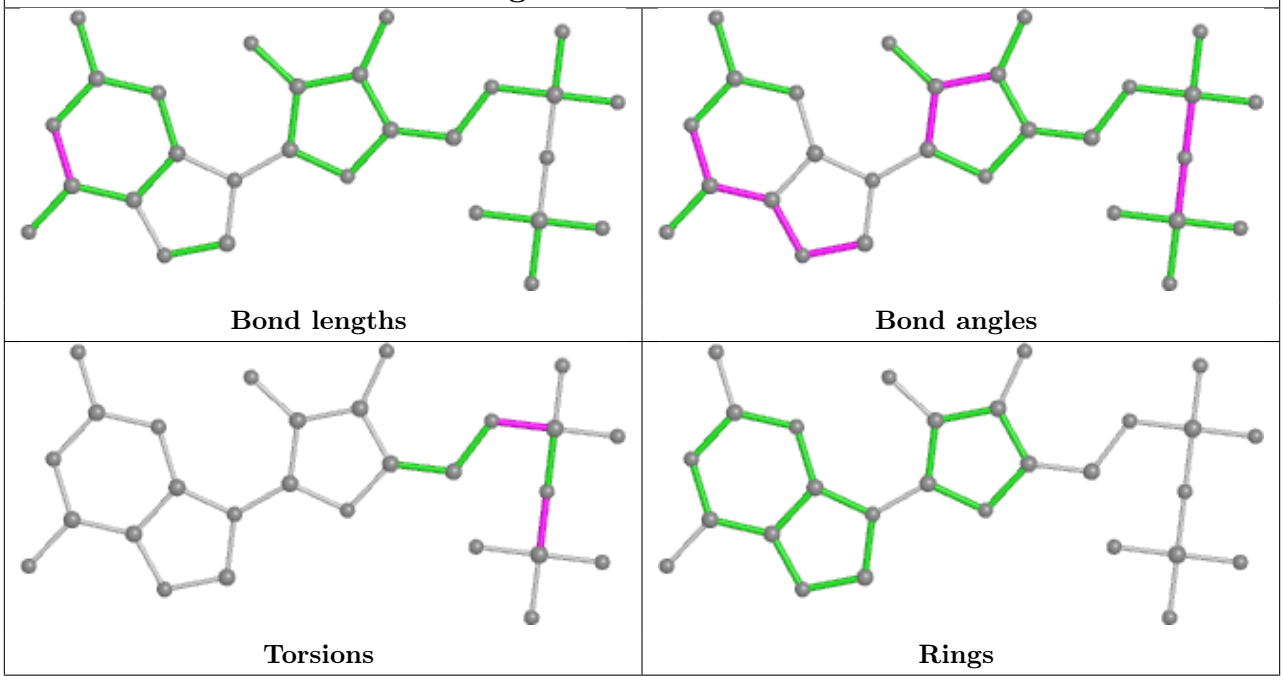
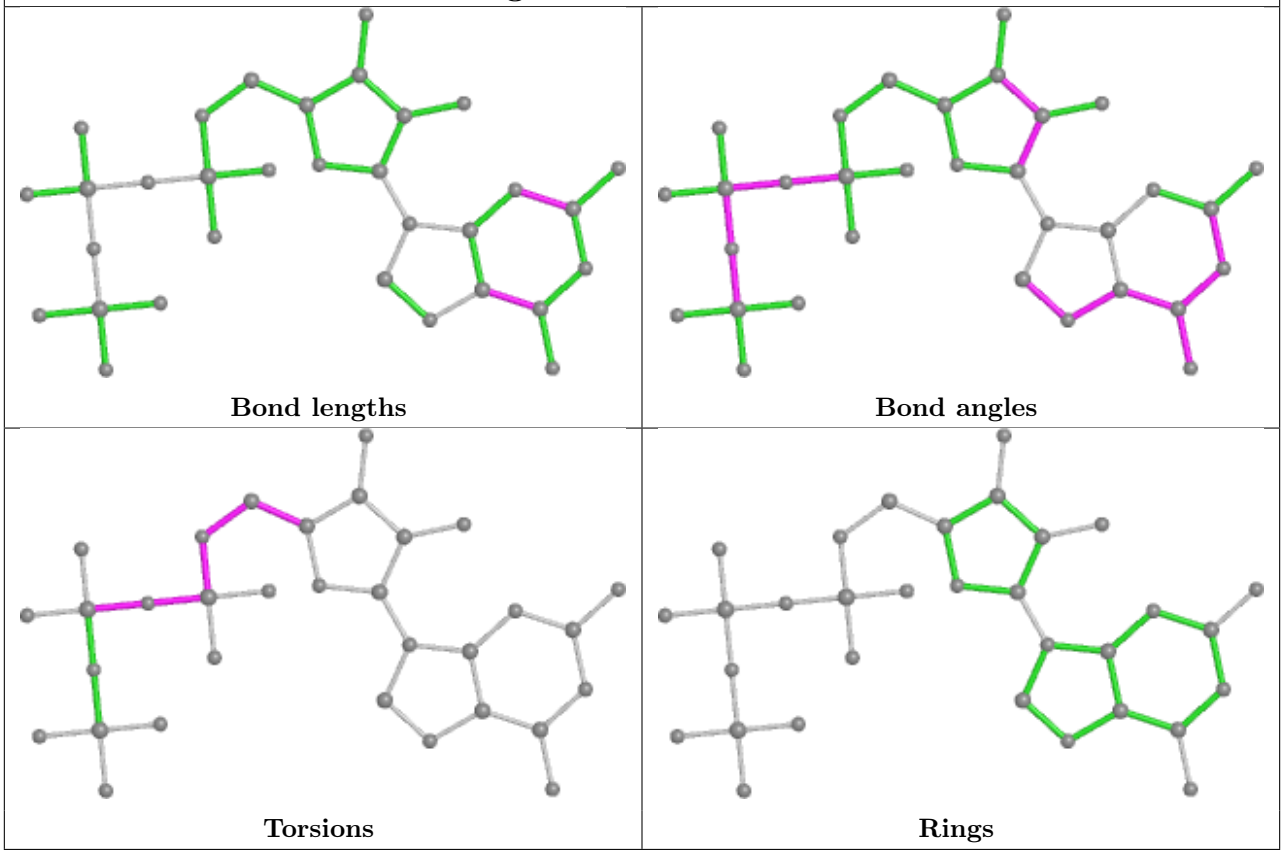


Rings

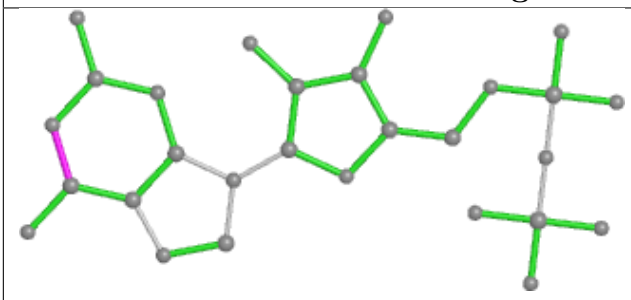
Ligand GDP BH 502



Ligand GTP OM 501



Ligand GDP EF 502



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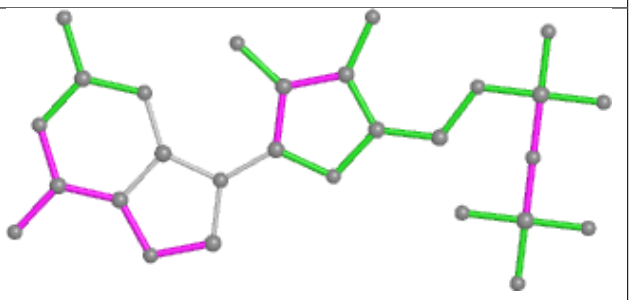
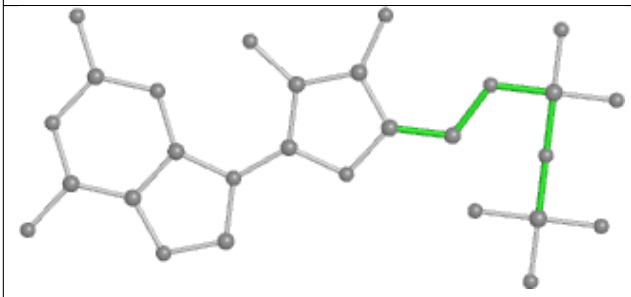


Bond angles



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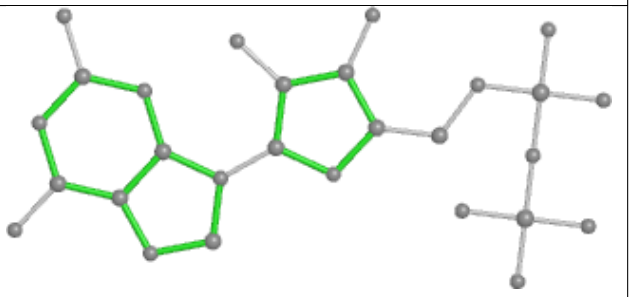
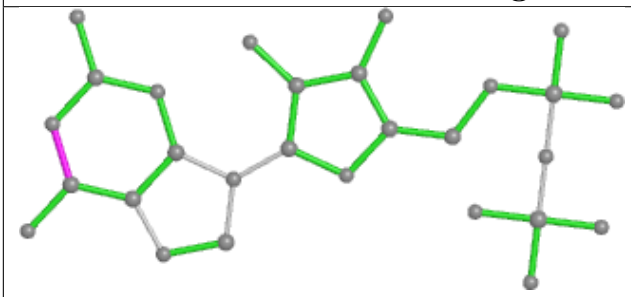


Rings

Ligand GDP SN 502



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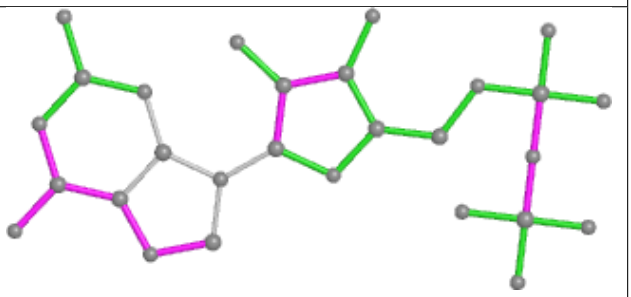
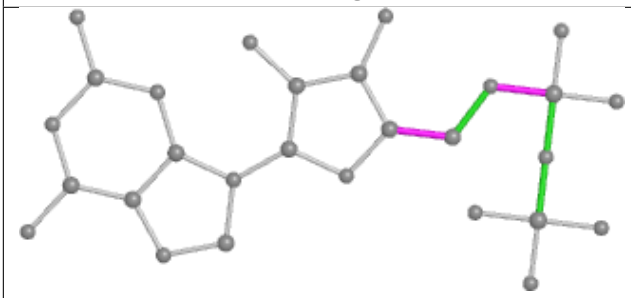
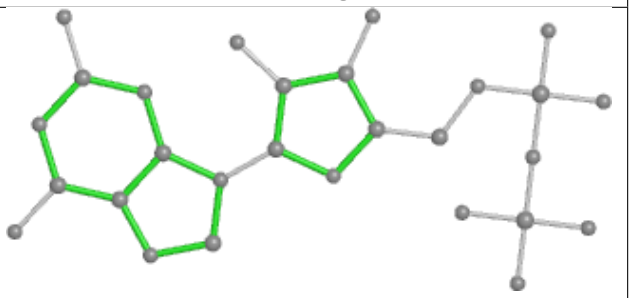


Bond angles

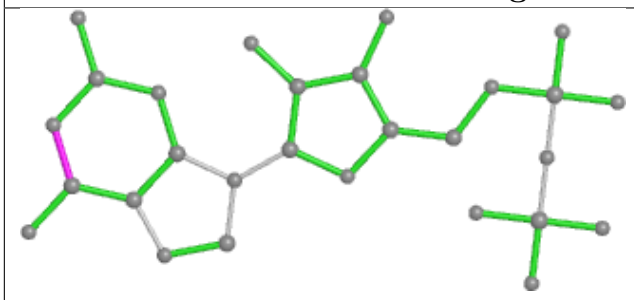


Torsions

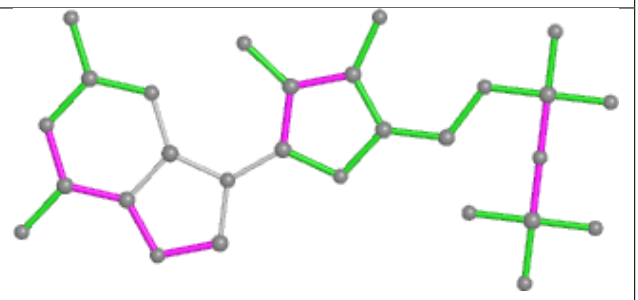


Rings

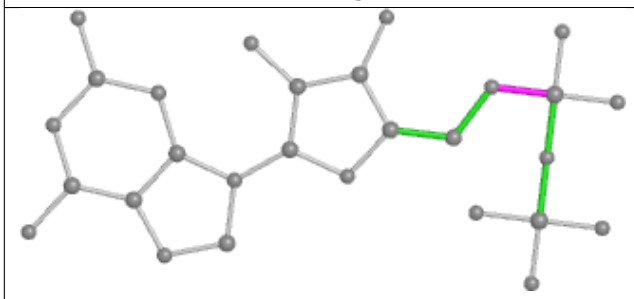
Ligand GDP UP 502



Bond lengths



Bond angles



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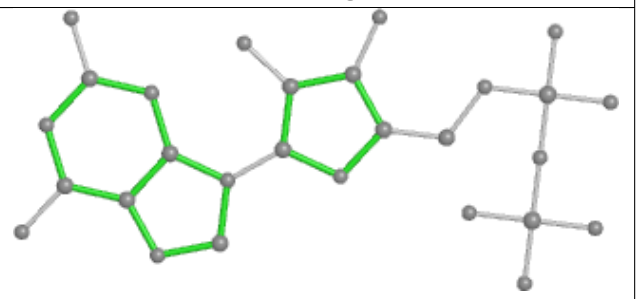
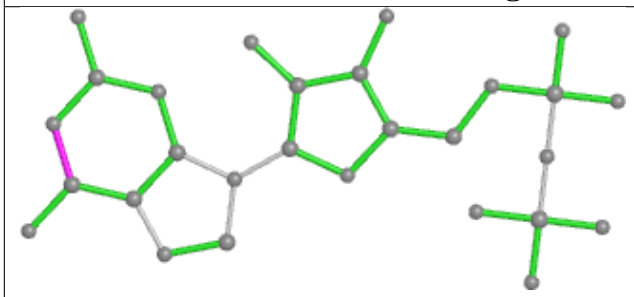
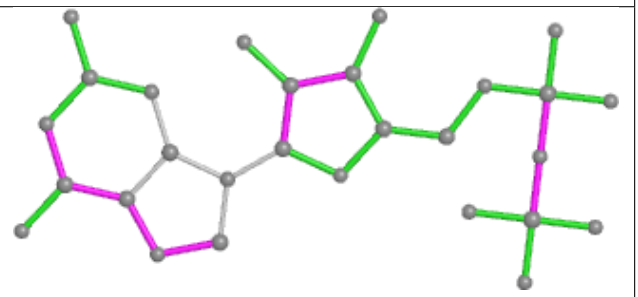


Rings

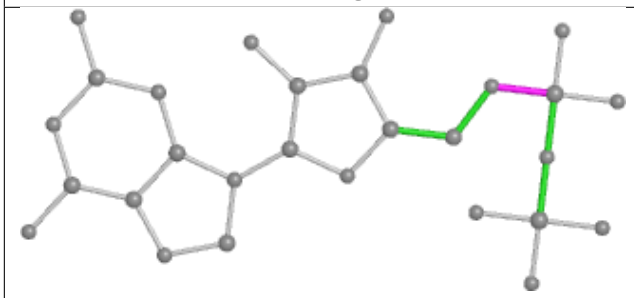
Ligand GDP MH 502



Bond lengths



Bond angles



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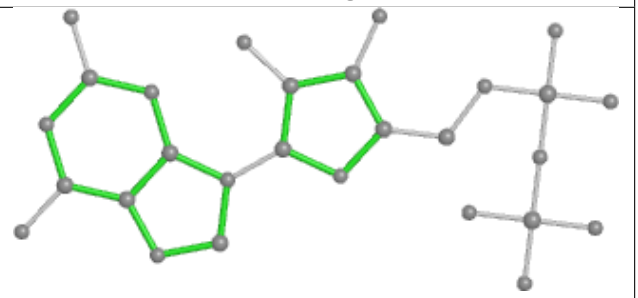
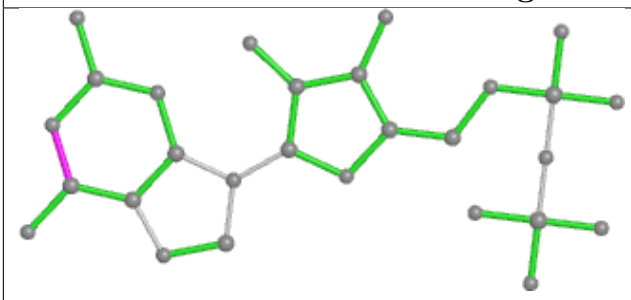
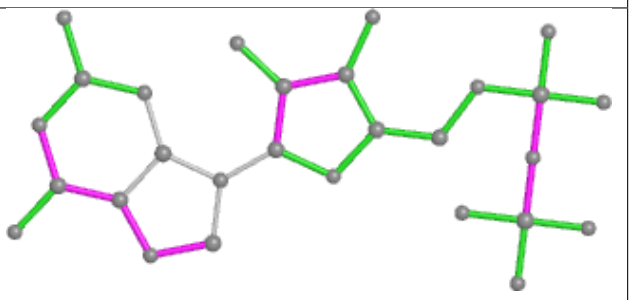


Rings

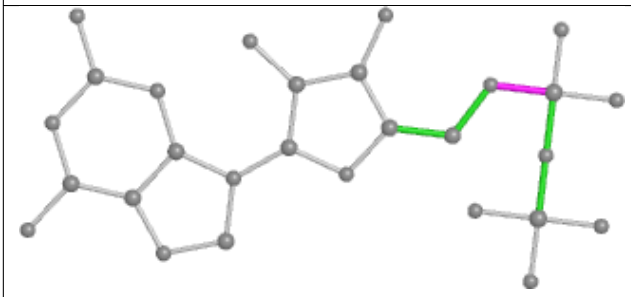
Ligand GDP IL 502



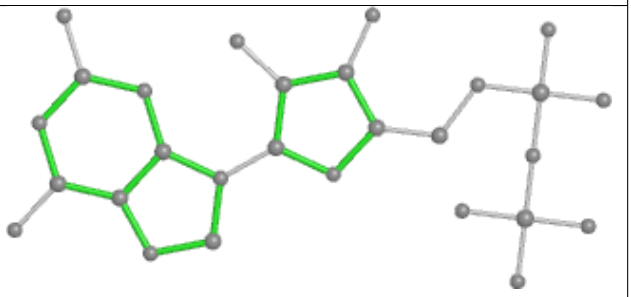
Bond lengths



Bond angles

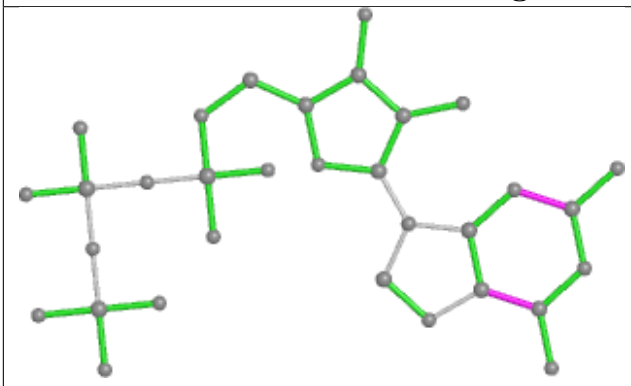


Torsions



Rings

Ligand GTP EC 501



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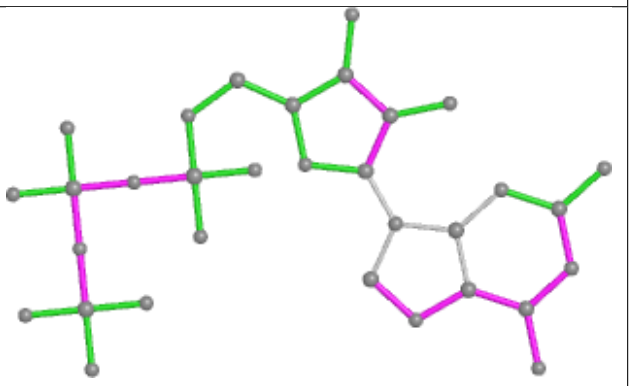

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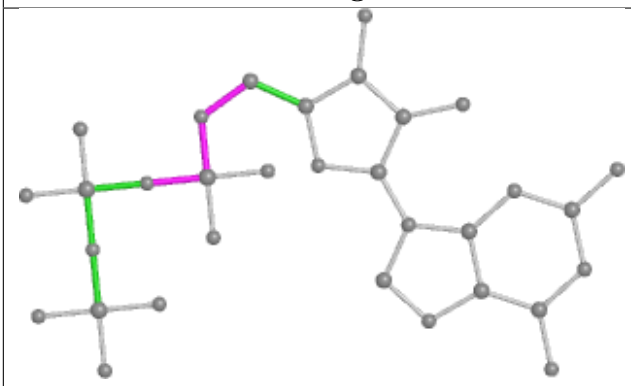

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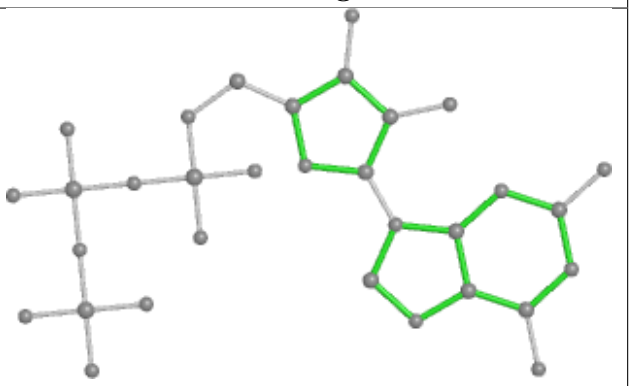
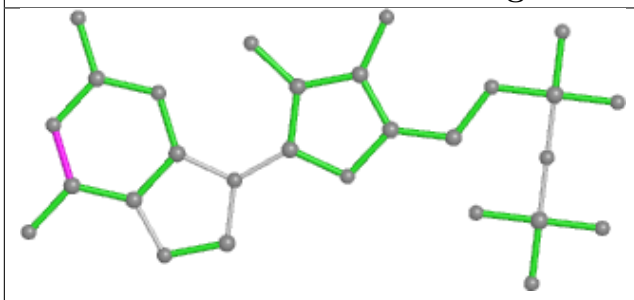


Rings

Ligand GDP MF 502



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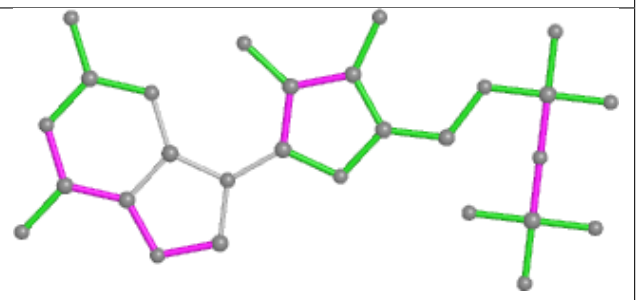

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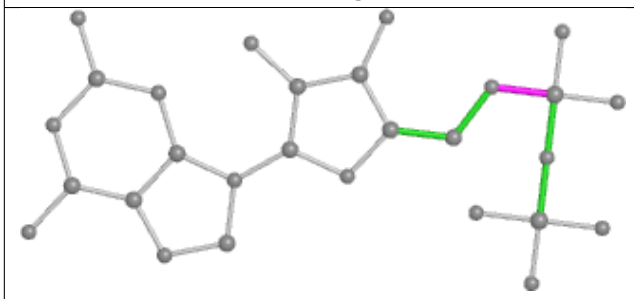

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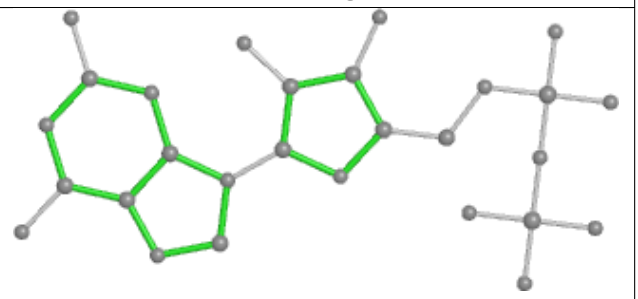
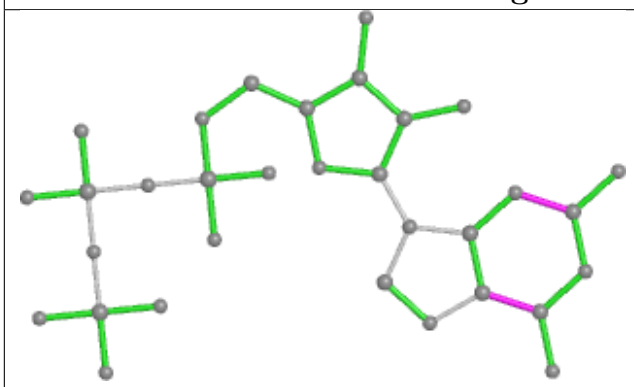


Rings

Ligand GTP DE 501



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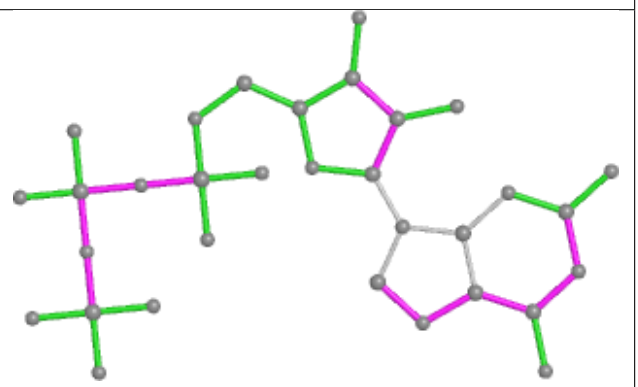

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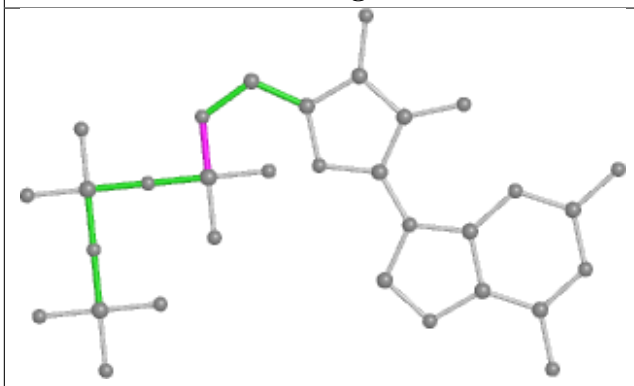

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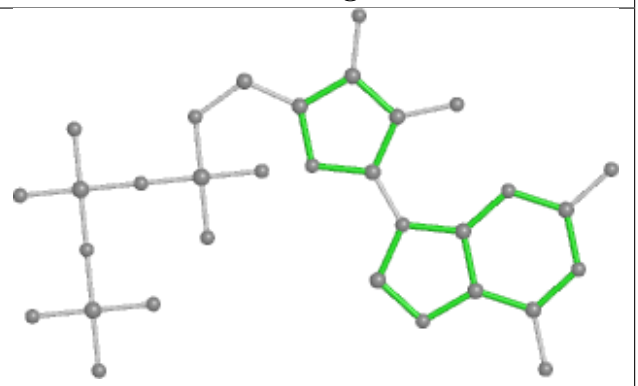
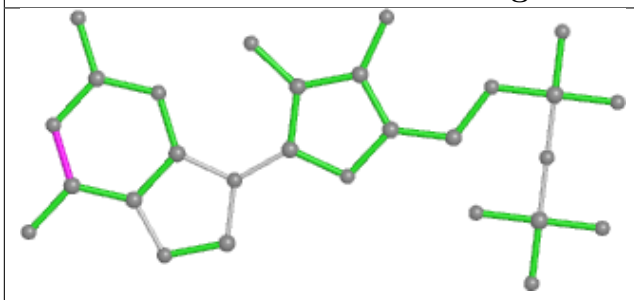


Rings

Ligand GDP DL 502



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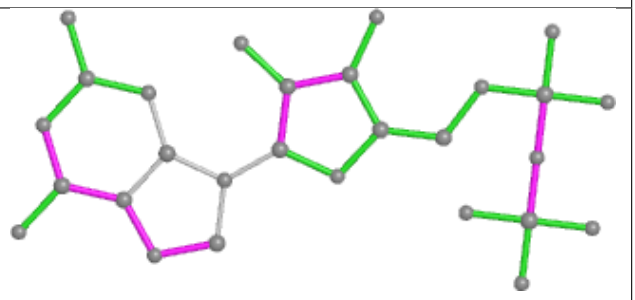

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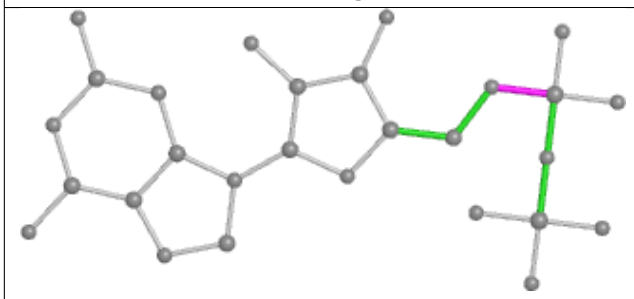

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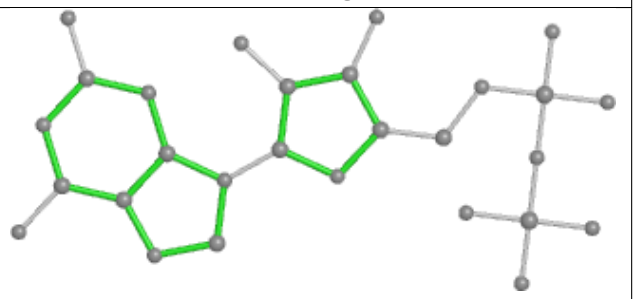
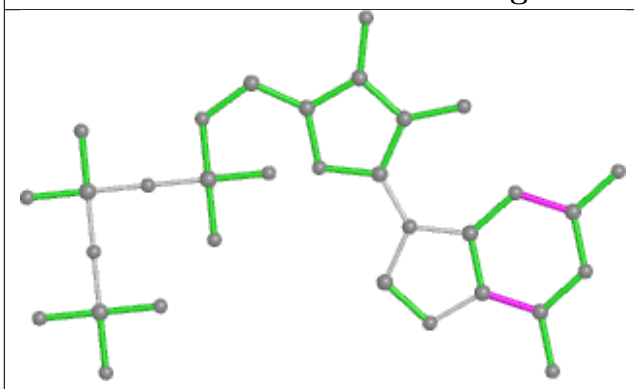


Rings

Ligand GTP QC 501



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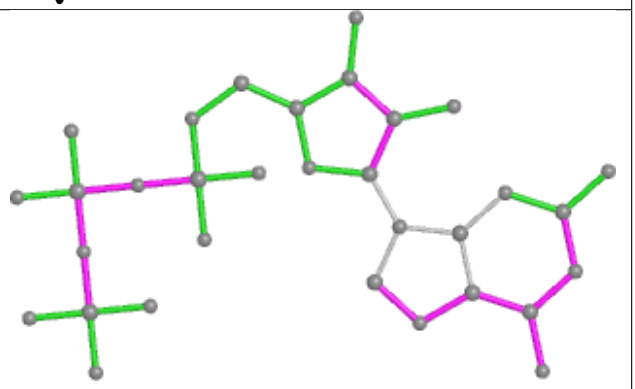

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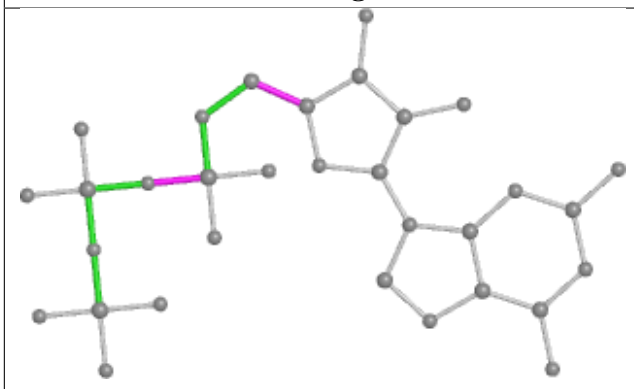

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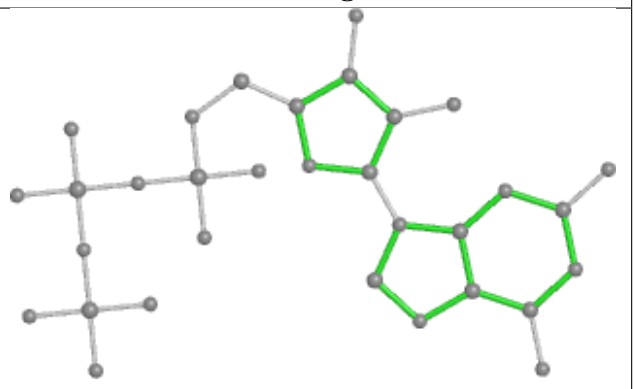
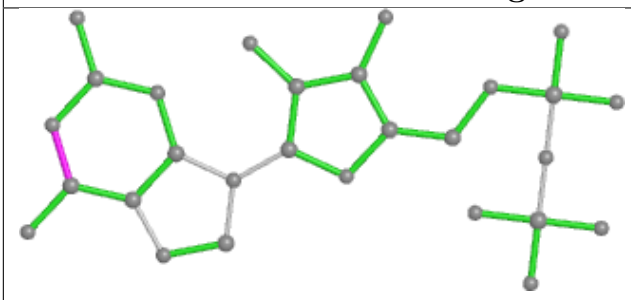


Rings

Ligand GDP DB 502



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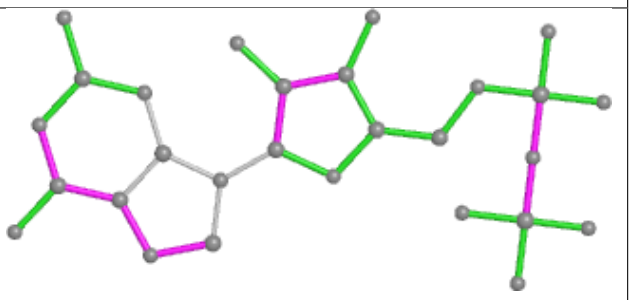

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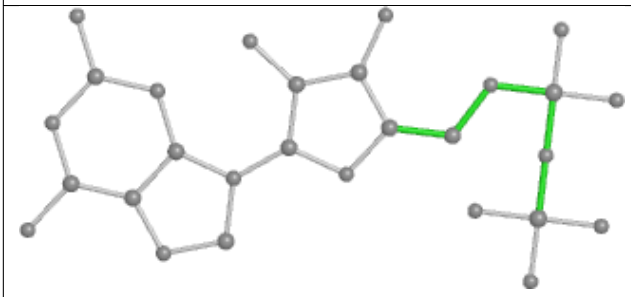

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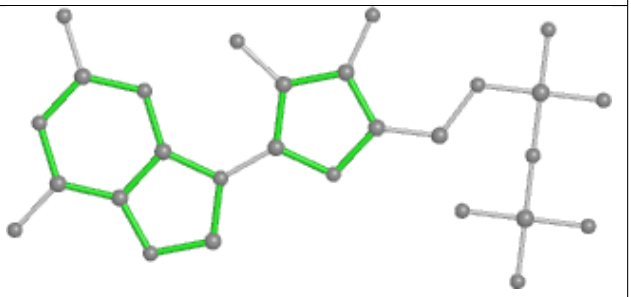
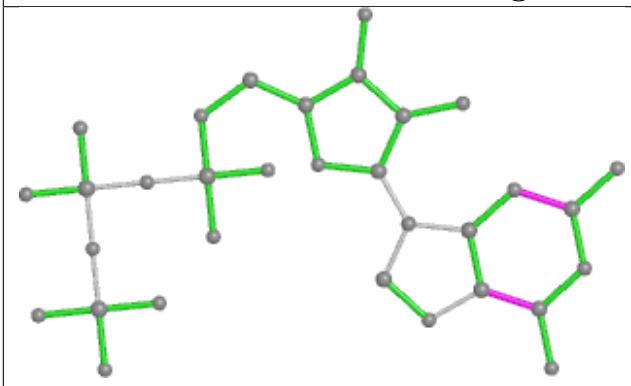


Rings

Ligand GTP KE 501



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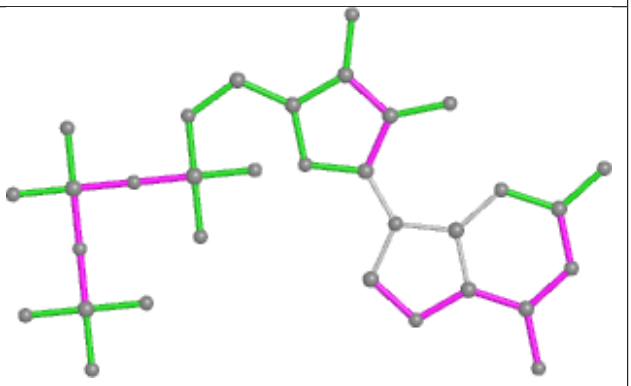

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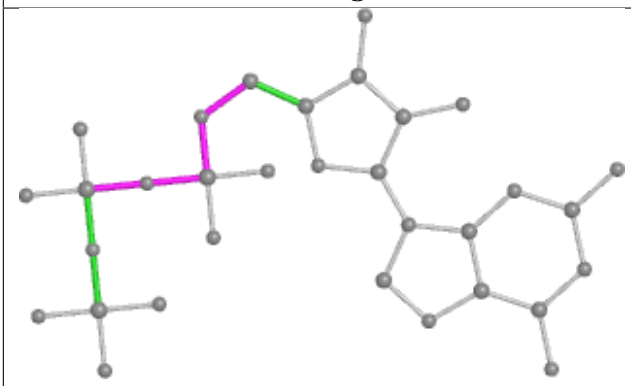

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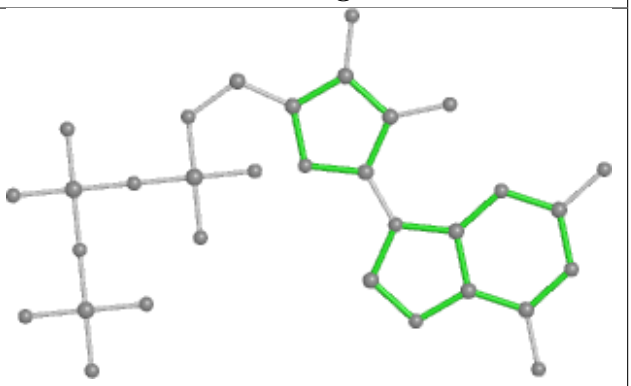
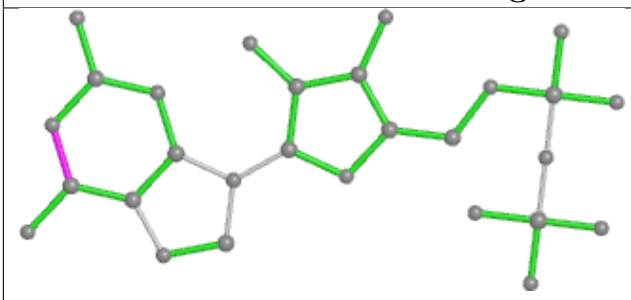


Rings

Ligand GDP DF 502



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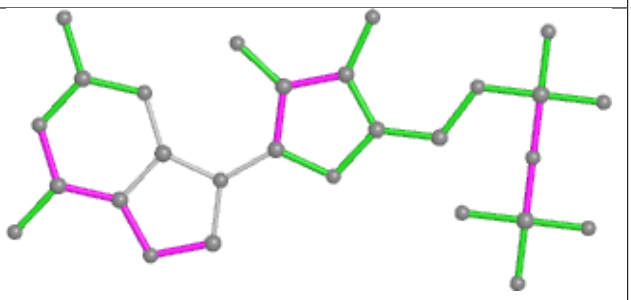

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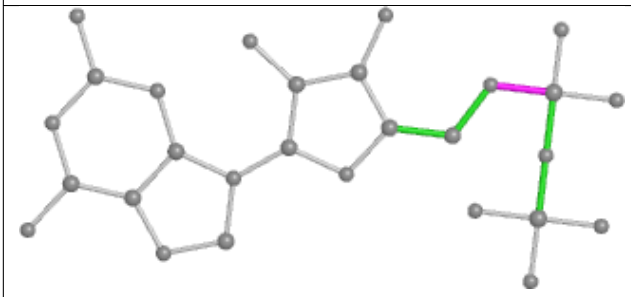

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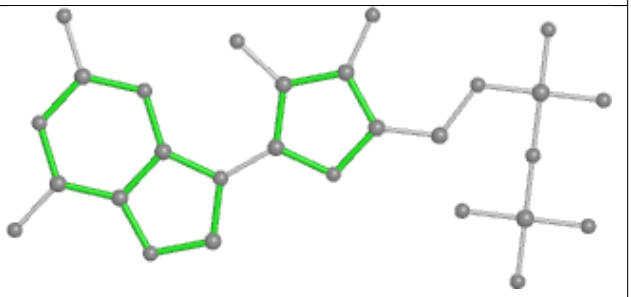
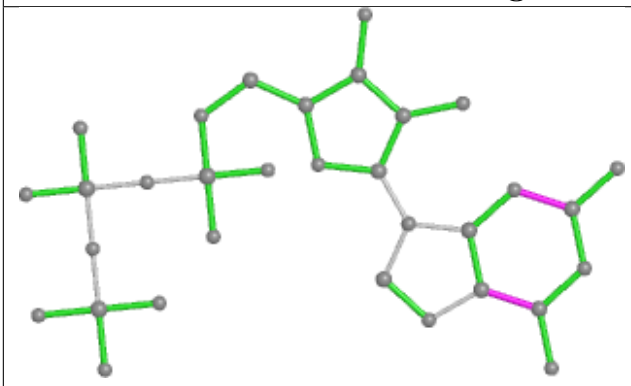


Rings

Ligand GTP NK 501



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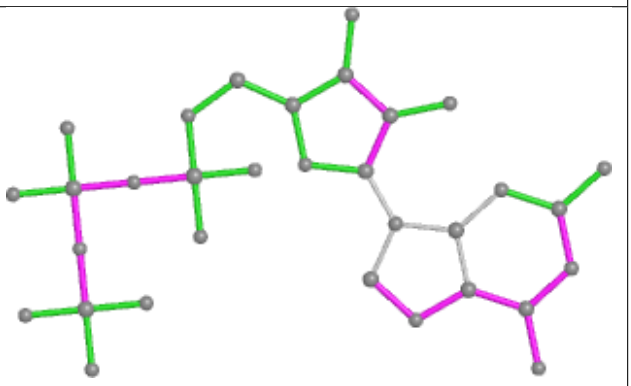
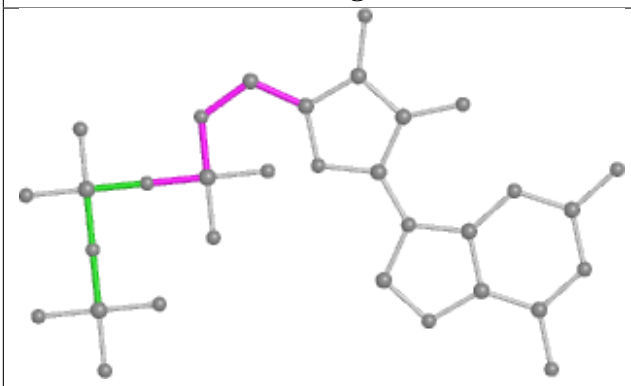


Bond angles



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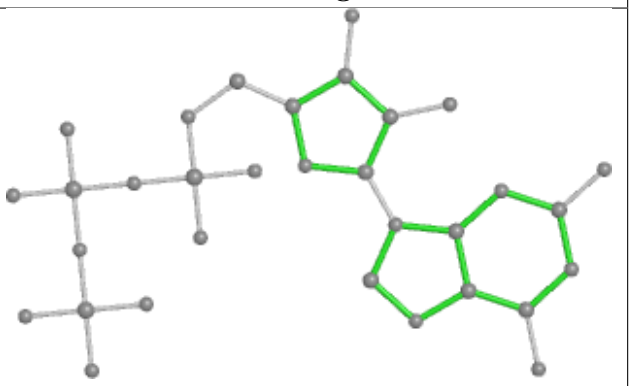
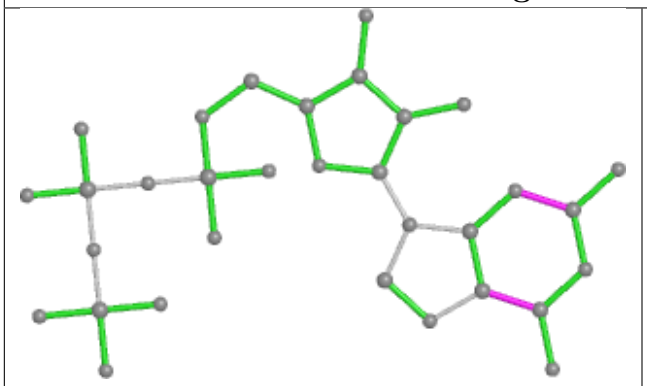


Rings

Ligand GTP EE 501



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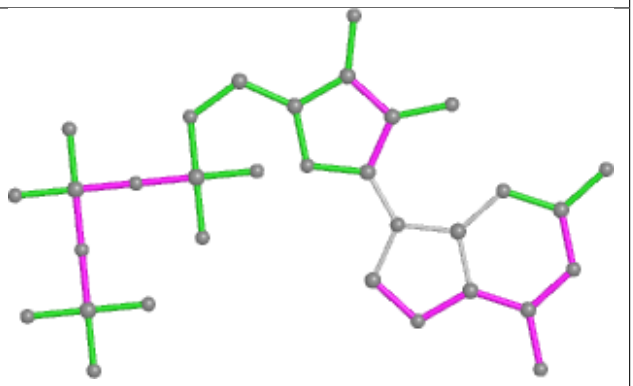

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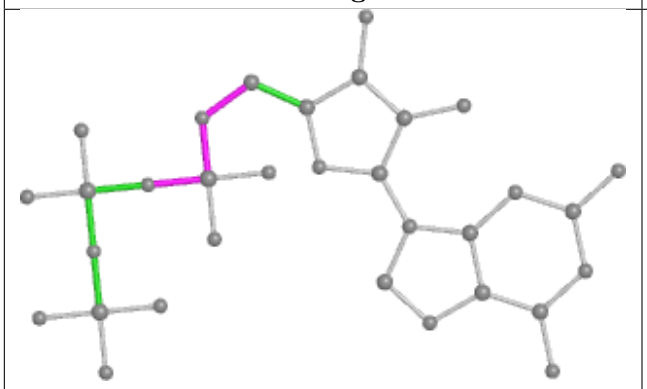

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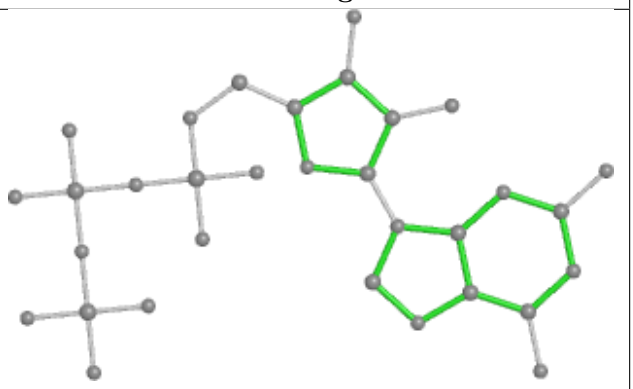
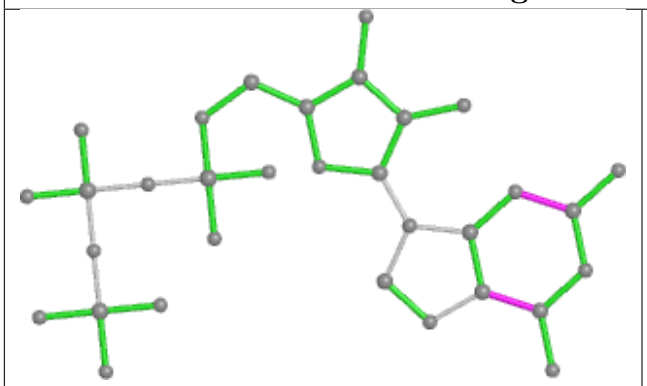


Rings

Ligand GTP RC 501



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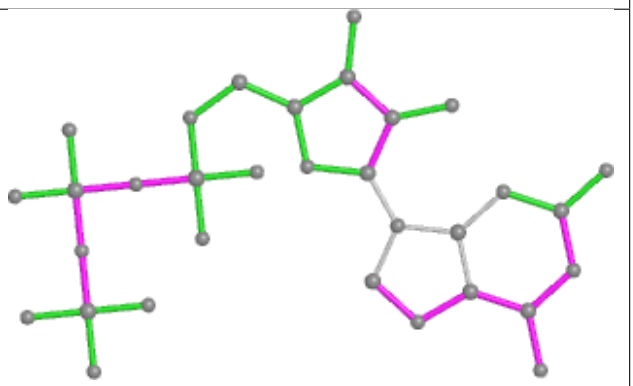

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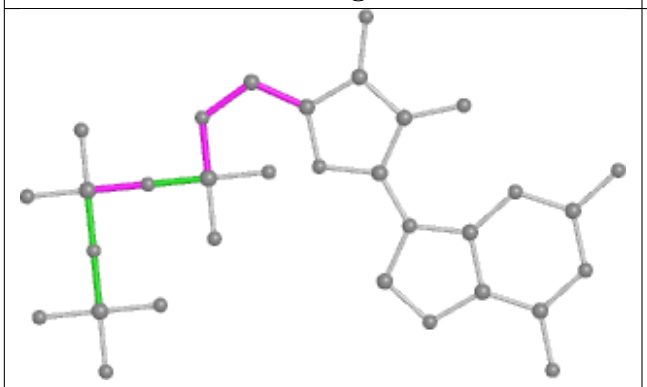

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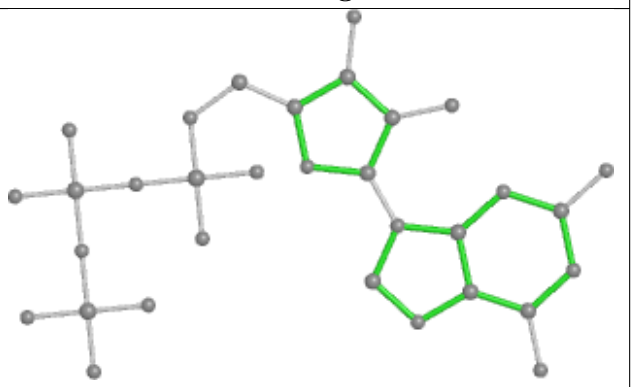
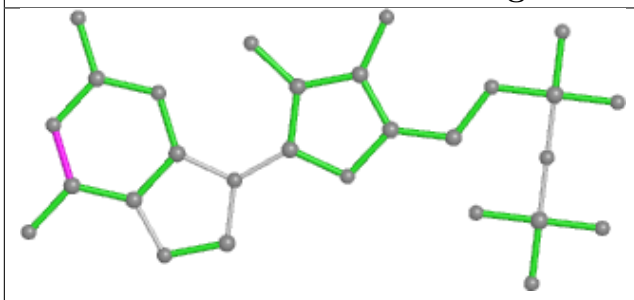


Rings

Ligand GDP ND 502



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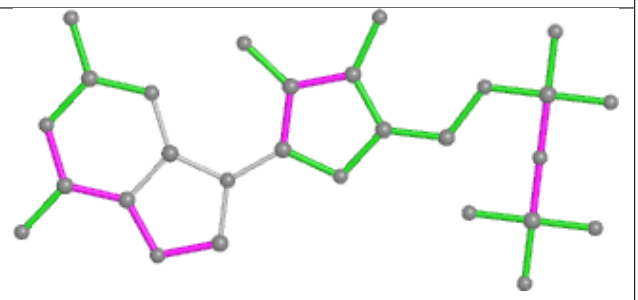

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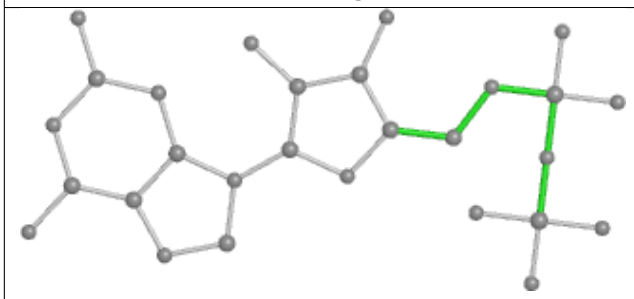

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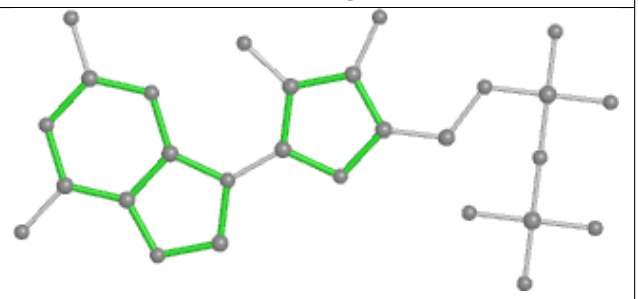
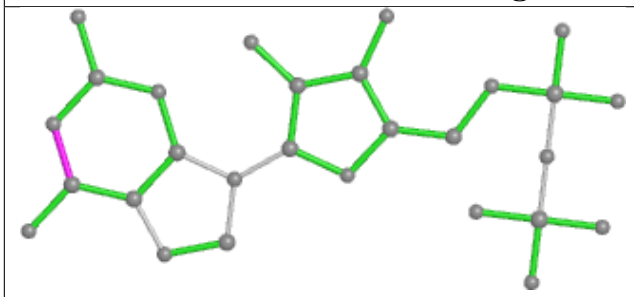


Rings

Ligand GDP EB 502



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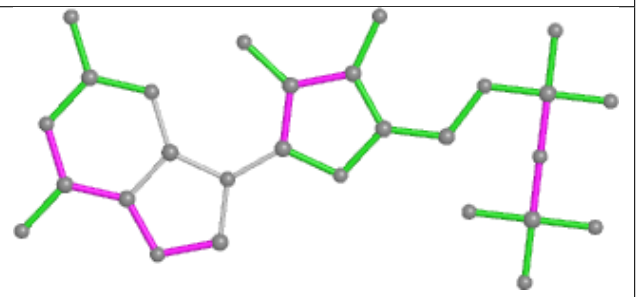

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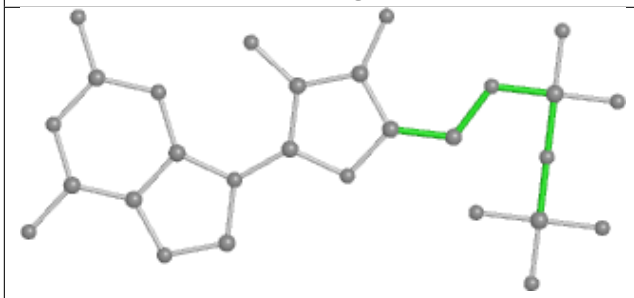

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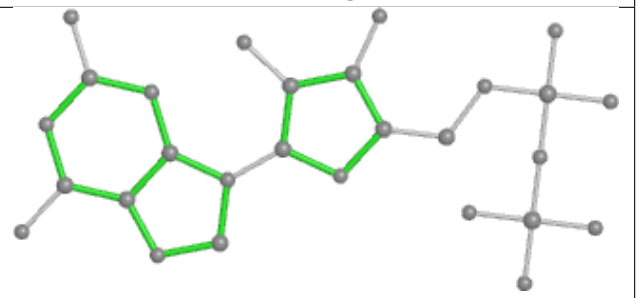
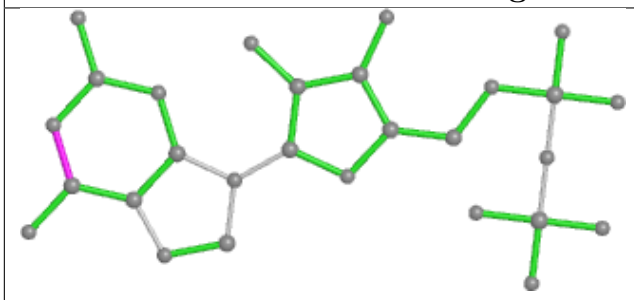


Rings

Ligand GDP PH 502



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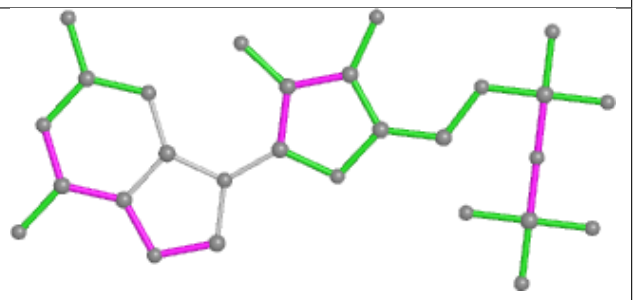

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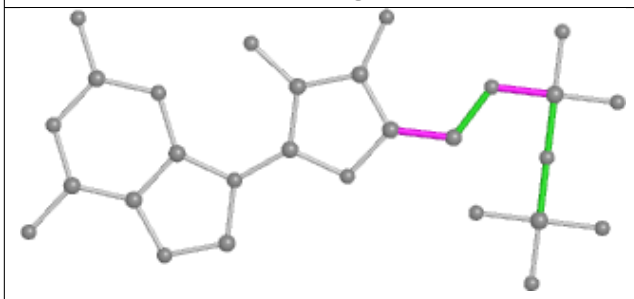

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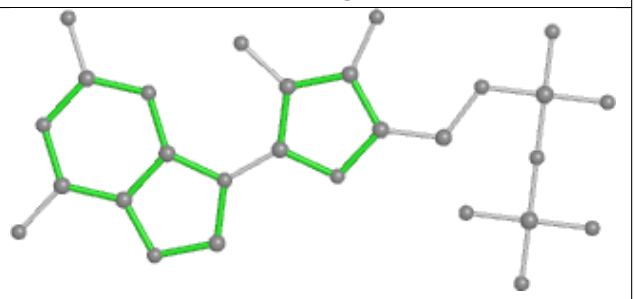
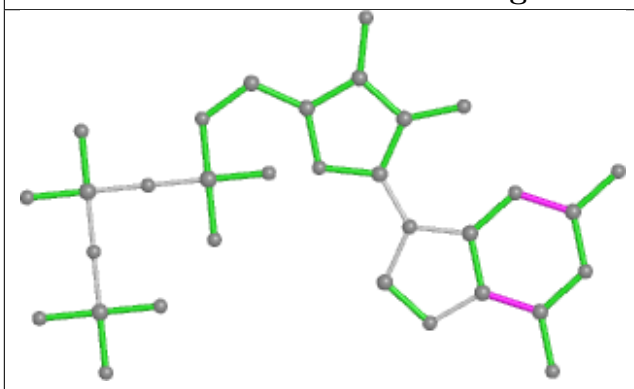
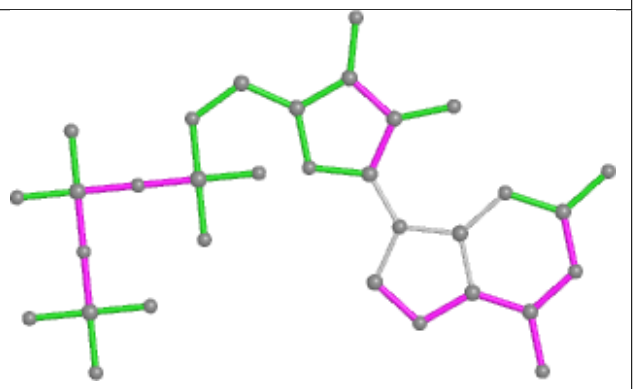


Rings

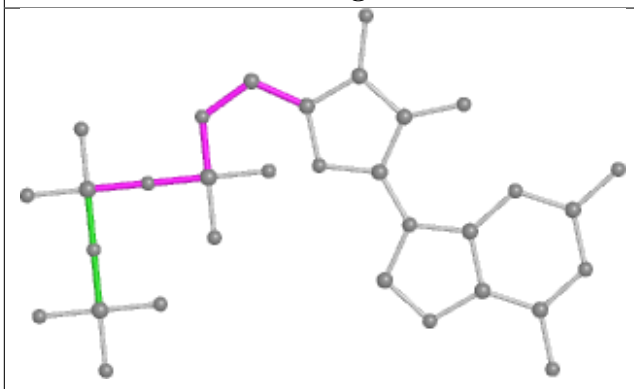
Ligand GTP VG 501



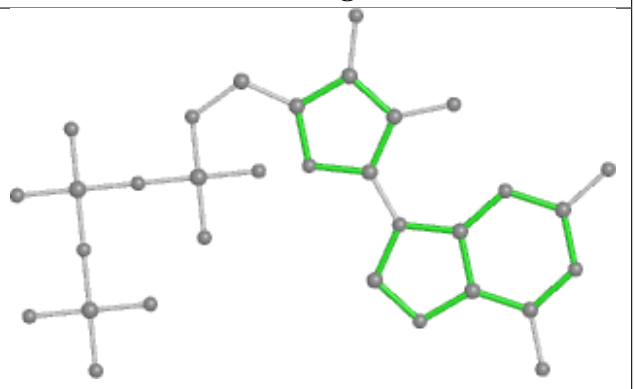
Bond lengths



Bond angles

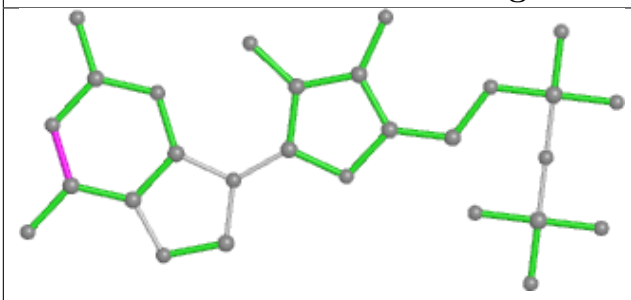


Torsions



Rings

Ligand GDP BB 502



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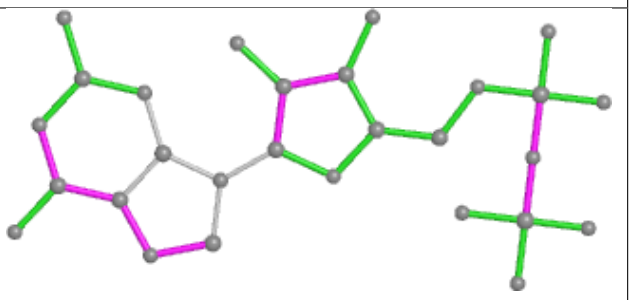
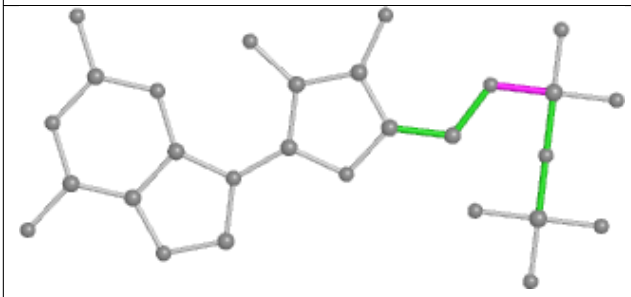


Bond angles



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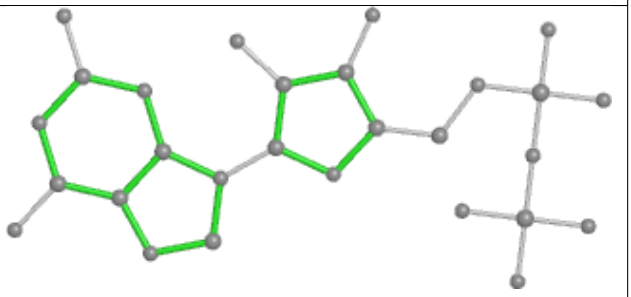
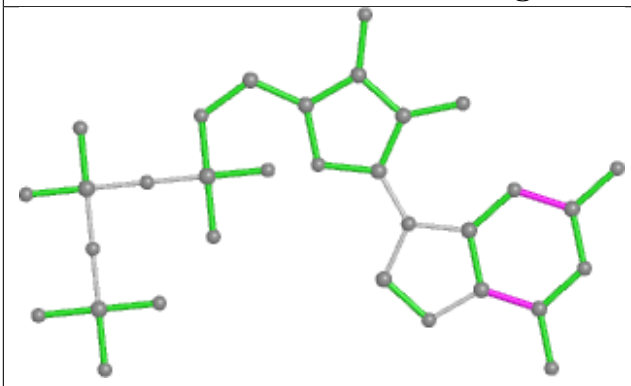


Rings

Ligand GTP SE 501



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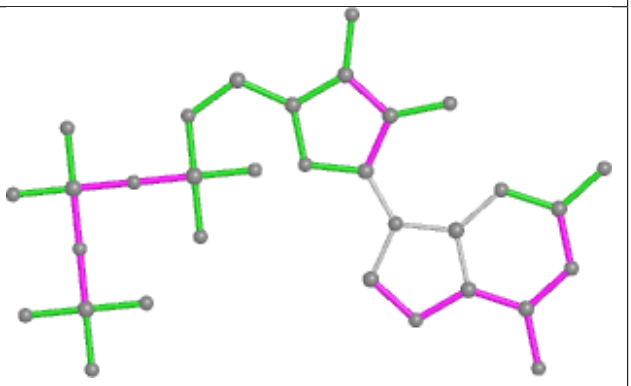
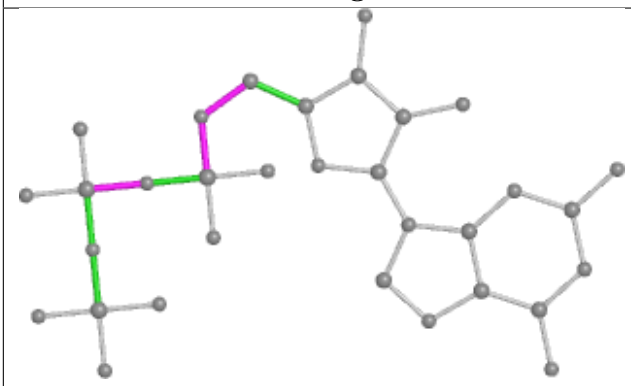
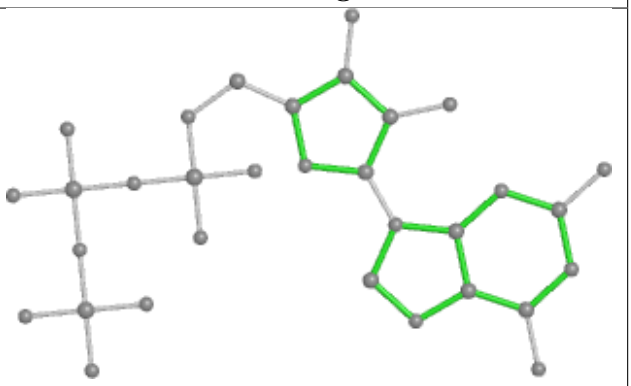


Bond angles

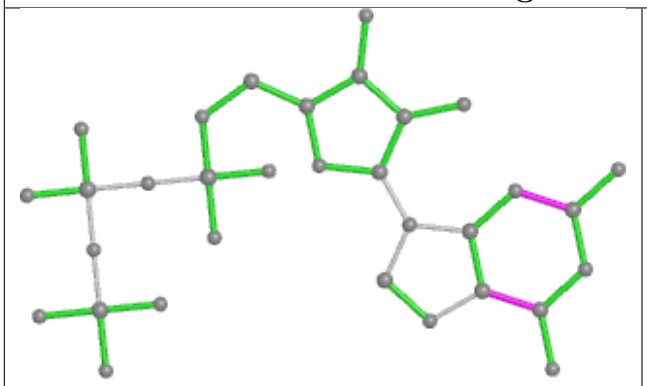


Torsions



Rings

Ligand GTP UI 501



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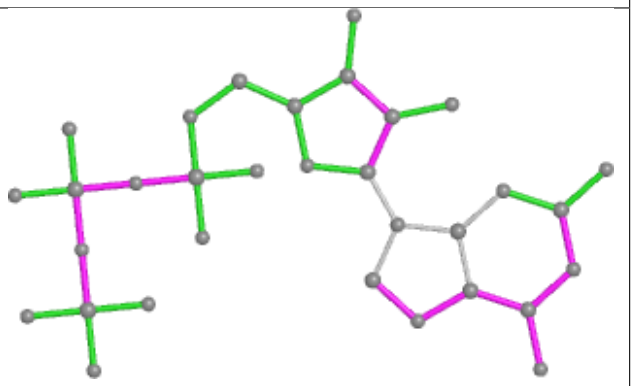
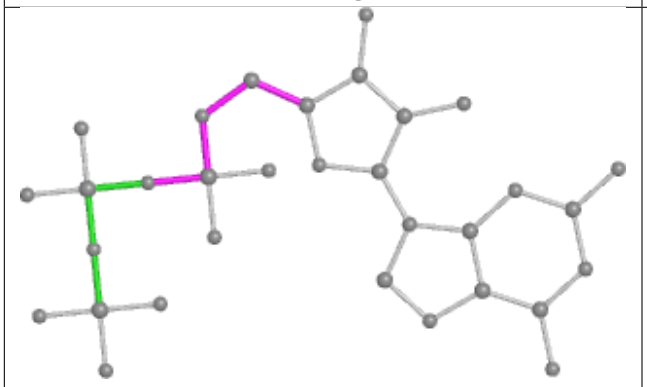
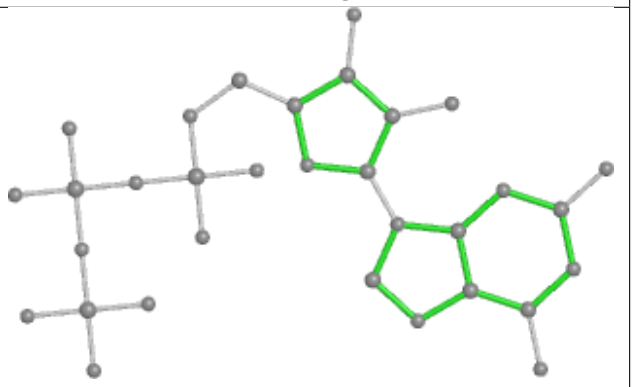


Bond angles

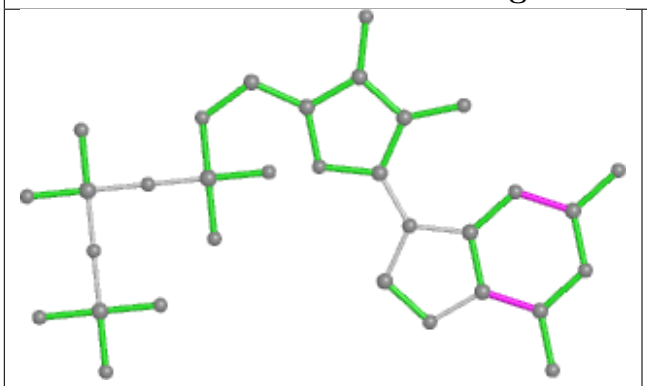


Torsions

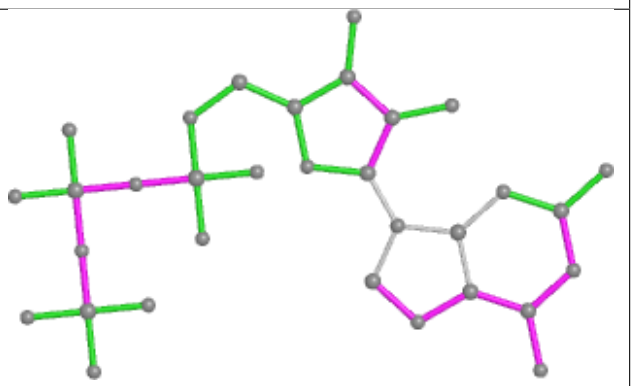


Rings

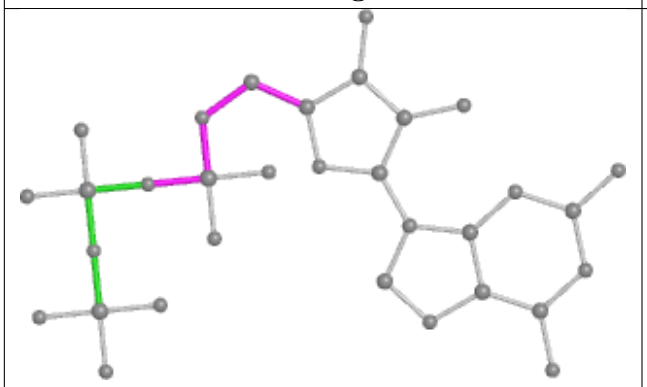
Ligand GTP UO 501



Bond lengths



Bond angles



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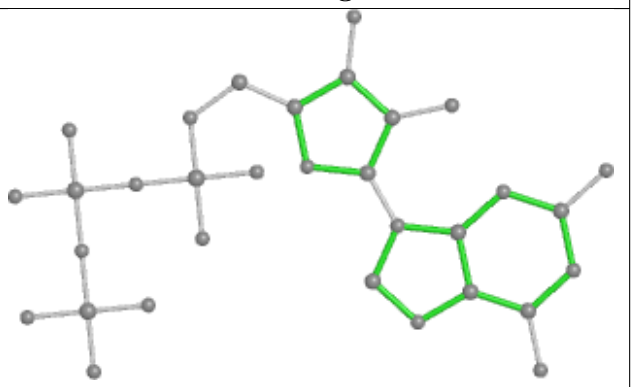
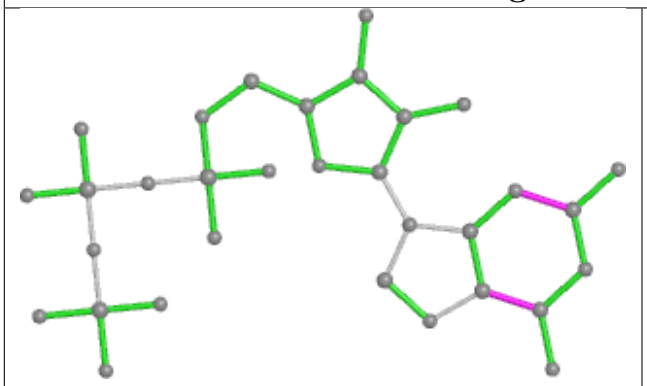


Rings

Ligand GTP UK 501



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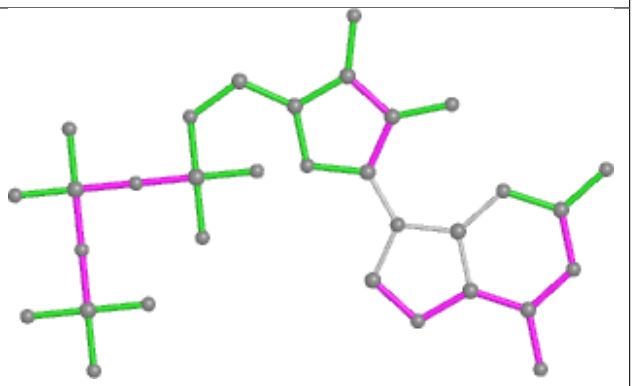

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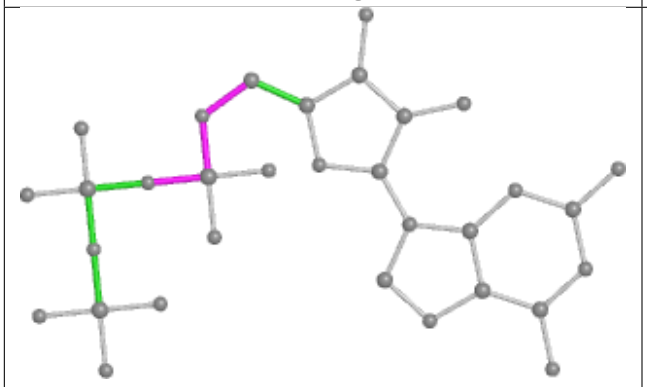

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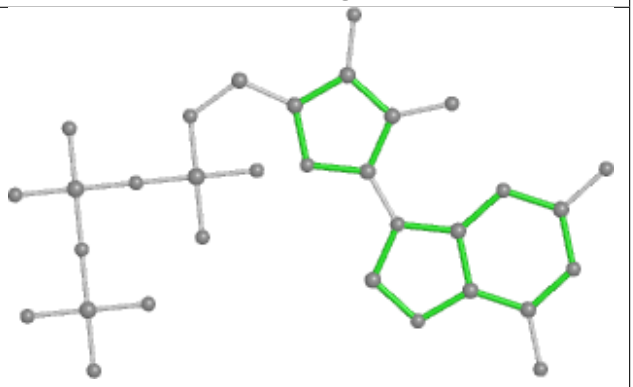
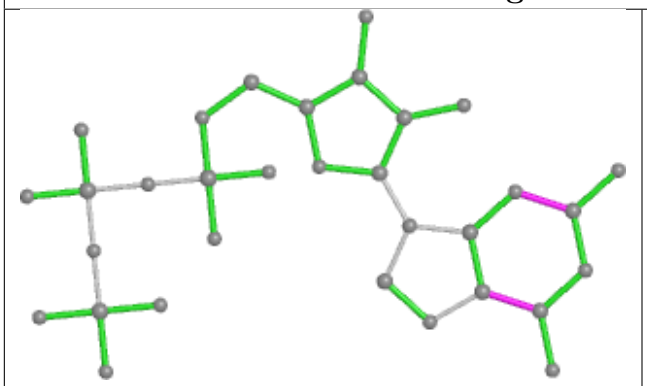
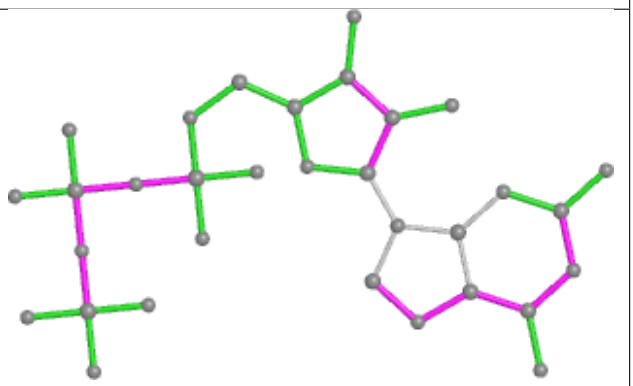


Rings

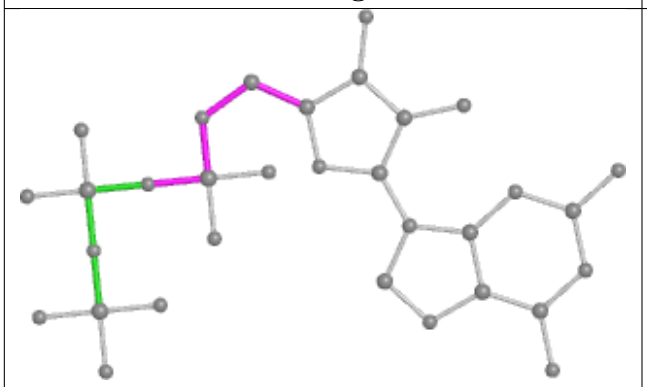
Ligand GTP WE 501



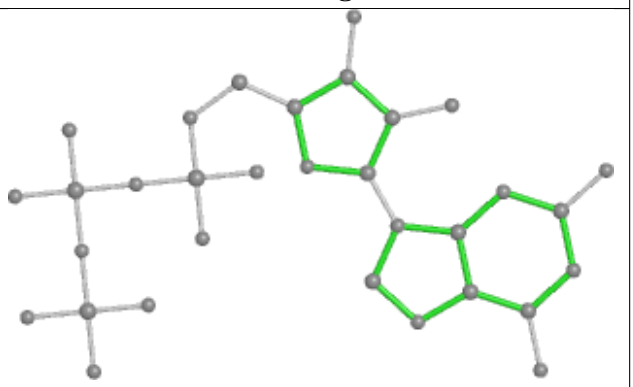
Bond lengths



Bond angles

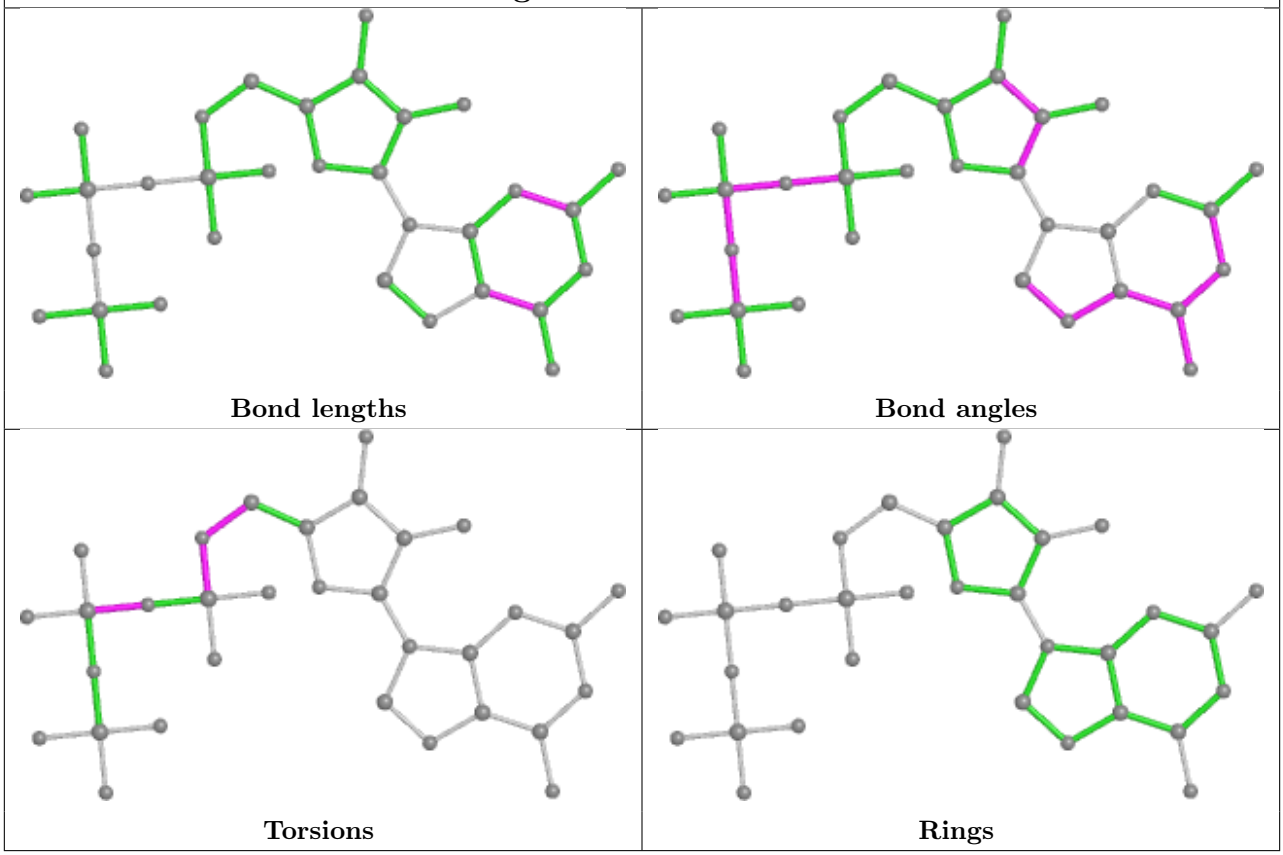


Torsions

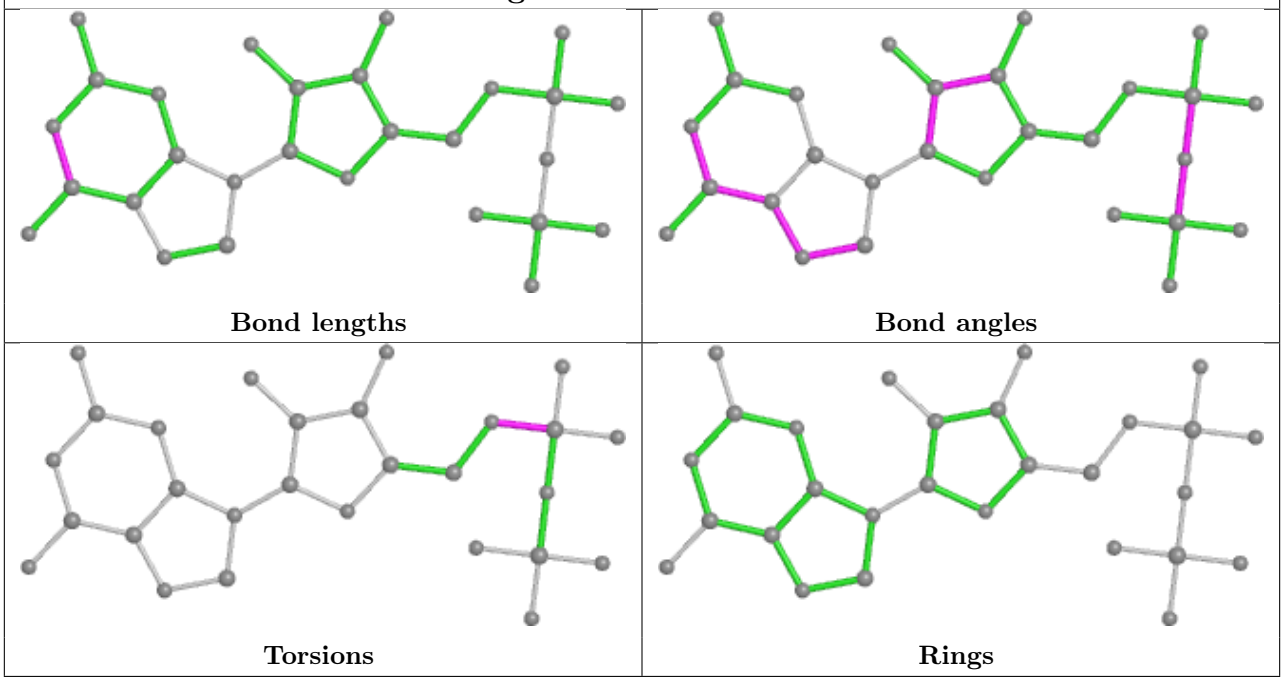


Rings

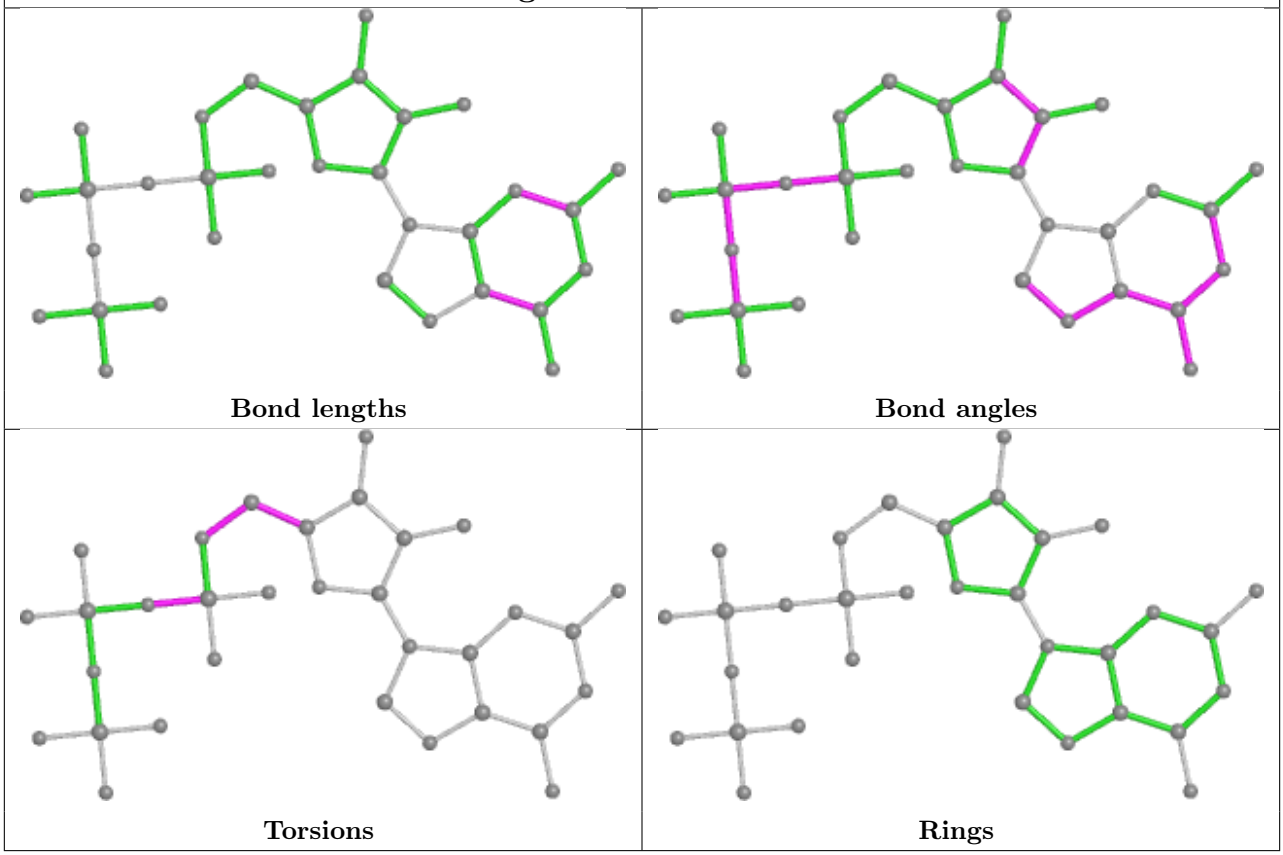
Ligand GTP JK 501



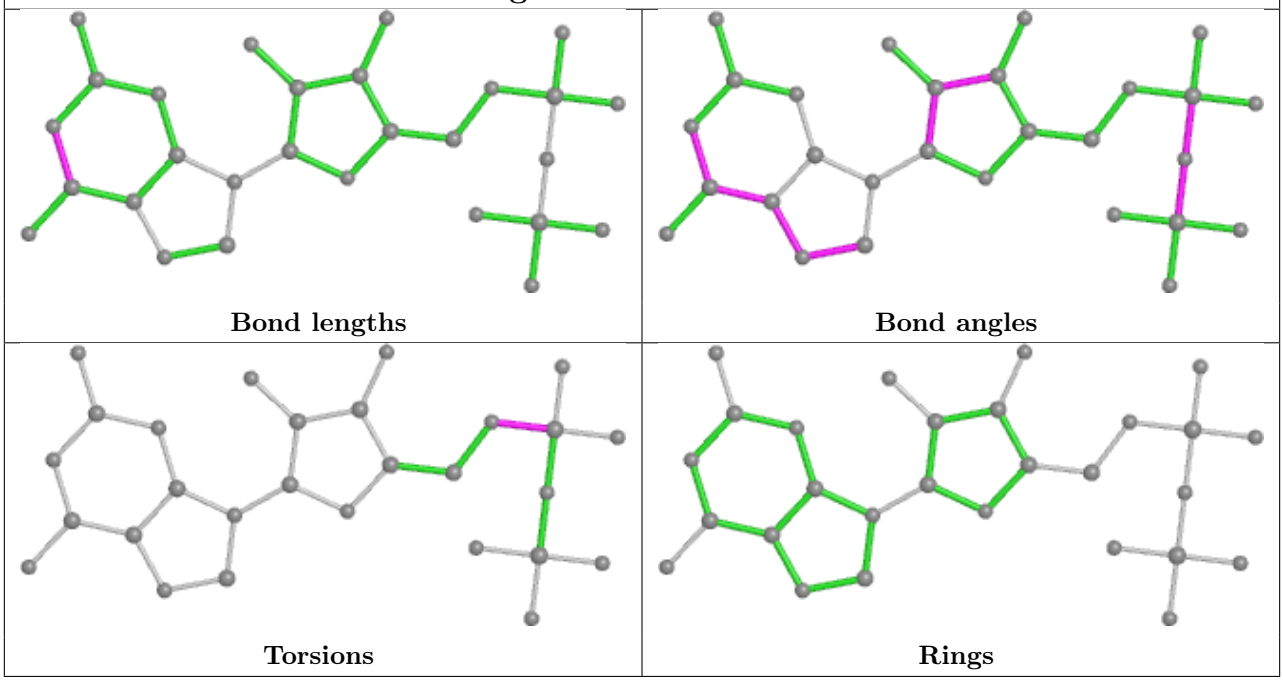
Ligand GDP DH 502



Ligand GTP IE 501



Ligand GDP EN 502



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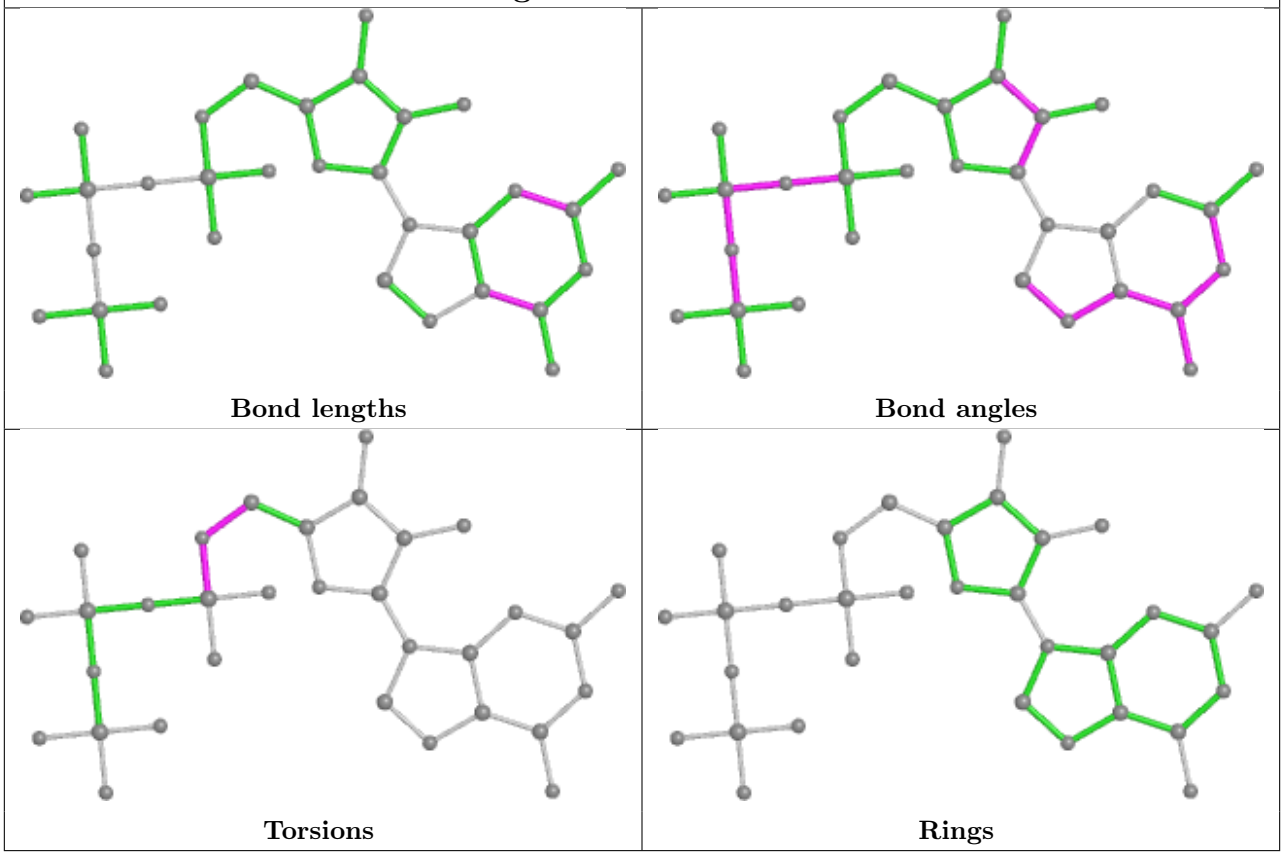
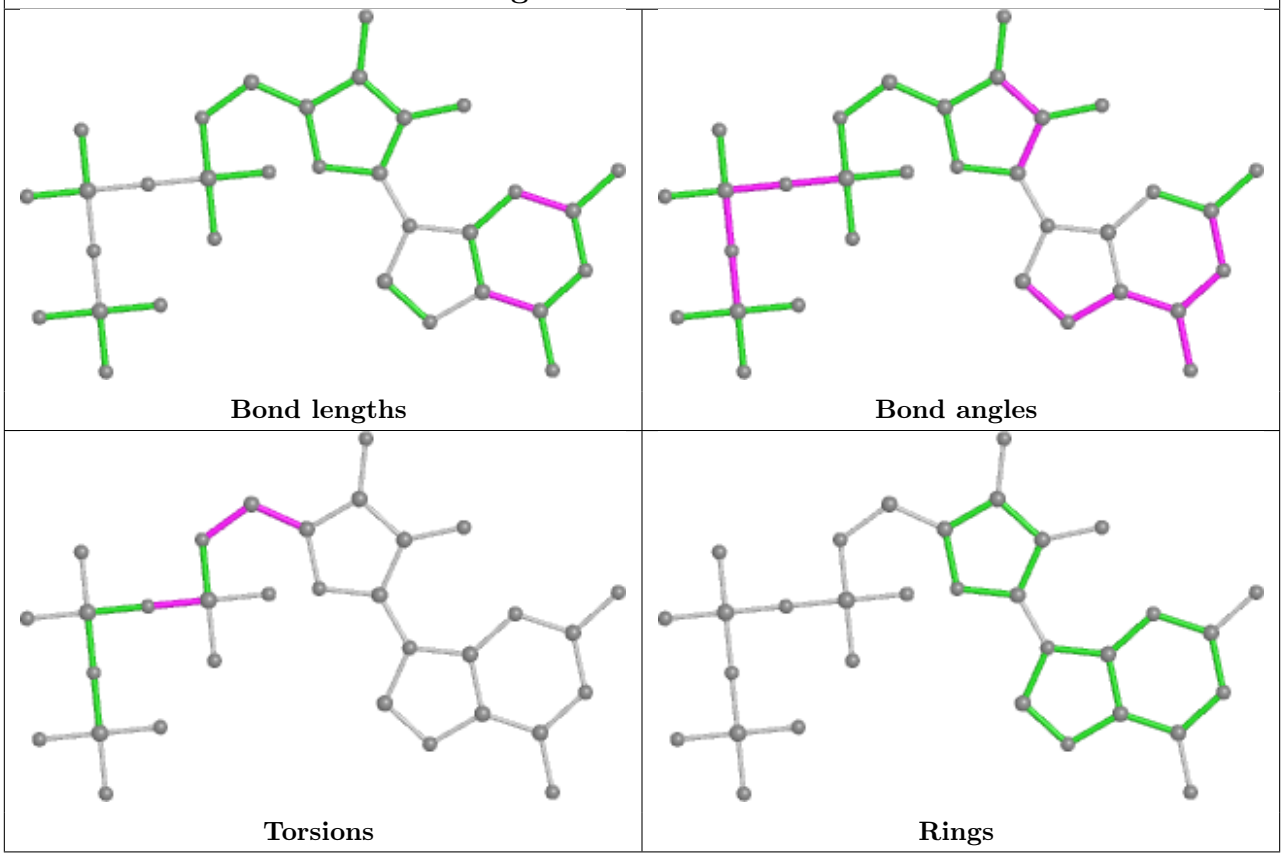
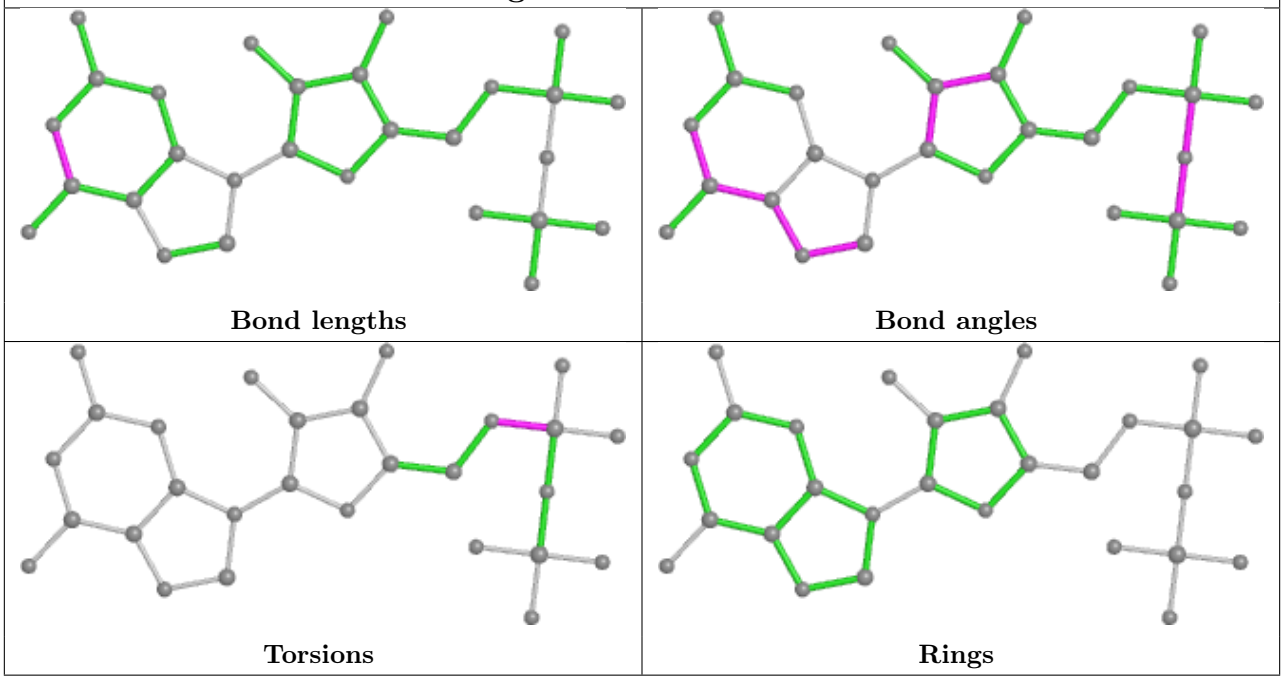


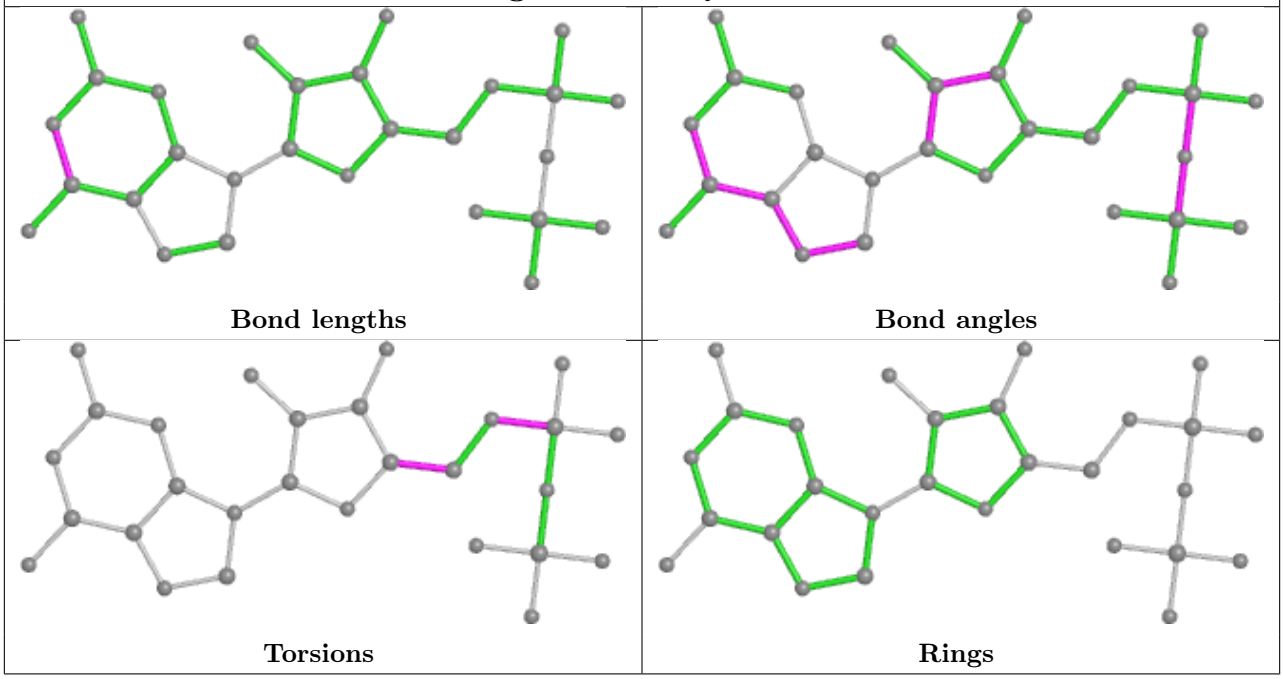
Ligand GTP UE 501



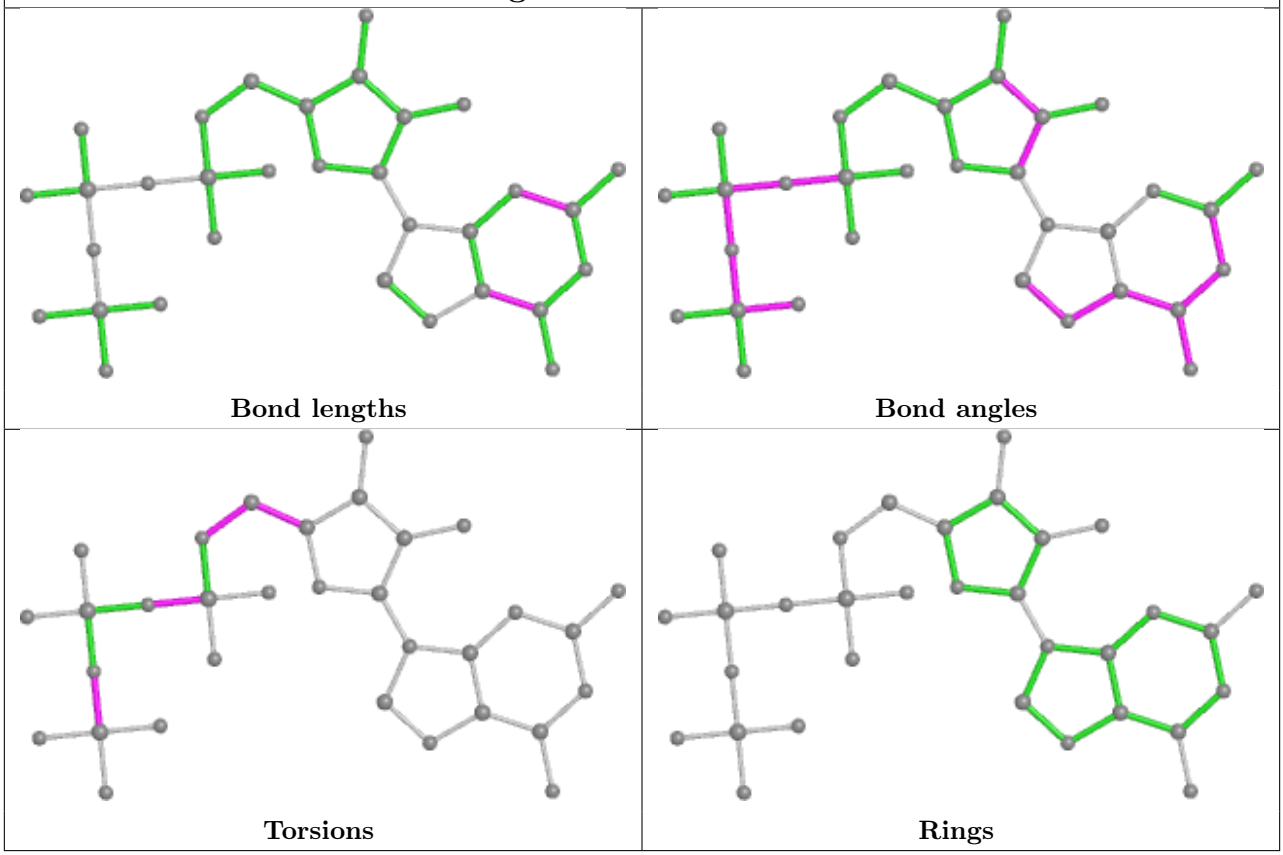
Ligand GDP HD 502



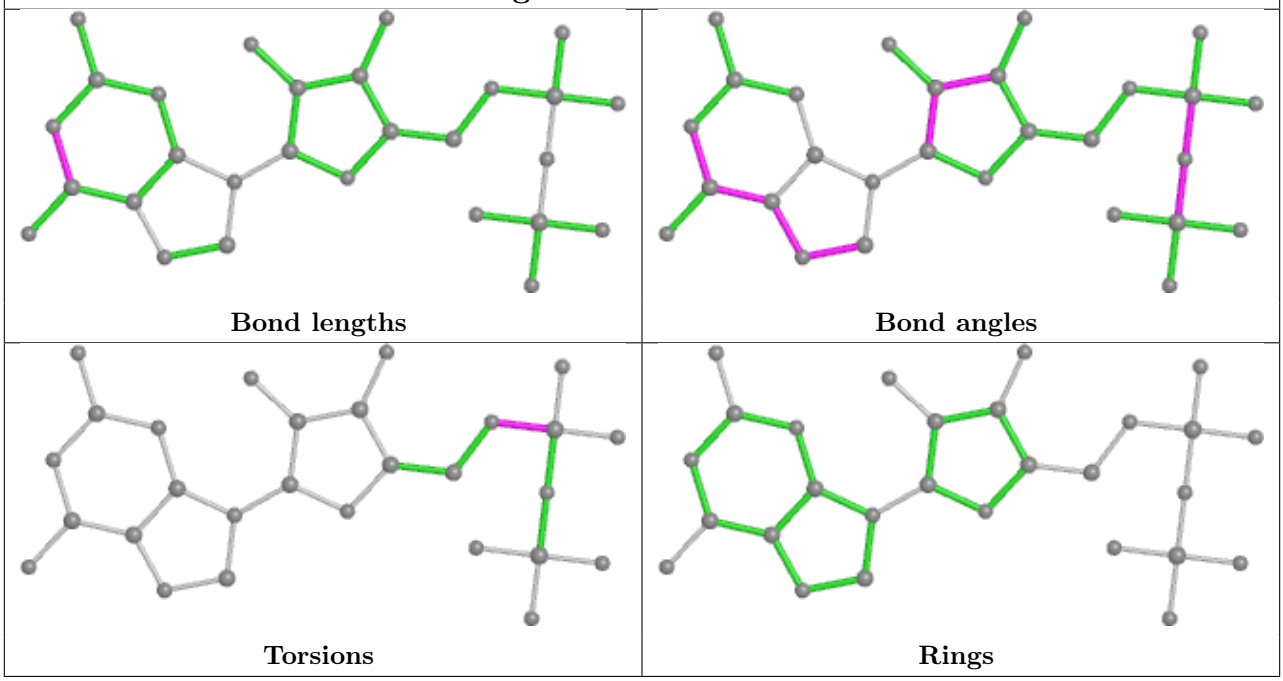
Ligand GDP QH 502



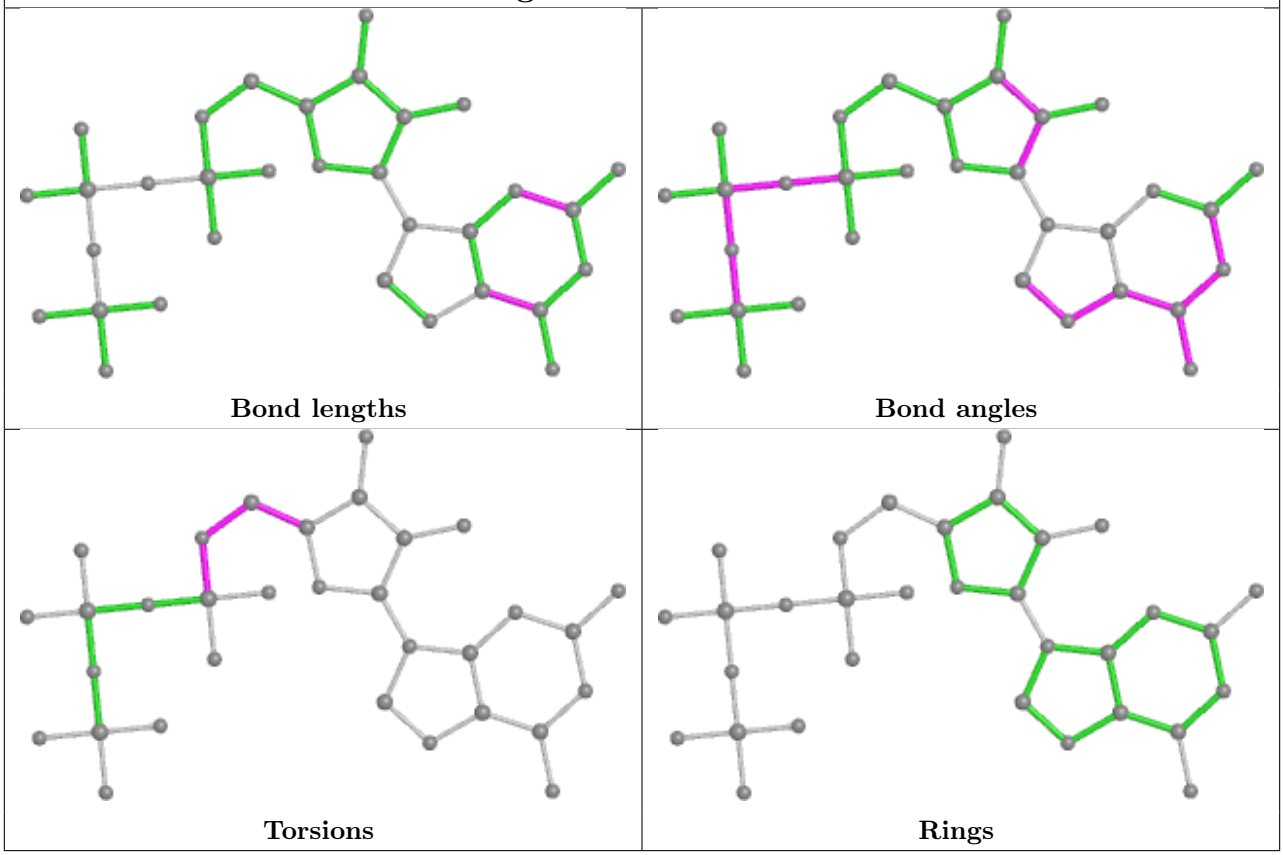
Ligand GTP NG 501



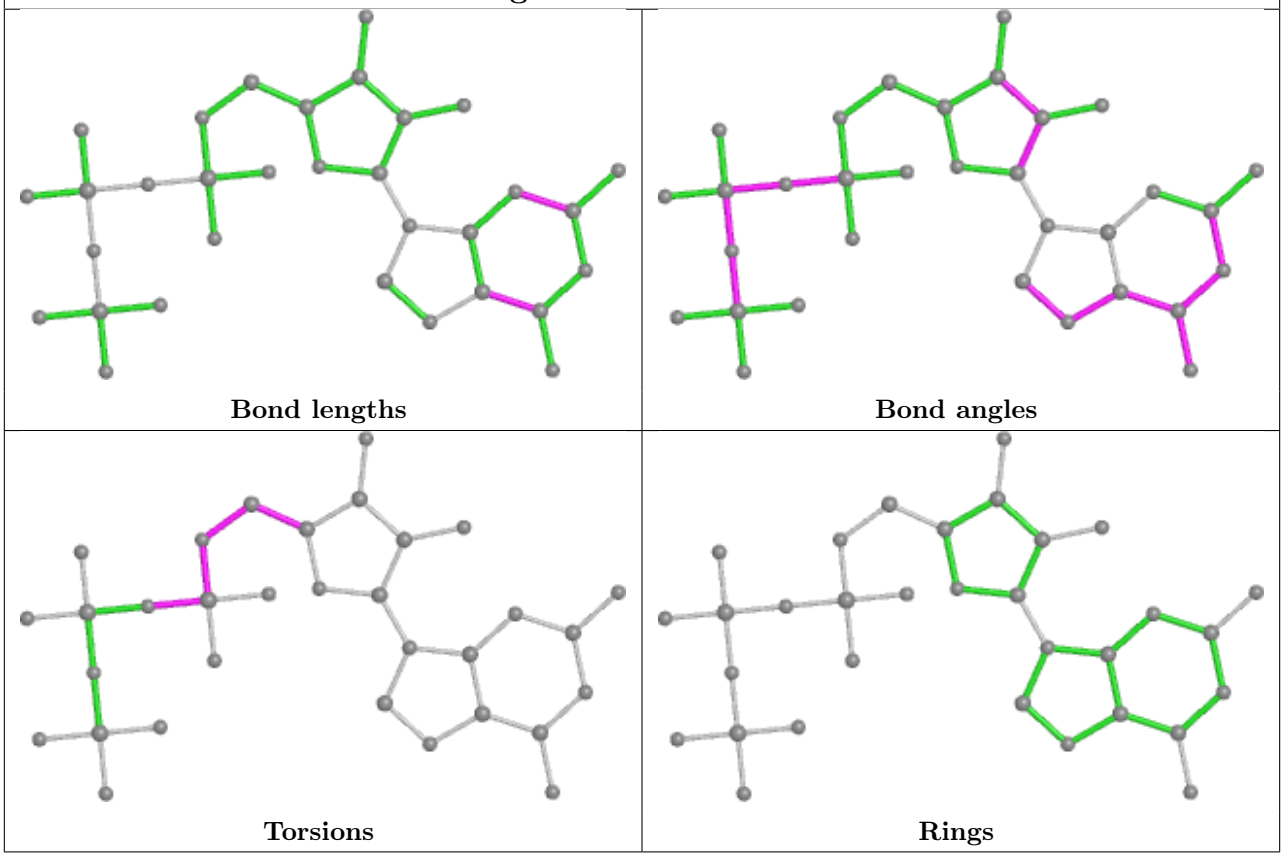
Ligand GDP VJ 502



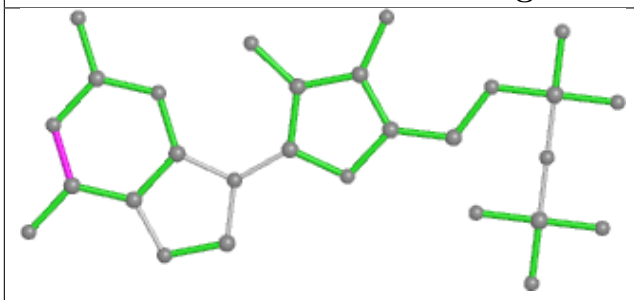
Ligand GTP RI 501



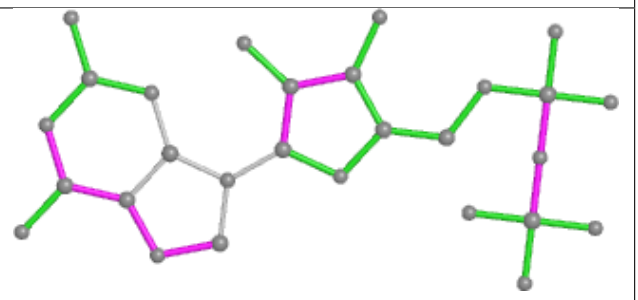
Ligand GTP TK 501



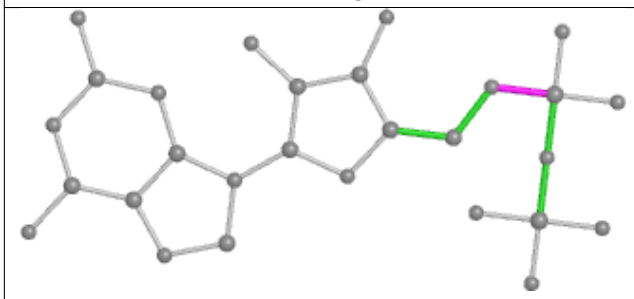
Ligand GDP IB 502



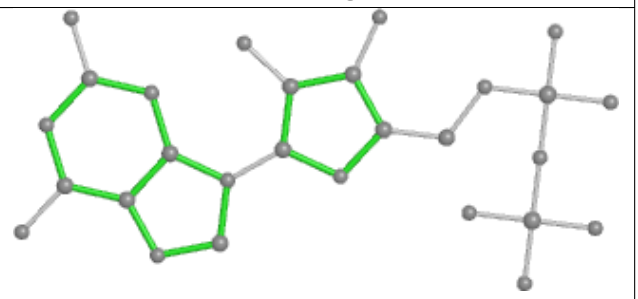
Bond lengths



Bond angles

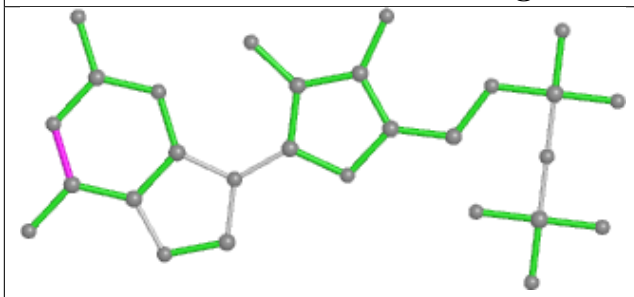


Torsions



Rings

Ligand GDP FJ 502



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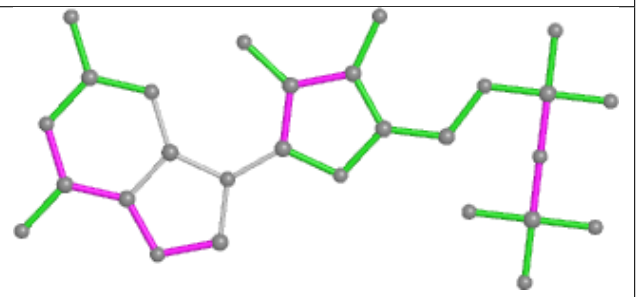
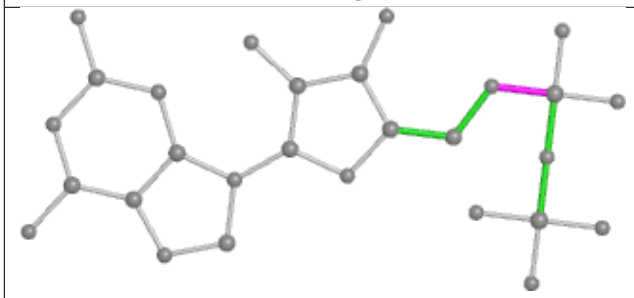


Bond angles



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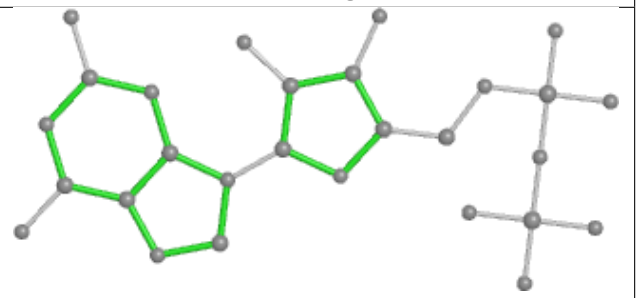
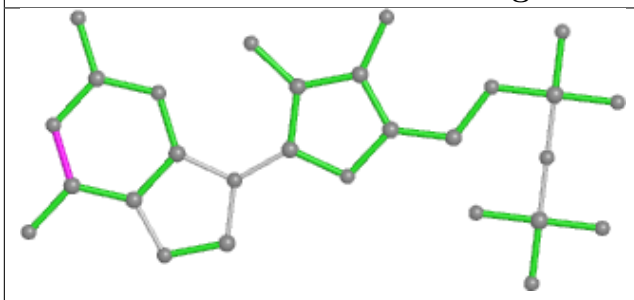
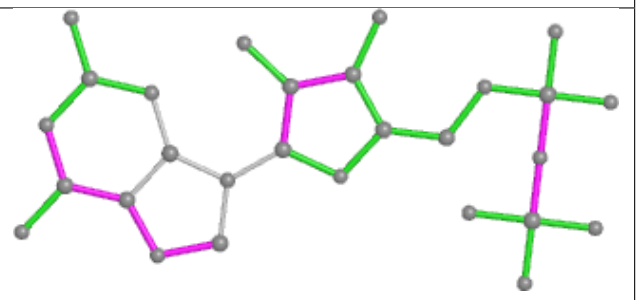


Rings

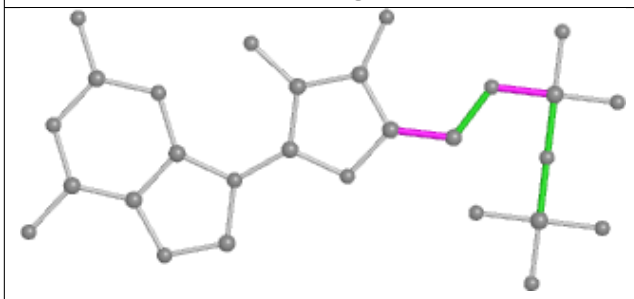
Ligand GDP LB 502



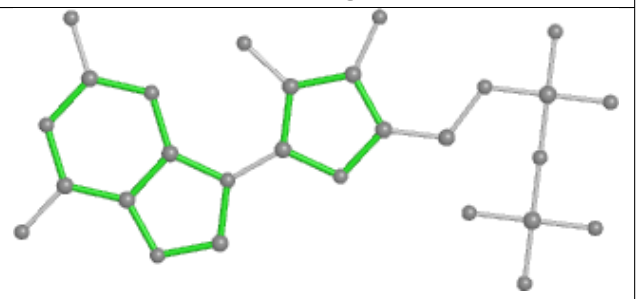
Bond lengths



Bond angles

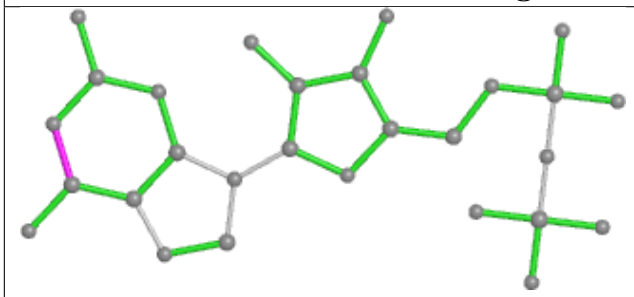


Torsions

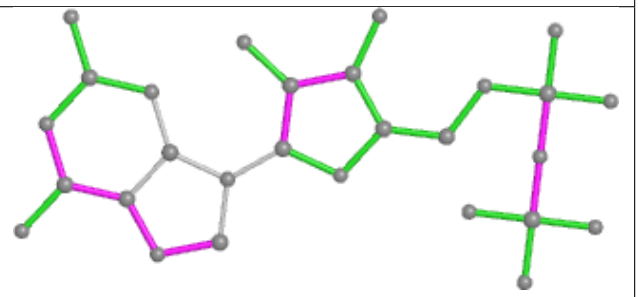


Rings

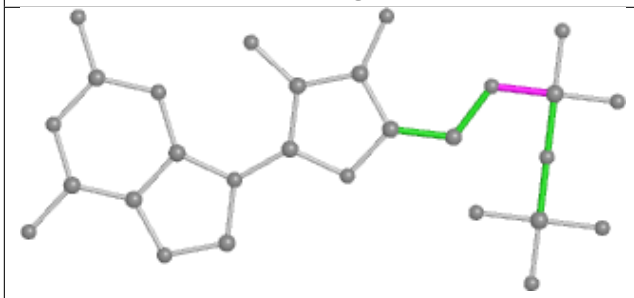
Ligand GDP ID 502



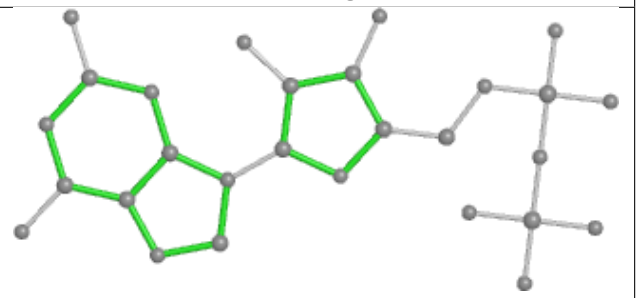
Bond lengths



Bond angles

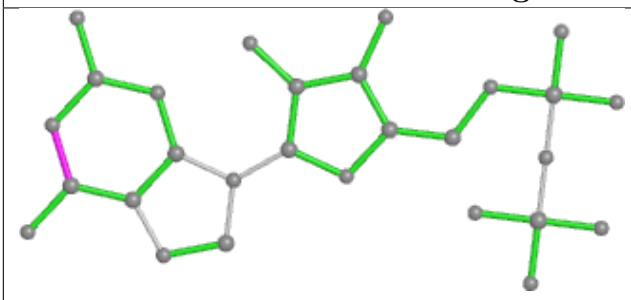


Torsions



Rings

Ligand GDP FL 502



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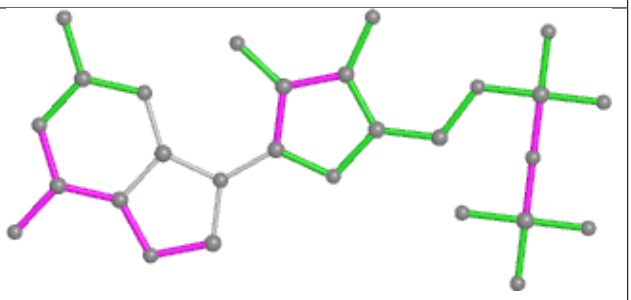
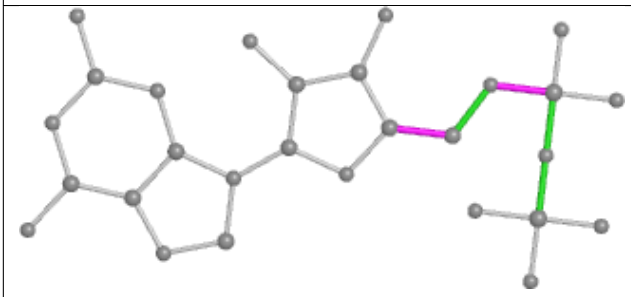


Bond angles



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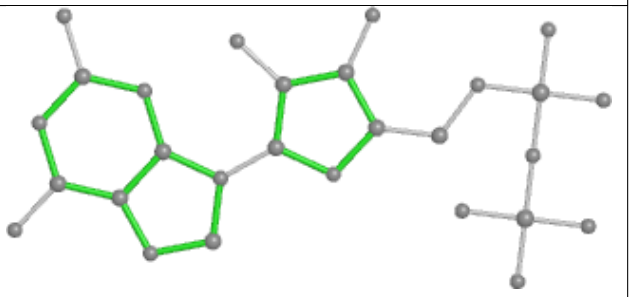
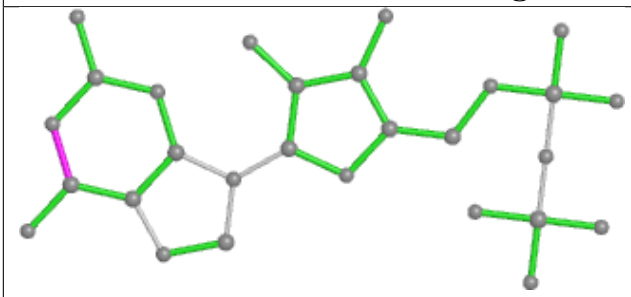


Rings

Ligand GDP JN 502



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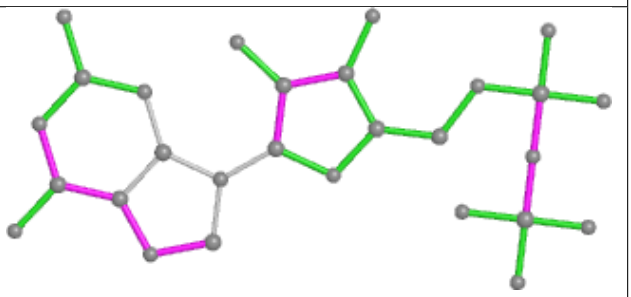
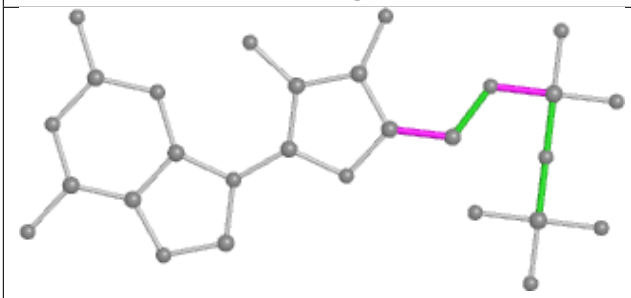
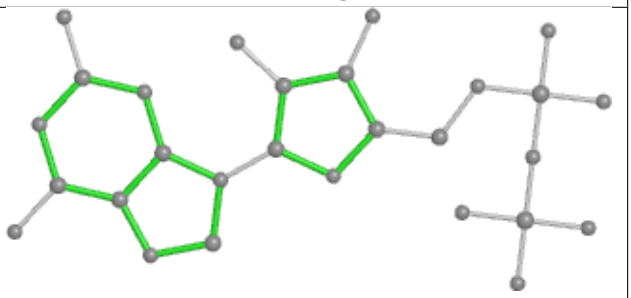


Bond angles

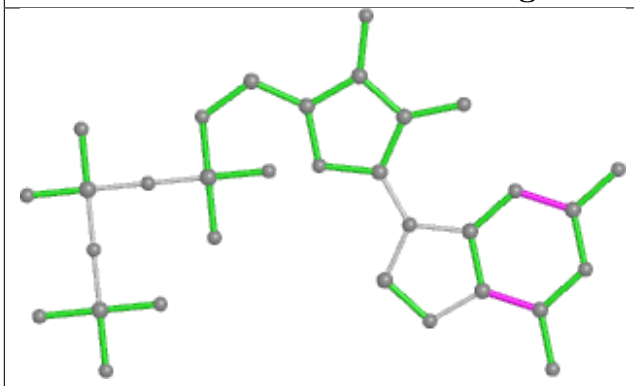


Torsions



Rings

Ligand GTP FI 501



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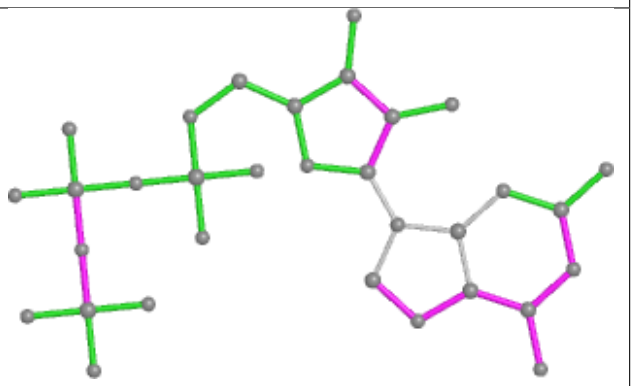

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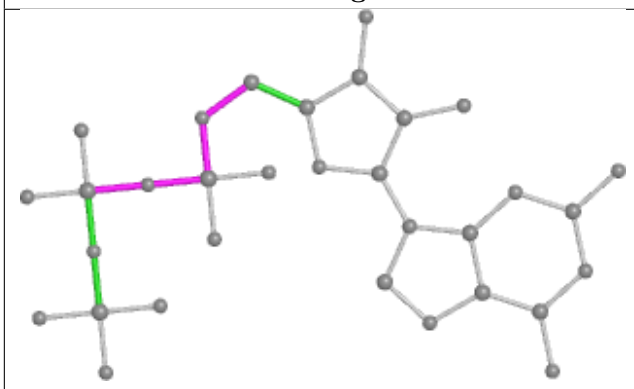

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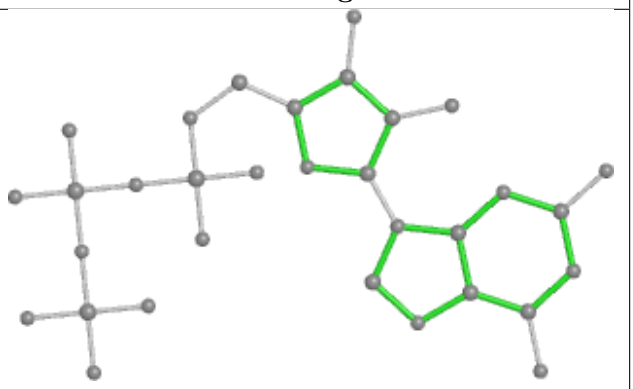
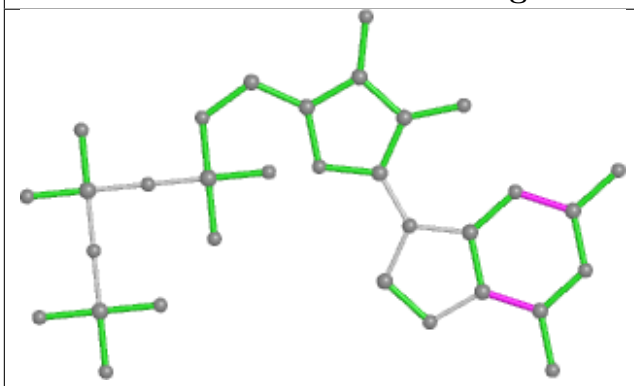


Rings

Ligand GTP RG 501



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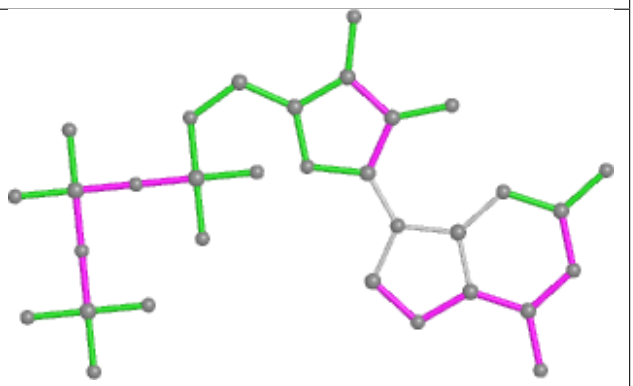

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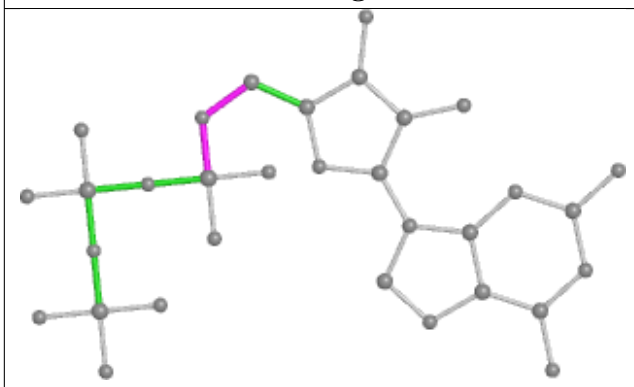

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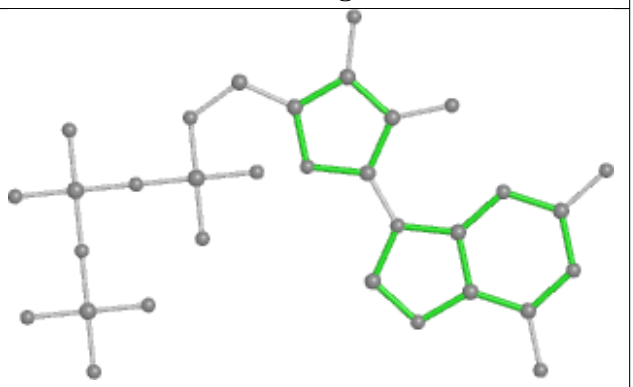
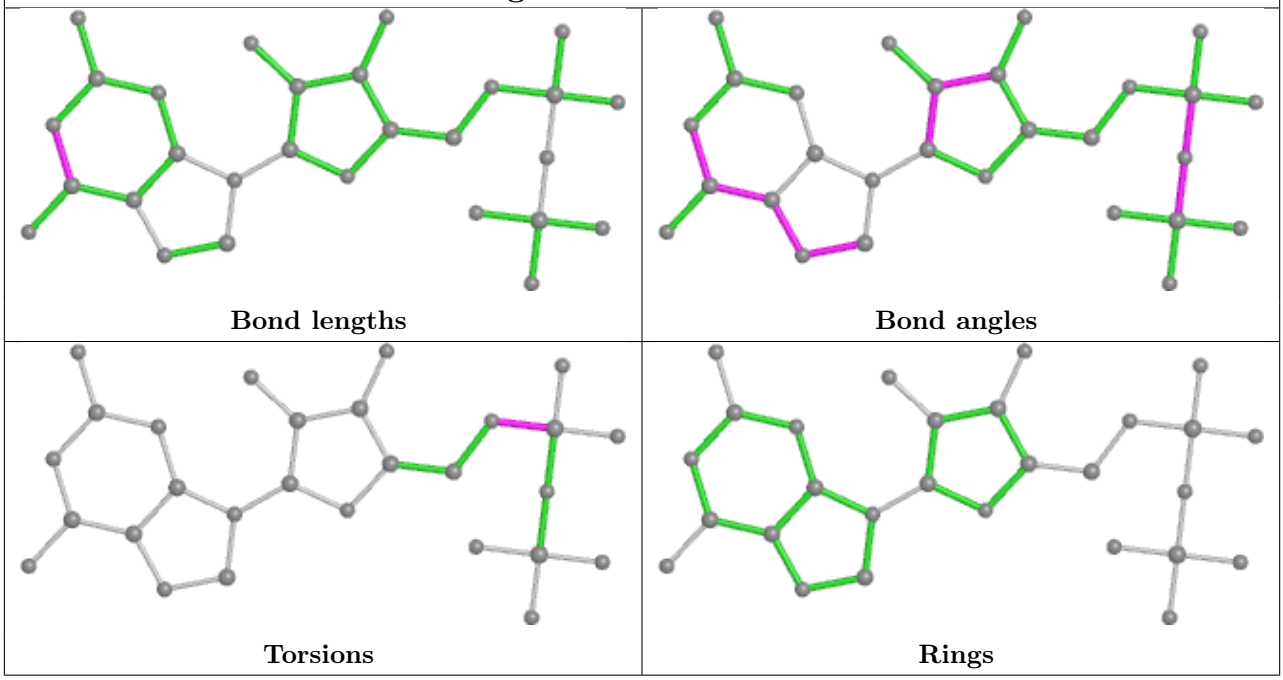


Rings

Ligand GDP HN 502



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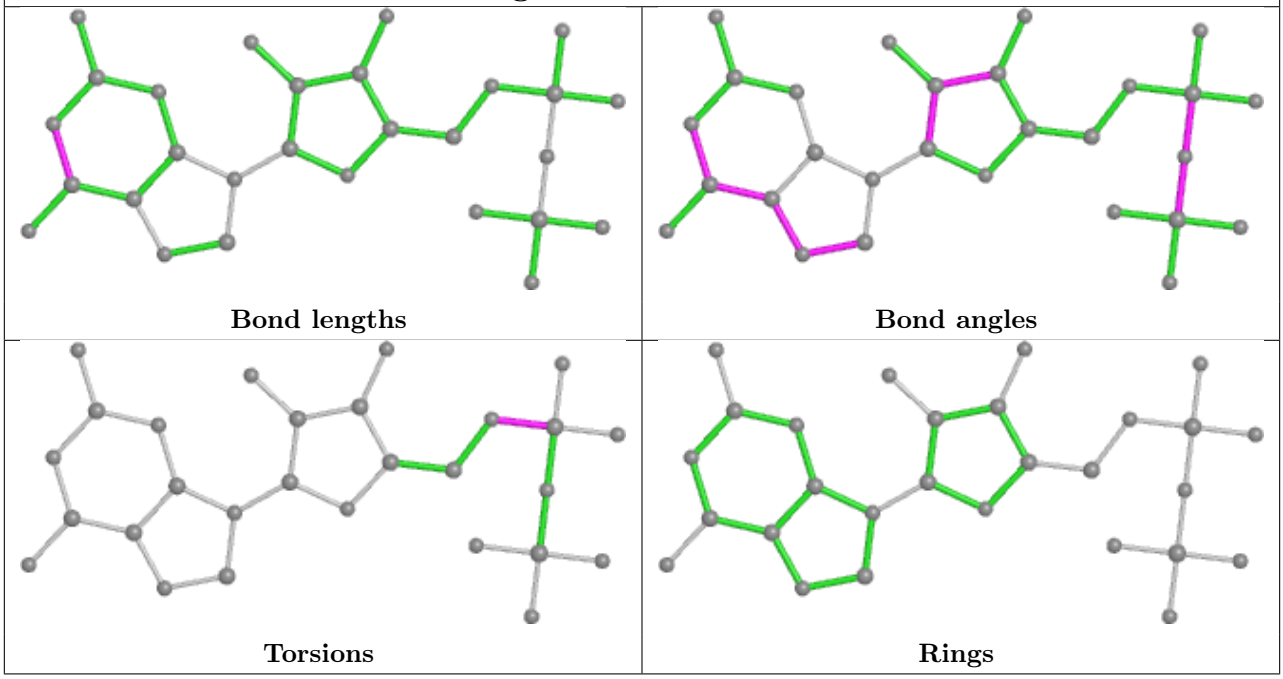
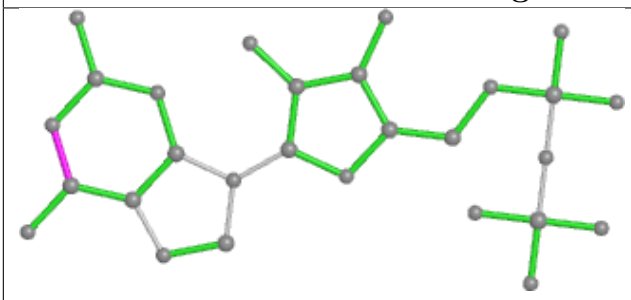


Ligand GDP RJ 502



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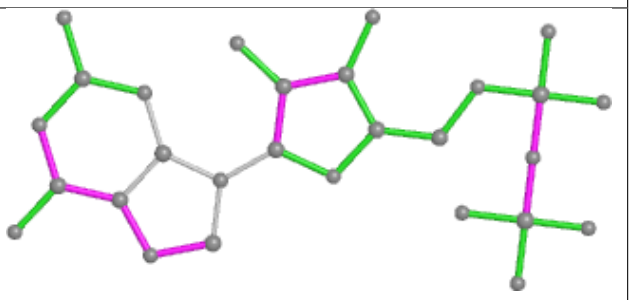

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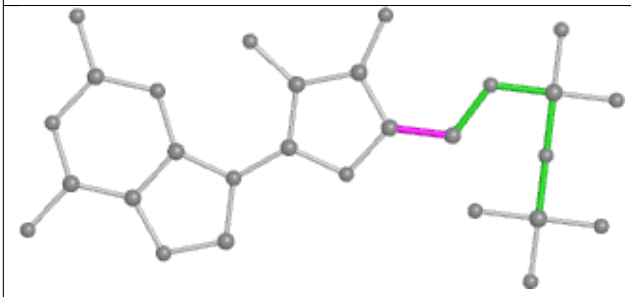

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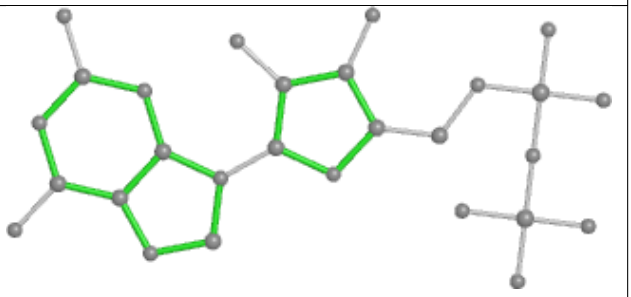
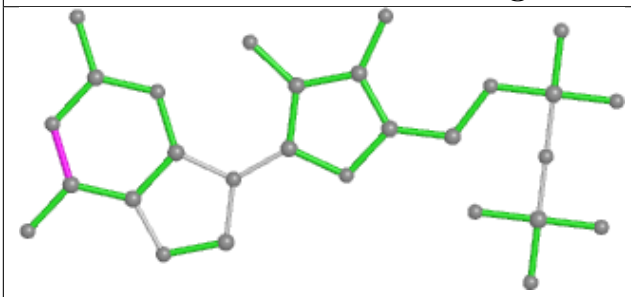


Rings

Ligand GDP NF 502



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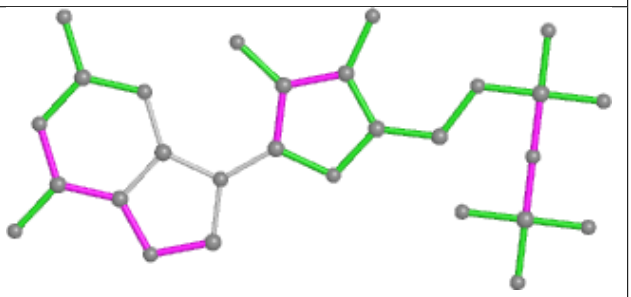

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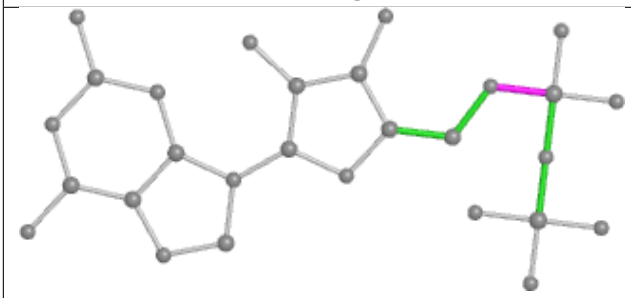

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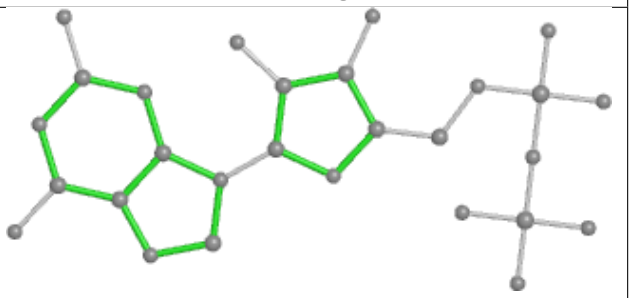
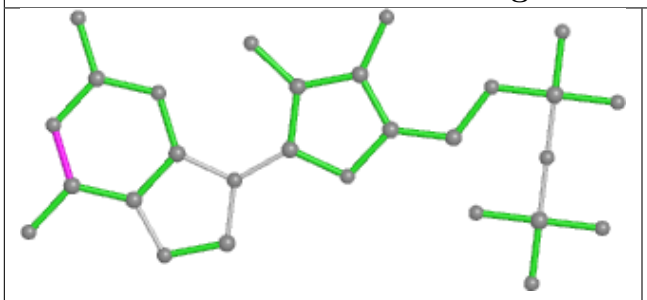


Rings

Ligand GDP VL 502



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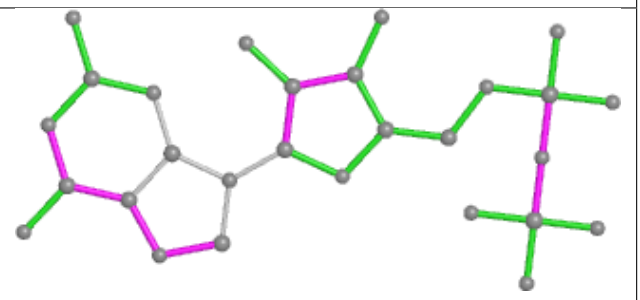

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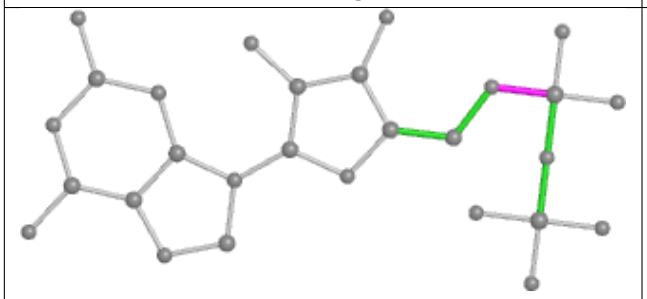

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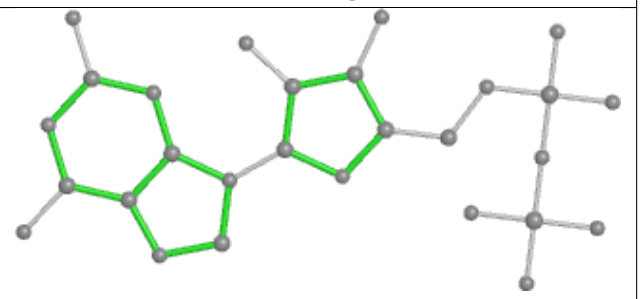
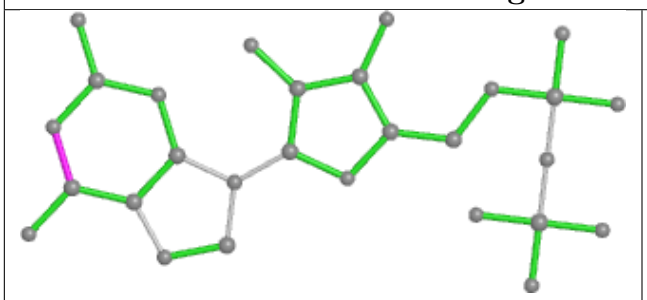


Rings

Ligand GDP KD 502



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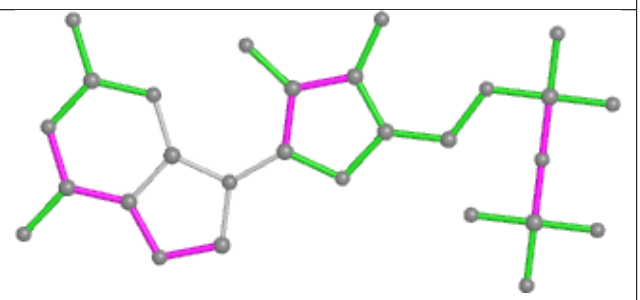

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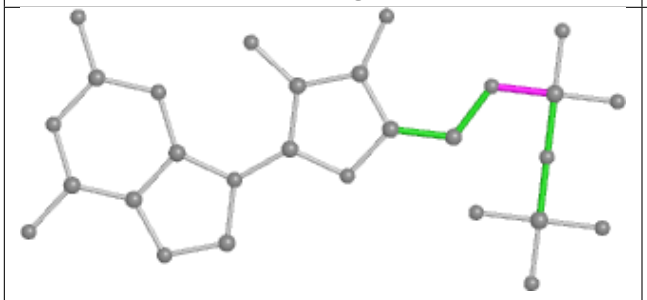

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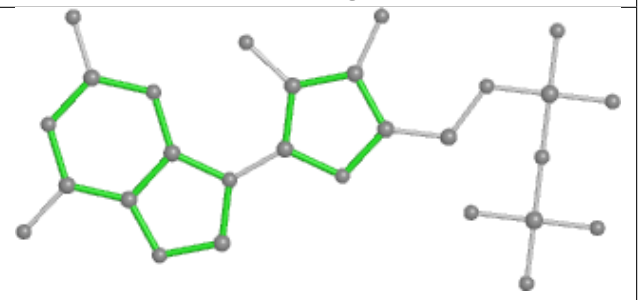
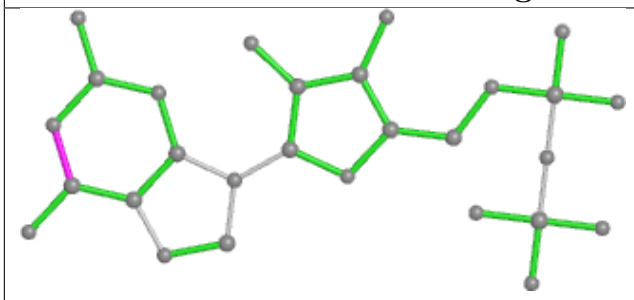


Rings

Ligand GDP IN 502



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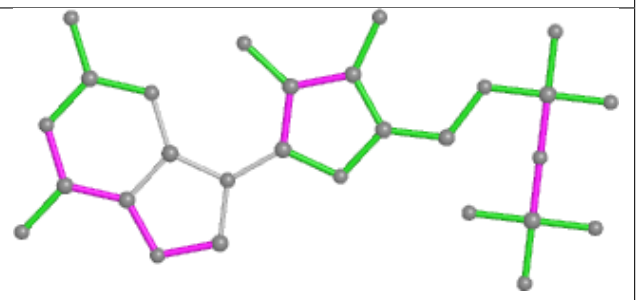

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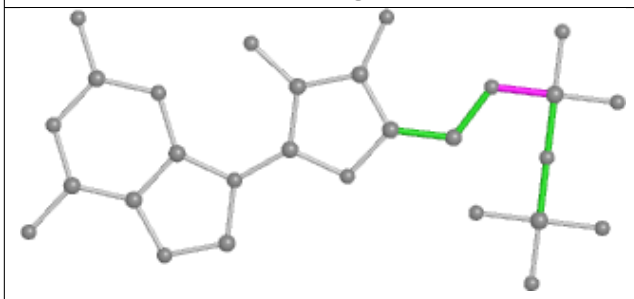

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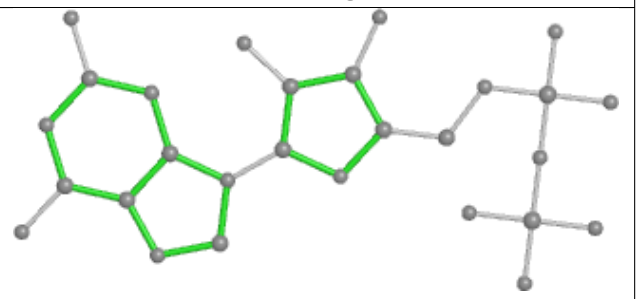
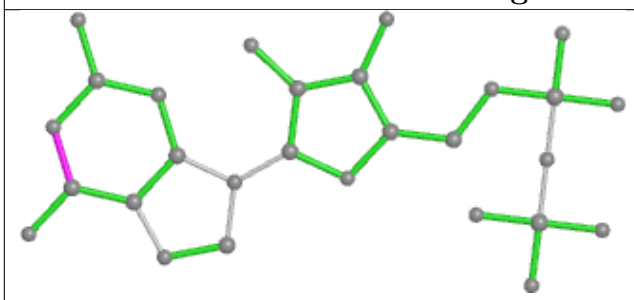


Rings

Ligand GDP UL 502



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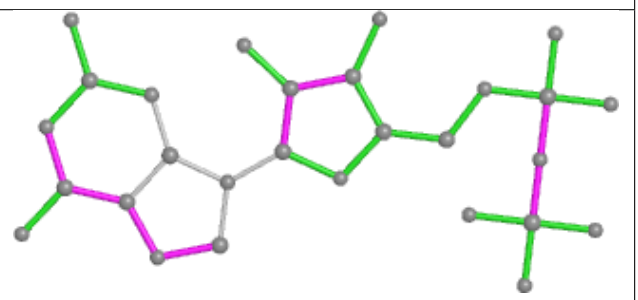

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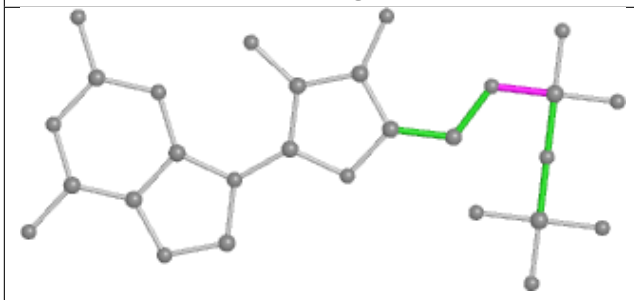

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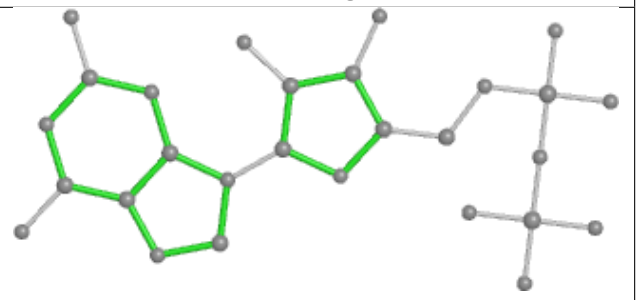
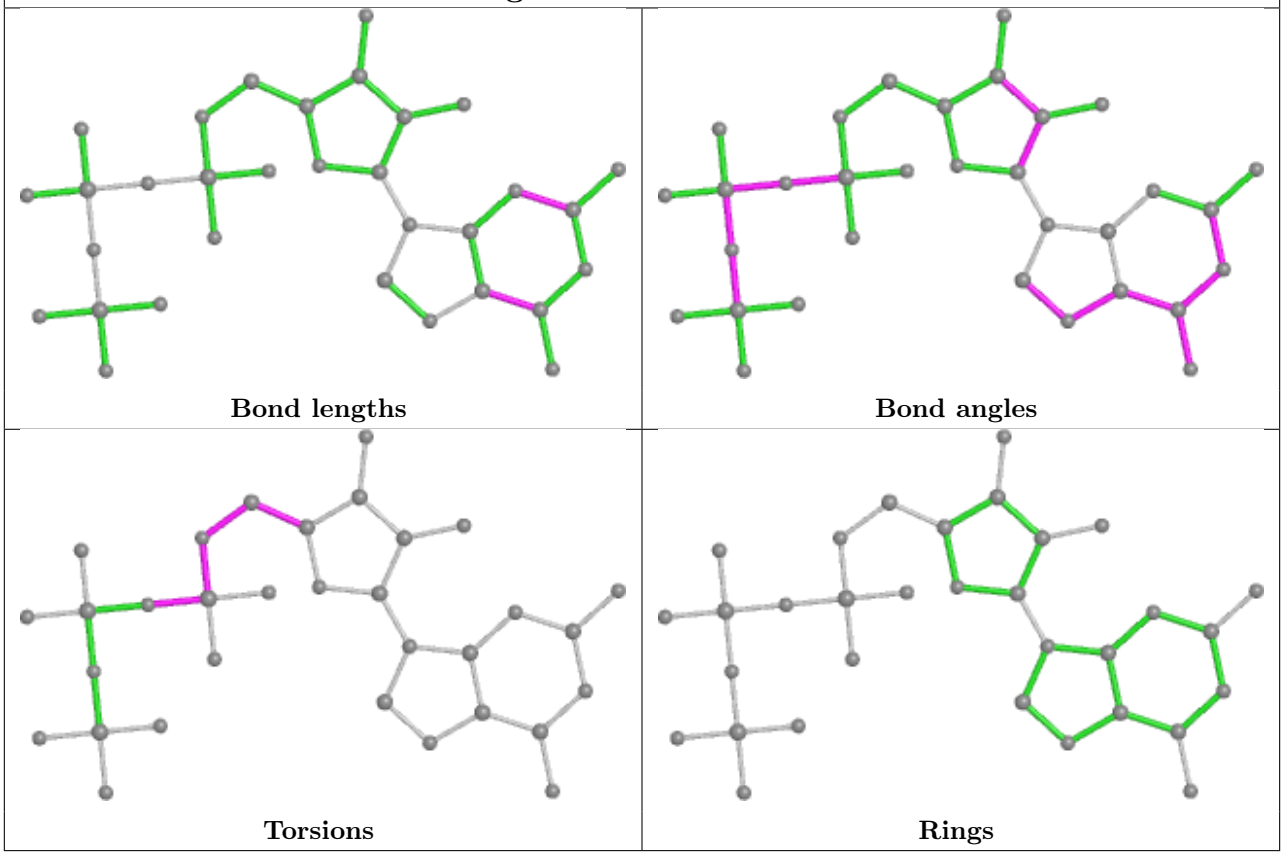
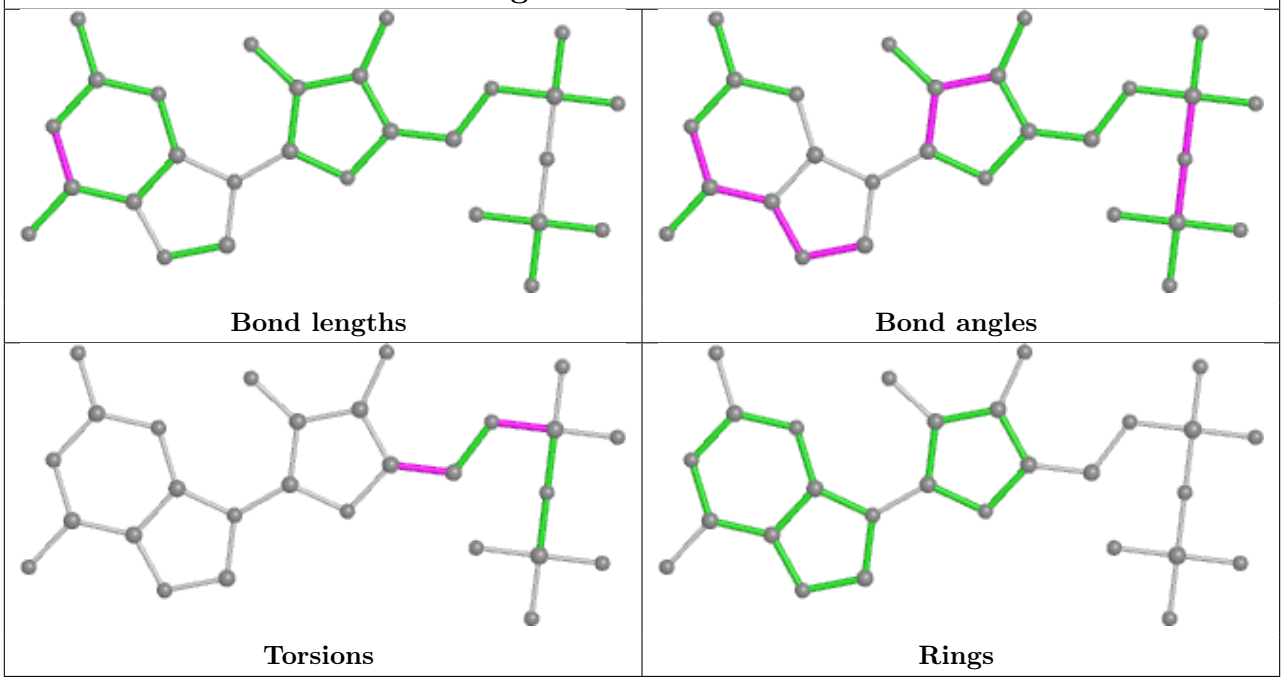


Rings

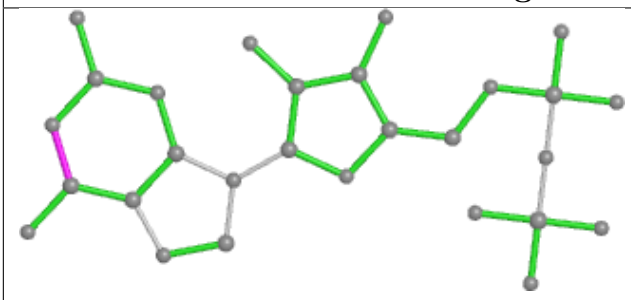
Ligand GTP UM 501



Ligand GDP LN 502



Ligand GDP LJ 502



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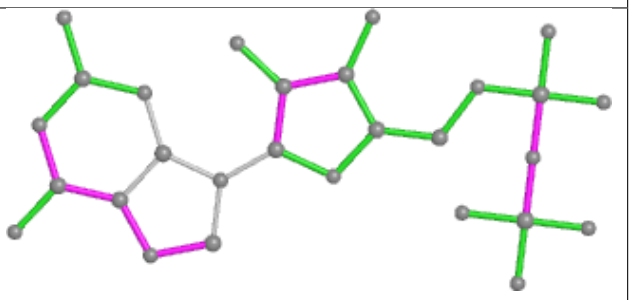

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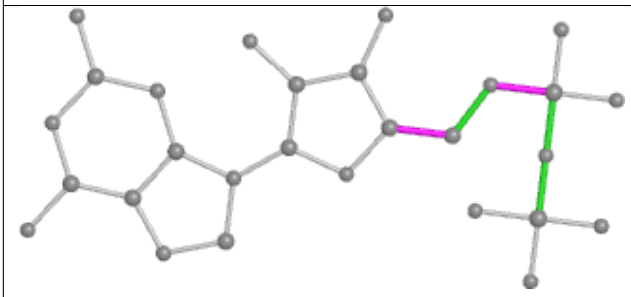

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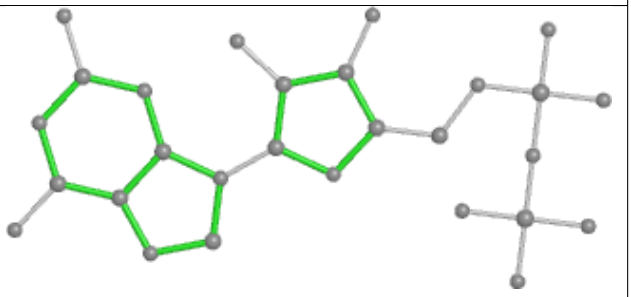
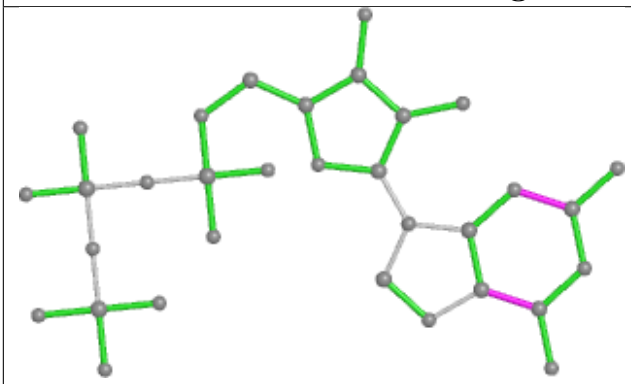


Rings

Ligand GTP AC 501



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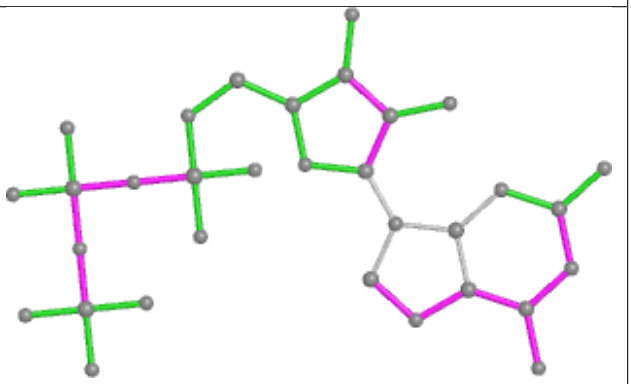

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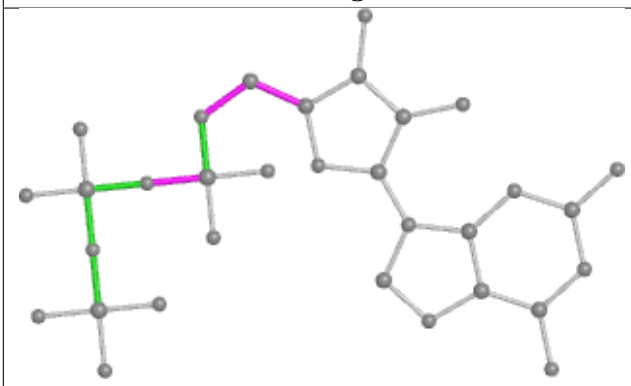

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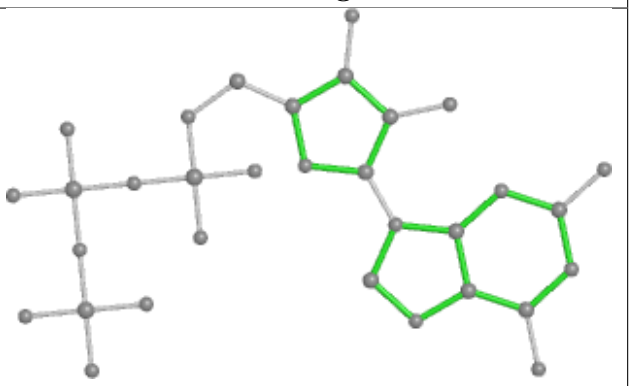
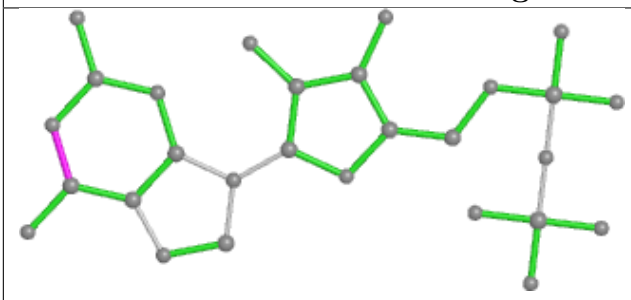


Rings

Ligand GDP AJ 502



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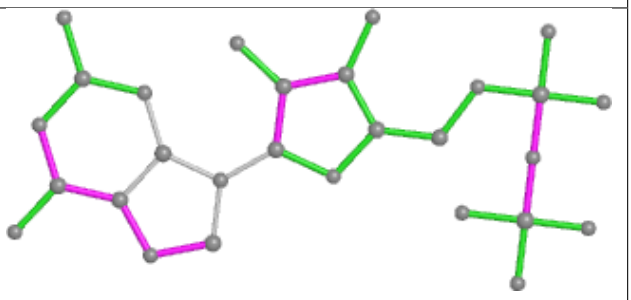

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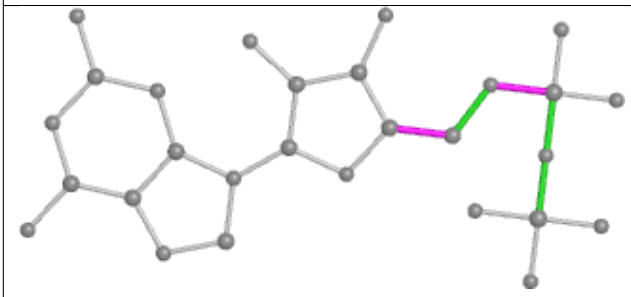

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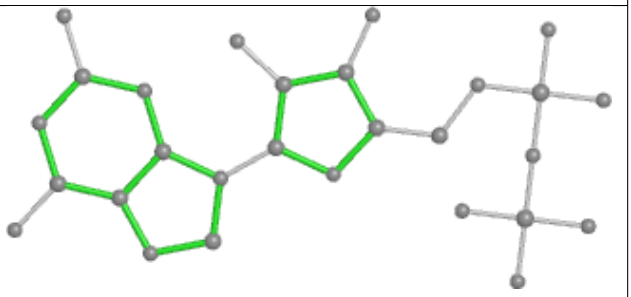
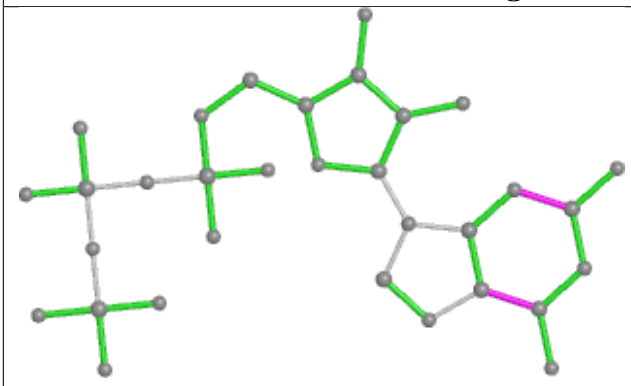


Rings

Ligand GTP DM 501



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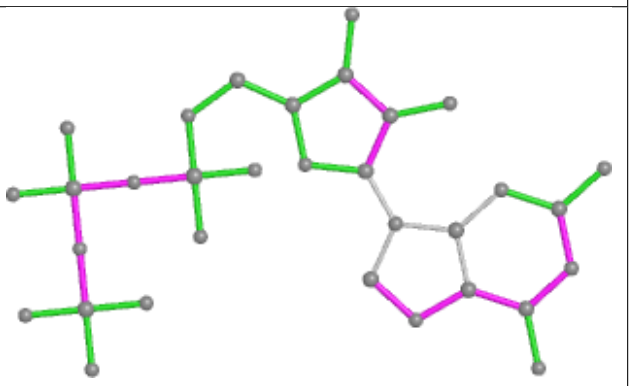

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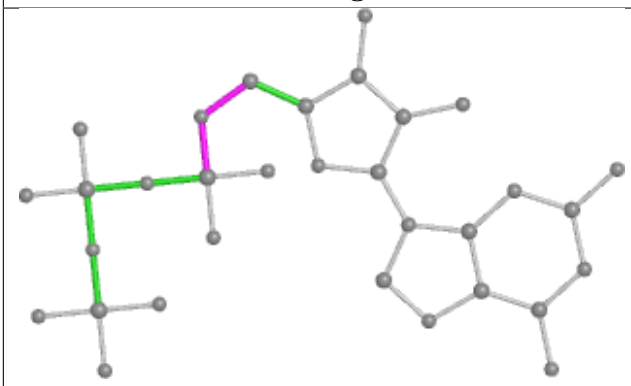

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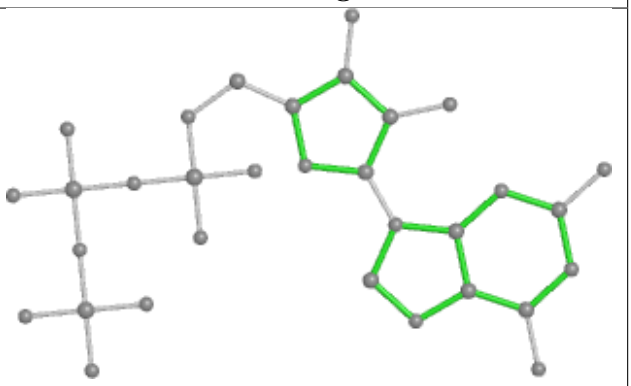
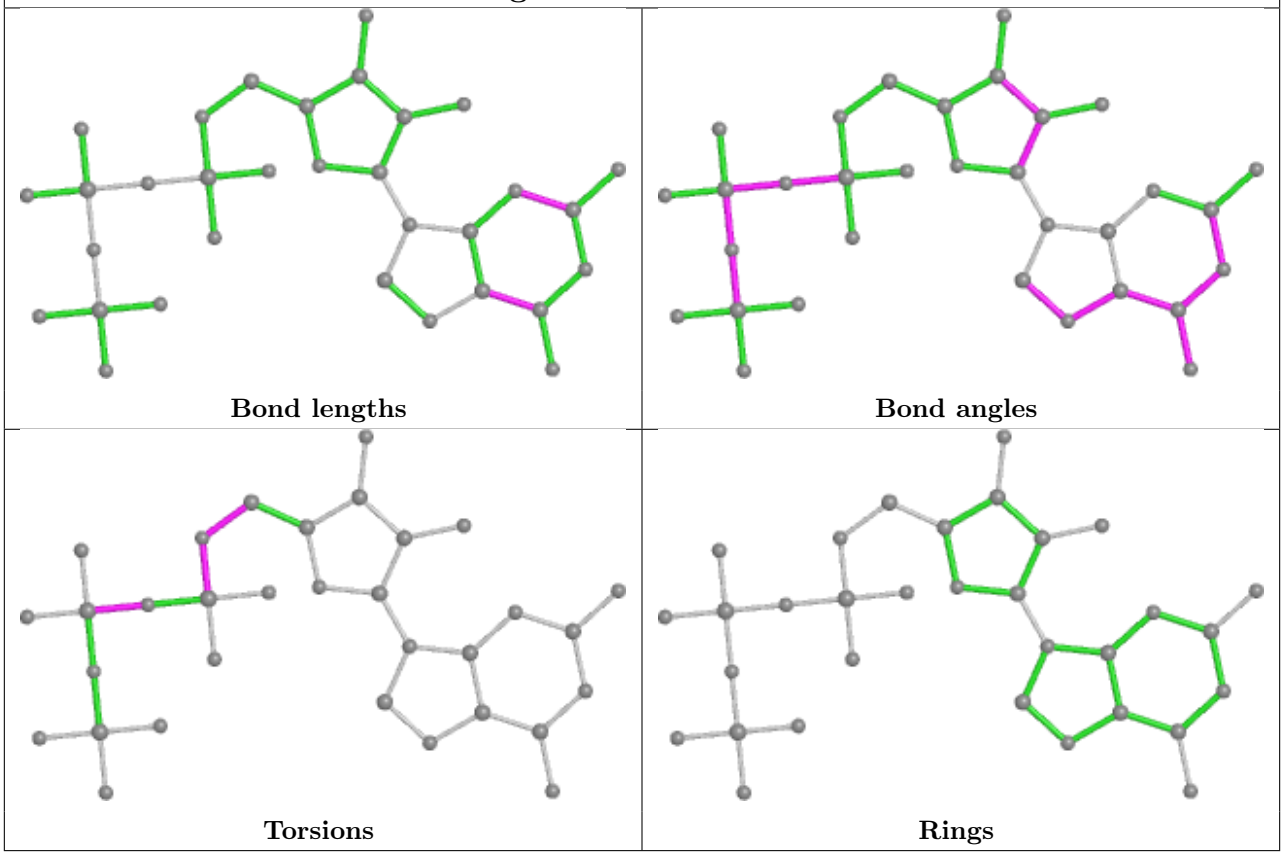
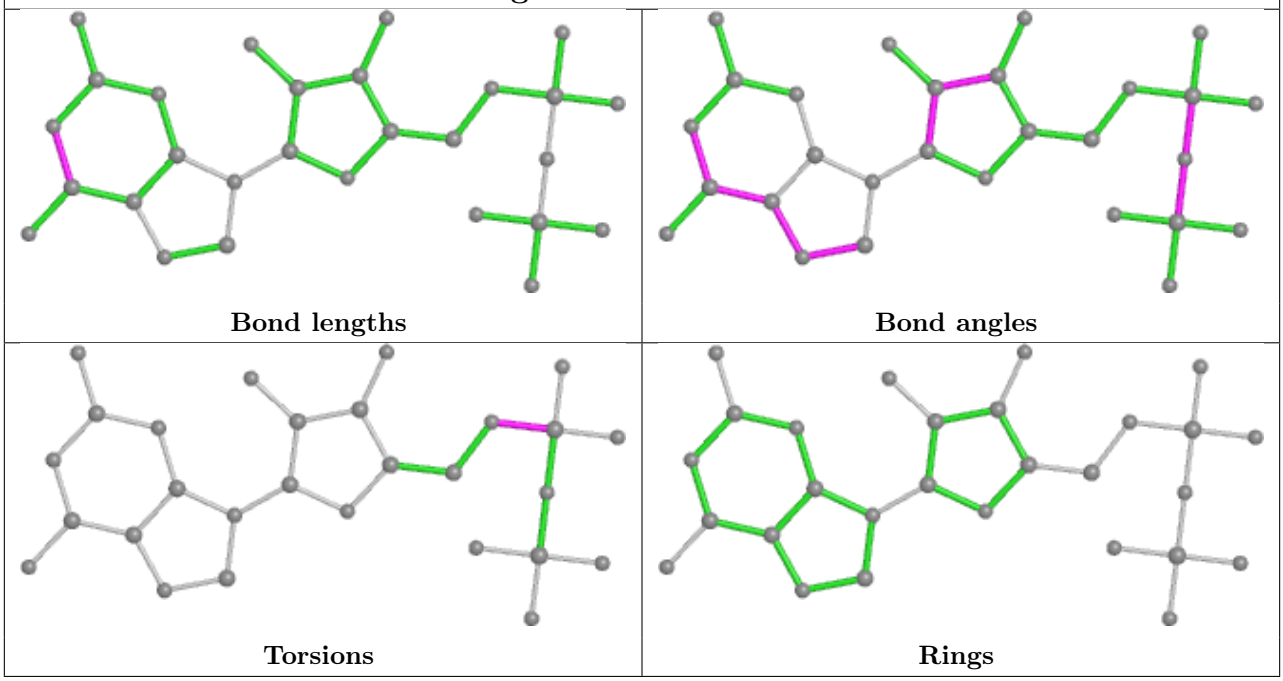


Rings

Ligand GTP SM 501



Ligand GDP AL 502



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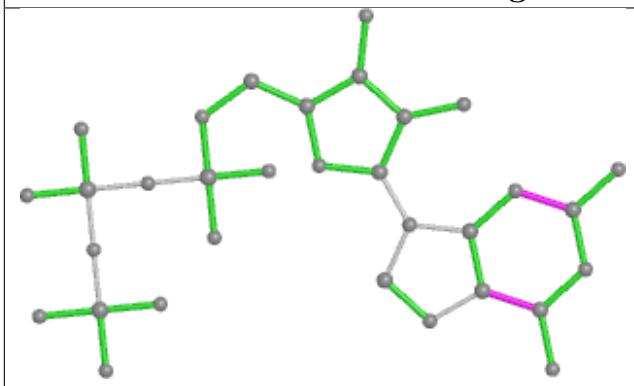

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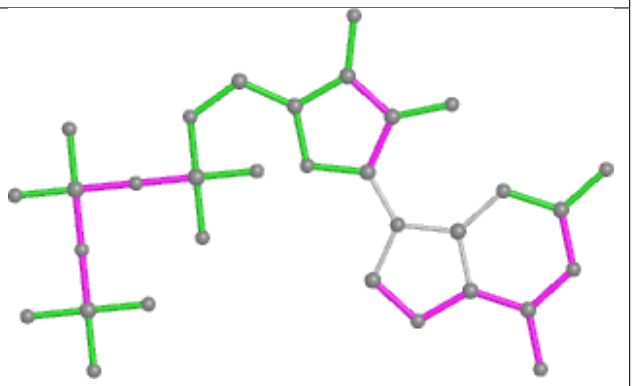
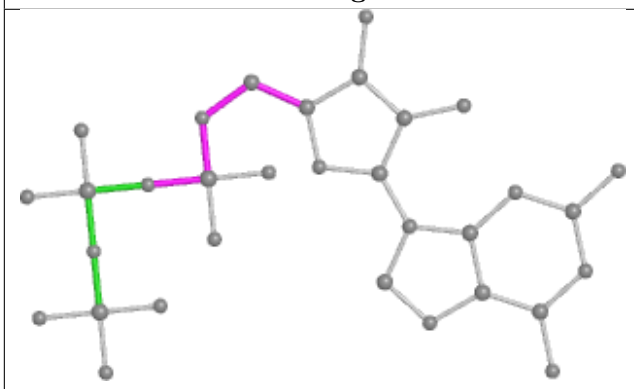
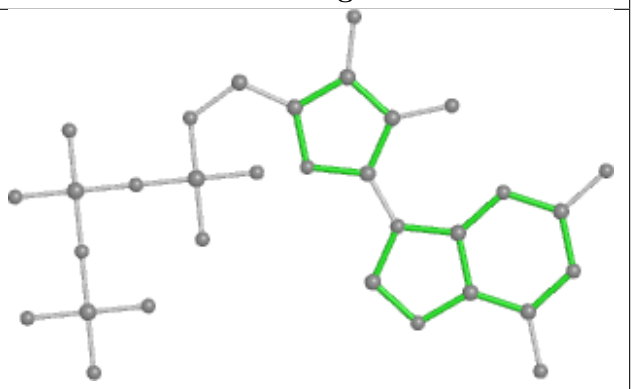


Bond angles

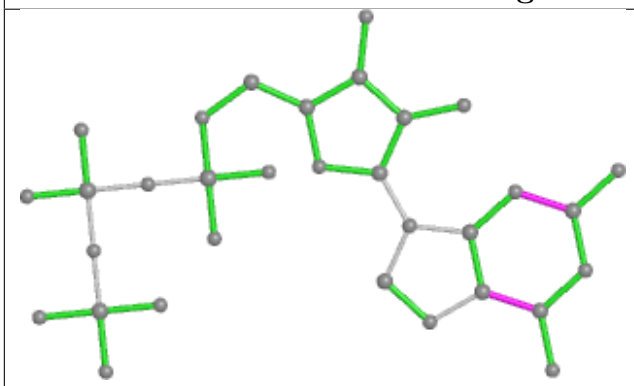


Torsions

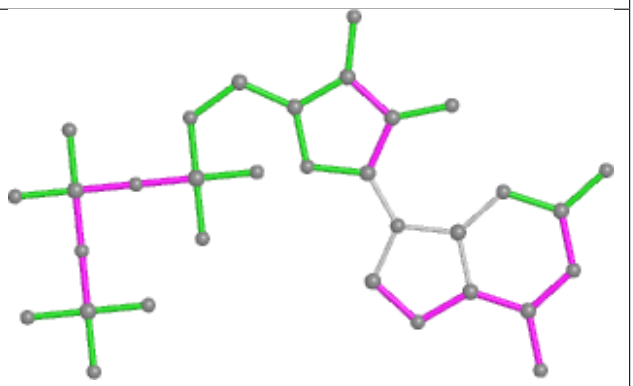


Rings

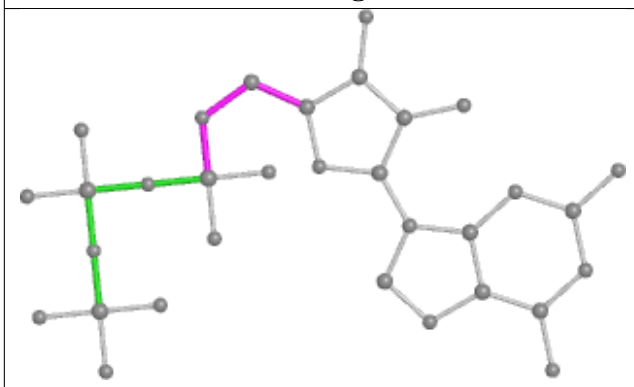
Ligand GTP IO 501



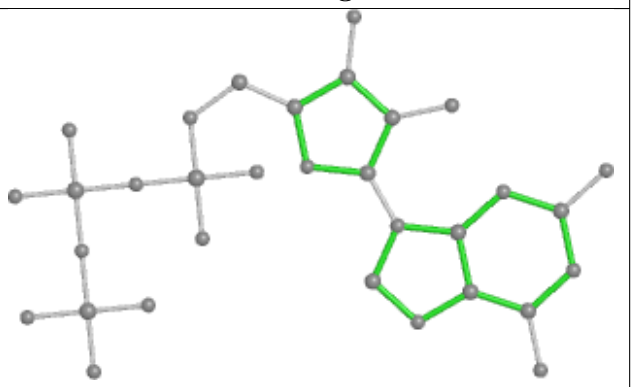
Bond lengths



Bond angles

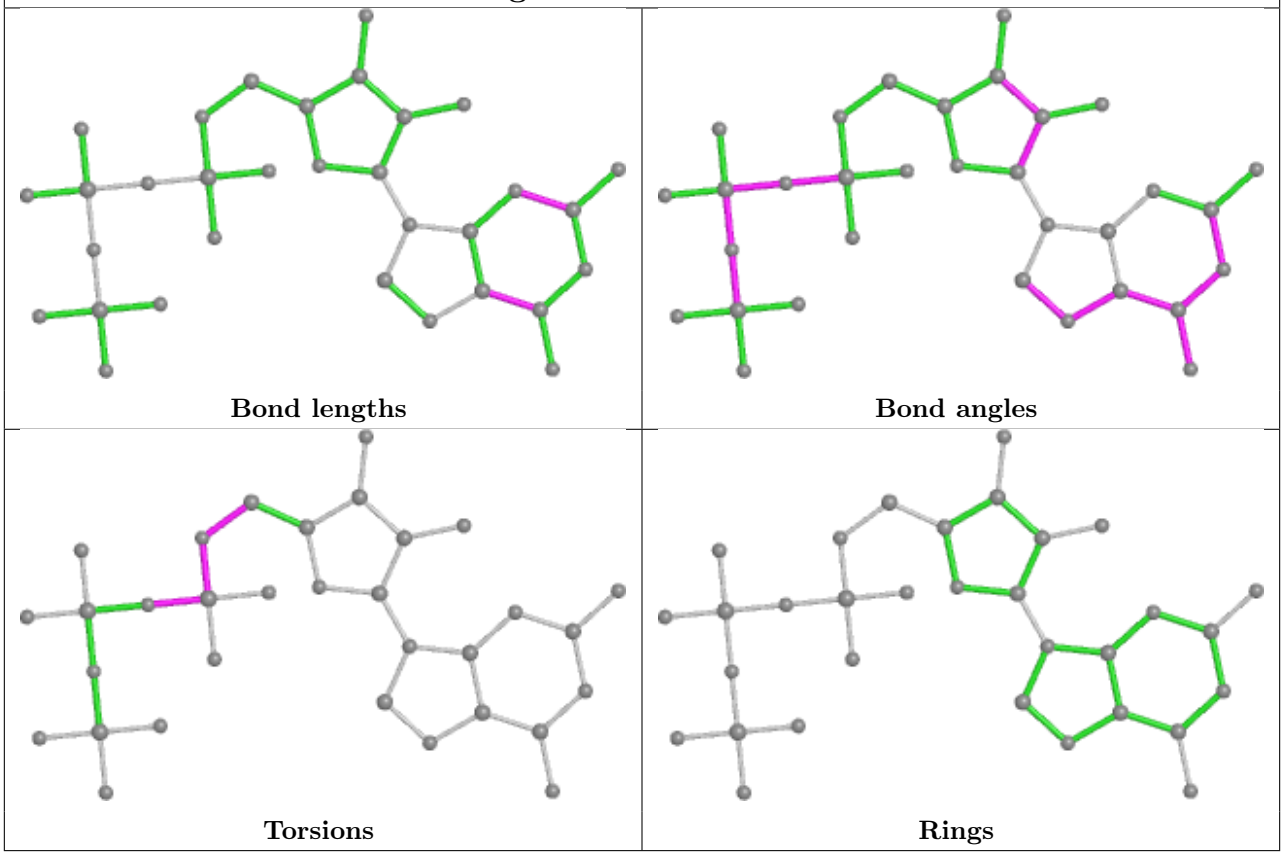


Torsions

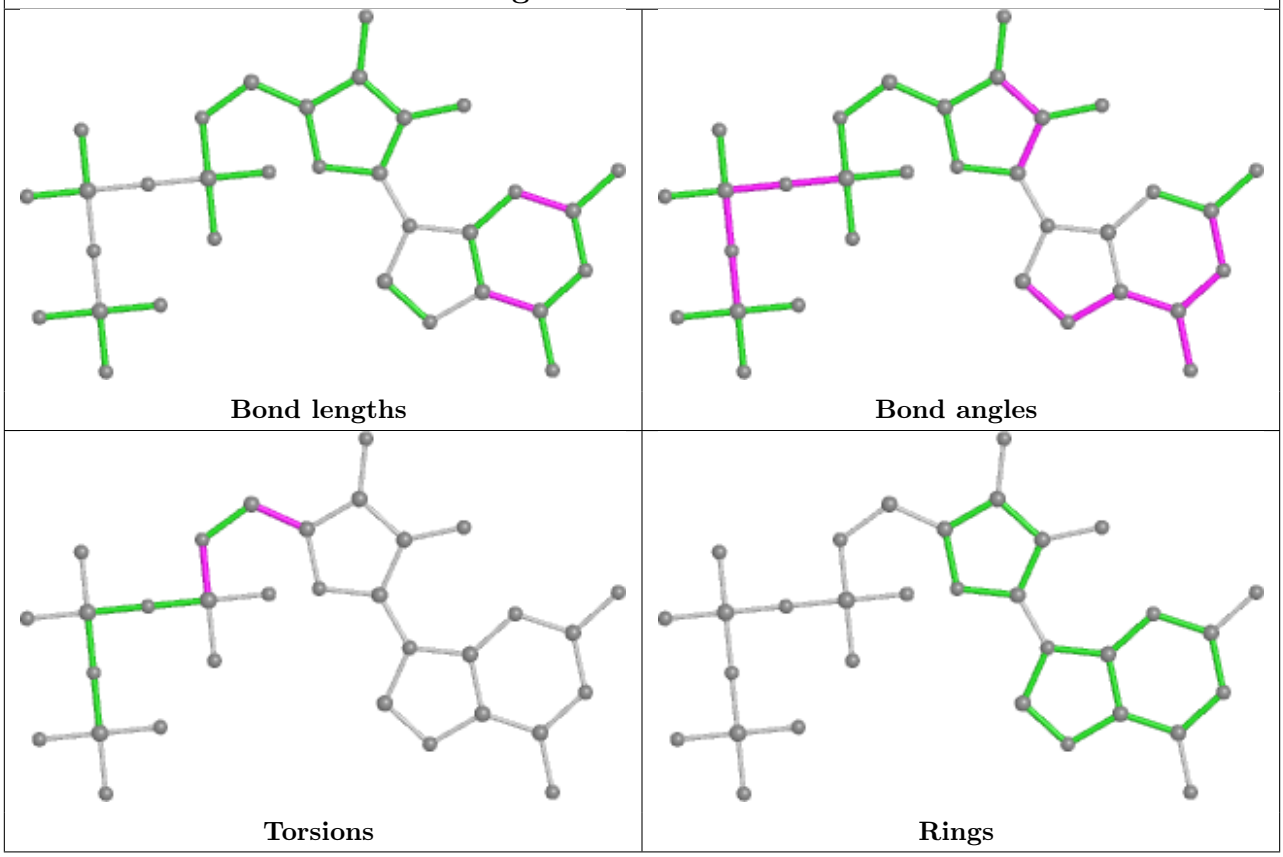


Rings

Ligand GTP AK 501



Ligand GTP CE 501



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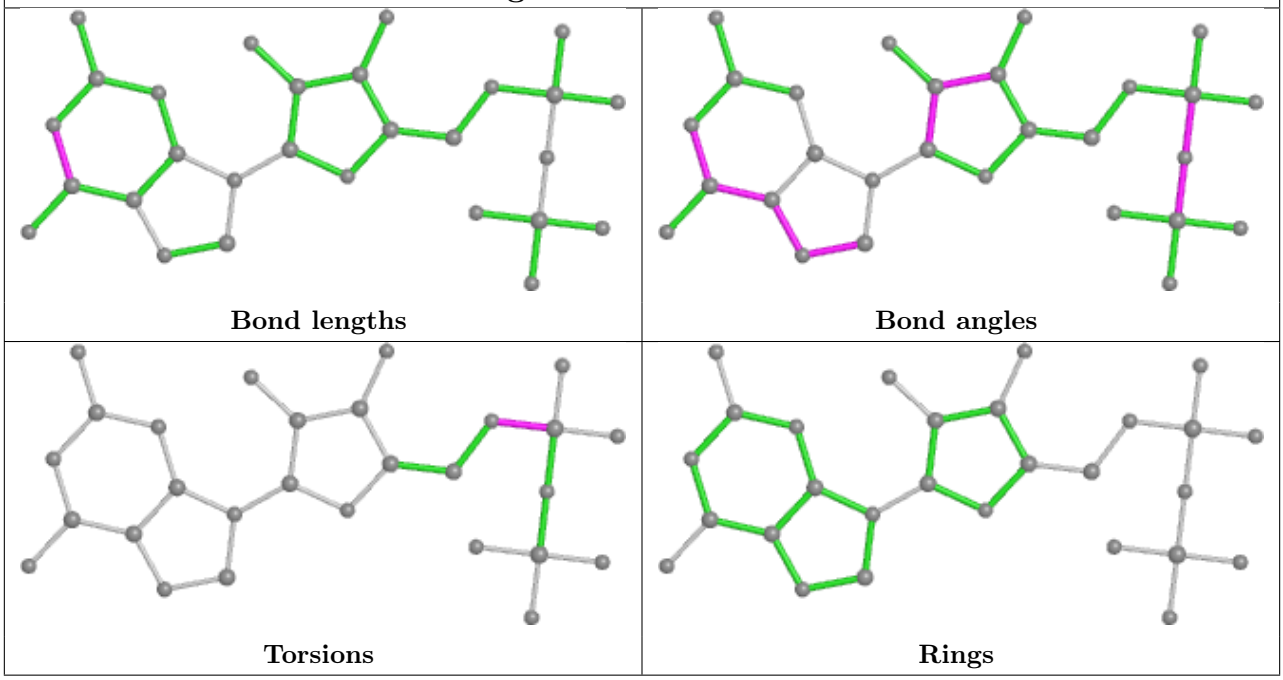
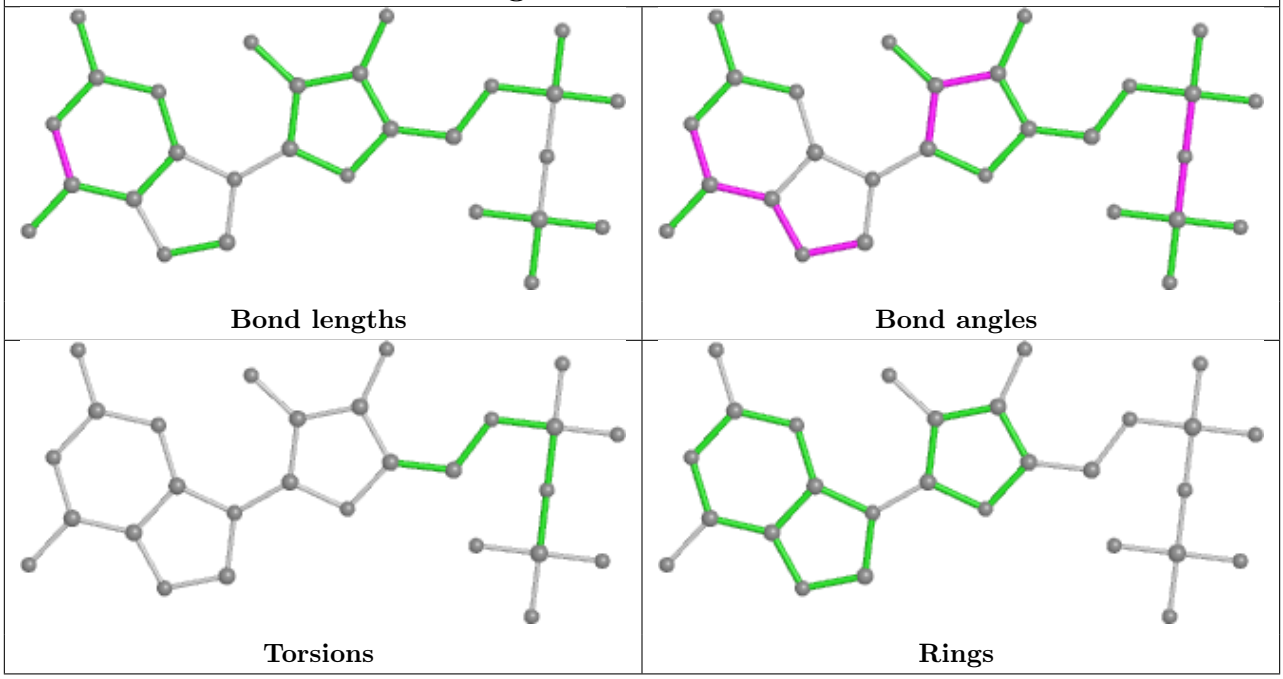
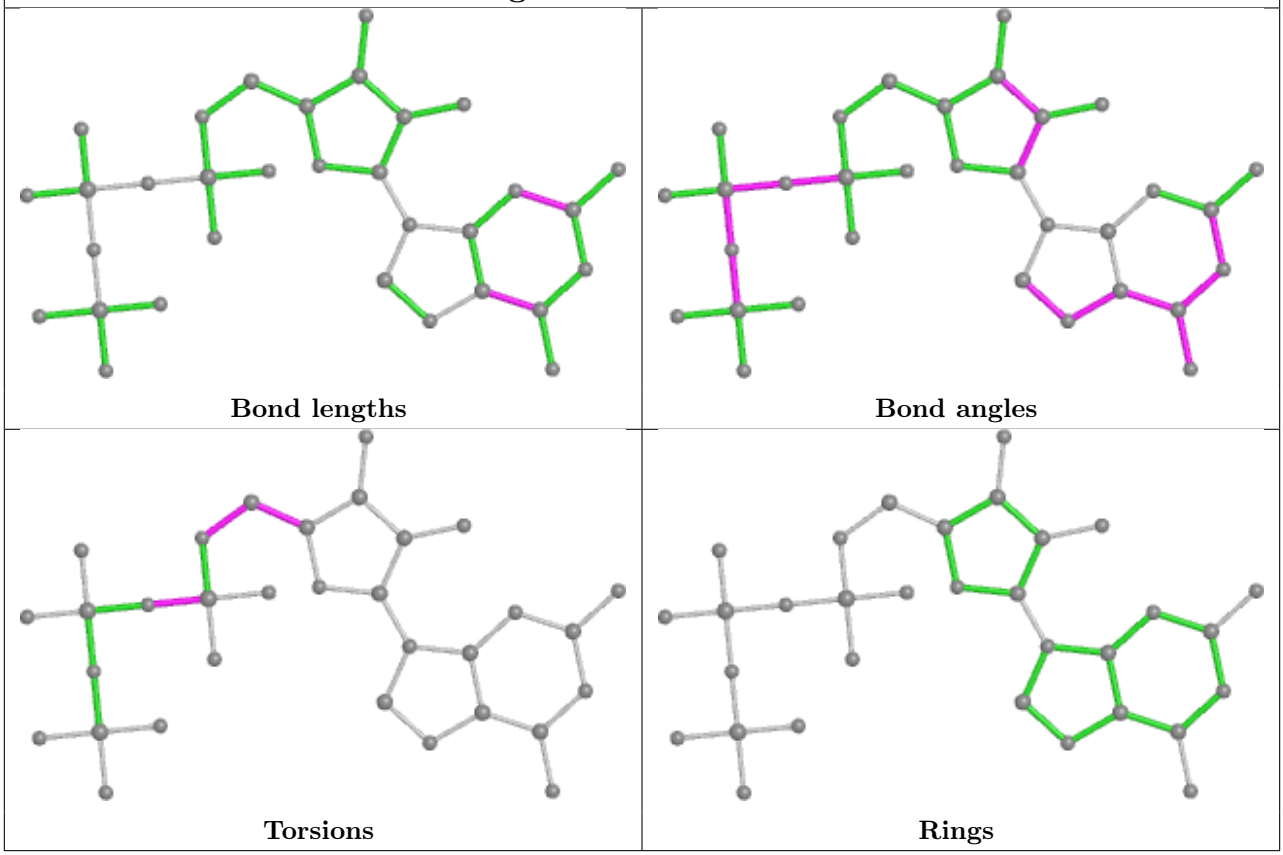


Ligand GDP VH 502



Ligand GTP HK 501



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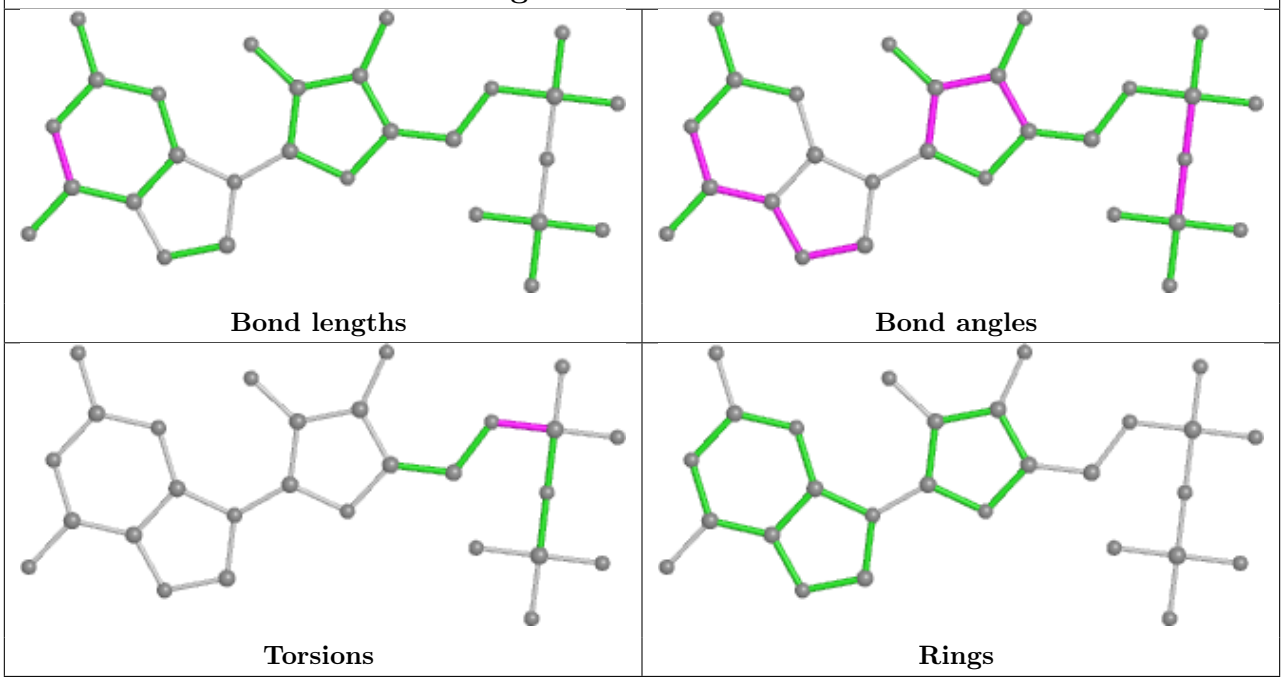

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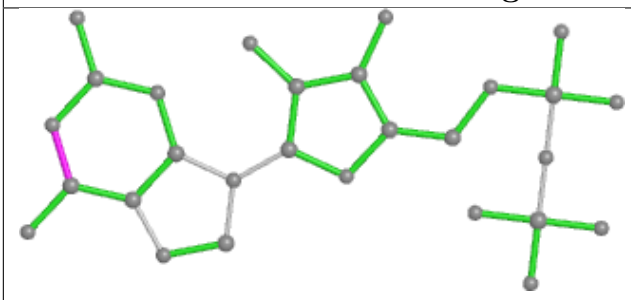
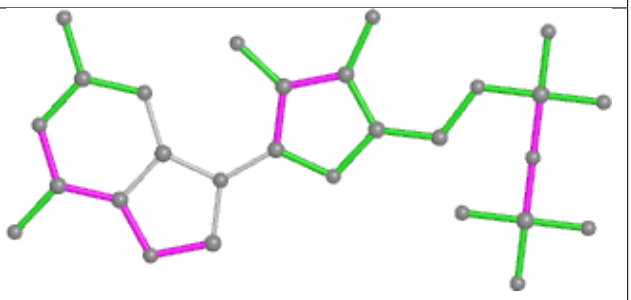
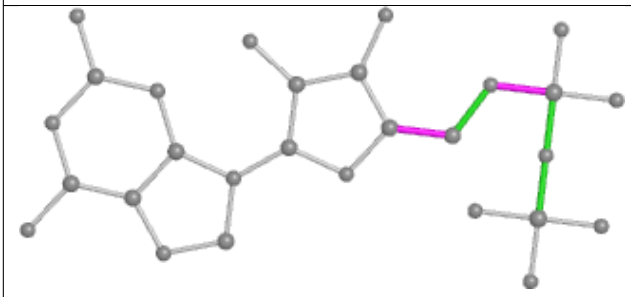


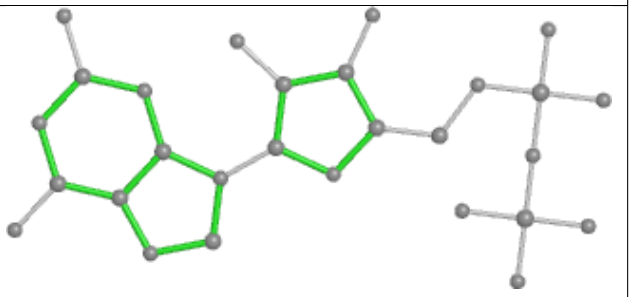
Bond lengths



Bond angles

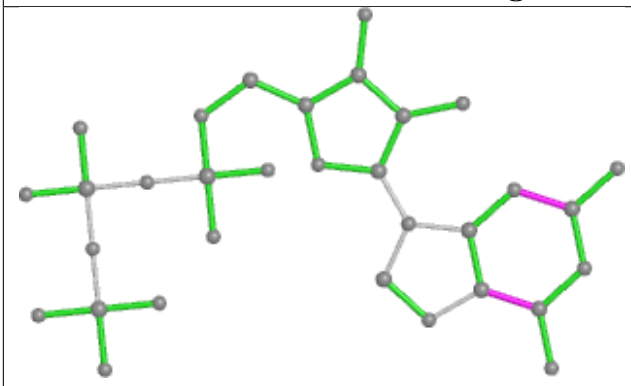


Torsions



Rings

Ligand GTP FM 501



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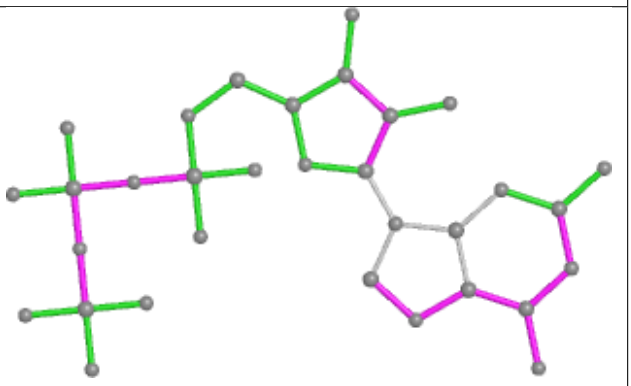
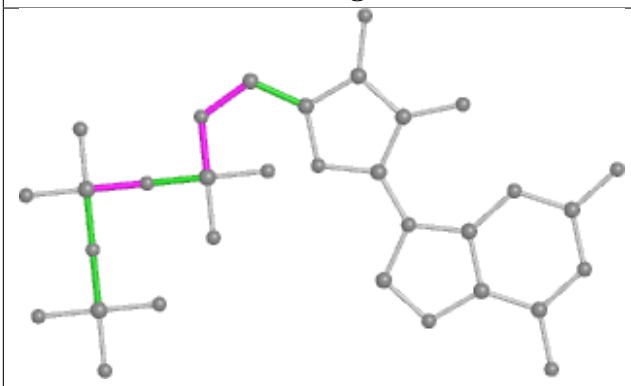


Bond angles



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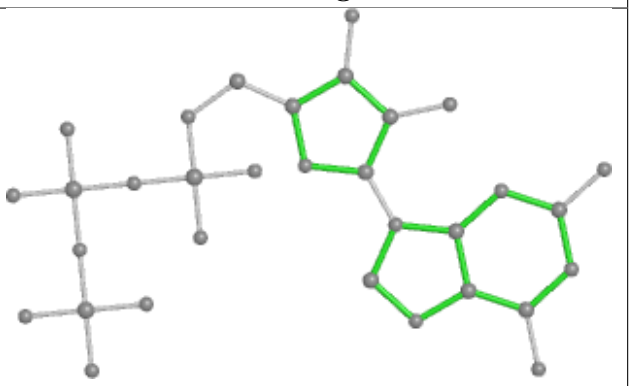
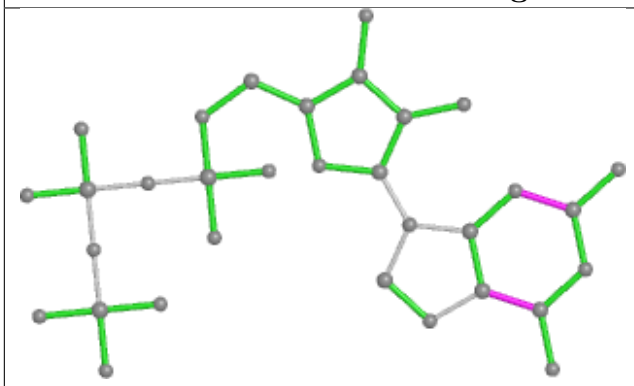


Rings

Ligand GTP JM 501



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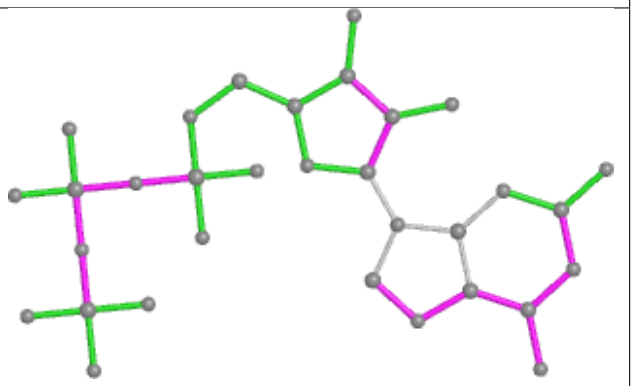
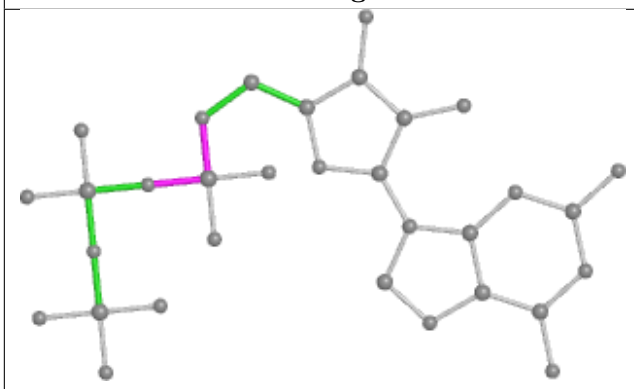


Bond angles



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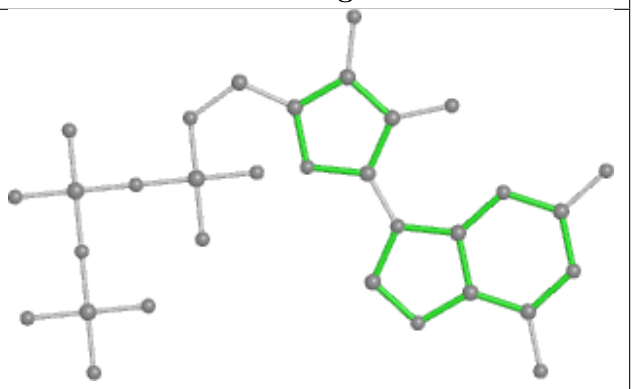
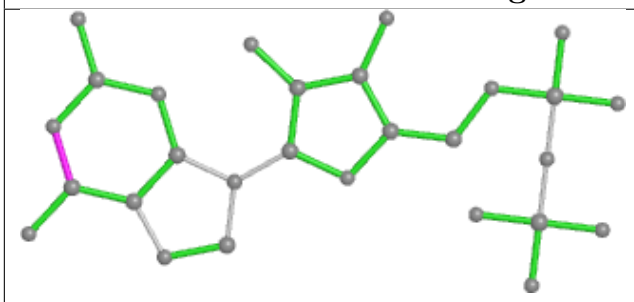
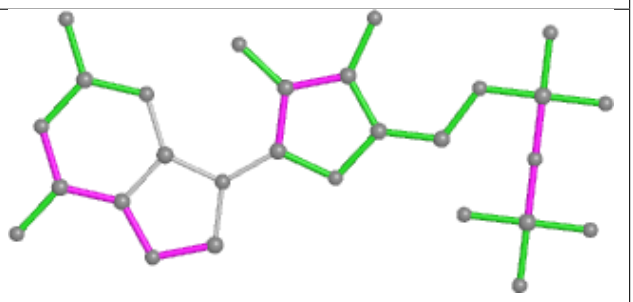


Rings

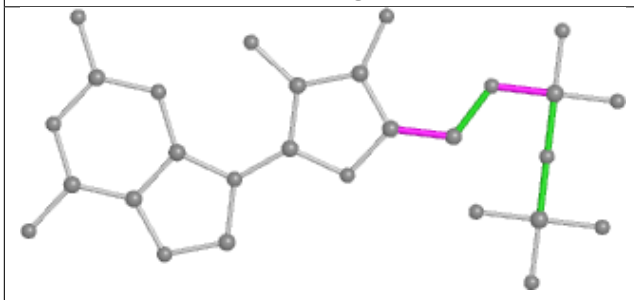
Ligand GDP CD 502



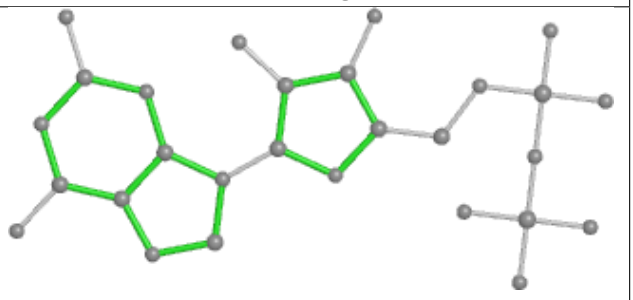
Bond lengths



Bond angles

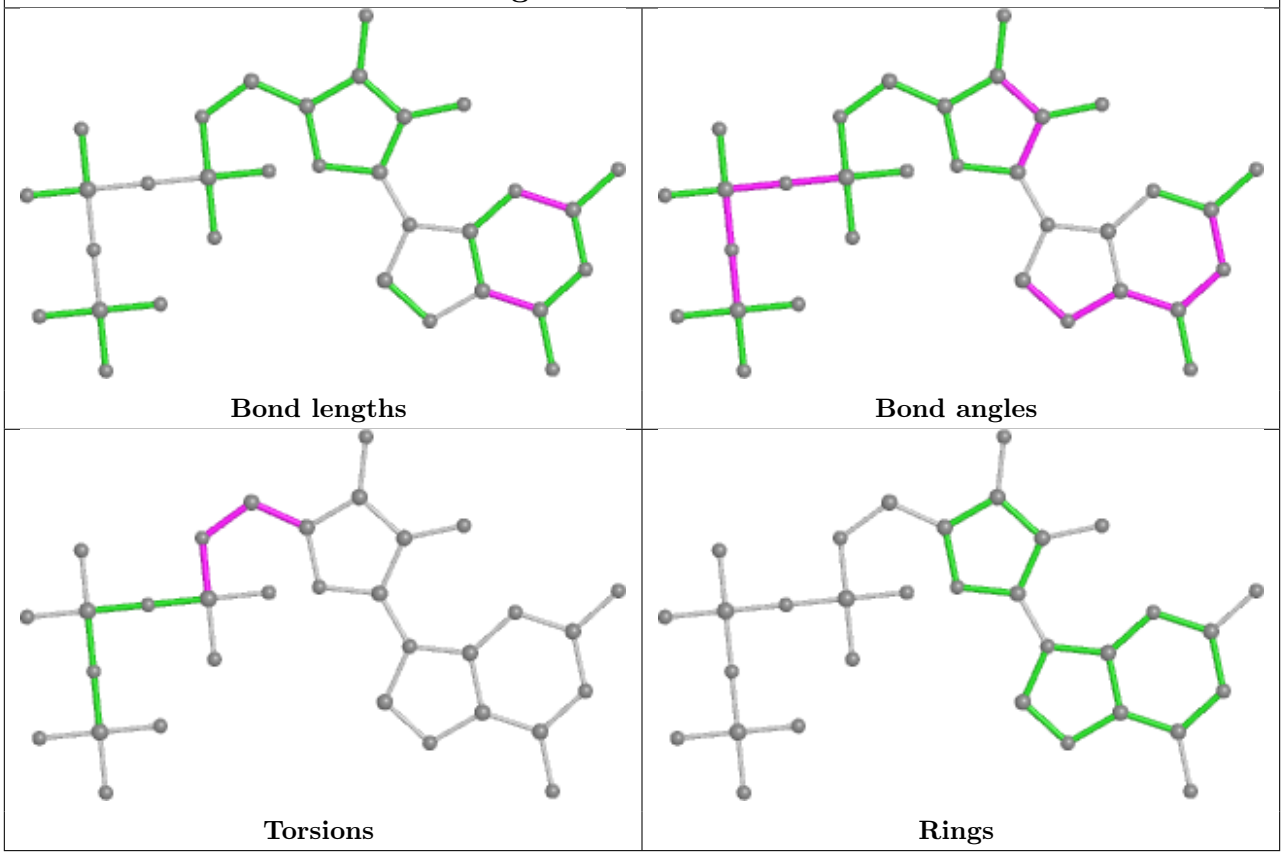


Torsions

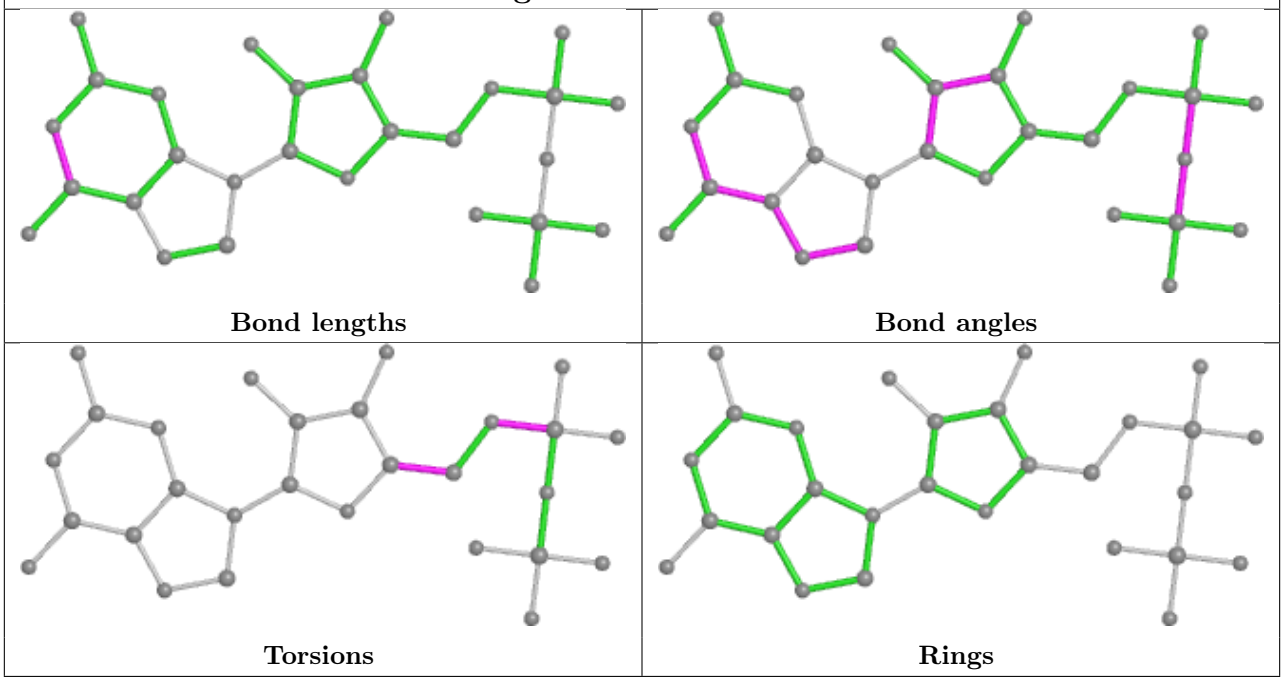


Rings

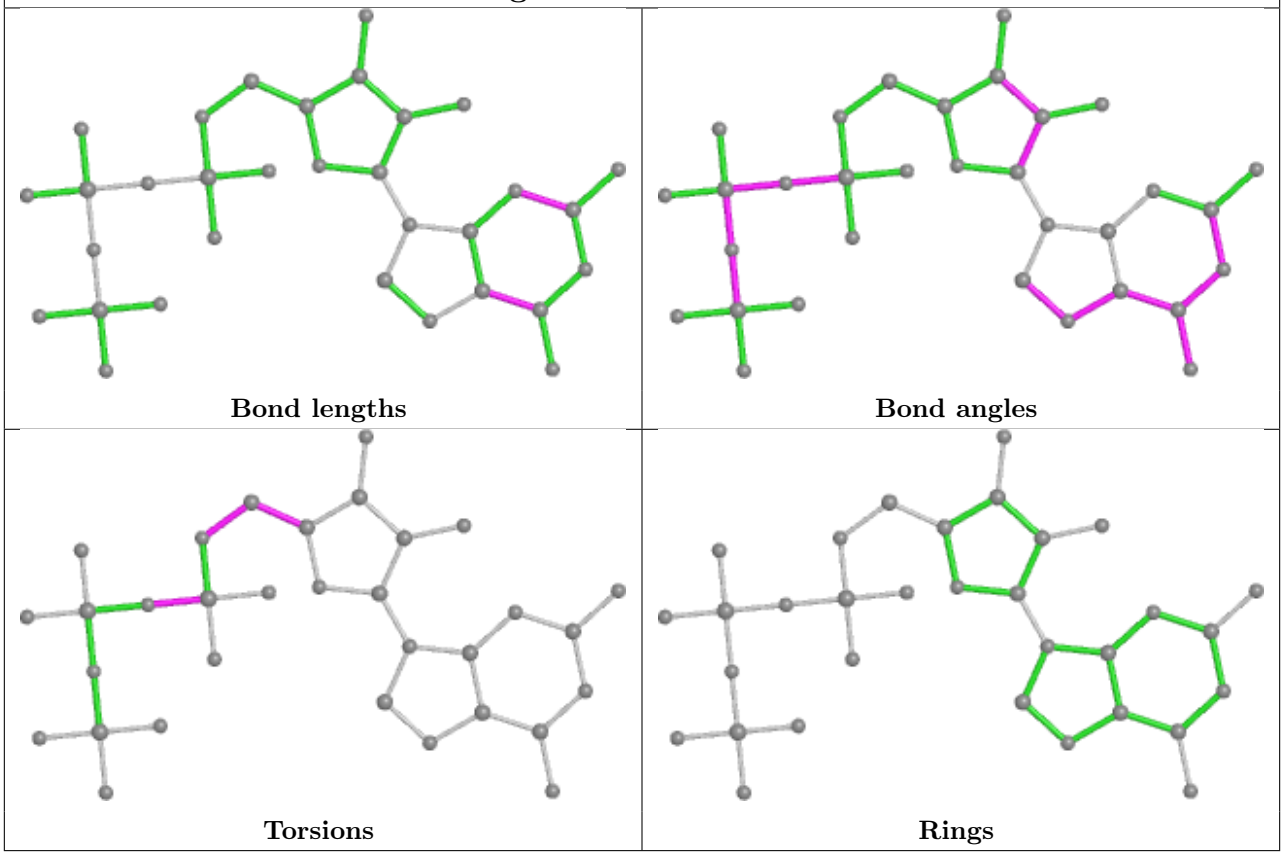
Ligand GTP WI 501



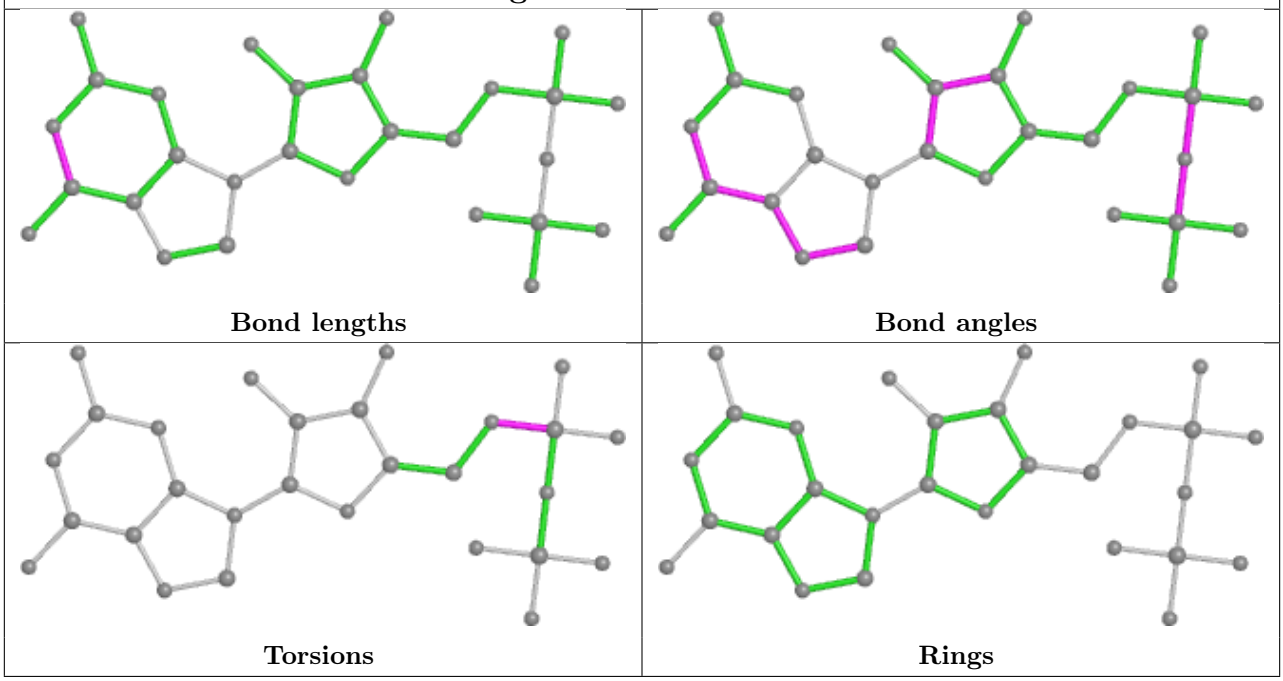
Ligand GDP TJ 502



Ligand GTP AA 501



Ligand GDP CB 502



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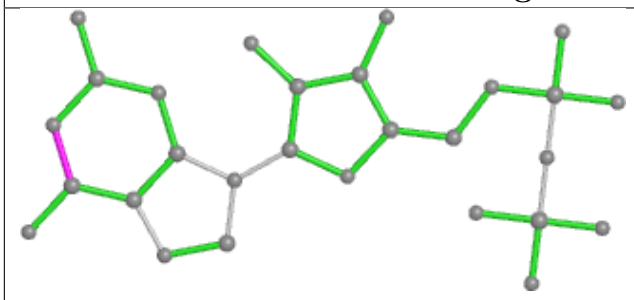
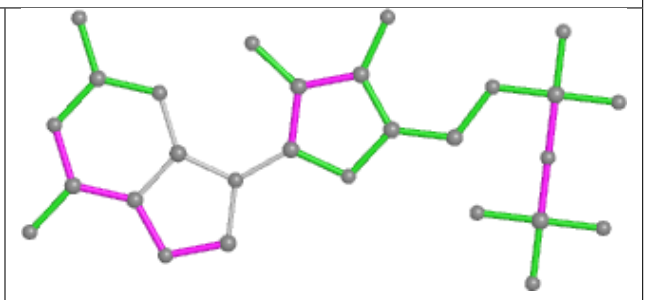
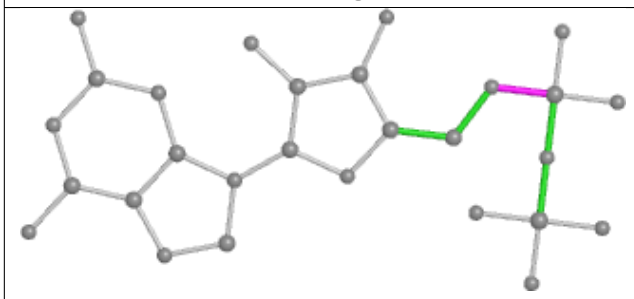


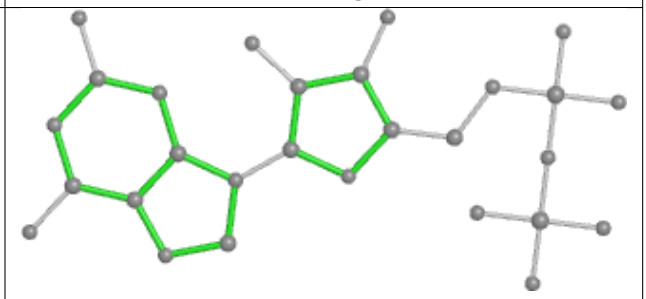
Bond lengths



Bond angles

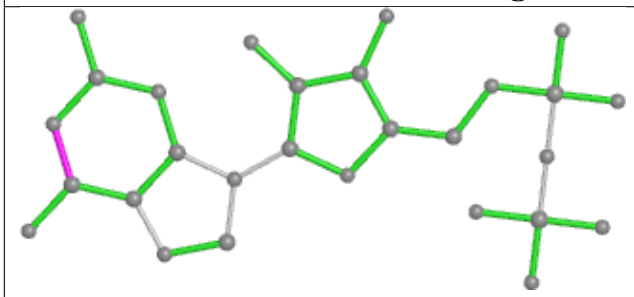


Torsions

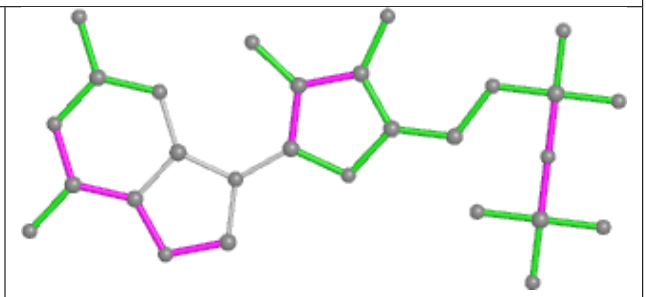


Rings

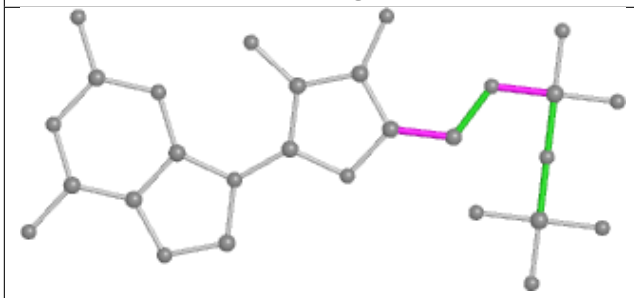
Ligand GDP TD 502



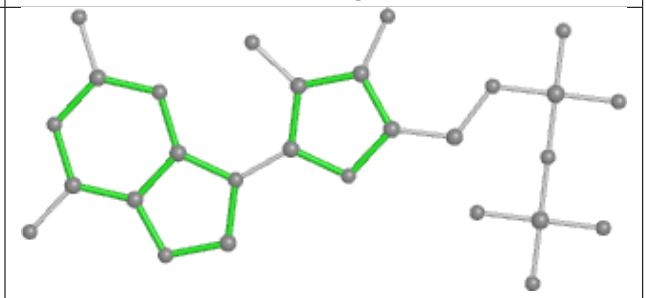
Bond lengths



Bond angles

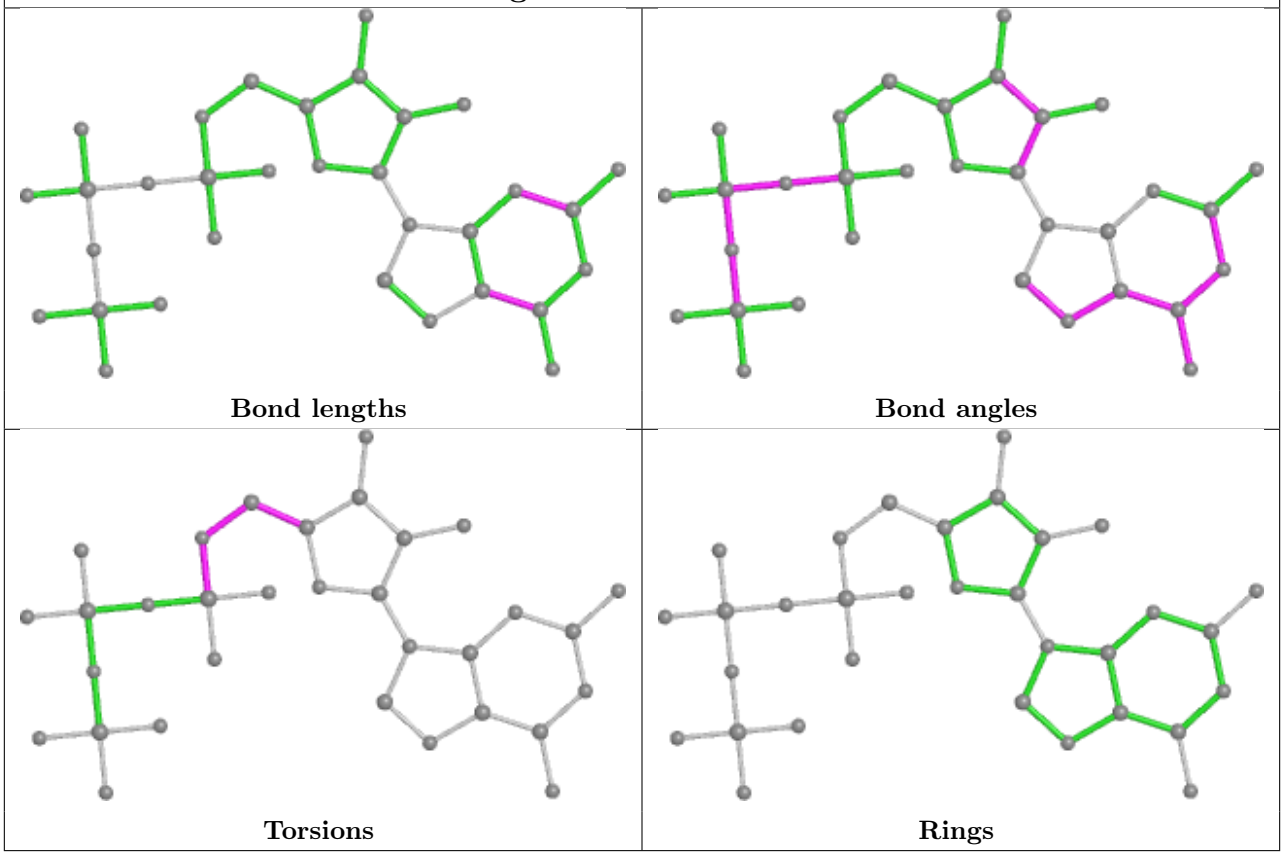


Torsions

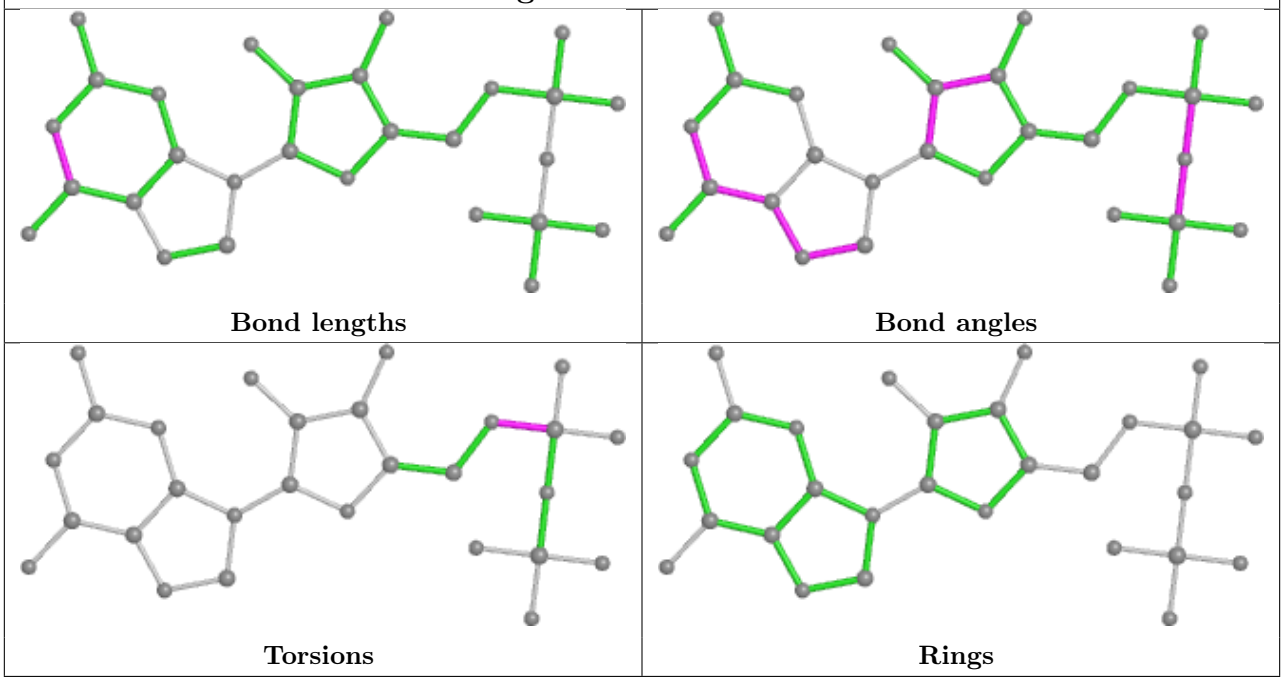


Rings

Ligand GTP CG 501



Ligand GDP JJ 502



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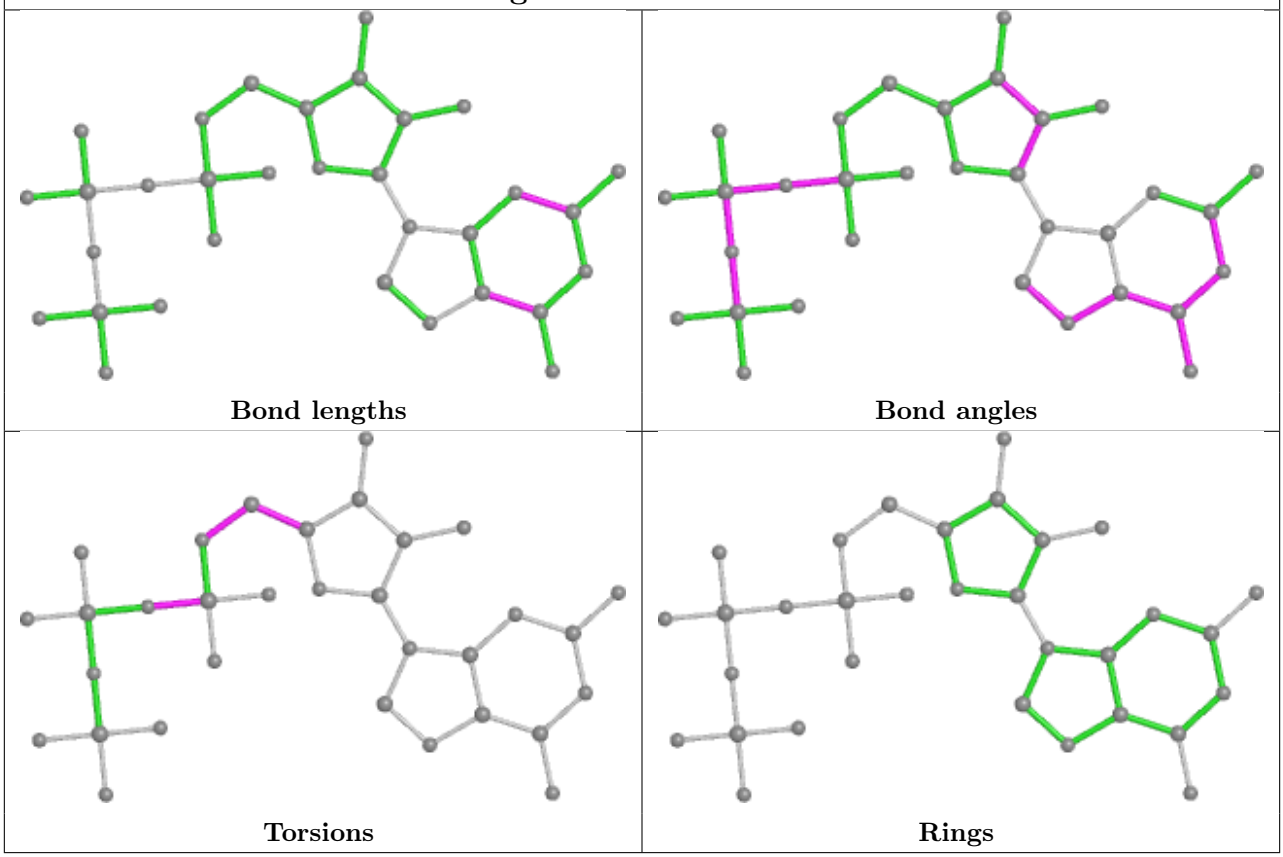

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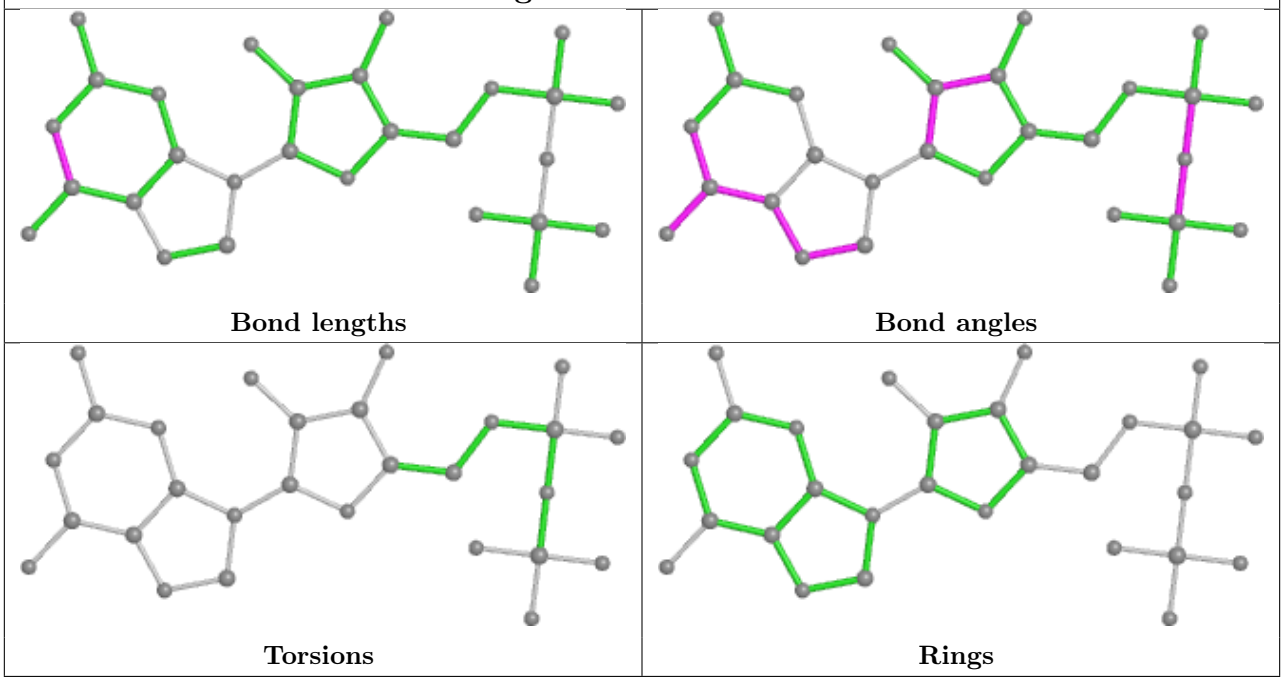
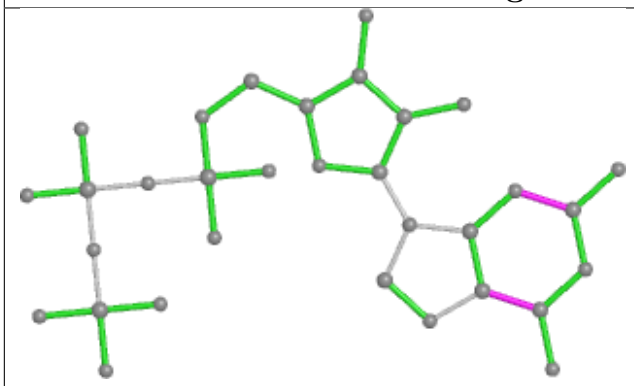
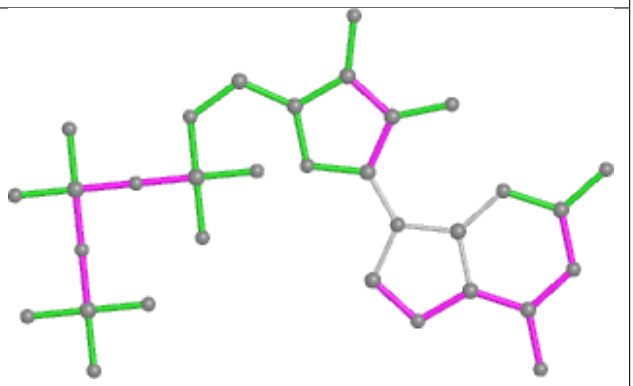


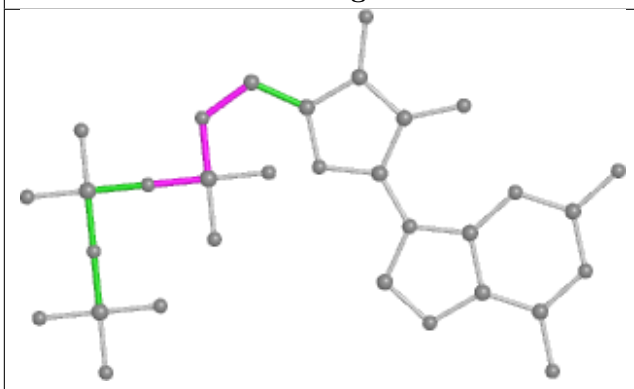
Ligand GTP RM 501



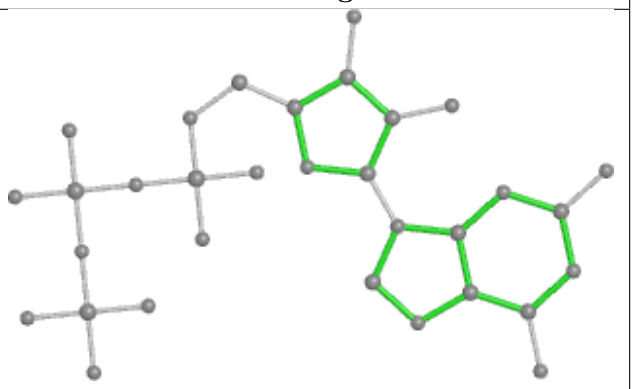
Bond lengths



Bond angles

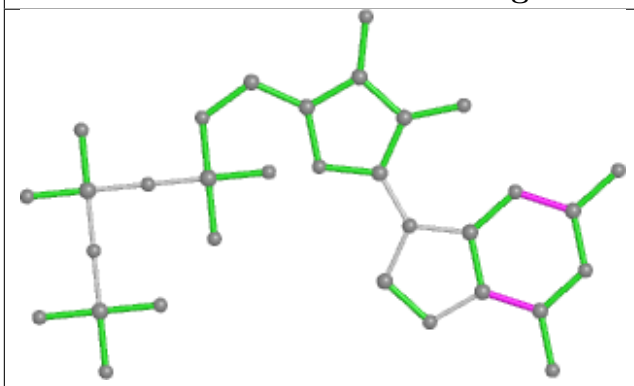


Torsions

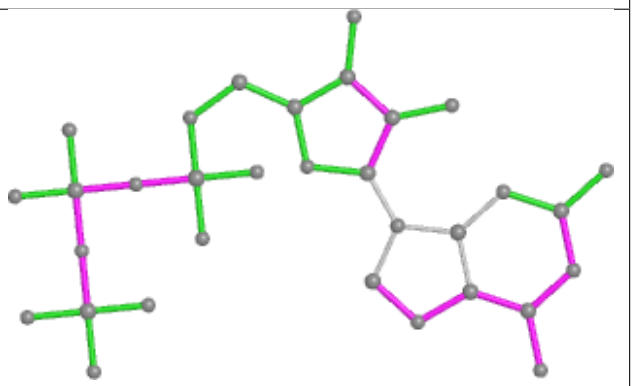


Rings

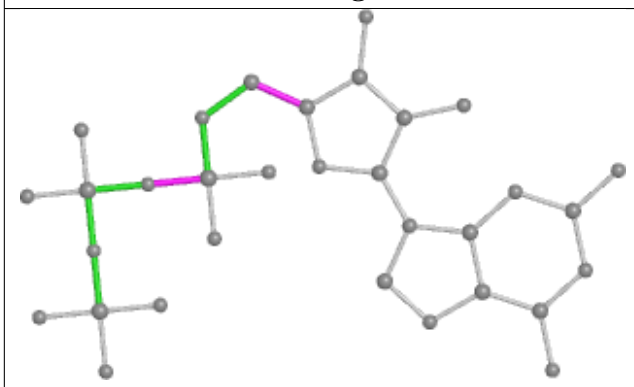
Ligand GTP AE 501



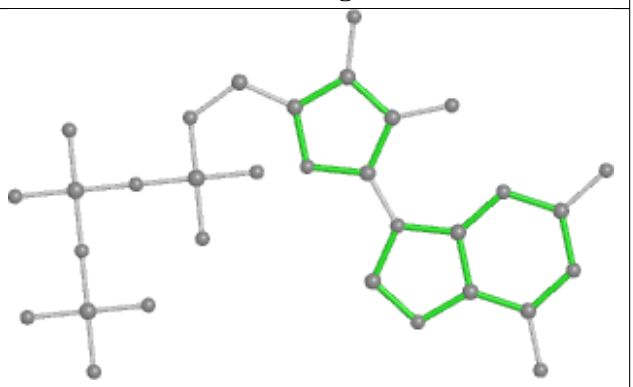
Bond lengths



Bond angles

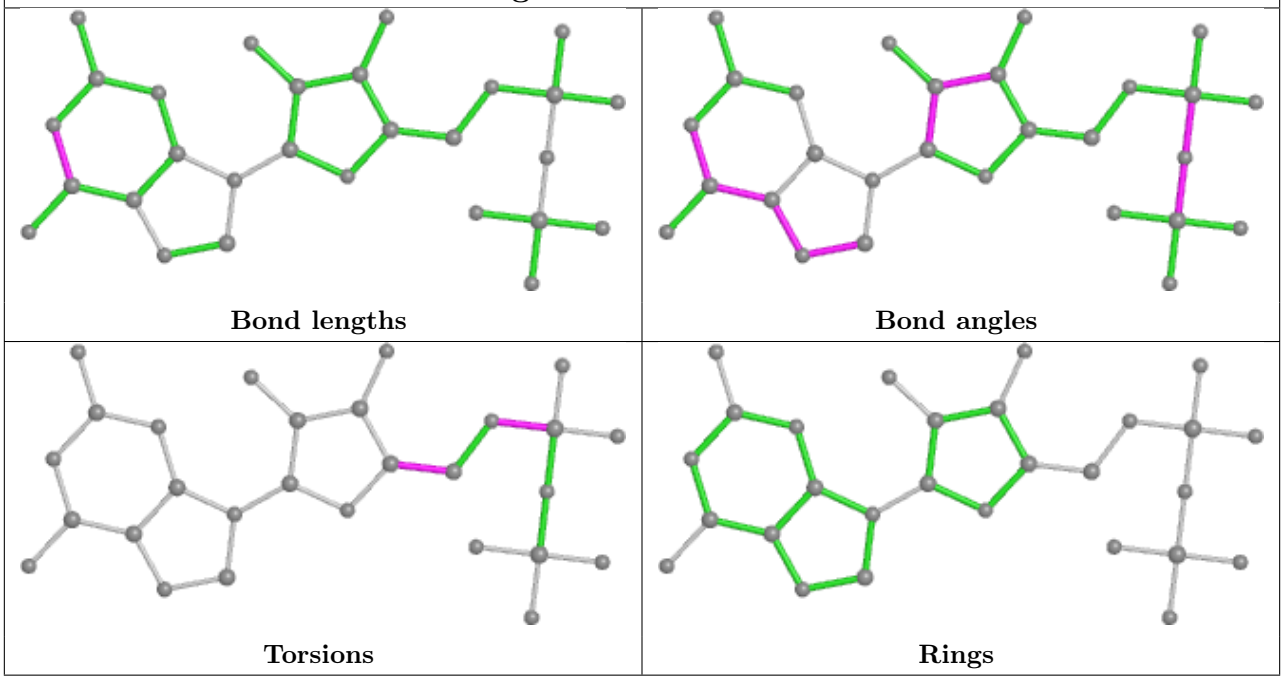


Torsions

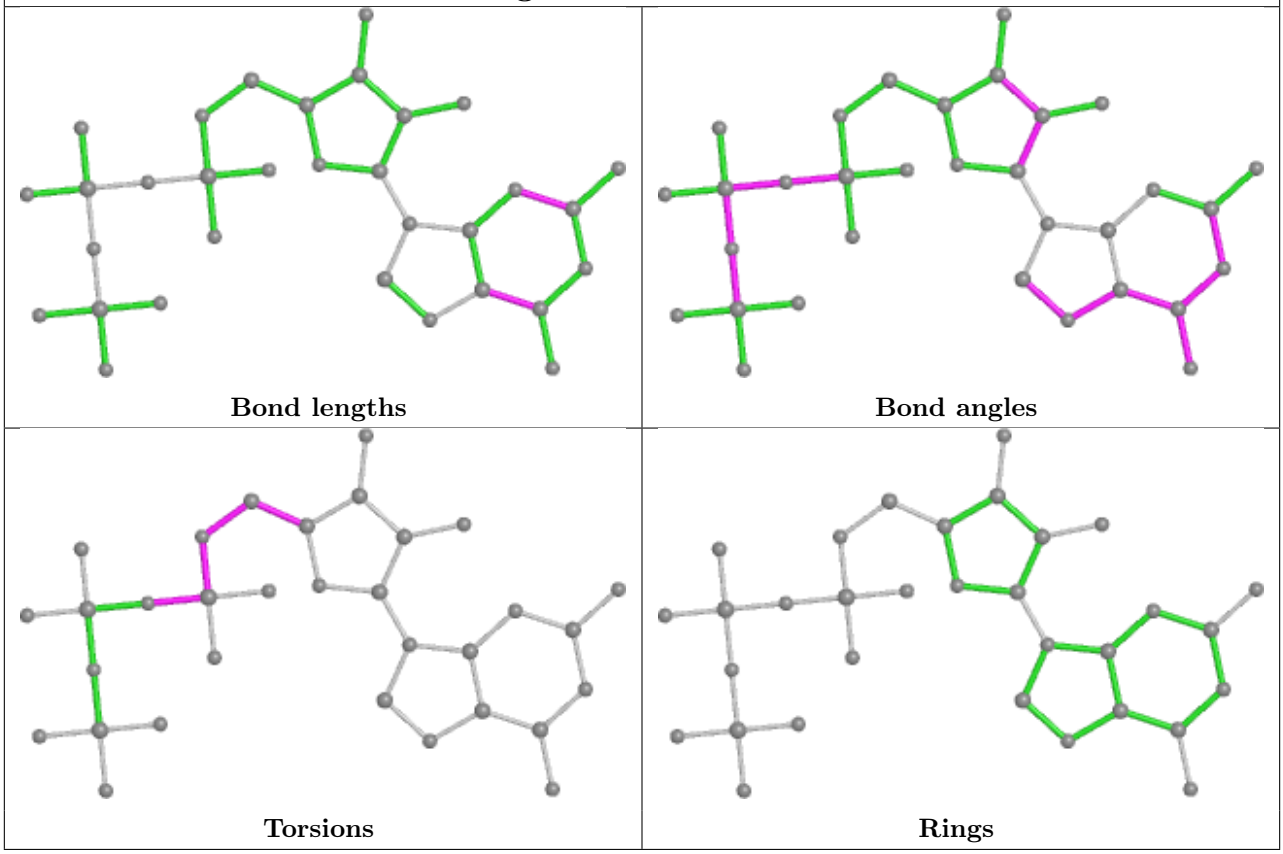


Rings

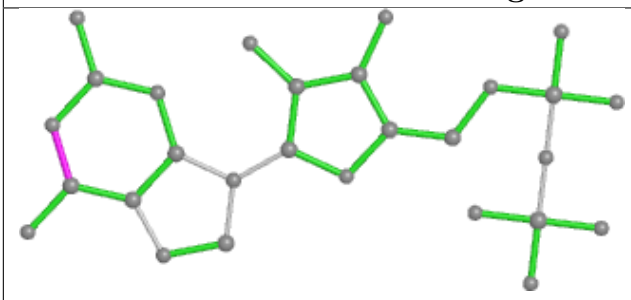
Ligand GDP GJ 502



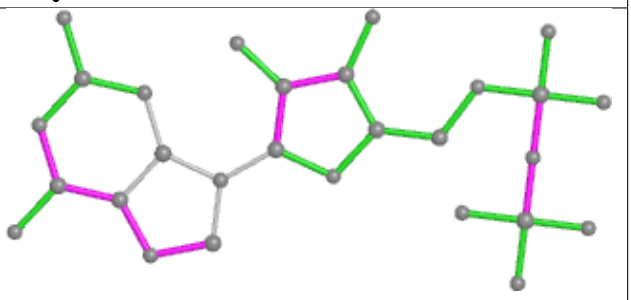
Ligand GTP IK 501



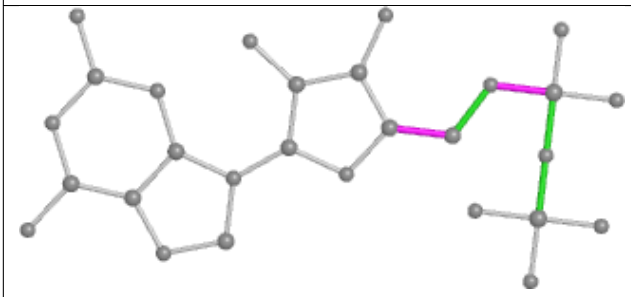
Ligand GDP QD 502



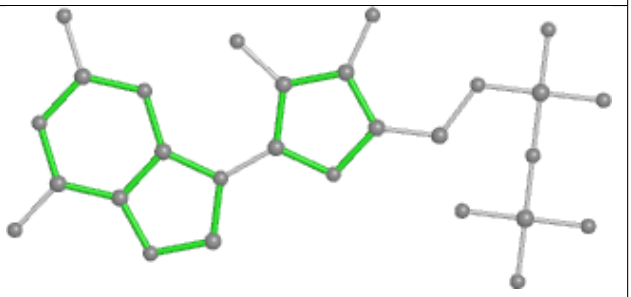
Bond lengths



Bond angles

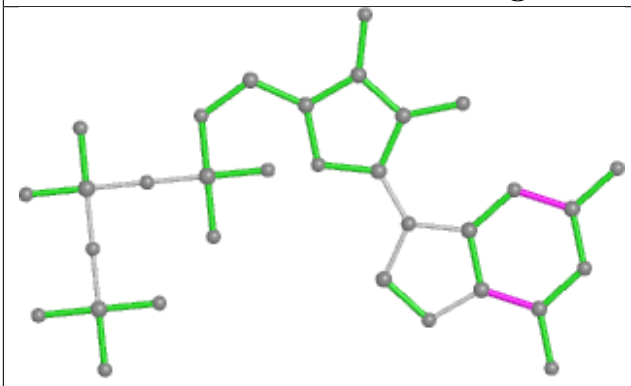


Torsions

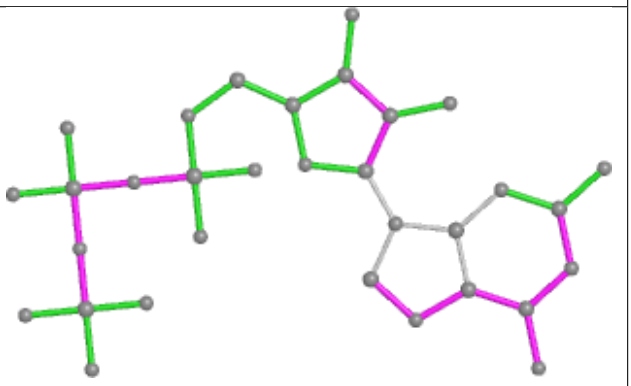


Rings

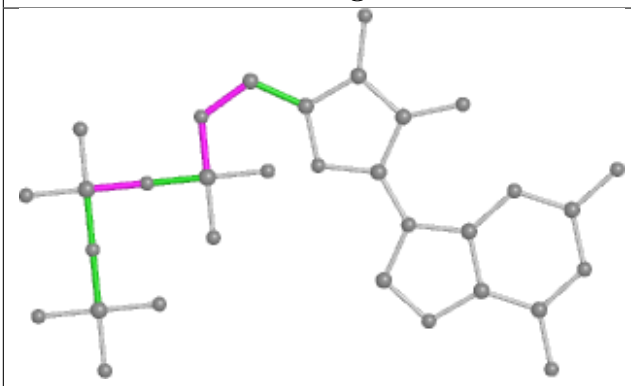
Ligand GTP TG 501



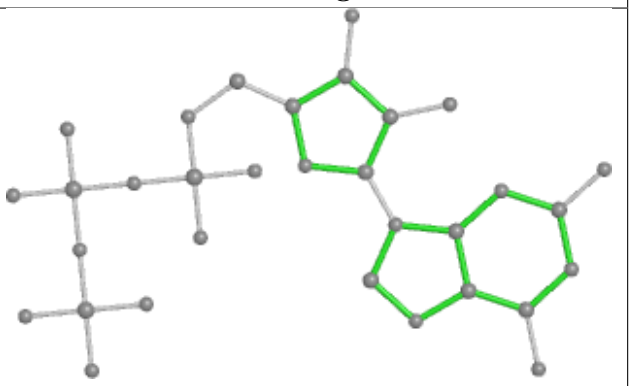
Bond lengths



Bond angles

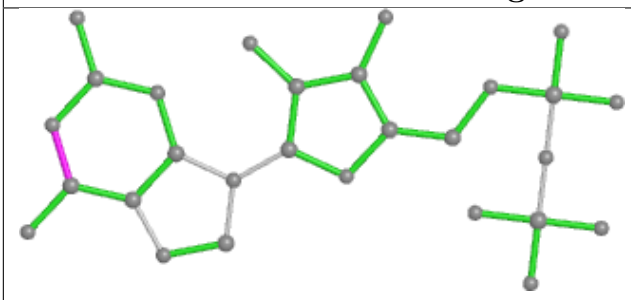


Torsions

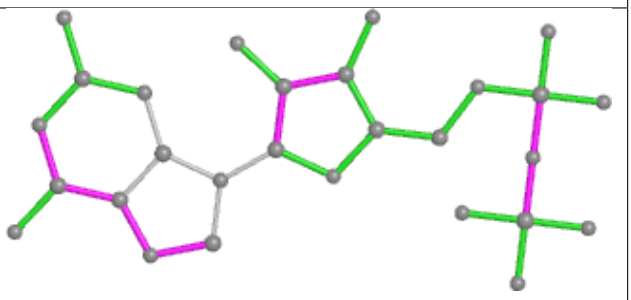


Rings

Ligand GDP KB 502



Bond lengths



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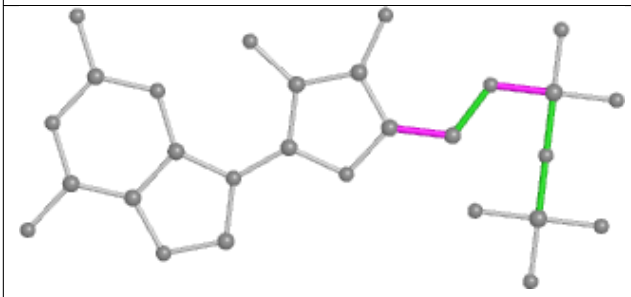

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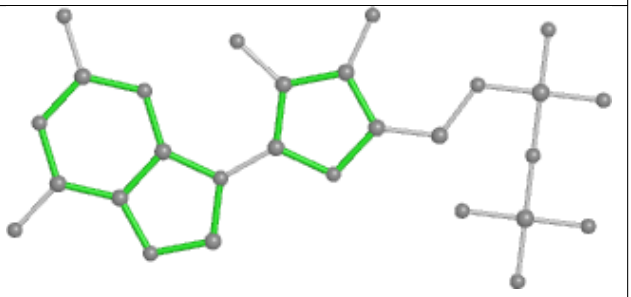
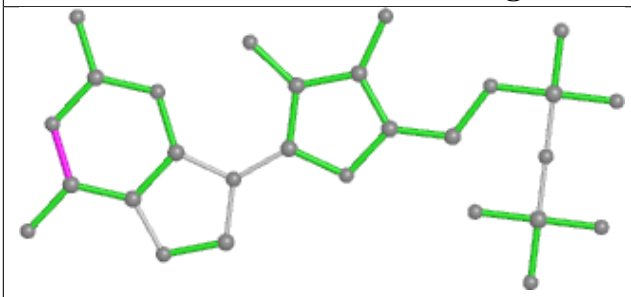


Rings

Ligand GDP MB 502



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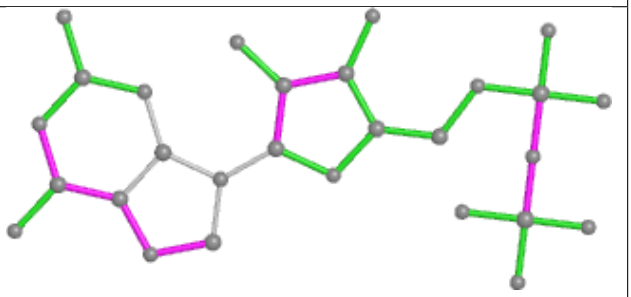
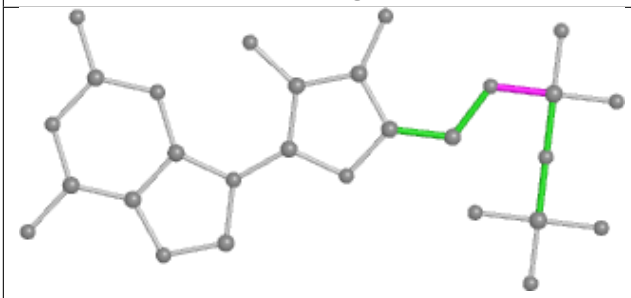


Bond angles



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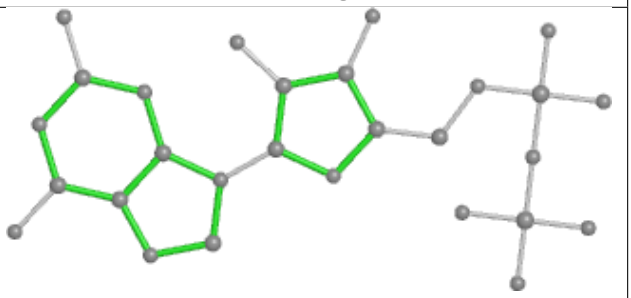
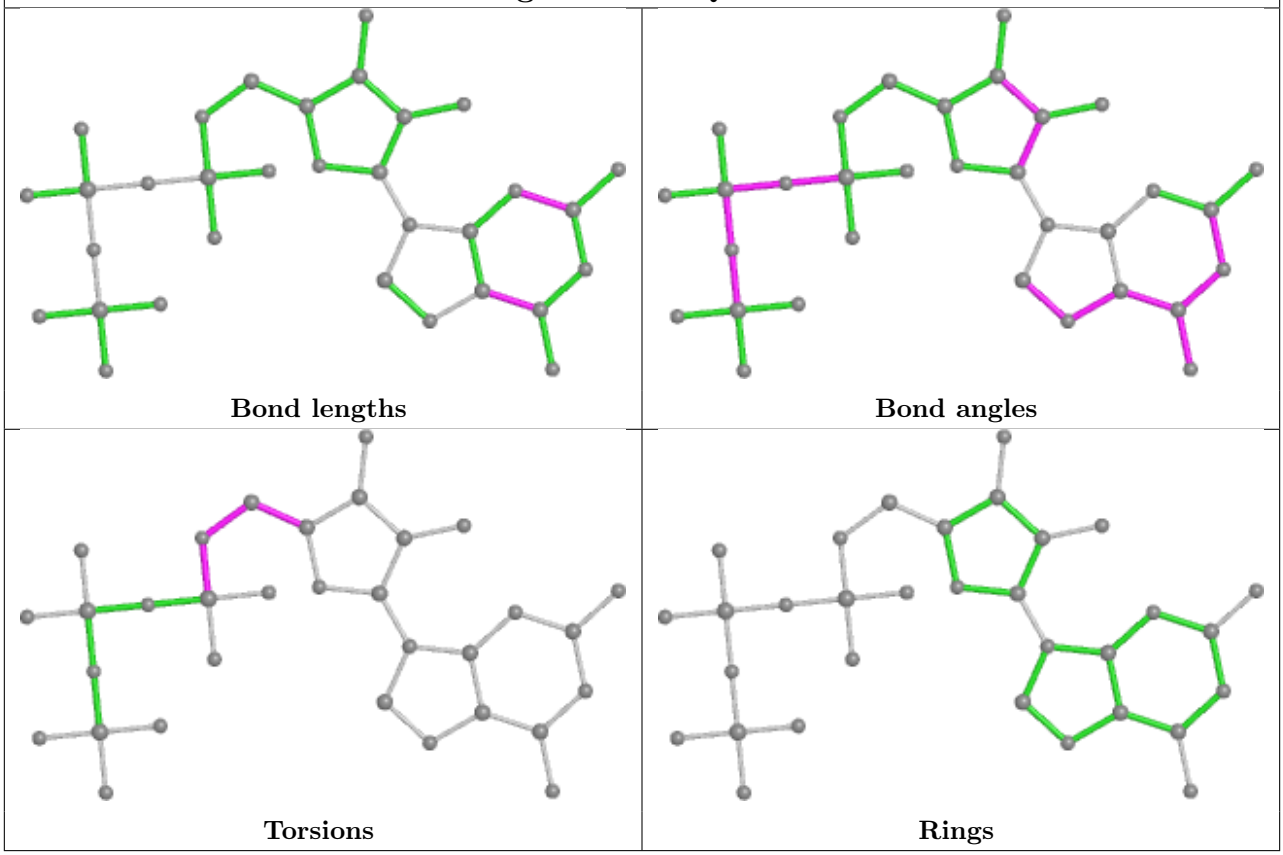


Rings

Ligand GTP QI 501



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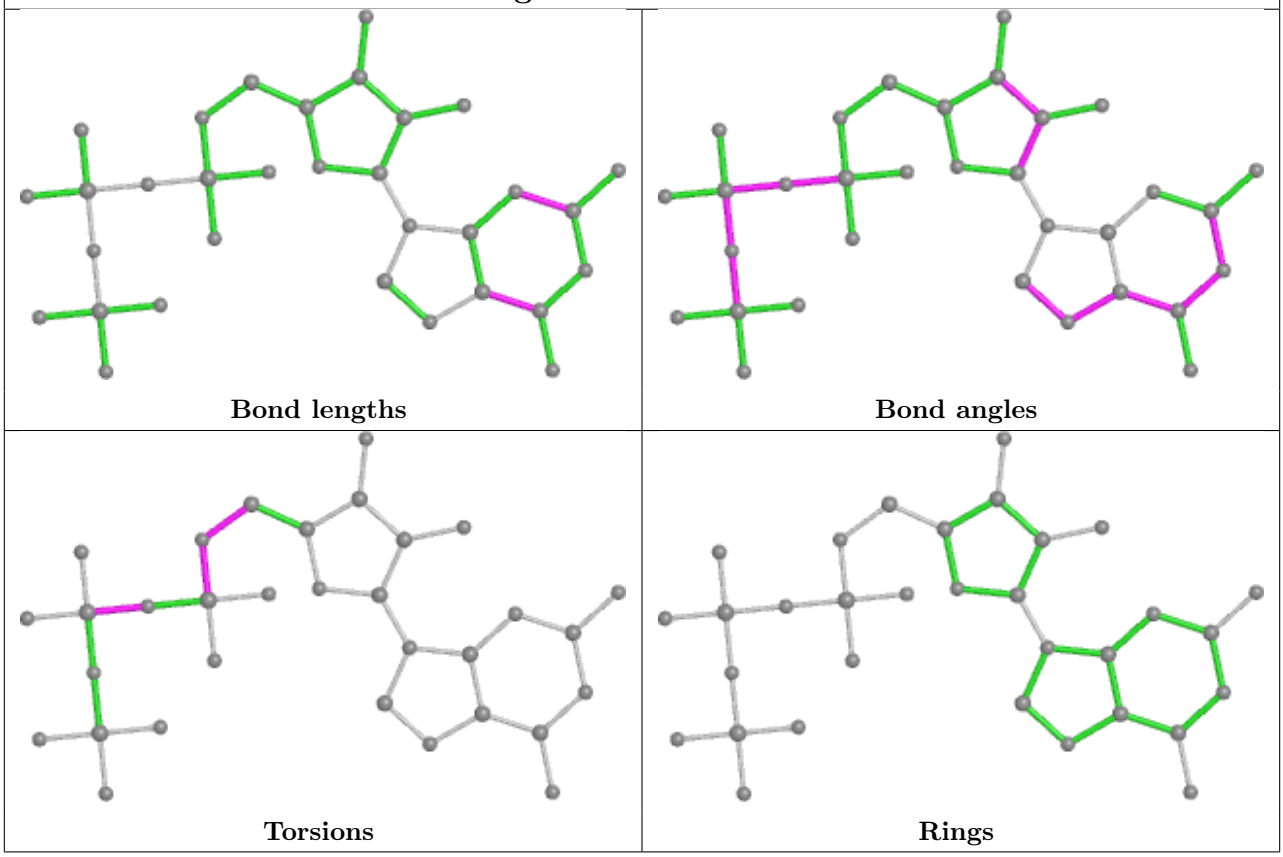

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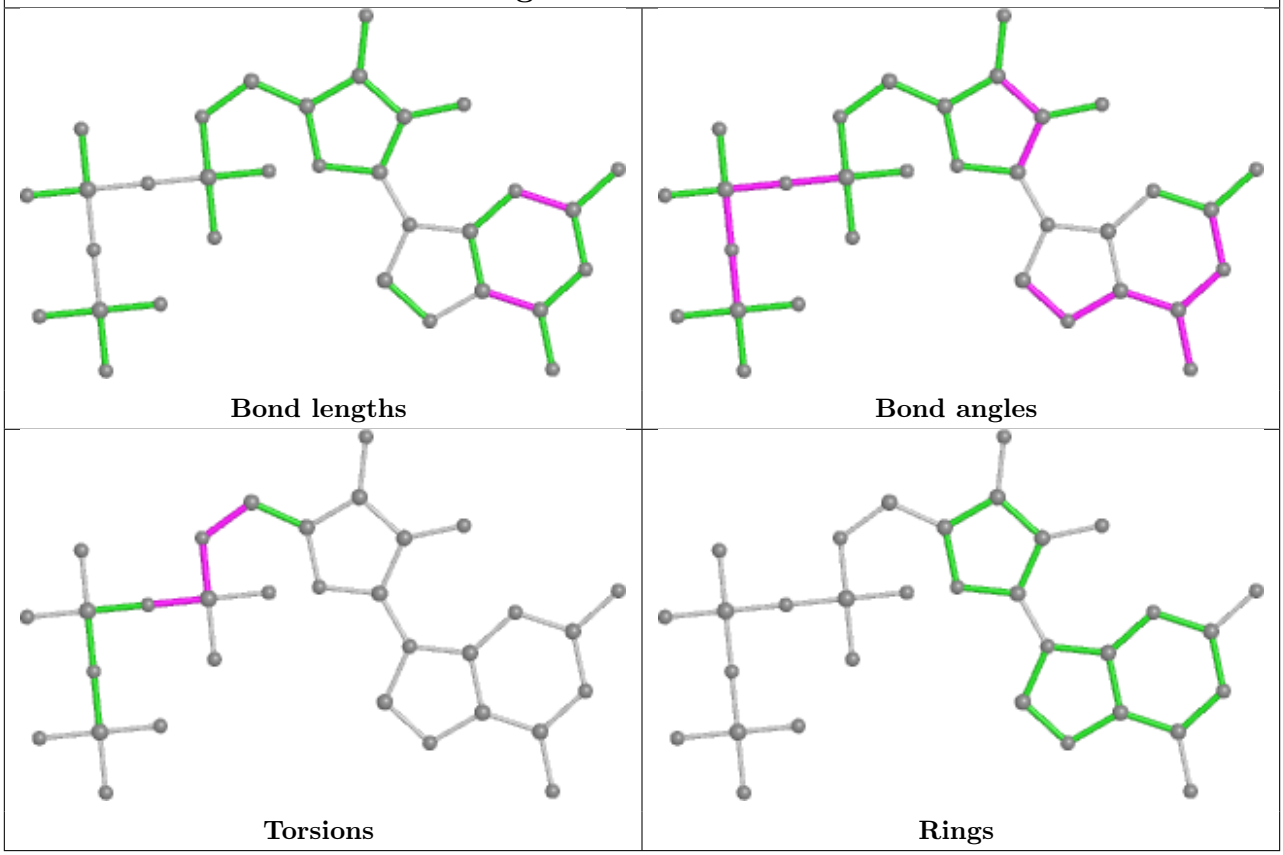
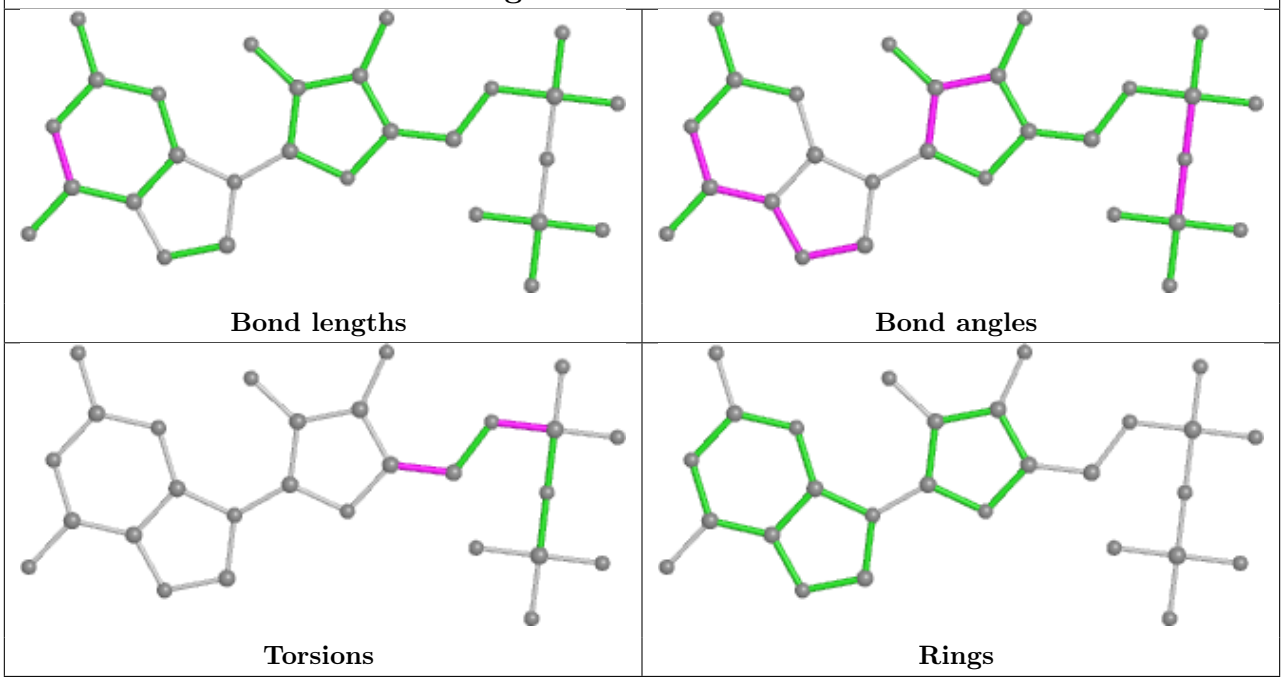
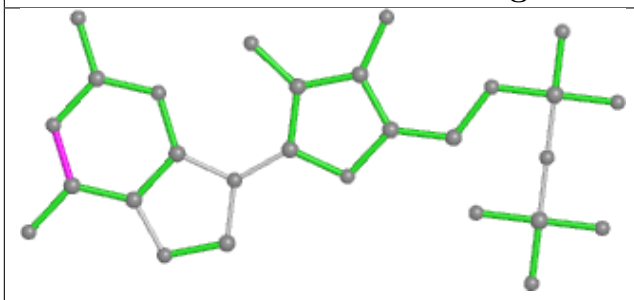


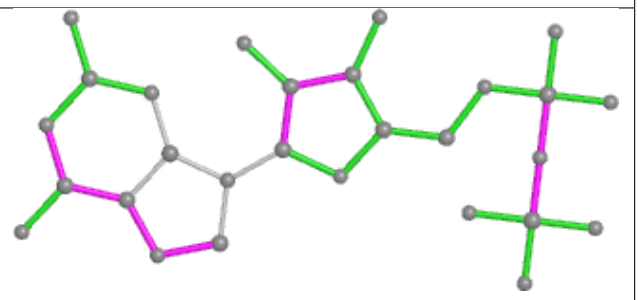
Ligand GDP WP 502



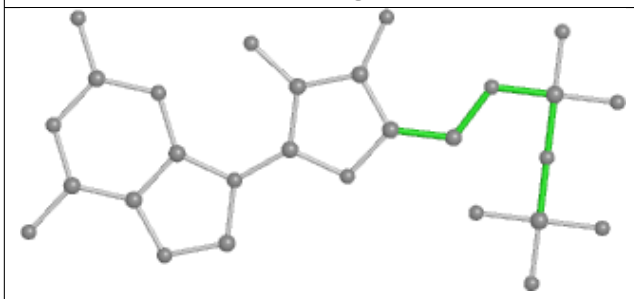
Ligand GDP HF 502



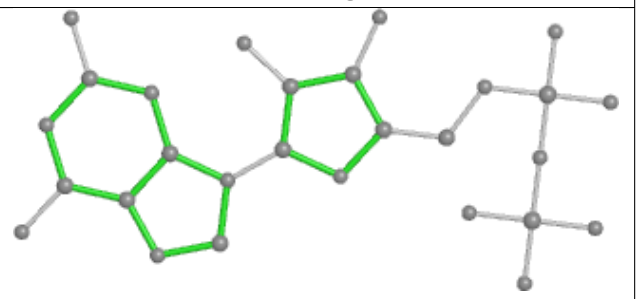
Bond lengths



Bond angles

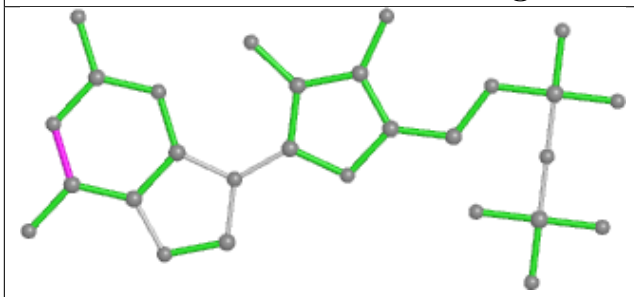


Torsions



Rings

Ligand GDP SD 502



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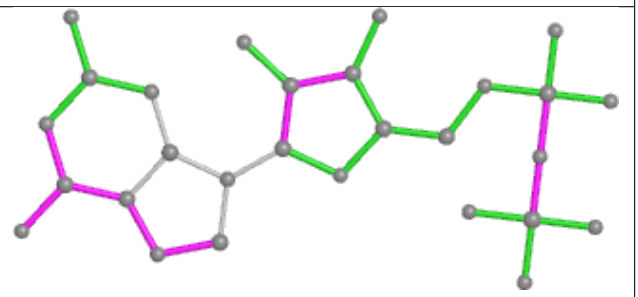

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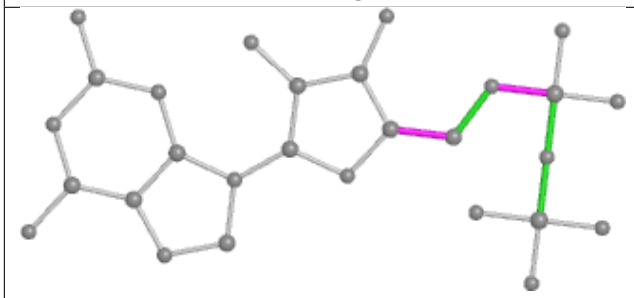

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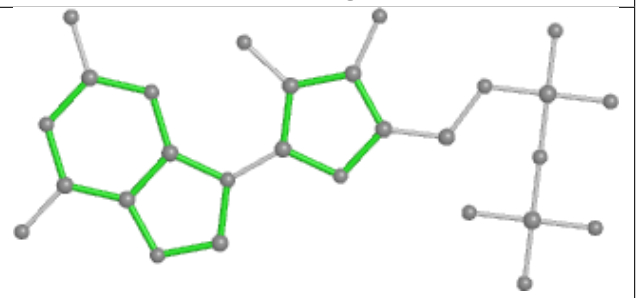
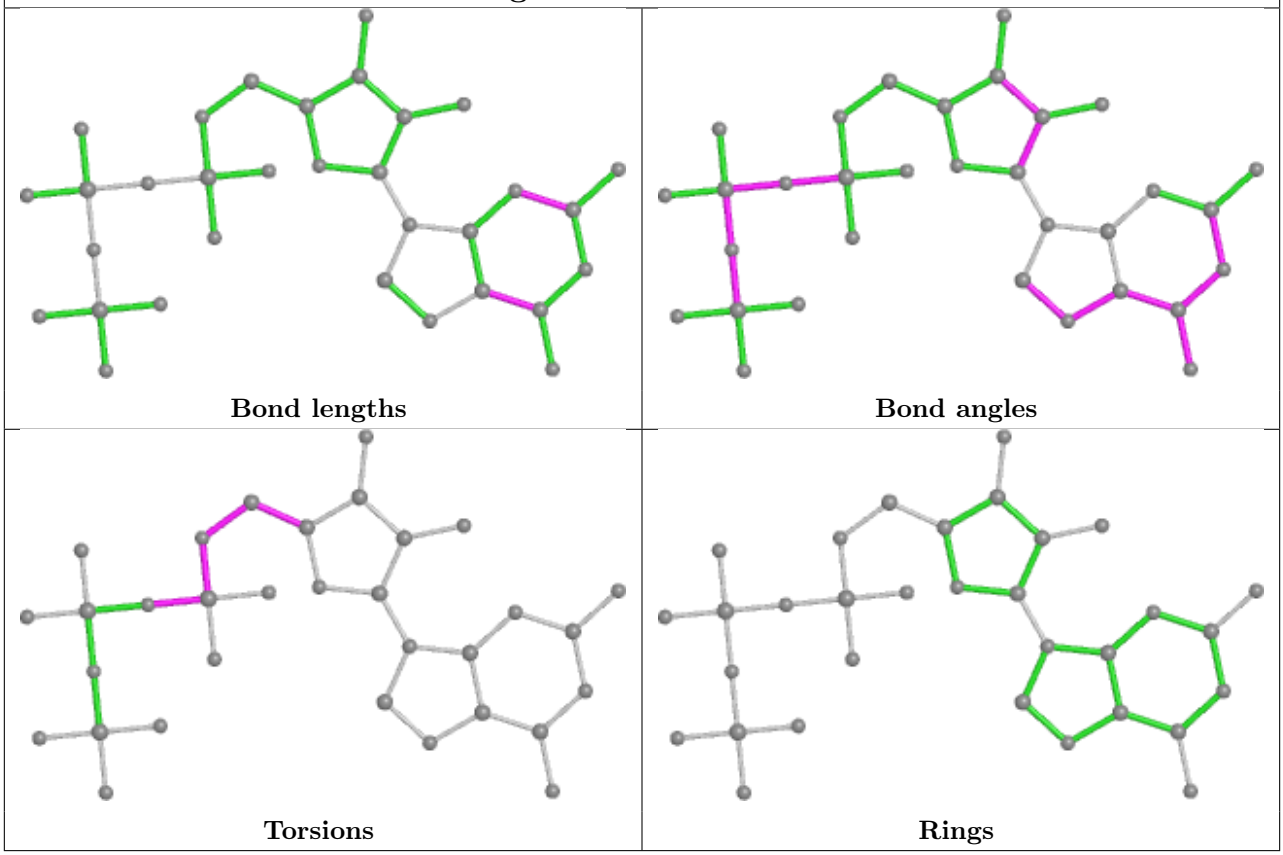
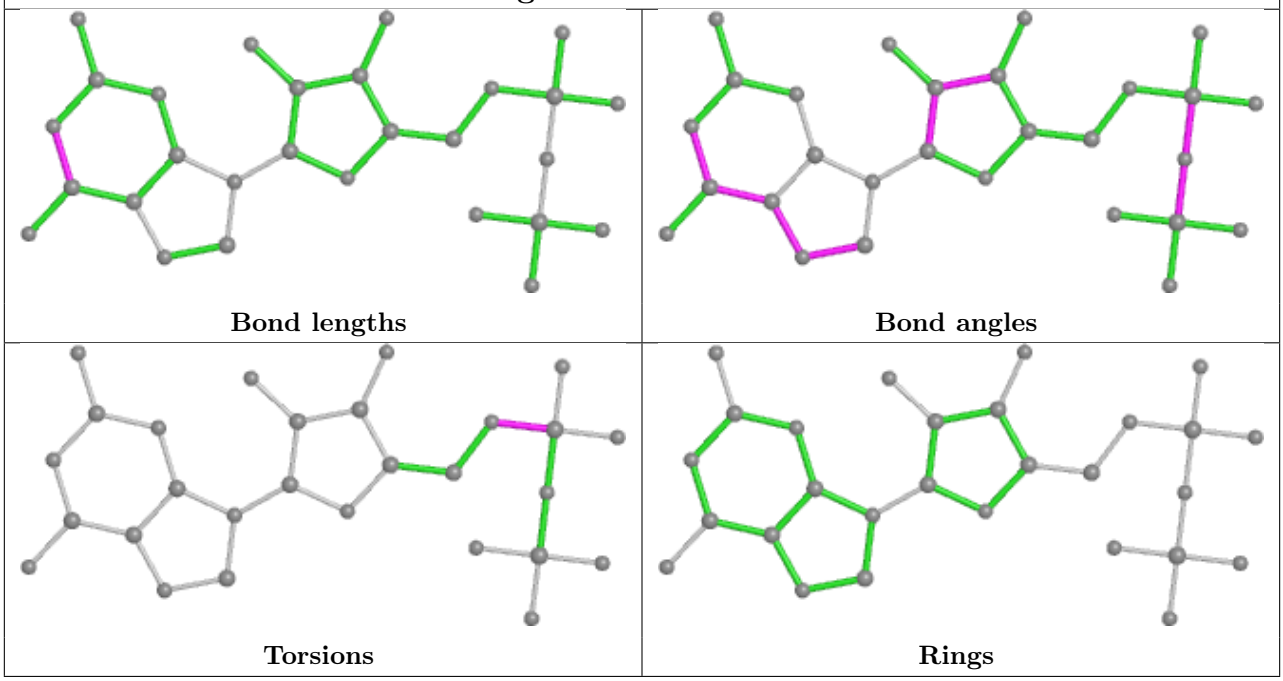


Rings

Ligand GTP GC 501



Ligand GDP IF 502



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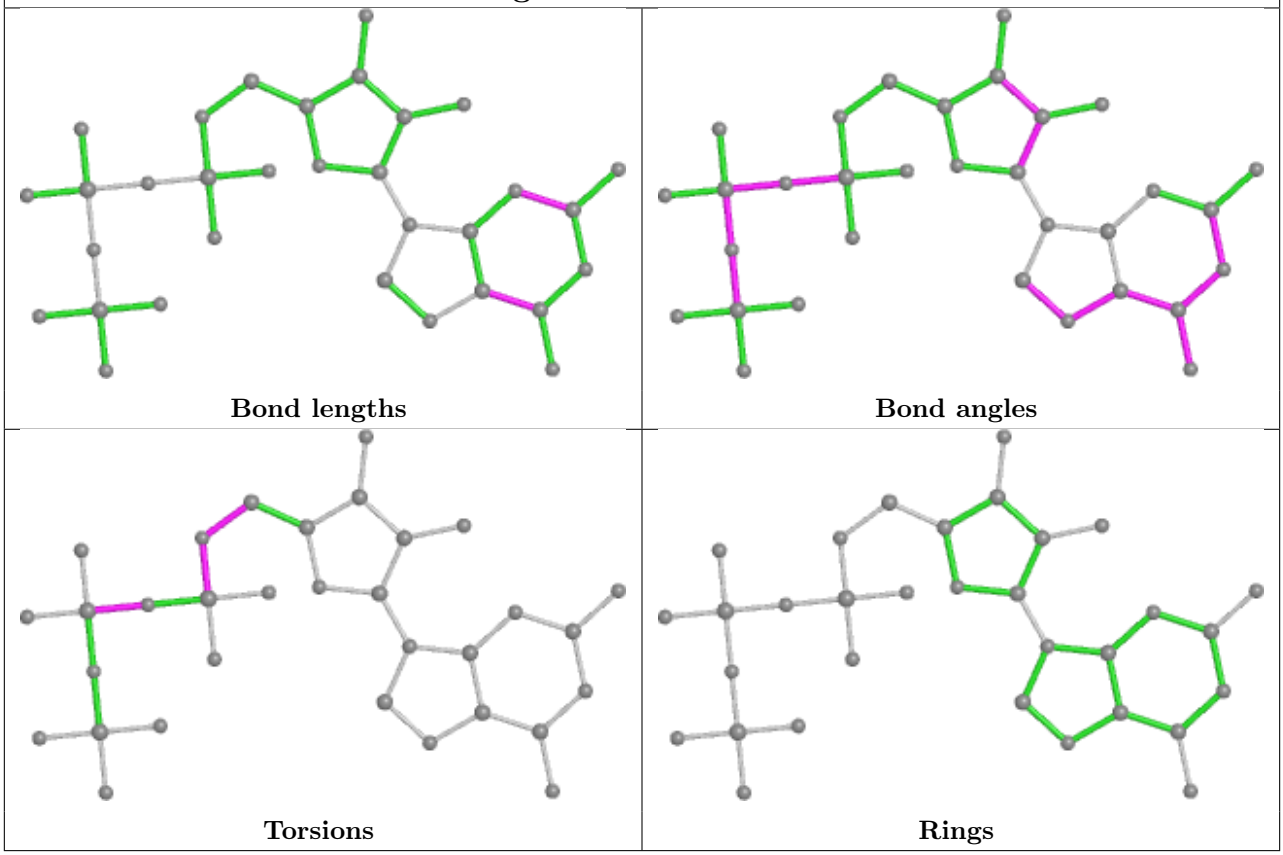
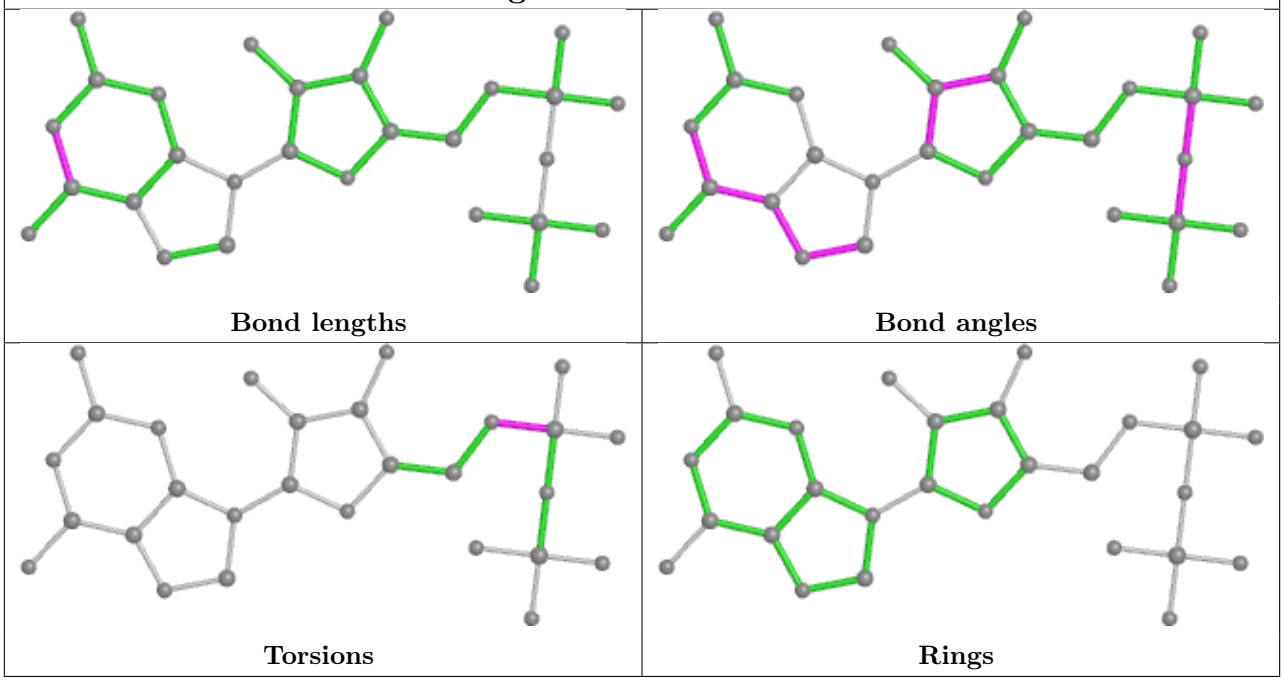
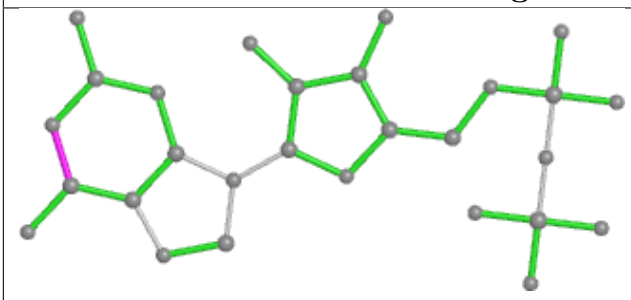


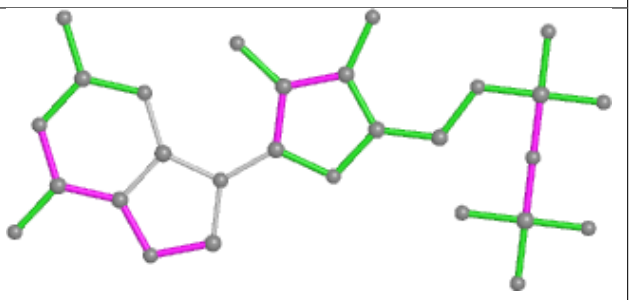
Ligand GDP CH 502



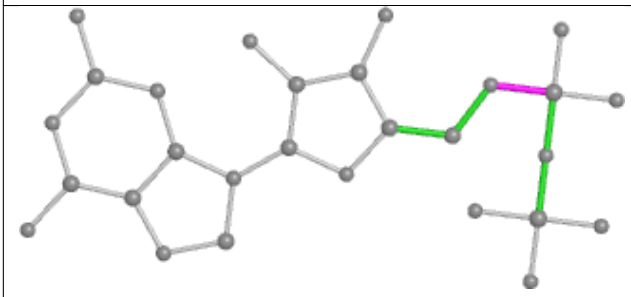
Ligand GDP HJ 502



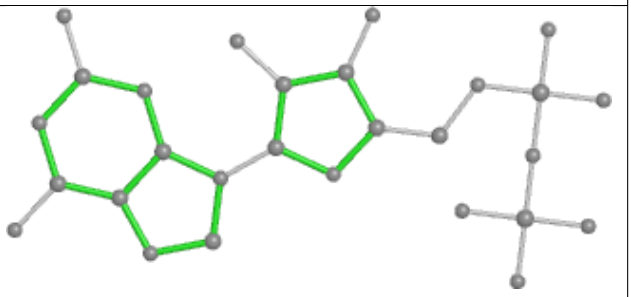
Bond lengths



Bond angles

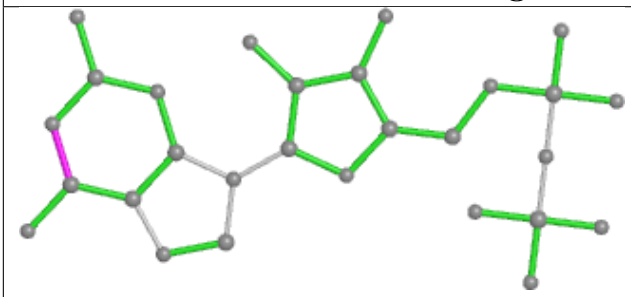


Torsions



Rings

Ligand GDP BD 502



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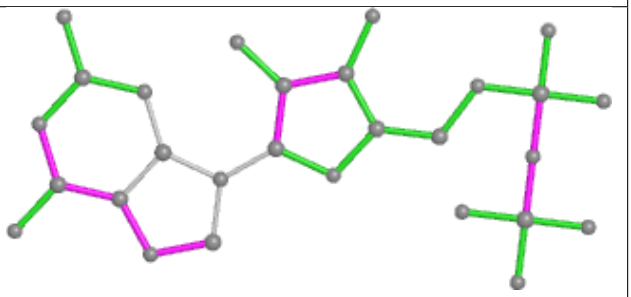
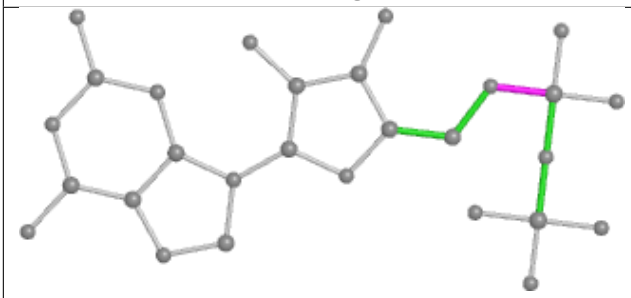
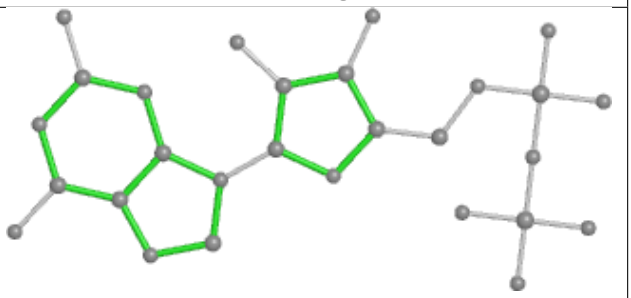


Bond angles

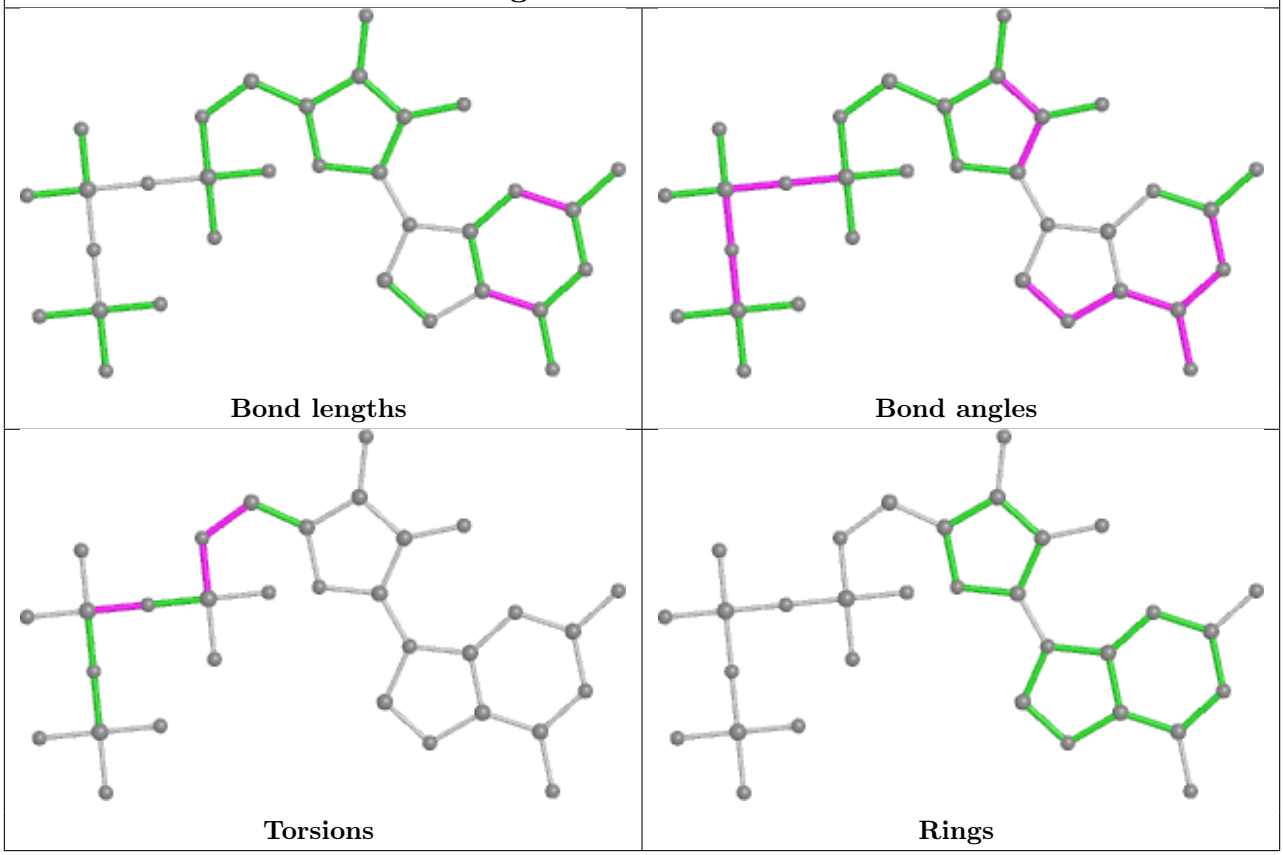


Torsions

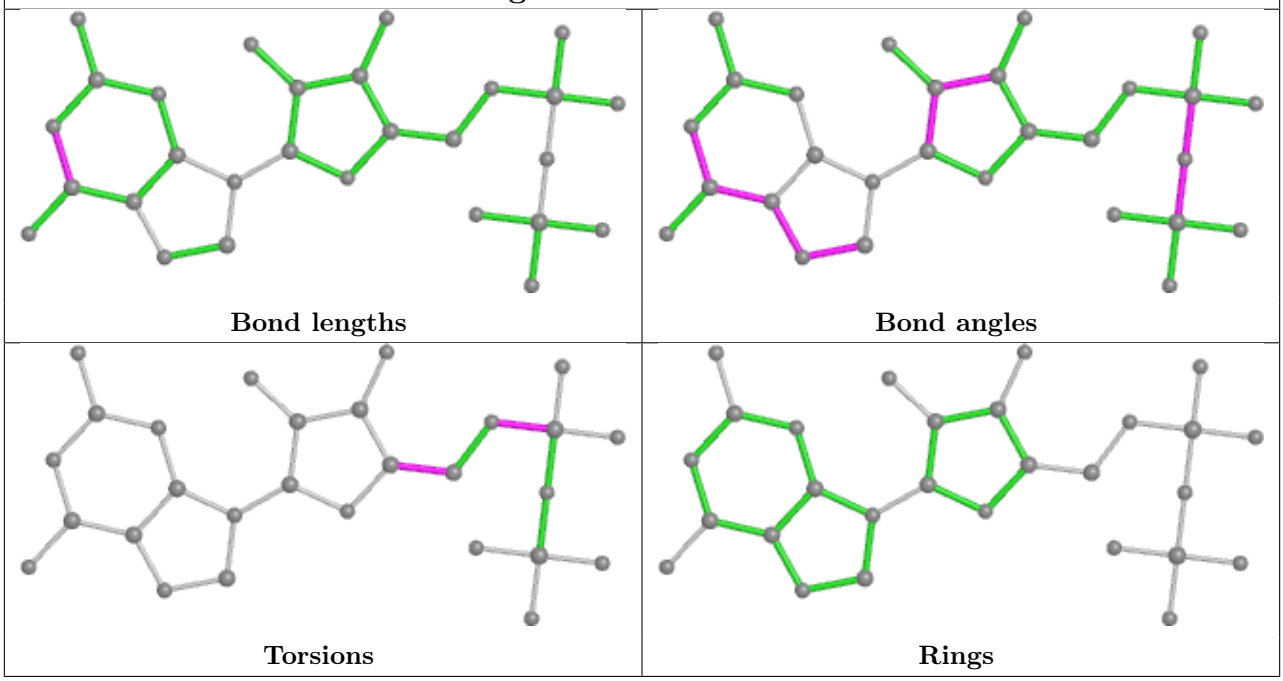


Rings

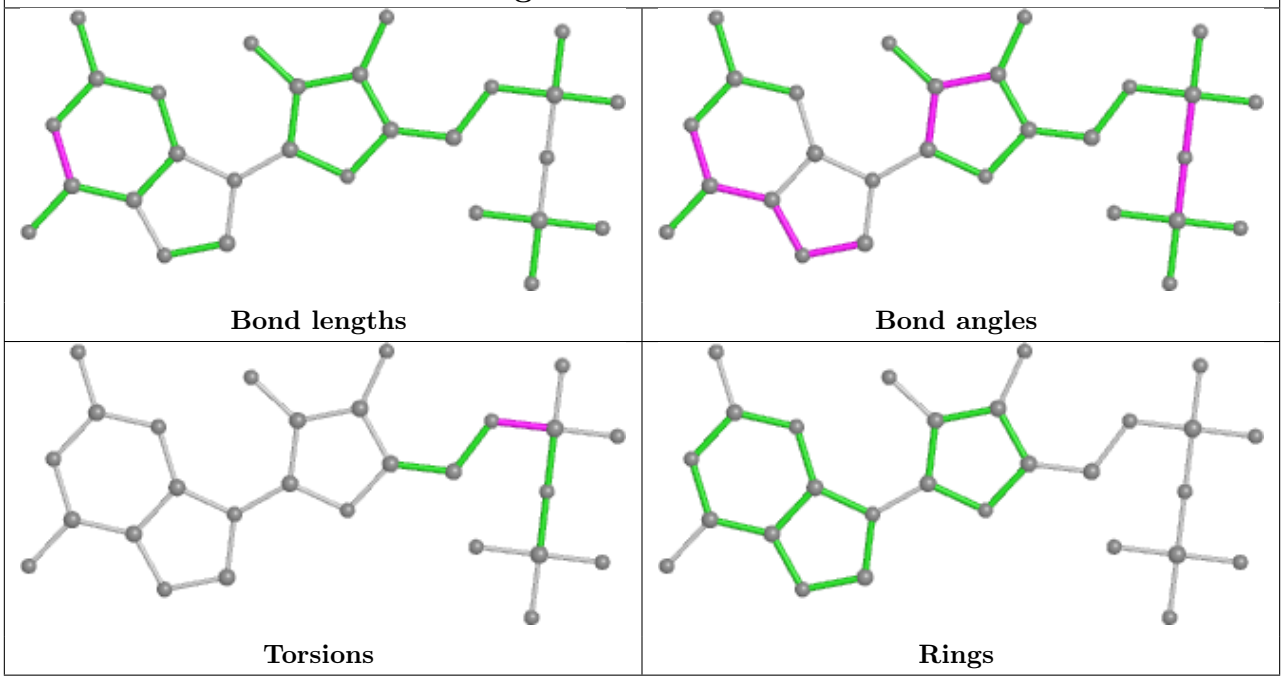
Ligand GTP KC 501



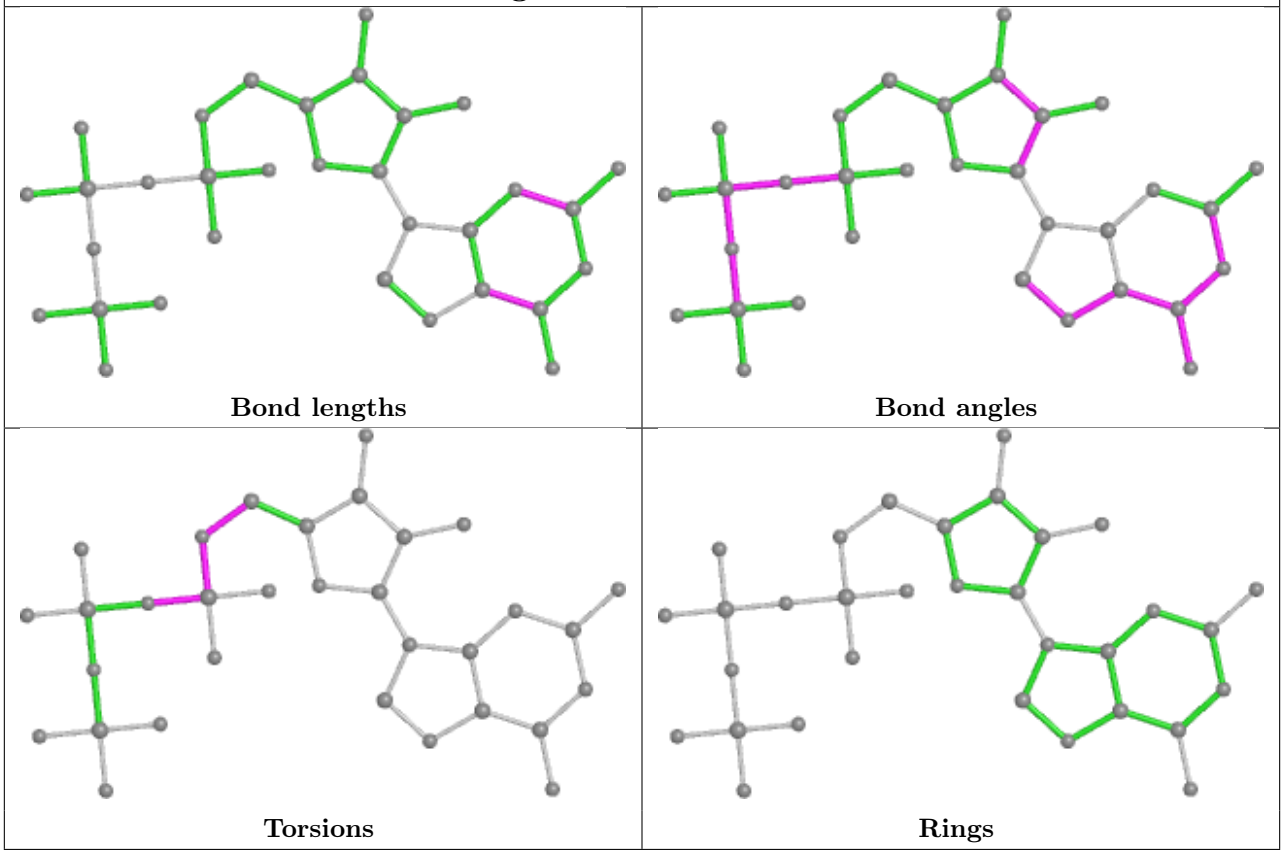
Ligand GDP GB 502



Ligand GDP IH 502



Ligand GTP EG 501



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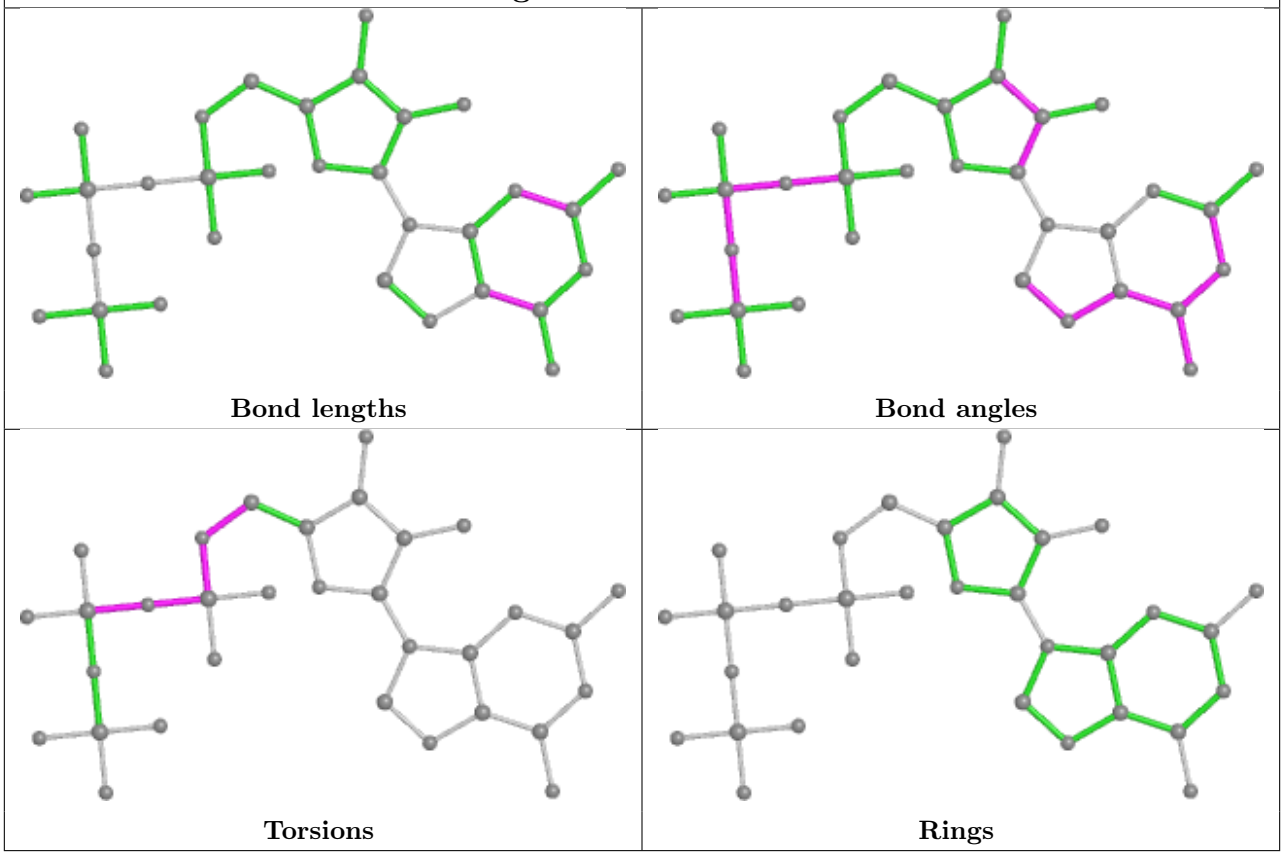
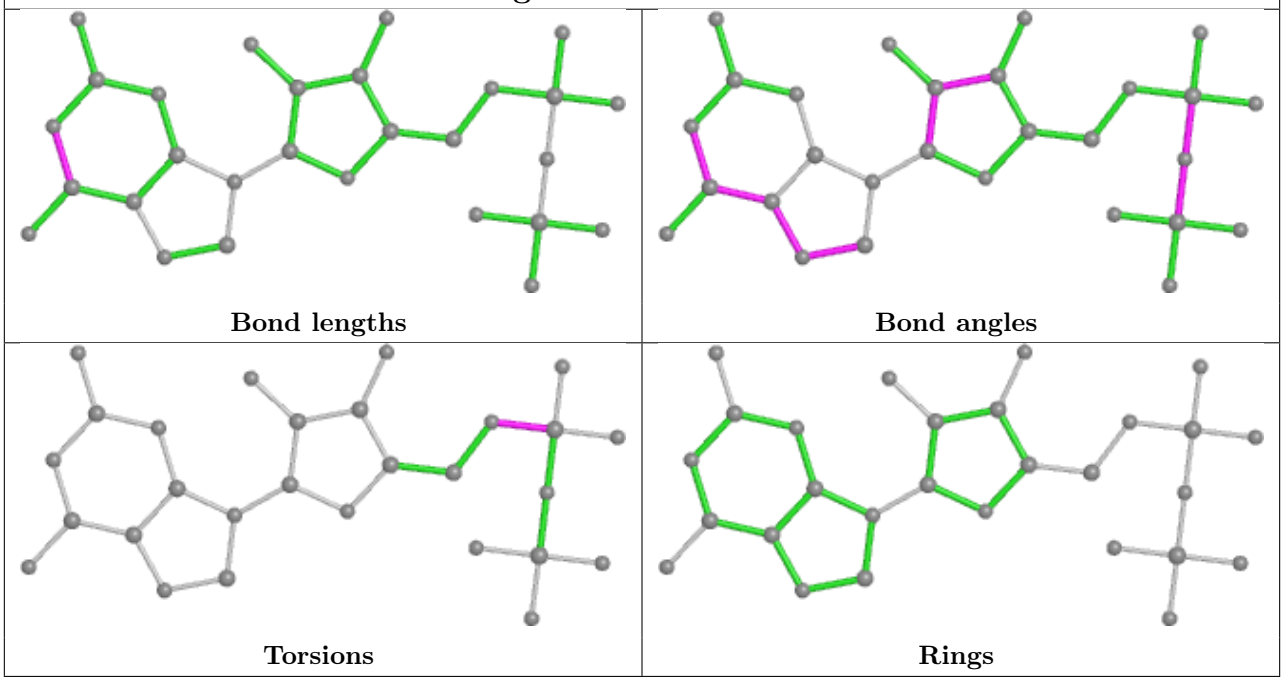


Ligand GDP JB 502



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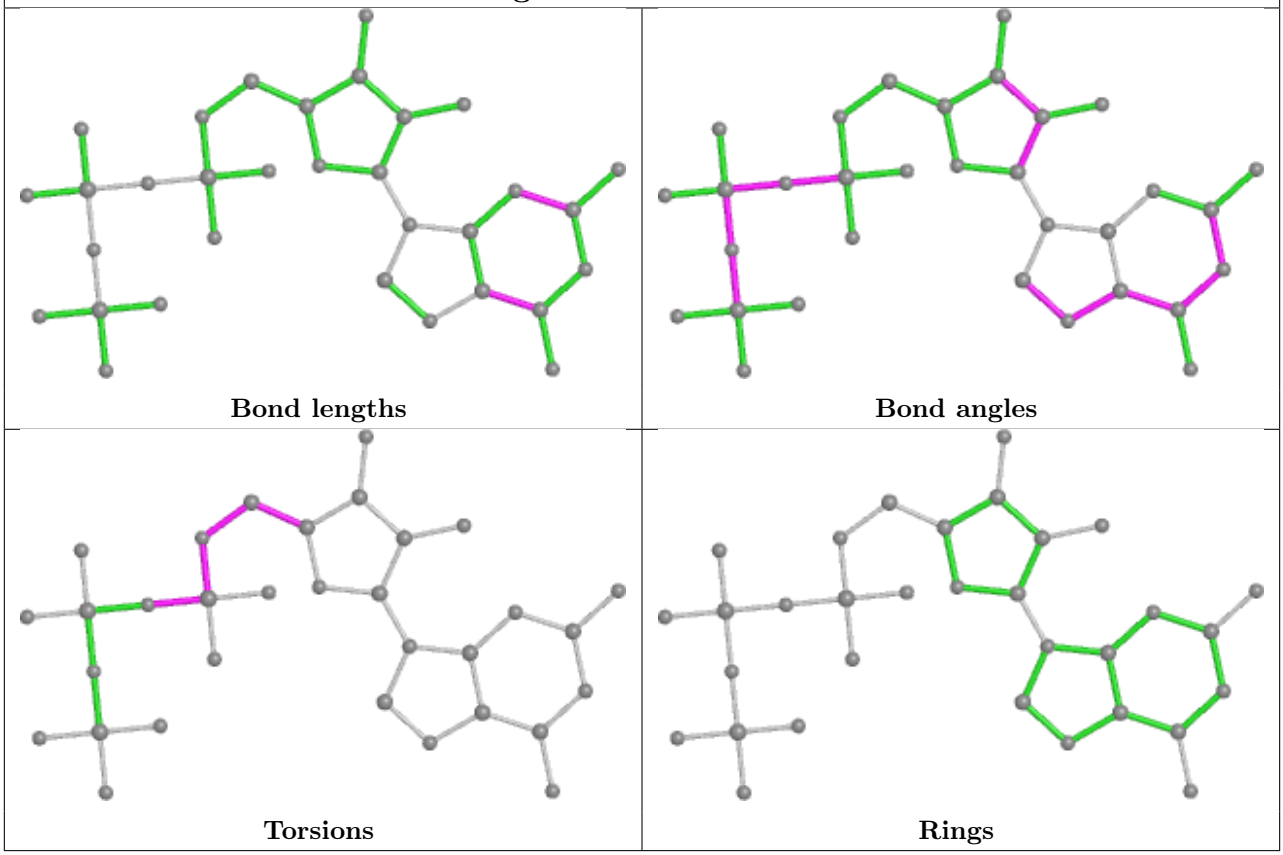
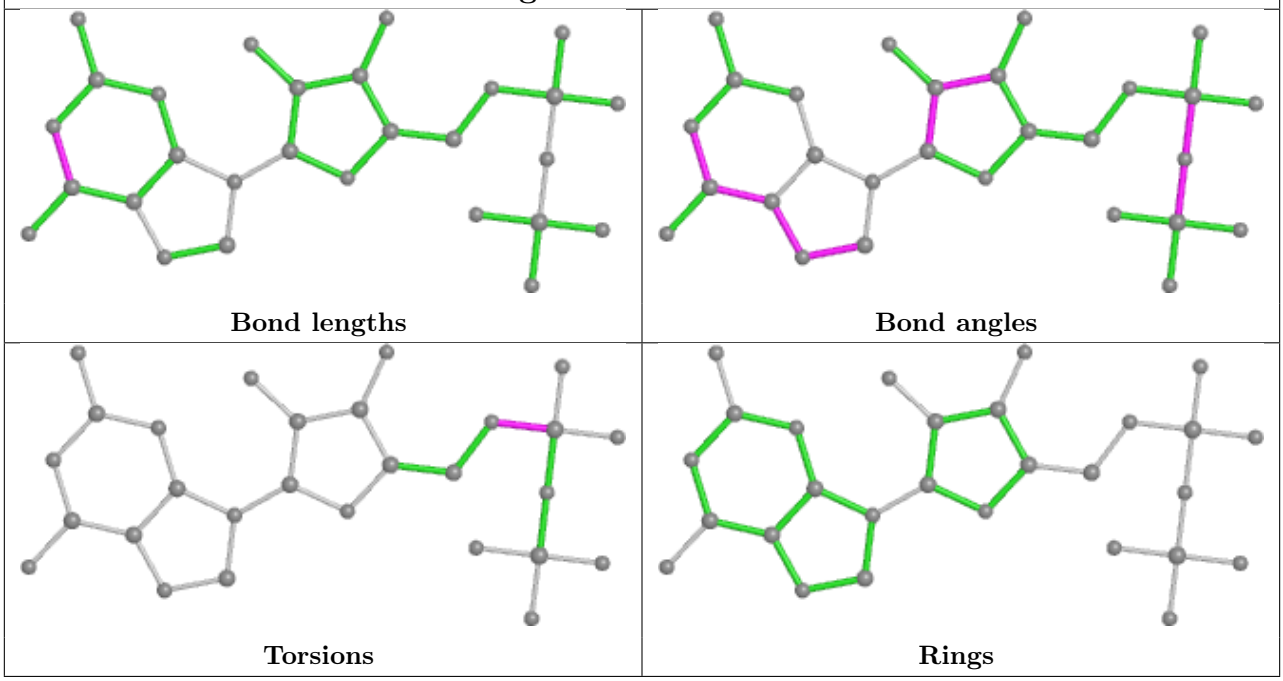
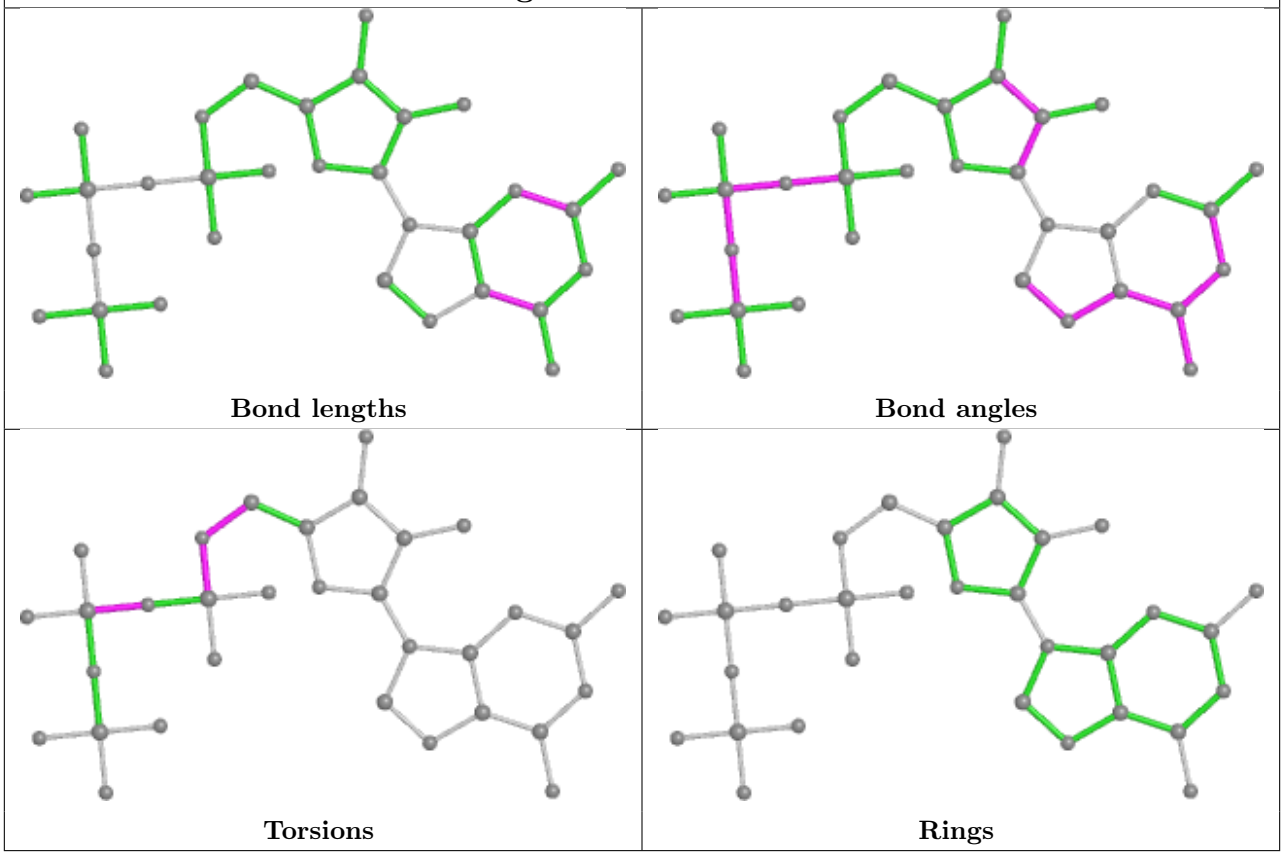


Ligand GDP IJ 502



Ligand GTP KI 501



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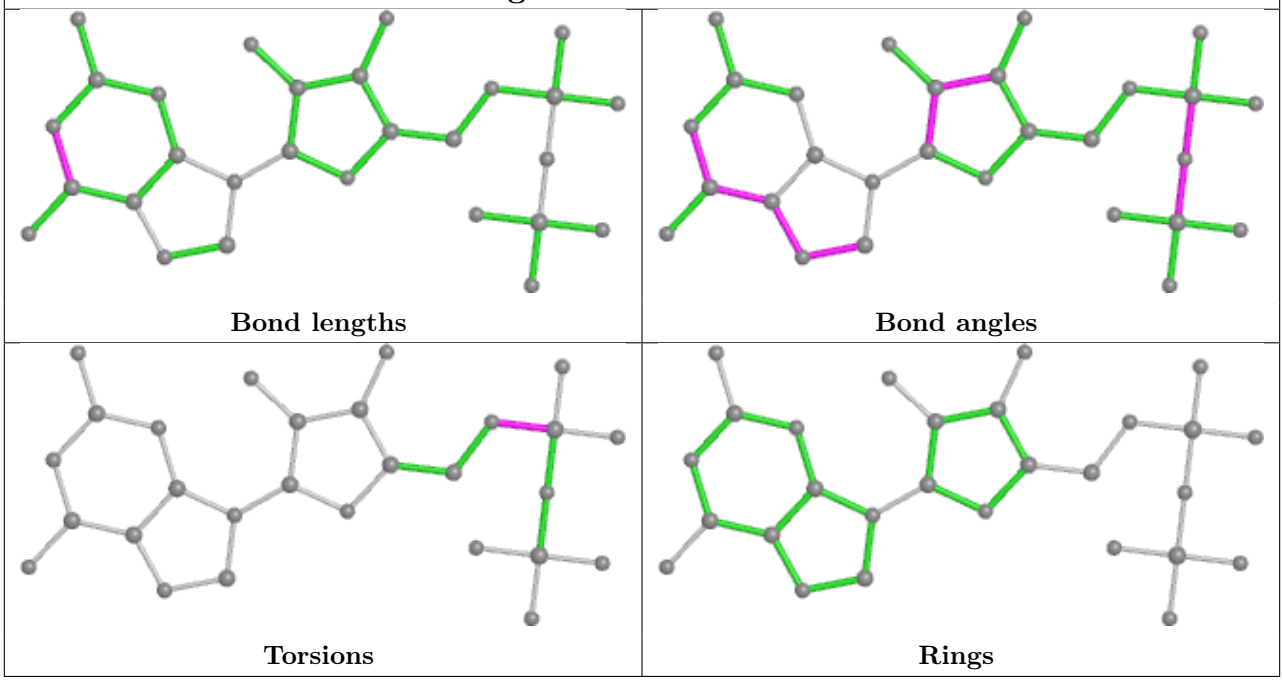
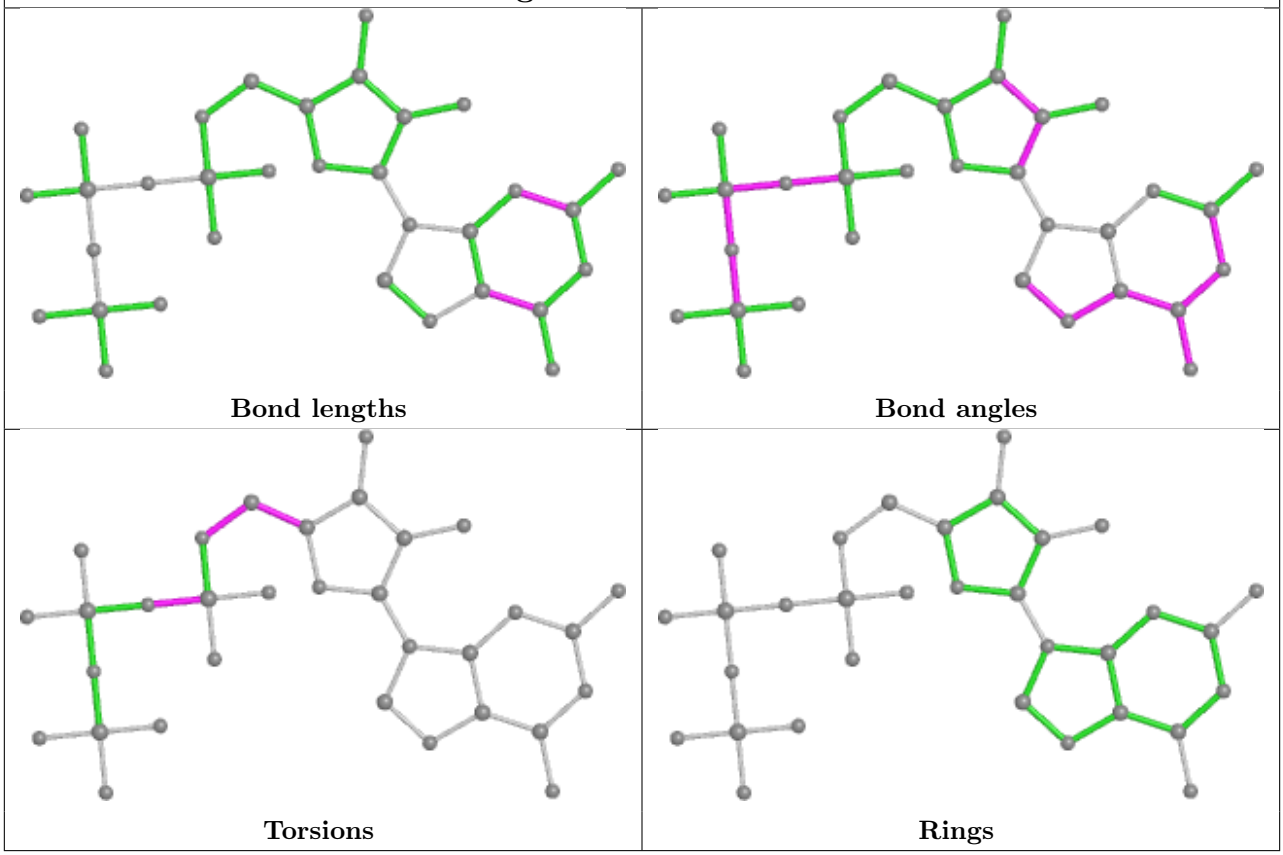


Ligand GTP AI 501



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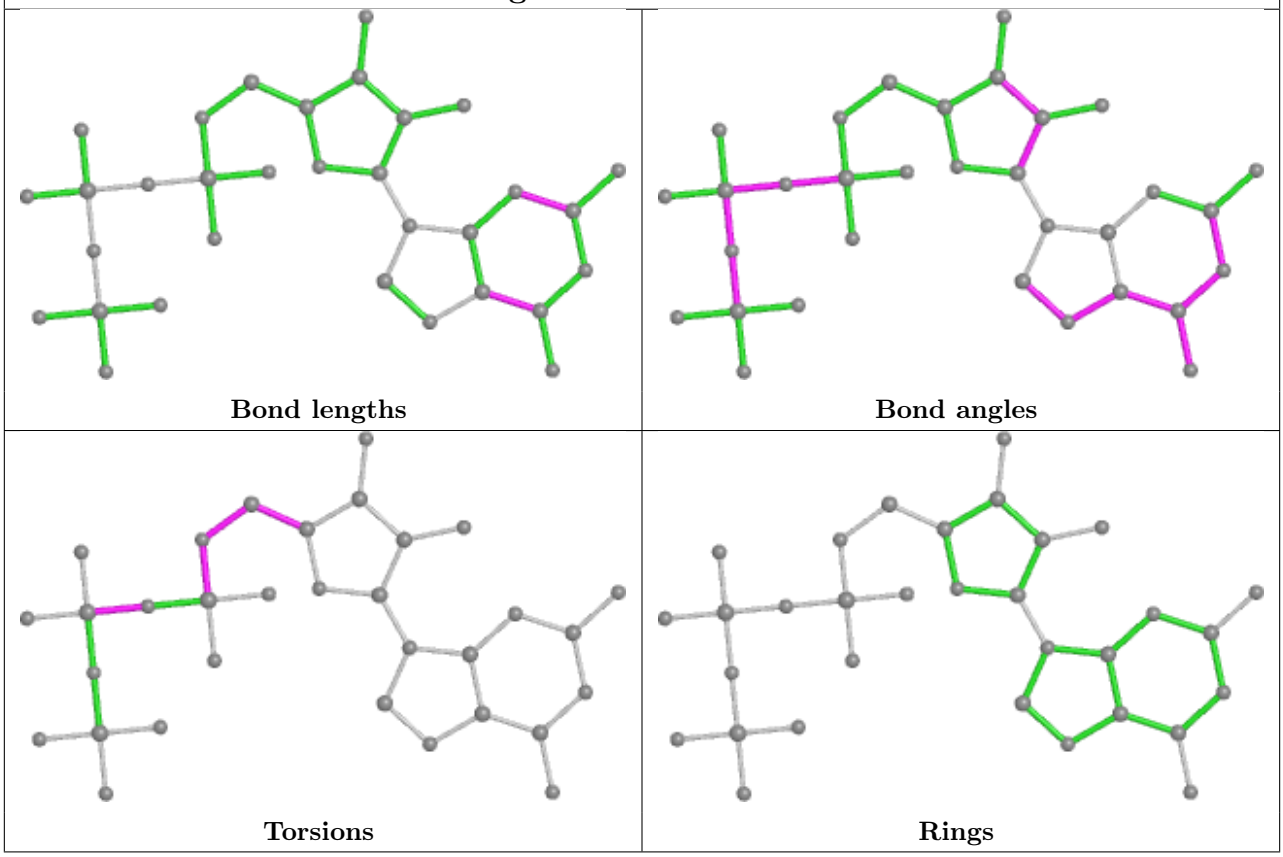

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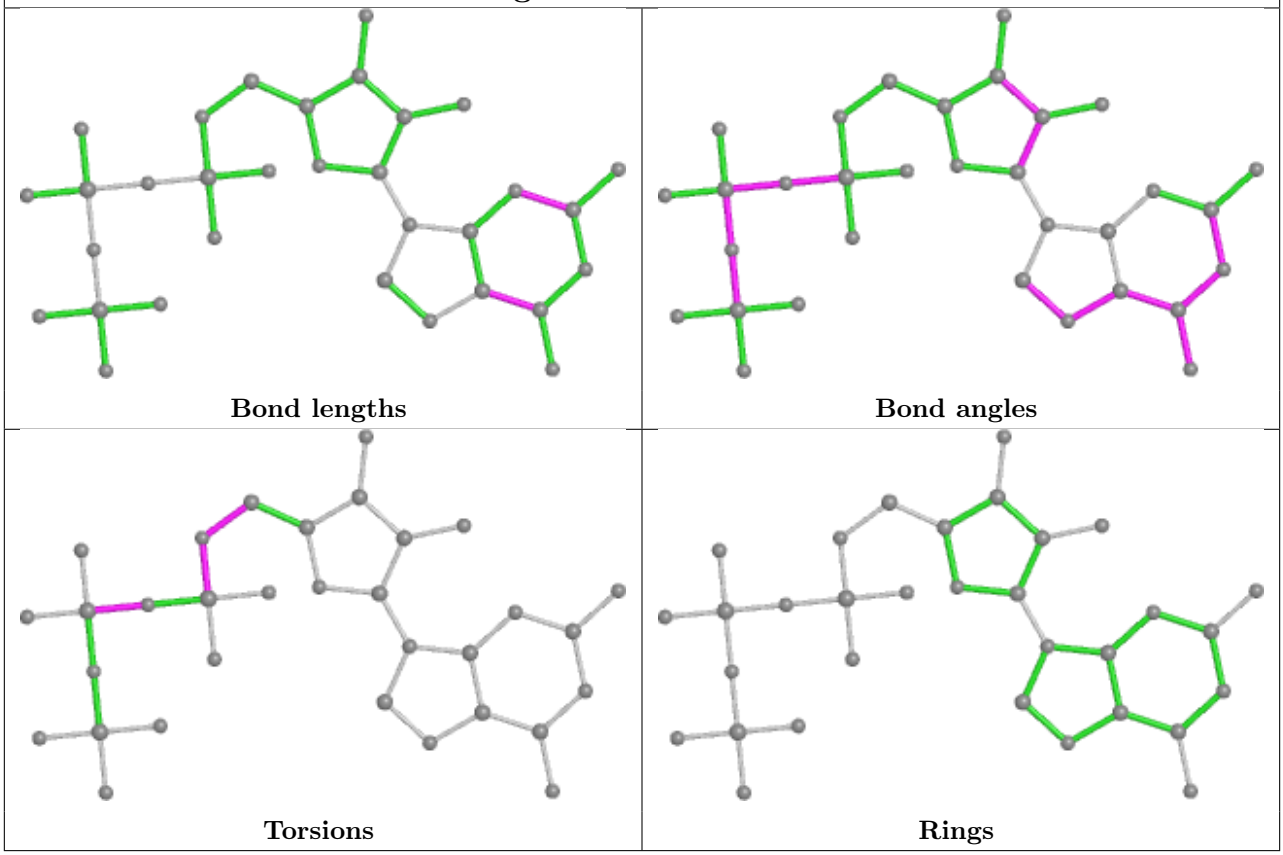

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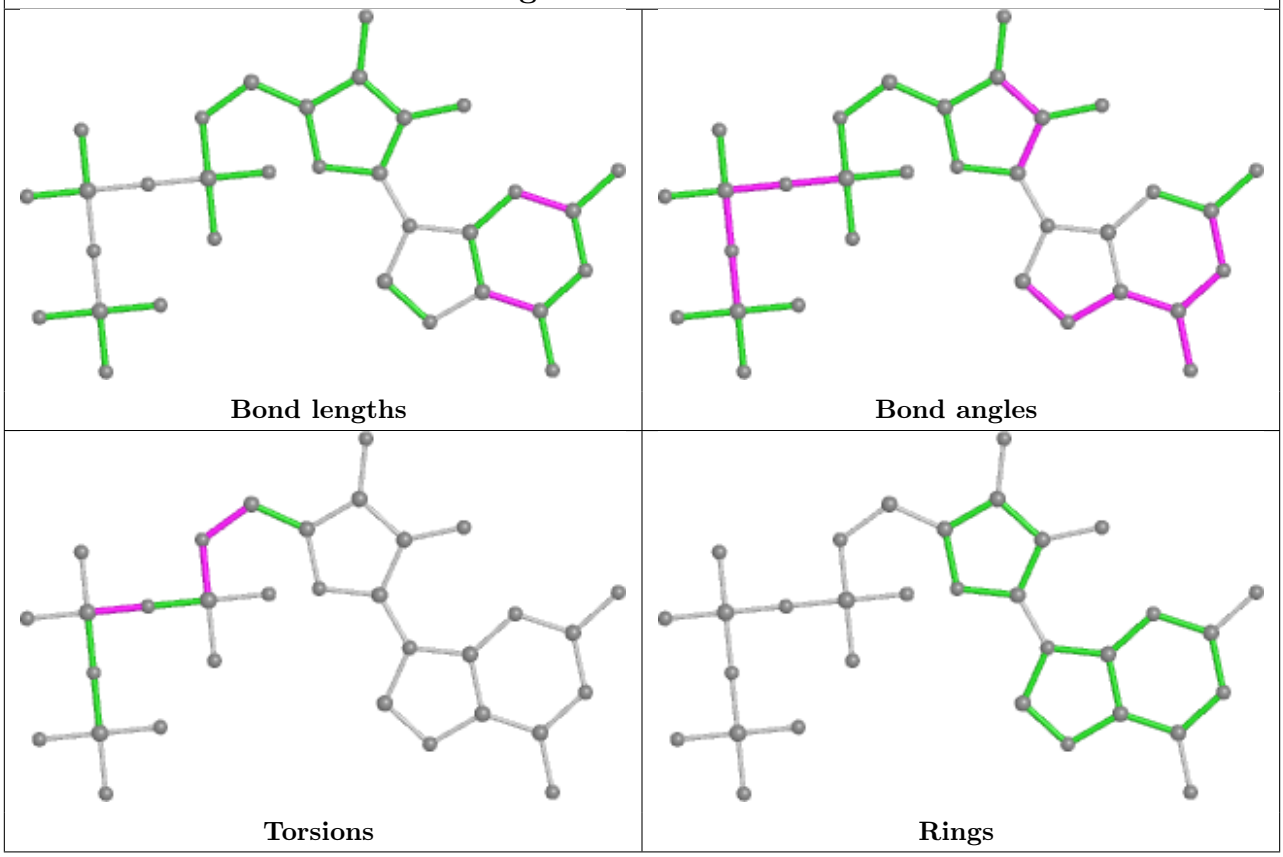

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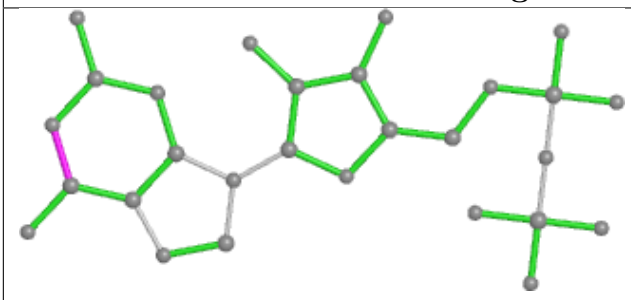
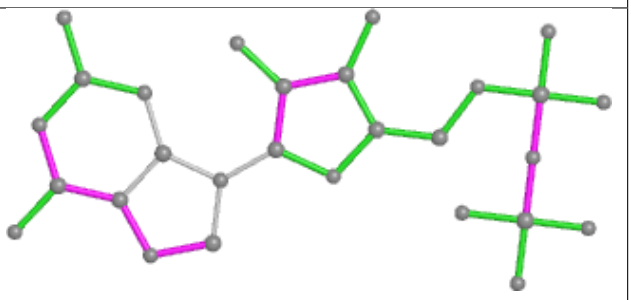
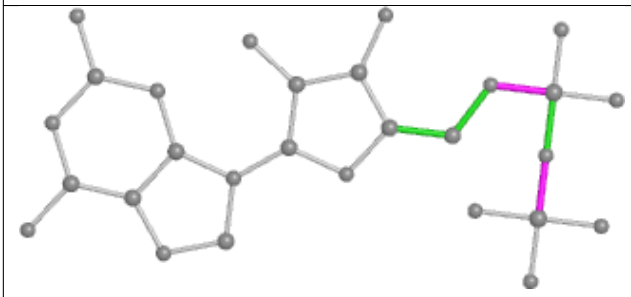


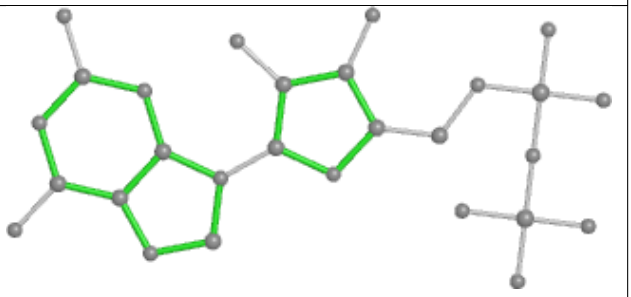
Bond lengths



Bond angles

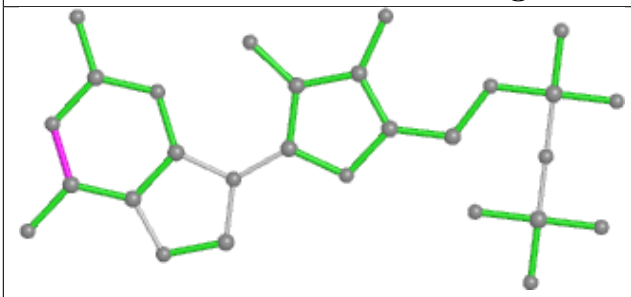


Torsions



Rings

Ligand GDP NL 502



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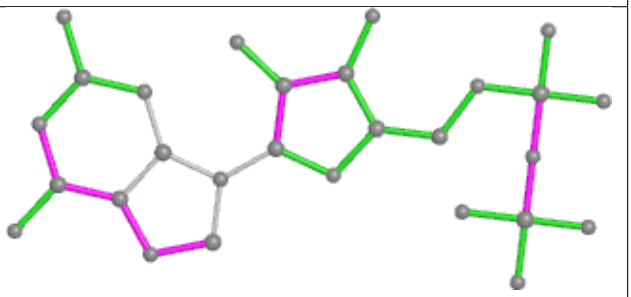
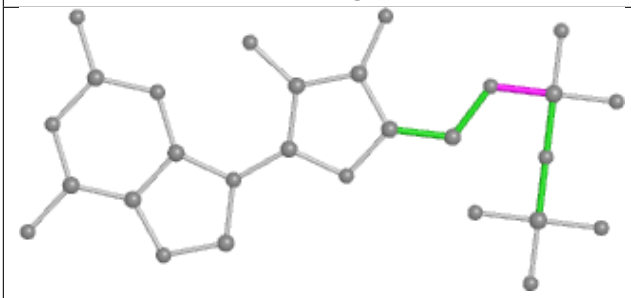


Bond angles



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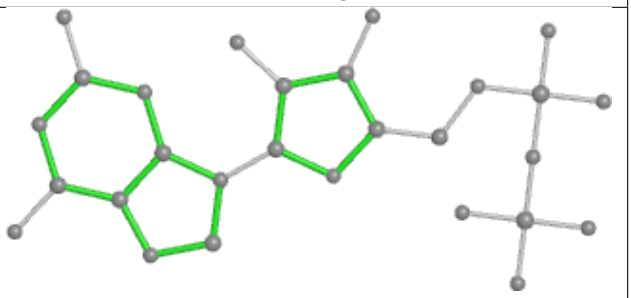
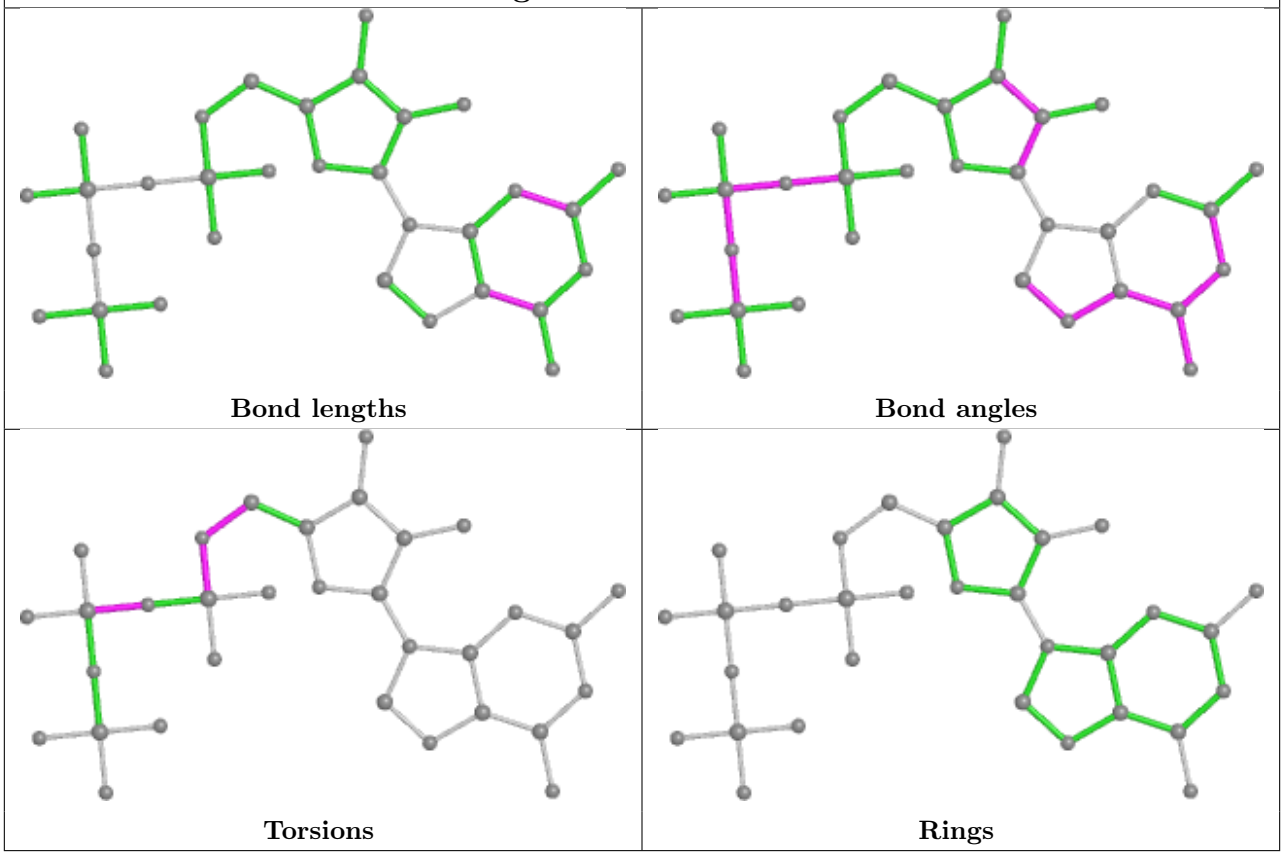
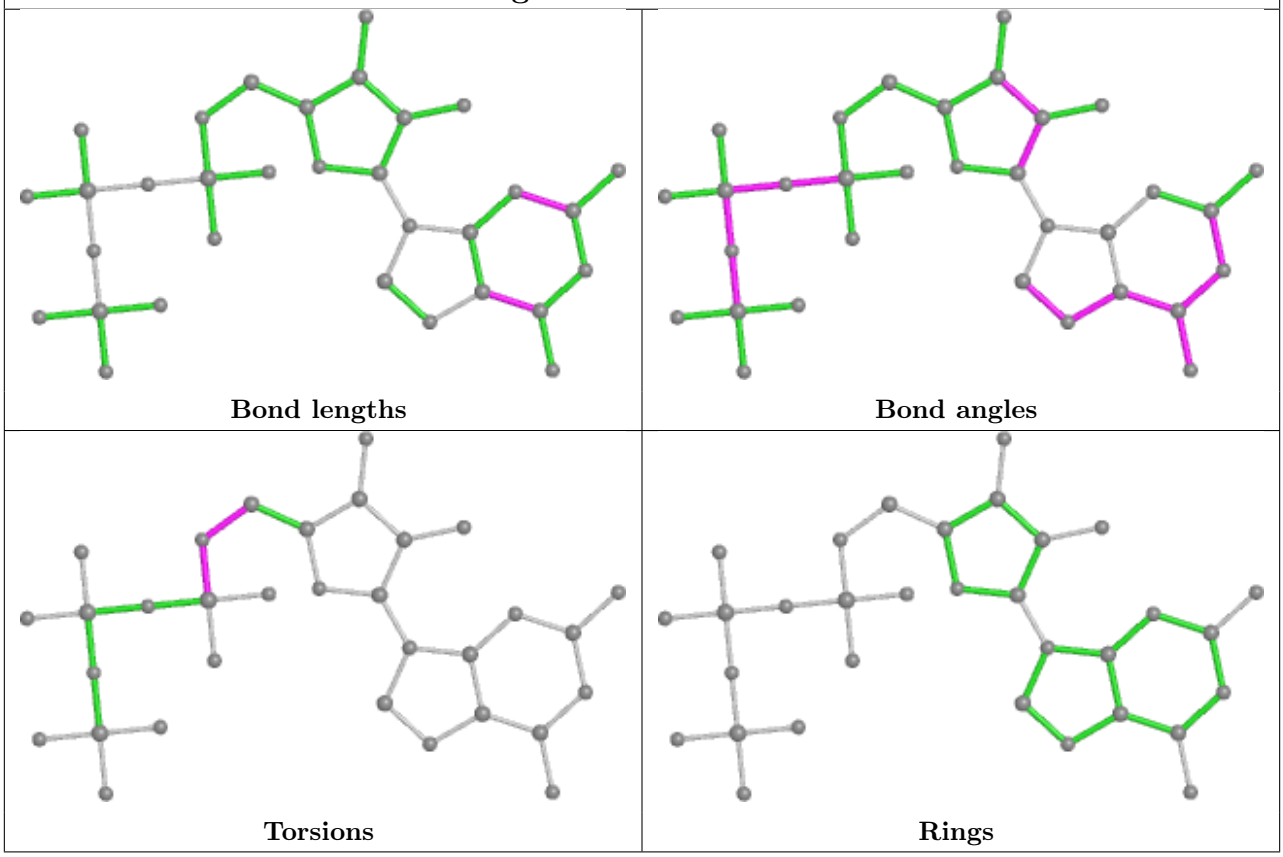


Rings

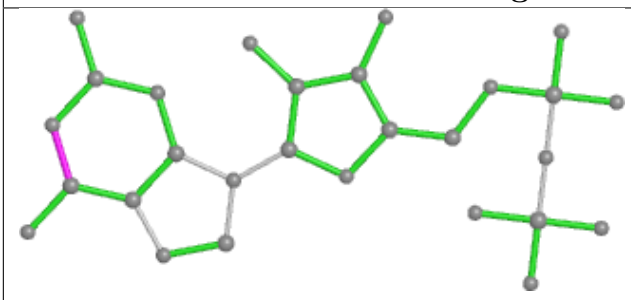
Ligand GTP MI 501



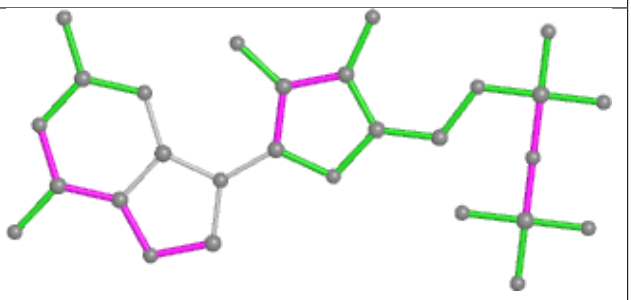
Ligand GTP RE 501



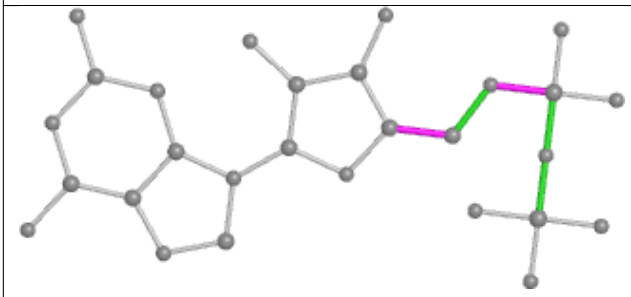
Ligand GDP TL 502



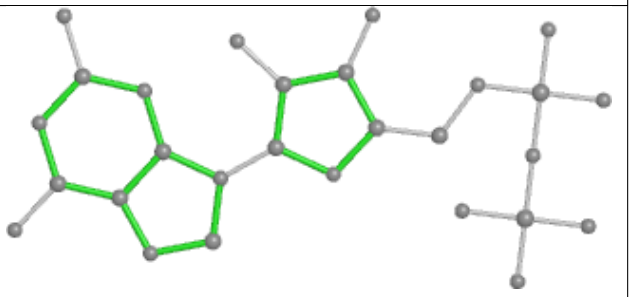
Bond lengths



Bond angles

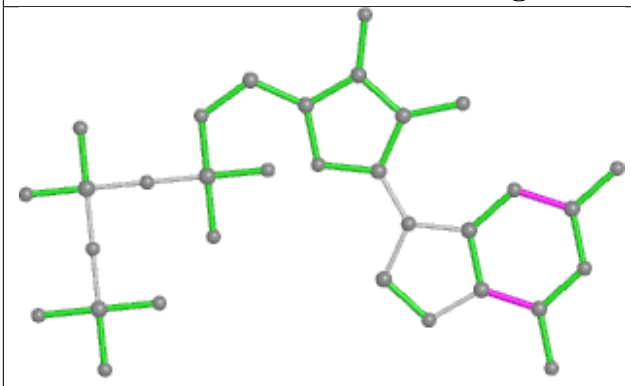


Torsions

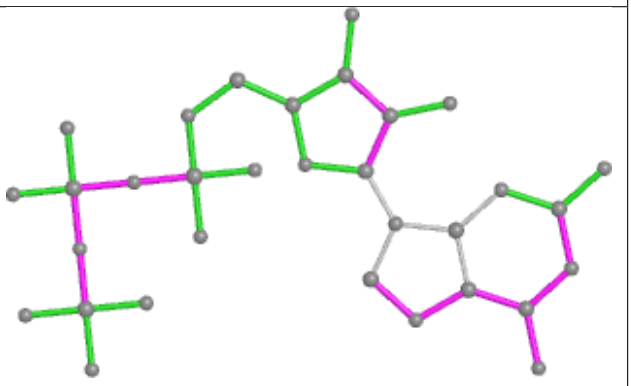


Rings

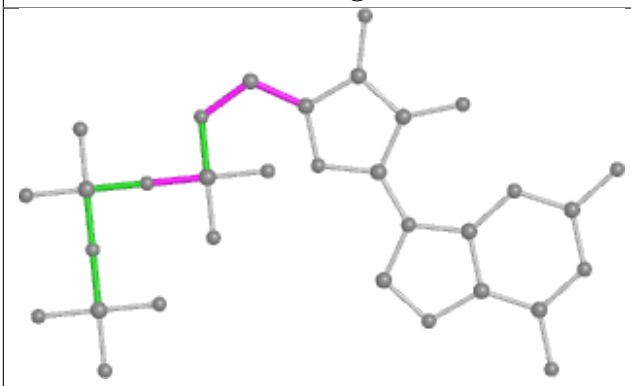
Ligand GTP OE 501



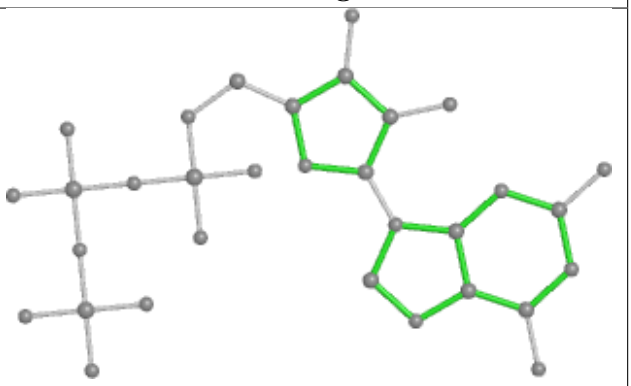
Bond lengths



Bond angles

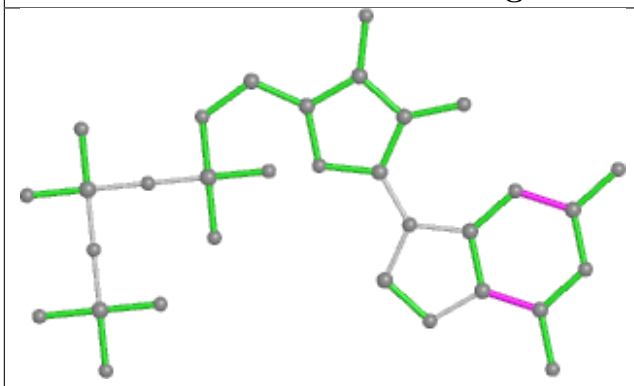


Torsions

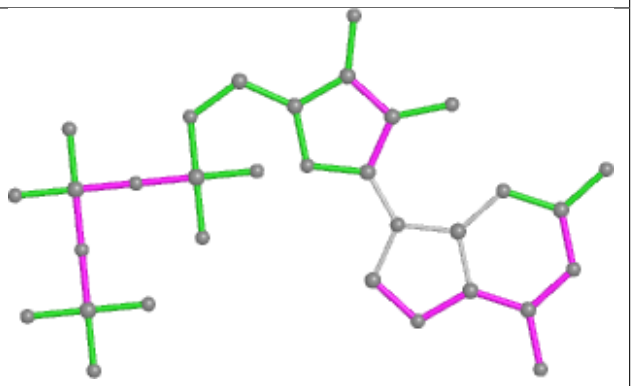


Rings

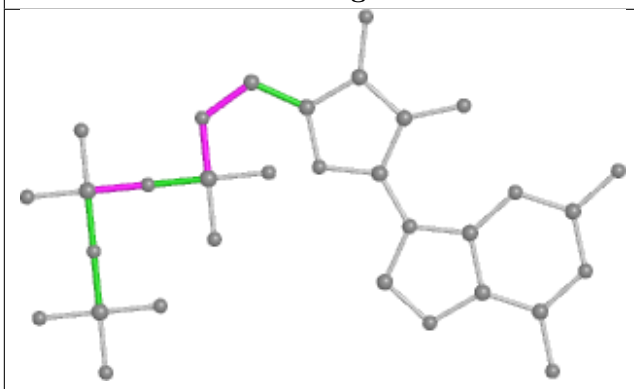
Ligand GTP MG 501



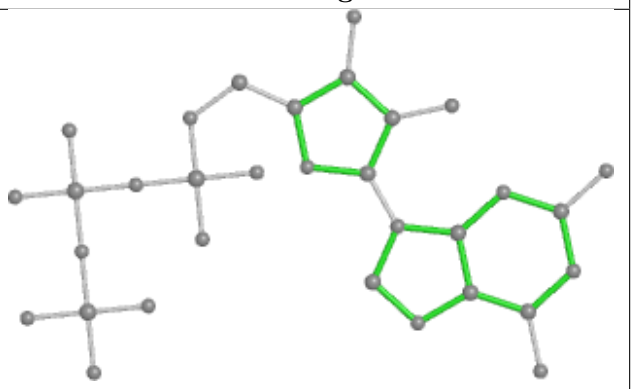
Bond lengths



Bond angles

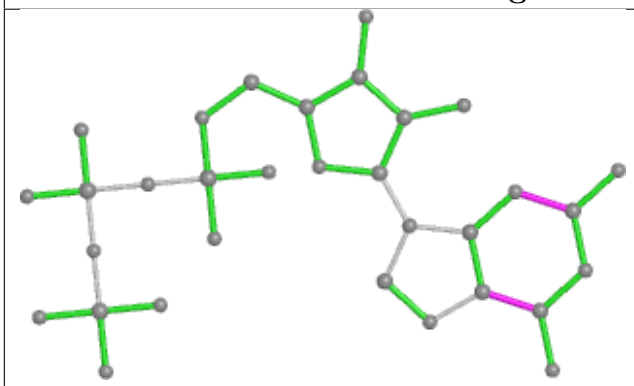


Torsions

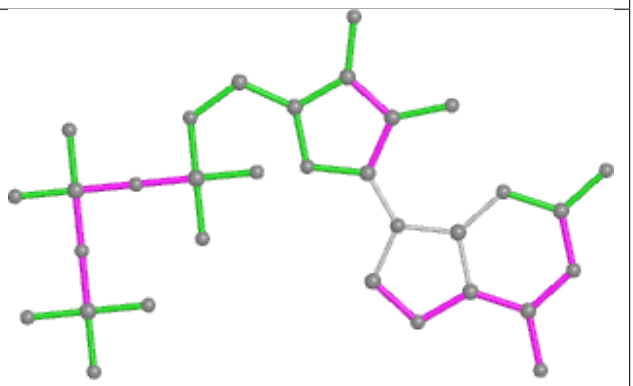


Rings

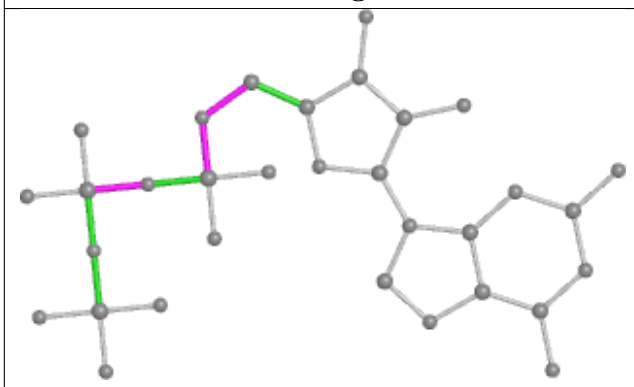
Ligand GTP KG 501



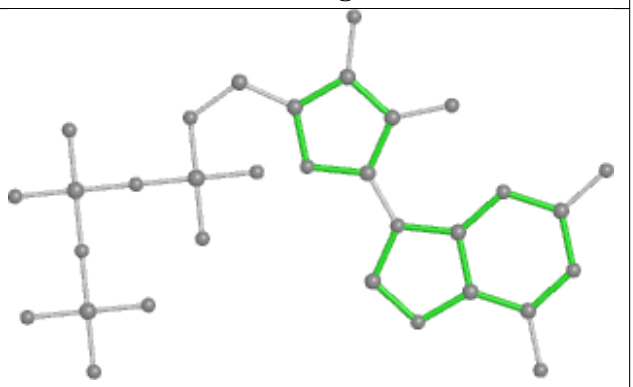
Bond lengths



Bond angles

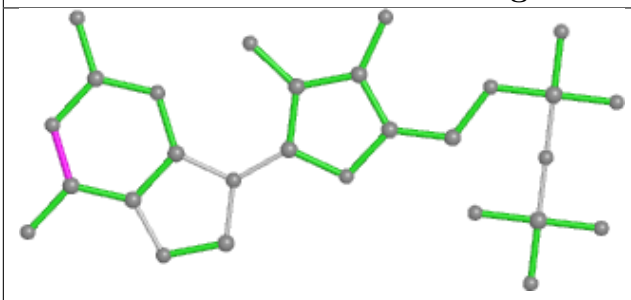


Torsions

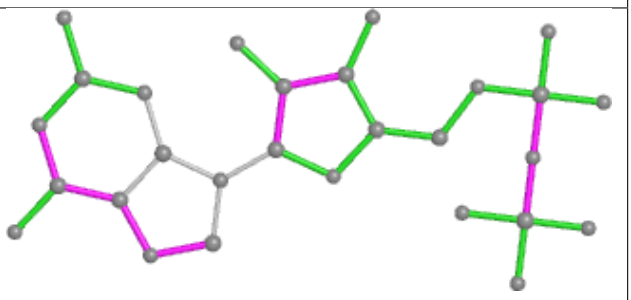


Rings

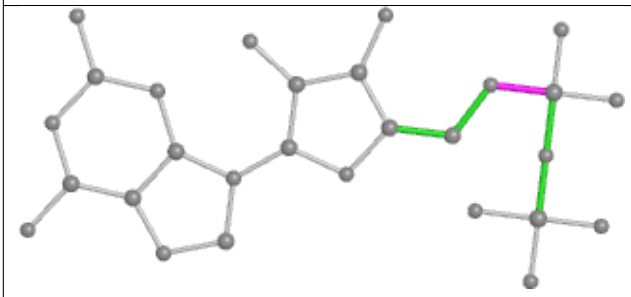
Ligand GDP FB 502



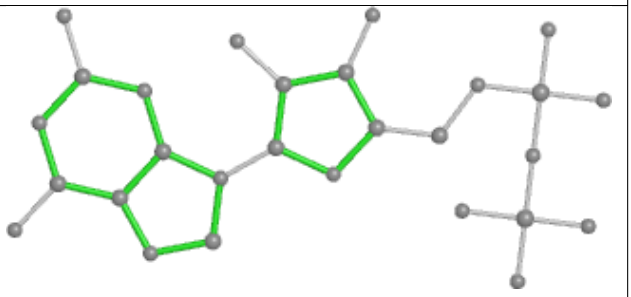
Bond lengths



Bond angles

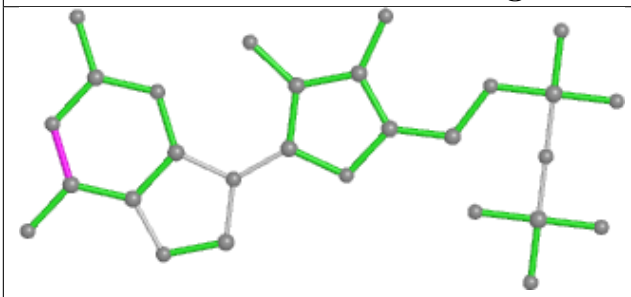


Torsions

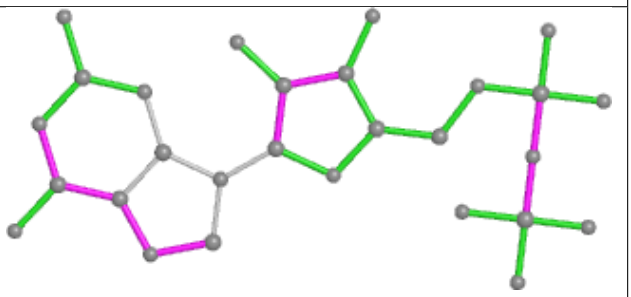


Rings

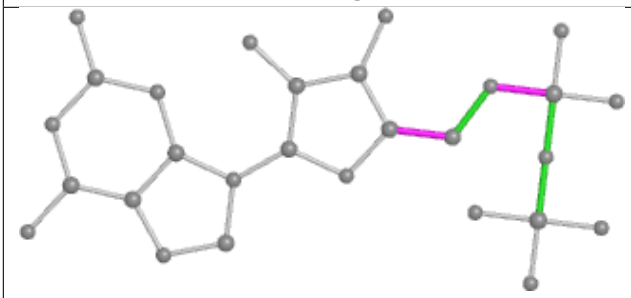
Ligand GDP KN 502



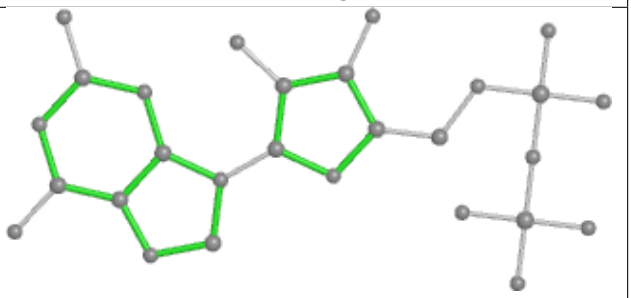
Bond lengths



Bond angles

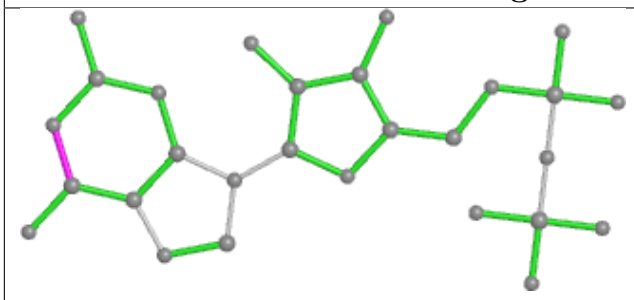


Torsions

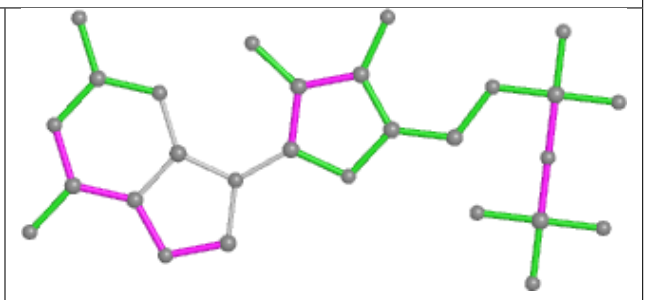


Rings

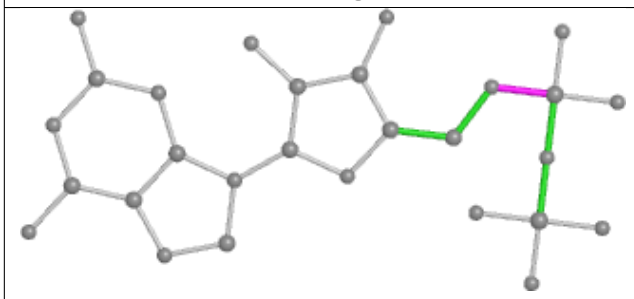
Ligand GDP KL 502



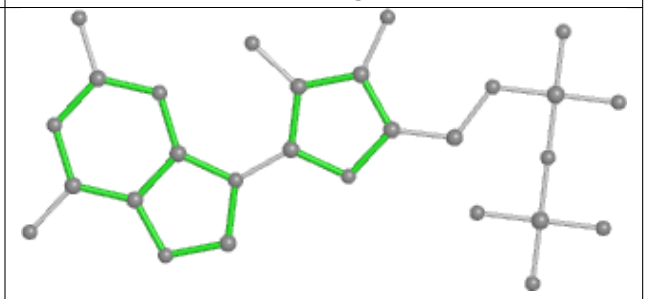
Bond lengths



Bond angles

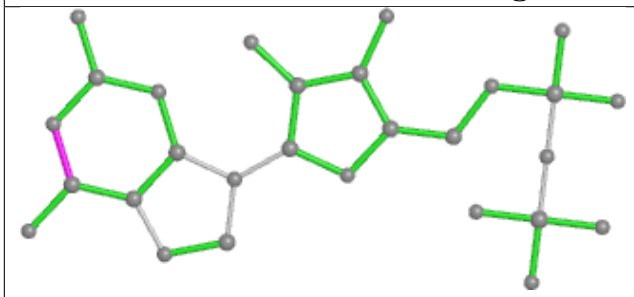


Torsions

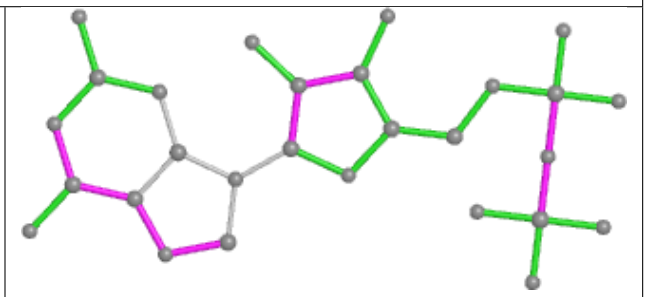


Rings

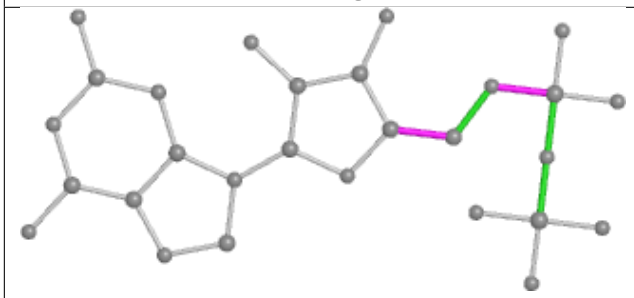
Ligand GDP OL 502



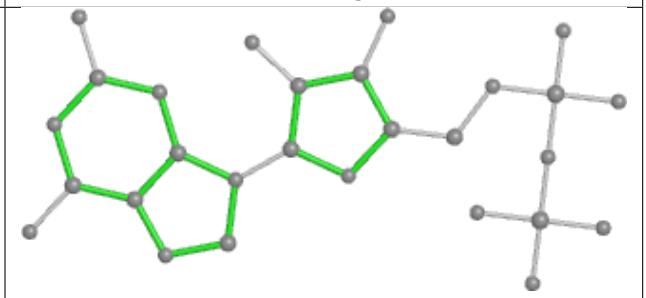
Bond lengths



Bond angles

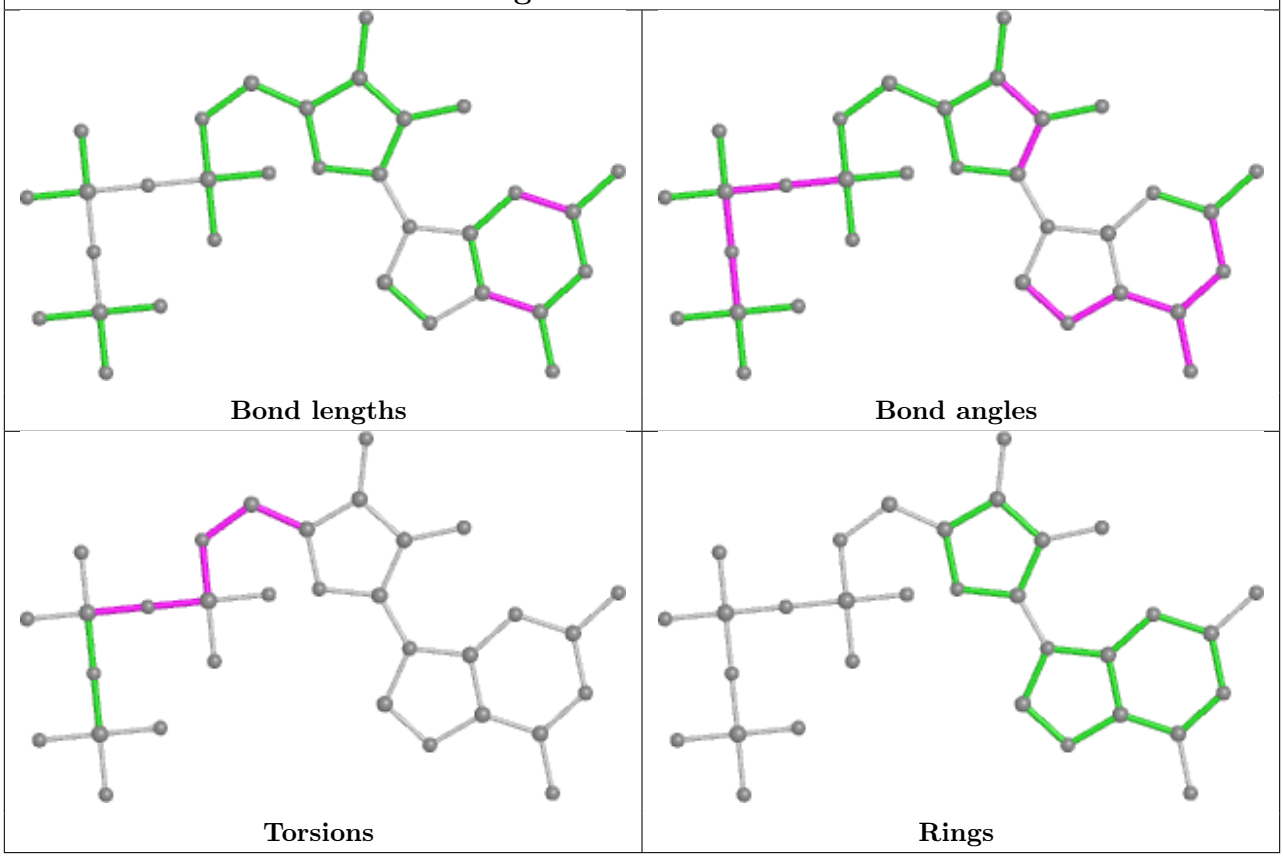


Torsions



Rings

Ligand GTP LE 501



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

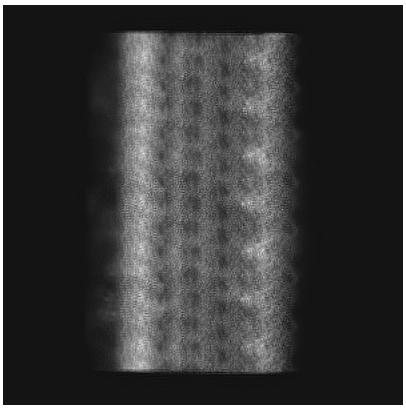
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-26624. These allow visual inspection of the internal detail of the map and identification of artifacts.

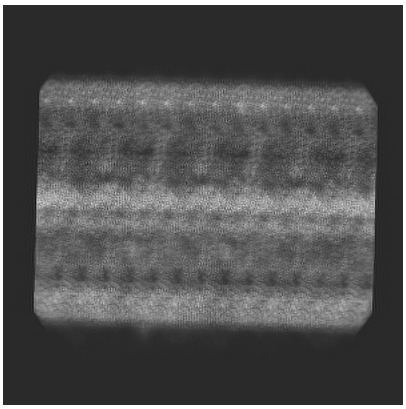
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

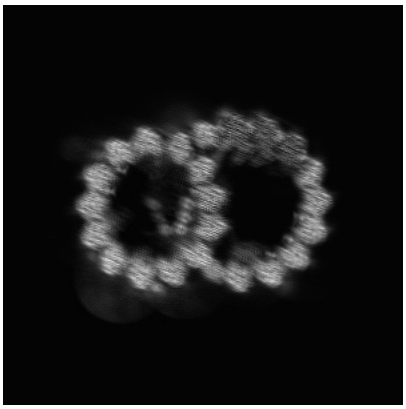
6.1.1 Primary map



X

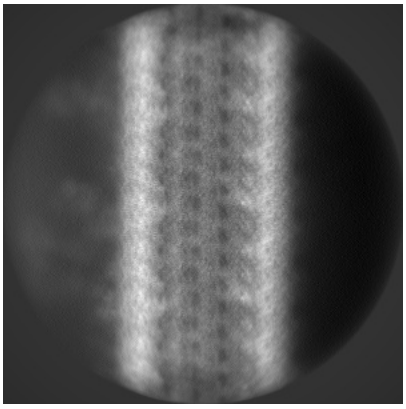


Y

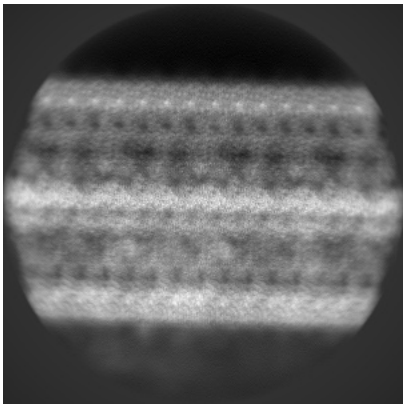


Z

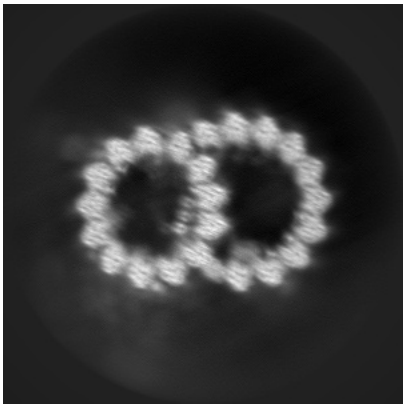
6.1.2 Raw map



X



Y

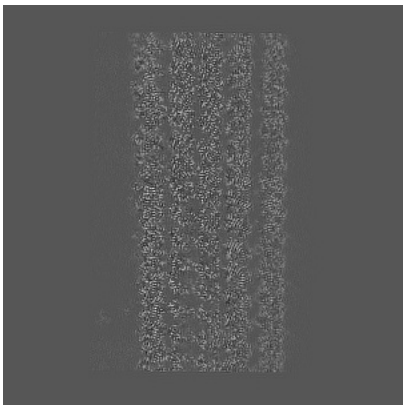


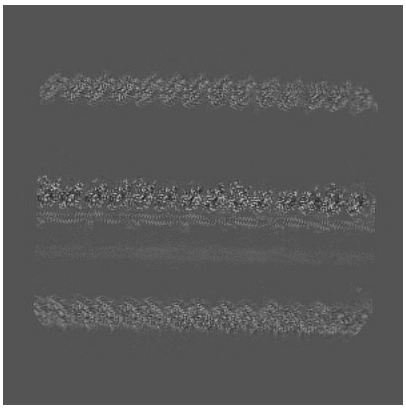
Z

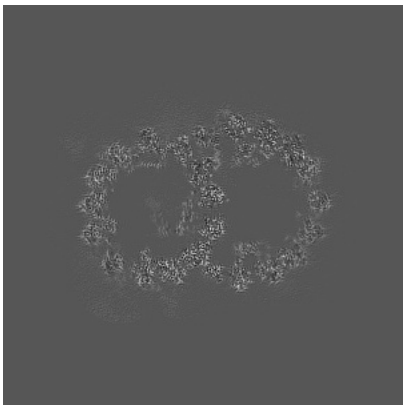
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

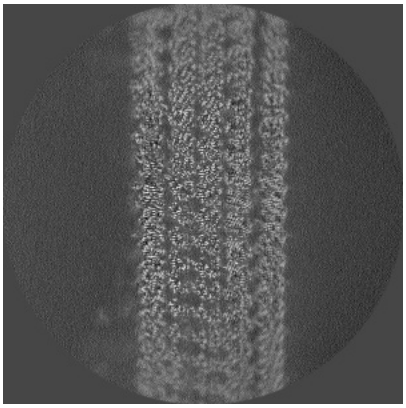
6.2.1 Primary map

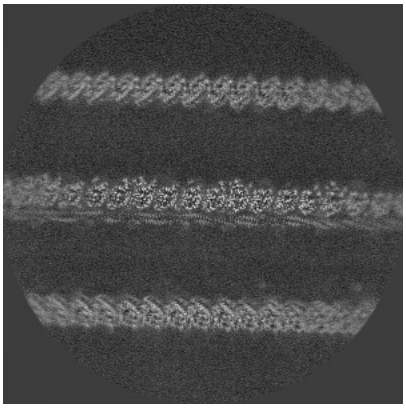

X Index: 256

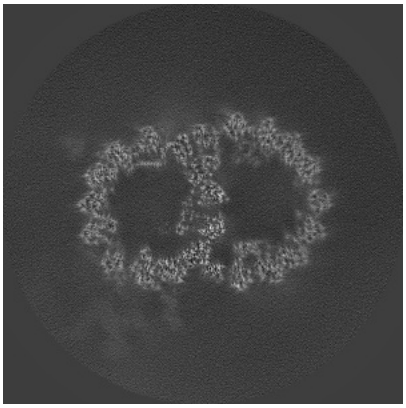

Y Index: 256


Z Index: 256

6.2.2 Raw map


X Index: 256

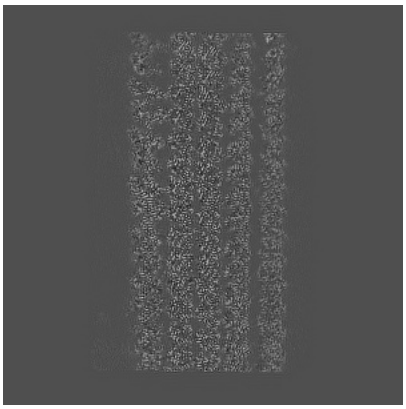

Y Index: 256

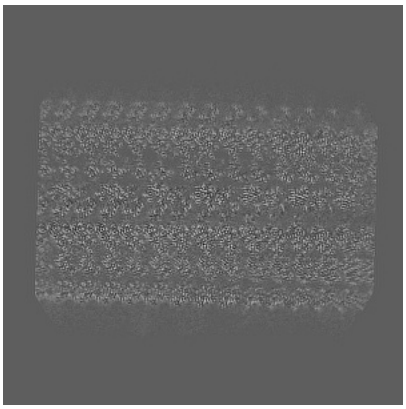

Z Index: 256

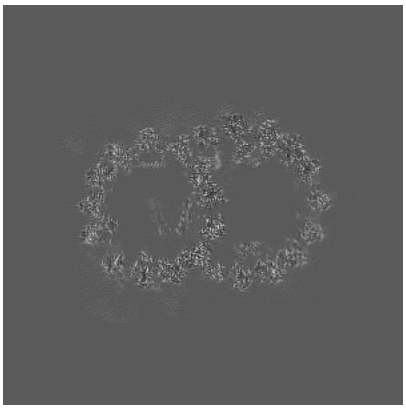
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

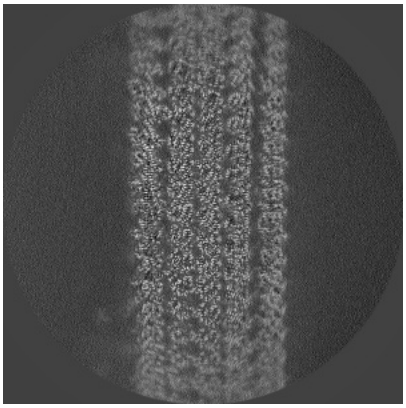
6.3.1 Primary map

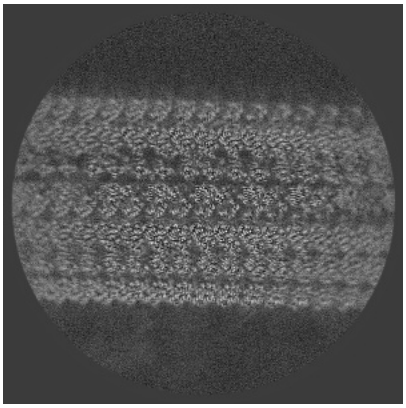

X Index: 261

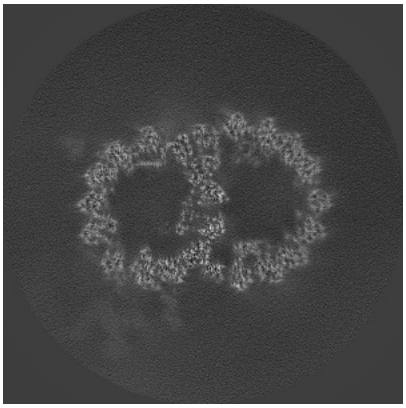

Y Index: 176


Z Index: 257

6.3.2 Raw map


X Index: 259

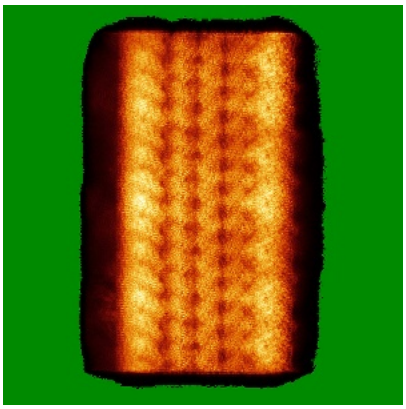

Y Index: 177


Z Index: 256

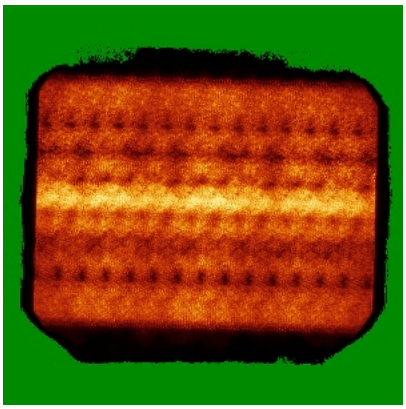
The images above show the largest variance slices of the map in three orthogonal directions.

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

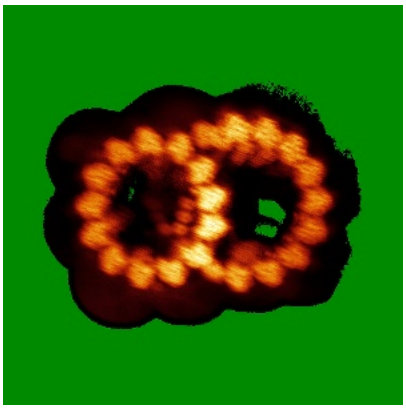
6.4.1 Primary map



X

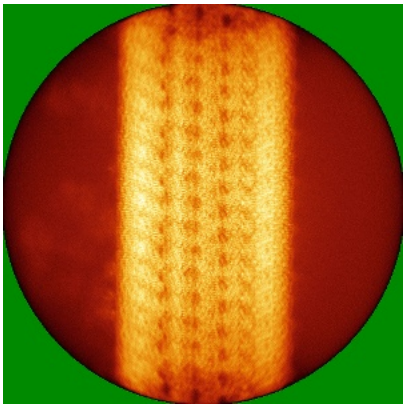


Y

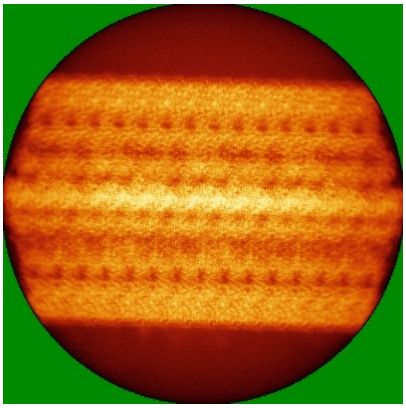


Z

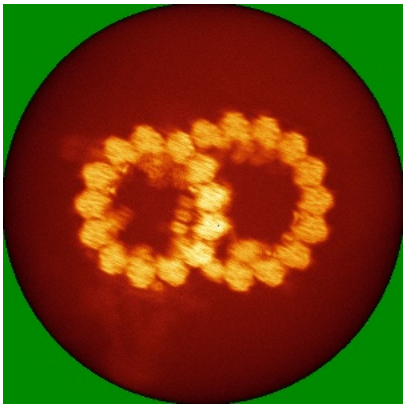
6.4.2 Raw map



X



Y

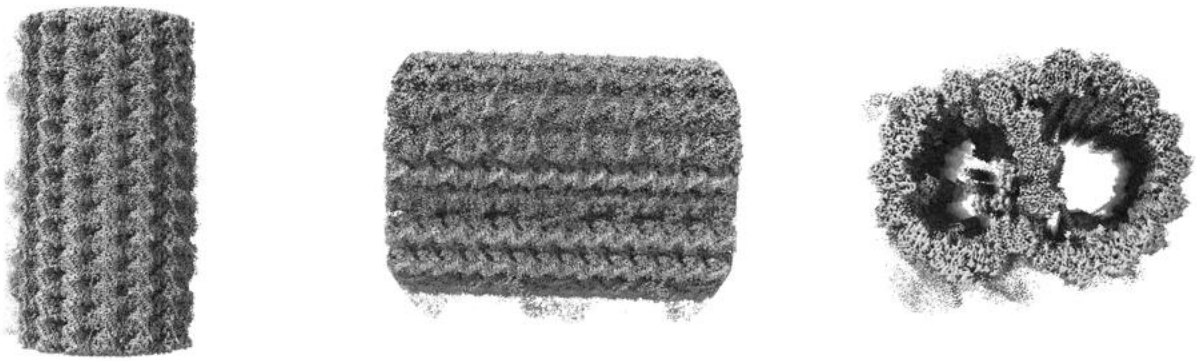


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

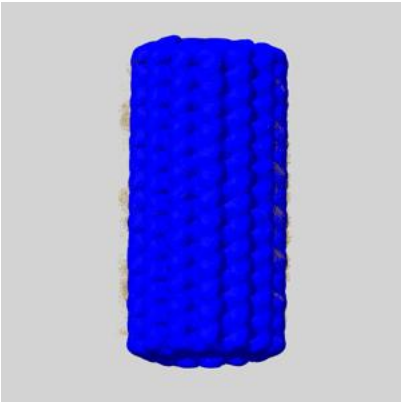
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

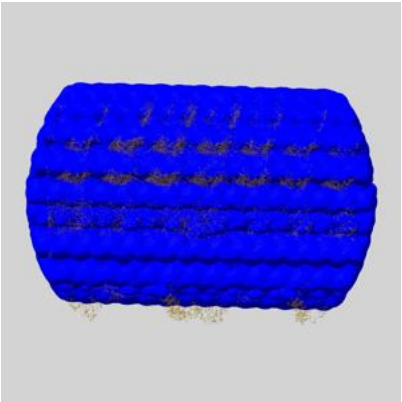
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

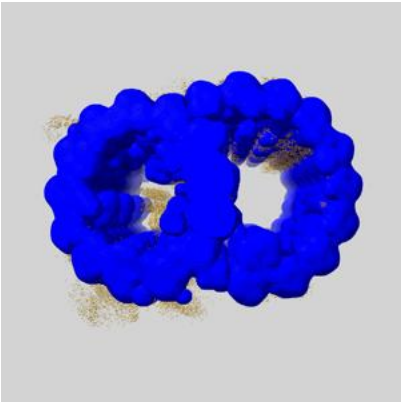
6.6.1 emd_26624_msk_1.map (i)



X



Y

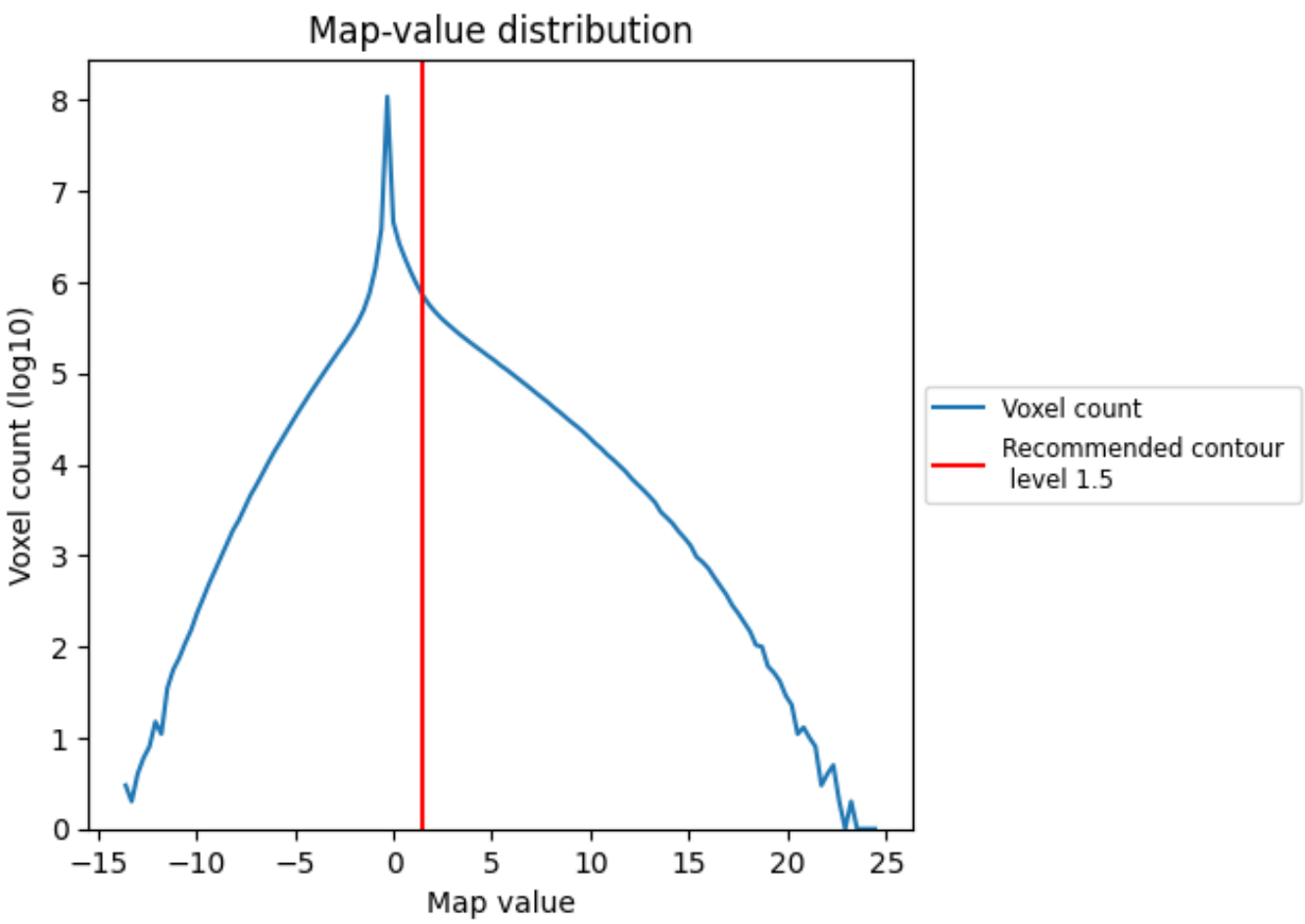


Z

7 Map analysis (i)

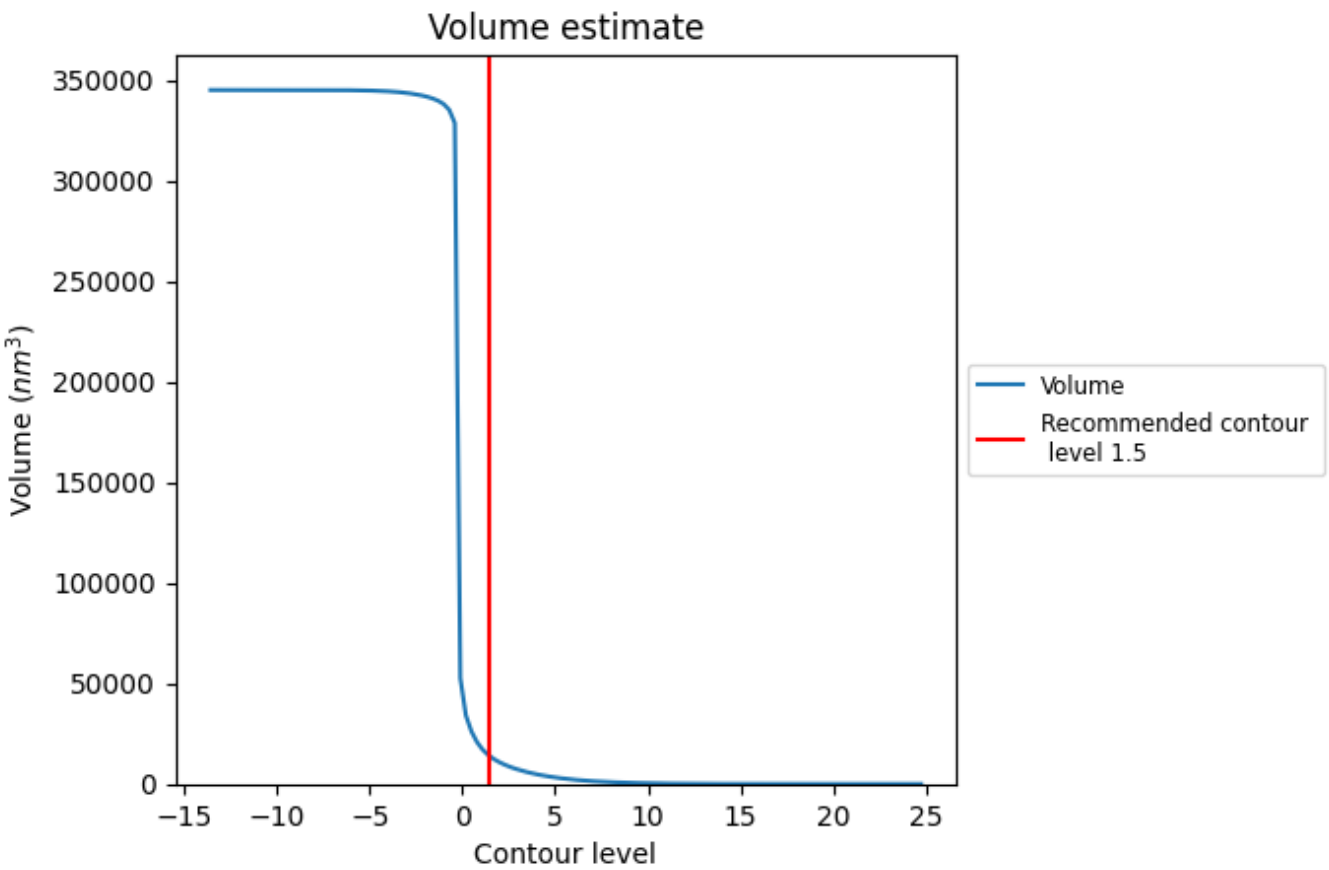
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

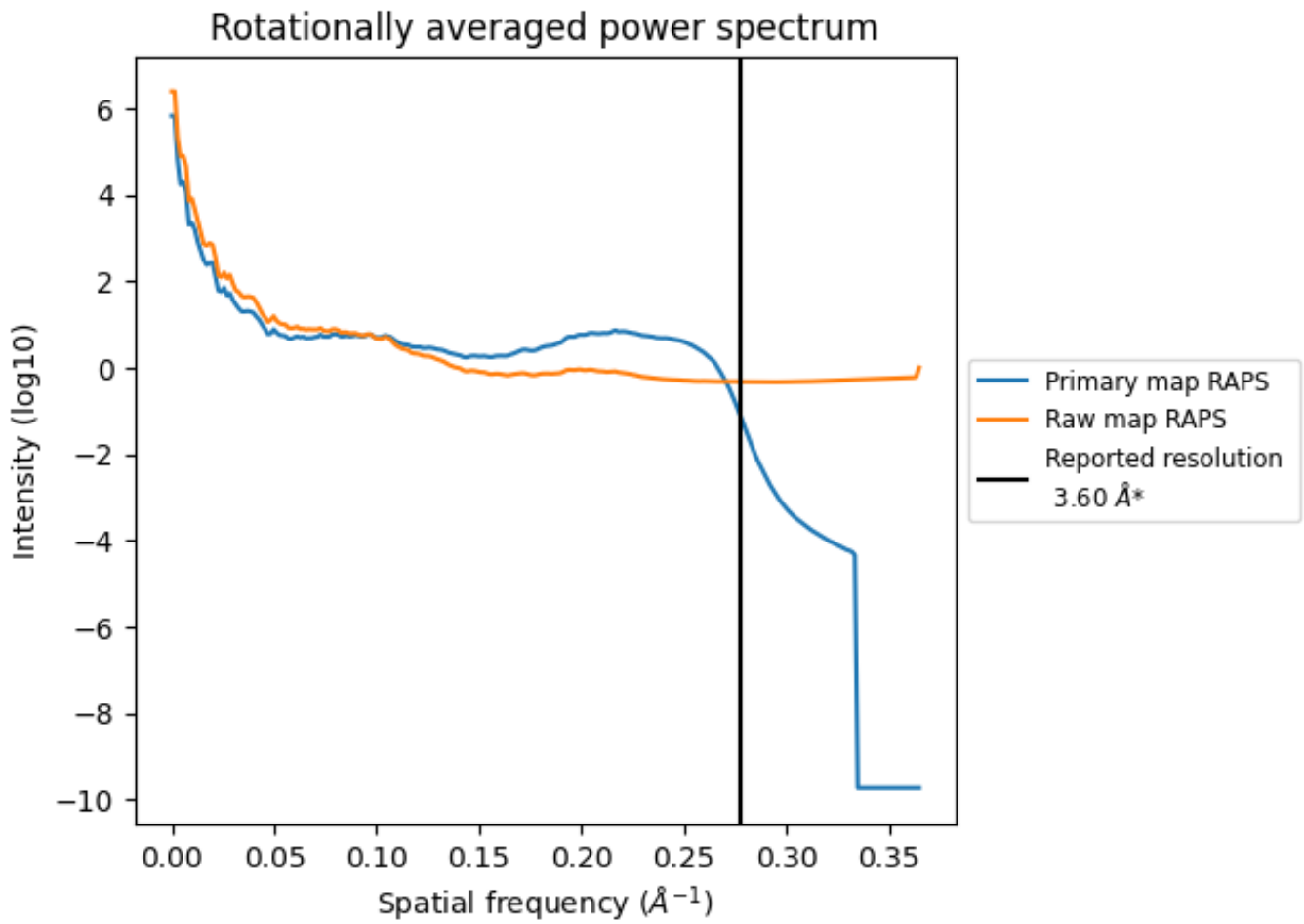
7.2 Volume estimate (i)



The volume at the recommended contour level is 13718 nm^3; this corresponds to an approximate mass of 12392 kDa.

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

7.3 Rotationally averaged power spectrum (i)

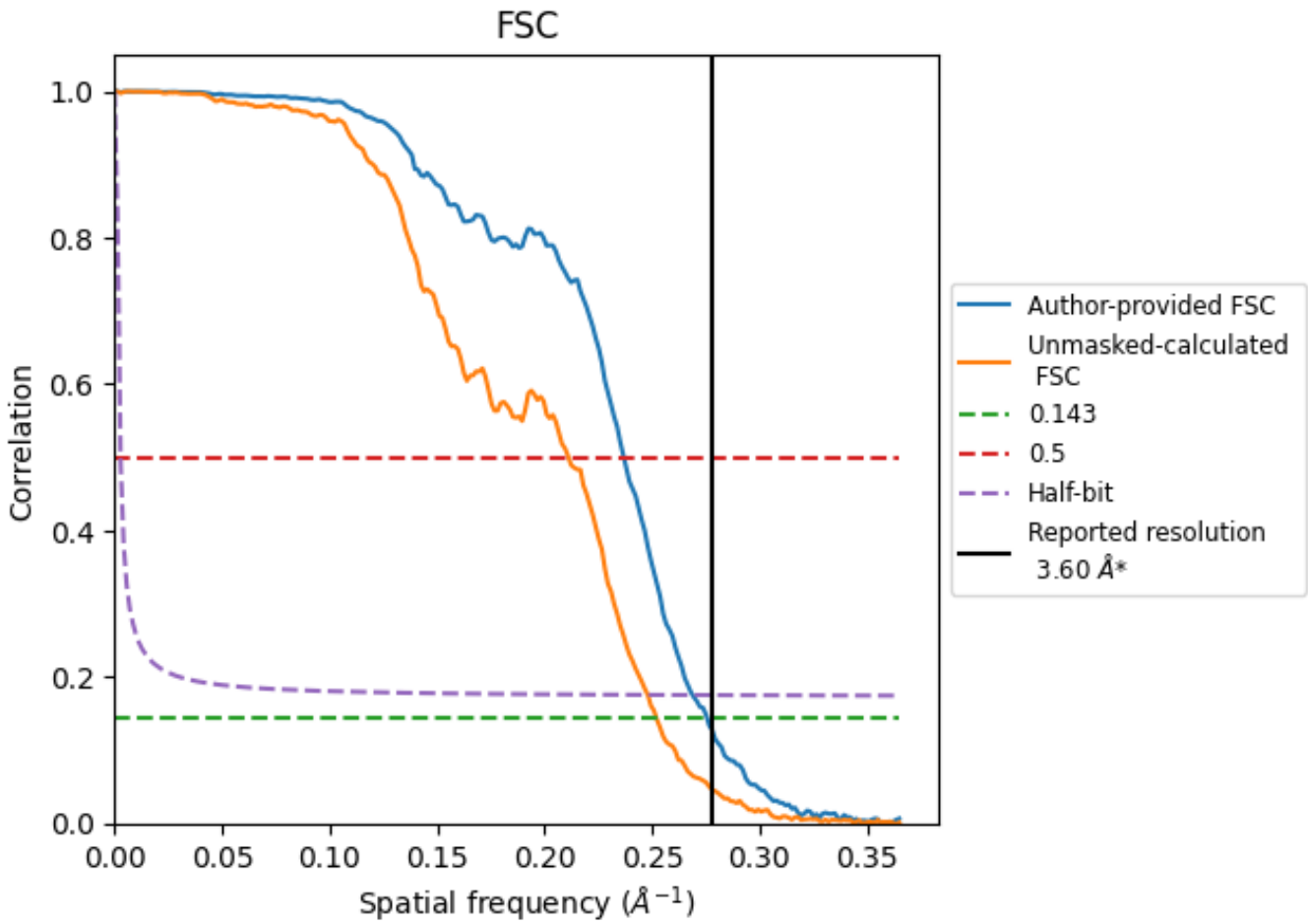


*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8.2 Resolution estimates (i)

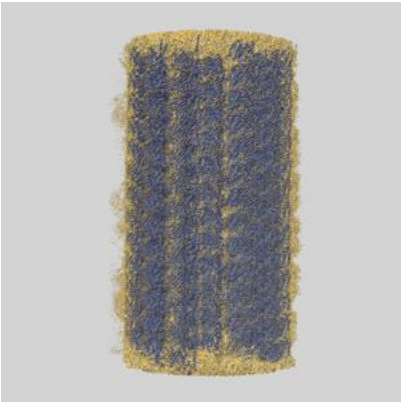
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.63	4.22	3.72
Unmasked-calculated*	3.97	4.74	4.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.97 differs from the reported value 3.6 by more than 10 %

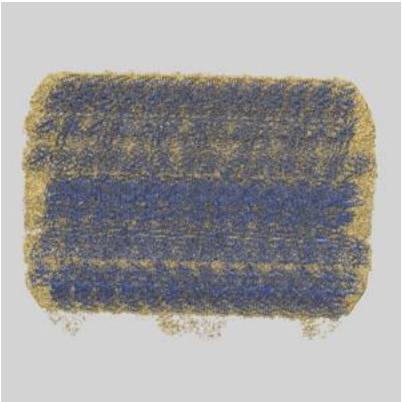
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-26624 and PDB model 7UNG. Per-residue inclusion information can be found in section 3 on page 68.

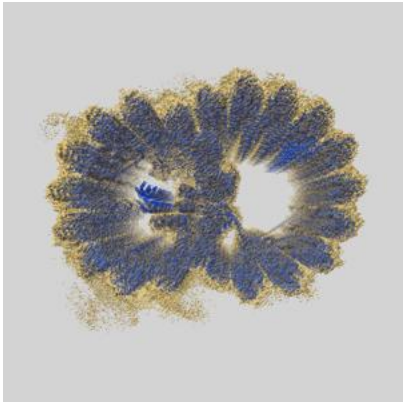
9.1 Map-model overlay (i)



X



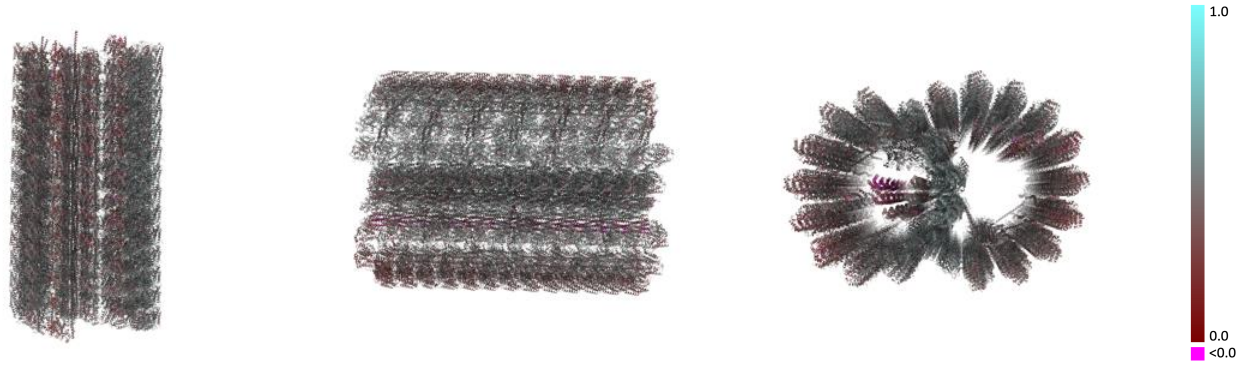
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

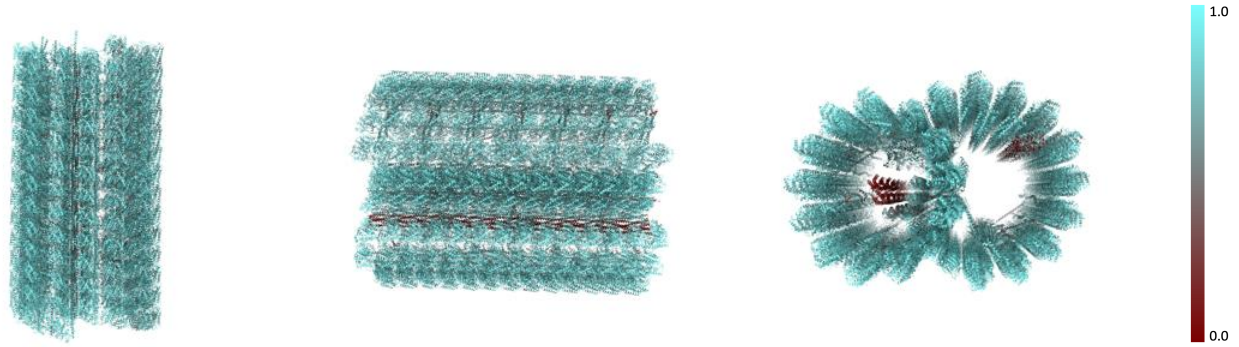
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

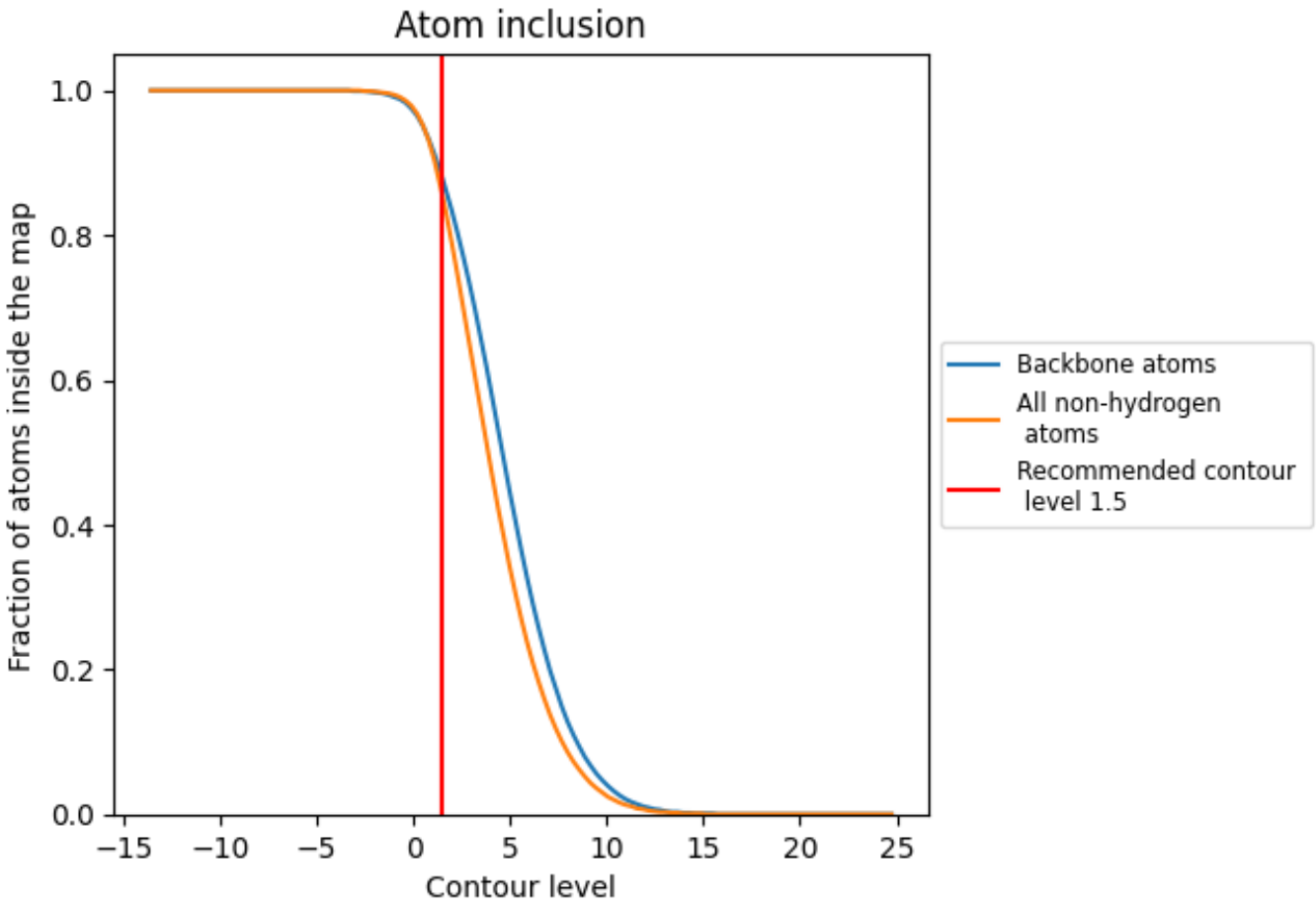
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (1.5).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8550	0.4460
0	0.8360	0.4810
1	0.7510	0.4290
2	0.8060	0.4540
3	0.7360	0.3800
4	0.7410	0.3840
5	0.8090	0.4610
6	0.8270	0.4530
7	0.7460	0.4420
8	0.8130	0.4580
9	0.8470	0.4510
A	0.8060	0.4430
A0	0.7690	0.4190
A1	0.7950	0.4320
A2	0.8040	0.4390
A3	0.8090	0.4370
A4	0.8380	0.4290
AA	0.9310	0.5070
AB	0.9190	0.5000
AC	0.9260	0.5130
AD	0.9260	0.5000
AE	0.9430	0.5210
AF	0.9250	0.5080
AG	0.9340	0.5250
AH	0.9240	0.5120
AI	0.9360	0.5170
AJ	0.9060	0.5020
AK	0.9230	0.5210
AL	0.9150	0.5010
AM	0.9410	0.5170
B	0.7340	0.4020
B0	0.7880	0.4240
B1	0.8060	0.4330
B2	0.8130	0.4440
B3	0.8050	0.4380

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Chain	Atom inclusion	Q-score
B4	0.8500	0.4480
B5	0.0240	0.2130
B6	0.1080	0.2200
B7	0.1380	0.2550
B8	0.1390	0.2410
B9	0.1080	0.2350
BA	0.9000	0.4570
BB	0.9120	0.4900
BC	0.9120	0.4880
BD	0.9210	0.4860
BE	0.9190	0.4740
BF	0.9200	0.4930
BG	0.9240	0.4950
BH	0.9240	0.4960
BI	0.9150	0.4790
BJ	0.9100	0.4750
BK	0.9100	0.4910
BL	0.9210	0.4940
BM	0.9110	0.4760
C	0.6900	0.3900
C0	0.5680	0.3630
C1	0.5290	0.3350
C2	0.6150	0.3650
C3	0.6080	0.3670
C4	0.5970	0.3660
CA	0.9010	0.4060
CB	0.9090	0.4340
CC	0.9090	0.4490
CD	0.8990	0.4430
CE	0.9040	0.4390
CF	0.9090	0.4580
CG	0.9130	0.4670
CH	0.9120	0.4610
CI	0.9140	0.4450
CJ	0.9080	0.4540
CK	0.9120	0.4710
CL	0.9010	0.4620
CM	0.9130	0.4450
D	0.7690	0.4540
D0	0.7340	0.4010
D1	0.7750	0.4220
D2	0.7750	0.4300

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Chain	Atom inclusion	Q-score
D3	0.7780	0.4200
D5	0.0300	0.1300
D6	0.0830	0.1470
D7	0.1000	0.1630
D8	0.0510	0.1500
DA	0.8690	0.3030
DB	0.9010	0.3850
DC	0.8960	0.3940
DD	0.8910	0.4070
DE	0.8790	0.3880
DF	0.8910	0.4130
DG	0.8920	0.4270
DH	0.9040	0.4320
DI	0.8980	0.4080
DJ	0.9120	0.4150
DK	0.9050	0.4210
DL	0.9100	0.4170
DM	0.9180	0.4080
E	0.8450	0.4790
EB	0.8810	0.3580
EC	0.8600	0.3720
ED	0.8680	0.3900
EE	0.8630	0.3790
EF	0.8750	0.3940
EG	0.8780	0.4130
EH	0.8820	0.4150
EI	0.8720	0.3970
EJ	0.8760	0.3830
EK	0.8560	0.3870
EL	0.8810	0.3940
EM	0.8610	0.3770
EN	0.8700	0.3030
F	0.7960	0.4630
F0	0.8720	0.4380
F1	0.8190	0.4250
F2	0.4080	0.3270
F3	0.8890	0.4460
F4	0.8030	0.4320
F5	0.2070	0.3030
F6	0.9420	0.4520
F7	0.9280	0.4570
F8	0.5270	0.3490

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Chain	Atom inclusion	Q-score
FB	0.8620	0.3550
FC	0.8780	0.3850
FD	0.8760	0.3910
FE	0.8760	0.3810
FF	0.8590	0.3820
FG	0.8670	0.4010
FH	0.8680	0.4030
FI	0.8730	0.3960
FJ	0.8670	0.3730
FK	0.8700	0.3840
FL	0.8550	0.3710
FM	0.8600	0.3660
FN	0.8330	0.3050
G	0.6740	0.3620
G0	0.9360	0.4770
G1	0.8520	0.4490
G2	0.4210	0.3190
G3	0.9250	0.4420
G4	0.9240	0.4420
G5	0.7450	0.3880
G6	0.8870	0.4530
G7	0.8010	0.4450
G8	0.1640	0.2890
GB	0.8740	0.3840
GC	0.8760	0.4050
GD	0.8860	0.4300
GE	0.8930	0.4180
GF	0.8800	0.4020
GG	0.8720	0.4110
GH	0.8850	0.4260
GI	0.8890	0.4230
GJ	0.8800	0.3960
GK	0.8750	0.3980
GL	0.8710	0.3900
GM	0.8570	0.3750
GN	0.8530	0.3440
H	0.7750	0.4560
H0	0.8740	0.4530
H1	0.8460	0.4470
H2	0.5860	0.3820
HB	0.9080	0.4390
HC	0.9150	0.4630

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Chain	Atom inclusion	Q-score
HD	0.9100	0.4690
HE	0.9020	0.4650
HF	0.9030	0.4480
HG	0.9050	0.4450
HH	0.9070	0.4660
HI	0.9060	0.4590
HJ	0.8930	0.4350
HK	0.8970	0.4270
HL	0.8920	0.4360
HM	0.9020	0.4340
HN	0.8650	0.3770
HO	0.8750	0.3580
I	0.3790	0.3310
I1	0.8220	0.4920
IB	0.8990	0.4370
IC	0.8940	0.4650
ID	0.9030	0.4830
IE	0.9120	0.4800
IF	0.9070	0.4540
IG	0.9050	0.4690
IH	0.9050	0.4830
II	0.9170	0.4860
IJ	0.8900	0.4540
IK	0.9030	0.4600
IL	0.8930	0.4500
IM	0.9010	0.4540
IN	0.8850	0.4180
IO	0.8710	0.3890
J	0.7410	0.4300
J1	0.8750	0.4650
J2	0.9200	0.4720
J3	0.9220	0.4680
J4	0.9250	0.4630
J5	0.9280	0.5010
JB	0.9080	0.4870
JC	0.8850	0.4860
JD	0.9060	0.4990
JE	0.8890	0.4770
JF	0.8980	0.4880
JG	0.8960	0.4920
JH	0.9110	0.4930
JI	0.8910	0.4840

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Chain	Atom inclusion	Q-score
JJ	0.8950	0.4740
JK	0.8680	0.4510
JL	0.9010	0.4730
JM	0.8850	0.4590
JN	0.8950	0.4410
K	0.4650	0.3750
K1	0.7990	0.4100
KB	0.9280	0.5170
KC	0.9210	0.5200
KD	0.9210	0.5250
KE	0.9260	0.5350
KF	0.9310	0.5350
KG	0.9200	0.5240
KH	0.9170	0.5280
KI	0.9150	0.5290
KJ	0.9280	0.5400
KK	0.9160	0.5240
KL	0.9110	0.5250
KM	0.9210	0.5410
KN	0.9330	0.5440
KO	0.9300	0.5250
L	0.7280	0.4230
L1	0.7810	0.4340
L2	0.8090	0.4420
LB	0.9240	0.5180
LC	0.9140	0.5230
LD	0.9190	0.5340
LE	0.9130	0.5330
LF	0.9090	0.5240
LG	0.9120	0.5320
LH	0.9210	0.5380
LI	0.9020	0.5240
LJ	0.9020	0.5250
LK	0.9100	0.5230
LL	0.9170	0.5310
LM	0.9210	0.5330
LN	0.9090	0.5200
M	0.5150	0.3930
M1	0.6180	0.3960
M2	0.7590	0.4620
M3	0.7070	0.4420
M4	0.7320	0.4490

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Chain	Atom inclusion	Q-score
MB	0.9200	0.4910
MC	0.9030	0.4900
MD	0.9030	0.4950
ME	0.8970	0.4910
MF	0.9050	0.4950
MG	0.8950	0.4980
MH	0.9000	0.4960
MI	0.8990	0.4970
MJ	0.9030	0.4950
MK	0.9000	0.4850
ML	0.9010	0.4790
MM	0.9020	0.4790
MN	0.9060	0.4740
N	0.6990	0.4200
NB	0.8640	0.4460
NC	0.8590	0.4520
ND	0.8730	0.4640
NE	0.8720	0.4730
NF	0.8810	0.4600
NG	0.8820	0.4730
NH	0.8690	0.4680
NI	0.8730	0.4740
NJ	0.8720	0.4520
NK	0.8820	0.4580
NL	0.8710	0.4540
NM	0.8670	0.4550
NN	0.8560	0.4280
O	0.8900	0.4650
OB	0.7960	0.4710
OC	0.8200	0.4870
OD	0.8320	0.4970
OE	0.8300	0.4960
OF	0.8300	0.4900
OG	0.8450	0.4940
OH	0.8480	0.5060
OI	0.8490	0.5030
OJ	0.8300	0.4940
OK	0.8370	0.5020
OL	0.8310	0.4980
OM	0.8310	0.4990
ON	0.8130	0.4900
OO	0.7930	0.4740

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Chain	Atom inclusion	Q-score
P	0.8460	0.4830
PC	0.7970	0.4760
PD	0.8200	0.4860
PE	0.8210	0.4920
PF	0.8070	0.4800
PG	0.8360	0.4870
PH	0.8480	0.5130
PI	0.8450	0.5110
PJ	0.8100	0.4850
PK	0.8270	0.4810
PL	0.8140	0.4870
PM	0.8270	0.5080
PN	0.8030	0.4910
PO	0.7920	0.4840
Q	0.8700	0.4660
QC	0.7450	0.4440
QD	0.8040	0.4710
QE	0.8000	0.4770
QF	0.7900	0.4760
QG	0.8130	0.4750
QH	0.8280	0.5000
QI	0.8320	0.4840
QJ	0.7870	0.4740
QK	0.7960	0.4650
QL	0.8100	0.4900
QM	0.8110	0.4840
QN	0.8030	0.4850
QO	0.7640	0.4570
R	0.5140	0.3780
RC	0.7800	0.3630
RD	0.8420	0.4170
RE	0.8400	0.4210
RF	0.8310	0.4000
RG	0.8380	0.3940
RH	0.8650	0.4210
RI	0.8520	0.4230
RJ	0.8290	0.3990
RK	0.8230	0.3910
RL	0.8600	0.4130
RM	0.8420	0.4240
RN	0.8470	0.4430
RO	0.8260	0.4300

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Chain	Atom inclusion	Q-score
S	0.5100	0.3910
SD	0.8510	0.3920
SE	0.8460	0.3880
SF	0.8560	0.3970
SG	0.8570	0.3730
SH	0.8580	0.3810
SI	0.8590	0.3950
SJ	0.8550	0.3920
SK	0.8770	0.3960
SL	0.8770	0.3930
SM	0.8870	0.4290
SN	0.8850	0.4350
SO	0.8930	0.4420
T	0.8530	0.4620
TD	0.8330	0.3450
TE	0.8300	0.3520
TF	0.8430	0.3700
TG	0.8670	0.3600
TH	0.8720	0.3700
TI	0.8710	0.3950
TJ	0.8640	0.3950
TK	0.8730	0.3840
TL	0.8900	0.3900
TM	0.8810	0.3980
TN	0.8740	0.4030
TO	0.8700	0.4000
TP	0.8520	0.3780
U	0.8680	0.4770
UD	0.8710	0.3940
UE	0.8690	0.4110
UF	0.8810	0.4210
UG	0.8980	0.4210
UH	0.8970	0.4280
UI	0.8910	0.4350
UJ	0.9060	0.4550
UK	0.9050	0.4440
UL	0.8930	0.4300
UM	0.8970	0.4410
UN	0.8990	0.4510
UO	0.9020	0.4520
UP	0.8730	0.4170
V	0.8590	0.4620

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Chain	Atom inclusion	Q-score
VD	0.8960	0.4110
VE	0.8950	0.4280
VF	0.8900	0.4360
VG	0.8880	0.4260
VH	0.9010	0.4440
VI	0.8960	0.4540
VJ	0.9030	0.4730
VK	0.9070	0.4680
VL	0.8930	0.4410
VM	0.8900	0.4480
VN	0.9020	0.4710
VO	0.9100	0.4690
VP	0.9100	0.4600
W	0.7910	0.4280
WD	0.8970	0.4260
WE	0.8880	0.4410
WF	0.9030	0.4510
WG	0.8970	0.4550
WH	0.9010	0.4580
WI	0.8860	0.4500
WJ	0.9080	0.4750
WK	0.8890	0.4560
WL	0.8830	0.4430
WM	0.8850	0.4460
WN	0.9040	0.4760
WO	0.8930	0.4670
WP	0.8940	0.4530
X	0.8030	0.4500
XA	0.9160	0.4780
XB	0.9210	0.4910
XC	0.9120	0.4920
XD	0.9060	0.4970
XE	0.9130	0.4890
XF	0.9010	0.4970
XG	0.9080	0.4870
Y	0.8030	0.4340
YB	0.9160	0.5020
YC	0.9180	0.5050
YD	0.9230	0.5120
YE	0.9000	0.5010
YF	0.9100	0.5090
YG	0.8200	0.4780

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Chain	Atom inclusion	Q-score
Z	0.7690	0.3870
a	0.7000	0.3840
b	0.6700	0.3810
c	0.6370	0.3560
d	0.6820	0.3850
e	0.8390	0.4470
f	0.8510	0.4750
g	0.8540	0.4830
h	0.8160	0.4460
i	0.7810	0.4640
j	0.7740	0.4550
k	0.8280	0.4810
l	0.9080	0.5150
m	0.8970	0.5200
n	0.8980	0.5240
o	0.7210	0.3900
o1	0.7690	0.4440
p	0.7930	0.4170
q	0.8500	0.4830
r	0.8550	0.4690
s	0.8360	0.4600
y	0.8590	0.4070
z	0.8380	0.4030