wwPDB EM Validation Summary Report

Mar 8, 2026 – 02:51 PM UTC

PDB ID	:	9E78 / pdb_00009e78
EMDB ID	:	EMD-47661
Title	:	48-nm repeat of the Leishmania tarentolae doublet microtubule
Authors	:	Doran, M.H.; Ren, P.; Hoog, J.L.; Brown, A.
Deposited on	:	2024-11-01
Resolution	:	2.90 Å(reported)
Based on initial model	:	.

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

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

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

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

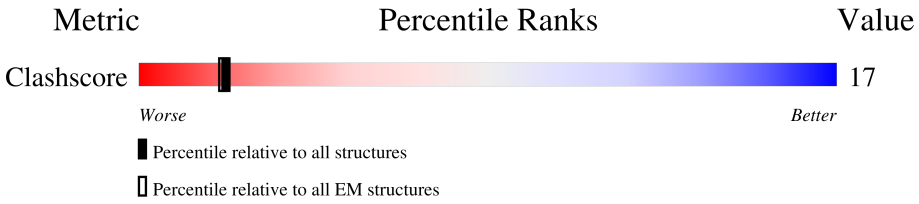
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

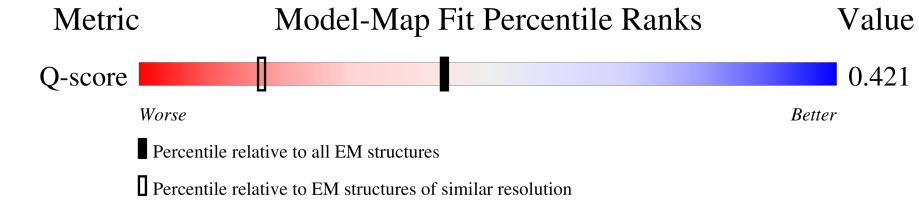
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	A	443	57% 40% .
1	AB	443	. 55% 39% 5%
1	AD	443	61% 35% .
1	AF	443	58% 39% .
1	AH	443	61% 36% .
1	AJ	443	61% 36% .

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Mol	Chain	Length	Quality of chain
1	AL	443	62% 35%
1	AN	443	57% 37% 5%
1	B	443	63% 32% 6%
1	BB	443	62% 35%
1	BD	443	65% 32%
1	BF	443	62% 35%
1	BH	443	60% 36%
1	BJ	443	61% 35%
1	BL	443	61% 35%
1	BN	443	62% 35%
1	CA	443	57% 39%
1	CC	443	67% 30%
1	CE	443	59% 38%
1	CG	443	68% 29%
1	CI	443	60% 36%
1	CK	443	59% 38%
1	CM	443	57% 39%
1	DA	443	67% 30%
1	DC	443	63% 34%
1	DE	443	62% 35%
1	DG	443	65% 31%
1	DI	443	65% 32%
1	DK	443	62% 35%
1	DM	443	55% 42%
1	E	443	61% 36%

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Mol	Chain	Length	Quality of chain
1	EB	443	60% 37%
1	ED	443	64% 33%
1	EF	443	67% 30%
1	EH	443	61% 36%
1	EJ	443	65% 32%
1	EL	443	54% 43%
1	F	443	60% 37%
1	FB	443	62% 35%
1	FD	443	60% 36%
1	FF	443	58% 39%
1	FH	443	62% 35%
1	FJ	443	63% 34%
1	FL	443	61% 35%
1	G	443	5% 64% 33%
1	GB	443	58% 39%
1	GD	443	58% 38%
1	GF	443	60% 37%
1	GH	443	58% 39%
1	GJ	443	60% 36%
1	GL	443	59% 38%
1	H	443	5% 60% 36%
1	HB	443	60% 36%
1	HD	443	58% 39%
1	HF	443	60% 37%
1	HH	443	61% 35%

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Mol	Chain	Length	Quality of chain
1	HJ	443	60% 36%
1	HL	443	57% 40%
1	I	443	54% 43%
1	IB	443	64% 33%
1	ID	443	59% 38%
1	IF	443	60% 37%
1	IH	443	64% 33%
1	IJ	443	64% 33%
1	IL	443	56% 41%
1	JA	443	63% 34%
1	JC	443	61% 36%
1	JE	443	61% 35%
1	JG	443	64% 33%
1	JI	443	64% 33%
1	JK	443	51% 46%
1	JM	443	61% 35%
1	KA	443	66% 31%
1	KC	443	62% 35%
1	KE	443	59% 37%
1	KG	443	63% 34%
1	KI	443	63% 34%
1	KK	443	59% 38%
1	KM	443	59% 38%
1	LA	443	60% 37%
1	LC	443	61% 36%

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Mol	Chain	Length	Quality of chain
1	LE	443	58% 39%
1	LG	443	57% 40%
1	LI	443	57% 40%
1	LK	443	58% 39%
1	LM	443	58% 39%
1	LO	443	53% 44%
1	M	443	63% 34%
1	MB	443	60% 37%
1	MD	443	56% 41%
1	MF	443	57% 40%
1	MH	443	62% 35%
1	MJ	443	60% 37%
1	ML	443	63% 34%
1	MN	443	59% 38%
1	N	443	58% 37% 5%
1	NB	443	58% 37% 5%
1	ND	443	61% 35%
1	NF	443	57% 39%
1	NH	443	59% 37%
1	NJ	443	64% 33%
1	NL	443	55% 41%
1	O	443	54% 42%
1	OB	443	58% 38%
1	OD	443	60% 36%
1	OF	443	60% 37%

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Mol	Chain	Length	Quality of chain
1	OH	443	59% 37%
1	OJ	443	58% 39%
1	OL	443	50% 46%
1	P	443	57% 34% 9%
1	PB	443	65% 31%
1	PD	443	61% 36%
1	PF	443	64% 33%
1	PH	443	62% 34%
1	PJ	443	64% 33%
1	PL	443	54% 42%
1	QA	443	58% 38%
1	QC	443	61% 35%
1	QE	443	62% 34%
1	QG	443	64% 33%
1	QI	443	64% 32%
1	QK	443	58% 39%
1	RA	443	60% 36%
1	RC	443	62% 35%
1	RE	443	60% 37%
1	RG	443	62% 34%
1	RI	443	63% 33%
1	RK	443	63% 34%
1	S	443	64% 32%
1	SB	443	61% 35%
1	SD	443	58% 37%

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Mol	Chain	Length	Quality of chain
1	SF	443	59% 37%
1	SH	443	60% 36%
1	SJ	443	59% 37%
1	T	443	58% 39%
1	TB	443	60% 37%
1	TD	443	59% 37%
1	TF	443	57% 39%
1	TH	443	60% 36%
1	TJ	443	65% 32%
1	TL	443	56% 40%
1	U	443	60% 36%
1	UB	443	62% 34%
1	UD	443	62% 34%
1	UF	443	58% 38%
1	UH	443	63% 33%
1	UJ	443	69% 27%
1	UL	443	60% 36%
1	V	443	60% 36%
1	VB	443	62% 34%
1	VD	443	60% 36%
1	VF	443	67% 30%
1	VH	443	65% 31%
1	VJ	443	63% 33%
1	VL	443	60% 37%
1	W	443	62% 34%

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Mol	Chain	Length	Quality of chain
1	WB	443	62% 34%
1	WD	443	63% 33%
1	WF	443	61% 35%
1	WH	443	60% 36%
1	WJ	443	63% 33%
1	WL	443	63% 33%
2	AA	451	62% 34% 5%
2	AC	451	59% 37%
2	AE	451	61% 36%
2	AG	451	62% 34%
2	AI	451	61% 36%
2	AK	451	62% 35%
2	AM	451	63% 32% 5%
2	BA	451	60% 35% 5%
2	BC	451	56% 39% 5%
2	BE	451	64% 31% 5%
2	BG	451	59% 36% 5%
2	BI	451	60% 37%
2	BK	451	59% 36% 5%
2	BM	451	62% 33% 5%
2	C	451	62% 36%
2	CB	451	65% 32%
2	CD	451	59% 39%
2	CF	451	66% 30% 5%
2	CH	451	62% 35%

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Mol	Chain	Length	Quality of chain
2	CJ	451	64% 34%
2	CL	451	62% 35%
2	D	451	6% 62% 34% 5%
2	DB	451	63% 32% 5%
2	DD	451	68% 27% 5%
2	DF	451	64% 32%
2	DH	451	64% 32% 5%
2	DJ	451	62% 33% 5%
2	DL	451	59% 37% 5%
2	EA	451	67% 28% 5%
2	EC	451	65% 32%
2	EE	451	59% 37%
2	EG	451	61% 35%
2	EI	451	64% 32%
2	EK	451	64% 31%
2	FA	451	66% 31%
2	FC	451	61% 35%
2	FE	451	63% 33%
2	FG	451	61% 35%
2	FI	451	64% 31% 5%
2	FK	451	59% 37%
2	GA	451	63% 33% 5%
2	GC	451	57% 38% 5%
2	GE	451	61% 34%
2	GG	451	64% 31% 5%

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Mol	Chain	Length	Quality of chain
2	GI	451	60% 35% 5%
2	GK	451	60% 35% 5%
2	HA	451	56% 39% 5%
2	HC	451	59% 37% 5%
2	HE	451	64% 33%
2	HG	451	61% 34%
2	HI	451	61% 35%
2	HK	451	59% 37%
2	HM	451	57% 38% 5%
2	IA	451	58% 37% 5%
2	IC	451	62% 34%
2	IE	451	61% 36%
2	IG	451	60% 37%
2	II	451	62% 35%
2	IK	451	57% 38% 5%
2	IM	451	59% 36% 5%
2	J	451	54% 43%
2	JB	451	63% 34%
2	JD	451	62% 33% 5%
2	JF	451	61% 34% 5%
2	JH	451	59% 37%
2	JJ	451	61% 35%
2	JL	451	55% 41%
2	JN	451	54% 43%
2	K	451	62% 34%

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Mol	Chain	Length	Quality of chain
2	KB	451	60% 37%
2	KD	451	63% 32% 5%
2	KF	451	63% 34%
2	KH	451	56% 40%
2	KJ	451	61% 35%
2	KL	451	61% 37%
2	KN	451	63% 35%
2	L	451	68% 29%
2	LB	451	57% 38%
2	LD	451	62% 33% 5%
2	LF	451	61% 37%
2	LH	451	57% 40%
2	LJ	451	60% 37%
2	LL	451	64% 33%
2	LN	451	59% 37%
2	MA	451	63% 33%
2	MC	451	60% 37%
2	ME	451	59% 38%
2	MG	451	61% 36%
2	MI	451	60% 37%
2	MK	451	57% 40%
2	MM	451	58% 37%
2	NA	451	63% 35%
2	NC	451	5% 61% 37%
2	NE	451	62% 35%

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Mol	Chain	Length	Quality of chain
2	NG	451	66% 31%
2	NI	451	59% 38%
2	NK	451	62% 36%
2	NM	451	61% 37%
2	OA	451	57% 39%
2	OC	451	60% 36%
2	OE	451	60% 35%
2	OG	451	60% 37%
2	OI	451	62% 33% 5%
2	OK	451	57% 38% 5%
2	OM	451	50% 46%
2	PA	451	61% 35% 5%
2	PC	451	64% 31%
2	PE	451	61% 34%
2	PG	451	60% 37%
2	PI	451	58% 38%
2	PK	451	62% 34%
2	PM	451	56% 39%
2	Q	451	61% 36%
2	QB	451	59% 36% 5%
2	QD	451	56% 39% 5%
2	QF	451	60% 36% 5%
2	QH	451	59% 39%
2	QJ	451	57% 39%
2	QL	451	60% 36%

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Mol	Chain	Length	Quality of chain
2	R	451	62% 35%
2	RB	451	60% 35%
2	RD	451	60% 36%
2	RF	451	62% 33%
2	RH	451	61% 35% 5%
2	RJ	451	60% 35% 5%
2	RL	451	62% 34%
2	SA	451	57% 39%
2	SC	451	62% 33%
2	SE	451	65% 31%
2	SG	451	62% 33%
2	SI	451	62% 34% 5%
2	SK	451	56% 39%
2	TA	451	62% 34% 5%
2	TC	451	58% 37% 5%
2	TE	451	63% 33% 5%
2	TG	451	63% 32%
2	TI	451	63% 33% 5%
2	TK	451	56% 40%
2	UA	451	65% 30% 5%
2	UC	451	62% 33% 5%
2	UE	451	63% 33% 5%
2	UG	451	61% 34%
2	UI	451	62% 34% 5%
2	UK	451	60% 35% 5%

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Mol	Chain	Length	Quality of chain
2	VA	451	64% 31%
2	VC	451	61% 35%
2	VE	451	68% 27%
2	VG	451	62% 34%
2	VI	451	65% 31%
2	VK	451	60% 35% 5%
2	VM	451	59% 37%
2	WA	451	63% 34%
2	WC	451	58% 38%
2	WE	451	63% 35%
2	WG	451	61% 34%
2	WI	451	63% 34%
2	WK	451	64% 31%
2	WM	451	66% 31%
3	X	214	65% 21% 14%
3	XA	214	56% 29% 14%
3	XB	214	50% 36% 14%
3	XC	214	55% 31% 14%
3	XD	214	53% 33% 14%
3	XE	214	54% 32% 14%
3	XF	214	57% 29% 14%
4	XM	310	61% 23% 16%
4	XO	310	57% 27% 16%
4	XQ	310	61% 23% 16%
4	XR	310	61% 23% 16%

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Mol	Chain	Length	Quality of chain
5	XN	314	61% 25% 14%
5	XP	314	61% 25% 14%
6	0	264	65% 32%
6	0A	264	64% 34%
7	0C	408	20% 10% 70%
7	0D	408	59% 28% 13%
8	0F	480	28% 9% 63%
8	0G	480	52% 20% 27%
8	0H	480	94%
8	0I	480	43% 16% 41%
8	0J	480	5% 35% 12% 53%
9	0L	629	65% 34%
9	0M	629	62% 37%
9	0N	629	61% 38%
9	0O	629	31% 19% 51%
10	0R	490	42% 21% 37%
10	0S	490	34% 11% 55%
11	0U	337	67% 32%
12	0W	343	74% 25%
13	0Y	279	68% 15% 16%
13	0Z	279	66% 18% 16%
13	0a	279	16% 5% 79%
14	0c	370	43% 21% 36%
14	0d	370	49% 22% 28%
15	0f	277	35% 23% 42%

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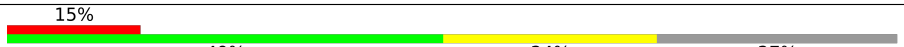
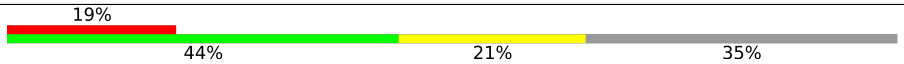
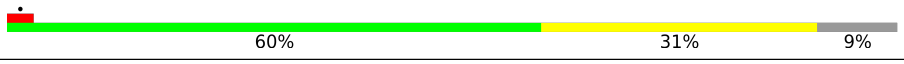
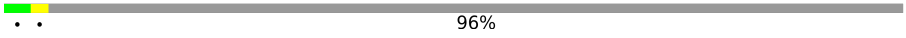
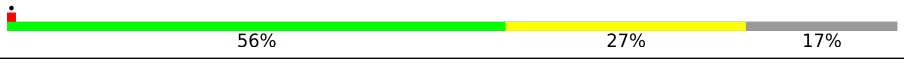
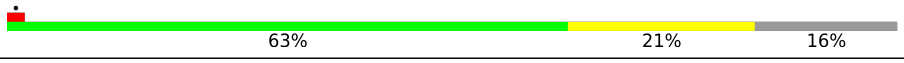
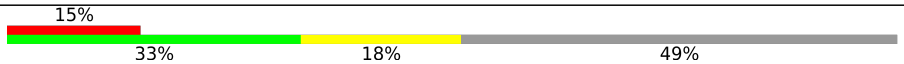
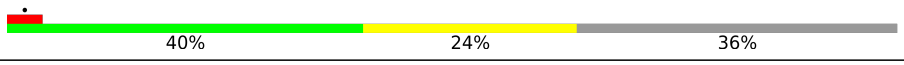
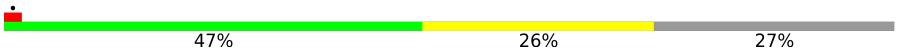
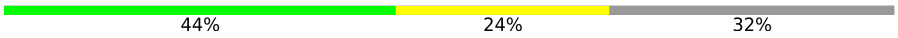
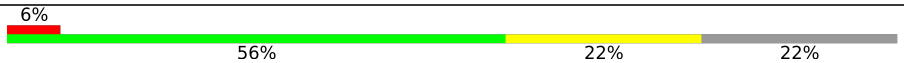
Mol	Chain	Length	Quality of chain
15	0g	277	
16	0k	979	
16	0l	979	
17	0m	446	
17	0n	446	
17	0o	446	
18	0p	305	
19	0r	306	
20	0t	295	
20	0u	295	
21	0v	533	
21	0w	533	
21	0x	533	
22	0z	282	
22	1w	282	
22	1x	282	
22	1y	282	
23	1A	397	
23	1B	397	
23	1D	397	
23	1E	397	
23	1F	397	
24	1H	756	
24	1I	756	
24	1J	756	

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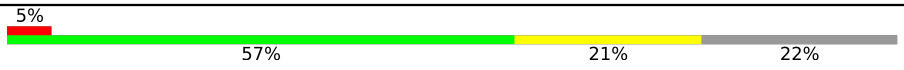
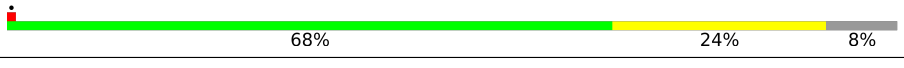
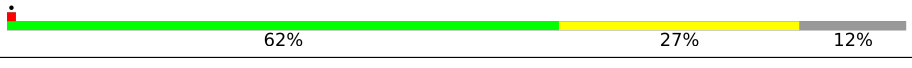
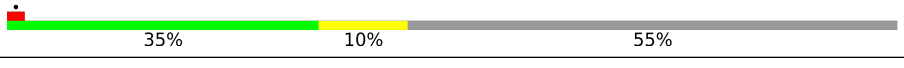
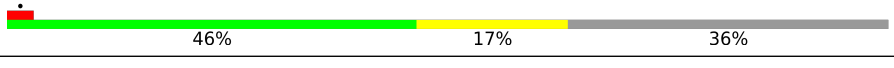
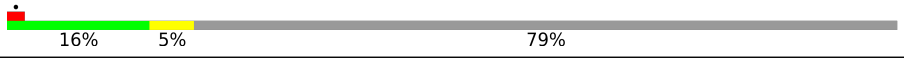
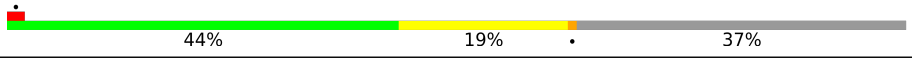
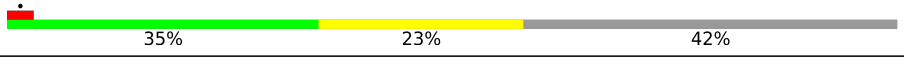
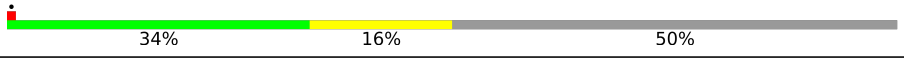
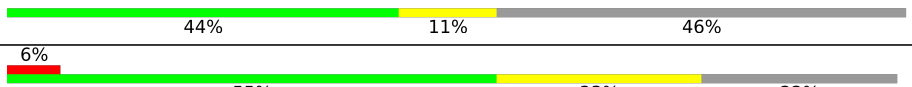
Mol	Chain	Length	Quality of chain
24	1K	756	
25	1O	774	
26	1Q	741	
27	1S	861	
27	1T	861	
28	1U	266	
28	1V	266	
28	1X	266	
28	1Y	266	
28	1a	266	
28	1b	266	
28	1c	266	
28	1d	266	
28	1e	266	
28	1g	266	
28	1h	266	
28	4V	266	
28	4W	266	
29	1j	226	
29	1k	226	
29	1l	226	
29	1m	226	
30	1o	236	
31	1q	275	
31	1r	275	

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Mol	Chain	Length	Quality of chain
31	1s	275	13% 52% 15% 33%
31	1t	275	8% 23% 5% 73%
32	2B	289	62% 25% 13%
32	2C	289	56% 24% 20%
33	2F	312	67% 24% 9%
33	2G	312	59% 32% 9%
33	2H	312	65% 27% 8%
33	2I	312	56% 21% 22%
34	2L	311	37% 18% 45%
35	2N	314	30% 13% 57%
35	2O	314	29% 22% 49%
36	2Q	338	63% 23% 14%
37	2S	358	45% 22% 34%
38	2U	352	40% 25% 35%
38	2V	352	23% 8% 69%
39	2X	352	50% 14% 36%
40	2Z	371	51% 25% 24%
41	2b	360	29% 5% 66%
41	2c	360	52% 16% 32%
41	2e	360	65% 25% 10%
41	2f	360	11% 86%
41	2h	360	48% 18% 34%
41	2i	360	31% 10% 59%
41	2k	360	36% 10% 54%
41	2l	360	54% 19% 27%

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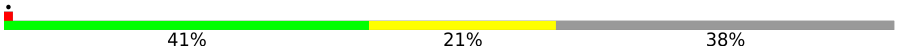
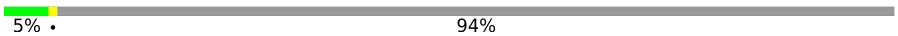
Mol	Chain	Length	Quality of chain
41	2n	360	
41	2o	360	
41	2p	360	
42	2r	410	
43	2t	343	
44	2v	413	
44	2w	413	
45	2y	430	
45	2z	430	
46	3B	439	
47	3D	457	
48	3F	468	
48	3G	468	
48	3H	468	
48	3I	468	
48	3L	468	
48	3M	468	
49	3P	588	
49	3Q	588	
50	3S	176	
51	X1	308	
52	3U	409	
53	3W	373	
53	3X	373	
54	3Z	443	

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Mol	Chain	Length	Quality of chain
54	3a	443	13% 7% 80%
54	4Y	443	96%
55	3b	183	60% 15% 26%
56	3d	261	5% 44% 12% 43%
57	3f	197	53% 30% 16%
57	3g	197	61% 23% 16%
57	3h	197	5% 62% 21% 16%
57	3i	197	46% 37% 16%
58	3m	195	56% 18% 26%
59	3o	306	13% 5% 82%
59	3p	306	34% 14% 52%
59	4O	306	42% 14% 43%
59	4P	306	18% 77%
59	4a	306	35% 15% 50%
59	4b	306	20% 77%
60	3r	158	56% 27% 18%
60	3s	158	51% 30% 18%
60	3t	158	28% 11% 60%
61	3w	288	42% 16% 42%
61	3x	288	34% 9% 56%
62	4A	480	94%
62	4B	480	30% 12% 58%
63	4I	590	5% 8% 5% 87%
64	5B	675	18% 7% 75%
64	5C	675	17% 8% 75%

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Mol	Chain	Length	Quality of chain
64	5D	675	94%
65	5G	617	20% 10% 70%
65	5H	617	18% 12% 70%
65	5I	617	6% 92%
66	5K	492	37% 17% 46%
66	5L	492	33% 21% 46%
67	5O	111	56% 41%
67	5P	111	18% 50% 46%
68	5S	176	5% 35% 16% 48%
68	5T	176	10% 38% 15% 48%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
72	ZN	1b	301	-	-	X	-

2 Entry composition (i)

There are 74 unique types of molecules in this entry. The entry contains 1371722 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AB	419	Total	C	N	O	S	0	0
			3283	2056	560	636	31		
1	AD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AN	419	Total	C	N	O	S	0	0
			3283	2056	560	636	31		
1	B	418	Total	C	N	O	S	0	0
			3270	2039	564	637	30		
1	BB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BD	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	BF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CA	424	Total	C	N	O	S	0	0
			3319	2076	568	643	32		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CC	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	CE	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	CG	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	CI	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	CK	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	CM	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DA	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DC	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DE	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DG	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DI	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DK	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	DM	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	E	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	EB	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	ED	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	EF	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	EH	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	EJ	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	EL	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	F	429	Total 3362	C 2101	N 578	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FJ	429	Total	C	N	O	S	0	0
			3361	2100	578	652	31		
1	FL	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	G	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GD	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	GF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GJ	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	GL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	H	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	I	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	IB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	ID	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JA	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JC	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JE	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JG	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JI	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JK	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JM	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	KA	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	KC	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KE	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KG	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KI	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KK	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KM	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LA	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	LC	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LE	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LG	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LI	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LK	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LM	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LO	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	M	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	MB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	MD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	MF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	MH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	MJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	ML	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	MN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	N	420	Total	C	N	O	S	0	0
			3290	2060	561	638	31		
1	NB	420	Total	C	N	O	S	0	0
			3290	2060	561	638	31		
1	ND	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	NF	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	NH	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	NJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	NL	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	O	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OB	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	OD	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OF	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OH	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OJ	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OL	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	P	401	Total	C	N	O	S	0	0
			3123	1946	540	609	28		
1	PB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	PD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	PF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	PH	426	Total	C	N	O	S	0	0
			3342	2089	575	647	31		
1	PJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	PL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	QA	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	QC	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	QE	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	QG	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	QI	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	QK	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	RA	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RC	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	RE	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RG	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RI	426	Total	C	N	O	S	0	0
			3342	2088	575	648	31		
1	RK	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	S	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SB	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SD	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SF	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SH	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	SJ	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	T	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	TB	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	TD	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	TF	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	TH	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	TJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	TL	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	U	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UB	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	UD	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UF	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UH	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UJ	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	UL	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	V	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	VB	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	VD	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	VF	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	VH	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	VJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	VL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	W	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	WB	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	WD	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	WF	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	WH	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	WJ	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	WL	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		

- Molecule 2 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	AC	433	Total	C	N	O	S	0	0
			3353	2117	570	643	23		
2	AE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AG	433	Total	C	N	O	S	0	0
			3352	2116	571	642	23		
2	AI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AK	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BA	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BC	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BE	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BG	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	BK	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	C	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CB	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CD	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CF	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	CH	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CJ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CL	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	D	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	DB	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DF	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	DH	430	Total	C	N	O	S	0	0
			3328	2102	567	636	23		
2	DJ	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DL	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	EA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	EC	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	EE	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	EG	433	Total	C	N	O	S	0	0
			3351	2114	570	644	23		
2	EI	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	EK	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	FA	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	FC	434	Total	C	N	O	S	0	0
			3360	2119	571	647	23		
2	FE	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	FG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	FI	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	FK	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	GA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GC	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	GG	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HC	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	HG	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	HI	431	Total	C	N	O	S	0	0
			3336	2106	568	639	23		
2	HK	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	HM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IC	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	IE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	II	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	J	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	JB	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	JD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	JF	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	JH	432	Total	C	N	O	S	0	0
			3342	2110	569	640	23		
2	JJ	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	JL	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	JN	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	K	434	Total	C	N	O	S	0	0
			3358	2119	572	643	24		
2	KB	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	KF	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KH	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	KJ	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	KL	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KN	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	L	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LB	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	LD	429	Total	C	N	O	S	0	0
			3322	2097	566	637	22		
2	LF	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LH	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LJ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LL	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LN	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	MA	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	MC	437	Total	C	N	O	S	0	0
			3379	2133	575	647	24		
2	ME	436	Total	C	N	O	S	0	0
			3368	2124	573	647	24		
2	MG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MK	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MM	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	NA	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NC	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NK	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NM	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	OA	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	OC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	OE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	OG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	OI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	OK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	OM	433	Total	C	N	O	S	0	0
			3352	2115	570	644	23		
2	PA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	PC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	PI	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PK	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	PM	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	Q	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	QB	429	Total	C	N	O	S	0	0
			3323	2100	566	634	23		
2	QD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	QF	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	QH	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	QJ	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	QL	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	R	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	RB	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RD	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RF	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RH	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	RJ	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	RL	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SA	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	SC	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SE	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	SI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	SK	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	TA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TC	428	Total	C	N	O	S	0	0
			3314	2093	565	634	22		
2	TE	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	TI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TK	433	Total	C	N	O	S	0	0
			3353	2117	570	643	23		
2	UA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UC	429	Total	C	N	O	S	0	0
			3322	2097	566	637	22		
2	UE	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	UI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	VA	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	VI	432	Total	C	N	O	S	0	0
			3342	2109	569	641	23		
2	VK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	VM	434	Total	C	N	O	S	0	0
			3360	2119	571	647	23		
2	WA	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WK	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WM	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

- Molecule 3 is a protein called CFAP20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	X	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XA	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XB	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XC	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XD	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XE	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XF	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		

- Molecule 4 is a protein called PACRGA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	XM	259	Total	C	N	O	S	0	0
			2045	1307	360	370	8		
4	XO	260	Total	C	N	O	S	0	0
			2053	1311	361	373	8		
4	XQ	260	Total	C	N	O	S	0	0
			2053	1311	361	373	8		
4	XR	260	Total	C	N	O	S	0	0
			2056	1313	364	371	8		

- Molecule 5 is a protein called PACRGB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	XN	269	Total	C	N	O	S	0	0
			2116	1359	366	384	7		
5	XP	269	Total	C	N	O	S	0	0
			2116	1359	366	384	7		

- Molecule 6 is a protein called CCDC81.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	0A	257	Total	C	N	O	S	0	0
			2004	1261	359	371	13		
6	0	257	Total	C	N	O	S	0	0
			2004	1261	359	371	13		

- Molecule 7 is a protein called CFAP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	0C	121	Total	C	N	O	S	0	0
			935	584	159	188	4		
7	0D	354	Total	C	N	O	S	0	0
			2723	1683	492	537	11		

- Molecule 8 is a protein called CFAP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	0F	176	Total	C	N	O	S	0	0
			1439	859	288	280	12		
8	0G	349	Total	C	N	O	S	0	0
			2955	1772	596	570	17		
8	0H	28	Total	C	N	O		0	0
			229	146	41	42			

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	0I	285	Total	C	N	O	S	0	0
			2369	1421	471	459	18		
8	0J	226	Total	C	N	O	S	0	0
			1906	1147	379	373	7		

- Molecule 9 is a protein called CFAP52.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	0L	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0M	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0N	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0O	310	Total	C	N	O	S	0	0
			2357	1482	416	445	14		

- Molecule 10 is a protein called CFAP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	0R	309	Total	C	N	O	S	0	0
			2628	1579	535	501	13		
10	0S	221	Total	C	N	O	S	0	0
			1874	1148	360	359	7		

- Molecule 11 is a protein called CFAP67A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	0U	333	Total	C	N	O	S	0	0
			2570	1621	437	495	17		

- Molecule 12 is a protein called CFAP67B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	0W	339	Total	C	N	O	S	0	0
			2595	1647	427	501	20		

- Molecule 13 is a protein called CFAP106A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0Y	233	Total	C	N	O	S	0	0
			1836	1152	334	345	5		

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Mol	Chain	Residues	Atoms	AltConf	Trace
13	0Z	235	Total C N O S 1849 1160 337 347 5	0	0
13	0a	58	Total C N O 422 263 78 81	0	0

- Molecule 14 is a protein called CFAP106B.

Mol	Chain	Residues	Atoms	AltConf	Trace
14	0c	237	Total C N O S 1929 1221 337 362 9	0	0
14	0d	265	Total C N O S 2150 1359 378 404 9	0	0

- Molecule 15 is a protein called CFAP107.

Mol	Chain	Residues	Atoms	AltConf	Trace
15	0f	160	Total C N O S 1257 783 222 241 11	0	0
15	0g	30	Total C N O S 218 137 34 46 1	0	0

- Molecule 16 is a protein called CFAP115.

Mol	Chain	Residues	Atoms	AltConf	Trace
16	0l	640	Total C N O S 5045 3192 918 914 21	0	0
16	0k	710	Total C N O S 5599 3537 1026 1009 27	0	0

- Molecule 17 is a protein called CFAP127.

Mol	Chain	Residues	Atoms	AltConf	Trace
17	0m	142	Total C N O S 1155 704 220 227 4	0	0
17	0n	406	Total C N O S 3388 2054 668 654 12	0	0
17	0o	20	Total C N O 171 107 35 29	0	0

- Molecule 18 is a protein called CFAP141.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	0p	108	Total	C	N	O	S	0	0
			906	557	177	169	3		

- Molecule 19 is a protein called CFAP143.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	0r	254	Total	C	N	O	S	0	0
			2033	1246	376	396	15		

- Molecule 20 is a protein called CFAP161.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	0t	262	Total	C	N	O	S	0	0
			2062	1298	358	388	18		
20	0u	227	Total	C	N	O	S	0	0
			1769	1117	306	330	16		

- Molecule 21 is a protein called CFAP210.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0w	449	Total	C	N	O	S	0	0
			3715	2242	741	724	8		
21	0x	111	Total	C	N	O	S	0	0
			906	556	175	172	3		
21	0v	73	Total	C	N	O		0	0
			582	351	115	116			

- Molecule 22 is a protein called DMIP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0z	143	Total	C	N	O	S	0	0
			1160	716	220	219	5		
22	1w	180	Total	C	N	O	S	0	0
			1481	915	278	281	7		
22	1x	206	Total	C	N	O	S	0	0
			1680	1031	322	315	12		
22	1y	91	Total	C	N	O	S	0	0
			722	449	130	141	2		

- Molecule 23 is a protein called RIB43.

Mol	Chain	Residues	Atoms	AltConf	Trace
23	1A	270	Total C N O S 2286 1390 449 436 11	0	0
23	1B	195	Total C N O S 1667 1015 321 322 9	0	0
23	1D	54	Total C N O S 464 285 91 85 3	0	0
23	1E	362	Total C N O S 3050 1855 590 590 15	0	0
23	1F	74	Total C N O S 635 387 120 124 4	0	0

- Molecule 24 is a protein called RIB72A.

Mol	Chain	Residues	Atoms	AltConf	Trace
24	1H	588	Total C N O S 4698 2967 812 900 19	0	0
24	1I	659	Total C N O S 5276 3326 920 1003 27	0	0
24	1J	670	Total C N O S 5356 3372 940 1018 26	0	0
24	1K	588	Total C N O S 4697 2966 812 900 19	0	0

- Molecule 25 is a protein called RIB72B.

Mol	Chain	Residues	Atoms	AltConf	Trace
25	1O	710	Total C N O S 5751 3614 1021 1096 20	0	0

- Molecule 26 is a protein called RIB72C.

Mol	Chain	Residues	Atoms	AltConf	Trace
26	1Q	655	Total C N O S 5263 3323 927 988 25	0	0

- Molecule 27 is a protein called RIB72D.

Mol	Chain	Residues	Atoms	AltConf	Trace
27	1S	726	Total C N O S 5834 3696 1029 1076 33	0	0
27	1T	222	Total C N O S 1787 1125 315 335 12	0	0

- Molecule 28 is a protein called DMIP1.

Mol	Chain	Residues	Atoms	AltConf	Trace
28	1U	120	Total C N O S 942 594 162 181 5	0	0
28	1V	48	Total C N O S 371 229 68 69 5	0	0
28	1X	120	Total C N O S 942 594 162 181 5	0	0
28	1Y	169	Total C N O S 1325 829 237 252 7	0	0
28	1a	57	Total C N O S 446 279 80 84 3	0	0
28	1b	168	Total C N O S 1313 823 230 250 10	0	0
28	1c	35	Total C N O S 263 162 50 46 5	0	0
28	1d	120	Total C N O S 942 594 162 181 5	0	0
28	1e	48	Total C N O S 371 229 68 69 5	0	0
28	1g	120	Total C N O S 942 594 162 181 5	0	0
28	1h	155	Total C N O S 1218 767 214 230 7	0	0
28	4V	62	Total C N O S 486 305 86 91 4	0	0
28	4W	188	Total C N O S 1474 927 255 283 9	0	0

- Molecule 29 is a protein called DMIP2.

Mol	Chain	Residues	Atoms	AltConf	Trace
29	1j	113	Total C N O S 909 584 153 168 4	0	0
29	1k	103	Total C N O S 801 502 140 157 2	0	0
29	1l	113	Total C N O S 909 584 153 168 4	0	0
29	1m	53	Total C N O S 420 268 72 78 2	0	0

- Molecule 30 is a protein called DMIP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	1o	128	Total	C	N	O	S	0	0
			1035	645	193	192	5		

- Molecule 31 is a protein called DMIP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1q	214	Total	C	N	O	S	0	0
			1679	1025	322	321	11		
31	1r	106	Total	C	N	O	S	0	0
			868	532	166	165	5		
31	1s	183	Total	C	N	O	S	0	0
			1446	884	273	277	12		
31	1t	75	Total	C	N	O	S	0	0
			618	372	125	116	5		

- Molecule 32 is a protein called DMIP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	2B	251	Total	C	N	O	S	0	0
			1977	1231	357	377	12		
32	2C	230	Total	C	N	O	S	0	0
			1814	1130	329	344	11		

- Molecule 33 is a protein called DMIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2F	284	Total	C	N	O	S	0	0
			2253	1411	411	418	13		
33	2G	283	Total	C	N	O	S	0	0
			2245	1407	409	416	13		
33	2H	288	Total	C	N	O	S	0	0
			2281	1428	416	424	13		
33	2I	243	Total	C	N	O	S	0	0
			1937	1208	355	363	11		

- Molecule 34 is a protein called DMIP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2L	172	Total	C	N	O	S	0	0
			1433	904	254	269	6		

- Molecule 35 is a protein called DMIP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2N	135	Total	C	N	O	S	0	0
			1103	698	208	194	3		
35	2O	161	Total	C	N	O	S	0	0
			1324	827	251	240	6		

- Molecule 36 is a protein called DMIP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2Q	291	Total	C	N	O	S	0	0
			2320	1483	394	429	14		

- Molecule 37 is a protein called DMIP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2S	237	Total	C	N	O	S	0	0
			1800	1127	317	341	15		

- Molecule 38 is a protein called DMIP12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2U	229	Total	C	N	O	S	0	0
			1807	1111	329	355	12		
38	2V	109	Total	C	N	O	S	0	0
			870	530	167	169	4		

- Molecule 39 is a protein called DMIP13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2X	227	Total	C	N	O	S	0	0
			1774	1081	355	328	10		

- Molecule 40 is a protein called DMIP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	2Z	283	Total	C	N	O	S	0	0
			2258	1427	412	414	5		

- Molecule 41 is a protein called DMIP15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	2b	121	Total	C	N	O	S	0	0
			1006	613	195	194	4		

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Mol	Chain	Residues	Atoms	AltConf	Trace
41	2c	245	Total C N O S 2092 1254 418 408 12	0	0
41	2e	325	Total C N O S 2735 1649 546 526 14	0	0
41	2f	52	Total C N O S 454 275 89 88 2	0	0
41	2h	237	Total C N O S 1978 1187 396 385 10	0	0
41	2i	149	Total C N O S 1301 776 266 252 7	0	0
41	2k	167	Total C N O S 1369 834 266 262 7	0	0
41	2l	264	Total C N O S 2228 1338 445 432 13	0	0
41	2n	42	Total C N O 361 219 72 70	0	0
41	2o	287	Total C N O S 2453 1473 490 478 12	0	0
41	2p	49	Total C N O S 425 257 86 80 2	0	0

- Molecule 42 is a protein called DMIP16.

Mol	Chain	Residues	Atoms	AltConf	Trace
42	2r	315	Total C N O S 2473 1564 439 460 10	0	0

- Molecule 43 is a protein called DMIP17.

Mol	Chain	Residues	Atoms	AltConf	Trace
43	2t	214	Total C N O S 1713 1075 302 324 12	0	0

- Molecule 44 is a protein called DMIP18.

Mol	Chain	Residues	Atoms	AltConf	Trace
44	2v	280	Total C N O S 2264 1438 391 425 10	0	0
44	2w	412	Total C N O S 3291 2082 565 629 15	0	0

- Molecule 45 is a protein called DMIP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2y	287	Total	C	N	O	S	0	0
			2316	1424	424	460	8		
45	2z	187	Total	C	N	O	S	0	0
			1435	890	257	287	1		

- Molecule 46 is a protein called DMIP20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3B	418	Total	C	N	O	S	0	0
			3308	2069	596	631	12		

- Molecule 47 is a protein called DMIP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3D	412	Total	C	N	O	S	0	0
			3212	1986	586	628	12		

- Molecule 48 is a protein called DMIP22.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	3I	80	Total	C	N	O	S	0	0
			640	400	114	122	4		
48	3F	155	Total	C	N	O	S	0	0
			1254	777	240	230	7		
48	3G	90	Total	C	N	O	S	0	0
			733	456	139	134	4		
48	3H	103	Total	C	N	O	S	0	0
			832	516	161	151	4		
48	3M	29	Total	C	N	O	S	0	0
			247	155	44	45	3		
48	3L	29	Total	C	N	O	S	0	0
			247	155	44	45	3		

- Molecule 49 is a protein called DMIP23.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3P	256	Total	C	N	O	S	0	0
			2002	1260	351	380	11		
49	3Q	490	Total	C	N	O	S	0	0
			3825	2406	666	735	18		

- Molecule 50 is a protein called DMIP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3S	25	Total	C	N	O	S	0	0
			182	109	36	33	4		

- Molecule 51 is a protein called DMIP24.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	X1	39	Total	C	N	O	0	0
			304	183	58	63		

- Molecule 52 is a protein called DMIP25.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3U	140	Total	C	N	O	S	0	0
			1074	681	186	203	4		

- Molecule 53 is a protein called DMIP26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3X	49	Total	C	N	O	S	0	0
			386	239	74	70	3		
53	3W	153	Total	C	N	O	S	0	0
			1264	786	231	239	8		

- Molecule 54 is a protein called DMIP27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3Z	181	Total	C	N	O	S	0	0
			1405	862	264	271	8		
54	3a	87	Total	C	N	O	S	0	0
			712	442	130	136	4		
54	4Y	16	Total	C	N	O	S	0	0
			122	75	18	28	1		

- Molecule 55 is a protein called ArcMAP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	3b	136	Total	C	N	O	S	0	0
			1126	695	204	223	4		

- Molecule 56 is a protein called ArcMAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	3d	148	Total	C	N	O	S	0	0
			1240	765	229	240	6		

- Molecule 57 is a protein called ArcMAP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	3f	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
57	3g	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
57	3h	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
57	3i	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		

- Molecule 58 is a protein called ArcMAP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	3m	144	Total	C	N	O	S	0	0
			1216	745	236	231	4		

- Molecule 59 is a protein called CFAP96.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	3o	55	Total	C	N	O	S	0	0
			459	293	79	85	2		
59	3p	148	Total	C	N	O	S	0	0
			1159	744	201	212	2		
59	4O	175	Total	C	N	O	S	0	0
			1399	899	245	253	2		
59	4P	69	Total	C	N	O	S	0	0
			529	346	84	98	1		
59	4a	154	Total	C	N	O	S	0	0
			1233	796	213	223	1		
59	4b	69	Total	C	N	O	S	0	0
			529	346	84	98	1		

- Molecule 60 is a protein called CFAP97.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	3r	130	Total	C	N	O	S	0	0
			1098	668	221	205	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
60	3s	130	Total	C	N	O	S	0	0
			1098	668	221	205	4		
60	3t	63	Total	C	N	O	S	0	0
			533	326	105	98	4		

- Molecule 61 is a protein called DMAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	3w	166	Total	C	N	O	S	0	0
			1362	872	235	249	6		
61	3x	126	Total	C	N	O	S	0	0
			987	626	178	182	1		

- Molecule 62 is a protein called DMAP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	4A	29	Total	C	N	O	S	0	0
			229	142	43	43	1		
62	4B	201	Total	C	N	O	S	0	0
			1584	1003	275	302	4		

- Molecule 63 is a protein called DMAP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	4I	77	Total	C	N	O	S	0	0
			620	385	128	106	1		

- Molecule 64 is a protein called distal DC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	5B	168	Total	C	N	O	S	0	0
			1348	828	258	257	5		
64	5C	168	Total	C	N	O	S	0	0
			1348	828	258	257	5		
64	5D	40	Total	C	N	O	S	0	0
			321	196	61	61	3		

- Molecule 65 is a protein called distal DC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	5G	185	Total	C	N	O	S	0	0
			1541	942	295	296	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
65	5H	185	Total	C	N	O	S	0	0
			1541	942	295	296	8		
65	5I	47	Total	C	N	O	S	0	0
			401	251	77	72	1		

- Molecule 66 is a protein called distal DC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	5K	266	Total	C	N	O	S	0	0
			2155	1372	377	393	13		
66	5L	266	Total	C	N	O	S	0	0
			2155	1372	377	393	13		

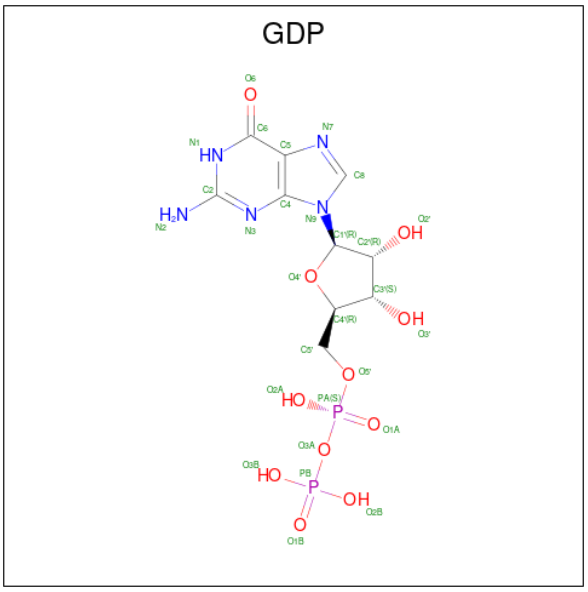
- Molecule 67 is a protein called DC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	5O	107	Total	C	N	O	S	0	0
			809	523	130	152	4		
67	5P	107	Total	C	N	O	S	0	0
			809	523	130	152	4		

- Molecule 68 is a protein called DC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	5S	92	Total	C	N	O	S	0	0
			749	470	137	133	9		
68	5T	92	Total	C	N	O	S	0	0
			749	470	137	133	9		

- Molecule 69 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



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

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Mol	Chain	Residues	Atoms					AltConf
69	BN	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CG	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CK	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	CM	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DG	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DK	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	DM	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	E	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	EB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	ED	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	EF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	EH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	EJ	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
69	EL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	F	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	FB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	FD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	FF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	FH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	FJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	FL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	G	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	GB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	GD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	GF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	GH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	GJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	GL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	H	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	HB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	HD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	HF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	HH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	HJ	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
69	HL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	I	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	IB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	ID	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	IF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	IH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	IJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	IL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JG	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JK	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	JM	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	KA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	KC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	KE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	KG	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	KI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	KK	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
69	KM	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LG	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LK	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LM	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	LO	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	M	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	MB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	MD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	MF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	MH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	MJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	ML	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	MN	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	N	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	NB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	ND	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	NF	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
69	NH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	NJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	NL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	O	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	OB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	OD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	OF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	OH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	OJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	OL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	P	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	PB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	PD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	PF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	PH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	PJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	PL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	QA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	QC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	QE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	QG	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
69	QI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	QK	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	RA	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	RC	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	RE	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	RG	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	RI	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	RK	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	S	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	SB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	SD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	SF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	SH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	SJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	T	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	TB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	TD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	TF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	TH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	TJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	TL	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
69	U	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	UB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	UD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	UF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	UH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	UJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	UL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	V	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	VB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	VD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	VF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	VH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	VJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	VL	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	W	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	WB	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	WD	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	WF	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	WH	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	WJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
69	WL	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 70 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
70	AA	1	Total Mg 1 1	0
70	AC	1	Total Mg 1 1	0
70	AE	1	Total Mg 1 1	0
70	AG	1	Total Mg 1 1	0
70	AI	1	Total Mg 1 1	0
70	AK	1	Total Mg 1 1	0
70	AM	1	Total Mg 1 1	0
70	BA	1	Total Mg 1 1	0
70	BC	1	Total Mg 1 1	0
70	BE	1	Total Mg 1 1	0
70	BG	1	Total Mg 1 1	0
70	BI	1	Total Mg 1 1	0
70	BK	1	Total Mg 1 1	0
70	BM	1	Total Mg 1 1	0
70	C	1	Total Mg 1 1	0
70	CB	1	Total Mg 1 1	0
70	CD	1	Total Mg 1 1	0
70	CF	1	Total Mg 1 1	0
70	CH	1	Total Mg 1 1	0
70	CJ	1	Total Mg 1 1	0
70	CL	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
70	D	1	Total Mg 1 1	0
70	DB	1	Total Mg 1 1	0
70	DD	1	Total Mg 1 1	0
70	DF	1	Total Mg 1 1	0
70	DH	1	Total Mg 1 1	0
70	DJ	1	Total Mg 1 1	0
70	DL	1	Total Mg 1 1	0
70	EA	1	Total Mg 1 1	0
70	EC	1	Total Mg 1 1	0
70	EE	1	Total Mg 1 1	0
70	EG	1	Total Mg 1 1	0
70	EI	1	Total Mg 1 1	0
70	EK	1	Total Mg 1 1	0
70	FA	1	Total Mg 1 1	0
70	FC	1	Total Mg 1 1	0
70	FE	1	Total Mg 1 1	0
70	FG	1	Total Mg 1 1	0
70	FI	1	Total Mg 1 1	0
70	FK	1	Total Mg 1 1	0
70	GA	1	Total Mg 1 1	0
70	GC	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
70	GE	1	Total Mg 1 1	0
70	GG	1	Total Mg 1 1	0
70	GI	1	Total Mg 1 1	0
70	GK	1	Total Mg 1 1	0
70	HA	1	Total Mg 1 1	0
70	HC	1	Total Mg 1 1	0
70	HE	1	Total Mg 1 1	0
70	HG	1	Total Mg 1 1	0
70	HI	1	Total Mg 1 1	0
70	HK	1	Total Mg 1 1	0
70	HM	1	Total Mg 1 1	0
70	IA	1	Total Mg 1 1	0
70	IC	1	Total Mg 1 1	0
70	IE	1	Total Mg 1 1	0
70	IG	1	Total Mg 1 1	0
70	II	1	Total Mg 1 1	0
70	IK	1	Total Mg 1 1	0
70	IM	1	Total Mg 1 1	0
70	J	1	Total Mg 1 1	0
70	JB	1	Total Mg 1 1	0
70	JD	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
70	JF	1	Total Mg 1 1	0
70	JH	1	Total Mg 1 1	0
70	JJ	1	Total Mg 1 1	0
70	JL	1	Total Mg 1 1	0
70	JN	1	Total Mg 1 1	0
70	K	1	Total Mg 1 1	0
70	KB	1	Total Mg 1 1	0
70	KD	1	Total Mg 1 1	0
70	KF	1	Total Mg 1 1	0
70	KH	1	Total Mg 1 1	0
70	KJ	1	Total Mg 1 1	0
70	KL	1	Total Mg 1 1	0
70	KN	1	Total Mg 1 1	0
70	L	1	Total Mg 1 1	0
70	LB	1	Total Mg 1 1	0
70	LD	1	Total Mg 1 1	0
70	LF	1	Total Mg 1 1	0
70	LH	1	Total Mg 1 1	0
70	LJ	1	Total Mg 1 1	0
70	LL	1	Total Mg 1 1	0
70	LN	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
70	MA	1	Total Mg 1 1	0
70	MC	1	Total Mg 1 1	0
70	ME	1	Total Mg 1 1	0
70	MG	1	Total Mg 1 1	0
70	MI	1	Total Mg 1 1	0
70	MK	1	Total Mg 1 1	0
70	MM	1	Total Mg 1 1	0
70	NA	1	Total Mg 1 1	0
70	NC	1	Total Mg 1 1	0
70	NE	1	Total Mg 1 1	0
70	NG	1	Total Mg 1 1	0
70	NI	1	Total Mg 1 1	0
70	NK	1	Total Mg 1 1	0
70	NM	1	Total Mg 1 1	0
70	OA	1	Total Mg 1 1	0
70	OC	1	Total Mg 1 1	0
70	OE	1	Total Mg 1 1	0
70	OG	1	Total Mg 1 1	0
70	OI	1	Total Mg 1 1	0
70	OK	1	Total Mg 1 1	0
70	OM	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
70	PA	1	Total Mg 1 1	0
70	PC	1	Total Mg 1 1	0
70	PE	1	Total Mg 1 1	0
70	PG	1	Total Mg 1 1	0
70	PI	1	Total Mg 1 1	0
70	PK	1	Total Mg 1 1	0
70	PM	1	Total Mg 1 1	0
70	Q	1	Total Mg 1 1	0
70	QB	1	Total Mg 1 1	0
70	QD	1	Total Mg 1 1	0
70	QF	1	Total Mg 1 1	0
70	QH	1	Total Mg 1 1	0
70	QJ	1	Total Mg 1 1	0
70	QL	1	Total Mg 1 1	0
70	R	1	Total Mg 1 1	0
70	RB	1	Total Mg 1 1	0
70	RD	1	Total Mg 1 1	0
70	RF	1	Total Mg 1 1	0
70	RH	1	Total Mg 1 1	0
70	RJ	1	Total Mg 1 1	0
70	RL	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
70	SA	1	Total Mg 1 1	0
70	SC	1	Total Mg 1 1	0
70	SE	1	Total Mg 1 1	0
70	SG	1	Total Mg 1 1	0
70	SI	1	Total Mg 1 1	0
70	SK	1	Total Mg 1 1	0
70	TA	1	Total Mg 1 1	0
70	TC	1	Total Mg 1 1	0
70	TE	1	Total Mg 1 1	0
70	TG	1	Total Mg 1 1	0
70	TI	1	Total Mg 1 1	0
70	TK	1	Total Mg 1 1	0
70	UA	1	Total Mg 1 1	0
70	UC	1	Total Mg 1 1	0
70	UE	1	Total Mg 1 1	0
70	UG	1	Total Mg 1 1	0
70	UI	1	Total Mg 1 1	0
70	UK	1	Total Mg 1 1	0
70	VA	1	Total Mg 1 1	0
70	VC	1	Total Mg 1 1	0
70	VE	1	Total Mg 1 1	0

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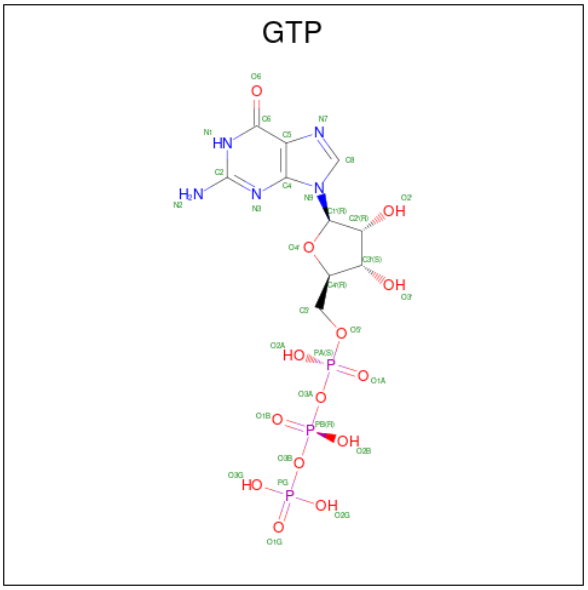
Mol	Chain	Residues	Atoms	AltConf
70	VG	1	Total Mg 1 1	0
70	VI	1	Total Mg 1 1	0
70	VK	1	Total Mg 1 1	0
70	VM	1	Total Mg 1 1	0
70	WA	1	Total Mg 1 1	0
70	WC	1	Total Mg 1 1	0
70	WE	1	Total Mg 1 1	0
70	WG	1	Total Mg 1 1	0
70	WI	1	Total Mg 1 1	0
70	WK	1	Total Mg 1 1	0
70	WM	1	Total Mg 1 1	0

- Molecule 71 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
71	AA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	AC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	AE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	AG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	AI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	AK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	AM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	BM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	C	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	CB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	CD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	CF	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	CJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	CL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	D	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	DB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	DD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	DF	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	DH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	DJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	DL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	EA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	EC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	EE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	EG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	EI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	EK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	FA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	FC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	FE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	FG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	FI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	FK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	GA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	GC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	GE	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	GG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	GI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	GK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	HM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	IA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	IC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	IE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	IG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	II	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	IK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	IM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	J	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	JB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	JD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	JF	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	JH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	JJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	JL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	JN	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	K	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KF	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	KN	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	L	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LF	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	LN	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	MA	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	MC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	ME	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	MG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	MI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	MK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	MM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	NM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	OM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	PA	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	PC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	PE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	PG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	PI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	PK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	PM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	Q	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	QB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	QD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	QF	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	QH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	QJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	QL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	R	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	RB	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	RD	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	RF	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	RH	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	RL	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	SA	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	SC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	SE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	SG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	SI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	SK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	TA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	TC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	TE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	TG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	TI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	TK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	UA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	UC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	UE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	UG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	UI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	UK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	VA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	VC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	VE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	VG	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
71	VI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	VK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	VM	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WA	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WC	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WE	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WG	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WI	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WK	1	Total	C	N	O	P	0
			32	10	5	14	3	
71	WM	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 72 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
72	0A	1	Total	Zn	0
			1	1	
72	0	1	Total	Zn	0
			1	1	
72	0z	1	Total	Zn	0
			1	1	
72	1V	2	Total	Zn	0
			2	2	
72	1Y	2	Total	Zn	0
			2	2	
72	1b	2	Total	Zn	0
			2	2	
72	1c	2	Total	Zn	0
			2	2	
72	1e	2	Total	Zn	0
			2	2	
72	1h	2	Total	Zn	0
			2	2	

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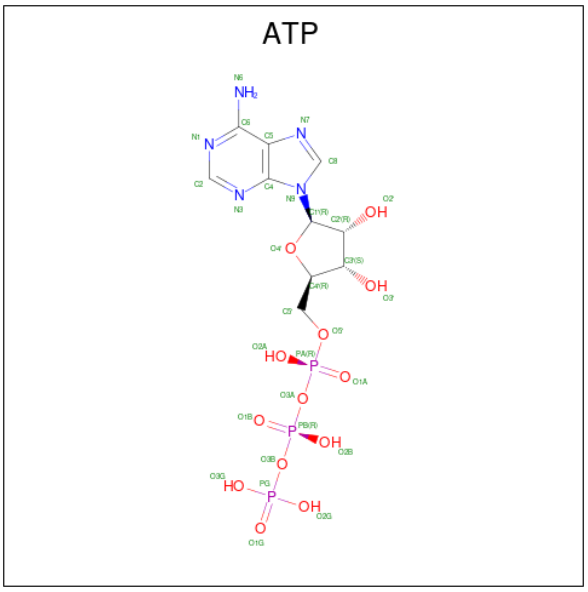
Mol	Chain	Residues	Atoms	AltConf
72	1q	3	Total Zn 3 3	0
72	1s	1	Total Zn 1 1	0
72	1t	1	Total Zn 1 1	0
72	1w	2	Total Zn 2 2	0
72	1x	2	Total Zn 2 2	0
72	3S	1	Total Zn 1 1	0
72	4W	2	Total Zn 2 2	0
72	5S	1	Total Zn 1 1	0
72	5T	1	Total Zn 1 1	0

- Molecule 73 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	AltConf
73	1S	1	Total Ca 1 1	0
73	2v	1	Total Ca 1 1	0
73	2w	1	Total Ca 1 1	0

- Molecule 74 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



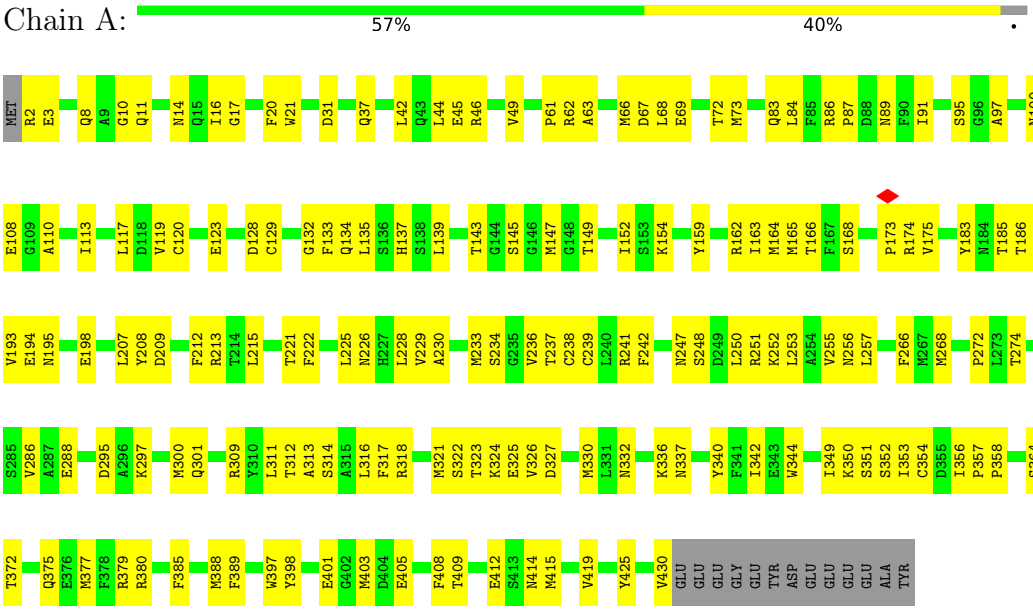
Mol	Chain	Residues	Atoms					AltConf
74	2v	1	Total	C	N	O	P	0
			31	10	5	13	3	
74	2w	1	Total	C	N	O	P	0
			31	10	5	13	3	

3 Residue-property plots (i)

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

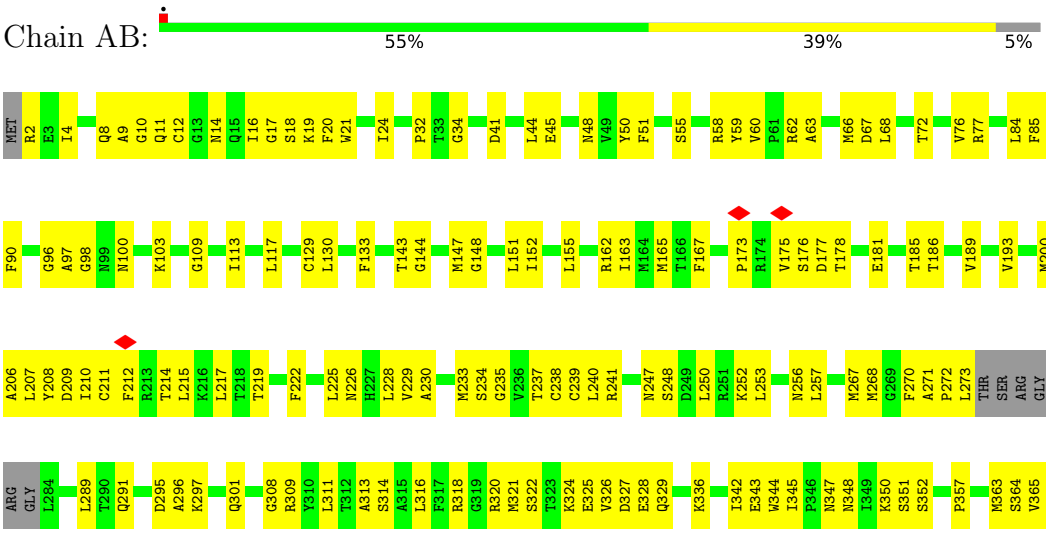
• Molecule 1: Tubulin beta chain

Chain A:



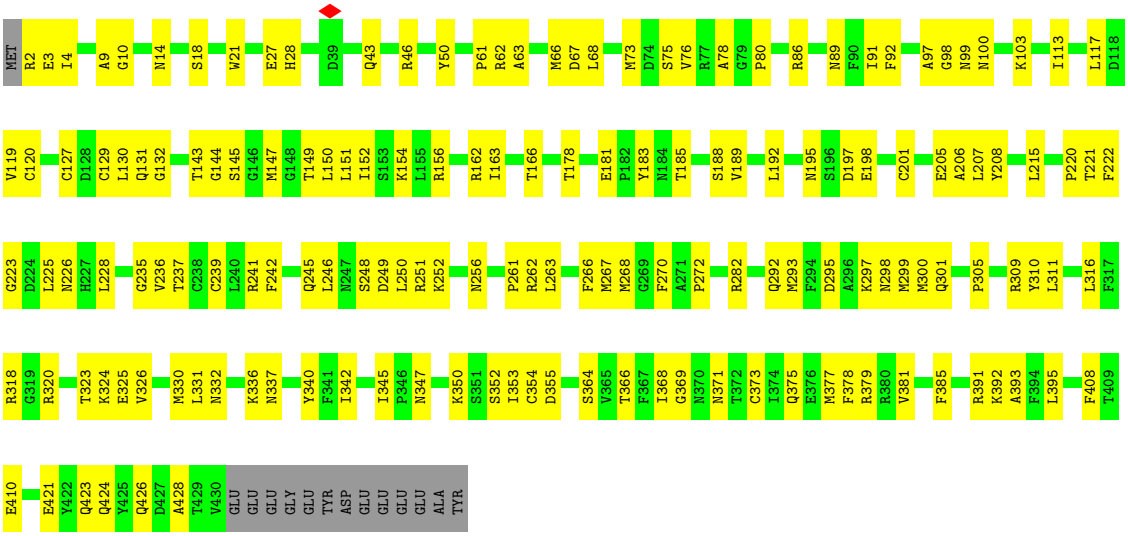
• Molecule 1: Tubulin beta chain

Chain AB:



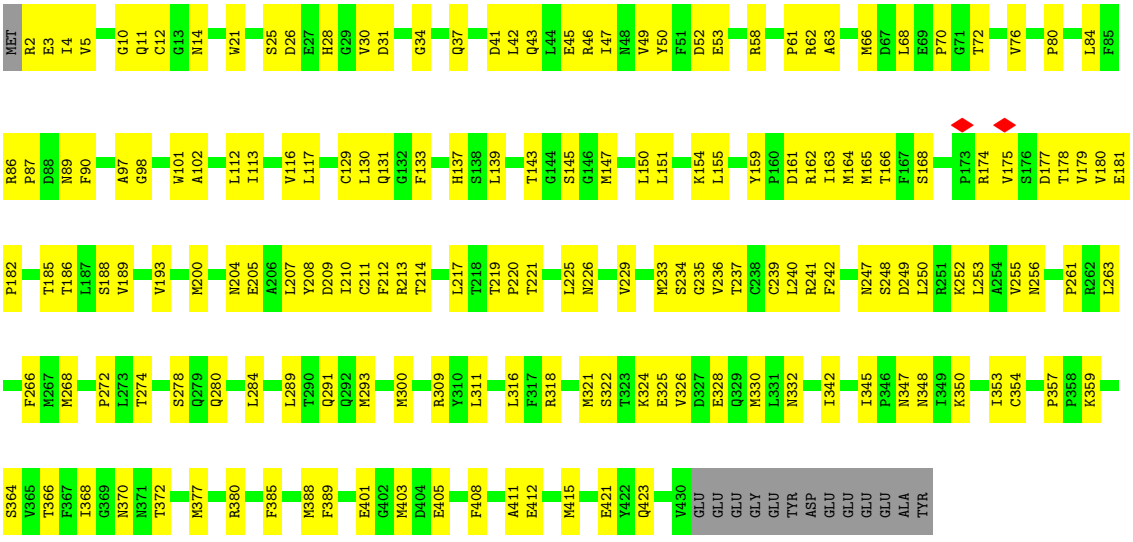
• Molecule 1: Tubulin beta chain

Chain AD:



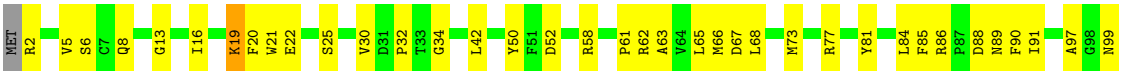
• Molecule 1: Tubulin beta chain

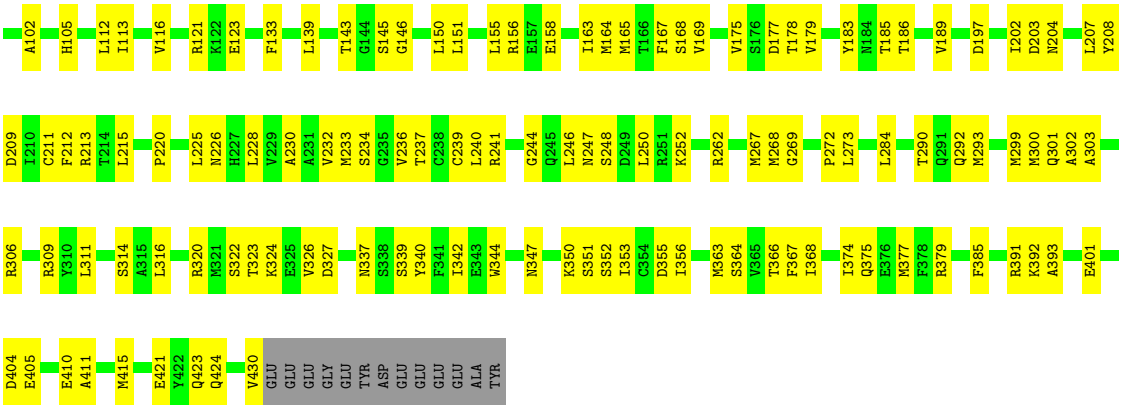
Chain AF:



• Molecule 1: Tubulin beta chain

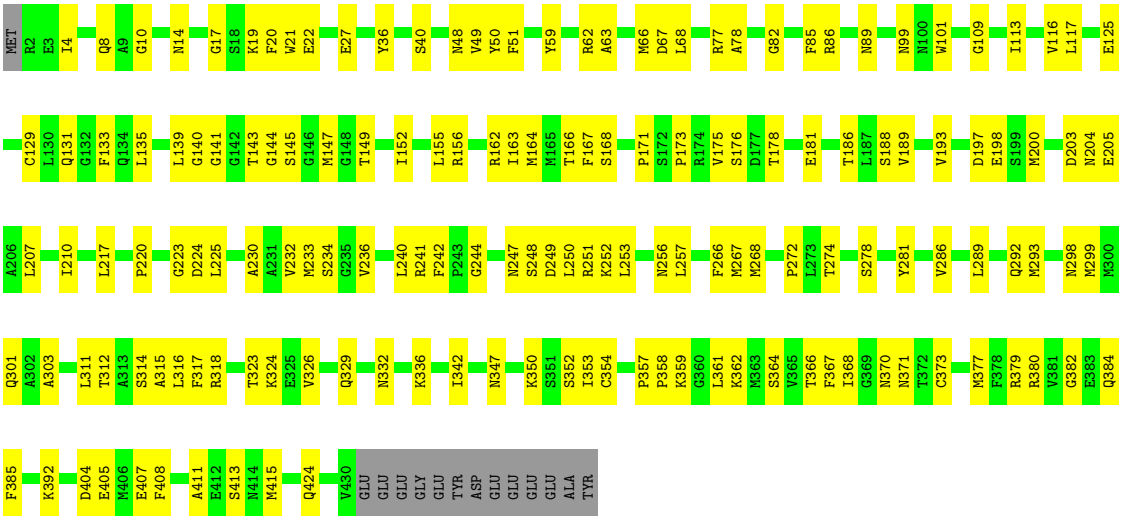
Chain AH:





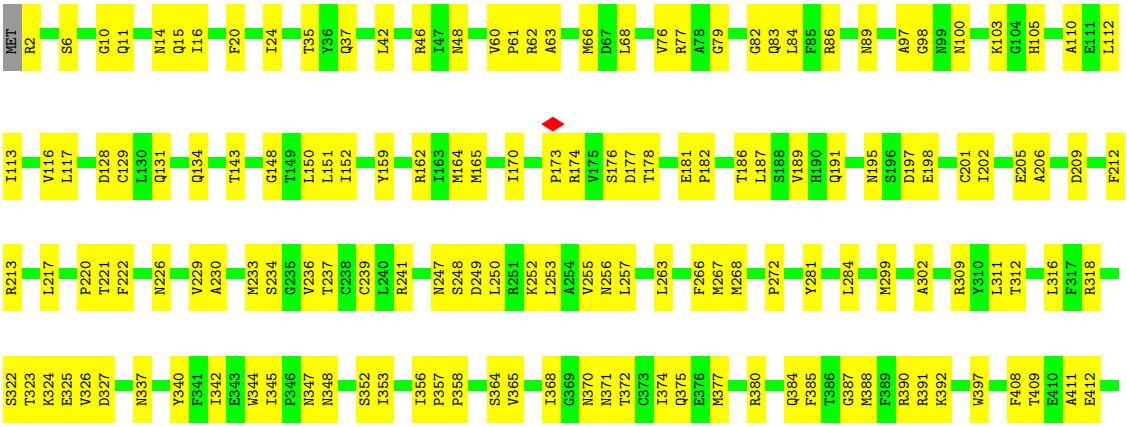
• Molecule 1: Tubulin beta chain

Chain AJ:



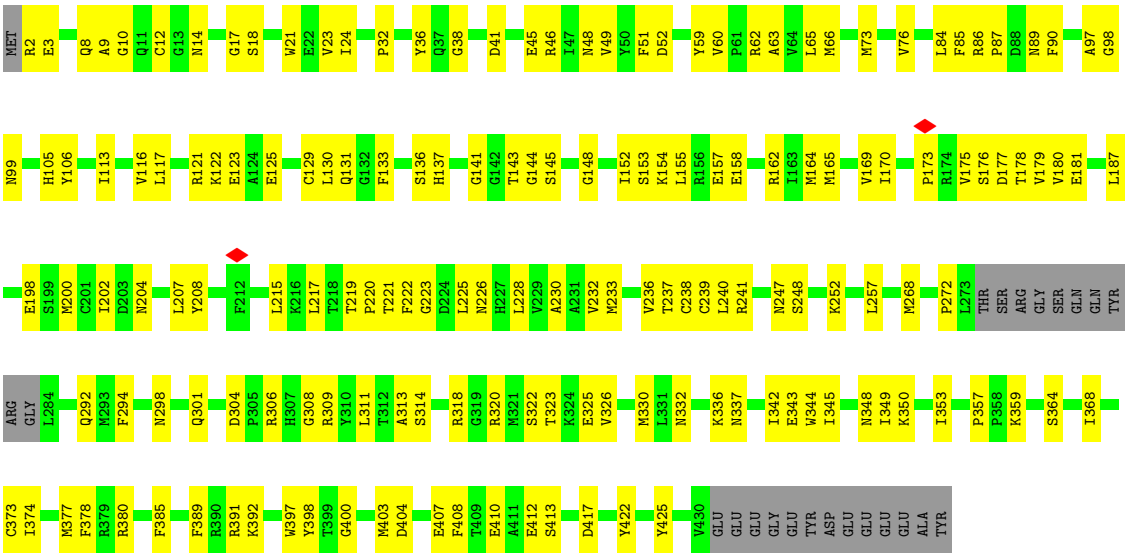
• Molecule 1: Tubulin beta chain

Chain AL:



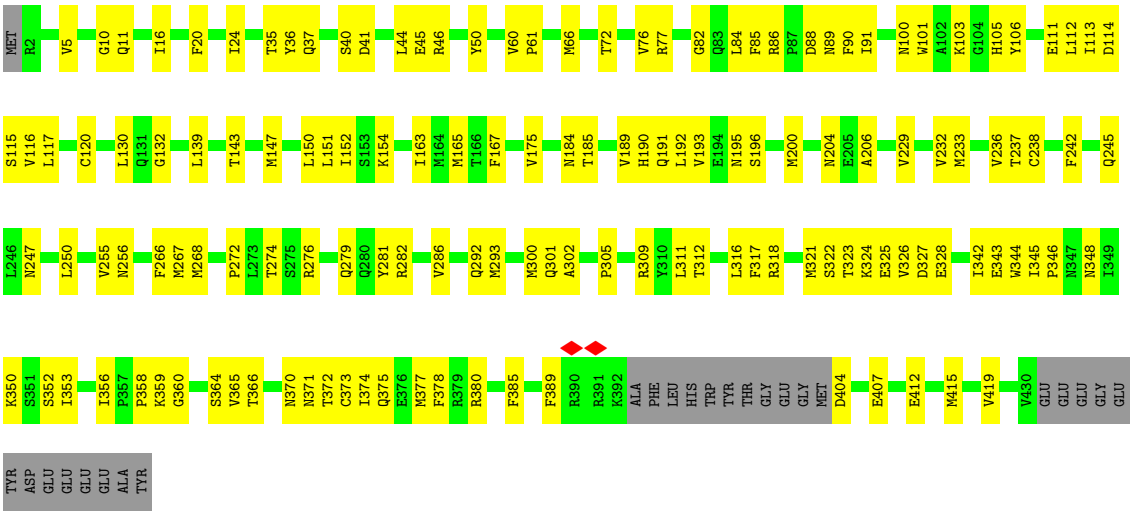
• Molecule 1: Tubulin beta chain

Chain AN:



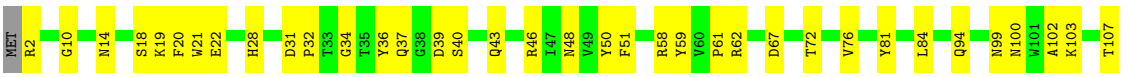
• Molecule 1: Tubulin beta chain

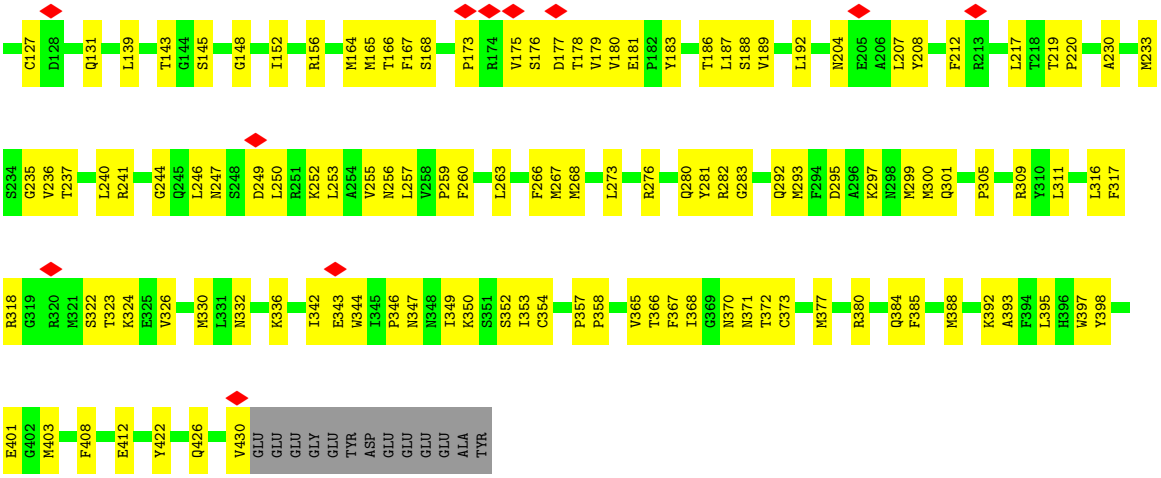
Chain B:



• Molecule 1: Tubulin beta chain

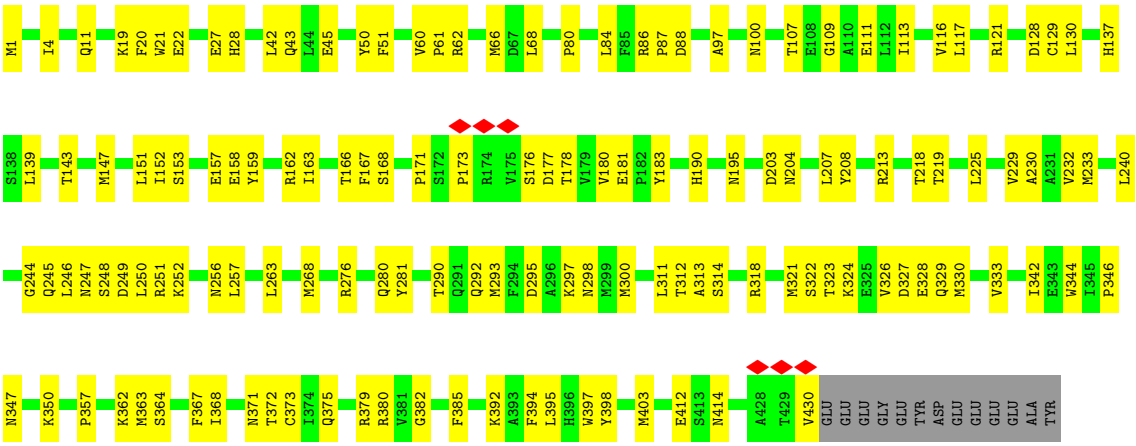
Chain BB:





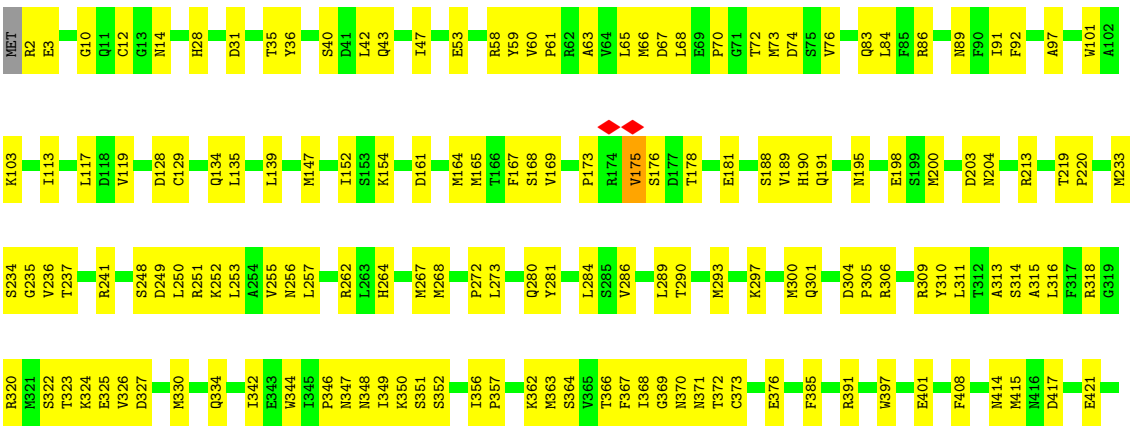
• Molecule 1: Tubulin beta chain

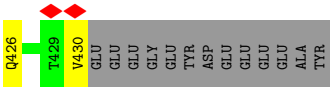
Chain BD:



• Molecule 1: Tubulin beta chain

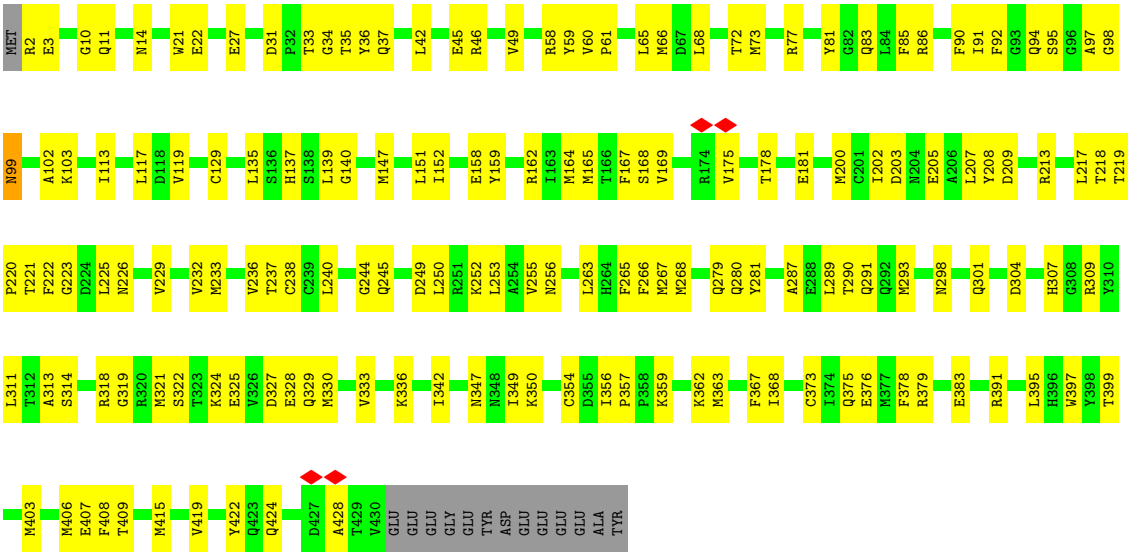
Chain BF:





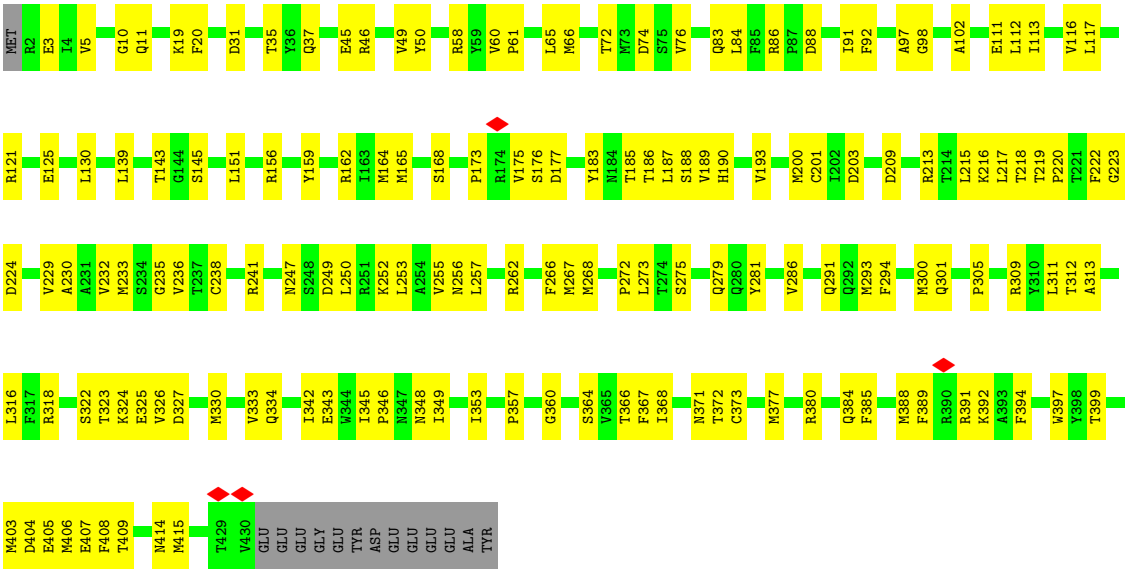
• Molecule 1: Tubulin beta chain

Chain BH:



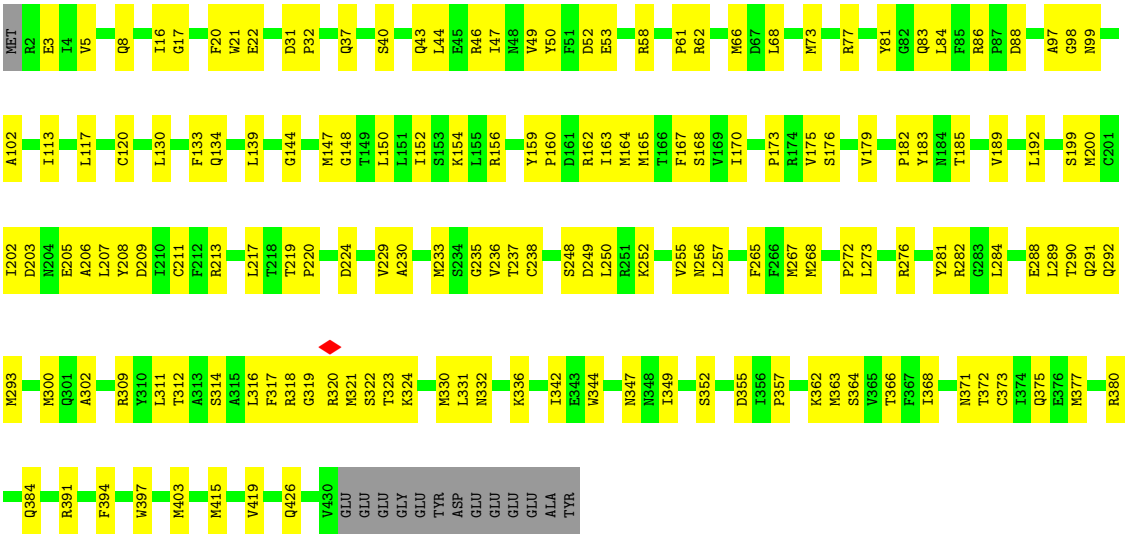
• Molecule 1: Tubulin beta chain

Chain BJ:



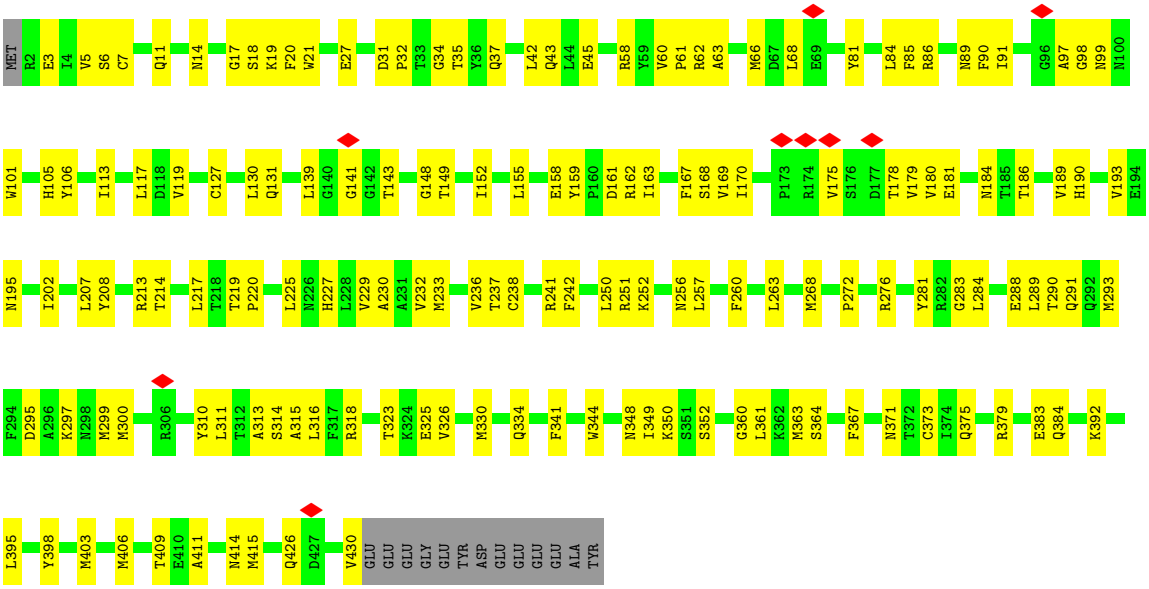
• Molecule 1: Tubulin beta chain

Chain BL:



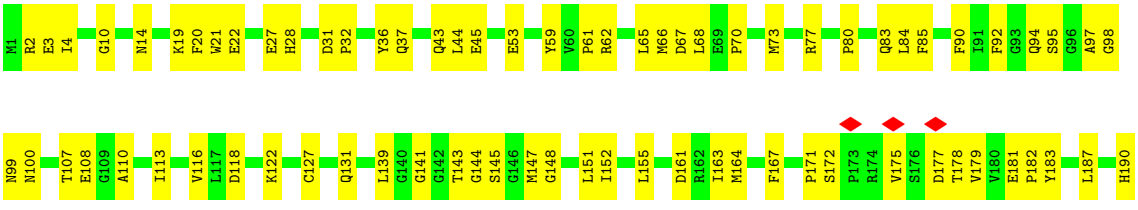
• Molecule 1: Tubulin beta chain

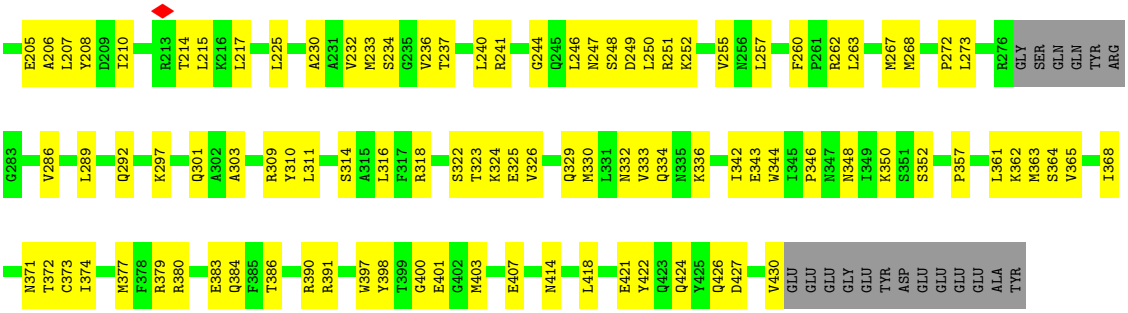
Chain BN:



• Molecule 1: Tubulin beta chain

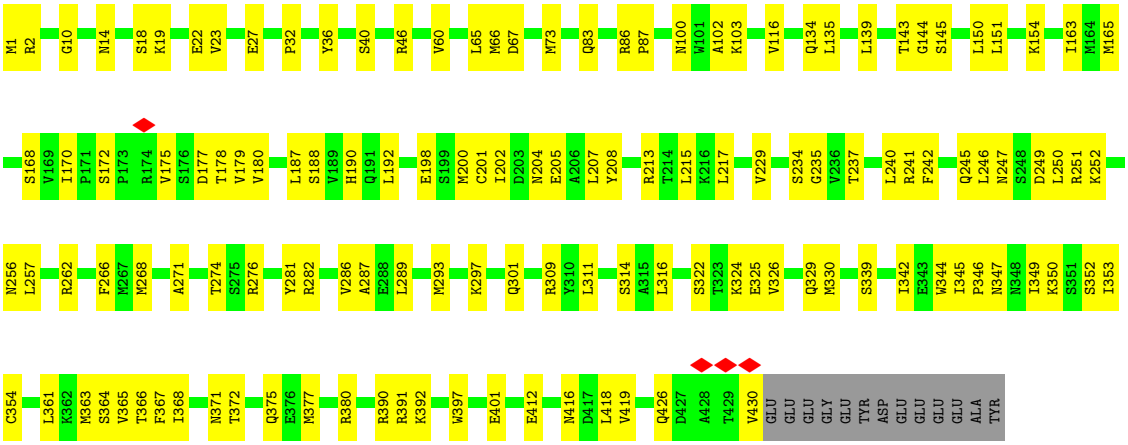
Chain CA:





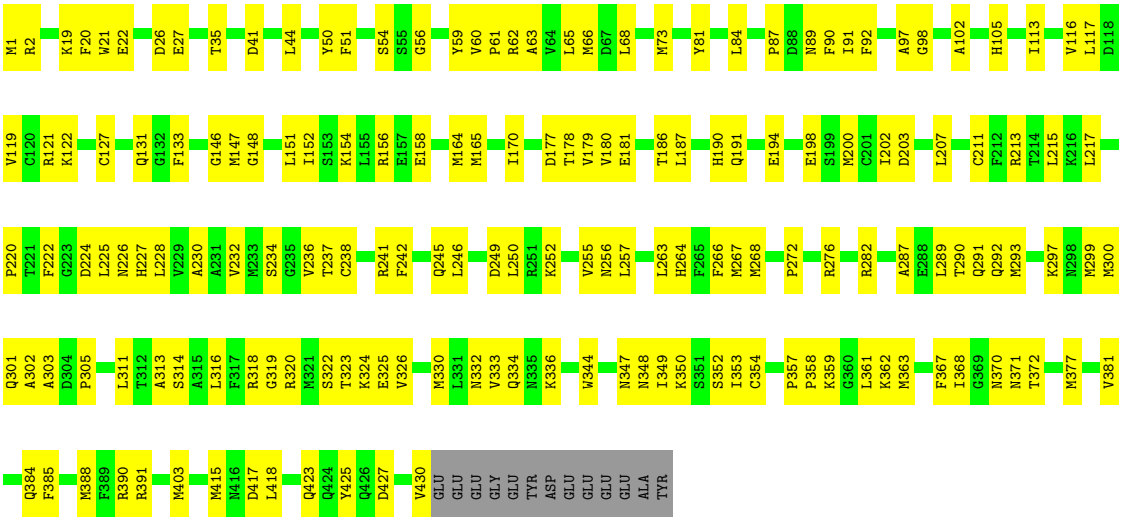
• Molecule 1: Tubulin beta chain

Chain CC:



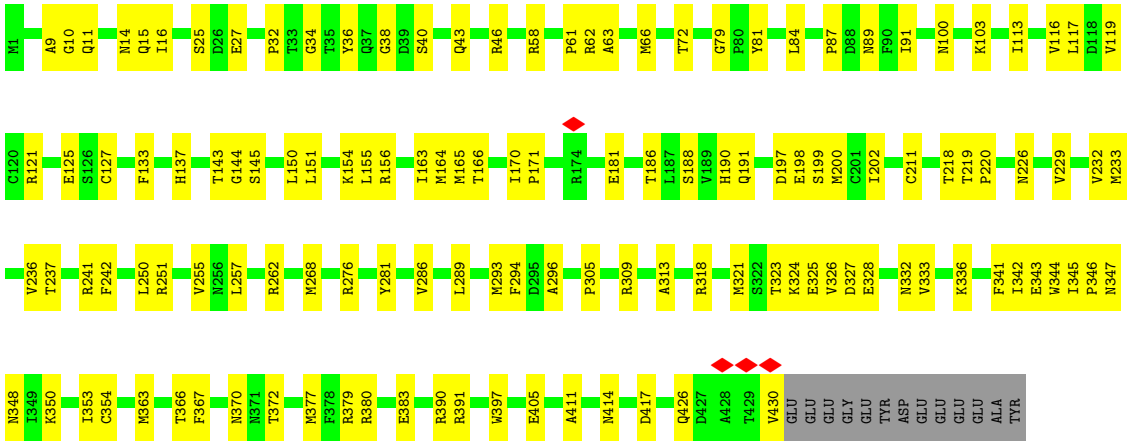
• Molecule 1: Tubulin beta chain

Chain CE:



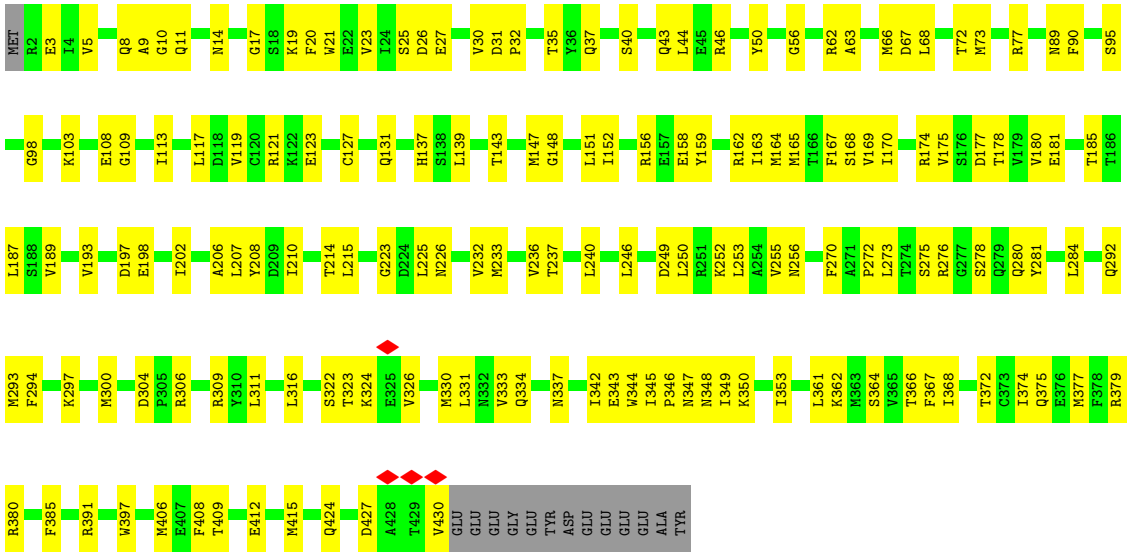
• Molecule 1: Tubulin beta chain

Chain CG:



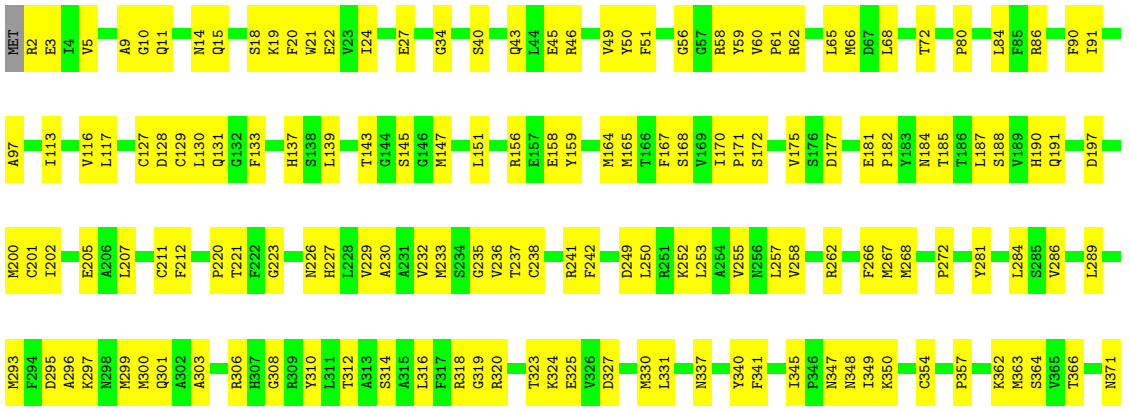
• Molecule 1: Tubulin beta chain

Chain CI:



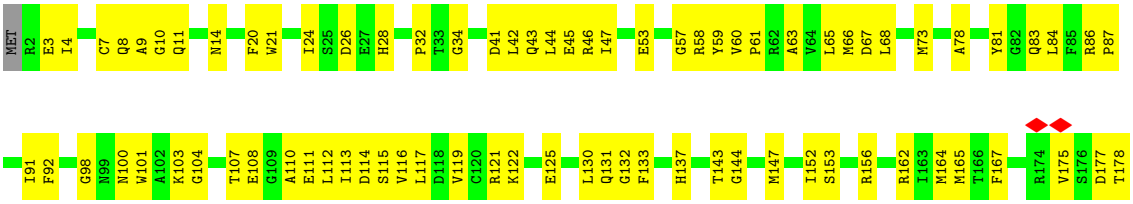
• Molecule 1: Tubulin beta chain

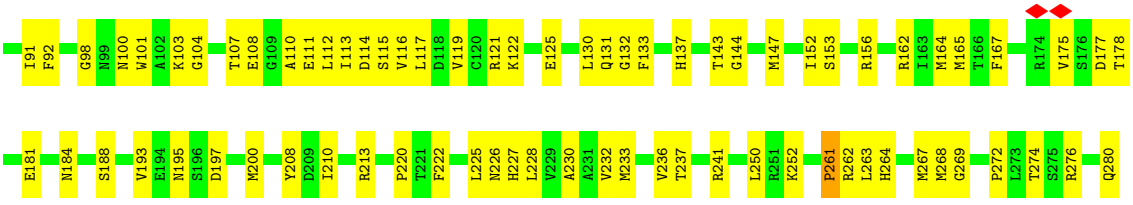
Chain CK:

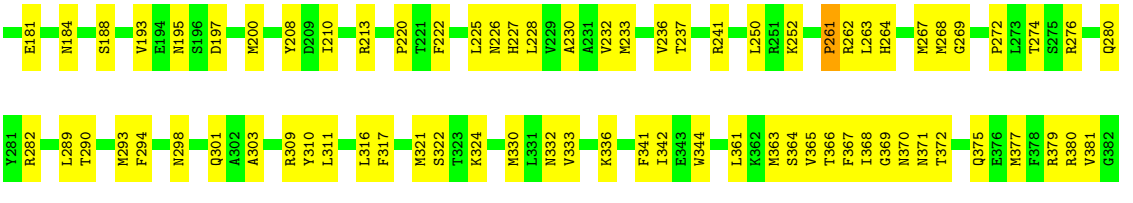


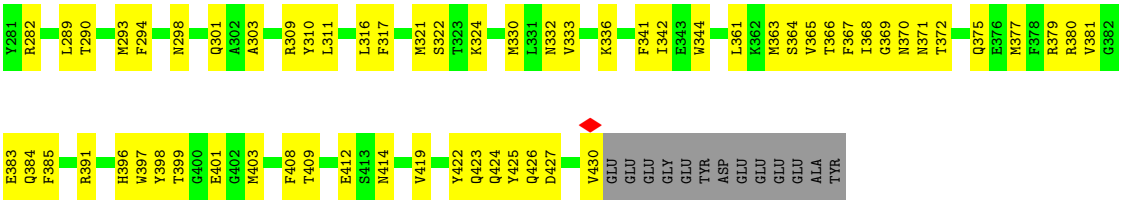
• Molecule 1: Tubulin beta chain

Chain CM:



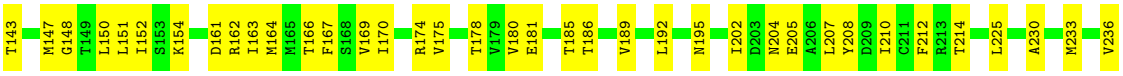


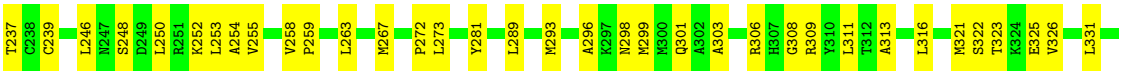




• Molecule 1: Tubulin beta chain

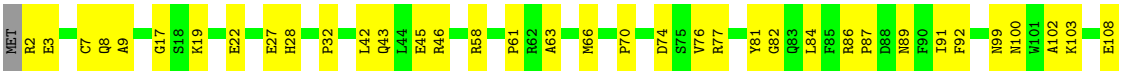
Chain DA:

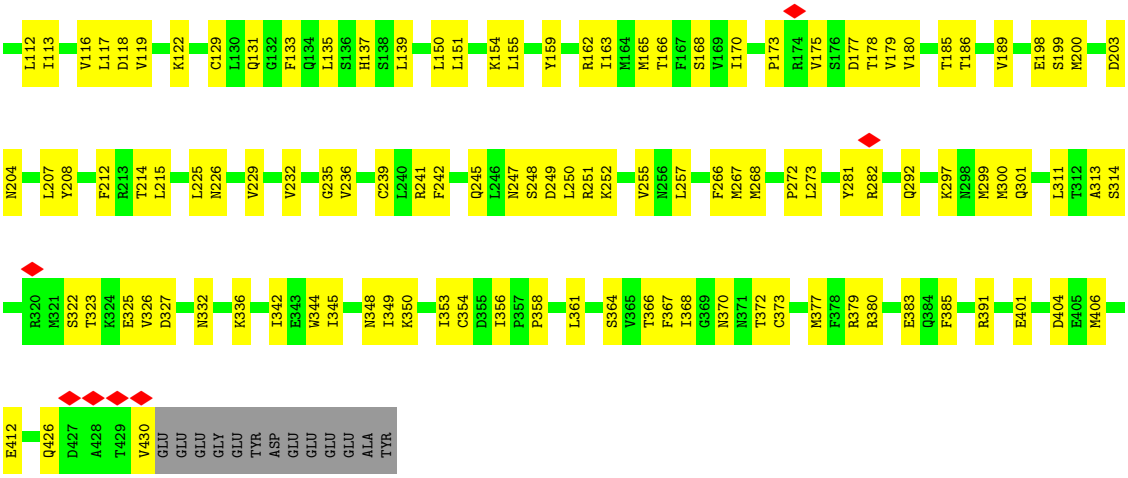




• Molecule 1: Tubulin beta chain

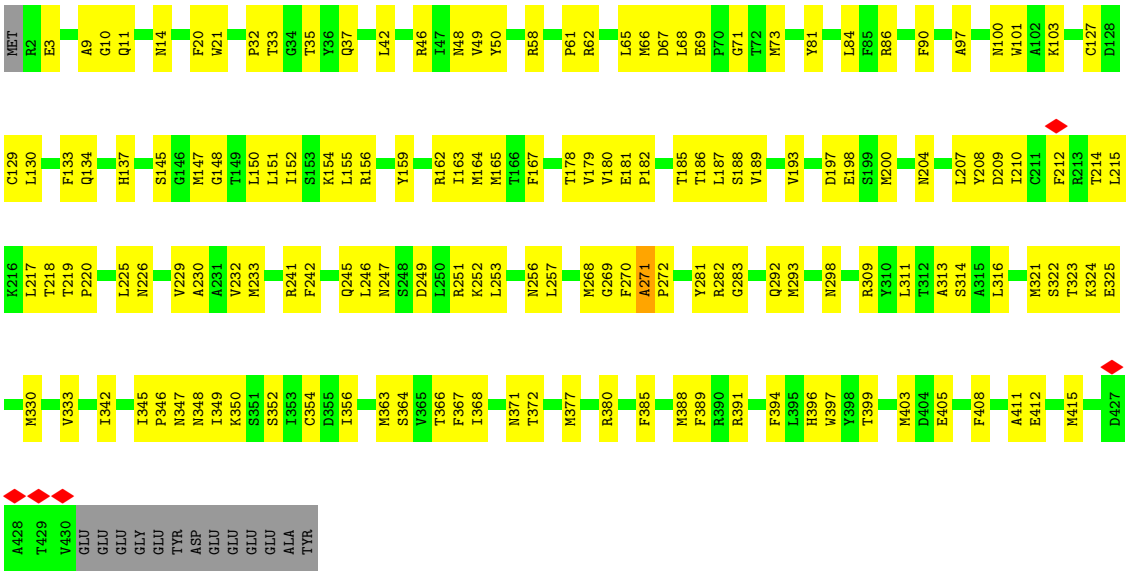
Chain DC:





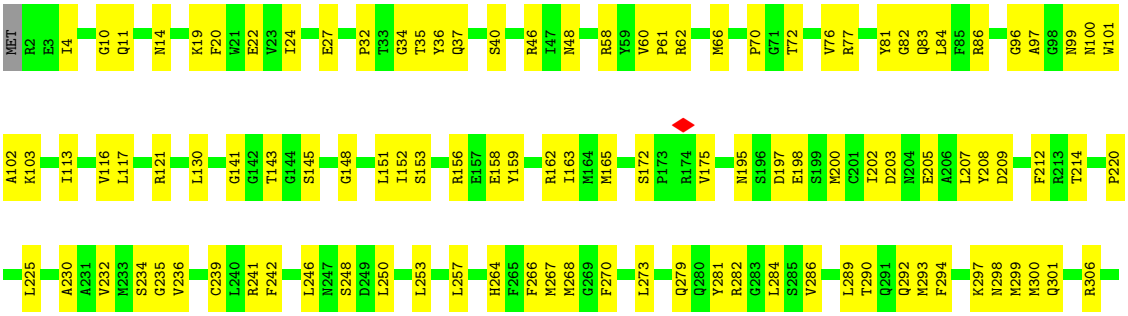
• Molecule 1: Tubulin beta chain

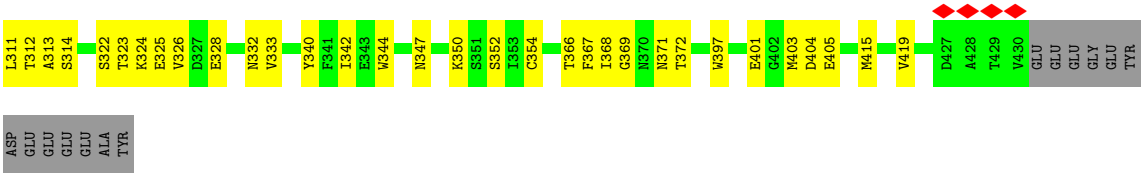
Chain DE:



• Molecule 1: Tubulin beta chain

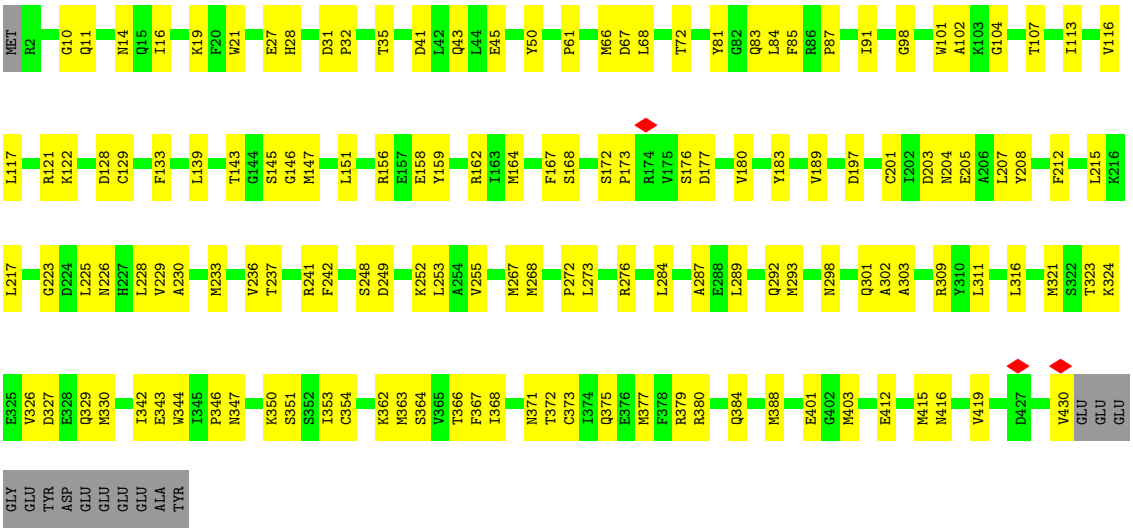
Chain DG:





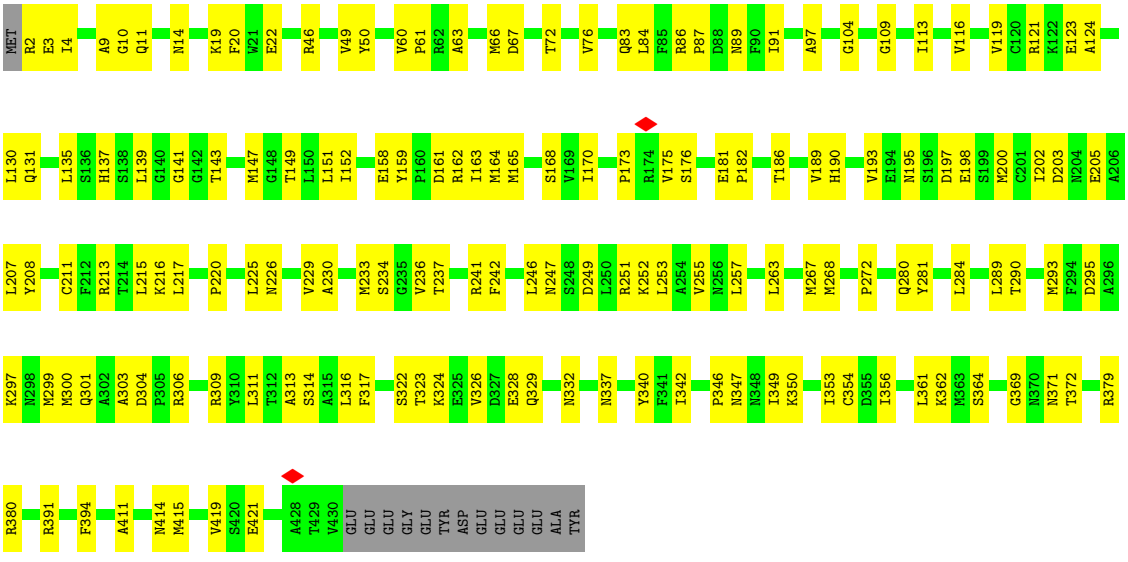
• Molecule 1: Tubulin beta chain

Chain DI:



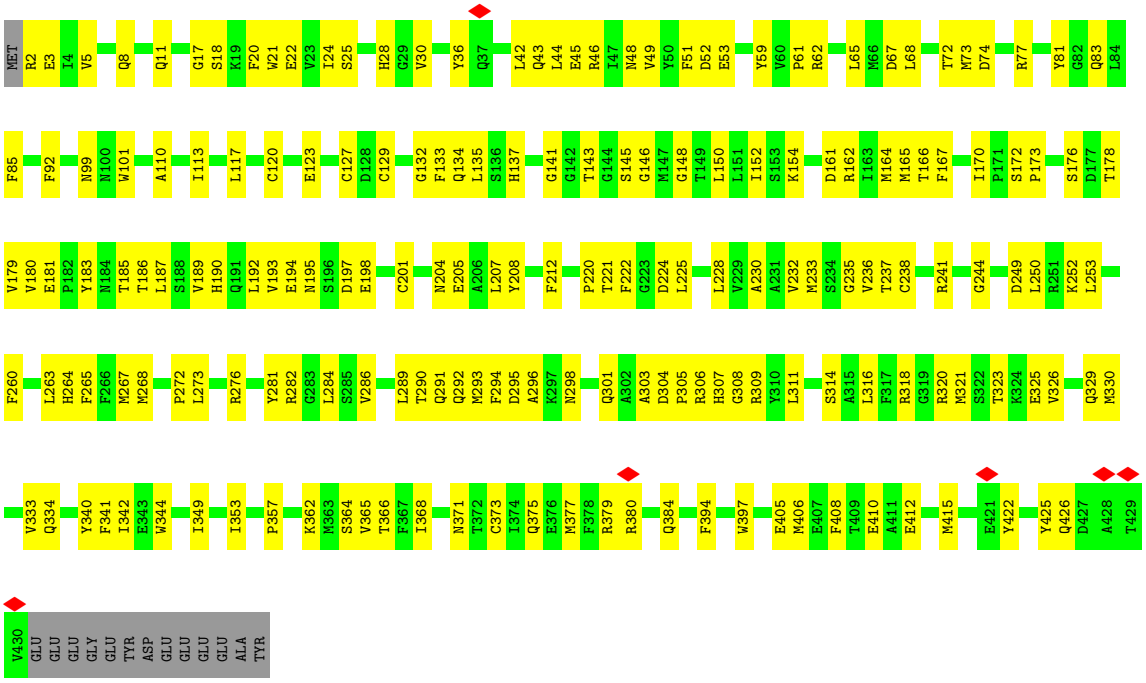
• Molecule 1: Tubulin beta chain

Chain DK:



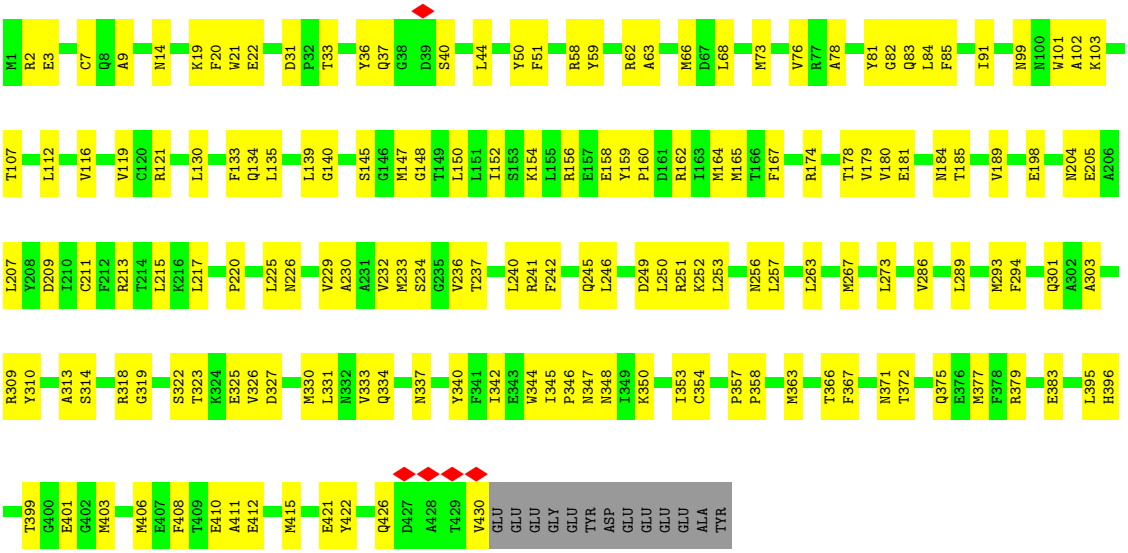
• Molecule 1: Tubulin beta chain

Chain DM:



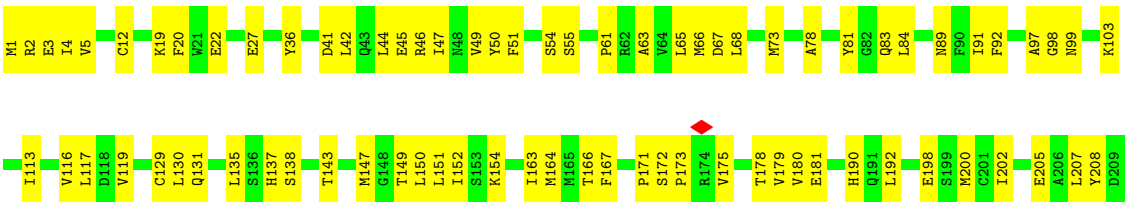
• Molecule 1: Tubulin beta chain

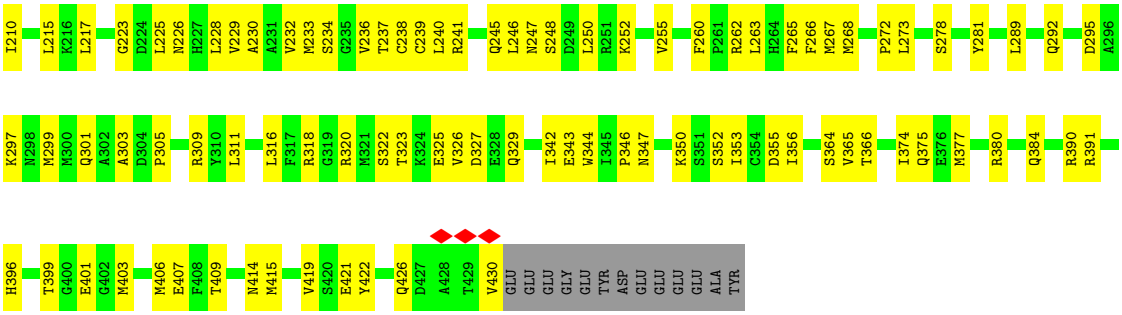
Chain E:



• Molecule 1: Tubulin beta chain

Chain EB:



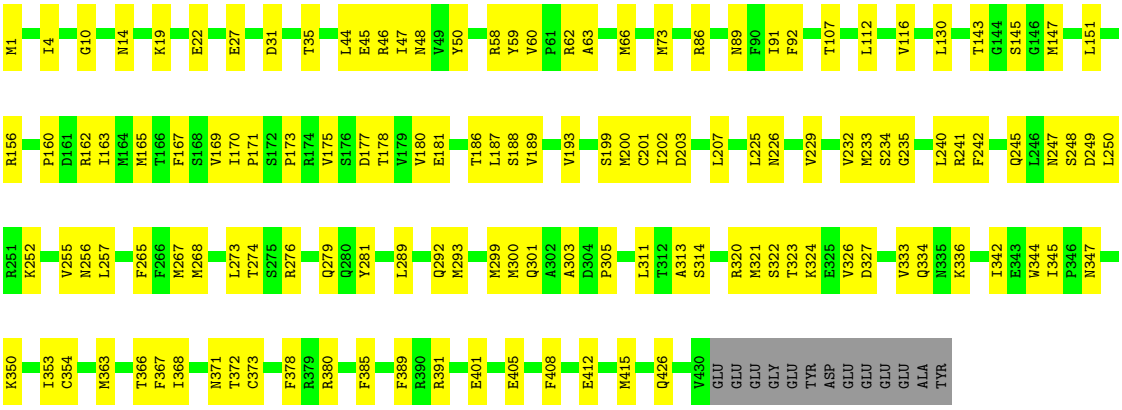


• Molecule 1: Tubulin beta chain

Chain ED:

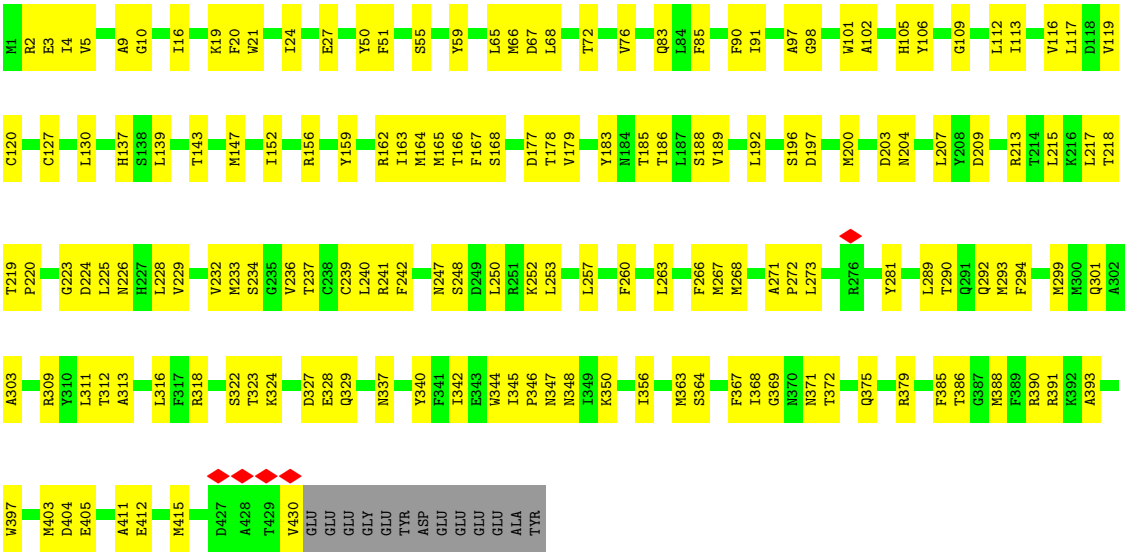
• Molecule 1: Tubulin beta chain

Chain EF:



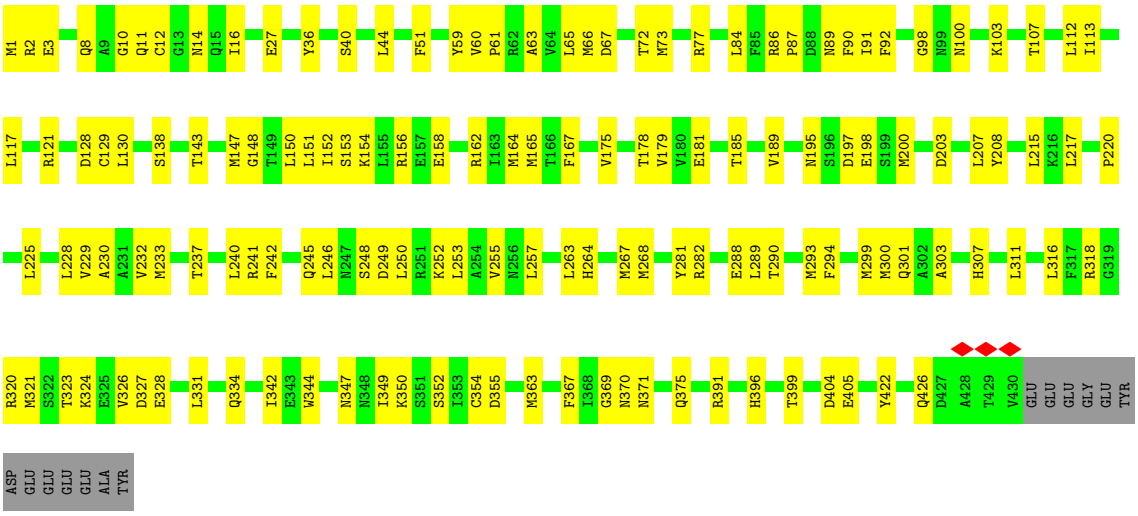
• Molecule 1: Tubulin beta chain

Chain EH:



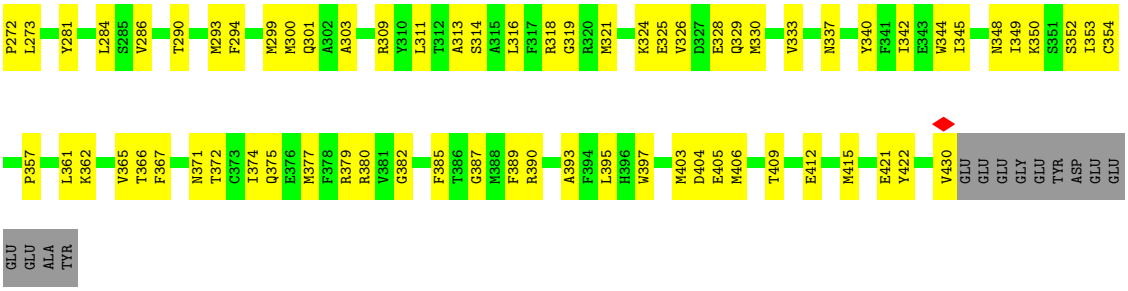
• Molecule 1: Tubulin beta chain

Chain EJ:



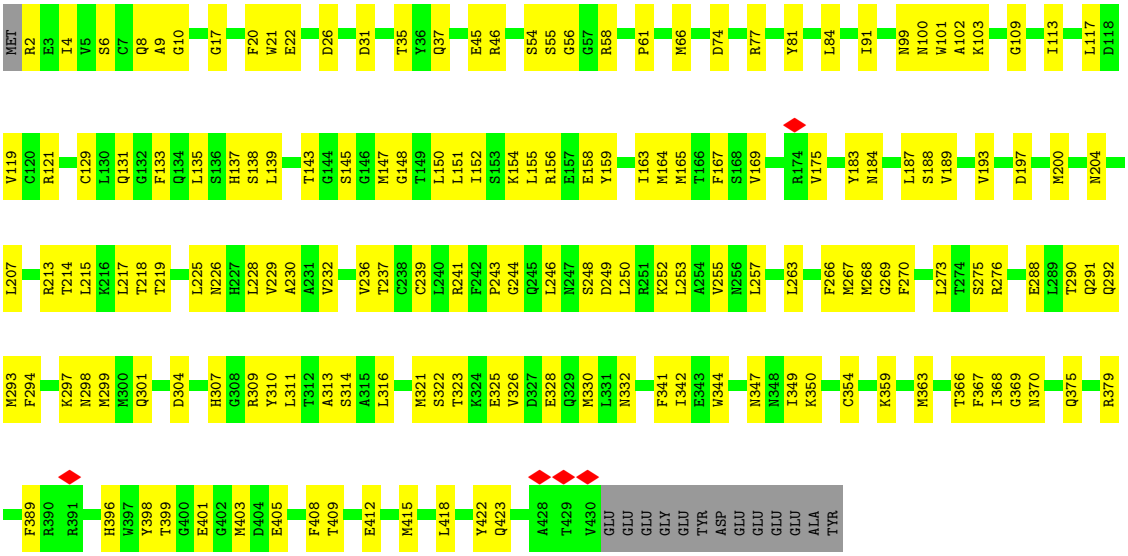
• Molecule 1: Tubulin beta chain

Chain EL:



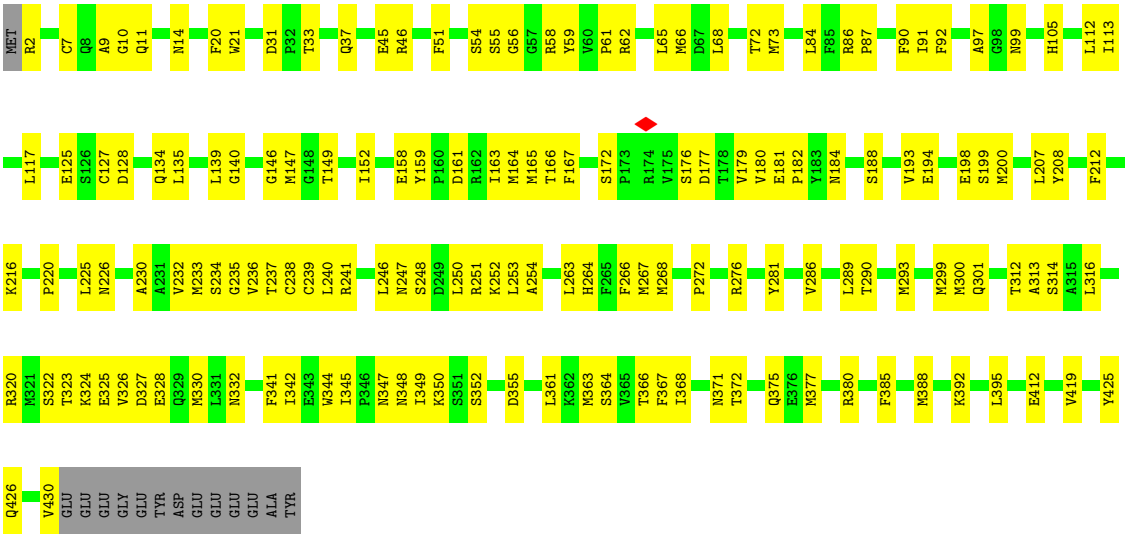
• Molecule 1: Tubulin beta chain

Chain F:



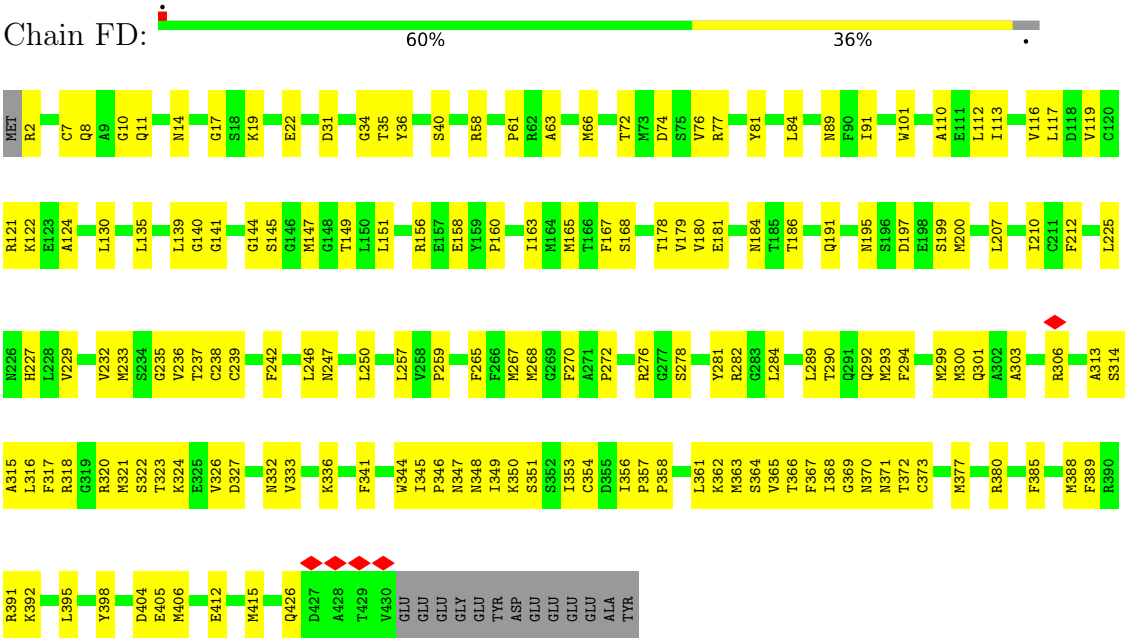
• Molecule 1: Tubulin beta chain

Chain FB:



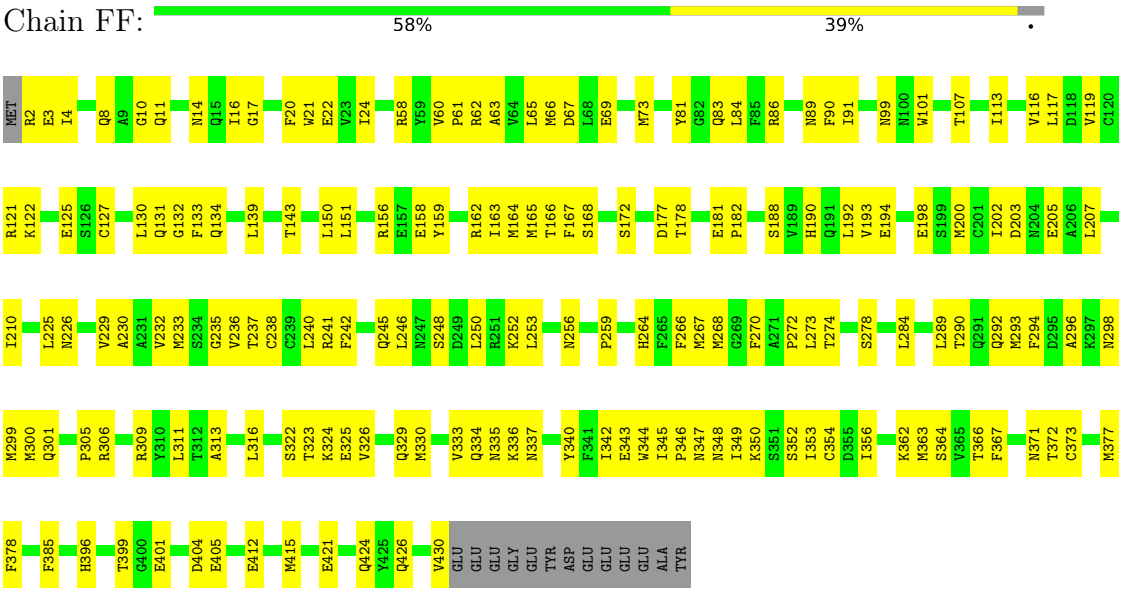
• Molecule 1: Tubulin beta chain

Chain FD:



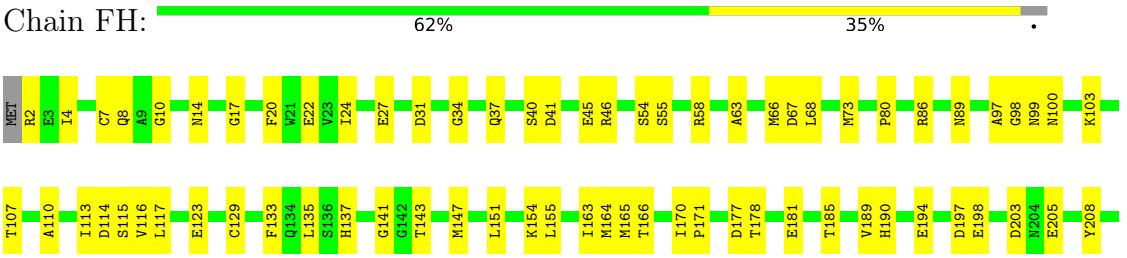
• Molecule 1: Tubulin beta chain

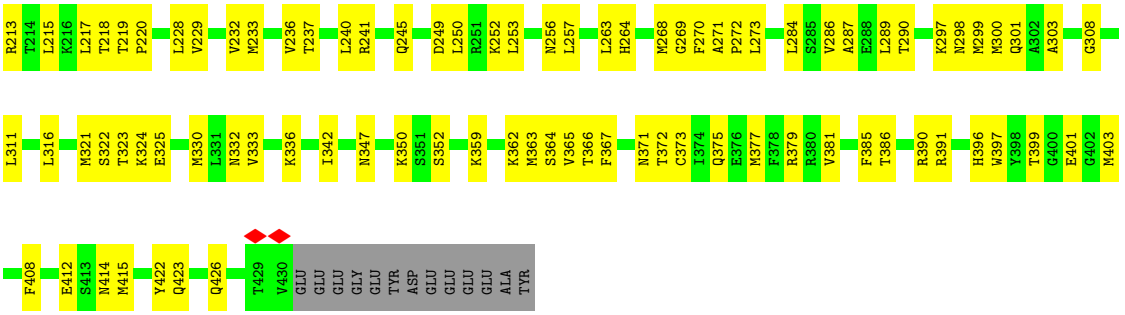
Chain FF:



• Molecule 1: Tubulin beta chain

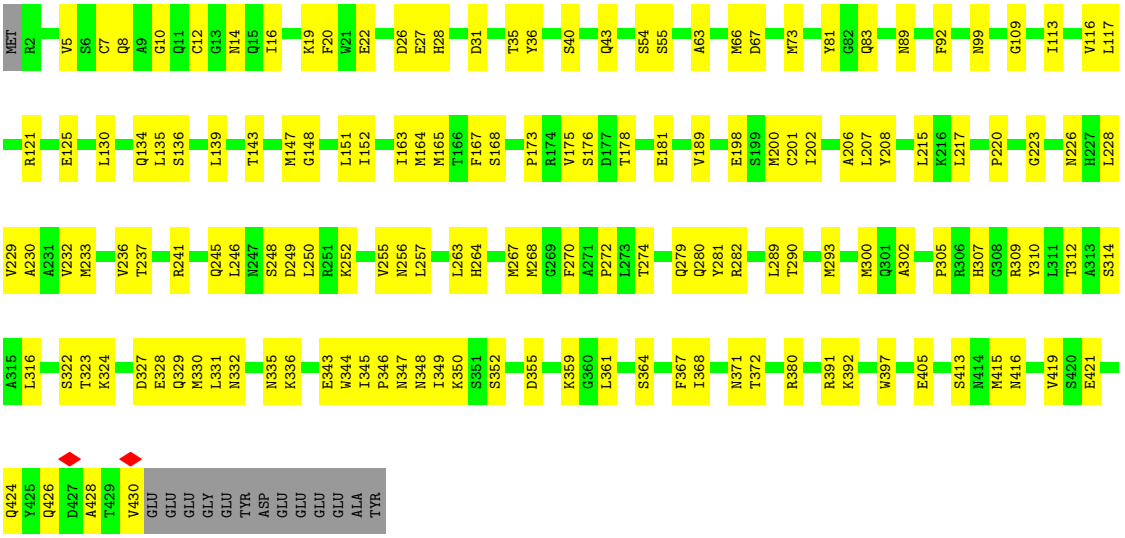
Chain FH:





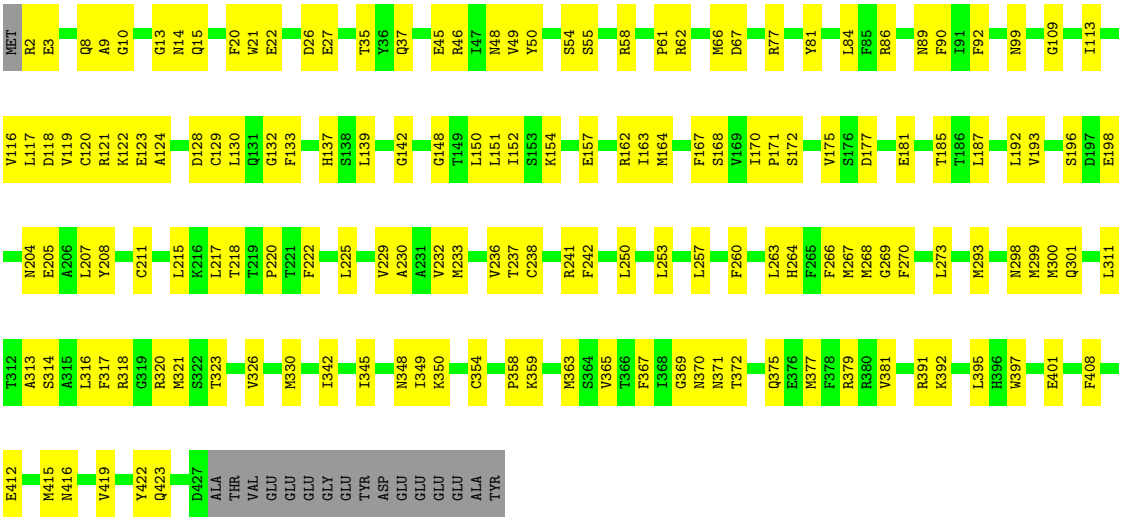
• Molecule 1: Tubulin beta chain

Chain FJ:



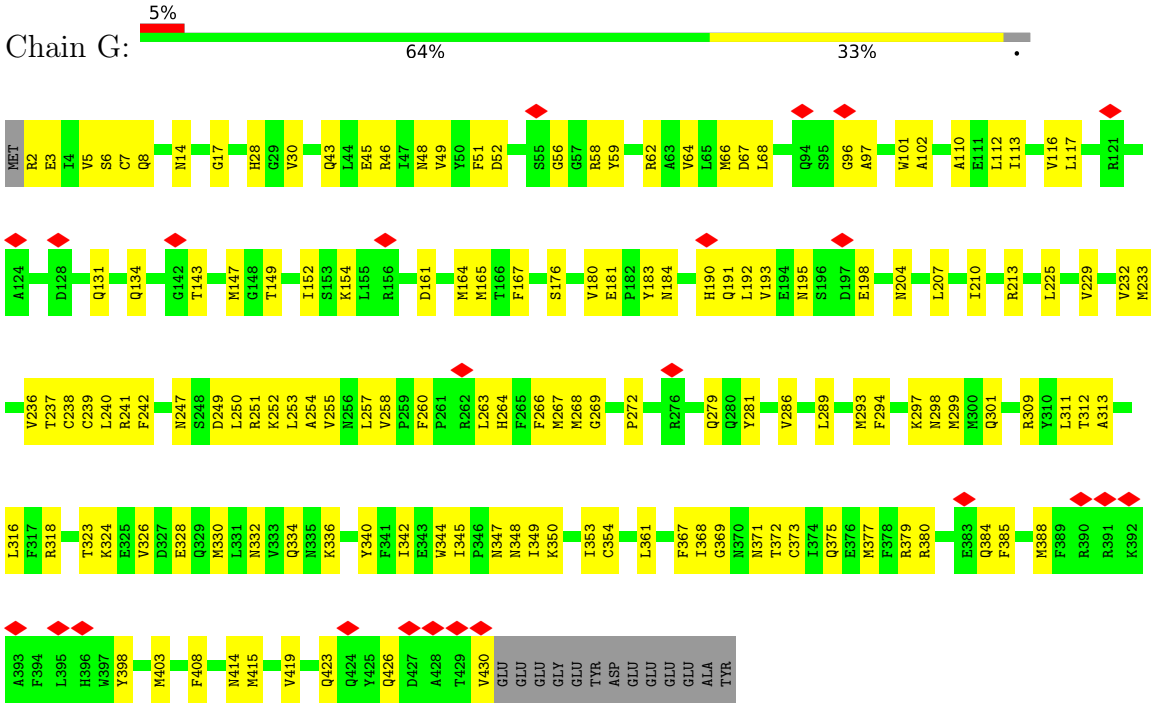
• Molecule 1: Tubulin beta chain

Chain FL:



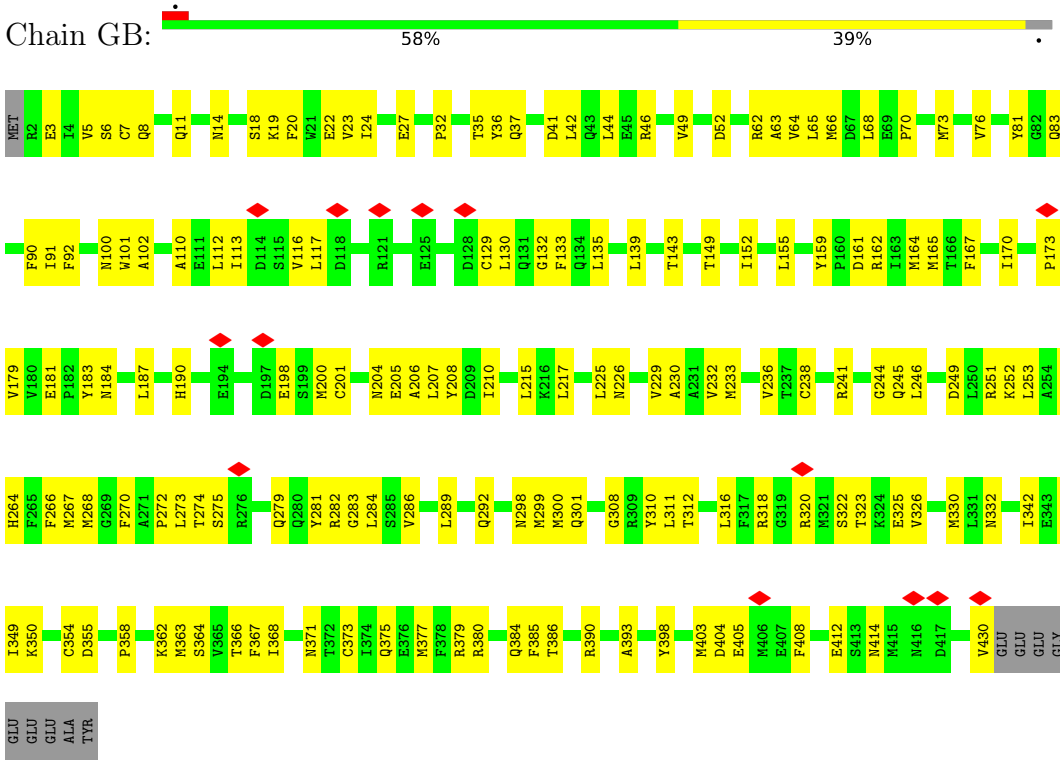
• Molecule 1: Tubulin beta chain

Chain G:



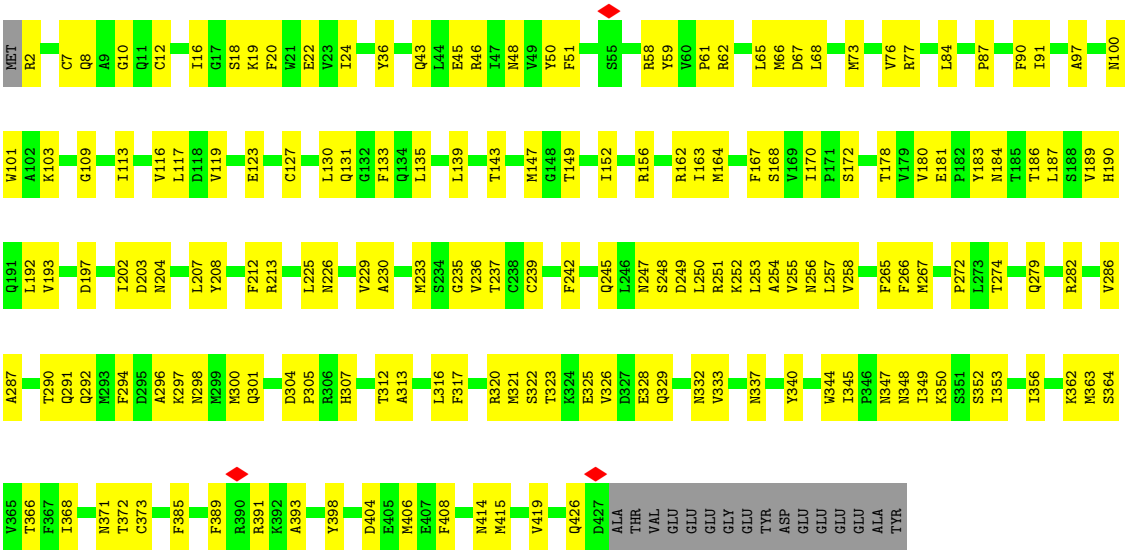
• Molecule 1: Tubulin beta chain

Chain GB:



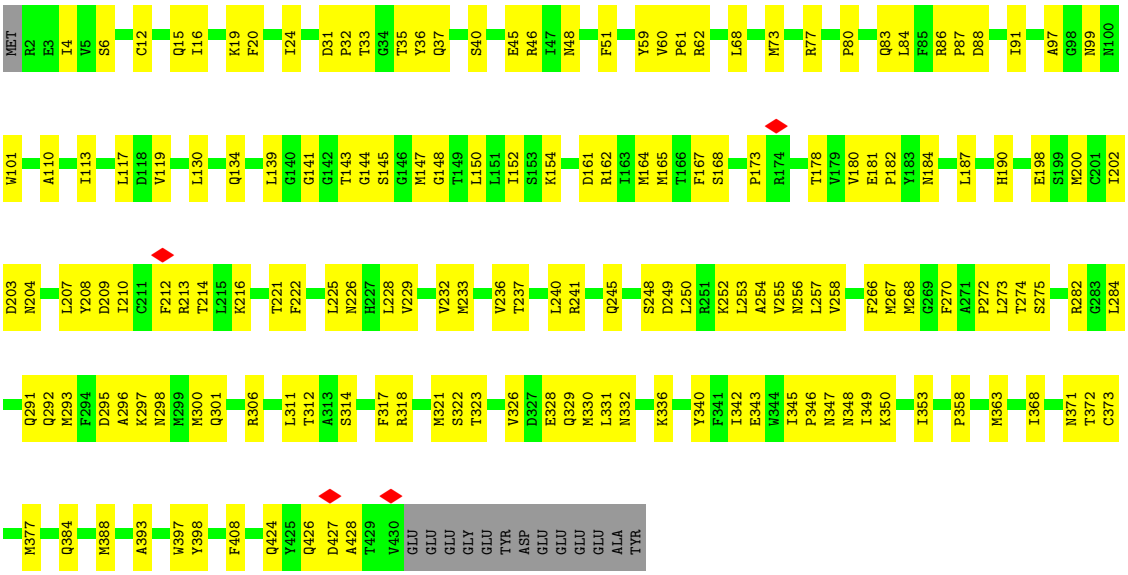
• Molecule 1: Tubulin beta chain

Chain GD:



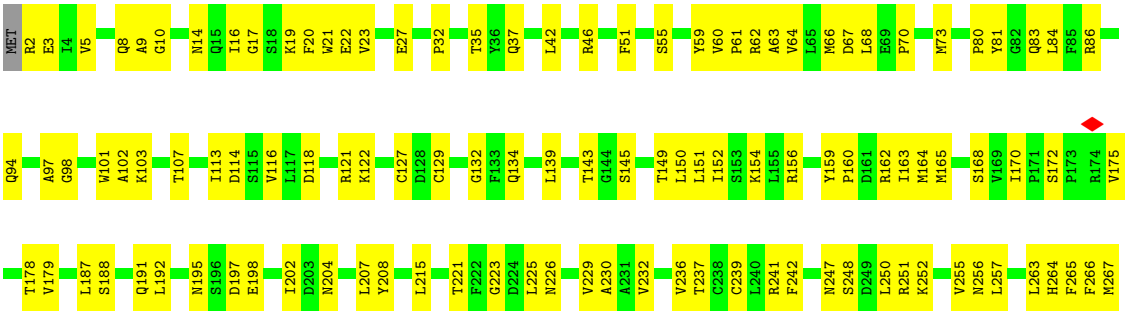
• Molecule 1: Tubulin beta chain

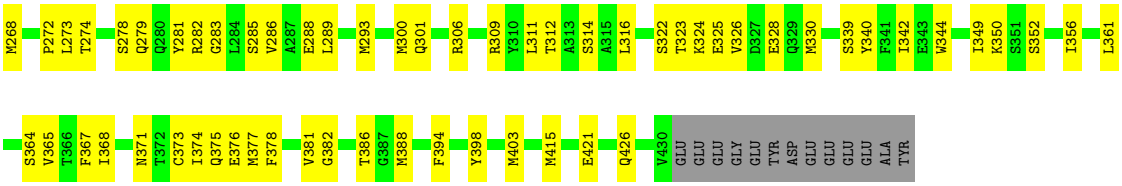
Chain GF:



• Molecule 1: Tubulin beta chain

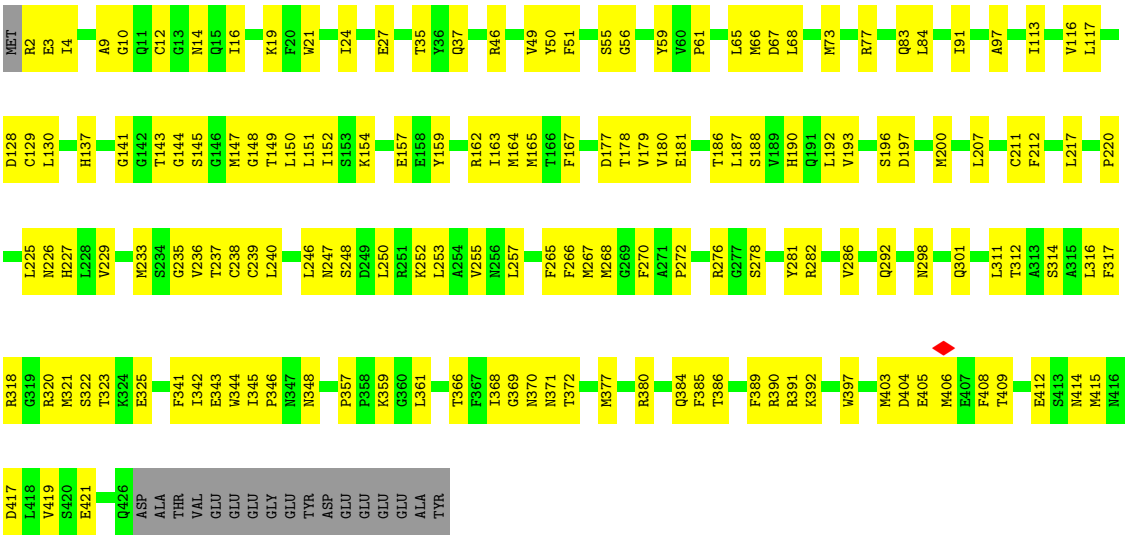
Chain GH:





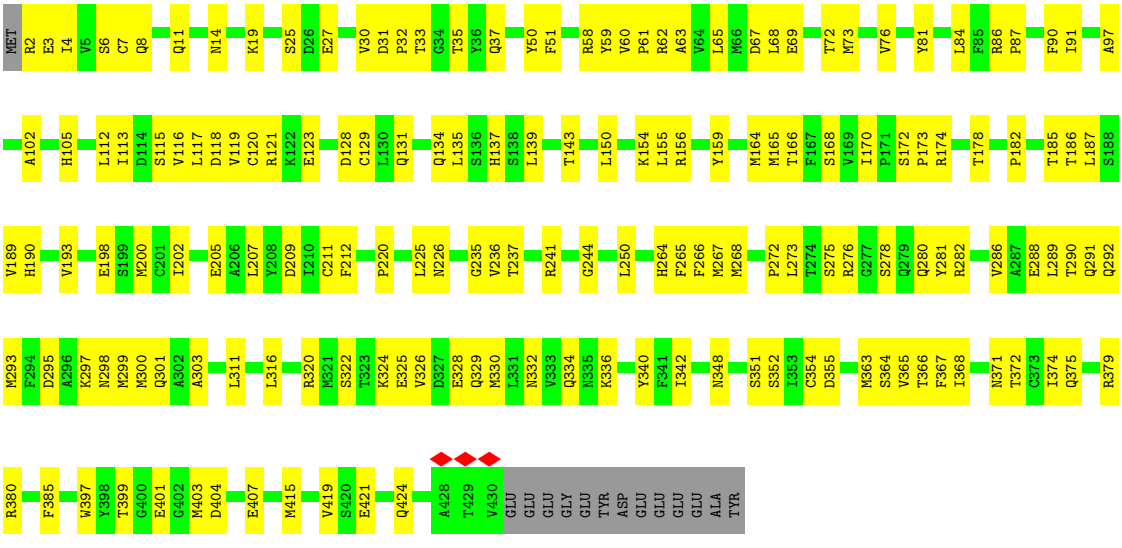
• Molecule 1: Tubulin beta chain

Chain GJ:



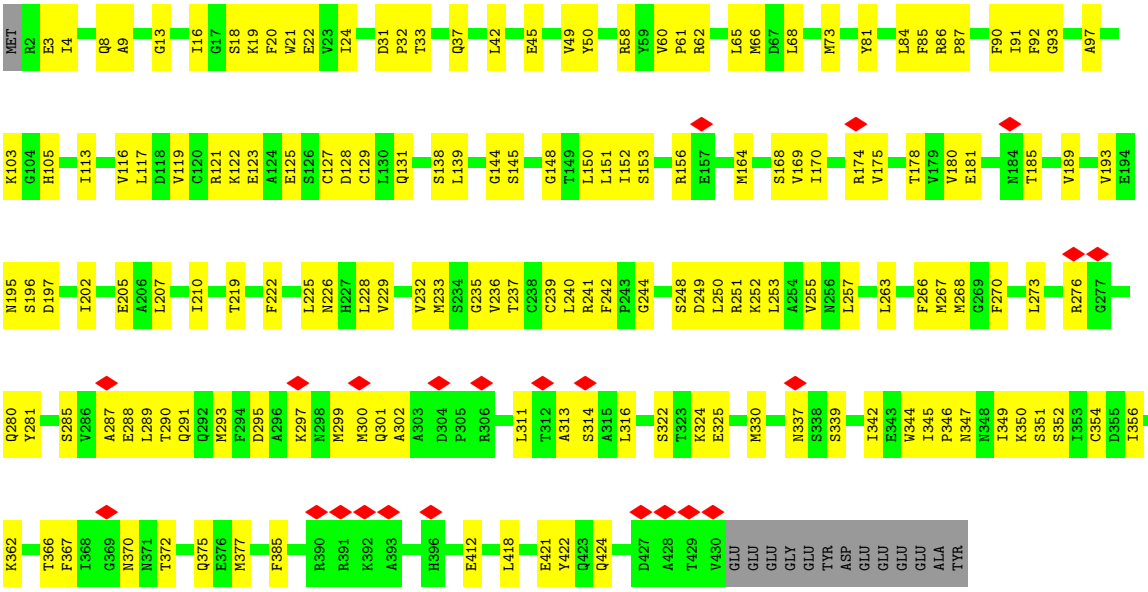
• Molecule 1: Tubulin beta chain

Chain GL:



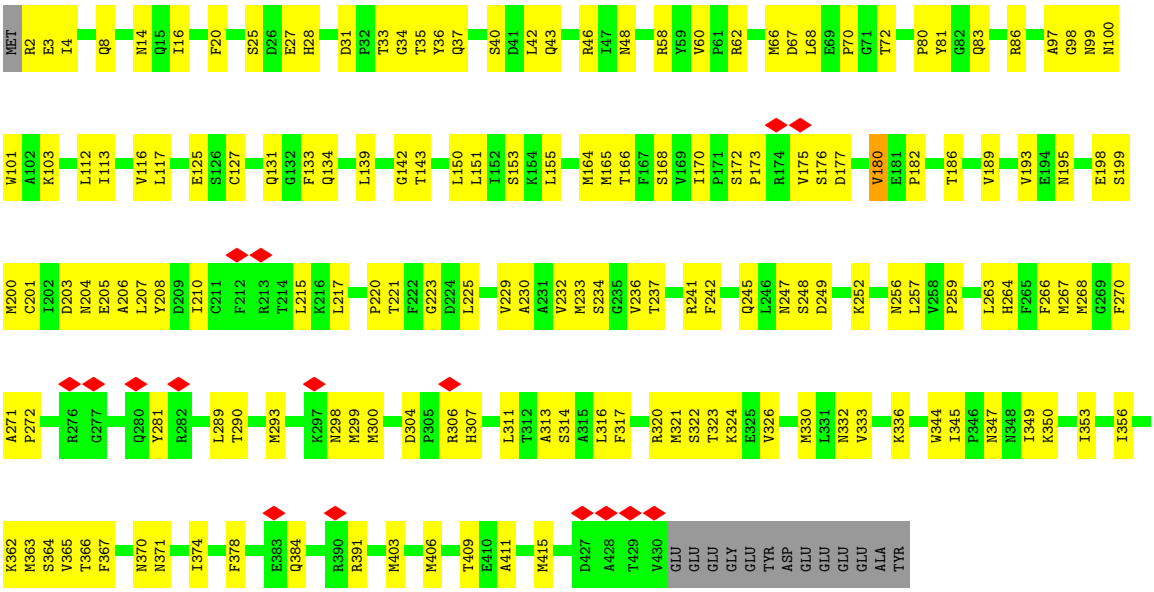
• Molecule 1: Tubulin beta chain

Chain H:



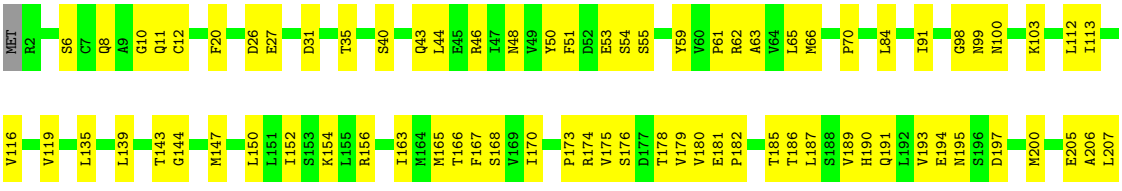
• Molecule 1: Tubulin beta chain

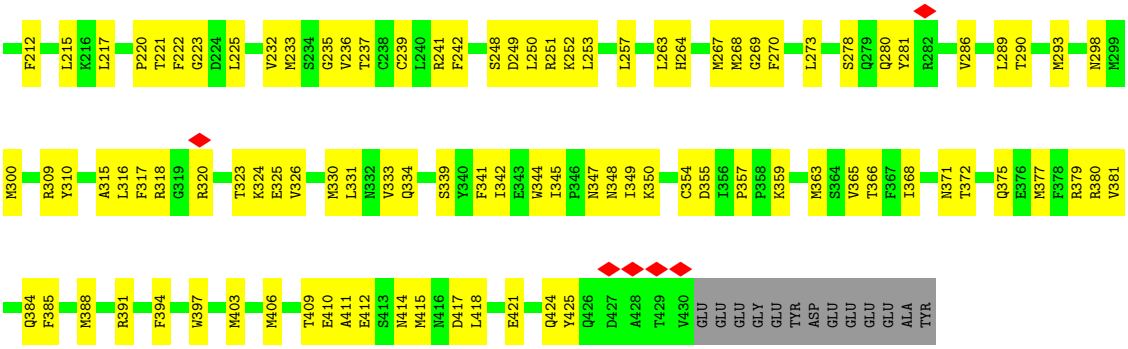
Chain HB:



• Molecule 1: Tubulin beta chain

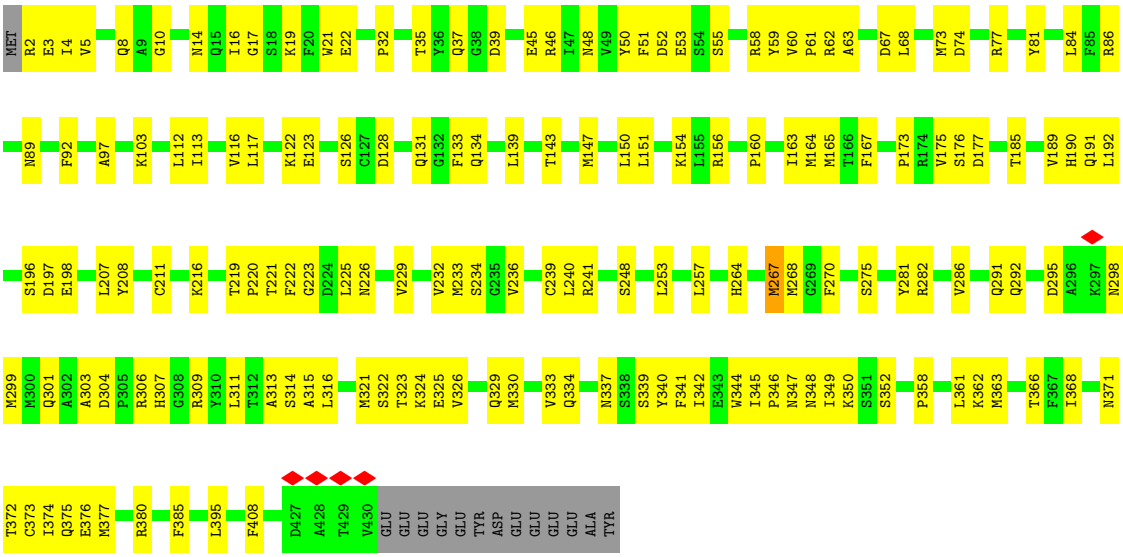
Chain HD:





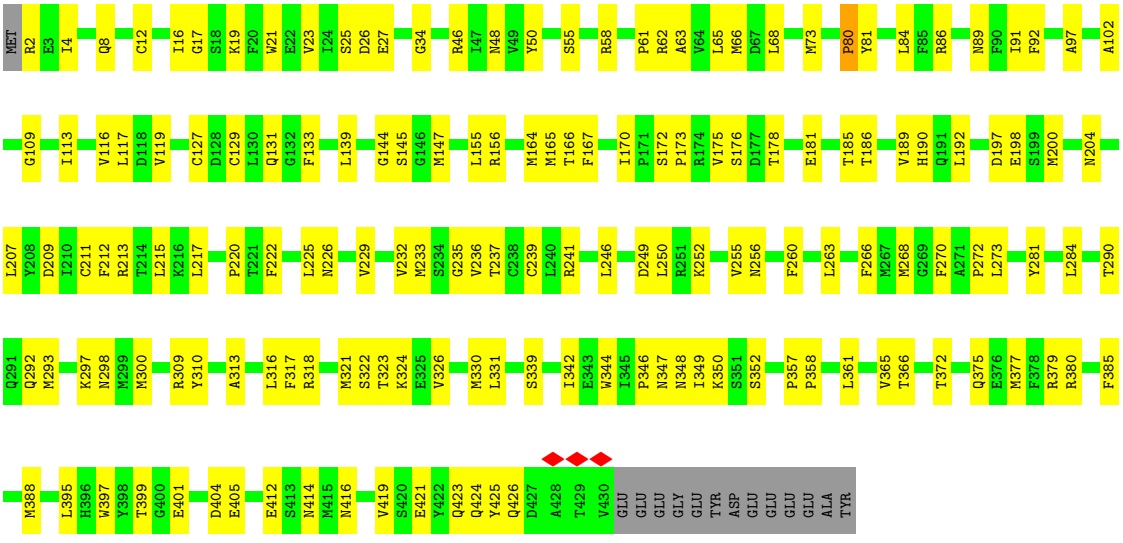
• Molecule 1: Tubulin beta chain

Chain HF:



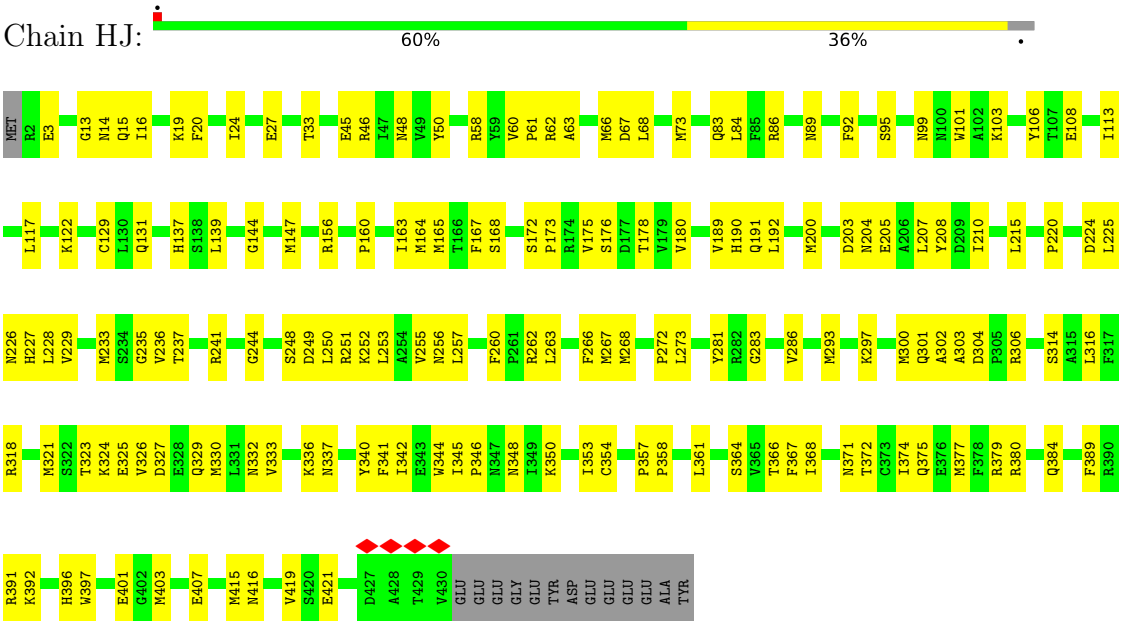
• Molecule 1: Tubulin beta chain

Chain HH:



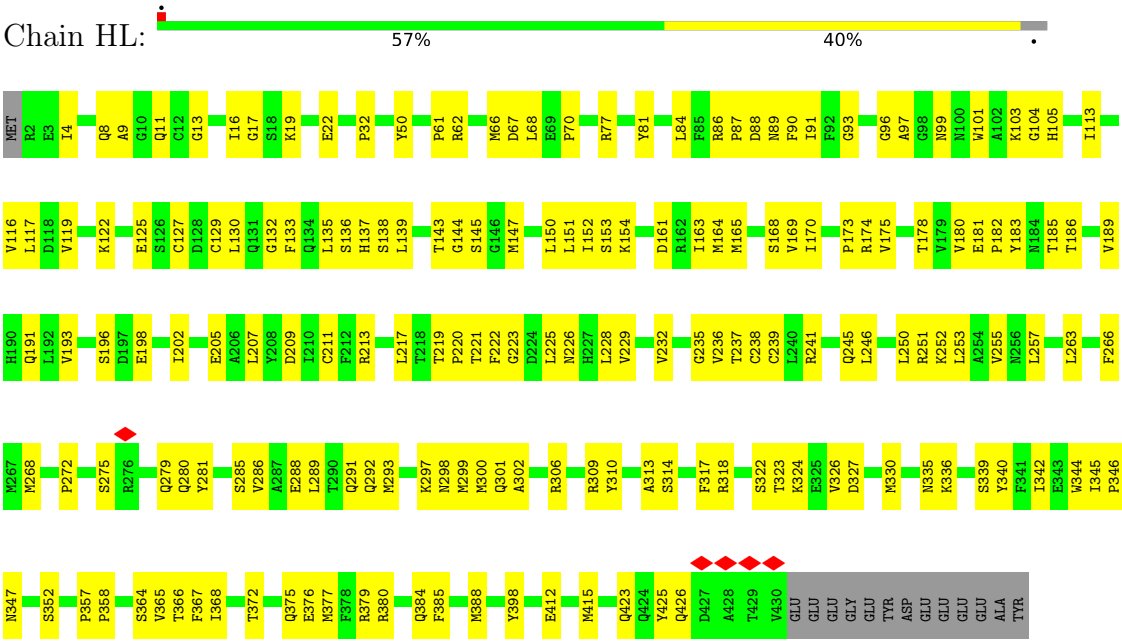
• Molecule 1: Tubulin beta chain

Chain HJ:



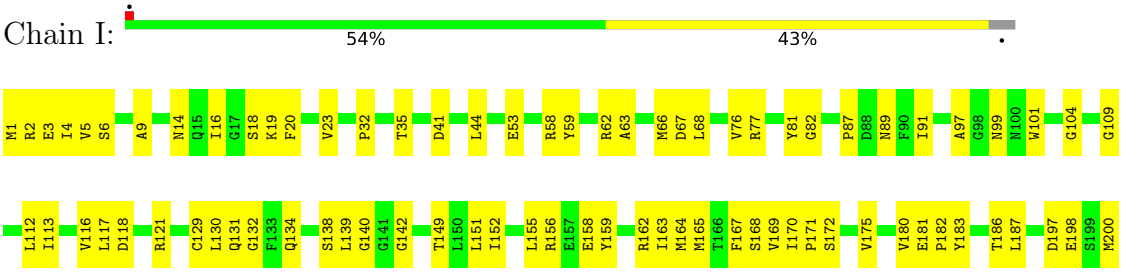
• Molecule 1: Tubulin beta chain

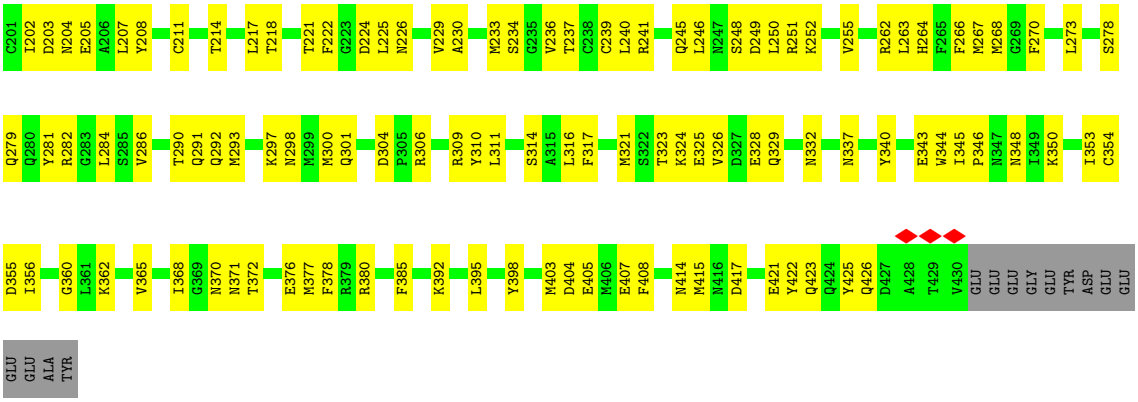
Chain HL:



• Molecule 1: Tubulin beta chain

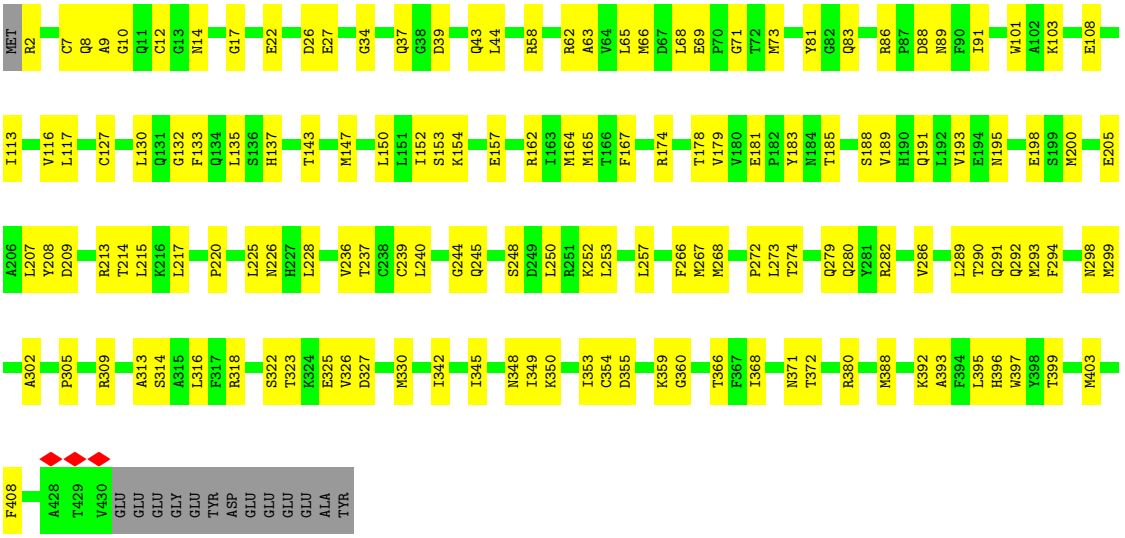
Chain I:





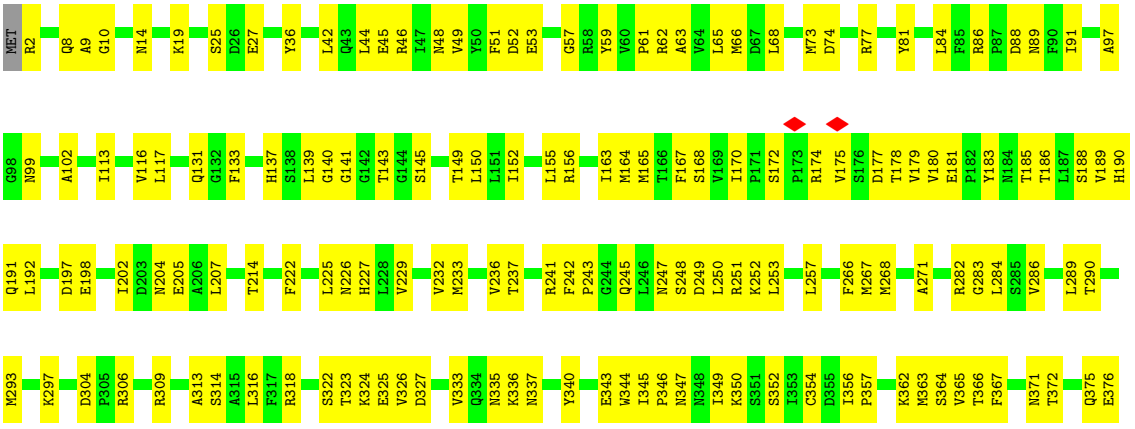
• Molecule 1: Tubulin beta chain

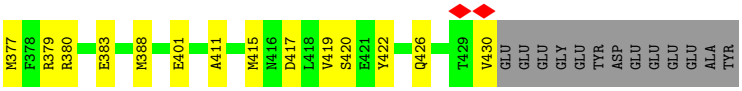
Chain IB:



• Molecule 1: Tubulin beta chain

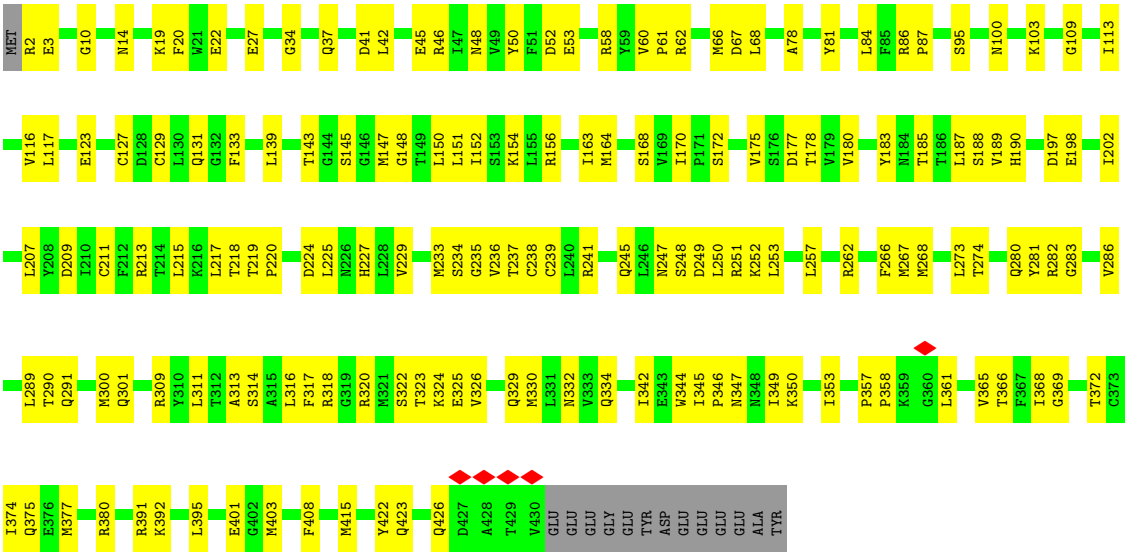
Chain ID:





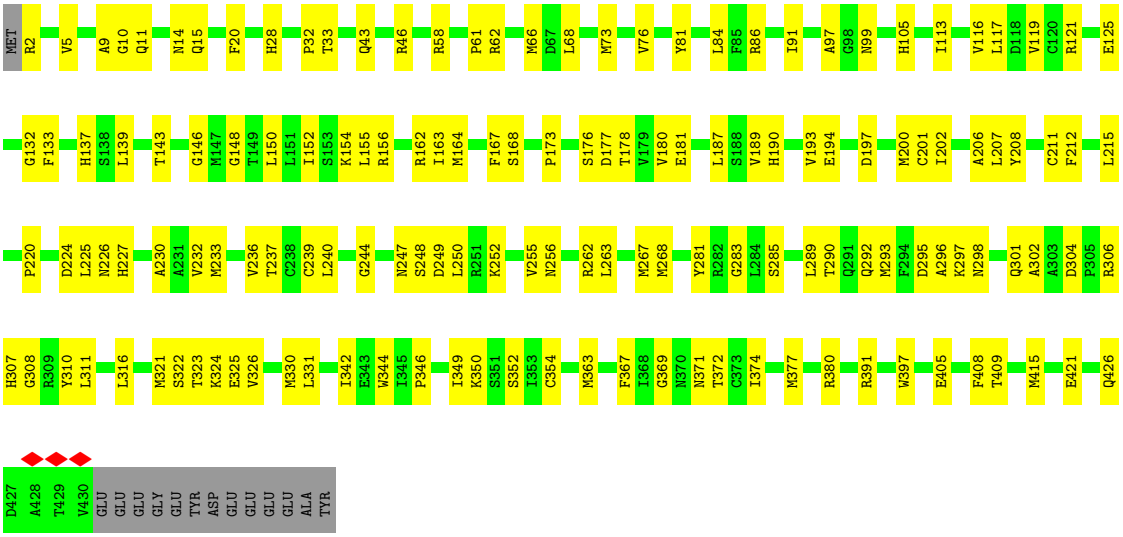
• Molecule 1: Tubulin beta chain

Chain IF:



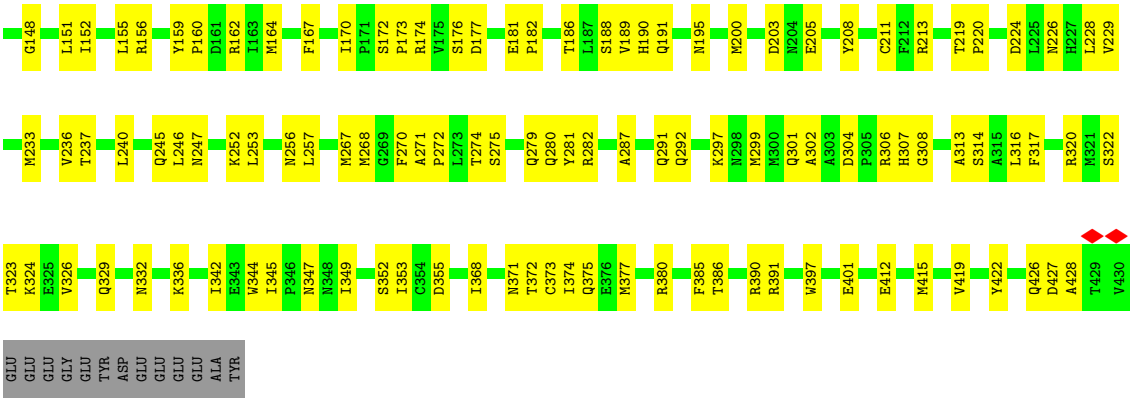
• Molecule 1: Tubulin beta chain

Chain IH:



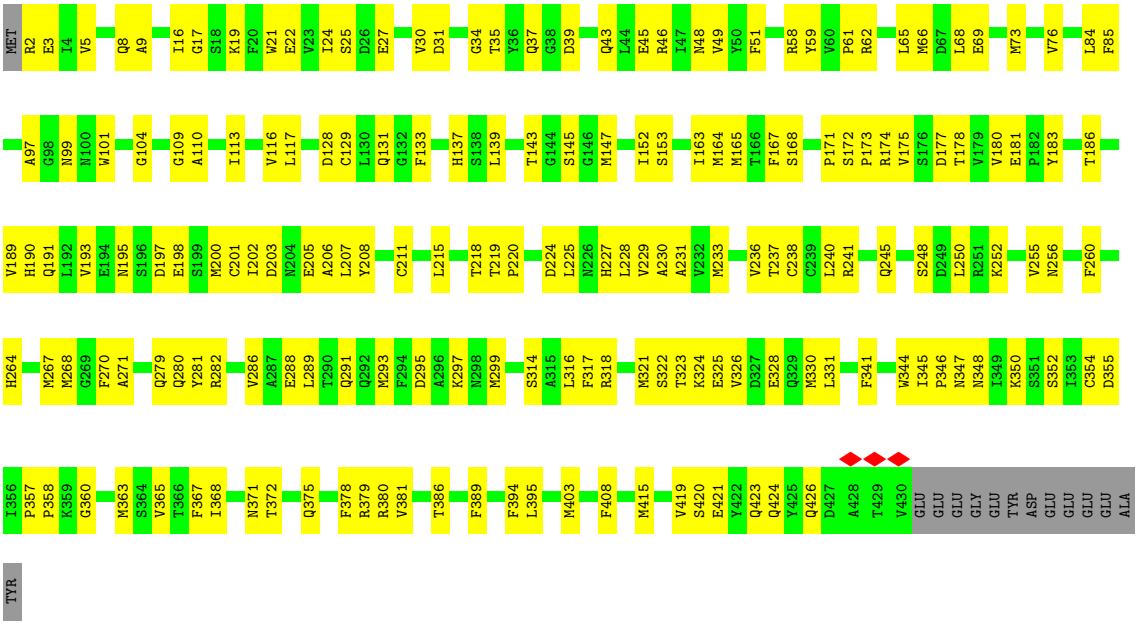
• Molecule 1: Tubulin beta chain

Chain IJ:



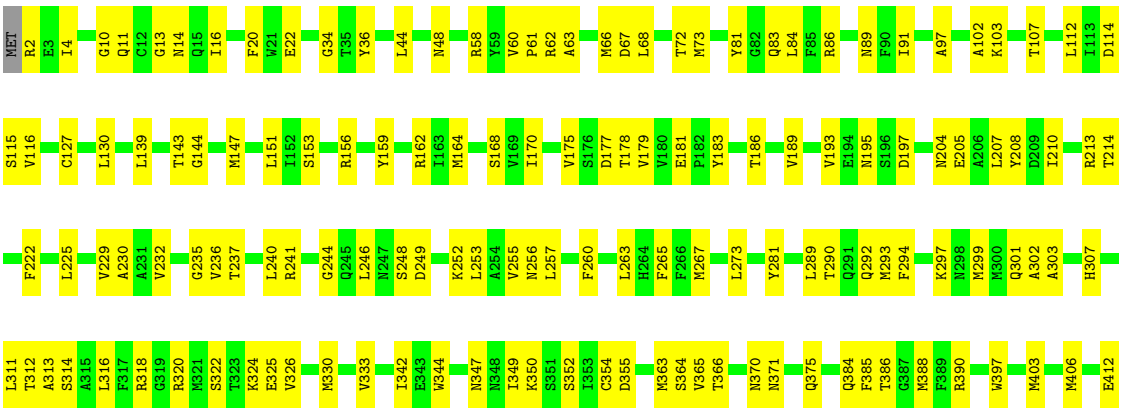
• Molecule 1: Tubulin beta chain

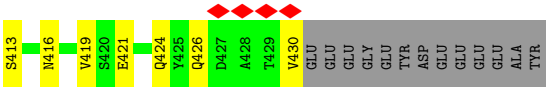
Chain IL:



• Molecule 1: Tubulin beta chain

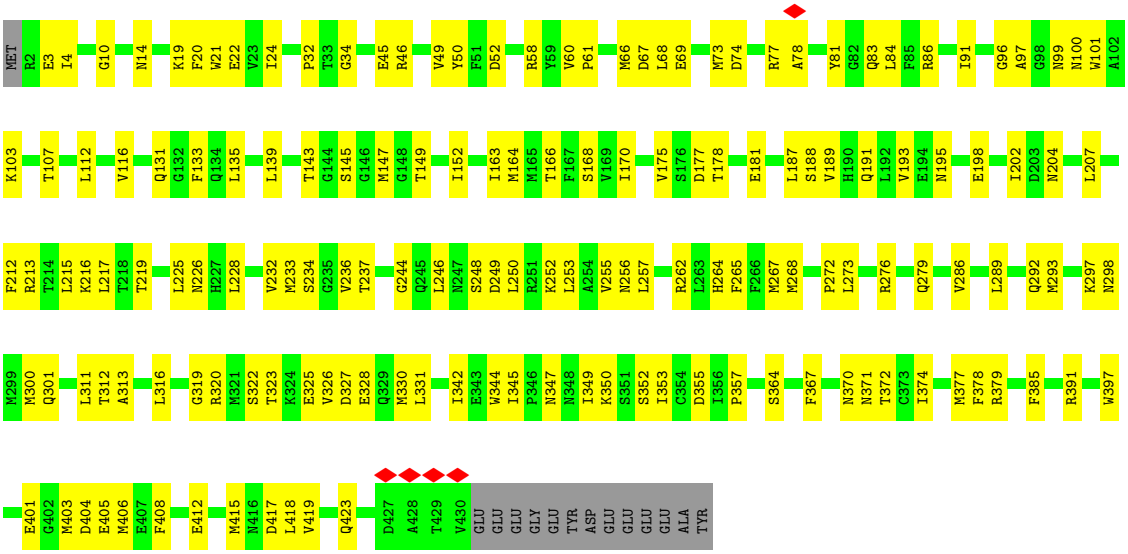
Chain JA:





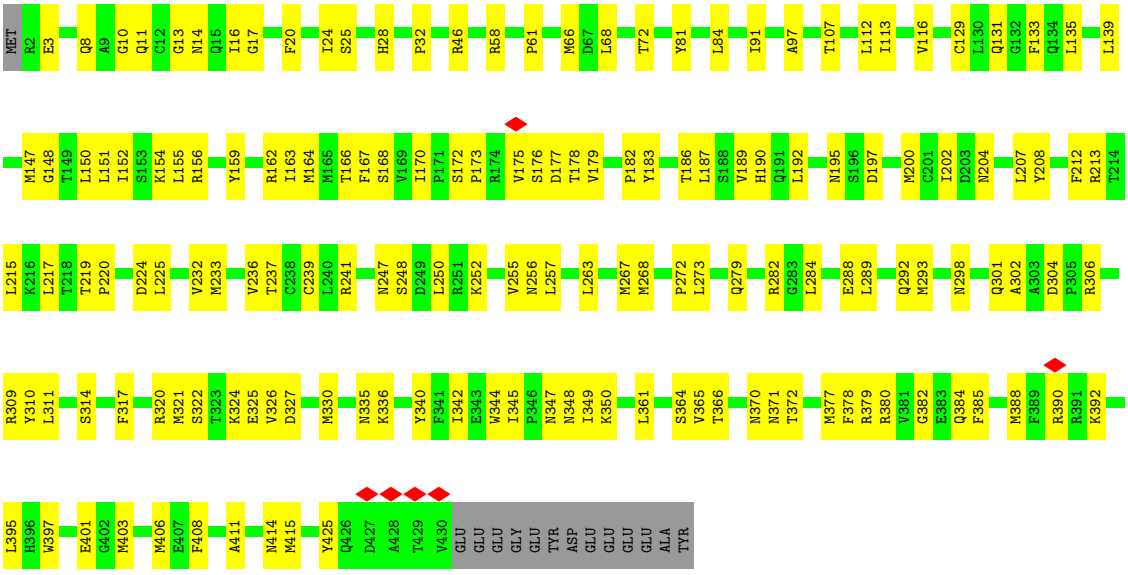
• Molecule 1: Tubulin beta chain

Chain JC:



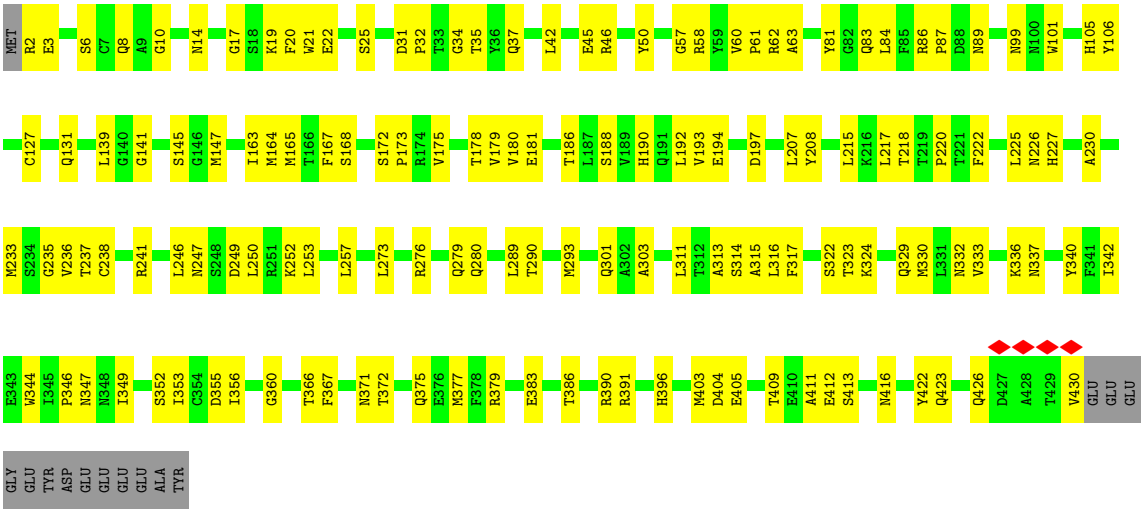
• Molecule 1: Tubulin beta chain

Chain JE:



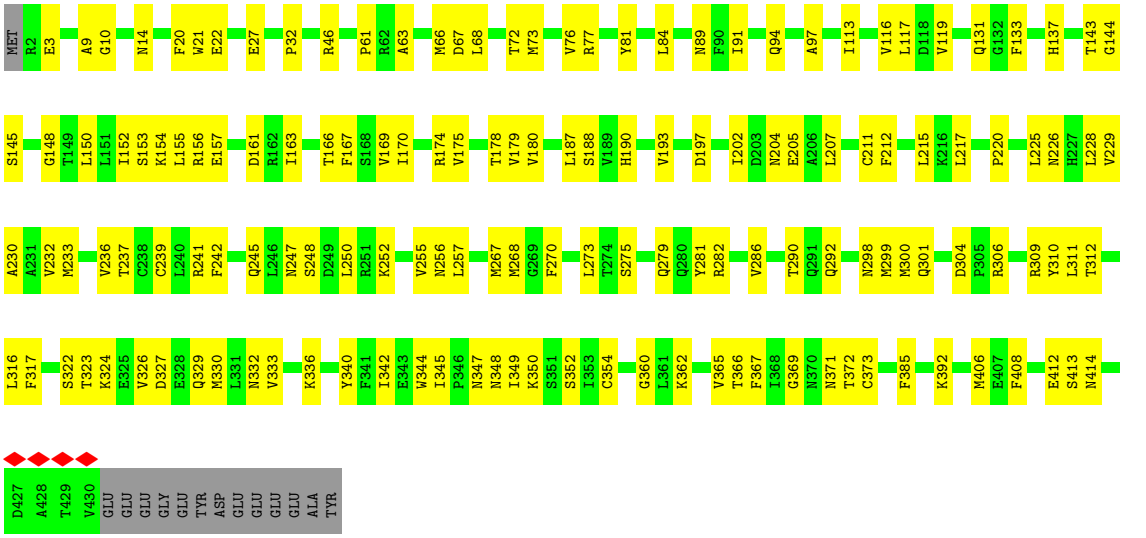
• Molecule 1: Tubulin beta chain

Chain JG:



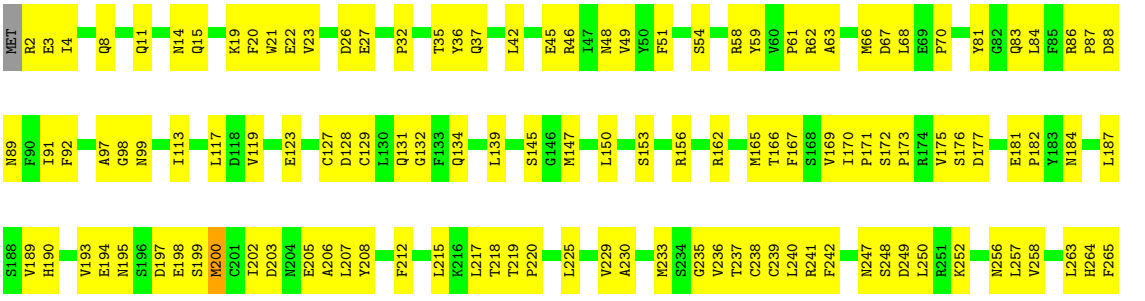
• Molecule 1: Tubulin beta chain

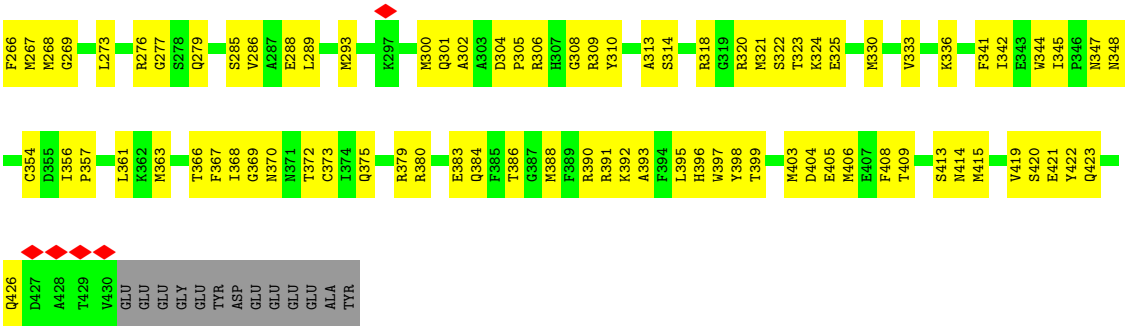
Chain JI:



• Molecule 1: Tubulin beta chain

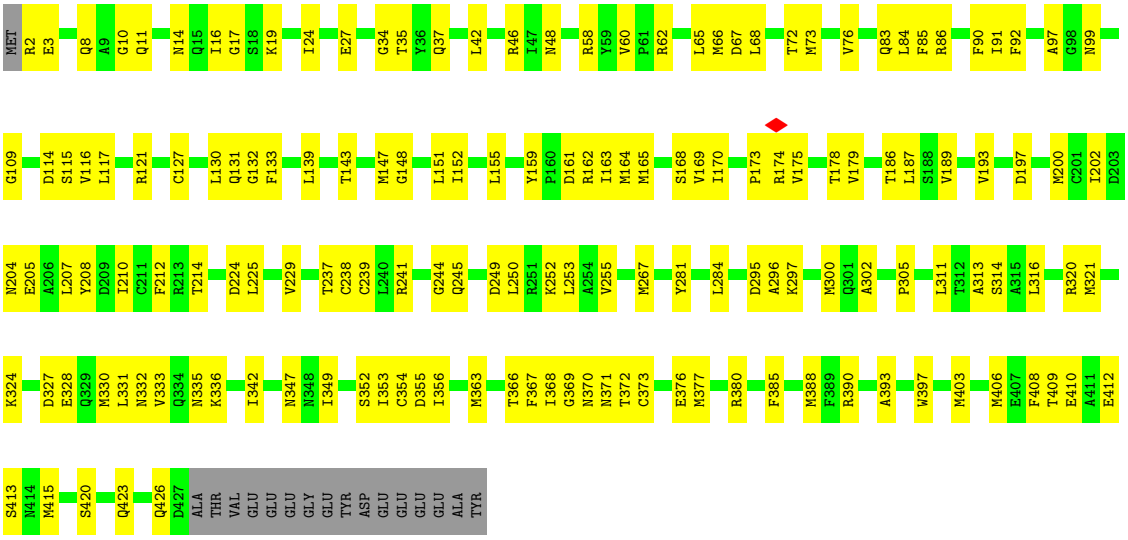
Chain JK:





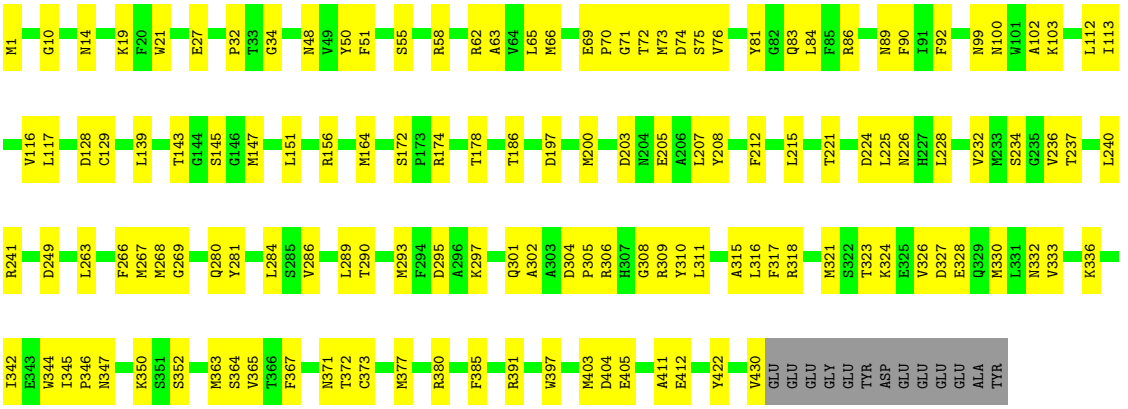
• Molecule 1: Tubulin beta chain

Chain JM:



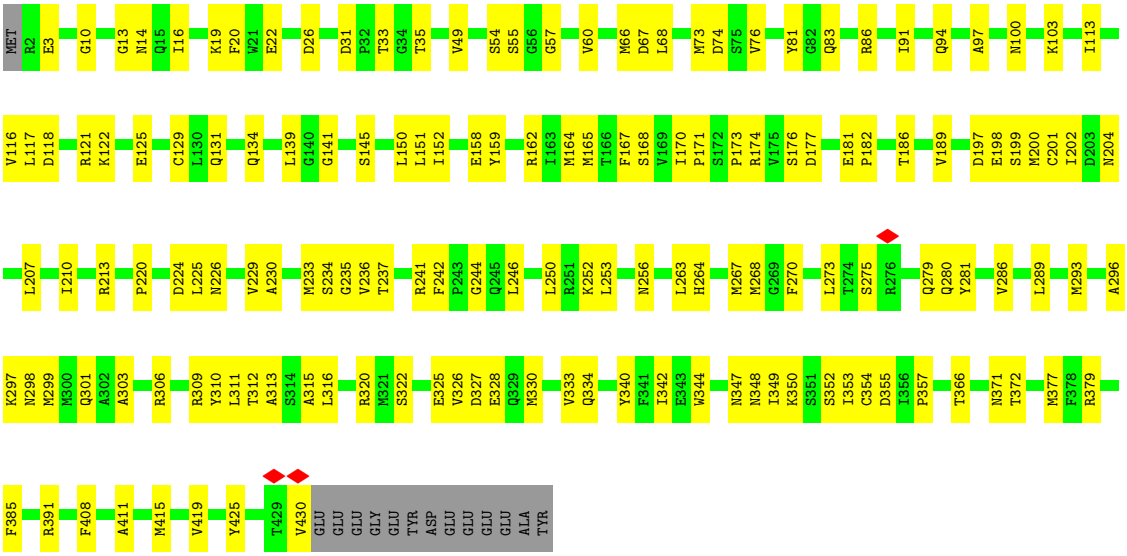
• Molecule 1: Tubulin beta chain

Chain KA:



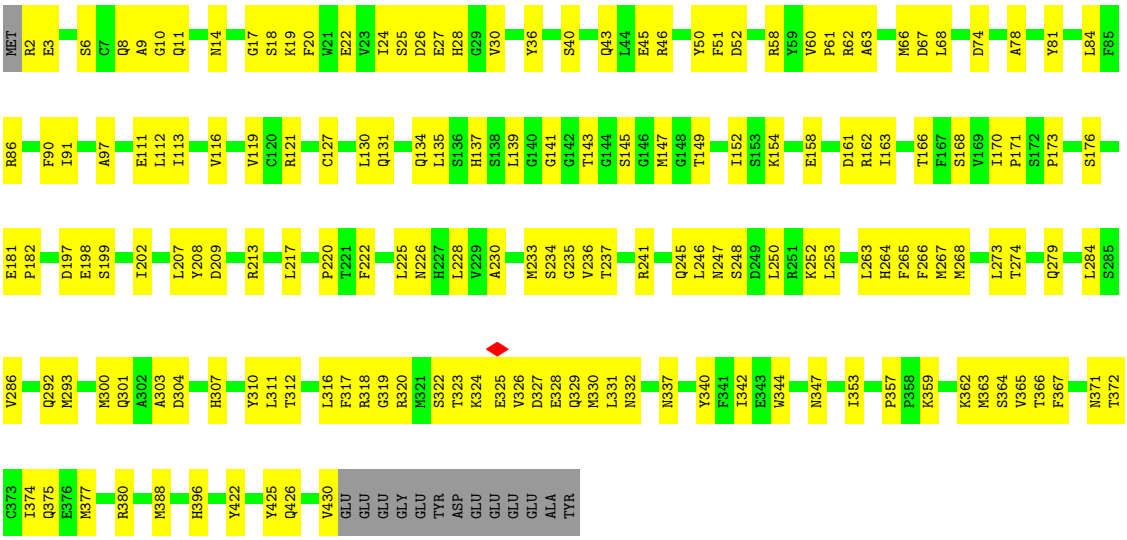
• Molecule 1: Tubulin beta chain

Chain KC:



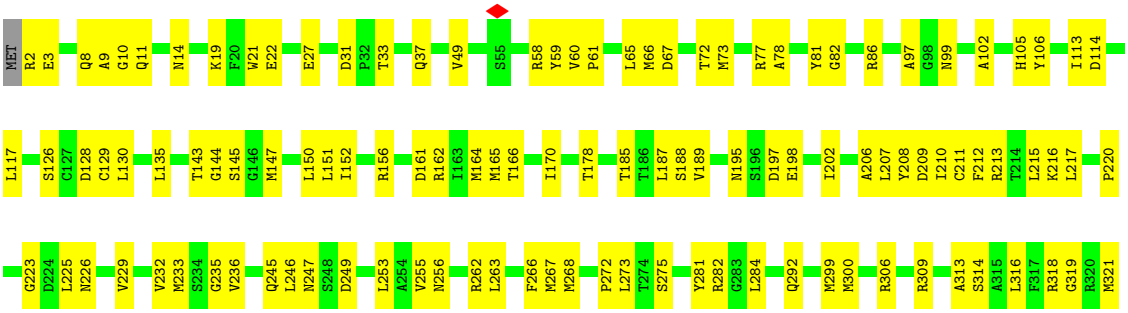
• Molecule 1: Tubulin beta chain

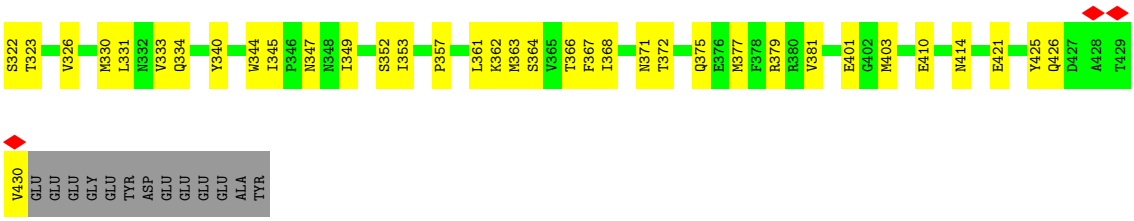
Chain KE:



• Molecule 1: Tubulin beta chain

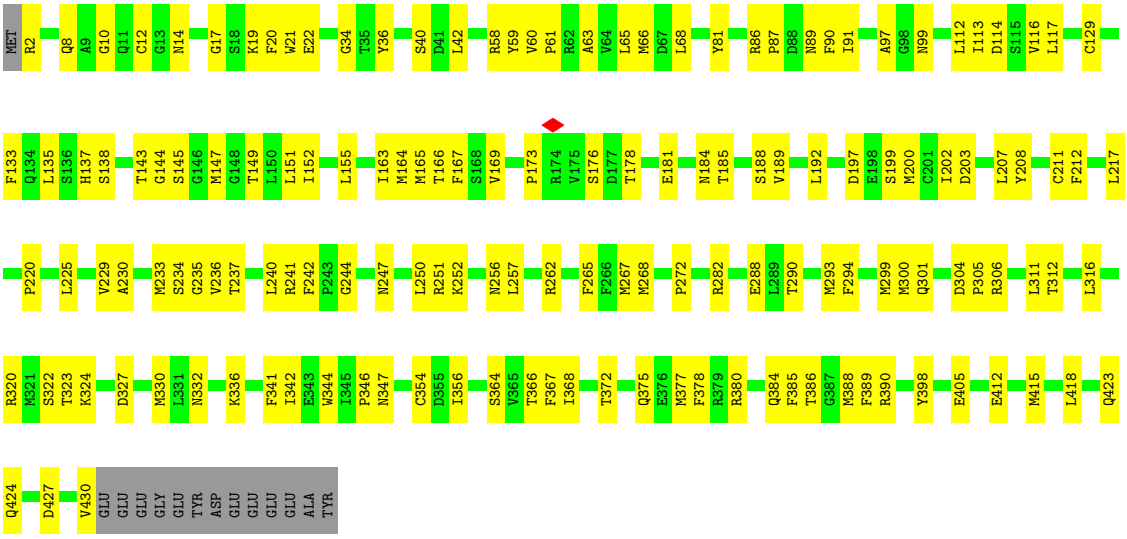
Chain KG:





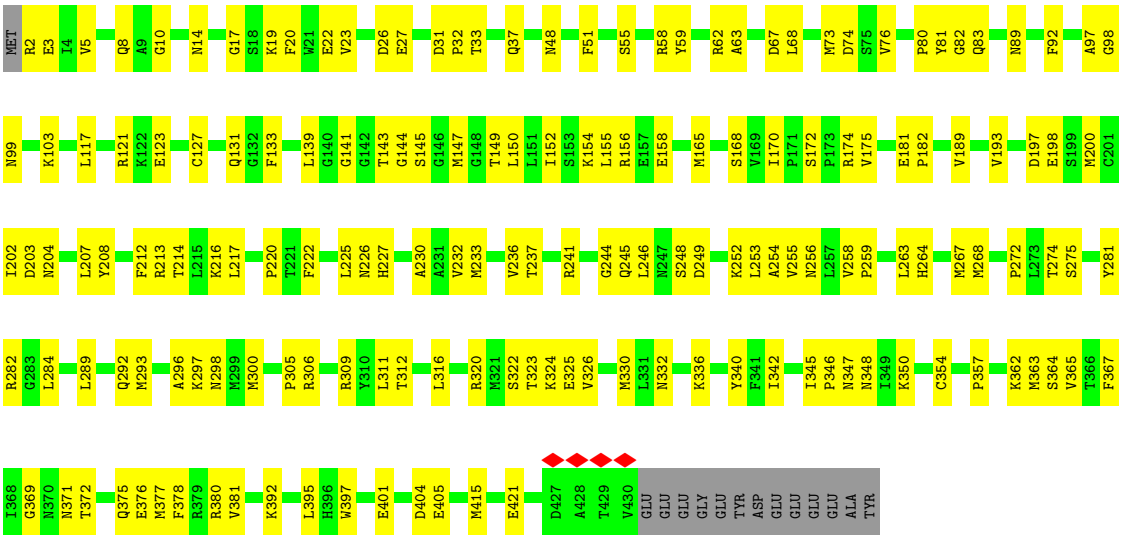
• Molecule 1: Tubulin beta chain

Chain KI:



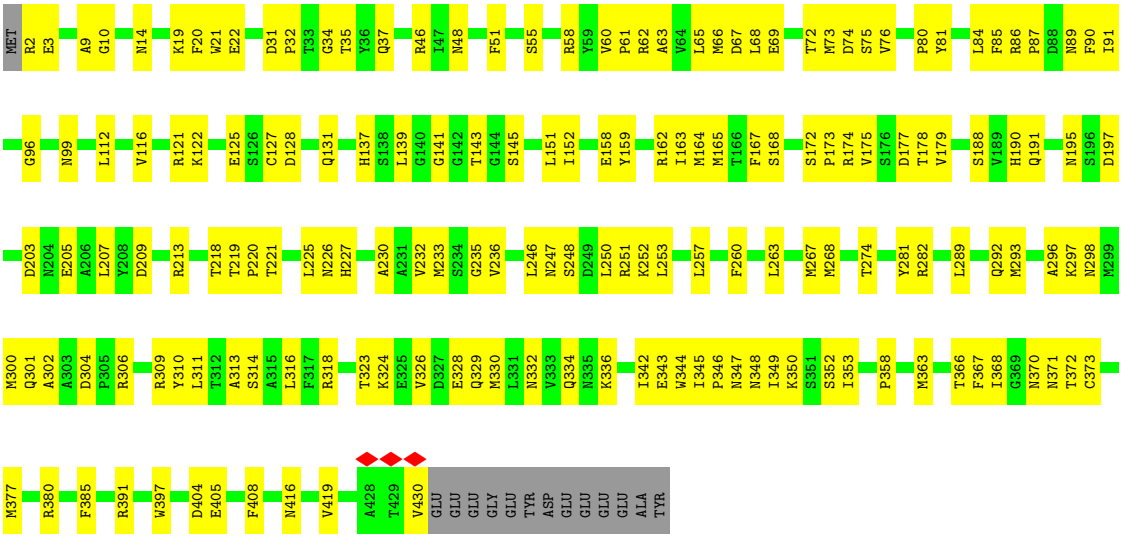
• Molecule 1: Tubulin beta chain

Chain KK:



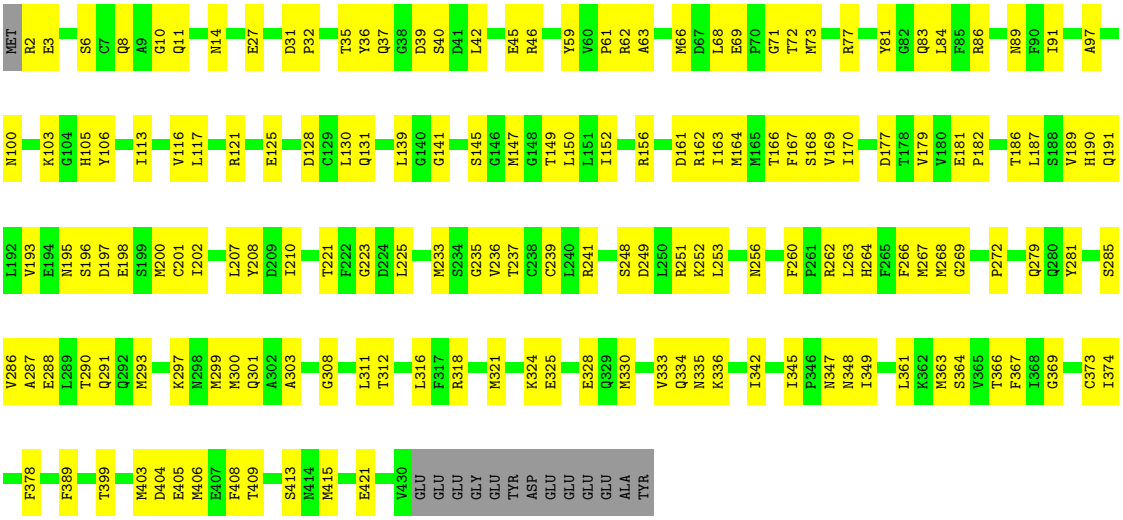
• Molecule 1: Tubulin beta chain

Chain KM:



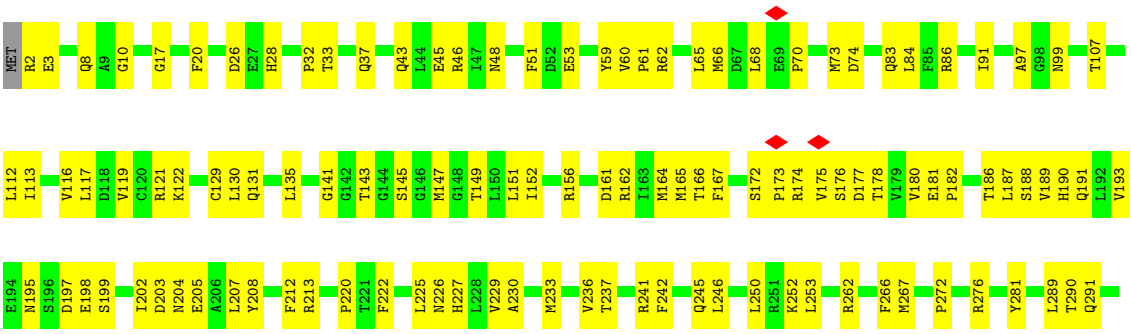
• Molecule 1: Tubulin beta chain

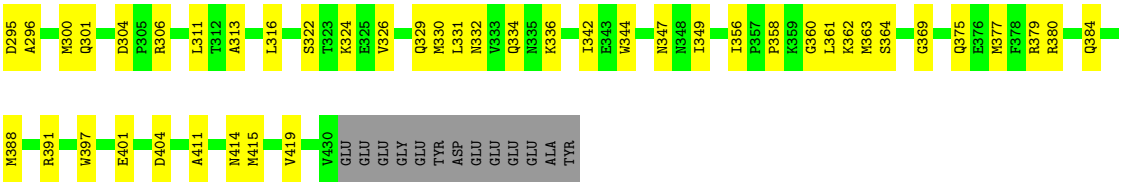
Chain LA:



• Molecule 1: Tubulin beta chain

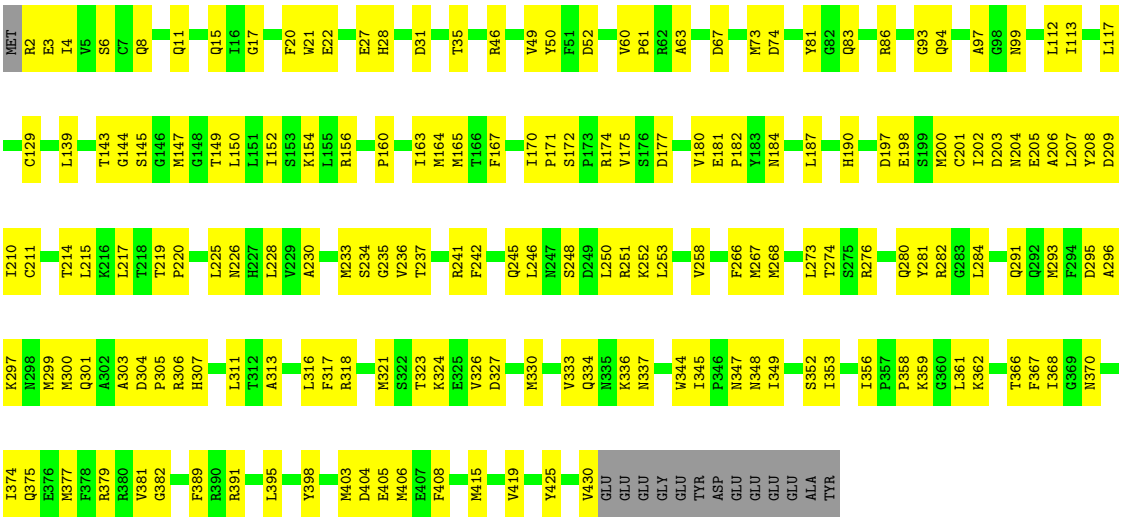
Chain LC:





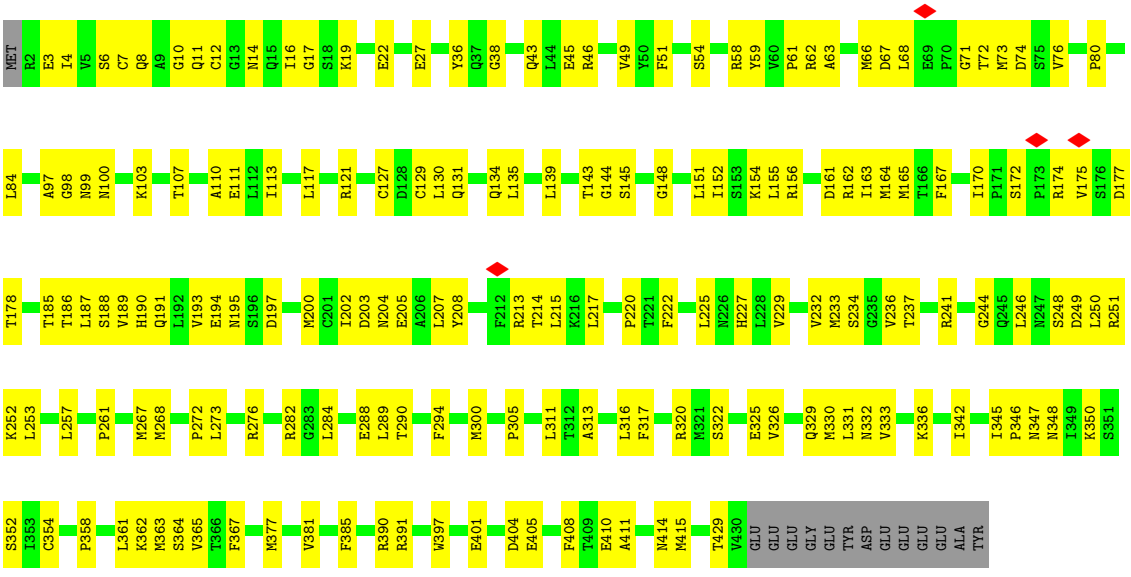
• Molecule 1: Tubulin beta chain

Chain LE:



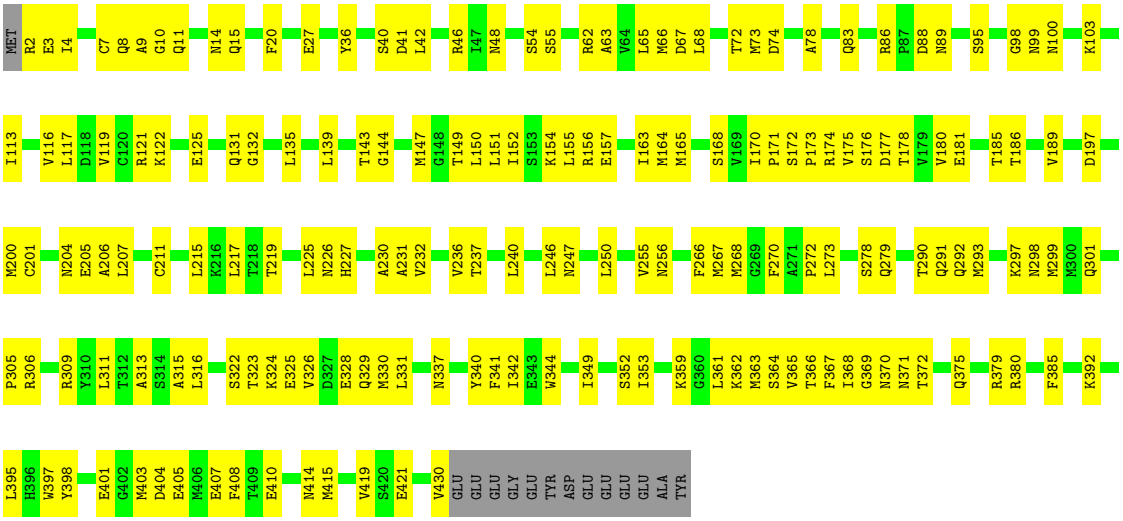
• Molecule 1: Tubulin beta chain

Chain LG:



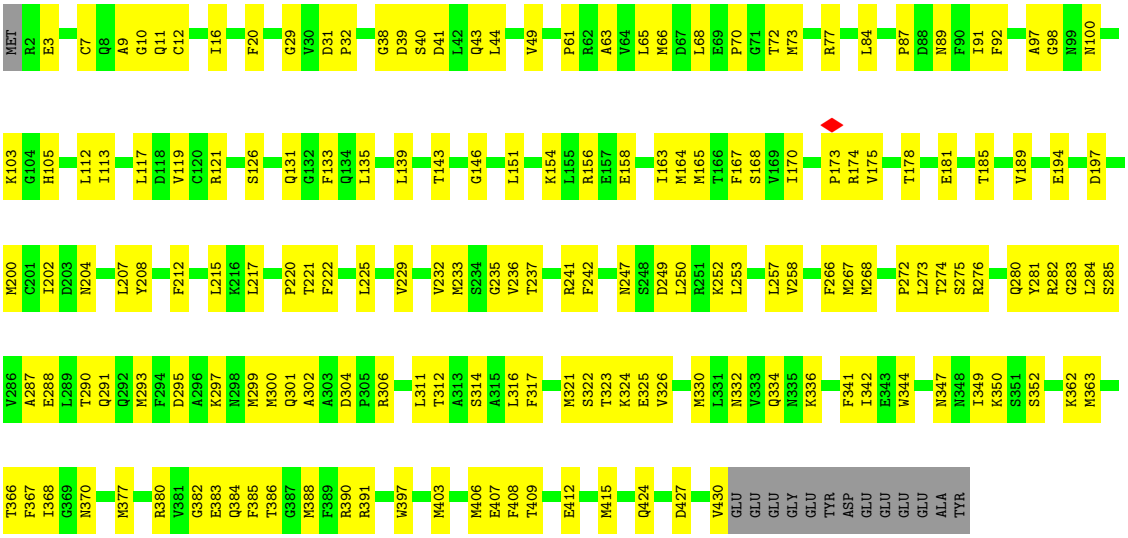
• Molecule 1: Tubulin beta chain

Chain LI:



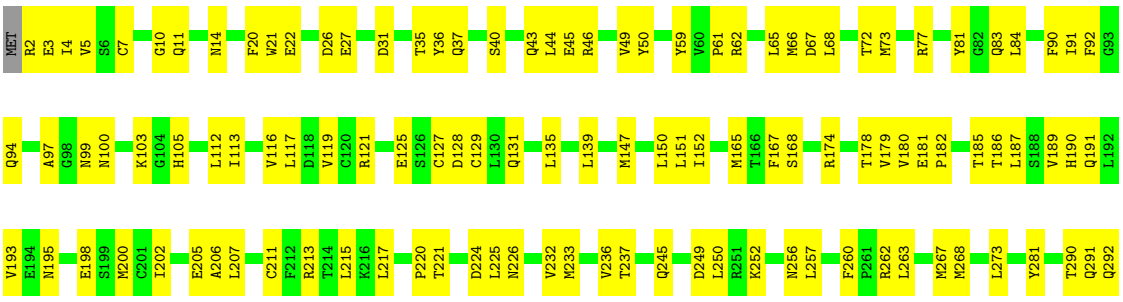
• Molecule 1: Tubulin beta chain

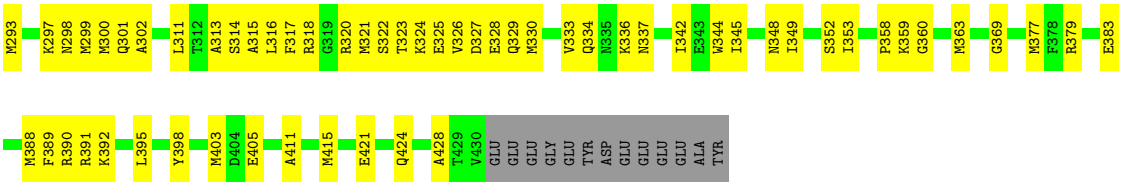
Chain LK:



• Molecule 1: Tubulin beta chain

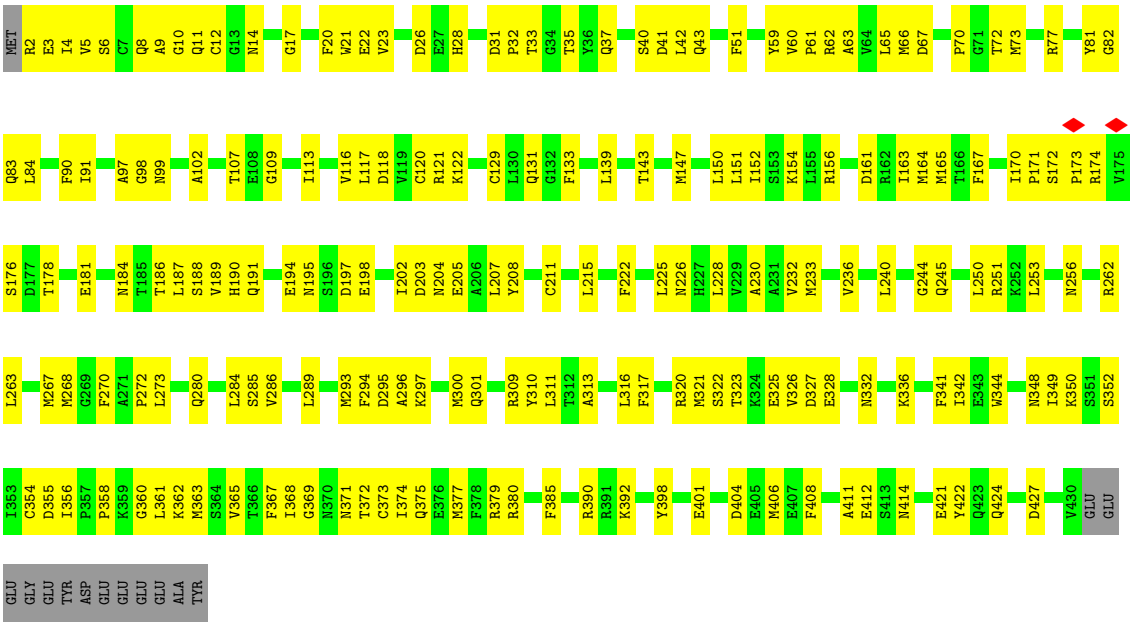
Chain LM:





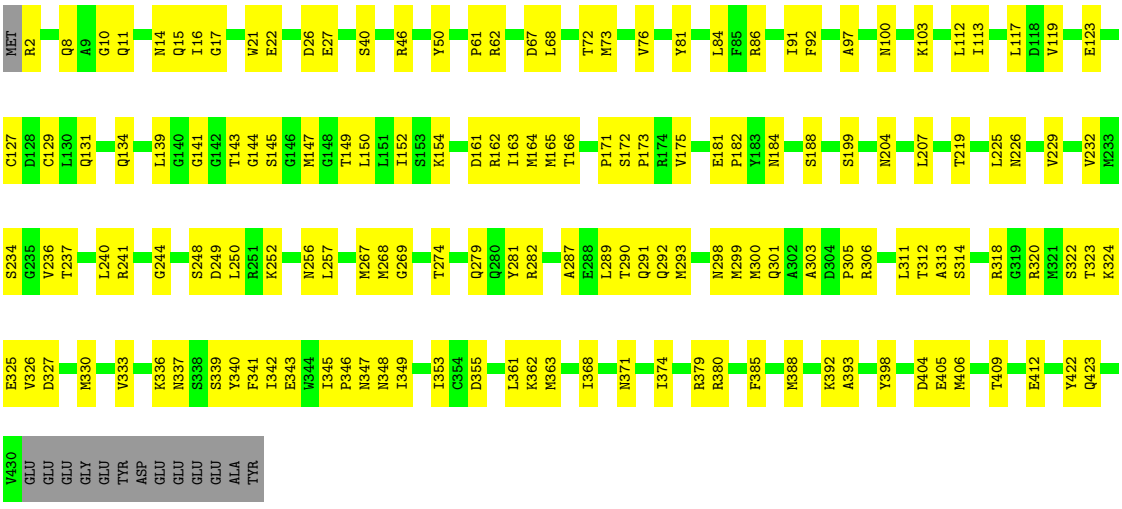
• Molecule 1: Tubulin beta chain

Chain LO:



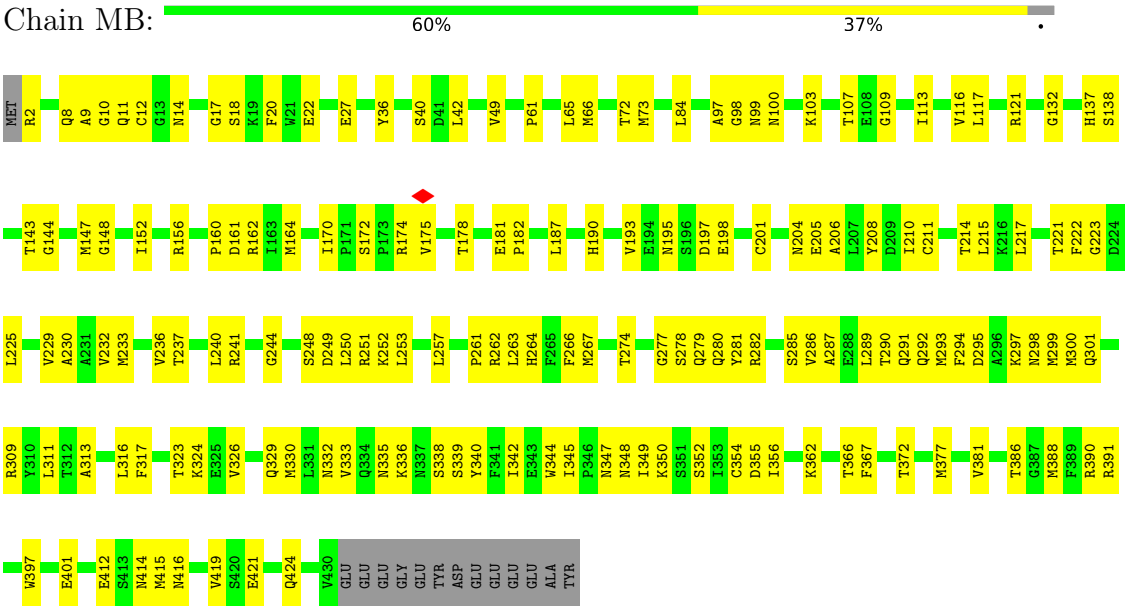
• Molecule 1: Tubulin beta chain

Chain M:



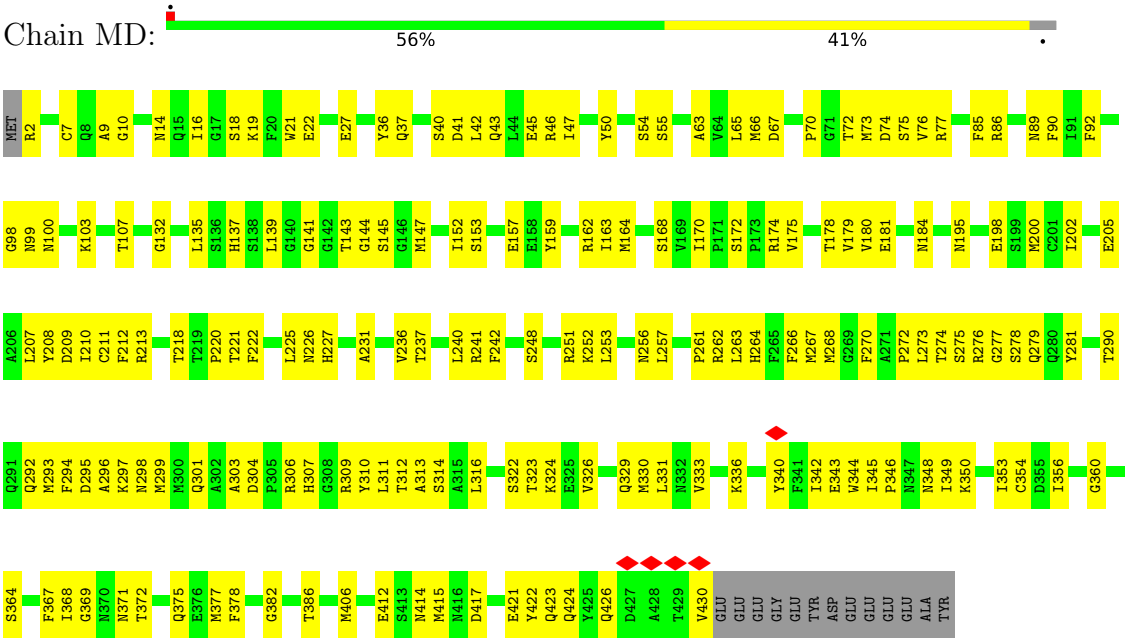
• Molecule 1: Tubulin beta chain

Chain MB:



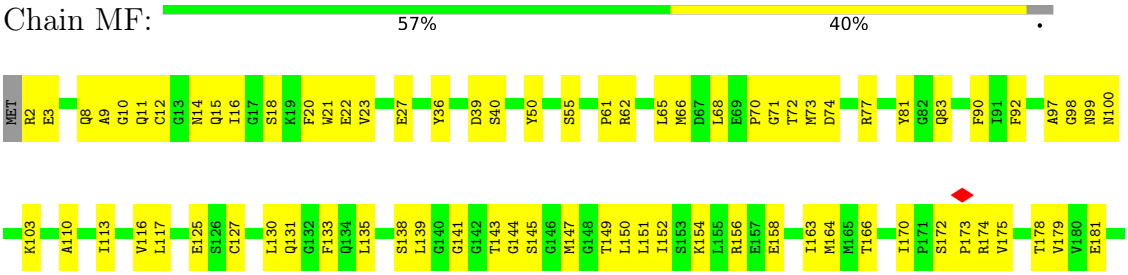
• Molecule 1: Tubulin beta chain

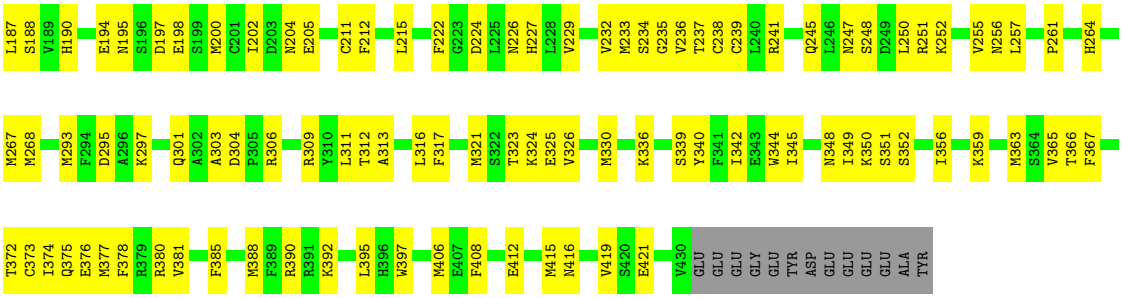
Chain MD:



• Molecule 1: Tubulin beta chain

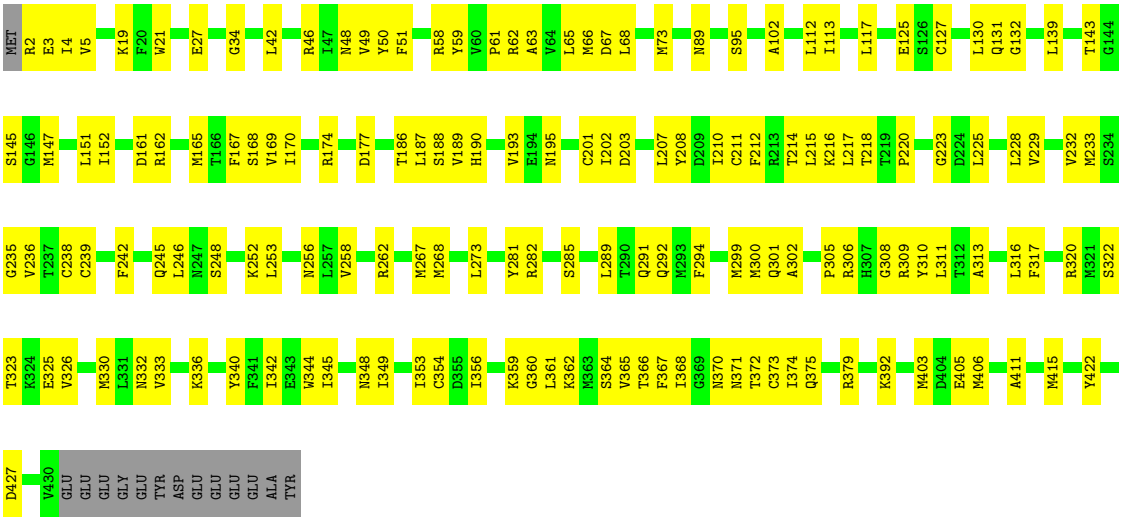
Chain MF:





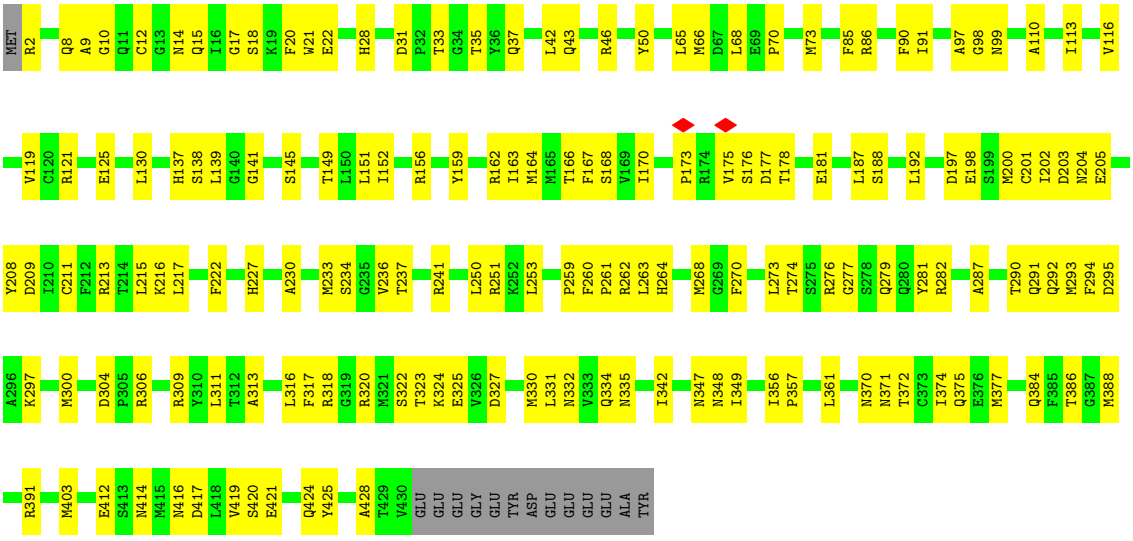
• Molecule 1: Tubulin beta chain

Chain MH:



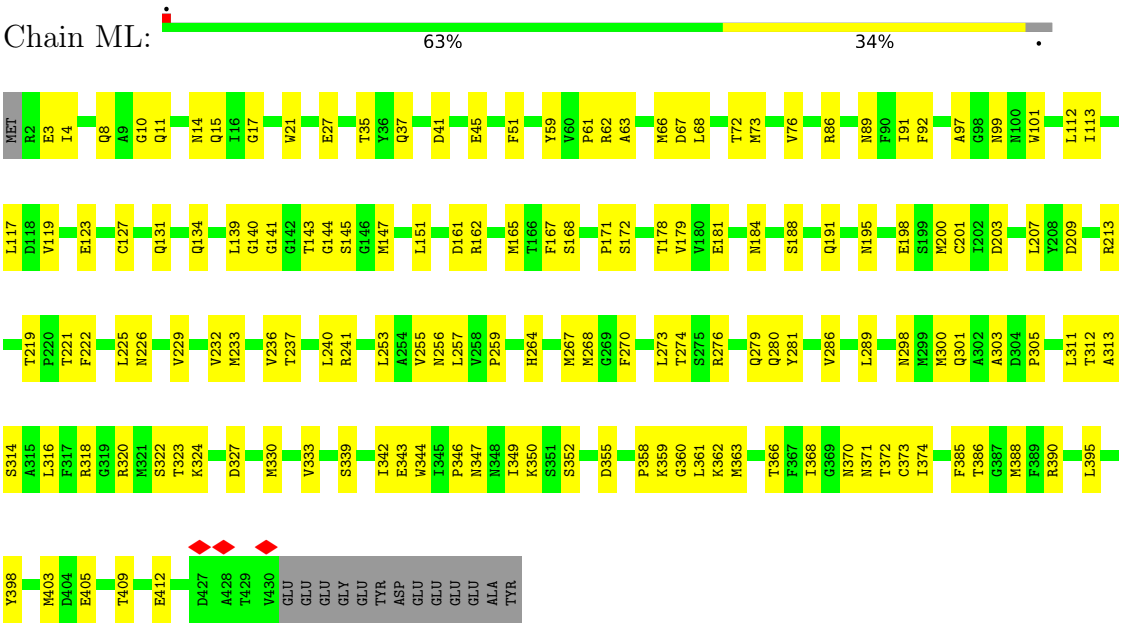
• Molecule 1: Tubulin beta chain

Chain MJ:



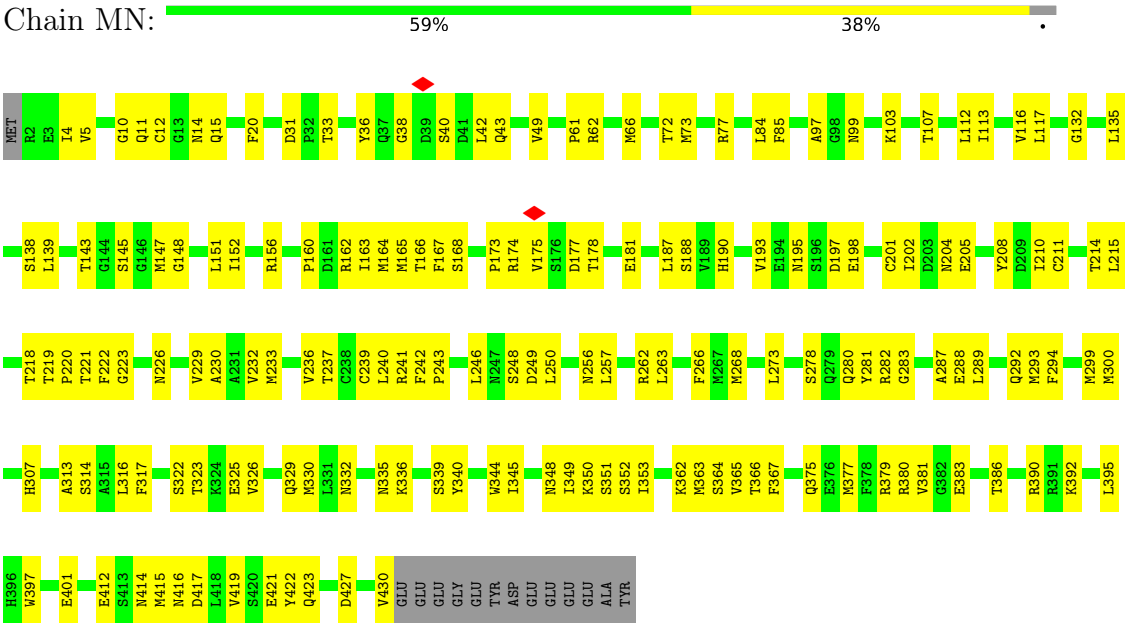
• Molecule 1: Tubulin beta chain

Chain ML:



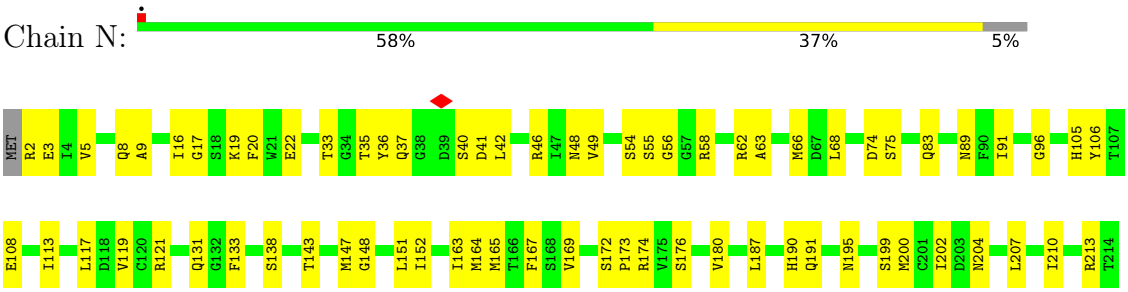
• Molecule 1: Tubulin beta chain

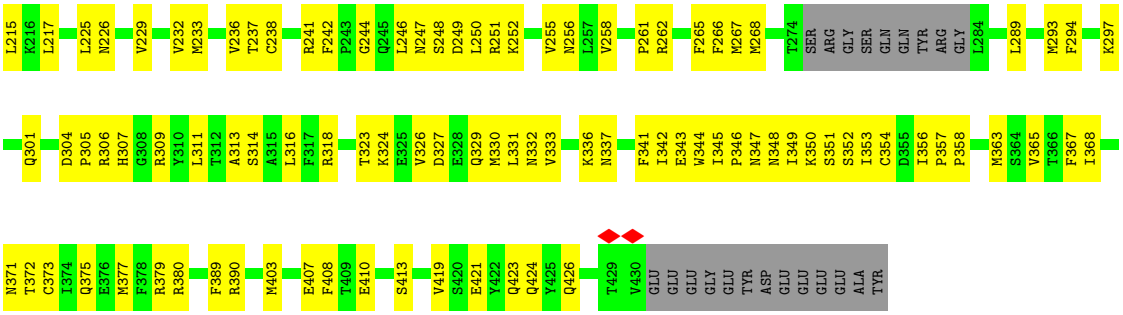
Chain MN:



• Molecule 1: Tubulin beta chain

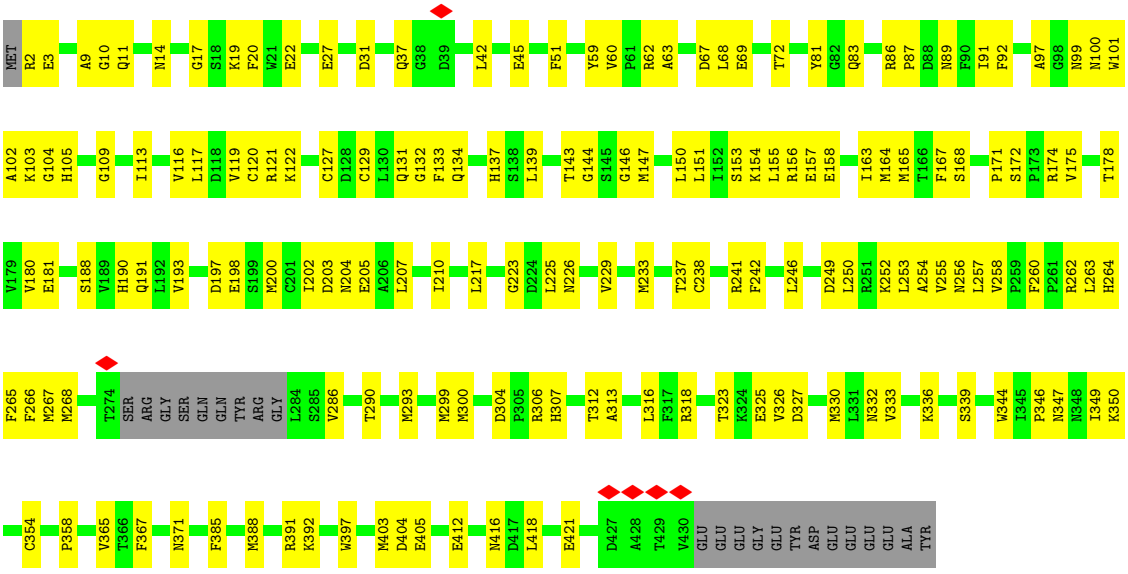
Chain N:





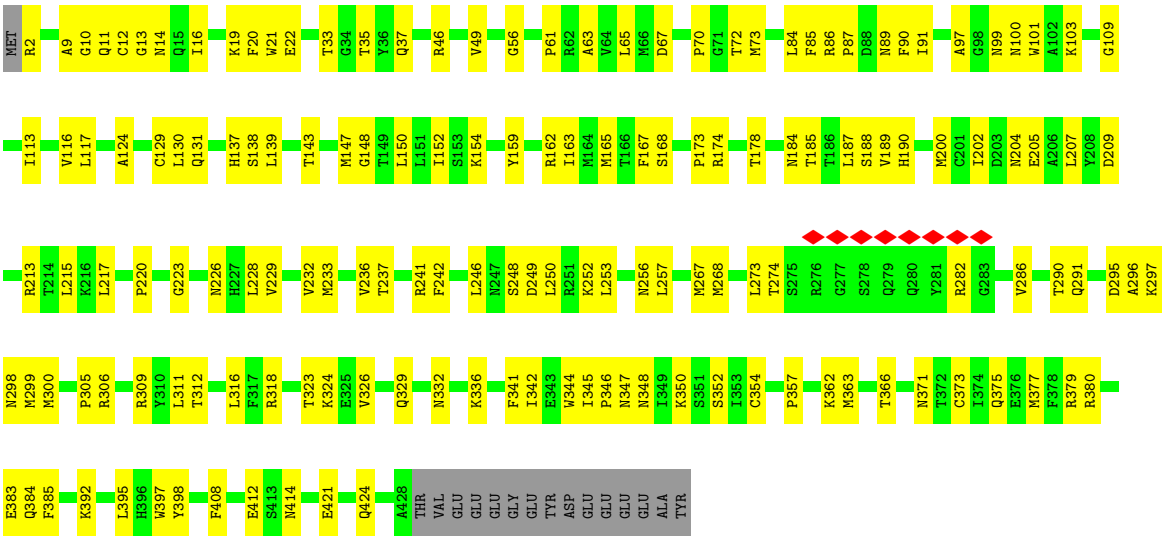
• Molecule 1: Tubulin beta chain

Chain NB:



• Molecule 1: Tubulin beta chain

Chain ND:



• Molecule 1: Tubulin beta chain

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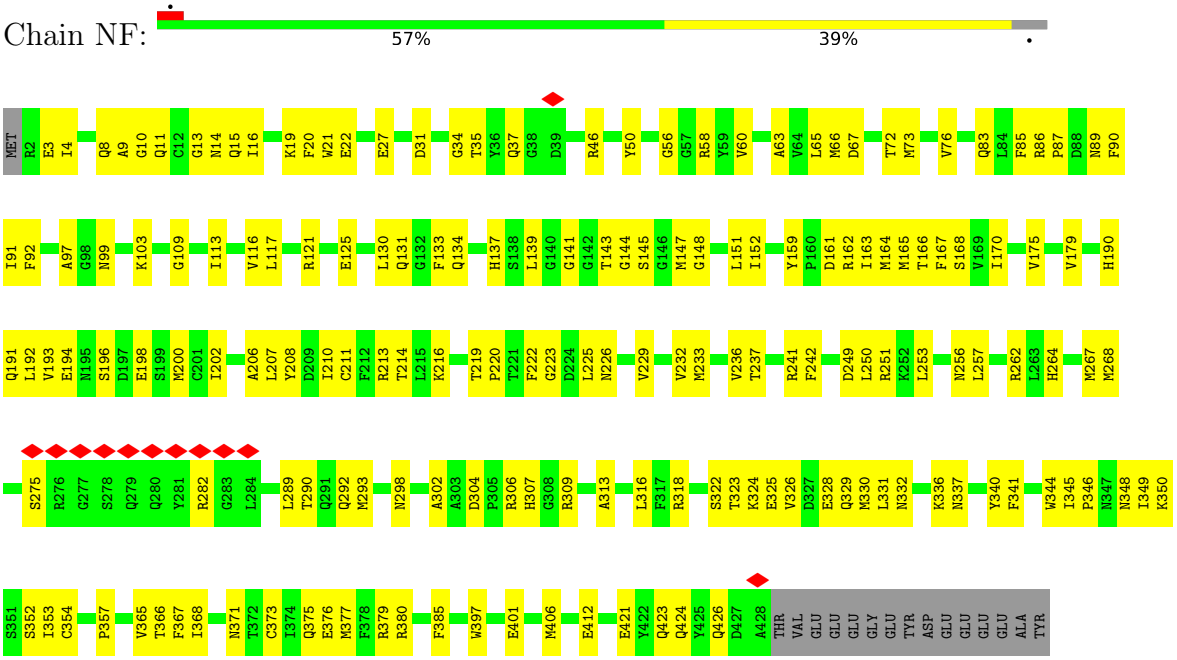
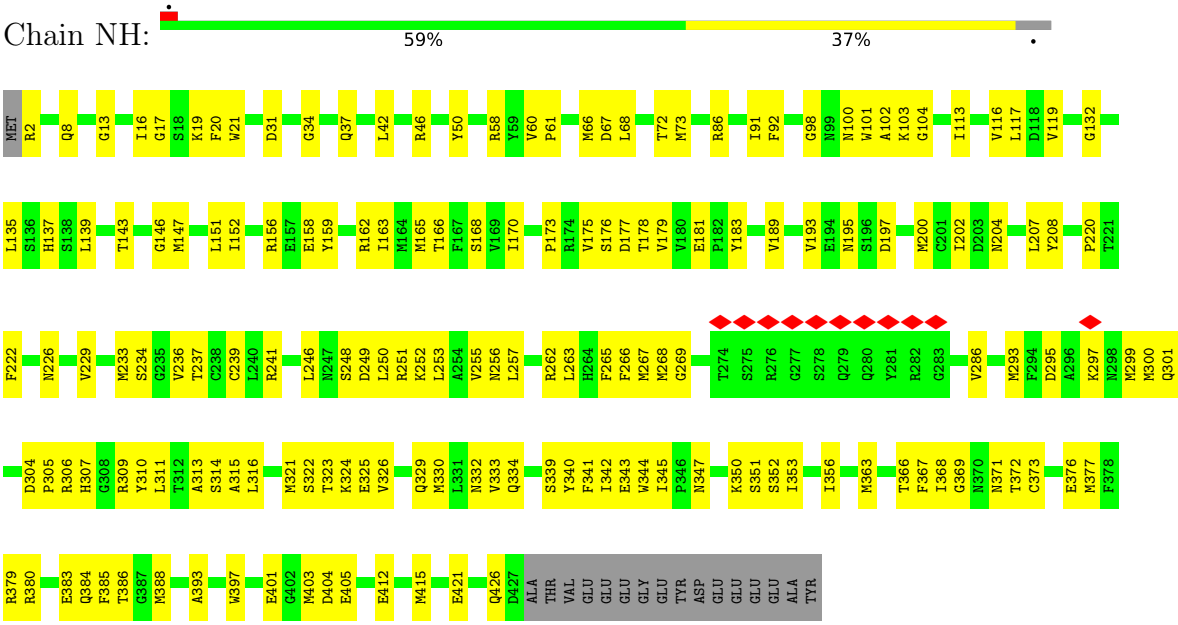


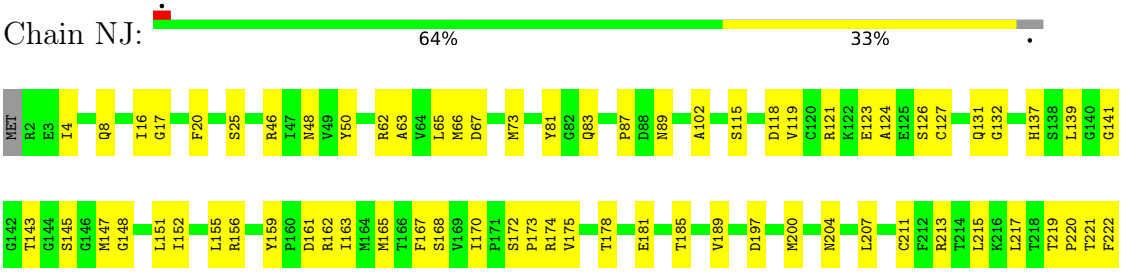
• Molecule 1: Tubulin beta chain

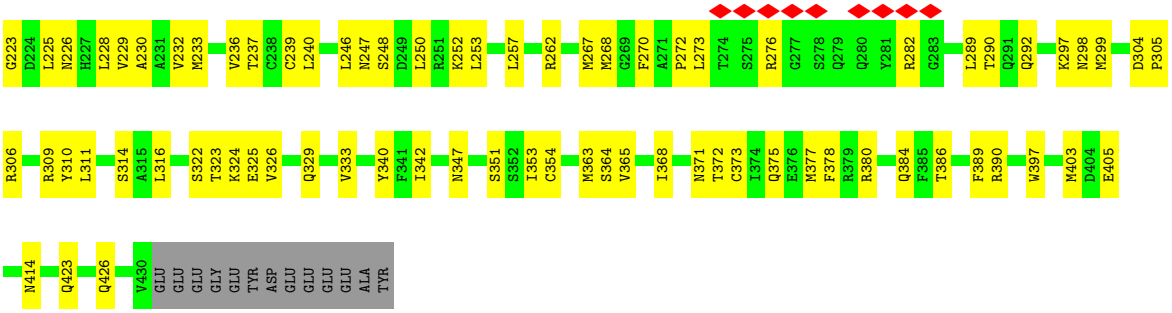
Chain NH:



• Molecule 1: Tubulin beta chain

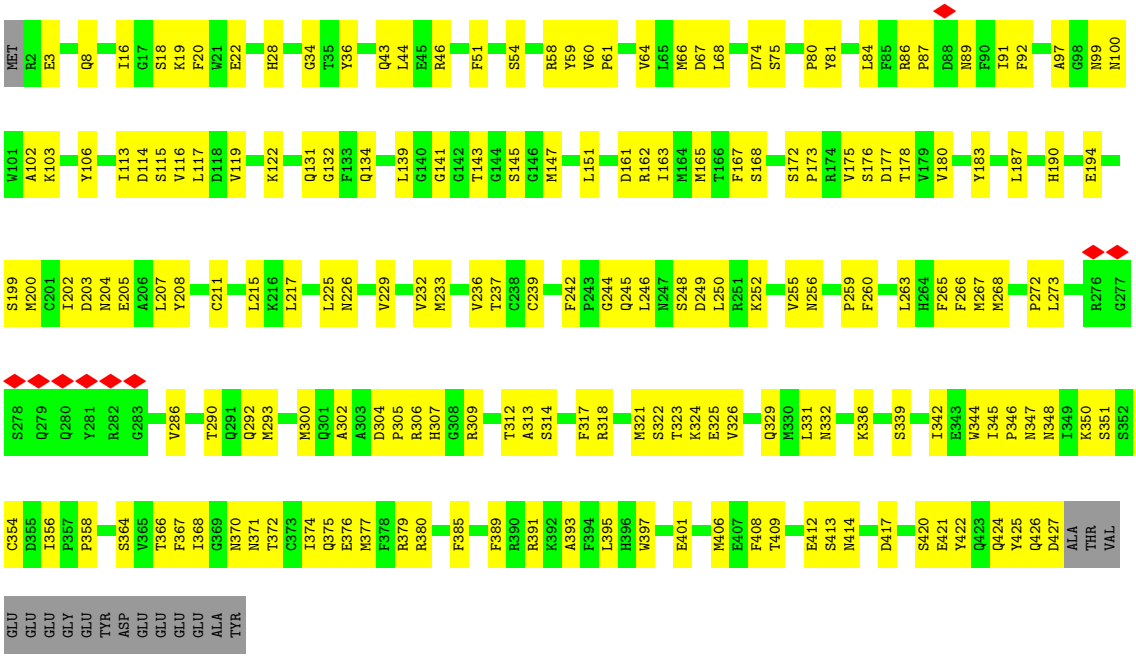
Chain NJ:





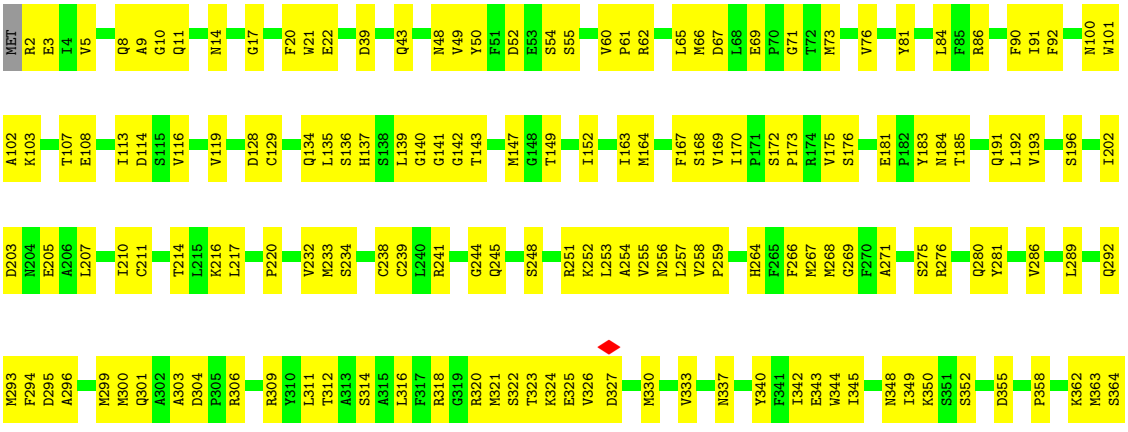
• Molecule 1: Tubulin beta chain

Chain NL:



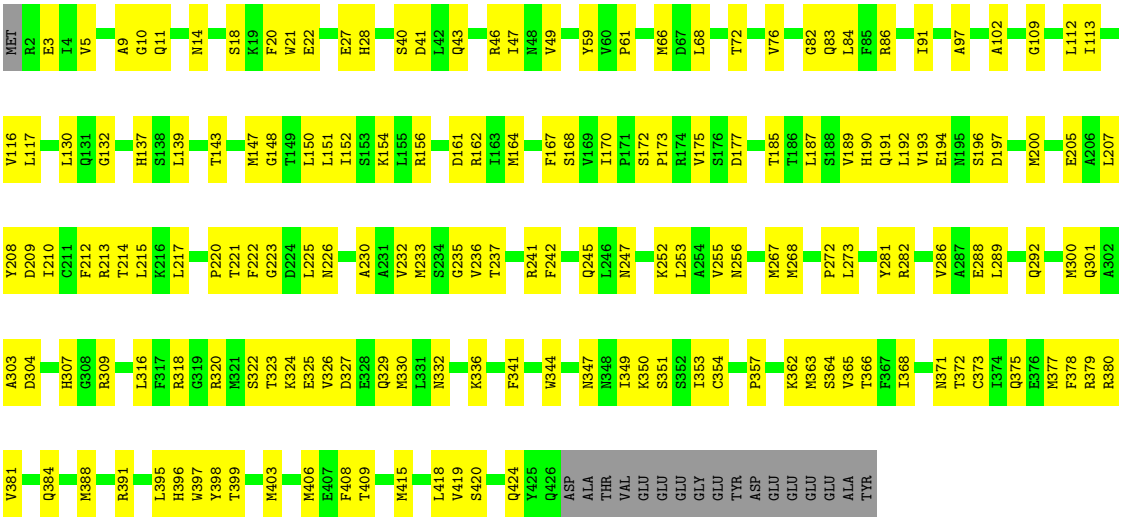
• Molecule 1: Tubulin beta chain

Chain O:



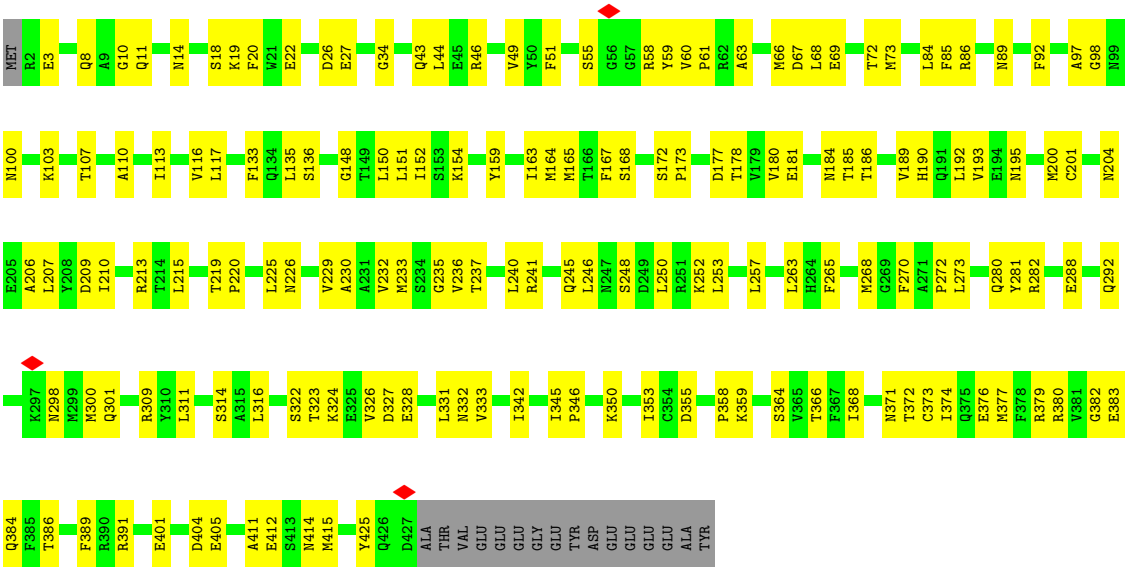
• Molecule 1: Tubulin beta chain

Chain OB:



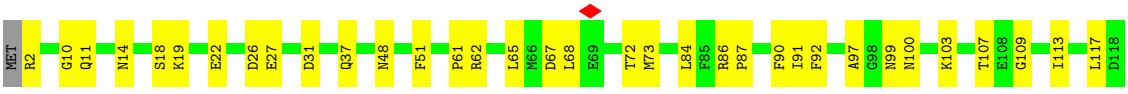
• Molecule 1: Tubulin beta chain

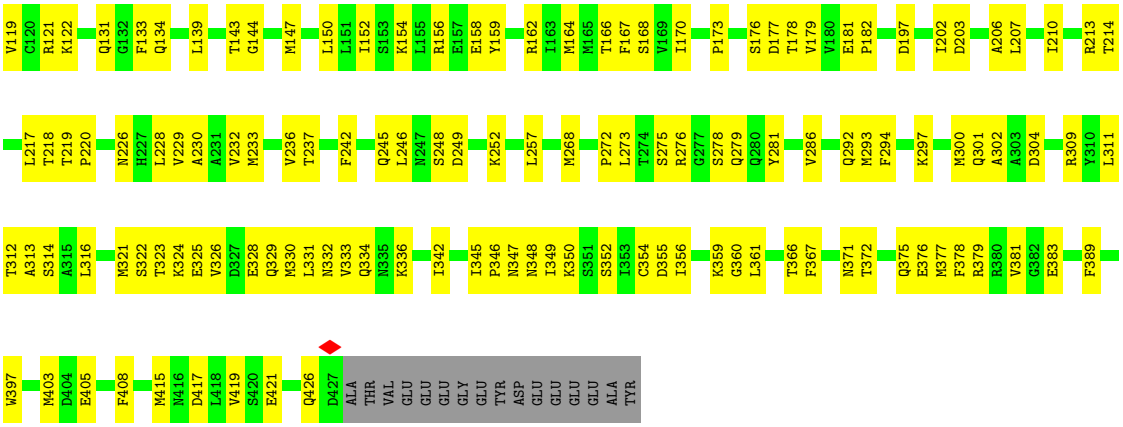
Chain OD:



• Molecule 1: Tubulin beta chain

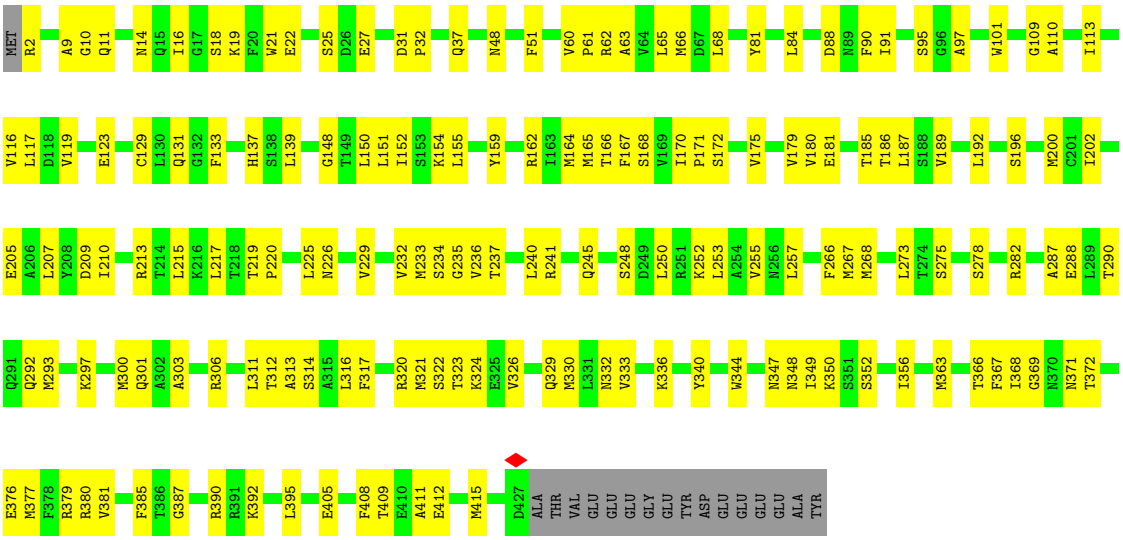
Chain OF:





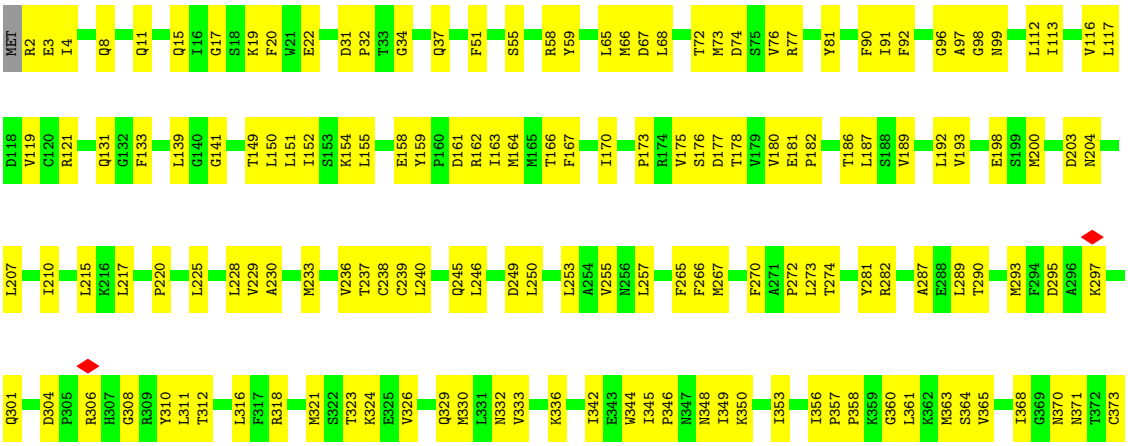
• Molecule 1: Tubulin beta chain

Chain OH:



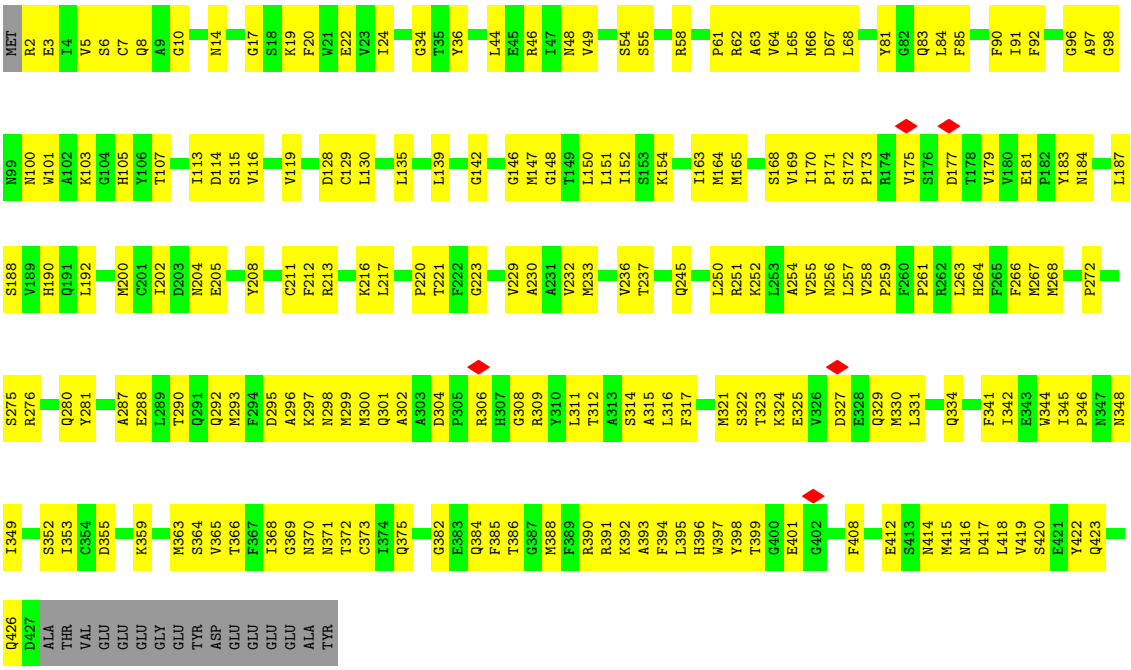
• Molecule 1: Tubulin beta chain

Chain OJ:



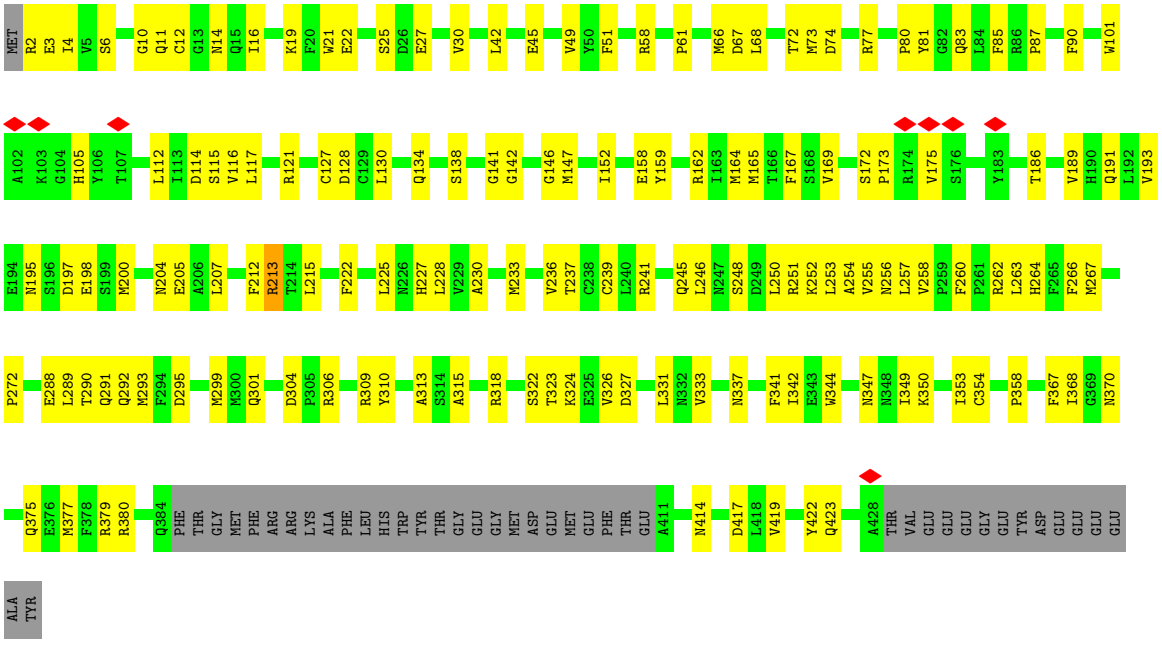
• Molecule 1: Tubulin beta chain

Chain OL:



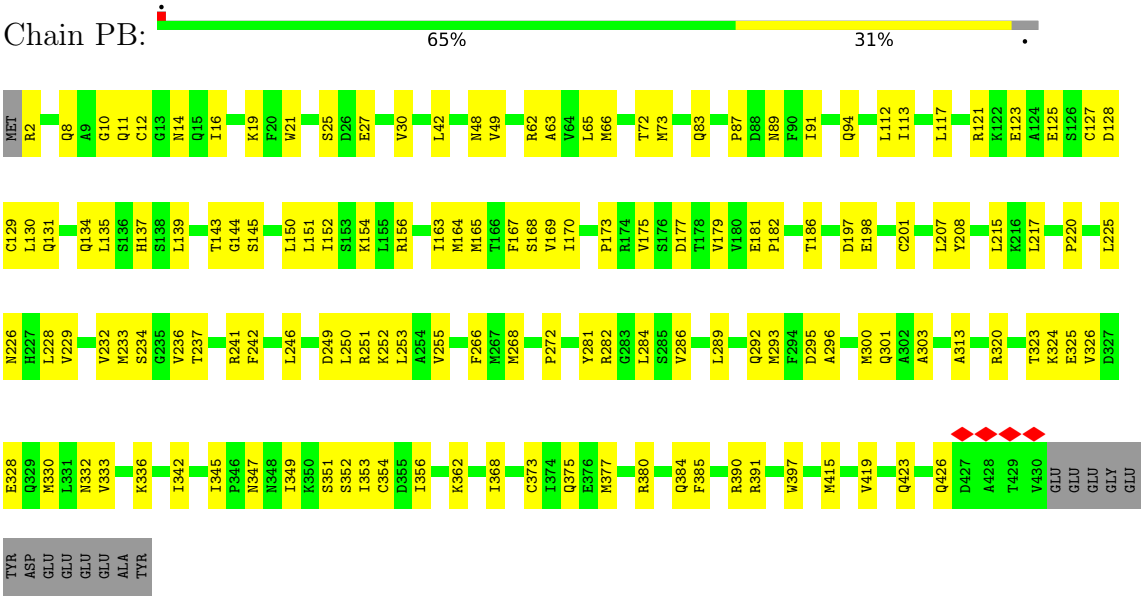
• Molecule 1: Tubulin beta chain

Chain P:



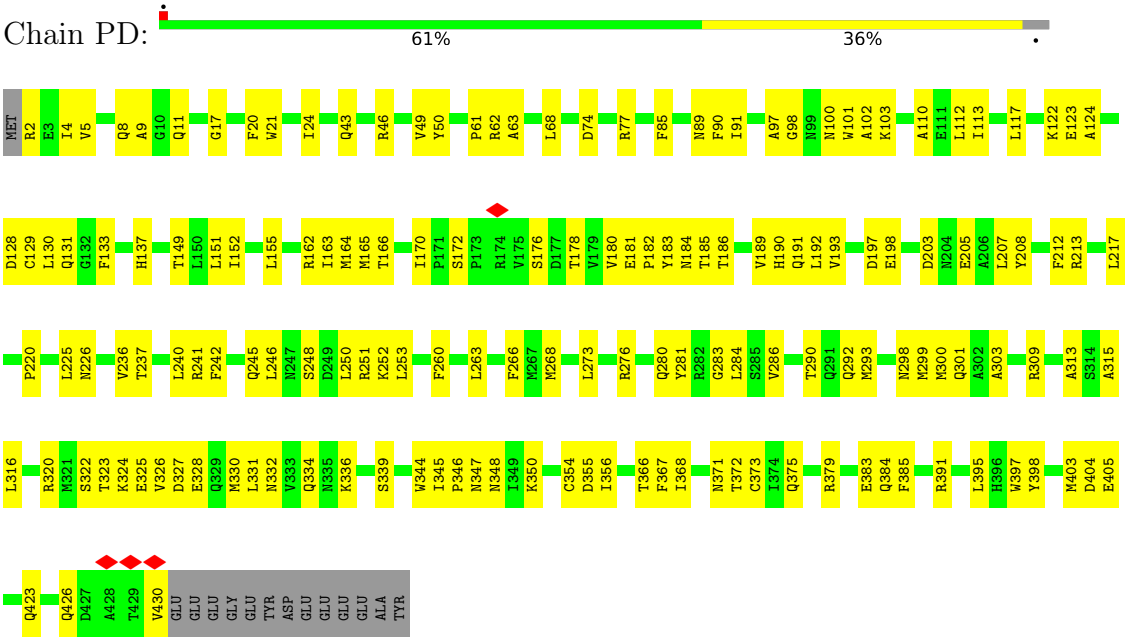
• Molecule 1: Tubulin beta chain

Chain PB:



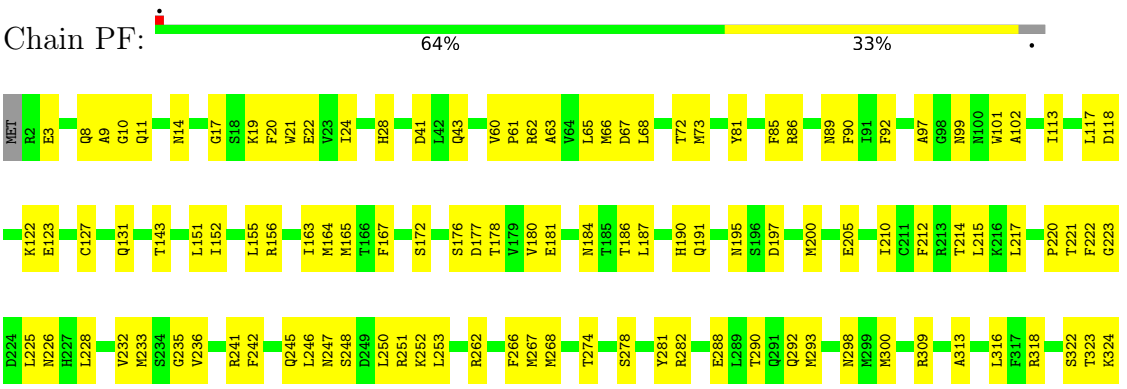
• Molecule 1: Tubulin beta chain

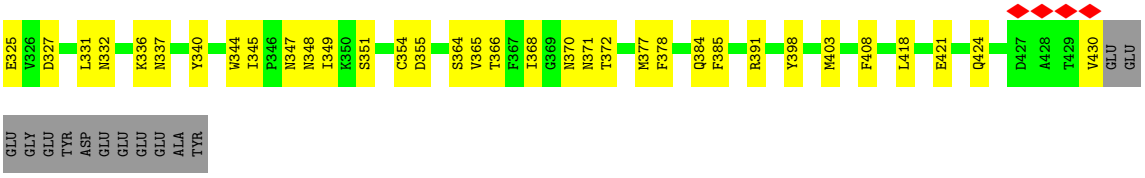
Chain PD:



• Molecule 1: Tubulin beta chain

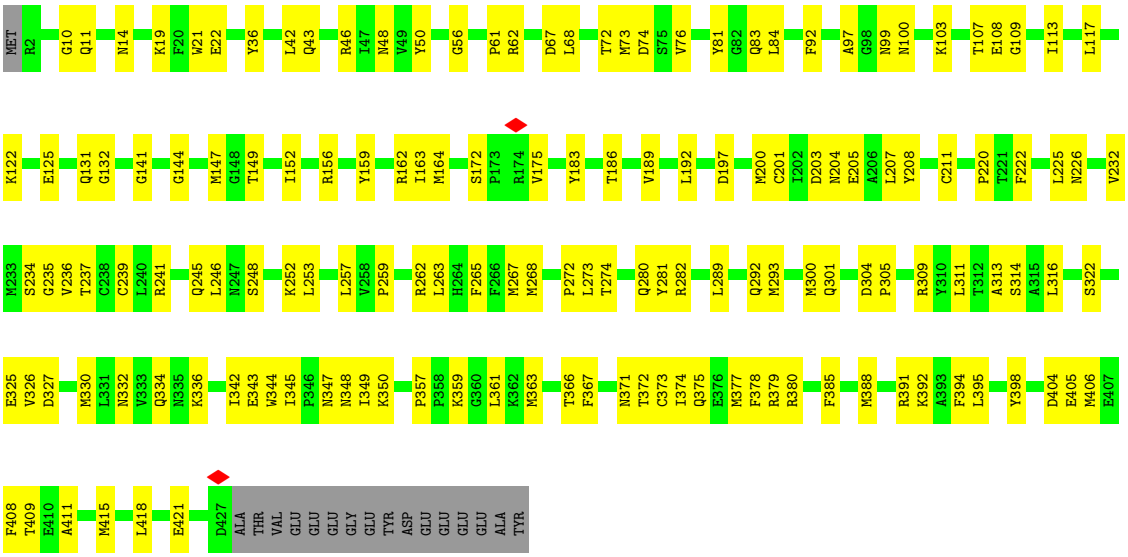
Chain PF:





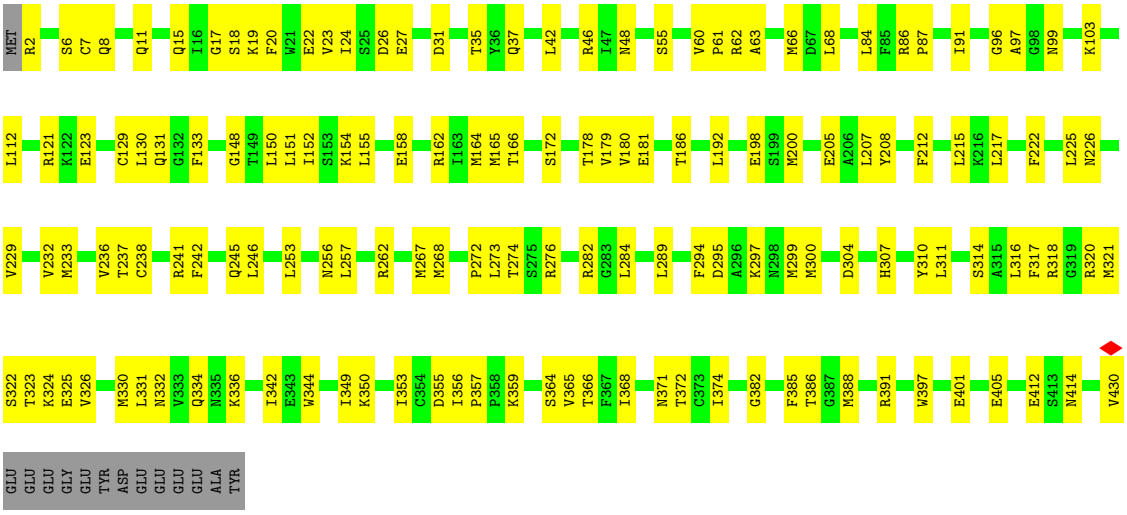
• Molecule 1: Tubulin beta chain

Chain PH:



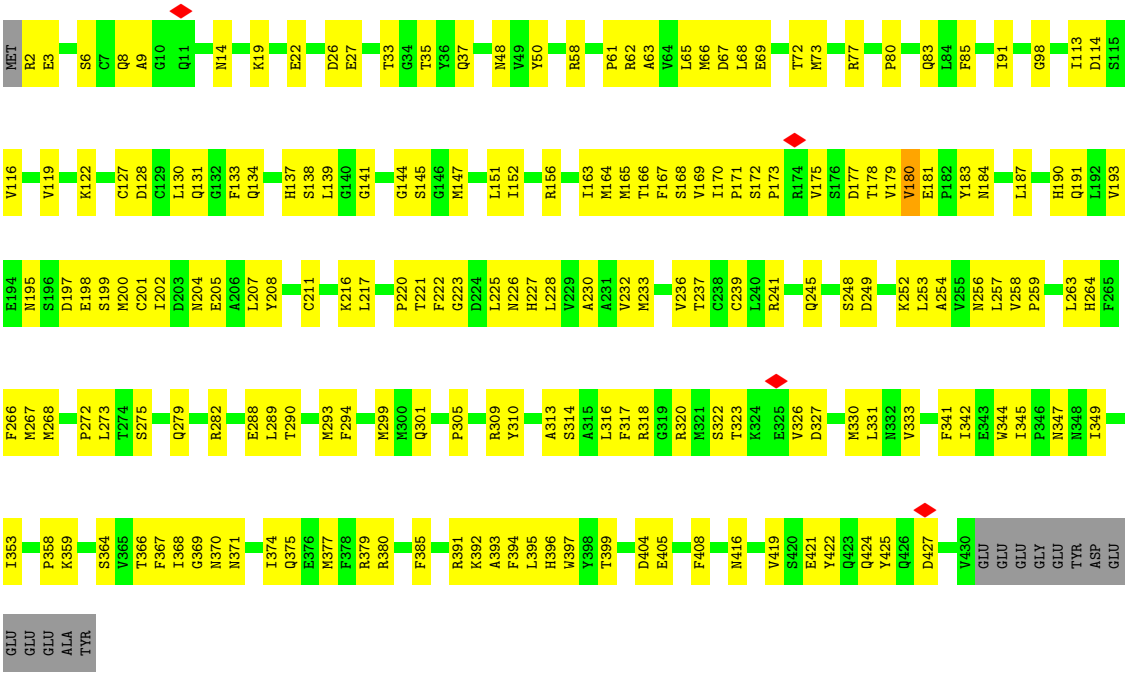
• Molecule 1: Tubulin beta chain

Chain PJ:



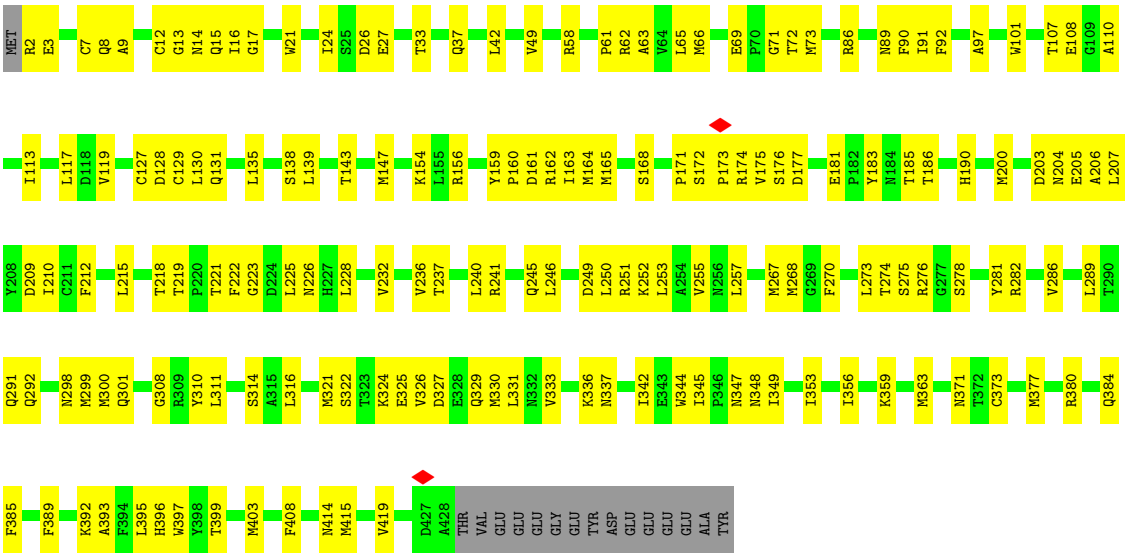
• Molecule 1: Tubulin beta chain

Chain PL:



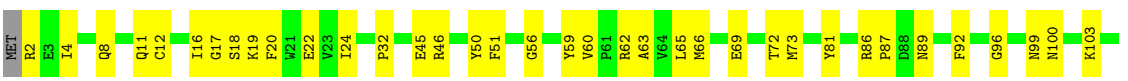
• Molecule 1: Tubulin beta chain

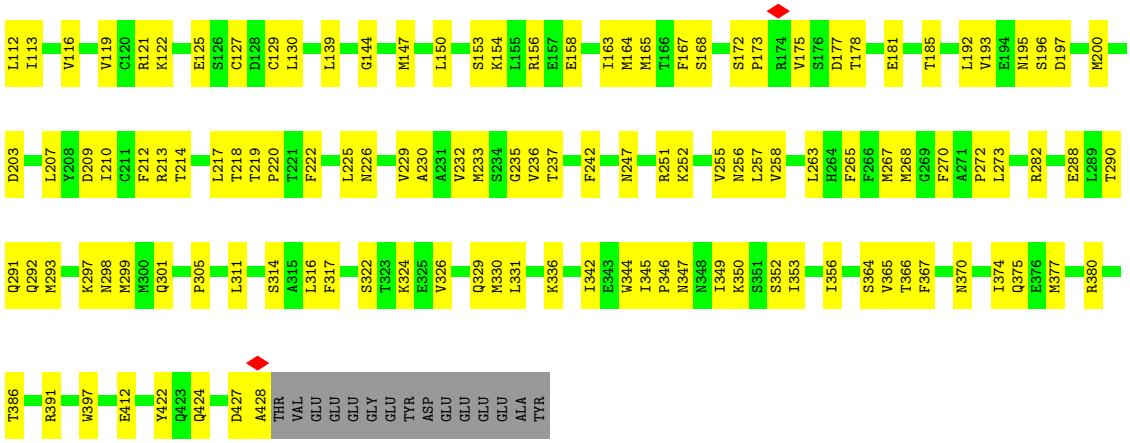
Chain QA:



• Molecule 1: Tubulin beta chain

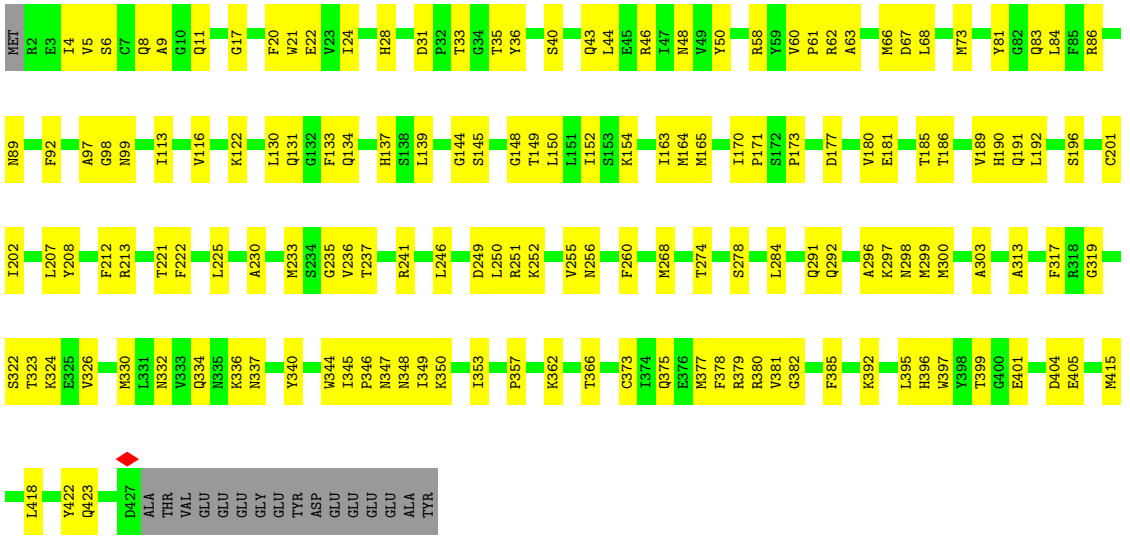
Chain QC:





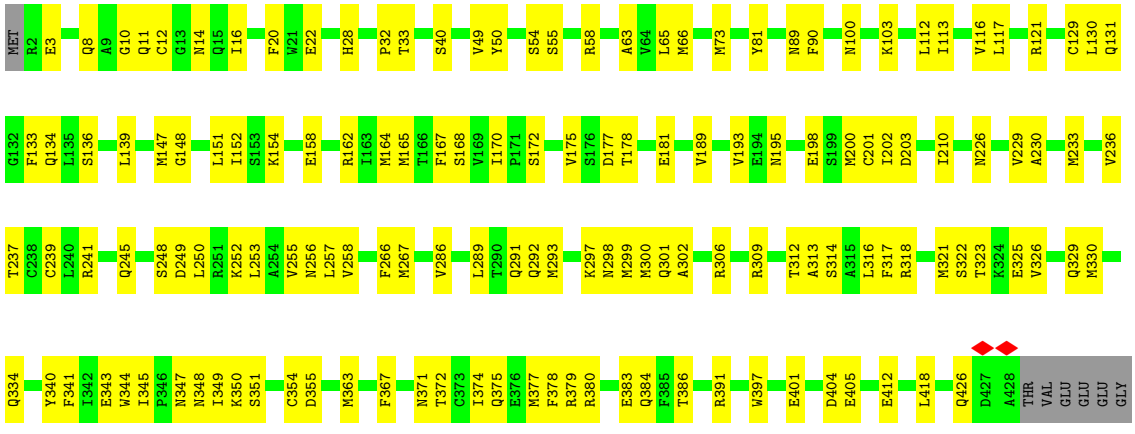
• Molecule 1: Tubulin beta chain

Chain QE:



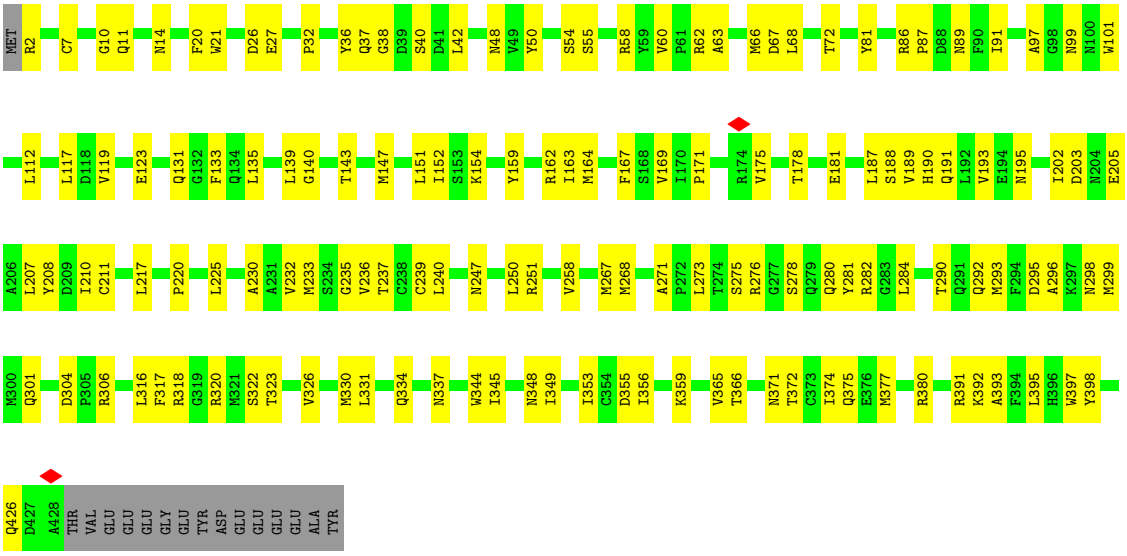
• Molecule 1: Tubulin beta chain

Chain QG:



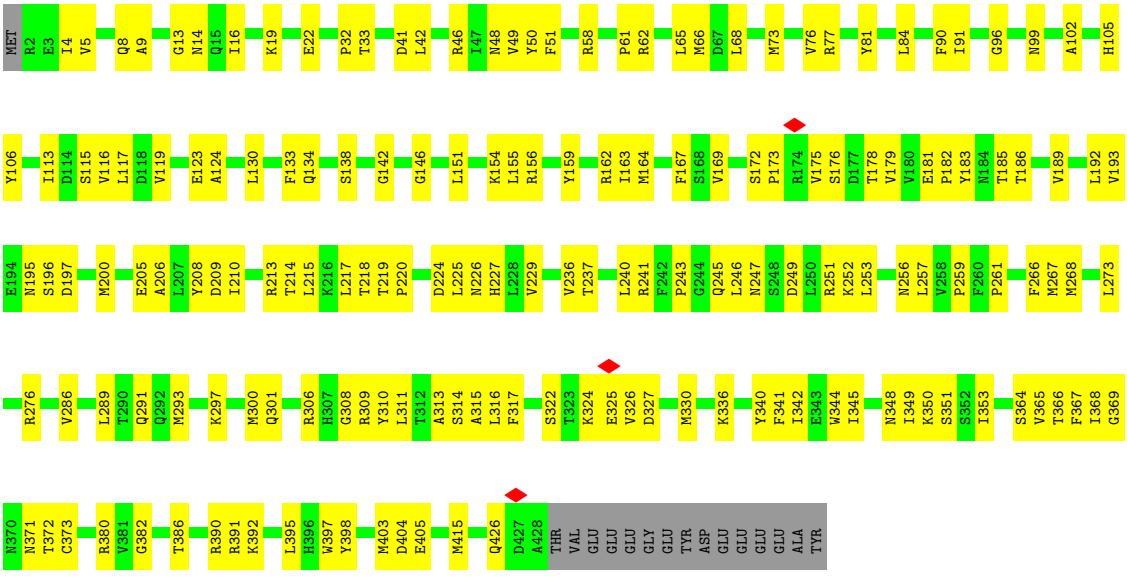
• Molecule 1: Tubulin beta chain

Chain QI:



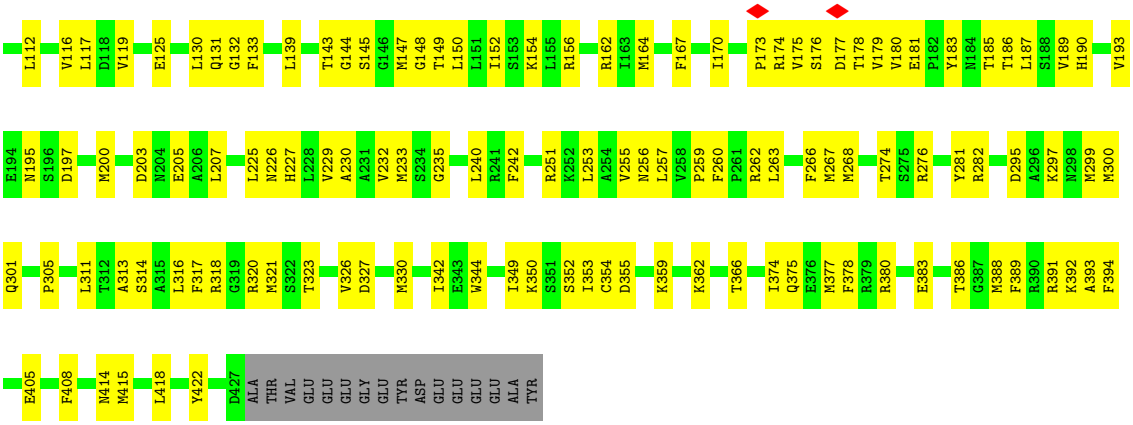
• Molecule 1: Tubulin beta chain

Chain QK:



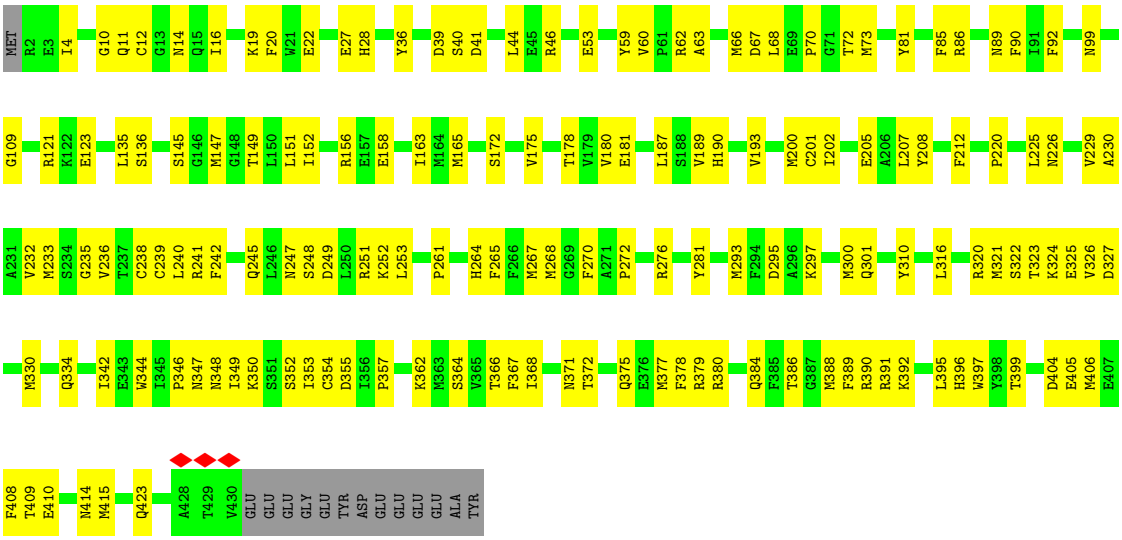
• Molecule 1: Tubulin beta chain

Chain RA:



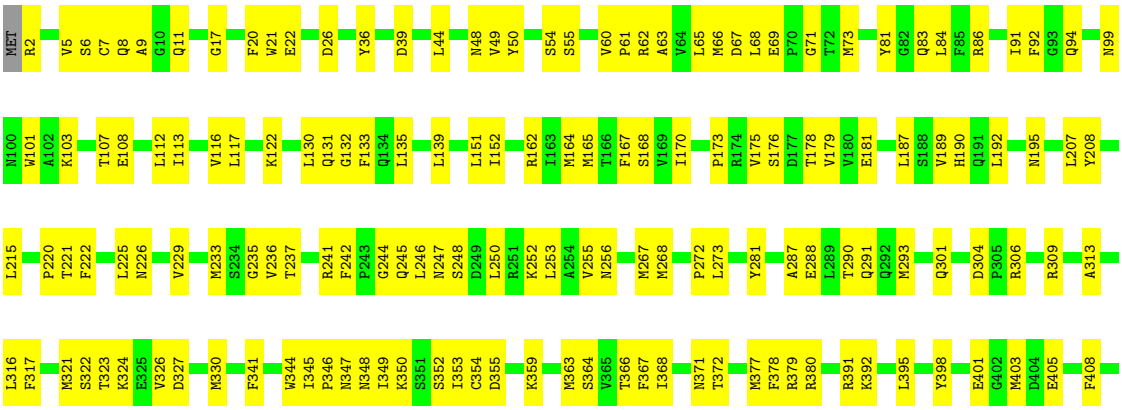
• Molecule 1: Tubulin beta chain

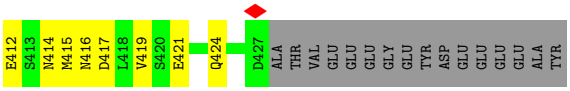
Chain RC:



• Molecule 1: Tubulin beta chain

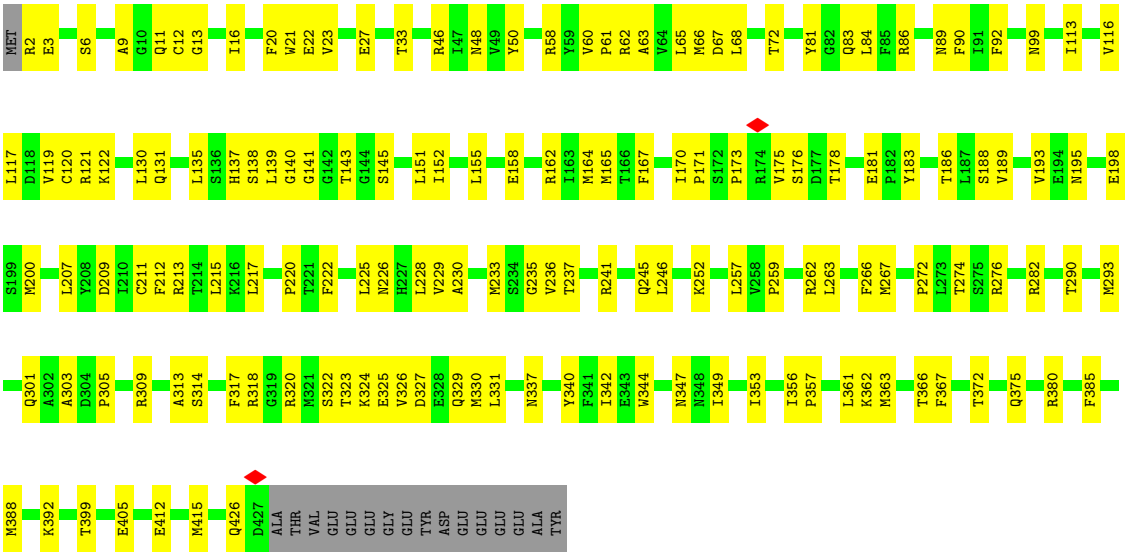
Chain RE:





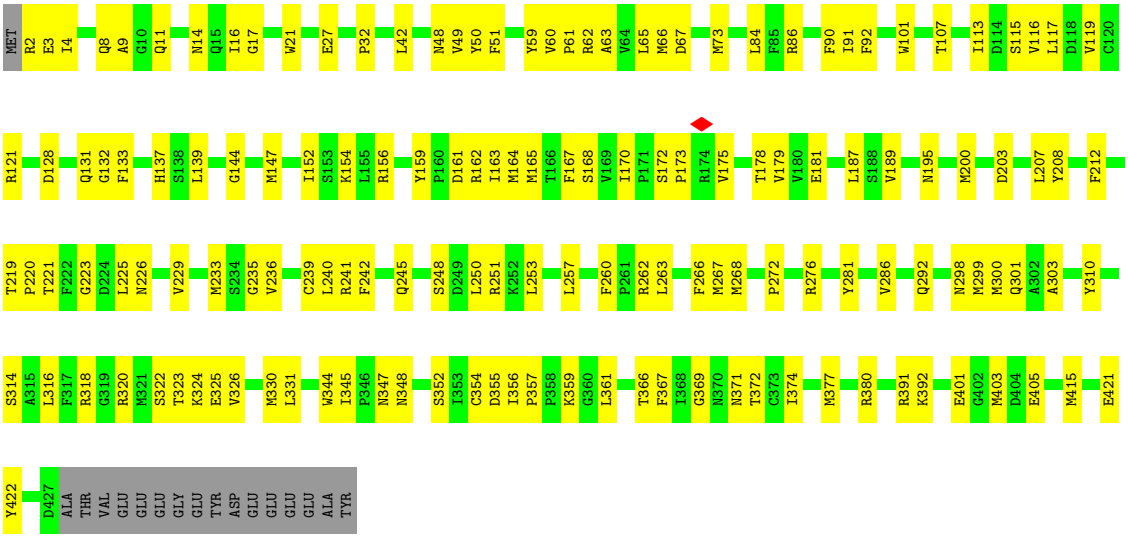
• Molecule 1: Tubulin beta chain

Chain RG:



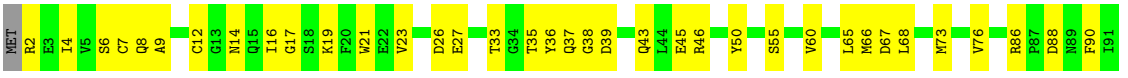
• Molecule 1: Tubulin beta chain

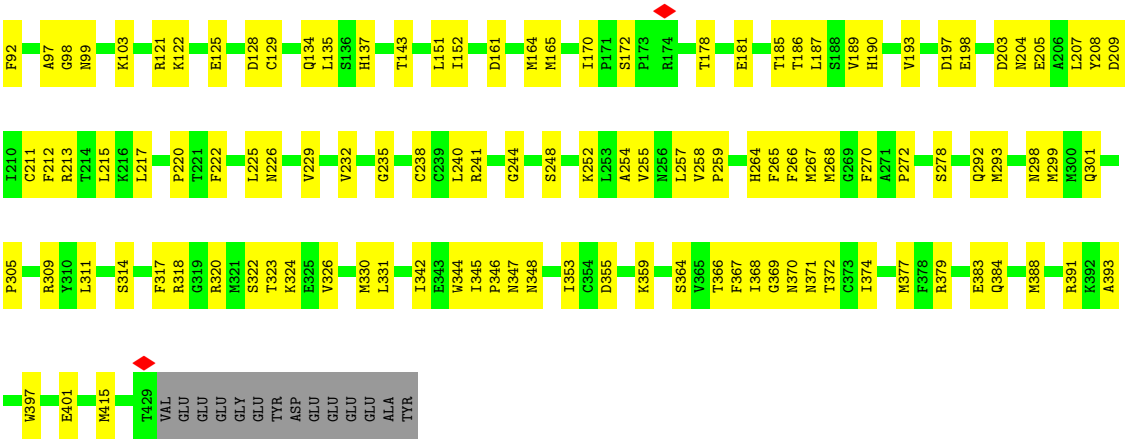
Chain RI:



• Molecule 1: Tubulin beta chain

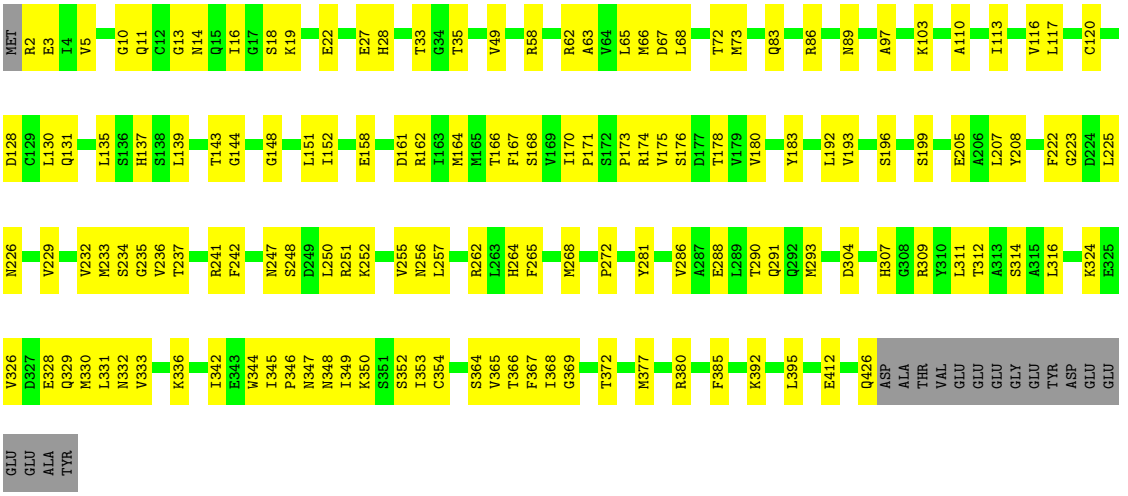
Chain RK:





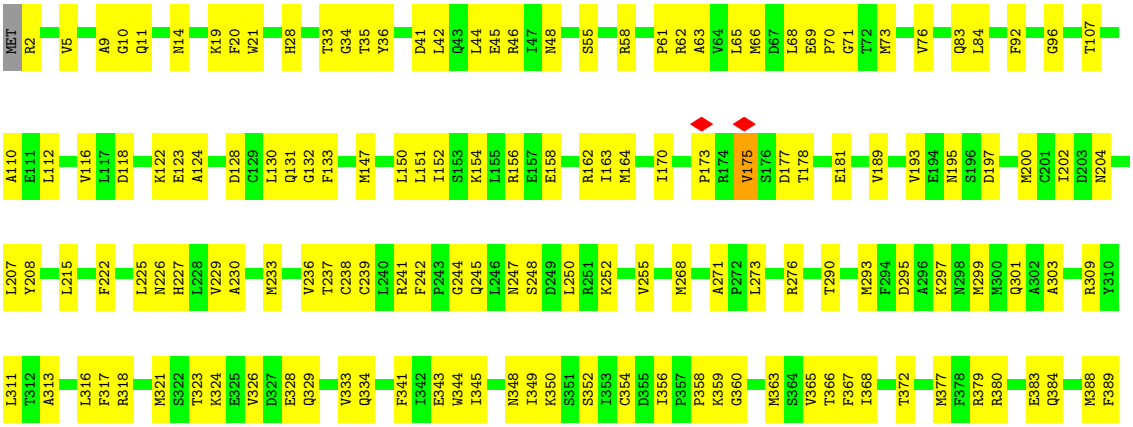
• Molecule 1: Tubulin beta chain

Chain S:



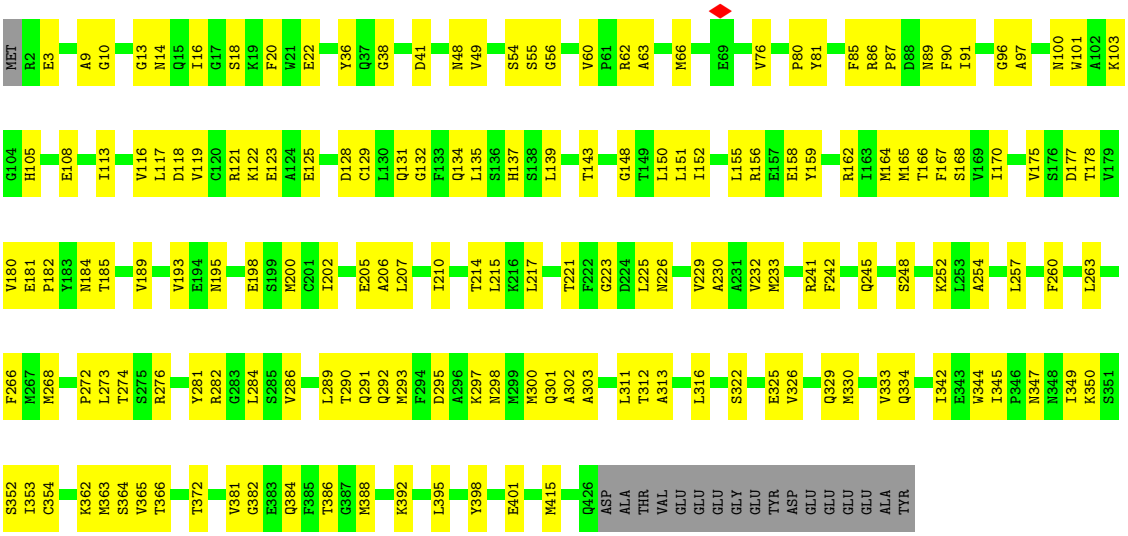
• Molecule 1: Tubulin beta chain

Chain SB:



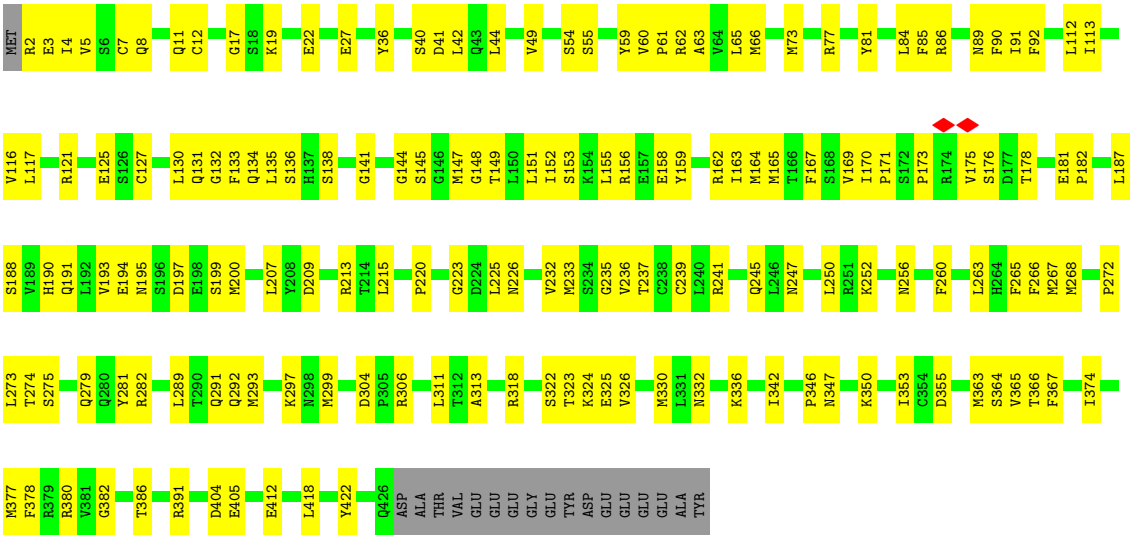
• Molecule 1: Tubulin beta chain

Chain SD:



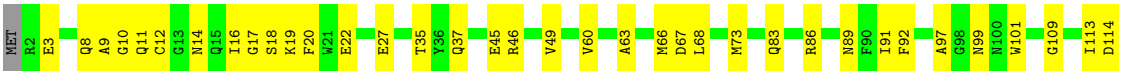
• Molecule 1: Tubulin beta chain

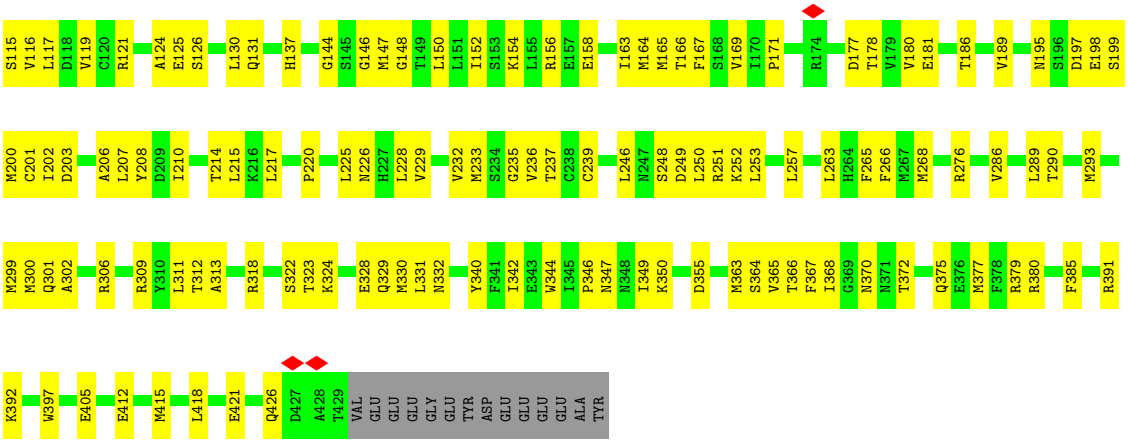
Chain SF:



• Molecule 1: Tubulin beta chain

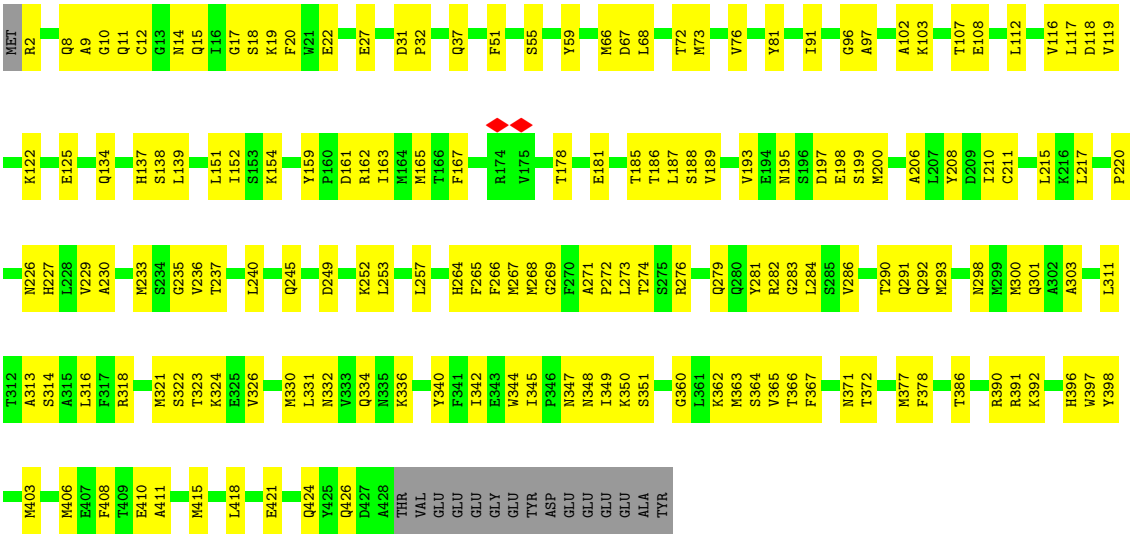
Chain SH:





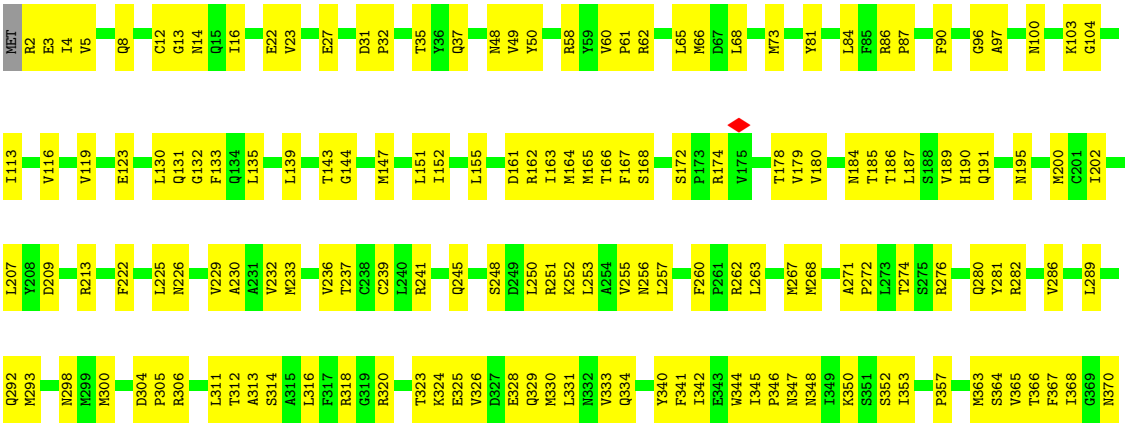
• Molecule 1: Tubulin beta chain

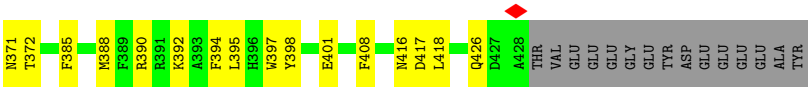
Chain SJ:



• Molecule 1: Tubulin beta chain

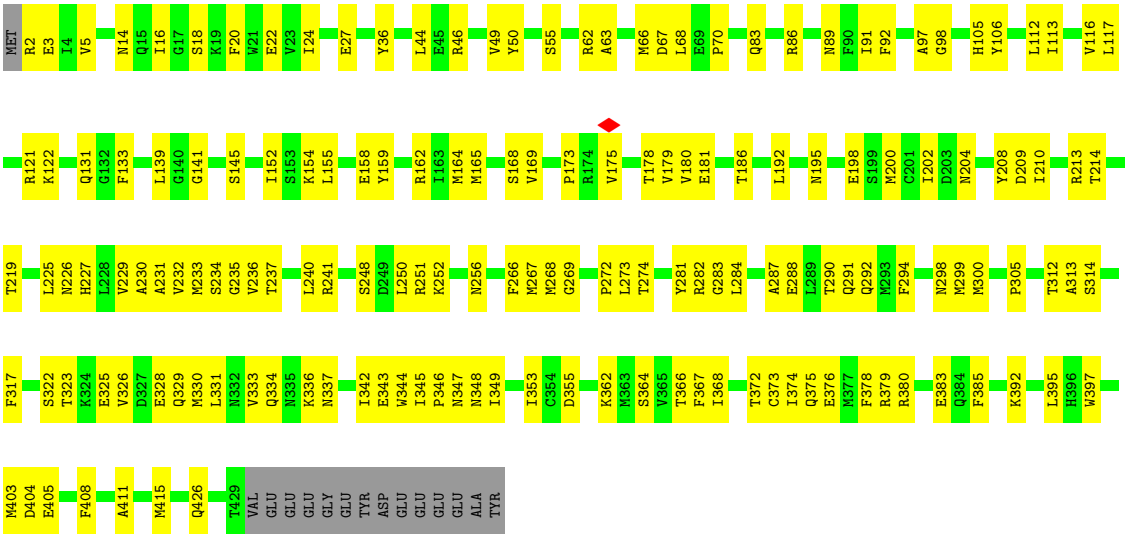
Chain T:





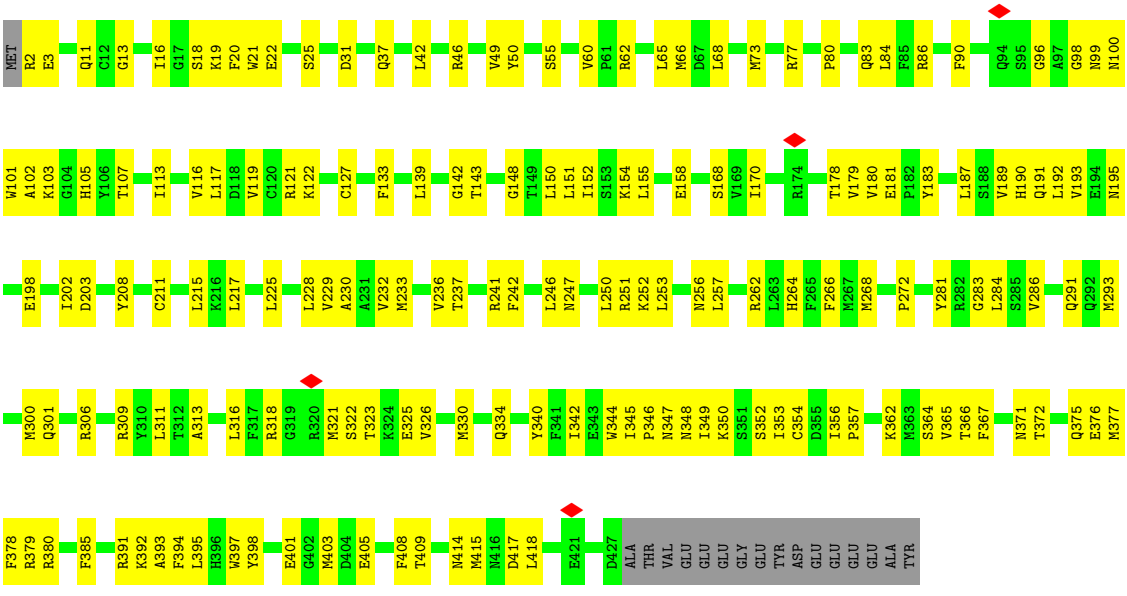
• Molecule 1: Tubulin beta chain

Chain TB:



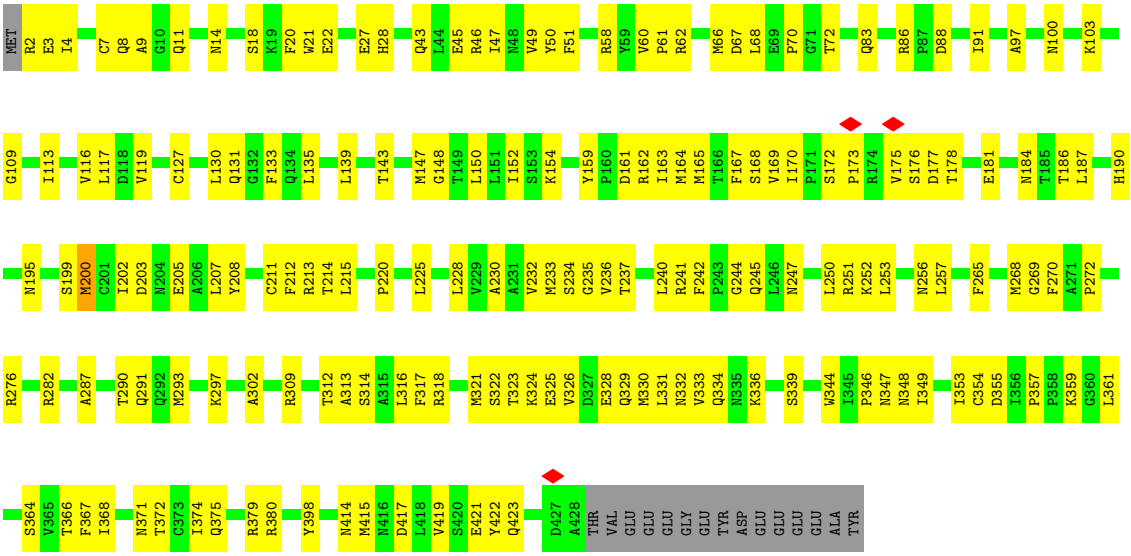
• Molecule 1: Tubulin beta chain

Chain TD:



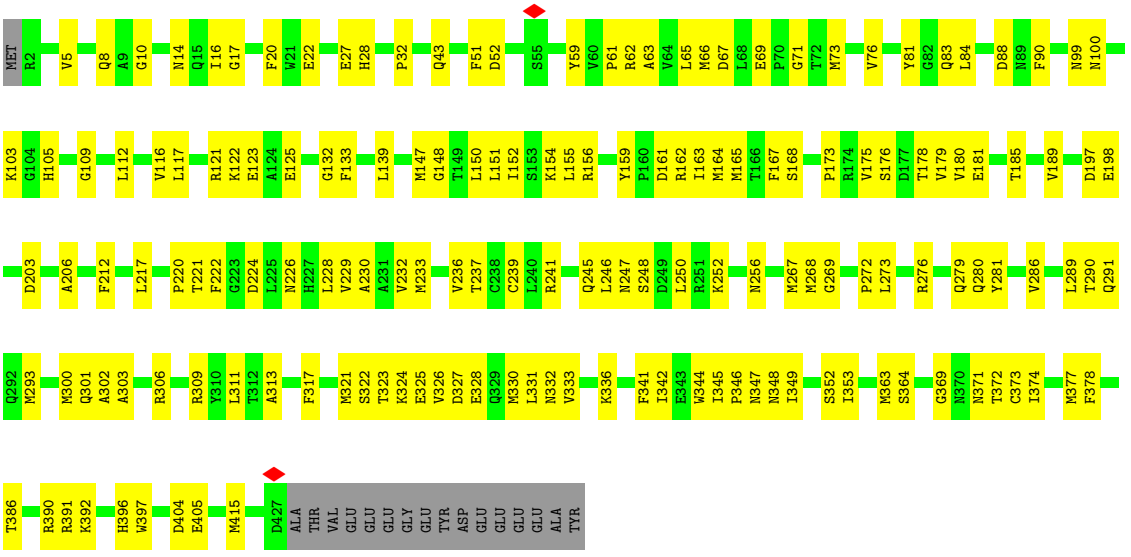
• Molecule 1: Tubulin beta chain

Chain TF:



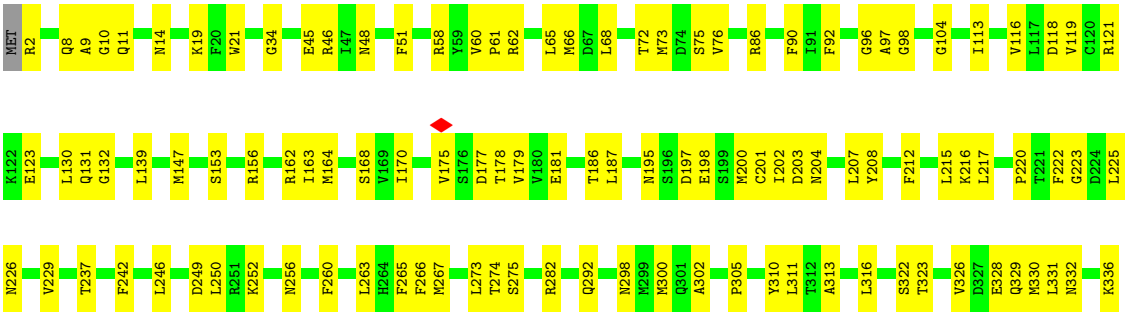
• Molecule 1: Tubulin beta chain

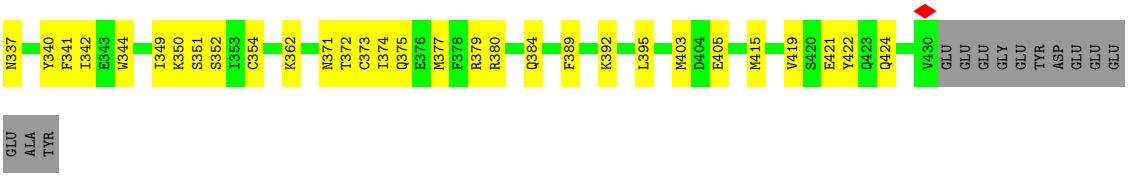
Chain TH:



• Molecule 1: Tubulin beta chain

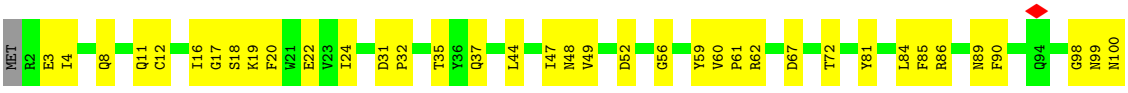
Chain TJ:

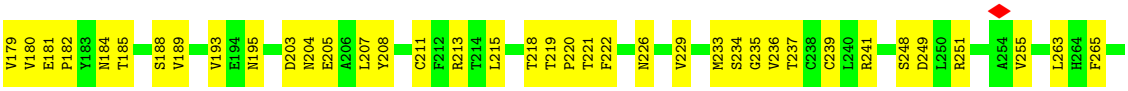


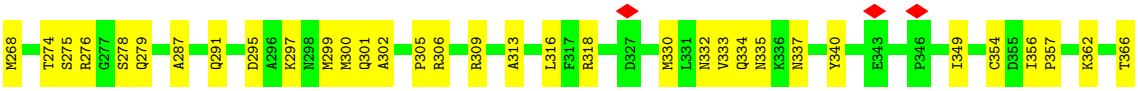


• Molecule 1: Tubulin beta chain

Chain TL:

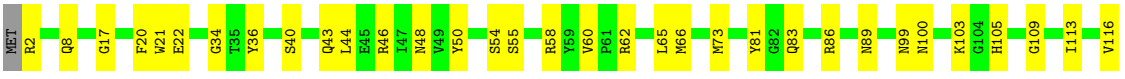


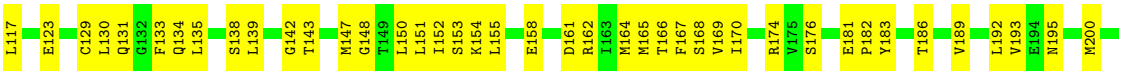


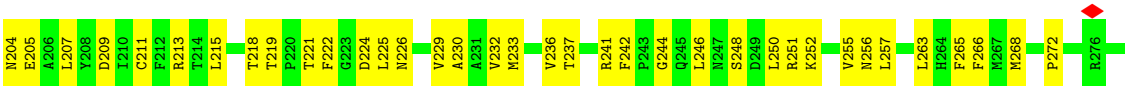


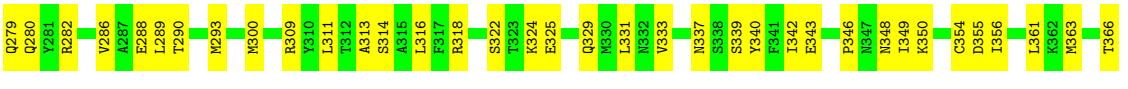
• Molecule 1: Tubulin beta chain

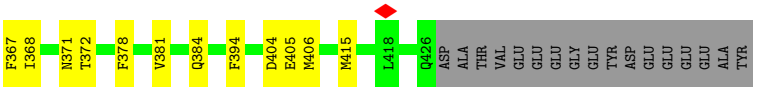
Chain U:





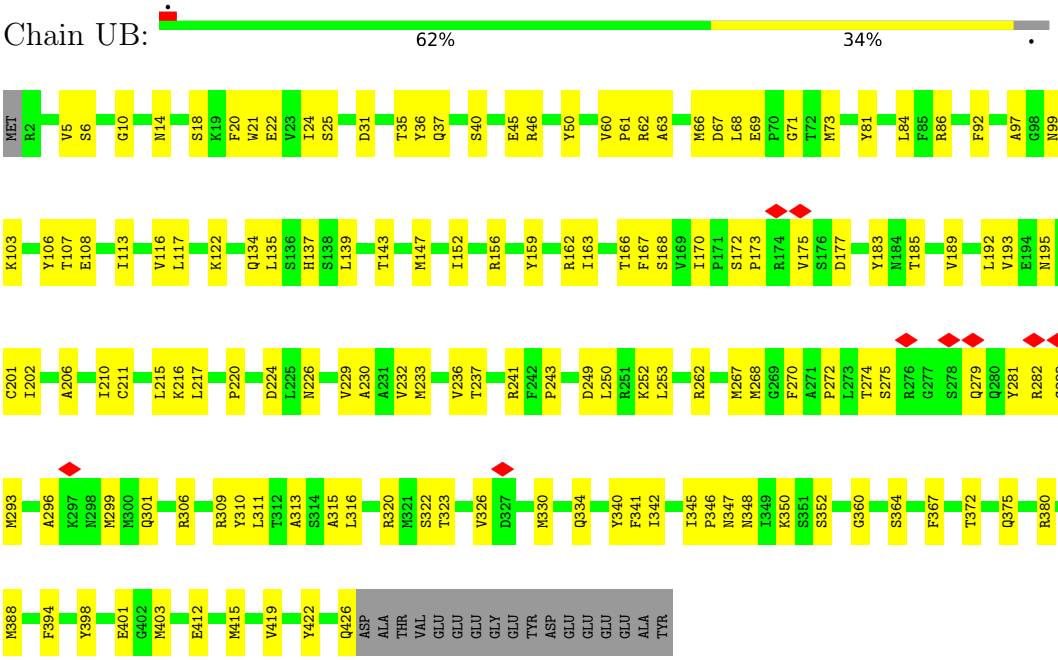






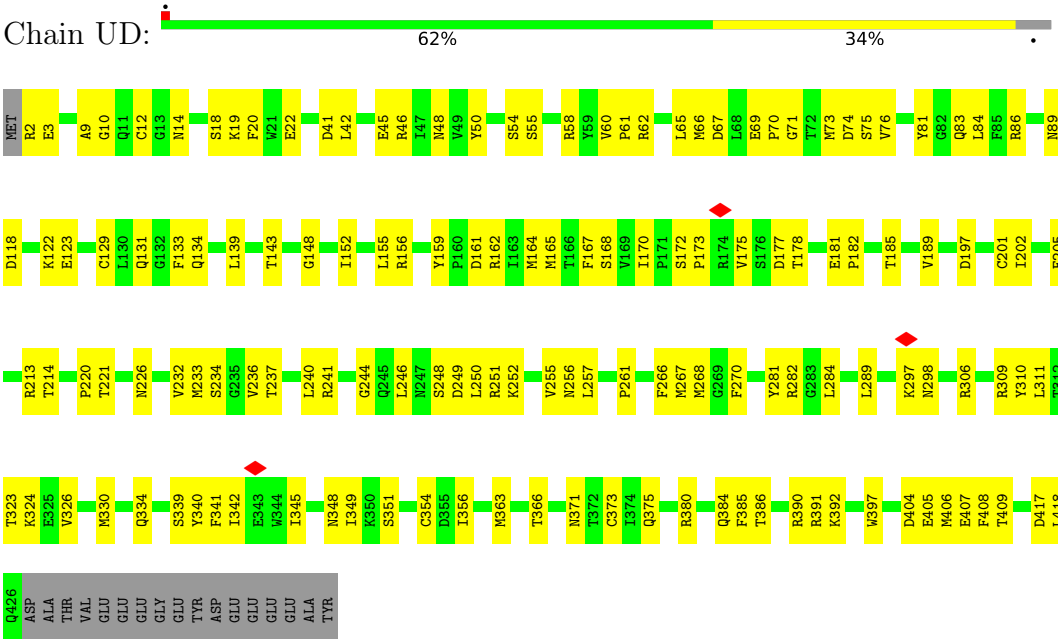
• Molecule 1: Tubulin beta chain

Chain UB:



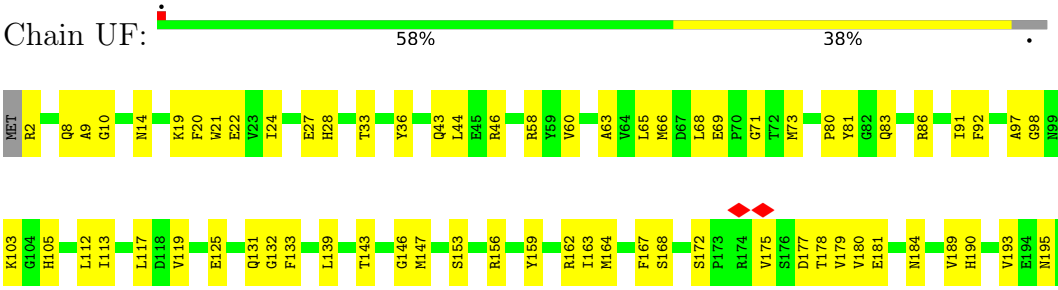
• Molecule 1: Tubulin beta chain

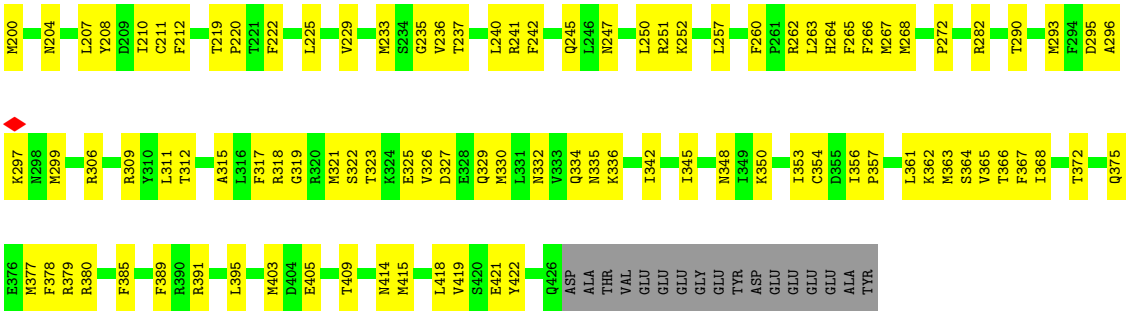
Chain UD:



• Molecule 1: Tubulin beta chain

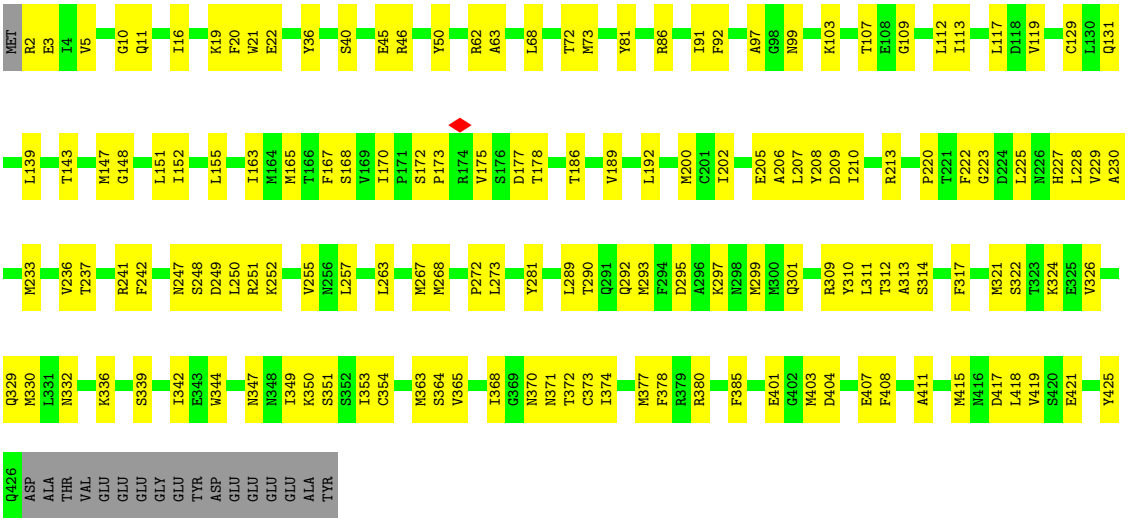
Chain UF:





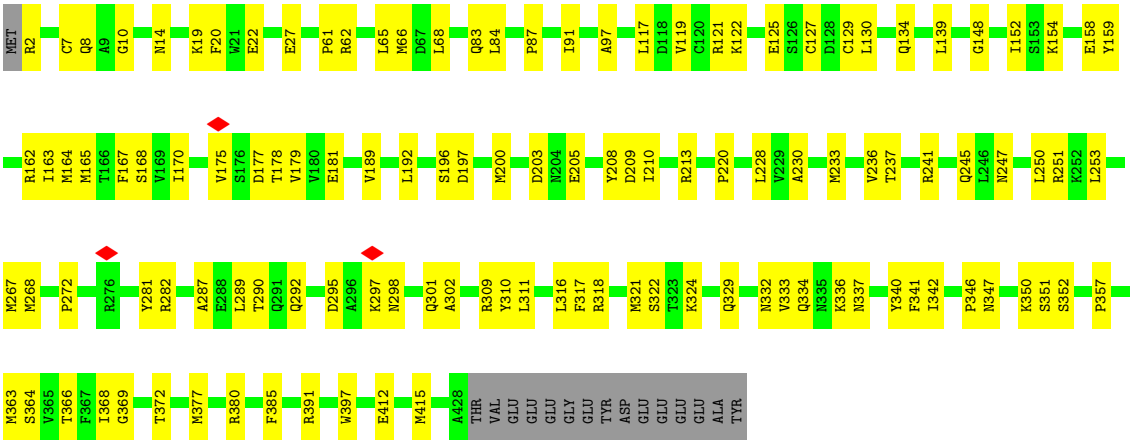
• Molecule 1: Tubulin beta chain

Chain UH:



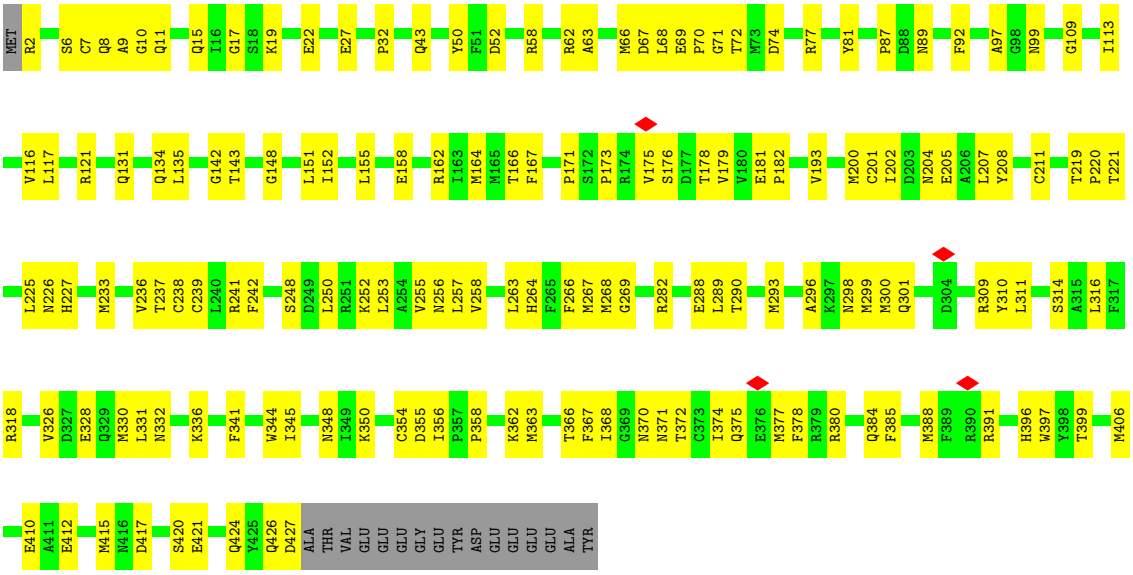
• Molecule 1: Tubulin beta chain

Chain UJ:



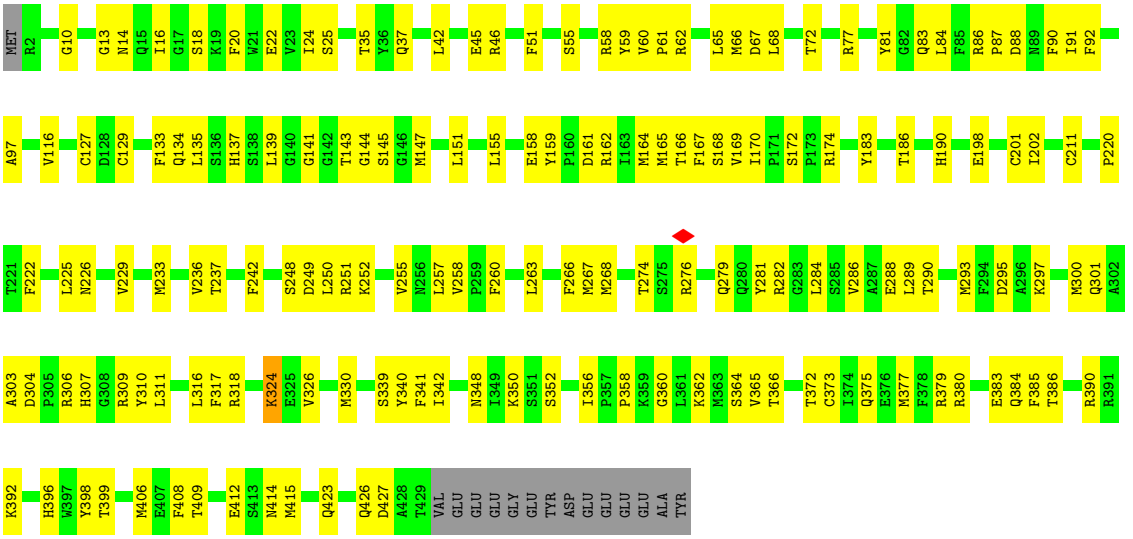
• Molecule 1: Tubulin beta chain

Chain UL:



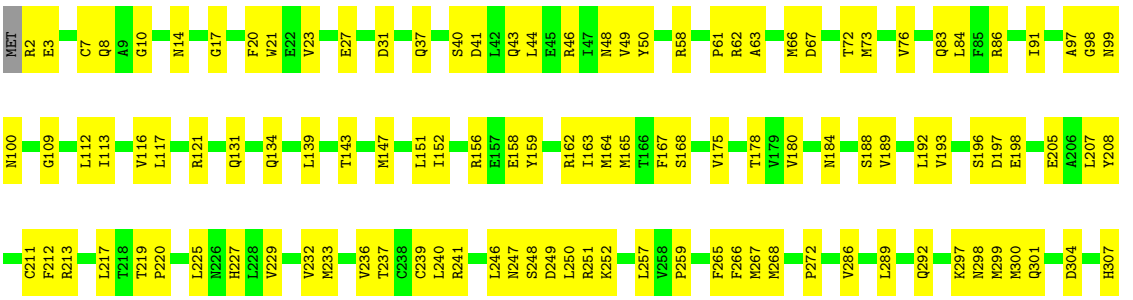
• Molecule 1: Tubulin beta chain

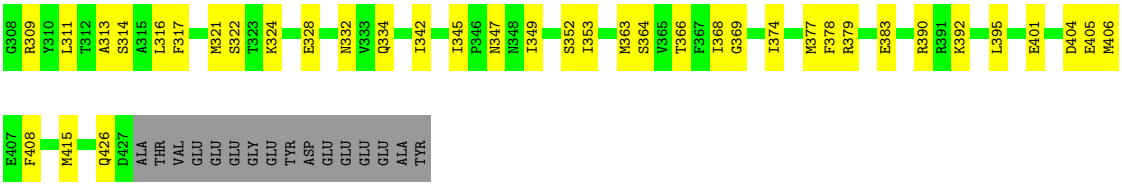
Chain V:



• Molecule 1: Tubulin beta chain

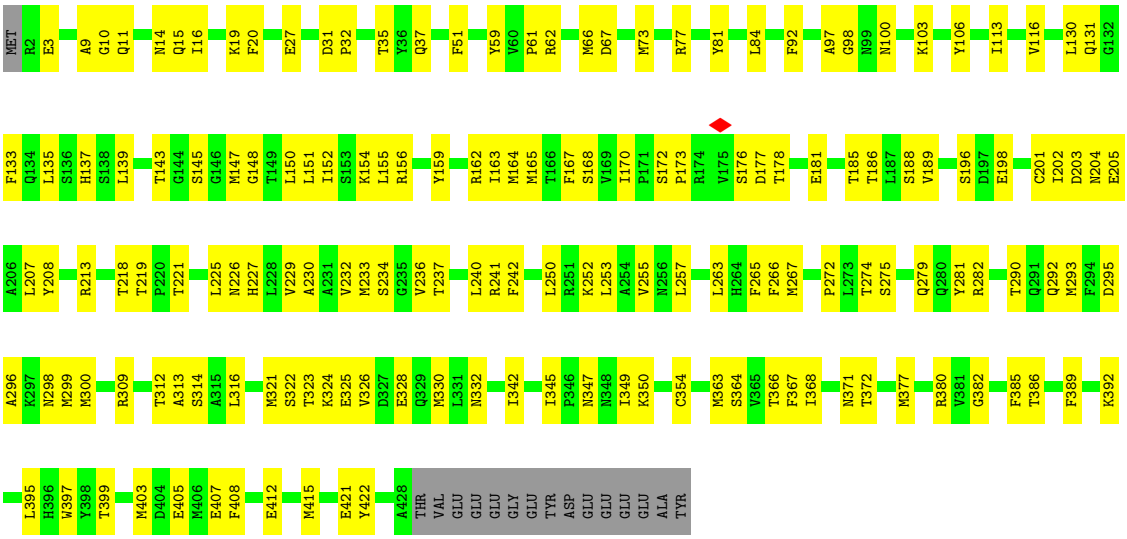
Chain VB:





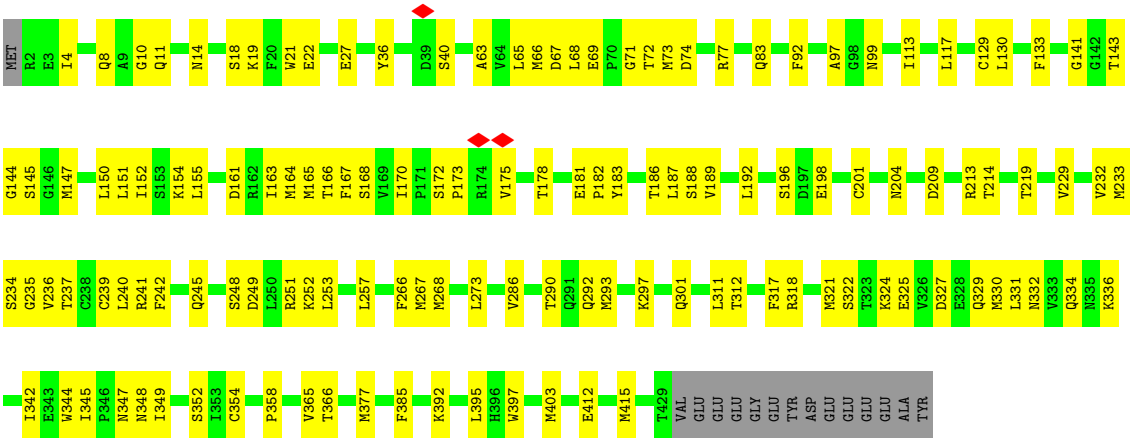
• Molecule 1: Tubulin beta chain

Chain VD:



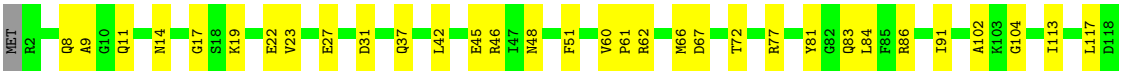
• Molecule 1: Tubulin beta chain

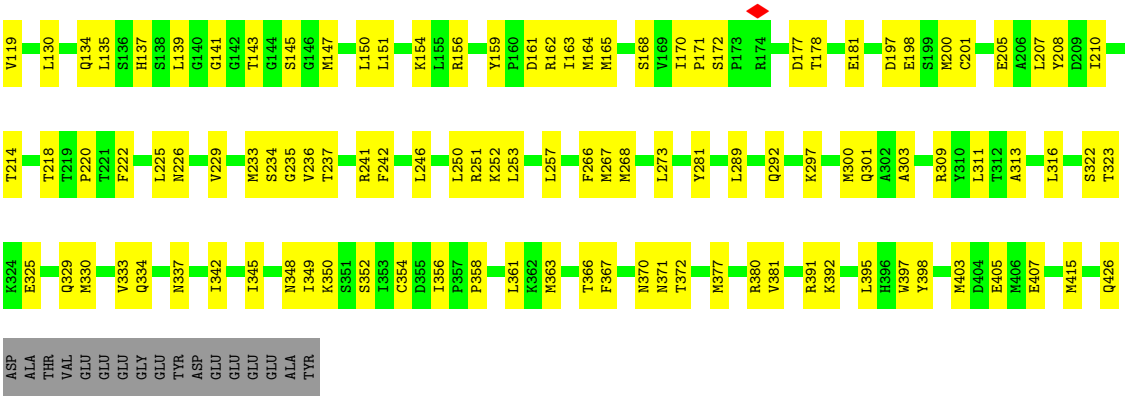
Chain VF:



• Molecule 1: Tubulin beta chain

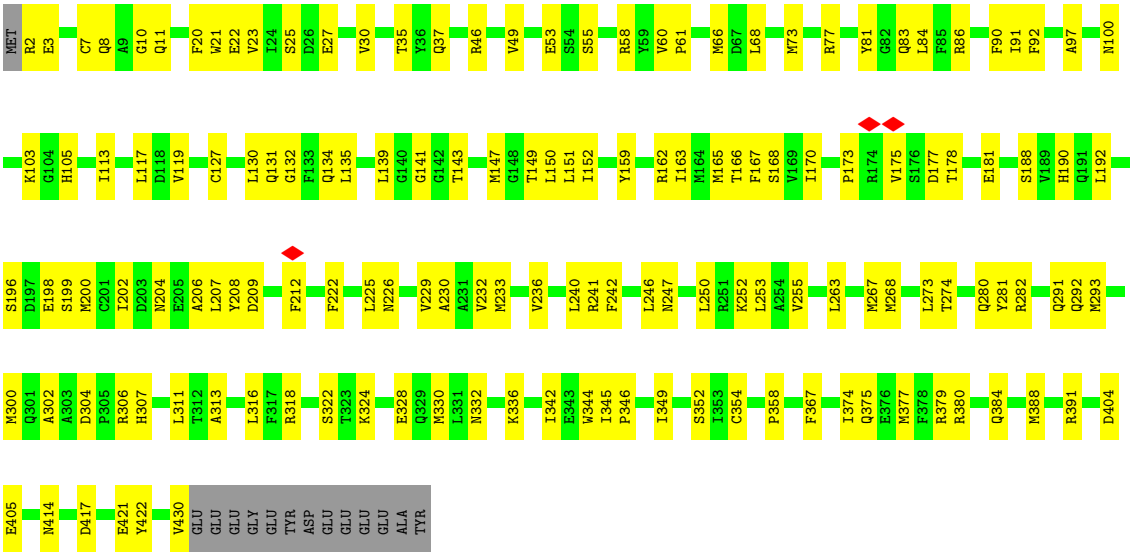
Chain VH:





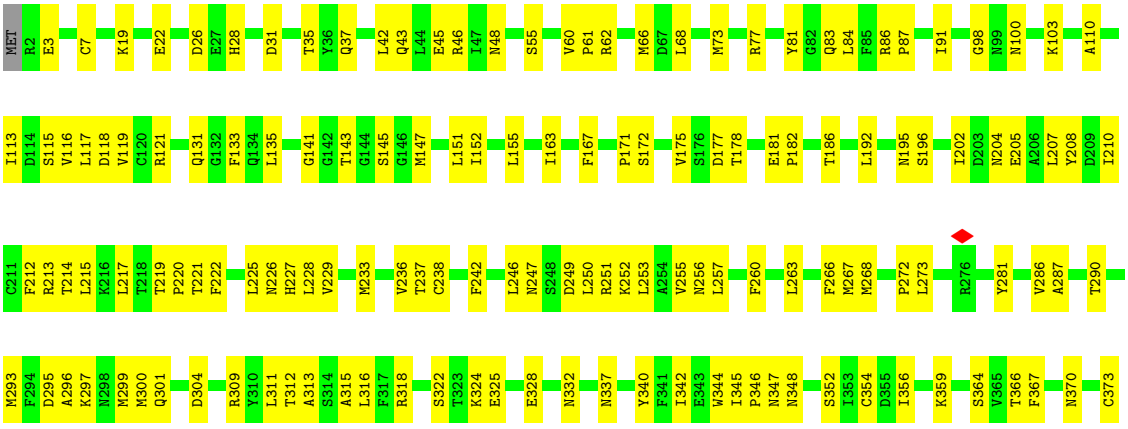
• Molecule 1: Tubulin beta chain

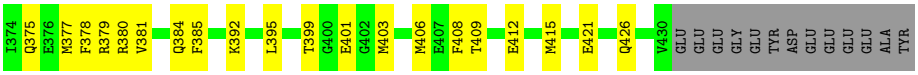
Chain VJ:



• Molecule 1: Tubulin beta chain

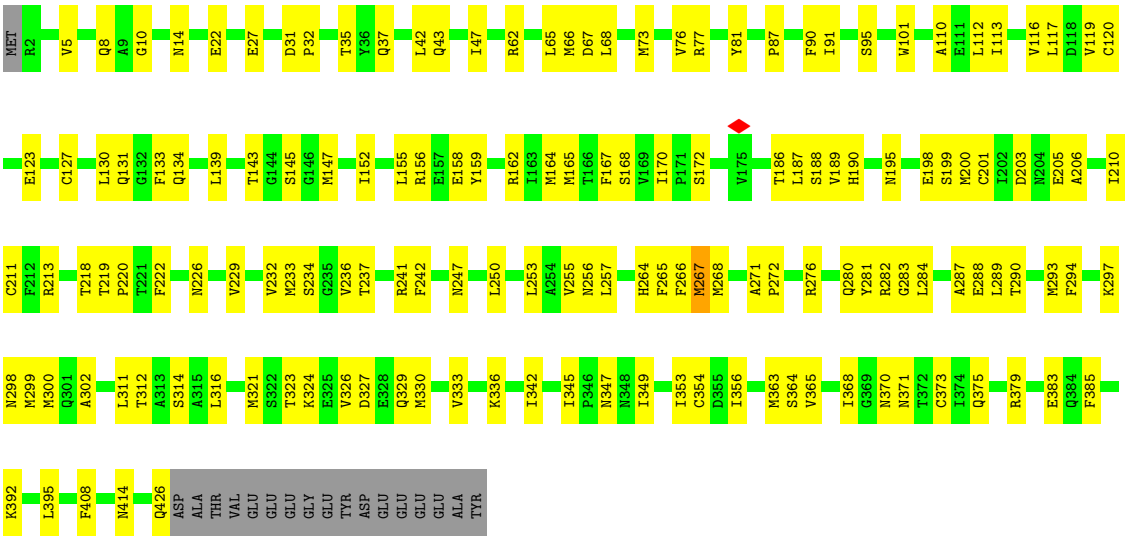
Chain VL:





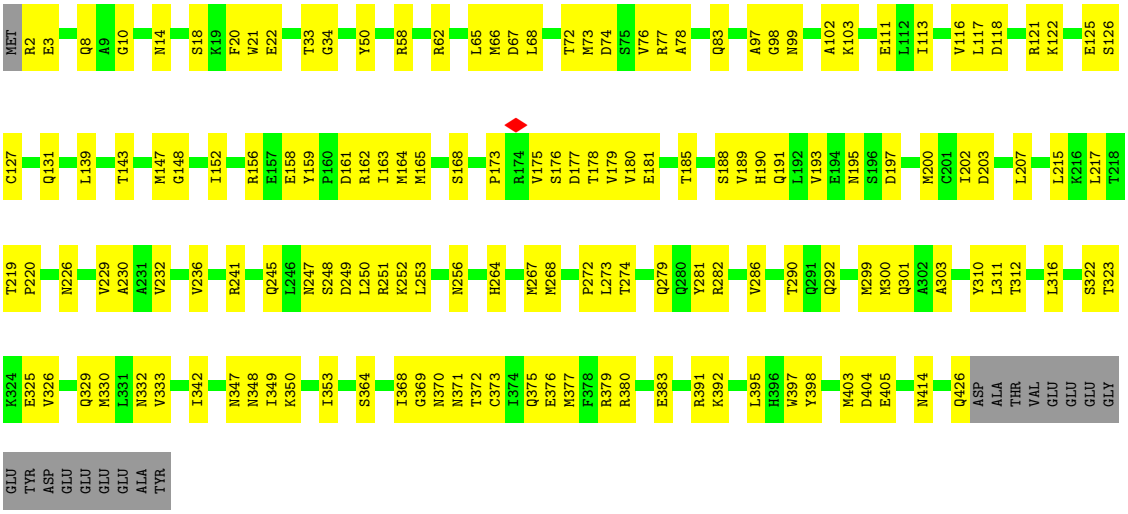
• Molecule 1: Tubulin beta chain

Chain W:



• Molecule 1: Tubulin beta chain

Chain WB:

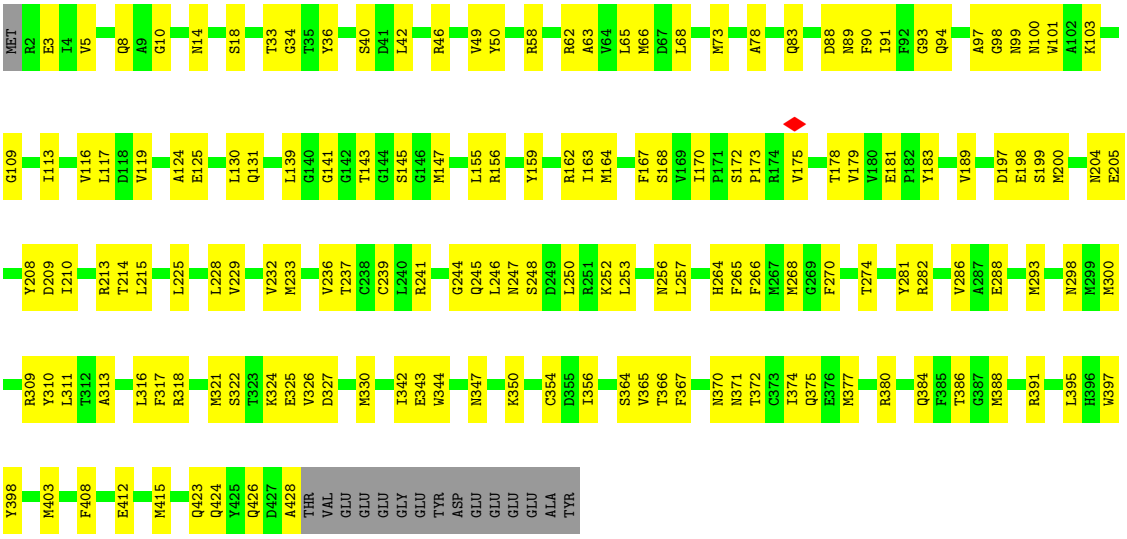


• Molecule 1: Tubulin beta chain

Chain WD:

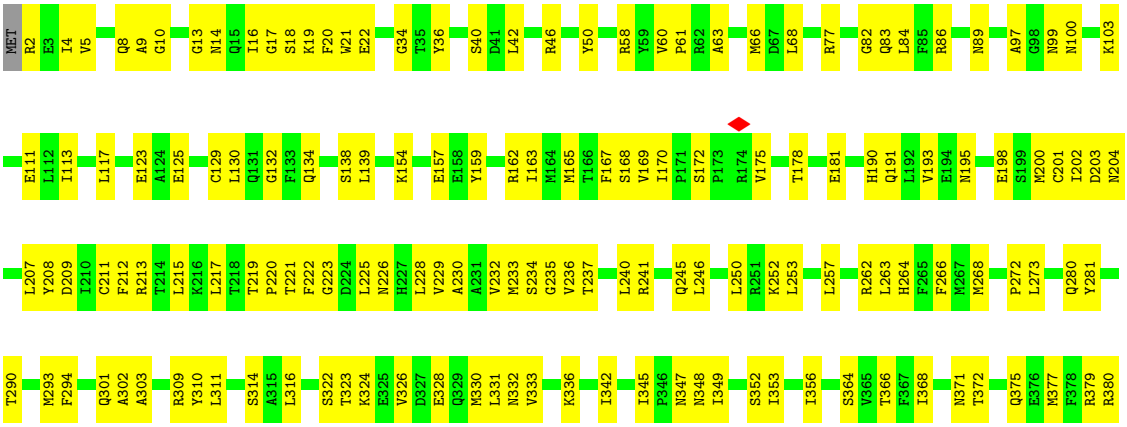
• Molecule 1: Tubulin beta chain

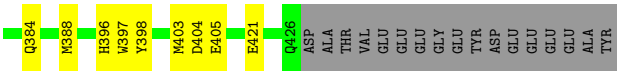
Chain WF:



• Molecule 1: Tubulin beta chain

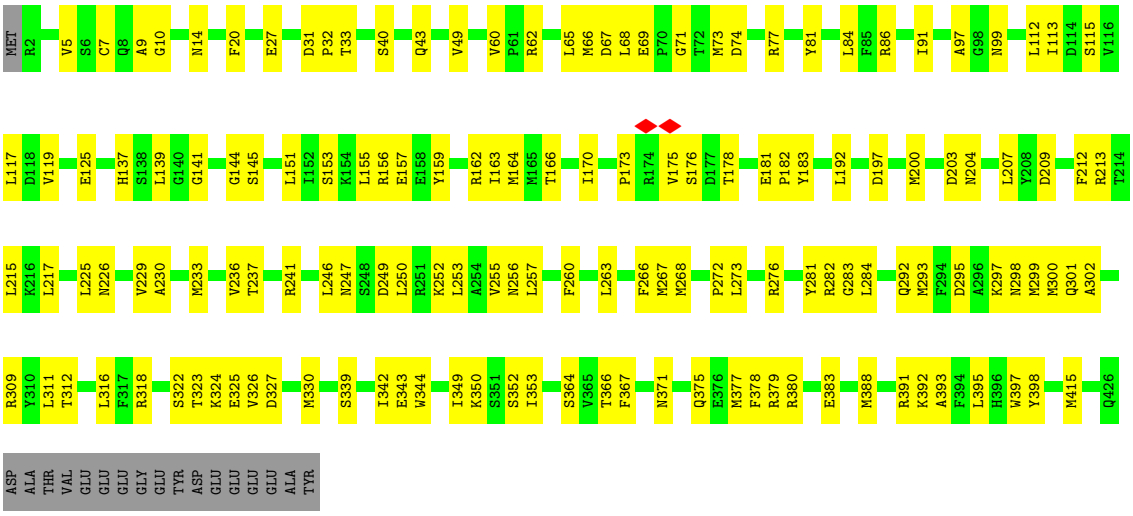
Chain WH:





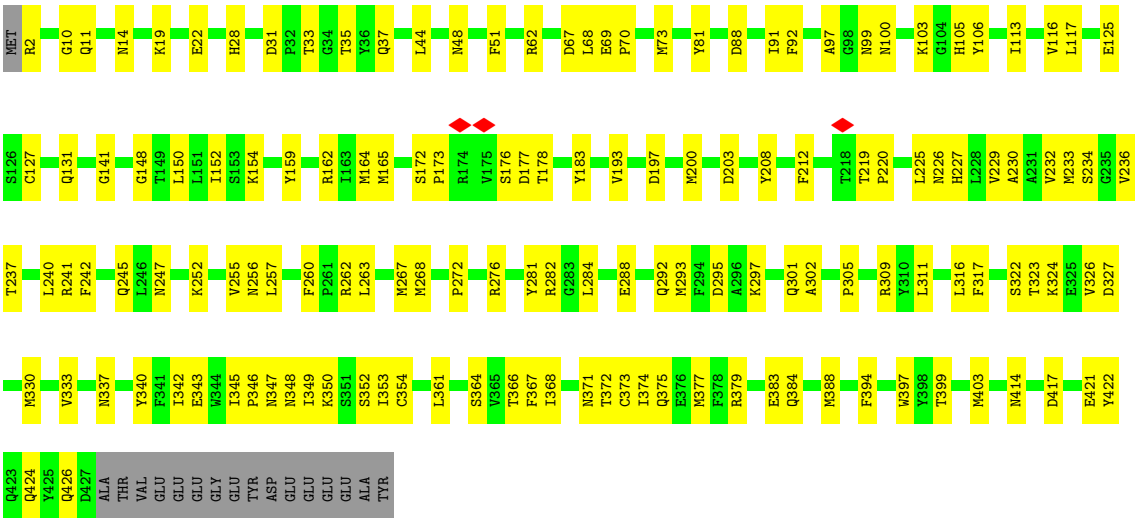
• Molecule 1: Tubulin beta chain

Chain WJ:



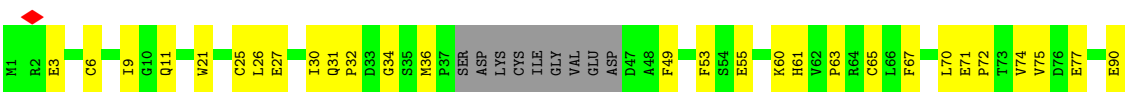
• Molecule 1: Tubulin beta chain

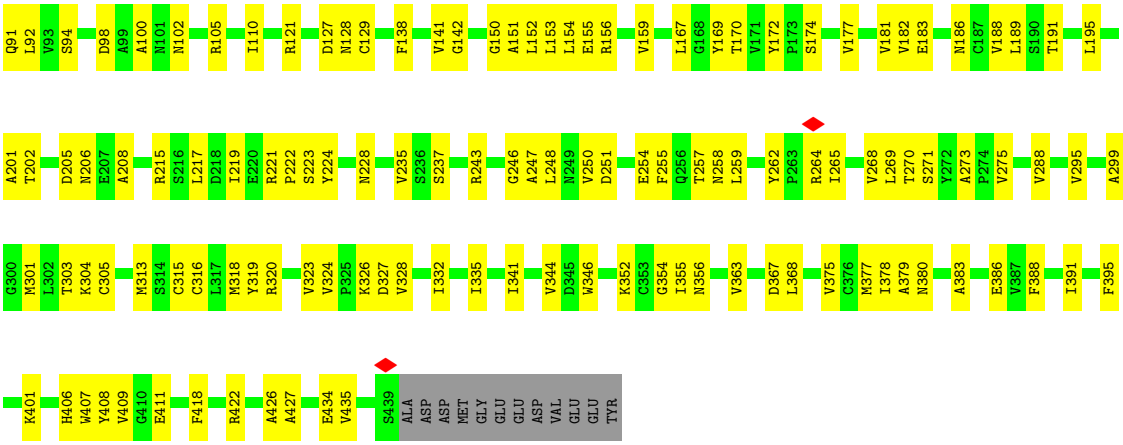
Chain WL:



• Molecule 2: Tubulin alpha chain

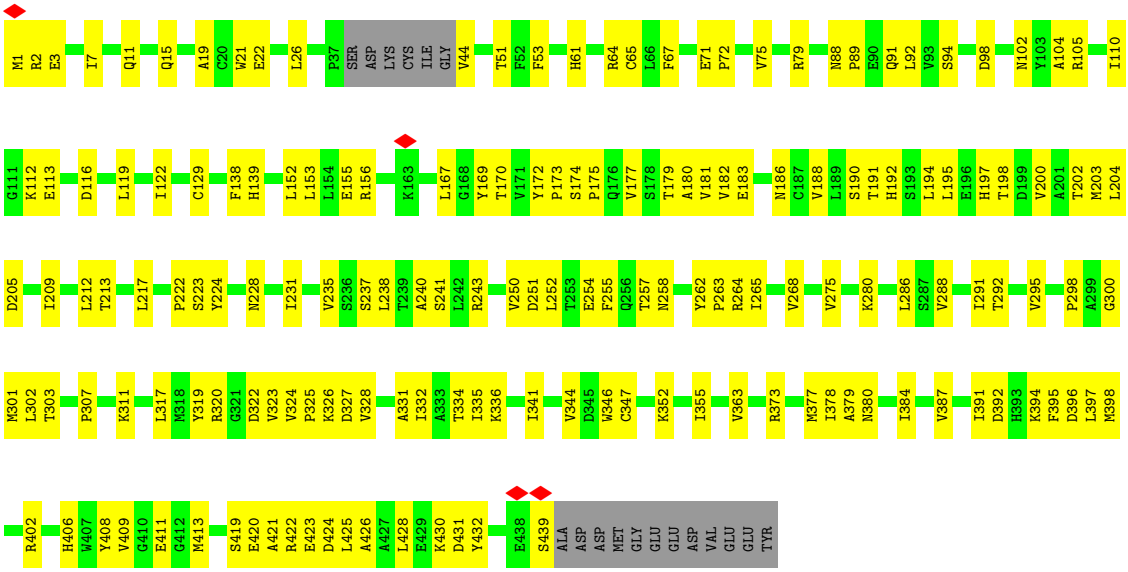
Chain AA:





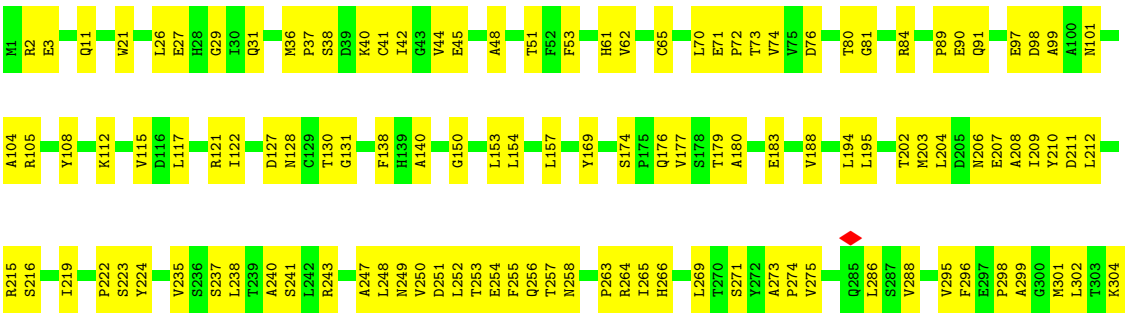
• Molecule 2: Tubulin alpha chain

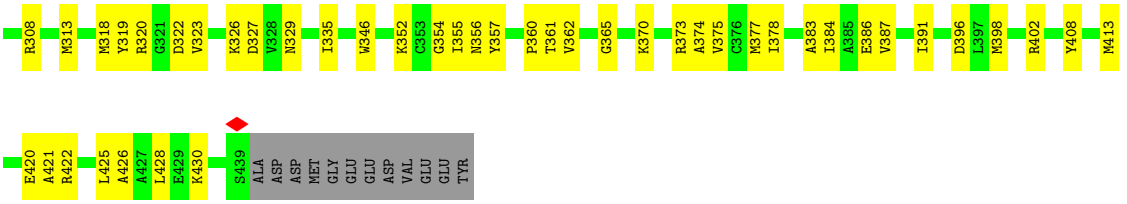
Chain AC:



• Molecule 2: Tubulin alpha chain

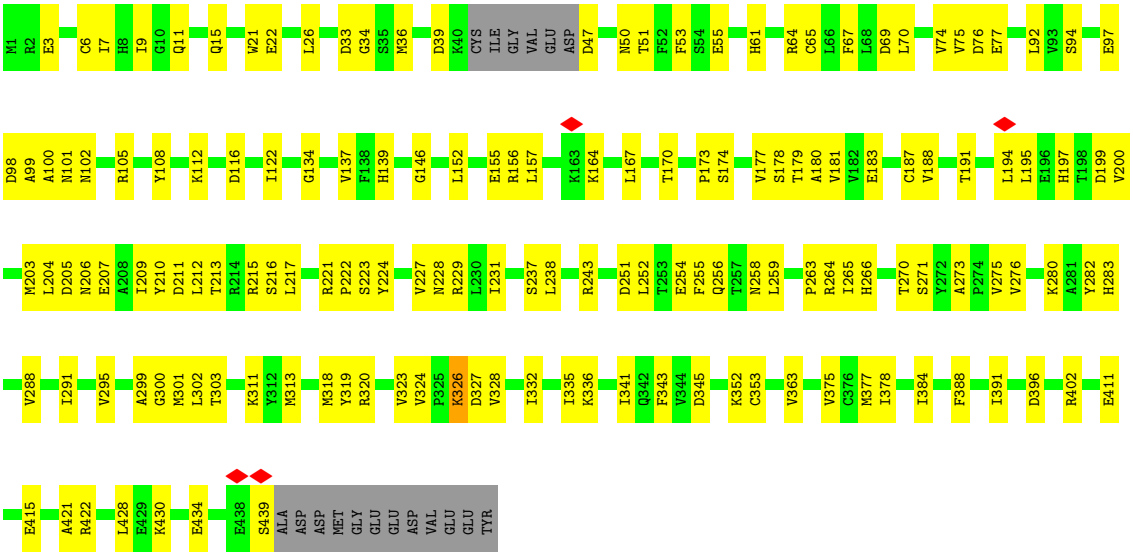
Chain AE:





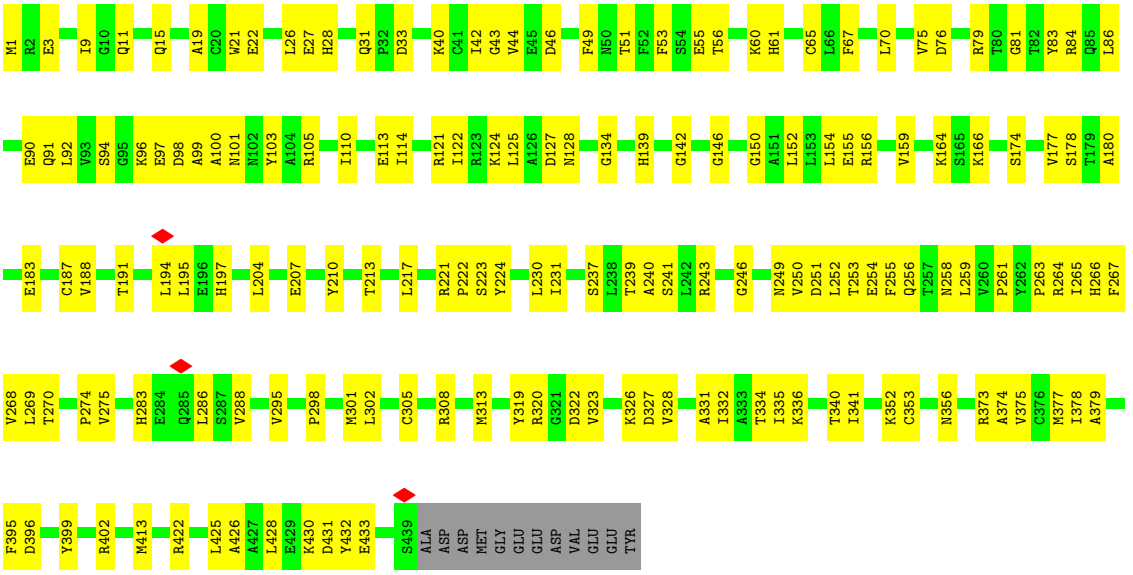
• Molecule 2: Tubulin alpha chain

Chain AG:



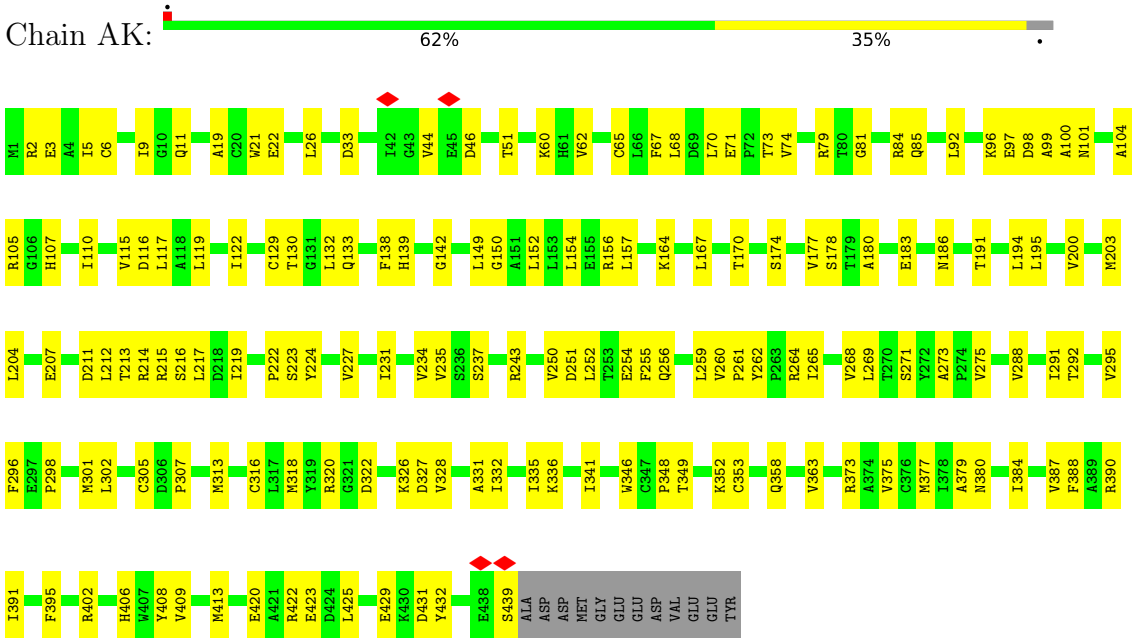
• Molecule 2: Tubulin alpha chain

Chain AI:



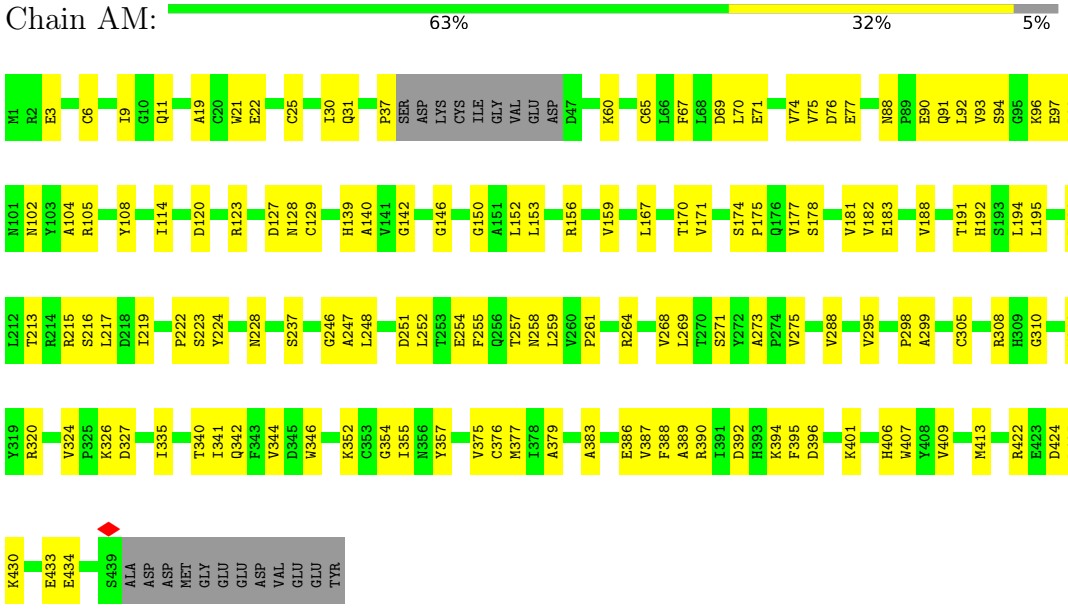
• Molecule 2: Tubulin alpha chain

Chain AK:



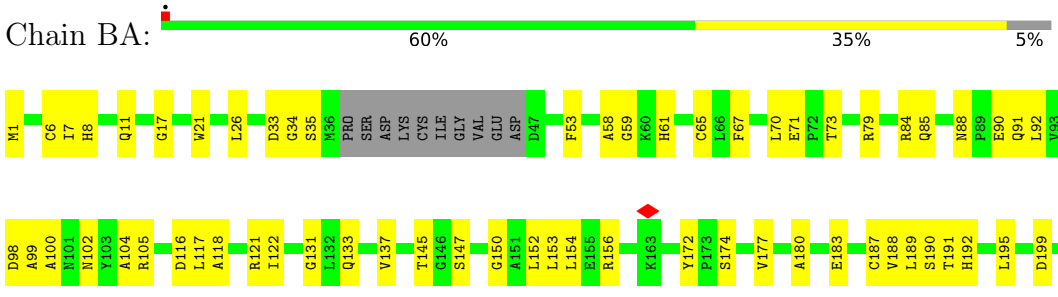
• Molecule 2: Tubulin alpha chain

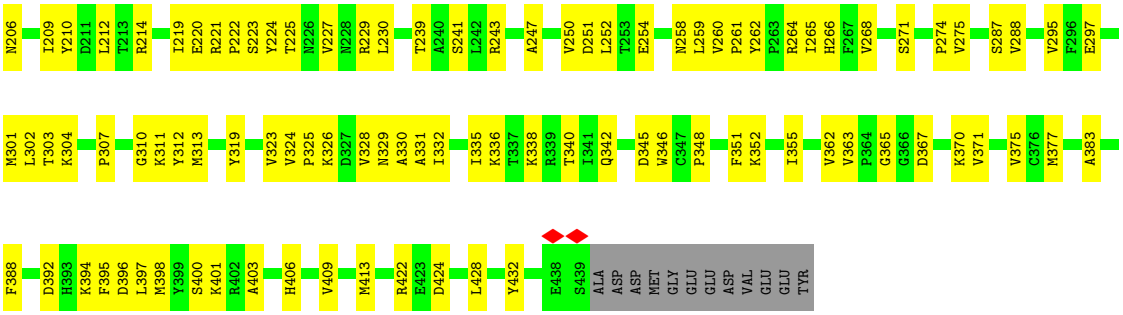
Chain AM:



• Molecule 2: Tubulin alpha chain

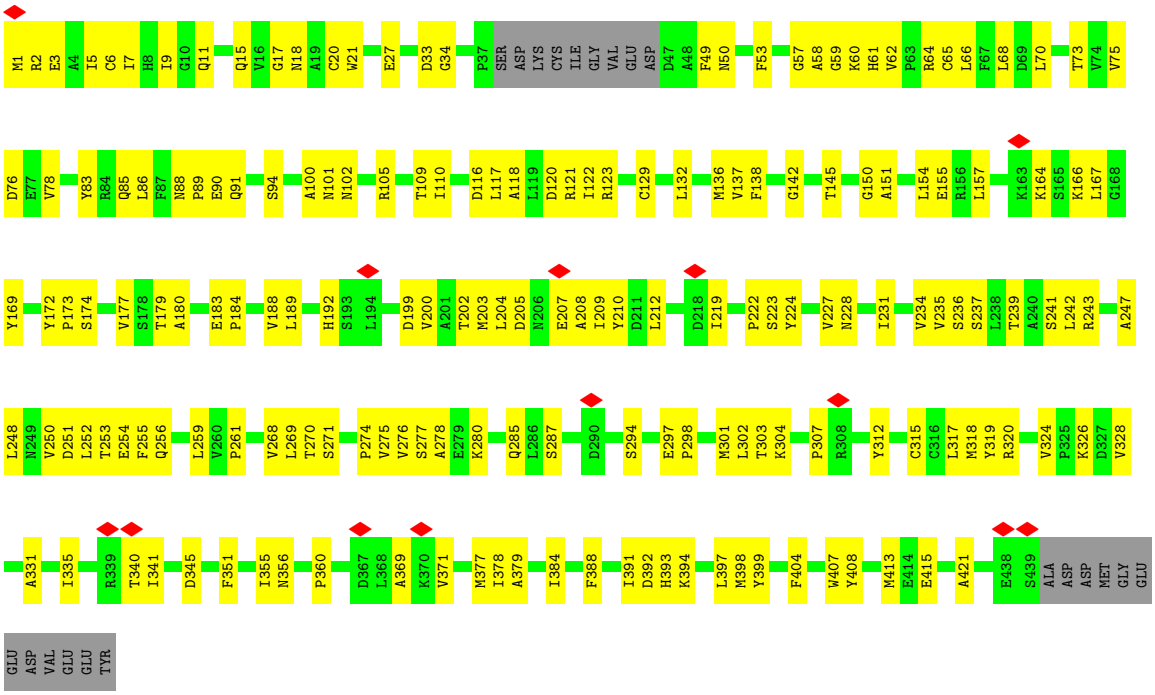
Chain BA:





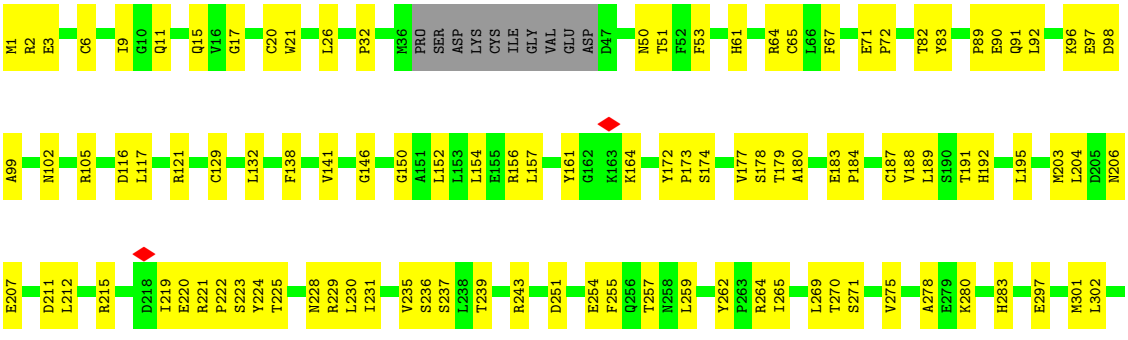
• Molecule 2: Tubulin alpha chain

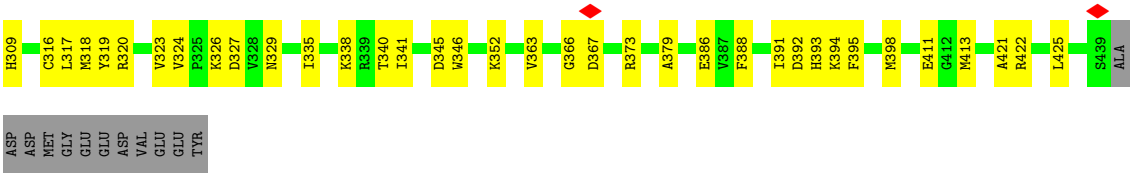
Chain BC:



• Molecule 2: Tubulin alpha chain

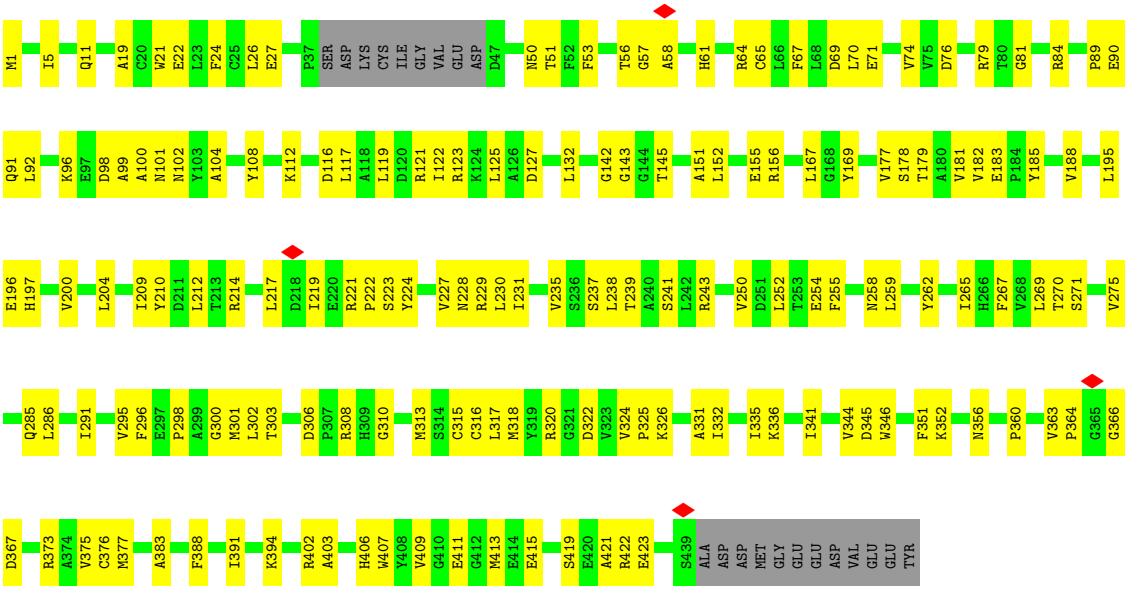
Chain BE:





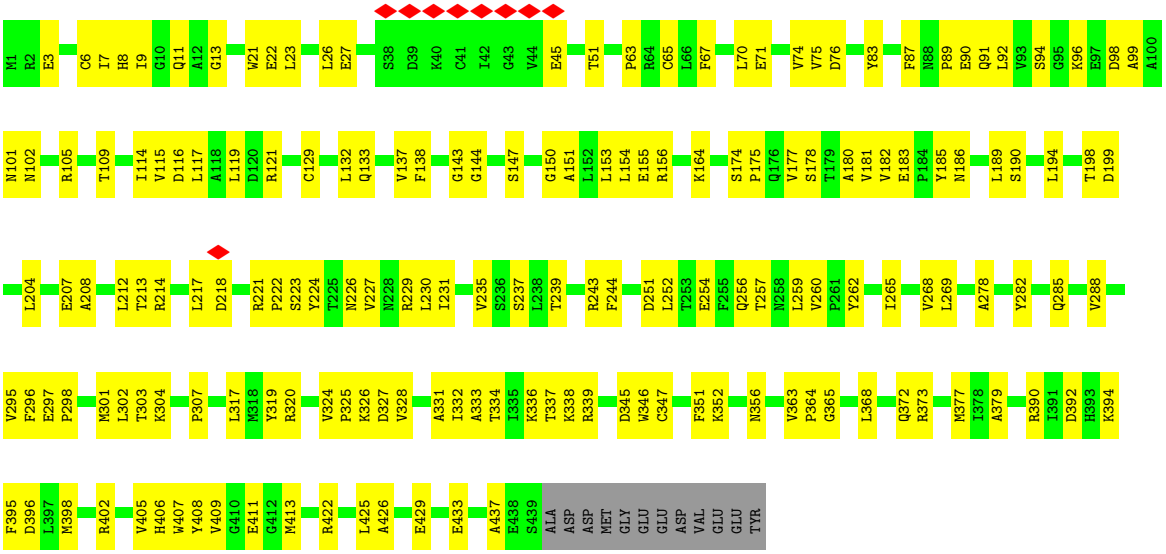
• Molecule 2: Tubulin alpha chain

Chain BG:



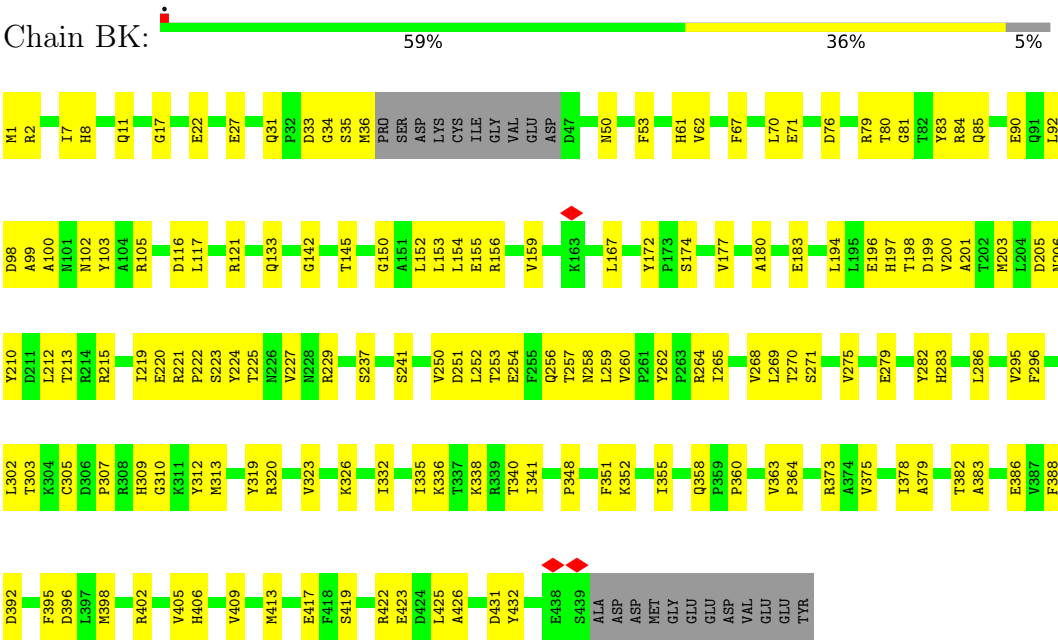
• Molecule 2: Tubulin alpha chain

Chain BI:



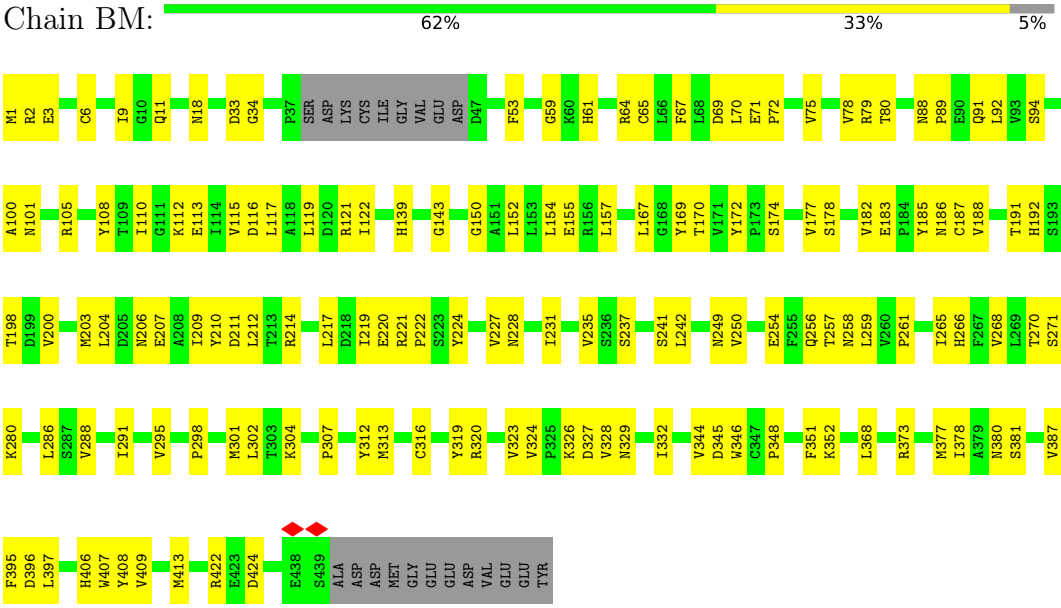
• Molecule 2: Tubulin alpha chain

Chain BK:



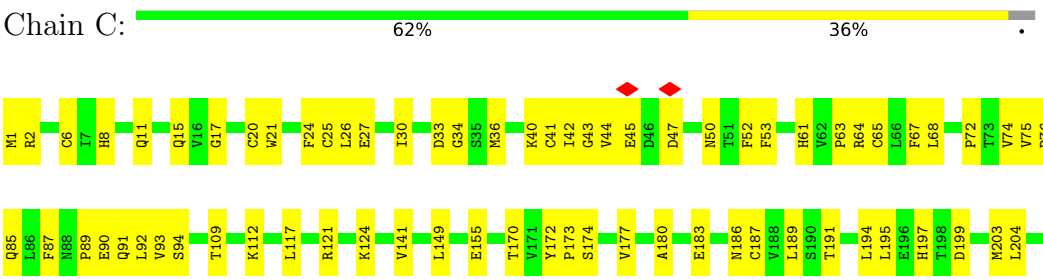
• Molecule 2: Tubulin alpha chain

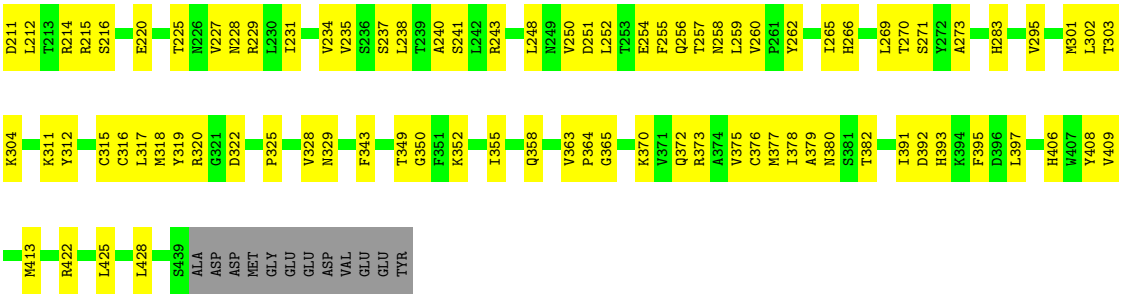
Chain BM:



• Molecule 2: Tubulin alpha chain

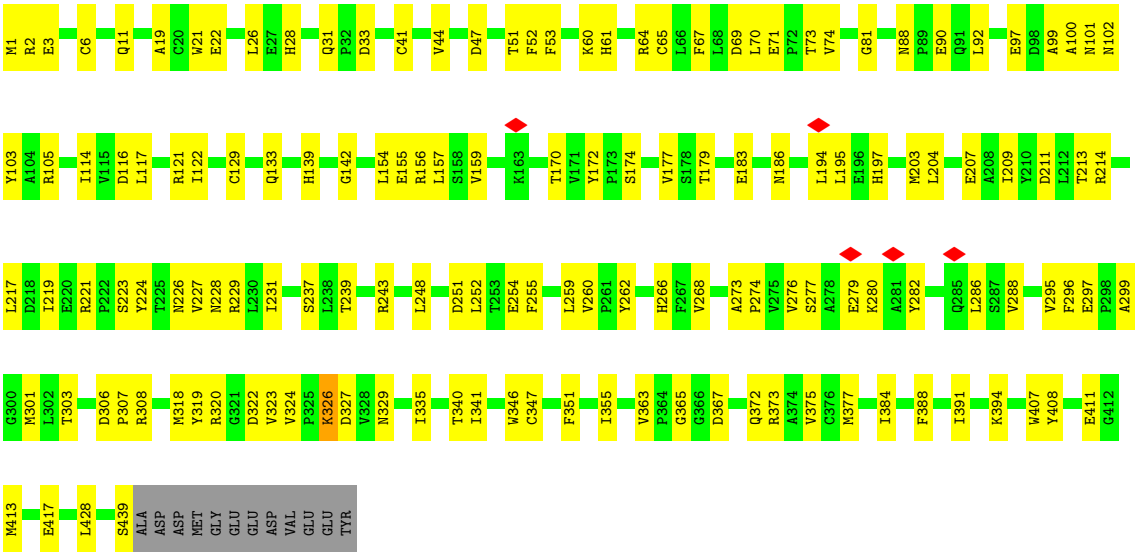
Chain C:





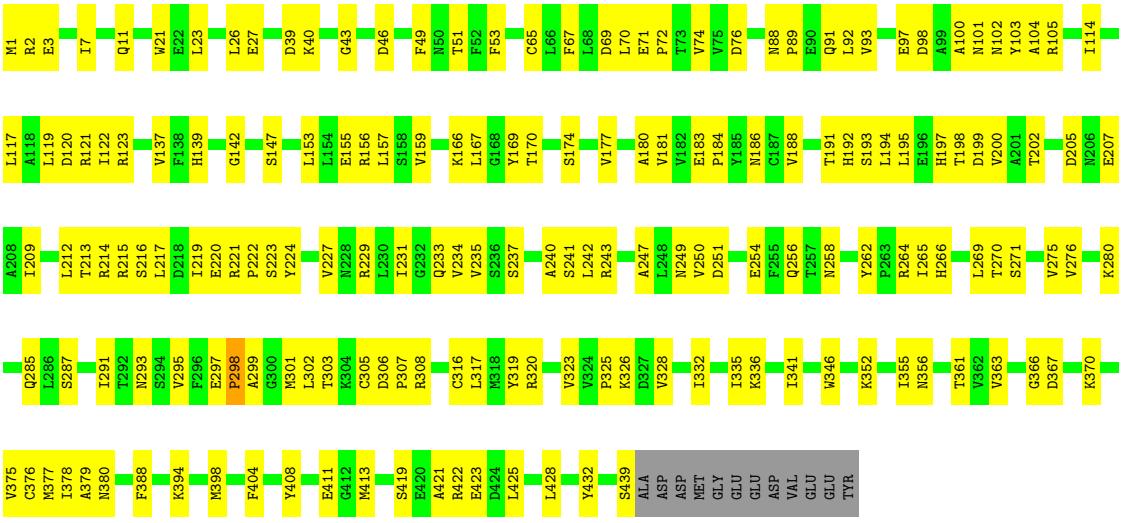
• Molecule 2: Tubulin alpha chain

Chain CB:



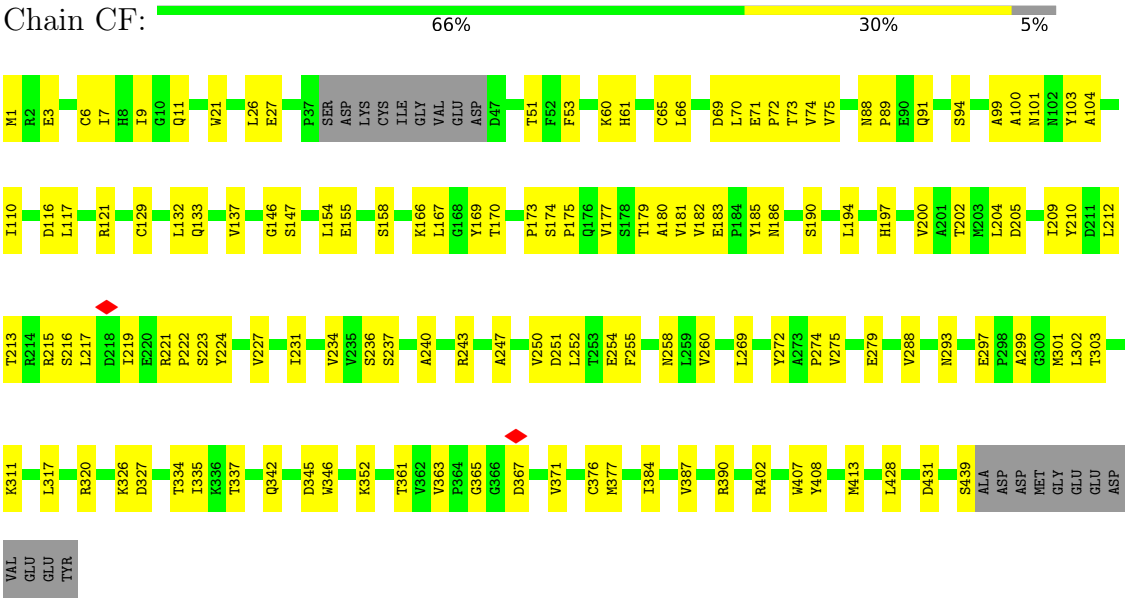
• Molecule 2: Tubulin alpha chain

Chain CD:



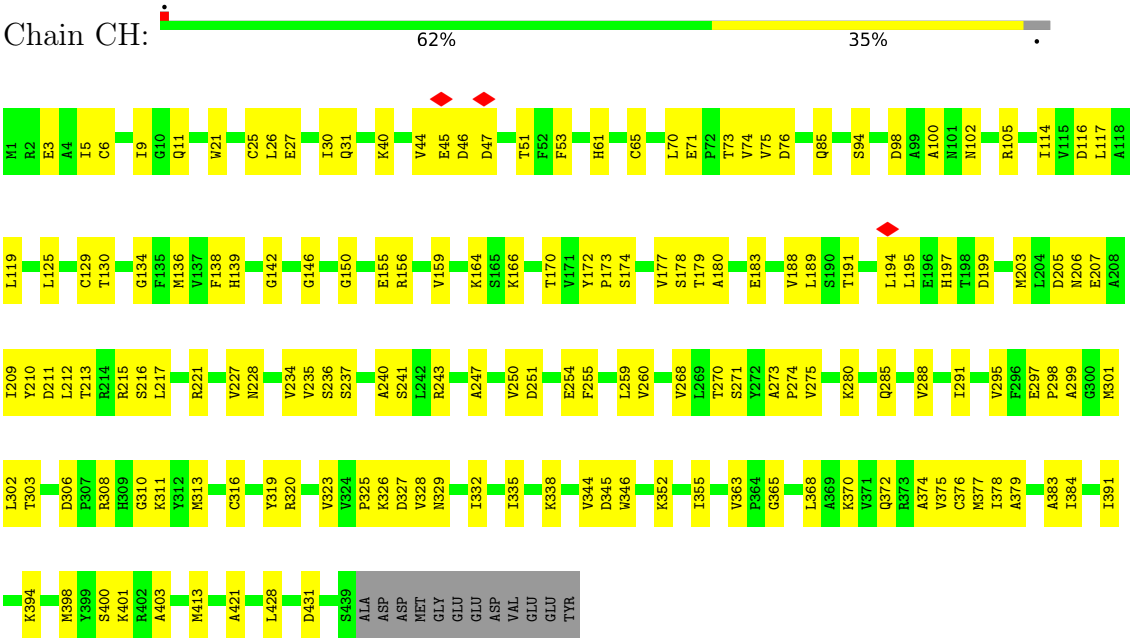
• Molecule 2: Tubulin alpha chain

Chain CF:



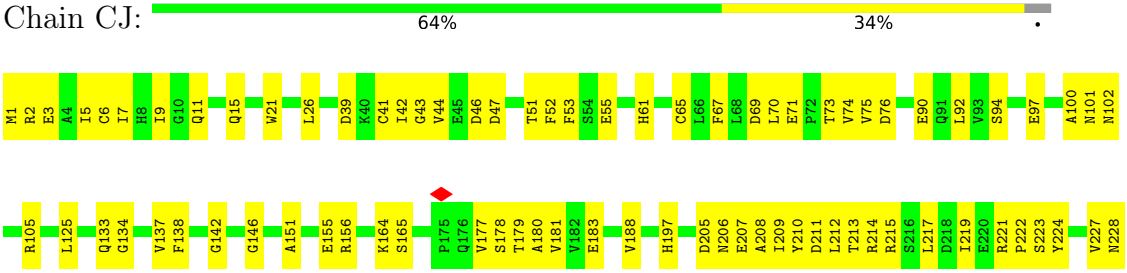
• Molecule 2: Tubulin alpha chain

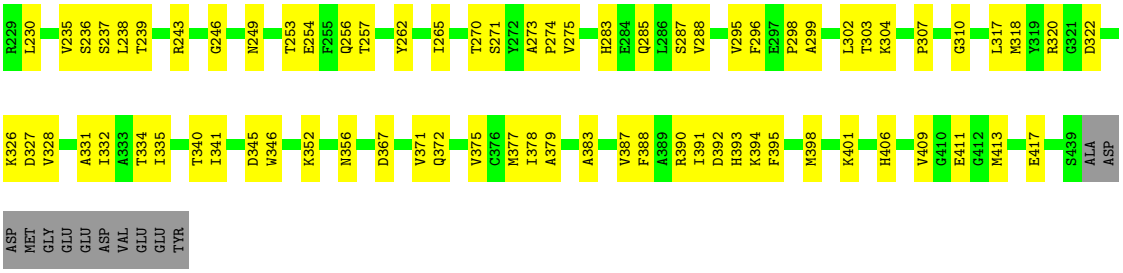
Chain CH:



• Molecule 2: Tubulin alpha chain

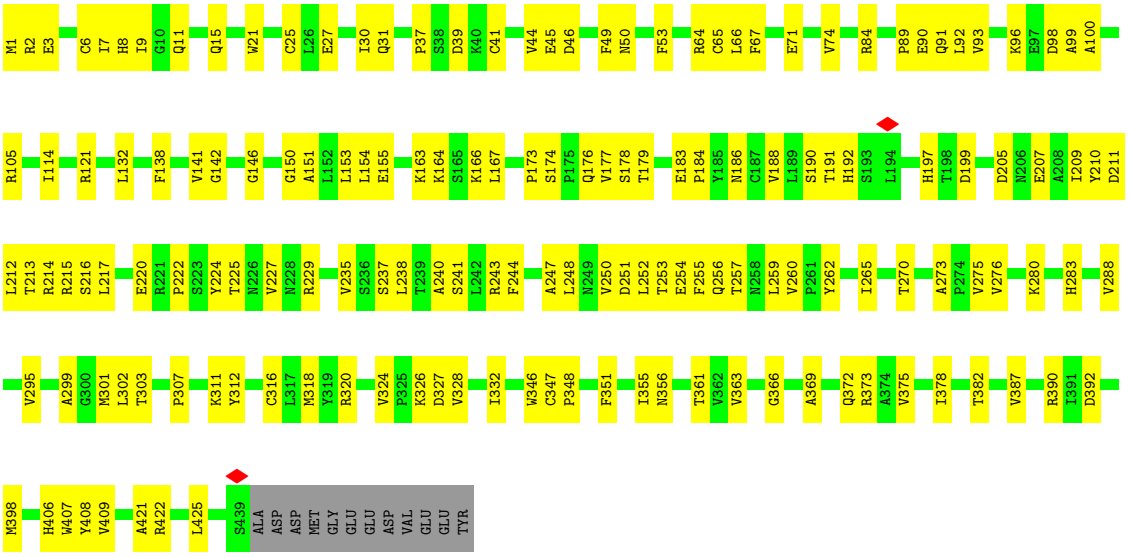
Chain CJ:





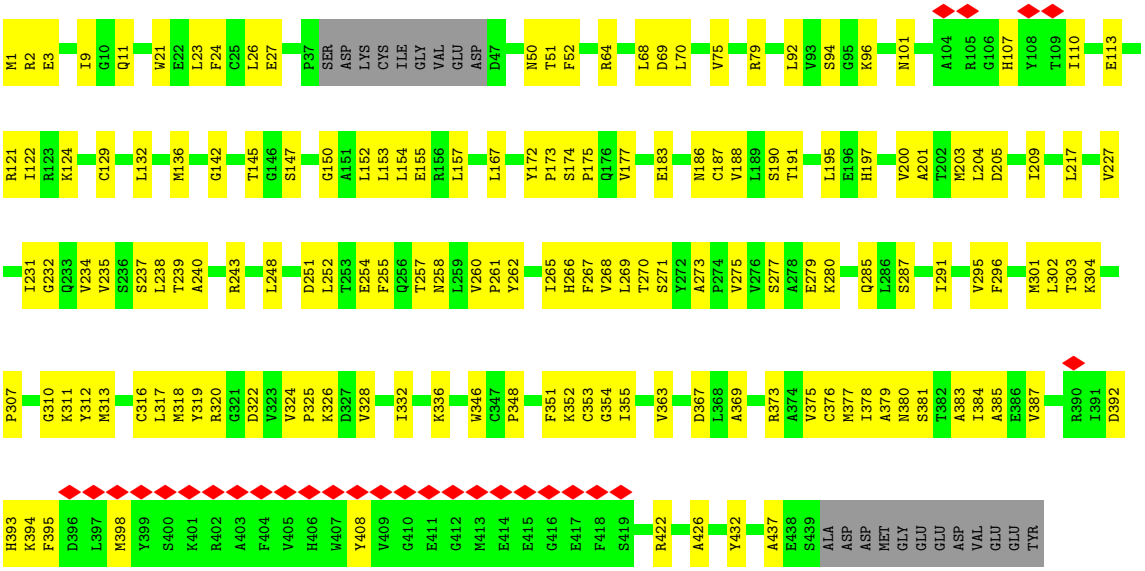
• Molecule 2: Tubulin alpha chain

Chain CL:



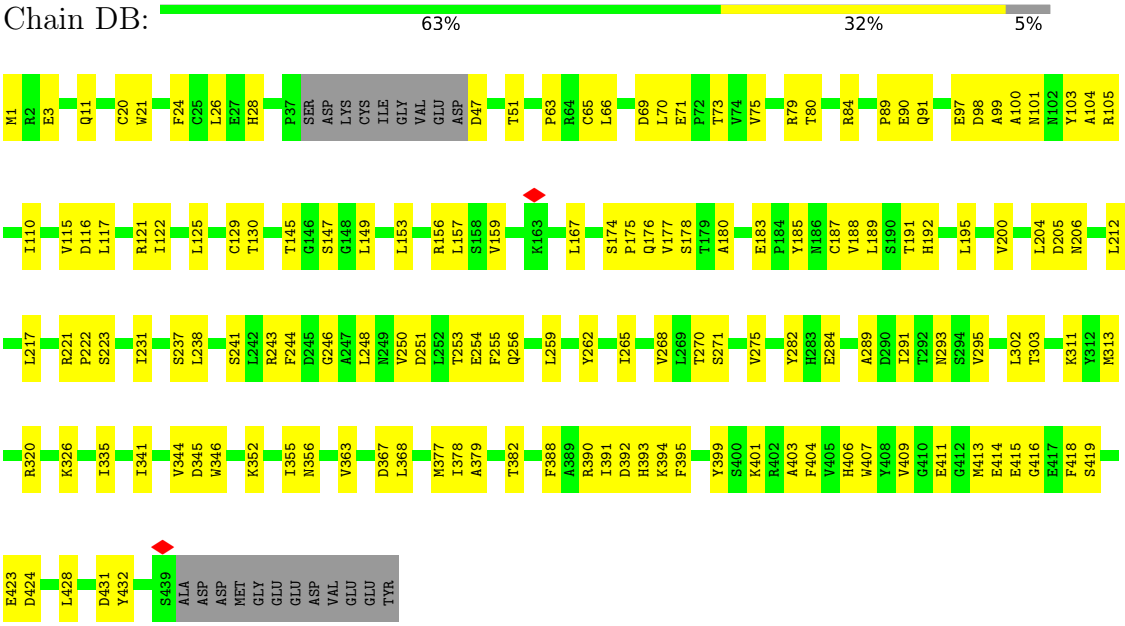
• Molecule 2: Tubulin alpha chain

Chain D:



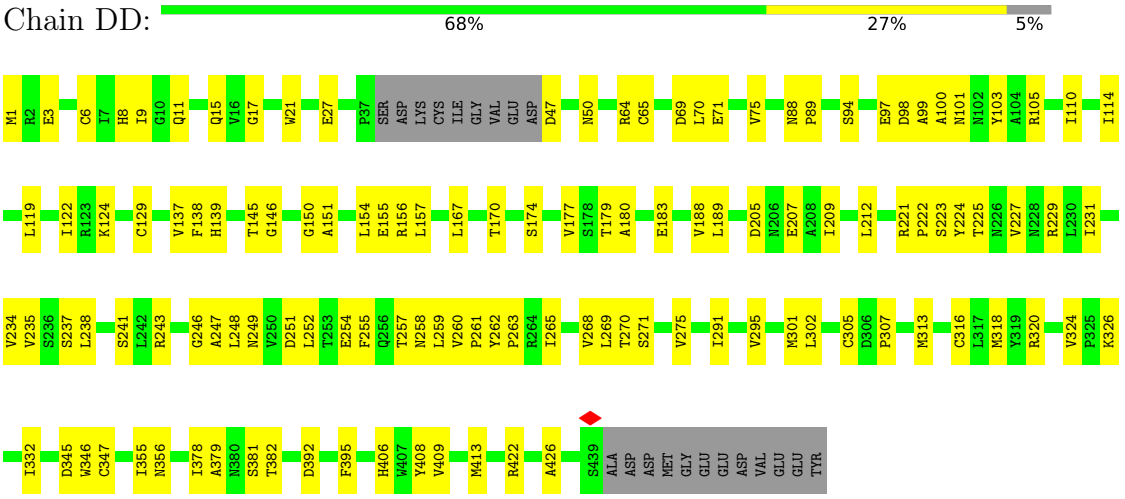
• Molecule 2: Tubulin alpha chain

Chain DB:



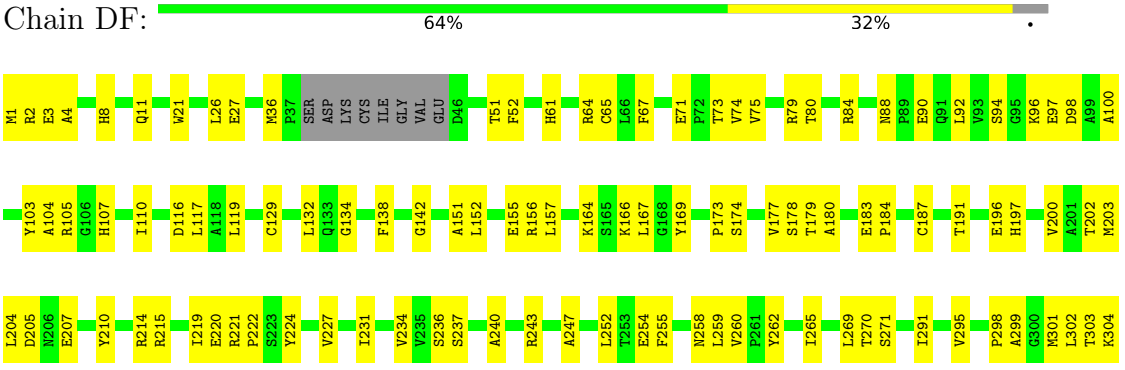
• Molecule 2: Tubulin alpha chain

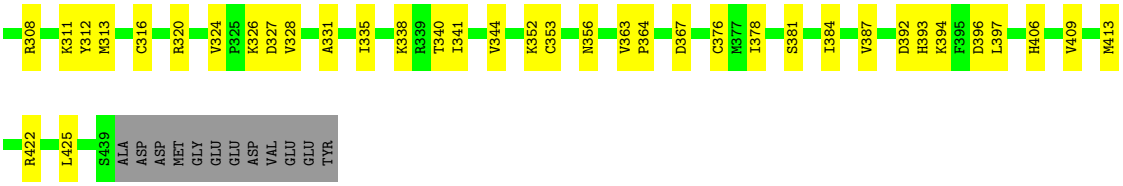
Chain DD:



• Molecule 2: Tubulin alpha chain

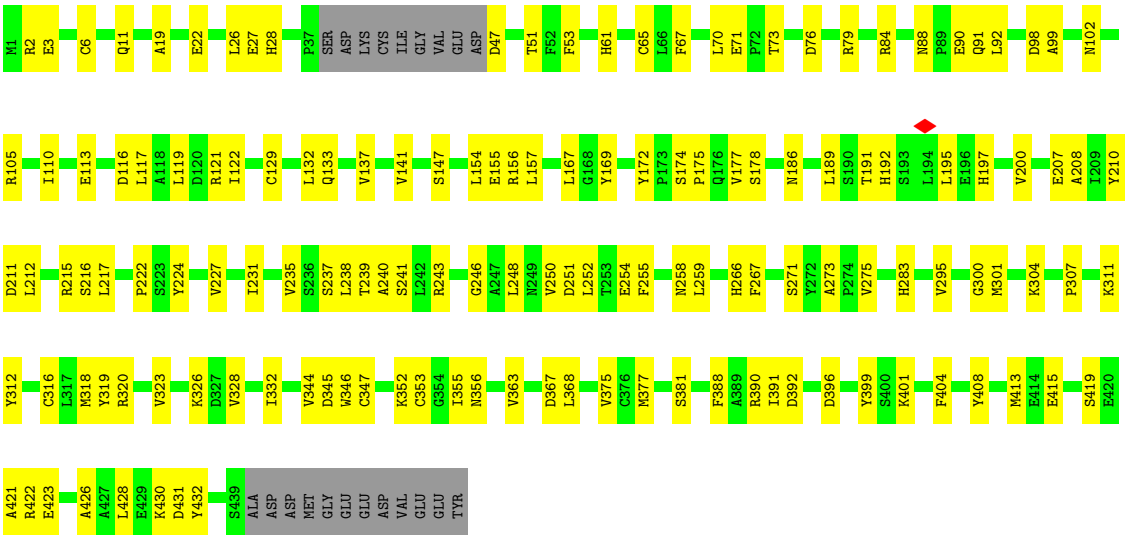
Chain DF:





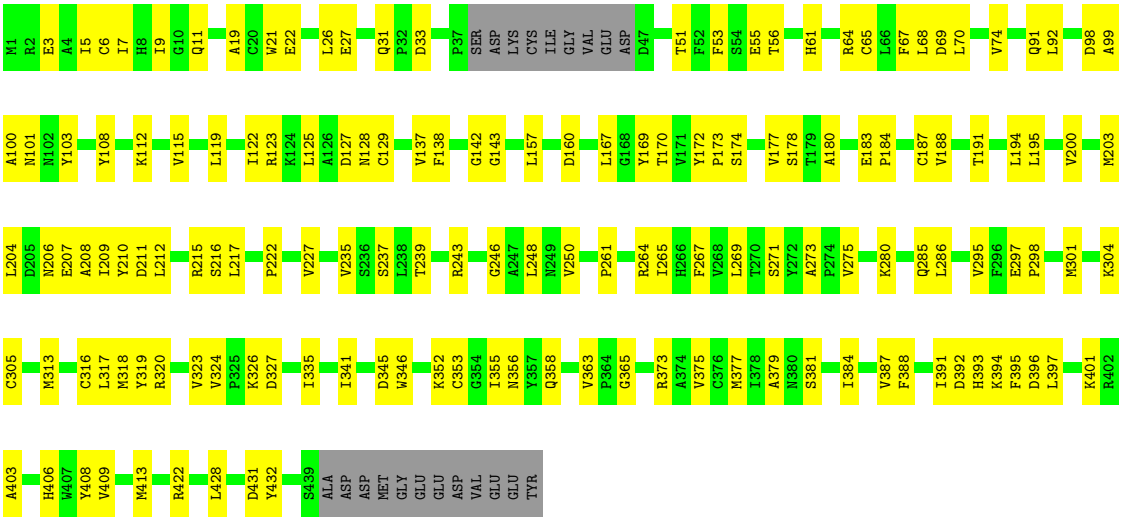
• Molecule 2: Tubulin alpha chain

Chain DH:



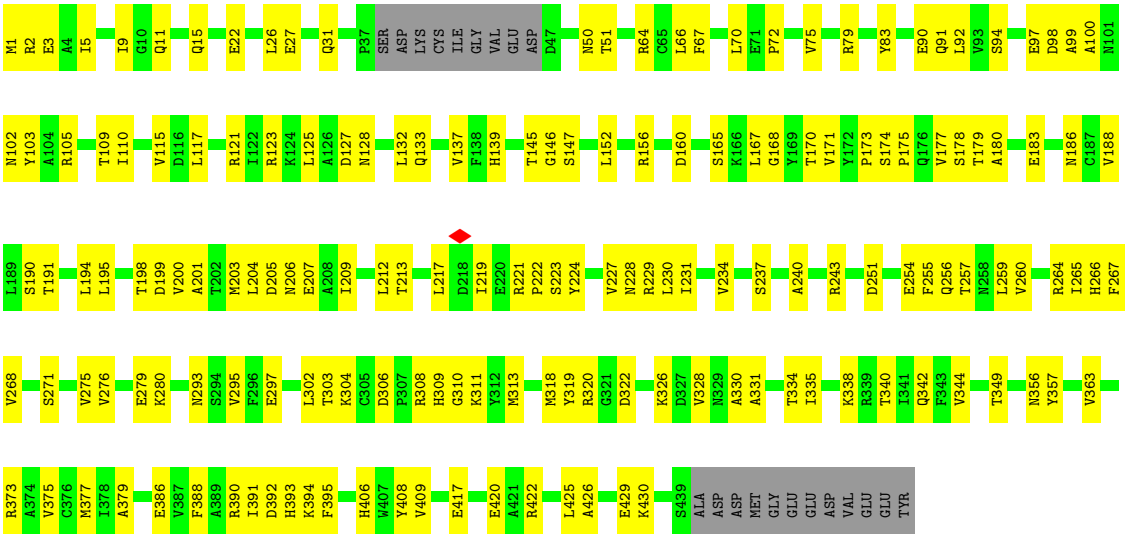
• Molecule 2: Tubulin alpha chain

Chain DJ:



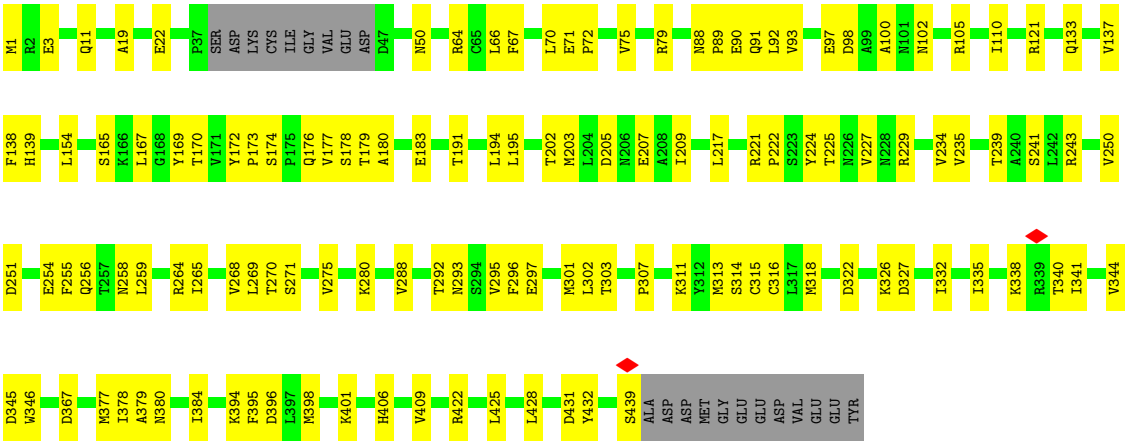
• Molecule 2: Tubulin alpha chain

Chain DL:



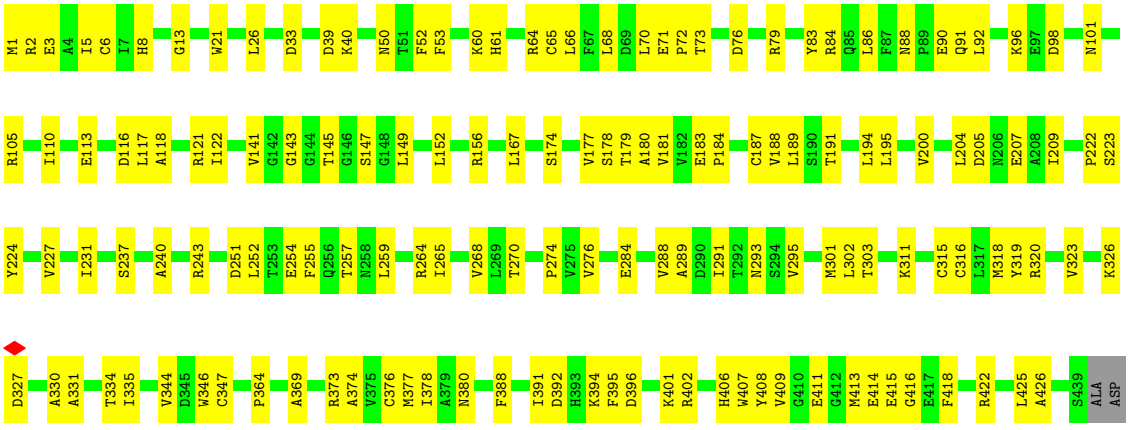
• Molecule 2: Tubulin alpha chain

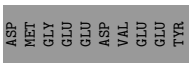
Chain EA:



• Molecule 2: Tubulin alpha chain

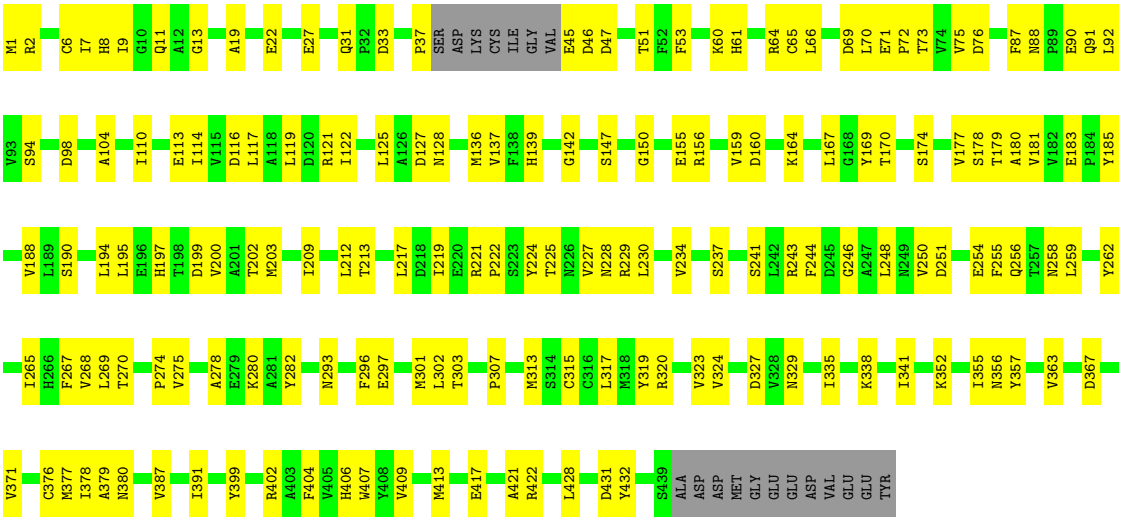
Chain EC:





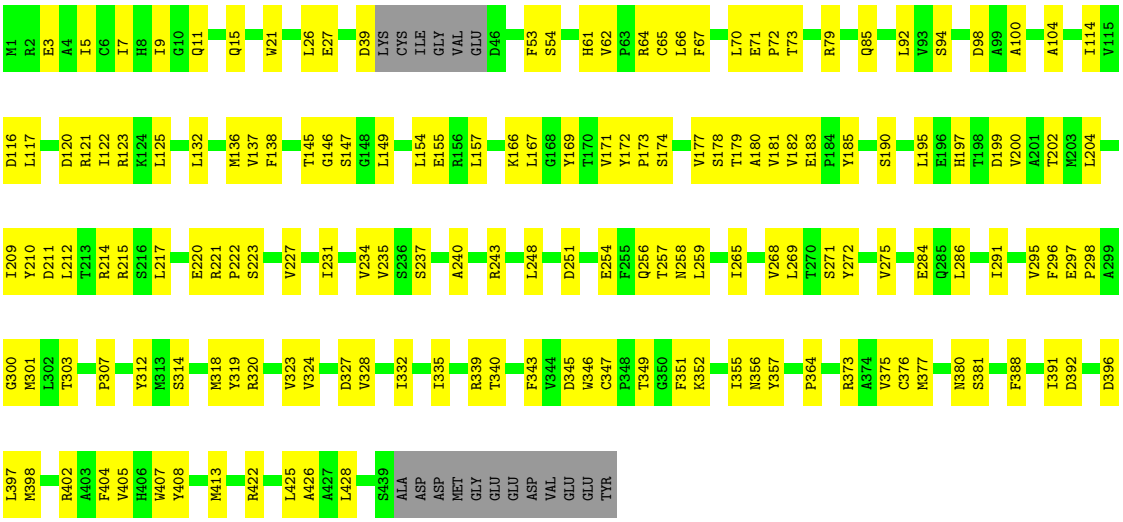
• Molecule 2: Tubulin alpha chain

Chain EE:



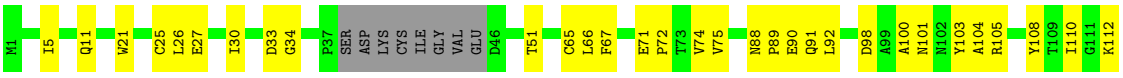
• Molecule 2: Tubulin alpha chain

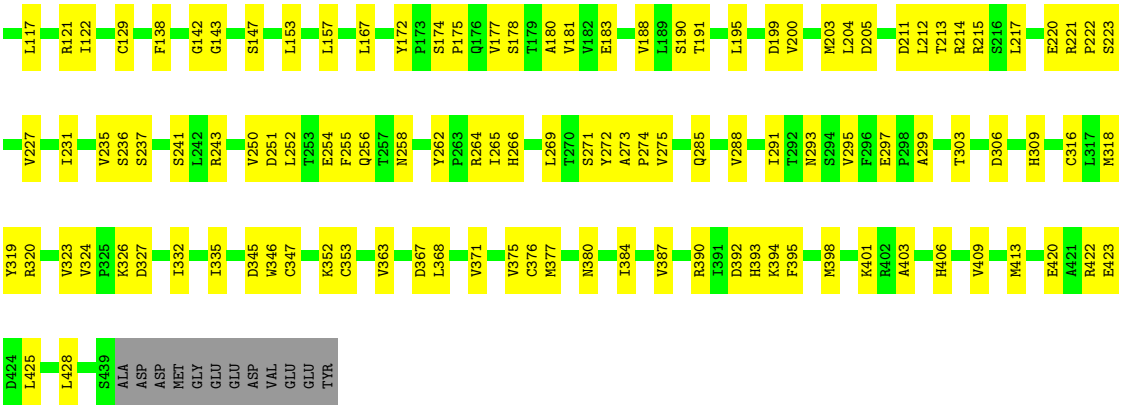
Chain EG:



• Molecule 2: Tubulin alpha chain

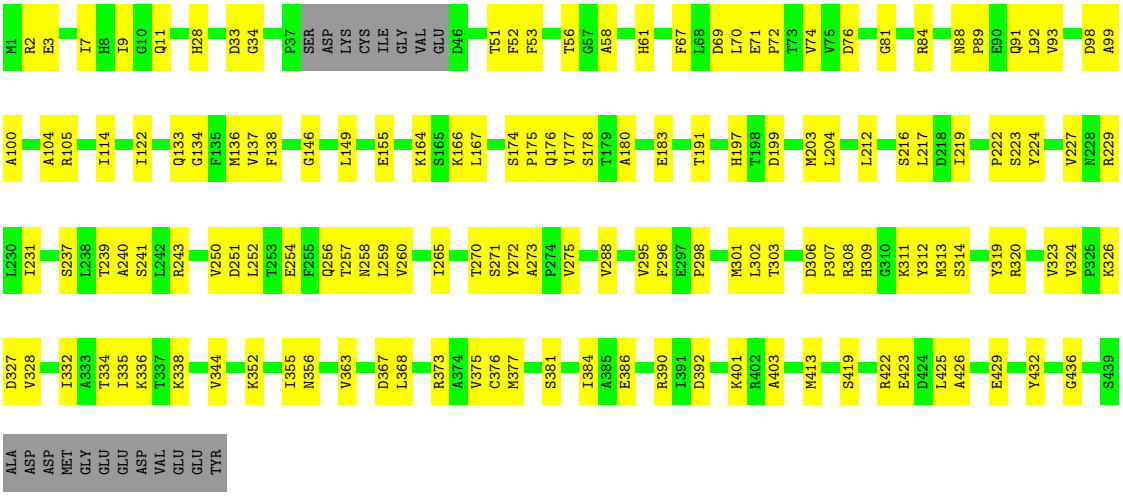
Chain EI:





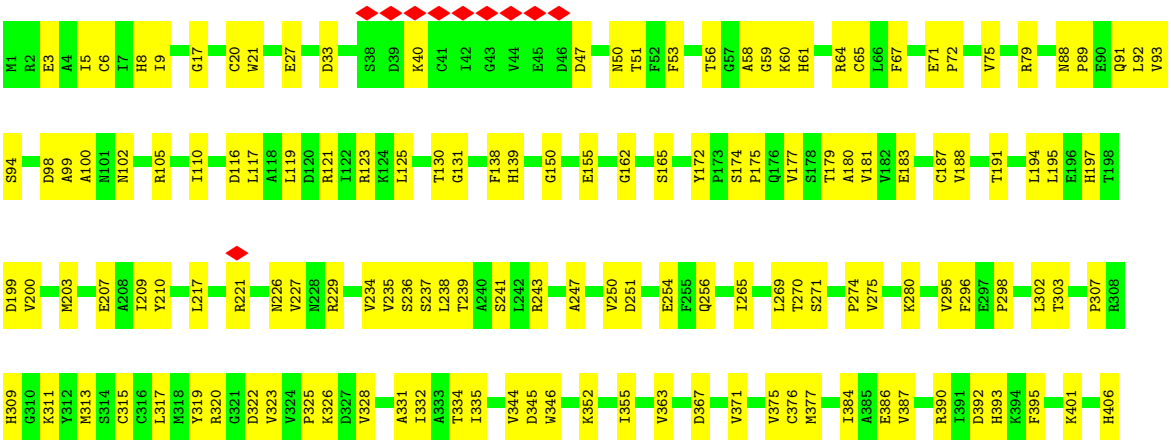
• Molecule 2: Tubulin alpha chain

Chain EK:



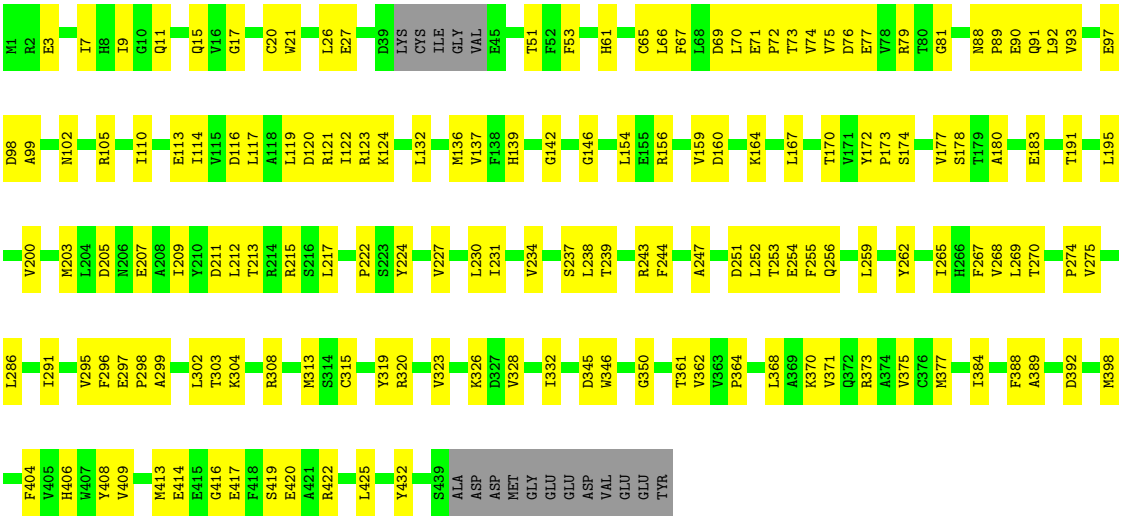
• Molecule 2: Tubulin alpha chain

Chain FA:



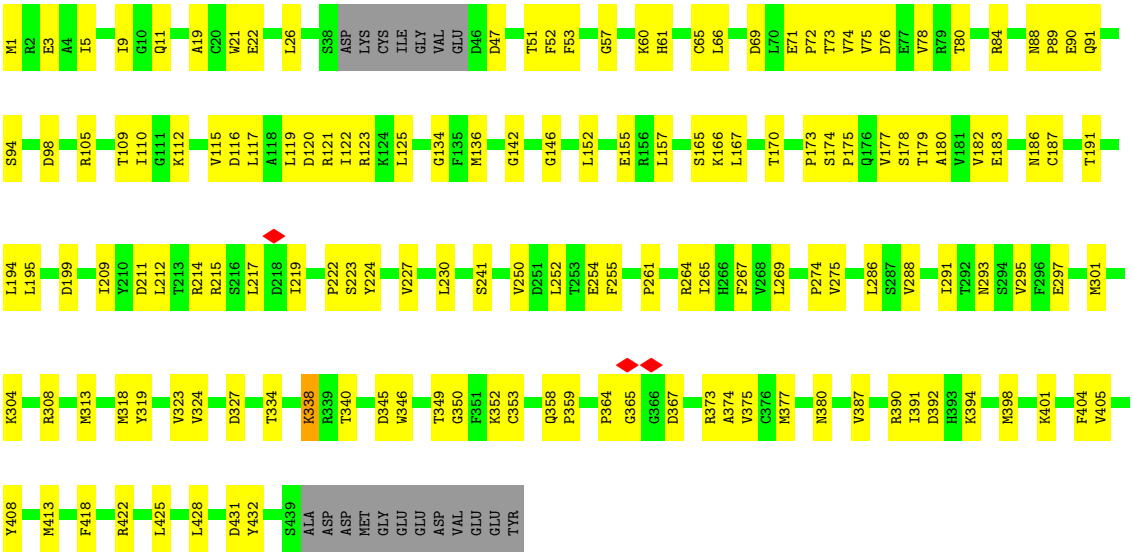
• Molecule 2: Tubulin alpha chain

Chain FC:



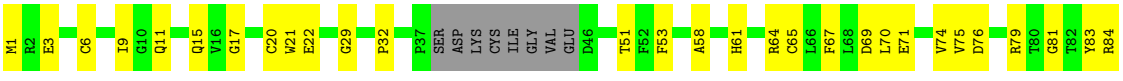
• Molecule 2: Tubulin alpha chain

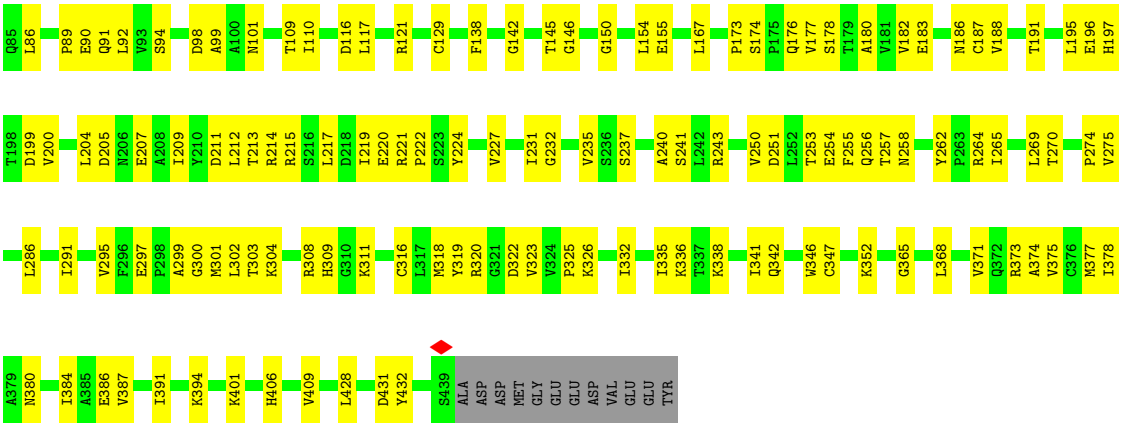
Chain FE:



• Molecule 2: Tubulin alpha chain

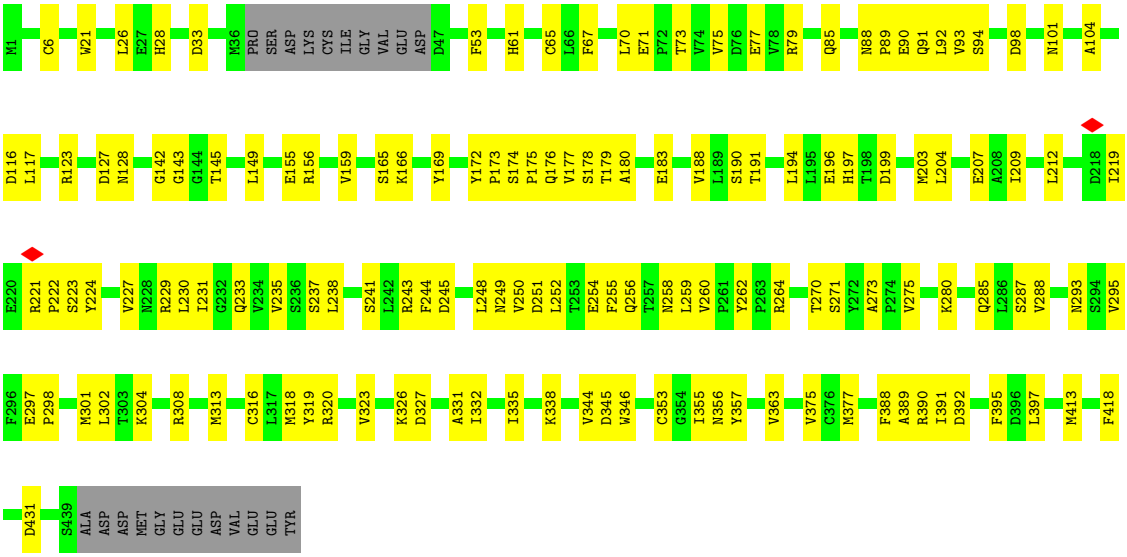
Chain FG:





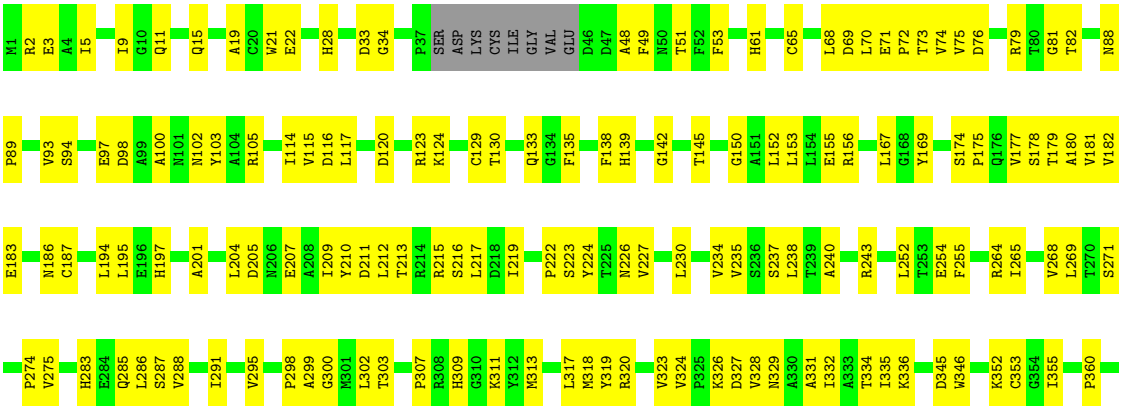
• Molecule 2: Tubulin alpha chain

Chain FI:



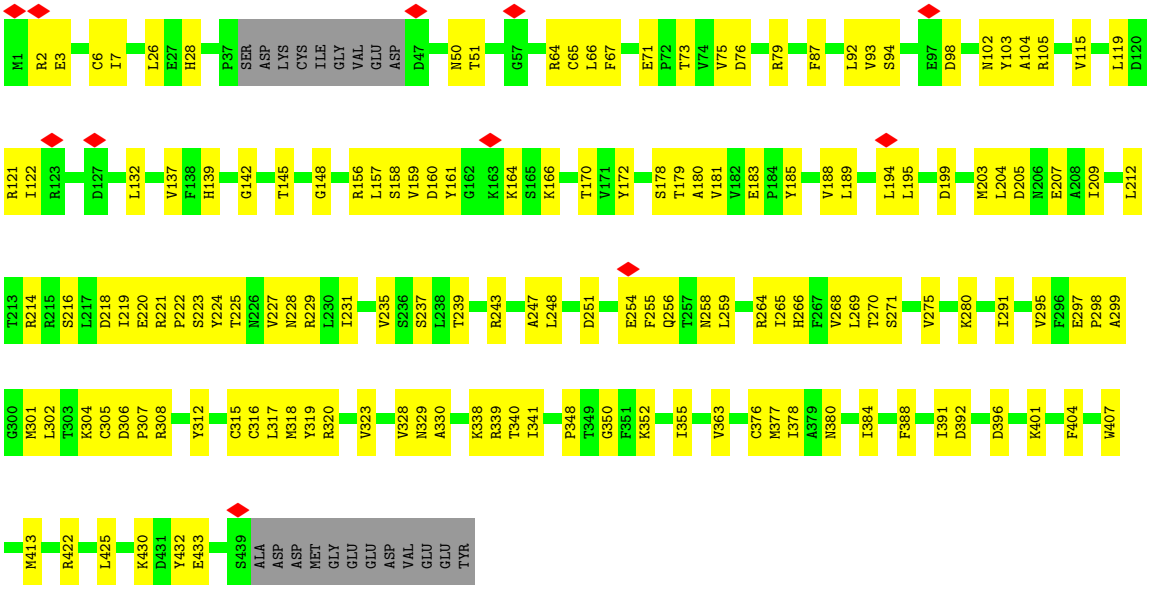
• Molecule 2: Tubulin alpha chain

Chain FK:



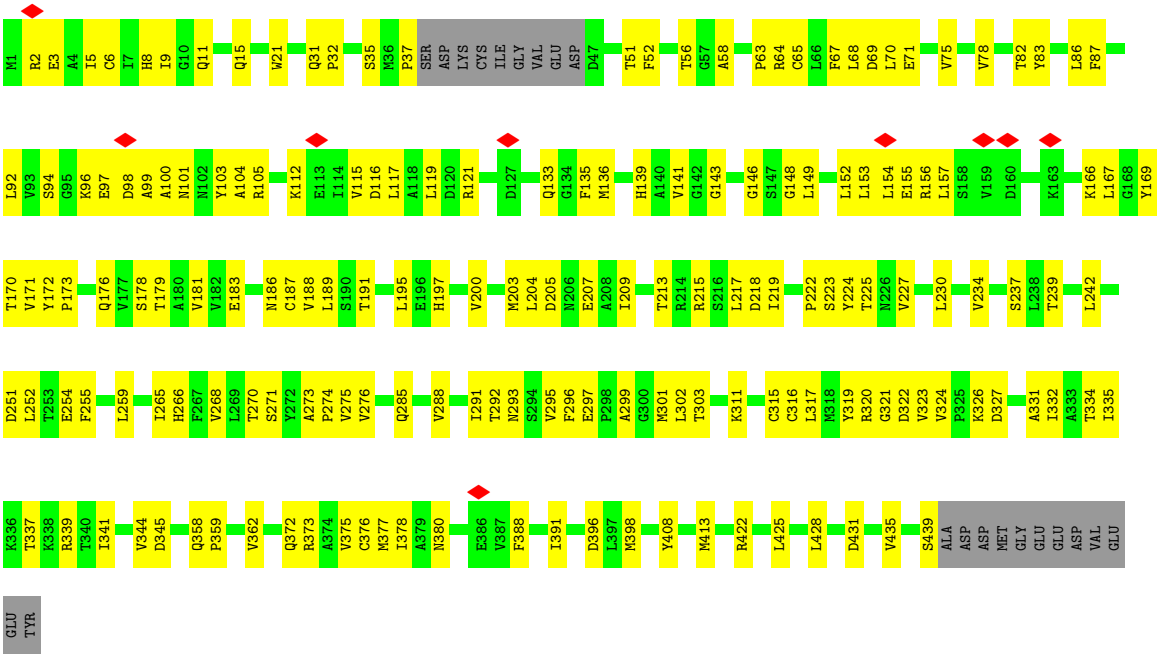
• Molecule 2: Tubulin alpha chain

Chain GA:



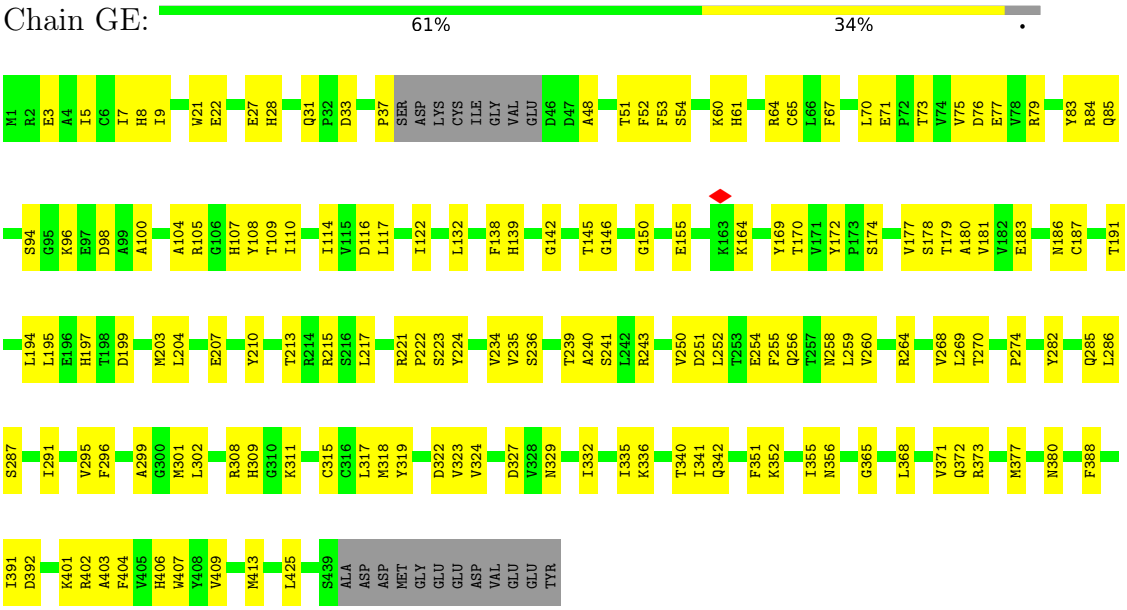
• Molecule 2: Tubulin alpha chain

Chain GC:



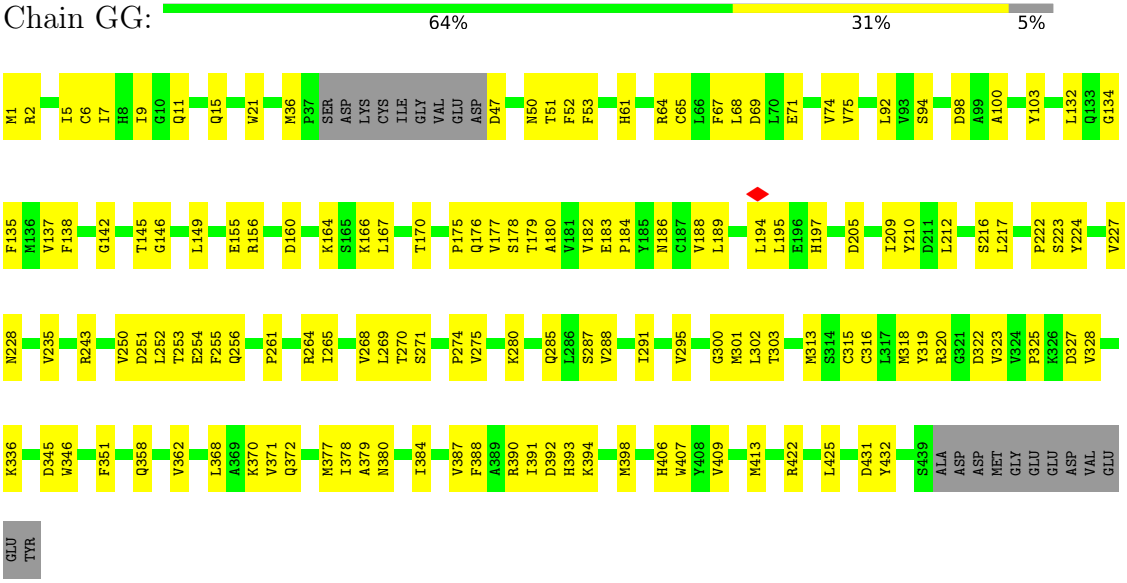
• Molecule 2: Tubulin alpha chain

Chain GE:



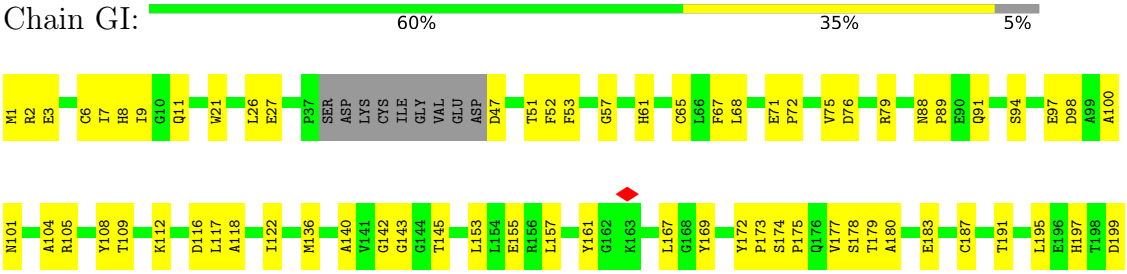
• Molecule 2: Tubulin alpha chain

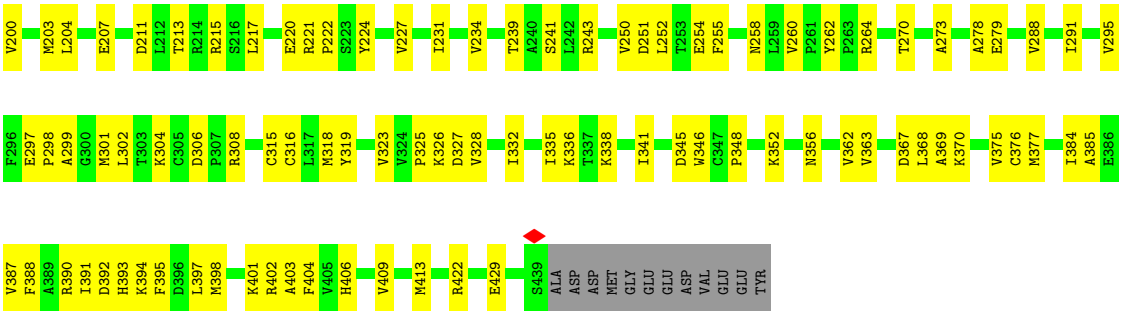
Chain GG:



• Molecule 2: Tubulin alpha chain

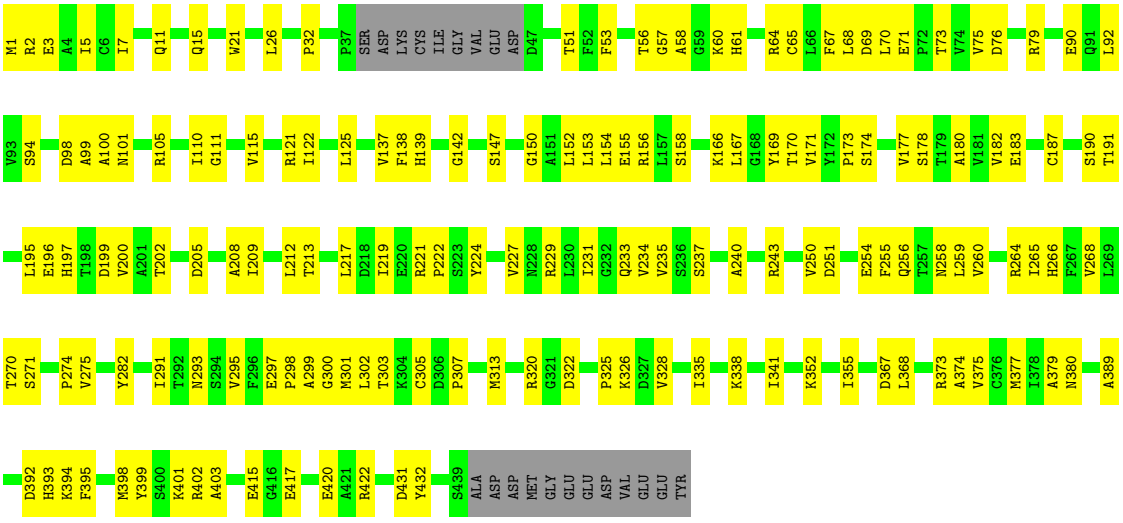
Chain GI:





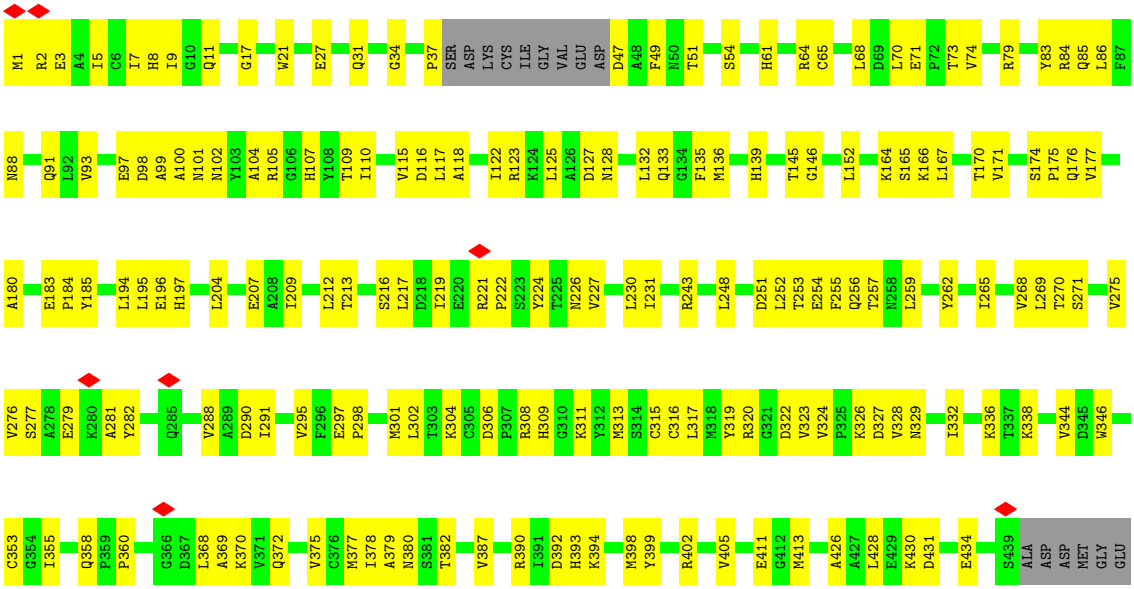
• Molecule 2: Tubulin alpha chain

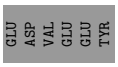
Chain GK:



• Molecule 2: Tubulin alpha chain

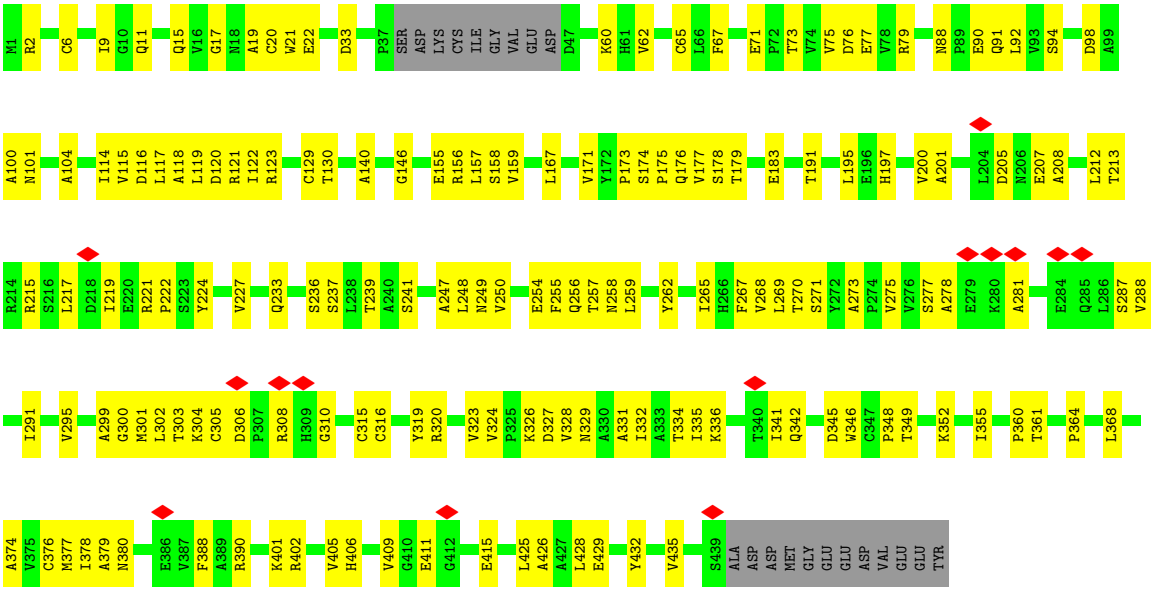
Chain HA:





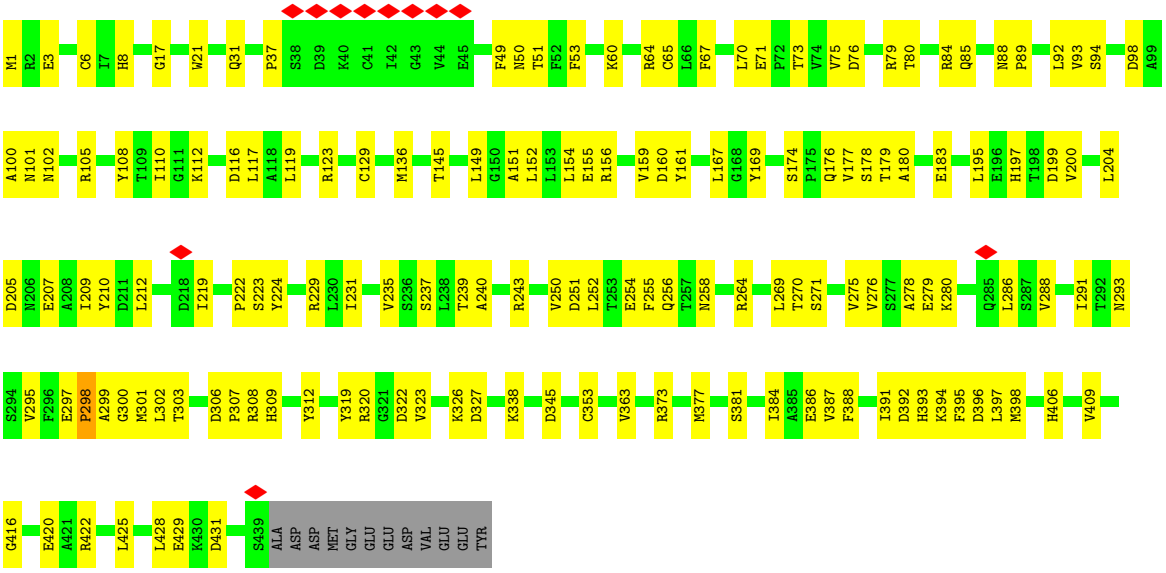
• Molecule 2: Tubulin alpha chain

Chain HC:



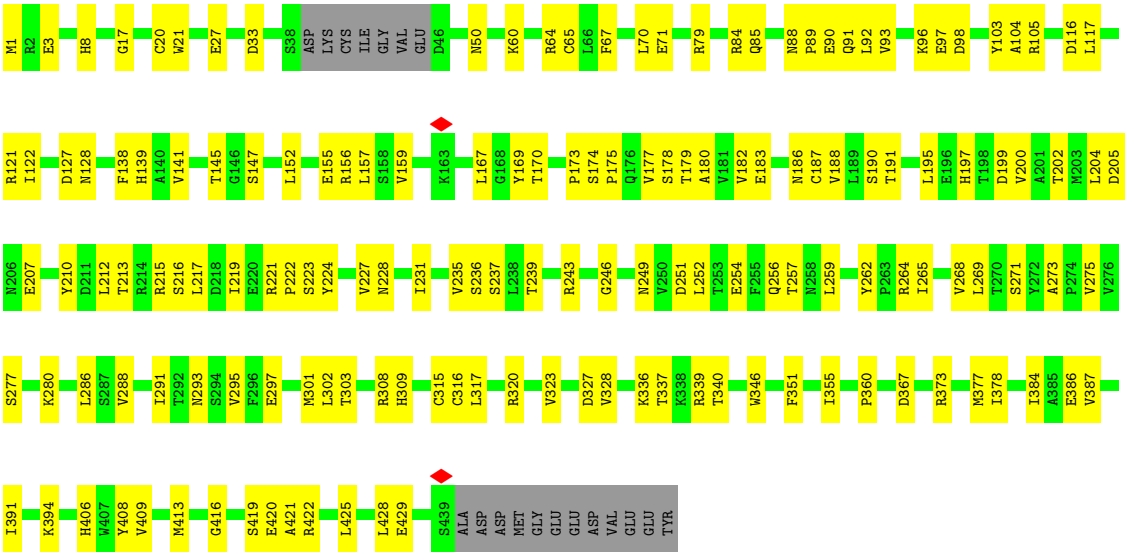
• Molecule 2: Tubulin alpha chain

Chain HE:



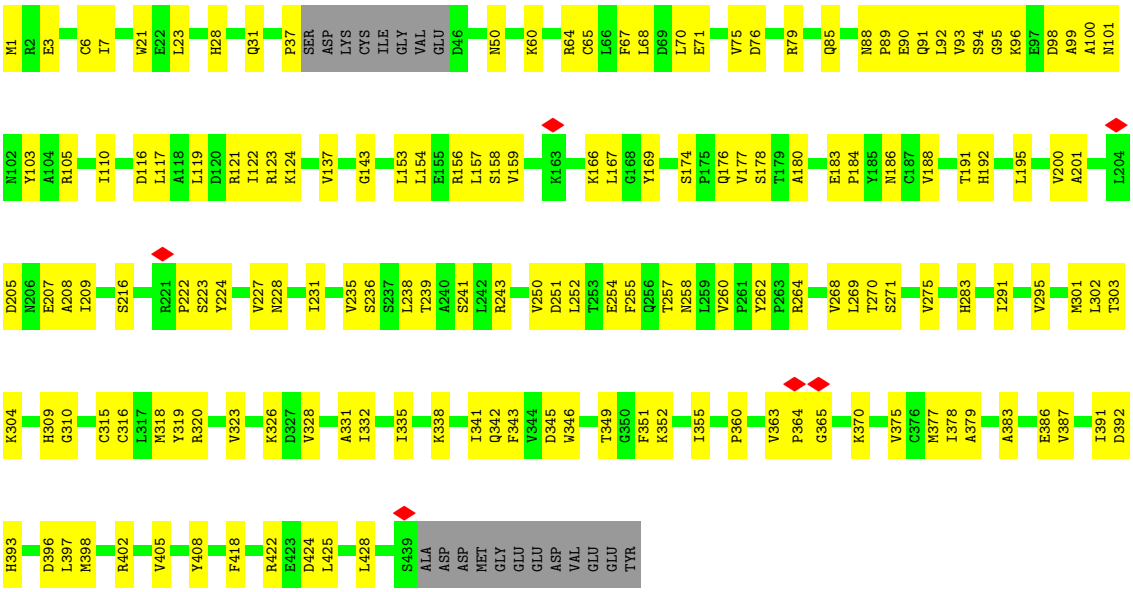
• Molecule 2: Tubulin alpha chain

Chain HG:



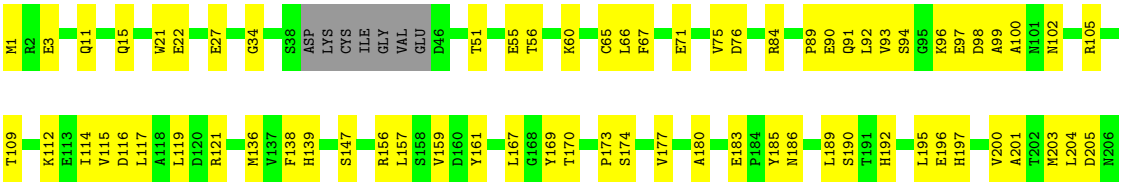
• Molecule 2: Tubulin alpha chain

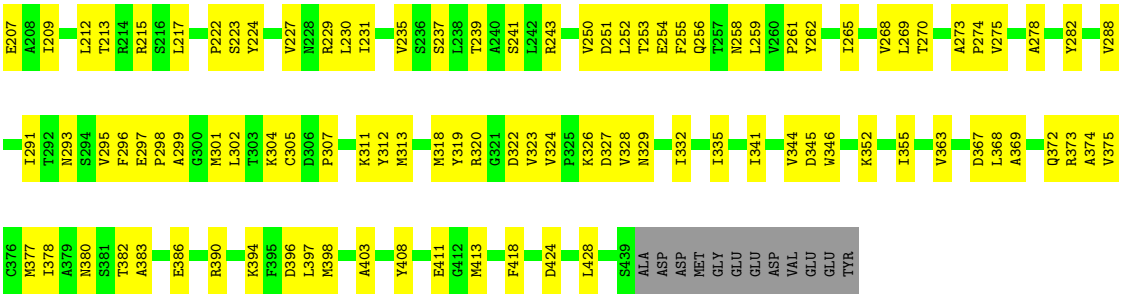
Chain HI:



• Molecule 2: Tubulin alpha chain

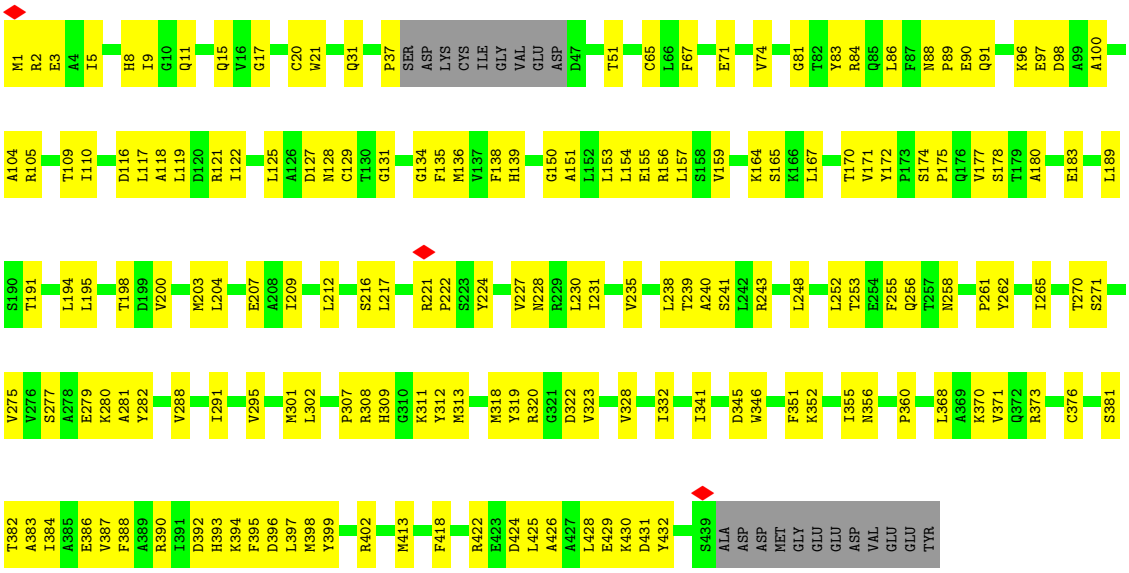
Chain HK:





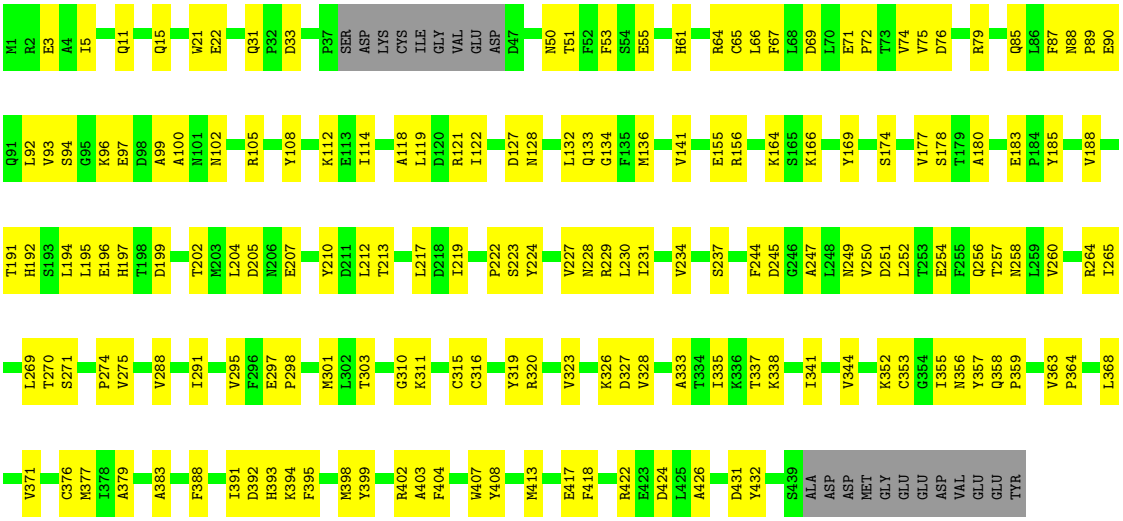
• Molecule 2: Tubulin alpha chain

Chain HM:



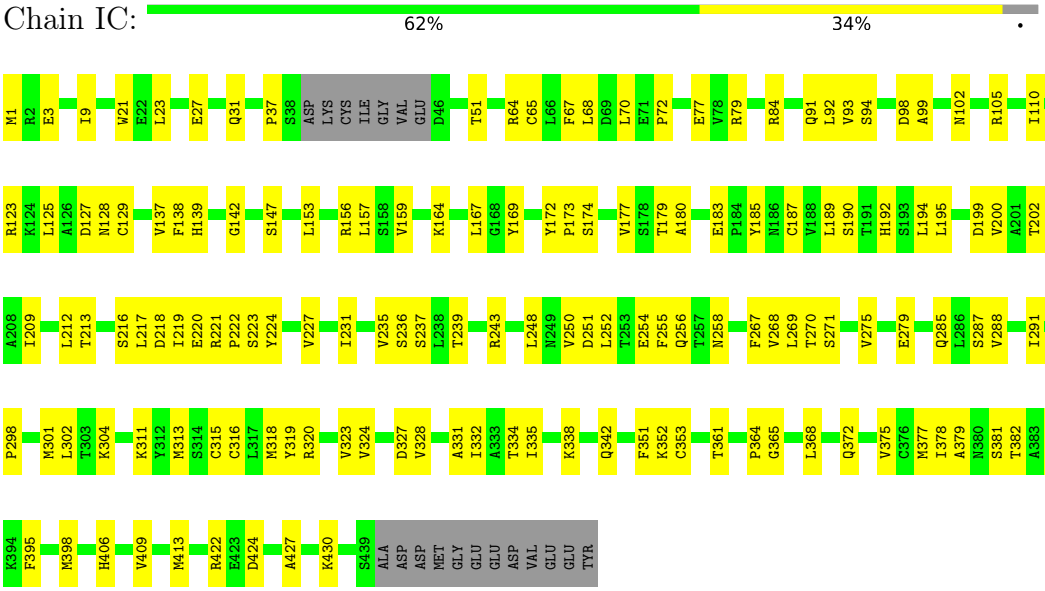
• Molecule 2: Tubulin alpha chain

Chain IA:



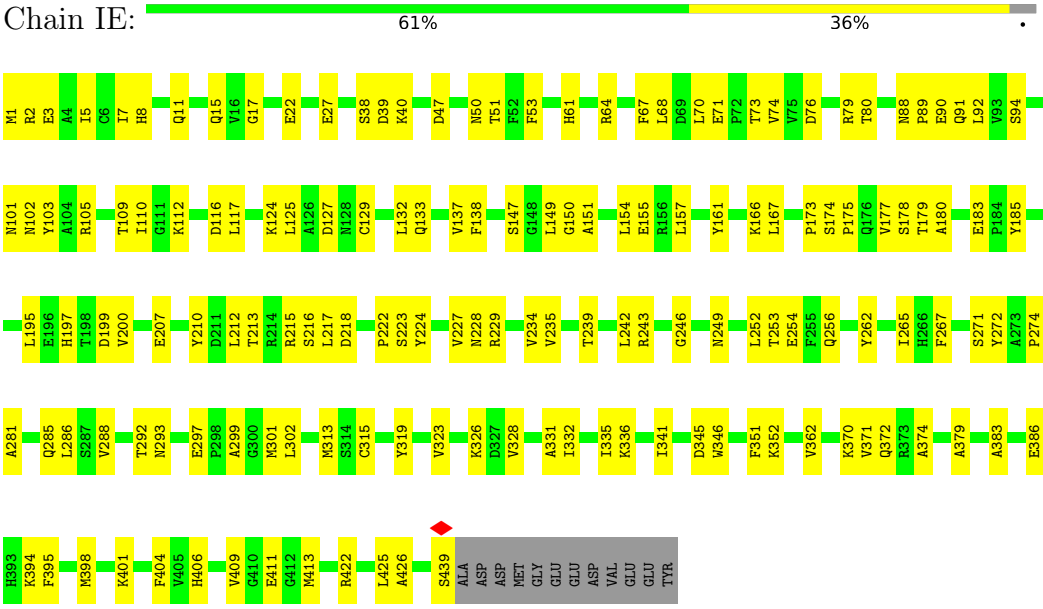
• Molecule 2: Tubulin alpha chain

Chain IC:



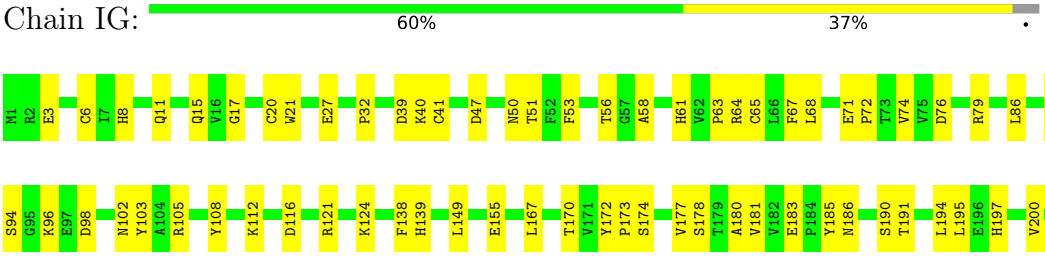
• Molecule 2: Tubulin alpha chain

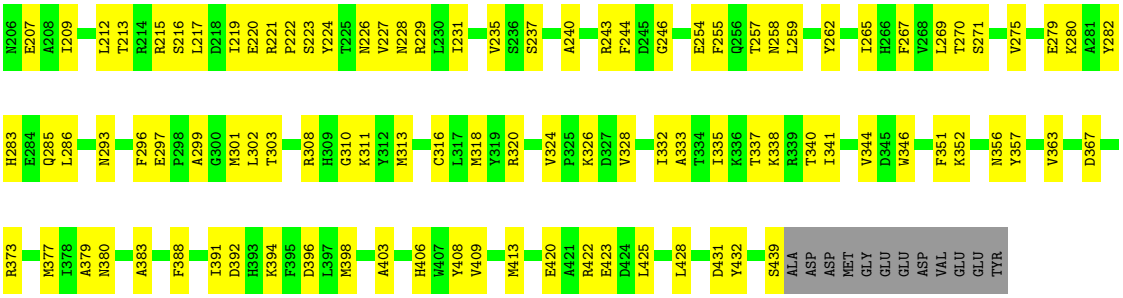
Chain IE:



• Molecule 2: Tubulin alpha chain

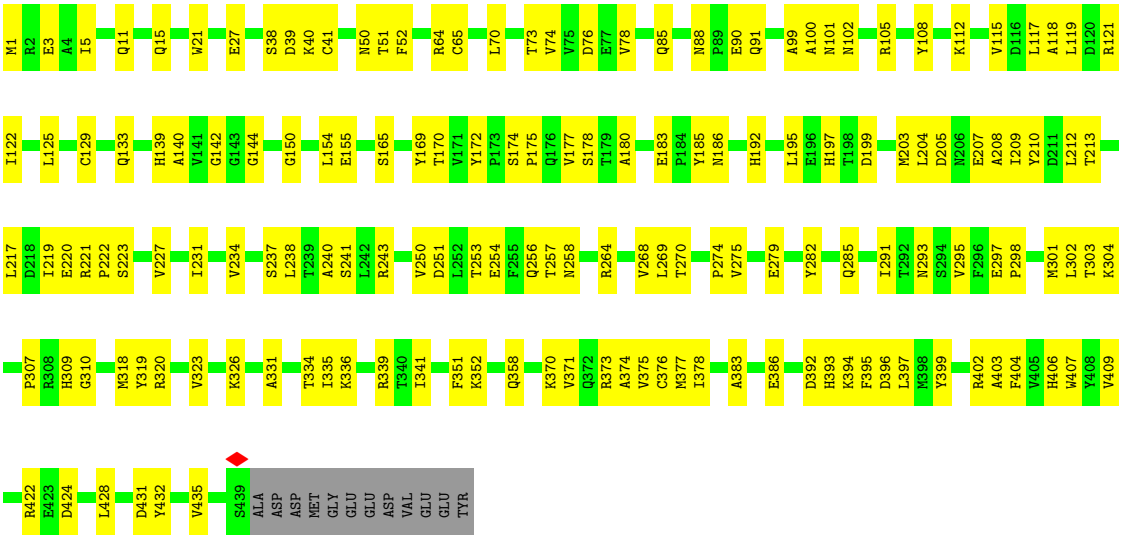
Chain IG:





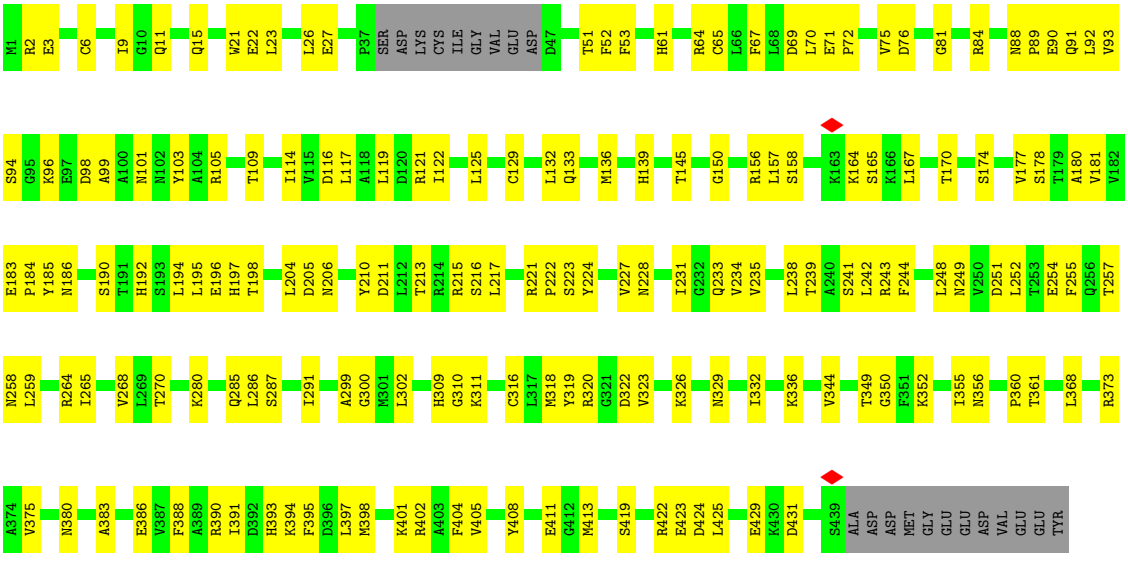
• Molecule 2: Tubulin alpha chain

Chain II:



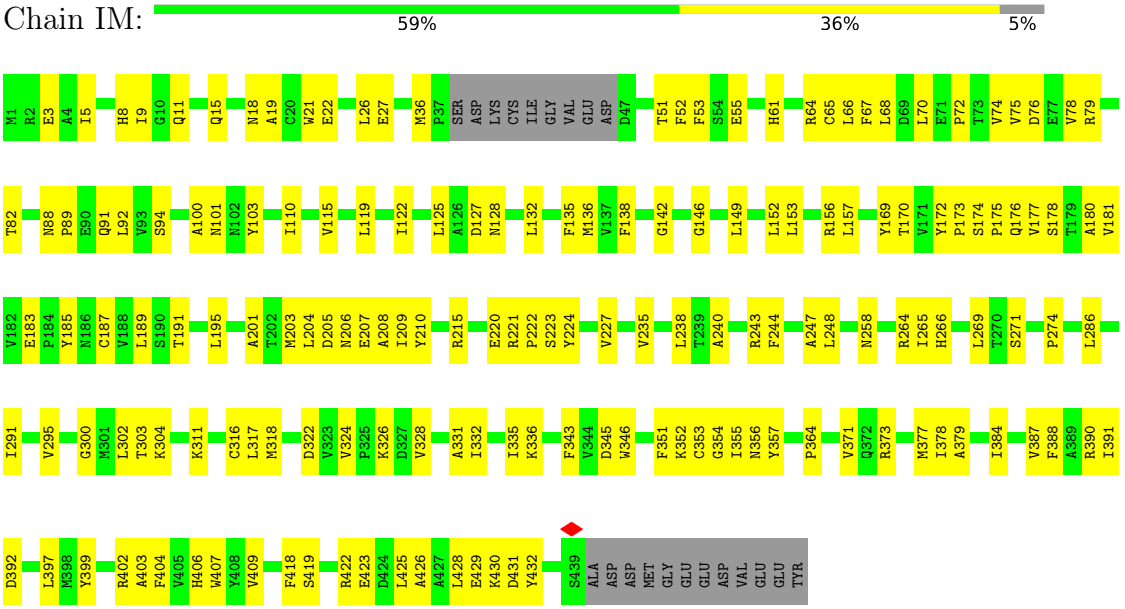
• Molecule 2: Tubulin alpha chain

Chain IK:



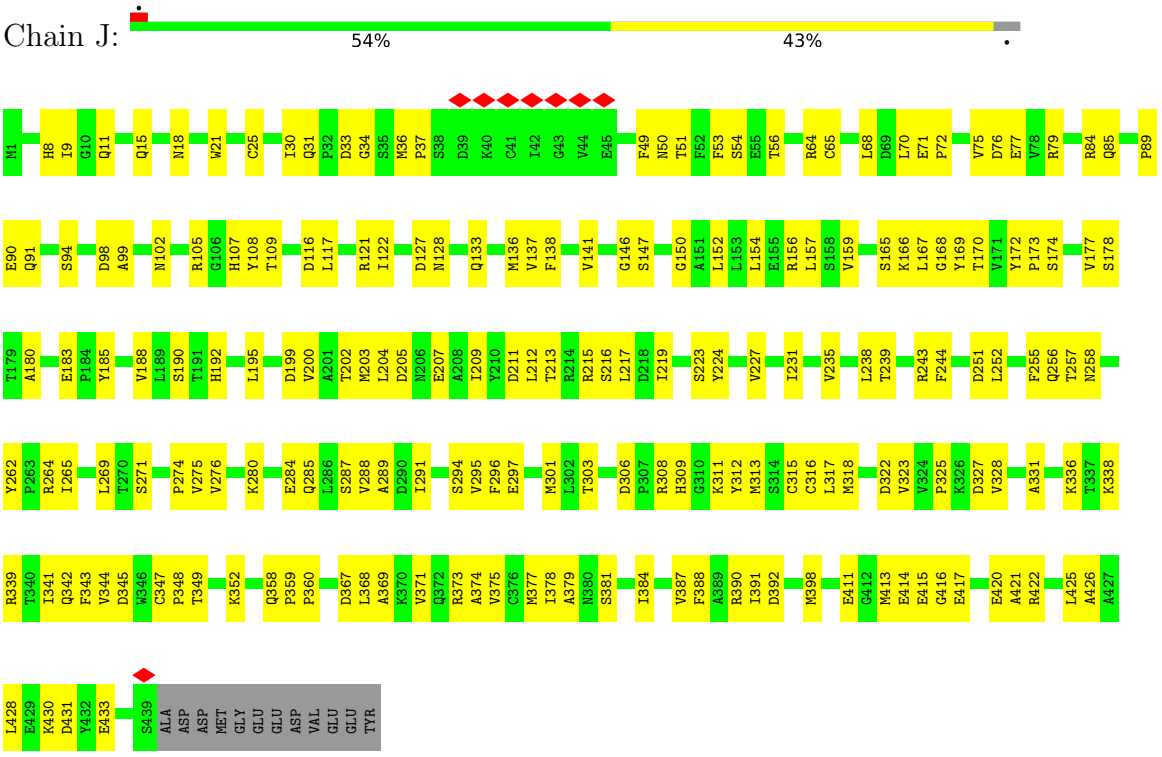
• Molecule 2: Tubulin alpha chain

Chain IM:



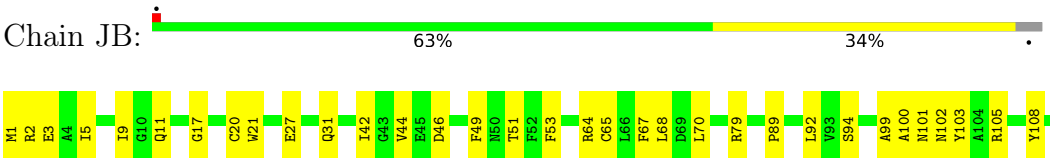
• Molecule 2: Tubulin alpha chain

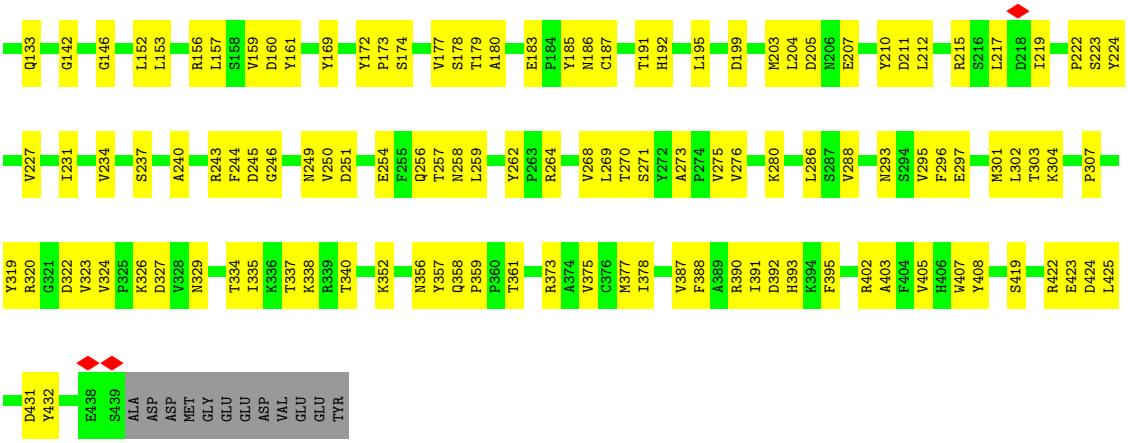
Chain J:



• Molecule 2: Tubulin alpha chain

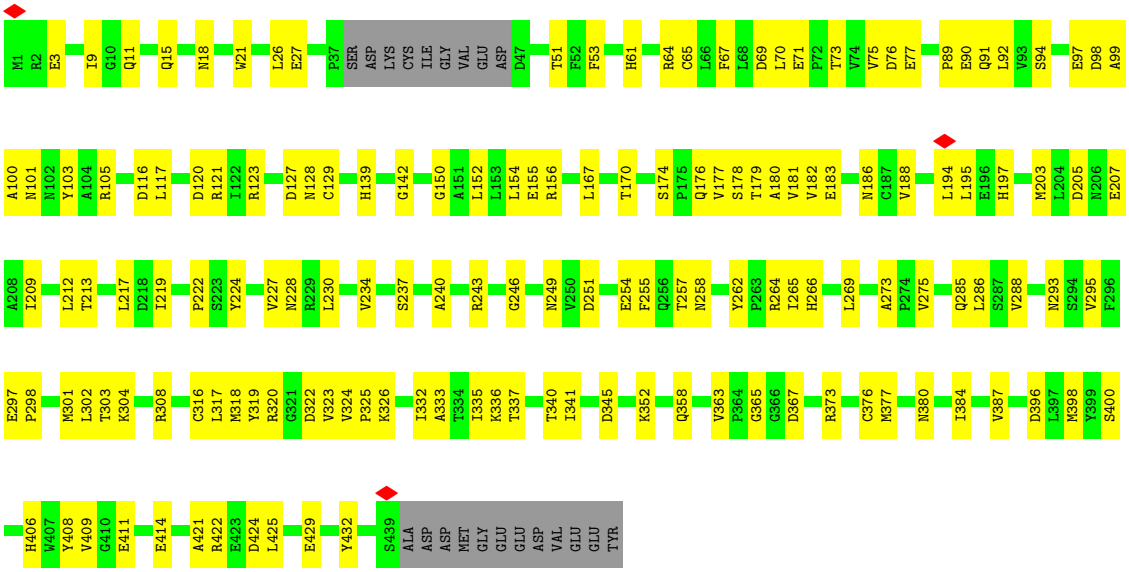
Chain JB:





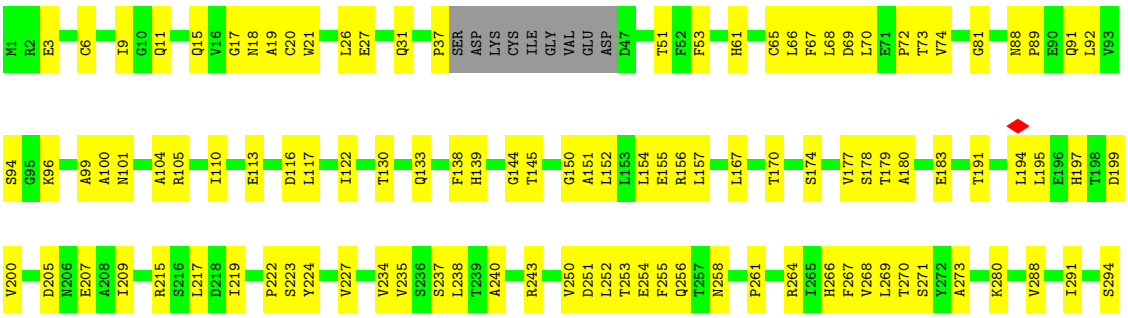
• Molecule 2: Tubulin alpha chain

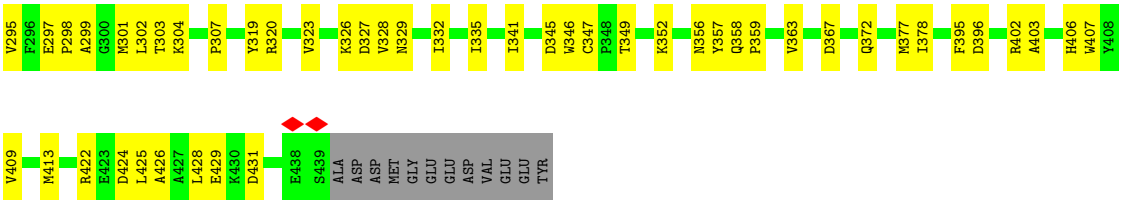
Chain JD:



• Molecule 2: Tubulin alpha chain

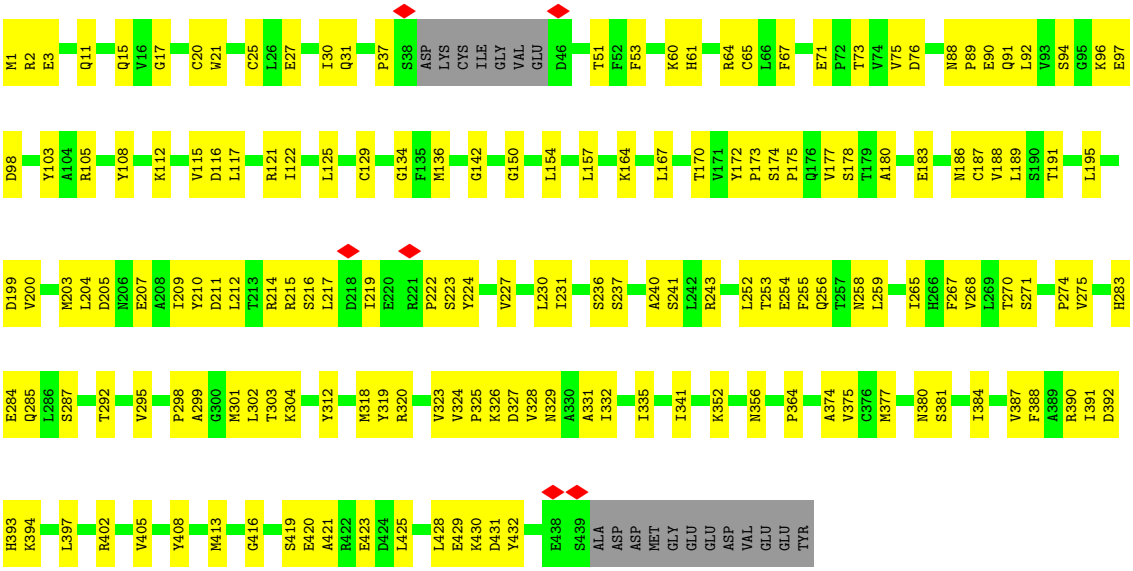
Chain JF:





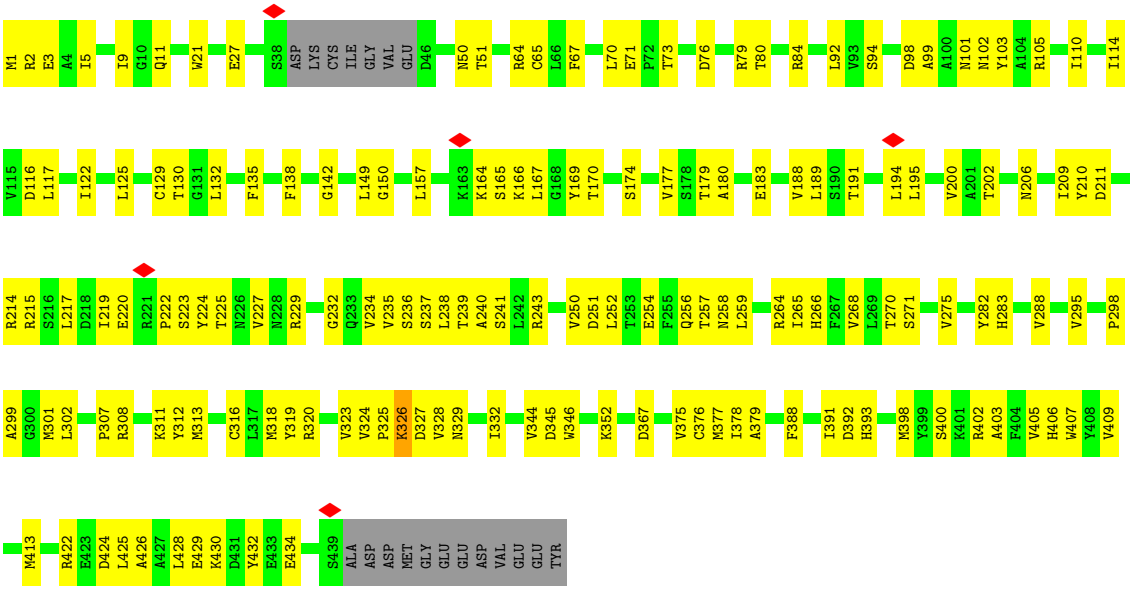
• Molecule 2: Tubulin alpha chain

Chain JH:



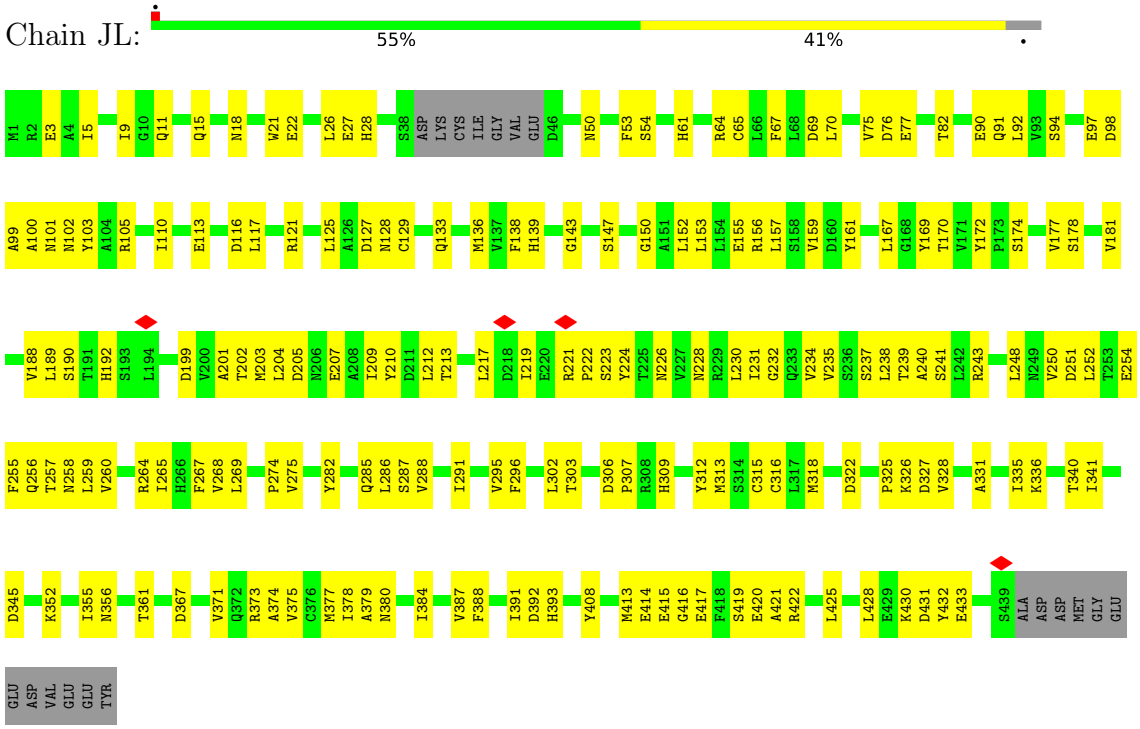
• Molecule 2: Tubulin alpha chain

Chain JJ:



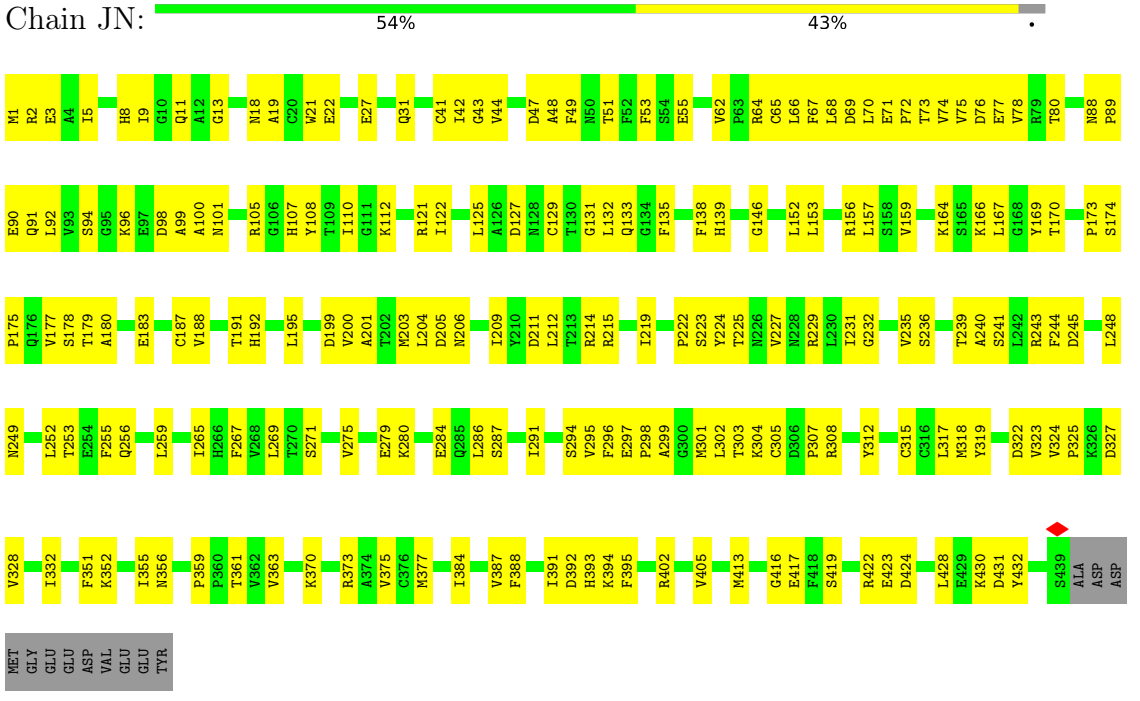
• Molecule 2: Tubulin alpha chain

Chain JL:



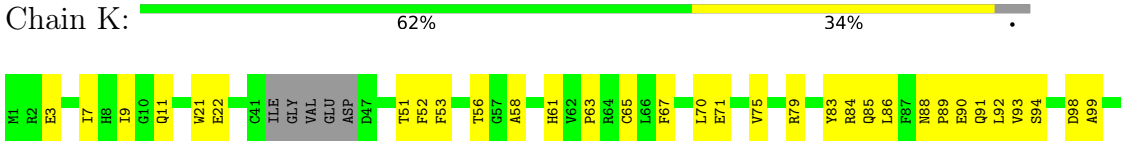
• Molecule 2: Tubulin alpha chain

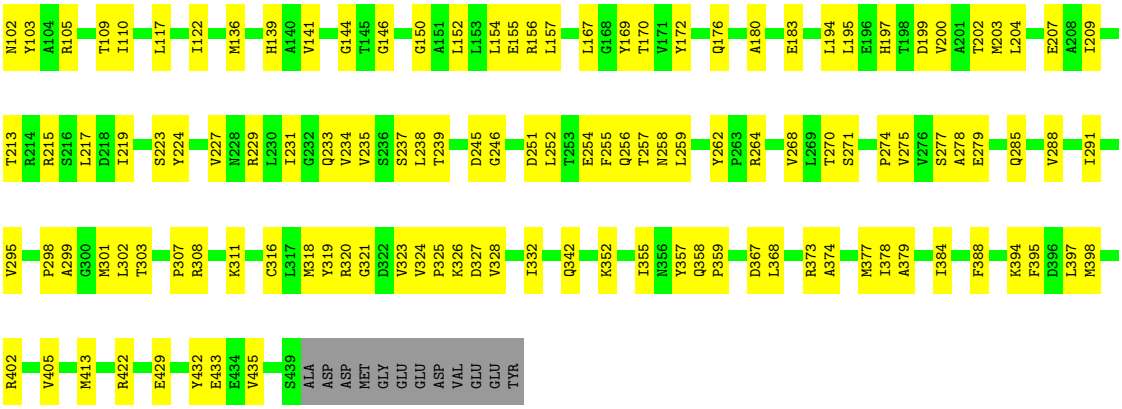
Chain JN:



• Molecule 2: Tubulin alpha chain

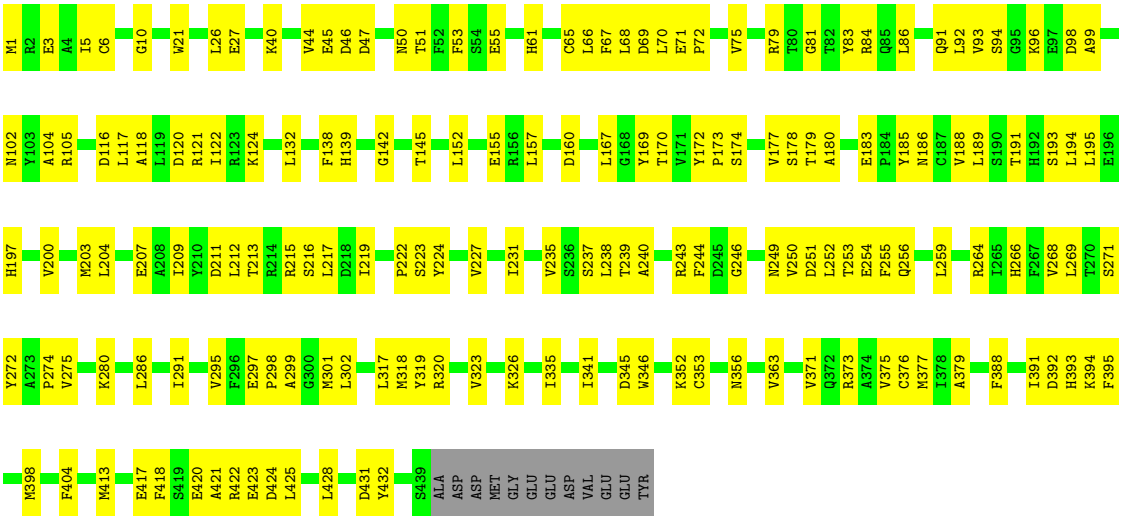
Chain K:





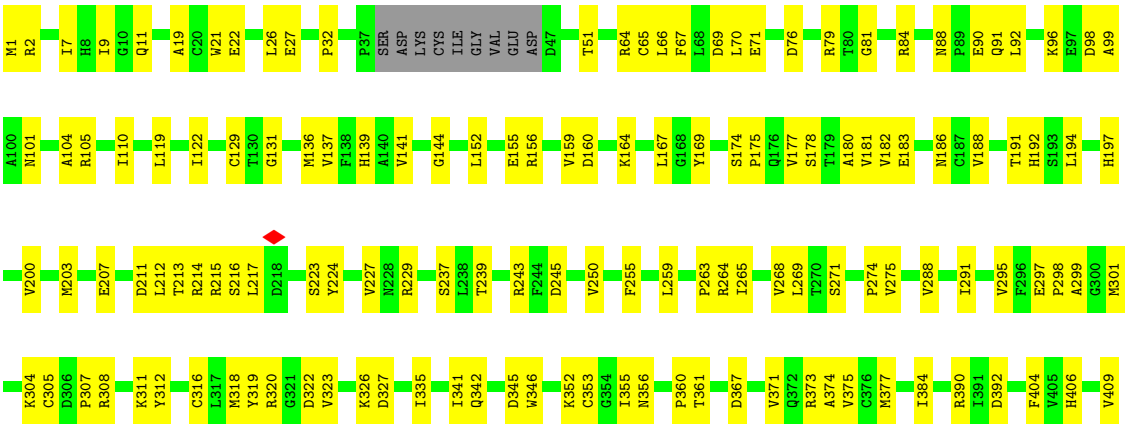
• Molecule 2: Tubulin alpha chain

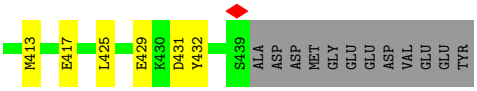
Chain KB:



• Molecule 2: Tubulin alpha chain

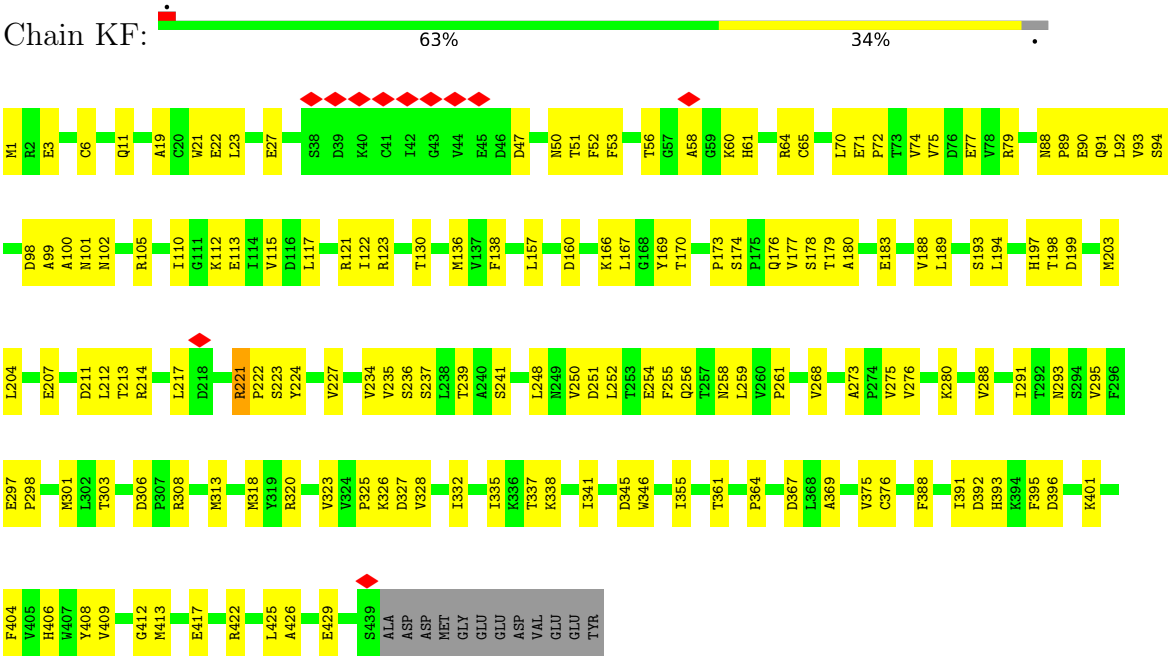
Chain KD:





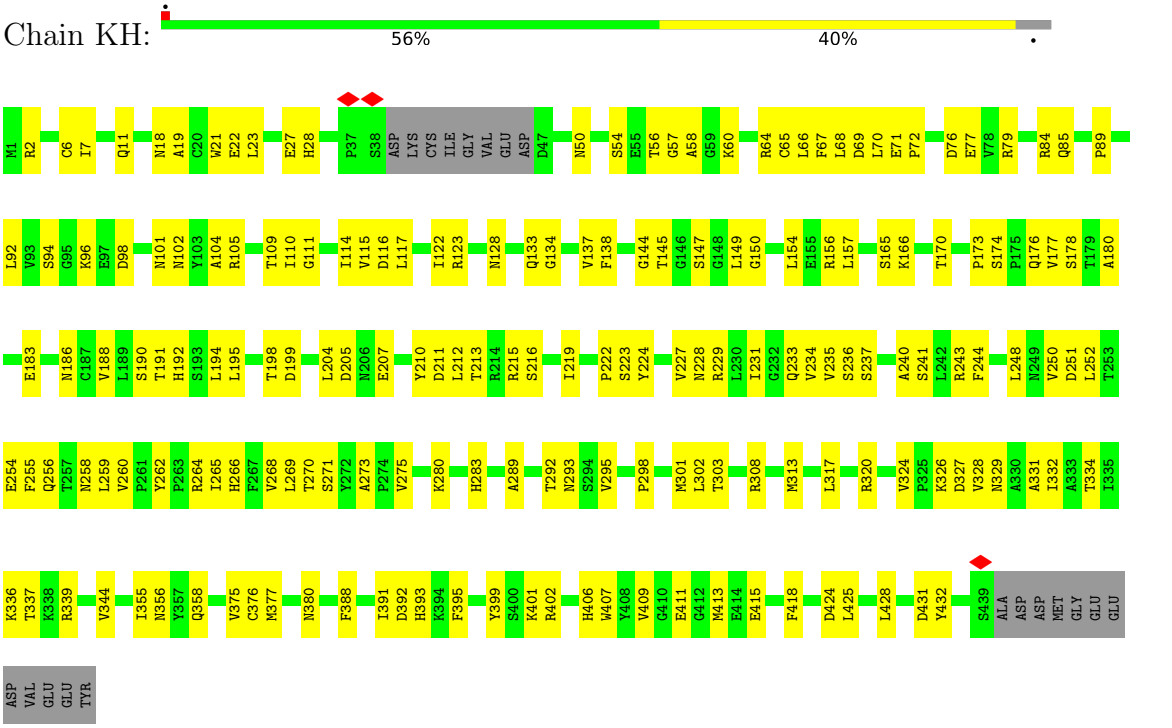
• Molecule 2: Tubulin alpha chain

Chain KF:



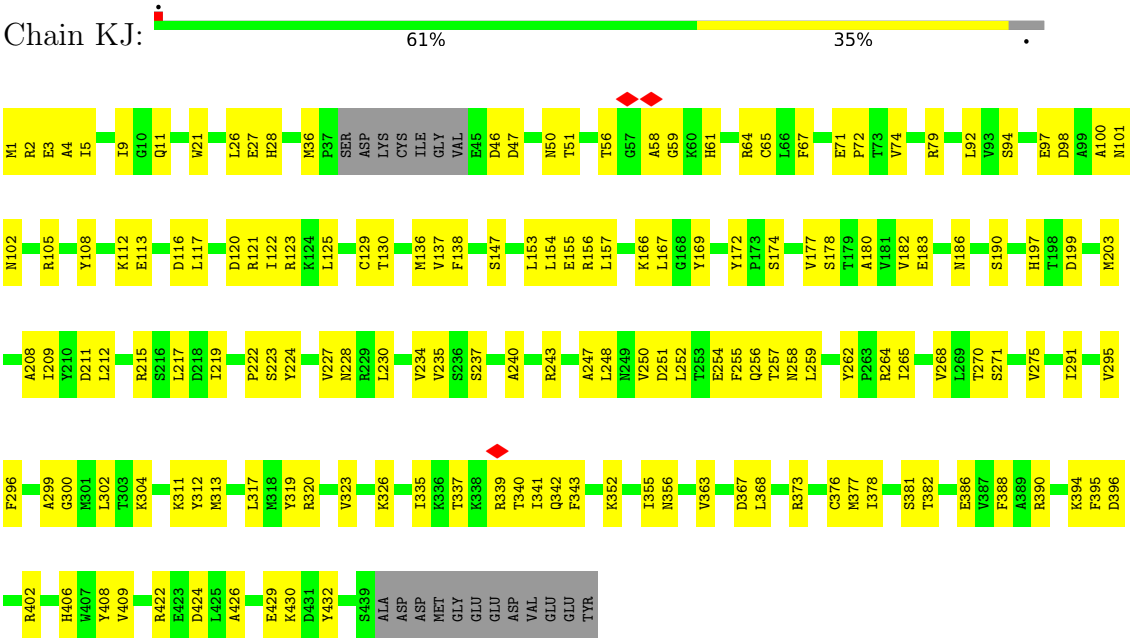
• Molecule 2: Tubulin alpha chain

Chain KH:



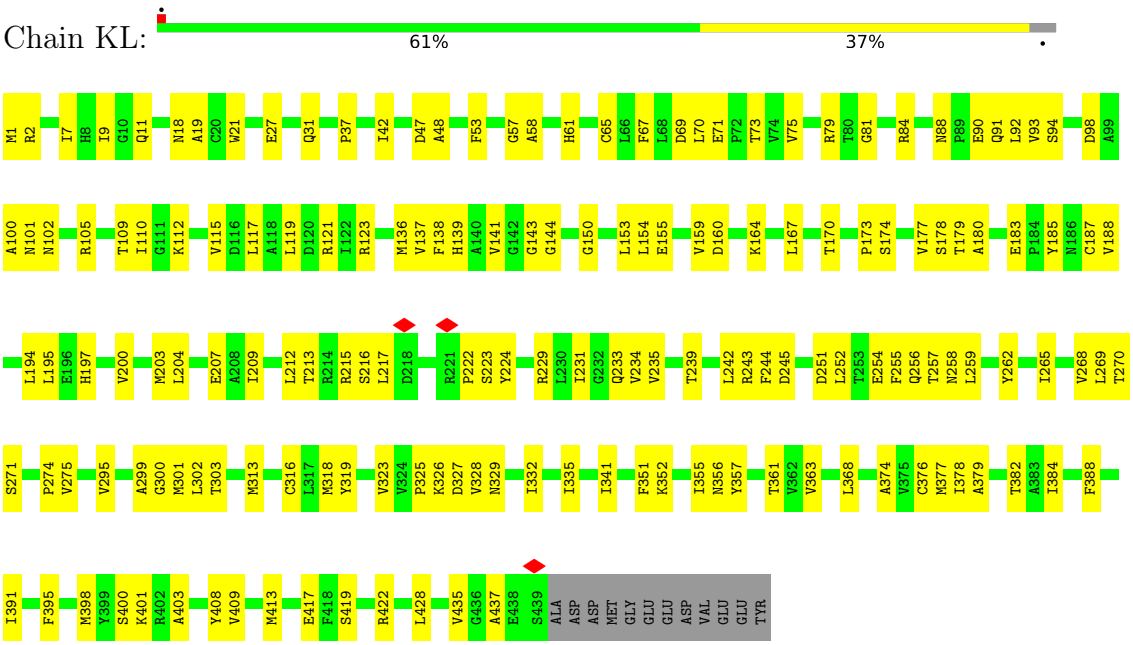
• Molecule 2: Tubulin alpha chain

Chain KJ:



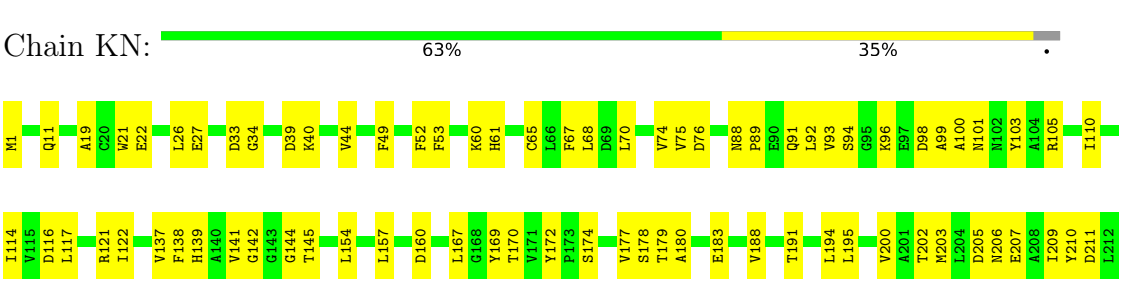
- Molecule 2: Tubulin alpha chain

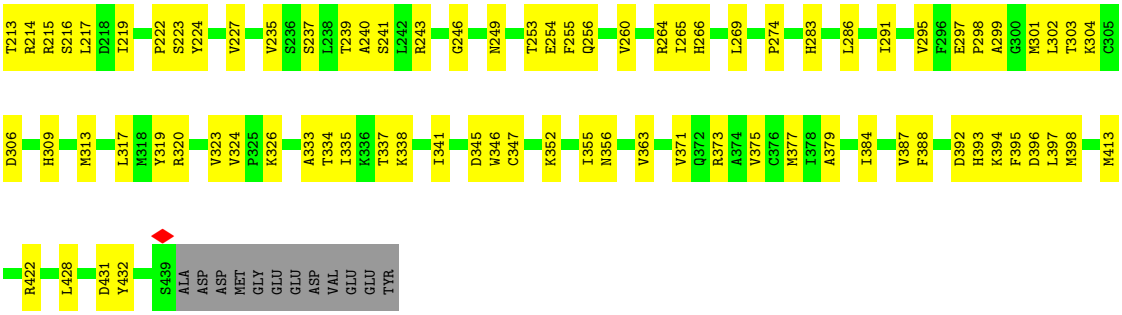
Chain KL:



- Molecule 2: Tubulin alpha chain

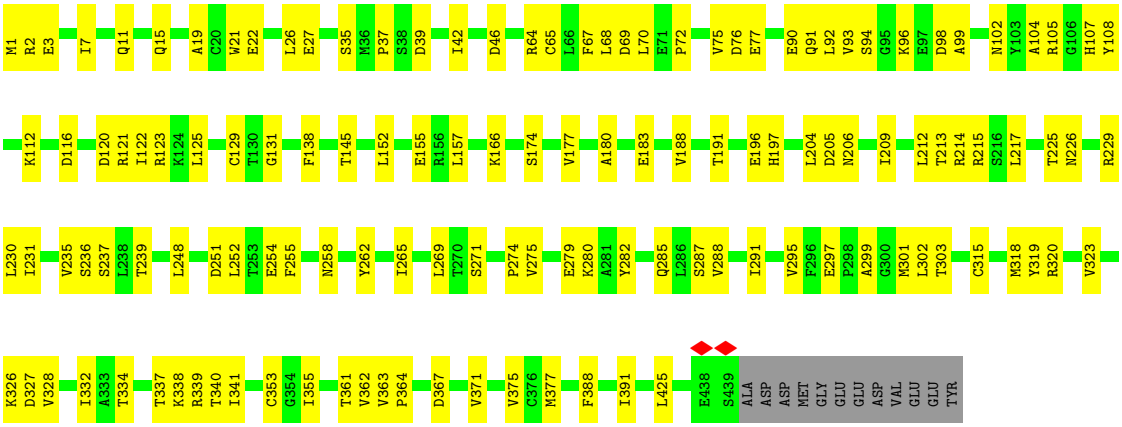
Chain KN:





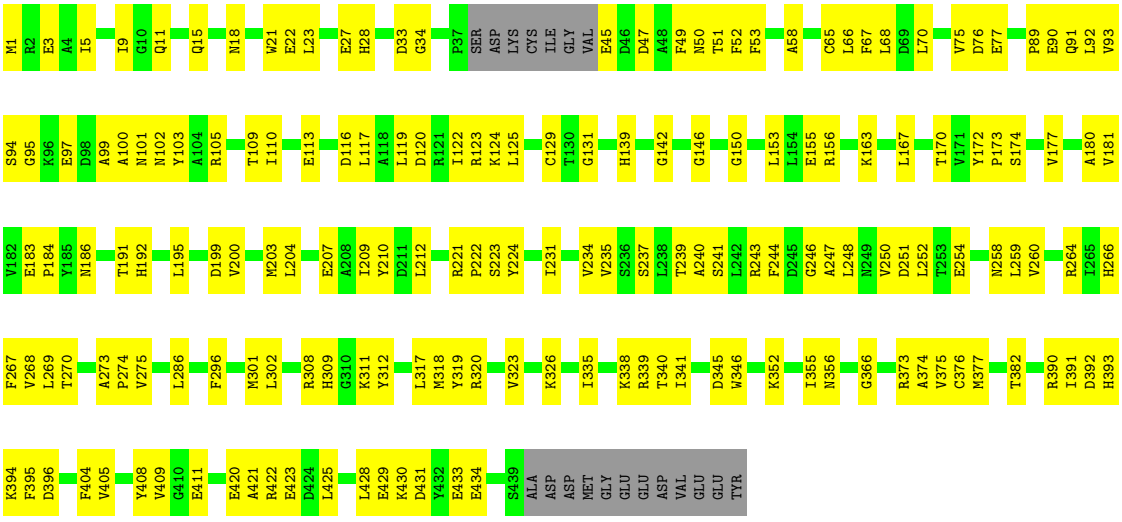
• Molecule 2: Tubulin alpha chain

Chain L:



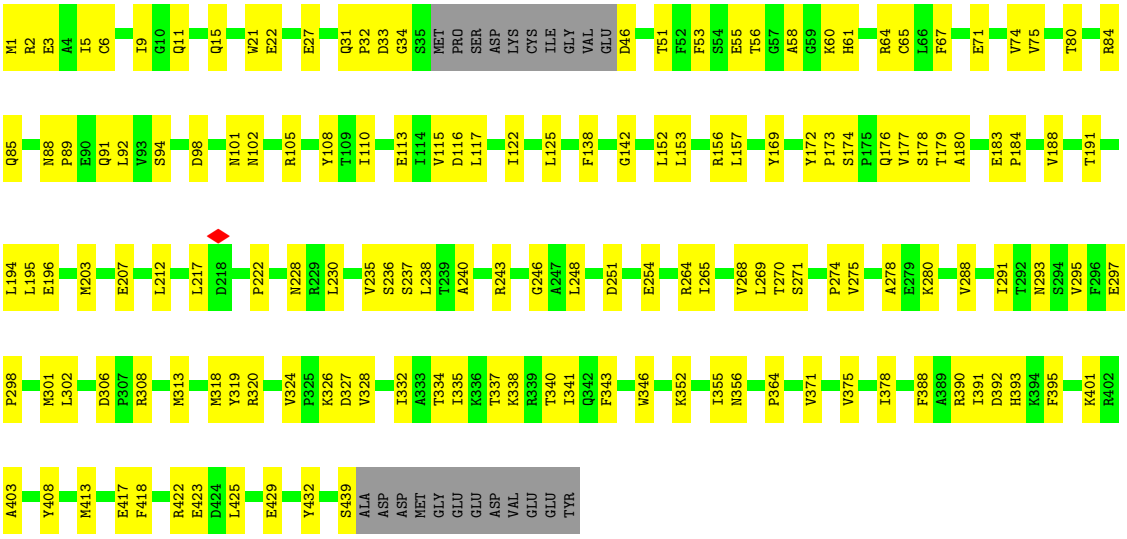
• Molecule 2: Tubulin alpha chain

Chain LB:



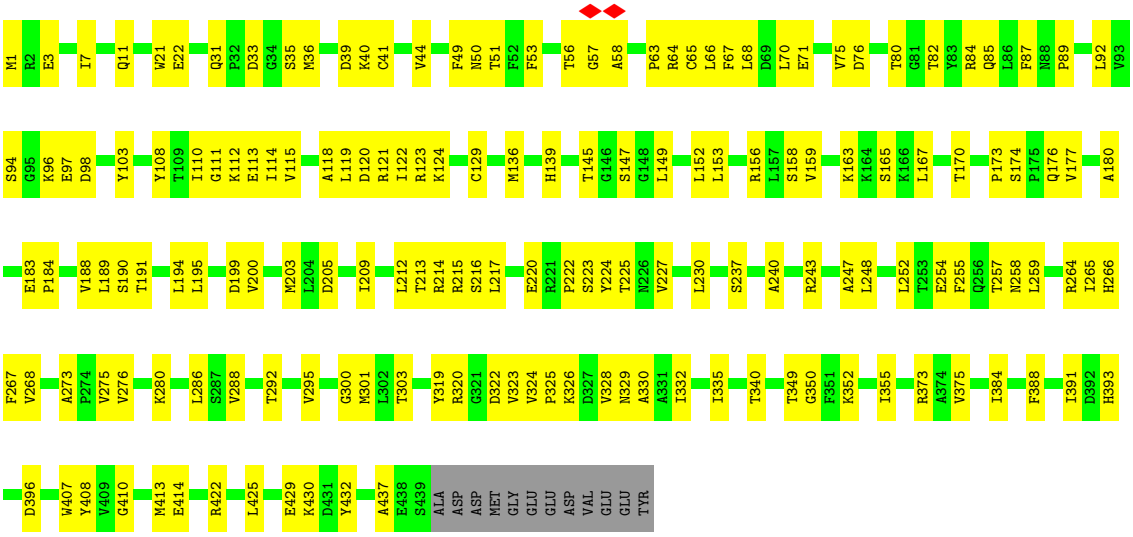
• Molecule 2: Tubulin alpha chain

Chain LD:



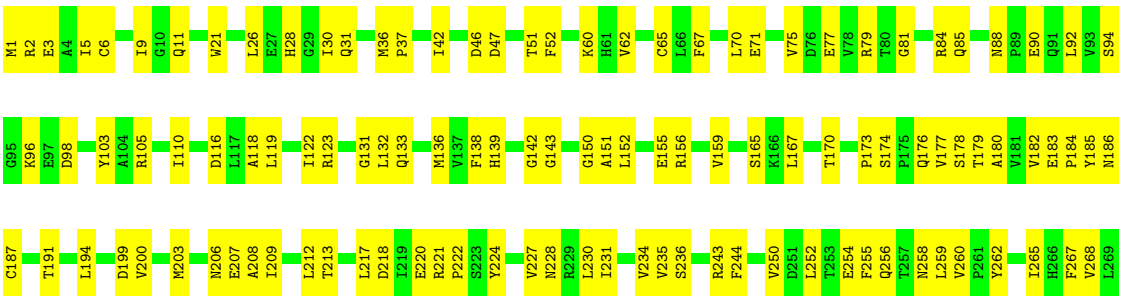
• Molecule 2: Tubulin alpha chain

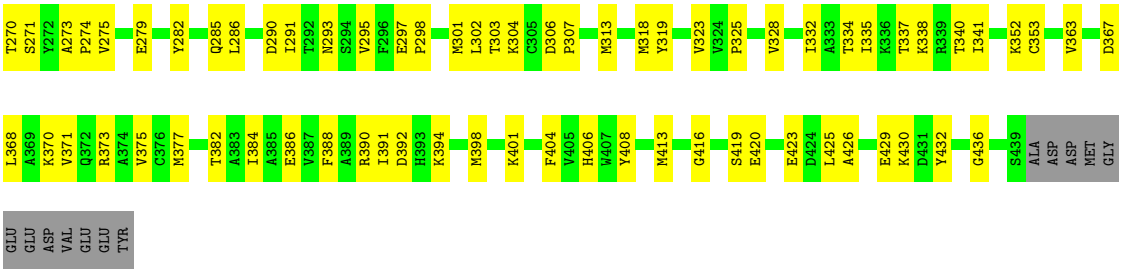
Chain LF:



• Molecule 2: Tubulin alpha chain

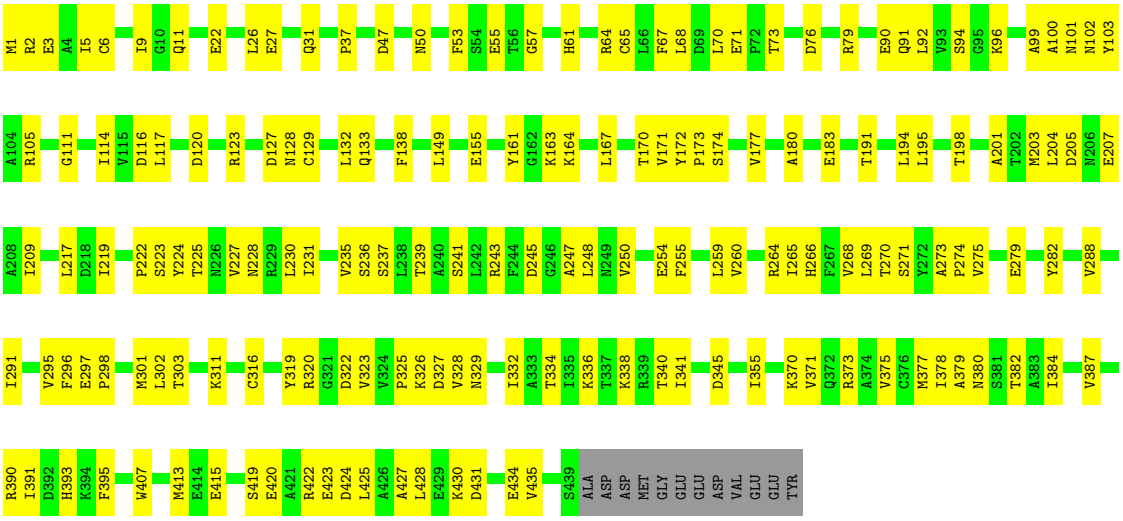
Chain LH:





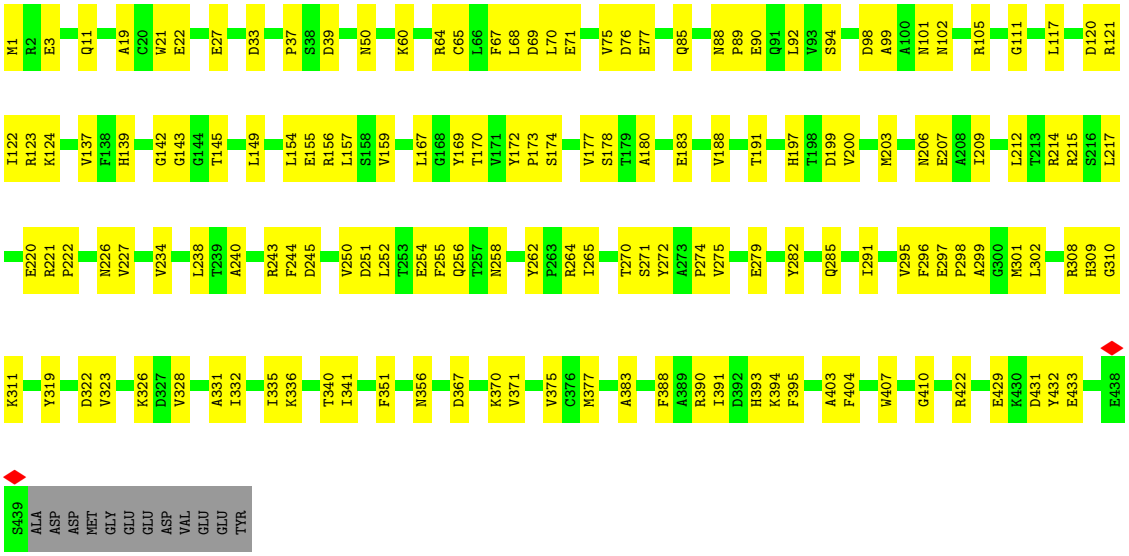
• Molecule 2: Tubulin alpha chain

Chain LJ:



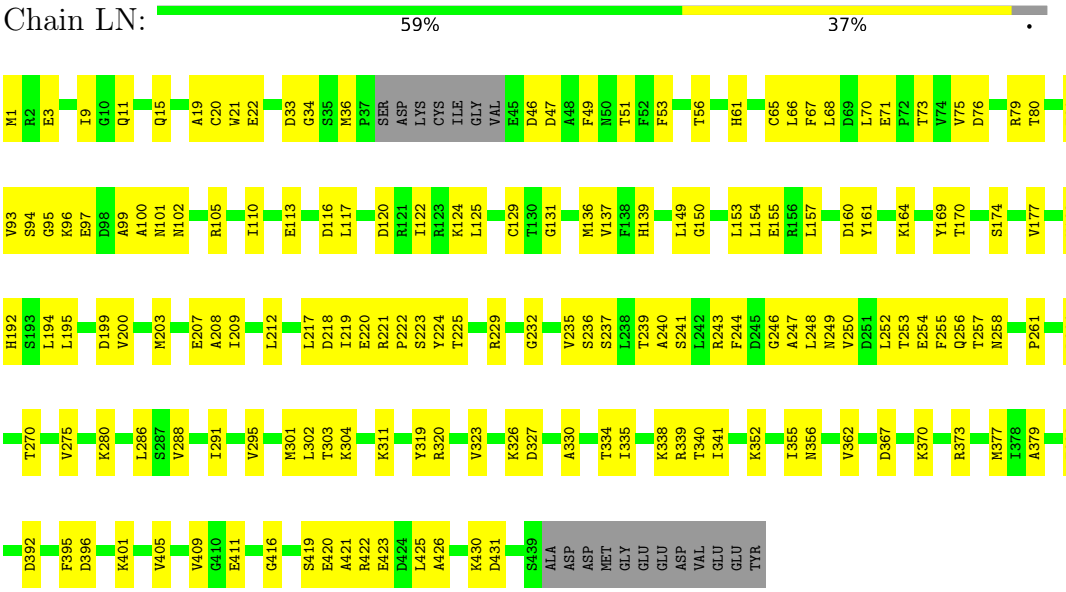
• Molecule 2: Tubulin alpha chain

Chain LL:



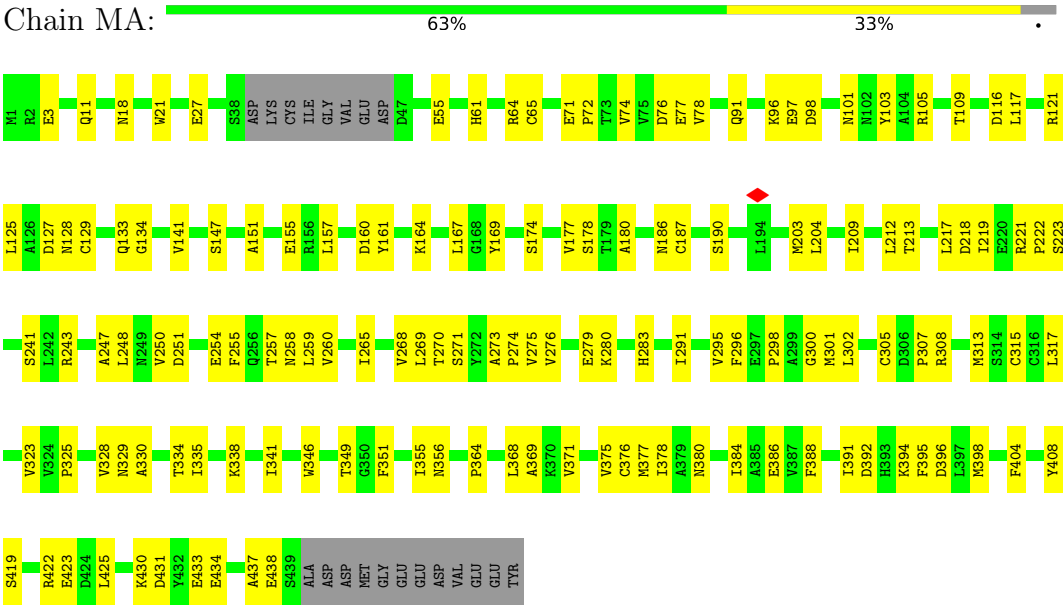
• Molecule 2: Tubulin alpha chain

Chain LN:



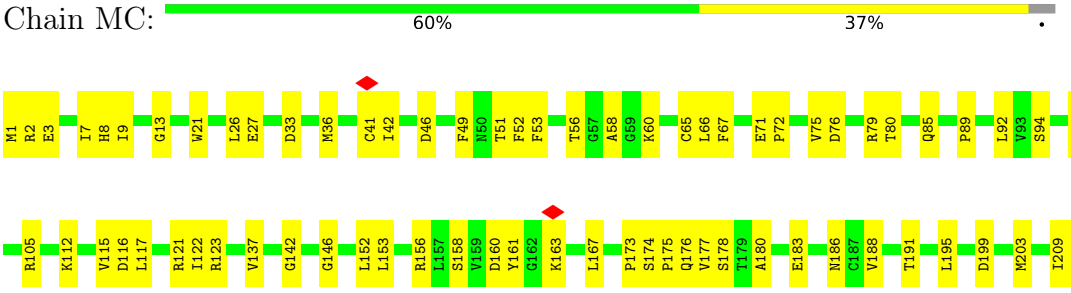
• Molecule 2: Tubulin alpha chain

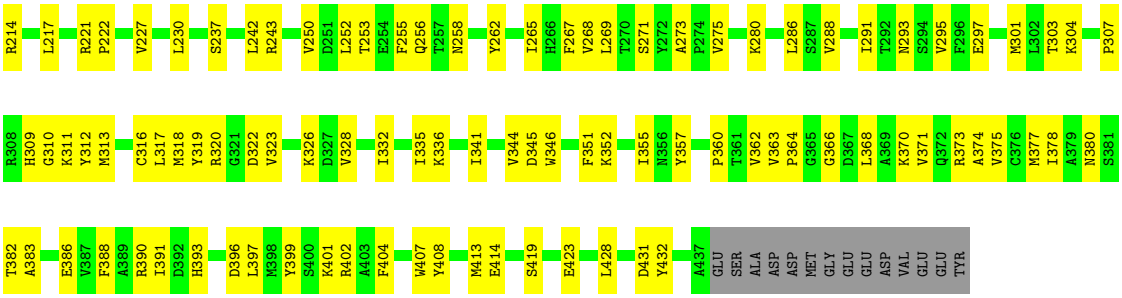
Chain MA:



• Molecule 2: Tubulin alpha chain

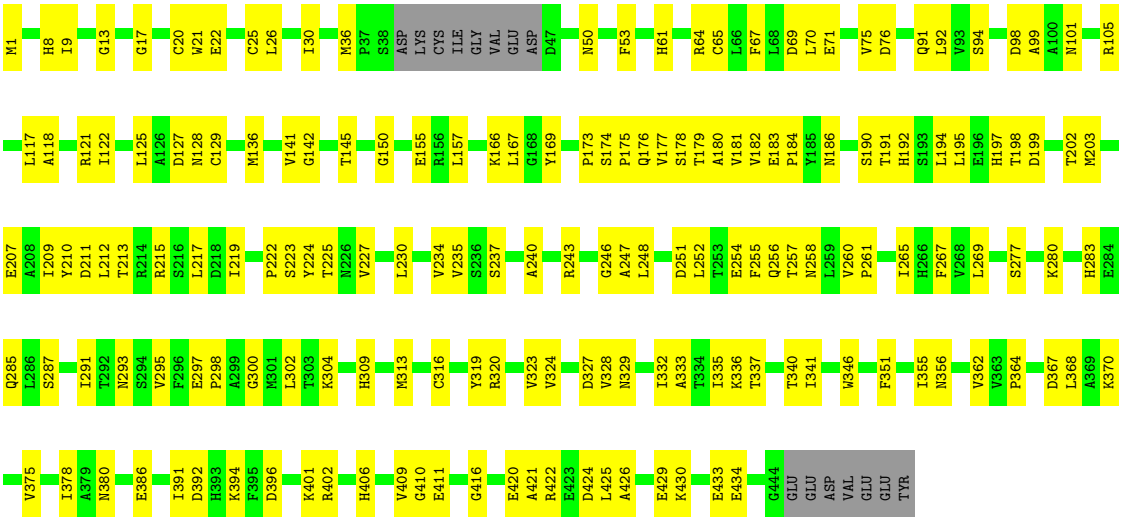
Chain MC:





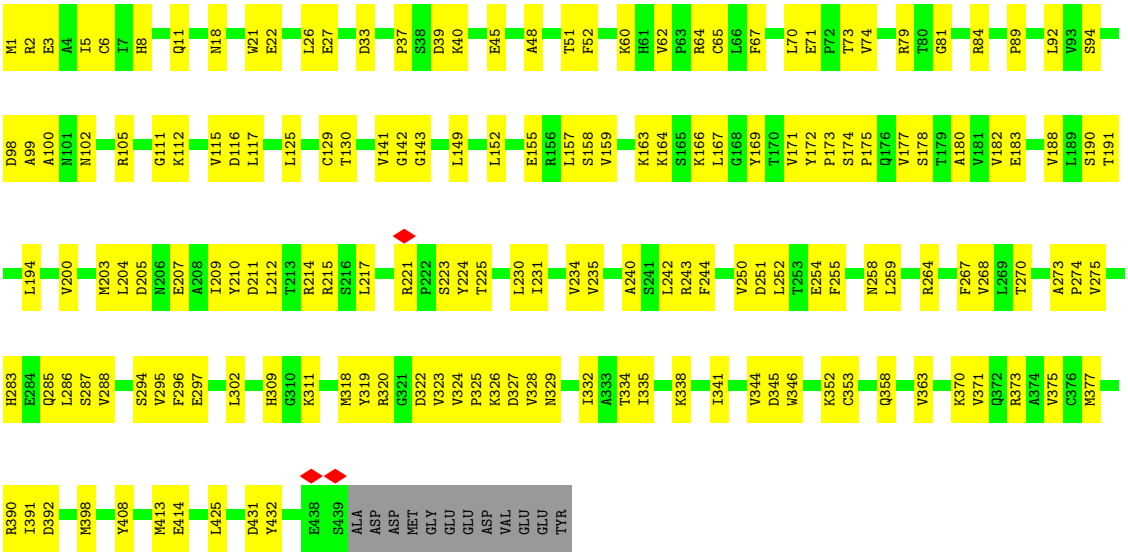
• Molecule 2: Tubulin alpha chain

Chain ME:



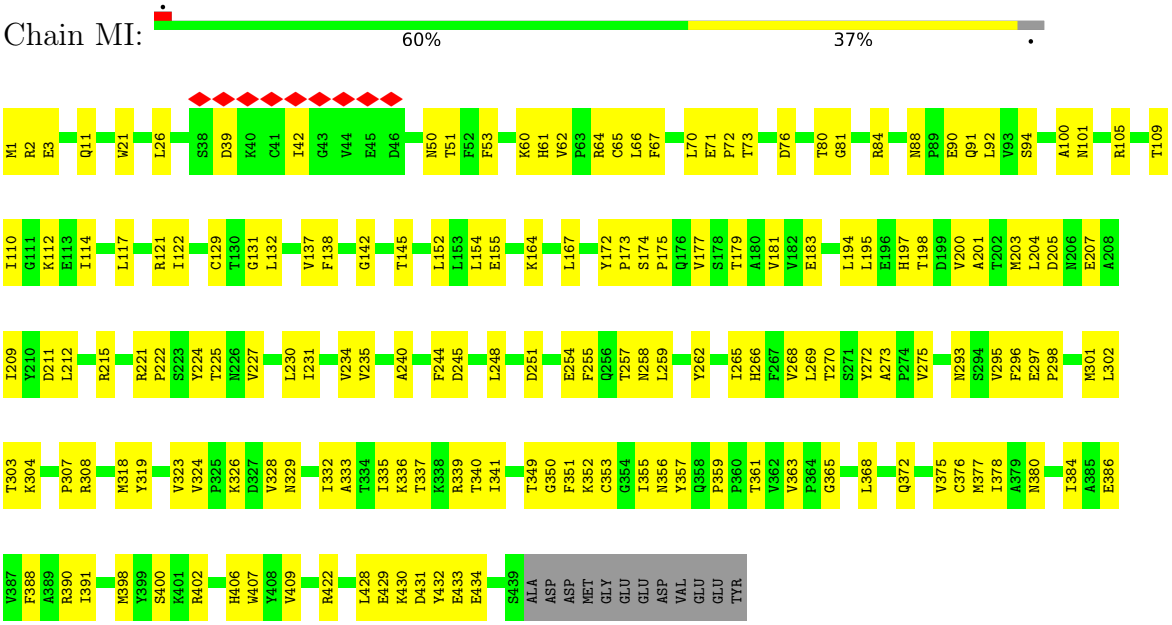
• Molecule 2: Tubulin alpha chain

Chain MG:



• Molecule 2: Tubulin alpha chain

Chain MI:



• Molecule 2: Tubulin alpha chain

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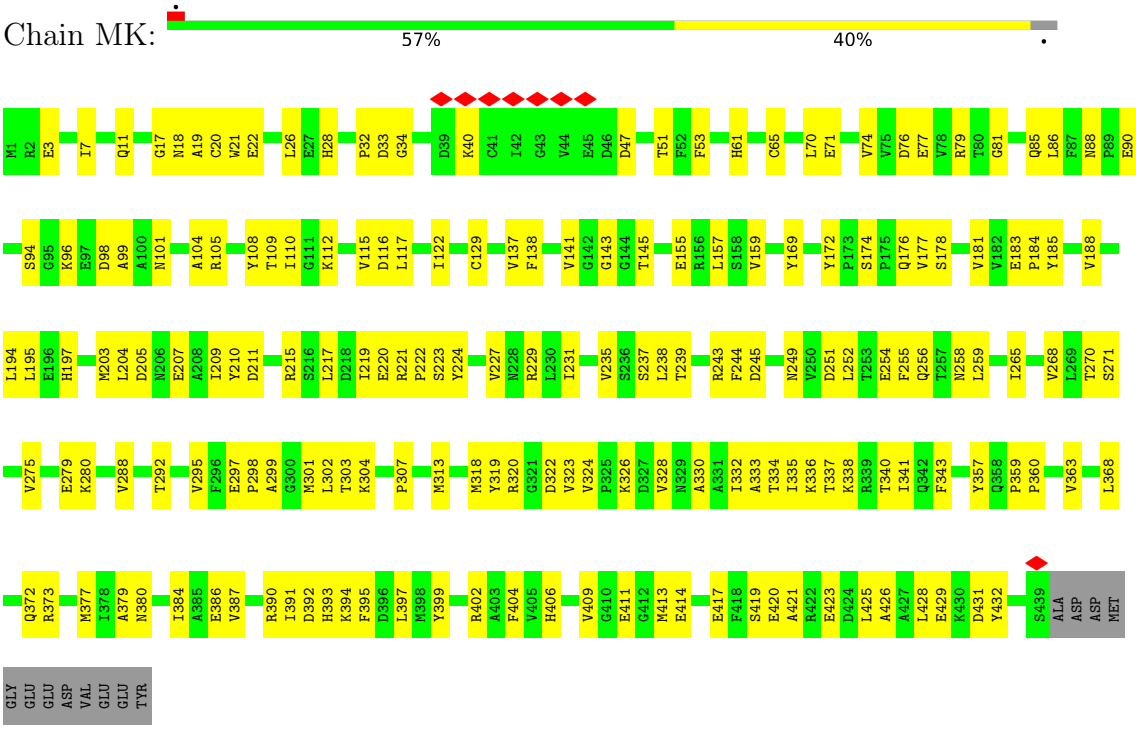
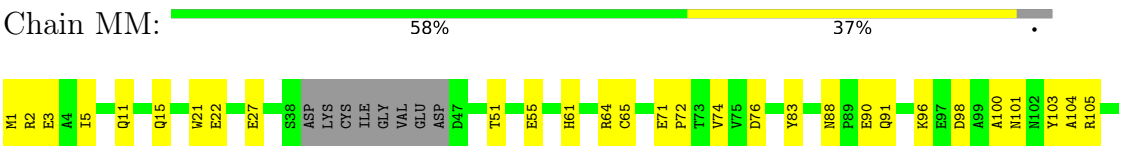
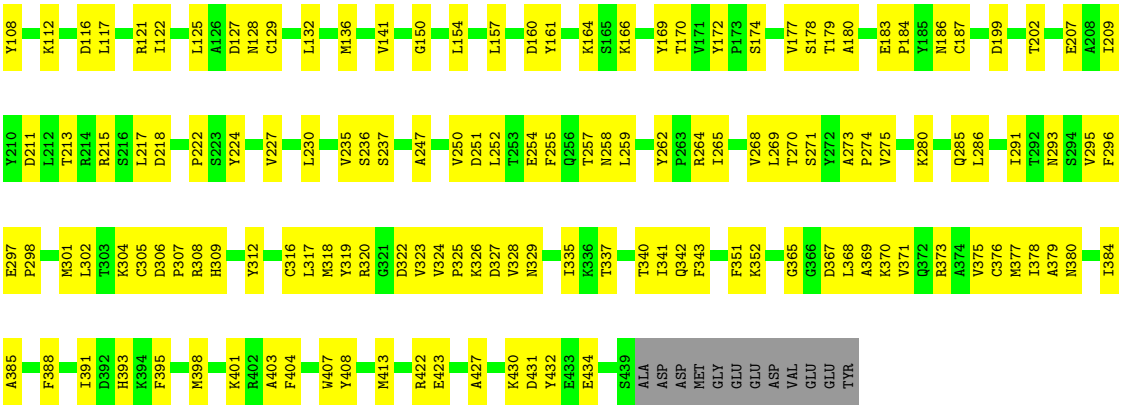


• Molecule 2: Tubulin alpha chain

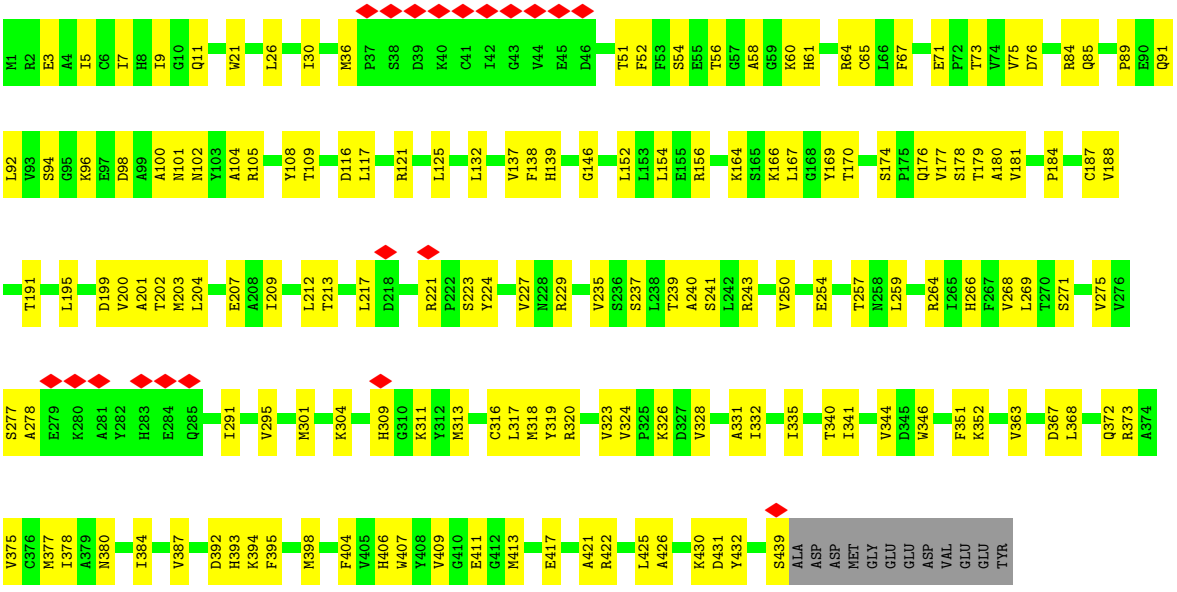
Chain MM:





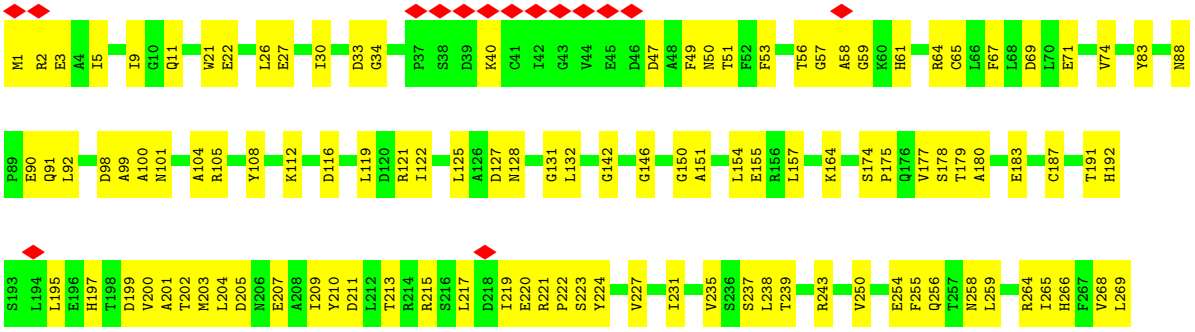
• Molecule 2: Tubulin alpha chain

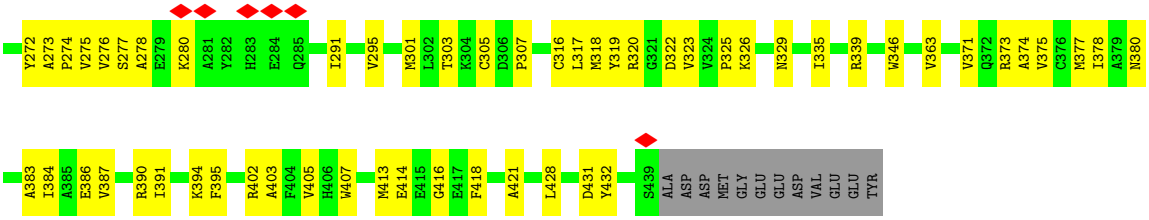
Chain NA:



• Molecule 2: Tubulin alpha chain

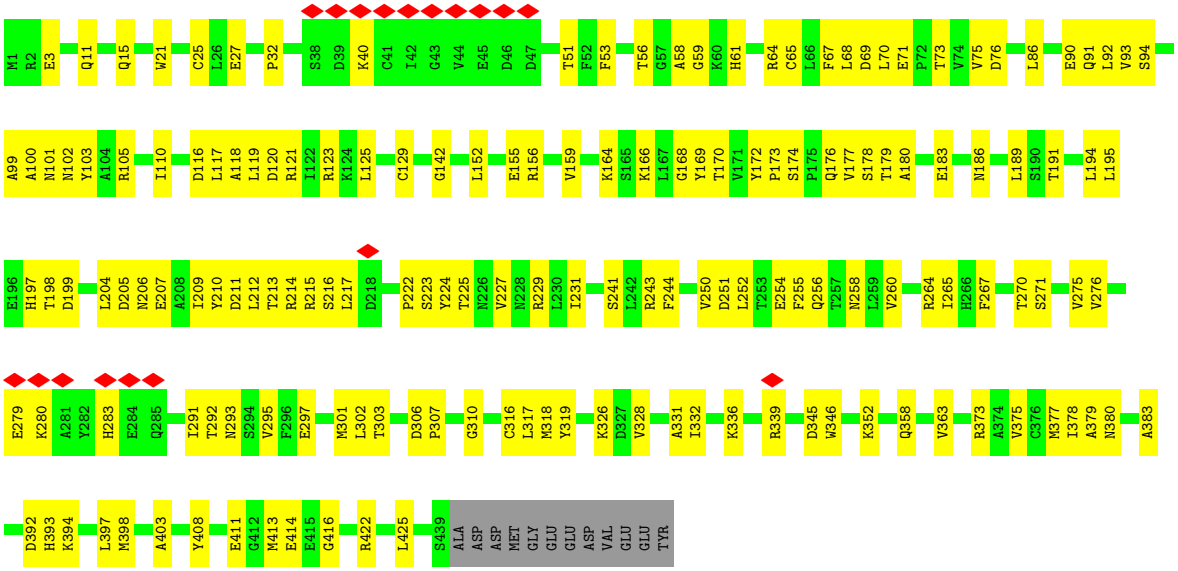
Chain NC:





• Molecule 2: Tubulin alpha chain

Chain NE:



• Molecule 2: Tubulin alpha chain

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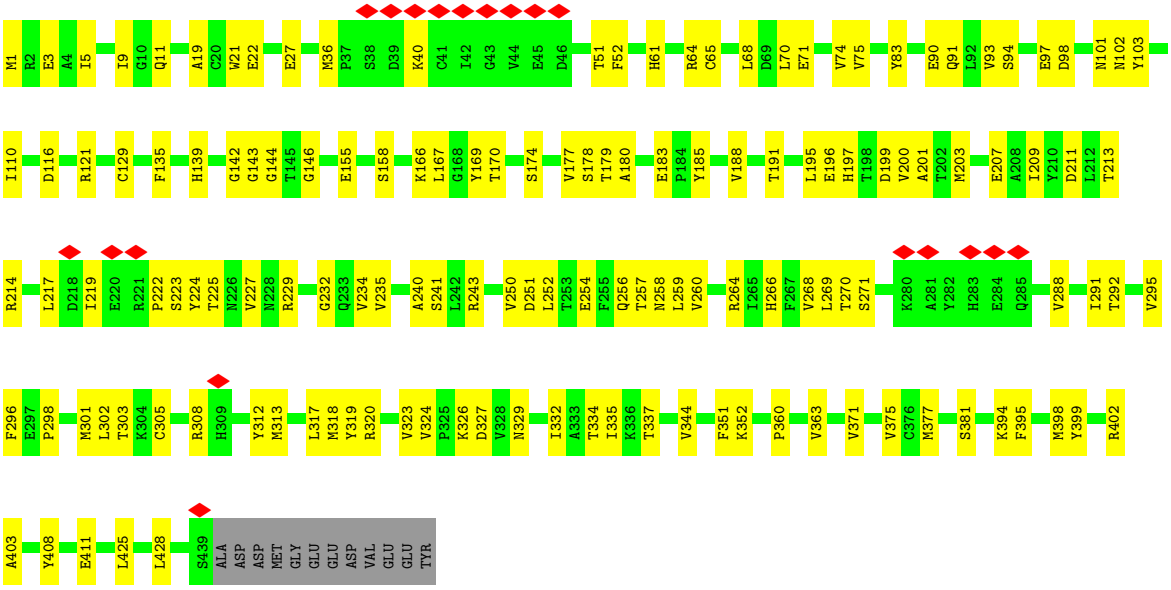

• Molecule 2: Tubulin alpha chain

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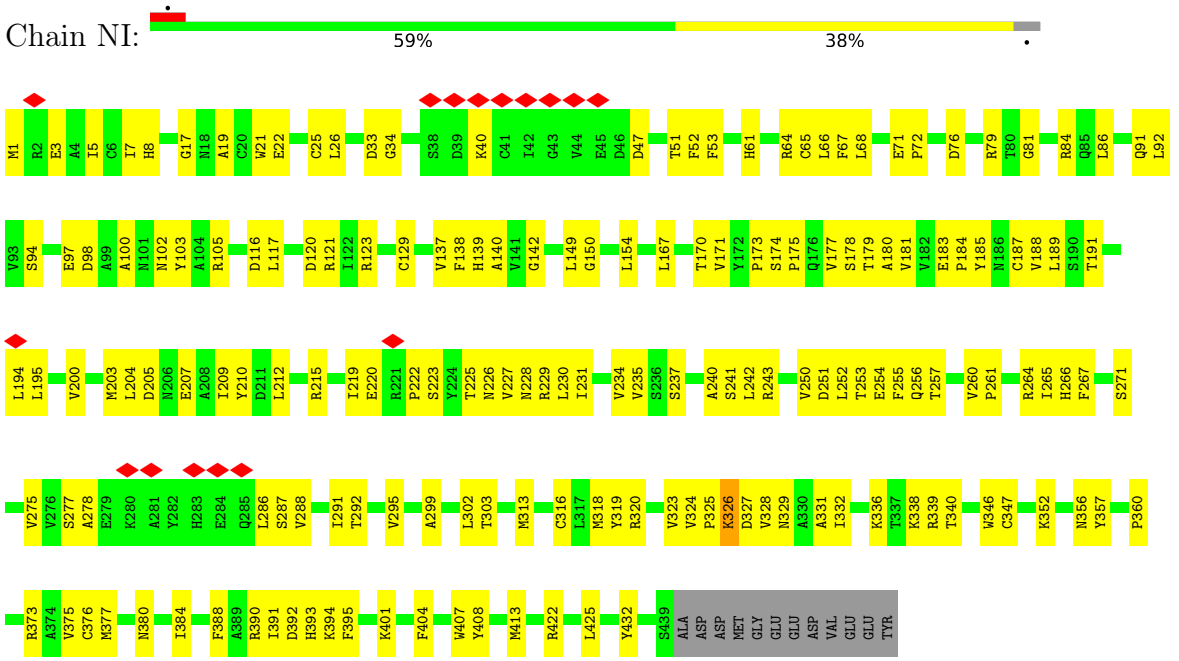

• Molecule 2: Tubulin alpha chain

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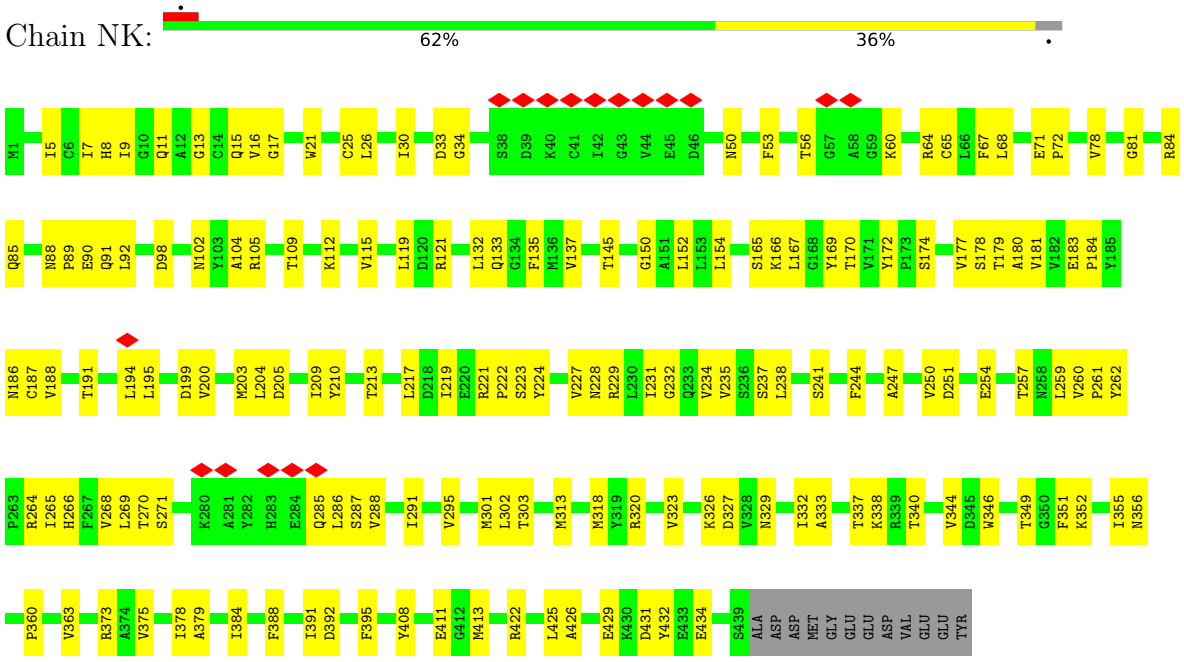

• Molecule 2: Tubulin alpha chain

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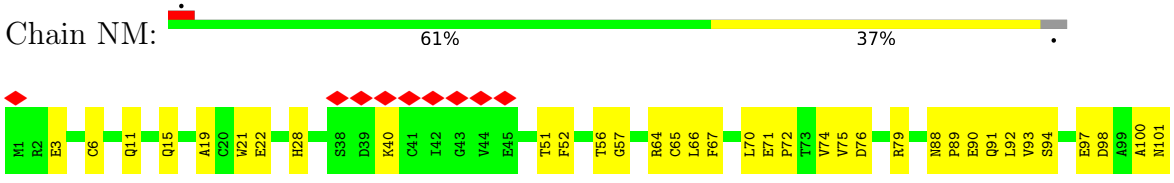
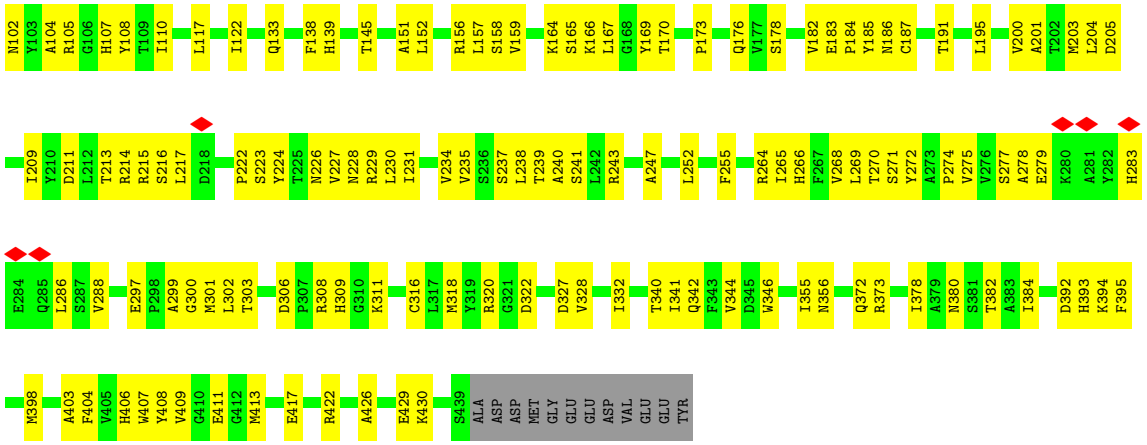
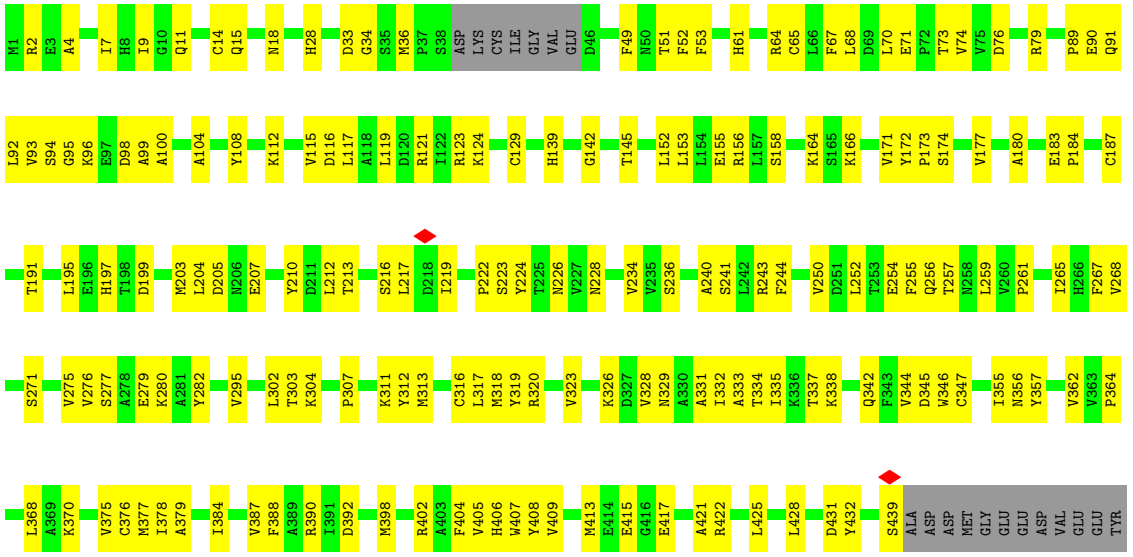




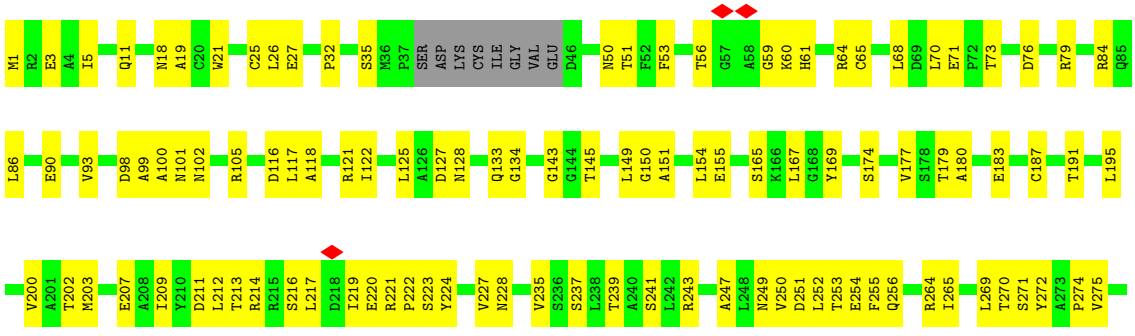
• Molecule 2: Tubulin alpha chain

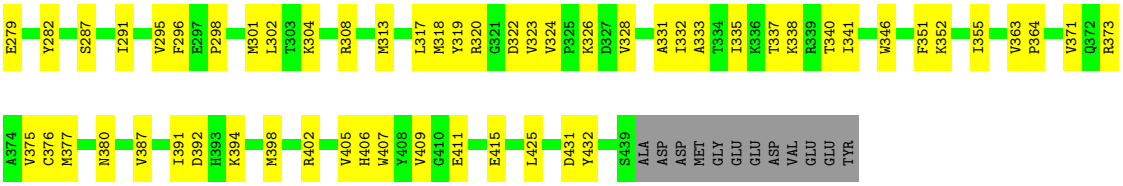
Chain OA:



• Molecule 2: Tubulin alpha chain

Chain OC:





• Molecule 2: Tubulin alpha chain

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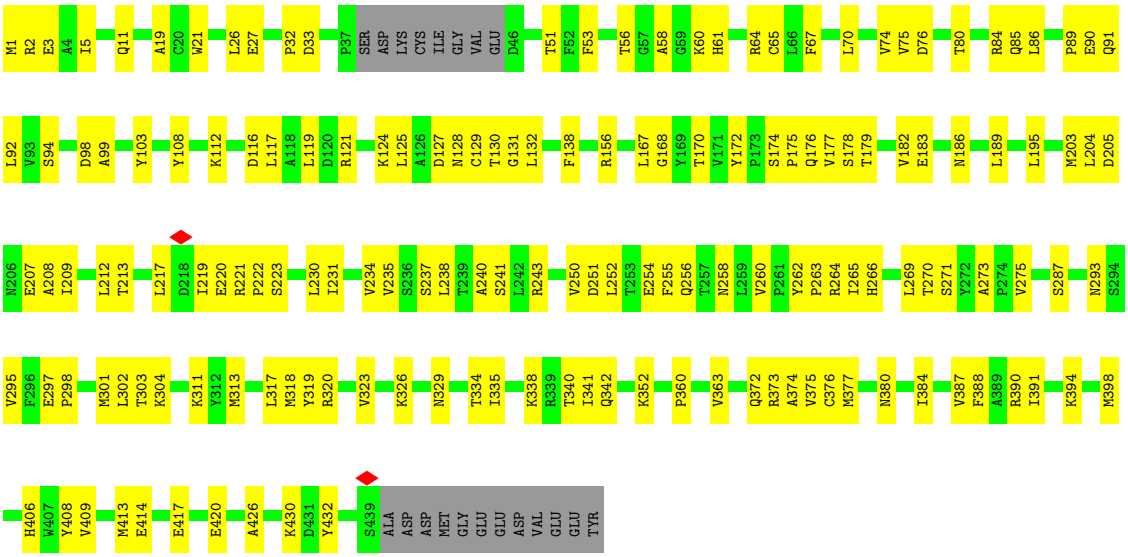
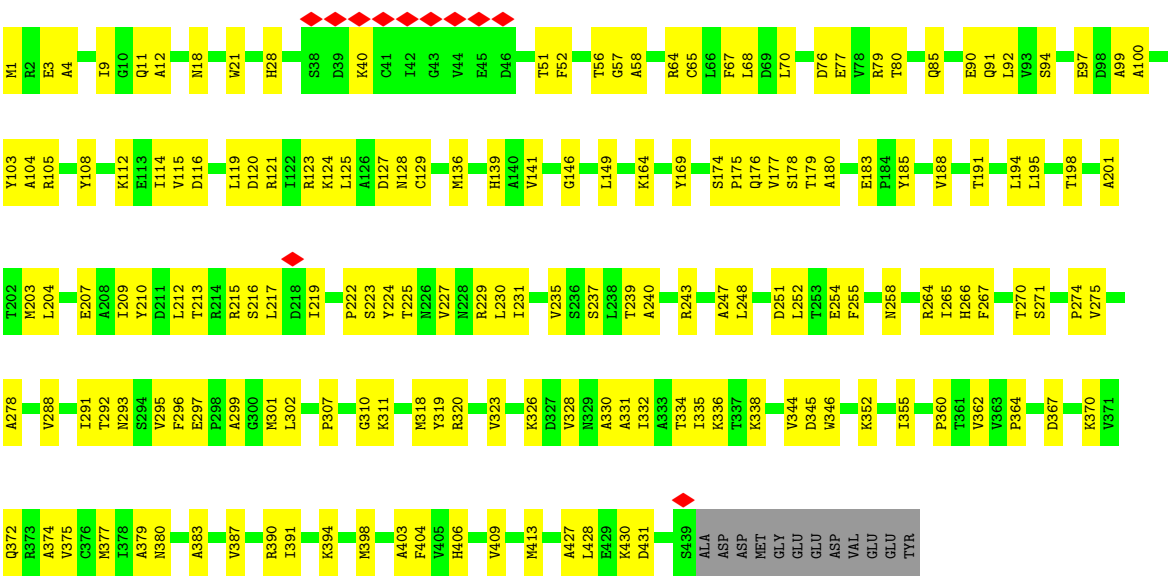


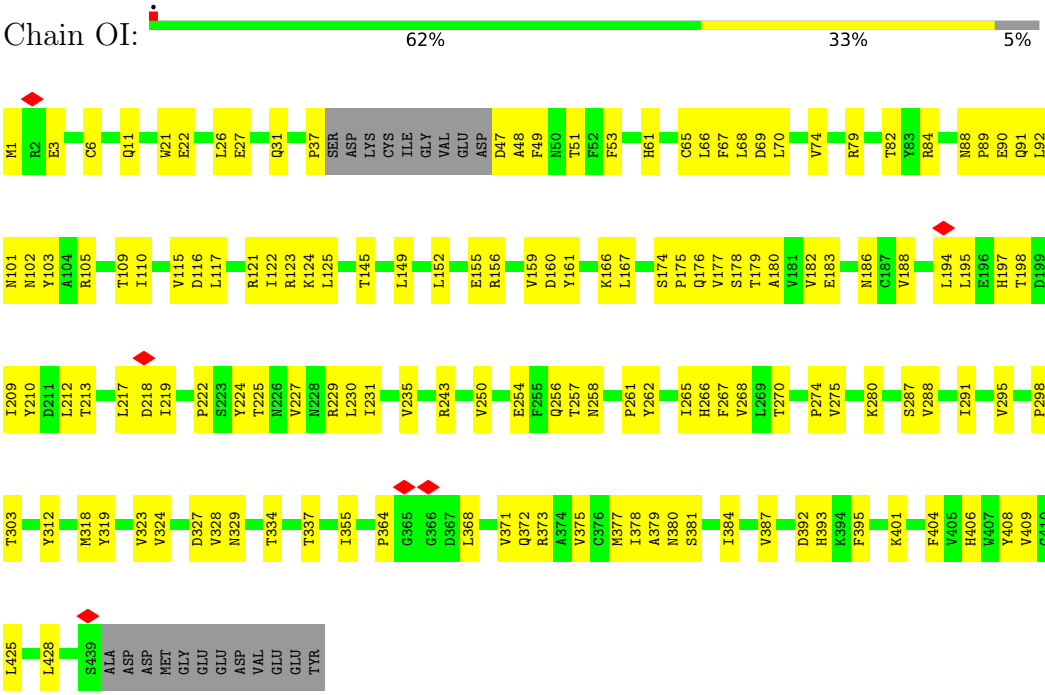
• Molecule 2: Tubulin alpha chain

Chain OG:



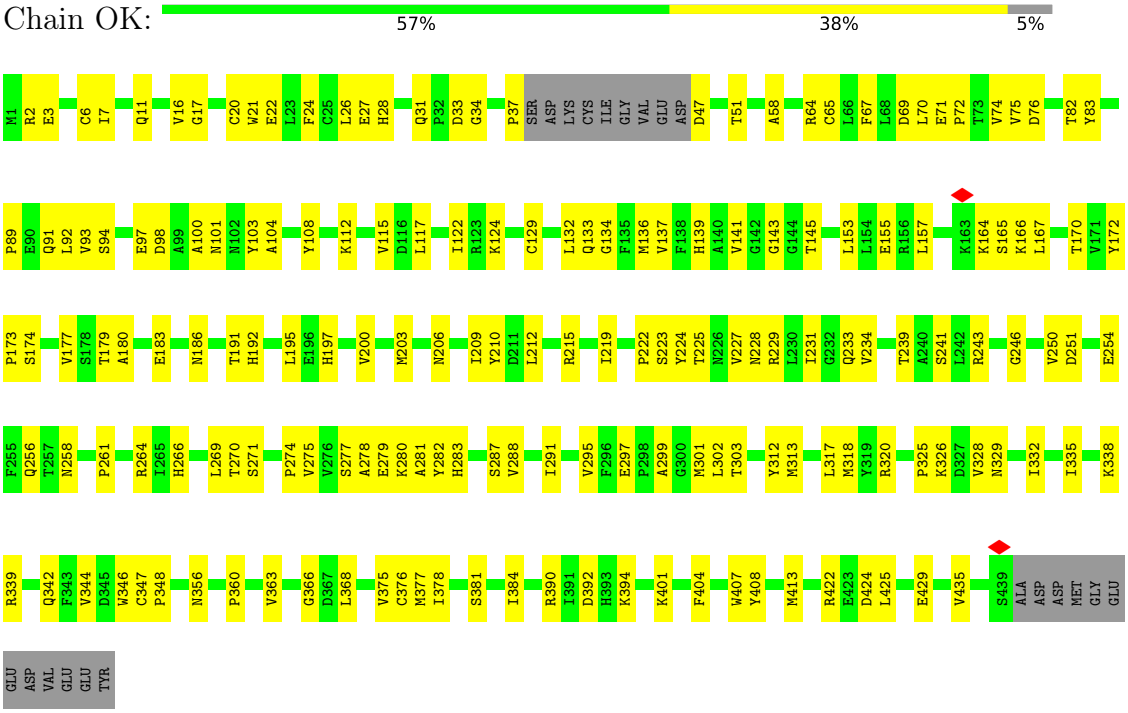
• Molecule 2: Tubulin alpha chain

Chain OI:



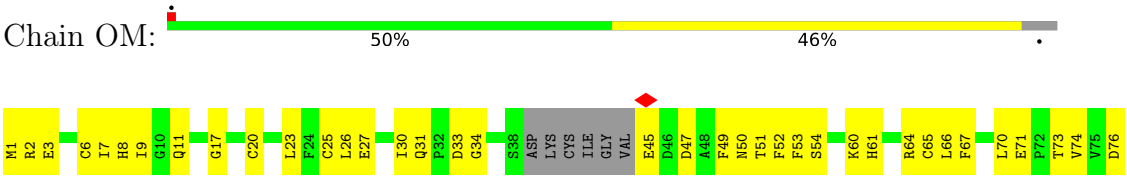
• Molecule 2: Tubulin alpha chain

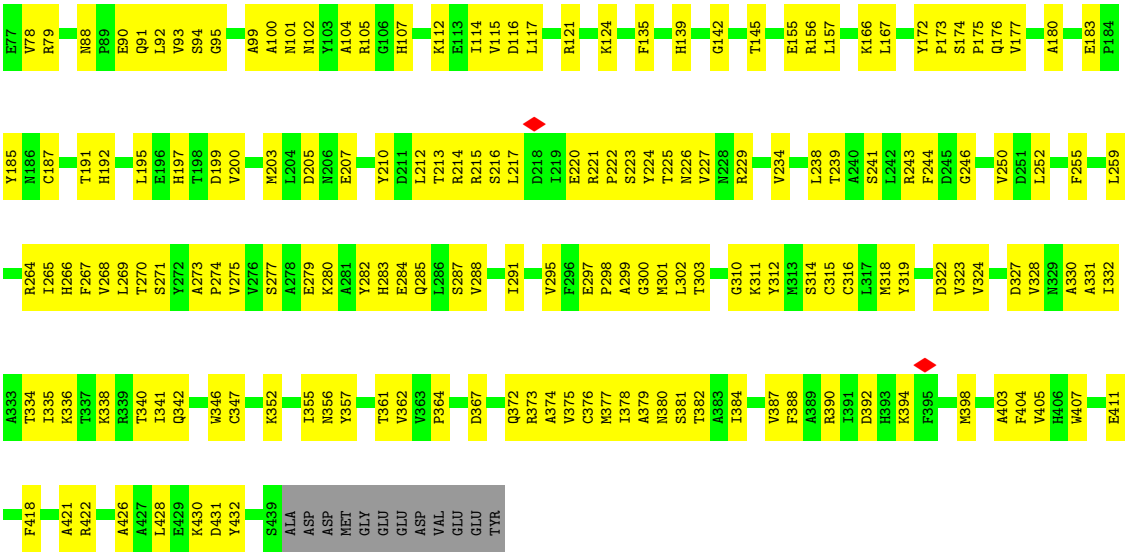
Chain OK:



• Molecule 2: Tubulin alpha chain

Chain OM:





• Molecule 2: Tubulin alpha chain

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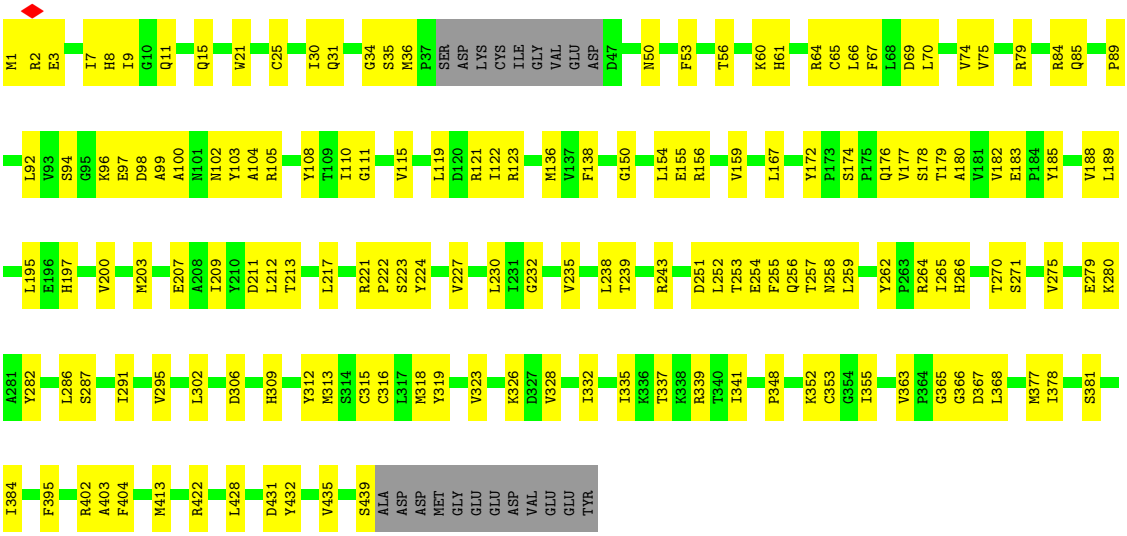
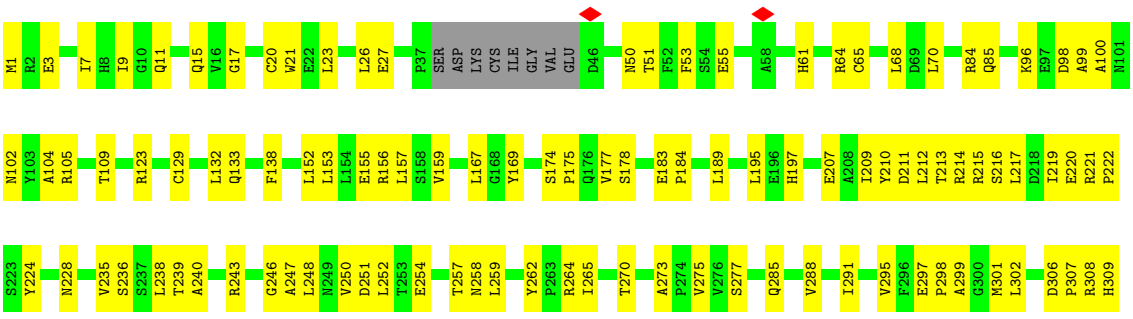
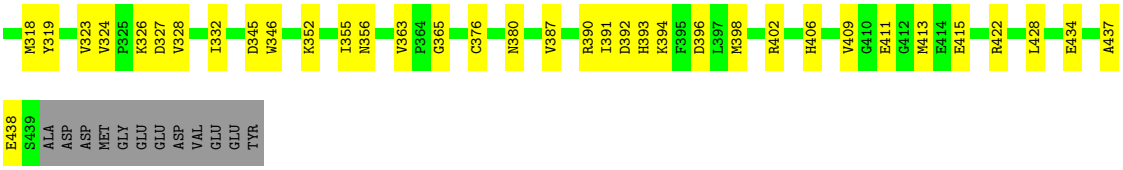


• Molecule 2: Tubulin alpha chain

Chain PC:





• Molecule 2: Tubulin alpha chain

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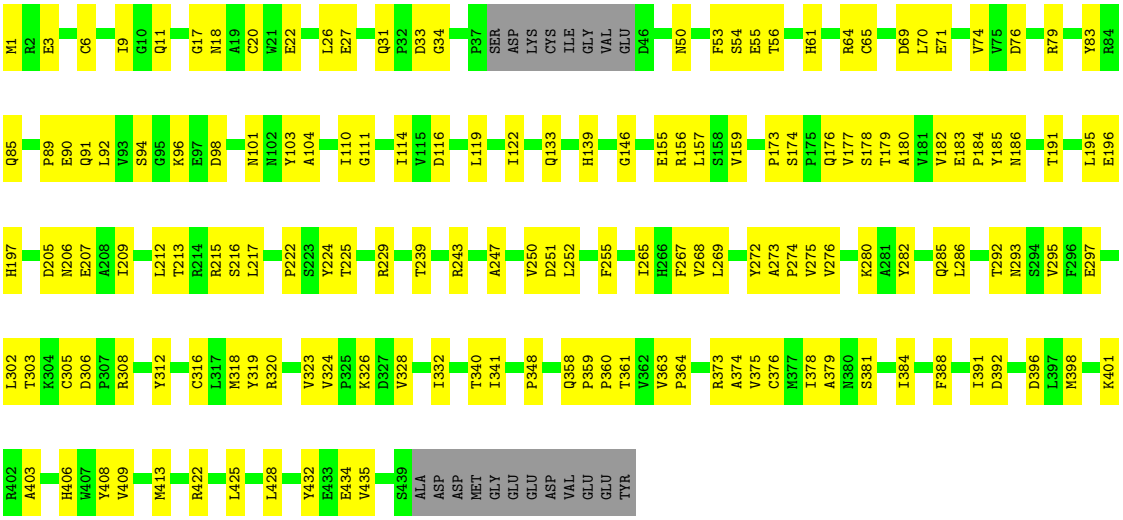
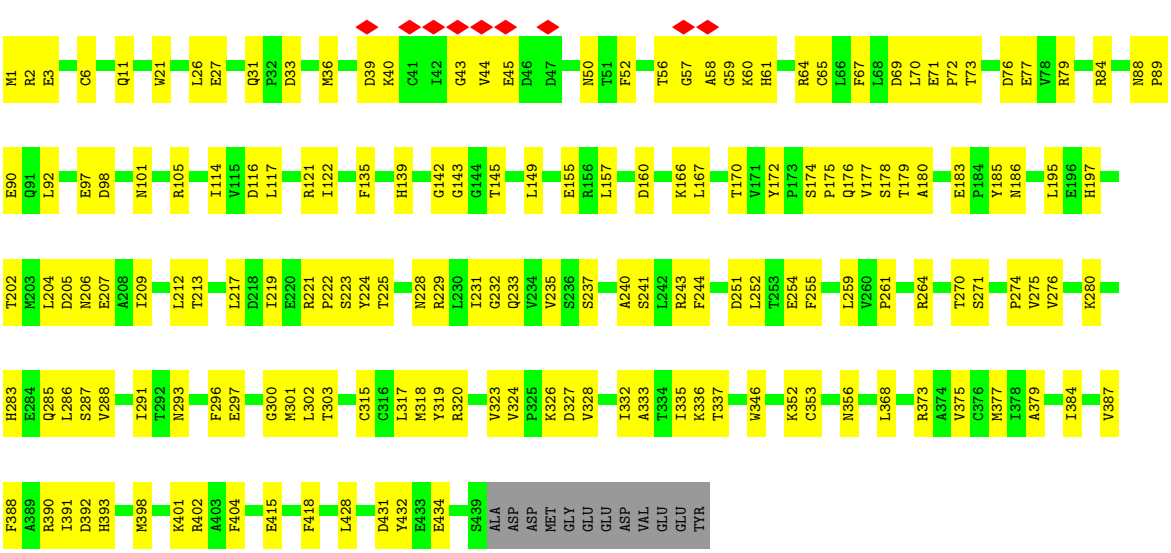


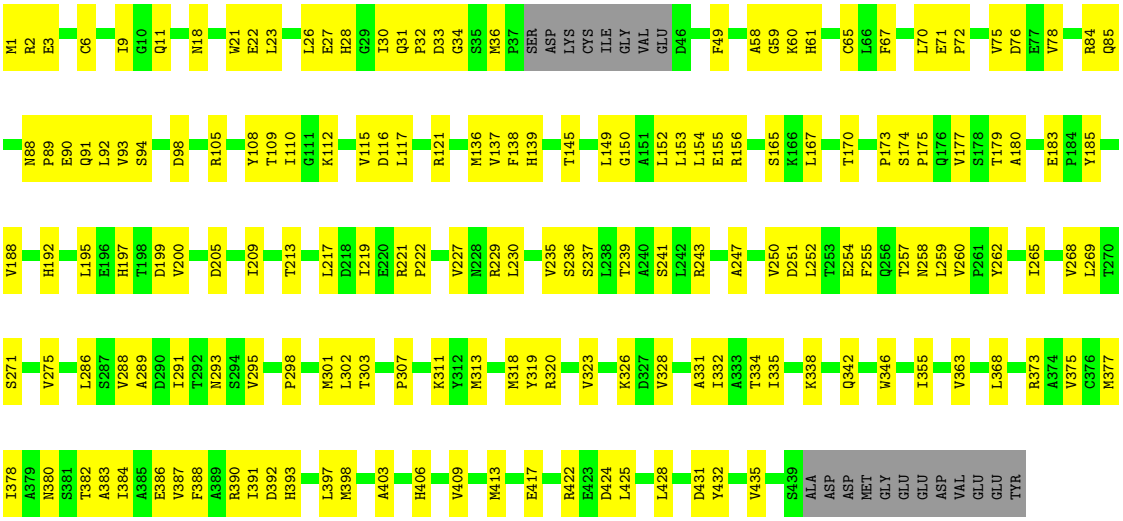
• Molecule 2: Tubulin alpha chain

Chain PG:



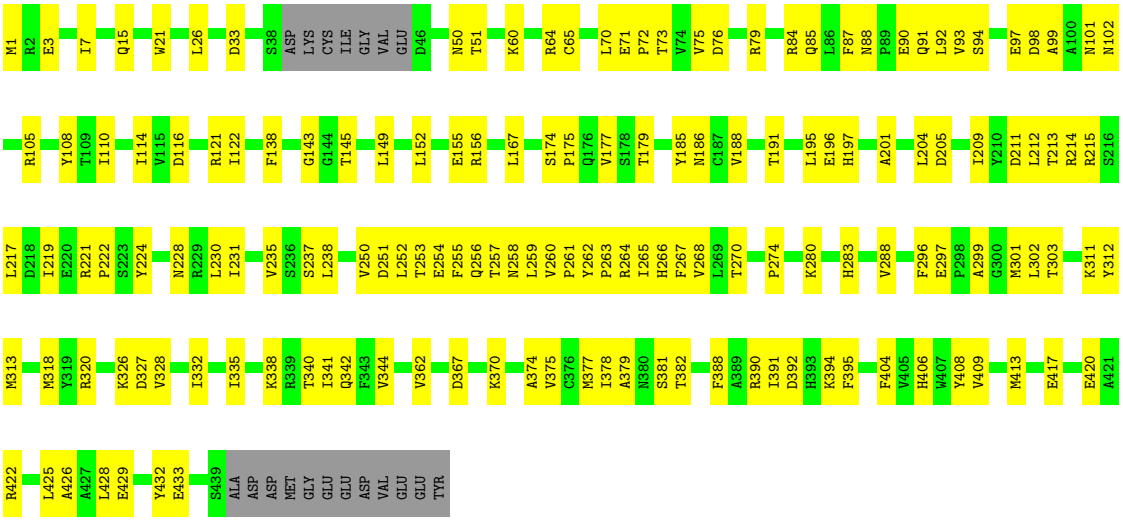
• Molecule 2: Tubulin alpha chain

Chain PI:



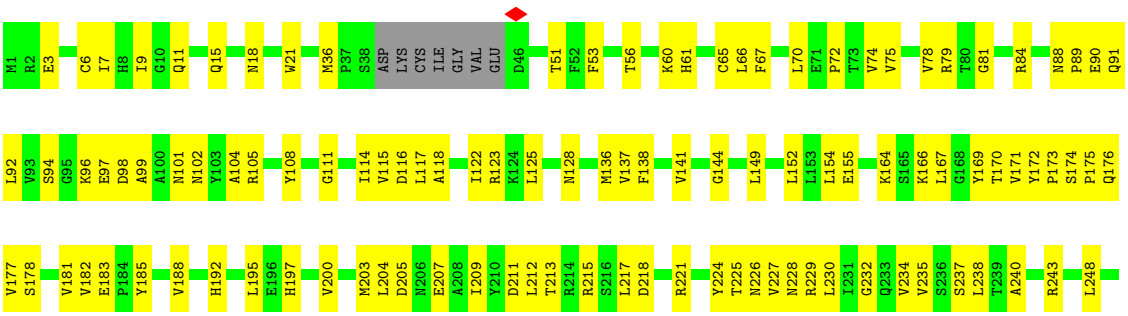
• Molecule 2: Tubulin alpha chain

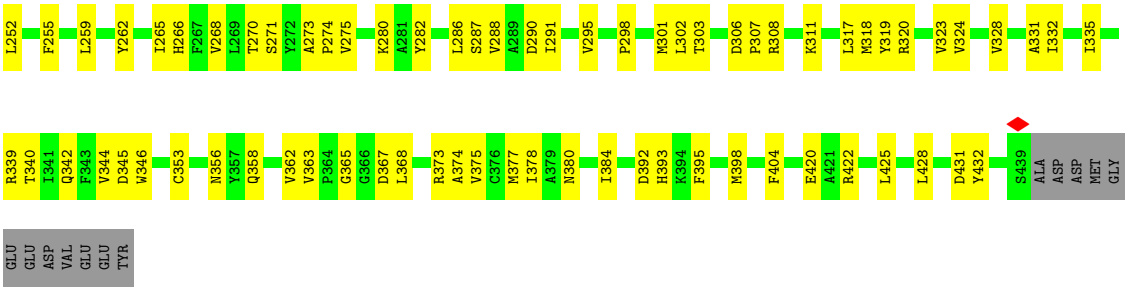
Chain PK:



• Molecule 2: Tubulin alpha chain

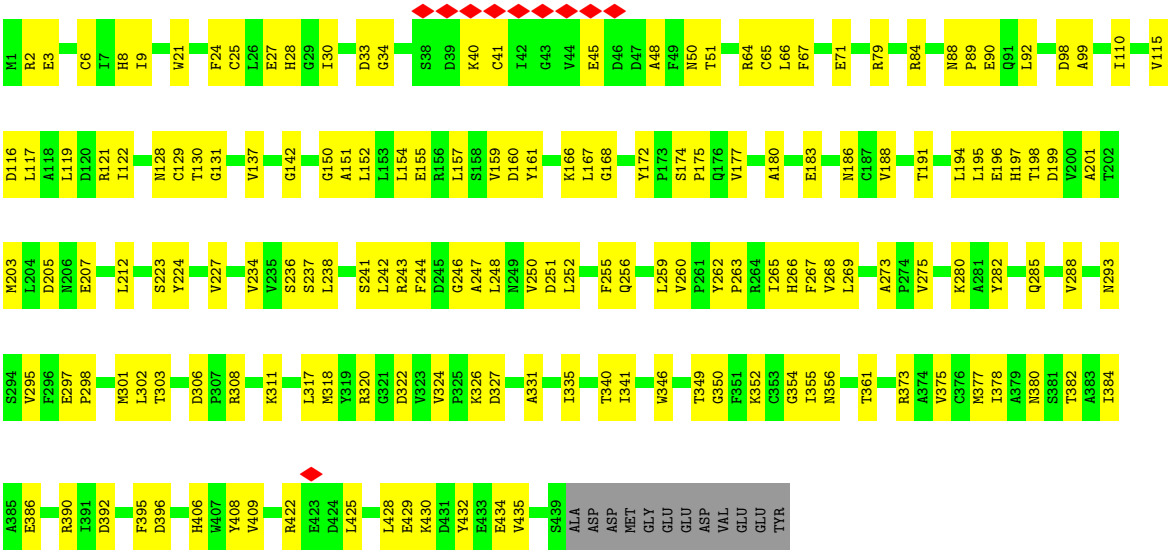
Chain PM:





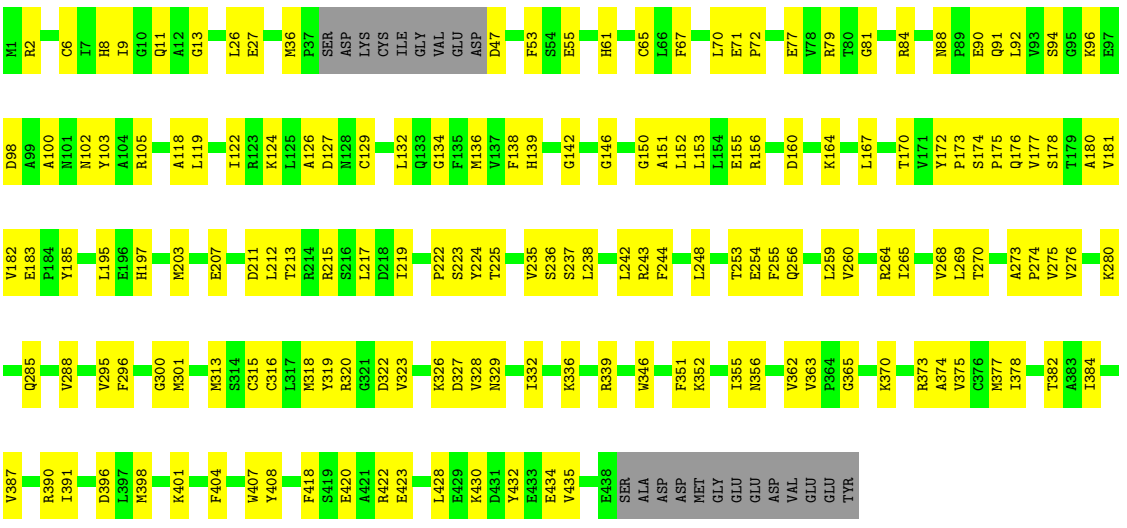
• Molecule 2: Tubulin alpha chain

Chain Q:



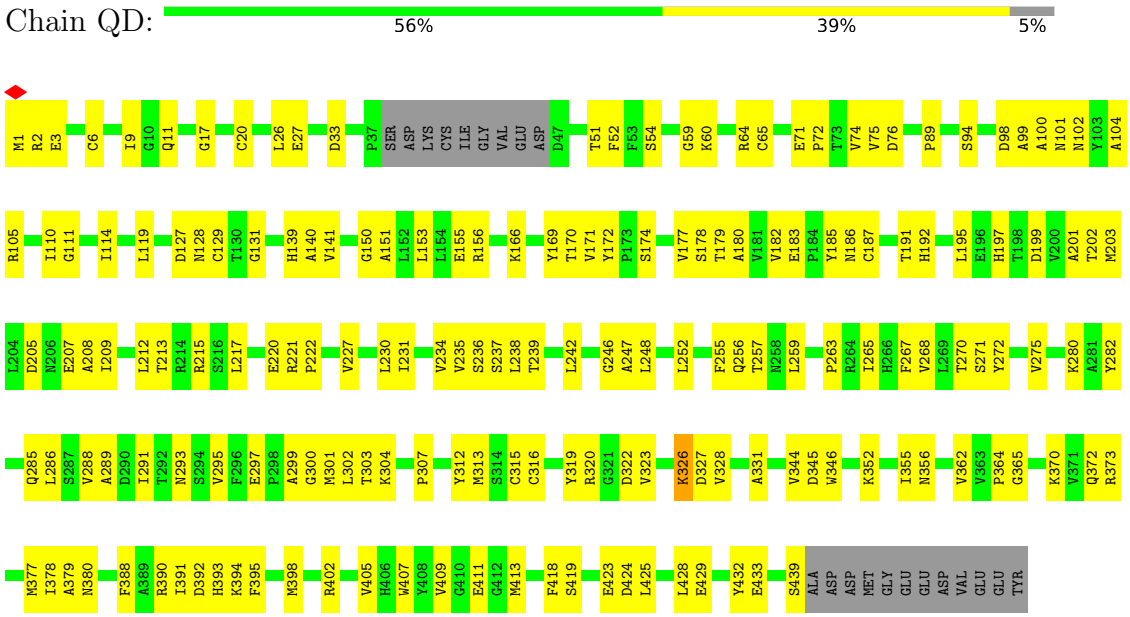
• Molecule 2: Tubulin alpha chain

Chain QB:



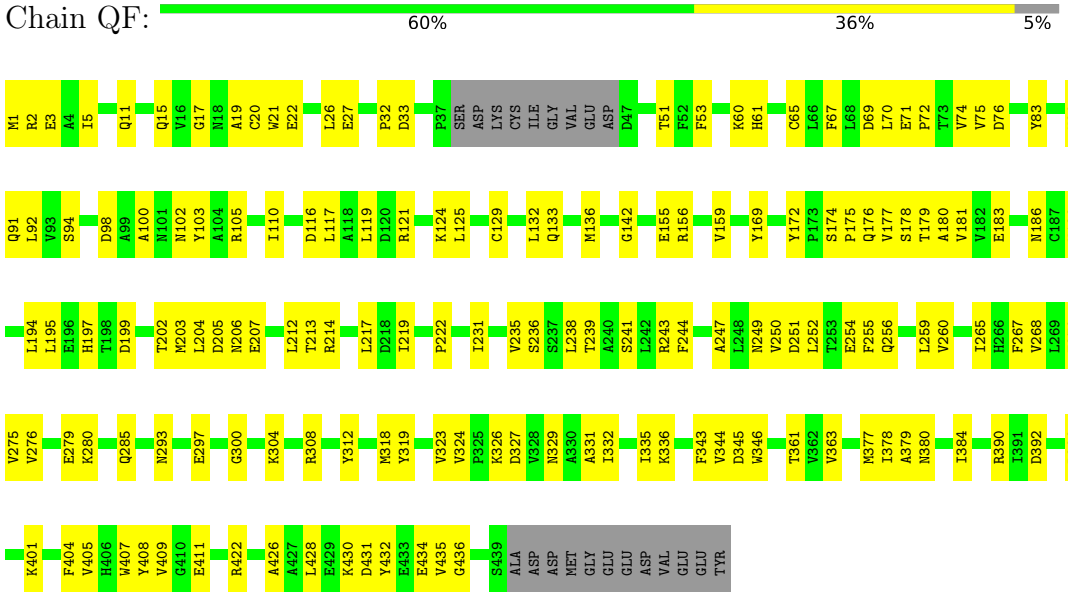
• Molecule 2: Tubulin alpha chain

Chain QD:



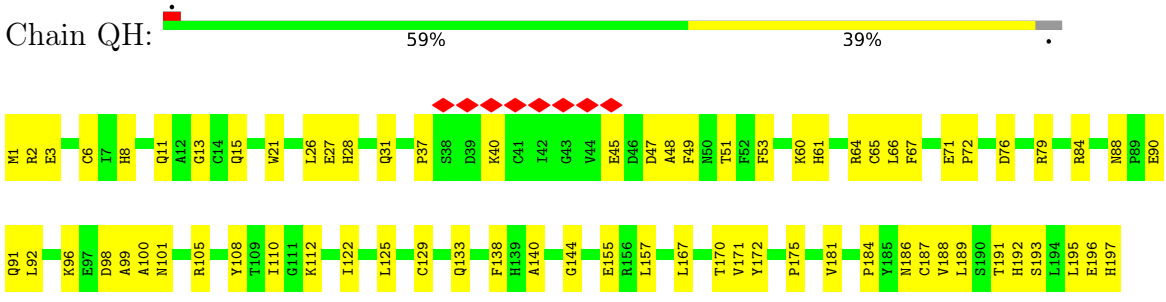
• Molecule 2: Tubulin alpha chain

Chain QF:



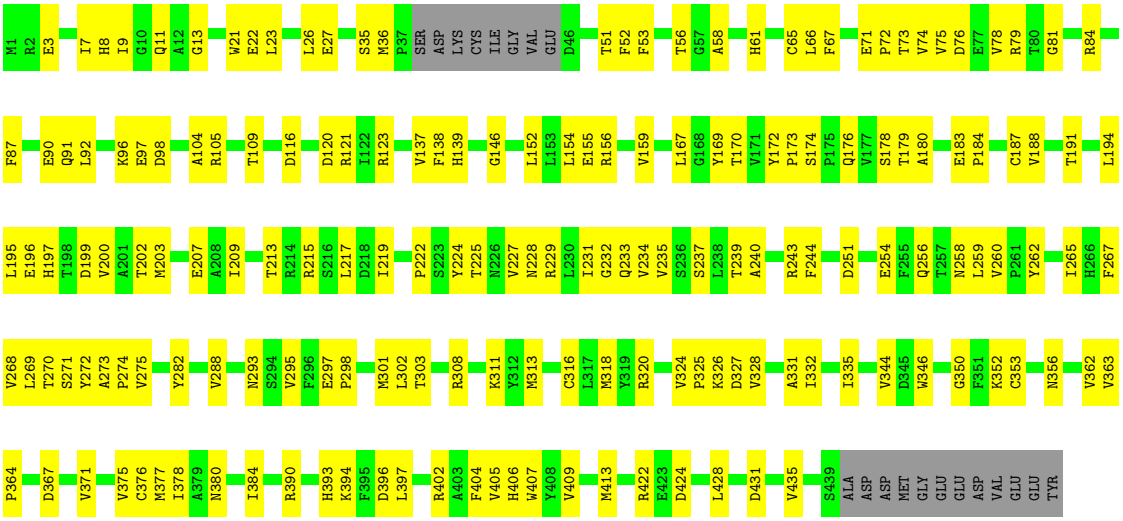
• Molecule 2: Tubulin alpha chain

Chain QH:



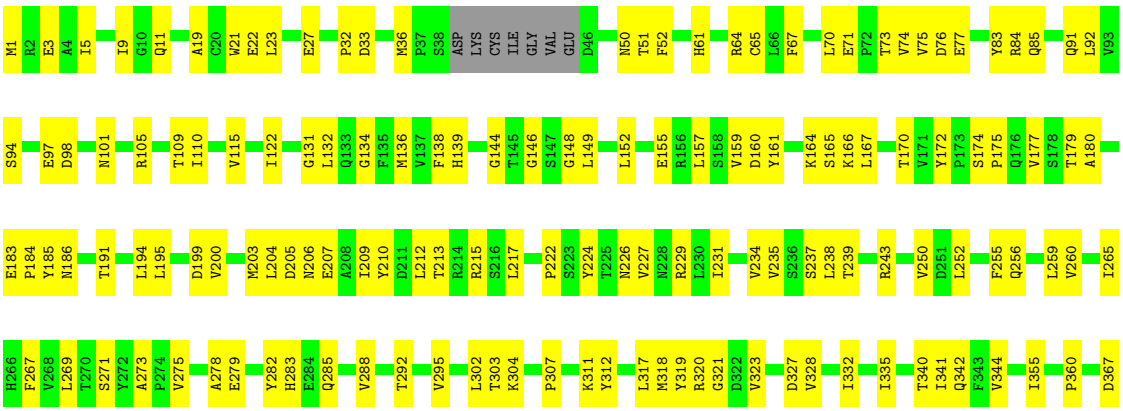
• Molecule 2: Tubulin alpha chain

Chain QJ:



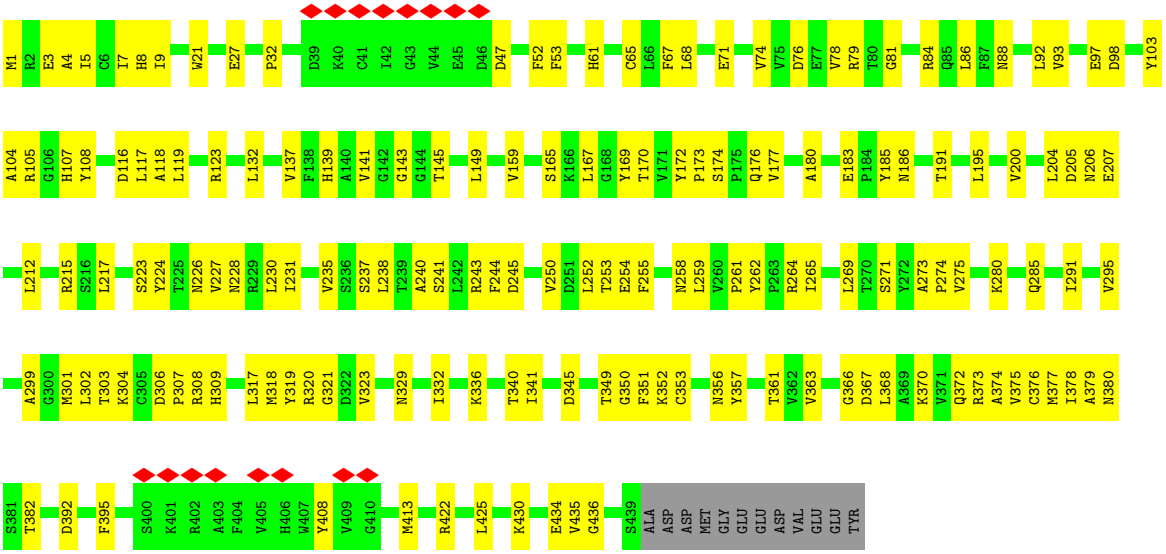
• Molecule 2: Tubulin alpha chain

Chain QL:



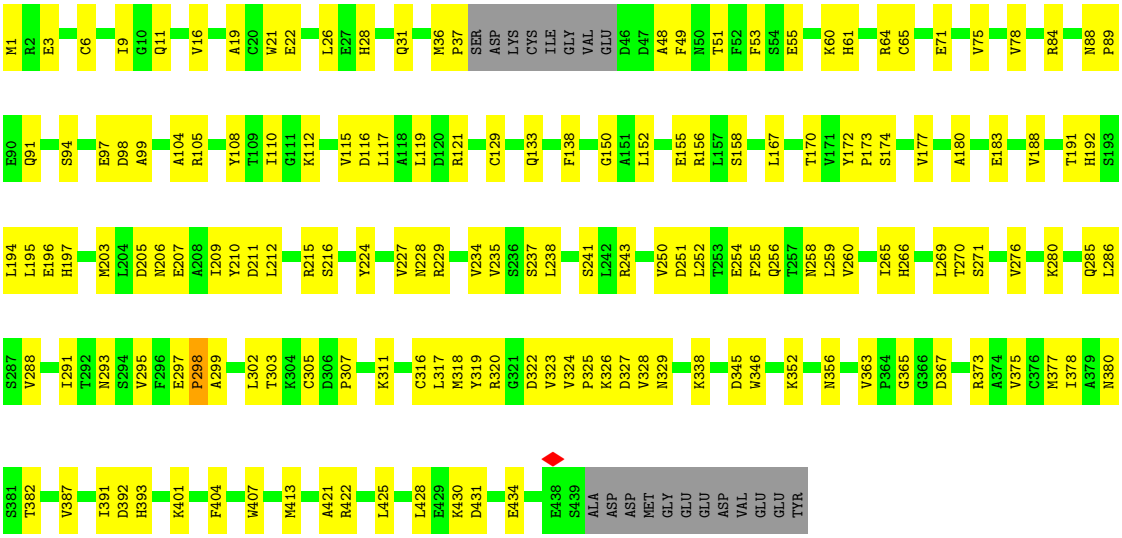
• Molecule 2: Tubulin alpha chain

Chain R:



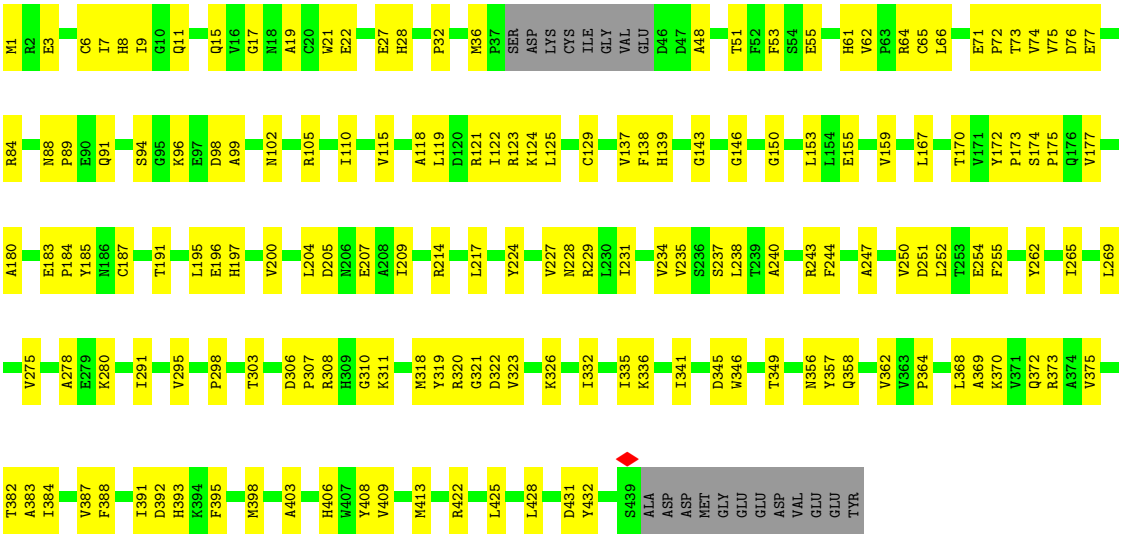
• Molecule 2: Tubulin alpha chain

Chain RB:



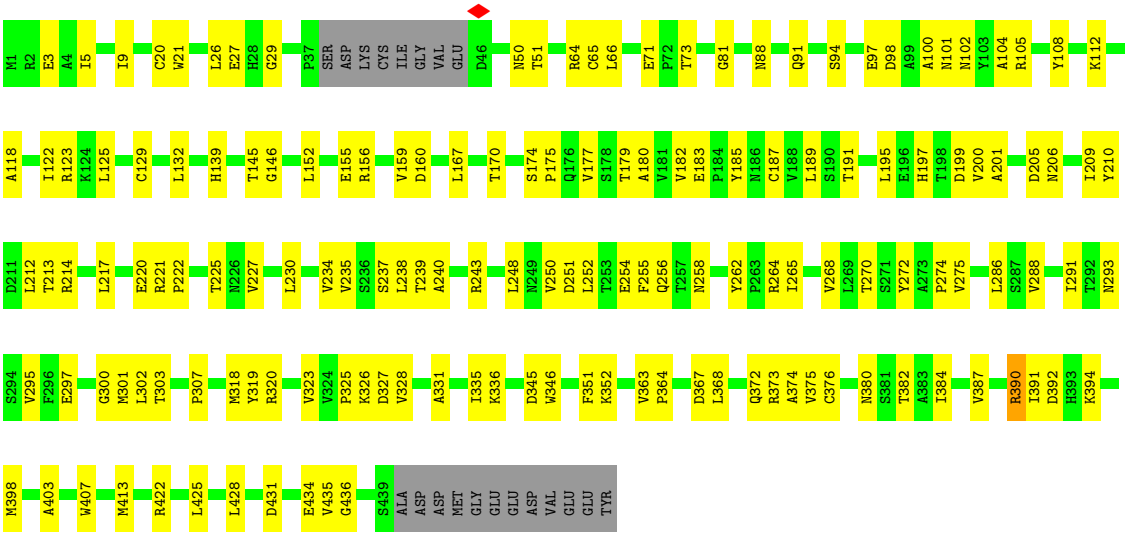
• Molecule 2: Tubulin alpha chain

Chain RD:



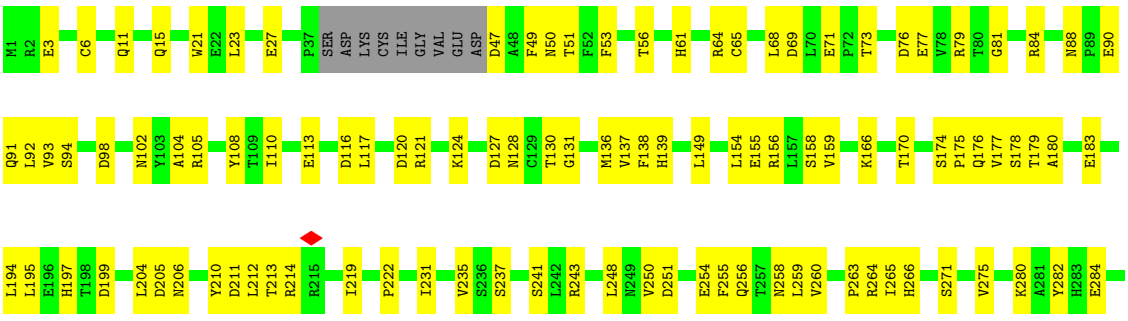
• Molecule 2: Tubulin alpha chain

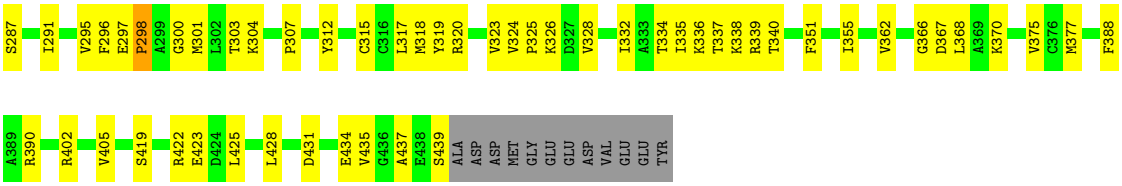
Chain RF:



• Molecule 2: Tubulin alpha chain

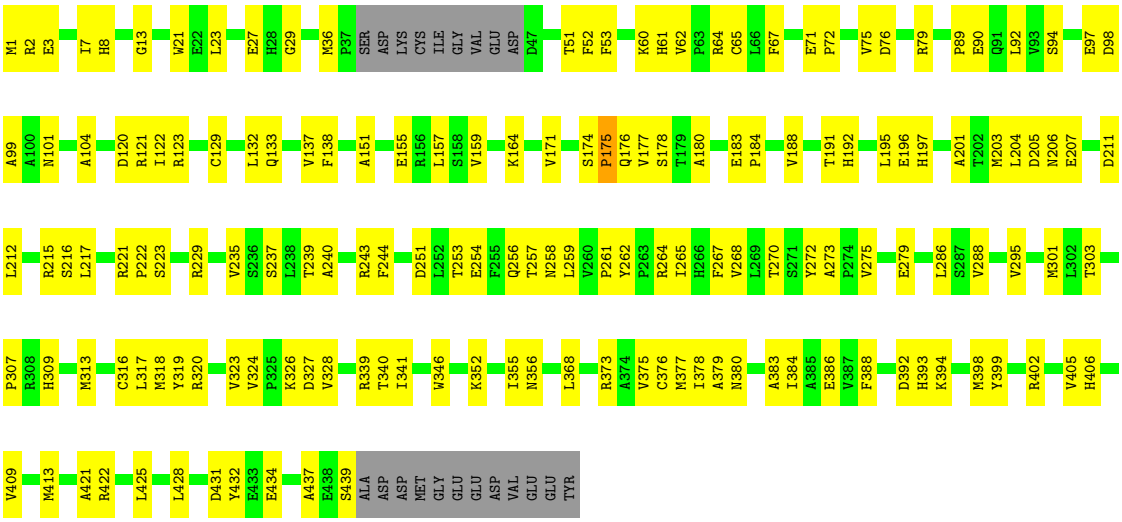
Chain RH:





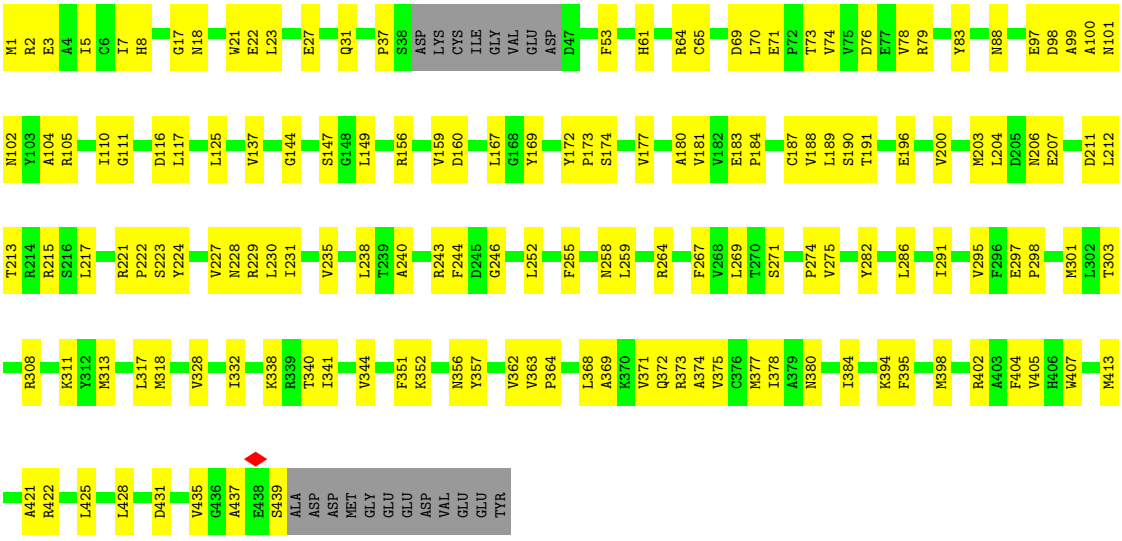
• Molecule 2: Tubulin alpha chain

Chain RJ:



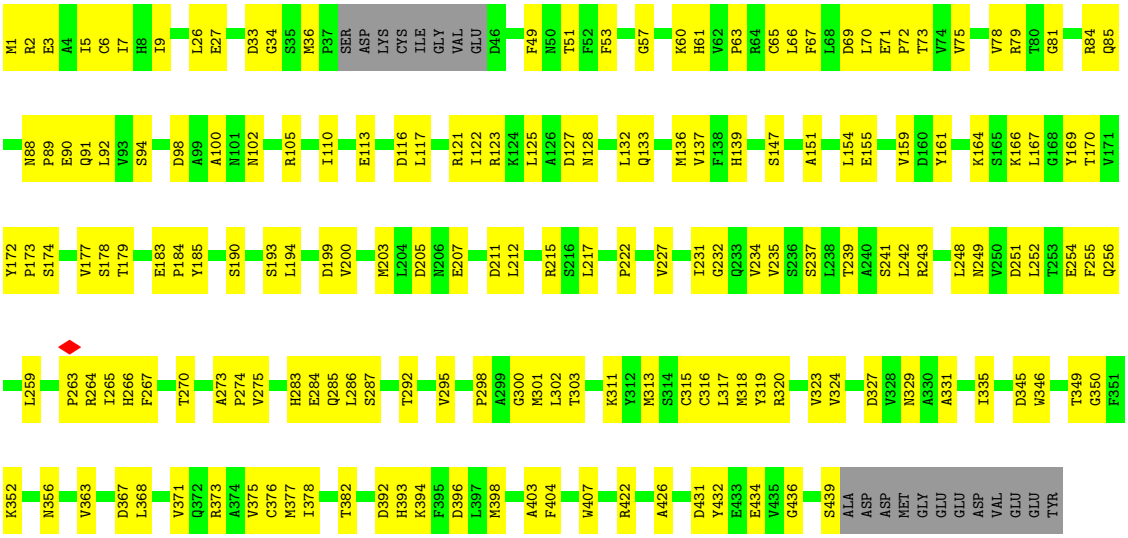
• Molecule 2: Tubulin alpha chain

Chain RL:



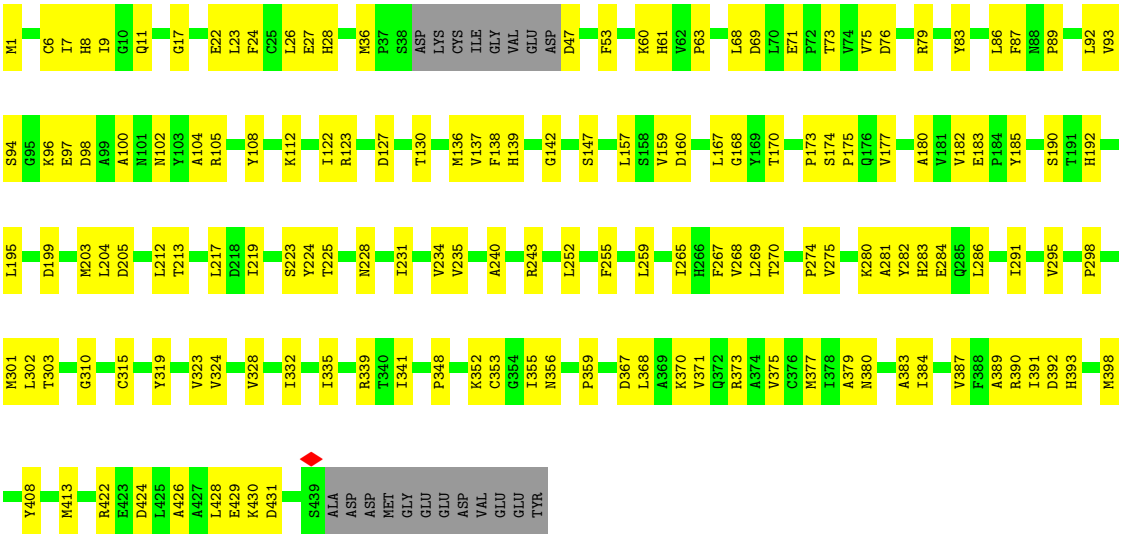
• Molecule 2: Tubulin alpha chain

Chain SA:



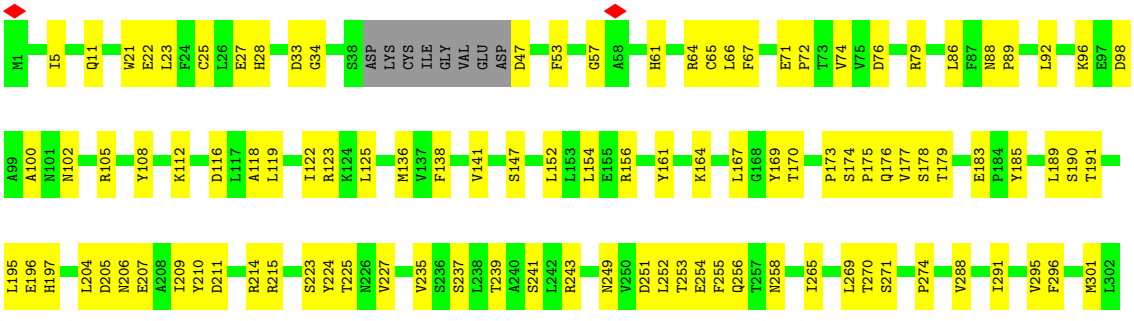
• Molecule 2: Tubulin alpha chain

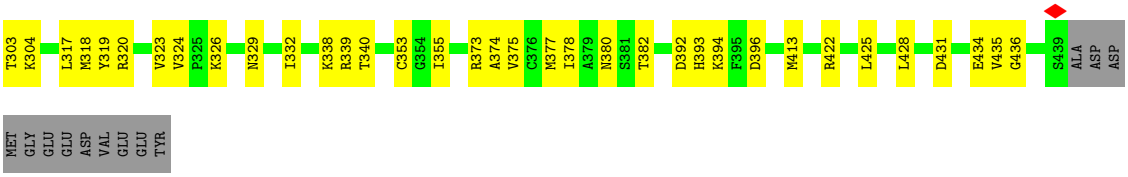
Chain SC:



• Molecule 2: Tubulin alpha chain

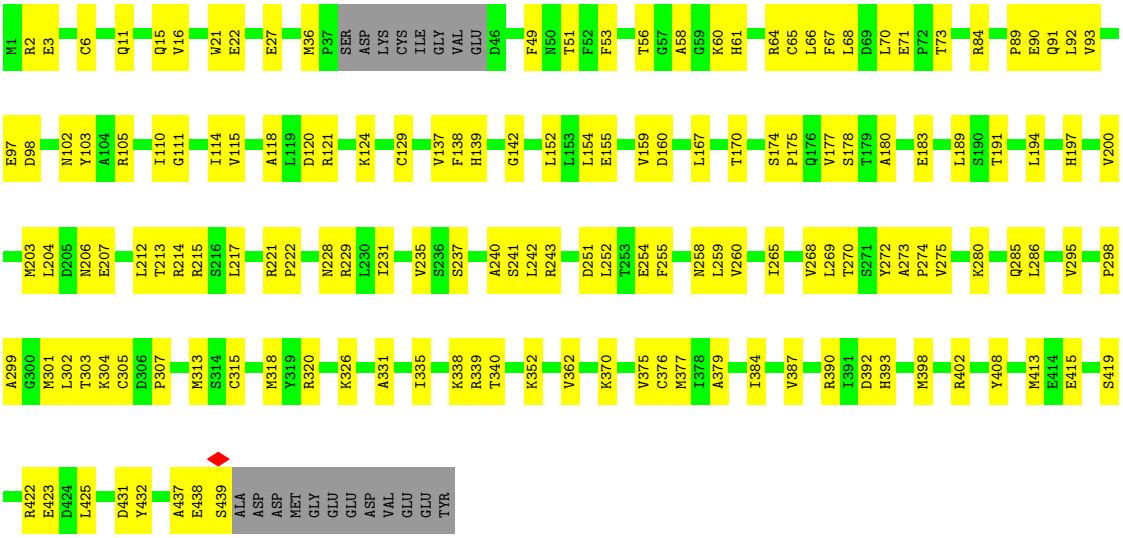
Chain SE:





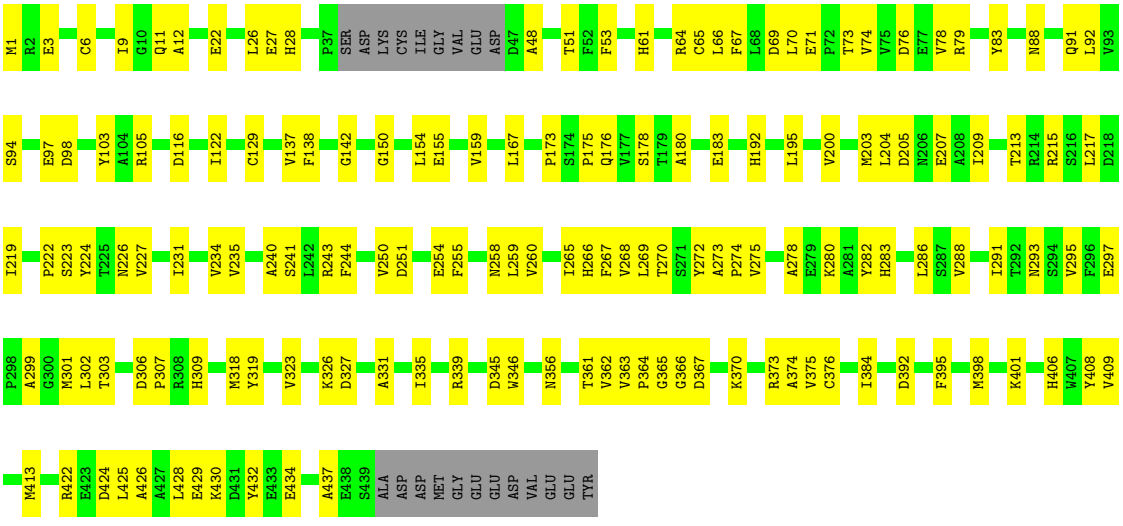
• Molecule 2: Tubulin alpha chain

Chain SG:



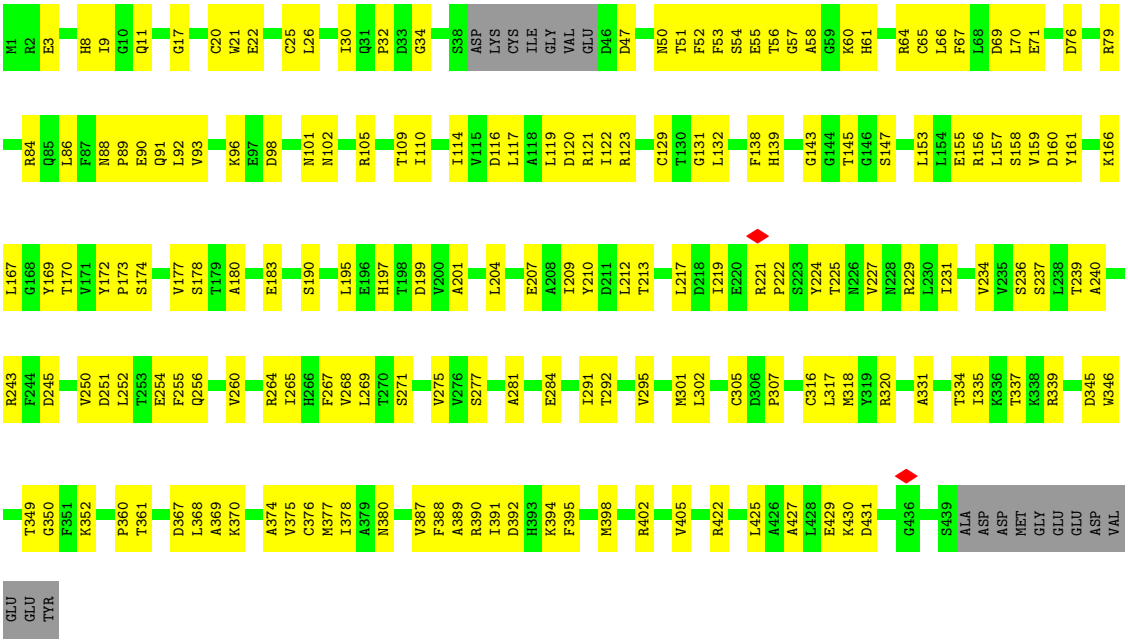
• Molecule 2: Tubulin alpha chain

Chain SI:



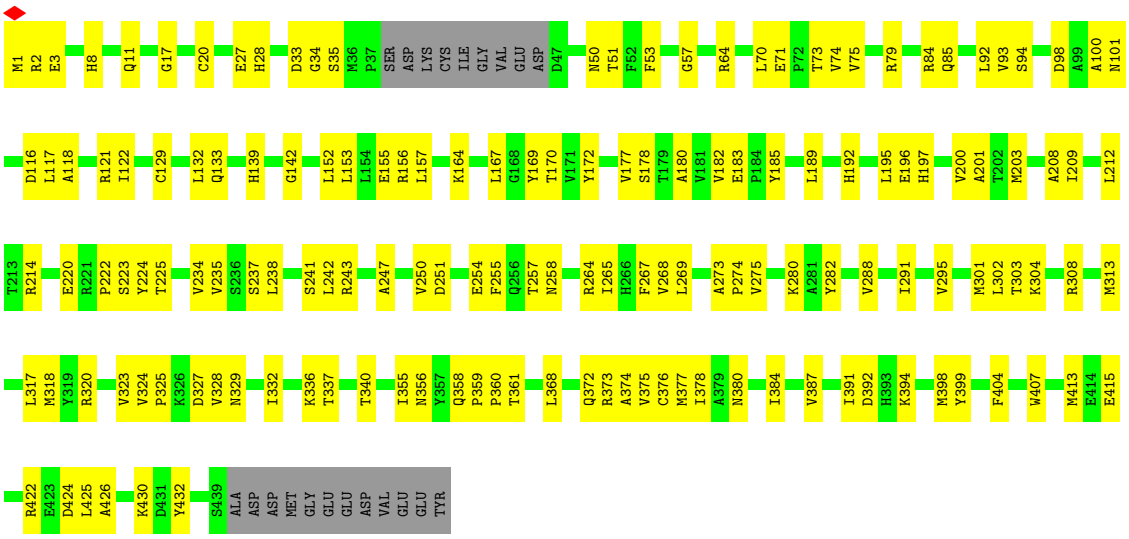
• Molecule 2: Tubulin alpha chain

Chain SK:



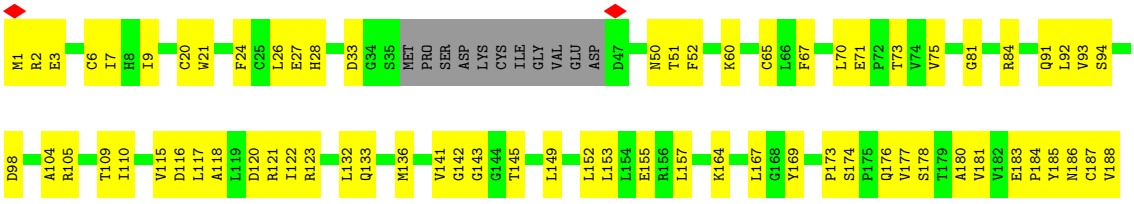
• Molecule 2: Tubulin alpha chain

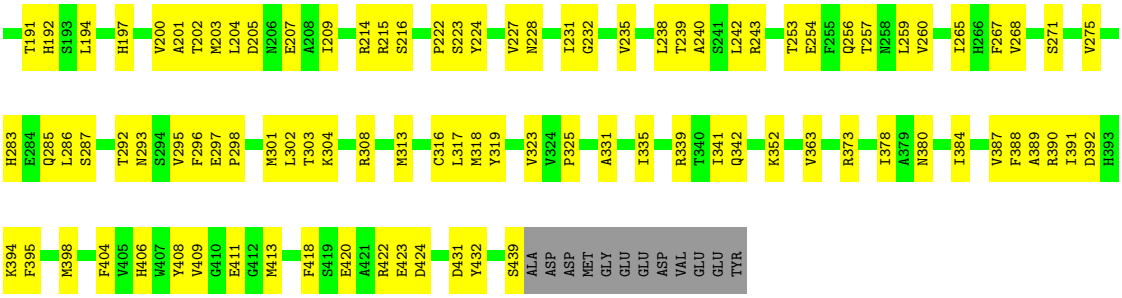
Chain TA:



• Molecule 2: Tubulin alpha chain

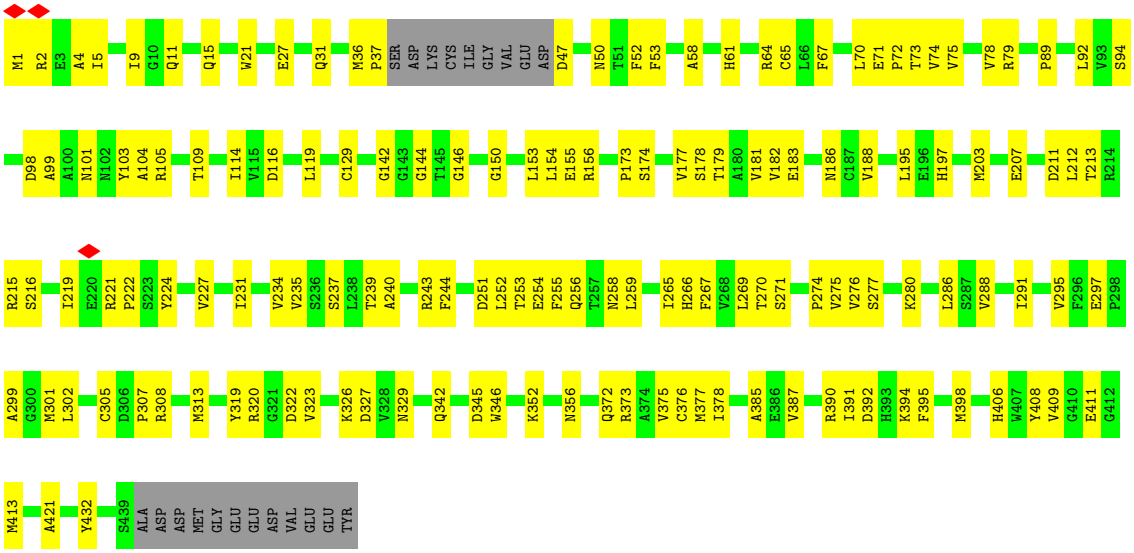
Chain TC:





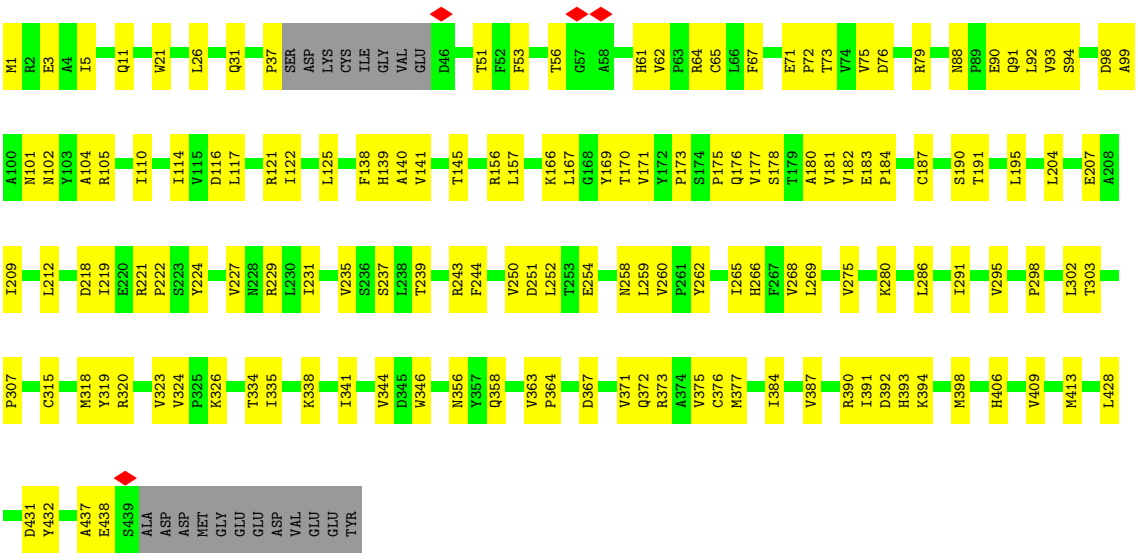
• Molecule 2: Tubulin alpha chain

Chain TE:



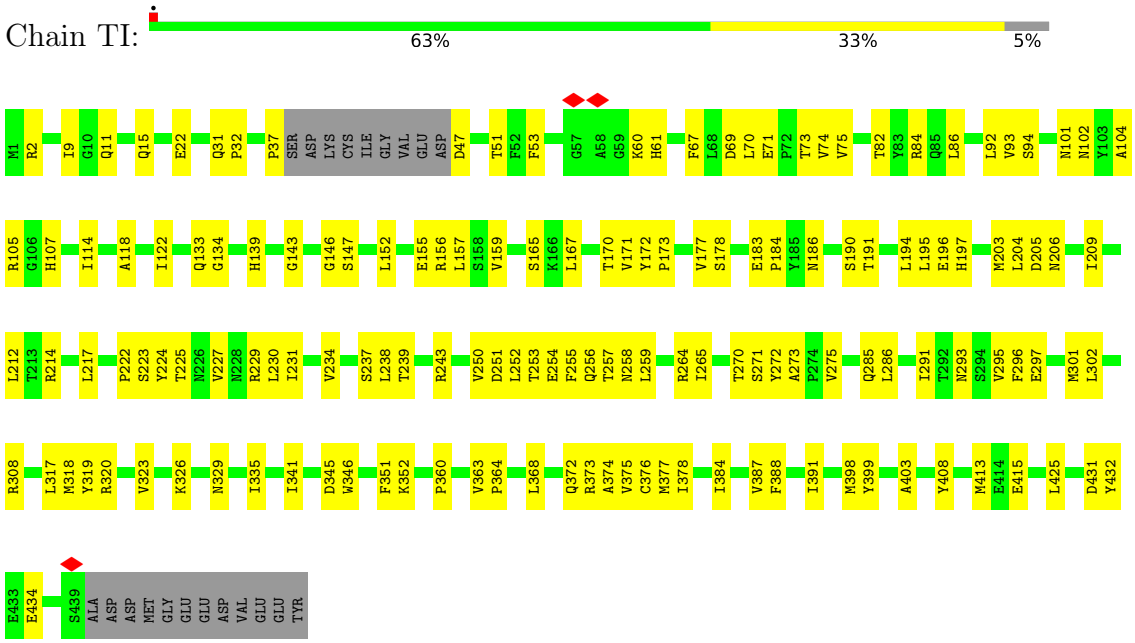
• Molecule 2: Tubulin alpha chain

Chain TG:



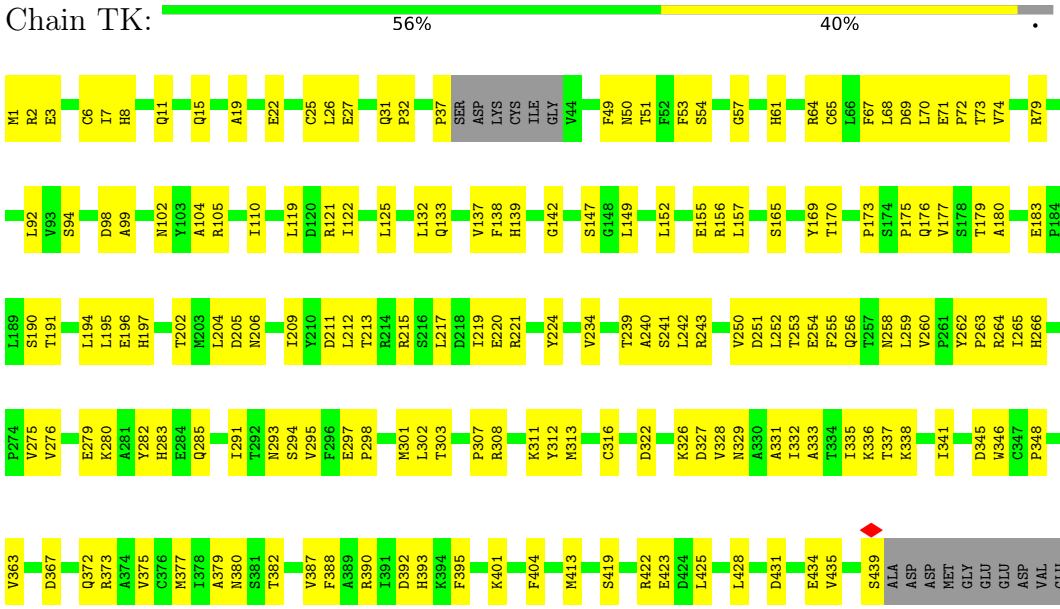
• Molecule 2: Tubulin alpha chain

Chain TI:



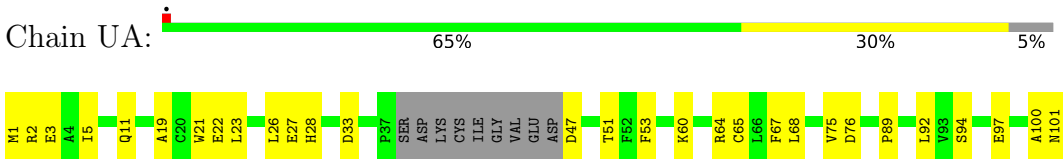
• Molecule 2: Tubulin alpha chain

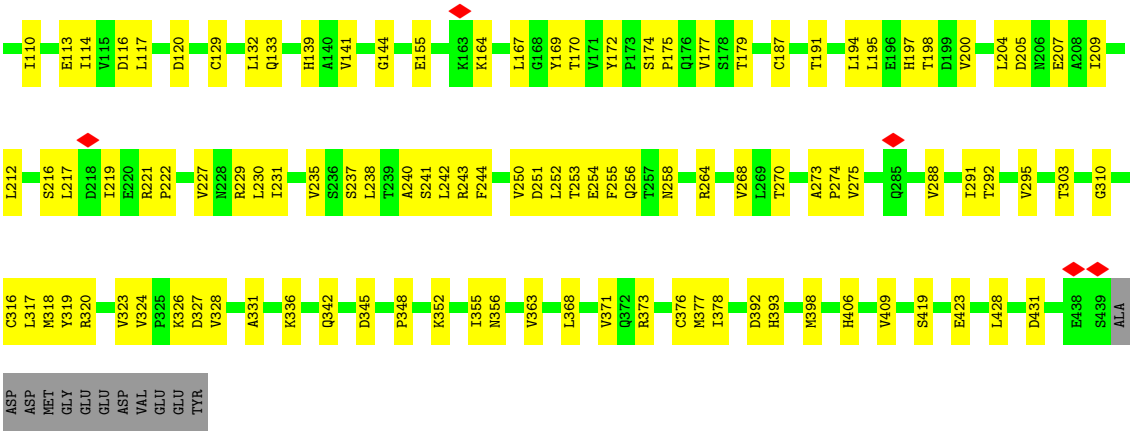
Chain TK:



• Molecule 2: Tubulin alpha chain

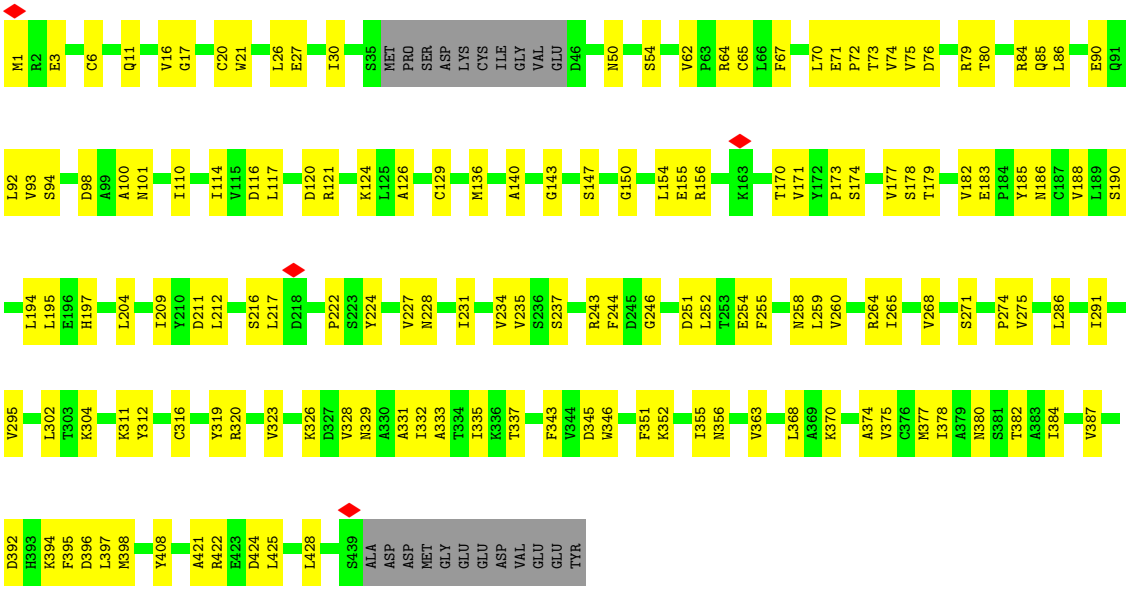
Chain UA:





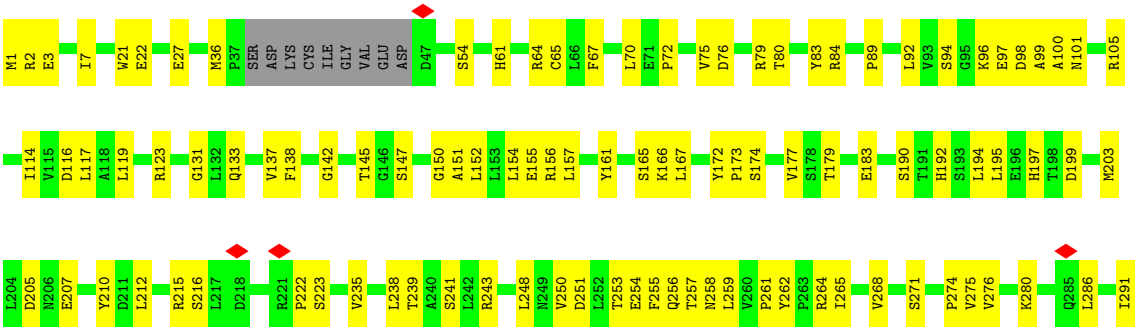
• Molecule 2: Tubulin alpha chain

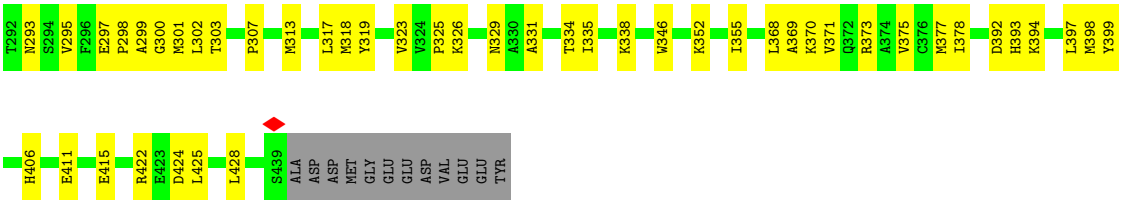
Chain UC:



• Molecule 2: Tubulin alpha chain

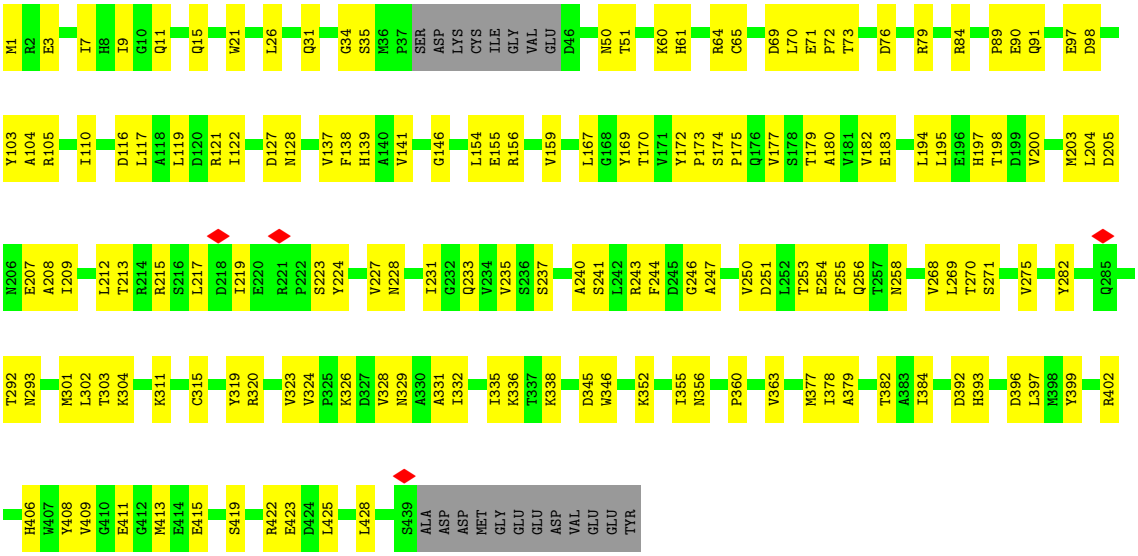
Chain UE:





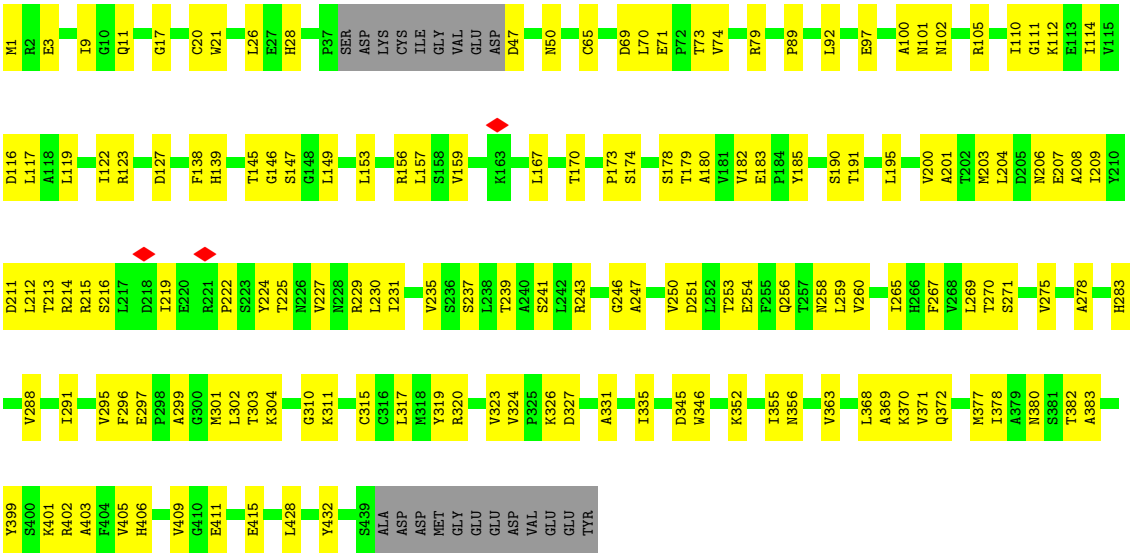
• Molecule 2: Tubulin alpha chain

Chain UG:



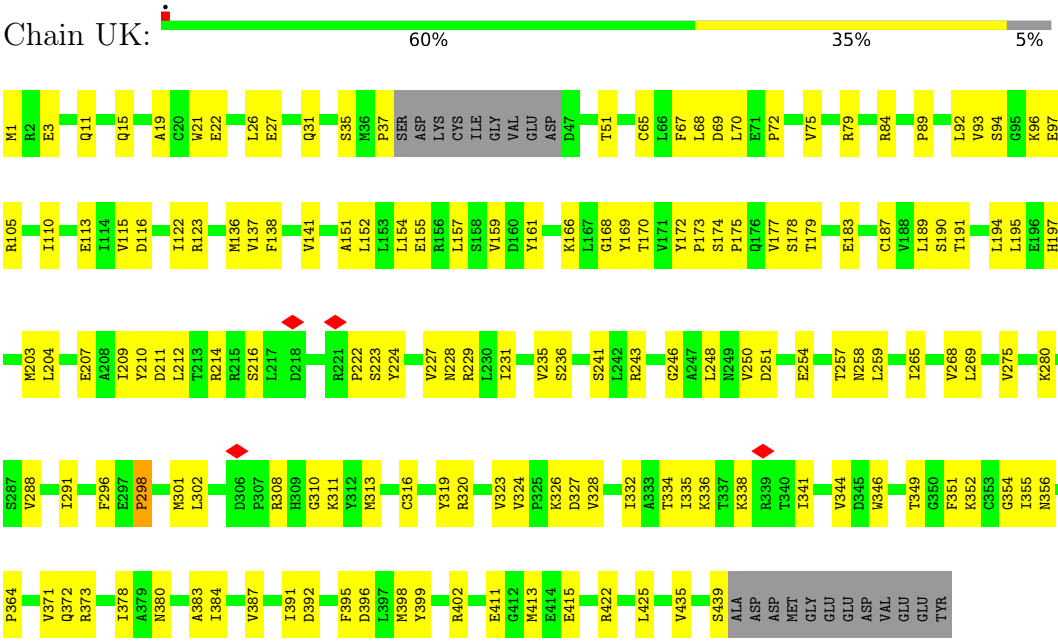
• Molecule 2: Tubulin alpha chain

Chain UI:



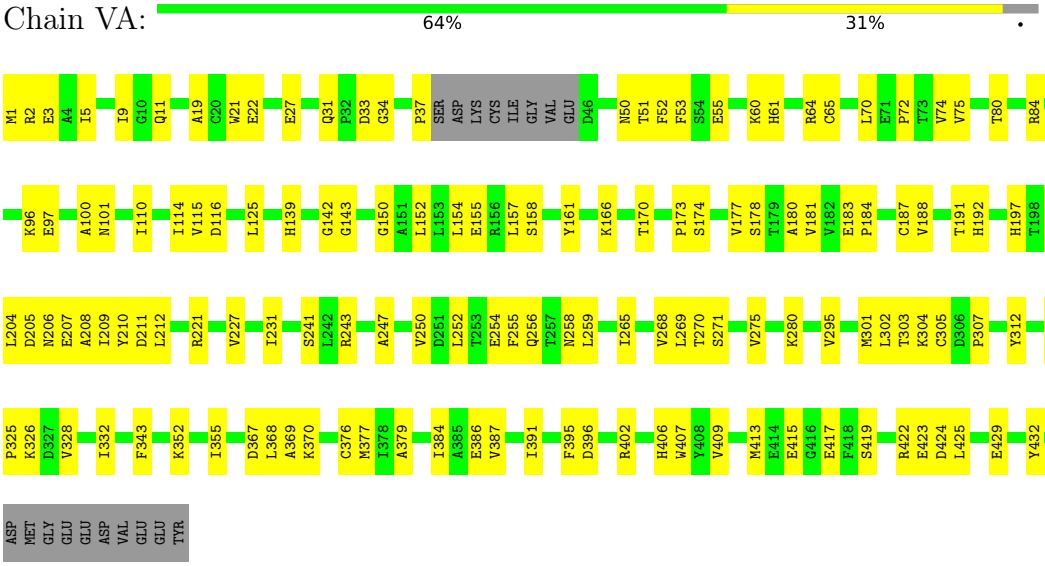
• Molecule 2: Tubulin alpha chain

Chain UK:



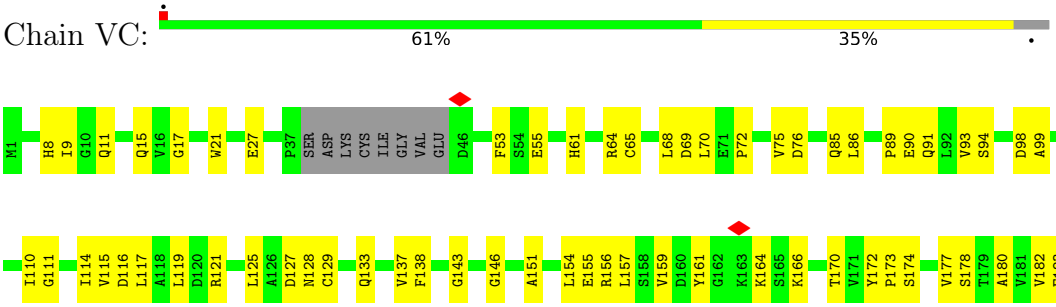
• Molecule 2: Tubulin alpha chain

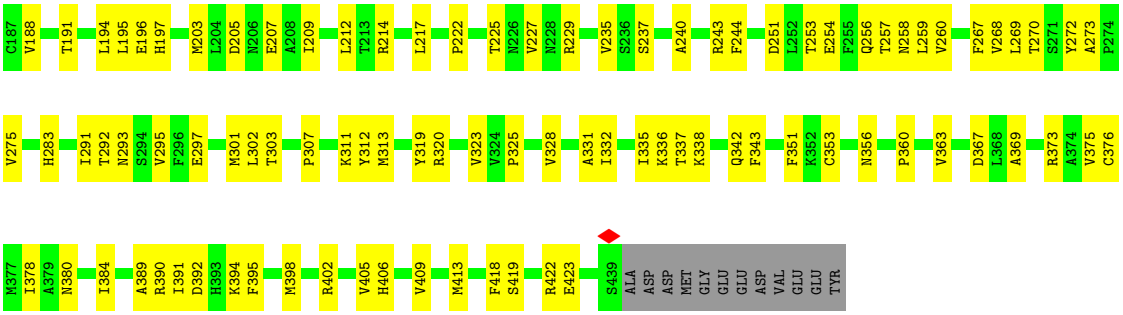
Chain VA:



• Molecule 2: Tubulin alpha chain

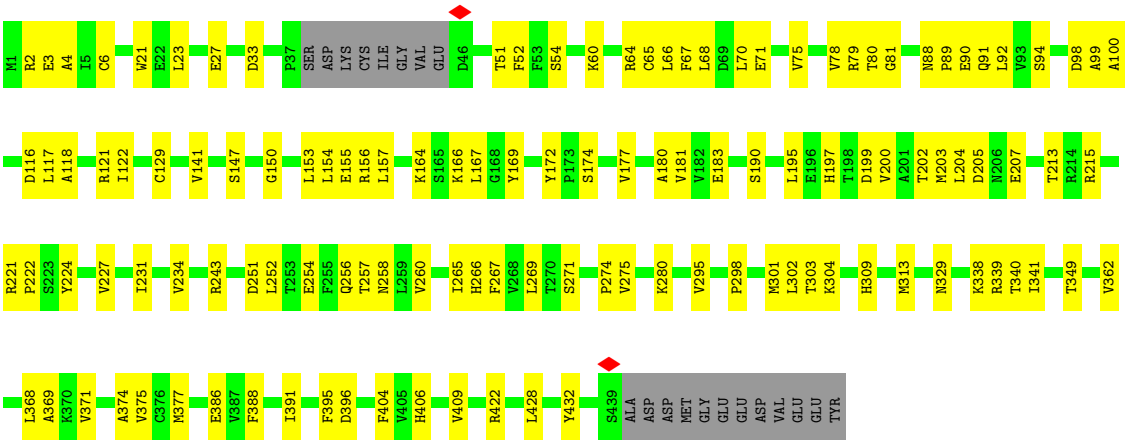
Chain VC:





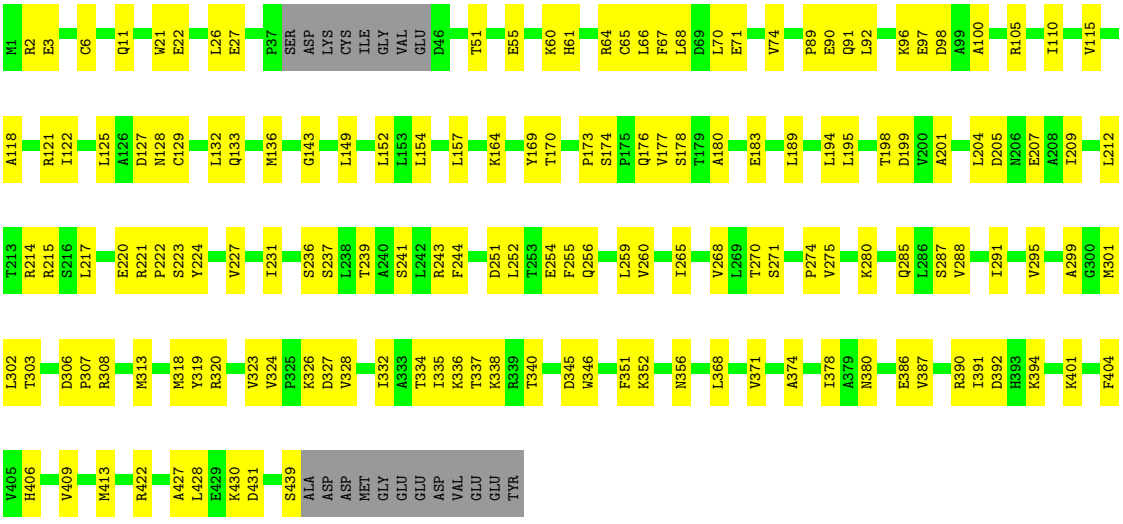
• Molecule 2: Tubulin alpha chain

Chain VE:



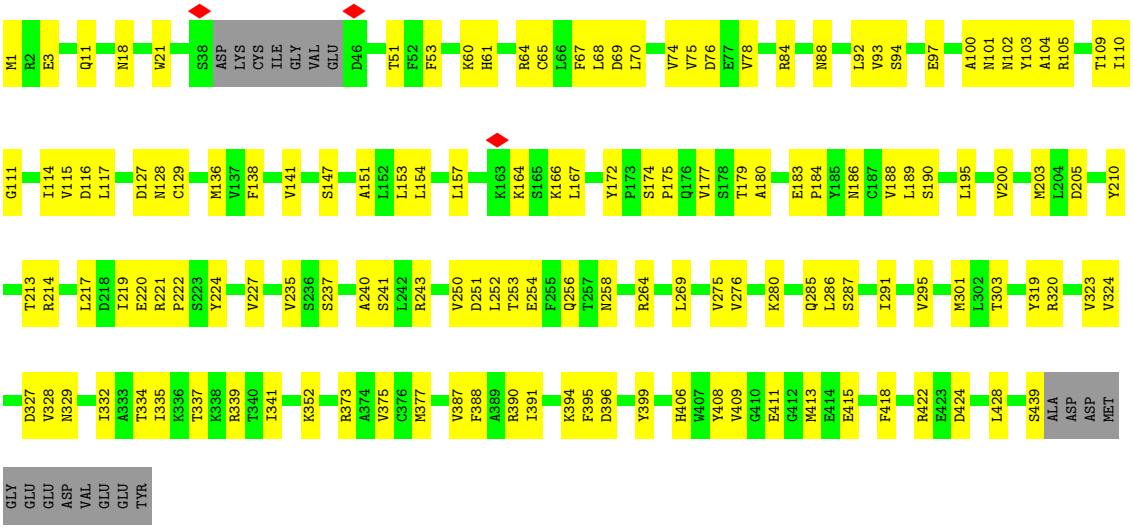
• Molecule 2: Tubulin alpha chain

Chain VG:



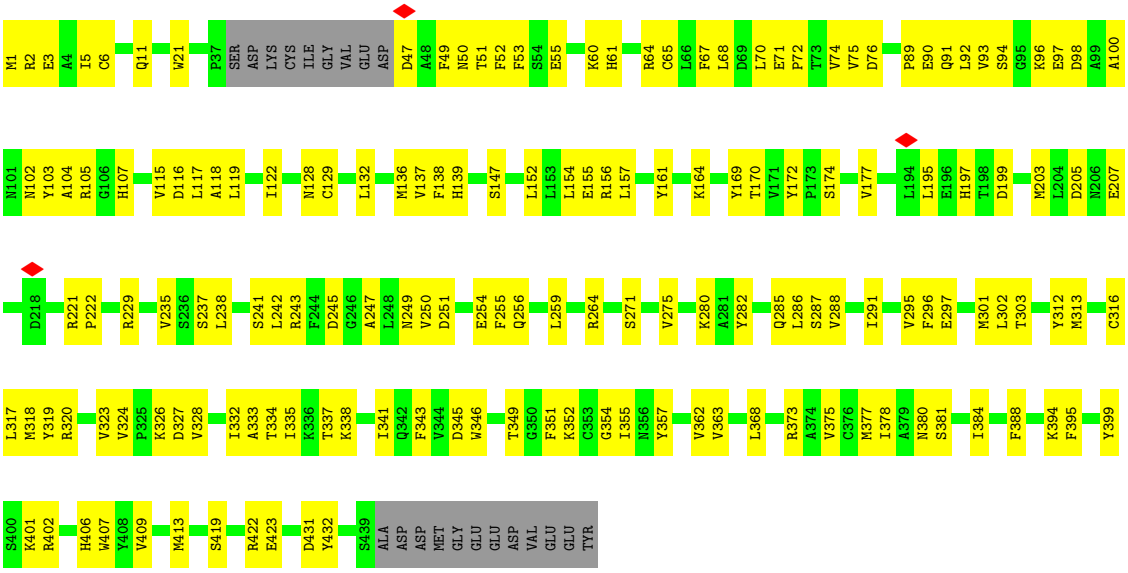
• Molecule 2: Tubulin alpha chain

Chain VI:



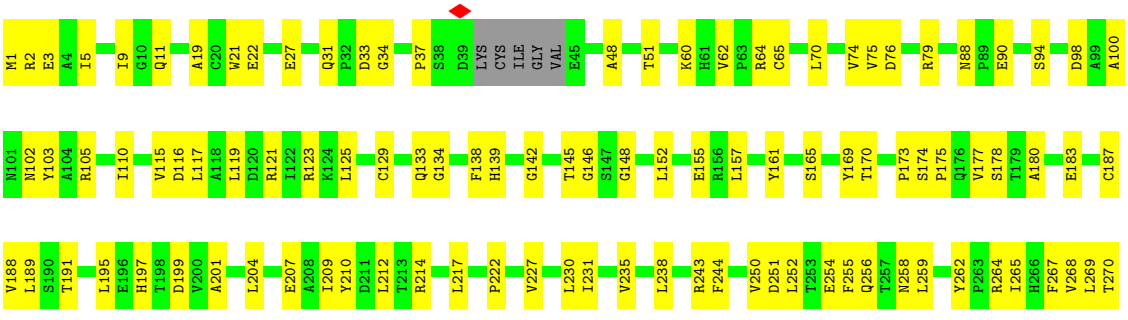
• Molecule 2: Tubulin alpha chain

Chain VK:



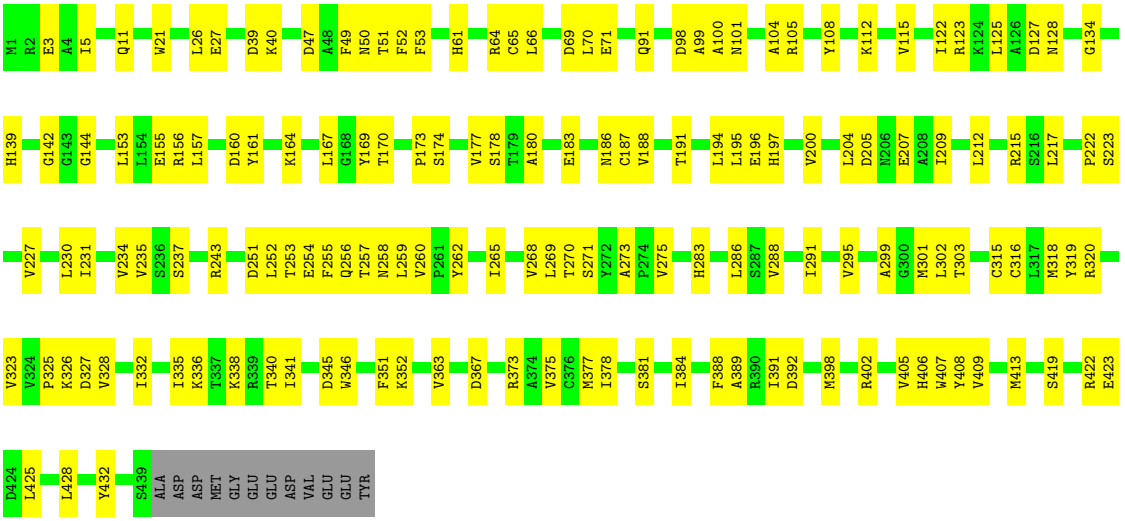
• Molecule 2: Tubulin alpha chain

Chain VM:



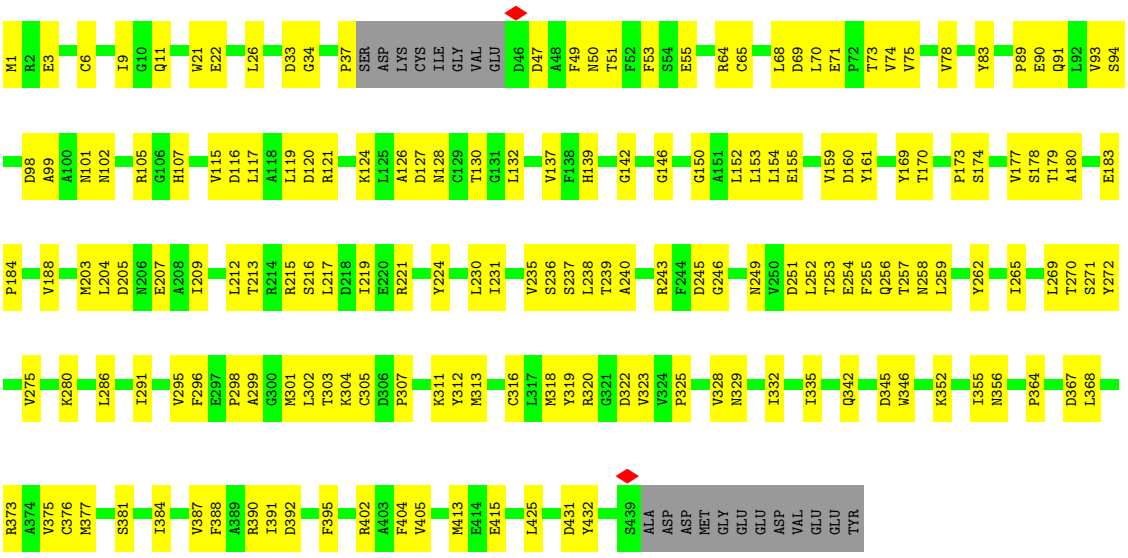
• Molecule 2: Tubulin alpha chain

Chain WA:



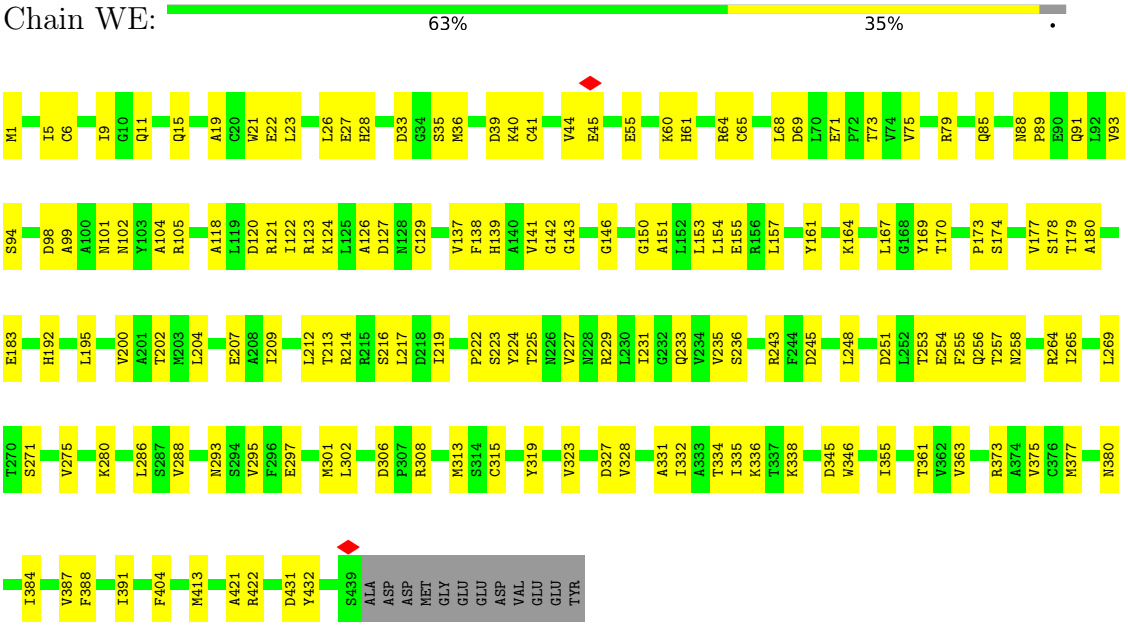
• Molecule 2: Tubulin alpha chain

Chain WC:



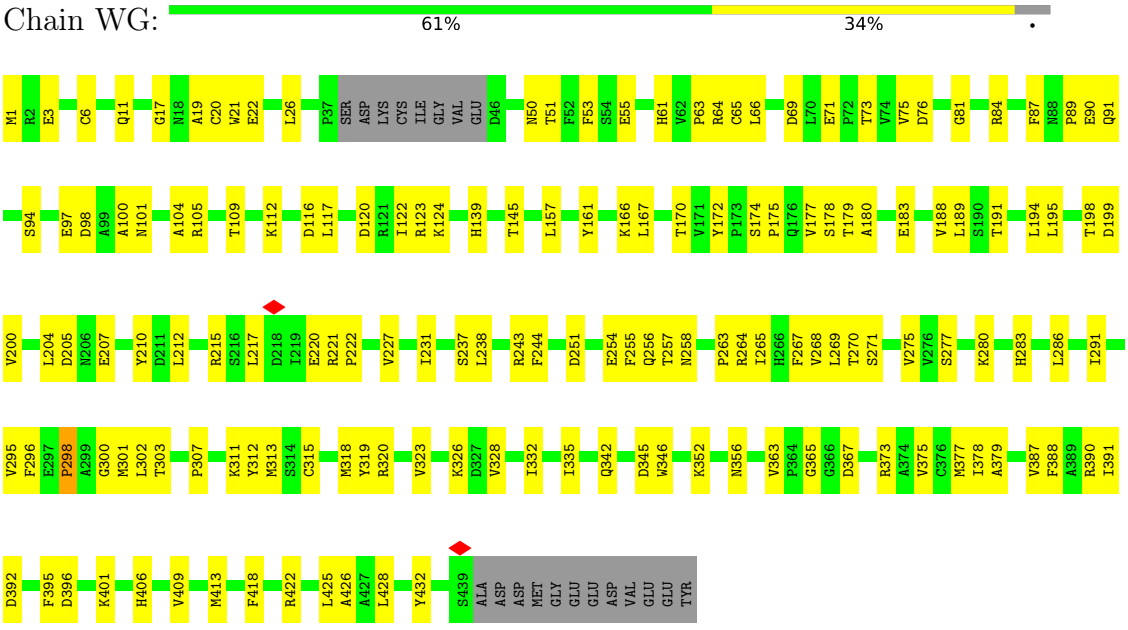
• Molecule 2: Tubulin alpha chain

Chain WE:



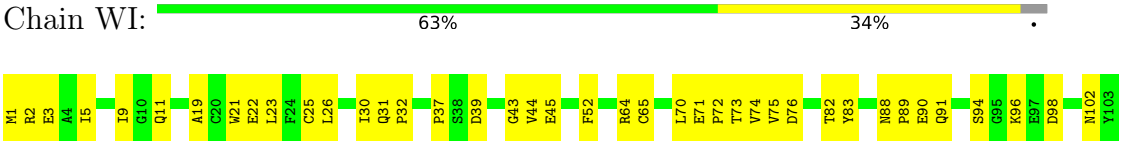
• Molecule 2: Tubulin alpha chain

Chain WG:



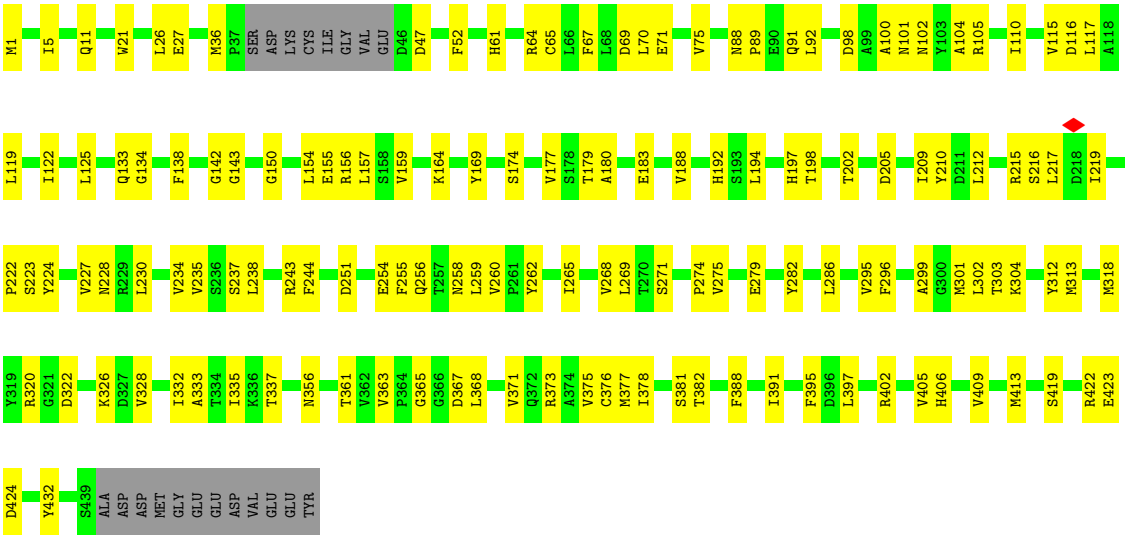
• Molecule 2: Tubulin alpha chain

Chain WI:



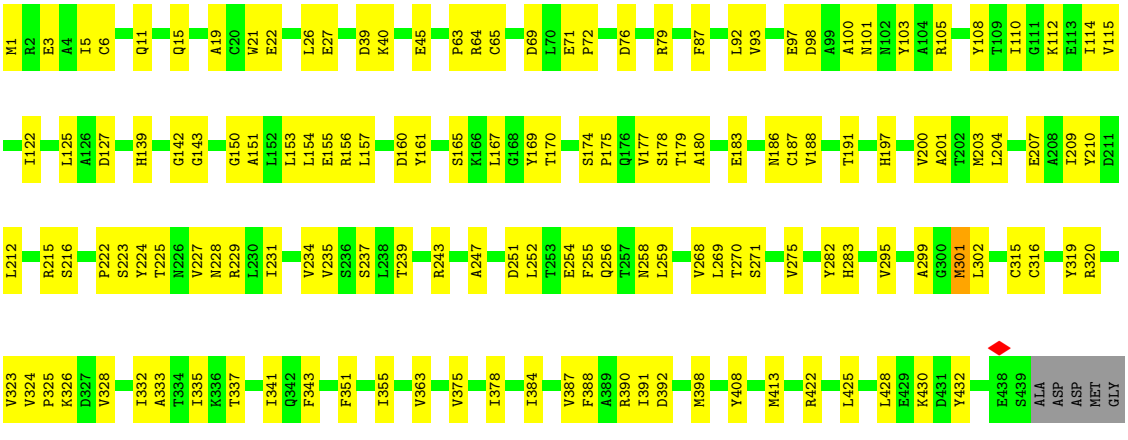
• Molecule 2: Tubulin alpha chain

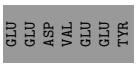
Chain WK:



• Molecule 2: Tubulin alpha chain

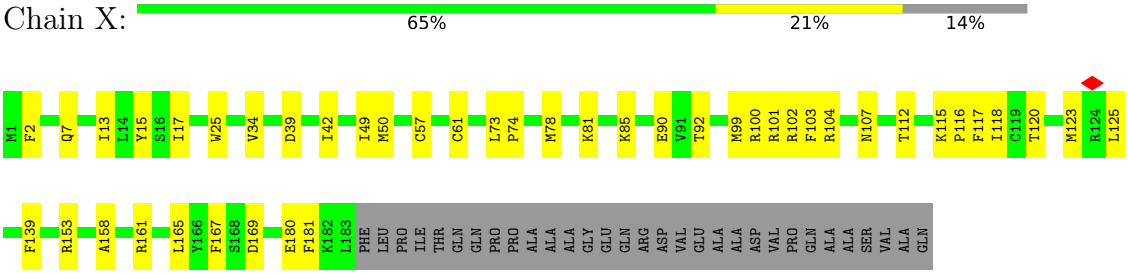
Chain WM:





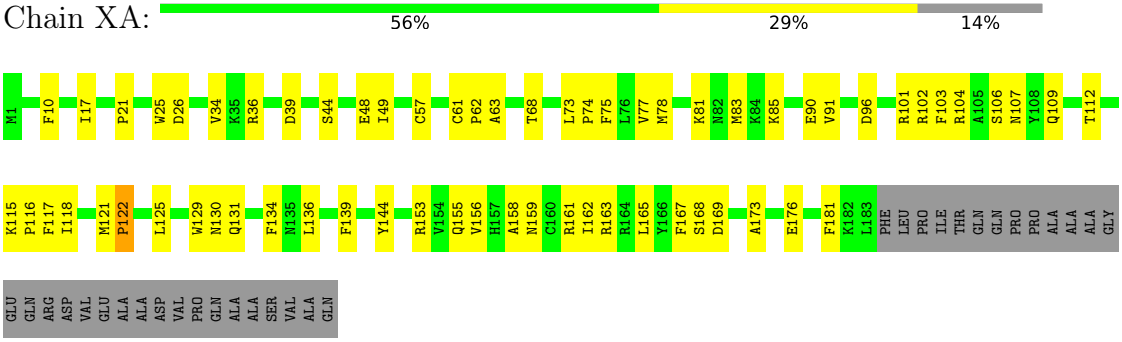
• Molecule 3: CFAP20

Chain X:



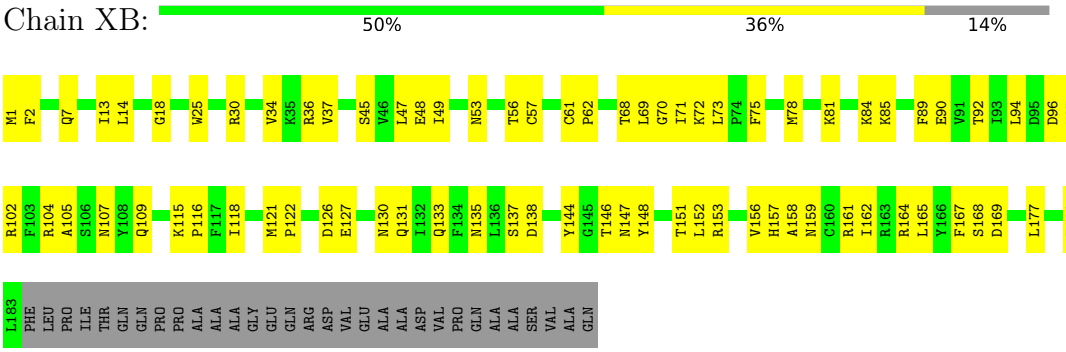
• Molecule 3: CFAP20

Chain XA:



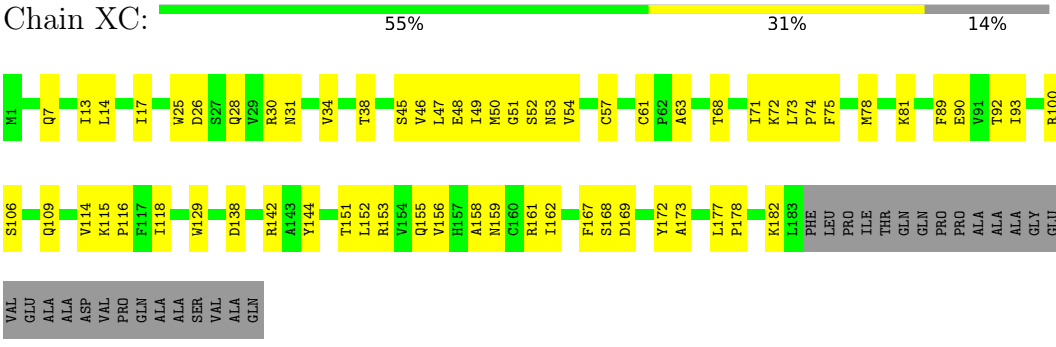
• Molecule 3: CFAP20

Chain XB:



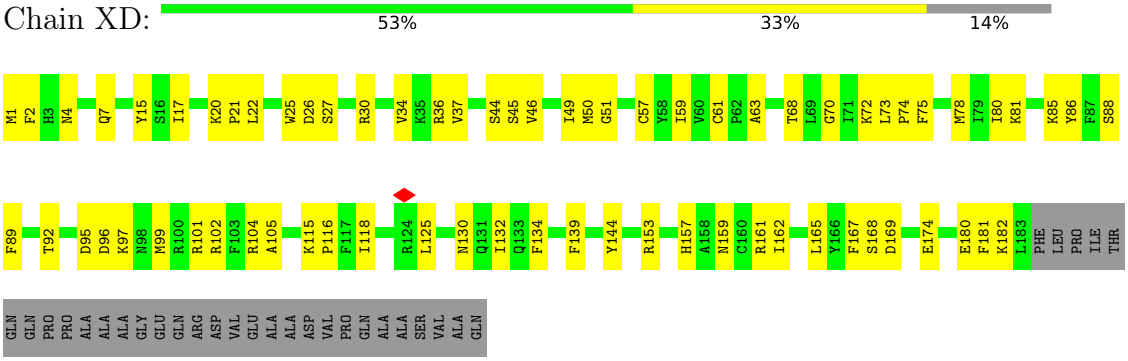
• Molecule 3: CFAP20

Chain XC:



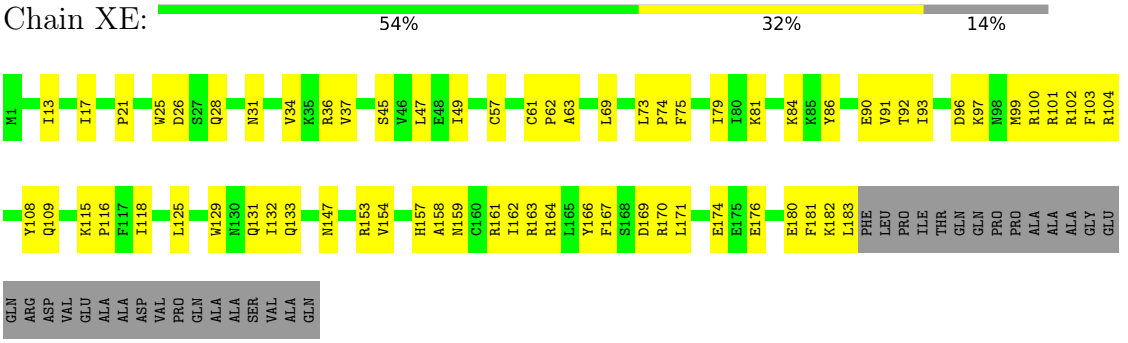
• Molecule 3: CFAP20

Chain XD:



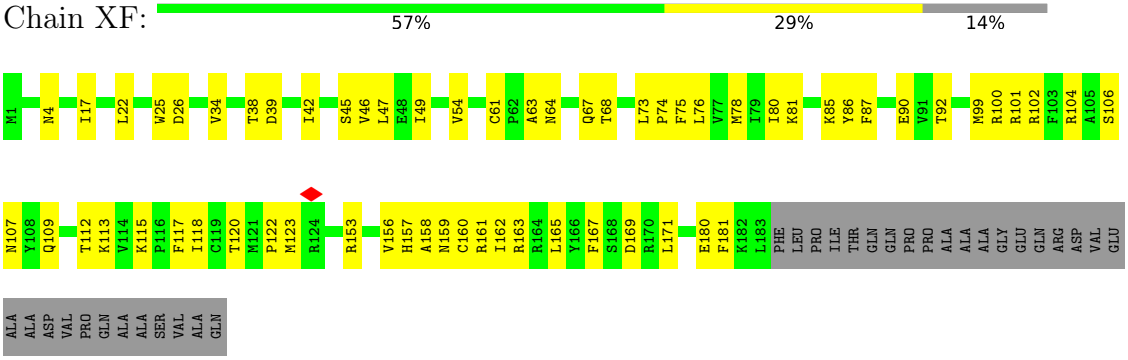
• Molecule 3: CFAP20

Chain XE:



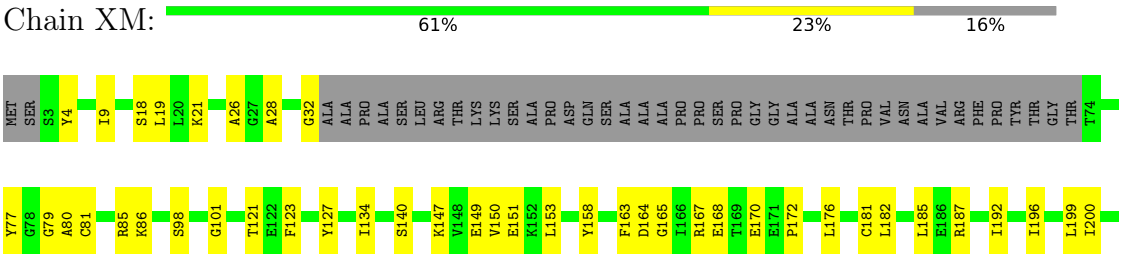
• Molecule 3: CFAP20

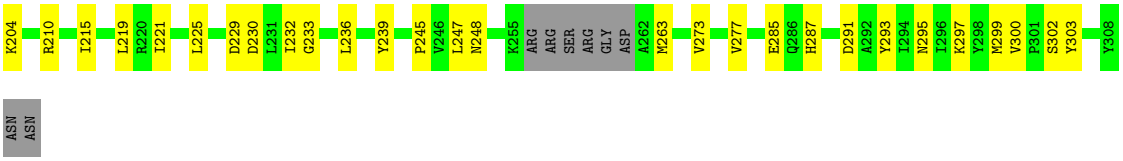
Chain XF:



• Molecule 4: PACRGA

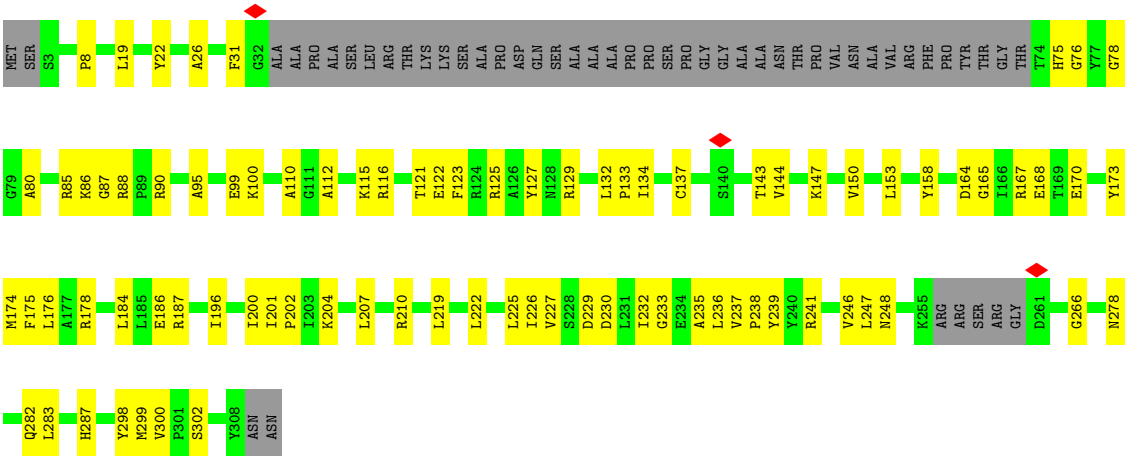
Chain XM:





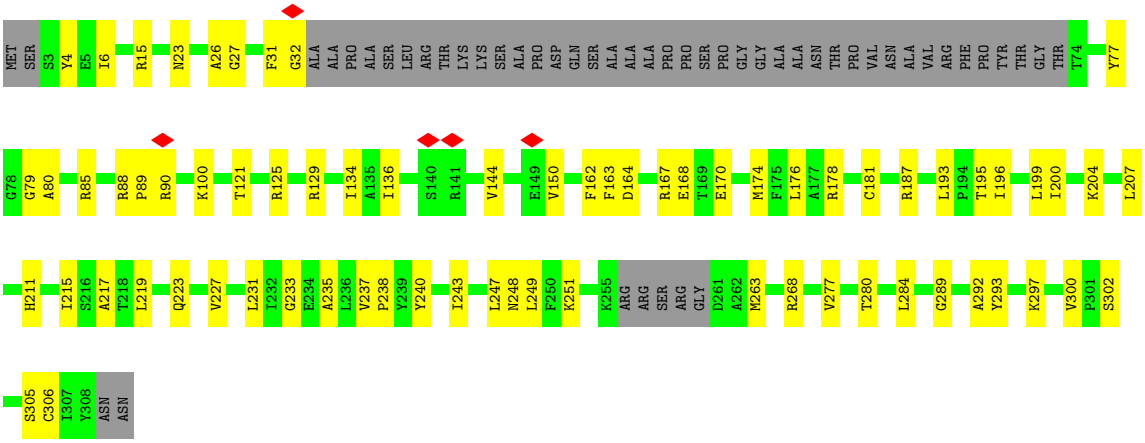
• Molecule 4: PACRGA

Chain XO:



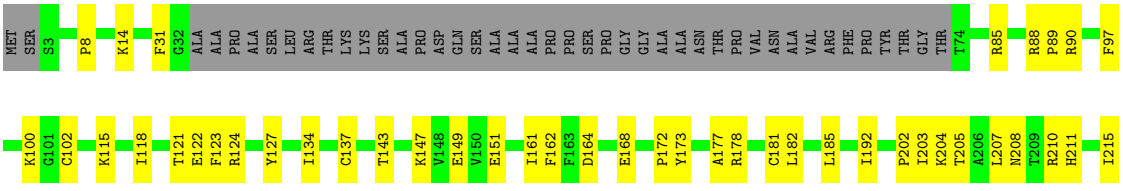
• Molecule 4: PACRGA

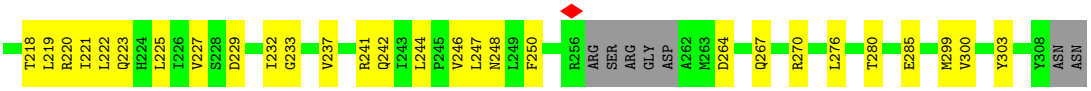
Chain XQ:



• Molecule 4: PACRGA

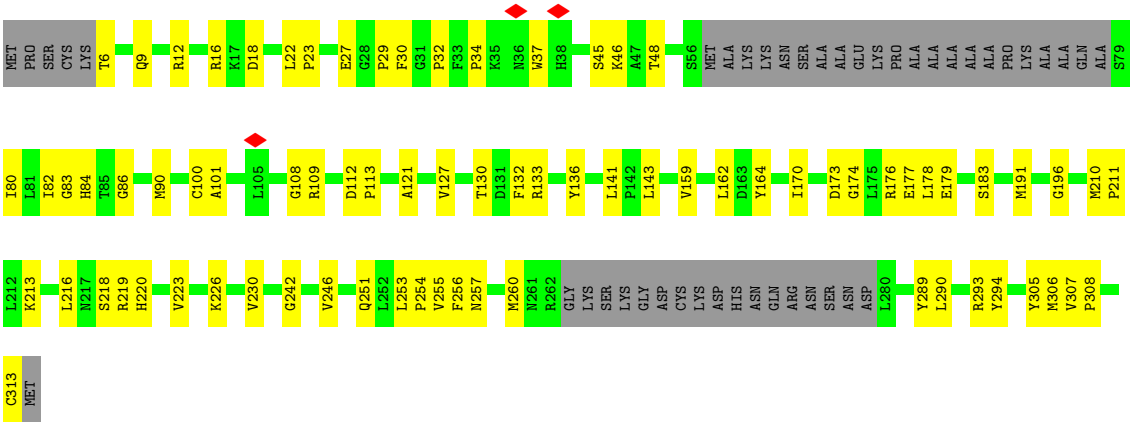
Chain XR:





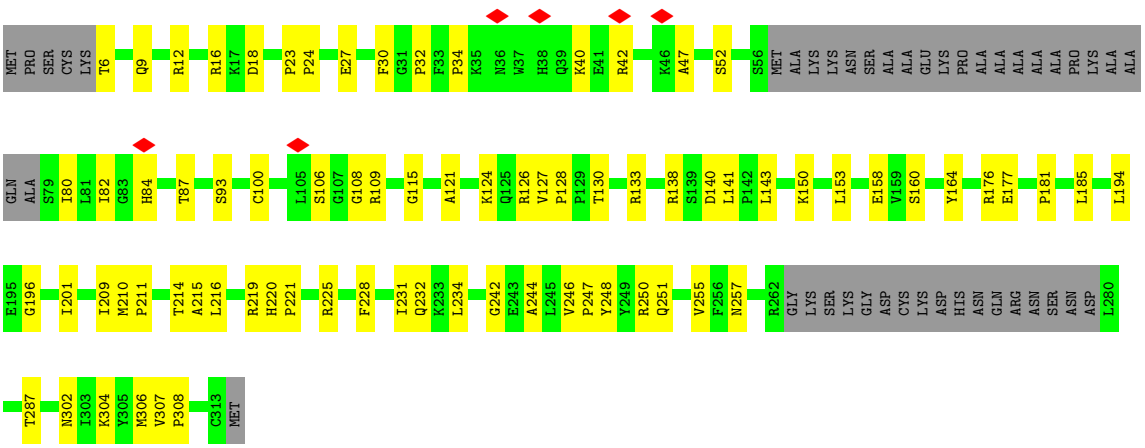
• Molecule 5: PACRGB

Chain XN:



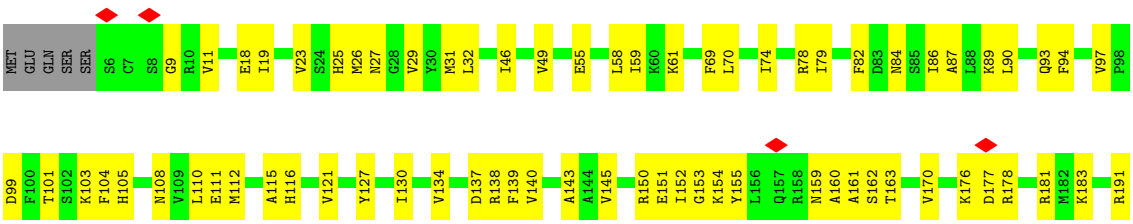
• Molecule 5: PACRGB

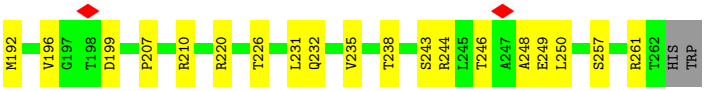
Chain XP:



• Molecule 6: CCDC81

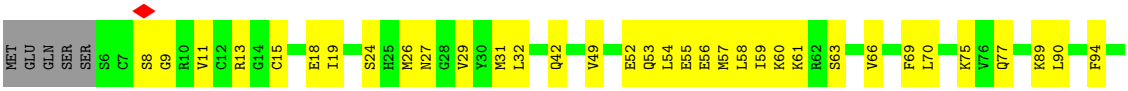
Chain 0A:

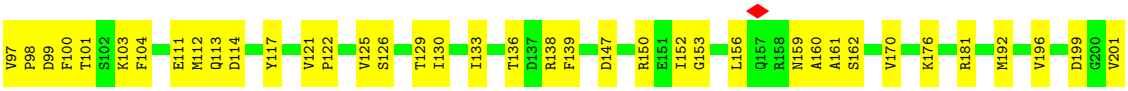


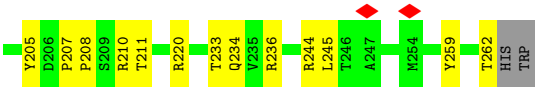


• Molecule 6: CCDC81

Chain 0:

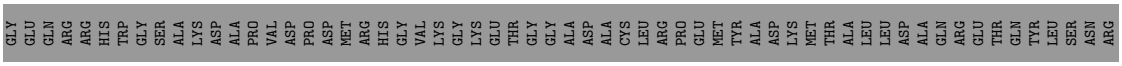






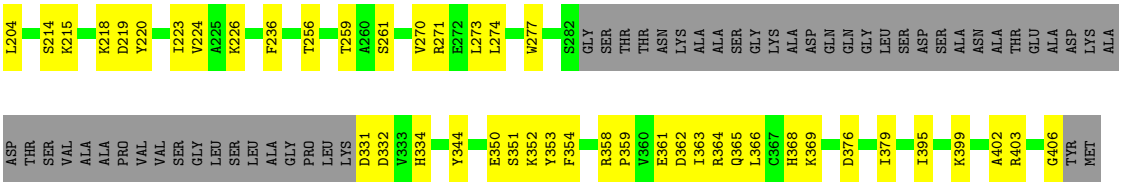
• Molecule 7: CFAP21

Chain 0C:



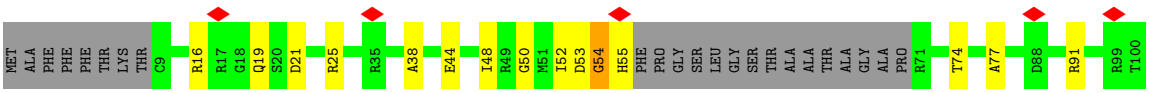
• Molecule 7: CFAP21

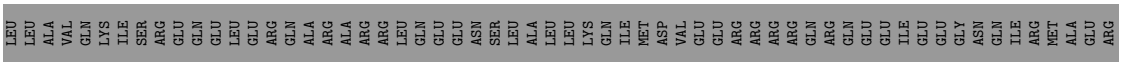
Chain 0D:



• Molecule 8: CFAP45

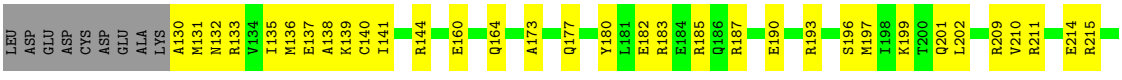
Chain 0F:

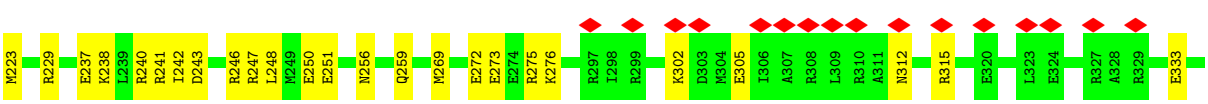


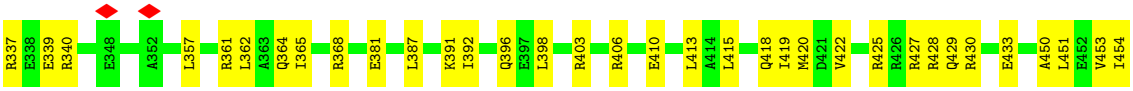


• Molecule 8: CFAP45

Chain 0G:

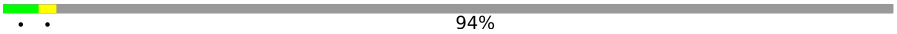


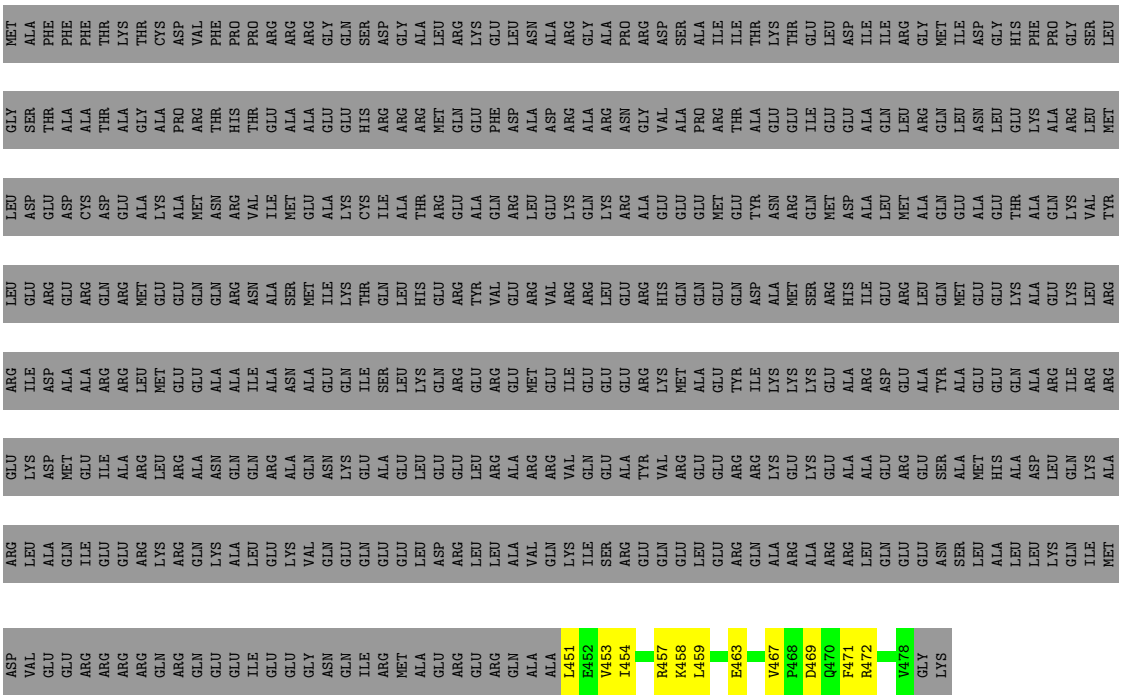




• Molecule 8: CFAP45

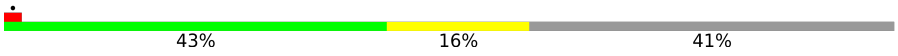
Chain 0H:

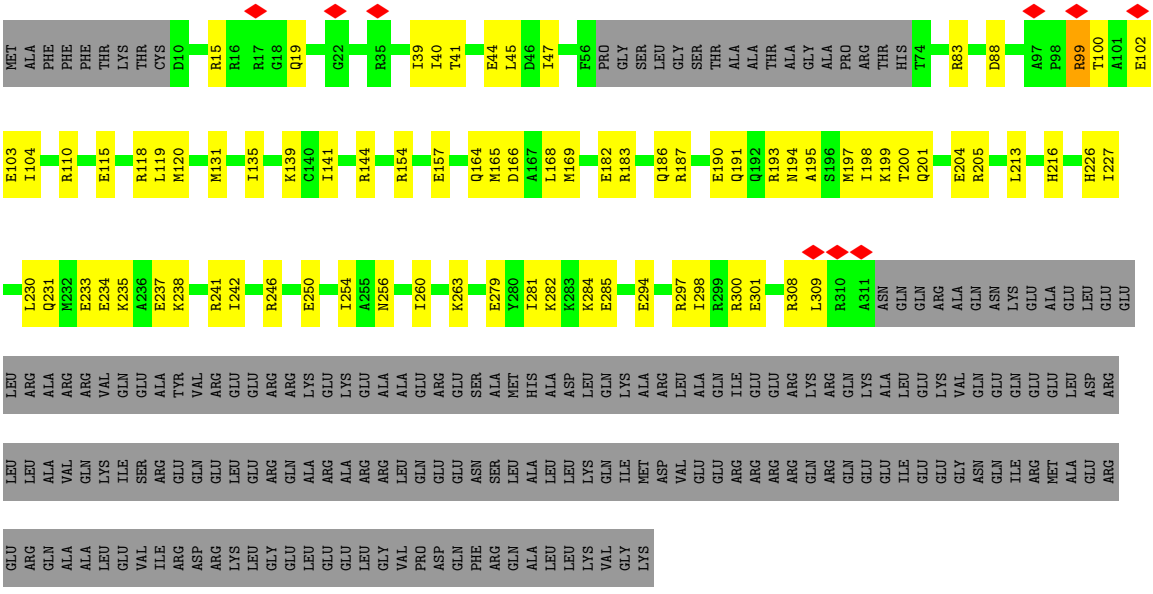




• Molecule 8: CFAP45

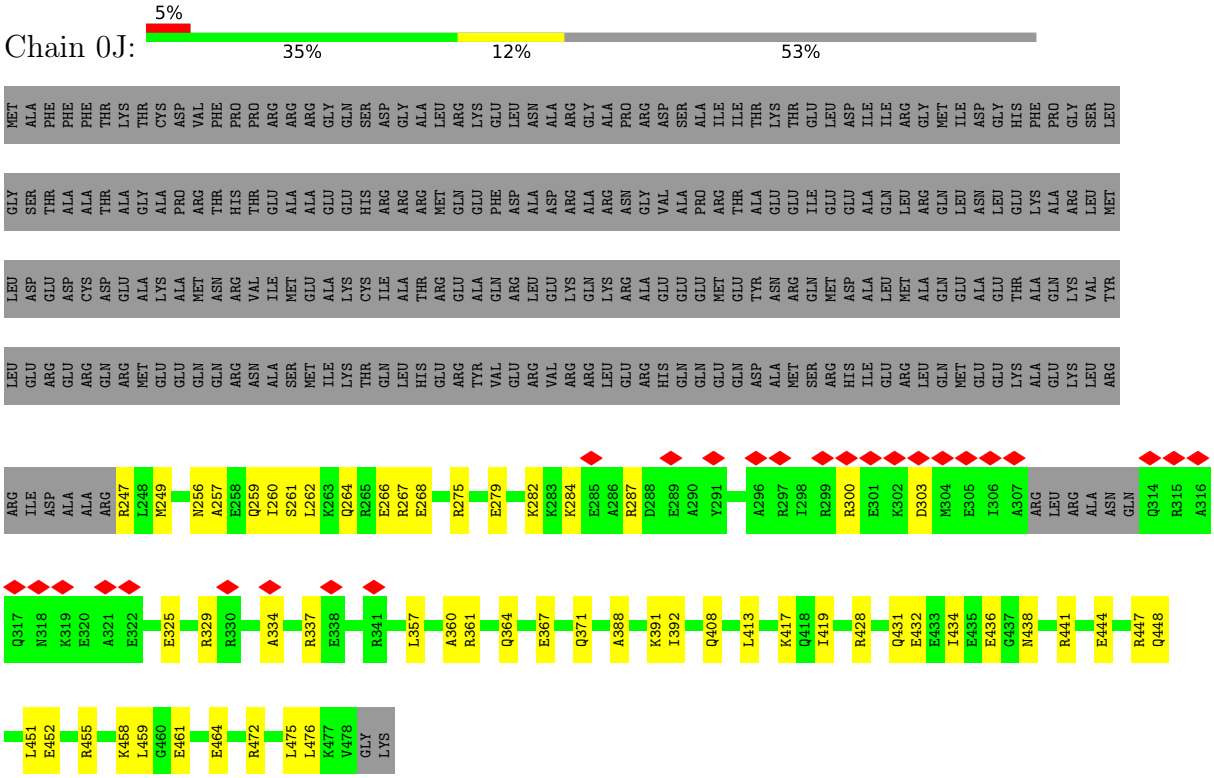
Chain 0I:





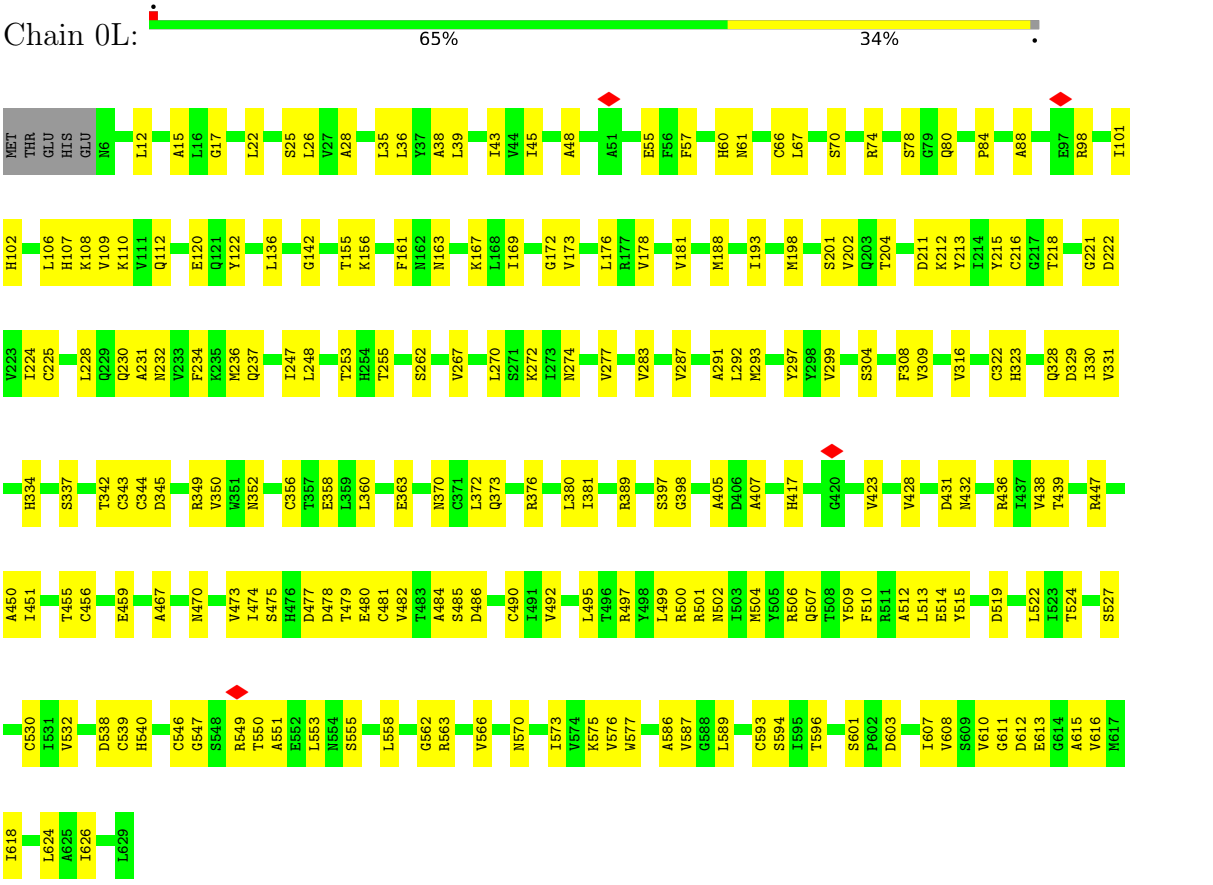
• Molecule 8: CFAP45

Chain 0J:



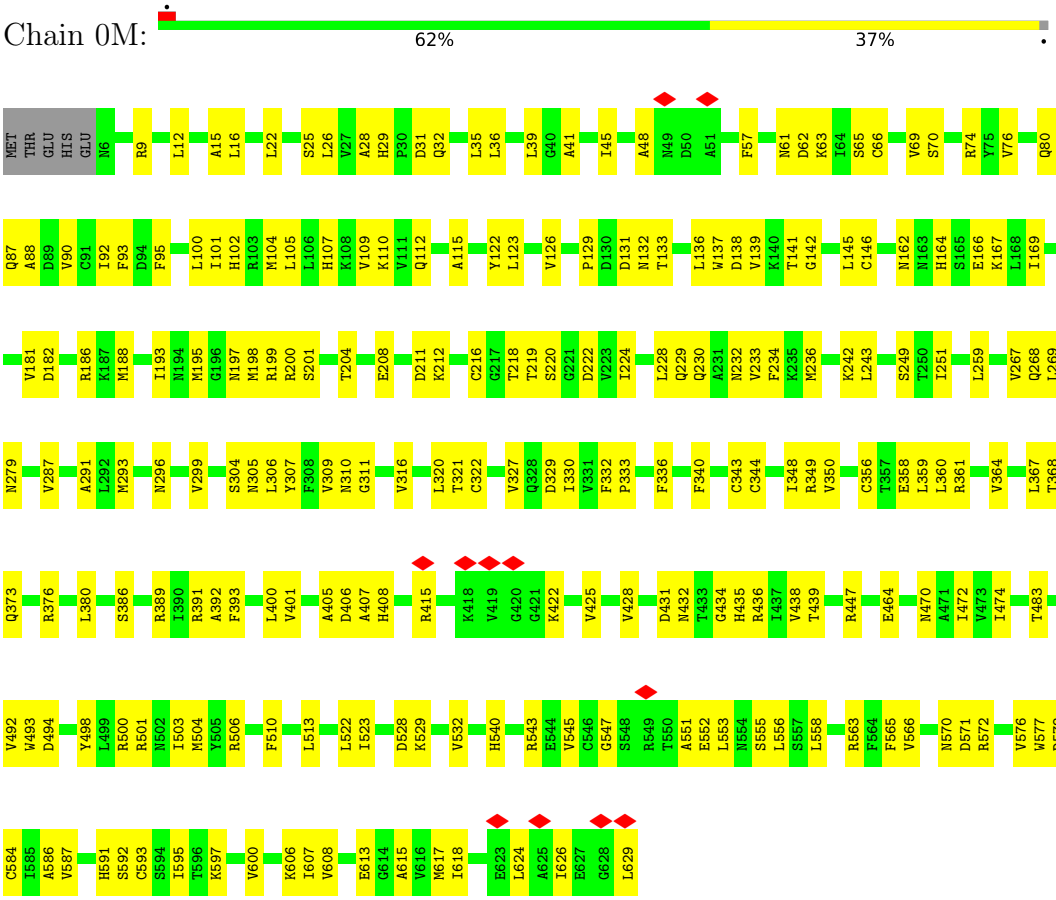
• Molecule 9: CFAP52

Chain 0L:



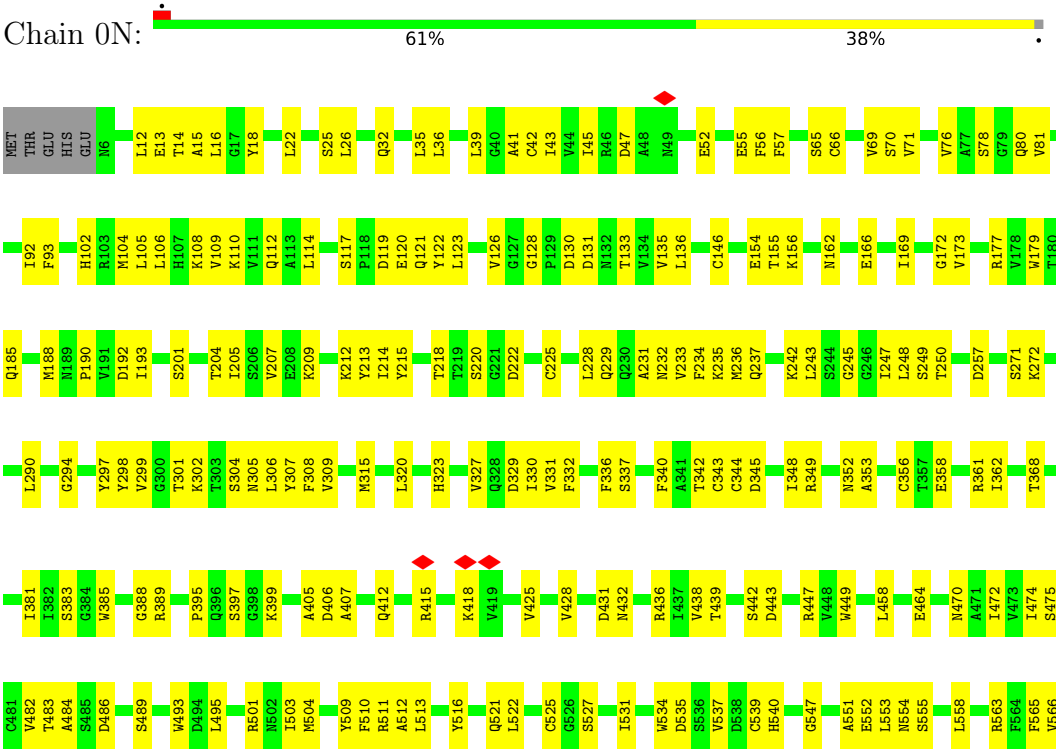
• Molecule 9: CFAP52

Chain 0M:



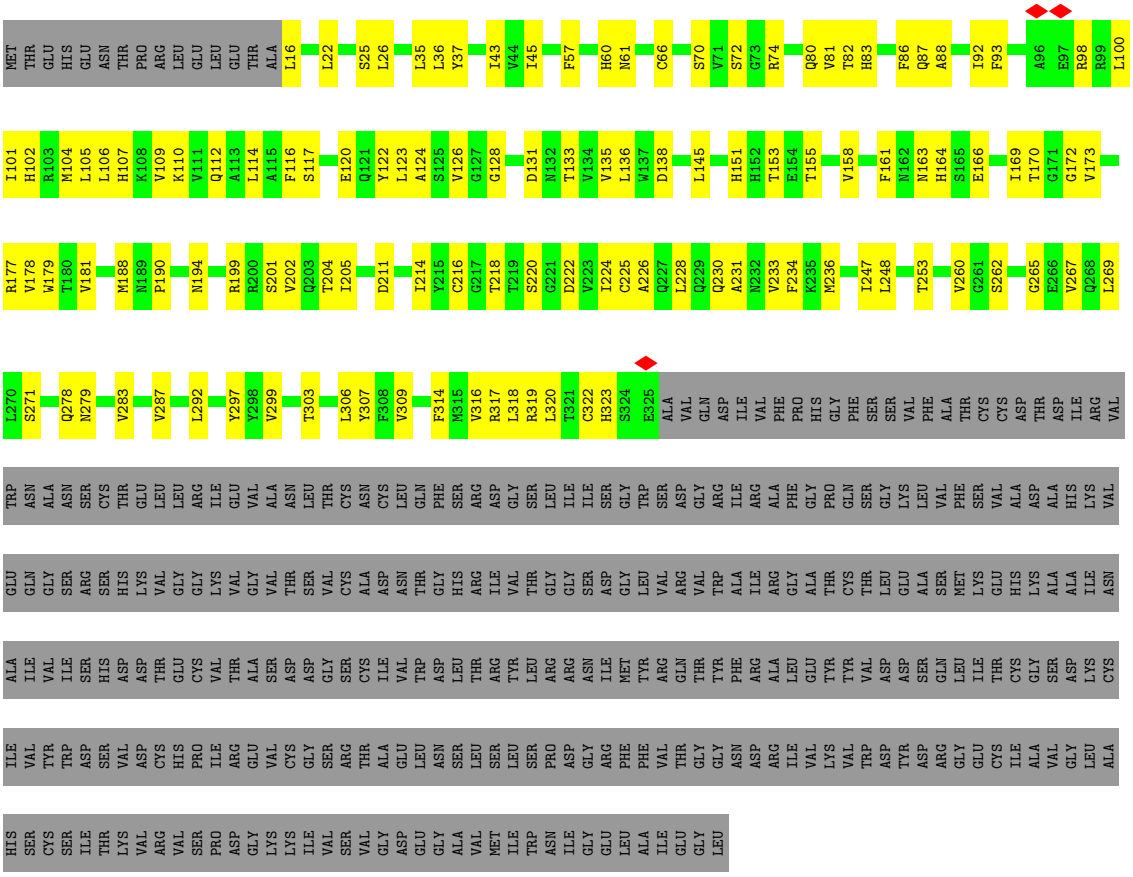
• Molecule 9: CFAP52

Chain 0N:



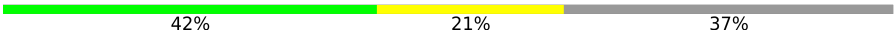
• Molecule 9: CFAP52

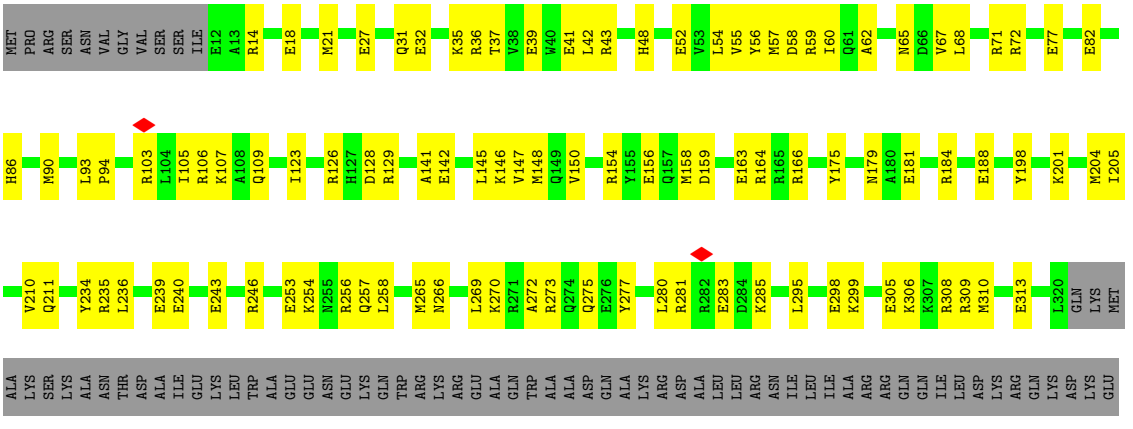
Chain 0O:

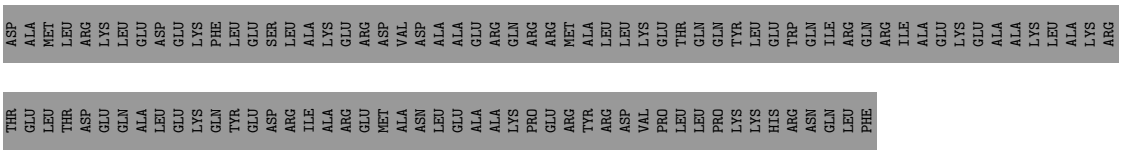


• Molecule 10: CFAP53

Chain 0R:

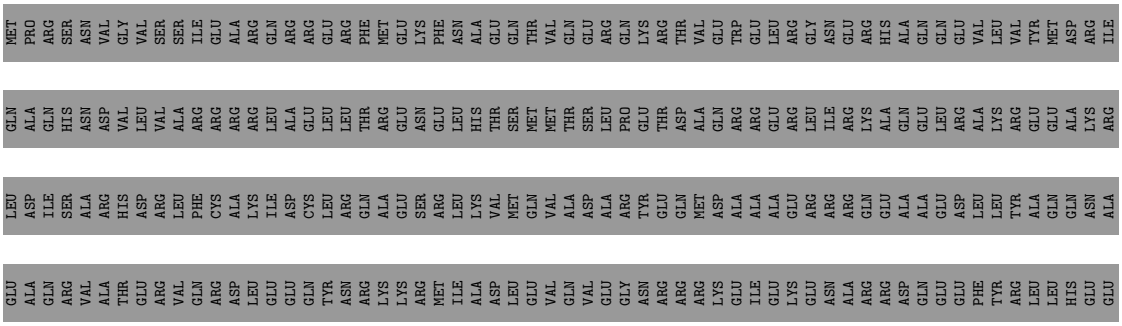


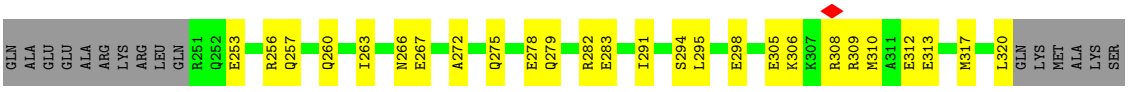


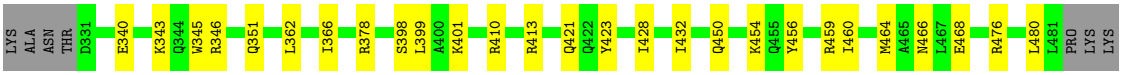


• Molecule 10: CFAP53

Chain 0S:

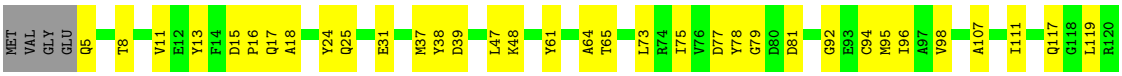


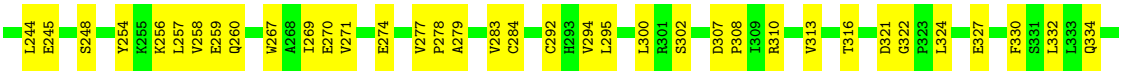




• Molecule 11: CFAP67A

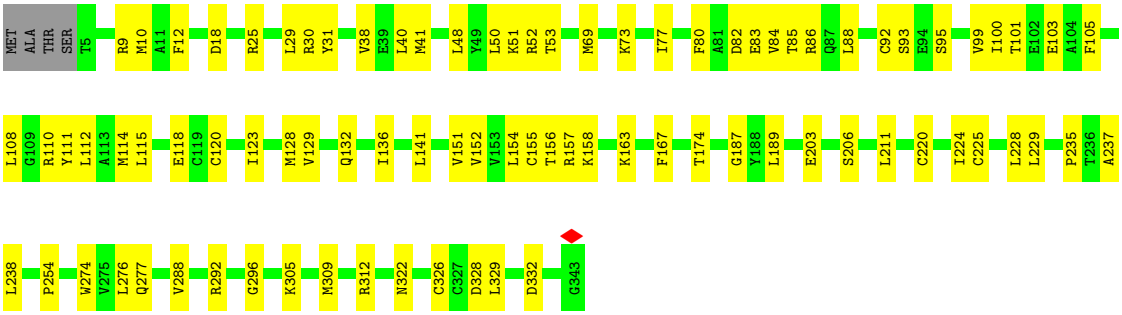
Chain 0U:





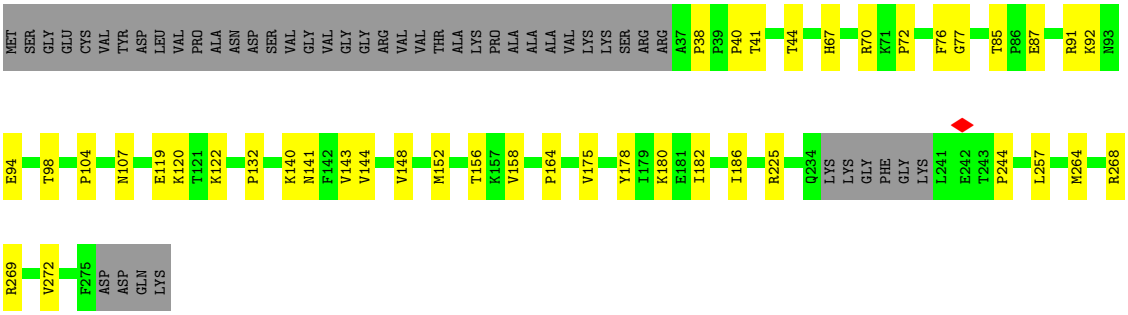
• Molecule 12: CFAP67B

Chain 0W:



• Molecule 13: CFAP106A

Chain 0Y:

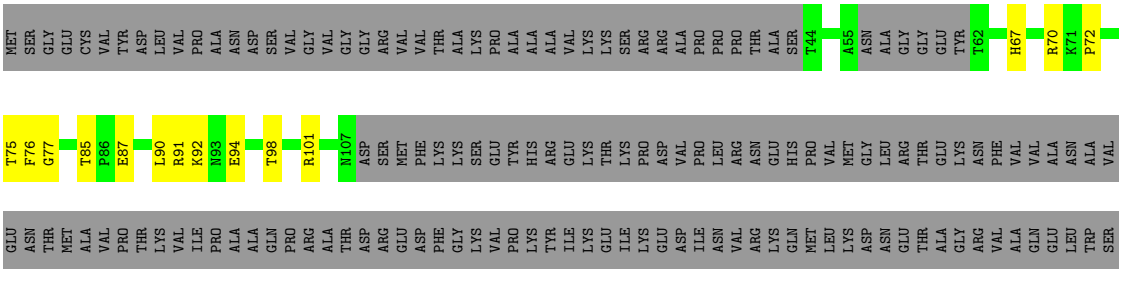


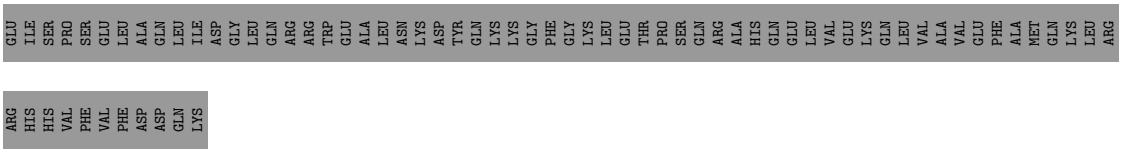
• Molecule 13: CFAP106A

Chain 0Z:

• Molecule 13: CFAP106A

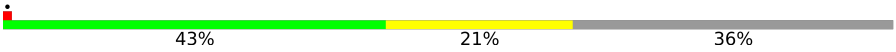
Chain 0a:

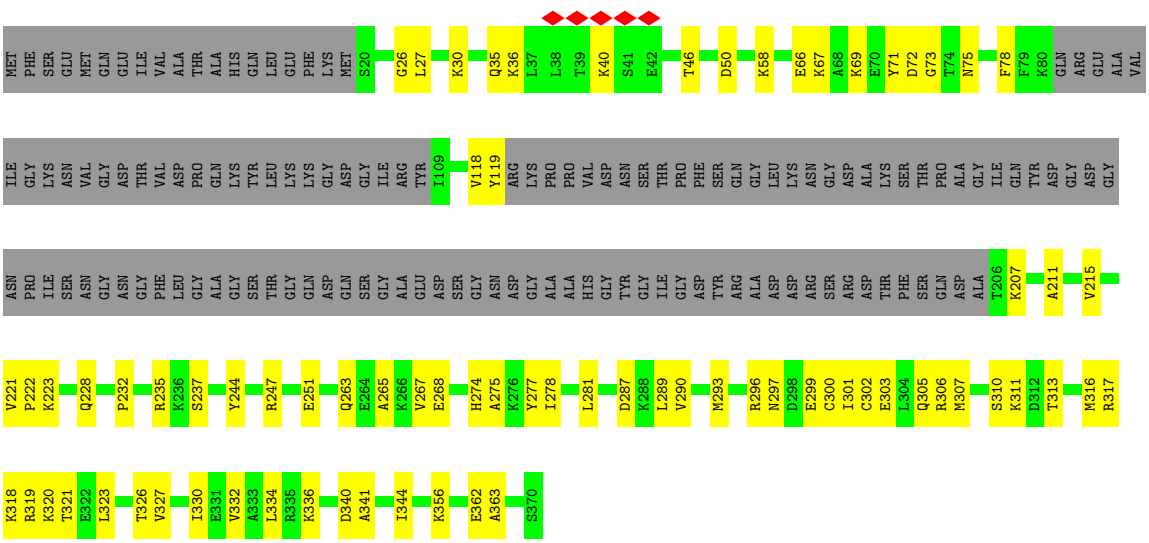




• Molecule 14: CFAP106B

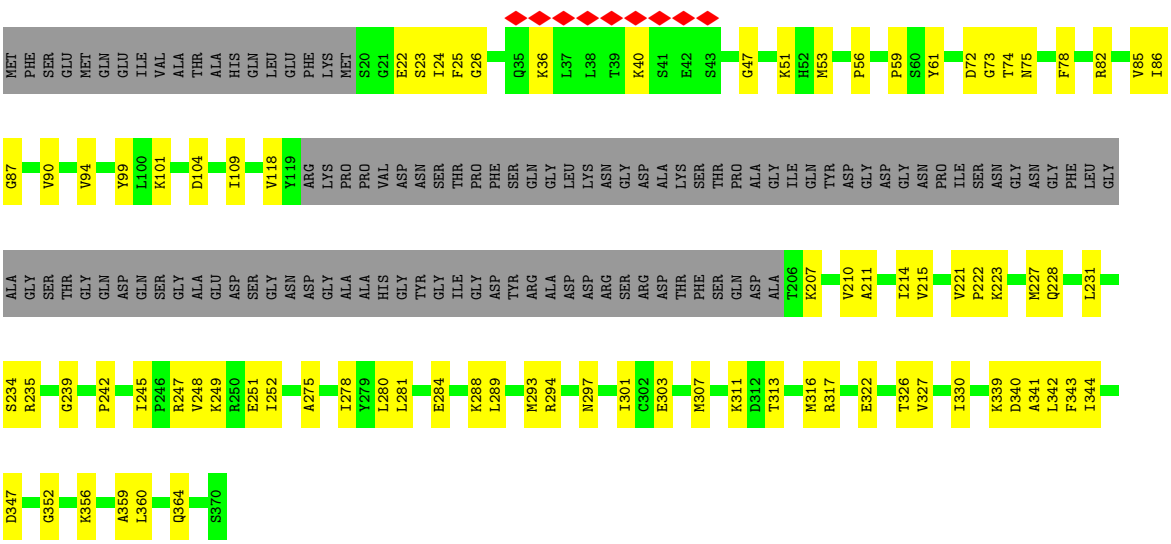
Chain 0c:





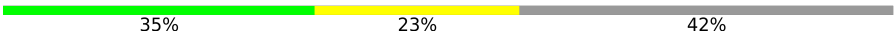
• Molecule 14: CFAP106B

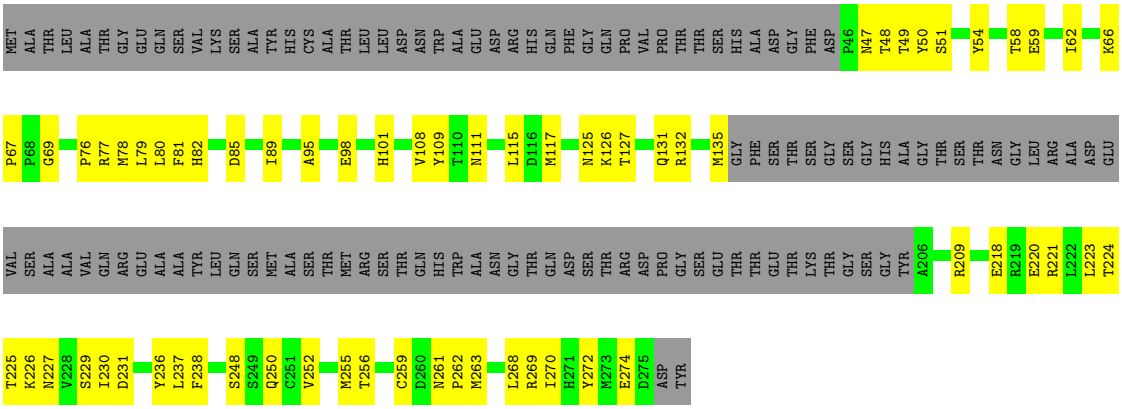
Chain 0d:



• Molecule 15: CFAP107

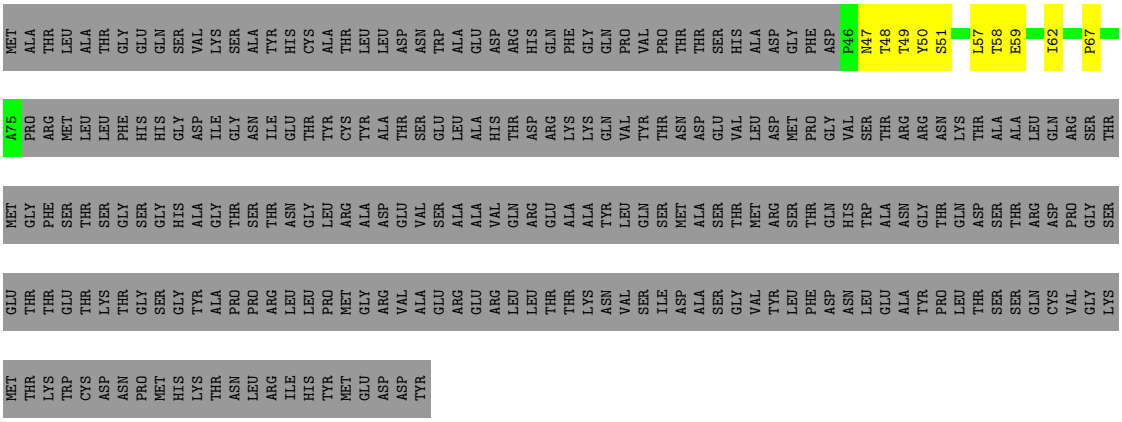
Chain 0f:





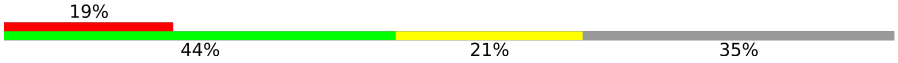
• Molecule 15: CFAP107

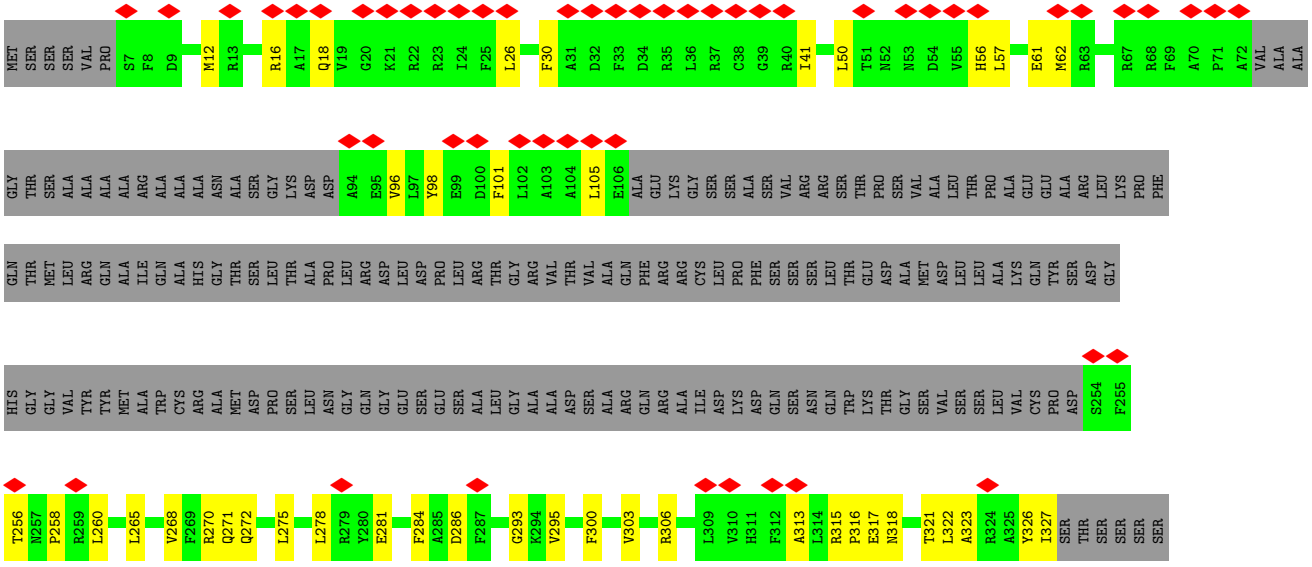
Chain 0g:

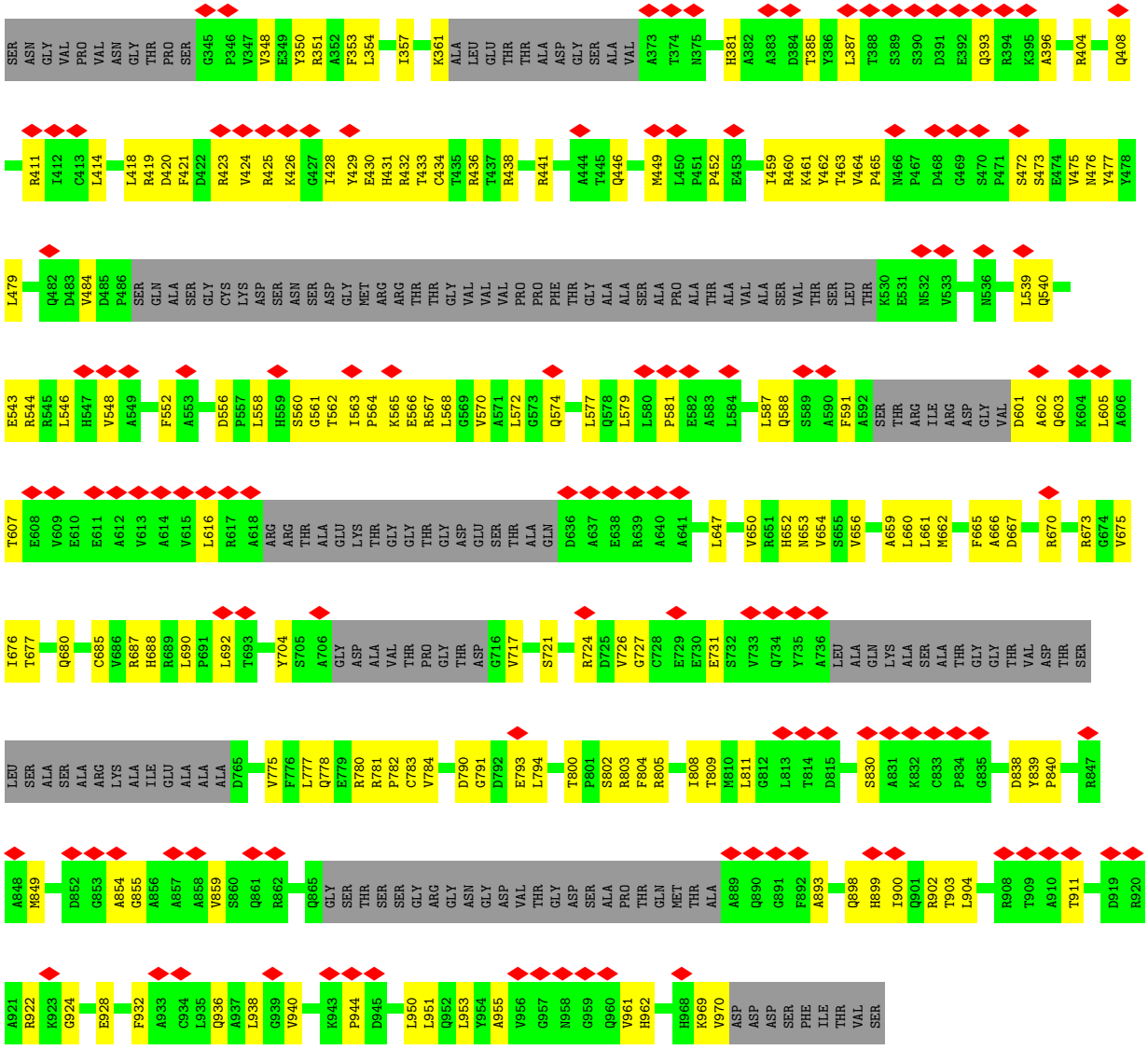


• Molecule 16: CFAP115

Chain 0l:

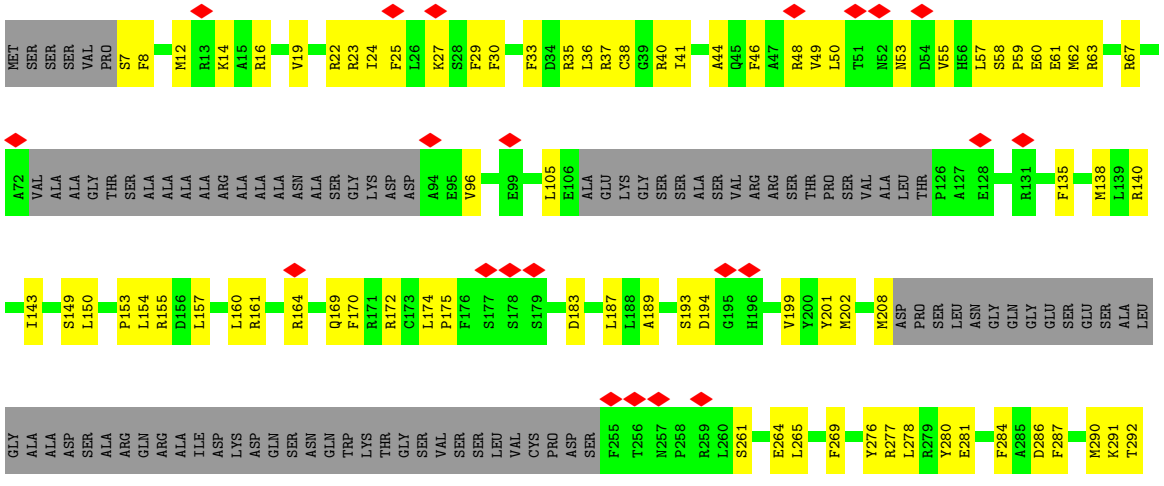


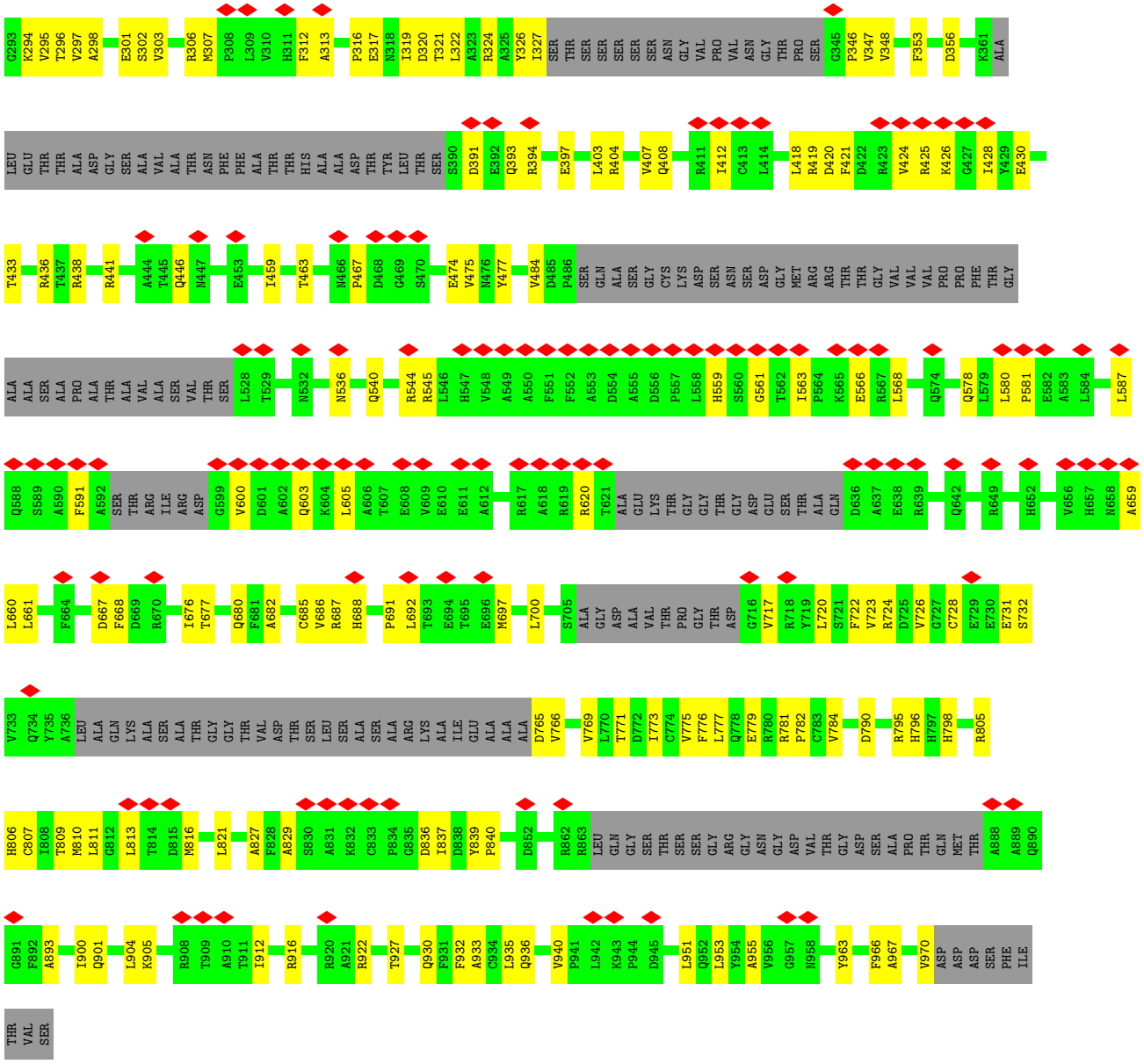




• Molecule 16: CFAP115

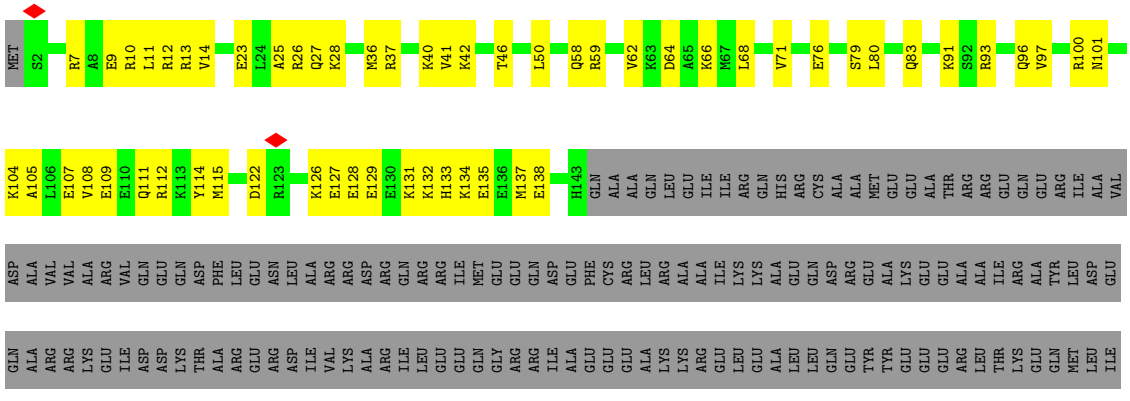
Chain 0k:

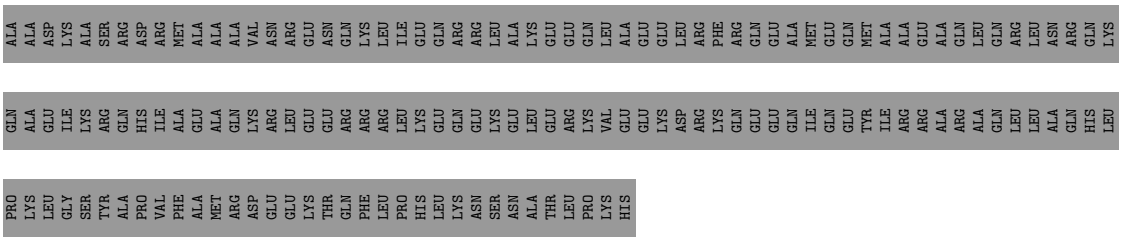




• Molecule 17: CFAP127

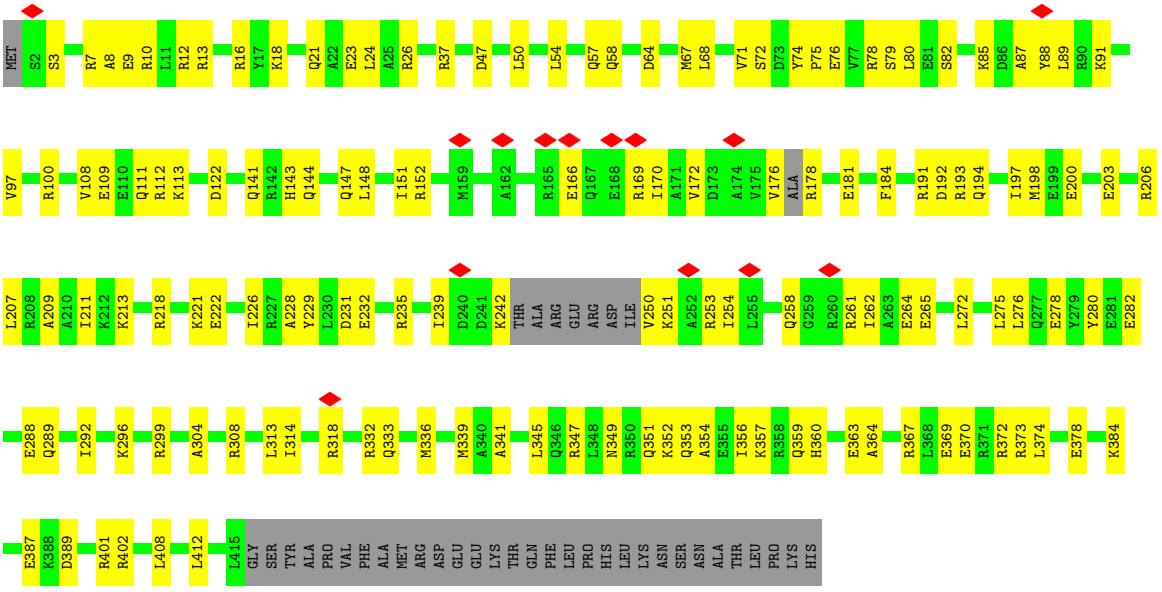
Chain 0m:





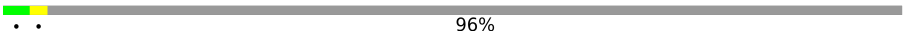
• Molecule 17: CFAP127

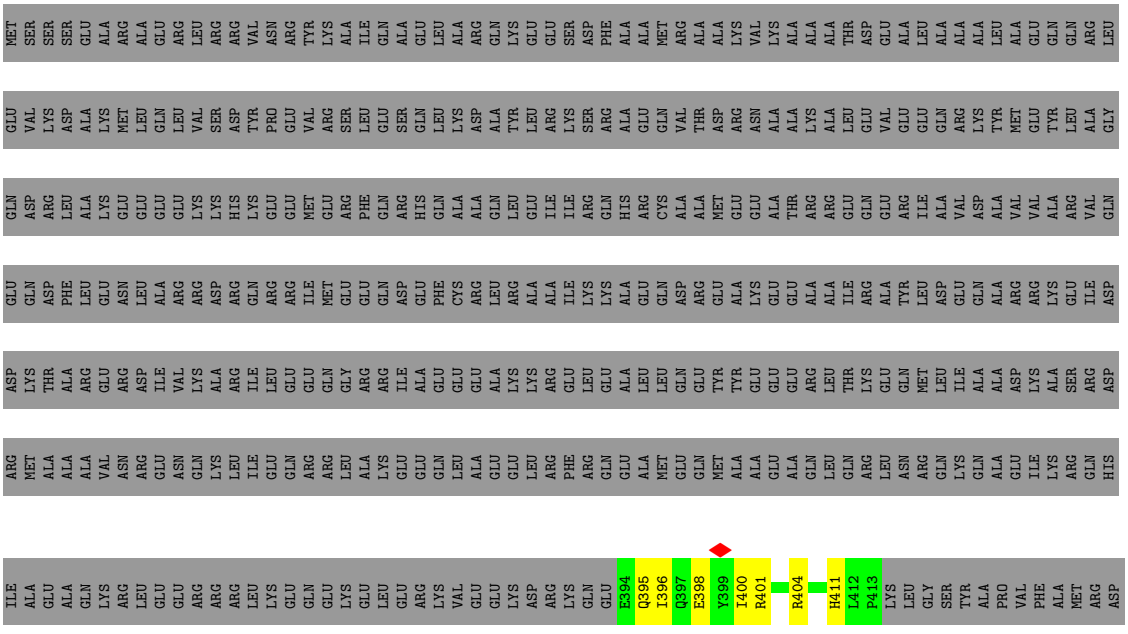
Chain 0n:



• Molecule 17: CFAP127

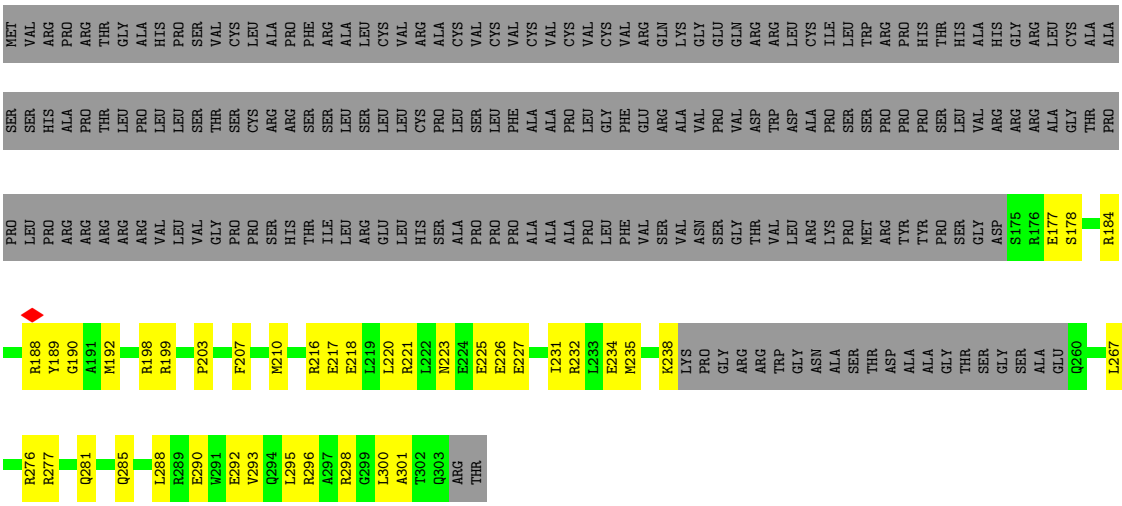
Chain 0o:





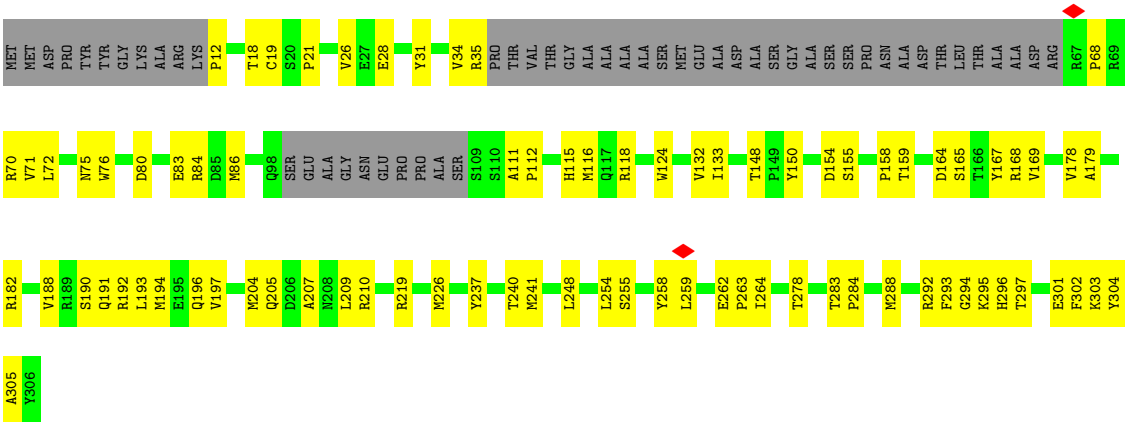
• Molecule 18: CFAP141

Chain 0p:



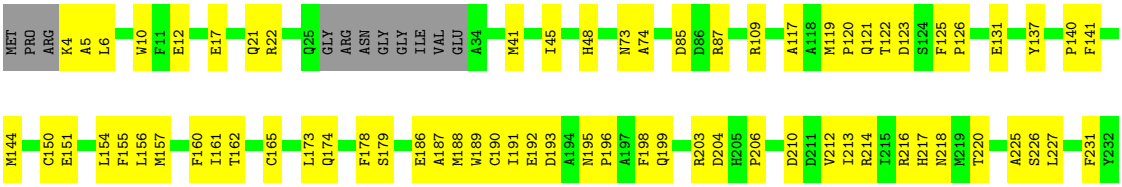
• Molecule 19: CFAP143

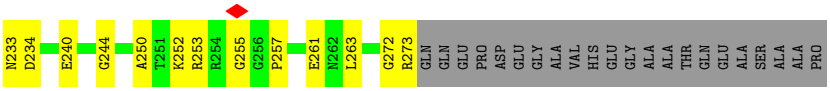
Chain 0r:



• Molecule 20: CFAP161

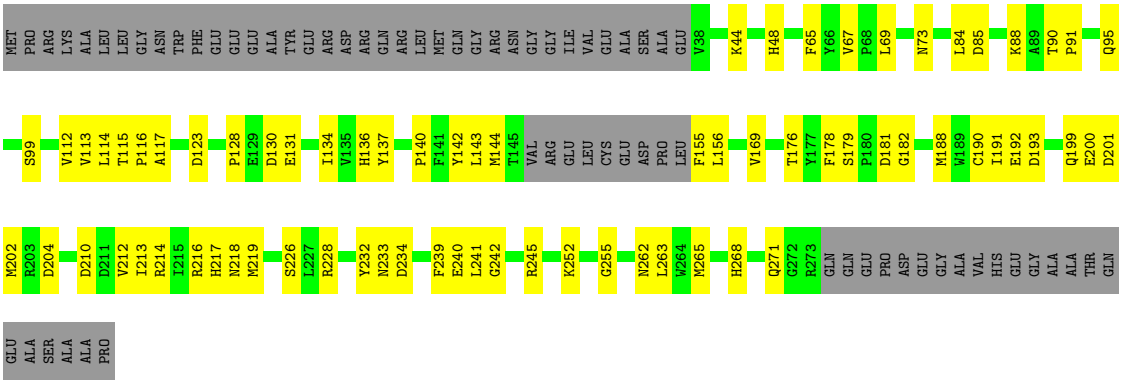
Chain 0t:





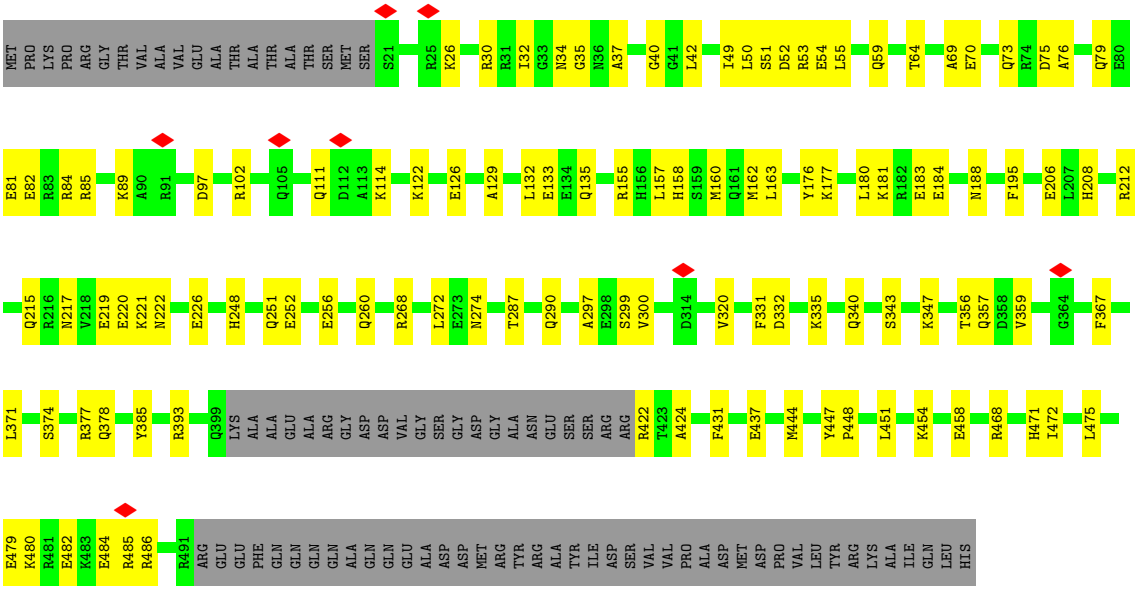
• Molecule 20: CFAP161

Chain 0u:



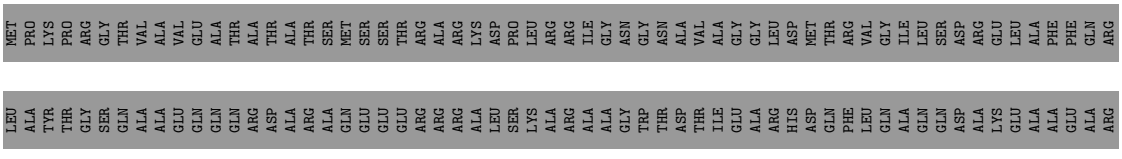
• Molecule 21: CFAP210

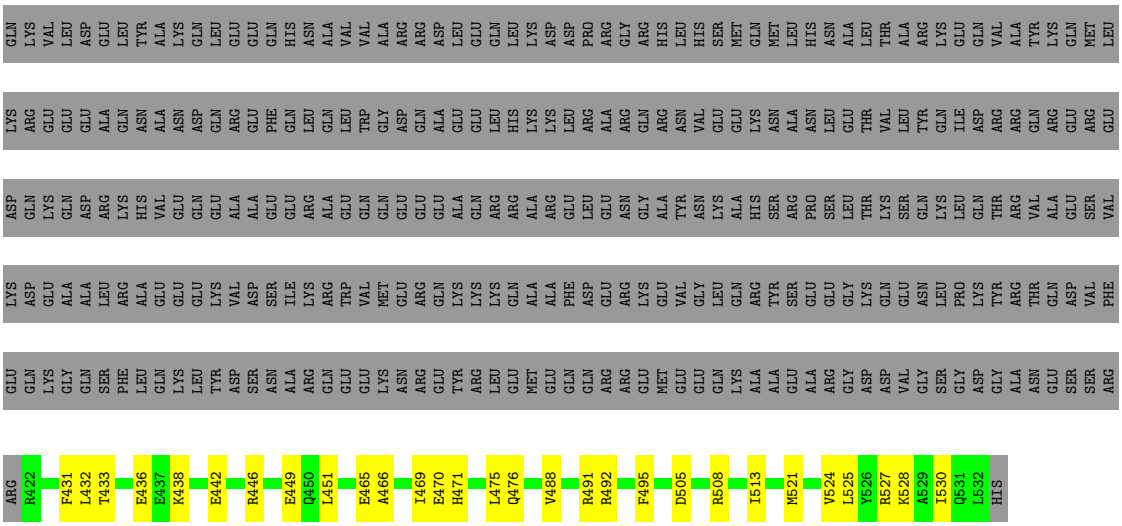
Chain 0w:



• Molecule 21: CFAP210

Chain 0x:



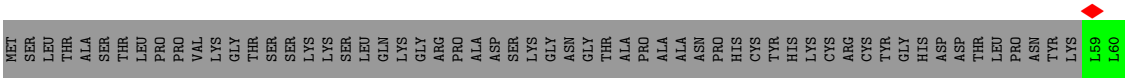


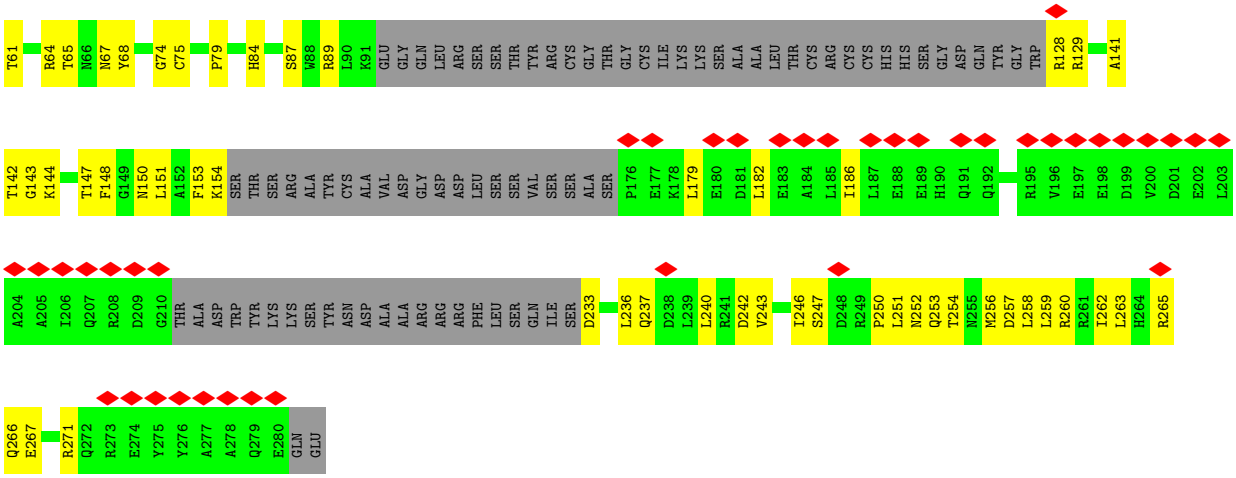
• Molecule 21: CFAP210

Chain 0v:

• Molecule 22: DMIP5

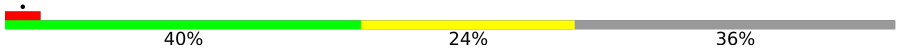
Chain 0z:

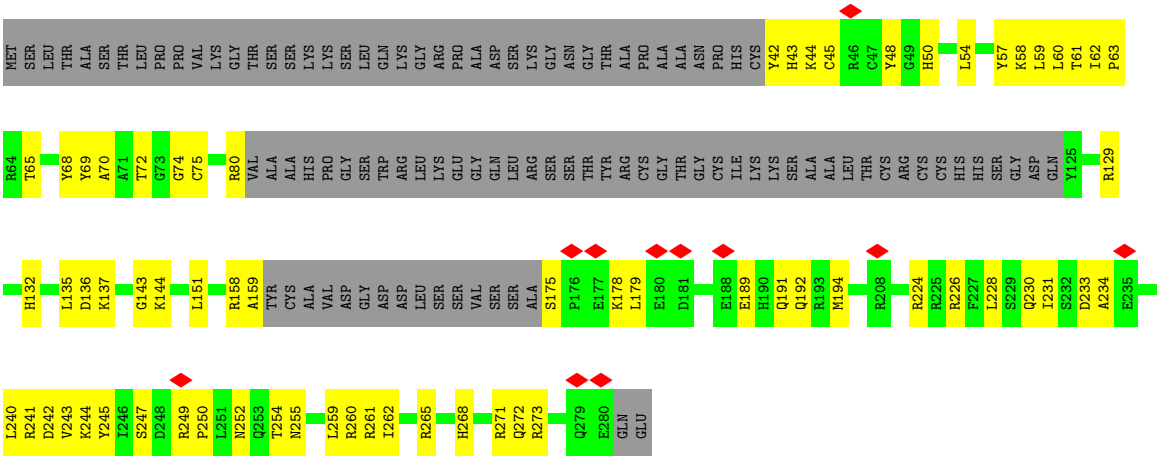




• Molecule 22: DMIP5

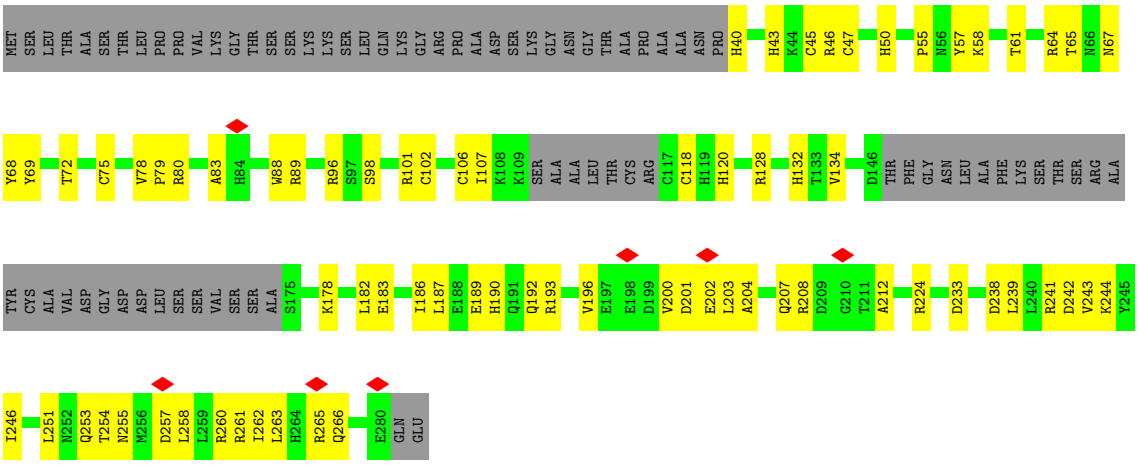
Chain 1w:





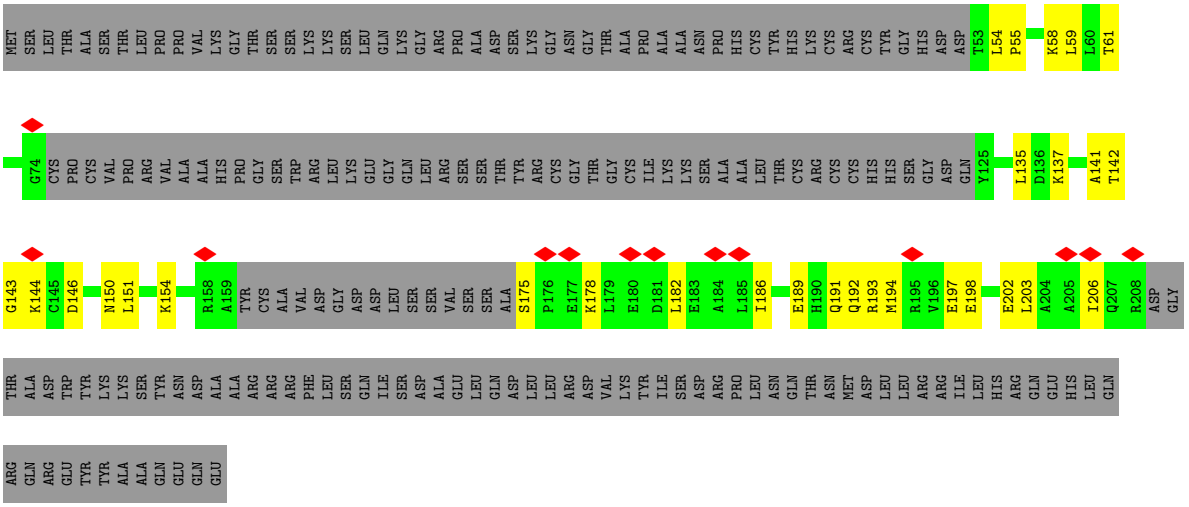
• Molecule 22: DMIP5

Chain 1x:



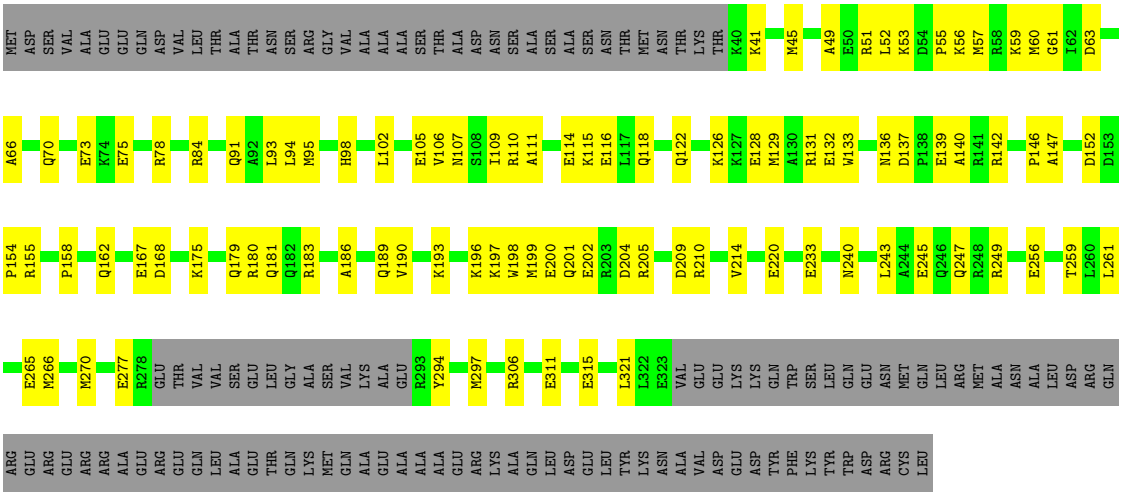
• Molecule 22: DMIP5

Chain 1y:



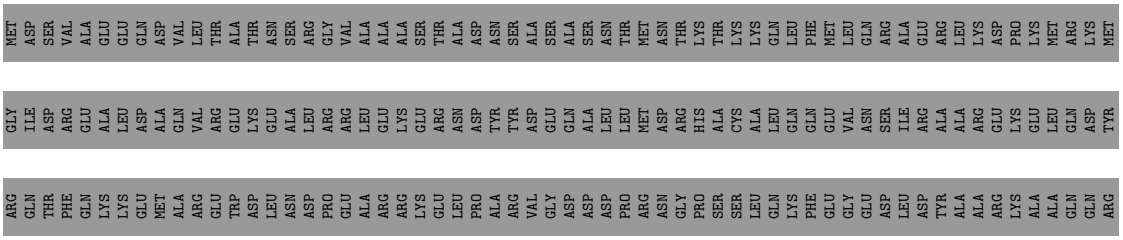
• Molecule 23: RIB43

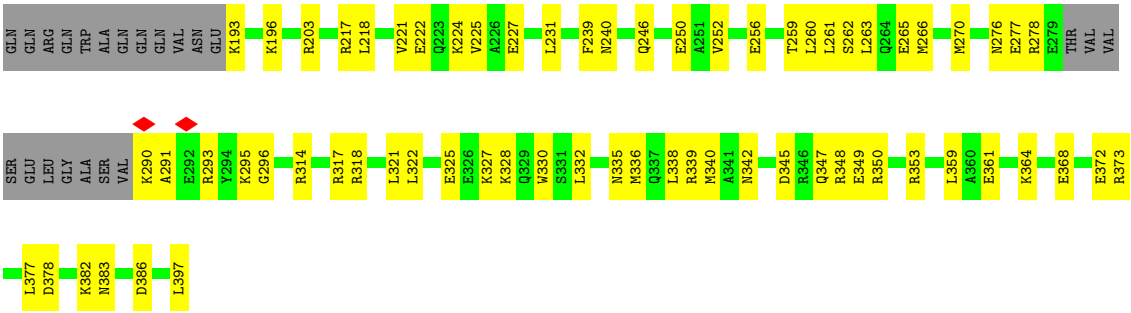
Chain 1A:



• Molecule 23: RIB43

Chain 1B:



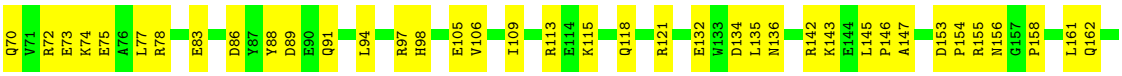


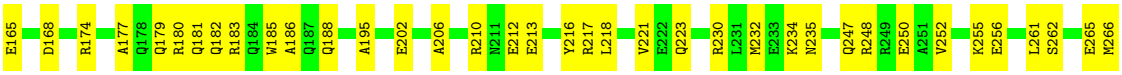
• Molecule 23: RIB43

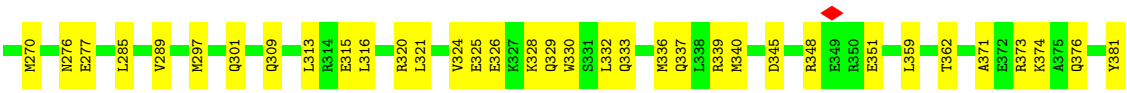
Chain 1D:

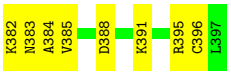
• Molecule 23: RIB43

Chain 1E:



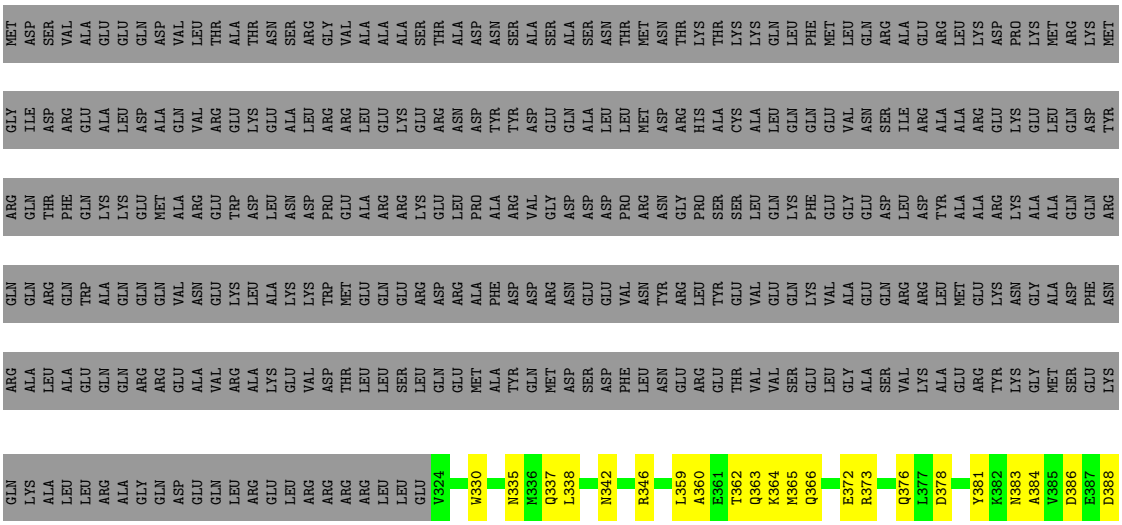






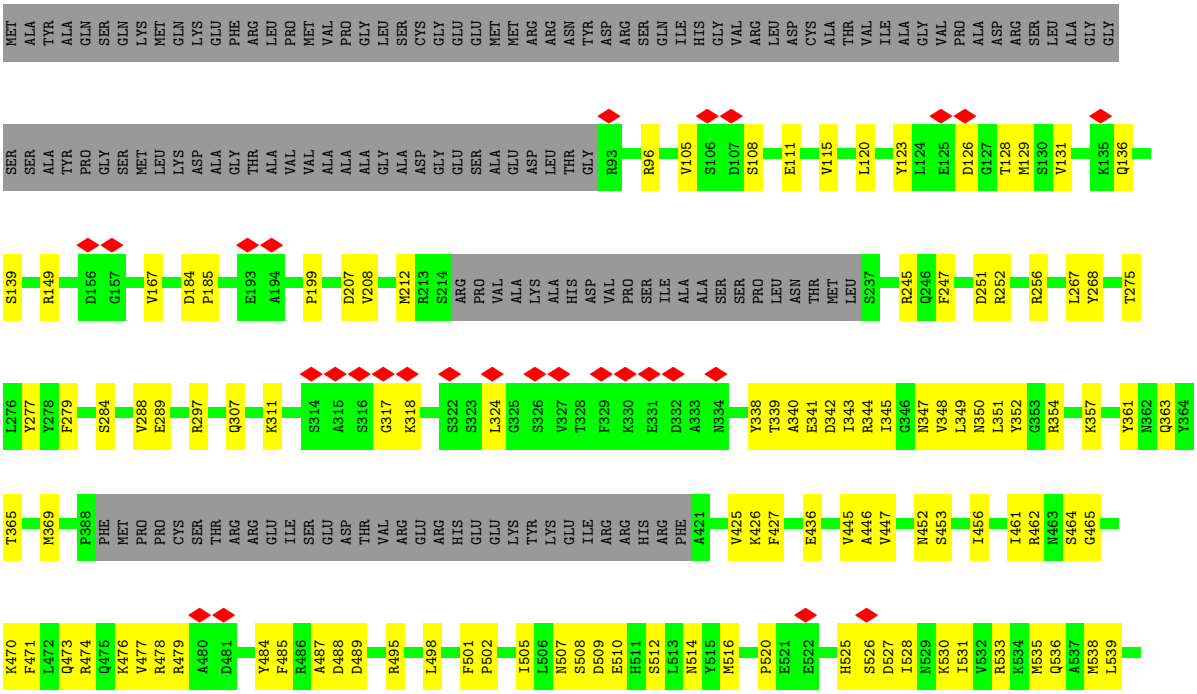
• Molecule 23: RIB43

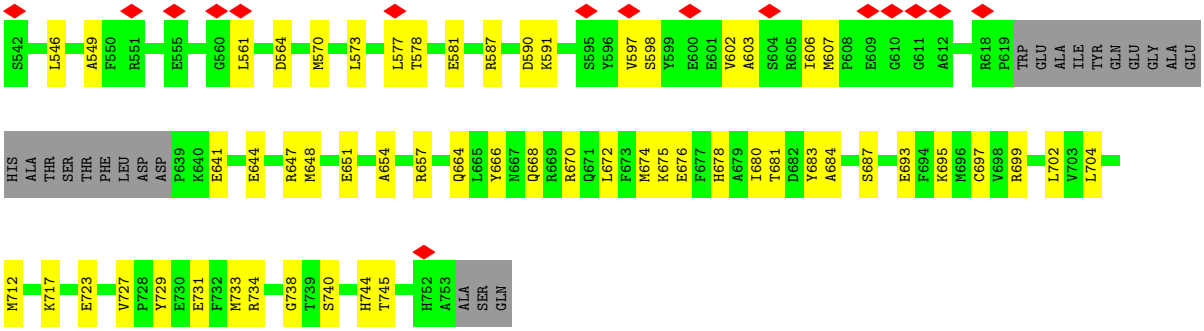
Chain 1F:



• Molecule 24: RIB72A

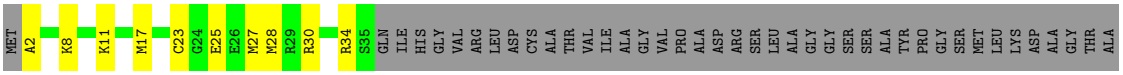
Chain 1H:

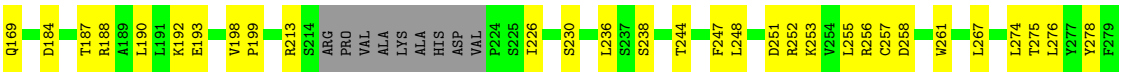


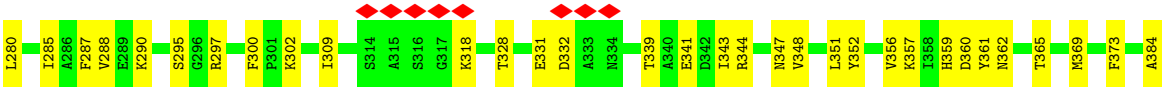


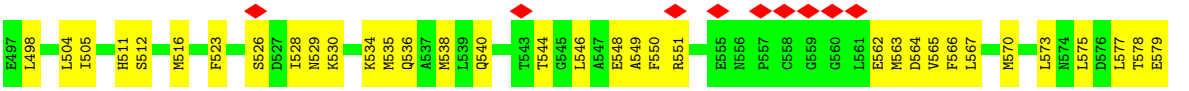
• Molecule 24: RIB72A

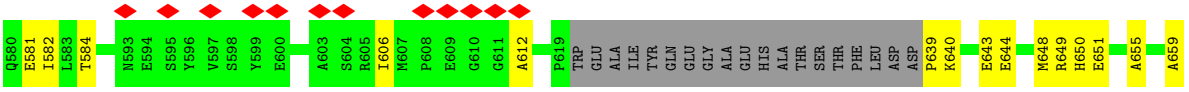
Chain 1I:

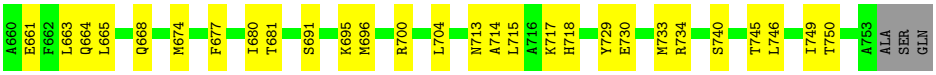






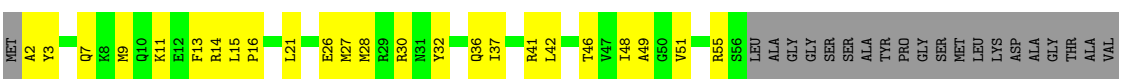


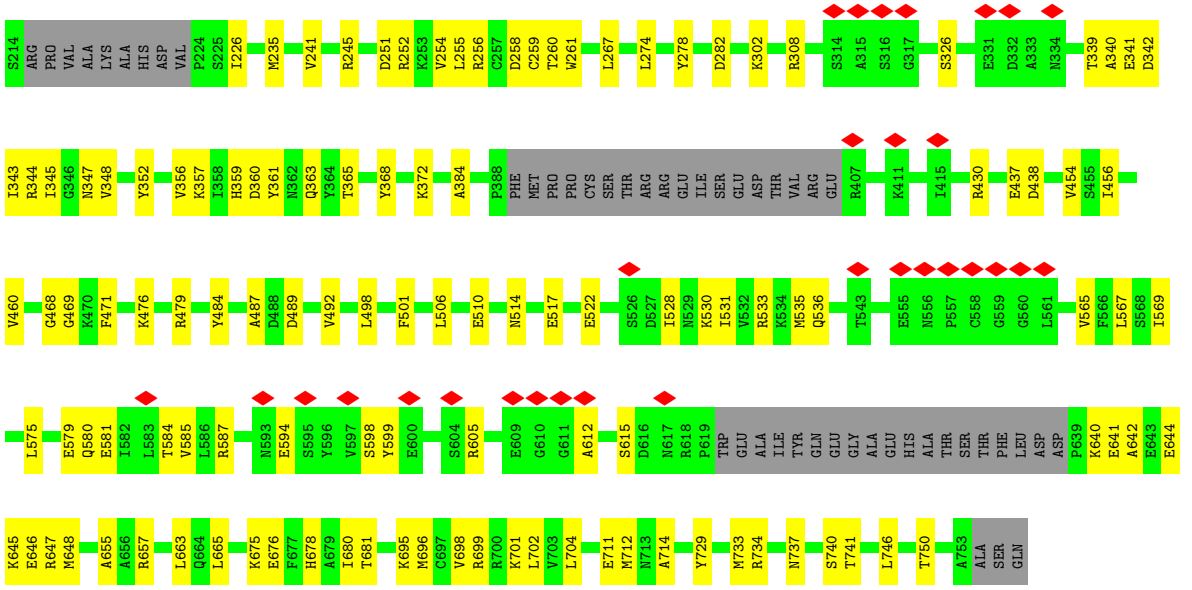




• Molecule 24: RIB72A

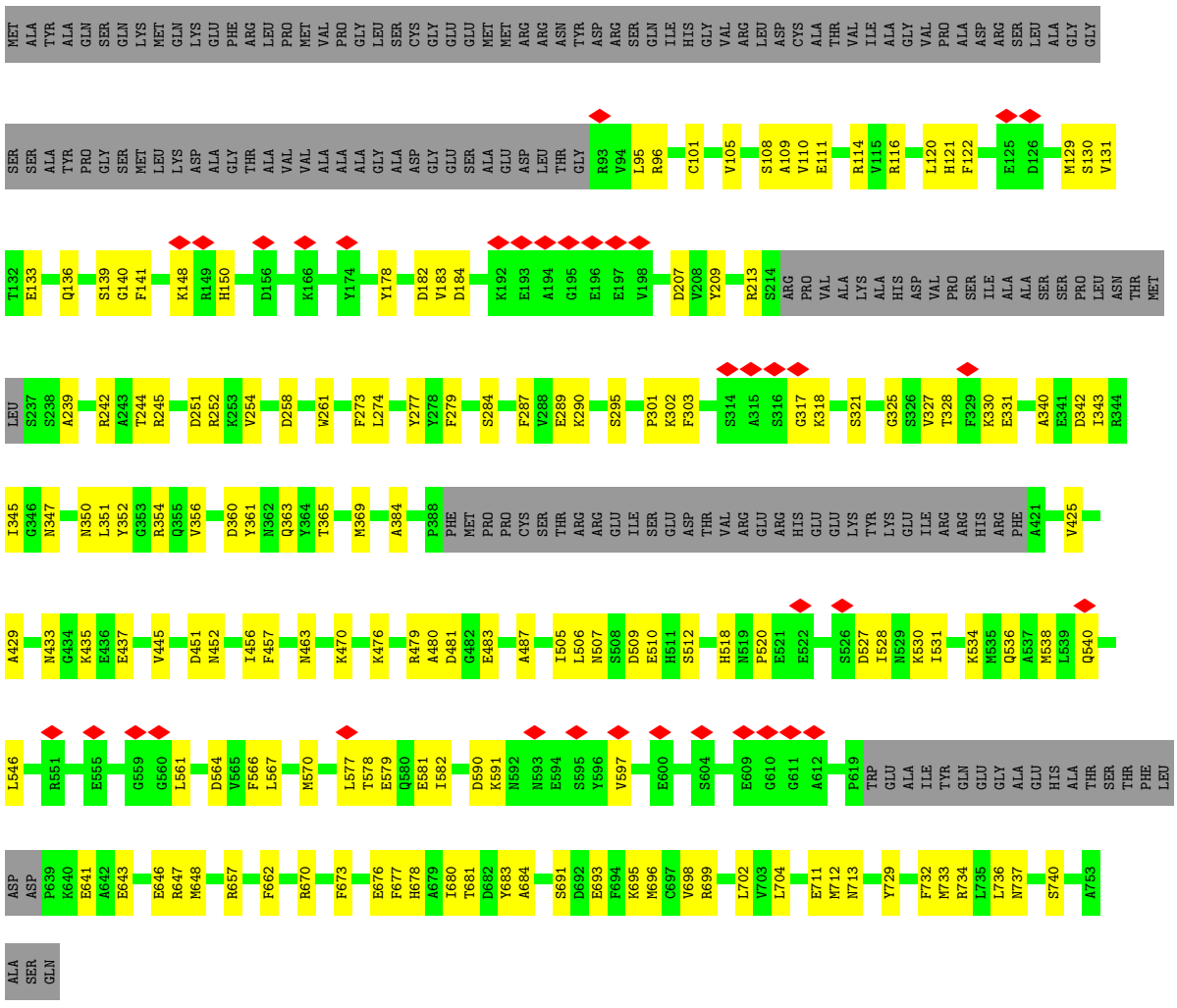
Chain 1J:





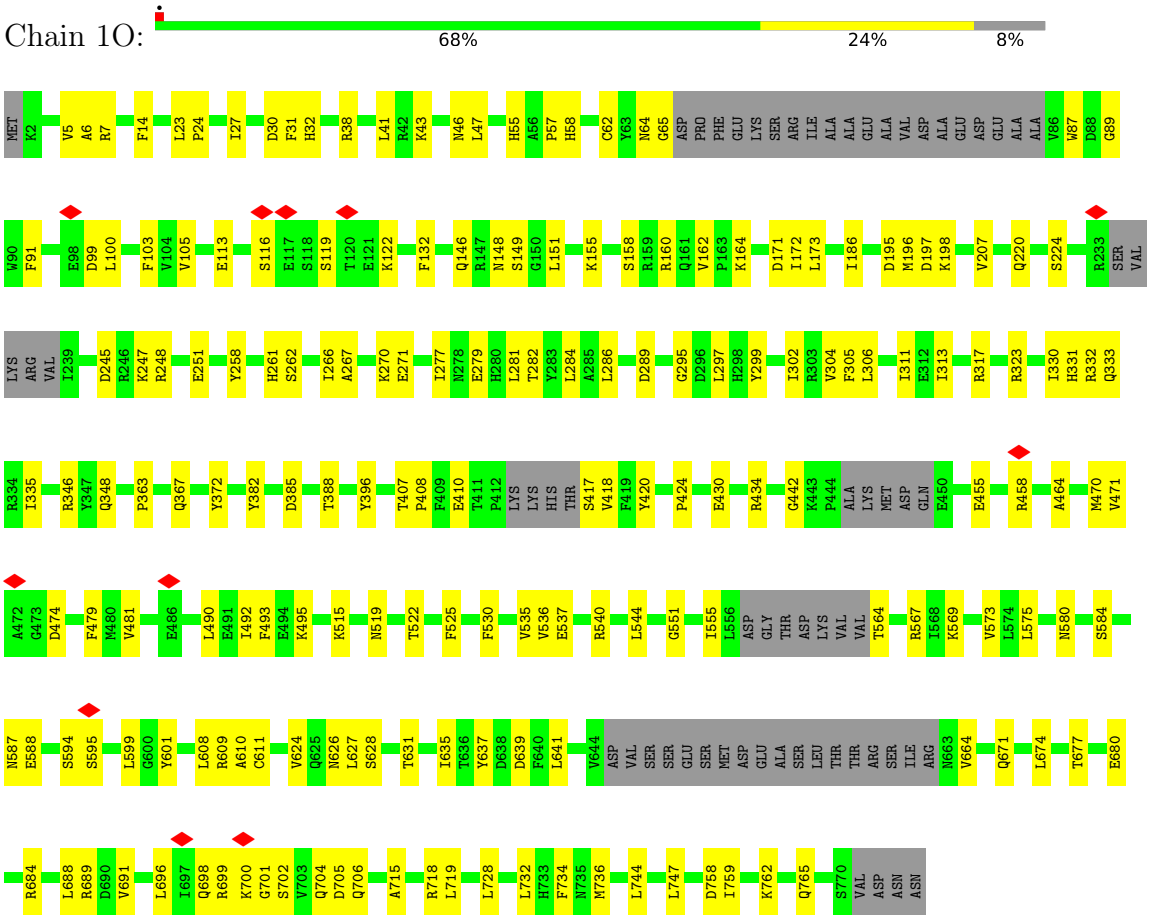
• Molecule 24: RIB72A

Chain 1K:



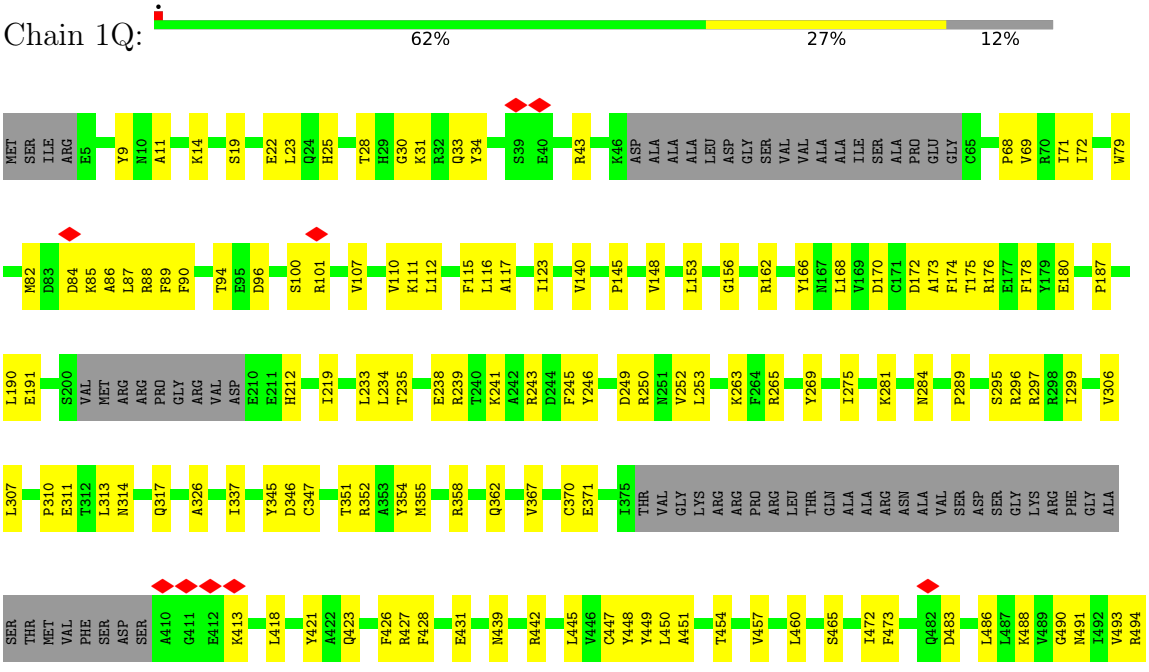
• Molecule 25: RIB72B

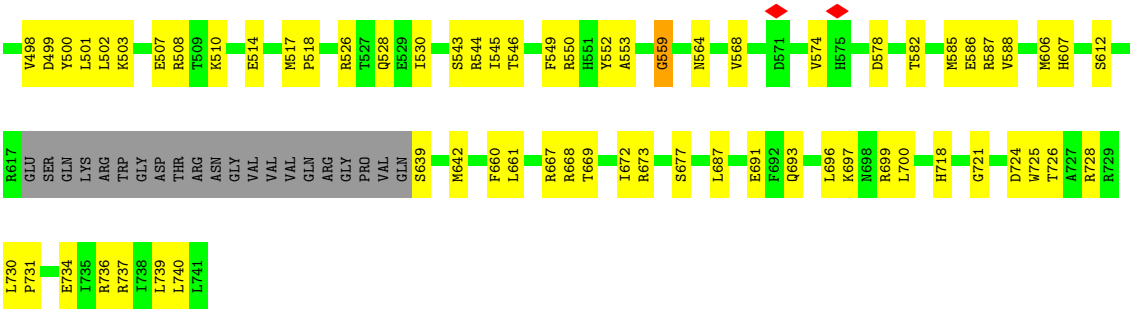
Chain 1O:



• Molecule 26: RIB72C

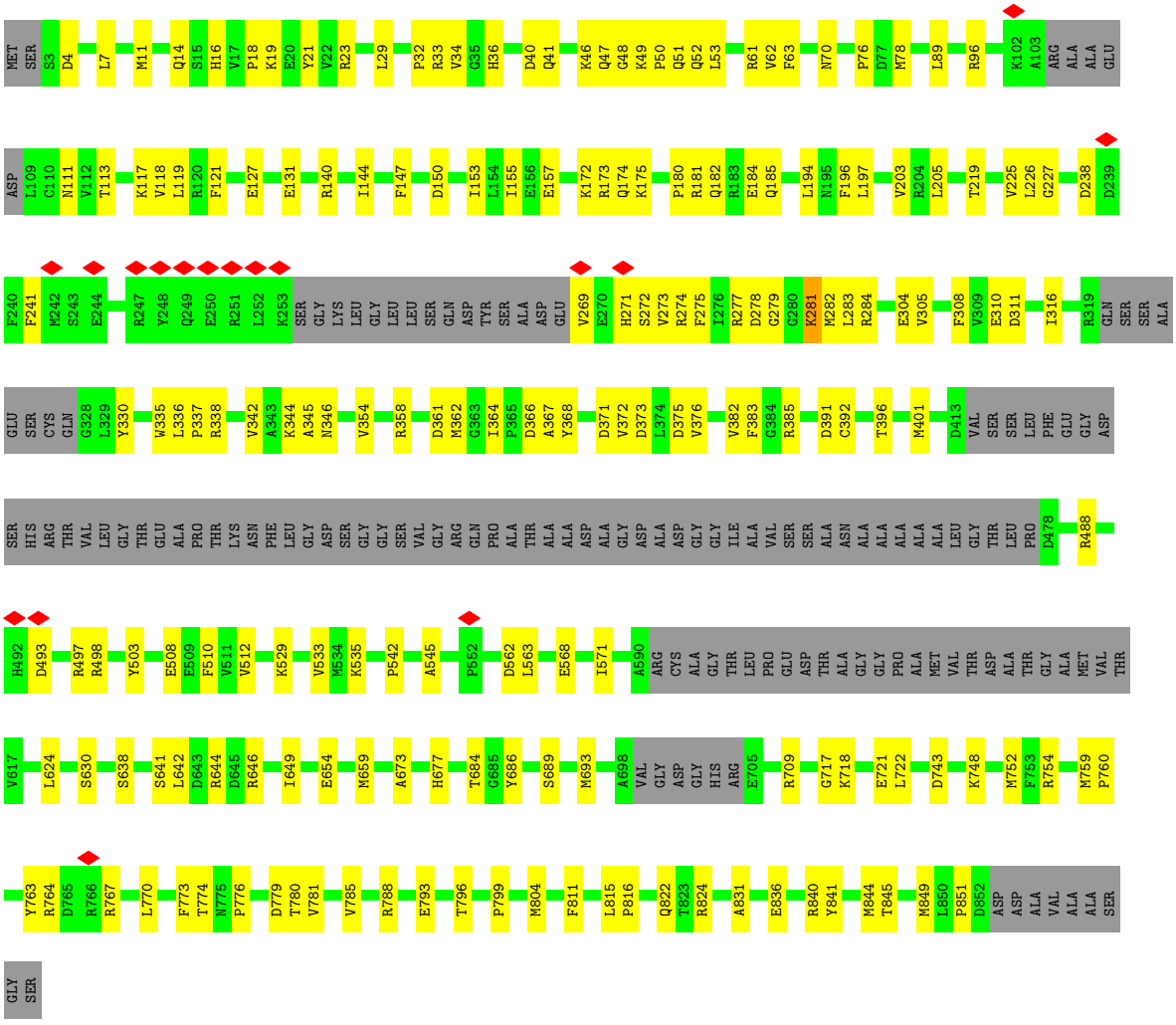
Chain 1Q:





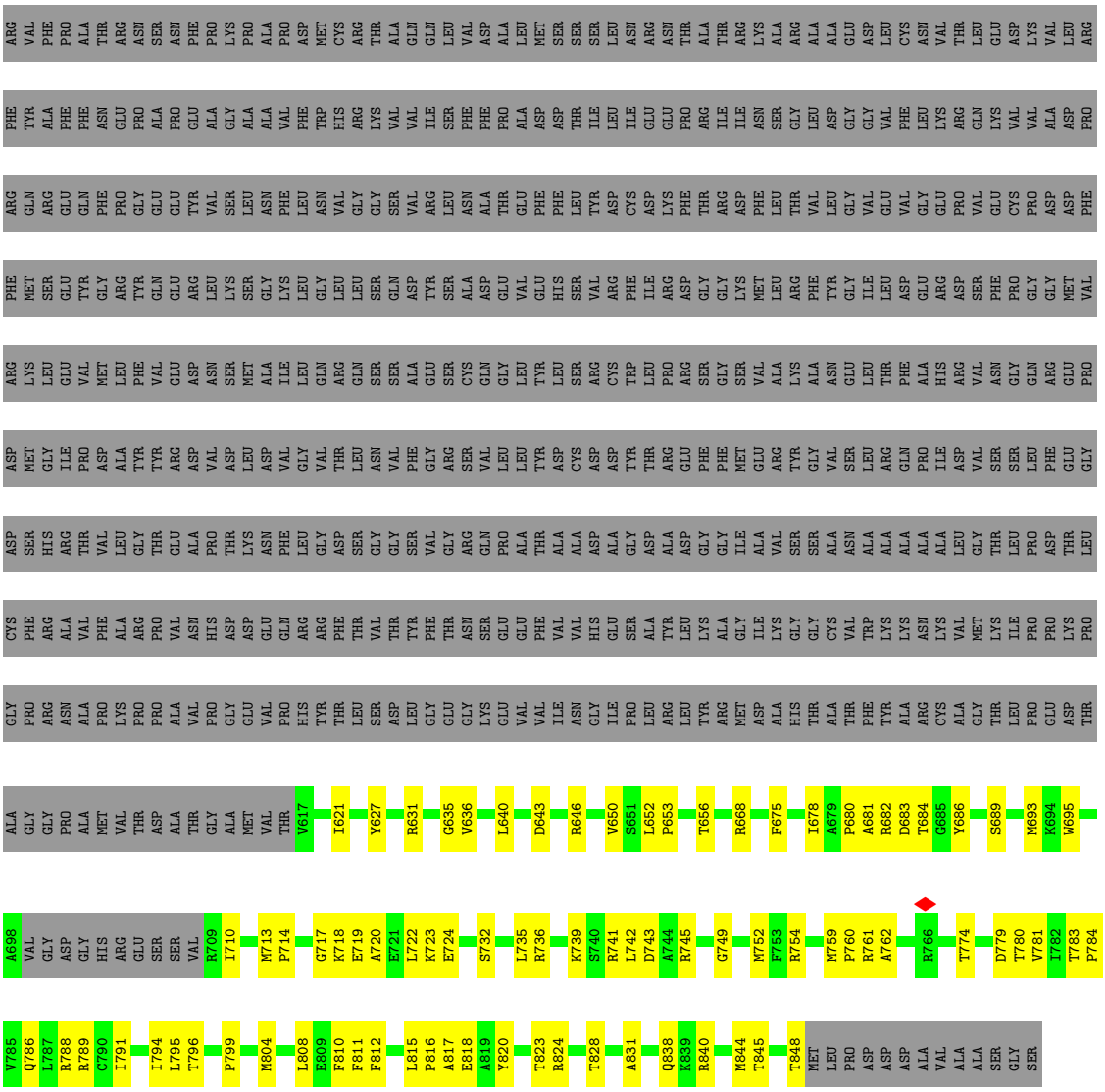
• Molecule 27: RIB72D

Chain 1S:



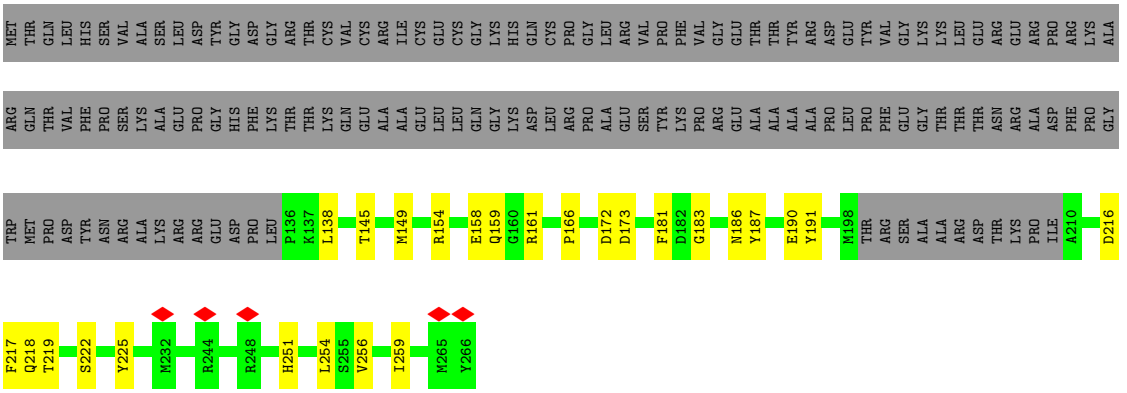
• Molecule 27: RIB72D

Chain 1T:



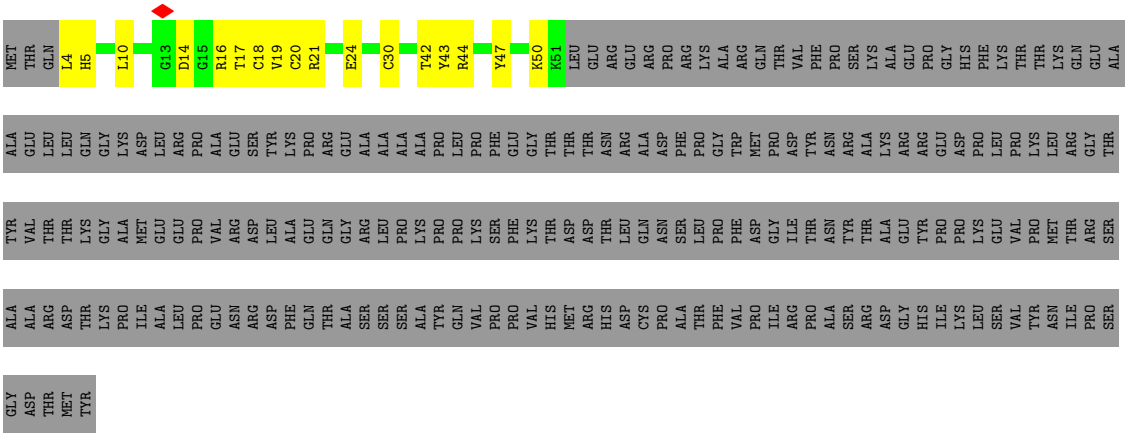
• Molecule 28: DMIP1

Chain 1U:



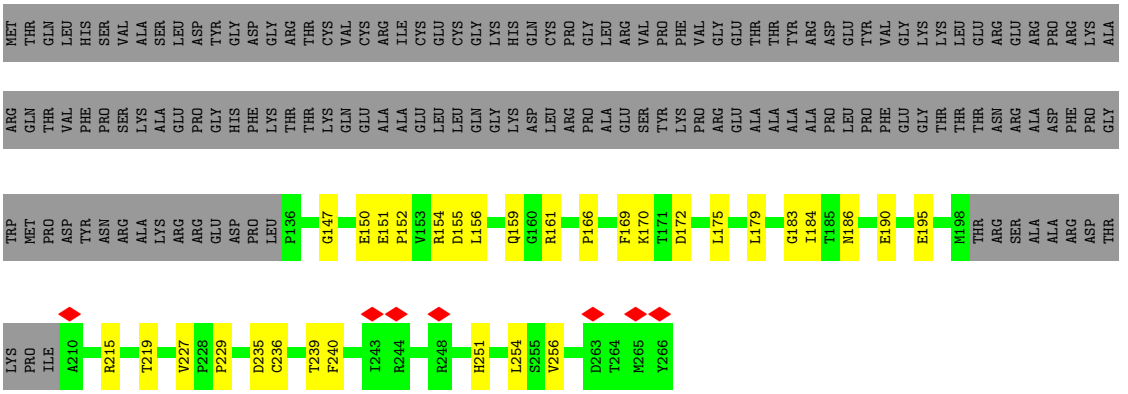
• Molecule 28: DMIP1

Chain 1V:



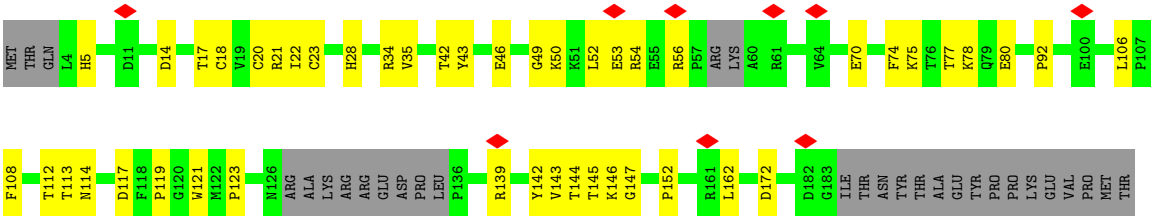
• Molecule 28: DMIP1

Chain 1X:



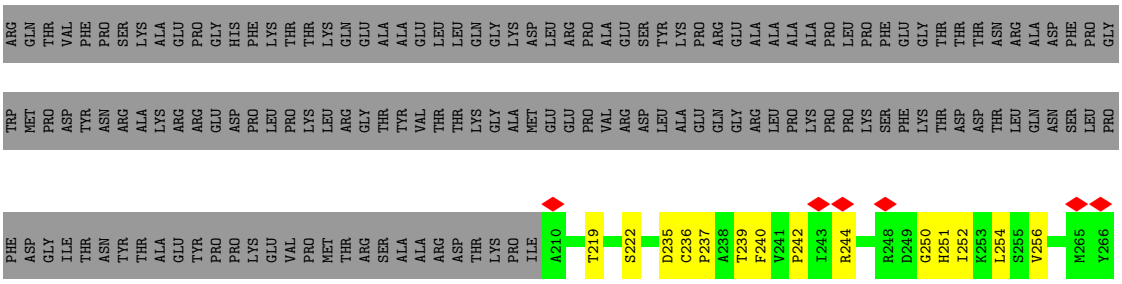
• Molecule 28: DMIP1

Chain 1Y:



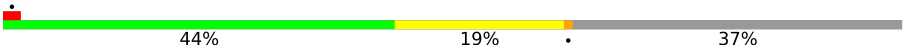
• Molecule 28: DMIP1

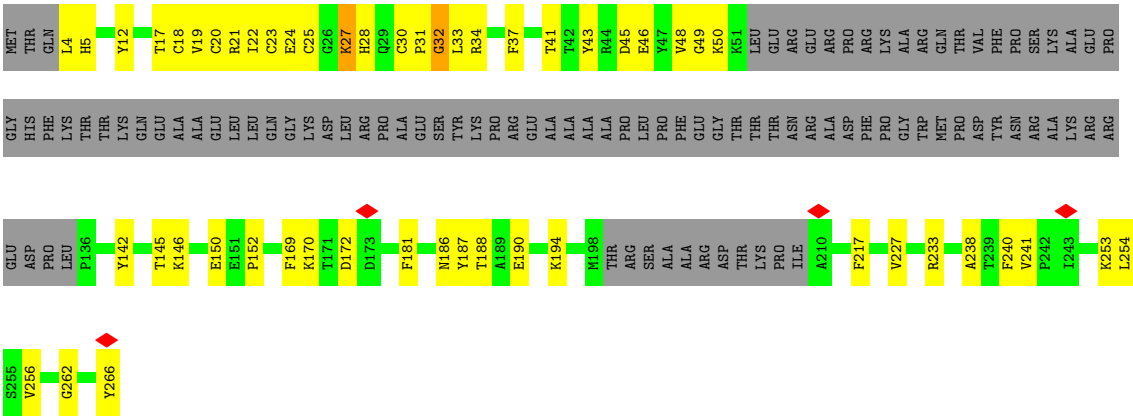
Chain 1a:



• Molecule 28: DMIP1

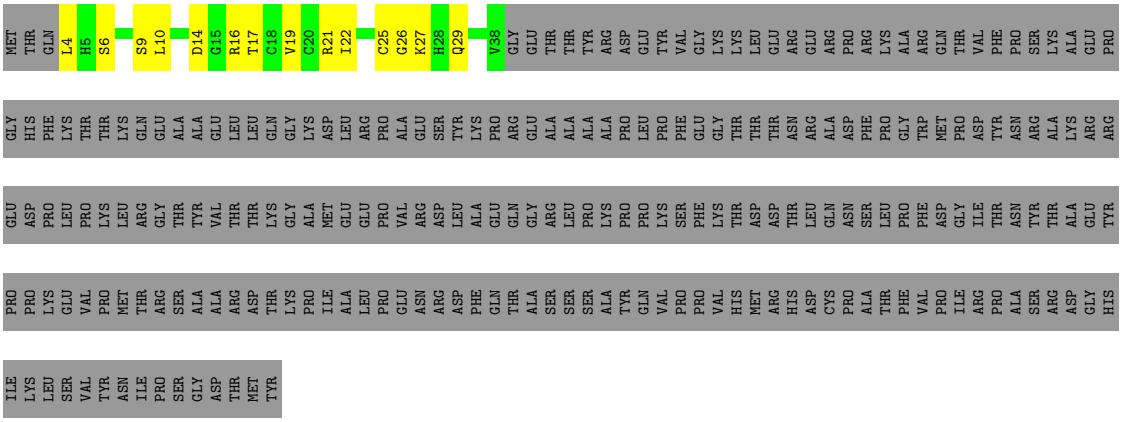
Chain 1b:





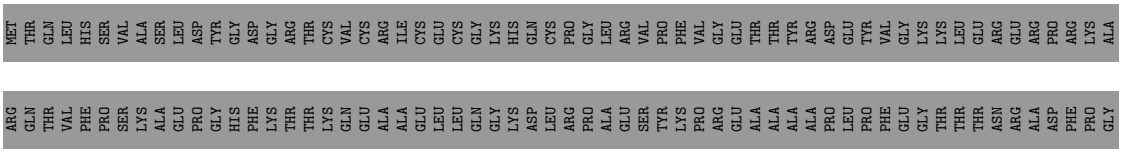
• Molecule 28: DMIP1

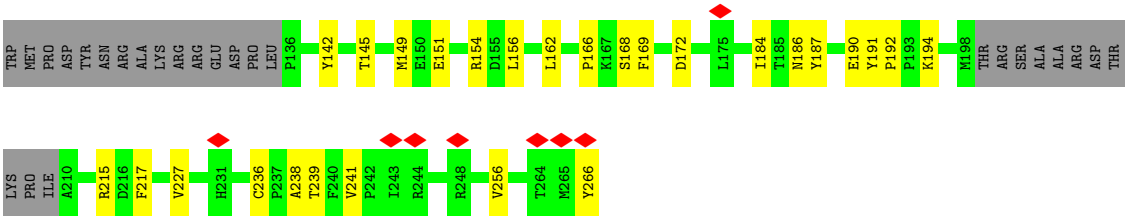
Chain 1c:



• Molecule 28: DMIP1

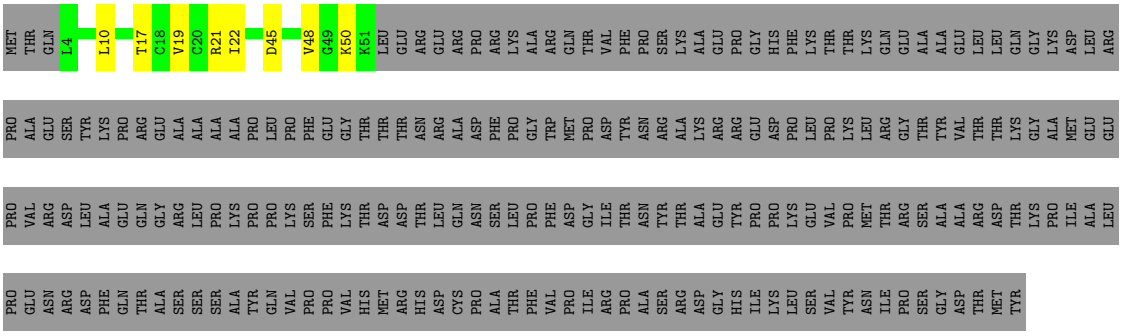
Chain 1d:





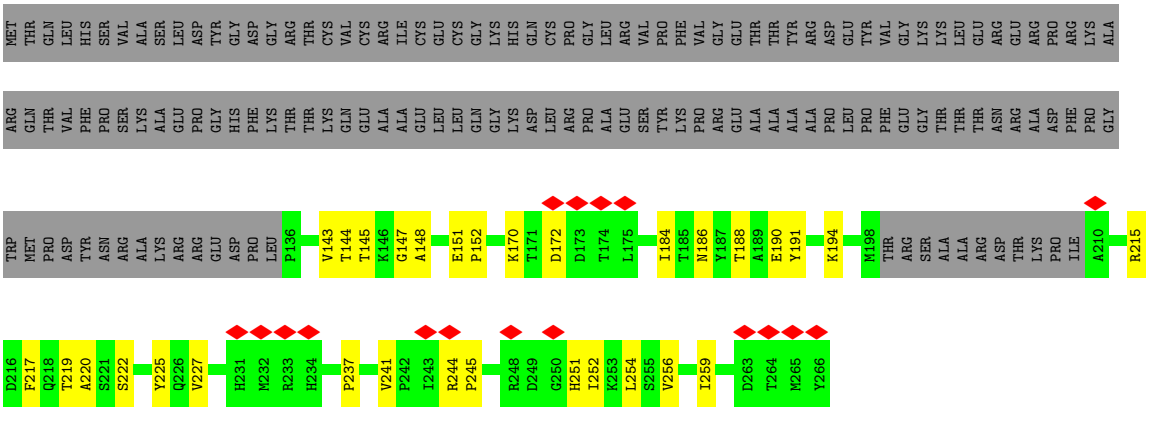
• Molecule 28: DMIP1

Chain 1e:



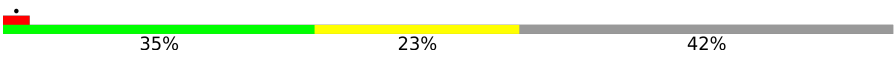
• Molecule 28: DMIP1

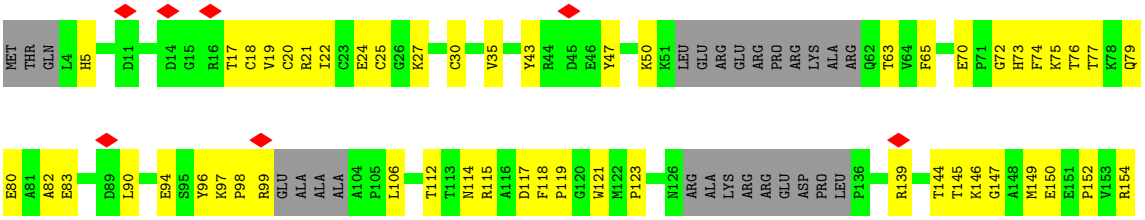
Chain 1g:

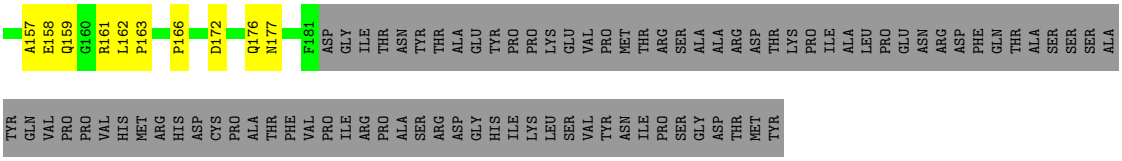


• Molecule 28: DMIP1

Chain 1h:

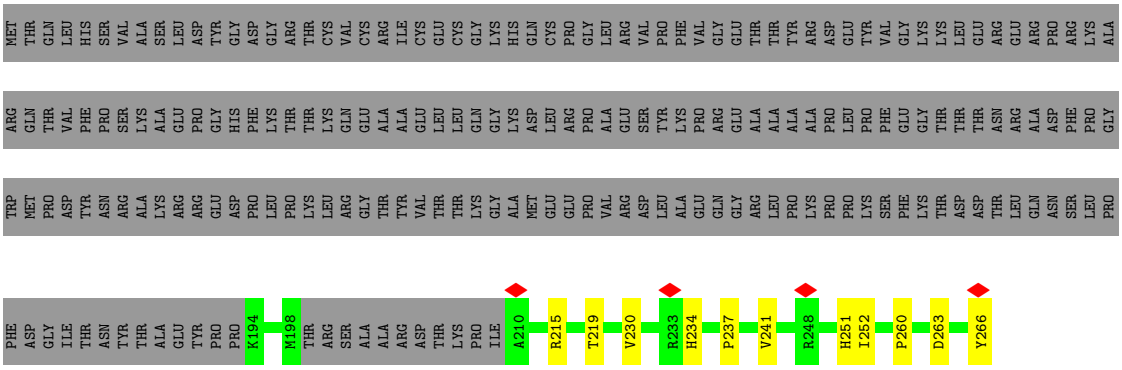






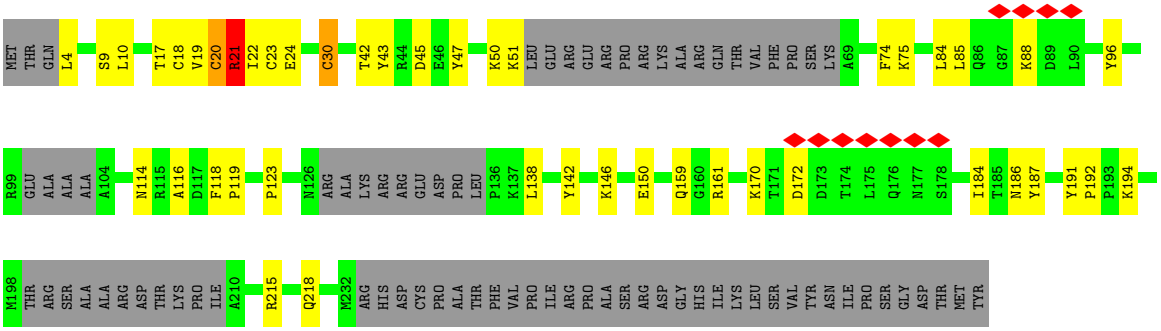
• Molecule 28: DMIP1

Chain 4V:



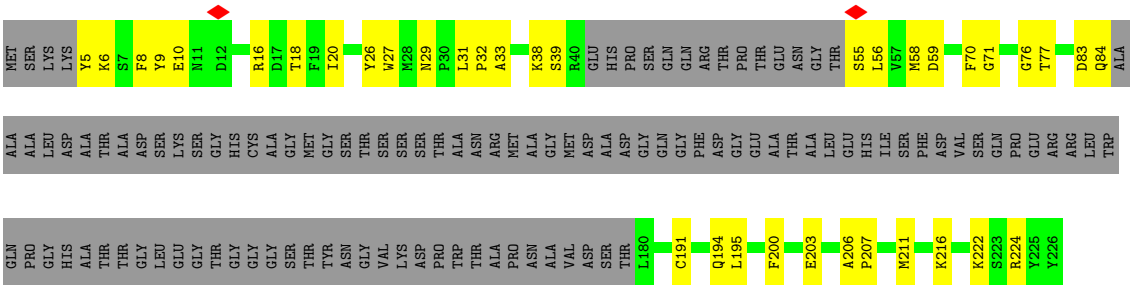
• Molecule 28: DMIP1

Chain 4W:



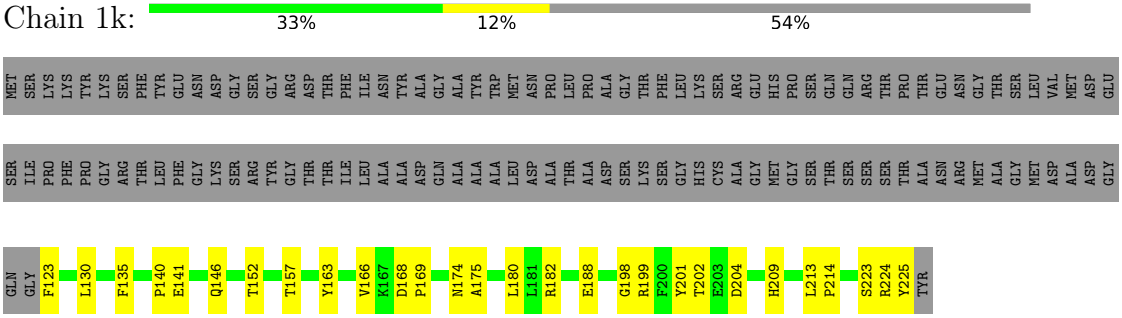
• Molecule 29: DMIP2

Chain 1j:



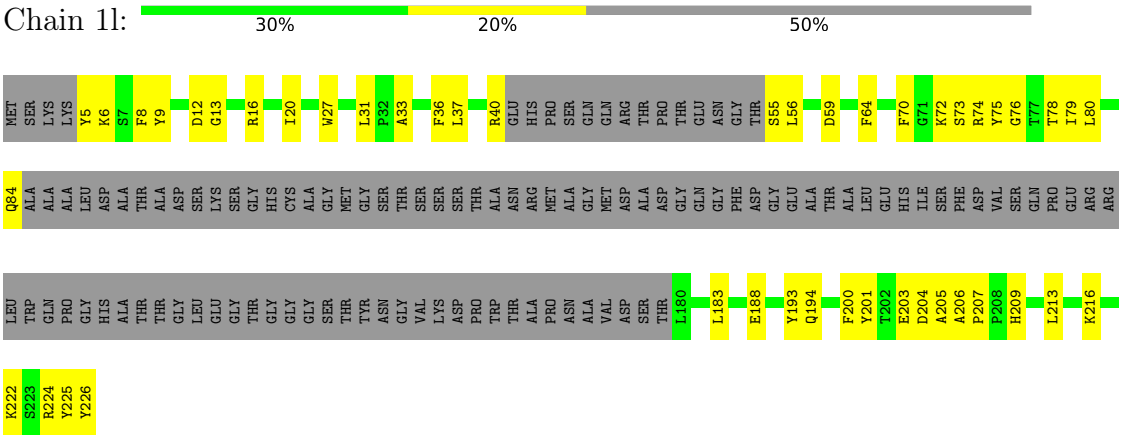
• Molecule 29: DMIP2

Chain 1k:



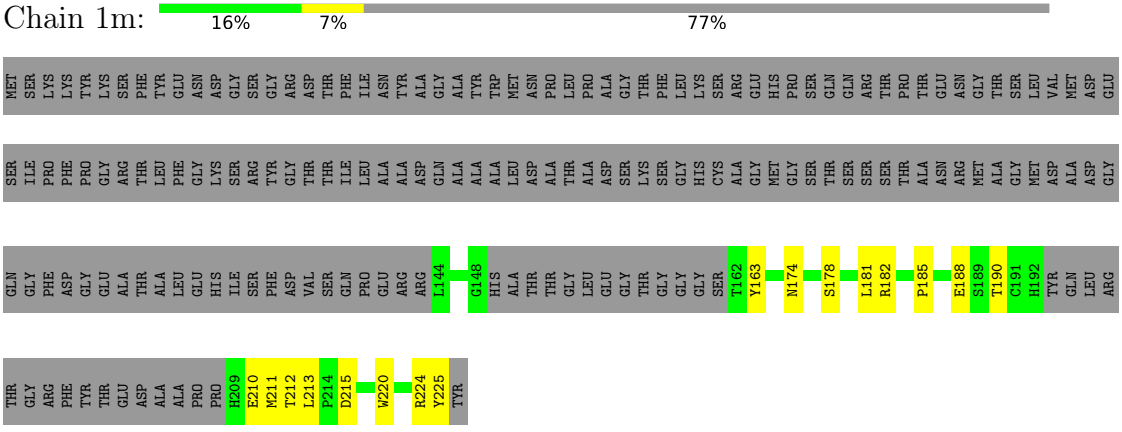
• Molecule 29: DMIP2

Chain 1l:



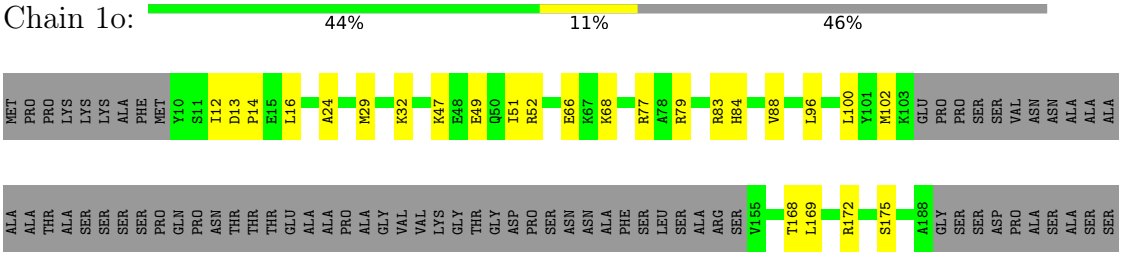
• Molecule 29: DMIP2

Chain 1m:



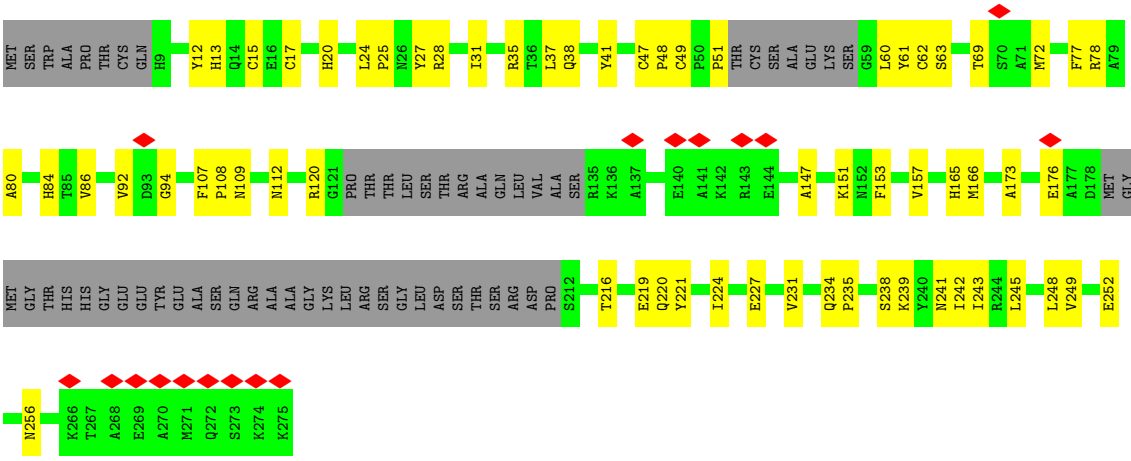
• Molecule 30: DMIP3

Chain 1o:



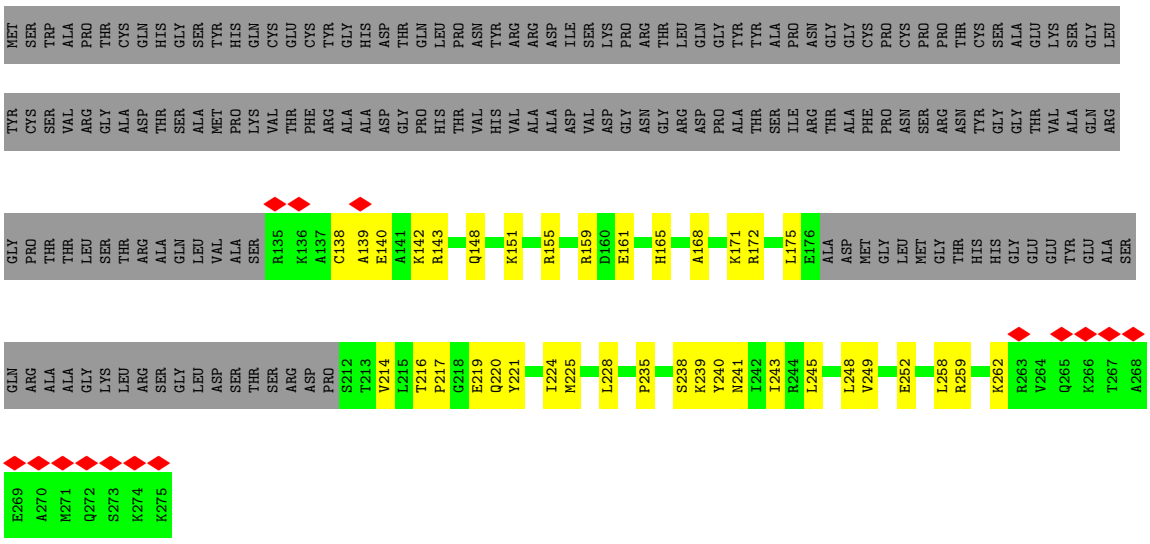
• Molecule 31: DMIP4

Chain 1q:



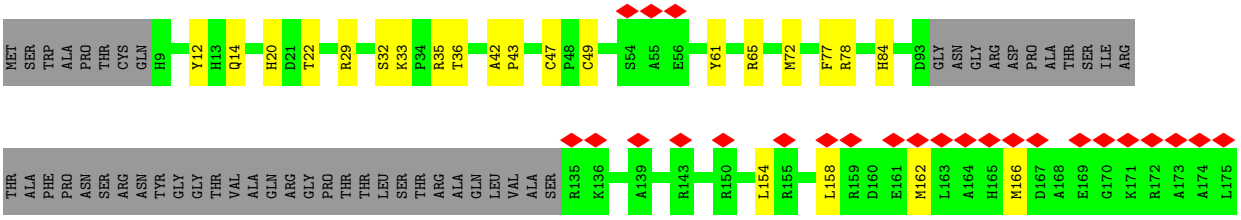
• Molecule 31: DMIP4

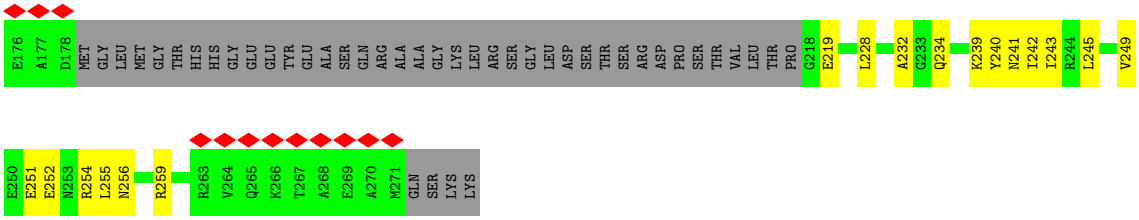
Chain 1r:



• Molecule 31: DMIP4

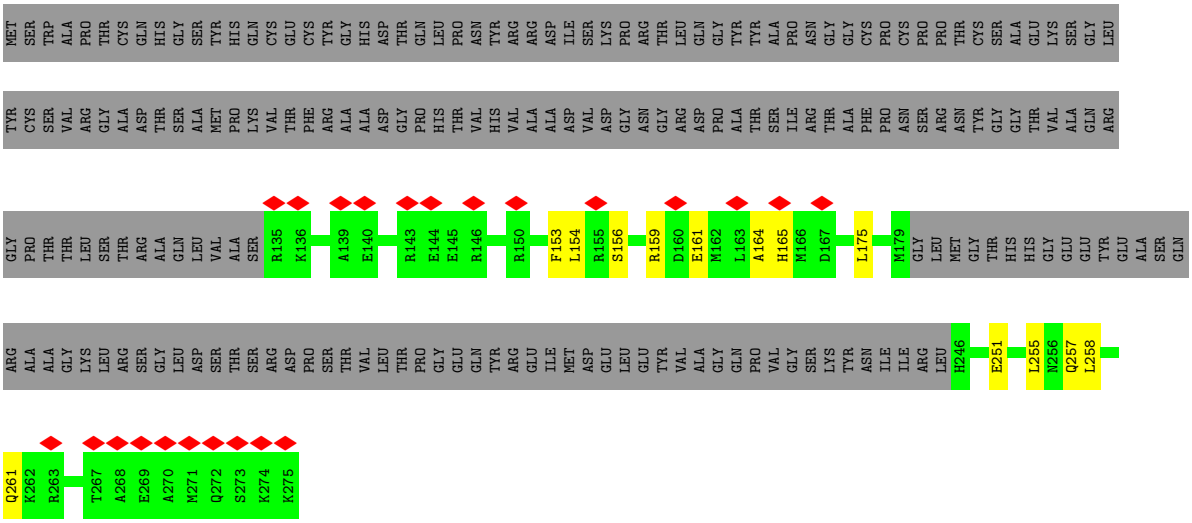
Chain 1s:





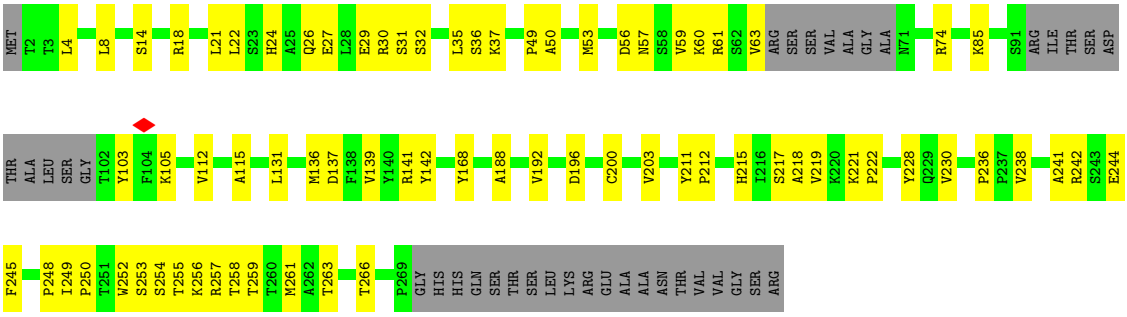
• Molecule 31: DMIP4

Chain 1t:



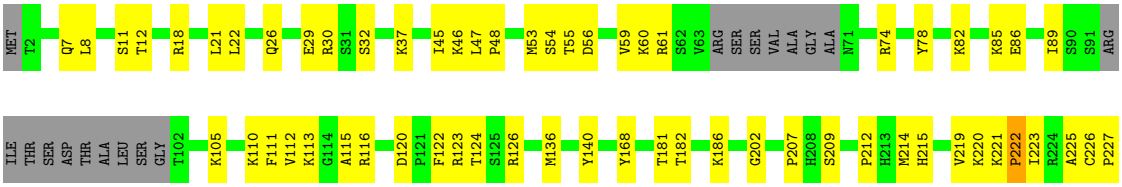
• Molecule 32: DMIP6

Chain 2B:



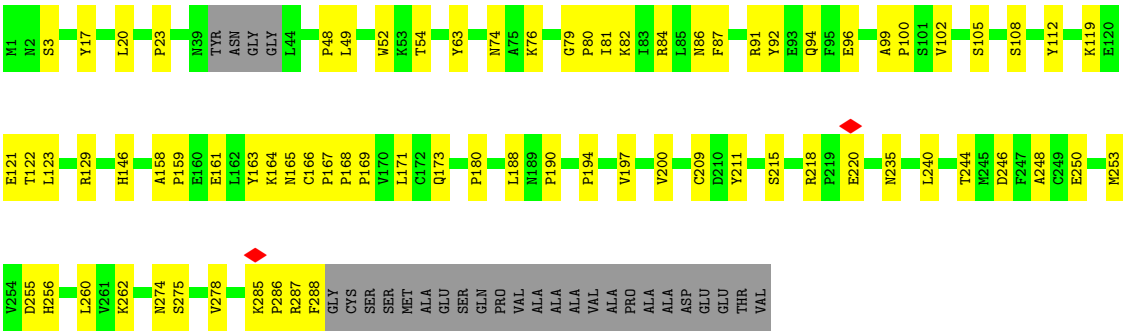
• Molecule 32: DMIP6

Chain 2C:



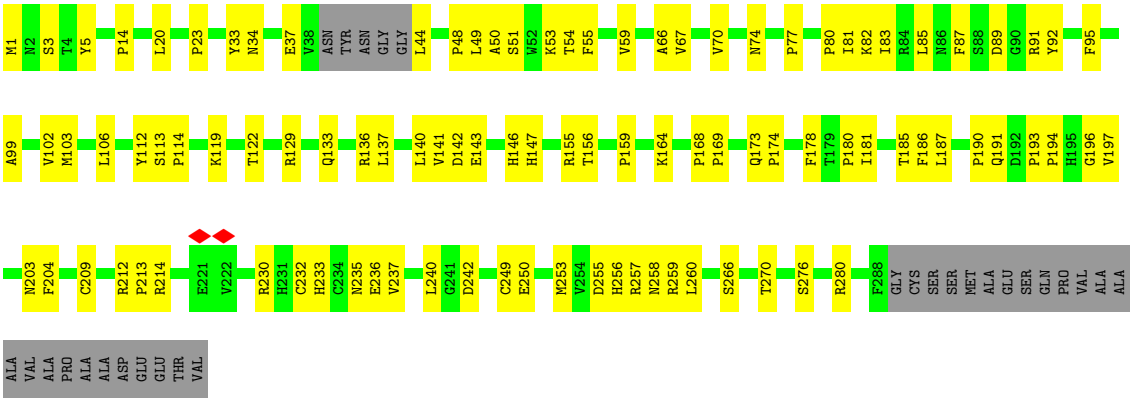
• Molecule 33: DMIP7

Chain 2F:



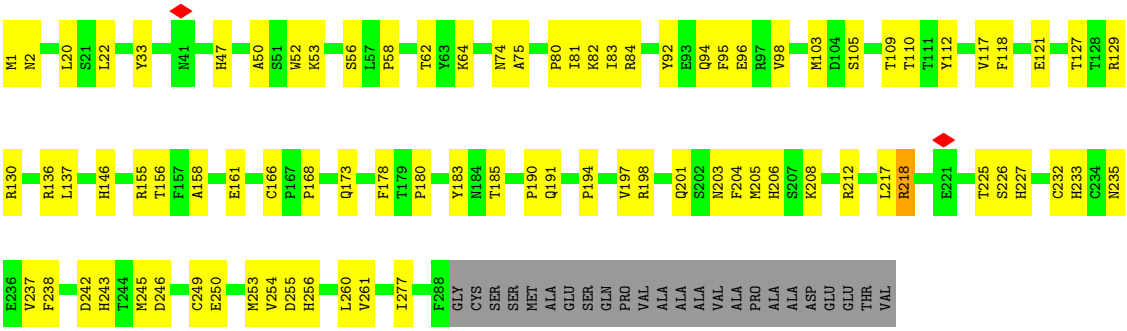
• Molecule 33: DMIP7

Chain 2G:



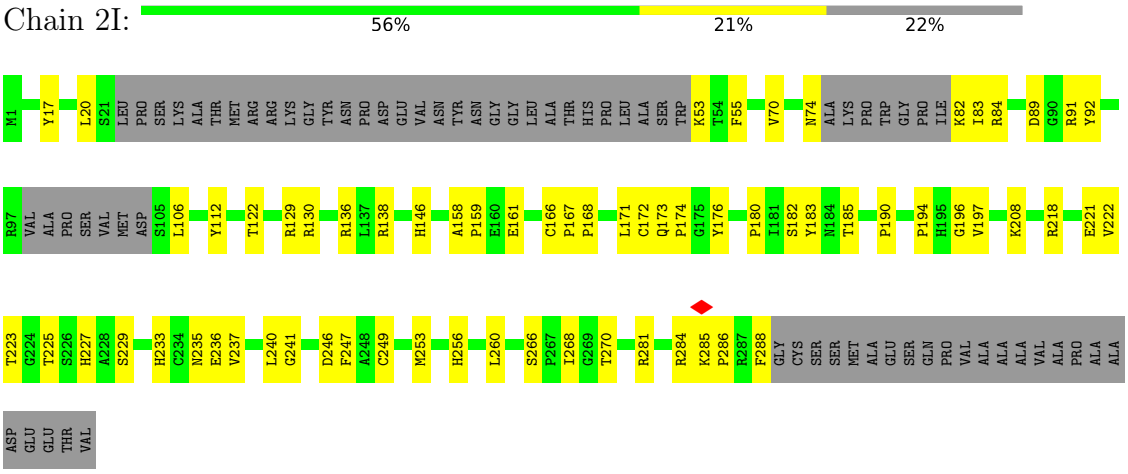
• Molecule 33: DMIP7

Chain 2H:



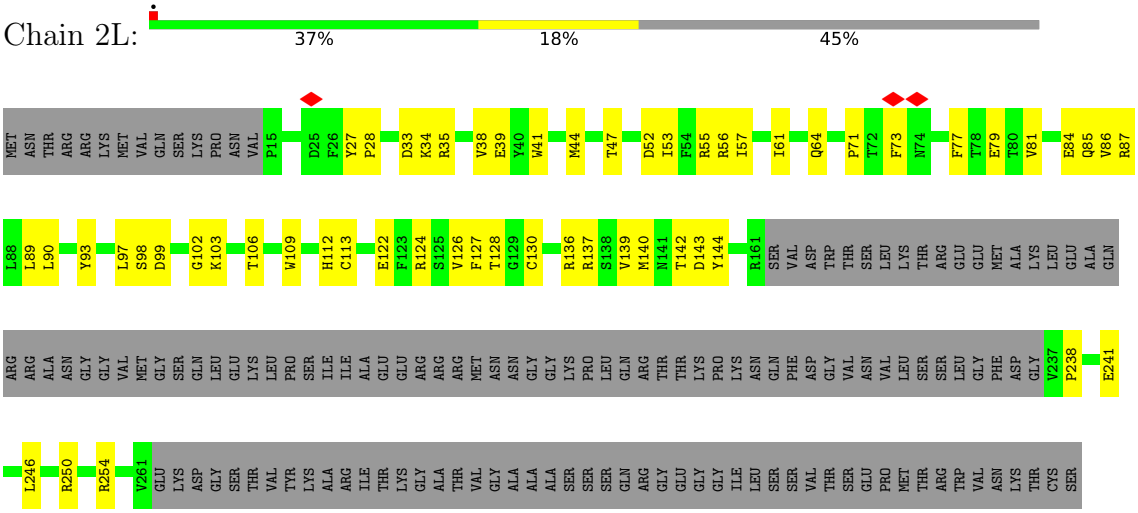
• Molecule 33: DMIP7

Chain 2I:



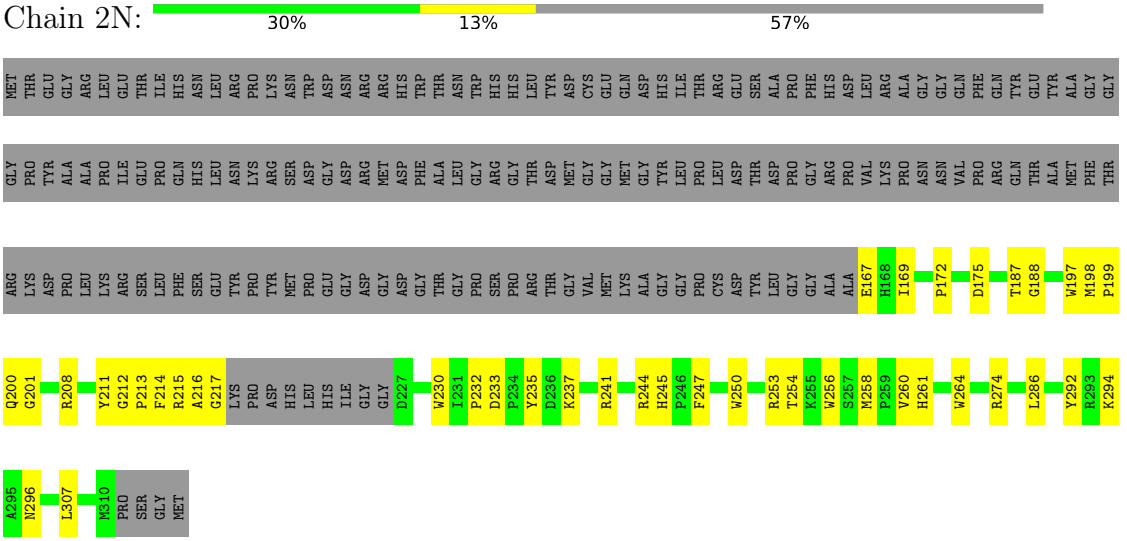
• Molecule 34: DMIP8

Chain 2L:



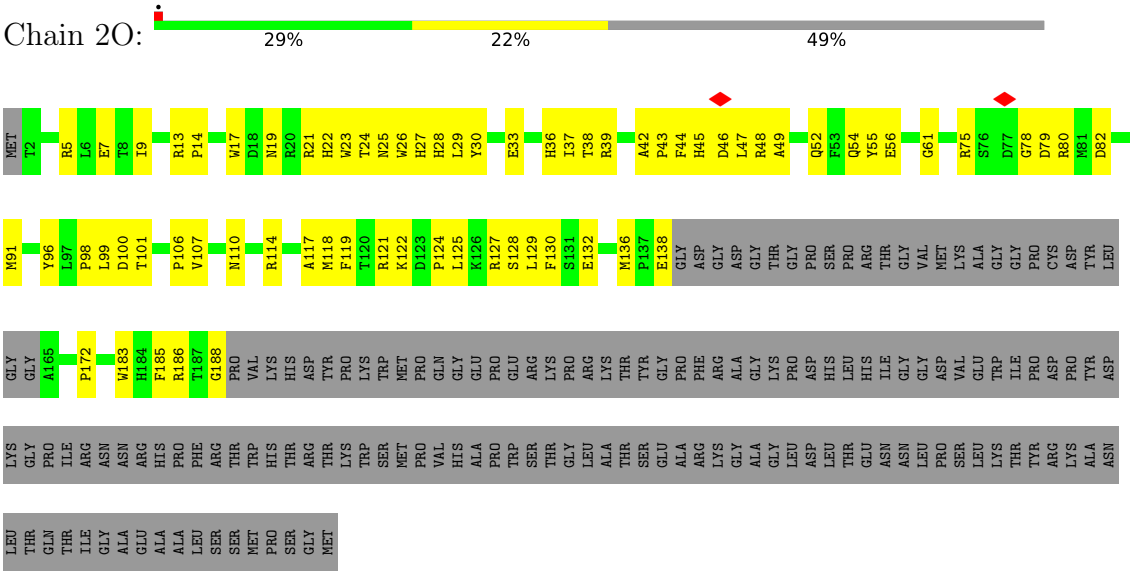
• Molecule 35: DMIP9

Chain 2N:



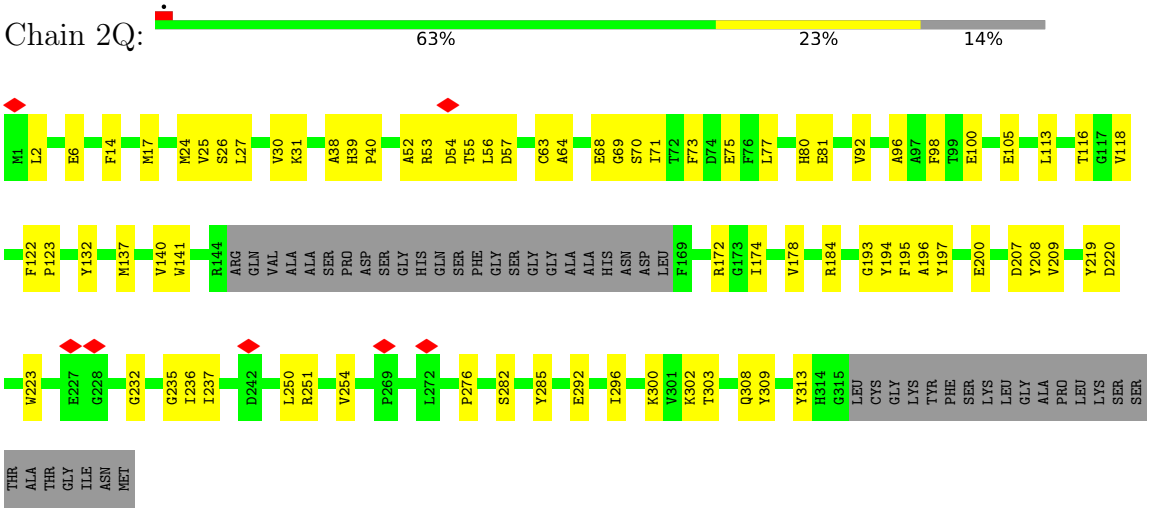
• Molecule 35: DMIP9

Chain 2O:



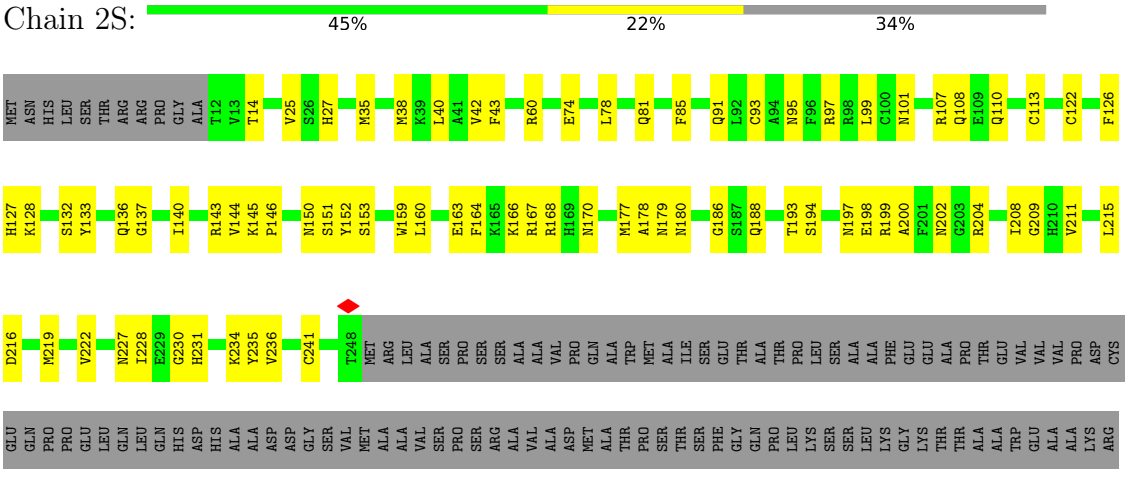
• Molecule 36: DMIP10

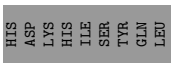
Chain 2Q:



• Molecule 37: DMIP11

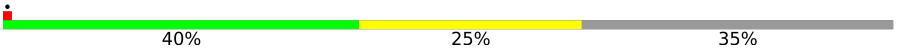
Chain 2S:

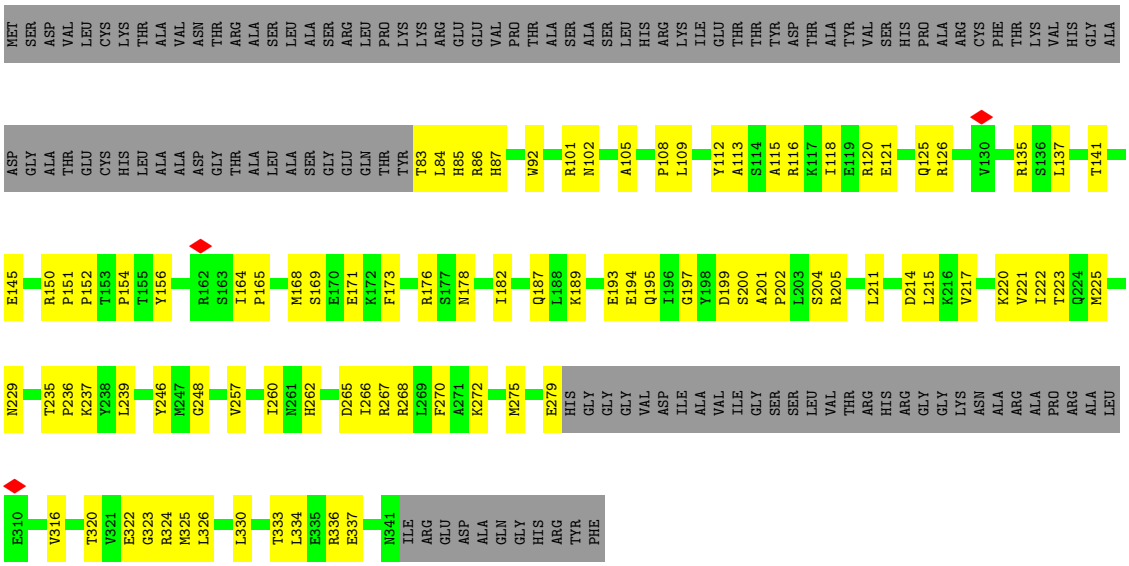




• Molecule 38: DMIP12

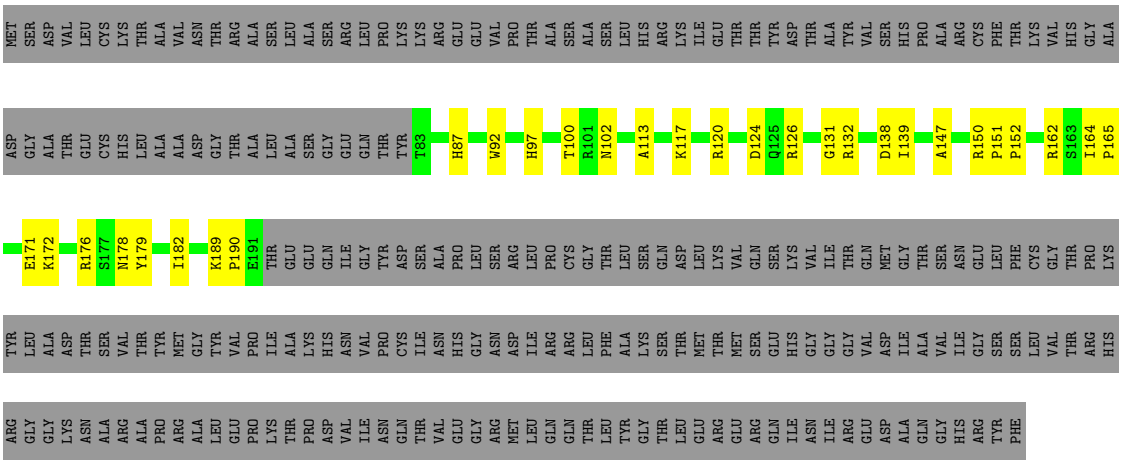
Chain 2U:





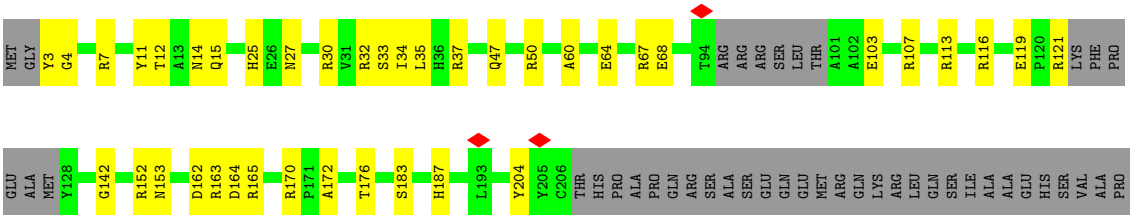
• Molecule 38: DMIP12

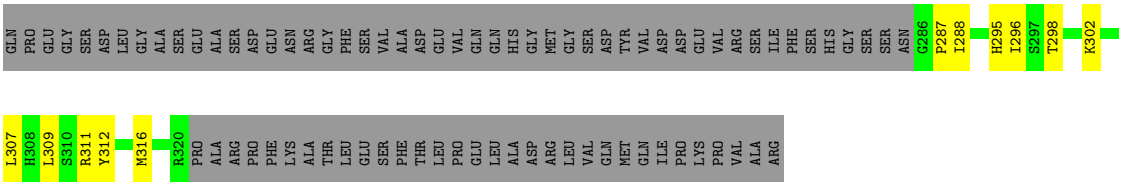
Chain 2V:



• Molecule 39: DMIP13

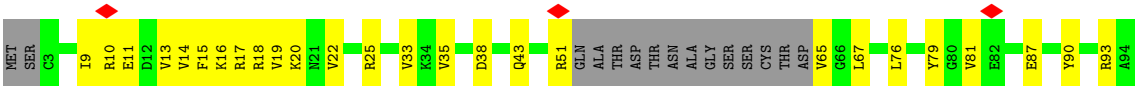
Chain 2X:





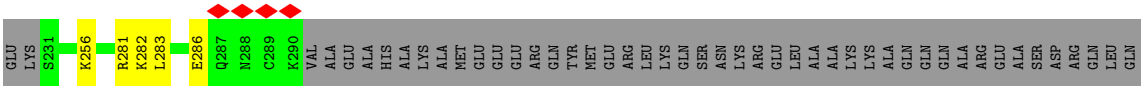
• Molecule 40: DMIP14

Chain 2Z:



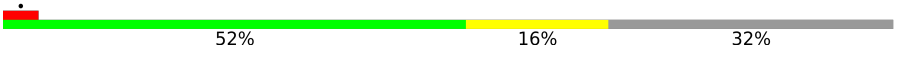
• Molecule 41: DMIP15

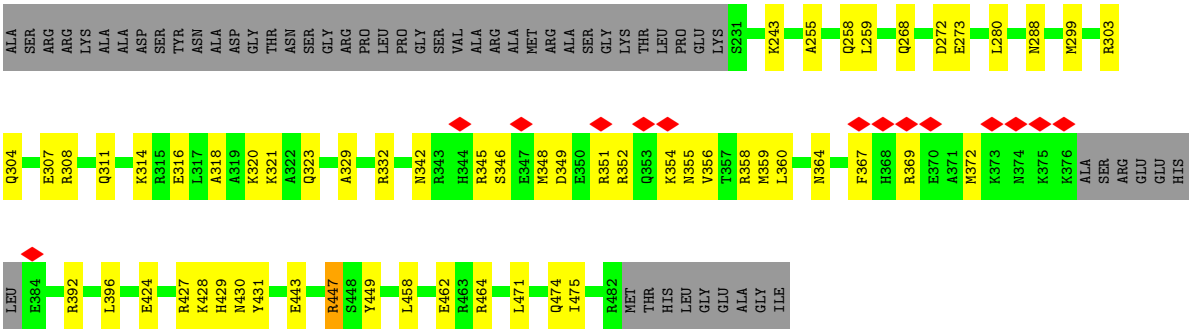
Chain 2b:



• Molecule 41: DMIP15

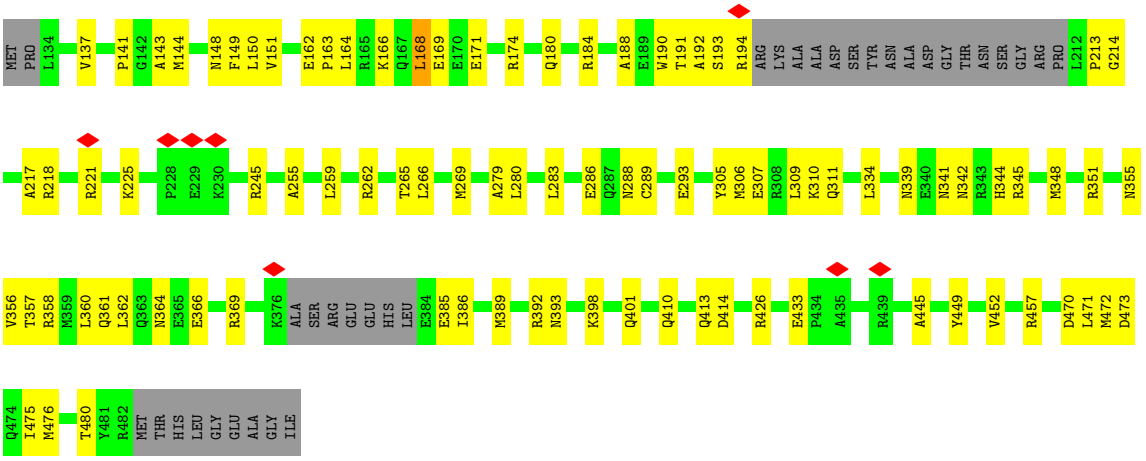
Chain 2c:





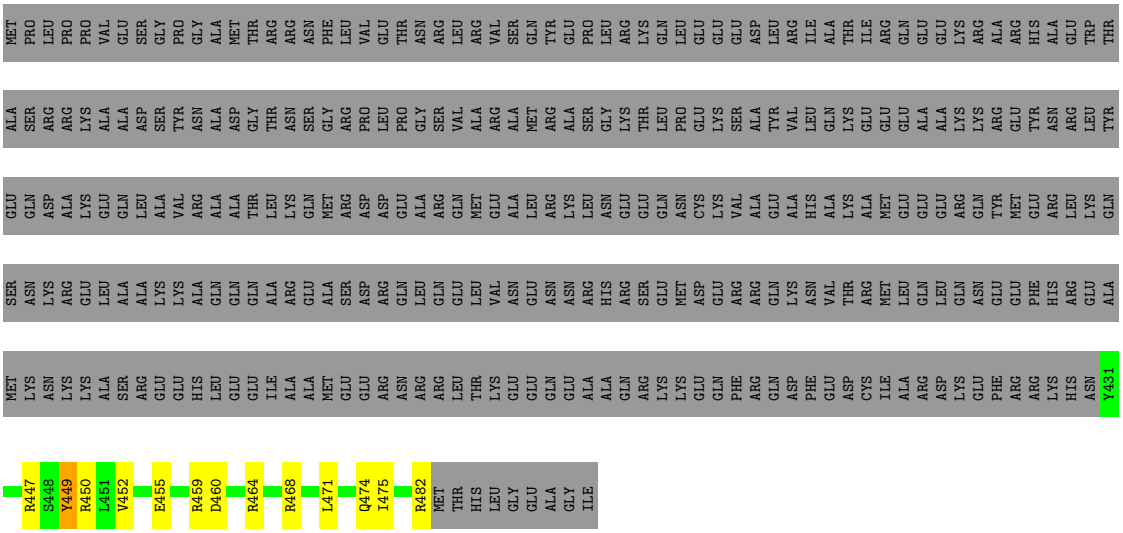
• Molecule 41: DMIP15

Chain 2e:



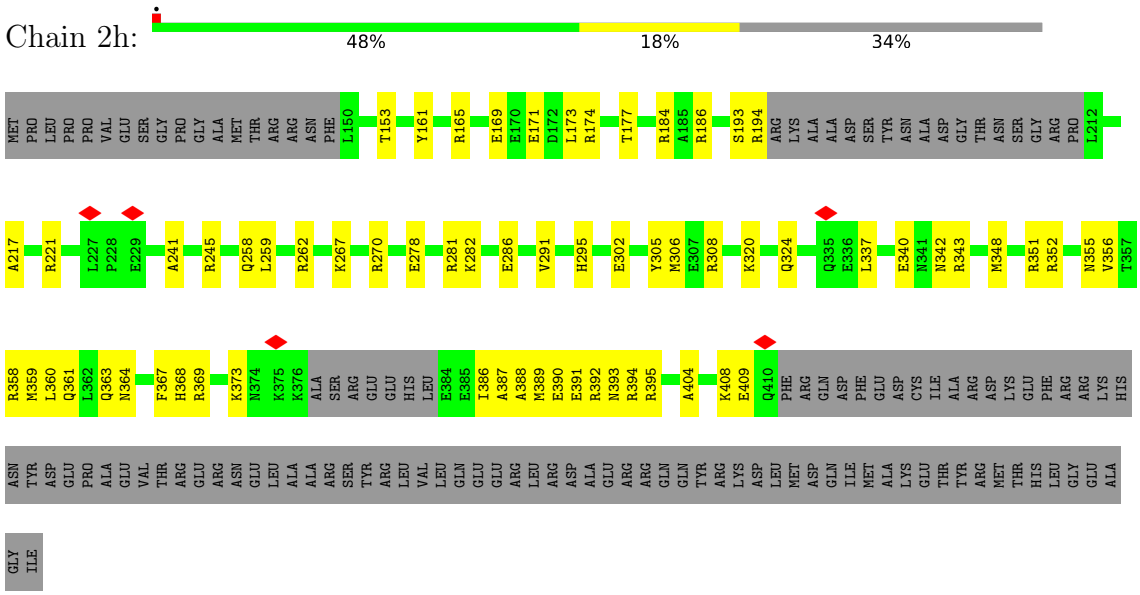
• Molecule 41: DMIP15

Chain 2f:



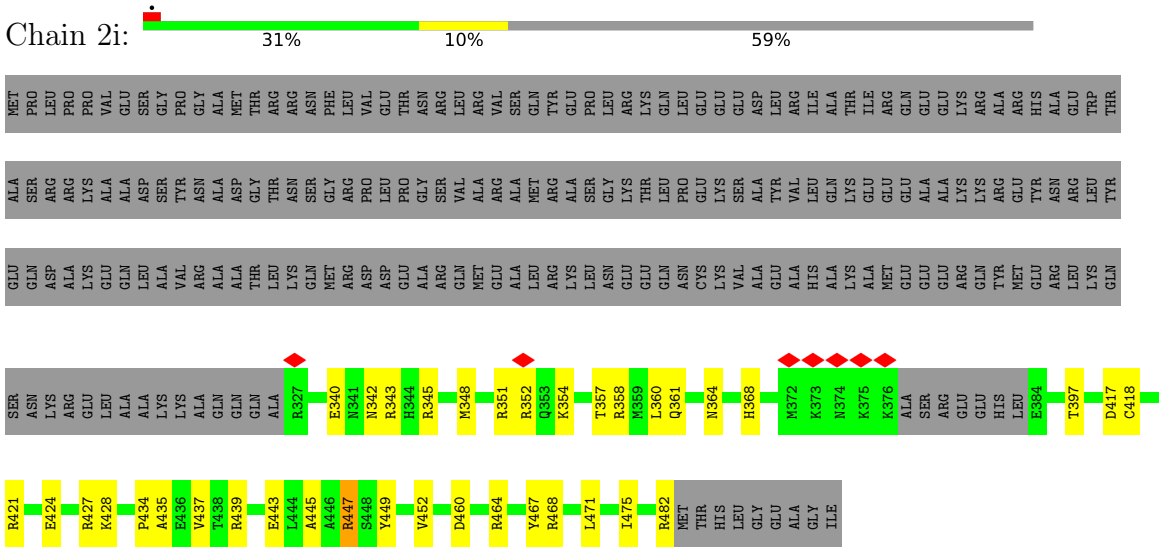
• Molecule 41: DMIP15

Chain 2h:



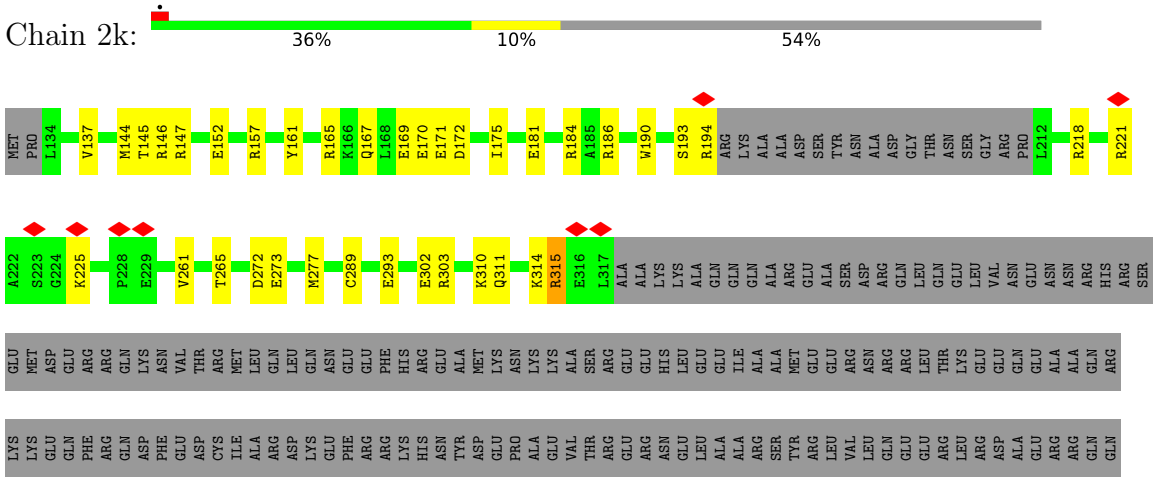
• Molecule 41: DMIP15

Chain 2i:



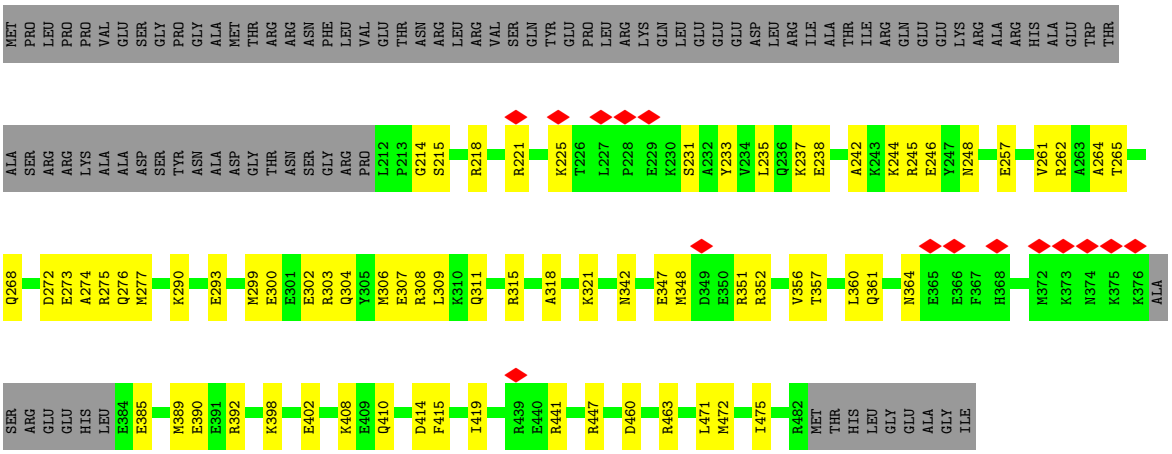
• Molecule 41: DMIP15

Chain 2k:



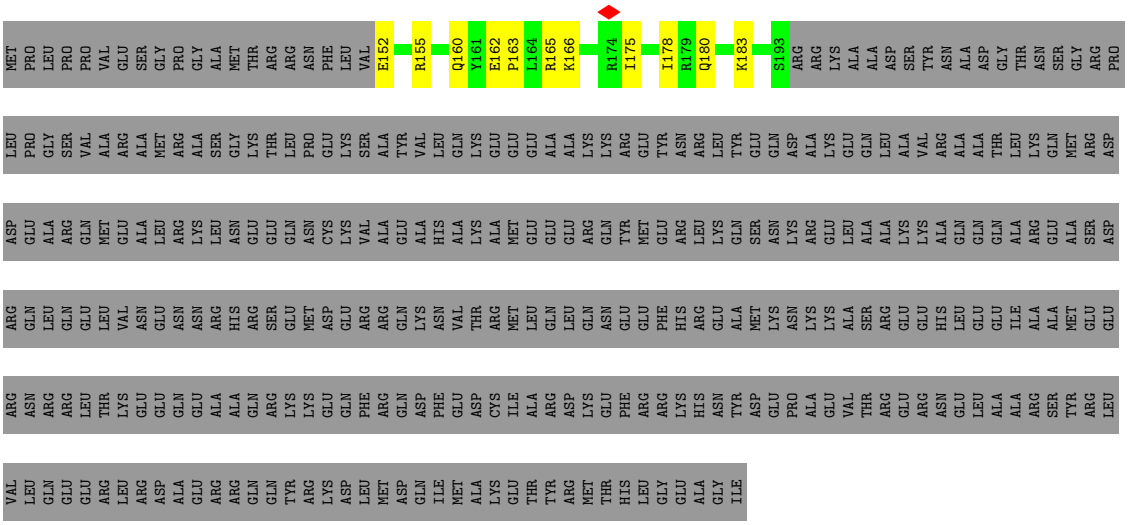
• Molecule 41: DMIP15

Chain 2l:



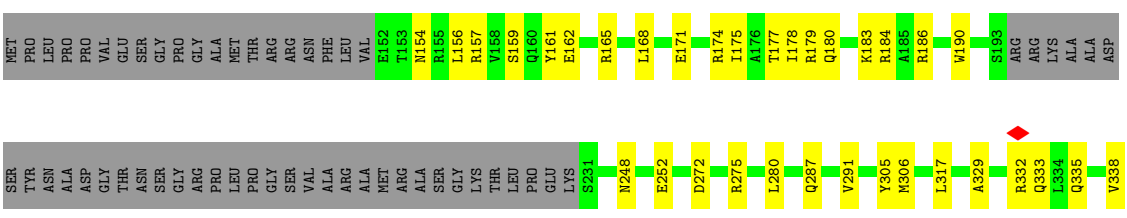
• Molecule 41: DMIP15

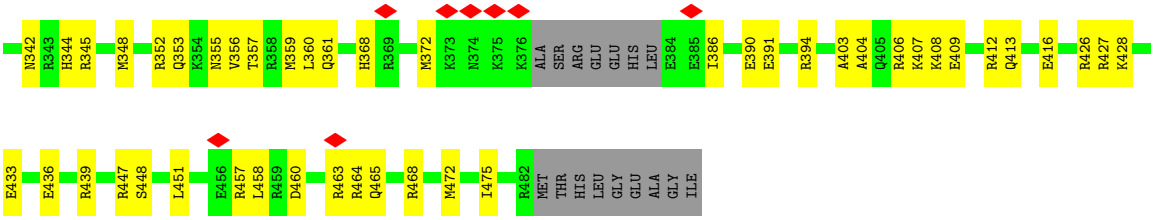
Chain 2n:



• Molecule 41: DMIP15

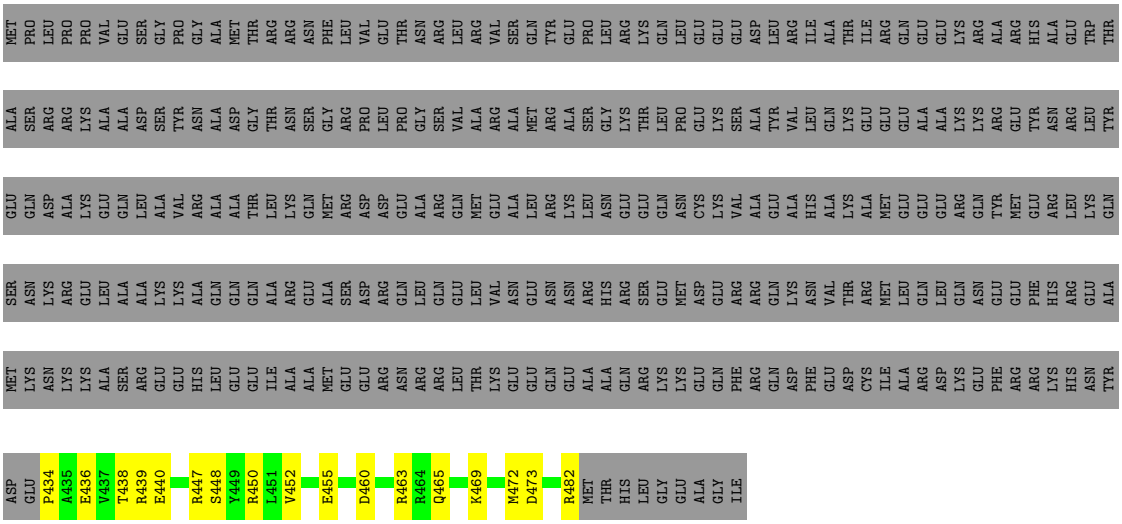
Chain 2o:





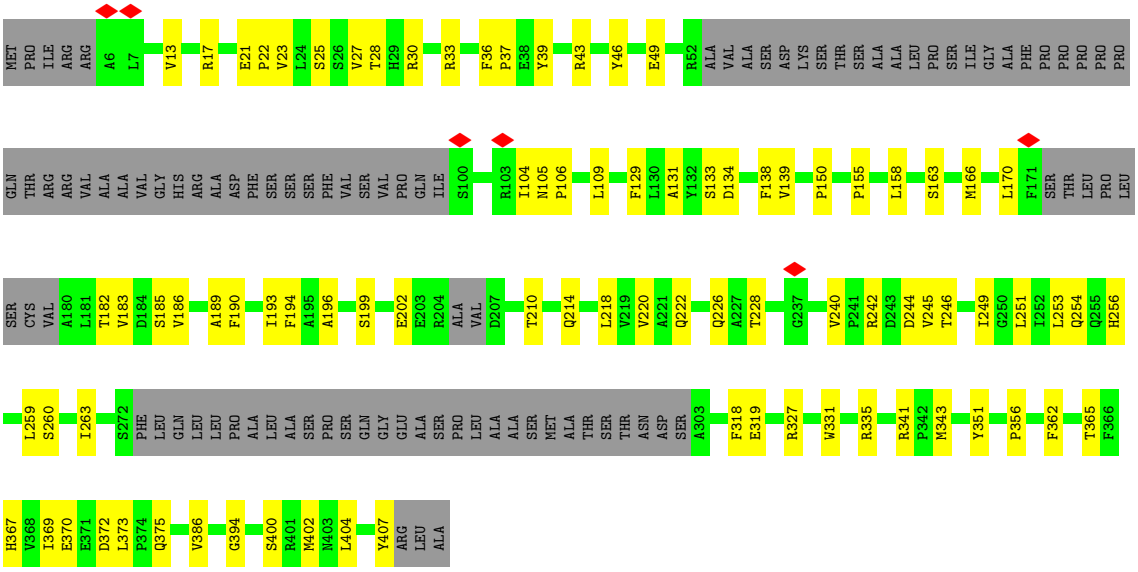
• Molecule 41: DMIP15

Chain 2p: 9% 5% 86%



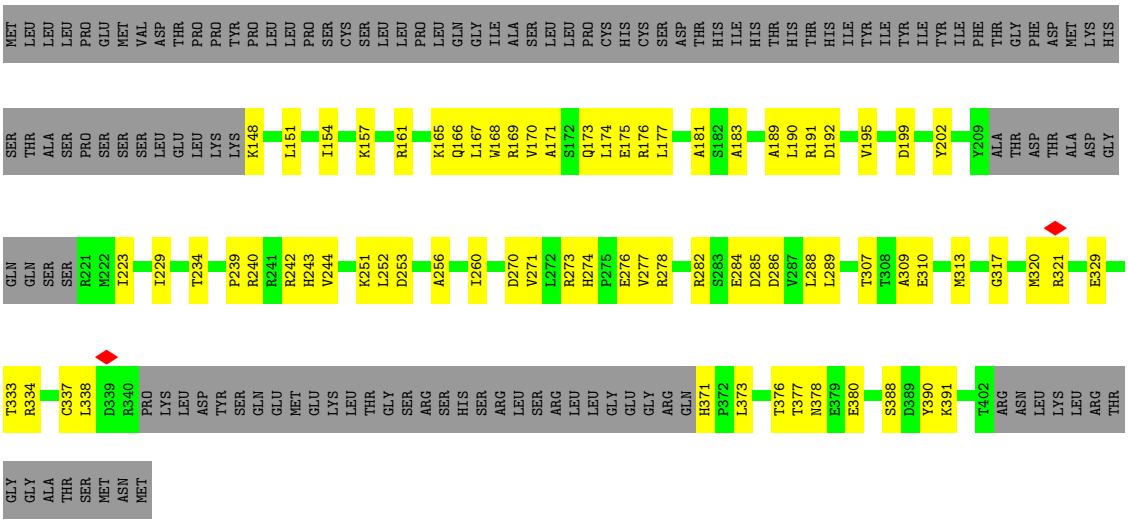
• Molecule 42: DMIP16

Chain 2r: 56% 21% 23%



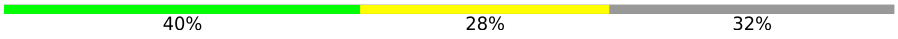
• Molecule 43: DMIP17

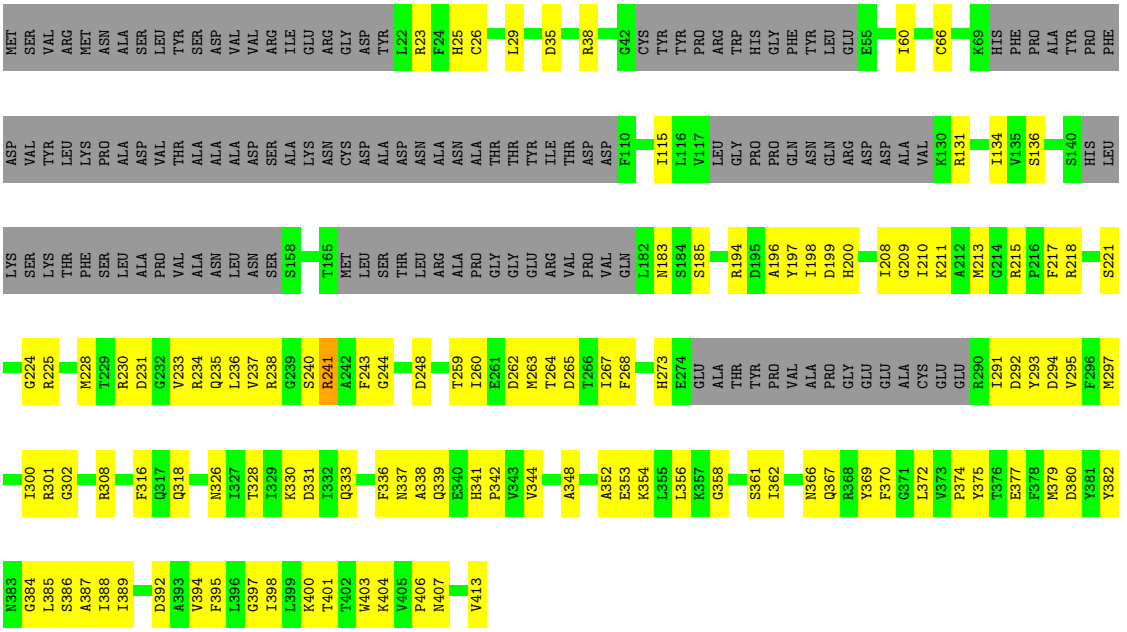
Chain 2t: 41% 21% 38%



• Molecule 44: DMIP18

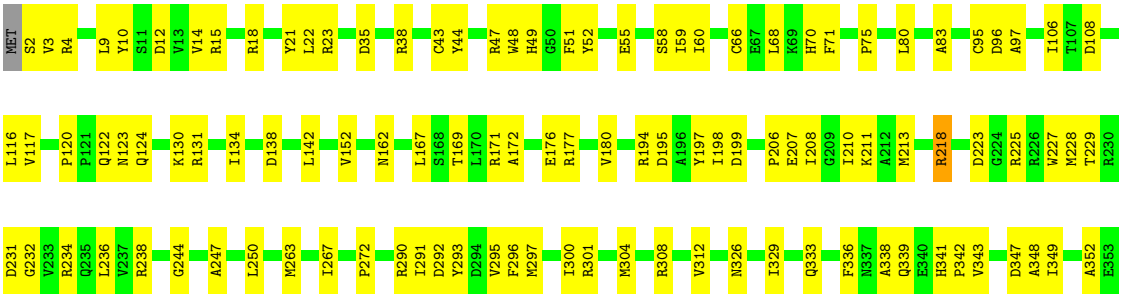
Chain 2v:

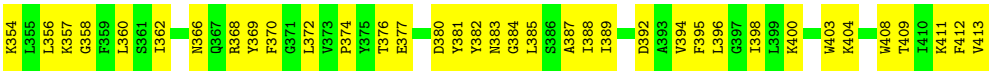




• Molecule 44: DMIP18

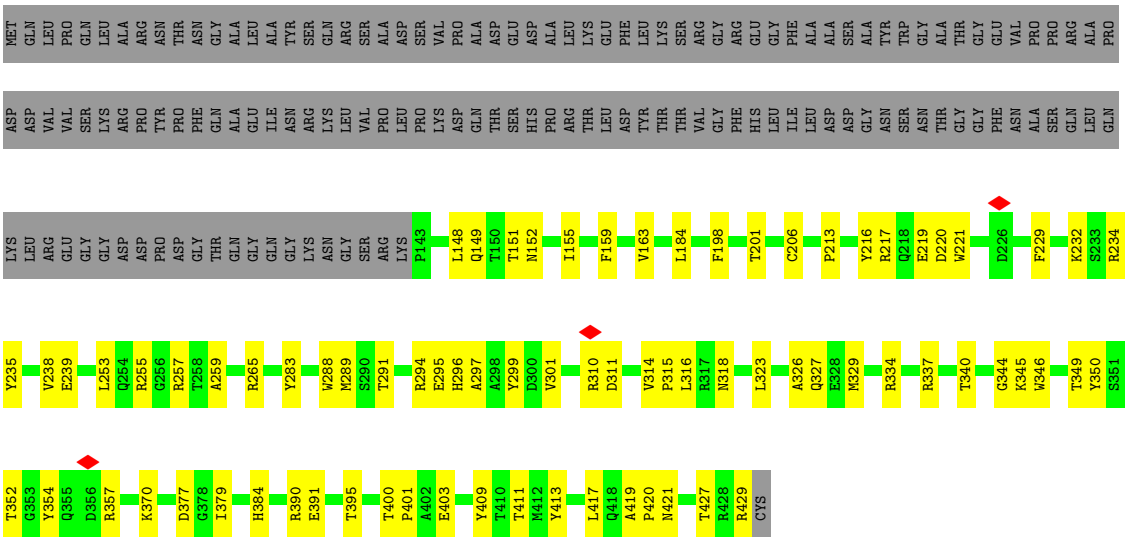
Chain 2w:





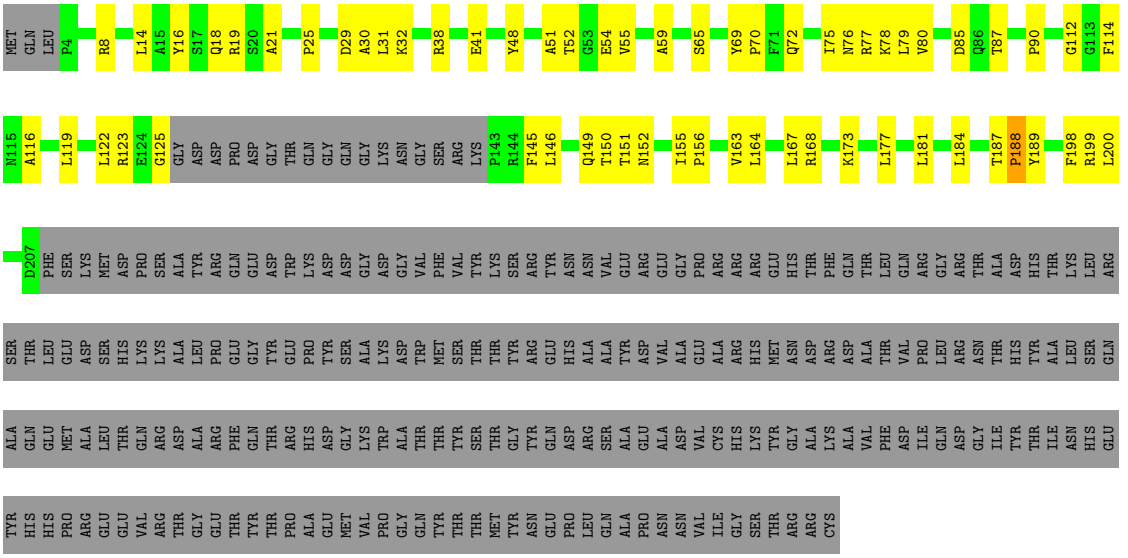
• Molecule 45: DMIP19

Chain 2y:



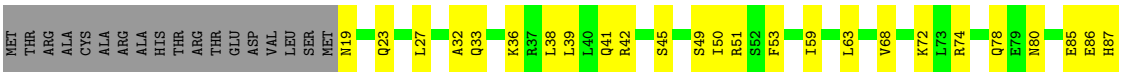
• Molecule 45: DMIP19

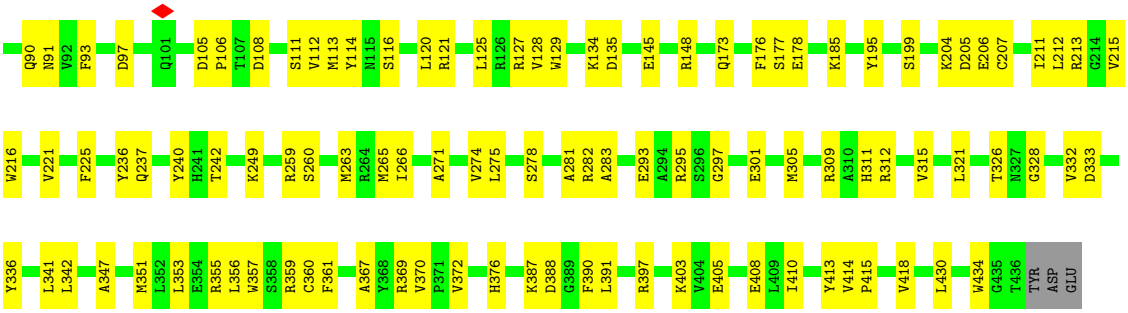
Chain 2z:



• Molecule 46: DMIP20

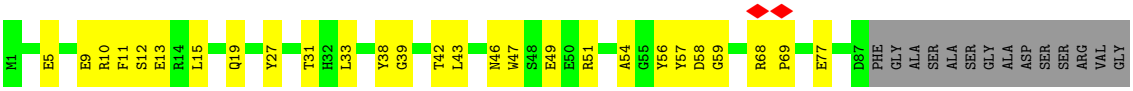
Chain 3B:

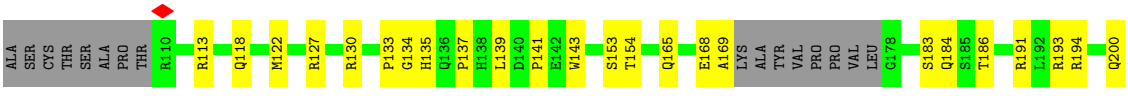


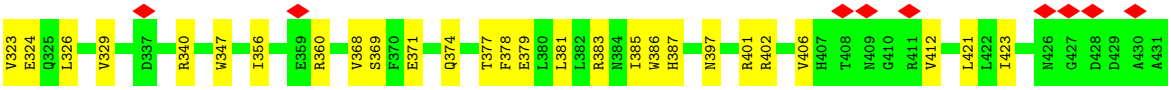


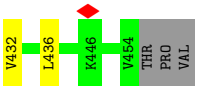
• Molecule 47: DMIP21

Chain 3D:



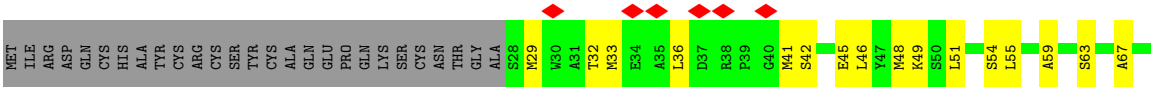


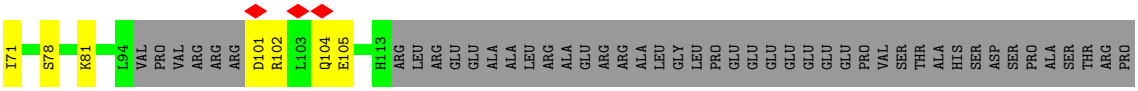


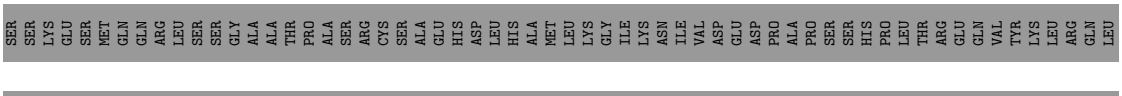


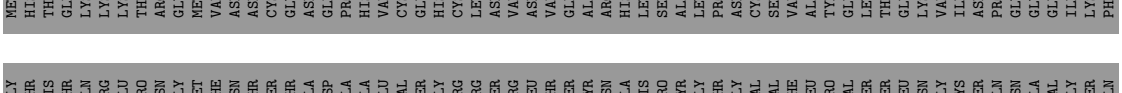
• Molecule 48: DMIP22

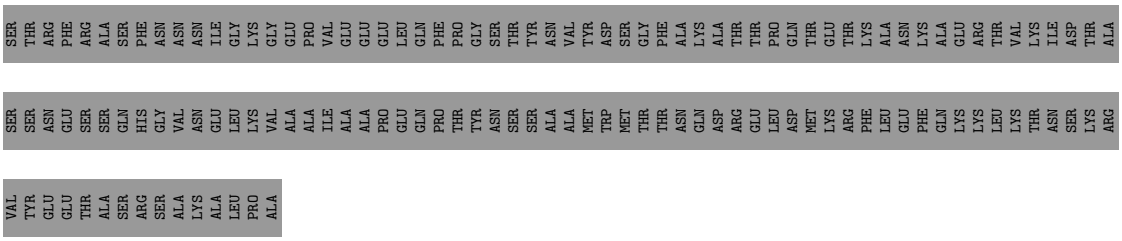
Chain 3I:





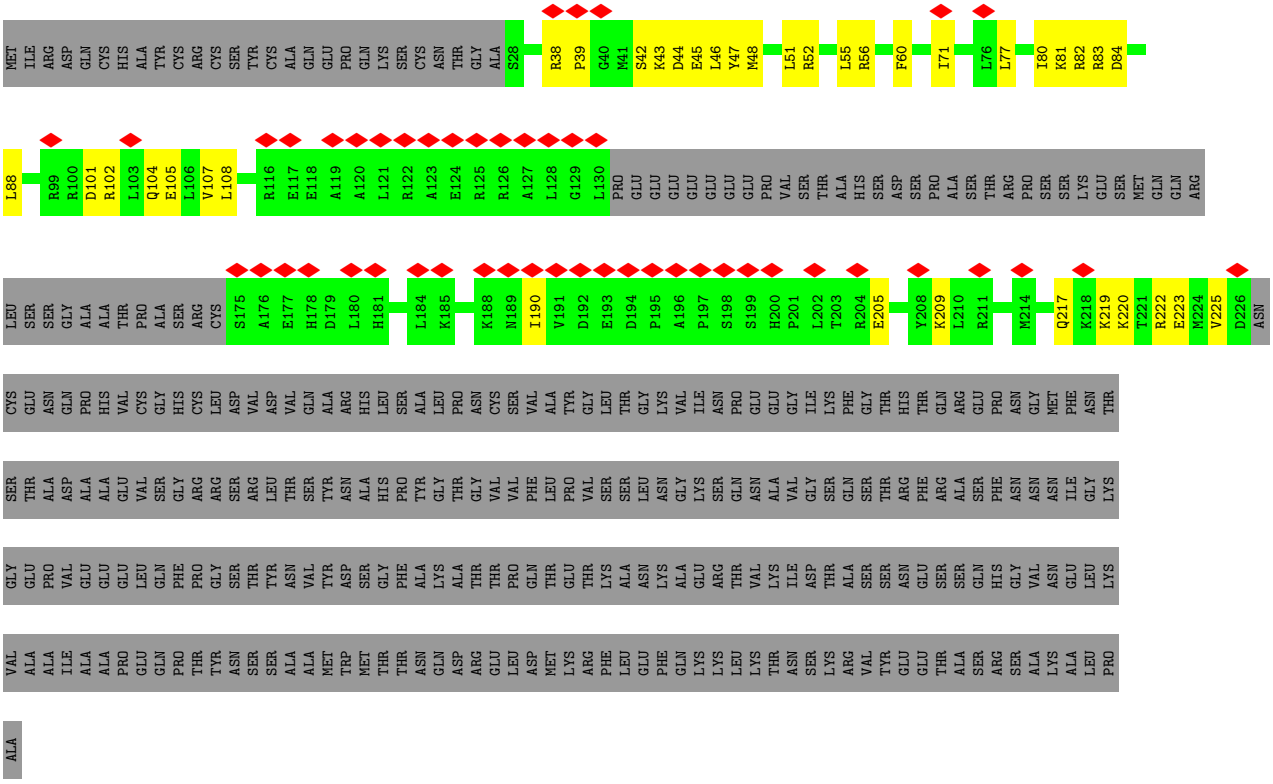






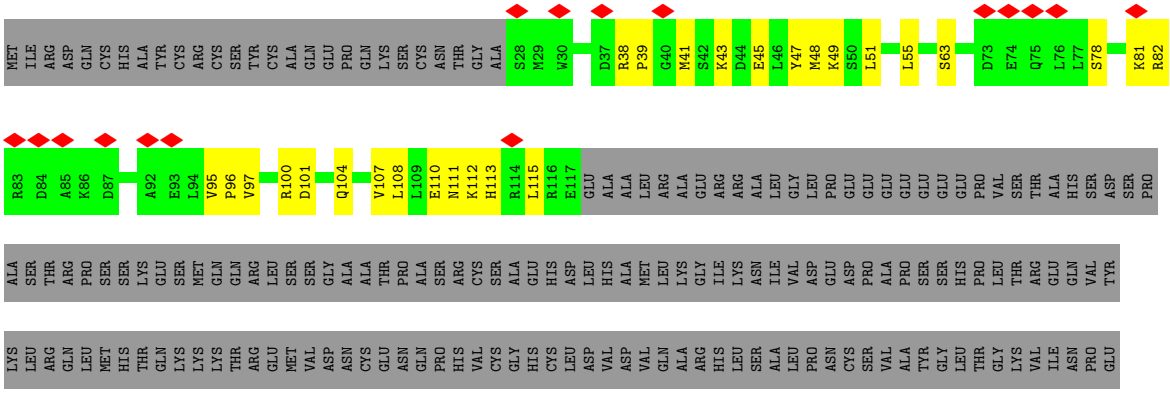
• Molecule 48: DMIP22

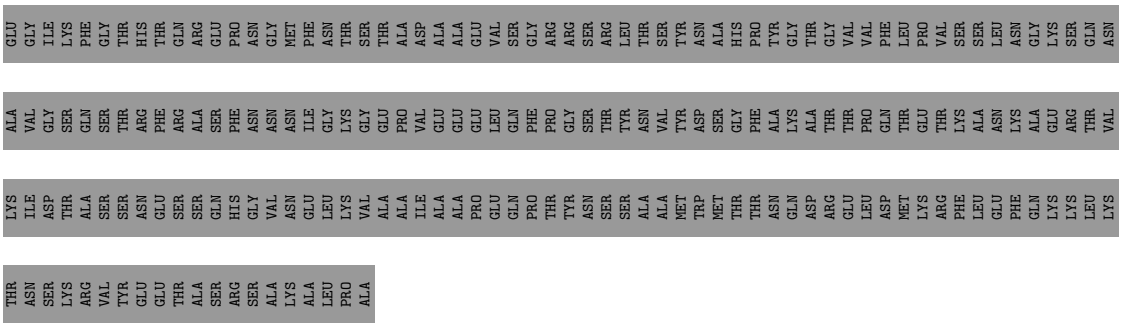
Chain 3F:



• Molecule 48: DMIP22

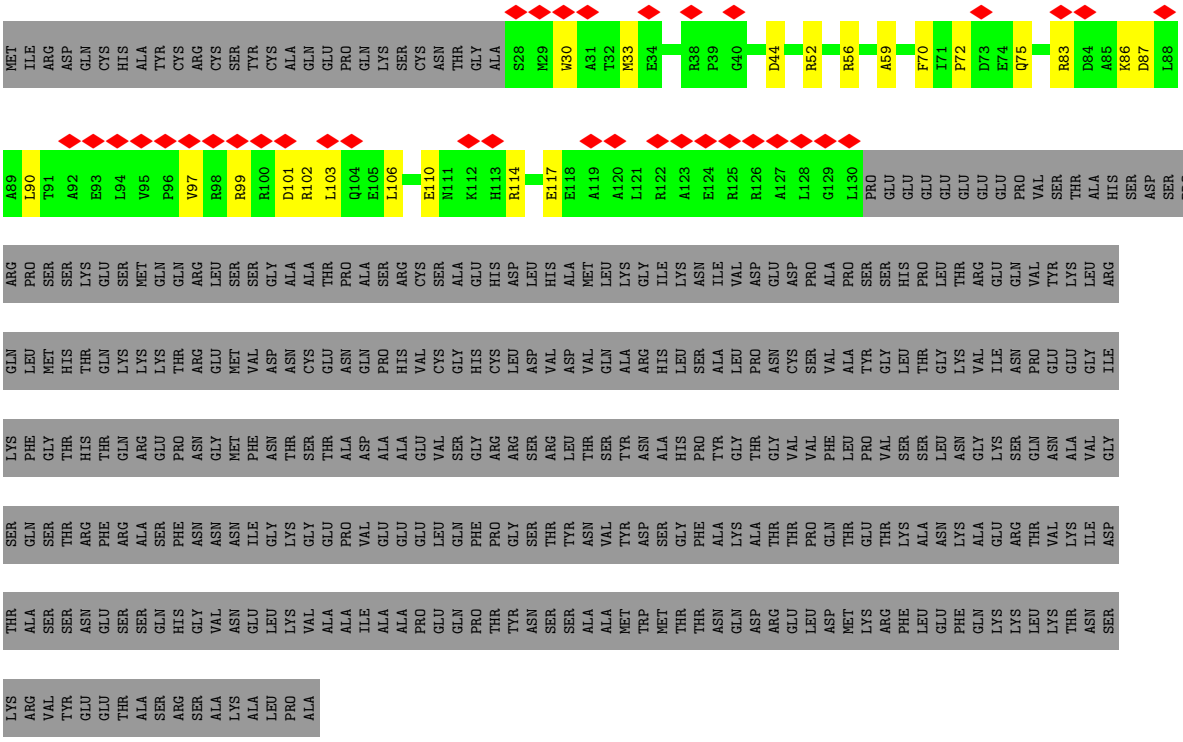
Chain 3G:





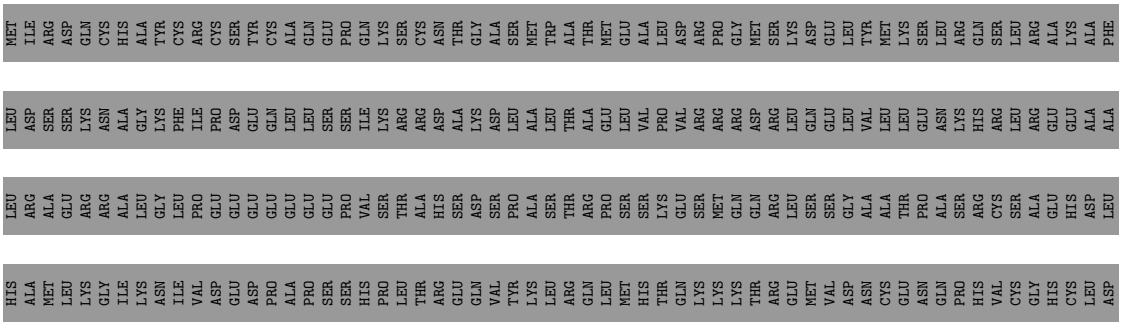
- Molecule 48: DMIP22

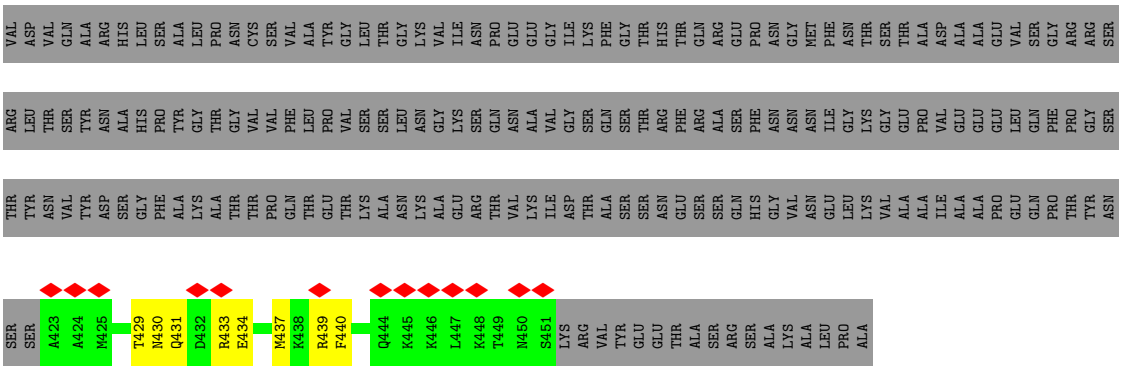
Chain 3H:



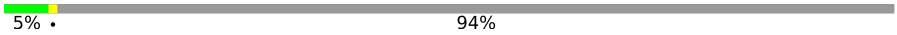
- Molecule 48: DMIP22

Chain 3M:



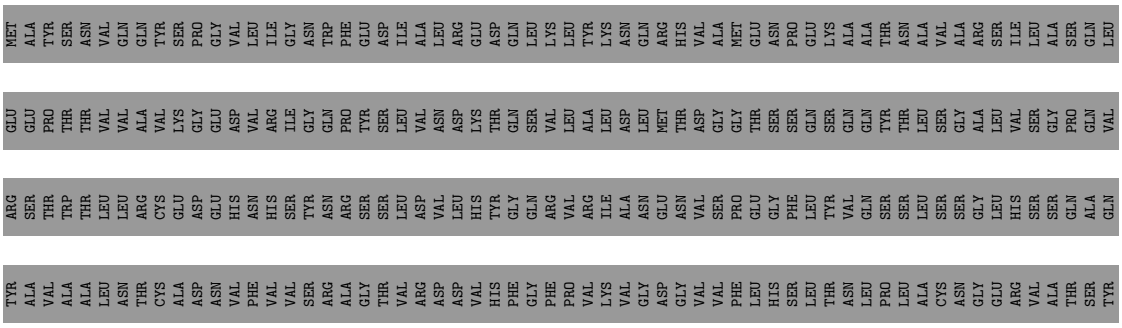


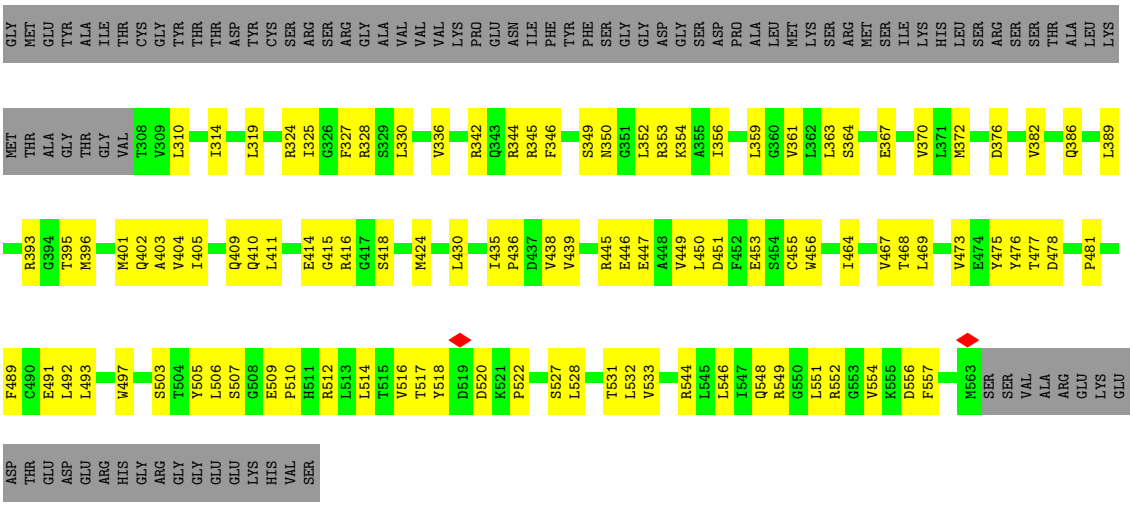
• Molecule 48: DMIP22

Chain 3L: 

• Molecule 49: DMIP23

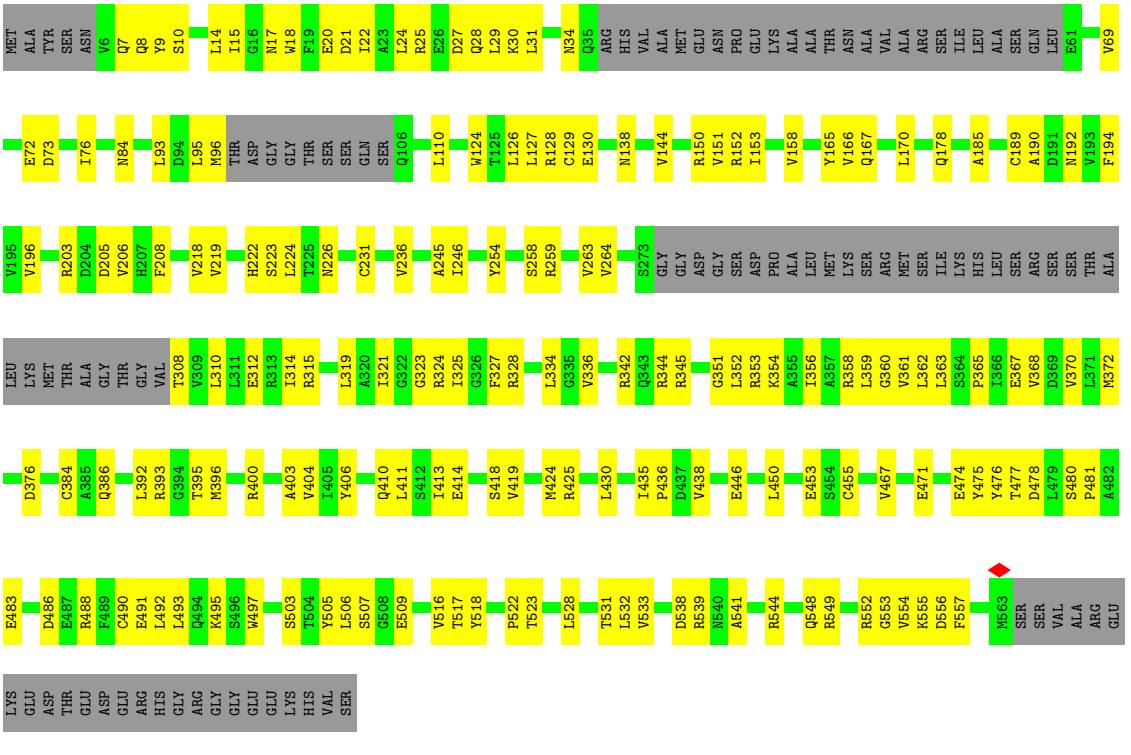
Chain 3P:





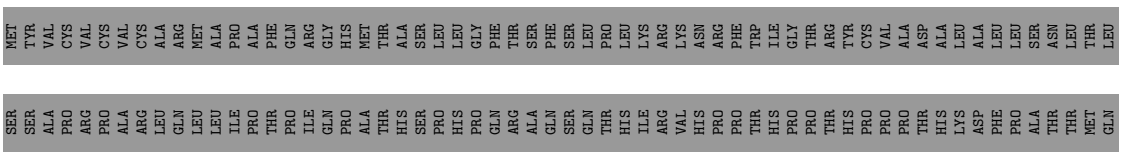
• Molecule 49: DMIP23

Chain 3Q:



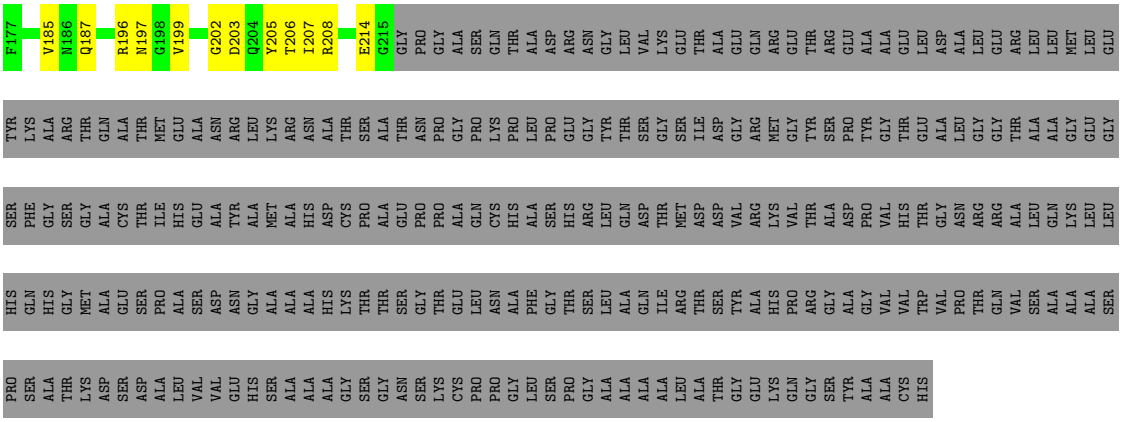
• Molecule 50: DMIP24

Chain 3S:



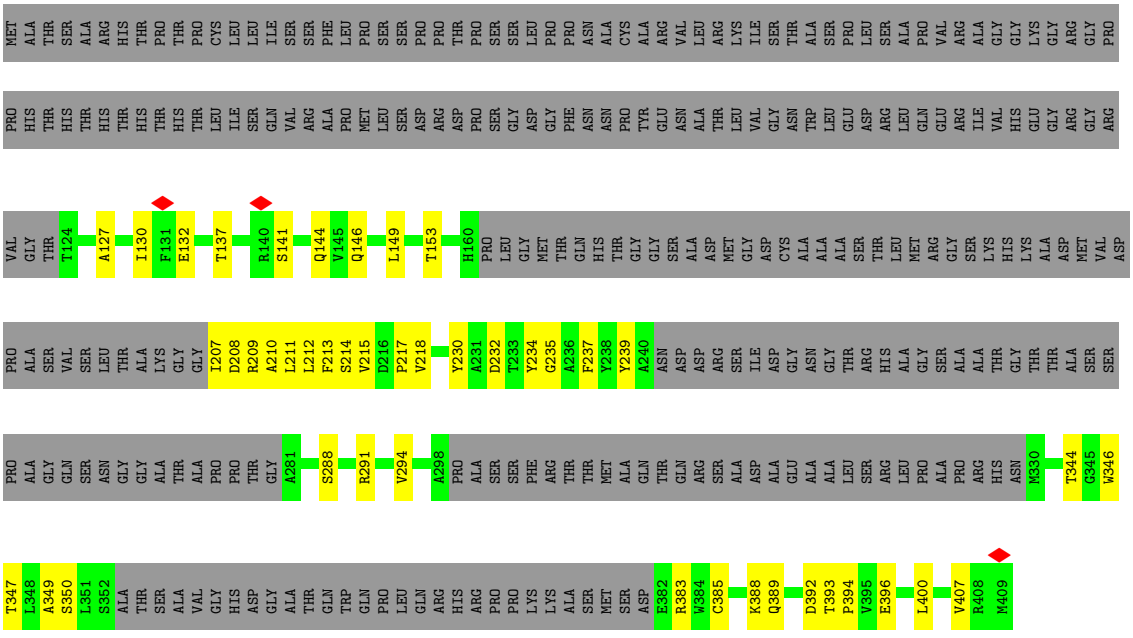
• Molecule 51: DMIP24

Chain X1:



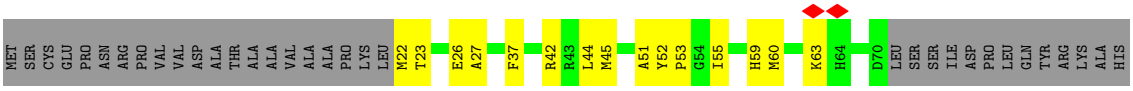
• Molecule 52: DMIP25

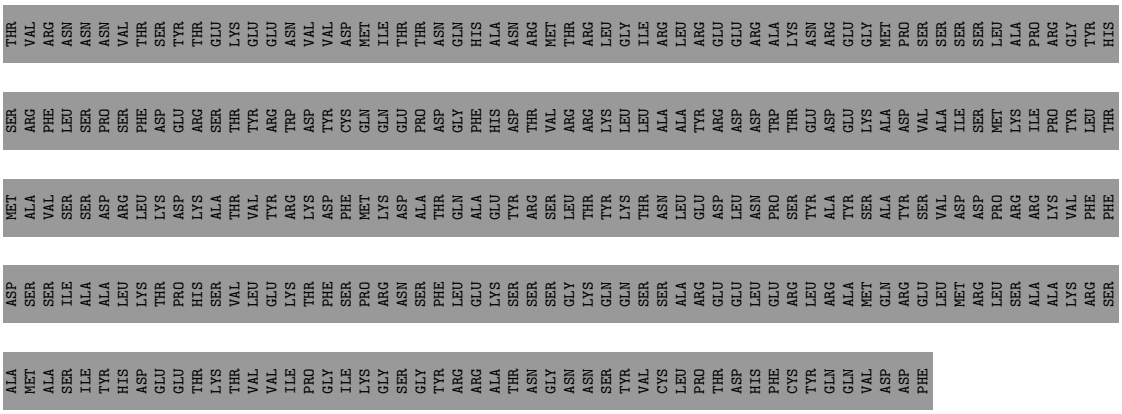
Chain 3U:



• Molecule 53: DMIP26

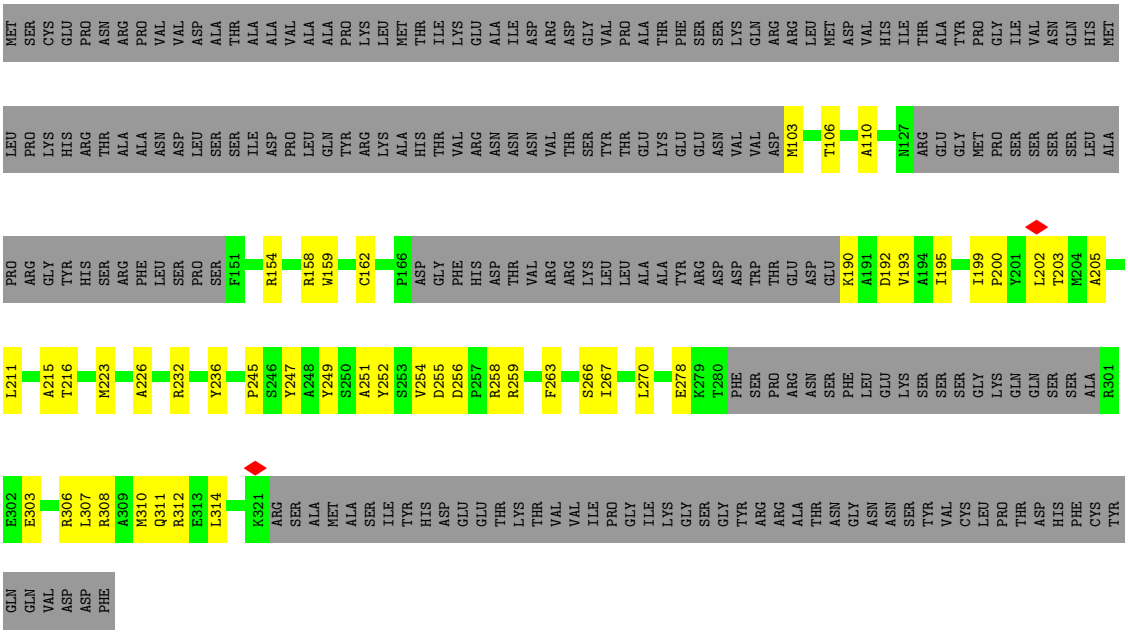
Chain 3X:





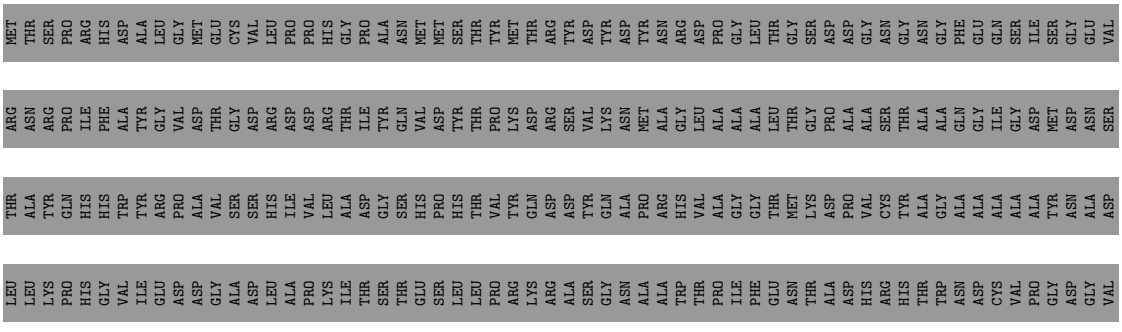
- Molecule 53: DMIP26

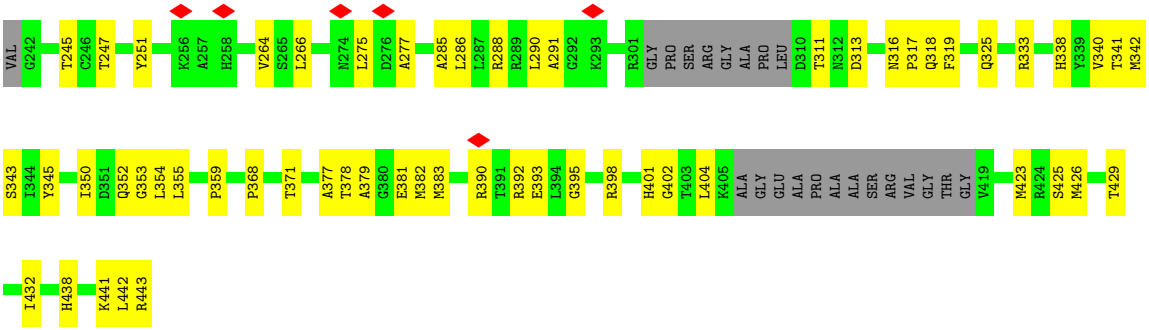
Chain 3W:



- Molecule 54: DMIP27

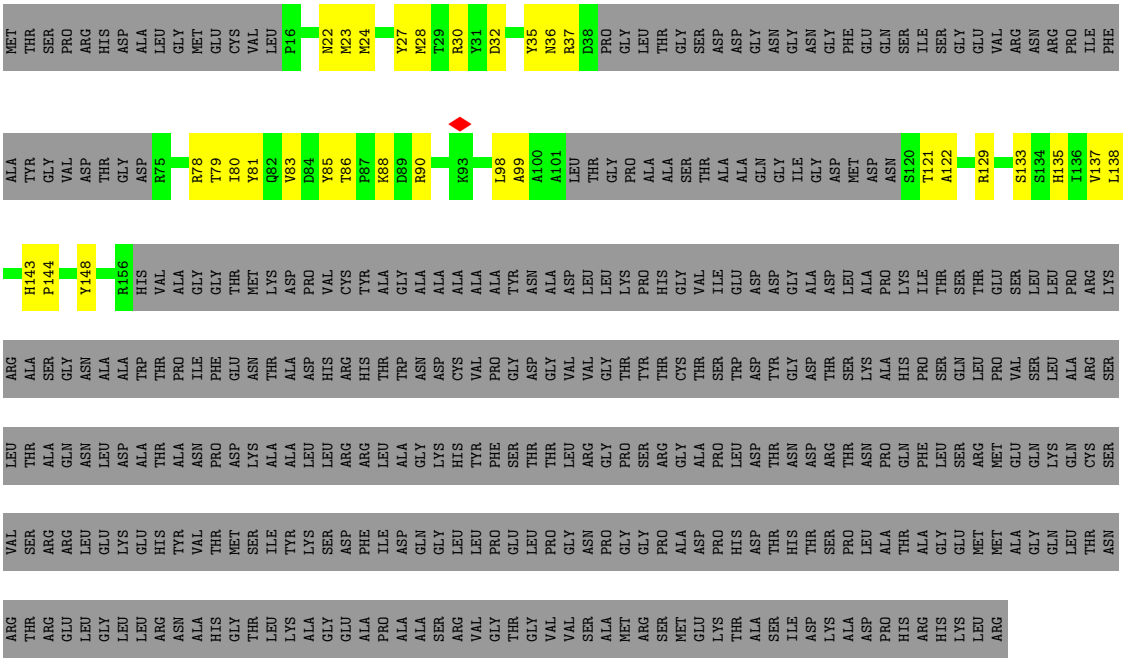
Chain 3Z:





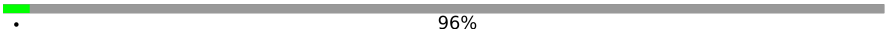
• Molecule 54: DMIP27

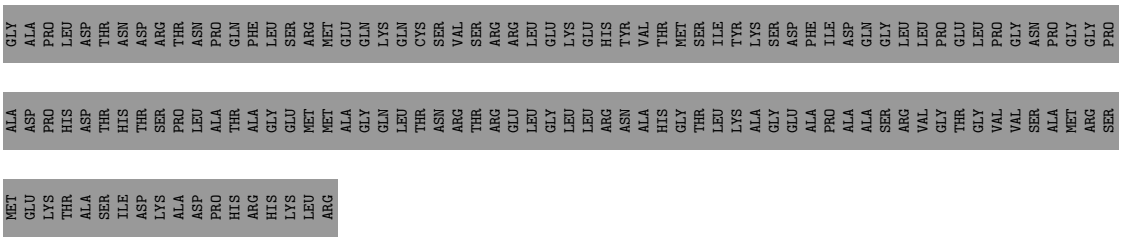
Chain 3a:



• Molecule 54: DMIP27

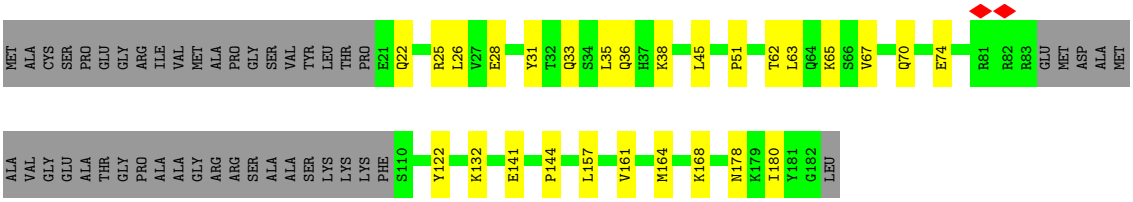
Chain 4Y:





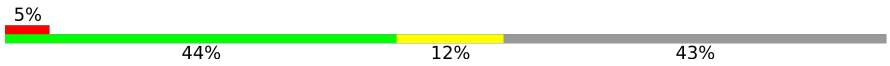
• Molecule 55: ArcMAP2

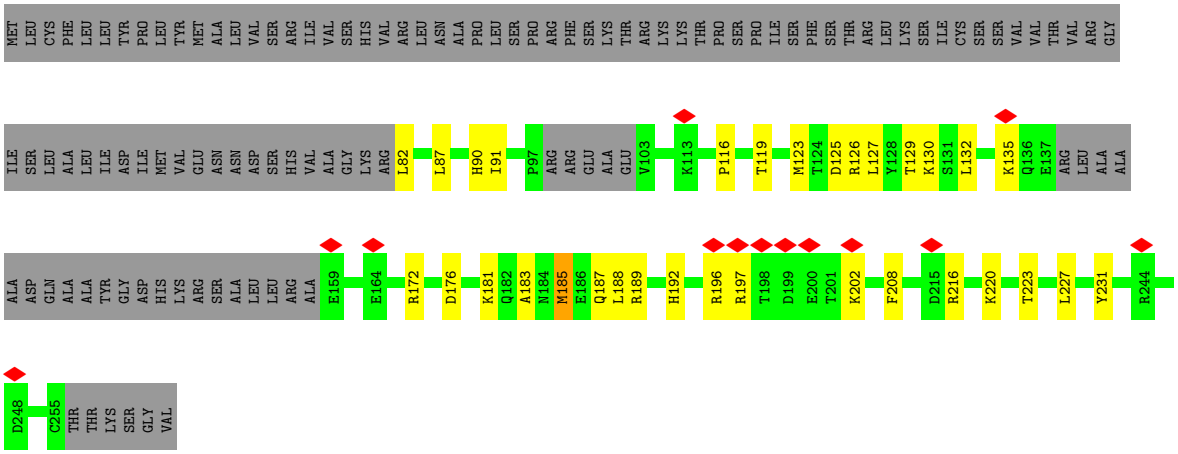
Chain 3b:



• Molecule 56: ArcMAP1

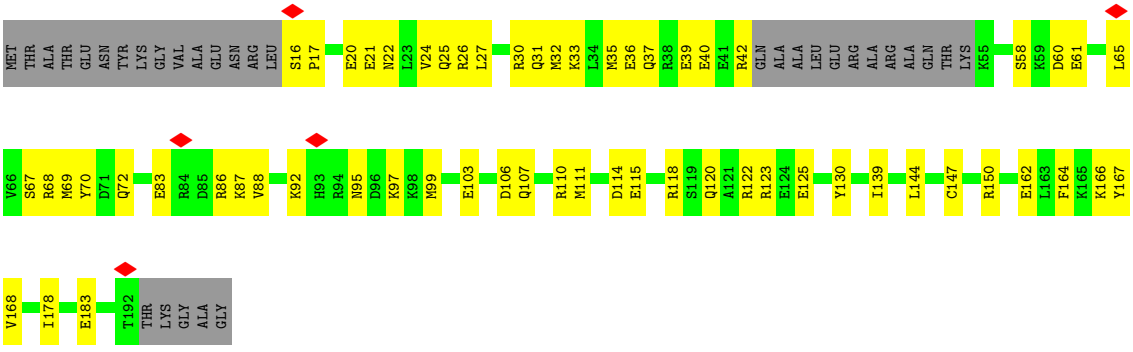
Chain 3d:





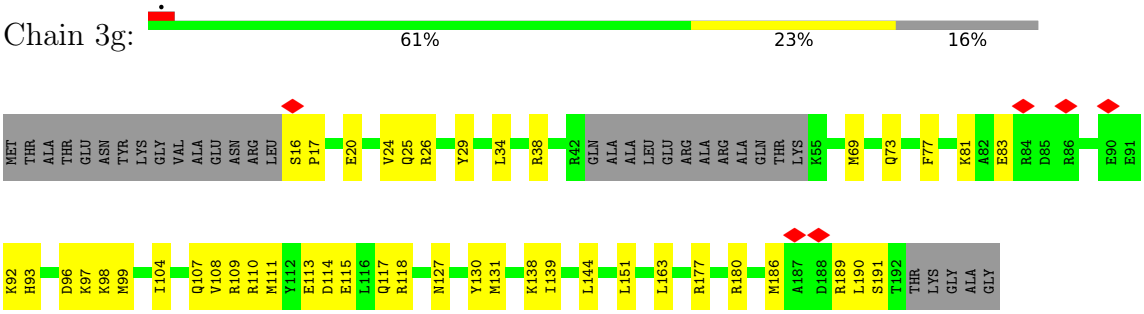
• Molecule 57: ArcMAP4

Chain 3f:



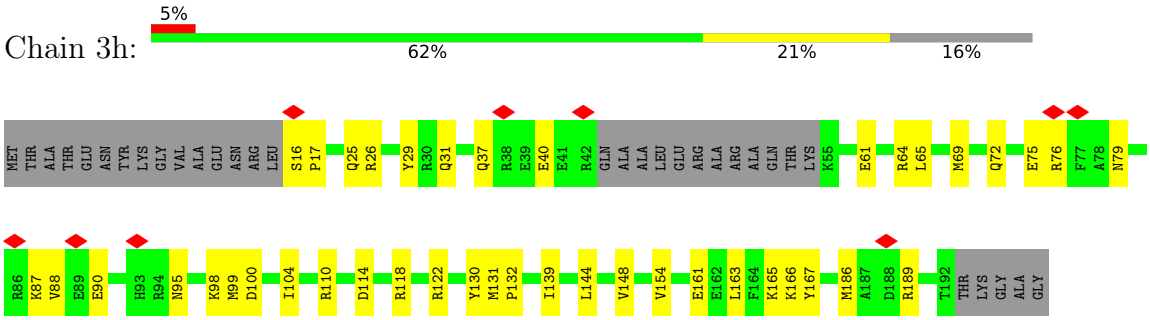
• Molecule 57: ArcMAP4

Chain 3g:



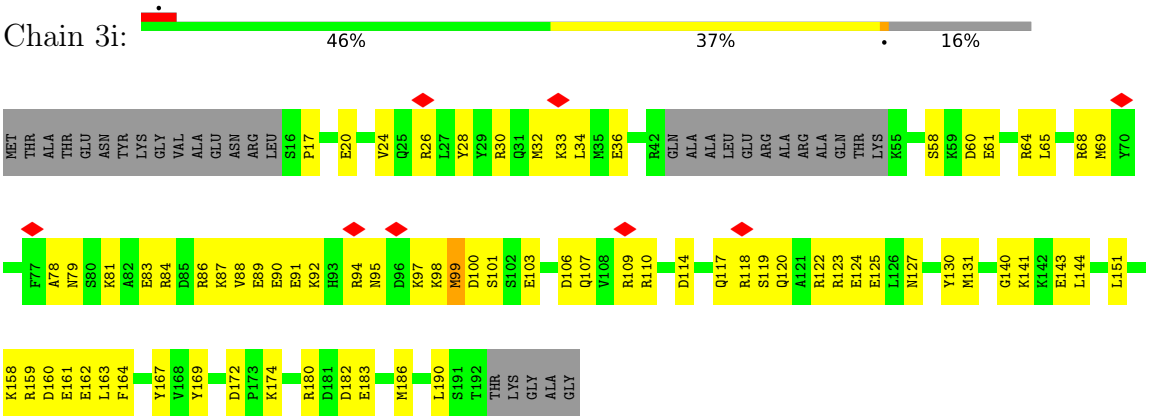
• Molecule 57: ArcMAP4

Chain 3h:



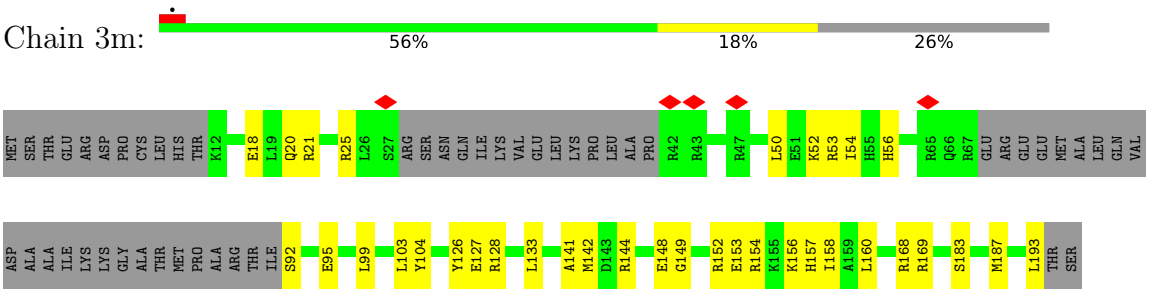
• Molecule 57: ArcMAP4

Chain 3i:



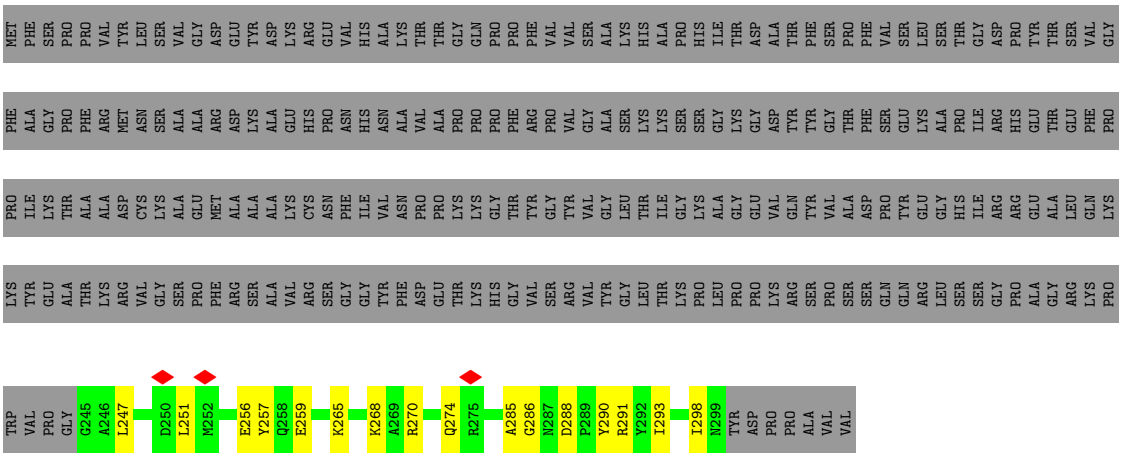
• Molecule 58: ArcMAP3

Chain 3m:



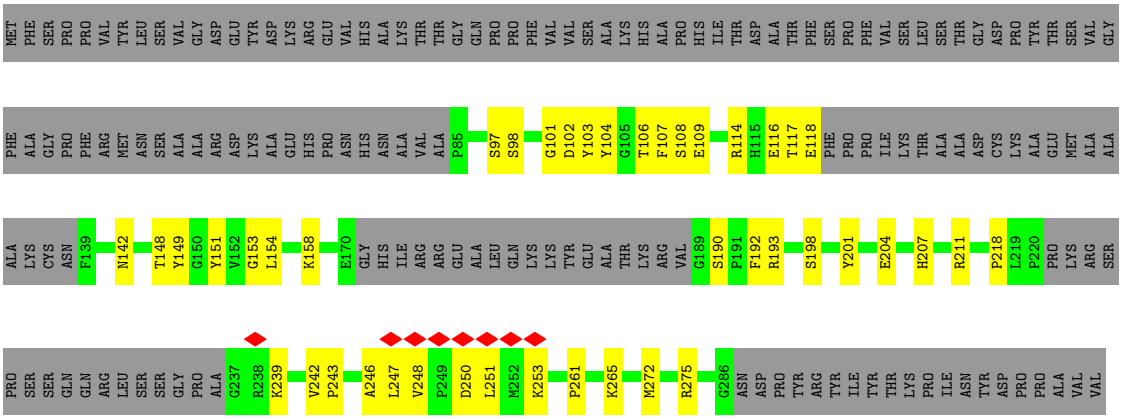
• Molecule 59: CFAP96

Chain 3o:



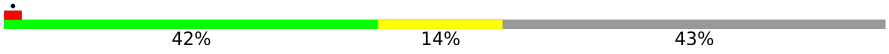
• Molecule 59: CFAP96

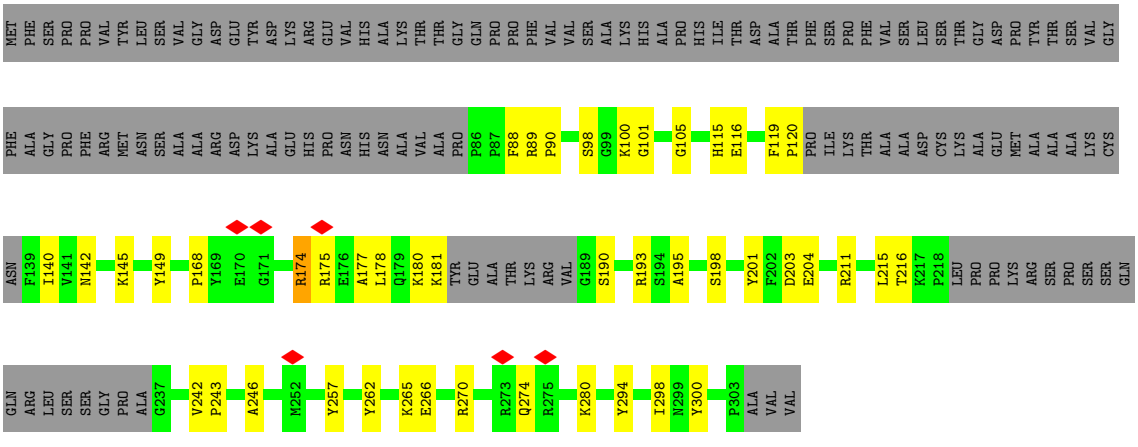
Chain 3p:



• Molecule 59: CFAP96

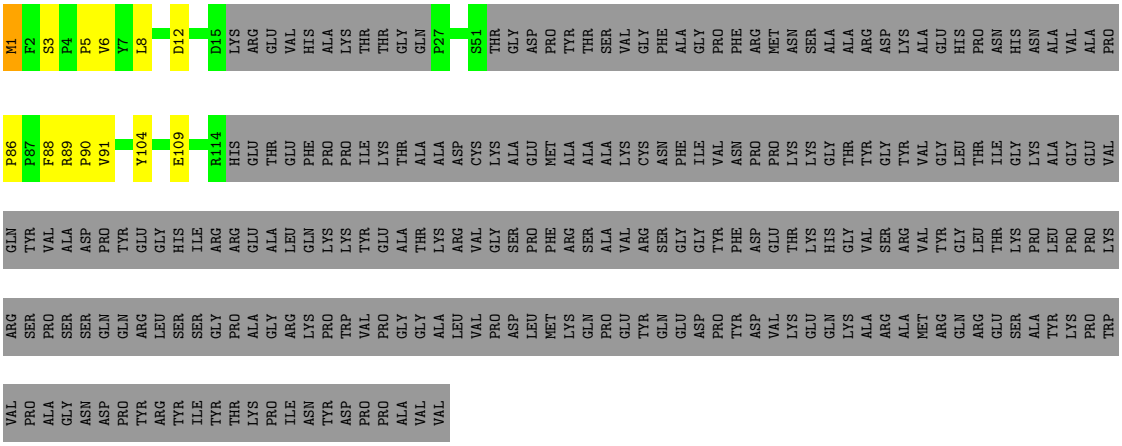
Chain 4O:





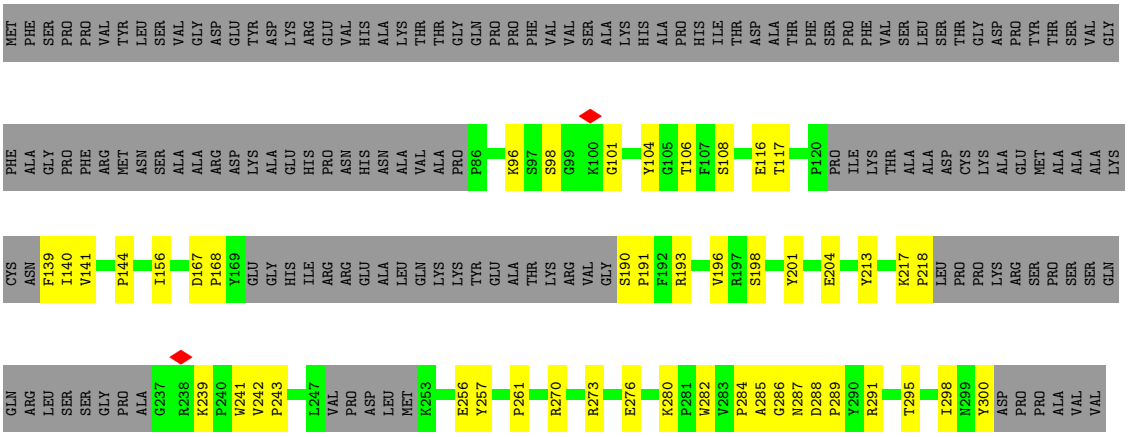
• Molecule 59: CFAP96

Chain 4P:



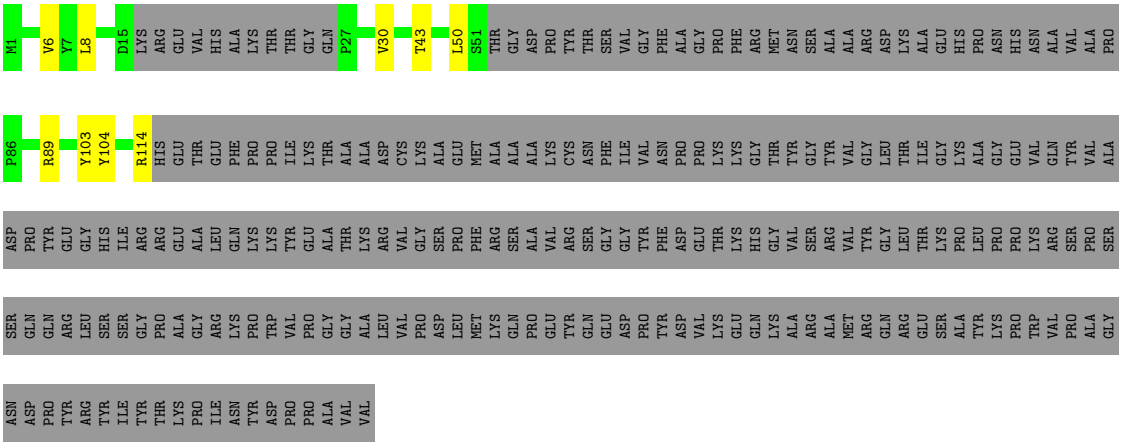
• Molecule 59: CFAP96

Chain 4a:



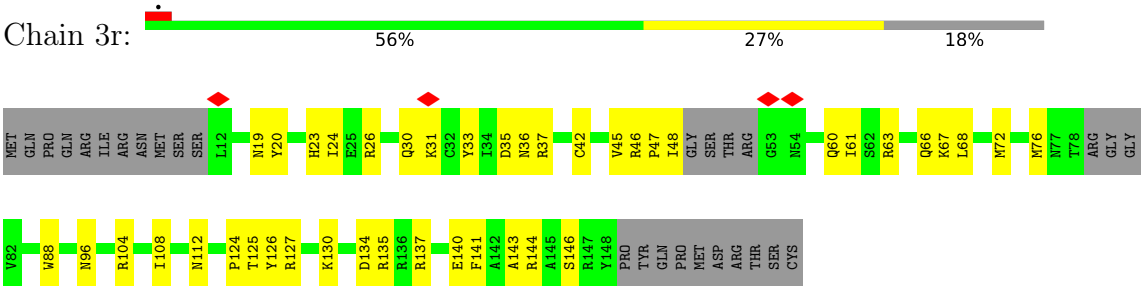
• Molecule 59: CFAP96

Chain 4b:



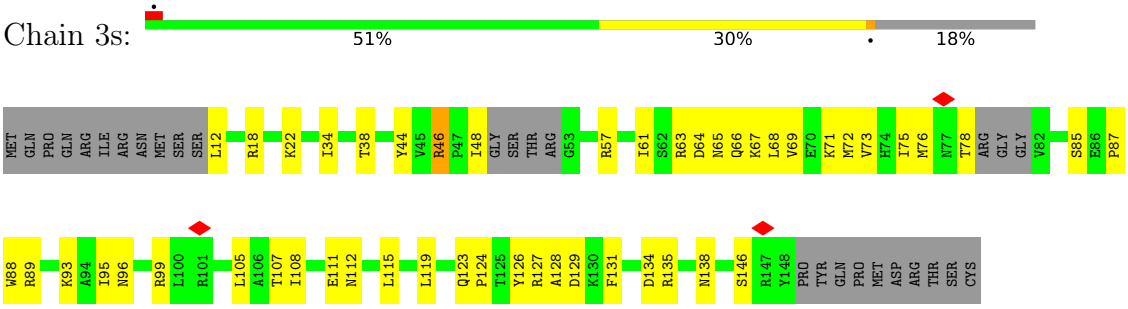
• Molecule 60: CFAP97

Chain 3r:



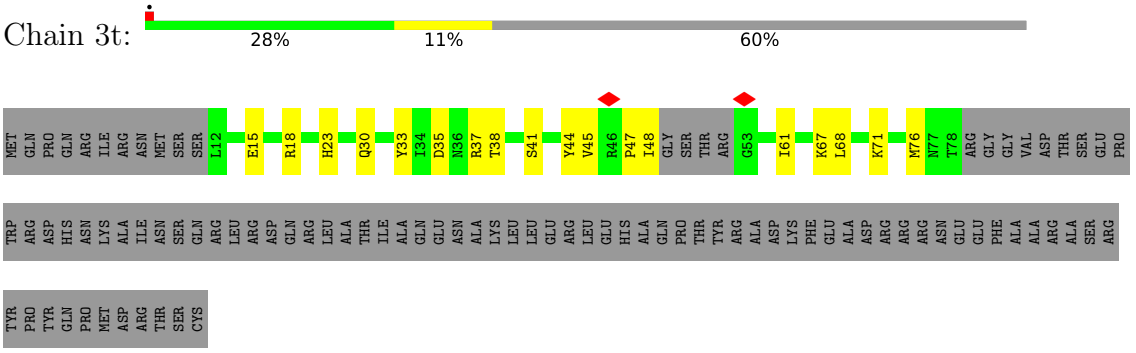
• Molecule 60: CFAP97

Chain 3s:



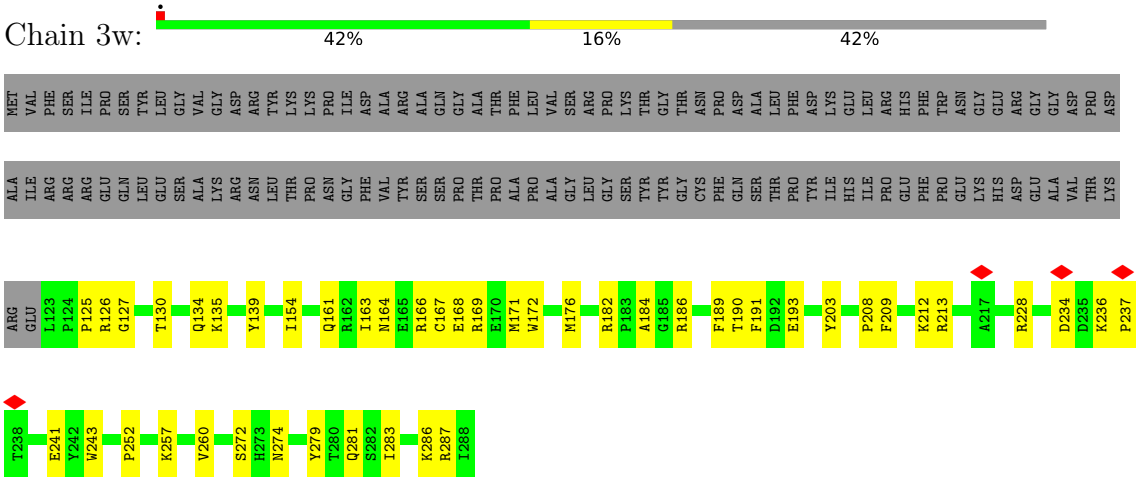
• Molecule 60: CFAP97

Chain 3t:



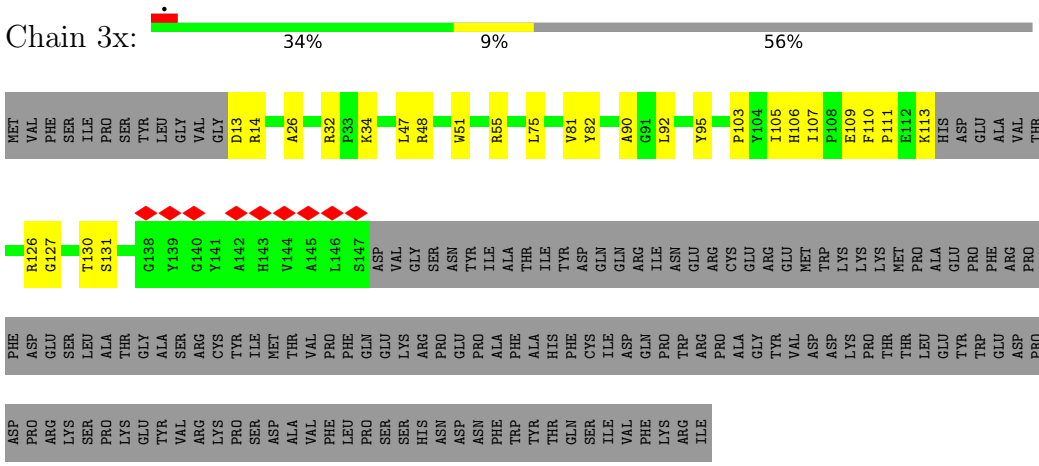
• Molecule 61: DMAP1

Chain 3w:



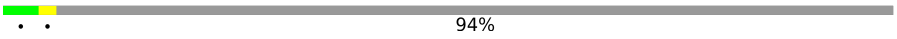
• Molecule 61: DMAP1

Chain 3x:



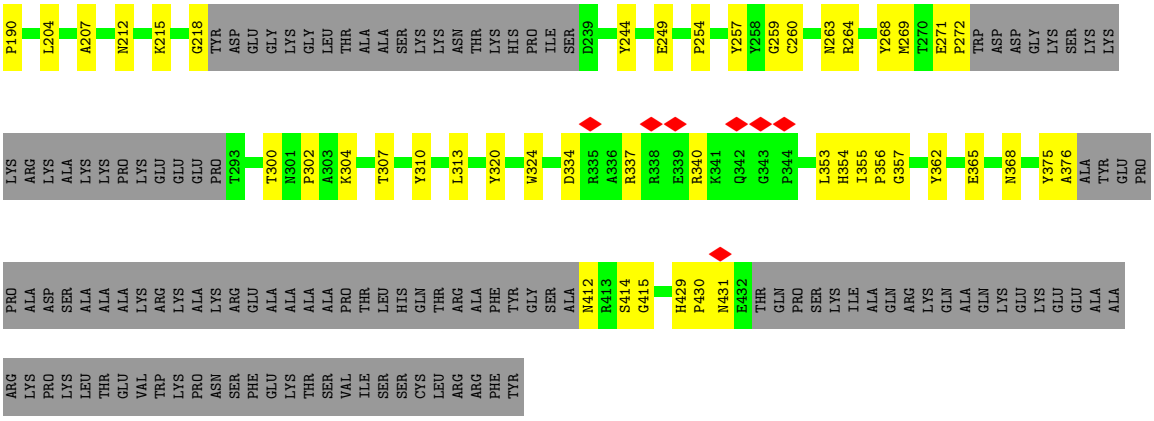
• Molecule 62: DMAP2

Chain 4A:



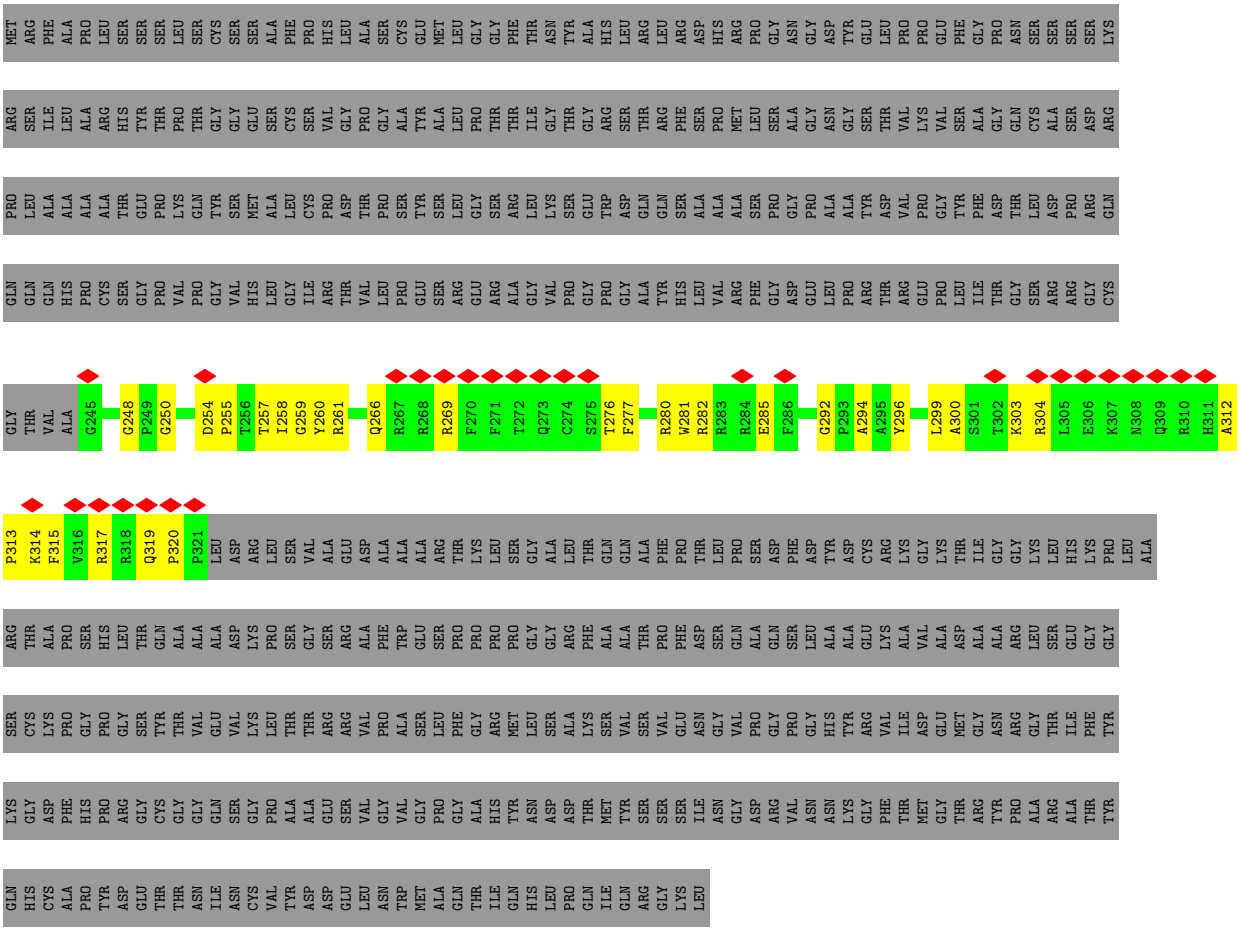
• Molecule 62: DMAP2

Chain 4B:



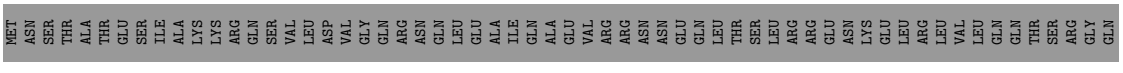
• Molecule 63: DMAP7

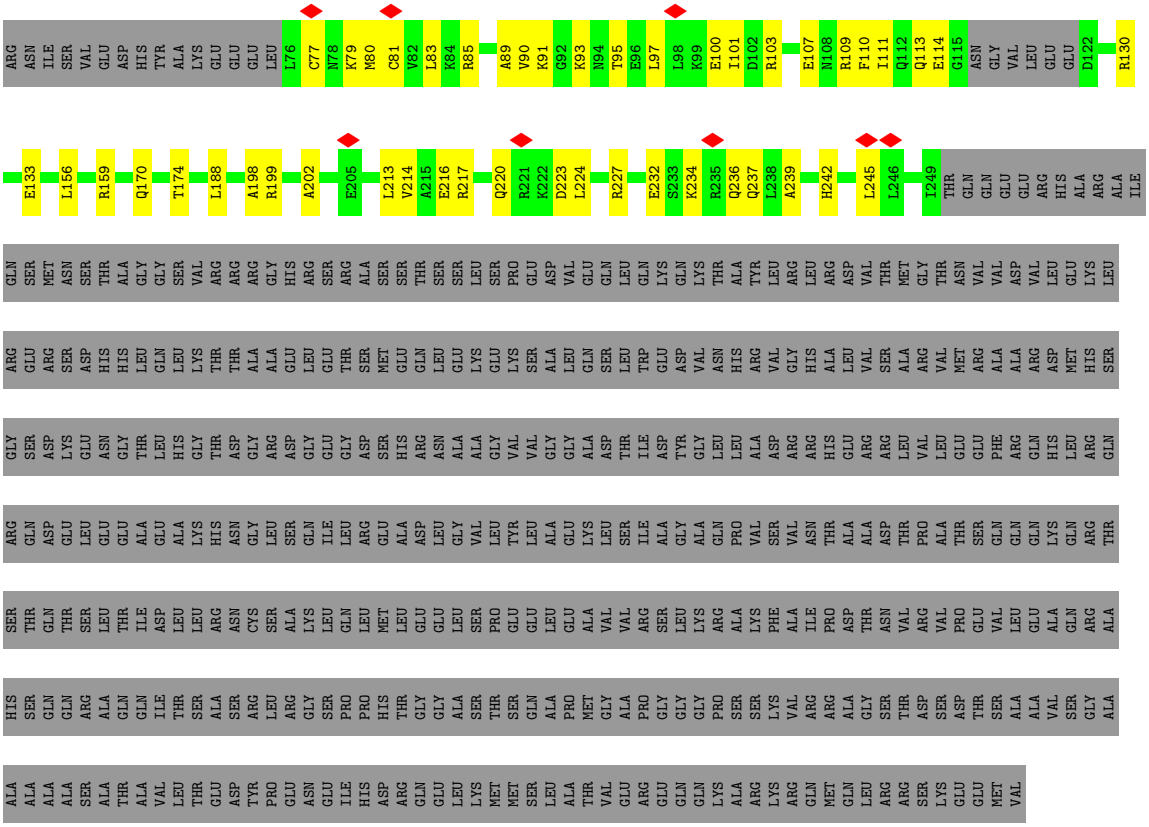
Chain 4I:



• Molecule 64: distal DC1

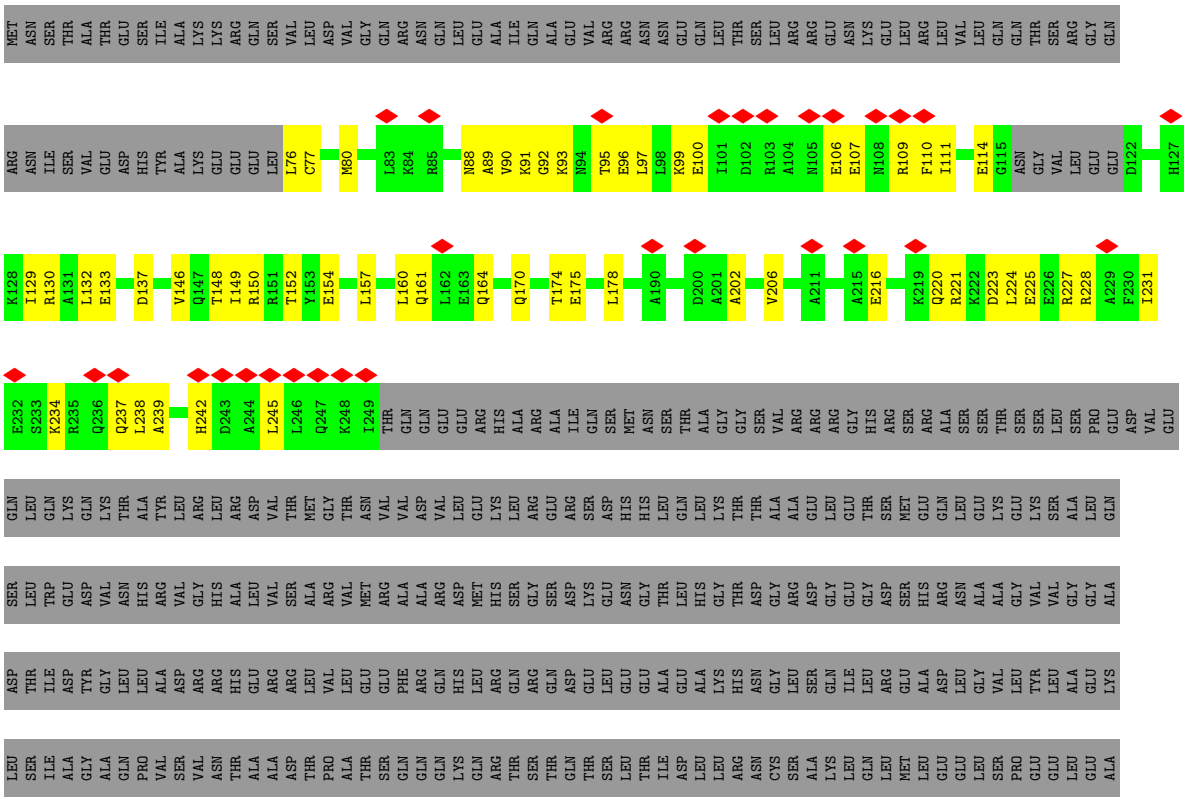
Chain 5B:

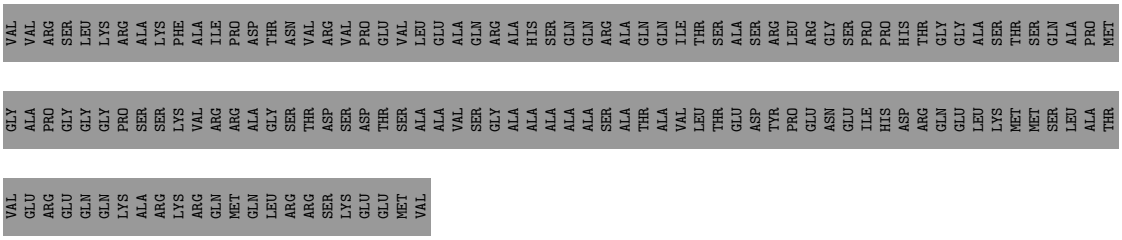




• Molecule 64: distal DC1

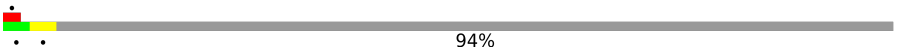
Chain 5C:

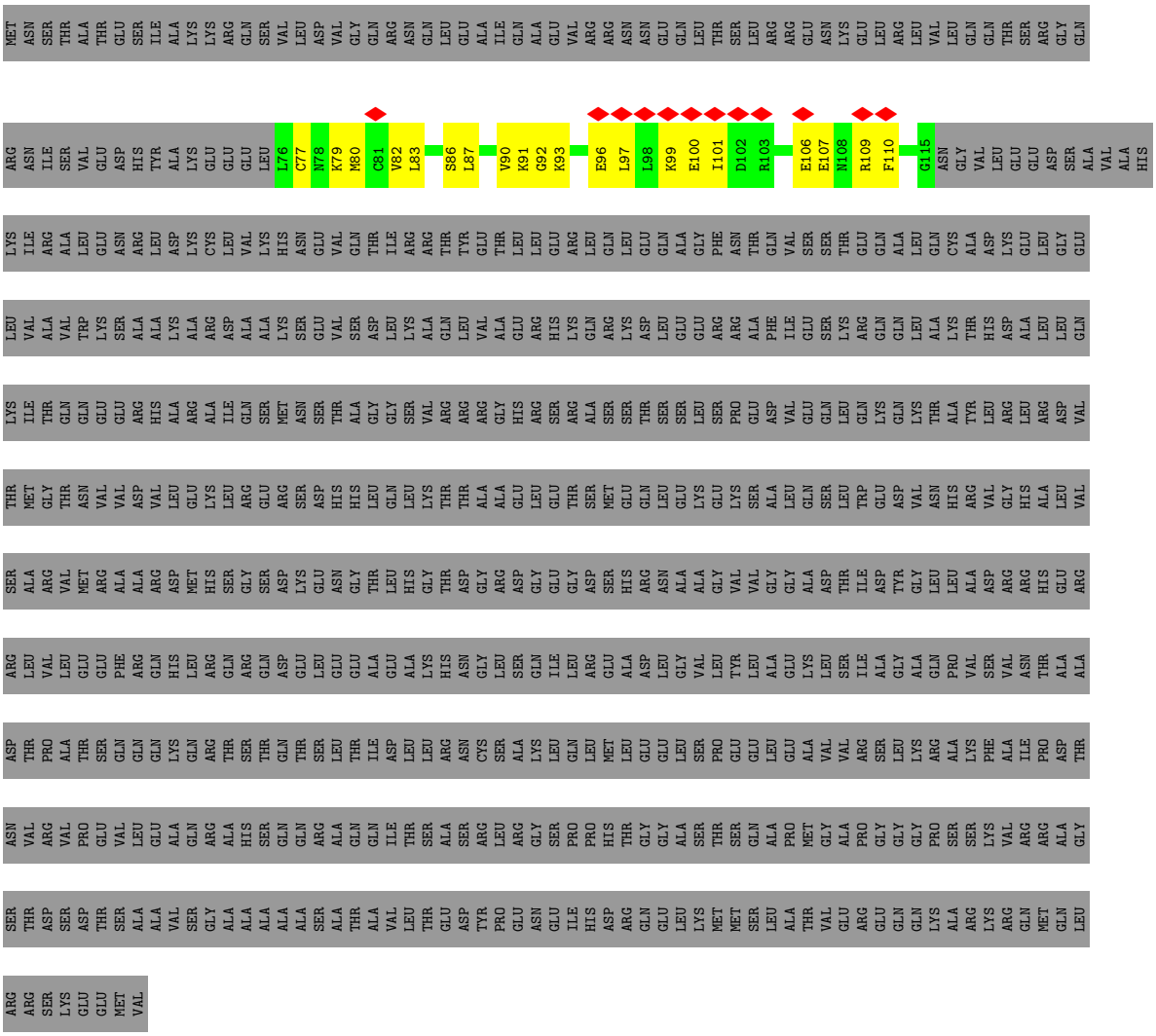




• Molecule 64: distal DC1

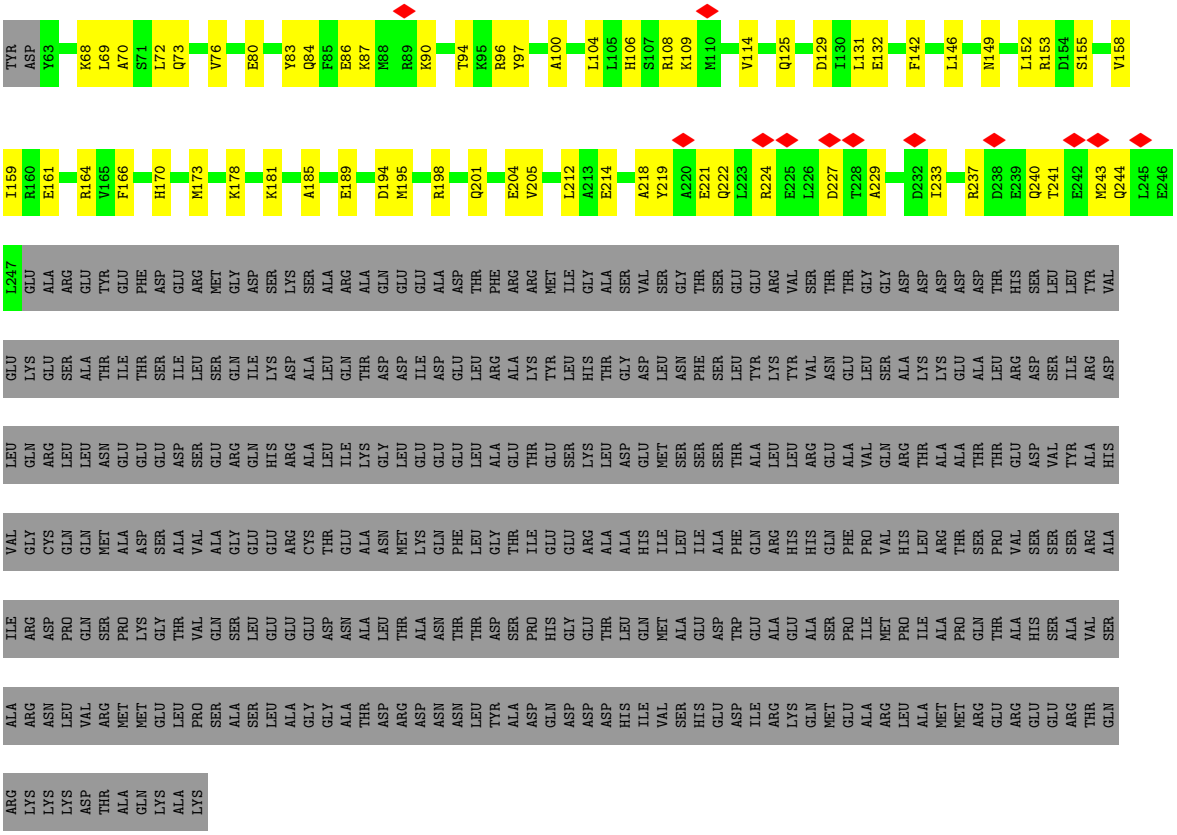
Chain 5D:





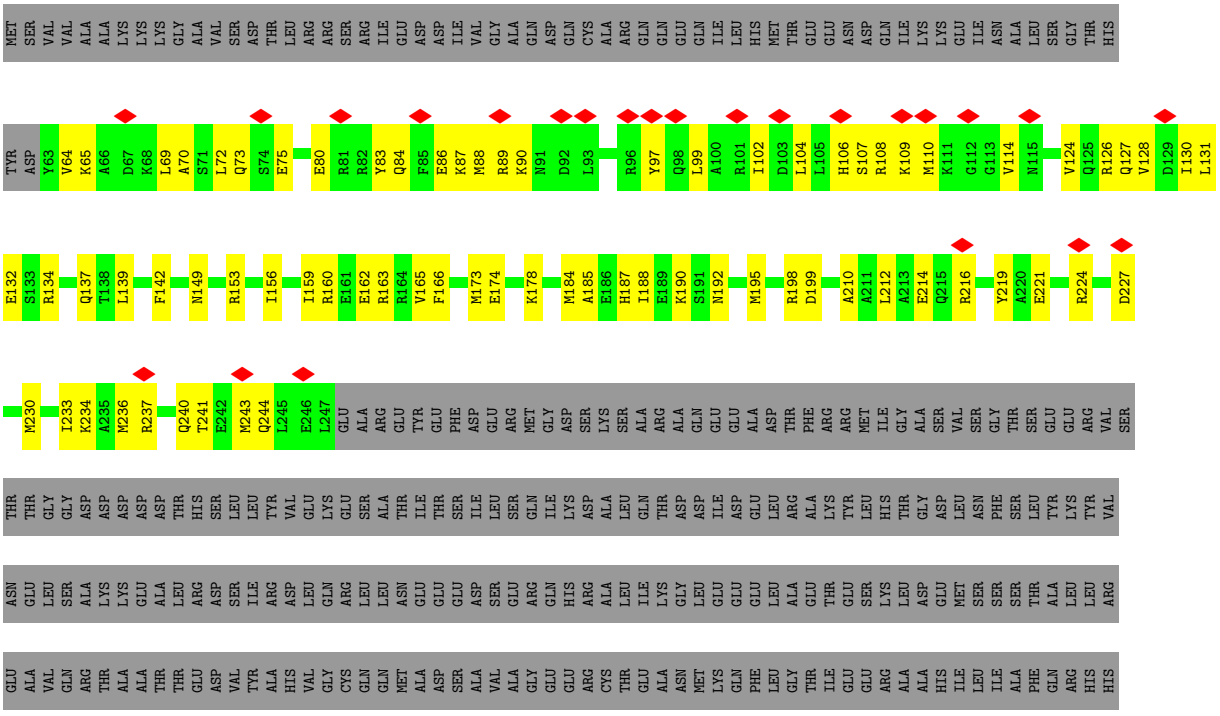
• Molecule 65: distal DC2

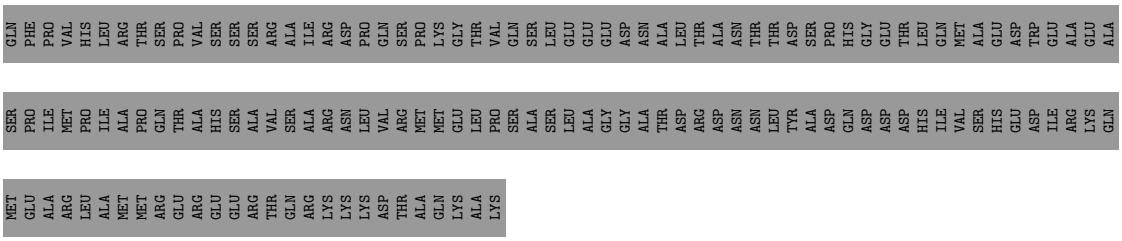
Chain 5G:



• Molecule 65: distal DC2

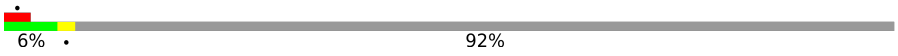
Chain 5H:

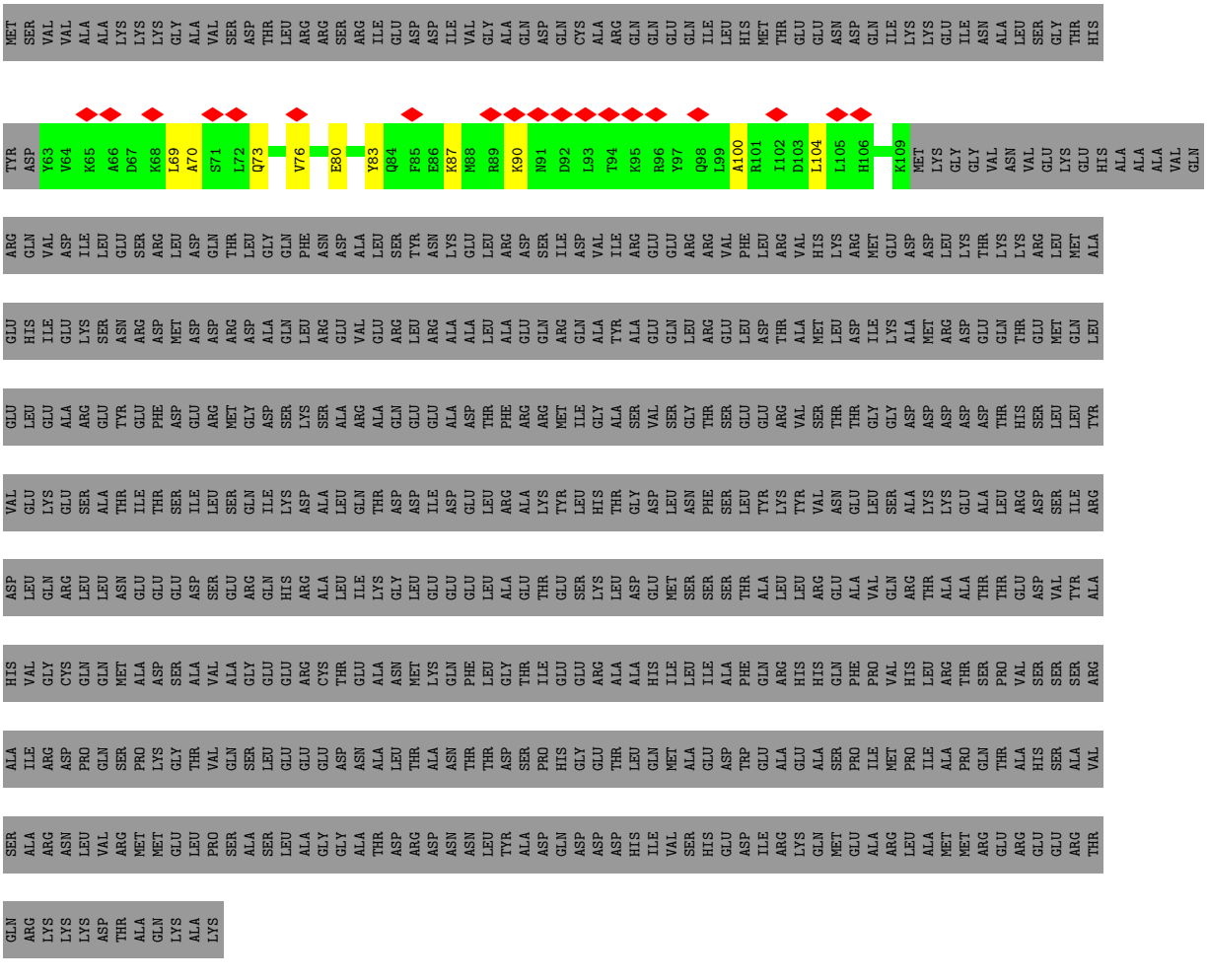




• Molecule 65: distal DC2

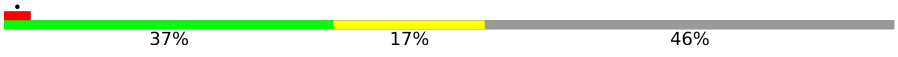
Chain 5I:

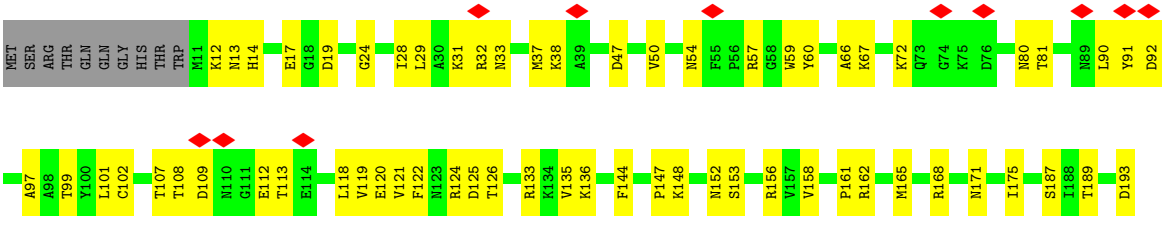


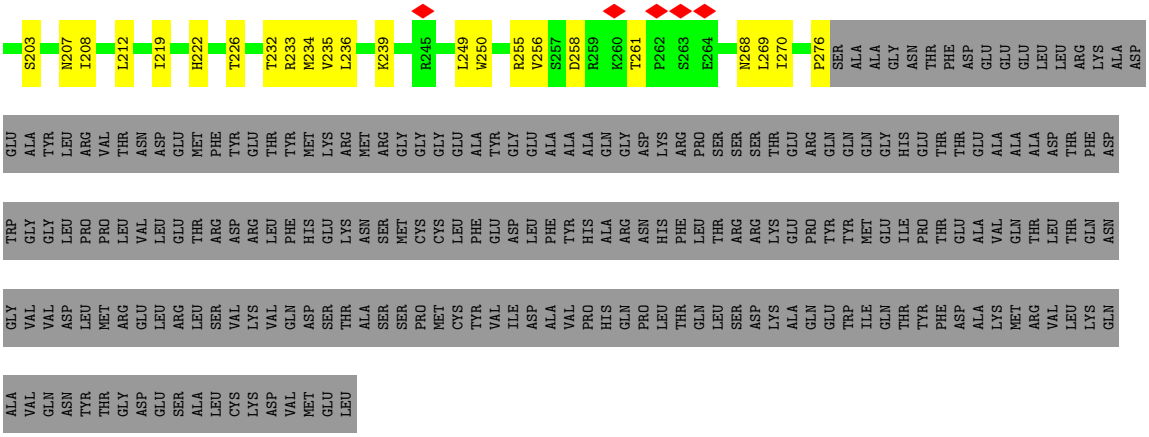


• Molecule 66: distal DC4

Chain 5K:

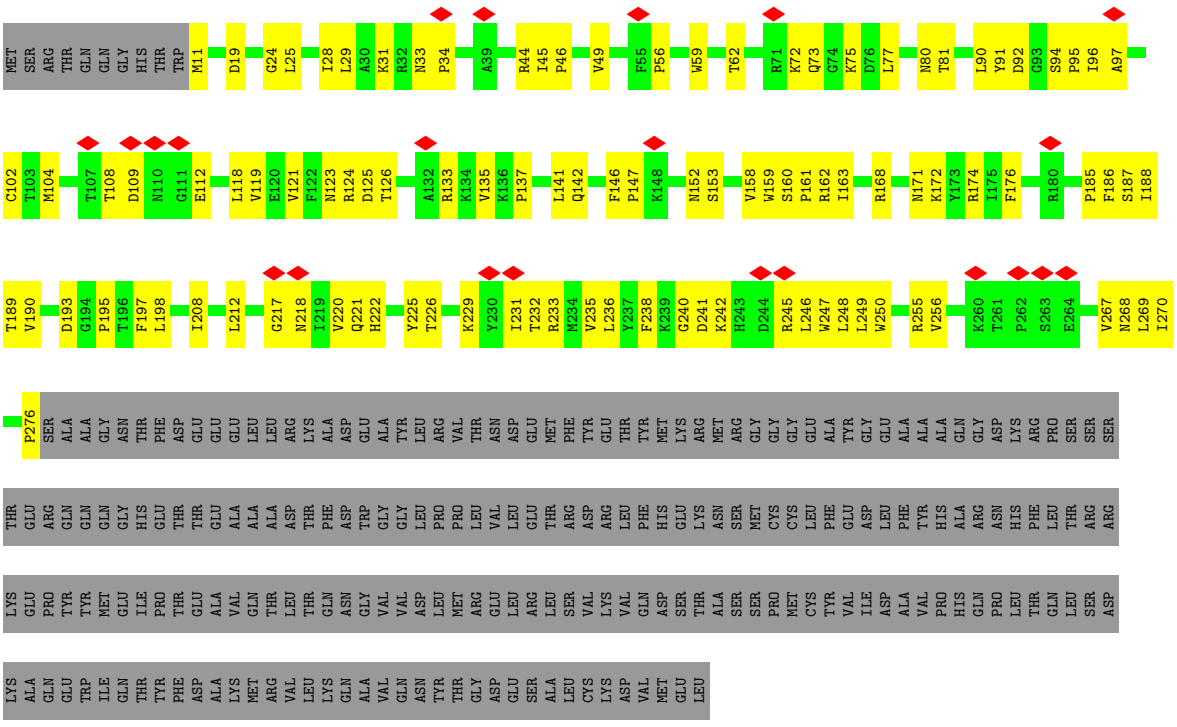






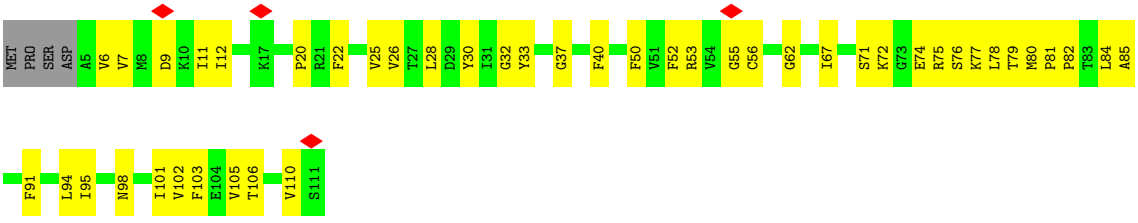
• Molecule 66: distal DC4

Chain 5L:



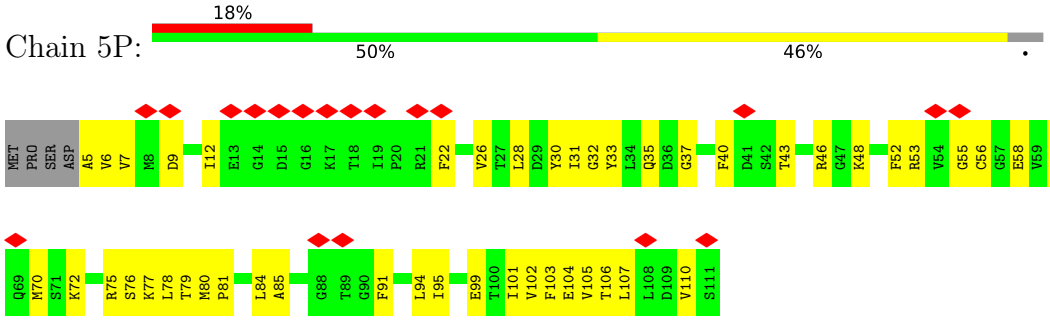
• Molecule 67: DC5

Chain 5O:



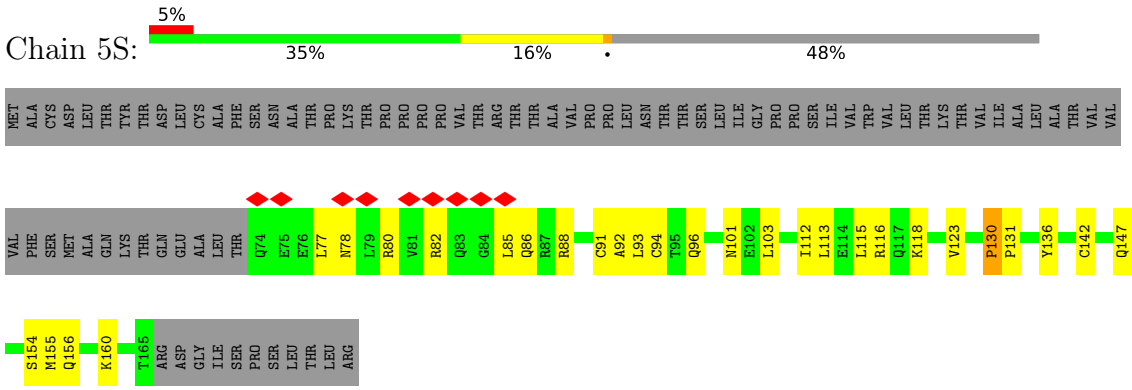
• Molecule 67: DC5

Chain 5P:



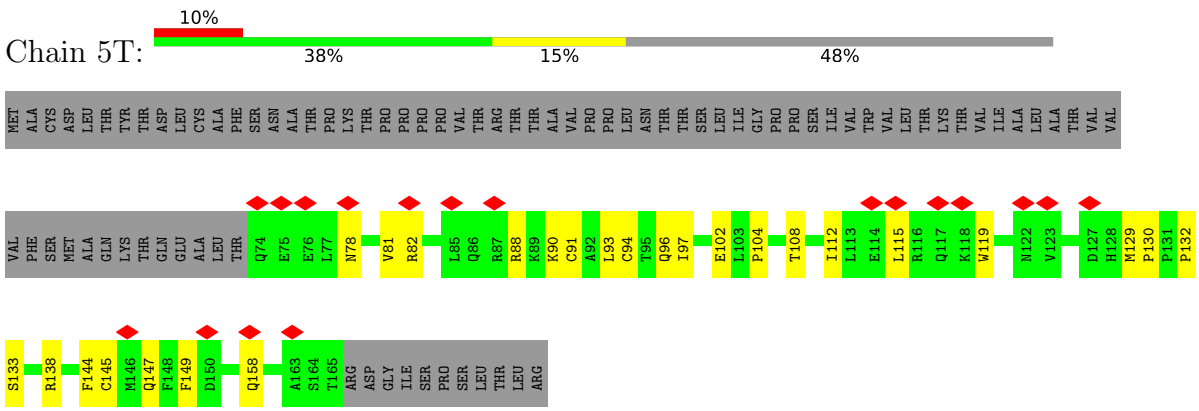
• Molecule 68: DC6

Chain 5S:



• Molecule 68: DC6

Chain 5T:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	533420	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	62.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.841	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.0435	Depositor
Map size (Å)	680.96, 680.96, 680.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, ATP, GTP, ZN, 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	A	0.15	0/3432	0.36	0/4637
1	AB	0.15	0/3351	0.36	0/4528
1	AD	0.15	0/3432	0.35	0/4637
1	AF	0.14	0/3432	0.34	0/4637
1	AH	0.19	0/3432	0.40	2/4637 (0.0%)
1	AJ	0.15	0/3432	0.35	0/4637
1	AL	0.14	0/3432	0.37	0/4637
1	AN	0.15	0/3351	0.35	0/4528
1	B	0.15	0/3334	0.34	0/4502
1	BB	0.14	0/3432	0.34	0/4637
1	BD	0.15	0/3440	0.38	0/4647
1	BF	0.14	0/3432	0.35	1/4637 (0.0%)
1	BH	0.29	0/3432	0.53	1/4637 (0.0%)
1	BJ	0.15	0/3432	0.37	0/4637
1	BL	0.15	0/3432	0.38	0/4637
1	BN	0.15	0/3432	0.40	0/4637
1	CA	0.16	0/3387	0.39	0/4575
1	CC	0.16	0/3440	0.39	0/4647
1	CE	0.15	0/3440	0.37	0/4647
1	CG	0.13	0/3440	0.36	0/4647
1	CI	0.14	0/3432	0.35	0/4637
1	CK	0.14	0/3432	0.34	0/4637
1	CM	0.17	0/3432	0.46	1/4637 (0.0%)
1	DA	0.15	0/3432	0.35	0/4637
1	DC	0.15	0/3432	0.36	0/4637
1	DE	0.15	0/3432	0.38	0/4637
1	DG	0.15	0/3432	0.37	0/4637
1	DI	0.14	0/3432	0.33	0/4637
1	DK	0.13	0/3432	0.34	0/4637
1	DM	0.17	0/3432	0.41	0/4637
1	E	0.16	0/3440	0.38	0/4647
1	EB	0.15	0/3440	0.37	0/4647

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	ED	0.16	0/3440	0.38	0/4647
1	EF	0.14	0/3440	0.36	0/4647
1	EH	0.14	0/3440	0.34	0/4647
1	EJ	0.15	0/3440	0.36	0/4647
1	EL	0.18	0/3432	0.44	0/4637
1	F	0.17	0/3432	0.40	0/4637
1	FB	0.16	0/3432	0.35	0/4637
1	FD	0.16	0/3432	0.37	0/4637
1	FF	0.16	0/3432	0.37	0/4637
1	FH	0.15	0/3432	0.36	0/4637
1	FJ	0.14	0/3430	0.36	0/4633
1	FL	0.17	0/3413	0.40	0/4610
1	G	0.13	0/3432	0.38	0/4637
1	GB	0.14	0/3432	0.35	0/4637
1	GD	0.16	0/3413	0.39	0/4610
1	GF	0.16	0/3432	0.41	0/4637
1	GH	0.15	0/3432	0.37	0/4637
1	GJ	0.16	0/3405	0.40	0/4599
1	GL	0.14	0/3432	0.39	0/4637
1	H	0.15	0/3432	0.37	0/4637
1	HB	0.17	0/3432	0.41	1/4637 (0.0%)
1	HD	0.16	0/3432	0.39	0/4637
1	HF	0.15	0/3432	0.36	0/4637
1	HH	0.15	0/3432	0.36	1/4637 (0.0%)
1	HJ	0.14	0/3432	0.36	0/4637
1	HL	0.15	0/3432	0.38	0/4637
1	I	0.16	0/3440	0.40	0/4647
1	IB	0.15	0/3432	0.37	0/4637
1	ID	0.14	0/3432	0.36	1/4637 (0.0%)
1	IF	0.14	0/3432	0.37	0/4637
1	IH	0.14	0/3432	0.34	0/4637
1	IJ	0.15	0/3432	0.36	0/4637
1	IL	0.18	0/3432	0.45	0/4637
1	JA	0.15	0/3432	0.36	0/4637
1	JC	0.15	0/3432	0.38	0/4637
1	JE	0.15	0/3432	0.40	0/4637
1	JG	0.15	0/3432	0.37	0/4637
1	JI	0.14	0/3432	0.34	0/4637
1	JK	0.17	0/3432	0.44	0/4637
1	JM	0.15	0/3413	0.37	0/4610
1	KA	0.15	0/3440	0.34	0/4647
1	KC	0.14	0/3432	0.36	0/4637
1	KE	0.15	0/3432	0.35	0/4637

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	KG	0.14	0/3432	0.34	0/4637
1	KI	0.14	0/3432	0.33	0/4637
1	KK	0.15	0/3432	0.40	0/4637
1	KM	0.14	0/3432	0.37	0/4637
1	LA	0.15	0/3432	0.38	0/4637
1	LC	0.14	0/3432	0.36	1/4637 (0.0%)
1	LE	0.16	0/3432	0.39	0/4637
1	LG	0.16	0/3432	0.39	0/4637
1	LI	0.14	0/3432	0.35	0/4637
1	LK	0.15	0/3432	0.36	0/4637
1	LM	0.17	0/3432	0.42	0/4637
1	LO	0.16	0/3432	0.40	0/4637
1	M	0.15	0/3432	0.35	0/4637
1	MB	0.15	0/3432	0.37	0/4637
1	MD	0.15	0/3432	0.36	0/4637
1	MF	0.16	0/3432	0.40	0/4637
1	MH	0.15	0/3432	0.37	0/4637
1	MJ	0.16	0/3432	0.43	0/4637
1	ML	0.15	0/3432	0.35	0/4637
1	MN	0.15	0/3432	0.36	0/4637
1	N	0.16	0/3358	0.41	0/4538
1	NB	0.14	0/3358	0.36	0/4538
1	ND	0.16	0/3418	0.40	0/4617
1	NF	0.14	0/3418	0.36	0/4617
1	NH	0.18	0/3413	0.39	1/4610 (0.0%)
1	NJ	0.14	0/3432	0.35	0/4637
1	NL	0.16	0/3413	0.42	0/4610
1	O	0.16	0/3413	0.40	0/4610
1	OB	0.15	0/3405	0.37	0/4599
1	OD	0.13	0/3413	0.34	0/4610
1	OF	0.15	0/3413	0.38	0/4610
1	OH	0.15	0/3413	0.37	0/4610
1	OJ	0.16	0/3413	0.39	0/4610
1	OL	0.18	0/3413	0.43	0/4610
1	P	0.16	0/3184	0.40	1/4303 (0.0%)
1	PB	0.15	0/3432	0.37	0/4637
1	PD	0.16	0/3432	0.39	0/4637
1	PF	0.15	0/3432	0.36	0/4637
1	PH	0.16	0/3412	0.39	0/4608
1	PJ	0.15	0/3432	0.34	0/4637
1	PL	0.17	0/3432	0.40	1/4637 (0.0%)
1	QA	0.16	0/3418	0.39	0/4617
1	QC	0.15	0/3418	0.34	0/4617

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	QE	0.16	0/3413	0.36	0/4610
1	QG	0.15	0/3418	0.34	0/4617
1	QI	0.15	0/3418	0.36	0/4617
1	QK	0.16	0/3418	0.39	0/4617
1	RA	0.16	0/3413	0.38	0/4610
1	RC	0.15	0/3432	0.36	0/4637
1	RE	0.15	0/3413	0.33	0/4610
1	RG	0.15	0/3413	0.34	0/4610
1	RI	0.14	0/3411	0.34	0/4606
1	RK	0.15	0/3425	0.38	0/4627
1	S	0.14	0/3405	0.37	0/4599
1	SB	0.16	0/3405	0.38	1/4599 (0.0%)
1	SD	0.16	0/3405	0.36	0/4599
1	SF	0.15	0/3405	0.36	0/4599
1	SH	0.15	0/3425	0.37	0/4627
1	SJ	0.15	0/3418	0.38	0/4617
1	T	0.16	0/3418	0.38	0/4617
1	TB	0.17	0/3425	0.39	0/4627
1	TD	0.17	0/3413	0.41	0/4610
1	TF	0.16	0/3418	0.38	0/4617
1	TH	0.14	0/3413	0.37	0/4610
1	TJ	0.16	0/3432	0.39	0/4637
1	TL	0.17	0/3418	0.44	0/4617
1	U	0.15	0/3405	0.35	0/4599
1	UB	0.14	0/3405	0.34	0/4599
1	UD	0.14	0/3405	0.35	0/4599
1	UF	0.15	0/3405	0.36	0/4599
1	UH	0.14	0/3405	0.36	0/4599
1	UJ	0.15	0/3418	0.36	0/4617
1	UL	0.16	0/3413	0.39	0/4610
1	V	0.17	0/3425	0.39	1/4627 (0.0%)
1	VB	0.14	0/3413	0.36	0/4610
1	VD	0.15	0/3418	0.38	0/4617
1	VF	0.14	0/3425	0.34	0/4627
1	VH	0.15	0/3405	0.36	0/4599
1	VJ	0.16	0/3432	0.38	0/4637
1	VL	0.14	0/3432	0.34	0/4637
1	W	0.15	0/3405	0.35	0/4599
1	WB	0.14	0/3405	0.36	0/4599
1	WD	0.14	0/3405	0.34	0/4599
1	WF	0.15	0/3418	0.36	0/4617
1	WH	0.14	0/3405	0.35	0/4599
1	WJ	0.14	0/3405	0.35	0/4599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	WL	0.14	0/3413	0.35	0/4610
2	AA	0.14	0/3400	0.35	0/4614
2	AC	0.15	0/3424	0.37	0/4647
2	AE	0.14	0/3466	0.36	0/4704
2	AG	0.14	0/3423	0.38	1/4644 (0.0%)
2	AI	0.14	0/3466	0.37	0/4704
2	AK	0.15	0/3466	0.37	0/4704
2	AM	0.15	0/3400	0.37	0/4614
2	BA	0.13	0/3392	0.33	0/4602
2	BC	0.15	0/3400	0.40	0/4614
2	BE	0.13	0/3392	0.34	0/4602
2	BG	0.15	0/3400	0.38	0/4614
2	BI	0.17	0/3466	0.41	1/4704 (0.0%)
2	BK	0.14	0/3392	0.35	0/4602
2	BM	0.15	0/3400	0.37	0/4614
2	C	0.16	0/3466	0.35	0/4704
2	CB	0.15	0/3466	0.36	1/4704 (0.0%)
2	CD	0.16	0/3466	0.39	1/4704 (0.0%)
2	CF	0.12	0/3400	0.32	0/4614
2	CH	0.14	0/3466	0.37	0/4704
2	CJ	0.13	0/3466	0.33	0/4704
2	CL	0.16	0/3466	0.39	0/4704
2	D	0.15	0/3400	0.36	0/4614
2	DB	0.15	0/3400	0.34	0/4614
2	DD	0.15	0/3400	0.36	0/4614
2	DF	0.13	0/3408	0.33	0/4625
2	DH	0.14	0/3398	0.34	0/4610
2	DJ	0.13	0/3400	0.33	0/4614
2	DL	0.15	0/3400	0.38	0/4614
2	EA	0.15	0/3400	0.35	0/4614
2	EC	0.15	0/3466	0.35	0/4704
2	EE	0.13	0/3417	0.33	0/4637
2	EG	0.15	0/3422	0.36	0/4644
2	EI	0.14	0/3408	0.35	0/4625
2	EK	0.14	0/3408	0.36	0/4625
2	FA	0.15	0/3466	0.38	0/4704
2	FC	0.15	0/3431	0.39	0/4656
2	FE	0.16	0/3414	0.39	0/4633
2	FG	0.17	0/3408	0.37	0/4625
2	FI	0.14	0/3392	0.35	0/4602
2	FK	0.16	0/3408	0.41	1/4625 (0.0%)
2	GA	0.15	0/3400	0.37	0/4614
2	GC	0.14	0/3400	0.38	0/4614

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	GE	0.16	0/3408	0.36	0/4625
2	GG	0.14	0/3400	0.35	0/4614
2	GI	0.15	0/3400	0.37	0/4614
2	GK	0.15	0/3400	0.38	0/4614
2	HA	0.15	0/3400	0.40	0/4614
2	HC	0.13	0/3400	0.37	1/4614 (0.0%)
2	HE	0.15	0/3466	0.39	1/4704 (0.0%)
2	HG	0.15	0/3414	0.40	1/4633 (0.0%)
2	HI	0.15	0/3406	0.38	0/4621
2	HK	0.16	0/3414	0.39	0/4633
2	HM	0.16	0/3400	0.42	0/4614
2	IA	0.16	0/3400	0.39	0/4614
2	IC	0.15	0/3414	0.37	0/4633
2	IE	0.14	0/3466	0.37	0/4704
2	IG	0.13	0/3466	0.35	0/4704
2	II	0.14	0/3466	0.36	0/4704
2	IK	0.17	0/3400	0.40	0/4614
2	IM	0.15	0/3400	0.40	0/4614
2	J	0.18	0/3466	0.42	0/4704
2	JB	0.14	0/3466	0.37	0/4704
2	JD	0.15	0/3400	0.38	1/4614 (0.0%)
2	JF	0.15	0/3400	0.37	0/4614
2	JH	0.14	0/3413	0.36	0/4631
2	JJ	0.16	0/3414	0.37	1/4633 (0.0%)
2	JL	0.17	0/3414	0.40	0/4633
2	JN	0.17	0/3466	0.45	0/4704
2	K	0.16	0/3429	0.40	0/4652
2	KB	0.14	0/3466	0.36	0/4704
2	KD	0.14	0/3400	0.35	0/4614
2	KF	0.15	0/3466	0.37	2/4704 (0.0%)
2	KH	0.16	0/3406	0.38	0/4622
2	KJ	0.14	0/3417	0.36	1/4637 (0.0%)
2	KL	0.16	0/3466	0.39	0/4704
2	KN	0.15	0/3466	0.37	0/4704
2	L	0.14	0/3466	0.36	0/4704
2	LB	0.15	0/3417	0.37	0/4637
2	LD	0.15	0/3392	0.36	0/4603
2	LF	0.15	0/3466	0.38	1/4704 (0.0%)
2	LH	0.19	0/3466	0.41	0/4704
2	LJ	0.15	0/3466	0.38	0/4704
2	LL	0.16	0/3466	0.36	0/4704
2	LN	0.15	0/3417	0.37	0/4637
2	MA	0.14	0/3406	0.37	0/4622

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	MC	0.15	0/3451	0.36	0/4684
2	ME	0.15	0/3439	0.37	0/4666
2	MG	0.14	0/3466	0.37	0/4704
2	MI	0.14	0/3466	0.36	0/4704
2	MK	0.16	0/3466	0.40	0/4704
2	MM	0.16	0/3406	0.40	0/4622
2	NA	0.14	0/3466	0.37	0/4704
2	NC	0.14	0/3466	0.36	0/4704
2	NE	0.14	0/3466	0.36	0/4704
2	NG	0.14	0/3466	0.37	0/4704
2	NI	0.16	0/3466	0.39	1/4704 (0.0%)
2	NK	0.16	0/3466	0.41	0/4704
2	NM	0.16	0/3466	0.43	0/4704
2	OA	0.15	0/3414	0.38	0/4633
2	OC	0.14	0/3408	0.37	0/4625
2	OE	0.14	0/3408	0.36	0/4625
2	OG	0.16	0/3466	0.38	0/4704
2	OI	0.15	0/3400	0.38	0/4614
2	OK	0.16	0/3400	0.41	0/4614
2	OM	0.17	0/3423	0.40	0/4645
2	PA	0.15	0/3400	0.38	0/4614
2	PC	0.14	0/3408	0.35	0/4625
2	PE	0.16	0/3408	0.35	0/4625
2	PG	0.15	0/3466	0.37	0/4704
2	PI	0.16	0/3408	0.38	0/4625
2	PK	0.17	0/3414	0.37	0/4633
2	PM	0.18	0/3414	0.43	0/4633
2	Q	0.16	0/3466	0.39	0/4704
2	QB	0.16	0/3394	0.39	0/4606
2	QD	0.17	0/3400	0.42	1/4614 (0.0%)
2	QF	0.15	0/3400	0.36	0/4614
2	QH	0.16	0/3466	0.37	0/4704
2	QJ	0.16	0/3408	0.36	0/4625
2	QL	0.17	0/3414	0.45	0/4633
2	R	0.15	0/3466	0.38	0/4704
2	RB	0.17	0/3408	0.40	2/4625 (0.0%)
2	RD	0.17	0/3408	0.38	0/4625
2	RF	0.16	0/3408	0.36	0/4625
2	RH	0.17	0/3400	0.40	1/4614 (0.0%)
2	RJ	0.17	0/3400	0.40	1/4614 (0.0%)
2	RL	0.16	0/3406	0.39	0/4622
2	SA	0.15	0/3408	0.35	0/4625
2	SC	0.15	0/3406	0.38	0/4622

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	SE	0.15	0/3406	0.36	0/4622
2	SG	0.14	0/3408	0.32	0/4625
2	SI	0.15	0/3400	0.36	0/4614
2	SK	0.18	1/3414 (0.0%)	0.41	0/4633
2	TA	0.15	0/3400	0.35	0/4614
2	TC	0.16	0/3384	0.39	0/4592
2	TE	0.14	0/3400	0.34	0/4614
2	TG	0.14	0/3408	0.33	0/4625
2	TI	0.14	0/3400	0.33	0/4614
2	TK	0.15	0/3424	0.38	0/4647
2	UA	0.15	0/3400	0.37	0/4614
2	UC	0.14	0/3392	0.35	0/4603
2	UE	0.15	0/3400	0.39	0/4614
2	UG	0.16	0/3408	0.36	0/4625
2	UI	0.14	0/3400	0.35	0/4614
2	UK	0.15	0/3400	0.36	1/4614 (0.0%)
2	VA	0.15	0/3408	0.38	0/4625
2	VC	0.15	0/3408	0.38	0/4625
2	VE	0.14	0/3408	0.34	0/4625
2	VG	0.13	0/3408	0.34	0/4625
2	VI	0.13	0/3412	0.33	0/4629
2	VK	0.15	0/3400	0.34	0/4614
2	VM	0.16	0/3431	0.41	0/4656
2	WA	0.14	0/3466	0.35	0/4704
2	WC	0.14	0/3408	0.35	0/4625
2	WE	0.13	0/3466	0.34	0/4704
2	WG	0.15	0/3408	0.36	1/4625 (0.0%)
2	WI	0.15	0/3466	0.39	0/4704
2	WK	0.13	0/3408	0.34	0/4625
2	WM	0.14	0/3466	0.36	0/4704
3	X	0.13	0/1544	0.33	0/2083
3	XA	0.15	0/1544	0.37	1/2083 (0.0%)
3	XB	0.13	0/1544	0.35	0/2083
3	XC	0.13	0/1544	0.36	0/2083
3	XD	0.13	0/1544	0.36	0/2083
3	XE	0.15	0/1544	0.39	0/2083
3	XF	0.13	0/1544	0.37	0/2083
4	XM	0.14	0/2094	0.33	0/2833
4	XO	0.15	0/2102	0.32	0/2844
4	XQ	0.13	0/2102	0.34	0/2844
4	XR	0.22	0/2105	0.40	0/2847
5	XN	0.14	0/2172	0.34	0/2940
5	XP	0.15	0/2172	0.36	0/2940

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
6	0	0.15	0/2040	0.38	0/2754
6	0A	0.23	0/2040	0.43	0/2754
7	0C	0.15	0/955	0.39	0/1293
7	0D	0.16	0/2785	0.43	1/3777 (0.0%)
8	0F	0.12	0/1449	0.34	1/1930 (0.1%)
8	0G	0.17	0/2966	0.40	0/3932
8	0H	0.16	0/230	0.48	0/307
8	0I	0.17	0/2384	0.44	0/3167
8	0J	0.17	0/1910	0.45	0/2530
9	0L	0.12	0/4845	0.35	0/6569
9	0M	0.12	0/4845	0.37	0/6569
9	0N	0.13	0/4845	0.39	0/6569
9	0O	0.17	0/2401	0.45	0/3253
10	0R	0.17	0/2646	0.45	0/3521
10	0S	0.18	0/1888	0.50	0/2513
11	0U	0.13	0/2621	0.35	0/3555
12	0W	0.12	0/2645	0.33	0/3600
13	0Y	0.12	0/1875	0.31	0/2538
13	0Z	0.13	0/1888	0.34	0/2554
13	0a	0.10	0/430	0.33	0/584
14	0c	0.17	0/1965	0.39	1/2631 (0.0%)
14	0d	0.20	0/2190	0.44	0/2934
15	0f	0.14	0/1283	0.37	0/1737
15	0g	0.11	0/223	0.30	0/303
16	0k	0.14	0/5705	0.37	0/7710
16	0l	0.13	0/5141	0.33	1/6953 (0.0%)
17	0m	0.18	0/1164	0.50	0/1550
17	0n	0.25	0/3406	0.54	0/4525
17	0o	0.11	0/173	0.33	0/232
18	0p	0.16	0/915	0.38	0/1222
19	0r	0.18	0/2076	0.41	0/2806
20	0t	0.14	0/2117	0.38	0/2877
20	0u	0.14	0/1819	0.36	0/2476
21	0v	0.13	0/588	0.35	0/788
21	0w	0.16	0/3753	0.40	0/5006
21	0x	0.13	0/917	0.32	0/1228
22	0z	0.31	0/1177	0.53	0/1585
22	1w	0.14	0/1509	0.37	0/2035
22	1x	0.21	0/1714	0.44	0/2310
22	1y	0.20	0/733	0.43	0/989
23	1A	0.16	0/2310	0.41	0/3075
23	1B	0.18	0/1682	0.45	0/2236
23	1D	0.16	0/467	0.43	0/616

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
23	1E	0.16	0/3083	0.38	0/4112
23	1F	0.18	0/642	0.42	0/856
24	1H	0.12	0/4800	0.32	0/6491
24	1I	0.12	0/5391	0.33	0/7280
24	1J	0.12	0/5470	0.33	0/7387
24	1K	0.13	0/4799	0.33	0/6489
25	1O	0.12	0/5862	0.31	0/7901
26	1Q	0.13	0/5371	0.35	1/7261 (0.0%)
27	1S	0.14	0/5967	0.34	0/8066
27	1T	0.15	0/1822	0.41	0/2458
28	1U	0.14	0/969	0.33	0/1318
28	1V	0.13	0/378	0.34	0/508
28	1X	0.13	0/969	0.32	0/1318
28	1Y	0.14	0/1357	0.36	0/1833
28	1a	0.11	0/460	0.27	0/627
28	1b	0.45	0/1347	0.74	2/1826 (0.1%)
28	1c	0.15	0/268	0.41	0/361
28	1d	0.13	0/969	0.31	0/1318
28	1e	0.10	0/378	0.25	0/508
28	1g	0.14	0/969	0.36	0/1318
28	1h	0.25	0/1248	0.48	0/1685
28	4V	0.13	0/500	0.30	0/679
28	4W	0.34	0/1512	0.68	6/2048 (0.3%)
29	1j	0.12	0/936	0.29	0/1267
29	1k	0.15	0/826	0.37	0/1128
29	1l	0.10	0/936	0.32	0/1267
29	1m	0.14	0/433	0.38	0/591
30	1o	0.11	0/1059	0.32	0/1435
31	1q	0.14	0/1708	0.37	2/2297 (0.1%)
31	1r	0.14	0/875	0.31	0/1164
31	1s	0.15	0/1471	0.28	0/1978
31	1t	0.15	0/620	0.45	0/817
32	2B	0.16	0/2020	0.35	0/2728
32	2C	0.15	0/1852	0.38	1/2496 (0.0%)
33	2F	0.24	0/2316	0.46	0/3146
33	2G	0.23	0/2308	0.44	1/3135 (0.0%)
33	2H	0.24	0/2346	0.43	0/3188
33	2I	0.28	0/1986	0.45	0/2689
34	2L	0.14	0/1473	0.37	0/2003
35	2N	0.16	0/1143	0.33	0/1555
35	2O	0.14	0/1369	0.36	0/1856
36	2Q	0.14	0/2383	0.34	0/3232
37	2S	0.13	0/1845	0.36	0/2506

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	2U	0.13	0/1840	0.35	0/2491
38	2V	0.15	0/888	0.41	0/1202
39	2X	0.14	0/1809	0.32	0/2439
40	2Z	0.13	0/2305	0.36	0/3116
41	2b	0.22	0/1016	0.42	0/1358
41	2c	0.26	0/2107	0.46	0/2794
41	2e	0.25	0/2760	0.54	2/3672 (0.1%)
41	2f	0.38	0/458	0.68	1/611 (0.2%)
41	2h	0.21	0/1990	0.46	0/2642
41	2i	0.20	0/1311	0.41	0/1737
41	2k	0.29	0/1383	0.52	0/1846
41	2l	0.16	0/2245	0.37	0/2979
41	2n	0.17	0/365	0.53	0/489
41	2o	0.23	0/2472	0.49	0/3283
41	2p	0.35	0/428	0.74	0/569
42	2r	0.18	0/2528	0.36	0/3431
43	2t	0.13	0/1750	0.38	0/2372
44	2v	0.20	0/2308	0.46	1/3111 (0.0%)
44	2w	0.16	0/3370	0.40	0/4575
45	2y	0.12	0/2372	0.32	0/3216
45	2z	0.43	0/1465	0.66	2/1989 (0.1%)
46	3B	0.11	0/3375	0.31	0/4571
47	3D	0.21	0/3268	0.41	0/4423
48	3F	0.16	0/1269	0.43	0/1696
48	3G	0.13	0/741	0.38	0/989
48	3H	0.16	0/840	0.45	0/1121
48	3I	0.17	0/646	0.51	0/861
48	3L	0.12	0/250	0.33	0/331
48	3M	0.07	0/250	0.21	0/331
49	3P	0.15	0/2031	0.37	0/2750
49	3Q	0.16	0/3890	0.37	0/5277
50	3S	0.11	0/183	0.21	0/242
51	X1	0.16	0/310	0.30	0/422
52	3U	0.12	0/1100	0.32	0/1501
53	3W	0.12	0/1282	0.29	0/1717
53	3X	0.14	0/393	0.40	0/530
54	3Z	0.24	0/1431	0.41	0/1933
54	3a	0.12	0/734	0.34	0/998
54	4Y	0.08	0/125	0.22	0/170
55	3b	0.21	0/1139	0.44	0/1526
56	3d	0.16	0/1259	0.44	2/1692 (0.1%)
57	3f	0.13	0/1426	0.38	0/1897
57	3g	0.12	0/1426	0.32	0/1897

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
57	3h	0.10	0/1426	0.27	0/1897
57	3i	0.22	0/1426	0.66	1/1897 (0.1%)
58	3m	0.15	0/1229	0.38	0/1638
59	3o	0.14	0/473	0.49	0/642
59	3p	0.16	0/1195	0.40	0/1614
59	4O	0.26	0/1444	0.44	0/1951
59	4P	0.12	0/548	0.33	0/742
59	4a	0.14	0/1273	0.33	0/1719
59	4b	0.13	0/548	0.27	0/742
60	3r	0.23	0/1115	0.45	0/1497
60	3s	0.22	0/1115	0.46	0/1497
60	3t	0.32	0/541	0.60	0/726
61	3w	0.23	0/1410	0.40	0/1916
61	3x	0.30	0/1018	0.49	0/1381
62	4A	0.11	0/236	0.33	0/322
62	4B	0.28	0/1637	0.43	0/2225
63	4I	0.12	0/639	0.29	0/863
64	5B	0.11	0/1356	0.29	0/1811
64	5C	0.19	0/1356	0.51	0/1811
64	5D	0.29	0/321	0.70	0/425
65	5G	0.11	0/1552	0.29	0/2068
65	5H	0.17	0/1552	0.45	0/2068
65	5I	0.14	0/405	0.37	0/537
66	5K	0.11	0/2204	0.29	0/2980
66	5L	0.12	0/2204	0.35	0/2980
67	5O	0.13	0/826	0.32	0/1117
67	5P	0.14	0/826	0.38	0/1117
68	5S	0.27	1/762 (0.1%)	0.40	0/1022
68	5T	0.15	0/762	0.41	0/1022
All	All	0.16	2/1389933 (0.0%)	0.38	63/1880072 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AB	0	1
1	BH	0	1
1	DE	0	1
1	EH	0	1
1	HB	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	HF	0	1
1	JK	0	1
1	SH	0	1
1	SJ	0	1
1	TF	0	1
1	W	0	1
2	FE	0	1
2	MG	0	1
2	QD	0	1
2	RF	0	1
2	WM	0	1
6	0A	0	1
8	0I	0	1
9	0O	0	1
17	0n	0	2
27	1S	0	1
28	4W	0	1
33	2H	0	1
41	2c	0	1
41	2f	0	2
41	2i	0	1
41	2k	0	1
41	2l	0	1
41	2o	0	1
44	2v	0	1
44	2w	0	1
59	4O	0	1
59	4P	0	1
60	3s	0	1
All	All	0	36

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	5S	130	PRO	CA-C	5.41	1.54	1.51
2	SK	47	ASP	CA-CB	5.33	1.61	1.53

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	2z	188	PRO	CA-N-CD	-11.78	95.51	112.00
2	RH	298	PRO	CA-N-CD	-11.21	96.30	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	4W	20	CYS	CB-CA-C	-9.71	90.00	110.31
1	HH	80	PRO	CA-N-CD	-8.96	99.45	112.00
2	HE	298	PRO	CA-N-CD	-8.75	99.75	112.00

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AB	267	MET	Peptide
1	BH	77	ARG	Sidechain
1	DE	271	ALA	Peptide
1	EH	271	ALA	Peptide
2	FE	338	LYS	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3362	0	3235	147	0
1	AB	3283	0	3160	140	0
1	AD	3362	0	3233	136	0
1	AF	3362	0	3235	148	0
1	AH	3362	0	3235	151	0
1	AJ	3362	0	3235	137	0
1	AL	3362	0	3235	133	0
1	AN	3283	0	3160	126	0
1	B	3270	0	3155	125	0
1	BB	3362	0	3235	139	0
1	BD	3370	0	3247	113	0
1	BF	3362	0	3235	138	0
1	BH	3362	0	3235	156	0
1	BJ	3362	0	3235	142	0
1	BL	3362	0	3235	131	0
1	BN	3362	0	3235	113	0
1	CA	3319	0	3200	143	0
1	CC	3370	0	3246	111	0
1	CE	3370	0	3245	148	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CG	3370	0	3247	105	0
1	CI	3362	0	3235	127	0
1	CK	3362	0	3234	139	0
1	CM	3362	0	3235	136	0
1	DA	3362	0	3235	105	0
1	DC	3362	0	3235	116	0
1	DE	3362	0	3233	119	0
1	DG	3362	0	3235	121	0
1	DI	3362	0	3235	105	0
1	DK	3362	0	3235	117	0
1	DM	3362	0	3235	147	0
1	E	3370	0	3245	129	0
1	EB	3370	0	3247	139	0
1	ED	3370	0	3245	114	0
1	EF	3370	0	3247	126	0
1	EH	3370	0	3247	132	0
1	EJ	3370	0	3245	125	0
1	EL	3362	0	3233	145	0
1	F	3362	0	3235	145	0
1	FB	3362	0	3235	128	0
1	FD	3362	0	3235	138	0
1	FF	3362	0	3235	142	0
1	FH	3362	0	3235	132	0
1	FJ	3361	0	3230	126	0
1	FL	3343	0	3214	133	0
1	G	3362	0	3233	124	0
1	GB	3362	0	3235	142	0
1	GD	3343	0	3213	158	0
1	GF	3362	0	3235	149	0
1	GH	3362	0	3235	137	0
1	GJ	3335	0	3210	143	0
1	GL	3362	0	3235	132	0
1	H	3362	0	3235	139	0
1	HB	3362	0	3234	147	0
1	HD	3362	0	3235	146	0
1	HF	3362	0	3235	129	0
1	HH	3362	0	3235	127	0
1	HJ	3362	0	3235	126	0
1	HL	3362	0	3235	165	0
1	I	3370	0	3247	170	0
1	IB	3362	0	3235	121	0
1	ID	3362	0	3235	137	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	IF	3362	0	3235	146	0
1	IH	3362	0	3235	118	0
1	IJ	3362	0	3235	127	0
1	IL	3362	0	3235	174	0
1	JA	3362	0	3235	141	0
1	JC	3362	0	3235	148	0
1	JE	3362	0	3235	132	0
1	JG	3362	0	3235	133	0
1	JI	3362	0	3235	117	0
1	JK	3362	0	3234	176	0
1	JM	3343	0	3214	139	0
1	KA	3370	0	3247	119	0
1	KC	3362	0	3235	128	0
1	KE	3362	0	3235	145	0
1	KG	3362	0	3234	120	0
1	KI	3362	0	3235	110	0
1	KK	3362	0	3235	156	0
1	KM	3362	0	3235	142	0
1	LA	3362	0	3235	142	0
1	LC	3362	0	3235	135	0
1	LE	3362	0	3235	162	0
1	LG	3362	0	3235	176	0
1	LI	3362	0	3235	147	0
1	LK	3362	0	3235	179	0
1	LM	3362	0	3235	154	0
1	LO	3362	0	3235	162	0
1	M	3362	0	3235	122	0
1	MB	3362	0	3235	149	0
1	MD	3362	0	3235	174	0
1	MF	3362	0	3235	164	0
1	MH	3362	0	3235	130	0
1	MJ	3362	0	3234	151	0
1	ML	3362	0	3235	124	0
1	MN	3362	0	3235	137	0
1	N	3290	0	3167	155	0
1	NB	3290	0	3166	128	0
1	ND	3348	0	3219	138	0
1	NF	3348	0	3217	137	0
1	NH	3343	0	3214	145	0
1	NJ	3362	0	3235	117	0
1	NL	3343	0	3214	155	0
1	O	3343	0	3212	162	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	OB	3335	0	3210	151	0
1	OD	3343	0	3212	137	0
1	OF	3343	0	3214	129	0
1	OH	3343	0	3214	128	0
1	OJ	3343	0	3214	140	0
1	OL	3343	0	3214	195	0
1	P	3123	0	3016	130	0
1	PB	3362	0	3235	118	0
1	PD	3362	0	3235	138	0
1	PF	3362	0	3235	124	0
1	PH	3342	0	3212	138	0
1	PJ	3362	0	3235	117	0
1	PL	3362	0	3235	170	0
1	QA	3348	0	3219	156	0
1	QC	3348	0	3217	128	0
1	QE	3343	0	3214	116	0
1	QG	3348	0	3219	119	0
1	QI	3348	0	3217	120	0
1	QK	3348	0	3219	153	0
1	RA	3343	0	3214	131	0
1	RC	3362	0	3234	123	0
1	RE	3343	0	3214	136	0
1	RG	3343	0	3214	122	0
1	RI	3342	0	3209	120	0
1	RK	3355	0	3226	129	0
1	S	3335	0	3210	112	0
1	SB	3335	0	3210	126	0
1	SD	3335	0	3210	128	0
1	SF	3335	0	3210	127	0
1	SH	3355	0	3226	119	0
1	SJ	3348	0	3218	146	0
1	T	3348	0	3218	158	0
1	TB	3355	0	3226	136	0
1	TD	3343	0	3214	146	0
1	TF	3348	0	3219	140	0
1	TH	3343	0	3214	143	0
1	TJ	3362	0	3235	118	0
1	TL	3348	0	3219	183	0
1	U	3335	0	3210	119	0
1	UB	3335	0	3210	116	0
1	UD	3335	0	3210	117	0
1	UF	3335	0	3210	142	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	UH	3335	0	3210	130	0
1	UJ	3348	0	3219	95	0
1	UL	3343	0	3214	128	0
1	V	3355	0	3226	131	0
1	VB	3343	0	3214	118	0
1	VD	3348	0	3219	119	0
1	VF	3355	0	3226	108	0
1	VH	3335	0	3208	114	0
1	VJ	3362	0	3235	120	0
1	VL	3362	0	3235	135	0
1	W	3335	0	3210	123	0
1	WB	3335	0	3210	124	0
1	WD	3335	0	3210	120	0
1	WF	3348	0	3219	119	0
1	WH	3335	0	3210	132	0
1	WJ	3335	0	3210	112	0
1	WL	3343	0	3214	127	0
2	AA	3329	0	3257	118	0
2	AC	3353	0	3276	133	0
2	AE	3394	0	3318	135	0
2	AG	3352	0	3279	133	0
2	AI	3394	0	3318	136	0
2	AK	3394	0	3318	133	0
2	AM	3329	0	3257	113	0
2	BA	3322	0	3250	130	0
2	BC	3329	0	3257	143	0
2	BE	3322	0	3250	119	0
2	BG	3329	0	3257	147	0
2	BI	3394	0	3318	148	0
2	BK	3322	0	3250	129	0
2	BM	3329	0	3257	121	0
2	C	3394	0	3318	127	0
2	CB	3394	0	3318	120	0
2	CD	3394	0	3318	159	0
2	CF	3329	0	3257	102	0
2	CH	3394	0	3318	130	0
2	CJ	3394	0	3318	127	0
2	CL	3394	0	3318	136	0
2	D	3329	0	3257	119	0
2	DB	3329	0	3257	118	0
2	DD	3329	0	3257	103	0
2	DF	3337	0	3261	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	DH	3328	0	3253	110	0
2	DJ	3329	0	3257	115	0
2	DL	3329	0	3257	126	0
2	EA	3329	0	3257	110	0
2	EC	3394	0	3318	113	0
2	EE	3346	0	3267	127	0
2	EG	3351	0	3270	133	0
2	EI	3337	0	3261	116	0
2	EK	3337	0	3261	116	0
2	FA	3394	0	3318	116	0
2	FC	3360	0	3276	118	0
2	FE	3343	0	3266	121	0
2	FG	3337	0	3261	137	0
2	FI	3322	0	3250	123	0
2	FK	3337	0	3261	126	0
2	GA	3329	0	3257	127	0
2	GC	3329	0	3257	144	0
2	GE	3337	0	3261	136	0
2	GG	3329	0	3257	108	0
2	GI	3329	0	3257	135	0
2	GK	3329	0	3257	136	0
2	HA	3329	0	3257	155	0
2	HC	3329	0	3257	137	0
2	HE	3394	0	3318	125	0
2	HG	3343	0	3266	116	0
2	HI	3336	0	3259	134	0
2	HK	3343	0	3266	129	0
2	HM	3329	0	3257	141	0
2	IA	3329	0	3257	141	0
2	IC	3343	0	3266	128	0
2	IE	3394	0	3318	137	0
2	IG	3394	0	3318	139	0
2	II	3394	0	3318	136	0
2	IK	3329	0	3257	143	0
2	IM	3329	0	3257	142	0
2	J	3394	0	3318	148	0
2	JB	3394	0	3318	135	0
2	JD	3329	0	3257	125	0
2	JF	3329	0	3257	135	0
2	JH	3342	0	3266	143	0
2	JJ	3343	0	3266	140	0
2	JL	3343	0	3266	151	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	JN	3394	0	3318	163	0
2	K	3358	0	3284	117	0
2	KB	3394	0	3318	131	0
2	KD	3329	0	3257	119	0
2	KF	3394	0	3318	134	0
2	KH	3335	0	3262	153	0
2	KJ	3346	0	3267	135	0
2	KL	3394	0	3318	146	0
2	KN	3394	0	3318	123	0
2	L	3394	0	3318	101	0
2	LB	3346	0	3267	142	0
2	LD	3322	0	3245	128	0
2	LF	3394	0	3318	138	0
2	LH	3394	0	3318	159	0
2	LJ	3394	0	3318	165	0
2	LL	3394	0	3318	133	0
2	LN	3346	0	3267	161	0
2	MA	3335	0	3262	129	0
2	MC	3379	0	3307	137	0
2	ME	3368	0	3287	150	0
2	MG	3394	0	3318	141	0
2	MI	3394	0	3318	138	0
2	MK	3394	0	3318	152	0
2	MM	3335	0	3262	138	0
2	NA	3394	0	3318	134	0
2	NC	3394	0	3318	137	0
2	NE	3394	0	3318	135	0
2	NG	3394	0	3318	121	0
2	NI	3394	0	3318	137	0
2	NK	3394	0	3318	135	0
2	NM	3394	0	3318	135	0
2	OA	3343	0	3265	161	0
2	OC	3337	0	3261	150	0
2	OE	3337	0	3261	136	0
2	OG	3394	0	3318	137	0
2	OI	3329	0	3257	118	0
2	OK	3329	0	3257	143	0
2	OM	3352	0	3271	205	0
2	PA	3329	0	3257	132	0
2	PC	3337	0	3261	113	0
2	PE	3337	0	3261	136	0
2	PG	3394	0	3318	149	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	PI	3337	0	3261	135	0
2	PK	3343	0	3266	133	0
2	PM	3343	0	3266	142	0
2	Q	3394	0	3318	137	0
2	QB	3323	0	3252	142	0
2	QD	3329	0	3257	146	0
2	QF	3329	0	3257	128	0
2	QH	3394	0	3318	143	0
2	QJ	3337	0	3261	139	0
2	QL	3343	0	3266	145	0
2	R	3394	0	3318	132	0
2	RB	3337	0	3261	135	0
2	RD	3337	0	3261	131	0
2	RF	3337	0	3261	135	0
2	RH	3329	0	3257	134	0
2	RJ	3329	0	3257	142	0
2	RL	3335	0	3262	139	0
2	SA	3337	0	3261	146	0
2	SC	3335	0	3262	122	0
2	SE	3335	0	3262	101	0
2	SG	3337	0	3261	117	0
2	SI	3329	0	3257	126	0
2	SK	3343	0	3266	164	0
2	TA	3329	0	3257	122	0
2	TC	3314	0	3241	135	0
2	TE	3329	0	3257	110	0
2	TG	3337	0	3261	121	0
2	TI	3329	0	3257	119	0
2	TK	3353	0	3276	160	0
2	UA	3329	0	3257	111	0
2	UC	3322	0	3245	126	0
2	UE	3329	0	3257	120	0
2	UG	3337	0	3260	127	0
2	UI	3329	0	3257	126	0
2	UK	3329	0	3257	141	0
2	VA	3337	0	3261	119	0
2	VC	3337	0	3261	126	0
2	VE	3337	0	3261	105	0
2	VG	3337	0	3260	123	0
2	VI	3342	0	3264	98	0
2	VK	3329	0	3257	127	0
2	VM	3360	0	3276	132	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	WA	3394	0	3318	132	0
2	WC	3337	0	3261	128	0
2	WE	3394	0	3318	116	0
2	WG	3337	0	3261	126	0
2	WI	3394	0	3318	113	0
2	WK	3337	0	3261	108	0
2	WM	3394	0	3318	121	0
3	X	1510	0	1518	34	0
3	XA	1510	0	1518	47	0
3	XB	1510	0	1518	58	0
3	XC	1510	0	1518	53	0
3	XD	1510	0	1518	61	0
3	XE	1510	0	1518	59	0
3	XF	1510	0	1518	48	0
4	XM	2045	0	2058	56	0
4	XO	2053	0	2062	66	0
4	XQ	2053	0	2062	71	0
4	XR	2056	0	2071	56	0
5	XN	2116	0	2114	72	0
5	XP	2116	0	2114	67	0
6	0	2004	0	2023	67	0
6	0A	2004	0	2023	80	0
7	0C	935	0	882	37	0
7	0D	2723	0	2608	123	0
8	0F	1439	0	1417	60	0
8	0G	2955	0	2995	84	0
8	0H	229	0	243	10	0
8	0I	2369	0	2363	68	0
8	0J	1906	0	1937	47	0
9	0L	4757	0	4698	140	0
9	0M	4757	0	4698	171	0
9	0N	4757	0	4698	187	0
9	0O	2357	0	2349	95	0
10	0R	2628	0	2629	101	0
10	0S	1874	0	1901	47	0
11	0U	2570	0	2542	83	0
12	0W	2595	0	2596	64	0
13	0Y	1836	0	1837	45	0
13	0Z	1849	0	1853	56	0
13	0a	422	0	422	12	0
14	0c	1929	0	1952	68	0
14	0d	2150	0	2177	89	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	0f	1257	0	1238	63	0
15	0g	218	0	207	10	0
16	0k	5599	0	5578	212	0
16	0l	5045	0	5007	170	0
17	0m	1155	0	1160	68	0
17	0n	3388	0	3431	126	0
17	0o	171	0	175	8	0
18	0p	906	0	895	45	0
19	0r	2033	0	1951	95	0
20	0t	2062	0	1965	66	0
20	0u	1769	0	1687	54	0
21	0v	582	0	554	18	0
21	0w	3715	0	3660	99	0
21	0x	906	0	903	30	0
22	0z	1160	0	1141	84	0
22	1w	1481	0	1429	68	0
22	1x	1680	0	1614	79	0
22	1y	722	0	706	38	0
23	1A	2286	0	2263	97	0
23	1B	1667	0	1640	72	0
23	1D	464	0	483	17	0
23	1E	3050	0	3010	142	0
23	1F	635	0	613	33	0
24	1H	4698	0	4581	136	0
24	1I	5276	0	5158	161	0
24	1J	5356	0	5242	149	0
24	1K	4697	0	4577	124	0
25	1O	5751	0	5661	144	0
26	1Q	5263	0	5177	162	0
27	1S	5834	0	5732	157	0
27	1T	1787	0	1767	66	0
28	1U	942	0	920	25	0
28	1V	371	0	355	18	0
28	1X	942	0	920	31	0
28	1Y	1325	0	1292	50	0
28	1a	446	0	425	34	0
28	1b	1313	0	1278	101	0
28	1c	263	0	253	13	0
28	1d	942	0	920	27	0
28	1e	371	0	355	7	0
28	1g	942	0	920	52	0
28	1h	1218	0	1189	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	4V	486	0	467	15	0
28	4W	1474	0	1422	55	0
29	1j	909	0	866	31	0
29	1k	801	0	745	29	0
29	1l	909	0	866	41	0
29	1m	420	0	397	16	0
30	1o	1035	0	1002	26	0
31	1q	1679	0	1626	60	0
31	1r	868	0	881	37	0
31	1s	1446	0	1394	40	0
31	1t	618	0	629	15	0
32	2B	1977	0	1960	71	0
32	2C	1814	0	1800	57	0
33	2F	2253	0	2212	60	0
33	2G	2245	0	2206	84	0
33	2H	2281	0	2234	71	0
33	2I	1937	0	1892	70	0
34	2L	1433	0	1355	46	0
35	2N	1103	0	1066	58	0
35	2O	1324	0	1231	90	0
36	2Q	2320	0	2242	55	0
37	2S	1800	0	1729	69	0
38	2U	1807	0	1780	93	0
38	2V	870	0	847	29	0
39	2X	1774	0	1712	48	0
40	2Z	2258	0	2230	78	0
41	2b	1006	0	1007	18	0
41	2c	2092	0	2064	59	0
41	2e	2735	0	2721	83	0
41	2f	454	0	446	11	0
41	2h	1978	0	1984	77	0
41	2i	1301	0	1270	36	0
41	2k	1369	0	1383	55	0
41	2l	2228	0	2214	53	0
41	2n	361	0	357	12	0
41	2o	2453	0	2421	83	0
41	2p	425	0	428	15	0
42	2r	2473	0	2429	63	0
43	2t	1713	0	1664	59	0
44	2v	2264	0	2195	104	0
44	2w	3291	0	3163	148	0
45	2y	2316	0	2162	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	2z	1435	0	1380	91	0
46	3B	3308	0	3248	92	0
47	3D	3212	0	3119	93	0
48	3F	1254	0	1303	32	0
48	3G	733	0	767	24	0
48	3H	832	0	874	19	0
48	3I	640	0	659	16	0
48	3L	247	0	249	7	0
48	3M	247	0	249	7	0
49	3P	2002	0	2032	90	0
49	3Q	3825	0	3796	150	0
50	3S	182	0	175	6	0
51	X1	304	0	280	17	0
52	3U	1074	0	1031	42	0
53	3W	1264	0	1264	48	0
53	3X	386	0	389	11	0
54	3Z	1405	0	1388	66	0
54	3a	712	0	647	34	0
54	4Y	122	0	102	3	0
55	3b	1126	0	1135	31	0
56	3d	1240	0	1234	37	0
57	3f	1408	0	1382	52	0
57	3g	1408	0	1382	42	0
57	3h	1408	0	1382	41	0
57	3i	1408	0	1382	76	0
58	3m	1216	0	1223	47	0
59	3o	459	0	445	12	0
59	3p	1159	0	1135	45	0
59	4O	1399	0	1368	58	0
59	4P	529	0	513	19	0
59	4a	1233	0	1197	54	0
59	4b	529	0	513	14	0
60	3r	1098	0	1069	56	0
60	3s	1098	0	1069	55	0
60	3t	533	0	524	26	0
61	3w	1362	0	1292	57	0
61	3x	987	0	951	80	0
62	4A	229	0	214	8	0
62	4B	1584	0	1493	70	0
63	4I	620	0	604	41	0
64	5B	1348	0	1390	45	0
64	5C	1348	0	1390	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	5D	321	0	332	27	0
65	5G	1541	0	1562	58	0
65	5H	1541	0	1562	76	0
65	5I	401	0	417	15	0
66	5K	2155	0	2155	62	0
66	5L	2155	0	2155	81	0
67	5O	809	0	824	35	0
67	5P	809	0	824	43	0
68	5S	749	0	757	25	0
68	5T	749	0	757	25	0
69	A	28	0	12	1	0
69	AB	28	0	12	3	0
69	AD	28	0	12	1	0
69	AF	28	0	12	3	0
69	AH	28	0	12	3	0
69	AJ	28	0	12	2	0
69	AL	28	0	12	2	0
69	AN	28	0	12	3	0
69	BB	28	0	12	1	0
69	BD	28	0	12	1	0
69	BF	28	0	12	0	0
69	BH	28	0	12	2	0
69	BJ	28	0	12	0	0
69	BL	28	0	12	1	0
69	BN	28	0	12	0	0
69	CA	28	0	12	2	0
69	CC	28	0	12	1	0
69	CE	28	0	12	2	0
69	CG	28	0	12	3	0
69	CI	28	0	12	1	0
69	CK	28	0	12	1	0
69	CM	28	0	12	3	0
69	DA	28	0	12	1	0
69	DC	28	0	12	3	0
69	DE	28	0	12	1	0
69	DG	28	0	12	2	0
69	DI	28	0	12	3	0
69	DK	28	0	12	4	0
69	DM	28	0	12	2	0
69	E	28	0	12	1	0
69	EB	28	0	12	2	0
69	ED	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	EF	28	0	12	1	0
69	EH	28	0	12	2	0
69	EJ	28	0	12	1	0
69	EL	28	0	12	3	0
69	F	28	0	12	1	0
69	FB	28	0	12	2	0
69	FD	28	0	12	1	0
69	FF	28	0	12	2	0
69	FH	28	0	12	1	0
69	FJ	28	0	12	0	0
69	FL	28	0	12	1	0
69	G	28	0	12	0	0
69	GB	28	0	12	3	0
69	GD	28	0	12	0	0
69	GF	28	0	12	4	0
69	GH	28	0	12	1	0
69	GJ	28	0	12	1	0
69	GL	28	0	12	1	0
69	H	28	0	12	1	0
69	HB	28	0	12	1	0
69	HD	28	0	12	2	0
69	HF	28	0	12	1	0
69	HH	28	0	12	3	0
69	HJ	28	0	12	2	0
69	HL	28	0	12	4	0
69	I	28	0	12	4	0
69	IB	28	0	12	2	0
69	ID	28	0	12	2	0
69	IF	28	0	12	0	0
69	IH	28	0	12	1	0
69	IJ	28	0	12	1	0
69	IL	28	0	12	1	0
69	JA	28	0	12	2	0
69	JC	28	0	12	2	0
69	JE	28	0	12	1	0
69	JG	28	0	12	1	0
69	JI	28	0	12	3	0
69	JK	28	0	12	1	0
69	JM	28	0	12	1	0
69	KA	28	0	12	1	0
69	KC	28	0	12	1	0
69	KE	28	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	KG	28	0	12	3	0
69	KI	28	0	12	2	0
69	KK	28	0	12	5	0
69	KM	28	0	12	1	0
69	LA	28	0	12	0	0
69	LC	28	0	12	3	0
69	LE	28	0	12	3	0
69	LG	28	0	12	2	0
69	LI	28	0	12	3	0
69	LK	28	0	12	1	0
69	LM	28	0	12	1	0
69	LO	28	0	12	3	0
69	M	28	0	12	2	0
69	MB	28	0	12	3	0
69	MD	28	0	12	2	0
69	MF	28	0	12	6	0
69	MH	28	0	12	0	0
69	MJ	28	0	12	3	0
69	ML	28	0	12	2	0
69	MN	28	0	12	2	0
69	N	28	0	12	3	0
69	NB	28	0	12	4	0
69	ND	28	0	12	3	0
69	NF	28	0	12	2	0
69	NH	28	0	12	1	0
69	NJ	28	0	12	2	0
69	NL	28	0	12	3	0
69	O	28	0	12	3	0
69	OB	28	0	12	5	0
69	OD	28	0	12	2	0
69	OF	28	0	12	1	0
69	OH	28	0	12	1	0
69	OJ	28	0	12	1	0
69	OL	28	0	12	2	0
69	P	28	0	12	7	0
69	PB	28	0	12	2	0
69	PD	28	0	12	1	0
69	PF	28	0	12	2	0
69	PH	28	0	12	3	0
69	PJ	28	0	12	0	0
69	PL	28	0	12	2	0
69	QA	28	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	QC	28	0	12	2	0
69	QE	28	0	12	1	0
69	QG	28	0	12	2	0
69	QI	28	0	12	2	0
69	QK	28	0	12	7	0
69	RA	28	0	12	3	0
69	RC	28	0	12	2	0
69	RE	28	0	12	0	0
69	RG	28	0	12	0	0
69	RI	28	0	12	3	0
69	RK	28	0	12	1	0
69	S	28	0	12	1	0
69	SB	28	0	12	0	0
69	SD	28	0	12	1	0
69	SF	28	0	12	3	0
69	SH	28	0	12	2	0
69	SJ	28	0	12	0	0
69	T	28	0	12	1	0
69	TB	28	0	12	1	0
69	TD	28	0	12	2	0
69	TF	28	0	12	1	0
69	TH	28	0	12	1	0
69	TJ	28	0	12	1	0
69	TL	28	0	12	3	0
69	U	28	0	12	1	0
69	UB	28	0	12	1	0
69	UD	28	0	12	3	0
69	UF	28	0	12	1	0
69	UH	28	0	12	0	0
69	UJ	28	0	12	0	0
69	UL	28	0	12	3	0
69	V	28	0	12	2	0
69	VB	28	0	12	0	0
69	VD	28	0	12	1	0
69	VF	28	0	12	1	0
69	VH	28	0	12	1	0
69	VJ	28	0	12	3	0
69	VL	28	0	12	3	0
69	W	28	0	12	1	0
69	WB	28	0	12	1	0
69	WD	28	0	12	1	0
69	WF	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	WH	28	0	12	3	0
69	WJ	28	0	12	3	0
69	WL	28	0	12	2	0
70	AA	1	0	0	0	0
70	AC	1	0	0	0	0
70	AE	1	0	0	0	0
70	AG	1	0	0	0	0
70	AI	1	0	0	0	0
70	AK	1	0	0	0	0
70	AM	1	0	0	0	0
70	BA	1	0	0	0	0
70	BC	1	0	0	0	0
70	BE	1	0	0	0	0
70	BG	1	0	0	0	0
70	BI	1	0	0	0	0
70	BK	1	0	0	0	0
70	BM	1	0	0	0	0
70	C	1	0	0	0	0
70	CB	1	0	0	0	0
70	CD	1	0	0	0	0
70	CF	1	0	0	0	0
70	CH	1	0	0	0	0
70	CJ	1	0	0	0	0
70	CL	1	0	0	0	0
70	D	1	0	0	0	0
70	DB	1	0	0	0	0
70	DD	1	0	0	0	0
70	DF	1	0	0	0	0
70	DH	1	0	0	0	0
70	DJ	1	0	0	0	0
70	DL	1	0	0	0	0
70	EA	1	0	0	0	0
70	EC	1	0	0	0	0
70	EE	1	0	0	0	0
70	EG	1	0	0	0	0
70	EI	1	0	0	0	0
70	EK	1	0	0	0	0
70	FA	1	0	0	0	0
70	FC	1	0	0	0	0
70	FE	1	0	0	0	0
70	FG	1	0	0	0	0
70	FI	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	FK	1	0	0	0	0
70	GA	1	0	0	0	0
70	GC	1	0	0	0	0
70	GE	1	0	0	0	0
70	GG	1	0	0	0	0
70	GI	1	0	0	0	0
70	GK	1	0	0	0	0
70	HA	1	0	0	0	0
70	HC	1	0	0	0	0
70	HE	1	0	0	0	0
70	HG	1	0	0	0	0
70	HI	1	0	0	0	0
70	HK	1	0	0	0	0
70	HM	1	0	0	0	0
70	IA	1	0	0	0	0
70	IC	1	0	0	0	0
70	IE	1	0	0	0	0
70	IG	1	0	0	0	0
70	II	1	0	0	0	0
70	IK	1	0	0	0	0
70	IM	1	0	0	0	0
70	J	1	0	0	0	0
70	JB	1	0	0	0	0
70	JD	1	0	0	0	0
70	JF	1	0	0	0	0
70	JH	1	0	0	0	0
70	JJ	1	0	0	0	0
70	JL	1	0	0	0	0
70	JN	1	0	0	0	0
70	K	1	0	0	0	0
70	KB	1	0	0	0	0
70	KD	1	0	0	0	0
70	KF	1	0	0	0	0
70	KH	1	0	0	0	0
70	KJ	1	0	0	0	0
70	KL	1	0	0	0	0
70	KN	1	0	0	0	0
70	L	1	0	0	0	0
70	LB	1	0	0	0	0
70	LD	1	0	0	0	0
70	LF	1	0	0	0	0
70	LH	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	LJ	1	0	0	0	0
70	LL	1	0	0	0	0
70	LN	1	0	0	0	0
70	MA	1	0	0	0	0
70	MC	1	0	0	0	0
70	ME	1	0	0	0	0
70	MG	1	0	0	0	0
70	MI	1	0	0	0	0
70	MK	1	0	0	0	0
70	MM	1	0	0	0	0
70	NA	1	0	0	0	0
70	NC	1	0	0	0	0
70	NE	1	0	0	0	0
70	NG	1	0	0	0	0
70	NI	1	0	0	0	0
70	NK	1	0	0	0	0
70	NM	1	0	0	0	0
70	OA	1	0	0	0	0
70	OC	1	0	0	0	0
70	OE	1	0	0	0	0
70	OG	1	0	0	0	0
70	OI	1	0	0	0	0
70	OK	1	0	0	0	0
70	OM	1	0	0	0	0
70	PA	1	0	0	0	0
70	PC	1	0	0	0	0
70	PE	1	0	0	0	0
70	PG	1	0	0	0	0
70	PI	1	0	0	0	0
70	PK	1	0	0	0	0
70	PM	1	0	0	0	0
70	Q	1	0	0	0	0
70	QB	1	0	0	0	0
70	QD	1	0	0	0	0
70	QF	1	0	0	0	0
70	QH	1	0	0	0	0
70	QJ	1	0	0	0	0
70	QL	1	0	0	0	0
70	R	1	0	0	0	0
70	RB	1	0	0	0	0
70	RD	1	0	0	0	0
70	RF	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	RH	1	0	0	0	0
70	RJ	1	0	0	0	0
70	RL	1	0	0	0	0
70	SA	1	0	0	0	0
70	SC	1	0	0	0	0
70	SE	1	0	0	0	0
70	SG	1	0	0	0	0
70	SI	1	0	0	0	0
70	SK	1	0	0	0	0
70	TA	1	0	0	0	0
70	TC	1	0	0	0	0
70	TE	1	0	0	0	0
70	TG	1	0	0	0	0
70	TI	1	0	0	0	0
70	TK	1	0	0	0	0
70	UA	1	0	0	0	0
70	UC	1	0	0	0	0
70	UE	1	0	0	0	0
70	UG	1	0	0	0	0
70	UI	1	0	0	0	0
70	UK	1	0	0	0	0
70	VA	1	0	0	0	0
70	VC	1	0	0	0	0
70	VE	1	0	0	0	0
70	VG	1	0	0	0	0
70	VI	1	0	0	0	0
70	VK	1	0	0	0	0
70	VM	1	0	0	0	0
70	WA	1	0	0	0	0
70	WC	1	0	0	0	0
70	WE	1	0	0	0	0
70	WG	1	0	0	0	0
70	WI	1	0	0	0	0
70	WK	1	0	0	0	0
70	WM	1	0	0	0	0
71	AA	32	0	12	2	0
71	AC	32	0	12	2	0
71	AE	32	0	12	1	0
71	AG	32	0	12	1	0
71	AI	32	0	12	0	0
71	AK	32	0	12	1	0
71	AM	32	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	BA	32	0	12	0	0
71	BC	32	0	12	1	0
71	BE	32	0	12	2	0
71	BG	32	0	12	4	0
71	BI	32	0	12	0	0
71	BK	32	0	12	1	0
71	BM	32	0	12	4	0
71	C	32	0	12	0	0
71	CB	32	0	12	2	0
71	CD	32	0	12	0	0
71	CF	32	0	12	0	0
71	CH	32	0	12	3	0
71	CJ	32	0	12	1	0
71	CL	32	0	12	0	0
71	D	32	0	12	5	0
71	DB	32	0	12	2	0
71	DD	32	0	12	3	0
71	DF	32	0	12	0	0
71	DH	32	0	12	0	0
71	DJ	32	0	12	1	0
71	DL	32	0	12	2	0
71	EA	32	0	12	0	0
71	EC	32	0	12	0	0
71	EE	32	0	12	1	0
71	EG	32	0	12	1	0
71	EI	32	0	12	2	0
71	EK	32	0	12	0	0
71	FA	32	0	12	2	0
71	FC	32	0	12	0	0
71	FE	32	0	12	0	0
71	FG	32	0	12	0	0
71	FI	32	0	12	0	0
71	FK	32	0	12	1	0
71	GA	32	0	12	1	0
71	GC	32	0	12	4	0
71	GE	32	0	12	1	0
71	GG	32	0	12	3	0
71	GI	32	0	12	5	0
71	GK	32	0	12	1	0
71	HA	32	0	12	1	0
71	HC	32	0	12	0	0
71	HE	32	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	HG	32	0	12	1	0
71	HI	32	0	12	2	0
71	HK	32	0	12	2	0
71	HM	32	0	12	3	0
71	IA	32	0	12	1	0
71	IC	32	0	12	2	0
71	IE	32	0	12	2	0
71	IG	32	0	12	0	0
71	II	32	0	12	2	0
71	IK	32	0	12	3	0
71	IM	32	0	12	1	0
71	J	32	0	12	0	0
71	JB	32	0	12	1	0
71	JD	32	0	12	0	0
71	JF	32	0	12	1	0
71	JH	32	0	12	1	0
71	JJ	32	0	12	1	0
71	JL	32	0	12	2	0
71	JN	32	0	12	1	0
71	K	32	0	12	2	0
71	KB	32	0	12	1	0
71	KD	32	0	12	1	0
71	KF	32	0	12	2	0
71	KH	32	0	12	2	0
71	KJ	32	0	12	1	0
71	KL	32	0	12	1	0
71	KN	32	0	12	1	0
71	L	32	0	12	1	0
71	LB	32	0	12	1	0
71	LD	32	0	12	0	0
71	LF	32	0	12	1	0
71	LH	32	0	12	2	0
71	LJ	32	0	12	2	0
71	LL	32	0	12	1	0
71	LN	32	0	12	1	0
71	MA	32	0	12	0	0
71	MC	32	0	12	1	0
71	ME	32	0	12	2	0
71	MG	32	0	12	2	0
71	MI	32	0	12	2	0
71	MK	32	0	12	0	0
71	MM	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	NA	32	0	12	1	0
71	NC	32	0	12	1	0
71	NE	32	0	12	1	0
71	NG	32	0	12	1	0
71	NI	32	0	12	0	0
71	NK	32	0	12	2	0
71	NM	32	0	12	1	0
71	OA	32	0	12	3	0
71	OC	32	0	12	5	0
71	OE	32	0	12	0	0
71	OG	32	0	12	1	0
71	OI	32	0	12	0	0
71	OK	32	0	12	0	0
71	OM	32	0	12	1	0
71	PA	32	0	12	1	0
71	PC	32	0	12	2	0
71	PE	32	0	12	5	0
71	PG	32	0	12	4	0
71	PI	32	0	12	3	0
71	PK	32	0	12	2	0
71	PM	32	0	12	1	0
71	Q	32	0	12	0	0
71	QB	32	0	12	1	0
71	QD	32	0	12	0	0
71	QF	32	0	12	2	0
71	QH	32	0	12	3	0
71	QJ	32	0	12	1	0
71	QL	32	0	12	2	0
71	R	32	0	12	3	0
71	RB	32	0	12	1	0
71	RD	32	0	12	3	0
71	RF	32	0	12	3	0
71	RH	32	0	12	3	0
71	RJ	32	0	12	1	0
71	RL	32	0	12	2	0
71	SA	32	0	12	0	0
71	SC	32	0	12	0	0
71	SE	32	0	12	1	0
71	SG	32	0	12	1	0
71	SI	32	0	12	2	0
71	SK	32	0	12	2	0
71	TA	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	TC	32	0	12	0	0
71	TE	32	0	12	1	0
71	TG	32	0	12	2	0
71	TI	32	0	12	4	0
71	TK	32	0	12	1	0
71	UA	32	0	12	1	0
71	UC	32	0	12	2	0
71	UE	32	0	12	0	0
71	UG	32	0	12	2	0
71	UI	32	0	12	2	0
71	UK	32	0	12	1	0
71	VA	32	0	12	1	0
71	VC	32	0	12	1	0
71	VE	32	0	12	1	0
71	VG	32	0	12	1	0
71	VI	32	0	12	0	0
71	VK	32	0	12	1	0
71	VM	32	0	12	3	0
71	WA	32	0	12	0	0
71	WC	32	0	12	0	0
71	WE	32	0	12	0	0
71	WG	32	0	12	4	0
71	WI	32	0	12	3	0
71	WK	32	0	12	1	0
71	WM	32	0	12	2	0
72	0	1	0	0	0	0
72	0A	1	0	0	0	0
72	0z	1	0	0	0	0
72	1V	2	0	0	0	0
72	1Y	2	0	0	0	0
72	1b	2	0	0	3	0
72	1c	2	0	0	0	0
72	1e	2	0	0	0	0
72	1h	2	0	0	0	0
72	1q	3	0	0	0	0
72	1s	1	0	0	0	0
72	1t	1	0	0	0	0
72	1w	2	0	0	0	0
72	1x	2	0	0	0	0
72	3S	1	0	0	0	0
72	4W	2	0	0	1	0
72	5S	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	5T	1	0	0	0	0
73	1S	1	0	0	0	0
73	2v	1	0	0	0	0
73	2w	1	0	0	0	0
74	2v	31	0	10	1	0
74	2w	31	0	12	0	0
All	All	1371722	0	1329418	45747	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 45747 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:0F:50:GLY:HA2	8:0F:55:HIS:CD2	1.22	1.69
2:OC:60:LYS:CE	41:2k:194:ARG:NH1	1.75	1.49
2:LJ:264:ARG:NH1	22:0z:144:LYS:CD	1.75	1.48
1:SJ:122:LYS:NZ	61:3x:82:TYR:CE1	1.68	1.46
1:SJ:125:GLU:CD	61:3x:82:TYR:HB2	1.41	1.46

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

5.3.2 Protein sidechains

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

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 511 ligands modelled in this entry, 190 are monoatomic - leaving 321 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	$\#\|Z\| > 2$
69	GDP	NB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	SE	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.59	10 (20%)
71	GTP	QD	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.58	9 (18%)
71	GTP	TG	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
71	GTP	QH	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.63	10 (20%)
71	GTP	JH	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.58	9 (18%)
71	GTP	IG	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	IB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	ME	501	70	33,34,34	0.99	3 (9%)	50,54,54	1.57	9 (18%)
69	GDP	WL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	PH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	6 (13%)
71	GTP	WG	501	70	33,34,34	0.88	1 (3%)	50,54,54	1.58	9 (18%)
71	GTP	GA	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
69	GDP	IF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	FF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	OL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	PB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	UH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	NH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	UE	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.56	9 (18%)
69	GDP	RA	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	7 (15%)
71	GTP	LJ	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.59	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
71	GTP	UK	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
71	GTP	RL	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
69	GDP	AB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	MB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	5 (11%)
69	GDP	PF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
69	GDP	NJ	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	II	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.60	9 (18%)
69	GDP	AF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	6 (13%)
69	GDP	HF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
69	GDP	KK	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	UF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	DG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	AN	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	QJ	501	70	33,34,34	0.95	2 (6%)	50,54,54	1.58	10 (20%)
69	GDP	WD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	GF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	IM	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.57	8 (16%)
71	GTP	WM	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	KC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	RF	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
69	GDP	LG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	6 (13%)
71	GTP	LH	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
69	GDP	H	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	NE	501	70	33,34,34	0.99	2 (6%)	50,54,54	1.56	9 (18%)
71	GTP	AG	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.55	9 (18%)
71	GTP	EA	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.61	9 (18%)
71	GTP	DB	501	70	33,34,34	0.99	2 (6%)	50,54,54	1.56	8 (16%)
71	GTP	PK	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	DJ	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.58	9 (18%)
71	GTP	SI	501	70	33,34,34	0.89	1 (3%)	50,54,54	1.57	8 (16%)
69	GDP	LI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	CC	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	FE	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.54	9 (18%)
71	GTP	MG	501	70	33,34,34	0.89	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	KA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
69	GDP	ID	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	WJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	HJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	FA	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.55	9 (18%)
71	GTP	JF	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)
71	GTP	TI	501	70	33,34,34	0.98	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	RG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	AH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.69	7 (15%)
69	GDP	EL	500	-	29,30,30	1.17	2 (6%)	45,47,47	1.74	5 (11%)
71	GTP	L	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.56	8 (16%)
69	GDP	W	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	OF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	VG	501	70	33,34,34	1.00	3 (9%)	50,54,54	1.57	9 (18%)
71	GTP	SK	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.58	8 (16%)
71	GTP	OG	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)
71	GTP	KD	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.56	8 (16%)
71	GTP	C	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	KL	501	70	33,34,34	0.96	2 (6%)	50,54,54	1.58	9 (18%)
71	GTP	QF	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
69	GDP	JM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	M	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	CF	501	70	33,34,34	0.99	2 (6%)	50,54,54	1.56	8 (16%)
69	GDP	BF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	JJ	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	FH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	R	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	EG	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.60	10 (20%)
71	GTP	IE	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.62	9 (18%)
71	GTP	BG	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.58	9 (18%)
69	GDP	U	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
71	GTP	IK	501	70	33,34,34	1.24	5 (15%)	50,54,54	1.62	10 (20%)
71	GTP	GK	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.57	8 (16%)
69	GDP	ML	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	QI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	LC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
71	GTP	VE	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)
69	GDP	GH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
71	GTP	RJ	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.57	8 (16%)
71	GTP	OK	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.61	9 (18%)
71	GTP	LF	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	FC	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.56	9 (18%)
69	GDP	MF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	IC	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.61	9 (18%)
69	GDP	VB	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	LK	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	BM	501	70	33,34,34	1.00	3 (9%)	50,54,54	1.55	9 (18%)
69	GDP	IL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
71	GTP	LL	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.54	8 (16%)
69	GDP	LM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	BH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	D	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.60	10 (20%)
69	GDP	RE	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.80	8 (17%)
71	GTP	RD	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.55	8 (16%)
69	GDP	CI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	LB	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.56	8 (16%)
69	GDP	UJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	GJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	DH	501	70	33,34,34	0.87	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	UA	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.55	9 (18%)
69	GDP	JA	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	FJ	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	NG	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.60	9 (18%)
71	GTP	UI	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.59	9 (18%)
69	GDP	DI	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	OA	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.55	8 (16%)
69	GDP	QG	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	CA	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
71	GTP	HM	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.55	9 (18%)
69	GDP	BN	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.80	8 (17%)
71	GTP	AA	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.55	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
71	GTP	MI	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.54	8 (16%)
69	GDP	G	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	JG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	SD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)
69	GDP	KG	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	VJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	8 (17%)
71	GTP	KF	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.56	9 (18%)
69	GDP	DM	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	6 (13%)
71	GTP	CB	501	70	33,34,34	0.98	1 (3%)	50,54,54	1.55	8 (16%)
71	GTP	OI	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	HL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
69	GDP	KE	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	BB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	6 (13%)
71	GTP	J	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.55	8 (16%)
71	GTP	FI	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	UG	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.58	9 (18%)
71	GTP	OM	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.56	8 (16%)
71	GTP	SC	501	70	33,34,34	0.89	1 (3%)	50,54,54	1.57	8 (16%)
69	GDP	JC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	RI	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	LN	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.55	9 (18%)
69	GDP	JI	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	6 (13%)
69	GDP	OH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
69	GDP	MJ	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.73	7 (15%)
69	GDP	PJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	JD	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.54	8 (16%)
71	GTP	EE	501	70	33,34,34	1.02	3 (9%)	50,54,54	1.58	9 (18%)
69	GDP	JE	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	IH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	HC	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.59	9 (18%)
69	GDP	DK	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	AD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	QK	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.74	6 (13%)
69	GDP	DC	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	E	500	-	29,30,30	1.18	3 (10%)	45,47,47	1.73	5 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
71	GTP	HI	501	70	33,34,34	0.88	1 (3%)	50,54,54	1.55	9 (18%)
69	GDP	WH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	CM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.82	9 (20%)
71	GTP	TE	501	70	33,34,34	0.90	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	F	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
69	GDP	OB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	CH	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.61	10 (20%)
69	GDP	RK	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	LE	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	WC	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.56	9 (18%)
71	GTP	EC	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	NI	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.58	9 (18%)
71	GTP	BA	501	70	33,34,34	0.98	1 (3%)	50,54,54	1.55	8 (16%)
69	GDP	NF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	AC	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.56	9 (18%)
71	GTP	PE	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.59	8 (16%)
71	GTP	MA	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.56	8 (16%)
69	GDP	FL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	6 (13%)
71	GTP	CD	501	70	33,34,34	1.02	3 (9%)	50,54,54	1.58	9 (18%)
71	GTP	RB	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.55	8 (16%)
71	GTP	VI	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	FG	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
69	GDP	MN	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
71	GTP	BC	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.57	9 (18%)
71	GTP	AI	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	WK	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.56	9 (18%)
71	GTP	QB	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.59	8 (16%)
69	GDP	EF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	BI	501	70	33,34,34	1.00	3 (9%)	50,54,54	1.57	8 (16%)
71	GTP	MC	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	UB	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	I	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	ED	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	T	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	VC	501	70	33,34,34	0.99	2 (6%)	50,54,54	1.56	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
69	GDP	DE	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	CK	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.82	7 (15%)
69	GDP	IJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	VM	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.56	9 (18%)
71	GTP	BE	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	CG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	LD	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
71	GTP	WE	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.59	10 (20%)
69	GDP	TB	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
69	GDP	JK	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	GC	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	RH	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	BD	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	6 (13%)
69	GDP	O	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	DF	501	70	33,34,34	0.96	2 (6%)	50,54,54	1.61	10 (20%)
69	GDP	EJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	FK	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.60	9 (18%)
71	GTP	QL	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.57	8 (16%)
69	GDP	FB	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	PI	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.56	8 (16%)
71	GTP	TK	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.54	8 (16%)
71	GTP	KH	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.61	9 (18%)
69	GDP	QA	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	EI	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	QC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	GB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	GD	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	7 (15%)
69	GDP	HH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	BL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	K	501	70	33,34,34	0.97	2 (6%)	50,54,54	1.58	9 (18%)
69	GDP	LA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	HB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
74	ATP	2w	501	-	32,33,33	0.32	0	48,52,52	0.28	0
69	GDP	VF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	NK	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
69	GDP	NL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
71	GTP	SA	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.56	9 (18%)
69	GDP	P	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.82	7 (15%)
71	GTP	GE	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.58	9 (18%)
69	GDP	VD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	HE	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.55	9 (18%)
71	GTP	Q	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	UD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	PC	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.56	8 (16%)
71	GTP	KN	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.57	8 (16%)
71	GTP	IA	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
69	GDP	SJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	AJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	8 (17%)
71	GTP	JB	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.56	8 (16%)
71	GTP	HA	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.54	9 (18%)
69	GDP	SB	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	BK	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
71	GTP	PM	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.56	8 (16%)
71	GTP	NA	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	DD	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.56	9 (18%)
71	GTP	AK	501	70	33,34,34	0.98	1 (3%)	50,54,54	1.57	8 (16%)
71	GTP	JL	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
69	GDP	KI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	VL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	6 (13%)
69	GDP	MD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	OD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	AM	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	NM	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
69	GDP	EH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.72	7 (15%)
71	GTP	GI	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.58	9 (18%)
69	GDP	UL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	QE	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	WI	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.55	8 (16%)
71	GTP	PG	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.57	8 (16%)
69	GDP	RC	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
69	GDP	WF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	GL	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	GG	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
71	GTP	HG	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
71	GTP	VA	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	VH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	MK	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
69	GDP	ND	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	8 (17%)
69	GDP	LO	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	6 (13%)
69	GDP	TD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
71	GTP	CJ	501	70	33,34,34	0.98	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	EK	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.58	9 (18%)
71	GTP	OC	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	MH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	WB	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	A	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
71	GTP	HK	501	70	33,34,34	0.92	1 (3%)	50,54,54	1.60	9 (18%)
74	ATP	2v	501	-	32,33,33	0.29	0	48,52,52	0.31	0
71	GTP	SG	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.59	10 (20%)
71	GTP	KJ	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.58	8 (16%)
71	GTP	CL	501	70	33,34,34	1.00	3 (9%)	50,54,54	1.55	8 (16%)
71	GTP	DL	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.57	10 (20%)
69	GDP	SH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	BJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	PD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	TF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)
69	GDP	V	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
69	GDP	DA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.79	7 (15%)
69	GDP	N	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	EB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.72	6 (13%)
69	GDP	AL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	8 (17%)
71	GTP	NC	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	AE	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
71	GTP	UC	501	70	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
69	GDP	OJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
69	GDP	PL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
71	GTP	TC	501	70	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
69	GDP	TJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	6 (13%)
71	GTP	MM	501	70	33,34,34	0.96	1 (3%)	50,54,54	1.57	9 (18%)
69	GDP	FD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	OE	501	70	33,34,34	0.96	2 (6%)	50,54,54	1.59	10 (20%)
71	GTP	TA	501	70	33,34,34	0.98	2 (6%)	50,54,54	1.58	10 (20%)
71	GTP	PA	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.57	8 (16%)
69	GDP	CE	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	7 (15%)
69	GDP	SF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
71	GTP	VK	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.56	8 (16%)
69	GDP	HD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
71	GTP	WA	501	70	33,34,34	0.97	1 (3%)	50,54,54	1.56	9 (18%)
69	GDP	TL	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	7 (15%)
69	GDP	KM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
69	GDP	TH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
71	GTP	JN	501	70	33,34,34	0.93	1 (3%)	50,54,54	1.57	9 (18%)
71	GTP	KB	501	70	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
69	GDP	S	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GDP	NB	500	-	-	3/16/32/32	0/3/3/3
71	GTP	SE	501	70	-	5/22/38/38	0/3/3/3
71	GTP	QD	501	70	-	5/22/38/38	0/3/3/3
71	GTP	TG	501	70	-	1/22/38/38	0/3/3/3
71	GTP	QH	501	70	-	10/22/38/38	0/3/3/3
71	GTP	JH	501	70	-	5/22/38/38	0/3/3/3
71	GTP	IG	501	70	-	7/22/38/38	0/3/3/3
69	GDP	IB	500	-	-	3/16/32/32	0/3/3/3
71	GTP	ME	501	70	-	5/22/38/38	0/3/3/3
69	GDP	WL	500	-	-	1/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GDP	PH	500	-	-	1/16/32/32	0/3/3/3
71	GTP	WG	501	70	-	1/22/38/38	0/3/3/3
71	GTP	GA	501	70	-	8/22/38/38	0/3/3/3
69	GDP	IF	500	-	-	3/16/32/32	0/3/3/3
69	GDP	FF	500	-	-	2/16/32/32	0/3/3/3
69	GDP	OL	500	-	-	2/16/32/32	0/3/3/3
69	GDP	PB	500	-	-	1/16/32/32	0/3/3/3
69	GDP	UH	500	-	-	1/16/32/32	0/3/3/3
69	GDP	NH	500	-	-	2/16/32/32	0/3/3/3
71	GTP	UE	501	70	-	9/22/38/38	0/3/3/3
69	GDP	RA	500	-	-	1/16/32/32	0/3/3/3
71	GTP	LJ	501	70	-	4/22/38/38	0/3/3/3
71	GTP	UK	501	70	-	5/22/38/38	0/3/3/3
71	GTP	RL	501	70	-	9/22/38/38	0/3/3/3
69	GDP	AB	500	-	-	1/16/32/32	0/3/3/3
69	GDP	MB	500	-	-	2/16/32/32	0/3/3/3
69	GDP	PF	500	-	-	3/16/32/32	0/3/3/3
69	GDP	NJ	500	-	-	1/16/32/32	0/3/3/3
71	GTP	II	501	70	-	3/22/38/38	0/3/3/3
69	GDP	AF	500	-	-	1/16/32/32	0/3/3/3
69	GDP	HF	500	-	-	2/16/32/32	0/3/3/3
69	GDP	KK	500	-	-	1/16/32/32	0/3/3/3
69	GDP	UF	500	-	-	1/16/32/32	0/3/3/3
69	GDP	DG	500	-	-	2/16/32/32	0/3/3/3
69	GDP	AN	500	-	-	1/16/32/32	0/3/3/3
71	GTP	QJ	501	70	-	4/22/38/38	0/3/3/3
69	GDP	WD	500	-	-	2/16/32/32	0/3/3/3
69	GDP	GF	500	-	-	4/16/32/32	0/3/3/3
71	GTP	IM	501	70	-	4/22/38/38	0/3/3/3
71	GTP	WM	501	70	-	3/22/38/38	0/3/3/3
69	GDP	KC	500	-	-	1/16/32/32	0/3/3/3
71	GTP	RF	501	70	-	1/22/38/38	0/3/3/3
69	GDP	LG	500	-	-	2/16/32/32	0/3/3/3
71	GTP	LH	501	70	-	3/22/38/38	0/3/3/3
69	GDP	H	500	-	-	1/16/32/32	0/3/3/3
71	GTP	NE	501	70	-	4/22/38/38	0/3/3/3
71	GTP	AG	501	70	-	7/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	EA	501	70	-	8/22/38/38	0/3/3/3
71	GTP	DB	501	70	-	3/22/38/38	0/3/3/3
71	GTP	PK	501	70	-	3/22/38/38	0/3/3/3
71	GTP	DJ	501	70	-	4/22/38/38	0/3/3/3
71	GTP	SI	501	70	-	3/22/38/38	0/3/3/3
69	GDP	LI	500	-	-	3/16/32/32	0/3/3/3
69	GDP	CC	500	-	-	2/16/32/32	0/3/3/3
71	GTP	FE	501	70	-	5/22/38/38	0/3/3/3
71	GTP	MG	501	70	-	5/22/38/38	0/3/3/3
69	GDP	KA	500	-	-	3/16/32/32	0/3/3/3
69	GDP	ID	500	-	-	1/16/32/32	0/3/3/3
69	GDP	WJ	500	-	-	1/16/32/32	0/3/3/3
69	GDP	HJ	500	-	-	2/16/32/32	0/3/3/3
71	GTP	FA	501	70	-	3/22/38/38	0/3/3/3
71	GTP	JF	501	70	-	3/22/38/38	0/3/3/3
71	GTP	TI	501	70	-	4/22/38/38	0/3/3/3
69	GDP	RG	500	-	-	1/16/32/32	0/3/3/3
69	GDP	AH	500	-	-	2/16/32/32	0/3/3/3
69	GDP	EL	500	-	-	3/16/32/32	0/3/3/3
71	GTP	L	501	70	-	4/22/38/38	0/3/3/3
69	GDP	W	500	-	-	1/16/32/32	0/3/3/3
69	GDP	OF	500	-	-	1/16/32/32	0/3/3/3
71	GTP	VG	501	70	-	4/22/38/38	0/3/3/3
71	GTP	SK	501	70	-	0/22/38/38	0/3/3/3
71	GTP	OG	501	70	-	3/22/38/38	0/3/3/3
71	GTP	KD	501	70	-	3/22/38/38	0/3/3/3
71	GTP	C	501	70	-	6/22/38/38	0/3/3/3
71	GTP	KL	501	70	-	2/22/38/38	0/3/3/3
71	GTP	QF	501	70	-	2/22/38/38	0/3/3/3
69	GDP	JM	500	-	-	0/16/32/32	0/3/3/3
69	GDP	M	500	-	-	3/16/32/32	0/3/3/3
71	GTP	CF	501	70	-	7/22/38/38	0/3/3/3
69	GDP	BF	500	-	-	1/16/32/32	0/3/3/3
71	GTP	JJ	501	70	-	3/22/38/38	0/3/3/3
69	GDP	FH	500	-	-	1/16/32/32	0/3/3/3
71	GTP	R	501	70	-	6/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	EG	501	70	-	6/22/38/38	0/3/3/3
71	GTP	IE	501	70	-	2/22/38/38	0/3/3/3
71	GTP	BG	501	70	-	0/22/38/38	0/3/3/3
69	GDP	U	500	-	-	2/16/32/32	0/3/3/3
71	GTP	IK	501	70	-	3/22/38/38	0/3/3/3
71	GTP	GK	501	70	-	3/22/38/38	0/3/3/3
69	GDP	ML	500	-	-	1/16/32/32	0/3/3/3
69	GDP	QI	500	-	-	2/16/32/32	0/3/3/3
69	GDP	LC	500	-	-	2/16/32/32	0/3/3/3
71	GTP	VE	501	70	-	1/22/38/38	0/3/3/3
69	GDP	GH	500	-	-	3/16/32/32	0/3/3/3
71	GTP	RJ	501	-	-	1/22/38/38	0/3/3/3
71	GTP	OK	501	-	-	6/22/38/38	0/3/3/3
71	GTP	LF	501	70	-	2/22/38/38	0/3/3/3
71	GTP	FC	501	70	-	4/22/38/38	0/3/3/3
69	GDP	MF	500	-	-	3/16/32/32	0/3/3/3
71	GTP	IC	501	70	-	4/22/38/38	0/3/3/3
69	GDP	VB	500	-	-	1/16/32/32	0/3/3/3
69	GDP	LK	500	-	-	1/16/32/32	0/3/3/3
71	GTP	BM	501	70	-	6/22/38/38	0/3/3/3
69	GDP	IL	500	-	-	0/16/32/32	0/3/3/3
71	GTP	LL	501	70	-	4/22/38/38	0/3/3/3
69	GDP	LM	500	-	-	1/16/32/32	0/3/3/3
69	GDP	BH	500	-	-	2/16/32/32	0/3/3/3
71	GTP	D	501	-	-	12/22/38/38	0/3/3/3
69	GDP	RE	500	-	-	0/16/32/32	0/3/3/3
71	GTP	RD	501	70	-	7/22/38/38	0/3/3/3
69	GDP	CI	500	-	-	1/16/32/32	0/3/3/3
71	GTP	LB	501	70	-	3/22/38/38	0/3/3/3
69	GDP	UJ	500	-	-	1/16/32/32	0/3/3/3
69	GDP	GJ	500	-	-	2/16/32/32	0/3/3/3
71	GTP	DH	501	70	-	2/22/38/38	0/3/3/3
71	GTP	UA	501	70	-	5/22/38/38	0/3/3/3
69	GDP	JA	500	-	-	1/16/32/32	0/3/3/3
69	GDP	FJ	500	-	-	2/16/32/32	0/3/3/3
71	GTP	NG	501	-	-	6/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	UI	501	70	-	3/22/38/38	0/3/3/3
69	GDP	DI	500	-	-	2/16/32/32	0/3/3/3
71	GTP	OA	501	70	-	4/22/38/38	0/3/3/3
69	GDP	QG	500	-	-	1/16/32/32	0/3/3/3
69	GDP	CA	500	-	-	3/16/32/32	0/3/3/3
71	GTP	HM	501	70	-	3/22/38/38	0/3/3/3
69	GDP	BN	500	-	-	2/16/32/32	0/3/3/3
71	GTP	AA	501	70	-	4/22/38/38	0/3/3/3
71	GTP	MI	501	70	-	5/22/38/38	0/3/3/3
69	GDP	G	500	-	-	0/16/32/32	0/3/3/3
69	GDP	JG	500	-	-	2/16/32/32	0/3/3/3
69	GDP	SD	500	-	-	3/16/32/32	0/3/3/3
69	GDP	KG	500	-	-	2/16/32/32	0/3/3/3
69	GDP	VJ	500	-	-	2/16/32/32	0/3/3/3
71	GTP	KF	501	70	-	6/22/38/38	0/3/3/3
69	GDP	DM	500	-	-	1/16/32/32	0/3/3/3
71	GTP	CB	501	70	-	3/22/38/38	0/3/3/3
71	GTP	OI	501	70	-	6/22/38/38	0/3/3/3
69	GDP	HL	500	-	-	1/16/32/32	0/3/3/3
69	GDP	KE	500	-	-	1/16/32/32	0/3/3/3
69	GDP	BB	500	-	-	2/16/32/32	0/3/3/3
71	GTP	J	501	70	-	8/22/38/38	0/3/3/3
71	GTP	FI	501	70	-	3/22/38/38	0/3/3/3
71	GTP	UG	501	70	-	5/22/38/38	0/3/3/3
71	GTP	OM	501	70	-	5/22/38/38	0/3/3/3
71	GTP	SC	501	70	-	6/22/38/38	0/3/3/3
69	GDP	JC	500	-	-	2/16/32/32	0/3/3/3
69	GDP	RI	500	-	-	0/16/32/32	0/3/3/3
71	GTP	LN	501	70	-	3/22/38/38	0/3/3/3
69	GDP	JI	500	-	-	1/16/32/32	0/3/3/3
69	GDP	OH	500	-	-	3/16/32/32	0/3/3/3
69	GDP	MJ	500	-	-	3/16/32/32	0/3/3/3
69	GDP	PJ	500	-	-	3/16/32/32	0/3/3/3
71	GTP	JD	501	70	-	5/22/38/38	0/3/3/3
71	GTP	EE	501	70	-	5/22/38/38	0/3/3/3
69	GDP	JE	500	-	-	1/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GDP	IH	500	-	-	2/16/32/32	0/3/3/3
71	GTP	HC	501	70	-	7/22/38/38	0/3/3/3
69	GDP	DK	500	-	-	1/16/32/32	0/3/3/3
69	GDP	AD	500	-	-	2/16/32/32	0/3/3/3
69	GDP	QK	500	-	-	5/16/32/32	0/3/3/3
69	GDP	DC	500	-	-	1/16/32/32	0/3/3/3
69	GDP	E	500	-	-	4/16/32/32	0/3/3/3
71	GTP	HI	501	70	-	2/22/38/38	0/3/3/3
69	GDP	WH	500	-	-	2/16/32/32	0/3/3/3
69	GDP	CM	500	-	-	3/16/32/32	0/3/3/3
71	GTP	TE	501	70	-	6/22/38/38	0/3/3/3
69	GDP	F	500	-	-	3/16/32/32	0/3/3/3
69	GDP	OB	500	-	-	5/16/32/32	0/3/3/3
71	GTP	CH	501	70	-	5/22/38/38	0/3/3/3
69	GDP	RK	500	-	-	2/16/32/32	0/3/3/3
69	GDP	LE	500	-	-	2/16/32/32	0/3/3/3
71	GTP	WC	501	70	-	2/22/38/38	0/3/3/3
71	GTP	EC	501	70	-	4/22/38/38	0/3/3/3
71	GTP	NI	501	70	-	1/22/38/38	0/3/3/3
71	GTP	BA	501	70	-	3/22/38/38	0/3/3/3
69	GDP	NF	500	-	-	3/16/32/32	0/3/3/3
71	GTP	AC	501	70	-	4/22/38/38	0/3/3/3
71	GTP	PE	501	70	-	0/22/38/38	0/3/3/3
71	GTP	MA	501	70	-	0/22/38/38	0/3/3/3
69	GDP	FL	500	-	-	3/16/32/32	0/3/3/3
71	GTP	CD	501	70	-	3/22/38/38	0/3/3/3
71	GTP	RB	501	70	-	3/22/38/38	0/3/3/3
71	GTP	VI	501	70	-	4/22/38/38	0/3/3/3
71	GTP	FG	501	70	-	7/22/38/38	0/3/3/3
69	GDP	MN	500	-	-	2/16/32/32	0/3/3/3
71	GTP	BC	501	70	-	0/22/38/38	0/3/3/3
71	GTP	AI	501	70	-	0/22/38/38	0/3/3/3
71	GTP	WK	501	70	-	5/22/38/38	0/3/3/3
71	GTP	QB	501	70	-	2/22/38/38	0/3/3/3
69	GDP	EF	500	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	BI	501	70	-	6/22/38/38	0/3/3/3
71	GTP	MC	501	70	-	4/22/38/38	0/3/3/3
69	GDP	UB	500	-	-	3/16/32/32	0/3/3/3
69	GDP	I	500	-	-	0/16/32/32	0/3/3/3
69	GDP	ED	500	-	-	4/16/32/32	0/3/3/3
69	GDP	T	500	-	-	1/16/32/32	0/3/3/3
71	GTP	VC	501	70	-	6/22/38/38	0/3/3/3
69	GDP	DE	500	-	-	1/16/32/32	0/3/3/3
69	GDP	CK	500	-	-	3/16/32/32	0/3/3/3
69	GDP	IJ	500	-	-	2/16/32/32	0/3/3/3
71	GTP	VM	501	70	-	5/22/38/38	0/3/3/3
71	GTP	BE	501	70	-	9/22/38/38	0/3/3/3
69	GDP	CG	500	-	-	2/16/32/32	0/3/3/3
71	GTP	LD	501	70	-	6/22/38/38	0/3/3/3
71	GTP	WE	501	70	-	8/22/38/38	0/3/3/3
69	GDP	TB	500	-	-	3/16/32/32	0/3/3/3
69	GDP	JK	500	-	-	3/16/32/32	0/3/3/3
71	GTP	GC	501	70	-	3/22/38/38	0/3/3/3
71	GTP	RH	501	70	-	2/22/38/38	0/3/3/3
69	GDP	BD	500	-	-	1/16/32/32	0/3/3/3
69	GDP	O	500	-	-	2/16/32/32	0/3/3/3
71	GTP	DF	501	70	-	6/22/38/38	0/3/3/3
69	GDP	EJ	500	-	-	1/16/32/32	0/3/3/3
71	GTP	FK	501	-	-	3/22/38/38	0/3/3/3
71	GTP	QL	501	-	-	3/22/38/38	0/3/3/3
69	GDP	FB	500	-	-	0/16/32/32	0/3/3/3
71	GTP	PI	501	70	-	4/22/38/38	0/3/3/3
71	GTP	TK	501	70	-	5/22/38/38	0/3/3/3
71	GTP	KH	501	70	-	5/22/38/38	0/3/3/3
69	GDP	QA	500	-	-	1/16/32/32	0/3/3/3
71	GTP	EI	501	70	-	2/22/38/38	0/3/3/3
69	GDP	QC	500	-	-	2/16/32/32	0/3/3/3
69	GDP	GB	500	-	-	1/16/32/32	0/3/3/3
69	GDP	GD	500	-	-	1/16/32/32	0/3/3/3
69	GDP	HH	500	-	-	1/16/32/32	0/3/3/3
69	GDP	BL	500	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	K	501	70	-	2/22/38/38	0/3/3/3
69	GDP	LA	500	-	-	2/16/32/32	0/3/3/3
69	GDP	HB	500	-	-	3/16/32/32	0/3/3/3
74	ATP	2w	501	-	-	7/22/38/38	0/3/3/3
69	GDP	VF	500	-	-	1/16/32/32	0/3/3/3
71	GTP	NK	501	-	-	3/22/38/38	0/3/3/3
69	GDP	NL	500	-	-	1/16/32/32	0/3/3/3
71	GTP	SA	501	70	-	3/22/38/38	0/3/3/3
69	GDP	P	500	-	-	2/16/32/32	0/3/3/3
71	GTP	GE	501	70	-	4/22/38/38	0/3/3/3
69	GDP	VD	500	-	-	1/16/32/32	0/3/3/3
71	GTP	HE	501	70	-	4/22/38/38	0/3/3/3
71	GTP	Q	501	70	-	3/22/38/38	0/3/3/3
69	GDP	UD	500	-	-	3/16/32/32	0/3/3/3
71	GTP	PC	501	70	-	3/22/38/38	0/3/3/3
71	GTP	KN	501	70	-	3/22/38/38	0/3/3/3
71	GTP	IA	501	70	-	6/22/38/38	0/3/3/3
69	GDP	SJ	500	-	-	2/16/32/32	0/3/3/3
69	GDP	AJ	500	-	-	1/16/32/32	0/3/3/3
71	GTP	JB	501	70	-	2/22/38/38	0/3/3/3
71	GTP	HA	501	70	-	3/22/38/38	0/3/3/3
69	GDP	SB	500	-	-	3/16/32/32	0/3/3/3
71	GTP	BK	501	70	-	5/22/38/38	0/3/3/3
71	GTP	PM	501	70	-	3/22/38/38	0/3/3/3
71	GTP	NA	501	-	-	7/22/38/38	0/3/3/3
71	GTP	DD	501	70	-	3/22/38/38	0/3/3/3
71	GTP	AK	501	70	-	3/22/38/38	0/3/3/3
71	GTP	JL	501	70	-	3/22/38/38	0/3/3/3
69	GDP	KI	500	-	-	3/16/32/32	0/3/3/3
69	GDP	VL	500	-	-	1/16/32/32	0/3/3/3
69	GDP	MD	500	-	-	1/16/32/32	0/3/3/3
69	GDP	OD	500	-	-	2/16/32/32	0/3/3/3
71	GTP	AM	501	70	-	5/22/38/38	0/3/3/3
71	GTP	NM	501	70	-	4/22/38/38	0/3/3/3
69	GDP	EH	500	-	-	1/16/32/32	0/3/3/3
71	GTP	GI	501	70	-	0/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GDP	UL	500	-	-	1/16/32/32	0/3/3/3
69	GDP	QE	500	-	-	2/16/32/32	0/3/3/3
71	GTP	WI	501	70	-	3/22/38/38	0/3/3/3
71	GTP	PG	501	-	-	5/22/38/38	0/3/3/3
69	GDP	RC	500	-	-	1/16/32/32	0/3/3/3
69	GDP	WF	500	-	-	1/16/32/32	0/3/3/3
69	GDP	GL	500	-	-	3/16/32/32	0/3/3/3
71	GTP	GG	501	70	-	4/22/38/38	0/3/3/3
71	GTP	HG	501	70	-	3/22/38/38	0/3/3/3
71	GTP	VA	501	70	-	4/22/38/38	0/3/3/3
69	GDP	VH	500	-	-	1/16/32/32	0/3/3/3
71	GTP	MK	501	70	-	5/22/38/38	0/3/3/3
69	GDP	ND	500	-	-	0/16/32/32	0/3/3/3
69	GDP	LO	500	-	-	3/16/32/32	0/3/3/3
69	GDP	TD	500	-	-	1/16/32/32	0/3/3/3
71	GTP	CJ	501	70	-	3/22/38/38	0/3/3/3
71	GTP	EK	501	70	-	3/22/38/38	0/3/3/3
71	GTP	OC	501	70	-	1/22/38/38	0/3/3/3
69	GDP	MH	500	-	-	1/16/32/32	0/3/3/3
69	GDP	WB	500	-	-	1/16/32/32	0/3/3/3
69	GDP	A	500	-	-	2/16/32/32	0/3/3/3
71	GTP	HK	501	70	-	4/22/38/38	0/3/3/3
74	ATP	2v	501	-	-	5/22/38/38	0/3/3/3
71	GTP	SG	501	70	-	8/22/38/38	0/3/3/3
71	GTP	KJ	501	70	-	3/22/38/38	0/3/3/3
71	GTP	CL	501	70	-	8/22/38/38	0/3/3/3
71	GTP	DL	501	-	-	8/22/38/38	0/3/3/3
69	GDP	SH	500	-	-	2/16/32/32	0/3/3/3
69	GDP	BJ	500	-	-	2/16/32/32	0/3/3/3
69	GDP	PD	500	-	-	4/16/32/32	0/3/3/3
69	GDP	TF	500	-	-	1/16/32/32	0/3/3/3
69	GDP	V	500	-	-	1/16/32/32	0/3/3/3
69	GDP	DA	500	-	-	4/16/32/32	0/3/3/3
69	GDP	N	500	-	-	1/16/32/32	0/3/3/3
69	GDP	EB	500	-	-	4/16/32/32	0/3/3/3
69	GDP	AL	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	NC	501	70	-	3/22/38/38	0/3/3/3
71	GTP	AE	501	70	-	4/22/38/38	0/3/3/3
71	GTP	UC	501	70	-	3/22/38/38	0/3/3/3
69	GDP	OJ	500	-	-	3/16/32/32	0/3/3/3
69	GDP	PL	500	-	-	1/16/32/32	0/3/3/3
71	GTP	TC	501	70	-	5/22/38/38	0/3/3/3
69	GDP	TJ	500	-	-	2/16/32/32	0/3/3/3
71	GTP	MM	501	70	-	2/22/38/38	0/3/3/3
69	GDP	FD	500	-	-	2/16/32/32	0/3/3/3
71	GTP	OE	501	70	-	4/22/38/38	0/3/3/3
71	GTP	TA	501	70	-	7/22/38/38	0/3/3/3
71	GTP	PA	501	70	-	0/22/38/38	0/3/3/3
69	GDP	CE	500	-	-	1/16/32/32	0/3/3/3
69	GDP	SF	500	-	-	1/16/32/32	0/3/3/3
71	GTP	VK	501	70	-	5/22/38/38	0/3/3/3
69	GDP	HD	500	-	-	3/16/32/32	0/3/3/3
71	GTP	WA	501	70	-	2/22/38/38	0/3/3/3
69	GDP	TL	500	-	-	0/16/32/32	0/3/3/3
69	GDP	KM	500	-	-	2/16/32/32	0/3/3/3
69	GDP	TH	500	-	-	1/16/32/32	0/3/3/3
71	GTP	JN	501	70	-	3/22/38/38	0/3/3/3
71	GTP	KB	501	70	-	4/22/38/38	0/3/3/3
69	GDP	S	500	-	-	2/16/32/32	0/3/3/3

The worst 5 of 685 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
71	IK	501	GTP	PB-O3A	3.42	1.63	1.59
69	QK	500	GDP	C5-C4	3.14	1.47	1.38
69	CK	500	GDP	C5-C4	3.13	1.47	1.38
69	G	500	GDP	C5-C4	3.12	1.47	1.38
69	GB	500	GDP	C5-C4	3.11	1.47	1.38

The worst 5 of 2496 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
69	CK	500	GDP	C5-C4-N3	-6.44	118.14	128.39
69	P	500	GDP	C5-C4-N3	-6.37	118.25	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
69	QK	500	GDP	C5-C4-N3	-6.26	118.44	128.39
69	TL	500	GDP	C5-C4-N3	-6.23	118.47	128.39
69	DA	500	GDP	C5-C4-N3	-6.23	118.48	128.39

There are no chirality outliers.

5 of 946 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
69	AB	500	GDP	C5'-O5'-PA-O1A
69	AD	500	GDP	C5'-O5'-PA-O1A
69	AF	500	GDP	C5'-O5'-PA-O1A
69	AH	500	GDP	C5'-O5'-PA-O1A
69	AJ	500	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

264 monomers are involved in 509 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	NB	500	GDP	4	0
71	SE	501	GTP	1	0
71	TG	501	GTP	2	0
71	QH	501	GTP	3	0
71	JH	501	GTP	1	0
69	IB	500	GDP	2	0
71	ME	501	GTP	2	0
69	WL	500	GDP	2	0
69	PH	500	GDP	3	0
71	WG	501	GTP	4	0
71	GA	501	GTP	1	0
69	FF	500	GDP	2	0
69	OL	500	GDP	2	0
69	PB	500	GDP	2	0
69	NH	500	GDP	1	0
69	RA	500	GDP	3	0
71	LJ	501	GTP	2	0
71	UK	501	GTP	1	0
71	RL	501	GTP	2	0
69	AB	500	GDP	3	0
69	MB	500	GDP	3	0
69	PF	500	GDP	2	0
69	NJ	500	GDP	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	II	501	GTP	2	0
69	AF	500	GDP	3	0
69	HF	500	GDP	1	0
69	KK	500	GDP	5	0
69	UF	500	GDP	1	0
69	DG	500	GDP	2	0
69	AN	500	GDP	3	0
71	QJ	501	GTP	1	0
69	WD	500	GDP	1	0
69	GF	500	GDP	4	0
71	IM	501	GTP	1	0
71	WM	501	GTP	2	0
69	KC	500	GDP	1	0
71	RF	501	GTP	3	0
69	LG	500	GDP	2	0
71	LH	501	GTP	2	0
69	H	500	GDP	1	0
71	NE	501	GTP	1	0
71	AG	501	GTP	1	0
71	DB	501	GTP	2	0
71	PK	501	GTP	2	0
71	DJ	501	GTP	1	0
71	SI	501	GTP	2	0
69	LI	500	GDP	3	0
69	CC	500	GDP	1	0
71	MG	501	GTP	2	0
69	KA	500	GDP	1	0
69	ID	500	GDP	2	0
69	WJ	500	GDP	3	0
69	HJ	500	GDP	2	0
71	FA	501	GTP	2	0
71	JF	501	GTP	1	0
71	TI	501	GTP	4	0
69	AH	500	GDP	3	0
69	EL	500	GDP	3	0
71	L	501	GTP	1	0
69	W	500	GDP	1	0
69	OF	500	GDP	1	0
71	VG	501	GTP	1	0
71	SK	501	GTP	2	0
71	OG	501	GTP	1	0
71	KD	501	GTP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	KL	501	GTP	1	0
71	QF	501	GTP	2	0
69	JM	500	GDP	1	0
69	M	500	GDP	2	0
71	JJ	501	GTP	1	0
69	FH	500	GDP	1	0
71	R	501	GTP	3	0
71	EG	501	GTP	1	0
71	IE	501	GTP	2	0
71	BG	501	GTP	4	0
69	U	500	GDP	1	0
71	IK	501	GTP	3	0
71	GK	501	GTP	1	0
69	ML	500	GDP	2	0
69	QI	500	GDP	2	0
69	LC	500	GDP	3	0
71	VE	501	GTP	1	0
69	GH	500	GDP	1	0
71	RJ	501	GTP	1	0
71	LF	501	GTP	1	0
69	MF	500	GDP	6	0
71	IC	501	GTP	2	0
69	LK	500	GDP	1	0
71	BM	501	GTP	4	0
69	IL	500	GDP	1	0
71	LL	501	GTP	1	0
69	LM	500	GDP	1	0
69	BH	500	GDP	2	0
71	D	501	GTP	5	0
71	RD	501	GTP	3	0
69	CI	500	GDP	1	0
71	LB	501	GTP	1	0
69	GJ	500	GDP	1	0
71	UA	501	GTP	1	0
69	JA	500	GDP	2	0
71	NG	501	GTP	1	0
71	UI	501	GTP	2	0
69	DI	500	GDP	3	0
71	OA	501	GTP	3	0
69	QG	500	GDP	2	0
69	CA	500	GDP	2	0
71	HM	501	GTP	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	AA	501	GTP	2	0
71	MI	501	GTP	2	0
69	JG	500	GDP	1	0
69	SD	500	GDP	1	0
69	KG	500	GDP	3	0
69	VJ	500	GDP	3	0
71	KF	501	GTP	2	0
69	DM	500	GDP	2	0
71	CB	501	GTP	2	0
69	HL	500	GDP	4	0
69	KE	500	GDP	2	0
69	BB	500	GDP	1	0
71	UG	501	GTP	2	0
71	OM	501	GTP	1	0
69	JC	500	GDP	2	0
69	RI	500	GDP	3	0
71	LN	501	GTP	1	0
69	JI	500	GDP	3	0
69	OH	500	GDP	1	0
69	MJ	500	GDP	3	0
71	EE	501	GTP	1	0
69	JE	500	GDP	1	0
69	IH	500	GDP	1	0
69	DK	500	GDP	4	0
69	AD	500	GDP	1	0
69	QK	500	GDP	7	0
69	DC	500	GDP	3	0
69	E	500	GDP	1	0
71	HI	501	GTP	2	0
69	WH	500	GDP	3	0
69	CM	500	GDP	3	0
71	TE	501	GTP	1	0
69	F	500	GDP	1	0
69	OB	500	GDP	5	0
71	CH	501	GTP	3	0
69	RK	500	GDP	1	0
69	LE	500	GDP	3	0
69	NF	500	GDP	2	0
71	AC	501	GTP	2	0
71	PE	501	GTP	5	0
69	FL	500	GDP	1	0
71	RB	501	GTP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	MN	500	GDP	2	0
71	BC	501	GTP	1	0
71	WK	501	GTP	1	0
71	QB	501	GTP	1	0
69	EF	500	GDP	1	0
71	MC	501	GTP	1	0
69	UB	500	GDP	1	0
69	I	500	GDP	4	0
69	ED	500	GDP	1	0
69	T	500	GDP	1	0
71	VC	501	GTP	1	0
69	DE	500	GDP	1	0
69	CK	500	GDP	1	0
69	IJ	500	GDP	1	0
71	VM	501	GTP	3	0
71	BE	501	GTP	2	0
69	CG	500	GDP	3	0
69	TB	500	GDP	1	0
69	JK	500	GDP	1	0
71	GC	501	GTP	4	0
71	RH	501	GTP	3	0
69	BD	500	GDP	1	0
69	O	500	GDP	3	0
69	EJ	500	GDP	1	0
71	FK	501	GTP	1	0
71	QL	501	GTP	2	0
69	FB	500	GDP	2	0
71	PI	501	GTP	3	0
71	TK	501	GTP	1	0
71	KH	501	GTP	2	0
69	QA	500	GDP	2	0
71	EI	501	GTP	2	0
69	QC	500	GDP	2	0
69	GB	500	GDP	3	0
69	HH	500	GDP	3	0
69	BL	500	GDP	1	0
71	K	501	GTP	2	0
69	HB	500	GDP	1	0
69	VF	500	GDP	1	0
71	NK	501	GTP	2	0
69	NL	500	GDP	3	0
69	P	500	GDP	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	GE	501	GTP	1	0
69	VD	500	GDP	1	0
71	HE	501	GTP	1	0
69	UD	500	GDP	3	0
71	PC	501	GTP	2	0
71	KN	501	GTP	1	0
71	IA	501	GTP	1	0
69	AJ	500	GDP	2	0
71	JB	501	GTP	1	0
71	HA	501	GTP	1	0
71	BK	501	GTP	1	0
71	PM	501	GTP	1	0
71	NA	501	GTP	1	0
71	DD	501	GTP	3	0
71	AK	501	GTP	1	0
71	JL	501	GTP	2	0
69	KI	500	GDP	2	0
69	VL	500	GDP	3	0
69	MD	500	GDP	2	0
69	OD	500	GDP	2	0
71	AM	501	GTP	1	0
71	NM	501	GTP	1	0
69	EH	500	GDP	2	0
71	GI	501	GTP	5	0
69	UL	500	GDP	3	0
69	QE	500	GDP	1	0
71	WI	501	GTP	3	0
71	PG	501	GTP	4	0
69	RC	500	GDP	2	0
69	WF	500	GDP	1	0
69	GL	500	GDP	1	0
71	GG	501	GTP	3	0
71	HG	501	GTP	1	0
71	VA	501	GTP	1	0
69	VH	500	GDP	1	0
69	ND	500	GDP	3	0
69	LO	500	GDP	3	0
69	TD	500	GDP	2	0
71	CJ	501	GTP	1	0
71	OC	501	GTP	5	0
69	WB	500	GDP	1	0
69	A	500	GDP	1	0

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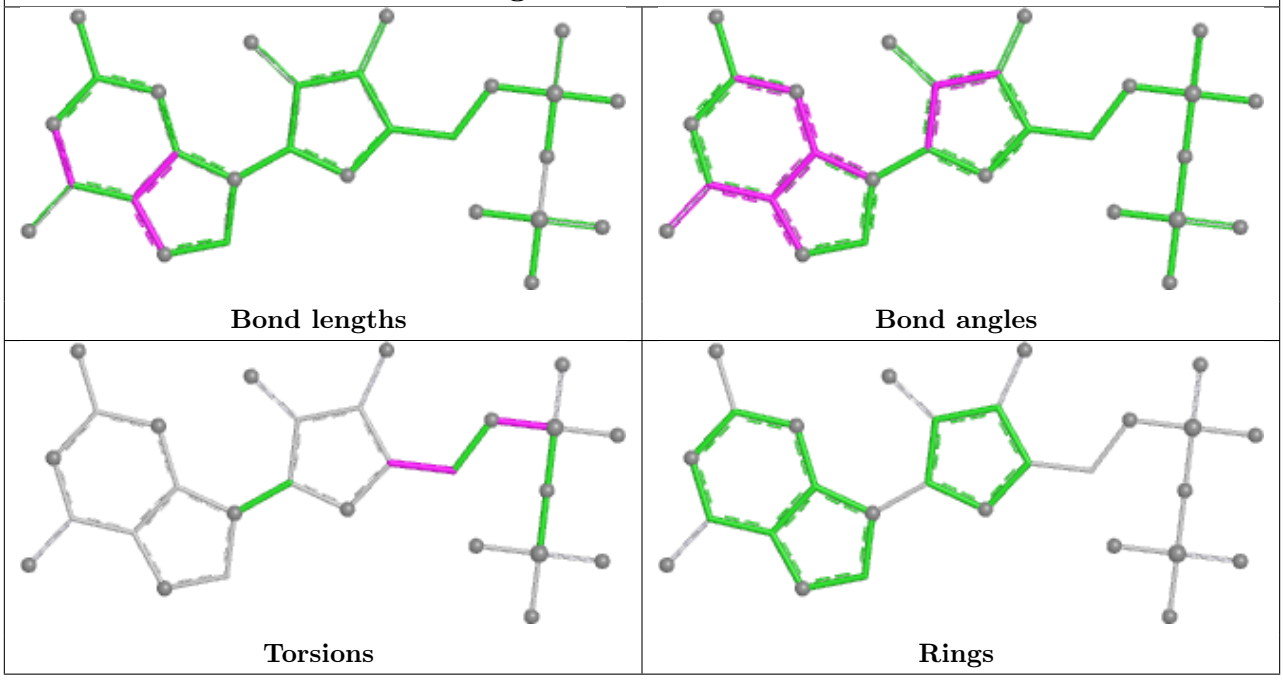
Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	HK	501	GTP	2	0
74	2v	501	ATP	1	0
71	SG	501	GTP	1	0
71	KJ	501	GTP	1	0
71	DL	501	GTP	2	0
69	SH	500	GDP	2	0
69	PD	500	GDP	1	0
69	TF	500	GDP	1	0
69	V	500	GDP	2	0
69	DA	500	GDP	1	0
69	N	500	GDP	3	0
69	EB	500	GDP	2	0
69	AL	500	GDP	2	0
71	NC	501	GTP	1	0
71	AE	501	GTP	1	0
71	UC	501	GTP	2	0
69	OJ	500	GDP	1	0
69	PL	500	GDP	2	0
69	TJ	500	GDP	1	0
69	FD	500	GDP	1	0
71	PA	501	GTP	1	0
69	CE	500	GDP	2	0
69	SF	500	GDP	3	0
71	VK	501	GTP	1	0
69	HD	500	GDP	2	0
69	TL	500	GDP	3	0
69	KM	500	GDP	1	0
69	TH	500	GDP	1	0
71	JN	501	GTP	1	0
71	KB	501	GTP	1	0
69	S	500	GDP	1	0

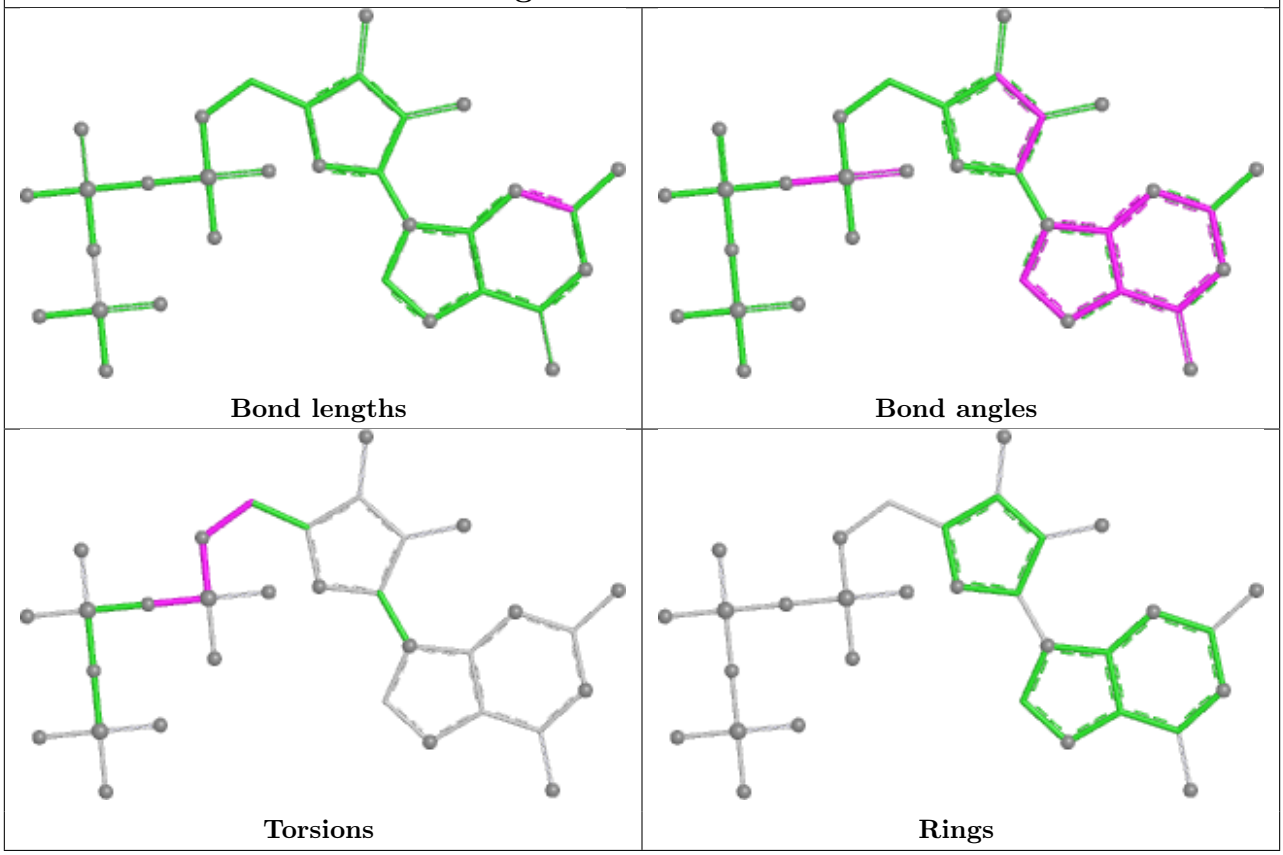
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

equivalents in the CSD to analyse the geometry.

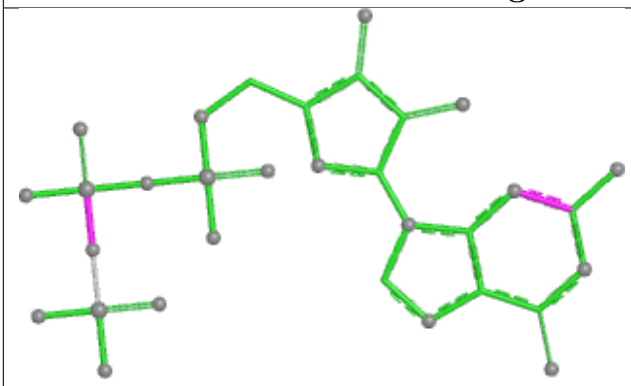
Ligand GDP NB 500



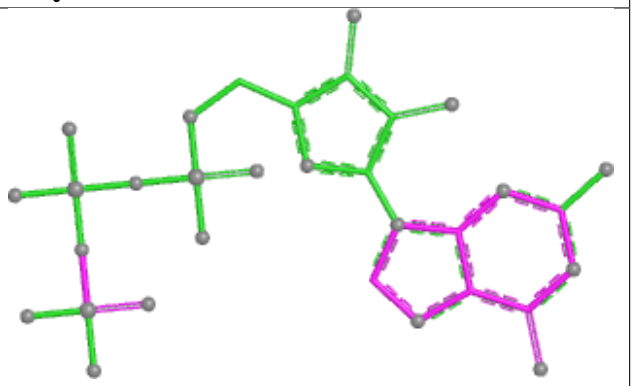
Ligand GTP SE 501



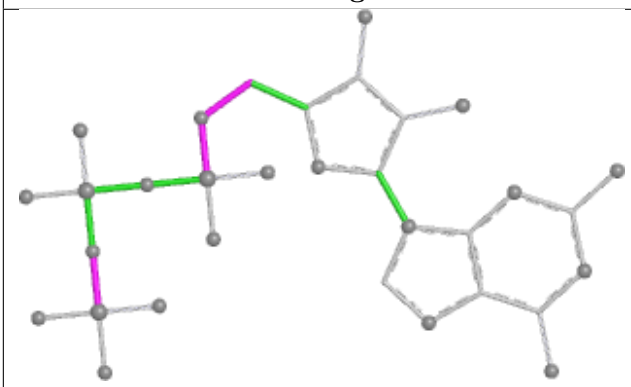
Ligand GTP QD 501



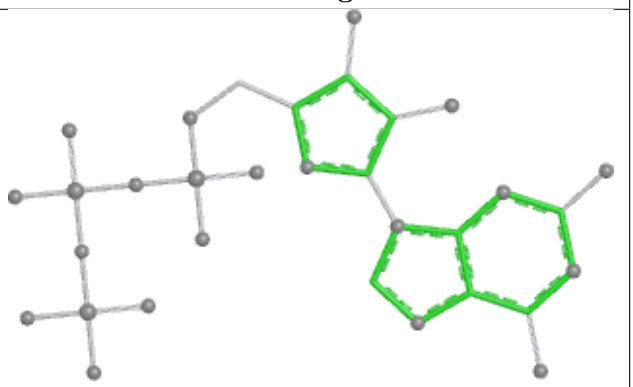
Bond lengths



Bond angles

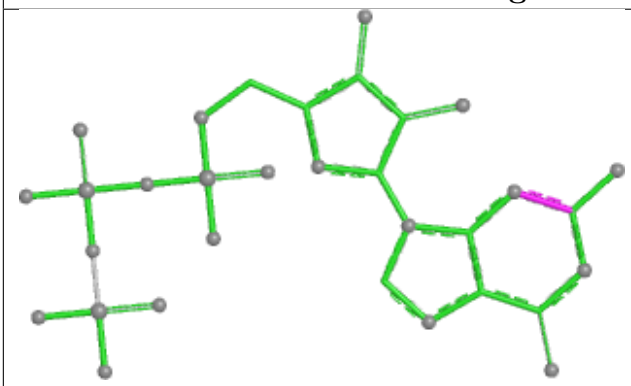


Torsions



Rings

Ligand GTP TG 501



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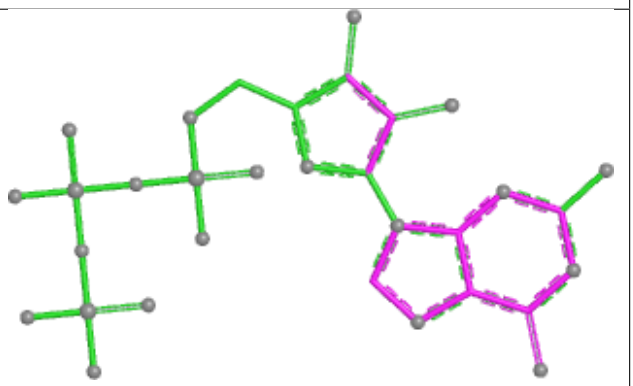

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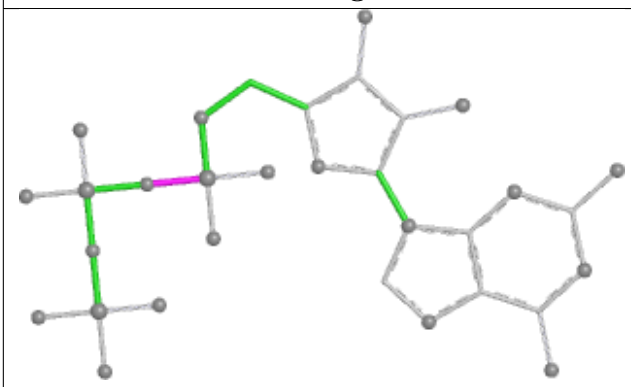

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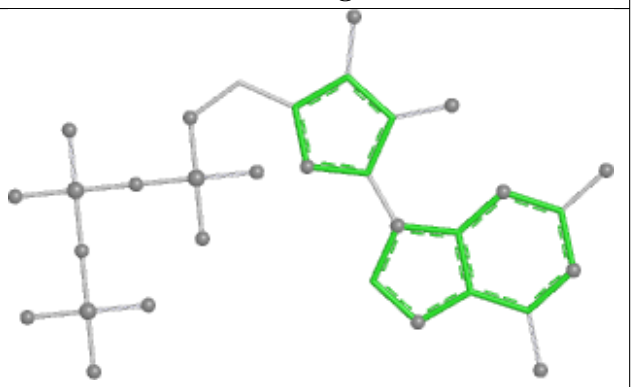
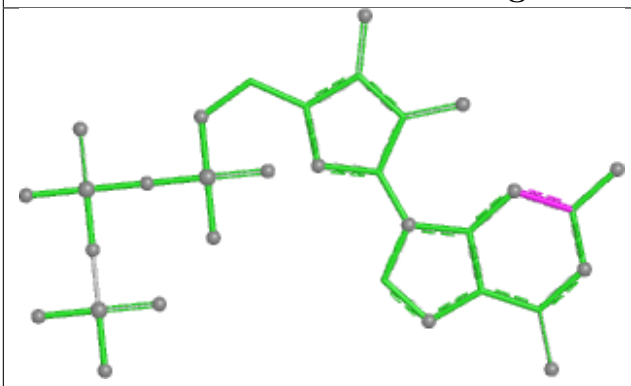


Rings

Ligand GTP QH 501



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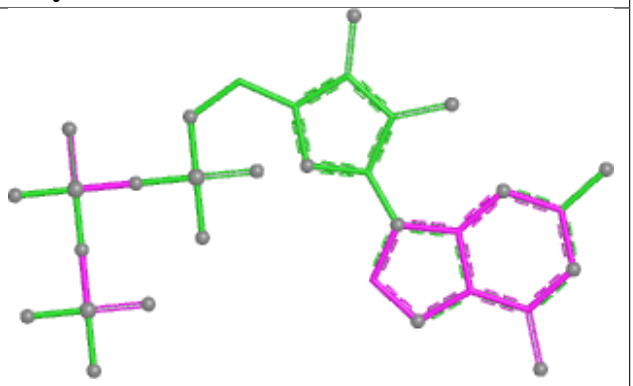

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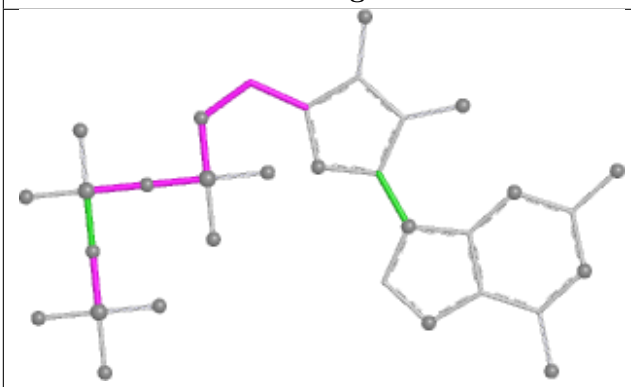

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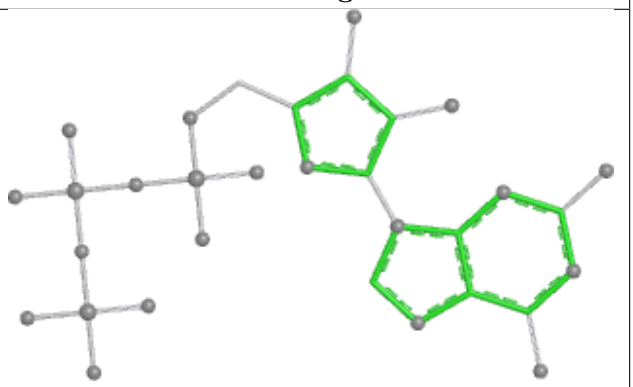
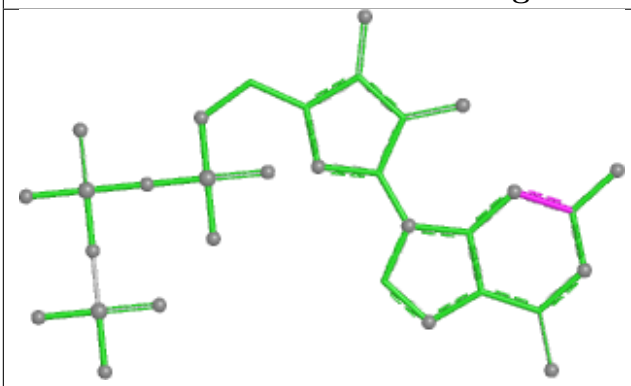


Rings

Ligand GTP JH 501



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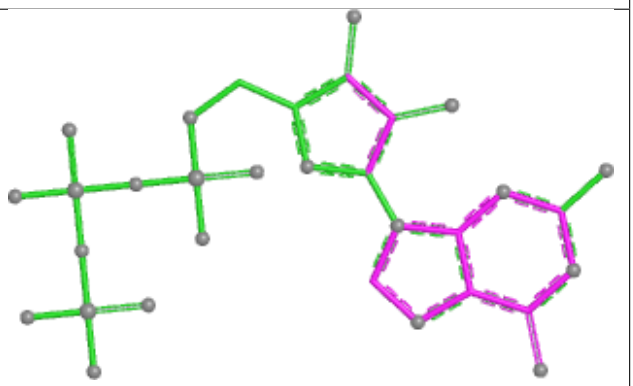

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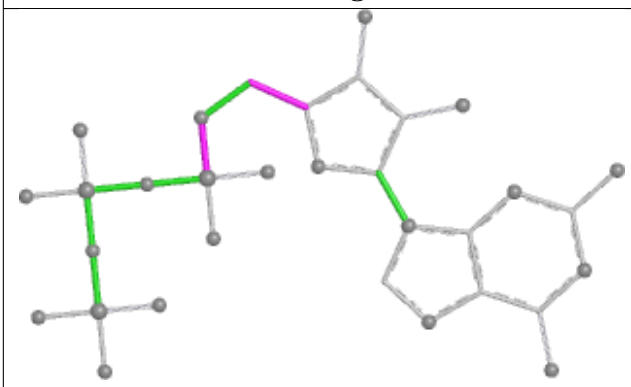

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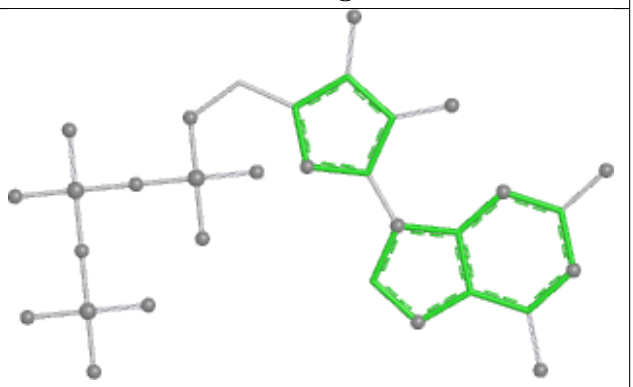
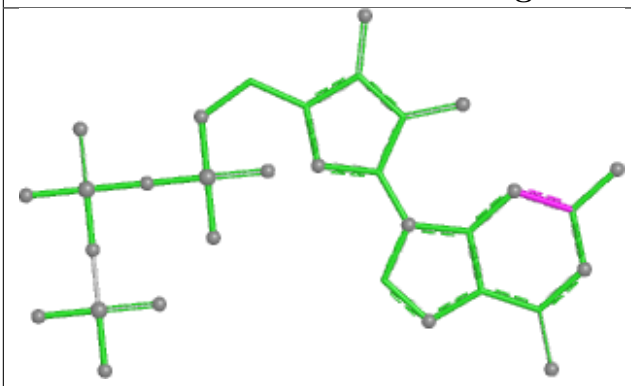


Rings

Ligand GTP IG 501



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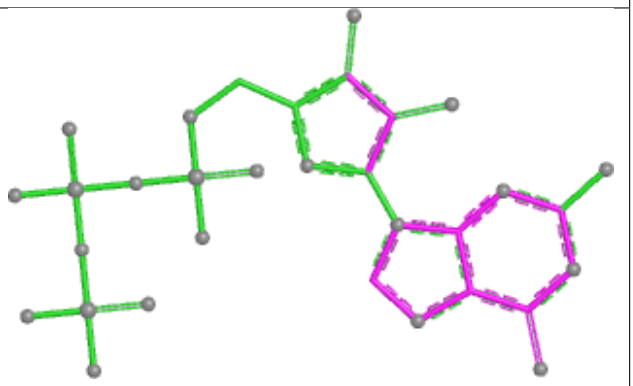

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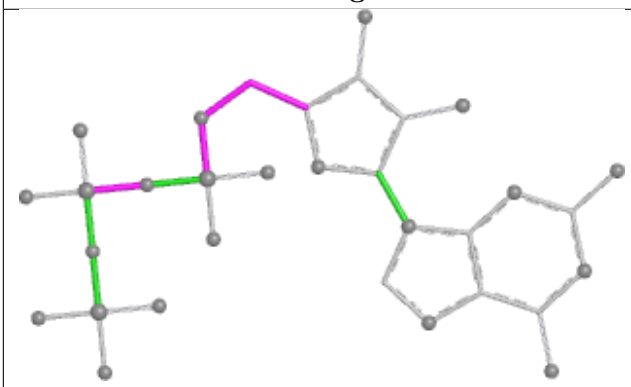

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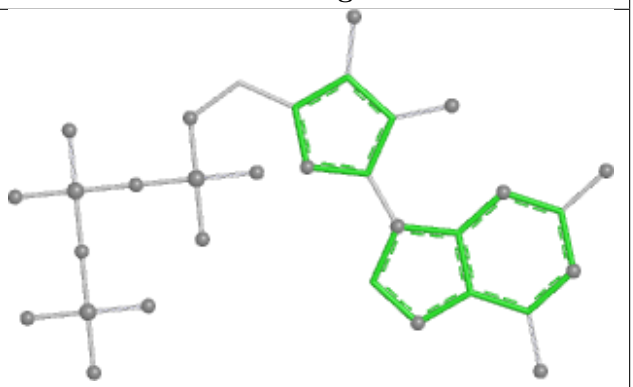
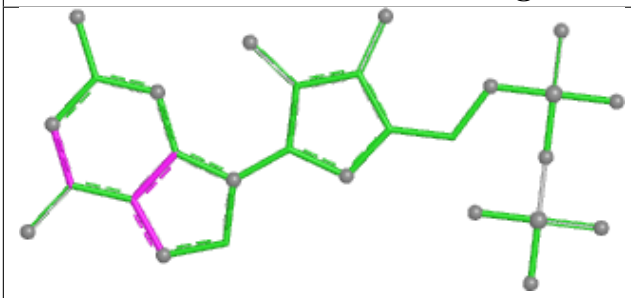


Rings

Ligand GDP IB 500



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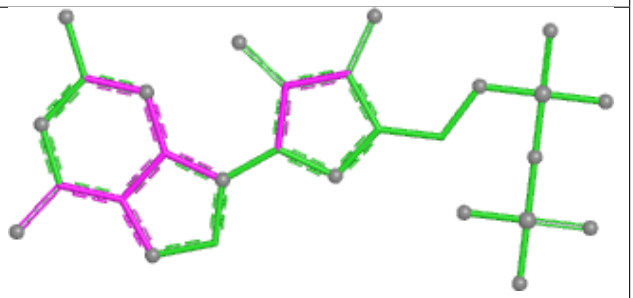

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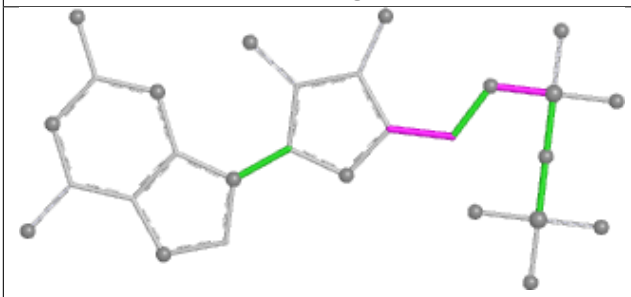

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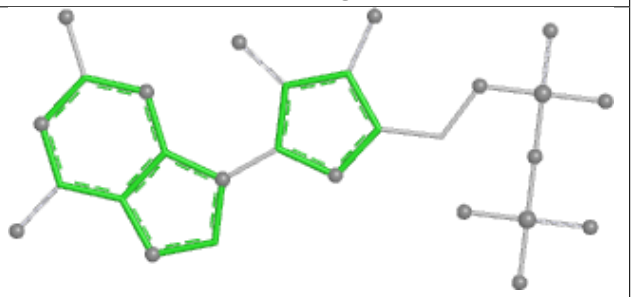

Rings

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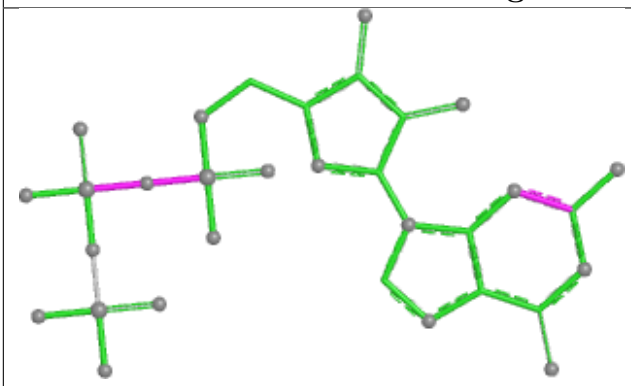

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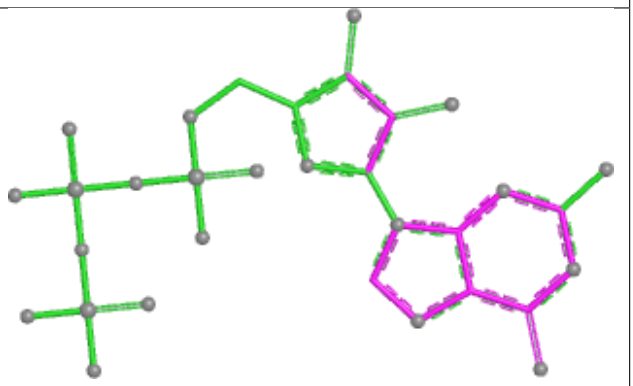

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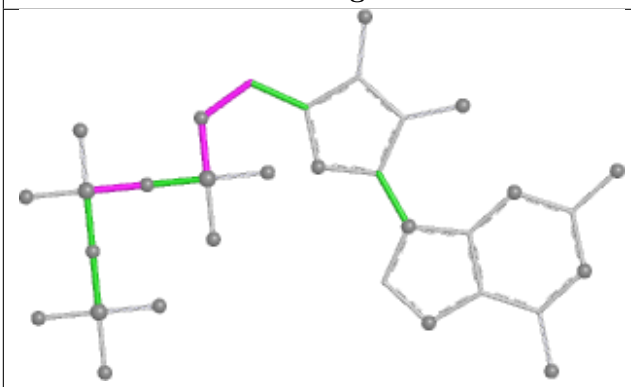

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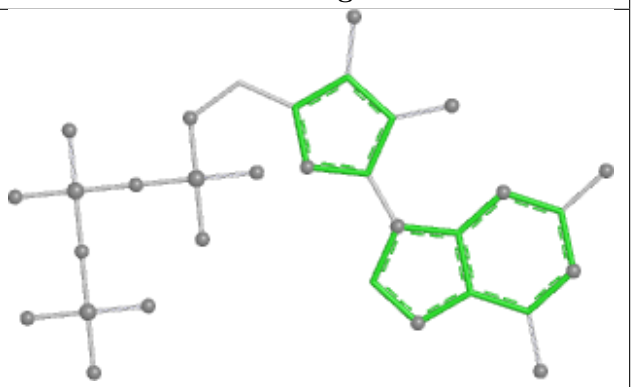
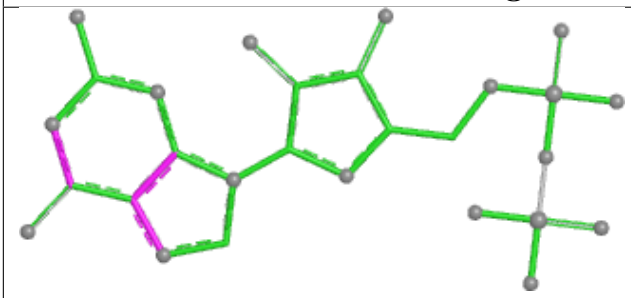


Rings

Ligand GDP WL 500



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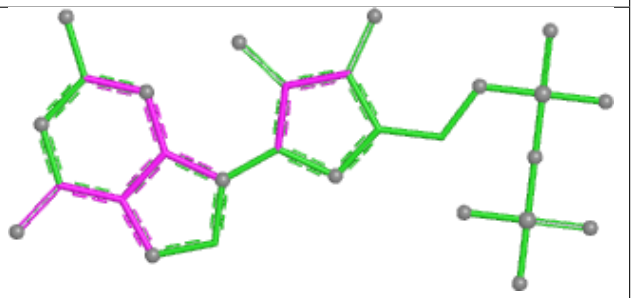

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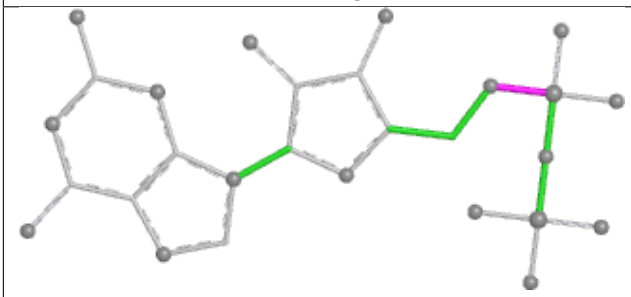

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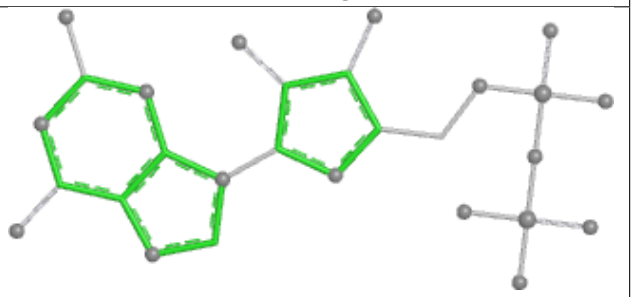
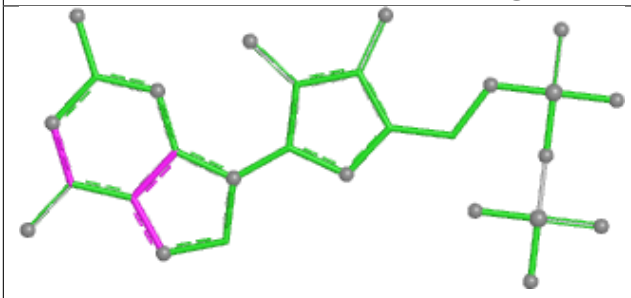


Rings

Ligand GDP PH 500



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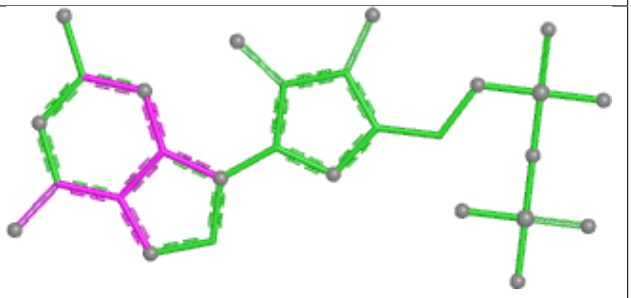

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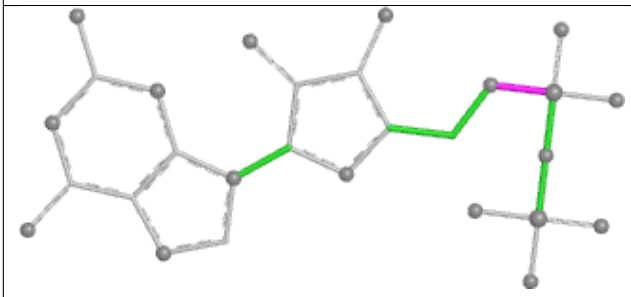

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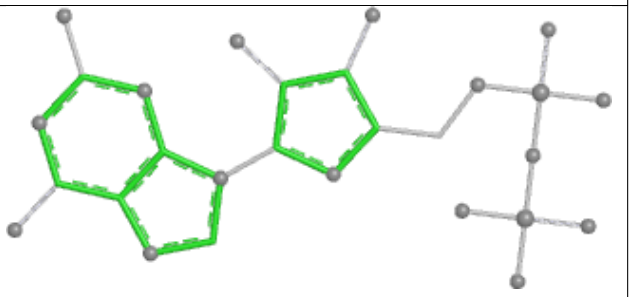
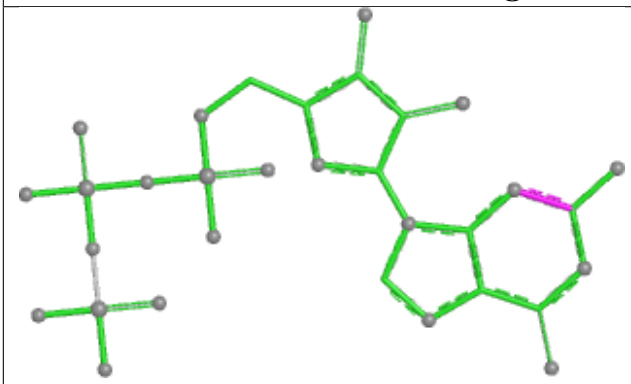


Rings

Ligand GTP WG 501



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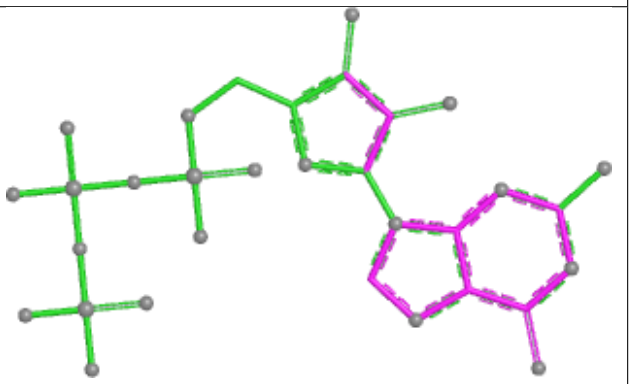

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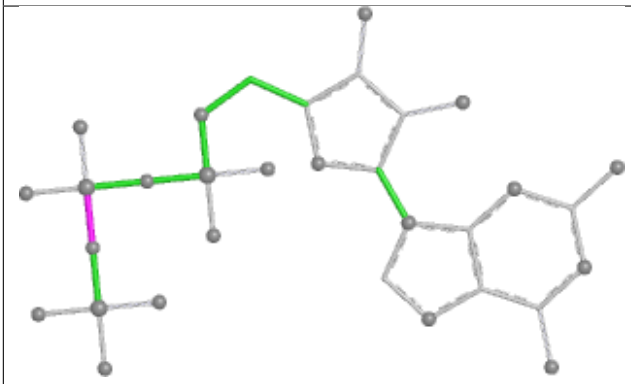

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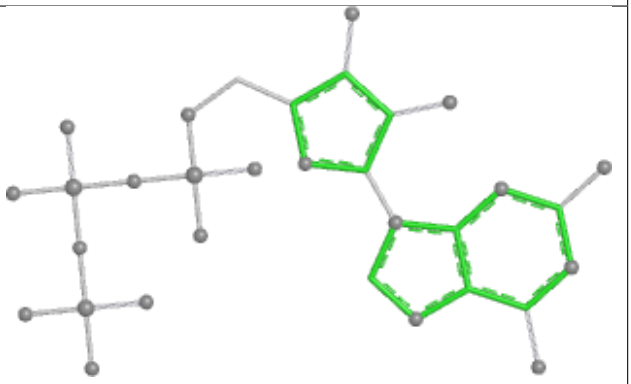
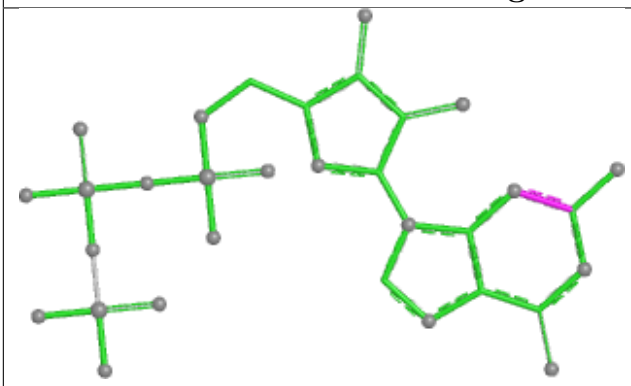


Rings

Ligand GTP GA 501



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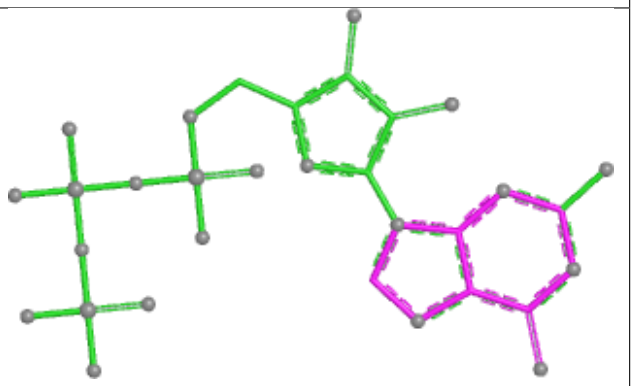

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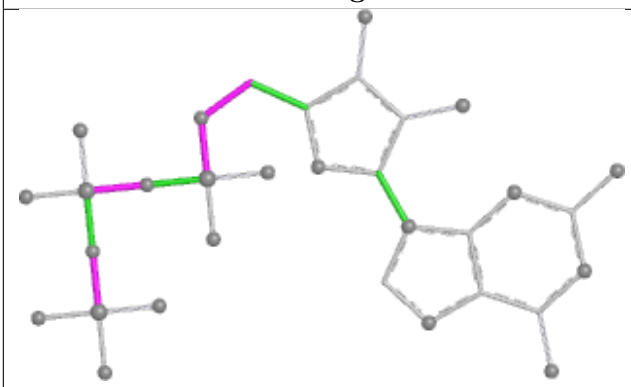

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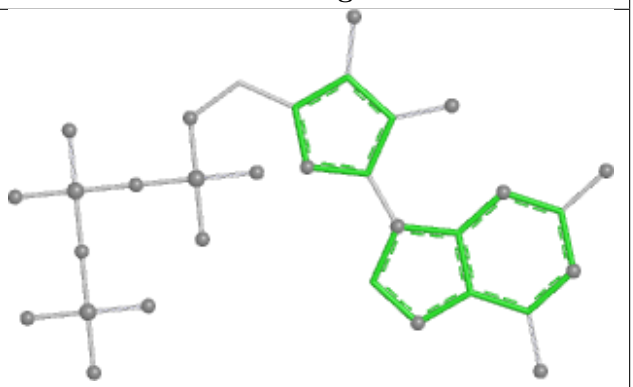
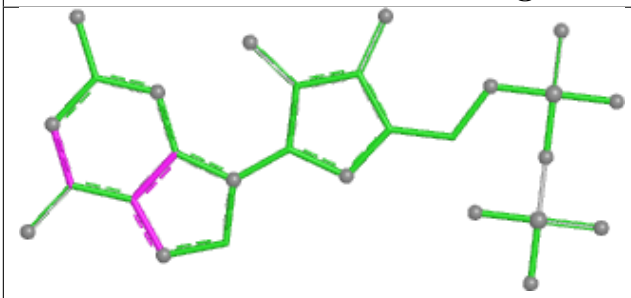


Rings

Ligand GDP IF 500



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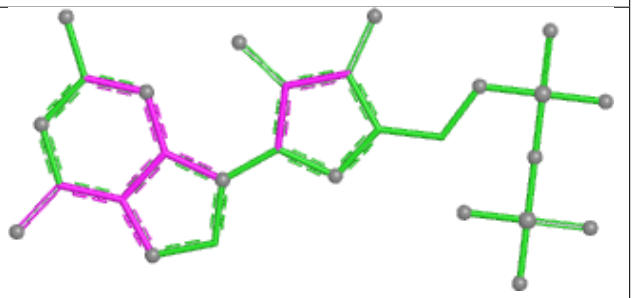

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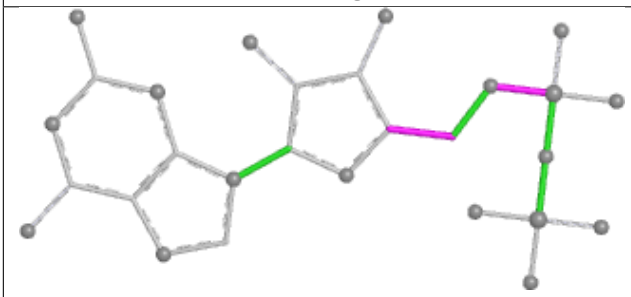

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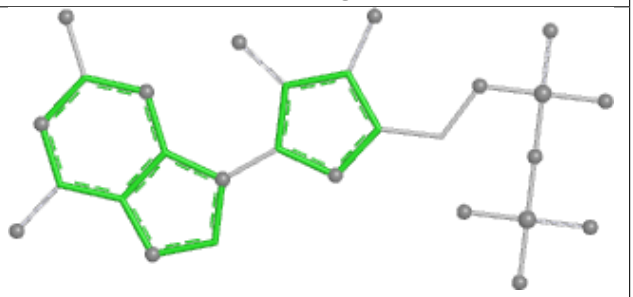
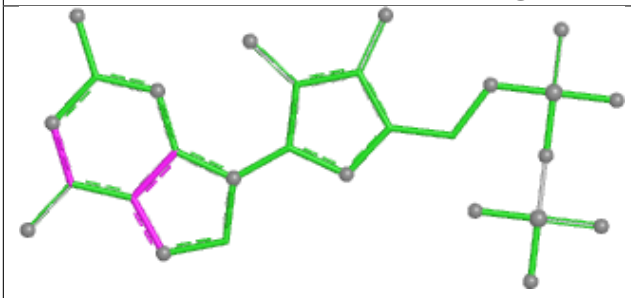
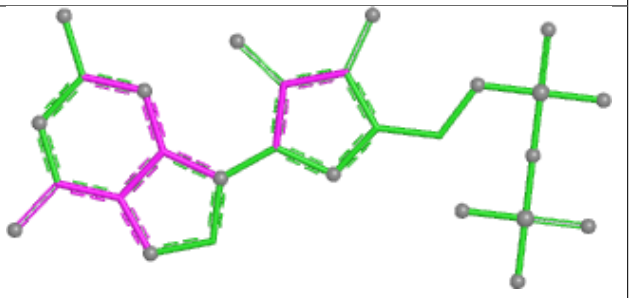
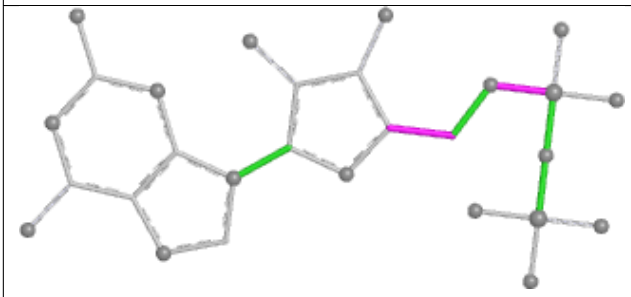
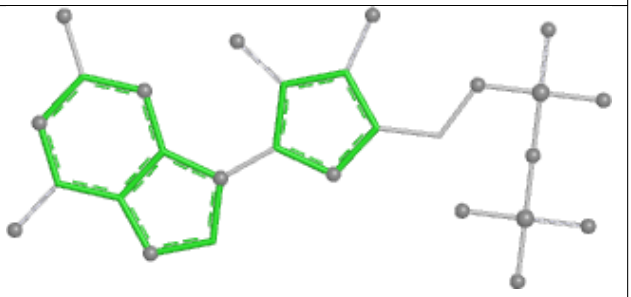
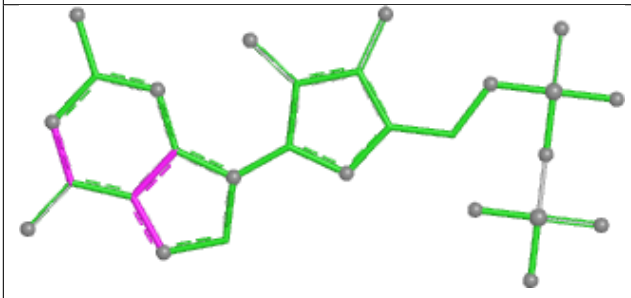
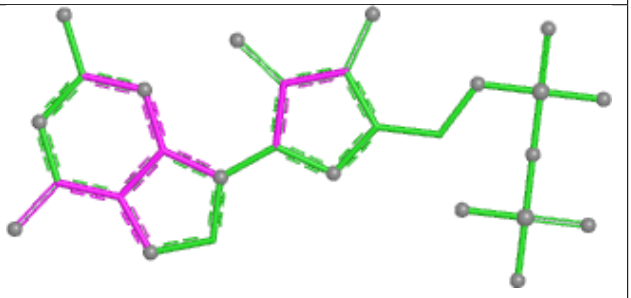
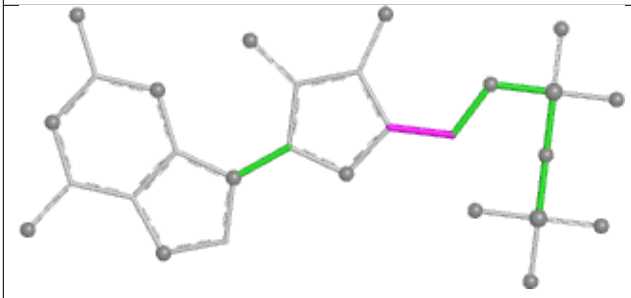
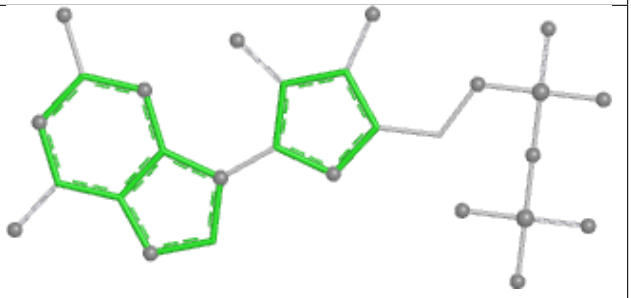
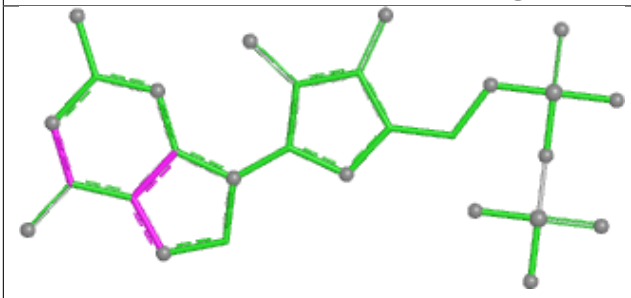


Rings

Ligand GDP FF 500	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP OL 500	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP PB 500



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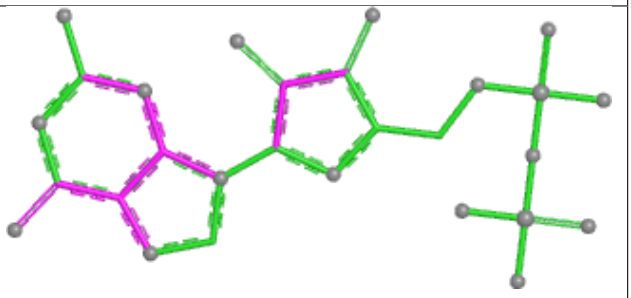

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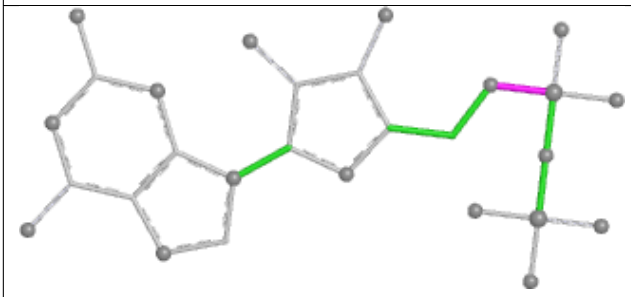
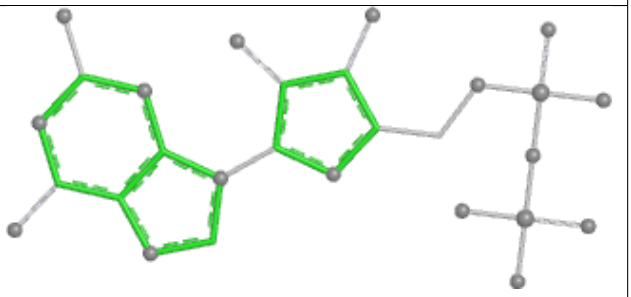
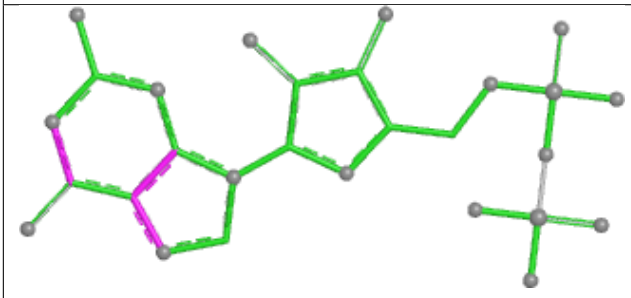


Torsions



Rings

Ligand GDP UH 500



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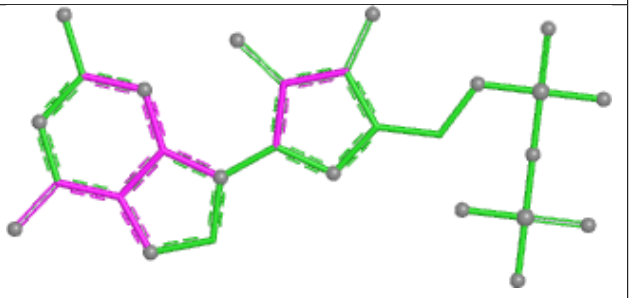

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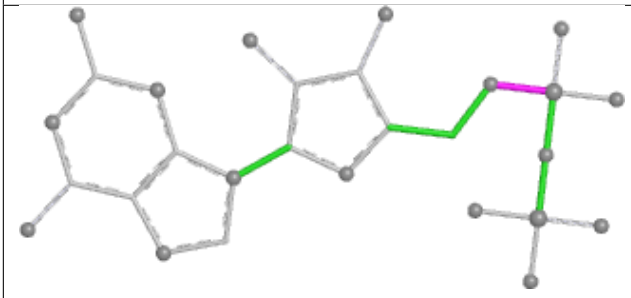

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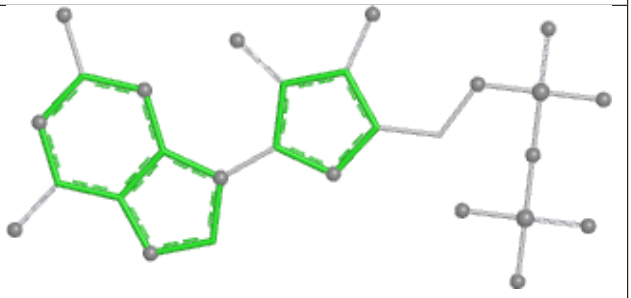
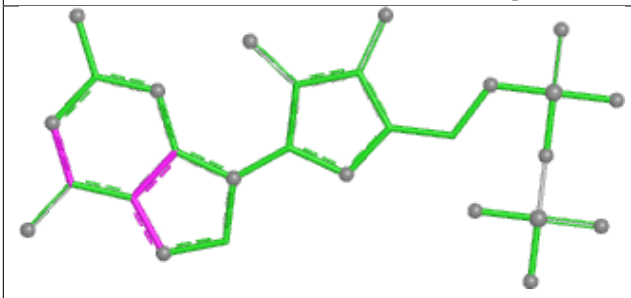


Rings

Ligand GDP NH 500



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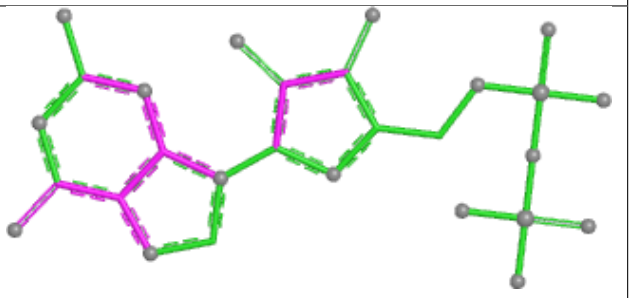

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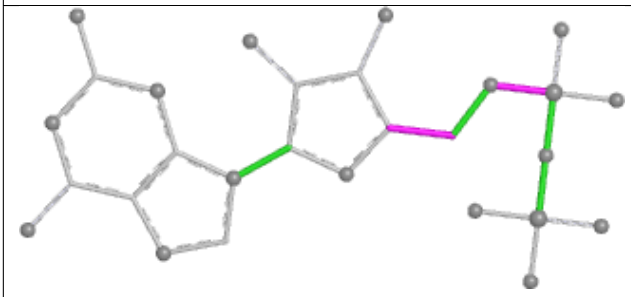

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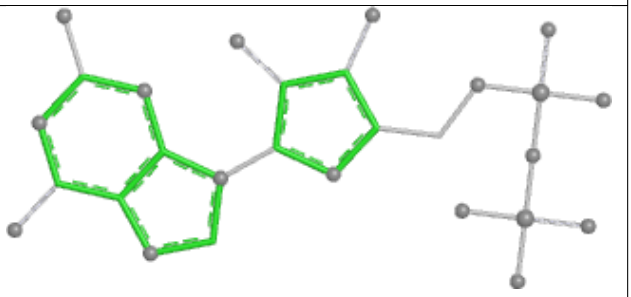
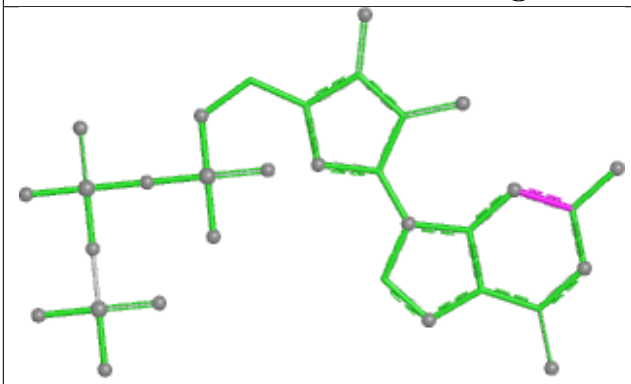


Rings

Ligand GTP UE 501



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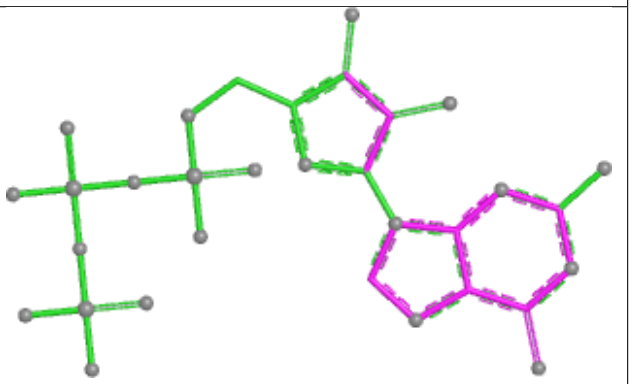

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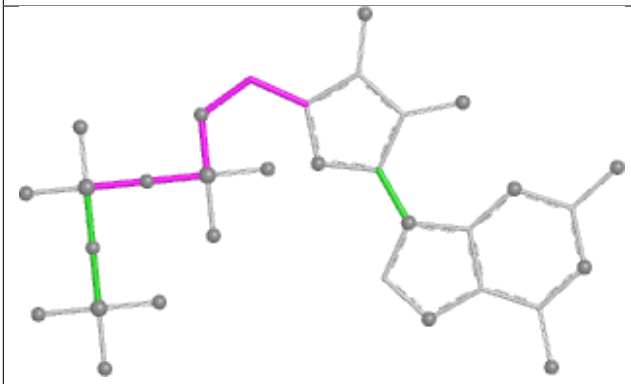

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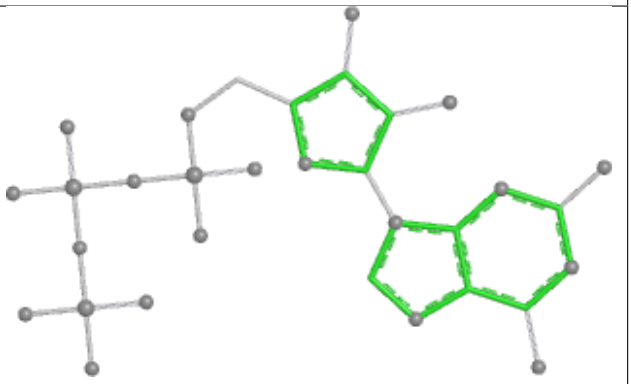
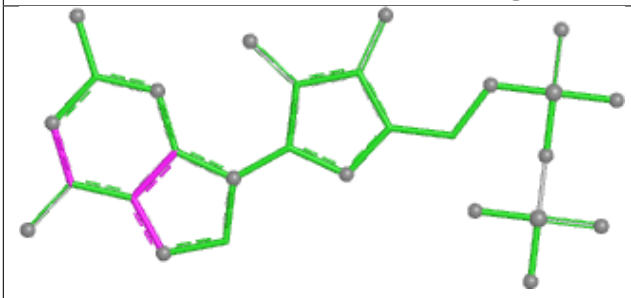


Rings

Ligand GDP RA 500



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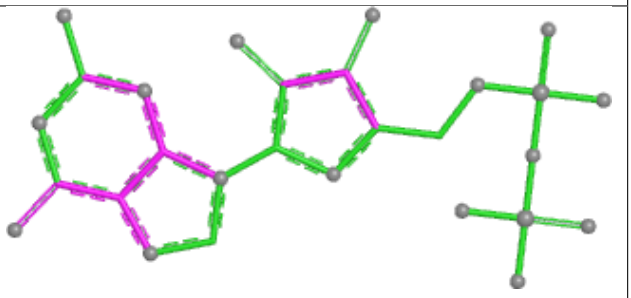

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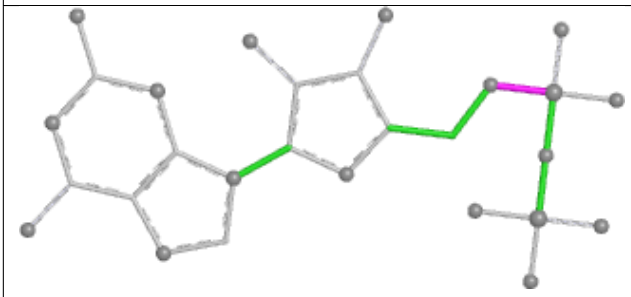

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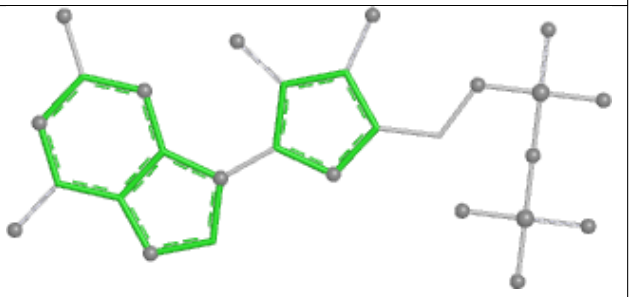
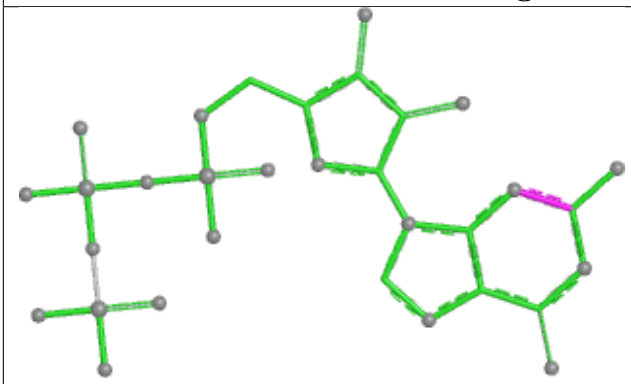


Rings

Ligand GTP LJ 501



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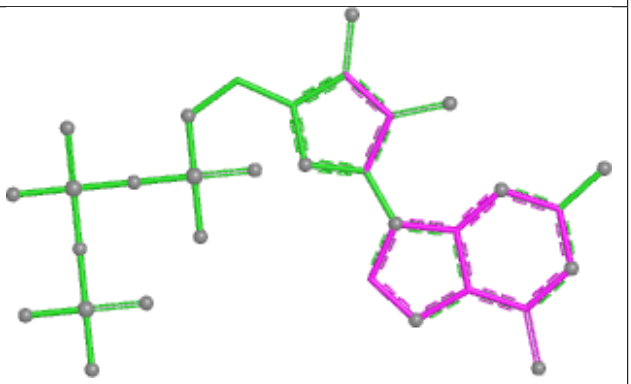

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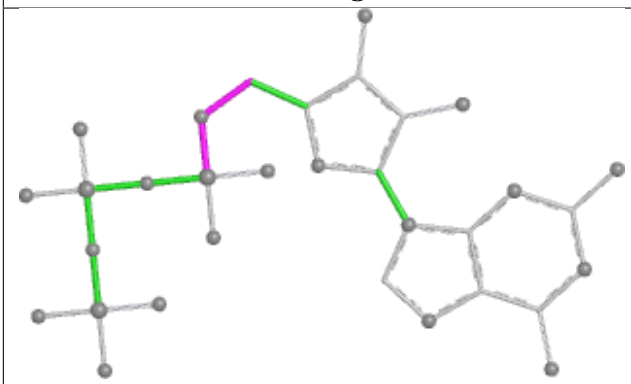

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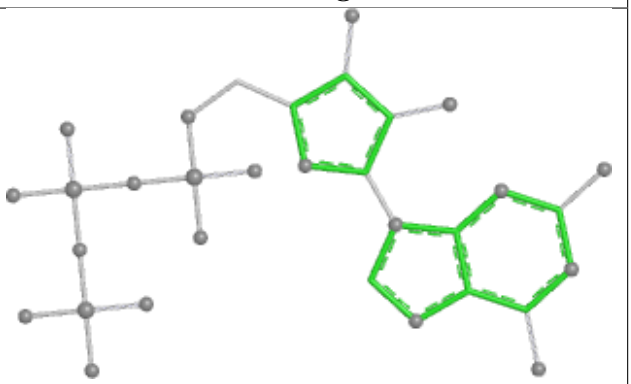
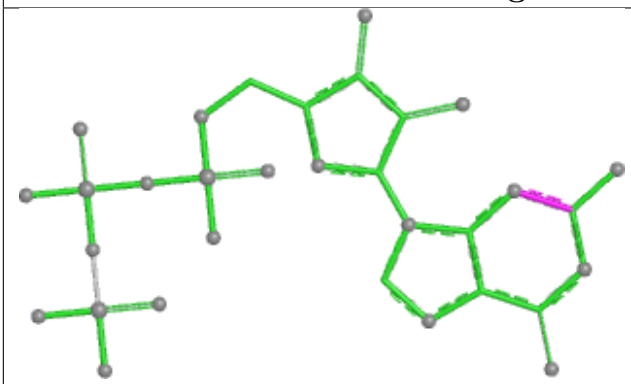


Rings

Ligand GTP UK 501



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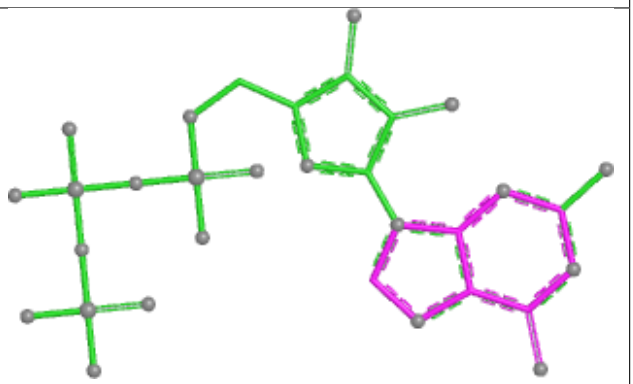

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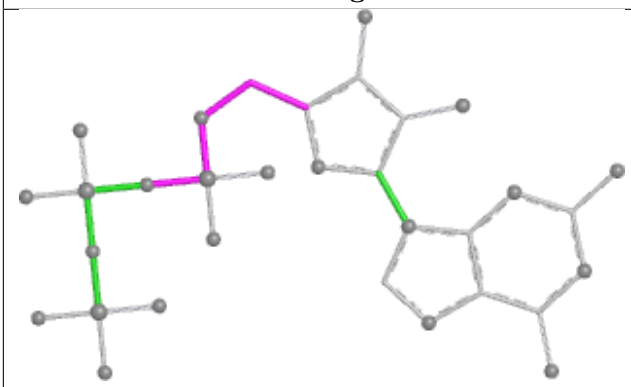

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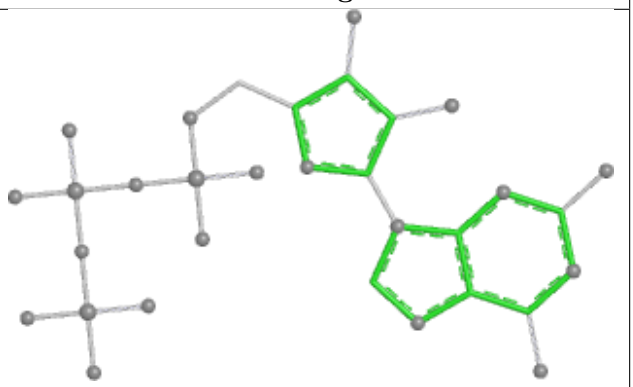
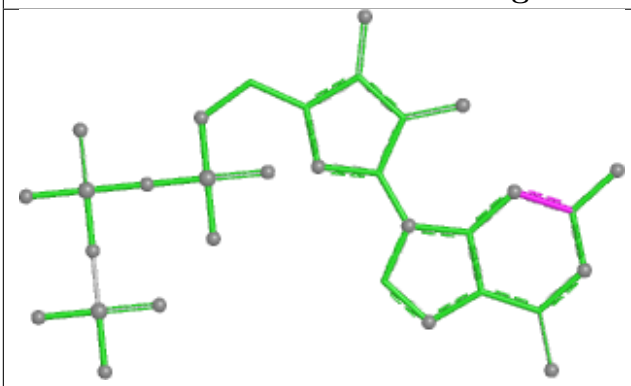


Rings

Ligand GTP RL 501



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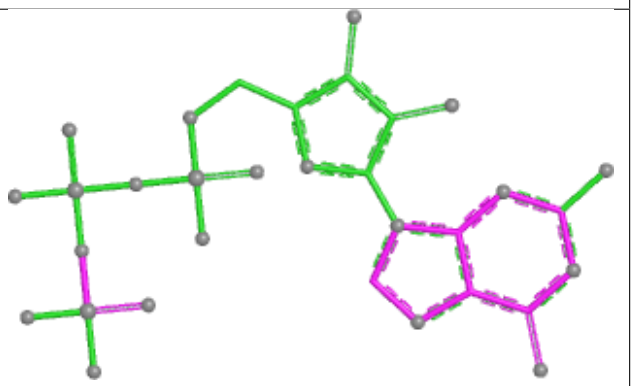

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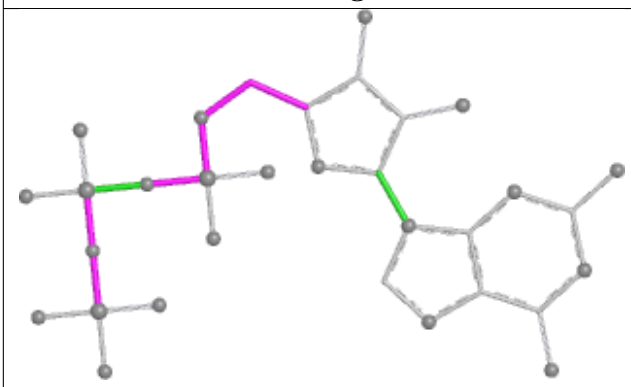

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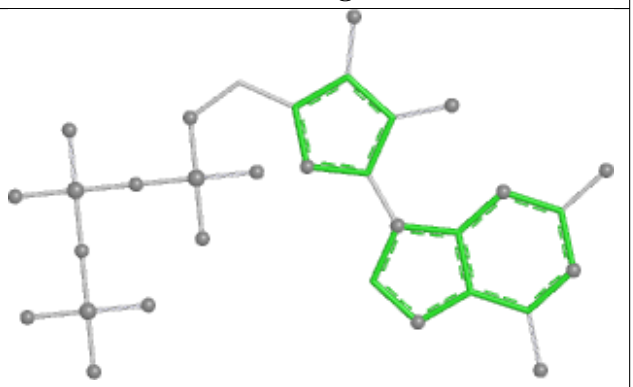
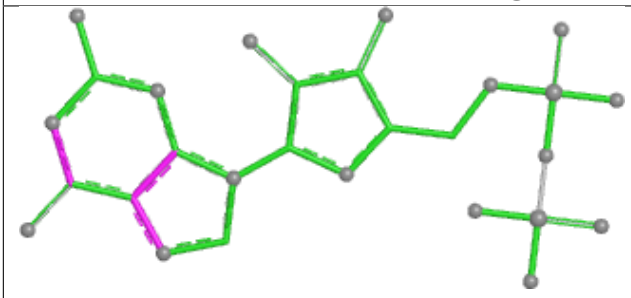


Rings

Ligand GDP AB 500



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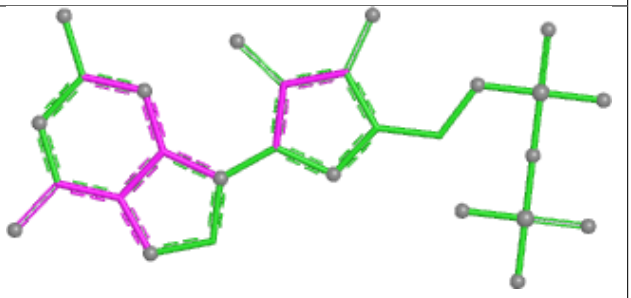

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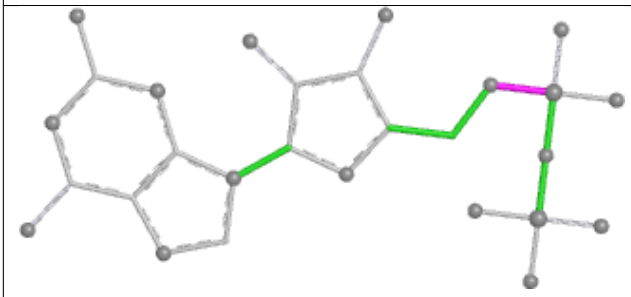

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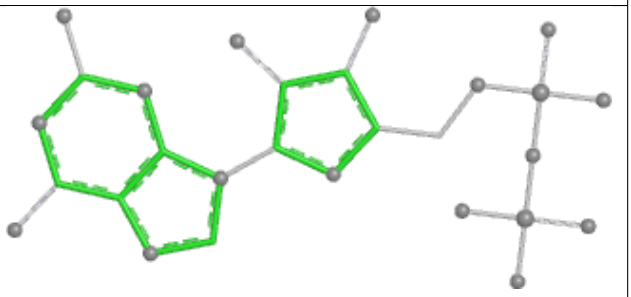
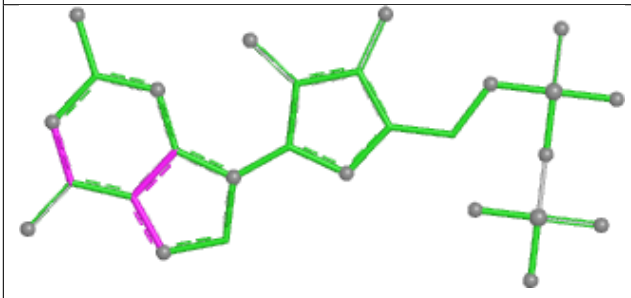


Rings

Ligand GDP MB 500



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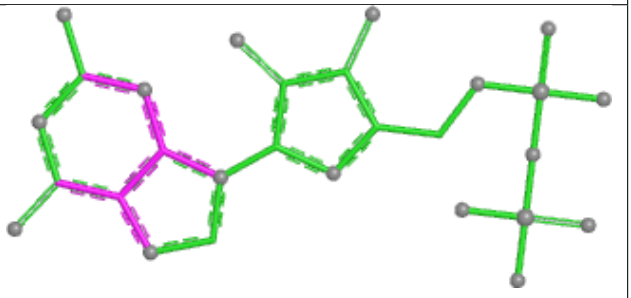

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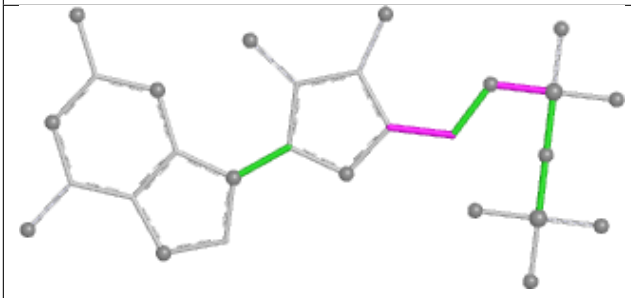

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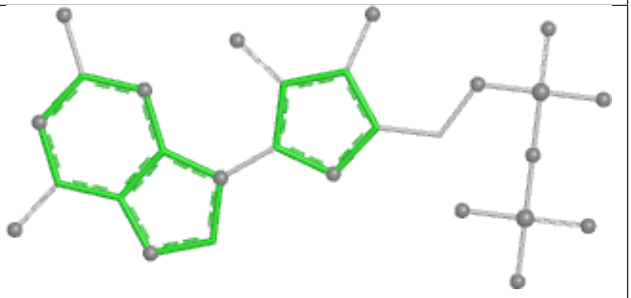

Rings

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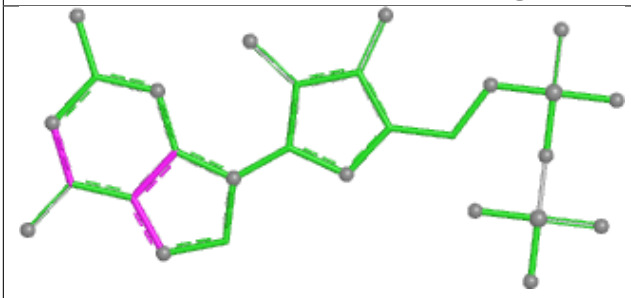

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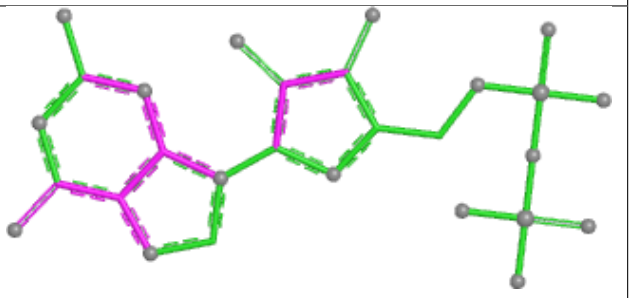

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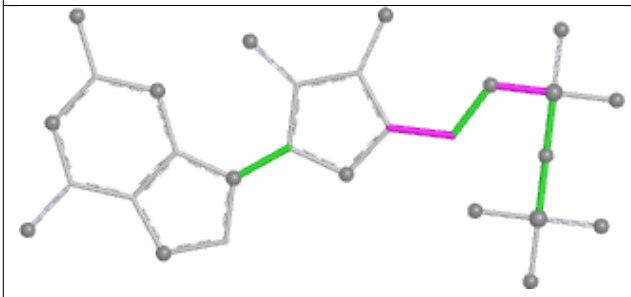

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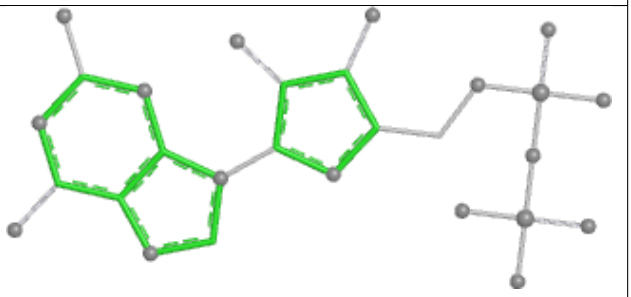
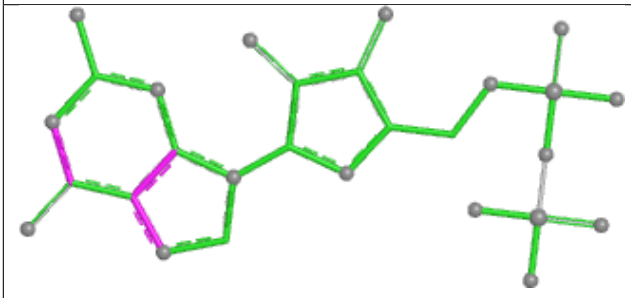


Rings

Ligand GDP NJ 500



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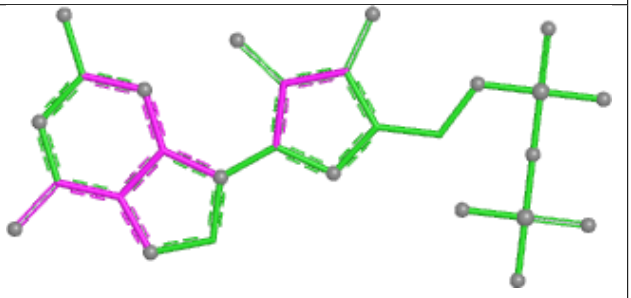

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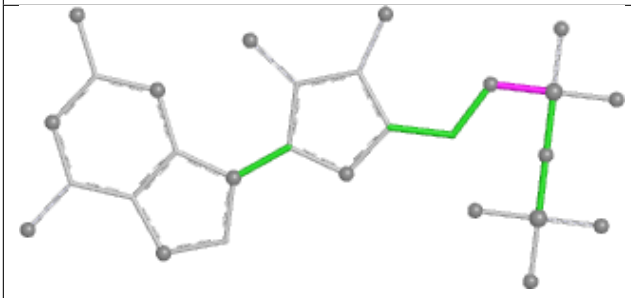

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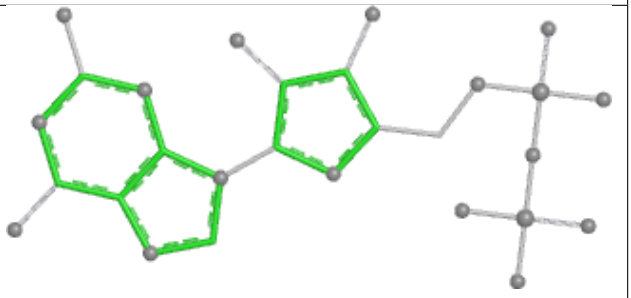
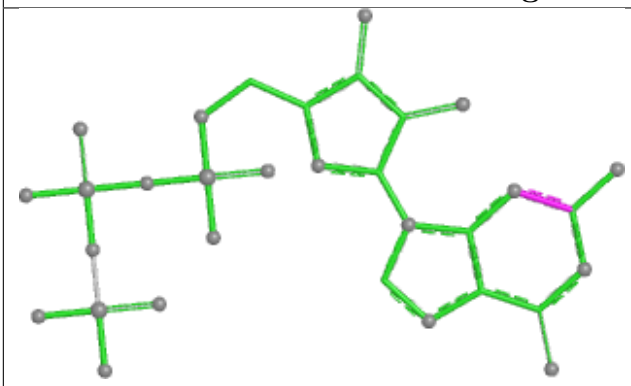


Rings

Ligand GTP II 501



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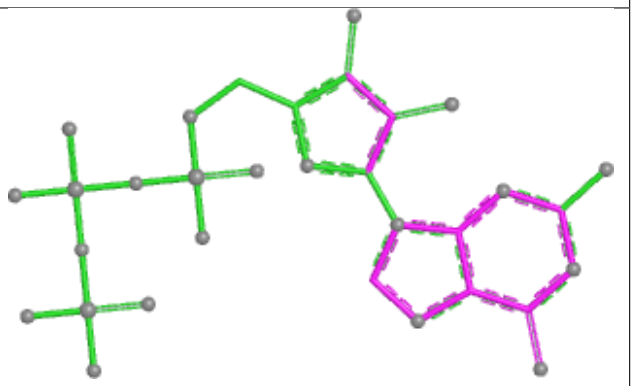

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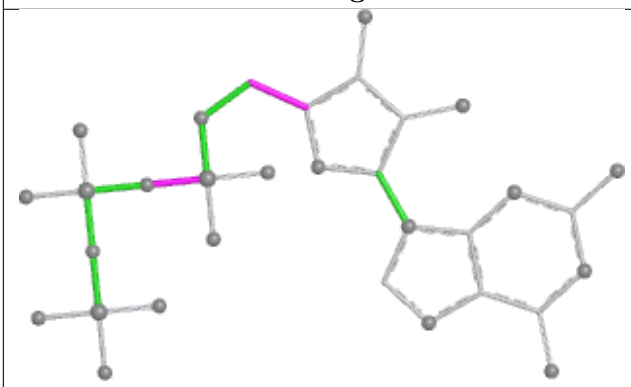

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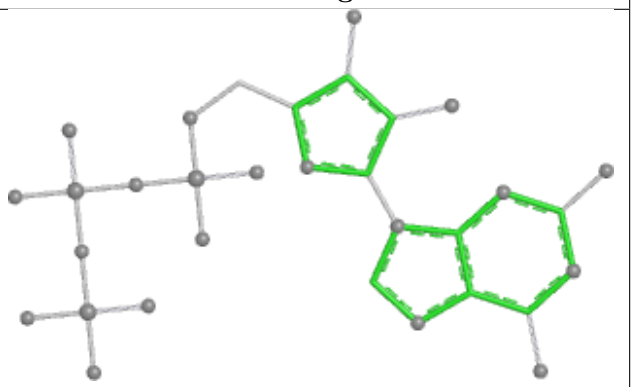
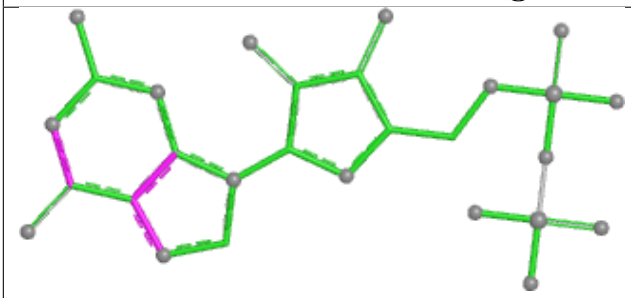


Rings

Ligand GDP AF 500



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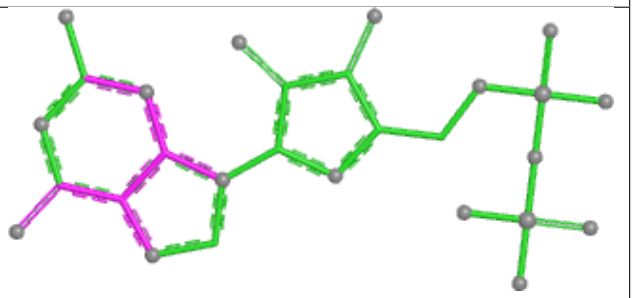
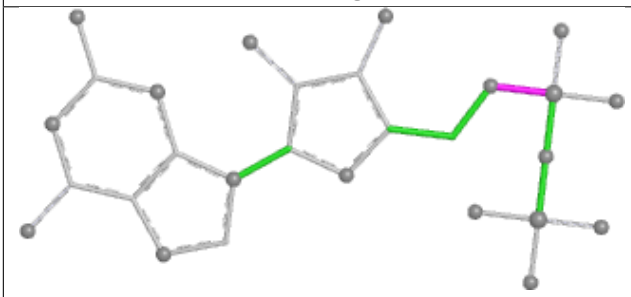


Bond angles



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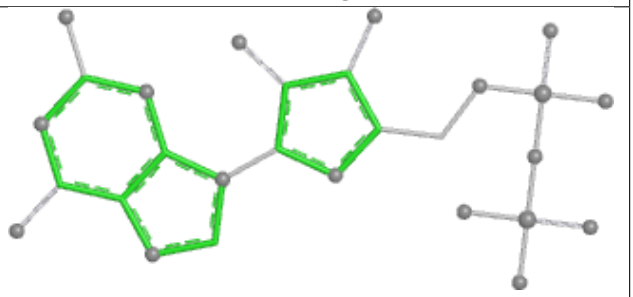
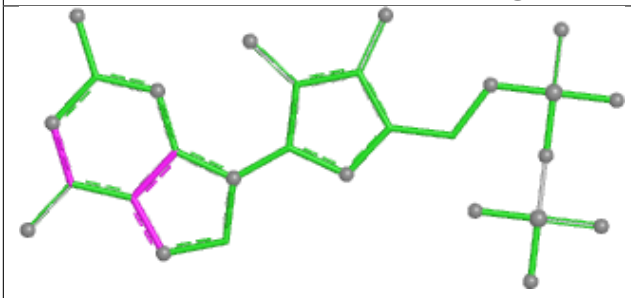


Rings

Ligand GDP HF 500



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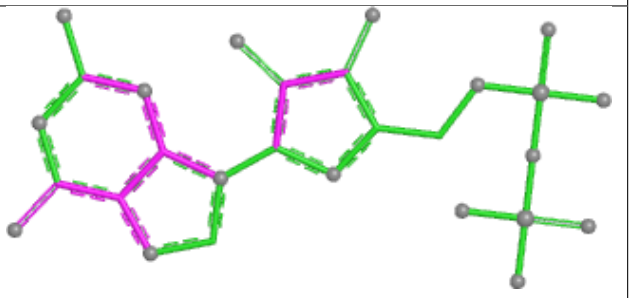
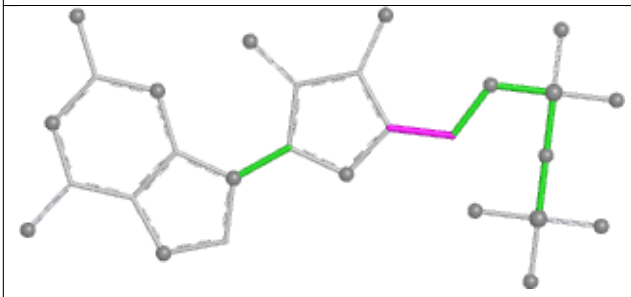
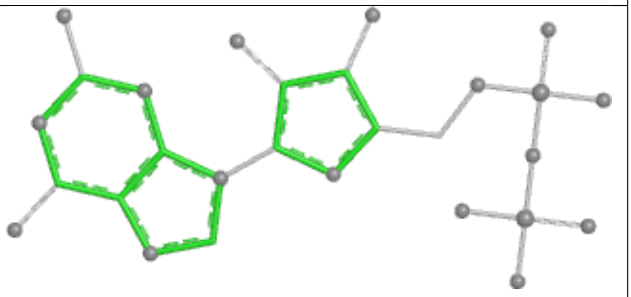


Bond angles

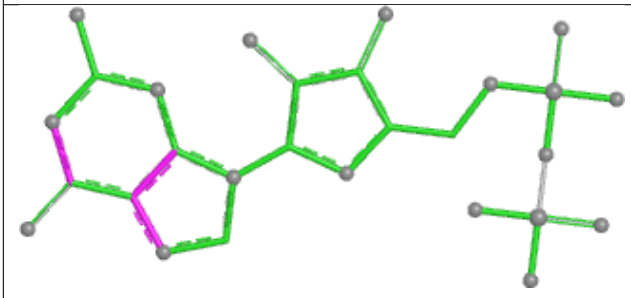


Torsions



Rings

Ligand GDP KK 500



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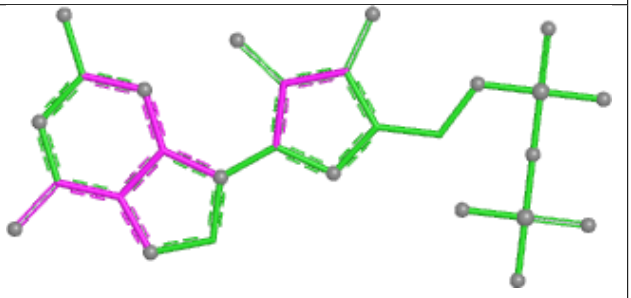

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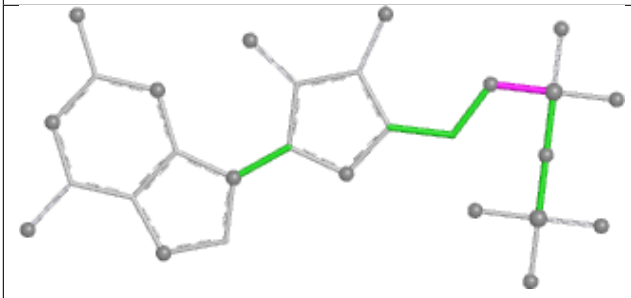

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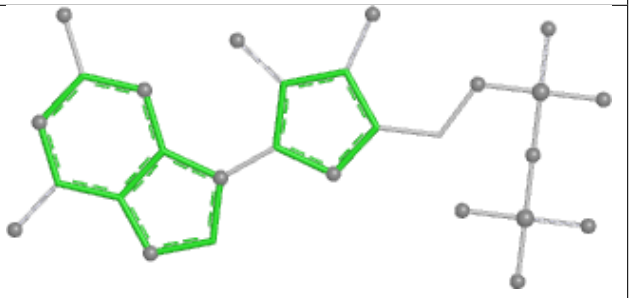
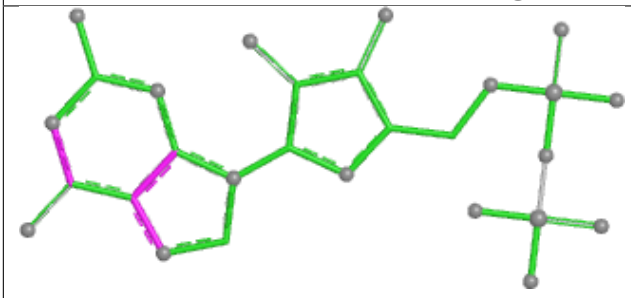


Rings

Ligand GDP UF 500



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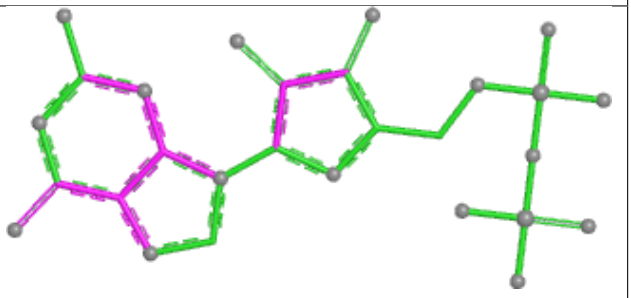

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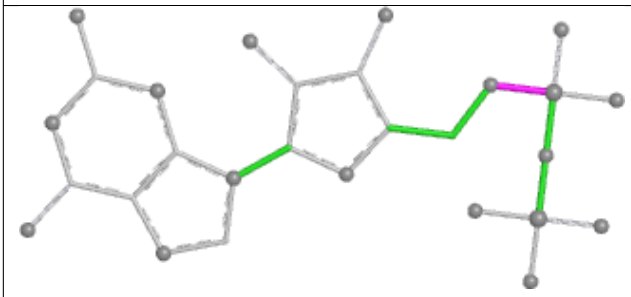

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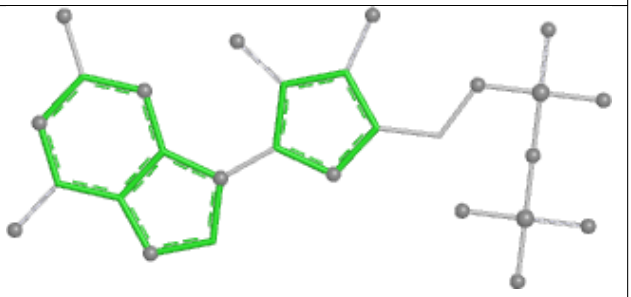
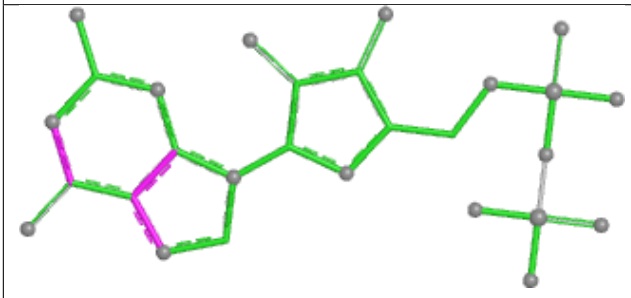


Rings

Ligand GDP DG 500



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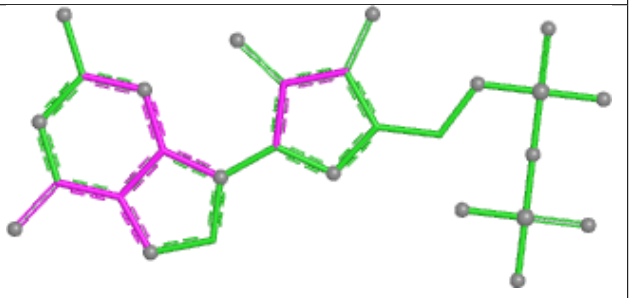

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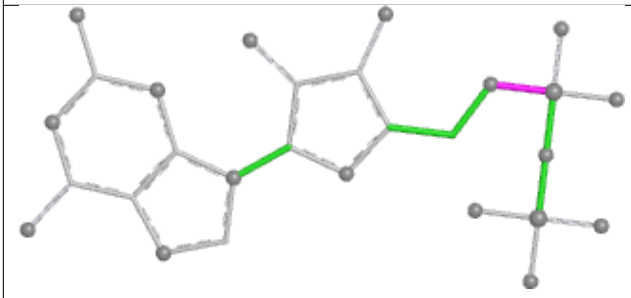

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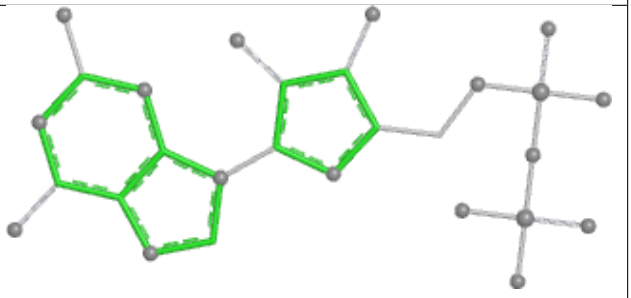
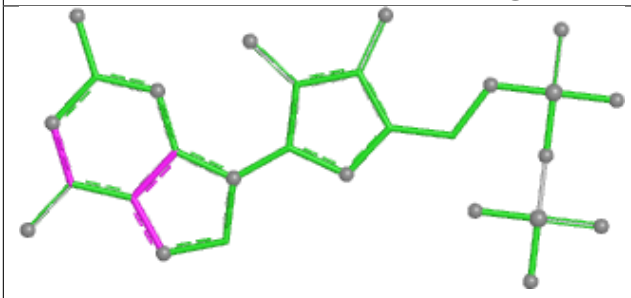


Rings

Ligand GDP AN 500



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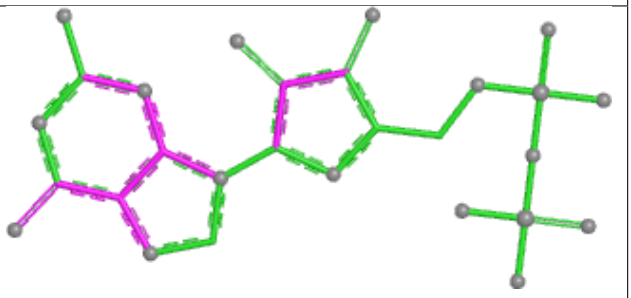

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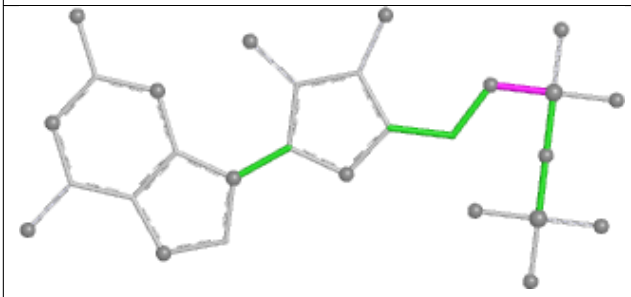

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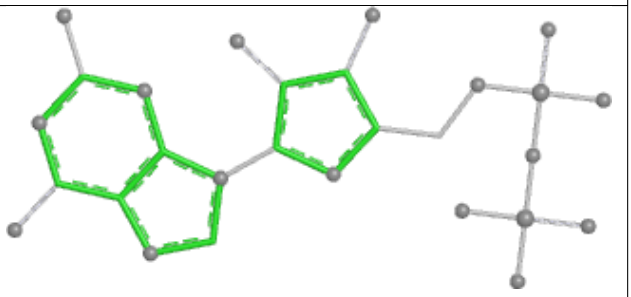
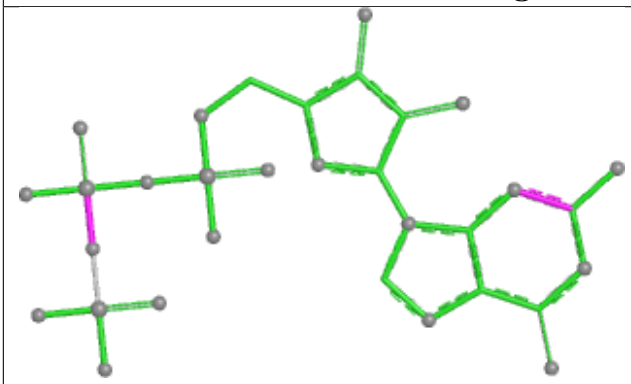


Rings

Ligand GTP QJ 501



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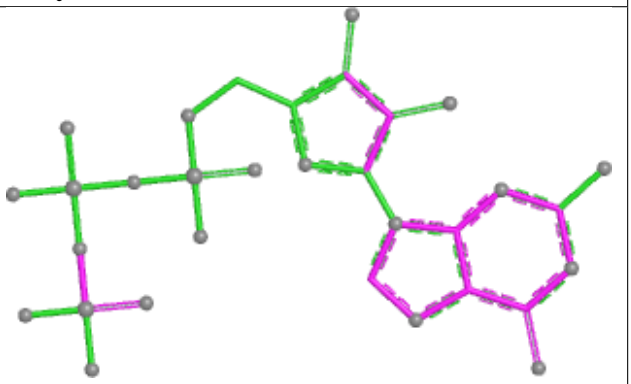

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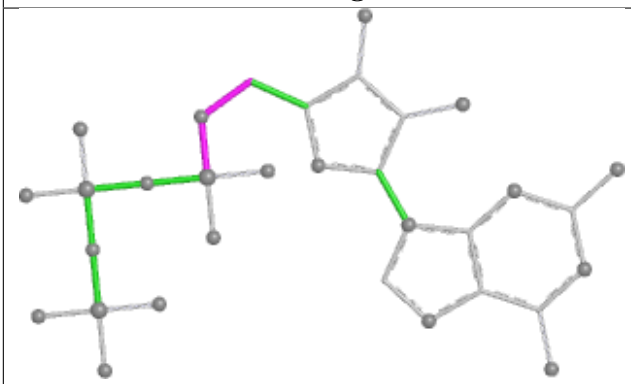

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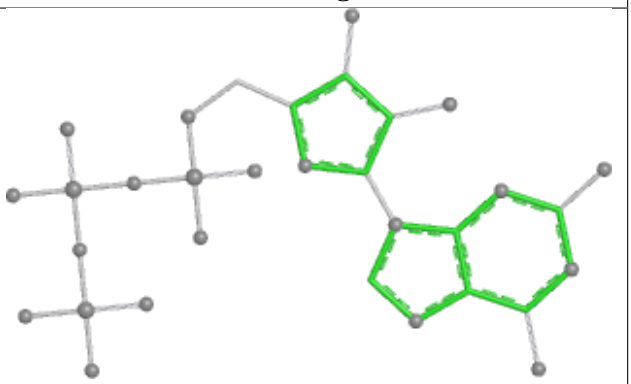
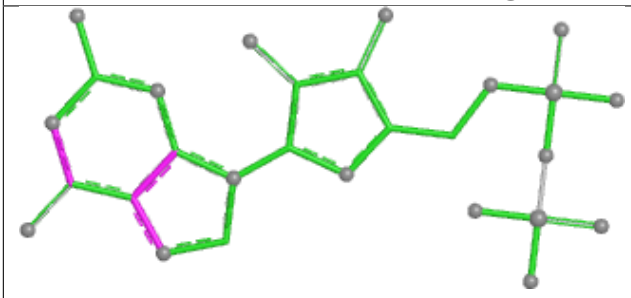


Rings

Ligand GDP WD 500



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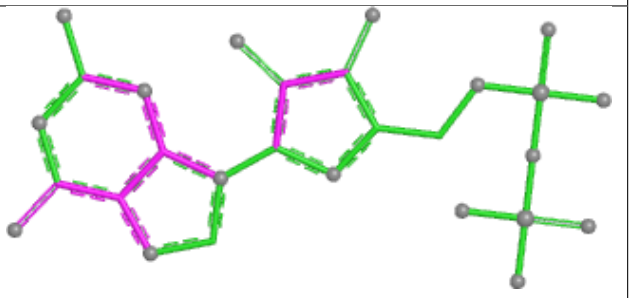

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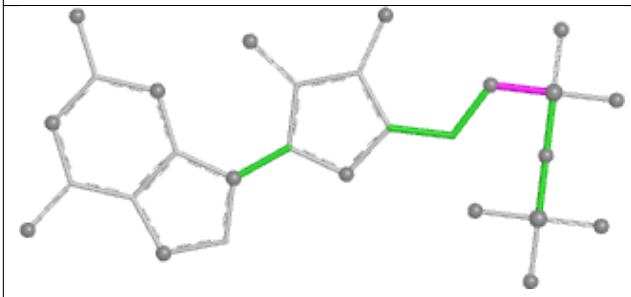

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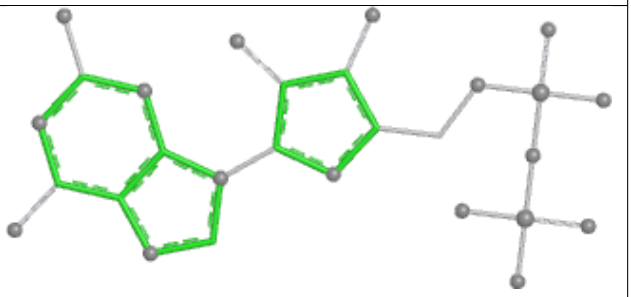
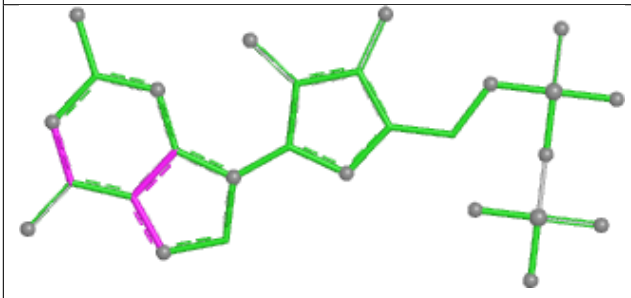


Rings

Ligand GDP GF 500



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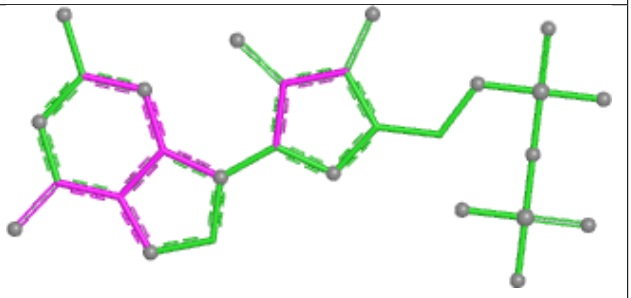

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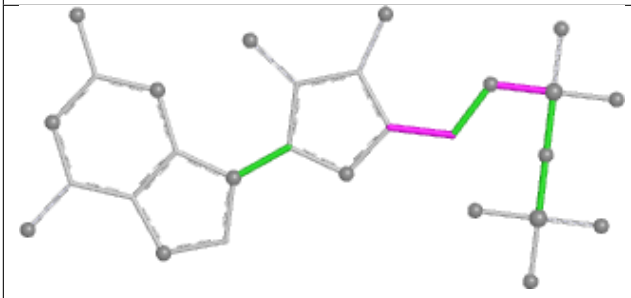

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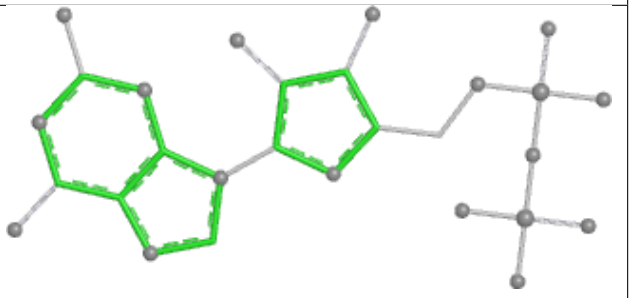
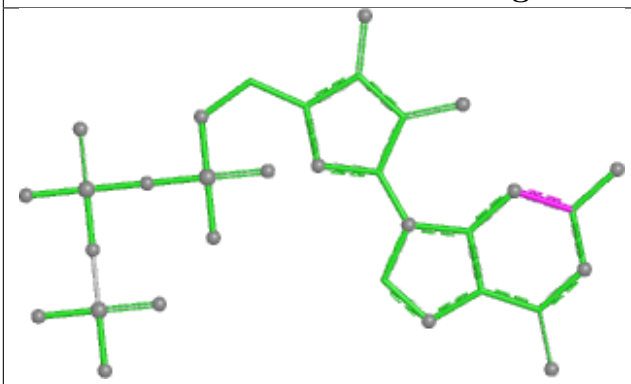


Rings

Ligand GTP IM 501



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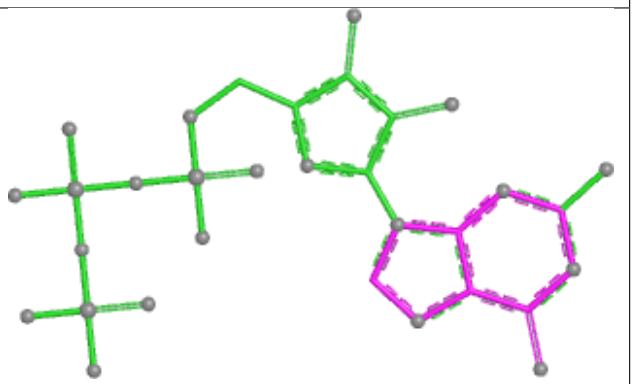

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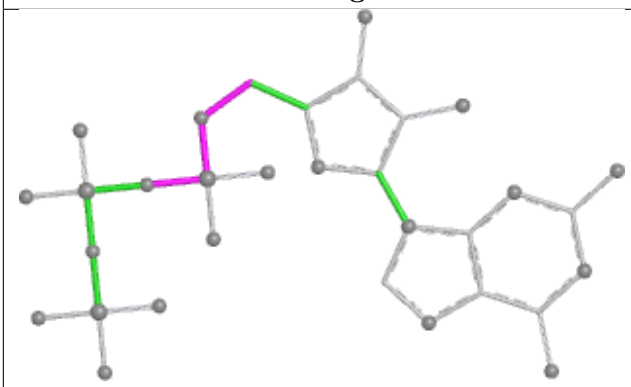

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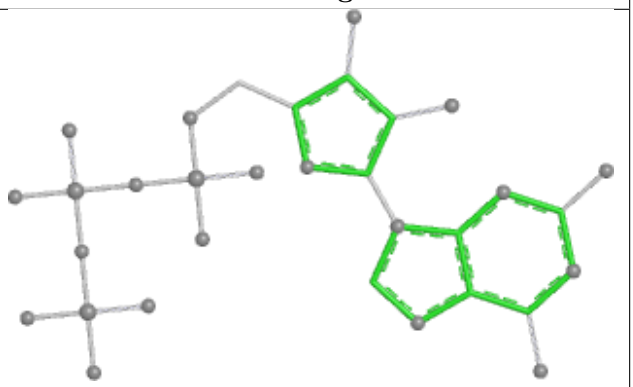
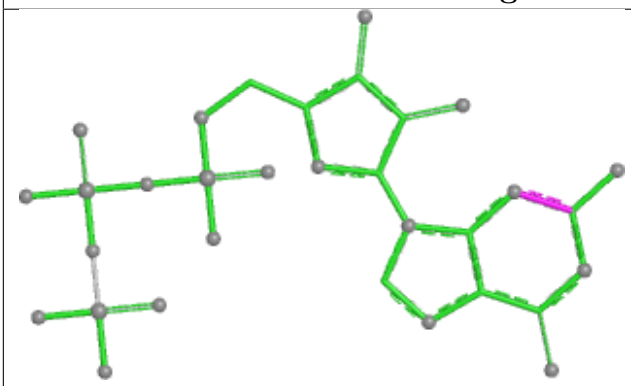


Rings

Ligand GTP WM 501



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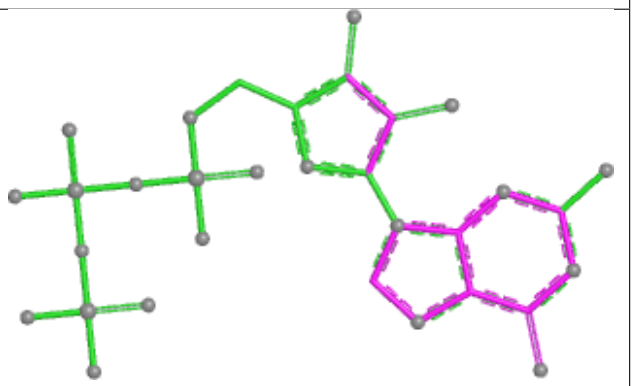

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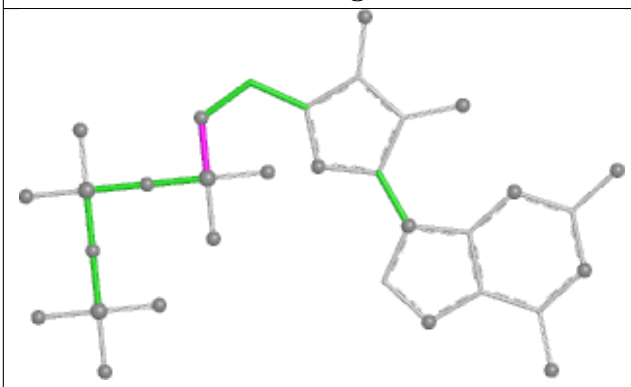

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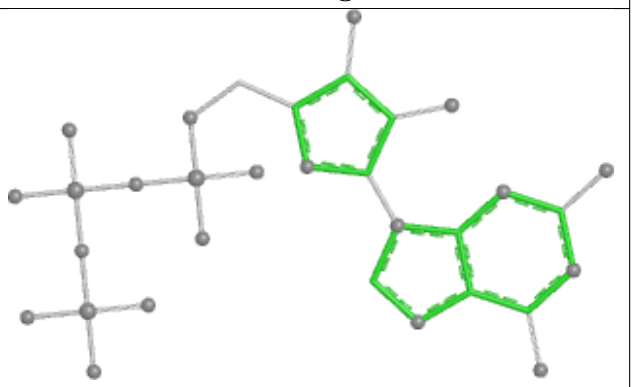
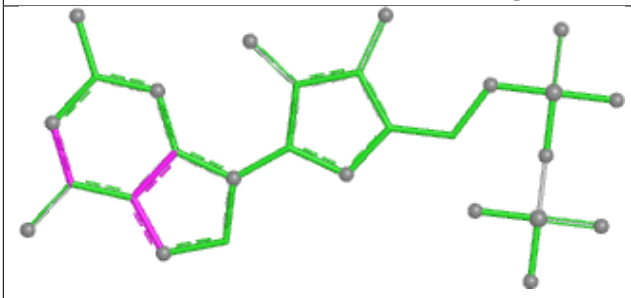


Rings

Ligand GDP KC 500



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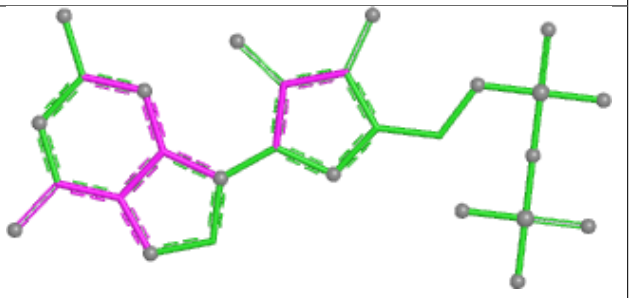

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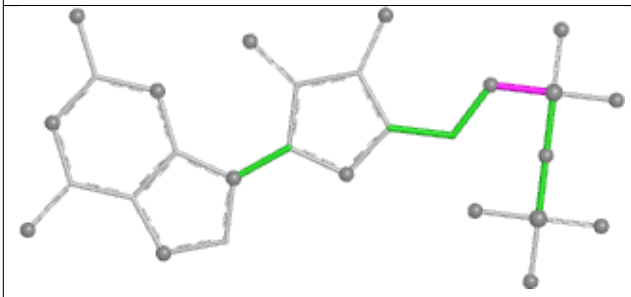

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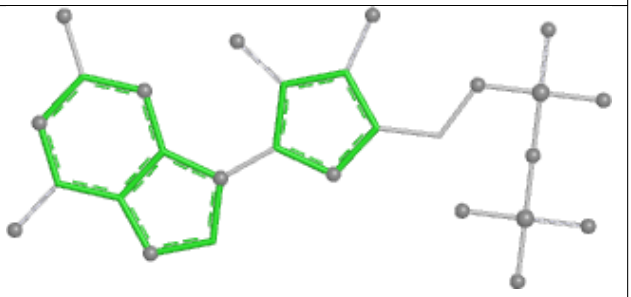
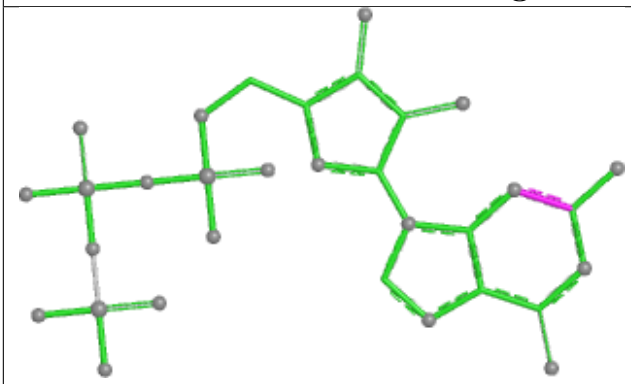


Rings

Ligand GTP RF 501



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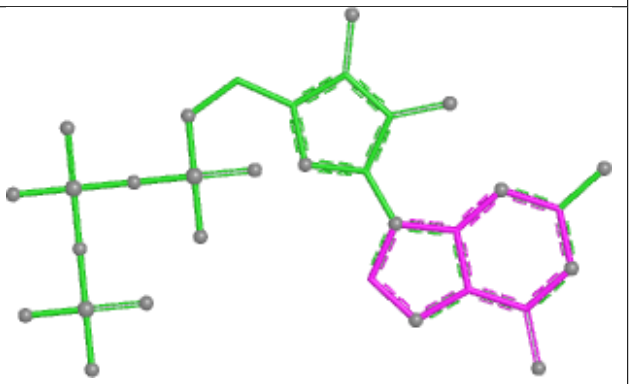

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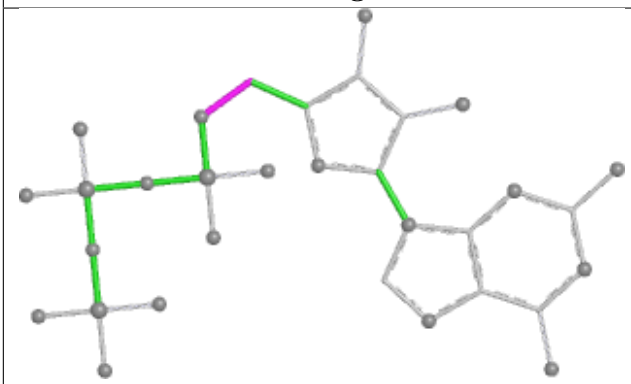

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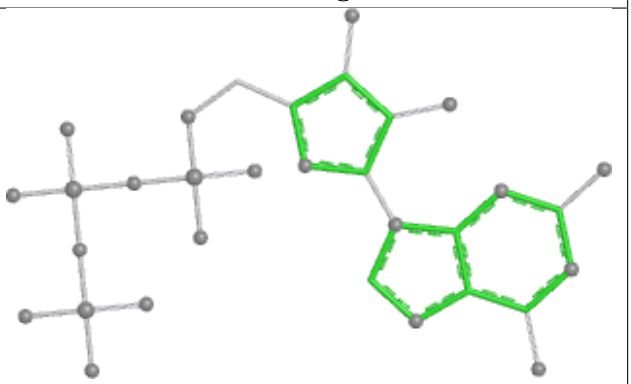
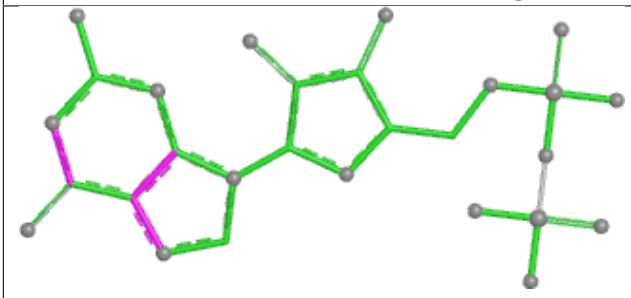


Rings

Ligand GDP LG 500



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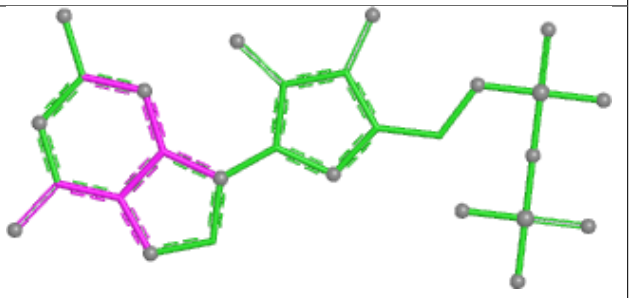

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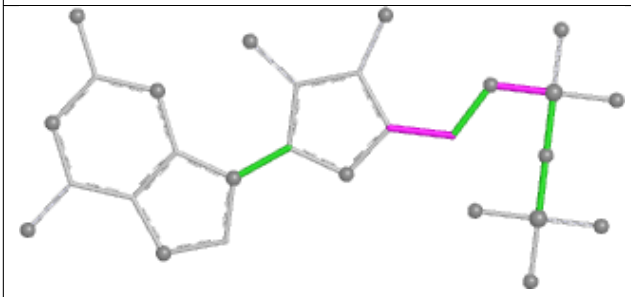

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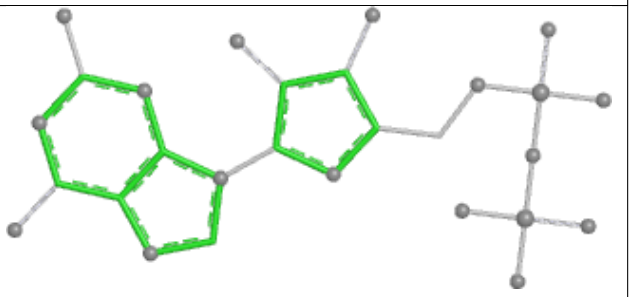
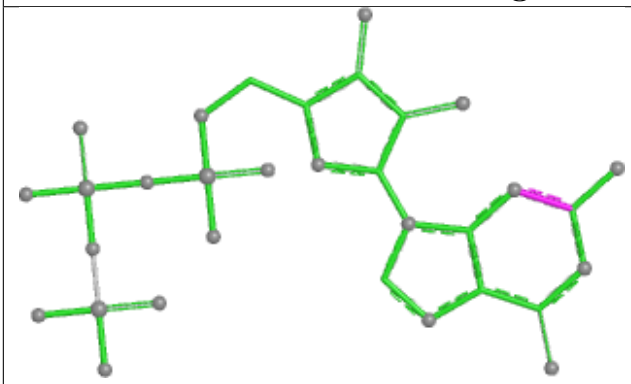


Rings

Ligand GTP LH 501



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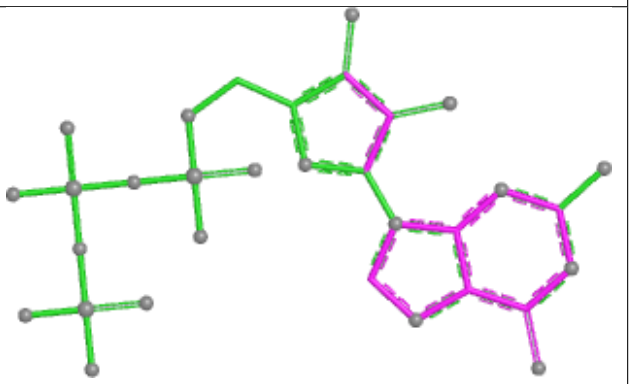
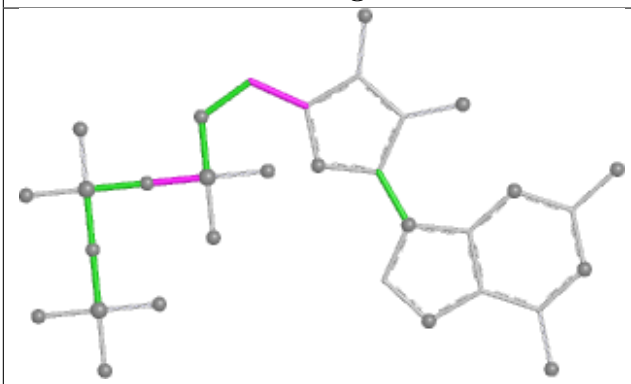


Bond angles



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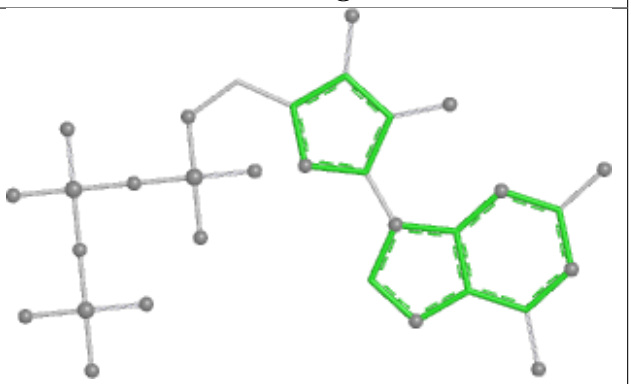
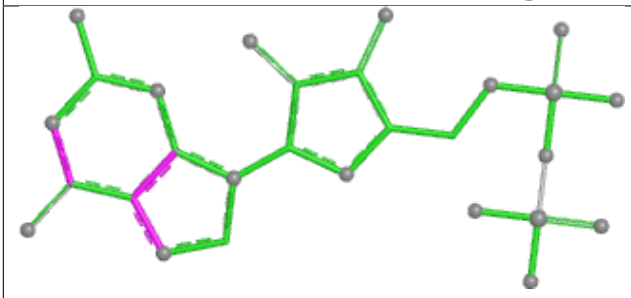
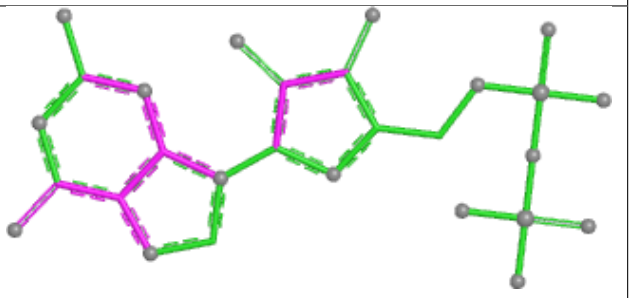


Rings

Ligand GDP H 500



Bond lengths



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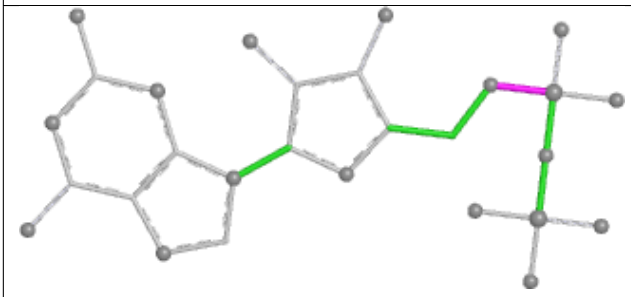

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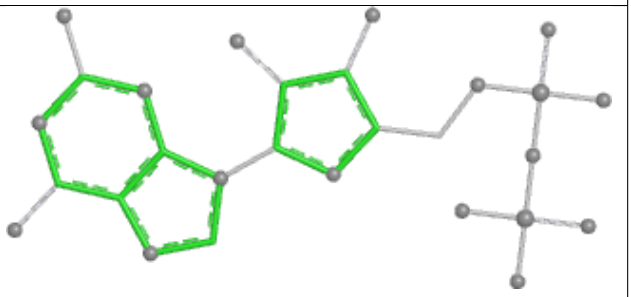
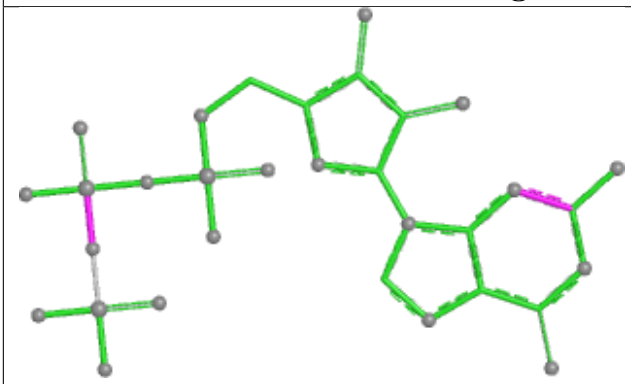


Rings

Ligand GTP NE 501



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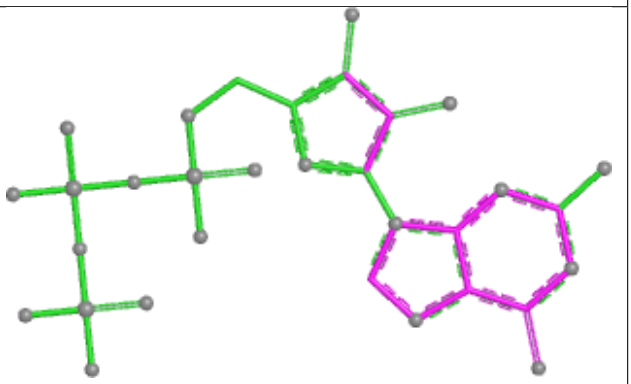

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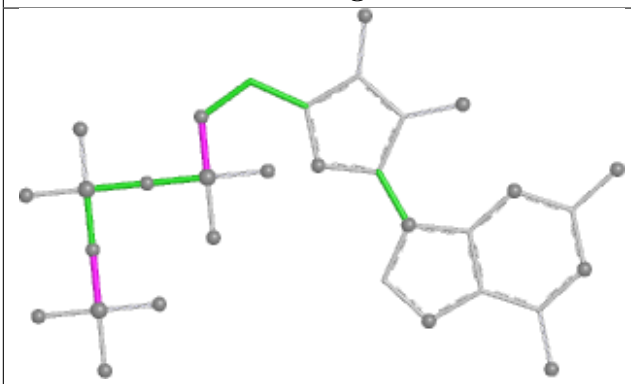

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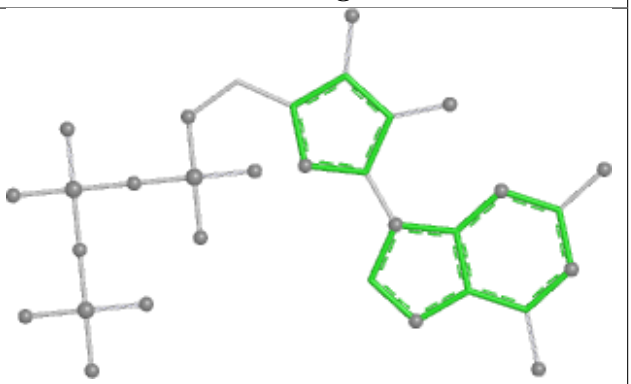
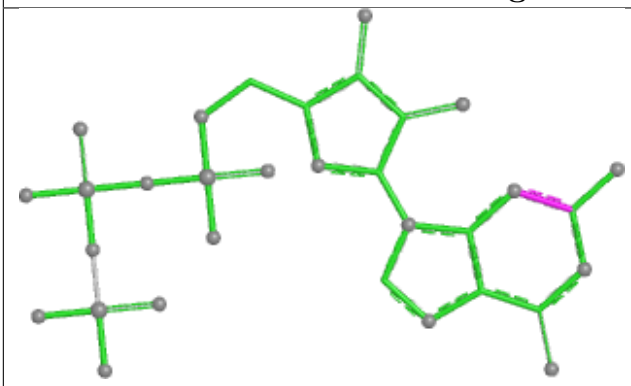


Rings

Ligand GTP AG 501



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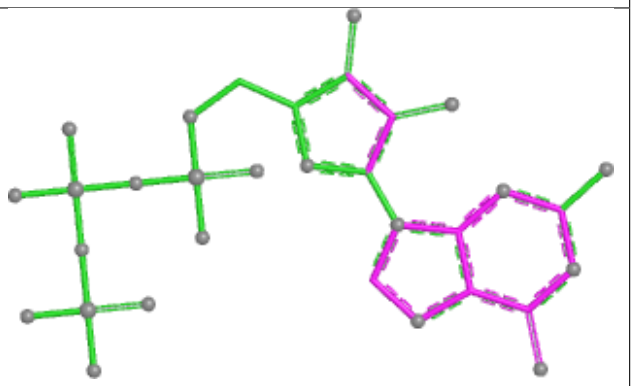

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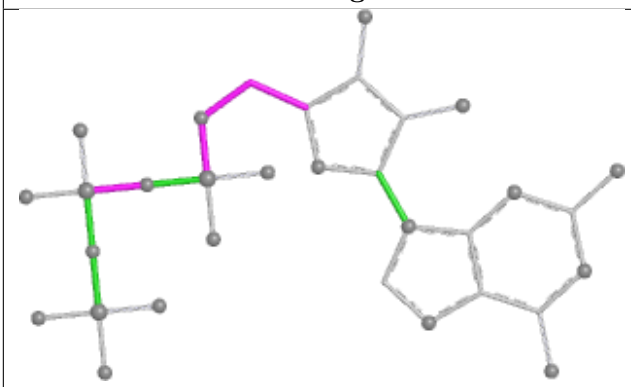

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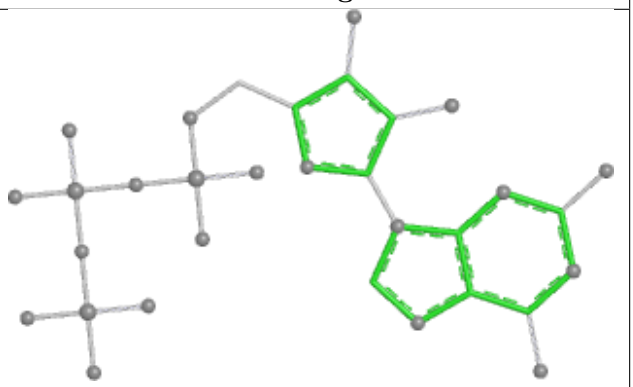

Rings

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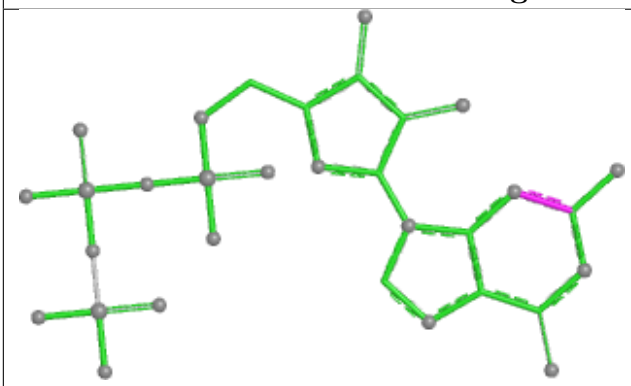

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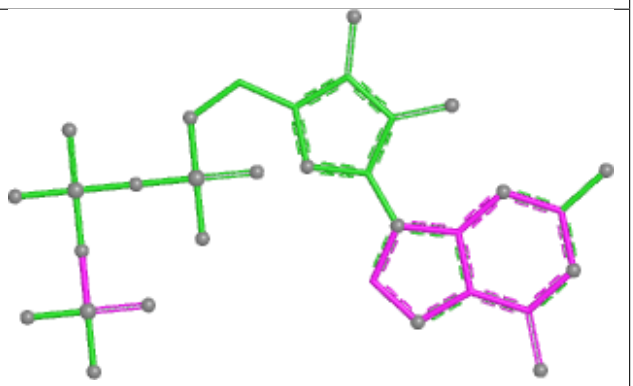

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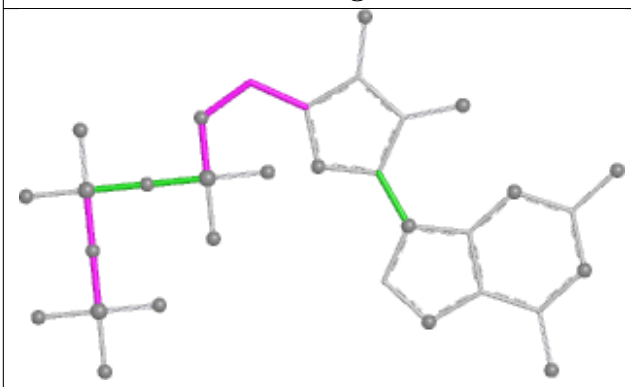

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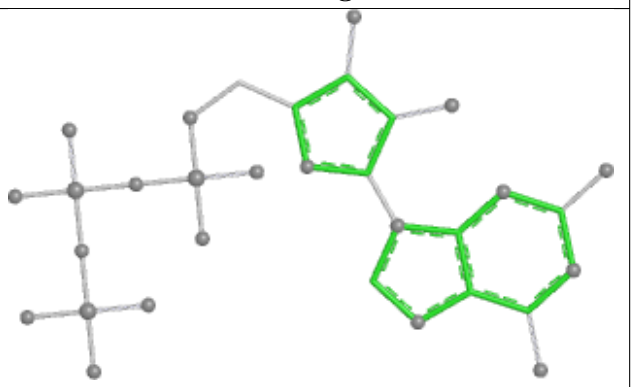

Rings

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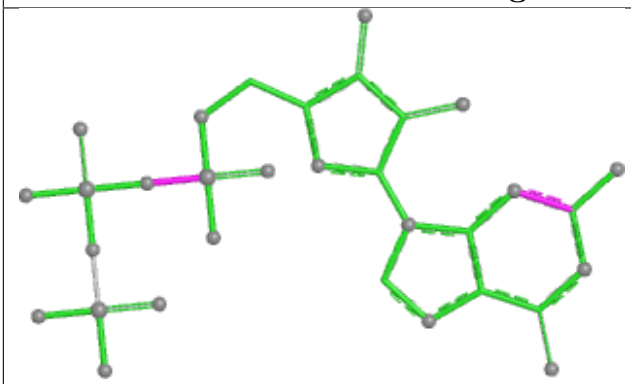

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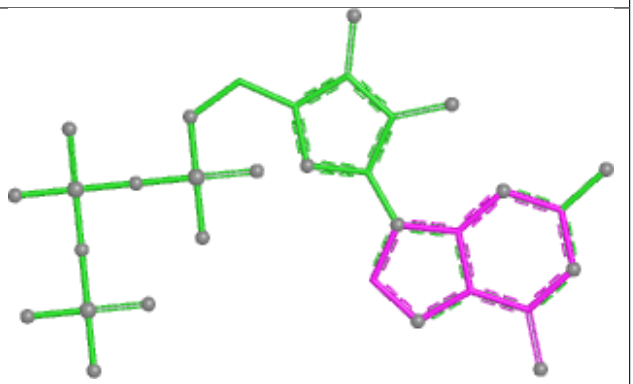

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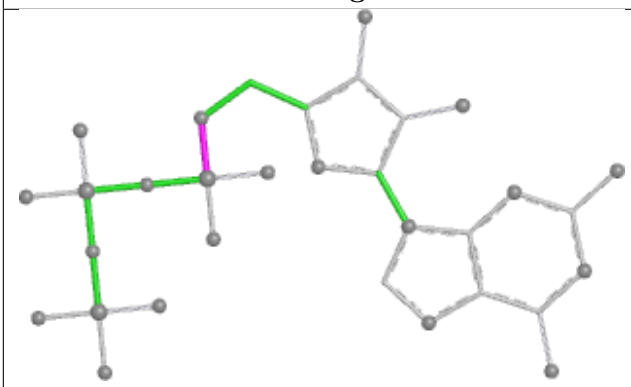

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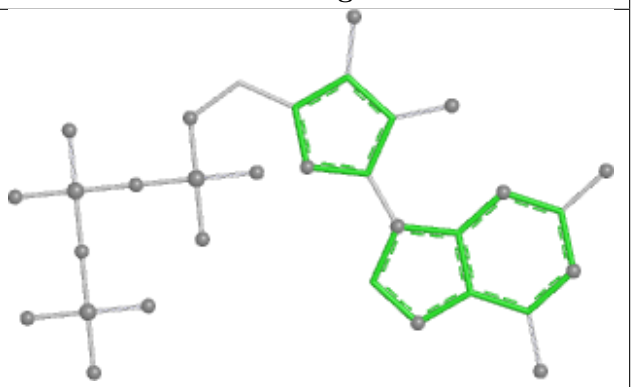
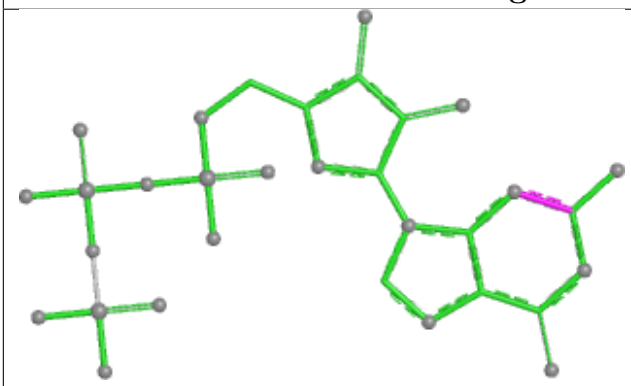


Rings

Ligand GTP PK 501



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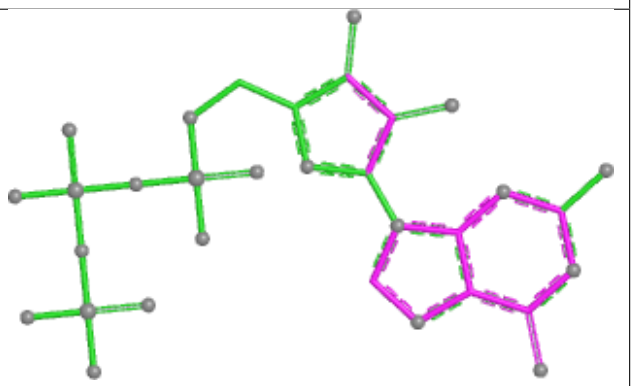

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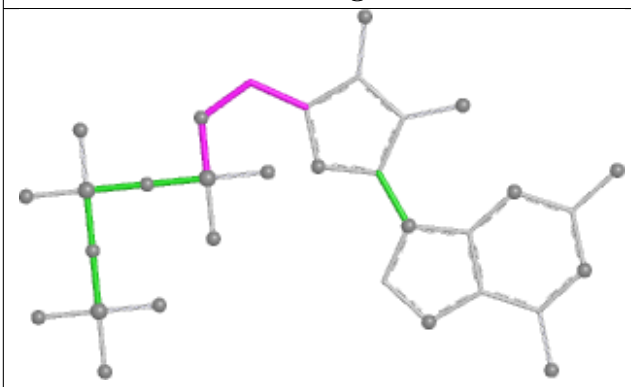

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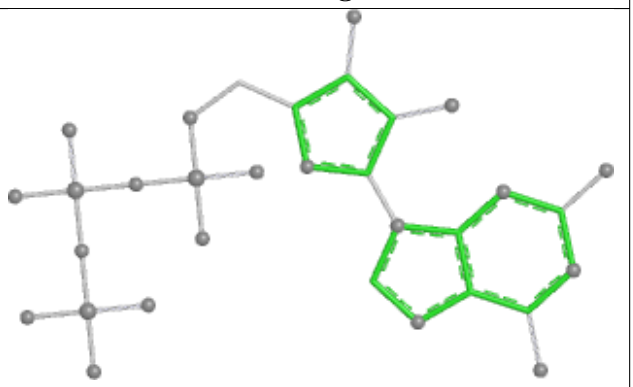

Rings

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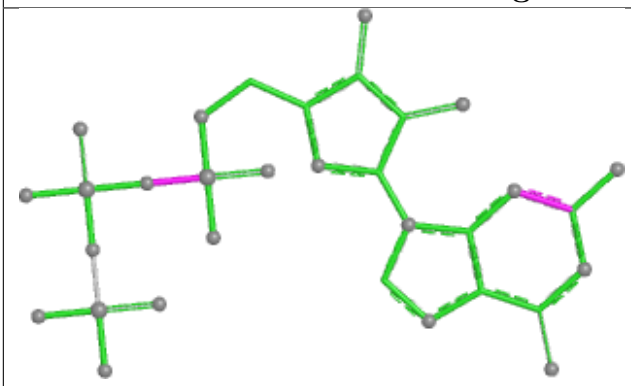

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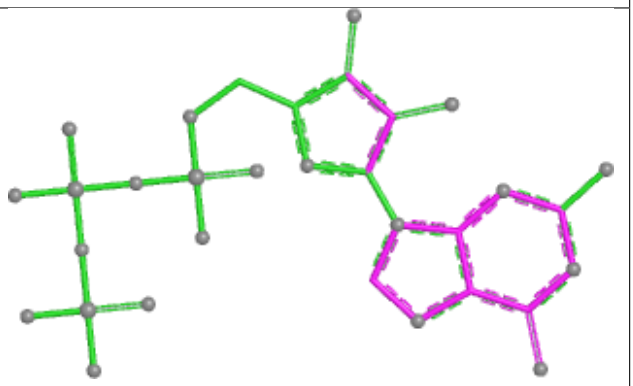

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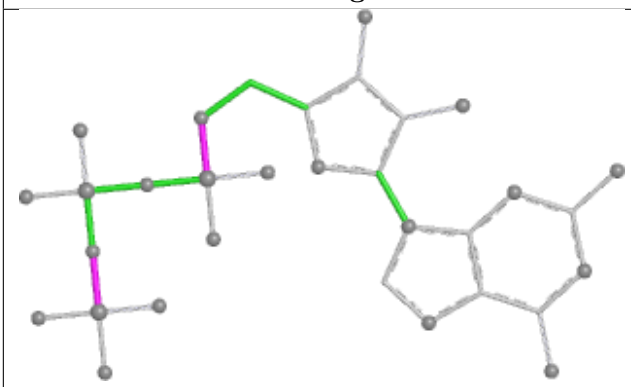

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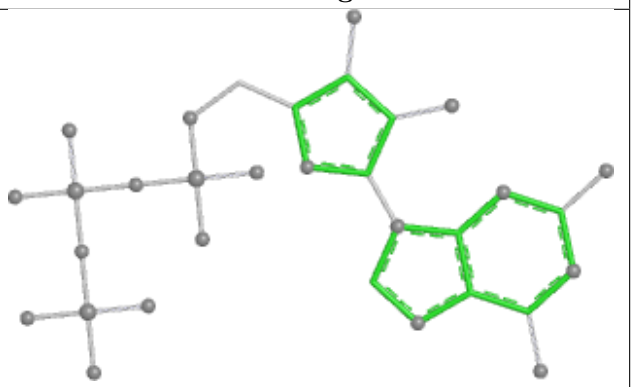
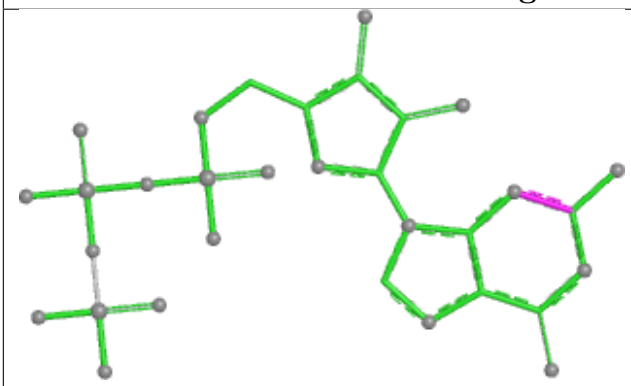


Rings

Ligand GTP SI 501



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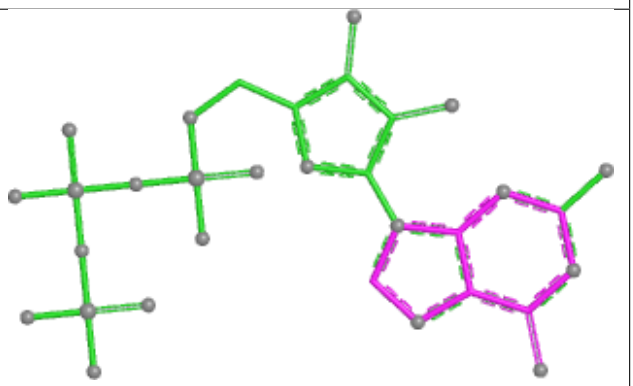

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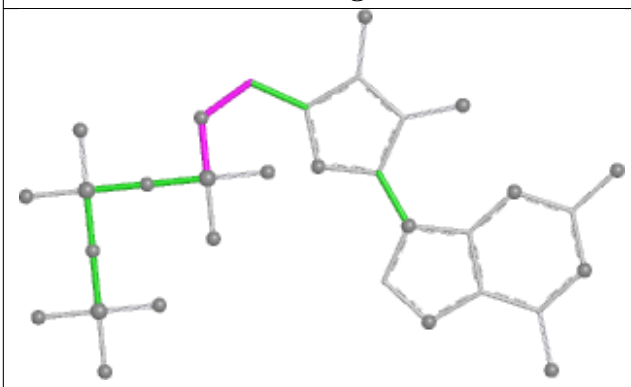

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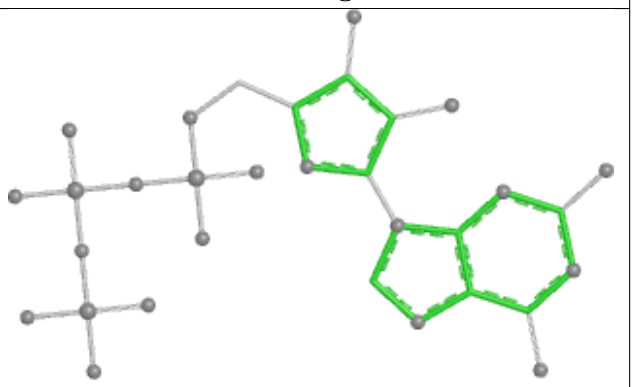
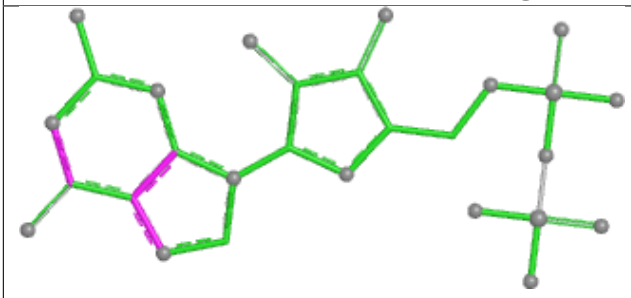


Rings

Ligand GDP LI 500



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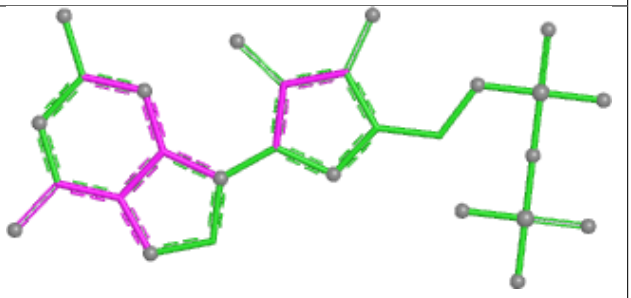

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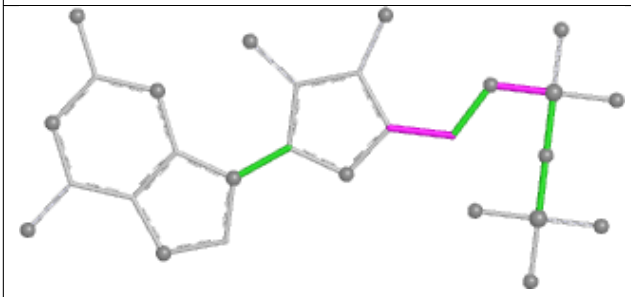

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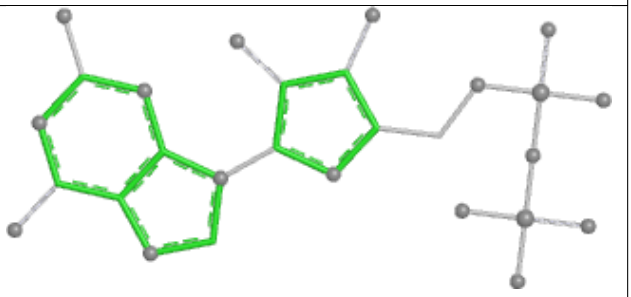
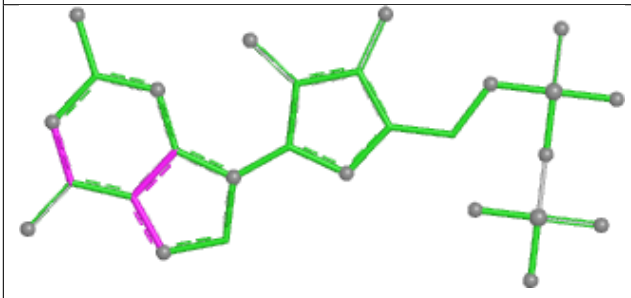


Rings

Ligand GDP CC 500



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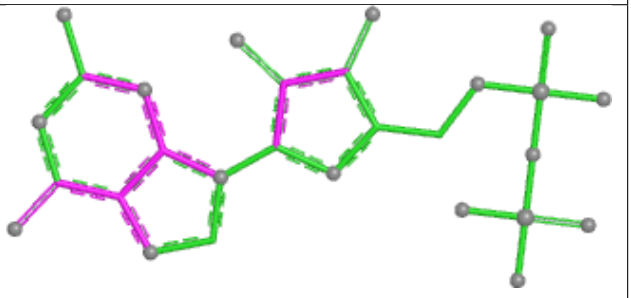

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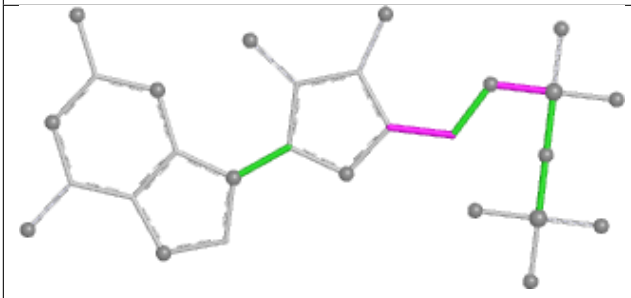

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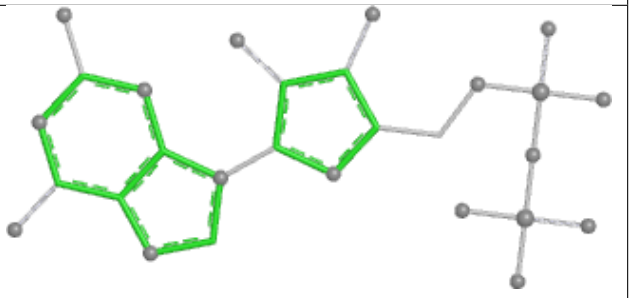

Rings

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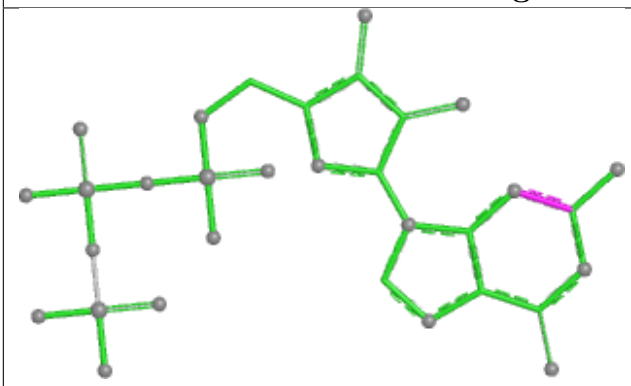

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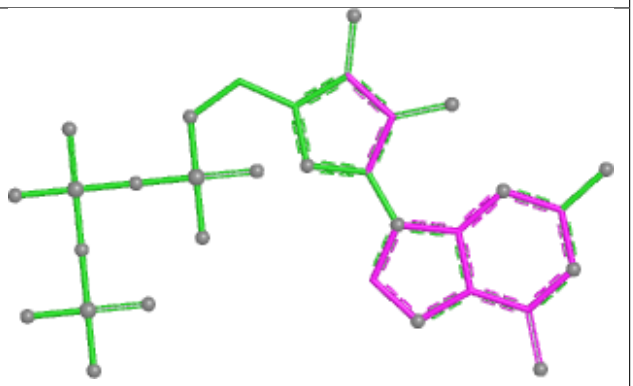

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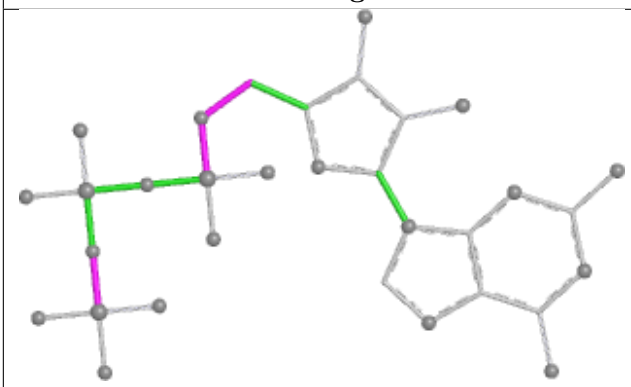

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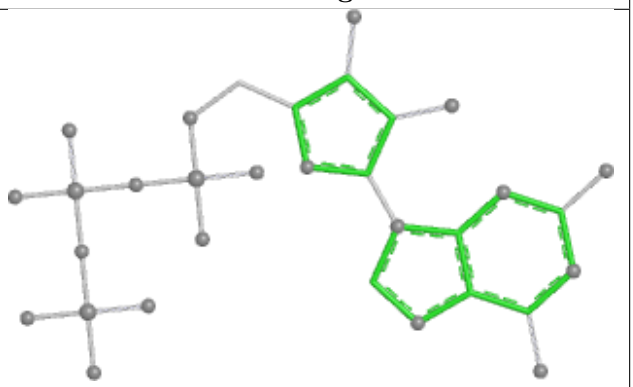
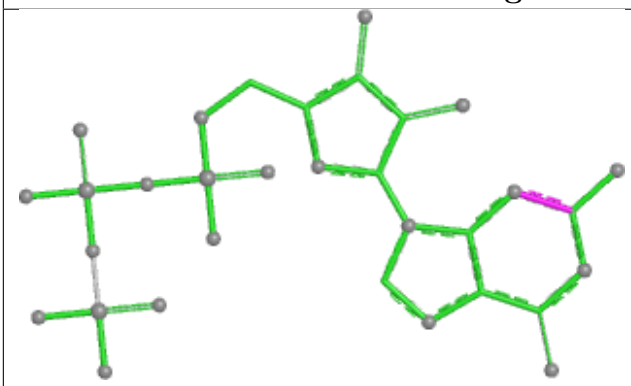


Rings

Ligand GTP MG 501



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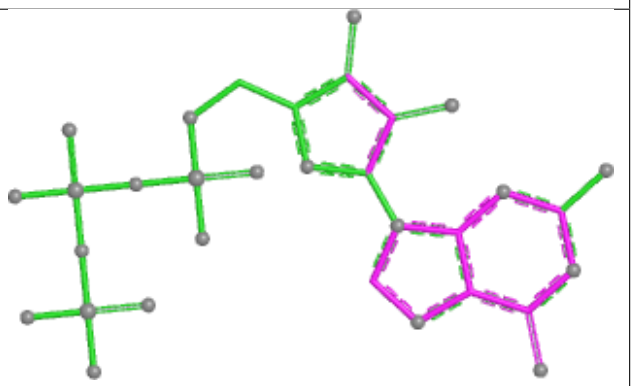

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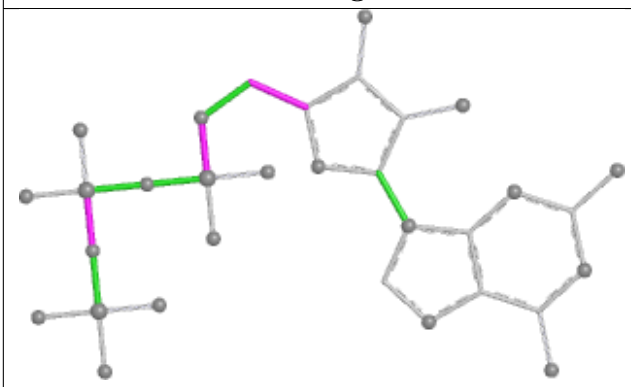

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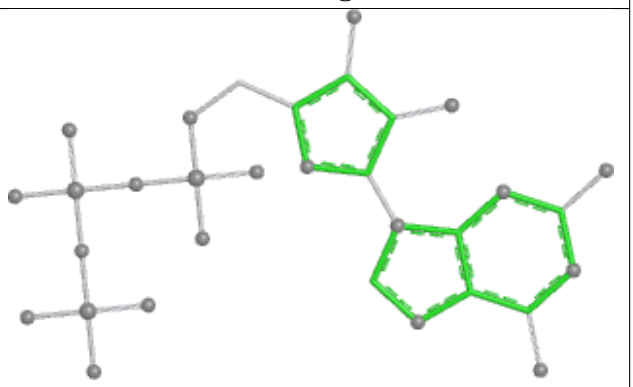
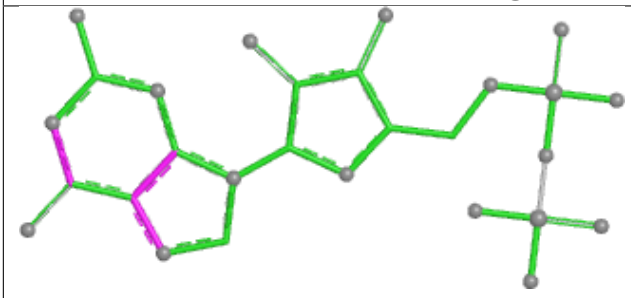


Rings

Ligand GDP KA 500



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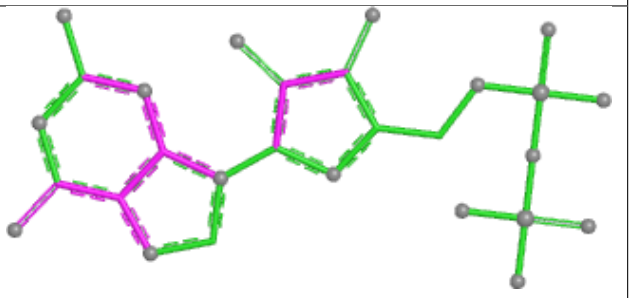

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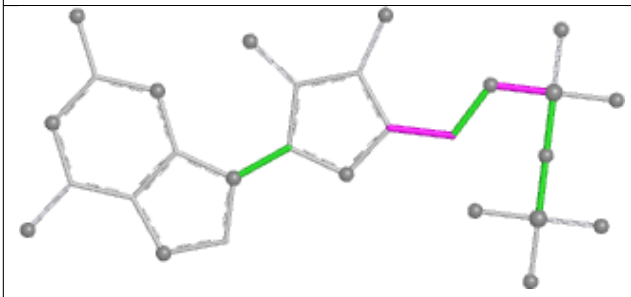

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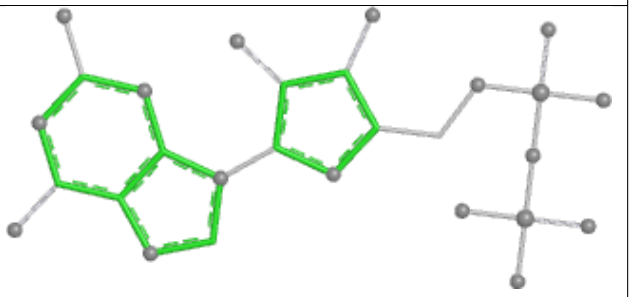
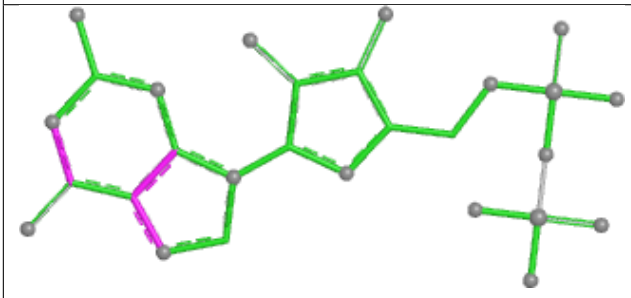


Rings

Ligand GDP ID 500



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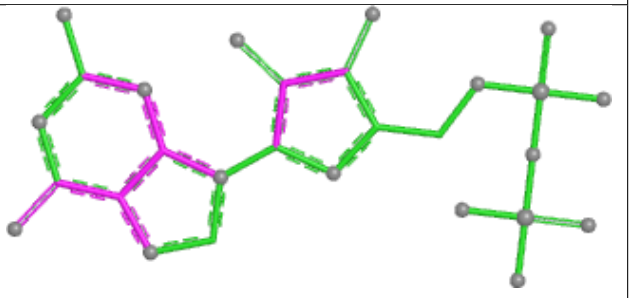
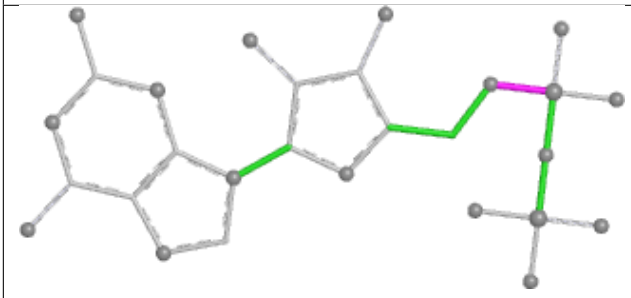


Bond angles



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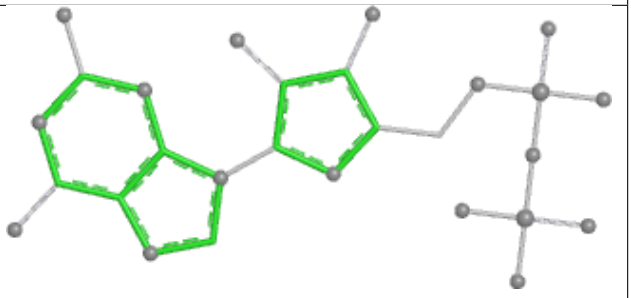
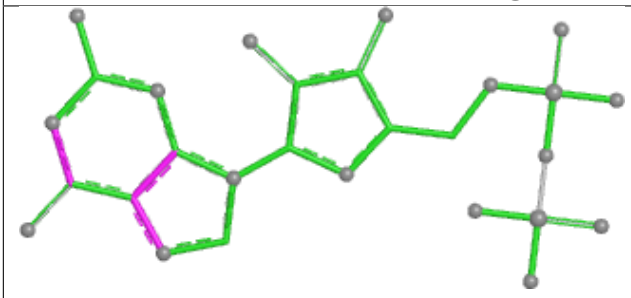


Rings

Ligand GDP WJ 500



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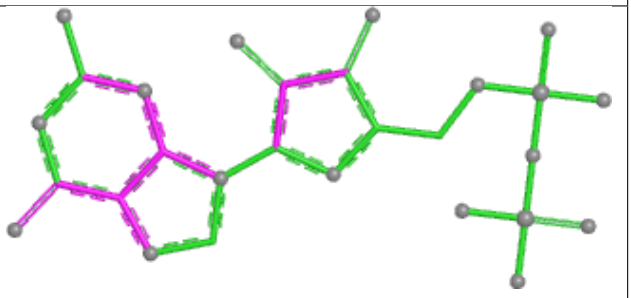

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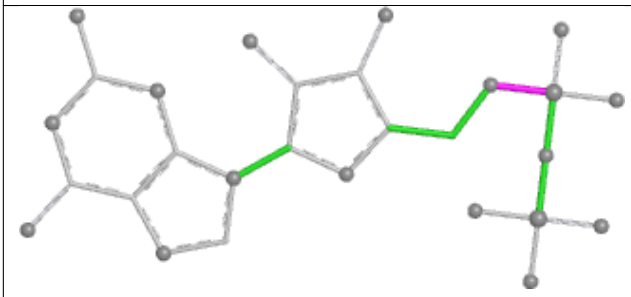
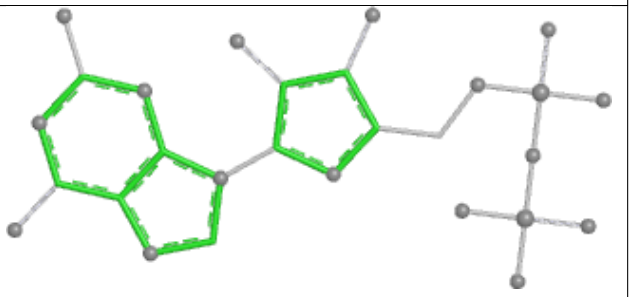
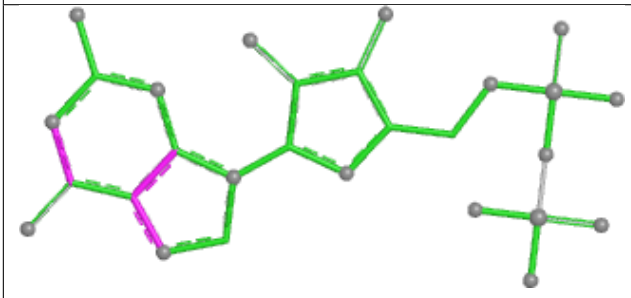


Torsions



Rings

Ligand GDP HJ 500



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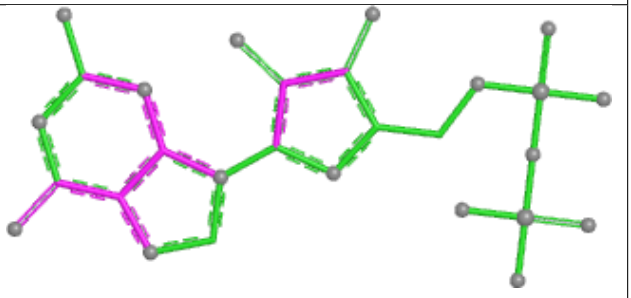

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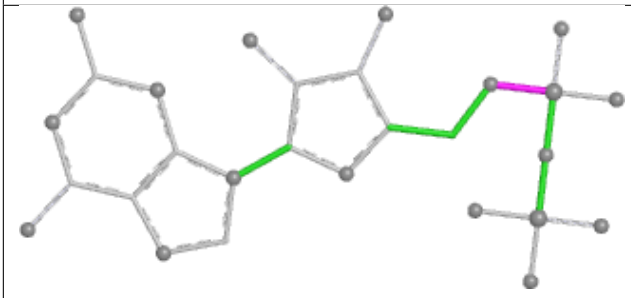

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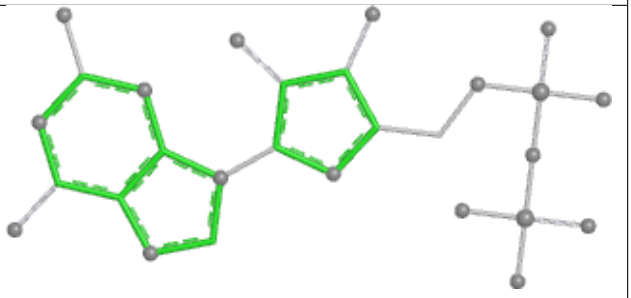
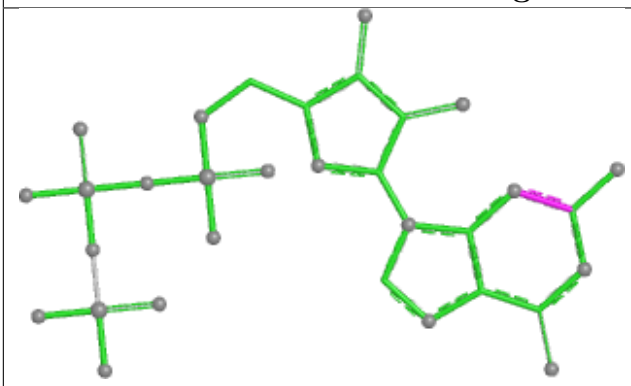


Rings

Ligand GTP FA 501



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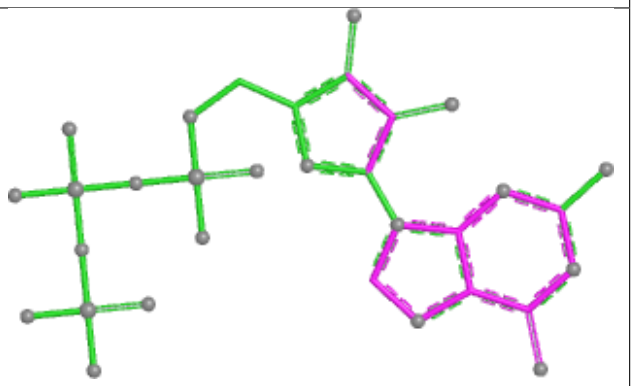

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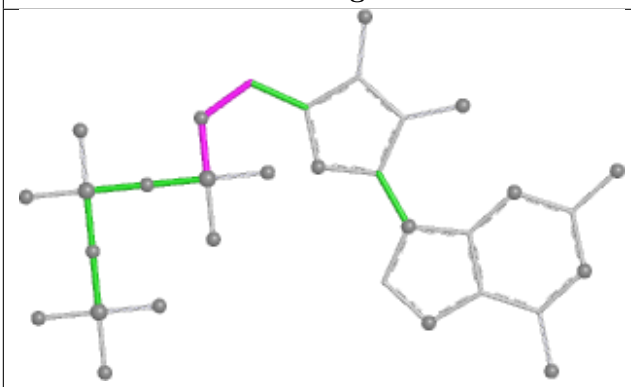

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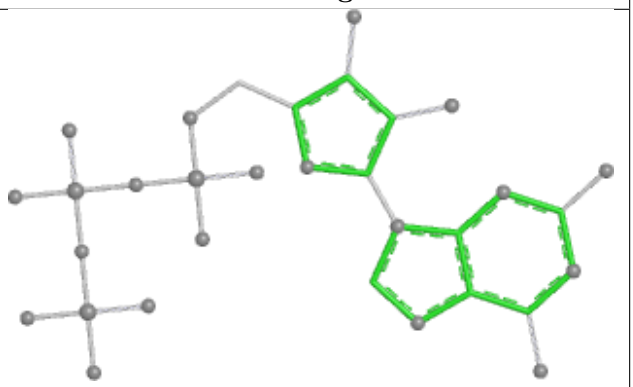

Rings

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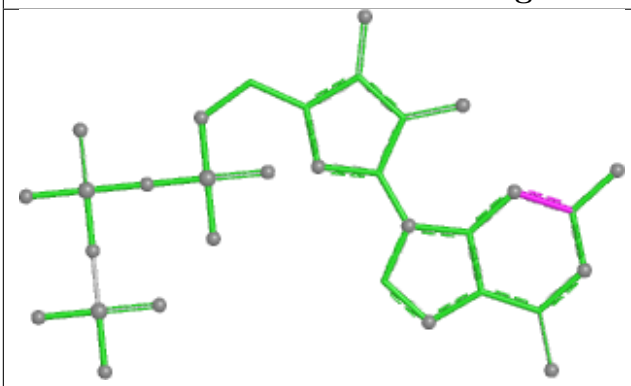

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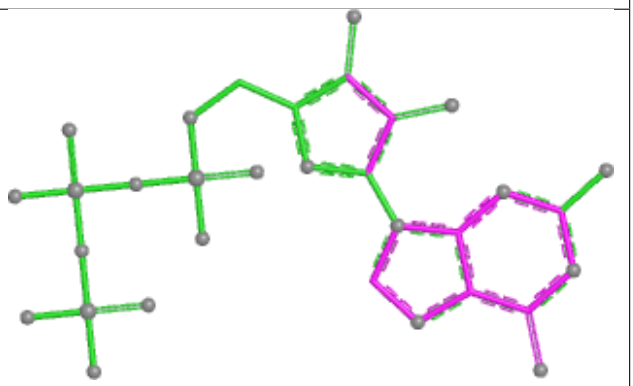

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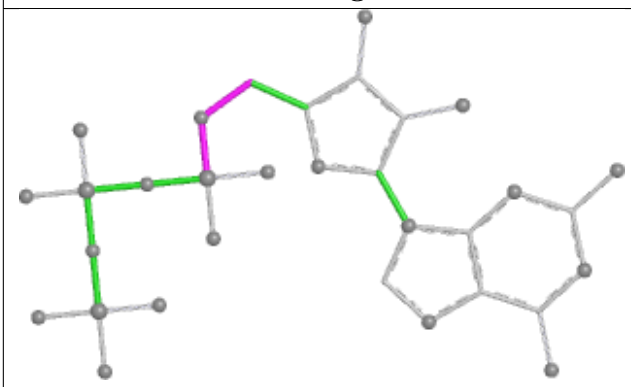

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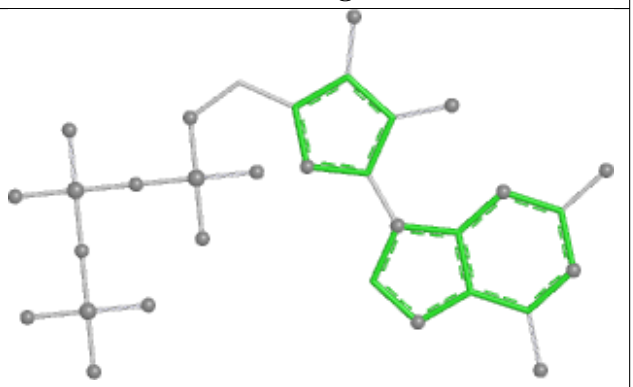

Rings

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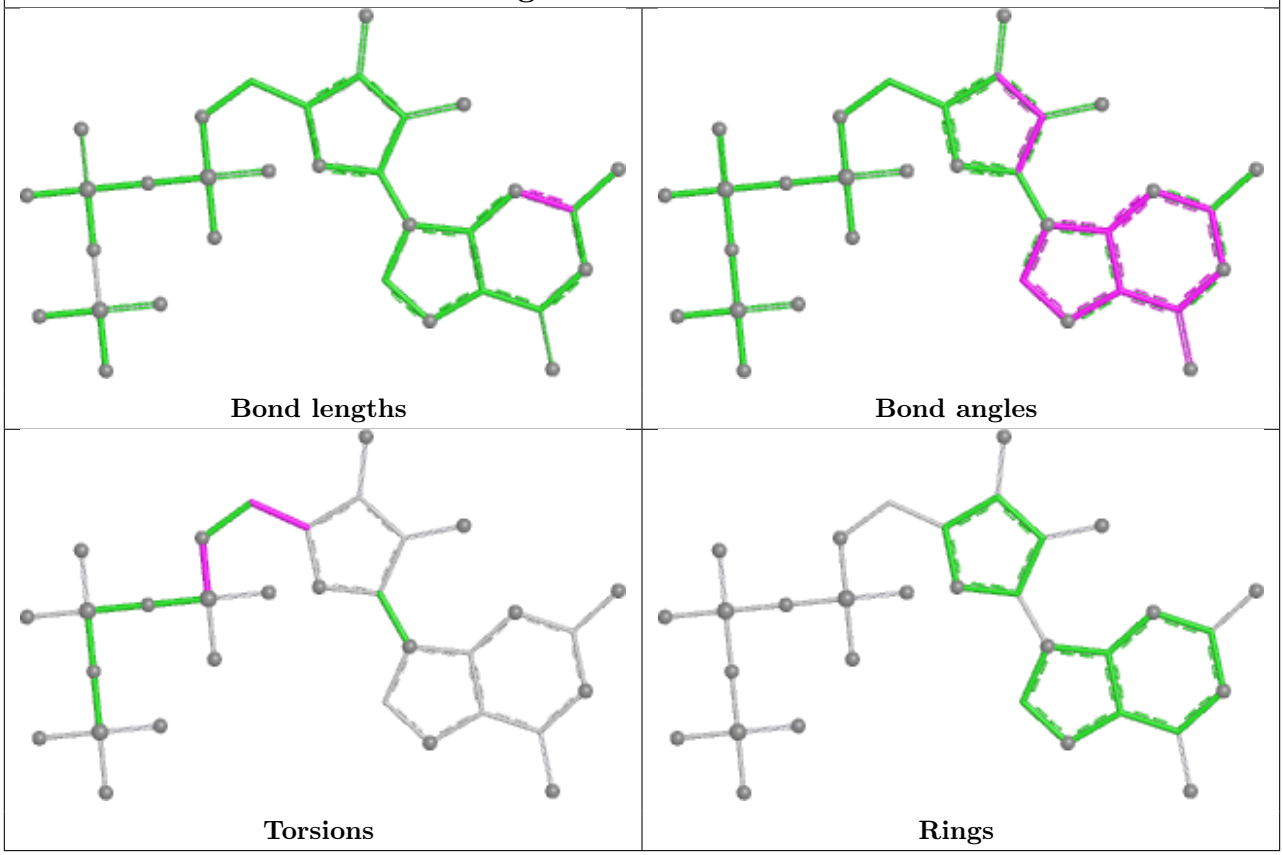

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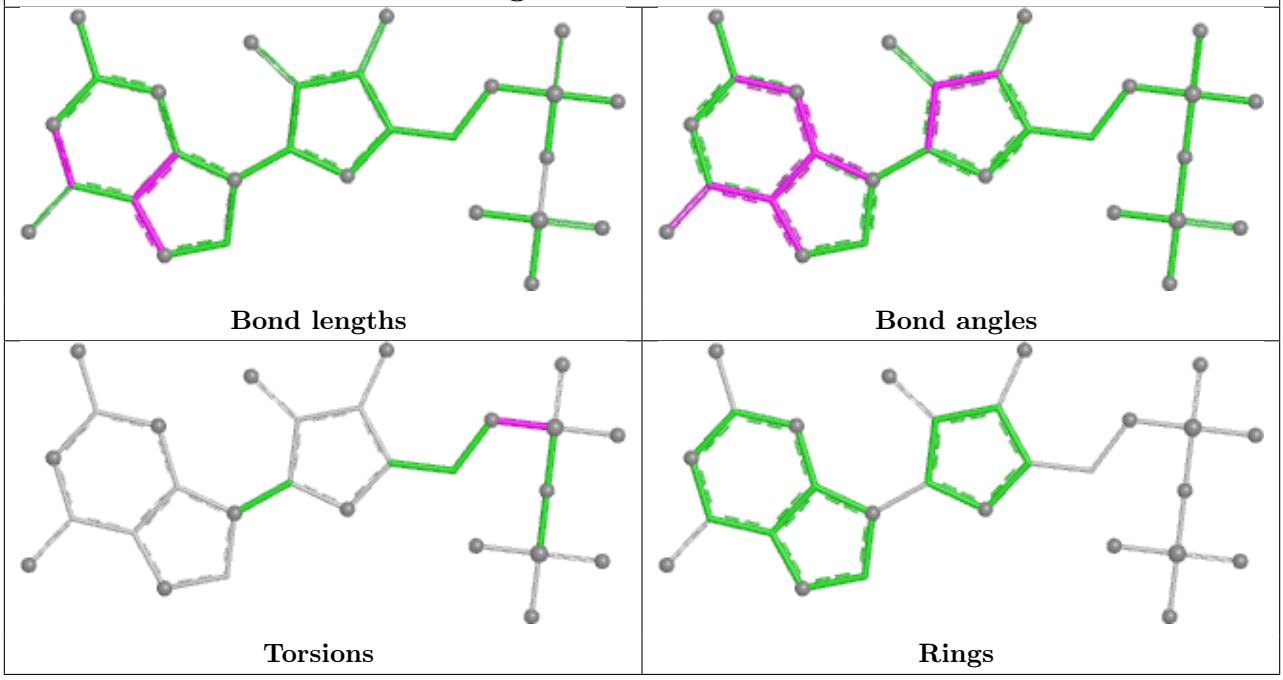

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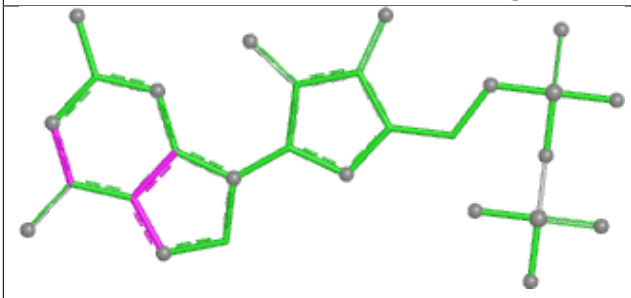

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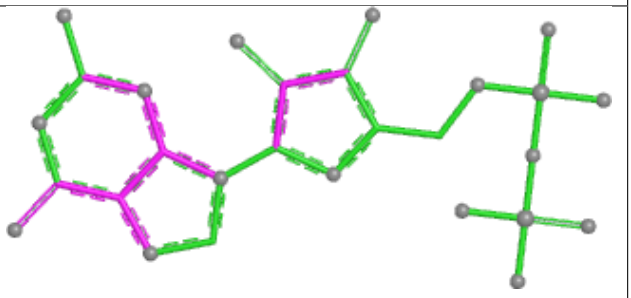

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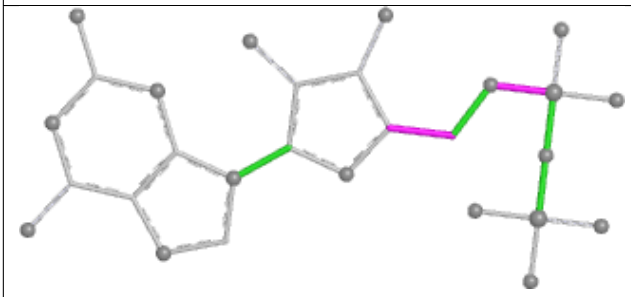

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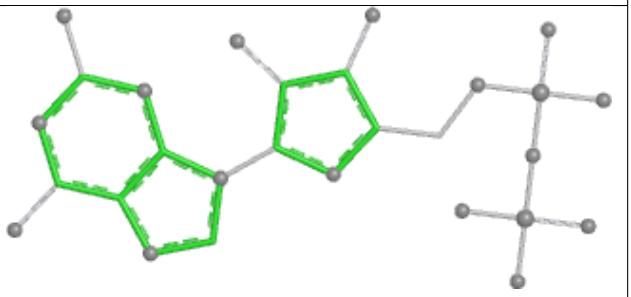
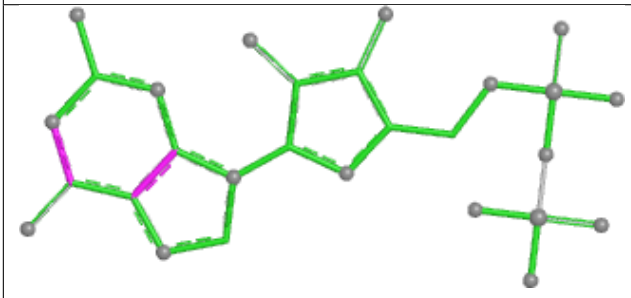


Rings

Ligand GDP EL 500



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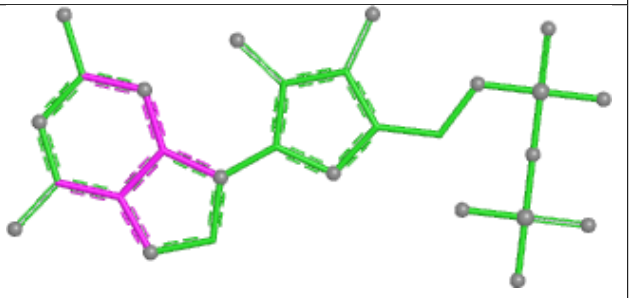

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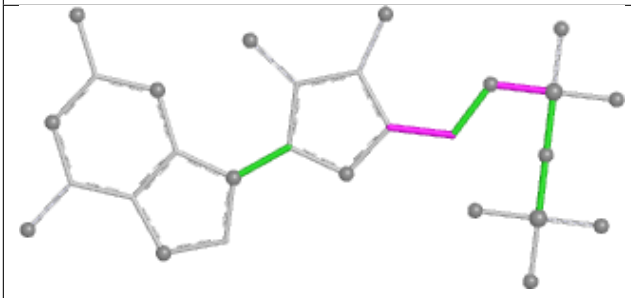

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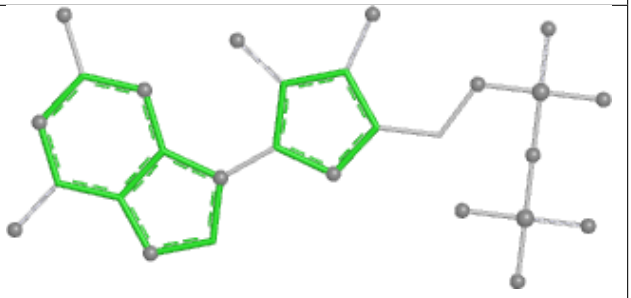
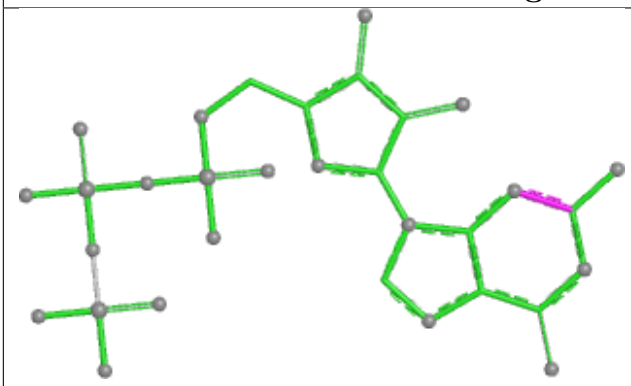


Rings

Ligand GTP L 501



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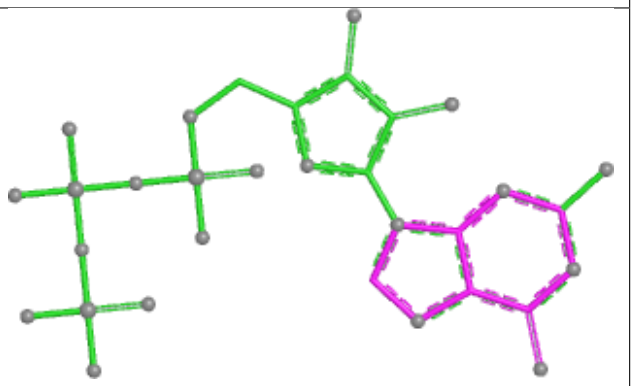

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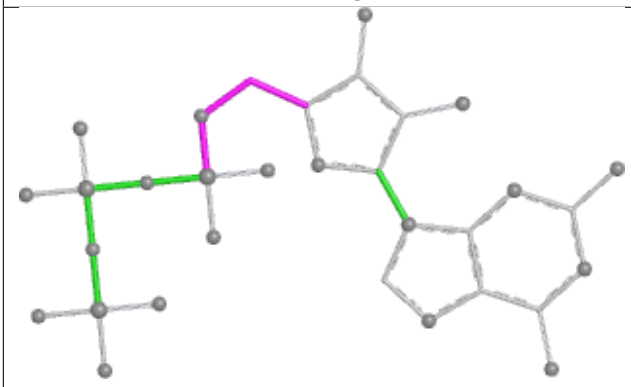

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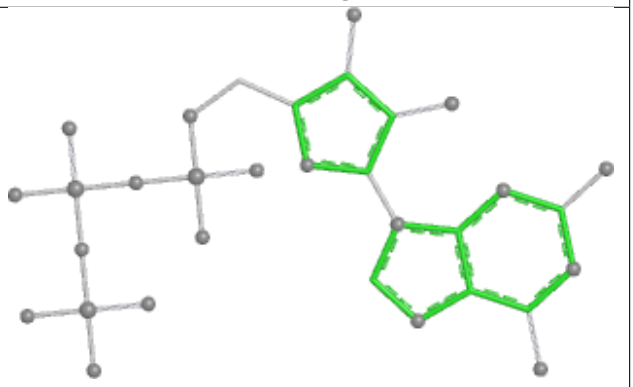
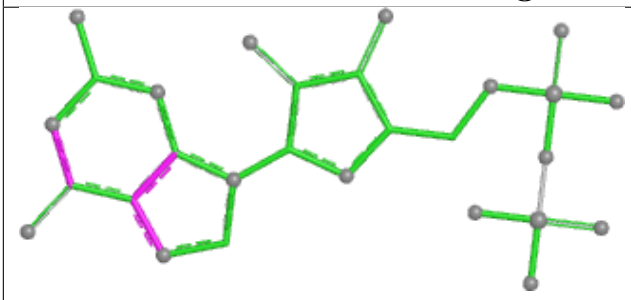


Rings

Ligand GDP W 500



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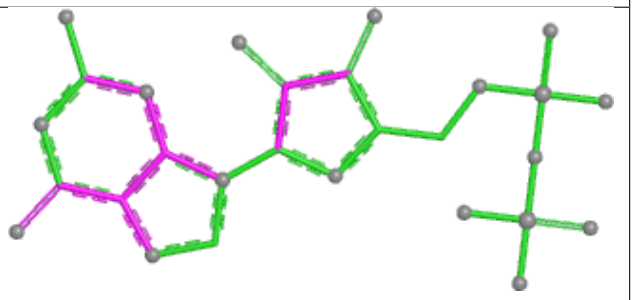

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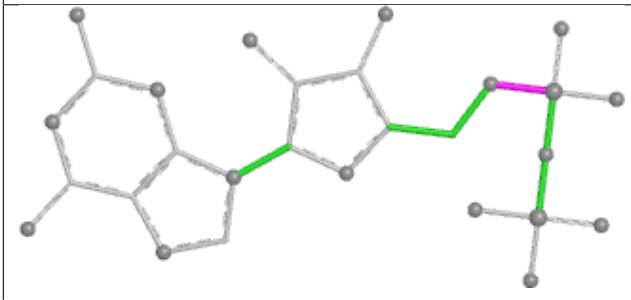

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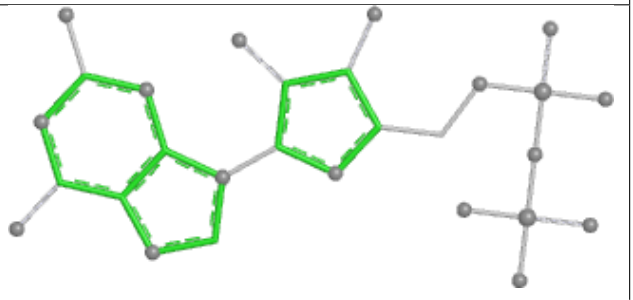
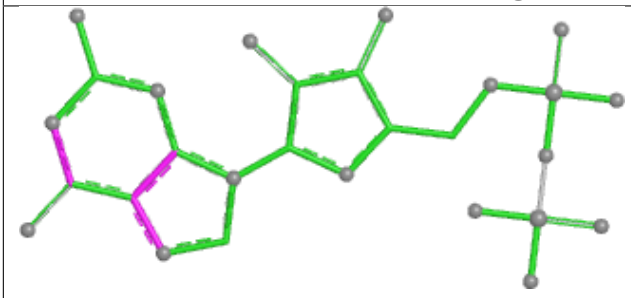


Rings

Ligand GDP OF 500



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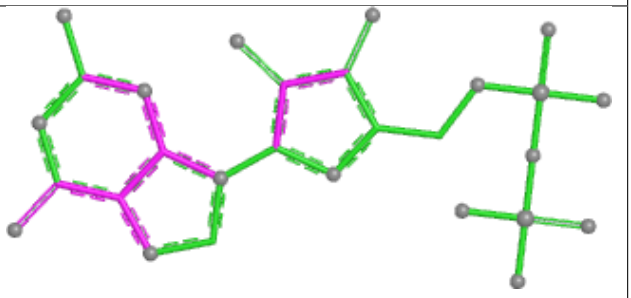

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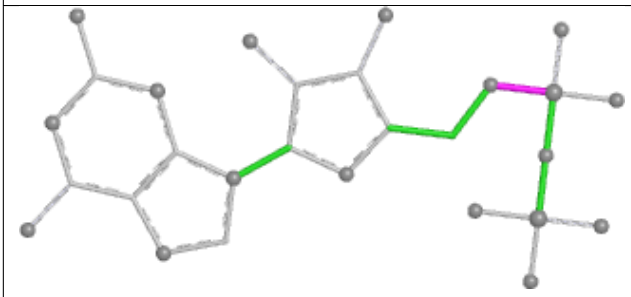

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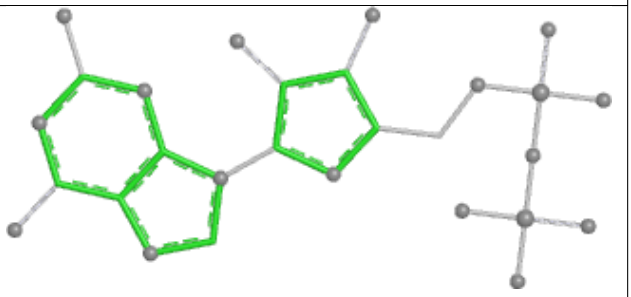

Rings

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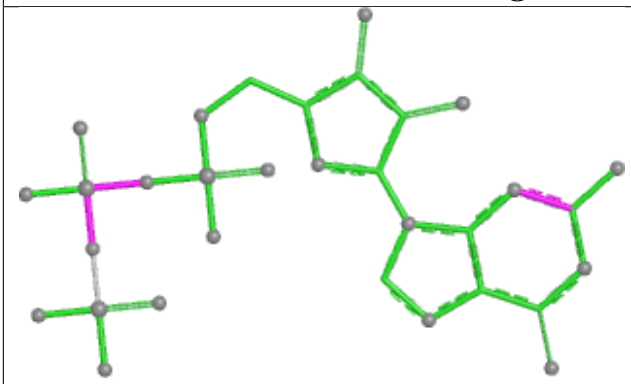

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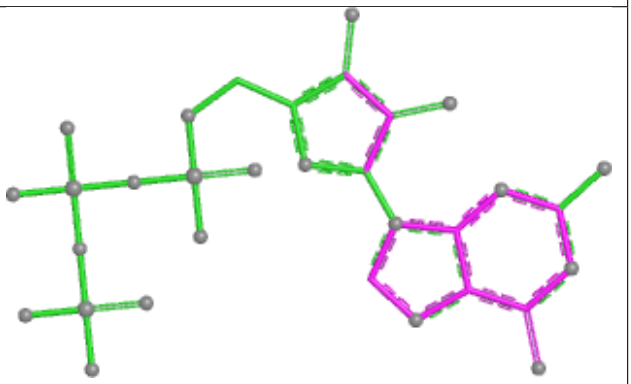

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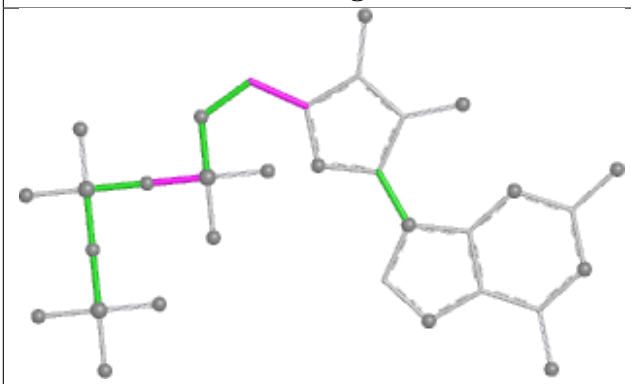

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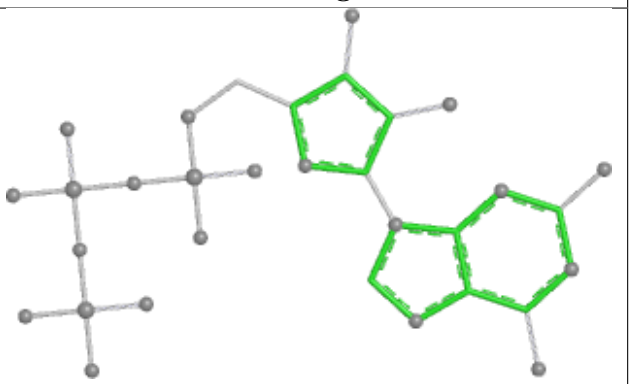

Rings

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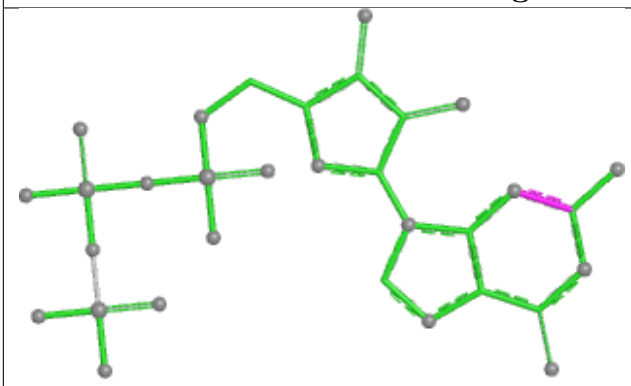

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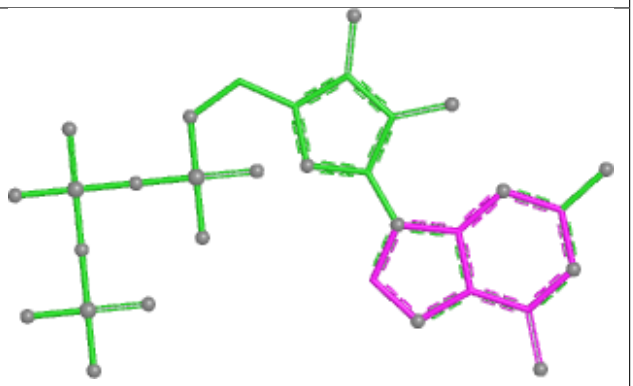

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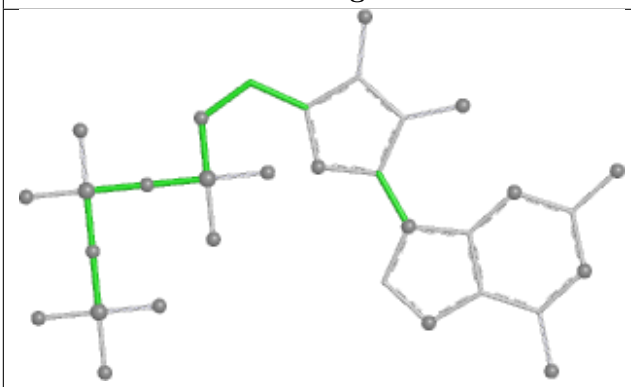

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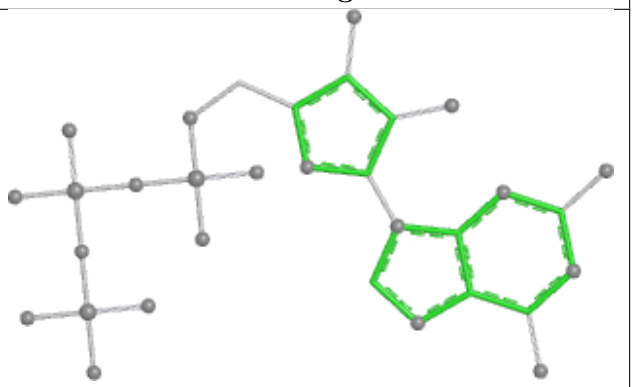

Rings

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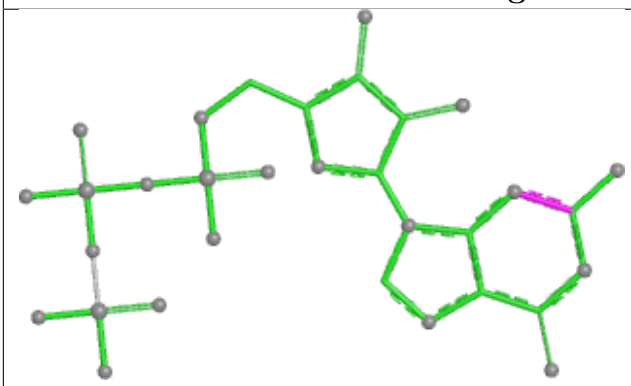

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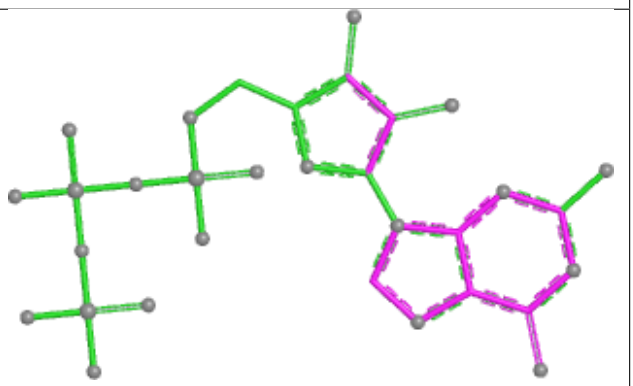

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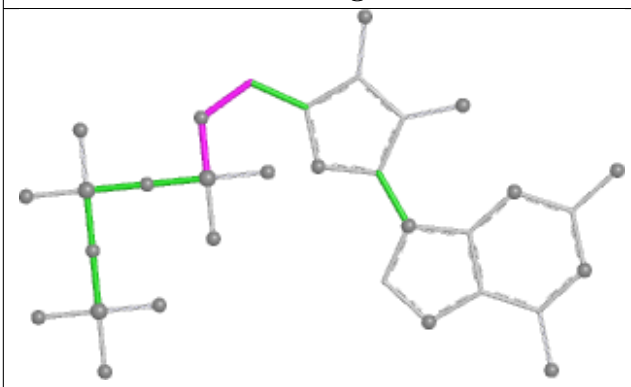

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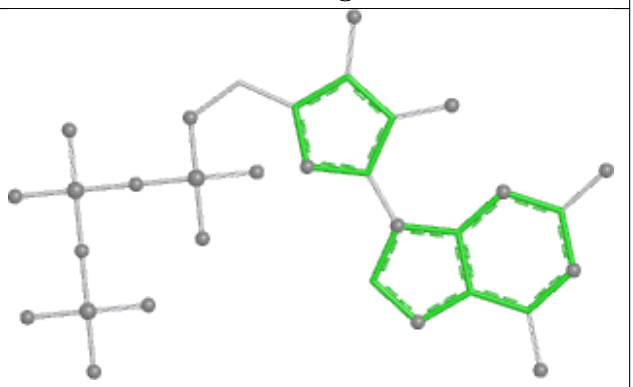

Rings

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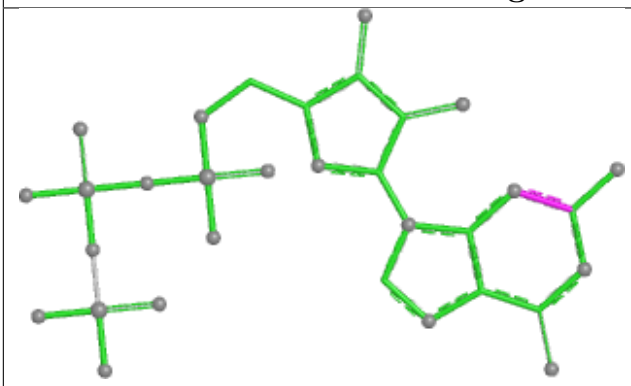

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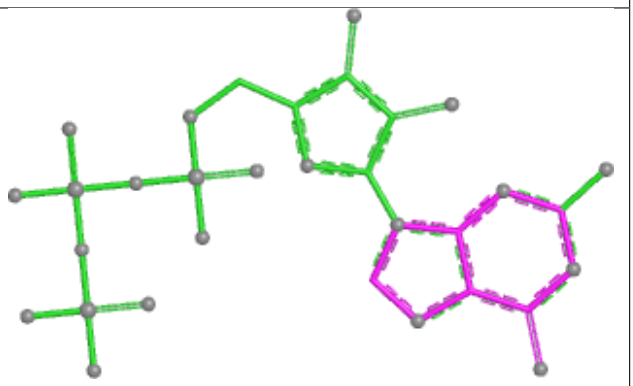
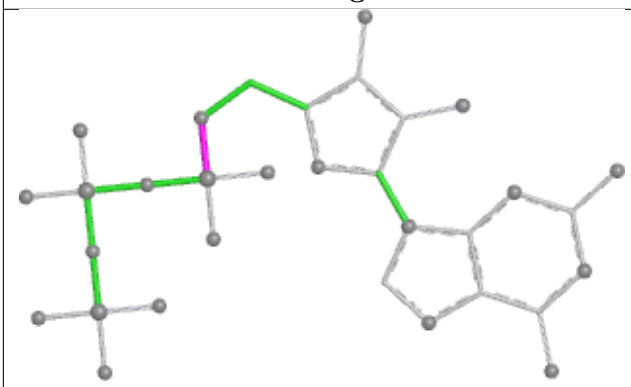


Bond angles



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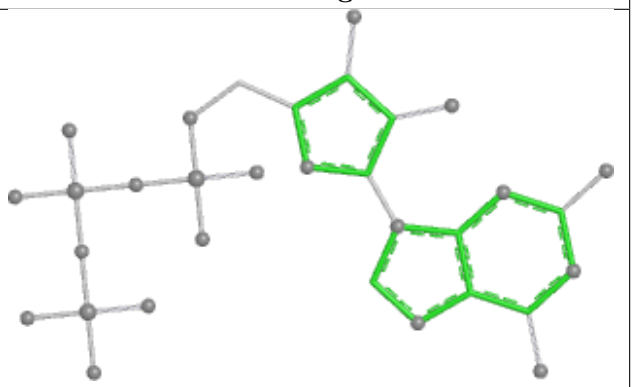

Rings

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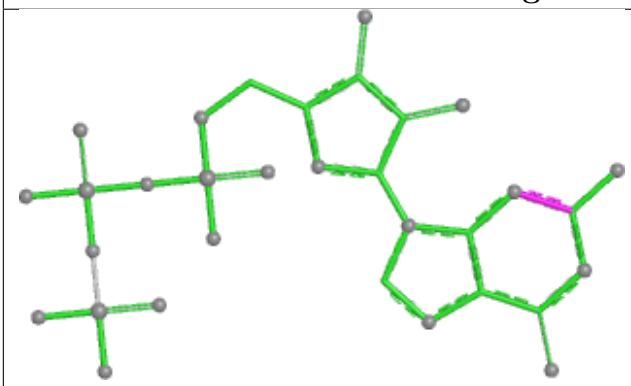

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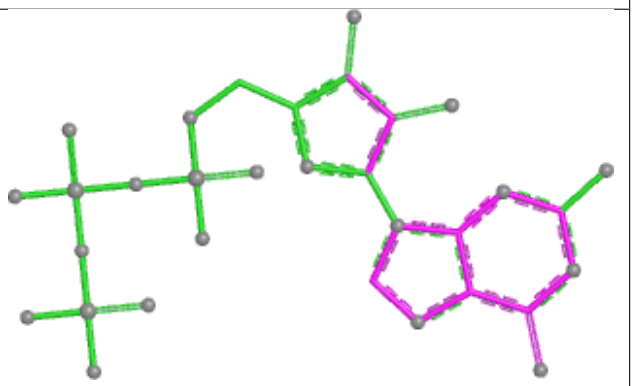
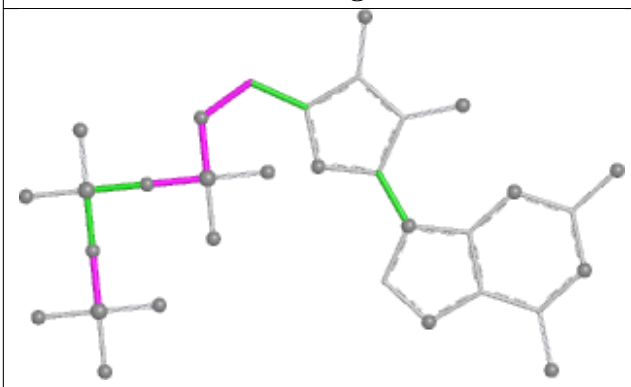
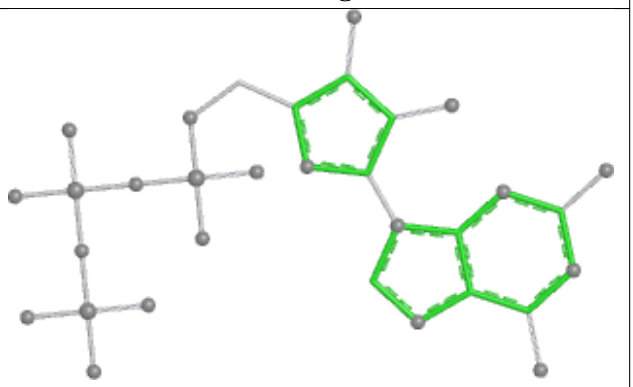


Bond angles

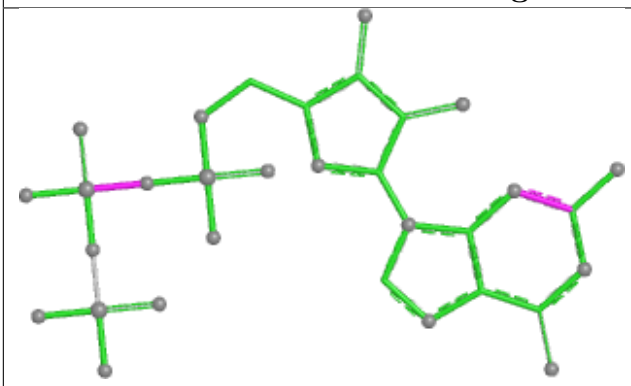


Torsions



Rings

Ligand GTP KL 501



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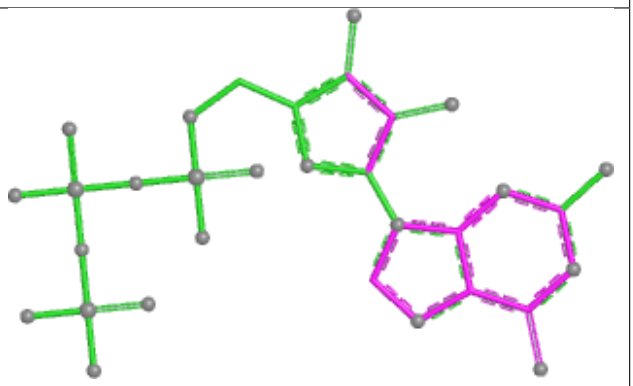

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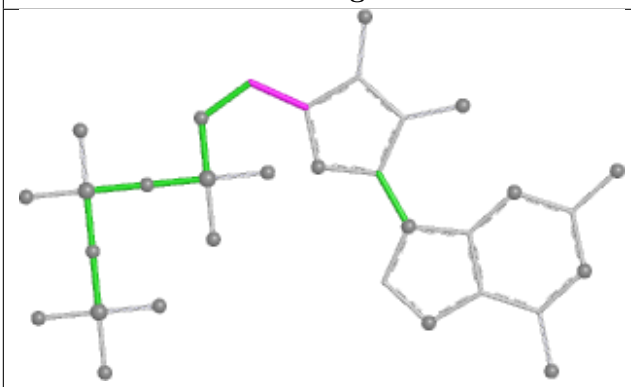

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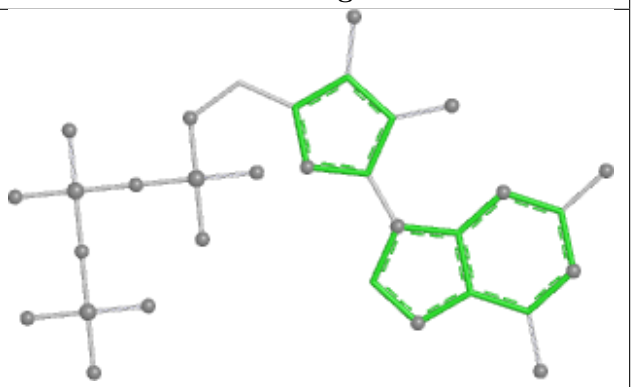
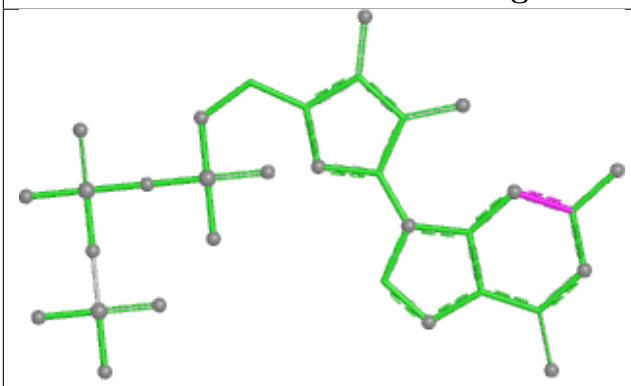


Rings

Ligand GTP QF 501



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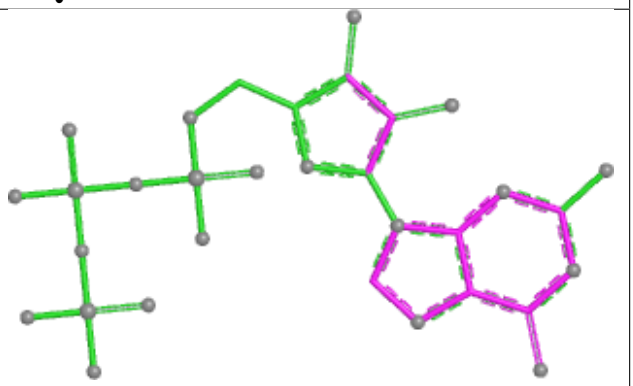

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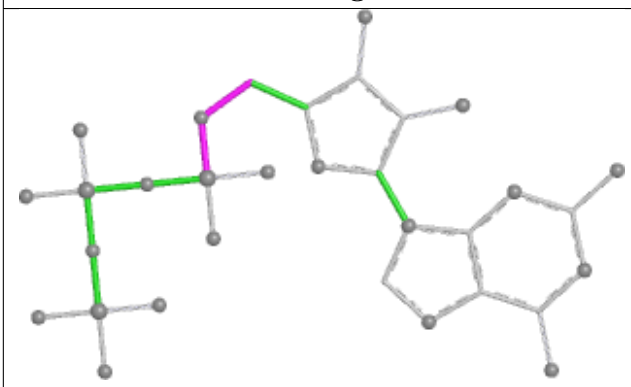

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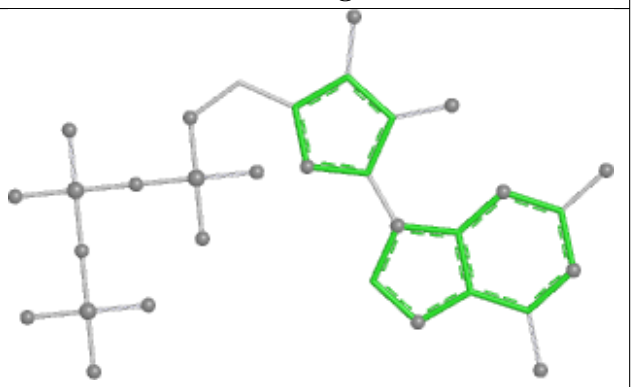
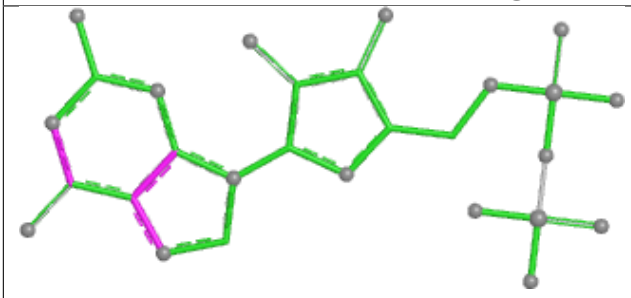


Rings

Ligand GDP JM 500



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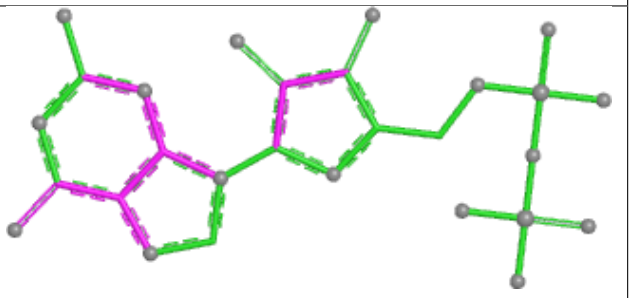

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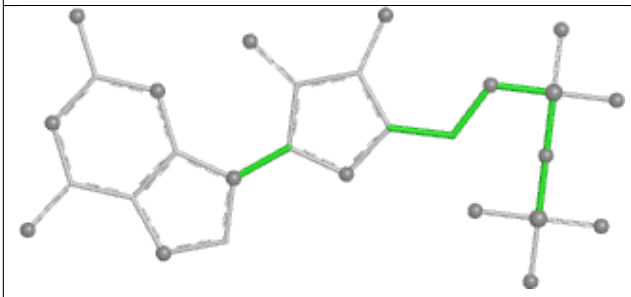

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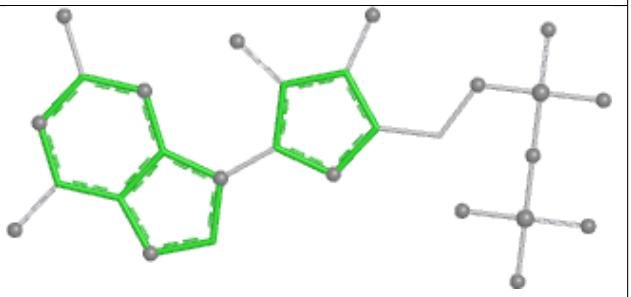
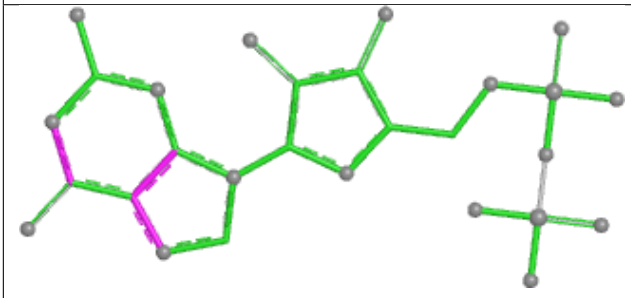


Rings

Ligand GDP M 500



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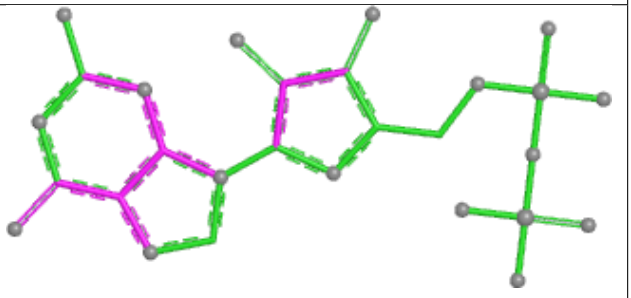

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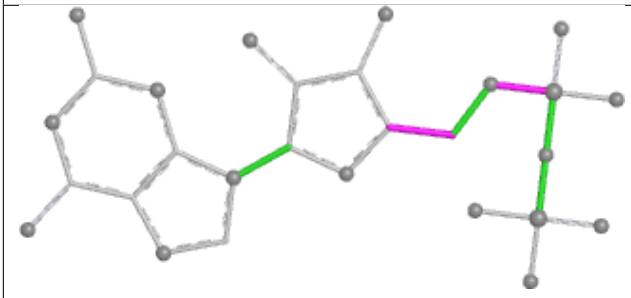

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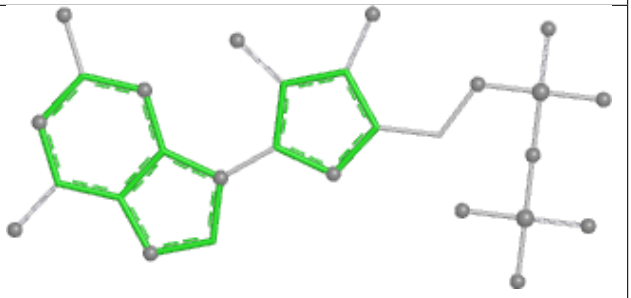
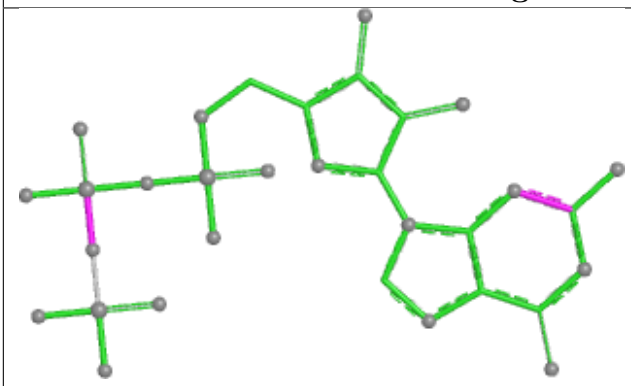


Rings

Ligand GTP CF 501



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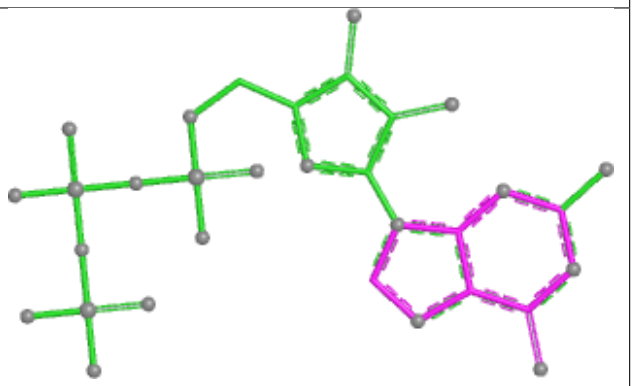

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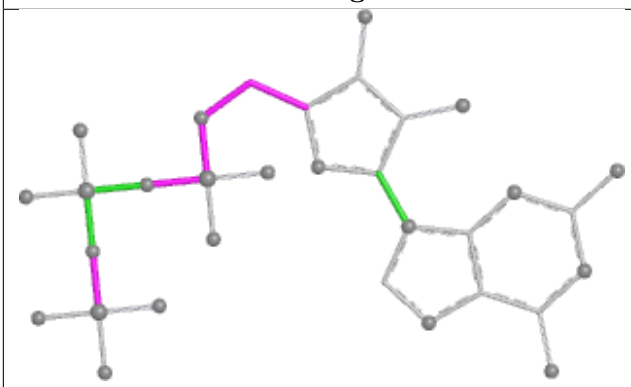

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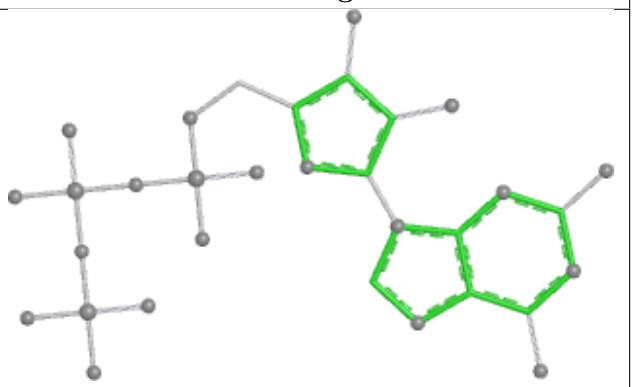
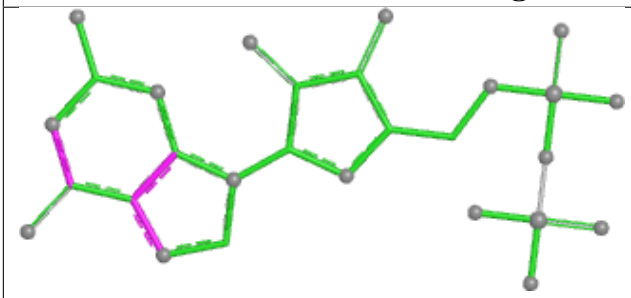


Rings

Ligand GDP BF 500



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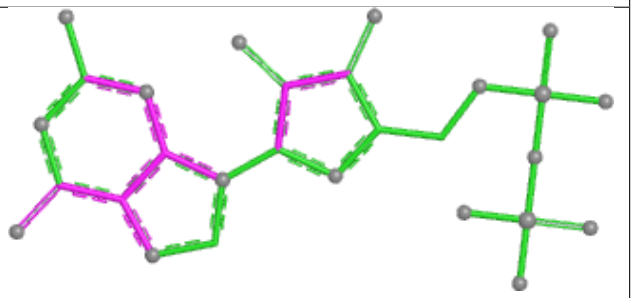

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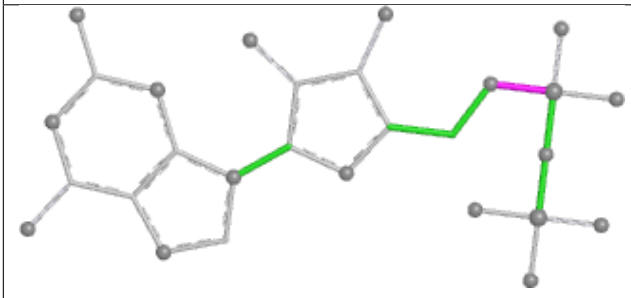

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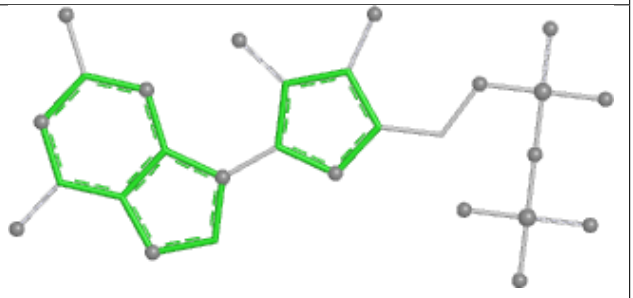
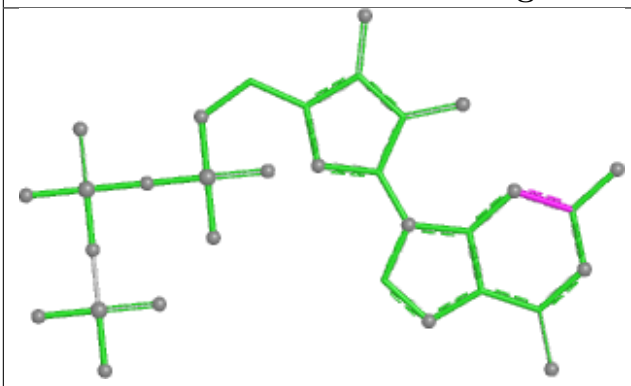


Rings

Ligand GTP JJ 501



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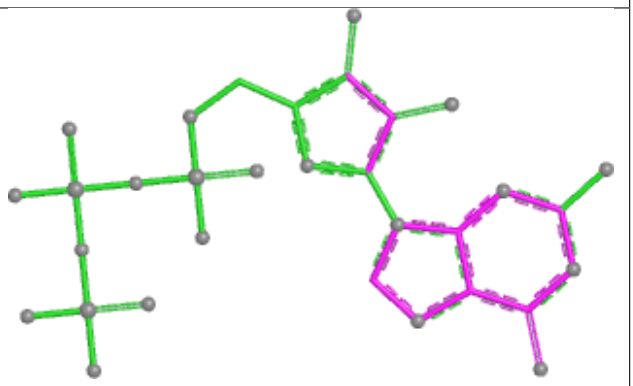

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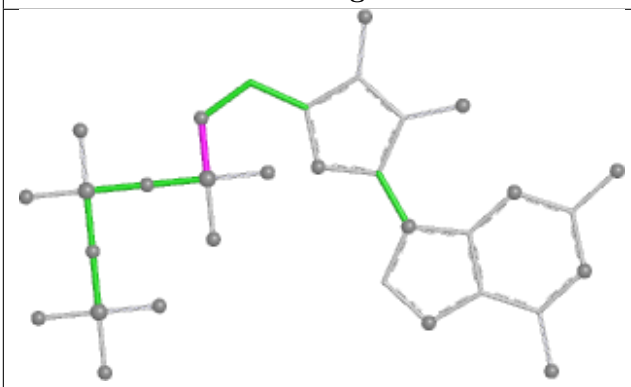

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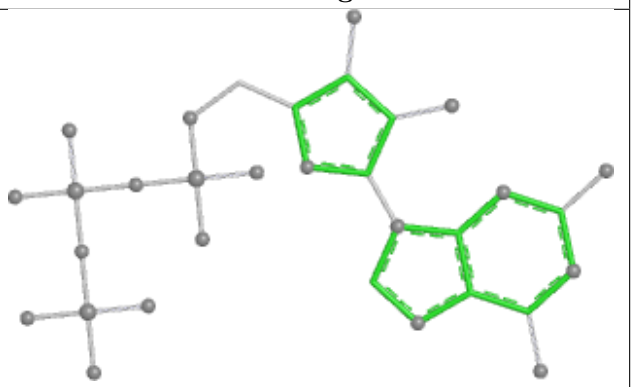
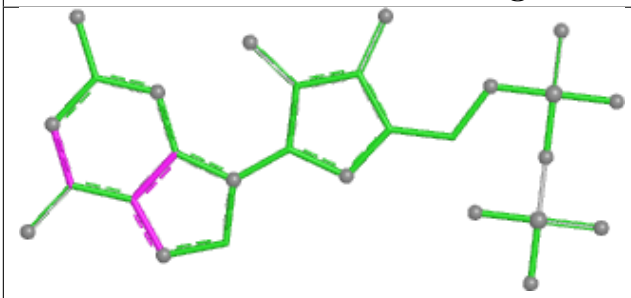


Rings

Ligand GDP FH 500



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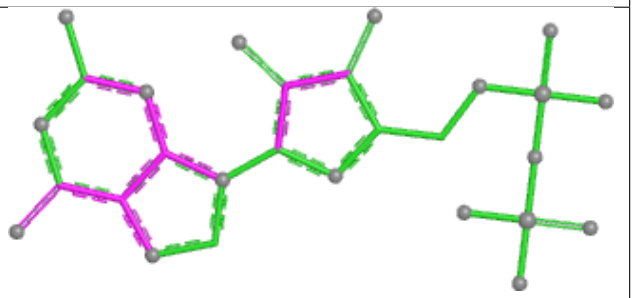

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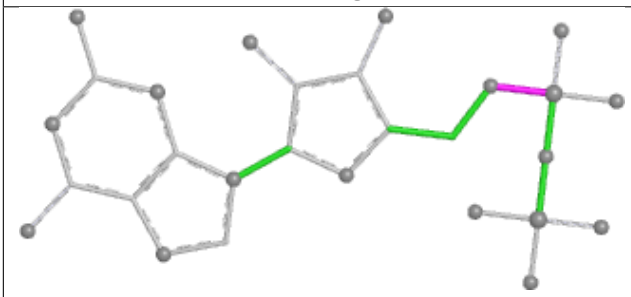

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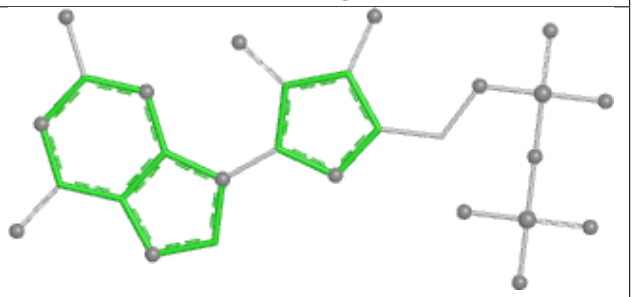
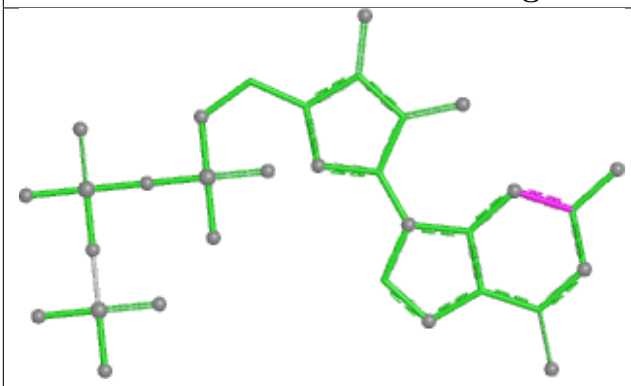


Rings

Ligand GTP R 501



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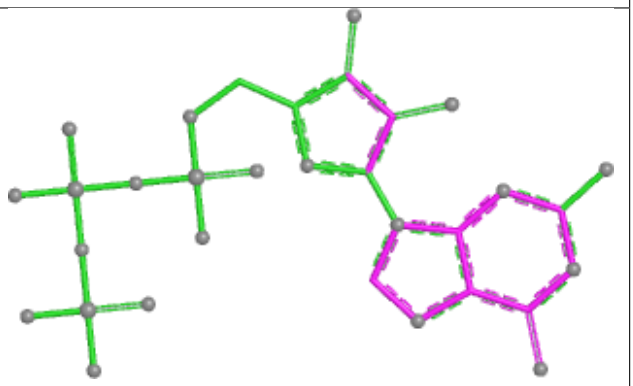

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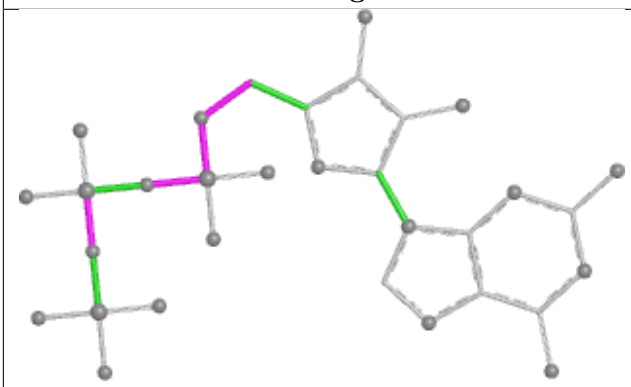

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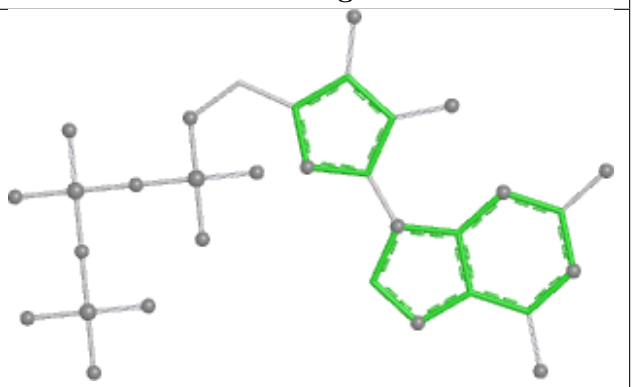

Rings

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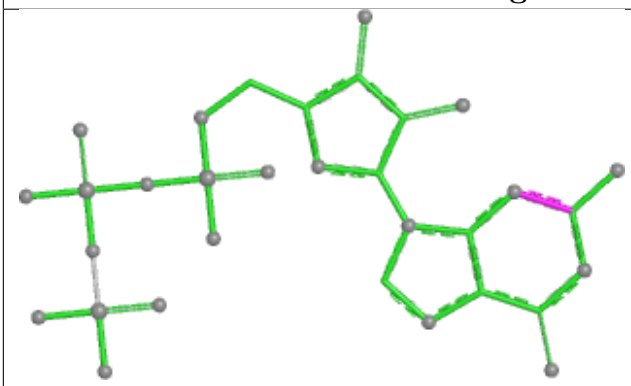

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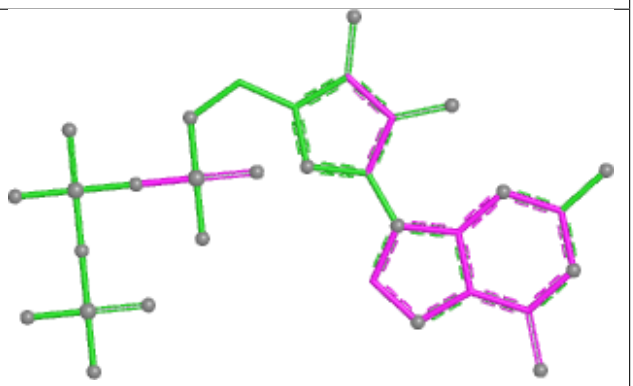

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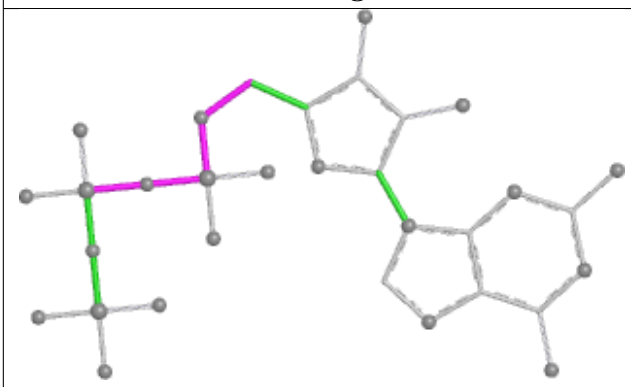

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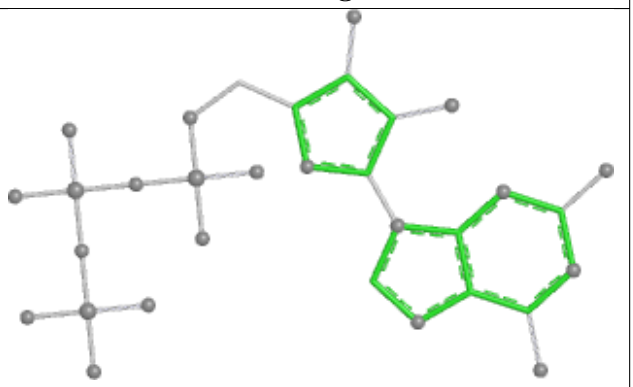
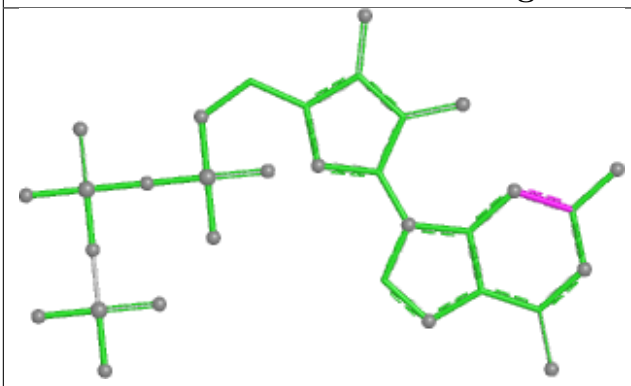


Rings

Ligand GTP IE 501



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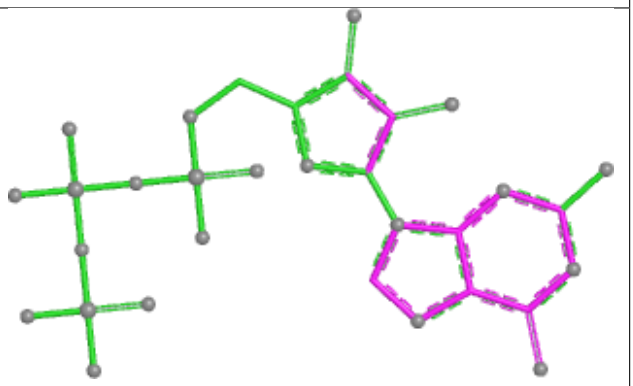

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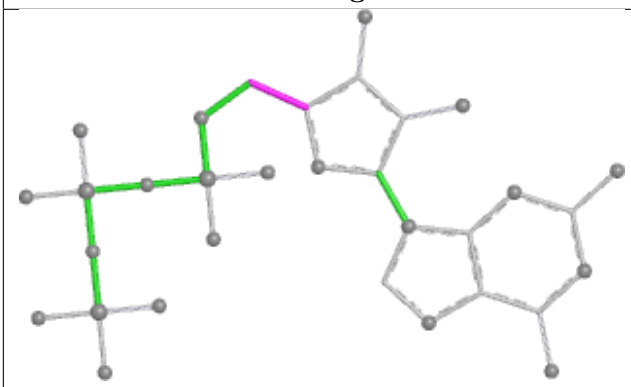

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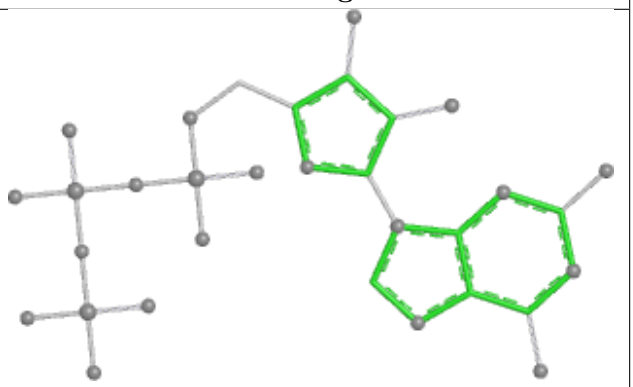
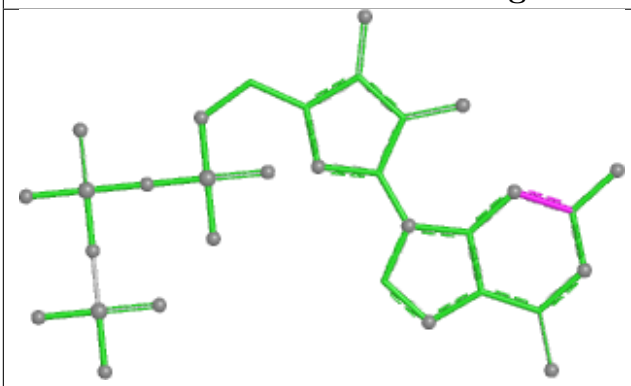


Rings

Ligand GTP BG 501



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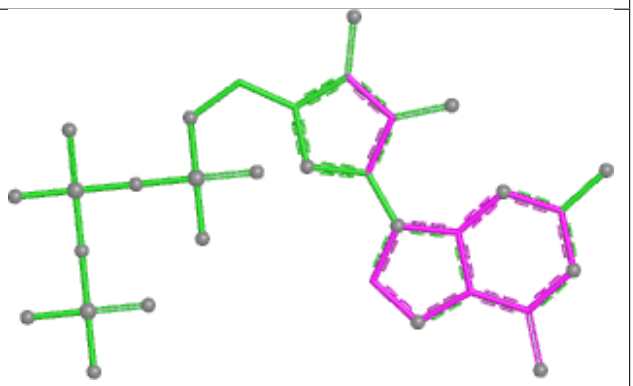

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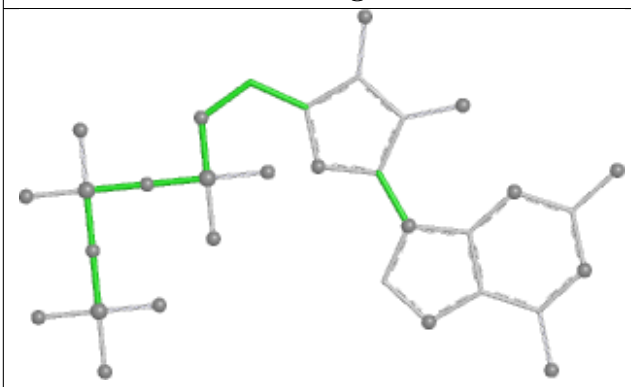

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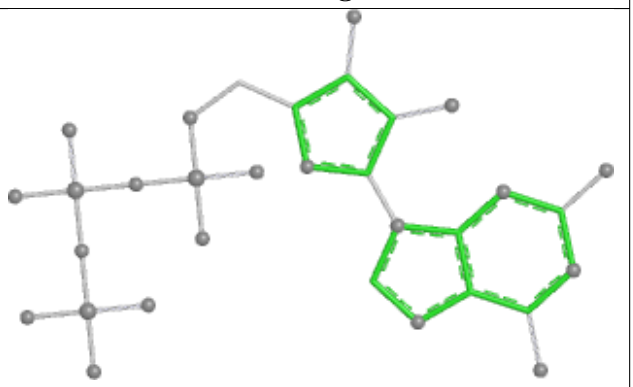
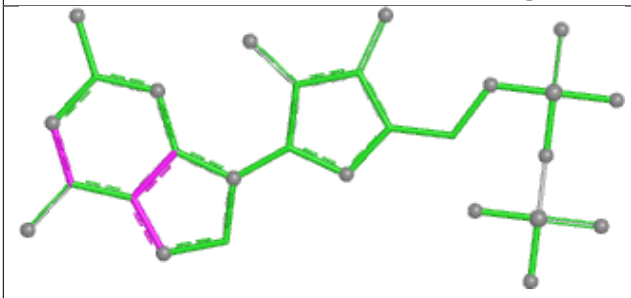


Rings

Ligand GDP U 500



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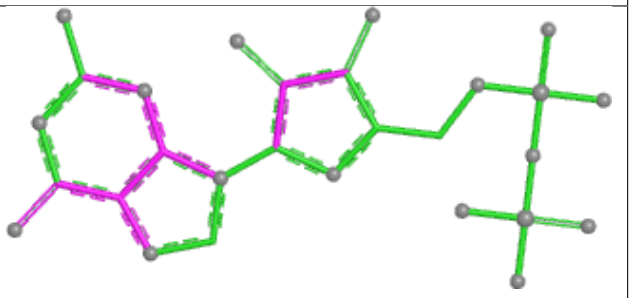
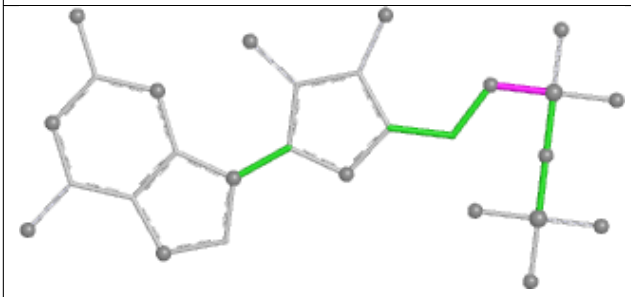


Bond angles



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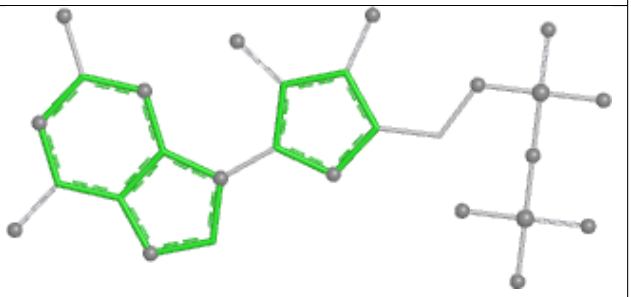
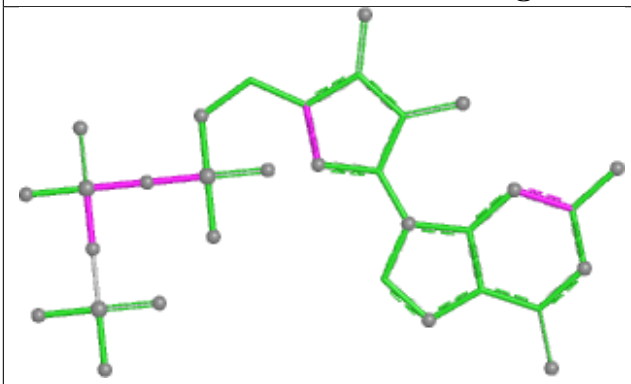


Rings

Ligand GTP IK 501



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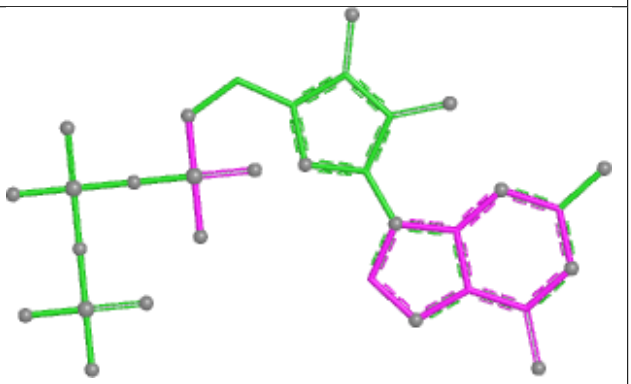
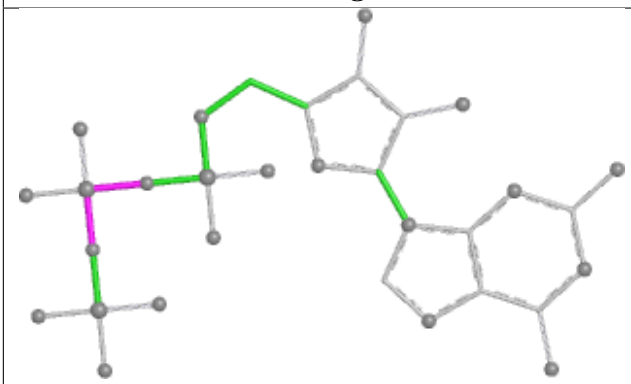
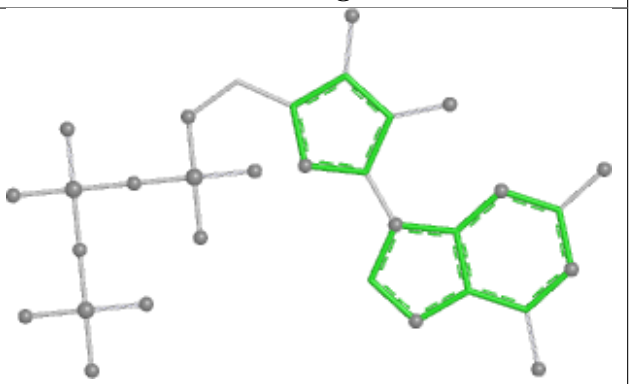


Bond angles

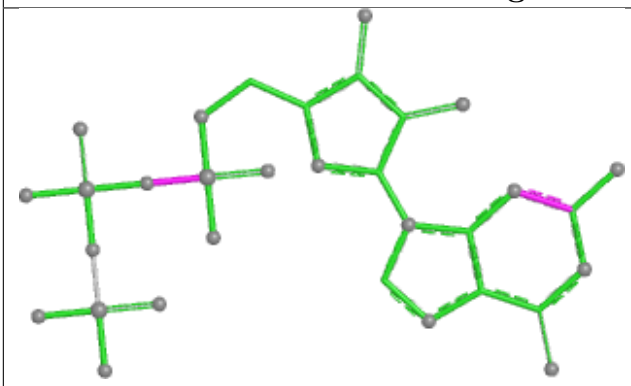


Torsions



Rings

Ligand GTP GK 501



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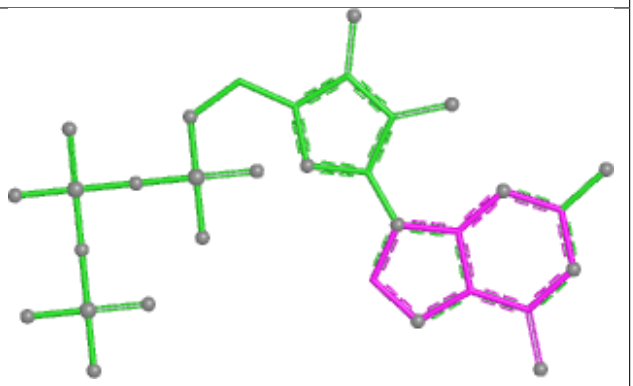

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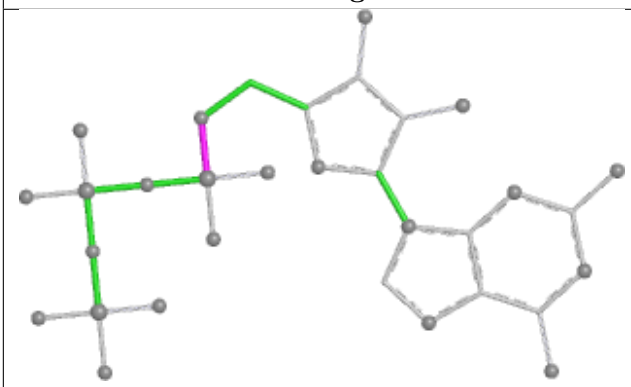

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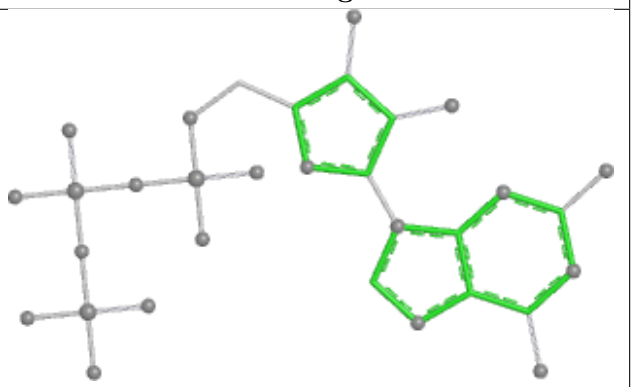
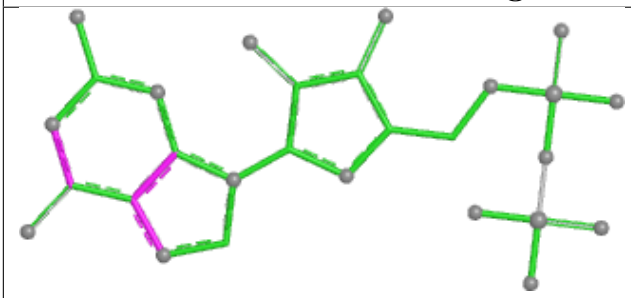


Rings

Ligand GDP ML 500



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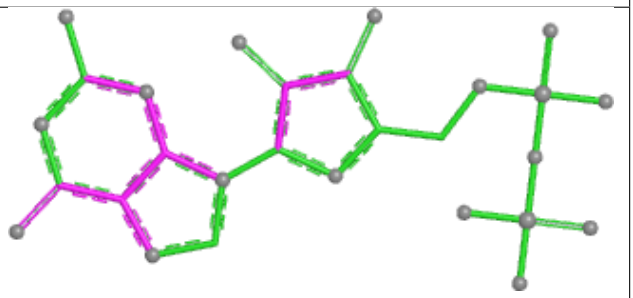

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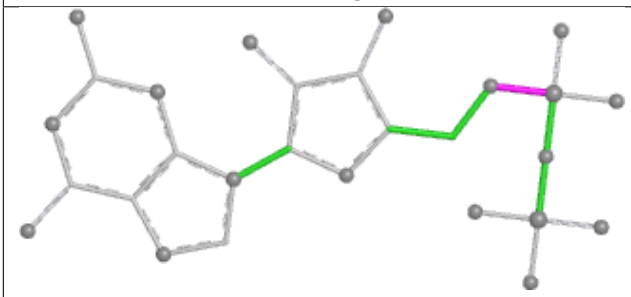

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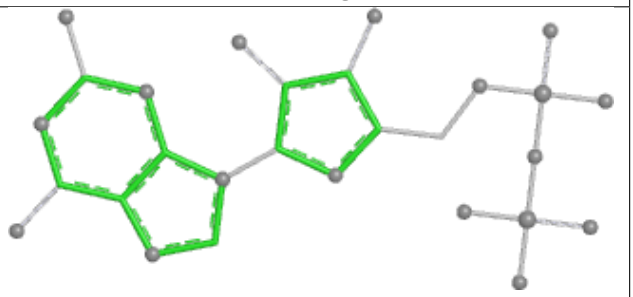
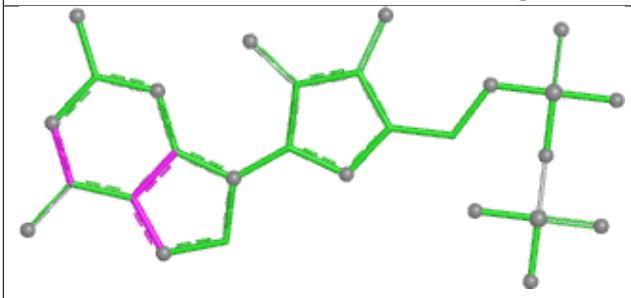


Rings

Ligand GDP QI 500



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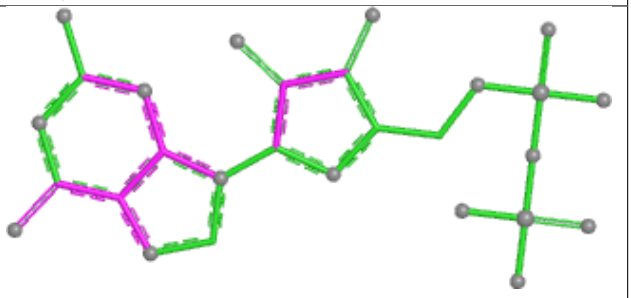

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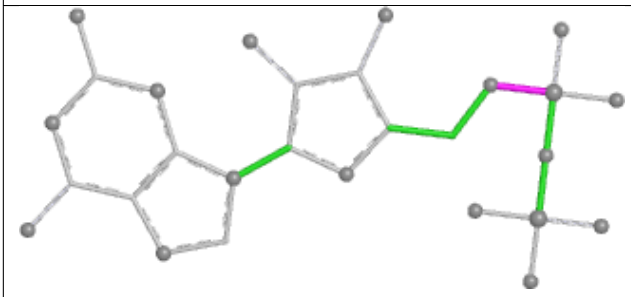

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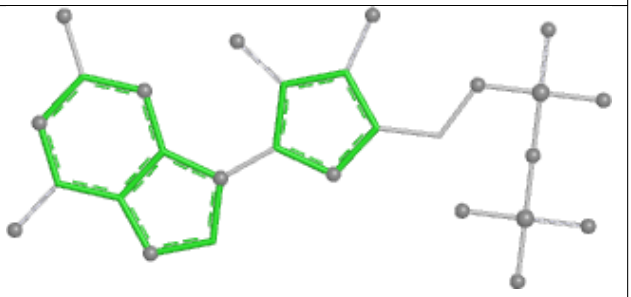
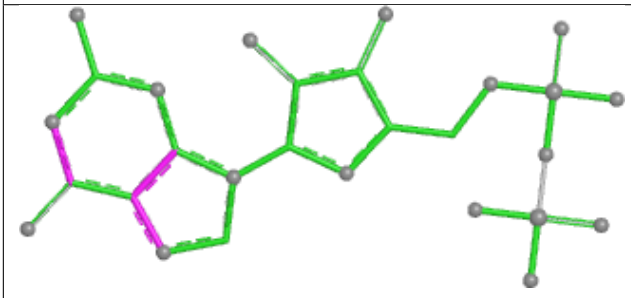


Rings

Ligand GDP LC 500



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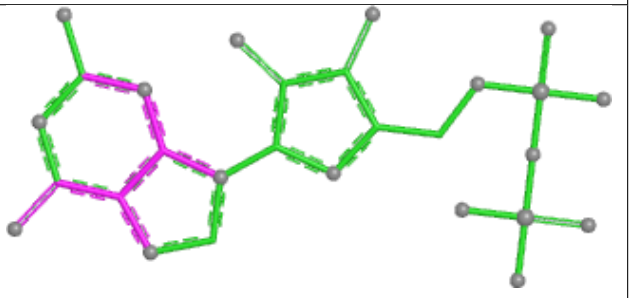

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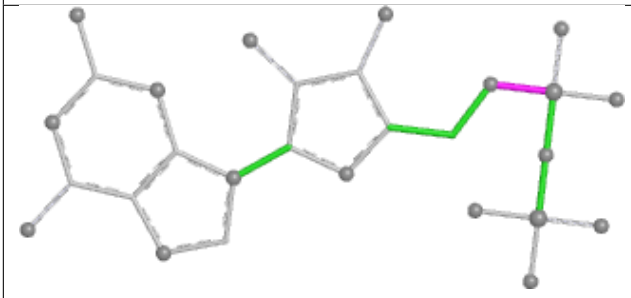

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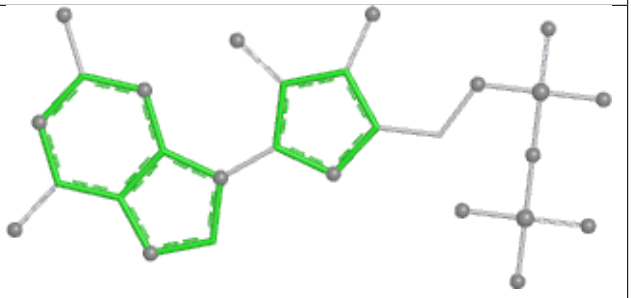
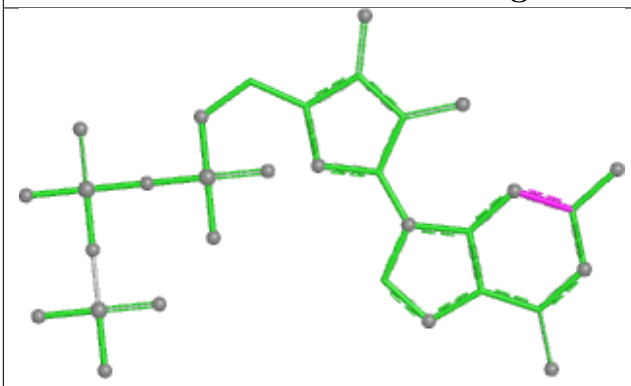


Rings

Ligand GTP VE 501



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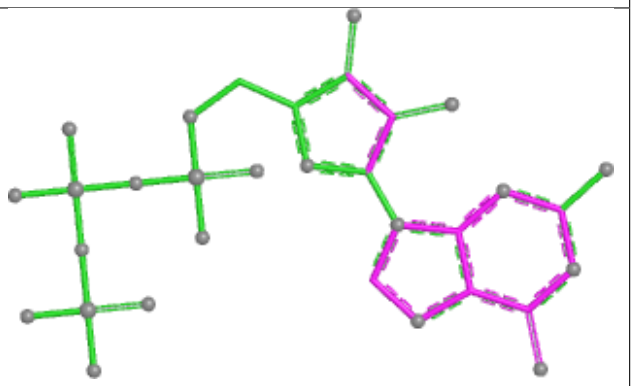

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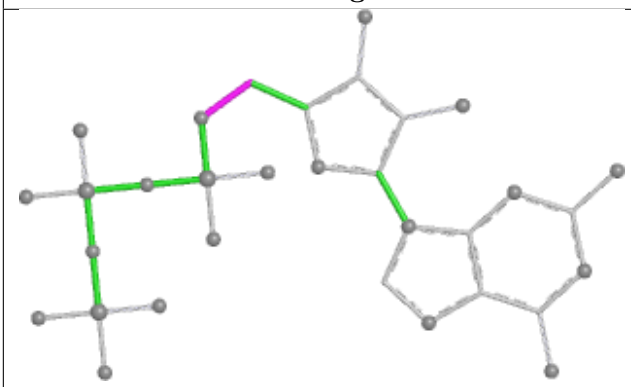

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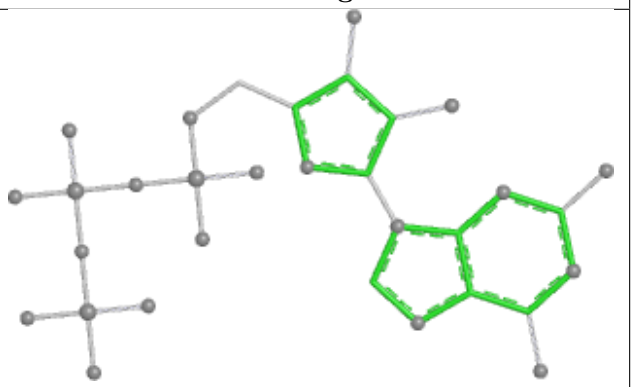
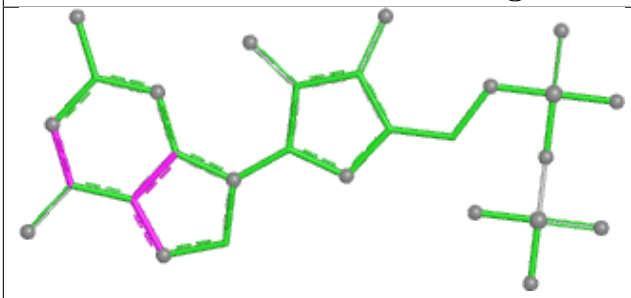


Rings

Ligand GDP GH 500



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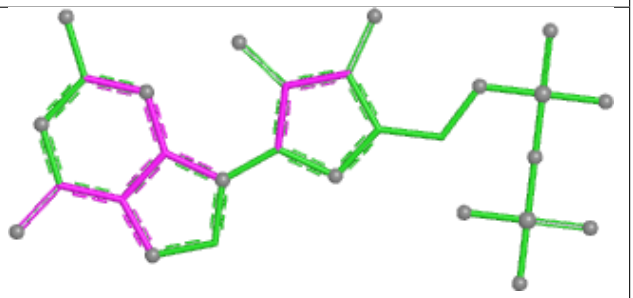

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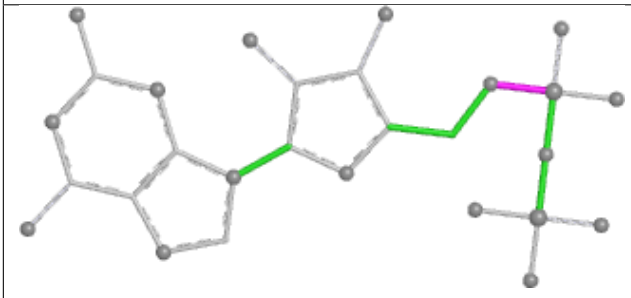

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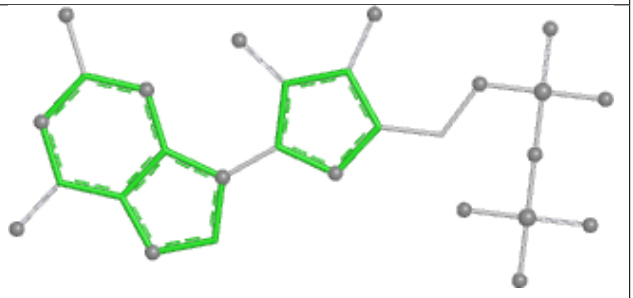
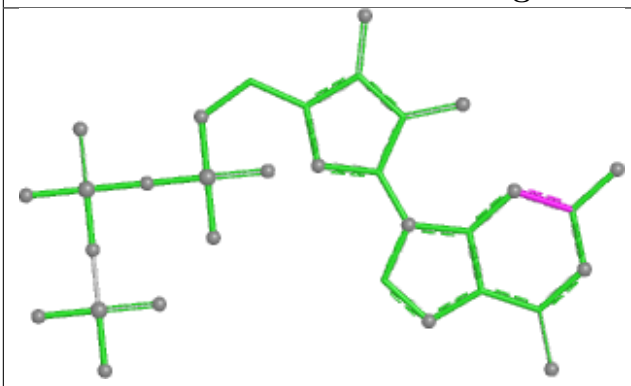


Rings

Ligand GTP RJ 501



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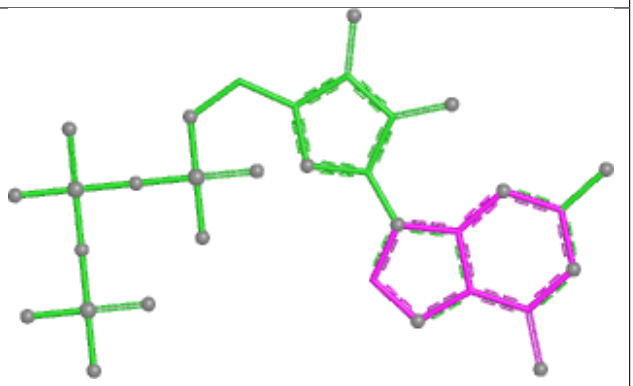

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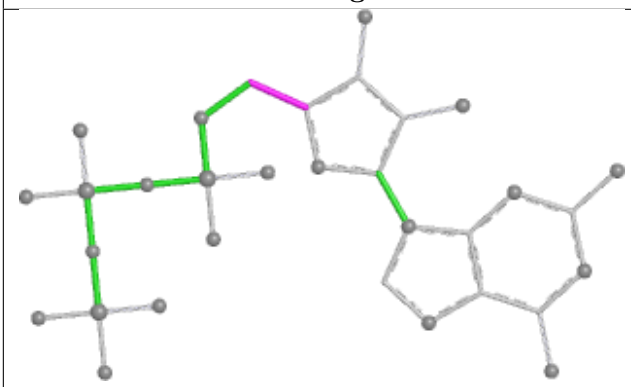

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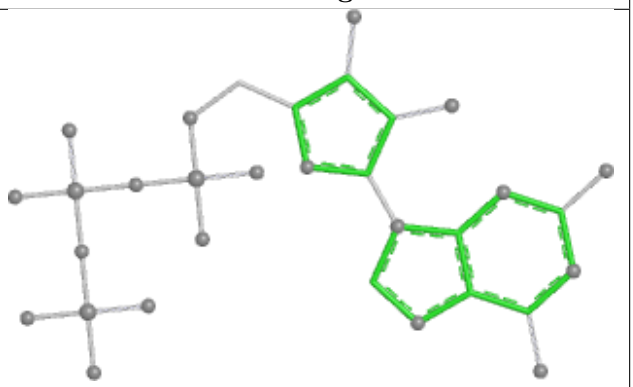
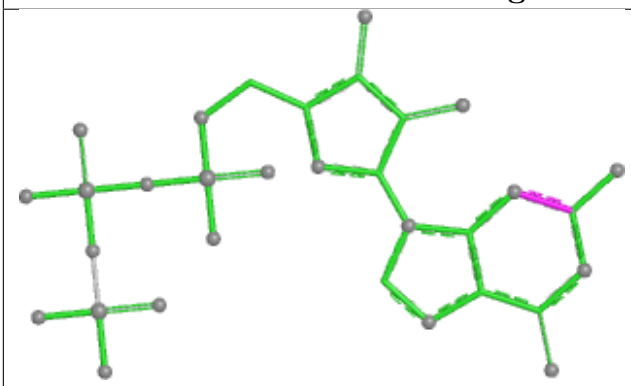


Rings

Ligand GTP OK 501



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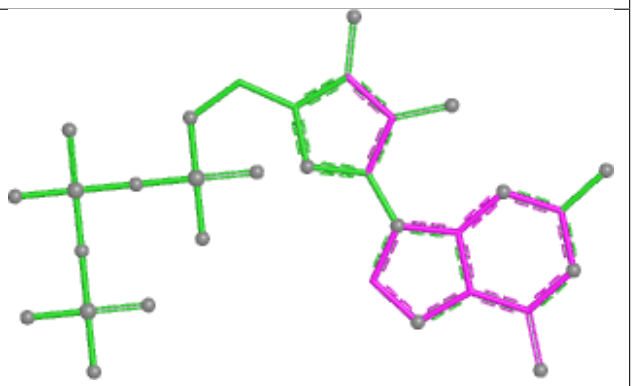

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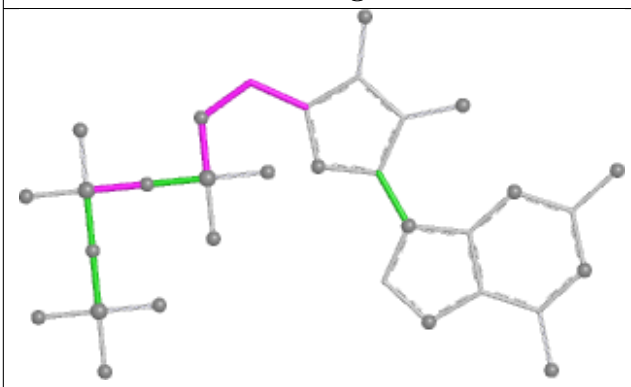

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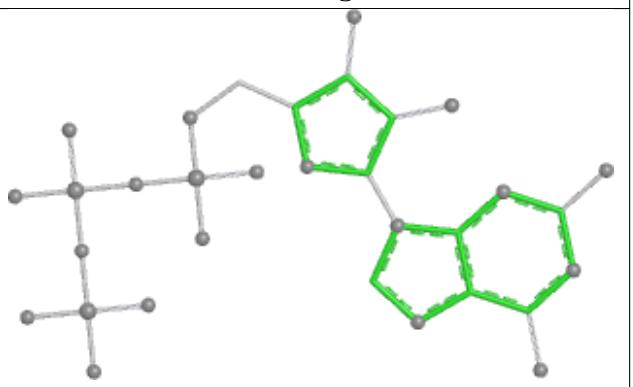
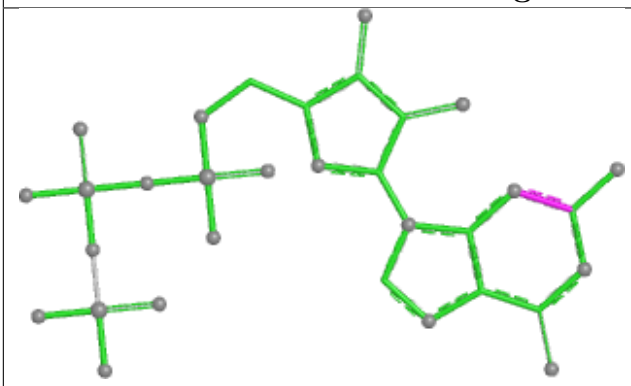


Rings

Ligand GTP LF 501



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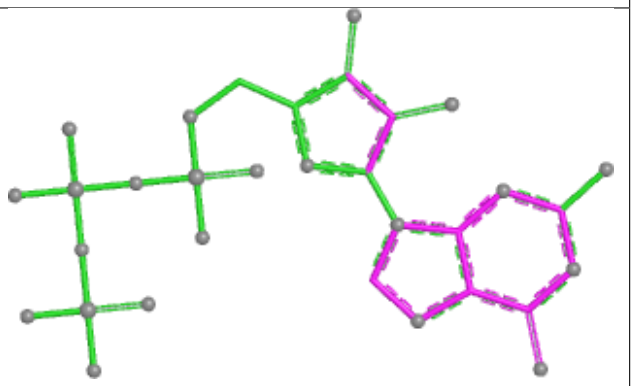

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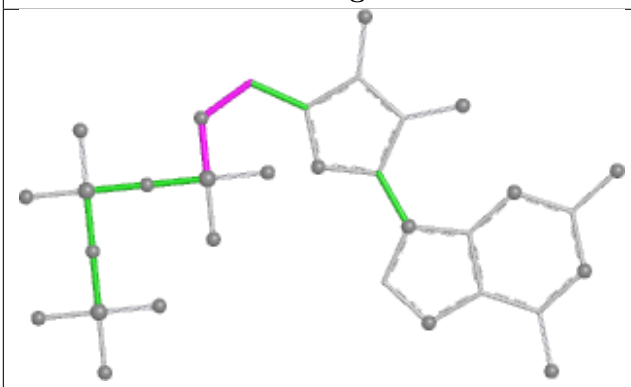

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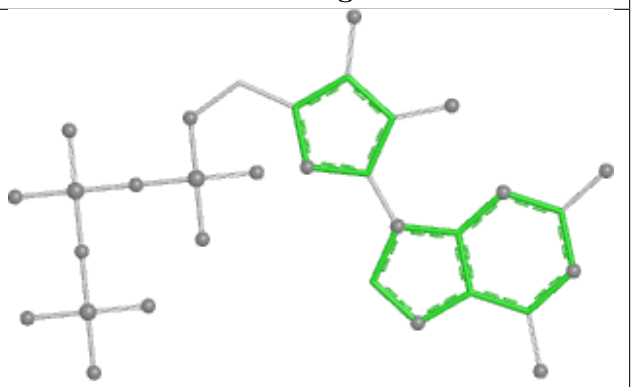
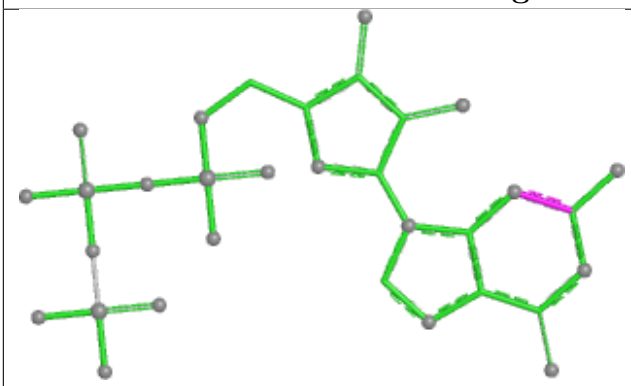


Rings

Ligand GTP FC 501



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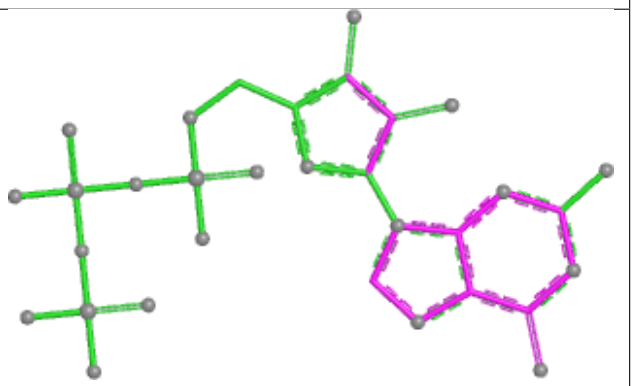

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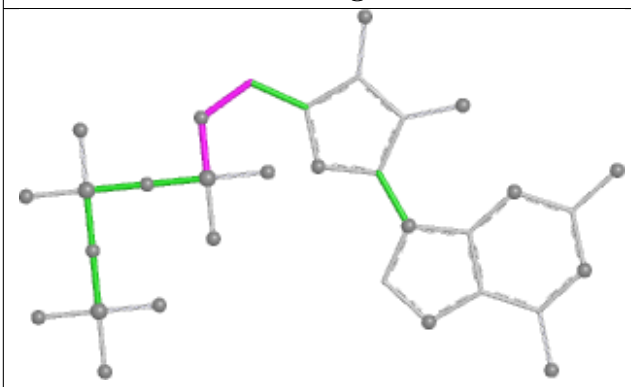

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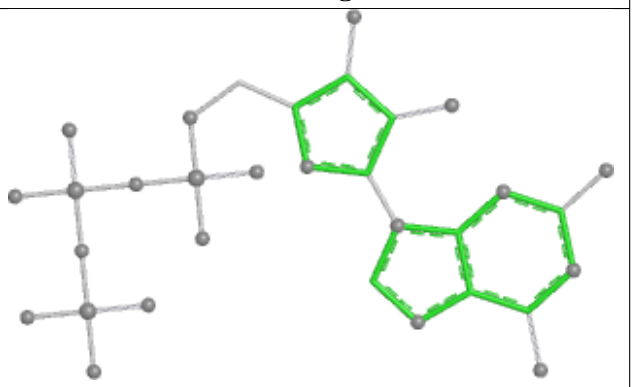
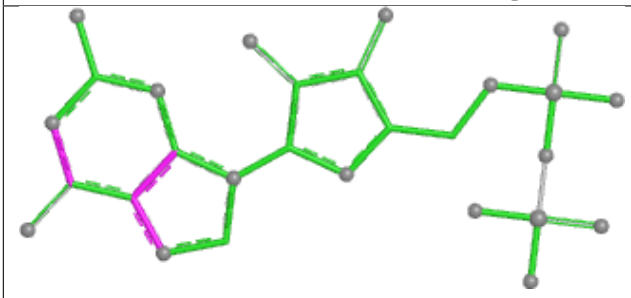


Rings

Ligand GDP MF 500



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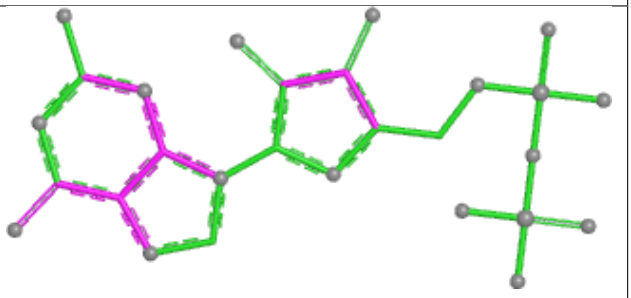

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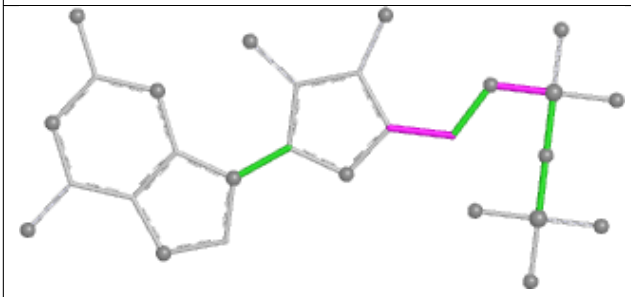

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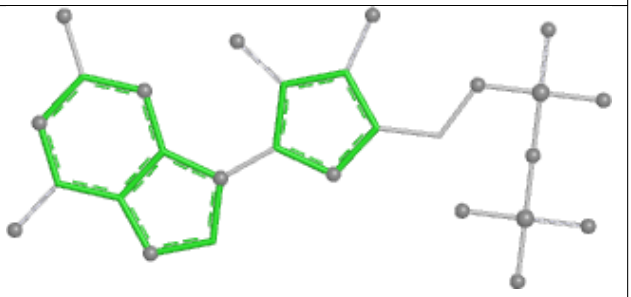
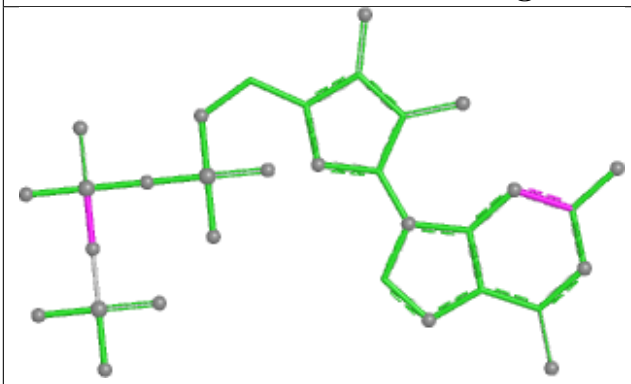


Rings

Ligand GTP IC 501



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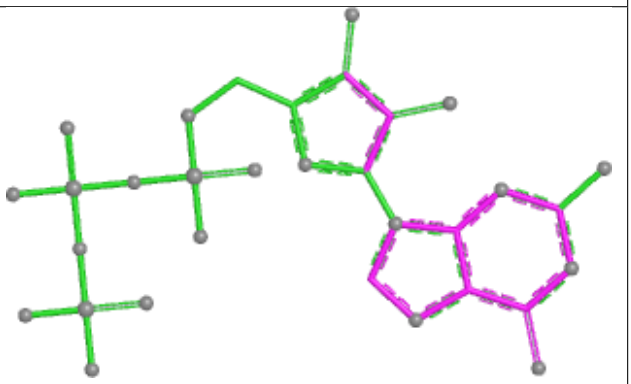

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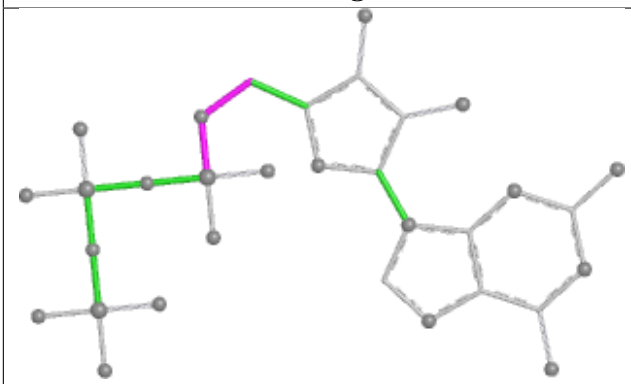
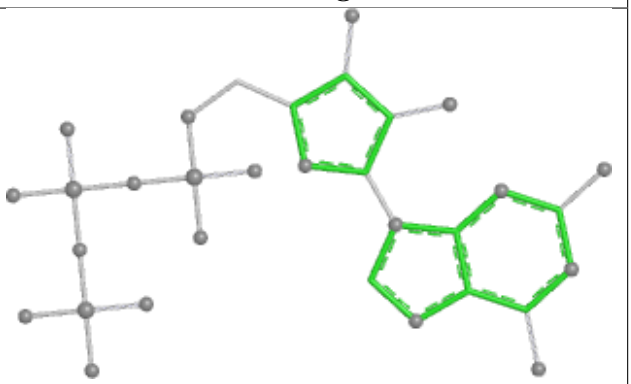
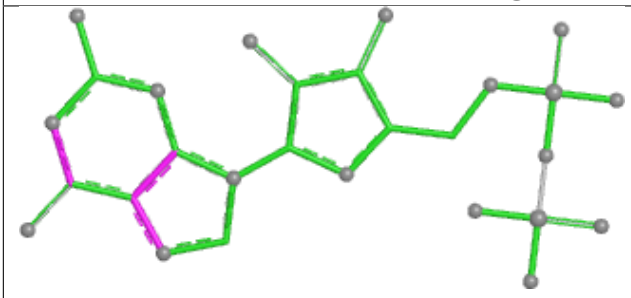


Torsions



Rings

Ligand GDP VB 500



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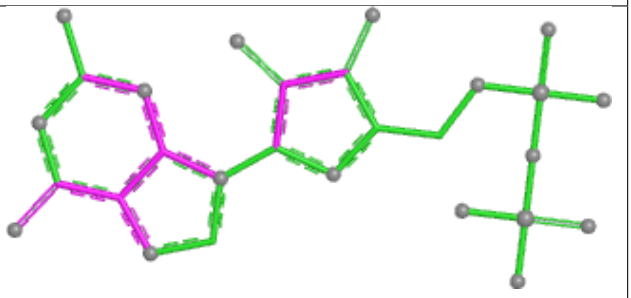
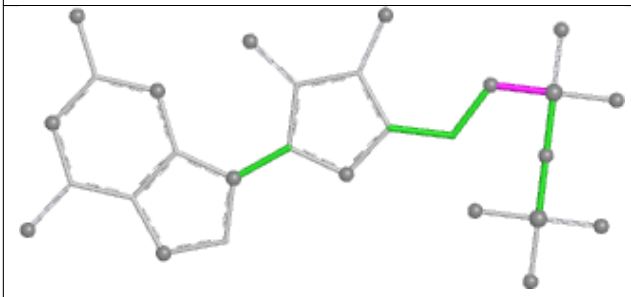


Bond angles



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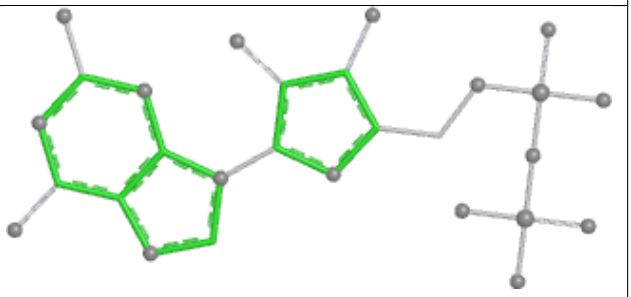
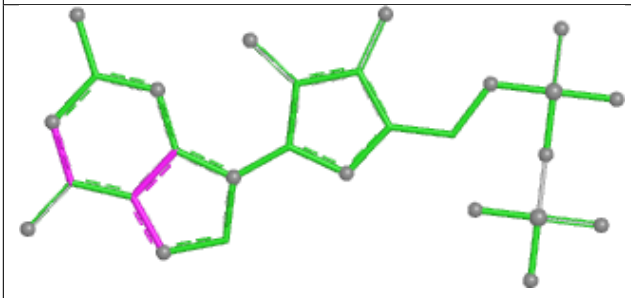
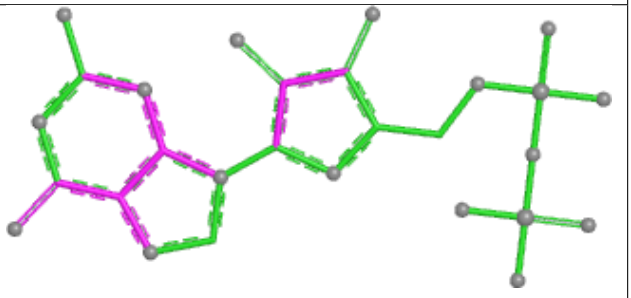


Rings

Ligand GDP LK 500



Bond lengths



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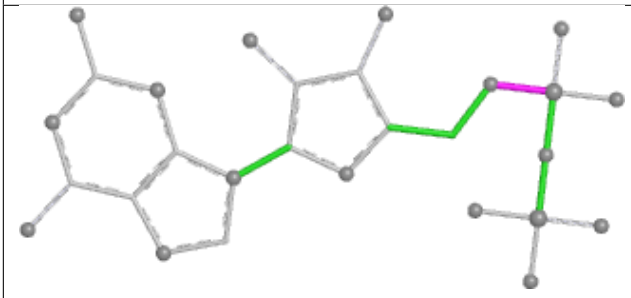
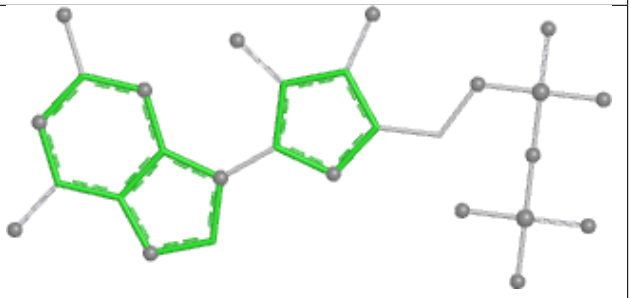
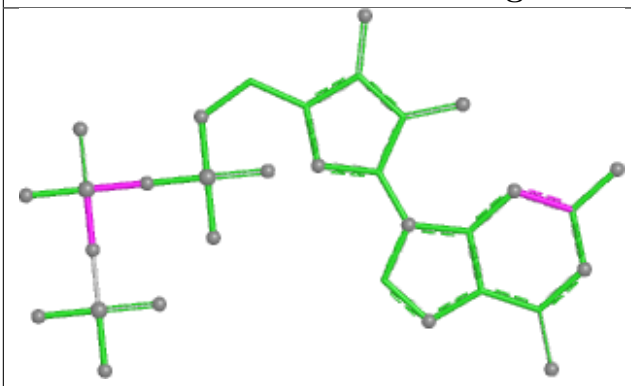


Torsions



Rings

Ligand GTP BM 501



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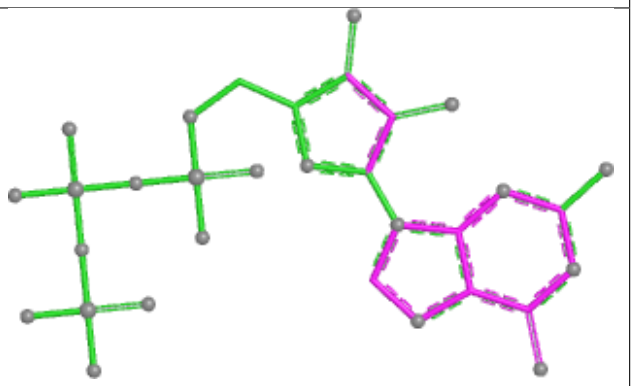

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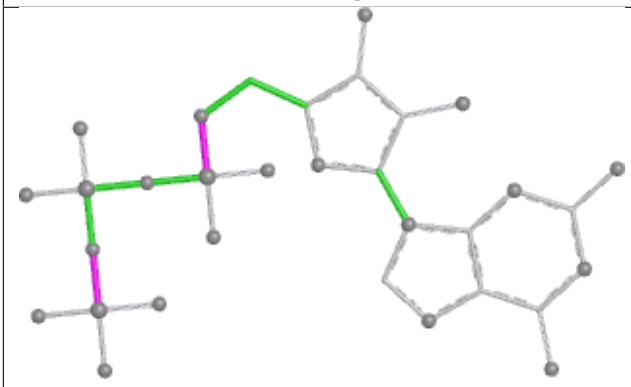

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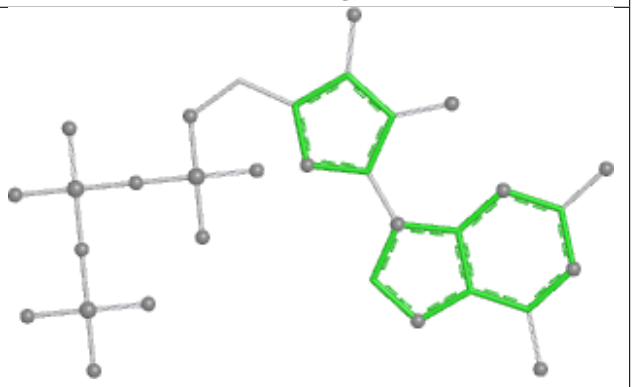
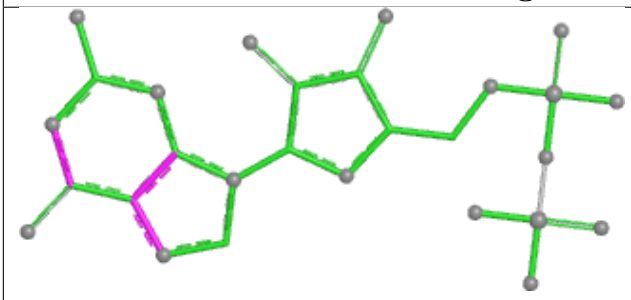


Rings

Ligand GDP IL 500



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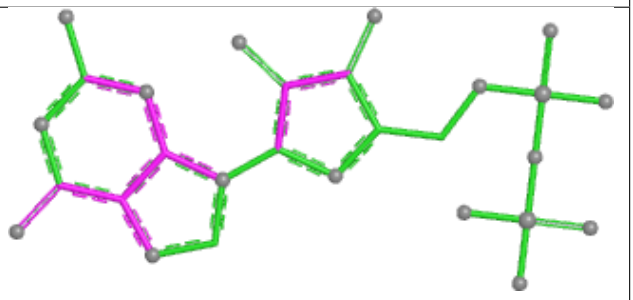

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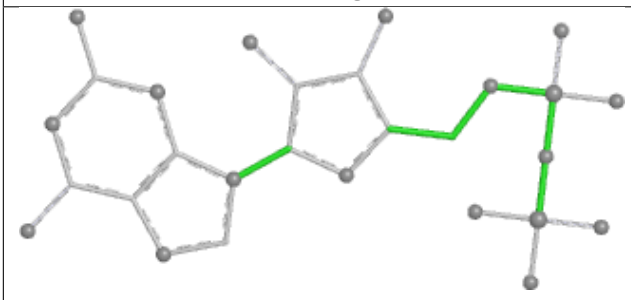

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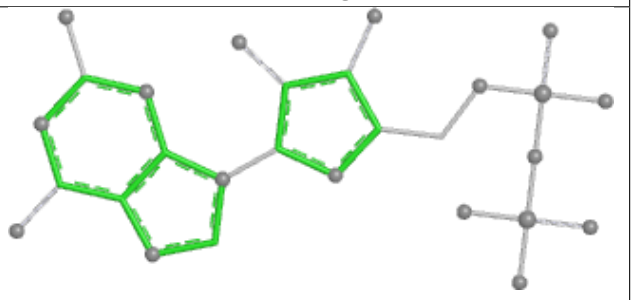
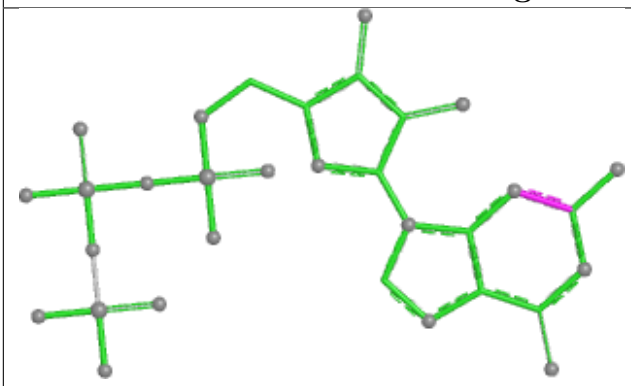


Rings

Ligand GTP LL 501



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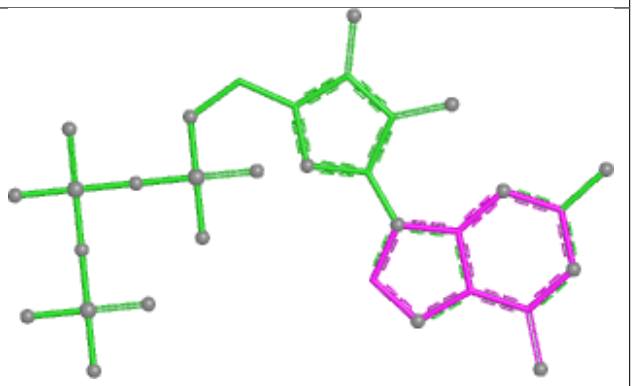

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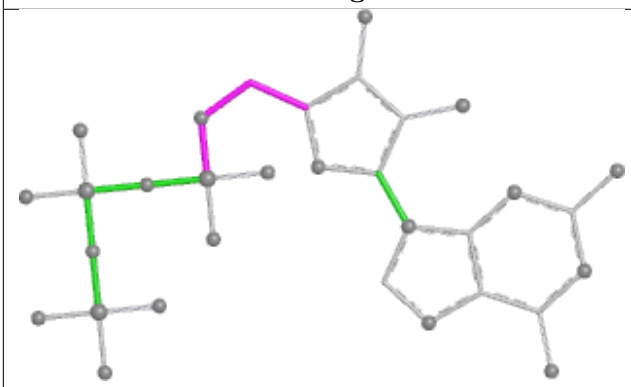

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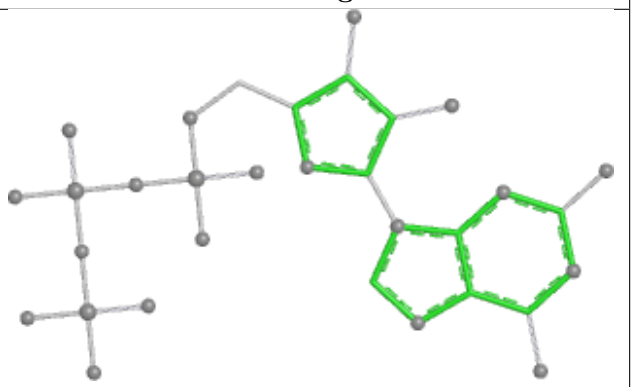
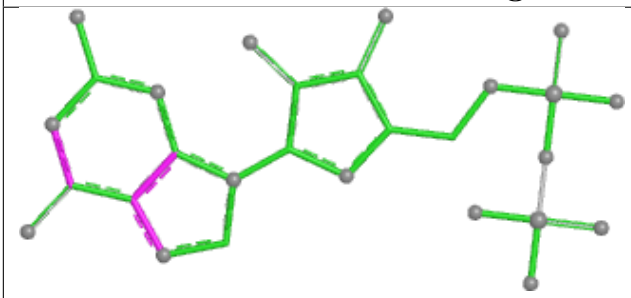


Rings

Ligand GDP LM 500



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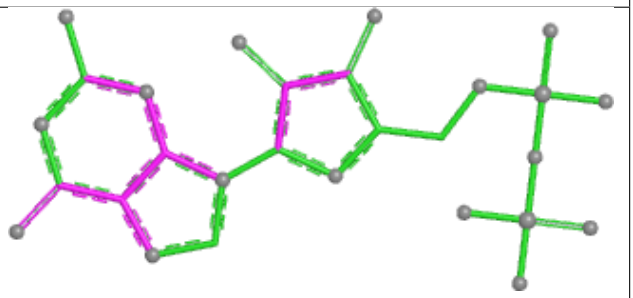

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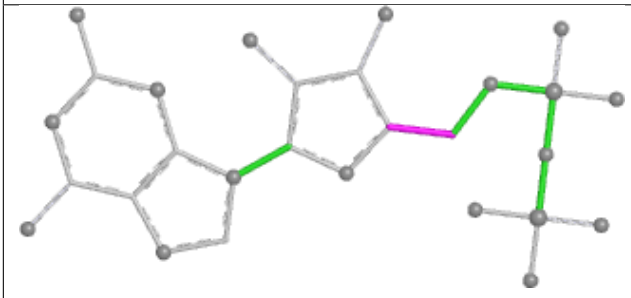

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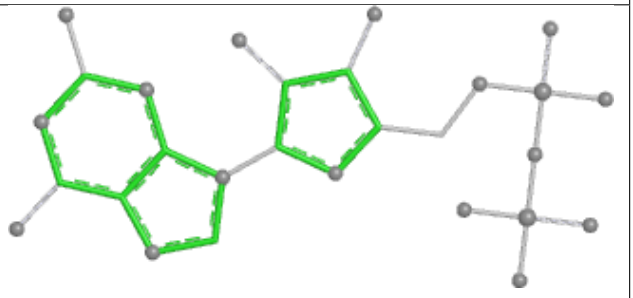
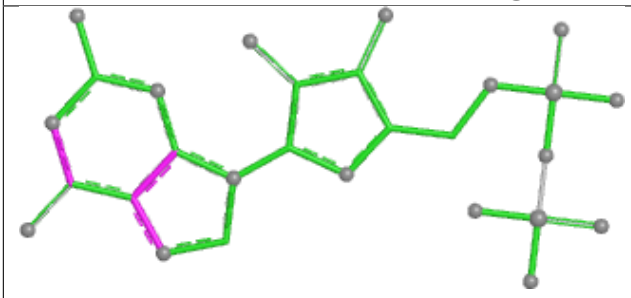


Rings

Ligand GDP BH 500



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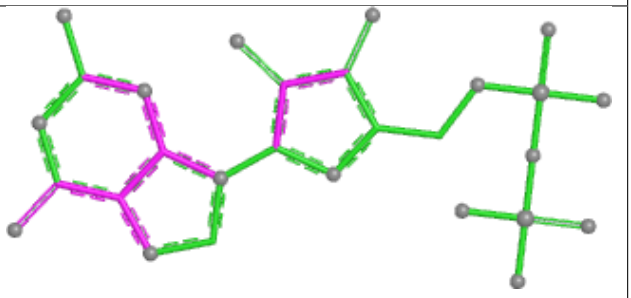

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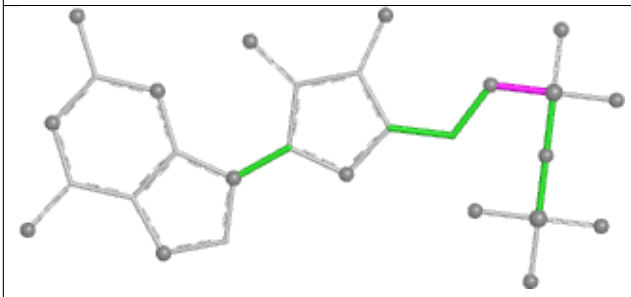

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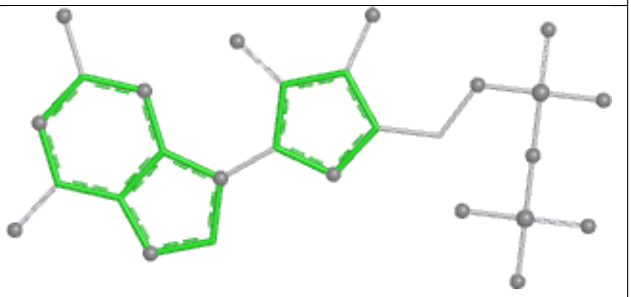
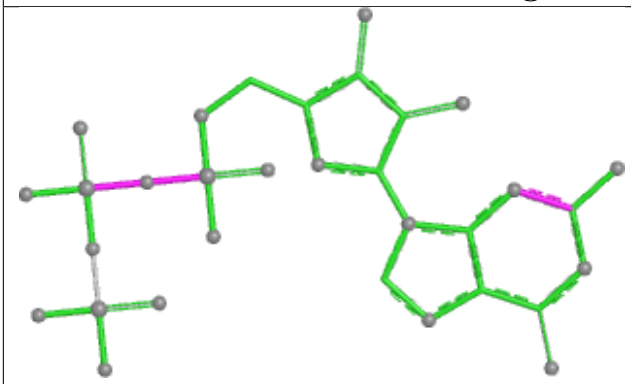


Rings

Ligand GTP D 501



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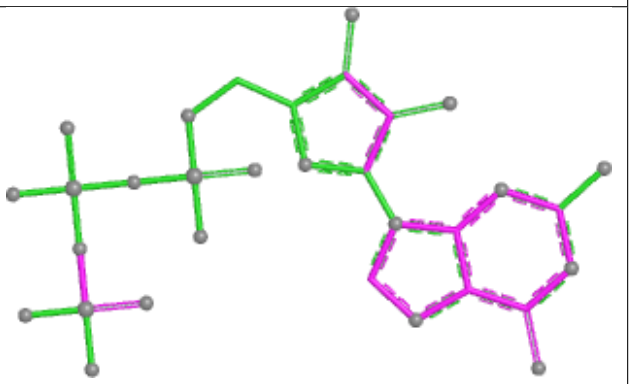

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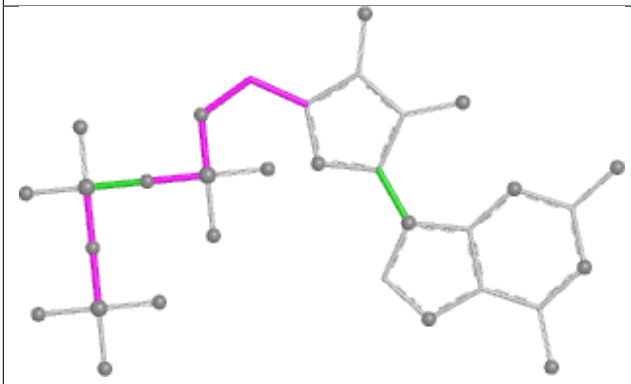

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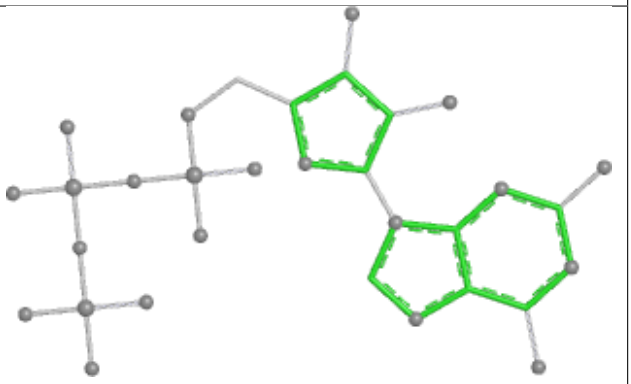
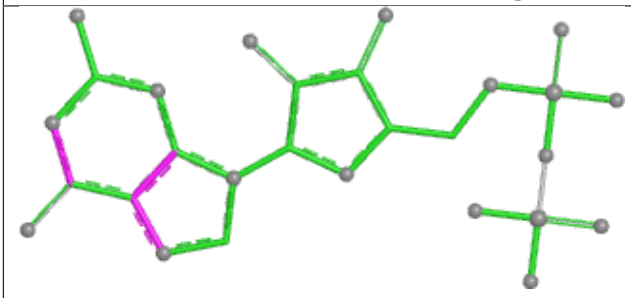


Rings

Ligand GDP RE 500



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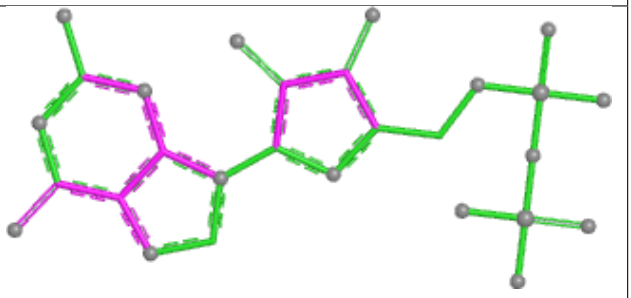

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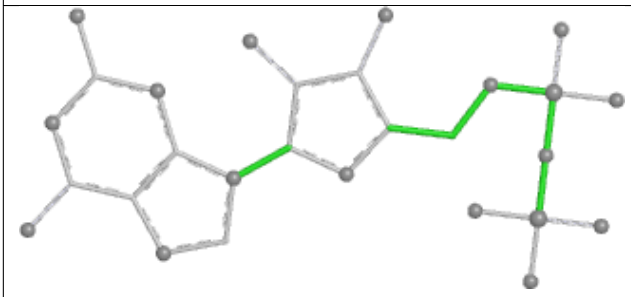

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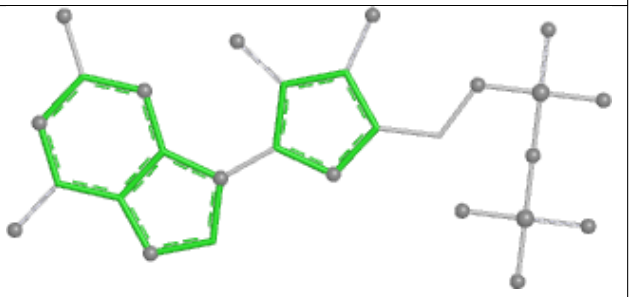
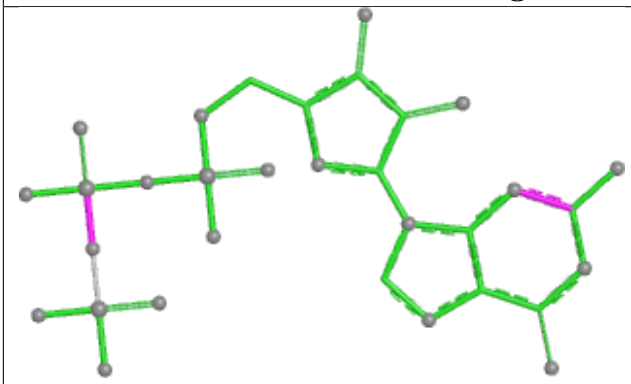


Rings

Ligand GTP RD 501



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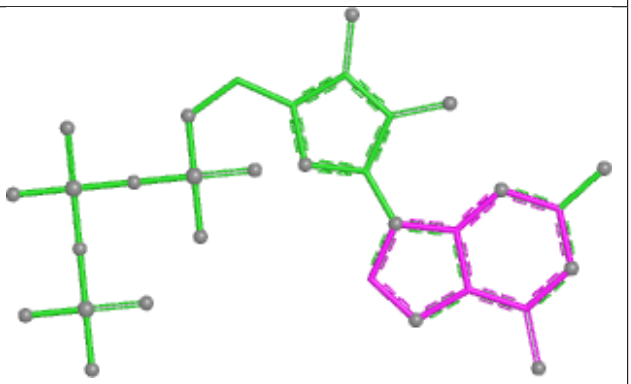

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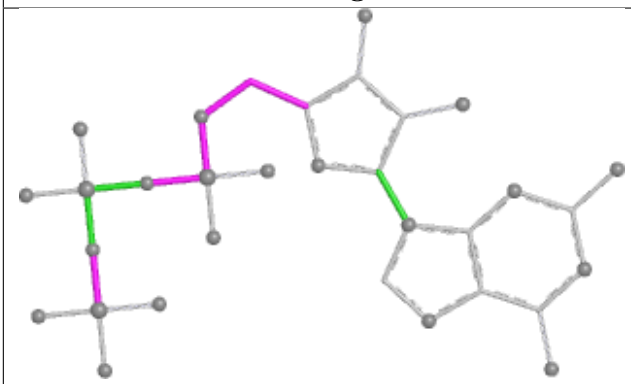

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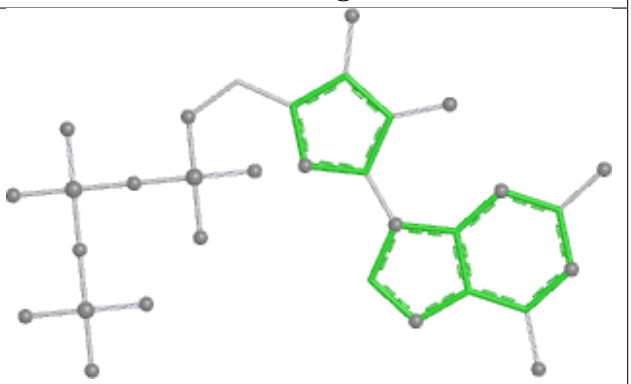
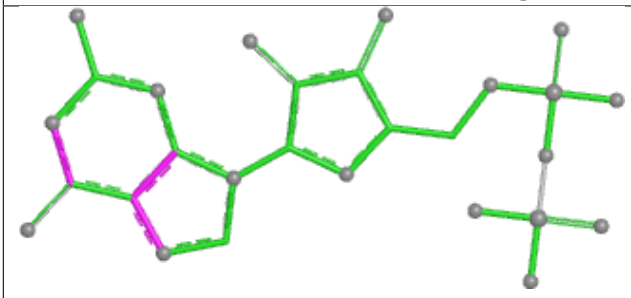


Rings

Ligand GDP CI 500



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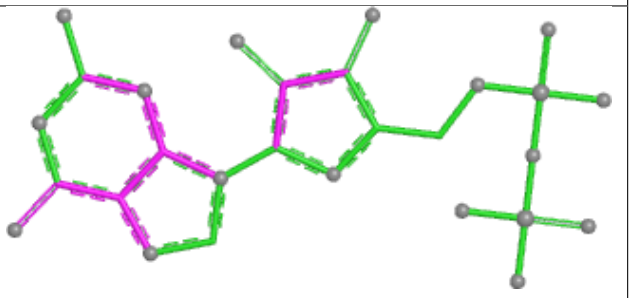

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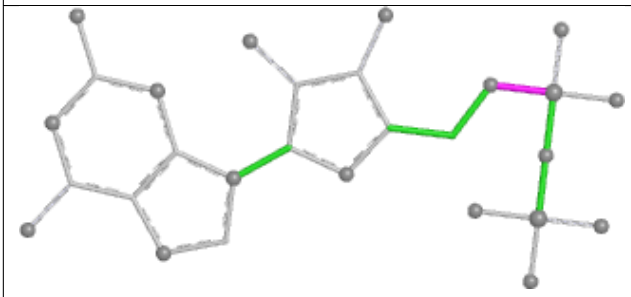

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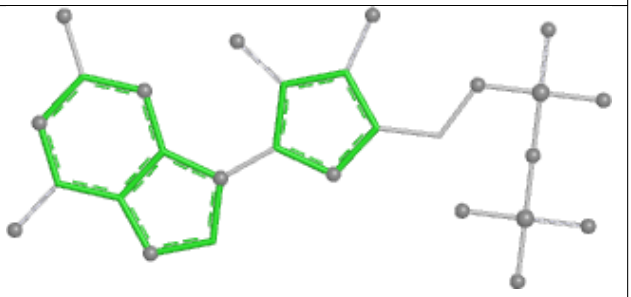
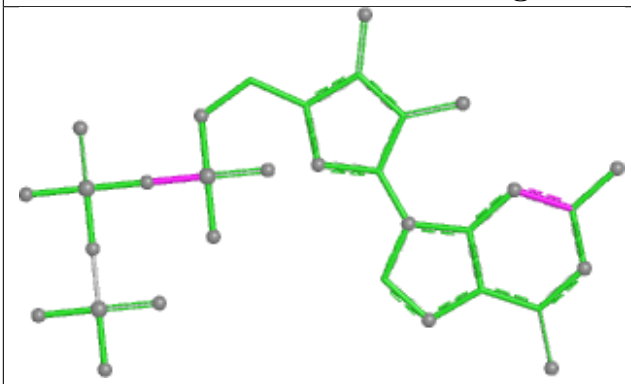


Rings

Ligand GTP LB 501



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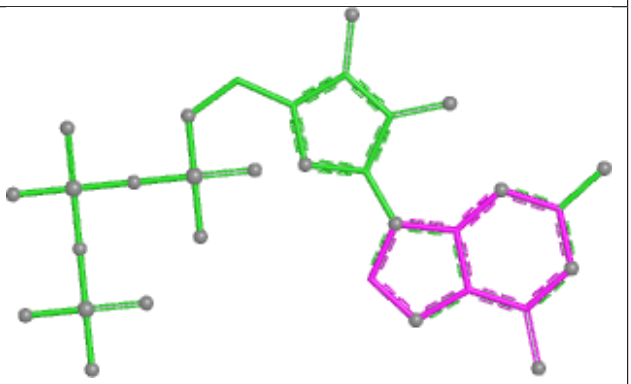

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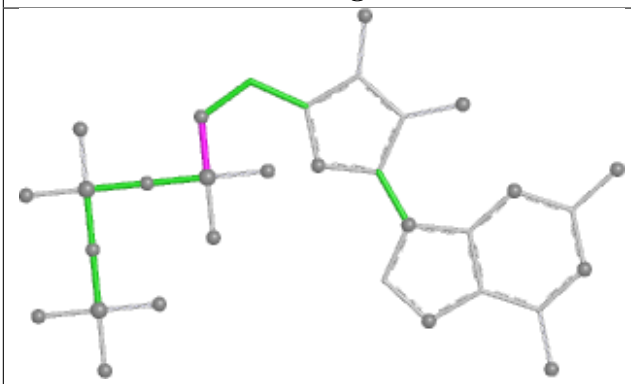

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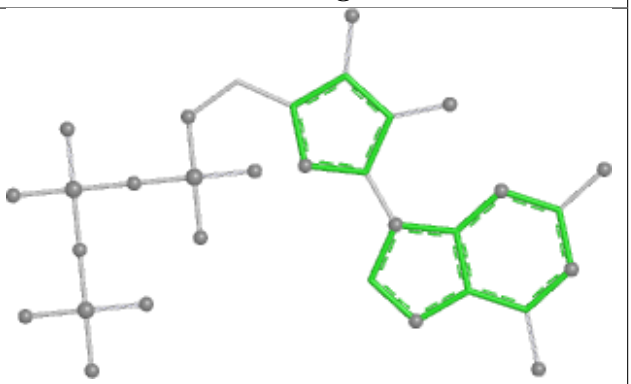
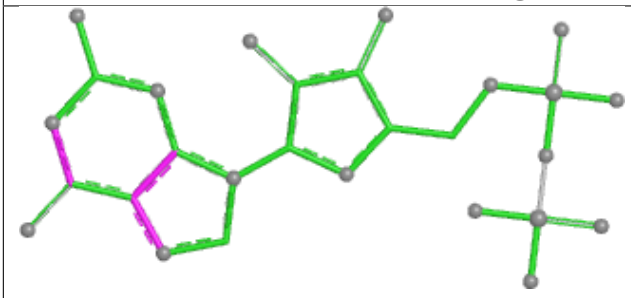


Rings

Ligand GDP UJ 500



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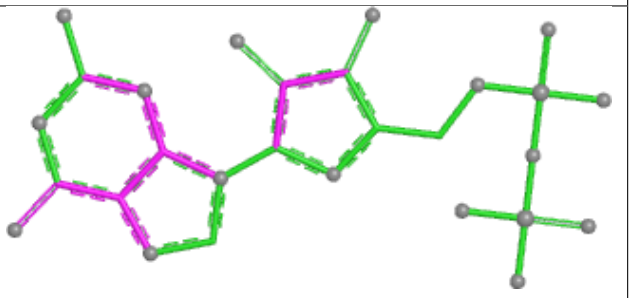

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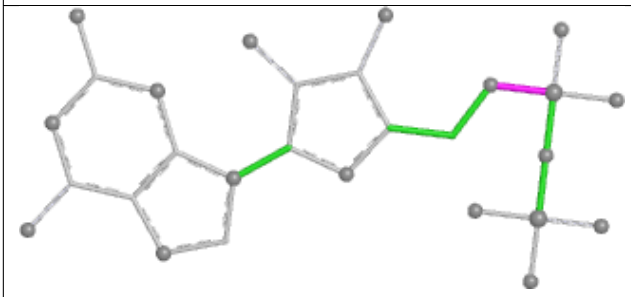

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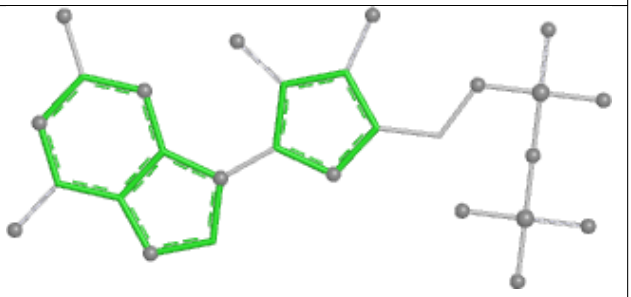
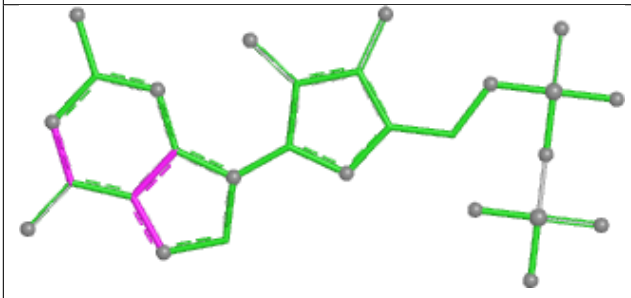


Rings

Ligand GDP GJ 500



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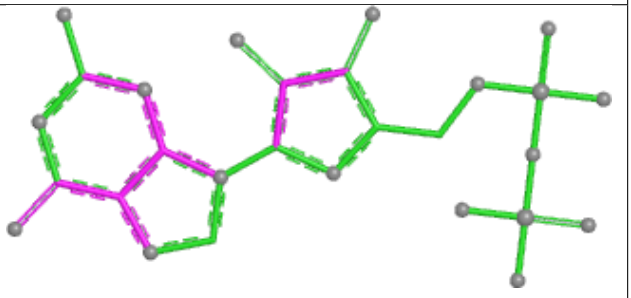

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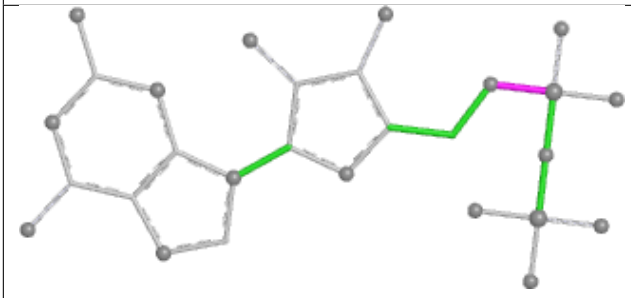

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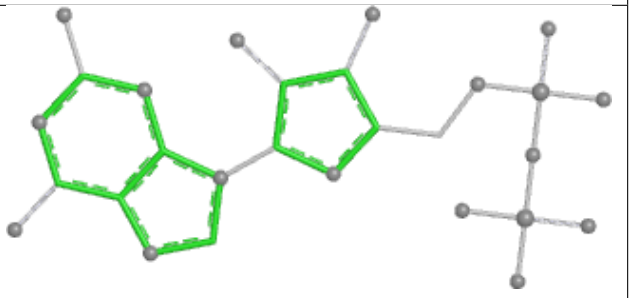
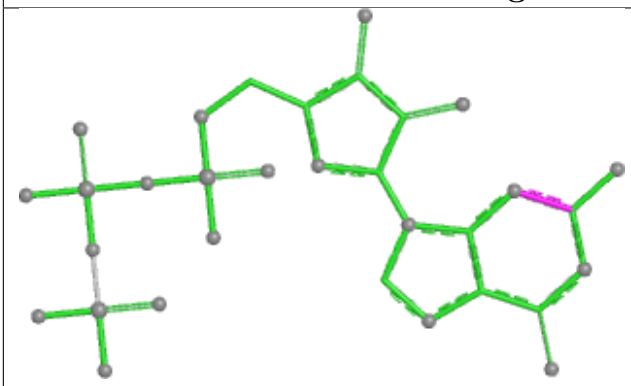


Rings

Ligand GTP DH 501



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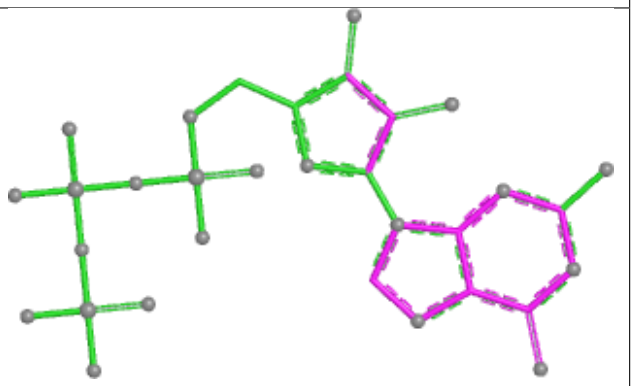

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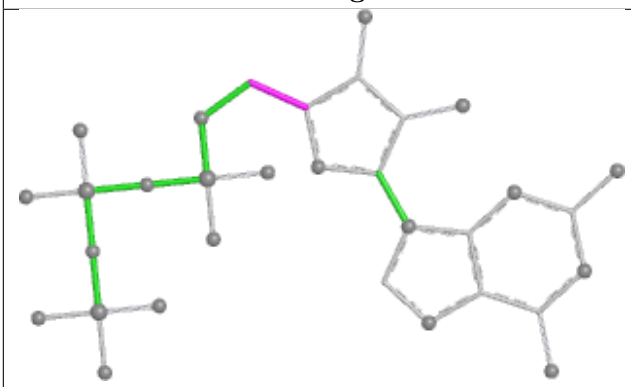

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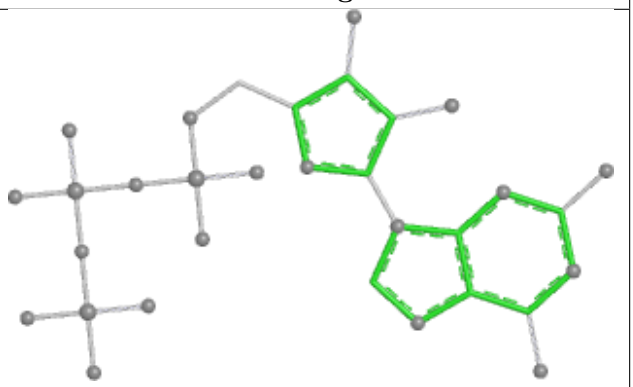
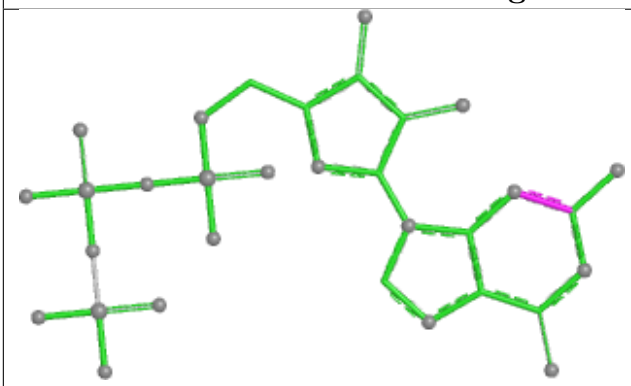
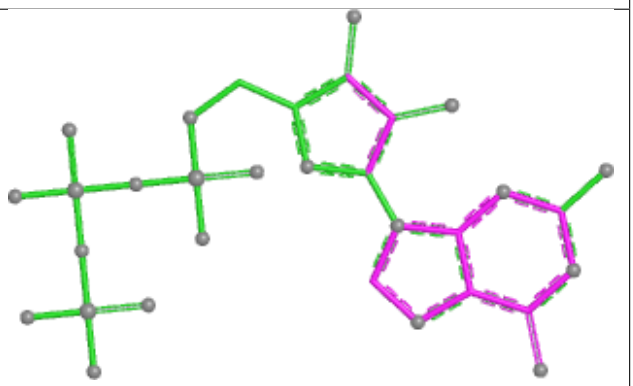


Rings

Ligand GTP UA 501



Bond lengths



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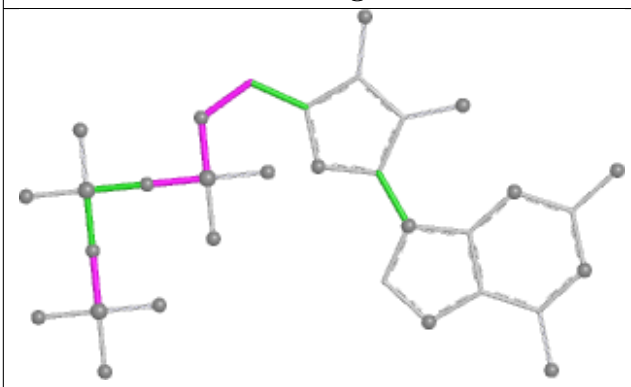
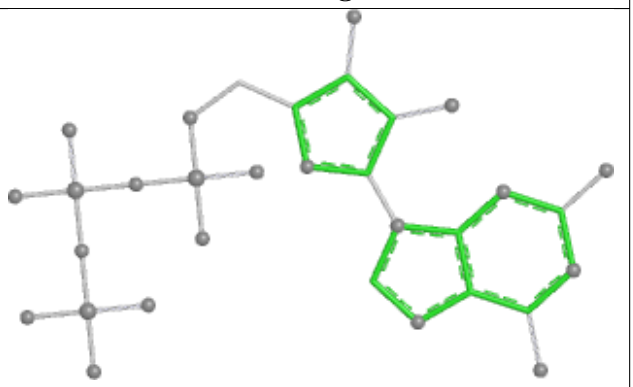
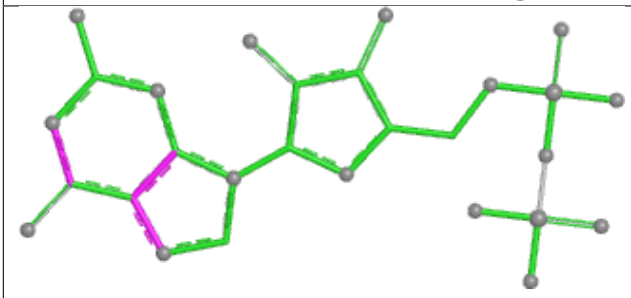


Torsions



Rings

Ligand GDP JA 500



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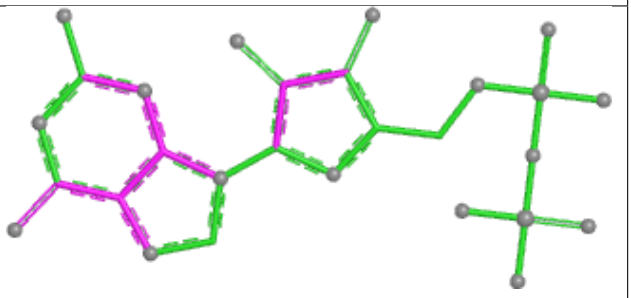

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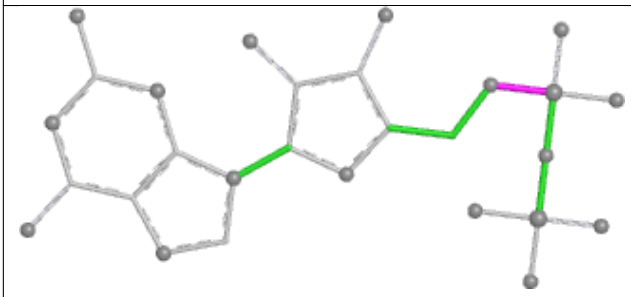

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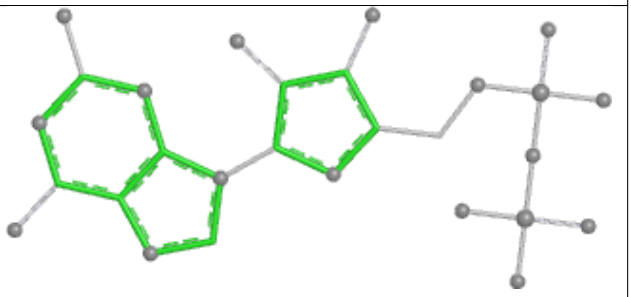
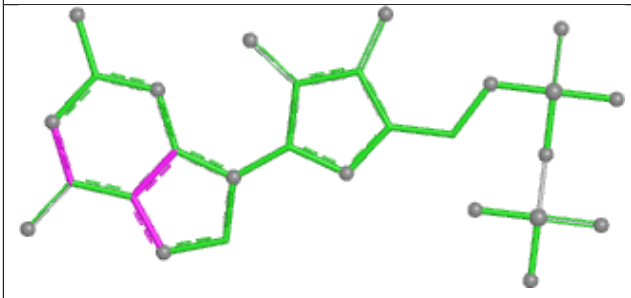


Rings

Ligand GDP FJ 500



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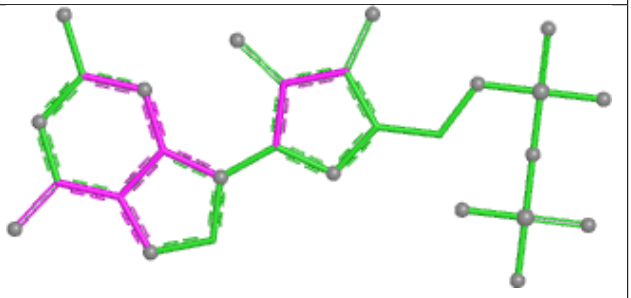

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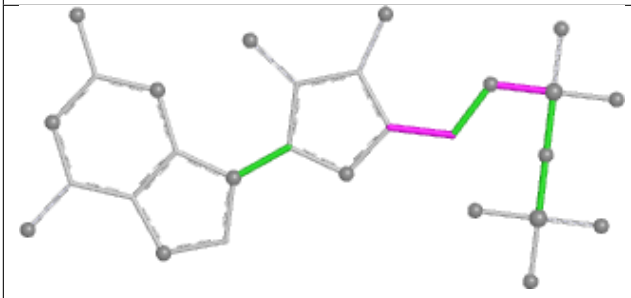

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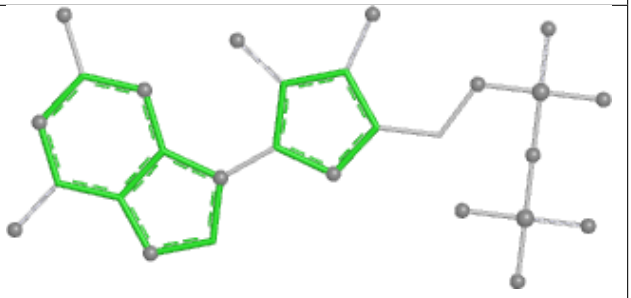
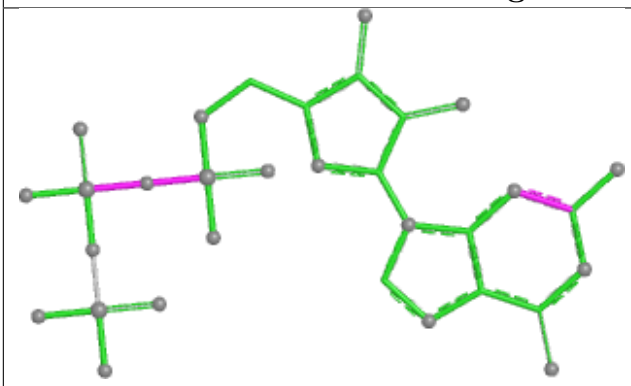


Rings

Ligand GTP NG 501



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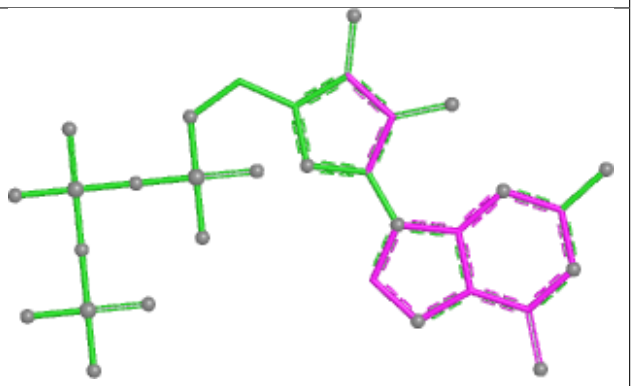

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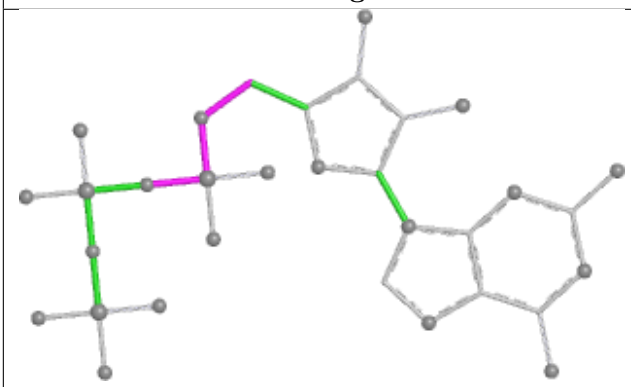

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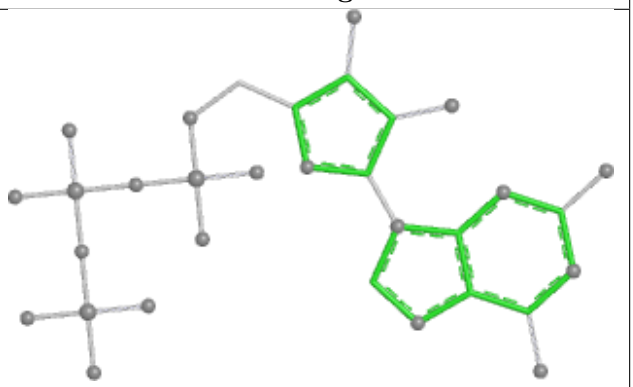
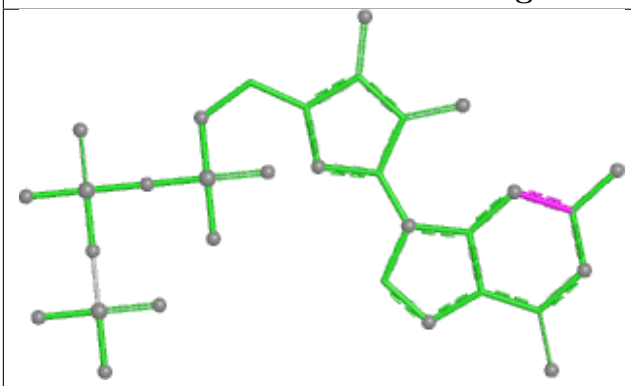


Rings

Ligand GTP UI 501



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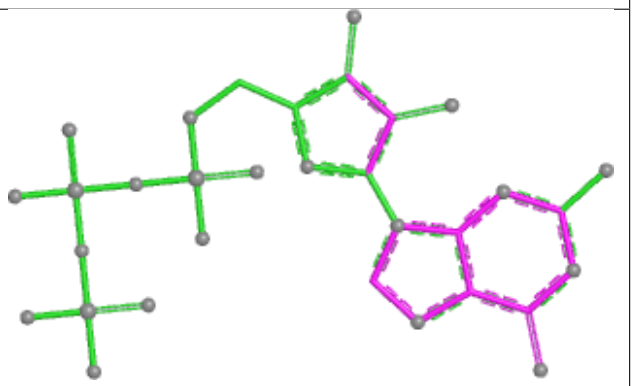

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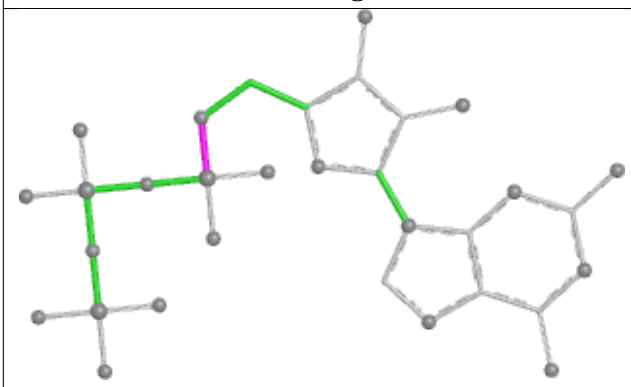

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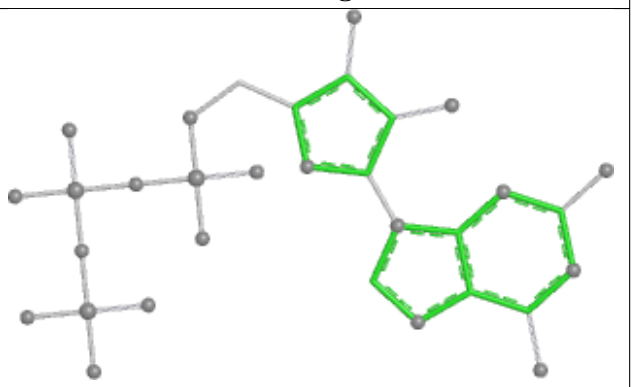
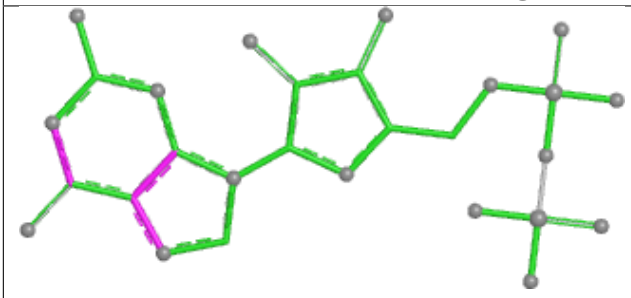


Rings

Ligand GDP DI 500



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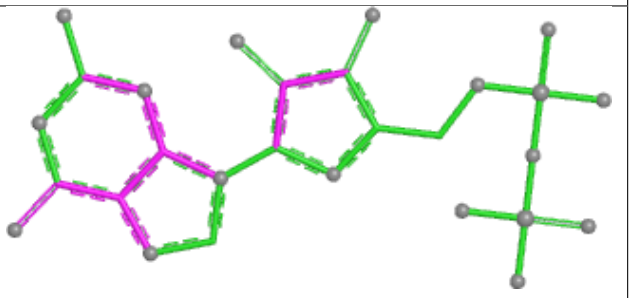

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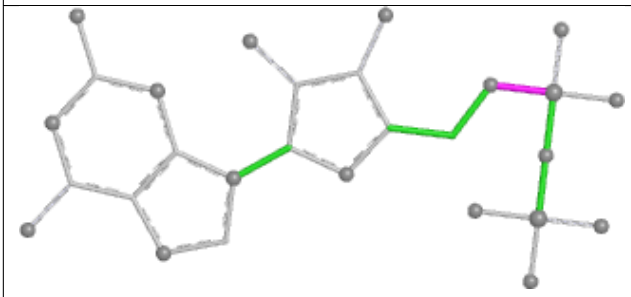

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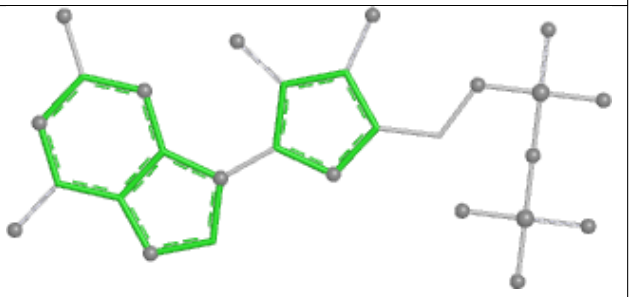
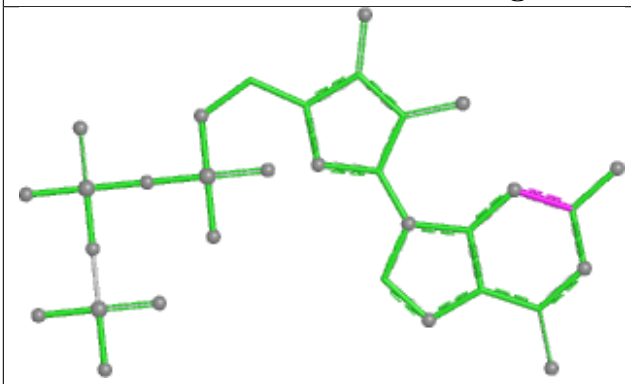


Rings

Ligand GTP OA 501



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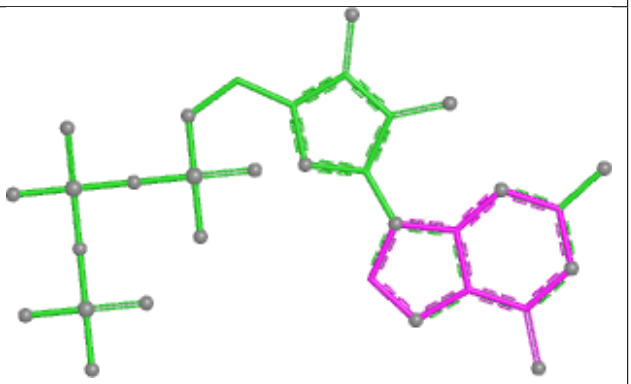

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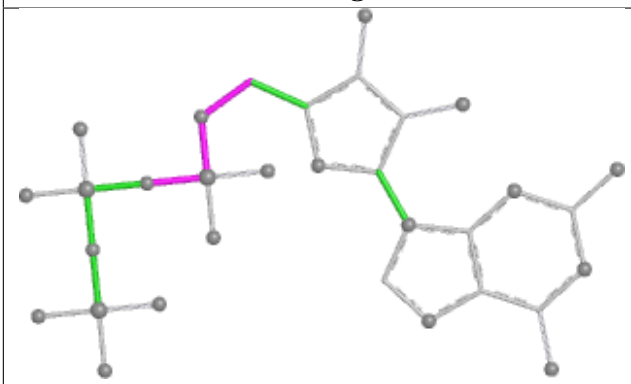

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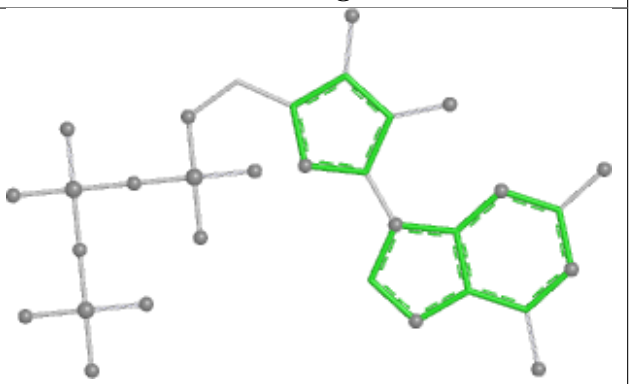
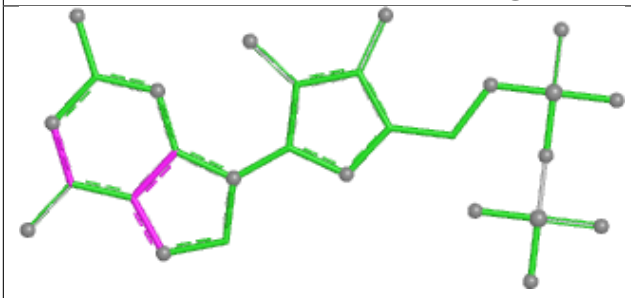


Rings

Ligand GDP QG 500



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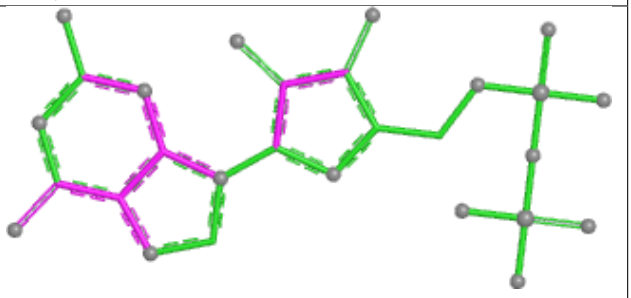

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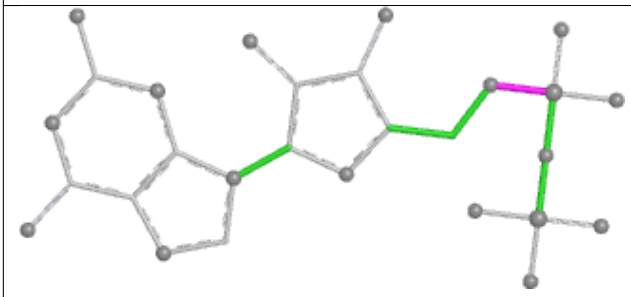

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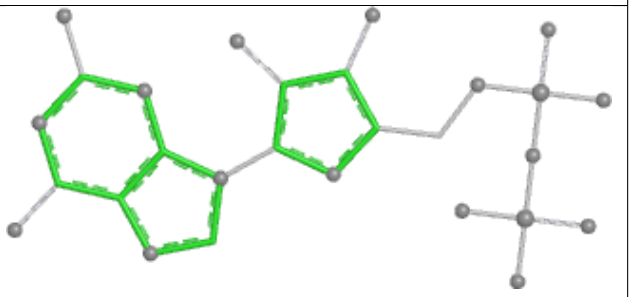
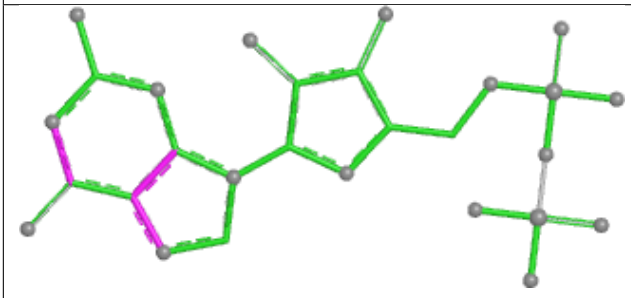


Rings

Ligand GDP CA 500



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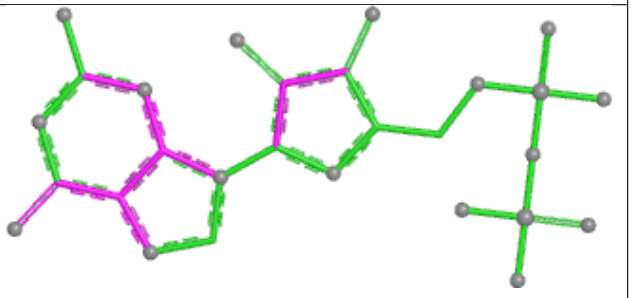

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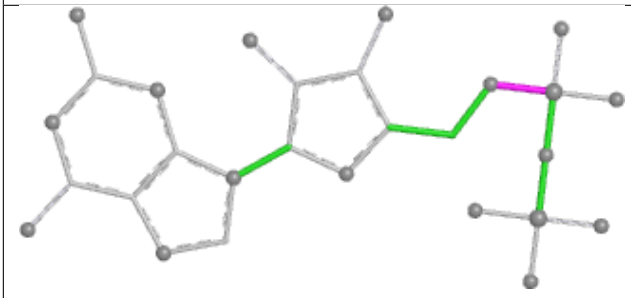

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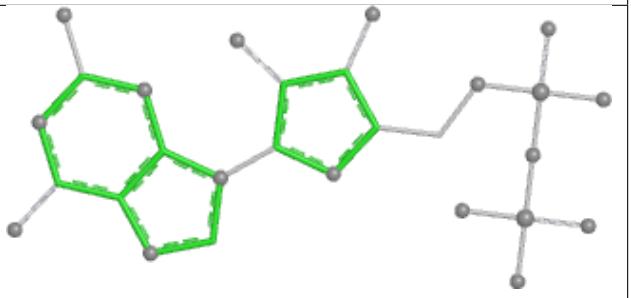
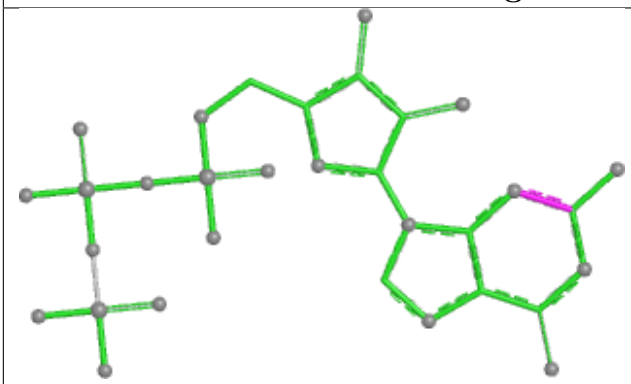


Rings

Ligand GTP HM 501



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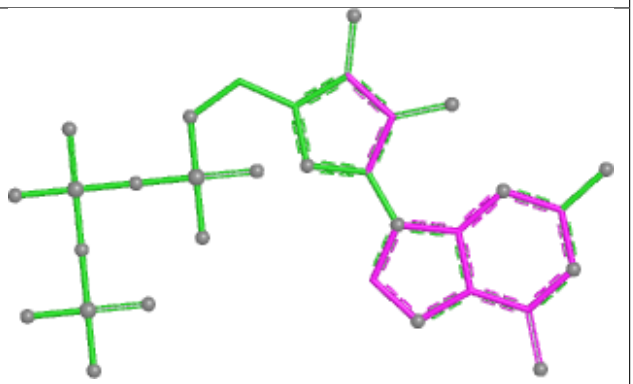

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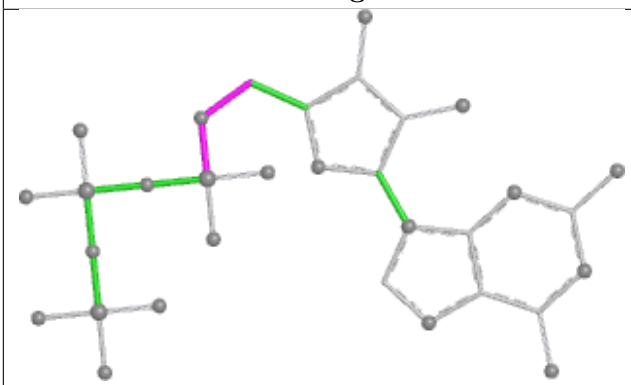

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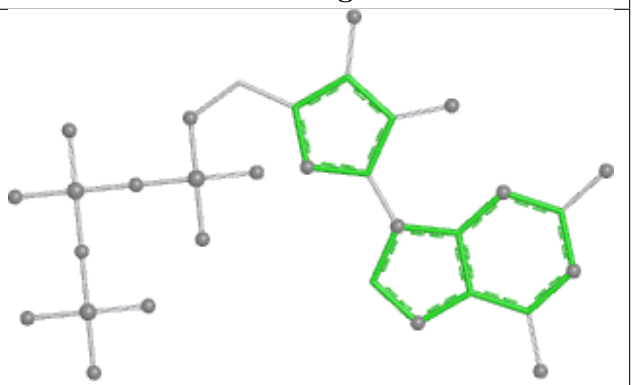
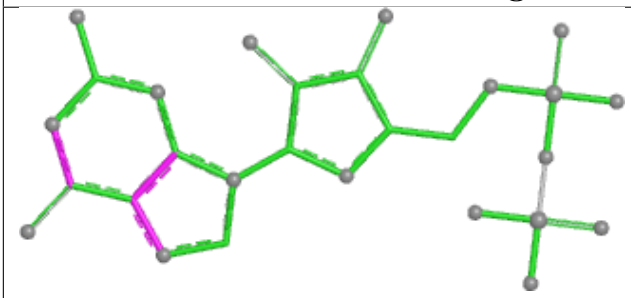


Rings

Ligand GDP BN 500



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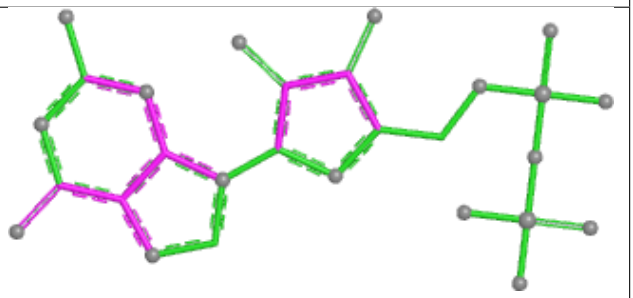

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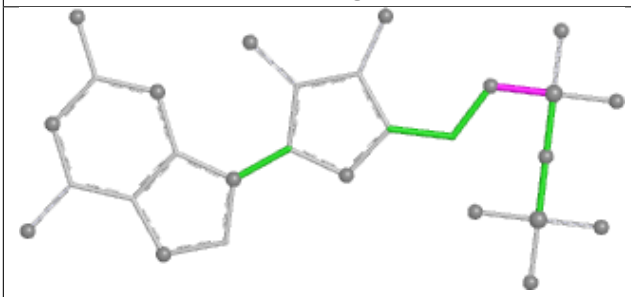

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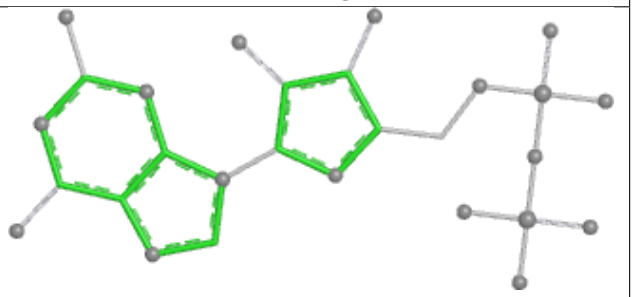

Rings

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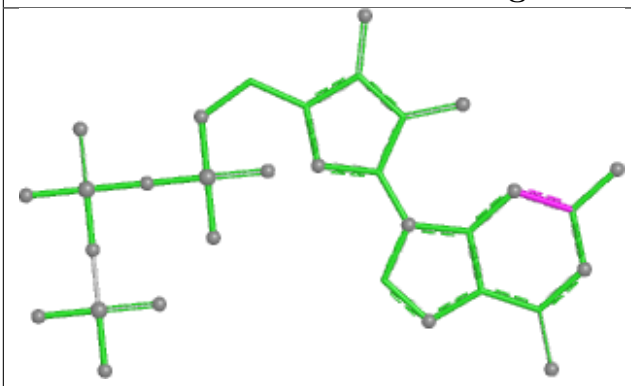

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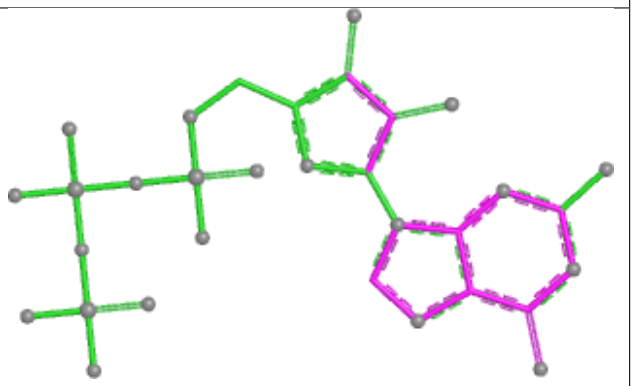

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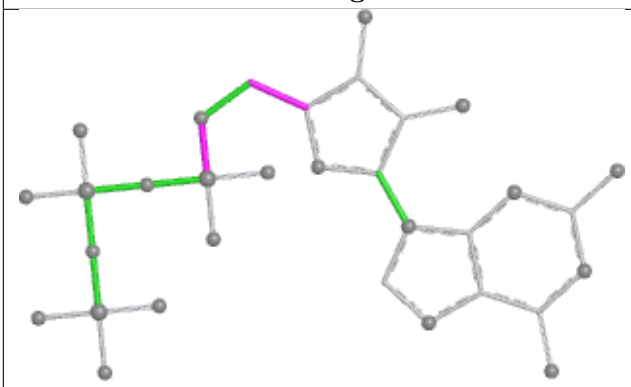

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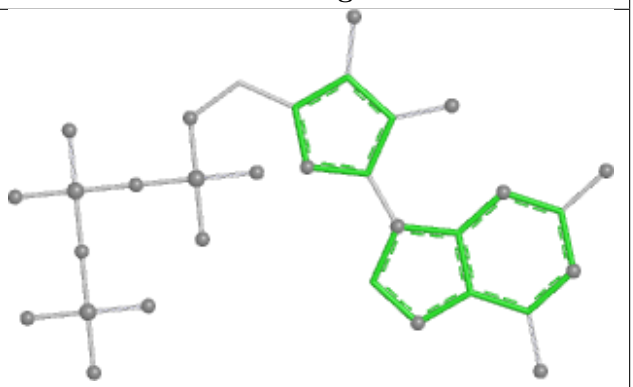

Rings

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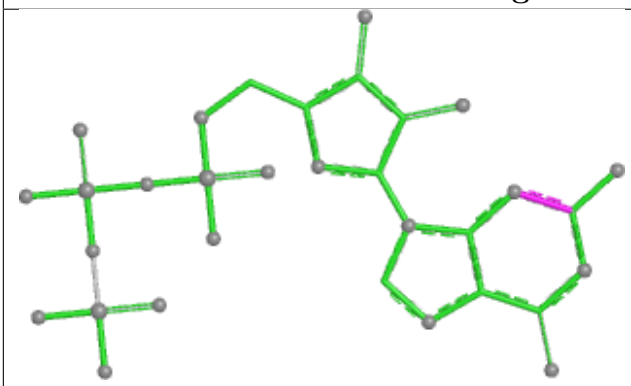

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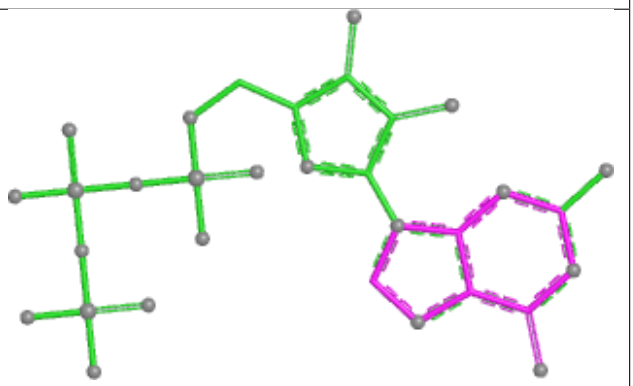

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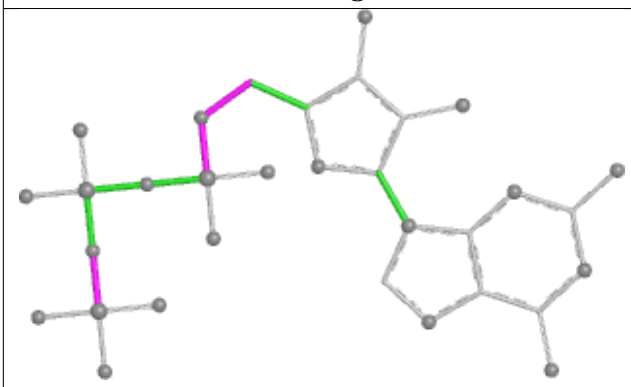

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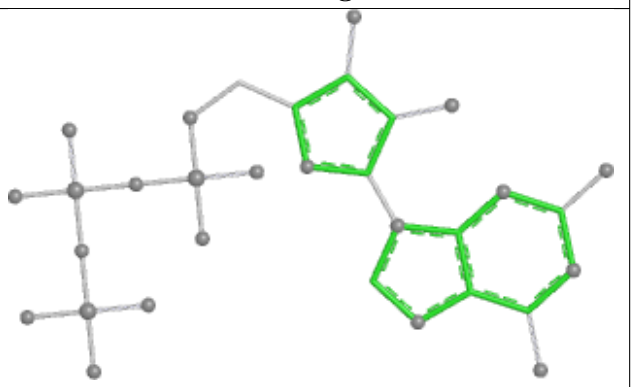
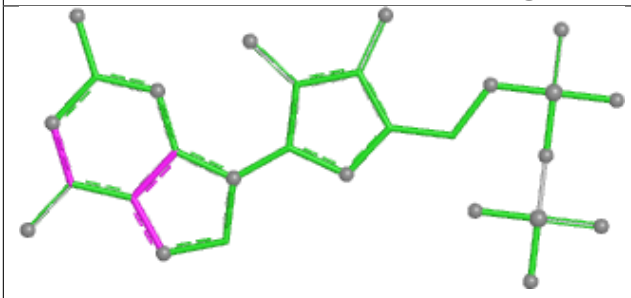
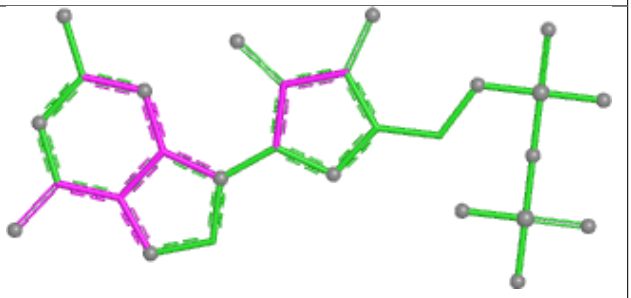
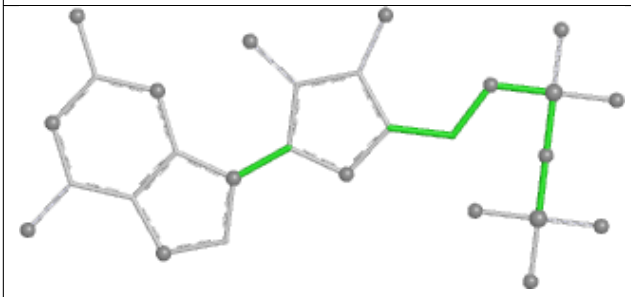
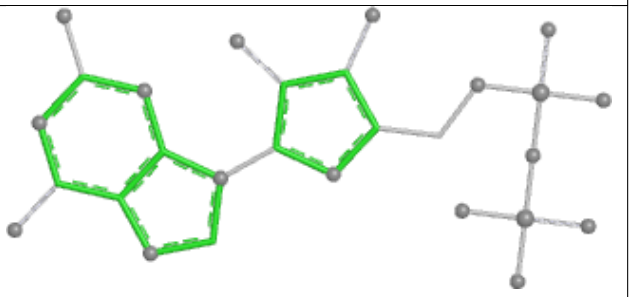
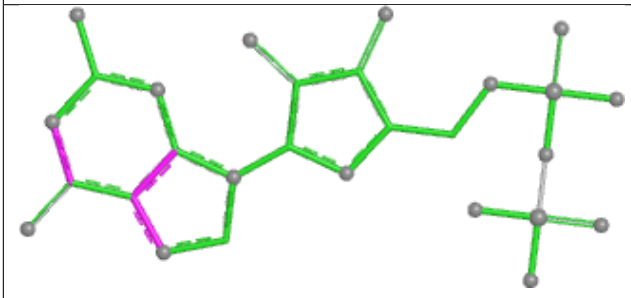
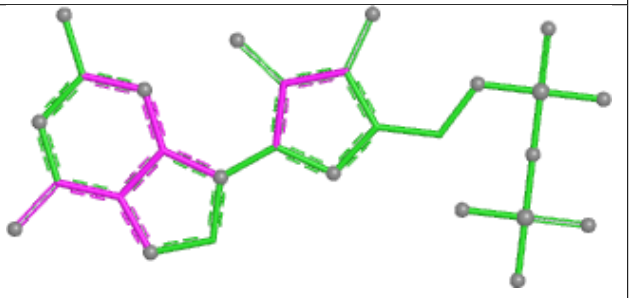


Rings

Ligand GDP G 500	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand GDP JG 500	
	
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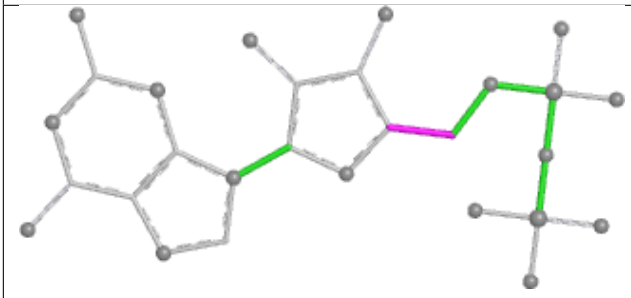
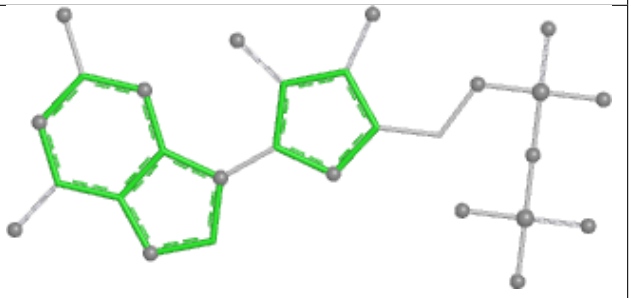
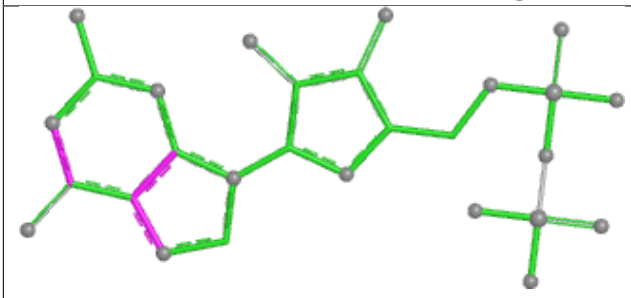
	
Torsions	Rings

Ligand GDP SD 500



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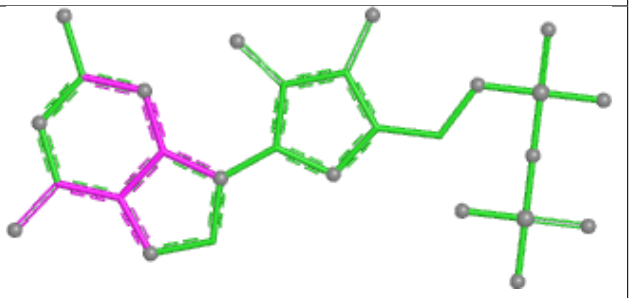

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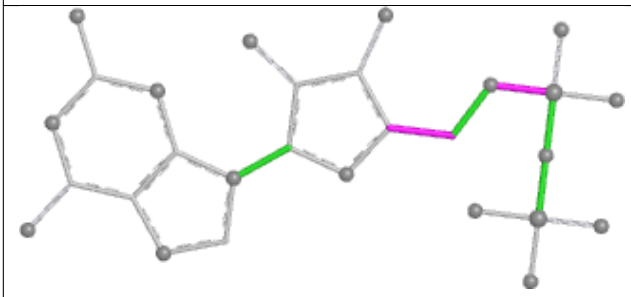

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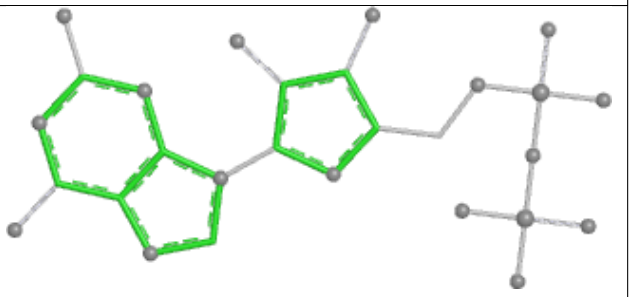
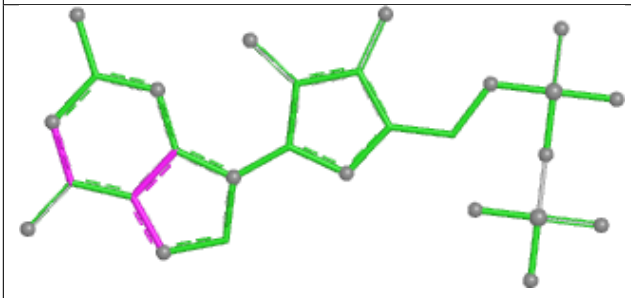


Rings

Ligand GDP KG 500



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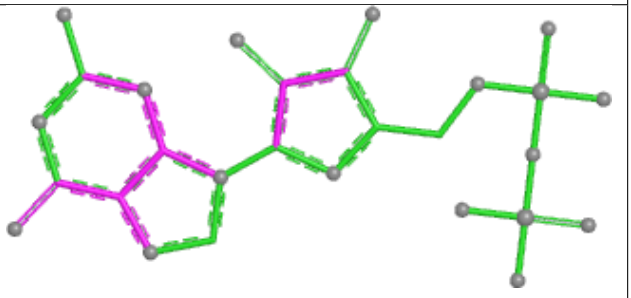

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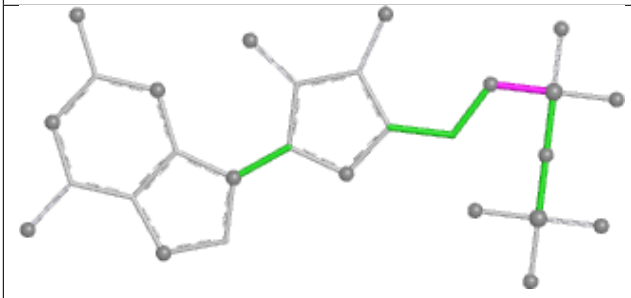

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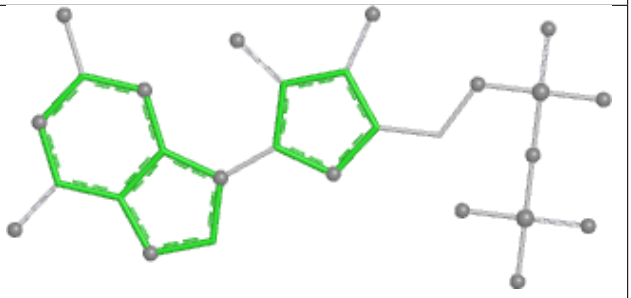
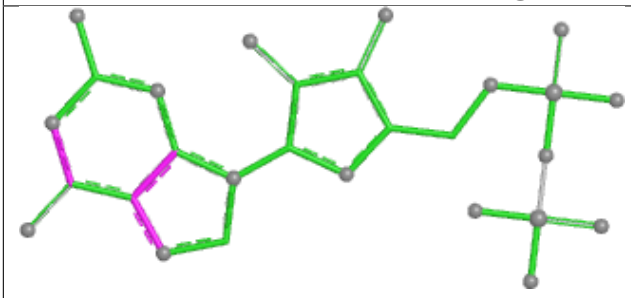


Rings

Ligand GDP VJ 500



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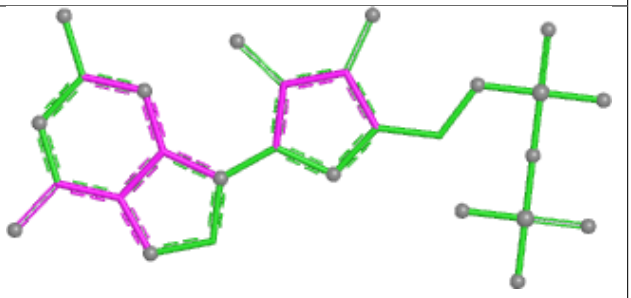

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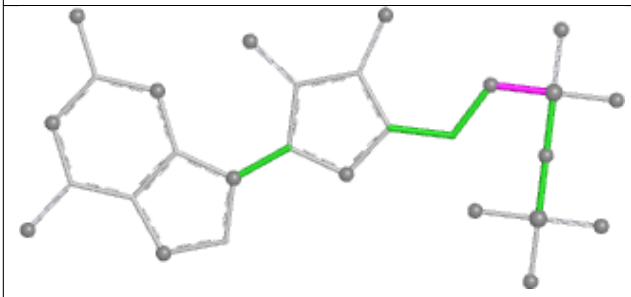

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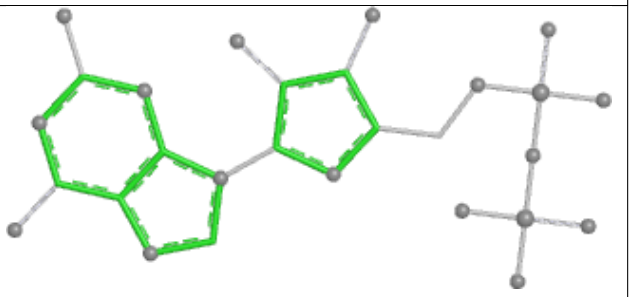
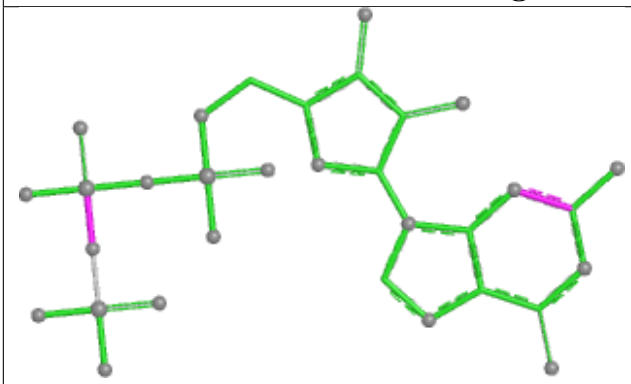


Rings

Ligand GTP KF 501



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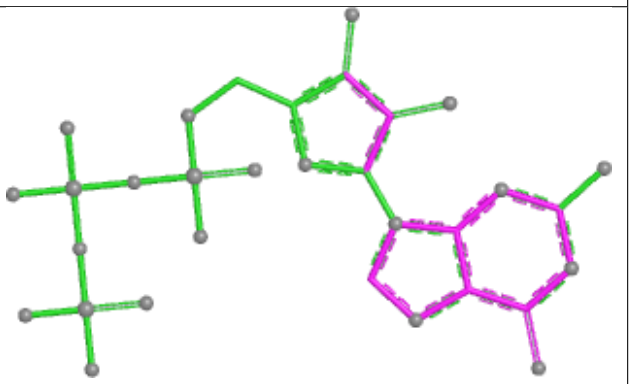

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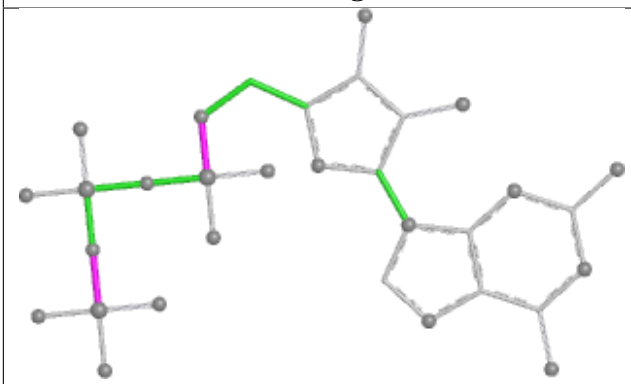

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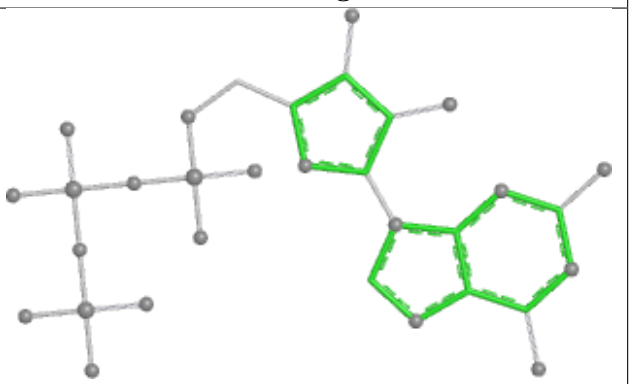
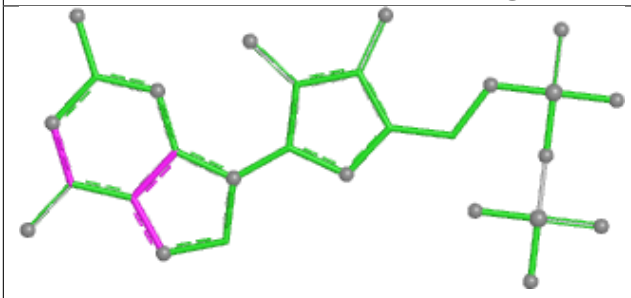


Rings

Ligand GDP DM 500



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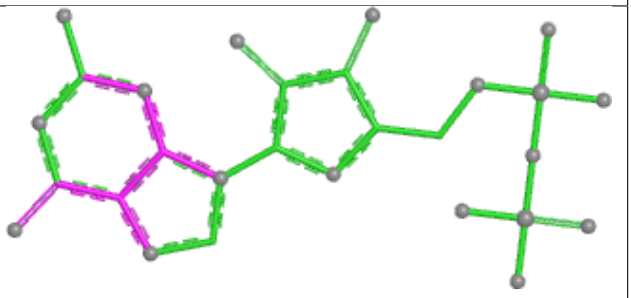

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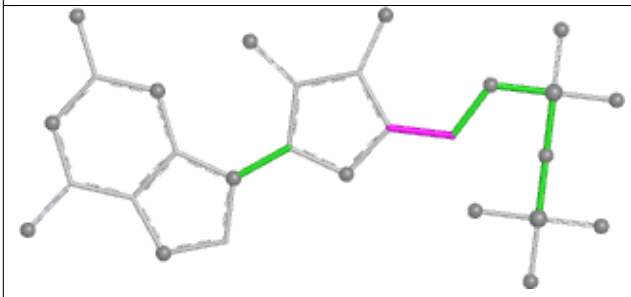

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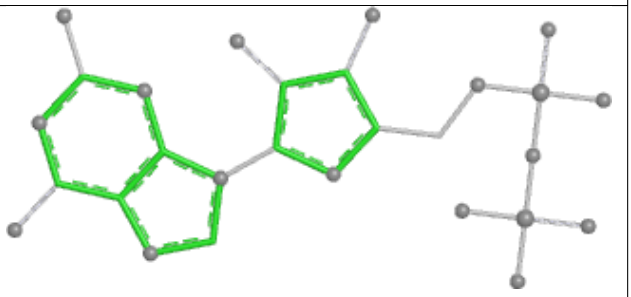
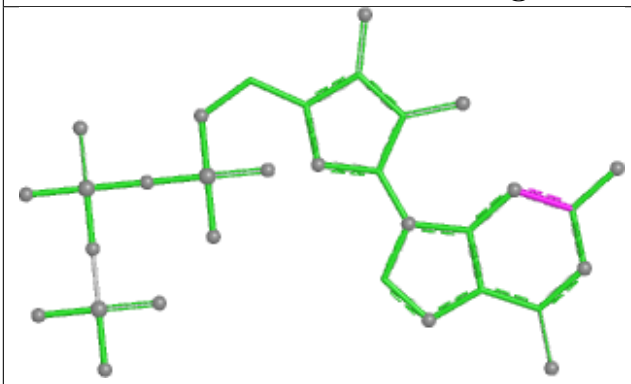


Rings

Ligand GTP CB 501



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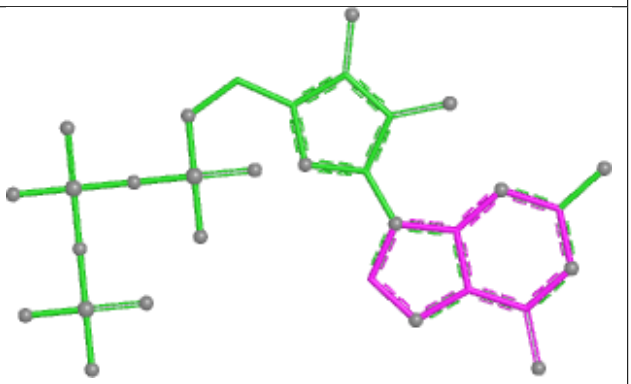

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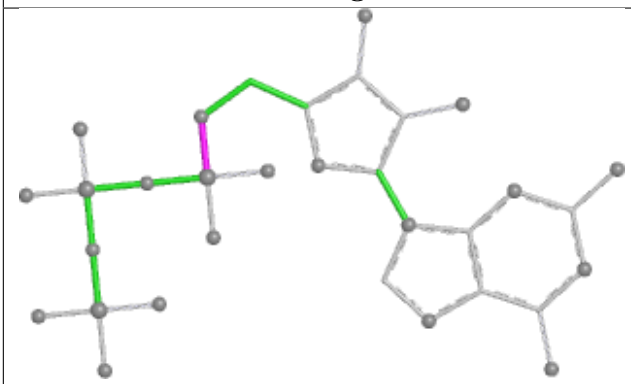

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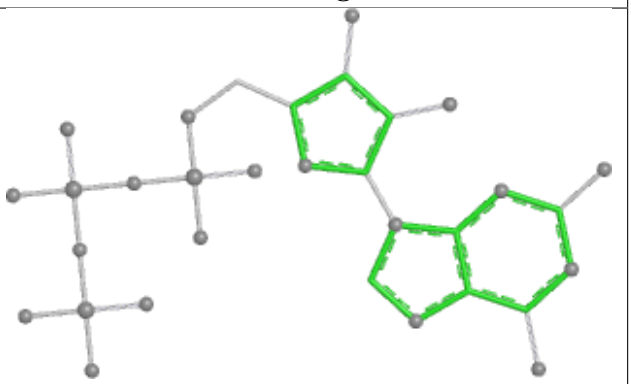
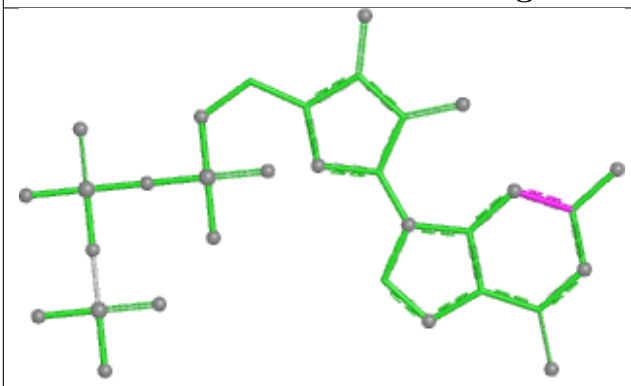


Rings

Ligand GTP OI 501



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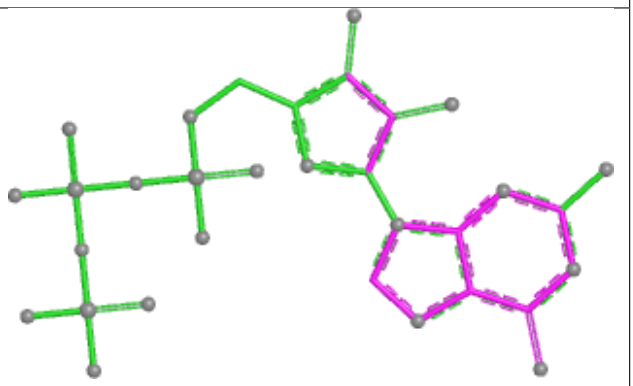

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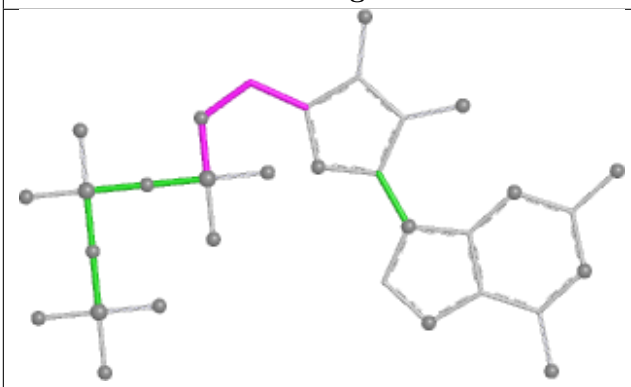

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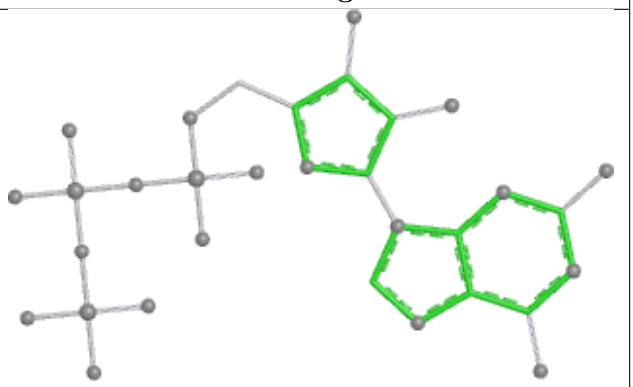
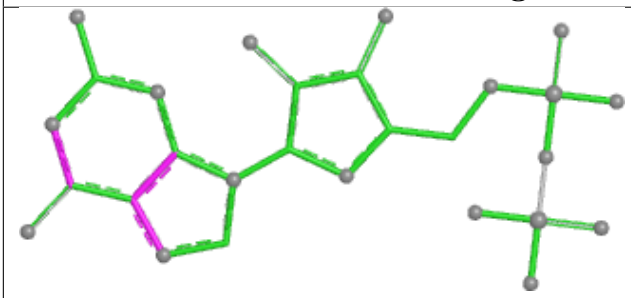


Rings

Ligand GDP HL 500



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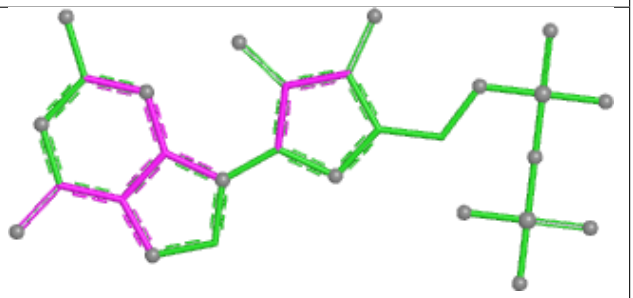

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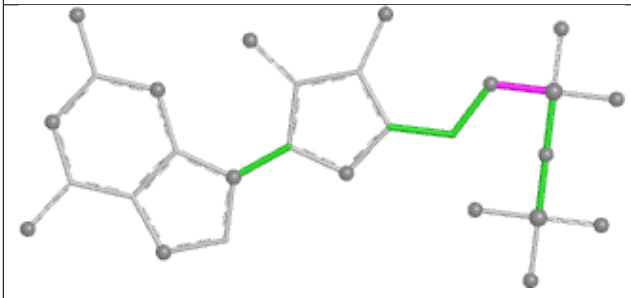

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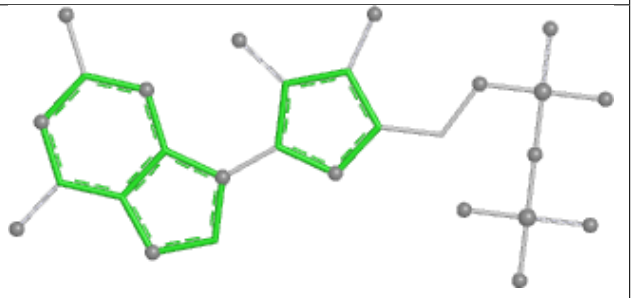
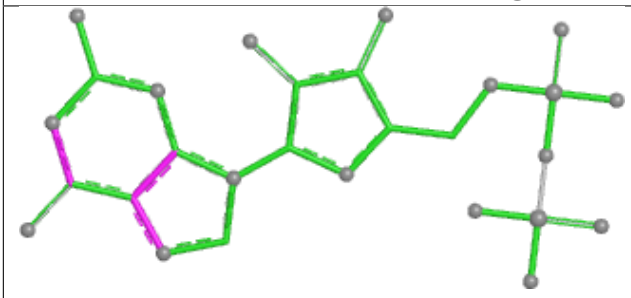


Rings

Ligand GDP KE 500



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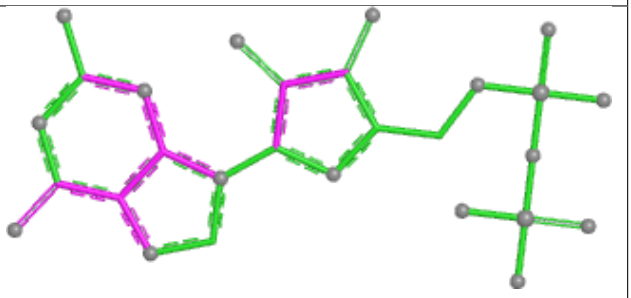

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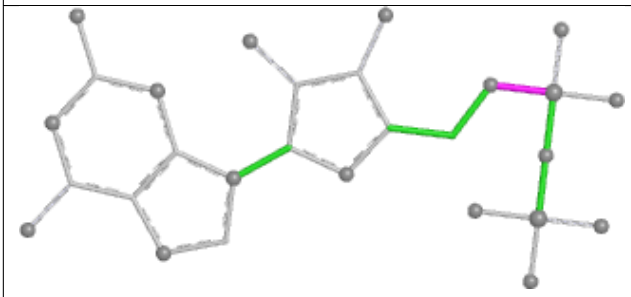

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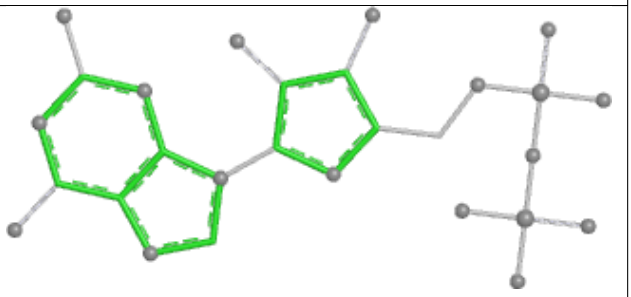
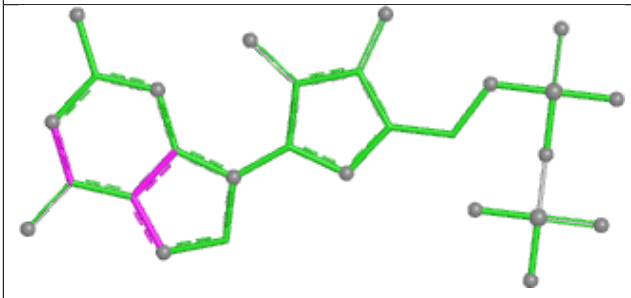


Rings

Ligand GDP BB 500



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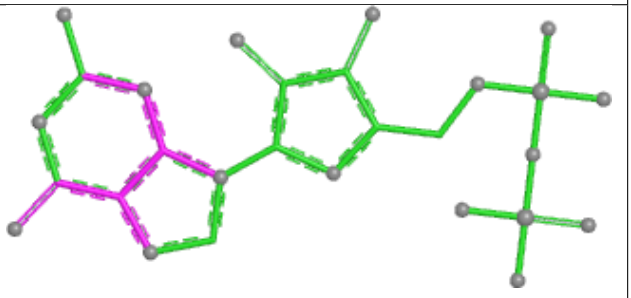

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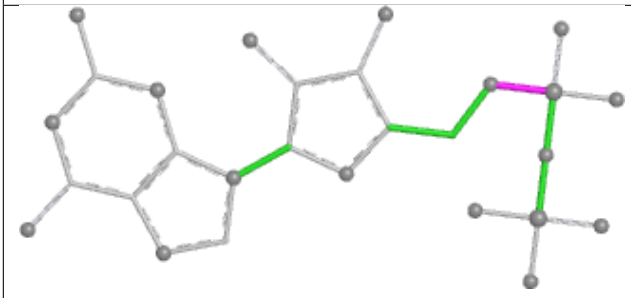

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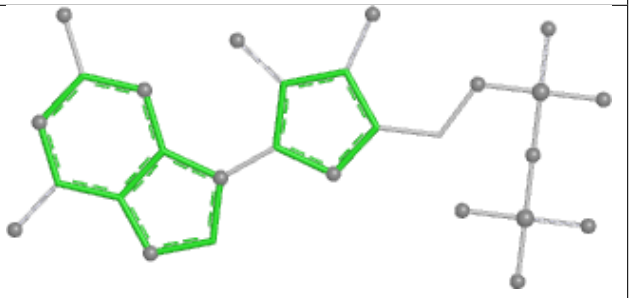
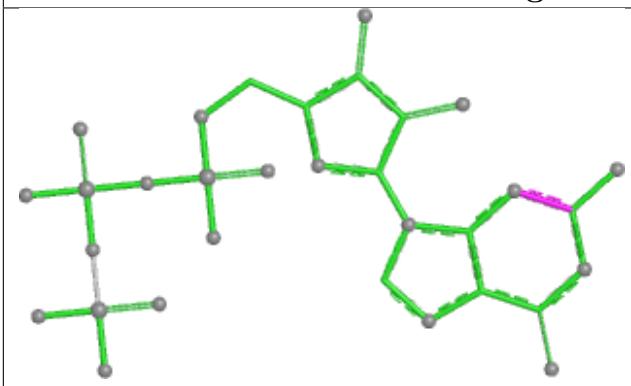


Rings

Ligand GTP J 501



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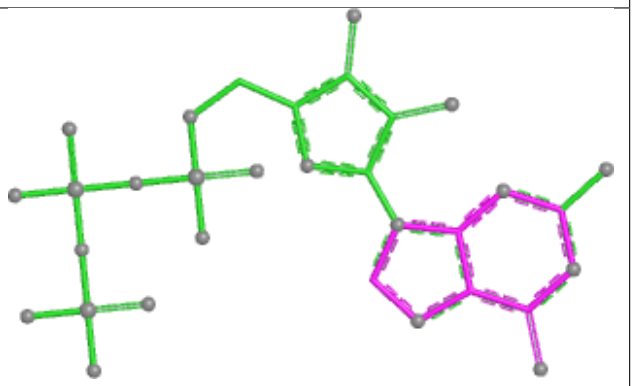

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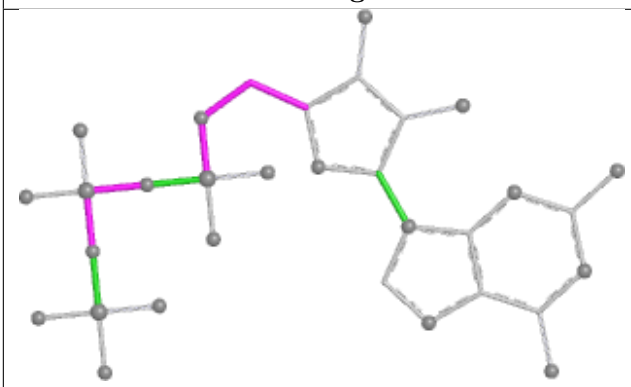

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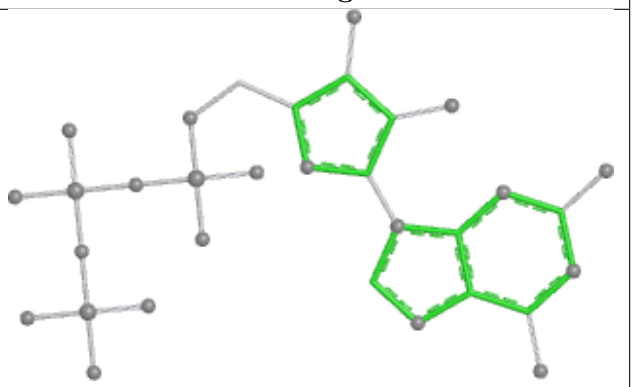
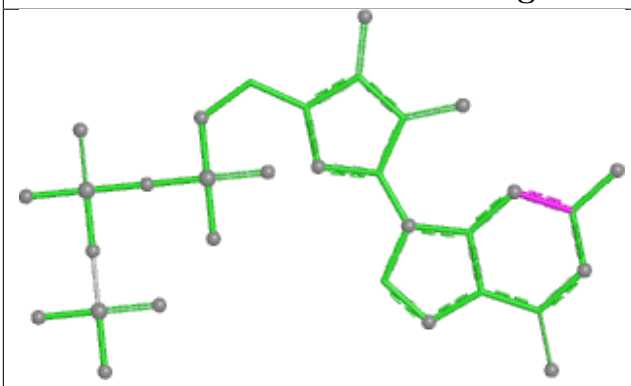


Rings

Ligand GTP FI 501



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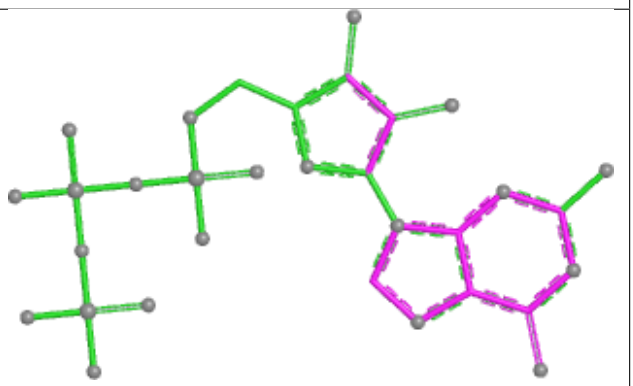
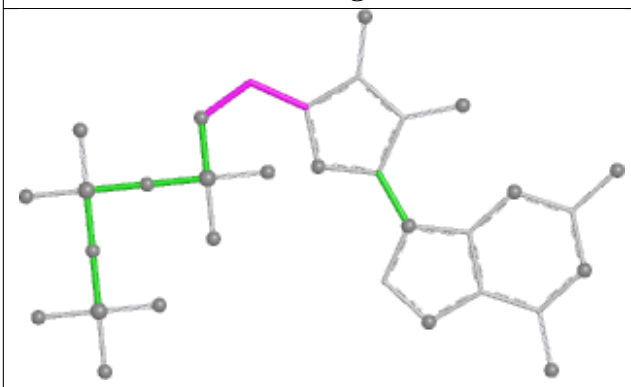
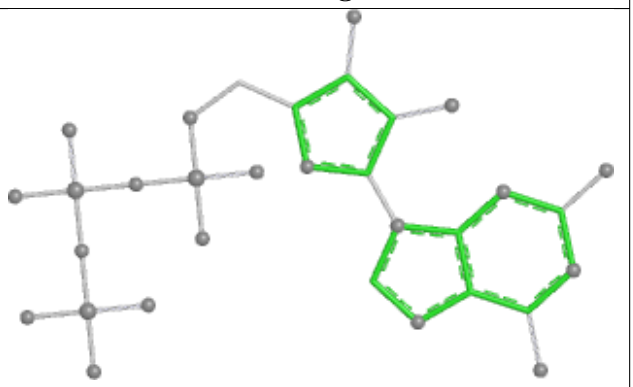


Bond angles

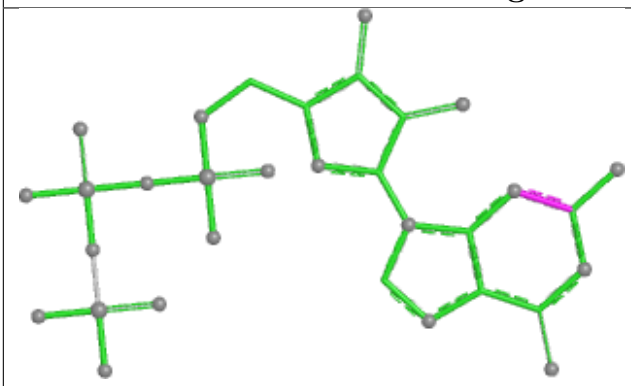


Torsions



Rings

Ligand GTP UG 501



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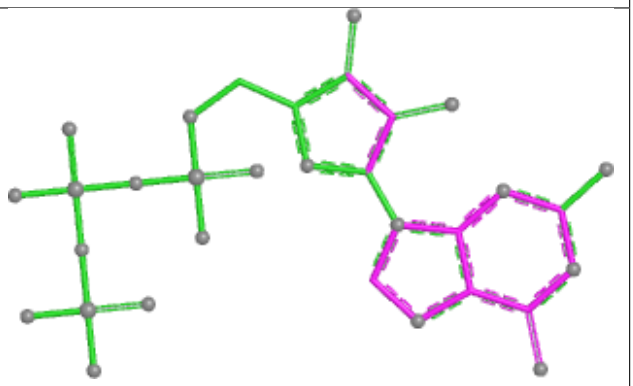

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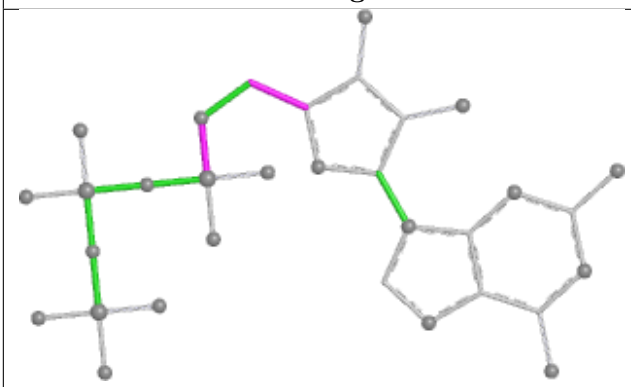

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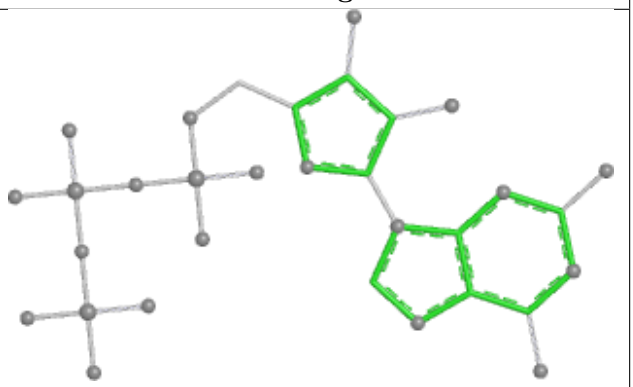
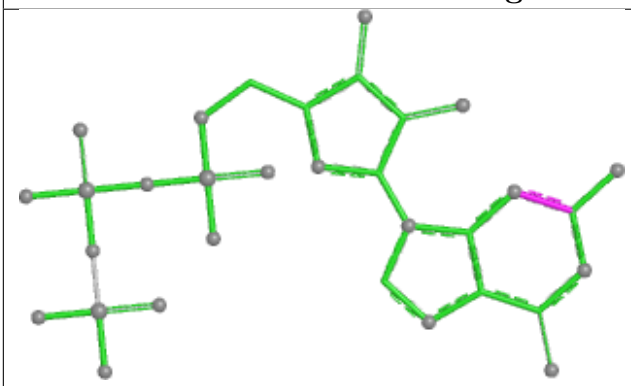


Rings

Ligand GTP OM 501



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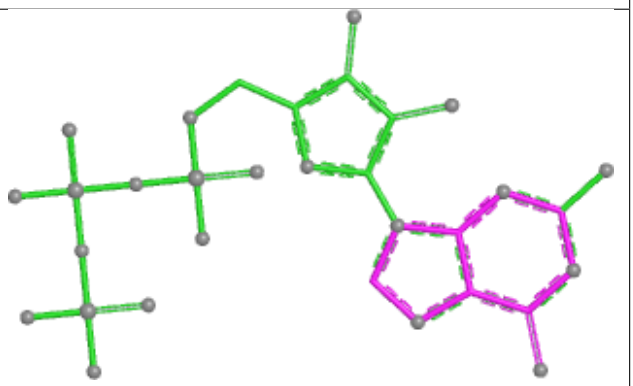

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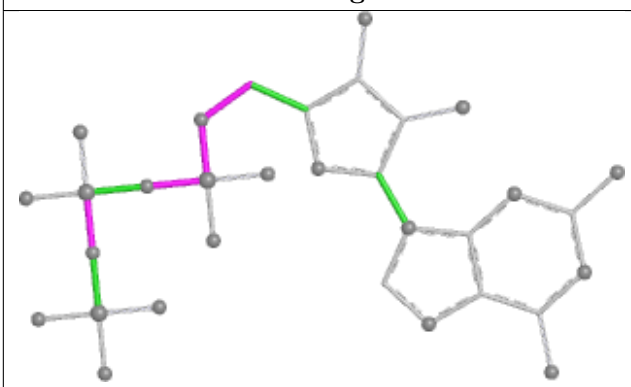
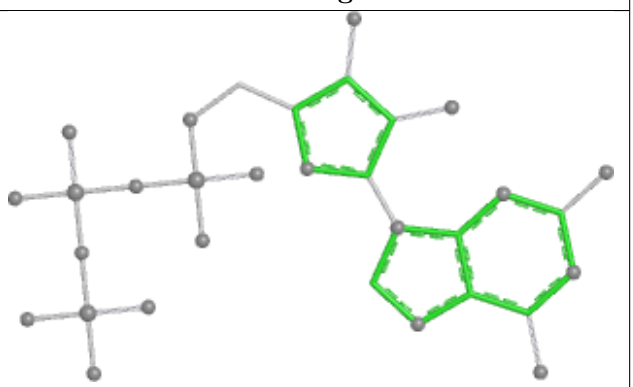
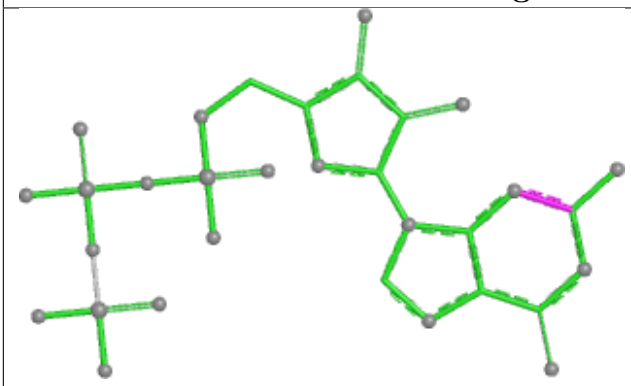


Torsions



Rings

Ligand GTP SC 501



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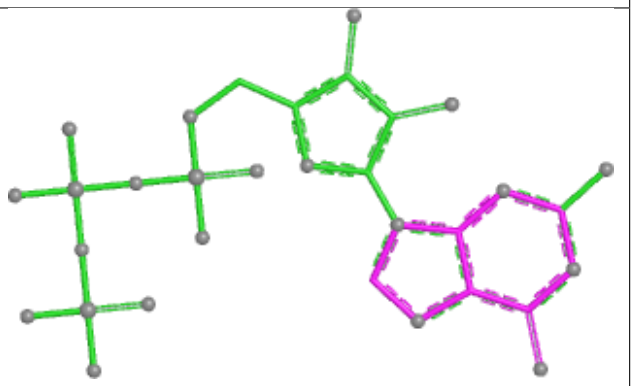

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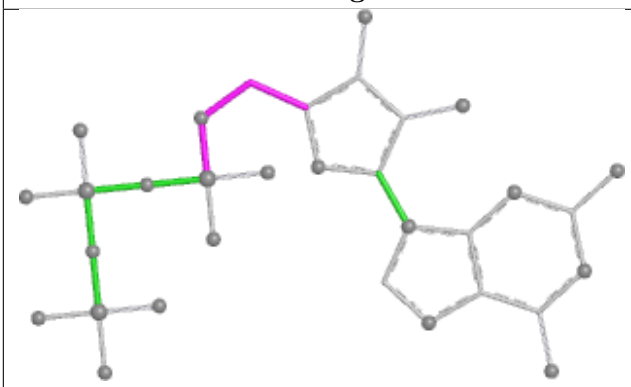

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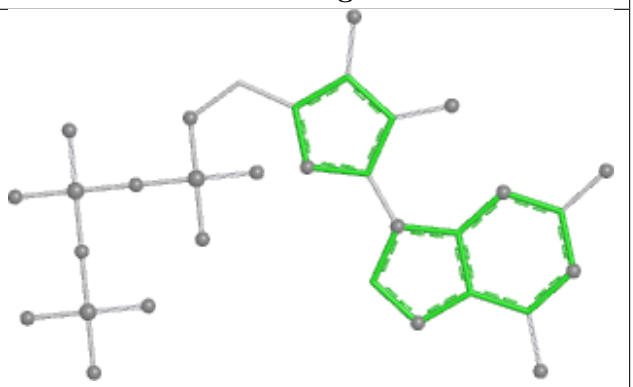
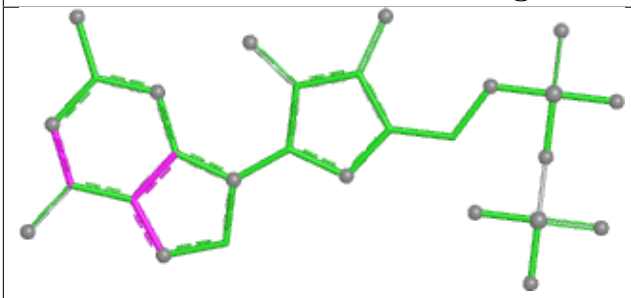


Rings

Ligand GDP JC 500



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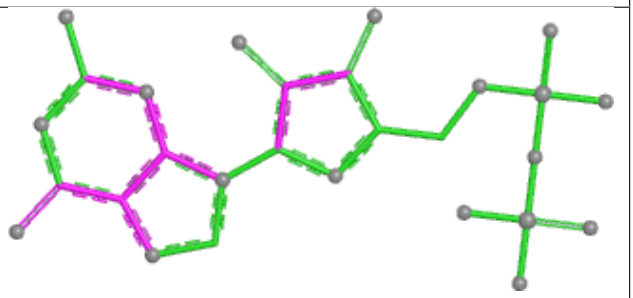

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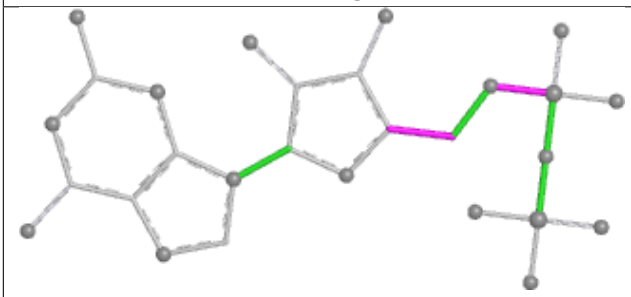

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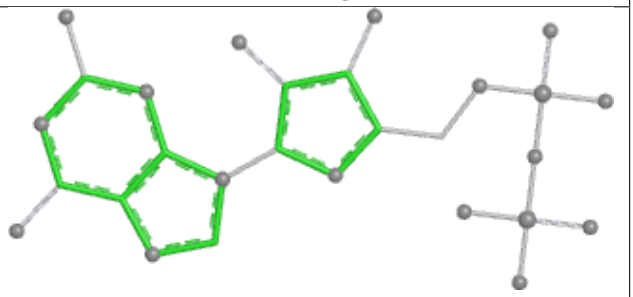
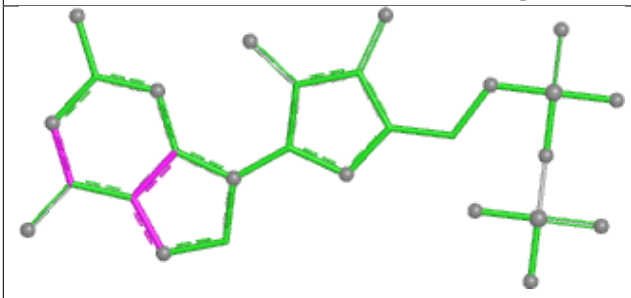


Rings

Ligand GDP RI 500



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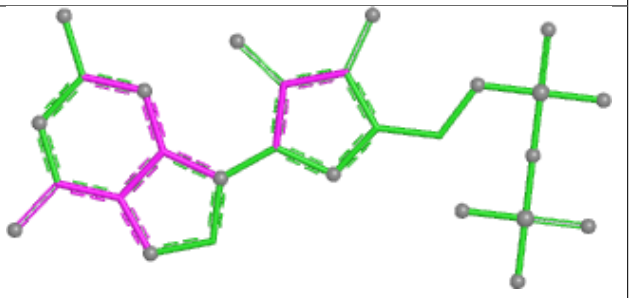

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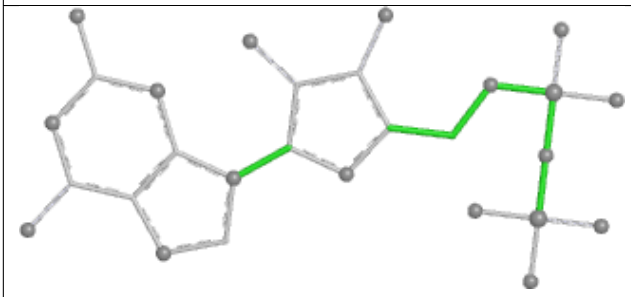

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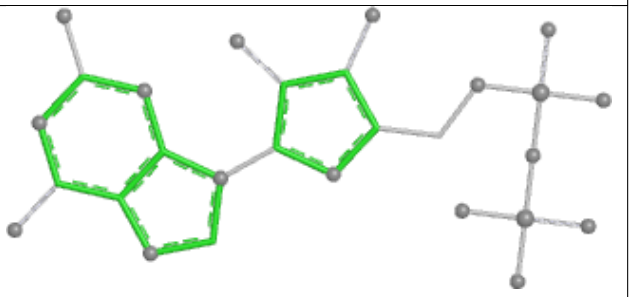
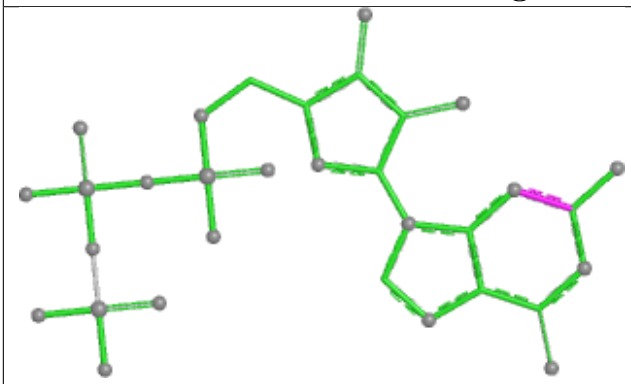


Rings

Ligand GTP LN 501



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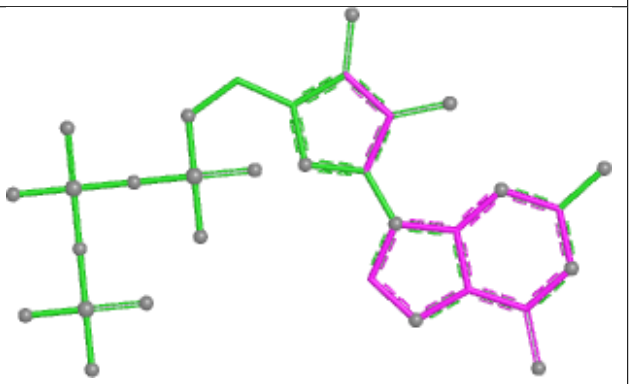

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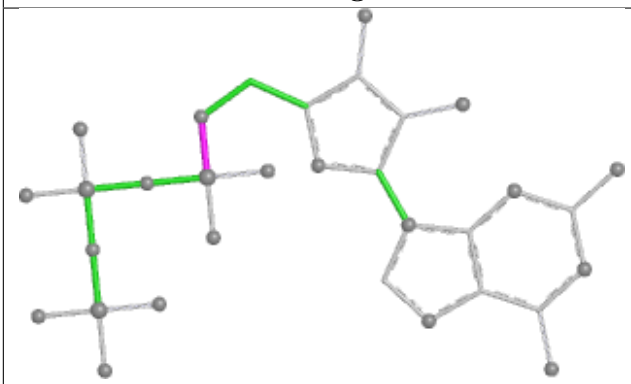

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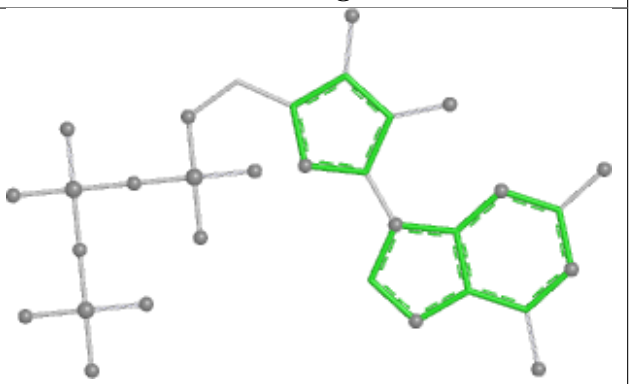
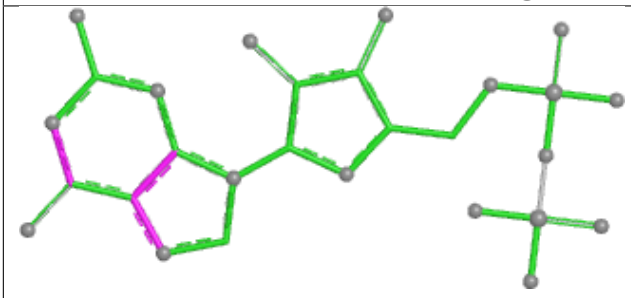


Rings

Ligand GDP JI 500



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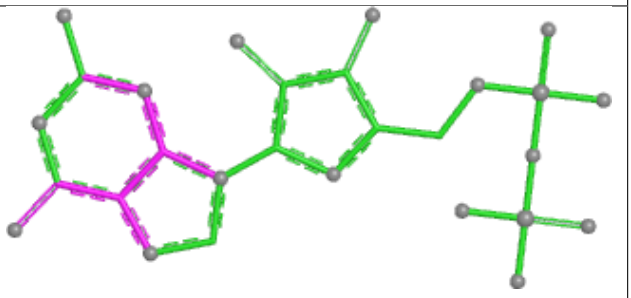

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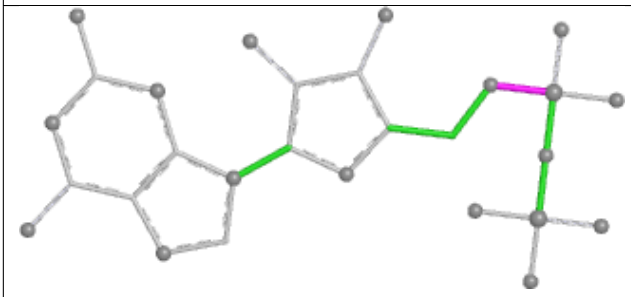

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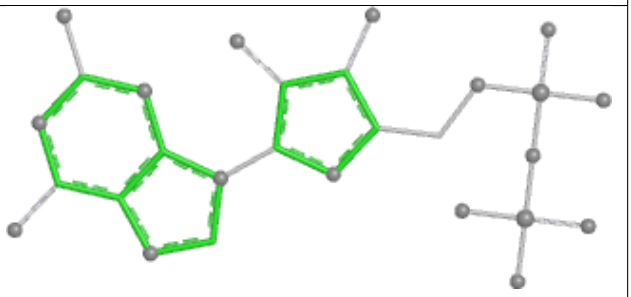
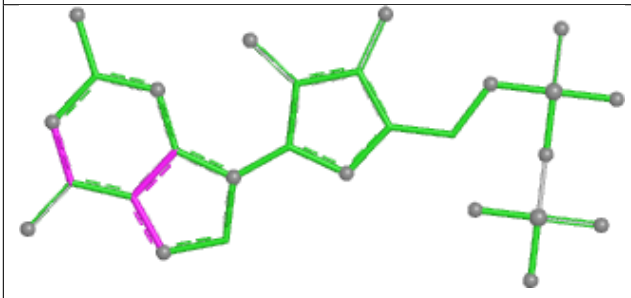


Rings

Ligand GDP OH 500



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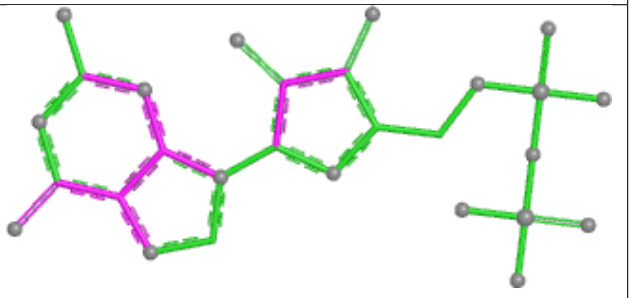

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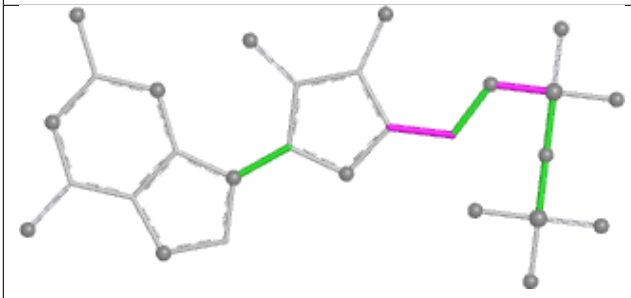

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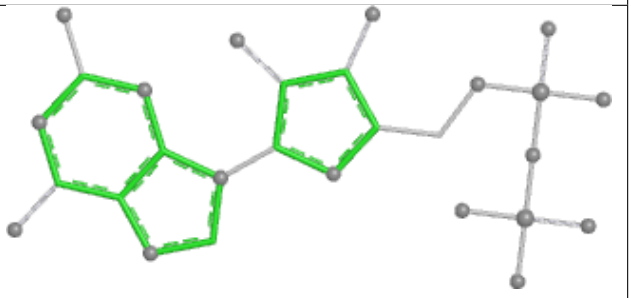
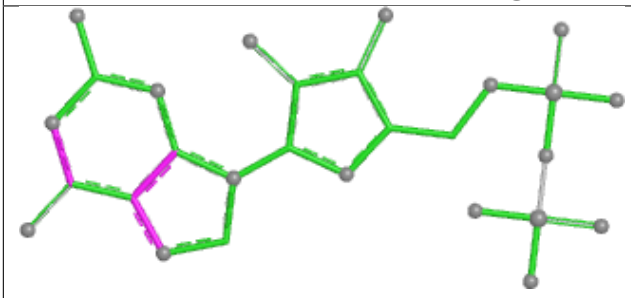


Rings

Ligand GDP MJ 500



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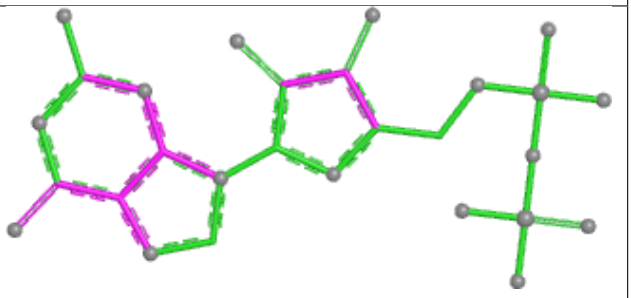

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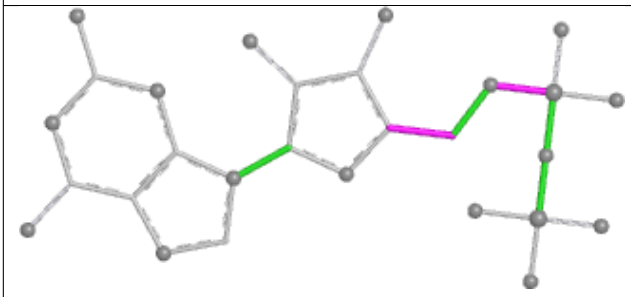

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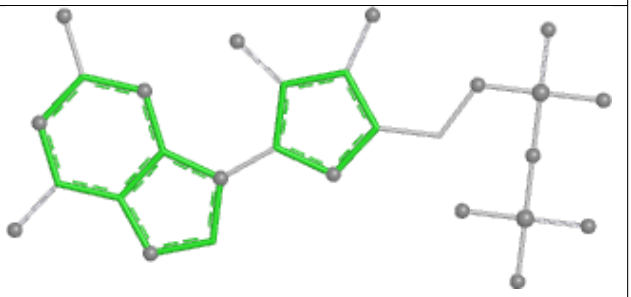
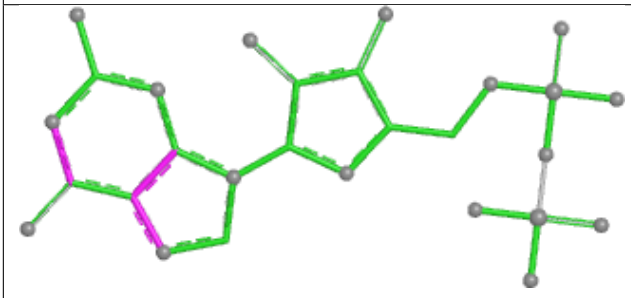


Rings

Ligand GDP PJ 500



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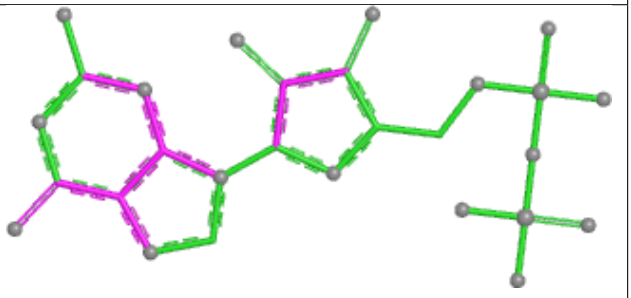

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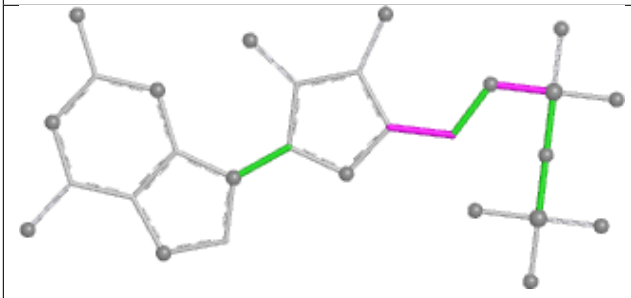

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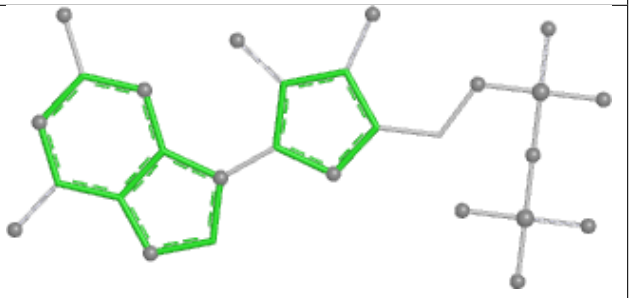
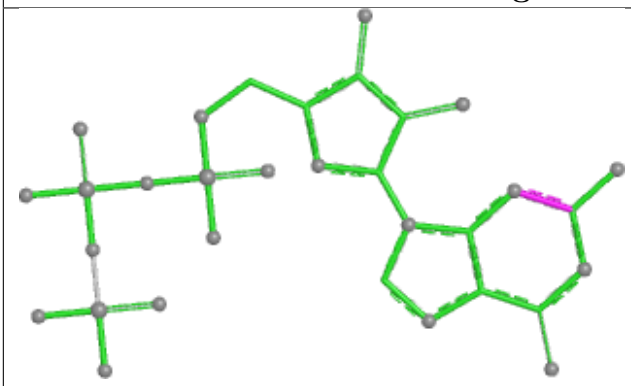


Rings

Ligand GTP JD 501



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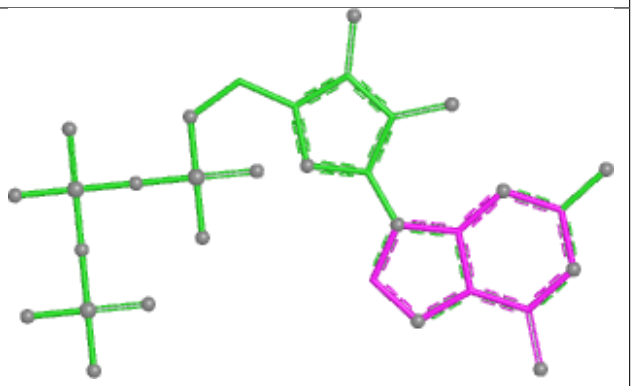

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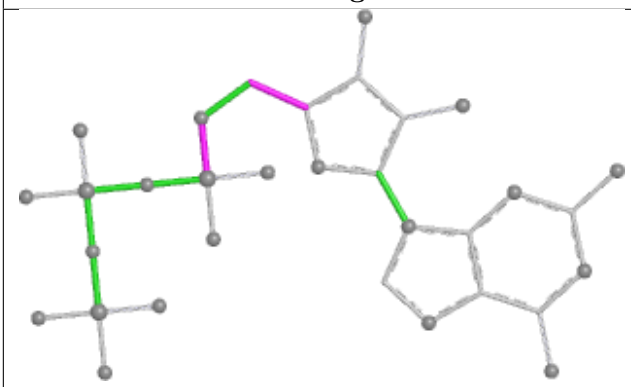

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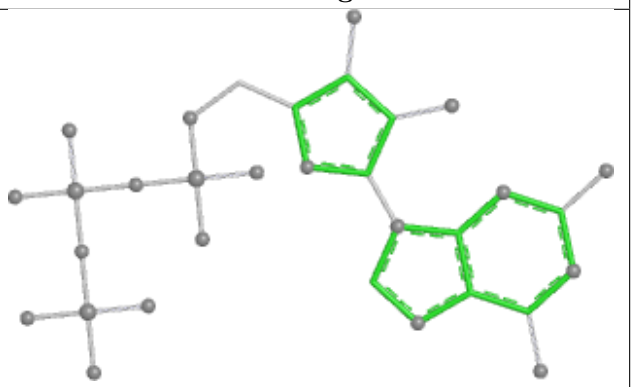
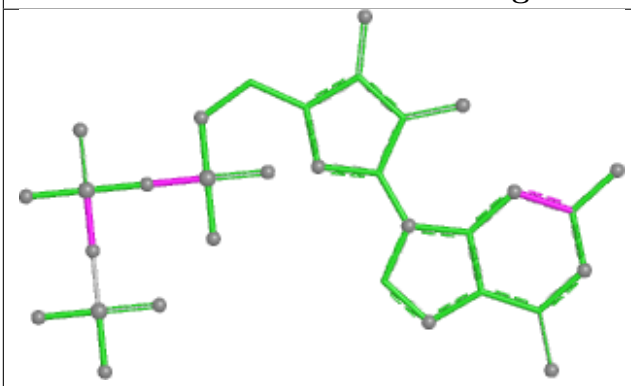


Rings

Ligand GTP EE 501



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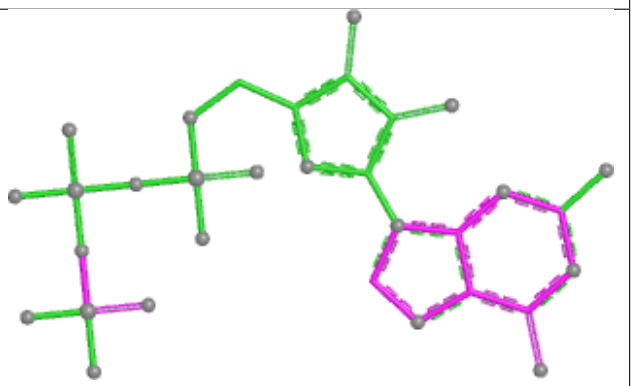

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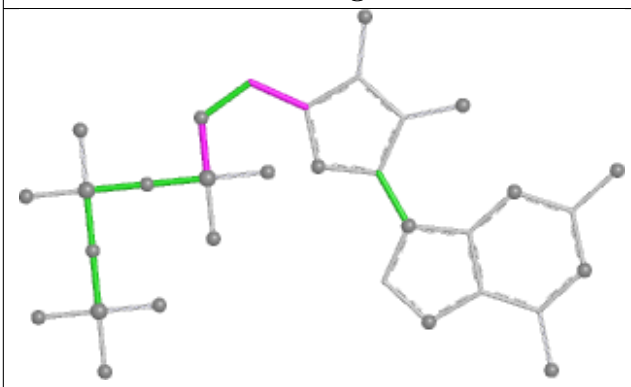

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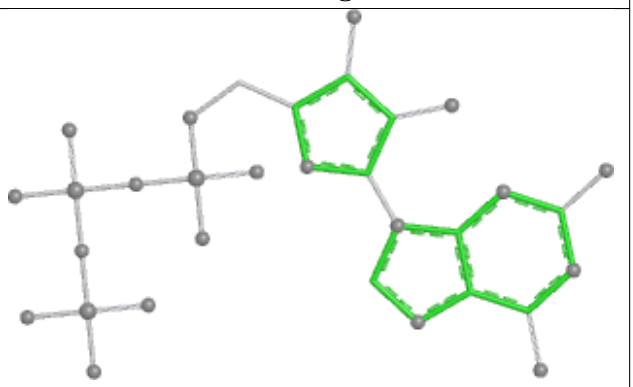
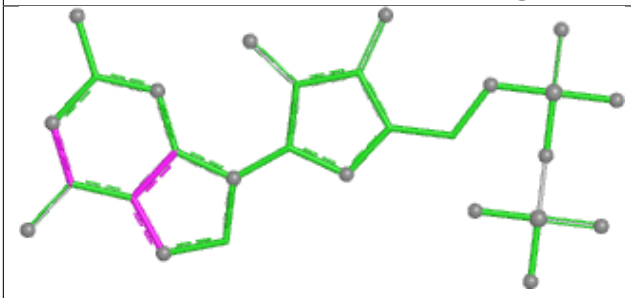
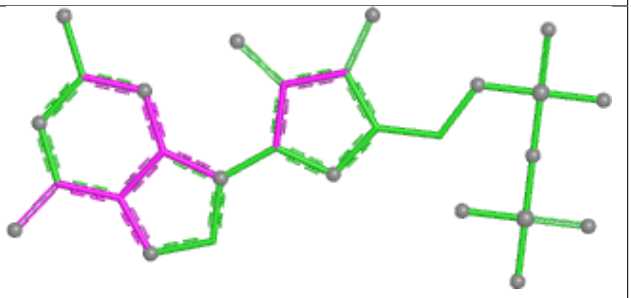
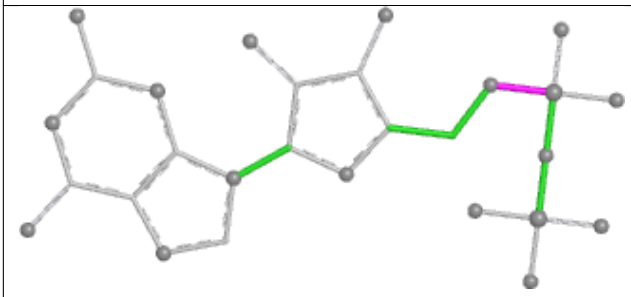
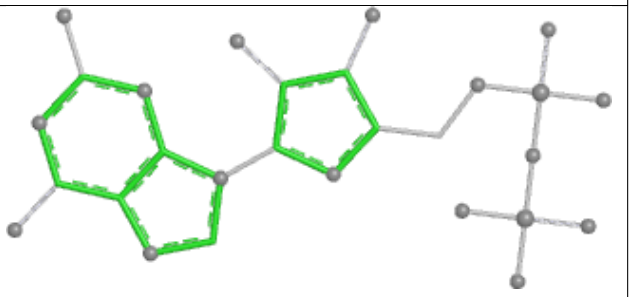
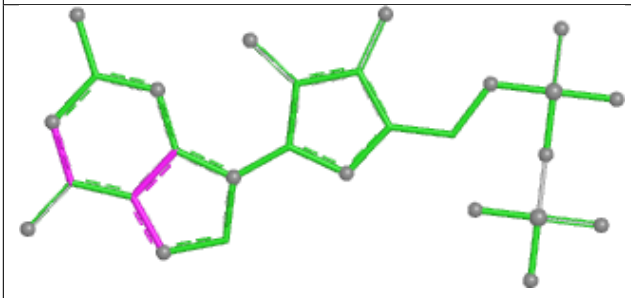
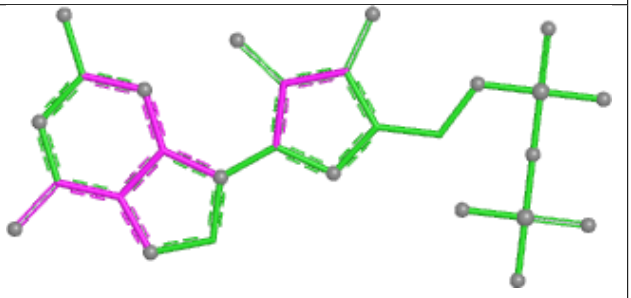
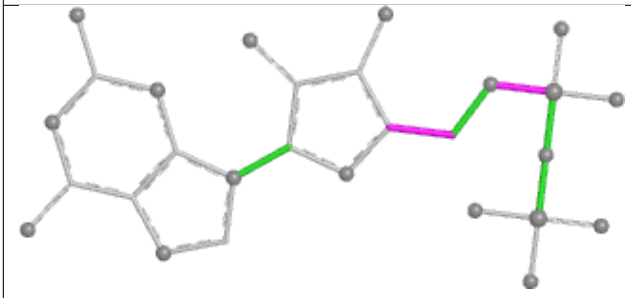
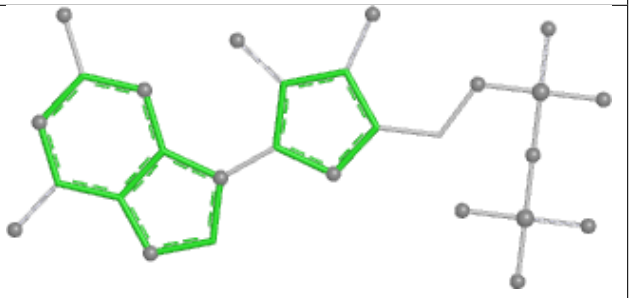
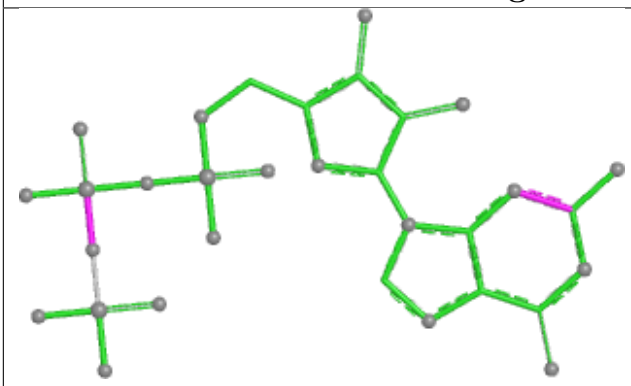


Rings

Ligand GDP JE 500	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP IH 500	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP HC 501



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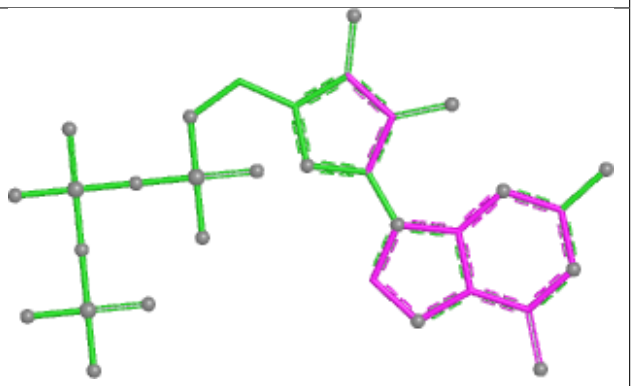

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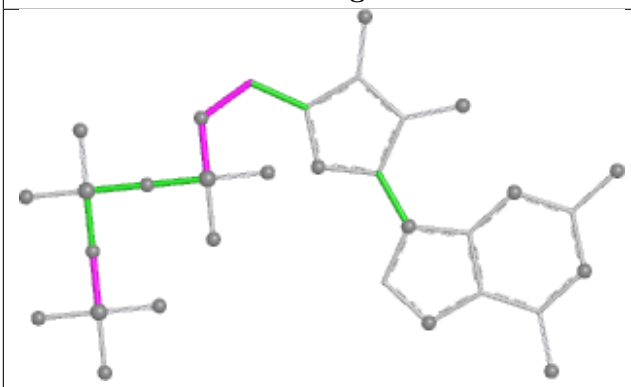

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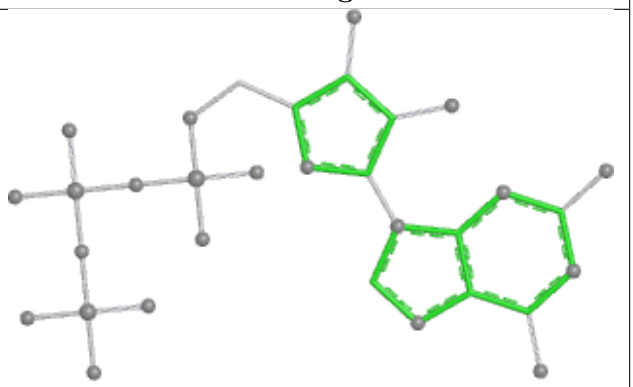
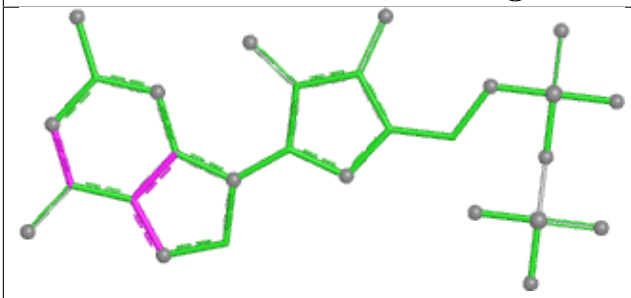


Rings

Ligand GDP DK 500



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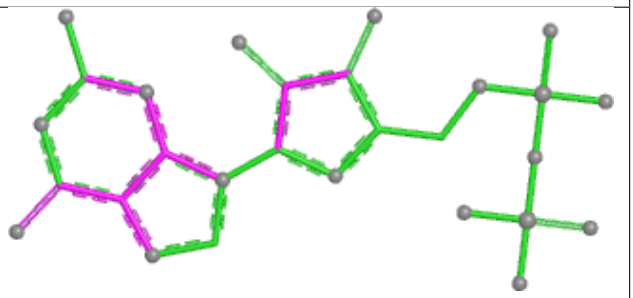

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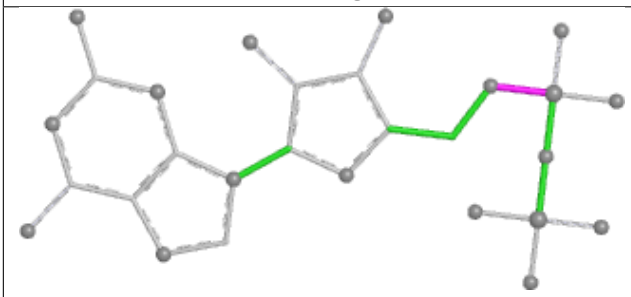

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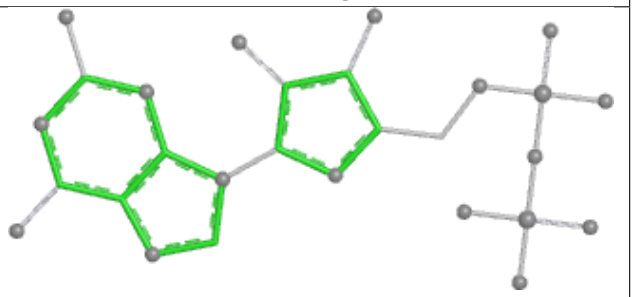
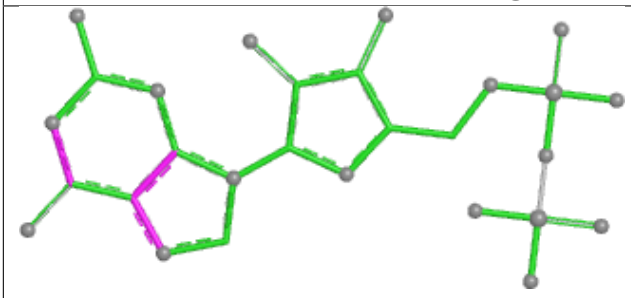


Rings

Ligand GDP AD 500



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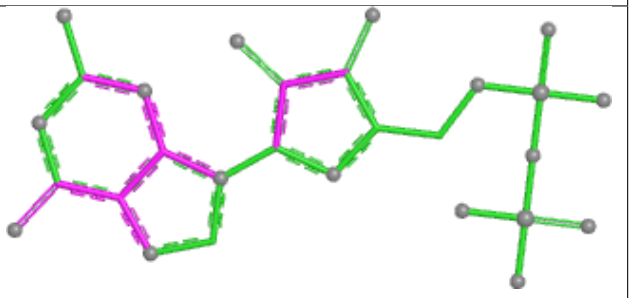

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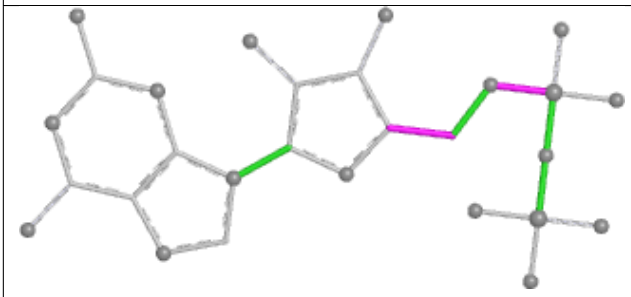

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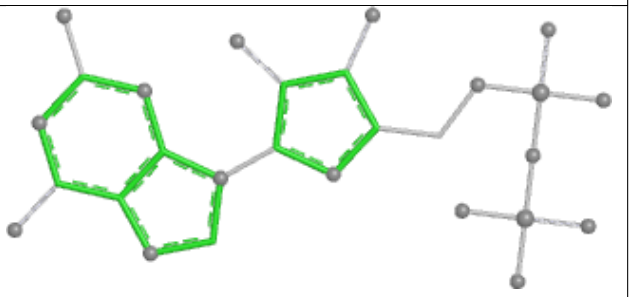
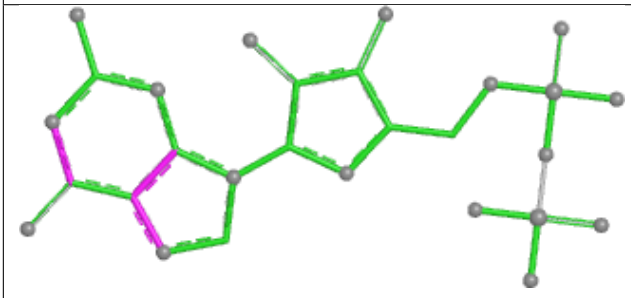


Rings

Ligand GDP QK 500



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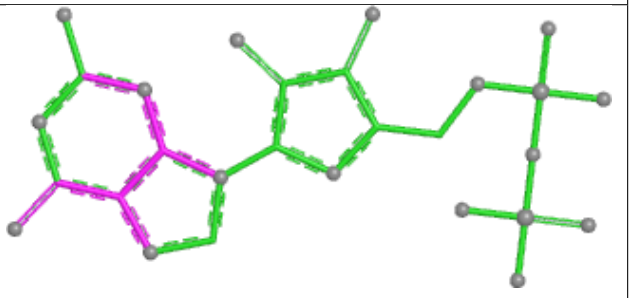

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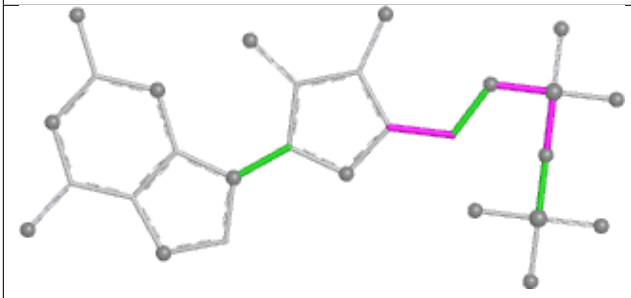

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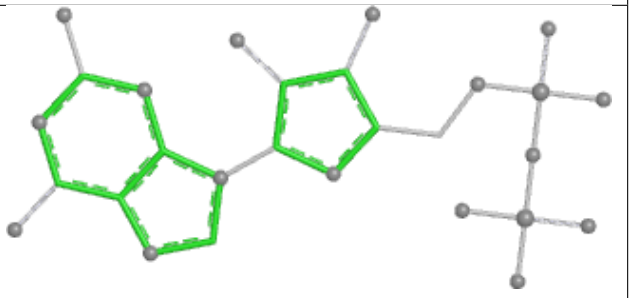
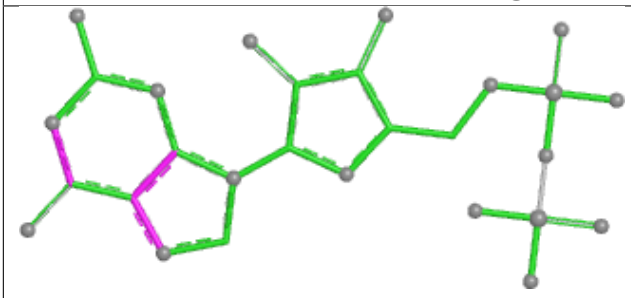


Rings

Ligand GDP DC 500



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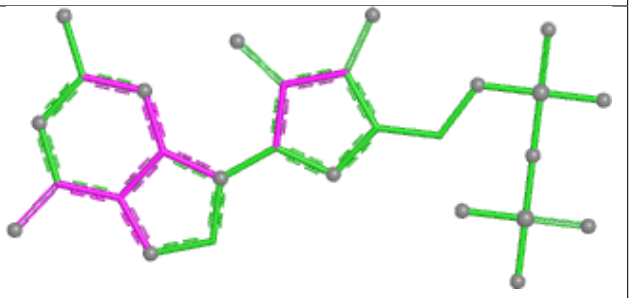

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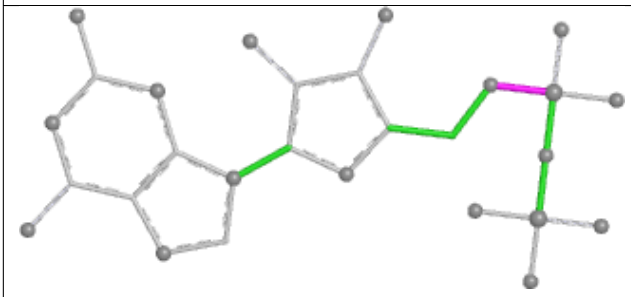

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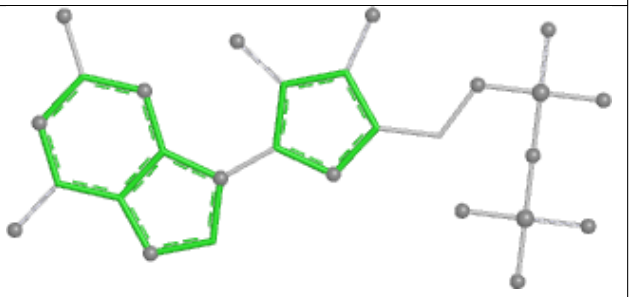
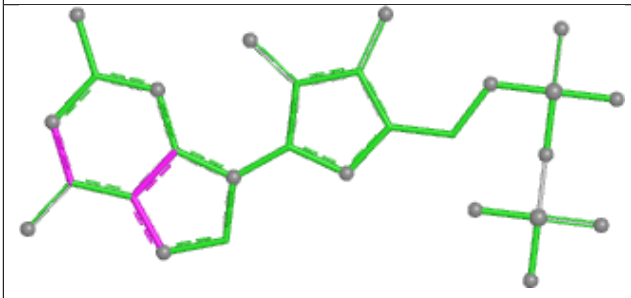


Rings

Ligand GDP E 500



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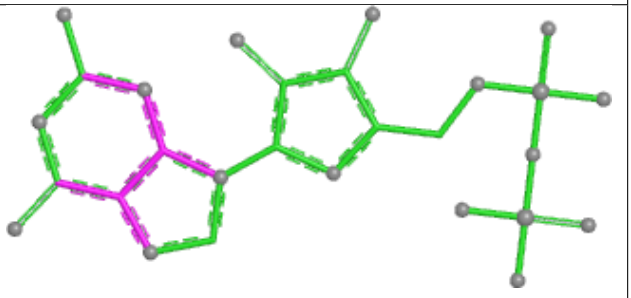

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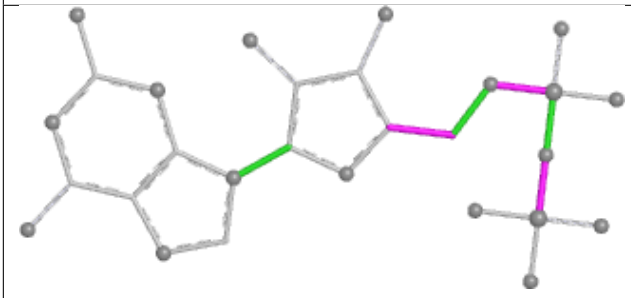

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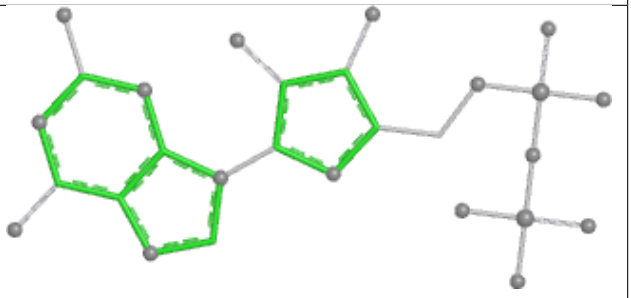
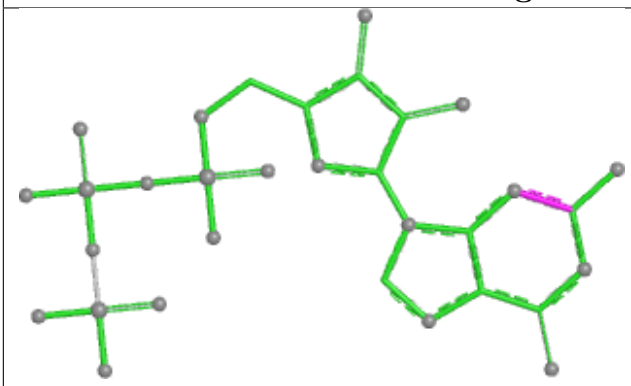


Rings

Ligand GTP HI 501



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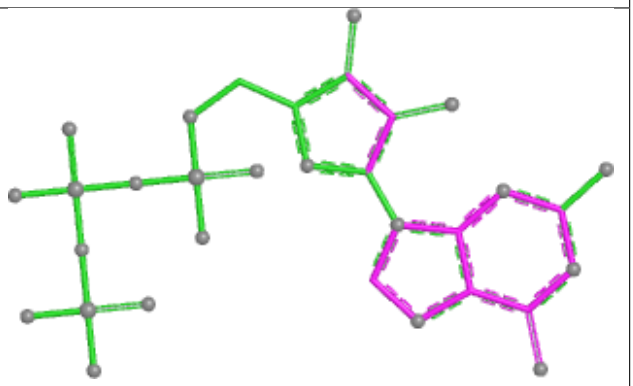

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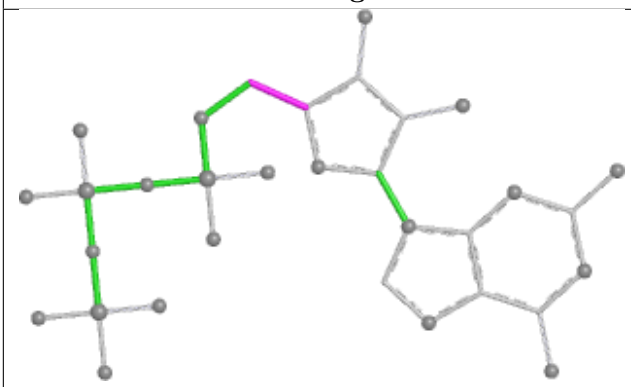

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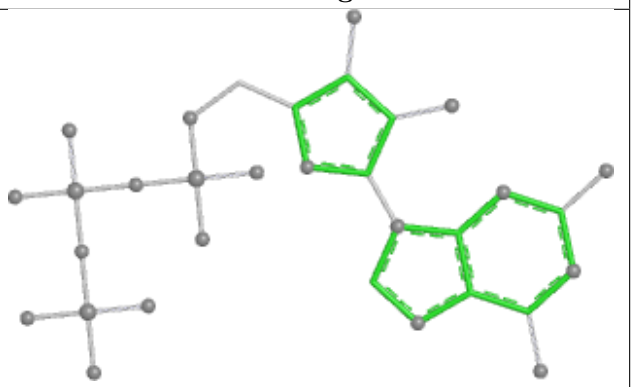
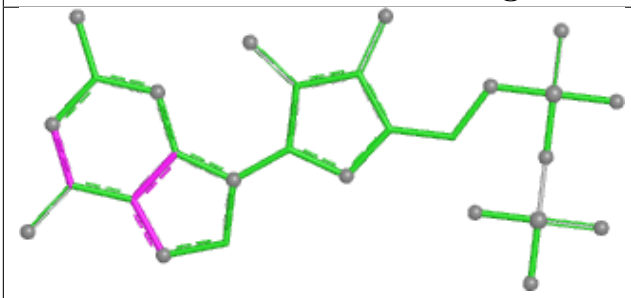


Rings

Ligand GDP WH 500



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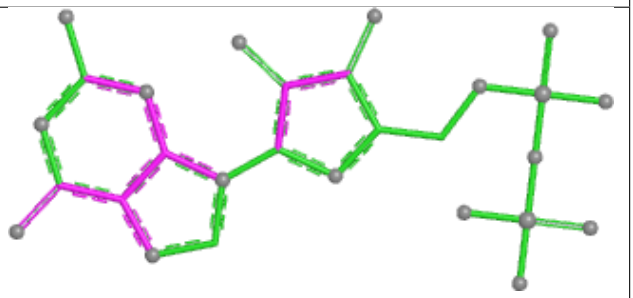

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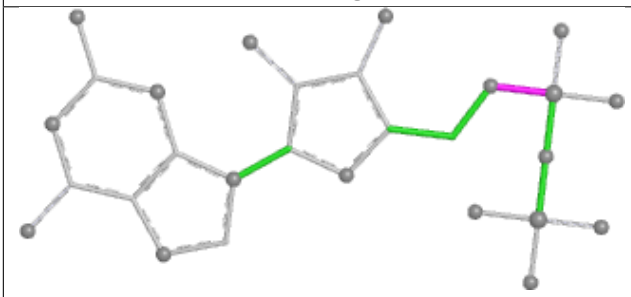

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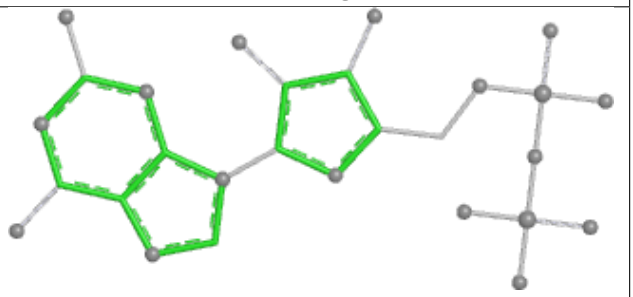
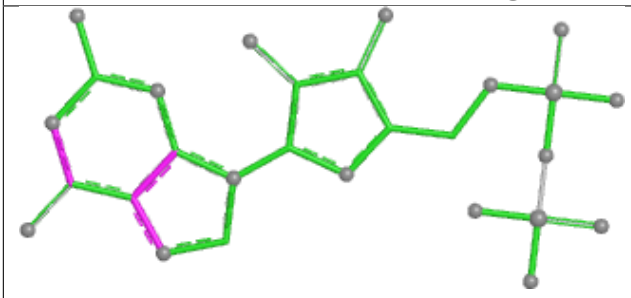


Rings

Ligand GDP CM 500



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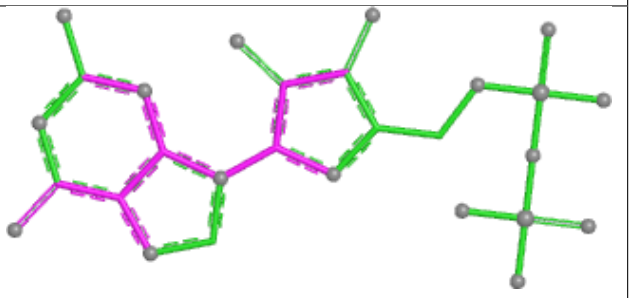

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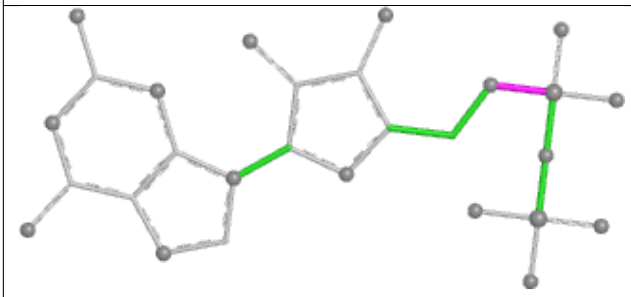

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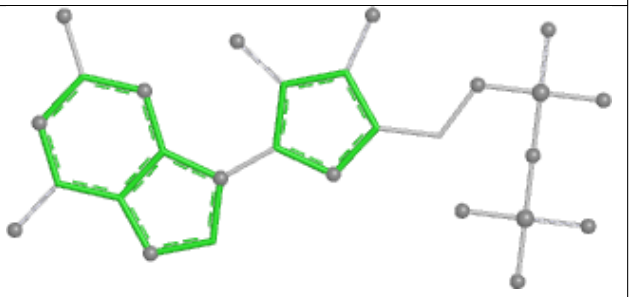
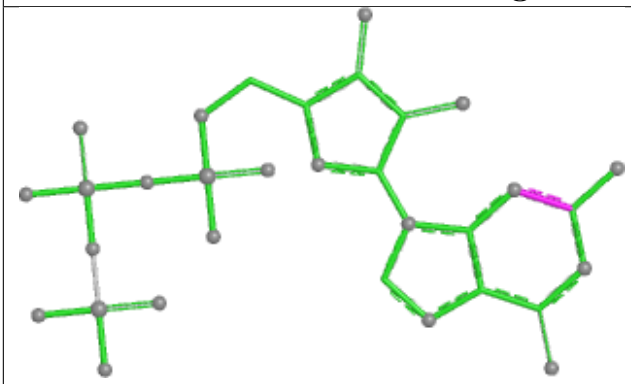


Rings

Ligand GTP TE 501



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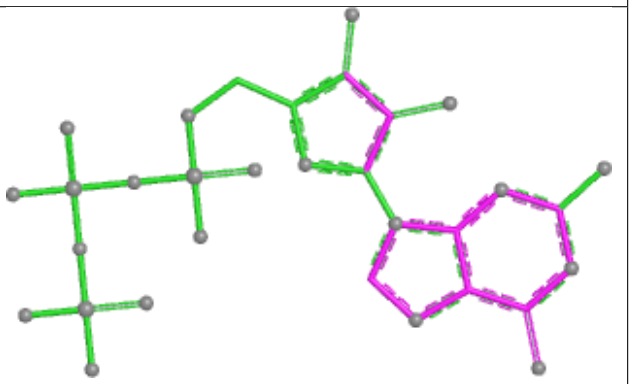

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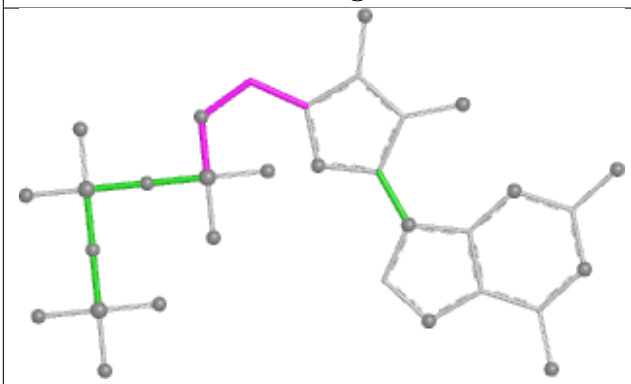

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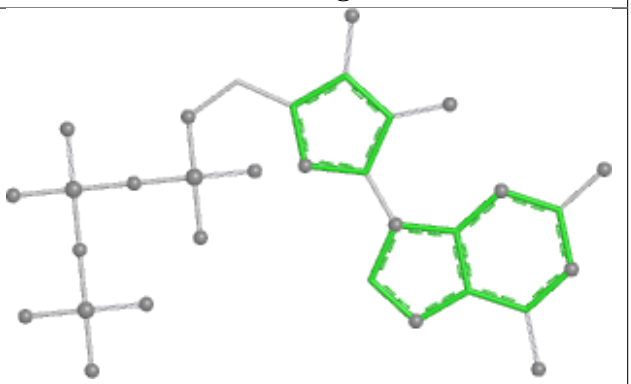
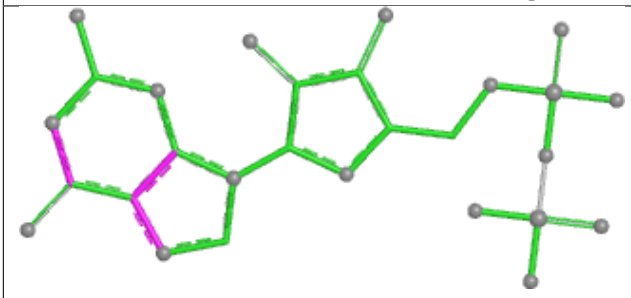


Rings

Ligand GDP F 500



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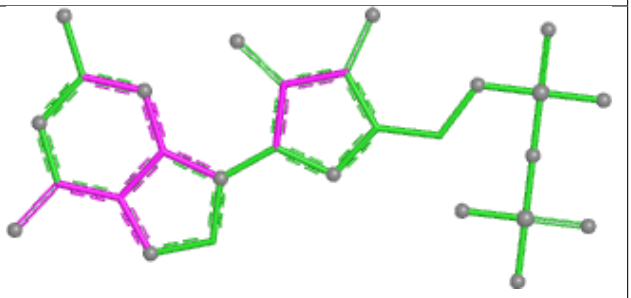

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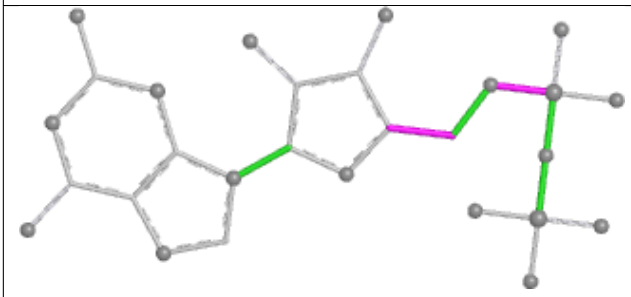

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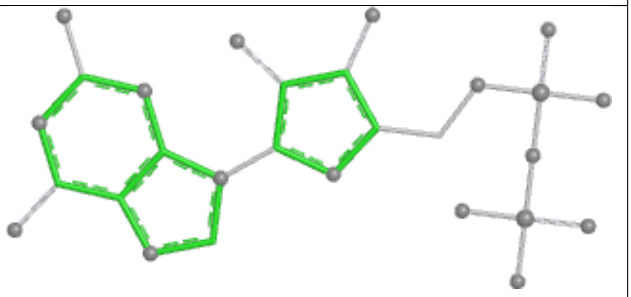
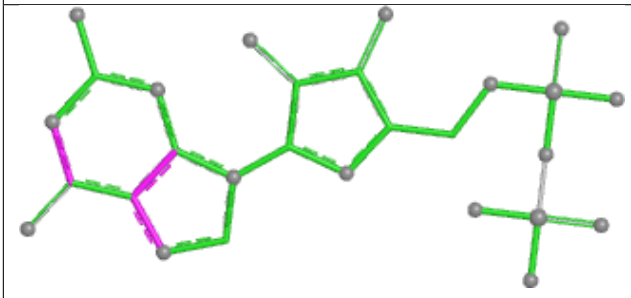


Rings

Ligand GDP OB 500



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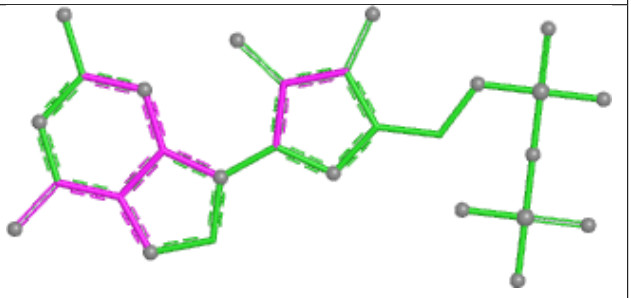

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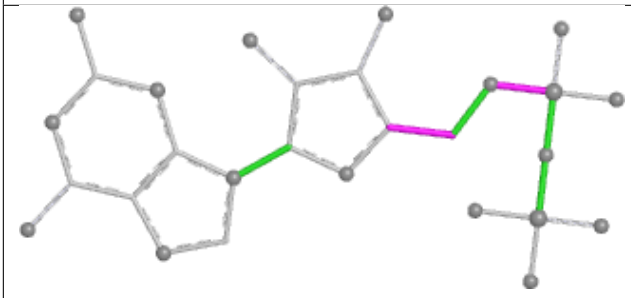

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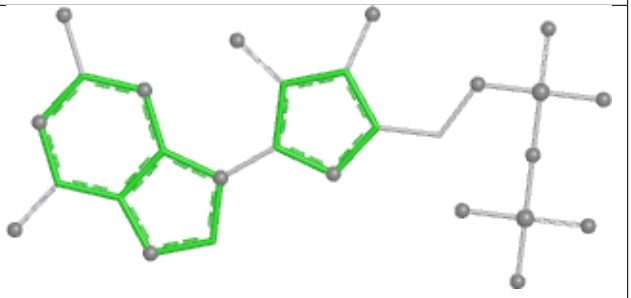
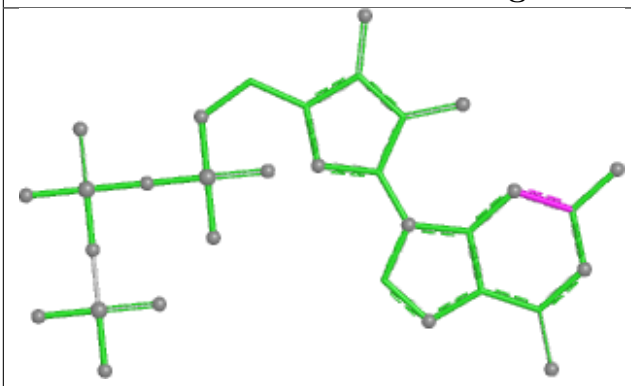


Rings

Ligand GTP CH 501



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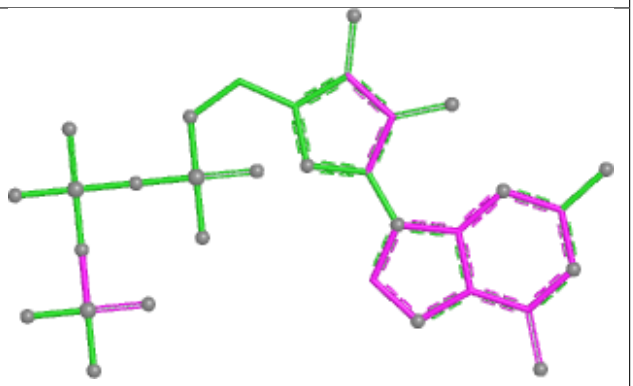

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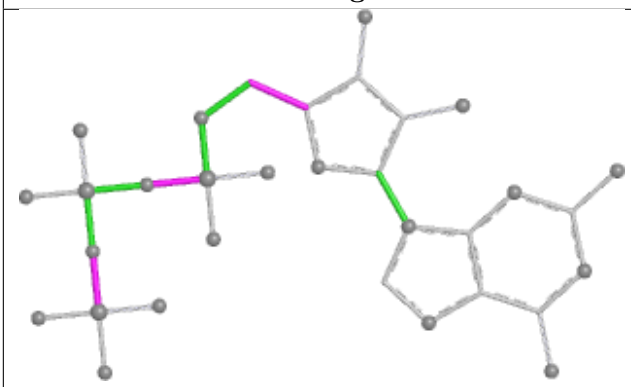

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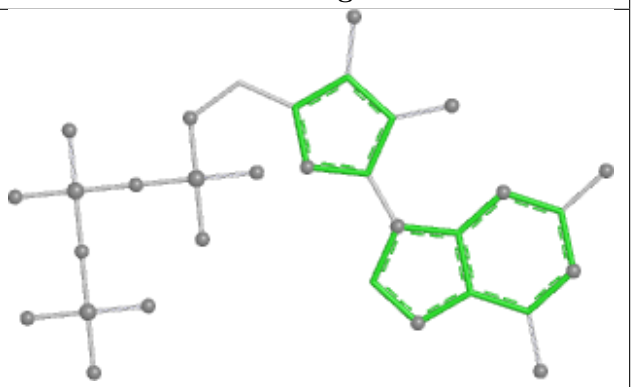
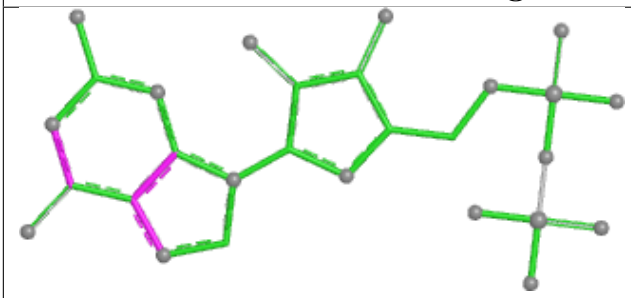


Rings

Ligand GDP RK 500



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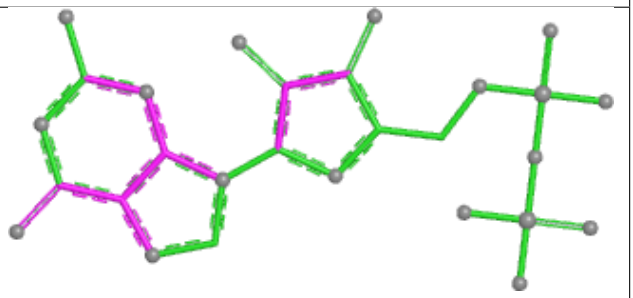

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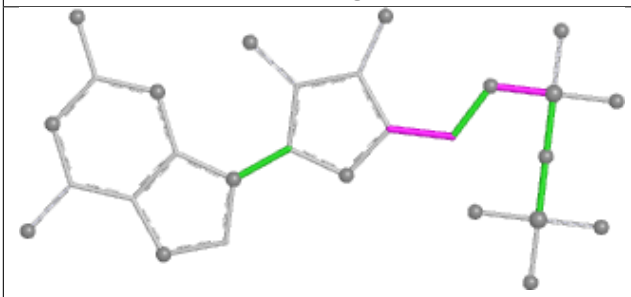

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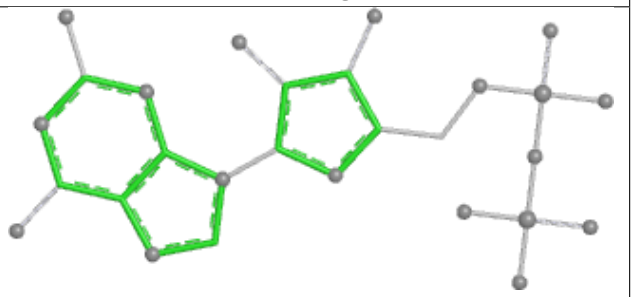
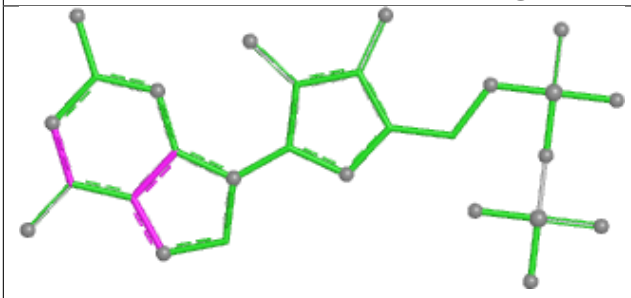


Rings

Ligand GDP LE 500



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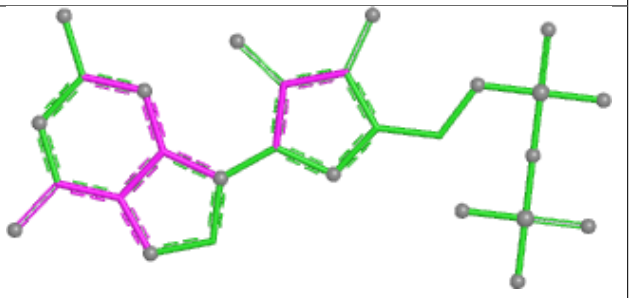
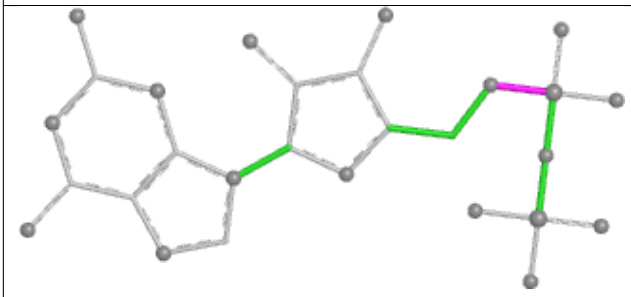


Bond angles



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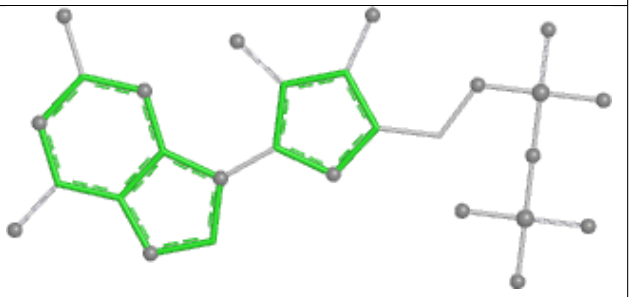
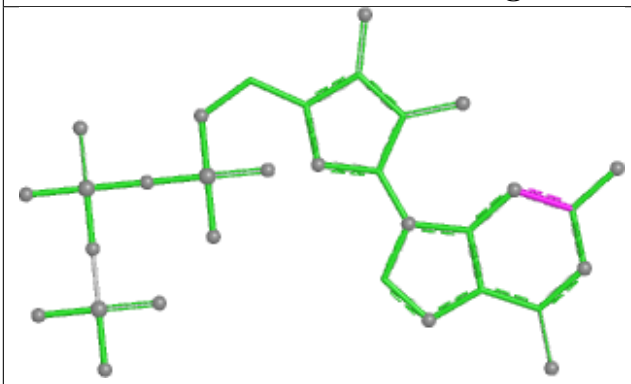


Rings

Ligand GTP WC 501



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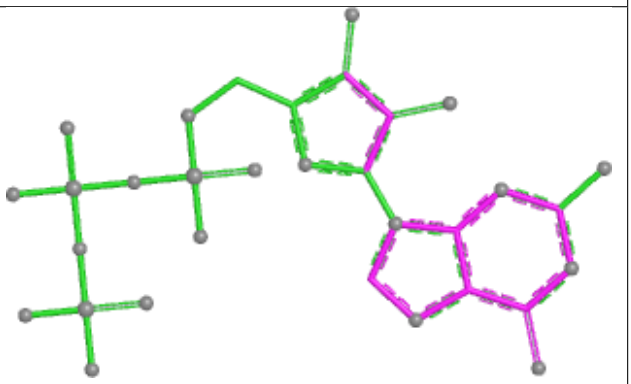

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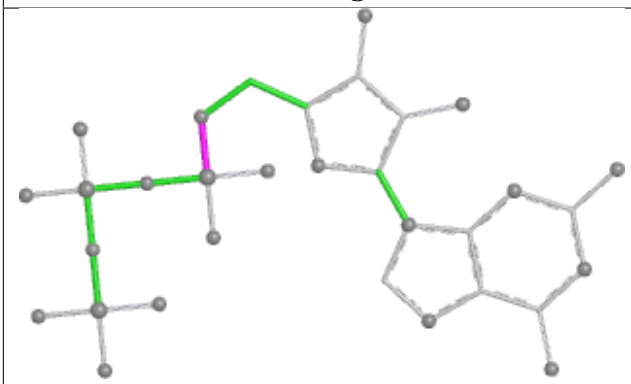
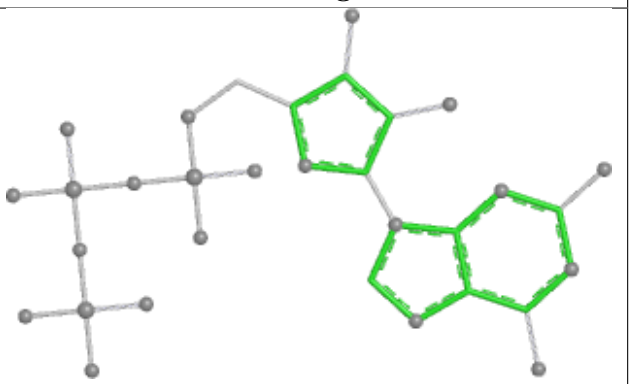
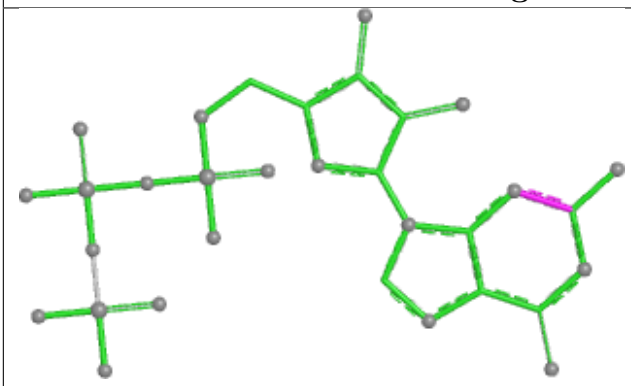


Torsions



Rings

Ligand GTP EC 501



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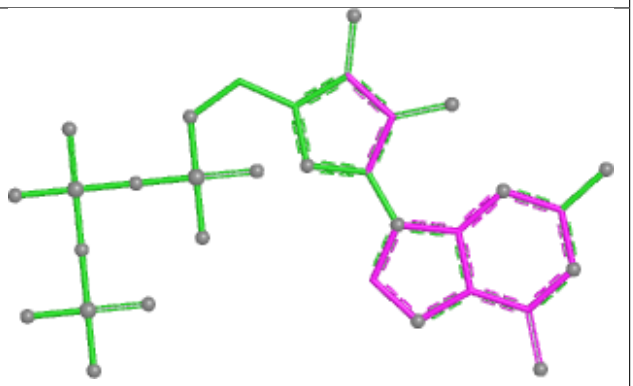

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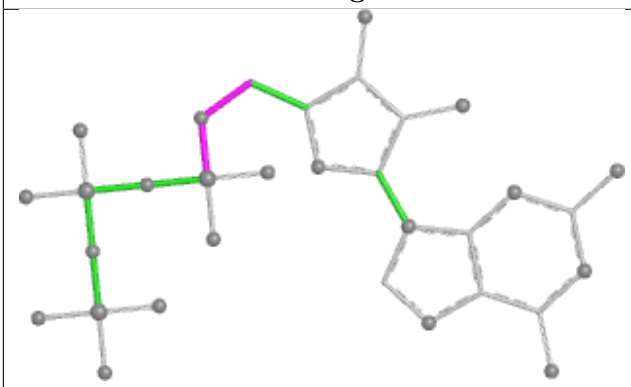

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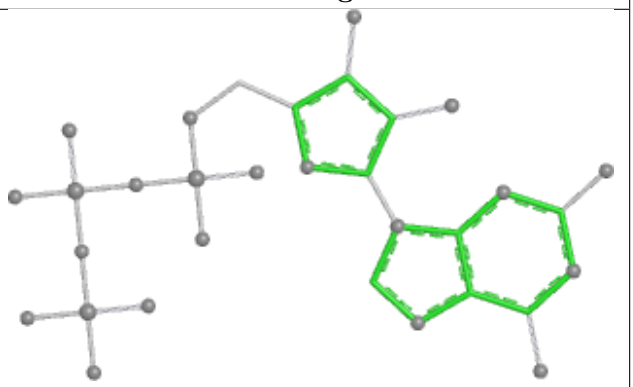
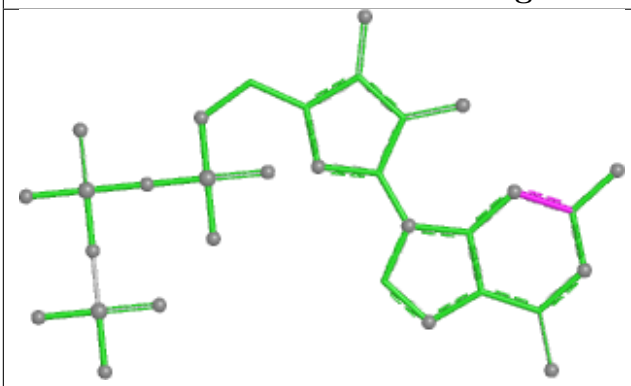


Rings

Ligand GTP NI 501



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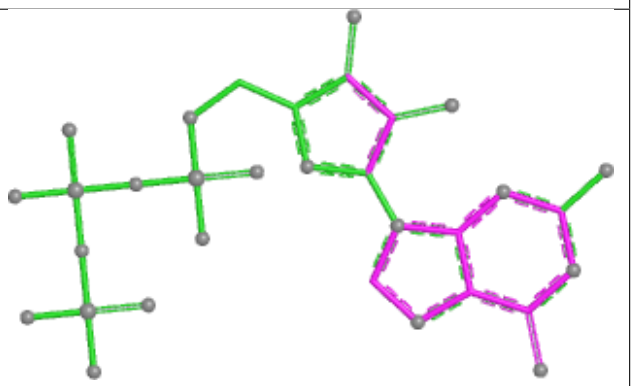

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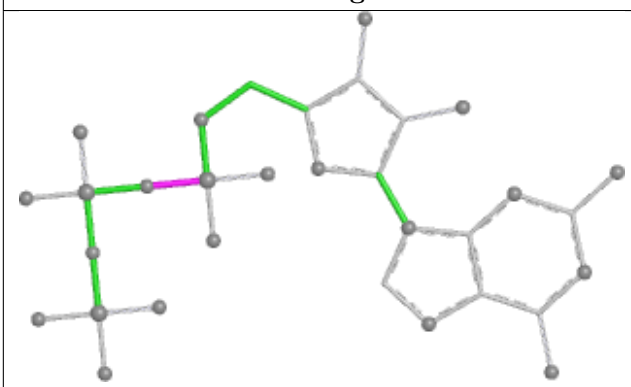

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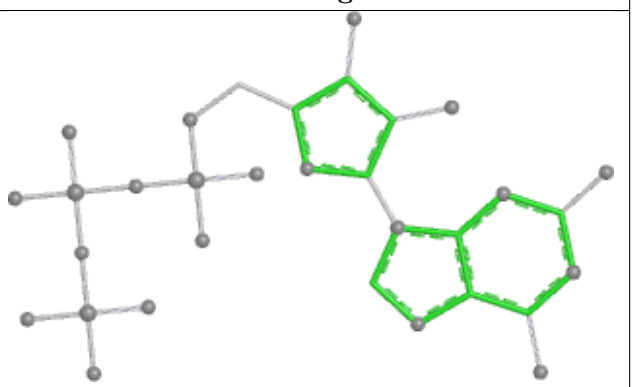

Rings

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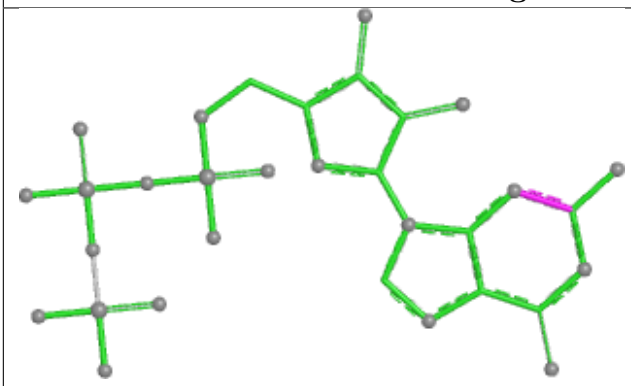

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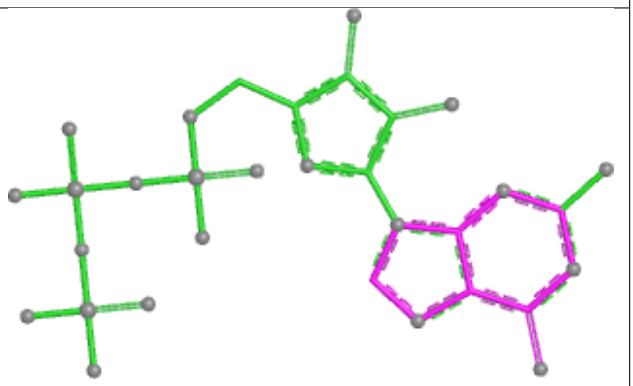

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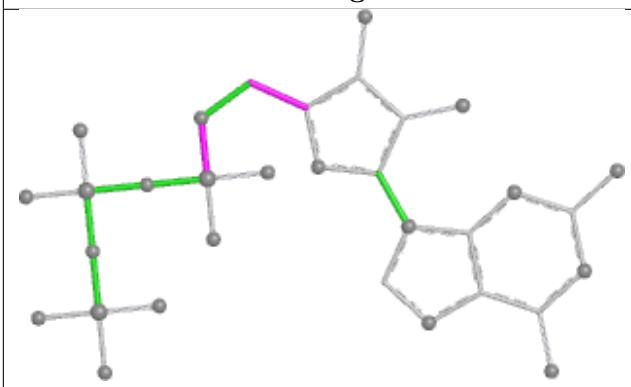

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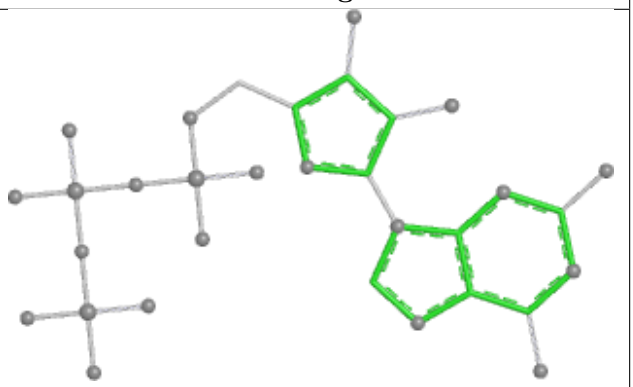
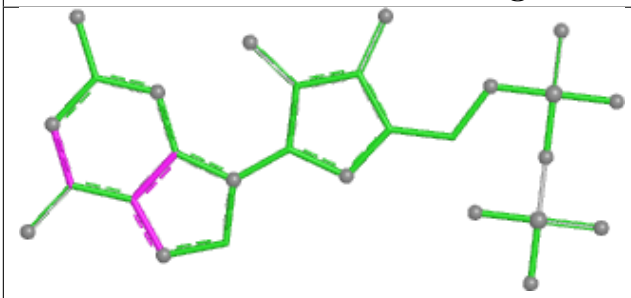


Rings

Ligand GDP NF 500



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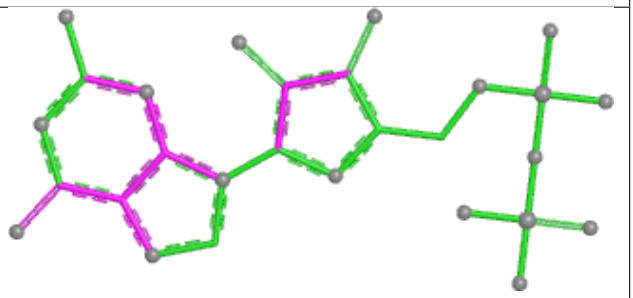

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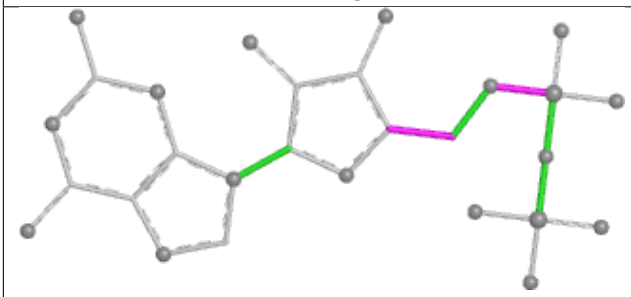

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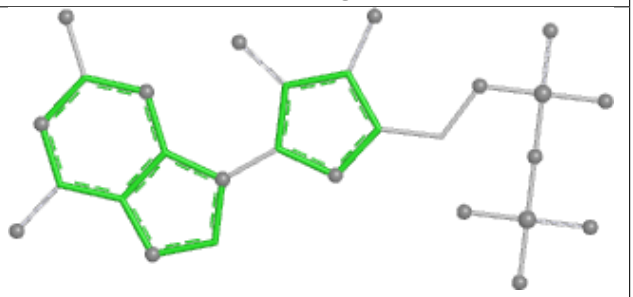
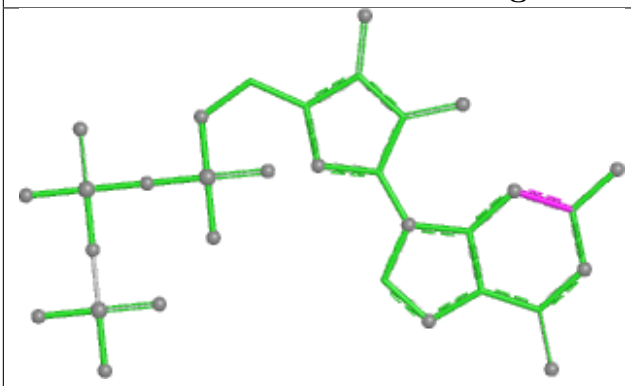


Rings

Ligand GTP AC 501



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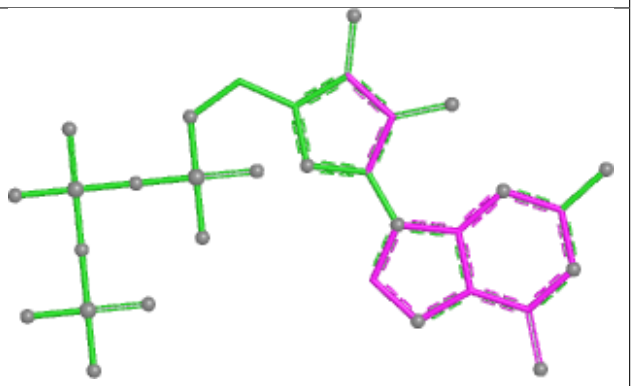

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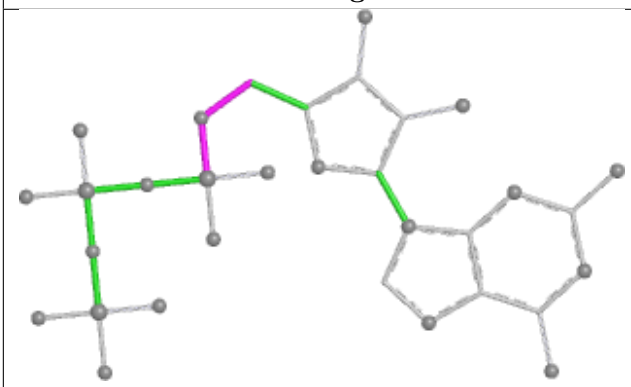

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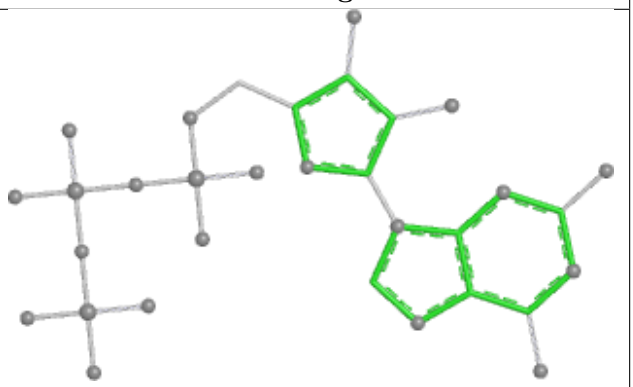

Rings

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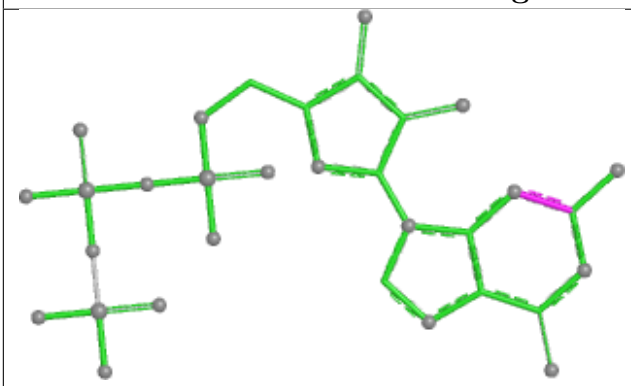

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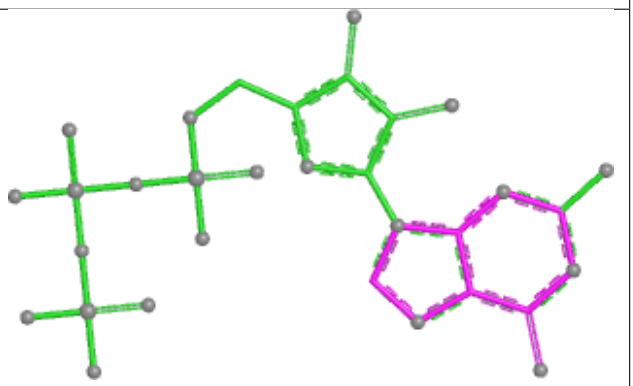

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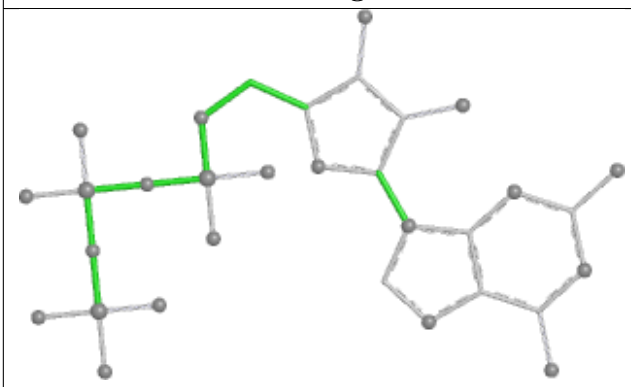

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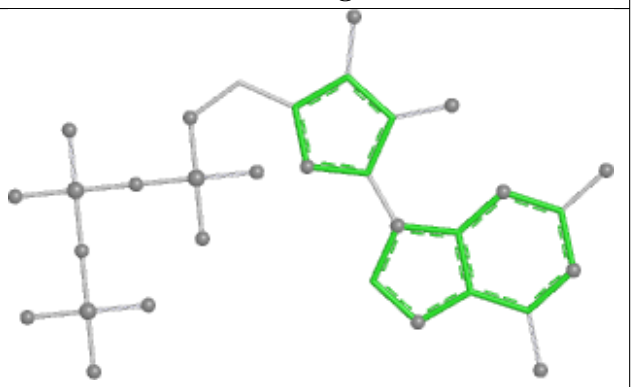

Rings

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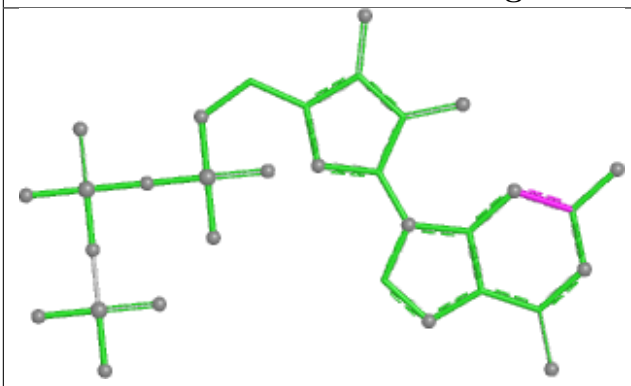

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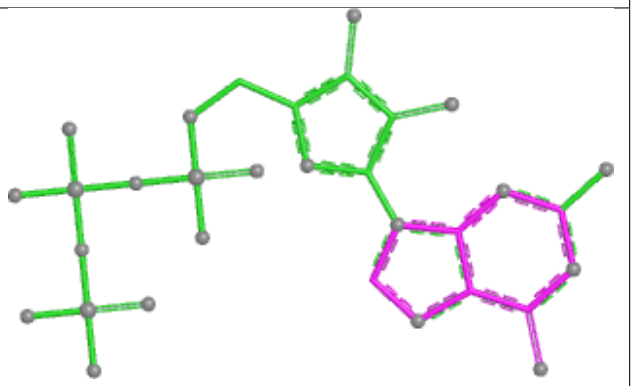

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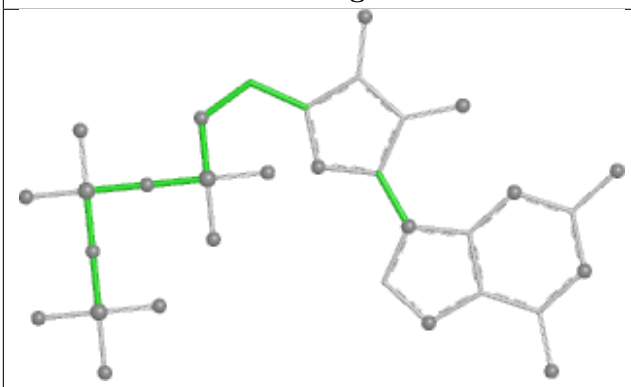

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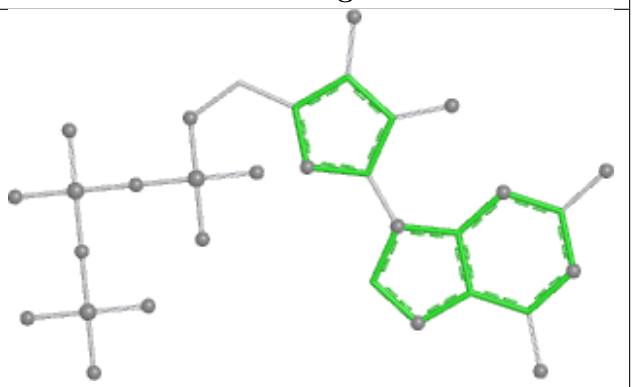
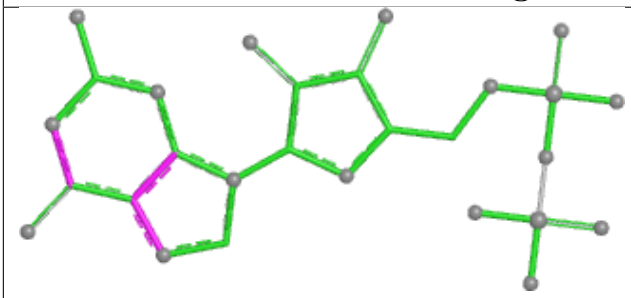


Rings

Ligand GDP FL 500



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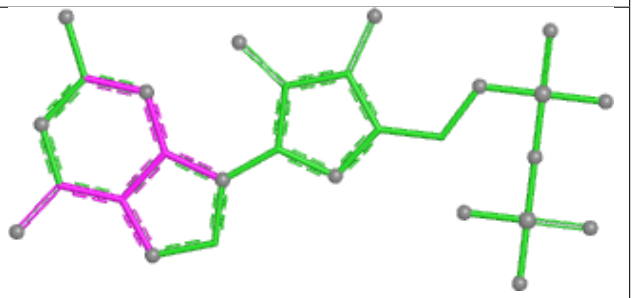

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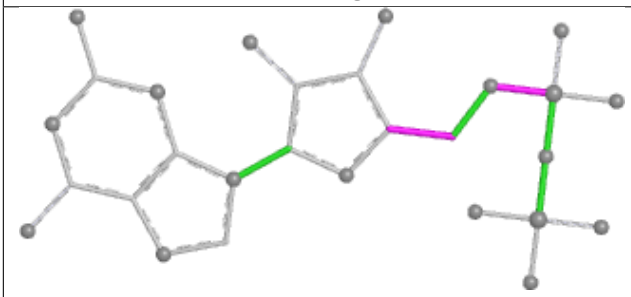

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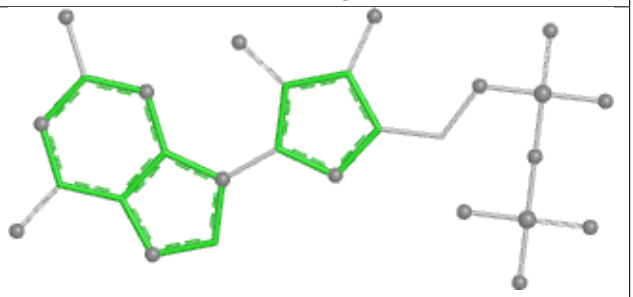

Rings

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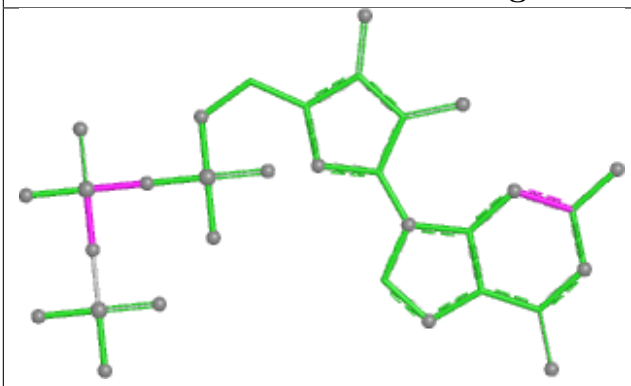

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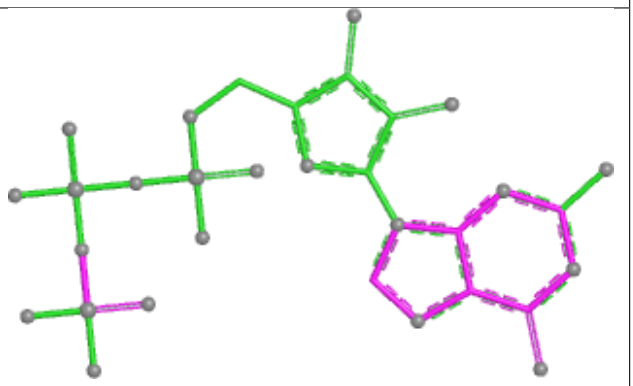

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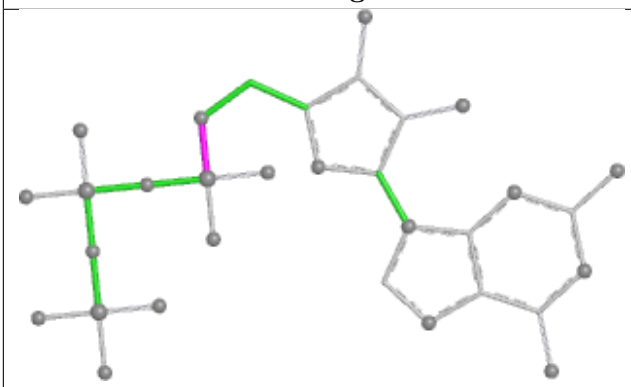

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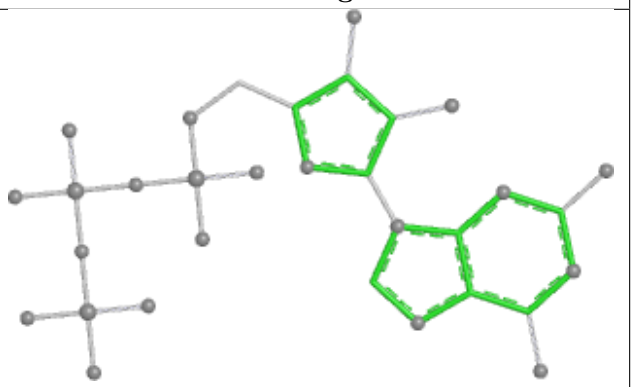
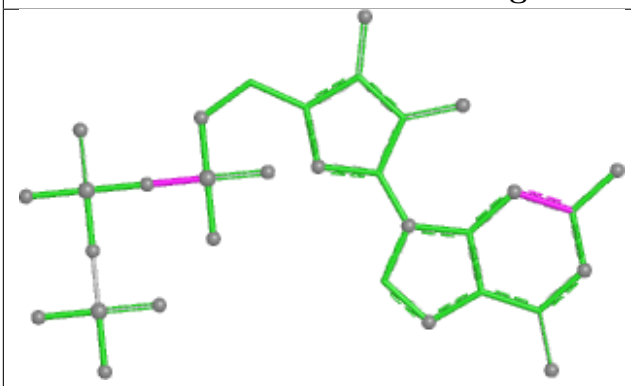


Rings

Ligand GTP RB 501



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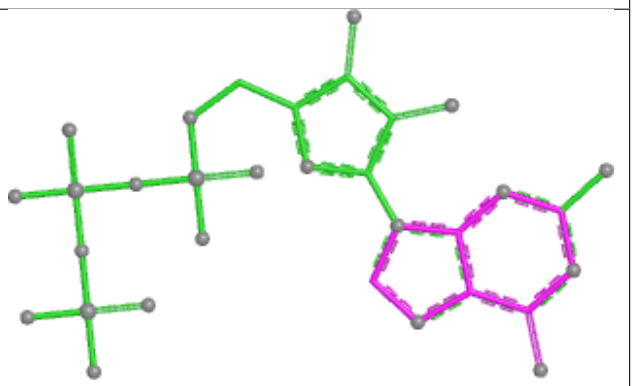

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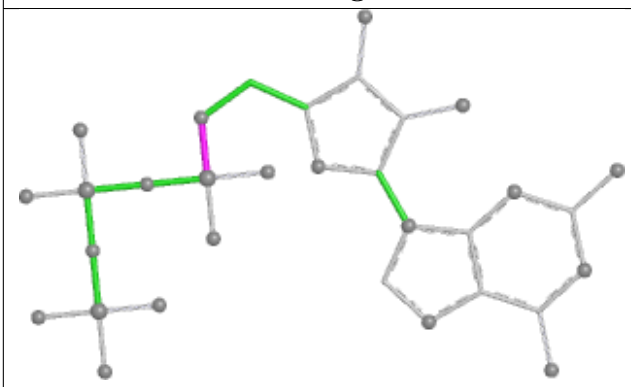

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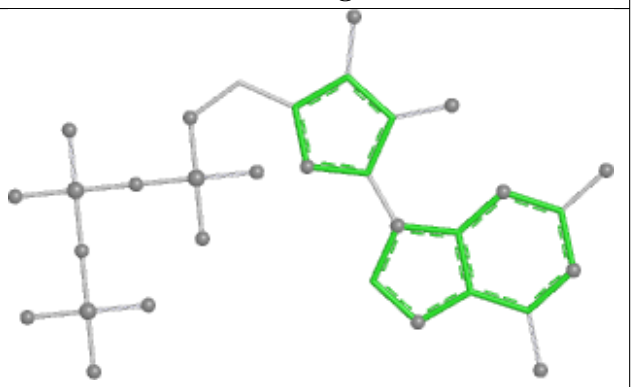
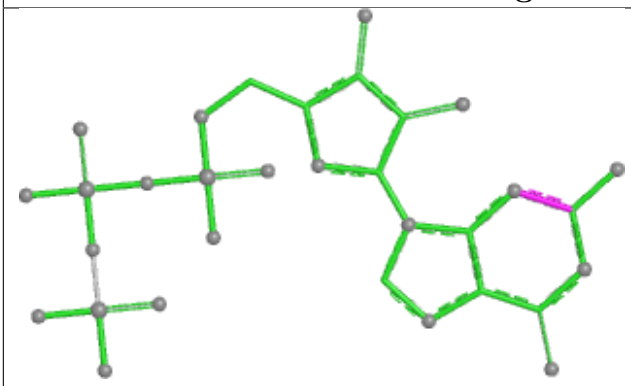


Rings

Ligand GTP VI 501



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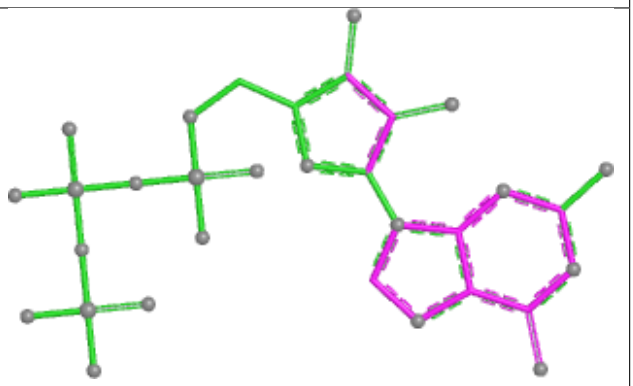

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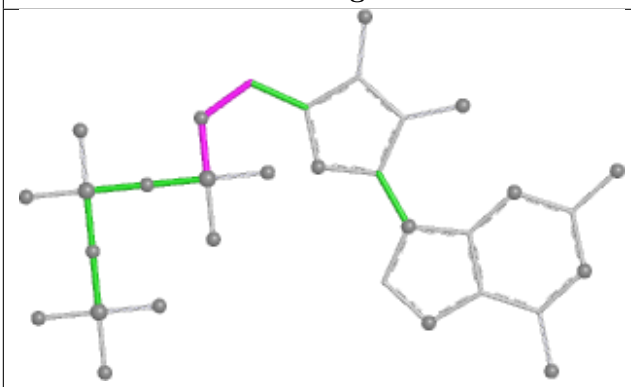

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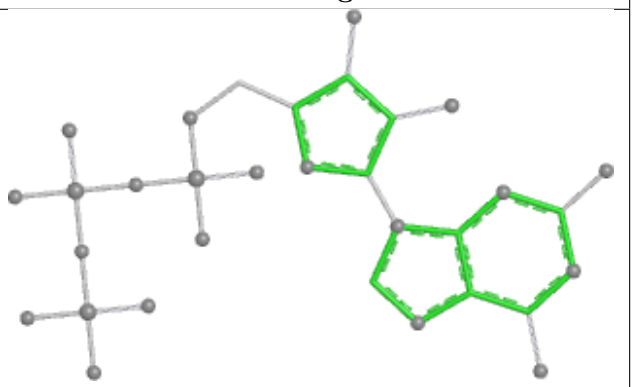
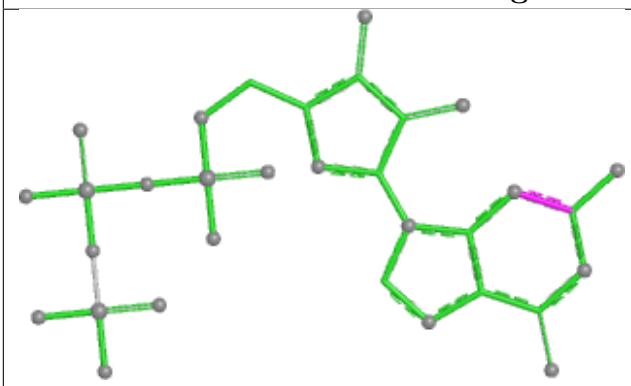


Rings

Ligand GTP FG 501



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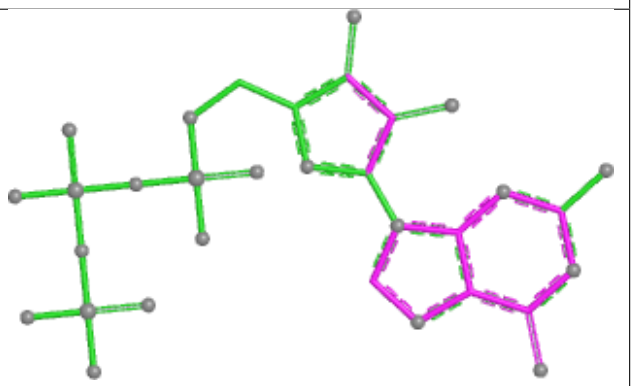
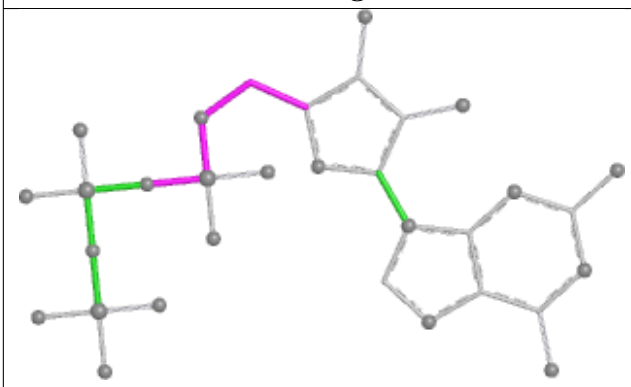


Bond angles



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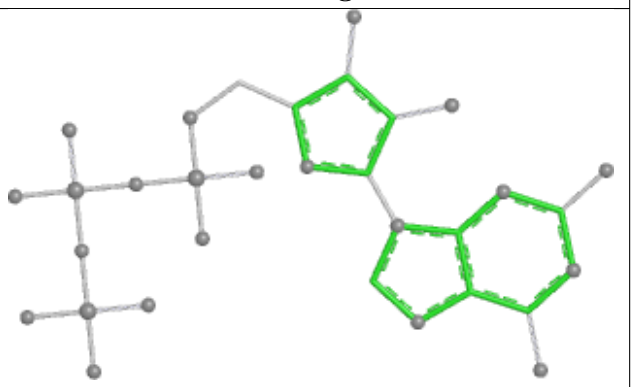
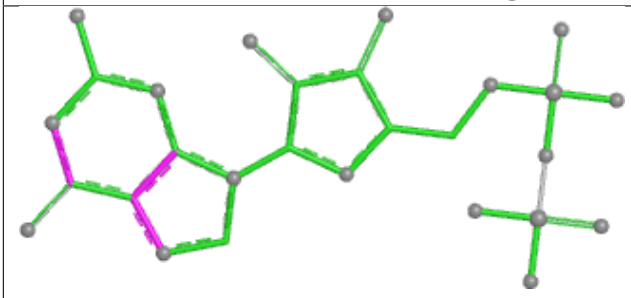


Rings

Ligand GDP MN 500



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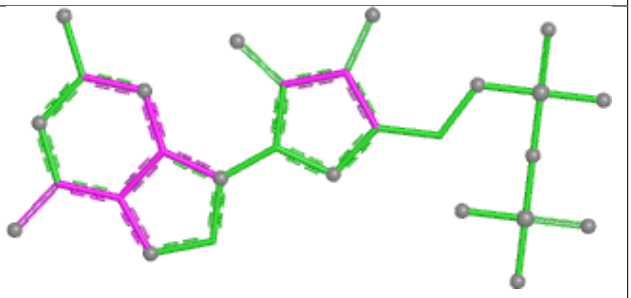

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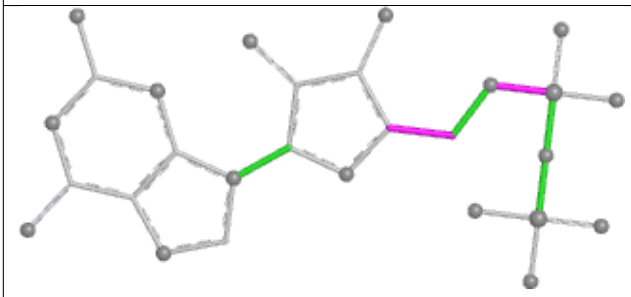

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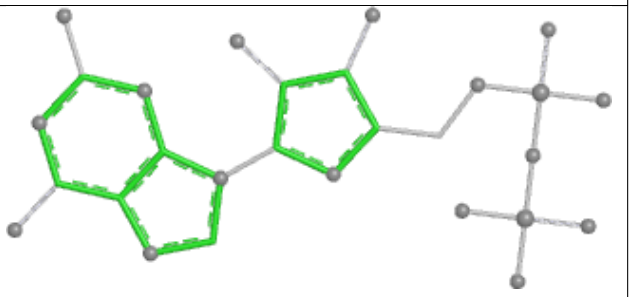
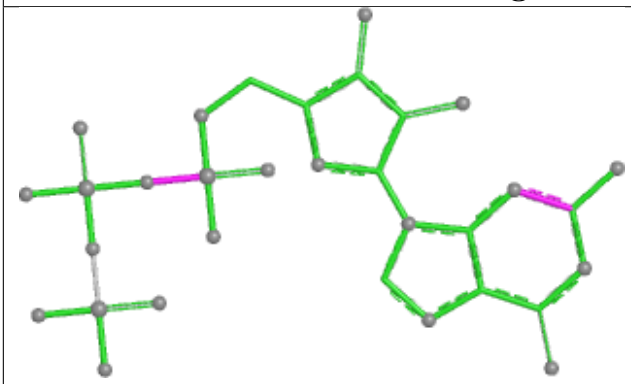


Rings

Ligand GTP BC 501



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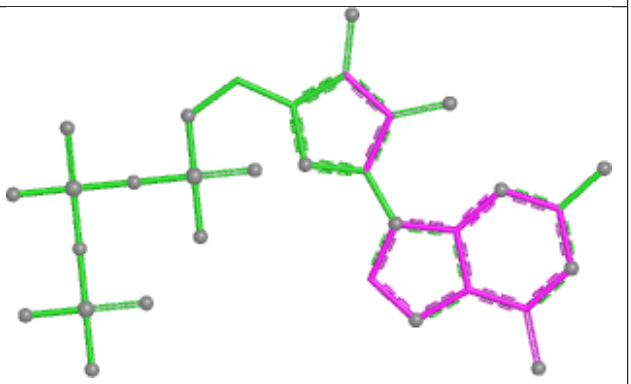

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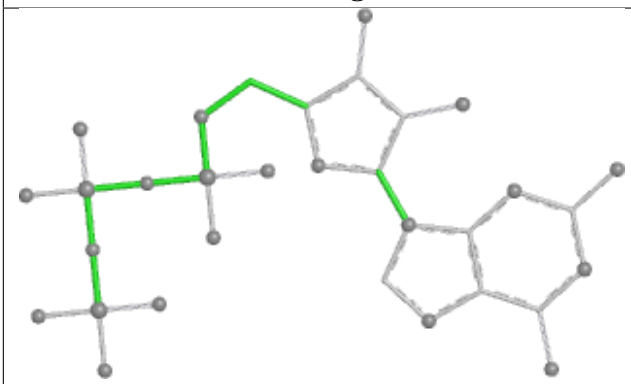

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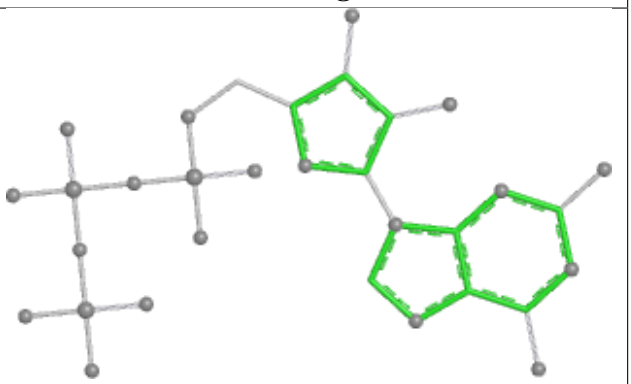
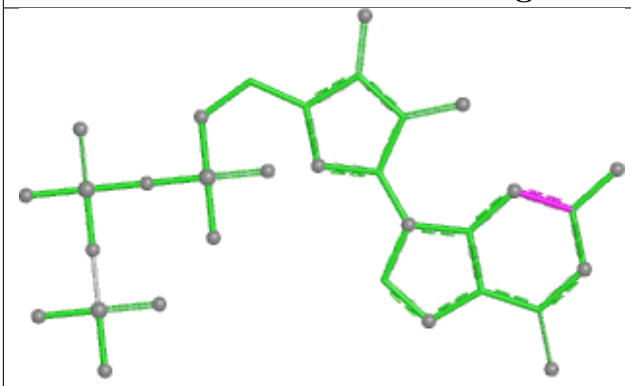


Rings

Ligand GTP AI 501



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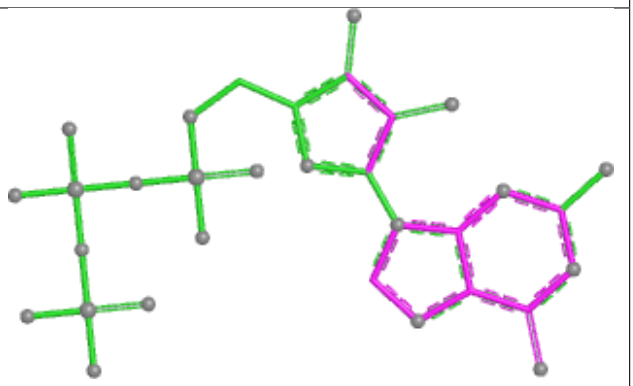

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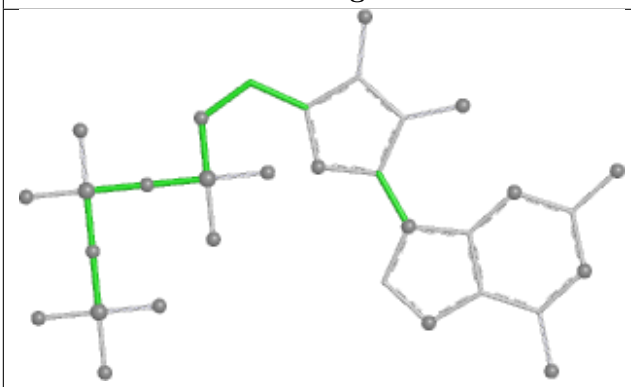

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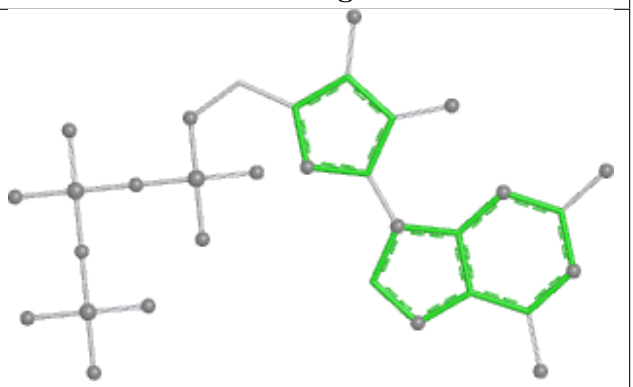
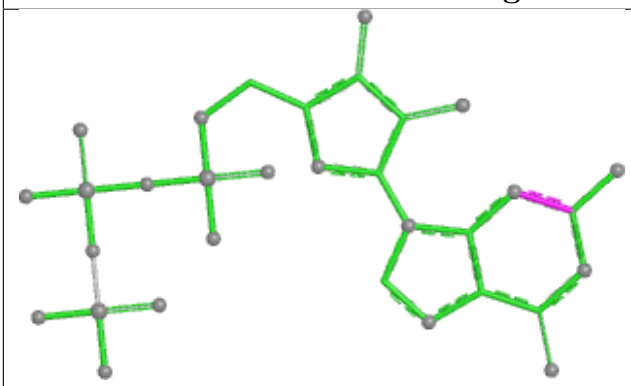


Rings

Ligand GTP WK 501



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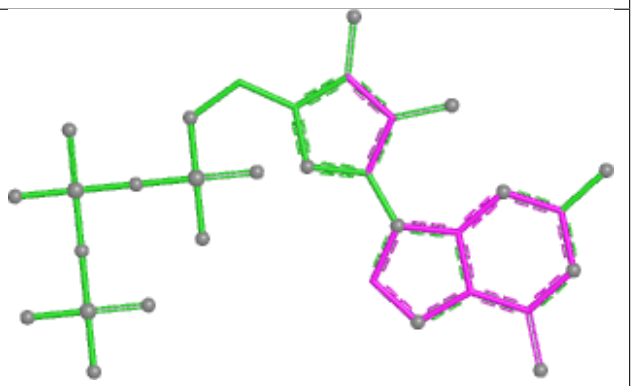

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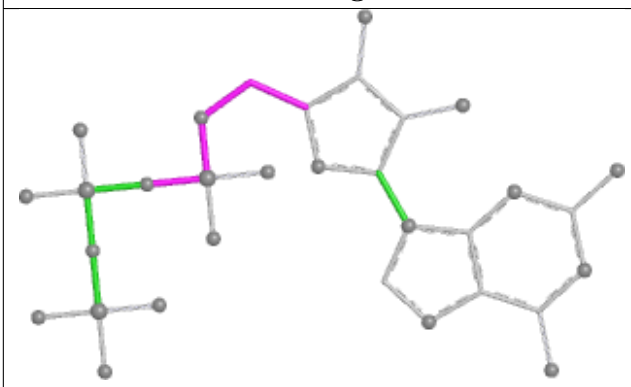

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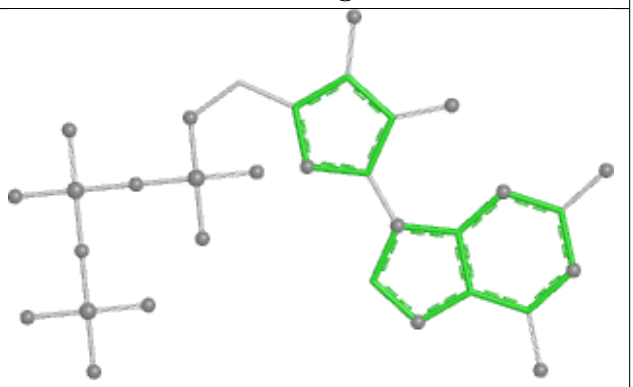
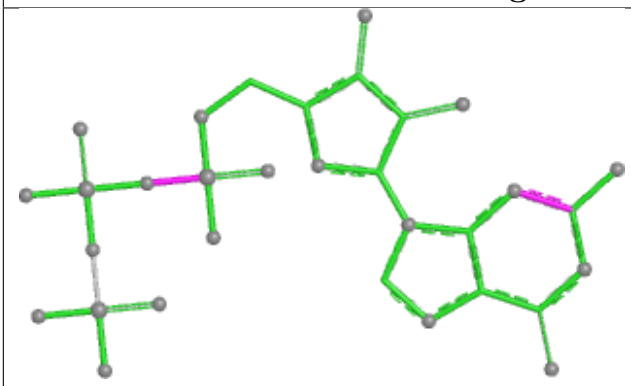


Rings

Ligand GTP QB 501



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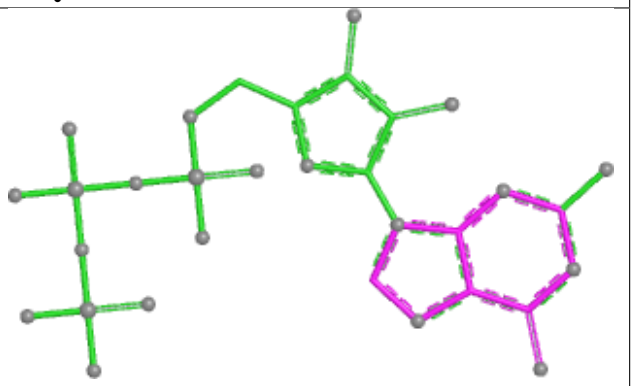

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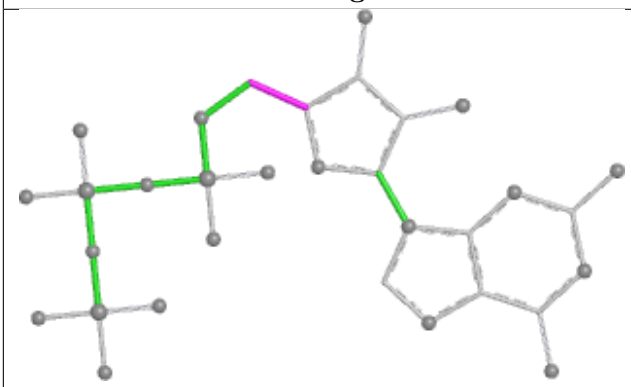

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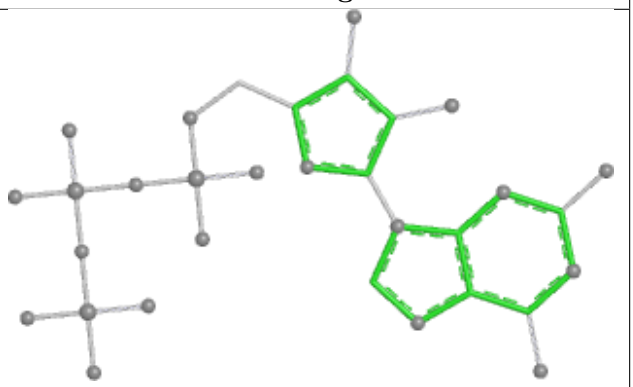
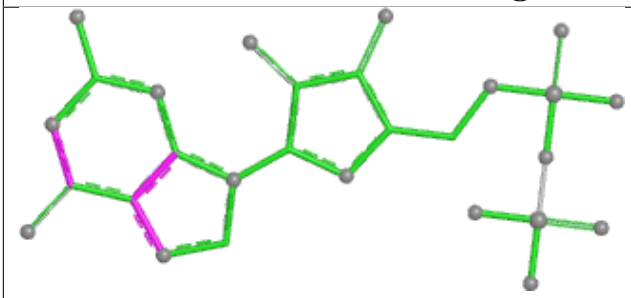


Rings

Ligand GDP EF 500



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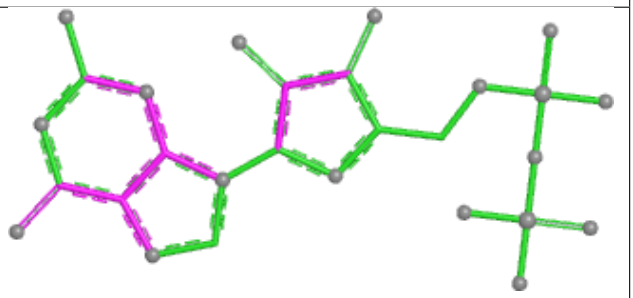

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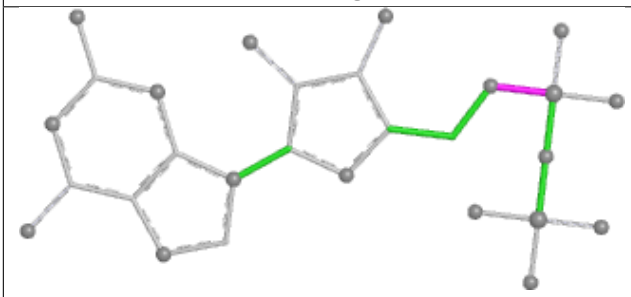

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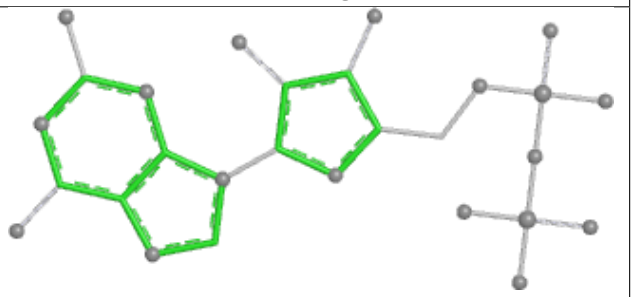
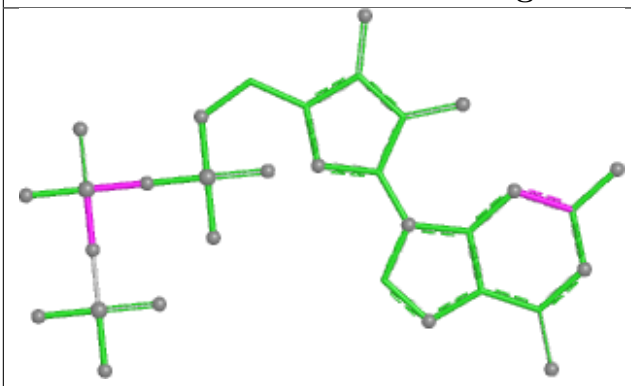


Rings

Ligand GTP BI 501



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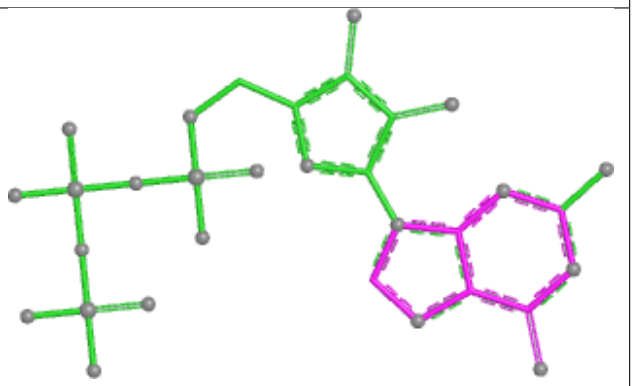

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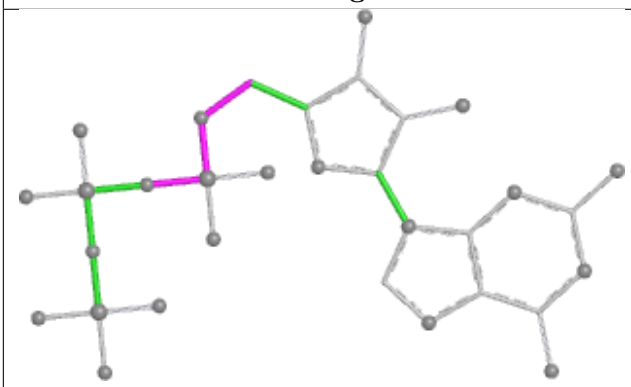

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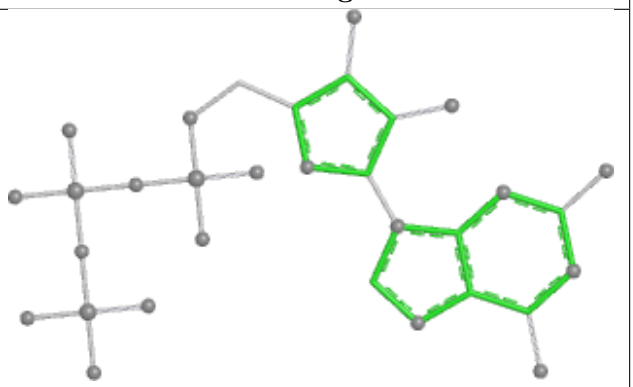
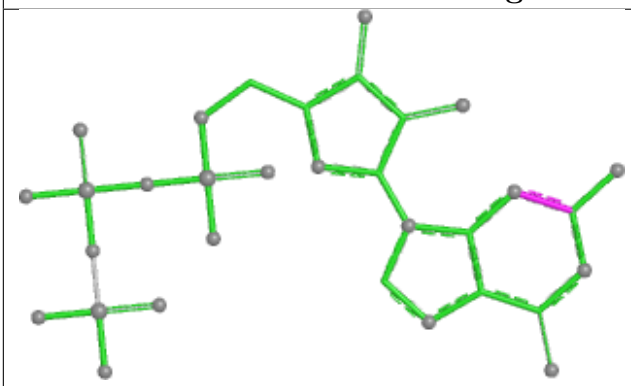


Rings

Ligand GTP MC 501



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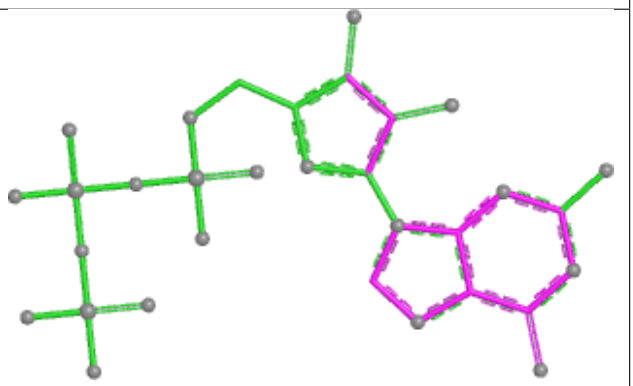

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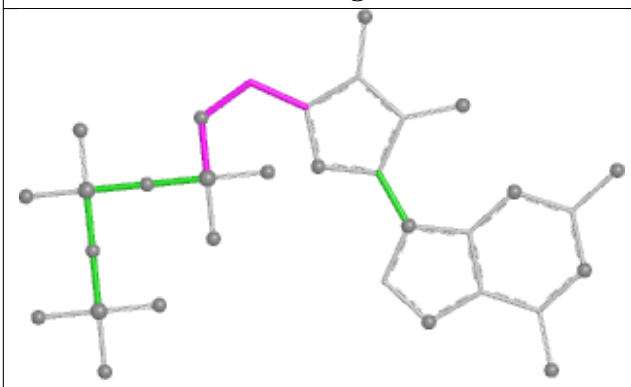

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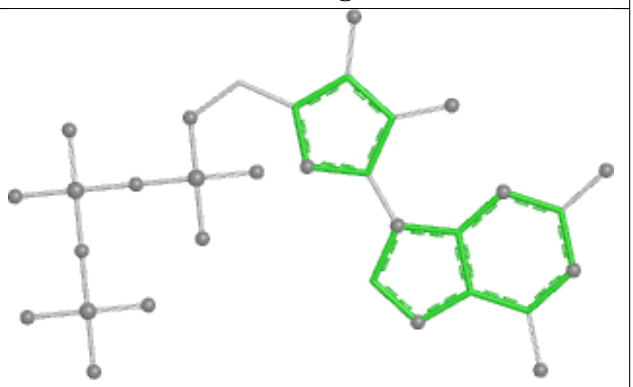
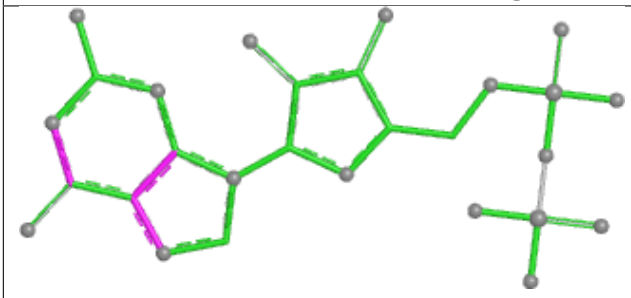


Rings

Ligand GDP UB 500



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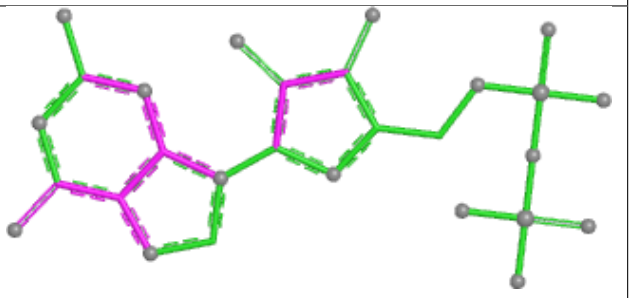

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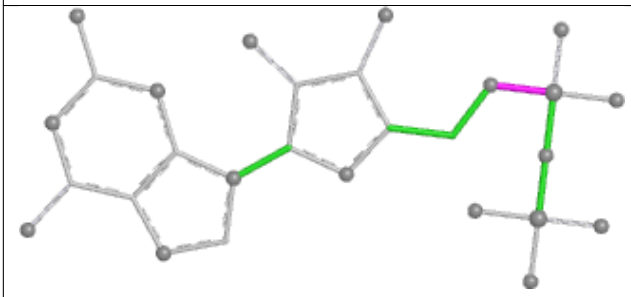

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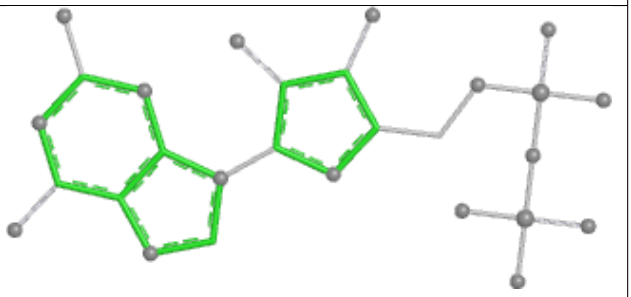
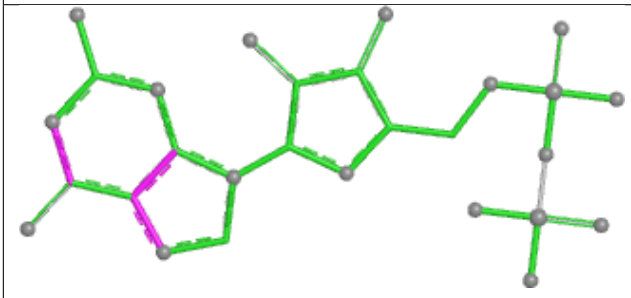


Rings

Ligand GDP I 500



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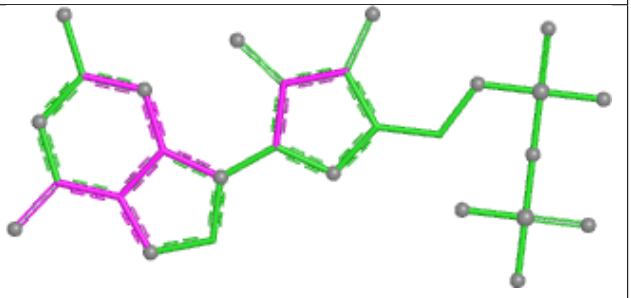

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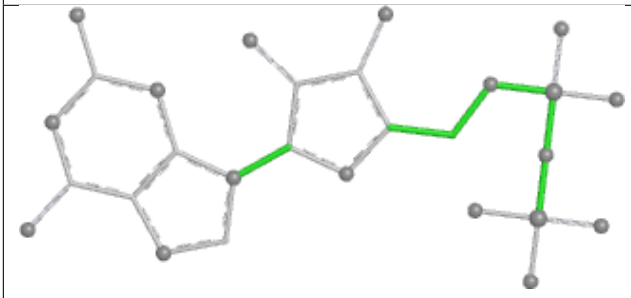

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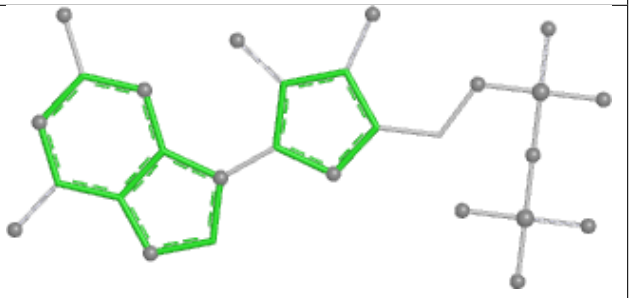
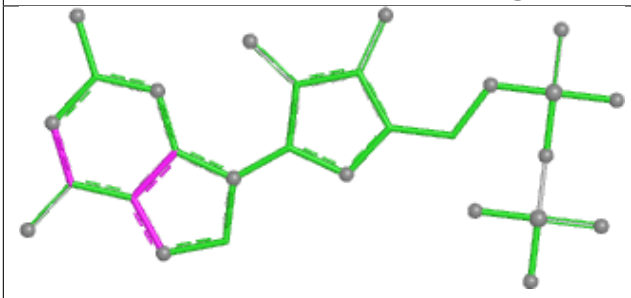


Rings

Ligand GDP ED 500



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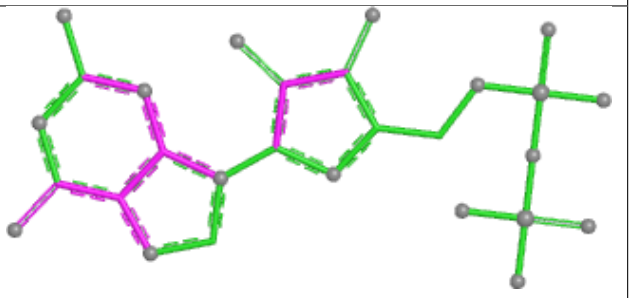

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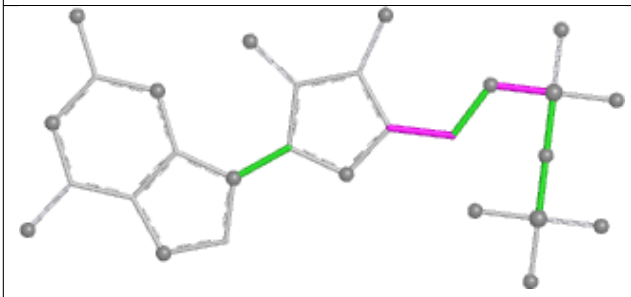

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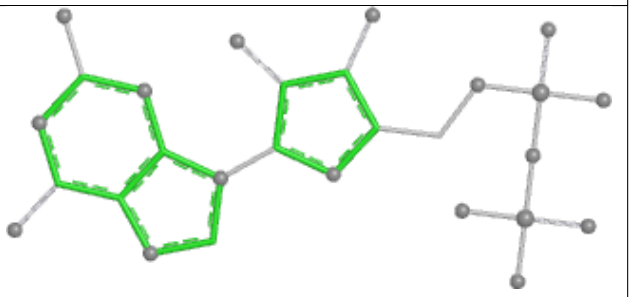
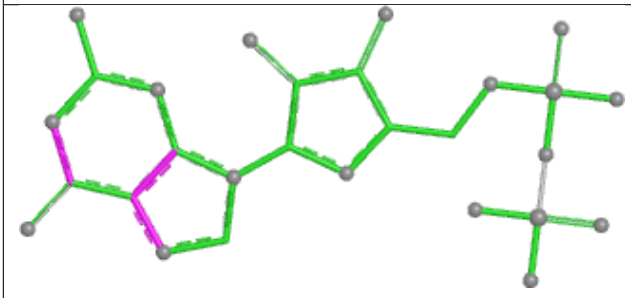


Rings

Ligand GDP T 500



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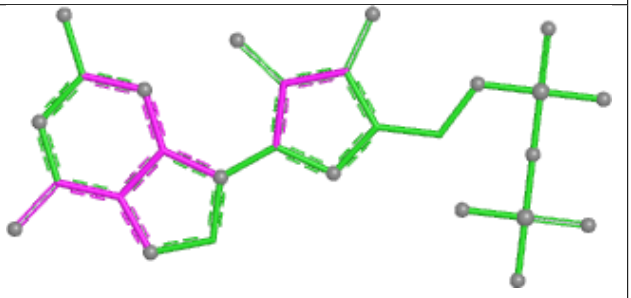

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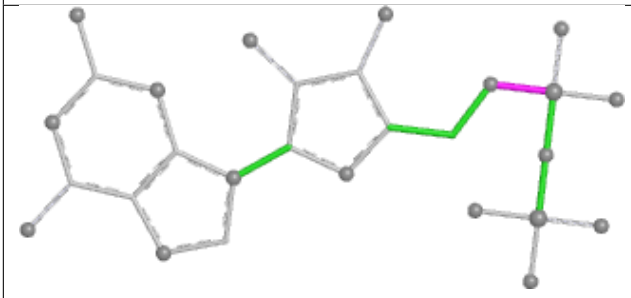

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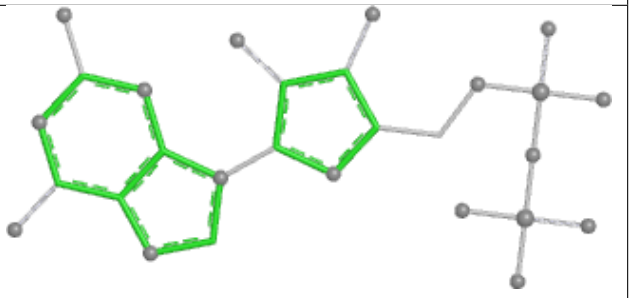
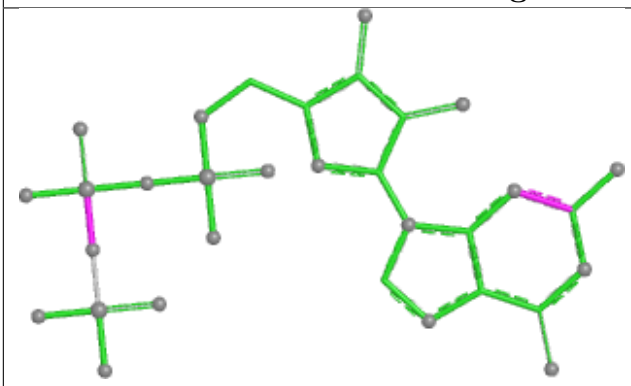


Rings

Ligand GTP VC 501



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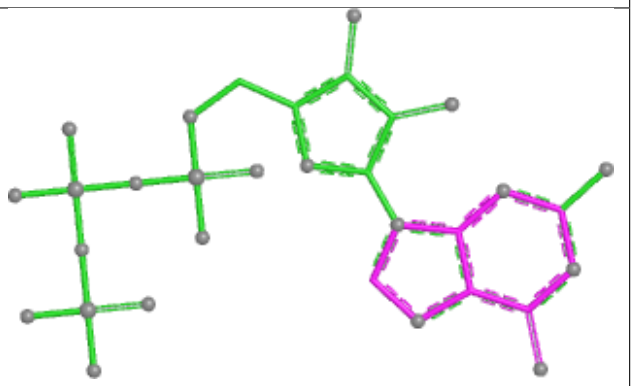

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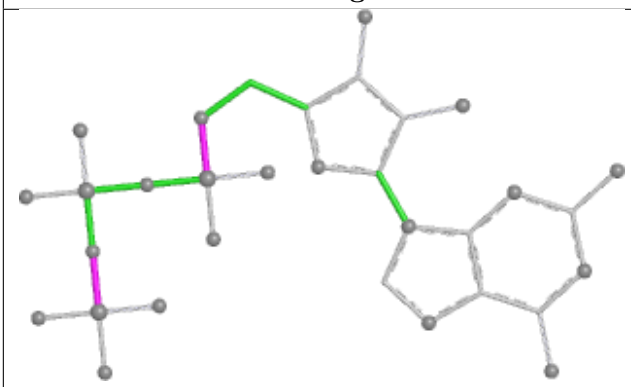

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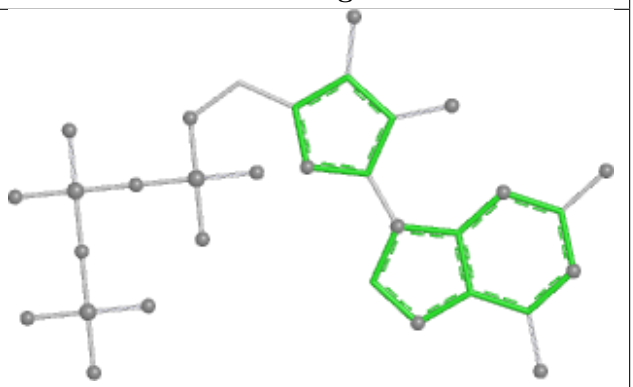
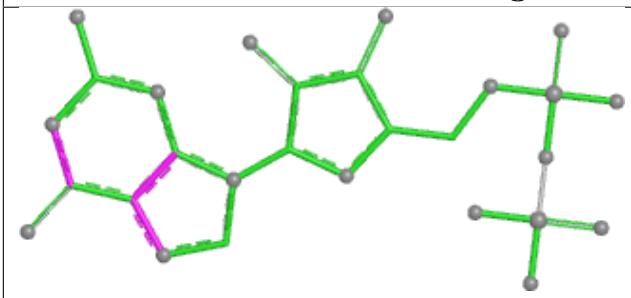


Rings

Ligand GDP DE 500



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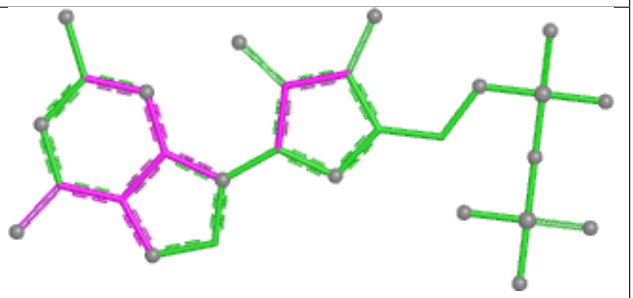

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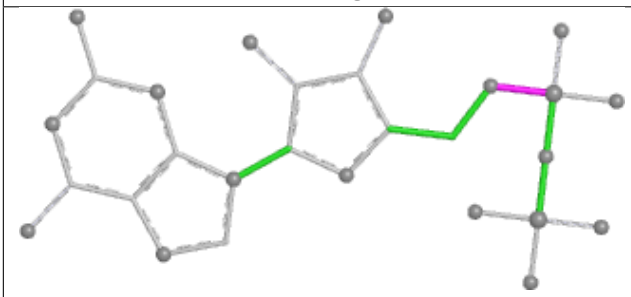

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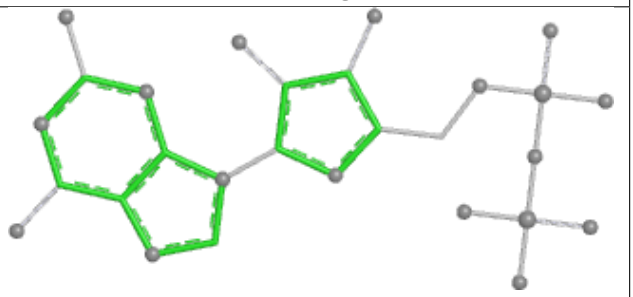
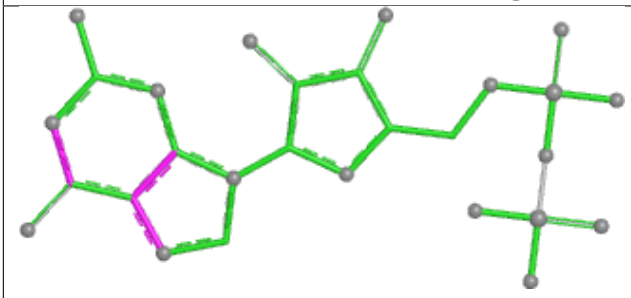


Rings

Ligand GDP CK 500



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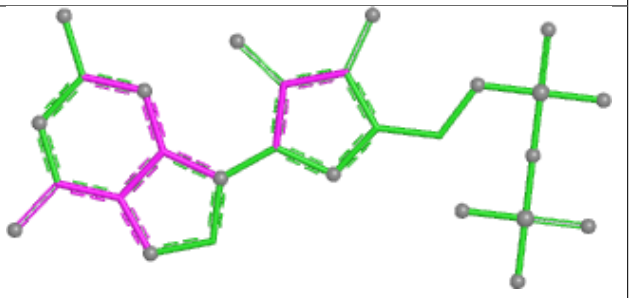

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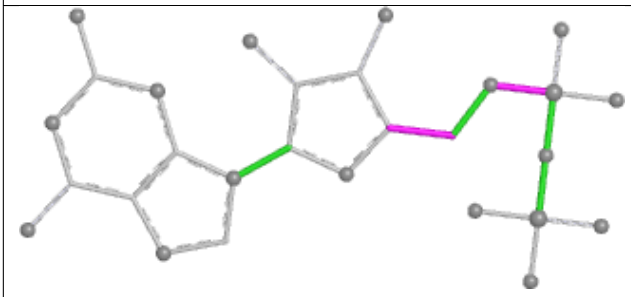

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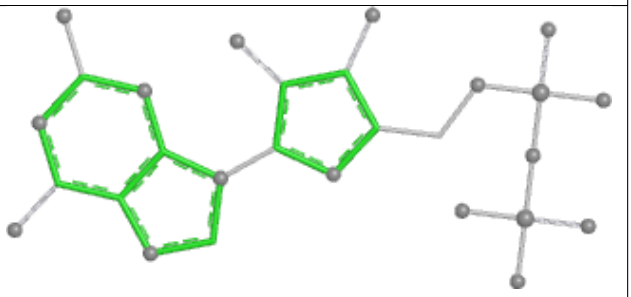
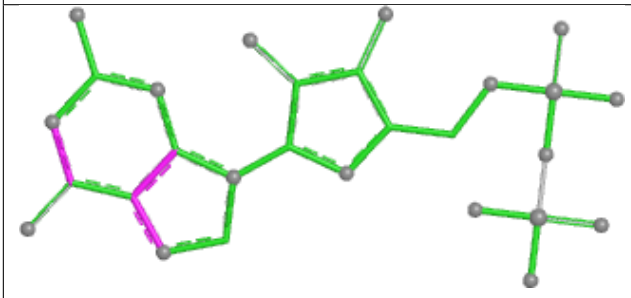


Rings

Ligand GDP IJ 500



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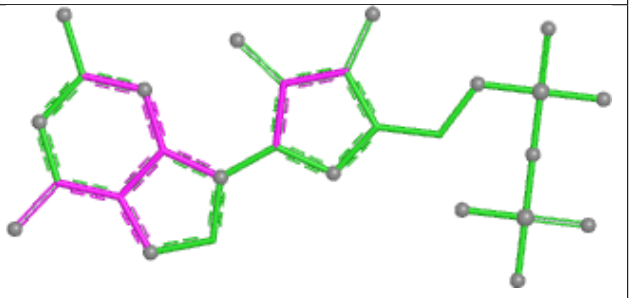

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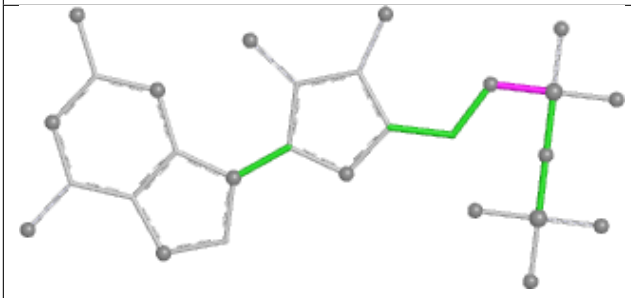
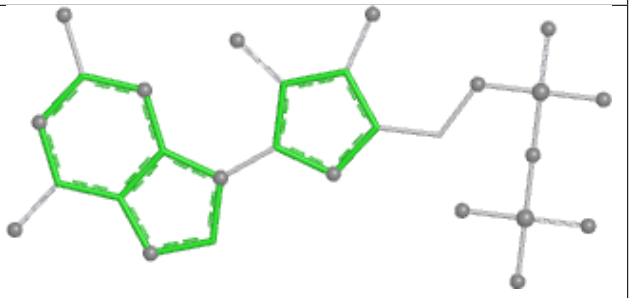
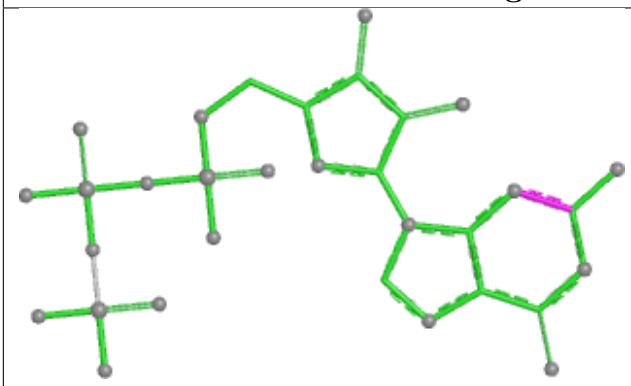


Torsions



Rings

Ligand GTP VM 501



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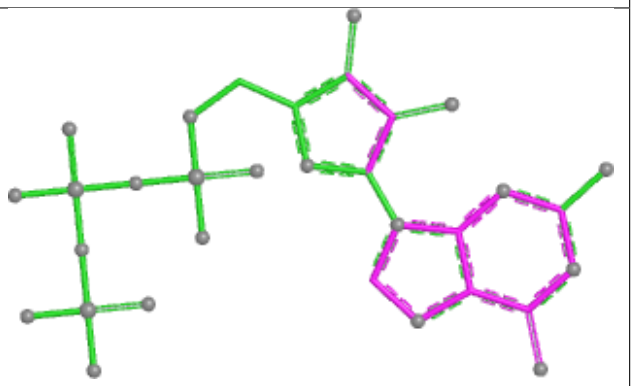

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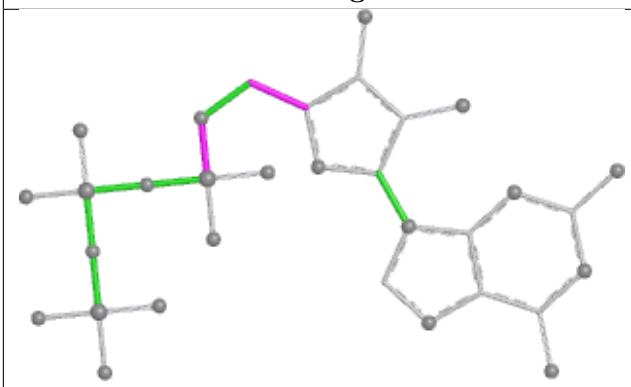

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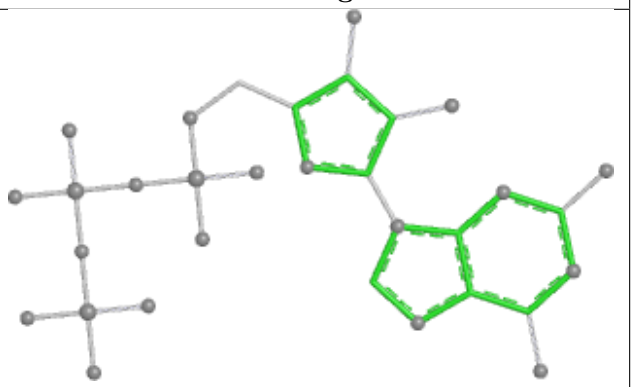
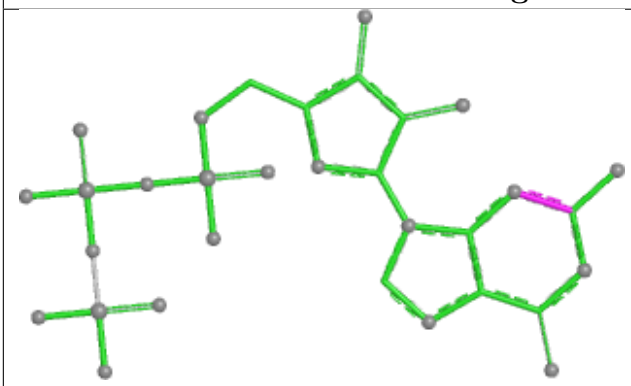


Rings

Ligand GTP BE 501



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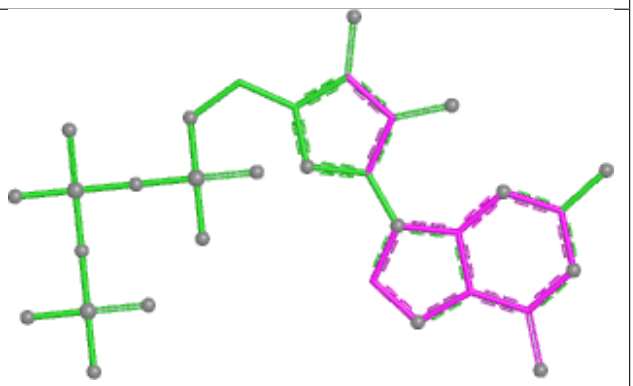

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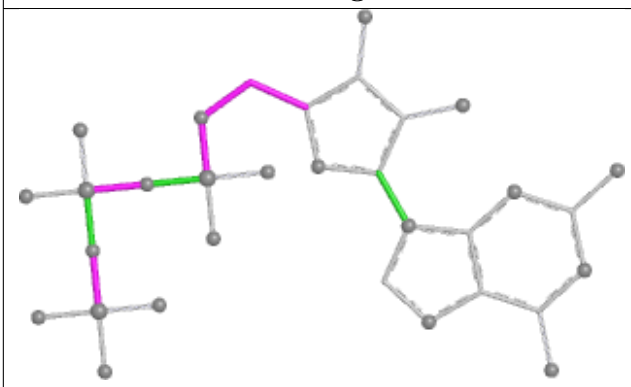

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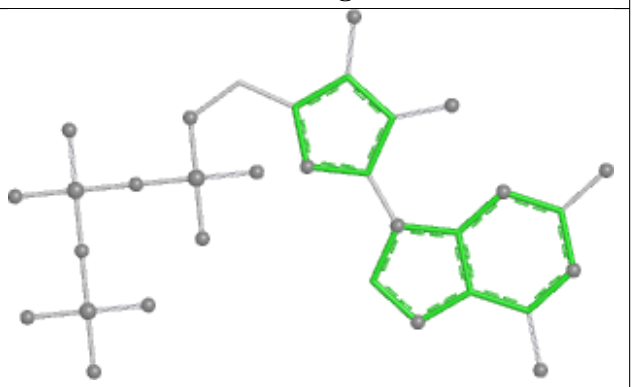
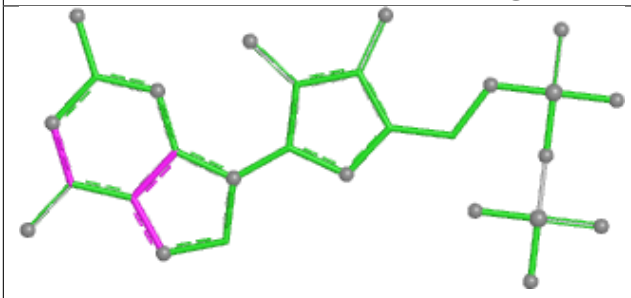


Rings

Ligand GDP CG 500



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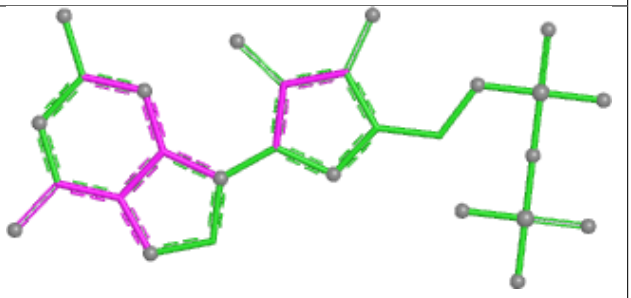

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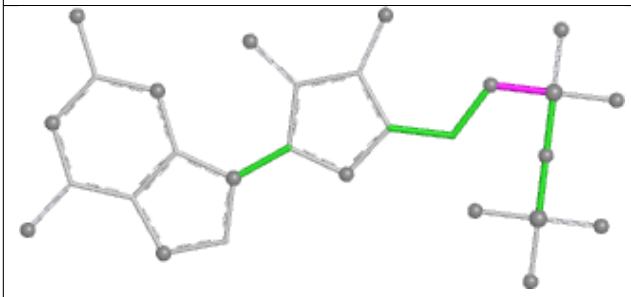

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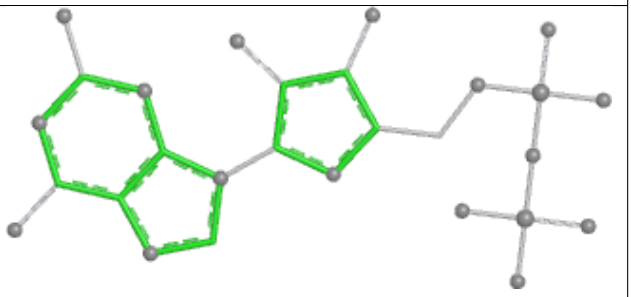

Rings

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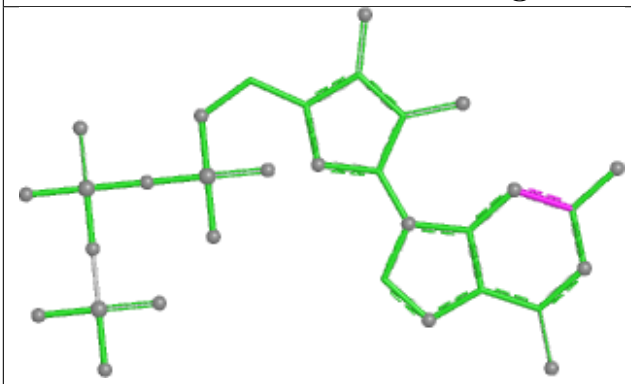

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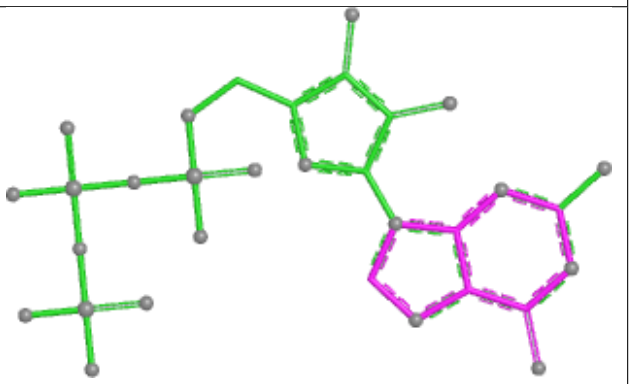

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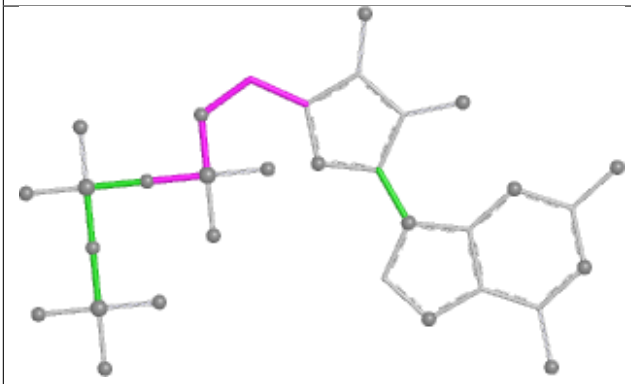

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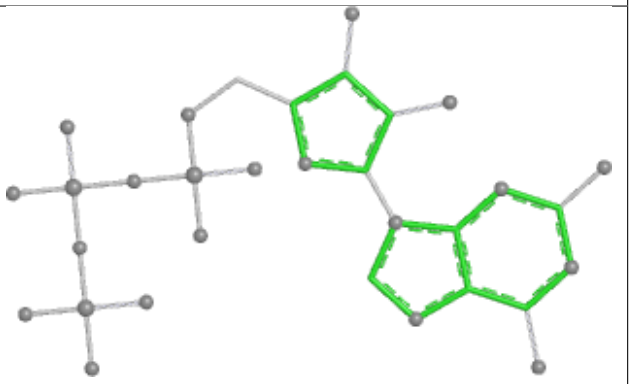
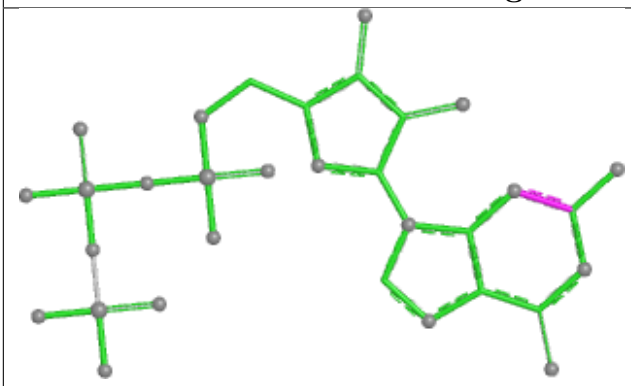


Rings

Ligand GTP WE 501



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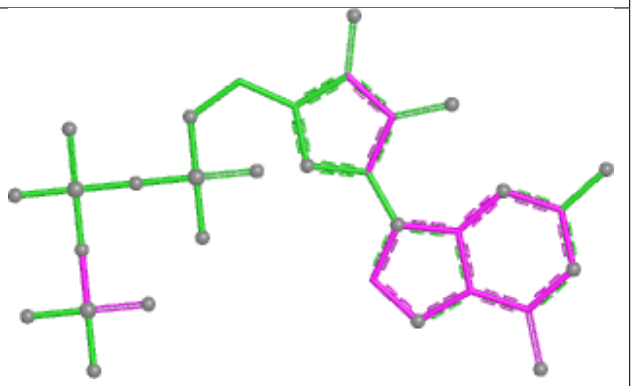

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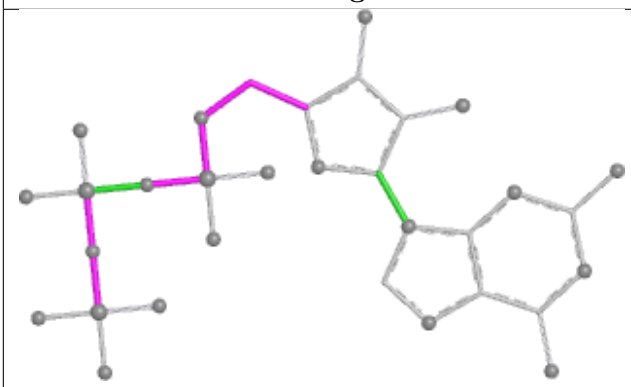

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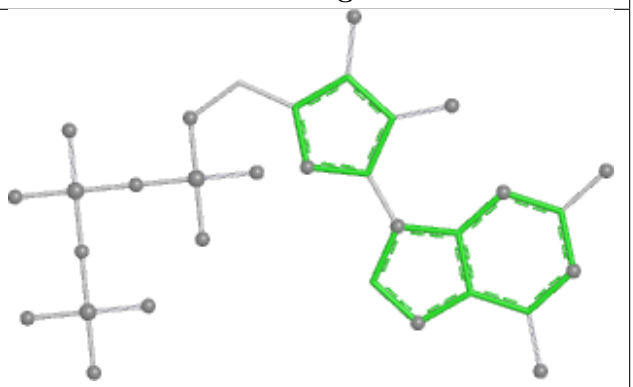
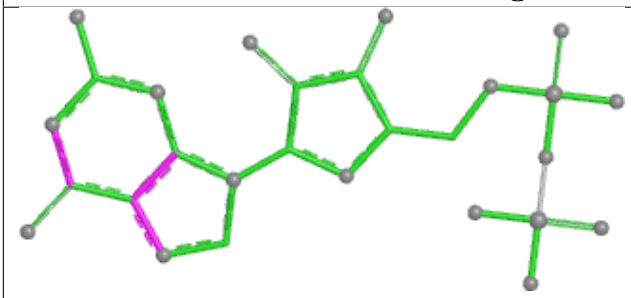


Rings

Ligand GDP TB 500



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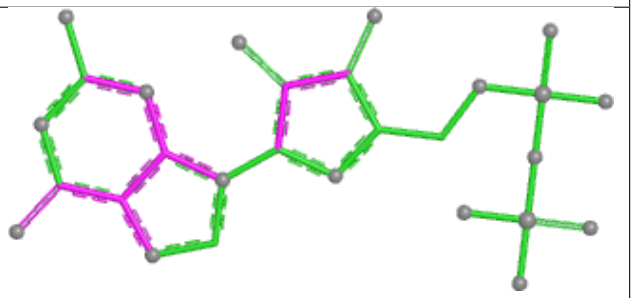

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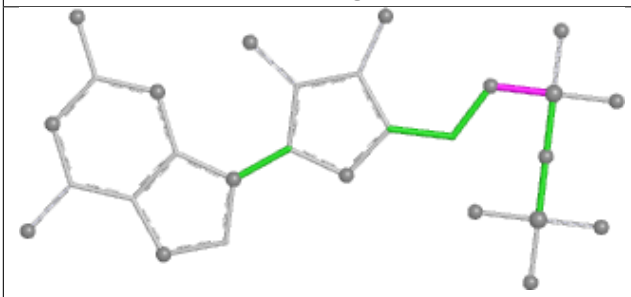

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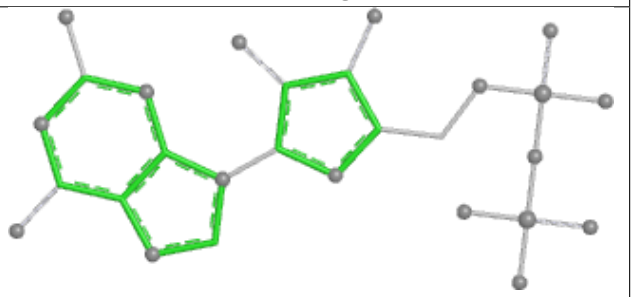
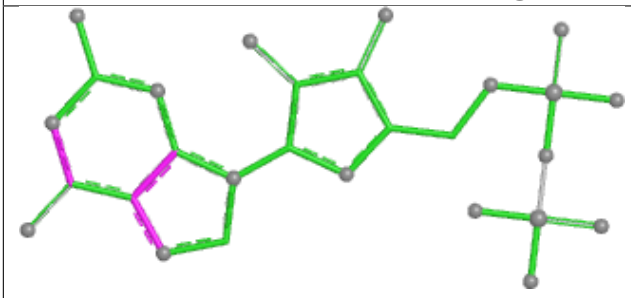


Rings

Ligand GDP JK 500



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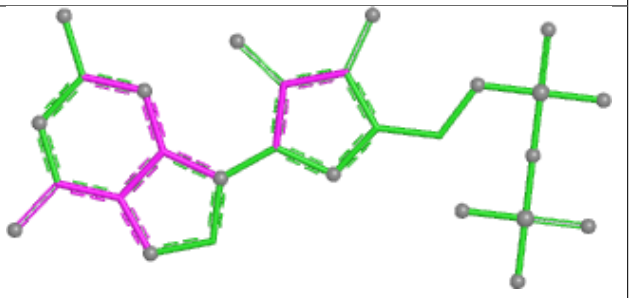

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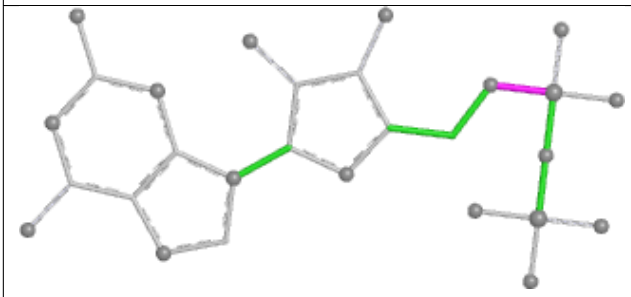

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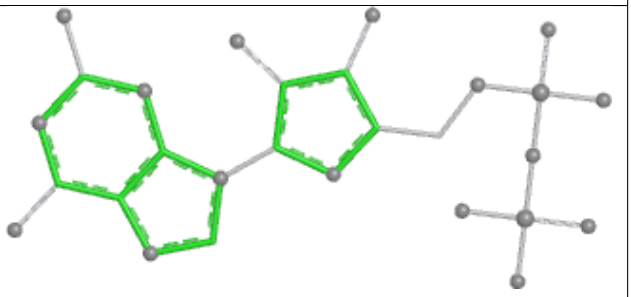
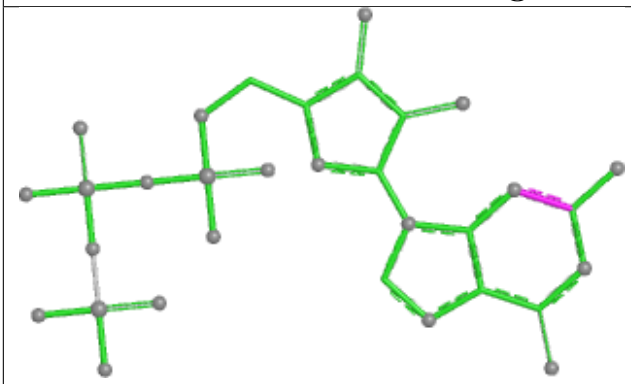


Rings

Ligand GTP GC 501



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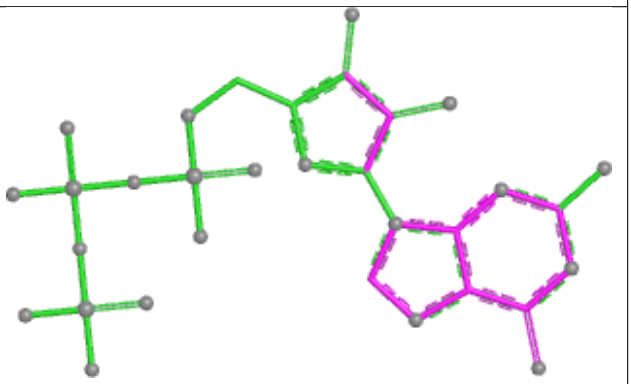

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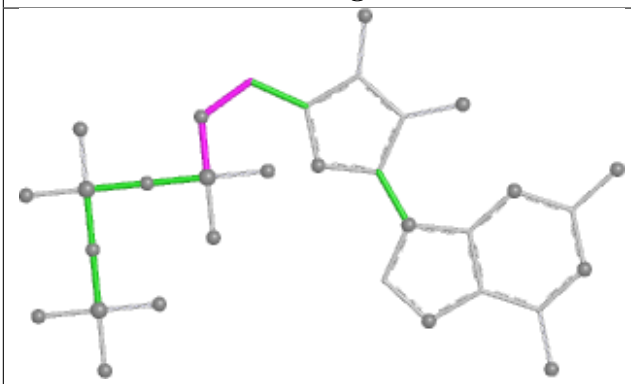

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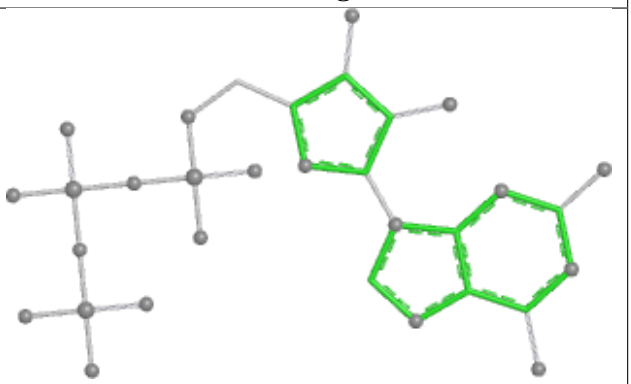

Rings

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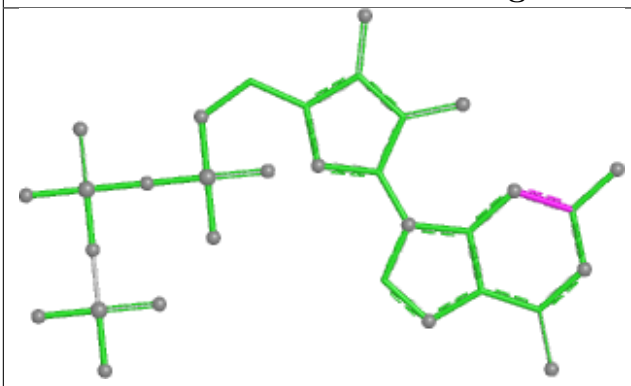

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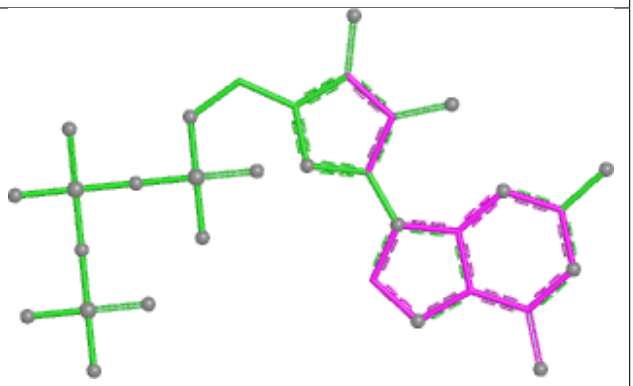

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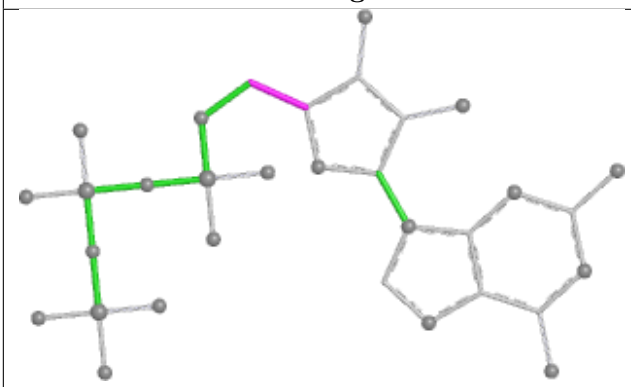

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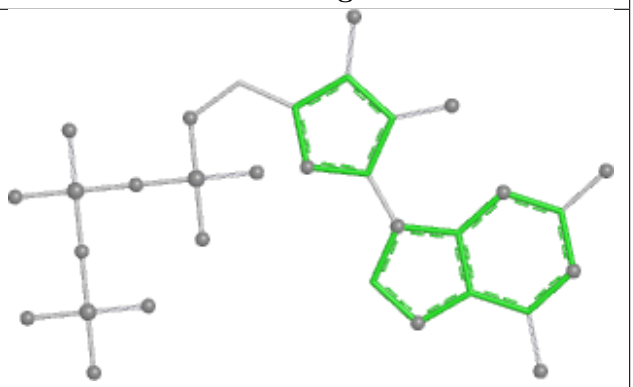
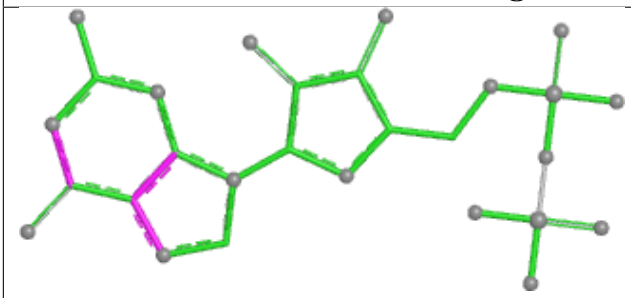


Rings

Ligand GDP BD 500



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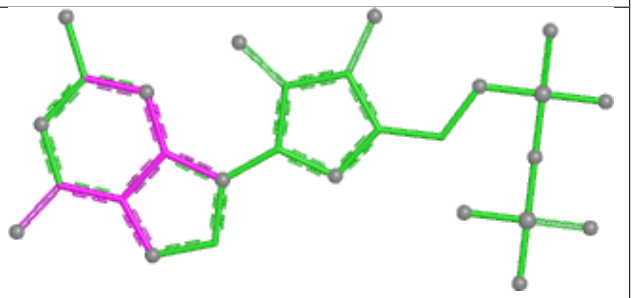

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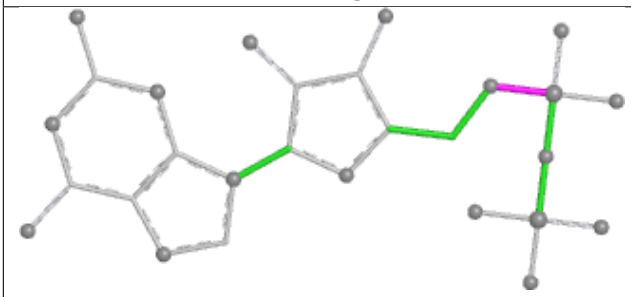

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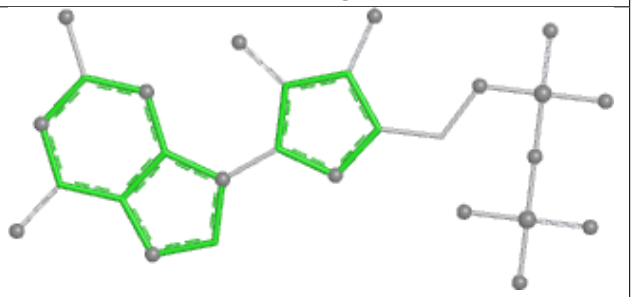
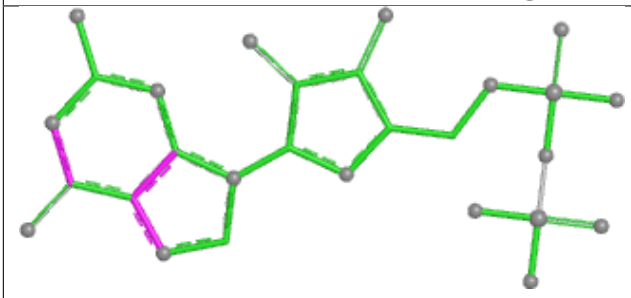


Rings

Ligand GDP O 500



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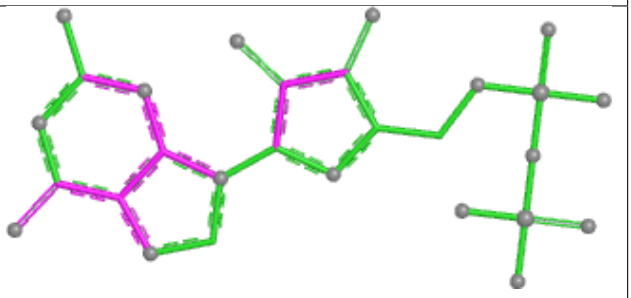

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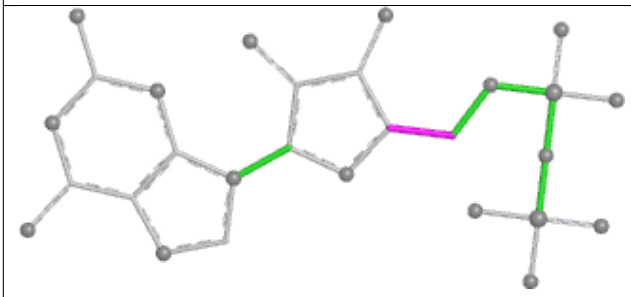

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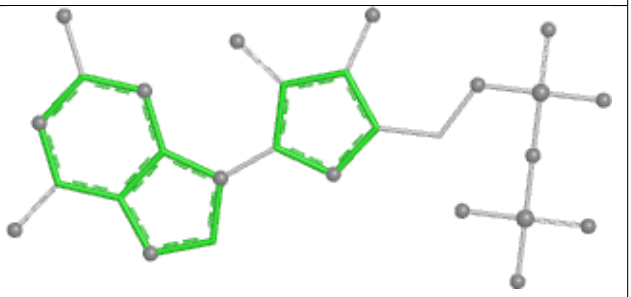
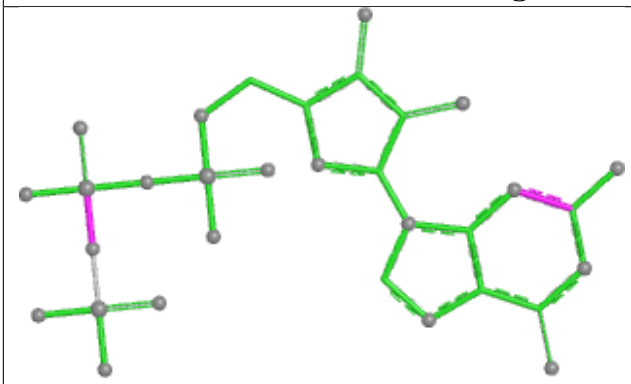


Rings

Ligand GTP DF 501



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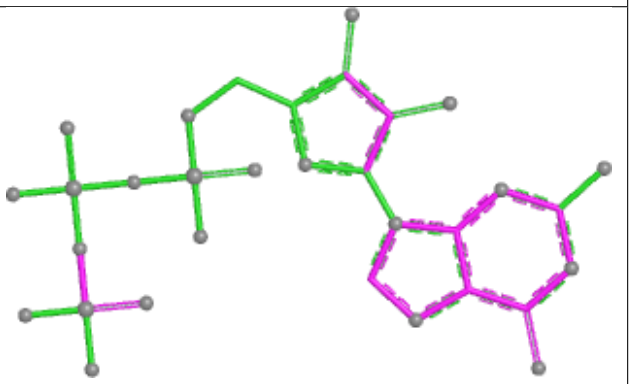

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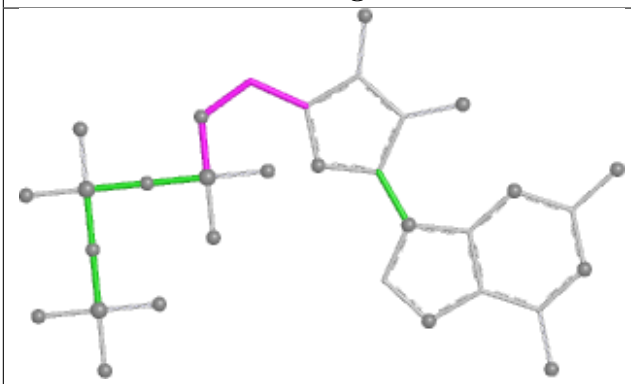

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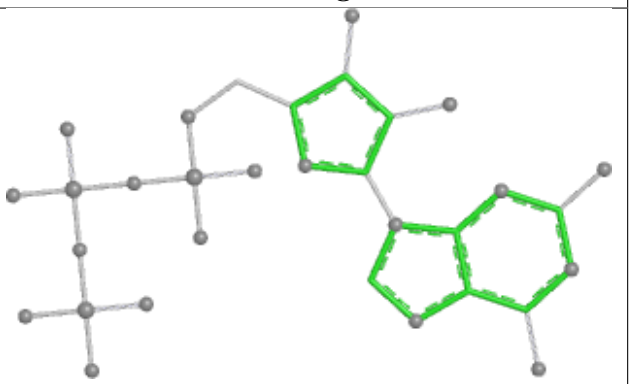
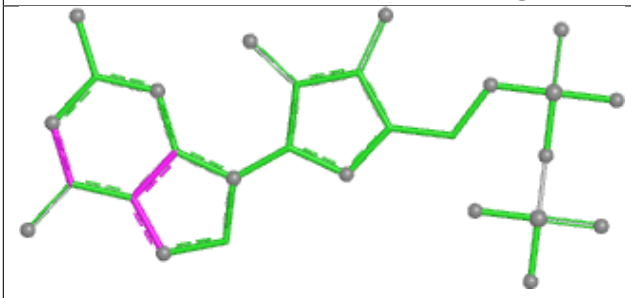


Rings

Ligand GDP EJ 500



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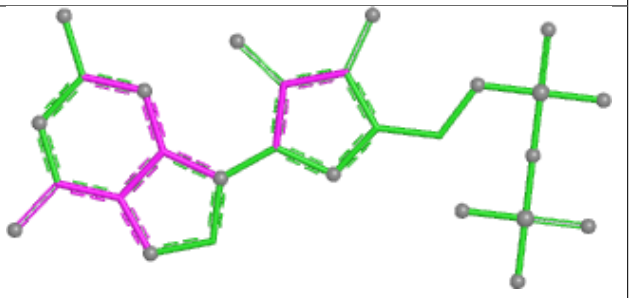

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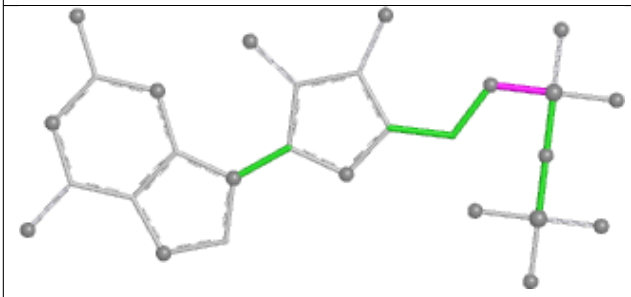

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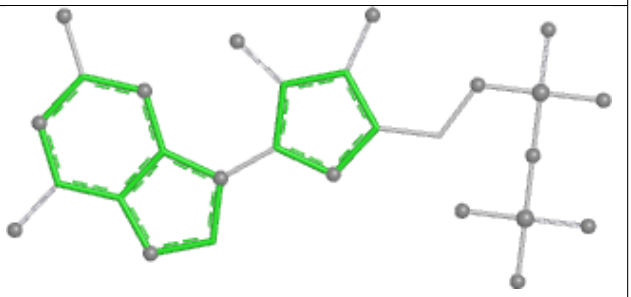
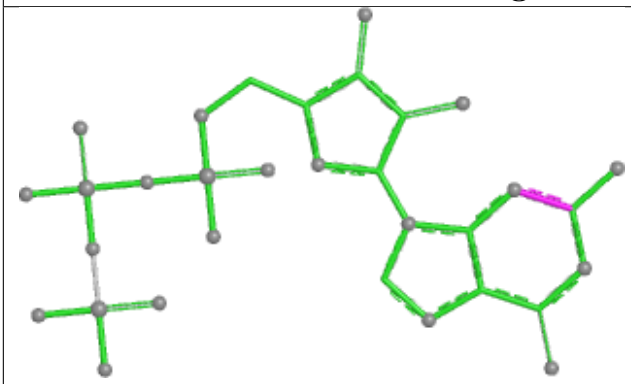


Rings

Ligand GTP FK 501



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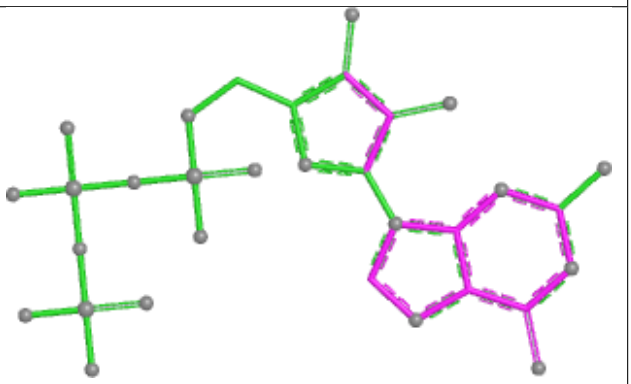

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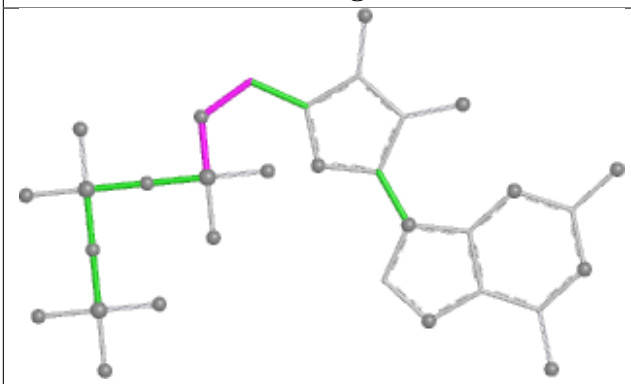
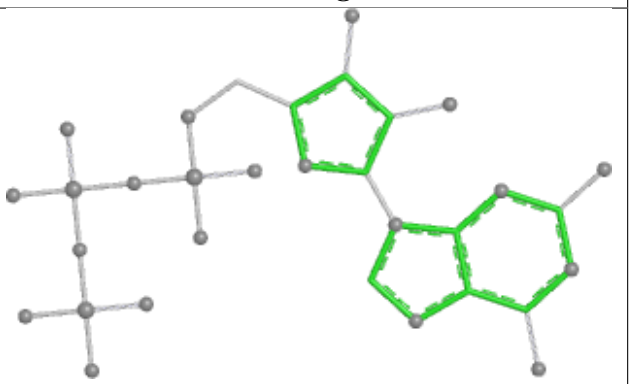
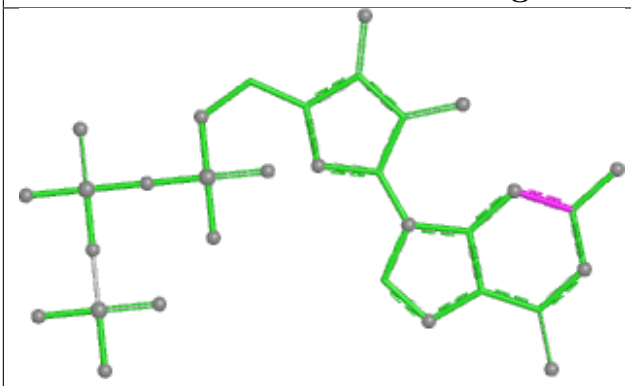


Torsions



Rings

Ligand GTP QL 501



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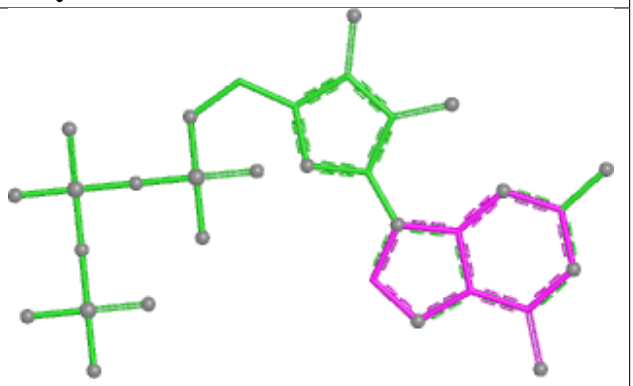

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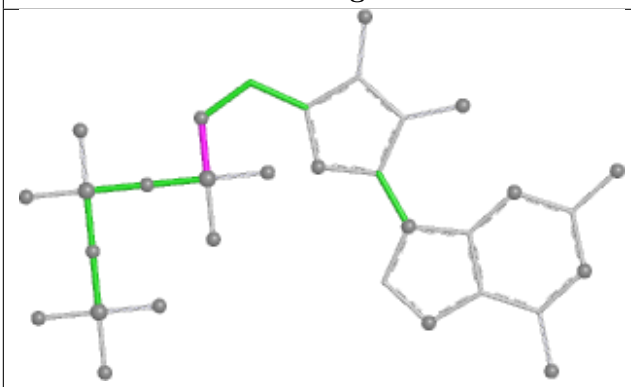

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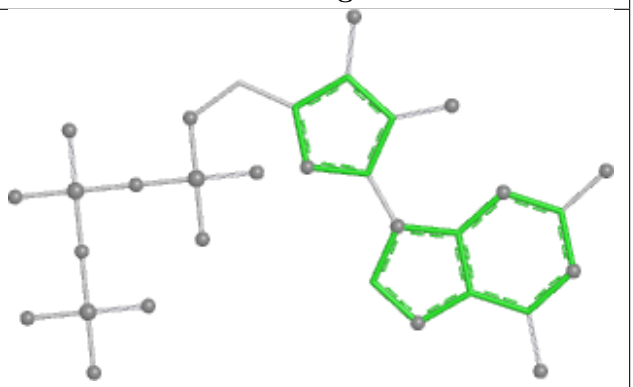
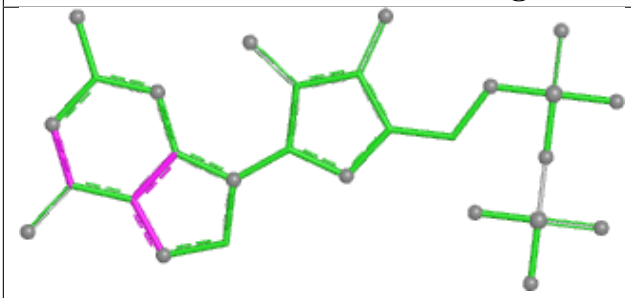


Rings

Ligand GDP FB 500



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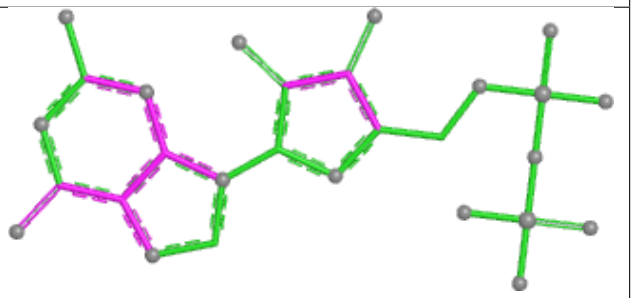

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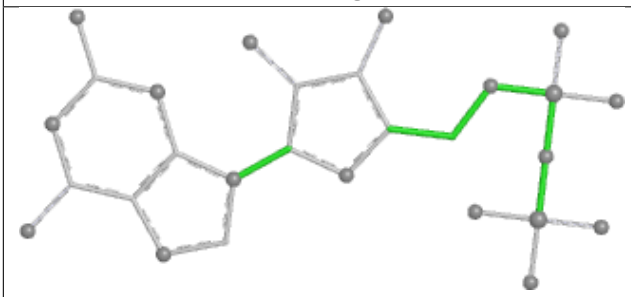

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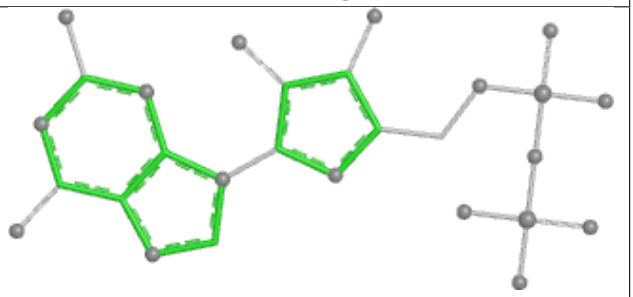
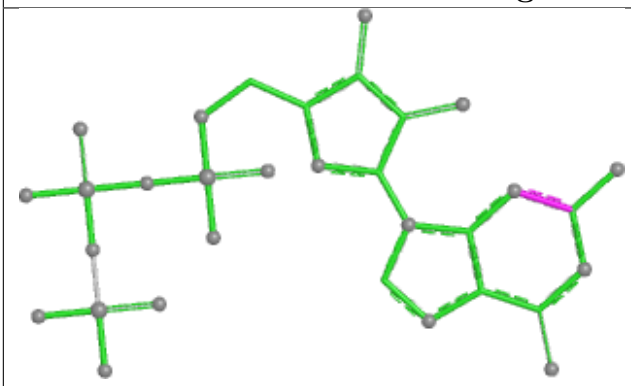


Rings

Ligand GTP PI 501



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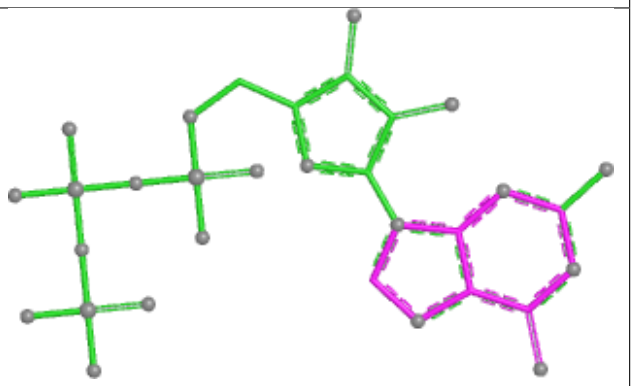

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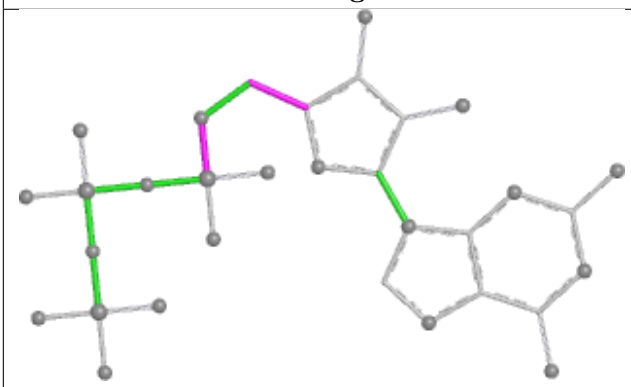

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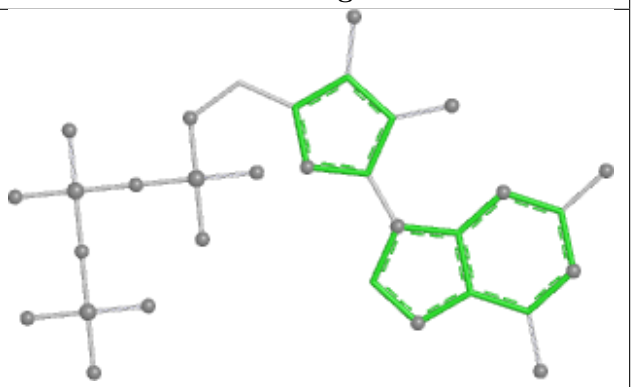
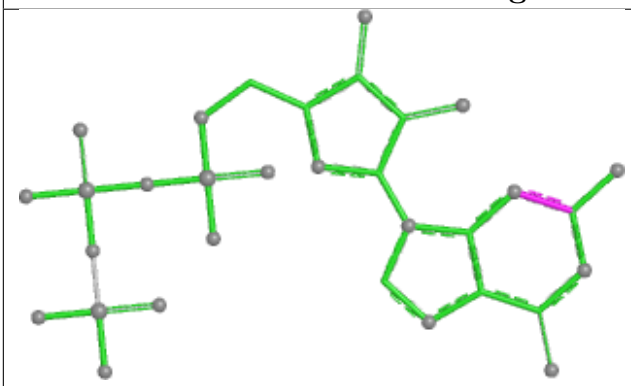


Rings

Ligand GTP TK 501



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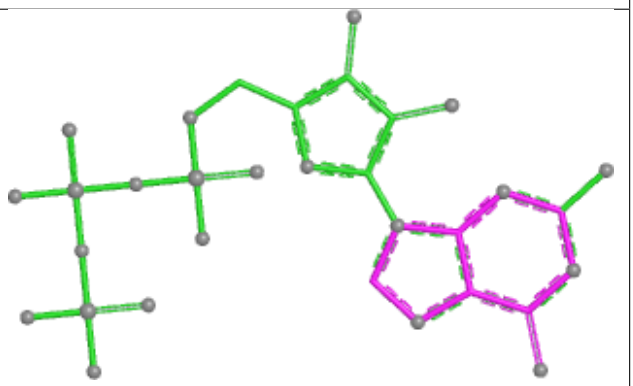

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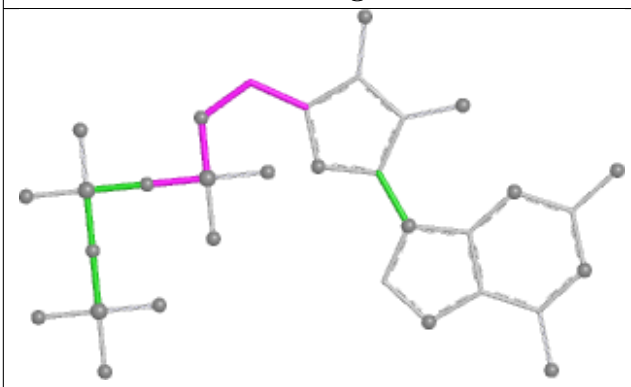

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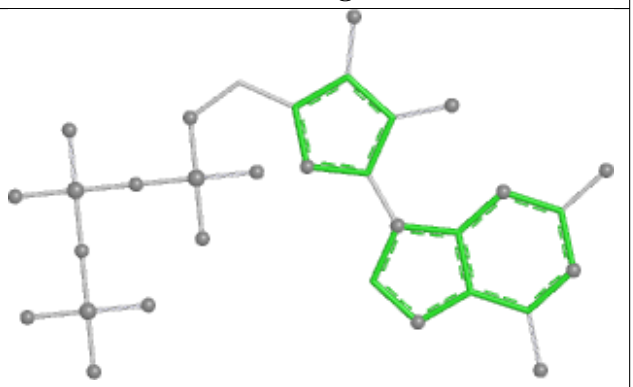
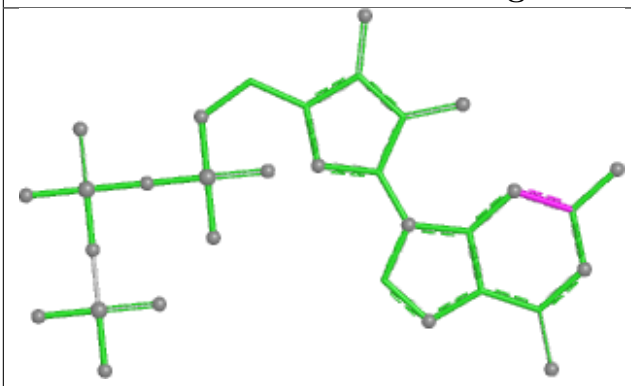


Rings

Ligand GTP KH 501



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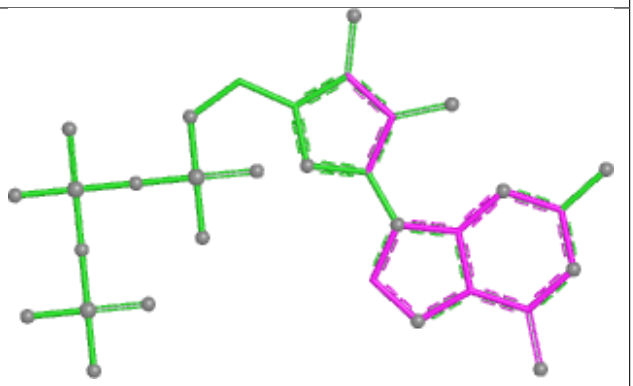

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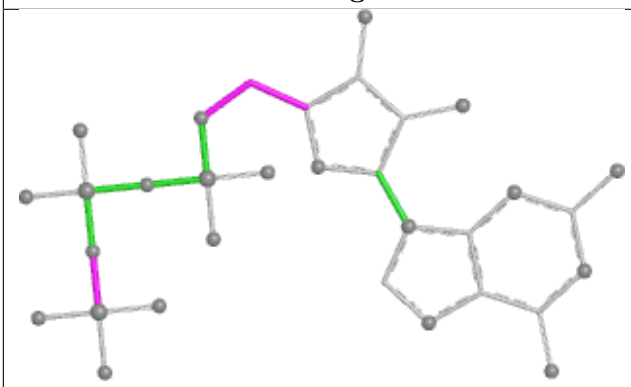

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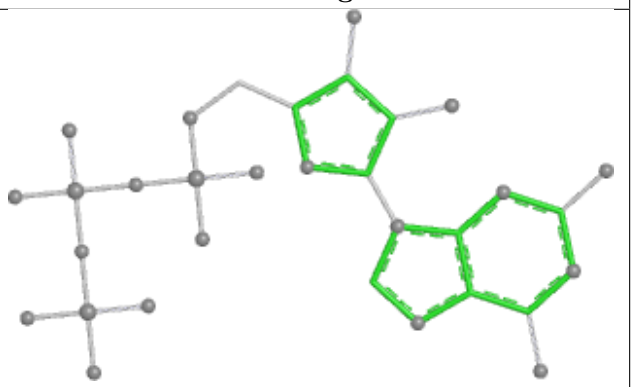
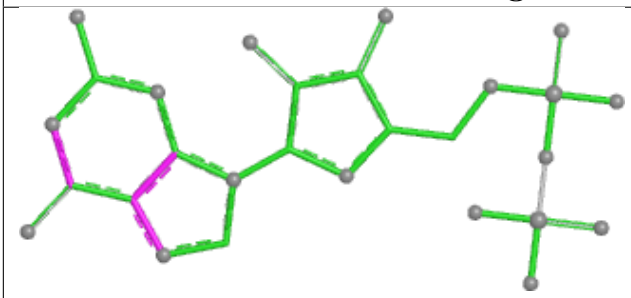


Rings

Ligand GDP QA 500



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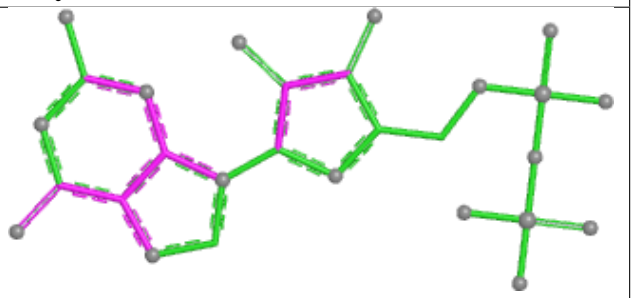

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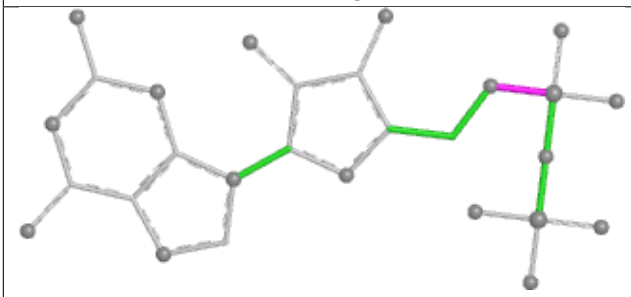

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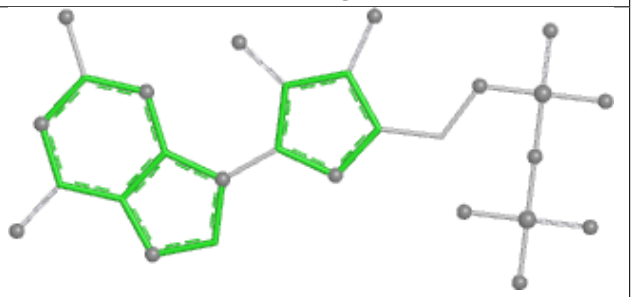

Rings

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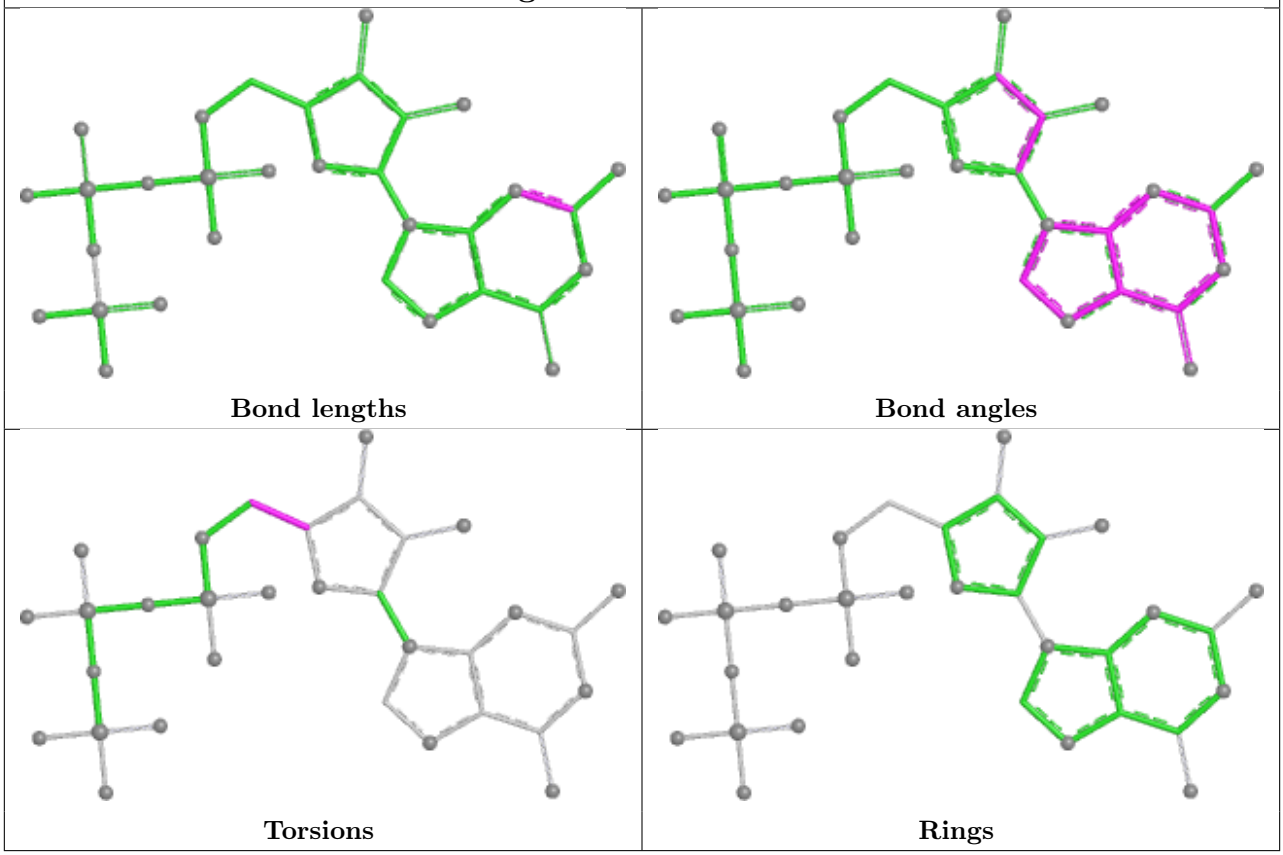

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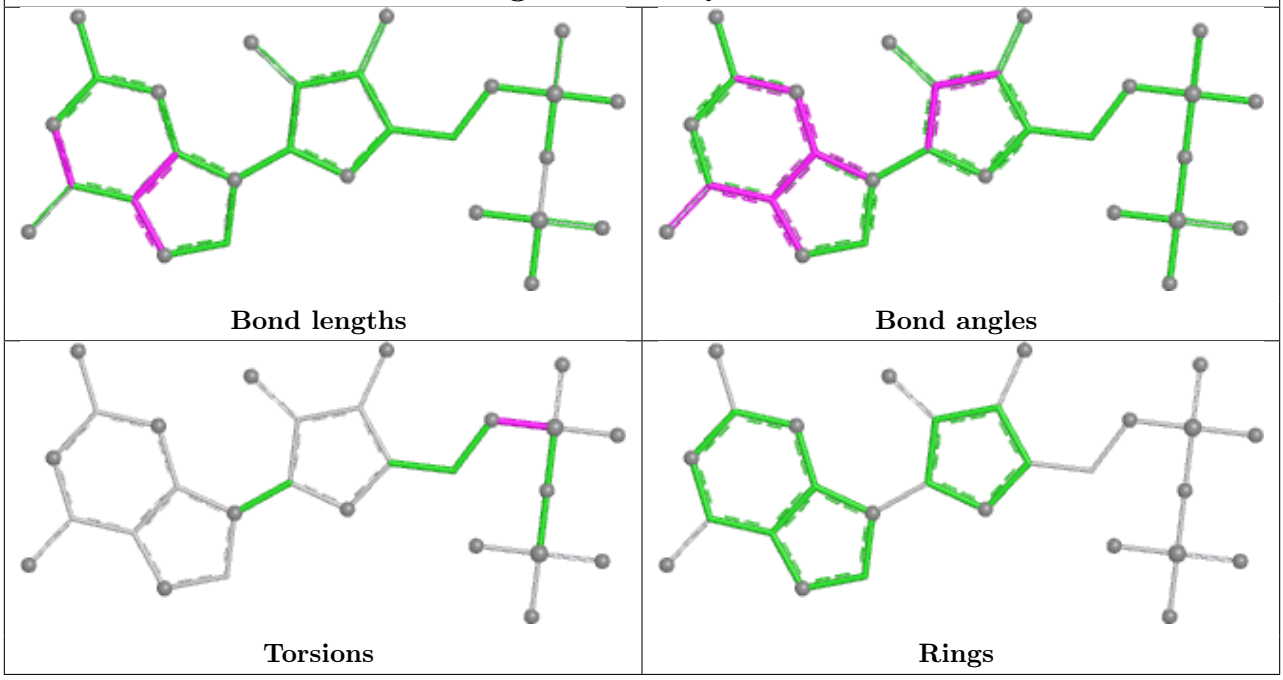

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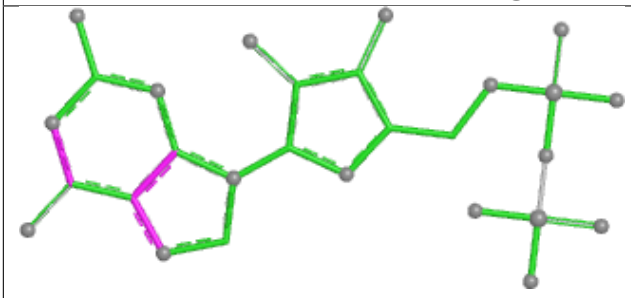

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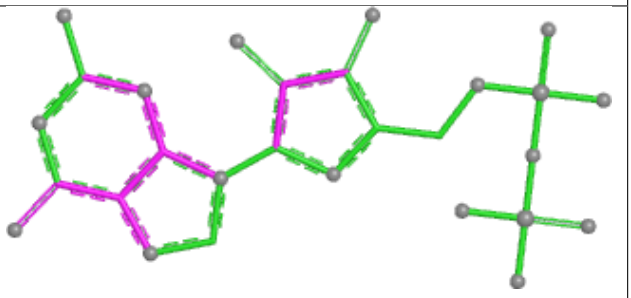

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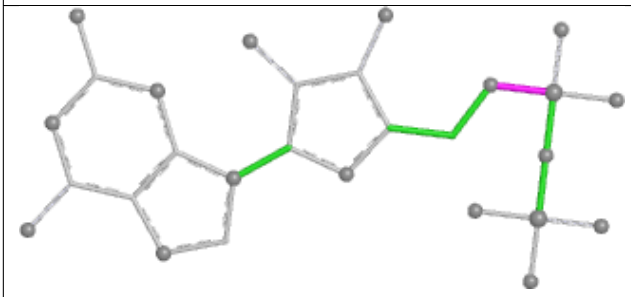

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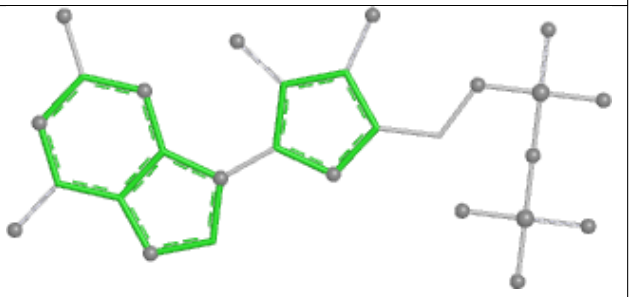
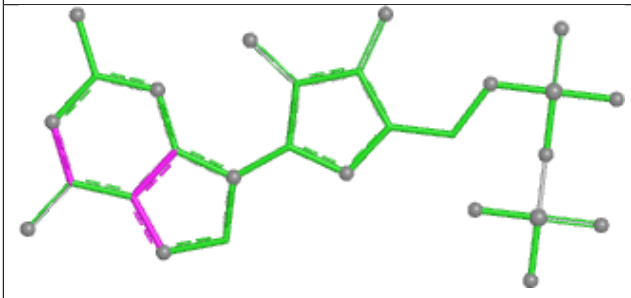


Rings

Ligand GDP GD 500



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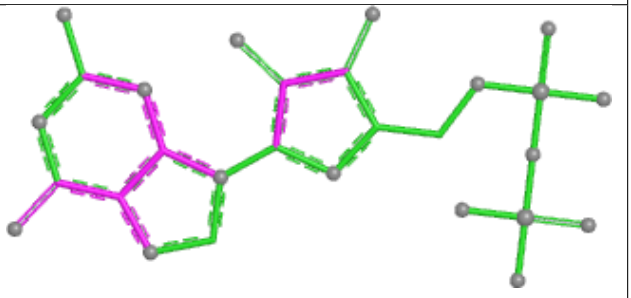

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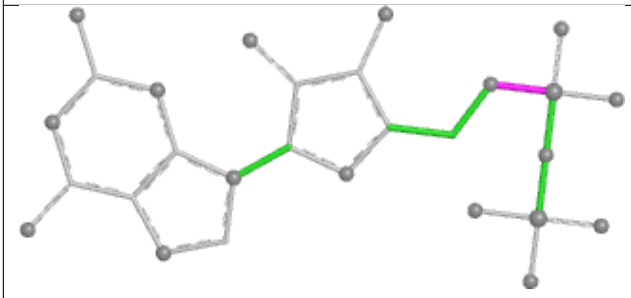

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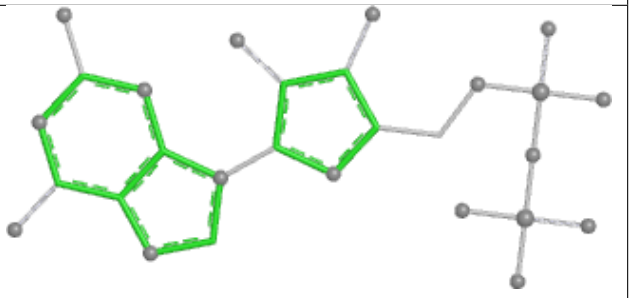
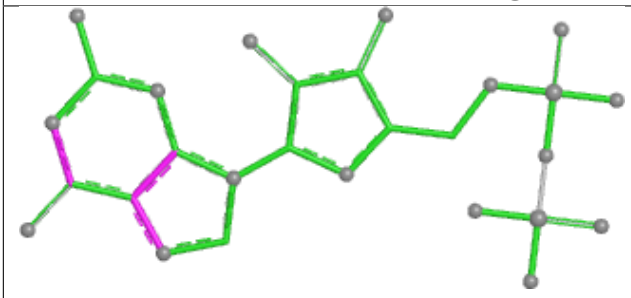


Rings

Ligand GDP HH 500



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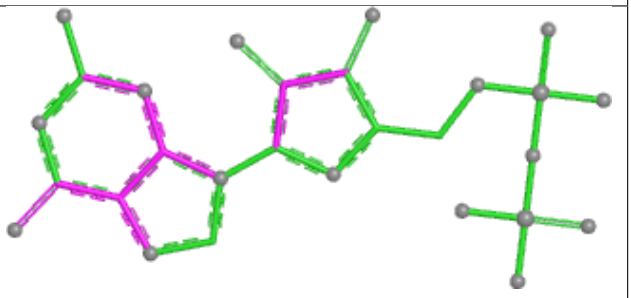

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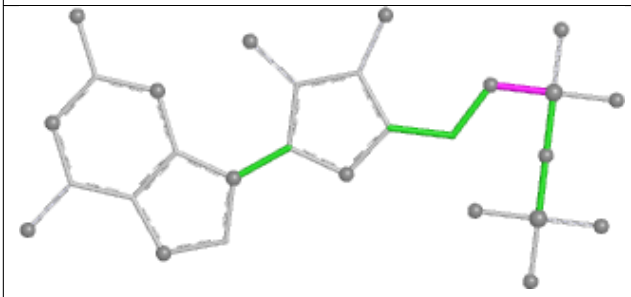

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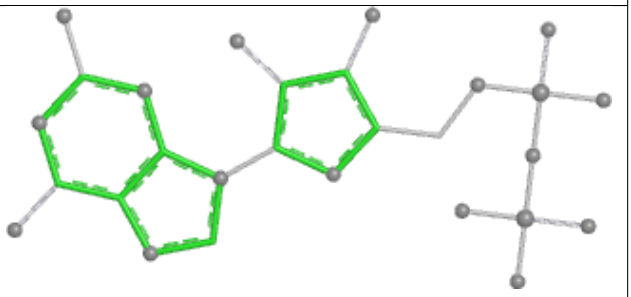
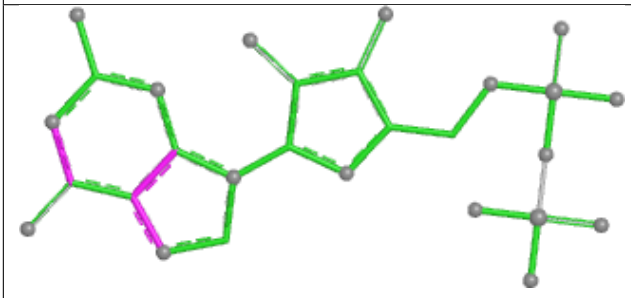


Rings

Ligand GDP BL 500



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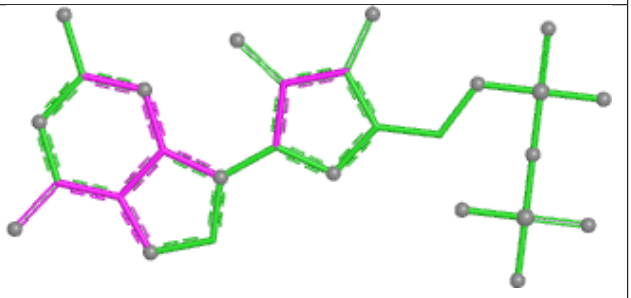

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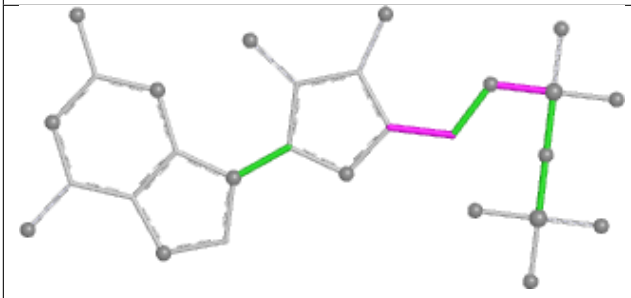

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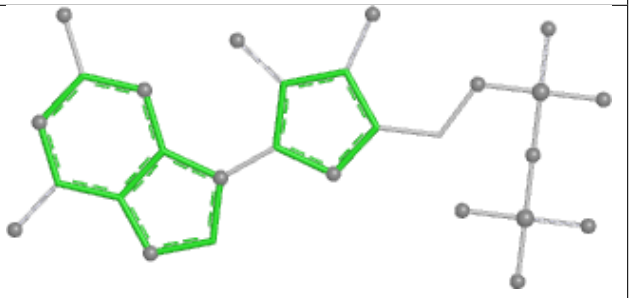
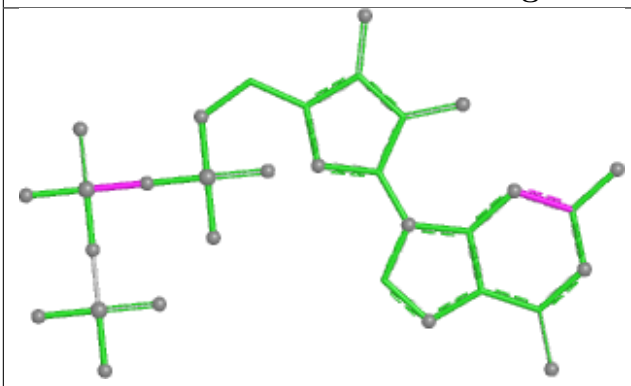


Rings

Ligand GTP K 501



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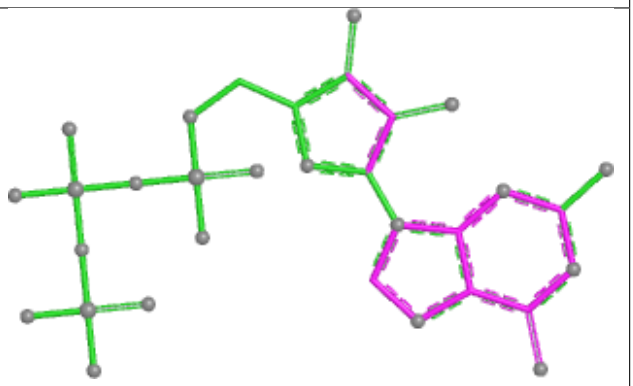

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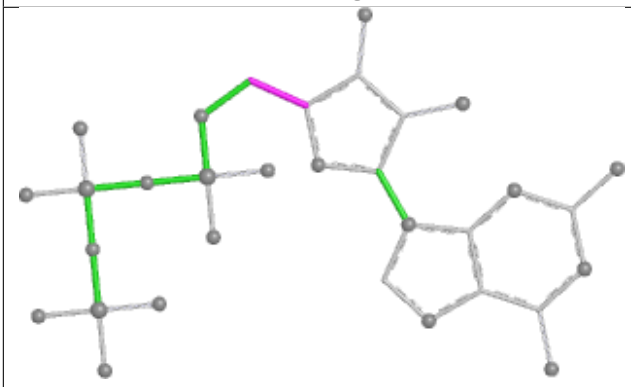

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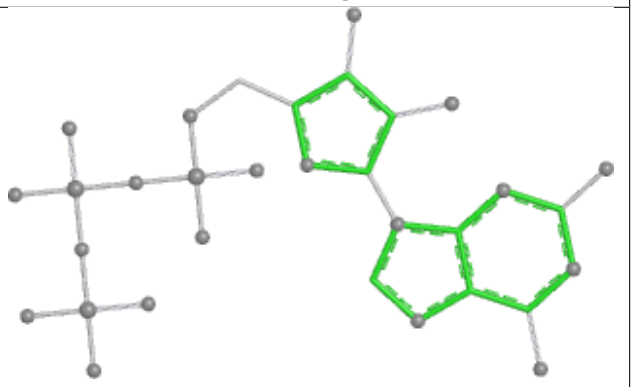
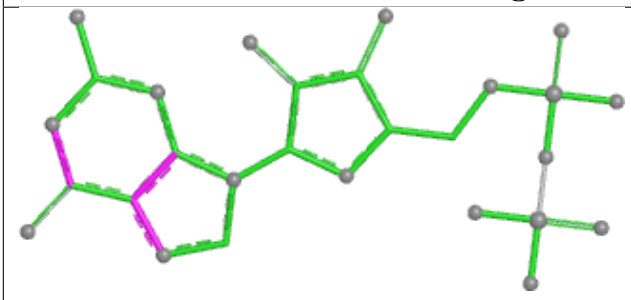


Rings

Ligand GDP LA 500



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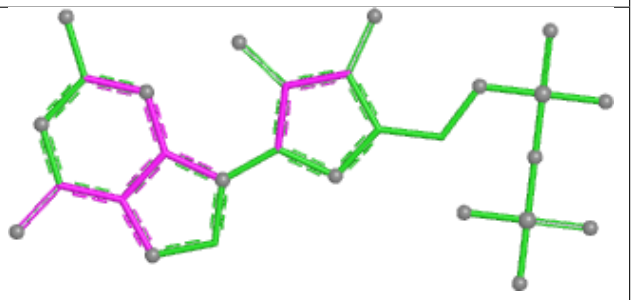
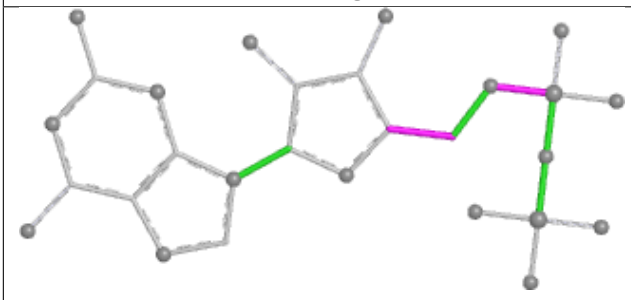


Bond angles



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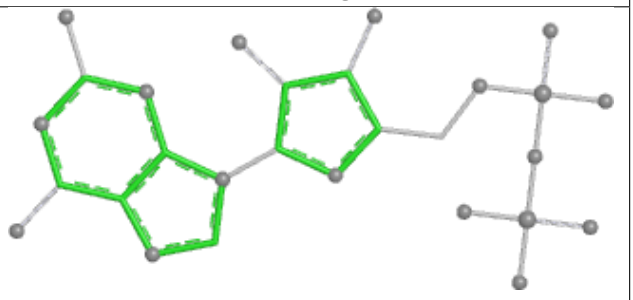
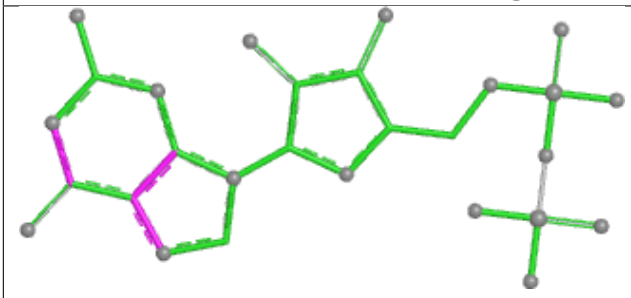


Rings

Ligand GDP HB 500



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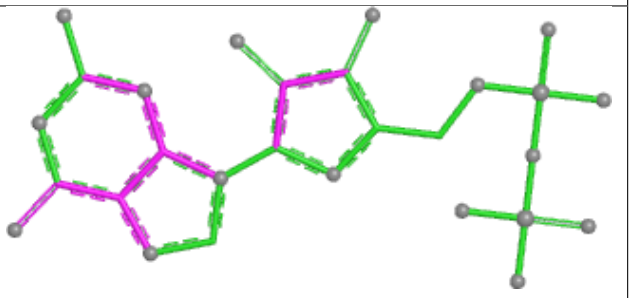
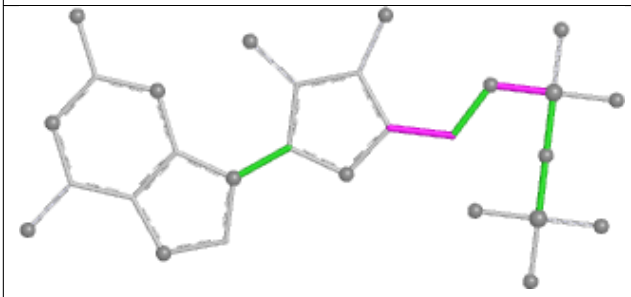
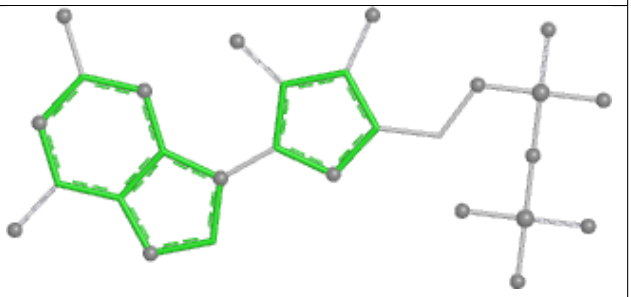


Bond angles

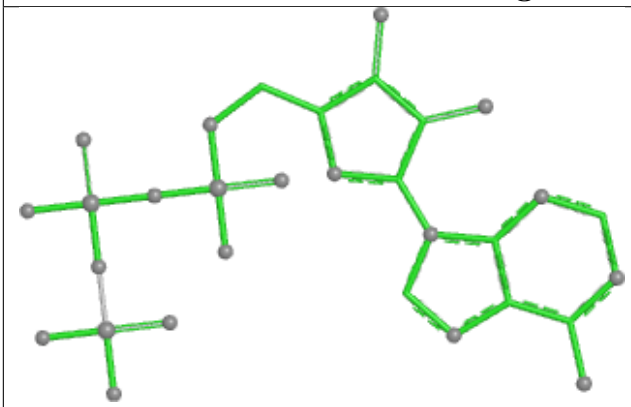


Torsions



Rings

Ligand ATP 2w 501



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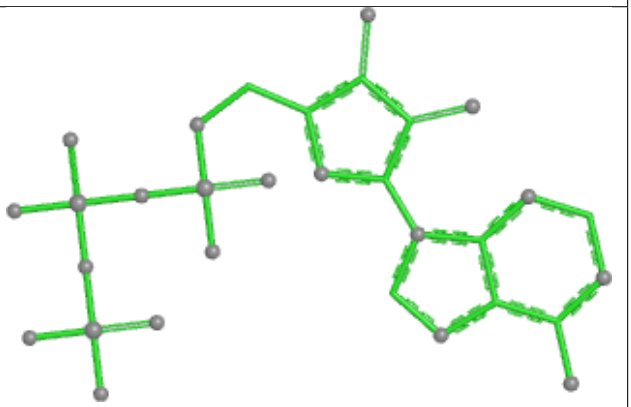

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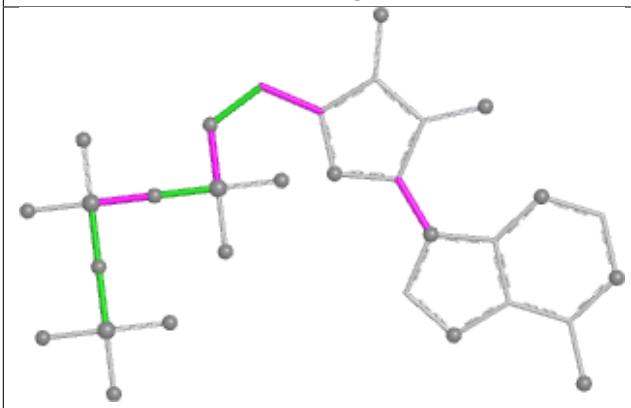

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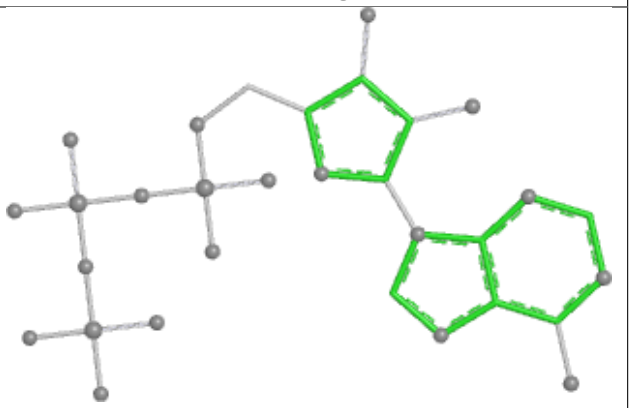
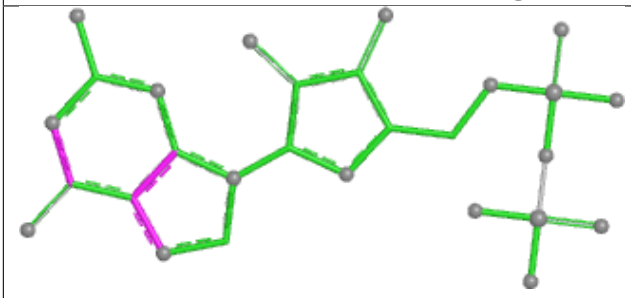


Rings

Ligand GDP VF 500



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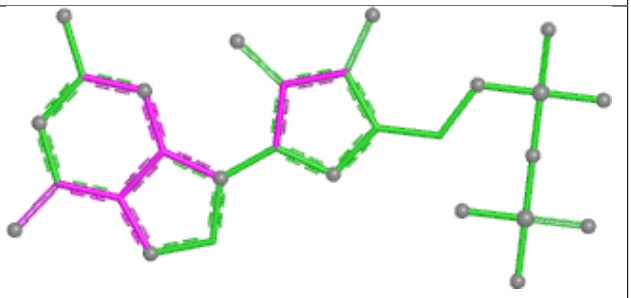

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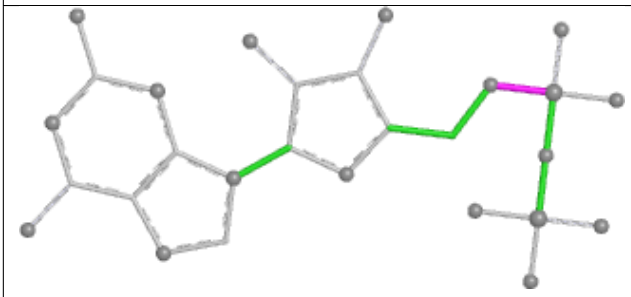

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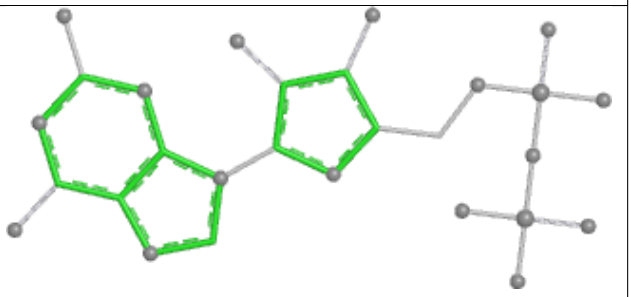

Rings

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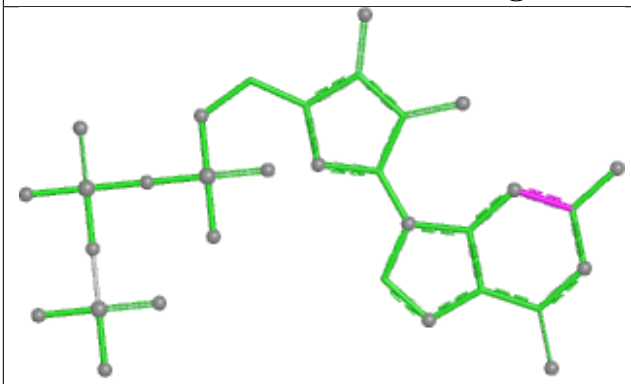

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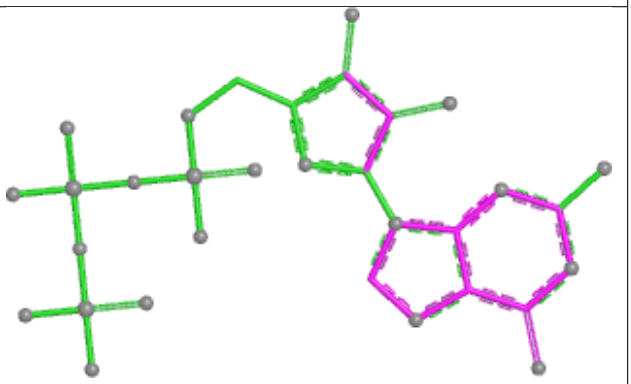

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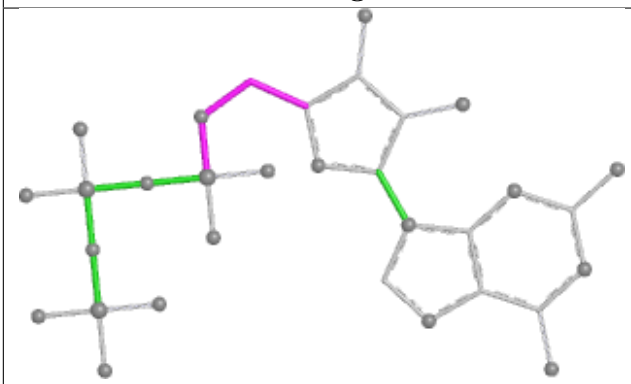

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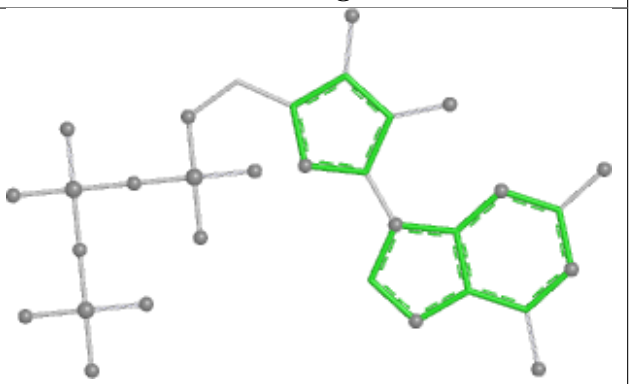

Rings

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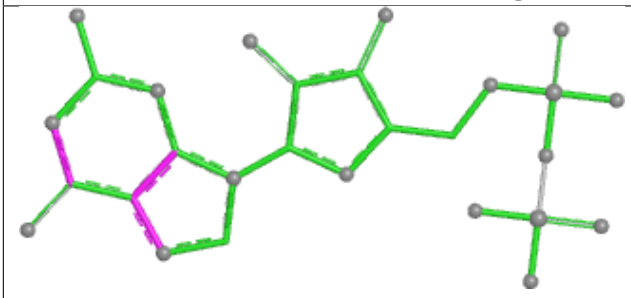

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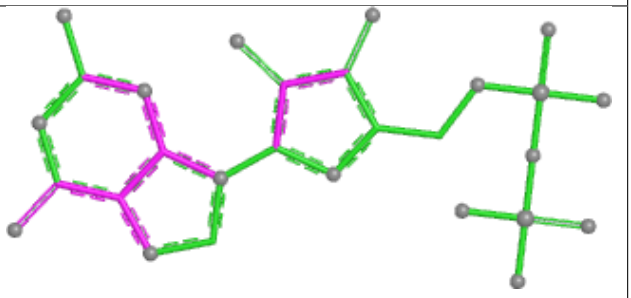

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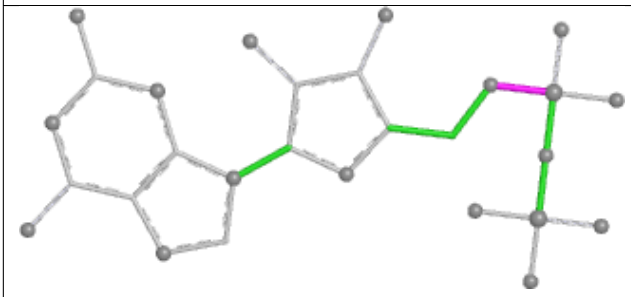

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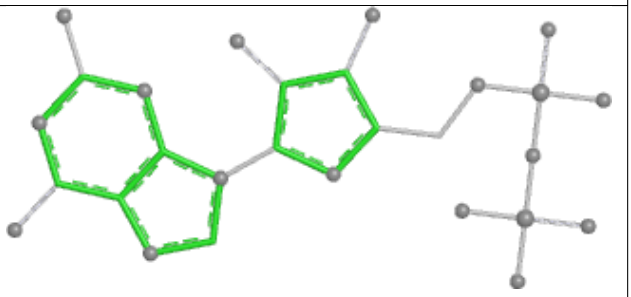
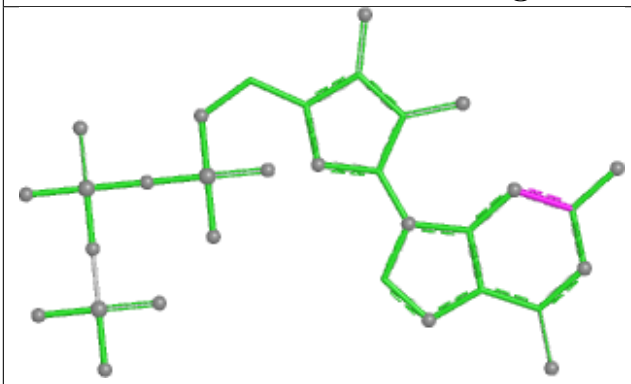


Rings

Ligand GTP SA 501



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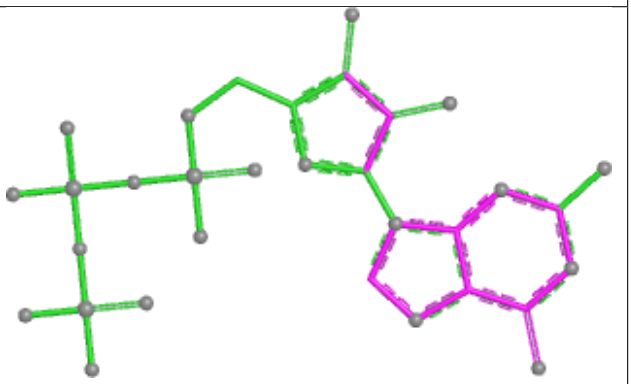

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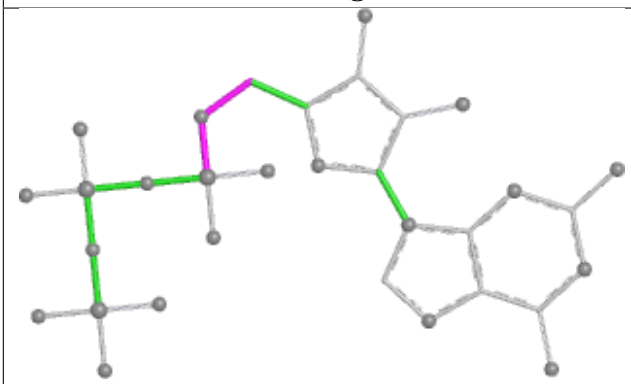

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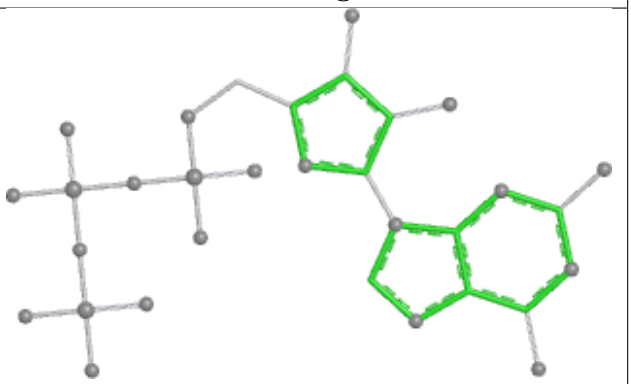
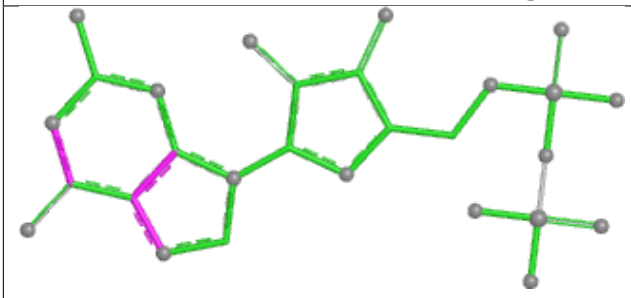


Rings

Ligand GDP P 500



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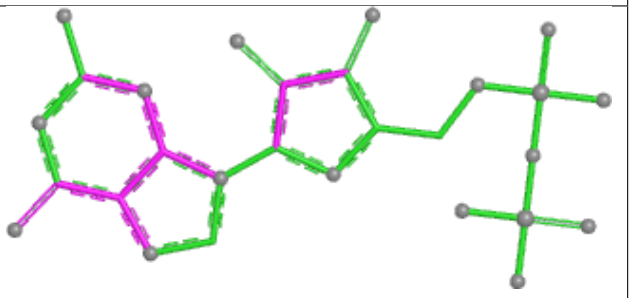

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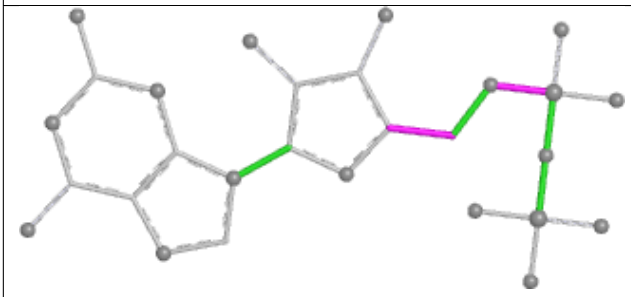

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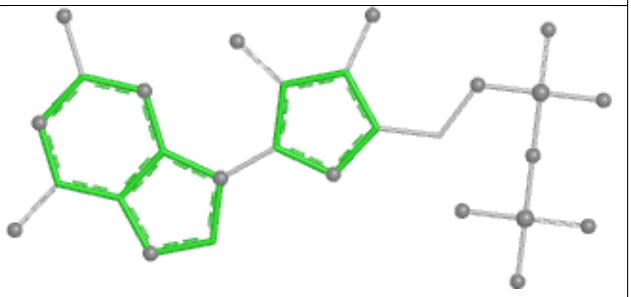
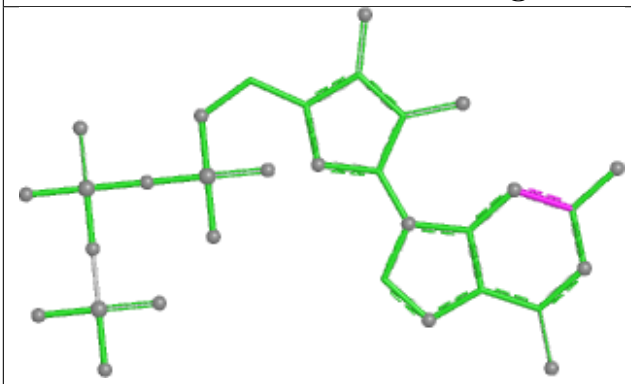


Rings

Ligand GTP GE 501



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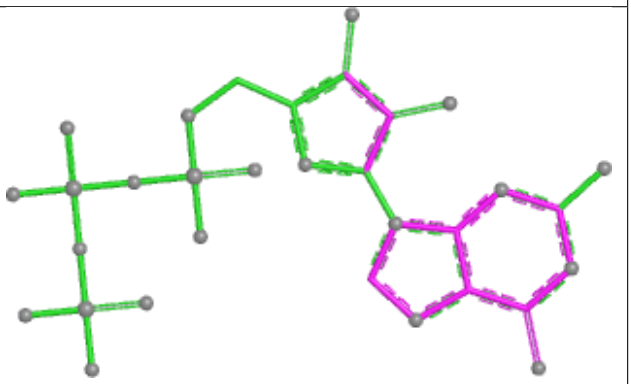

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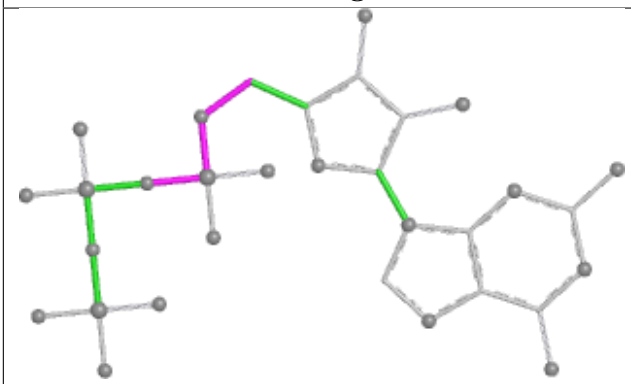

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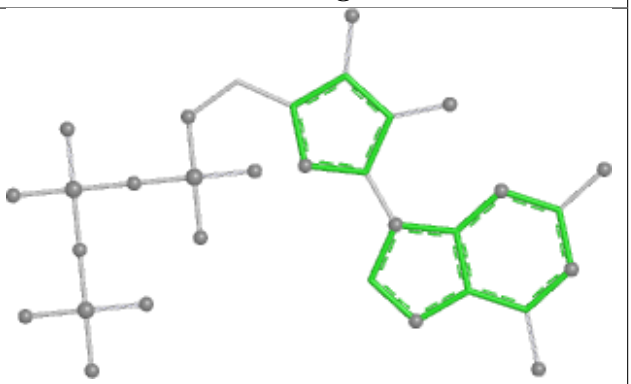
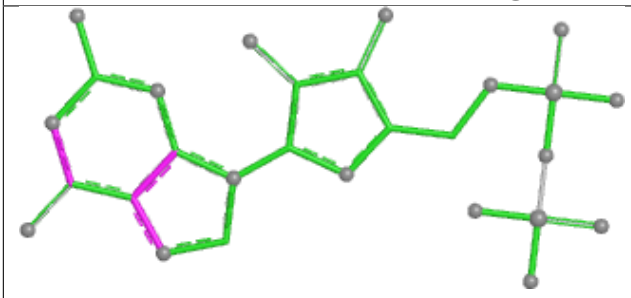


Rings

Ligand GDP VD 500



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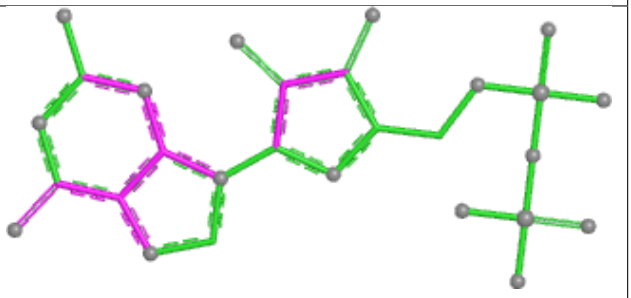

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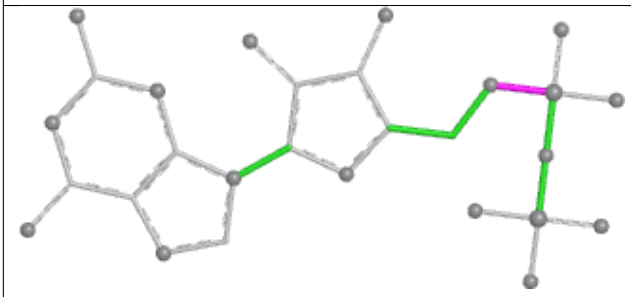

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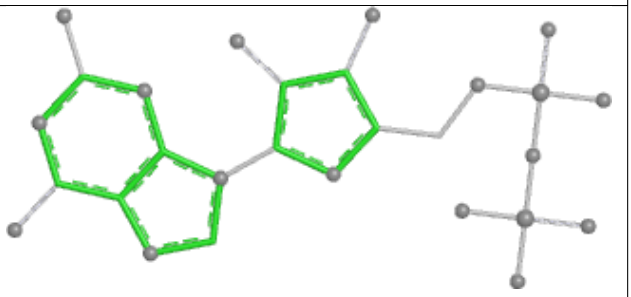

Rings

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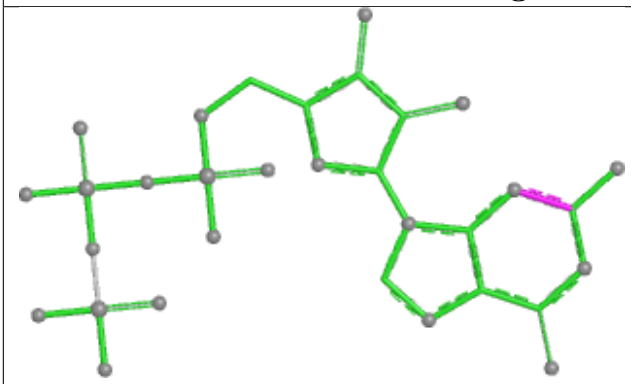

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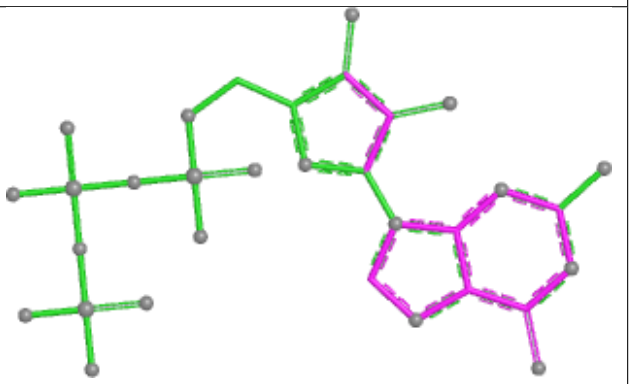

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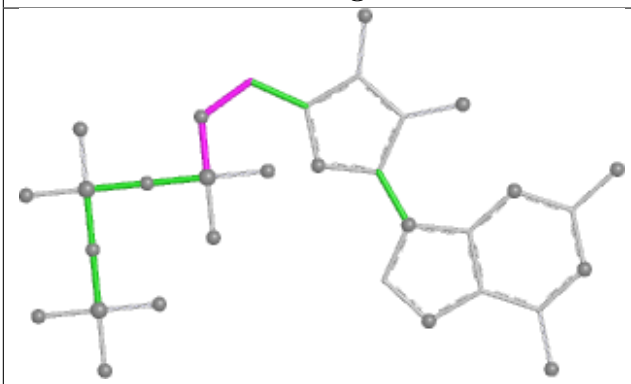

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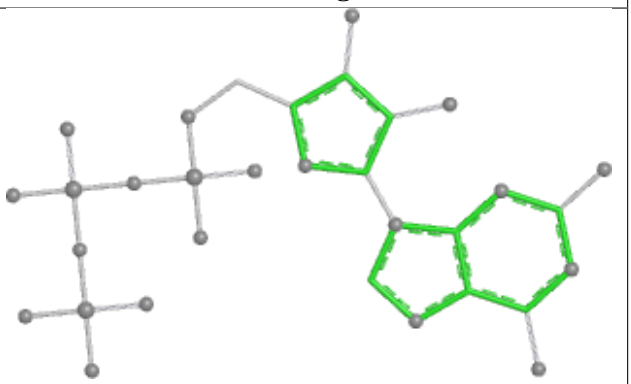

Rings

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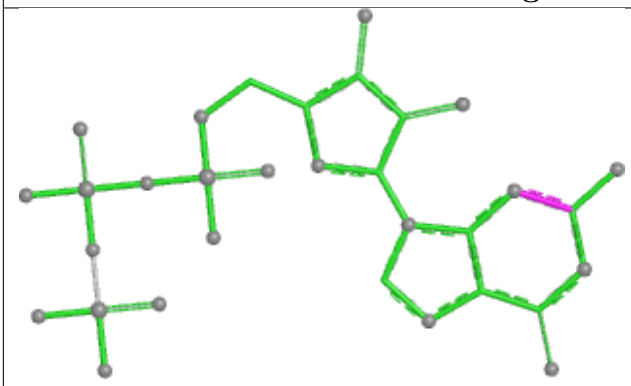

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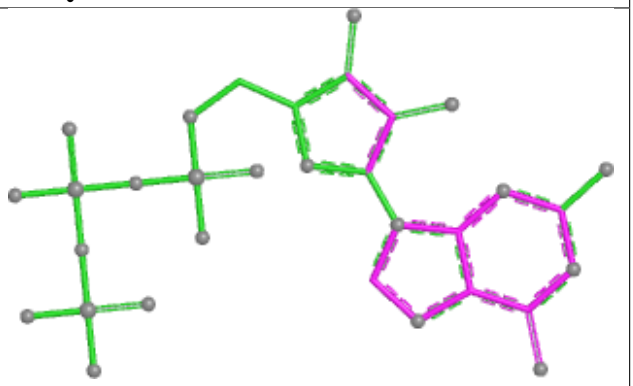

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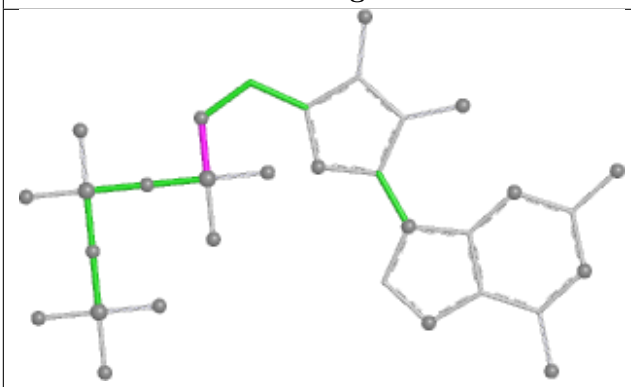

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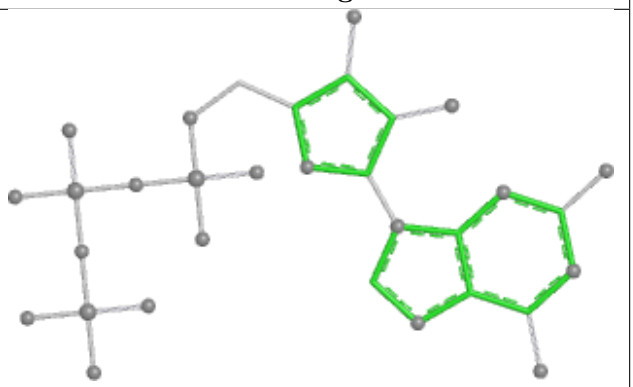
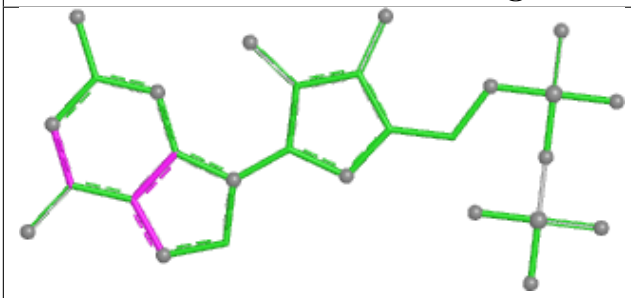


Rings

Ligand GDP UD 500



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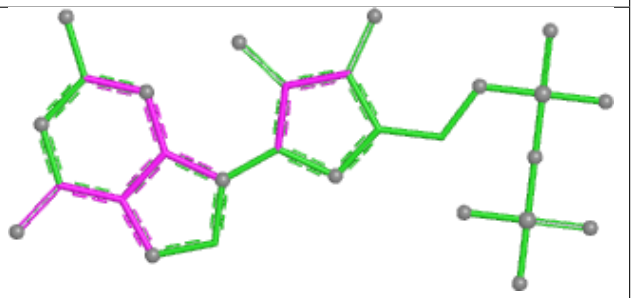

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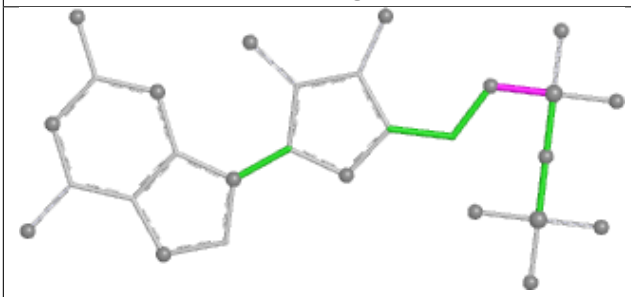

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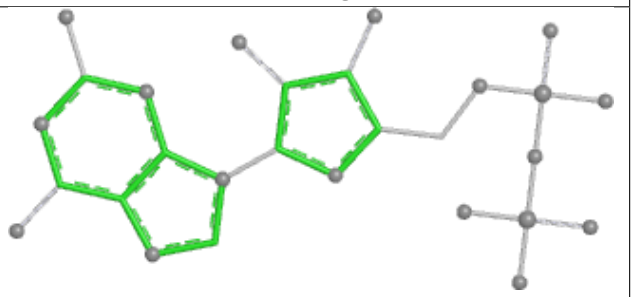

Rings

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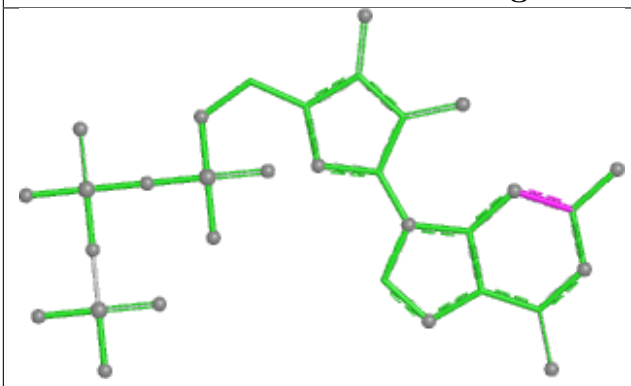

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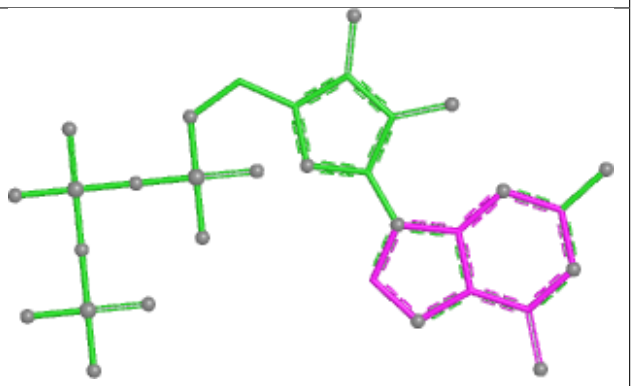

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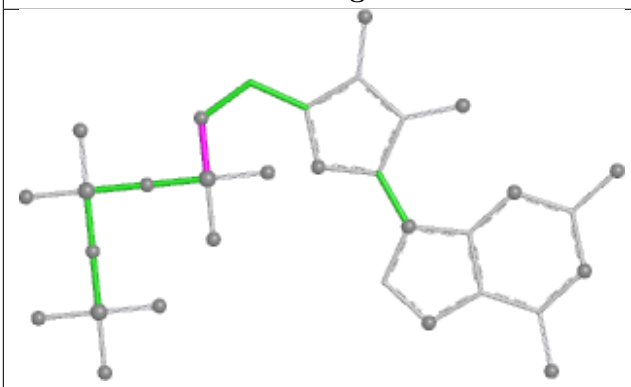

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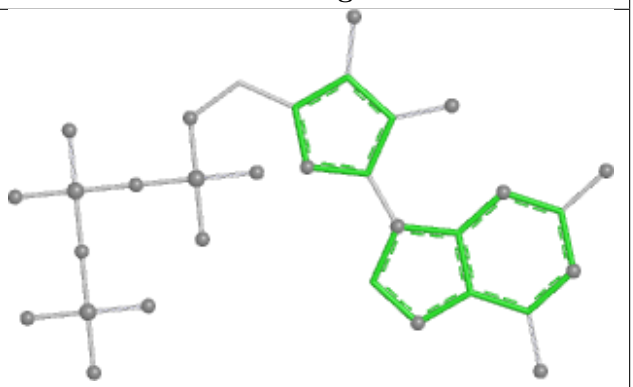
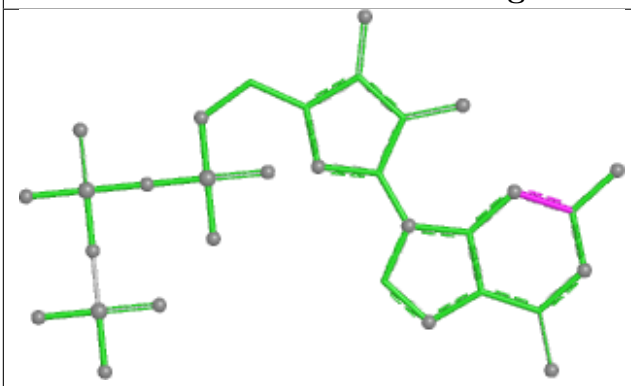


Rings

Ligand GTP KN 501



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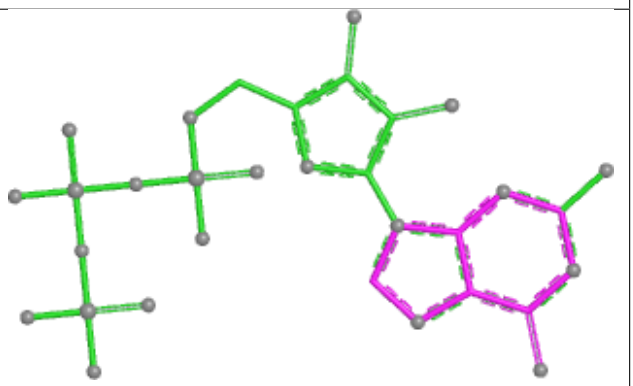

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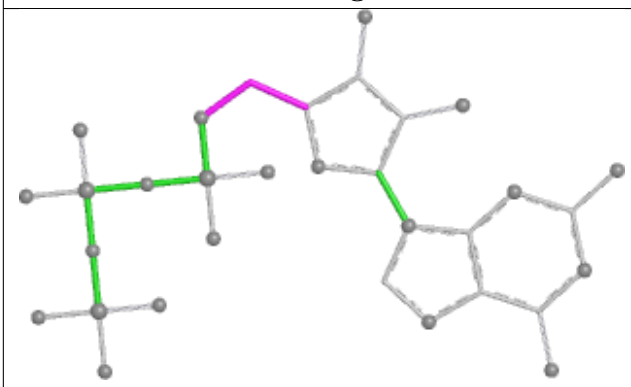

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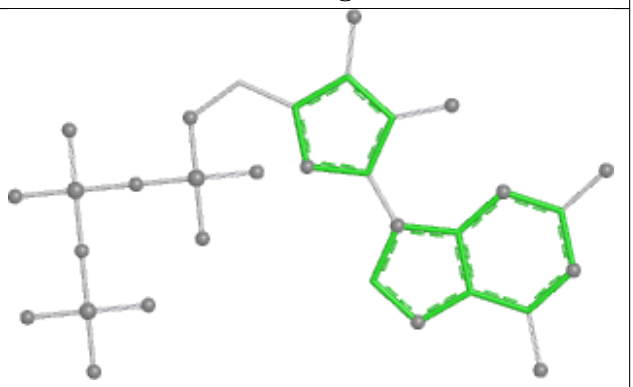
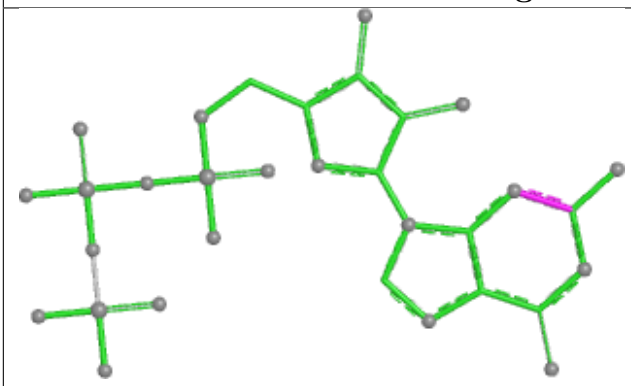


Rings

Ligand GTP IA 501



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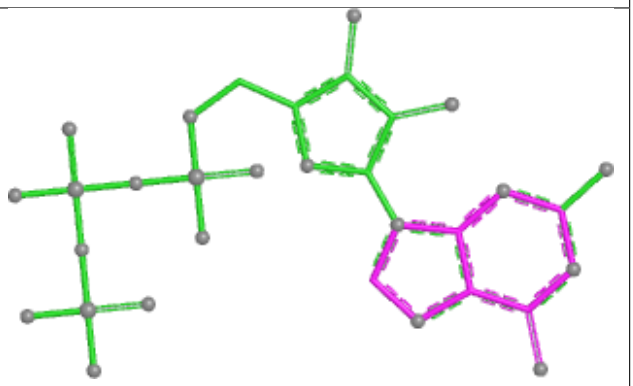

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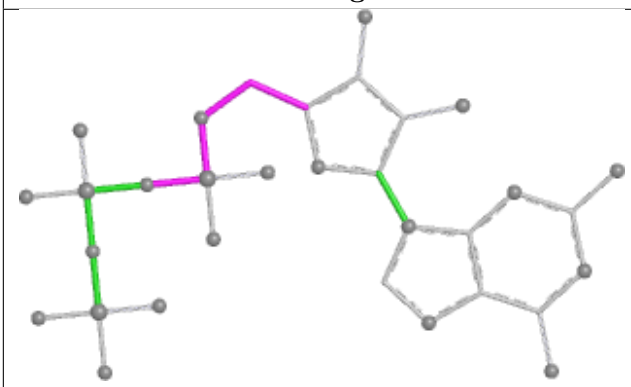

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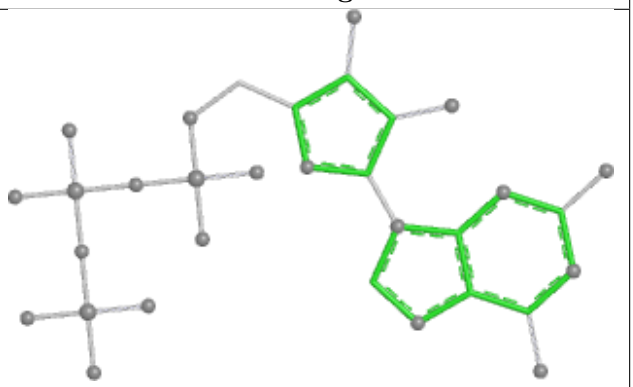
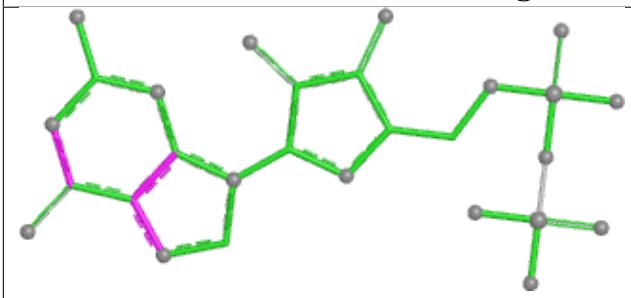


Rings

Ligand GDP SJ 500



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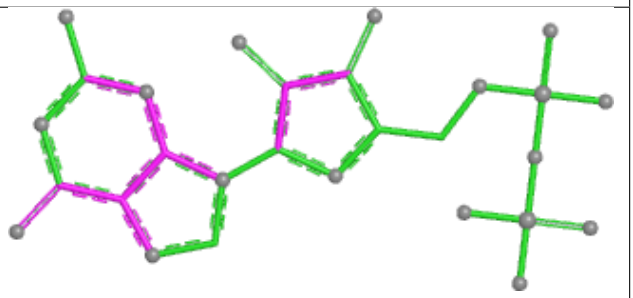

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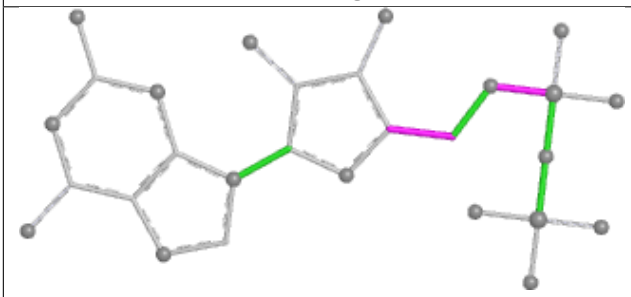

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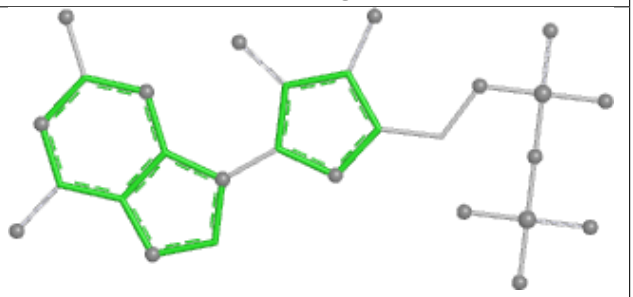
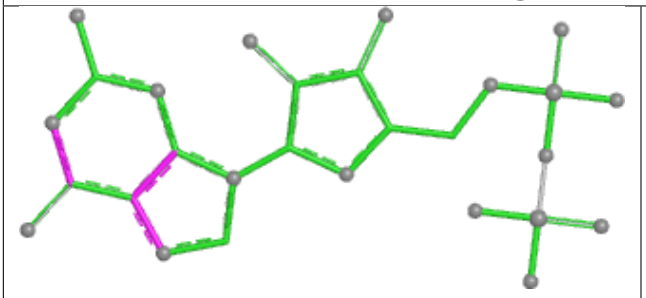


Rings

Ligand GDP AJ 500



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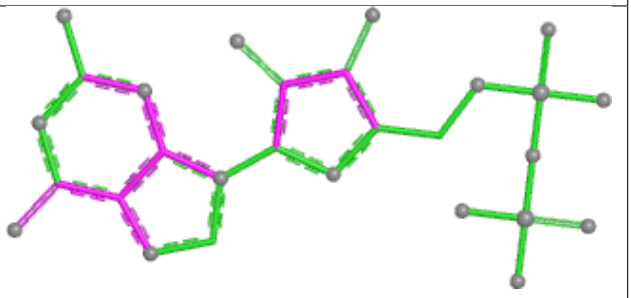

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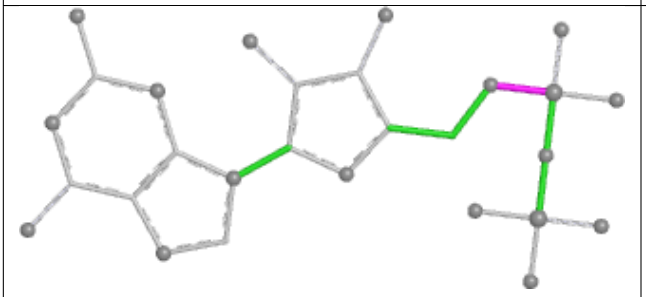

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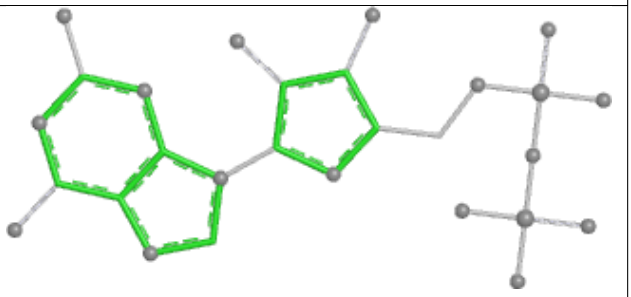
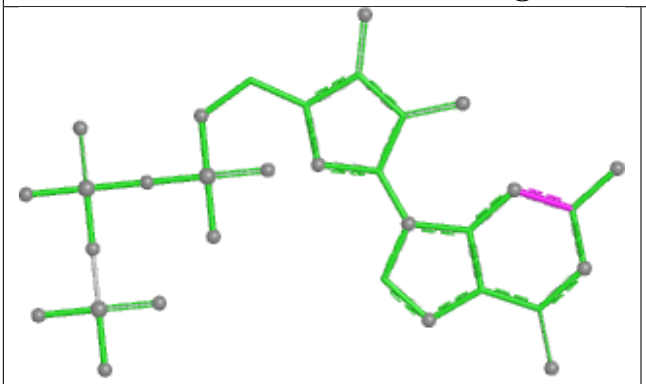


Rings

Ligand GTP JB 501



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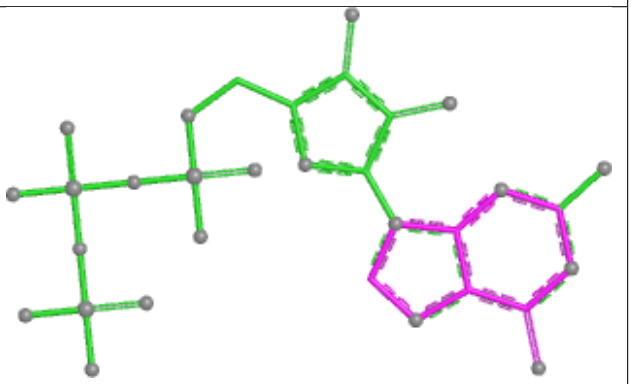

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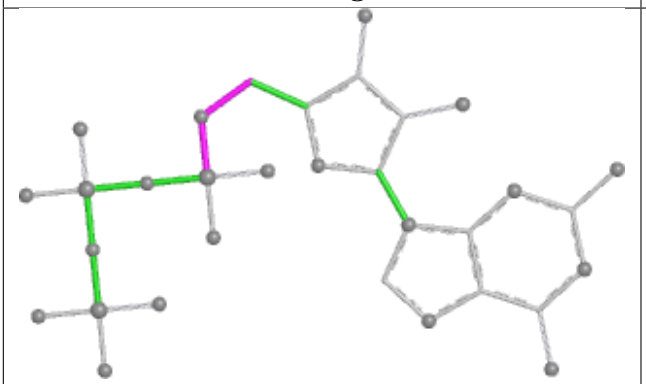

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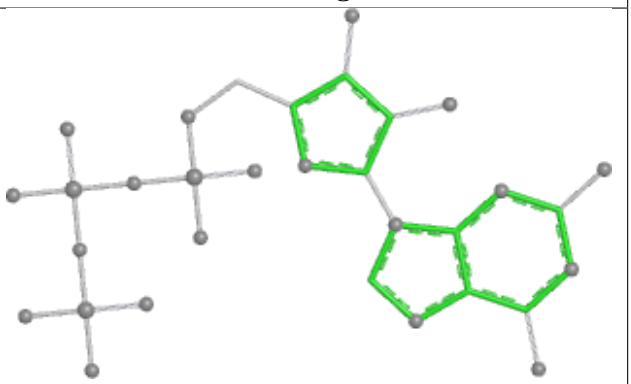
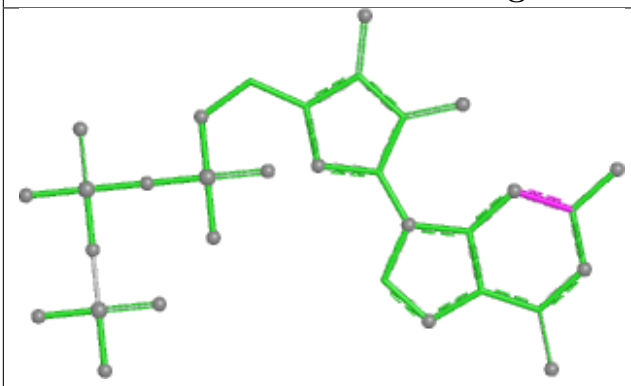


Rings

Ligand GTP HA 501



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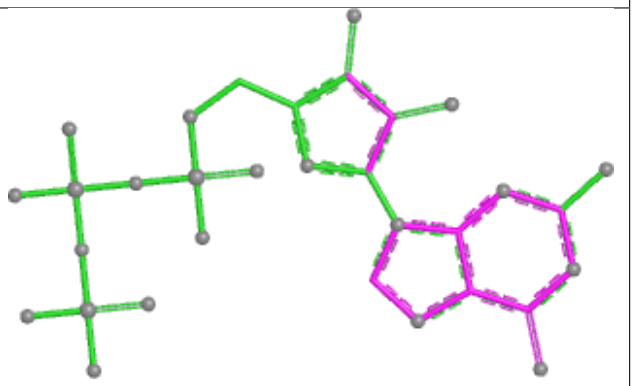

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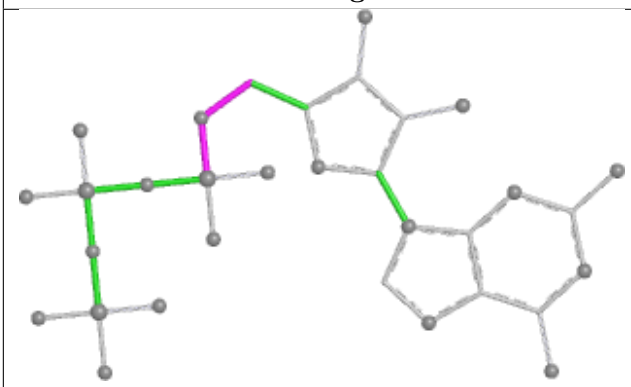

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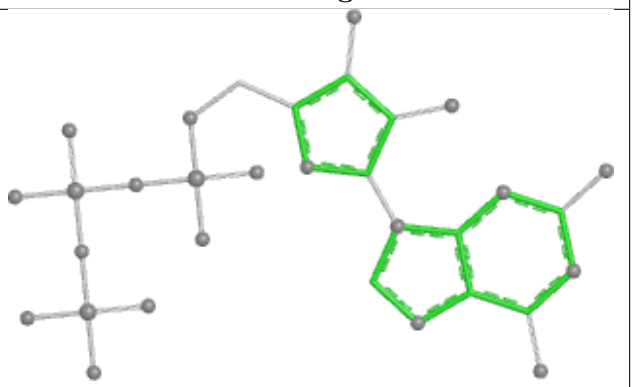
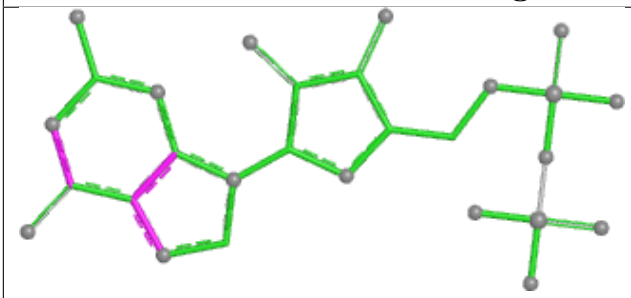


Rings

Ligand GDP SB 500



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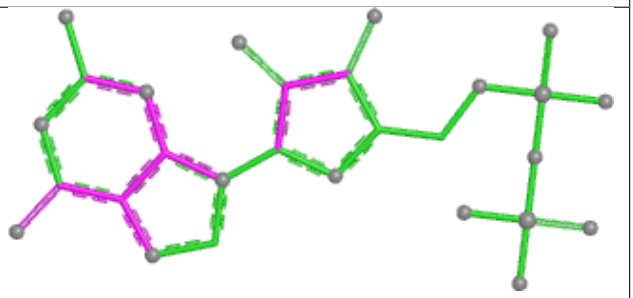

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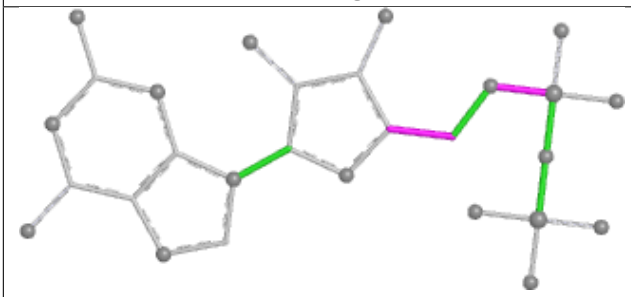

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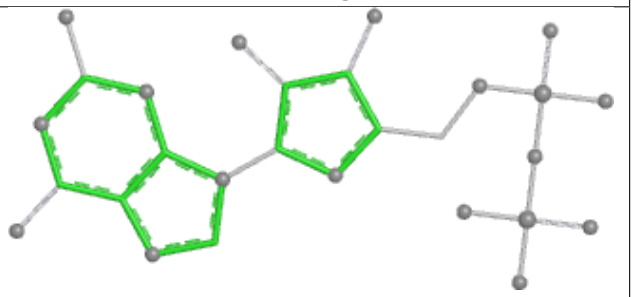
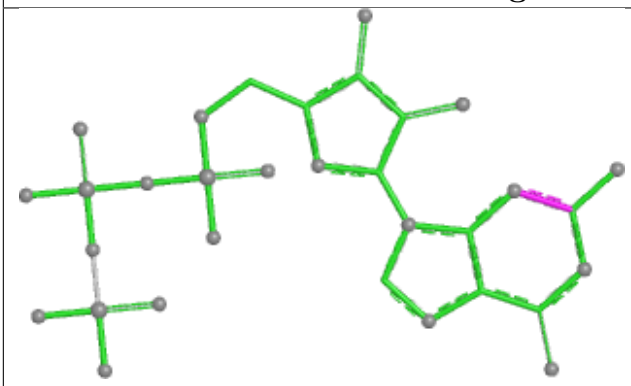


Rings

Ligand GTP BK 501



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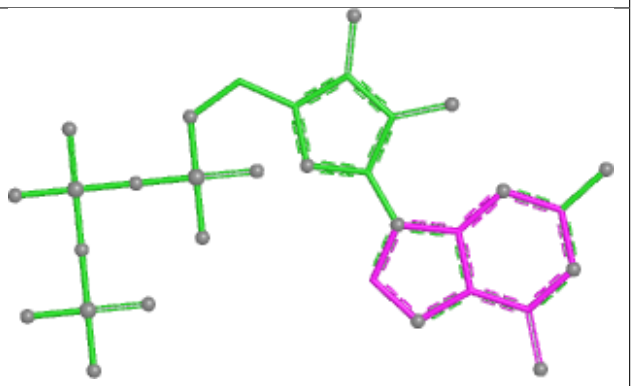

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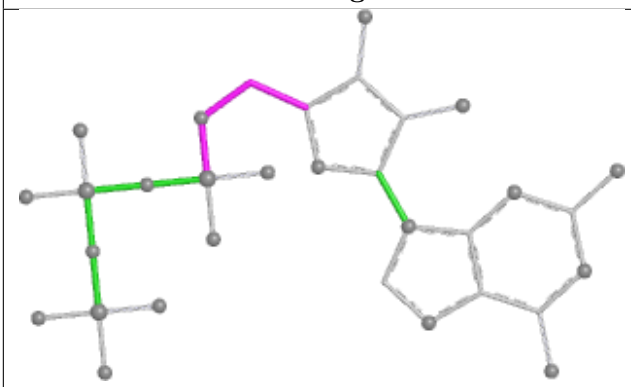

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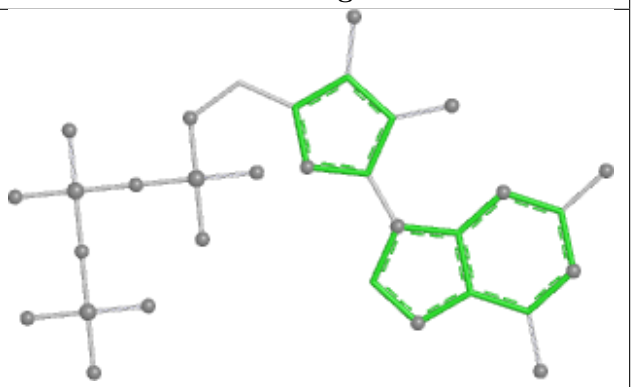
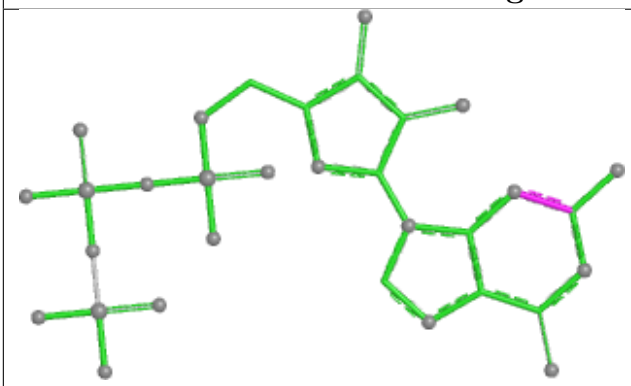


Rings

Ligand GTP PM 501



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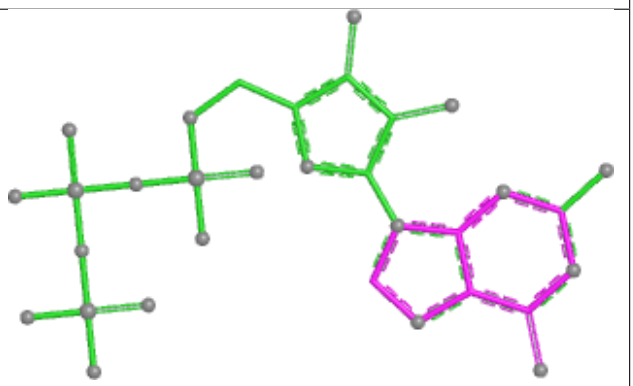

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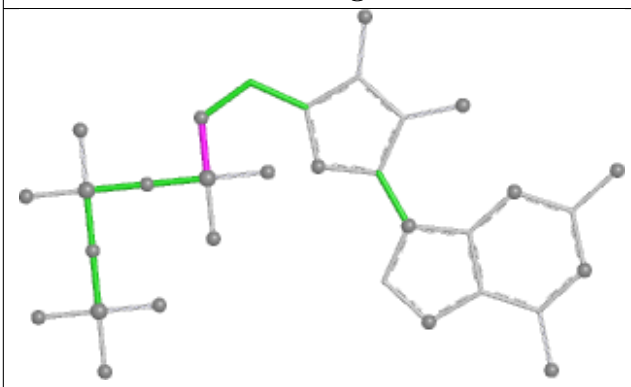

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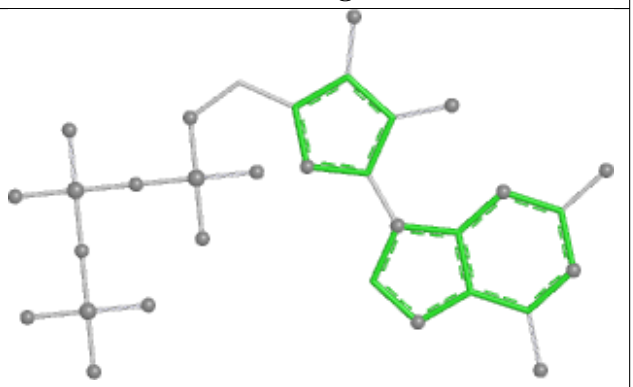
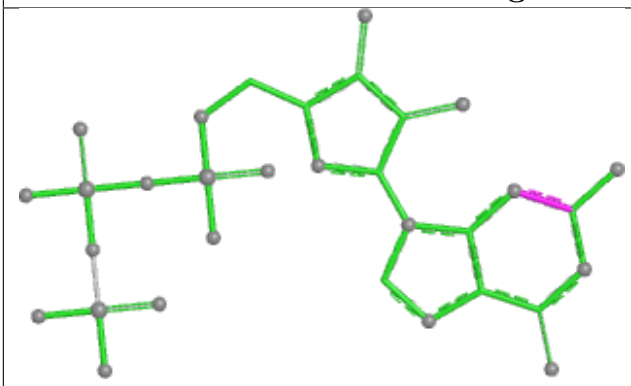


Rings

Ligand GTP NA 501



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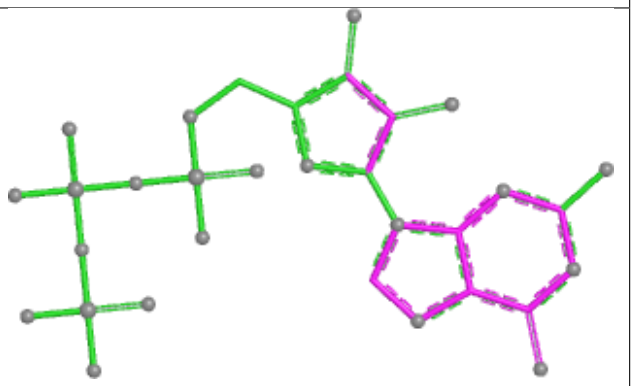

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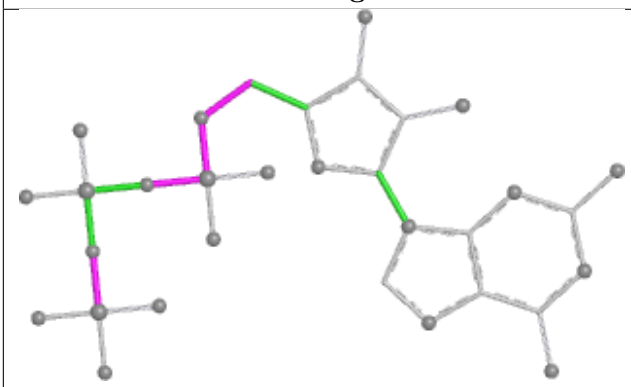

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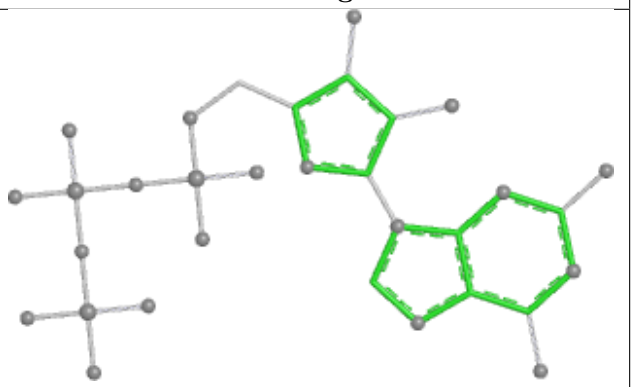

Rings

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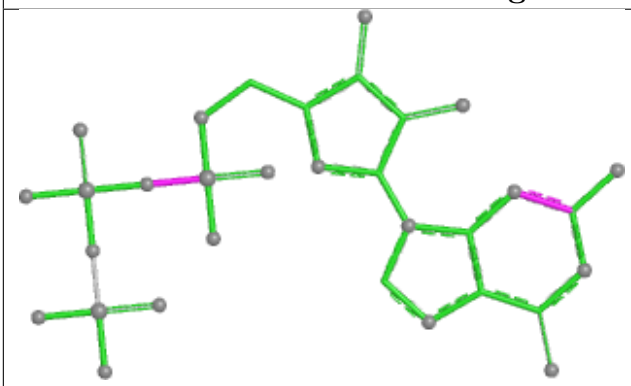

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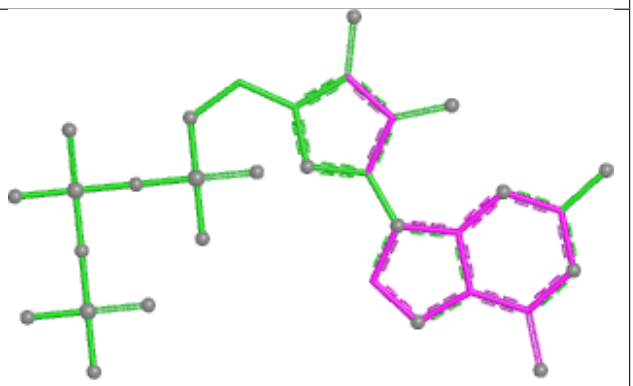

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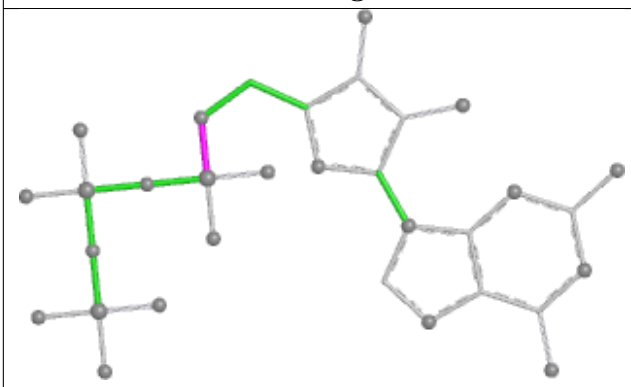

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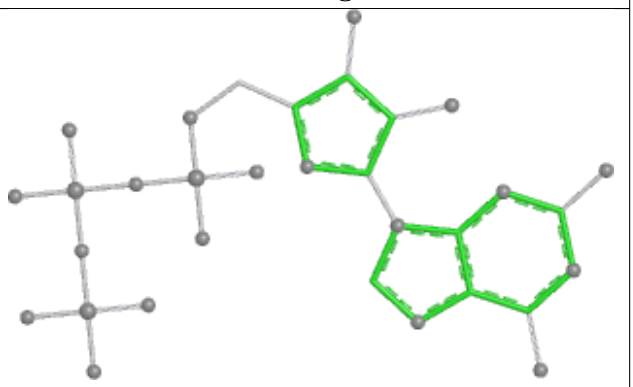
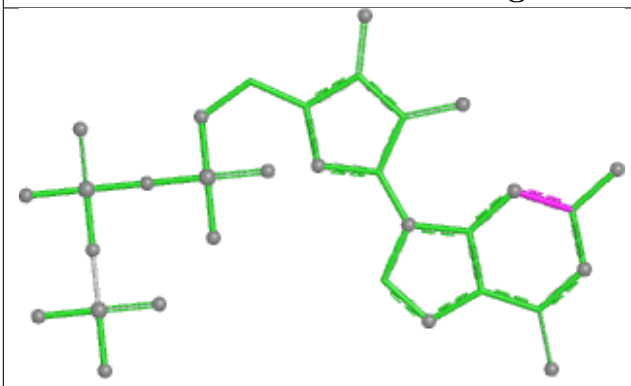


Rings

Ligand GTP AK 501



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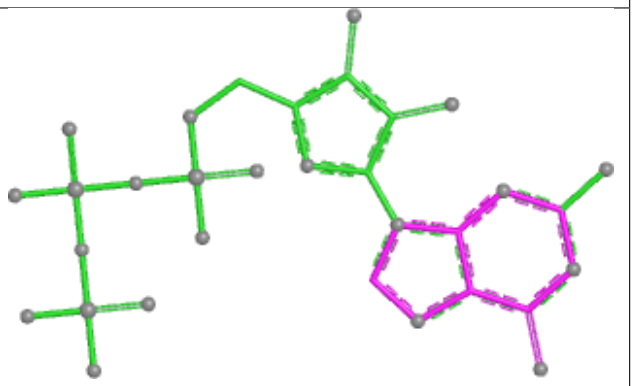

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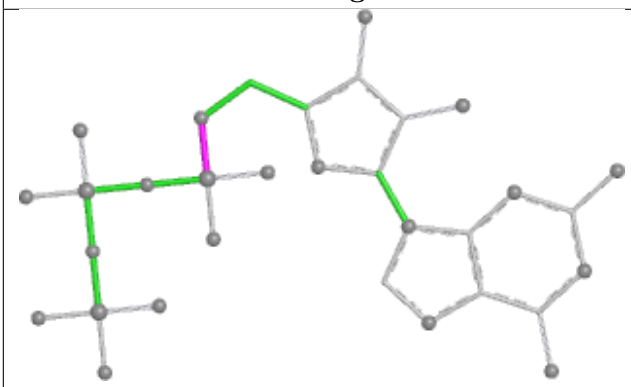

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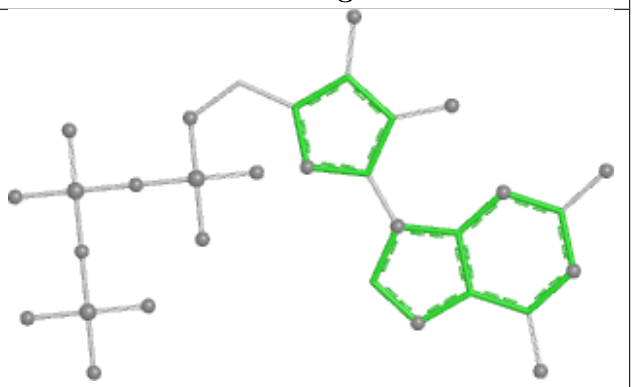
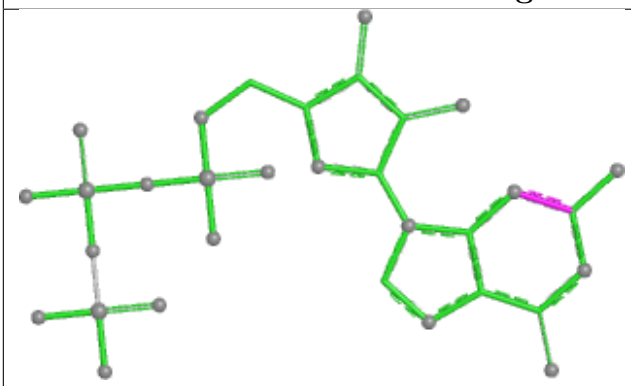


Rings

Ligand GTP JL 501



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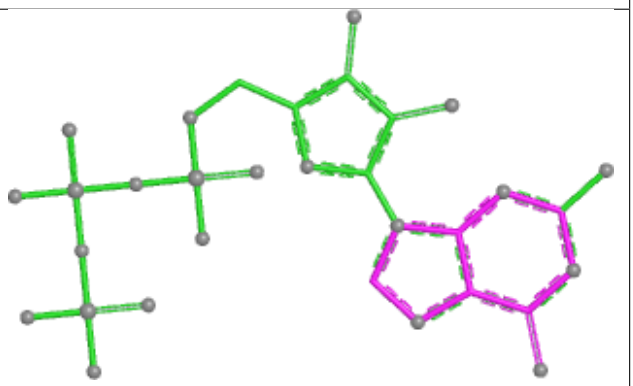

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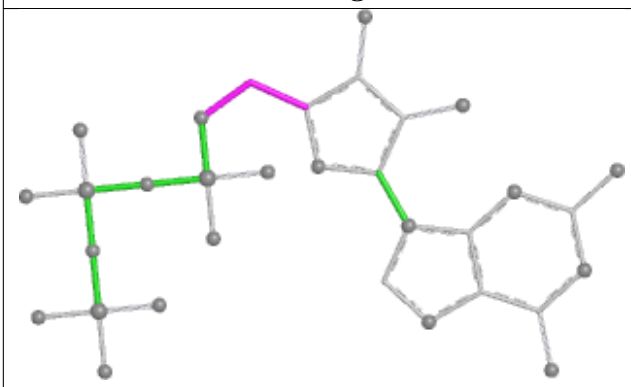

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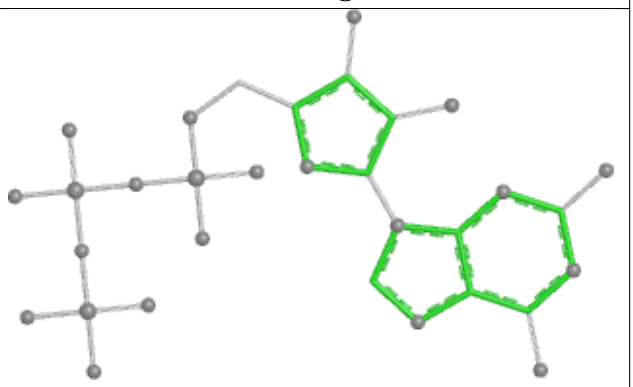
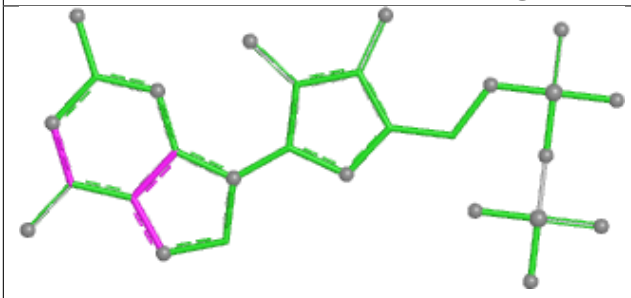


Rings

Ligand GDP KI 500



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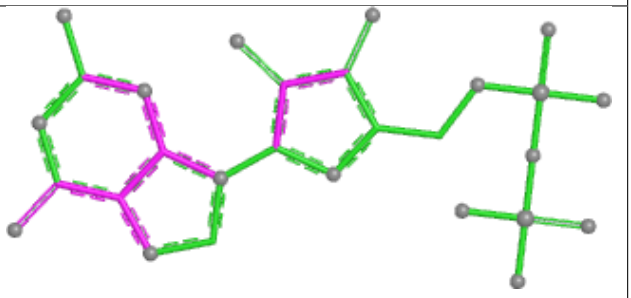

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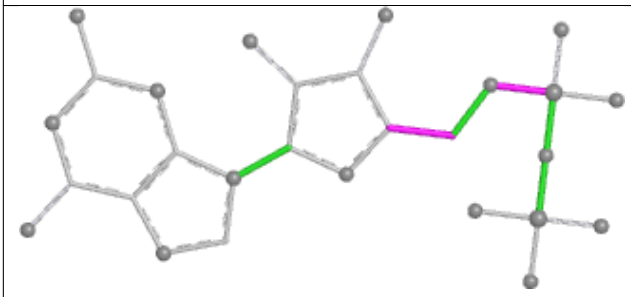
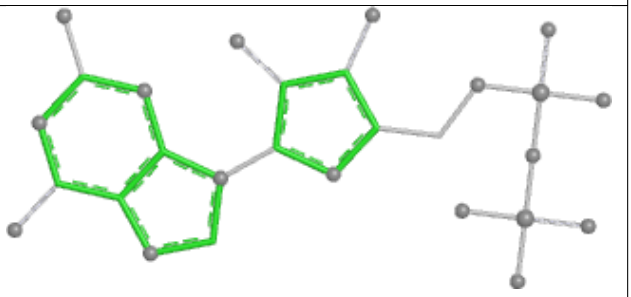
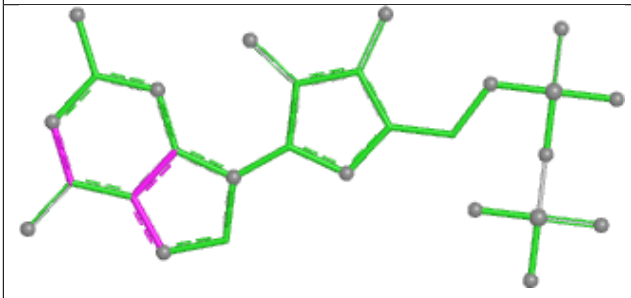


Torsions



Rings

Ligand GDP VL 500



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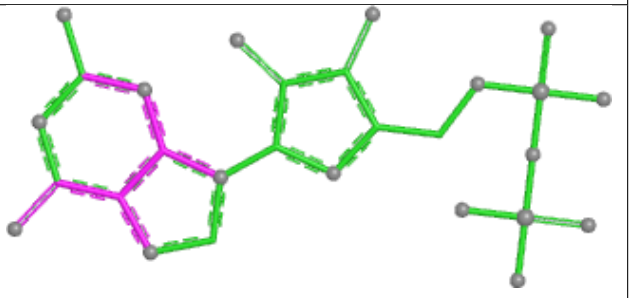
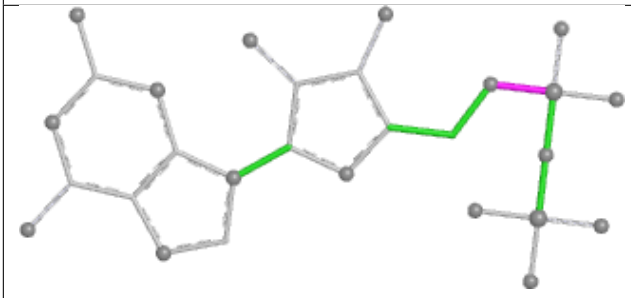


Bond angles



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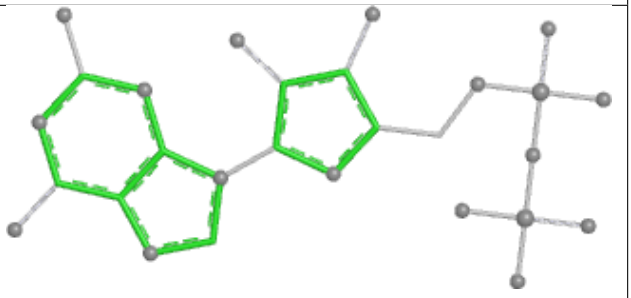
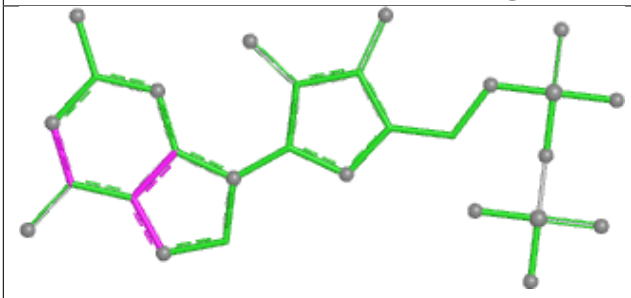


Rings

Ligand GDP MD 500



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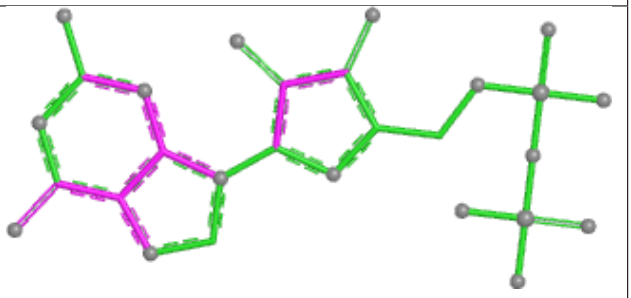

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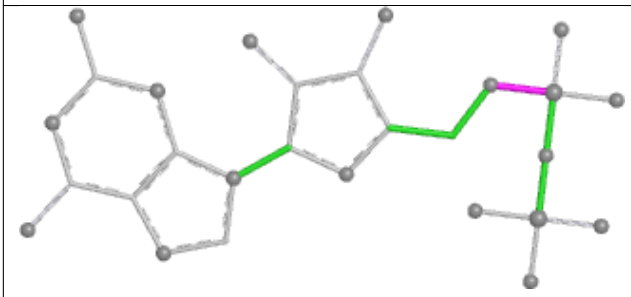
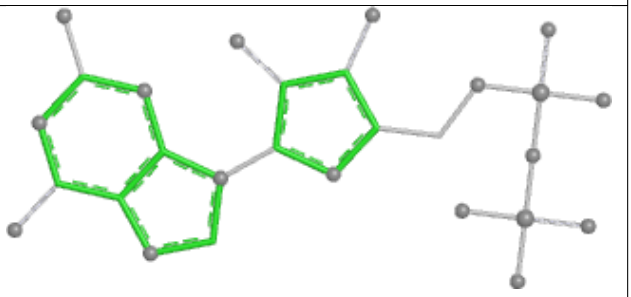
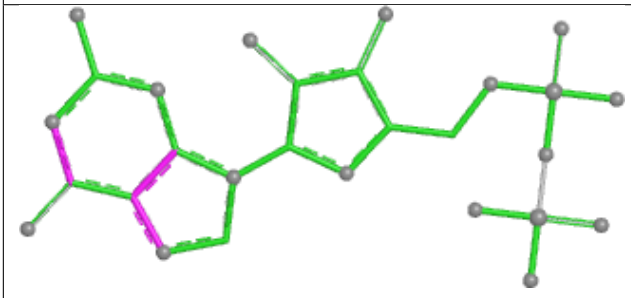


Torsions



Rings

Ligand GDP OD 500



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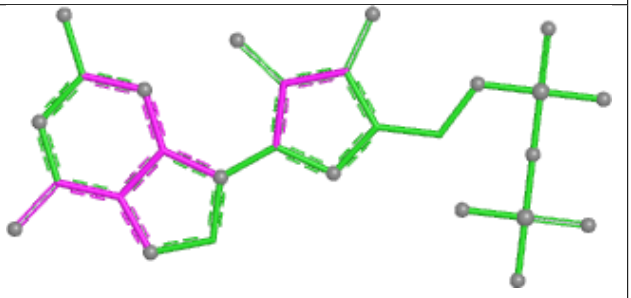

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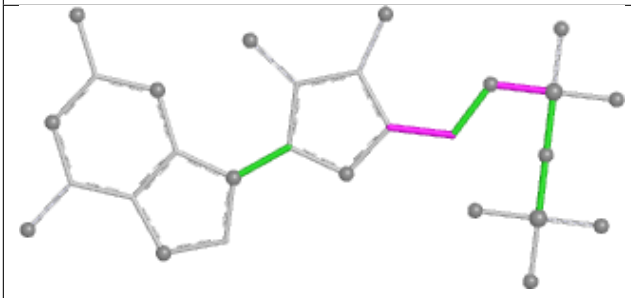

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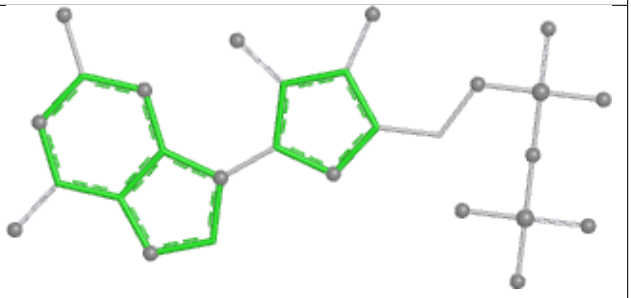
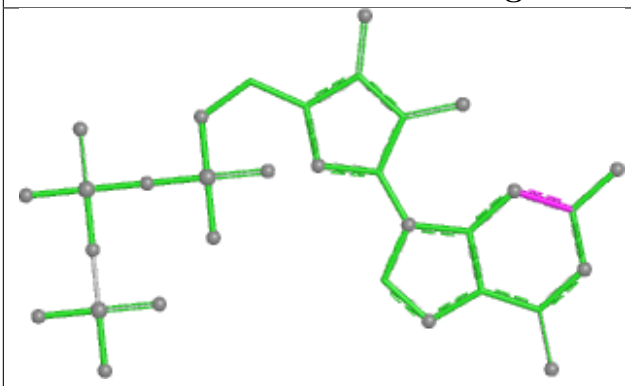


Rings

Ligand GTP AM 501



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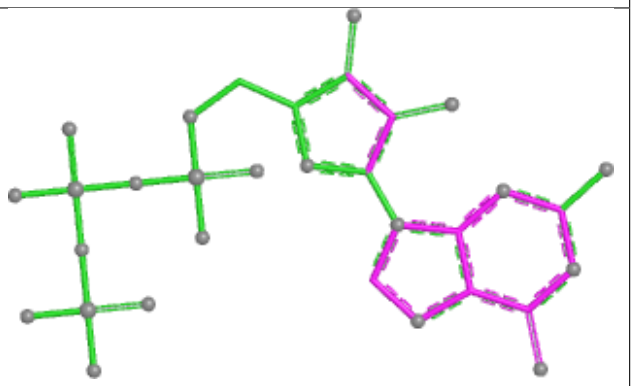

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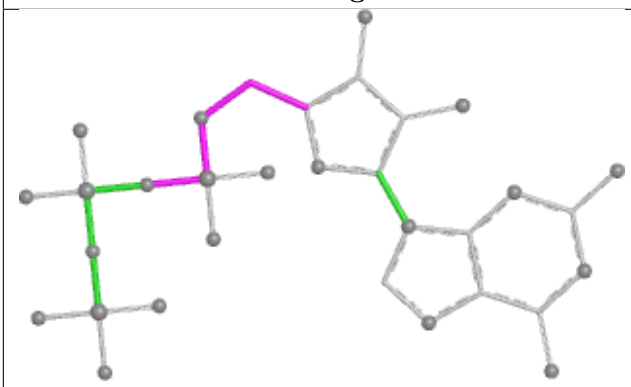

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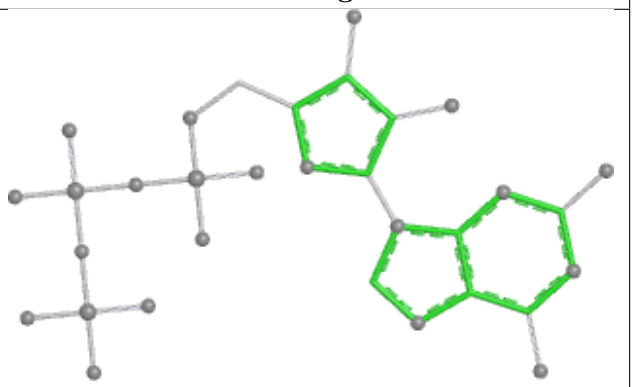
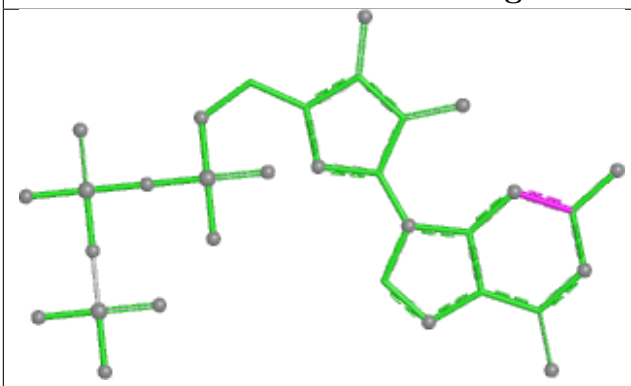


Rings

Ligand GTP NM 501



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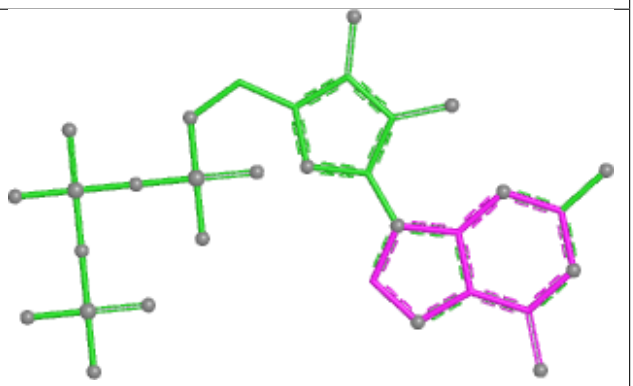

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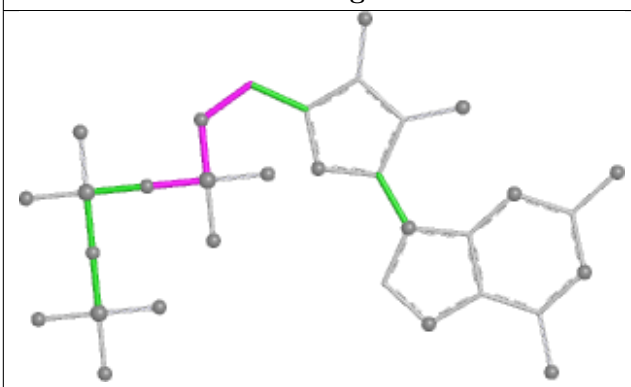

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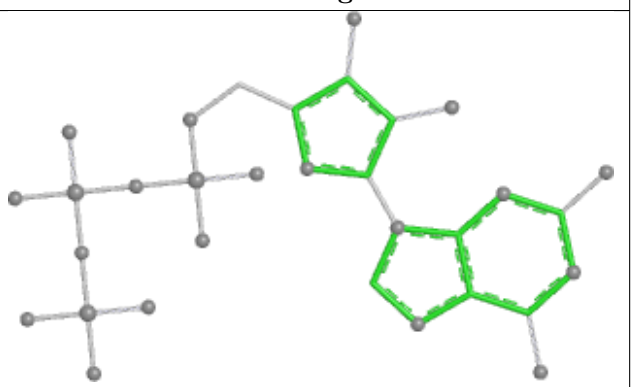
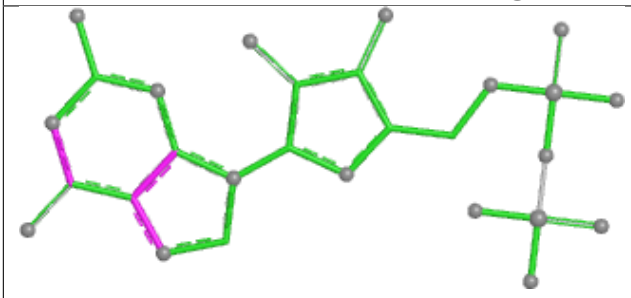


Rings

Ligand GDP EH 500



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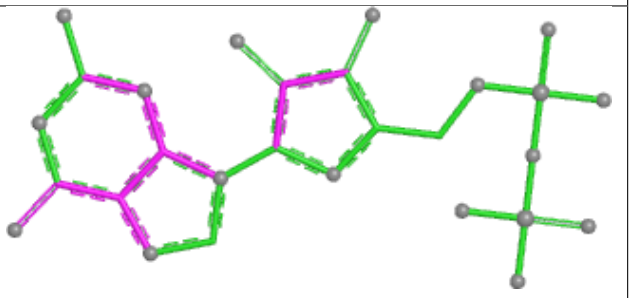

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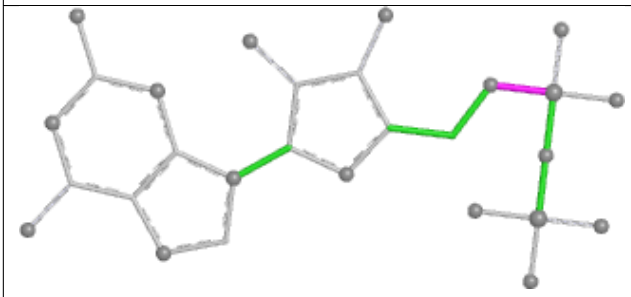

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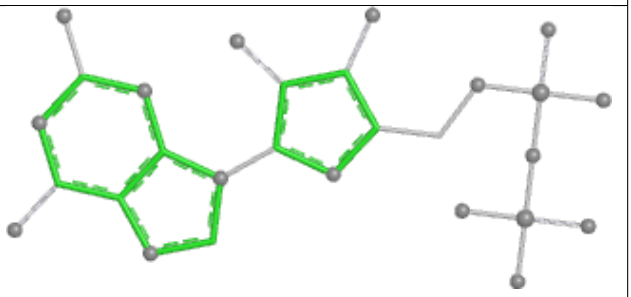
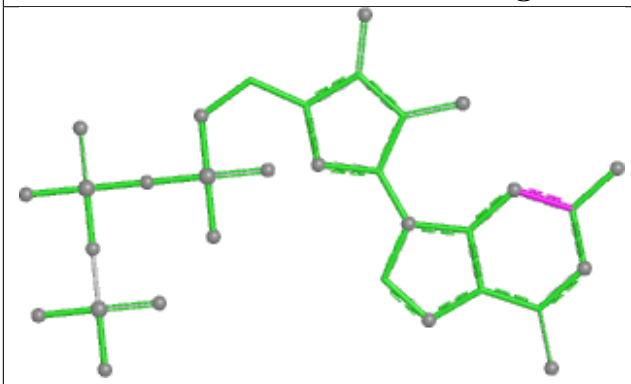


Rings

Ligand GTP GI 501



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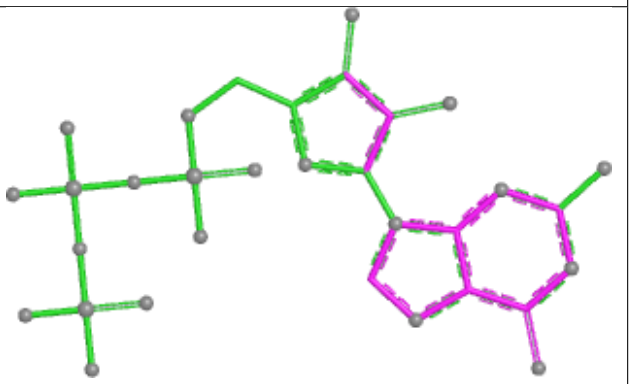

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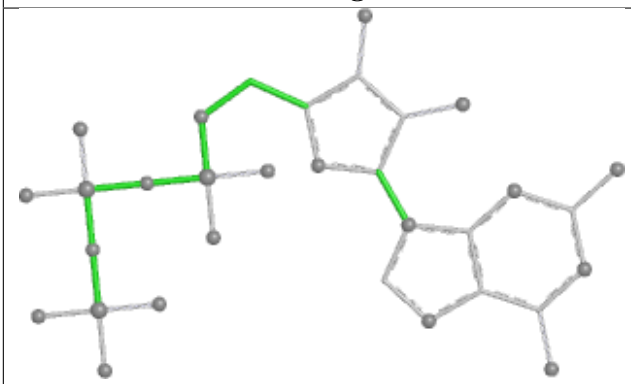

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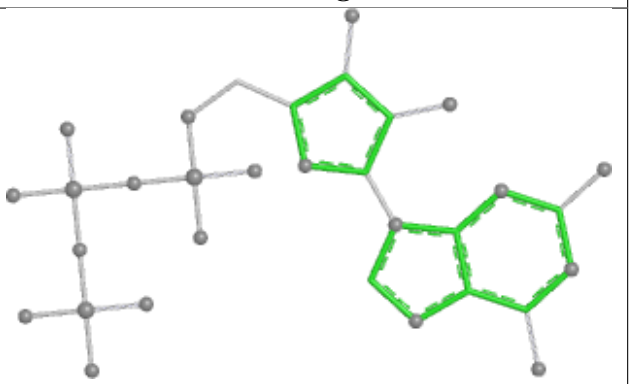
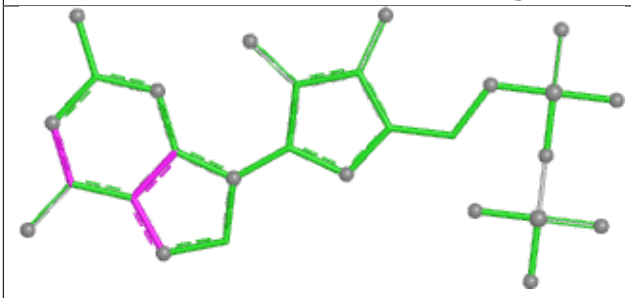


Rings

Ligand GDP UL 500



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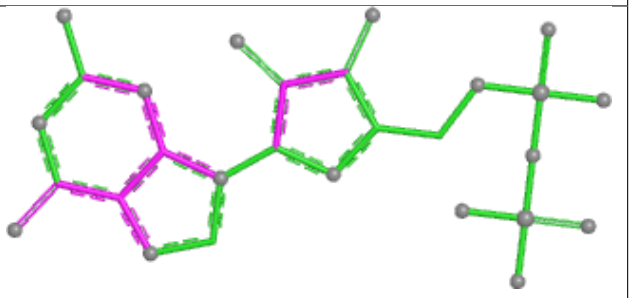

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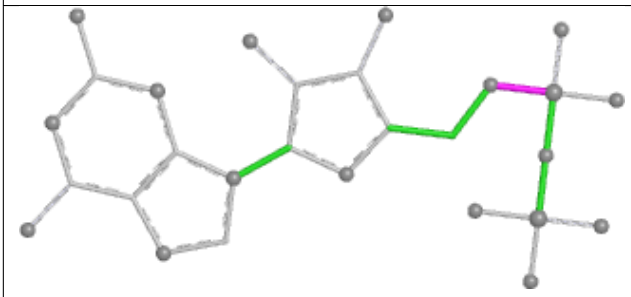

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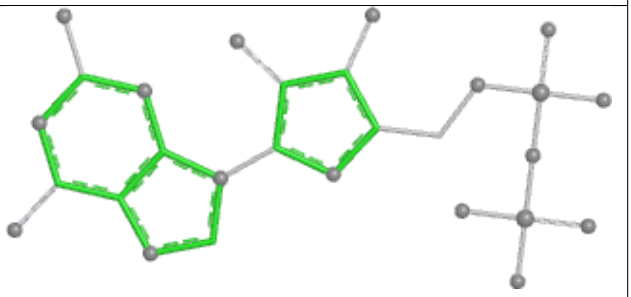
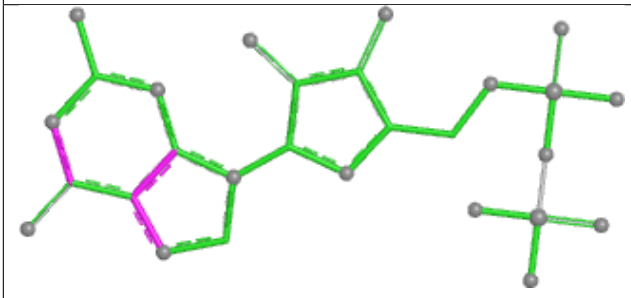


Rings

Ligand GDP QE 500



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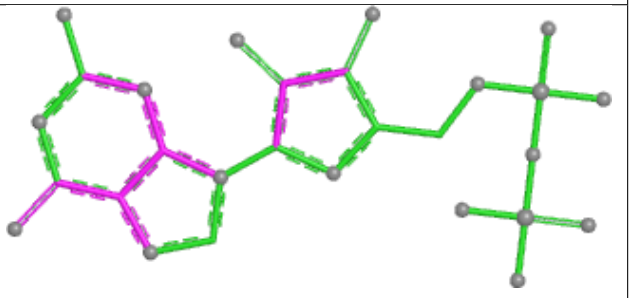

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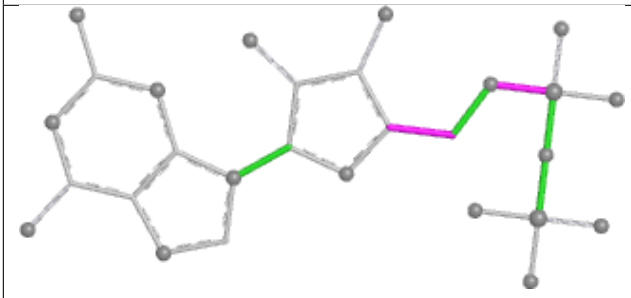

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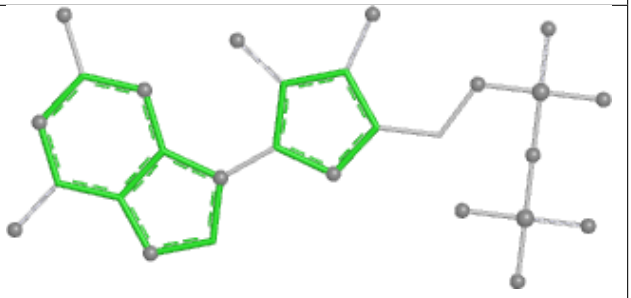
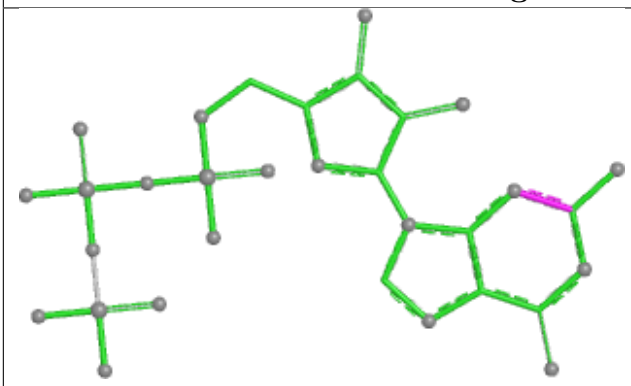


Rings

Ligand GTP WI 501



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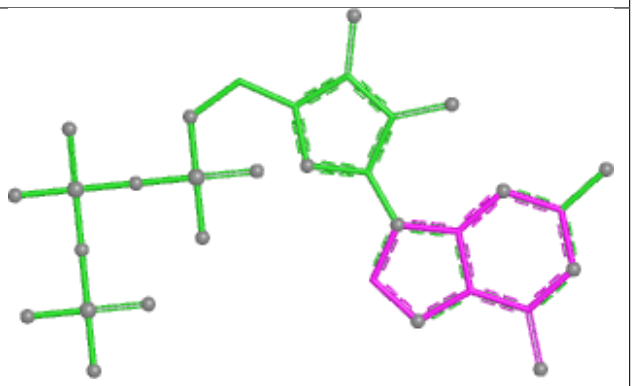

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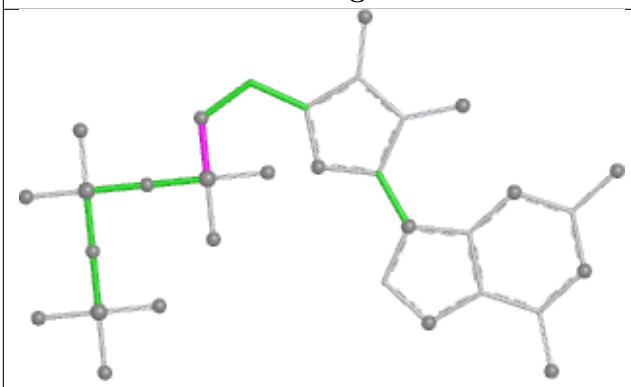

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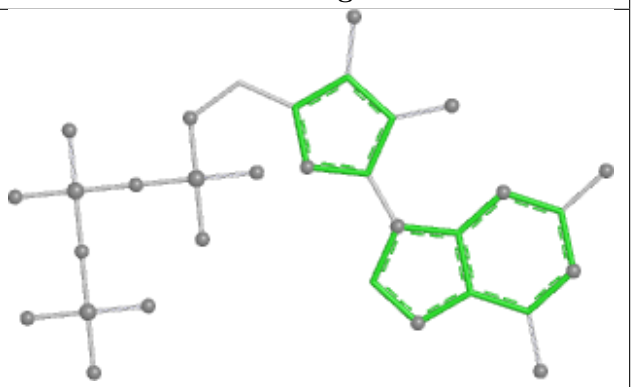
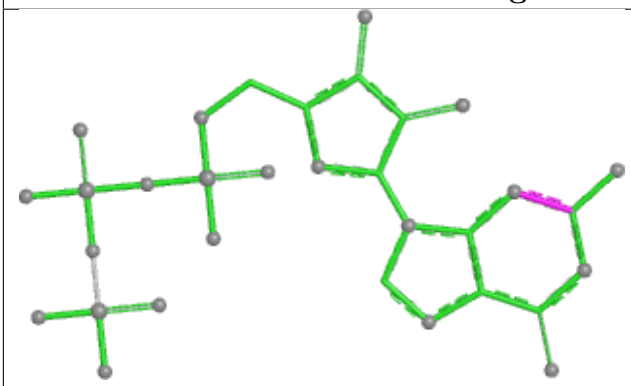


Rings

Ligand GTP PG 501



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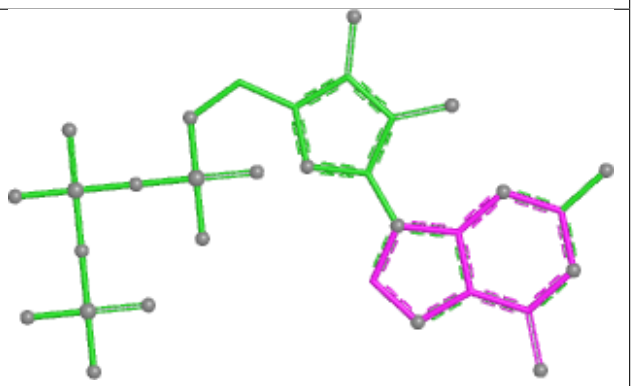

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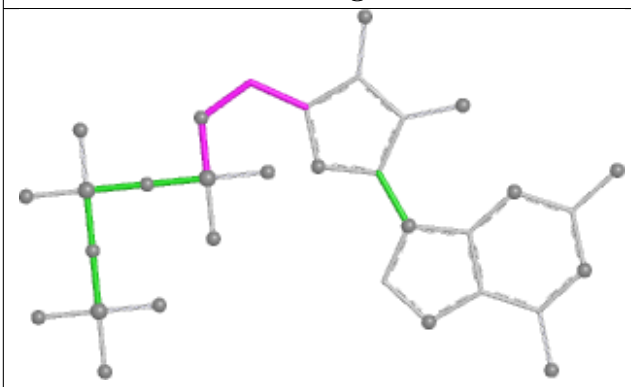

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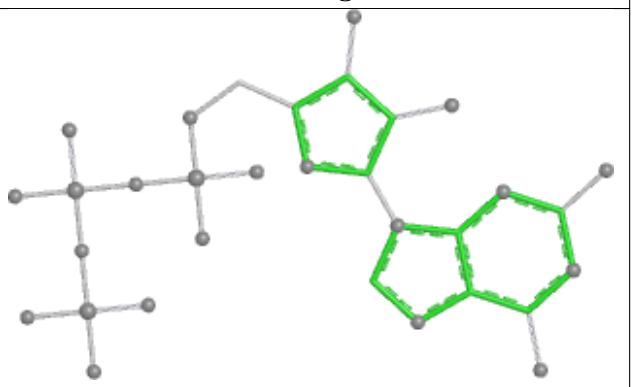
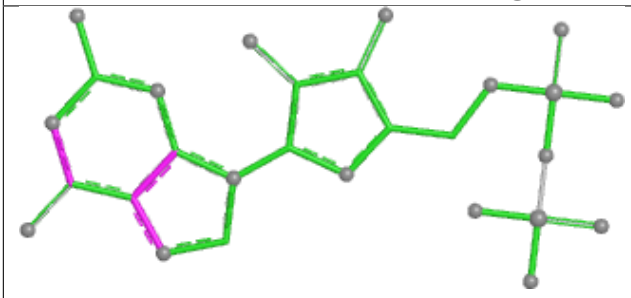
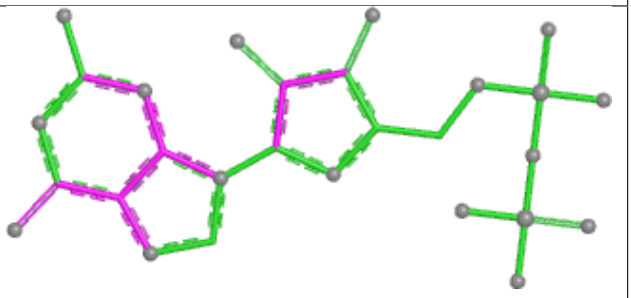
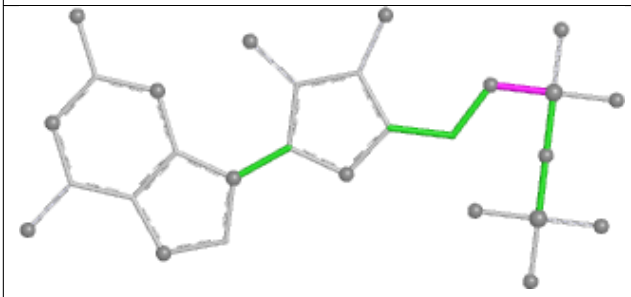
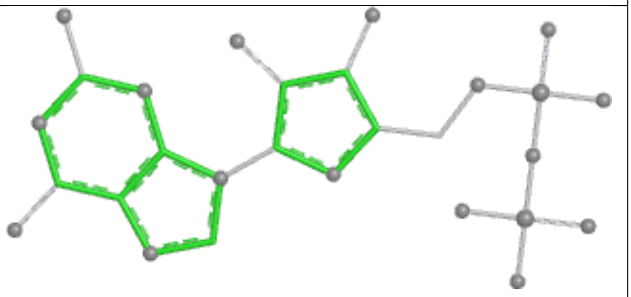
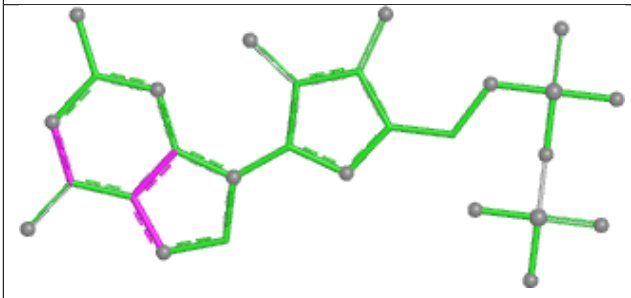
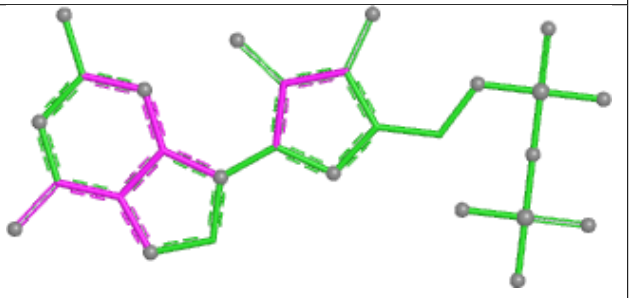
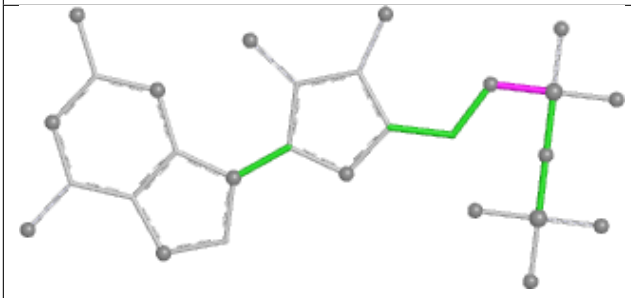
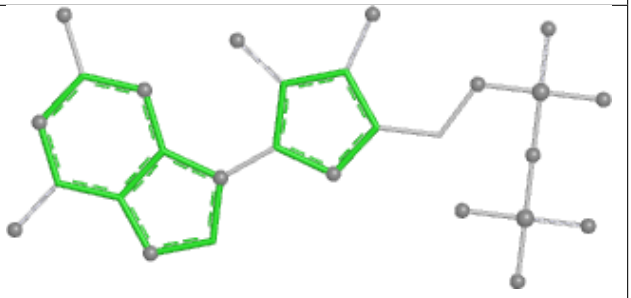
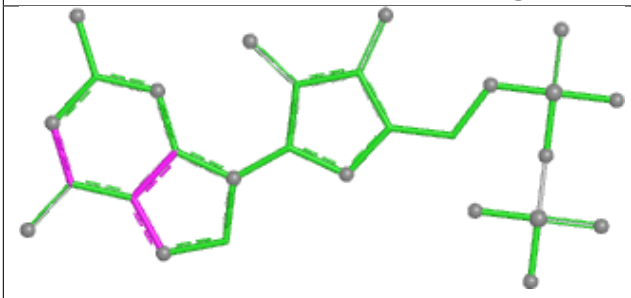


Rings

Ligand GDP RC 500	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP WF 500	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP GL 500



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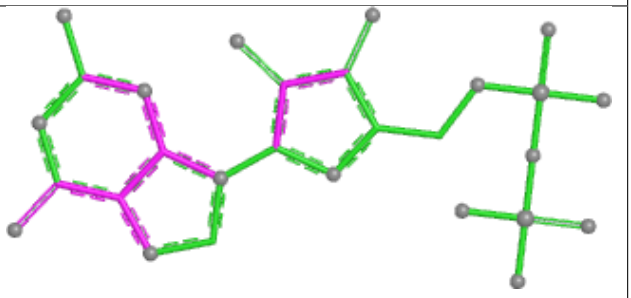

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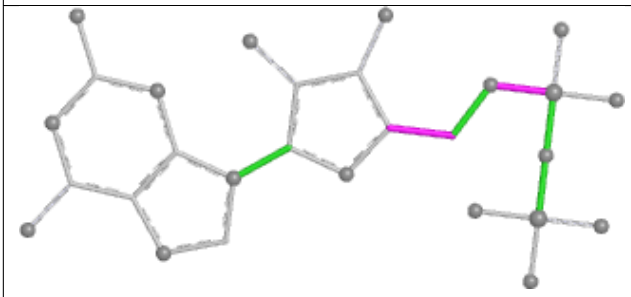
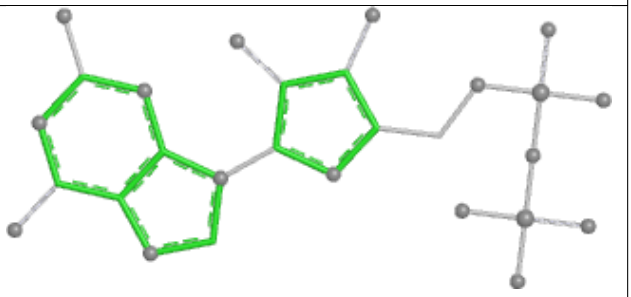
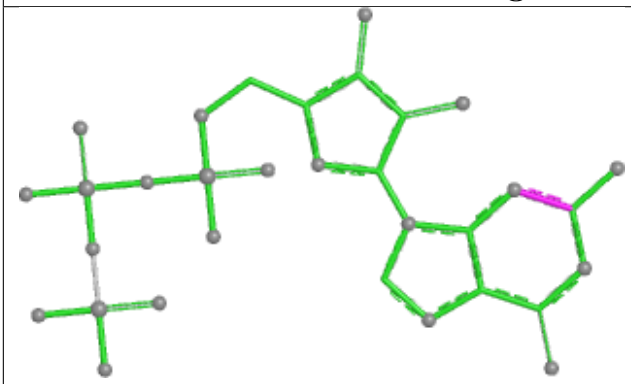


Torsions



Rings

Ligand GTP GG 501



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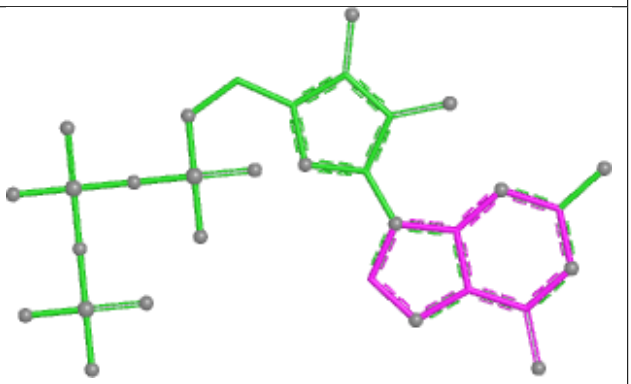

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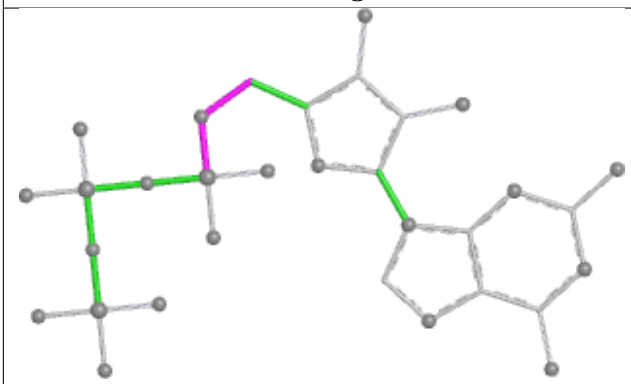

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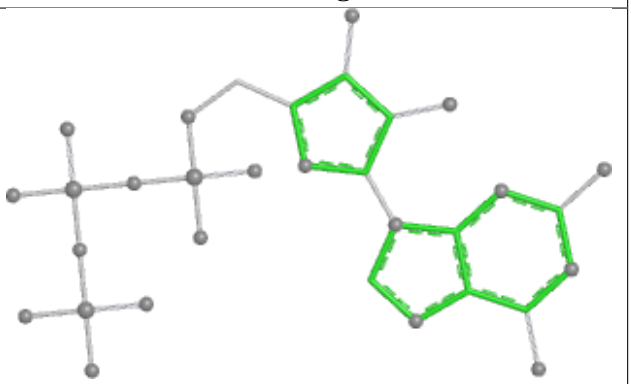
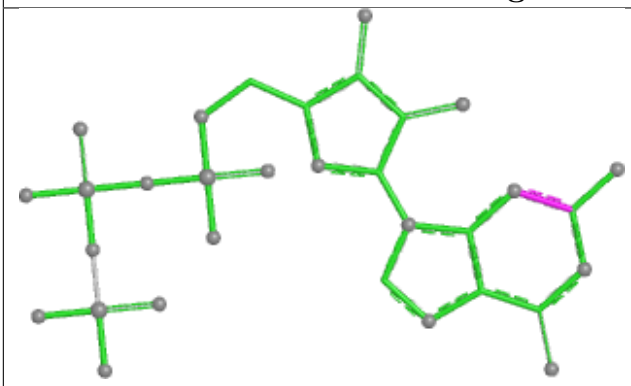


Rings

Ligand GTP HG 501



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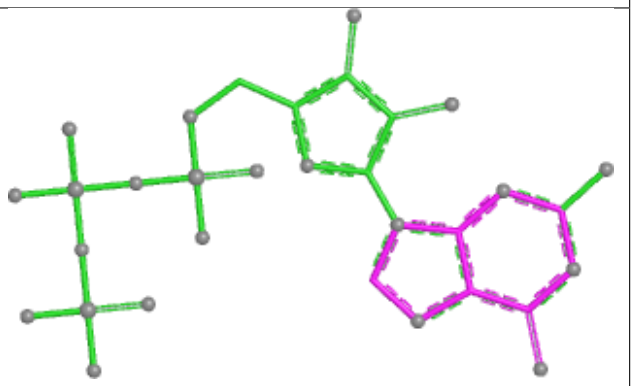

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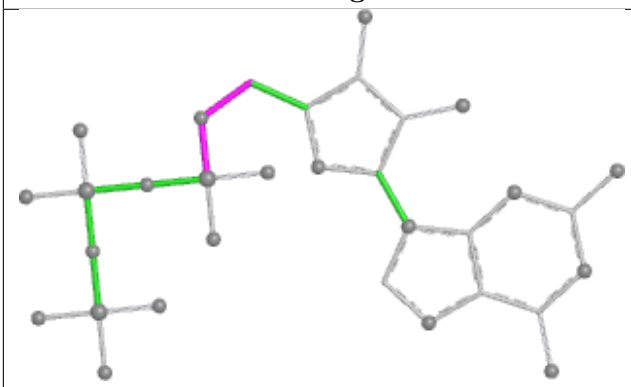
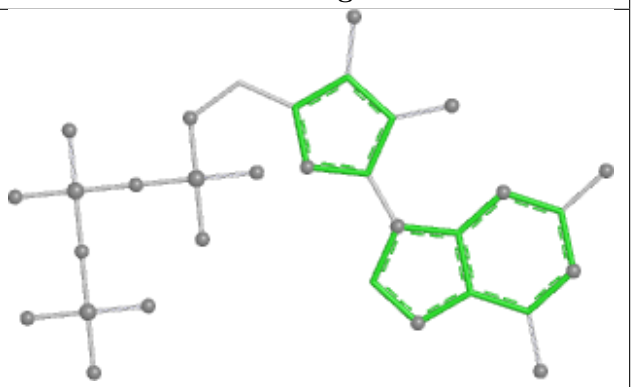
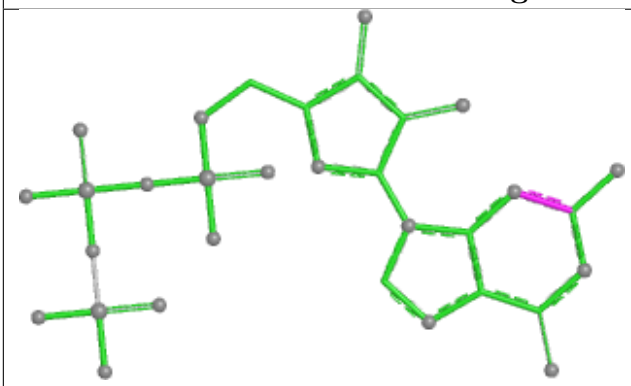


Torsions



Rings

Ligand GTP VA 501



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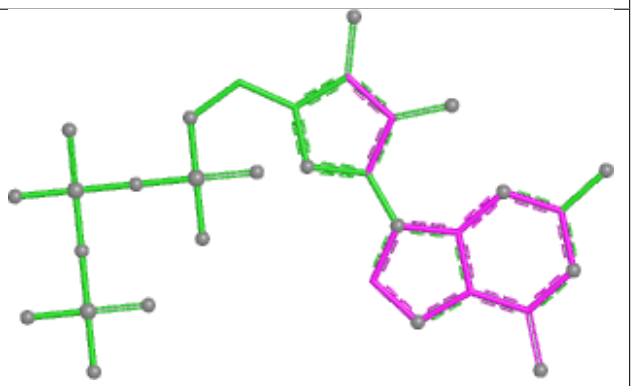

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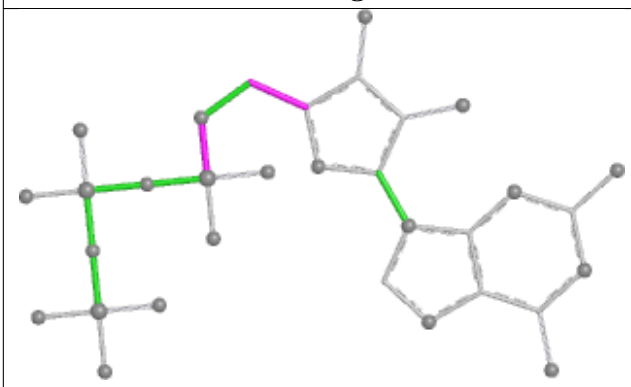

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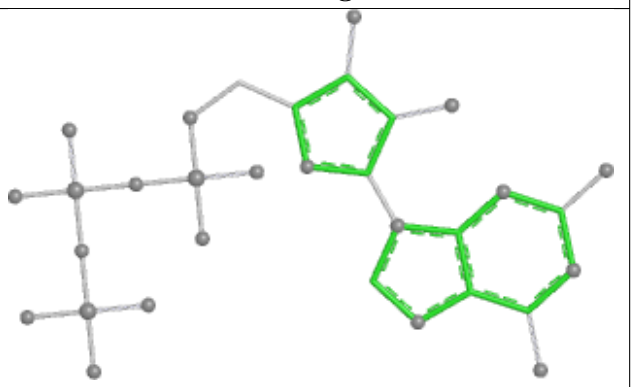
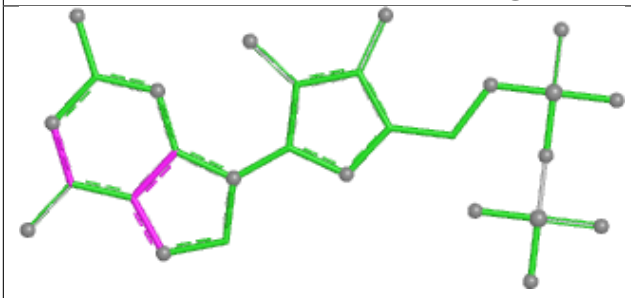


Rings

Ligand GDP VH 500



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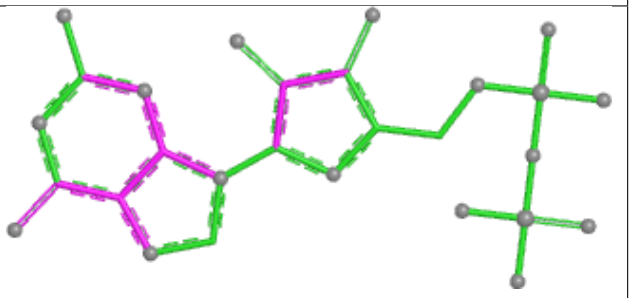

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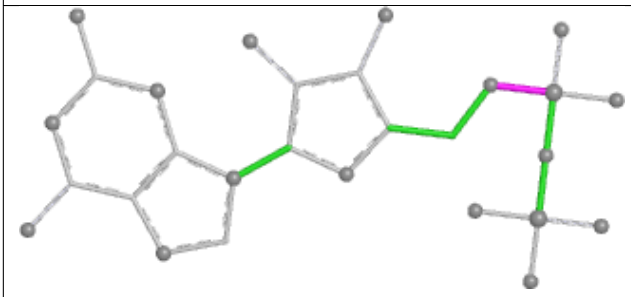

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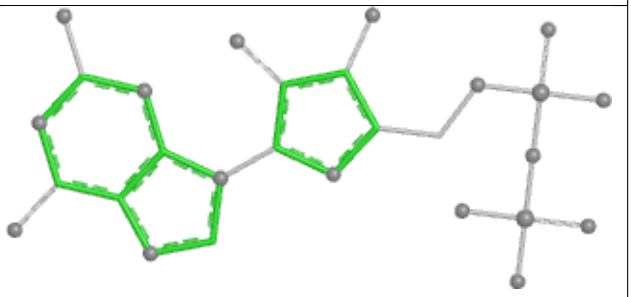

Rings

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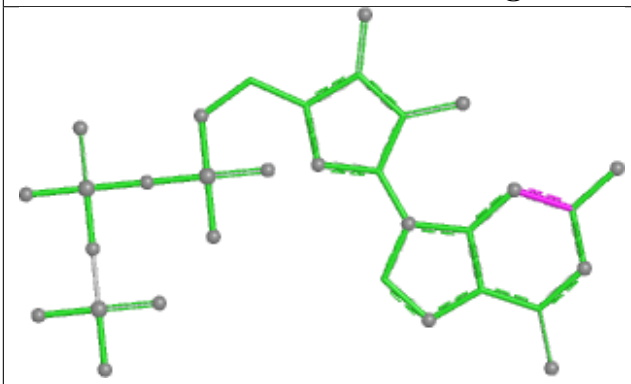

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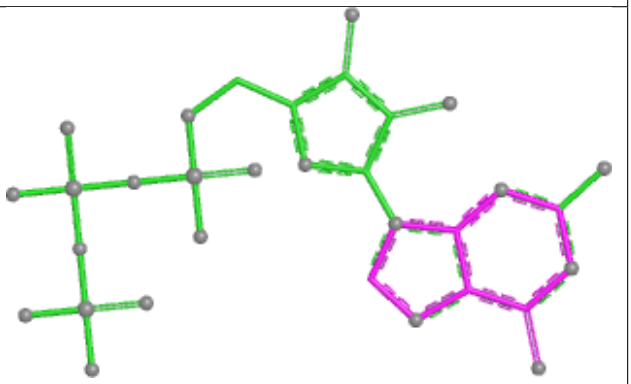

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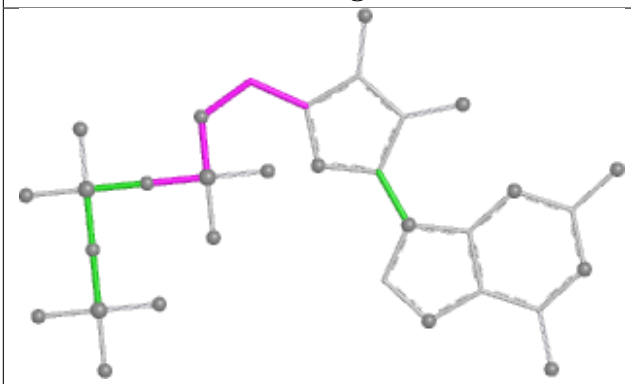

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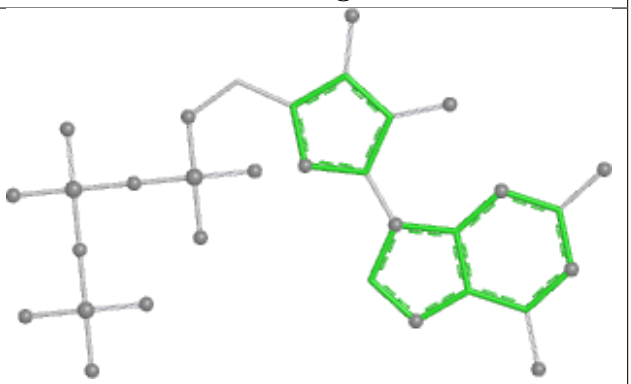
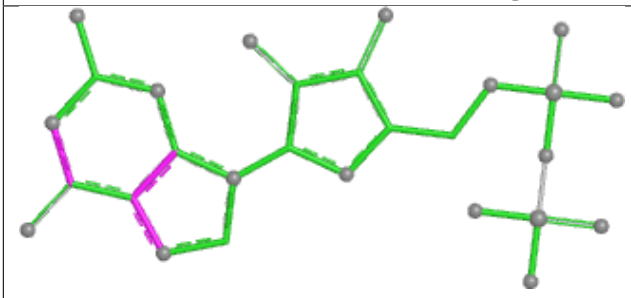


Rings

Ligand GDP ND 500



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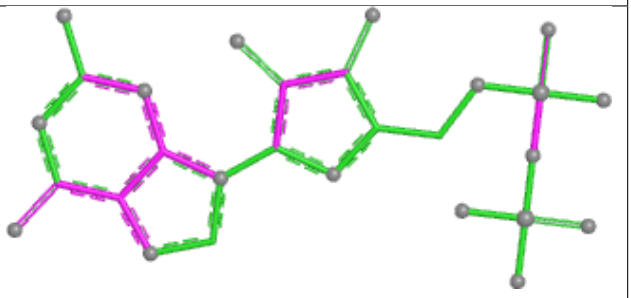

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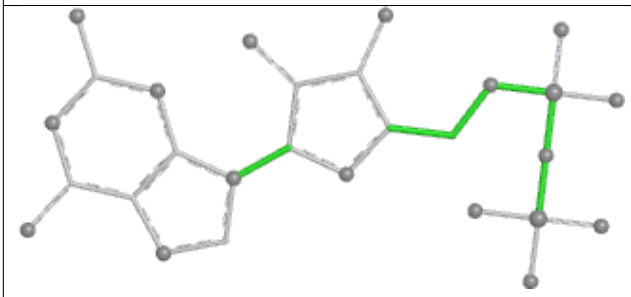

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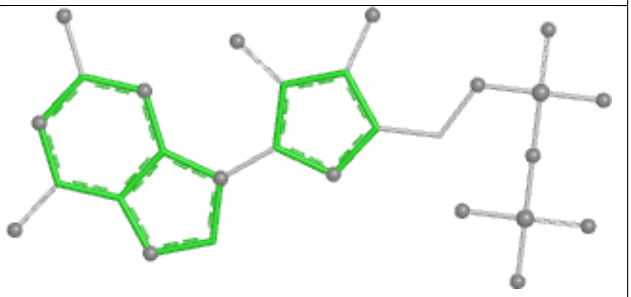

Rings

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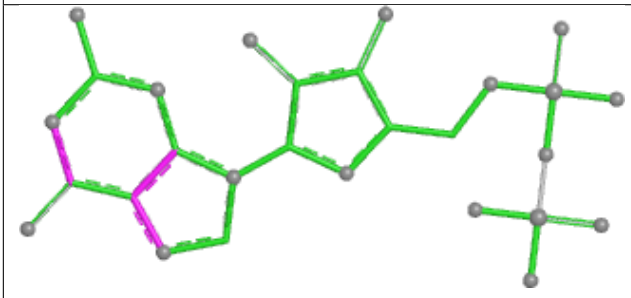

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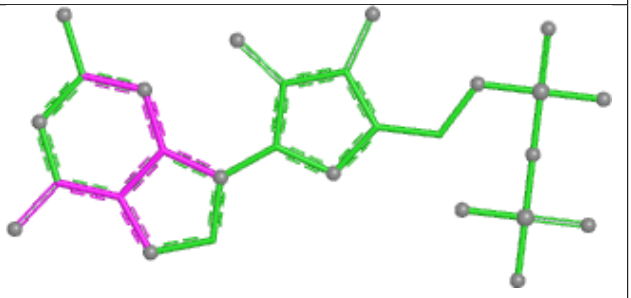

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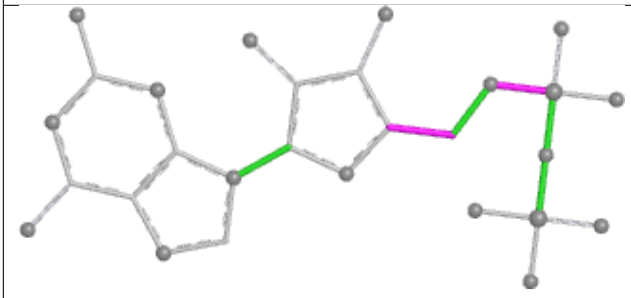

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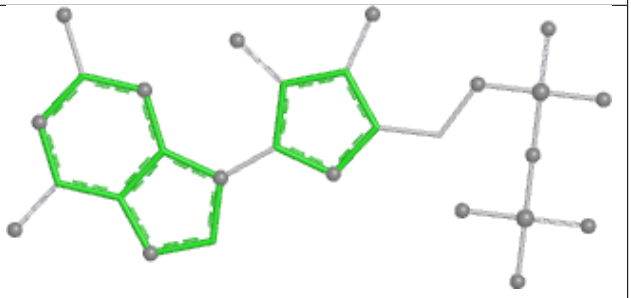

Rings

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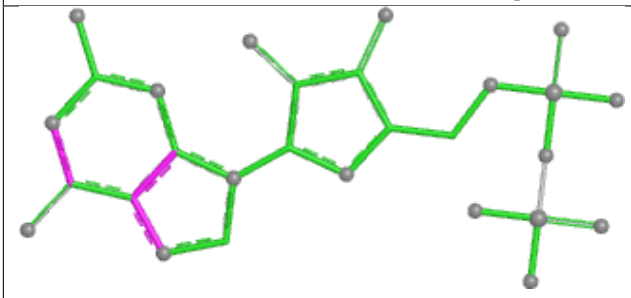

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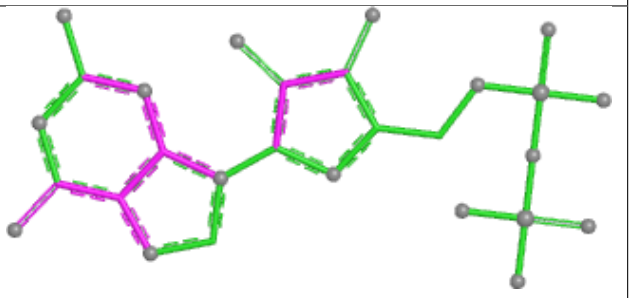

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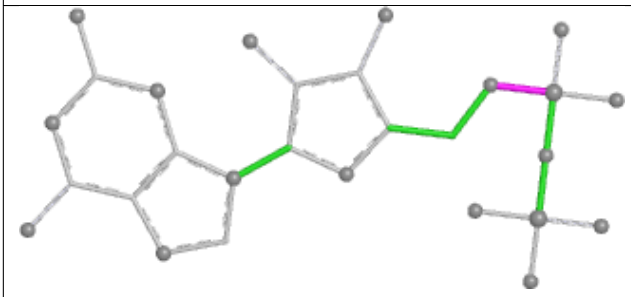

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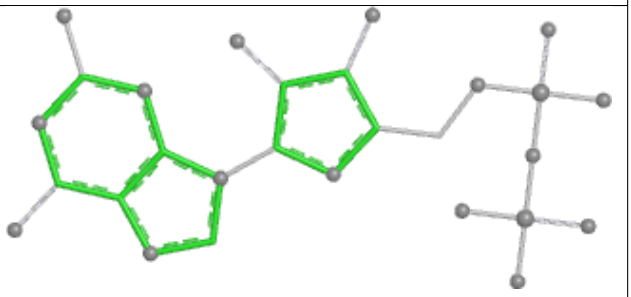
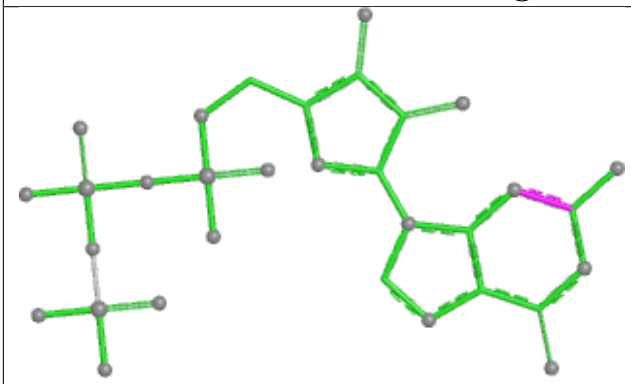


Rings

Ligand GTP CJ 501



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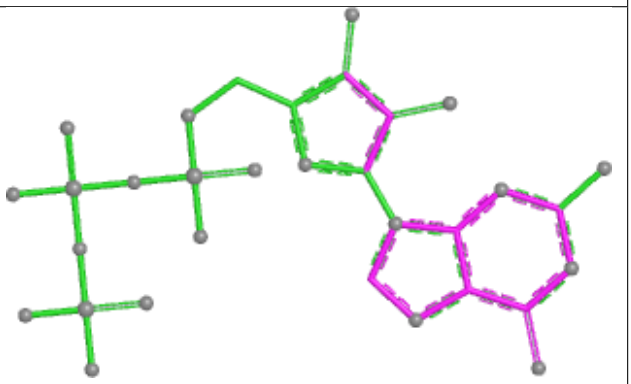

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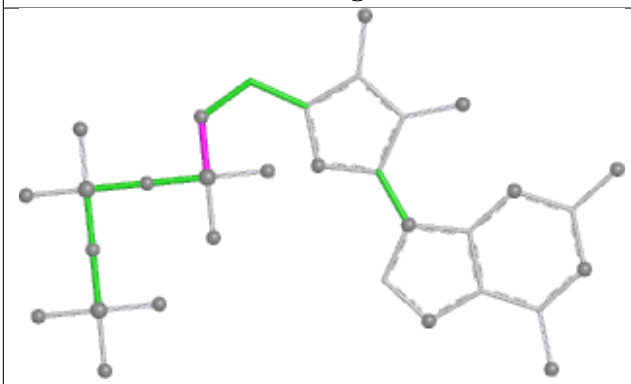

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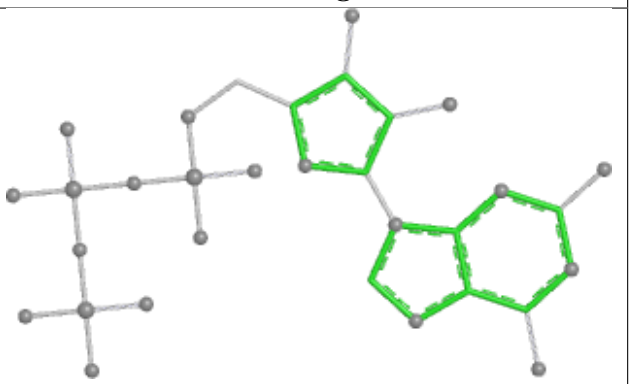
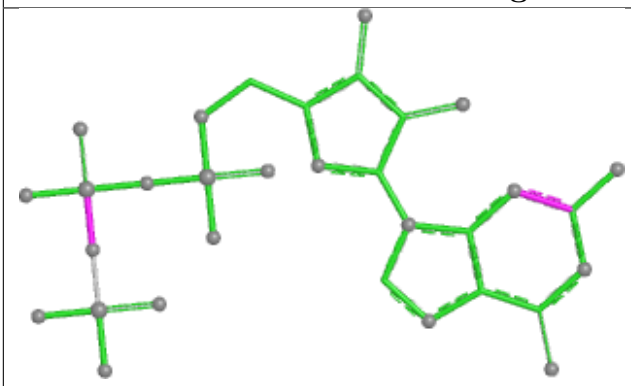


Rings

Ligand GTP EK 501



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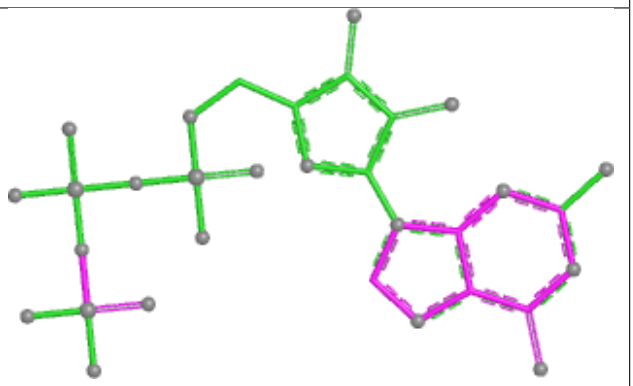

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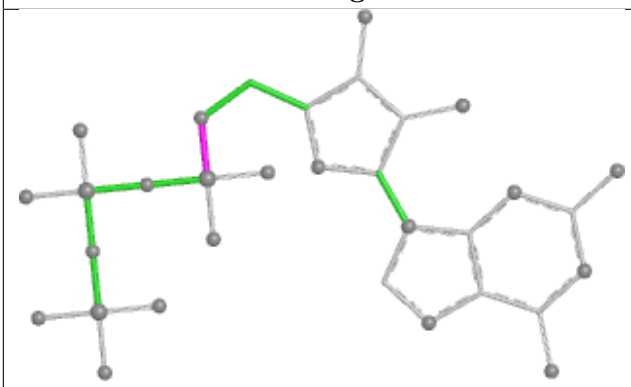

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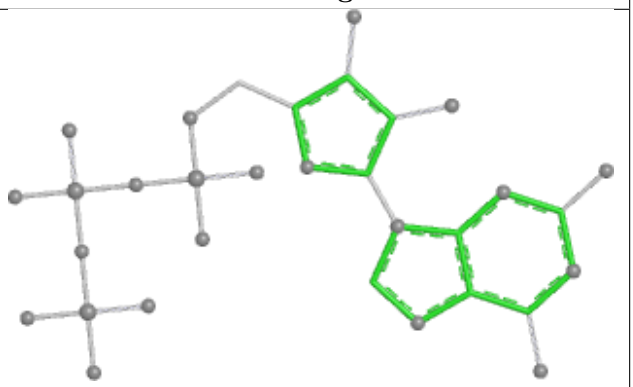
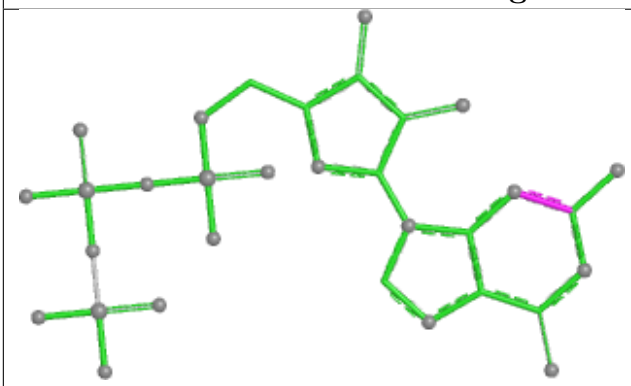


Rings

Ligand GTP OC 501



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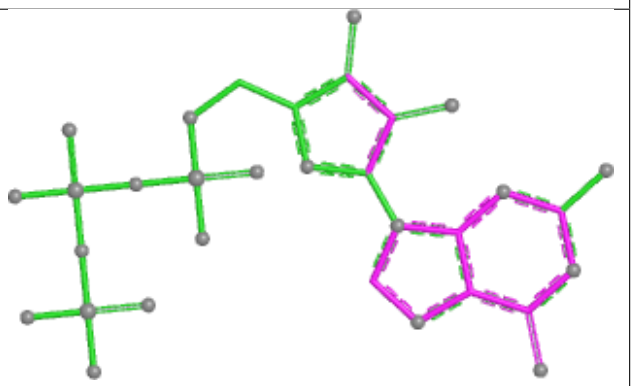

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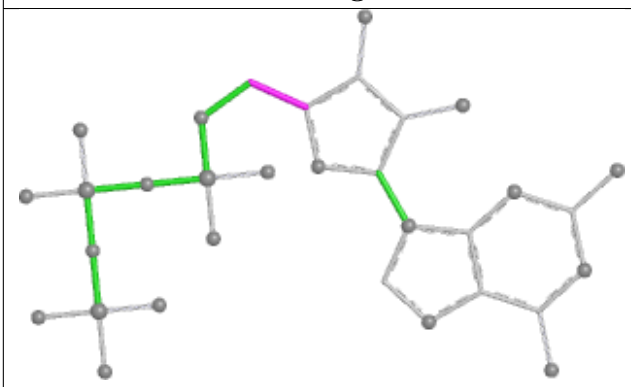

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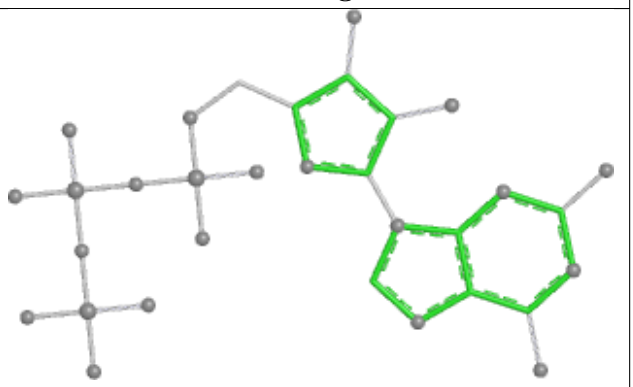
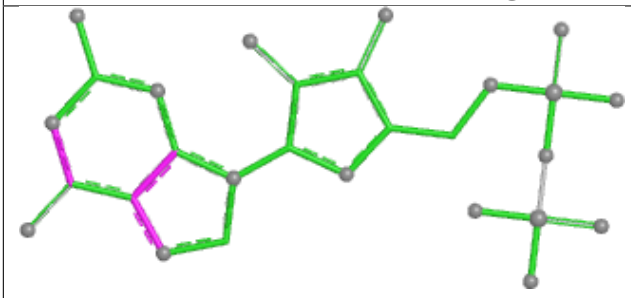


Rings

Ligand GDP MH 500



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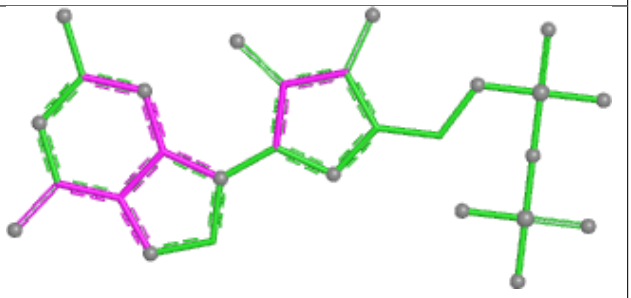

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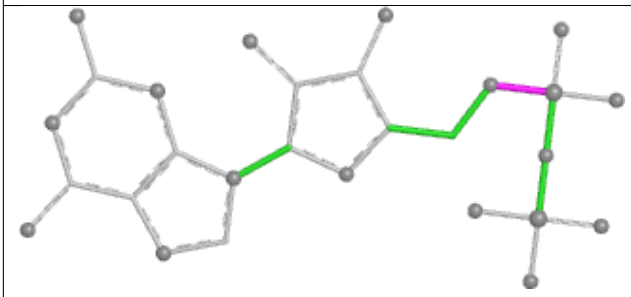

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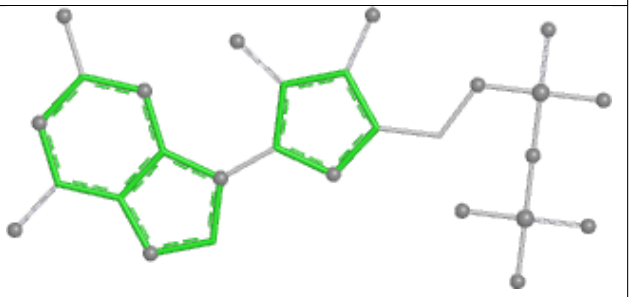
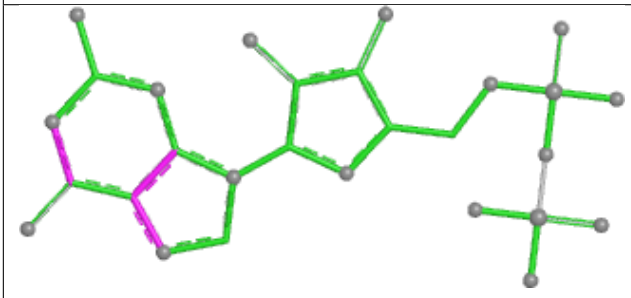


Rings

Ligand GDP WB 500



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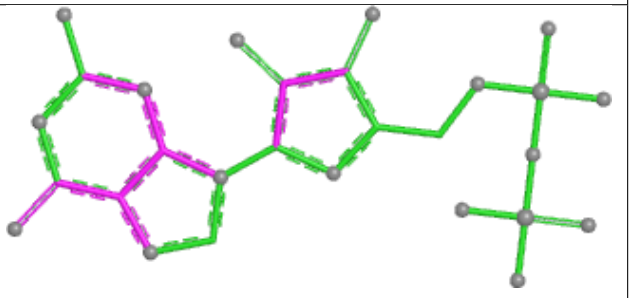
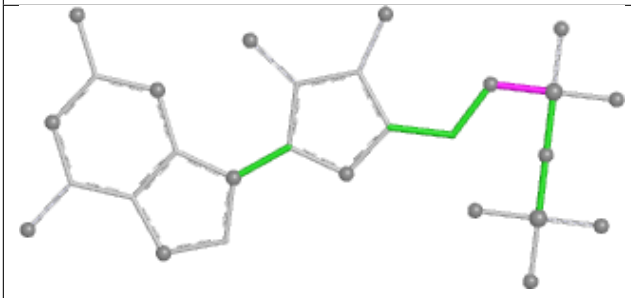


Bond angles



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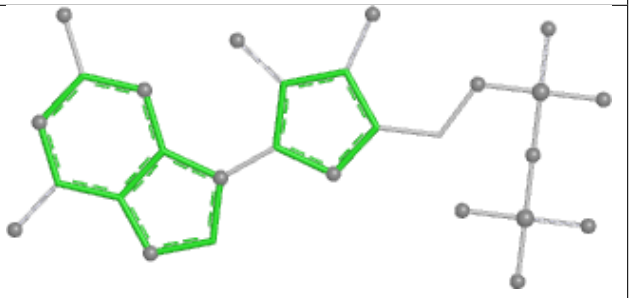
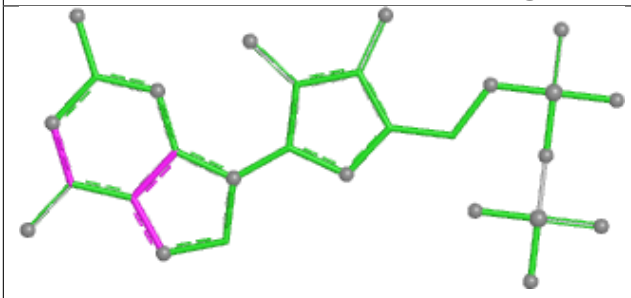


Rings

Ligand GDP A 500



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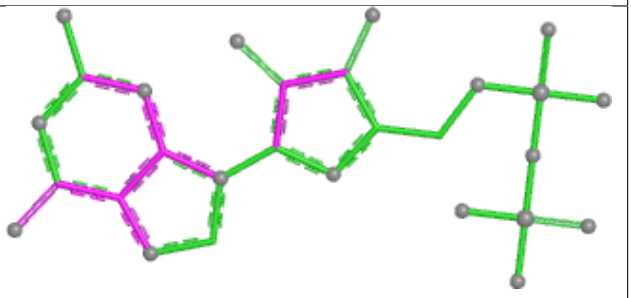
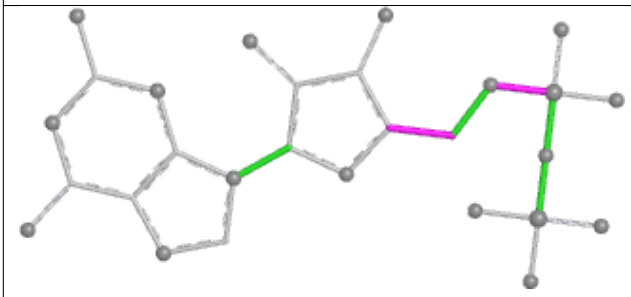


Bond angles



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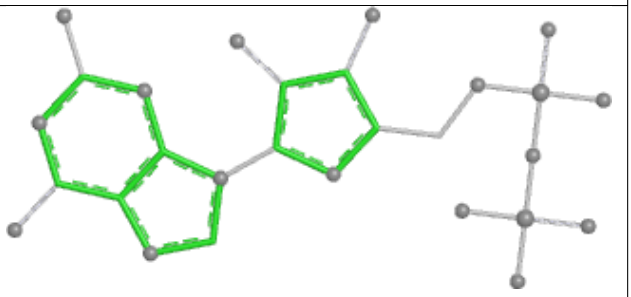
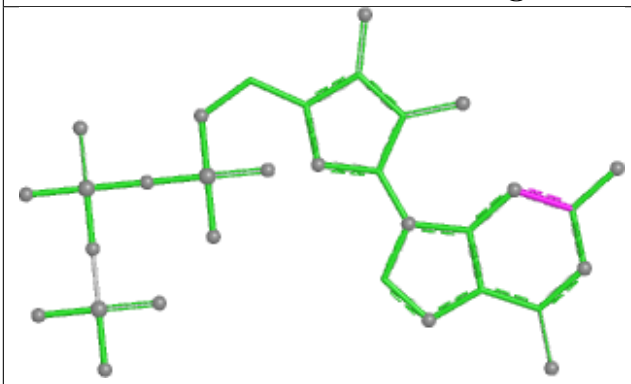


Rings

Ligand GTP HK 501



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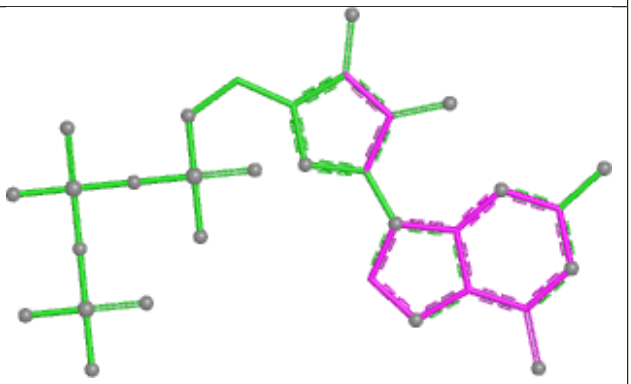
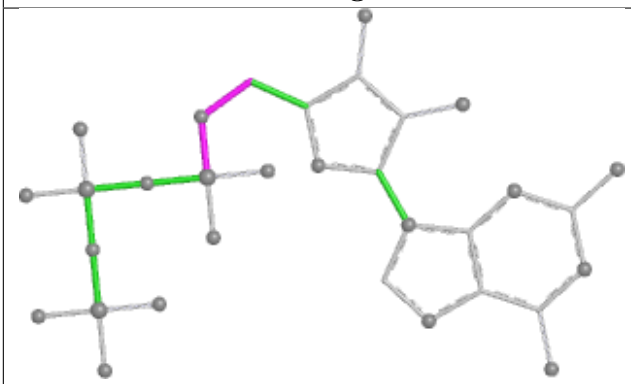


Bond angles



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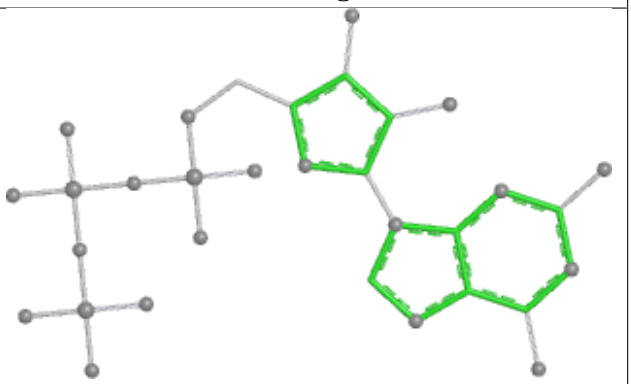
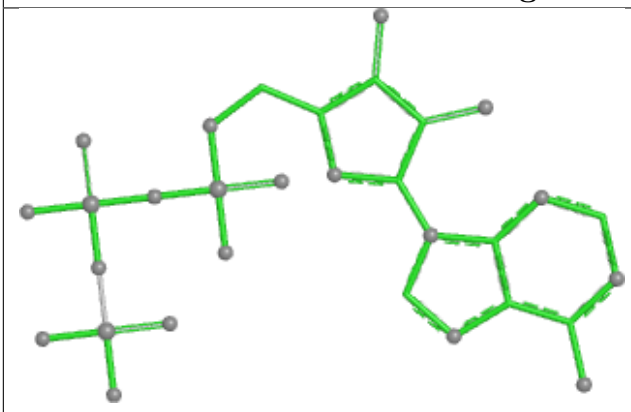


Rings

Ligand ATP 2v 501



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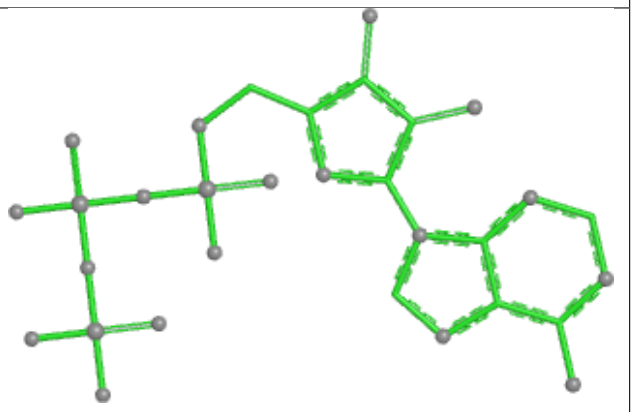

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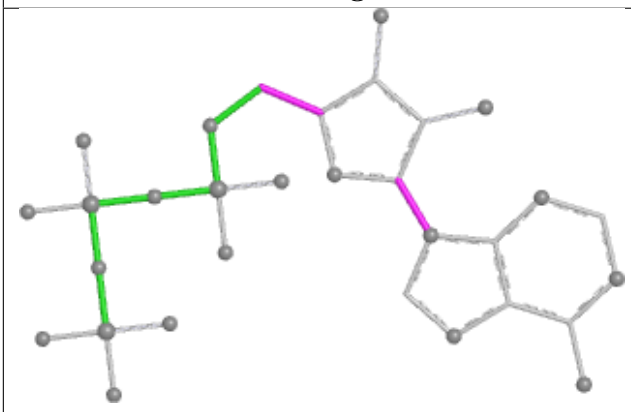

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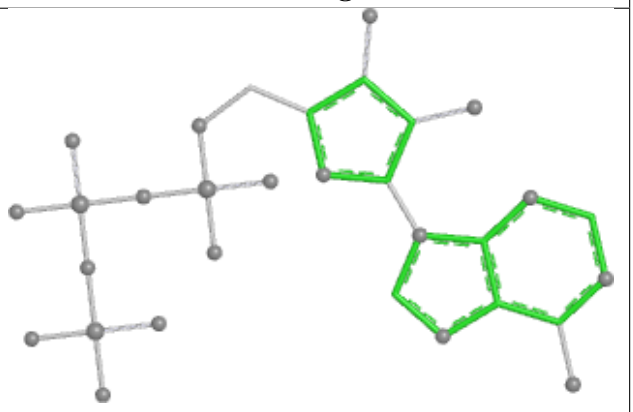
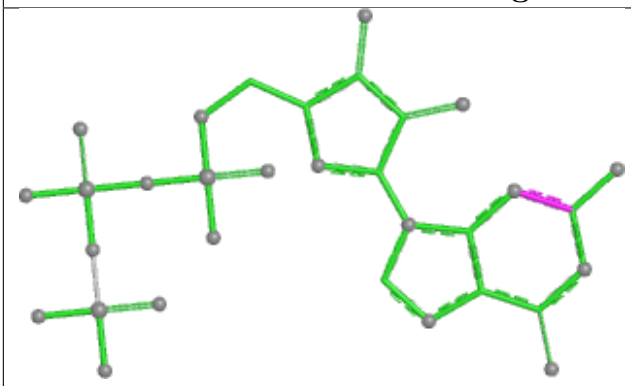


Rings

Ligand GTP SG 501



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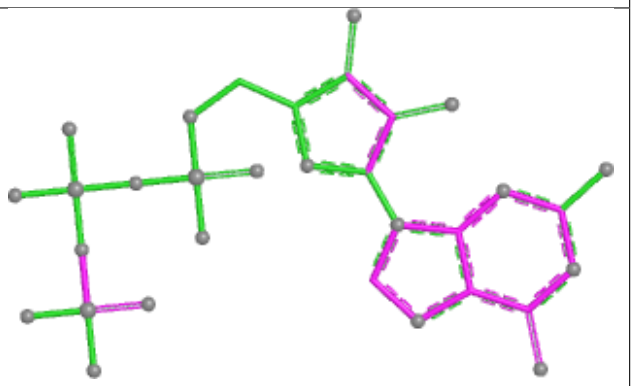

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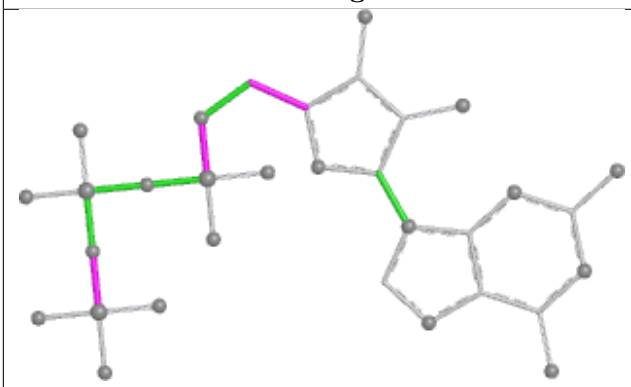

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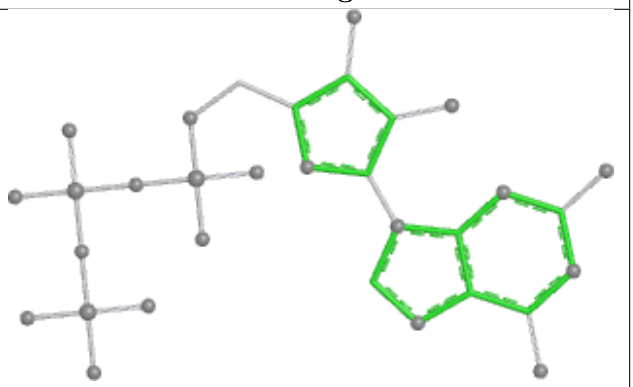
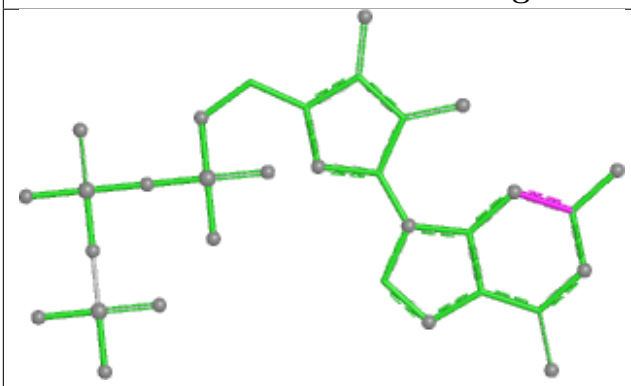


Rings

Ligand GTP KJ 501



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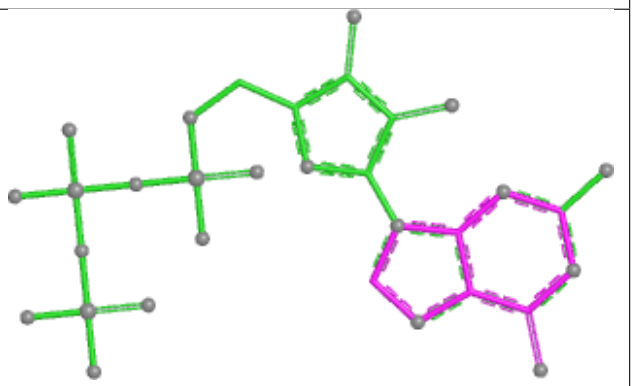

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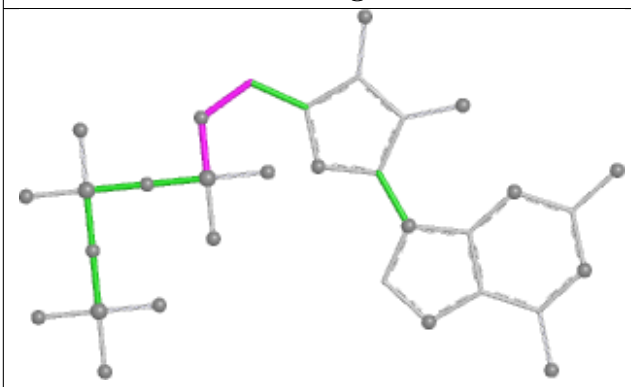

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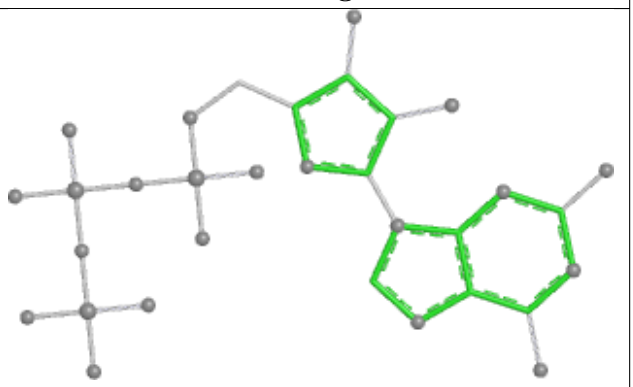

Rings

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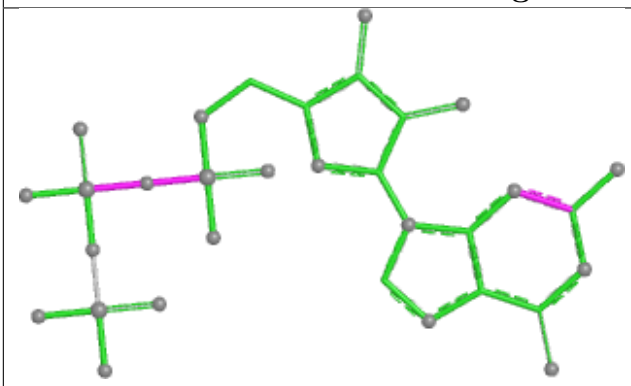

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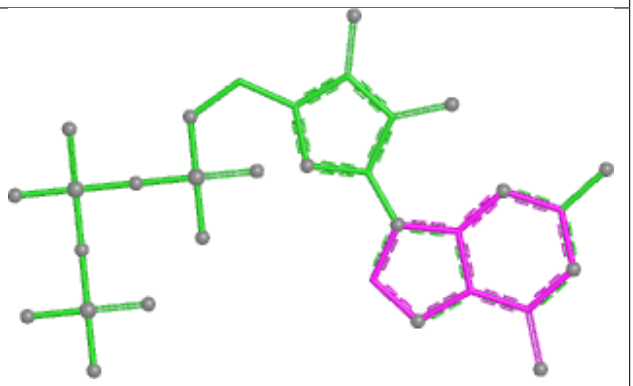

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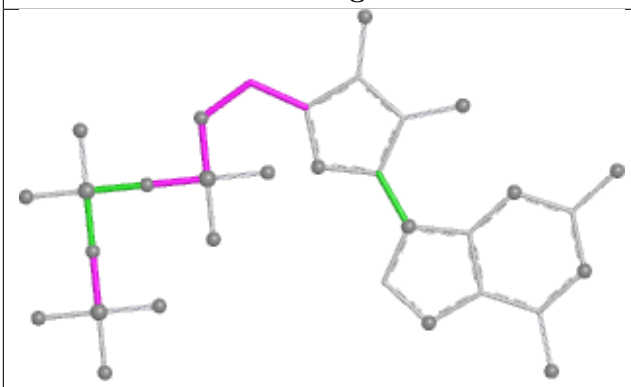

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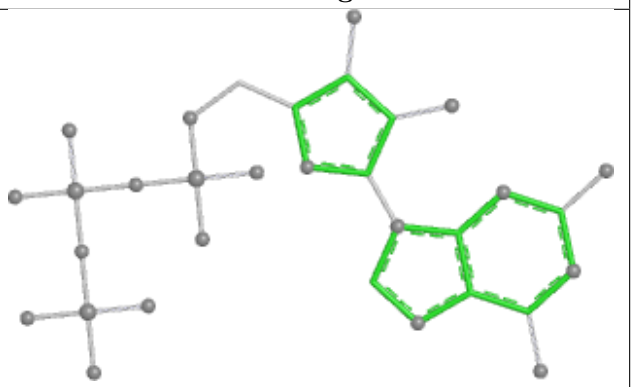

Rings

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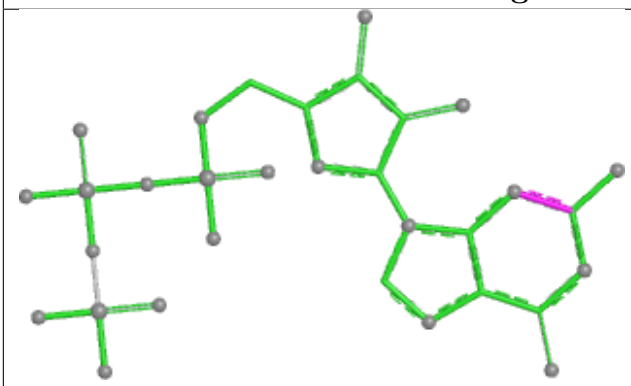

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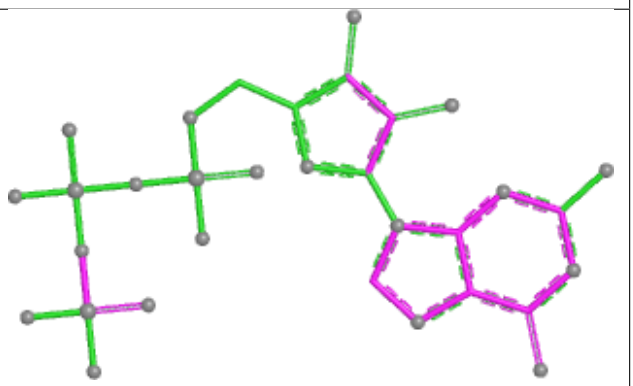

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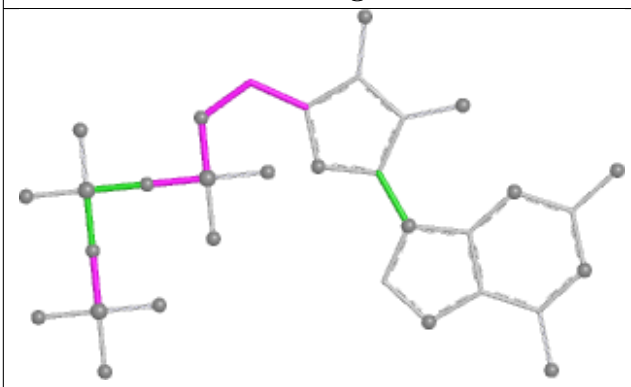

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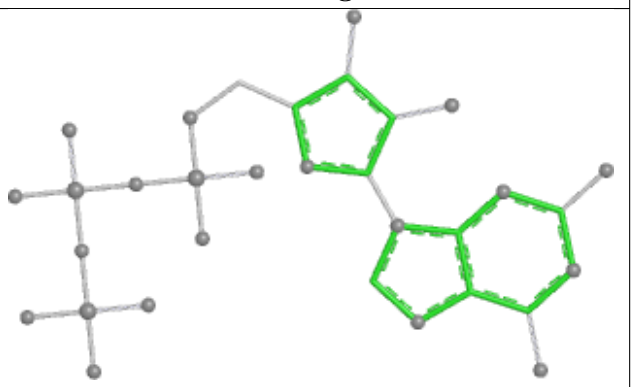
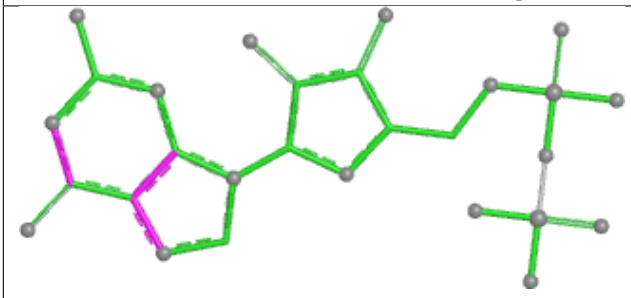


Rings

Ligand GDP SH 500



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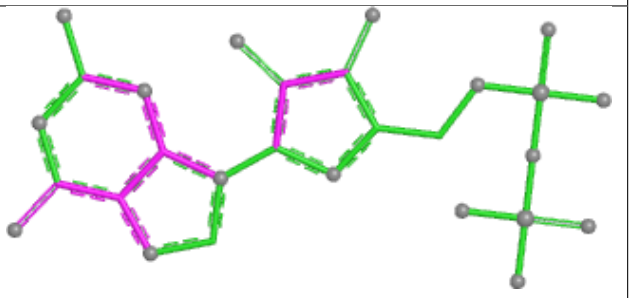

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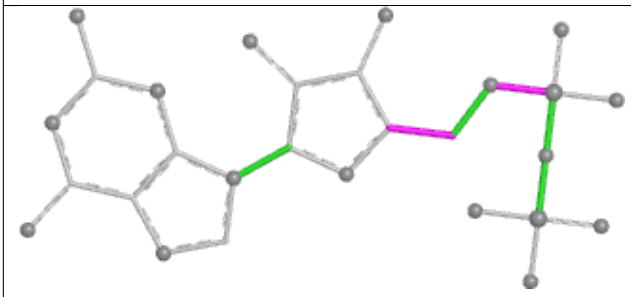

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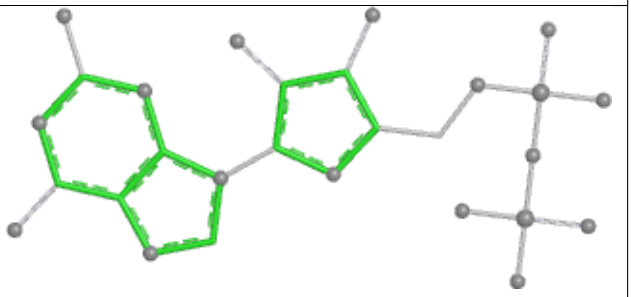
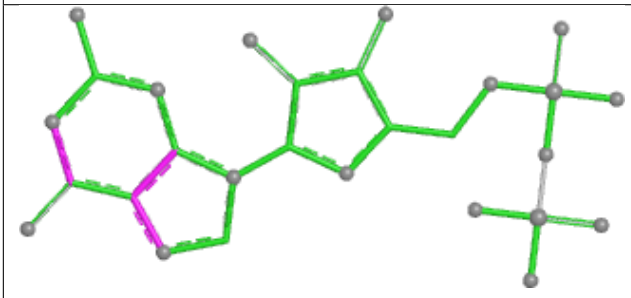


Rings

Ligand GDP BJ 500



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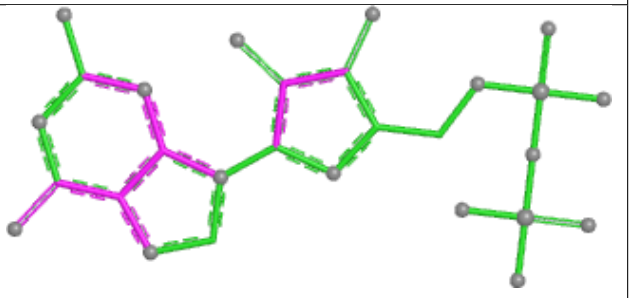

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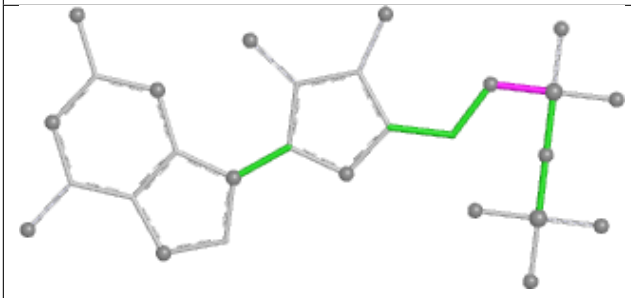

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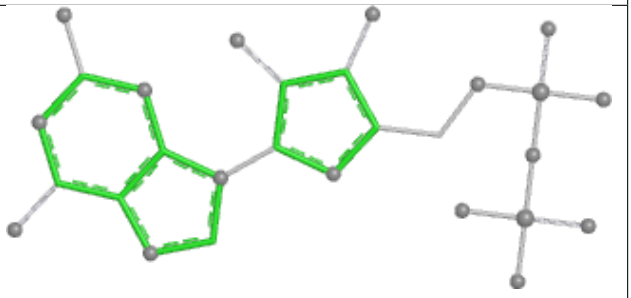
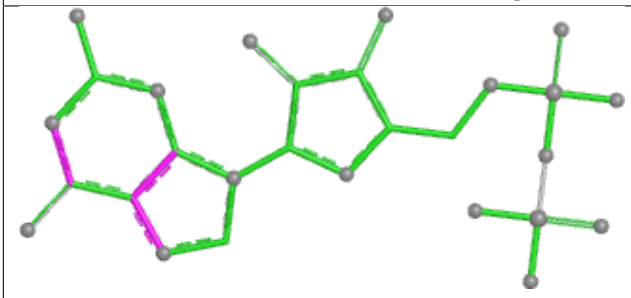


Rings

Ligand GDP PD 500



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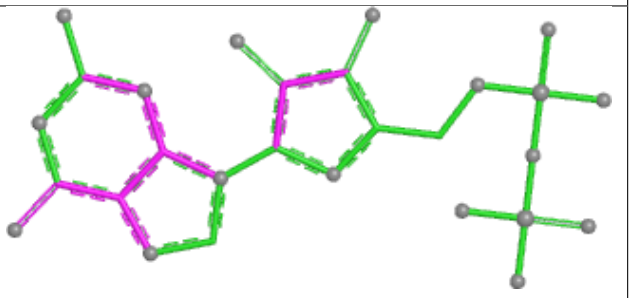

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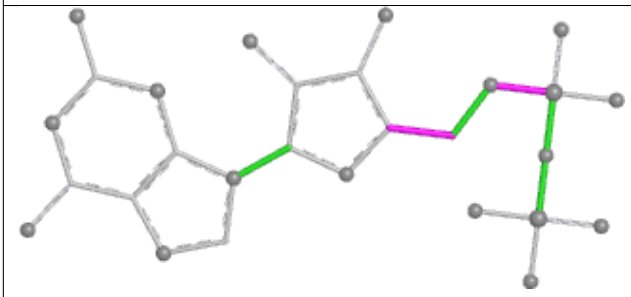

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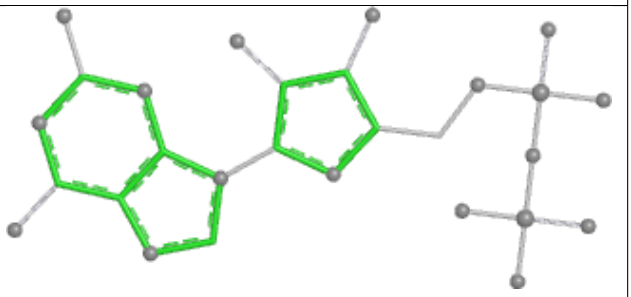
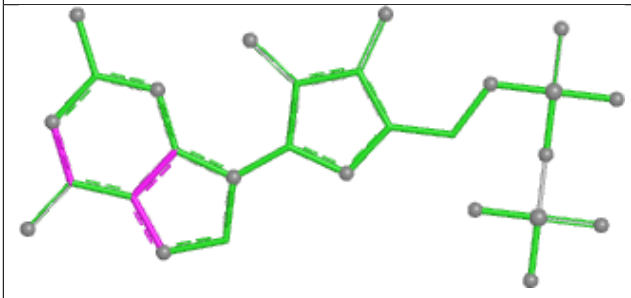


Rings

Ligand GDP TF 500



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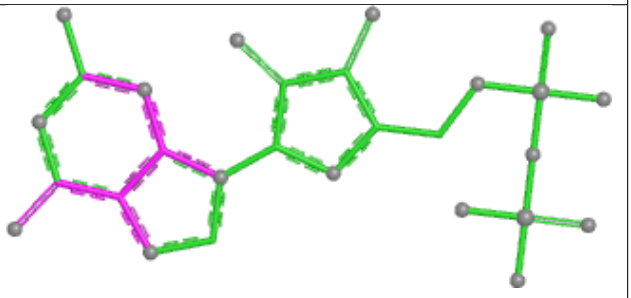

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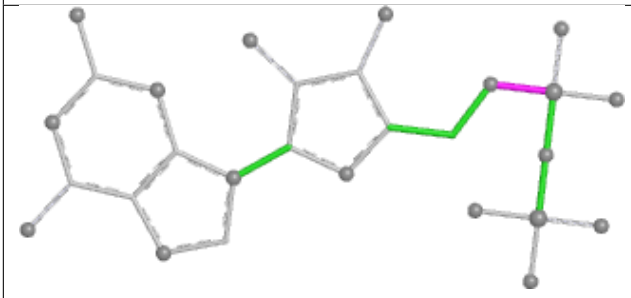

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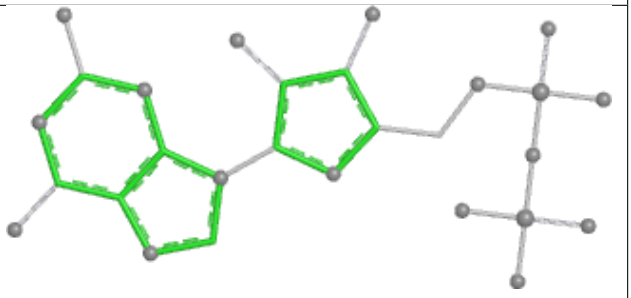
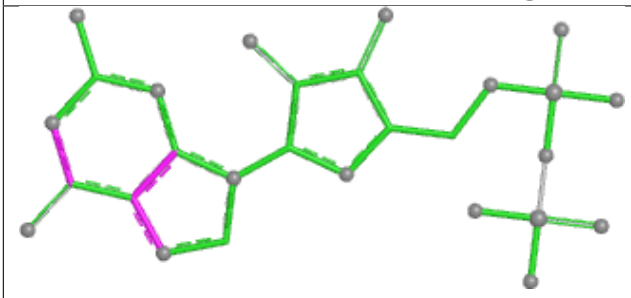


Rings

Ligand GDP V 500



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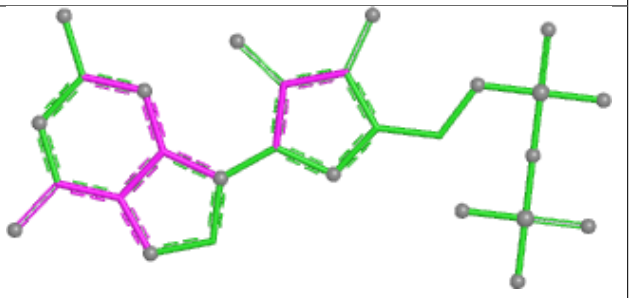

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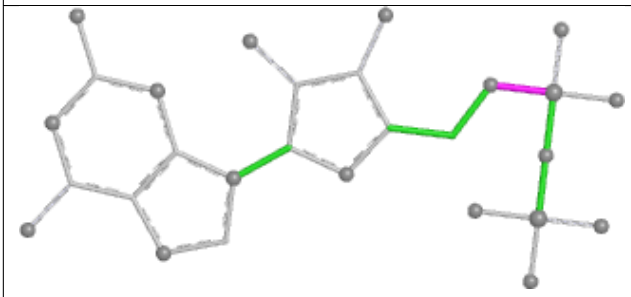

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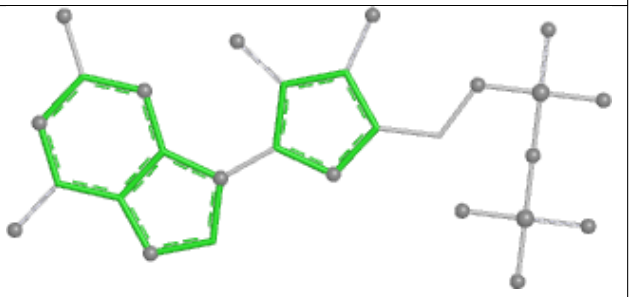
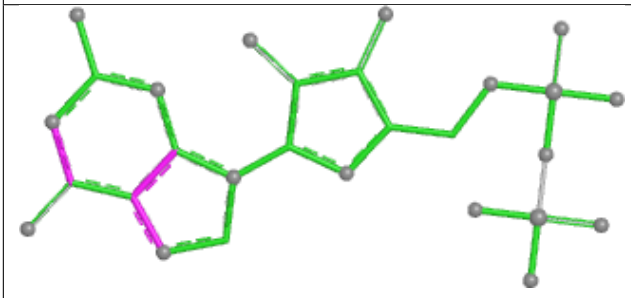


Rings

Ligand GDP DA 500



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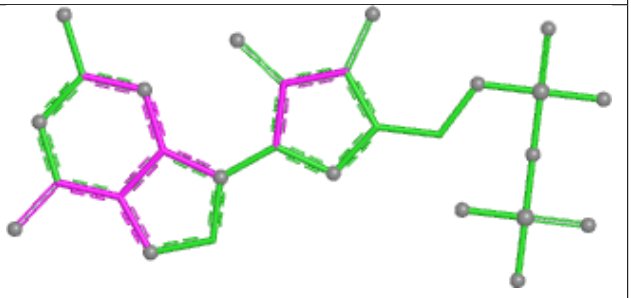

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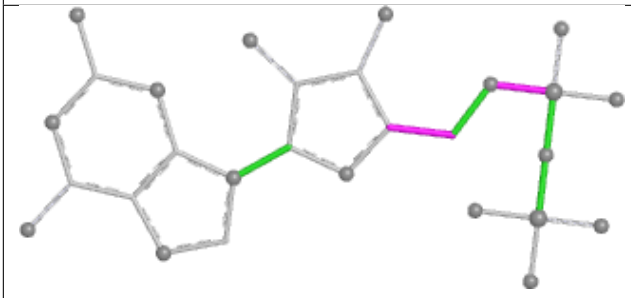

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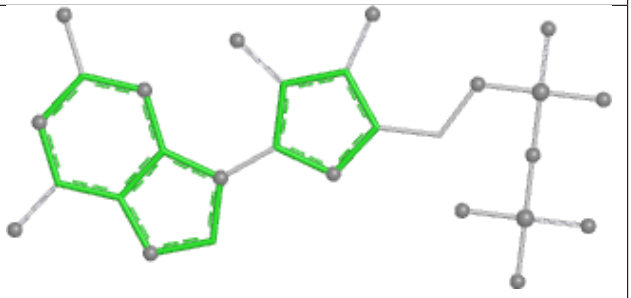
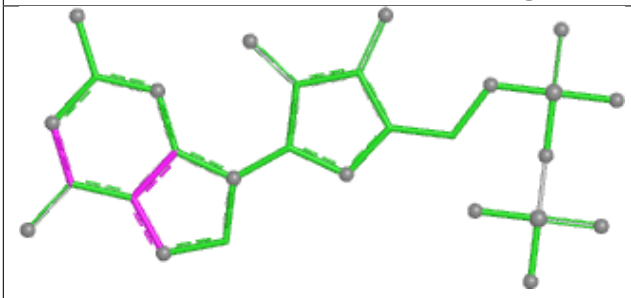


Rings

Ligand GDP N 500



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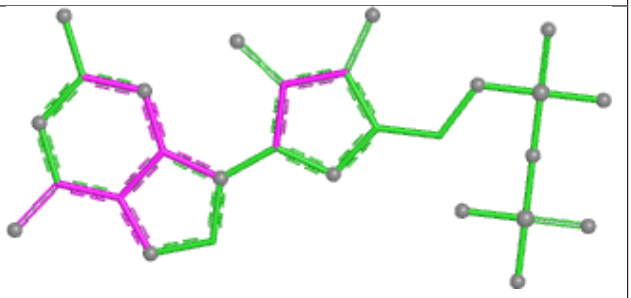

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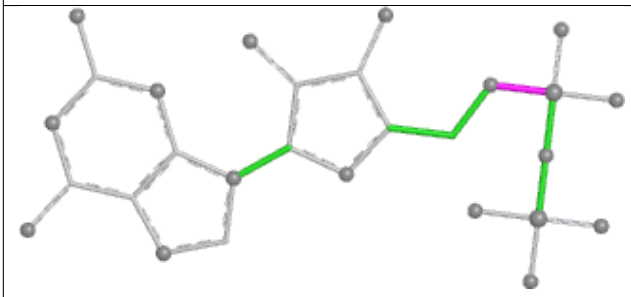

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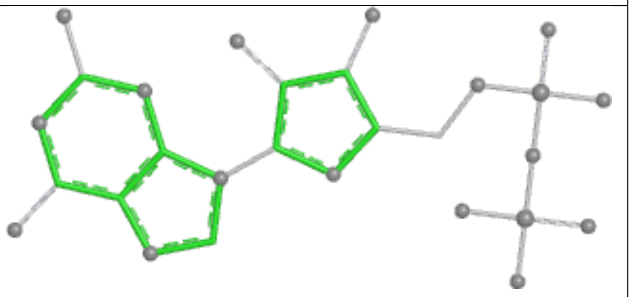
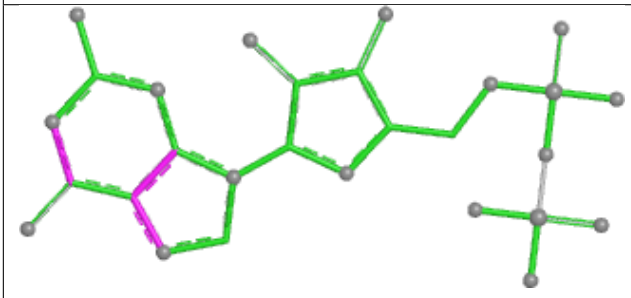


Rings

Ligand GDP EB 500



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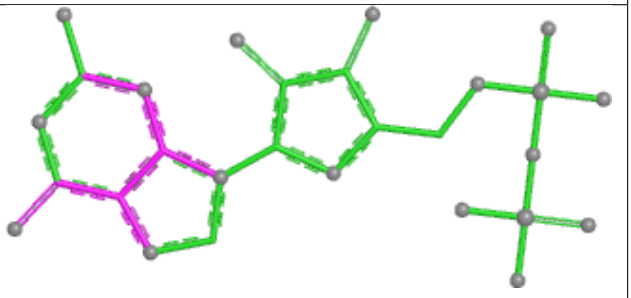

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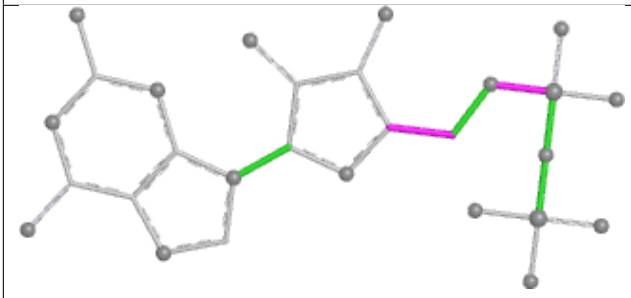

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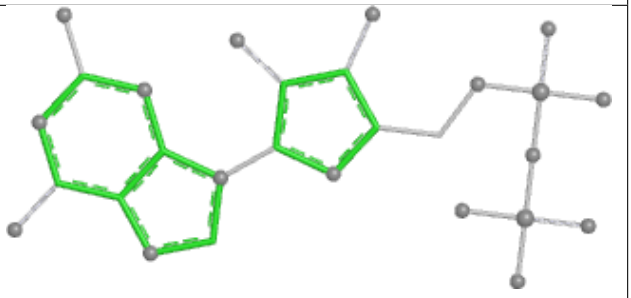
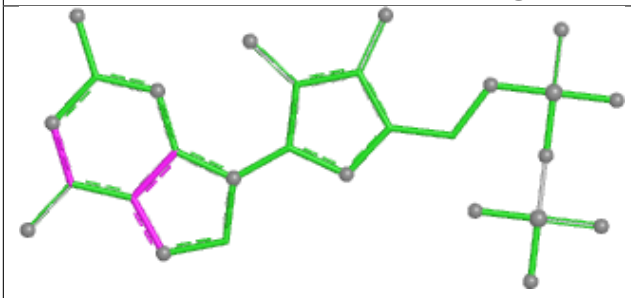


Rings

Ligand GDP AL 500



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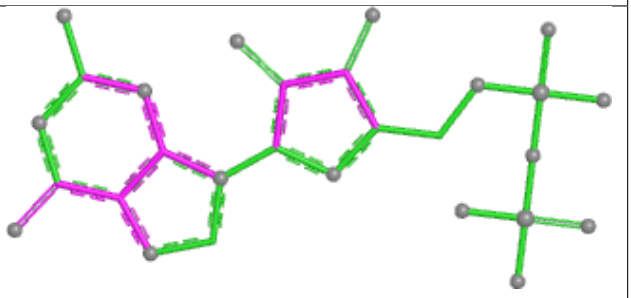
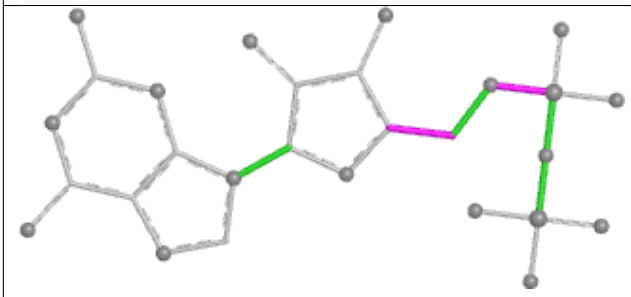


Bond angles



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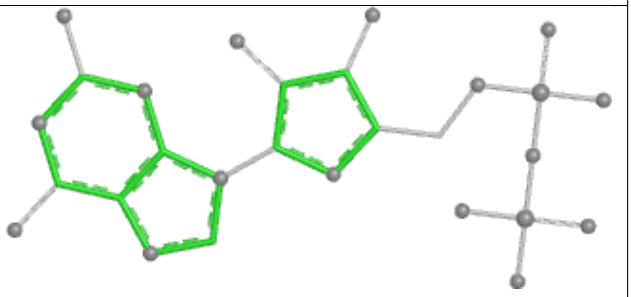
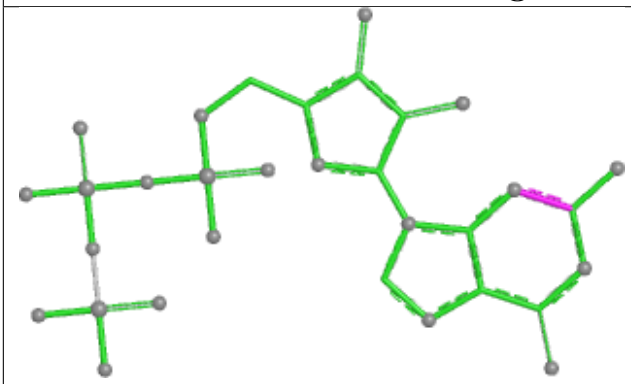


Rings

Ligand GTP NC 501



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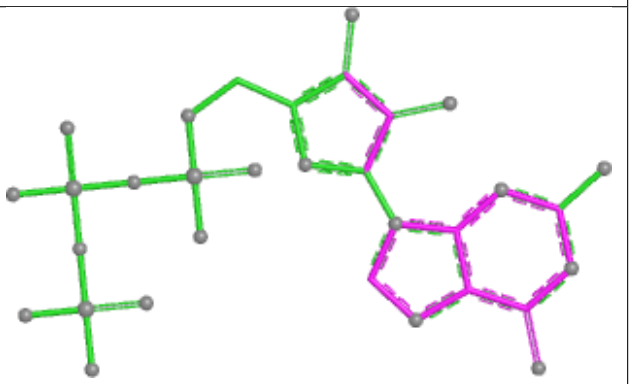

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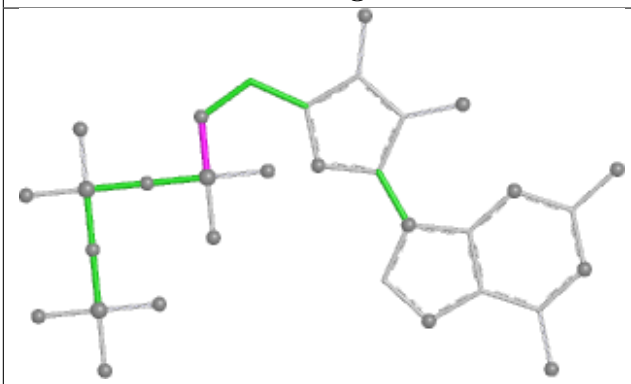
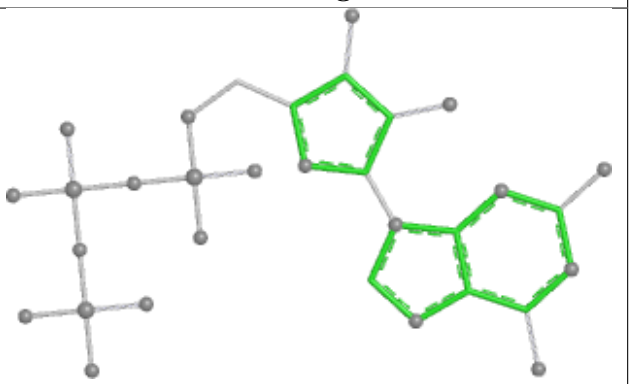
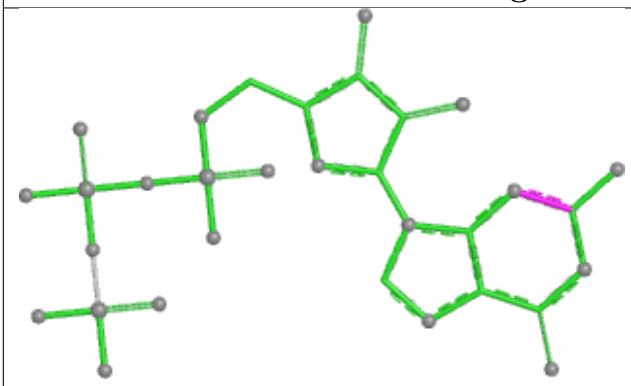


Torsions



Rings

Ligand GTP AE 501



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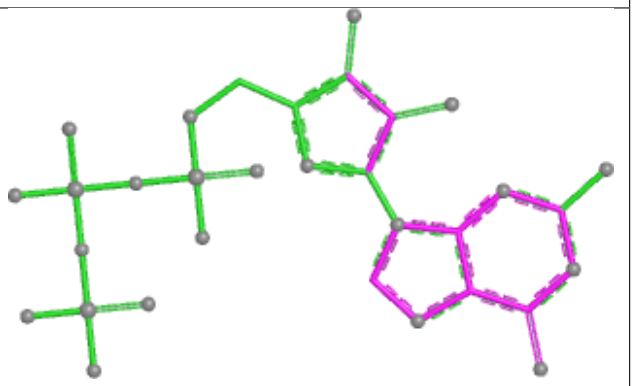

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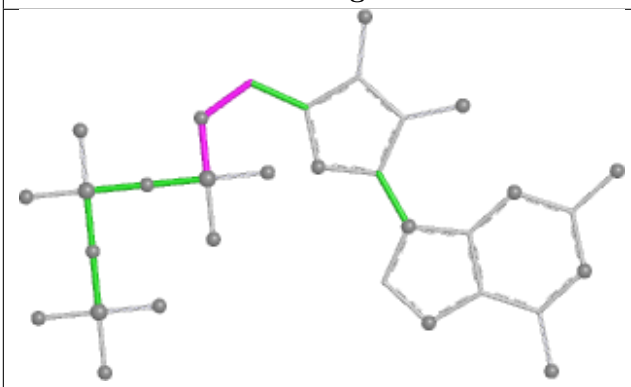

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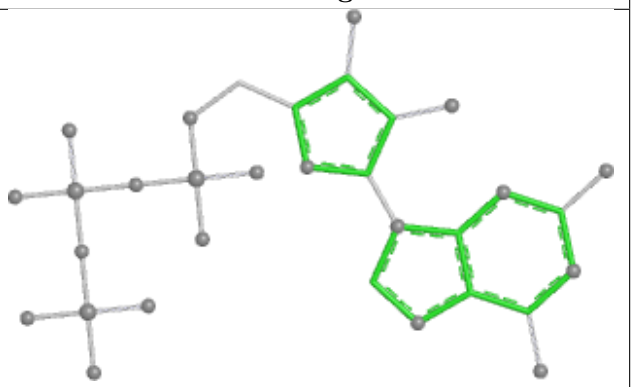
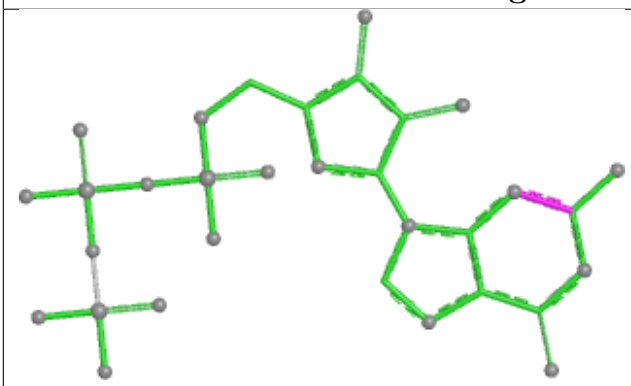


Rings

Ligand GTP UC 501



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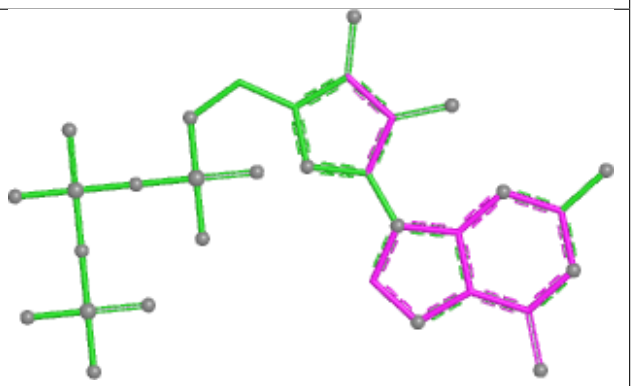

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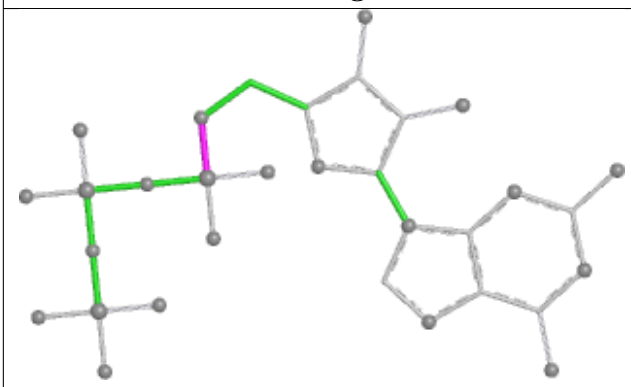

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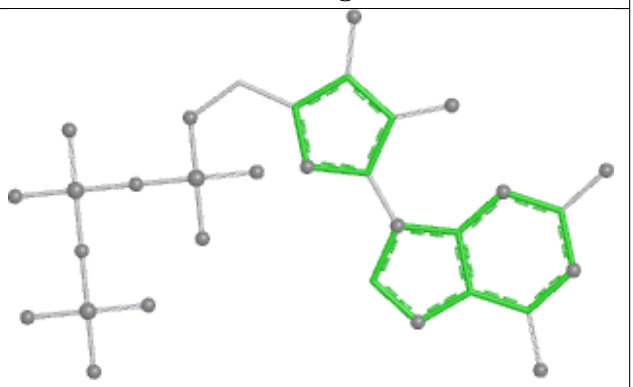
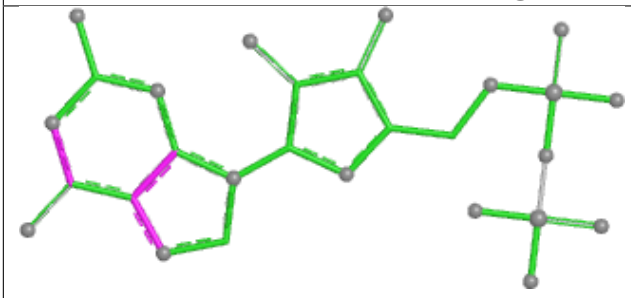


Rings

Ligand GDP OJ 500



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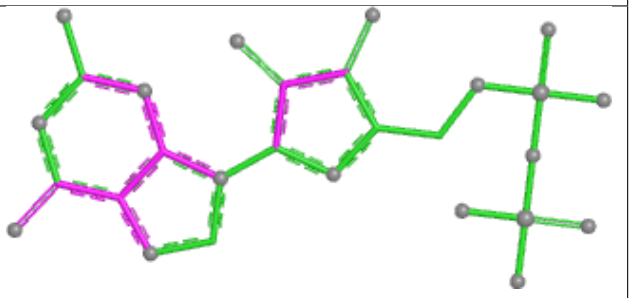

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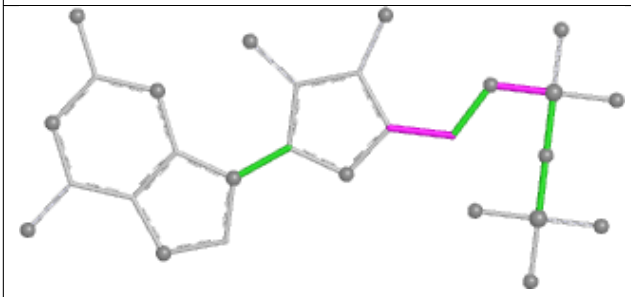

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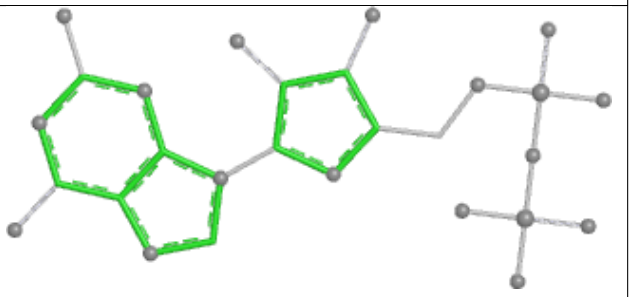
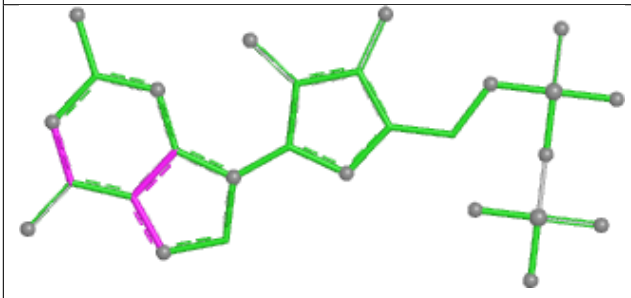


Rings

Ligand GDP PL 500



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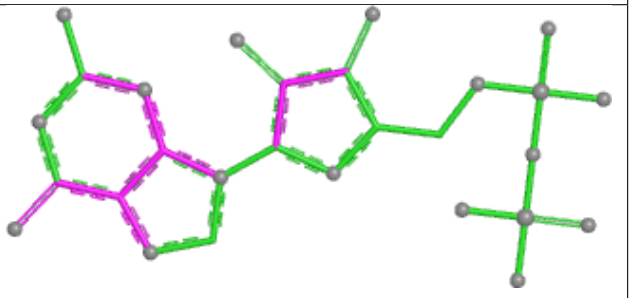

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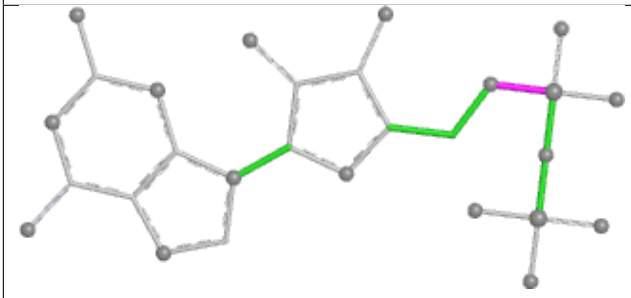

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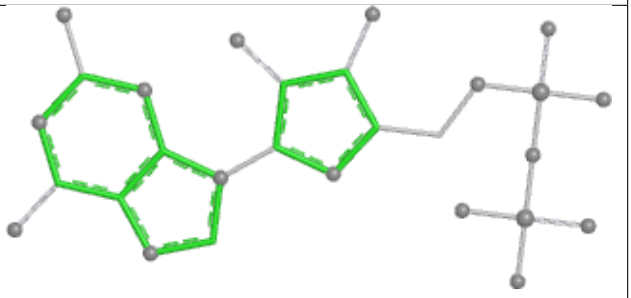

Rings

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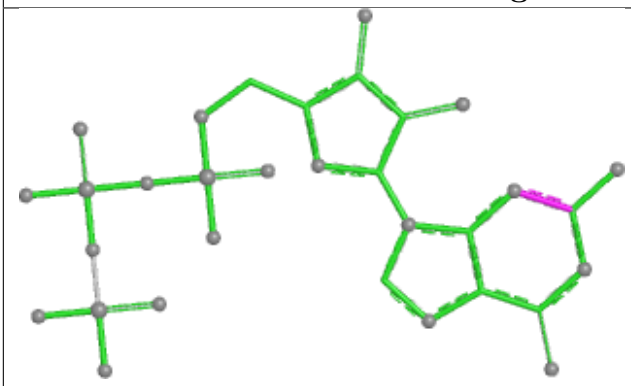

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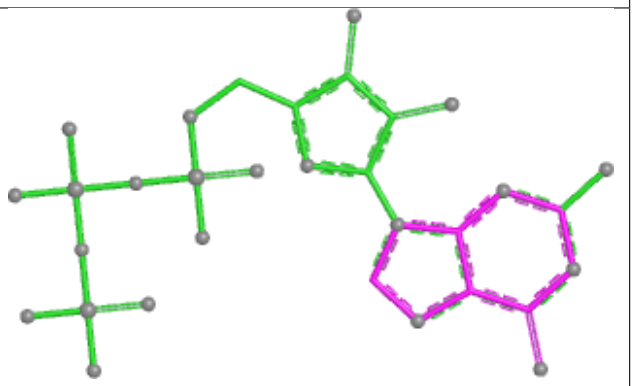

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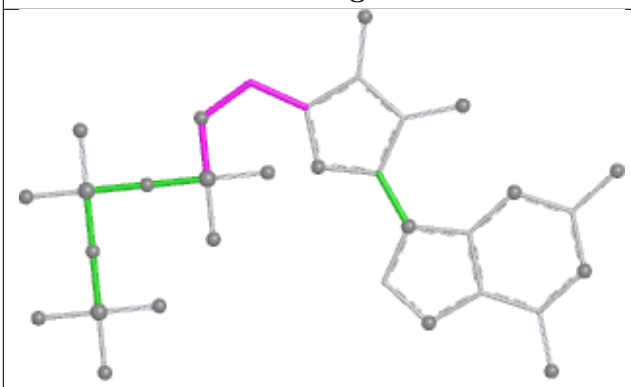

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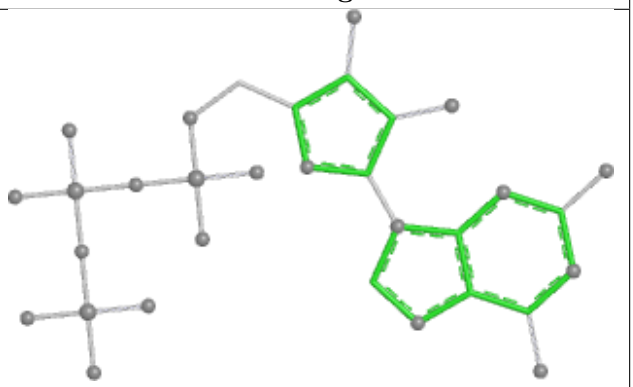
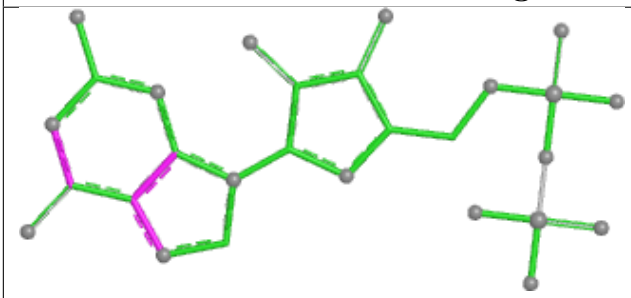


Rings

Ligand GDP TJ 500



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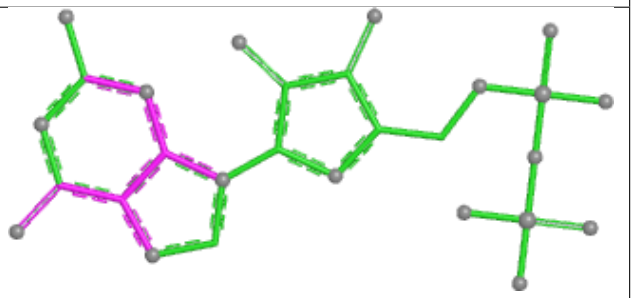

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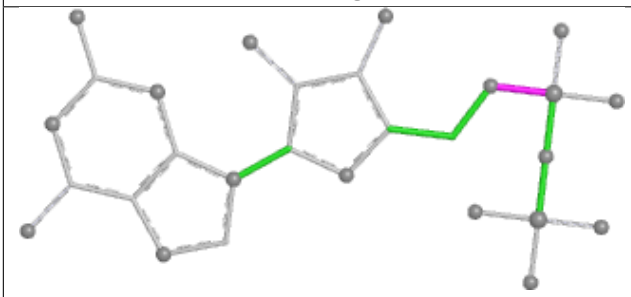

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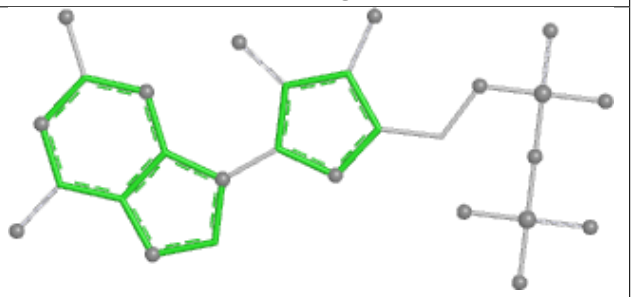
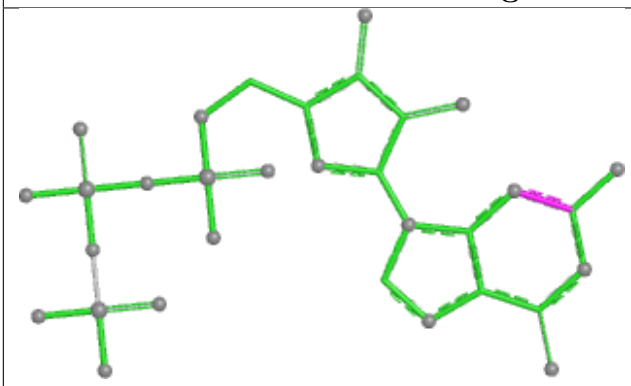


Rings

Ligand GTP MM 501



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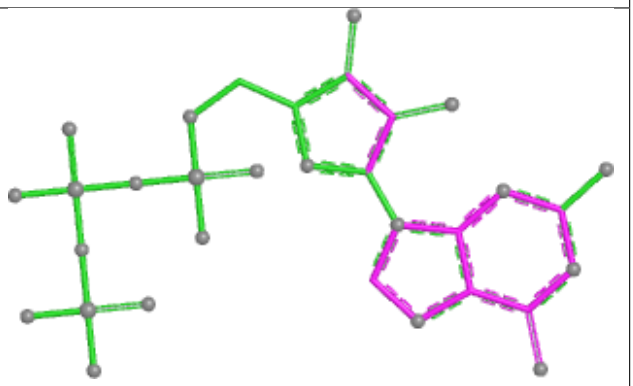

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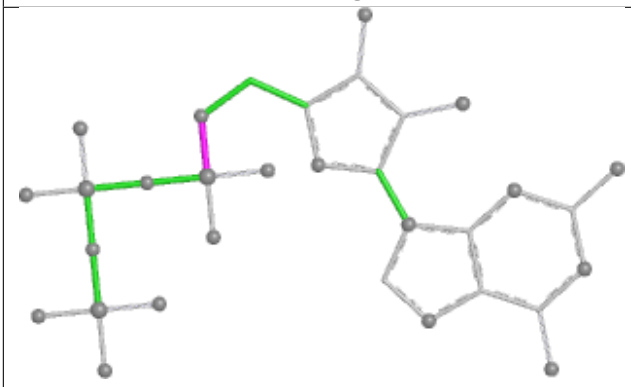

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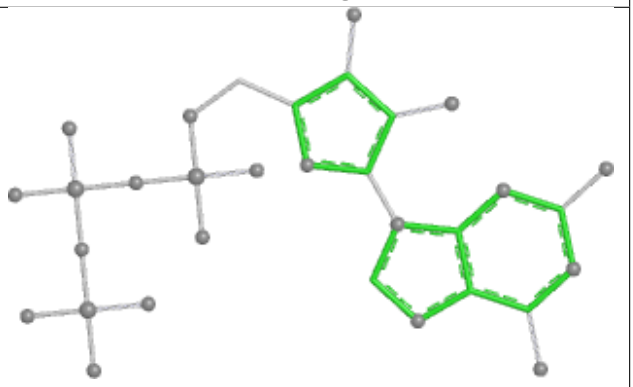
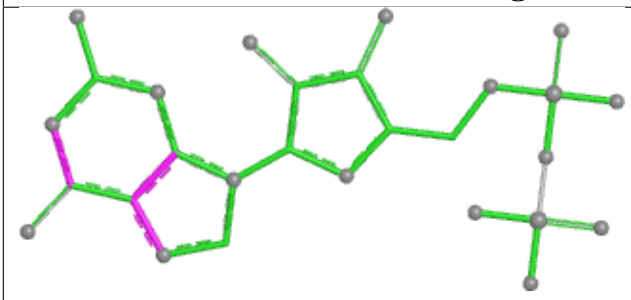


Rings

Ligand GDP FD 500



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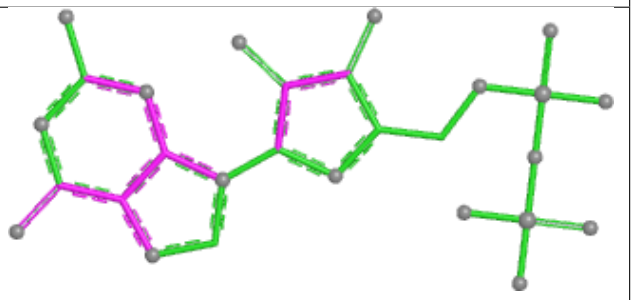

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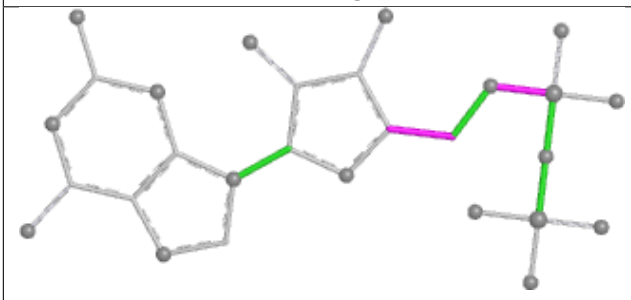

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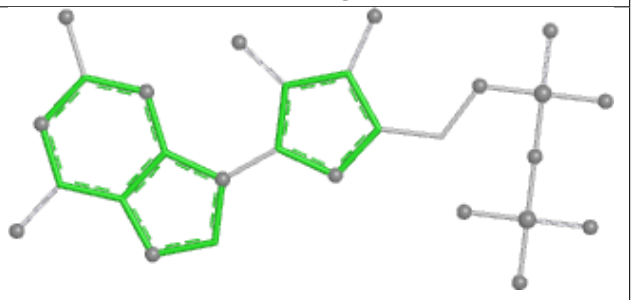
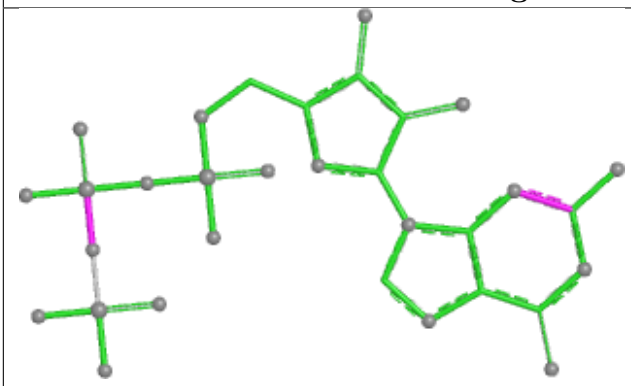


Rings

Ligand GTP OE 501



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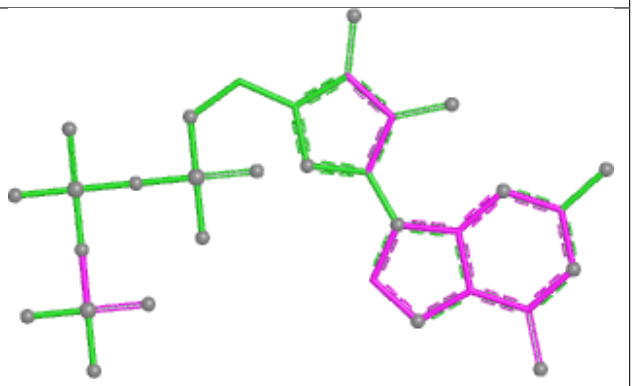

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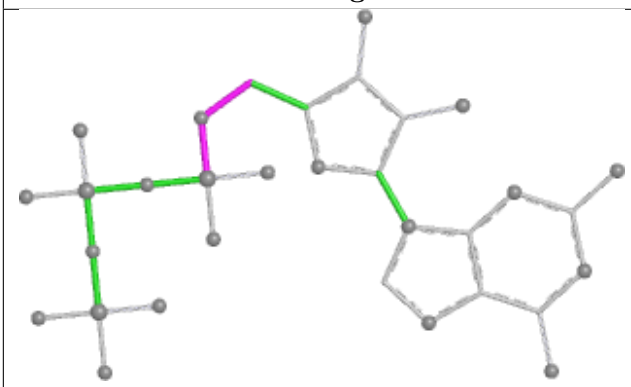

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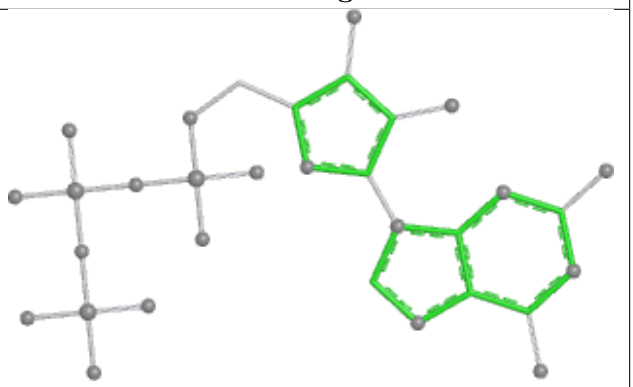
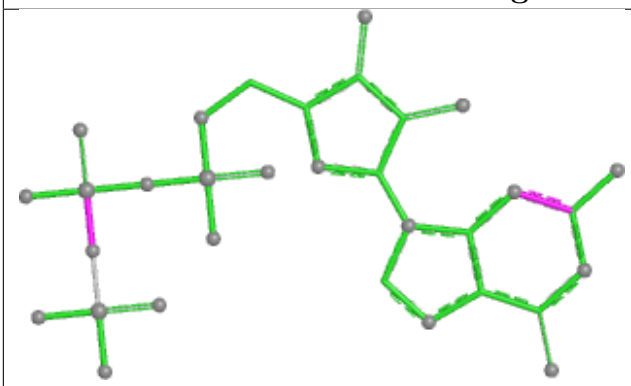


Rings

Ligand GTP TA 501



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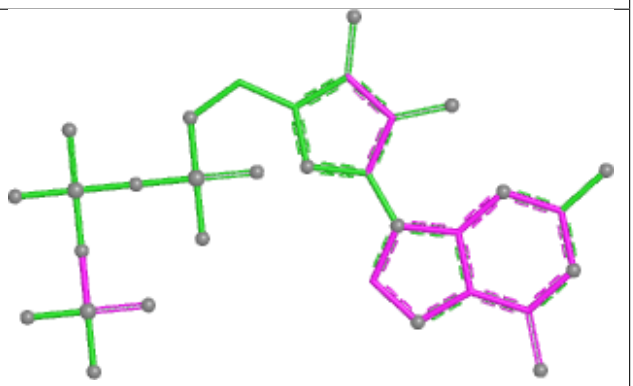

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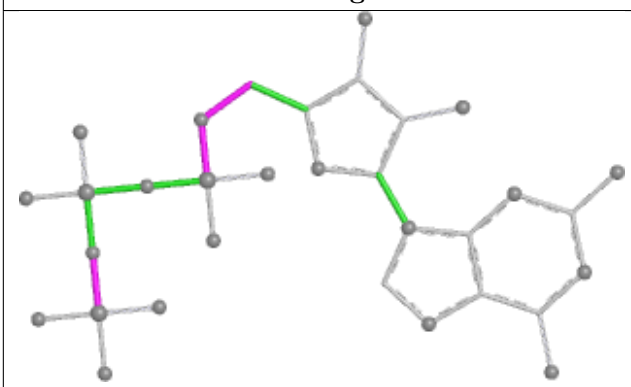

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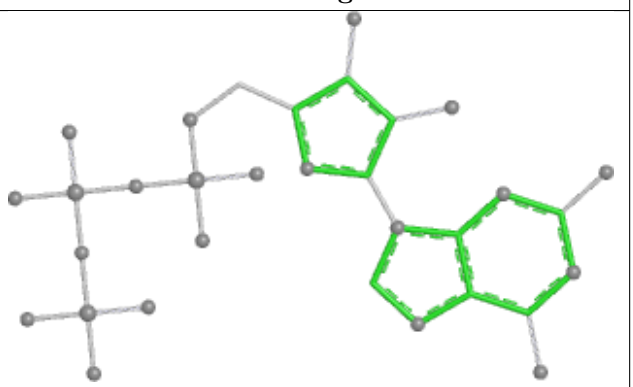
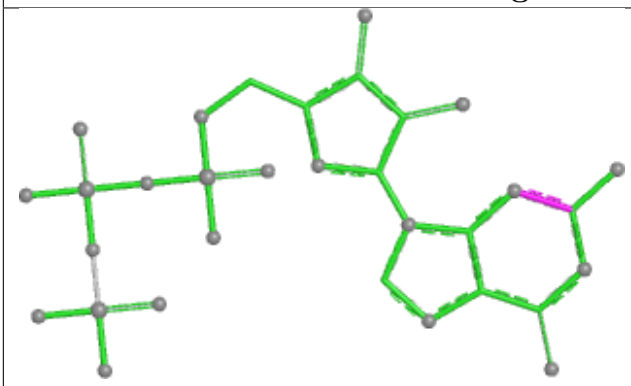


Rings

Ligand GTP PA 501



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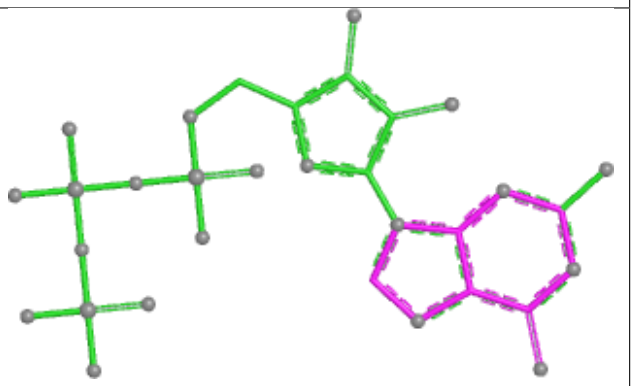

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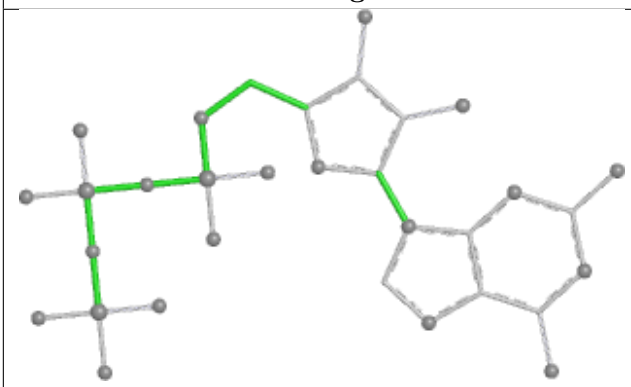

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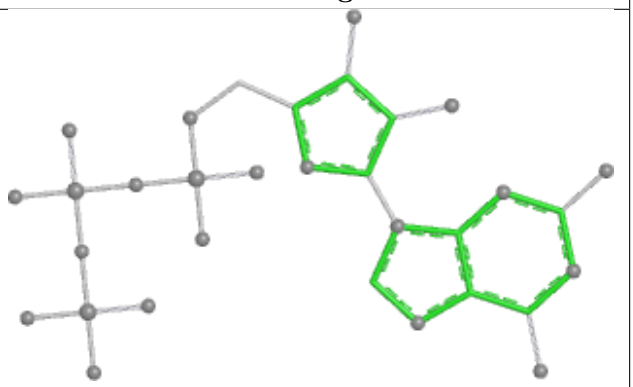
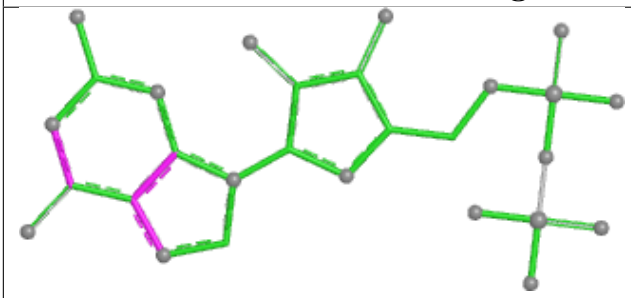


Rings

Ligand GDP CE 500



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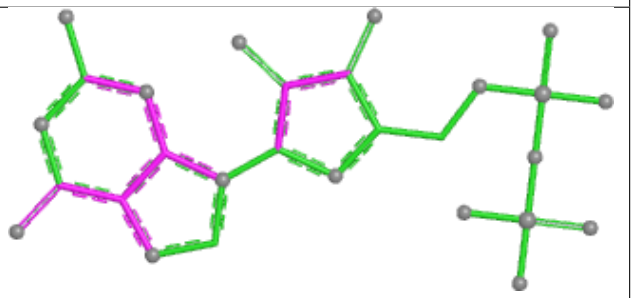
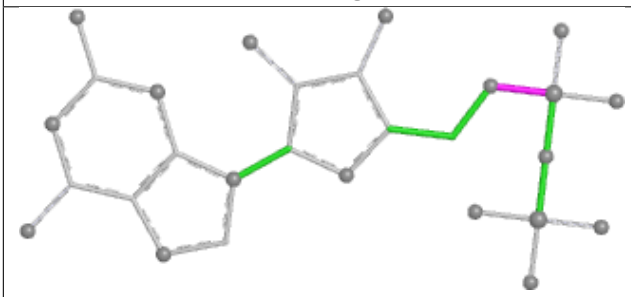


Bond angles



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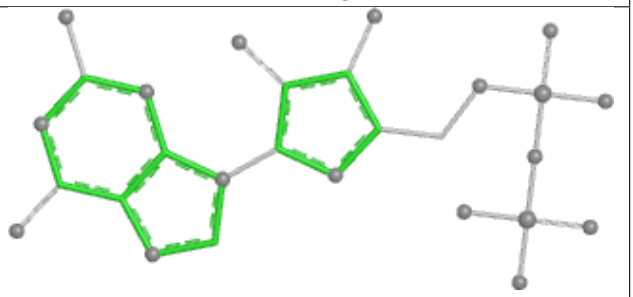
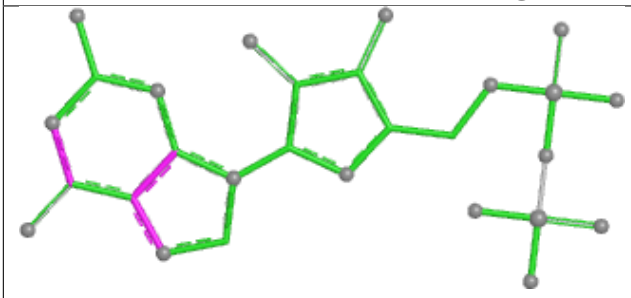


Rings

Ligand GDP SF 500



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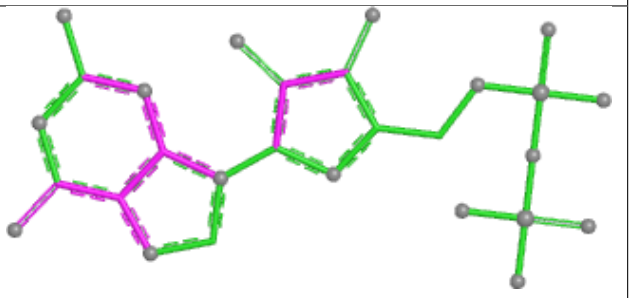

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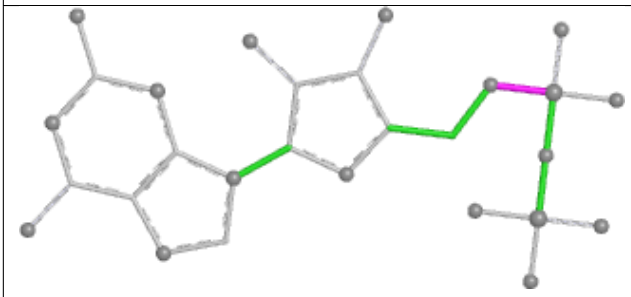
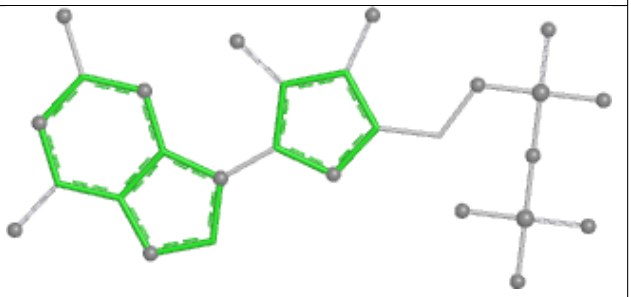
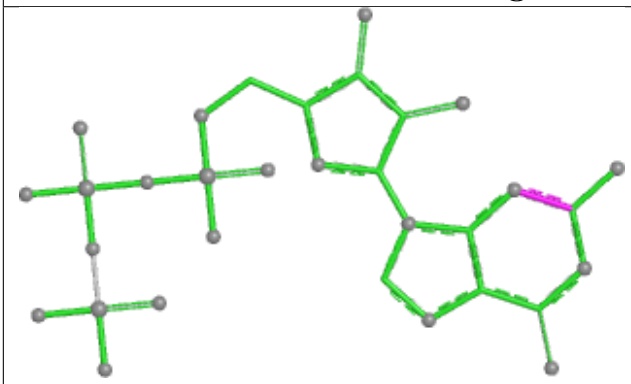


Torsions

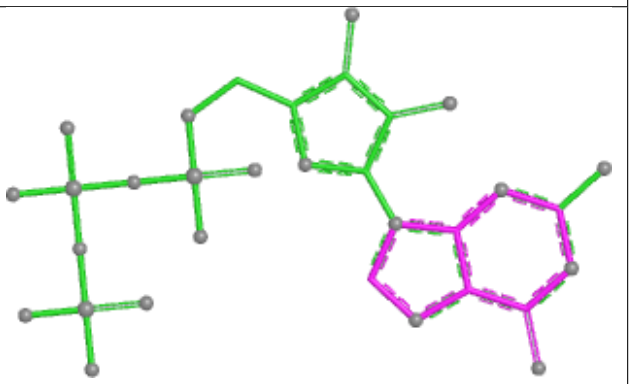


Rings

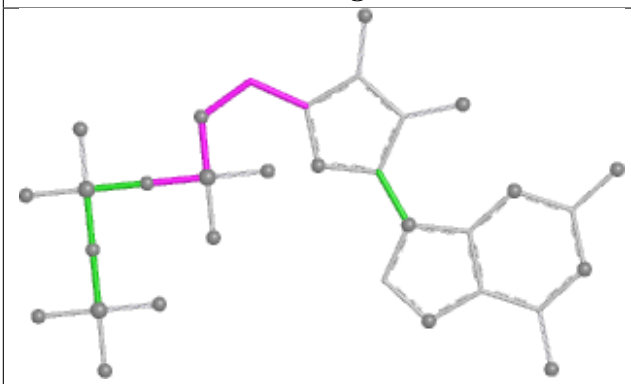
Ligand GTP VK 501



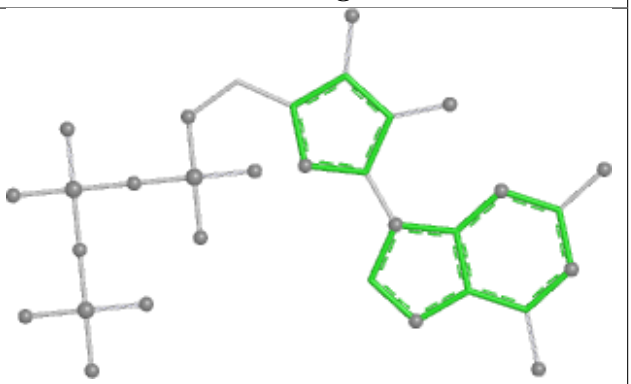
Bond lengths



Bond angles

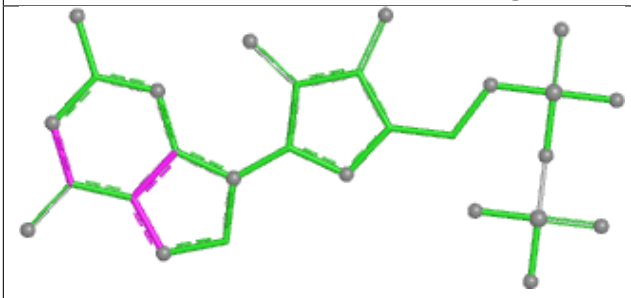


Torsions

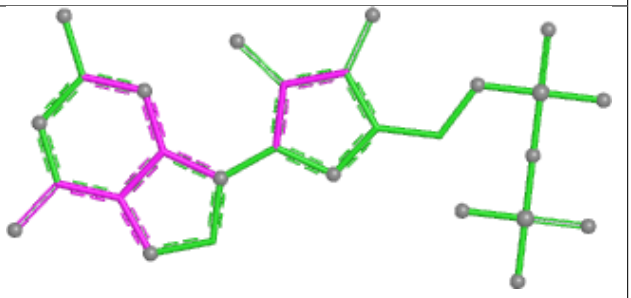


Rings

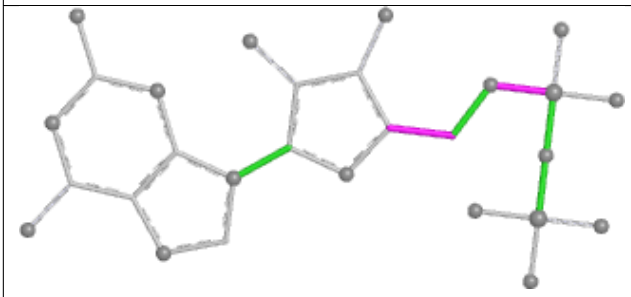
Ligand GDP HD 500



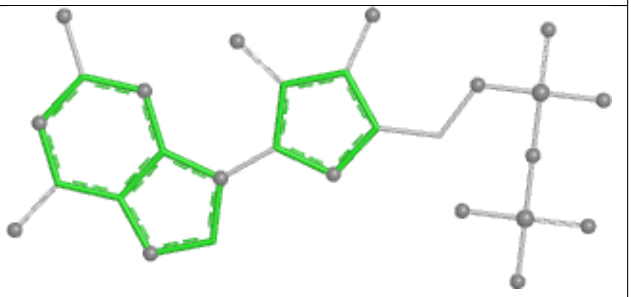
Bond lengths



Bond angles

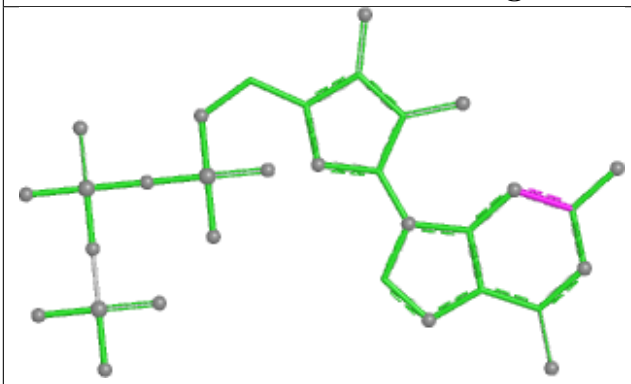


Torsions

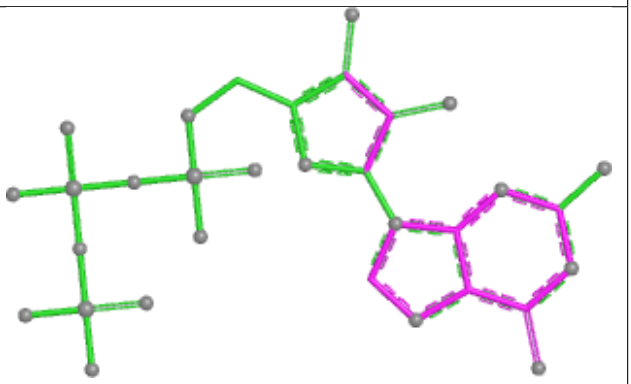


Rings

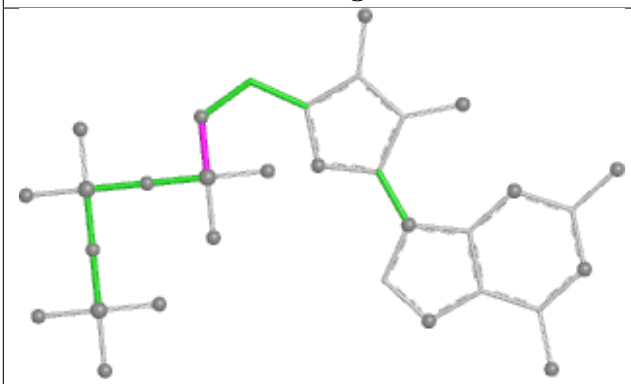
Ligand GTP WA 501



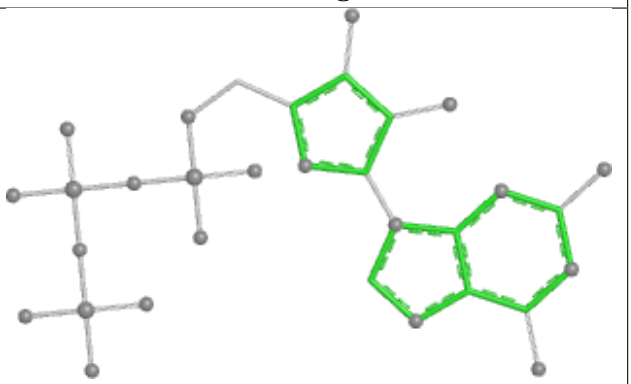
Bond lengths



Bond angles

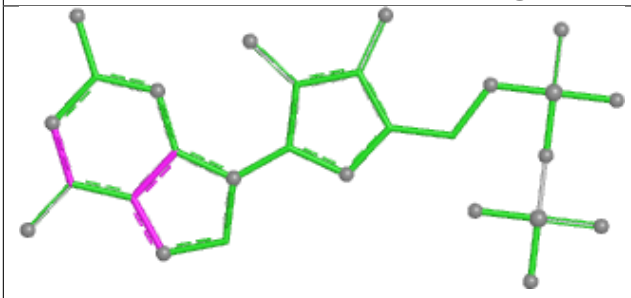


Torsions

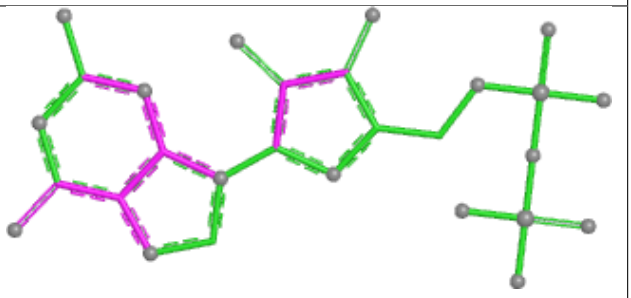


Rings

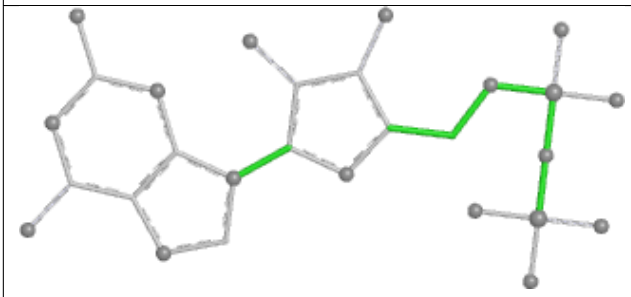
Ligand GDP TL 500



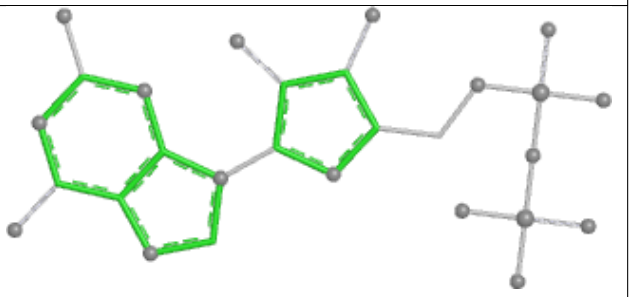
Bond lengths



Bond angles

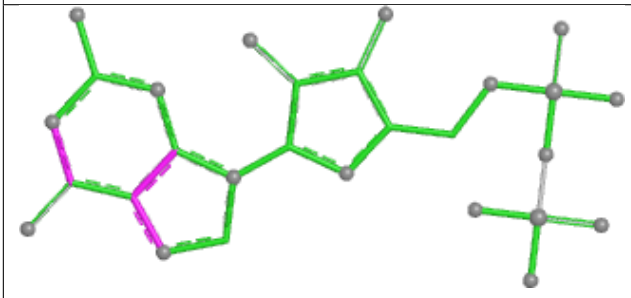


Torsions

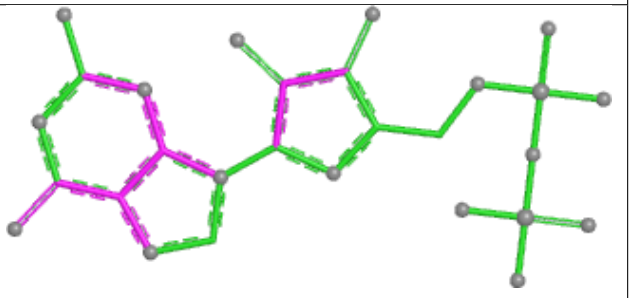


Rings

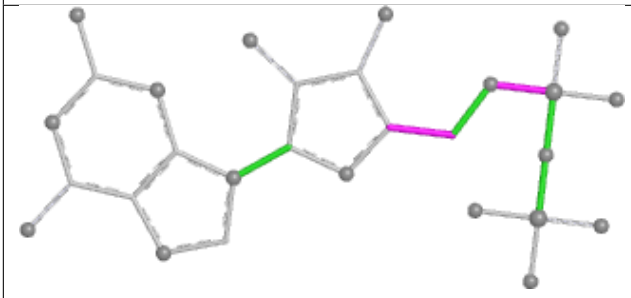
Ligand GDP KM 500



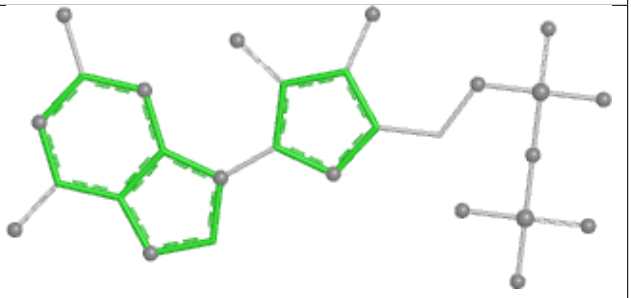
Bond lengths



Bond angles

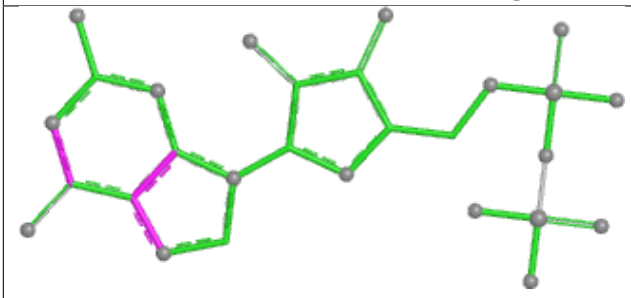


Torsions

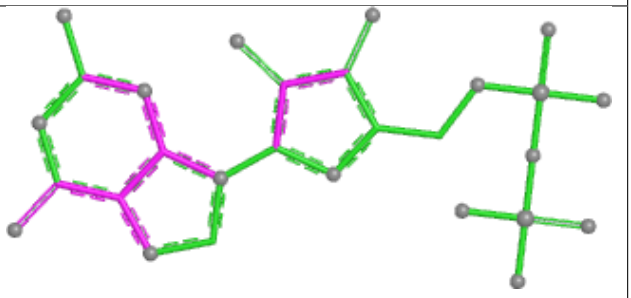


Rings

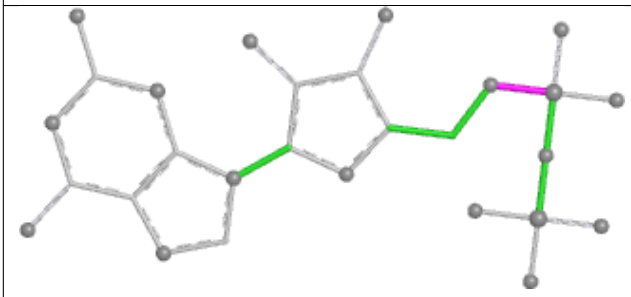
Ligand GDP TH 500



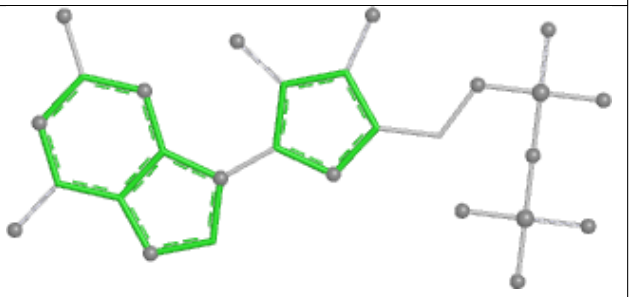
Bond lengths



Bond angles

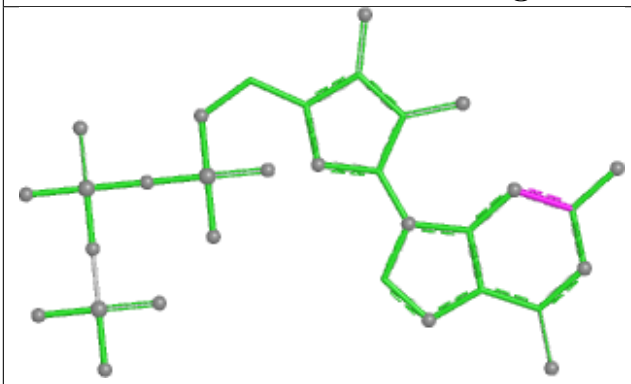


Torsions

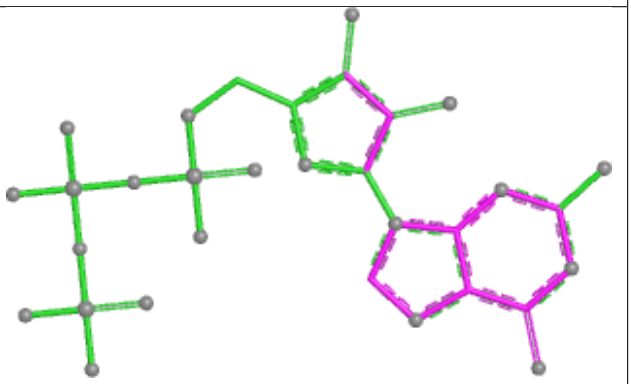


Rings

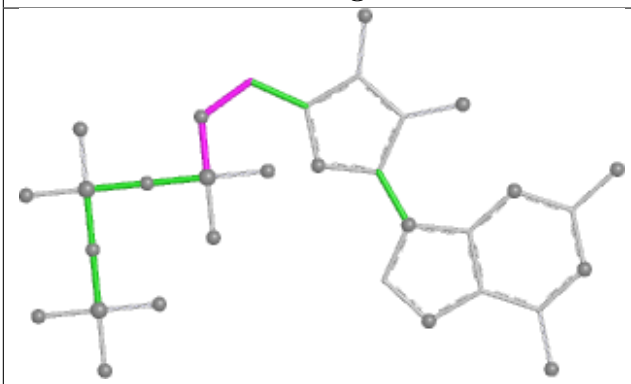
Ligand GTP JN 501



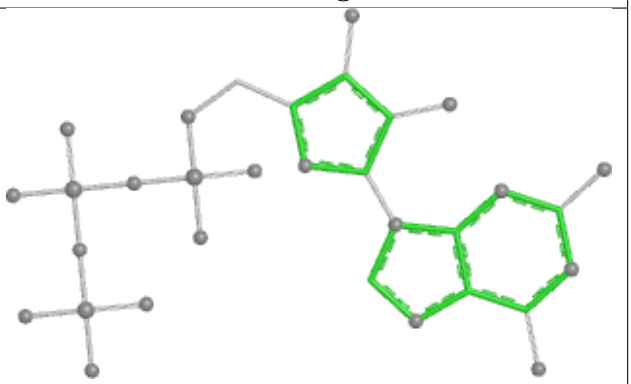
Bond lengths



Bond angles

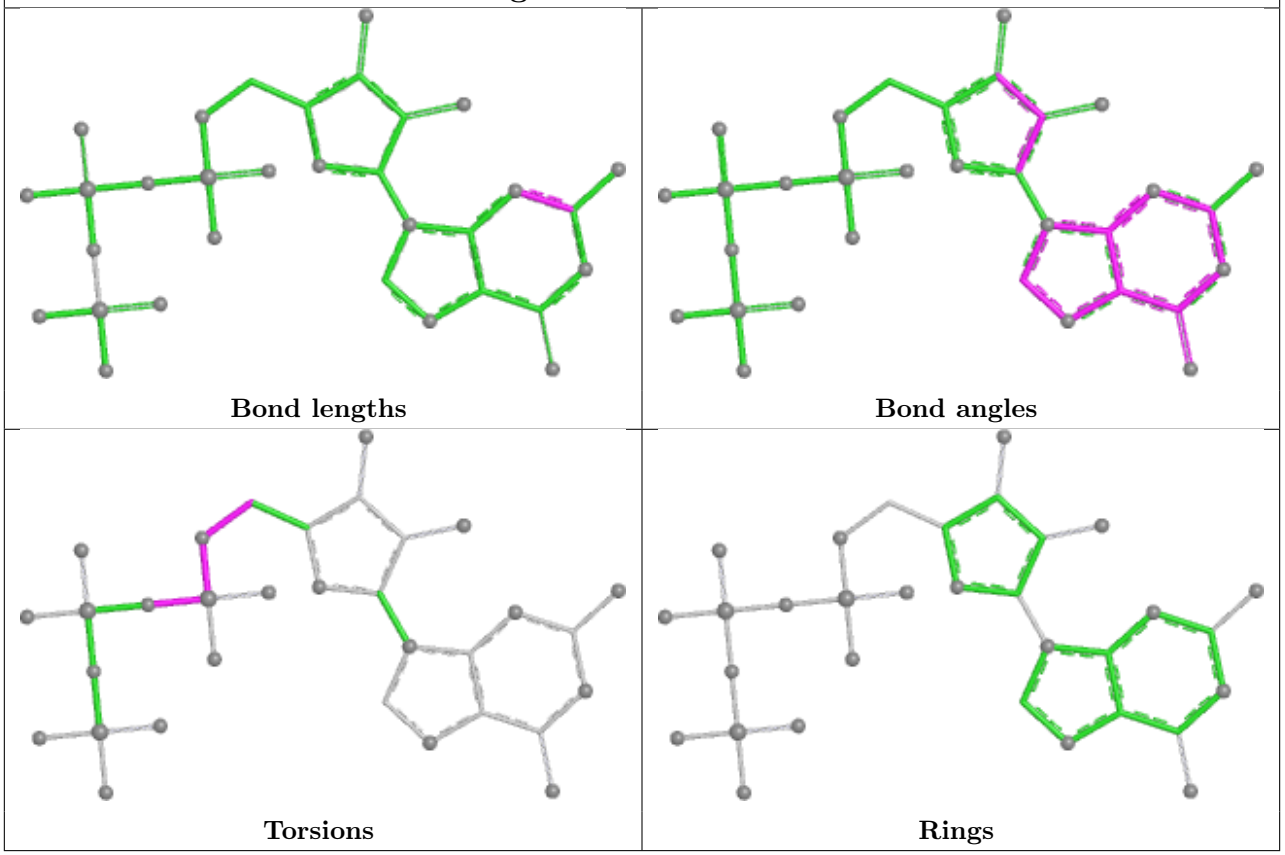


Torsions

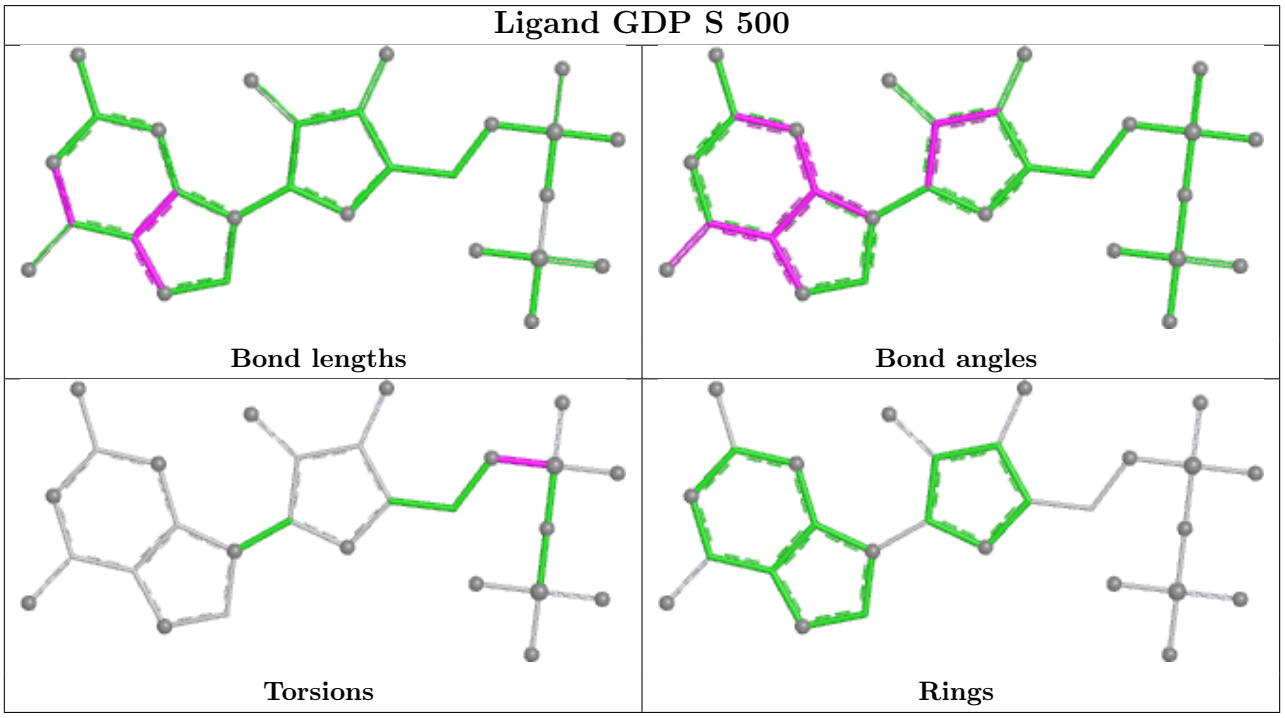


Rings

Ligand GTP KB 501



Ligand GDP S 500



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

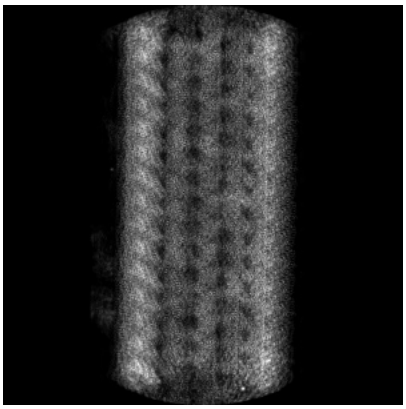
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47661. These allow visual inspection of the internal detail of the map and identification of artifacts.

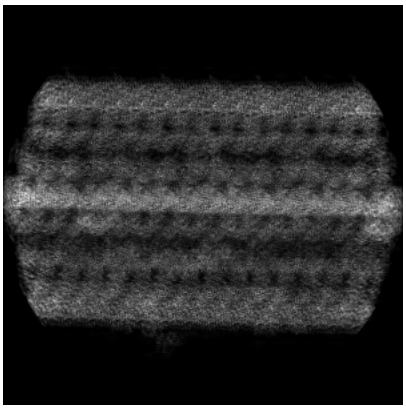
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

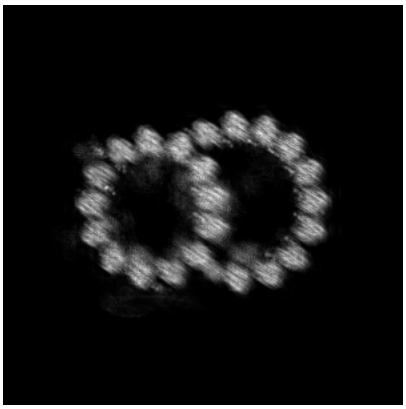
6.1.1 Primary map



X

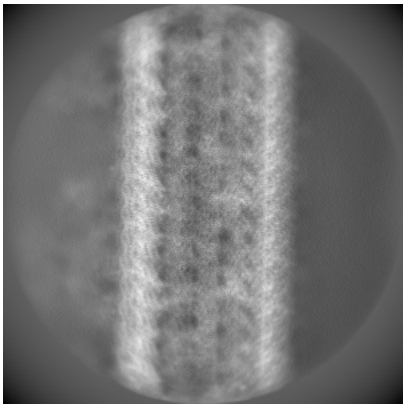


Y

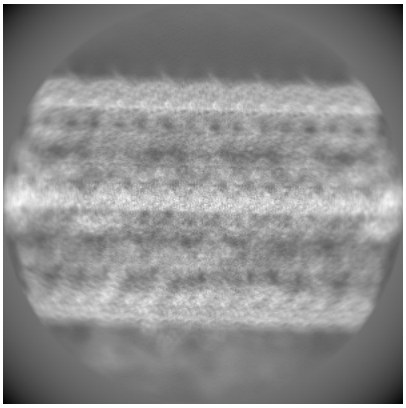


Z

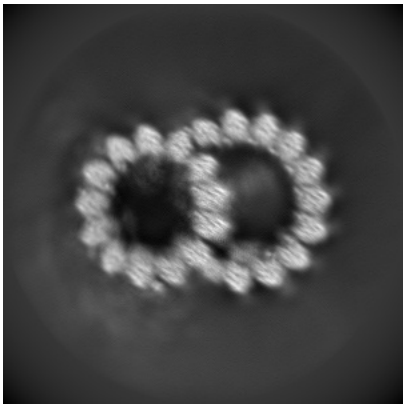
6.1.2 Raw map



X



Y

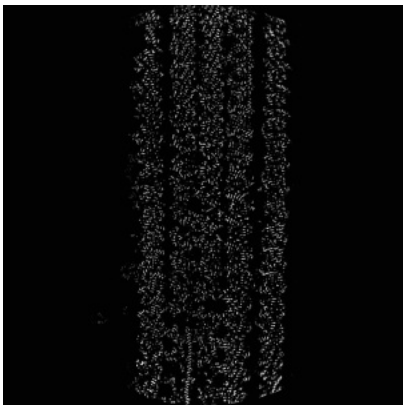


Z

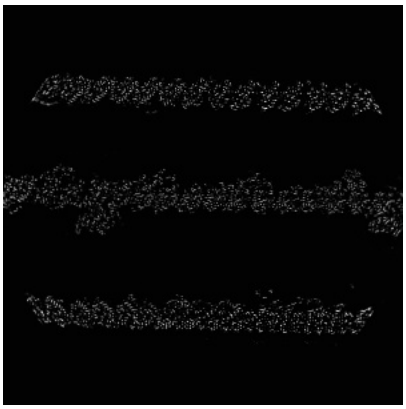
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

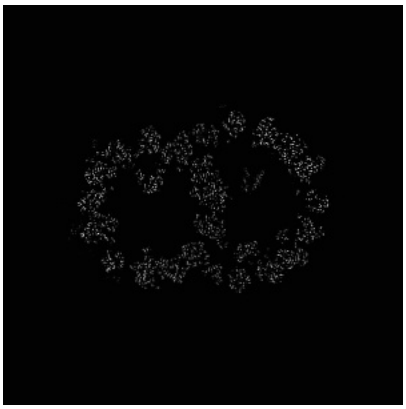
6.2.1 Primary map



X Index: 256

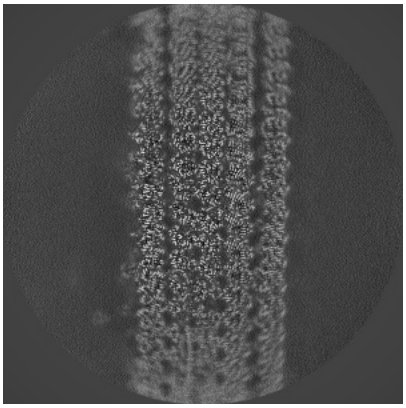


Y Index: 256

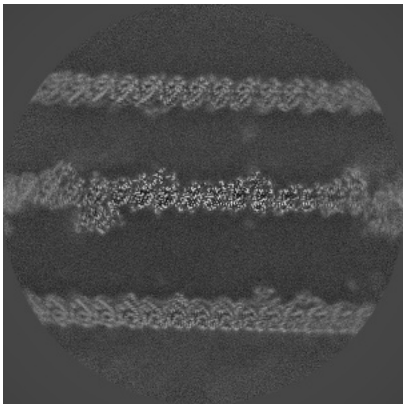


Z Index: 256

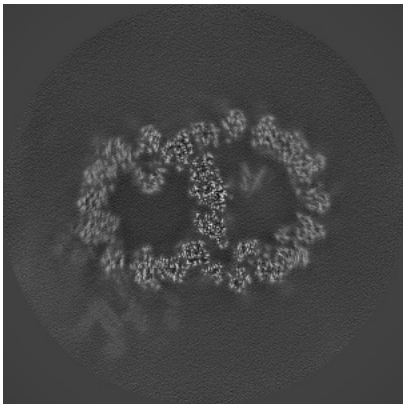
6.2.2 Raw map



X Index: 256



Y Index: 256

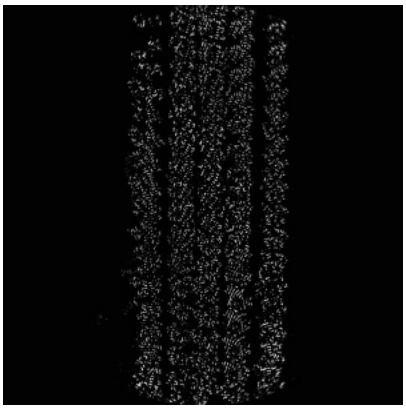


Z Index: 256

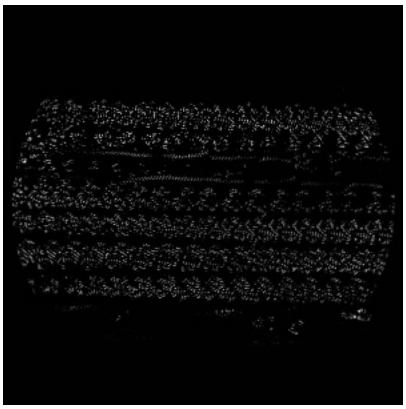
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

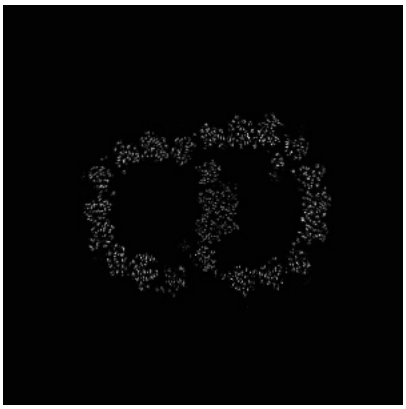
6.3.1 Primary map



X Index: 260

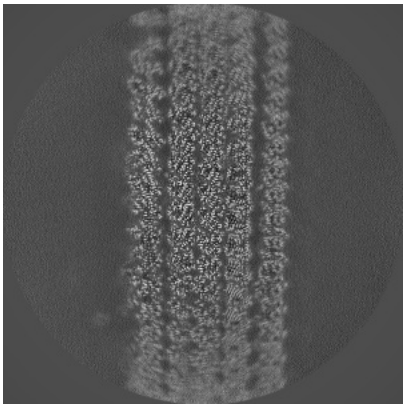


Y Index: 335

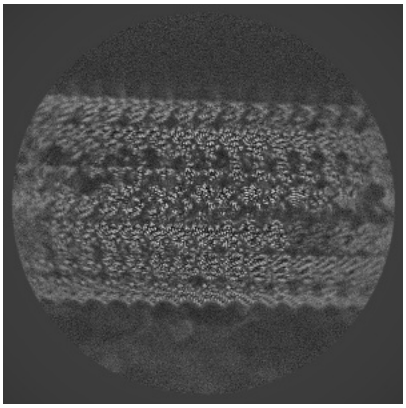


Z Index: 57

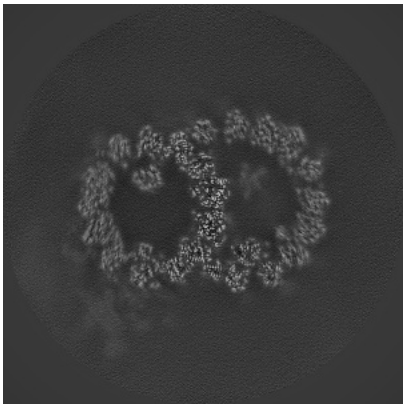
6.3.2 Raw map



X Index: 260



Y Index: 176

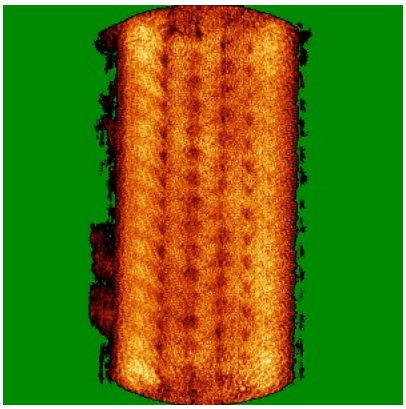


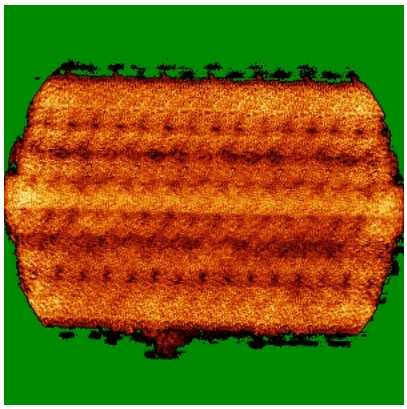
Z Index: 250

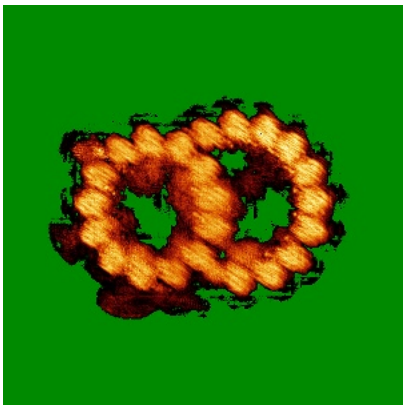
The images above show the largest variance slices of the map in three orthogonal directions.

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

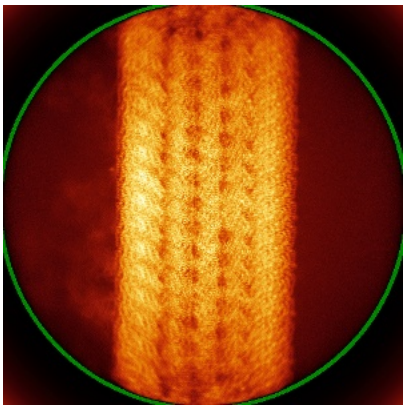
6.4.1 Primary map

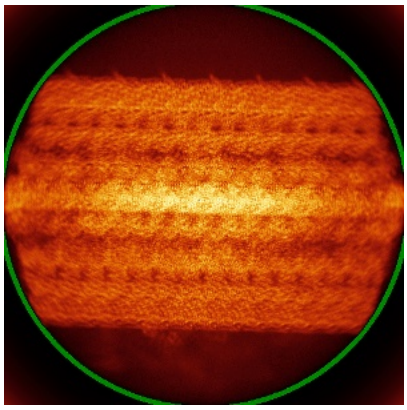

X

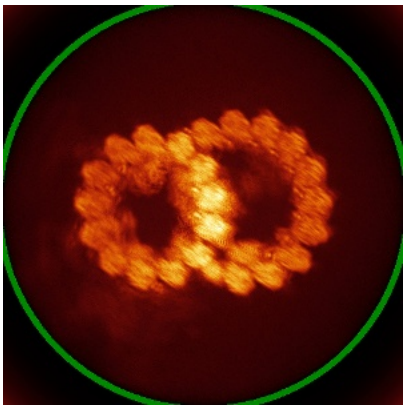

Y


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)

This section was not generated.

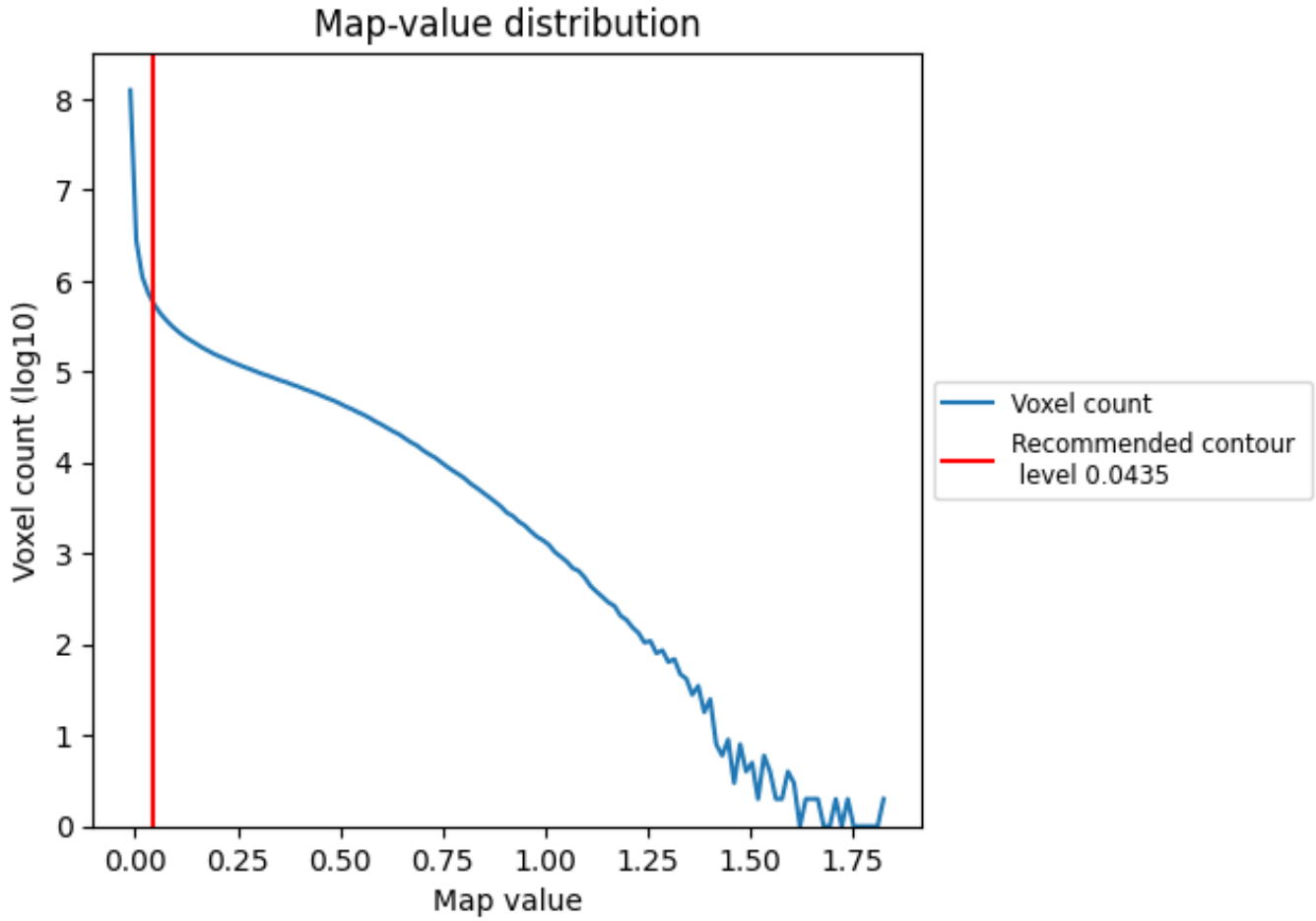
6.6 Mask visualisation (i)

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

7 Map analysis

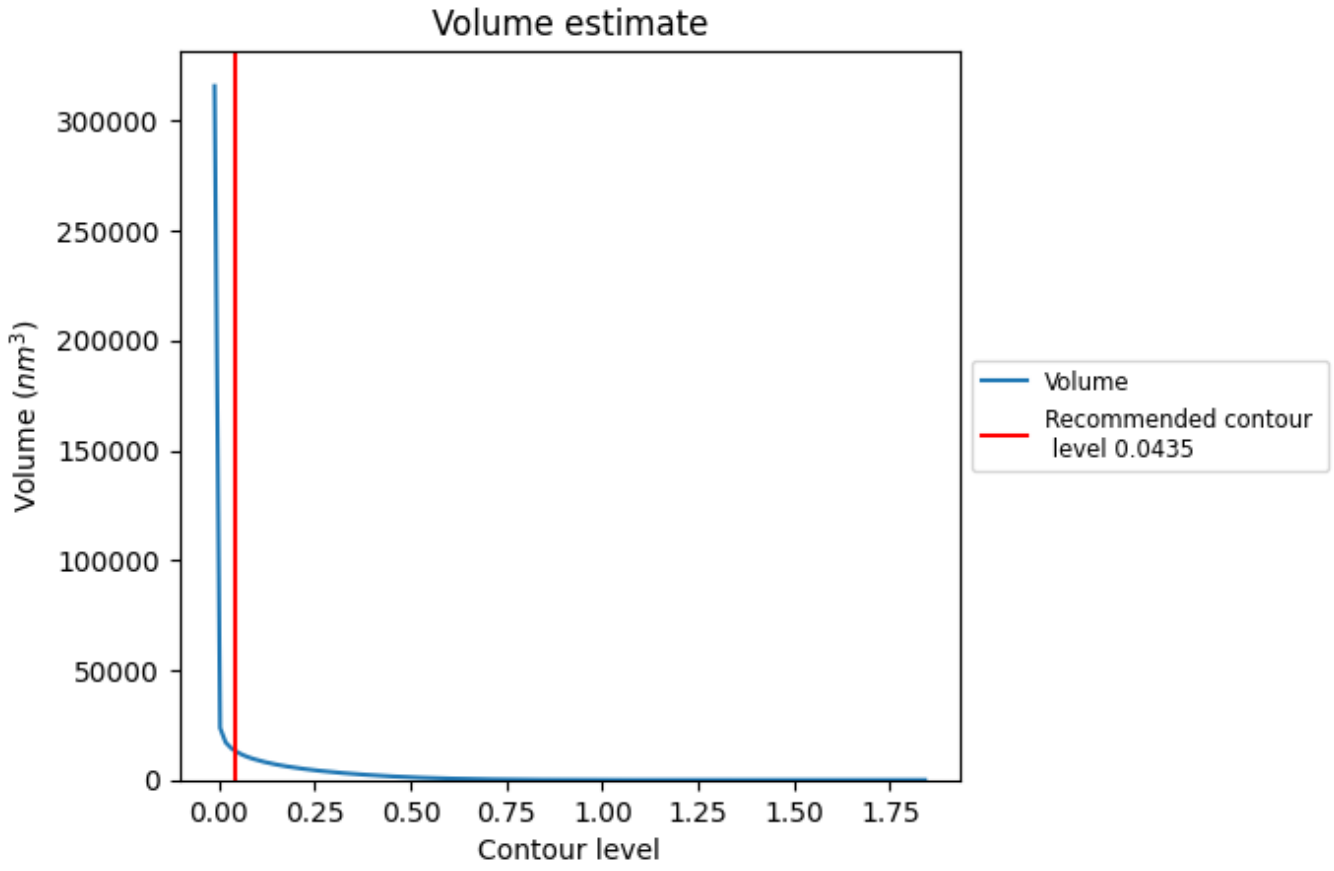
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

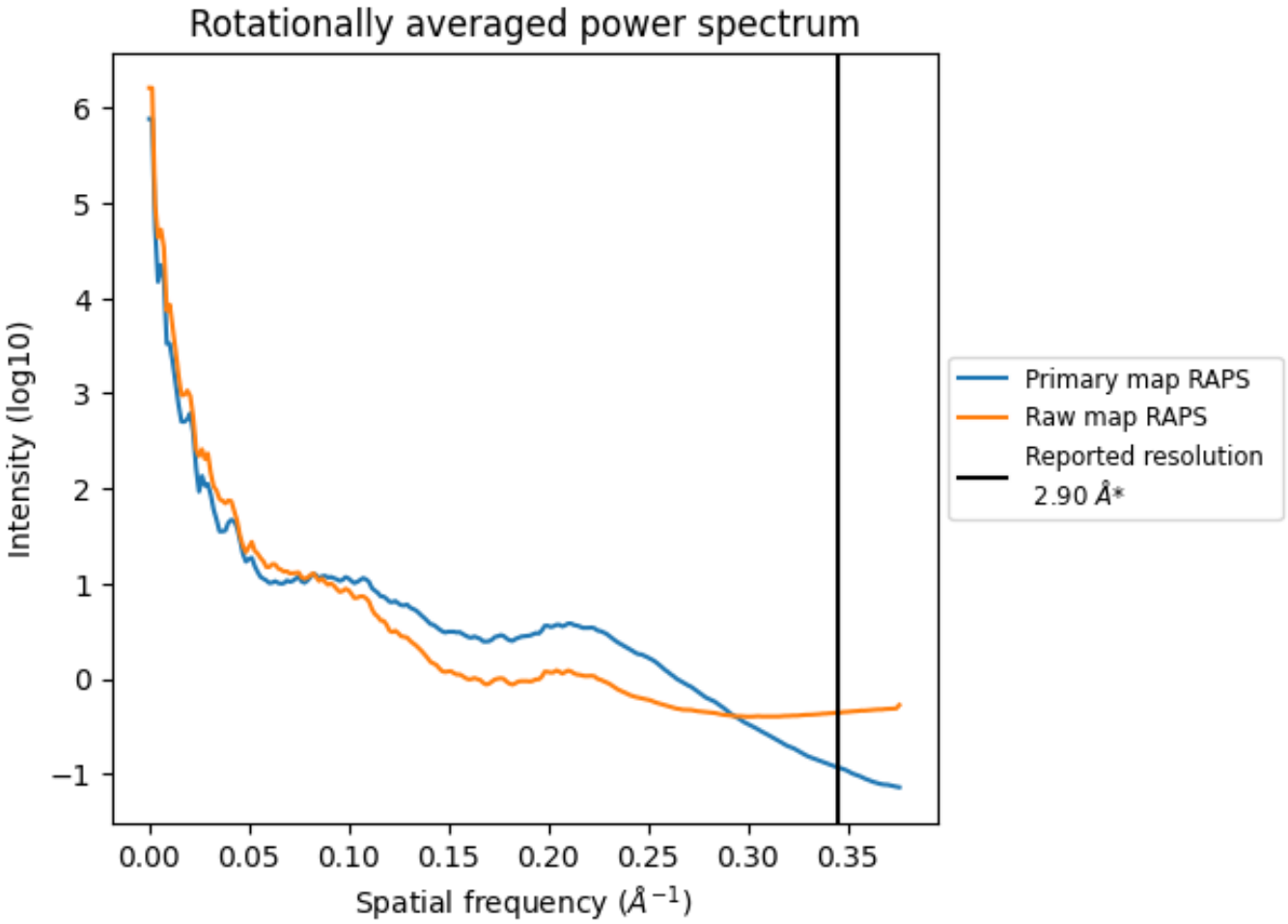
7.2 Volume estimate



The volume at the recommended contour level is 13083 nm^3; this corresponds to an approximate mass of 11818 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)

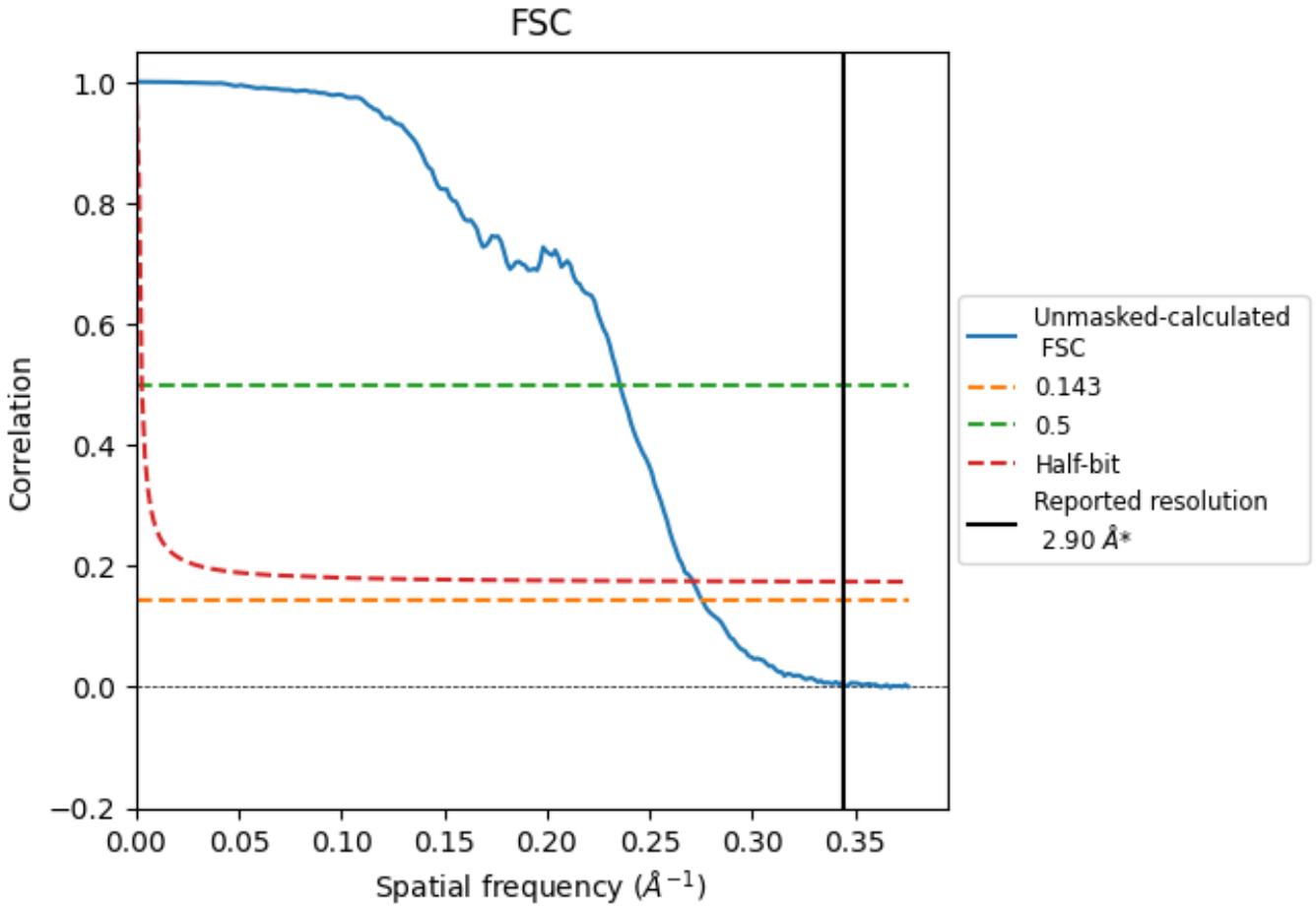


*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8.2 Resolution estimates (i)

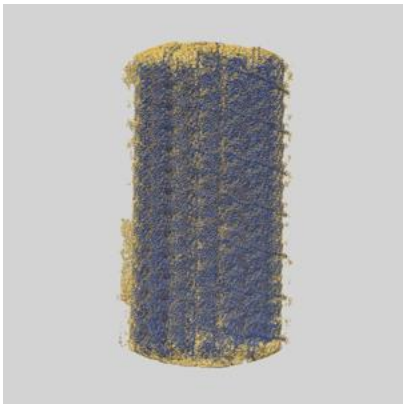
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.63	4.25	3.69

*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 3.63 differs from the reported value 2.9 by more than 10 %

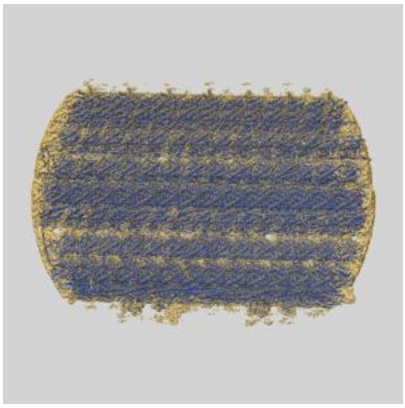
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47661 and PDB model 9E78. Per-residue inclusion information can be found in section 3 on page 79.

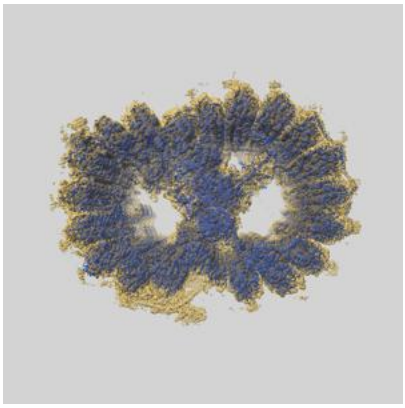
9.1 Map-model overlay



X



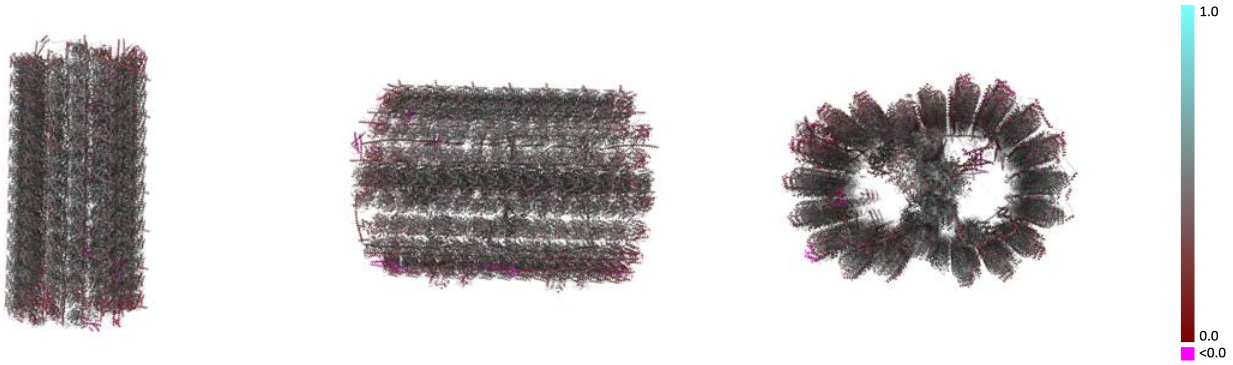
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0435 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)



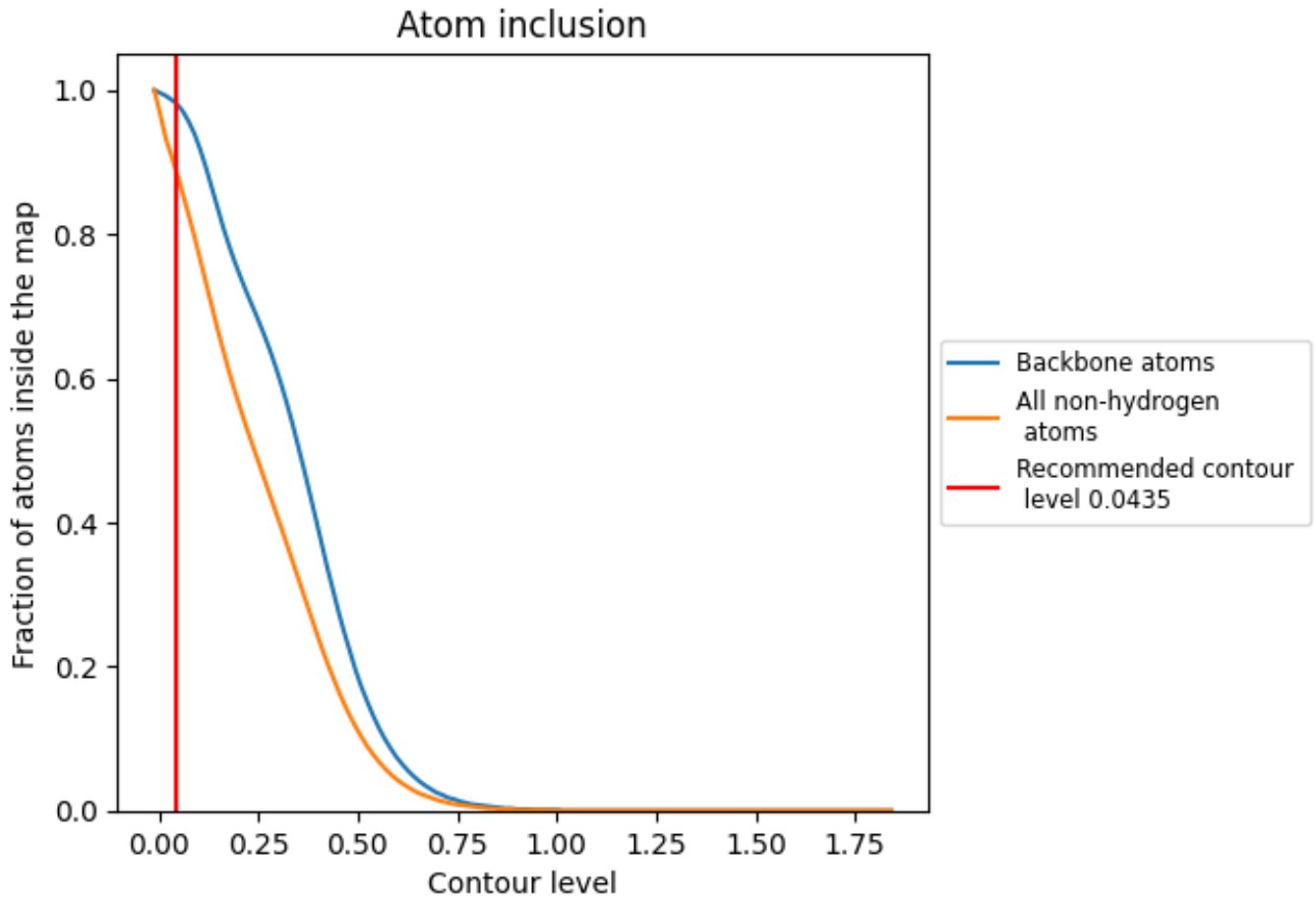
X Y Z

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)

This section was not generated.

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0435) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8880	0.4210
0	0.9160	0.4480
0A	0.8850	0.4350
0C	0.8910	0.3690
0D	0.8720	0.3660
0F	0.7950	0.3640
0G	0.7170	0.3190
0H	0.7580	0.2040
0I	0.7390	0.3240
0J	0.6720	0.2350
0L	0.8890	0.4600
0M	0.8840	0.4480
0N	0.8950	0.4530
0O	0.8840	0.3550
0R	0.8060	0.3460
0S	0.7640	0.2880
0U	0.9020	0.4490
0W	0.8800	0.4120
0Y	0.8680	0.4330
0Z	0.8530	0.4300
0a	0.9300	0.4500
0c	0.8520	0.3860
0d	0.8200	0.3890
0f	0.9100	0.4450
0g	0.9630	0.4340
0k	0.6530	0.3150
0l	0.6000	0.2870
0m	0.7810	0.3010
0n	0.7260	0.2490
0o	0.8230	0.2330
0p	0.7980	0.3660
0r	0.8720	0.4170
0t	0.9170	0.4450
0u	0.9330	0.3880
0v	0.8010	0.2720

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Chain	Atom inclusion	Q-score
0w	0.8000	0.3660
0x	0.8590	0.3840
0z	0.6470	0.2820
1A	0.9000	0.4510
1B	0.8750	0.4150
1D	0.9080	0.4130
1E	0.8990	0.4500
1F	0.9150	0.4370
1H	0.8070	0.3570
1I	0.8390	0.3890
1J	0.8380	0.3950
1K	0.8160	0.3610
1O	0.8620	0.4220
1Q	0.8580	0.4180
1S	0.8690	0.4380
1T	0.8940	0.3180
1U	0.7920	0.3710
1V	0.8590	0.3940
1X	0.8000	0.3550
1Y	0.8010	0.3670
1a	0.7680	0.3020
1b	0.8410	0.3670
1c	0.8800	0.3020
1d	0.7740	0.3520
1e	0.8810	0.4110
1g	0.7090	0.3340
1h	0.7740	0.3420
1j	0.9090	0.4510
1k	0.8890	0.4250
1l	0.9060	0.4540
1m	0.9510	0.4220
1o	0.8860	0.4380
1q	0.7780	0.3830
1r	0.6860	0.2710
1s	0.6750	0.2930
1t	0.5320	0.0680
1w	0.7560	0.3270
1x	0.7860	0.3480
1y	0.7280	0.2370
2B	0.8930	0.4620
2C	0.8960	0.4540
2F	0.9060	0.4620

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Chain	Atom inclusion	Q-score
2G	0.8950	0.4600
2H	0.8950	0.4490
2I	0.9160	0.4440
2L	0.8160	0.3620
2N	0.8980	0.4500
2O	0.8930	0.4300
2Q	0.8320	0.3880
2S	0.8920	0.4610
2U	0.8670	0.3950
2V	0.8510	0.3620
2X	0.8130	0.3930
2Z	0.8650	0.4380
2b	0.8390	0.3770
2c	0.7420	0.3070
2e	0.7770	0.3410
2f	0.8440	0.3040
2h	0.7640	0.3220
2i	0.7280	0.2720
2k	0.7740	0.3290
2l	0.7340	0.2760
2n	0.7450	0.2540
2o	0.7050	0.2880
2p	0.7240	0.1920
2r	0.8400	0.3680
2t	0.8660	0.3870
2v	0.9380	0.4070
2w	0.9270	0.4560
2y	0.8830	0.4480
2z	0.8970	0.4320
3B	0.8900	0.4300
3D	0.8480	0.4040
3F	0.5500	0.1620
3G	0.6840	0.2400
3H	0.5300	0.1880
3I	0.6770	0.2210
3L	0.8060	0.4230
3M	0.3800	0.2070
3P	0.9170	0.4040
3Q	0.9120	0.4390
3S	0.8660	0.4270
3U	0.8770	0.4240
3W	0.7950	0.3860

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Chain	Atom inclusion	Q-score
3X	0.7930	0.3590
3Z	0.7920	0.4000
3a	0.8620	0.4370
3b	0.8100	0.3510
3d	0.7290	0.3150
3f	0.7670	0.2750
3g	0.7660	0.3530
3h	0.7410	0.3130
3i	0.7600	0.2080
3m	0.7850	0.3700
3o	0.8040	0.3350
3p	0.8160	0.3940
3r	0.7720	0.3230
3s	0.7770	0.3470
3t	0.7420	0.2640
3w	0.8640	0.4210
3x	0.8260	0.3810
4A	0.8190	0.3750
4B	0.8280	0.4110
4I	0.5320	0.2360
4O	0.8310	0.3900
4P	0.8790	0.4120
4V	0.8320	0.3940
4W	0.8170	0.3940
4Y	0.7560	0.3100
4a	0.8030	0.3660
4b	0.8520	0.4110
5B	0.7560	0.2440
5C	0.6470	0.1700
5D	0.5490	0.0640
5G	0.7830	0.2690
5H	0.6710	0.1750
5I	0.5360	0.0410
5K	0.7980	0.3300
5L	0.7240	0.2430
5O	0.8050	0.3160
5P	0.6270	0.1820
5S	0.7540	0.3230
5T	0.6320	0.2100
A	0.9280	0.4400
AA	0.9150	0.4540
AB	0.9190	0.4630

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Chain	Atom inclusion	Q-score
AC	0.9080	0.4530
AD	0.9210	0.4610
AE	0.9100	0.4490
AF	0.9190	0.4580
AG	0.9000	0.4470
AH	0.9220	0.4510
AI	0.9140	0.4460
AJ	0.9210	0.4560
AK	0.9030	0.4480
AL	0.9250	0.4610
AM	0.9280	0.4610
AN	0.9270	0.4280
B	0.9080	0.4110
BA	0.9010	0.4380
BB	0.8440	0.4250
BC	0.8100	0.4050
BD	0.9030	0.4400
BE	0.9120	0.4380
BF	0.9110	0.4510
BG	0.9100	0.4370
BH	0.9120	0.4410
BI	0.8940	0.4200
BJ	0.9060	0.4360
BK	0.9100	0.4500
BL	0.9230	0.4550
BM	0.9160	0.4370
BN	0.8530	0.3720
C	0.9040	0.4260
CA	0.9150	0.4690
CB	0.9050	0.4580
CC	0.9090	0.4500
CD	0.9150	0.4340
CE	0.9150	0.4520
CF	0.9120	0.4510
CG	0.9090	0.4450
CH	0.9110	0.4270
CI	0.9150	0.4410
CJ	0.9160	0.4540
CK	0.9040	0.4350
CL	0.9130	0.4330
CM	0.9100	0.3410
D	0.8050	0.3160

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Chain	Atom inclusion	Q-score
DA	0.8960	0.4500
DB	0.8980	0.4630
DC	0.9000	0.4510
DD	0.9050	0.4450
DE	0.9100	0.4490
DF	0.9130	0.4570
DG	0.9070	0.4440
DH	0.9160	0.4430
DI	0.9190	0.4440
DJ	0.9180	0.4530
DK	0.9180	0.4490
DL	0.9160	0.4300
DM	0.8830	0.3200
E	0.8940	0.4210
EA	0.8950	0.4500
EB	0.8930	0.4610
EC	0.9010	0.4570
ED	0.9050	0.4560
EE	0.9030	0.4540
EF	0.9120	0.4600
EG	0.9140	0.4400
EH	0.9110	0.4340
EI	0.9070	0.4420
EJ	0.9070	0.4460
EK	0.9140	0.4360
EL	0.9040	0.3670
F	0.9040	0.4010
FA	0.8880	0.4290
FB	0.9090	0.4650
FC	0.9170	0.4680
FD	0.9010	0.4590
FE	0.9060	0.4660
FF	0.9220	0.4660
FG	0.9240	0.4580
FH	0.9230	0.4530
FI	0.9210	0.4520
FJ	0.9200	0.4490
FK	0.9210	0.4380
FL	0.9290	0.4100
G	0.7650	0.2810
GA	0.8330	0.3440
GB	0.8000	0.3760

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Chain	Atom inclusion	Q-score
GC	0.8420	0.3790
GD	0.8750	0.4130
GE	0.8940	0.4380
GF	0.8930	0.4410
GG	0.9000	0.4450
GH	0.9080	0.4350
GI	0.9060	0.4310
GJ	0.9070	0.4310
GK	0.9110	0.4320
GL	0.9020	0.3870
H	0.8110	0.2930
HA	0.8780	0.3640
HB	0.8430	0.3840
HC	0.8480	0.3890
HD	0.8810	0.4070
HE	0.8770	0.4100
HF	0.8910	0.4200
HG	0.8930	0.4230
HH	0.8970	0.4210
HI	0.8870	0.4120
HJ	0.8960	0.4160
HK	0.9110	0.4270
HL	0.8920	0.3840
HM	0.9110	0.3570
I	0.9050	0.3480
IA	0.9070	0.4040
IB	0.9200	0.4310
IC	0.9180	0.4330
ID	0.9100	0.4310
IE	0.9050	0.4260
IF	0.9050	0.4300
IG	0.9150	0.4450
IH	0.9120	0.4390
II	0.9070	0.4390
IJ	0.9100	0.4370
IK	0.9080	0.4180
IL	0.9030	0.3860
IM	0.9150	0.3820
J	0.9080	0.3680
JA	0.9170	0.4230
JB	0.9130	0.4330
JC	0.9130	0.4310

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Chain	Atom inclusion	Q-score
JD	0.9120	0.4360
JE	0.9120	0.4370
JF	0.9030	0.4410
JG	0.9050	0.4440
JH	0.8960	0.4340
JI	0.9050	0.4500
JJ	0.9020	0.4380
JK	0.9040	0.4190
JL	0.9090	0.4190
JM	0.9190	0.4020
JN	0.9210	0.3650
K	0.9360	0.4230
KA	0.9290	0.4480
KB	0.9280	0.4540
KC	0.9150	0.4550
KD	0.9230	0.4600
KE	0.9250	0.4590
KF	0.8960	0.4460
KG	0.9090	0.4570
KH	0.9000	0.4530
KI	0.9110	0.4650
KJ	0.9200	0.4600
KK	0.9110	0.4430
KL	0.9180	0.4360
KM	0.9210	0.4350
KN	0.9350	0.4250
L	0.9450	0.4420
LA	0.9500	0.4670
LB	0.9390	0.4660
LC	0.9340	0.4750
LD	0.9300	0.4680
LE	0.9330	0.4730
LF	0.9200	0.4730
LG	0.9140	0.4730
LH	0.9290	0.4770
LI	0.9350	0.4810
LJ	0.9240	0.4630
LK	0.9280	0.4720
LL	0.9320	0.4560
LM	0.9440	0.4620
LN	0.9420	0.4580
LO	0.9440	0.4340

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Chain	Atom inclusion	Q-score
M	0.9390	0.4720
MA	0.9330	0.4770
MB	0.9300	0.4780
MC	0.9160	0.4650
MD	0.9170	0.4610
ME	0.9240	0.4710
MF	0.9220	0.4710
MG	0.9050	0.4550
MH	0.9140	0.4560
MI	0.9060	0.4510
MJ	0.9270	0.4590
MK	0.9050	0.4380
ML	0.9150	0.4600
MM	0.9390	0.4680
MN	0.9400	0.4590
N	0.8900	0.3720
NA	0.8560	0.3730
NB	0.8830	0.4050
NC	0.8640	0.3980
ND	0.8830	0.4140
NE	0.8620	0.4020
NF	0.8600	0.4090
NG	0.8400	0.3940
NH	0.8730	0.4170
NI	0.8680	0.4170
NJ	0.8820	0.4230
NK	0.8640	0.3950
NL	0.8730	0.3780
NM	0.8660	0.3410
O	0.8820	0.3260
OA	0.9030	0.3900
OB	0.9070	0.4190
OC	0.9010	0.4210
OD	0.9040	0.4250
OE	0.9110	0.4310
OF	0.9010	0.4330
OG	0.8860	0.4200
OH	0.9090	0.4380
OI	0.8940	0.4370
OJ	0.8990	0.4300
OK	0.8870	0.4120
OL	0.8740	0.3610

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Chain	Atom inclusion	Q-score
OM	0.8740	0.3230
P	0.8820	0.3310
PA	0.9080	0.3870
PB	0.9120	0.4380
PC	0.9140	0.4440
PD	0.9130	0.4390
PE	0.9140	0.4380
PF	0.9100	0.4500
PG	0.8980	0.4460
PH	0.9110	0.4580
PI	0.9080	0.4590
PJ	0.9080	0.4590
PK	0.9050	0.4500
PL	0.8880	0.3930
PM	0.8900	0.3560
Q	0.8860	0.3640
QA	0.9160	0.4420
QB	0.9190	0.4540
QC	0.9150	0.4550
QD	0.9140	0.4460
QE	0.9130	0.4560
QF	0.9100	0.4560
QG	0.9150	0.4720
QH	0.8940	0.4530
QI	0.9130	0.4630
QJ	0.9240	0.4610
QK	0.8930	0.4020
QL	0.9100	0.3670
R	0.8710	0.3580
RA	0.9130	0.4400
RB	0.9140	0.4440
RC	0.9080	0.4450
RD	0.9100	0.4380
RE	0.9100	0.4500
RF	0.9080	0.4610
RG	0.9060	0.4690
RH	0.9060	0.4550
RI	0.9190	0.4530
RJ	0.9040	0.4310
RK	0.9040	0.4220
RL	0.9100	0.3860
S	0.9250	0.4520

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Chain	Atom inclusion	Q-score
SA	0.9210	0.4590
SB	0.9130	0.4540
SC	0.9160	0.4470
SD	0.9160	0.4610
SE	0.9140	0.4740
SF	0.9180	0.4760
SG	0.9240	0.4750
SH	0.9170	0.4470
SI	0.9210	0.4500
SJ	0.9110	0.4520
SK	0.9170	0.4210
T	0.9130	0.4200
TA	0.9000	0.4420
TB	0.9000	0.4420
TC	0.8910	0.4120
TD	0.8990	0.4220
TE	0.9120	0.4630
TF	0.9180	0.4650
TG	0.9140	0.4600
TH	0.9150	0.4440
TI	0.9130	0.4440
TJ	0.9130	0.4440
TK	0.9140	0.4340
TL	0.8410	0.2440
U	0.8820	0.3880
UA	0.8790	0.4190
UB	0.8760	0.4210
UC	0.8900	0.4210
UD	0.9020	0.4400
UE	0.8950	0.4400
UF	0.9010	0.4490
UG	0.9040	0.4410
UH	0.9030	0.4290
UI	0.9030	0.4310
UJ	0.8970	0.4320
UK	0.8920	0.4190
UL	0.8710	0.3490
V	0.9120	0.4190
VA	0.9070	0.4440
VB	0.9120	0.4620
VC	0.9150	0.4570
VD	0.9170	0.4550

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Chain	Atom inclusion	Q-score
VE	0.9070	0.4540
VF	0.9150	0.4660
VG	0.9070	0.4570
VH	0.9100	0.4530
VI	0.9140	0.4580
VJ	0.9180	0.4690
VK	0.9160	0.4680
VL	0.9160	0.4510
VM	0.8750	0.3870
W	0.9130	0.4280
WA	0.9160	0.4520
WB	0.9150	0.4580
WC	0.9160	0.4520
WD	0.9050	0.4400
WE	0.9100	0.4450
WF	0.9100	0.4480
WG	0.9080	0.4500
WH	0.9040	0.4460
WI	0.9120	0.4450
WJ	0.9160	0.4680
WK	0.9140	0.4680
WL	0.9030	0.4480
WM	0.9080	0.4230
X	0.9080	0.4630
X1	0.8840	0.4300
XA	0.8990	0.4670
XB	0.9250	0.4630
XC	0.9050	0.4600
XD	0.9140	0.4670
XE	0.9150	0.4710
XF	0.9140	0.4650
XM	0.8950	0.4500
XN	0.8770	0.4240
XO	0.8980	0.4450
XP	0.8640	0.4220
XQ	0.9010	0.4530
XR	0.9110	0.4260