wwPDB EM Validation Summary Report

Mar 6, 2026 – 09:10 AM UTC

PDB ID	:	8I7R / pdb_00008i7r
EMDB ID	:	EMD-35230
Title	:	In situ structure of axonemal doublet microtubules in mouse sperm with 48-nm repeat
Authors	:	Zhu, Y.; Yin, G.L.; Tai, L.H.; Sun, F.
Deposited on	:	2023-02-02
Resolution	:	6.50 Å(reported)

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

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

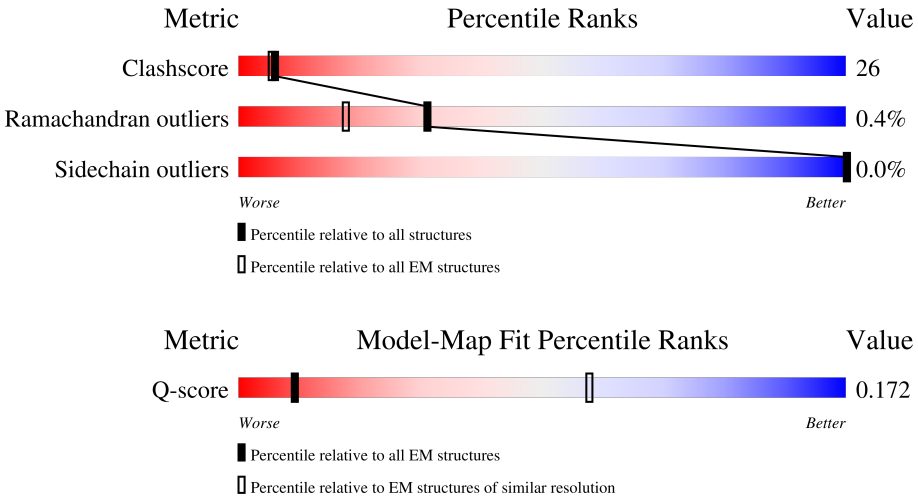
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

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

The reported resolution of this entry is 6.50 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	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	556 (6.00 - 7.00)

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	491	8% 32% 33% 36%
1	B	491	10% 19% 21% 60%
2	A1	418	39% 36% 25%
2	A2	418	49% 46% 5%

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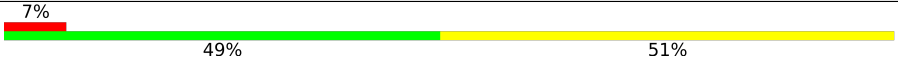
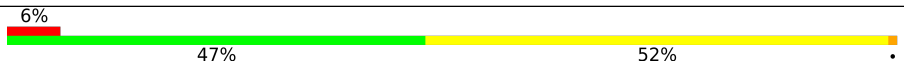
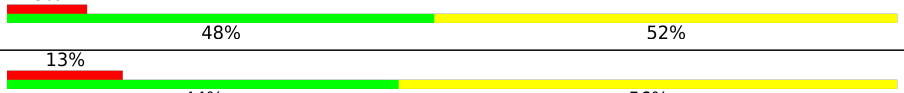
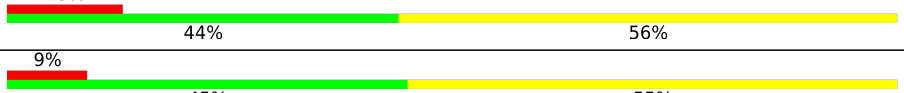
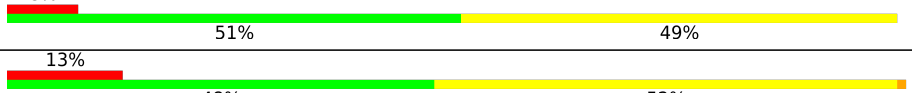
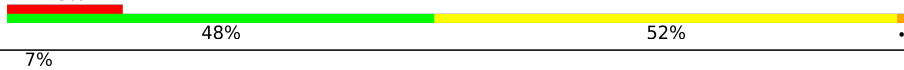
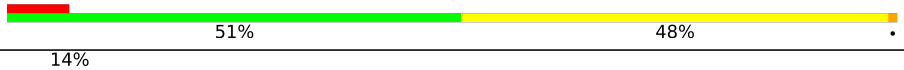
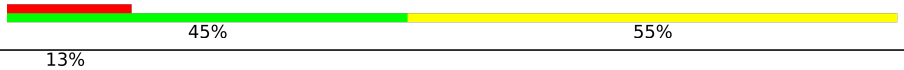
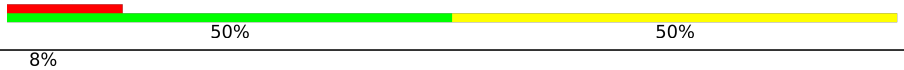
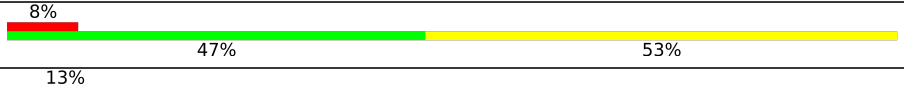
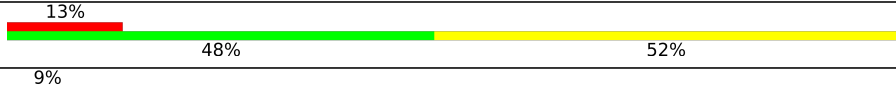
Mol	Chain	Length	Quality of chain
2	A3	418	
2	A4	418	
3	AB	427	
3	AD	427	
3	AF	427	
3	AH	427	
3	AJ	427	
3	AL	427	
3	BB	427	
3	BD	427	
3	BF	427	
3	BH	427	
3	BJ	427	
3	BL	427	
3	CB	427	
3	CD	427	
3	CF	427	
3	CH	427	
3	CJ	427	
3	CL	427	
3	DB	427	
3	DD	427	
3	DF	427	
3	DH	427	
3	DJ	427	

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Mol	Chain	Length	Quality of chain
3	DL	427	12% 52% 47%
3	EB	427	18% 48% 52%
3	ED	427	10% 45% 55%
3	EF	427	19% 52% 48%
3	EH	427	12% 52% 48%
3	EJ	427	25% 43% 56%
3	EL	427	21% 48% 52%
3	FB	427	21% 50% 49%
3	FD	427	14% 49% 51%
3	FF	427	23% 52% 48%
3	FH	427	16% 50% 49%
3	FJ	427	21% 51% 48%
3	FL	427	22% 50% 50%
3	GB	427	22% 45% 55%
3	GD	427	19% 47% 52%
3	GF	427	26% 50% 49%
3	GH	427	22% 49% 50%
3	GJ	427	22% 48% 52%
3	GL	427	27% 48% 52%
3	HB	427	28% 52% 48%
3	HD	427	20% 52% 48%
3	HF	427	27% 51% 48%
3	HH	427	21% 48% 51%
3	HJ	427	25% 47% 53%
3	HL	427	27% 45% 54%

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Mol	Chain	Length	Quality of chain
3	IB	427	19% 44% 55%
3	ID	427	18% 48% 52%
3	IF	427	20% 50% 49%
3	IH	427	17% 48% 52%
3	IJ	427	16% 49% 51%
3	IL	427	21% 48% 52%
3	JB	427	12% 52% 47%
3	JD	427	10% 50% 50%
3	JF	427	16% 56% 44%
3	JH	427	9% 49% 51%
3	JJ	427	15% 51% 48%
3	JL	427	16% 53% 47%
3	KB	427	12% 48% 52%
3	KD	427	7% 46% 53%
3	KF	427	9% 51% 48%
3	KH	427	6% 46% 54%
3	KJ	427	52% 48%
3	KL	427	16% 45% 55%
3	LB	427	14% 44% 56%
3	LD	427	6% 45% 54%
3	LF	427	5% 48% 52%
3	LH	427	5% 47% 52%
3	LJ	427	43% 57%
3	LL	427	11% 49% 50%
3	MB	427	13% 50% 50%

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Mol	Chain	Length	Quality of chain
3	MD	427	43% 57%
3	MF	427	49% 50%
3	MH	427	42% 58%
3	MJ	427	5% 52% 47%
3	ML	427	7% 46% 53%
3	NB	427	38% 58% 41%
3	ND	427	25% 54% 45%
3	NF	427	31% 53% 47%
3	NH	427	24% 49% 50%
3	NJ	427	37% 55% 44%
3	NL	427	35% 57% 42%
3	OB	427	64% 50% 49%
3	OD	427	53% 53% 46%
3	OF	427	53% 51% 48%
3	OH	427	48% 56% 44%
3	OJ	427	57% 53% 46%
3	OL	427	59% 57% 43%
3	PB	427	64% 54% 45%
3	PD	427	54% 51% 49%
3	PF	427	54% 52% 48%
3	PH	427	56% 51% 48%
3	PJ	427	53% 52% 47%
3	PL	427	67% 50% 50%
3	QB	427	70% 52% 47%
3	QD	427	56% 51% 49%

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Mol	Chain	Length	Quality of chain
3	QF	427	54% 51% 48%
3	QH	427	59% 53% 46%
3	QJ	427	58% 50% 50%
3	QL	427	70% 54% 46%
3	RB	427	74% 48% 51%
3	RD	427	67% 53% 46%
3	RF	427	55% 50% 49%
3	RH	427	64% 46% 54%
3	RJ	427	59% 53% 47%
3	RL	427	72% 53% 46%
3	SB	427	68% 50% 50%
3	SD	427	60% 53% 47%
3	SF	427	43% 53% 46%
3	SH	427	60% 52% 47%
3	SJ	427	53% 51% 48%
3	SL	427	70% 53% 46%
3	TB	427	68% 57% 43%
3	TD	427	60% 51% 48%
3	TF	427	40% 49% 50%
3	TH	427	57% 47% 52%
3	TJ	427	46% 52% 48%
3	TL	427	57% 48% 50%
3	TN	427	67% 51% 48%
3	UB	427	53% 53% 46%
3	UD	427	28% 52% 47%

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Mol	Chain	Length	Quality of chain
3	UF	427	40% 46% 53%
3	UH	427	35% 56% 44%
3	UJ	427	49% 50% 49%
3	UL	427	52% 57% 43%
3	VB	427	35% 48% 52%
3	VD	427	19% 52% 48%
3	VF	427	25% 50% 49%
3	VH	427	23% 55% 45%
3	VJ	427	30% 52% 47%
3	VL	427	40% 56% 43%
3	WB	427	20% 49% 51%
3	WD	427	16% 50% 49%
3	WF	427	15% 50% 50%
3	WH	427	15% 51% 48%
3	WJ	427	16% 51% 48%
3	WL	427	23% 54% 45%
4	AC	438	7% 44% 56%
4	AE	438	5% 45% 54%
4	AG	438	11% 47% 53%
4	AI	438	7% 45% 54%
4	AK	438	8% 47% 52%
4	AM	438	11% 46% 54%
4	BC	438	9% 49% 51%
4	BE	438	6% 45% 55%
4	BG	438	15% 48% 52%

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Mol	Chain	Length	Quality of chain
4	BI	438	8% 47% 53%
4	BK	438	10% 45% 55%
4	BM	438	12% 51% 49%
4	CC	438	13% 45% 55%
4	CE	438	13% 49% 51%
4	CG	438	18% 44% 56%
4	CI	438	13% 42% 58%
4	CK	438	14% 40% 59%
4	CM	438	16% 45% 54%
4	DA	438	20% 46% 54%
4	DC	438	12% 46% 54%
4	DE	438	17% 42% 57%
4	DG	438	17% 45% 55%
4	DI	438	15% 46% 54%
4	DK	438	19% 44% 55%
4	EA	438	21% 50% 50%
4	EC	438	16% 46% 54%
4	EE	438	19% 45% 54%
4	EG	438	21% 46% 54%
4	EI	438	14% 41% 59%
4	EK	438	25% 45% 55%
4	FA	438	31% 51% 49%
4	FC	438	20% 47% 53%
4	FE	438	18% 45% 54%
4	FG	438	27% 44% 56%

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Mol	Chain	Length	Quality of chain
4	FI	438	16% 46% 54%
4	FK	438	27% 44% 55%
4	GA	438	32% 50% 50%
4	GC	438	26% 44% 55%
4	GE	438	21% 42% 58%
4	GG	438	32% 45% 55%
4	GI	438	17% 42% 58%
4	GK	438	36% 49% 51%
4	HA	438	35% 44% 56%
4	HC	438	34% 45% 55%
4	HE	438	23% 44% 56%
4	HG	438	33% 45% 55%
4	HI	438	17% 41% 58%
4	HK	438	41% 47% 53%
4	IA	438	30% 46% 54%
4	IC	438	25% 47% 53%
4	IE	438	18% 45% 55%
4	IG	438	28% 45% 55%
4	II	438	16% 45% 55%
4	IK	438	27% 44% 56%
4	IM	438	24% 44% 56%
4	JA	438	20% 53% 47%
4	JC	438	13% 45% 55%
4	JE	438	16% 46% 53%
4	JG	438	17% 48% 52%

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Mol	Chain	Length	Quality of chain
4	JI	438	13% 47% 53%
4	JK	438	24% 47% 53%
4	KA	438	18% 45% 55%
4	KC	438	9% 43% 57%
4	KE	438	8% 44% 56%
4	KG	438	12% 47% 53%
4	KI	438	10% 41% 59%
4	KK	438	16% 43% 57%
4	LA	438	14% 46% 53%
4	LC	438	8% 42% 58%
4	LE	438	7% 45% 55%
4	LG	438	10% 45% 54%
4	LI	438	9% 46% 54%
4	LK	438	12% 46% 54%
4	MC	438	10% 40% 59%
4	ME	438	7% 46% 54%
4	MG	438	7% 45% 55%
4	MI	438	8% 46% 53%
4	MK	438	7% 44% 56%
4	MM	438	14% 46% 54%
4	NA	438	44% 56% 44%
4	NC	438	38% 50% 50%
4	NE	438	31% 48% 51%
4	NG	438	34% 49% 51%
4	NI	438	28% 50% 50%

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Mol	Chain	Length	Quality of chain
4	NK	438	41% 52% 48%
4	OA	438	72% 54% 45%
4	OC	438	66% 50% 50%
4	OE	438	50% 48% 51%
4	OG	438	56% 52% 48%
4	OI	438	47% 49% 50%
4	OK	438	62% 53% 47%
4	PA	438	71% 52% 48%
4	PC	438	67% 50% 50%
4	PE	438	46% 48% 52%
4	PG	438	58% 48% 52%
4	PI	438	53% 43% 57%
4	PK	438	71% 50% 50%
4	PM	438	68% 49% 51%
4	QC	438	67% 46% 54%
4	QE	438	48% 47% 53%
4	QG	438	57% 46% 54%
4	QI	438	53% 48% 52%
4	QK	438	64% 48% 51%
4	QM	438	71% 50% 50%
4	RC	438	76% 49% 51%
4	RE	438	54% 51% 49%
4	RG	438	66% 48% 52%
4	RI	438	60% 44% 55%
4	RK	438	63% 47% 53%

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Mol	Chain	Length	Quality of chain
4	RM	438	79% 50% 50%
4	SC	438	69% 48% 51%
4	SE	438	47% 48% 52%
4	SG	438	59% 46% 54%
4	SI	438	54% 42% 58%
4	SK	438	49% 49% 50%
4	SM	438	73% 50% 49%
4	TC	438	69% 47% 53%
4	TE	438	48% 52% 48%
4	TG	438	51% 49% 51%
4	TI	438	59% 50% 50%
4	TK	438	49% 48% 52%
4	TM	438	69% 50% 50%
4	UA	438	56% 53% 47%
4	UC	438	37% 48% 51%
4	UE	438	41% 45% 55%
4	UG	438	45% 45% 55%
4	UI	438	41% 48% 51%
4	UK	438	59% 51% 49%
4	VA	438	42% 52% 48%
4	VC	438	32% 49% 51%
4	VE	438	24% 46% 53%
4	VG	438	35% 47% 53%
4	VI	438	26% 50% 50%
4	VK	438	41% 48% 52%

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Mol	Chain	Length	Quality of chain
4	WA	438	29% 54% 45%
4	WC	438	24% 50% 50%
4	WE	438	19% 47% 53%
4	WG	438	23% 46% 54%
4	WI	438	24% 47% 53%
4	WK	438	30% 47% 52%
5	B1	430	29% 27% 45%
5	B2	430	53% 44%
5	B3	430	53% 43%
5	B4	430	43% 30% 27%
5	B5	430	7% 5% 89%
5	B6	430	46% 38% 16%
5	B7	430	51% 42% 6%
5	B8	430	52% 40% 7%
5	B9	430	13% 14% 73%
6	C	395	19% 42% 52% 6%
6	D	395	28% 45% 49% 6%
7	C1	490	10% 10% 80%
7	C2	490	41% 38% 21%
7	C3	490	39% 40% 21%
7	C4	490	37% 37% 26%
7	C5	490	5% 8% 87%
7	C6	490	25% 16% 59%
7	C7	490	42% 38% 20%
7	C8	490	44% 36% 20%

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Mol	Chain	Length	Quality of chain
7	C9	490	32% 29% 39%
7	Ca	490	24% 21% 55%
7	Cb	490	44% 35% 21%
7	Cc	490	42% 37% 21%
7	Cd	490	35% 19% 46%
8	D1	447	8% 5% 87%
8	D2	447	42% 40% 18%
8	D3	447	51% 44% 5%
8	D4	447	45% 50% 5%
8	D5	447	12% 17% 71%
8	D6	447	9% 8% 83%
8	D7	447	38% 44% 17%
8	D8	447	44% 45% 11%
8	D9	447	45% 43% 12%
8	Da	447	6% 7% 87%
9	E	853	7% 18% 13% 69%
9	F	853	5% 11% 6% 83%
10	E1	206	20% 50% 40% 9%
10	E2	206	23% 52% 37% 9%
10	E3	206	20% 55% 35% 9%
10	E4	206	6% 16% 12% 72%
11	F1	557	28% 23% 49%
11	F2	557	35% 36% 29%
11	F3	557	5% 33% 38% 29%
11	F4	557	21% 17% 62%

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Mol	Chain	Length	Quality of chain
11	F5	557	16% 23% 23% 54%
11	F6	557	23% 35% 35% 30%
11	F7	557	10% 35% 35% 30%
11	F8	557	6% 20% 21% 59%
11	F9	557	26% 18% 13% 69%
11	Fa	557	29% 39% 31% 30%
11	Fb	557	13% 36% 32% 30%
11	Fc	557	26% 30% 26% 43%
11	Fd	557	96%
11	Fe	557	14% 27% 16% 57%
11	Ff	557	22% 43% 27% 29%
11	Fg	557	26% 39% 17% 44%
11	Fh	557	12% 21% 11% 67%
11	Fi	557	33% 31% 18% 51%
11	Fj	557	15% 27% 23% 50%
11	Fk	557	11% 30% 30% 40%
11	Fl	557	12% 30% 30% 40%
11	Fm	557	12% 34% 25% 41%
12	G	514	11% 52% 36% 13%
12	H	514	5% 91%
13	G1	648	13% 40% 38% 21%
13	G2	648	15% 42% 34% 24%
13	G3	648	20% 45% 33% 21%
14	G4	750	20% 47% 53%
14	G5	750	22% 52% 47%

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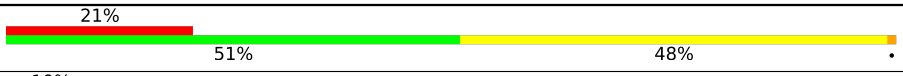
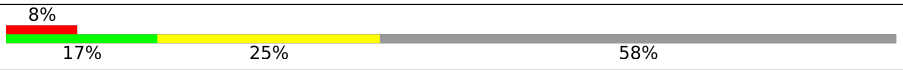
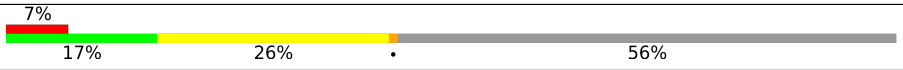
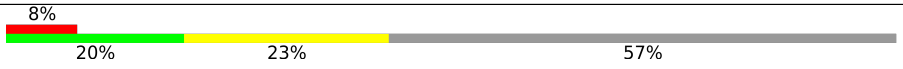
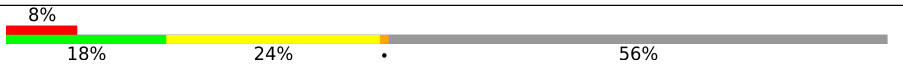
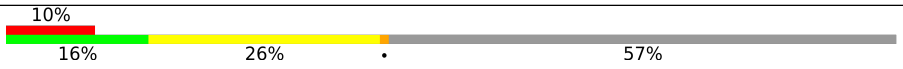
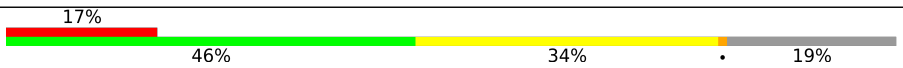
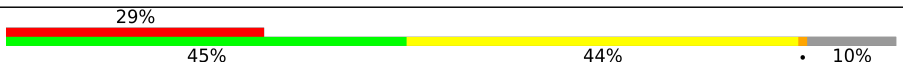
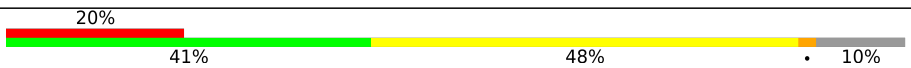
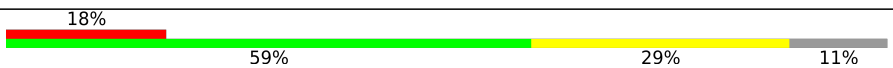
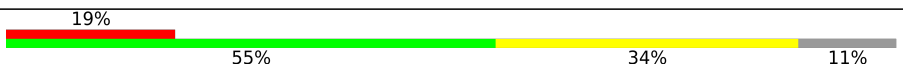
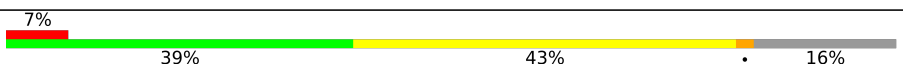
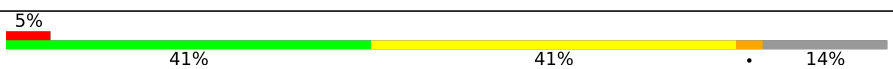
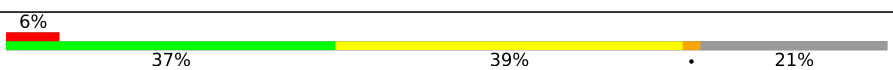
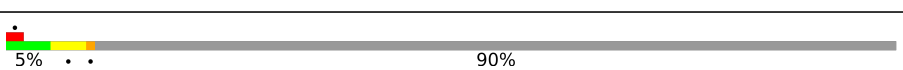
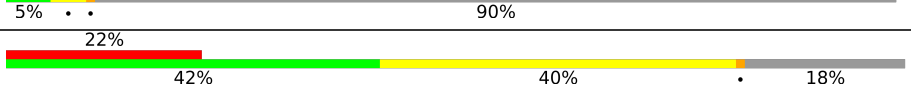
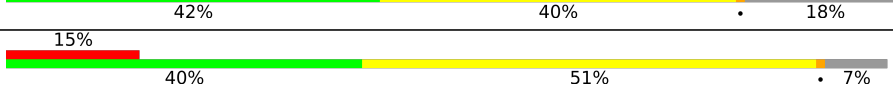
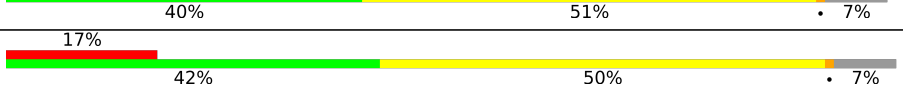
Mol	Chain	Length	Quality of chain
14	G6	750	
15	H1	319	
15	H2	319	
15	H3	319	
15	H4	319	
15	H5	319	
15	H6	319	
16	I	228	
17	I1	200	
17	I2	200	
17	I3	200	
18	J	196	
19	J1	189	
19	J2	189	
19	J3	189	
20	K	303	
20	L	303	
21	K1	499	
21	K2	499	
21	K3	499	
21	K4	499	
21	K5	499	
22	L1	255	
22	L2	255	
22	L3	255	

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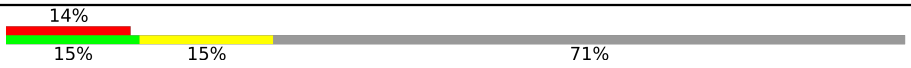
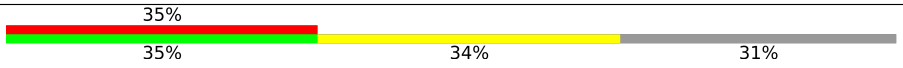
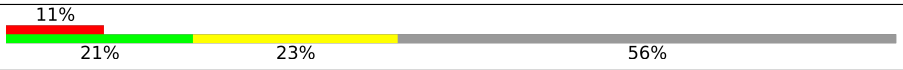
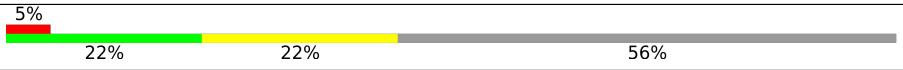
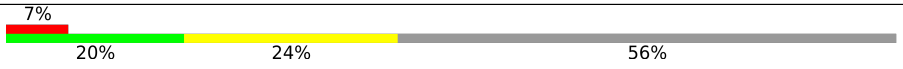
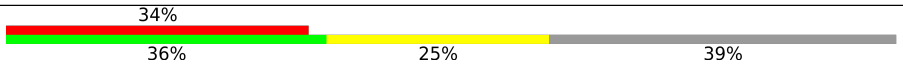
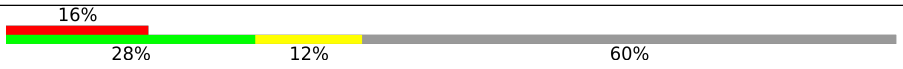
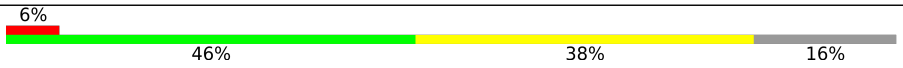
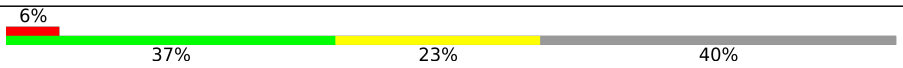
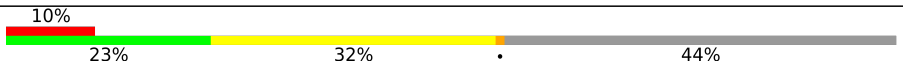
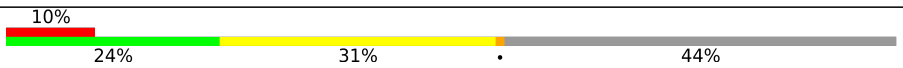
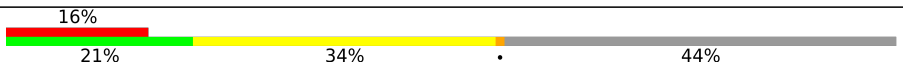
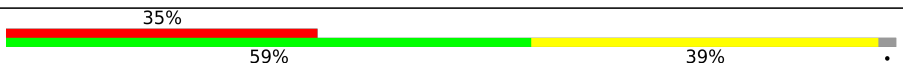
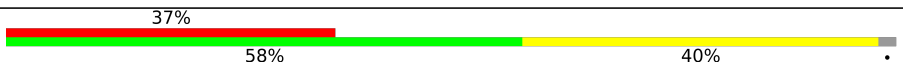
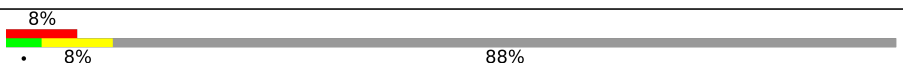
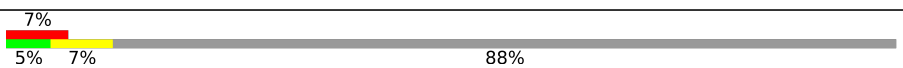
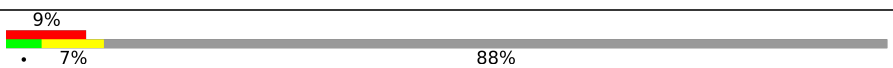
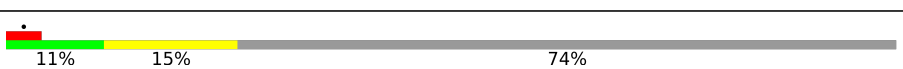
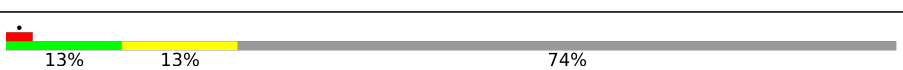
Mol	Chain	Length	Quality of chain
22	L4	255	
23	M	167	
24	M1	141	
24	M2	141	
24	M3	141	
25	N	122	
26	N1	168	
26	N2	168	
26	N3	168	
26	N4	168	
27	O	377	
27	P	377	
27	Q	377	
27	R	377	
28	O1	189	
28	O2	189	
28	O3	189	
29	P1	620	
29	P2	620	
29	P3	620	
30	Q1	1516	
30	Q2	1516	
30	Q3	1516	
31	R1	283	
31	R2	283	

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Mol	Chain	Length	Quality of chain
31	R3	283	7% 13% 12% 74%
32	S	470	6% 9% 7% 85%
32	T	470	9% 16% 7% 77%
33	U	551	52% 34% 32% 34%
33	V	551	11% 7% 5% 89%
33	W	551	32% 30% 29% 41%
33	X	551	15% 18% 14% 68%
34	XA	193	31% 45% 51%
34	XB	193	6% 47% 49%
34	XC	193	46% 50%
34	XD	193	10% 48% 48%
34	XE	193	7% 40% 56%
34	XF	193	12% 45% 51%
34	XG	193	9% 40% 55%
35	XH	241	15% 34% 39% 26%
35	XI	241	10% 34% 40% 26%
35	XJ	241	51% 35% 39% 26%
35	XK	241	9% 30% 43% 26%
35	XL	241	8% 36% 38% 26%
35	XM	241	11% 36% 38% 26%
36	Y	547	27% 26% 14% 61%
36	Z	547	41% 26% 25% 48%
37	YA	168	100% 60% 39%
37	YB	168	99% 43% 55%
37	YC	168	98% 56% 43%

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Mol	Chain	Length	Quality of chain
37	YD	168	98% 49% 50%
37	YE	168	98% 49% 51%
37	YF	168	96% 48% 52%
37	YG	168	96% 58% 42%
37	YH	168	92% 49% 51%
37	YI	168	99% 50% 49%
37	YJ	168	100% 61% 38%
37	YK	168	99% 49% 50%
37	YL	168	99% 48% 52%
37	YM	168	98% 45% 54%
37	YN	168	81% 48% 51%
37	YO	168	100% 56% 43%
37	YP	168	97% 44% 55%
37	YQ	168	96% 49% 51%
37	YR	168	100% 49% 51%
37	YS	168	100% 59% 40%
37	YT	168	99% 58% 41%
37	YU	168	100% 55% 45%
37	YV	168	100% 50% 49%
37	YW	168	100% 51% 49%
38	a	101	42% 49% 10%

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
39	GTP	AF	501	-	-	X	-
39	GTP	BF	501	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
39	GTP	BH	501	-	-	X	-
39	GTP	BK	501	-	-	X	-
39	GTP	BL	501	-	-	X	-
39	GTP	BM	501	-	-	X	-
39	GTP	CF	501	-	-	X	-
39	GTP	DC	501	-	-	X	-
39	GTP	EB	501	-	-	X	-
39	GTP	EE	501	-	-	X	-
39	GTP	EI	501	-	-	X	-
39	GTP	FK	501	-	-	X	-
39	GTP	GB	501	-	-	X	-
39	GTP	GC	501	-	-	X	-
39	GTP	GH	501	-	-	X	-
39	GTP	HH	501	-	-	X	-
39	GTP	IG	501	-	-	X	-
39	GTP	IJ	501	-	-	X	-
39	GTP	JH	501	-	-	X	-
39	GTP	JI	501	-	-	X	-
39	GTP	KD	501	-	-	X	-
39	GTP	KL	501	-	-	X	-
39	GTP	MC	501	-	-	X	-
39	GTP	MF	501	-	-	X	-
39	GTP	MJ	501	-	-	X	-
39	GTP	ML	501	-	-	X	-
39	GTP	NH	501	-	-	X	-
39	GTP	NI	501	-	-	X	-
39	GTP	PB	501	-	-	X	-
39	GTP	QB	501	-	-	X	-
39	GTP	RD	501	-	-	X	-
39	GTP	RH	501	-	-	X	-
39	GTP	SH	501	-	-	X	-
39	GTP	TJ	501	-	-	X	-
39	GTP	UF	501	-	-	X	-
39	GTP	UK	501	-	-	X	-
39	GTP	VF	501	-	-	X	-
39	GTP	VH	501	-	-	X	-
39	GTP	WD	501	-	-	X	-
39	GTP	WL	501	-	-	X	-

2 Entry composition (i)

There are 39 unique types of molecules in this entry. The entry contains 1283344 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 Meiosis-specific nuclear structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	315	Total	C	N	O	S	0	0
			2736	1673	516	534	13		
1	B	196	Total	C	N	O	S	0	0
			1673	1036	310	319	8		

- Molecule 2 is a protein called Tektin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A1	315	Total	C	N	O	S	0	0
			2578	1598	464	507	9		
2	A2	396	Total	C	N	O	S	0	0
			3251	2013	588	640	10		
2	A3	396	Total	C	N	O	S	0	0
			3251	2013	588	640	10		
2	A4	188	Total	C	N	O	S	0	0
			1563	971	277	314	1		

- Molecule 3 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	AD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	AF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	AH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	AJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	AL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	BB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	BD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	BF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	BH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	BJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	BL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	CB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	CD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	CF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	CH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	CJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	CL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	DB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	DD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	DF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	DH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	DJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	DL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	EB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	ED	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	EF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	EH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	EJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	EL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	FB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	FD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	FF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	FH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	FJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	FL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	GB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	GD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	GF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	GH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	GJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	GL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	HB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	HD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	HF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	HH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	HJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	HL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	IB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	ID	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	IF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	IH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	IJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	IL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	JB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	JD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	JF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	JH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	JJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	JL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	KB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	KD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	KF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	KH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	KJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	KL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	LB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	LD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	LF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	LH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	LJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	LL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	MB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	MD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	MF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	MH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	MJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	ML	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	NB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	ND	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	NF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	NH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	NJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	NL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	OB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	OD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	OF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	OH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	OJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	OL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	PB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	PD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	PF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	PH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	PJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	PL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	QB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	QD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	QF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	QH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	QJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	QL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	RB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	RD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	RF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	RH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	RJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	RL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	SB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	SD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	SF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	SH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	SJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	SL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	TN	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	UB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	UD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	UF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	UH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	UJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	UL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	VB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	VD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	VF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	VH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	VJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	VL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	WB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	WD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	WF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	WH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	WJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
3	WL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

- Molecule 4 is a protein called Detyrosinated tubulin alpha-3 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	AE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	AG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	AI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	AK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	AM	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	BC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	BE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	BG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	BI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	BK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	BM	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	CC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	CE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	CG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	CI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	CK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	CM	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	DA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	DC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	DE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	DG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	DI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	DK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	EA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	EC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	EE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	EG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	EI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	EK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	FA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	FC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	FE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	FG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	FI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	FK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	GA	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	GC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	GE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	GG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	GI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	GK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	HA	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	HC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	HE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	HG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	HI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	HK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	IA	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	IC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	IE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	IG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	II	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	IK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	IM	438	Total 3418	C 2166	N 581	O 649	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	JA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	JC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	JE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	JG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	JI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	JK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	KA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	KC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	KE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	KG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	KI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	KK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	LA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	LC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	LE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	LG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	LI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	LK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	MC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	ME	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	MG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	MI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	MK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	MM	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	NA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	NC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	NE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	NG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	NI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	NK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	OA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	OC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	OE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	OG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	OI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	OK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	PA	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	PC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	PE	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	PG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	PI	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
4	PK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	PM	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	QC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	QE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	QG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	QI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	QK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	QM	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	RC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	RE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	RG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	RI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	RK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	RM	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	SC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	SE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	SG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	SI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	SK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	SM	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	TC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	TE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	TG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	TI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	TK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	TM	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	UA	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	UC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	UE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	UG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	UI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	UK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	VA	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	VC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	VE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	VG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	VI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	VK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	WA	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	WC	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	WE	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	WG	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
4	WI	438	Total 3418	C 2166	N 581	O 649	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	WK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

- Molecule 5 is a protein called Tektin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B1	238	Total	C	N	O	S	0	0
			1941	1202	352	378	9		
5	B2	416	Total	C	N	O	S	0	0
			3417	2102	632	669	14		
5	B3	416	Total	C	N	O	S	0	0
			3417	2102	632	669	14		
5	B4	312	Total	C	N	O	S	0	0
			2553	1566	473	504	10		
5	B5	48	Total	C	N	O		0	0
			406	246	82	78			
5	B6	363	Total	C	N	O	S	0	0
			2977	1834	548	584	11		
5	B7	405	Total	C	N	O	S	0	0
			3324	2047	613	650	14		
5	B8	398	Total	C	N	O	S	0	0
			3271	2011	605	641	14		
5	B9	115	Total	C	N	O	S	0	0
			952	587	175	184	6		

- Molecule 6 is a protein called Nucleoside diphosphate kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	372	Total	C	N	O	S	0	0
			2945	1866	511	548	20		
6	D	372	Total	C	N	O	S	0	0
			2945	1866	511	548	20		

- Molecule 7 is a protein called Tektin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C1	98	Total	C	N	O	S	0	0
			803	485	157	160	1		
7	C2	388	Total	C	N	O	S	0	0
			3169	1942	586	627	14		
7	C3	388	Total	C	N	O	S	0	0
			3169	1942	586	627	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	C4	361	Total	C	N	O	S	0	0
			2934	1801	540	579	14		
7	C5	63	Total	C	N	O	S	0	0
			523	322	99	100	2		
7	C6	200	Total	C	N	O	S	0	0
			1633	990	311	328	4		
7	C7	394	Total	C	N	O	S	0	0
			3216	1972	595	635	14		
7	C8	394	Total	C	N	O	S	0	0
			3216	1972	595	635	14		
7	C9	298	Total	C	N	O	S	0	0
			2426	1496	440	477	13		
7	Ca	219	Total	C	N	O	S	0	0
			1797	1111	327	347	12		
7	Cb	388	Total	C	N	O	S	0	0
			3169	1942	586	627	14		
7	Cc	388	Total	C	N	O	S	0	0
			3169	1942	586	627	14		
7	Cd	264	Total	C	N	O	S	0	0
			2154	1314	402	430	8		

- Molecule 8 is a protein called Tektin-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D1	56	Total	C	N	O	S	0	0
			467	290	87	89	1		
8	D2	365	Total	C	N	O	S	0	0
			2997	1834	552	596	15		
8	D3	425	Total	C	N	O	S	0	0
			3488	2138	648	685	17		
8	D4	425	Total	C	N	O	S	0	0
			3488	2138	648	685	17		
8	D5	130	Total	C	N	O	S	0	0
			1063	652	199	206	6		
8	D6	75	Total	C	N	O	S	0	0
			612	376	116	118	2		
8	D7	369	Total	C	N	O	S	0	0
			3031	1852	566	597	16		
8	D8	398	Total	C	N	O	S	0	0
			3291	2017	613	645	16		
8	D9	394	Total	C	N	O	S	0	0
			3260	1998	608	638	16		

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Mol	Chain	Residues	Atoms	AltConf	Trace
8	Da	58	Total C N O 490 300 96 94	0	0

- Molecule 9 is a protein called EF-hand domain-containing family member B.

Mol	Chain	Residues	Atoms	AltConf	Trace
9	E	265	Total C N O S 2160 1360 390 405 5	0	0
9	F	149	Total C N O S 1182 762 209 206 5	0	0

- Molecule 10 is a protein called Tektin bundle-interacting protein 1.

Mol	Chain	Residues	Atoms	AltConf	Trace
10	E1	187	Total C N O S 1558 992 295 265 6	0	0
10	E2	187	Total C N O S 1558 992 295 265 6	0	0
10	E3	187	Total C N O S 1558 992 295 265 6	0	0
10	E4	57	Total C N O S 472 306 87 78 1	0	0

- Molecule 11 is a protein called Tektin-5.

Mol	Chain	Residues	Atoms	AltConf	Trace
11	F1	284	Total C N O S 2335 1443 428 444 20	0	0
11	F2	393	Total C N O S 3224 1994 590 616 24	0	0
11	F3	393	Total C N O S 3224 1994 590 616 24	0	0
11	F4	212	Total C N O S 1745 1064 326 343 12	0	0
11	F5	256	Total C N O S 2116 1296 396 411 13	0	0
11	F6	389	Total C N O S 3194 1973 586 612 23	0	0
11	F7	389	Total C N O S 3194 1973 586 612 23	0	0
11	F8	229	Total C N O S 1877 1170 340 350 17	0	0

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Mol	Chain	Residues	Atoms	AltConf	Trace
11	F9	173	Total C N O S 1412 885 254 262 11	0	0
11	Fa	389	Total C N O S 3194 1973 586 612 23	0	0
11	Fb	389	Total C N O S 3194 1973 586 612 23	0	0
11	Fc	315	Total C N O S 2585 1591 476 500 18	0	0
11	Fd	23	Total C N O 199 119 42 38	0	0
11	Fe	237	Total C N O S 1946 1201 354 375 16	0	0
11	Ff	393	Total C N O S 3224 1994 590 616 24	0	0
11	Fg	311	Total C N O S 2561 1587 465 488 21	0	0
11	Fh	183	Total C N O S 1495 941 266 275 13	0	0
11	Fi	272	Total C N O S 2235 1383 406 429 17	0	0
11	Fj	277	Total C N O S 2272 1406 409 441 16	0	0
11	Fk	332	Total C N O S 2721 1685 493 523 20	0	0
11	Fl	332	Total C N O S 2721 1685 493 523 20	0	0
11	Fm	327	Total C N O S 2677 1656 484 517 20	0	0

- Molecule 12 is a protein called Cilia- and flagella-associated protein 53.

Mol	Chain	Residues	Atoms	AltConf	Trace
12	G	448	Total C N O S 3804 2315 737 736 16	0	0
12	H	47	Total C N O S 387 234 74 77 2	0	0

- Molecule 13 is a protein called EF-hand domain-containing protein 1.

Mol	Chain	Residues	Atoms	AltConf	Trace
13	G1	510	Total C N O S 4192 2708 704 763 17	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	G2	495	Total	C	N	O	S	0	0
			4081	2634	687	743	17		
13	G3	511	Total	C	N	O	S	0	0
			4200	2712	706	765	17		

- Molecule 14 is a protein called EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G4	748	Total	C	N	O	S	0	0
			6177	3989	1028	1131	29		
14	G5	747	Total	C	N	O	S	0	0
			6169	3983	1027	1130	29		
14	G6	747	Total	C	N	O	S	0	0
			6169	3983	1027	1130	29		

- Molecule 15 is a protein called Protein FAM166A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H1	139	Total	C	N	O	S	0	0
			1138	727	203	202	6		
15	H2	135	Total	C	N	O	S	0	0
			1107	708	196	198	5		
15	H3	139	Total	C	N	O	S	0	0
			1138	727	203	202	6		
15	H4	138	Total	C	N	O	S	0	0
			1127	721	199	201	6		
15	H5	139	Total	C	N	O	S	0	0
			1138	727	203	202	6		
15	H6	136	Total	C	N	O	S	0	0
			1118	714	200	199	5		

- Molecule 16 is a protein called Cilia- and flagella-associated protein 95.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	96	Total	C	N	O	S	0	0
			781	490	130	157	4		

- Molecule 17 is a protein called Protein FAM166C.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I1	38	Total	C	N	O	S	0	0
			298	192	47	58	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	I2	38	Total	C	N	O	S	0	0
			298	192	47	58	1		
17	I3	38	Total	C	N	O	S	0	0
			298	192	47	58	1		

- Molecule 18 is a protein called Cilia- and flagella-associated protein 107.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	158	Total	C	N	O	S	0	0
			1323	851	236	231	5		

- Molecule 19 is a protein called Dual specificity phosphatase 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J1	171	Total	C	N	O	S	0	0
			1378	886	230	253	9		
19	J2	171	Total	C	N	O	S	0	0
			1378	886	230	253	9		
19	J3	171	Total	C	N	O	S	0	0
			1378	886	230	253	9		

- Molecule 20 is a protein called Cilia- and flagella-associated protein 161.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	270	Total	C	N	O	S	0	0
			2154	1357	382	400	15		
20	L	270	Total	C	N	O	S	0	0
			2154	1357	382	400	15		

- Molecule 21 is a protein called Coiled-coil domain-containing protein 105.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K1	103	Total	C	N	O	S	0	0
			847	527	168	144	8		
21	K2	421	Total	C	N	O	S	0	0
			3408	2110	663	609	26		
21	K3	428	Total	C	N	O	S	0	0
			3465	2147	674	618	26		
21	K4	394	Total	C	N	O	S	0	0
			3181	1971	614	571	25		
21	K5	50	Total	C	N	O	S	0	0
			400	251	80	65	4		

- Molecule 22 is a protein called Enkurin.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L1	210	Total	C	N	O	S	0	0
			1728	1102	306	313	7		
22	L2	236	Total	C	N	O	S	0	0
			1929	1231	340	349	9		
22	L3	236	Total	C	N	O	S	0	0
			1929	1231	340	349	9		
22	L4	75	Total	C	N	O	S	0	0
			609	392	112	101	4		

- Molecule 23 is a protein called Piercer of microtubule wall 1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	115	Total	C	N	O	S	0	0
			944	595	170	175	4		

- Molecule 24 is a protein called Testis-expressed protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	M1	62	Total	C	N	O	S	0	0
			510	327	89	89	5		
24	M2	62	Total	C	N	O	S	0	0
			510	327	89	89	5		
24	M3	62	Total	C	N	O	S	0	0
			510	327	89	89	5		

- Molecule 25 is a protein called Piercer of microtubule wall 2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	N	74	Total	C	N	O	S	0	0
			583	379	94	104	6		

- Molecule 26 is a protein called Cilia- and flagella-associated protein 276.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	N1	68	Total	C	N	O	0	0
			535	335	95	105		
26	N2	68	Total	C	N	O	0	0
			535	335	95	105		
26	N3	68	Total	C	N	O	0	0
			535	335	95	105		

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Mol	Chain	Residues	Atoms				AltConf	Trace
26	N4	68	Total 535	C 335	N 95	O 105	0	0

- Molecule 27 is a protein called RIB43A-like with coiled-coils protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	O	49	Total 413	C 256	N 83	O 73	S 1	0	0
27	P	317	Total 2693	C 1649	N 537	O 494	S 13	0	0
27	Q	183	Total 1541	C 942	N 305	O 284	S 10	0	0
27	R	226	Total 1922	C 1173	N 381	O 361	S 7	0	0

- Molecule 28 is a protein called Protein Flattop.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	O1	105	Total 825	C 524	N 148	O 152	S 1	0	0
28	O2	105	Total 825	C 524	N 148	O 152	S 1	0	0
28	O3	105	Total 825	C 524	N 148	O 152	S 1	0	0

- Molecule 29 is a protein called Cilia- and flagella-associated protein 52.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P1	608	Total 4696	C 2970	N 819	O 875	S 32	0	0
29	P2	608	Total 4696	C 2970	N 819	O 875	S 32	0	0
29	P3	608	Total 4696	C 2970	N 819	O 875	S 32	0	0

- Molecule 30 is a protein called EF-hand calcium-binding domain-containing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Q1	178	Total 1473	C 941	N 254	O 268	S 10	0	0
30	Q2	178	Total 1473	C 941	N 254	O 268	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
30	Q3	178	Total	C	N	O	S	0	0
			1473	941	254	268	10		

- Molecule 31 is a protein called Cilia and flagella-associated protein 77.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	R1	74	Total	C	N	O	S	0	0
			604	371	119	111	3		
31	R2	74	Total	C	N	O	S	0	0
			604	371	119	111	3		
31	R3	74	Total	C	N	O	S	0	0
			604	371	119	111	3		

- Molecule 32 is a protein called Sperm-associated antigen 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S	71	Total	C	N	O	S	0	0
			575	361	105	108	1		
32	T	109	Total	C	N	O	S	0	0
			904	559	166	174	5		

- Molecule 33 is a protein called Cilia- and flagella-associated protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	U	363	Total	C	N	O	S	0	0
			3125	1885	623	603	14		
33	V	63	Total	C	N	O	S	0	0
			537	328	107	101	1		
33	W	323	Total	C	N	O	S	0	0
			2733	1660	521	538	14		
33	X	176	Total	C	N	O	S	0	0
			1506	913	307	284	2		

- Molecule 34 is a protein called Cilia- and flagella-associated protein 20.

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

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

- Molecule 35 is a protein called Parkin coregulated gene protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	XH	178	Total	C	N	O	S	0	0
			1469	953	247	261	8		
35	XI	178	Total	C	N	O	S	0	0
			1469	953	247	261	8		
35	XJ	178	Total	C	N	O	S	0	0
			1469	953	247	261	8		
35	XK	178	Total	C	N	O	S	0	0
			1469	953	247	261	8		
35	XL	178	Total	C	N	O	S	0	0
			1469	953	247	261	8		
35	XM	178	Total	C	N	O	S	0	0
			1469	953	247	261	8		

- Molecule 36 is a protein called Cilia- and flagella-associated protein 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	214	Total	C	N	O	S	0	0
			1821	1124	345	346	6		
36	Z	283	Total	C	N	O	S	0	0
			2401	1487	429	476	9		

- Molecule 37 is a protein called Sperm acrosome-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	YA	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YB	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YC	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		

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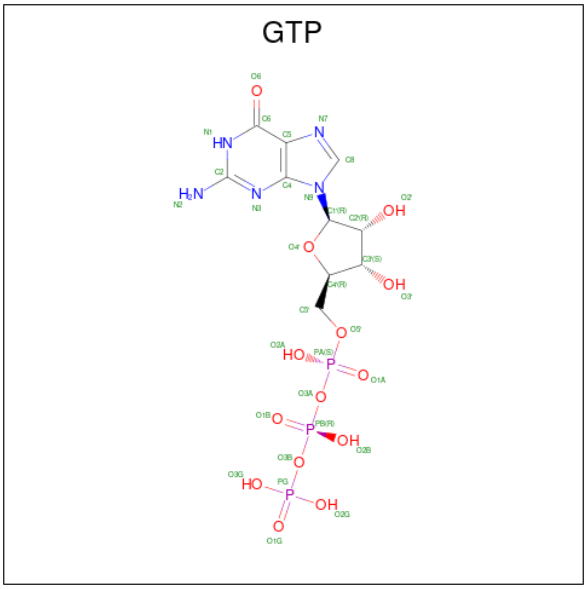
Mol	Chain	Residues	Atoms					AltConf	Trace
37	YD	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YE	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YF	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YG	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YH	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YI	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YJ	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YK	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YL	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YM	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YN	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YO	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YP	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YQ	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YR	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YS	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YT	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YU	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YV	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		
37	YW	168	Total	C	N	O	S	0	0
			1365	856	244	254	11		

- Molecule 38 is a protein called Cilia- and flagella-associated protein 141.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	a	91	Total	C	N	O	S	0	0
			782	492	146	140	4		

- Molecule 39 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
39	AB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	AL	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	AM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	BM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CI	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	CJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	CM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	DL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	ED	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EE	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	EF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	EL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	FL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GB	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	GC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	GL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	HK	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	HL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	ID	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	II	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	IM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JG	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	JH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	JL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	KL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LD	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	LE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	LL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	ML	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	MM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NA	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	NB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	ND	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	NL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	OK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	OL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	PM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QG	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	QH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	QL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	RM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SD	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	SE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	SM	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	TM	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
39	TN	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	UL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VH	1	Total	C	N	O	P	0
			32	10	5	14	3	

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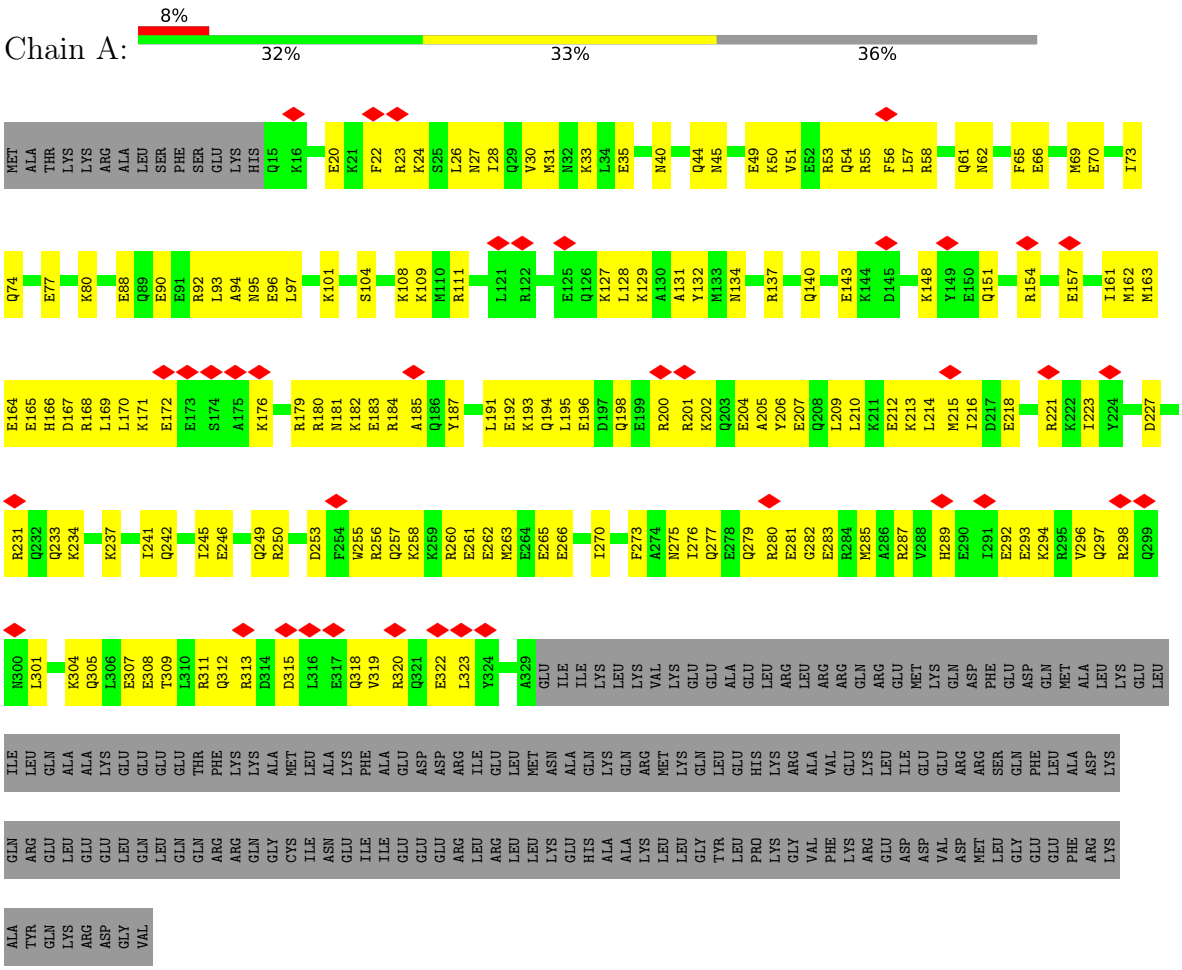
Mol	Chain	Residues	Atoms					AltConf
39	VI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	VL	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WA	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WB	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WC	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WD	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WE	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WF	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WG	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WH	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WI	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WK	1	Total	C	N	O	P	0
			32	10	5	14	3	
39	WL	1	Total	C	N	O	P	0
			32	10	5	14	3	

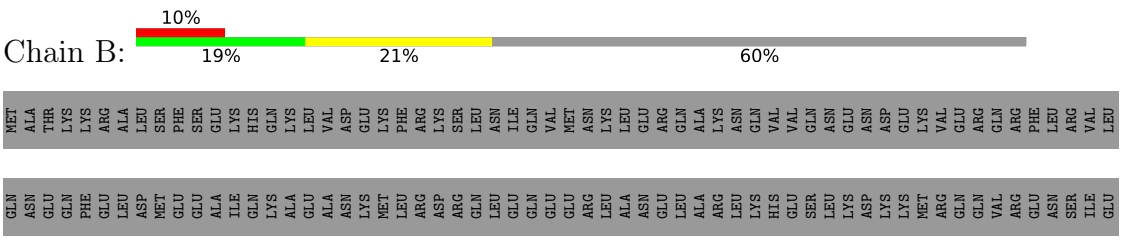
3 Residue-property plots

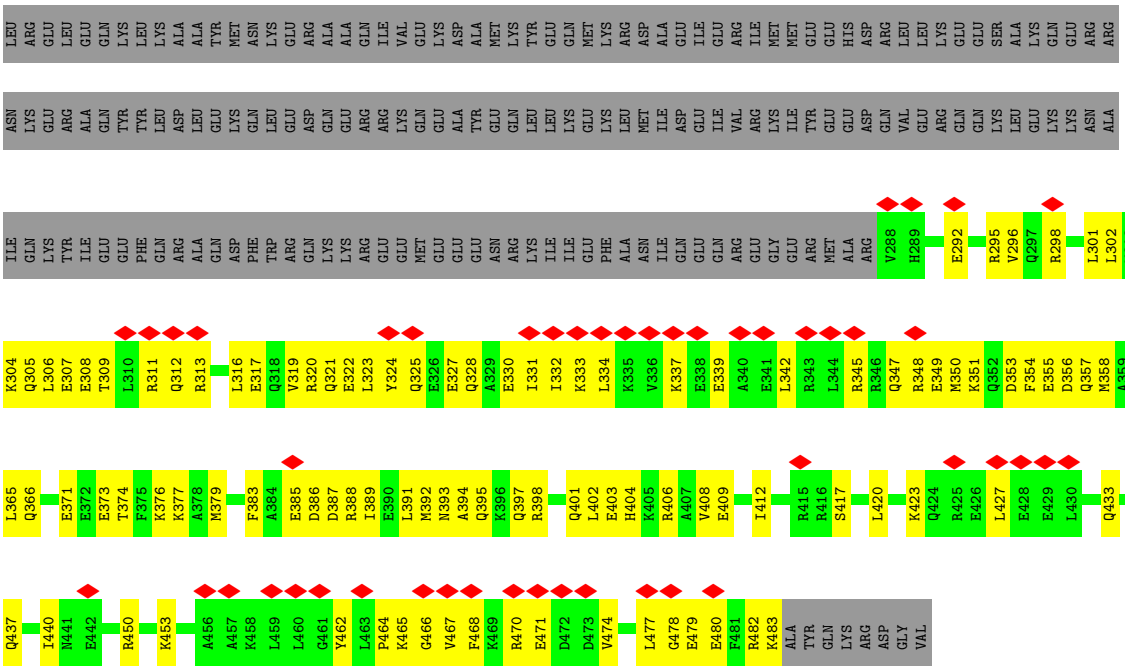
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Meiosis-specific nuclear structural protein 1



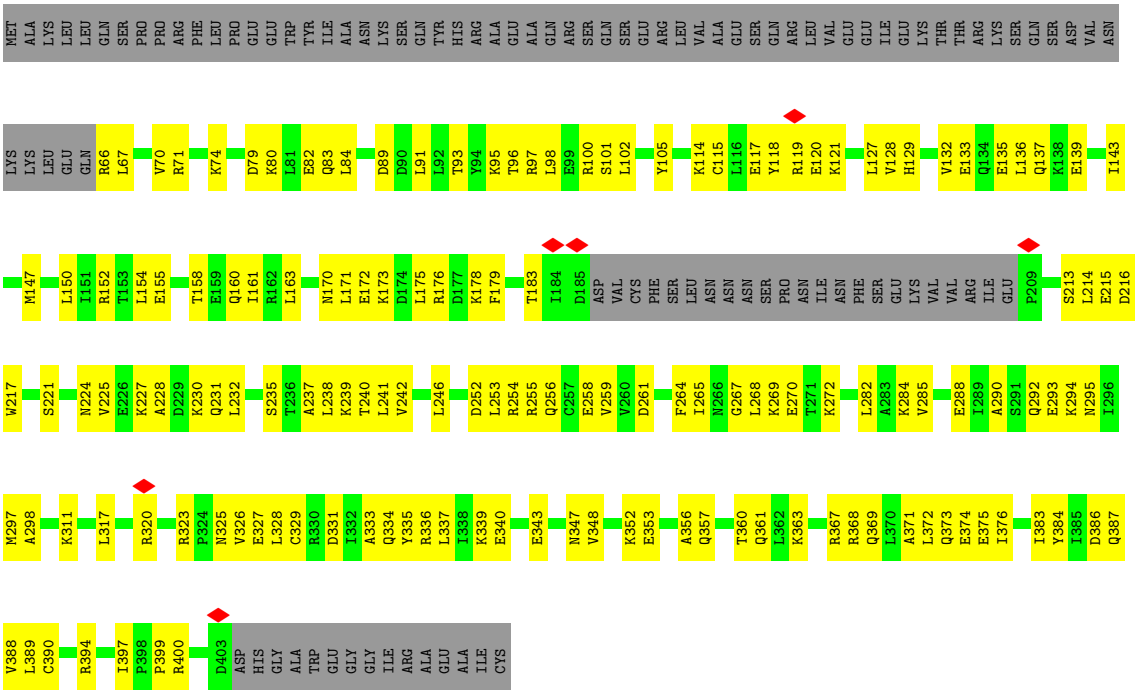
• Molecule 1: Meiosis-specific nuclear structural protein 1





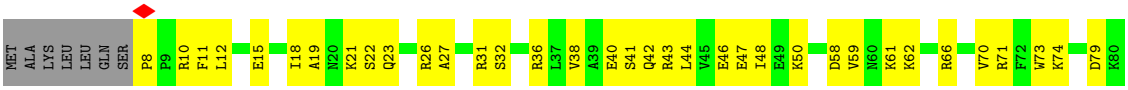
• Molecule 2: Tektin-1

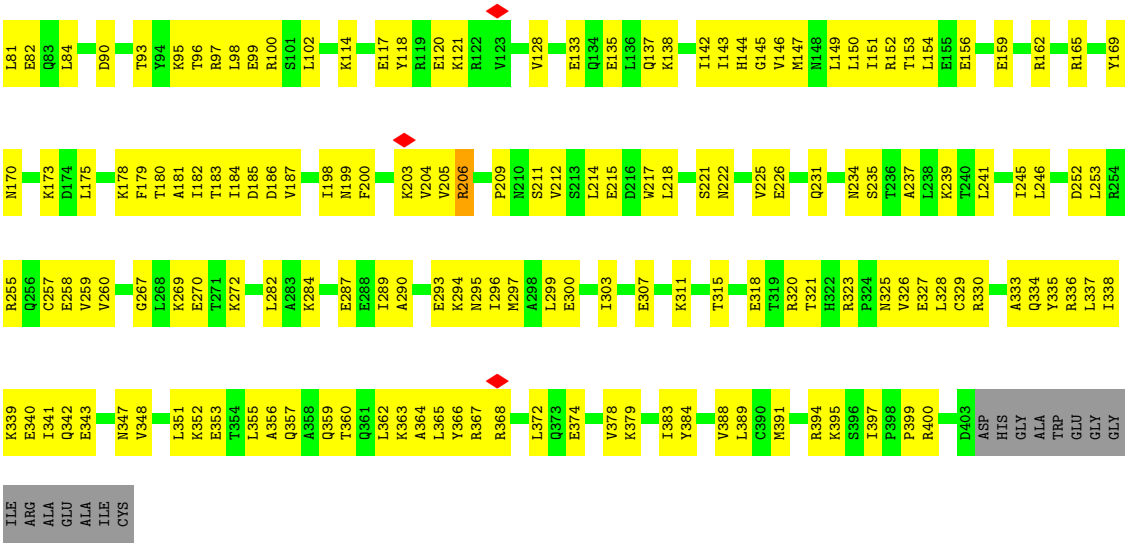
Chain A1:



• Molecule 2: Tektin-1

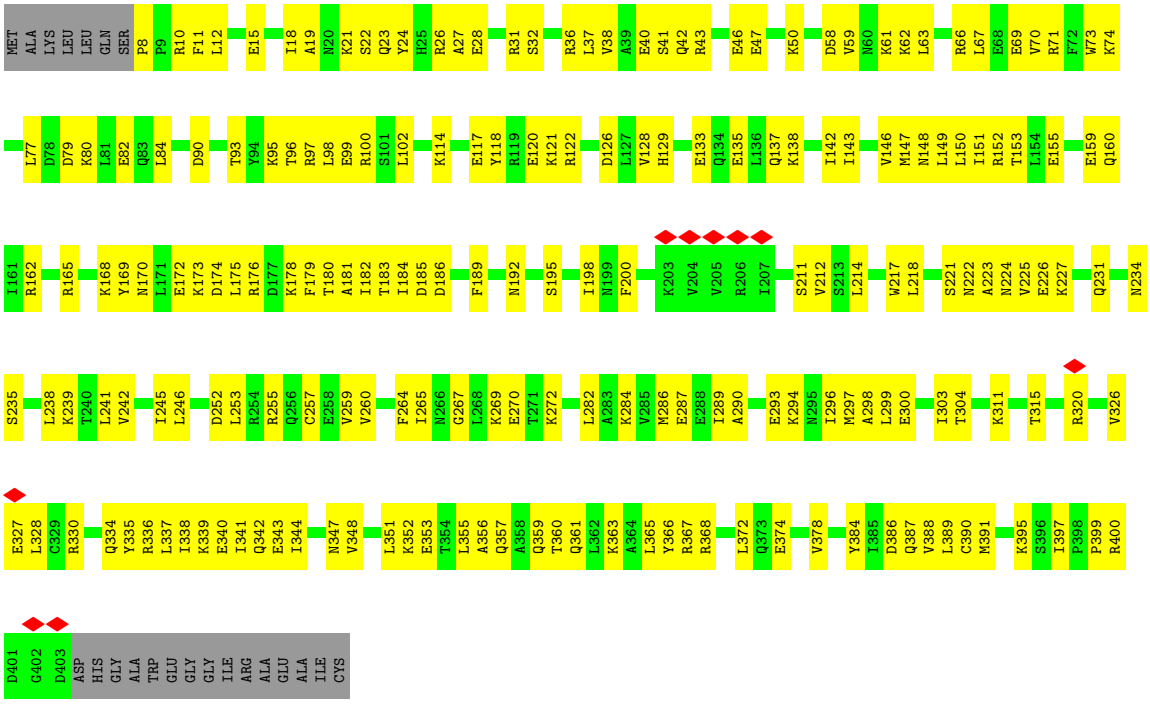
Chain A2:





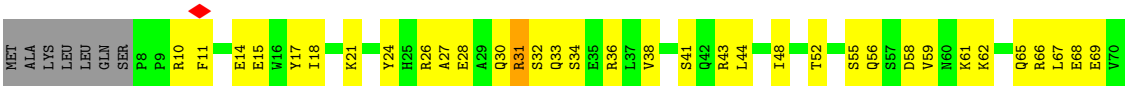
• Molecule 2: Tektin-1

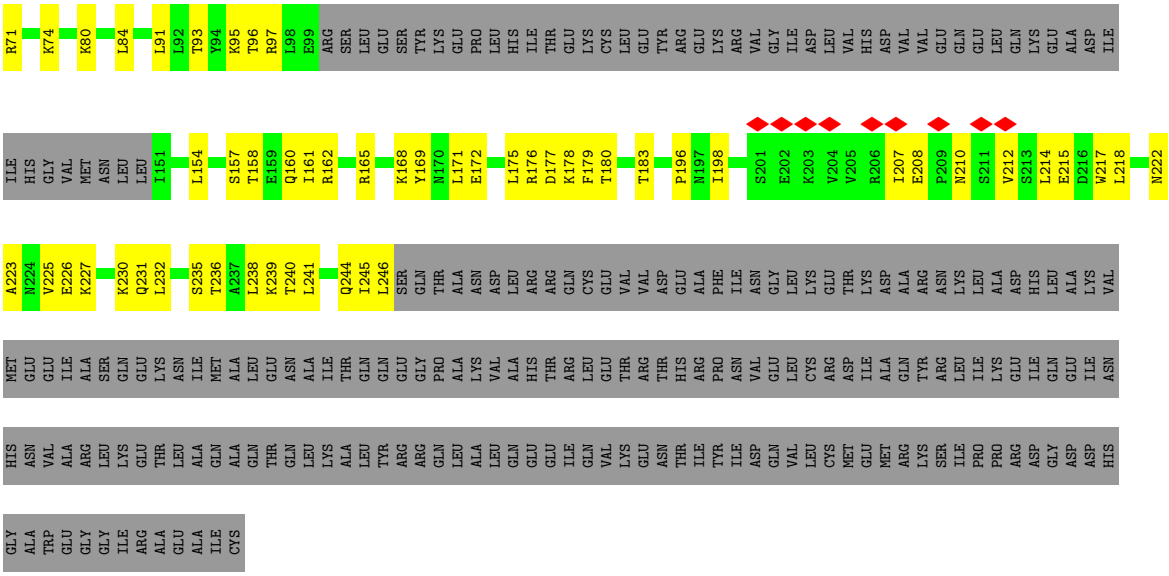
Chain A3:



• Molecule 2: Tektin-1

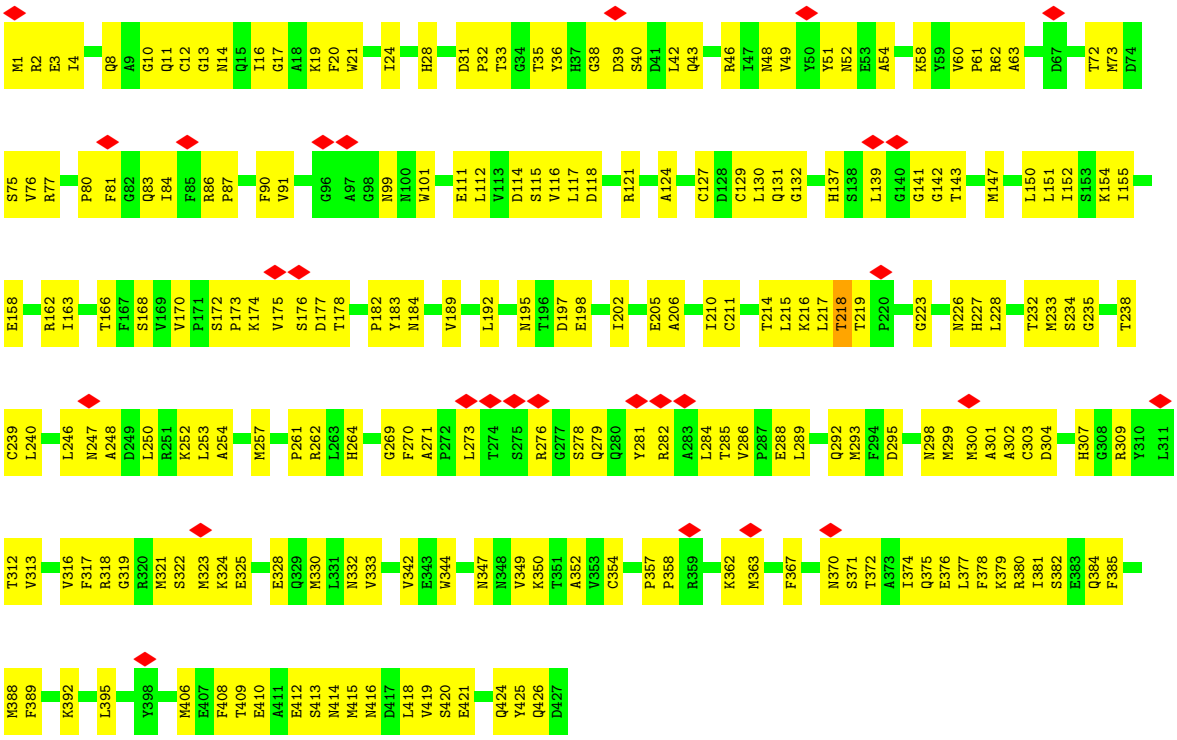
Chain A4:





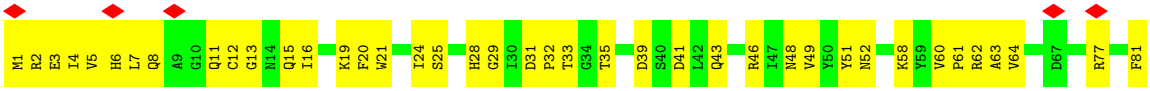
• Molecule 3: Tubulin beta-4B chain

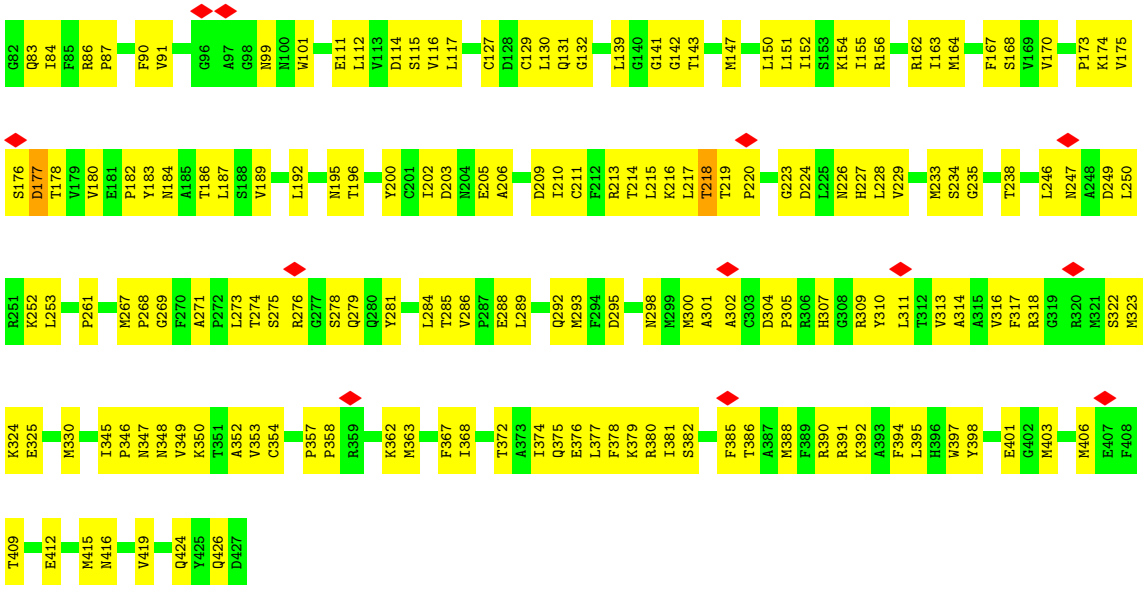
Chain AB:



• Molecule 3: Tubulin beta-4B chain

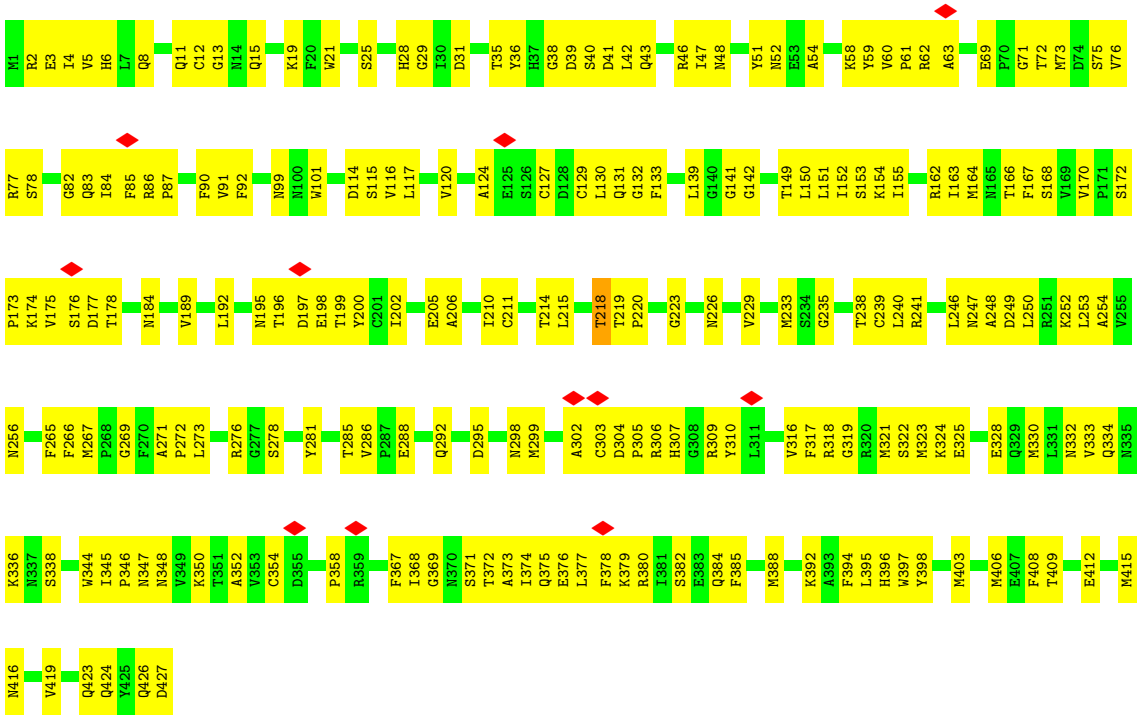
Chain AD:





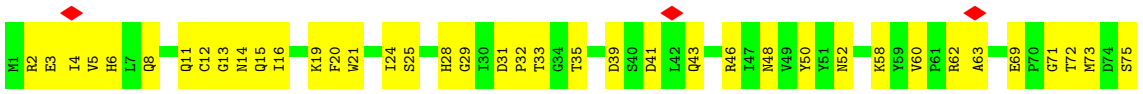
• Molecule 3: Tubulin beta-4B chain

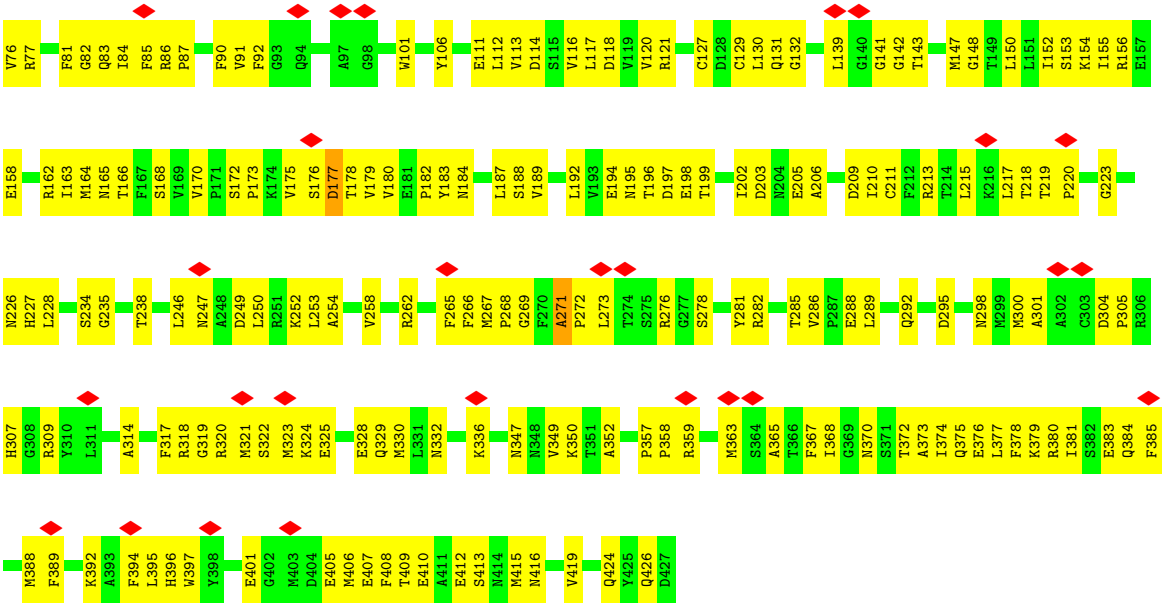
Chain AF:



• Molecule 3: Tubulin beta-4B chain

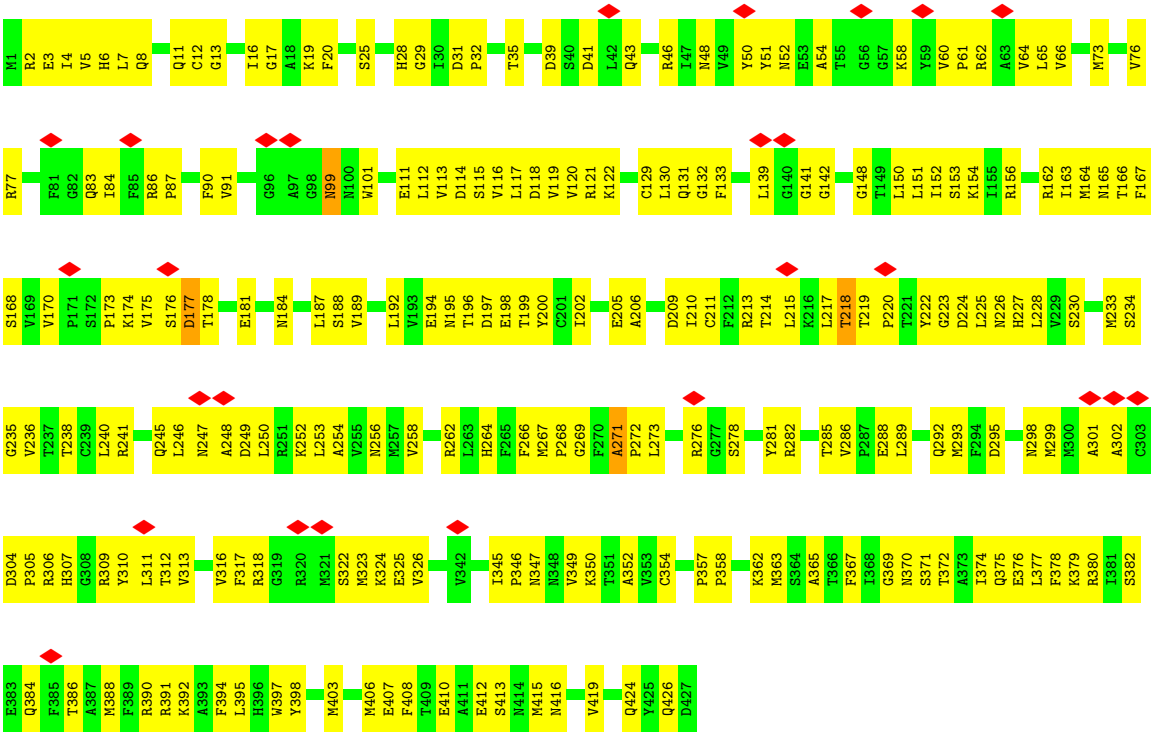
Chain AH:





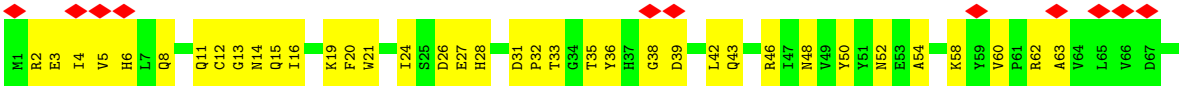
• Molecule 3: Tubulin beta-4B chain

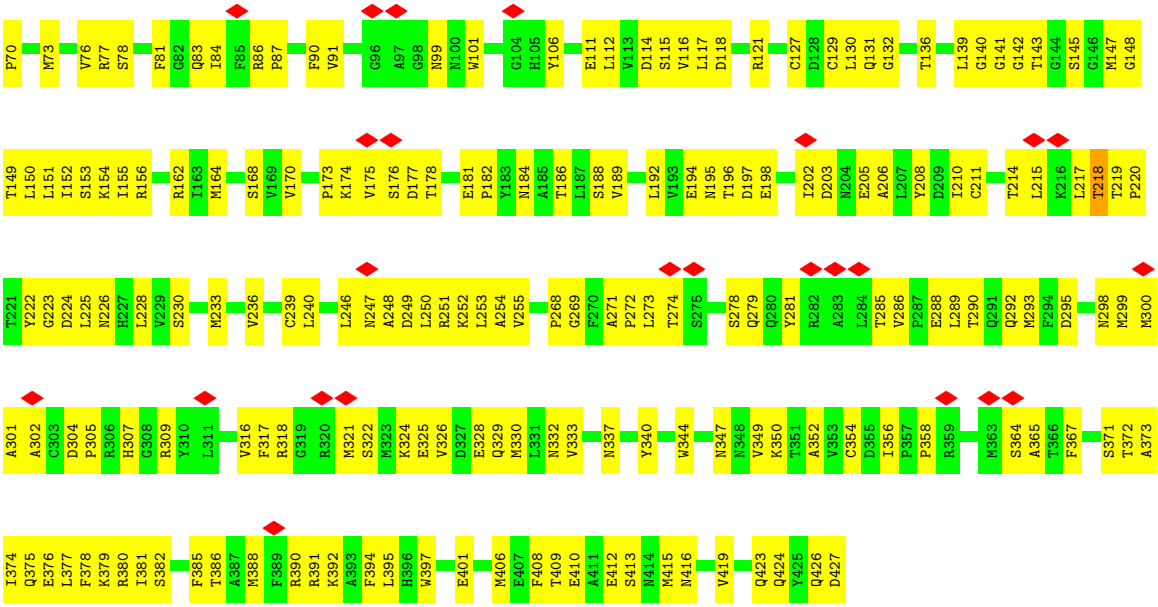
Chain AJ:



• Molecule 3: Tubulin beta-4B chain

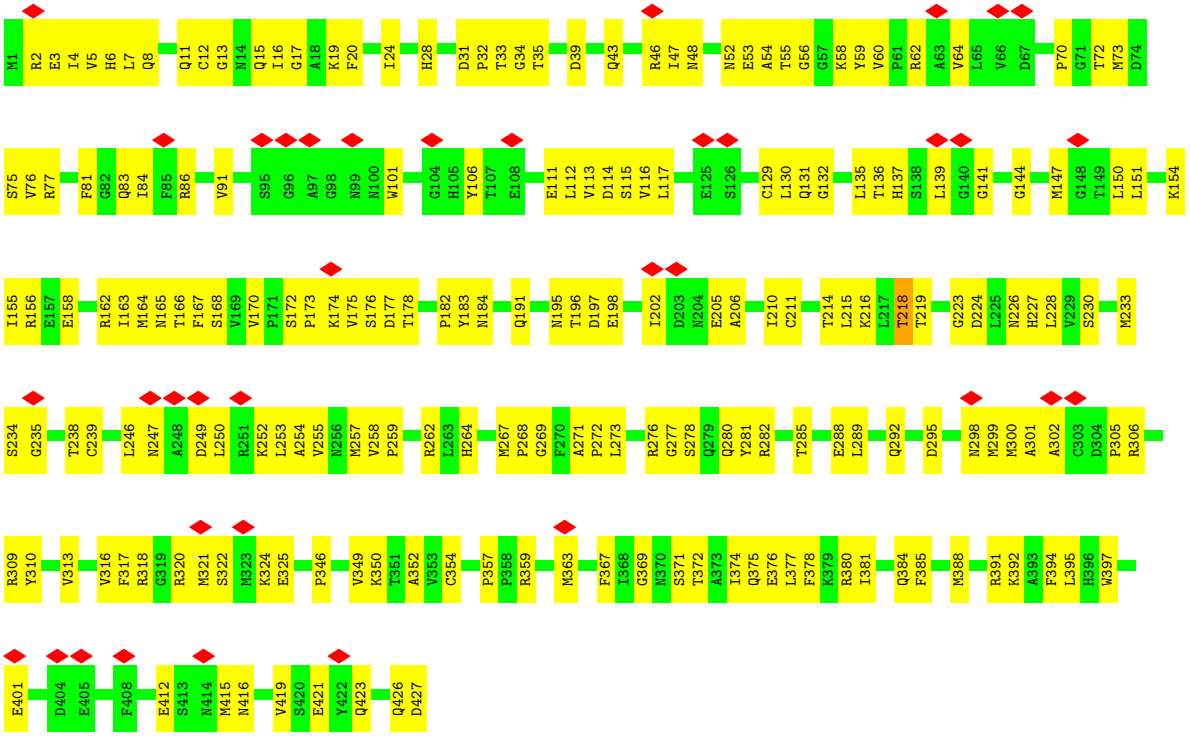
Chain AL:





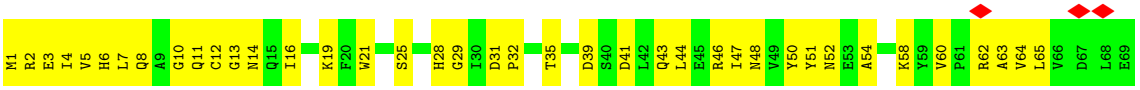
• Molecule 3: Tubulin beta-4B chain

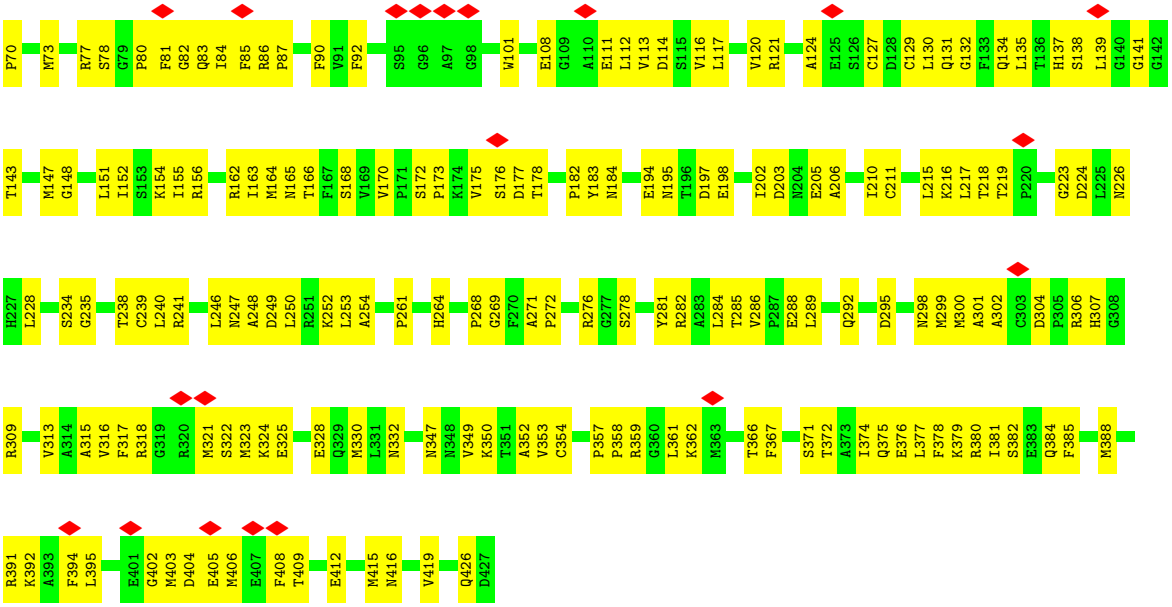
Chain BB:



• Molecule 3: Tubulin beta-4B chain

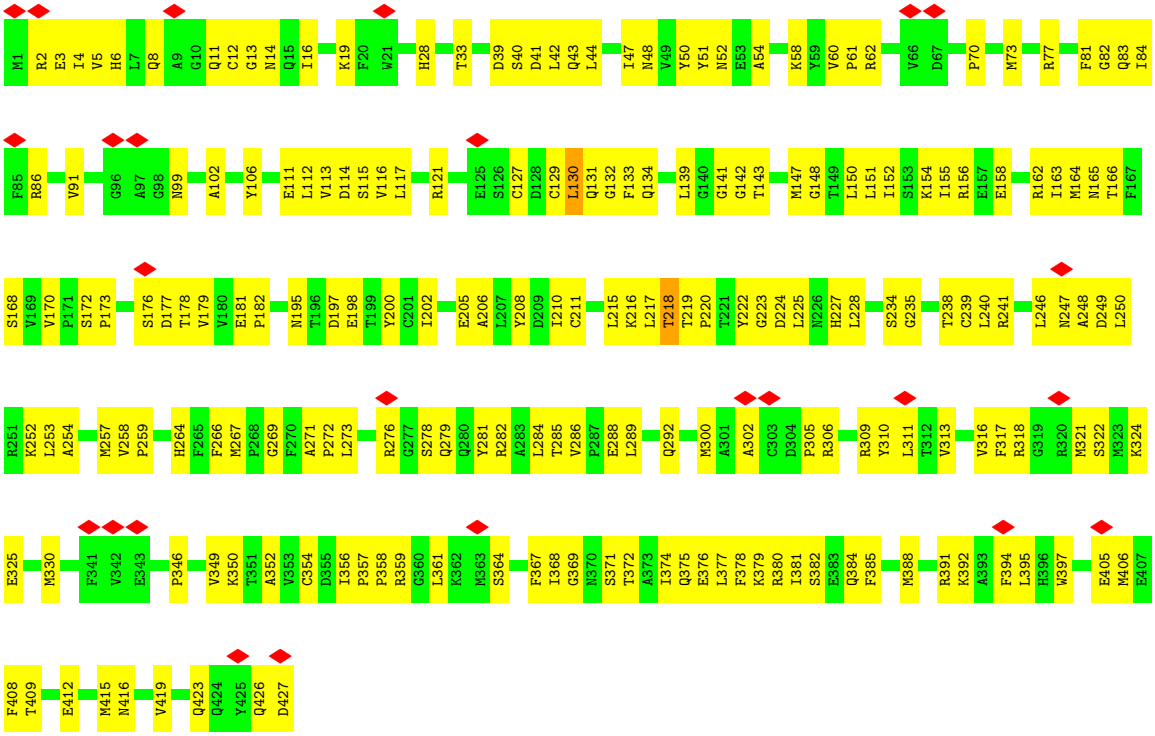
Chain BD:





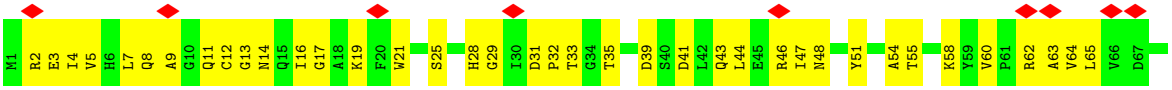
• Molecule 3: Tubulin beta-4B chain

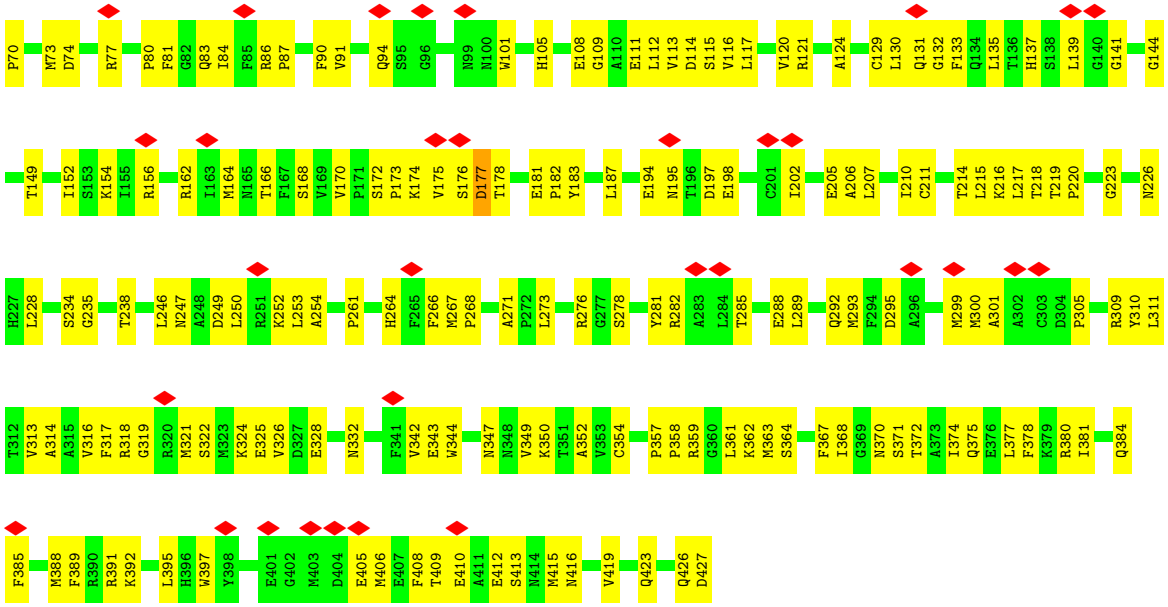
Chain BF:



• Molecule 3: Tubulin beta-4B chain

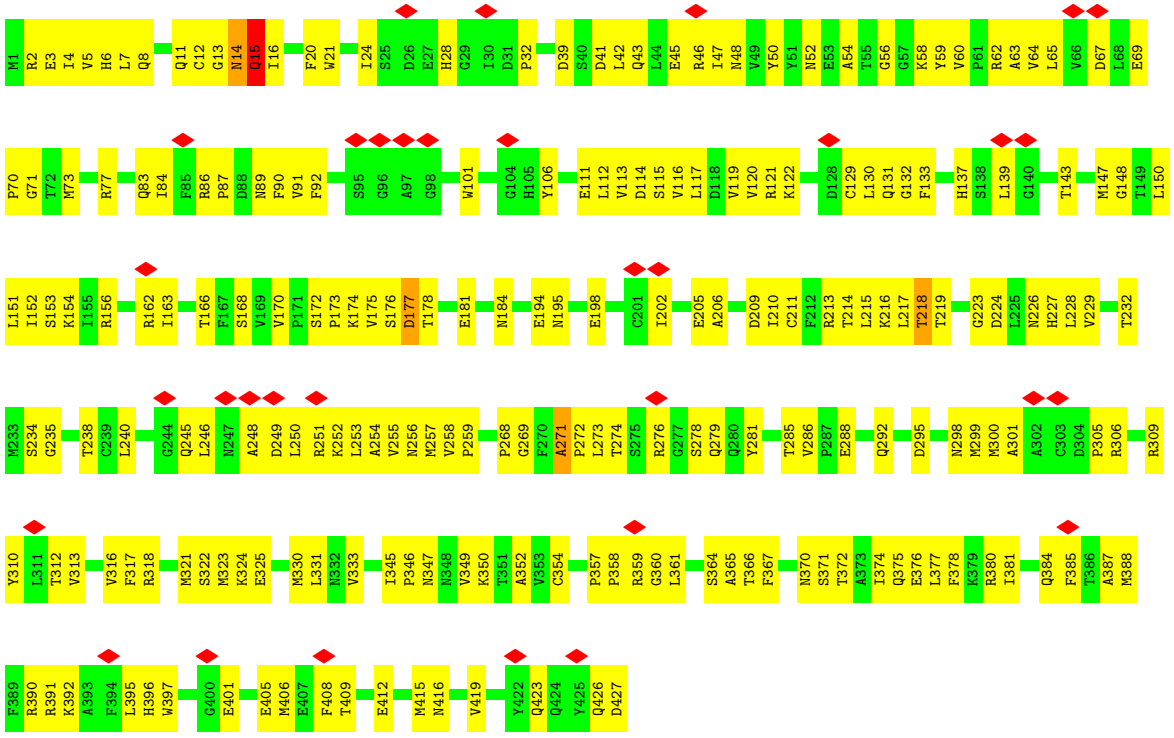
Chain BH:





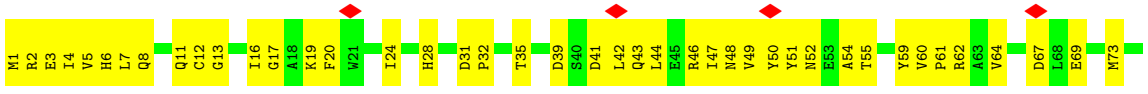
• Molecule 3: Tubulin beta-4B chain

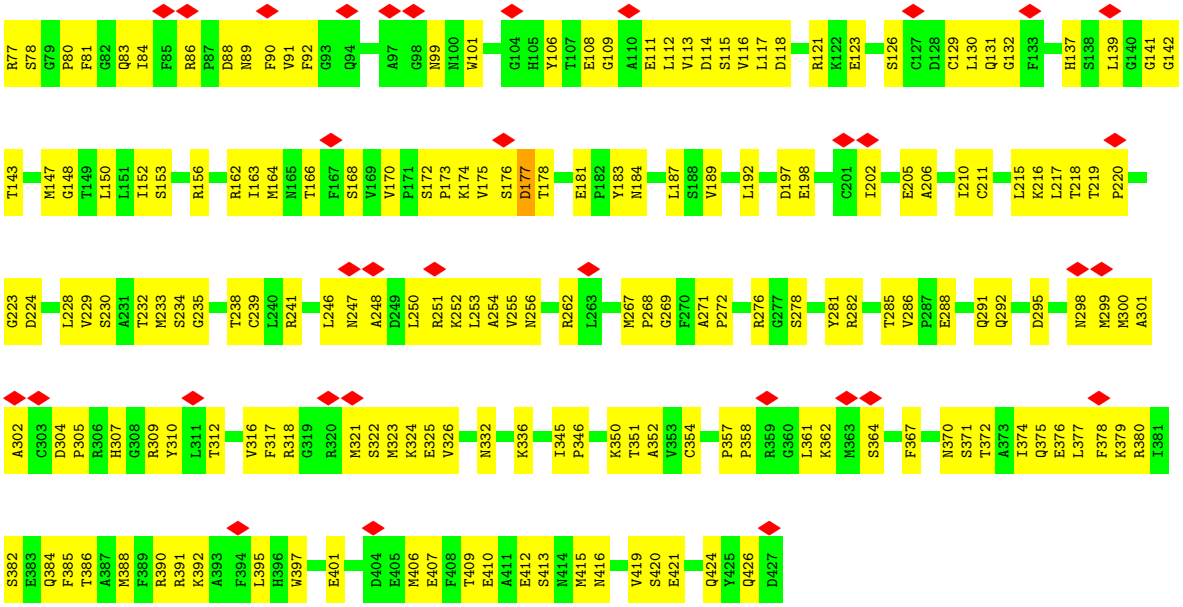
Chain BJ:



• Molecule 3: Tubulin beta-4B chain

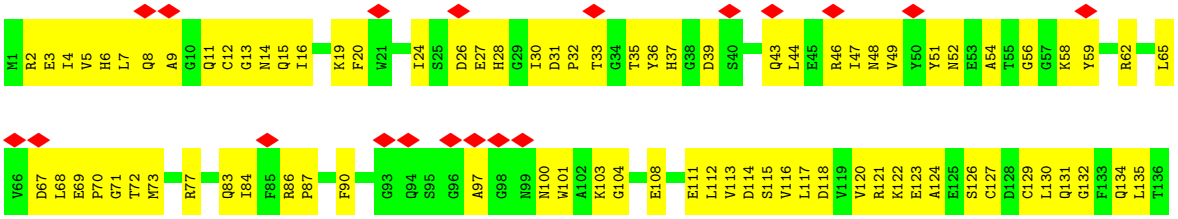
Chain BL:

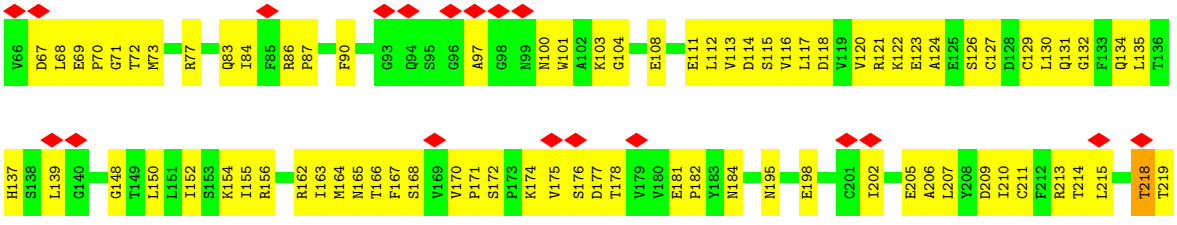


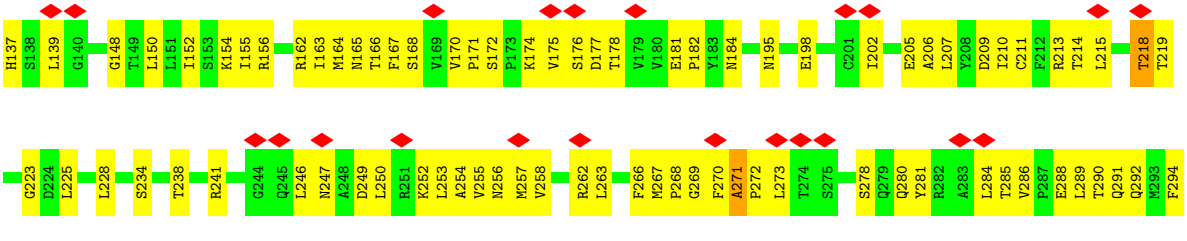


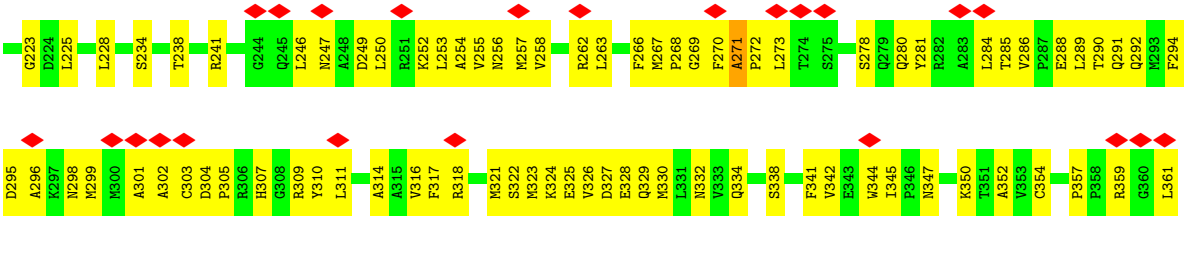
• Molecule 3: Tubulin beta-4B chain

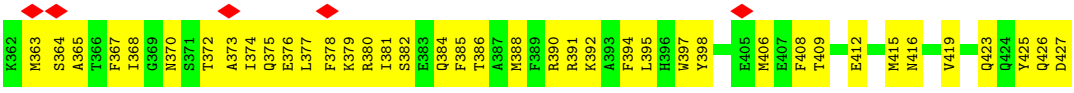
Chain CB:





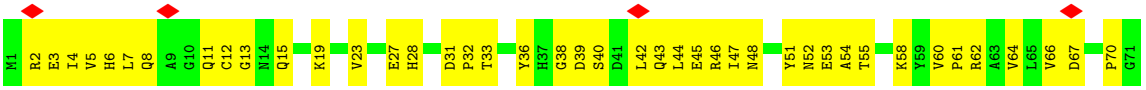


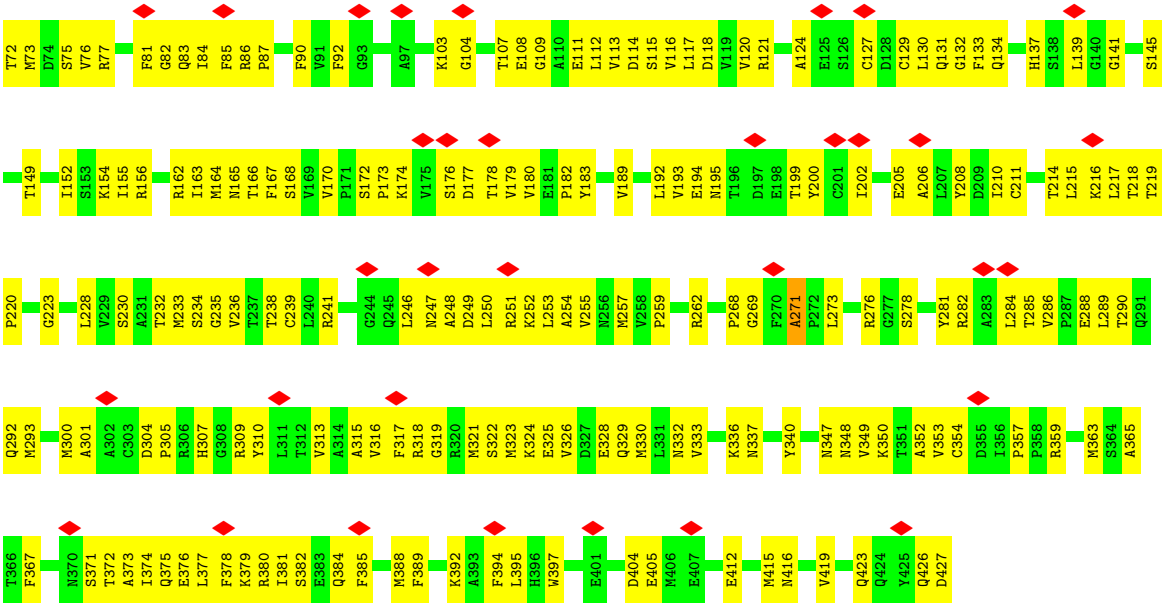




• Molecule 3: Tubulin beta-4B chain

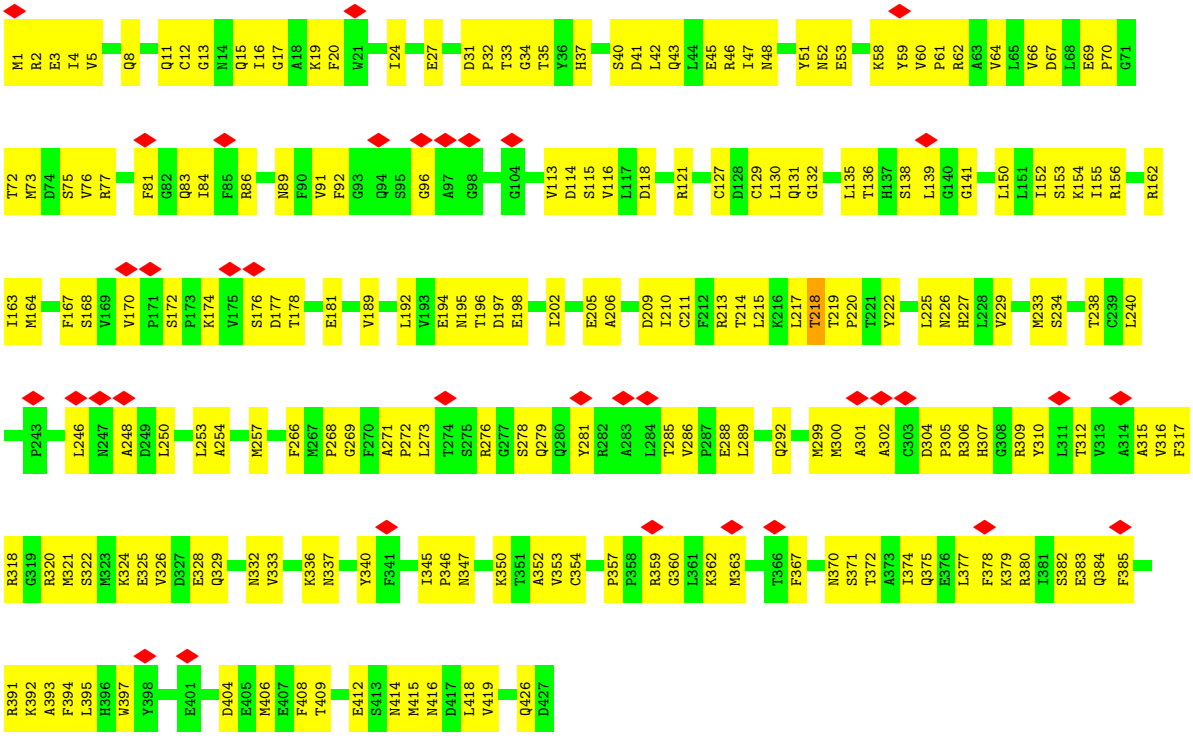
Chain CD:





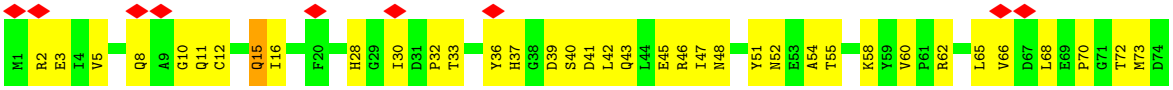
• Molecule 3: Tubulin beta-4B chain

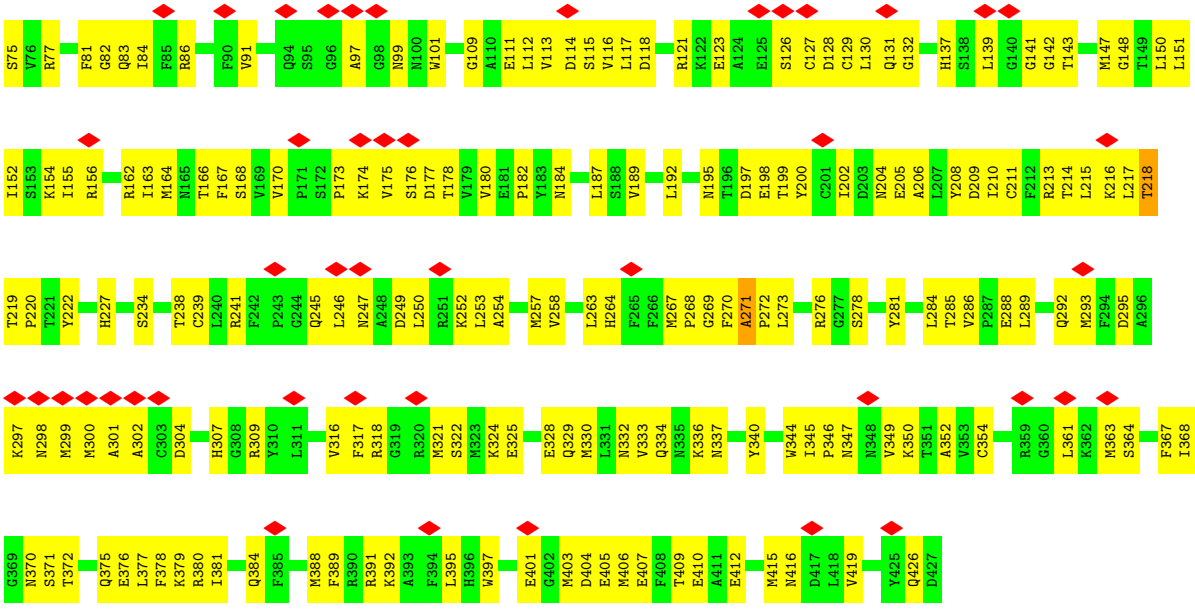
Chain CF:



• Molecule 3: Tubulin beta-4B chain

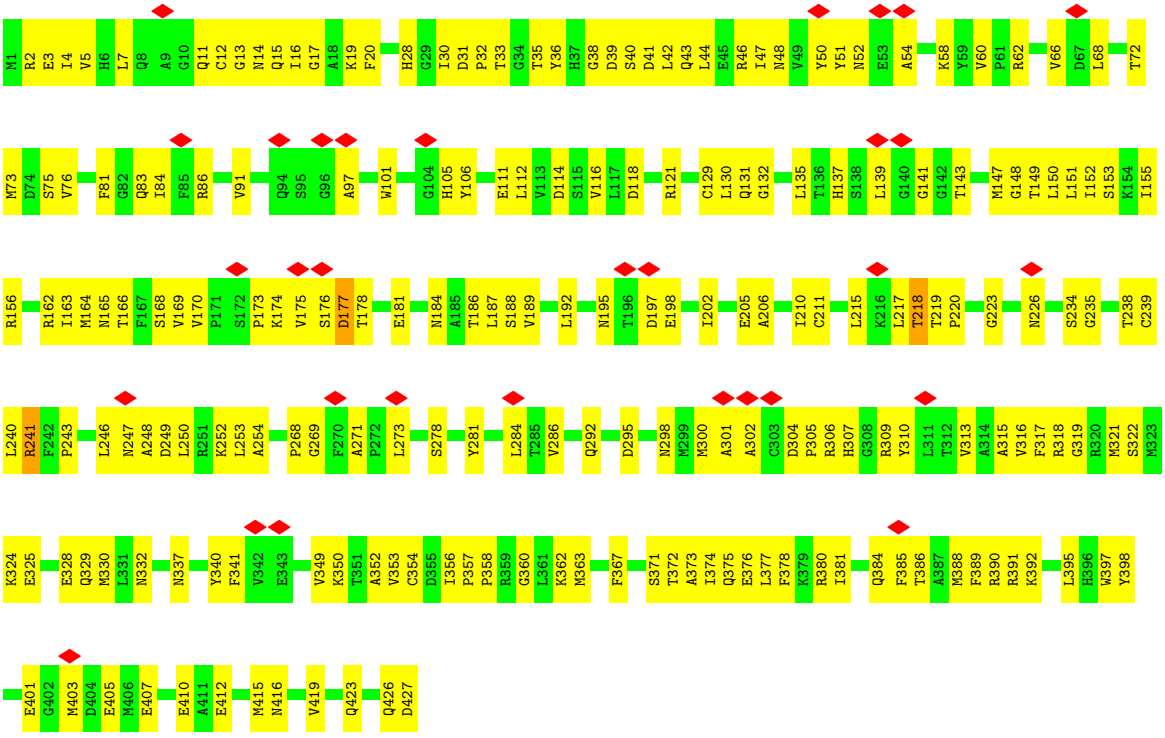
Chain CH:





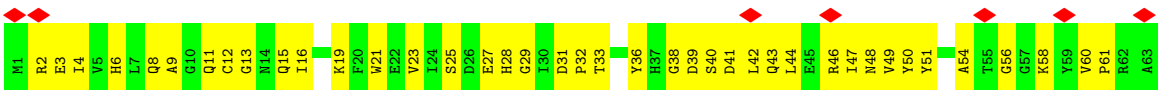
• Molecule 3: Tubulin beta-4B chain

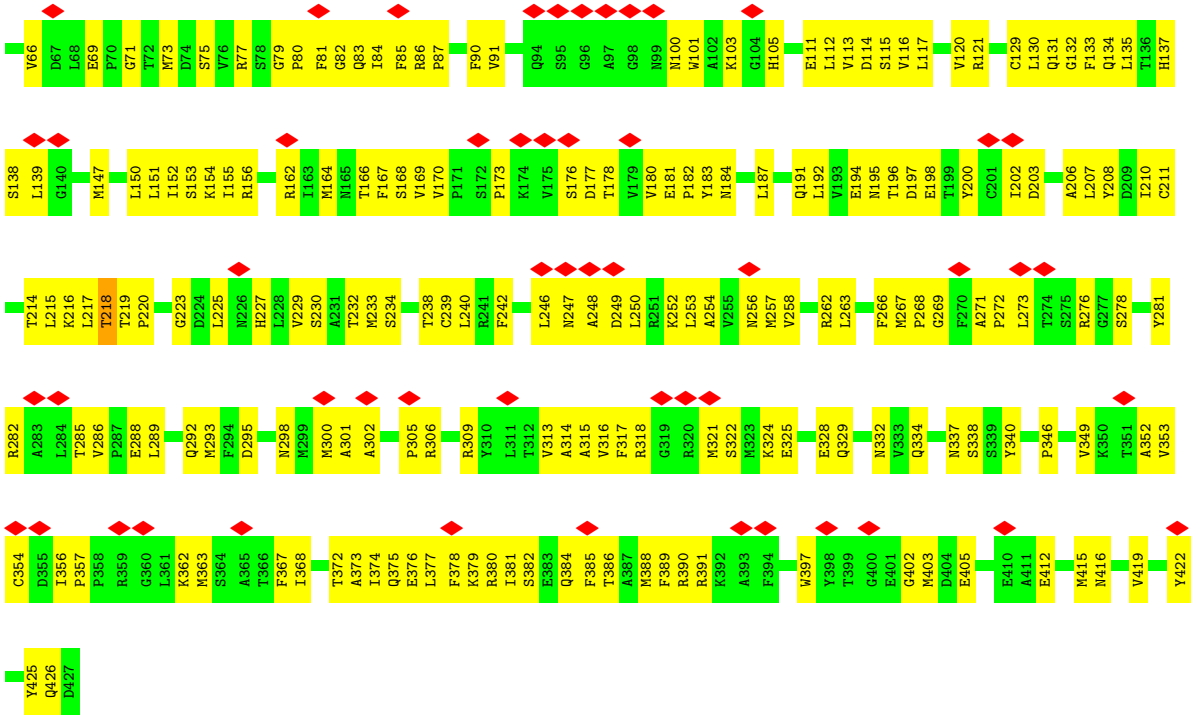
Chain CJ:



• Molecule 3: Tubulin beta-4B chain

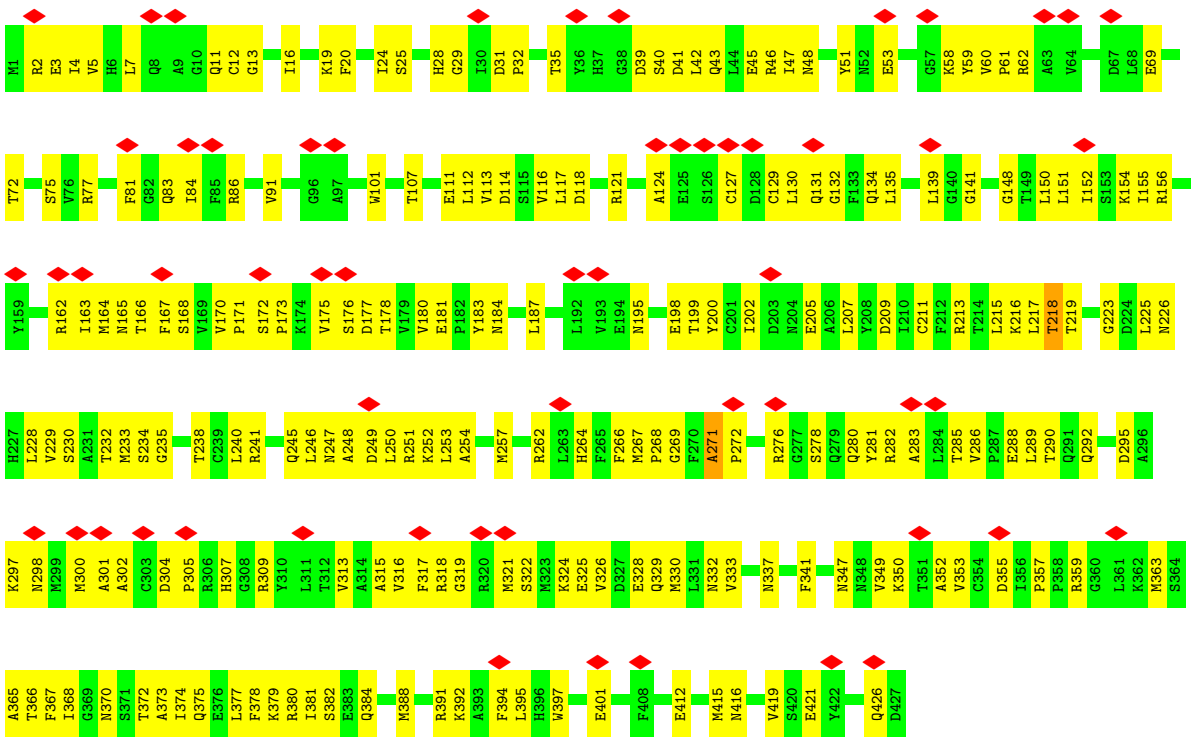
Chain CL:





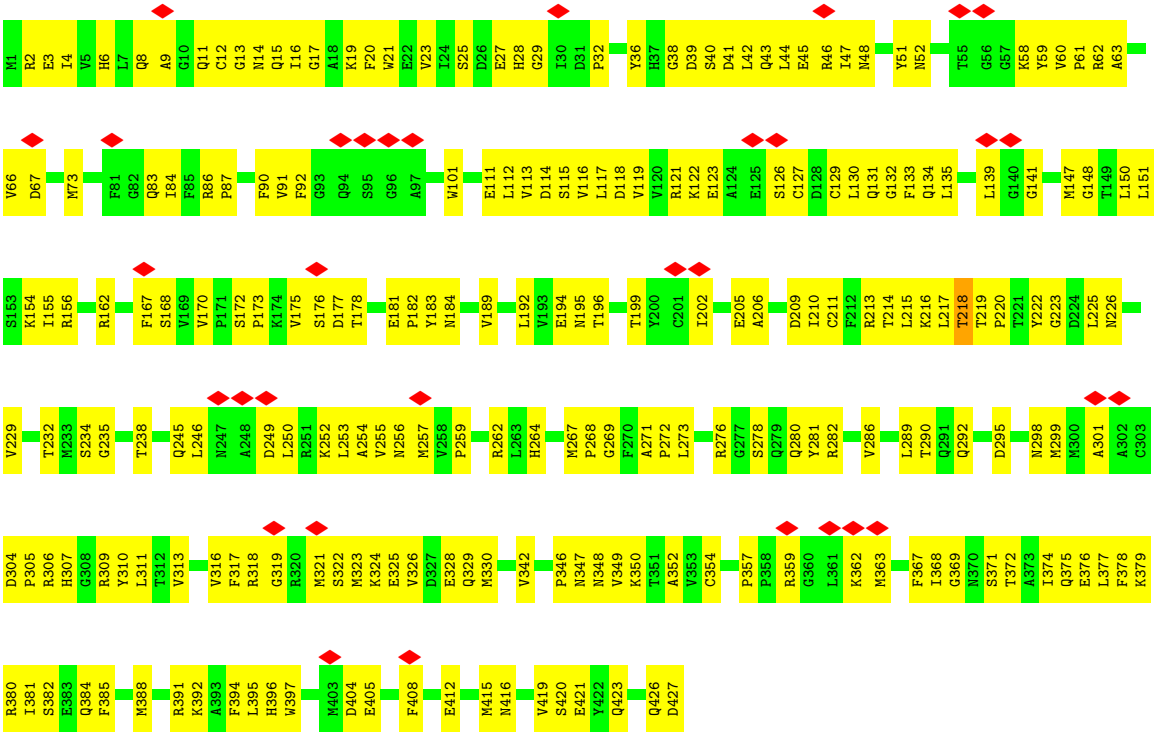
• Molecule 3: Tubulin beta-4B chain

Chain DB:



• Molecule 3: Tubulin beta-4B chain

Chain DD:



• Molecule 3: Tubulin beta-4B chain

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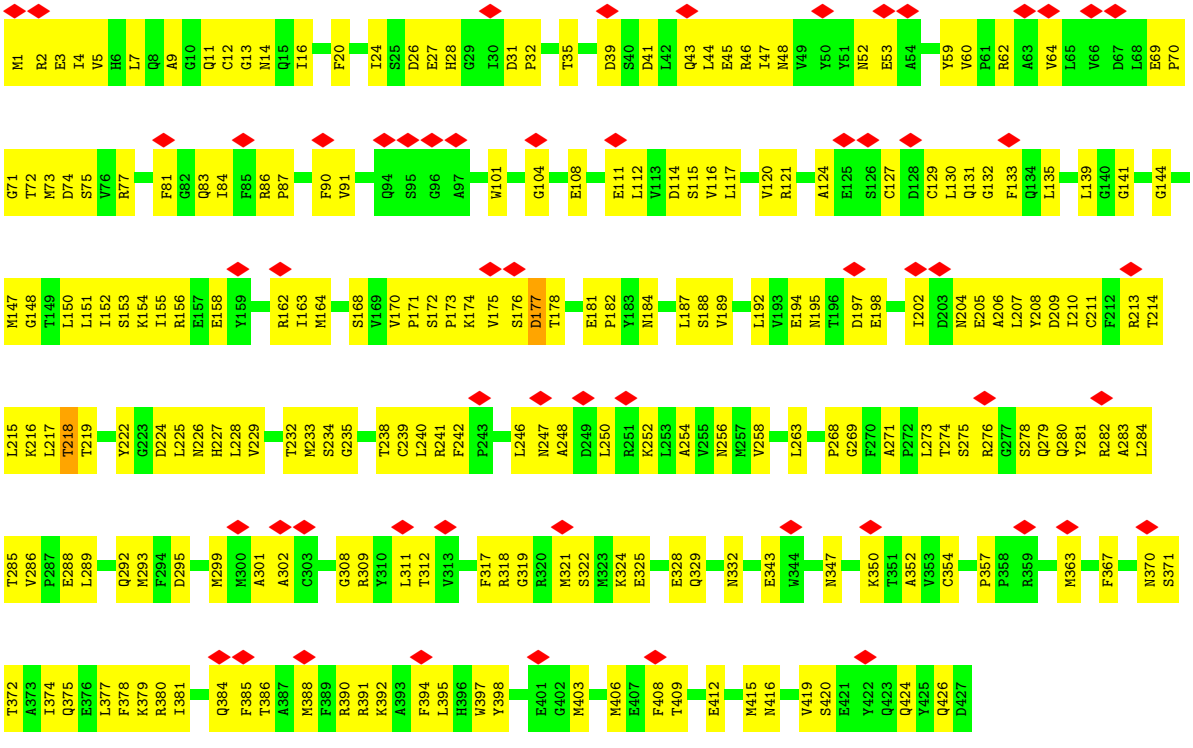
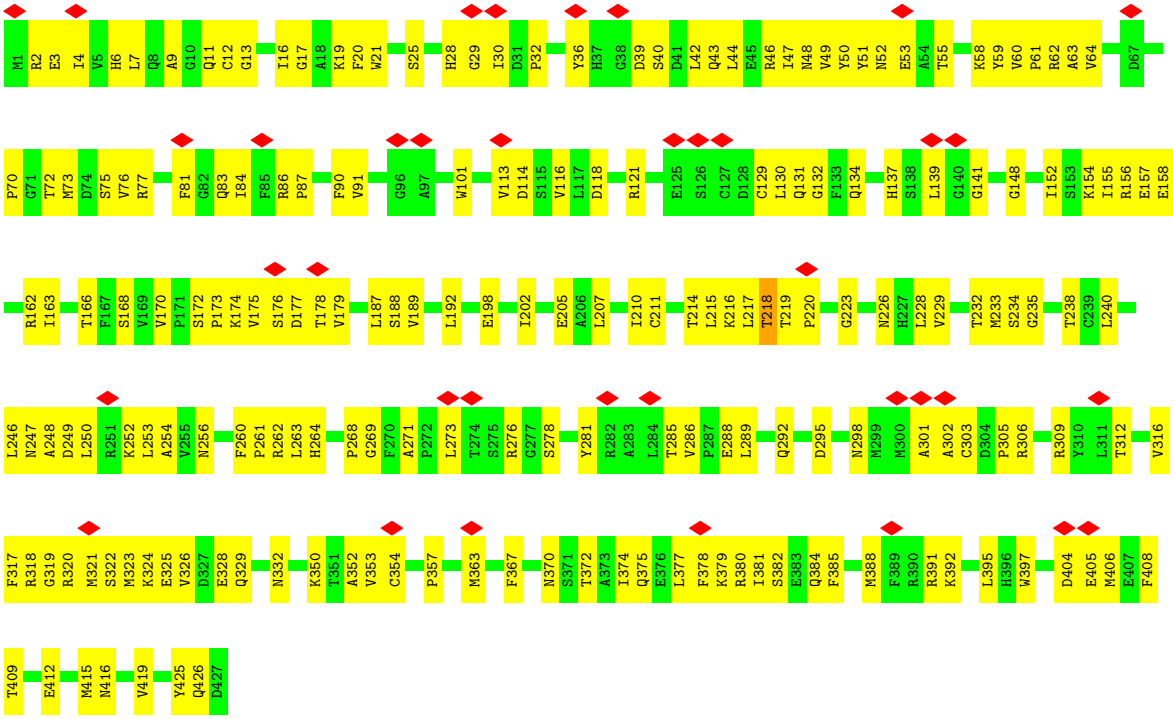


• Molecule 3: Tubulin beta-4B chain

Chain DH:



• Molecule 3: Tubulin beta-4B chain

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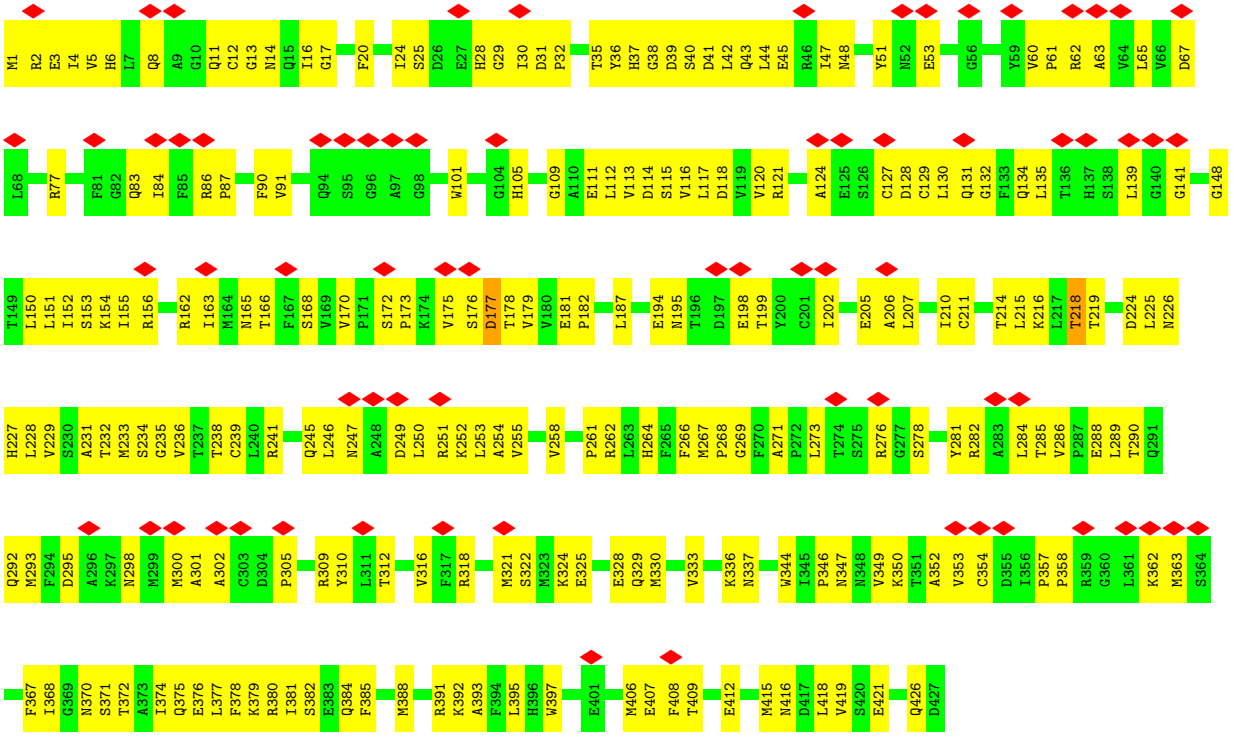

• Molecule 3: Tubulin beta-4B chain

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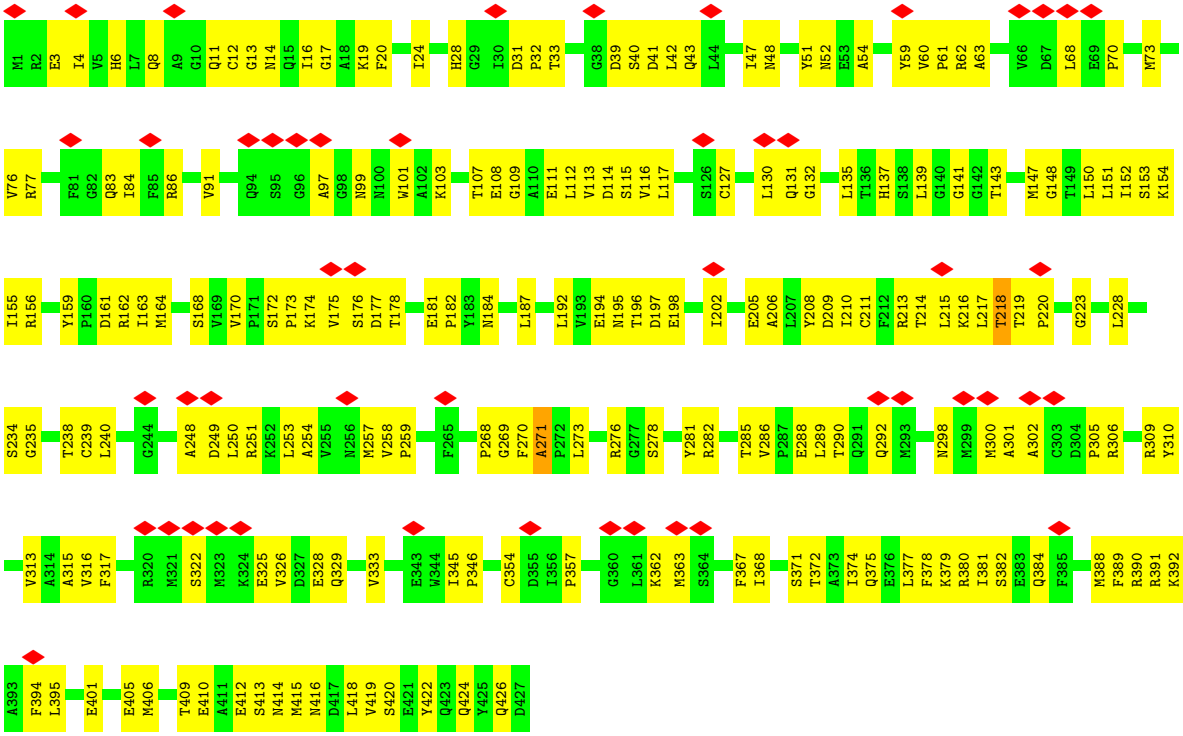

• Molecule 3: Tubulin beta-4B chain

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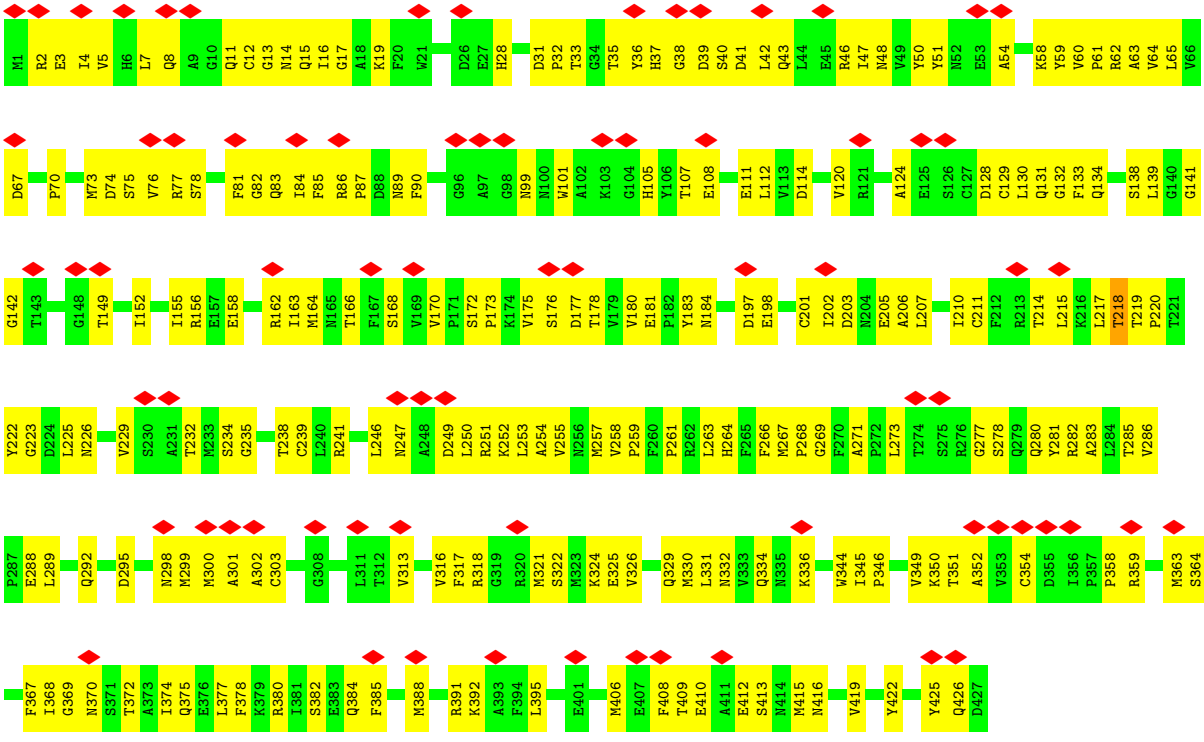
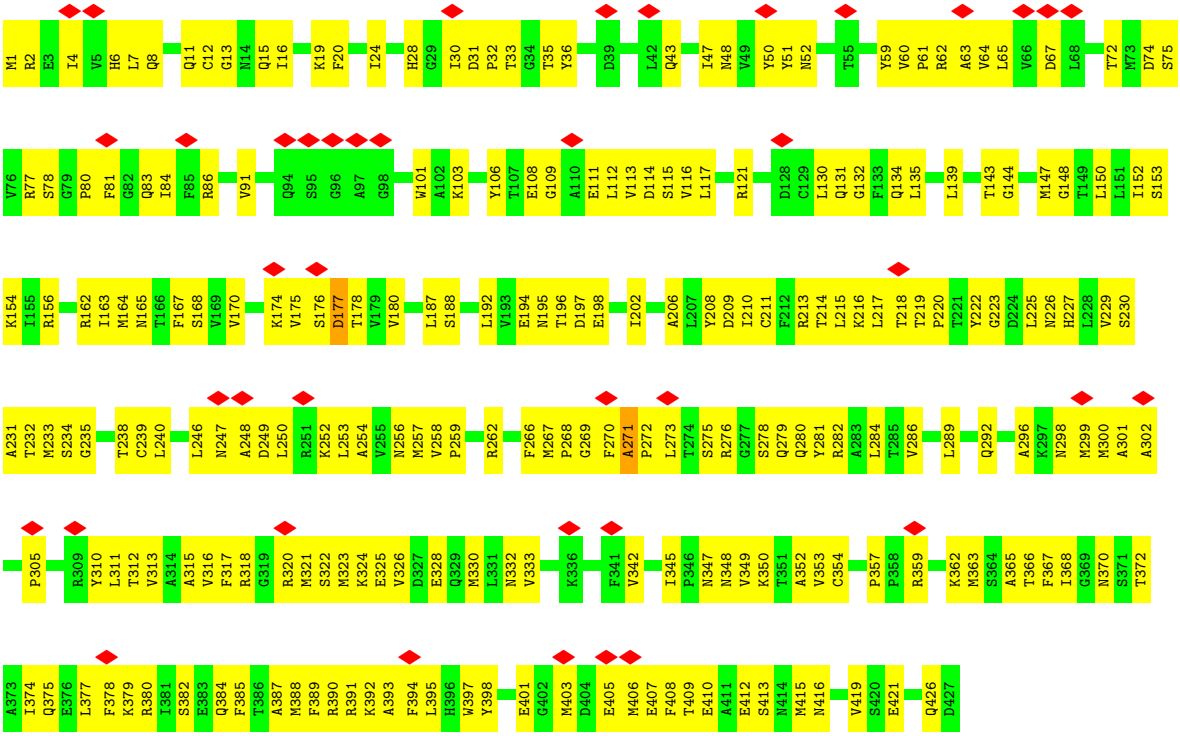


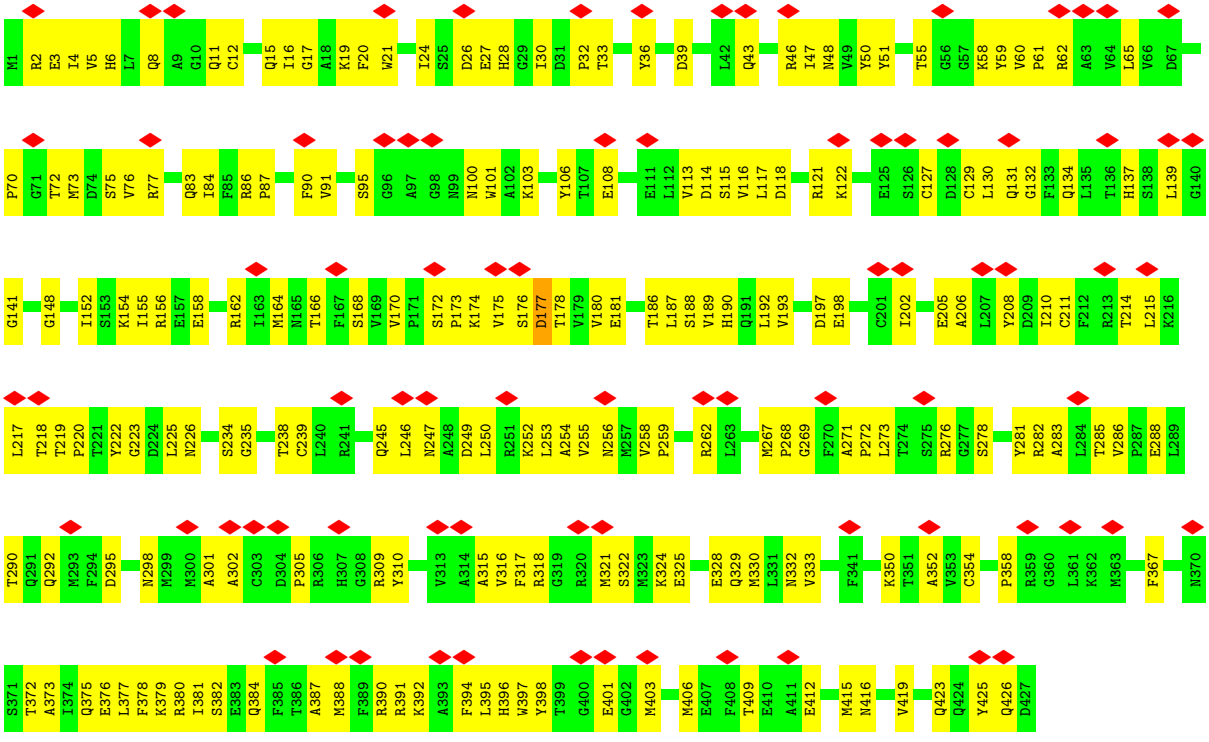
• Molecule 3: Tubulin beta-4B chain

Chain ED:



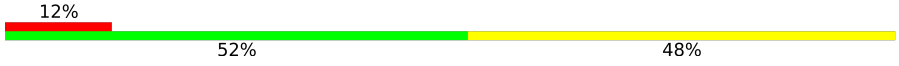
• Molecule 3: Tubulin beta-4B chain

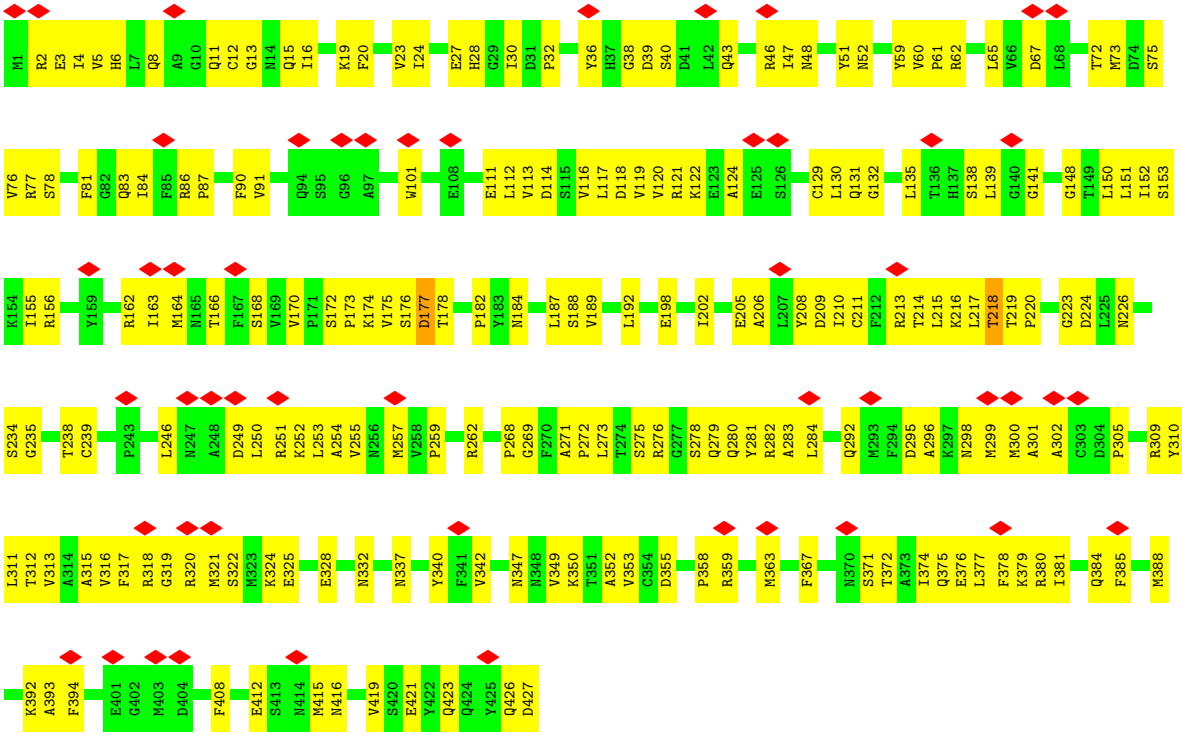
Chain EF:



• Molecule 3: Tubulin beta-4B chain

Chain EH:





• Molecule 3: Tubulin beta-4B chain

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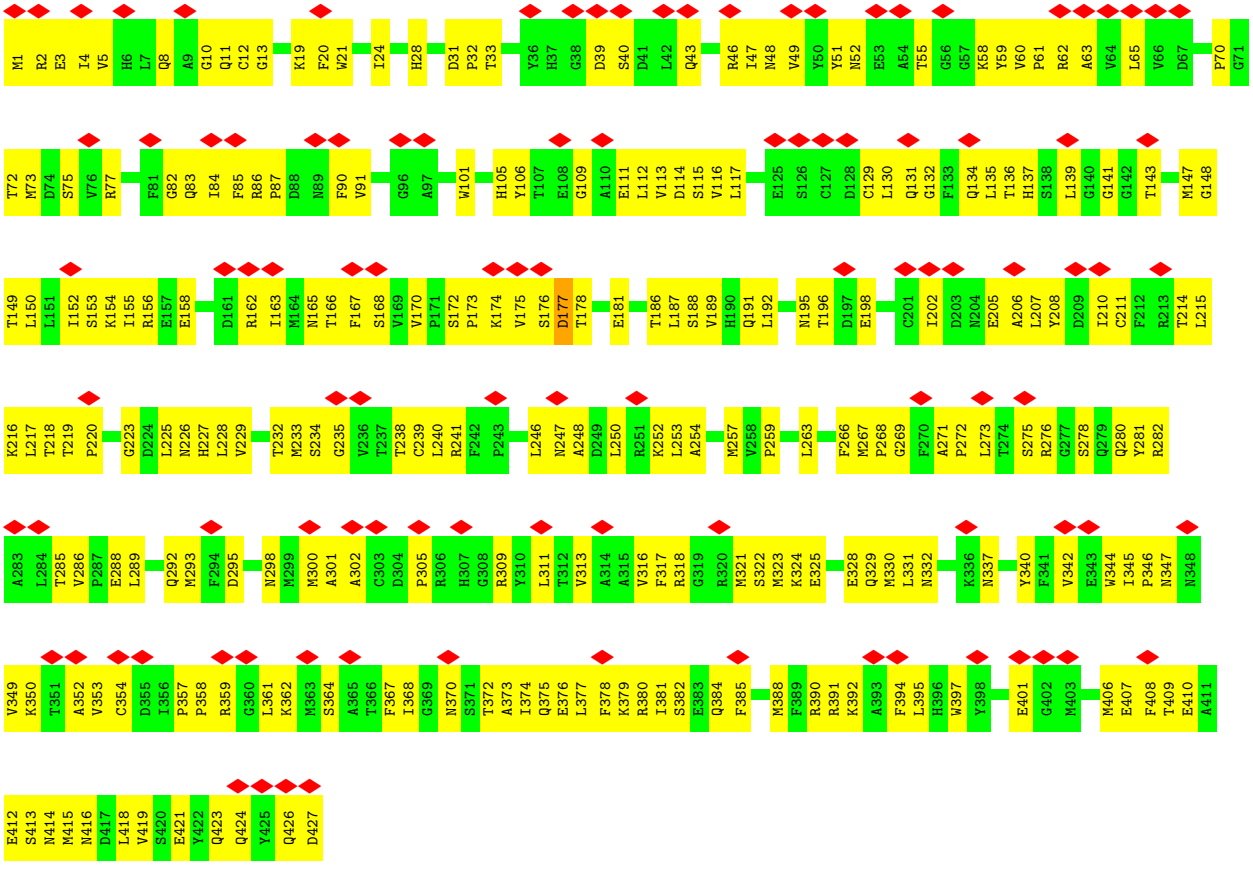

• Molecule 3: Tubulin beta-4B chain

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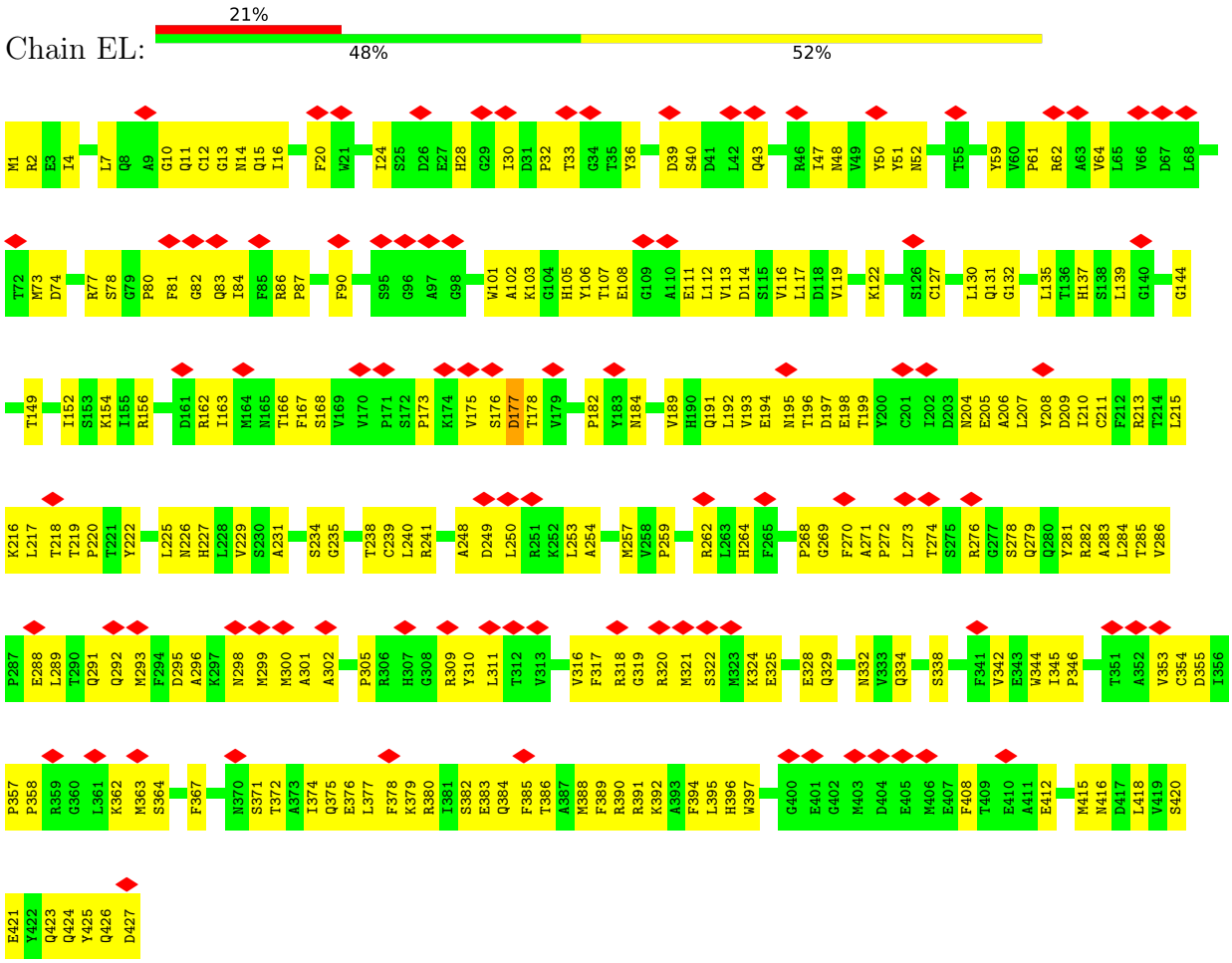
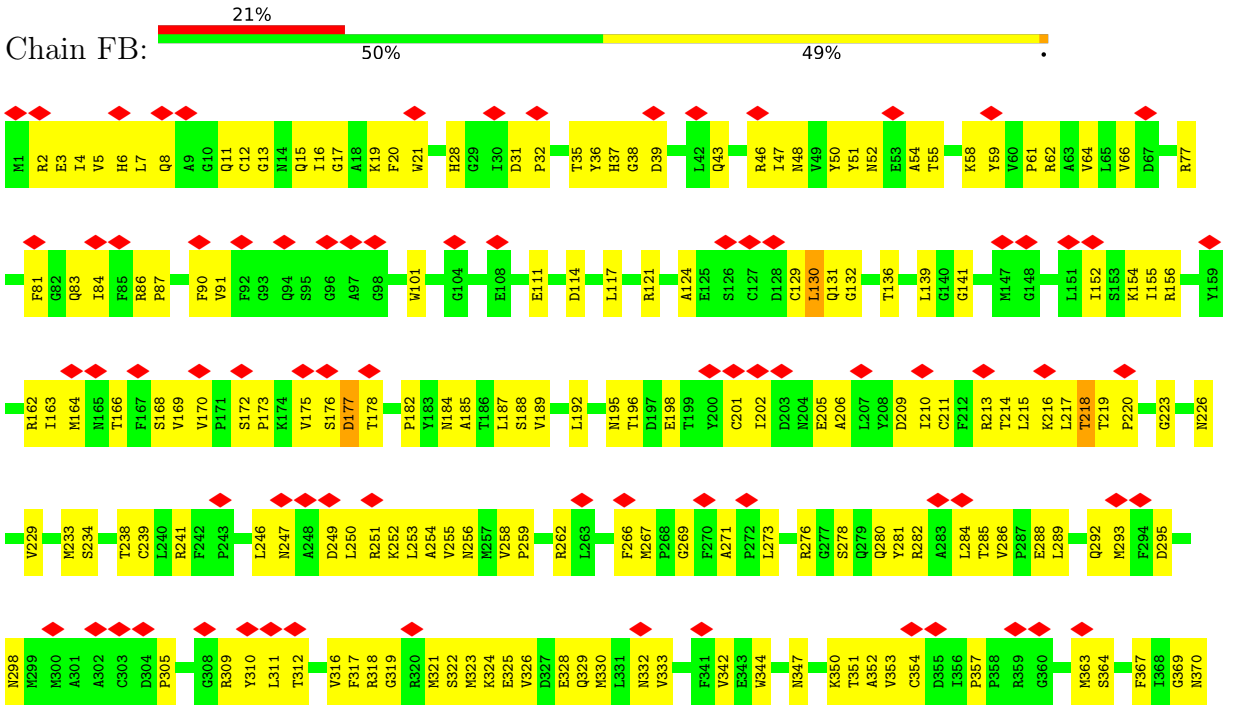
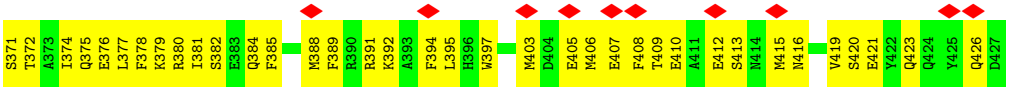


• Molecule 3: Tubulin beta-4B chain

Chain FB:





• Molecule 3: Tubulin beta-4B chain

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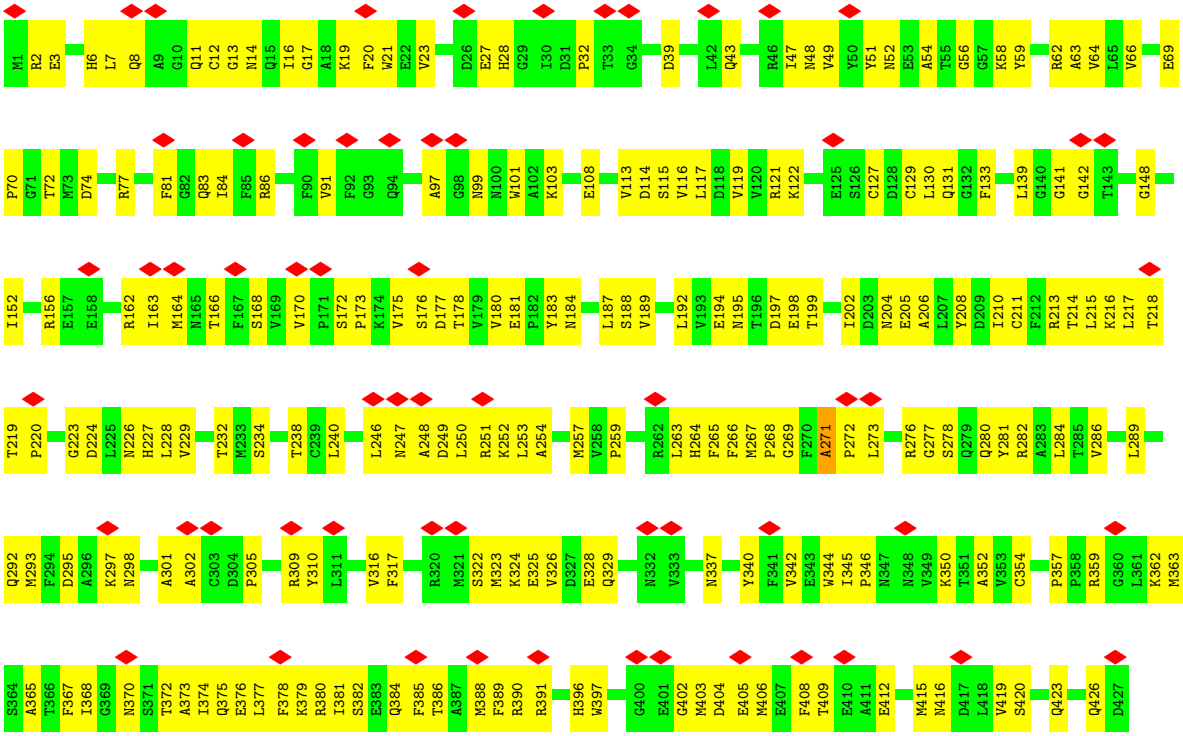

• Molecule 3: Tubulin beta-4B chain

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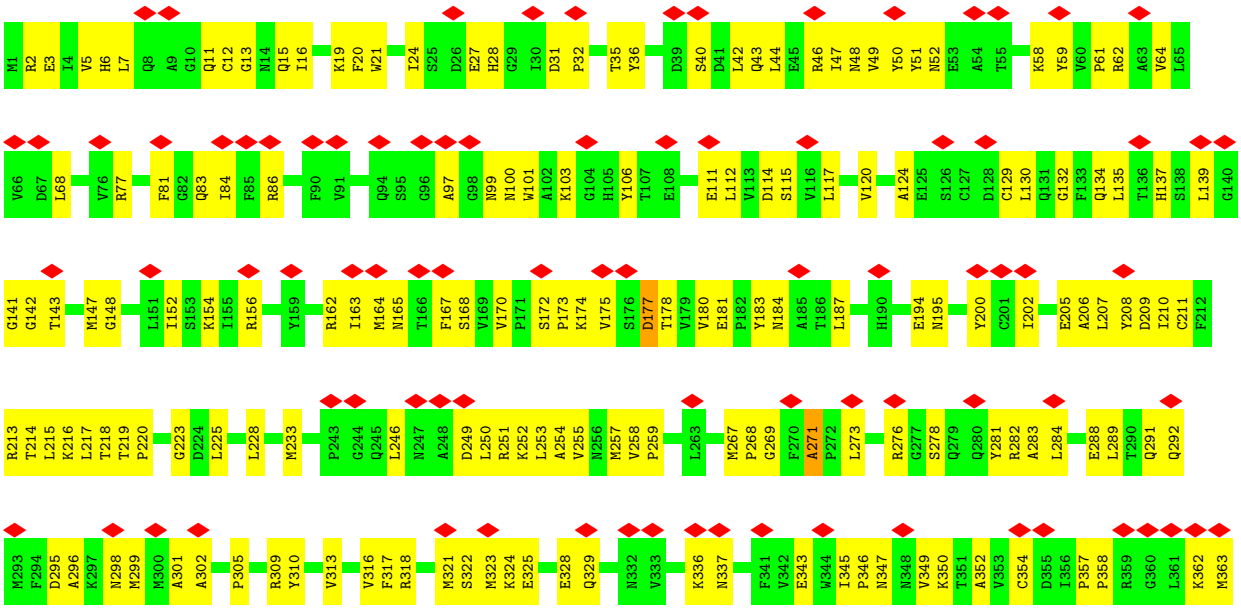

• Molecule 3: Tubulin beta-4B chain

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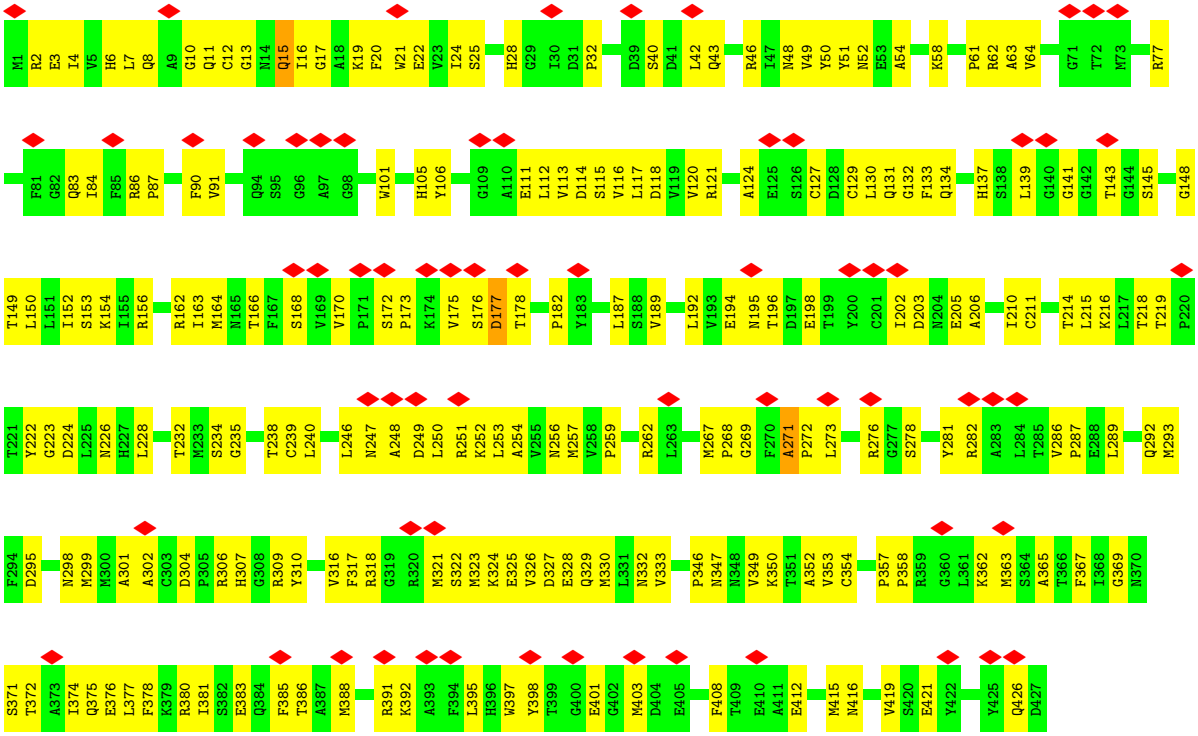

• Molecule 3: Tubulin beta-4B chain

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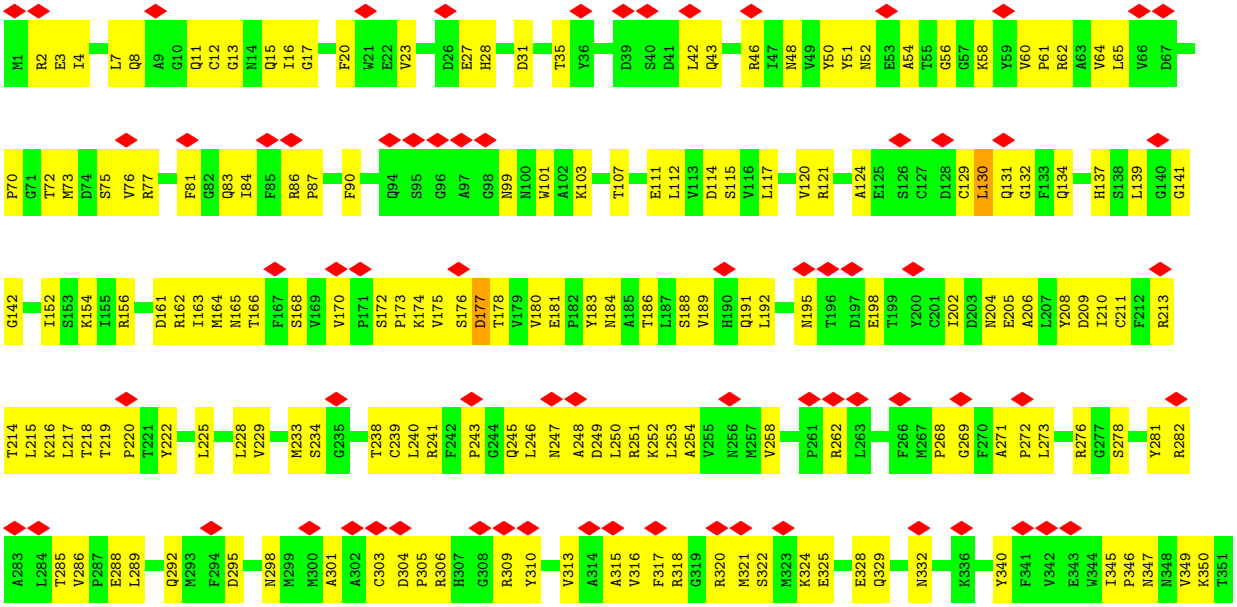

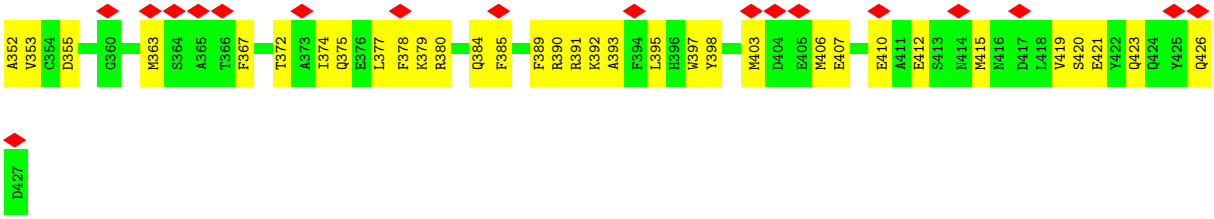

• Molecule 3: Tubulin beta-4B chain

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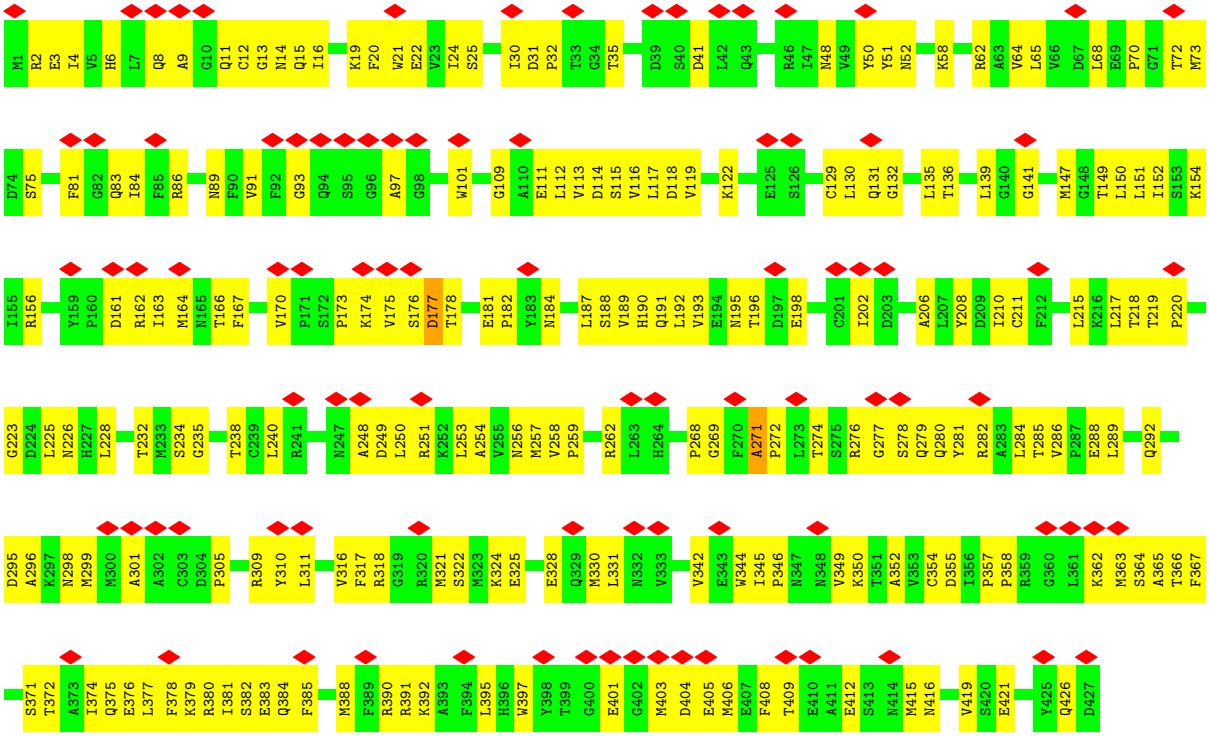

• Molecule 3: Tubulin beta-4B chain

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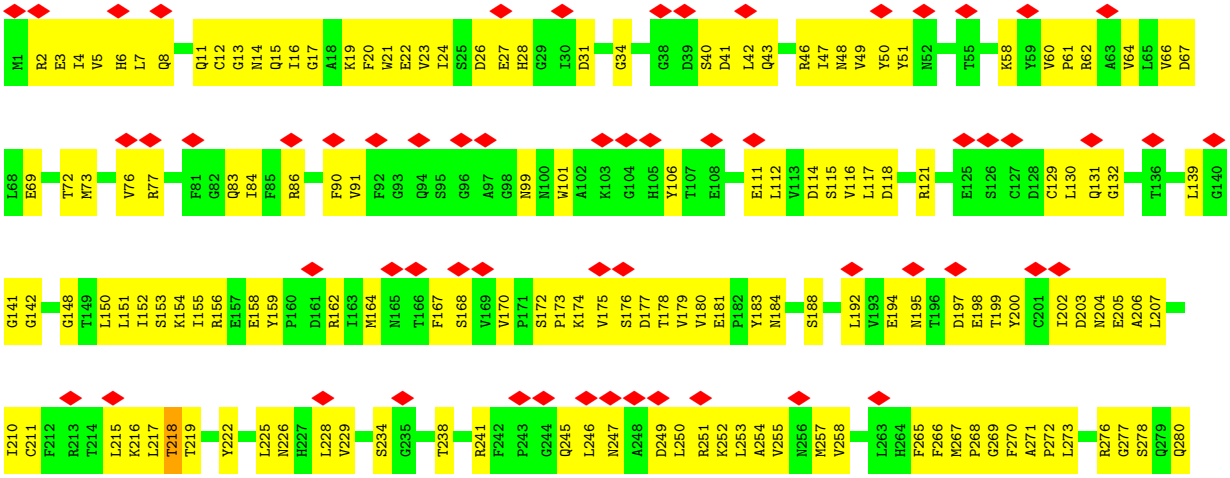

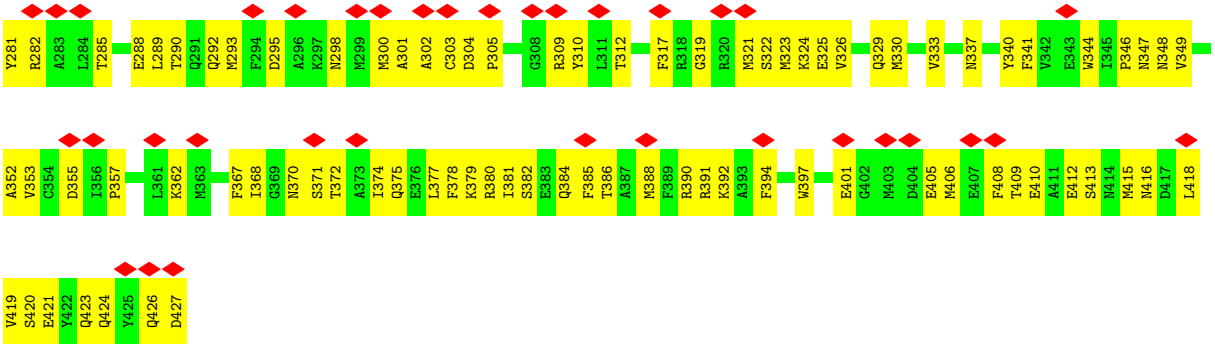

• Molecule 3: Tubulin beta-4B chain

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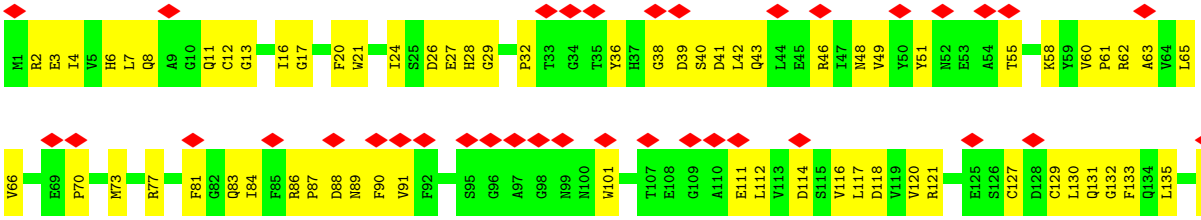
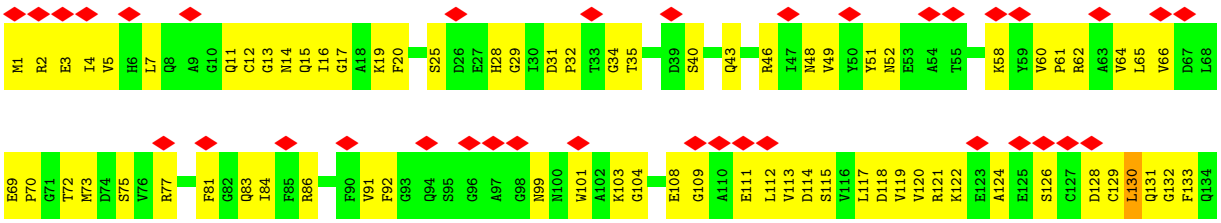
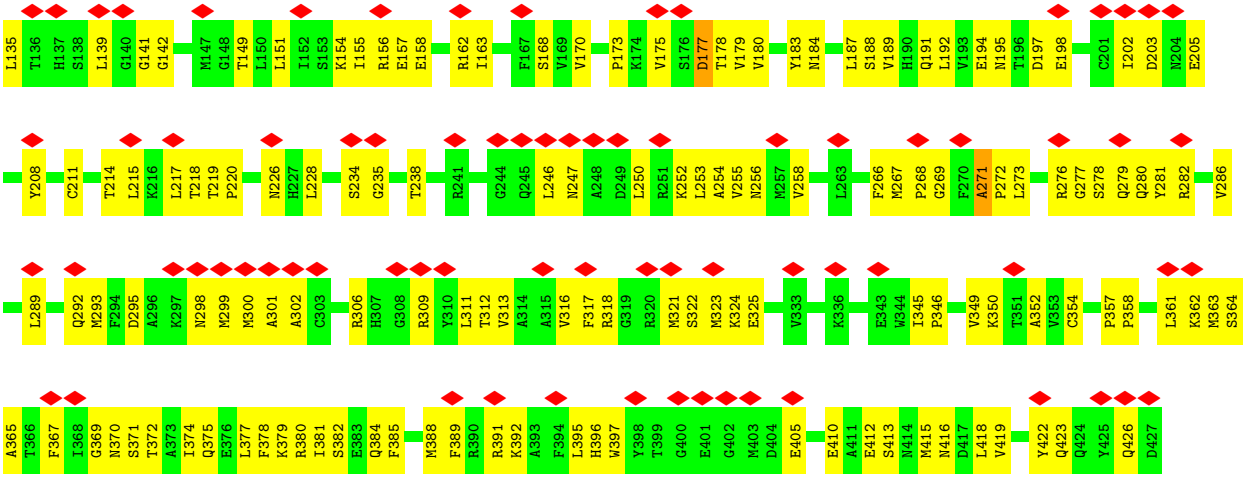


• Molecule 3: Tubulin beta-4B chain

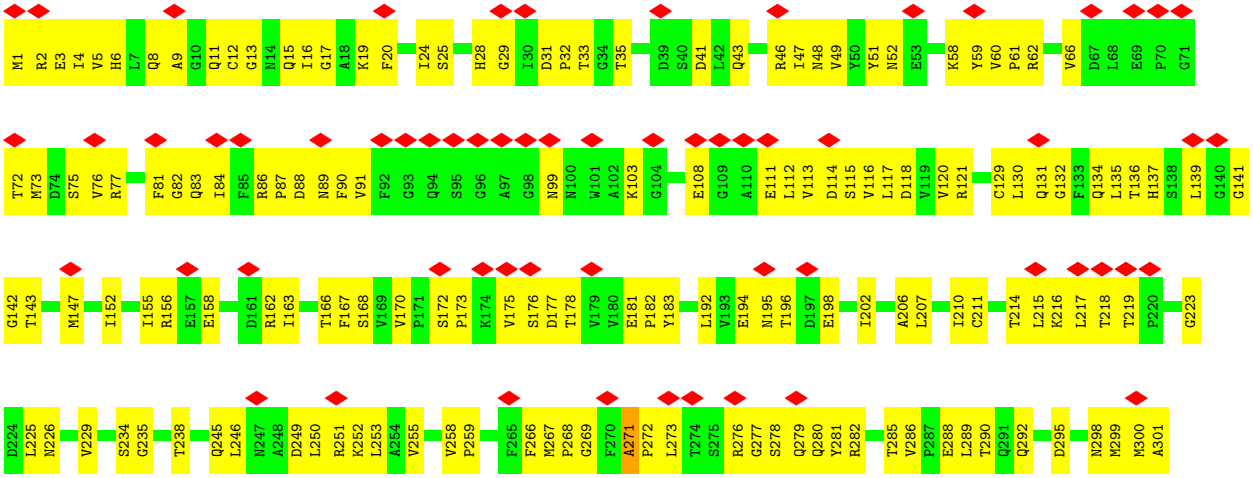
Chain GF:





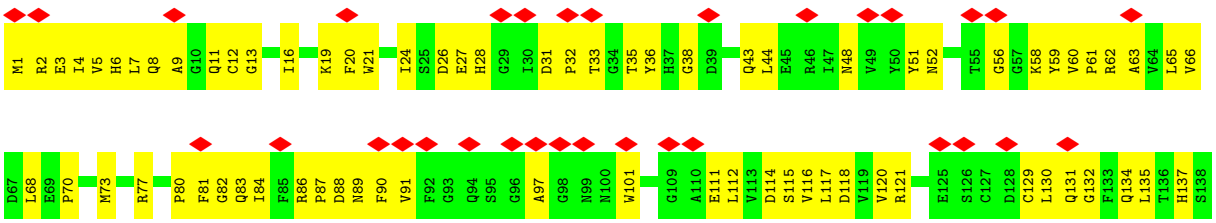
• Molecule 3: Tubulin beta-4B chain

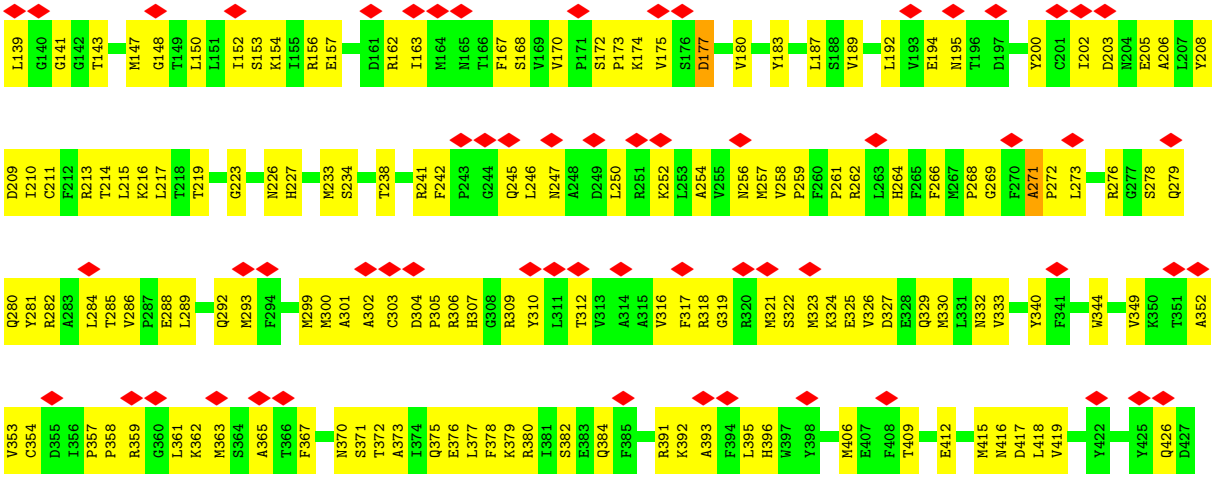
Chain GH:



• Molecule 3: Tubulin beta-4B chain

Chain GJ:



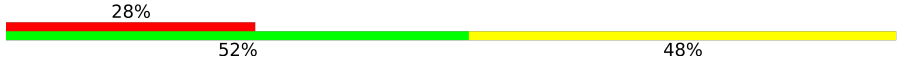


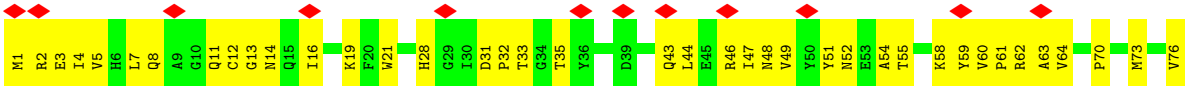
• Molecule 3: Tubulin beta-4B chain

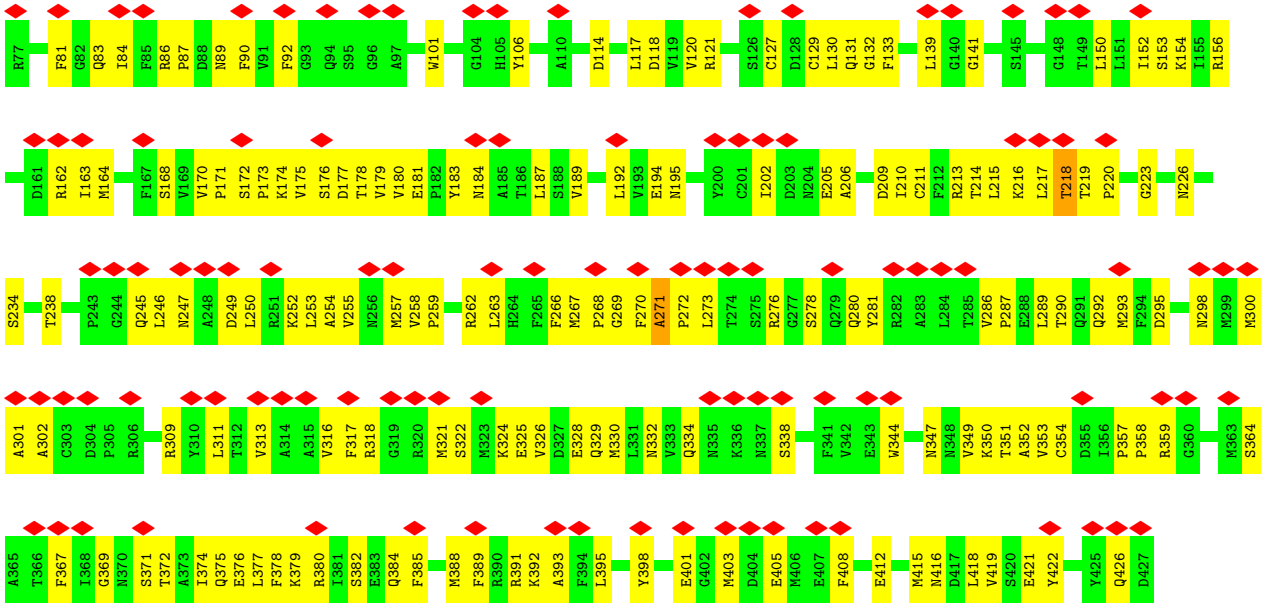
Chain GL:

• Molecule 3: Tubulin beta-4B chain

Chain HB:

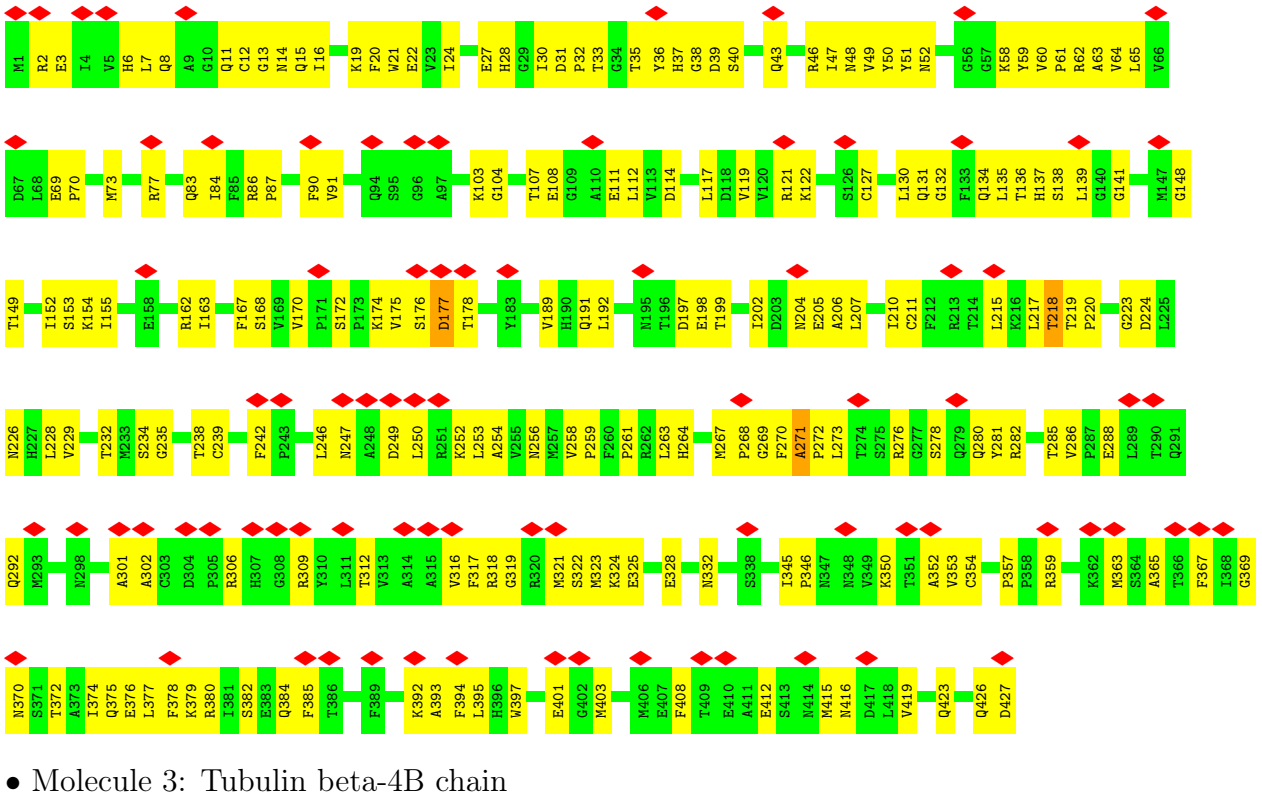






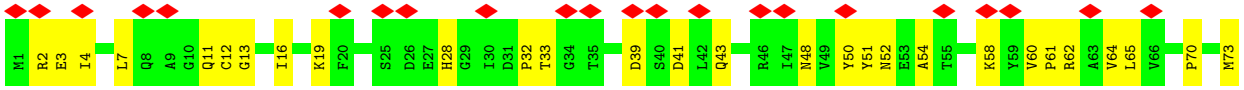
• Molecule 3: Tubulin beta-4B chain

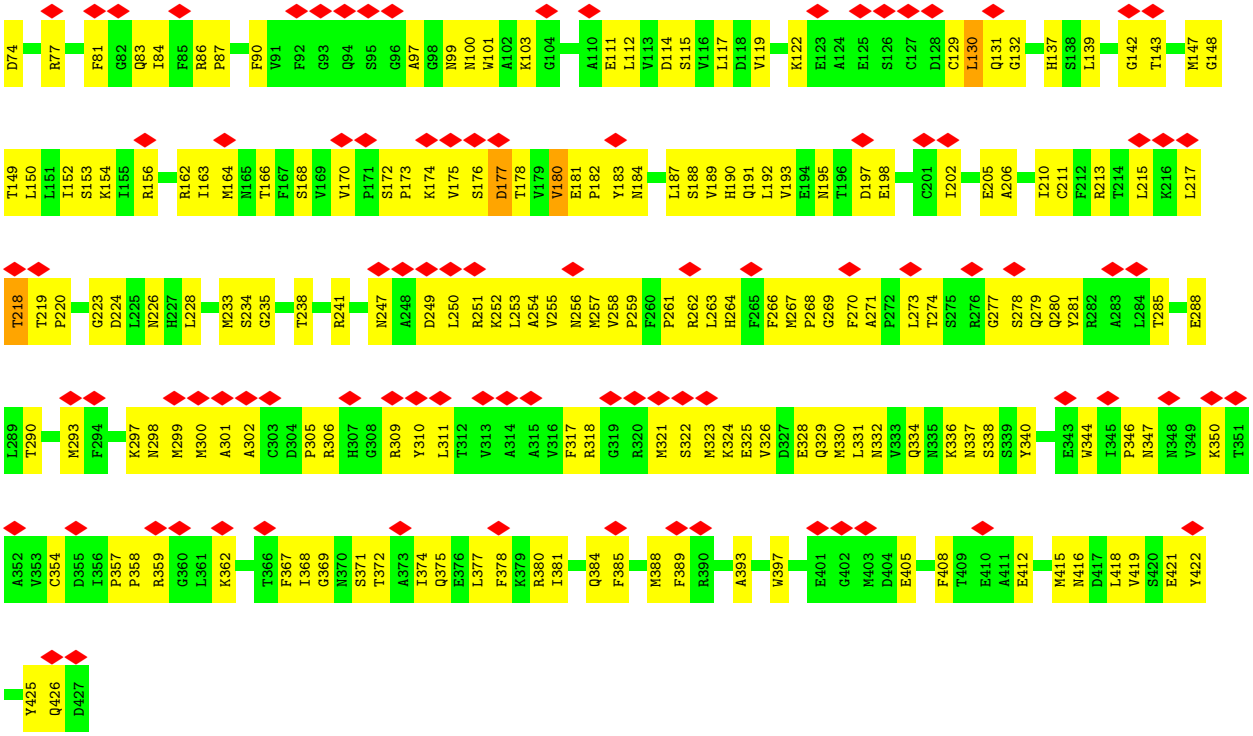
Chain HD:

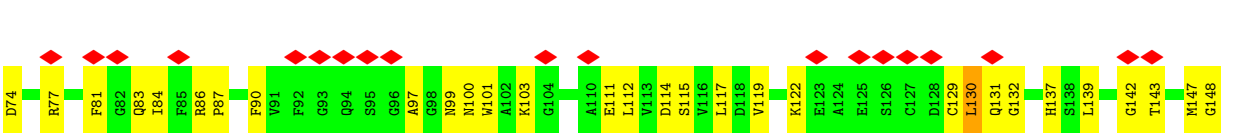


• Molecule 3: Tubulin beta-4B chain

Chain HF:

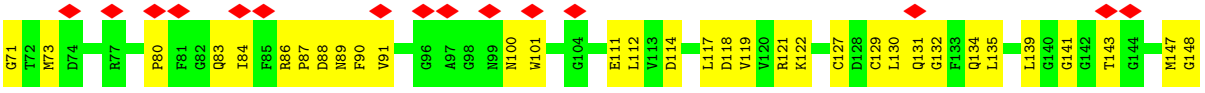


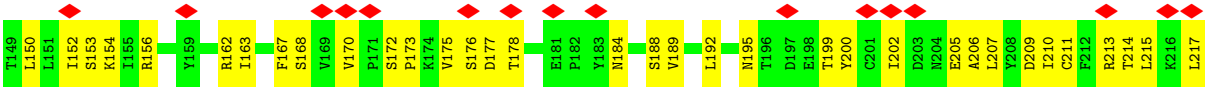


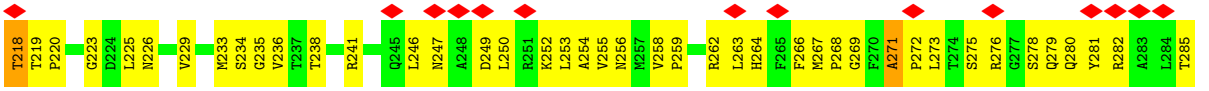


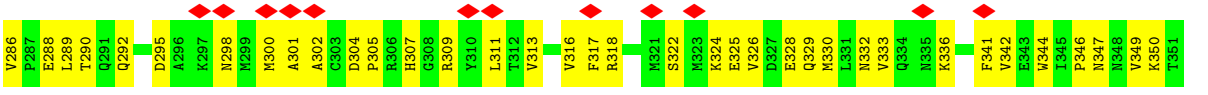
• Molecule 3: Tubulin beta-4B chain

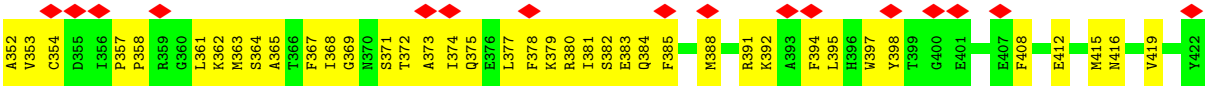
Chain HH:









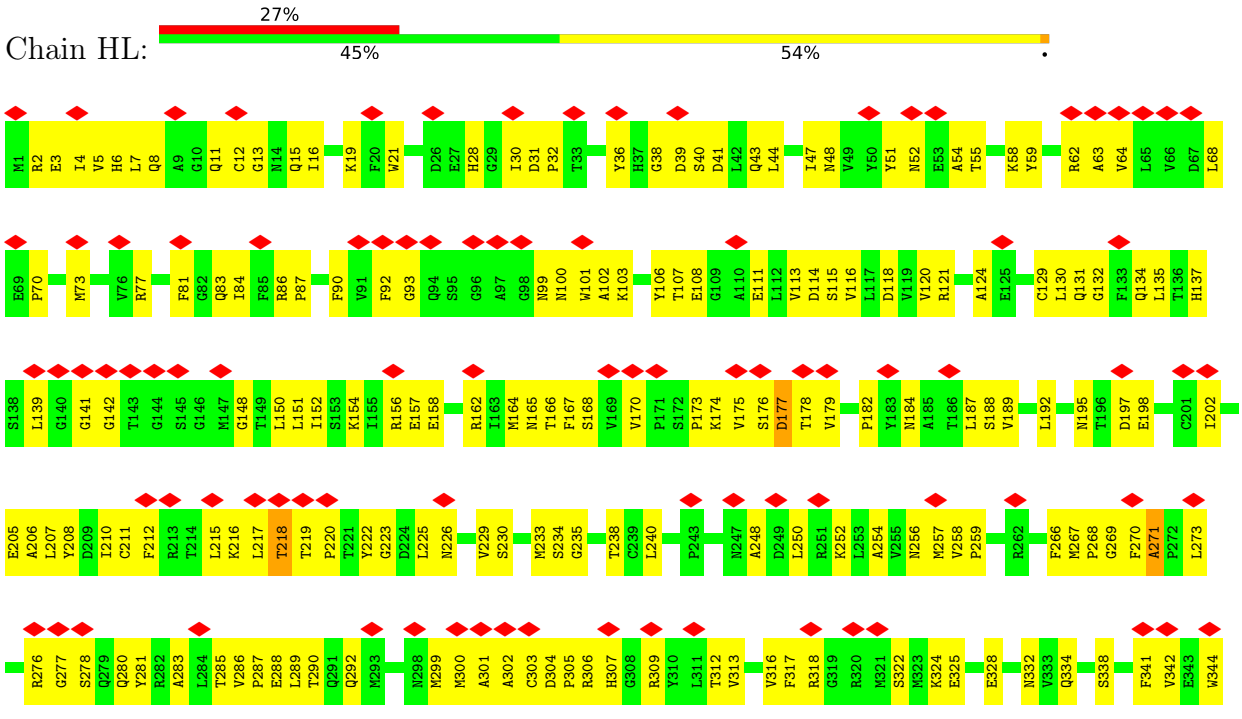


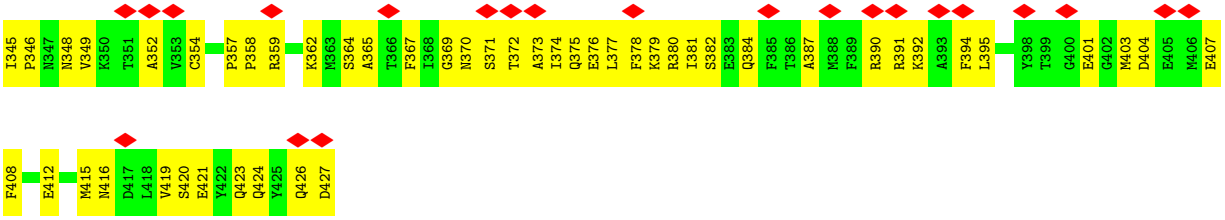
• Molecule 3: Tubulin beta-4B chain

Chain HJ:

• Molecule 3: Tubulin beta-4B chain

Chain HL:





• Molecule 3: Tubulin beta-4B chain

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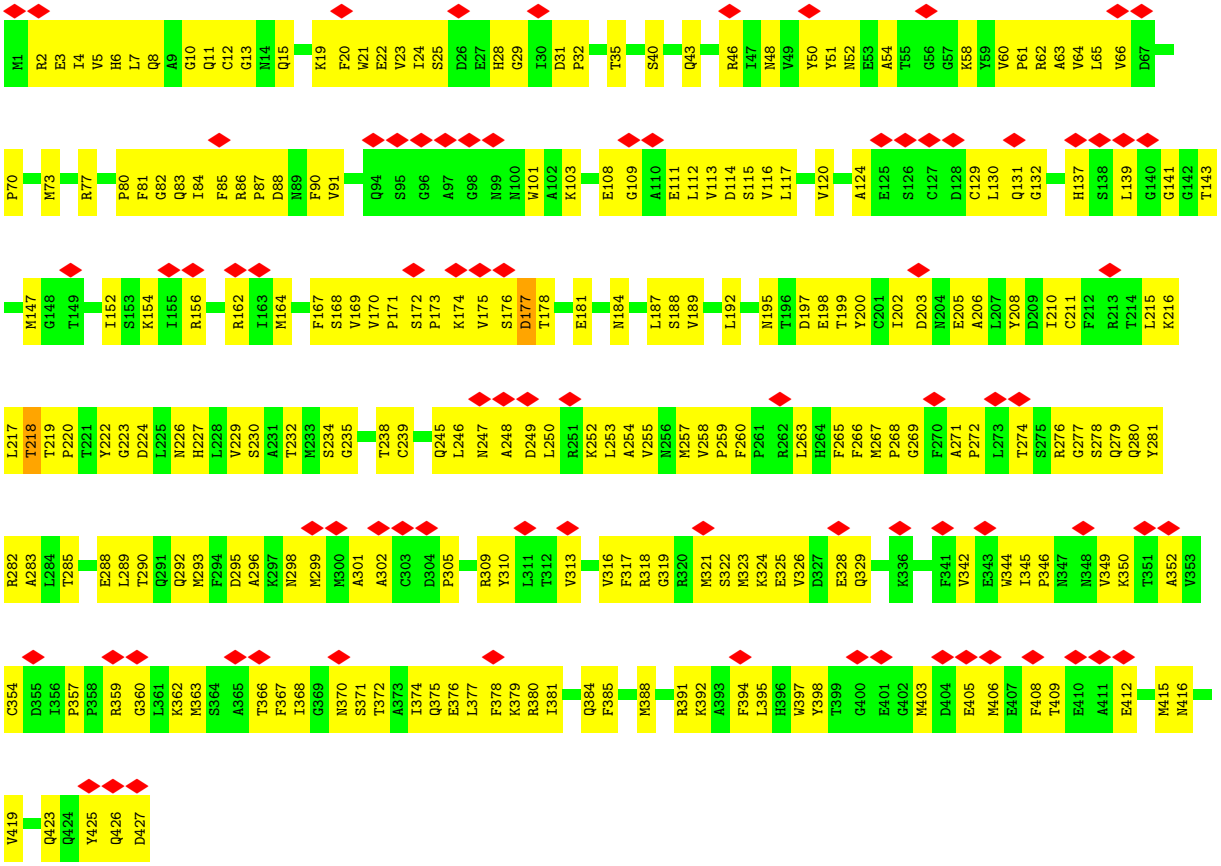

• Molecule 3: Tubulin beta-4B chain

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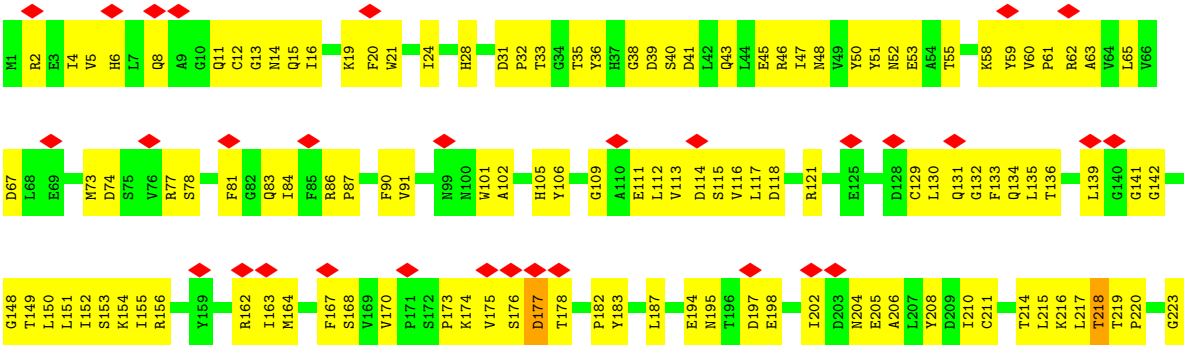
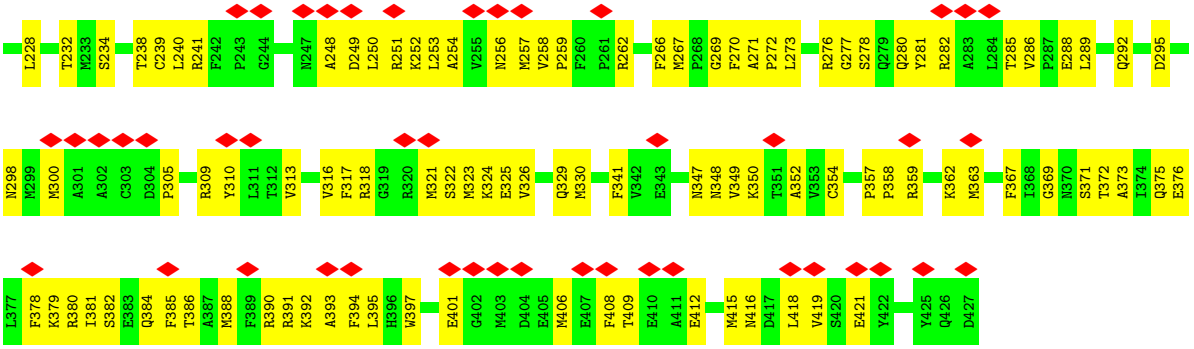
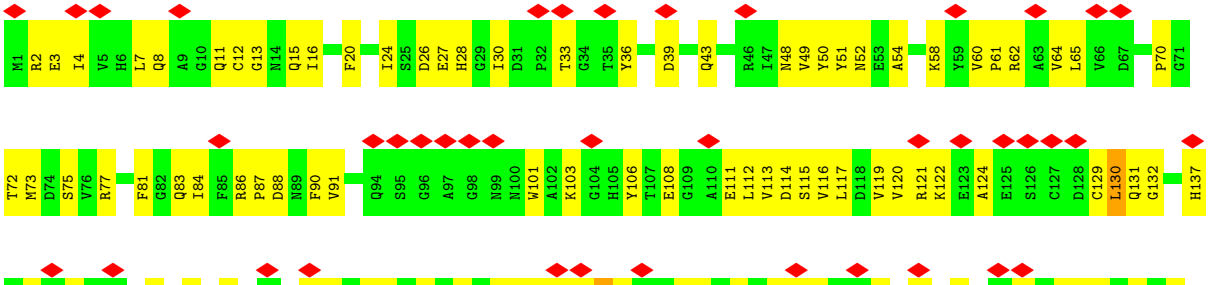




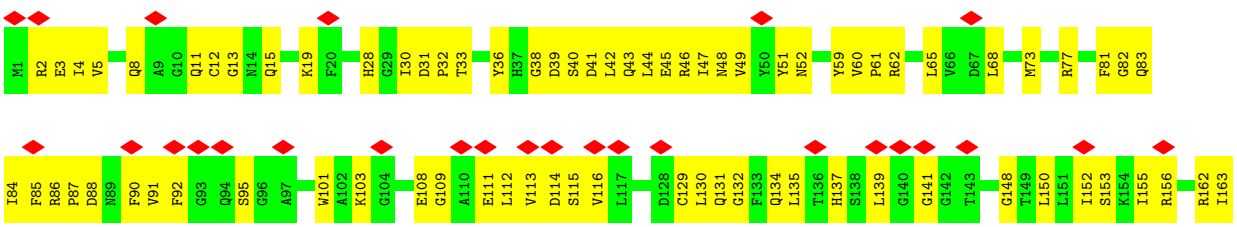
• Molecule 3: Tubulin beta-4B chain

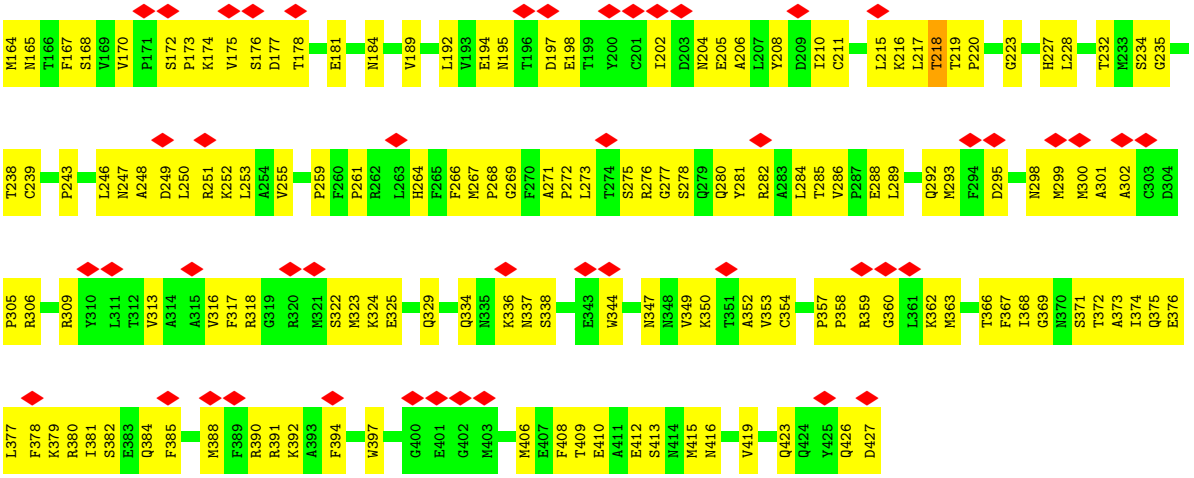
Chain IF:



• Molecule 3: Tubulin beta-4B chain

Chain IH:





• Molecule 3: Tubulin beta-4B chain

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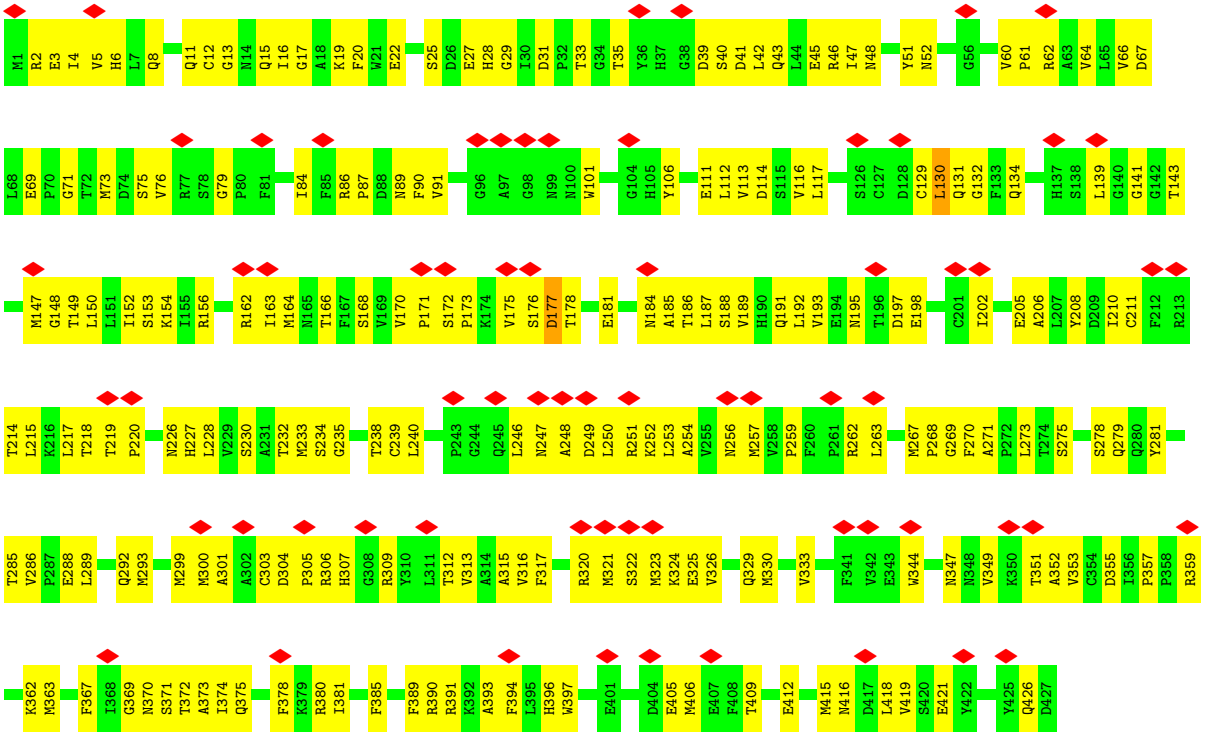

• Molecule 3: Tubulin beta-4B chain

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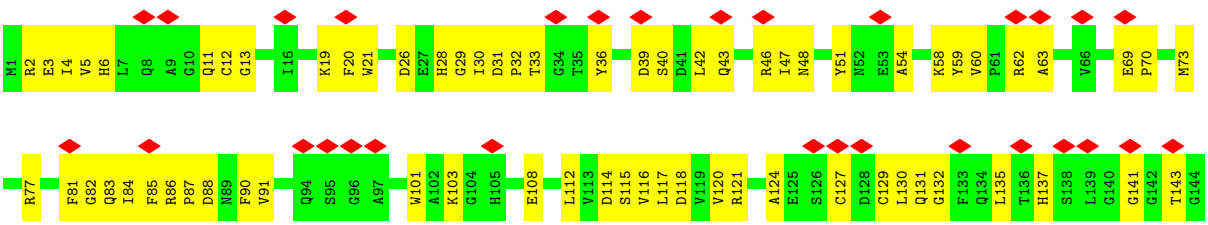
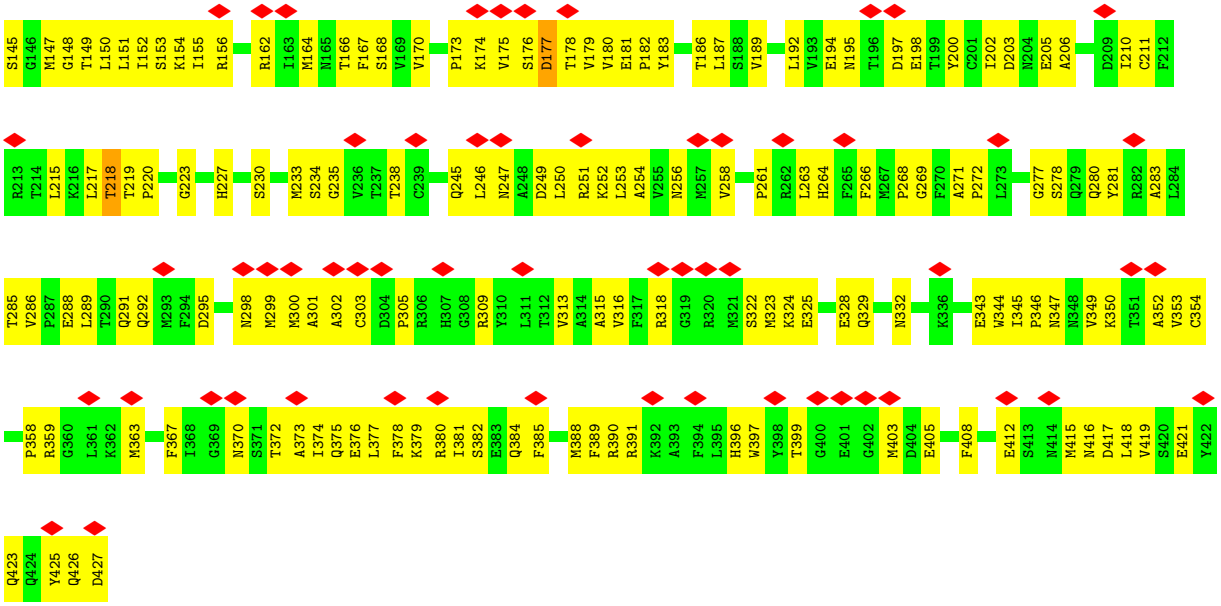
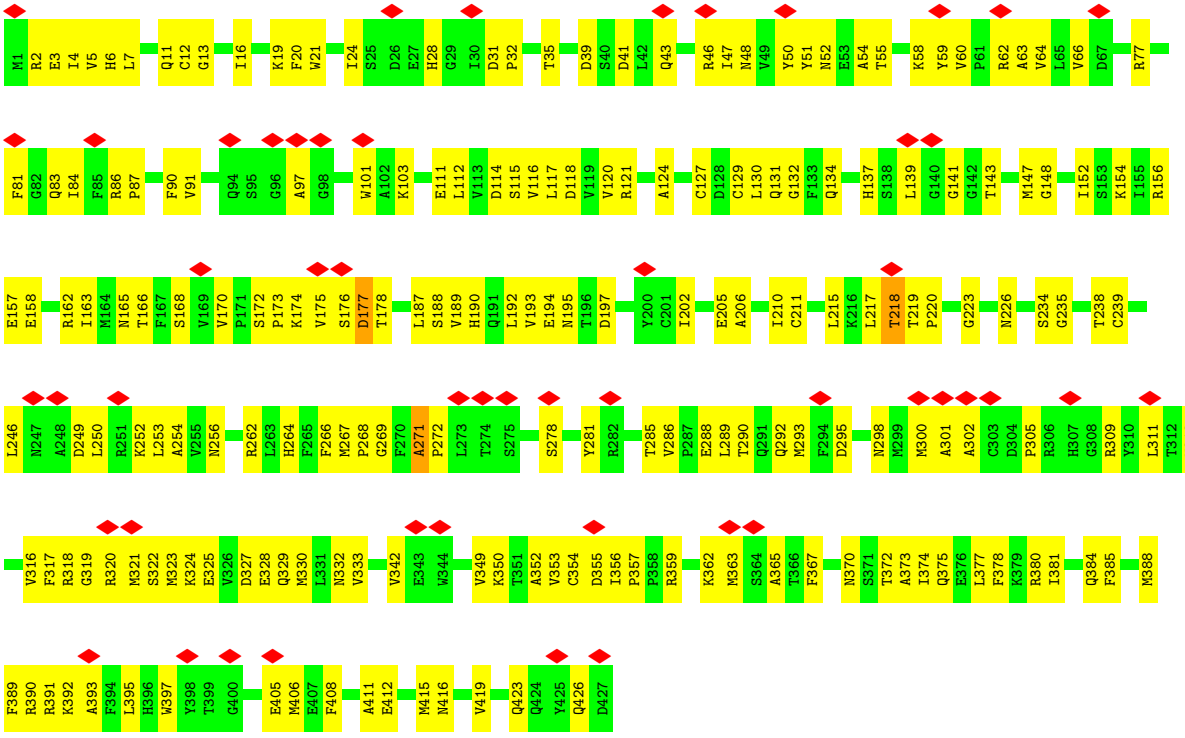




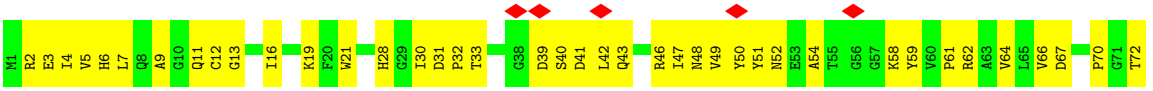
• Molecule 3: Tubulin beta-4B chain

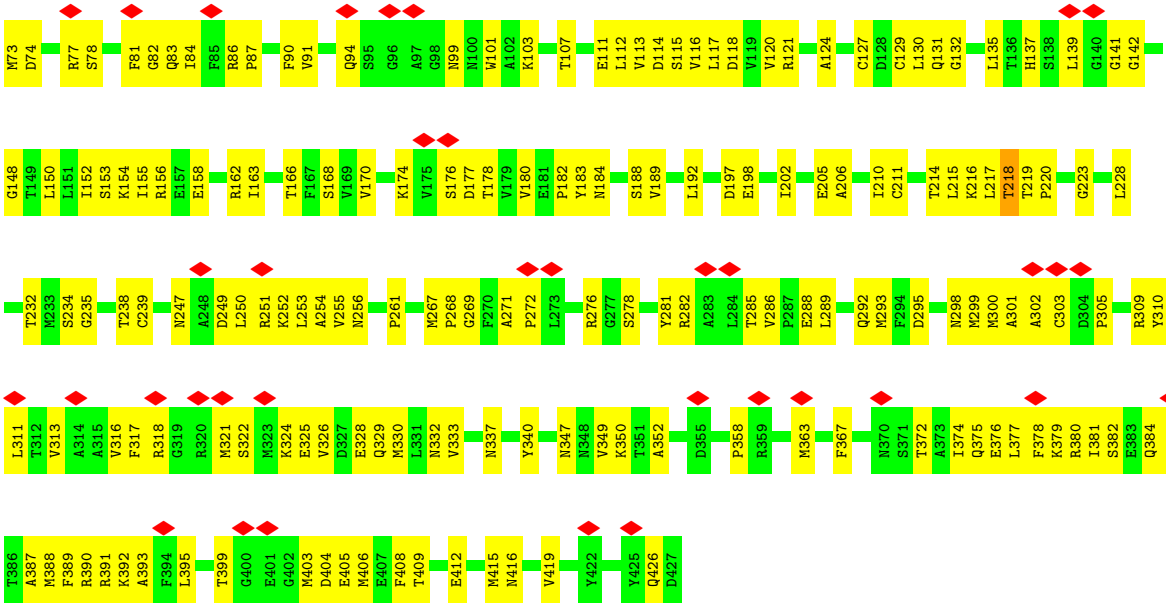
Chain JB:



• Molecule 3: Tubulin beta-4B chain

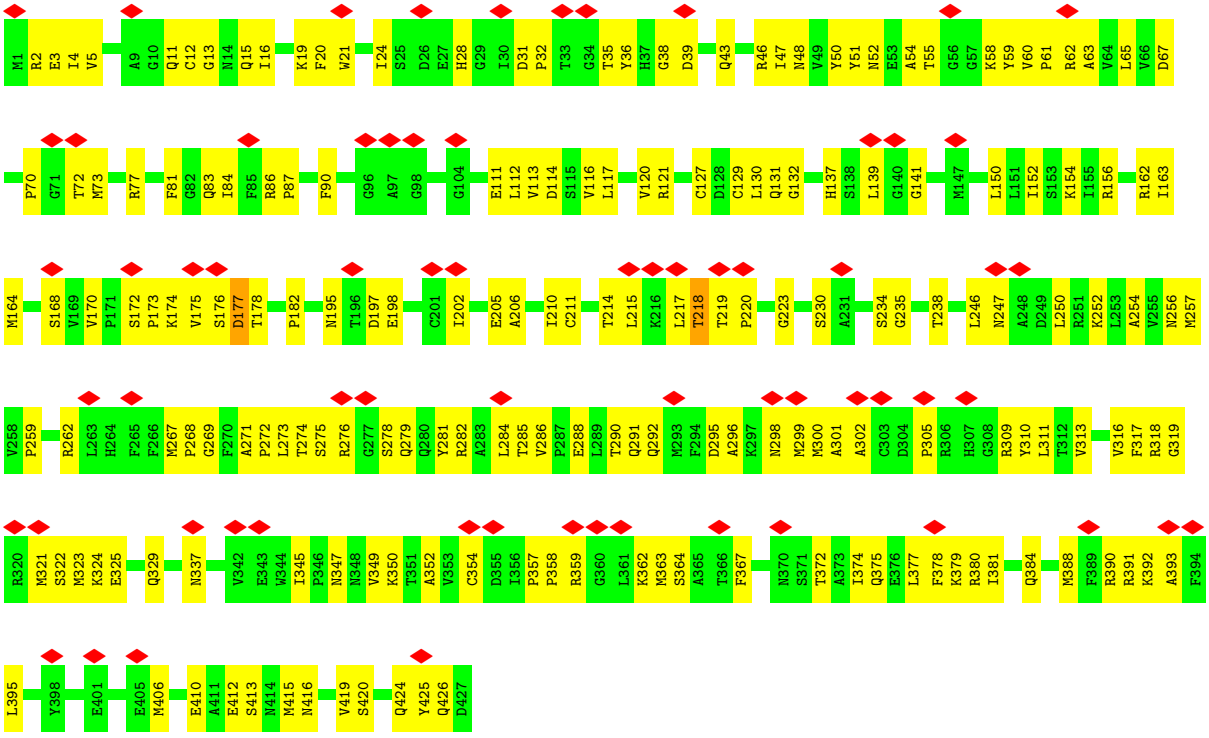
Chain JD:





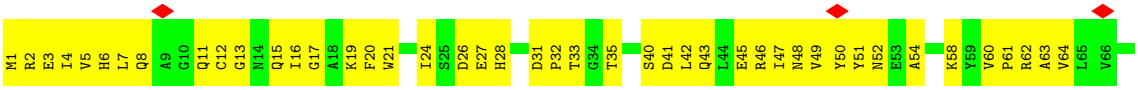
• Molecule 3: Tubulin beta-4B chain

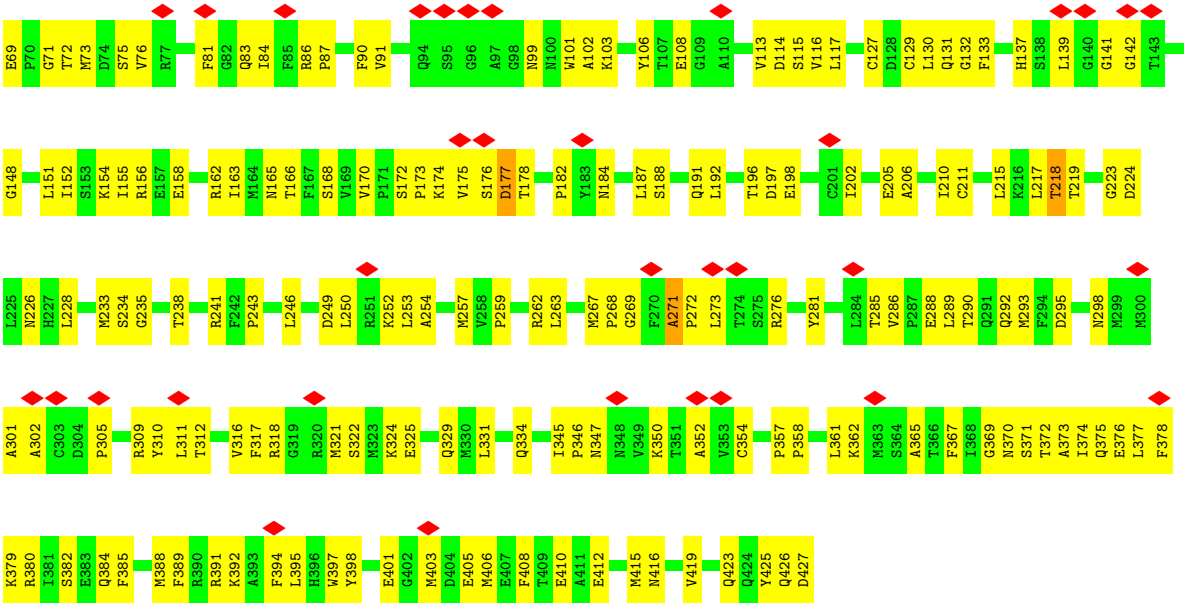
Chain JF:



• Molecule 3: Tubulin beta-4B chain

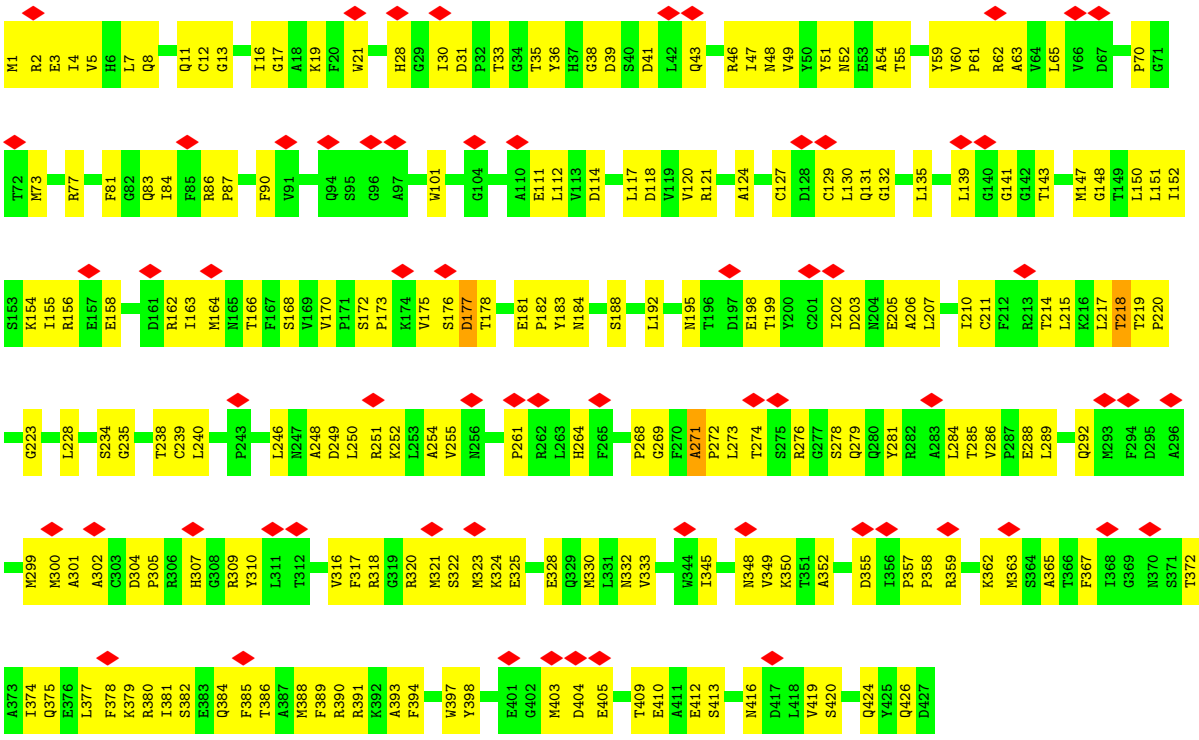
Chain JH:





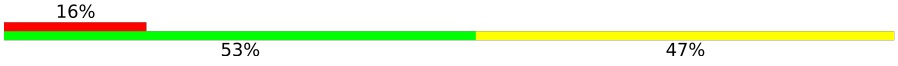
• Molecule 3: Tubulin beta-4B chain

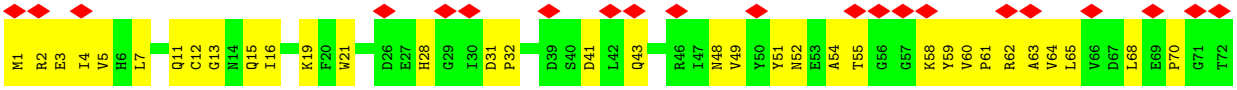
Chain JJ:

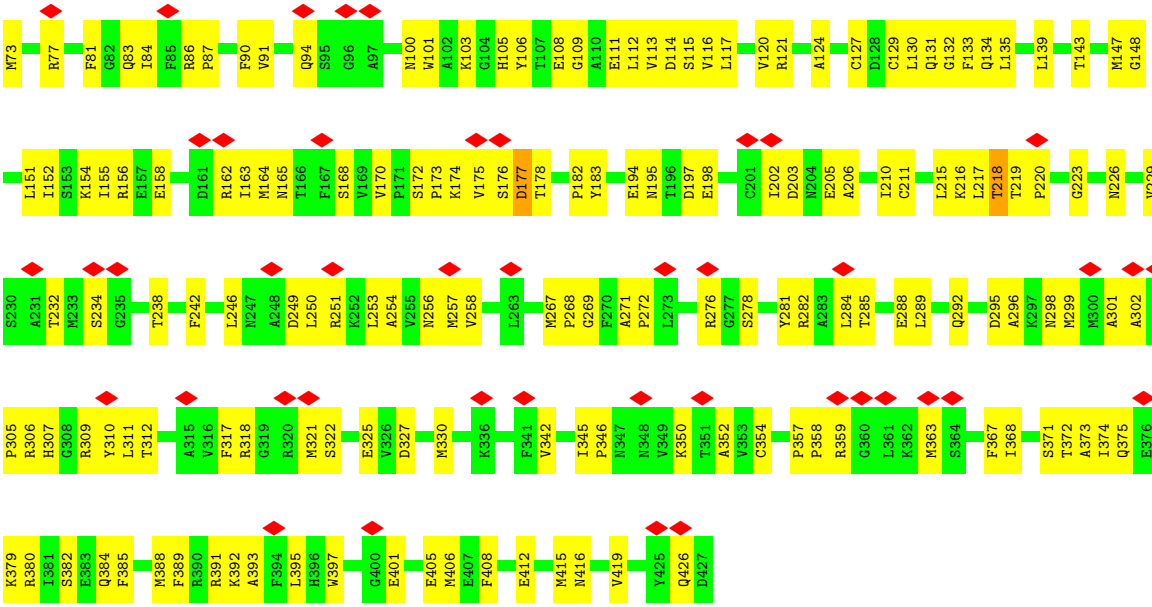


• Molecule 3: Tubulin beta-4B chain

Chain JL:

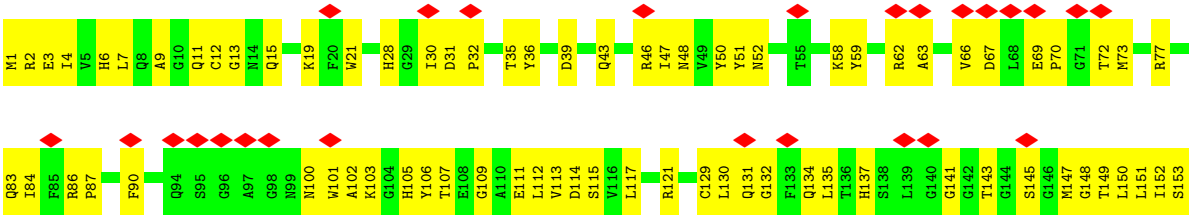






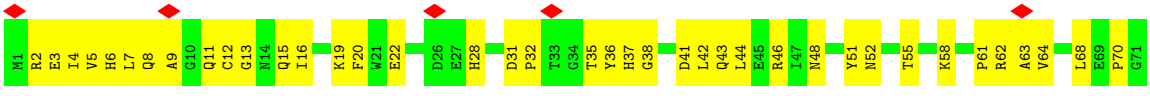
• Molecule 3: Tubulin beta-4B chain

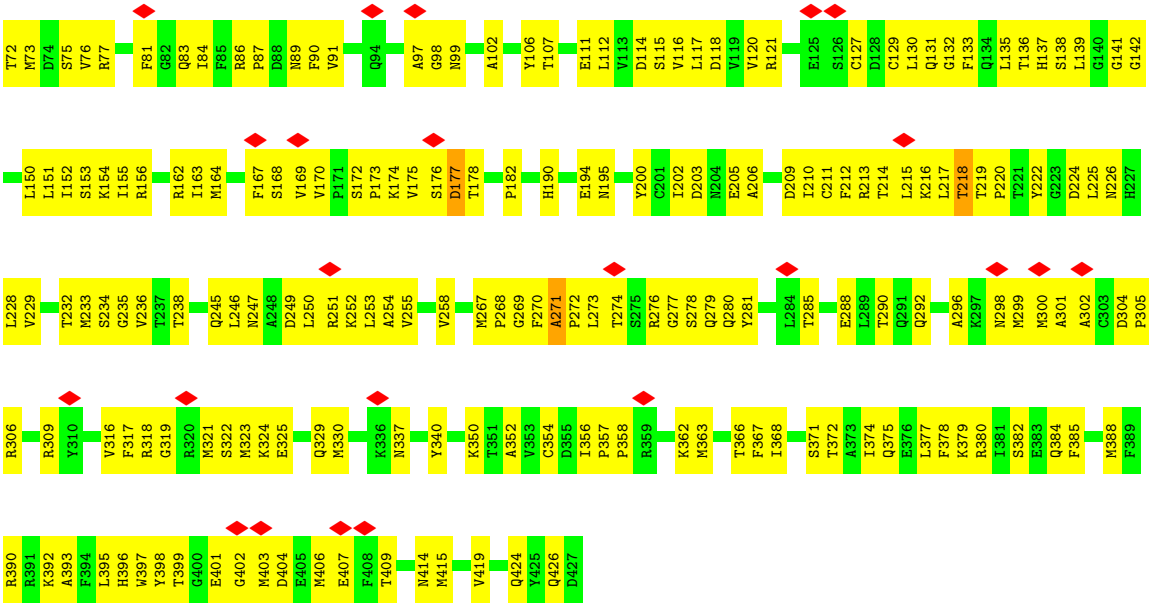
Chain KB:



• Molecule 3: Tubulin beta-4B chain

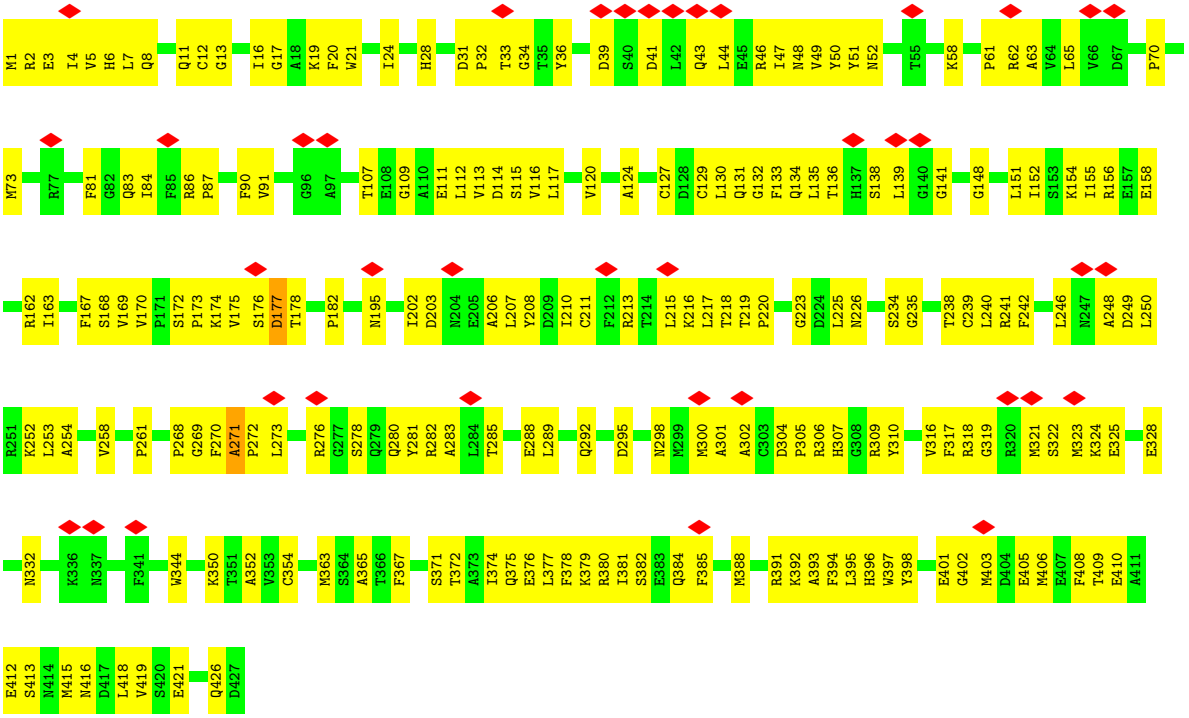
Chain KD:





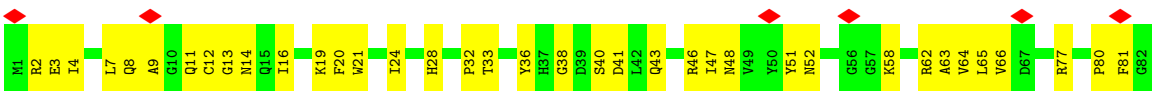
• Molecule 3: Tubulin beta-4B chain

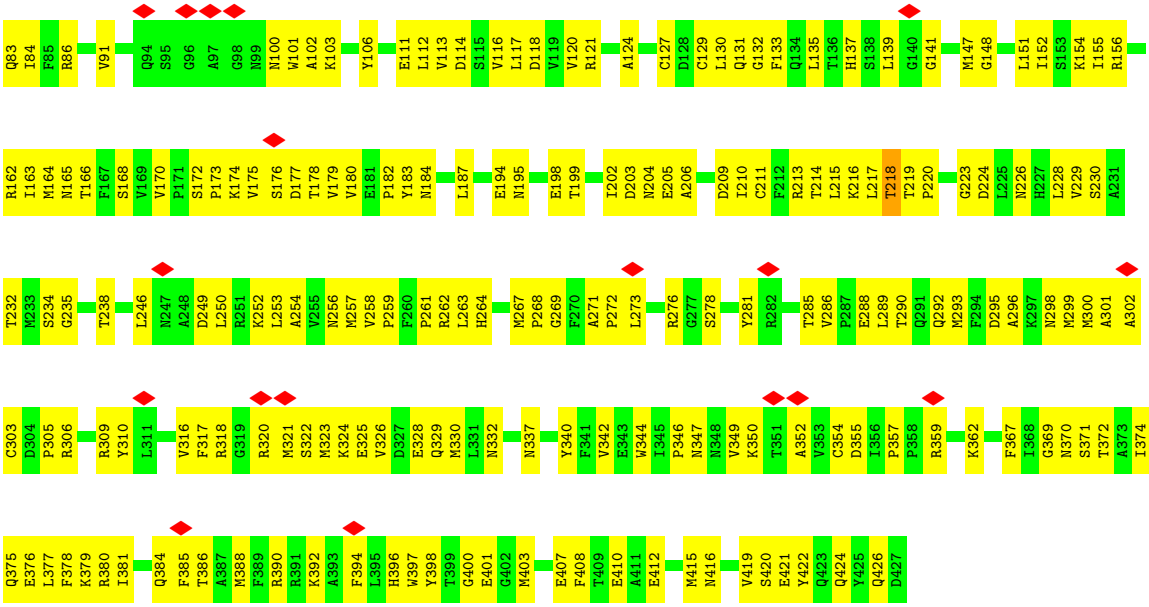
Chain KF:



• Molecule 3: Tubulin beta-4B chain

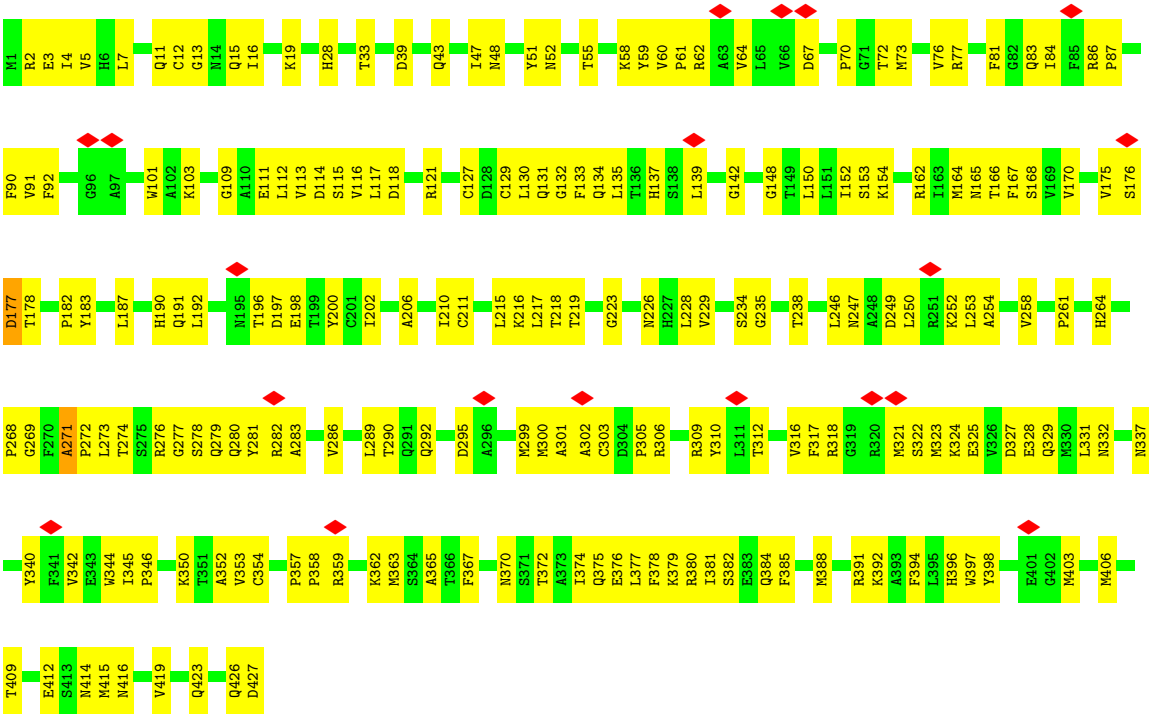
Chain KH:





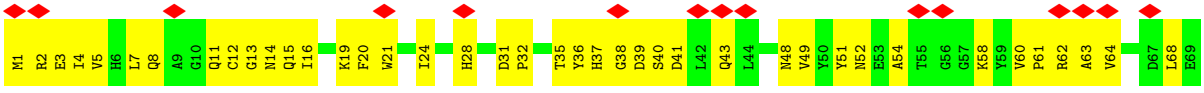
• Molecule 3: Tubulin beta-4B chain

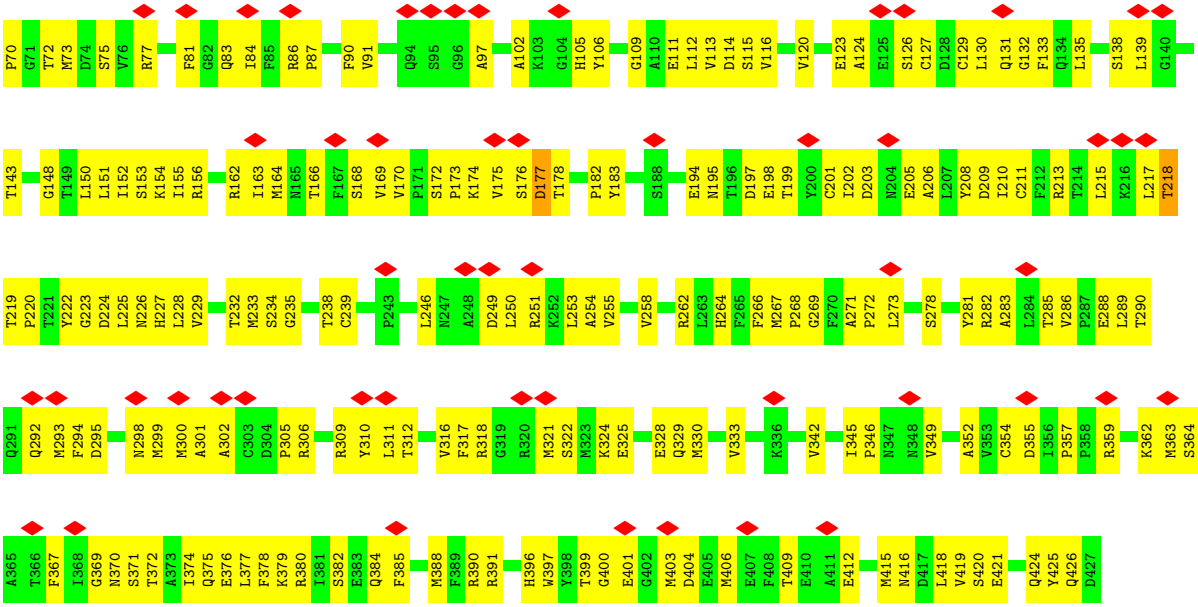
Chain KJ:



• Molecule 3: Tubulin beta-4B chain

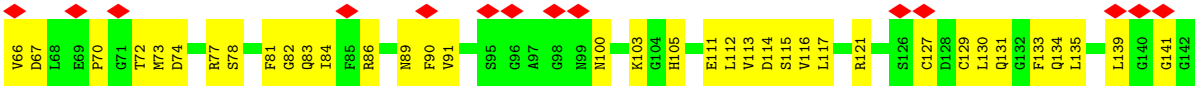
Chain KL:

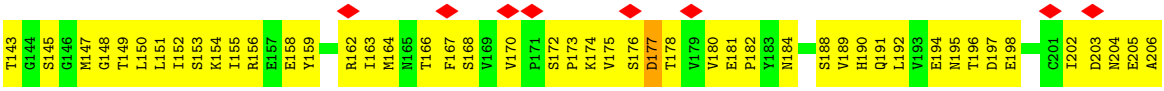


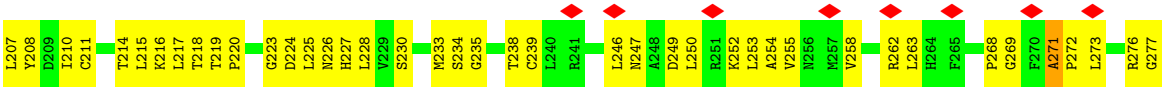


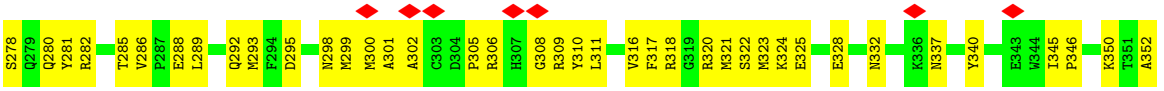
• Molecule 3: Tubulin beta-4B chain

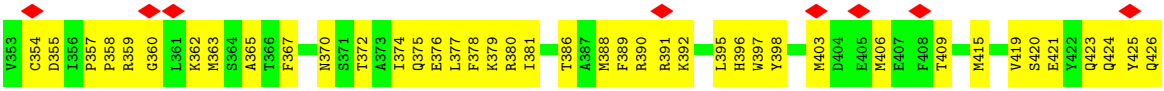
Chain LB:





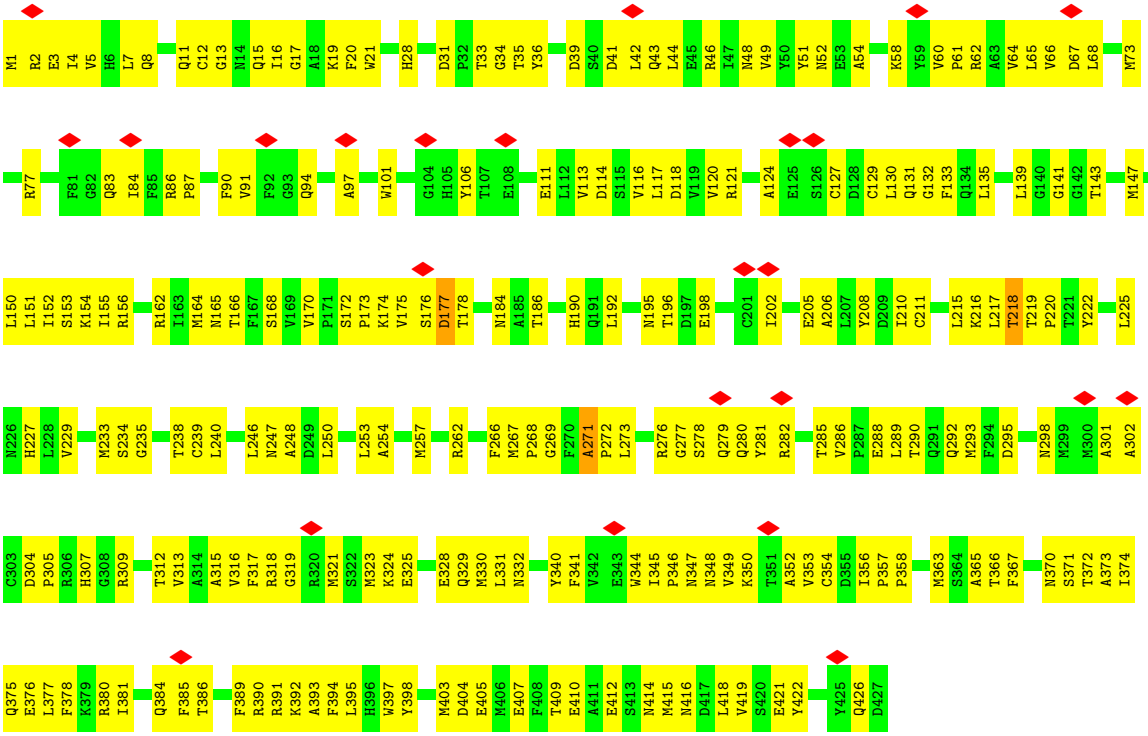






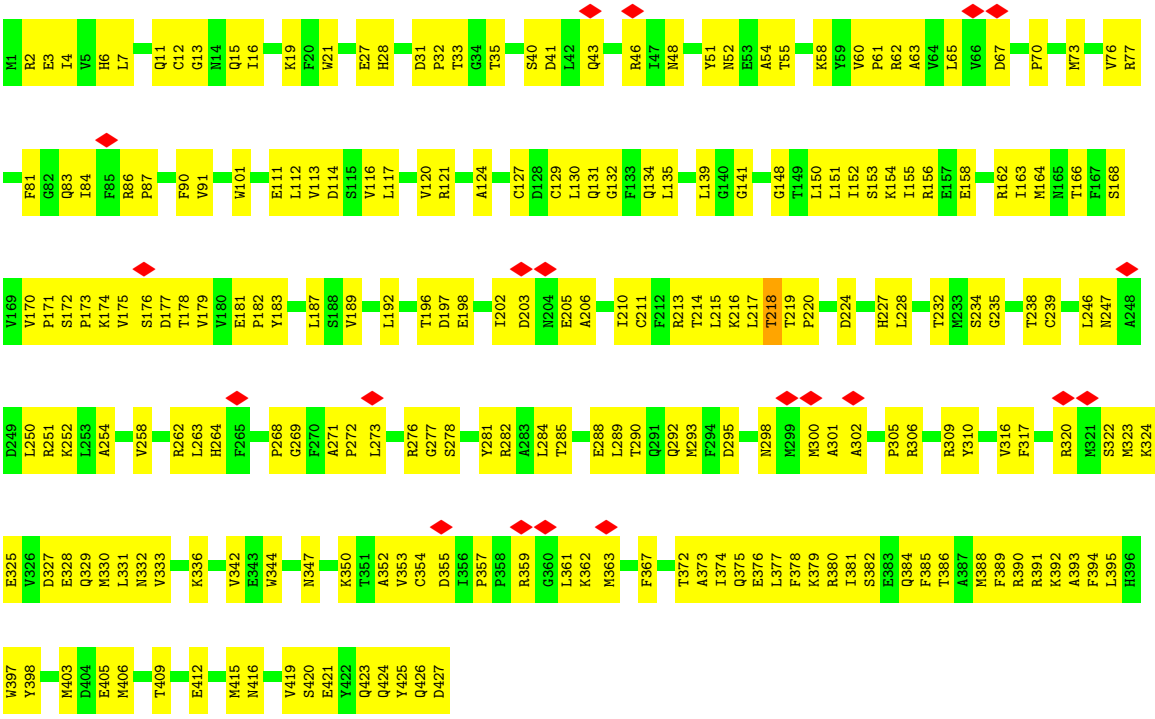
• Molecule 3: Tubulin beta-4B chain

Chain LD:



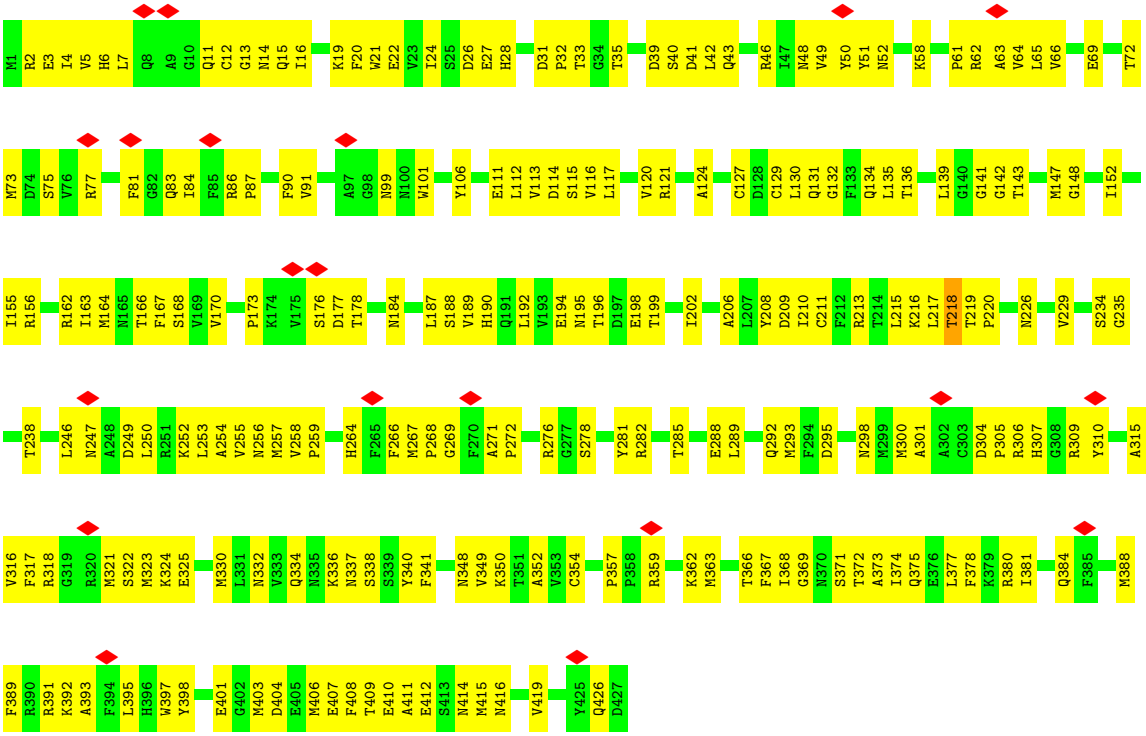
• Molecule 3: Tubulin beta-4B chain

Chain LF:



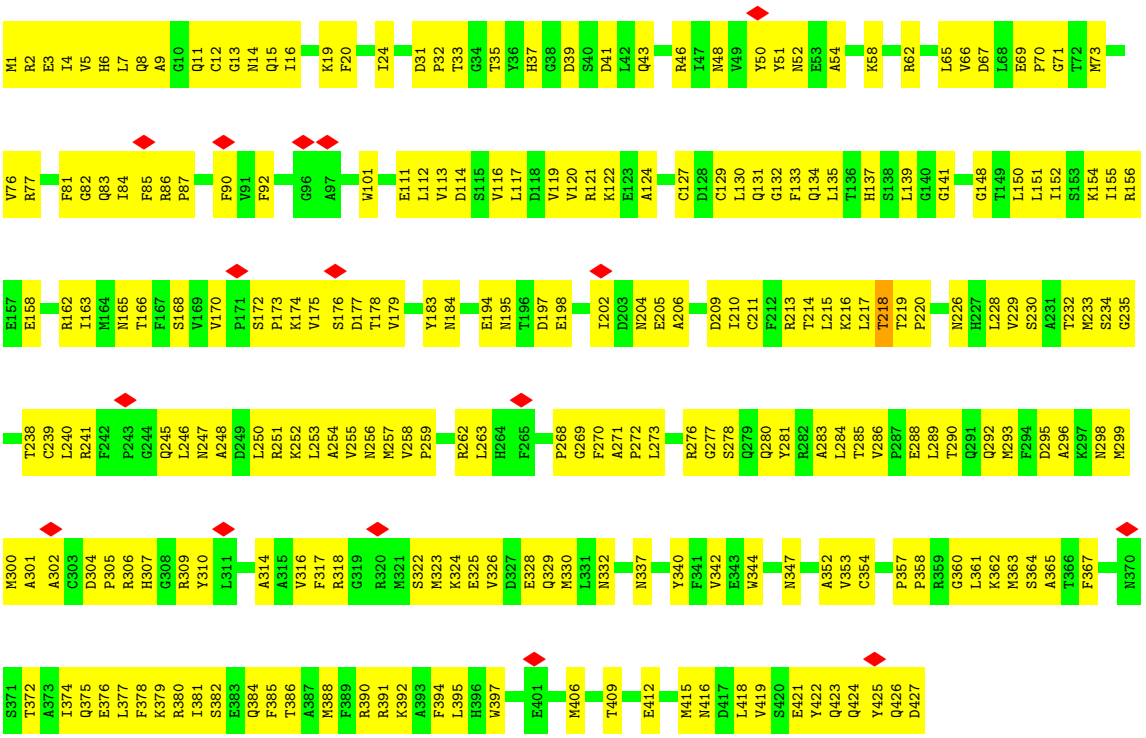
• Molecule 3: Tubulin beta-4B chain

Chain LH:



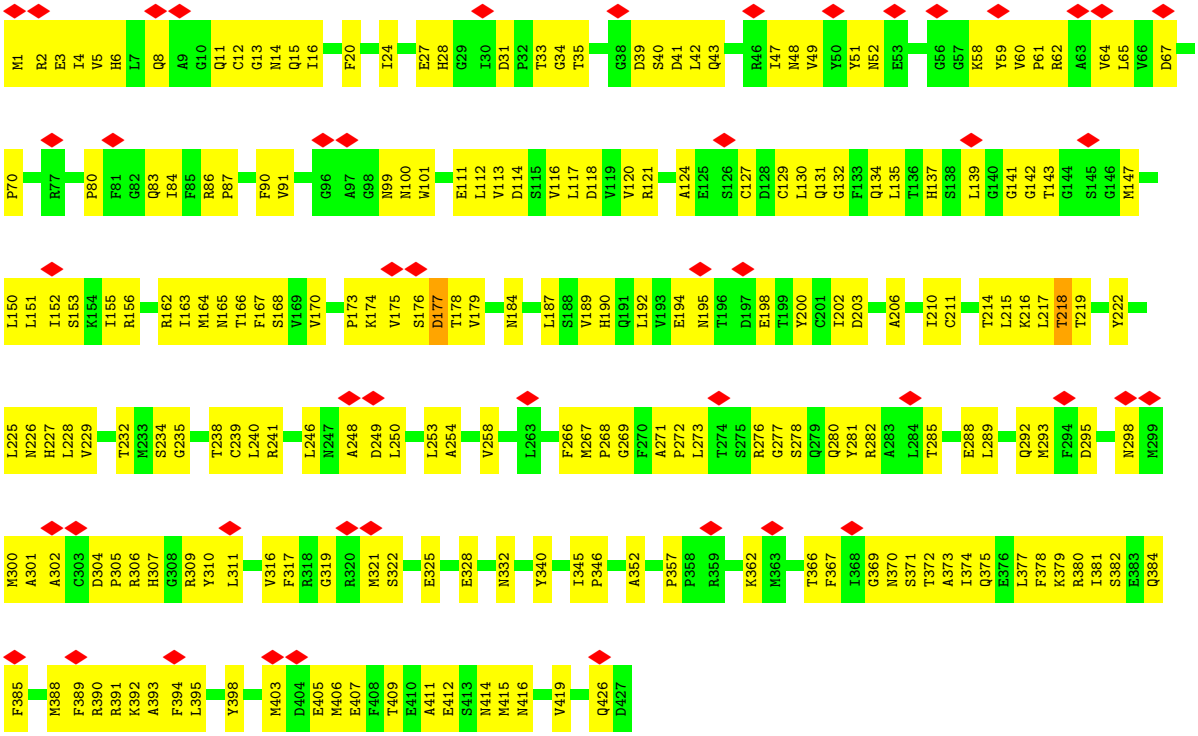
• Molecule 3: Tubulin beta-4B chain

Chain LJ:



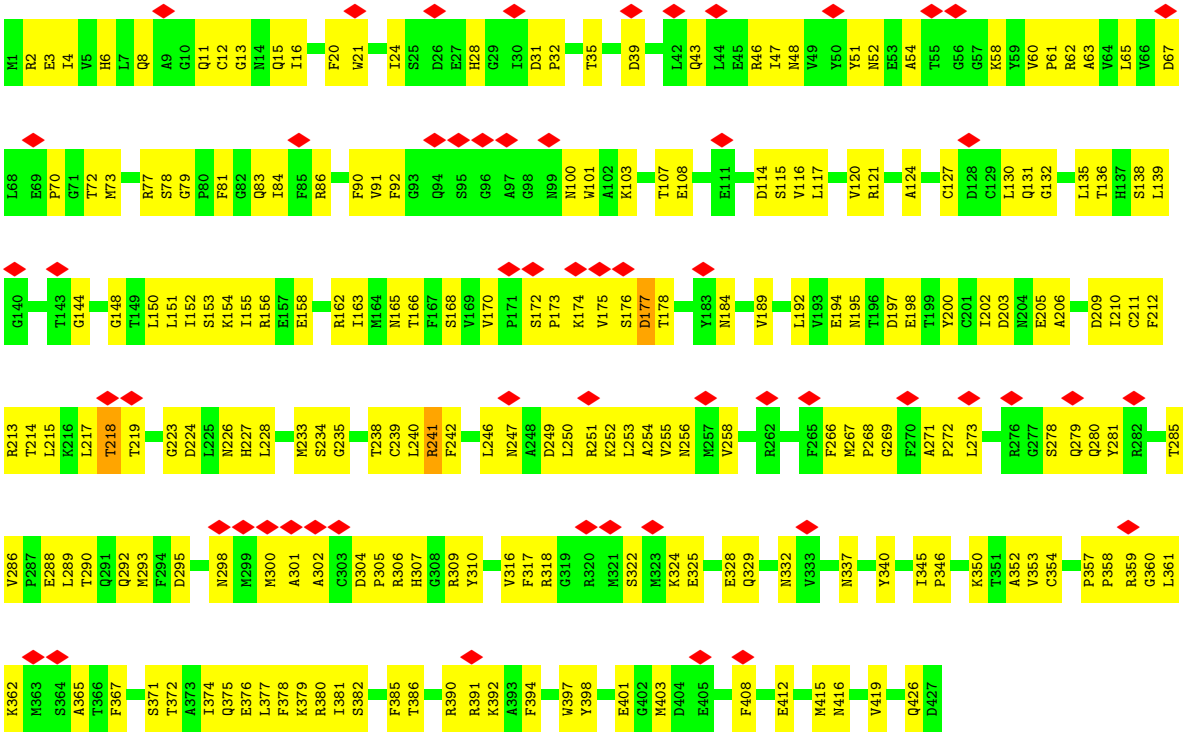
• Molecule 3: Tubulin beta-4B chain

Chain LL:



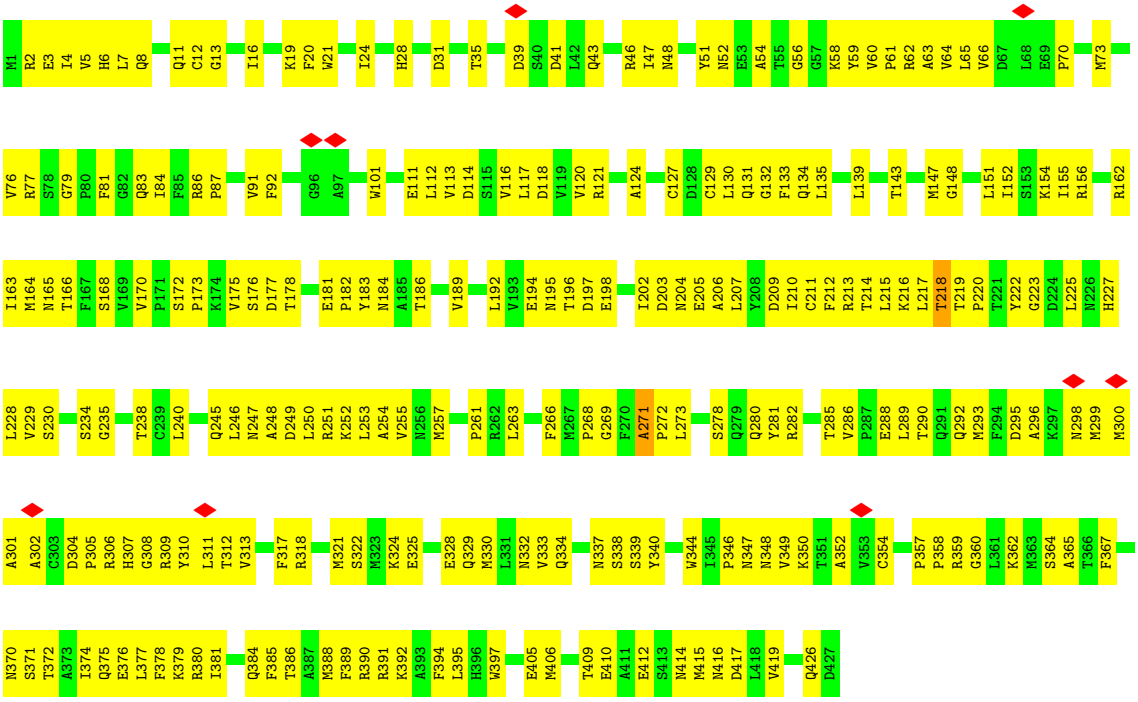
• Molecule 3: Tubulin beta-4B chain

Chain MB:



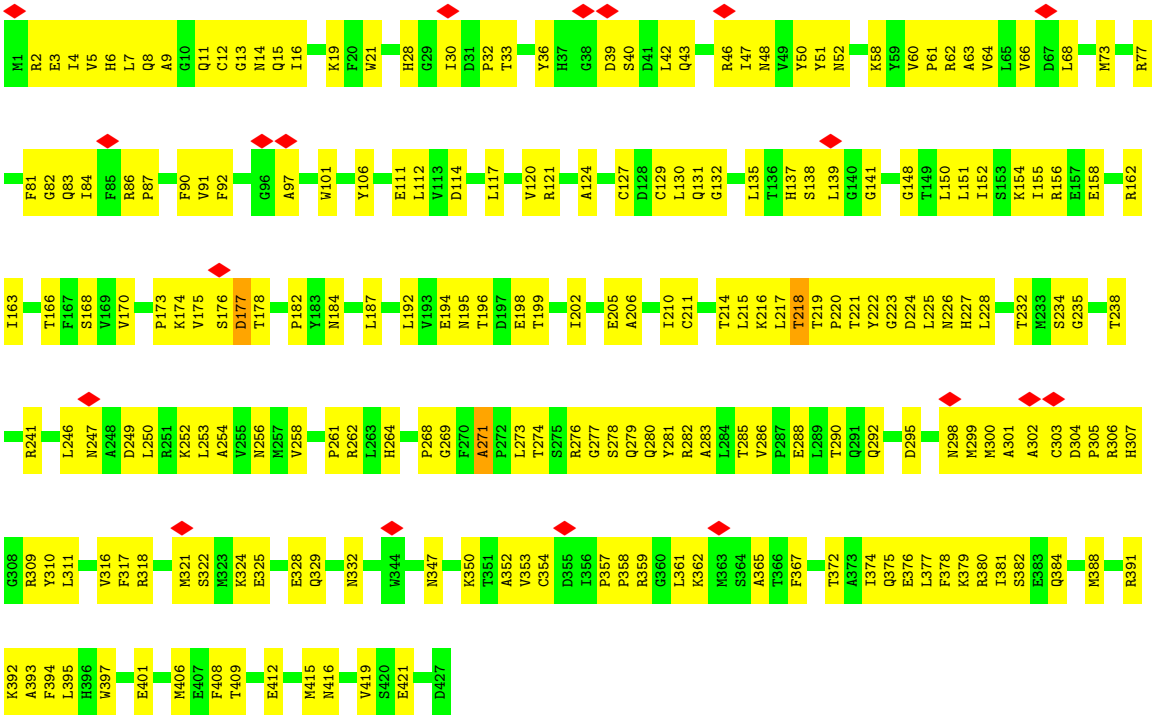
• Molecule 3: Tubulin beta-4B chain

Chain MD:



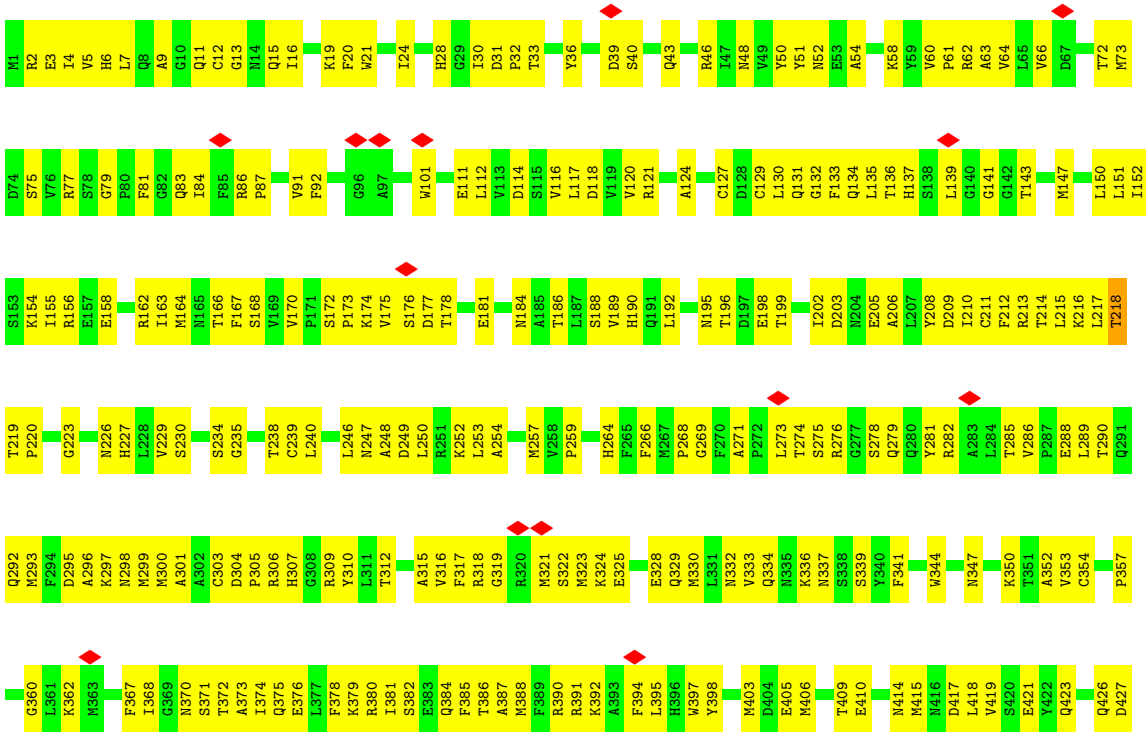
• Molecule 3: Tubulin beta-4B chain

Chain MF:



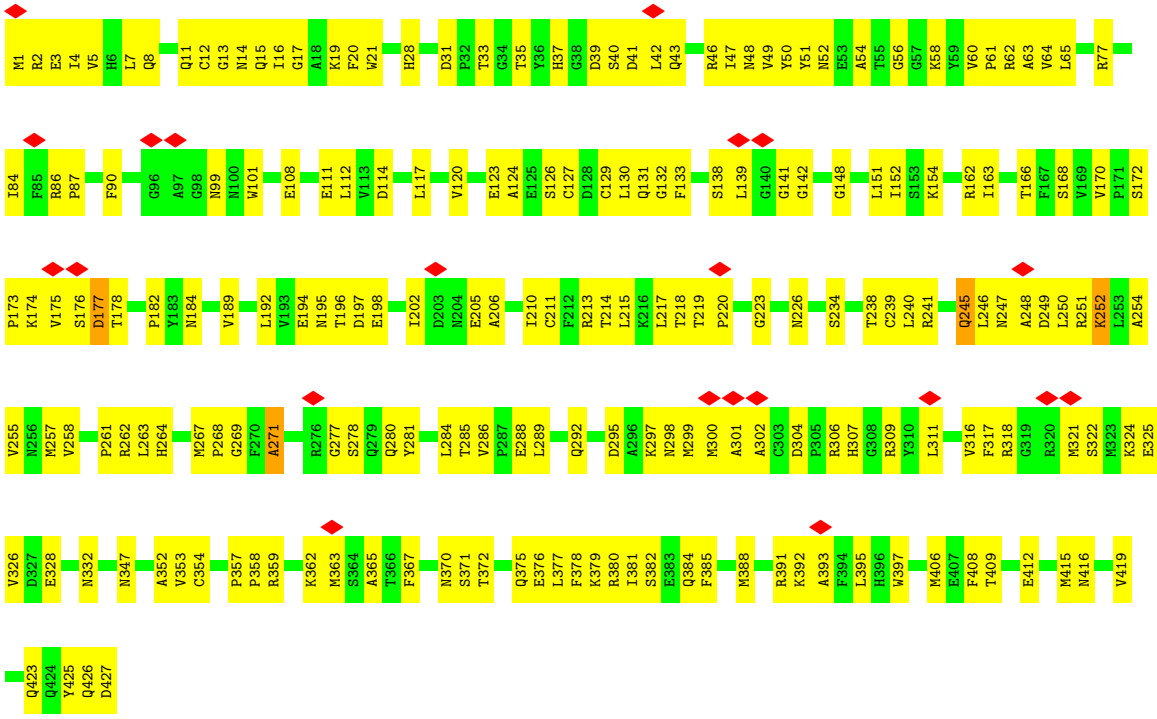
• Molecule 3: Tubulin beta-4B chain

Chain MH:



• Molecule 3: Tubulin beta-4B chain

Chain MJ:



• Molecule 3: Tubulin beta-4B chain

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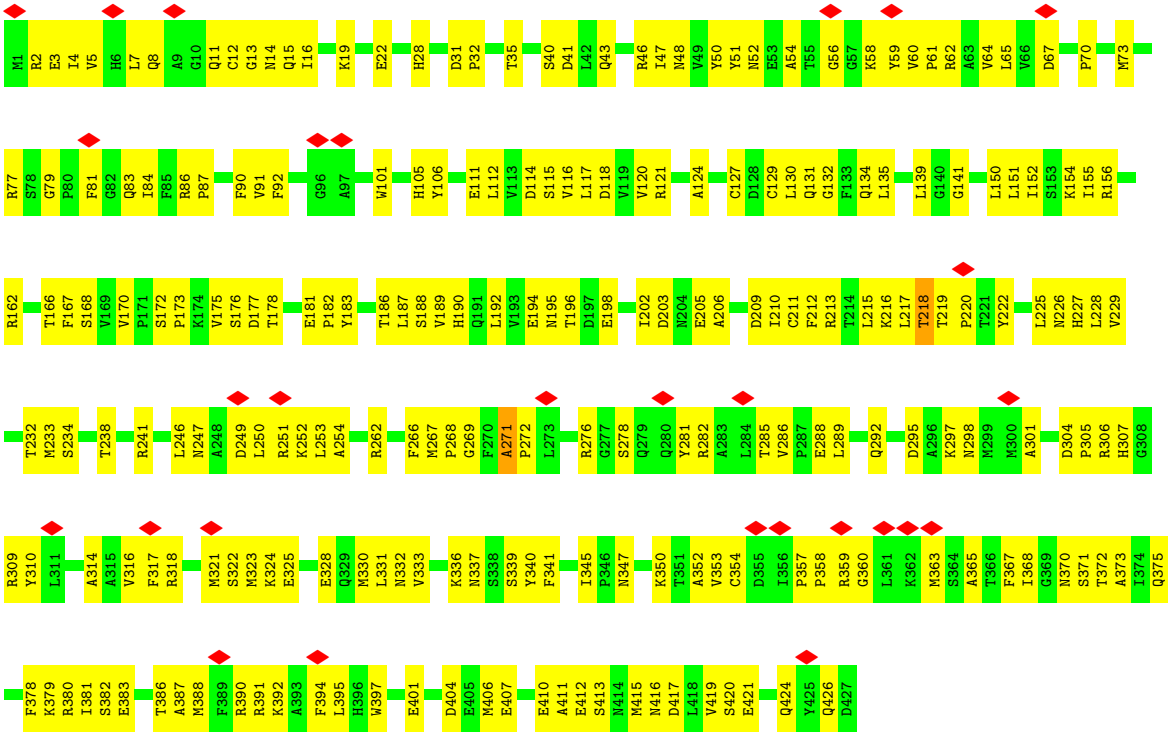

• Molecule 3: Tubulin beta-4B chain

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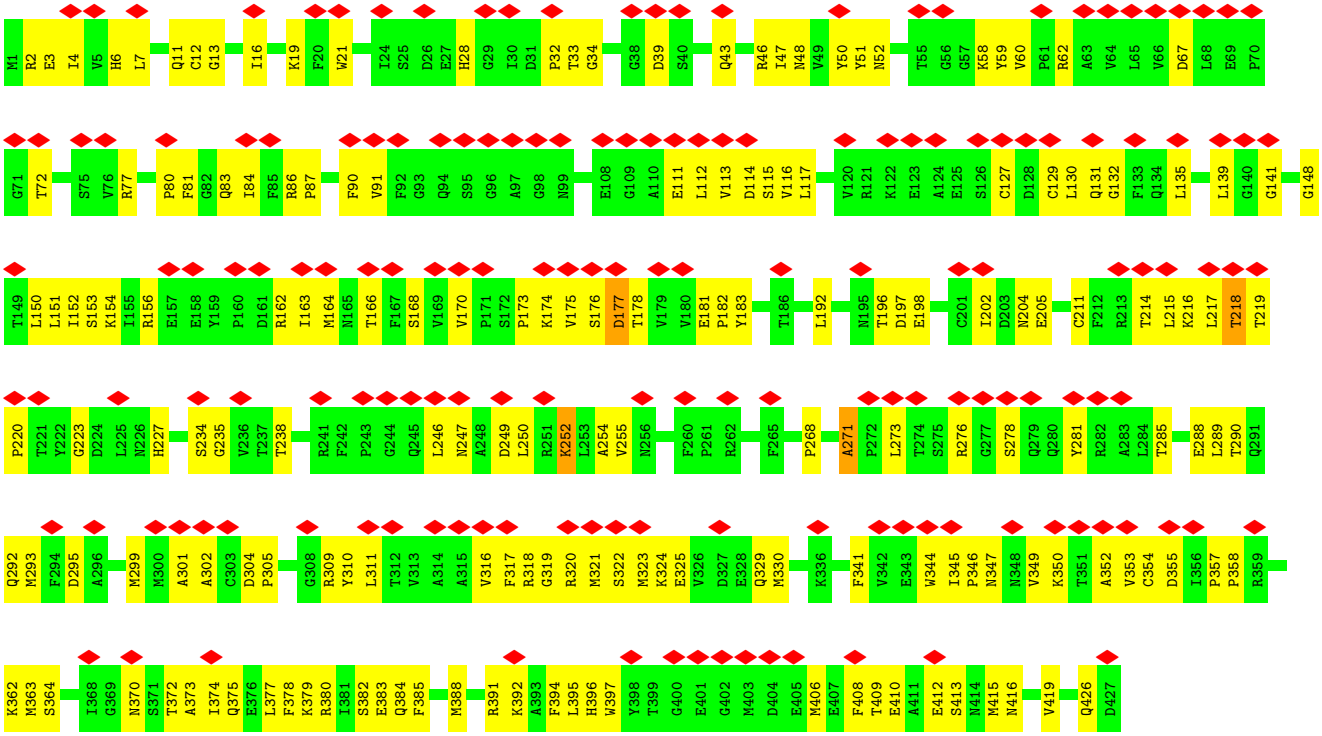
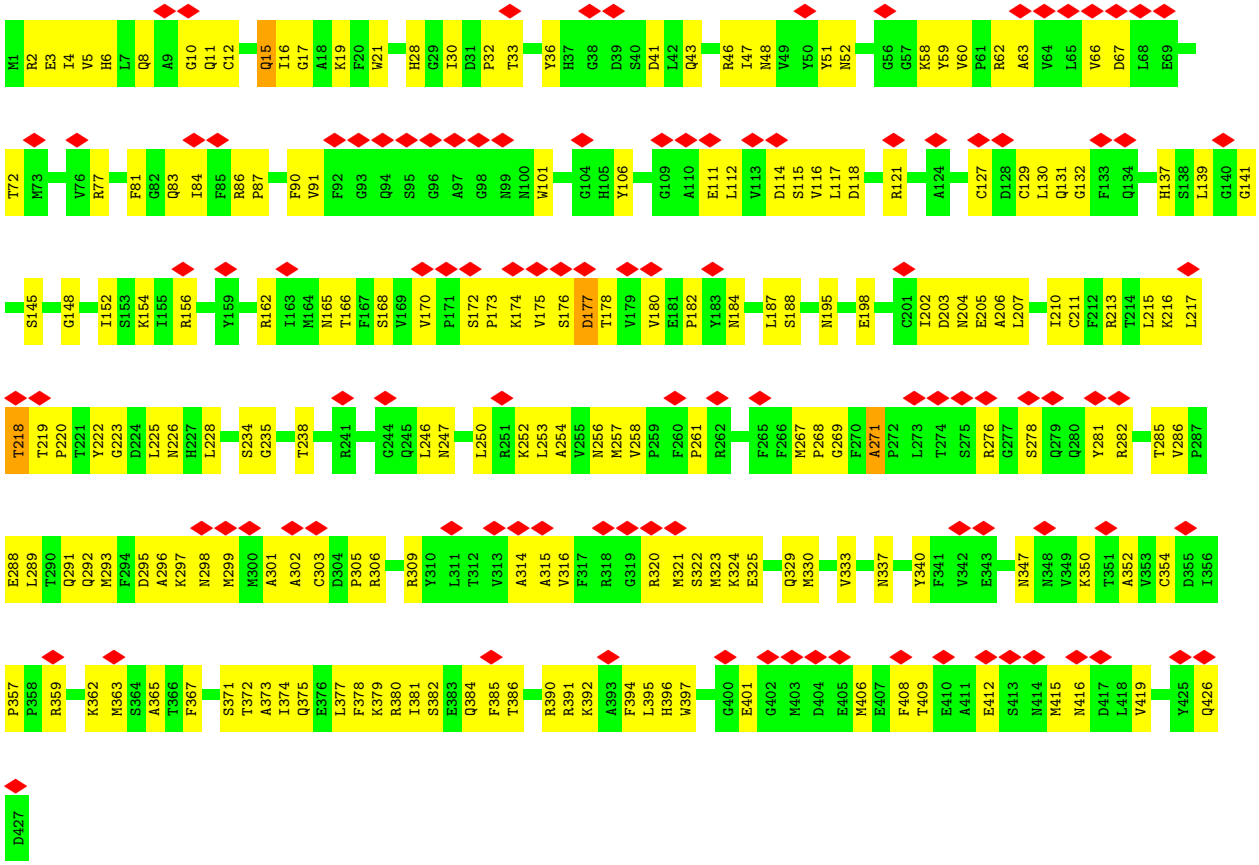


• Molecule 3: Tubulin beta-4B chain

Chain ND:



• Molecule 3: Tubulin beta-4B chain

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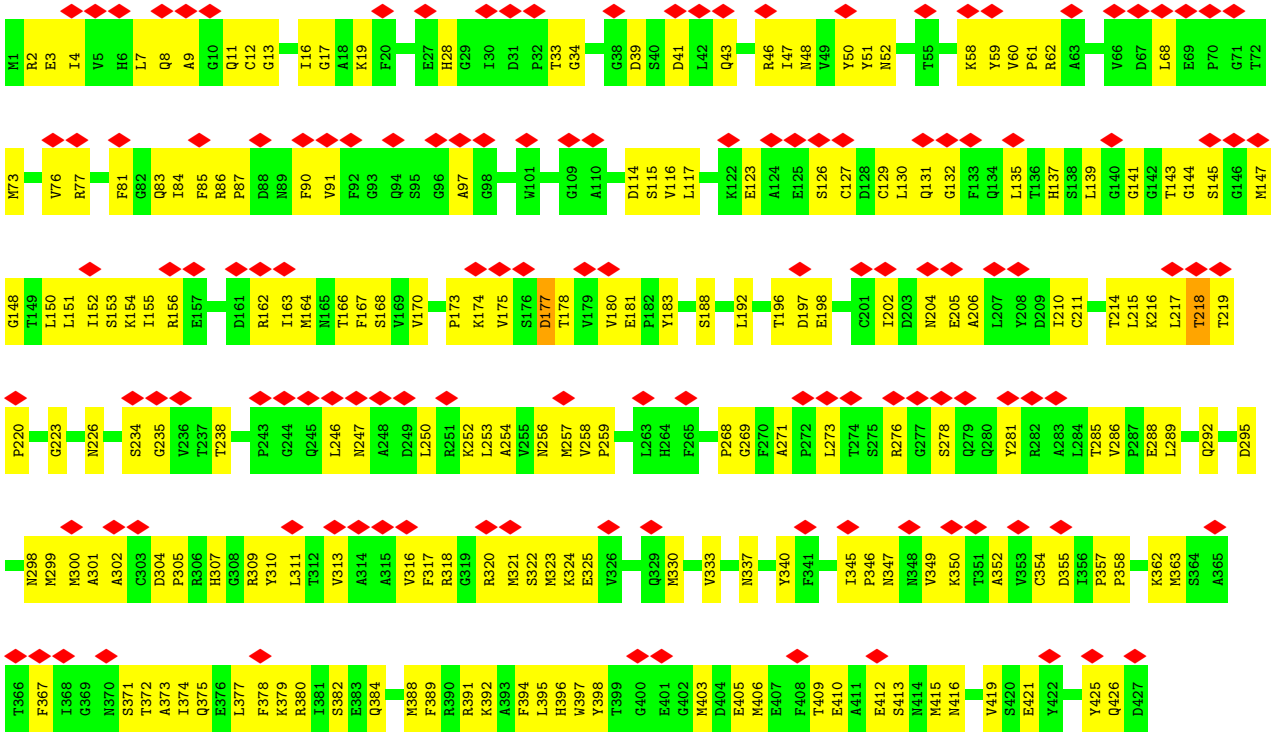
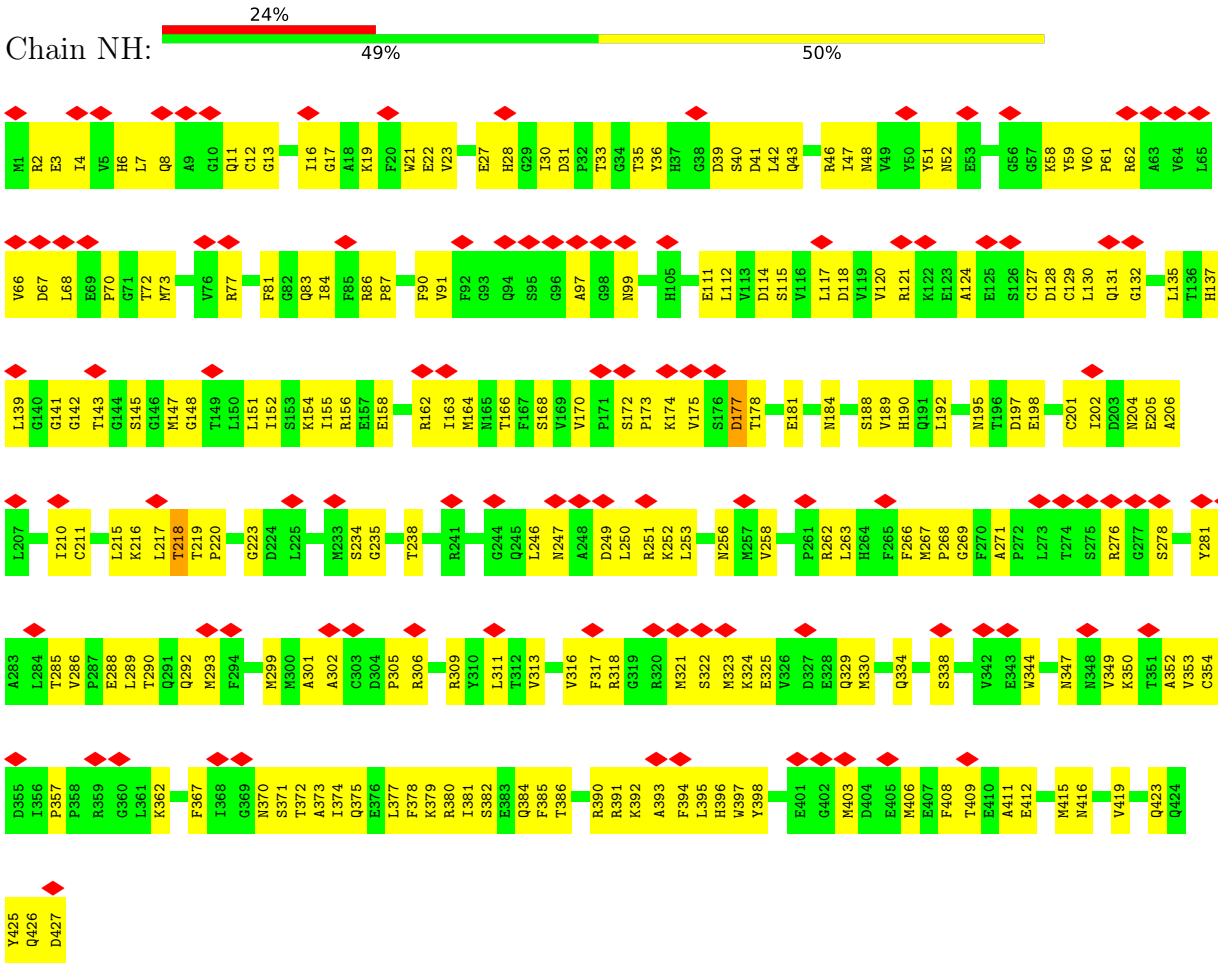


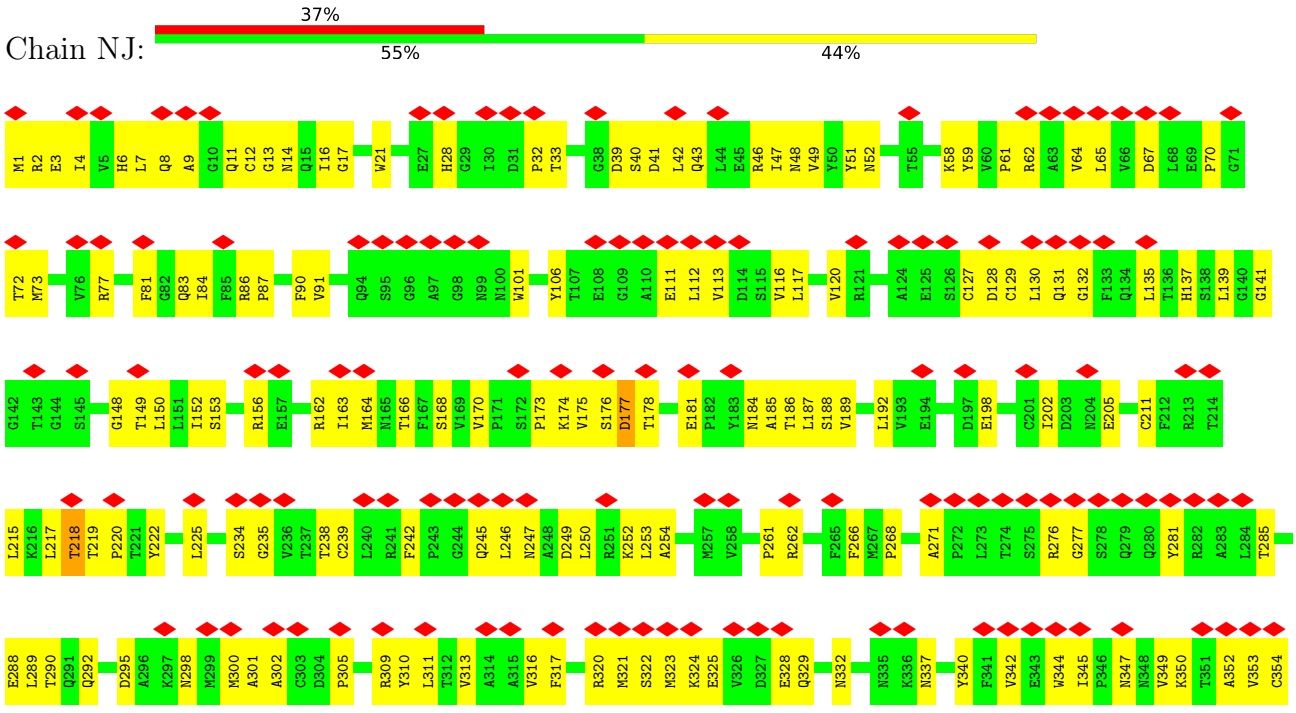
• Molecule 3: Tubulin beta-4B chain

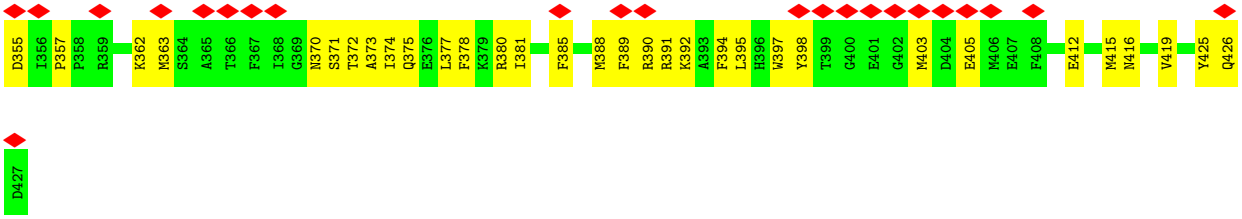
Chain NH:



• Molecule 3: Tubulin beta-4B chain

Chain NJ:





• Molecule 3: Tubulin beta-4B chain

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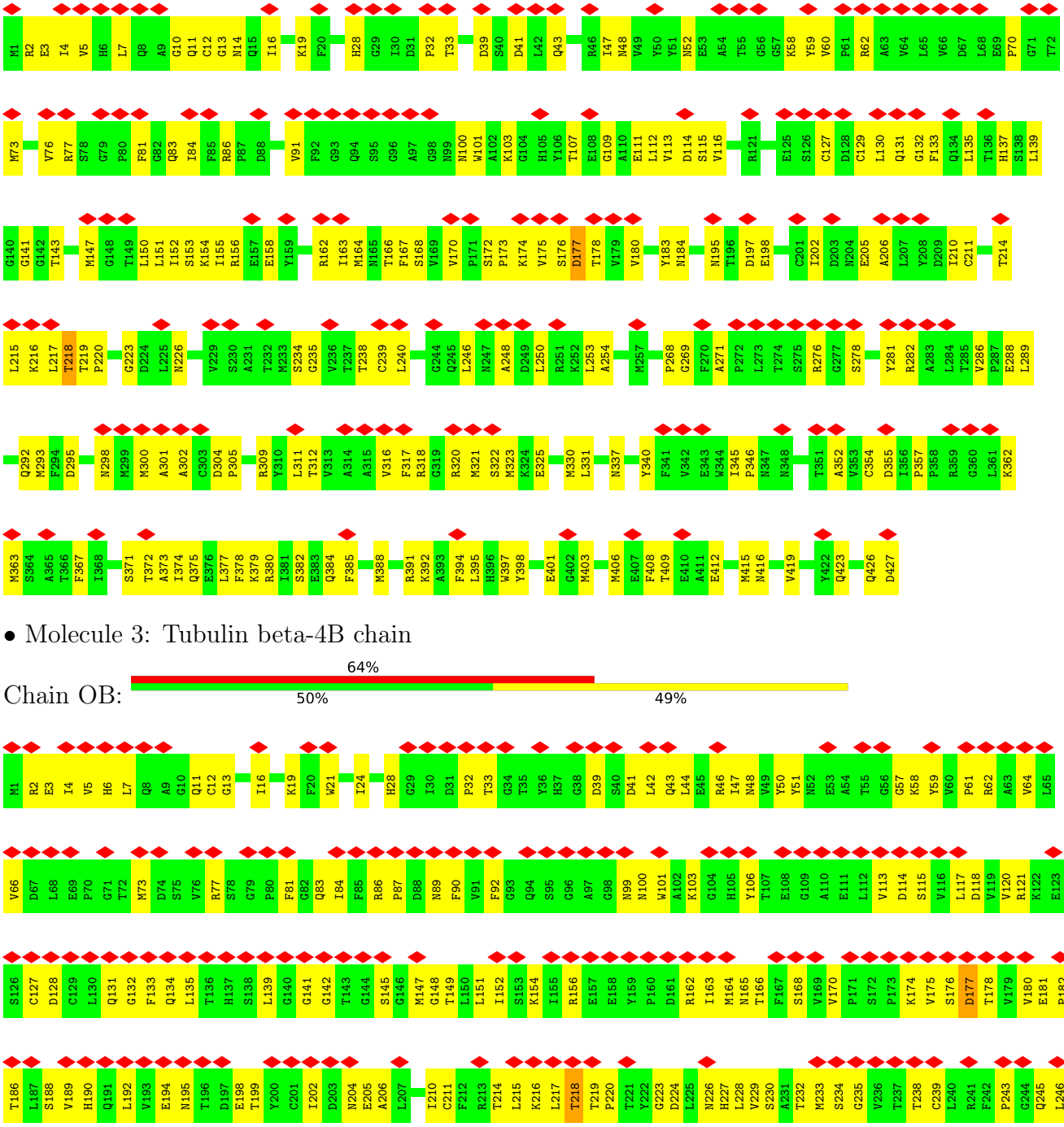

• Molecule 3: Tubulin beta-4B chain

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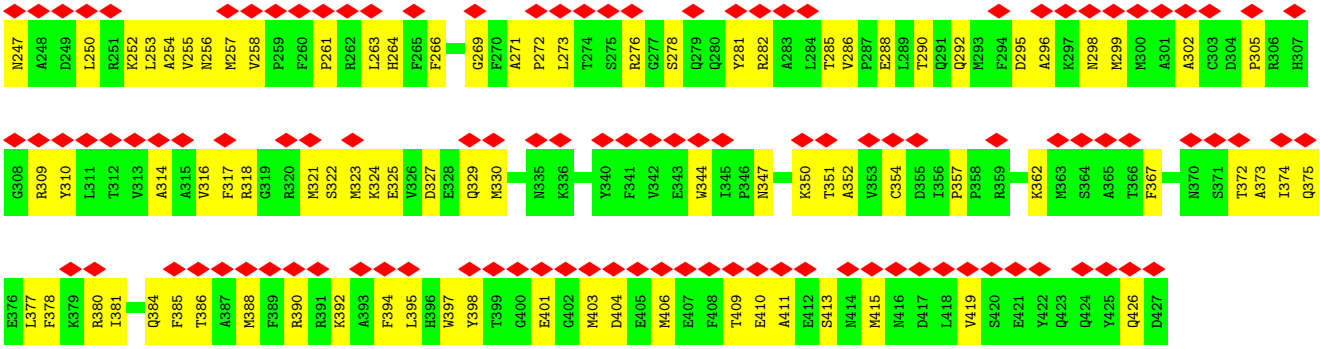
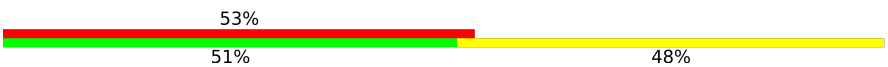


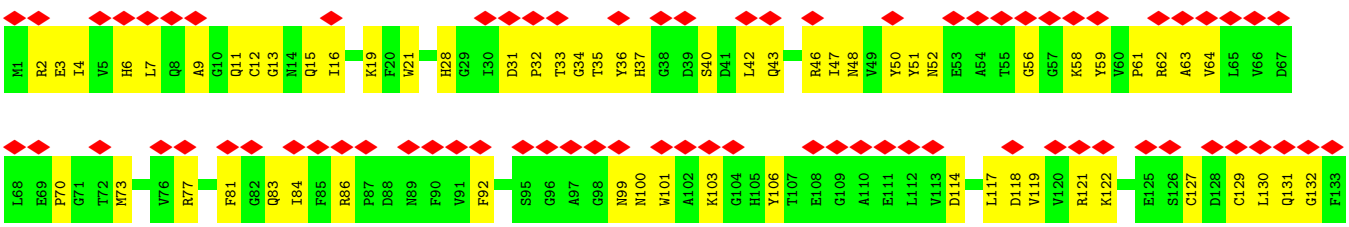
• Molecule 3: Tubulin beta-4B chain

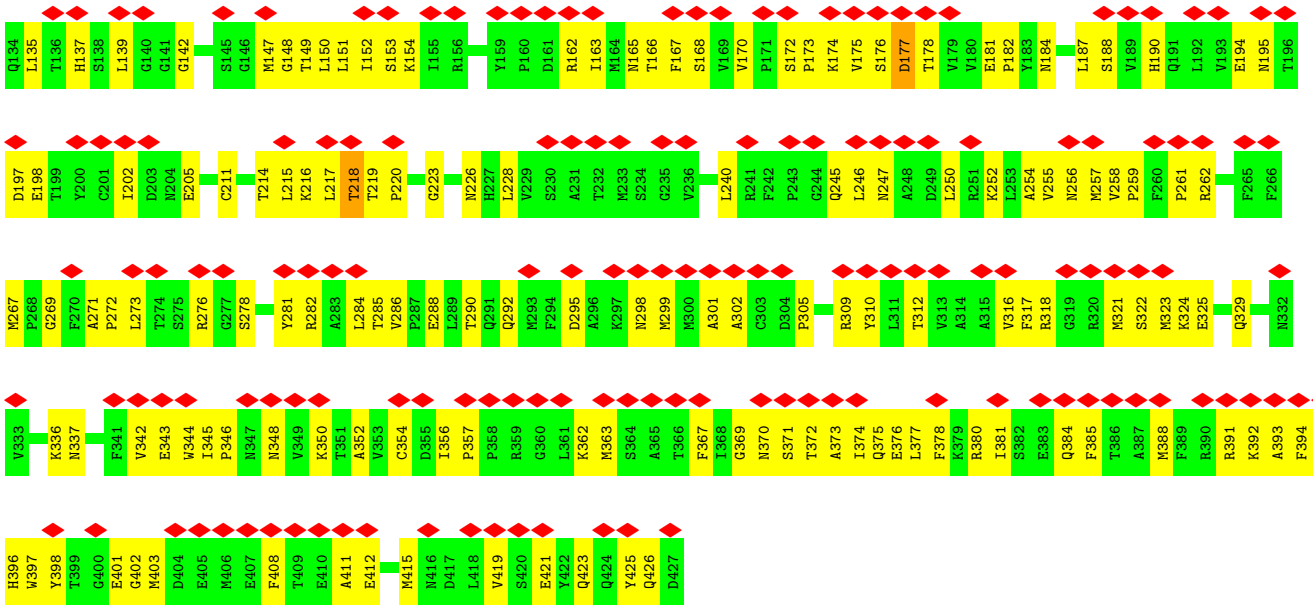
Chain OD:

• Molecule 3: Tubulin beta-4B chain

Chain OF:

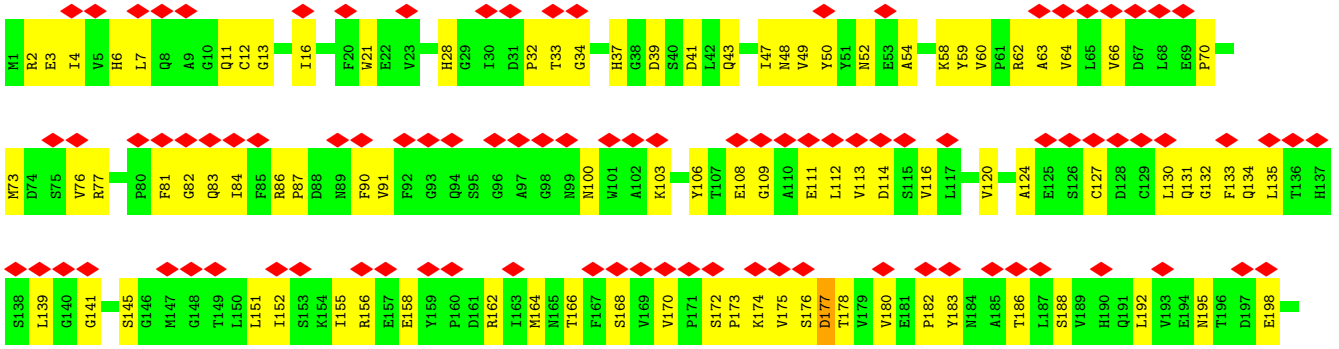






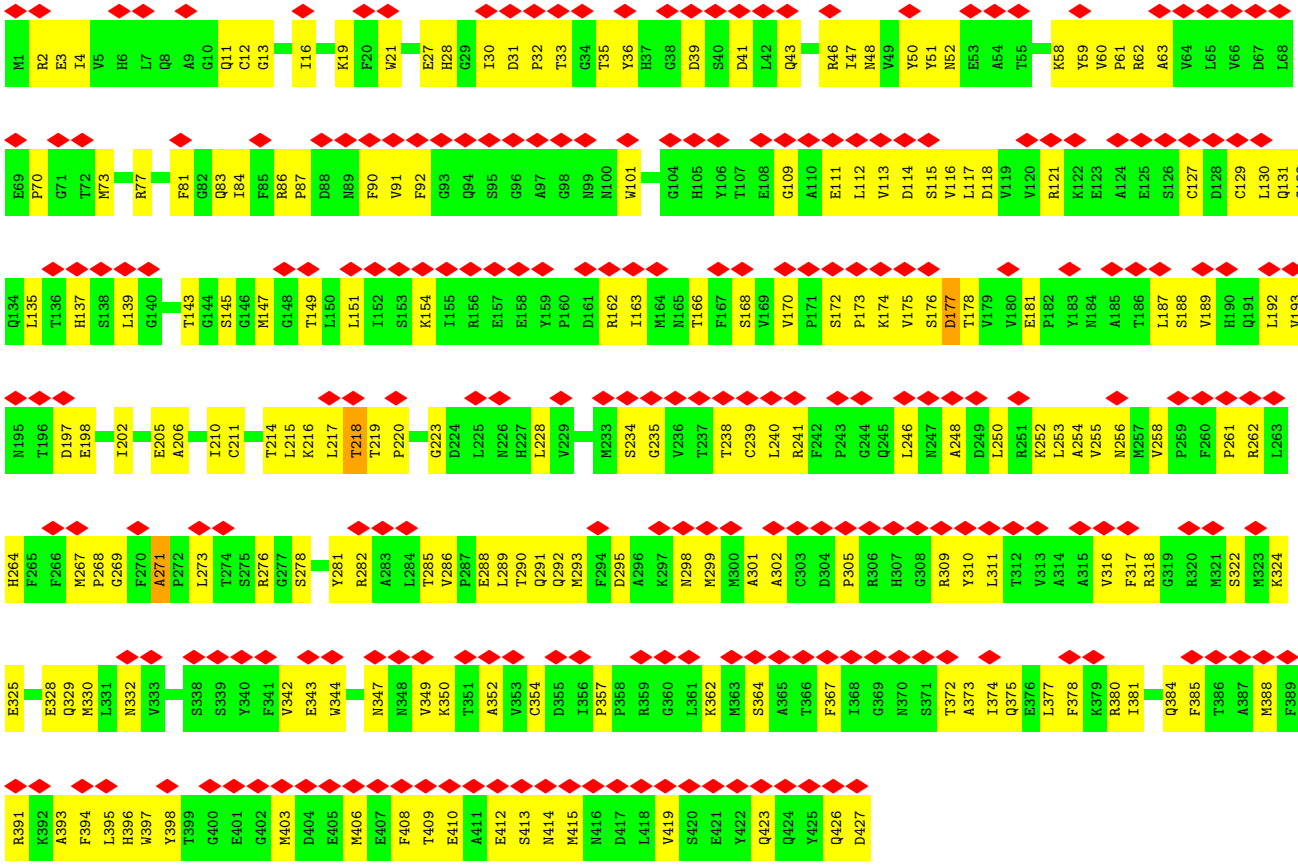
• Molecule 3: Tubulin beta-4B chain

Chain OH:



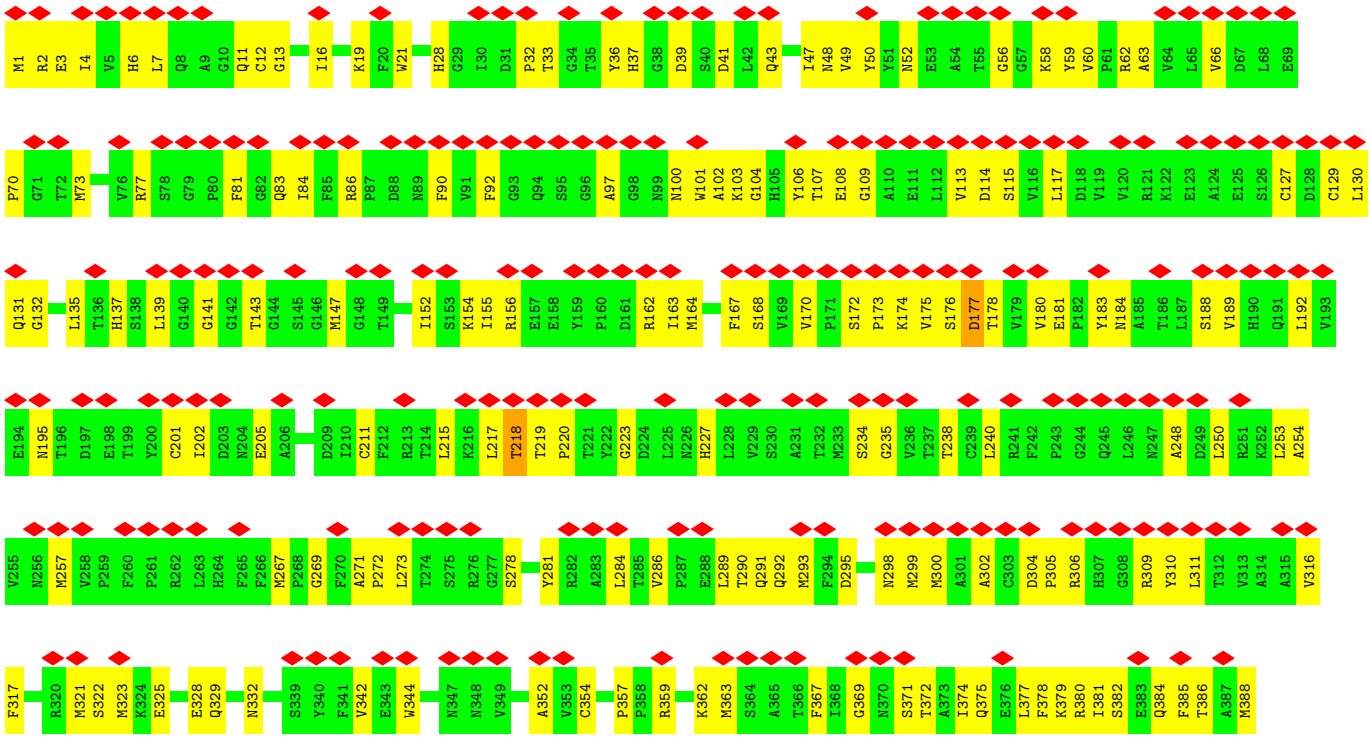
• Molecule 3: Tubulin beta-4B chain

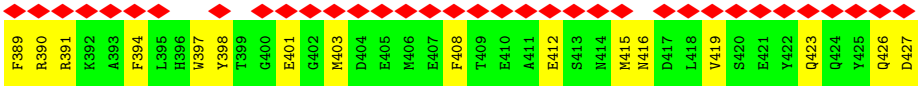
Chain OJ:



• Molecule 3: Tubulin beta-4B chain

Chain OL:



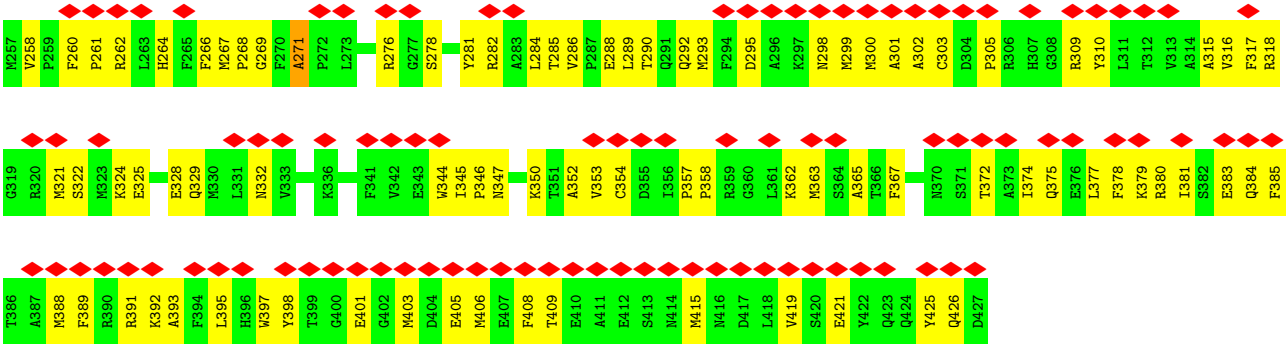


• Molecule 3: Tubulin beta-4B chain

Chain PB:

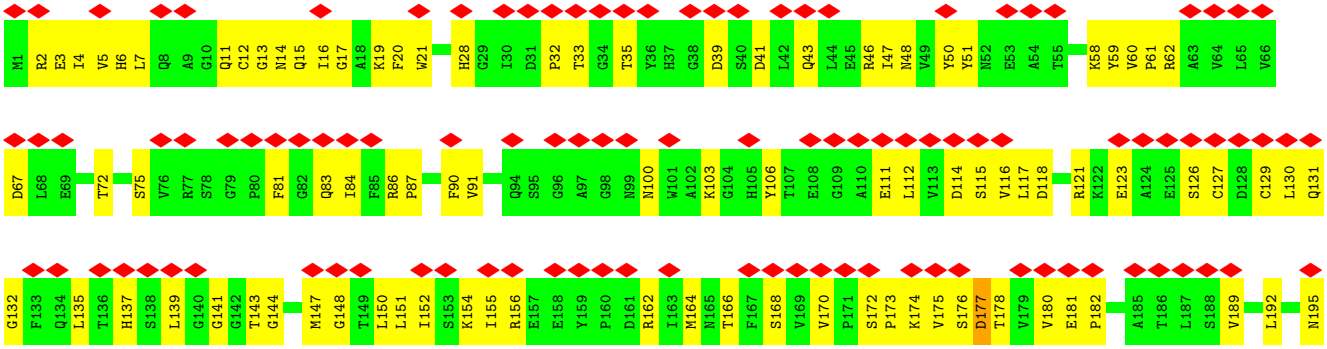
• Molecule 3: Tubulin beta-4B chain

Chain PD:



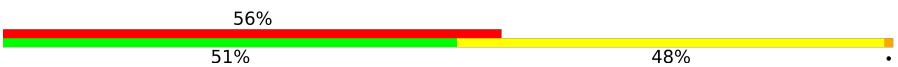
• Molecule 3: Tubulin beta-4B chain

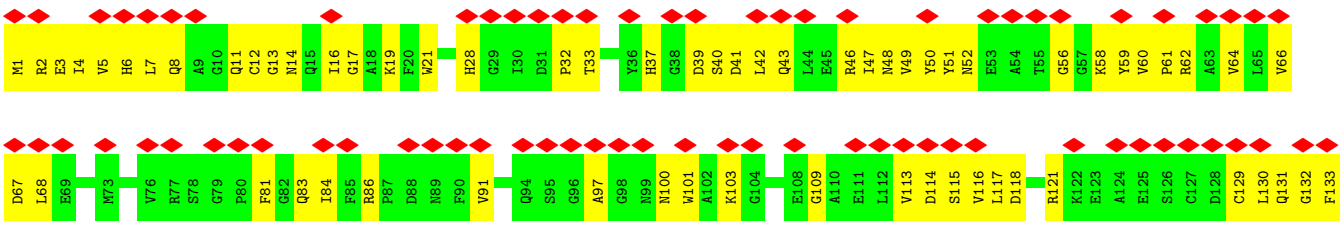
Chain PF:

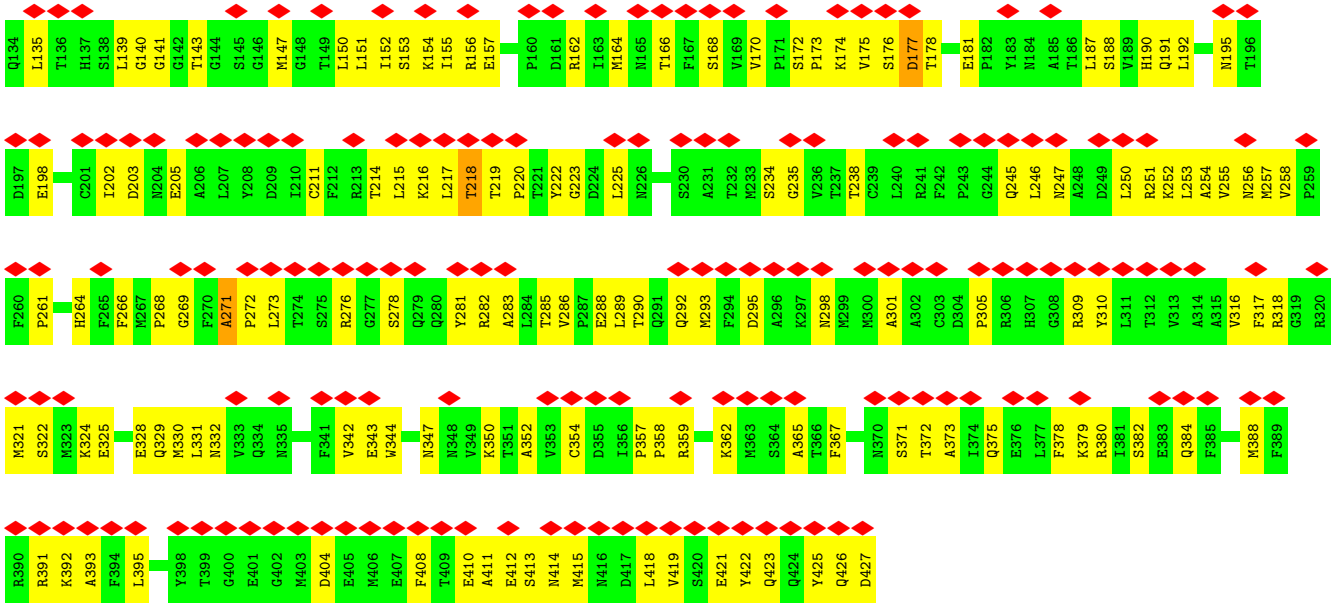


• Molecule 3: Tubulin beta-4B chain

Chain PH:

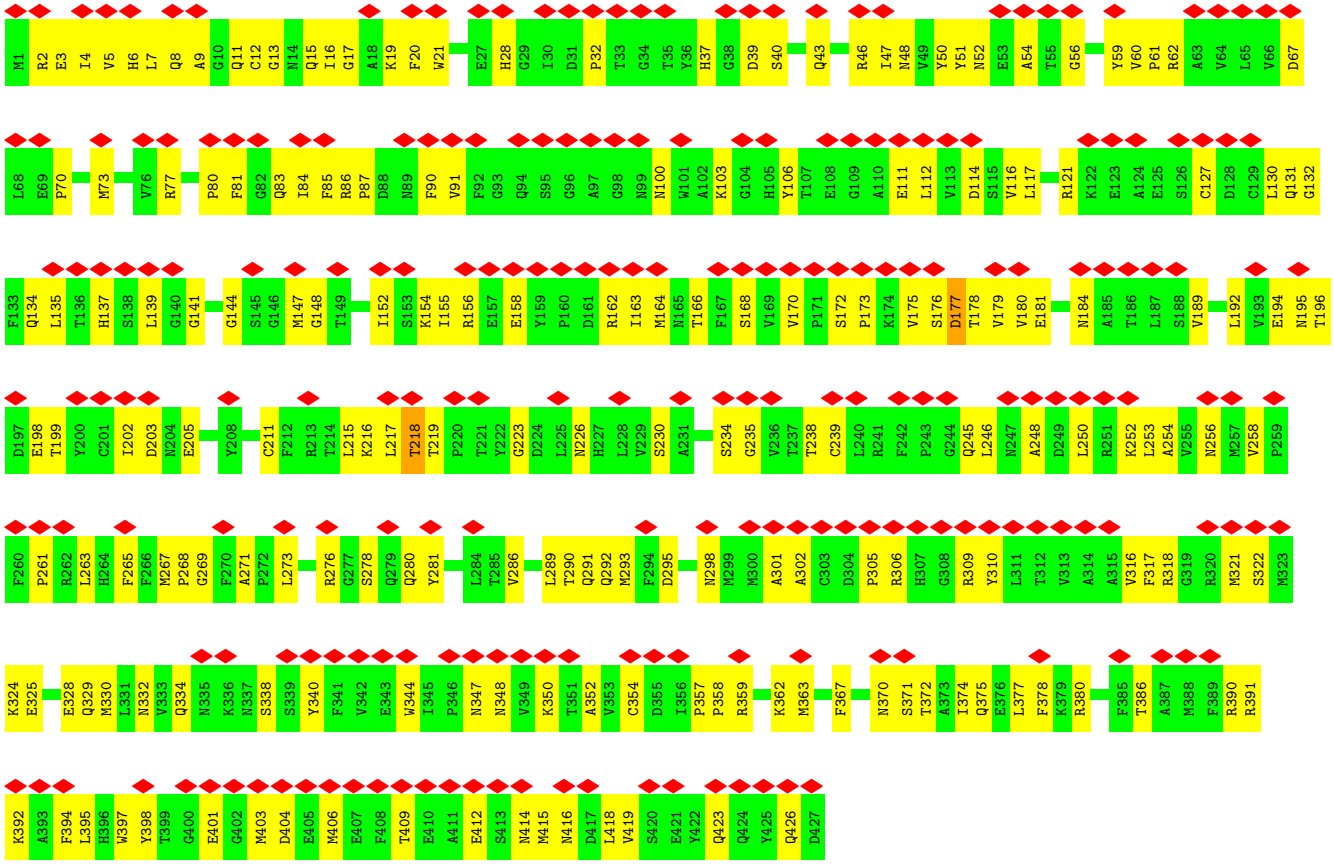






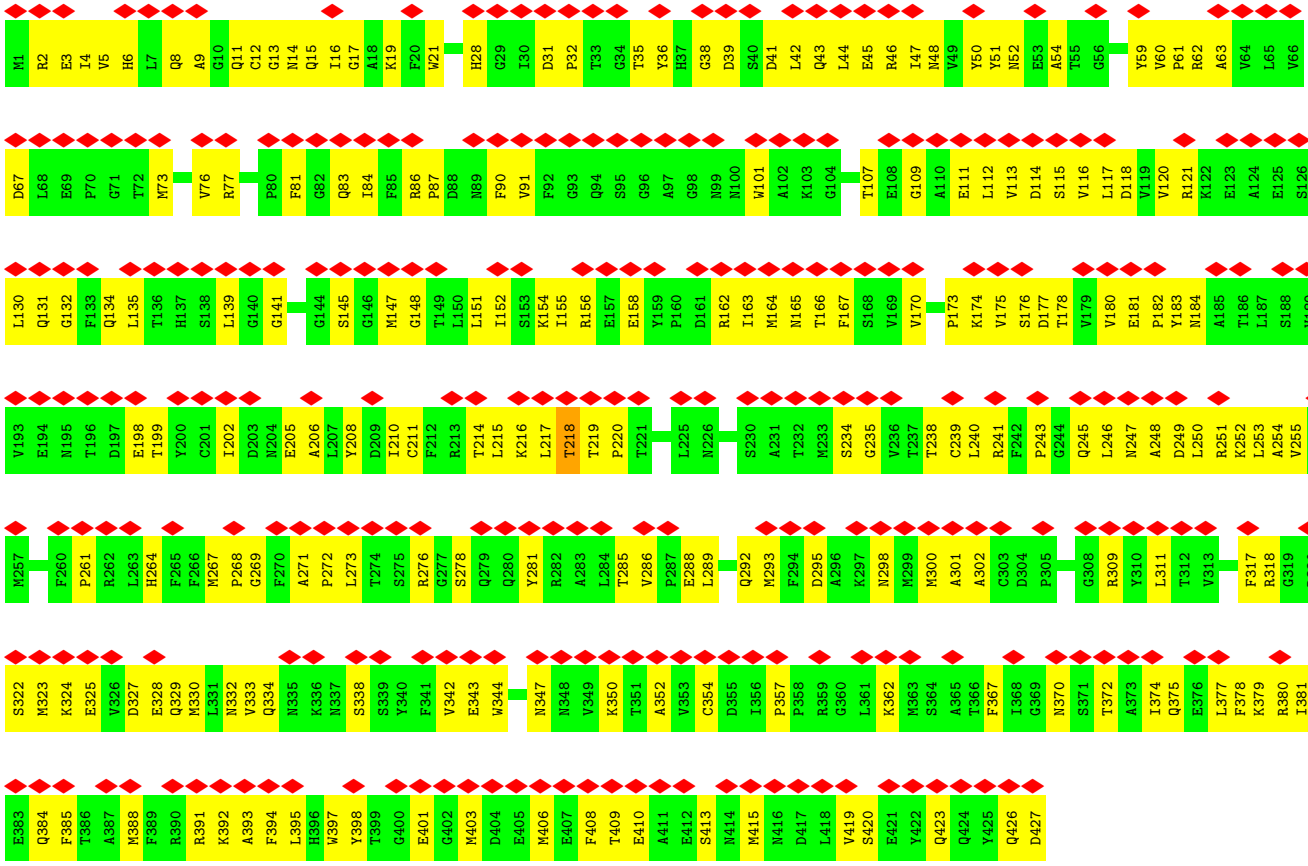
• Molecule 3: Tubulin beta-4B chain

Chain PJ:



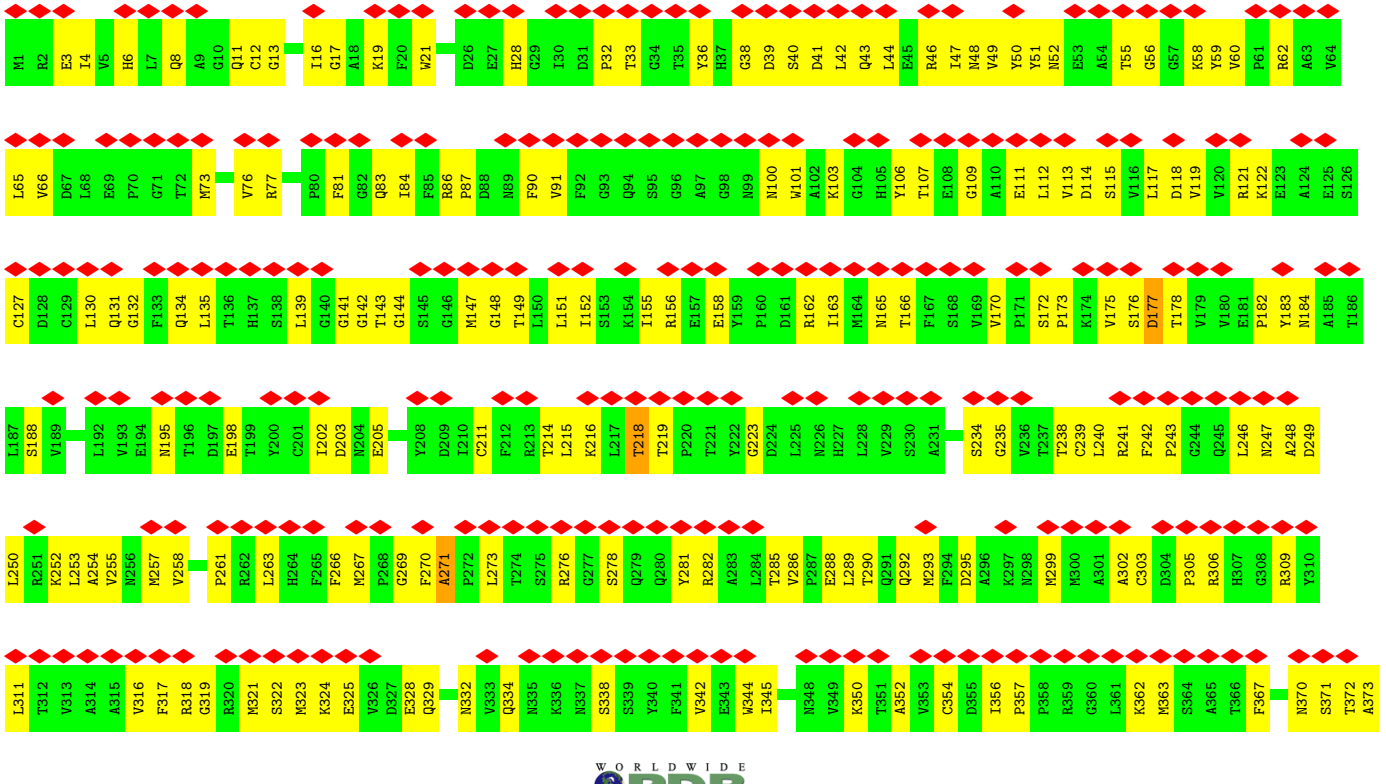
• Molecule 3: Tubulin beta-4B chain

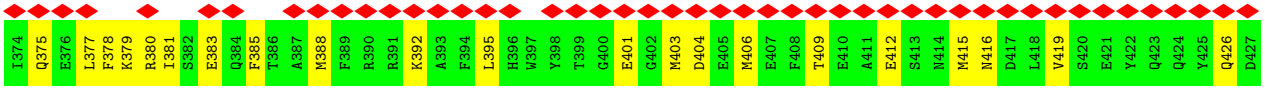
Chain PL:



• Molecule 3: Tubulin beta-4B chain

Chain QB:



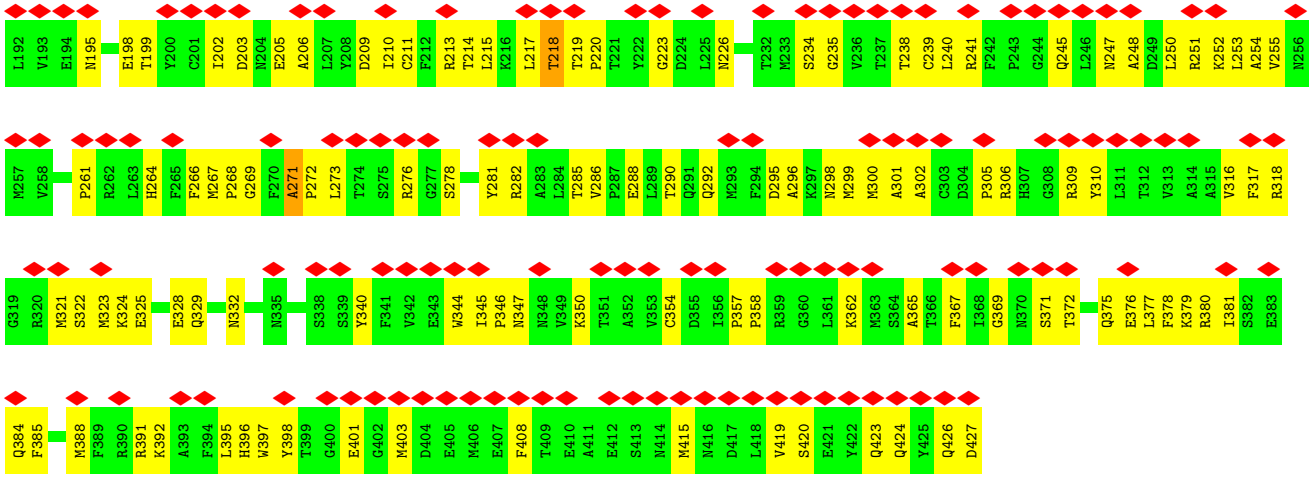


• Molecule 3: Tubulin beta-4B chain

Chain QD:

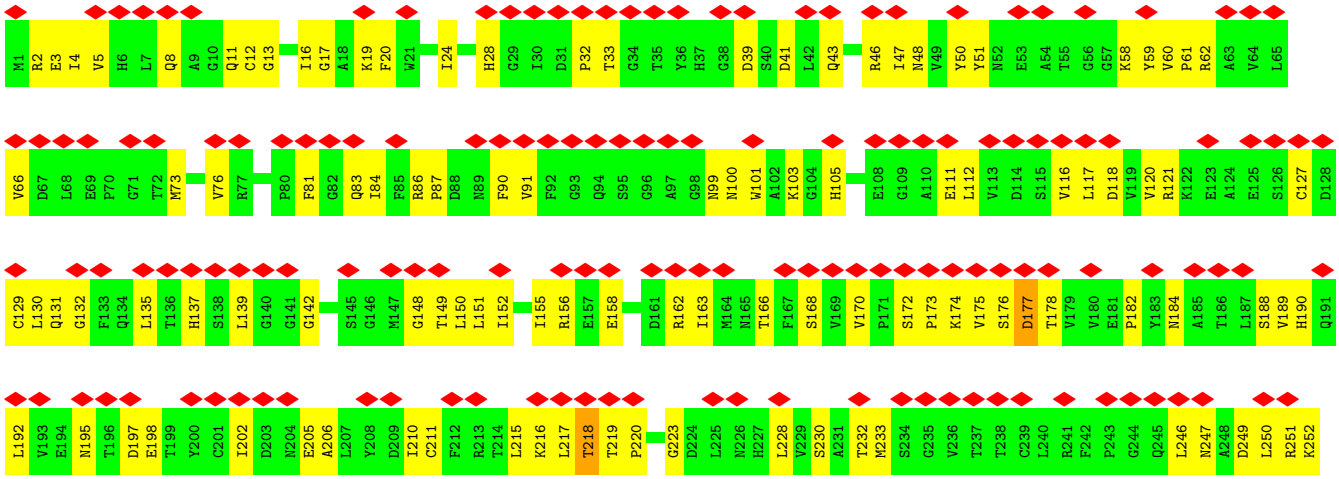
• Molecule 3: Tubulin beta-4B chain

Chain QF:



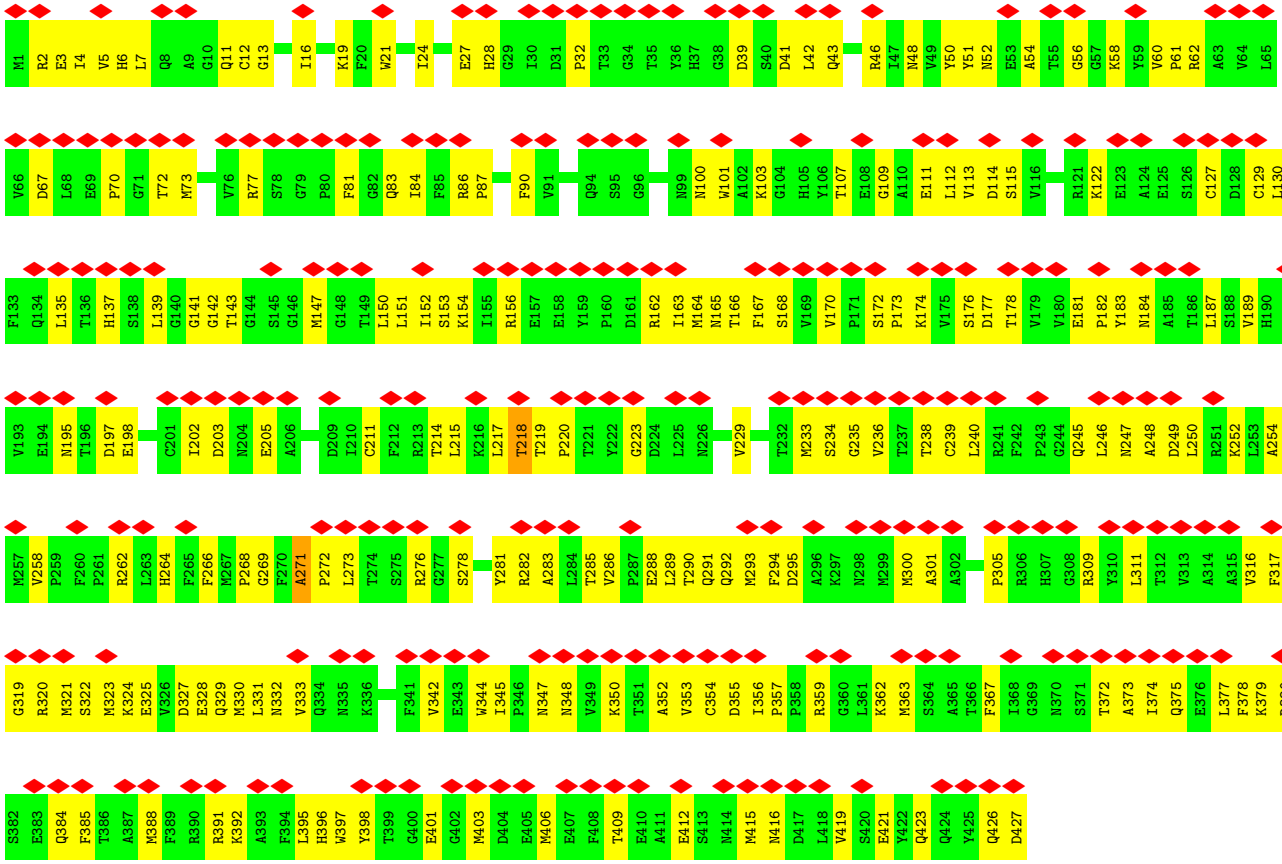
• Molecule 3: Tubulin beta-4B chain

Chain QH:



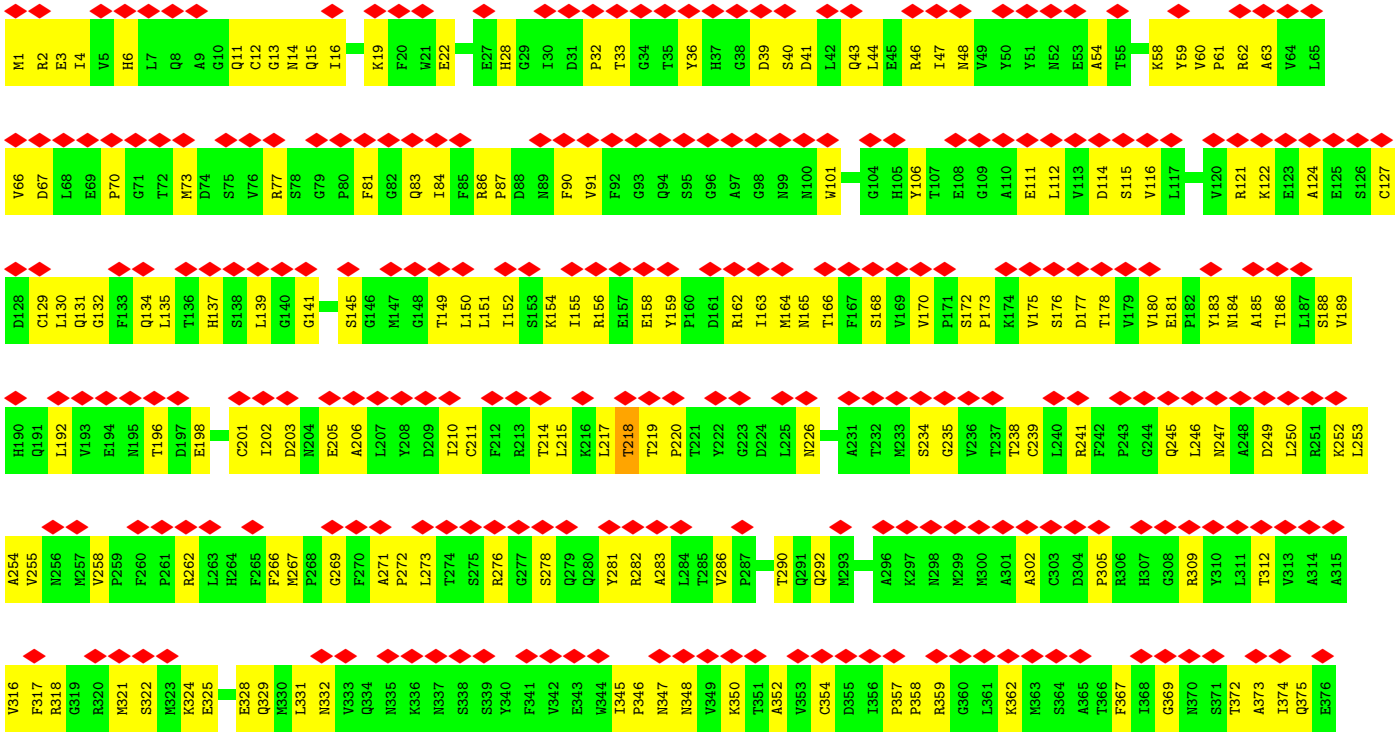
• Molecule 3: Tubulin beta-4B chain

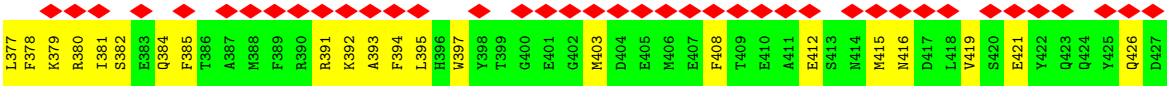
Chain QJ:



• Molecule 3: Tubulin beta-4B chain

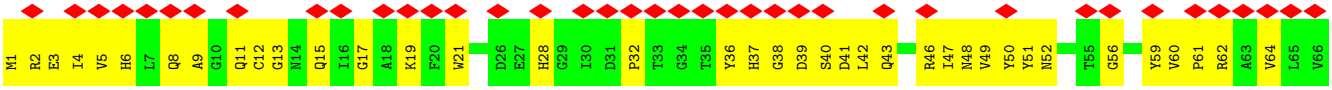
Chain QL:

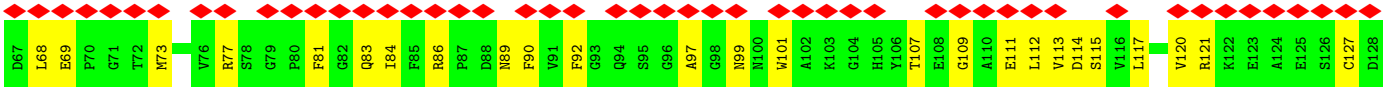


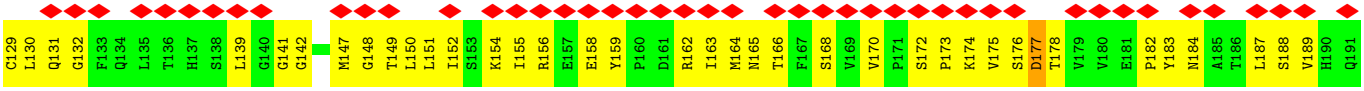


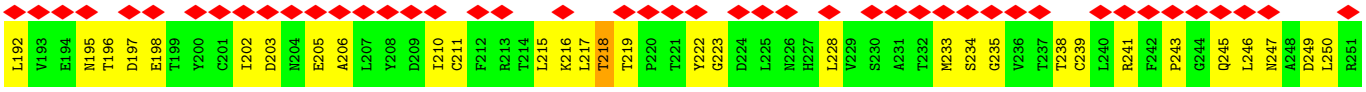
• Molecule 3: Tubulin beta-4B chain

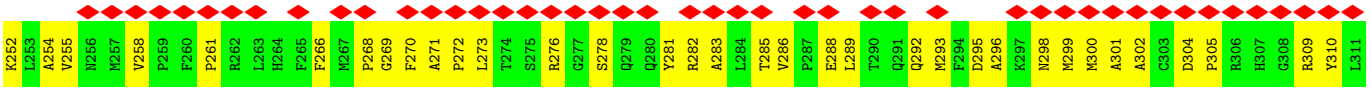
Chain RB:

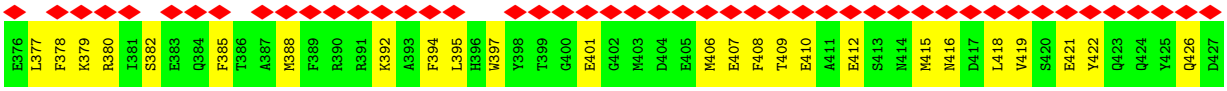






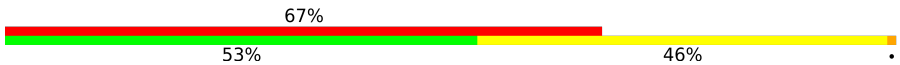


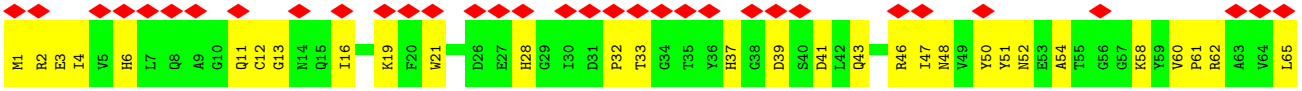


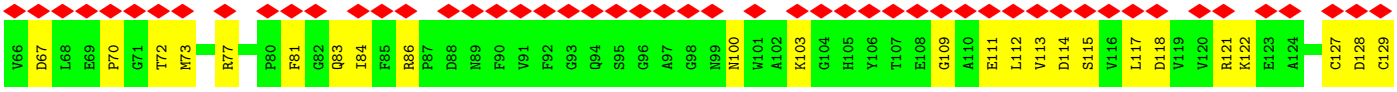


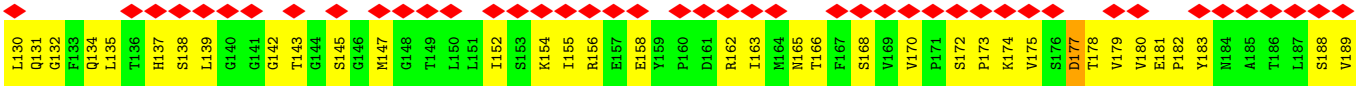
• Molecule 3: Tubulin beta-4B chain

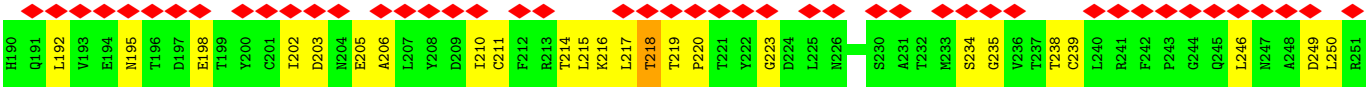
Chain RD:

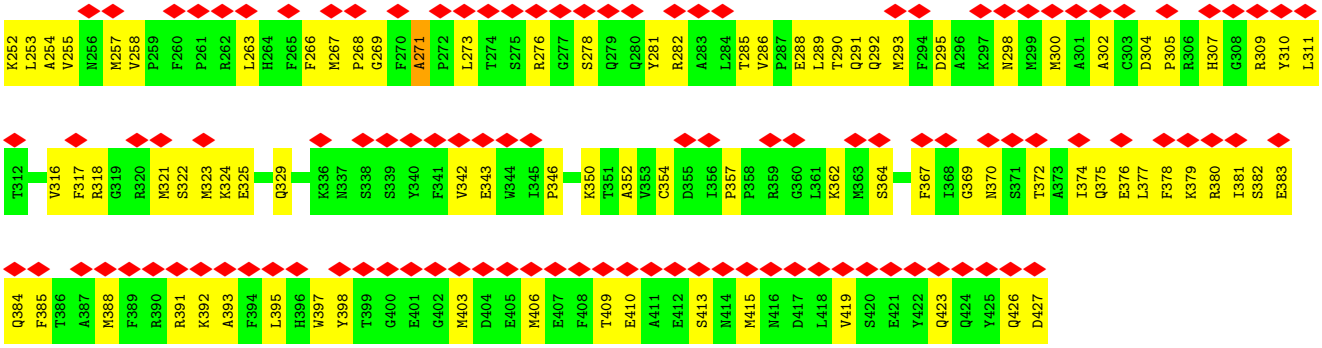






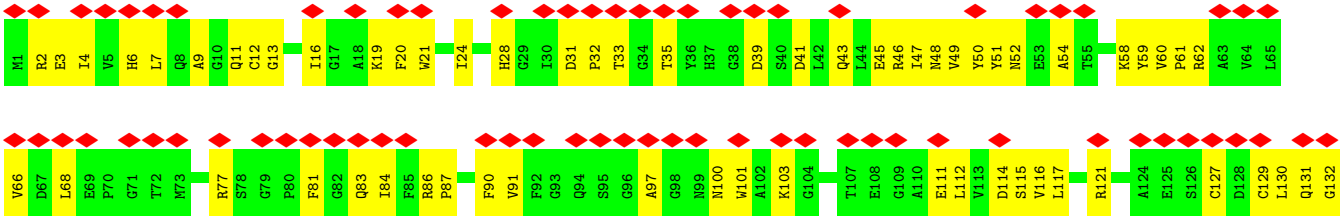






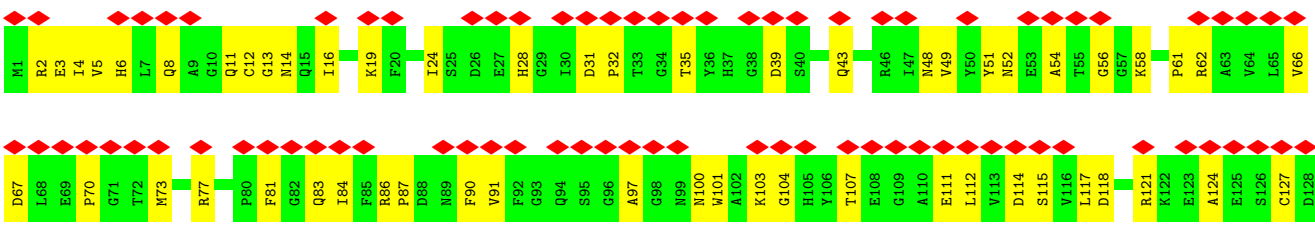
• Molecule 3: Tubulin beta-4B chain

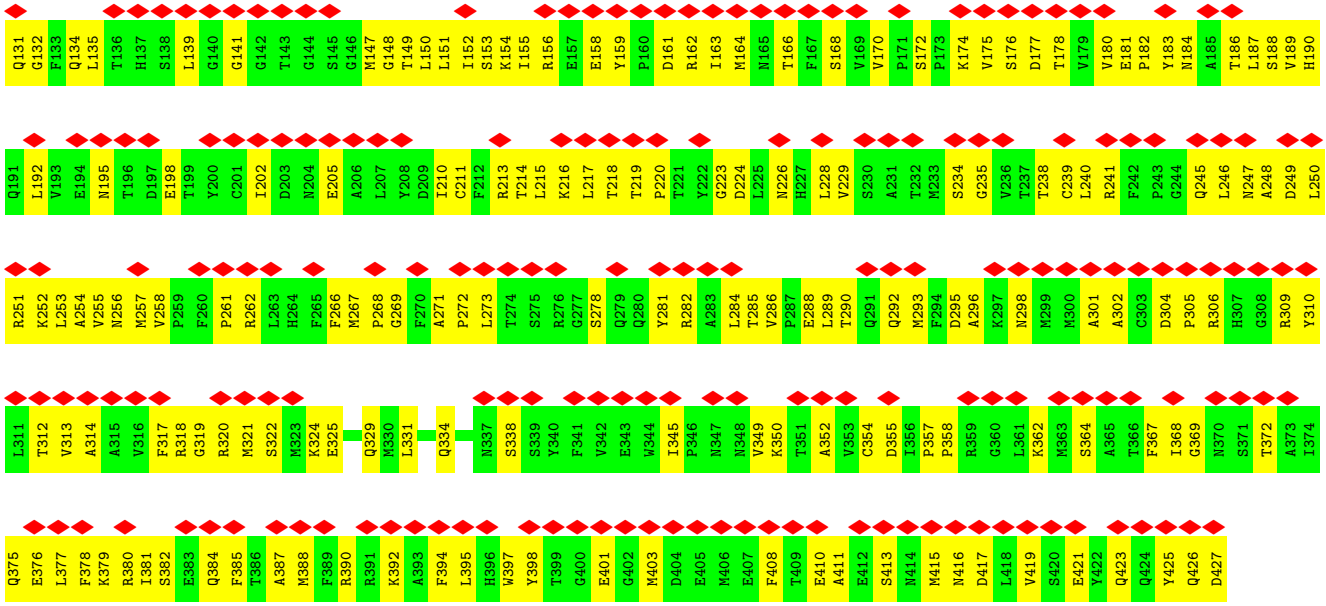
Chain RF:



• Molecule 3: Tubulin beta-4B chain

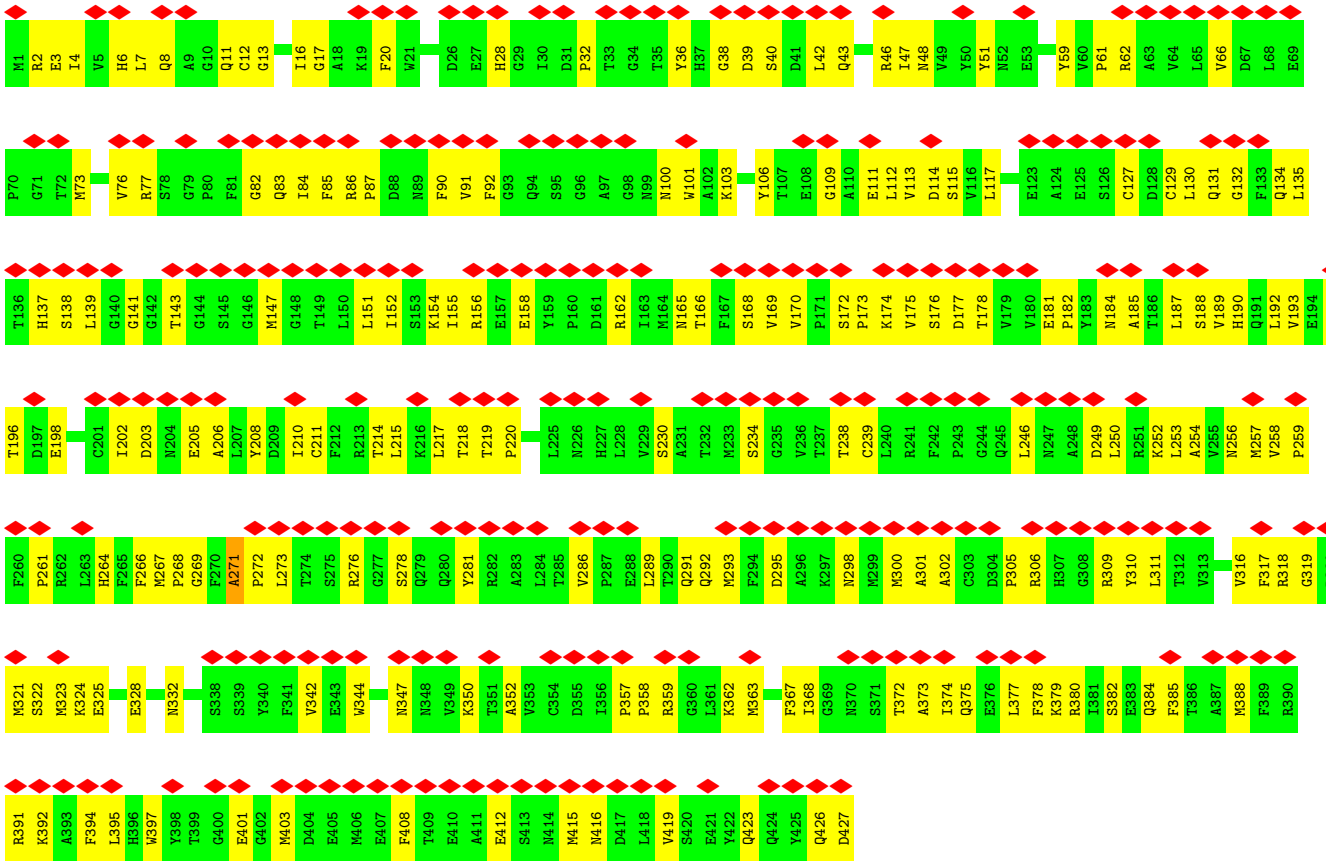
Chain RH:





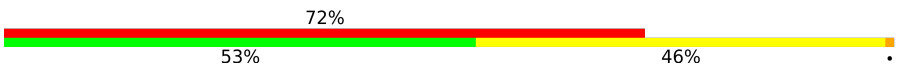
• Molecule 3: Tubulin beta-4B chain

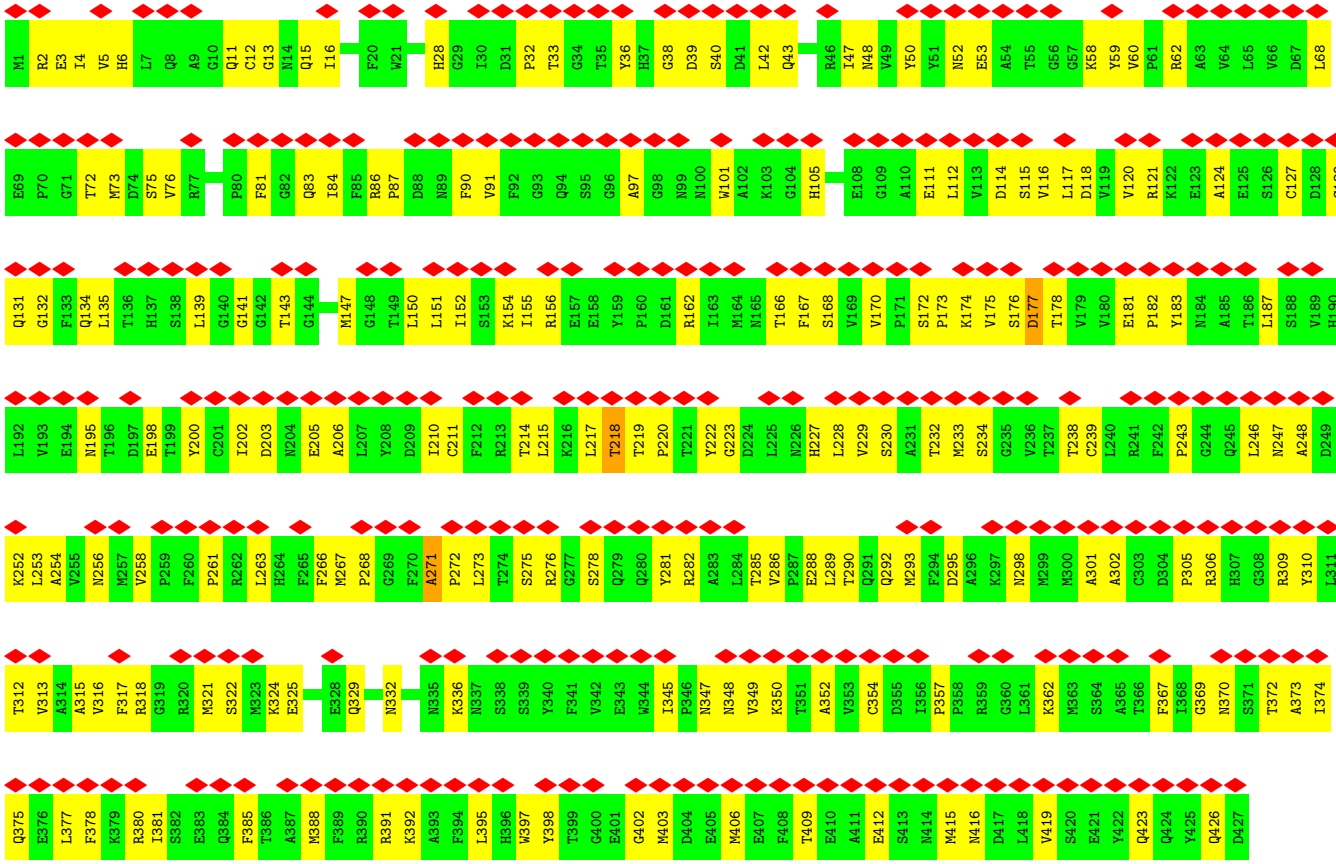
Chain RJ:



• Molecule 3: Tubulin beta-4B chain

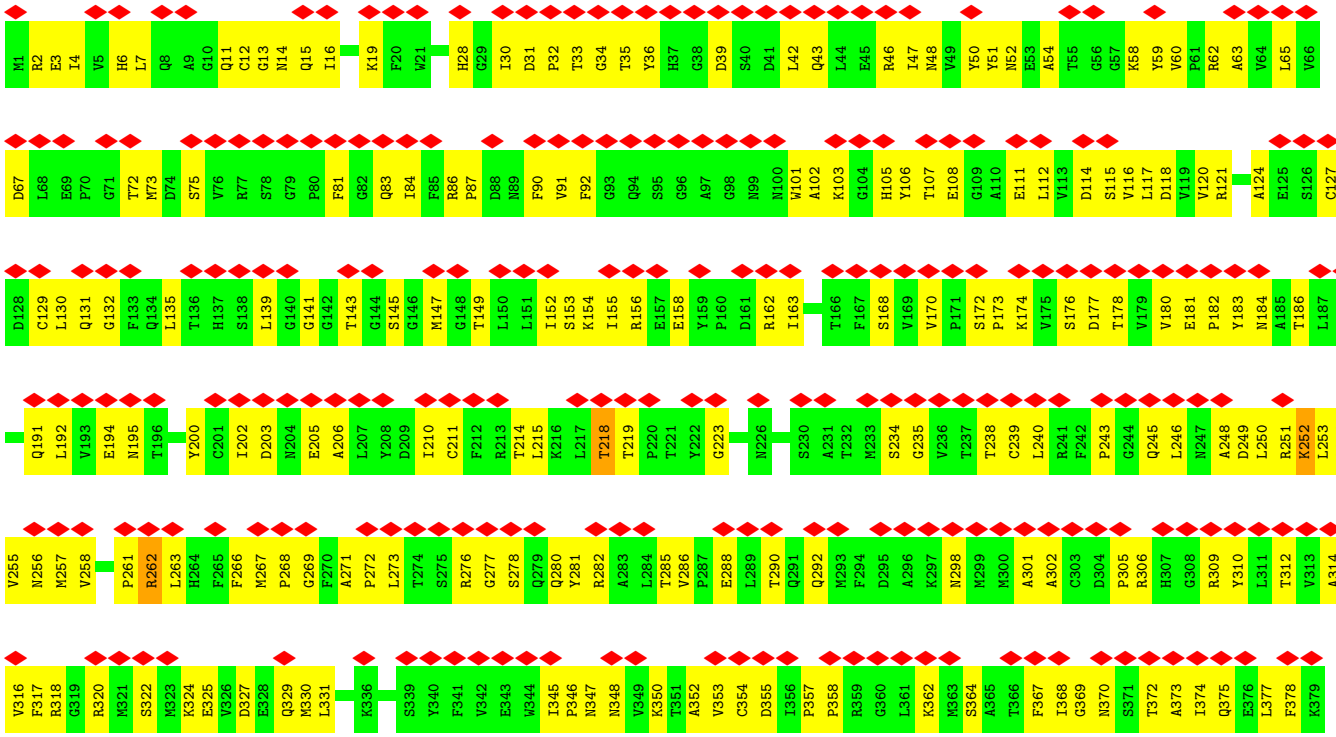
Chain RL:

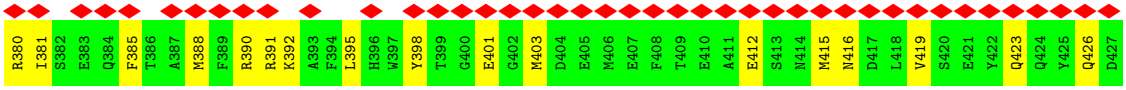




• Molecule 3: Tubulin beta-4B chain

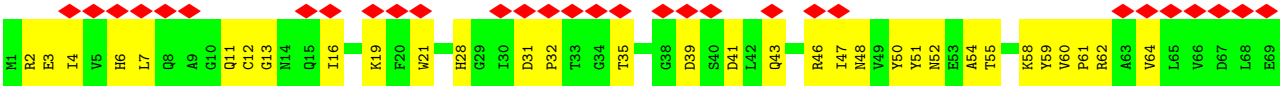
Chain SB:

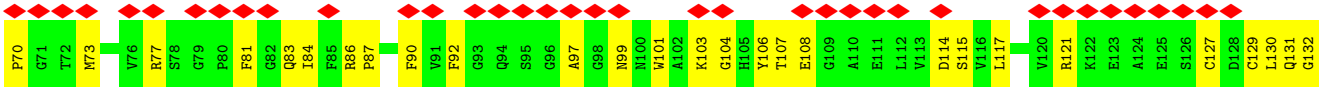


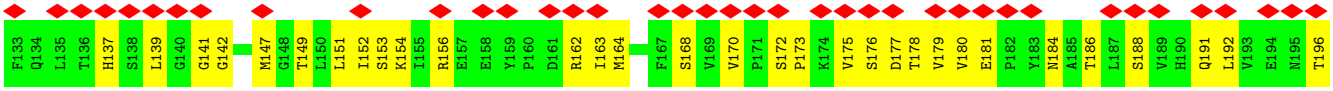


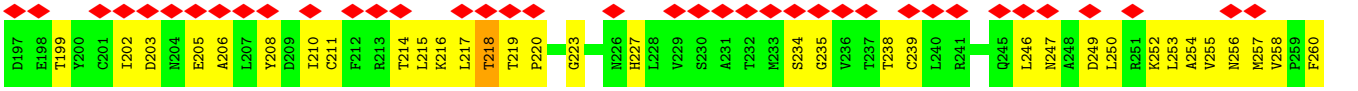
• Molecule 3: Tubulin beta-4B chain

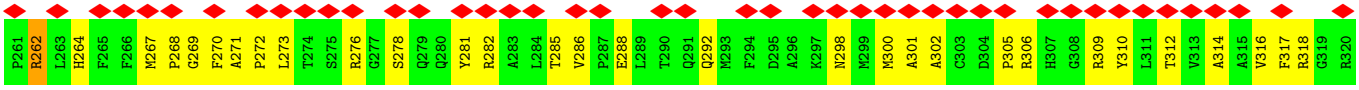
Chain SD:

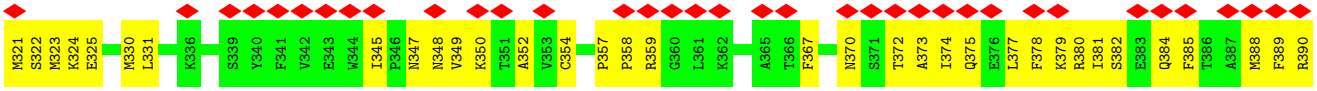


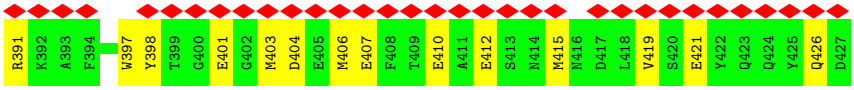






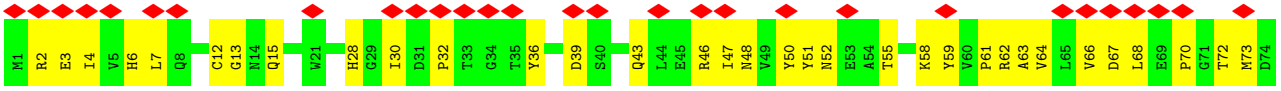


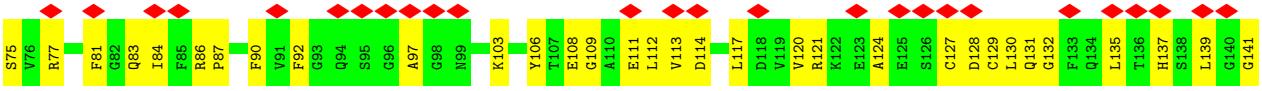


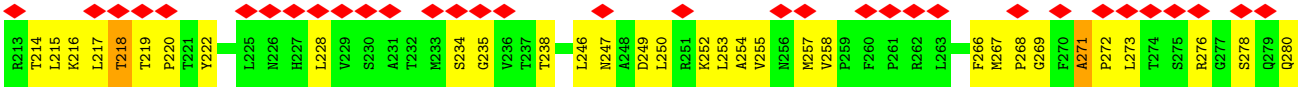


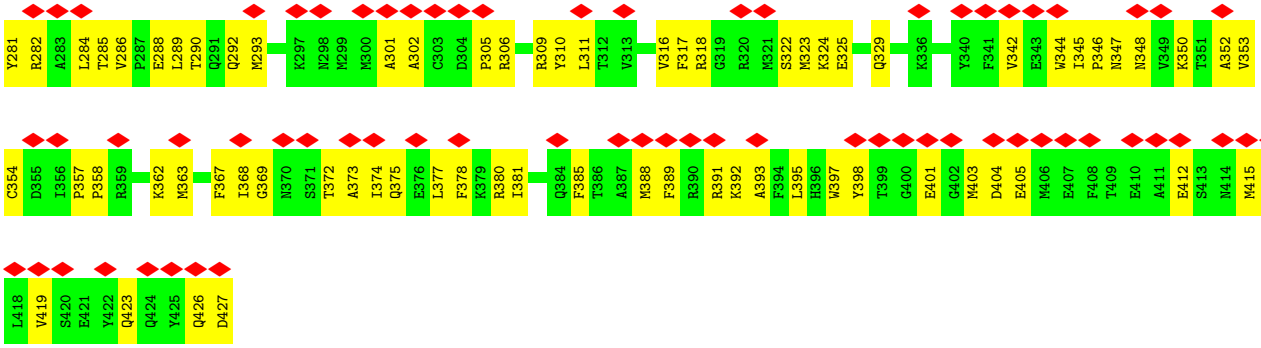
• Molecule 3: Tubulin beta-4B chain

Chain SF:



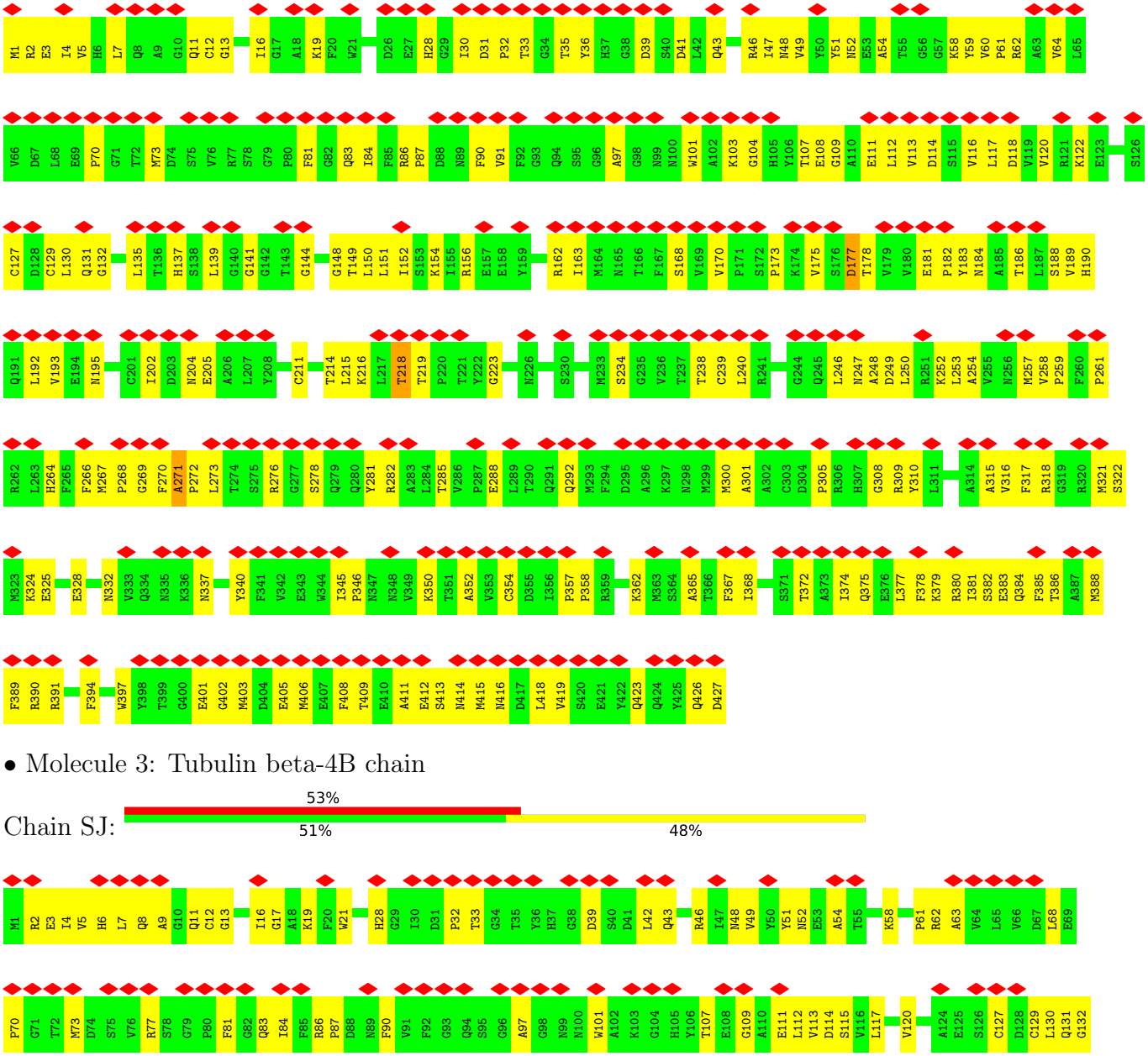






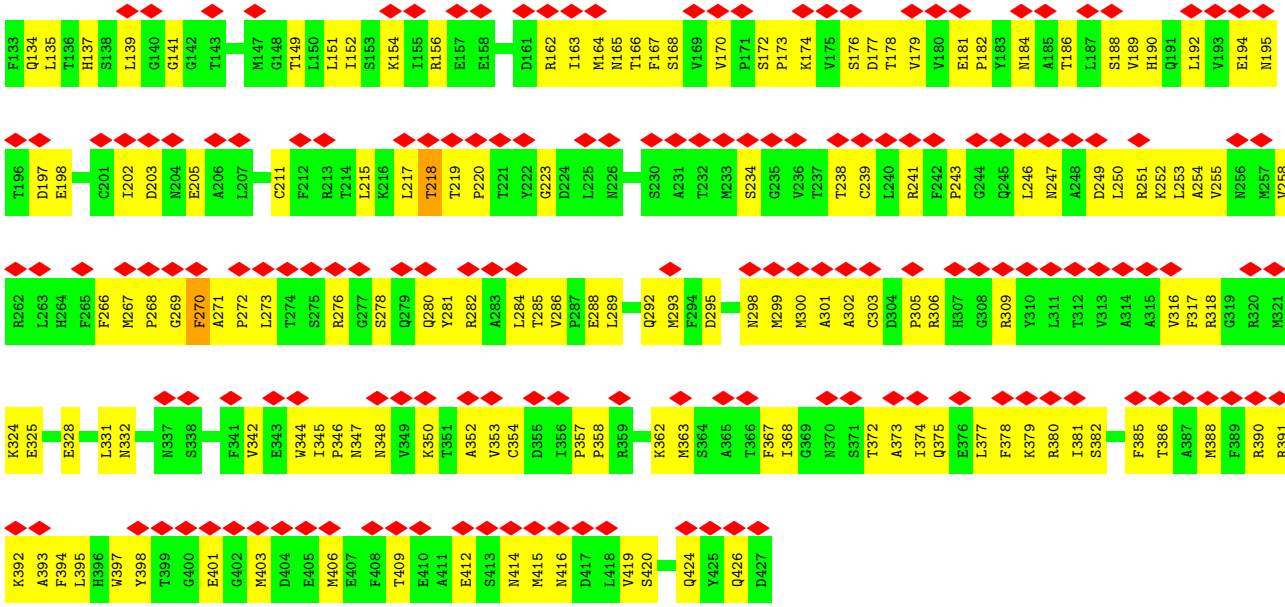
• Molecule 3: Tubulin beta-4B chain

Chain SH:



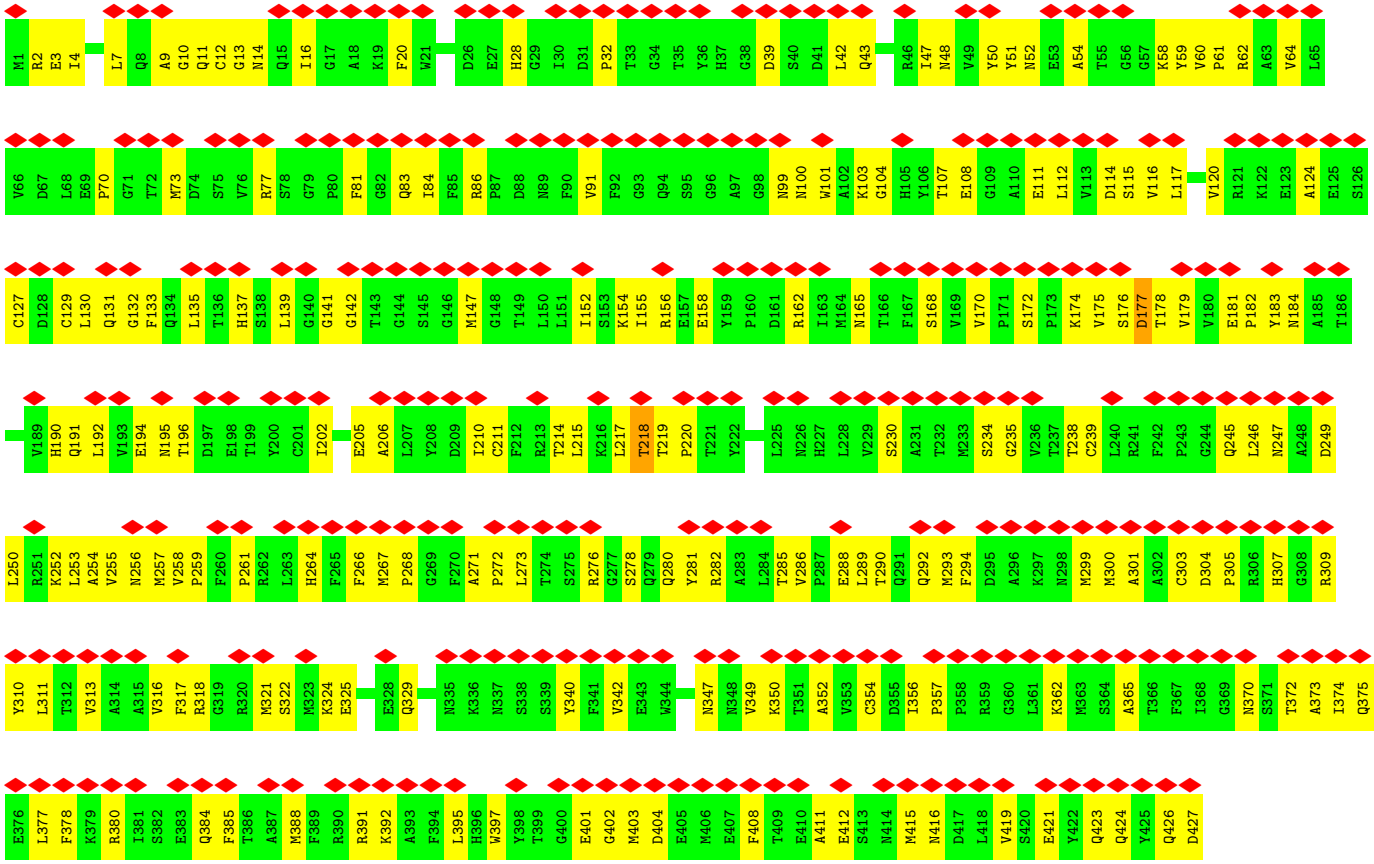
• Molecule 3: Tubulin beta-4B chain

Chain SJ:



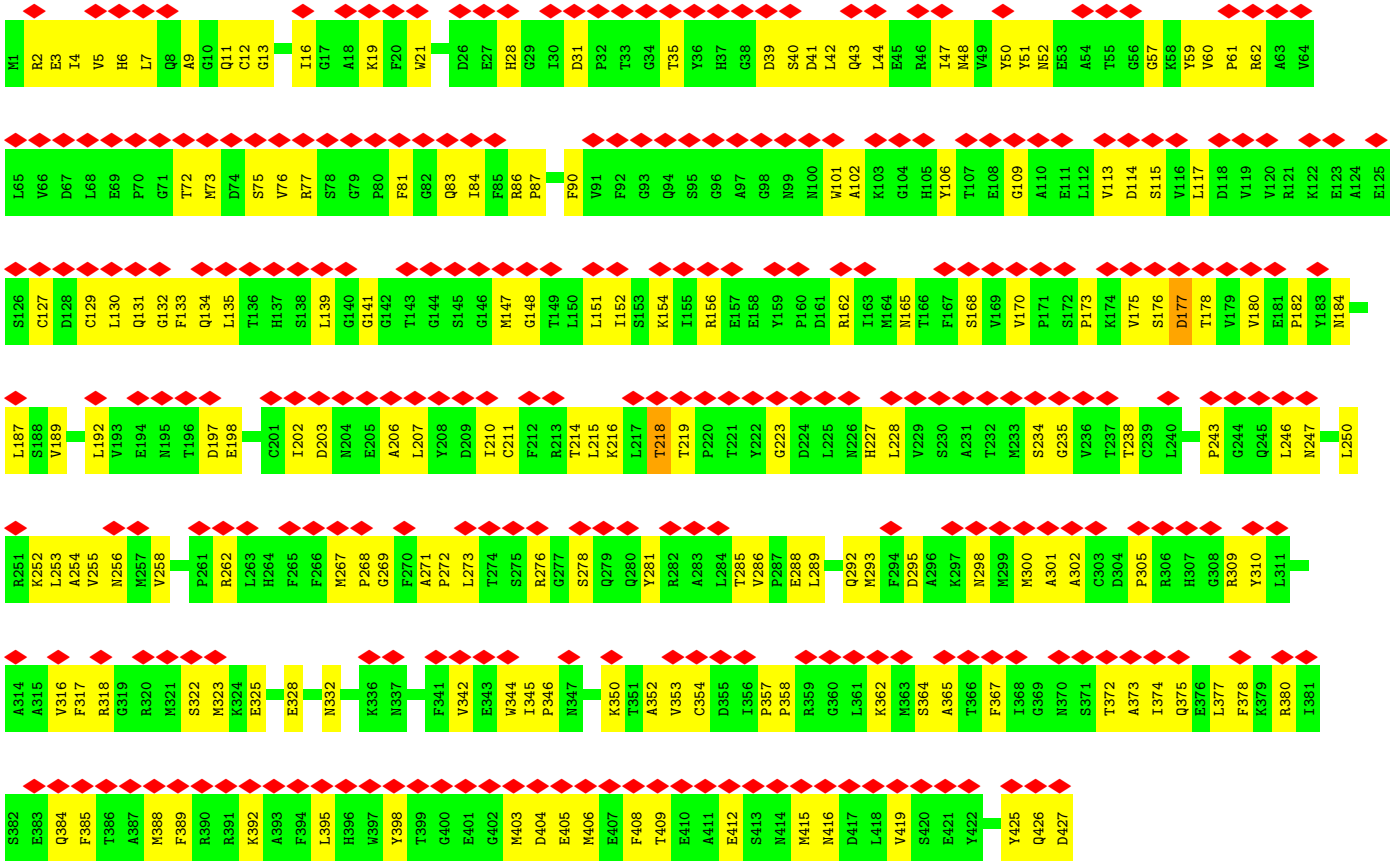
• Molecule 3: Tubulin beta-4B chain

Chain SL:



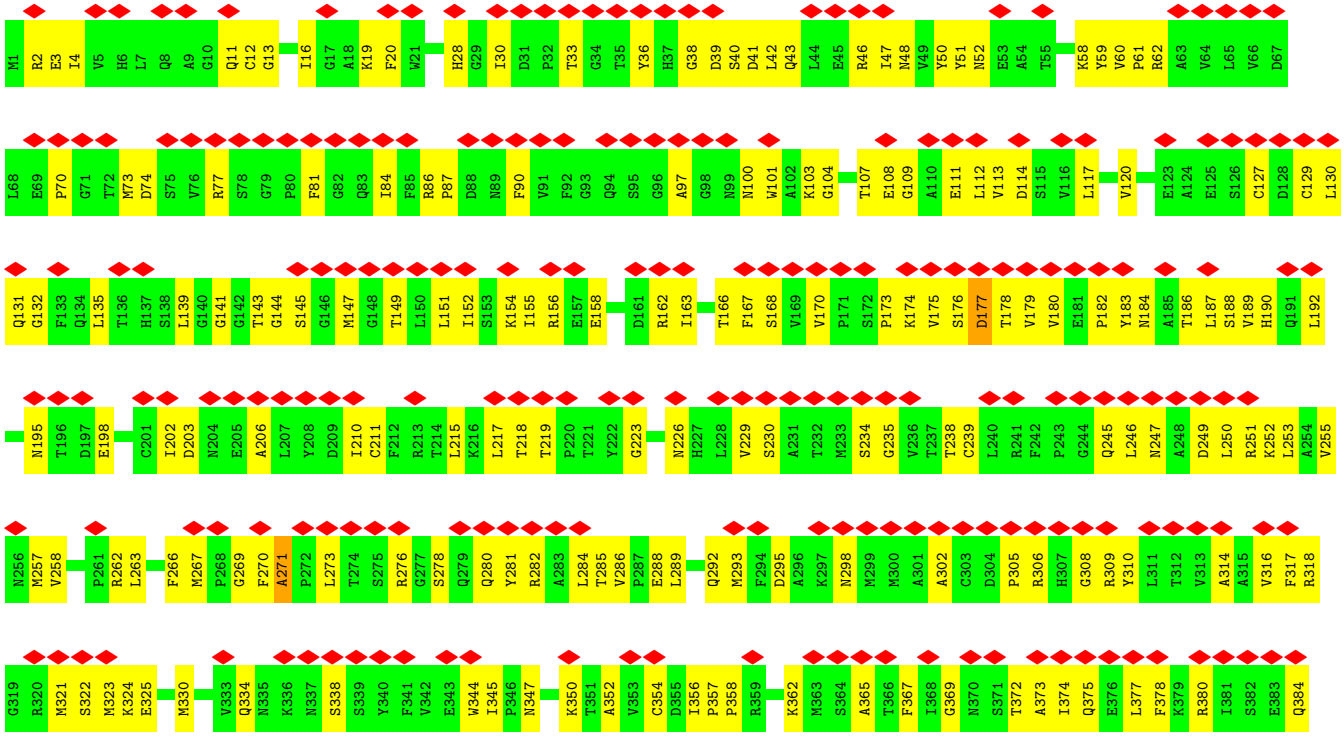
• Molecule 3: Tubulin beta-4B chain

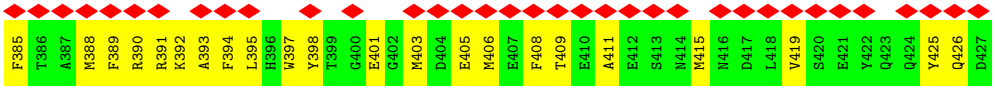
Chain TB:



• Molecule 3: Tubulin beta-4B chain

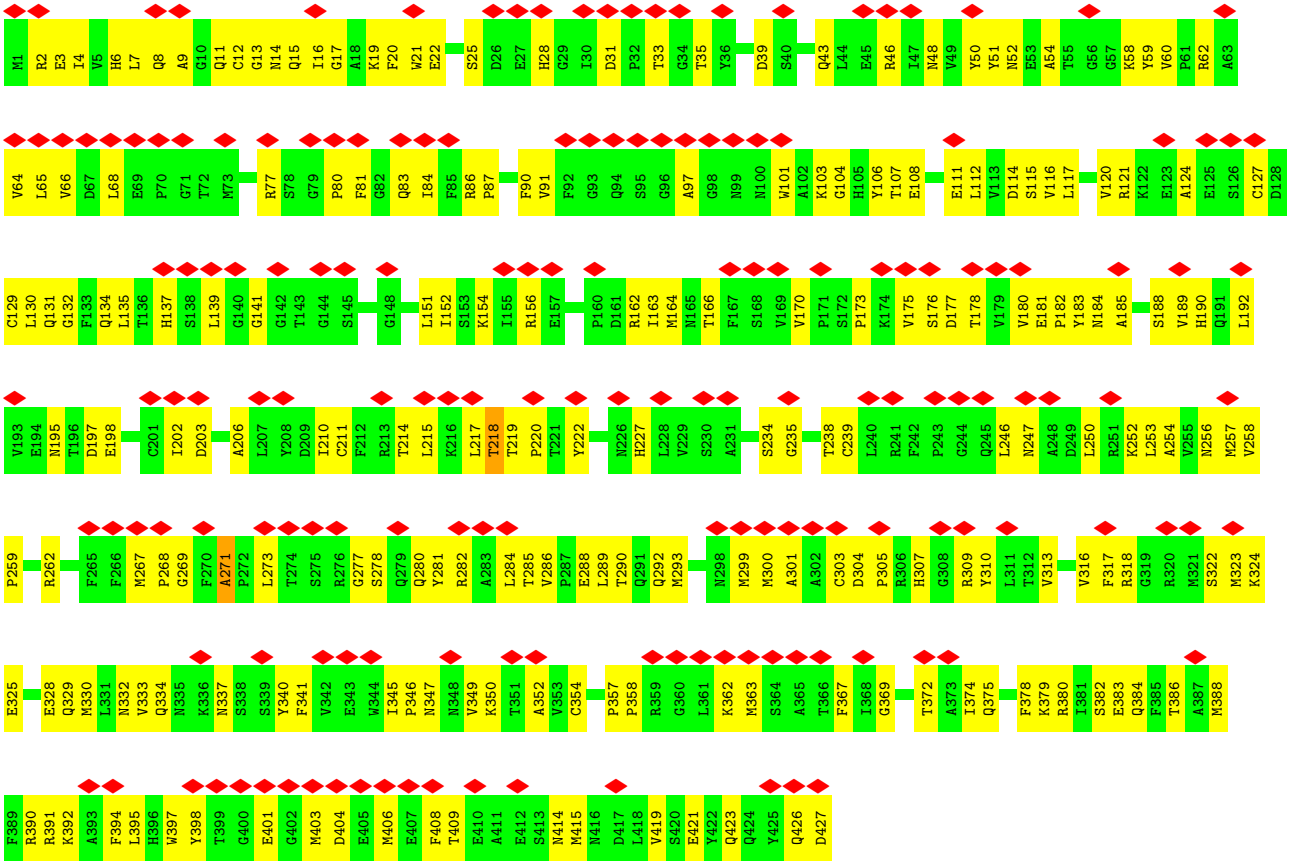
Chain TD:





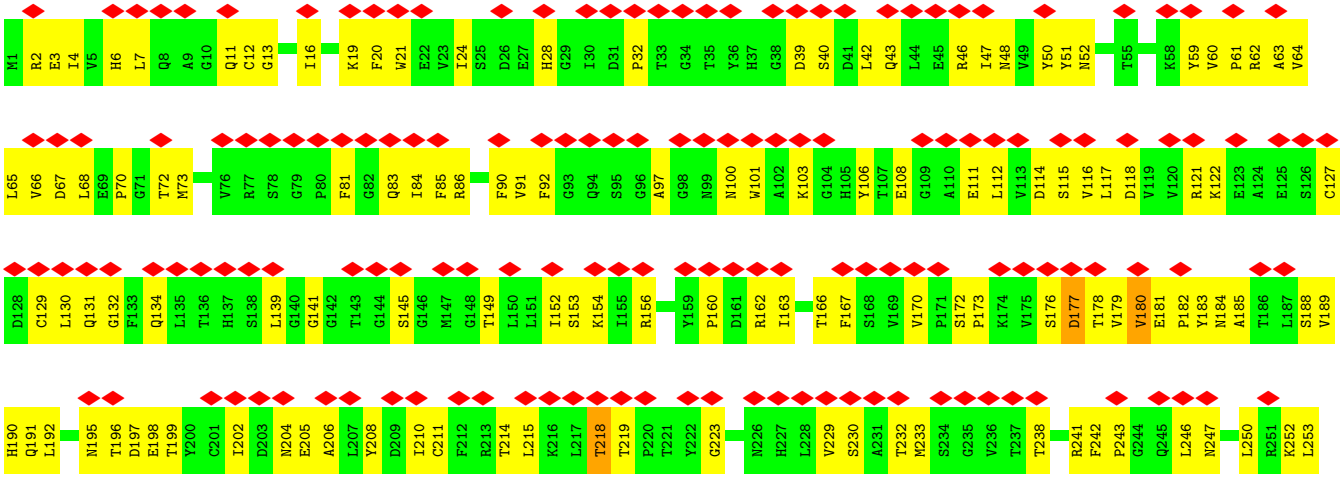
• Molecule 3: Tubulin beta-4B chain

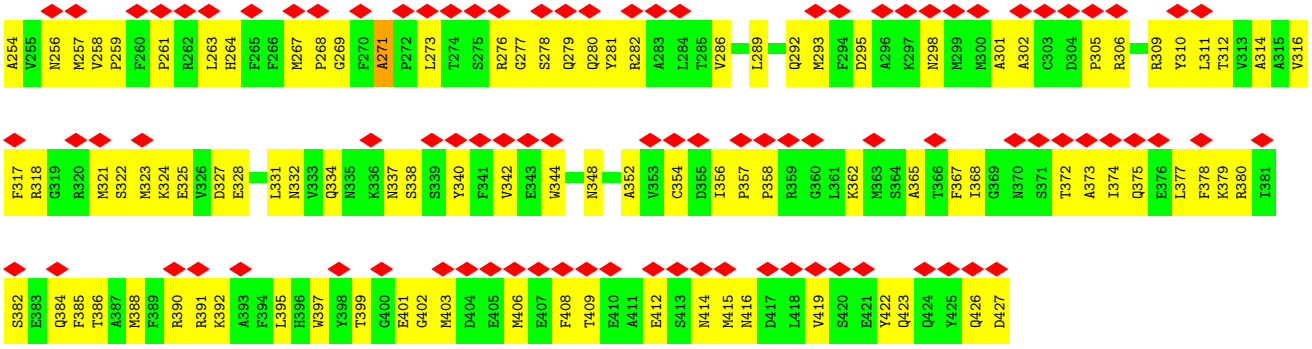
Chain TF:



• Molecule 3: Tubulin beta-4B chain

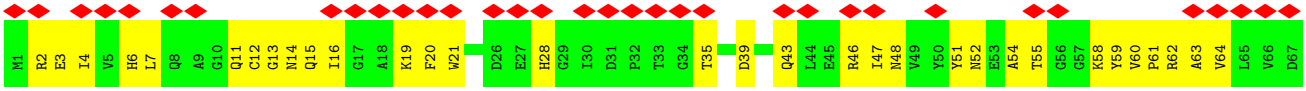
Chain TH:

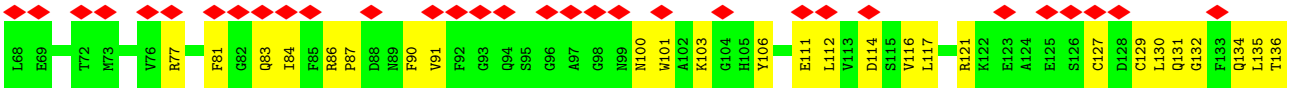


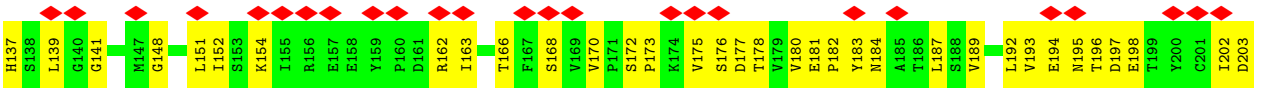


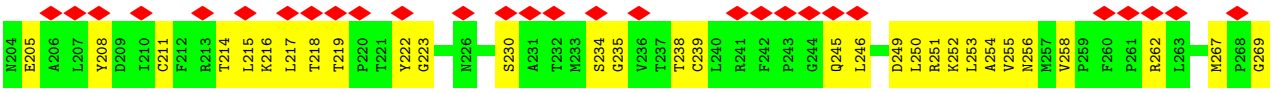
• Molecule 3: Tubulin beta-4B chain

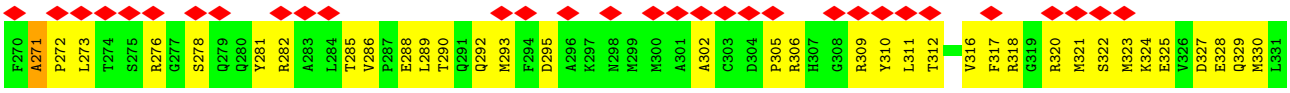
Chain TJ:

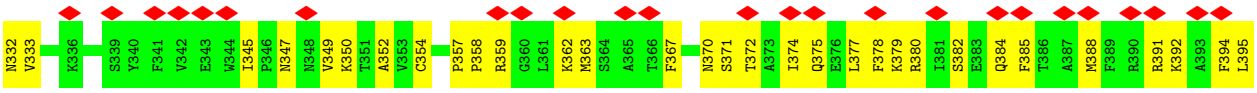


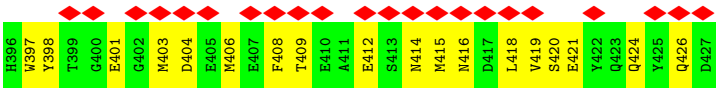






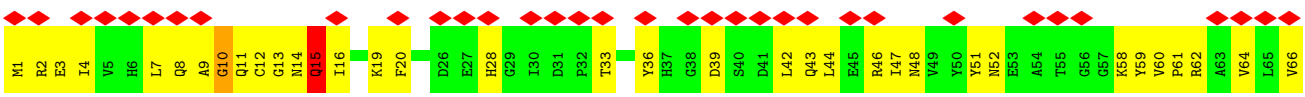


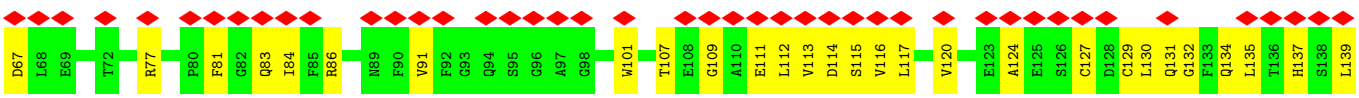


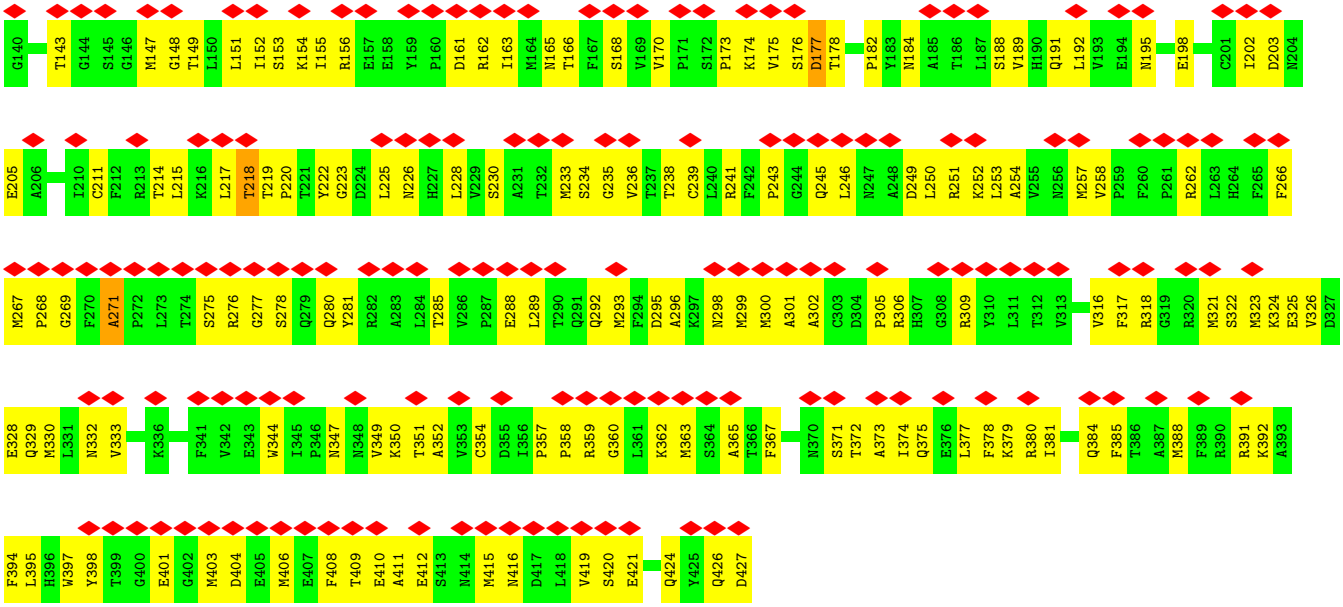


• Molecule 3: Tubulin beta-4B chain

Chain TL:

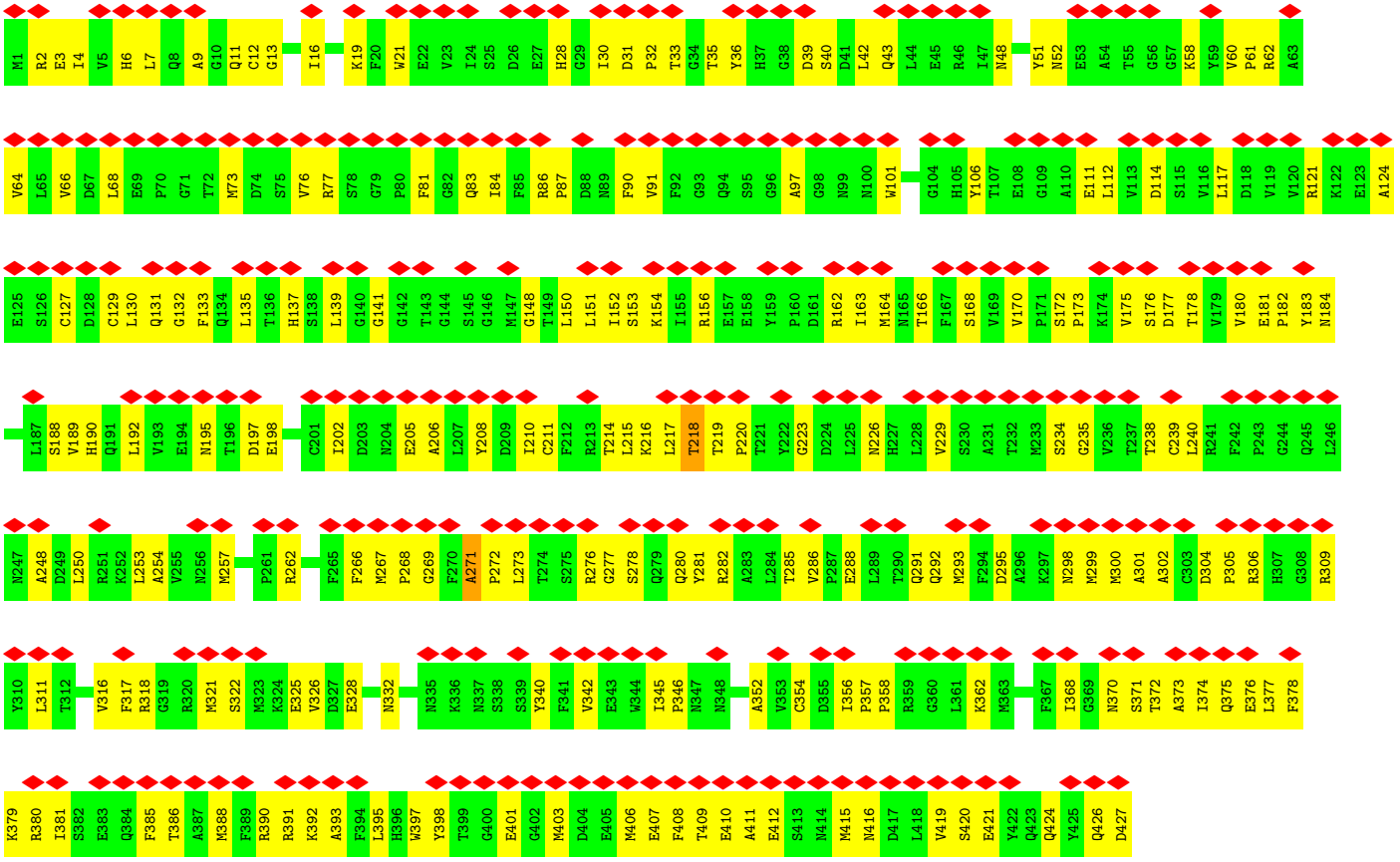






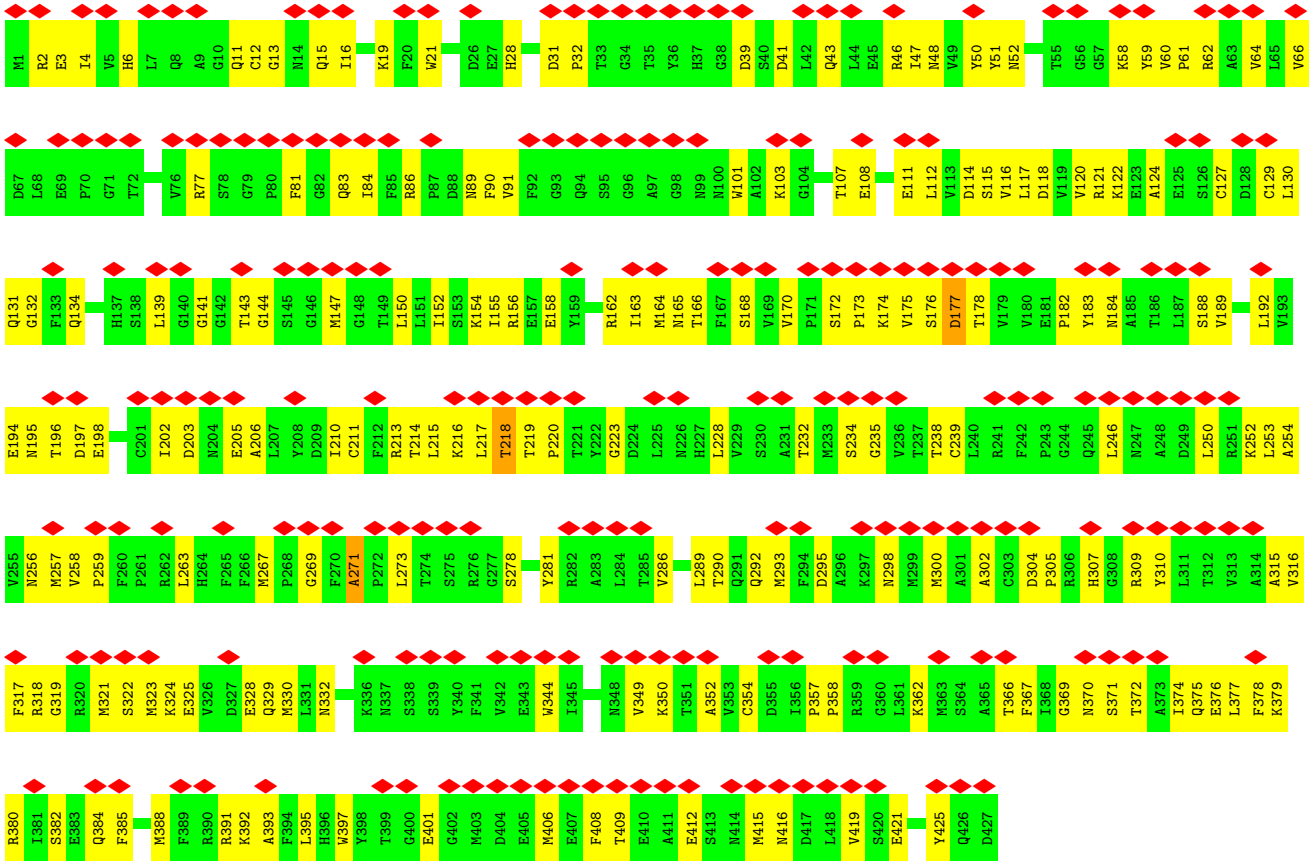
• Molecule 3: Tubulin beta-4B chain

Chain TN:



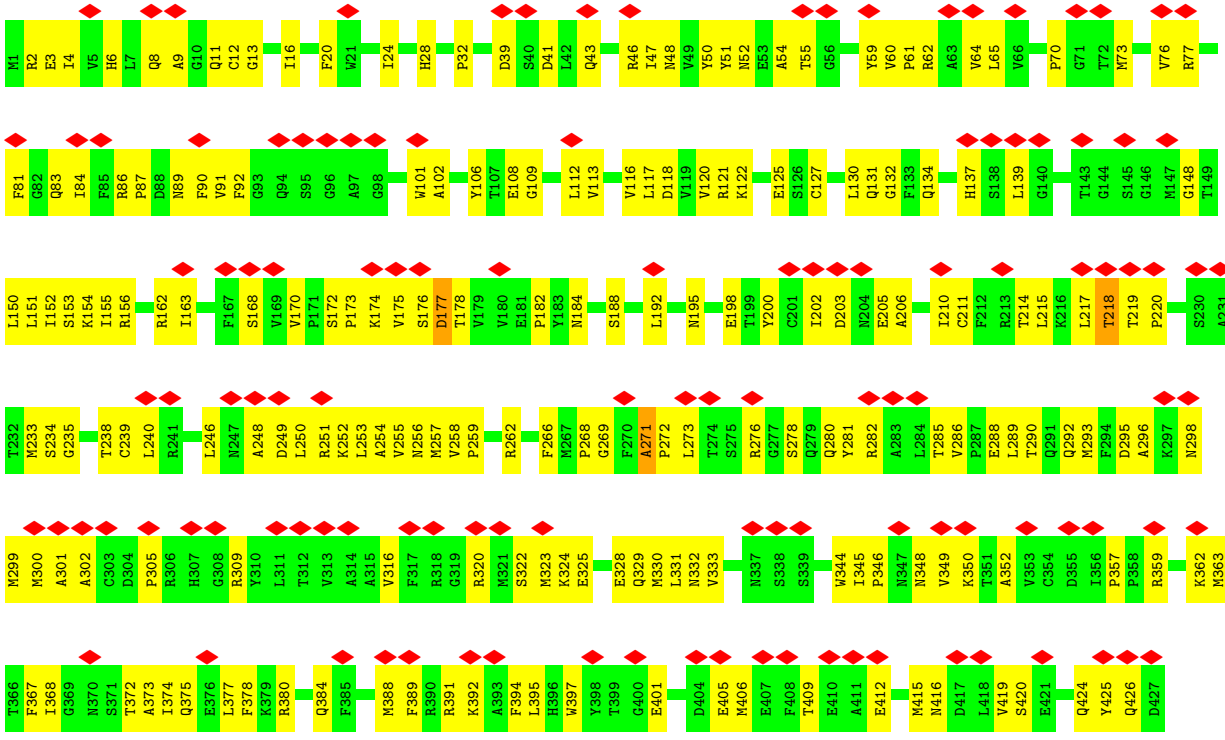
• Molecule 3: Tubulin beta-4B chain

Chain UB:



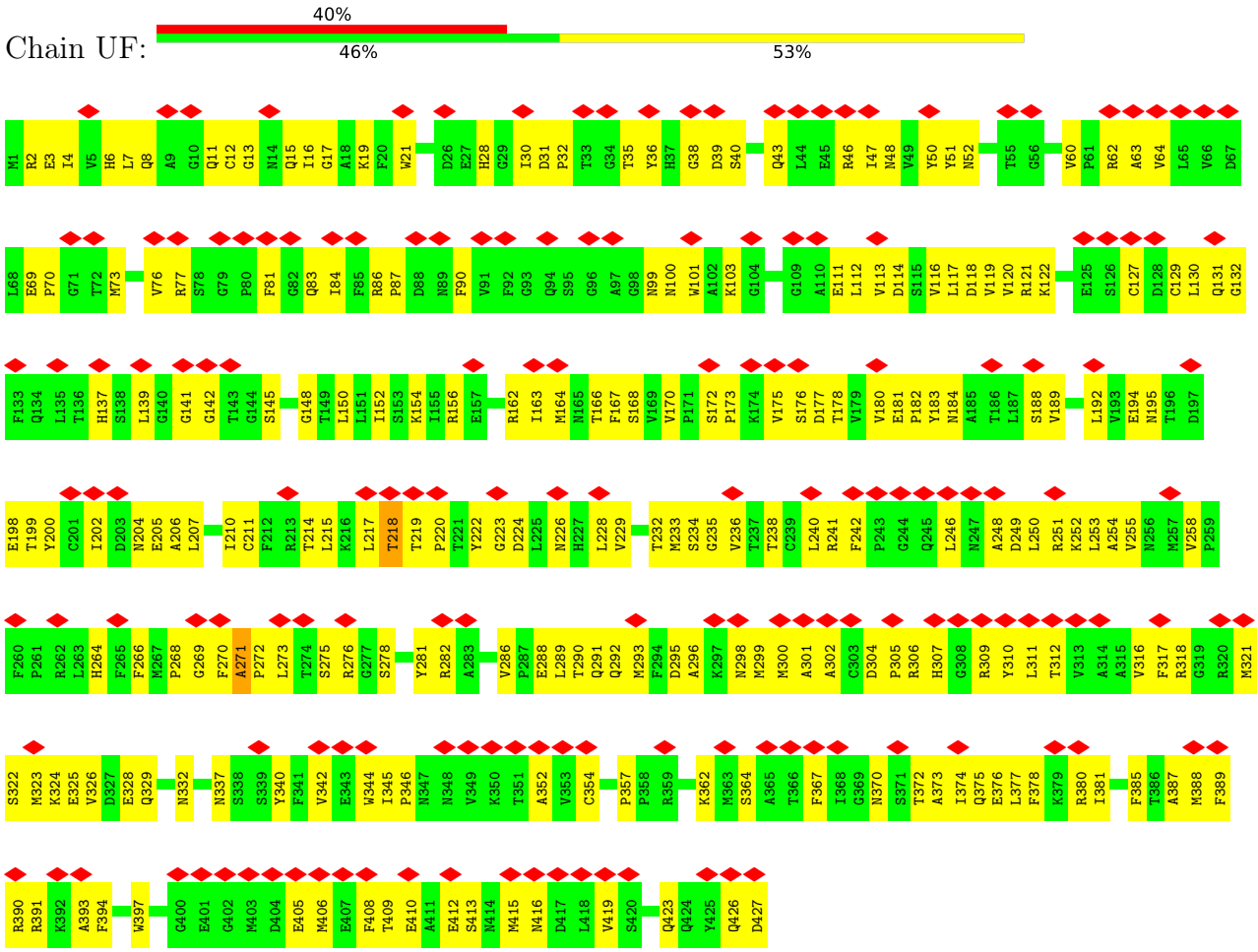
• Molecule 3: Tubulin beta-4B chain

Chain UD:



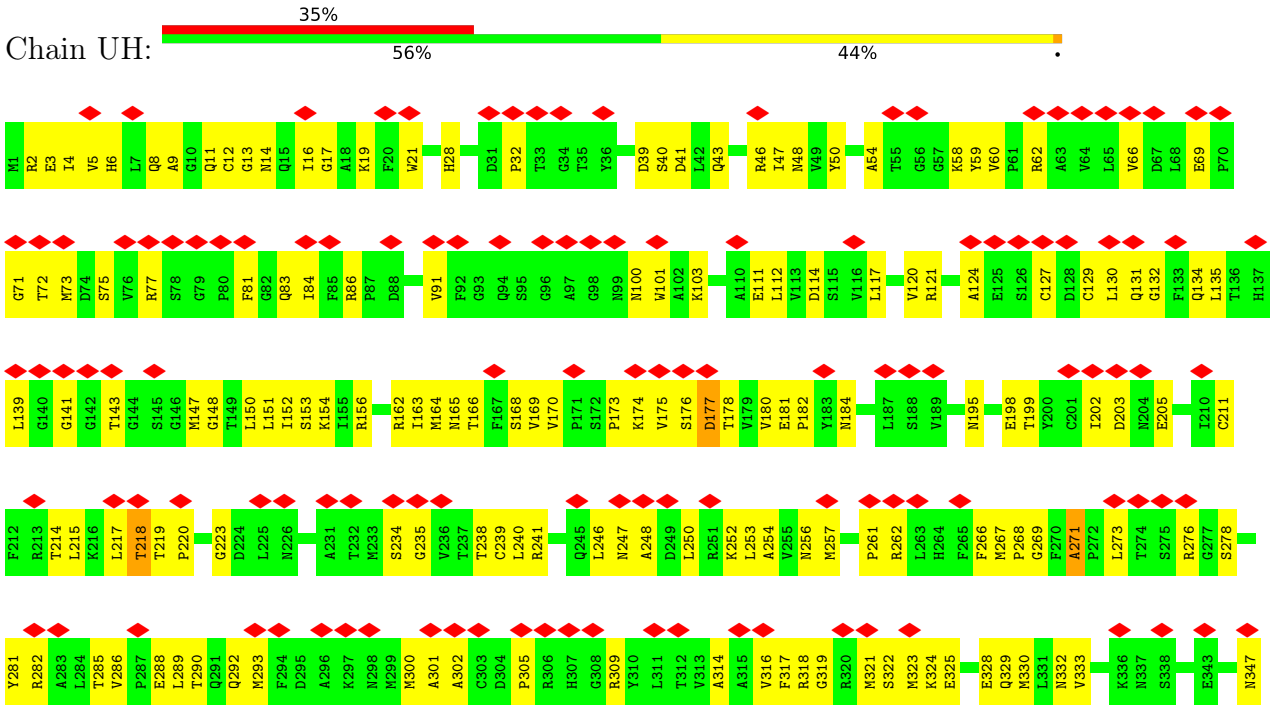
• Molecule 3: Tubulin beta-4B chain

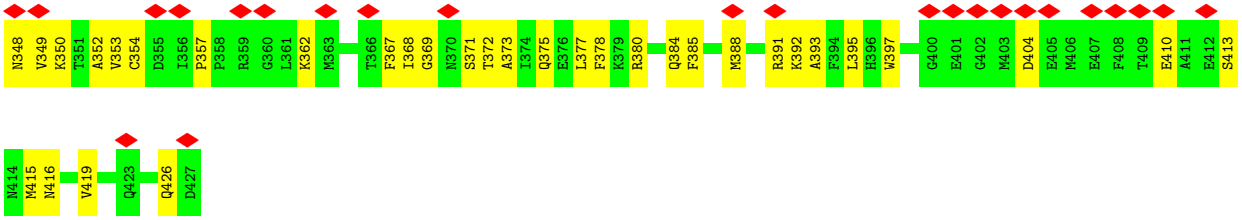
Chain UF:



• Molecule 3: Tubulin beta-4B chain

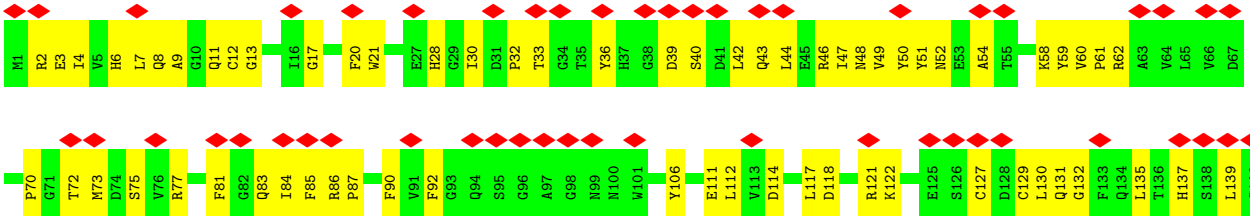
Chain UH:





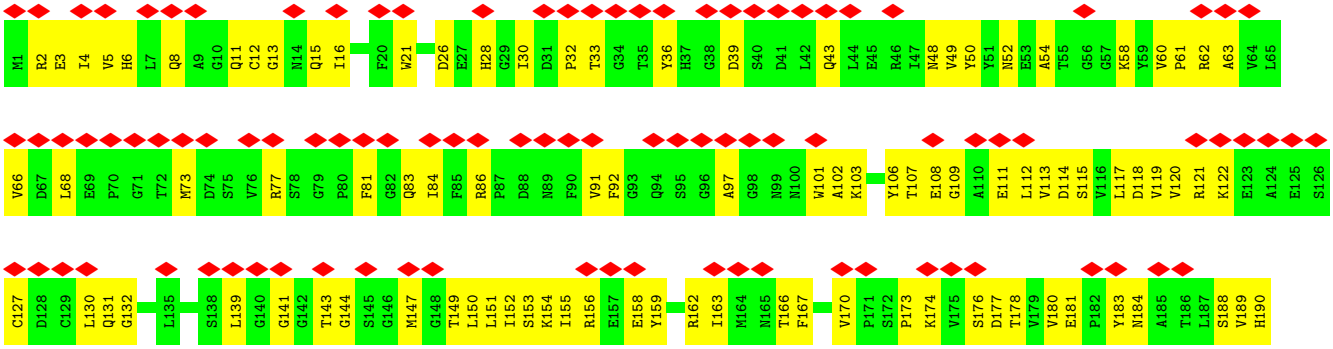
• Molecule 3: Tubulin beta-4B chain

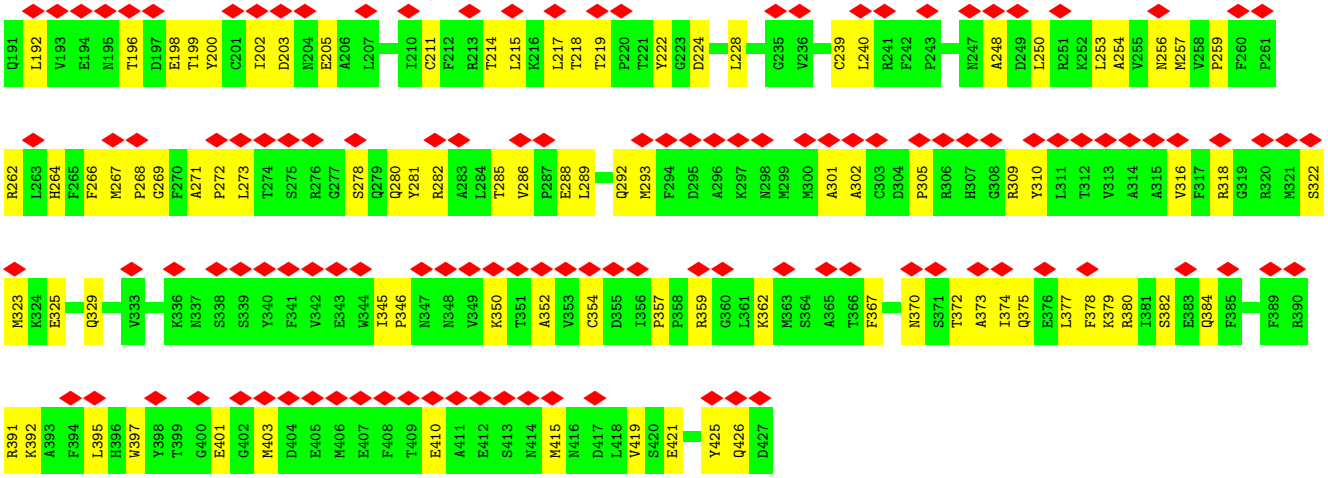
Chain UJ:



• Molecule 3: Tubulin beta-4B chain

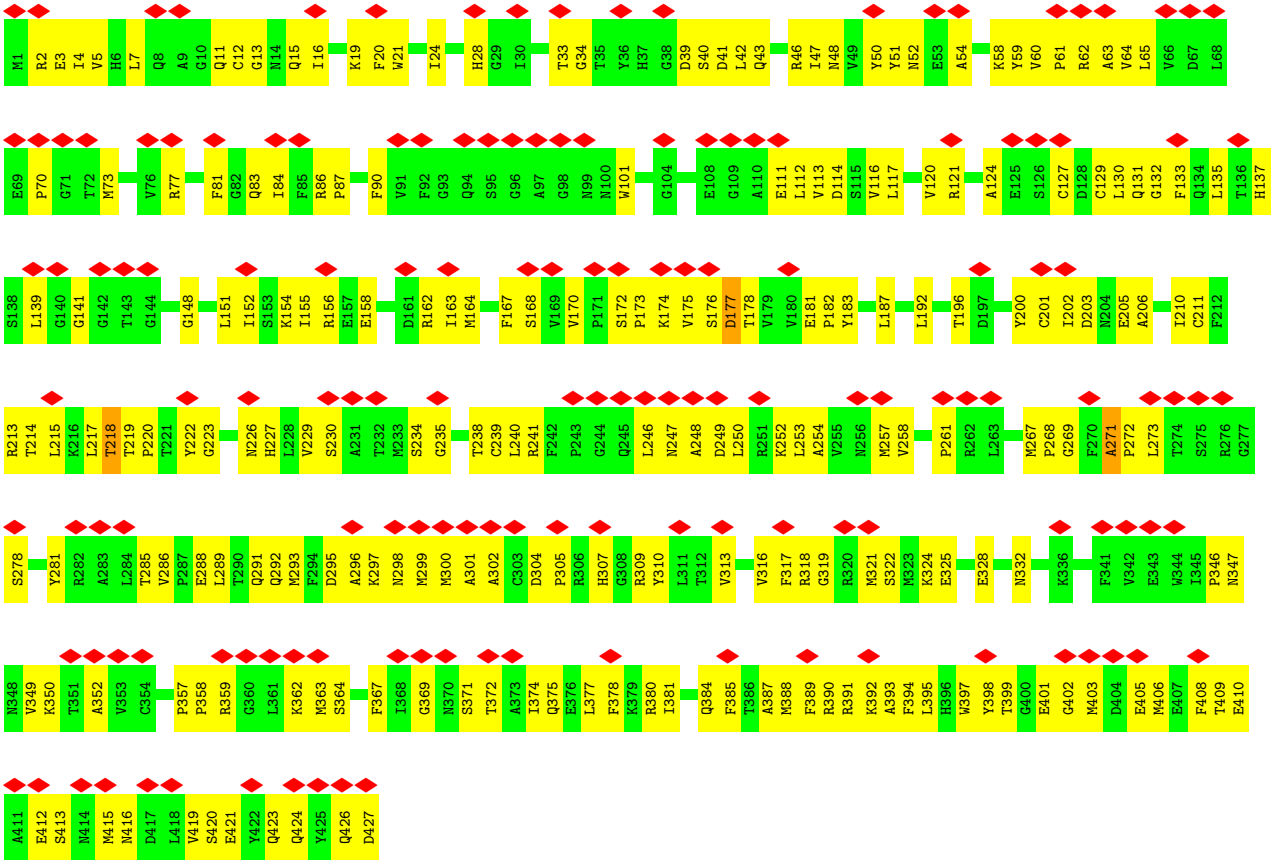
Chain UL:





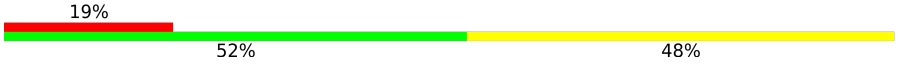
• Molecule 3: Tubulin beta-4B chain

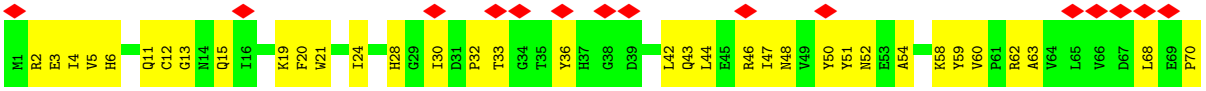
Chain VB:

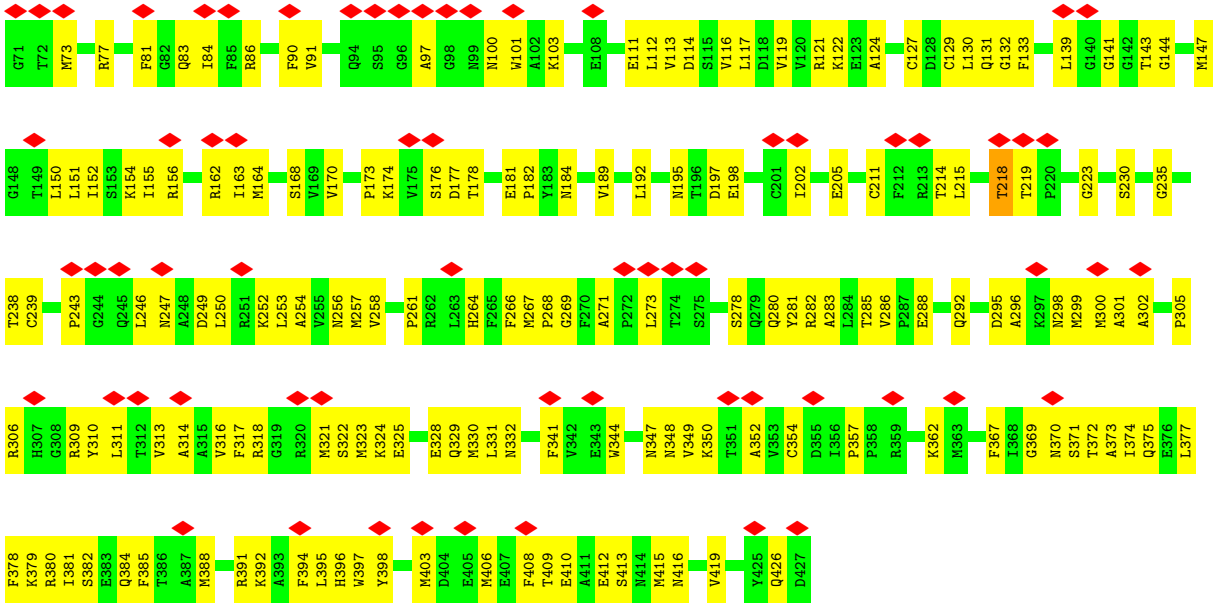


• Molecule 3: Tubulin beta-4B chain

Chain VD:

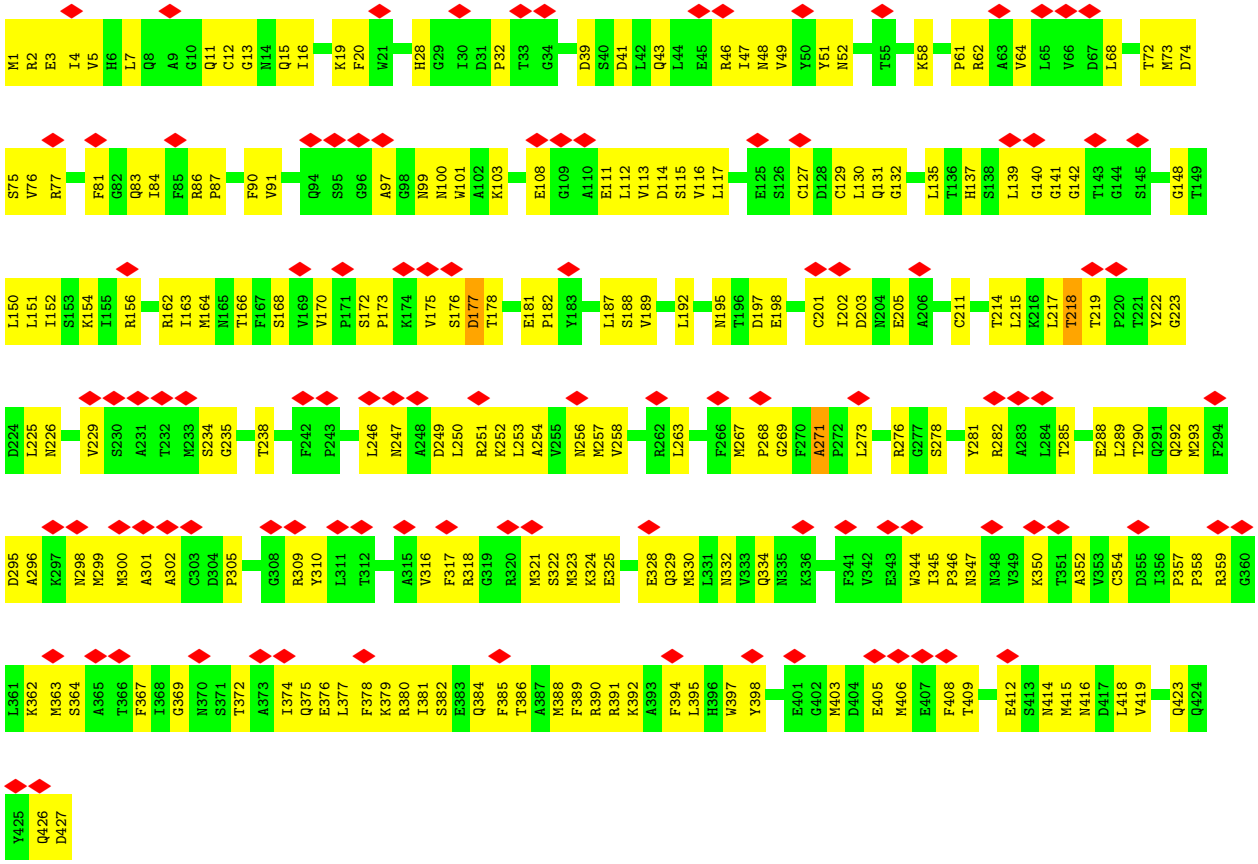






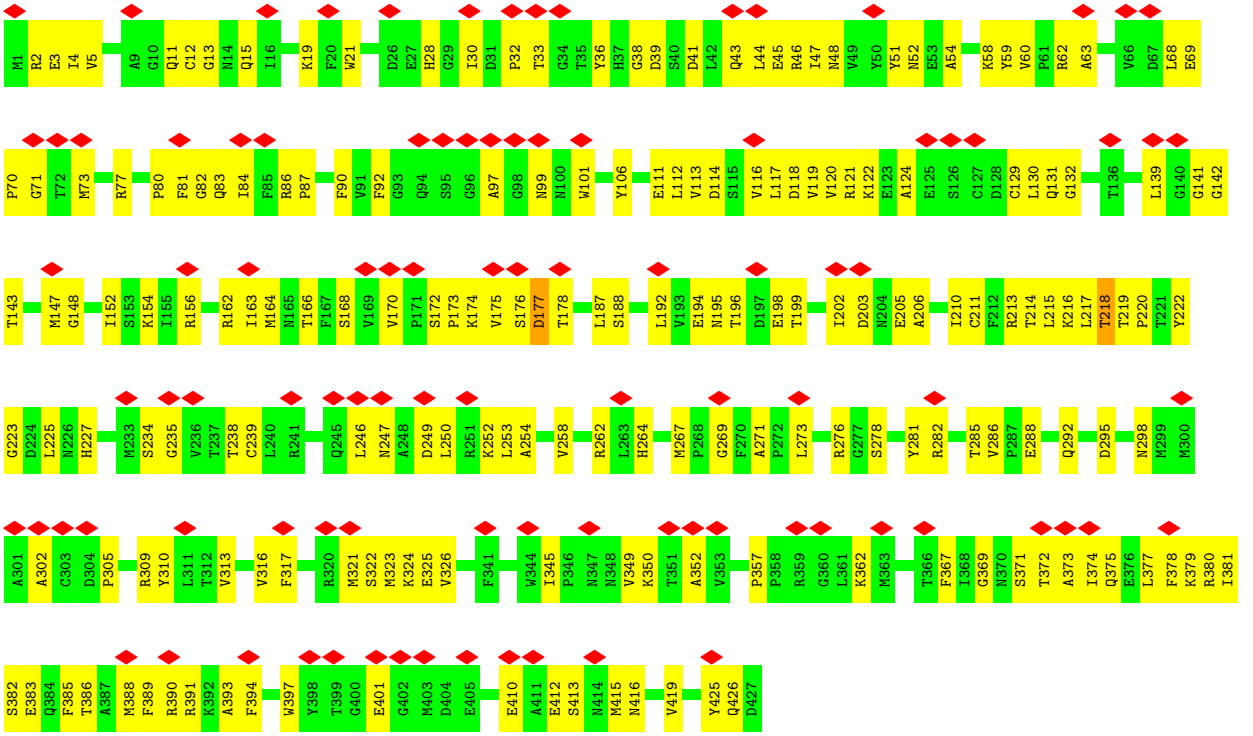
• Molecule 3: Tubulin beta-4B chain

Chain VF:



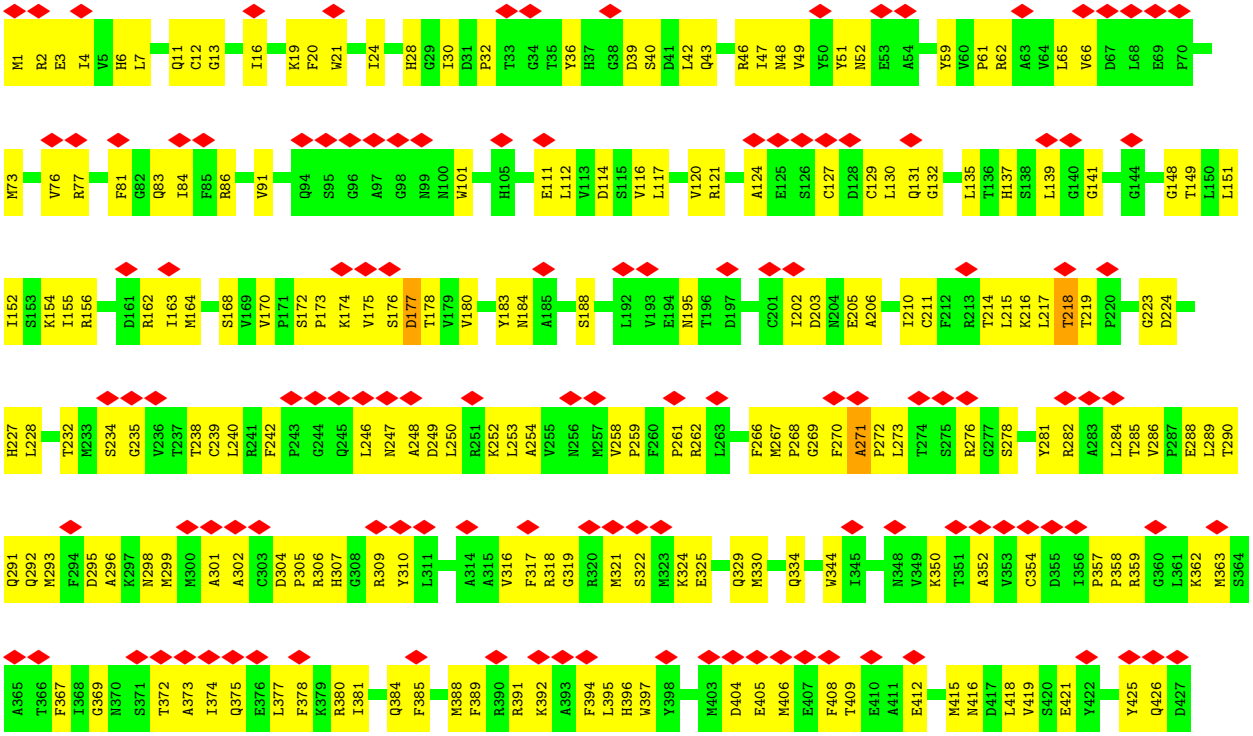
• Molecule 3: Tubulin beta-4B chain

Chain VH:



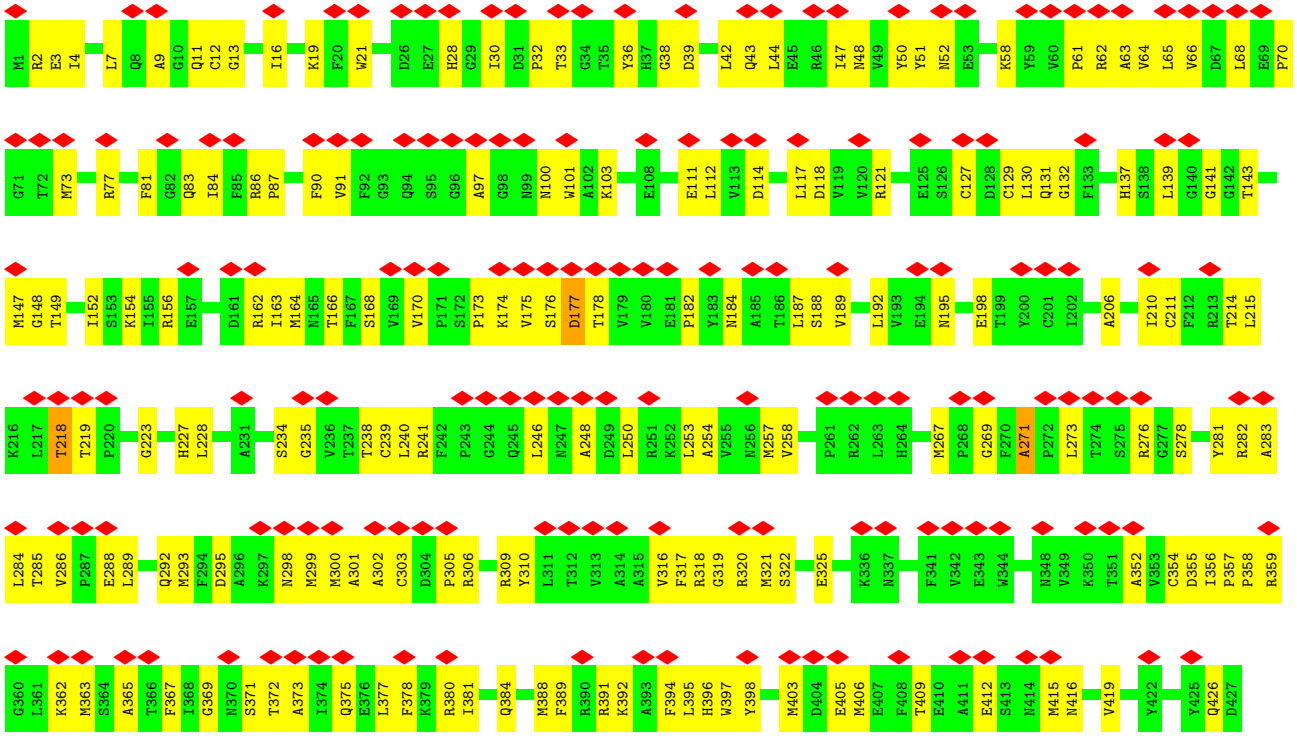
• Molecule 3: Tubulin beta-4B chain

Chain VJ:



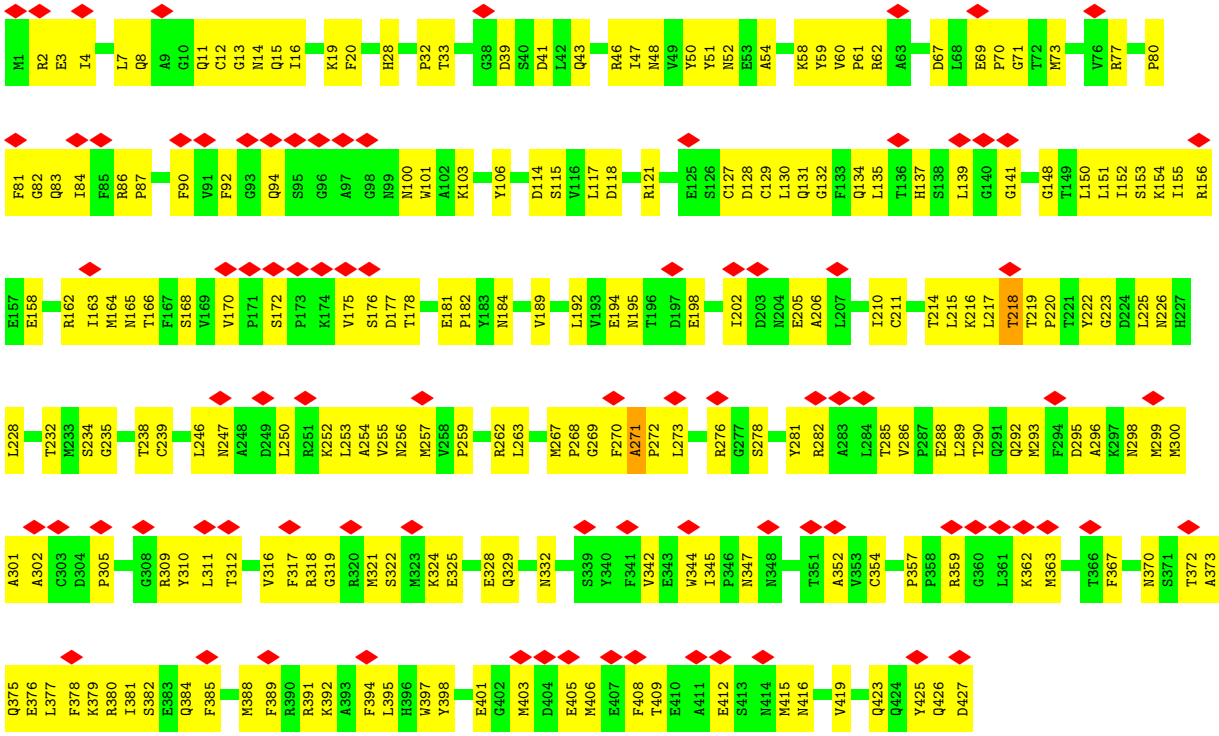
• Molecule 3: Tubulin beta-4B chain

Chain VL:



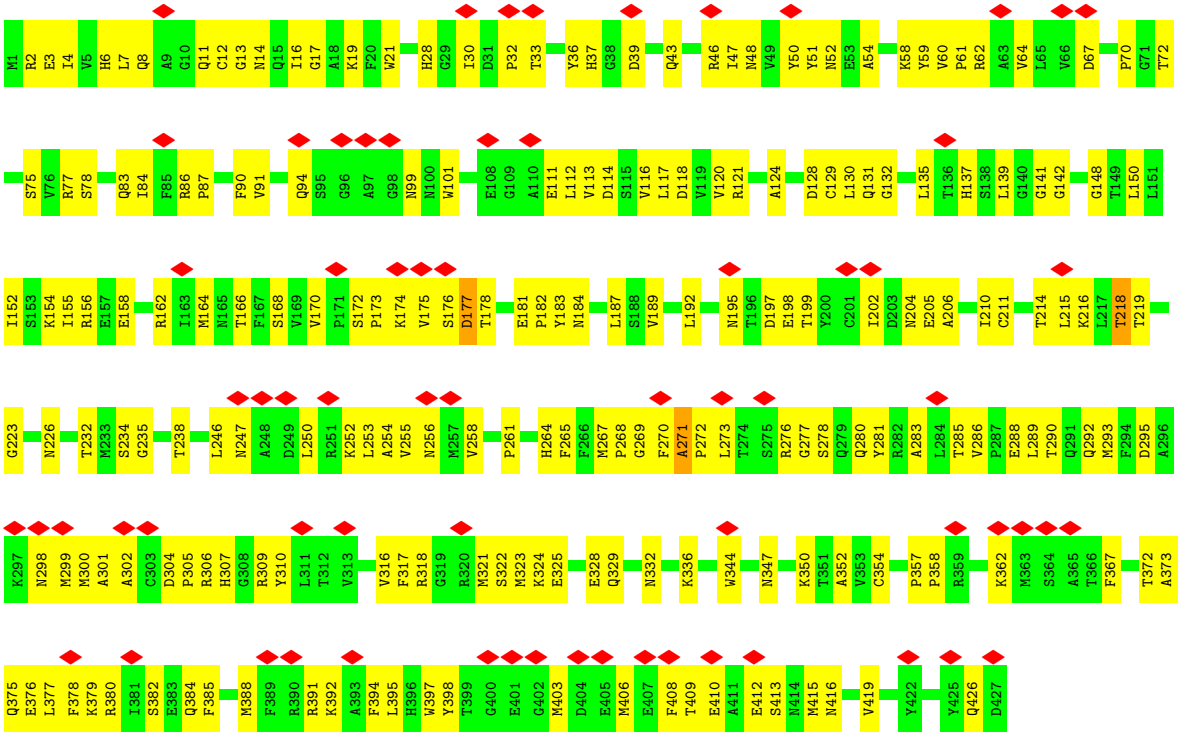
• Molecule 3: Tubulin beta-4B chain

Chain WB:



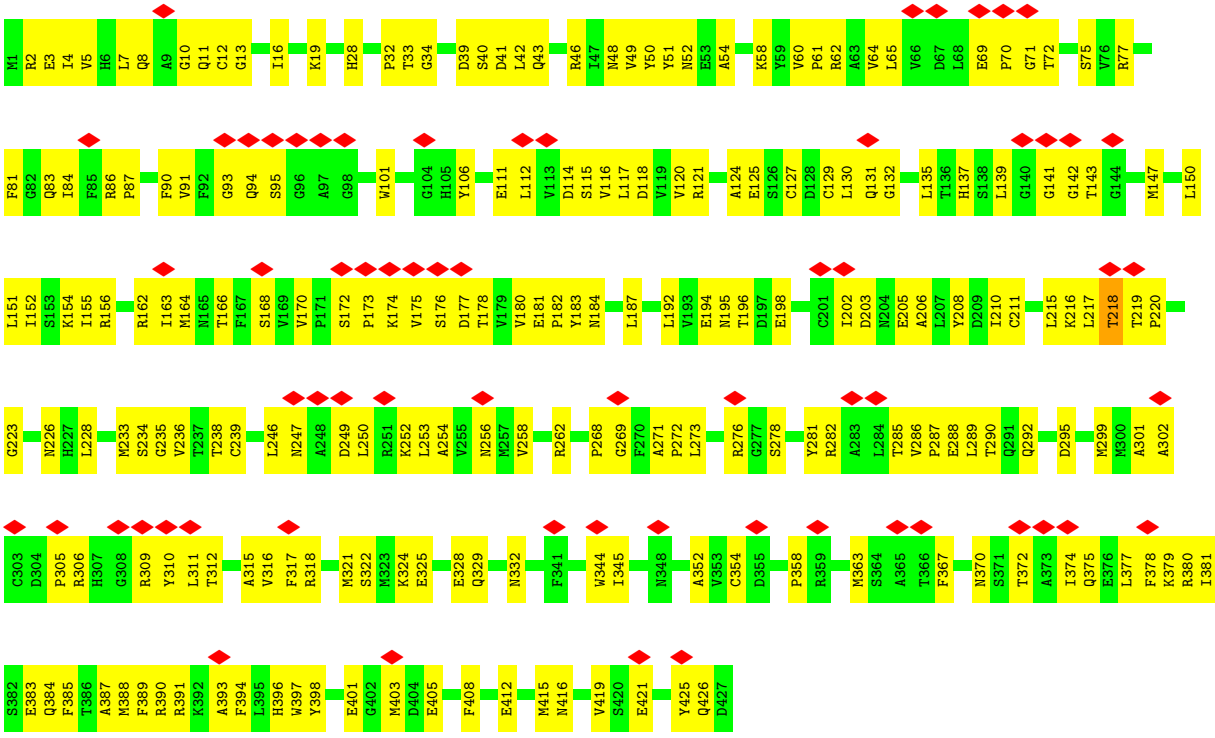
• Molecule 3: Tubulin beta-4B chain

Chain WD:



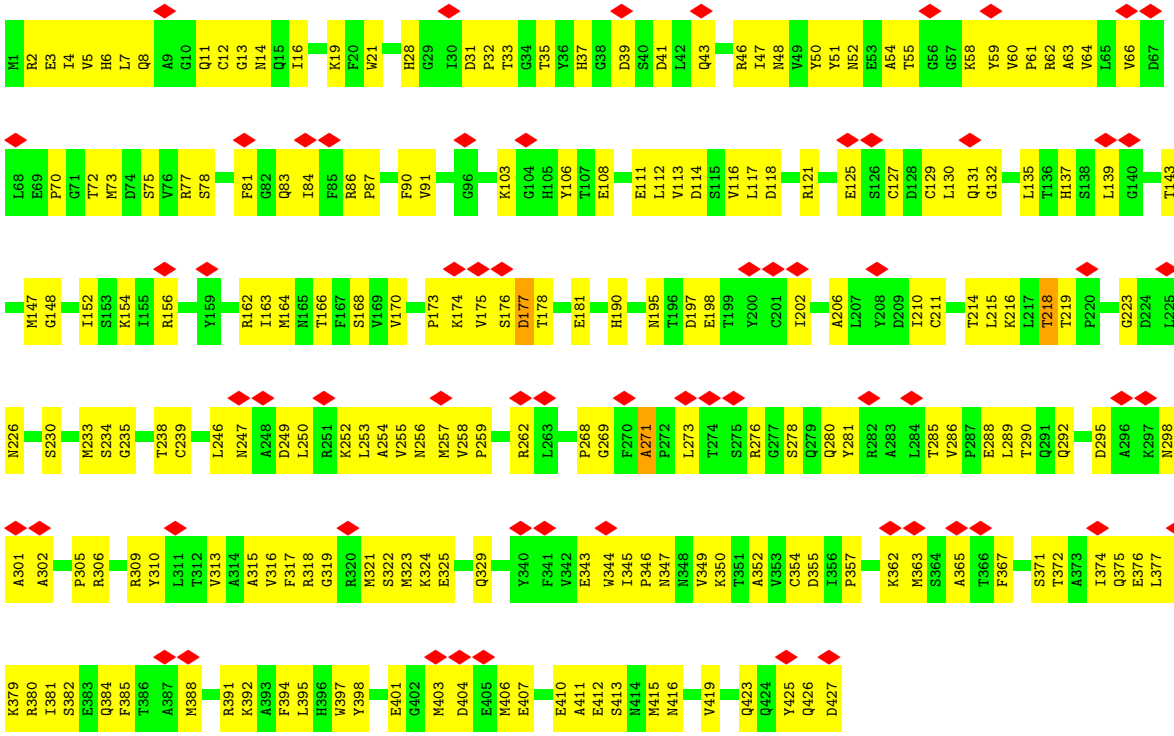
• Molecule 3: Tubulin beta-4B chain

Chain WF:



• Molecule 3: Tubulin beta-4B chain

Chain WH:



• Molecule 3: Tubulin beta-4B chain

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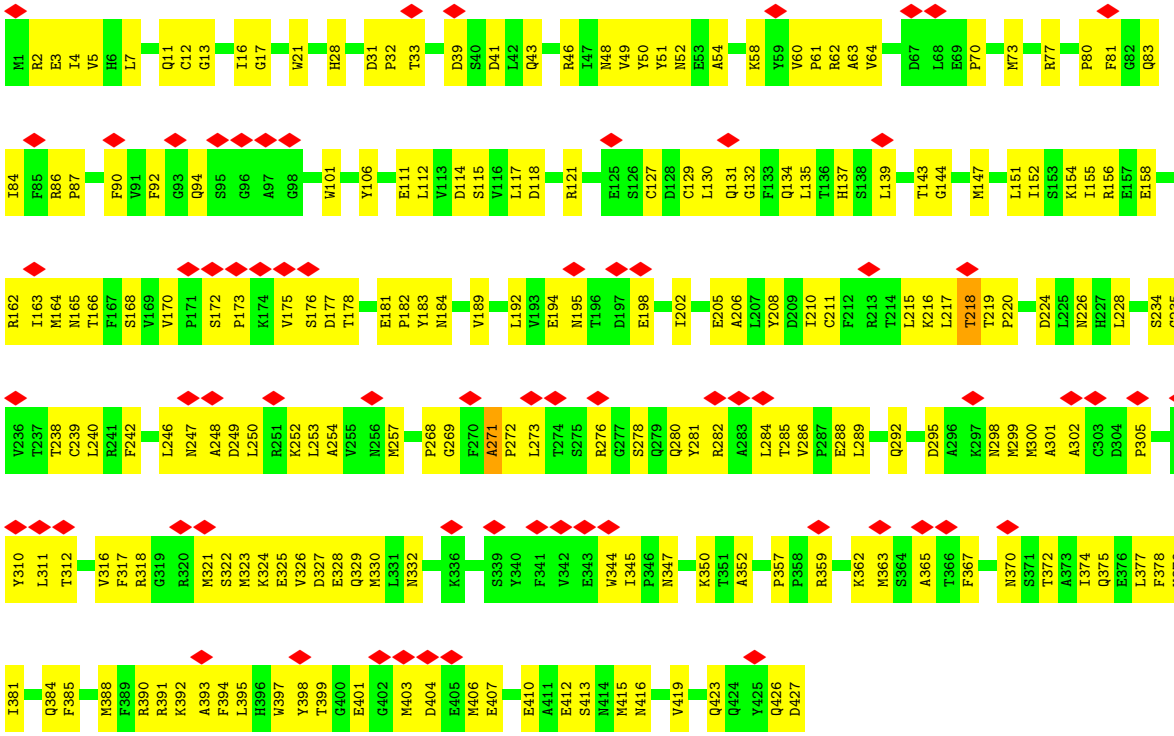
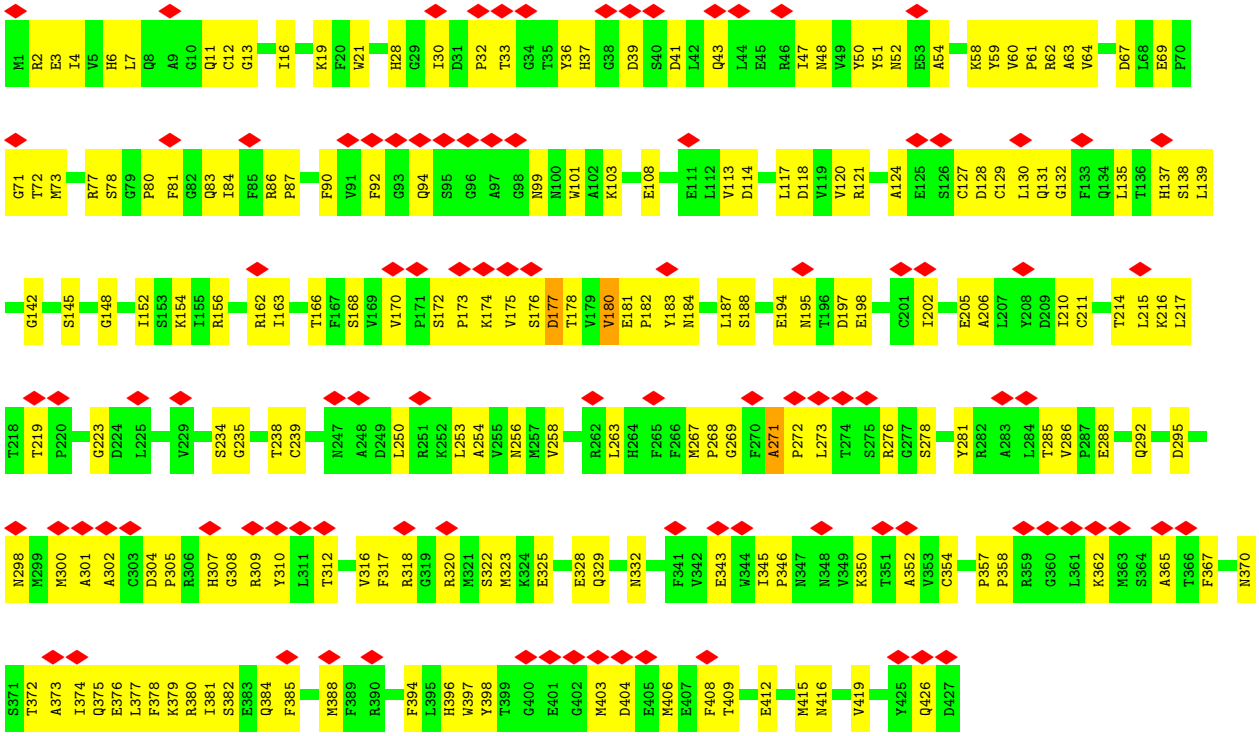


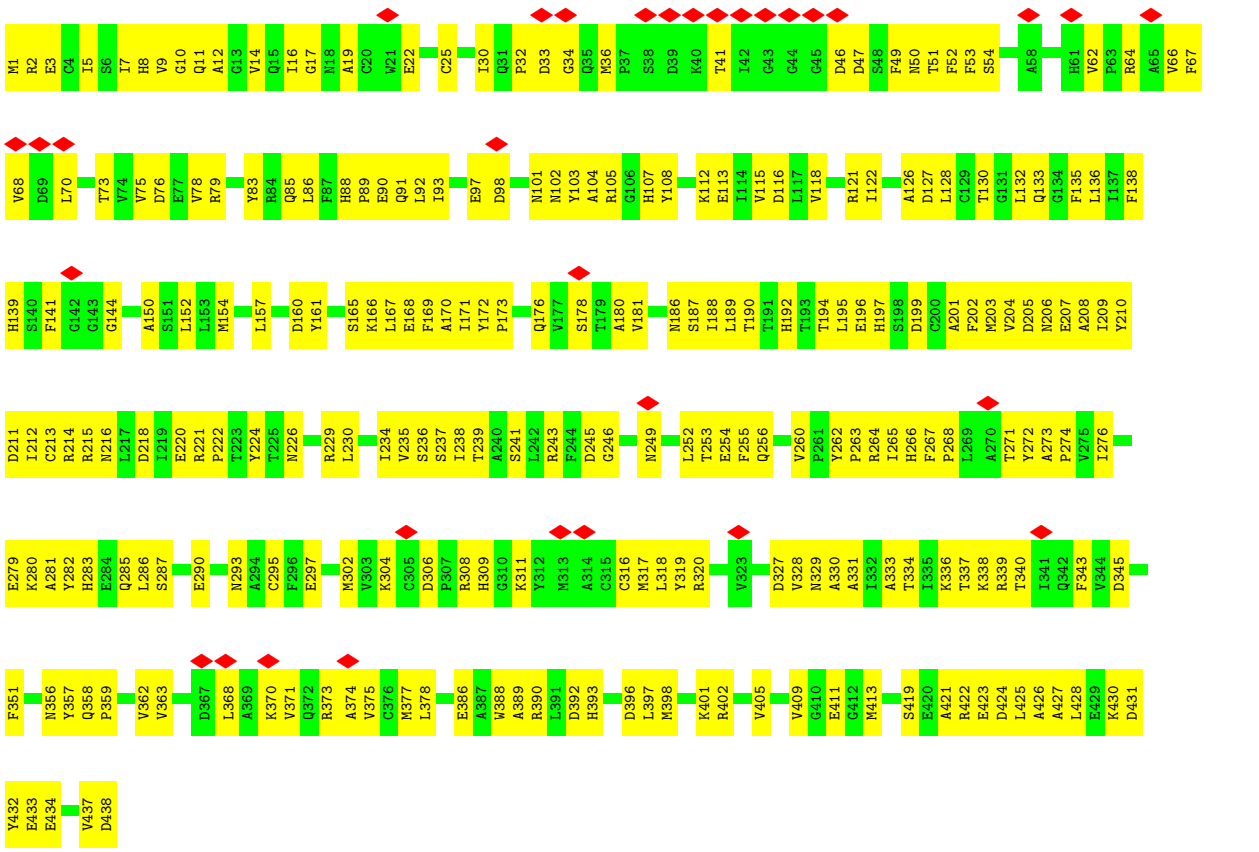
• Molecule 3: Tubulin beta-4B chain

Chain WL:



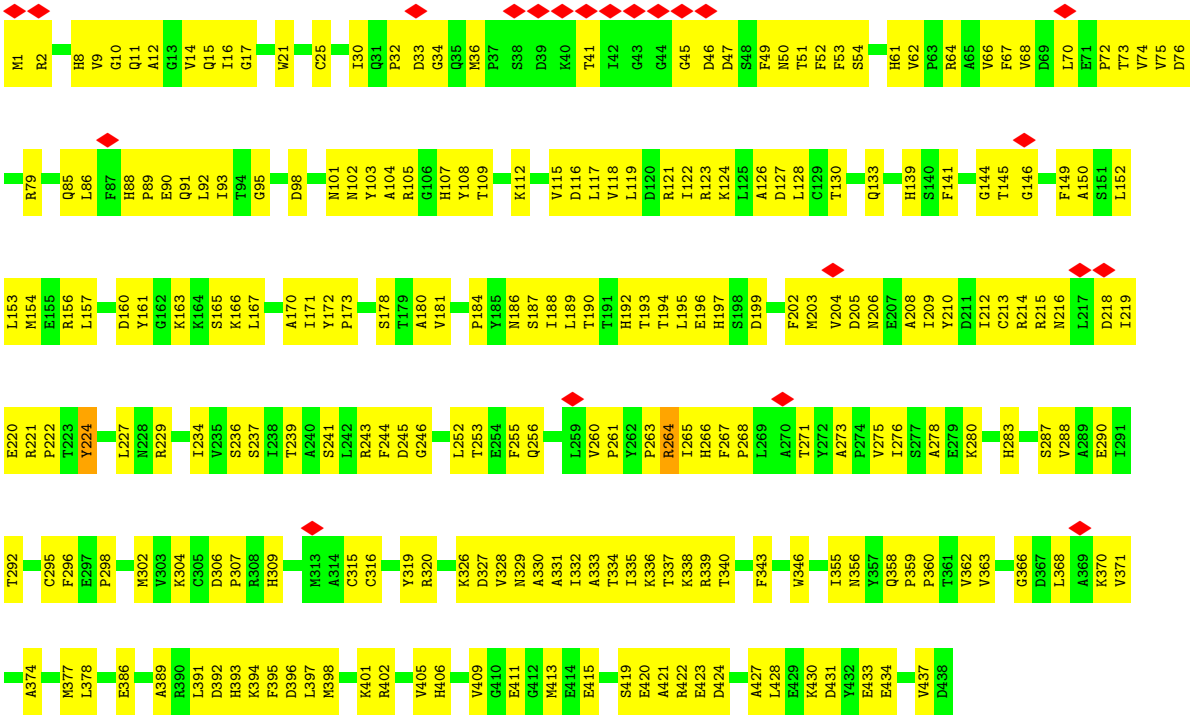
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain AC:



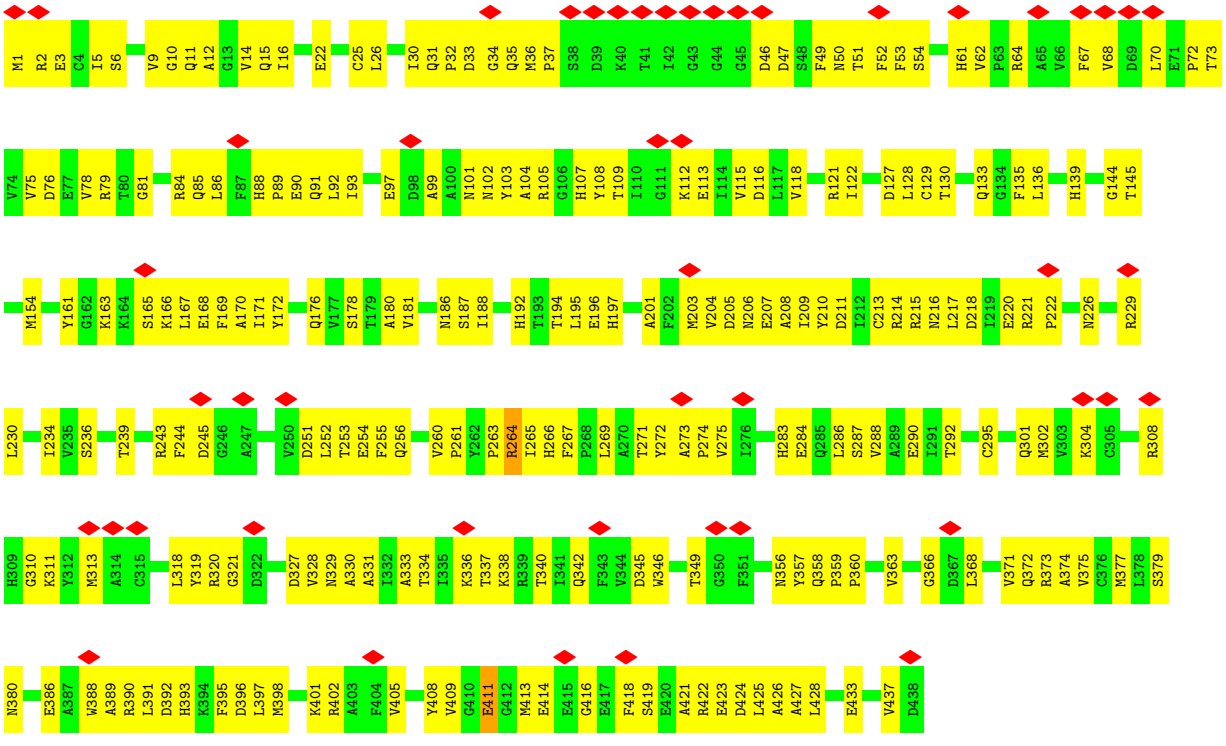
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain AE:



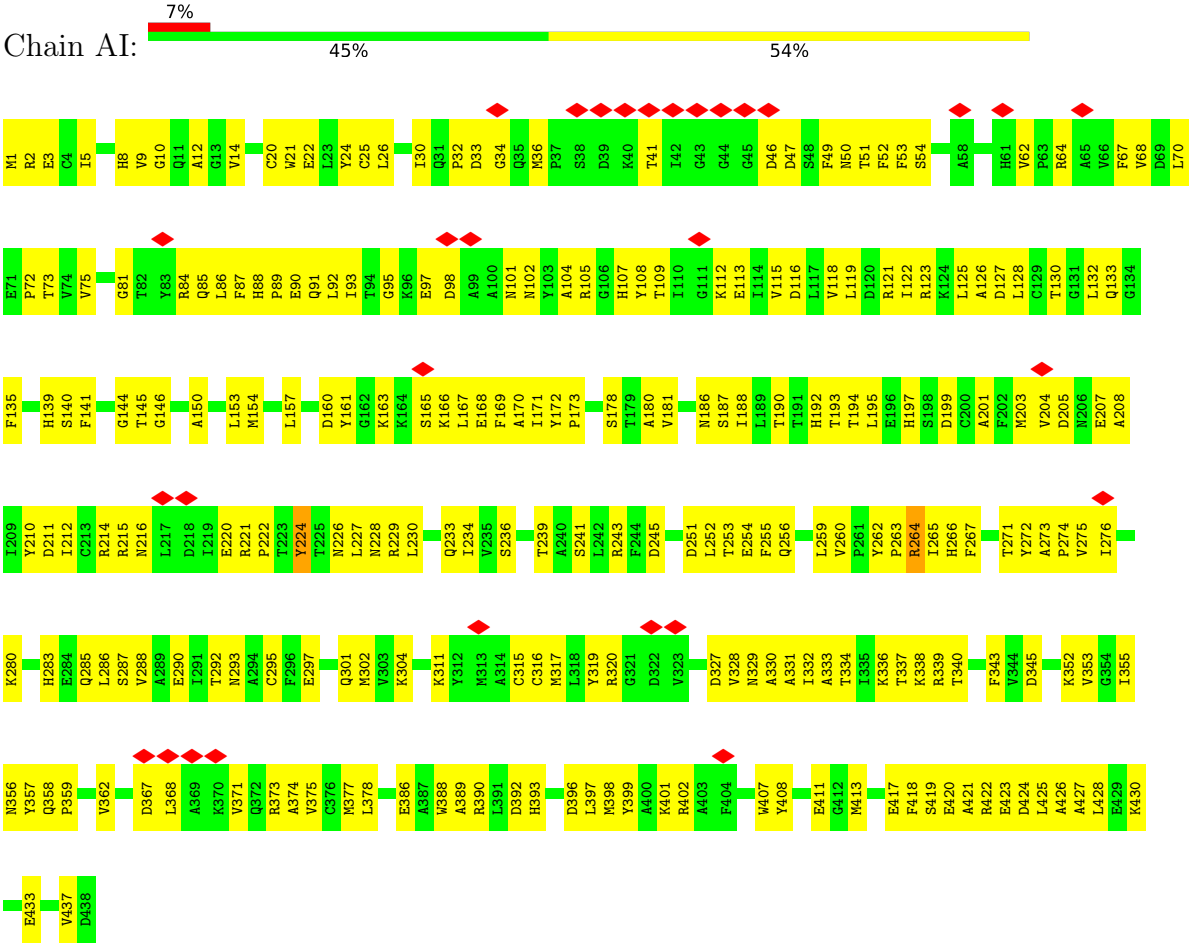
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain AG:



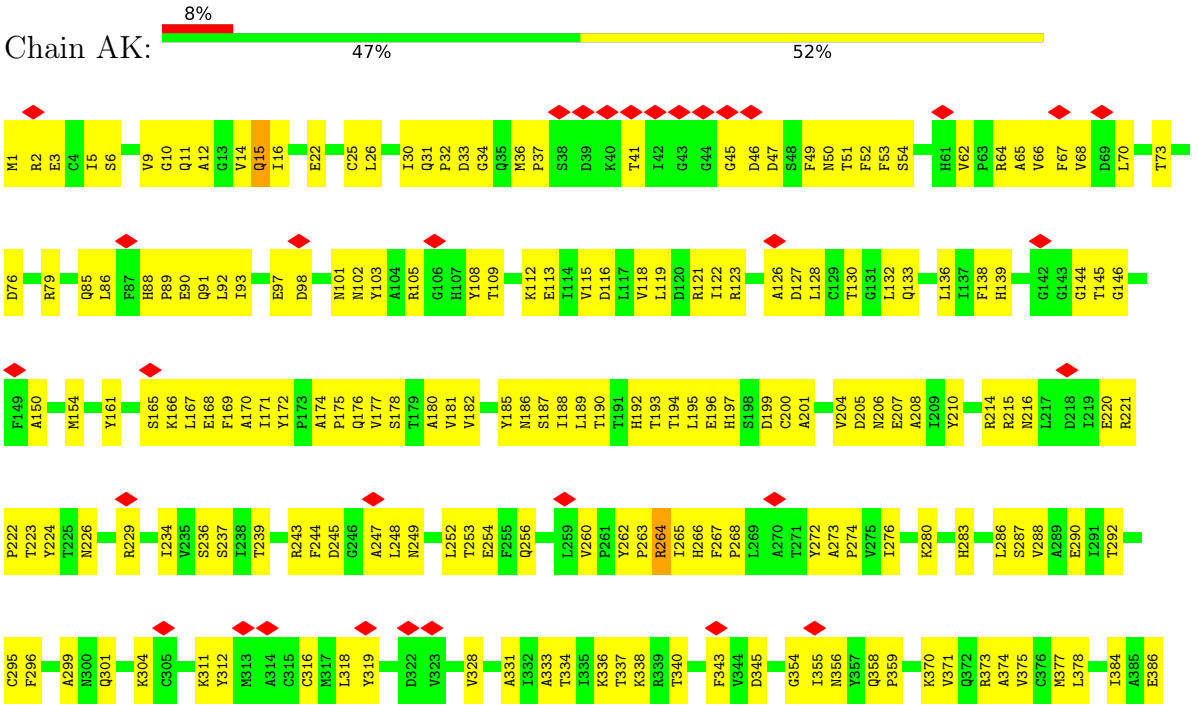
• Molecule 4: Detyrosinated tubulin alpha-3 chain

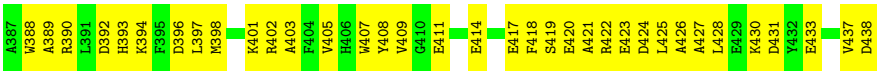
Chain AI:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

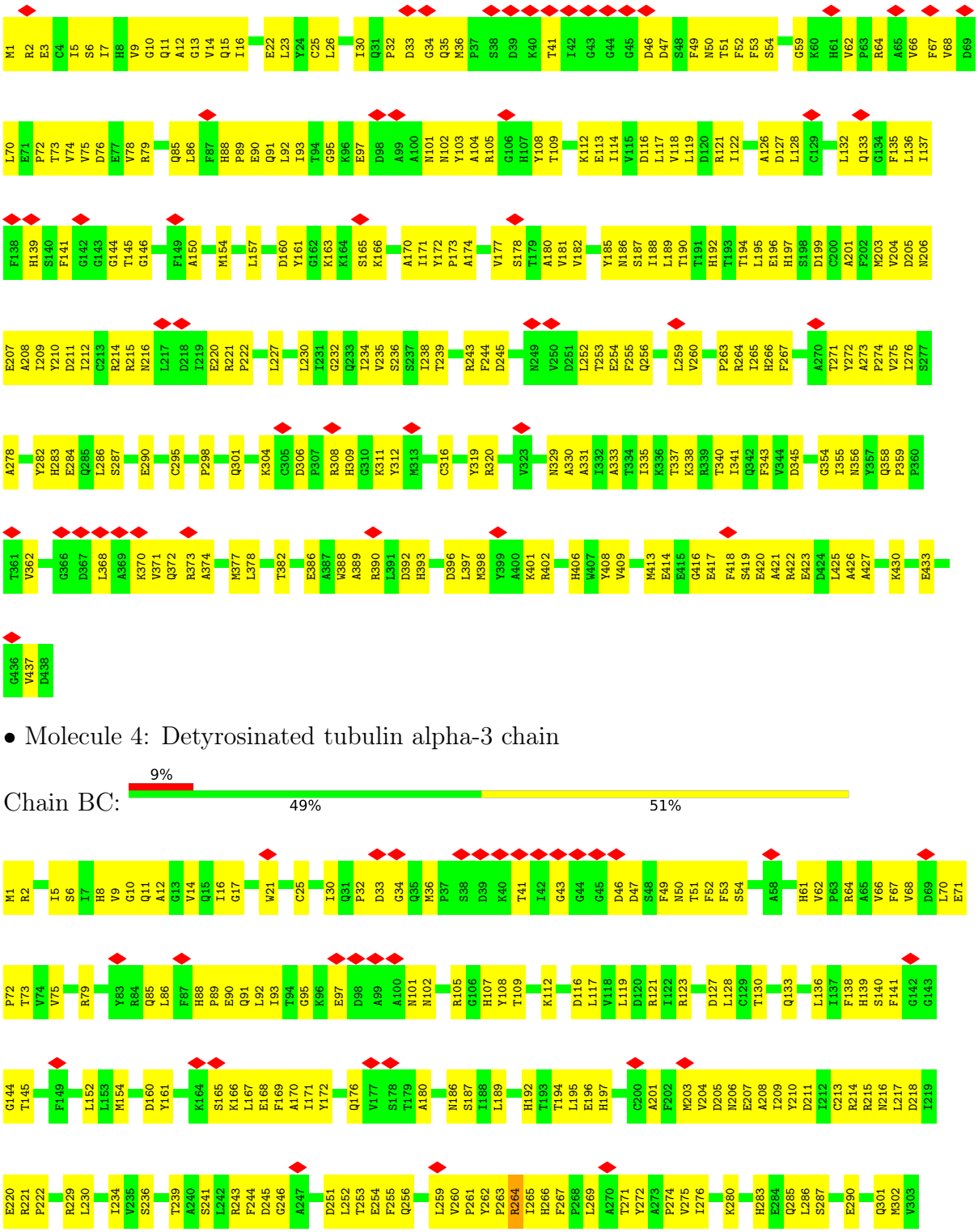
Chain AK:





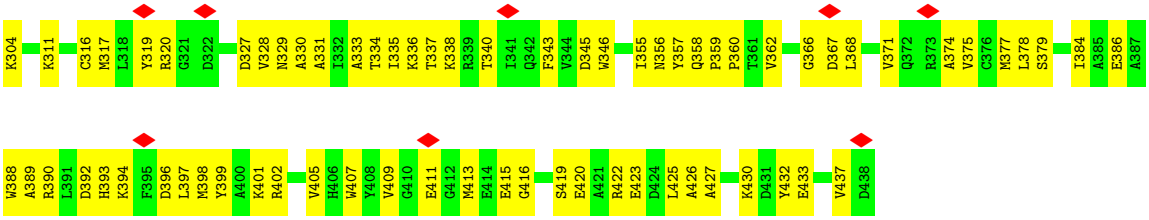
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain AM:



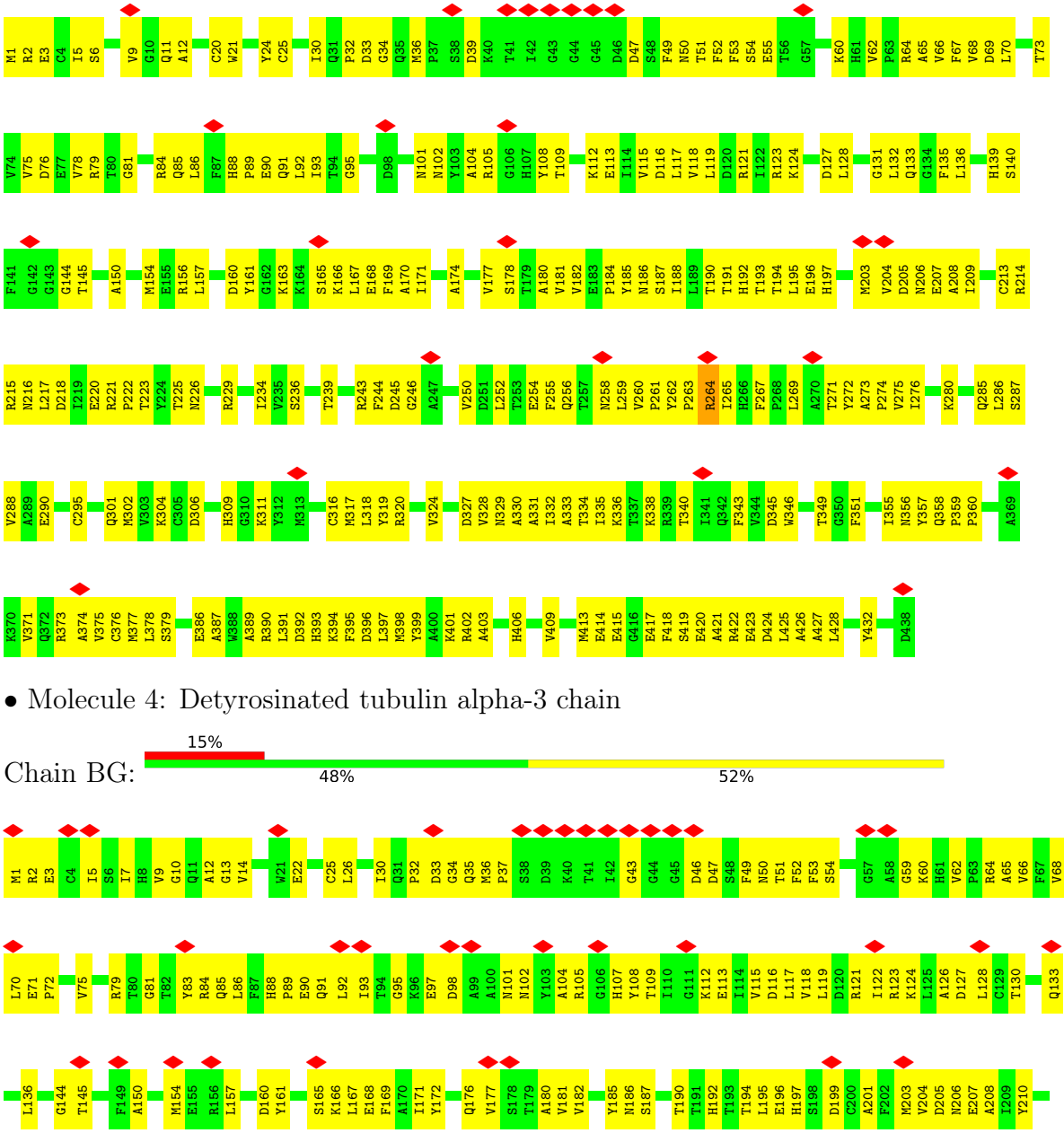
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain BC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain BE:

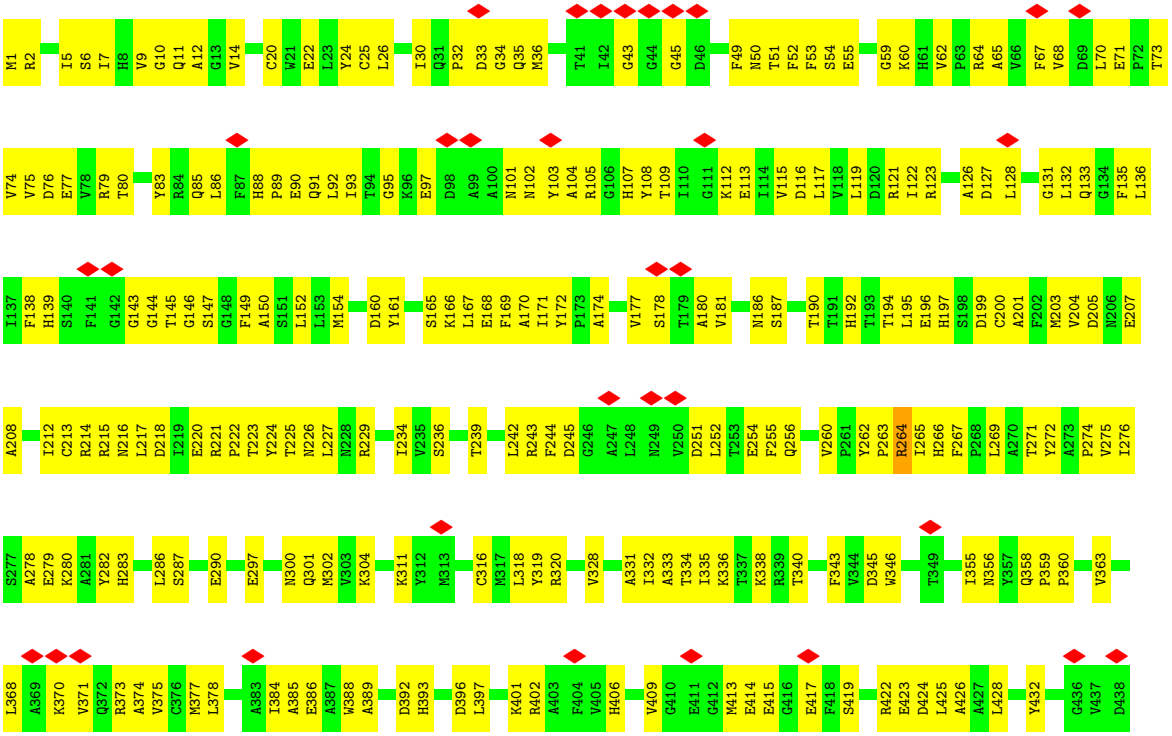


• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain BG:

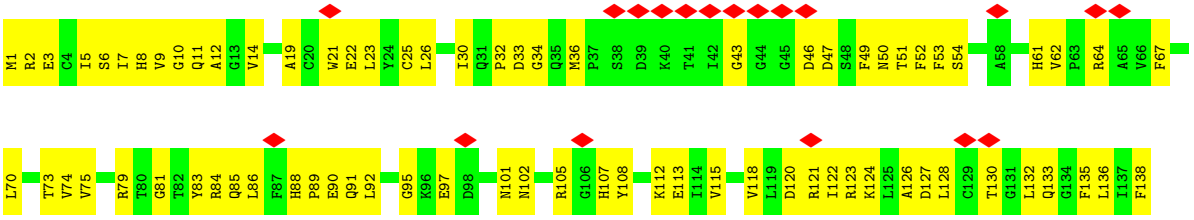
• Molecule 4: Detyrosinated tubulin alpha-3 chain

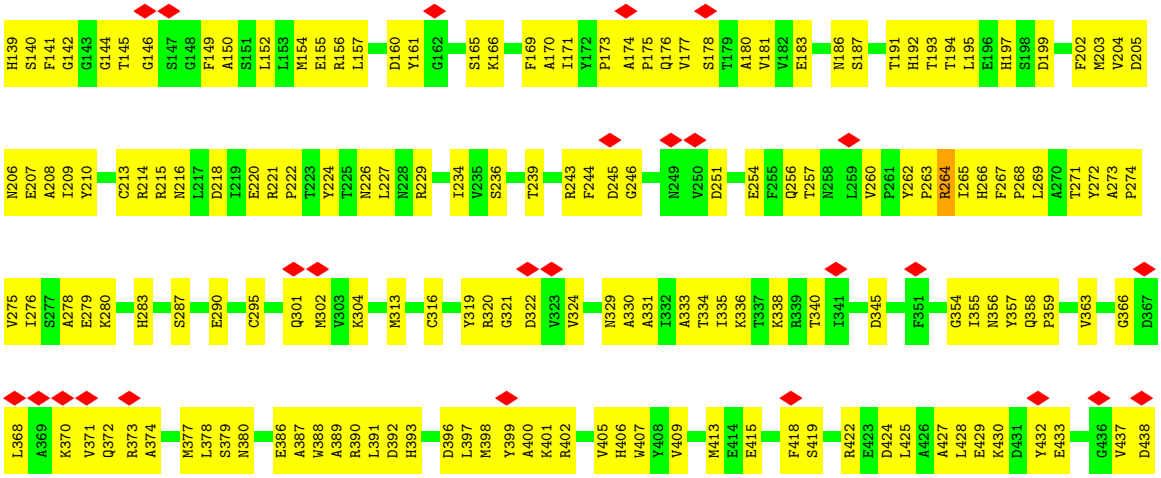
Chain BI:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

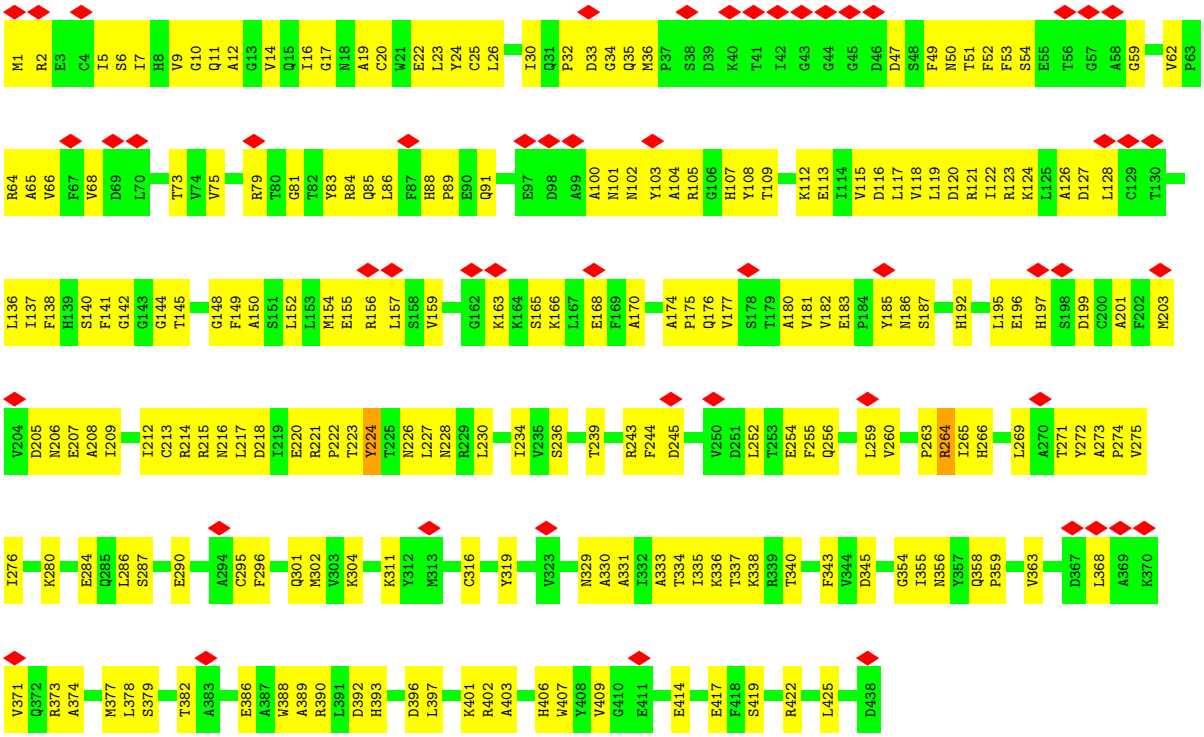
Chain BK:





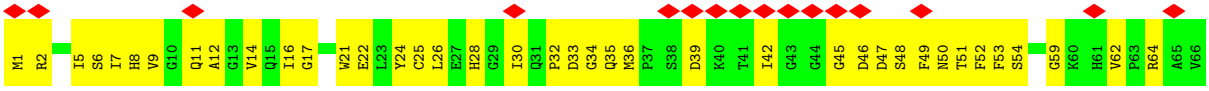
• Molecule 4: Detyrosinated tubulin alpha-3 chain

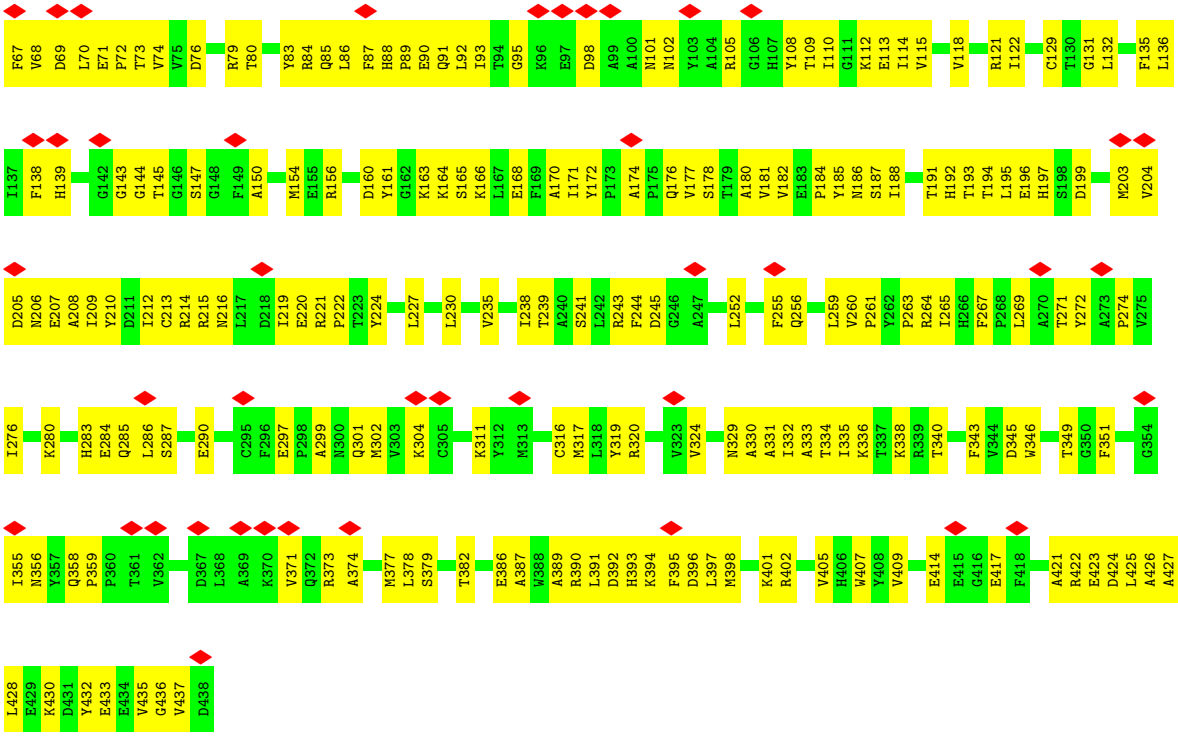
Chain BM:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

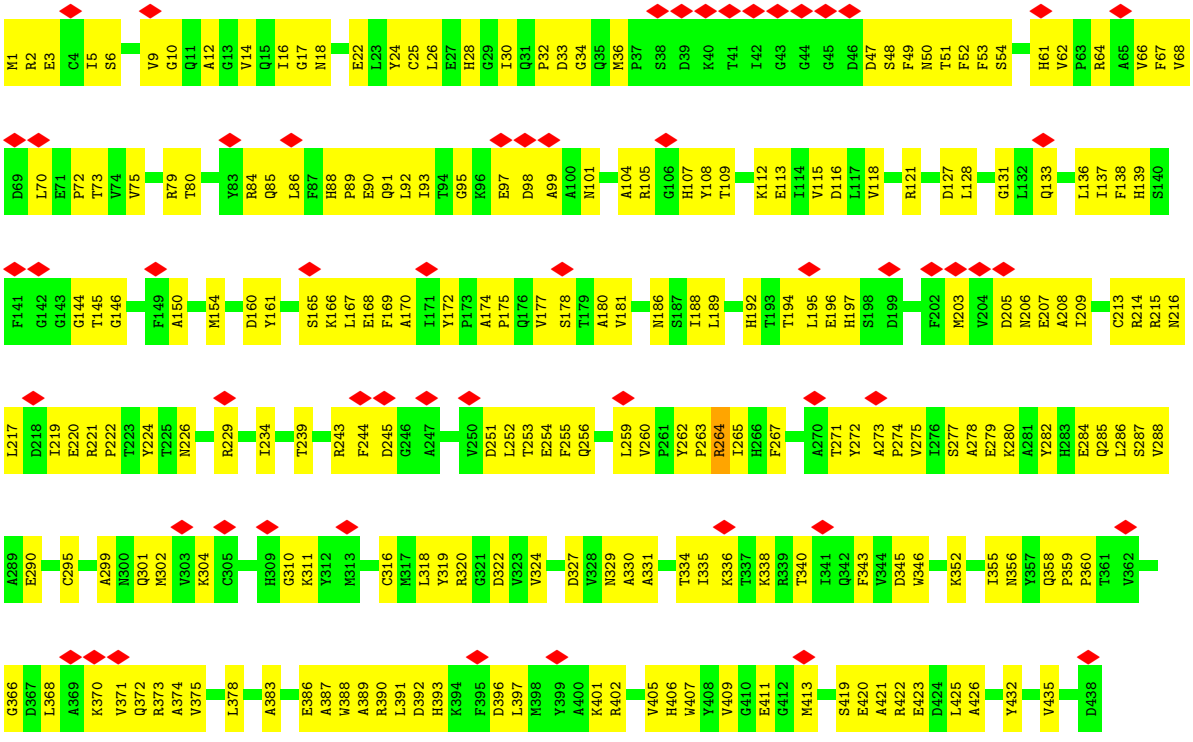
Chain CC:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain CE:

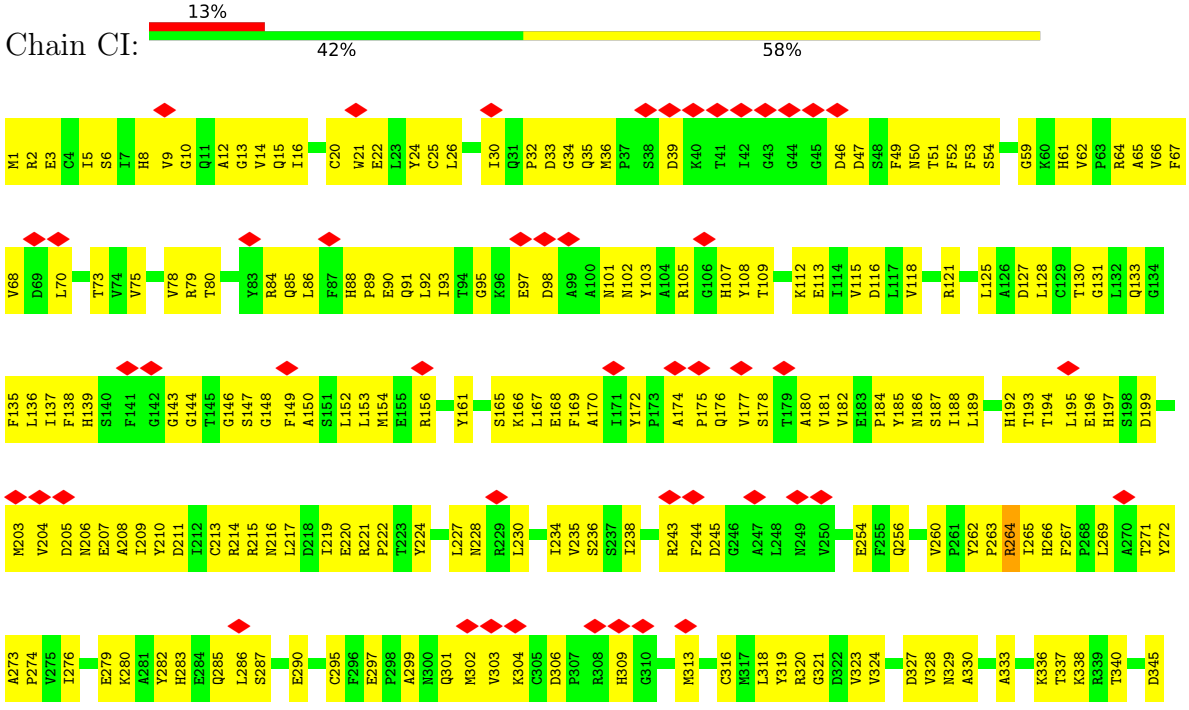


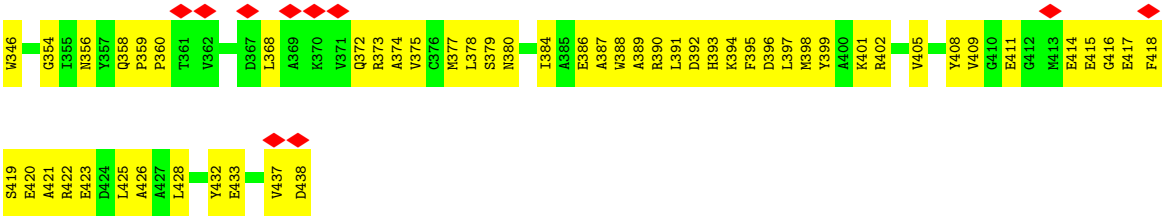
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain CG:

• Molecule 4: Detyrosinated tubulin alpha-3 chain

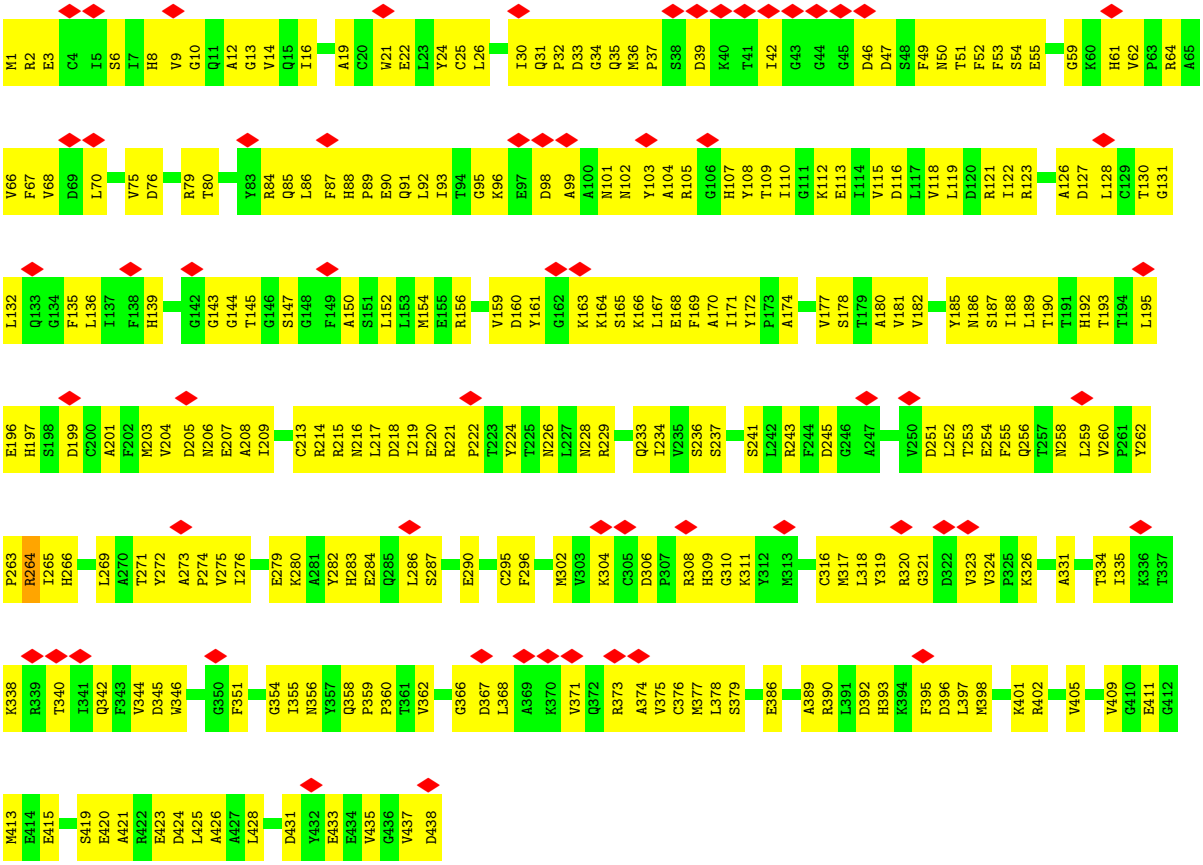
Chain CI:





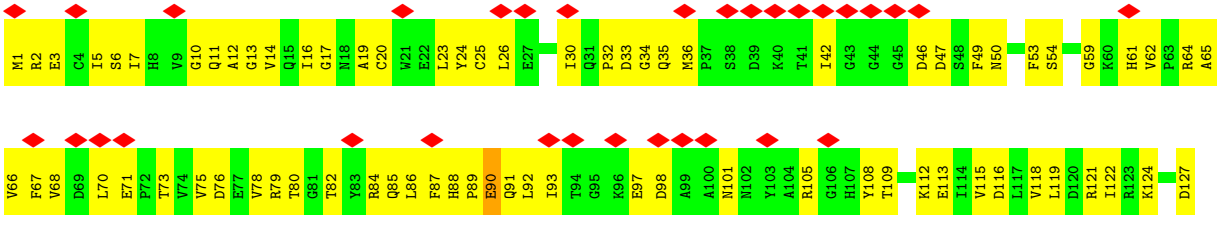
• Molecule 4: Detyrosinated tubulin alpha-3 chain

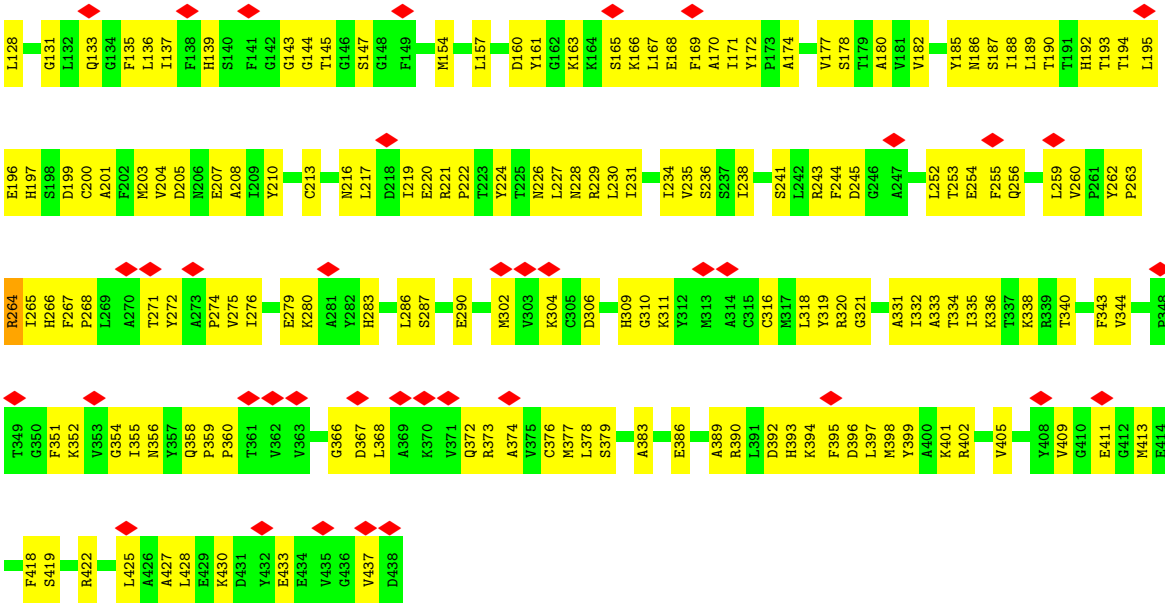
Chain CK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

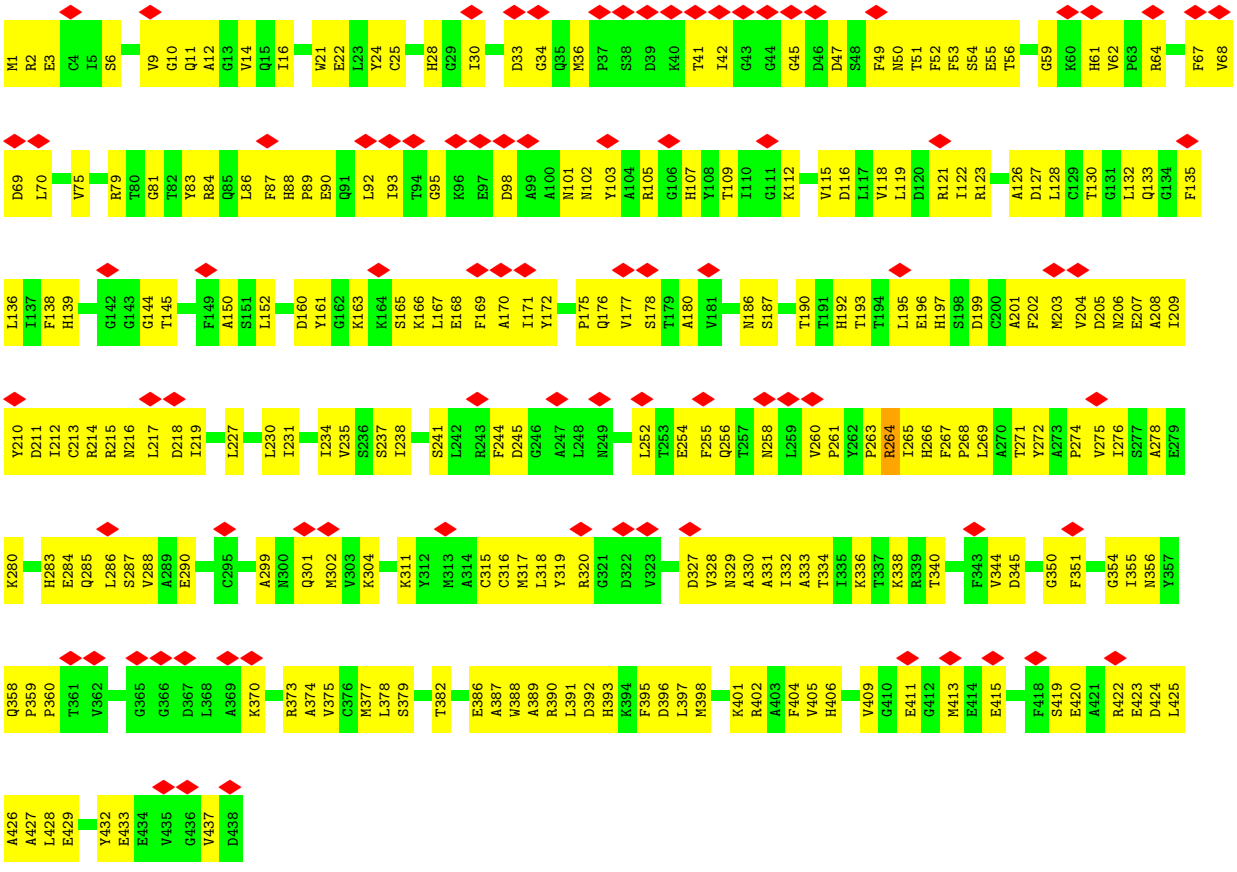
Chain CM:





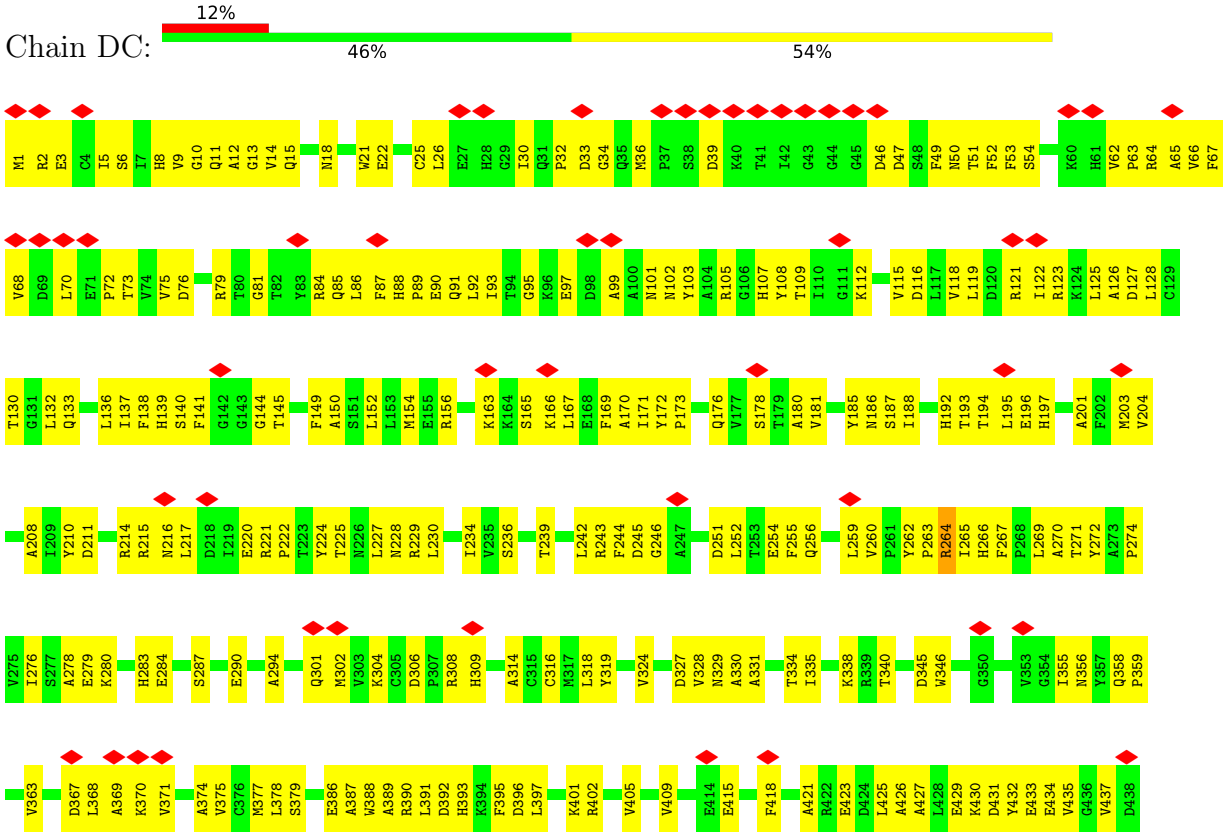
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain DA:



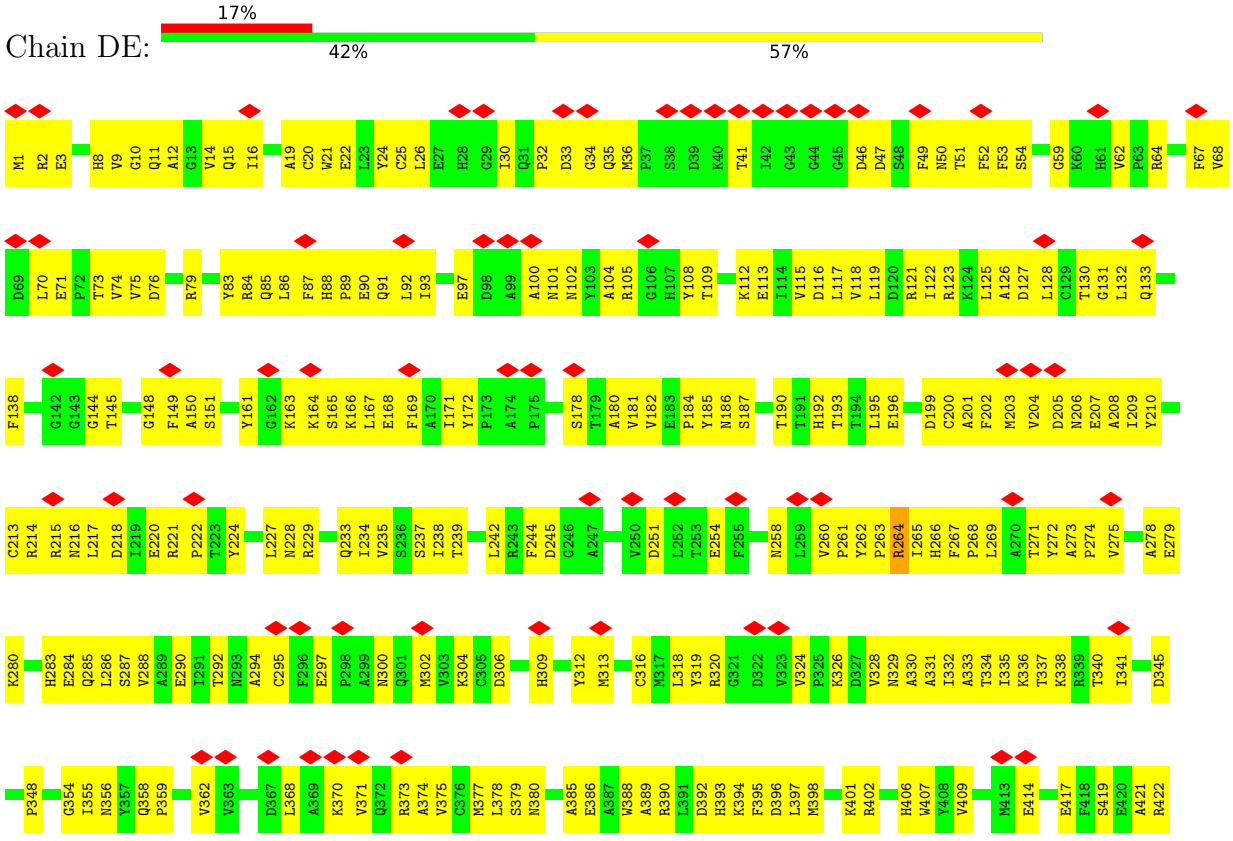
• Molecule 4: Detyrosinated tubulin alpha-3 chain

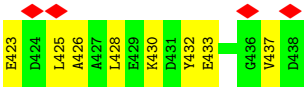
Chain DC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain DE:



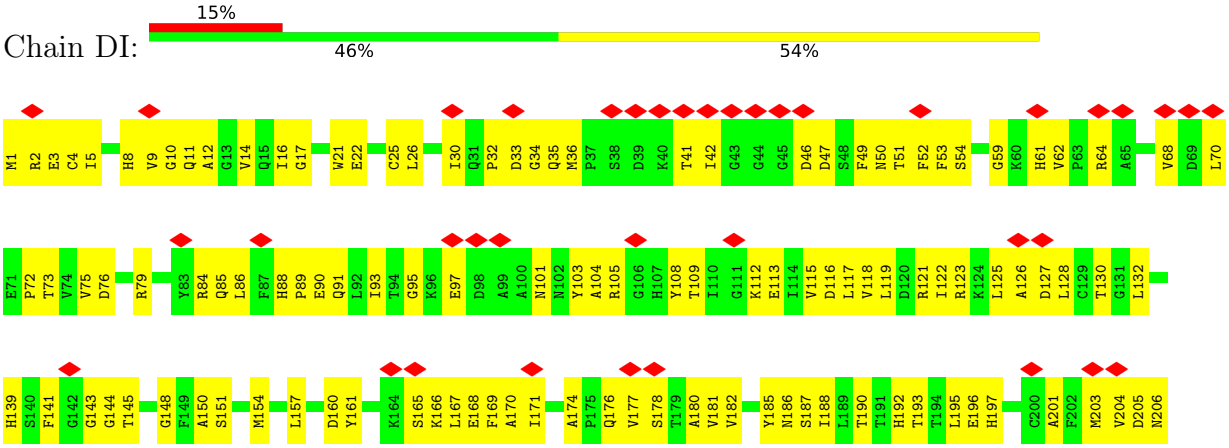


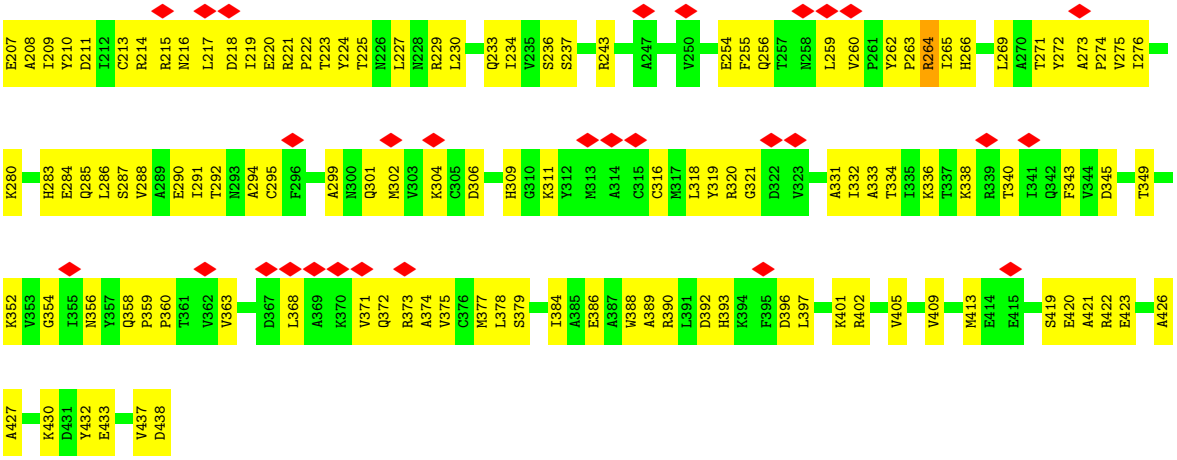
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain DG:

• Molecule 4: Detyrosinated tubulin alpha-3 chain

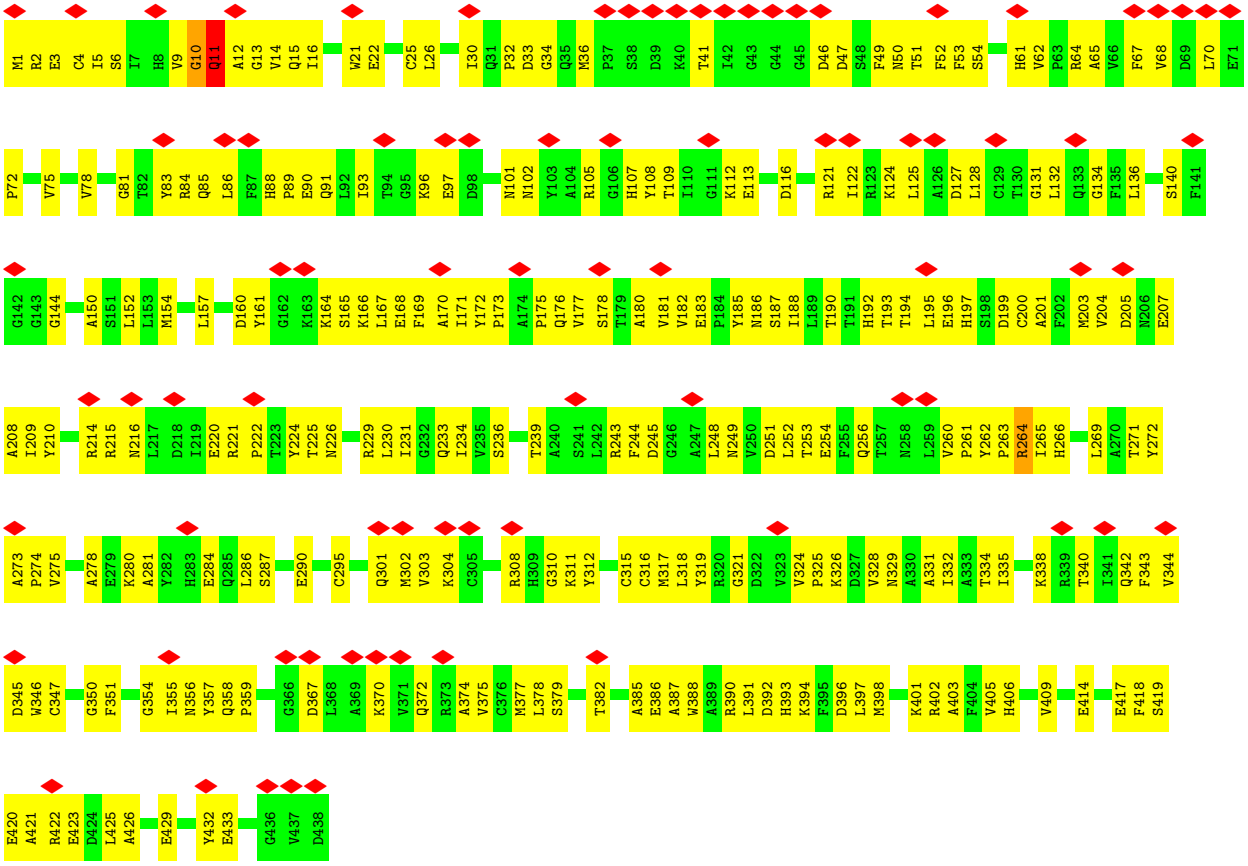
Chain DI:





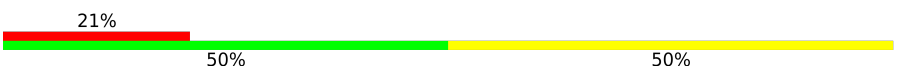
• Molecule 4: Detyrosinated tubulin alpha-3 chain

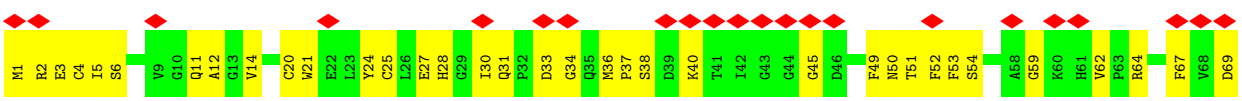
Chain DK:

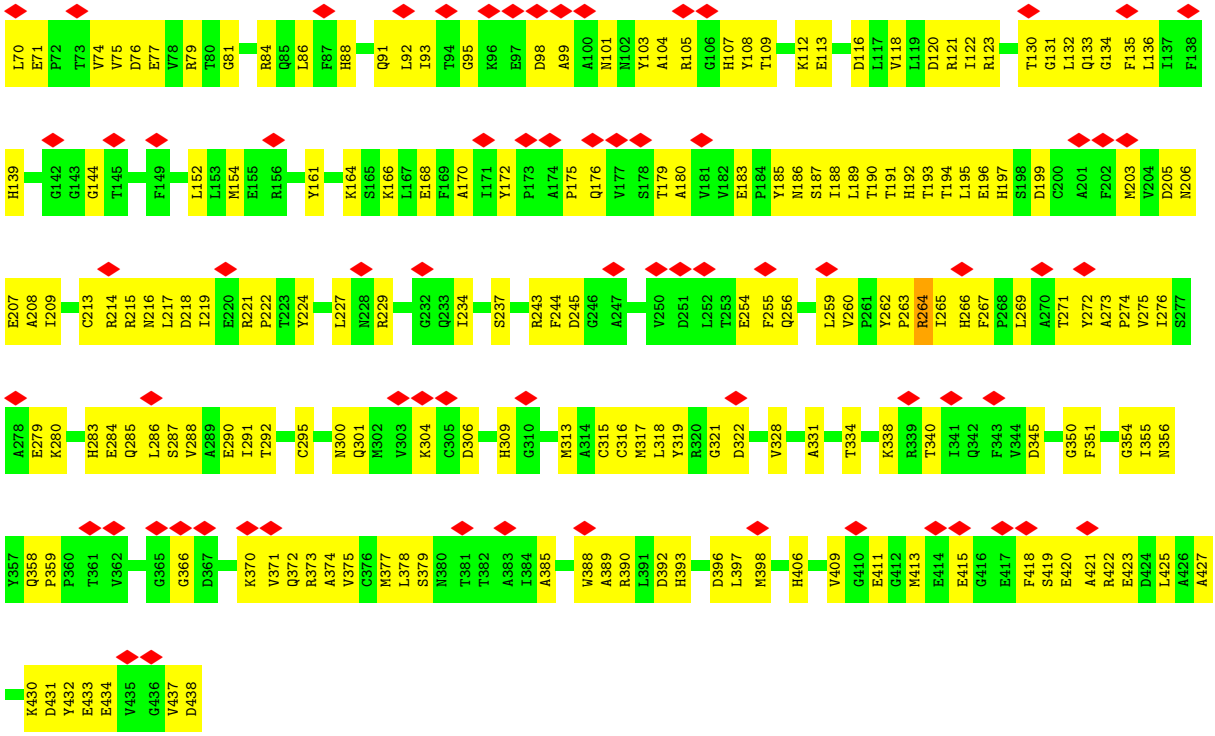


• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain EA:







• Molecule 4: Detyrosinated tubulin alpha-3 chain

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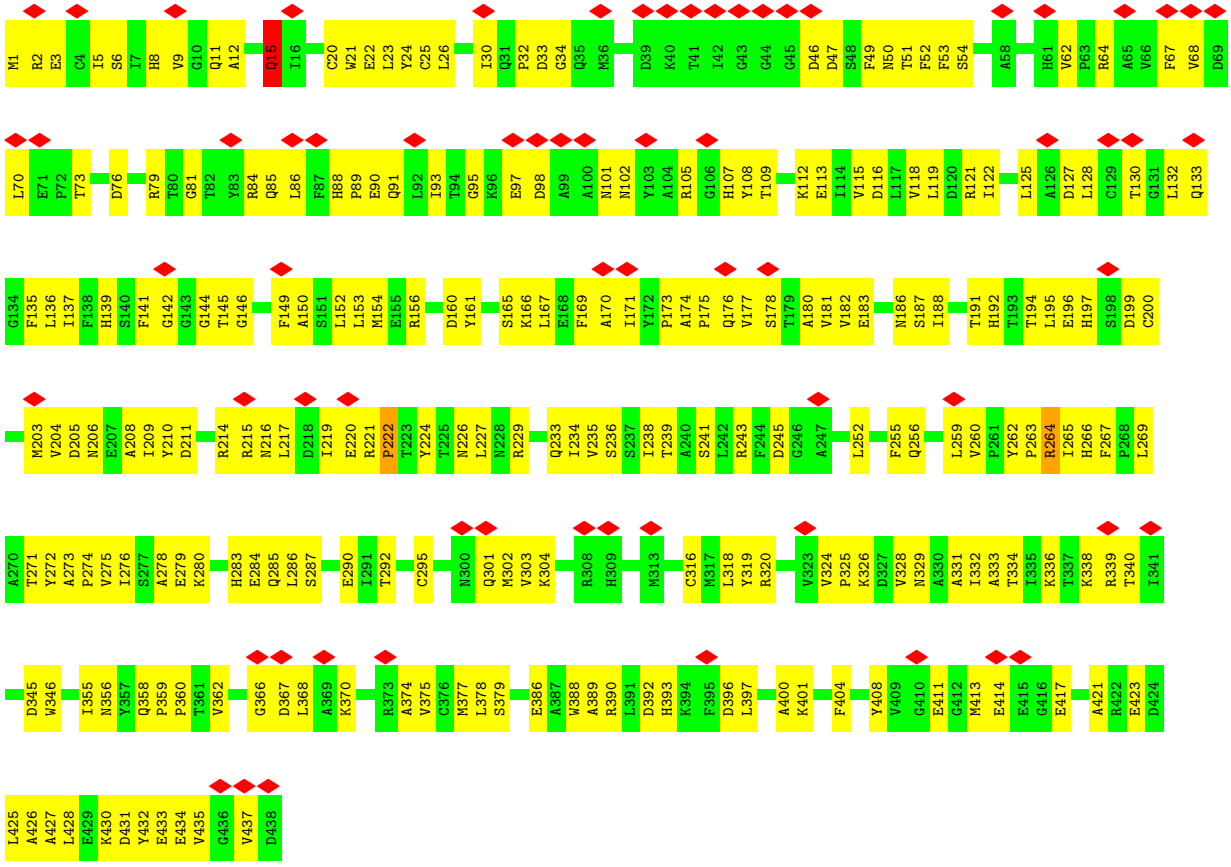
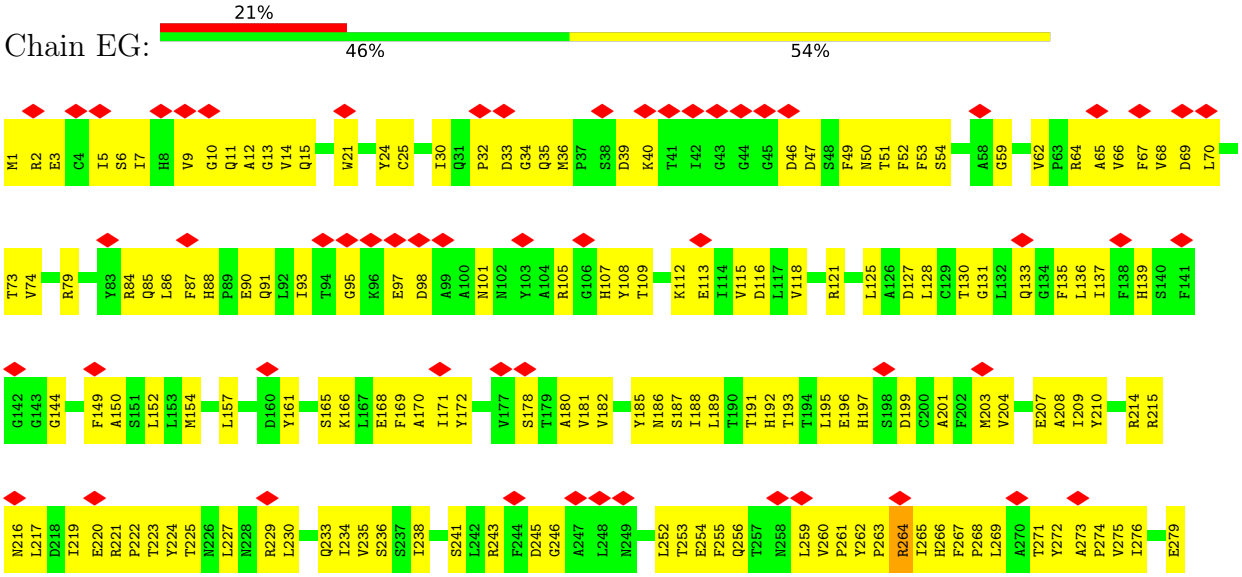


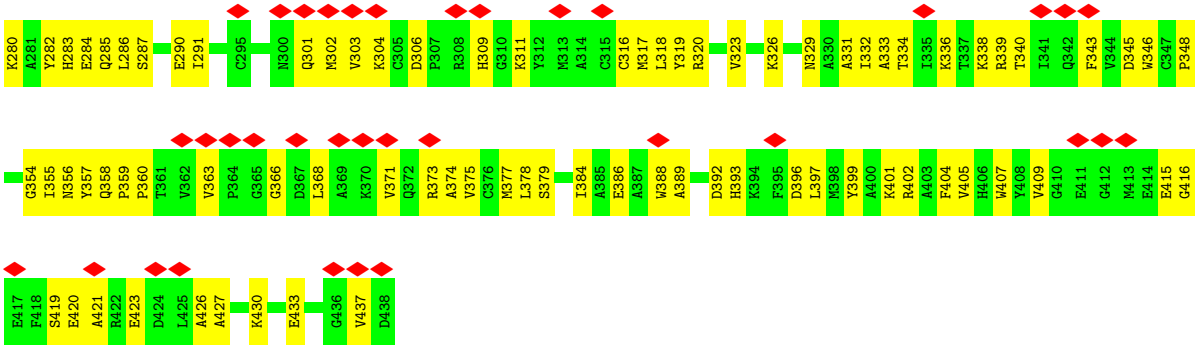
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain EE:

• Molecule 4: Detyrosinated tubulin alpha-3 chain

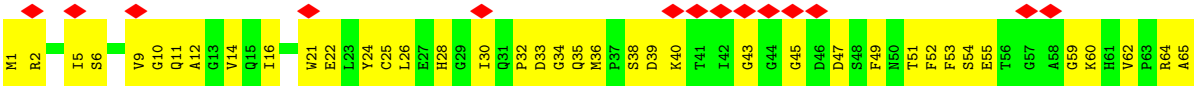
Chain EG:

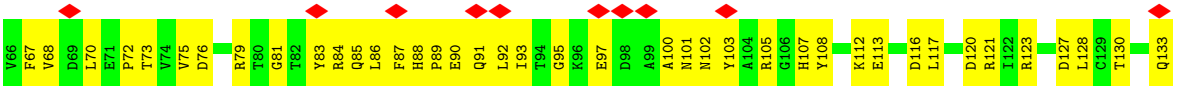


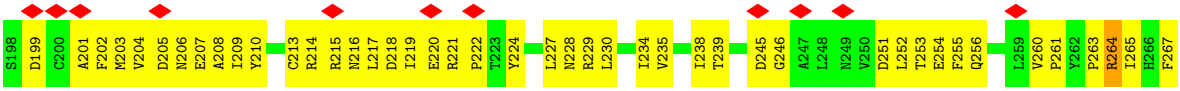


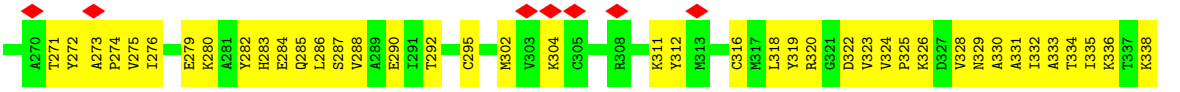
• Molecule 4: Detyrosinated tubulin alpha-3 chain

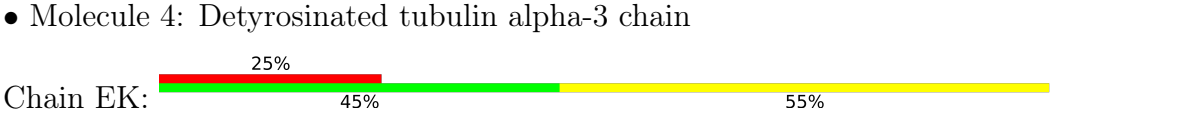
Chain EI:

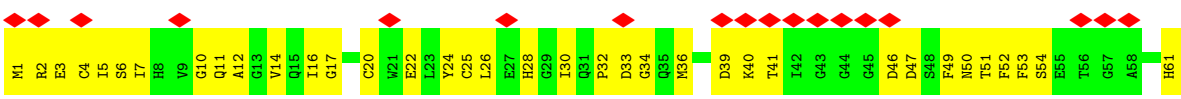






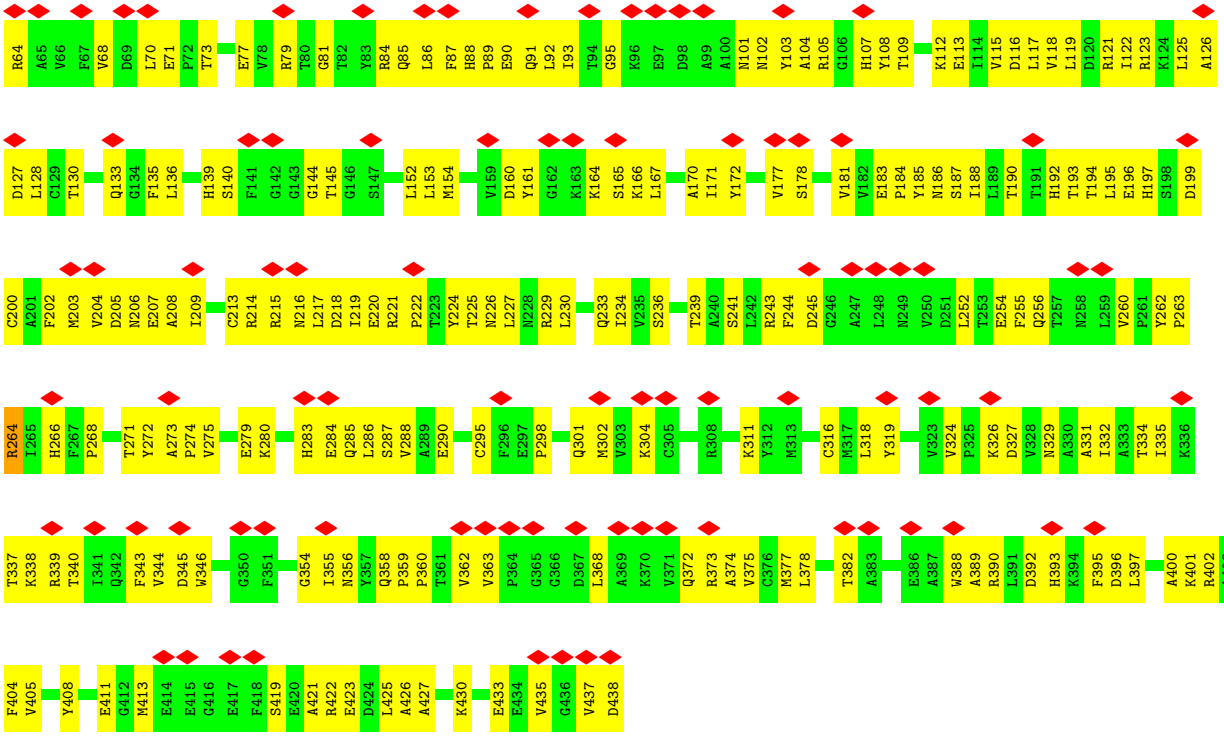






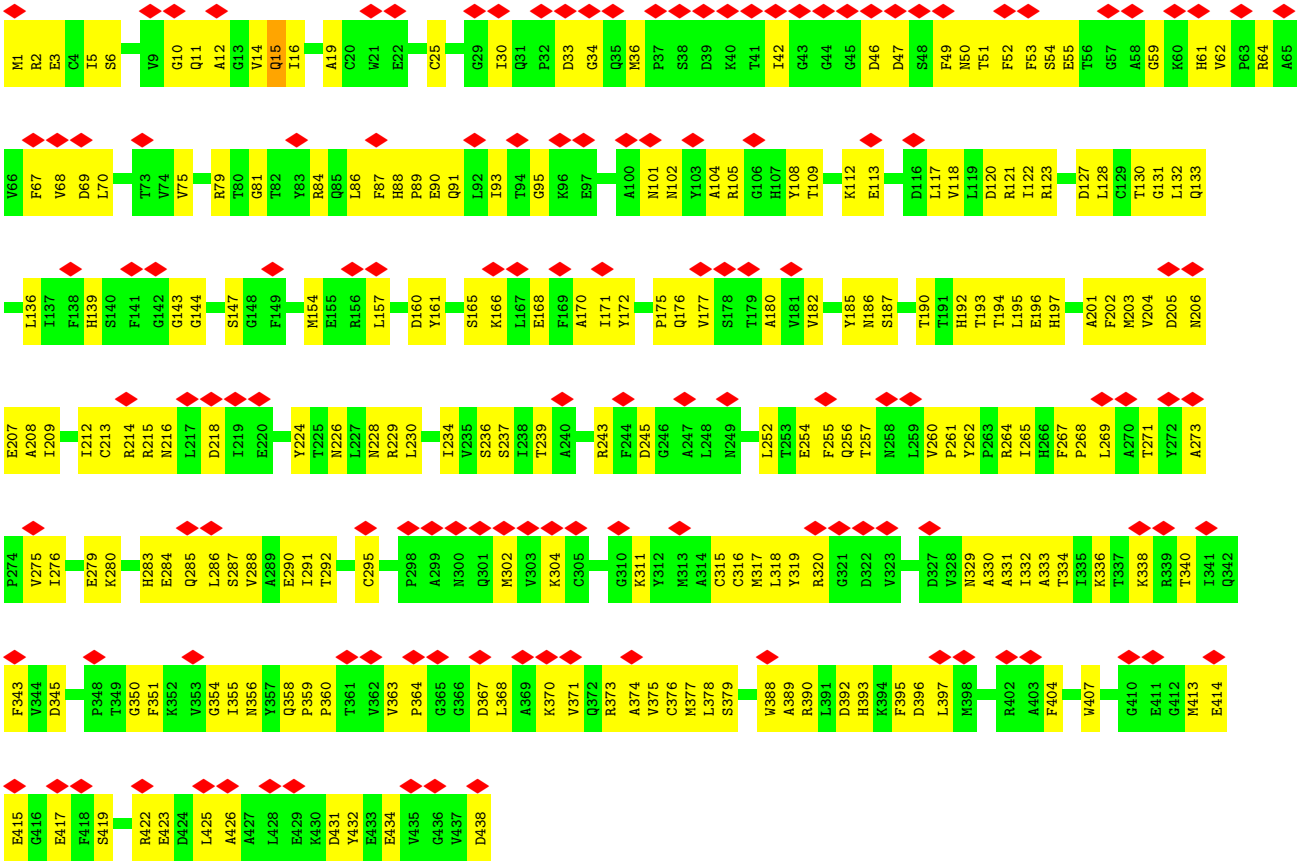
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain EK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain FA:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

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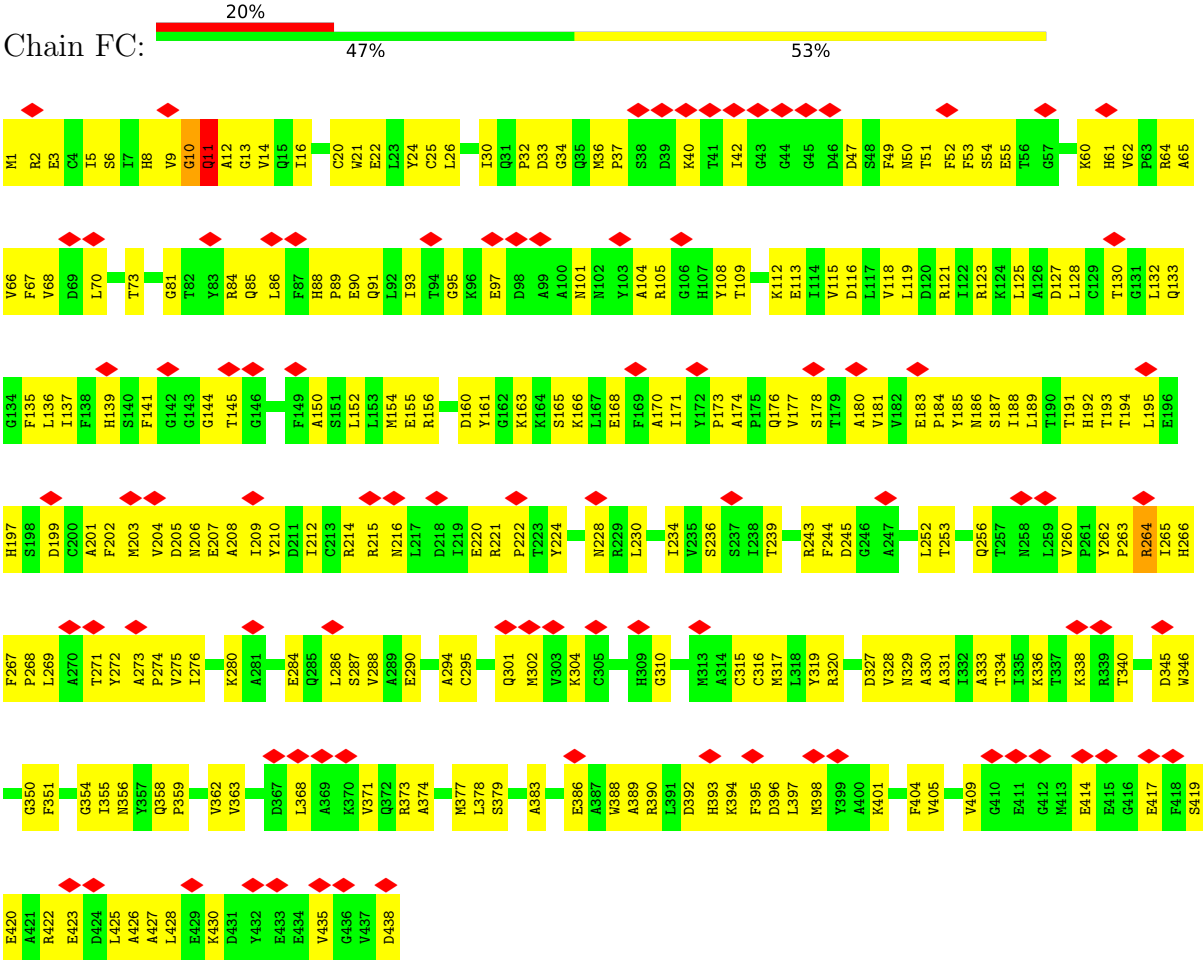
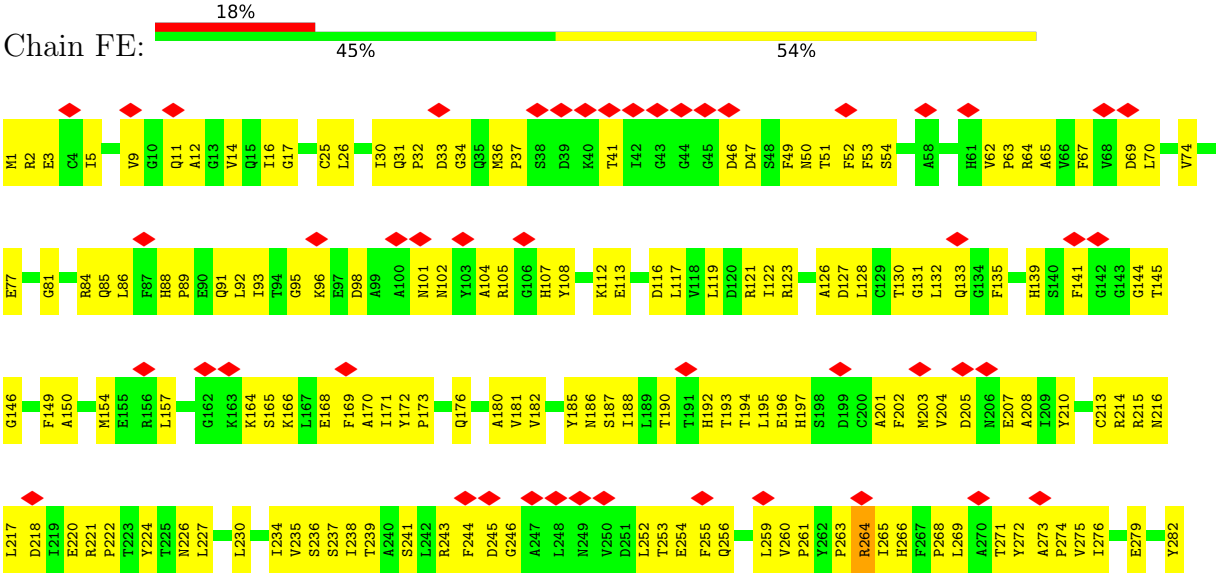
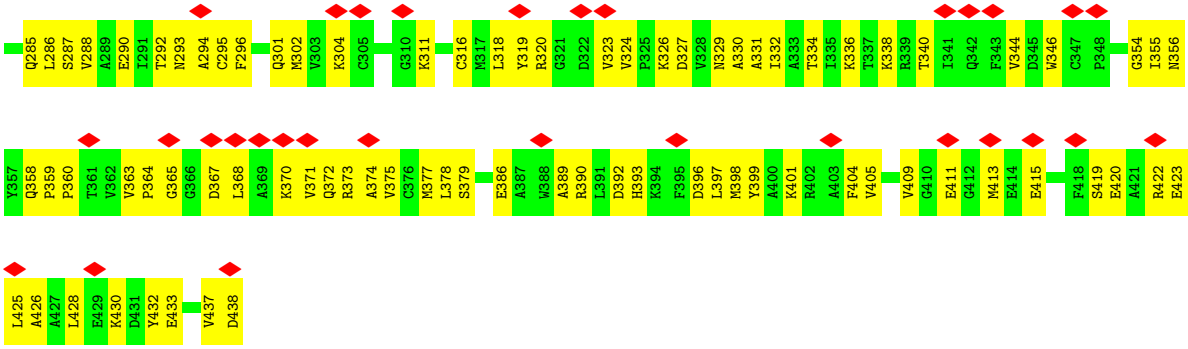


• Molecule 4: Detyrosinated tubulin alpha-3 chain

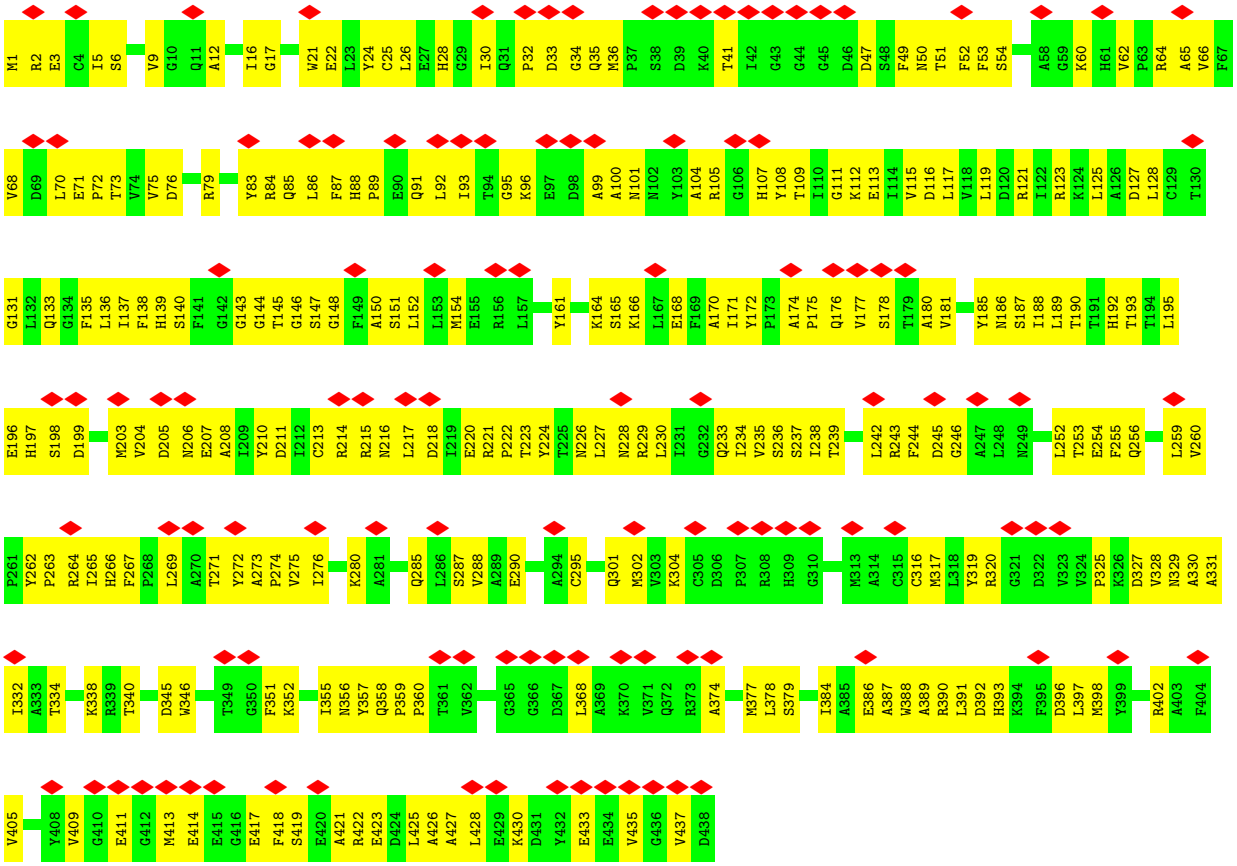
Chain FE:





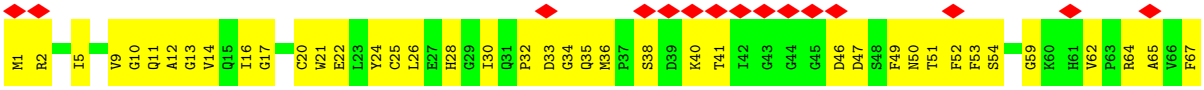
• Molecule 4: Detyrosinated tubulin alpha-3 chain

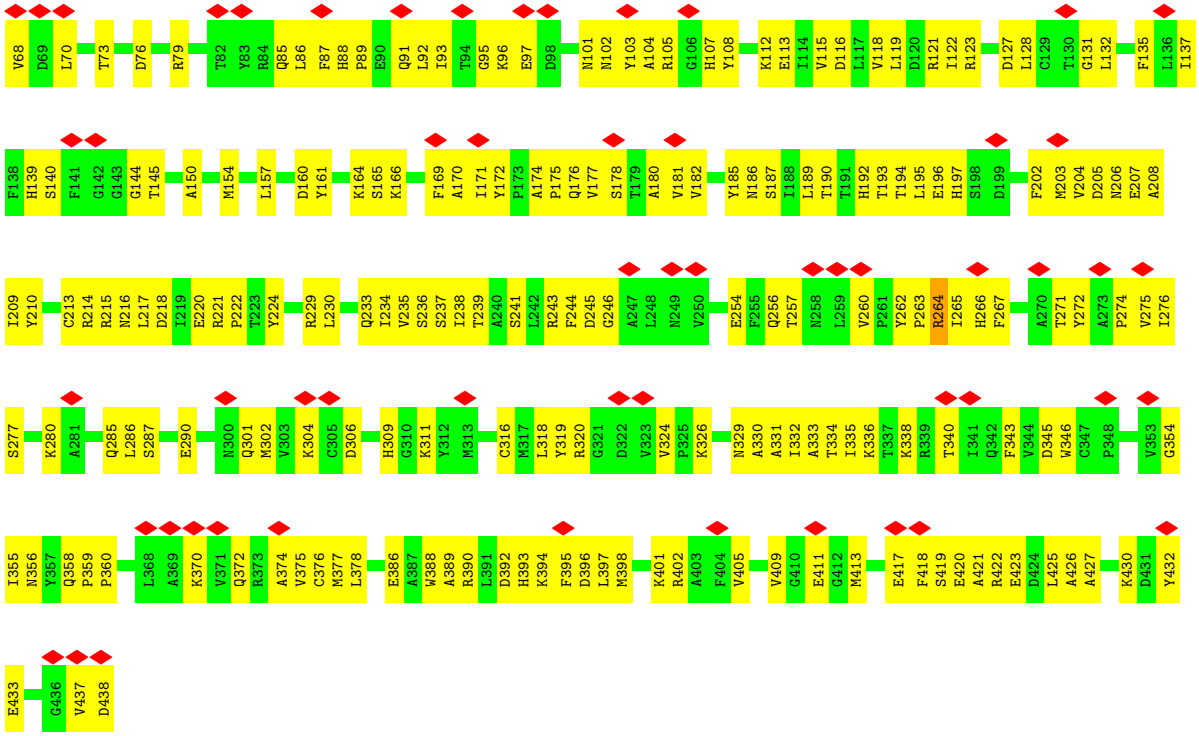
Chain FG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

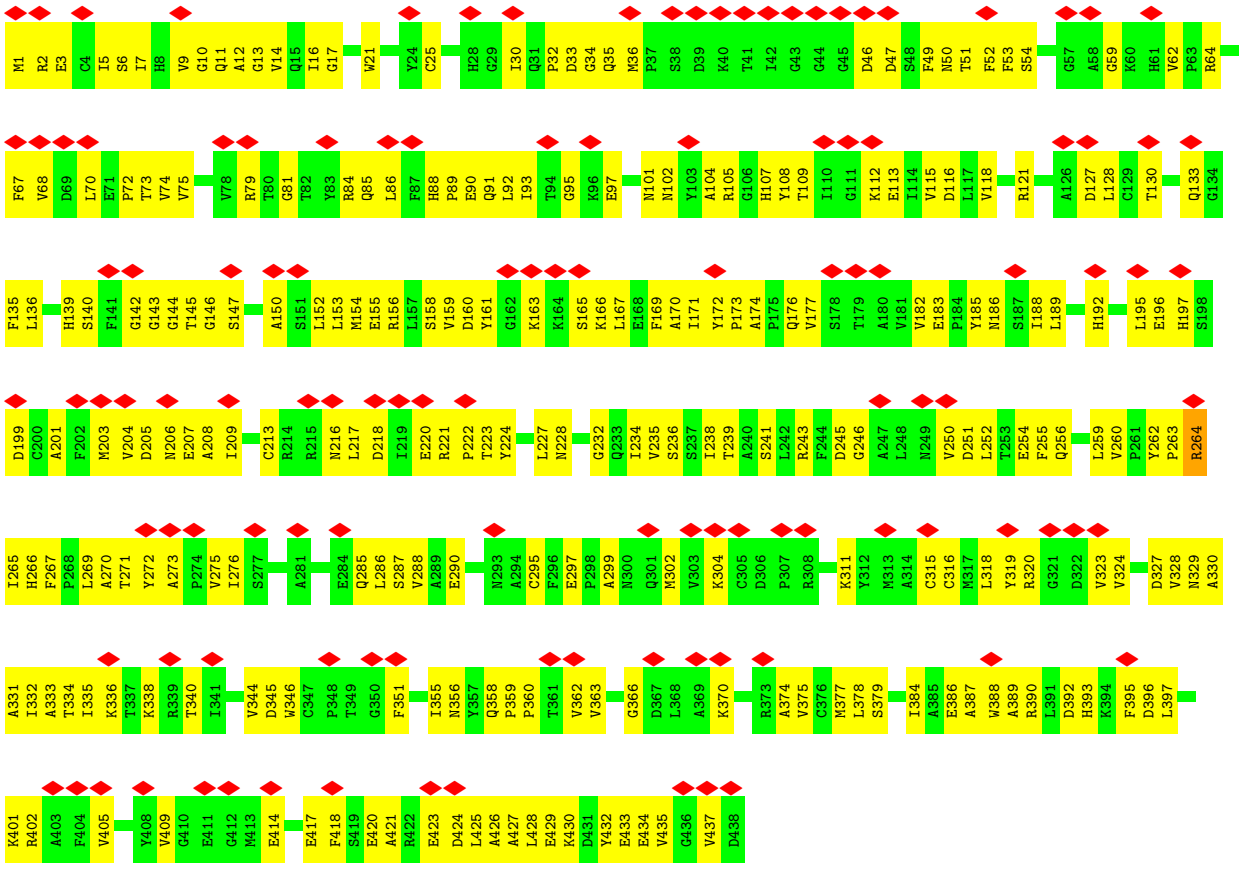
Chain FI:





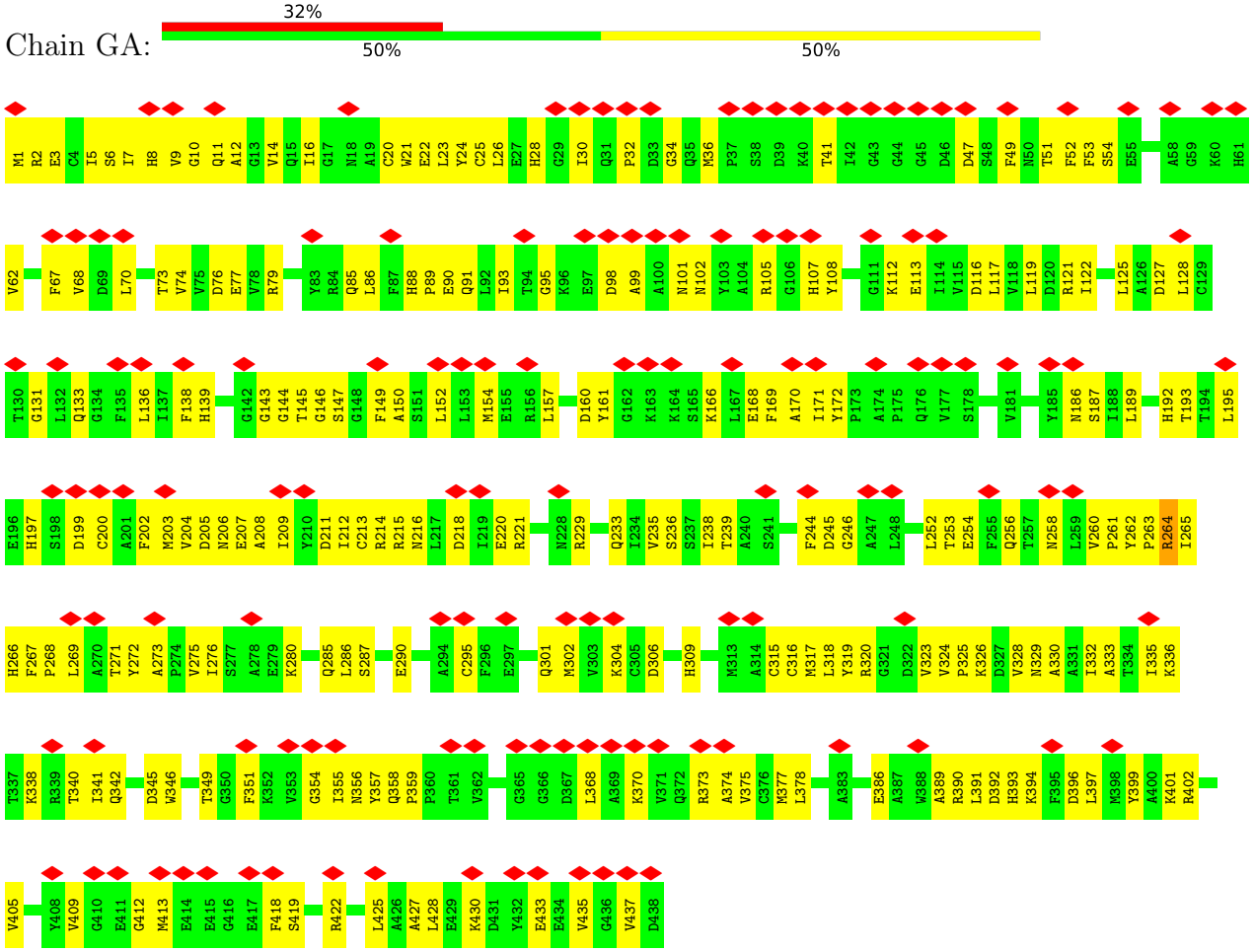
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain FK:



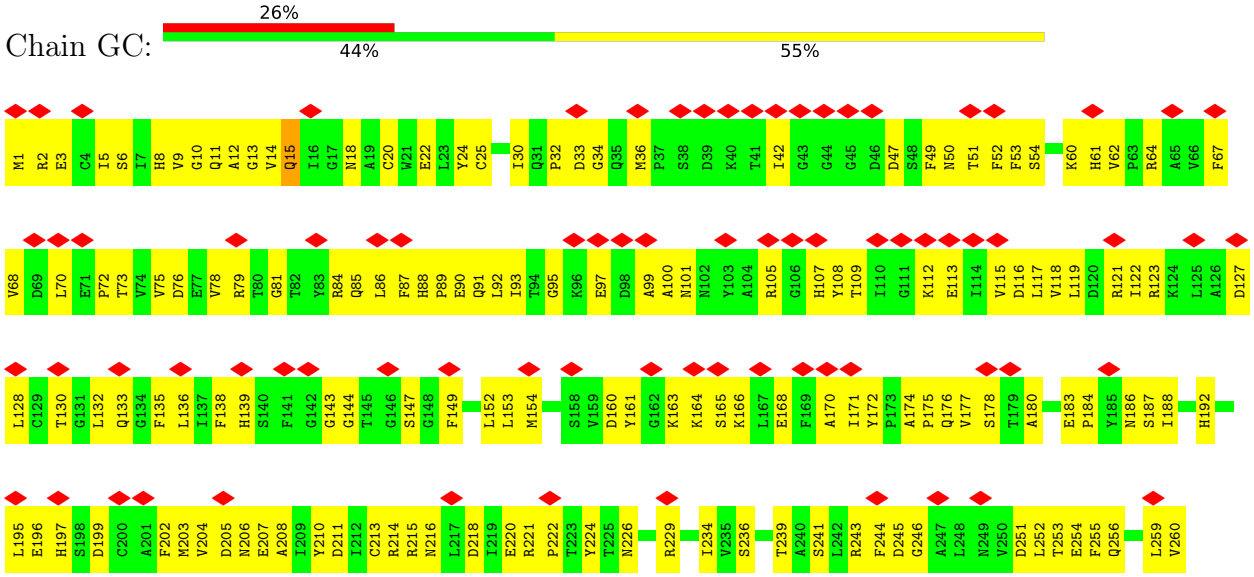
• Molecule 4: Detyrosinated tubulin alpha-3 chain

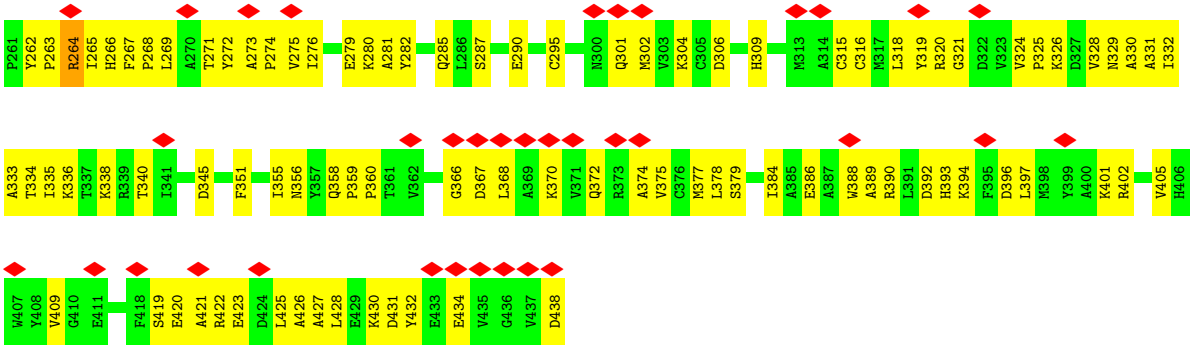
Chain GA:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

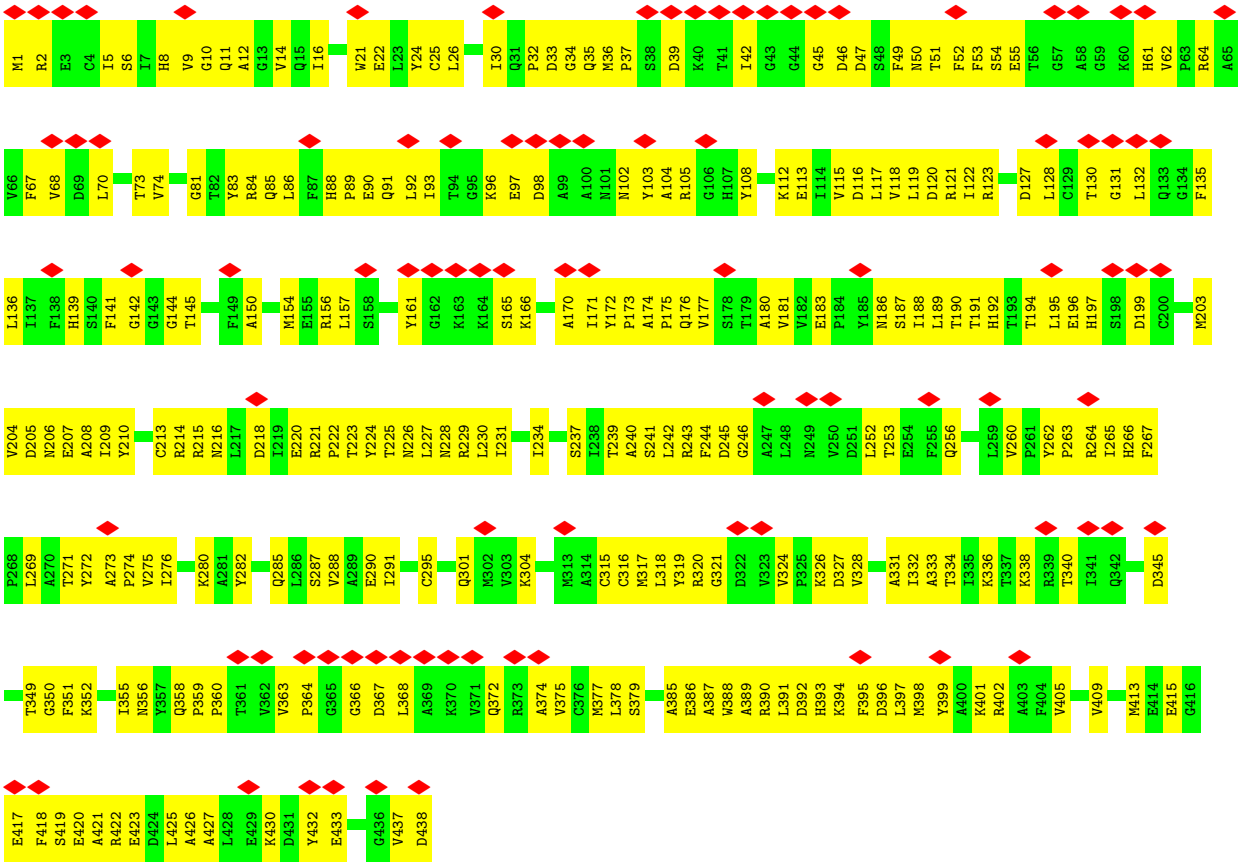
Chain GC:





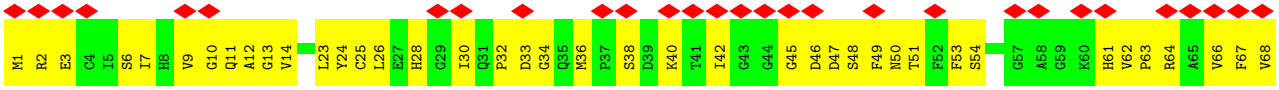
• Molecule 4: Detyrosinated tubulin alpha-3 chain

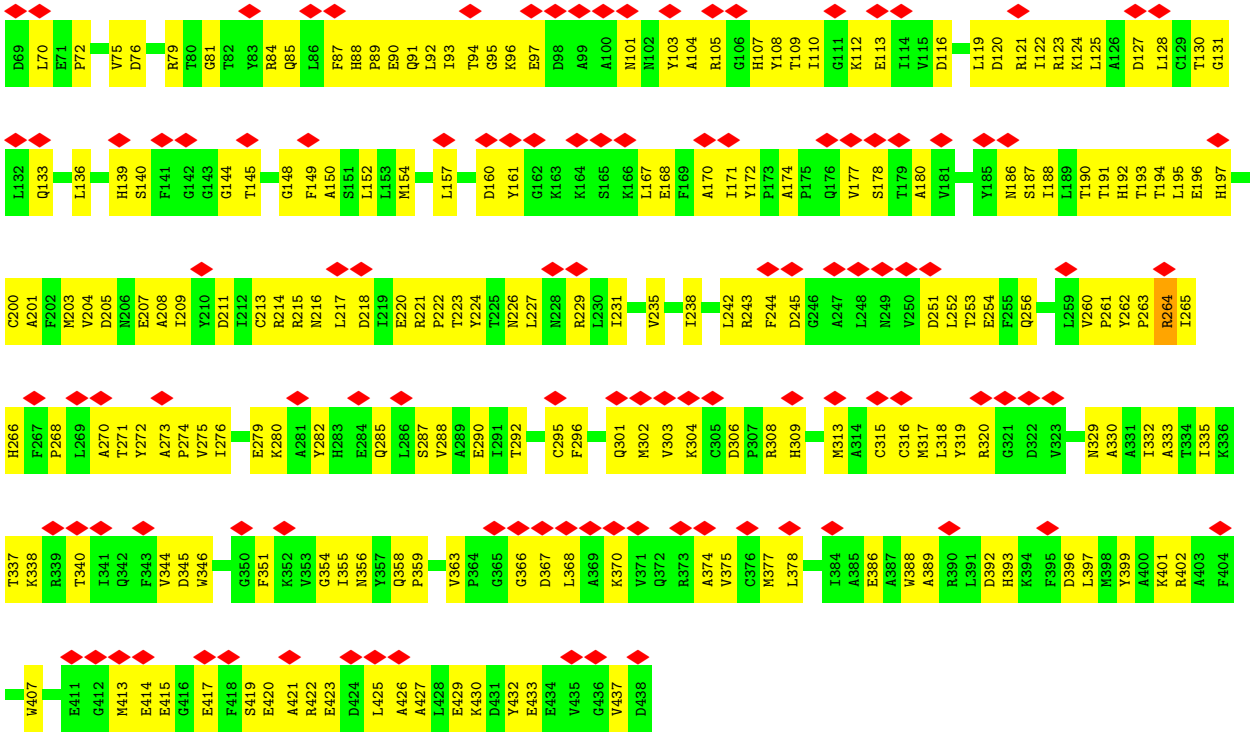
Chain GE:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

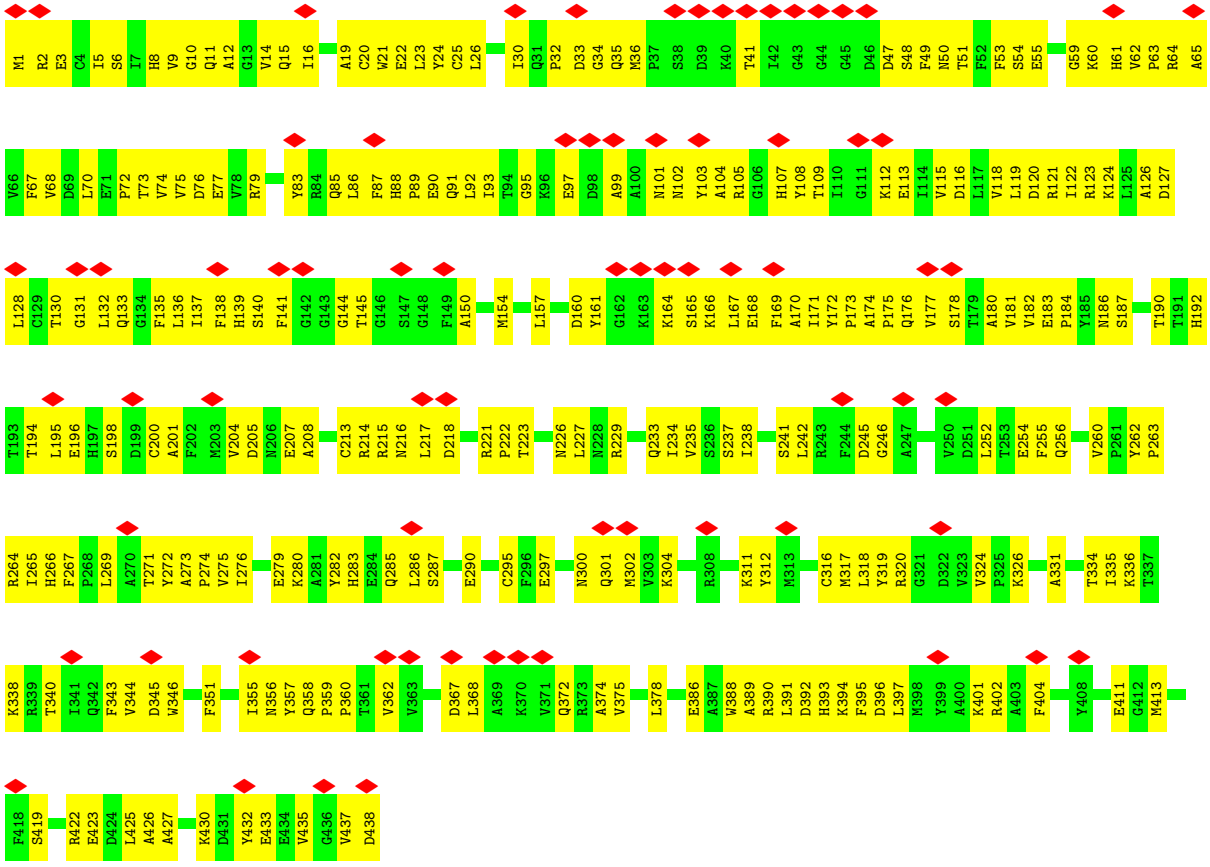
Chain GG:





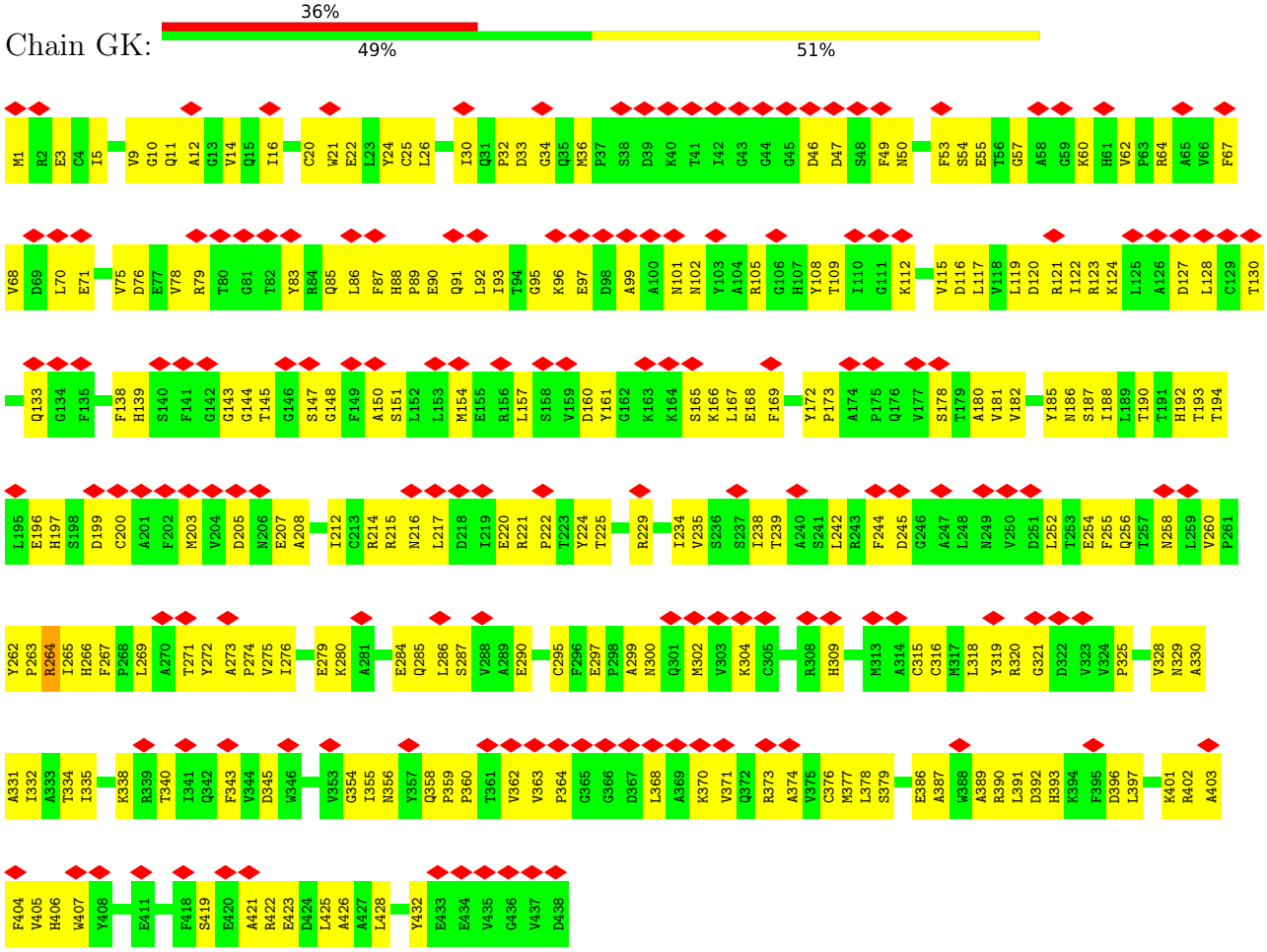
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain GI:



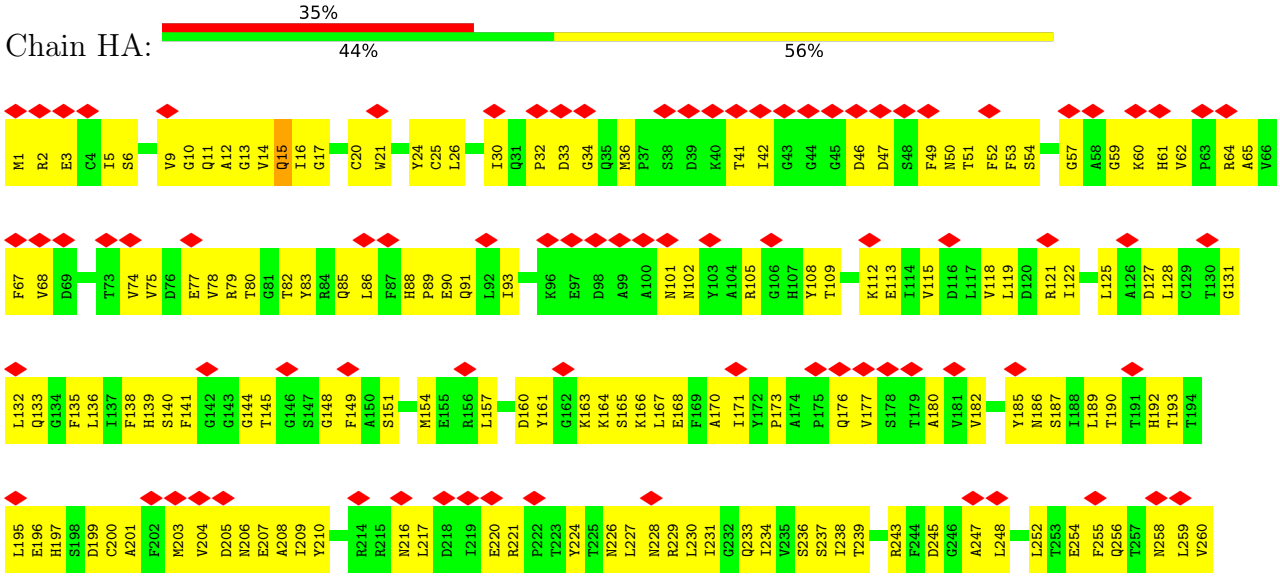
• Molecule 4: Detyrosinated tubulin alpha-3 chain

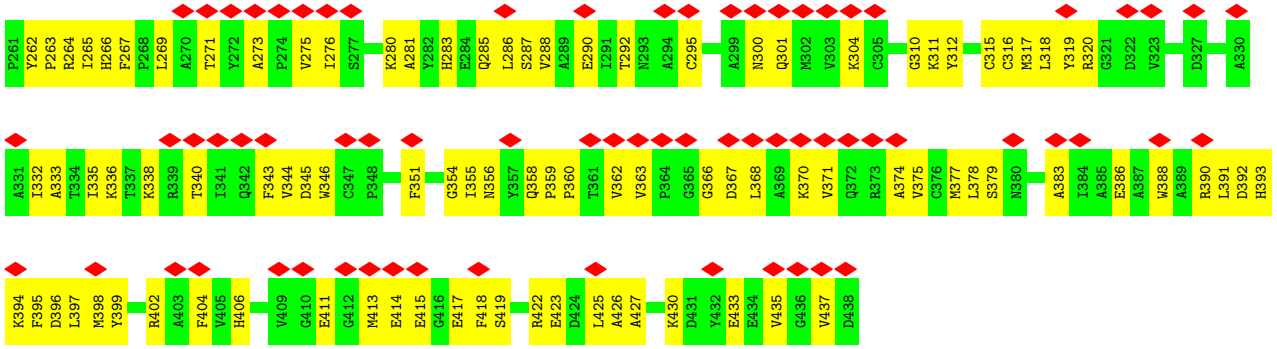
Chain GK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

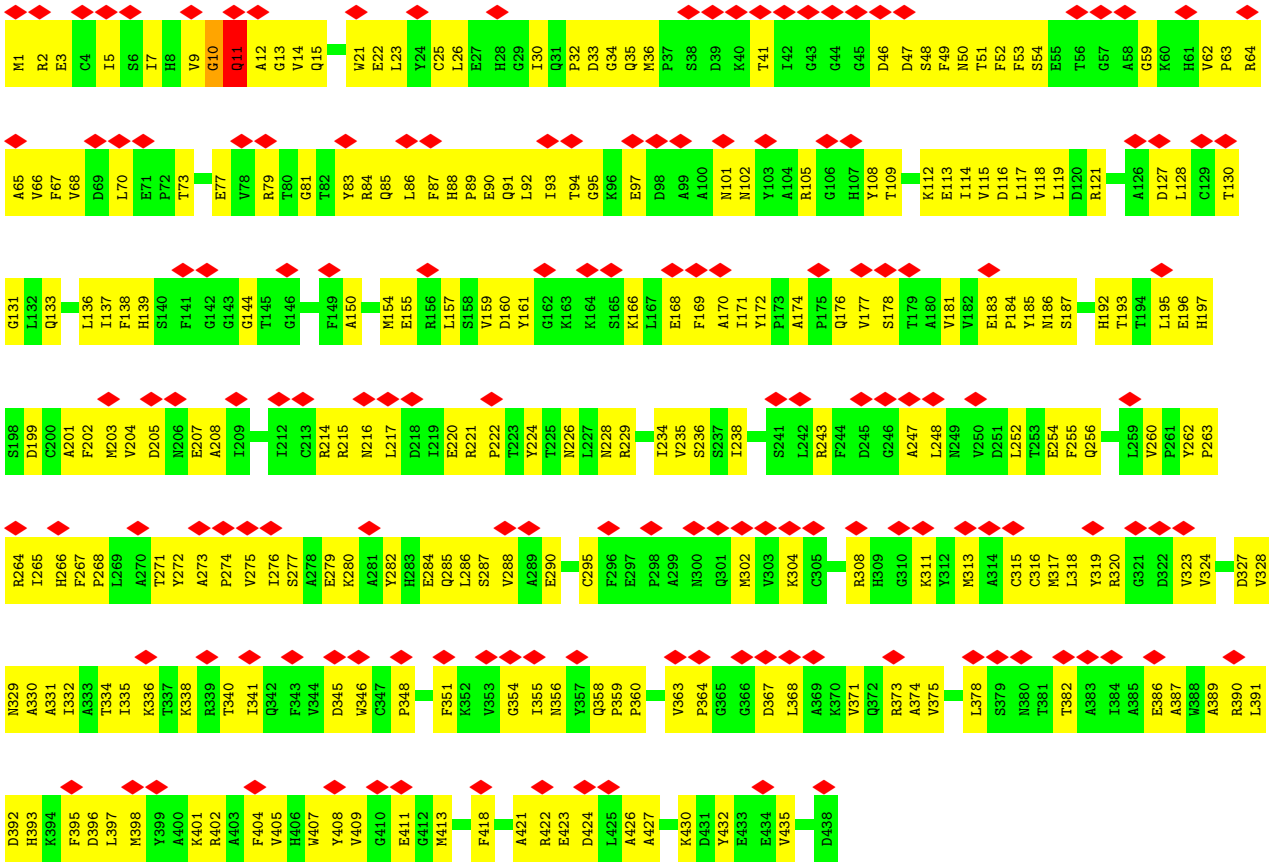
Chain HA:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain HC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

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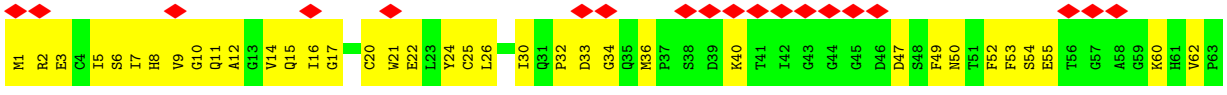

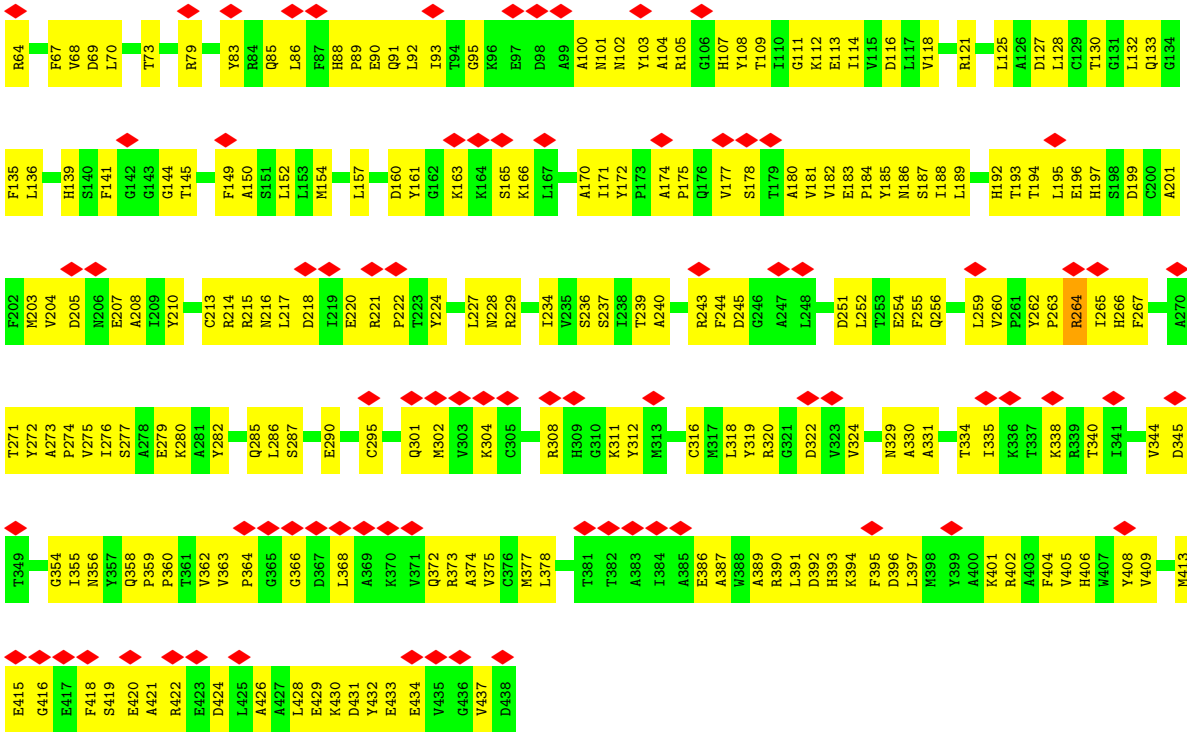

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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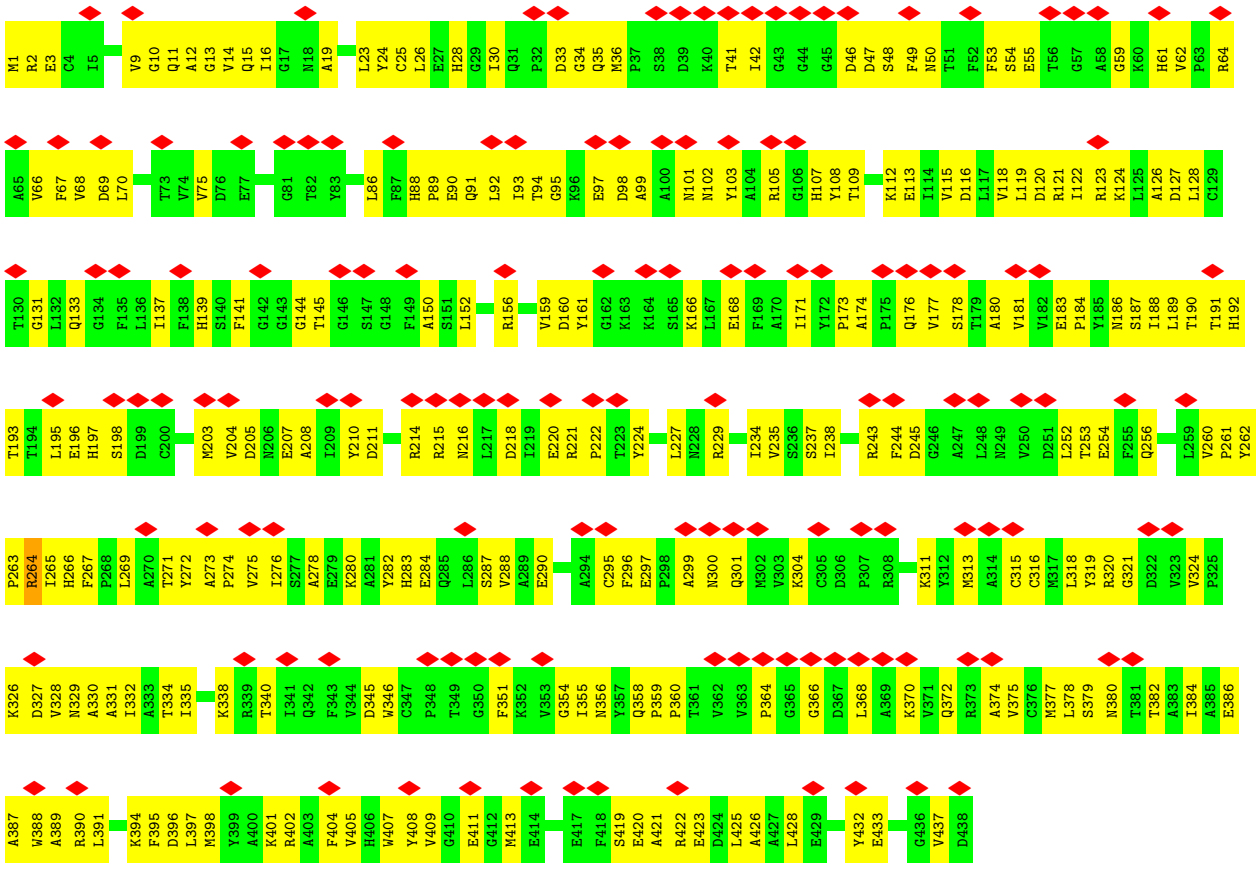

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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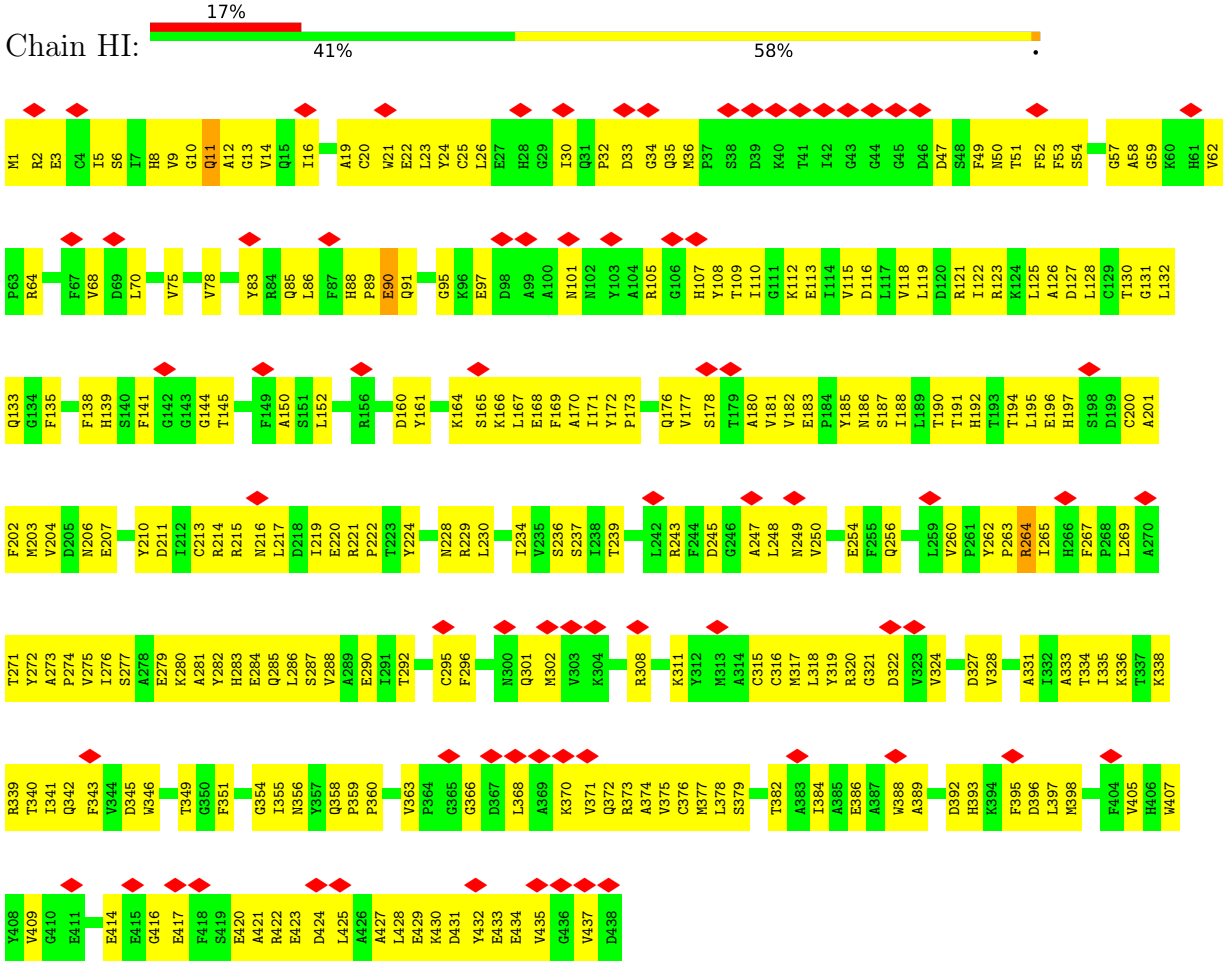

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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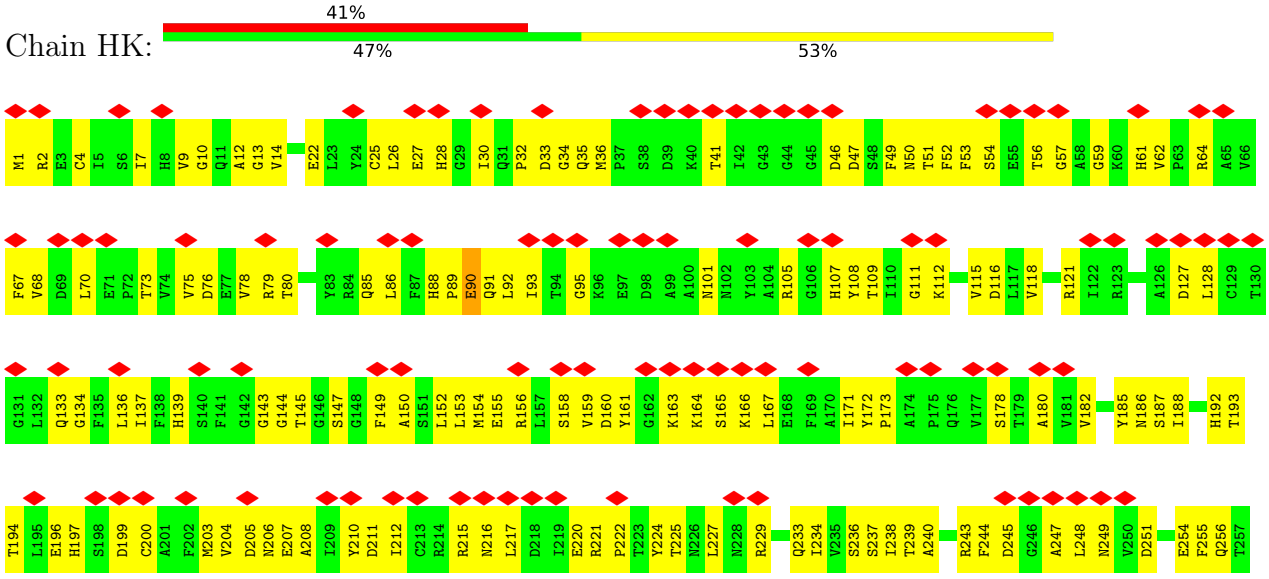
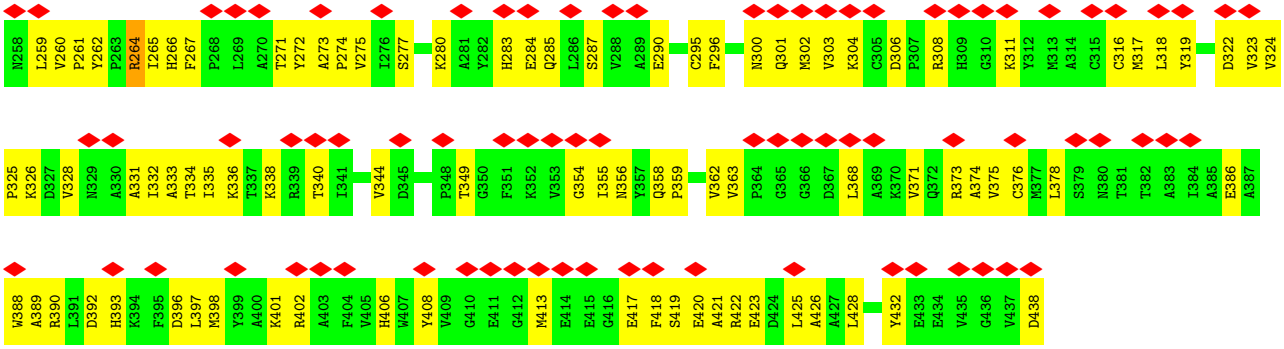
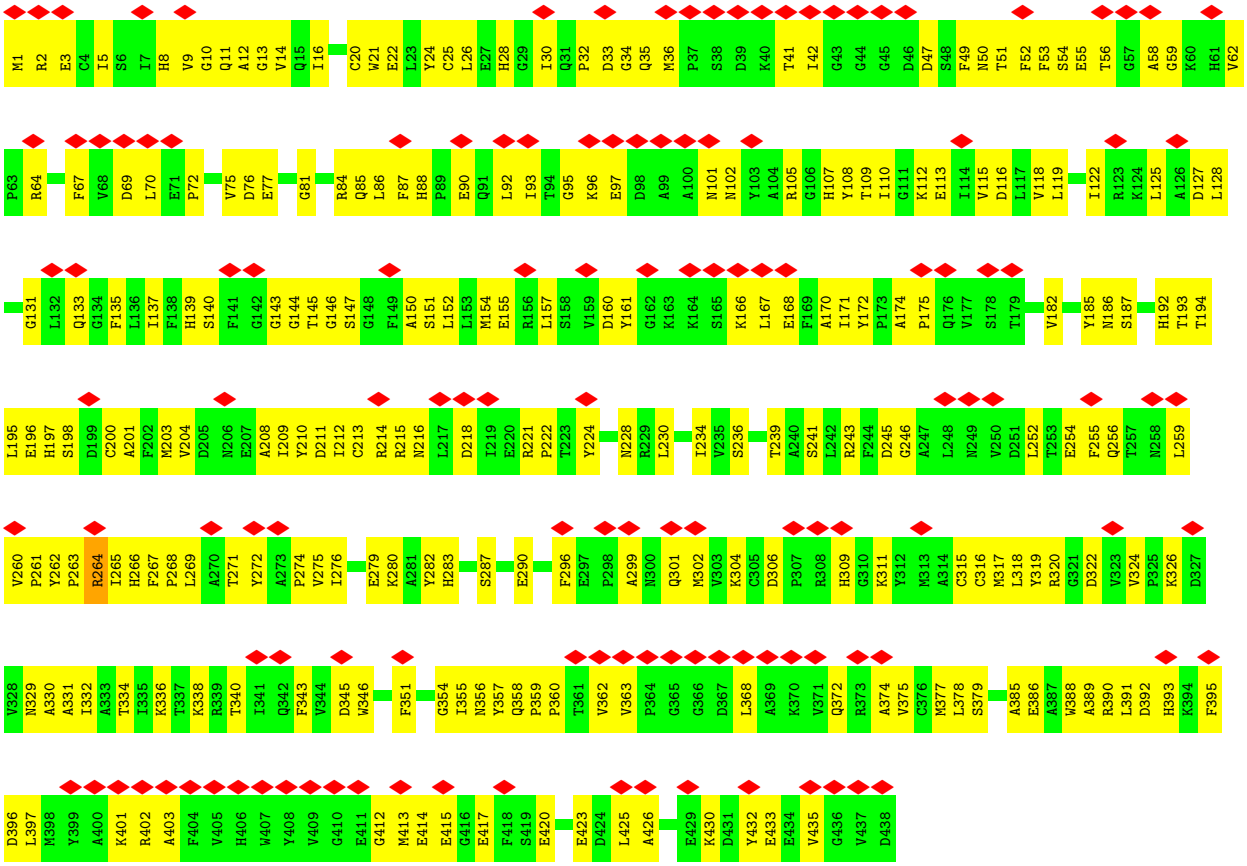




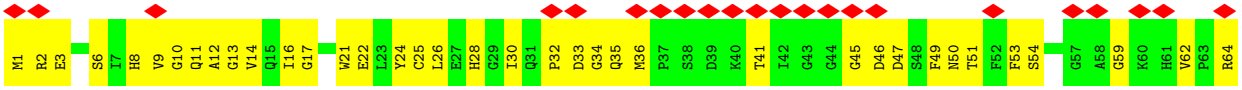
• Molecule 4: Detyrosinated tubulin alpha-3 chain

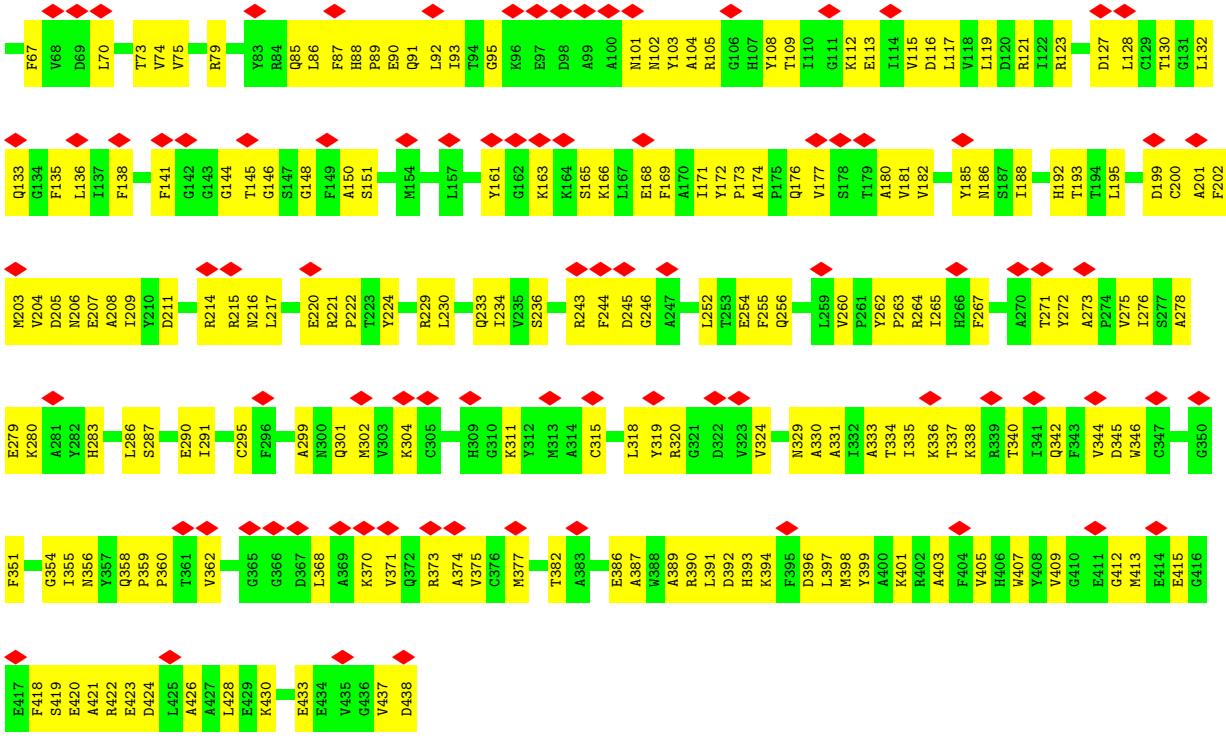
Chain IA:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

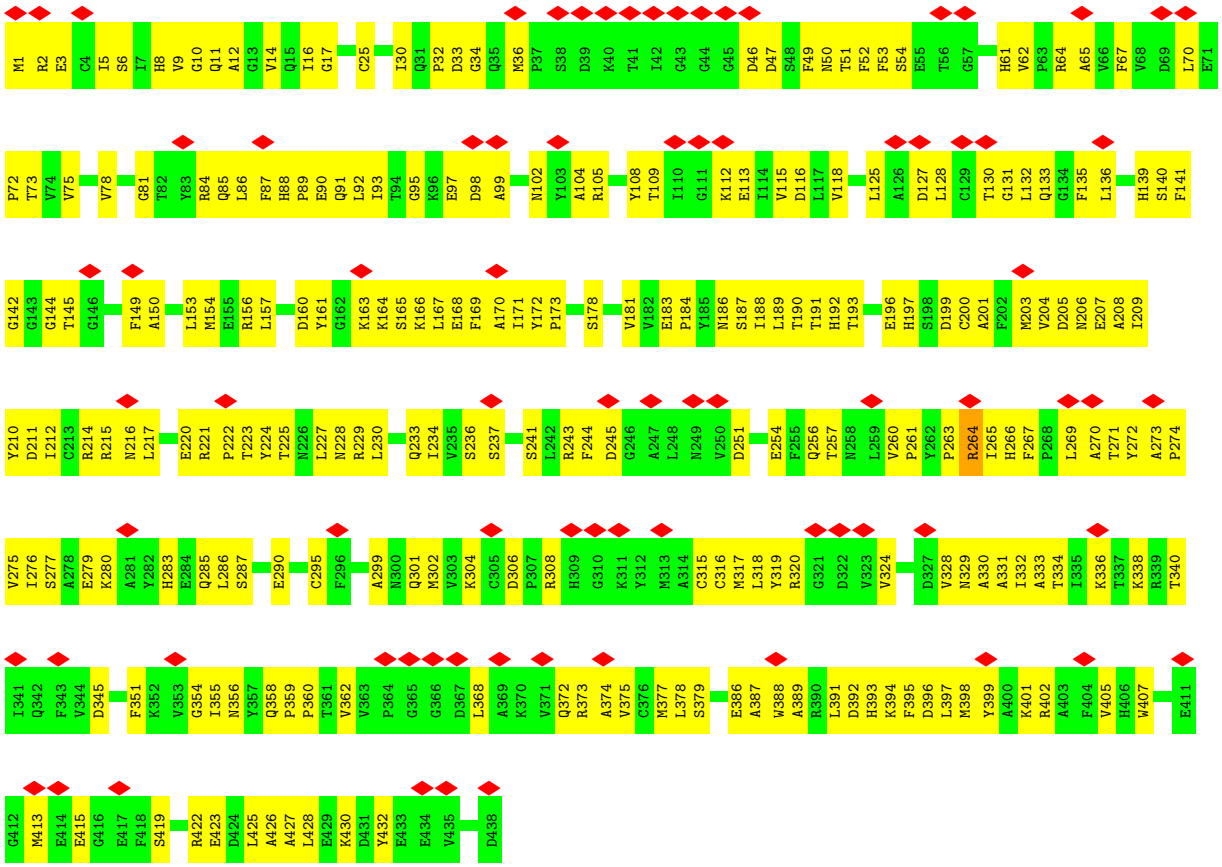
Chain IC:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain IE:

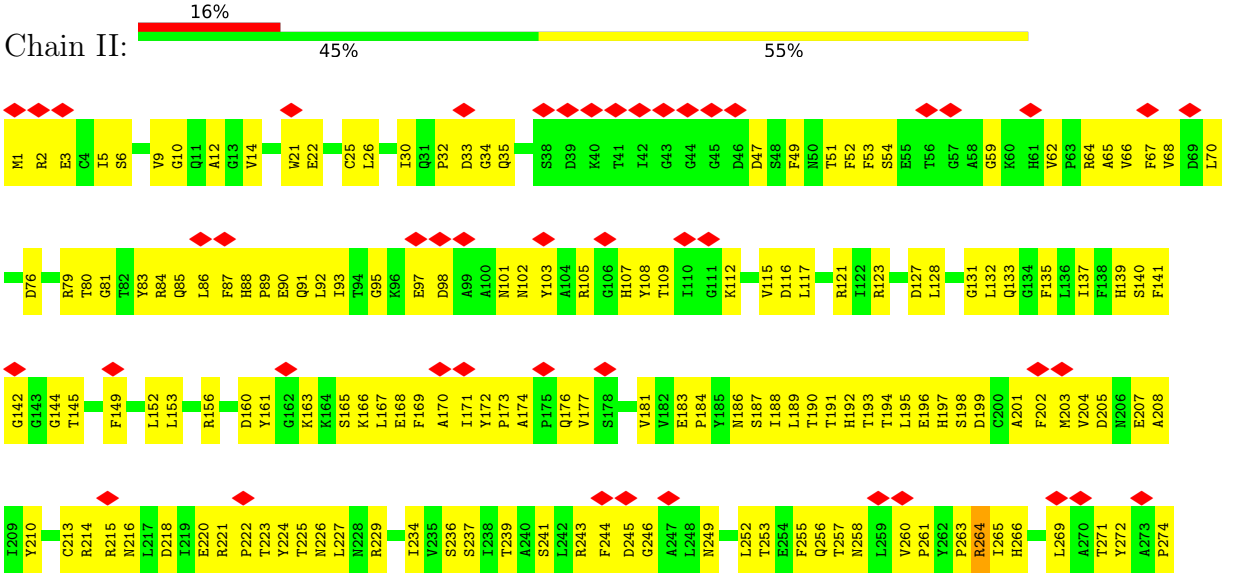


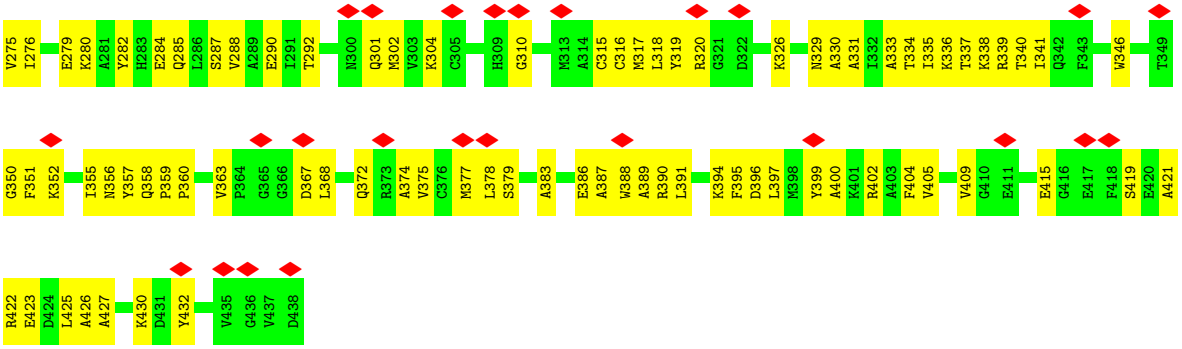
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain IG:

• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain II:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

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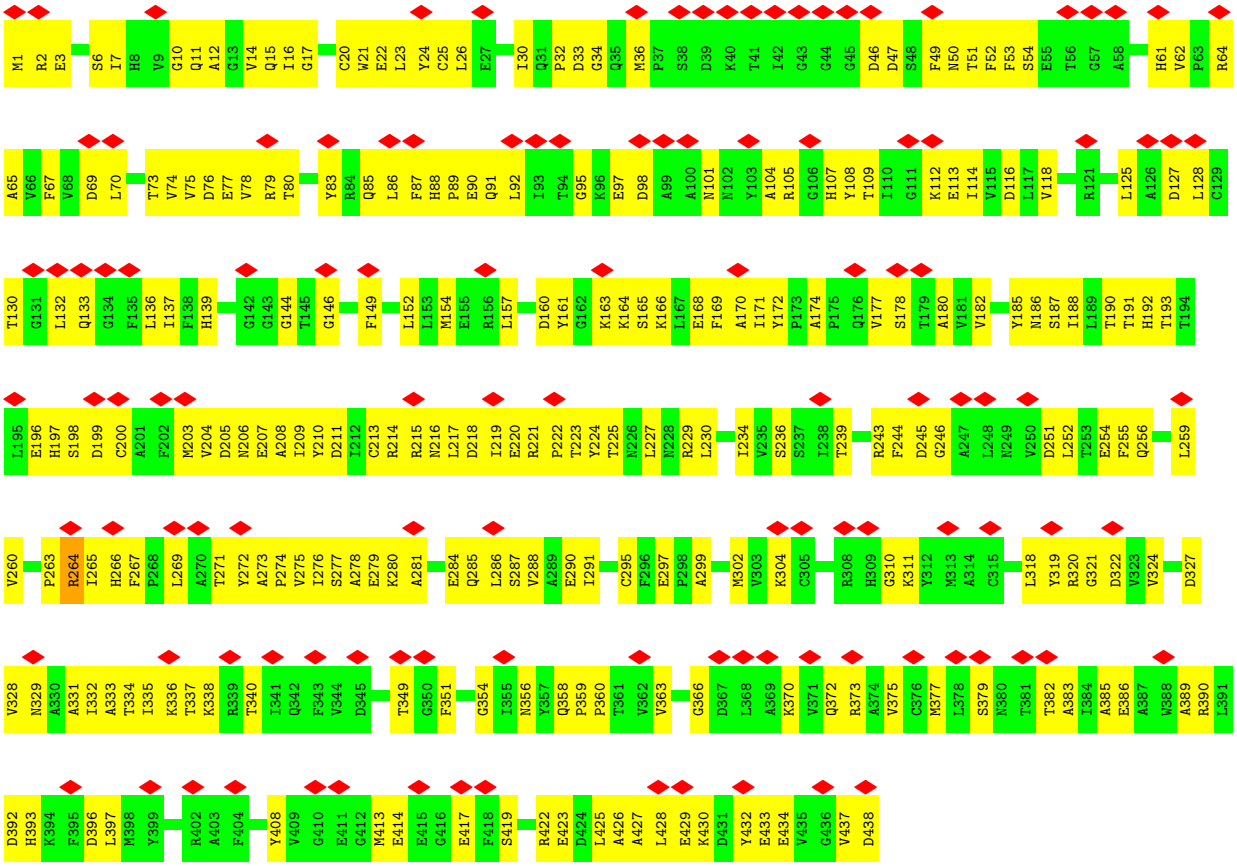

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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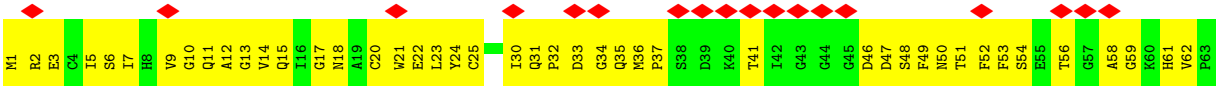
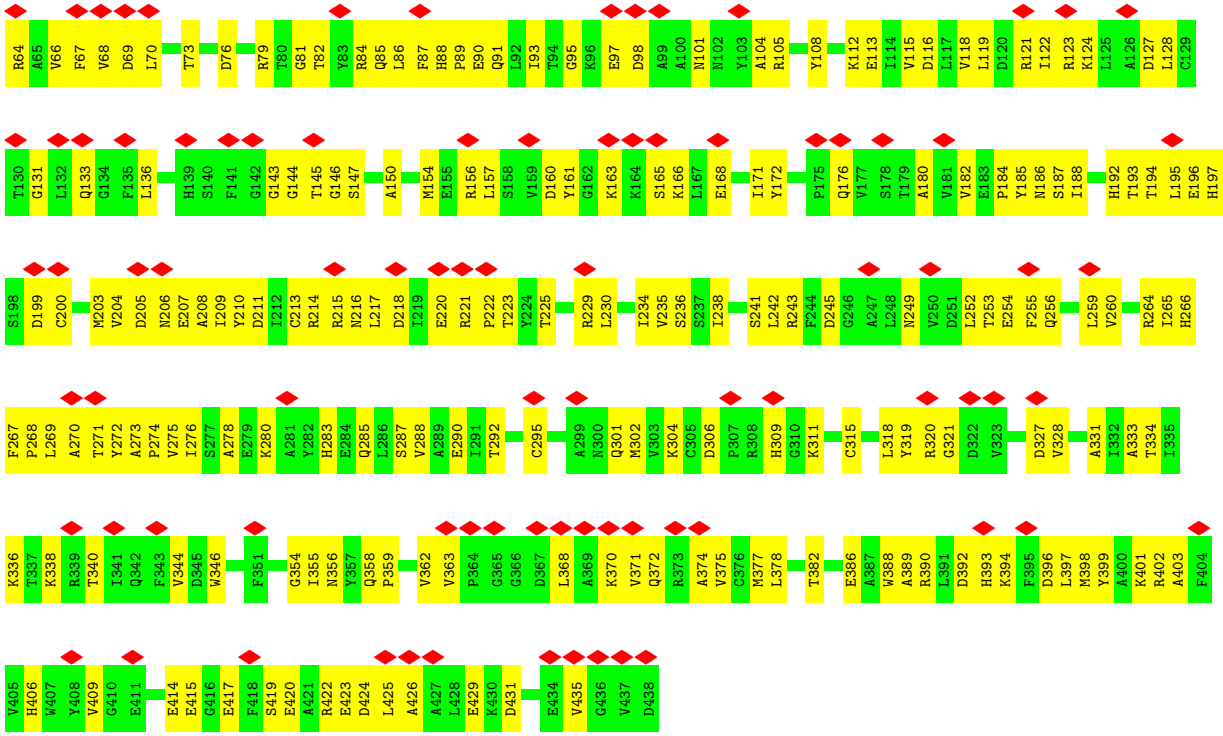
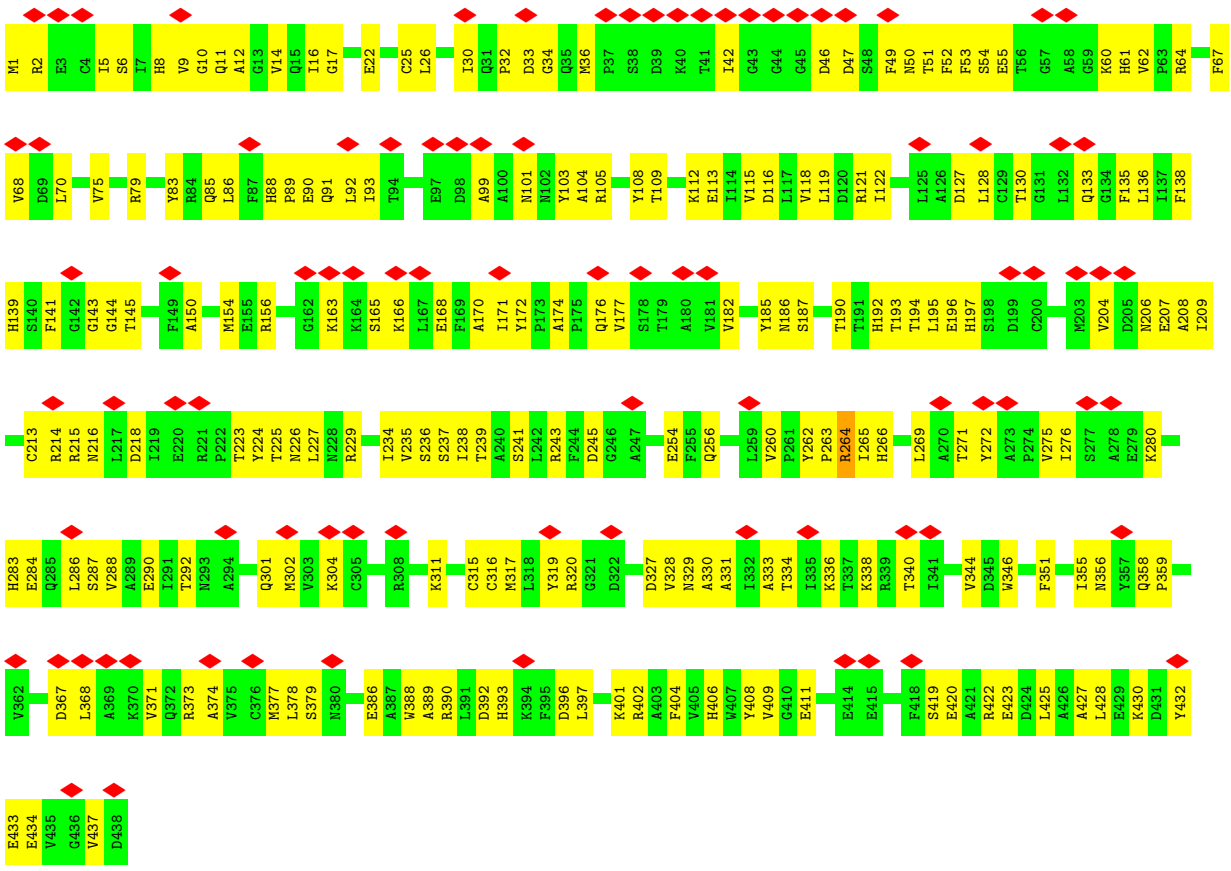




• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain JA:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

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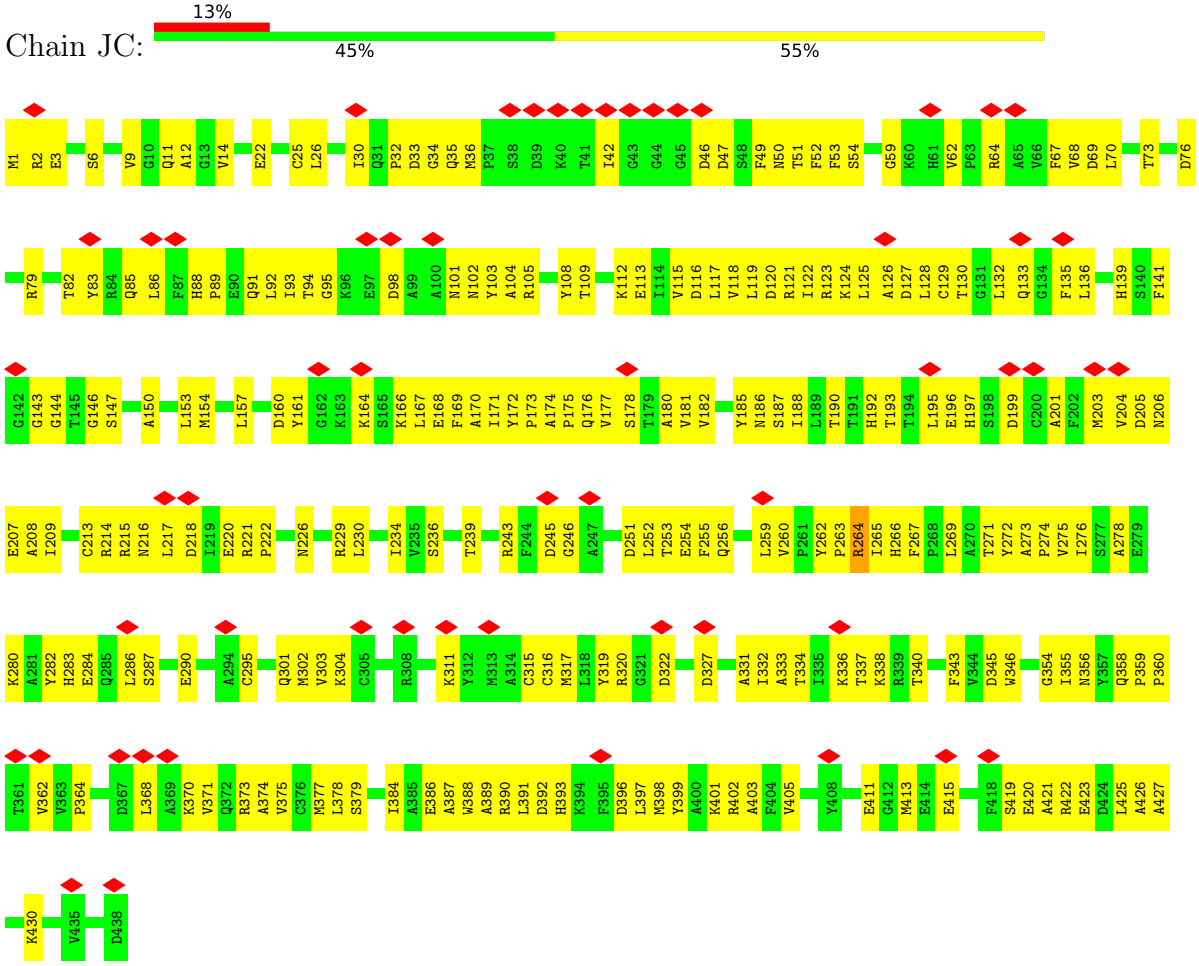
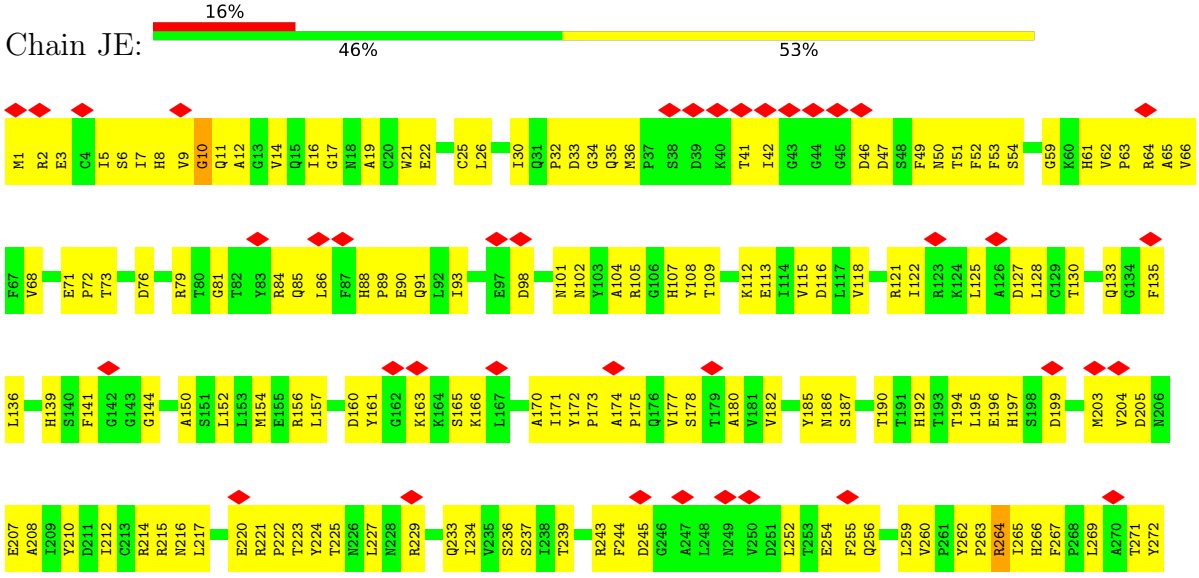
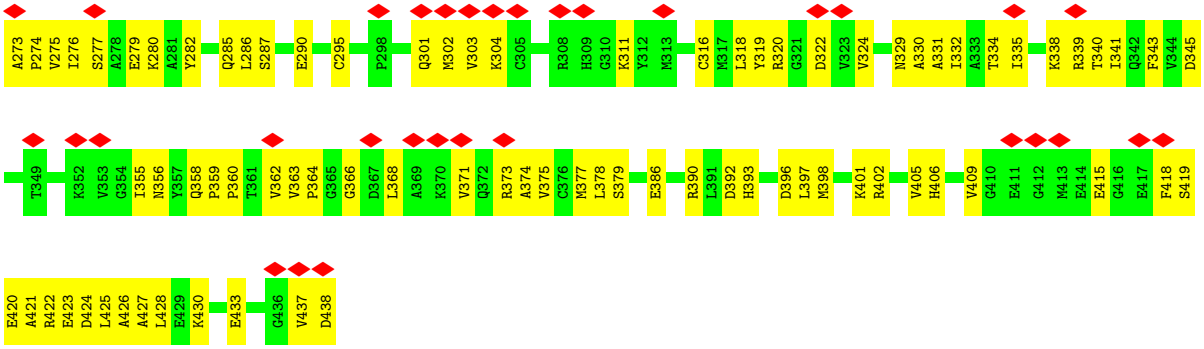


• Molecule 4: Detyrosinated tubulin alpha-3 chain

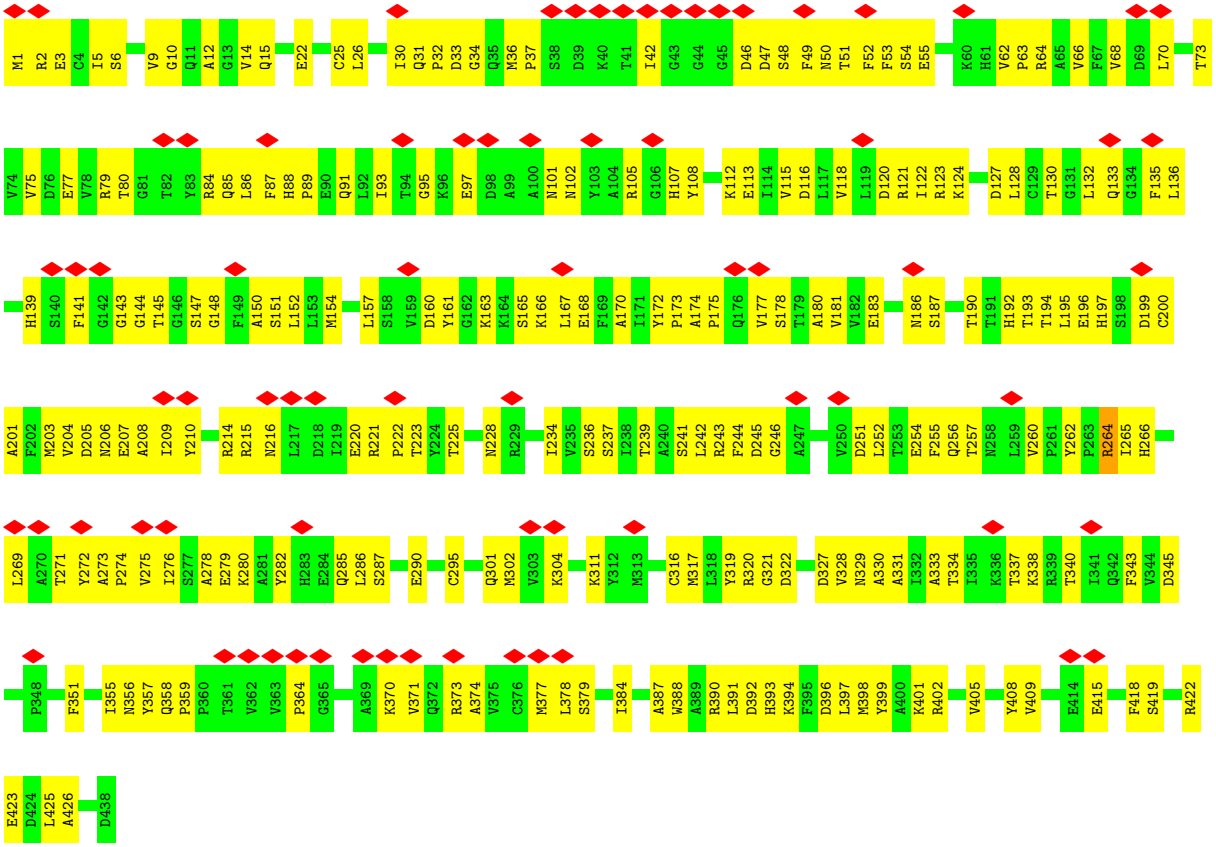
Chain JE:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain JG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

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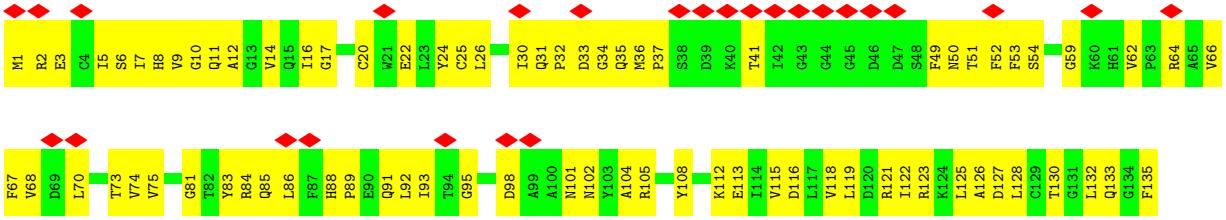
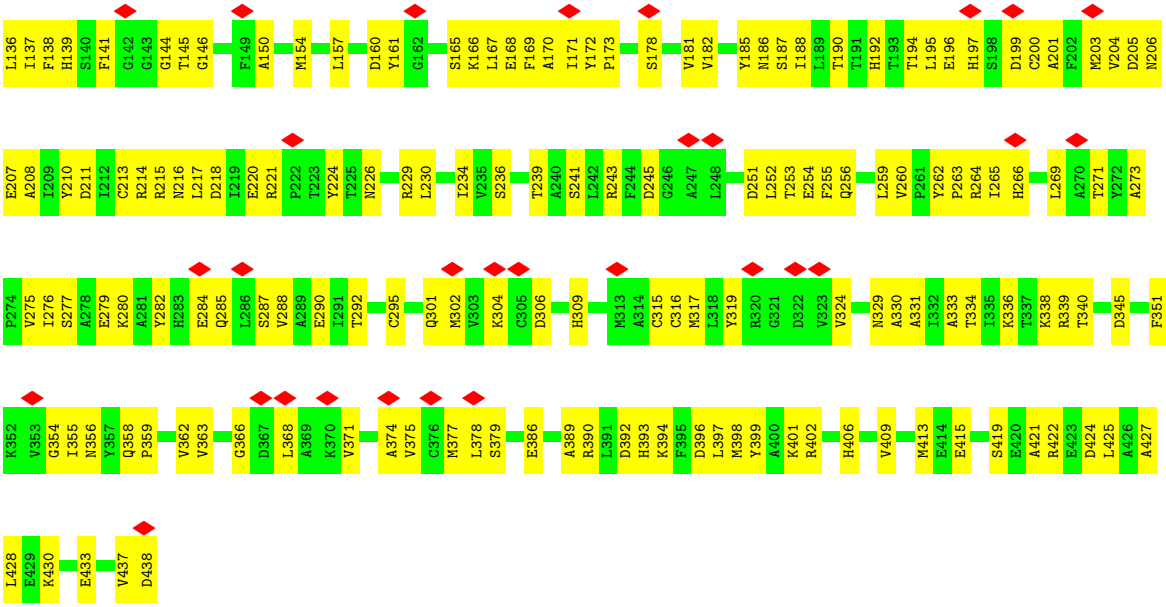
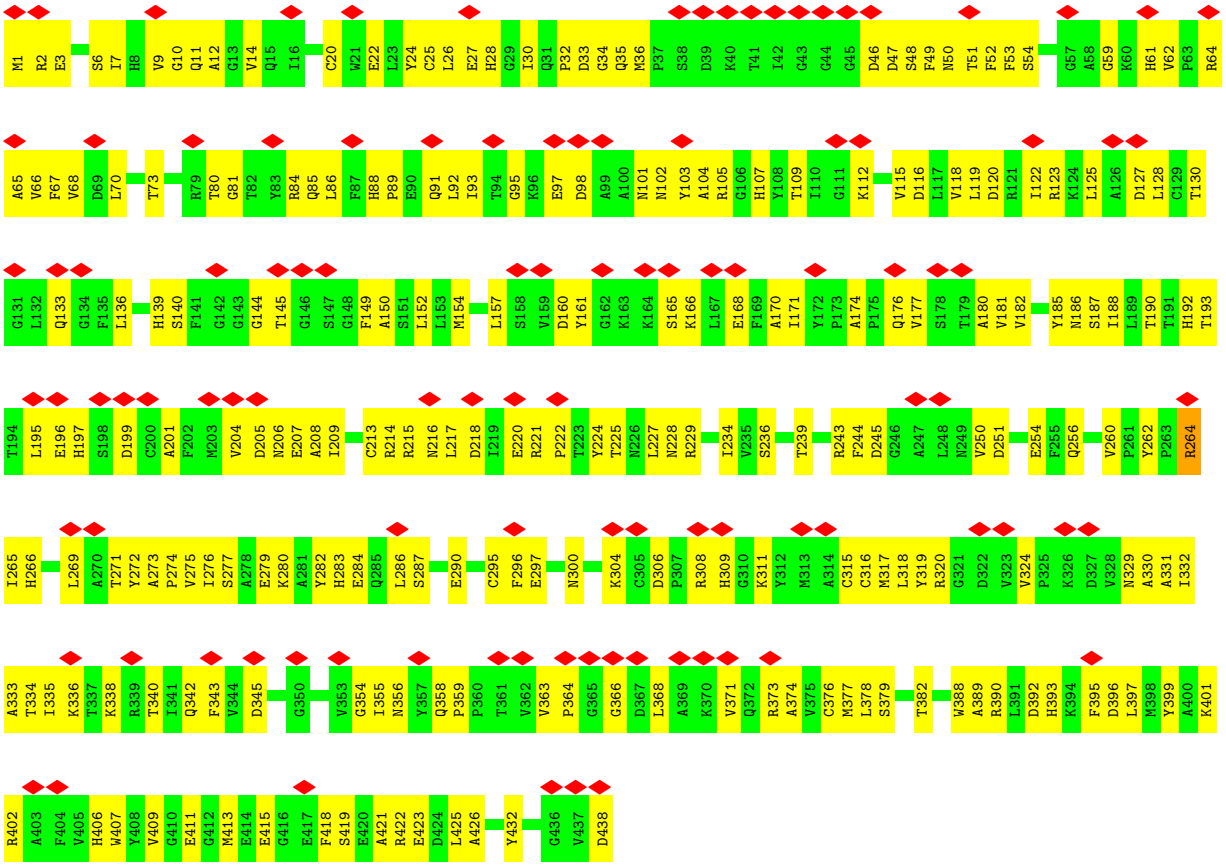




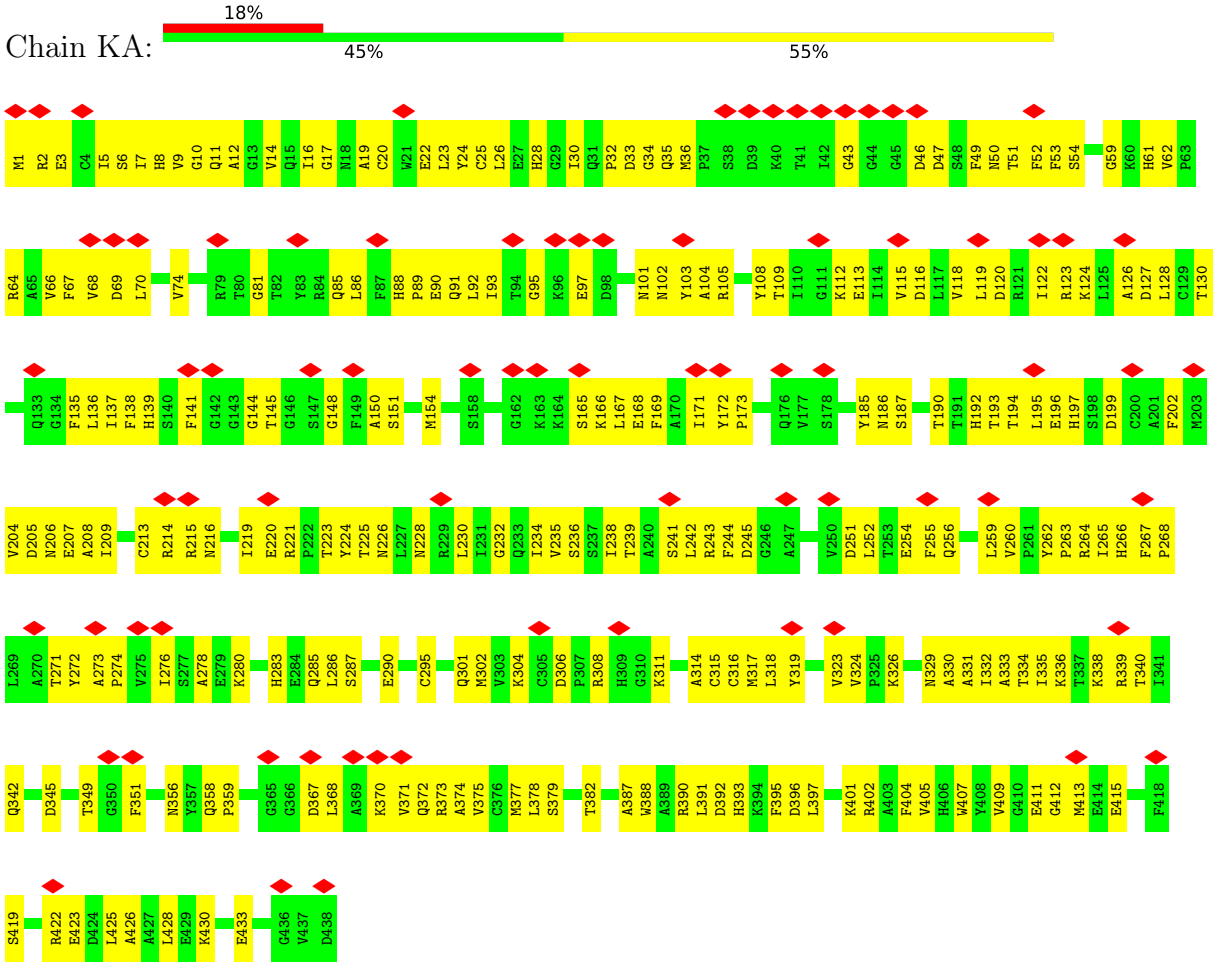
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain JK:



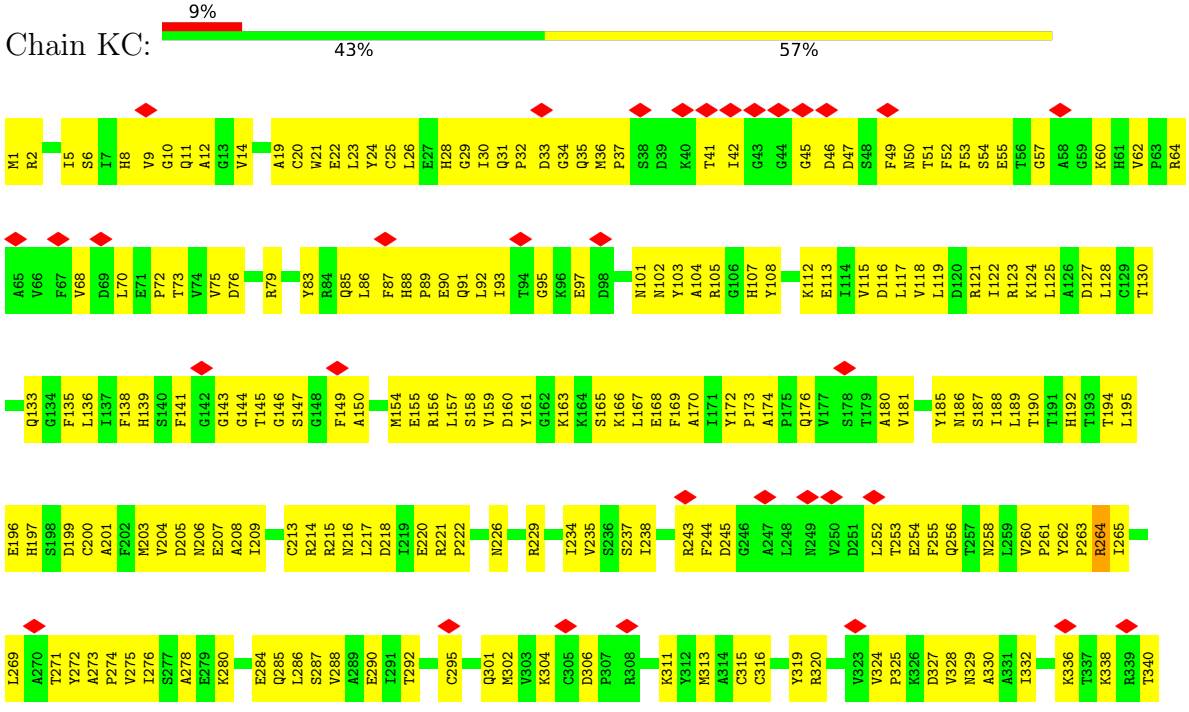
• Molecule 4: Detyrosinated tubulin alpha-3 chain

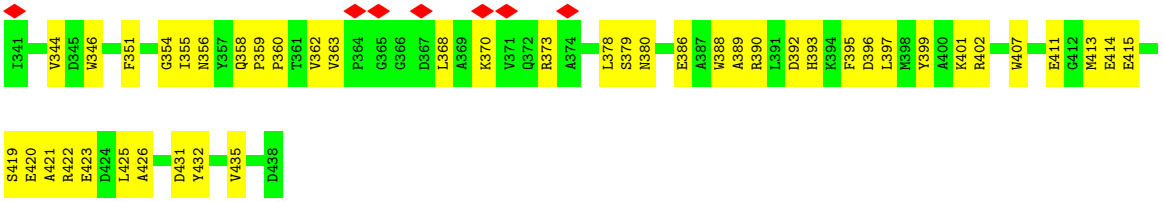
Chain KA:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain KC:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

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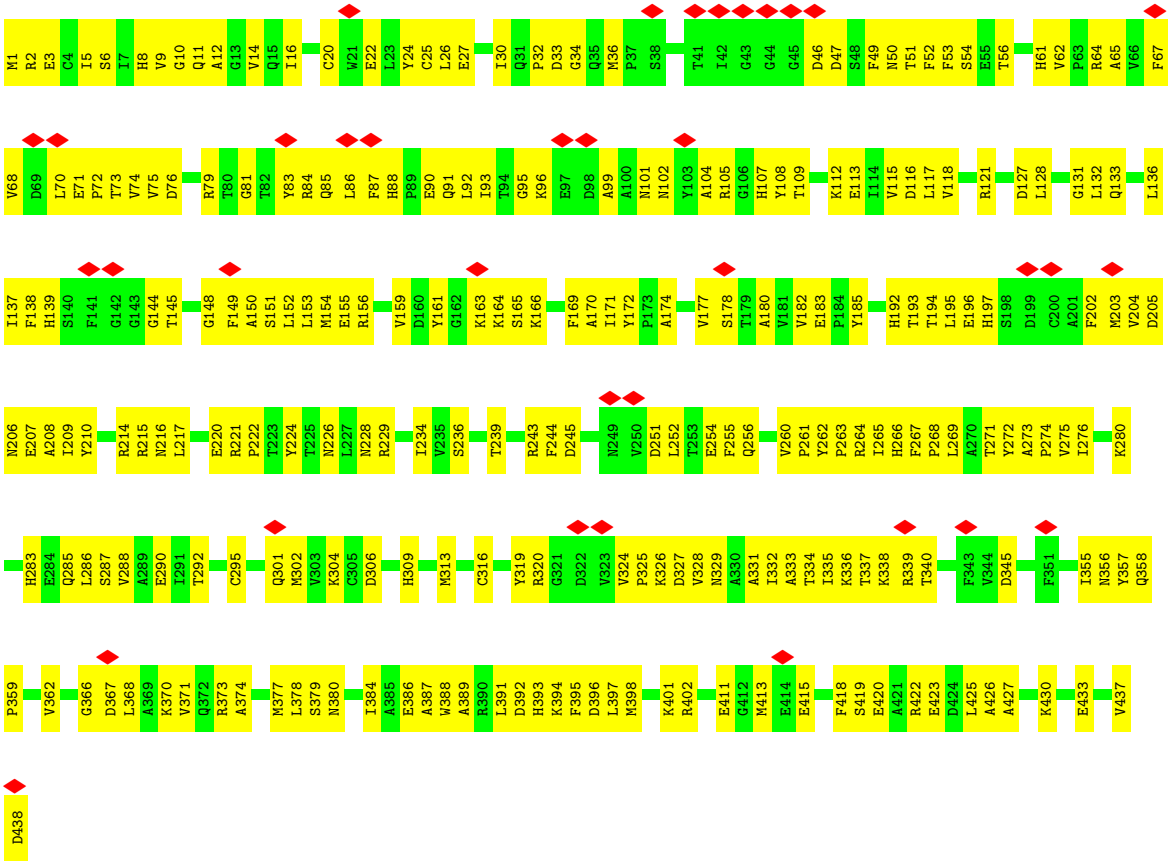
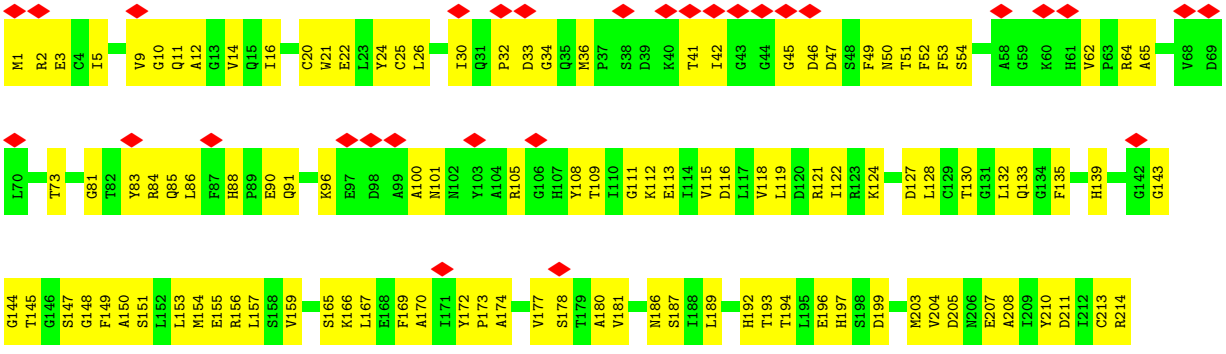
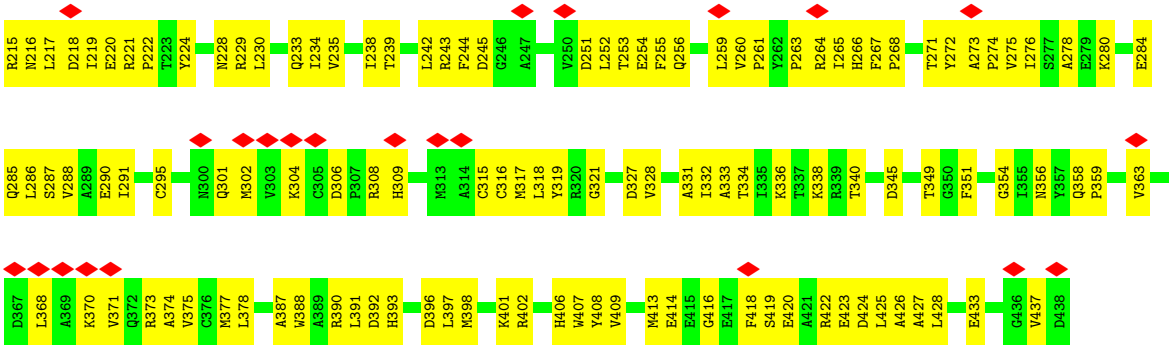


• Molecule 4: Detyrosinated tubulin alpha-3 chain

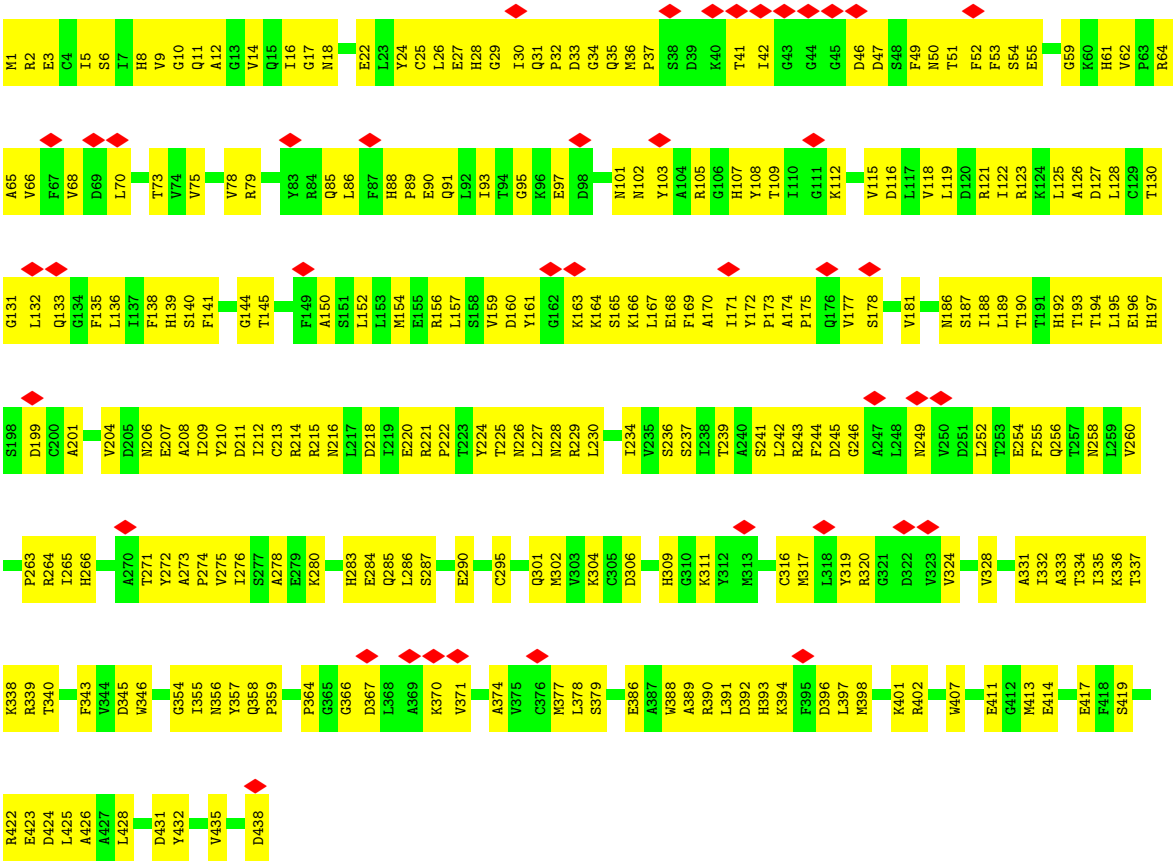
Chain KG:





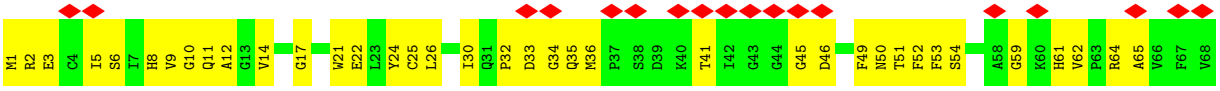
• Molecule 4: Detyrosinated tubulin alpha-3 chain

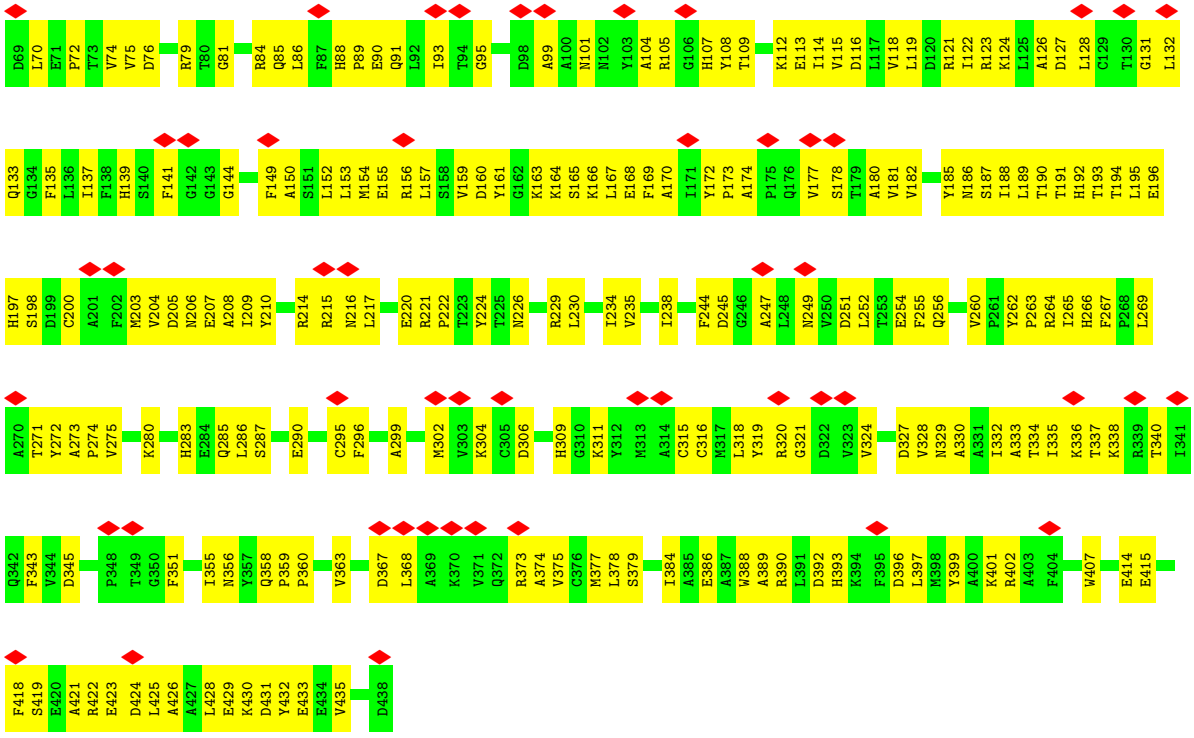
Chain KI:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

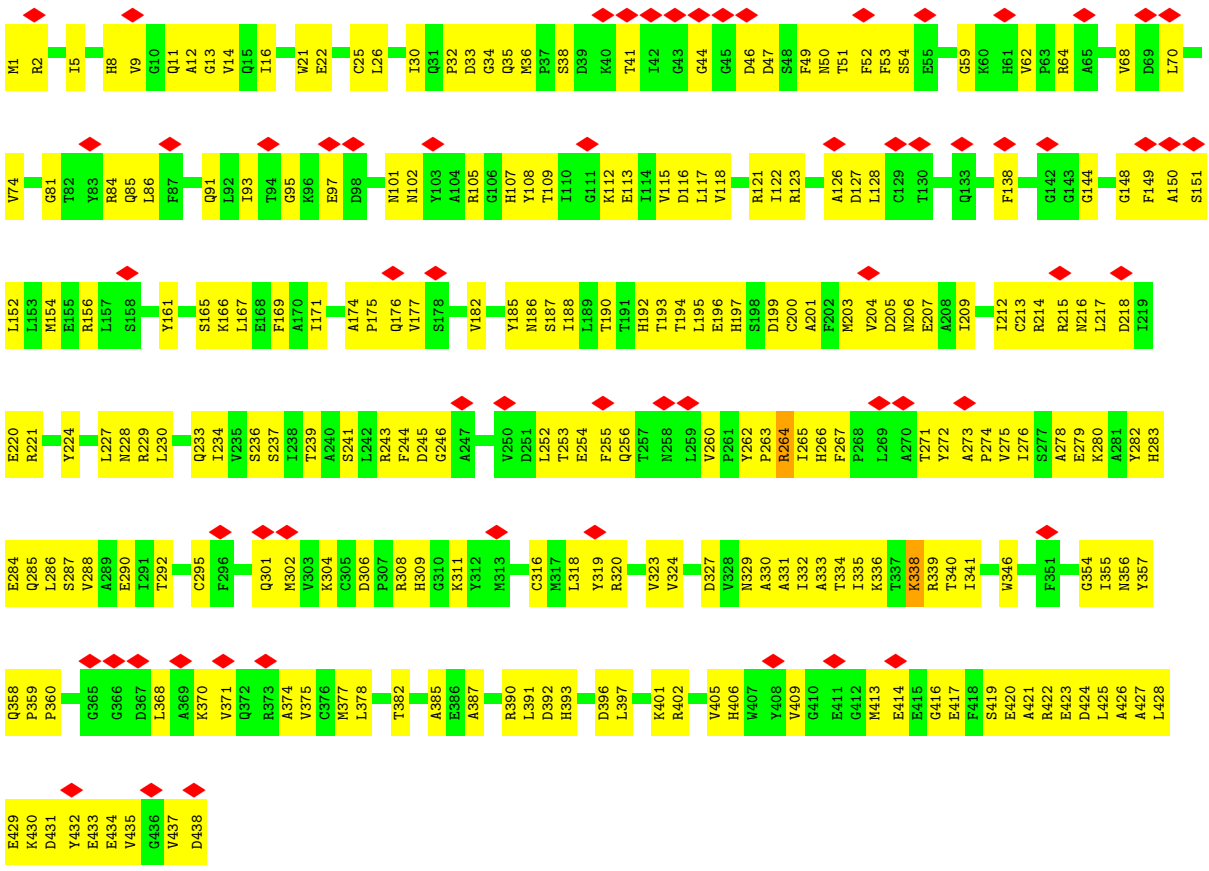
Chain KK:





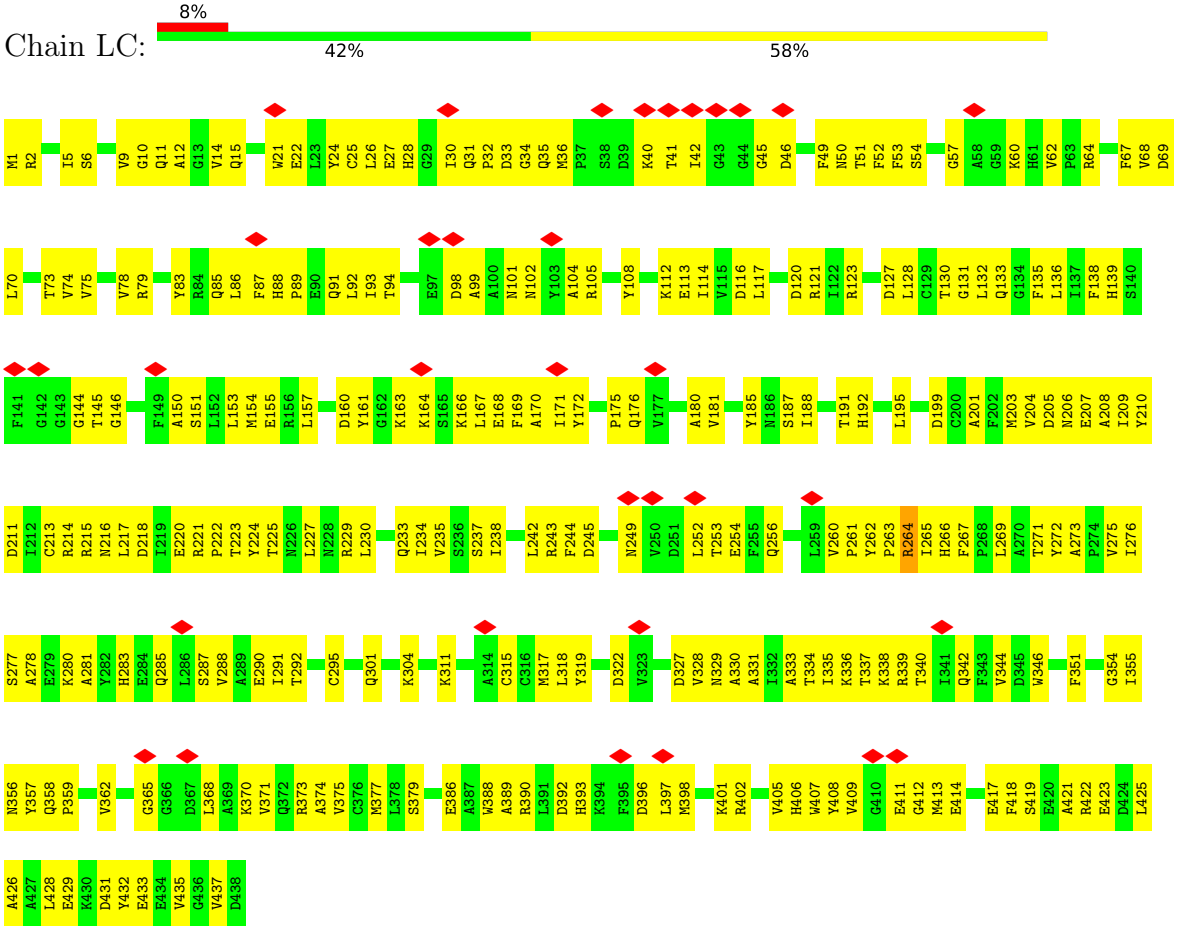
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain LA:



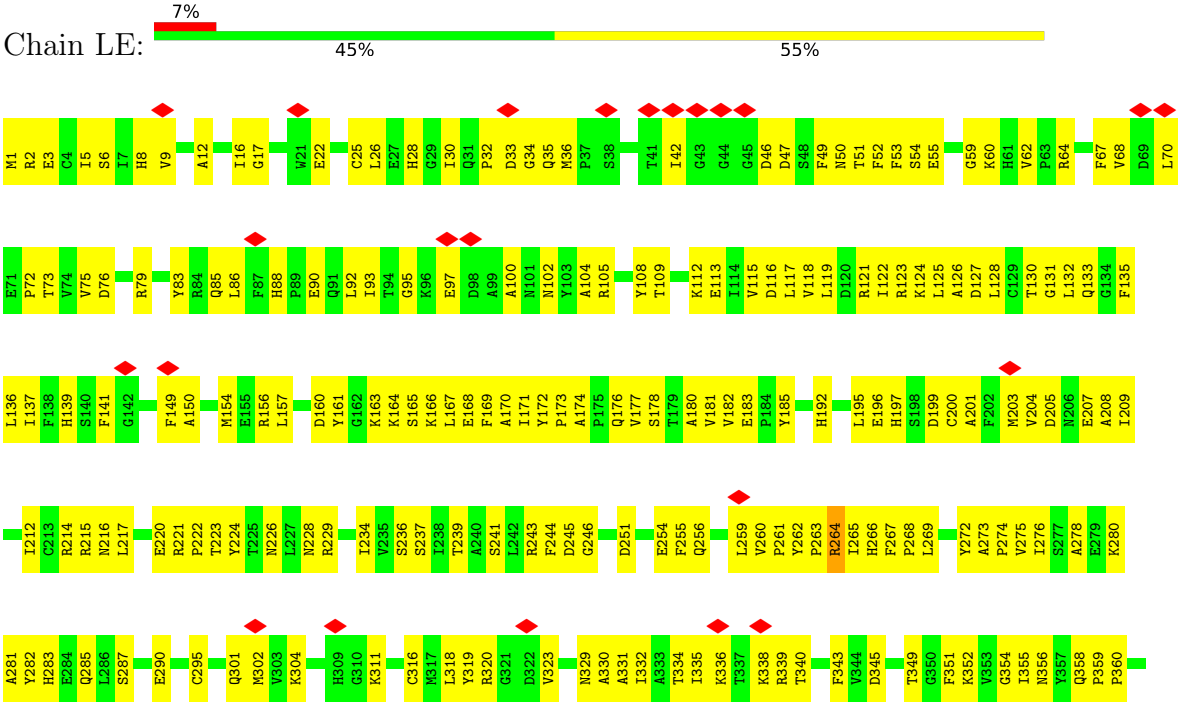
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain LC:



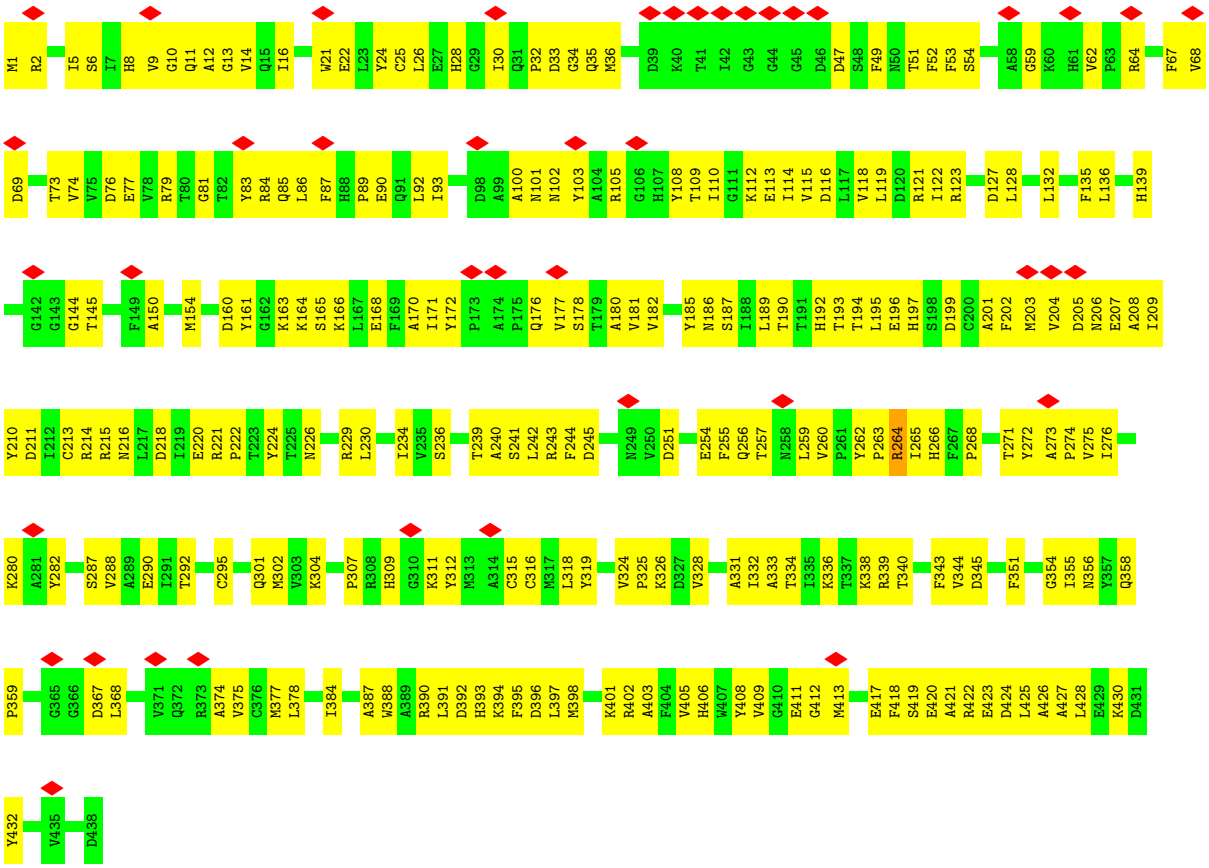
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain LE:



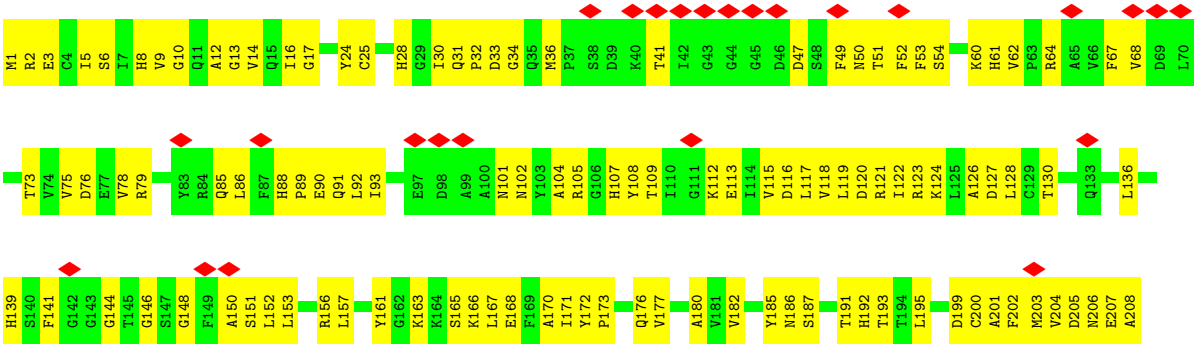
• Molecule 4: Detyrosinated tubulin alpha-3 chain

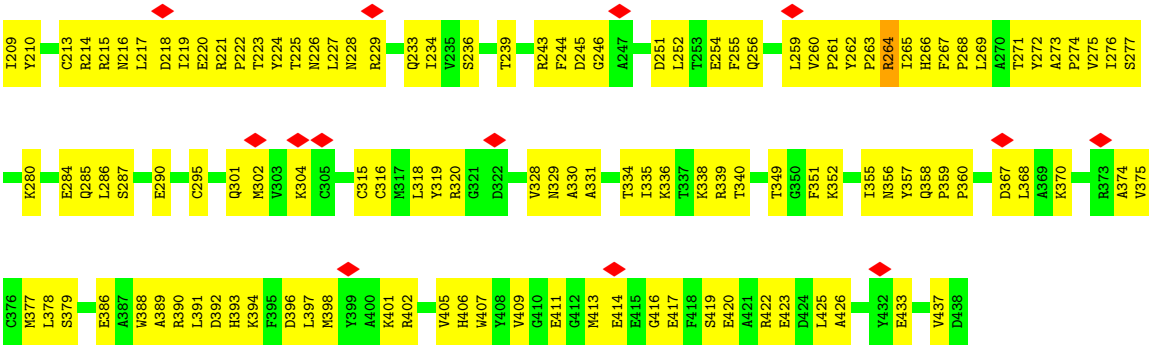
Chain LG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

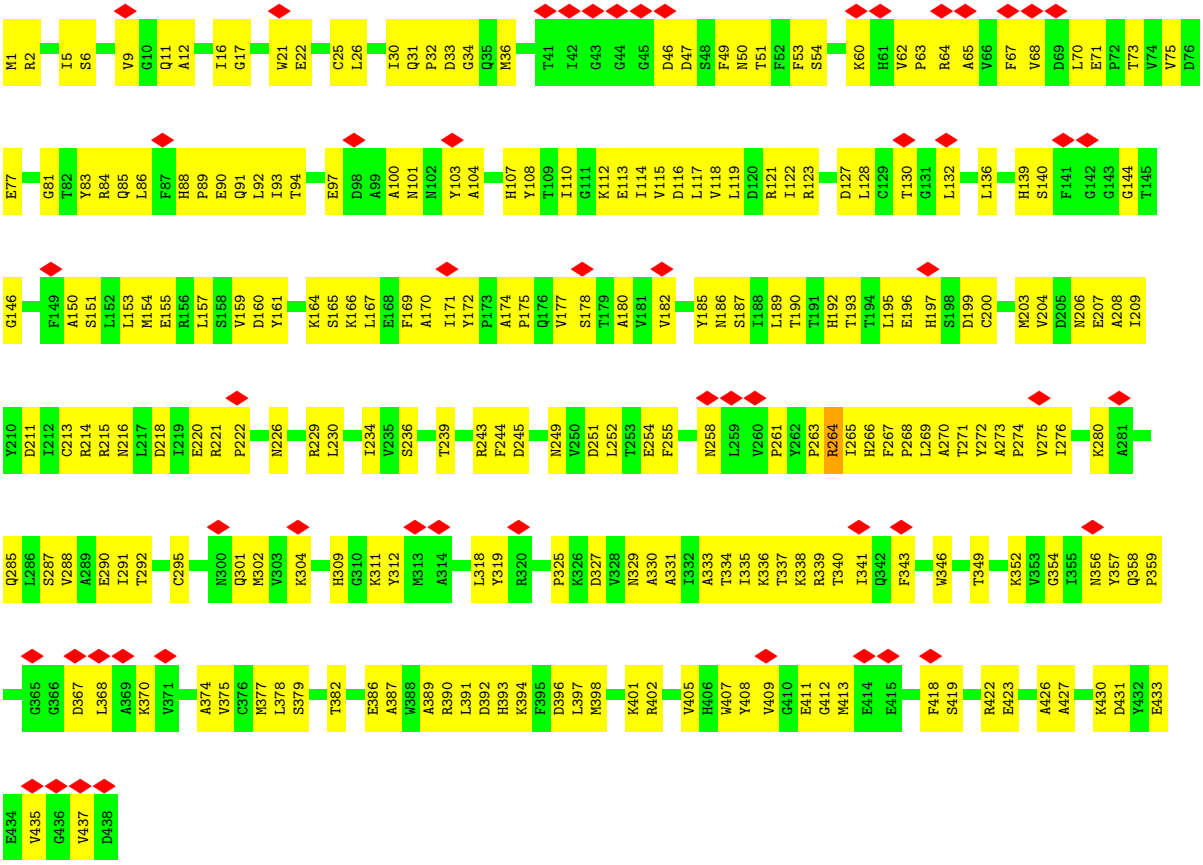
Chain LI:





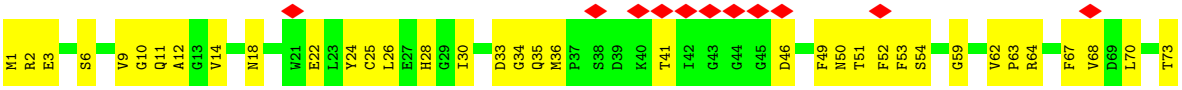
• Molecule 4: Detyrosinated tubulin alpha-3 chain

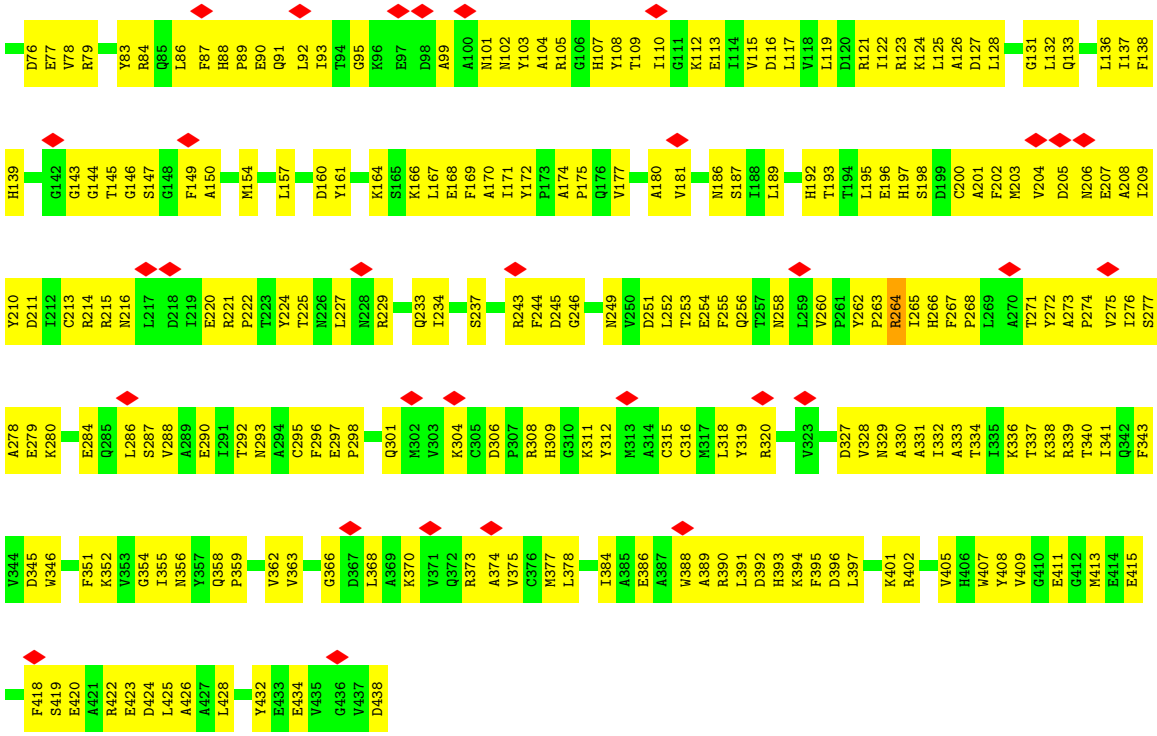
Chain LK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

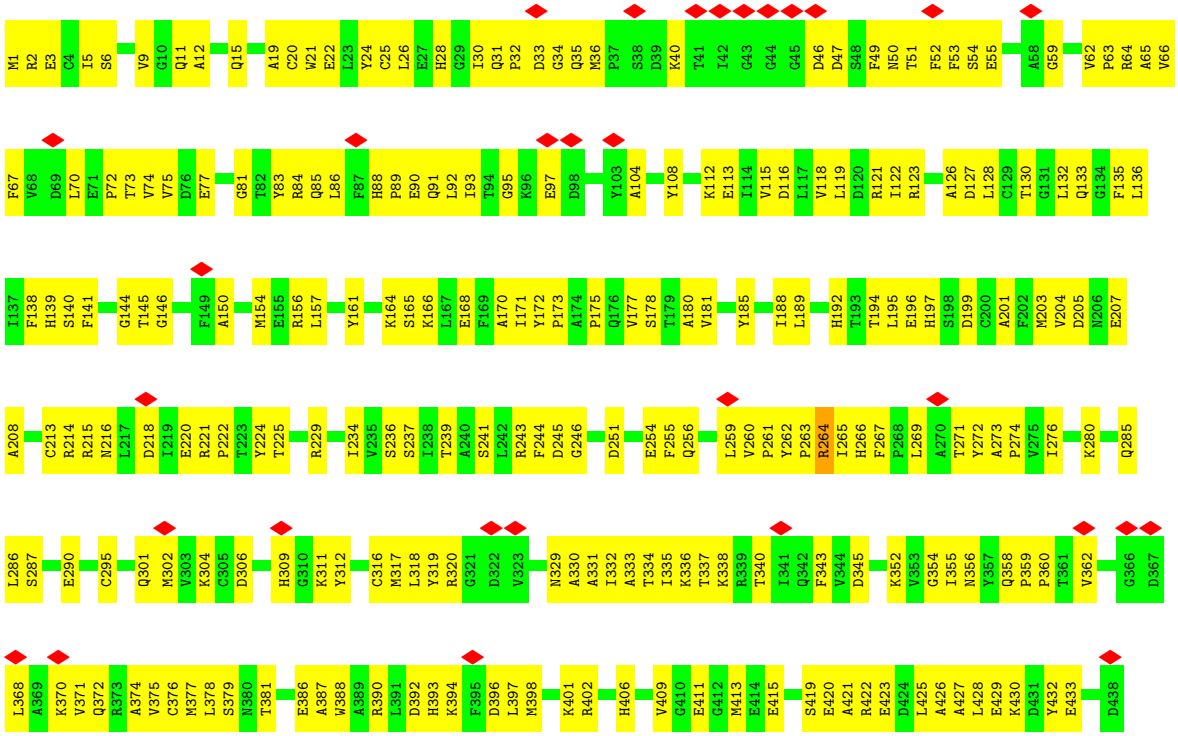
Chain MC:





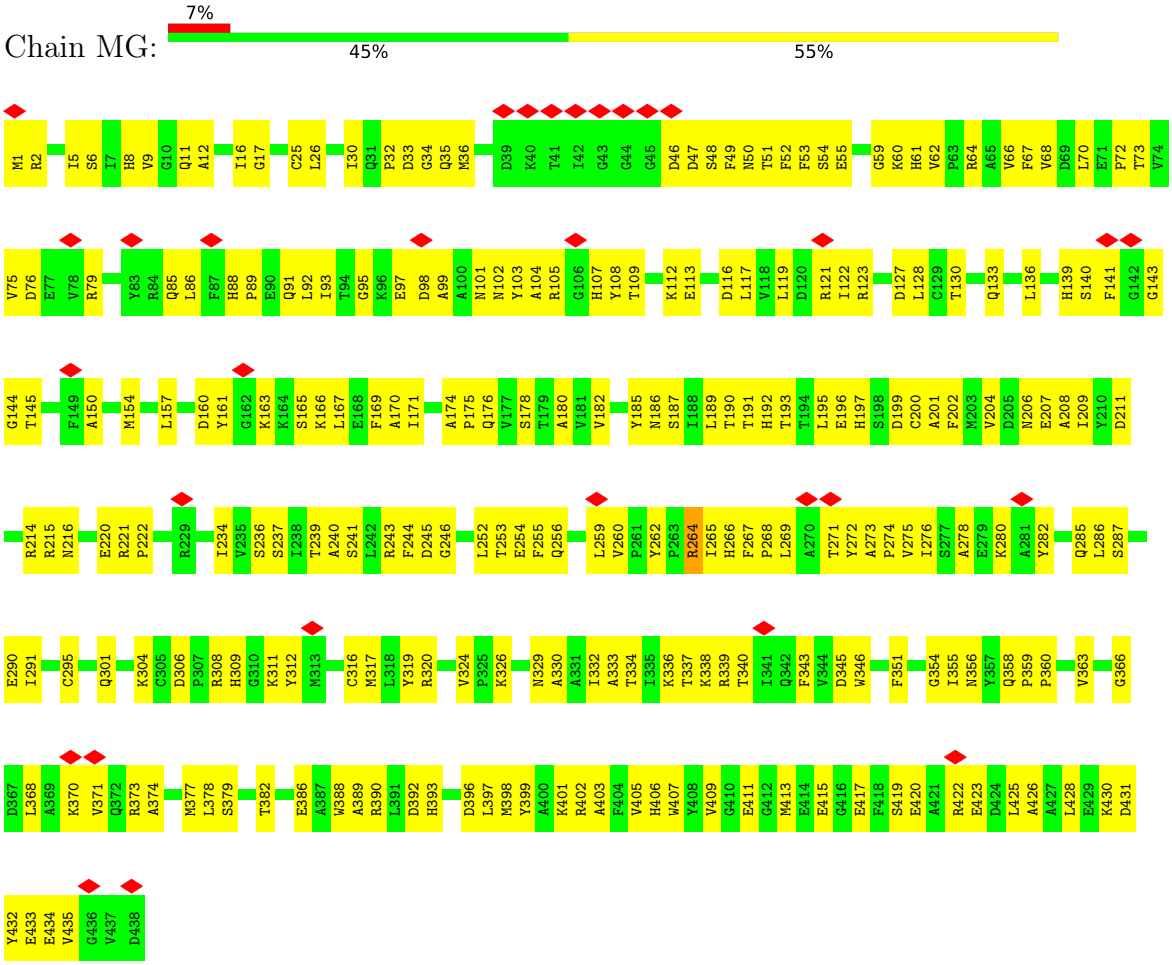
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain ME:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain MG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

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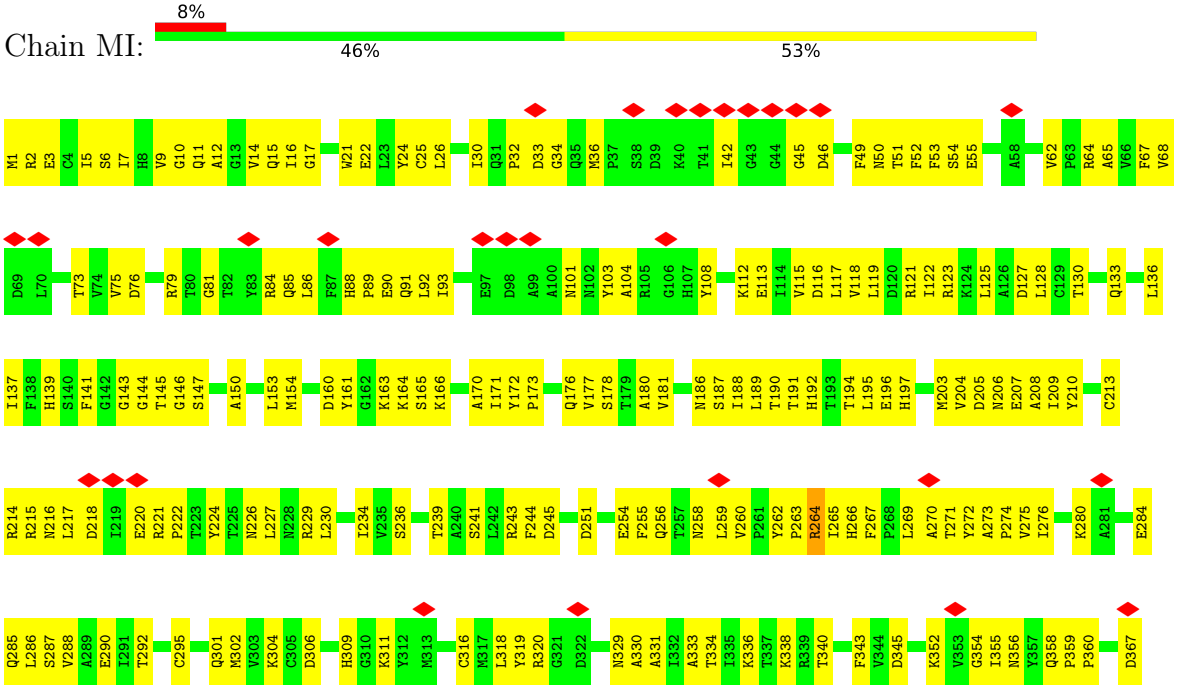

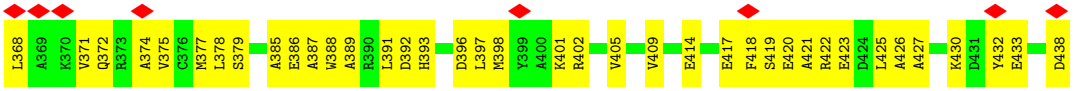

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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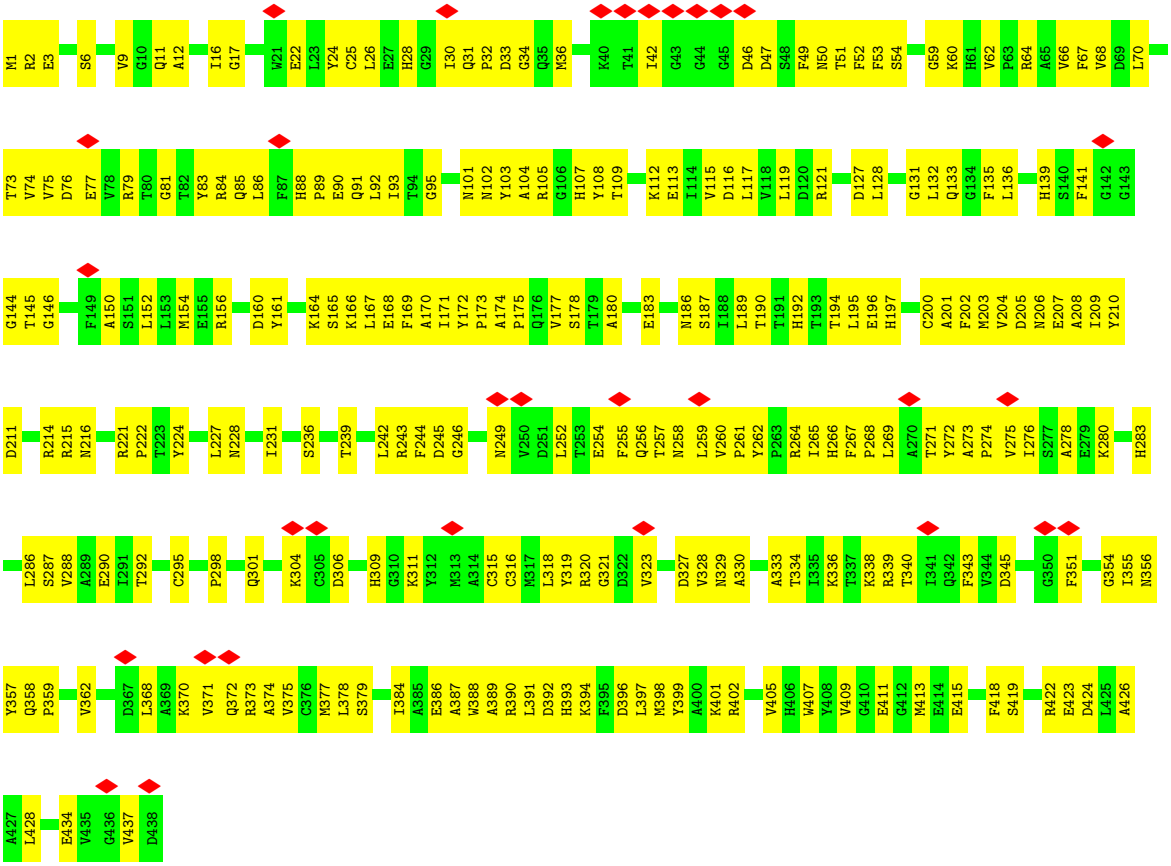

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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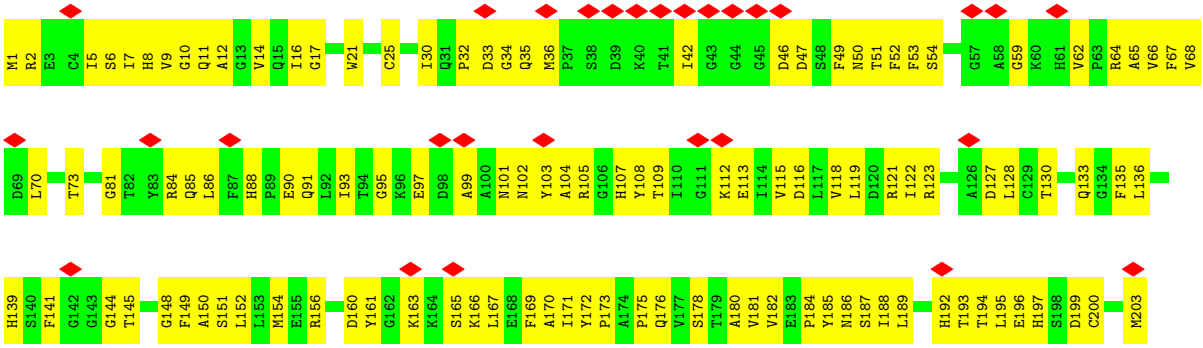

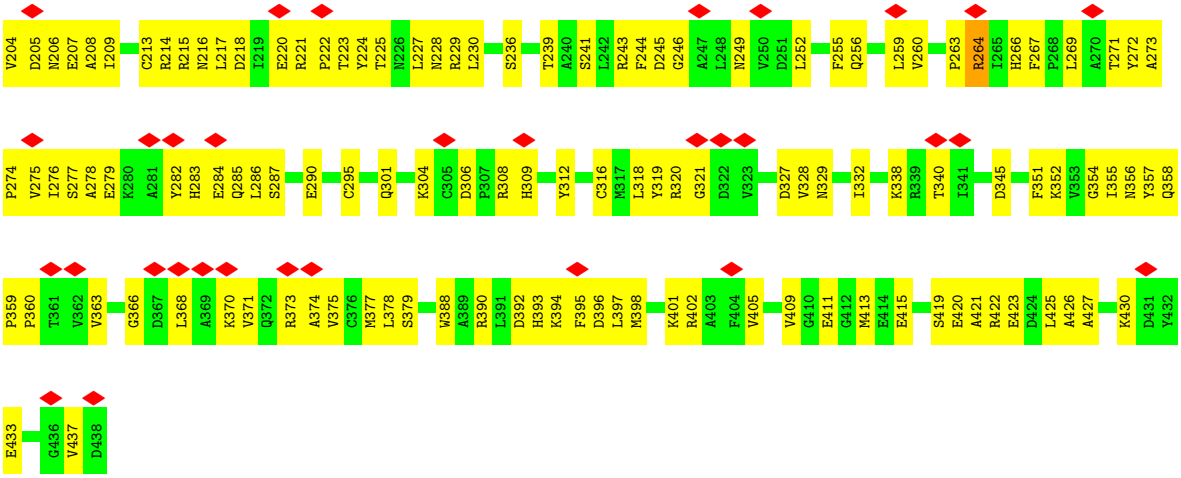

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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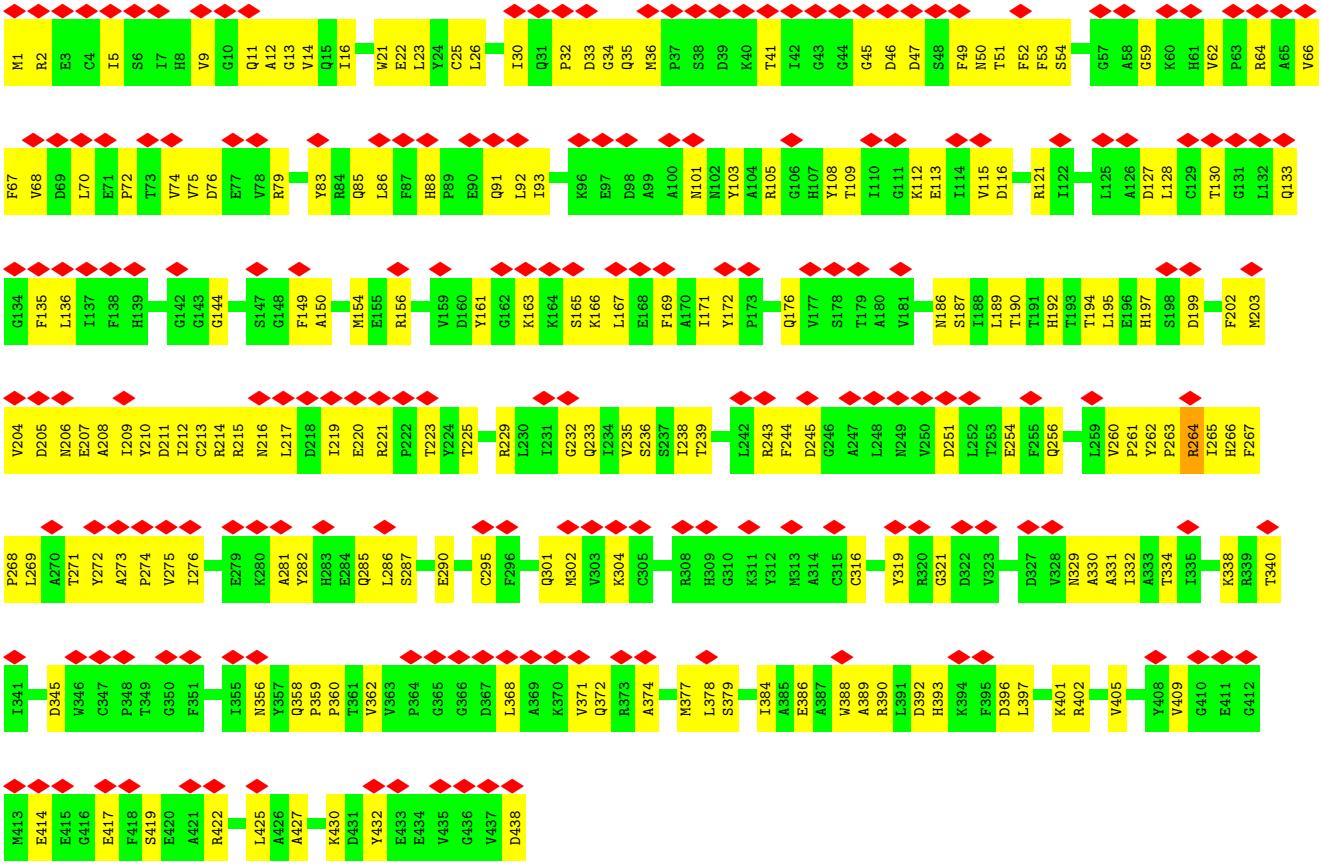
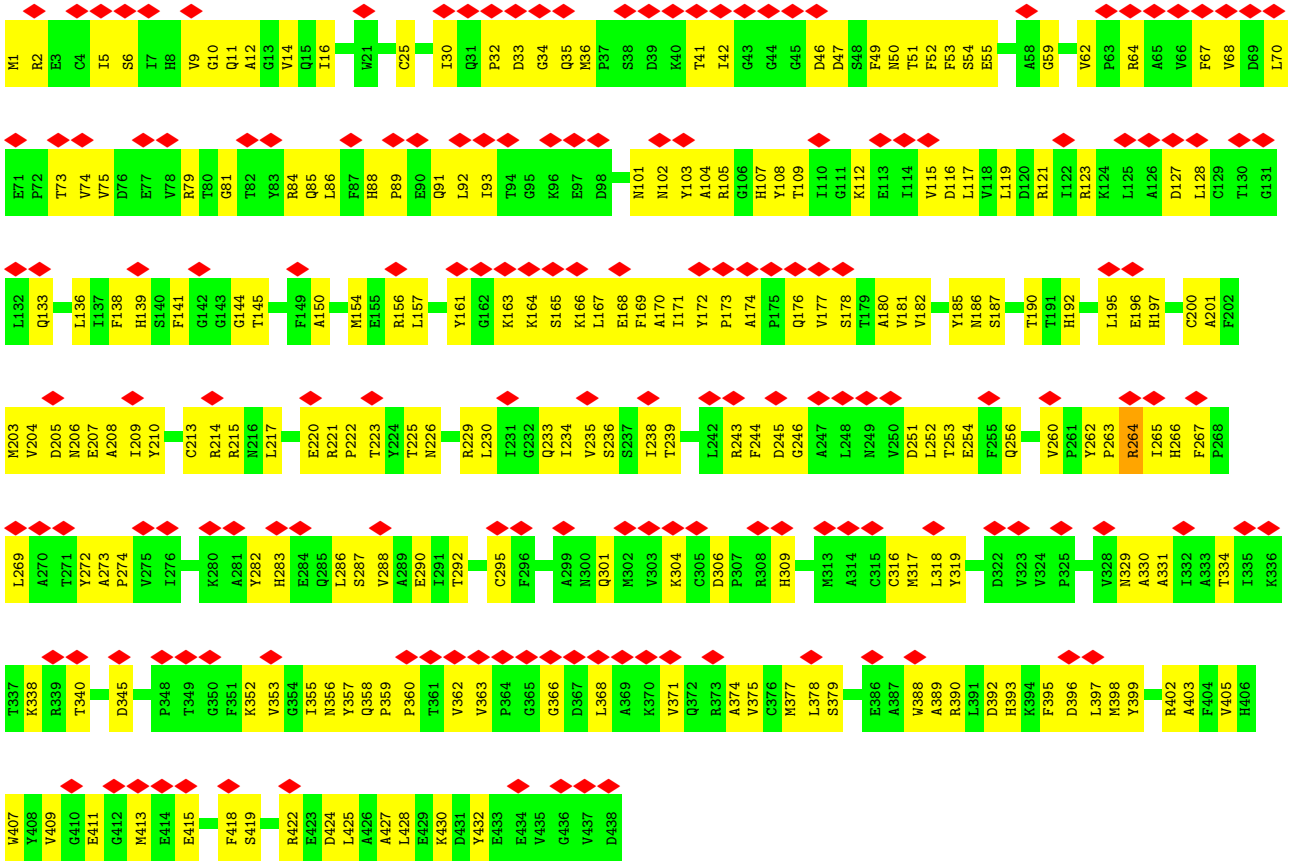


• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain NC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

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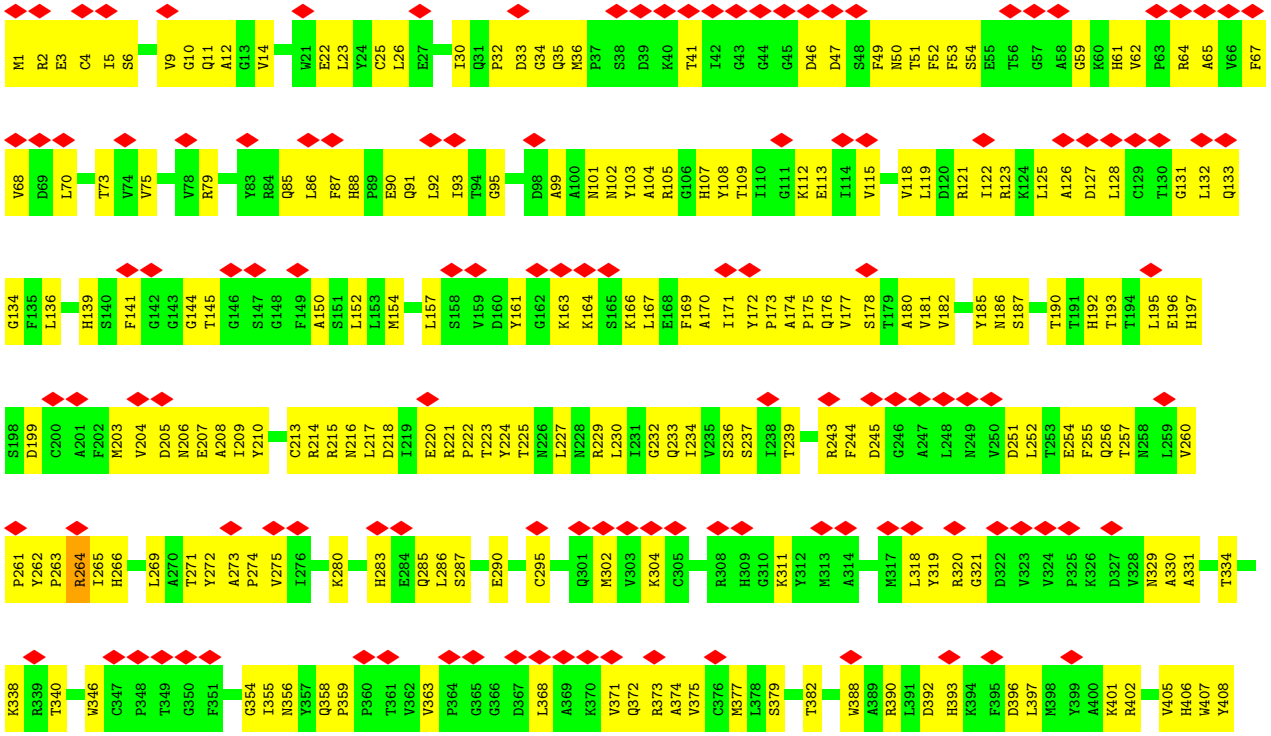

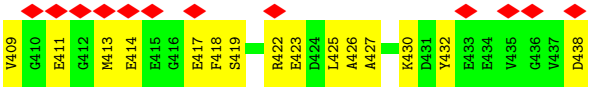

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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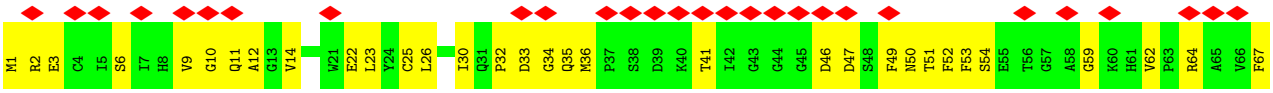
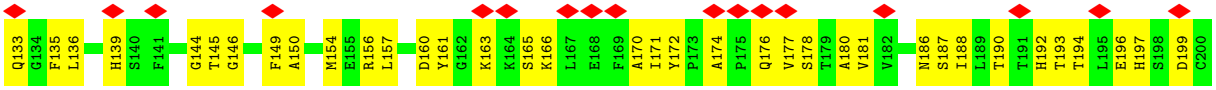
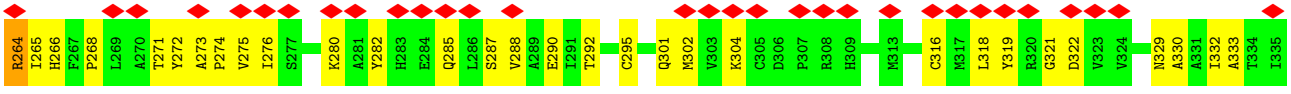
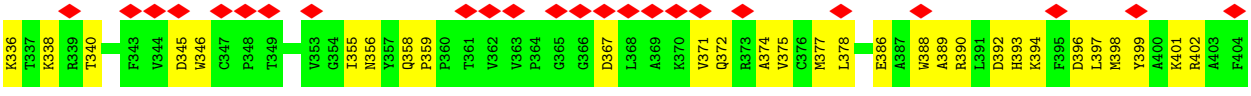
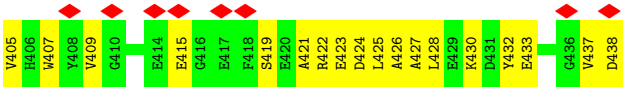




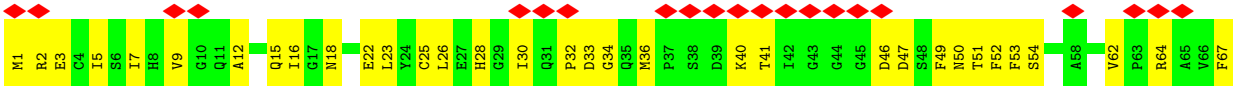


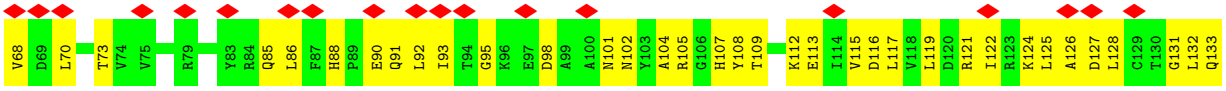


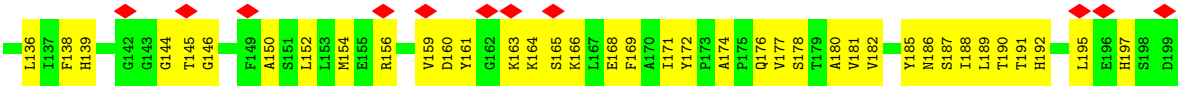


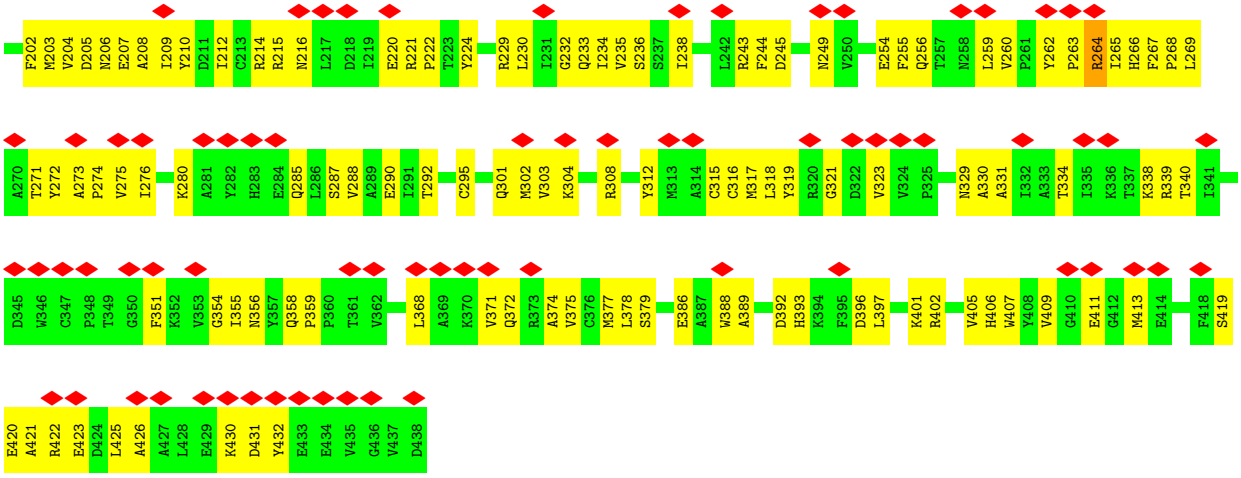
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain NI:









• Molecule 4: Detyrosinated tubulin alpha-3 chain

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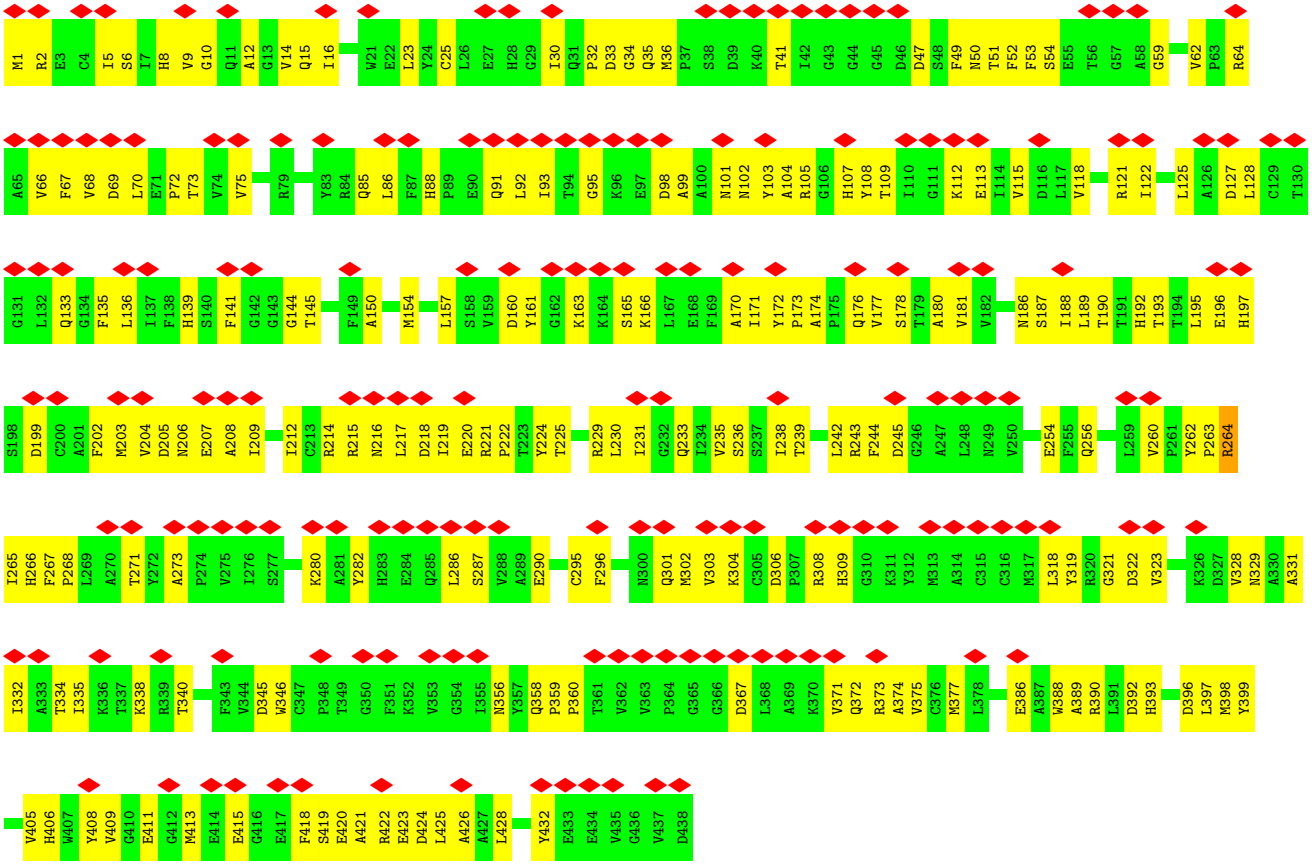

• Molecule 4: Detyrosinated tubulin alpha-3 chain

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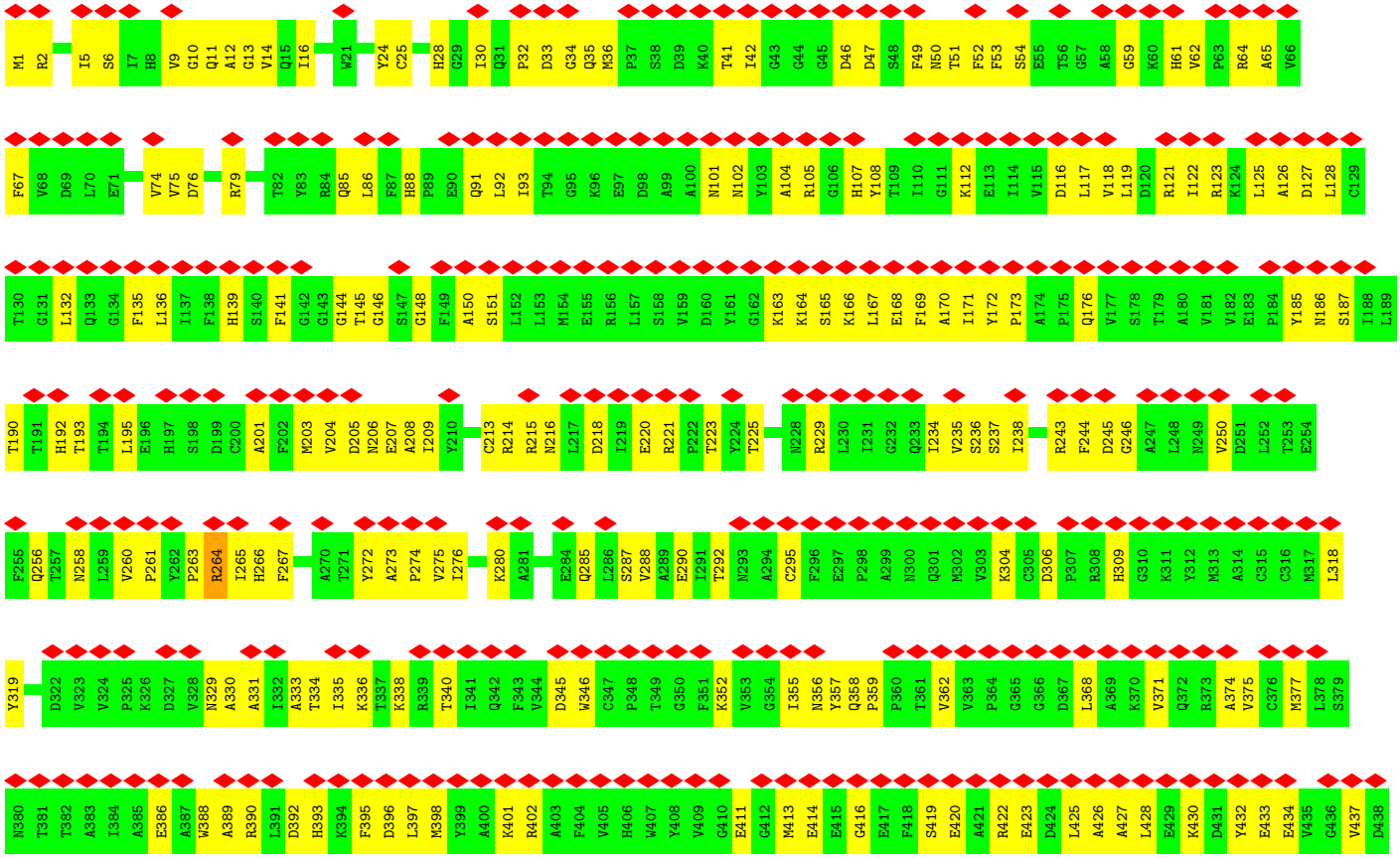
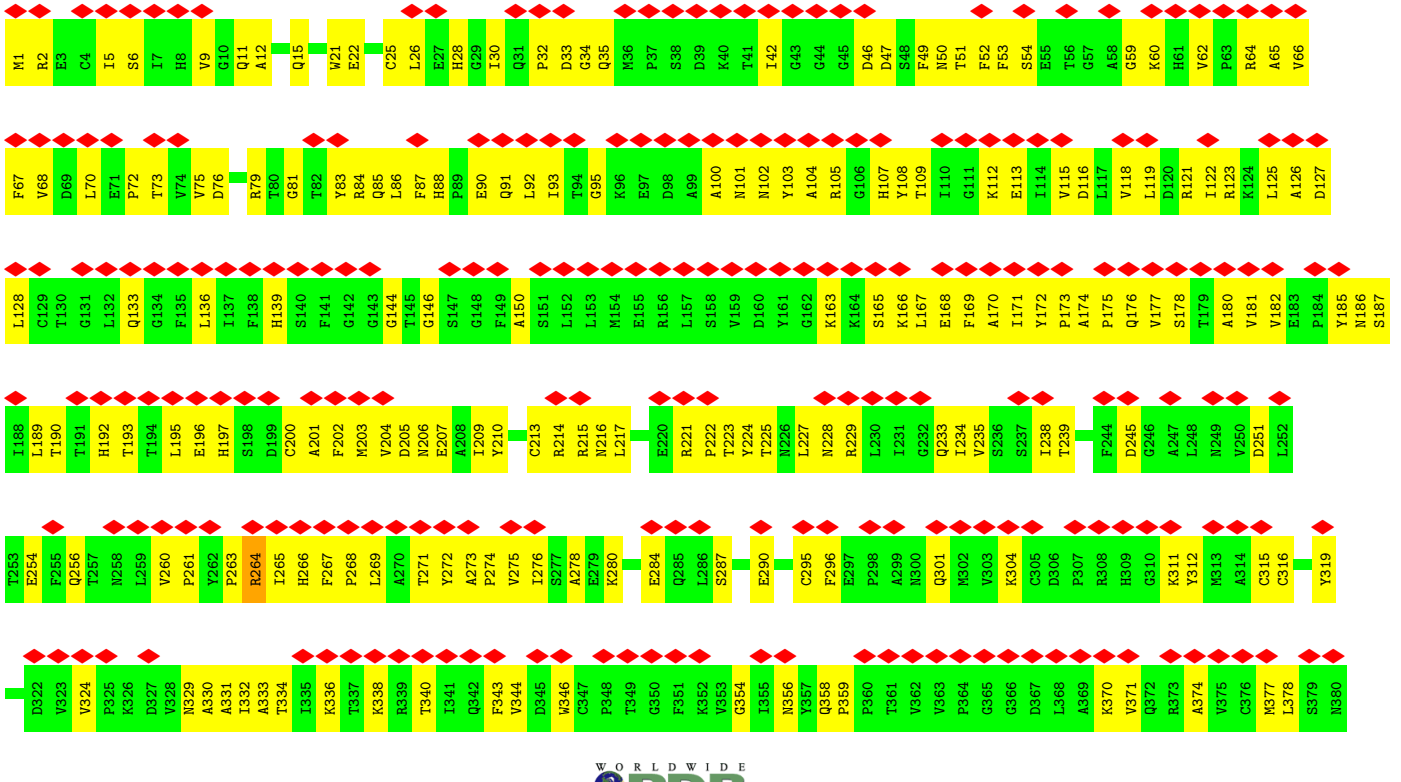
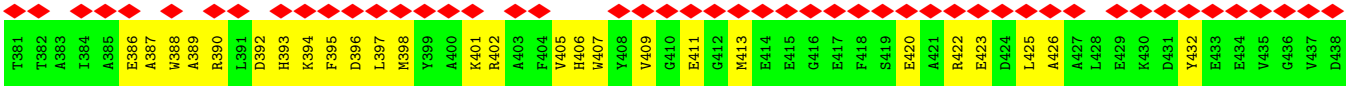


• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain OC:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

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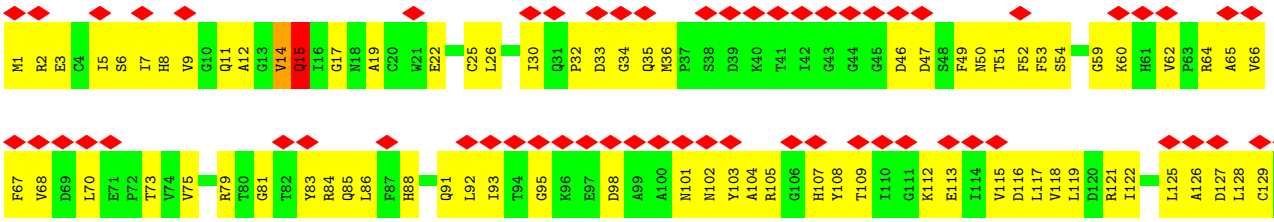
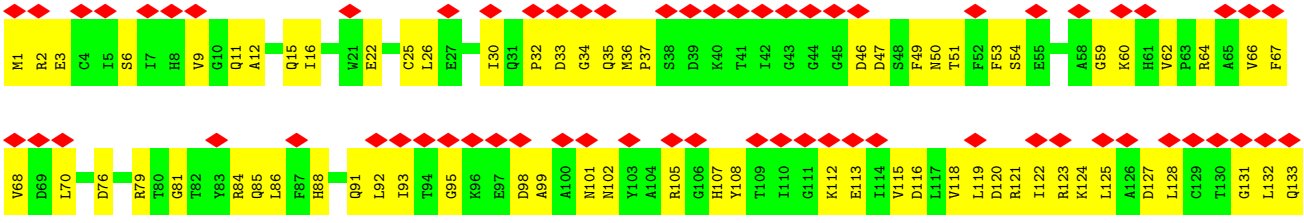
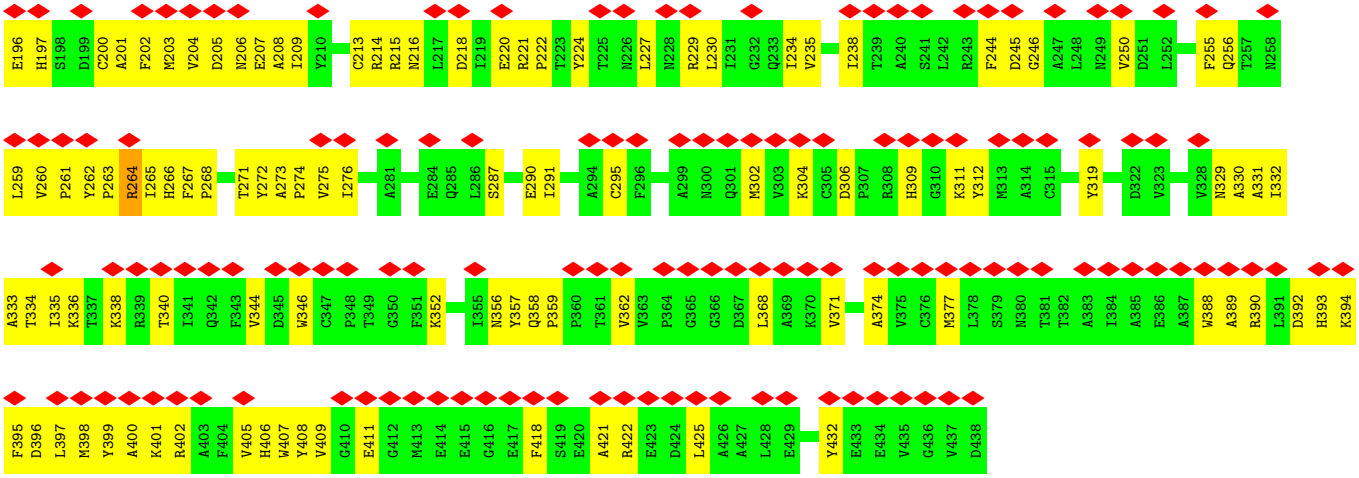


• Molecule 4: Detyrosinated tubulin alpha-3 chain

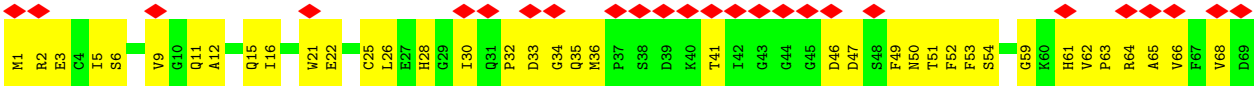
Chain OG:

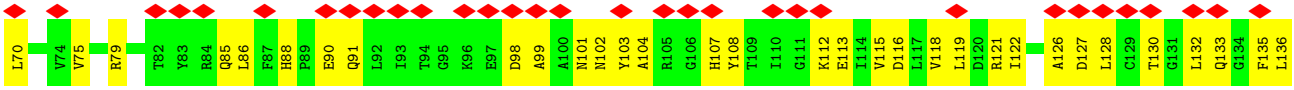


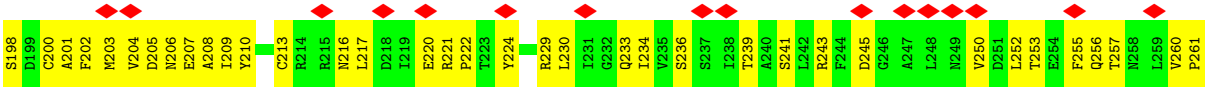


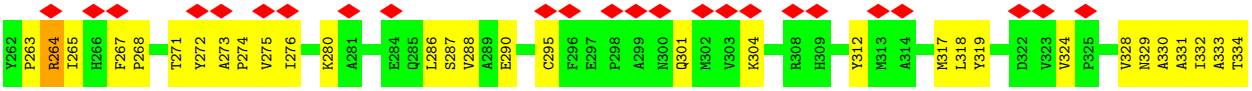
• Molecule 4: Detyrosinated tubulin alpha-3 chain

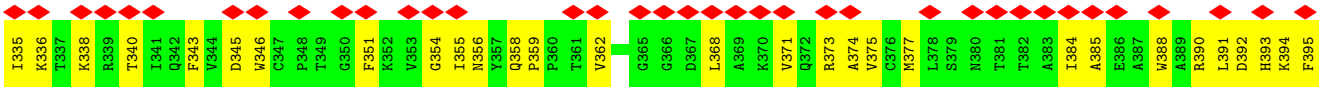
Chain OI:

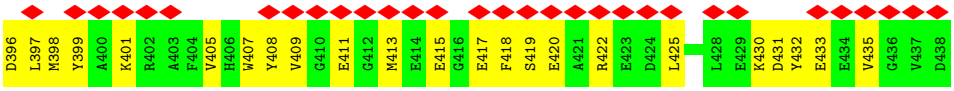






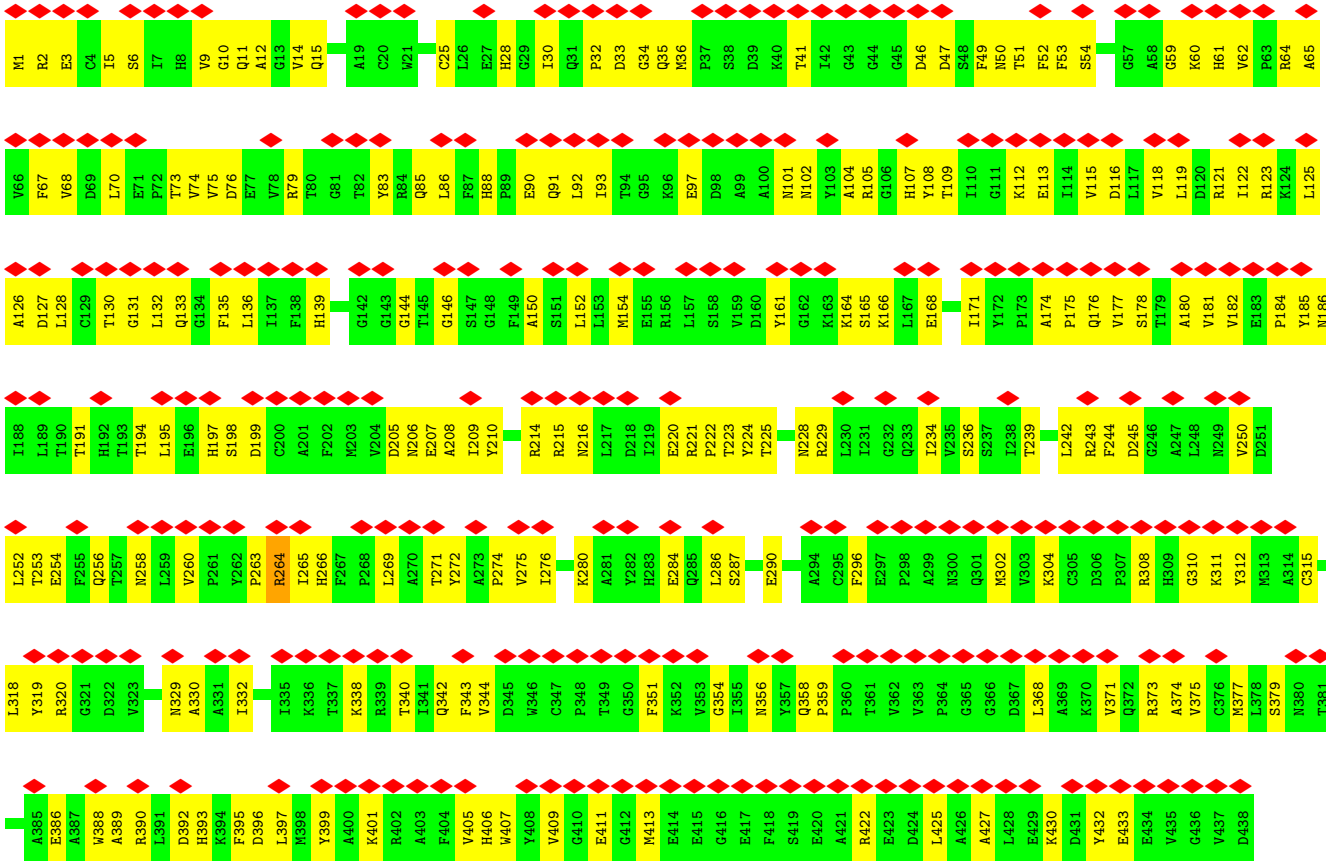






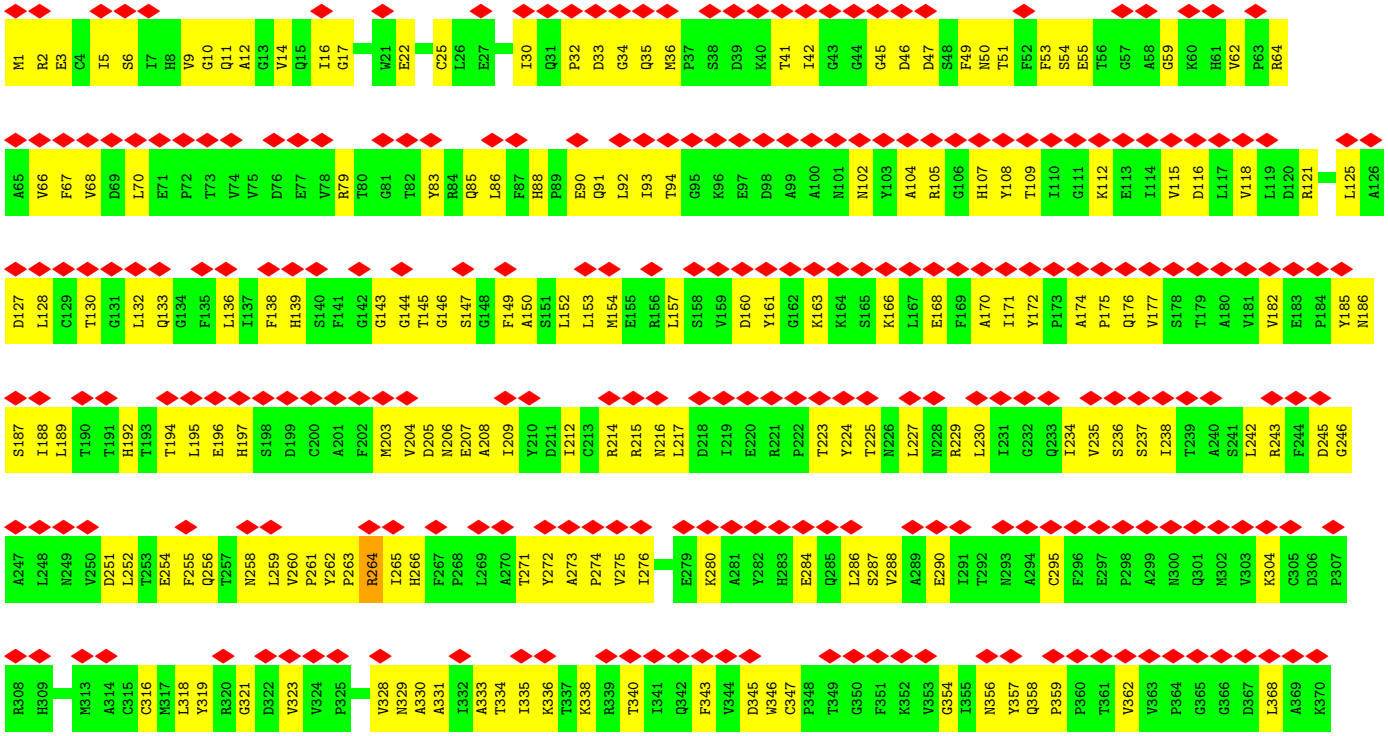
• Molecule 4: Detyrosinated tubulin alpha-3 chain

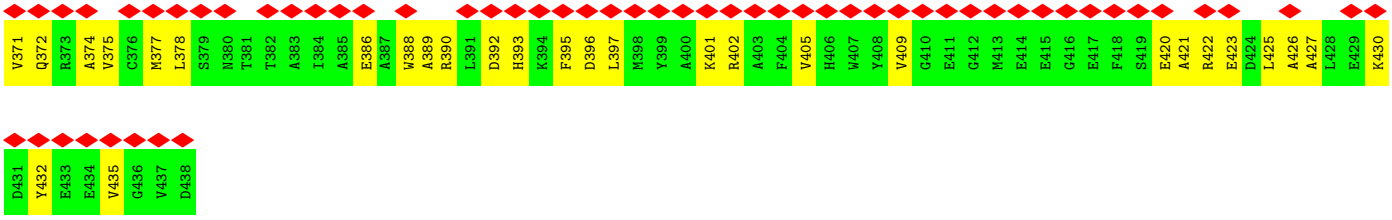
Chain OK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

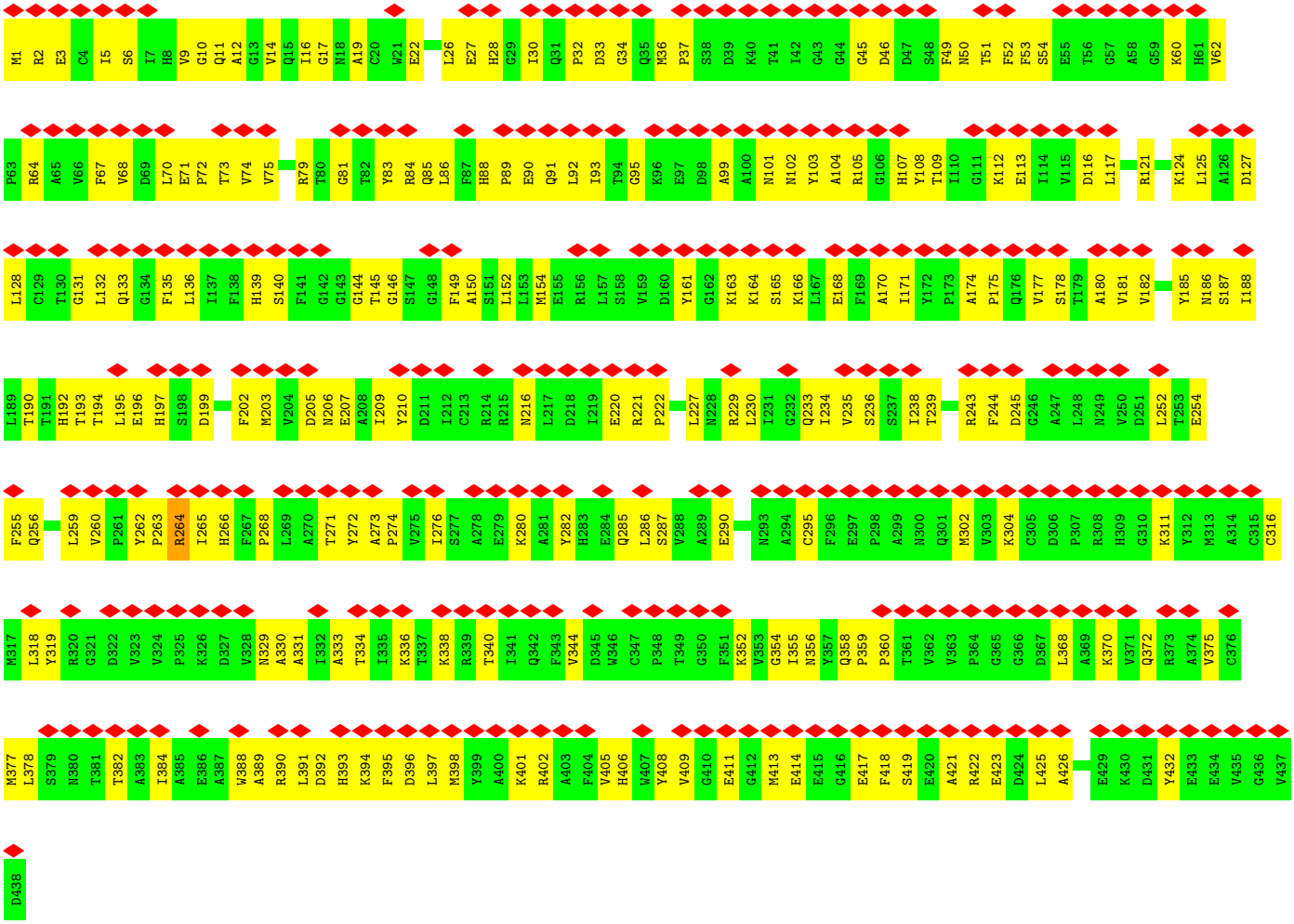
Chain PA:





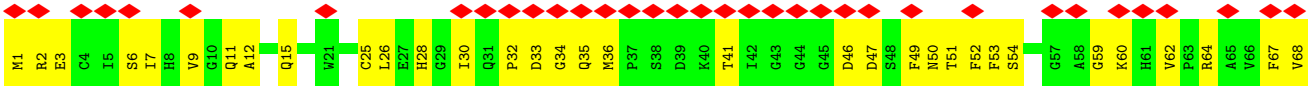
• Molecule 4: Detyrosinated tubulin alpha-3 chain

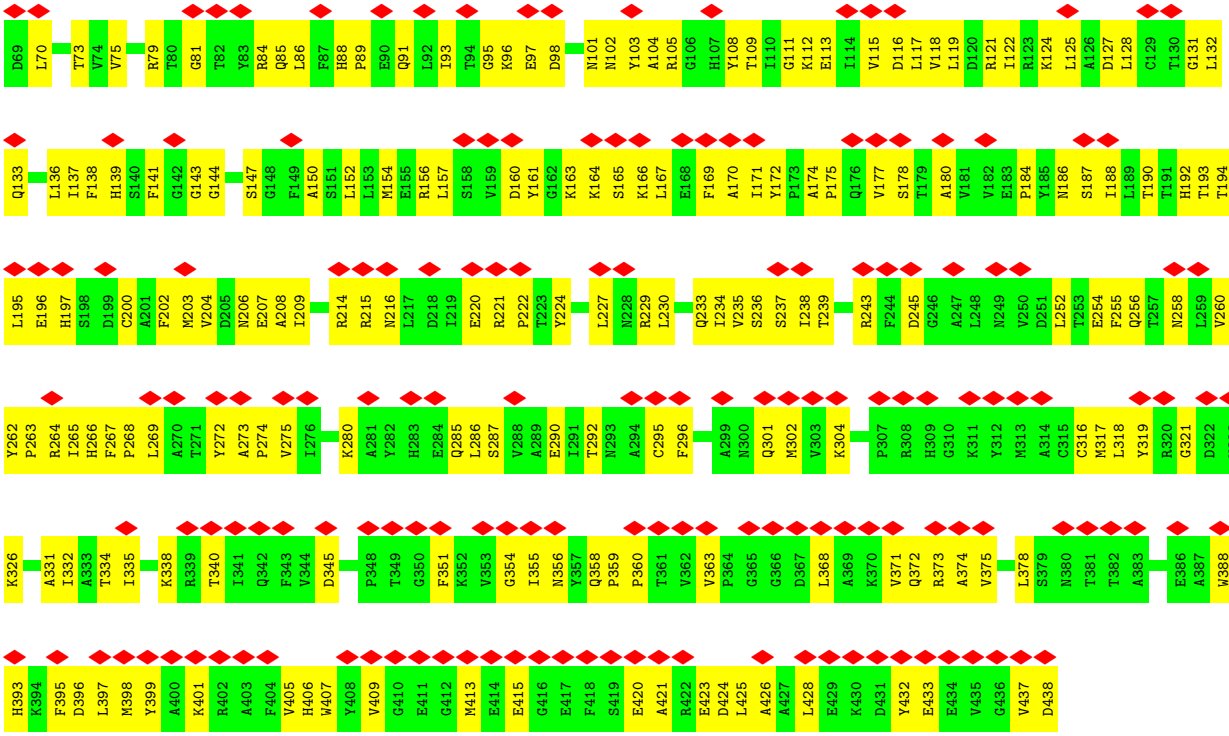
Chain PC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

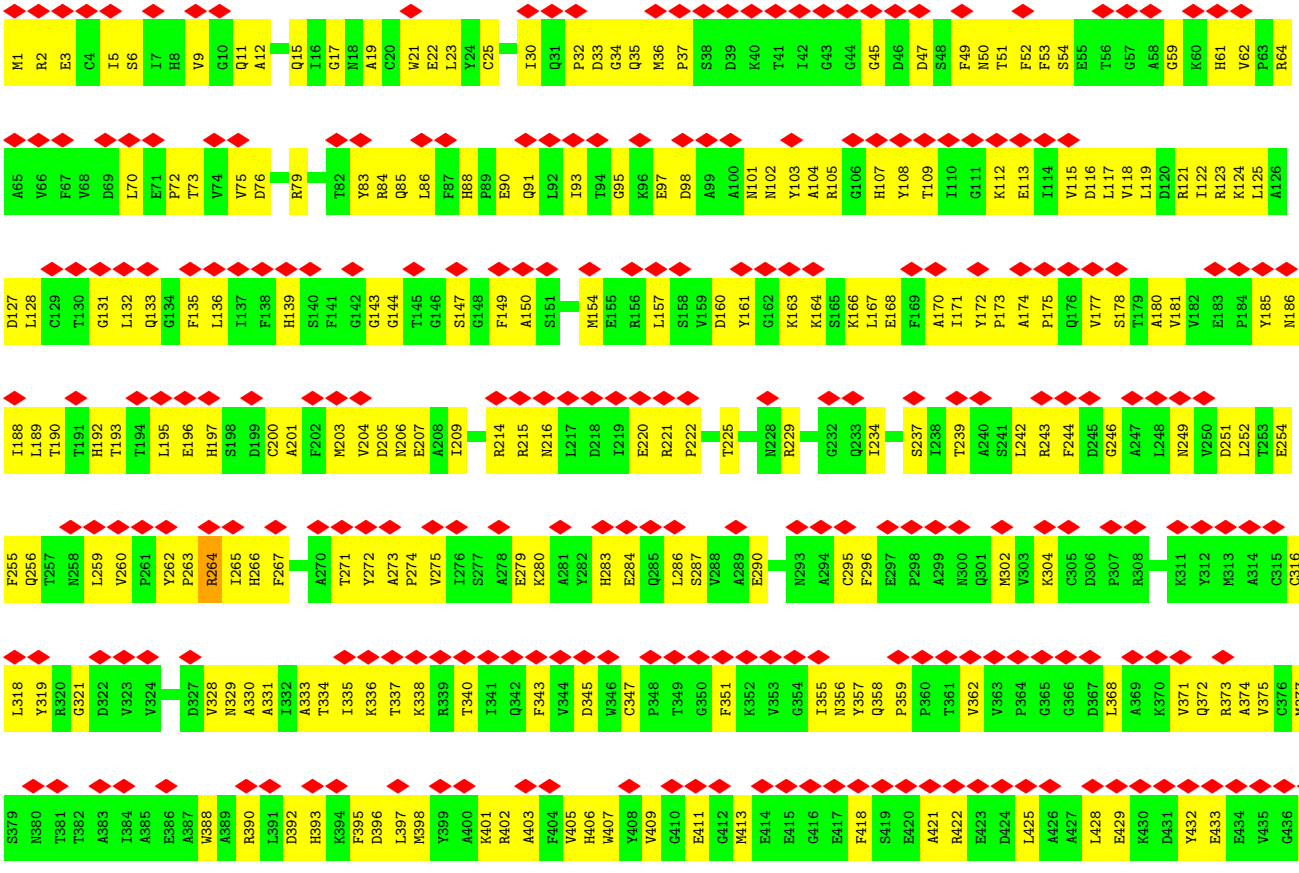
Chain PE:





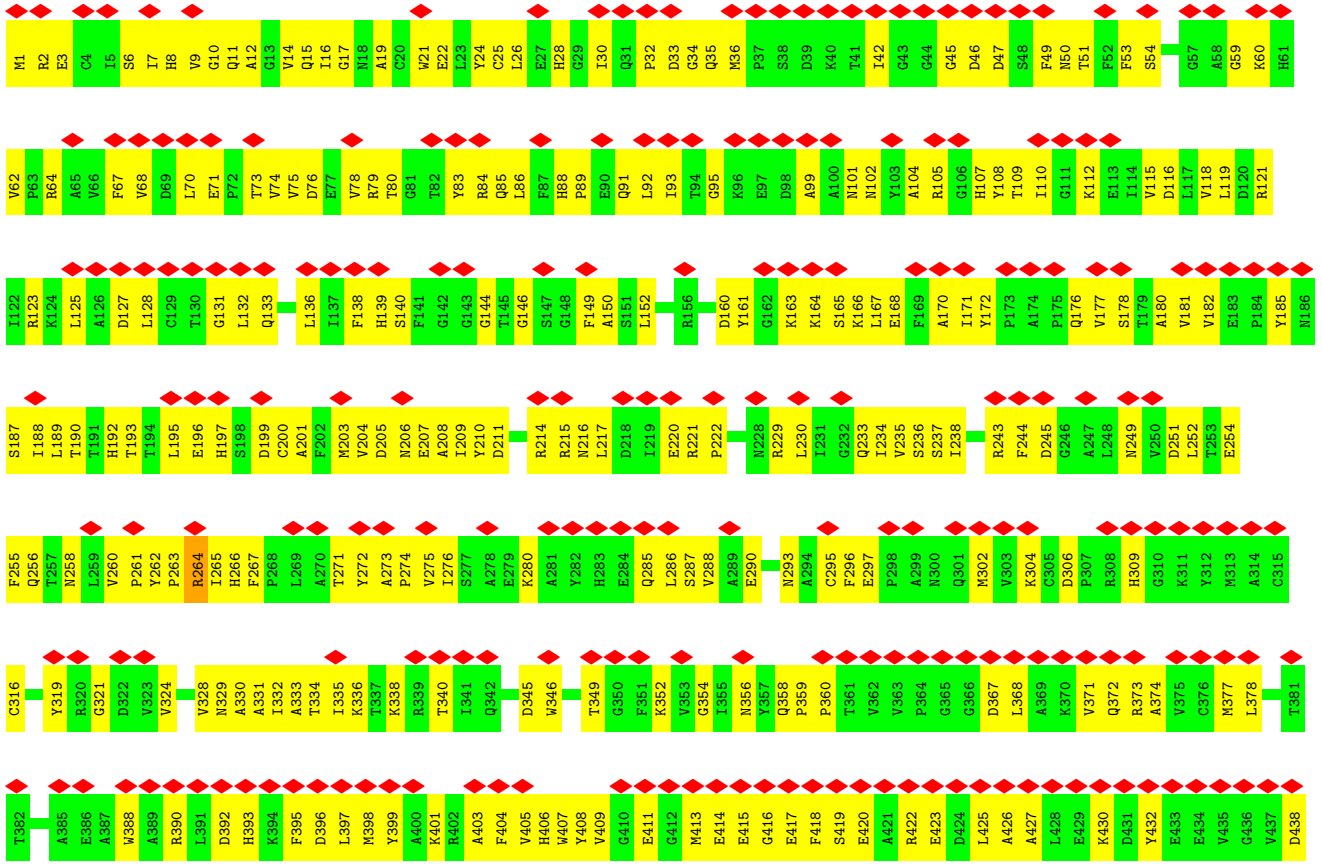
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain PG:



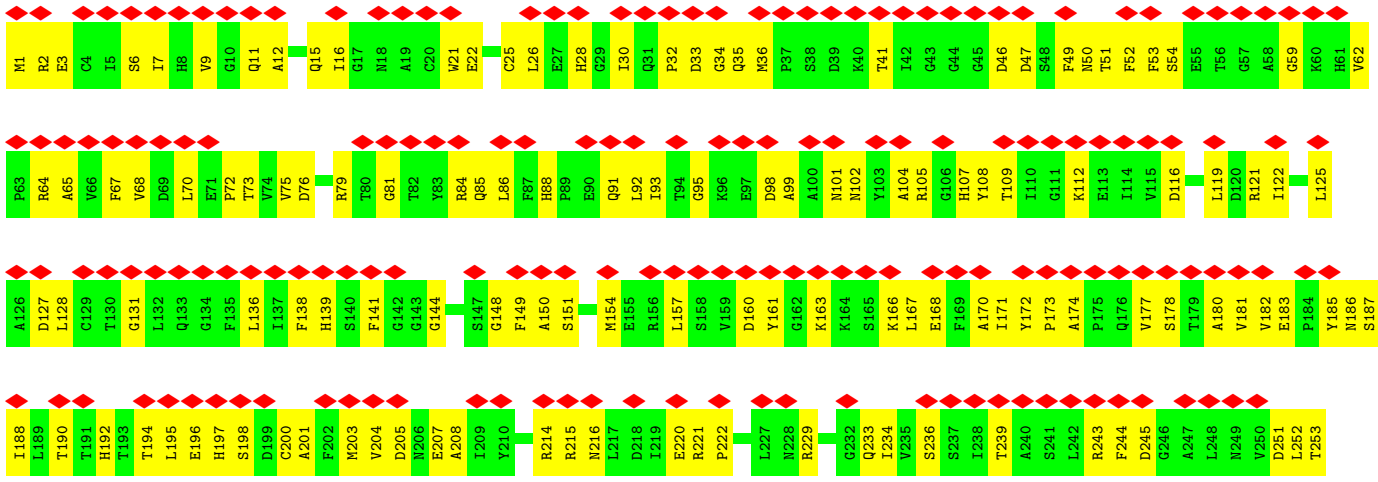
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain PI:



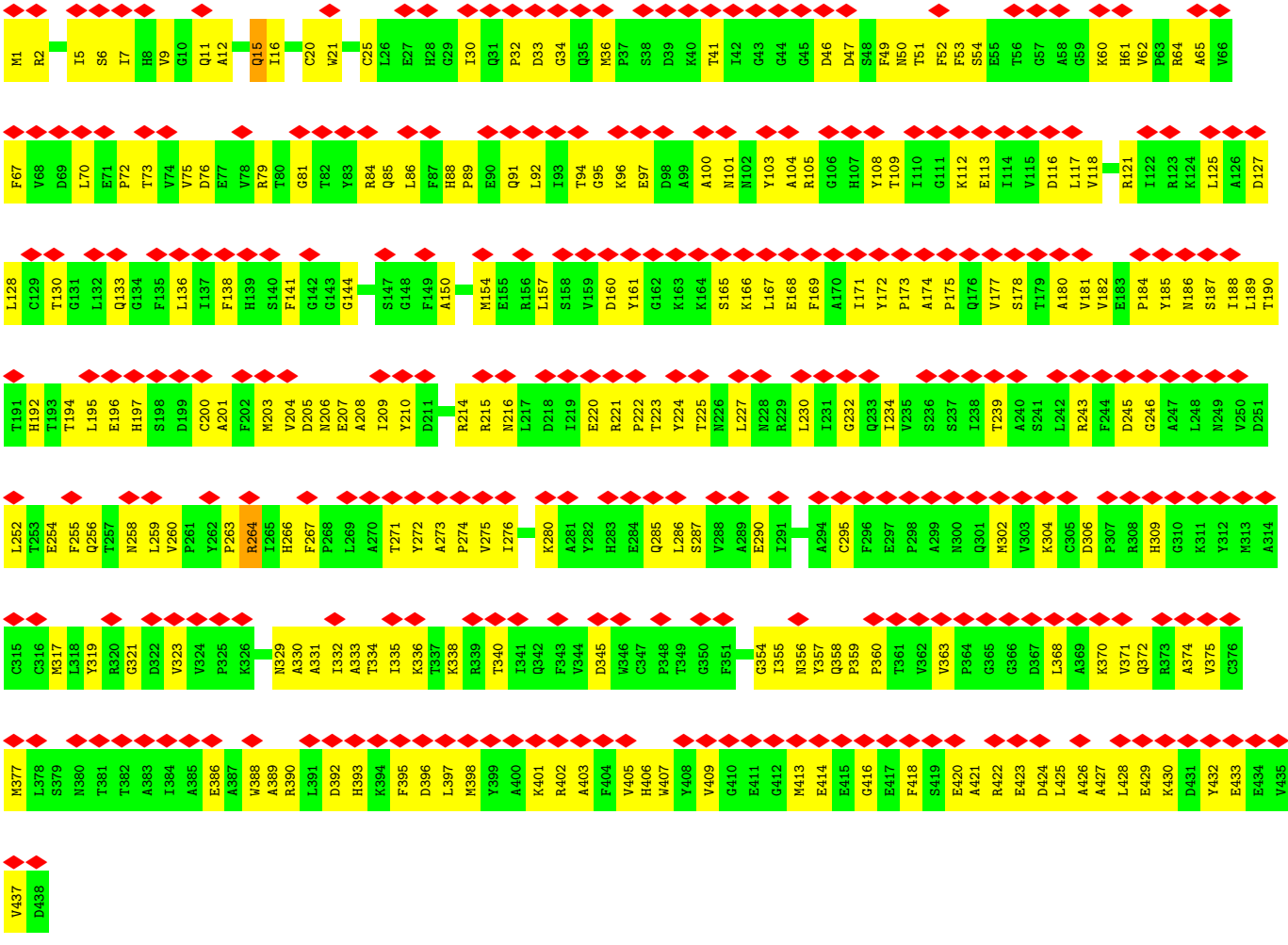
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain PK:



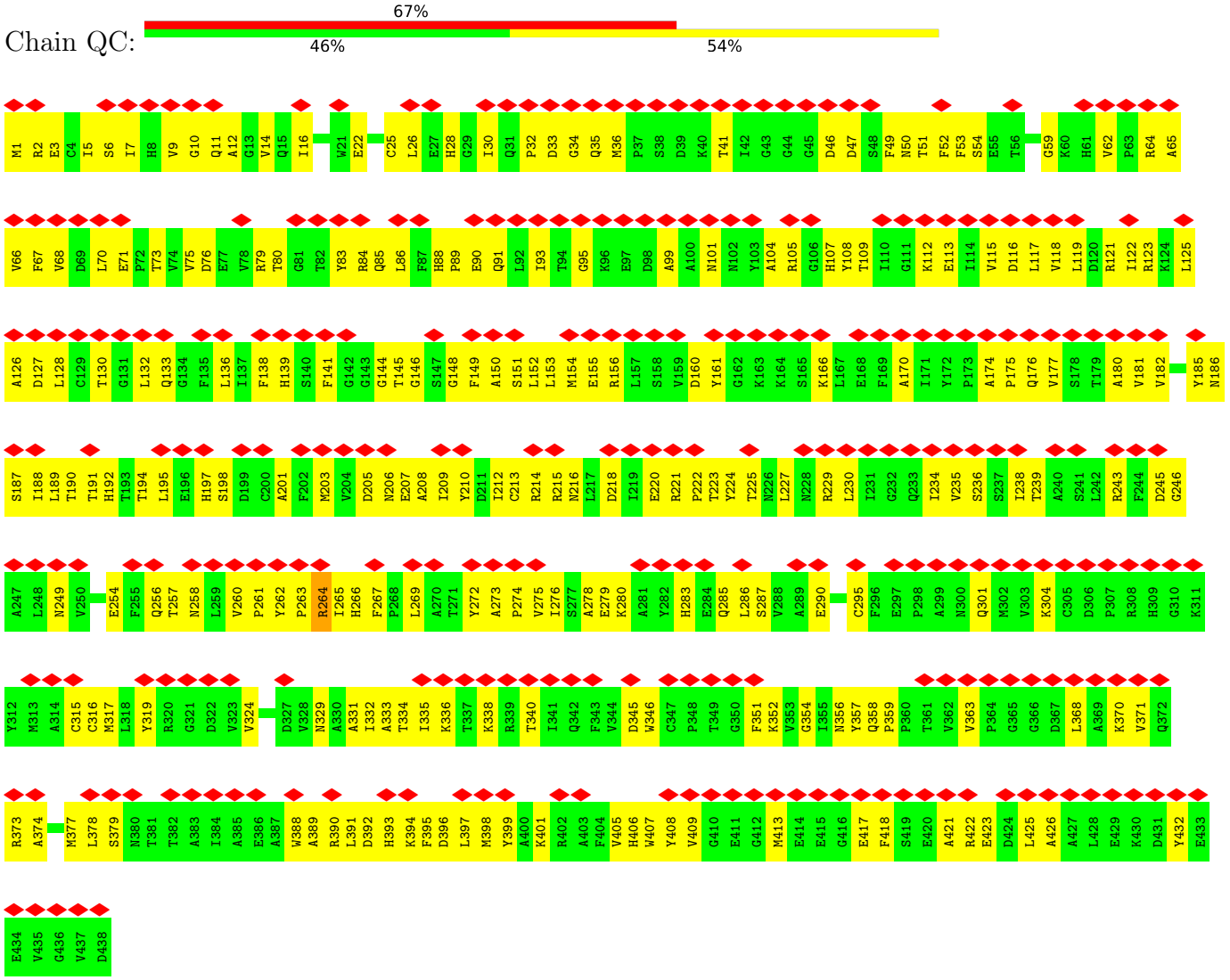
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain PM:



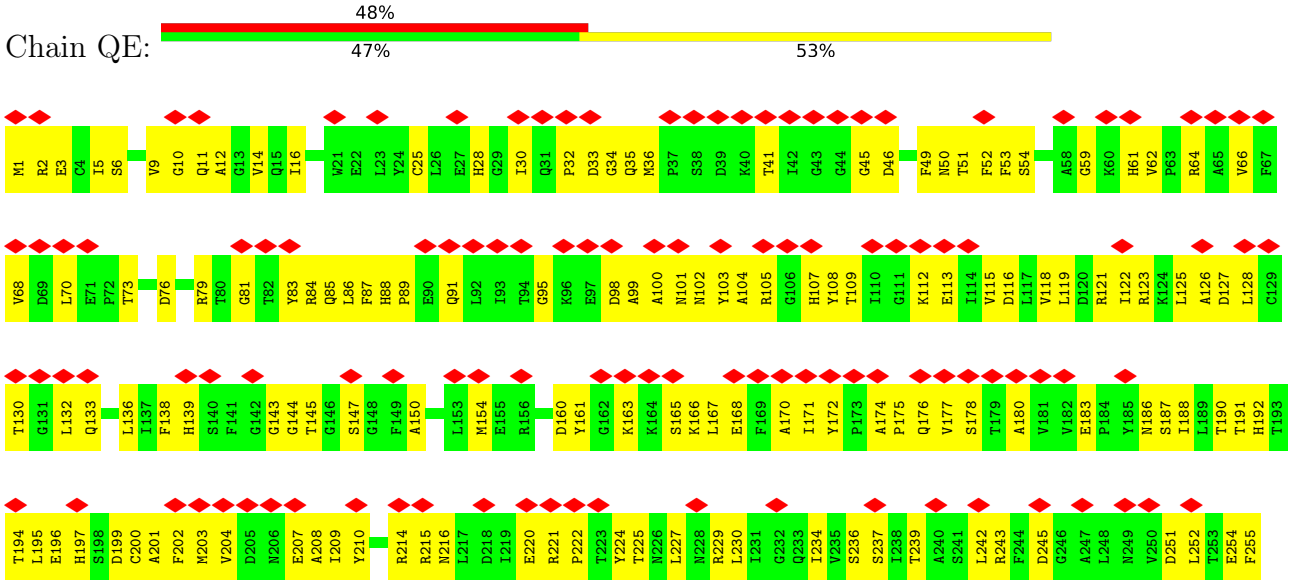
• Molecule 4: Detyrosinated tubulin alpha-3 chain

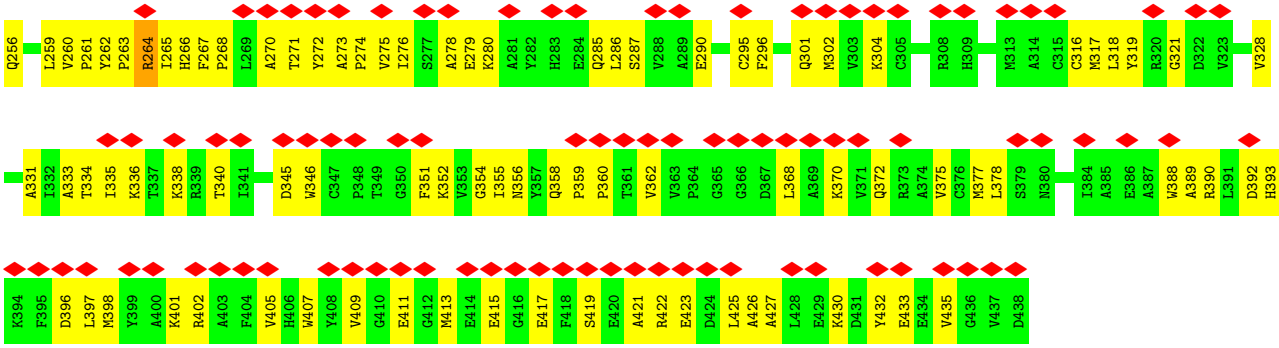
Chain QC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

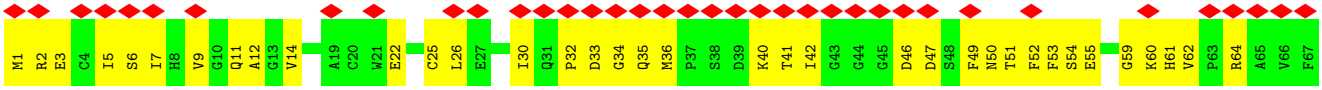
Chain QE:

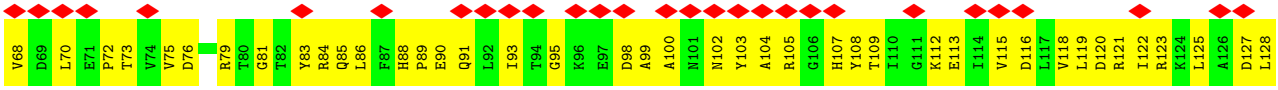


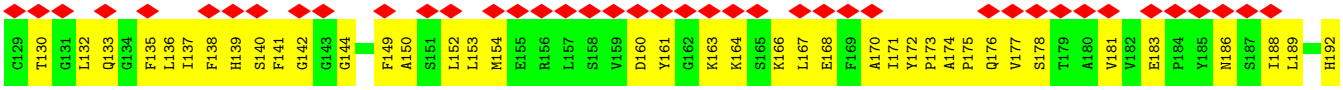


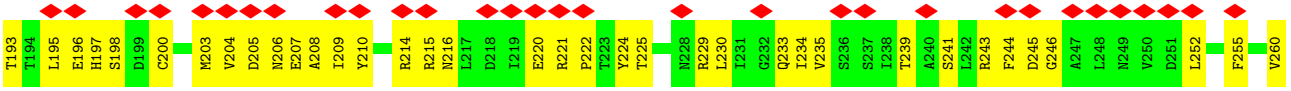
• Molecule 4: Detyrosinated tubulin alpha-3 chain

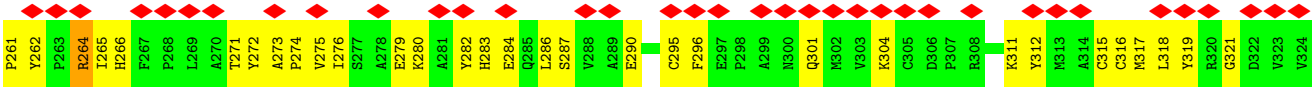
Chain QG:

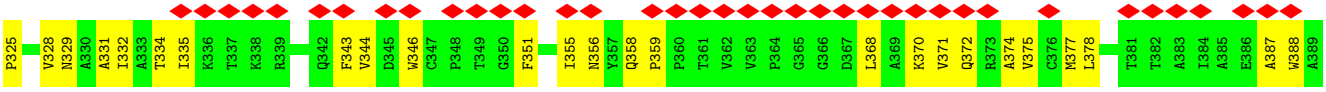


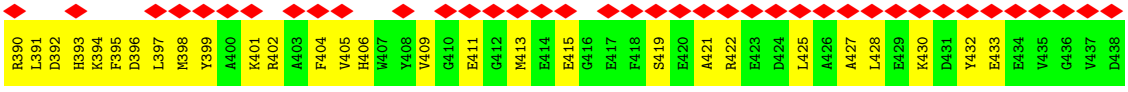






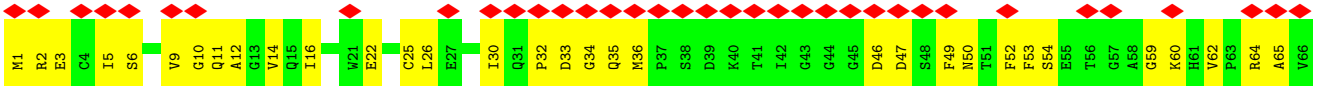


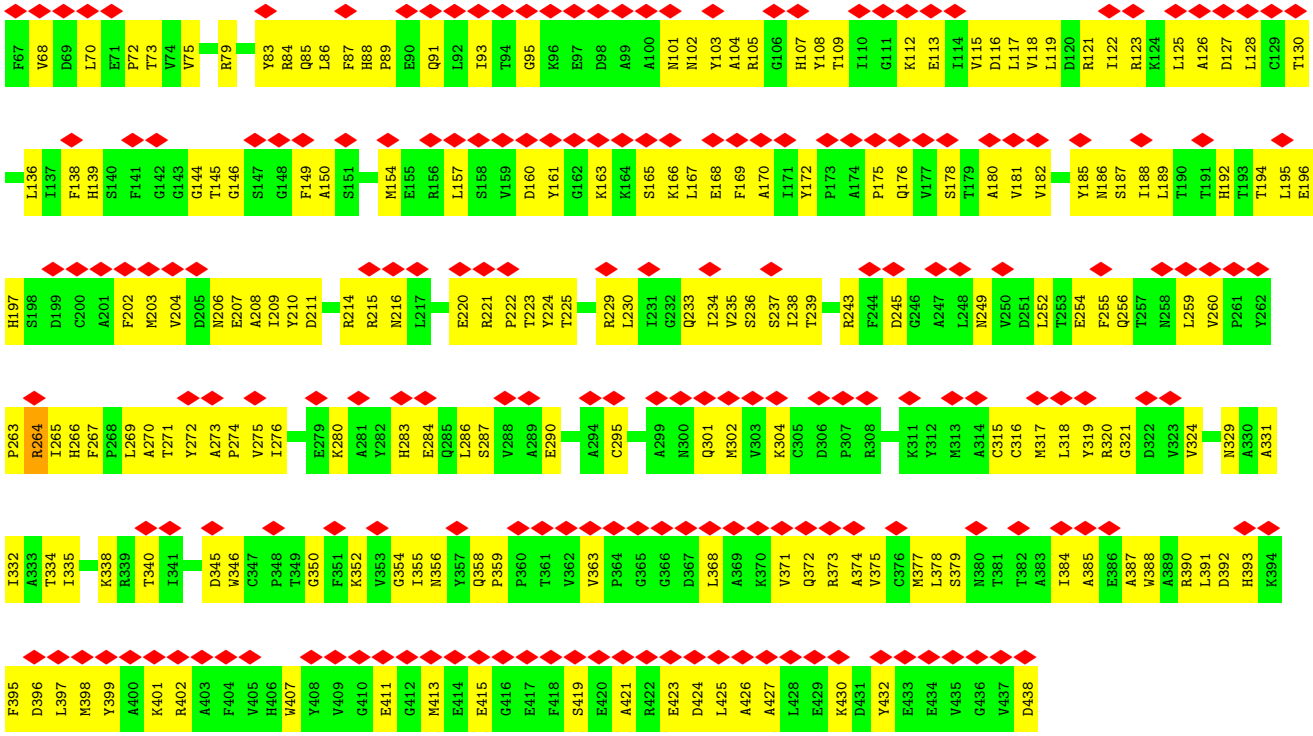




• Molecule 4: Detyrosinated tubulin alpha-3 chain

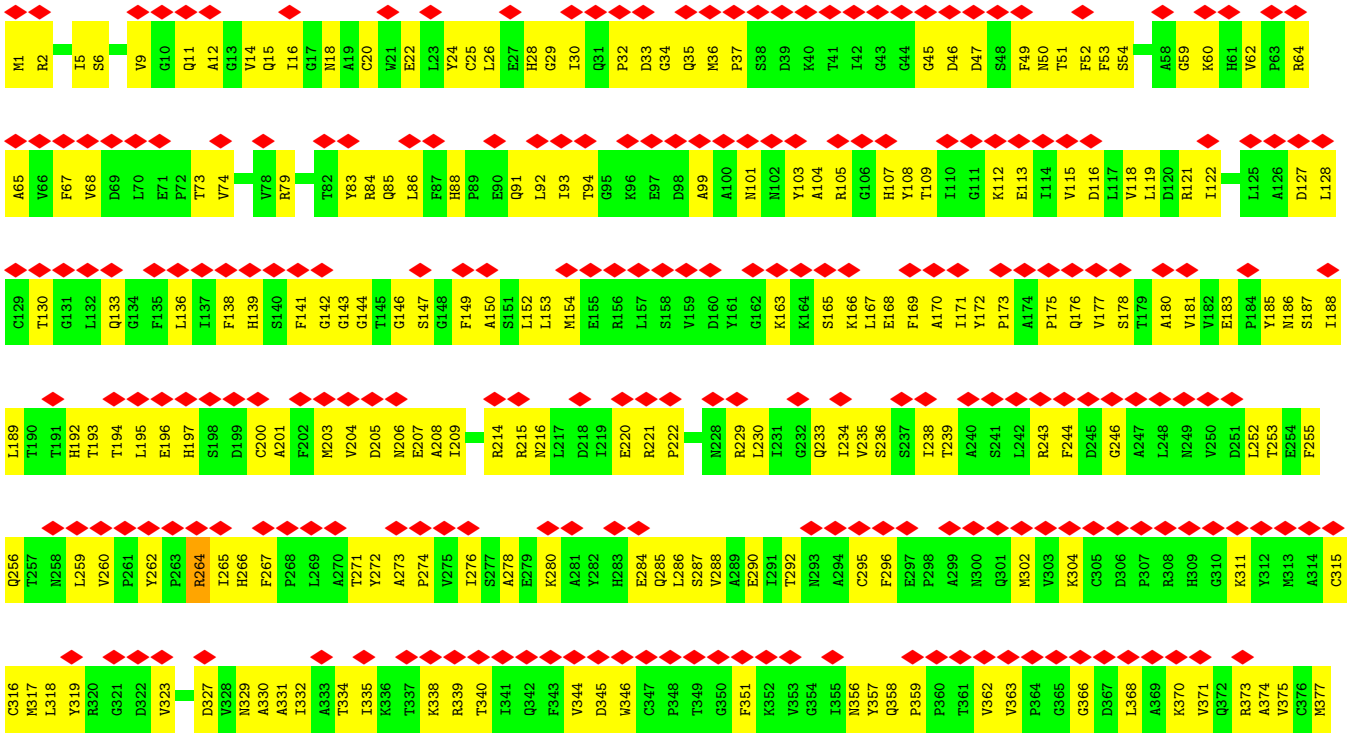
Chain QI:

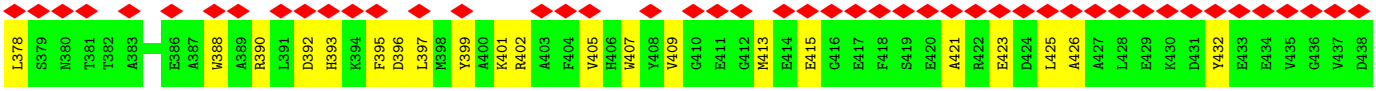




• Molecule 4: Detyrosinated tubulin alpha-3 chain

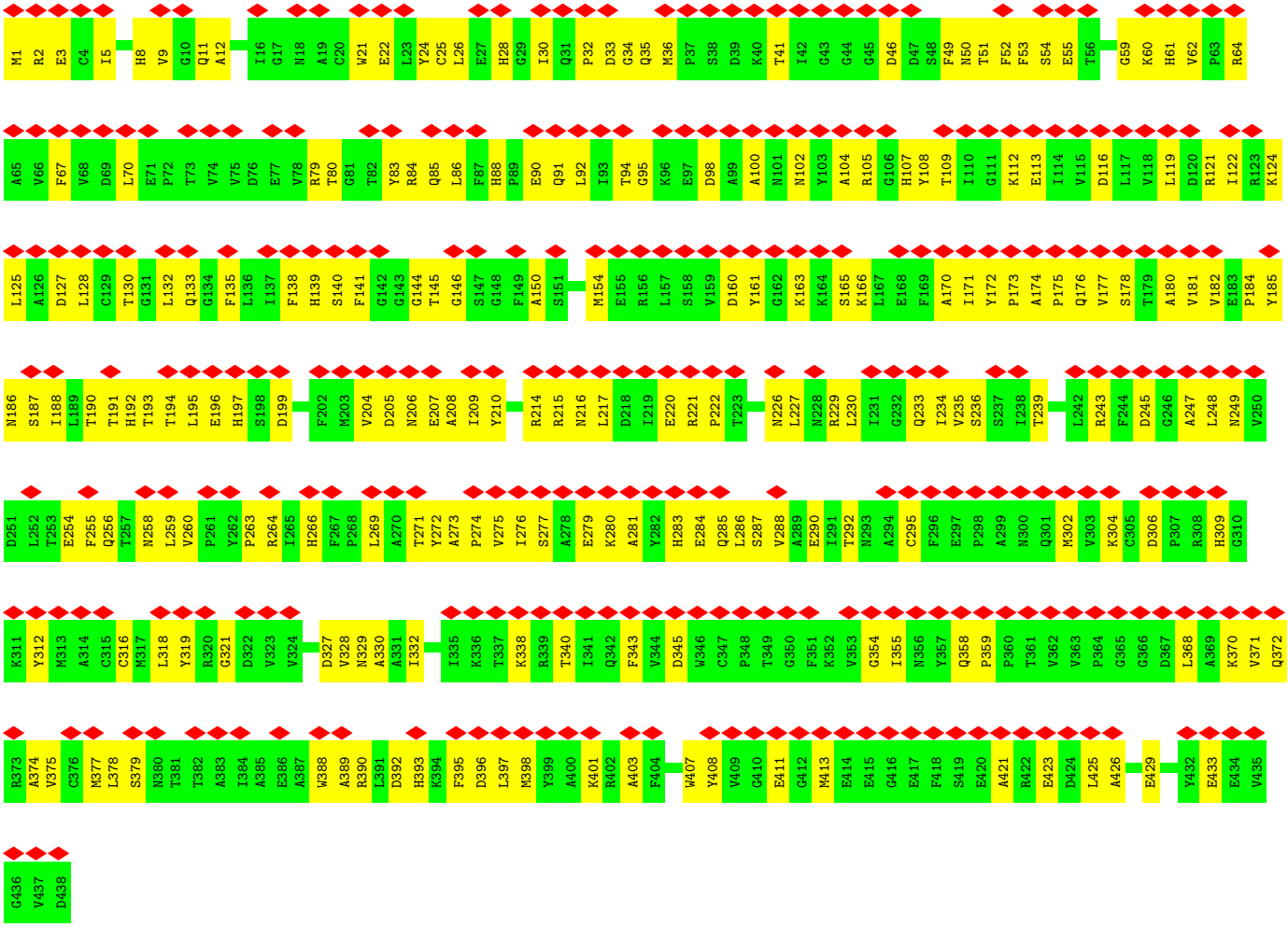
Chain QK:





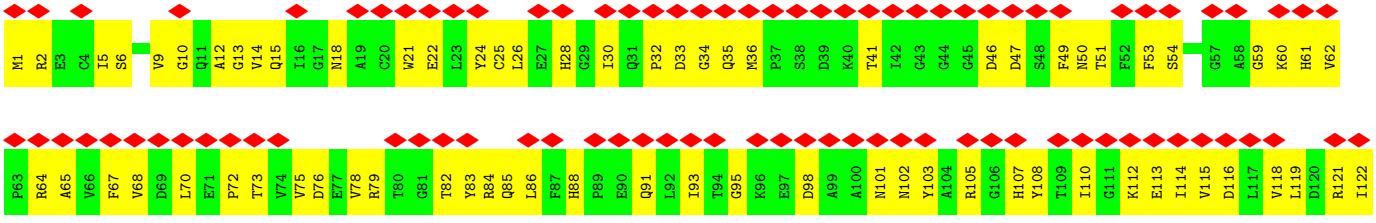
• Molecule 4: Detyrosinated tubulin alpha-3 chain

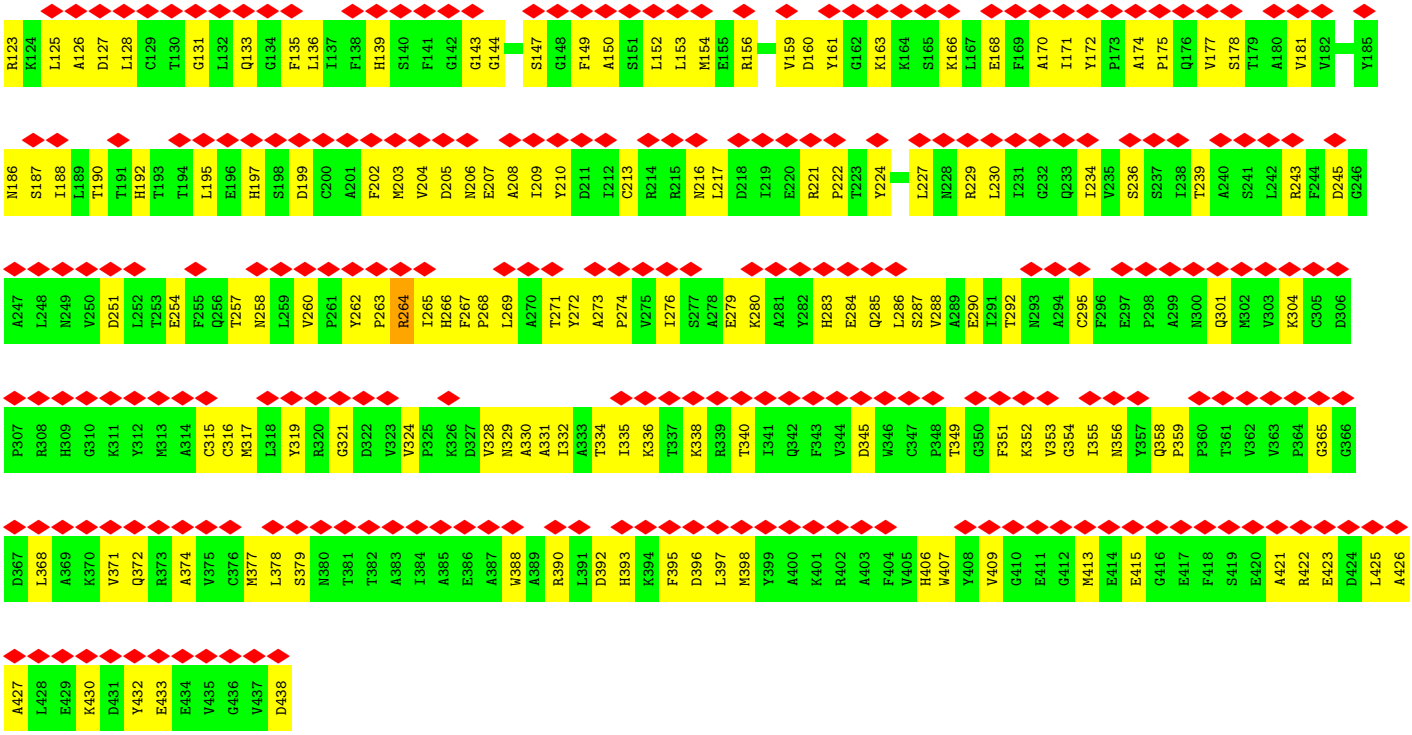
Chain QM:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

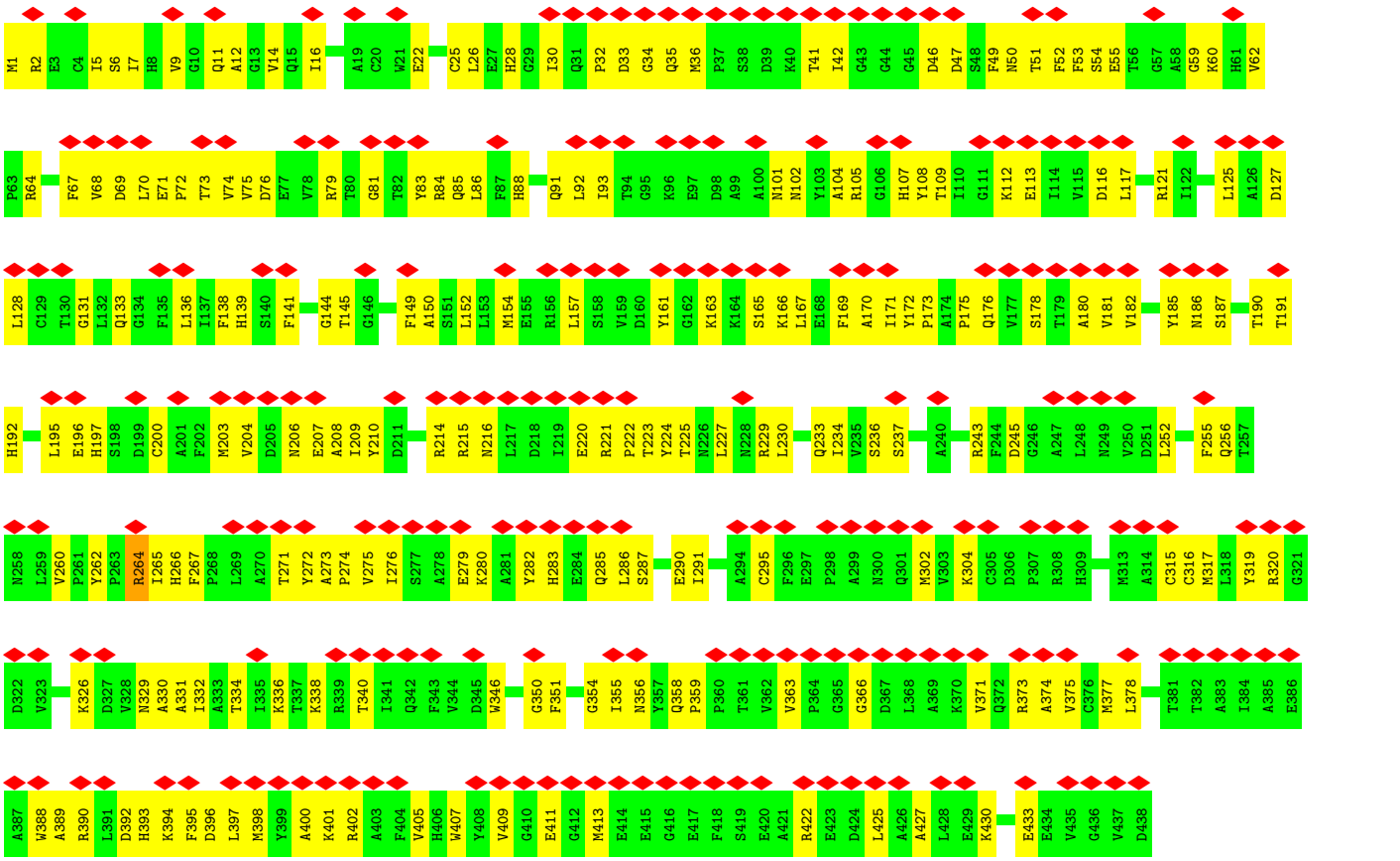
Chain RC:





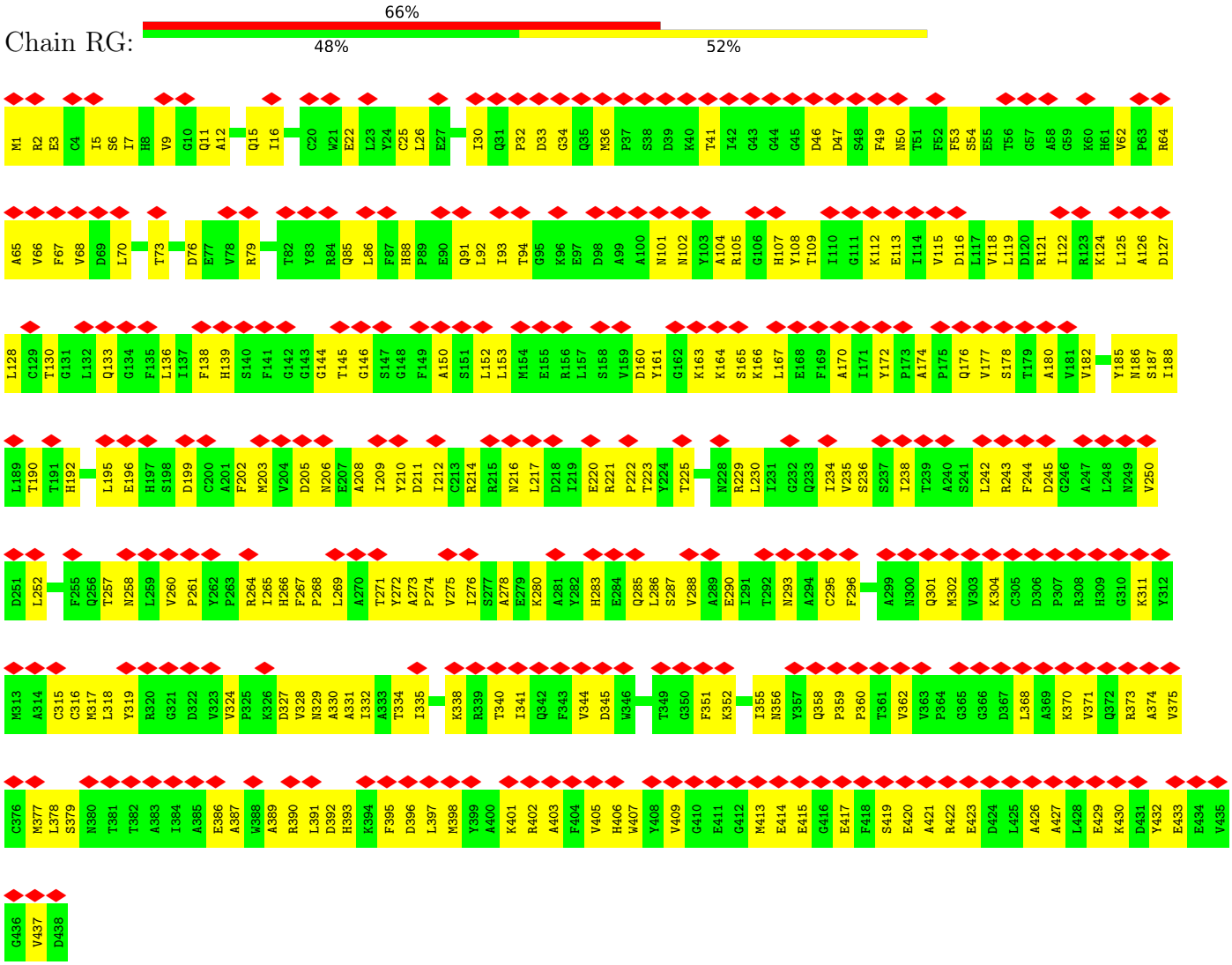
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain RE:



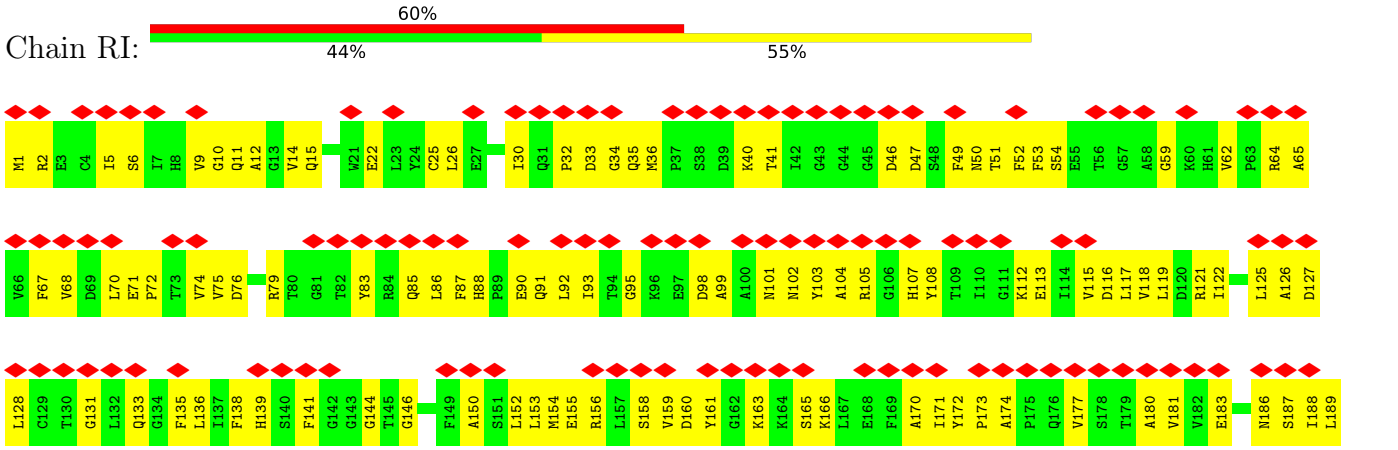
• Molecule 4: Detyrosinated tubulin alpha-3 chain

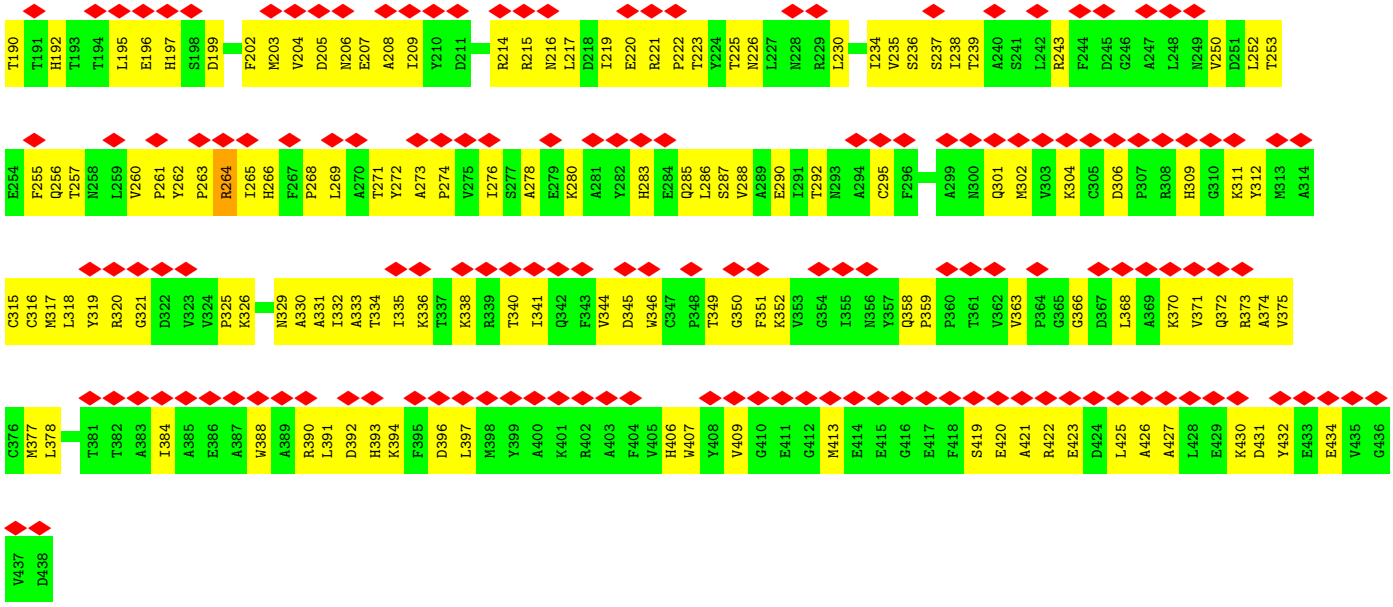
Chain RG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

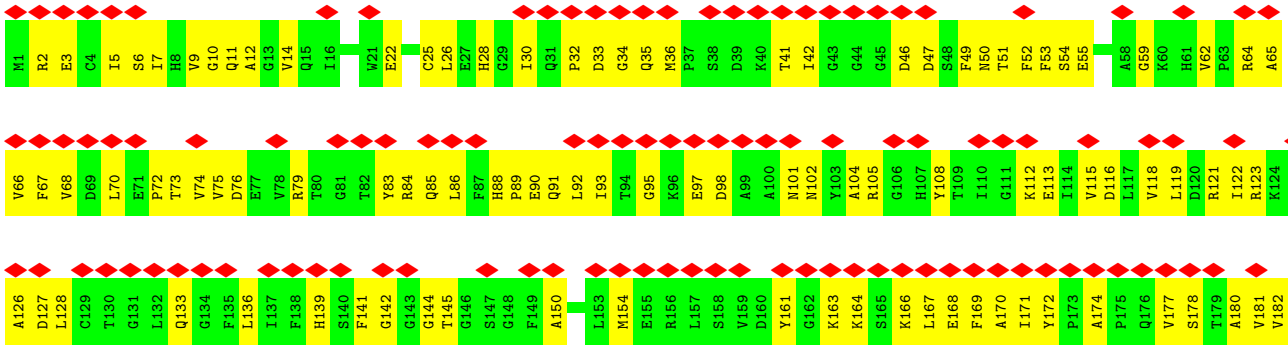
Chain RI:





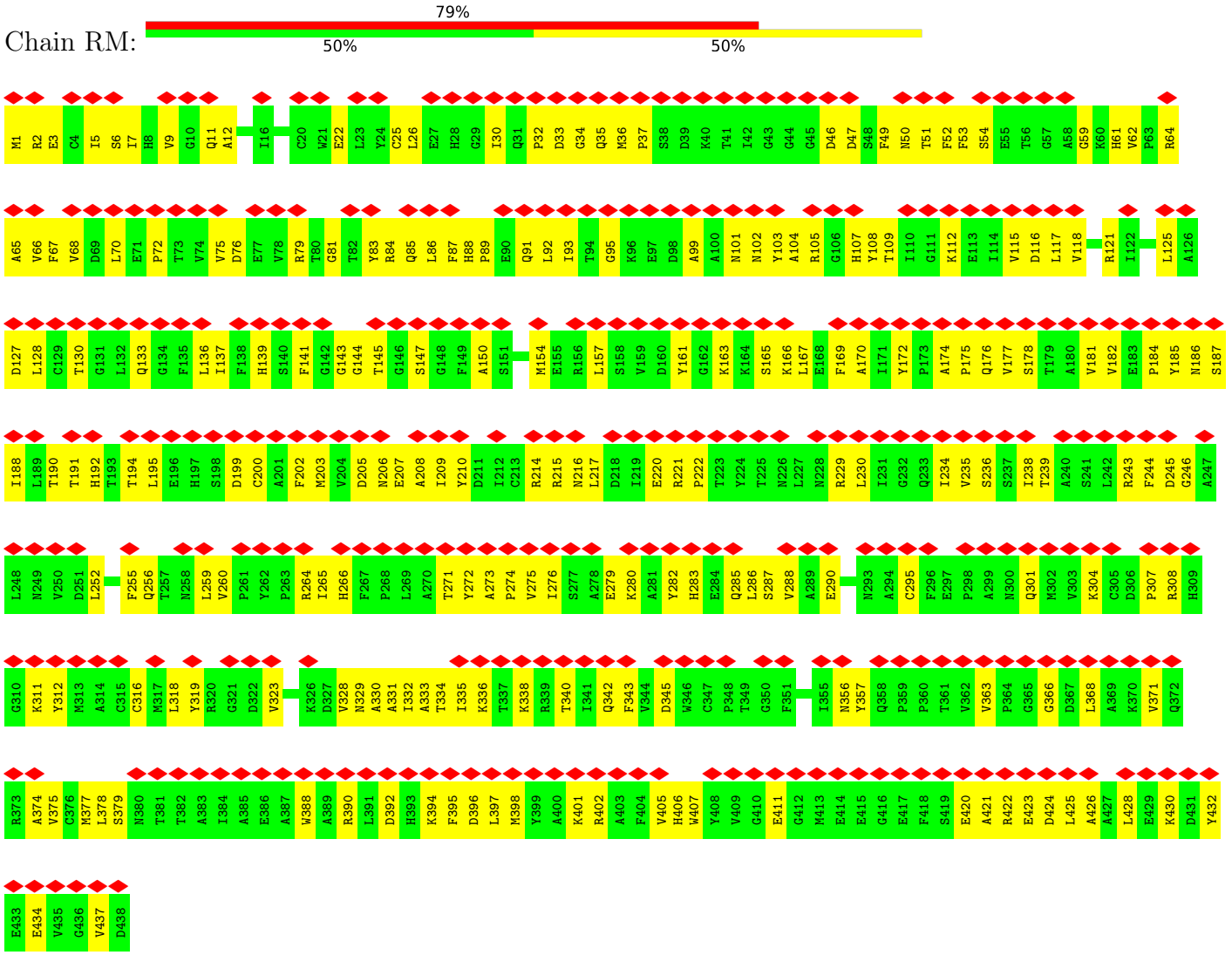
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain RK:



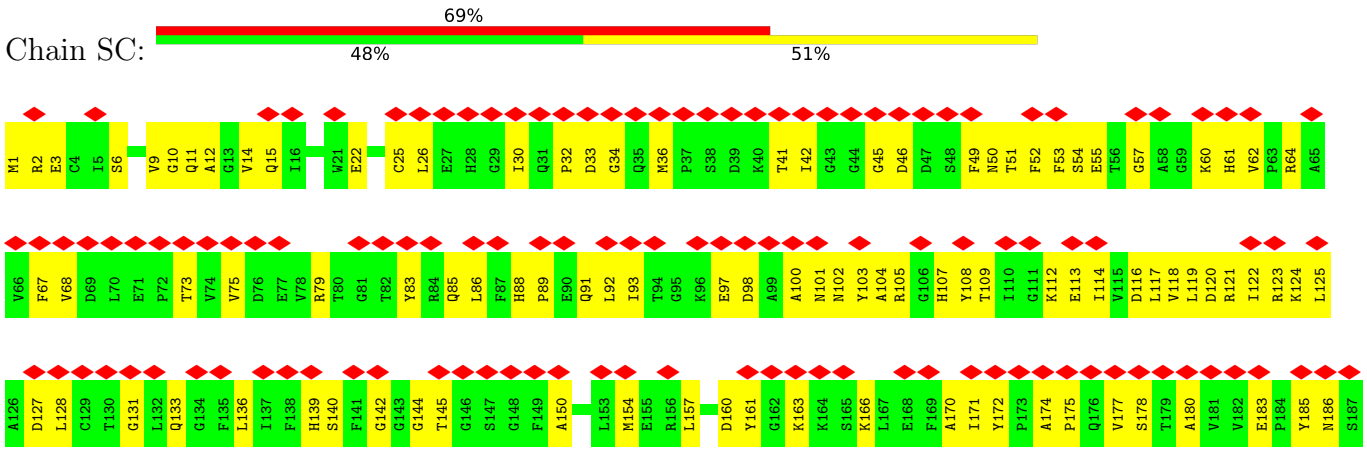
• Molecule 4: Detyrosinated tubulin alpha-3 chain

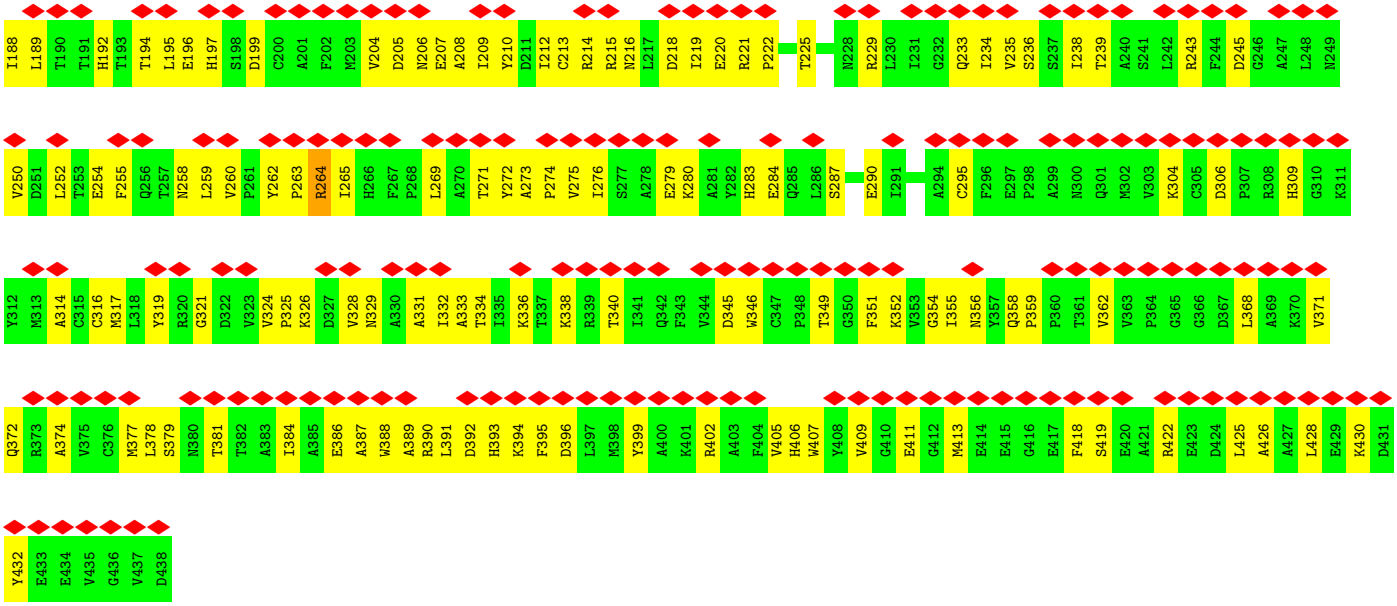
Chain RM:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

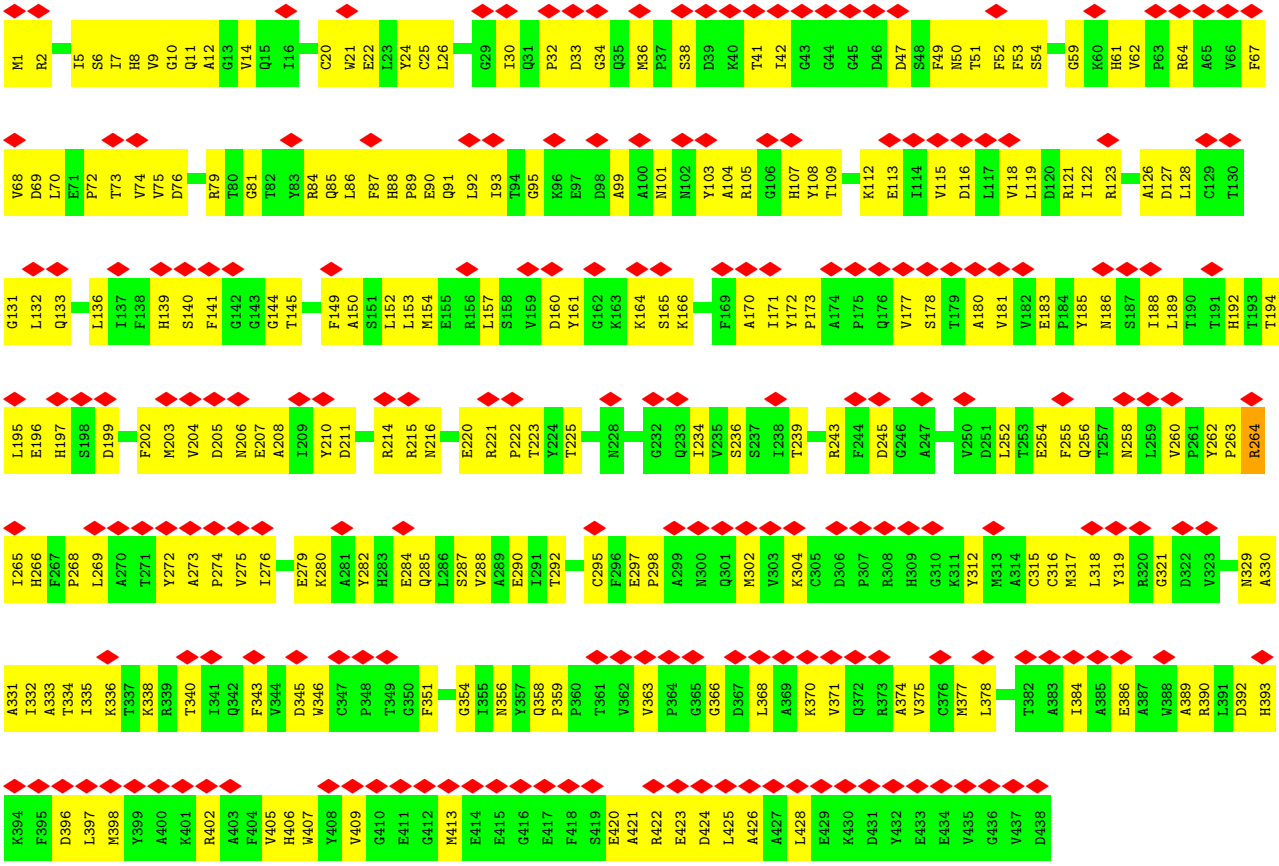
Chain SC:





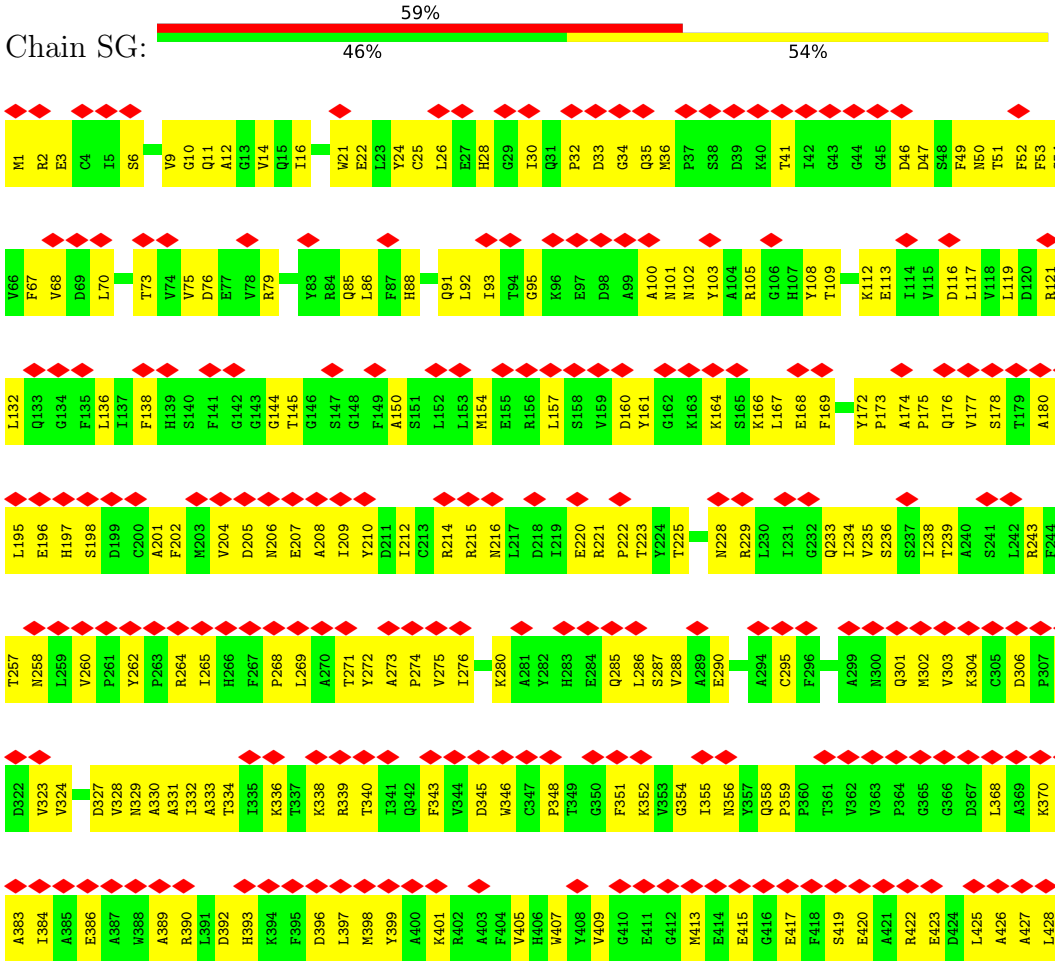
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain SE:



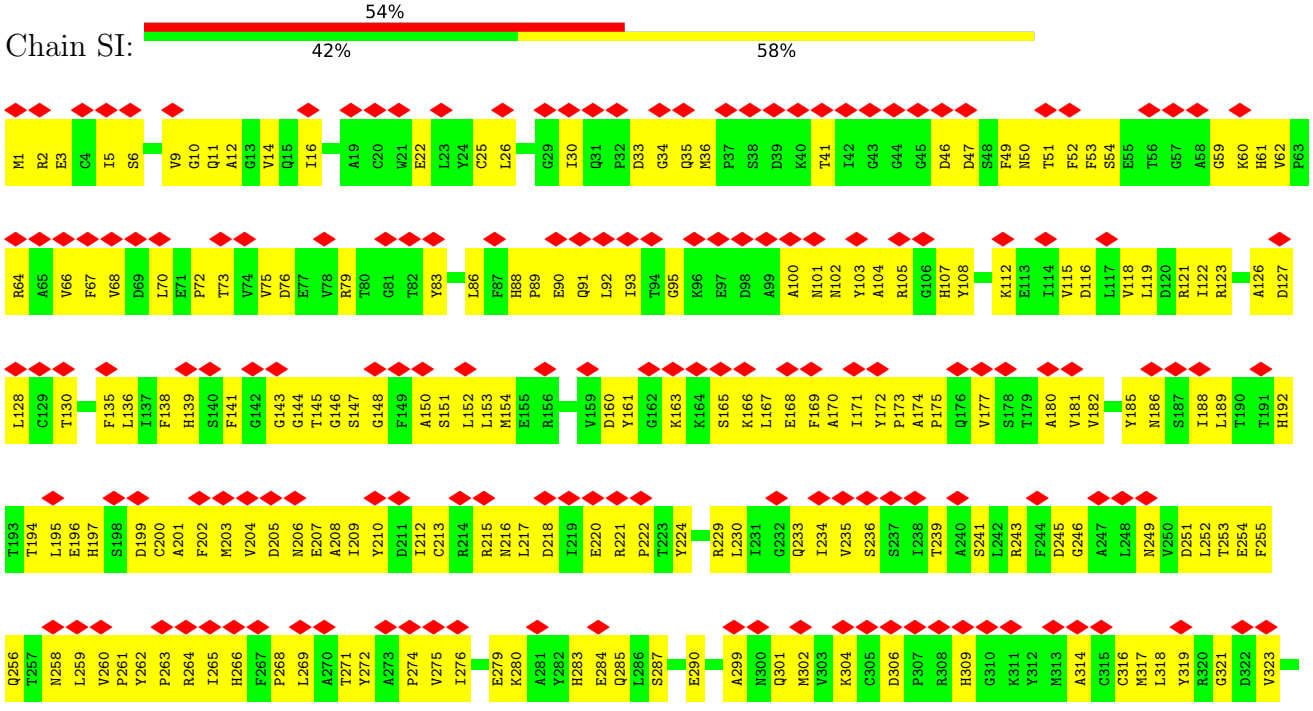
• Molecule 4: Detyrosinated tubulin alpha-3 chain

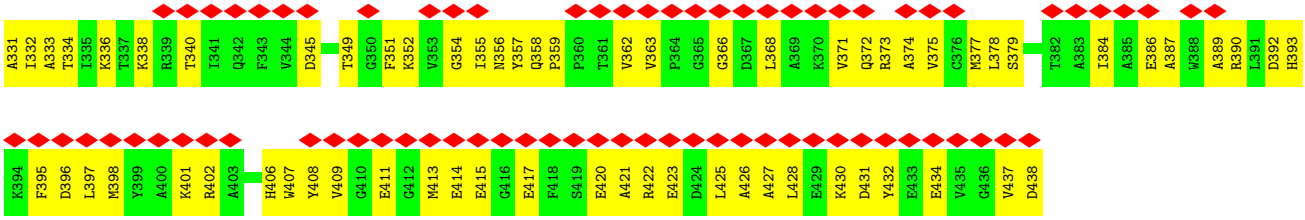
Chain SG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

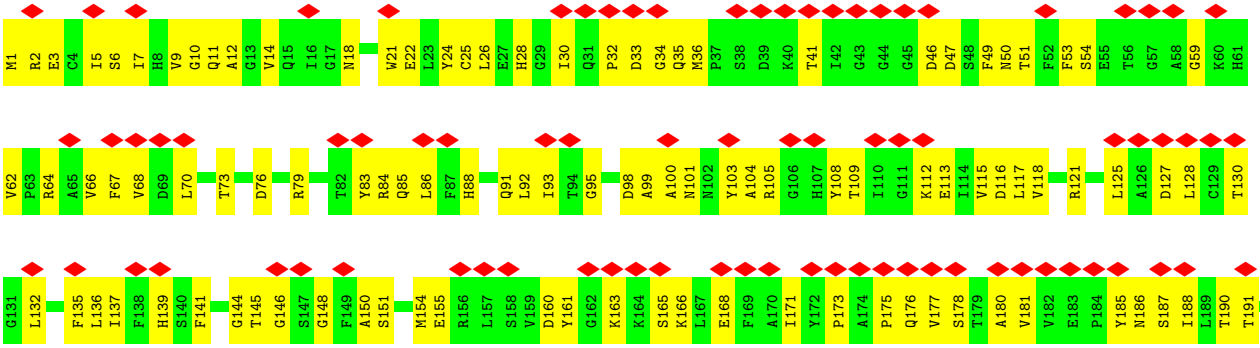
Chain SI:





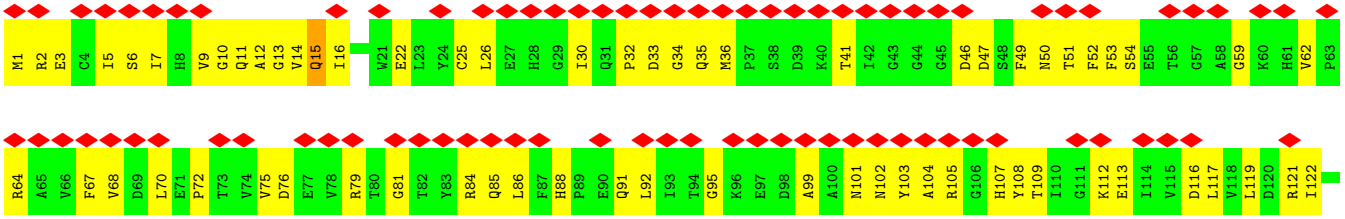
• Molecule 4: Detyrosinated tubulin alpha-3 chain

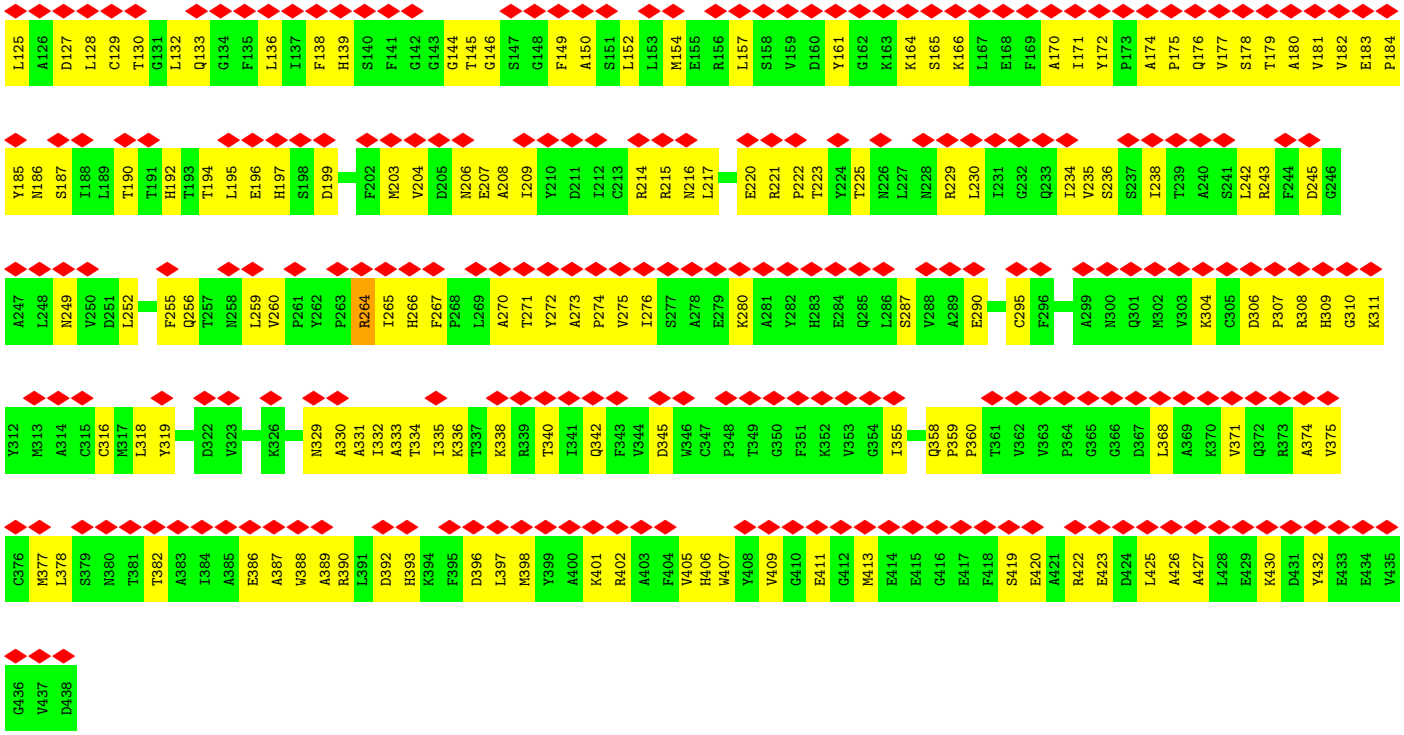
Chain SK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain SM:





• Molecule 4: Detyrosinated tubulin alpha-3 chain

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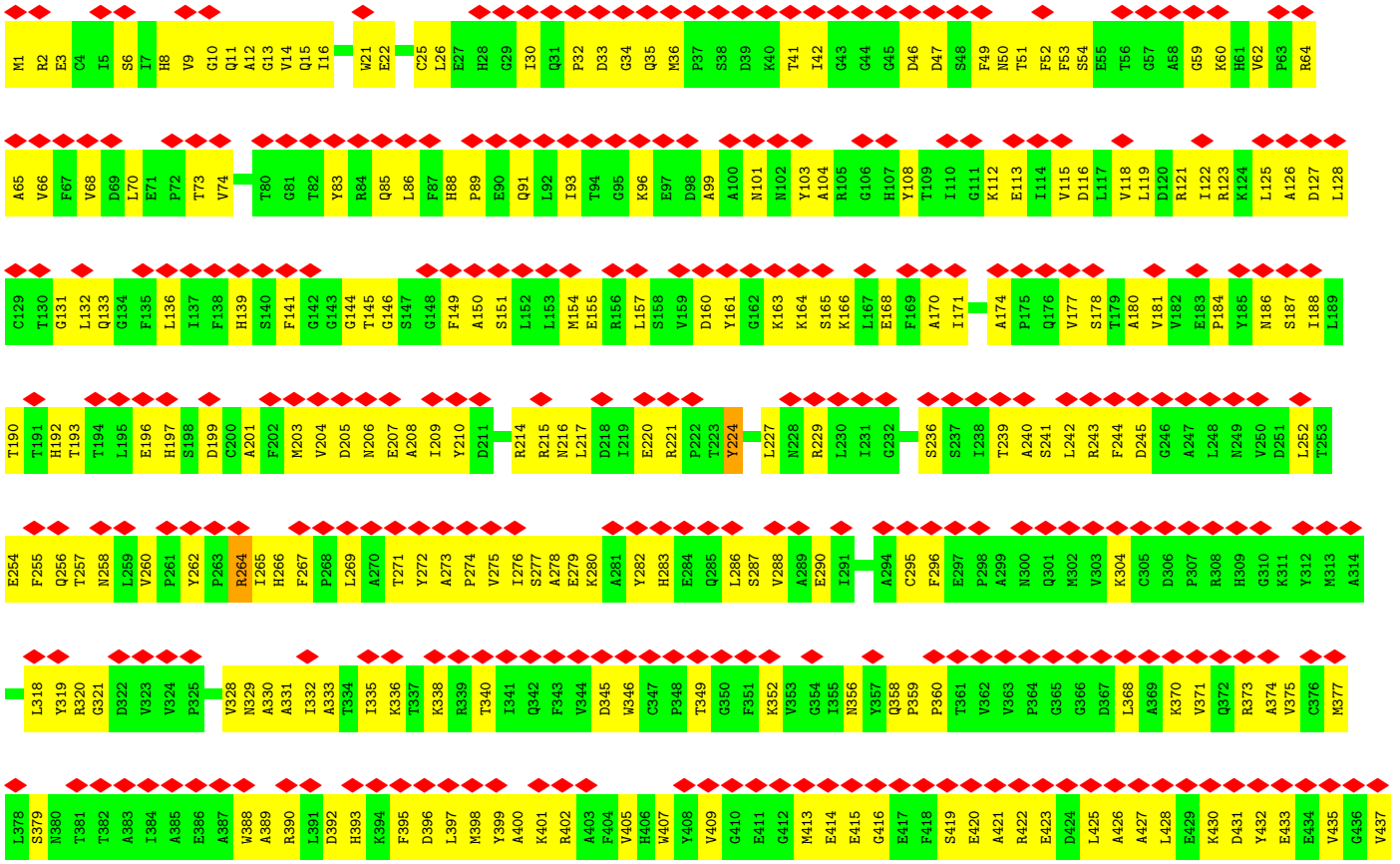
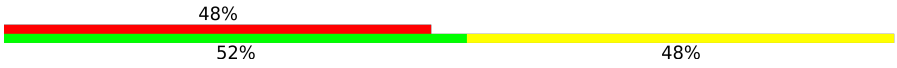
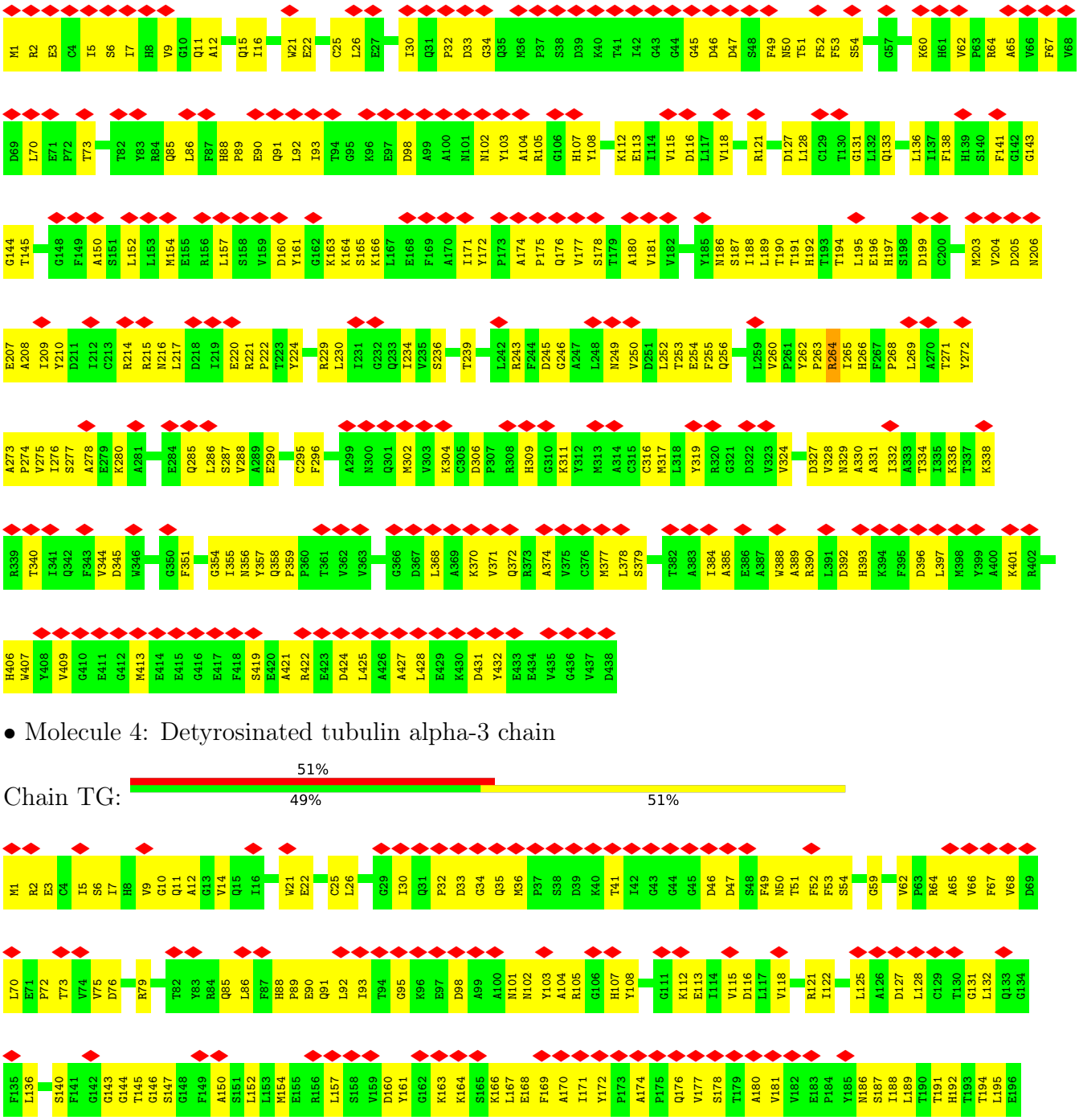


• Molecule 4: Detyrosinated tubulin alpha-3 chain

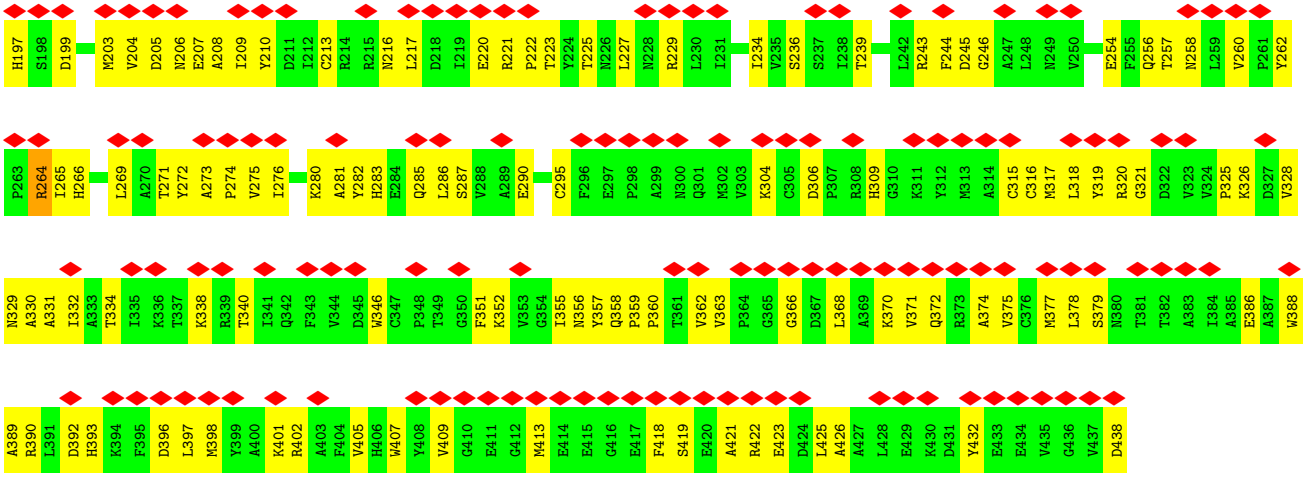
Chain TE:





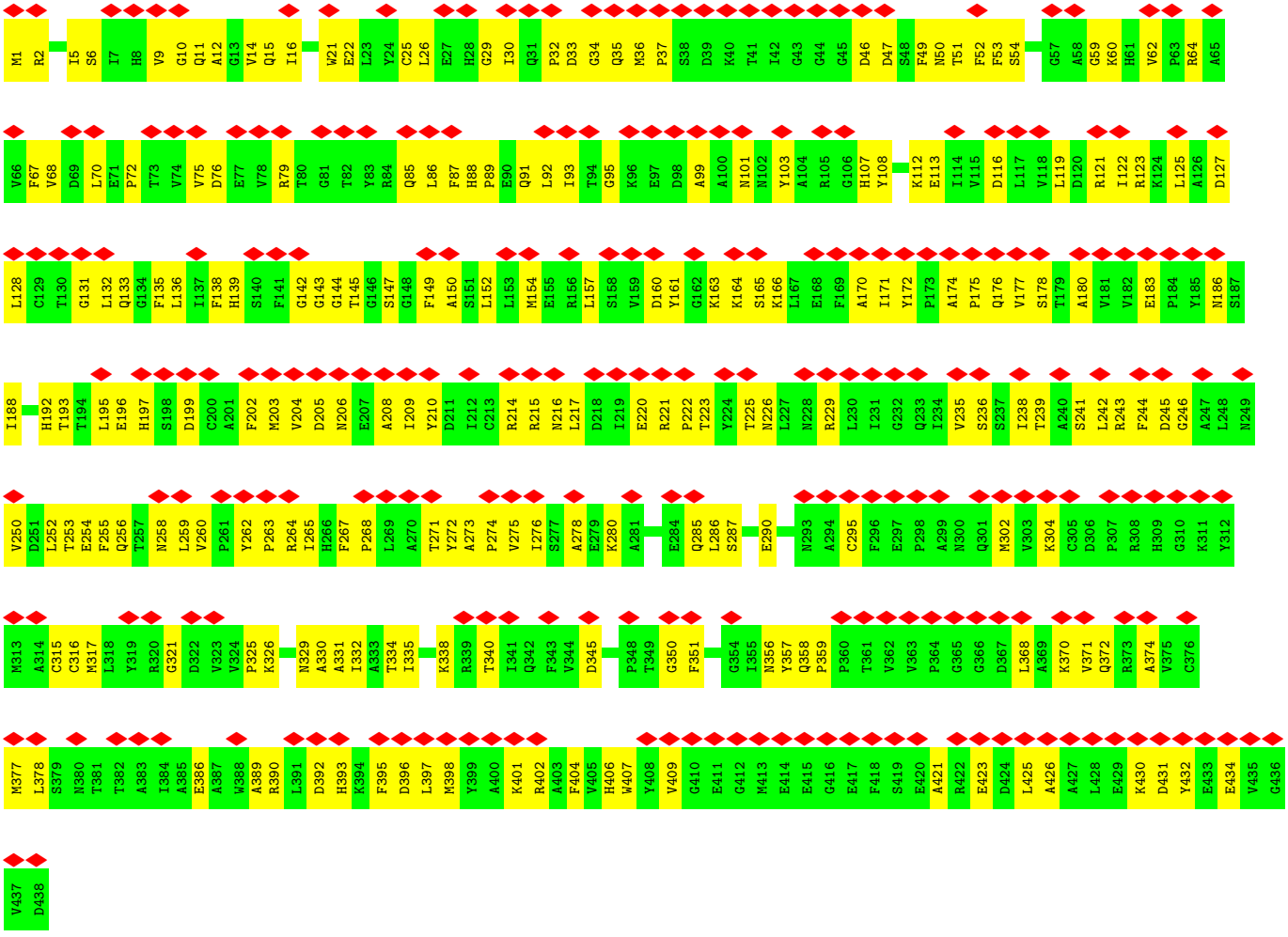
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain TG:



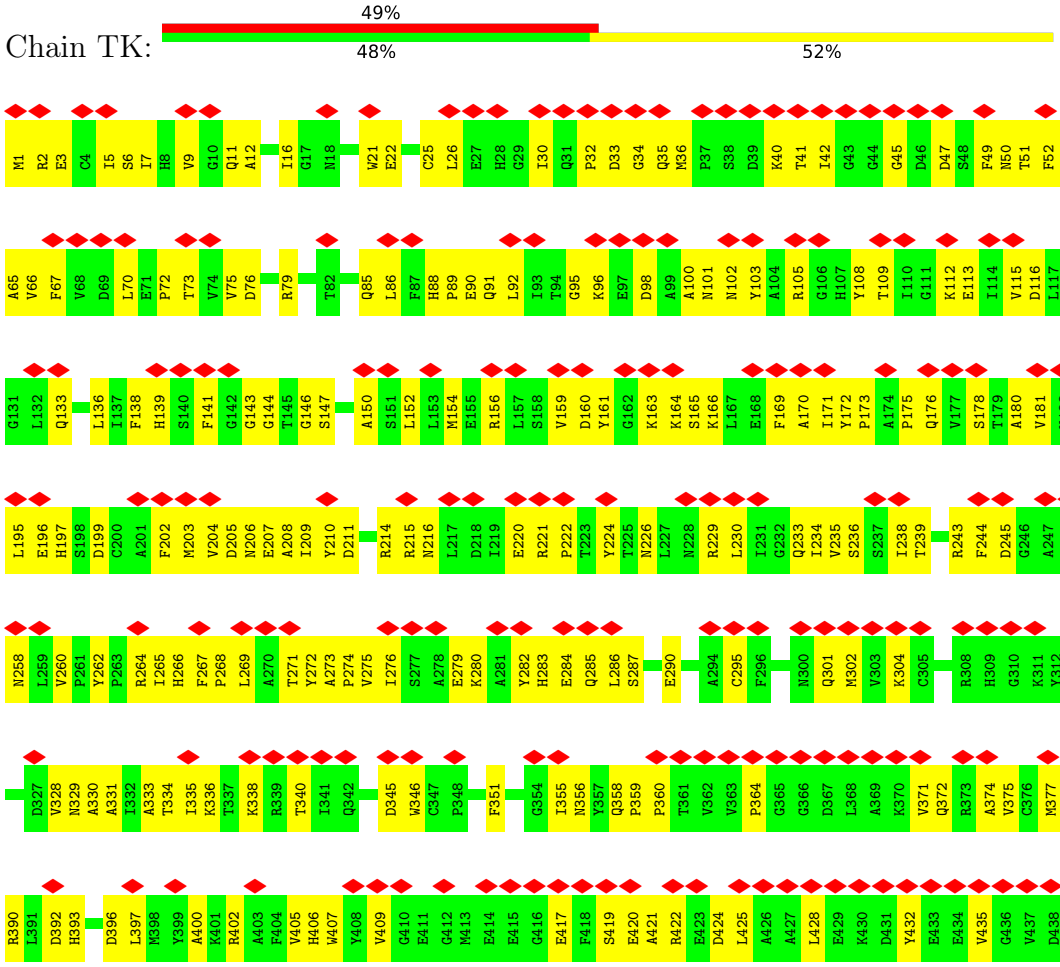
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain TI:



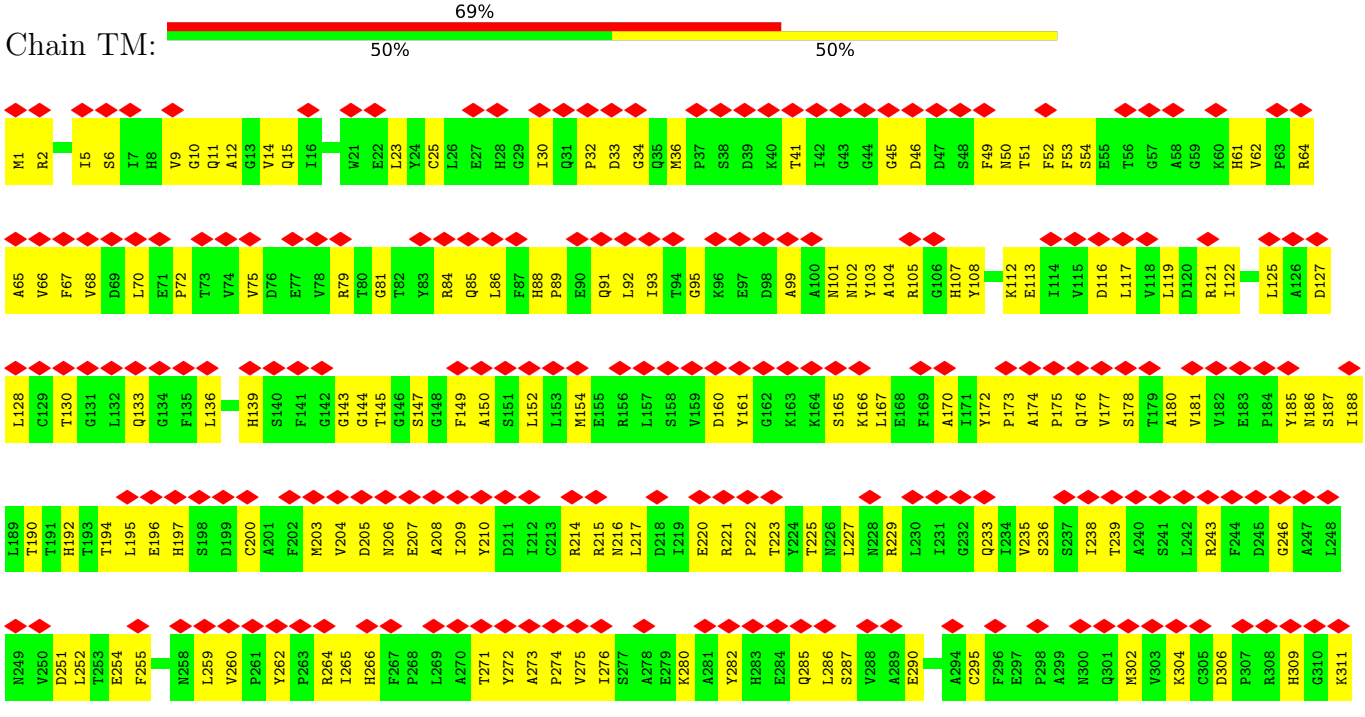
• Molecule 4: Detyrosinated tubulin alpha-3 chain

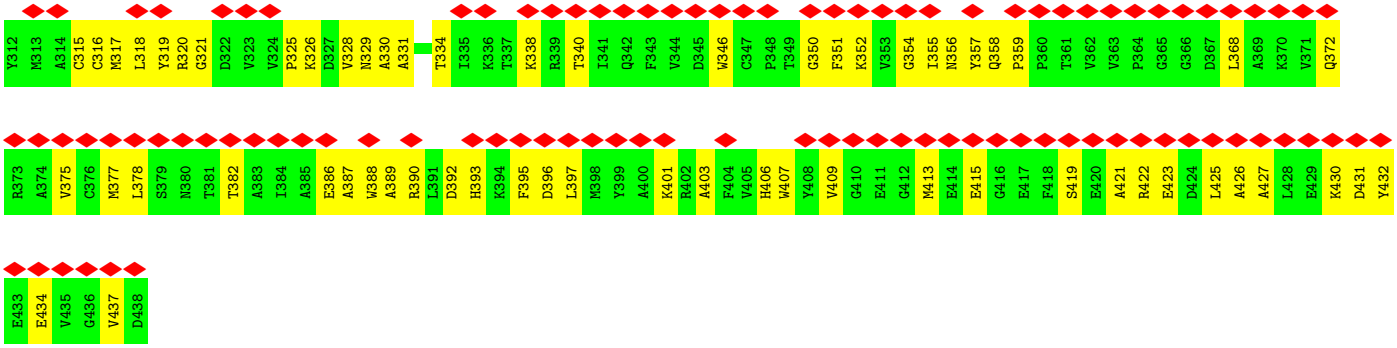
Chain TK:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

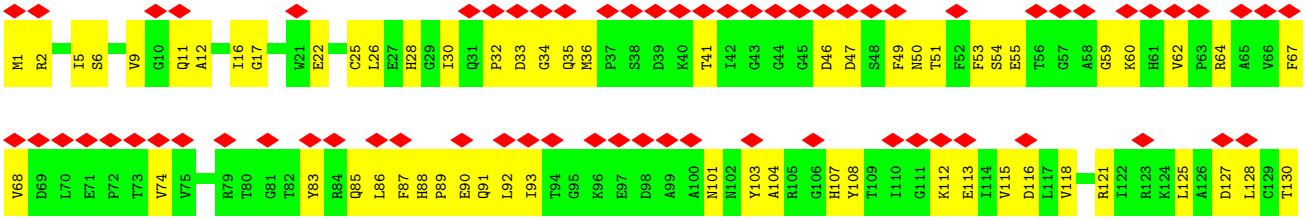
Chain TM:





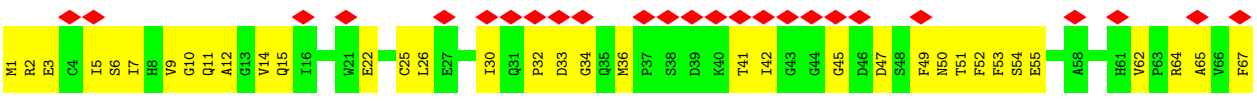
• Molecule 4: Detyrosinated tubulin alpha-3 chain

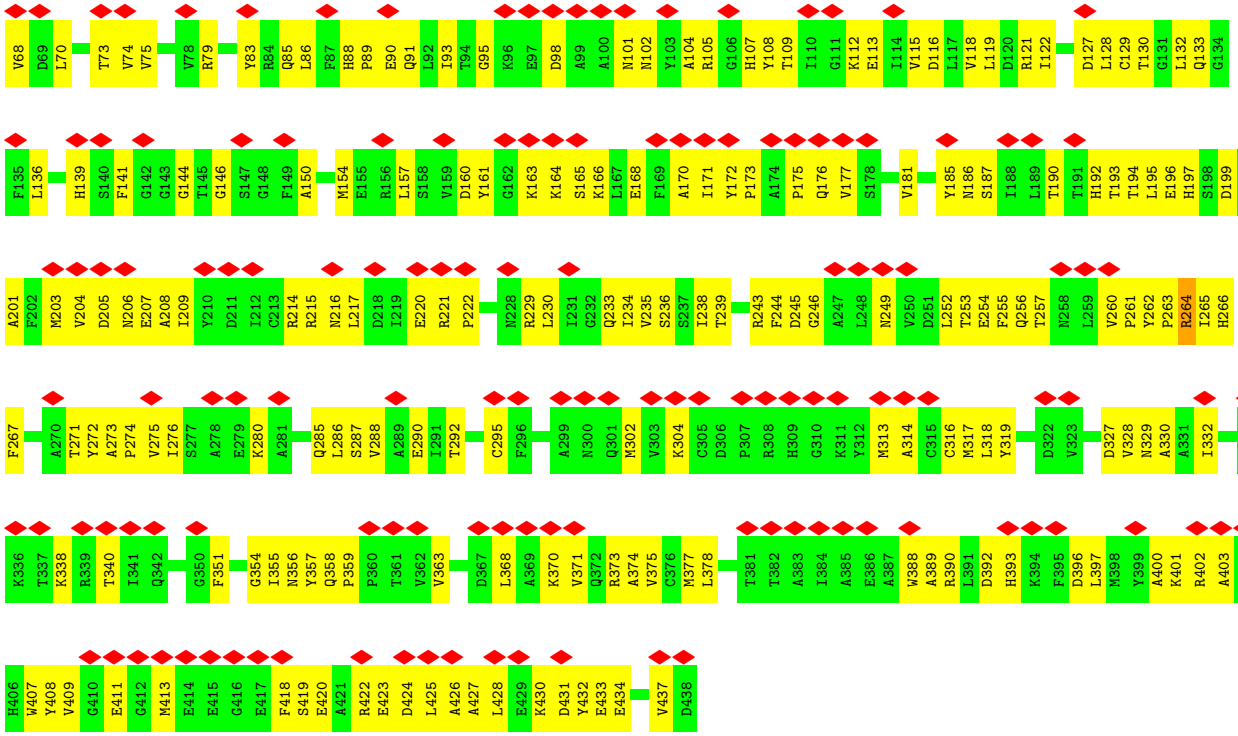
Chain UA:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

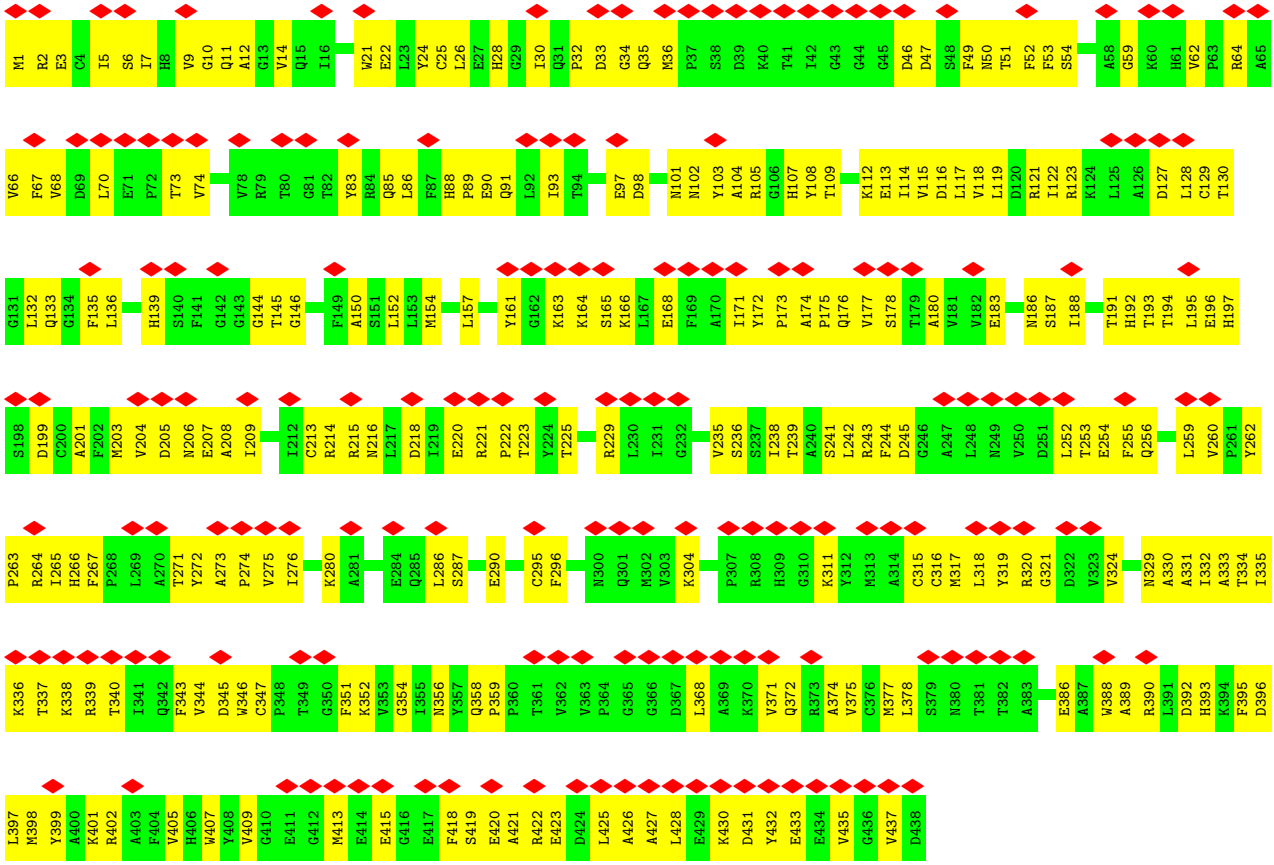
Chain UC:





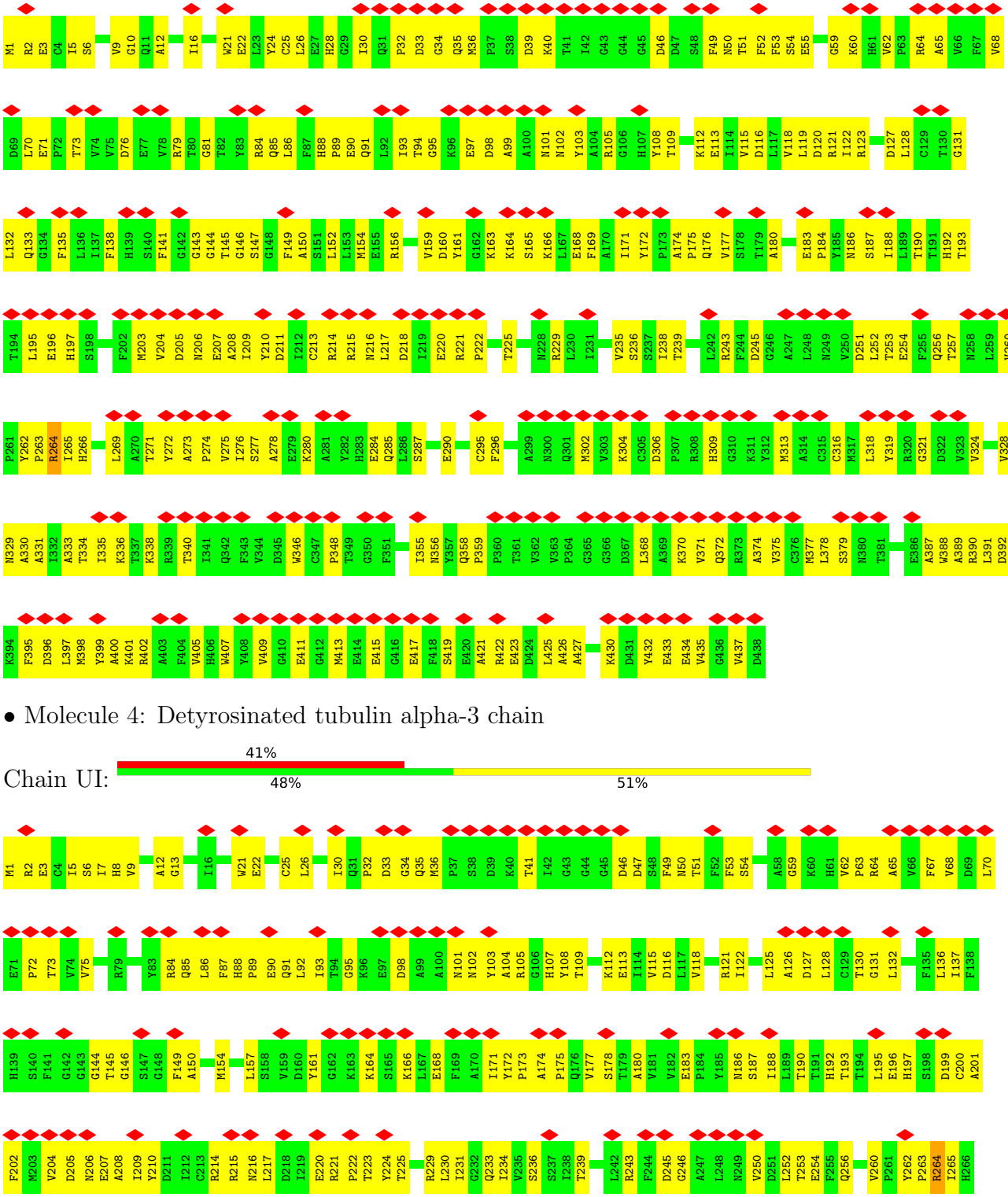
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain UE:



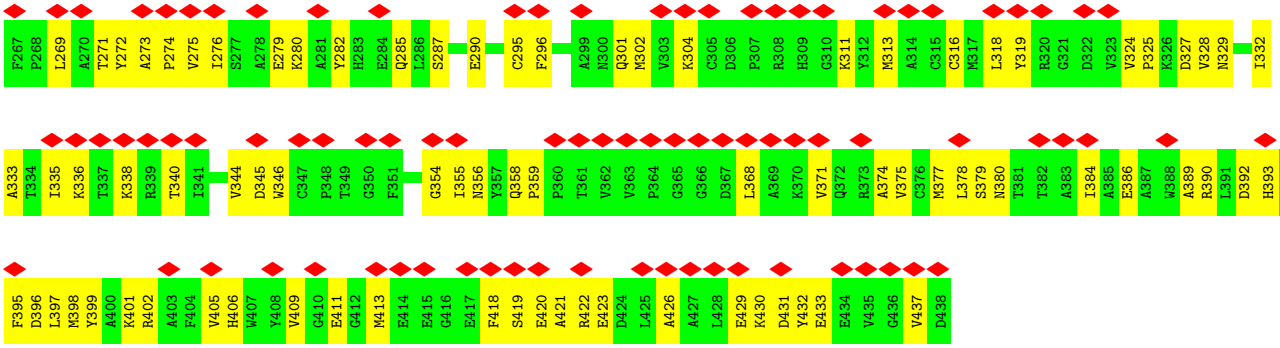
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain UG:



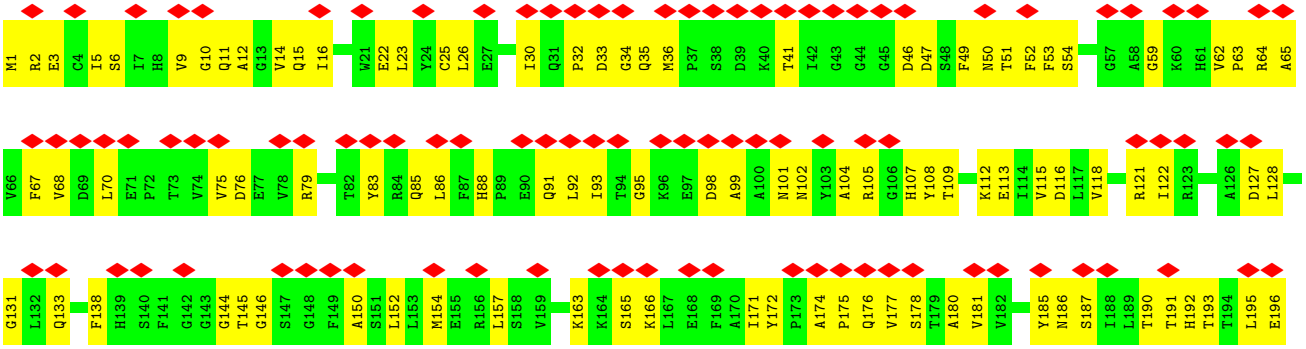
• Molecule 4: Detyrosinated tubulin alpha-3 chain

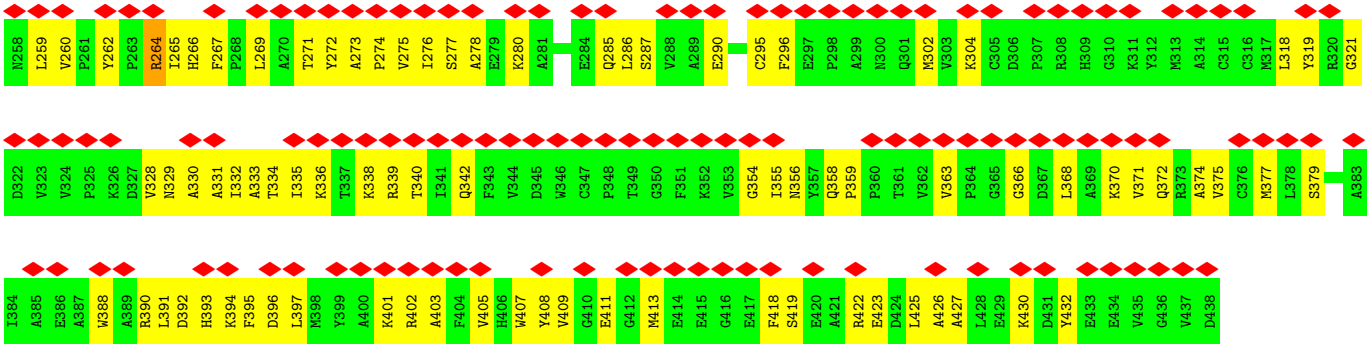
Chain UI:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

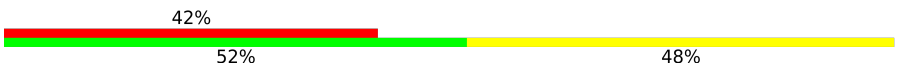
Chain UK:

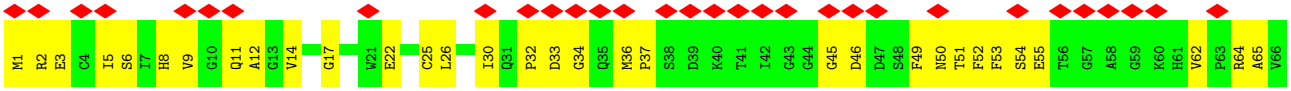


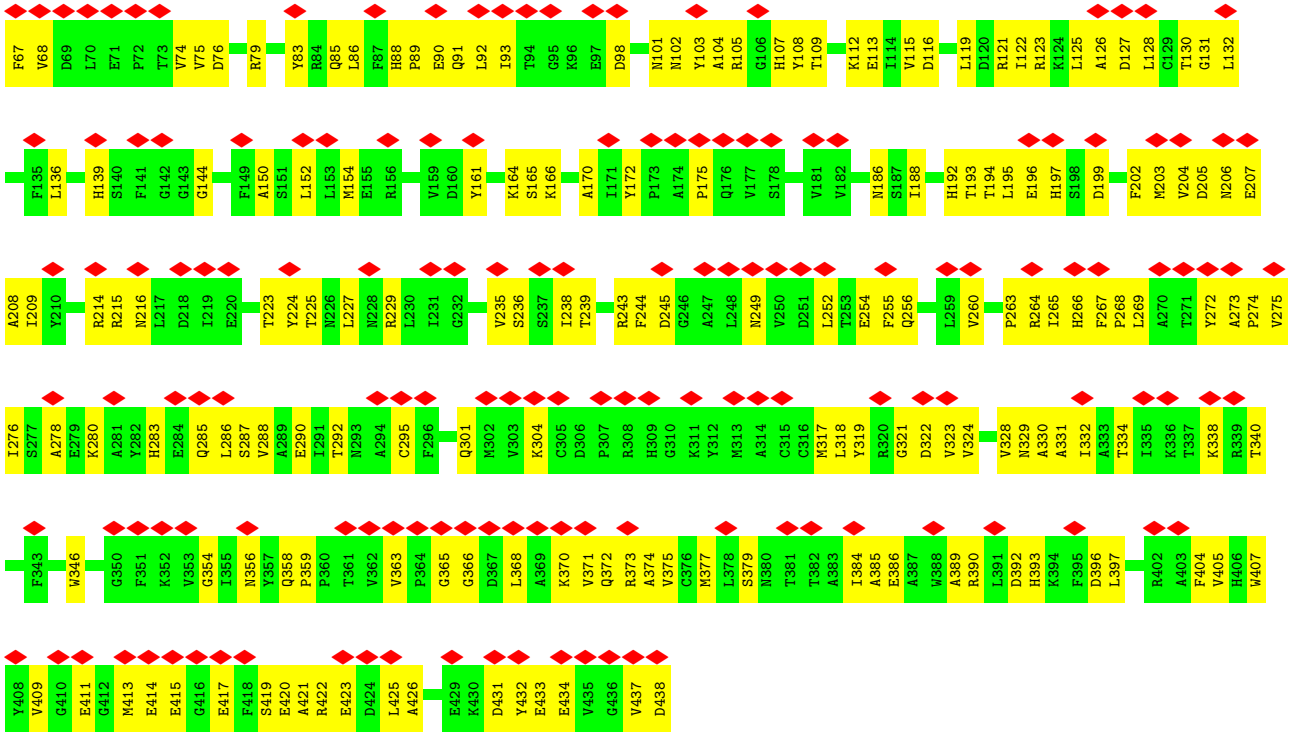


• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain VA:

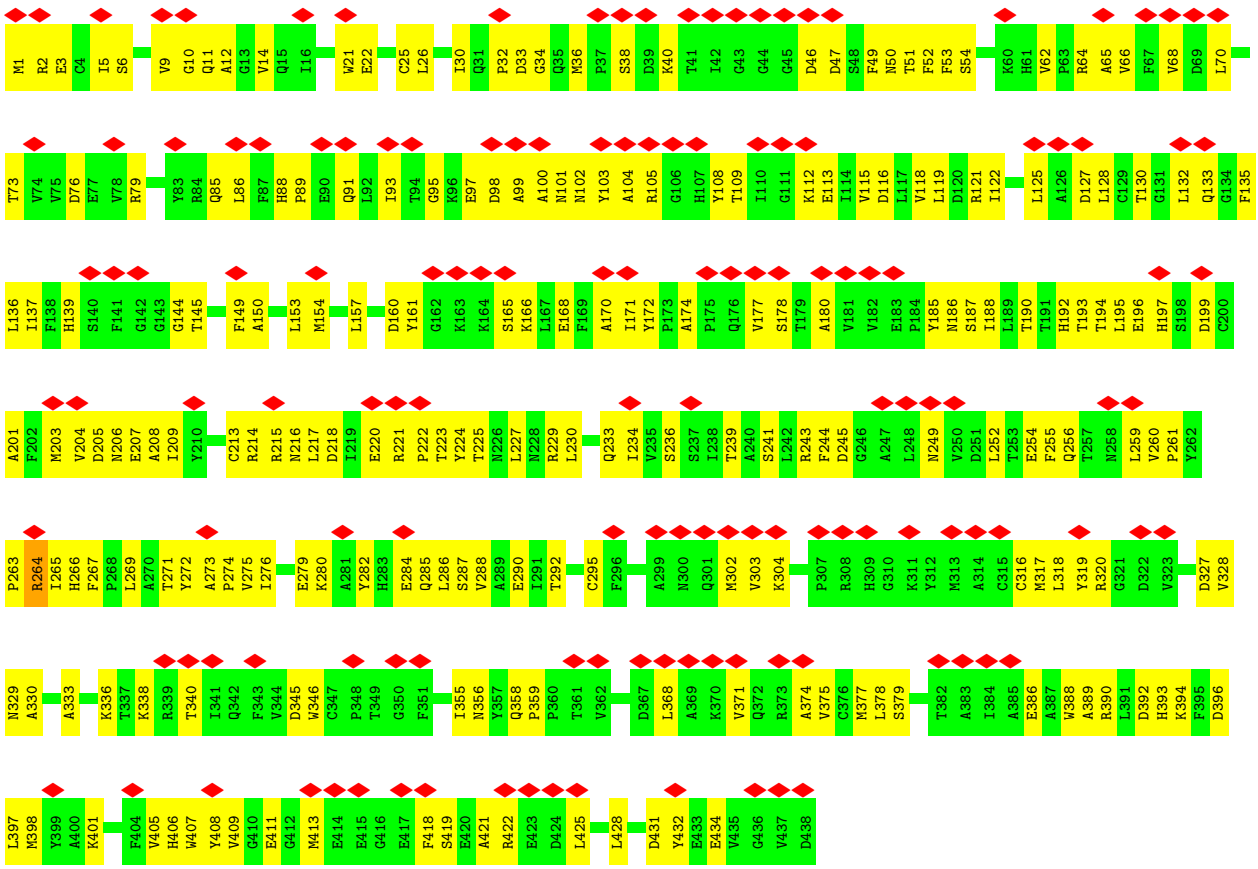






• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain VC:

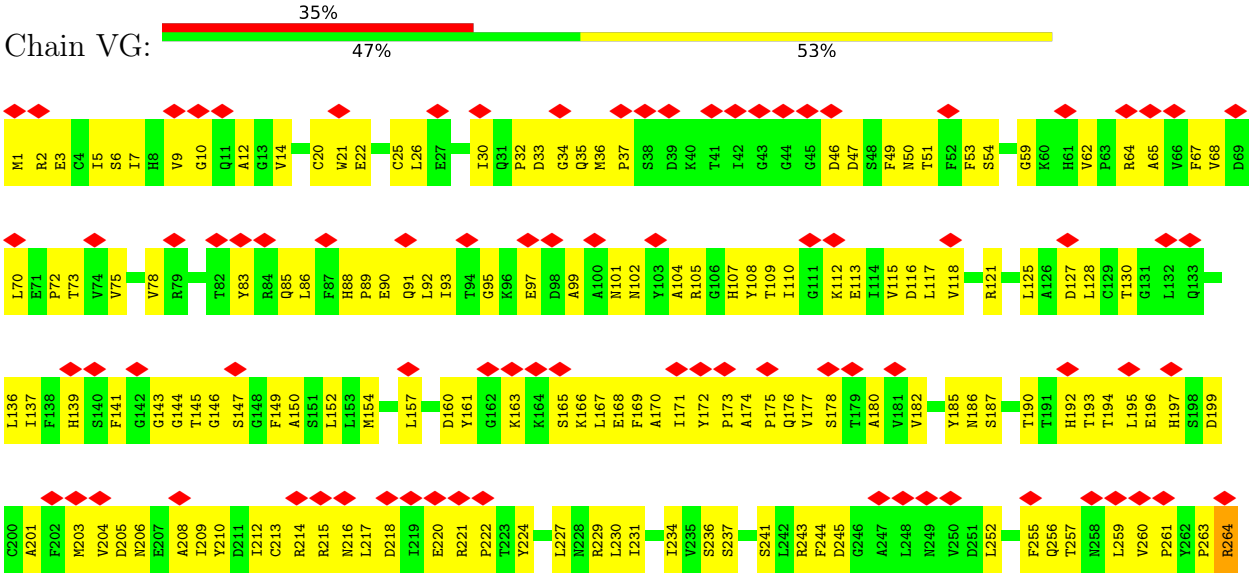


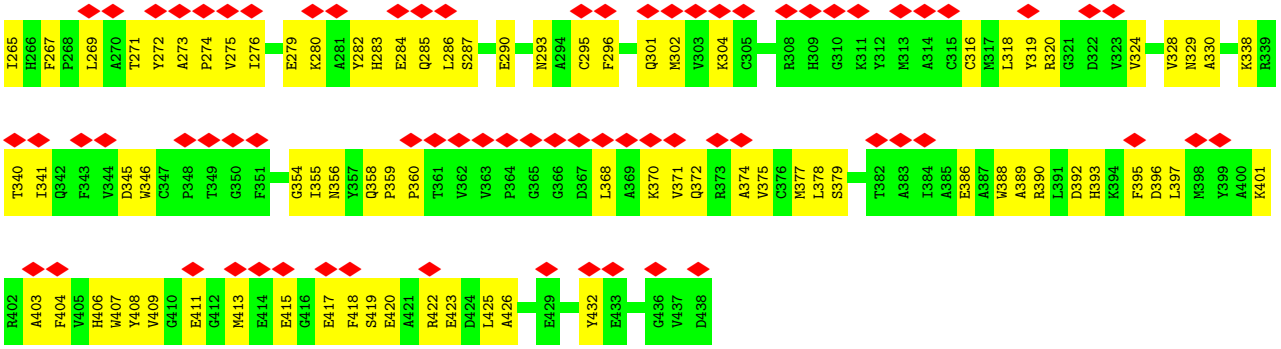
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain VE:

• Molecule 4: Detyrosinated tubulin alpha-3 chain

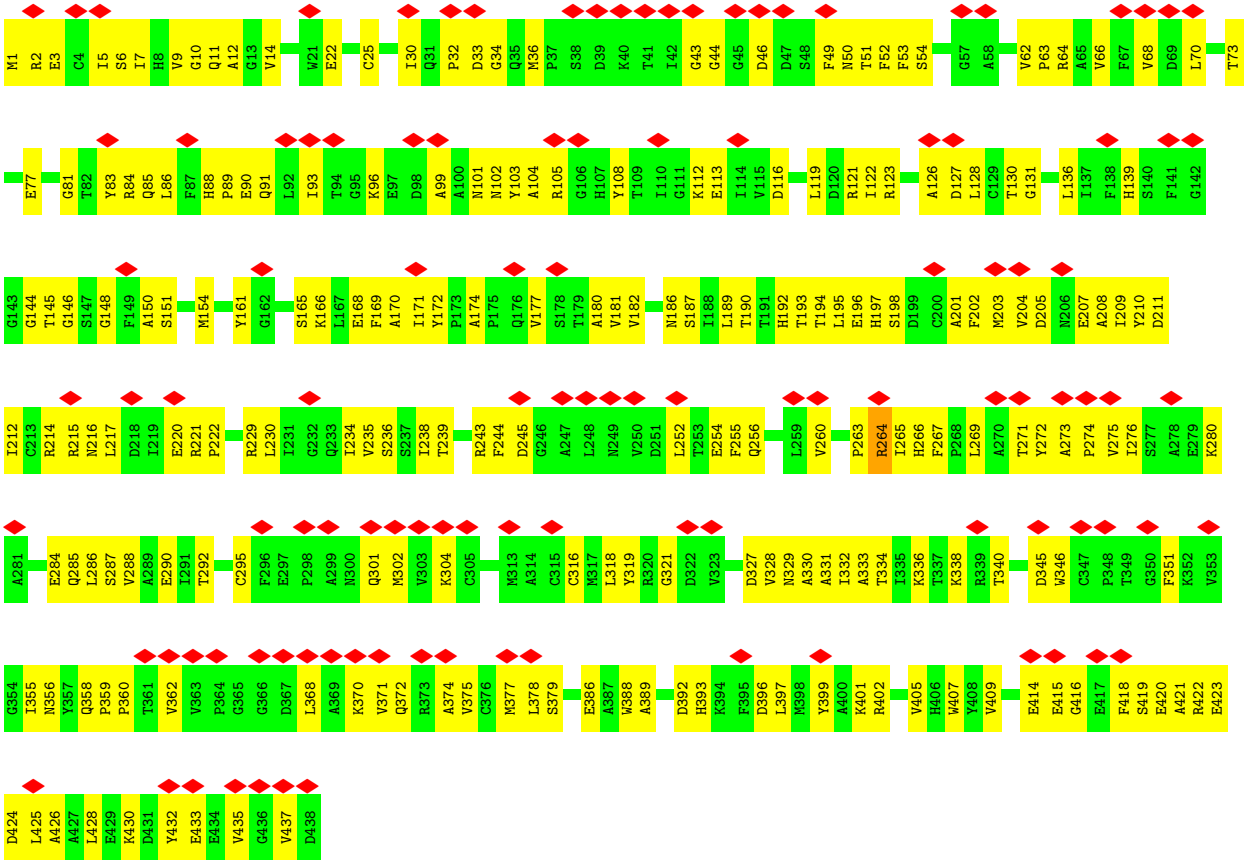
Chain VG:





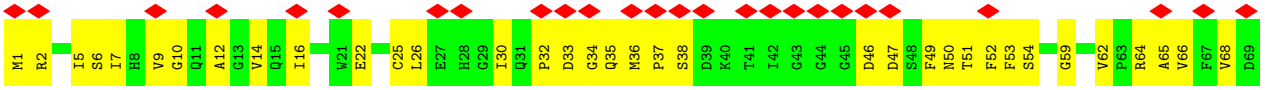
• Molecule 4: Detyrosinated tubulin alpha-3 chain

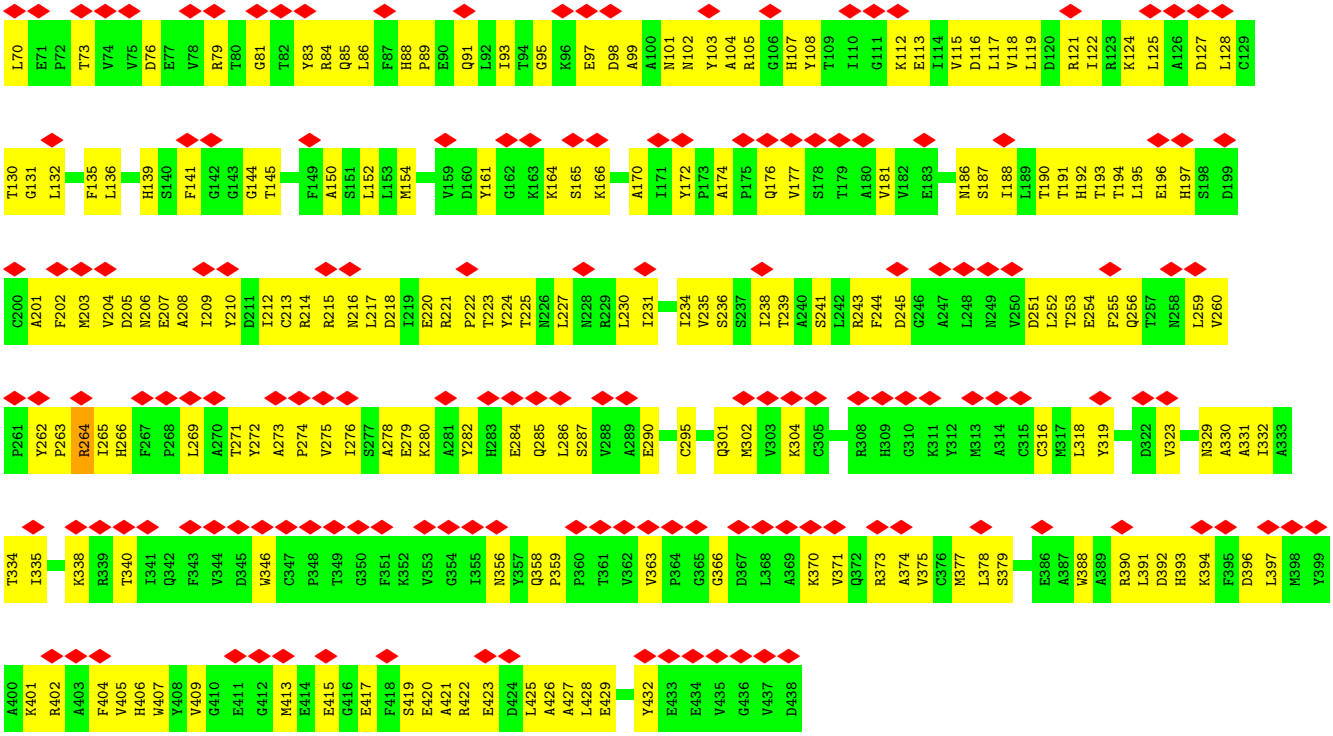
Chain VI:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

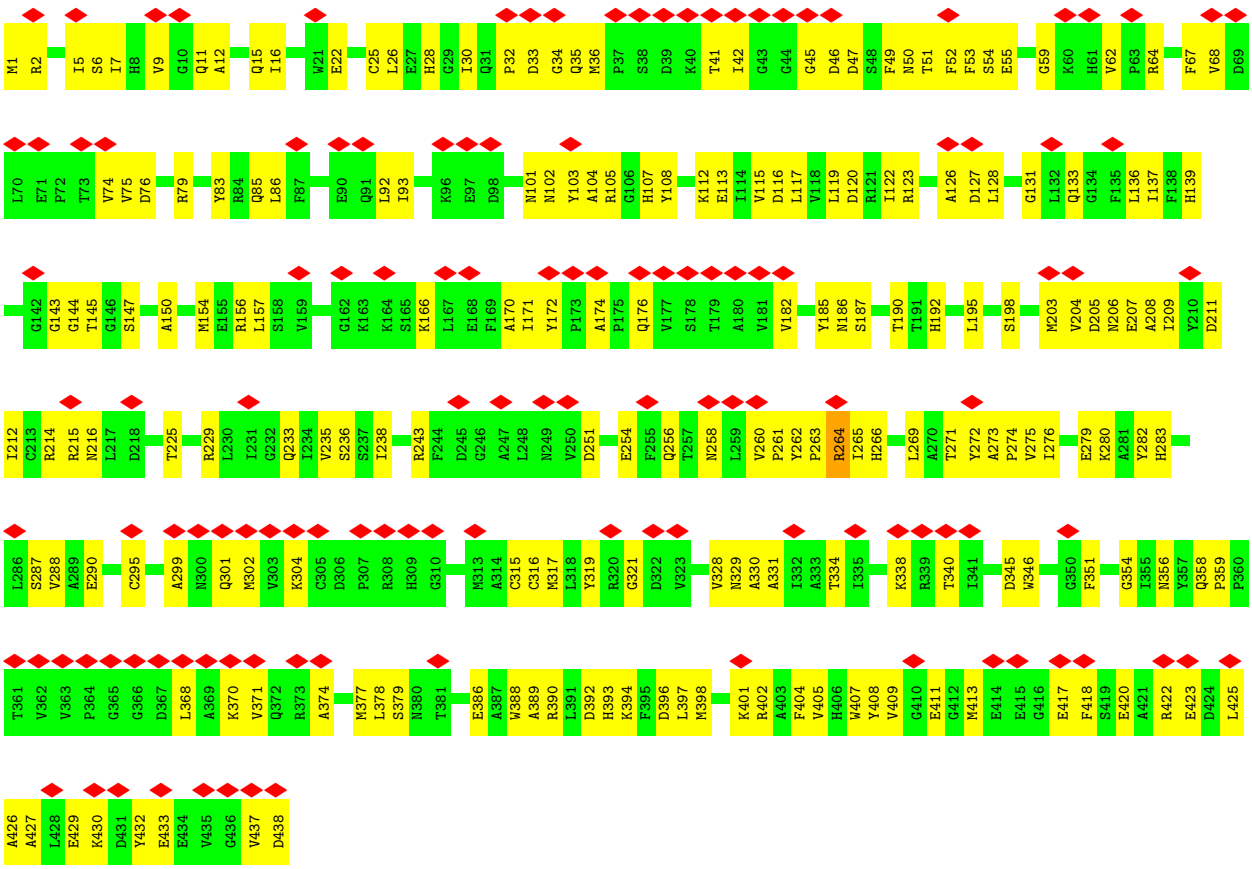
Chain VK:





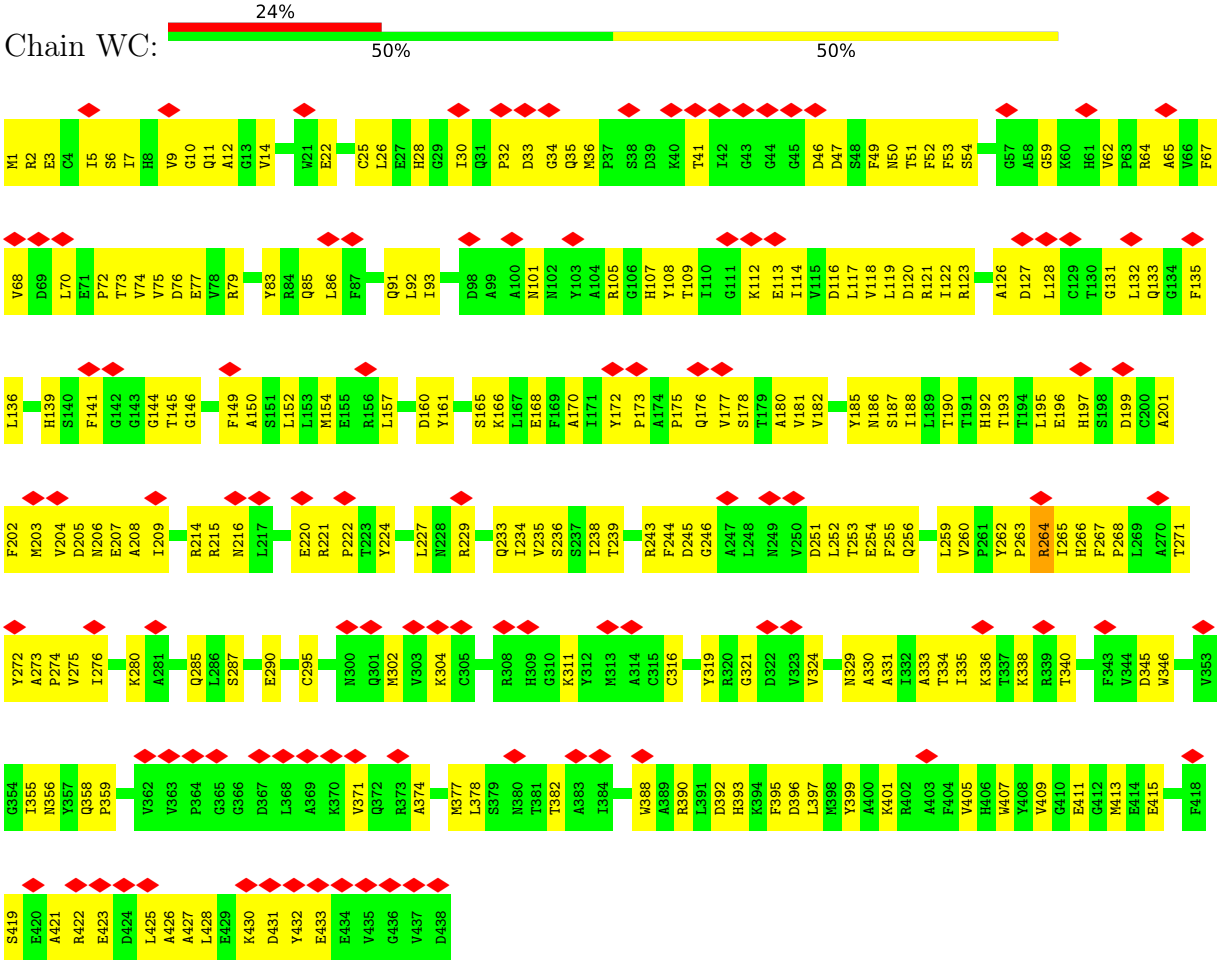
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain WA:



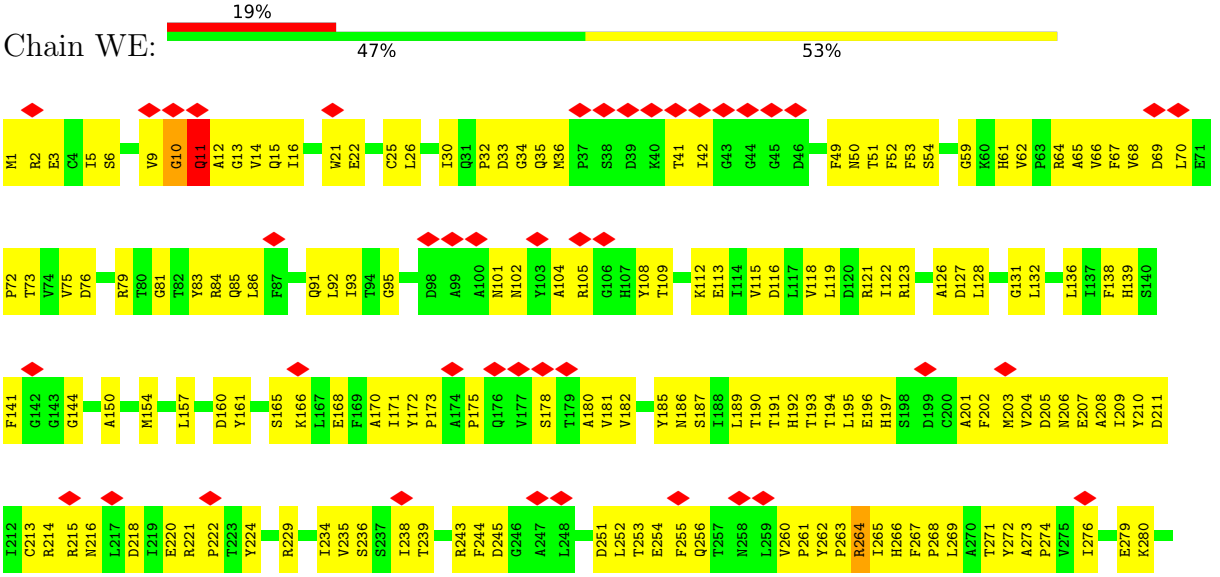
• Molecule 4: Detyrosinated tubulin alpha-3 chain

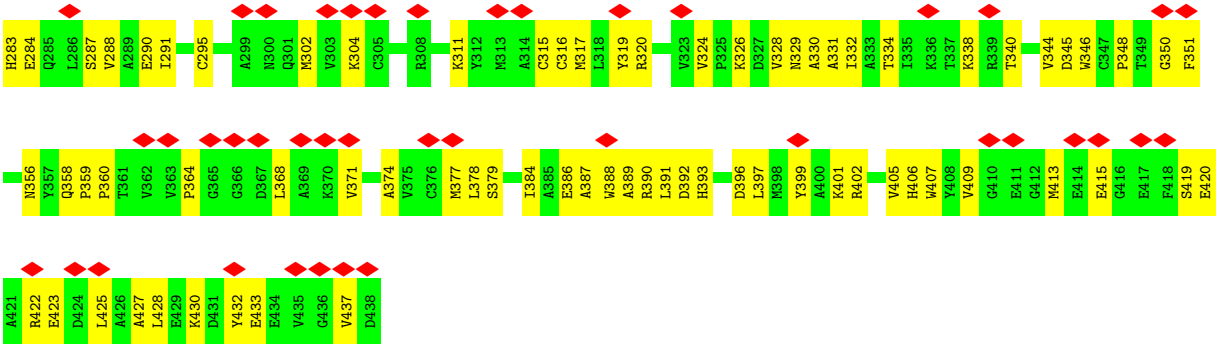
Chain WC:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

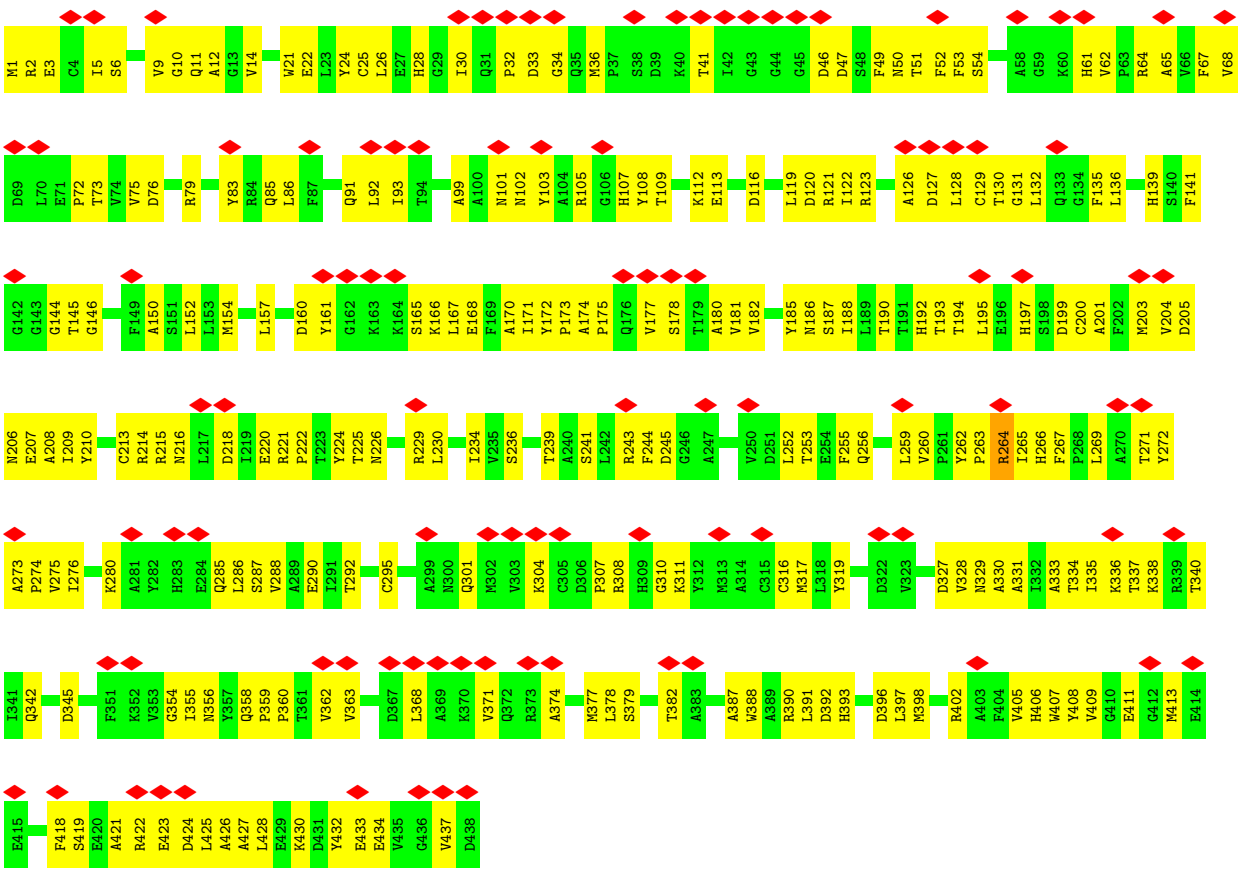
Chain WE:





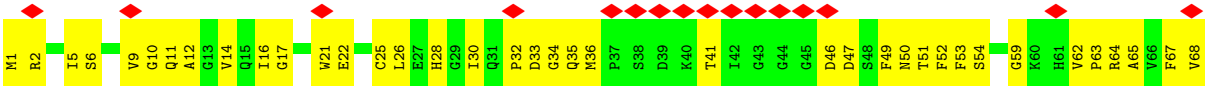
• Molecule 4: Detyrosinated tubulin alpha-3 chain

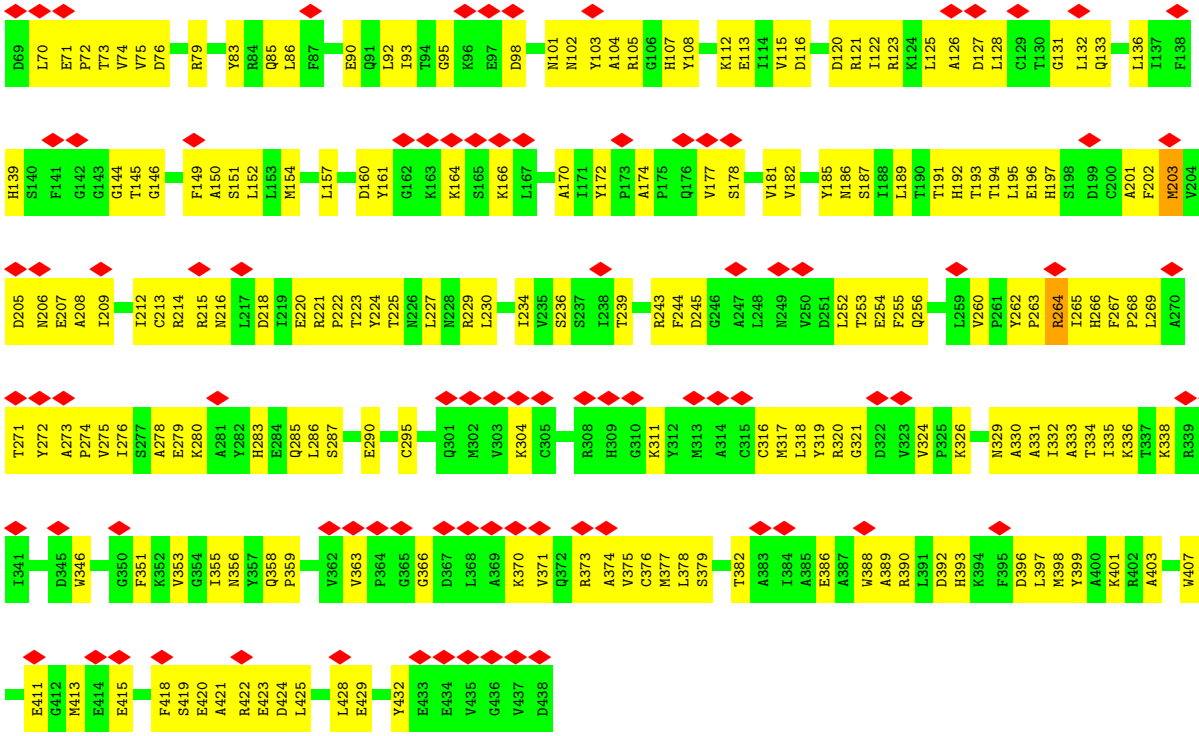
Chain WG:



• Molecule 4: Detyrosinated tubulin alpha-3 chain

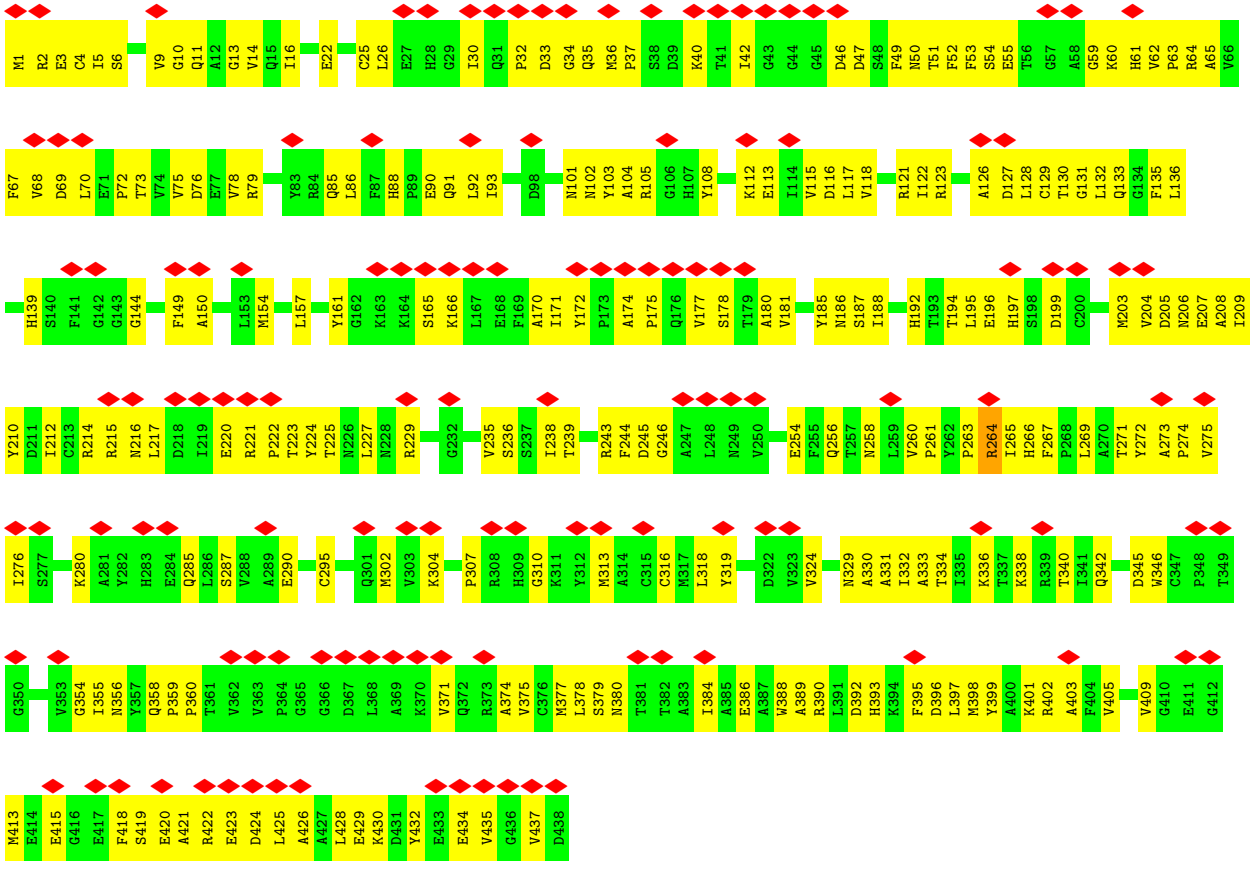
Chain WI:





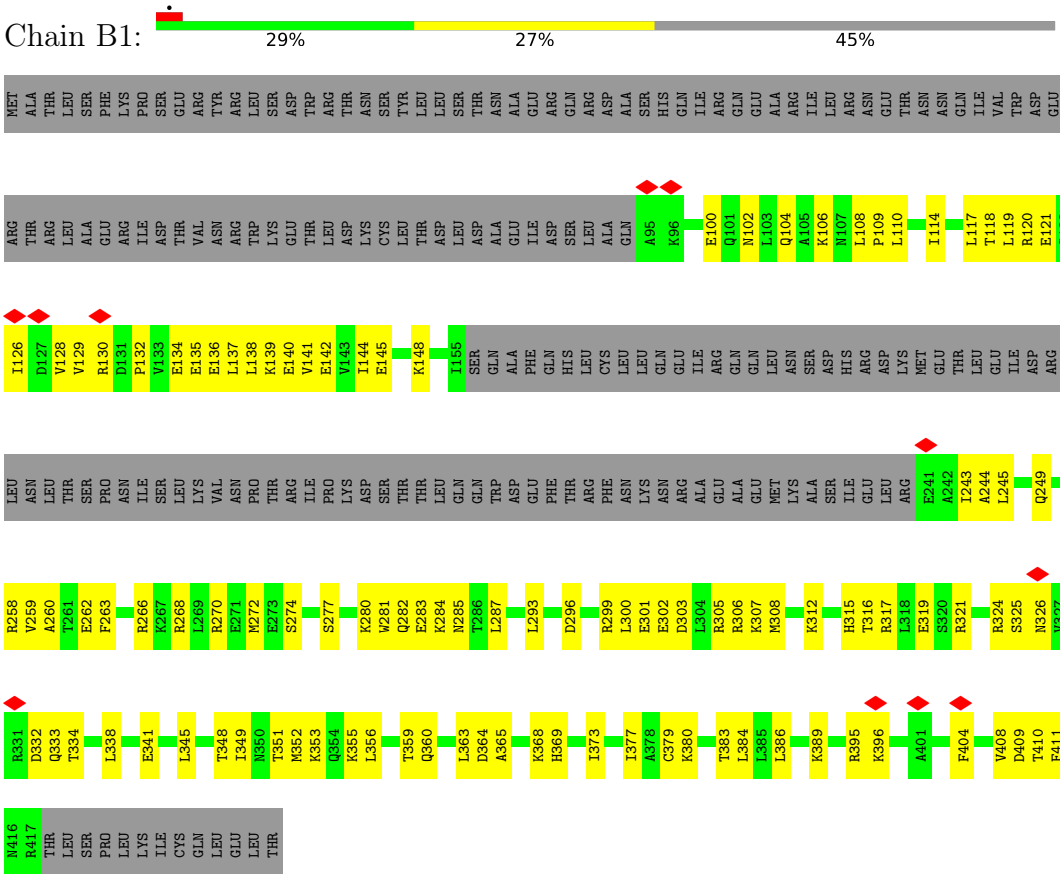
• Molecule 4: Detyrosinated tubulin alpha-3 chain

Chain WK:



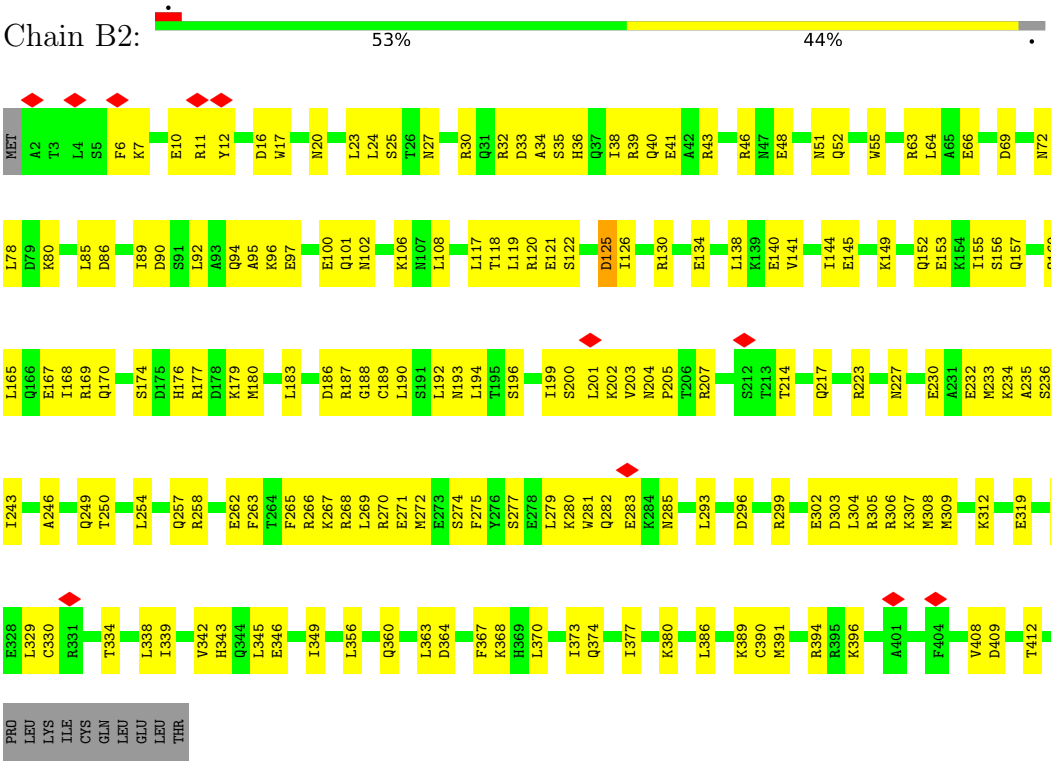
• Molecule 5: Tektin-2

Chain B1:



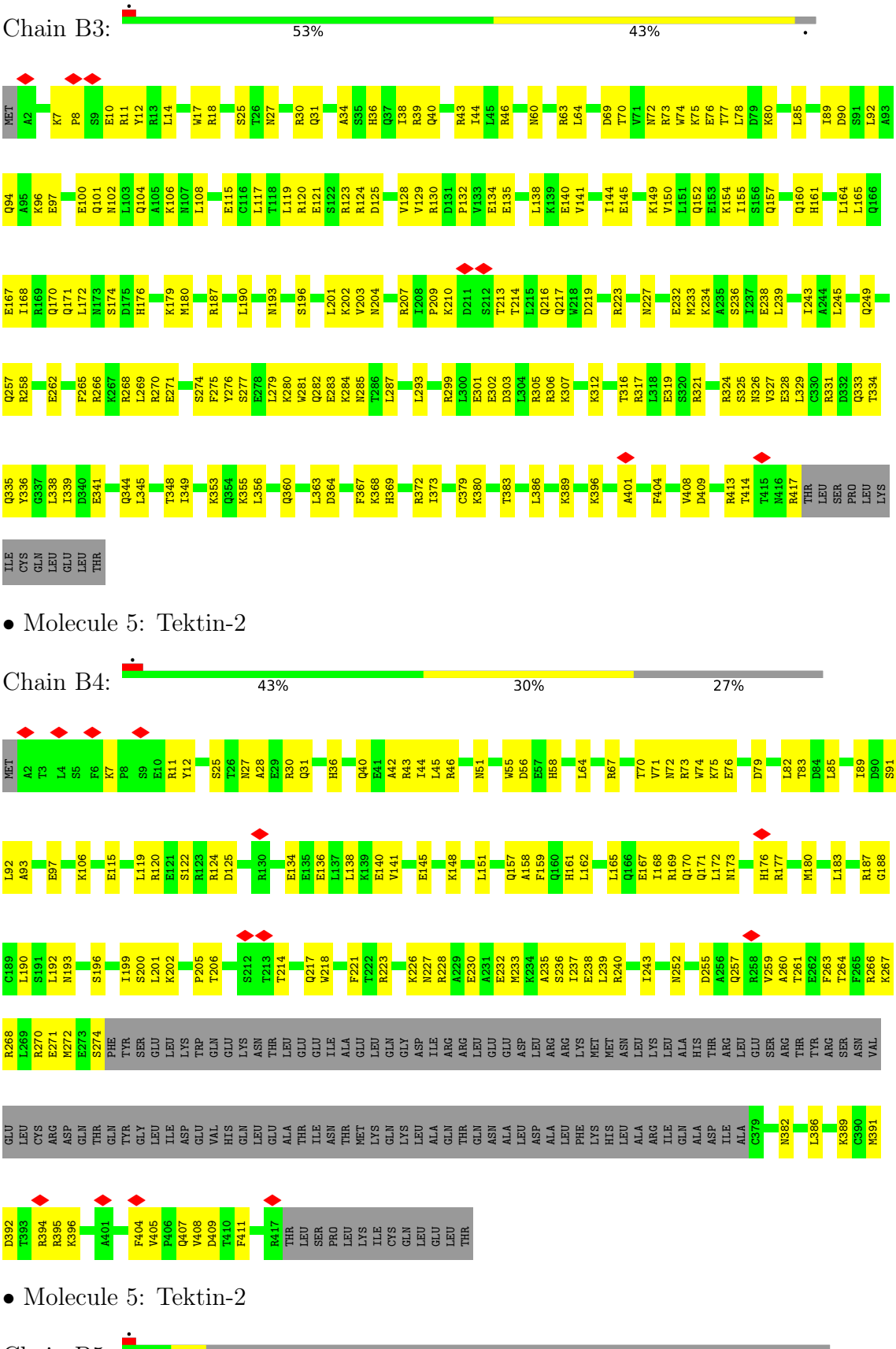
• Molecule 5: Tektin-2

Chain B2:



• Molecule 5: Tektin-2

Chain B3:

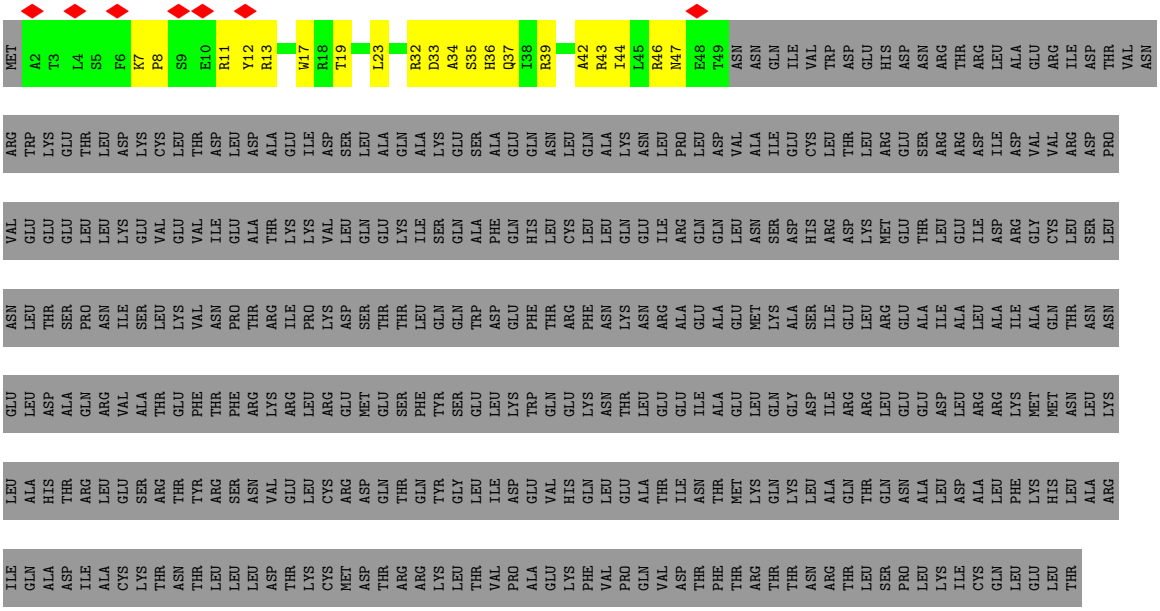


• Molecule 5: Tektin-2

Chain B4:

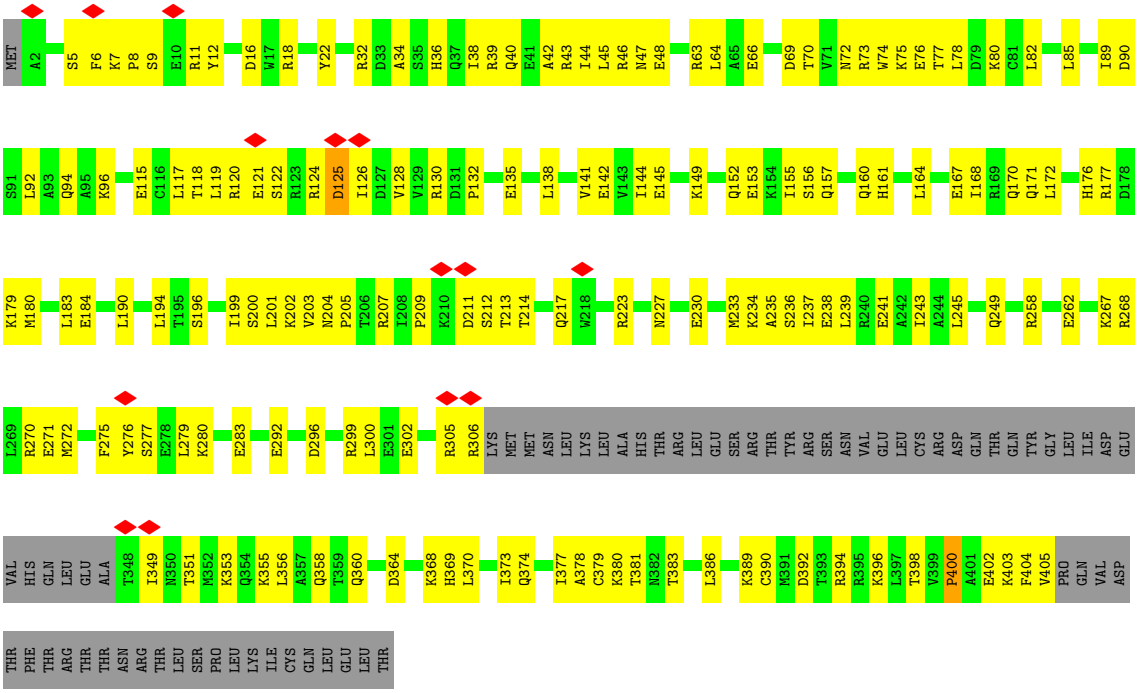
• Molecule 5: Tektin-2

Chain B5:



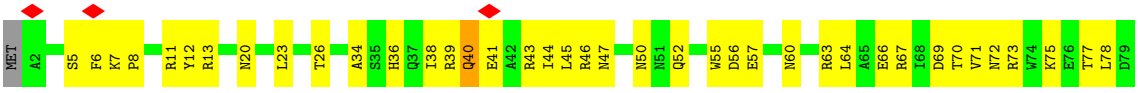
• Molecule 5: Tektin-2

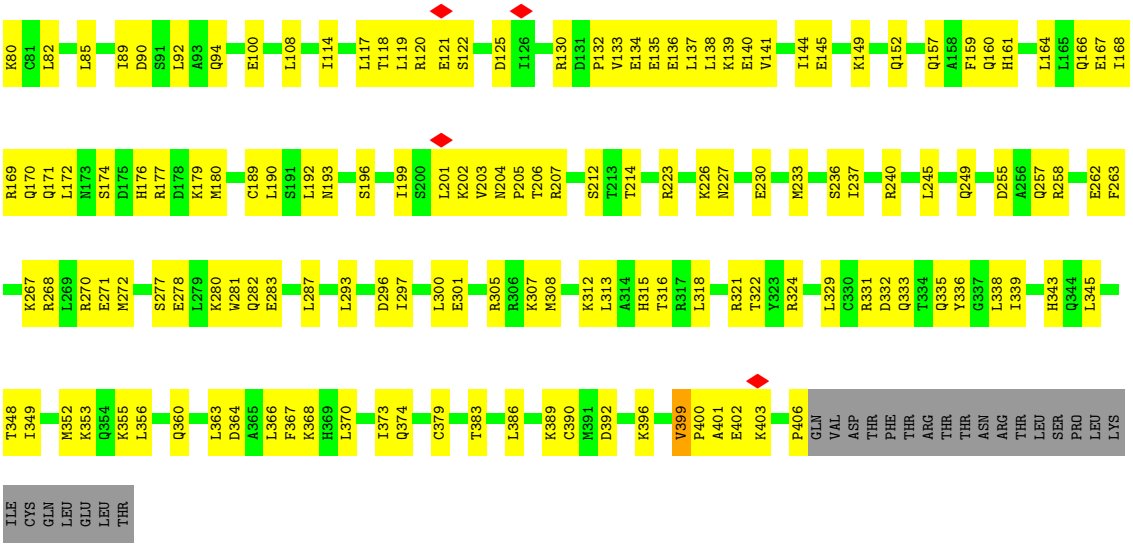
Chain B6:



• Molecule 5: Tektin-2

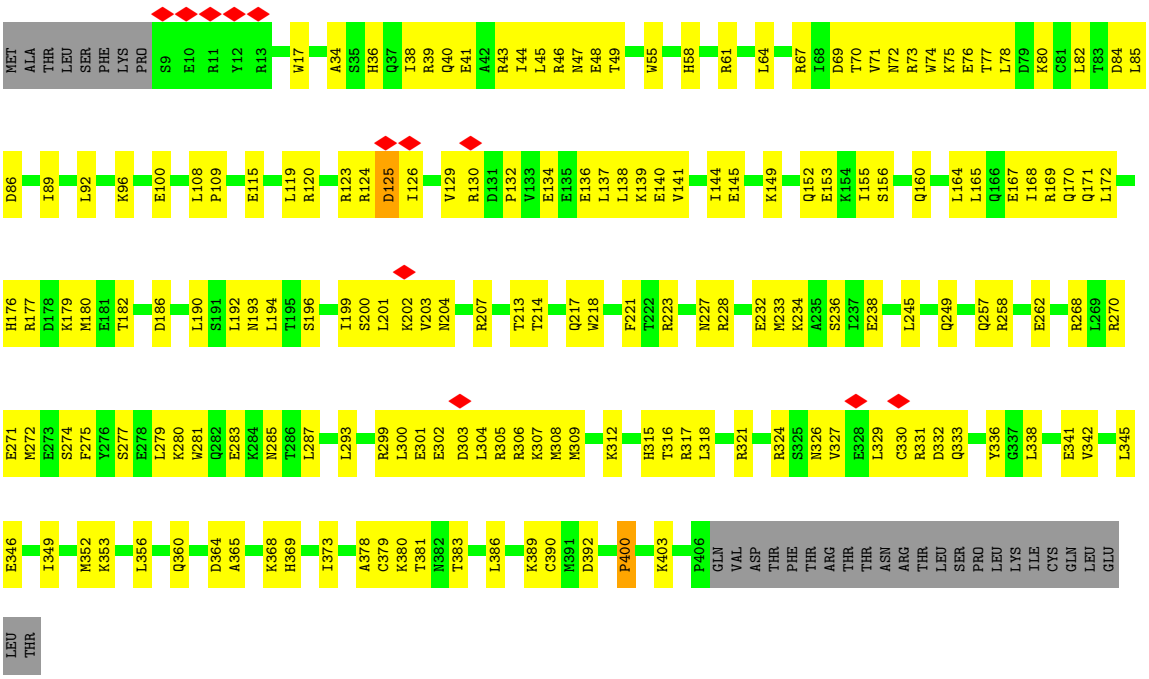
Chain B7:





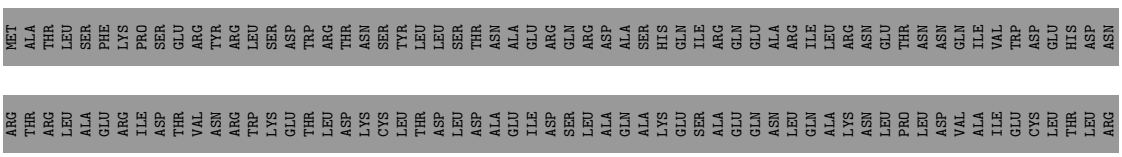
• Molecule 5: Tektin-2

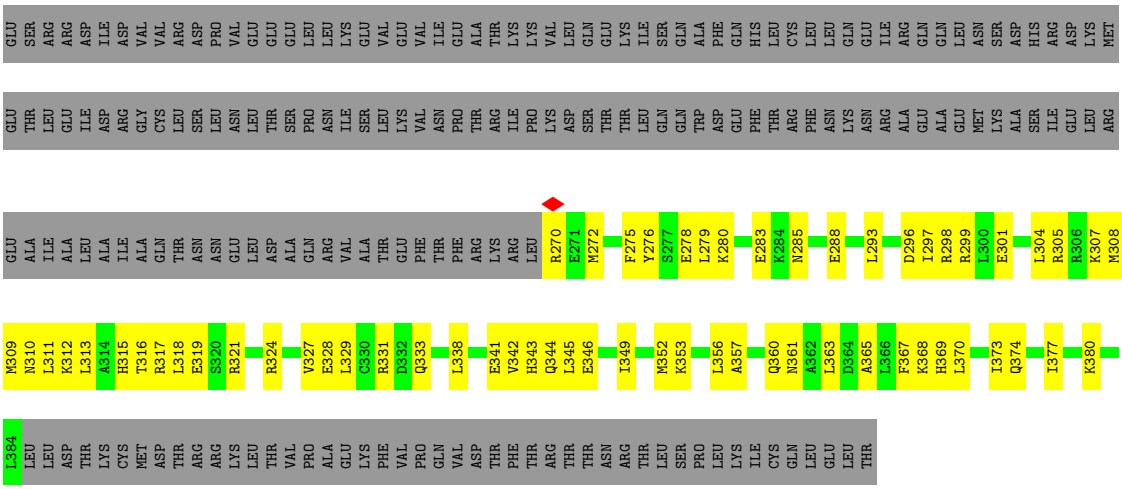
Chain B8:



• Molecule 5: Tektin-2

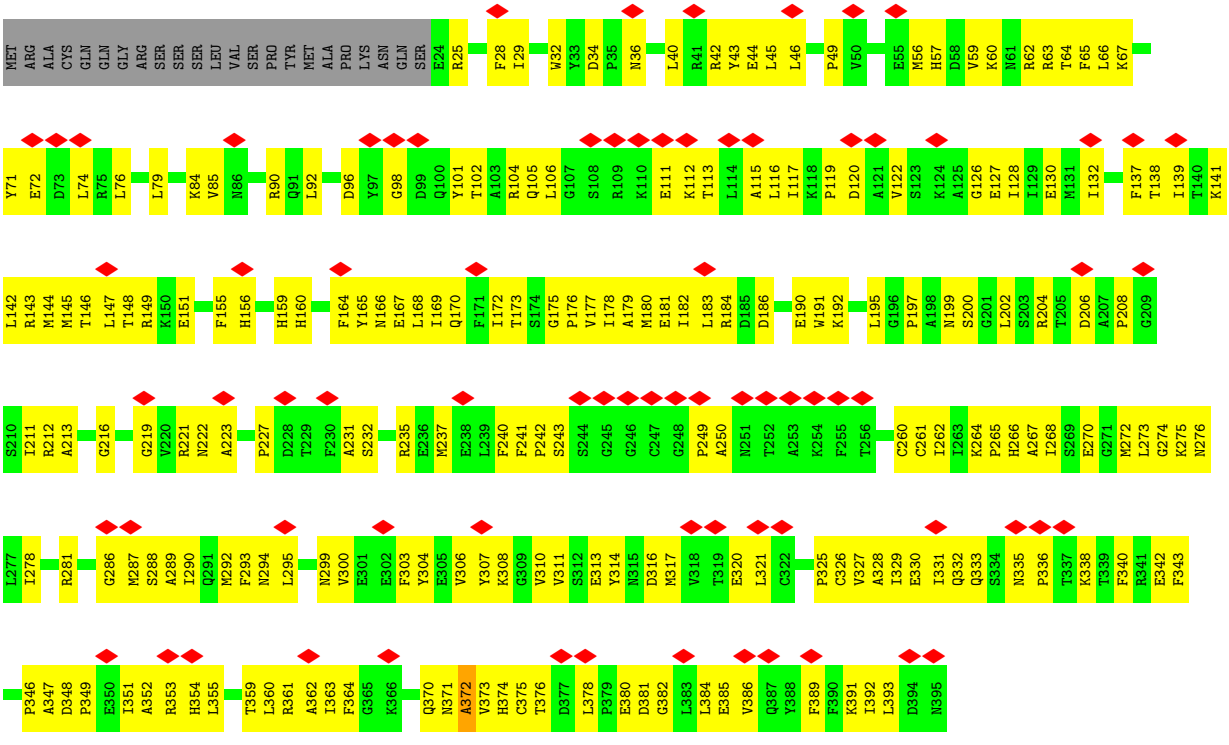
Chain B9:





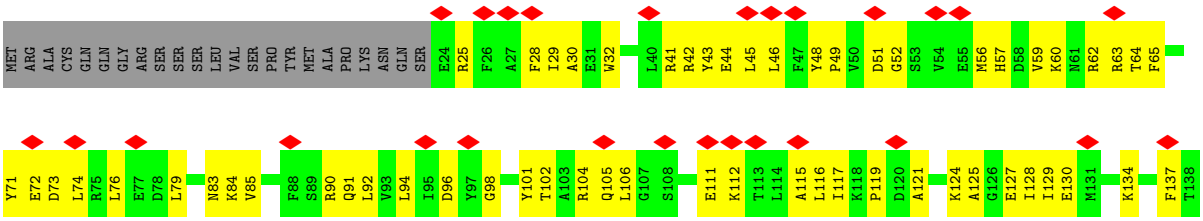
• Molecule 6: Nucleoside diphosphate kinase 7

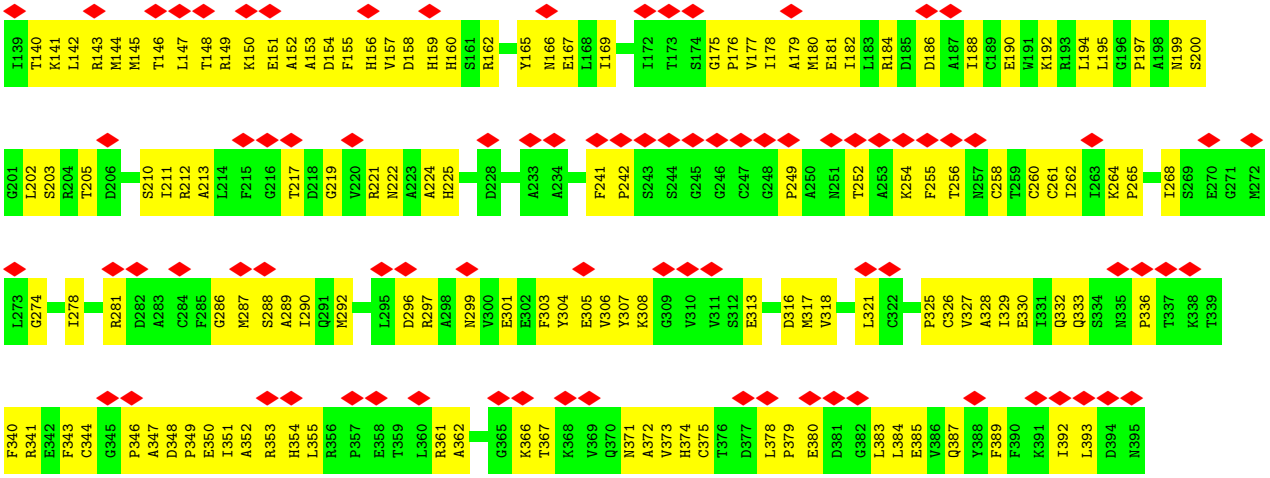
Chain C:



• Molecule 6: Nucleoside diphosphate kinase 7

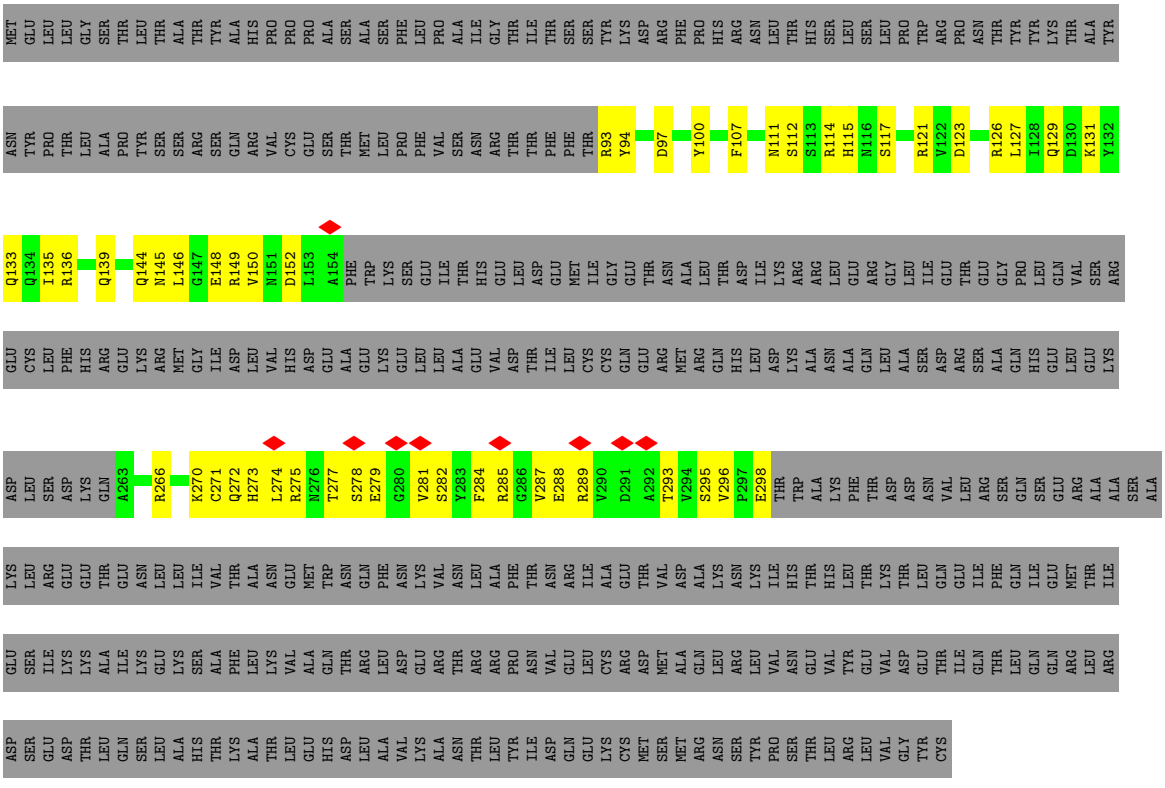
Chain D:





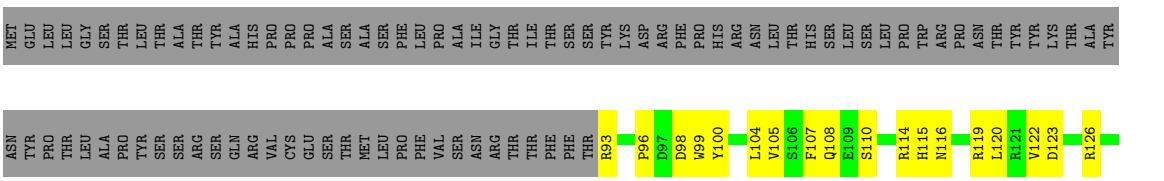
- Molecule 7: Tektin-3

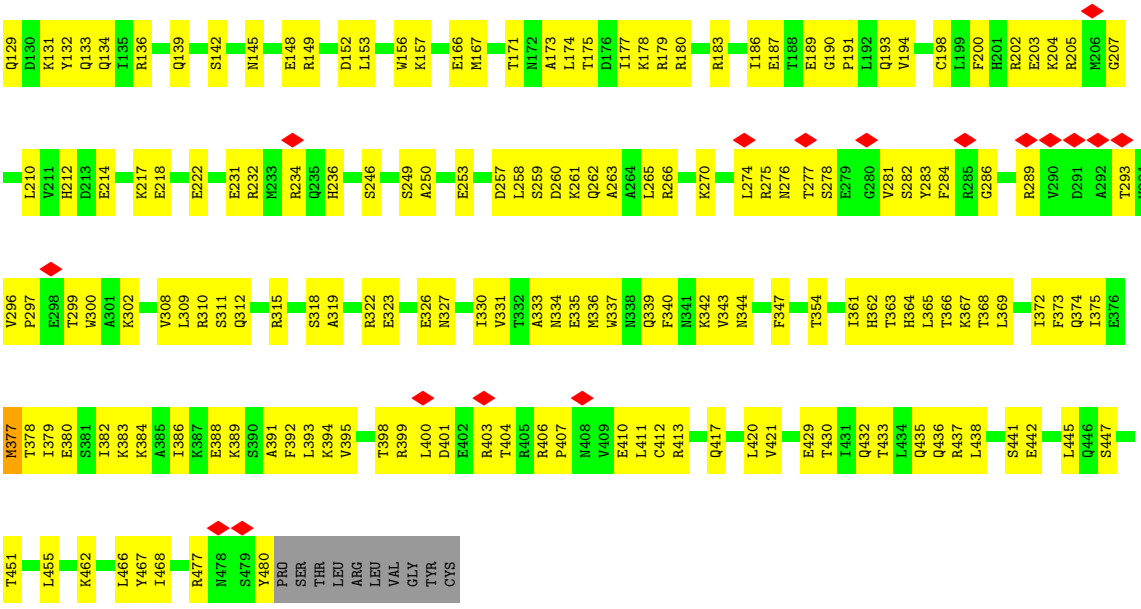
Chain C1:



- Molecule 7: Tektin-3

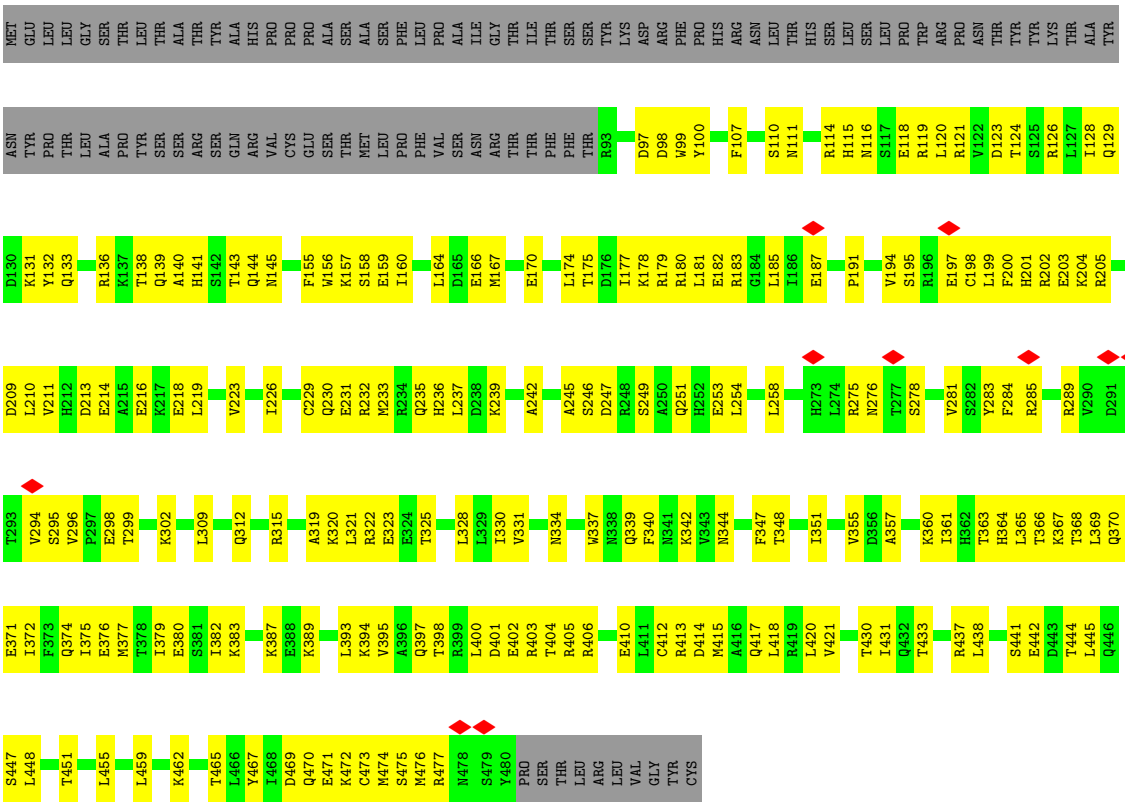
Chain C2:





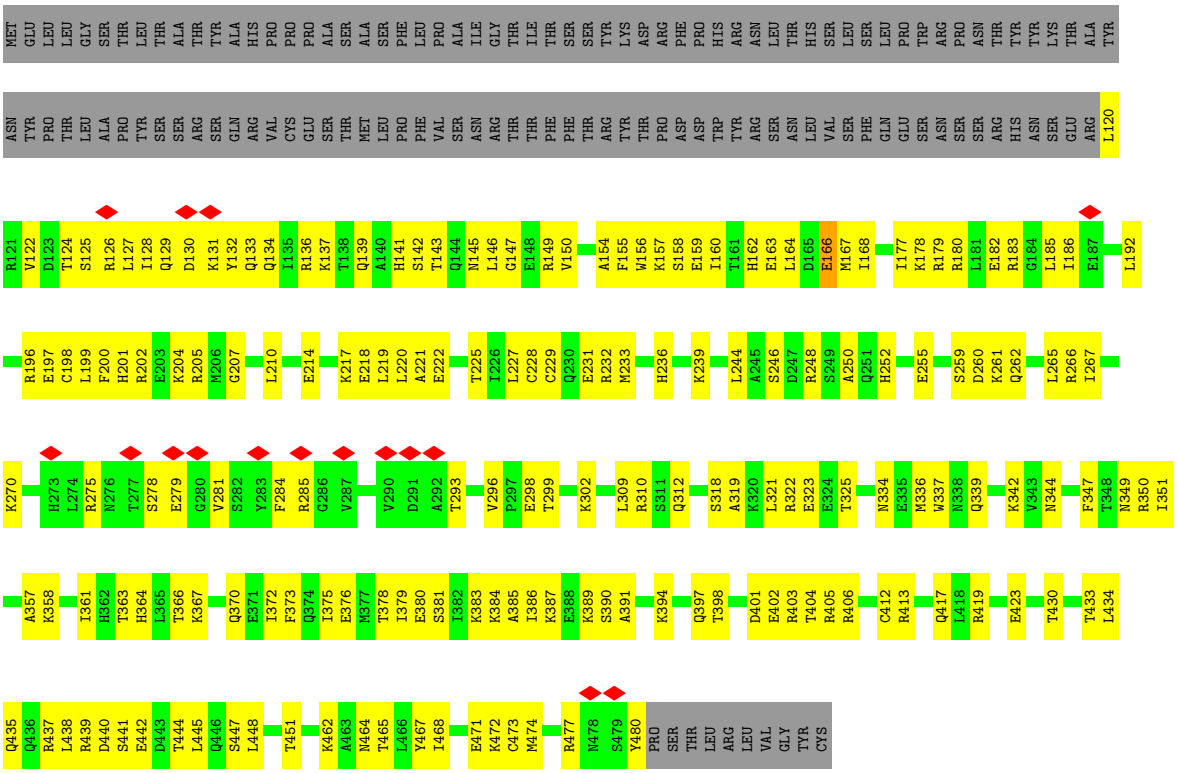
• Molecule 7: Tektin-3

Chain C3:



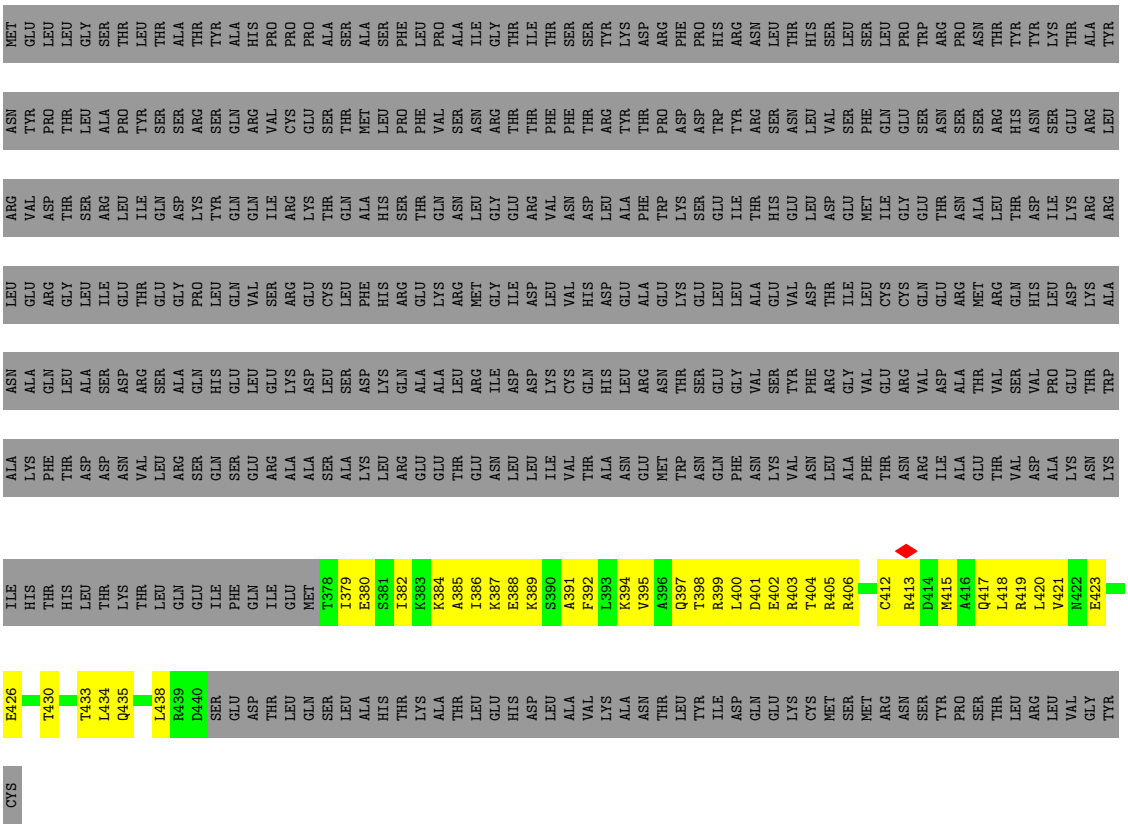
• Molecule 7: Tektin-3

Chain C4:



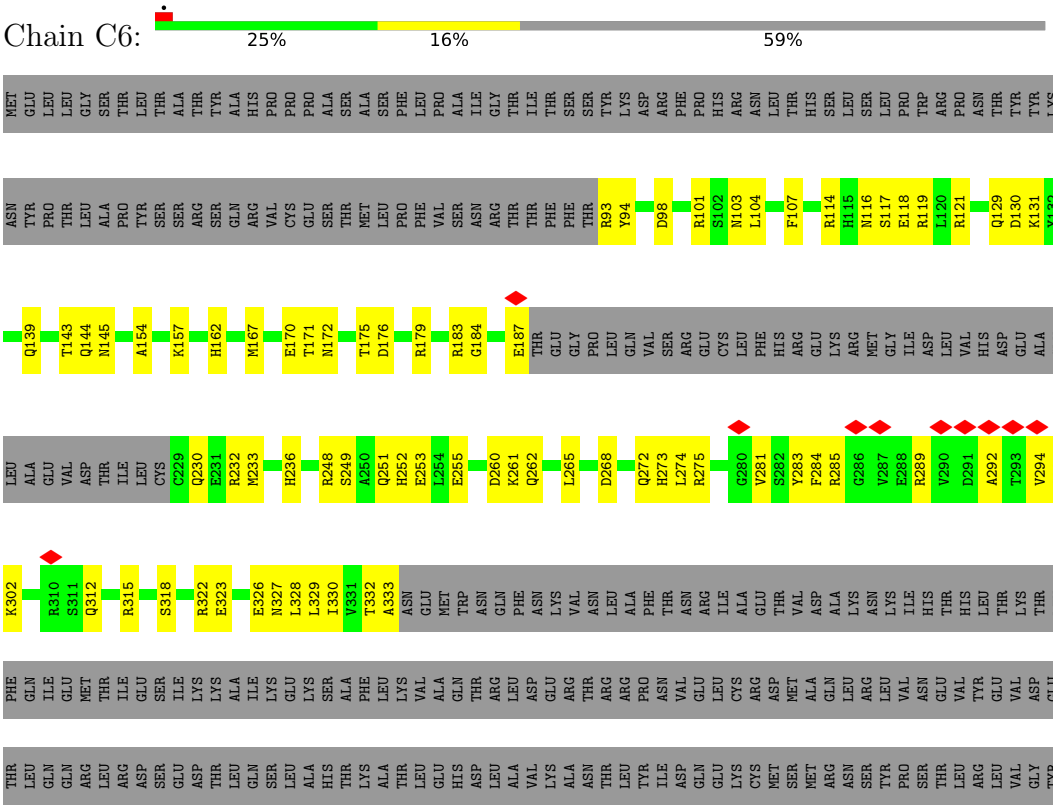
• Molecule 7: Tektin-3

Chain C5: 5% 8% 87%



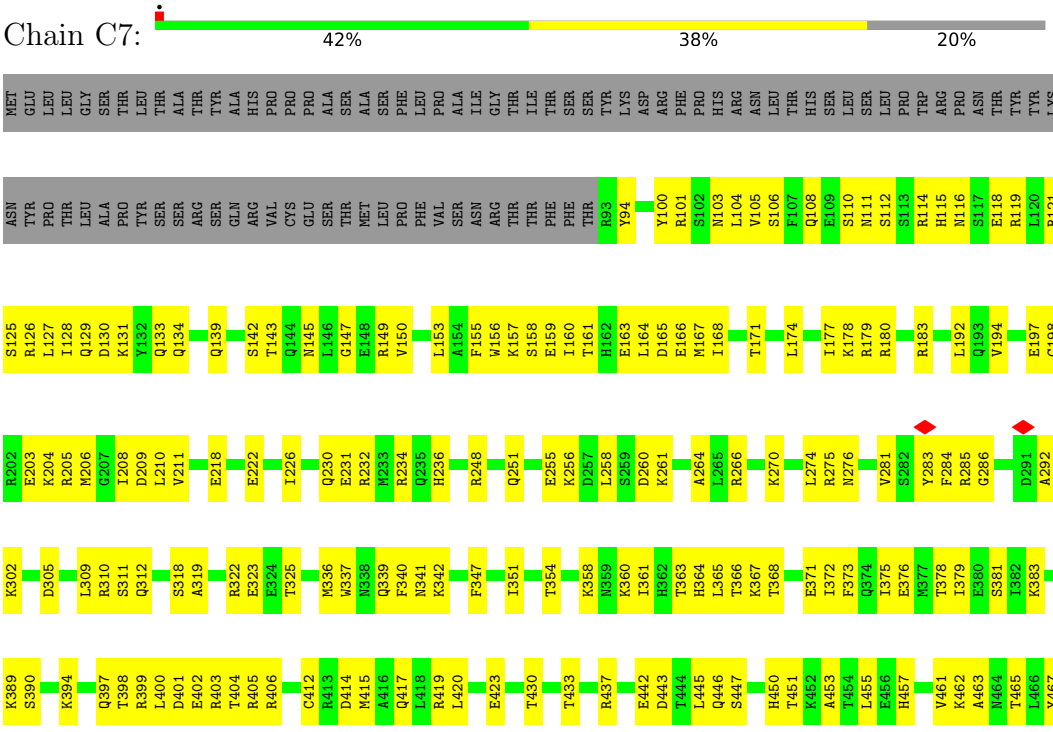
• Molecule 7: Tektin-3

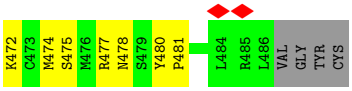
Chain C6:



• Molecule 7: Tektin-3

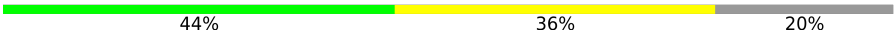
Chain C7:

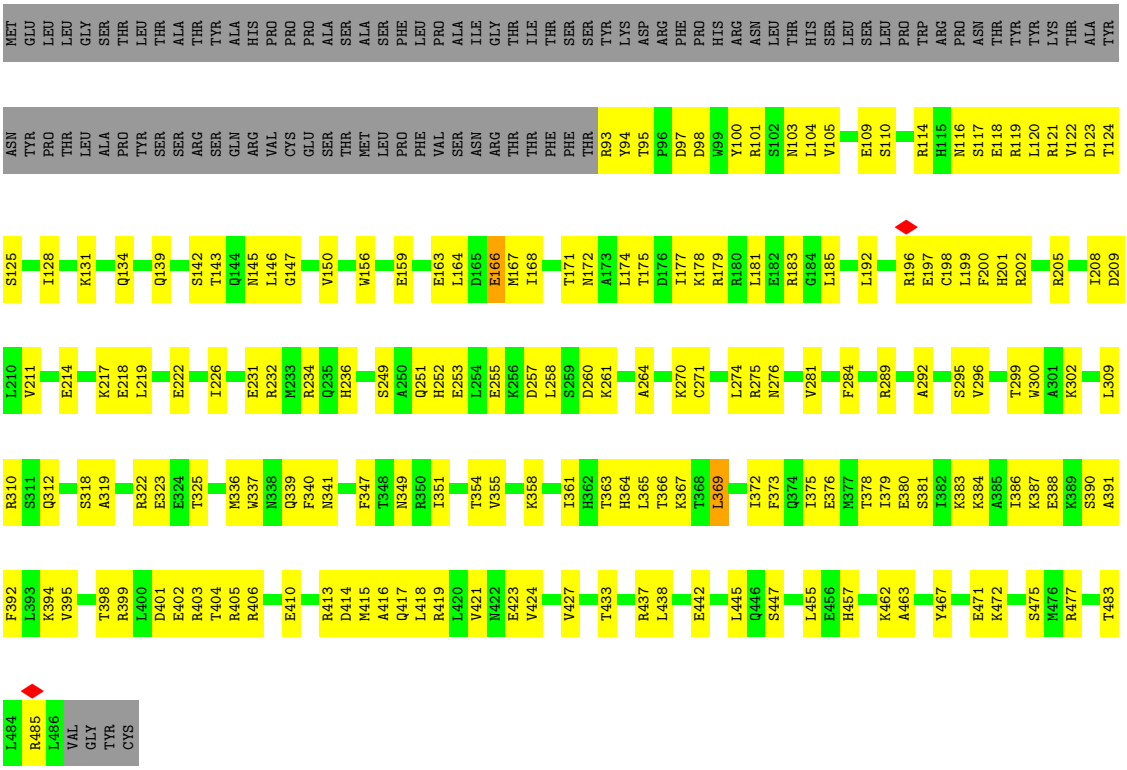




• Molecule 7: Tektin-3

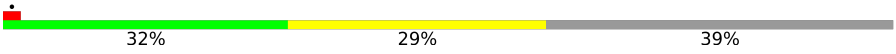
Chain C8:

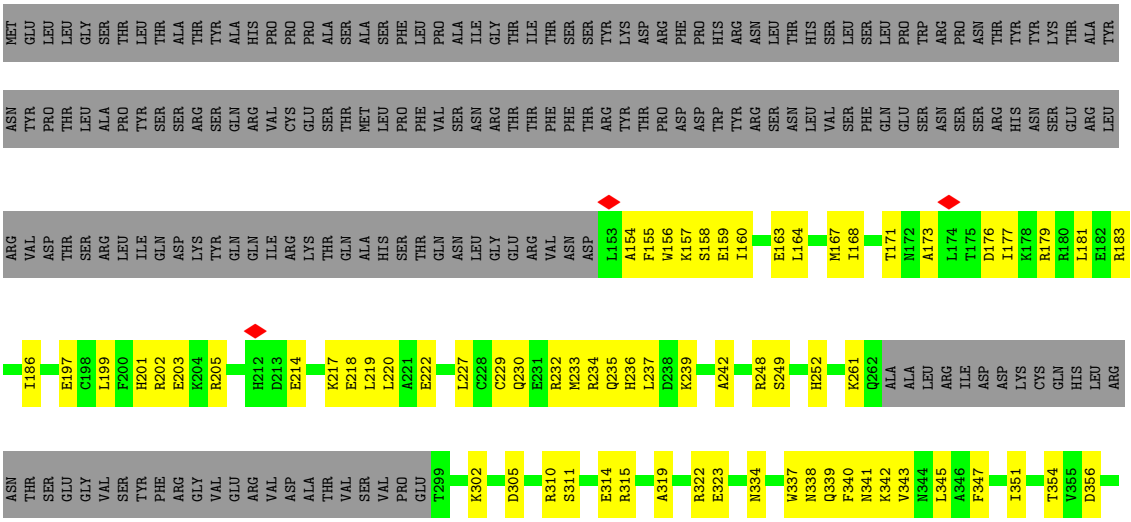


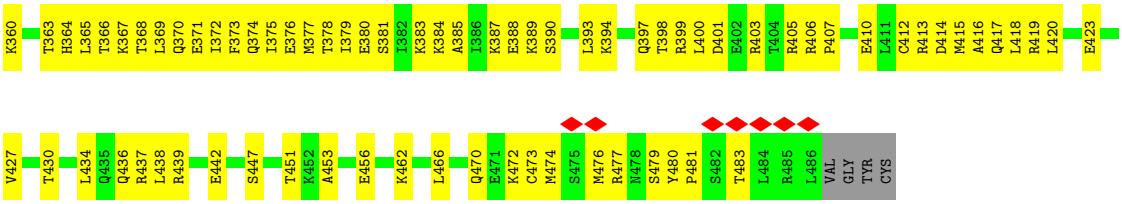


• Molecule 7: Tektin-3

Chain C9:

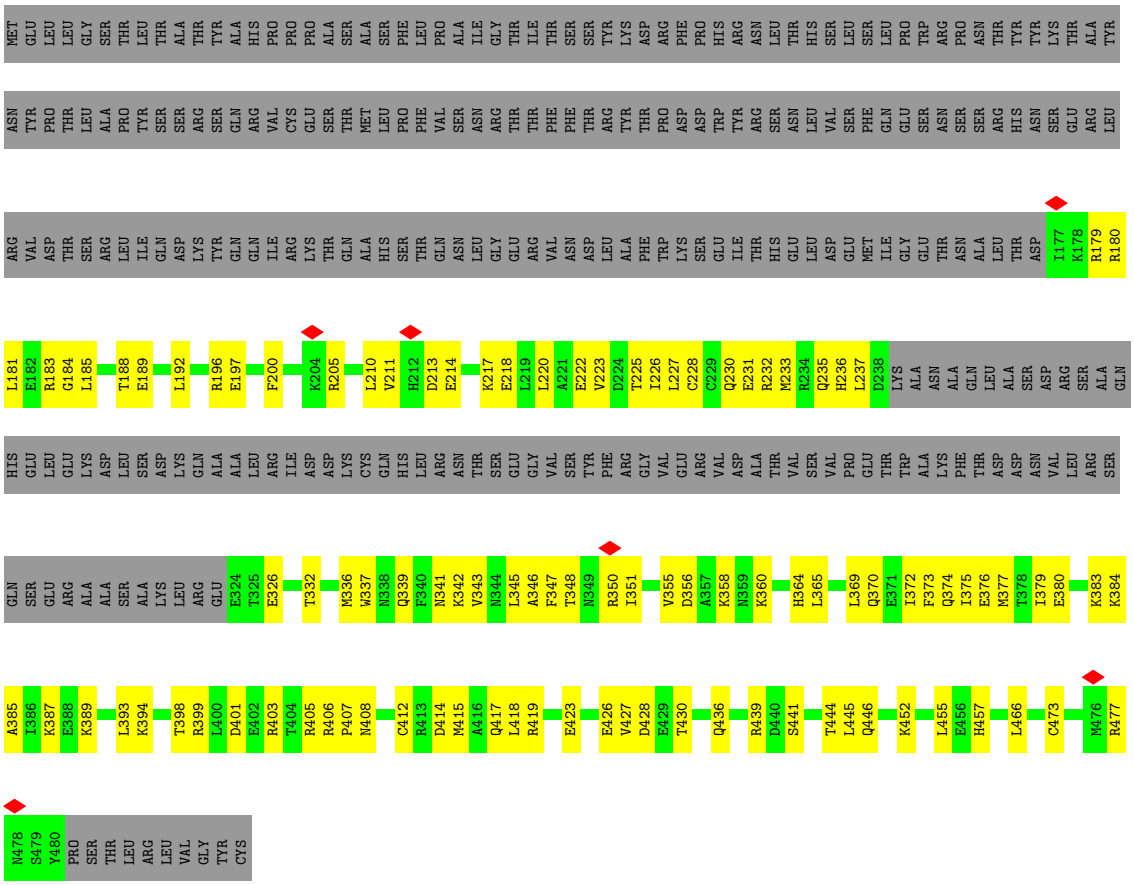






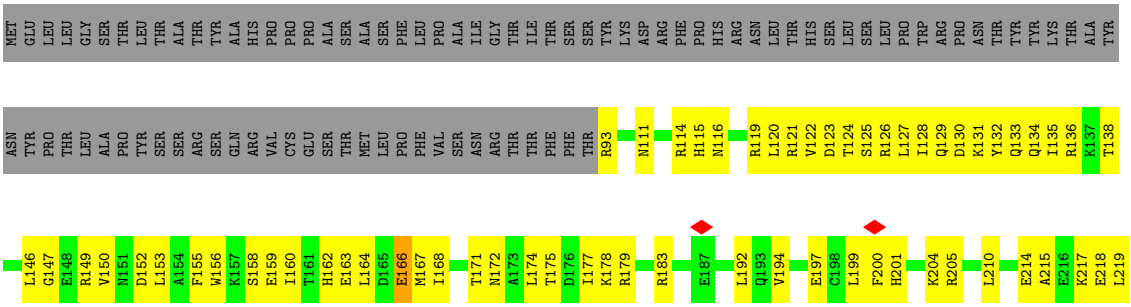
• Molecule 7: Tektin-3

Chain Ca:



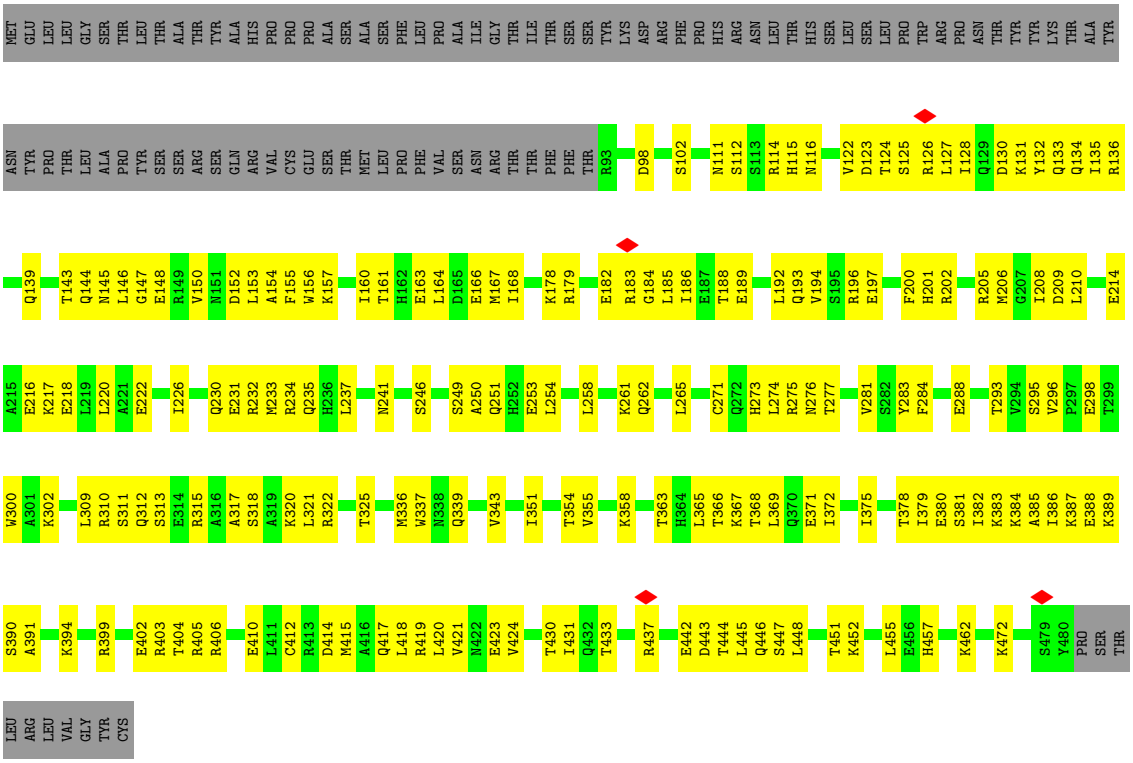
• Molecule 7: Tektin-3

Chain Cb:



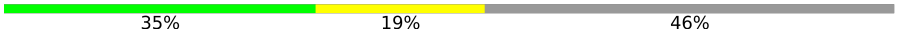
• Molecule 7: Tektin-3

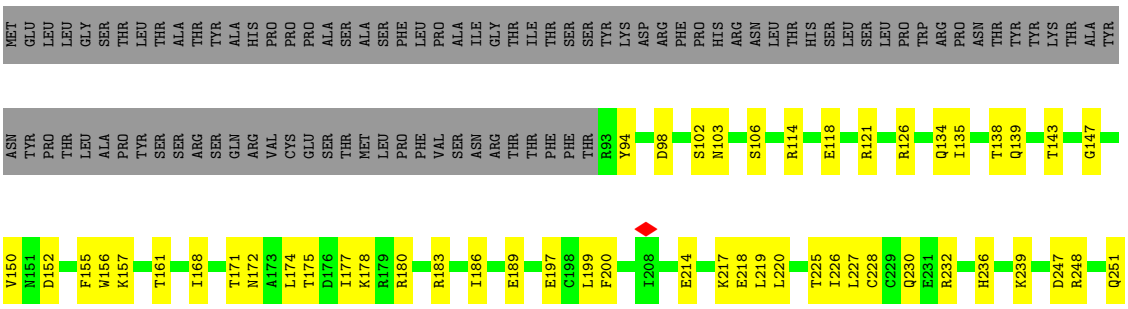
Chain Cc:

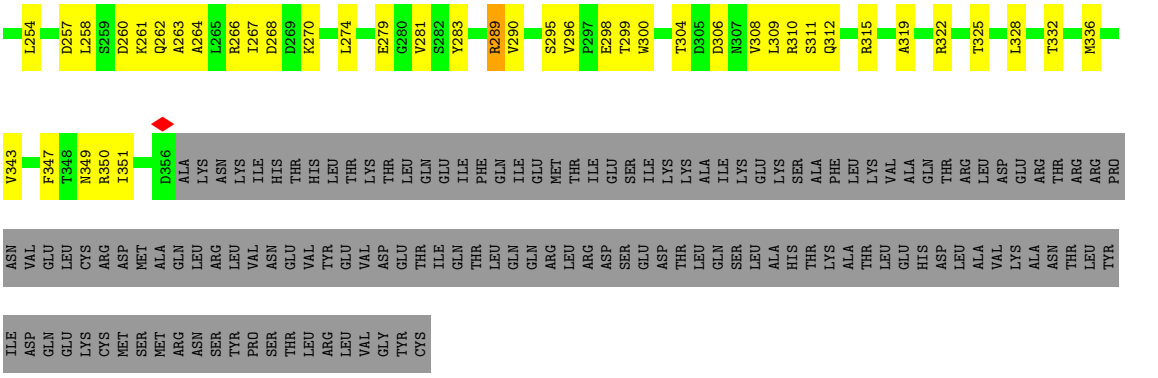


• Molecule 7: Tektin-3

Chain Cd:

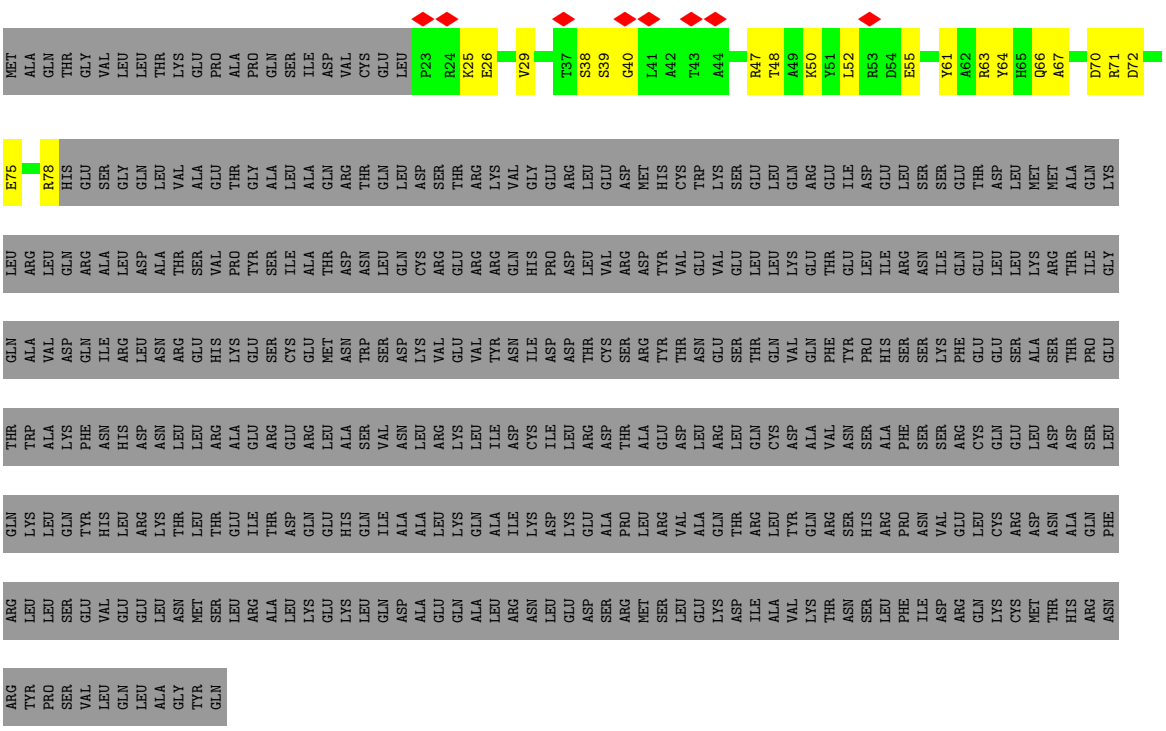






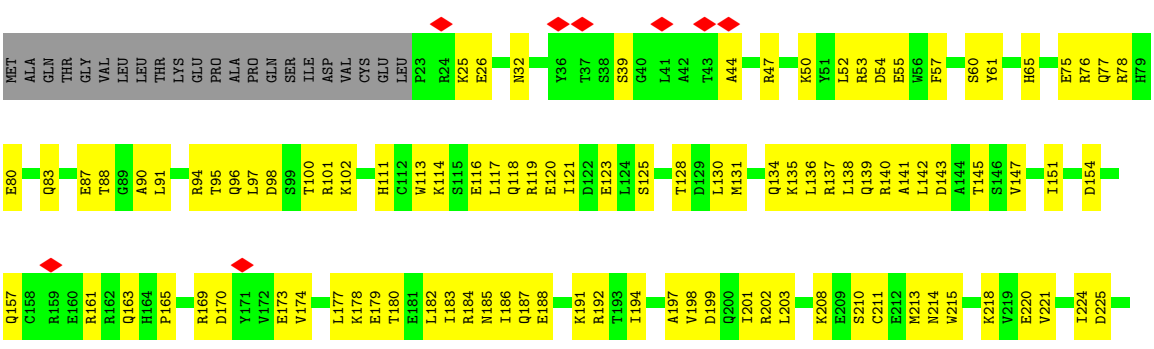
• Molecule 8: Tektin-4

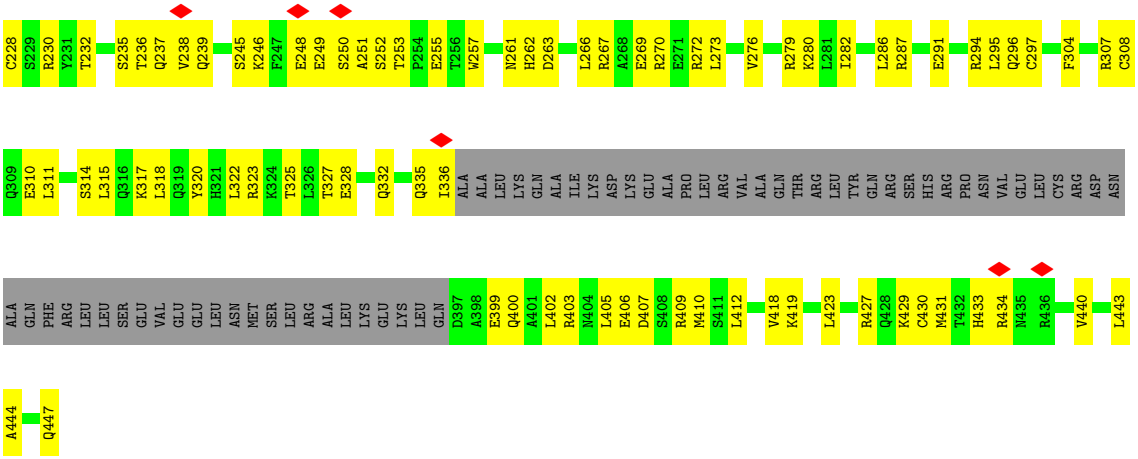
Chain D1:



• Molecule 8: Tektin-4

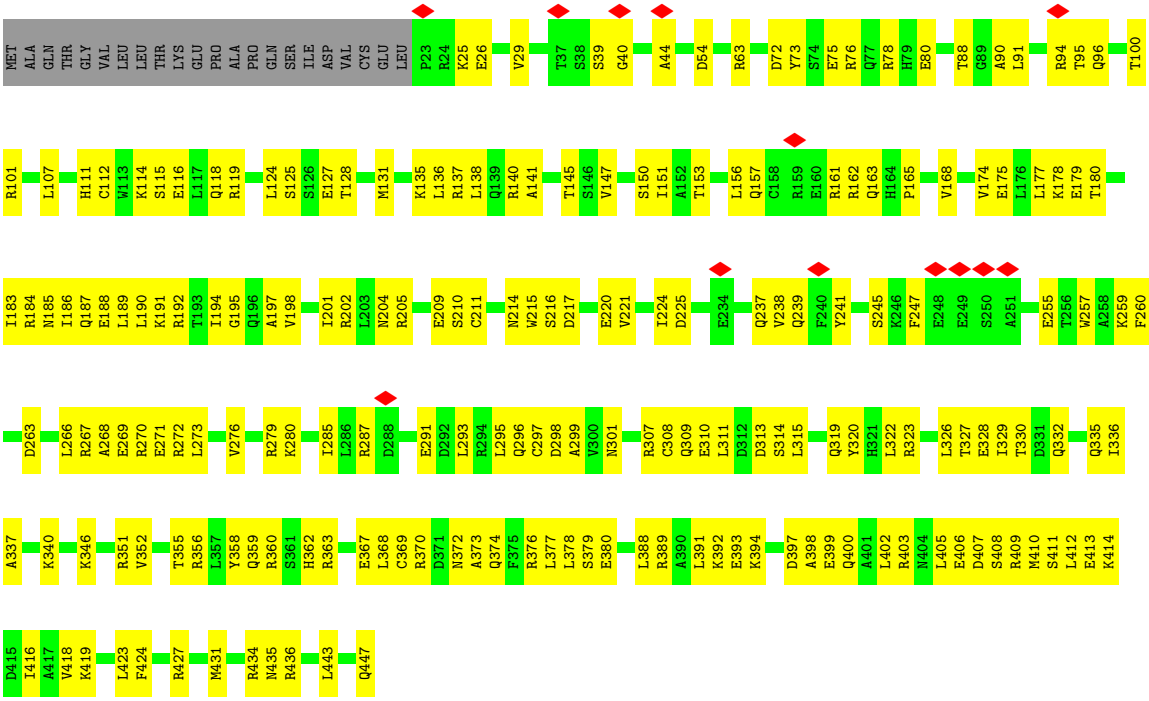
Chain D2:





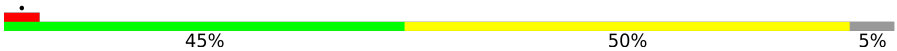
• Molecule 8: Tektin-4

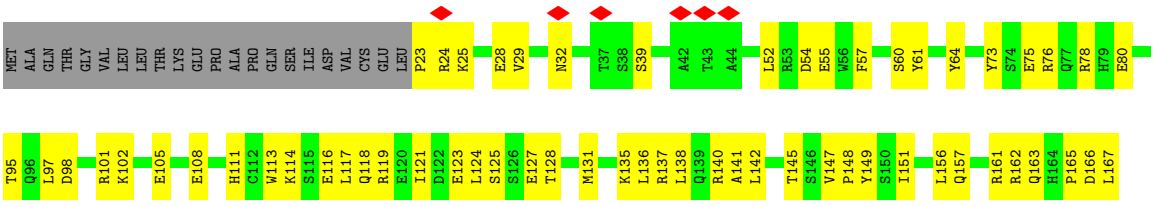
Chain D3:

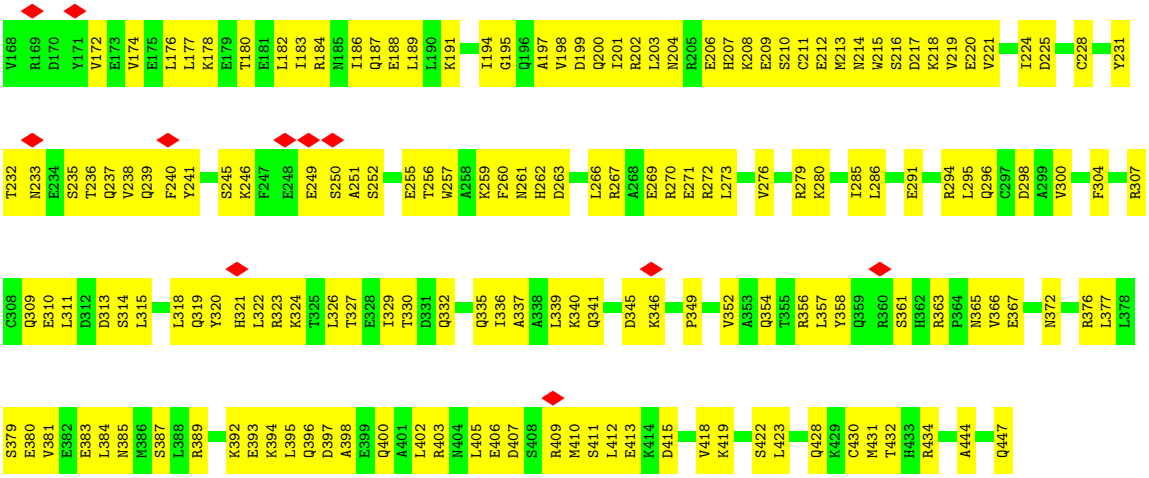


• Molecule 8: Tektin-4

Chain D4:

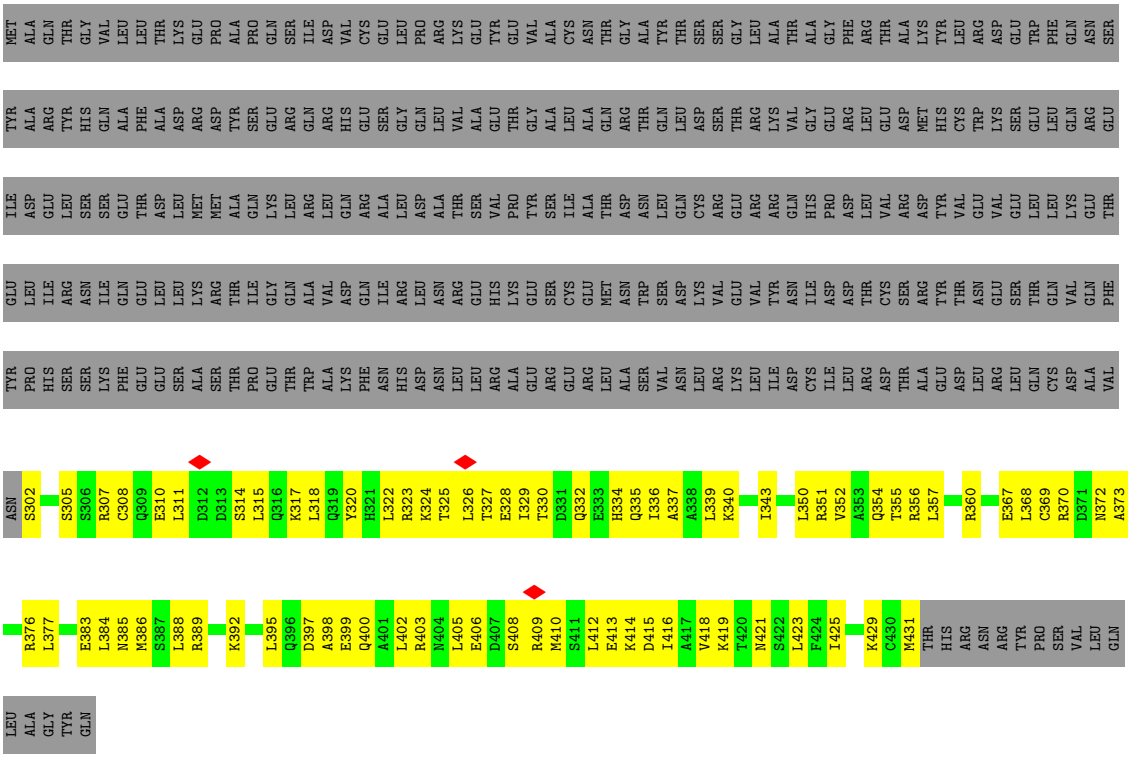






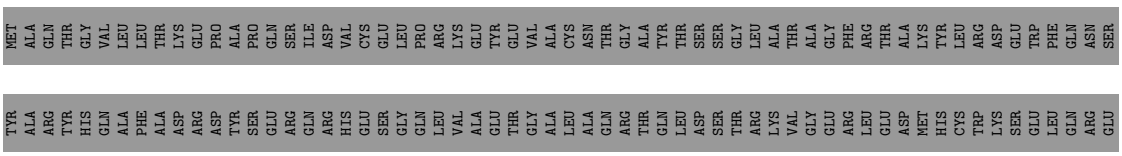
• Molecule 8: Tektin-4

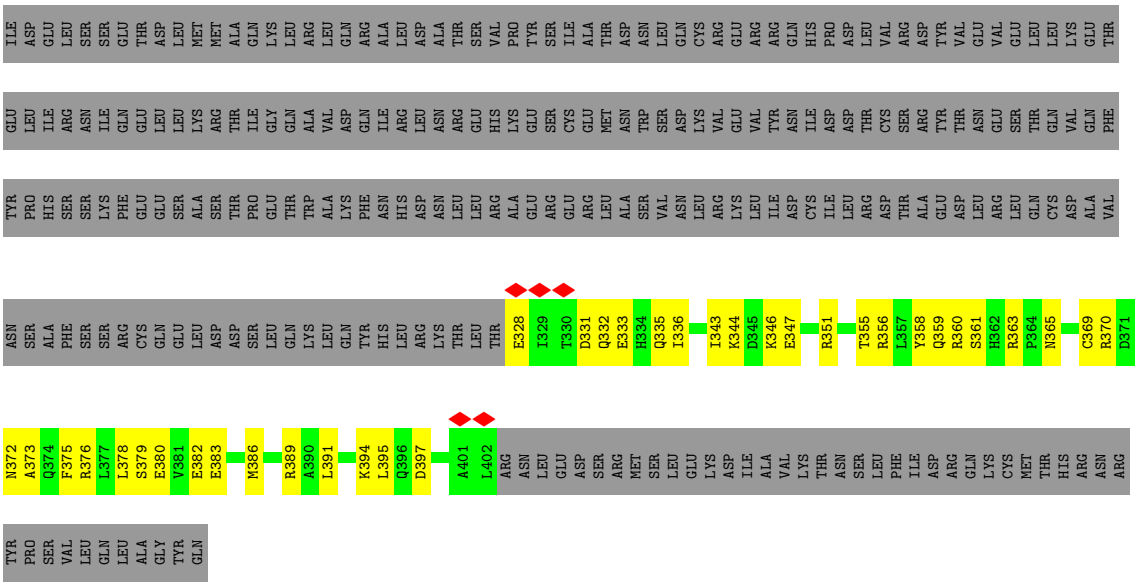
Chain D5:



• Molecule 8: Tektin-4

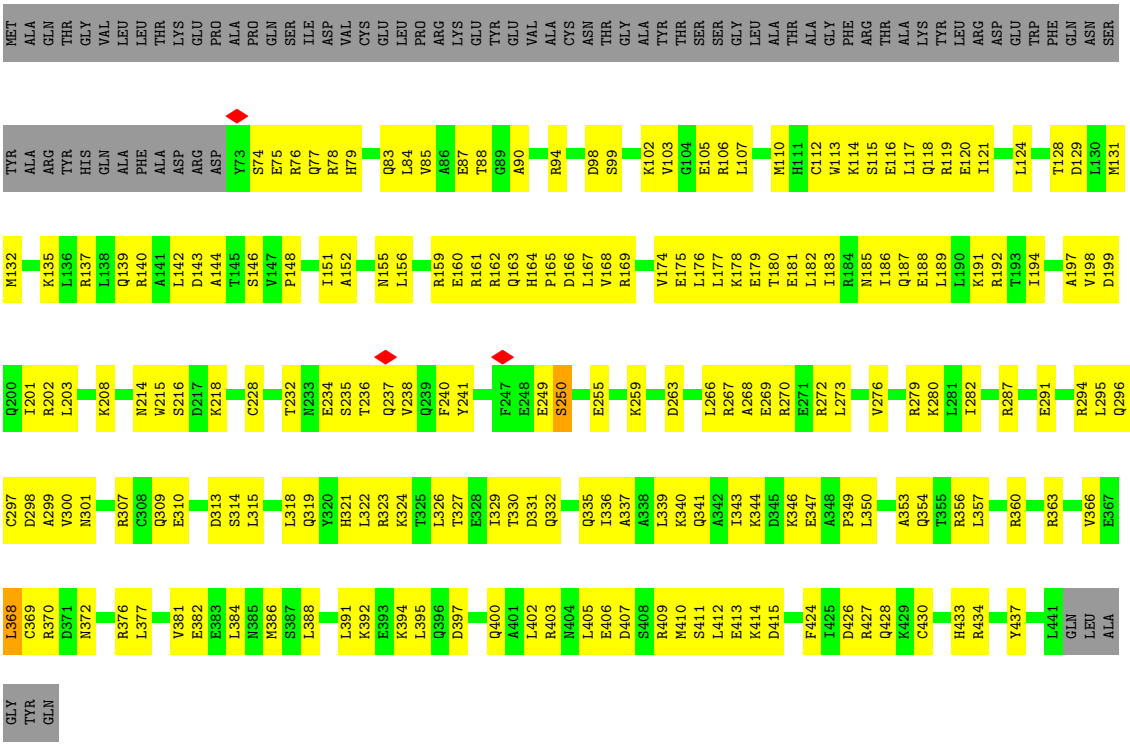
Chain D6:





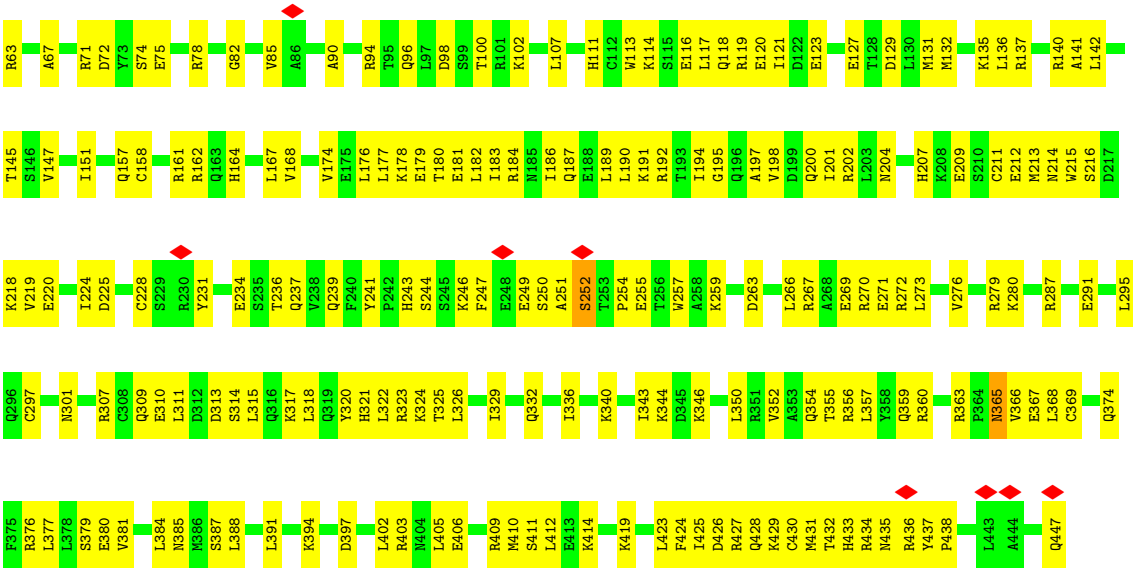
• Molecule 8: Tektin-4

Chain D7:



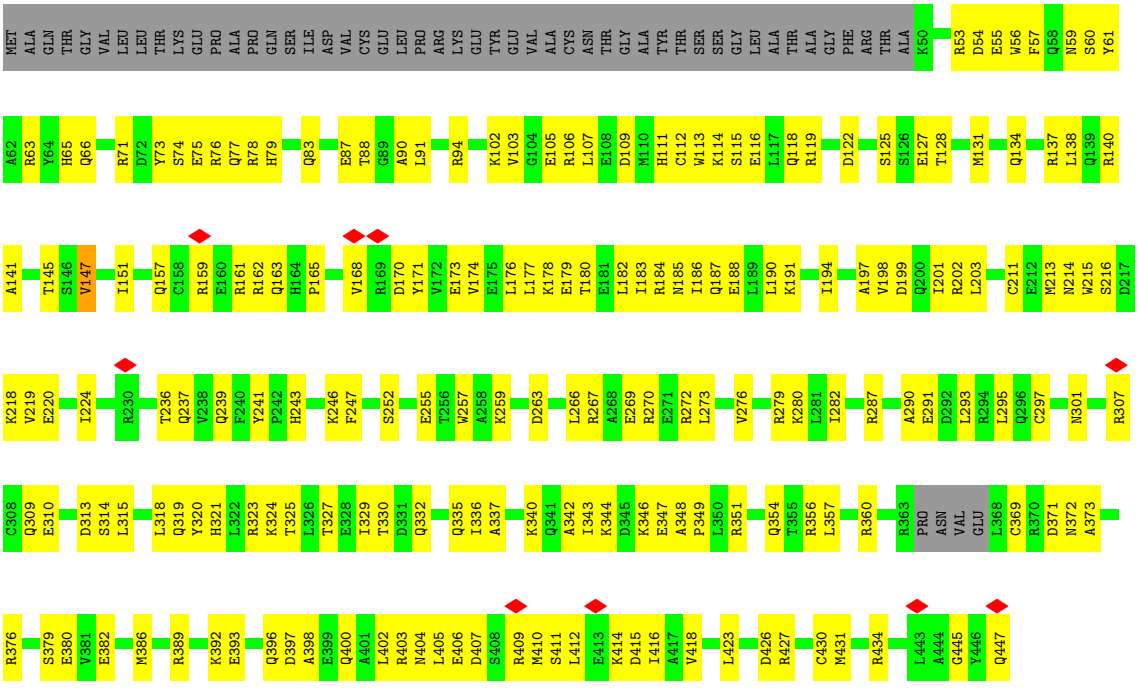
• Molecule 8: Tektin-4

Chain D8:



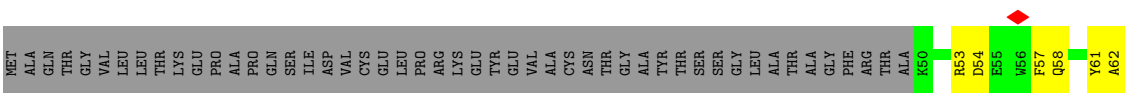
• Molecule 8: Tektin-4

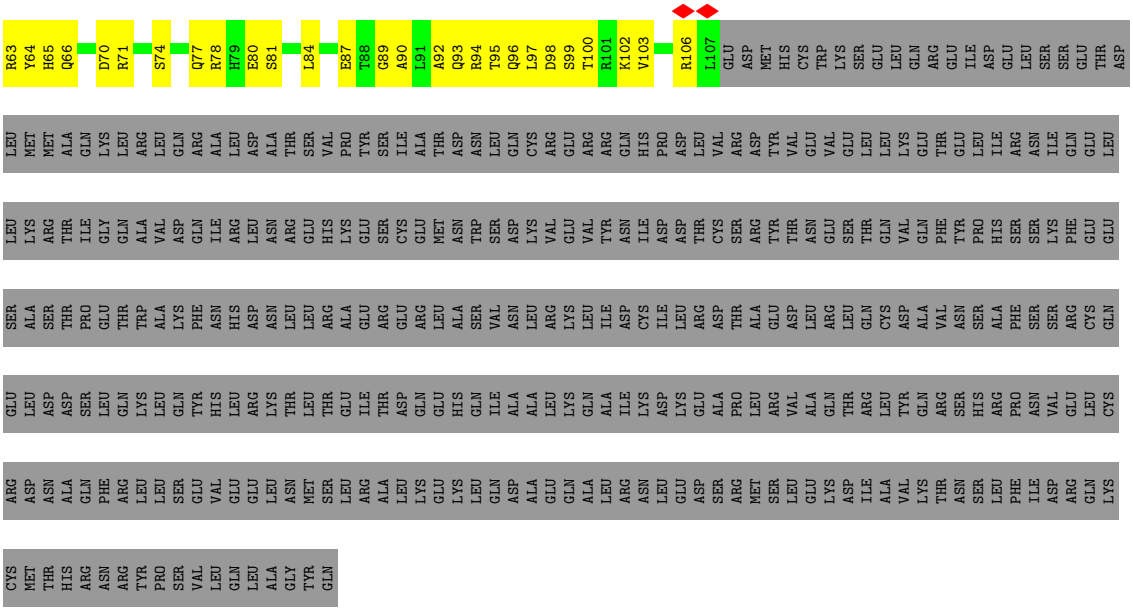
Chain D9:



• Molecule 8: Tektin-4

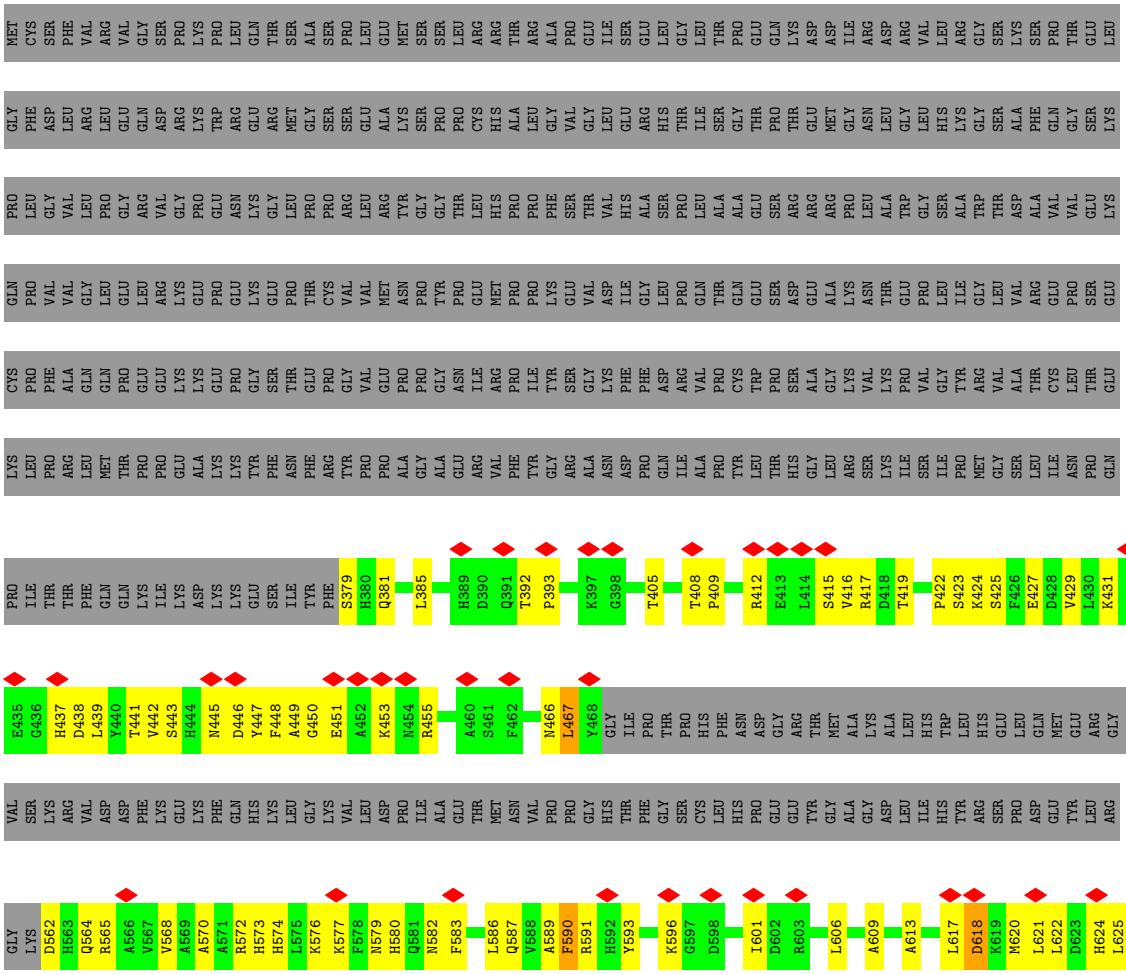
Chain Da:

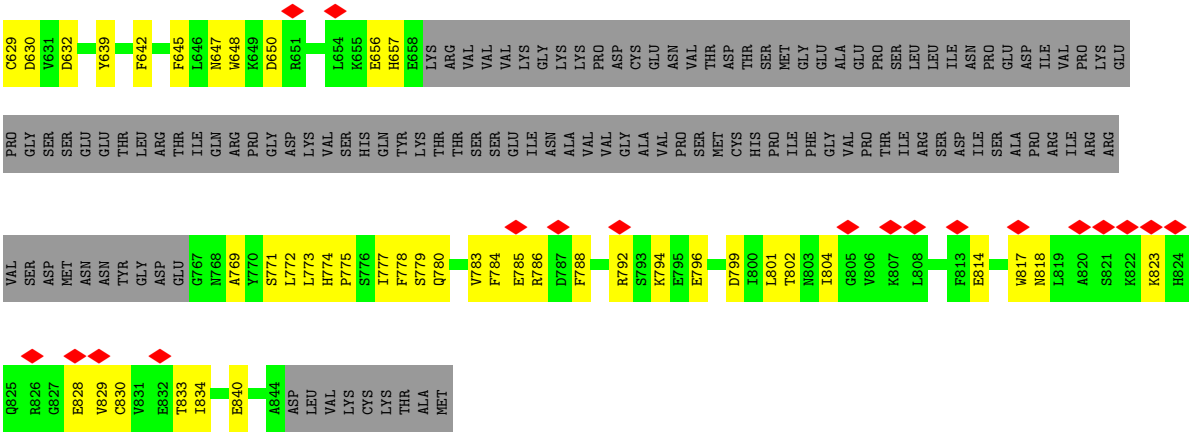




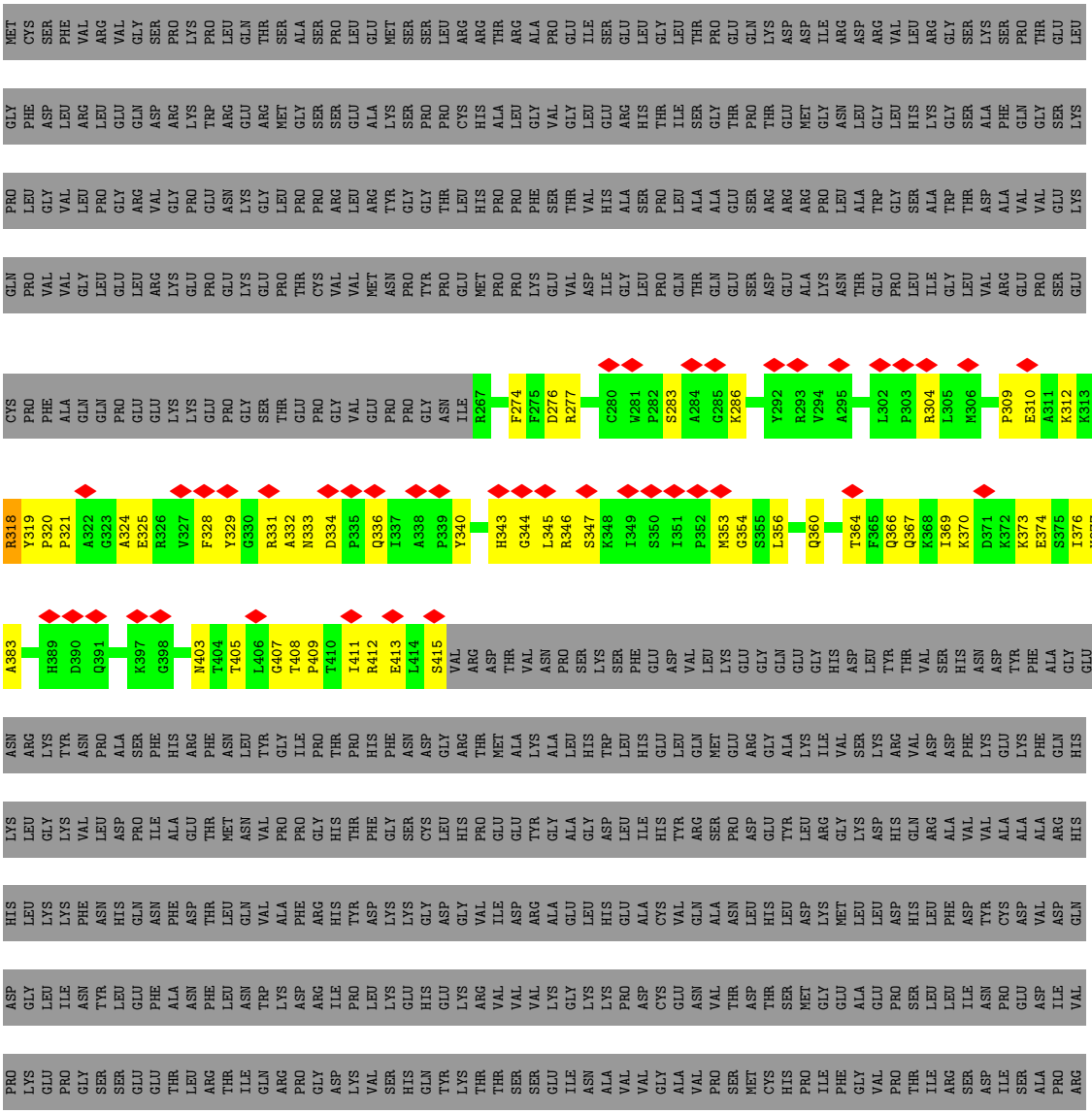
• Molecule 9: EF-hand domain-containing family member B

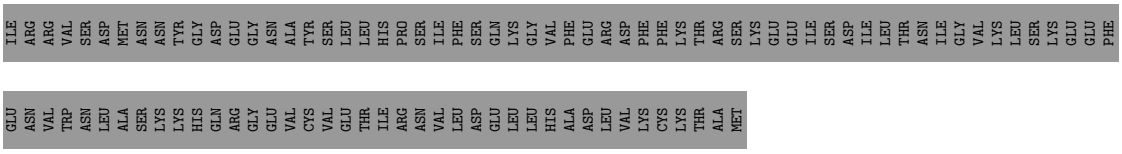
Chain E:





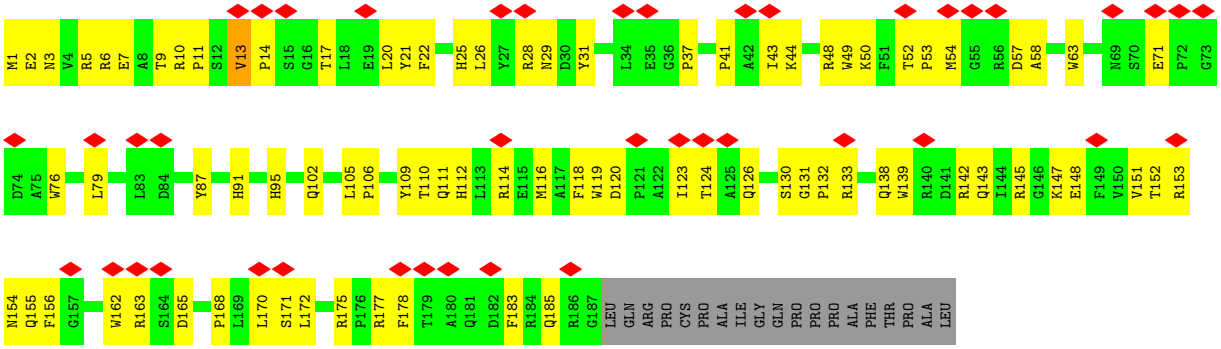
• Molecule 9: EF-hand domain-containing family member B





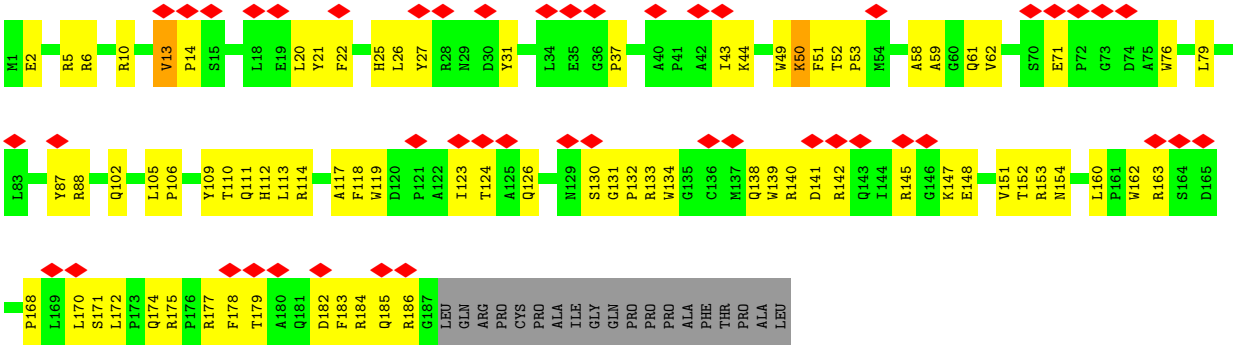
• Molecule 10: Tektin bundle-interacting protein 1

Chain E1:



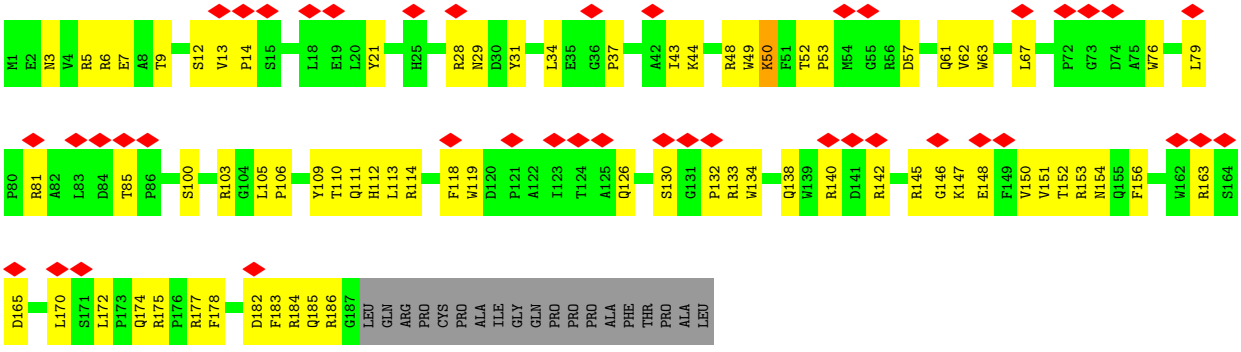
• Molecule 10: Tektin bundle-interacting protein 1

Chain E2:



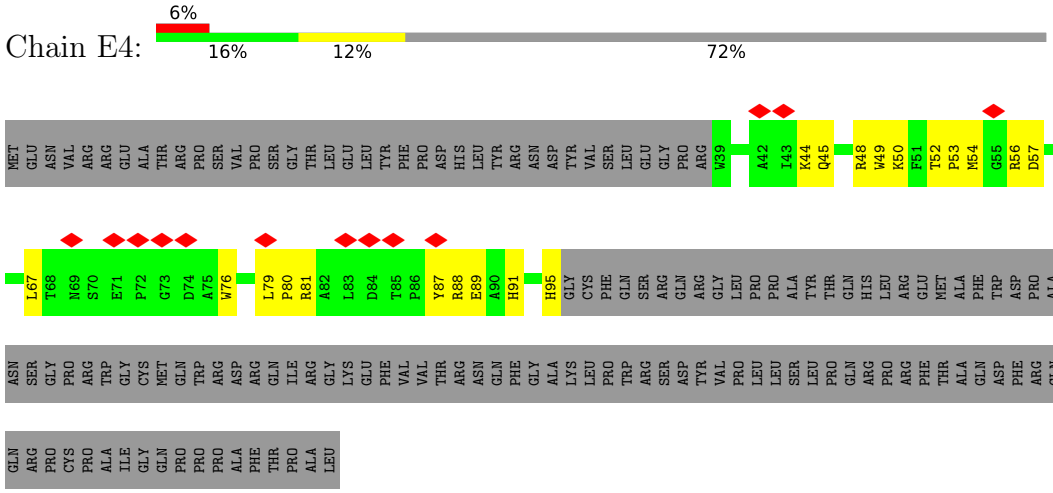
• Molecule 10: Tektin bundle-interacting protein 1

Chain E3:



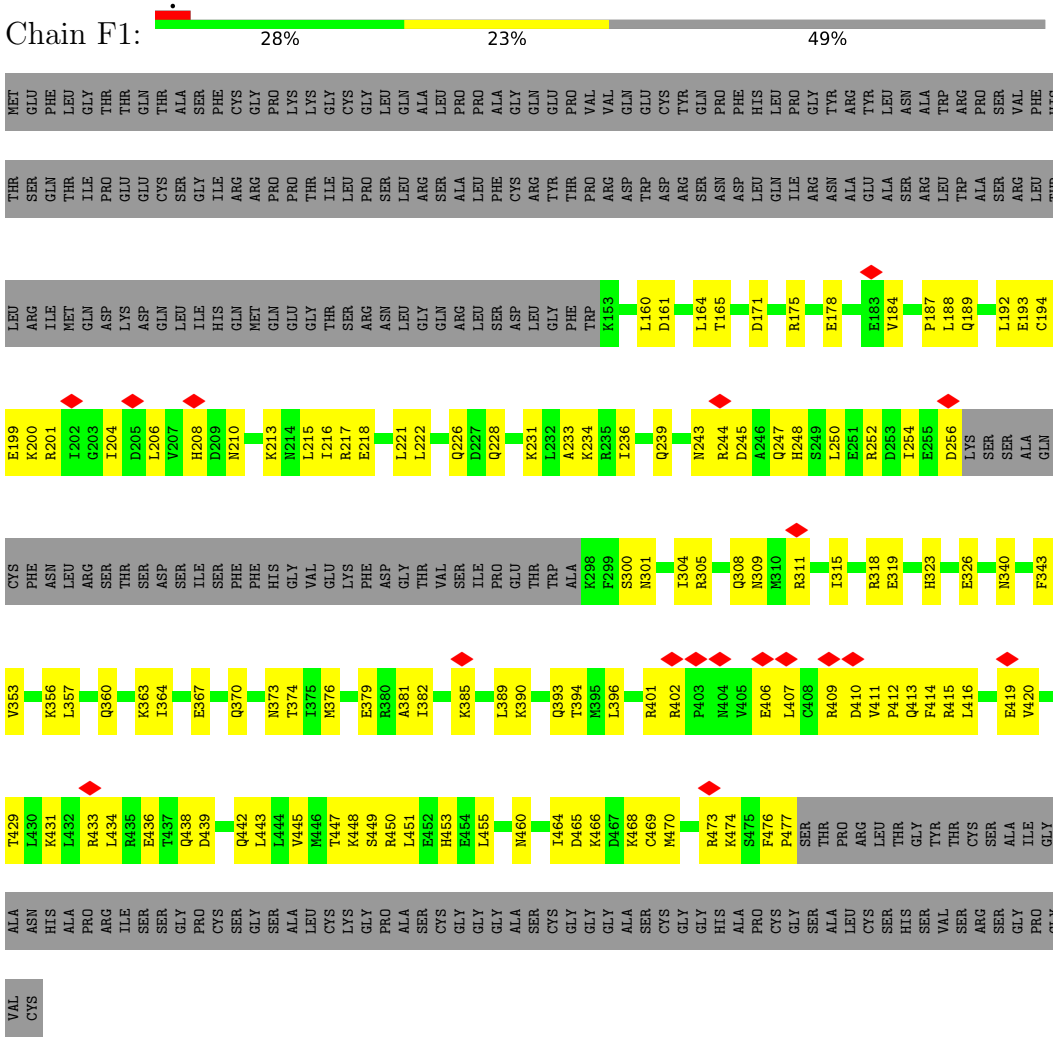
• Molecule 10: Tektin bundle-interacting protein 1

Chain E4:



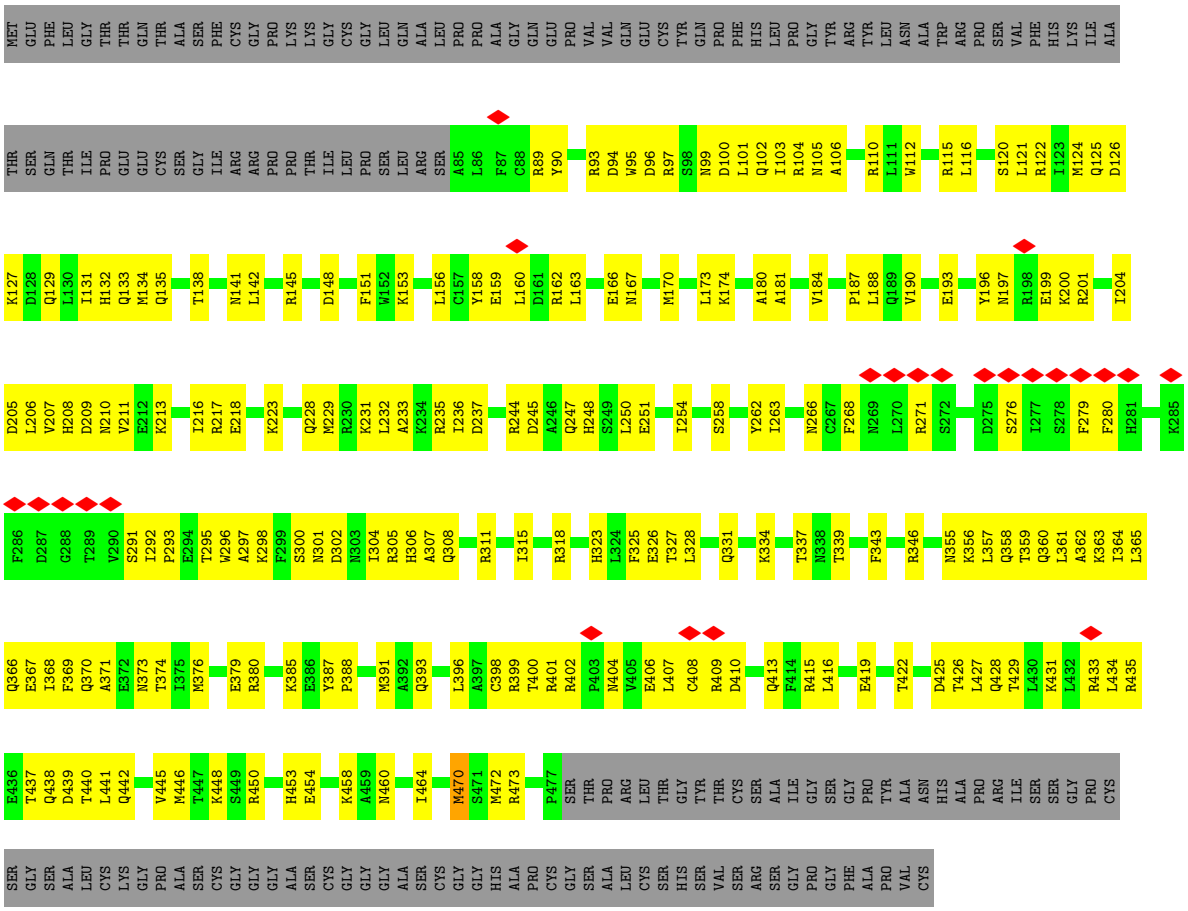
• Molecule 11: Tektin-5

Chain F1:



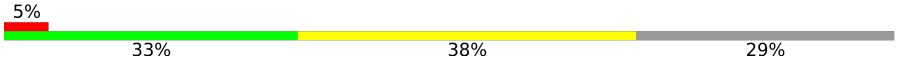
• Molecule 11: Tektin-5

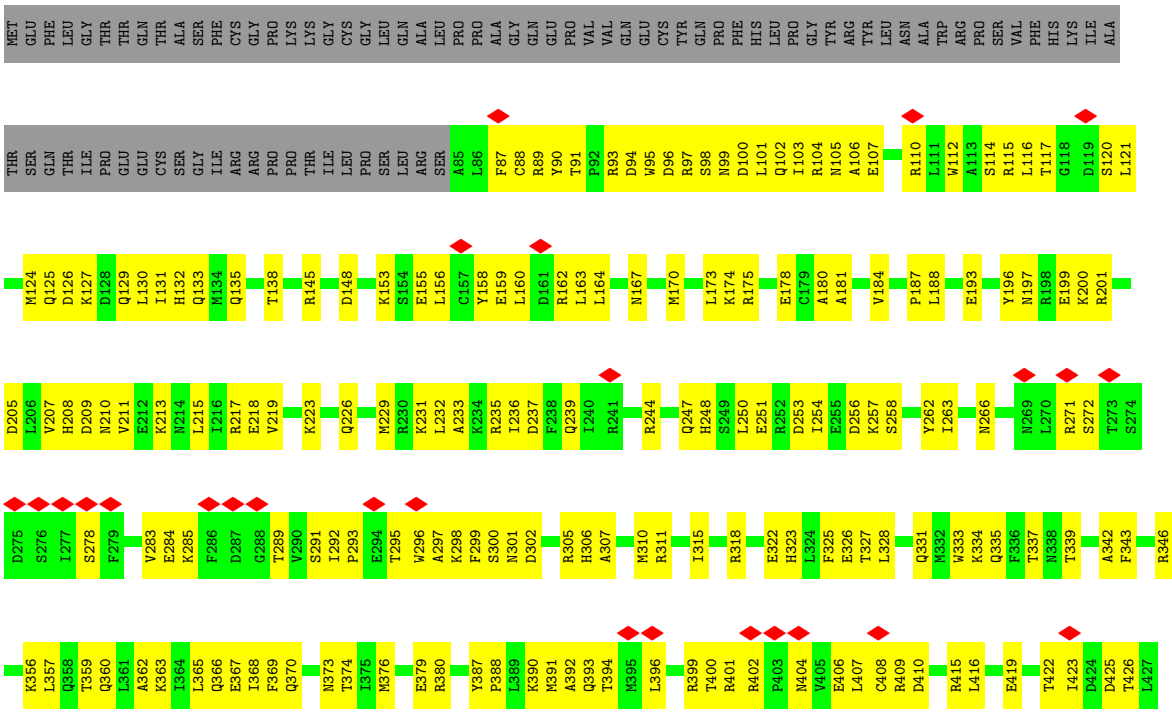
Chain F2:

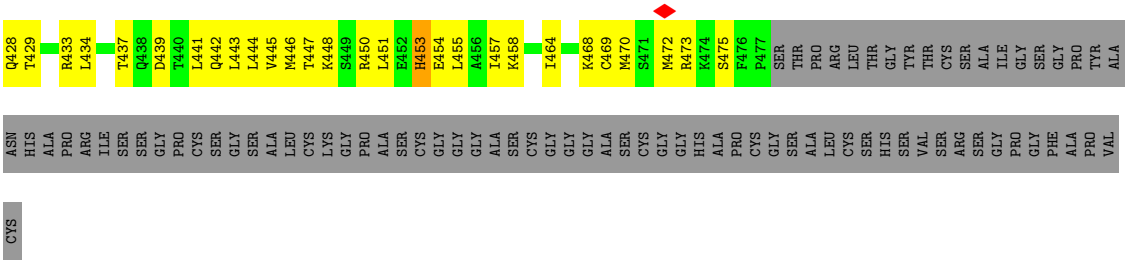


• Molecule 11: Tektin-5

Chain F3:

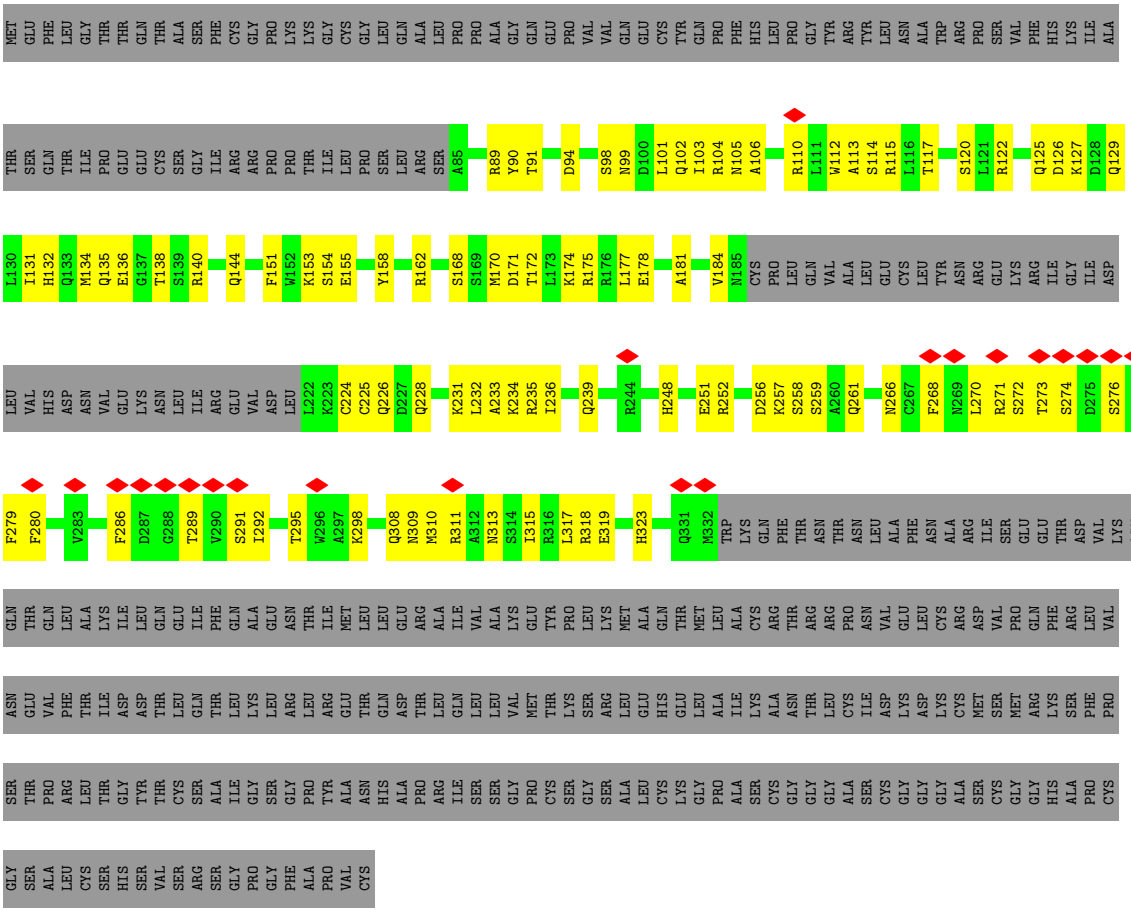






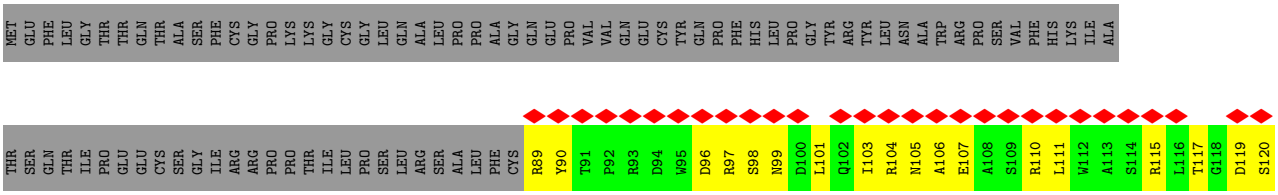
• Molecule 11: Tektin-5

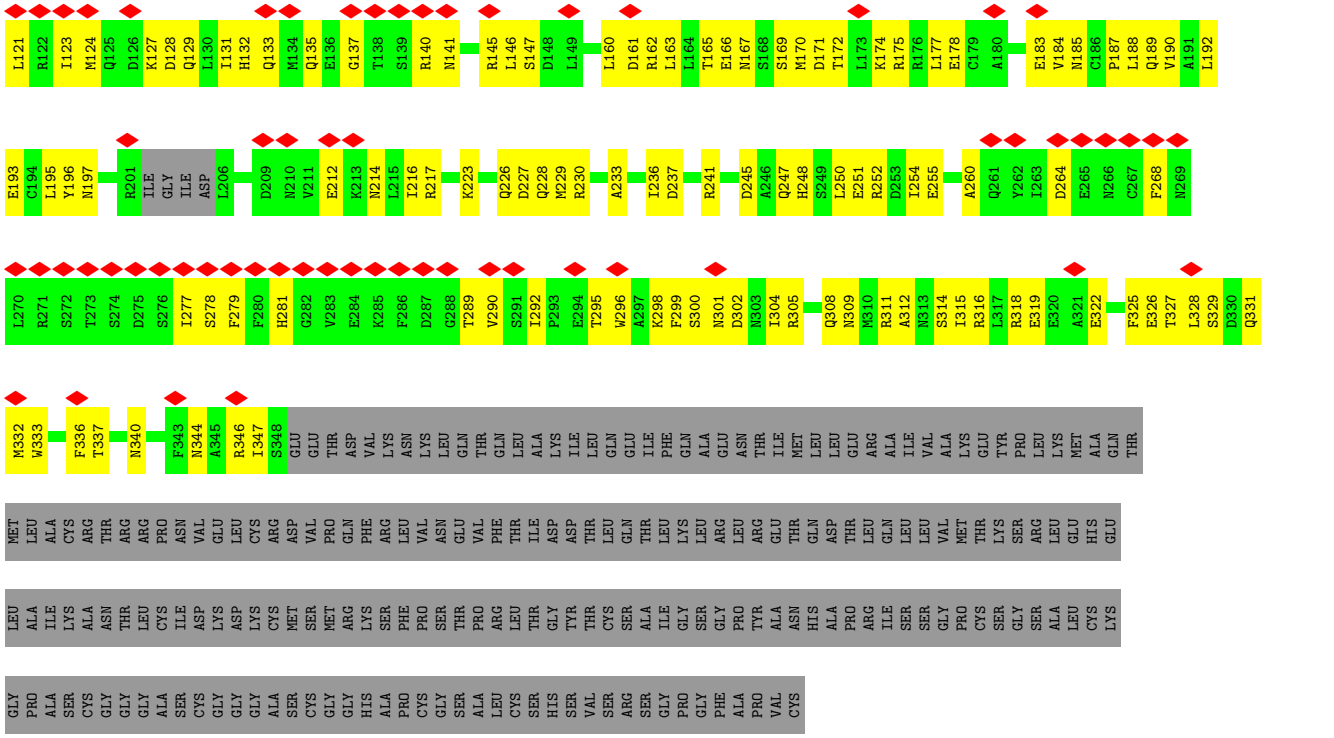
Chain F4:



• Molecule 11: Tektin-5

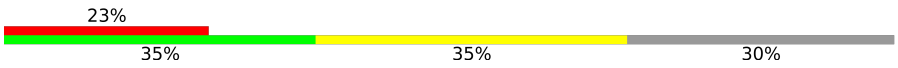
Chain F5:

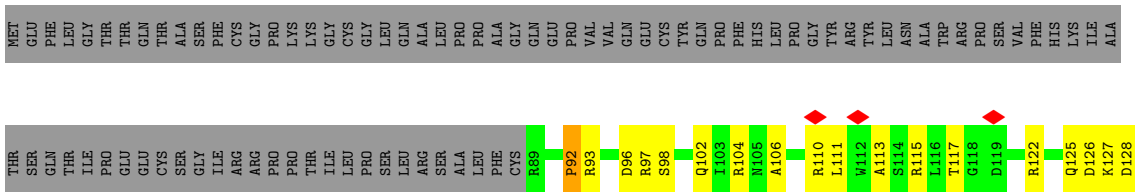


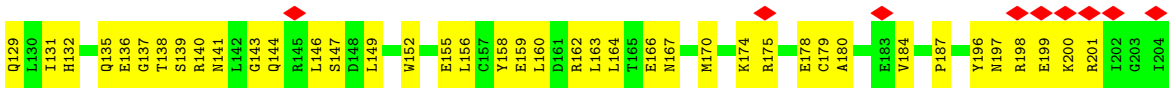


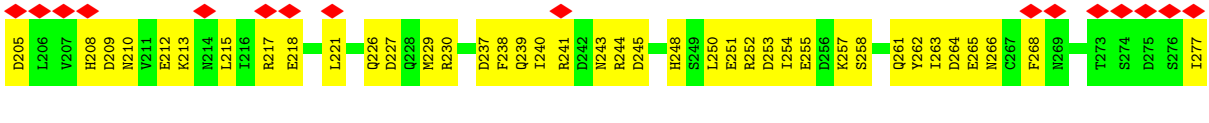
• Molecule 11: Tektin-5

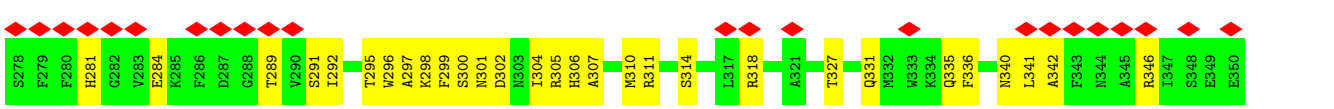
Chain F6:

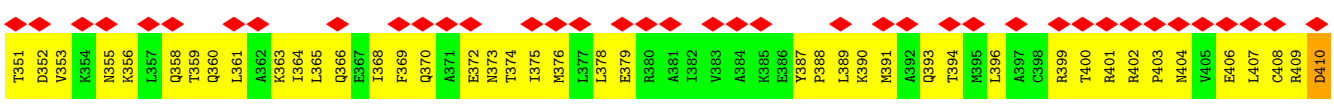


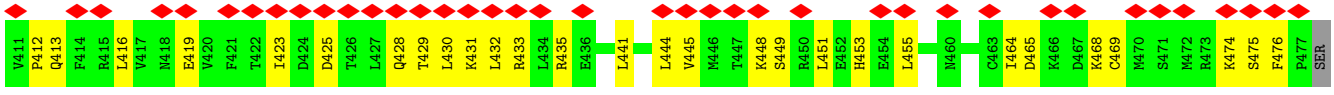


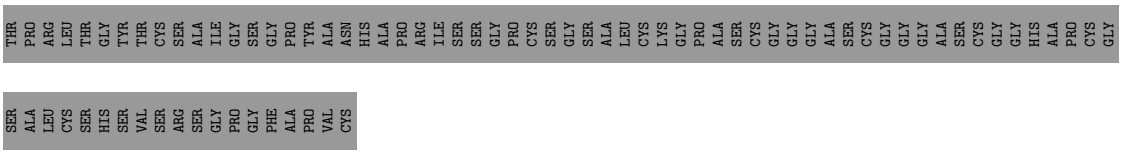






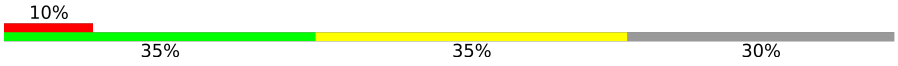


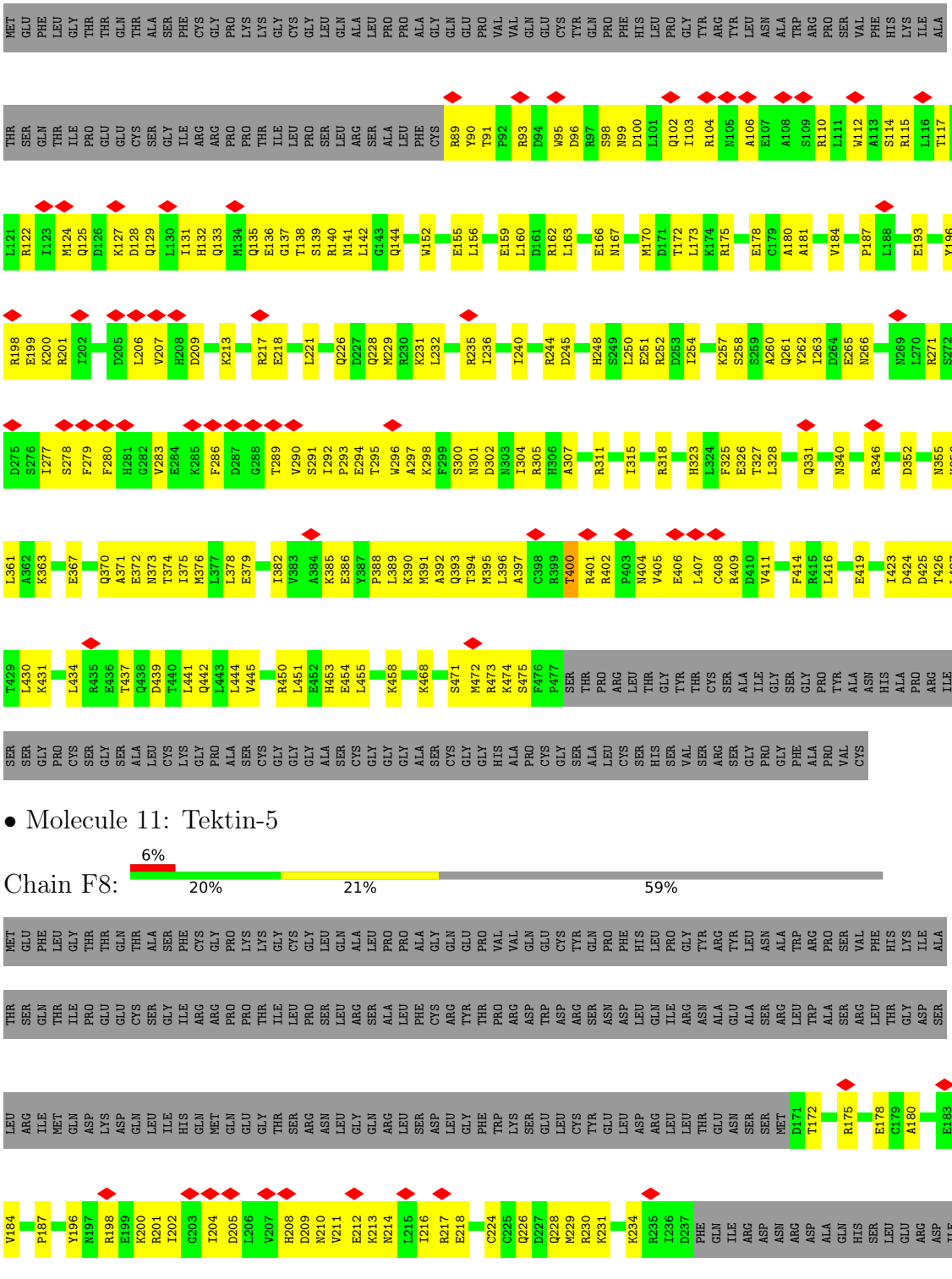




• Molecule 11: Tektin-5

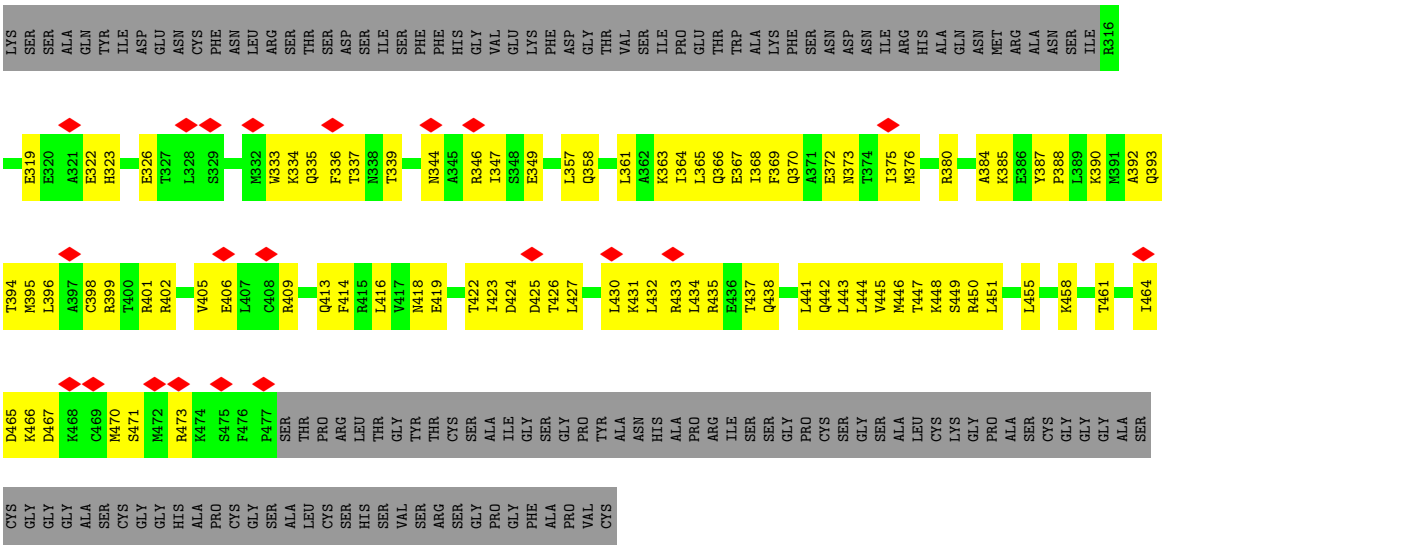
Chain F7:





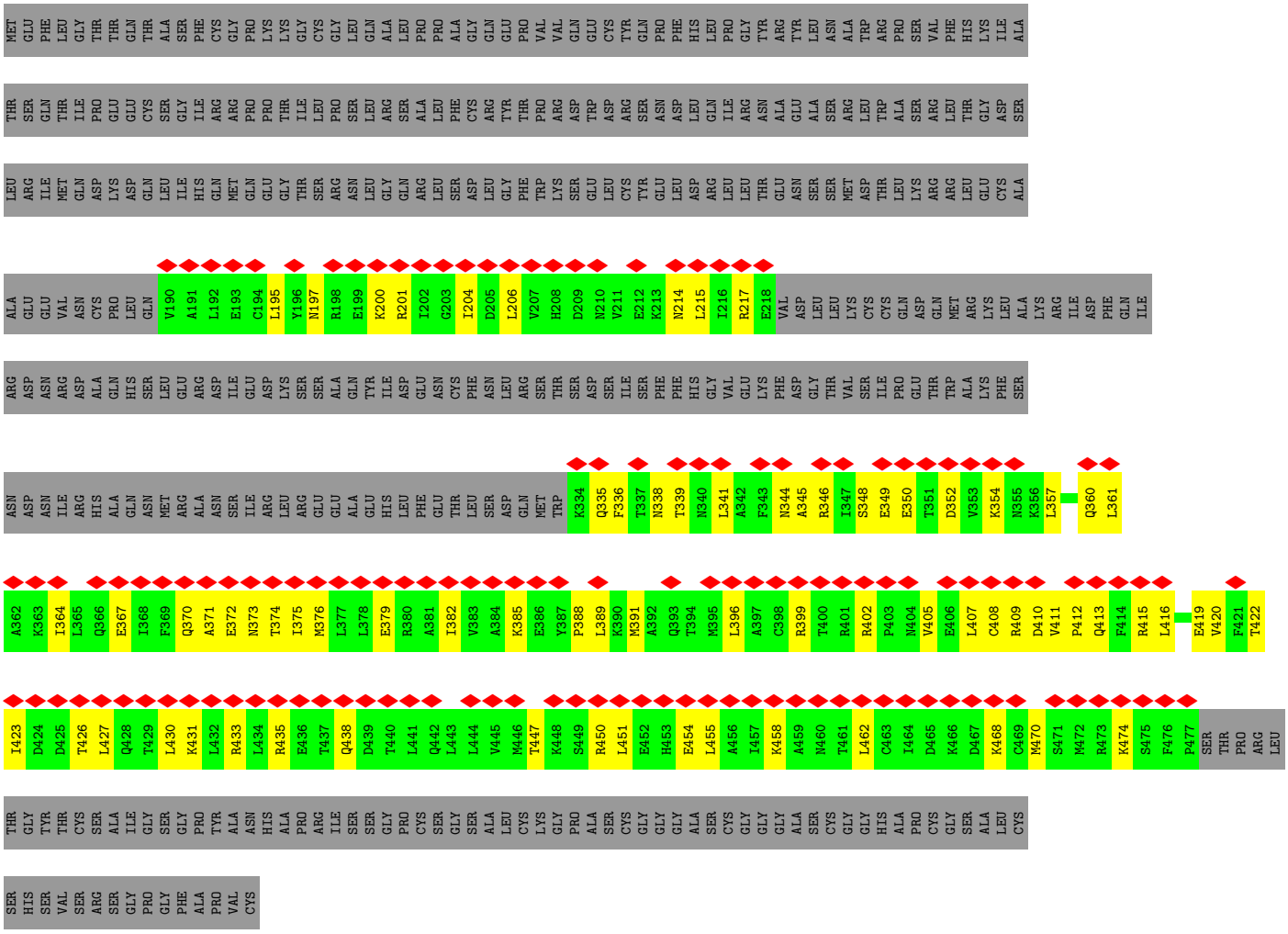
• Molecule 11: Tektin-5

Chain F8:



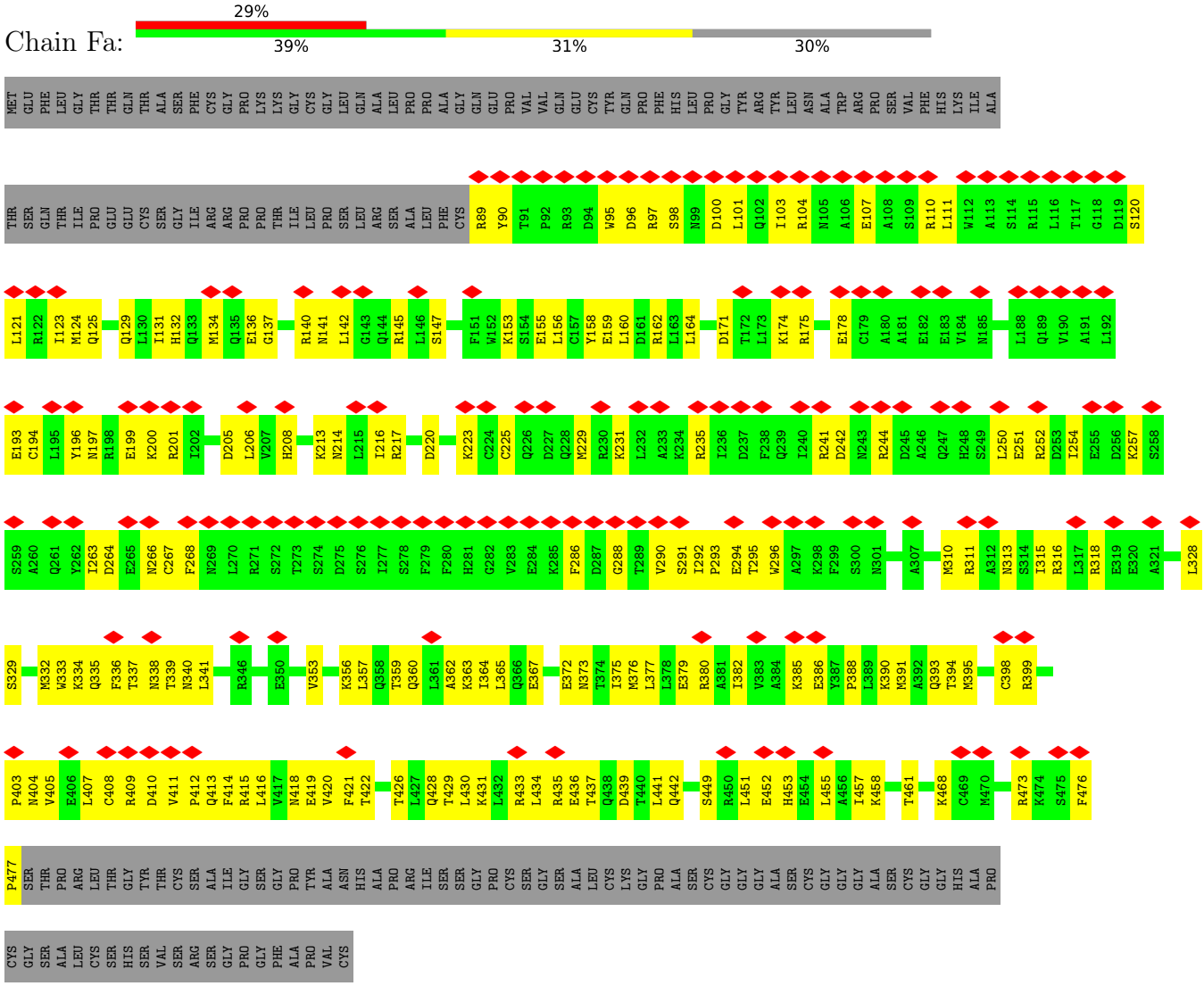
• Molecule 11: Tektin-5

Chain F9:



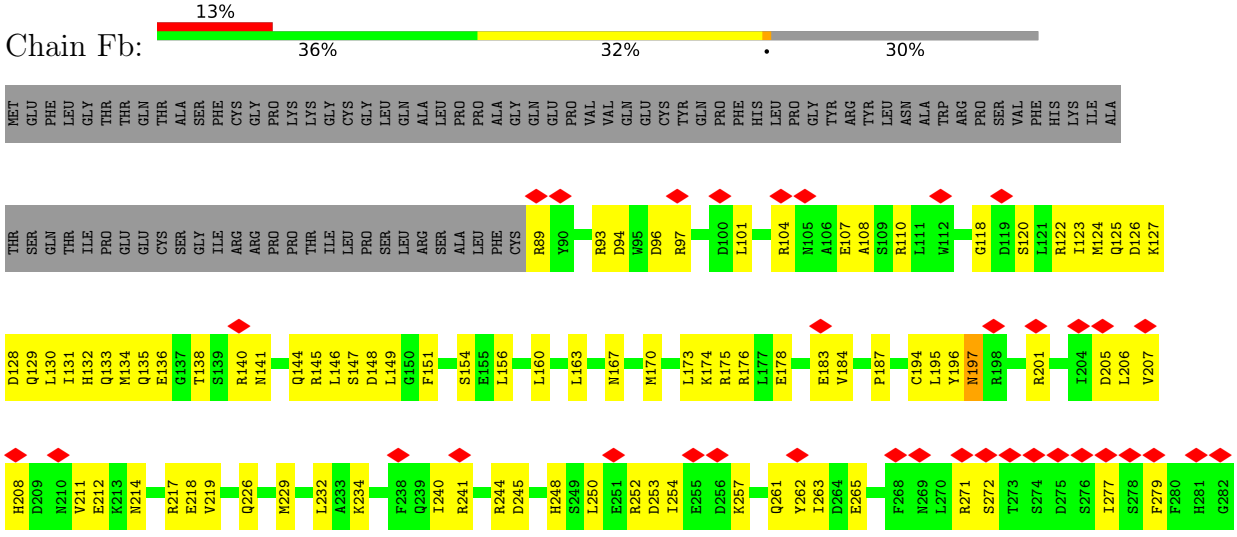
• Molecule 11: Tektin-5

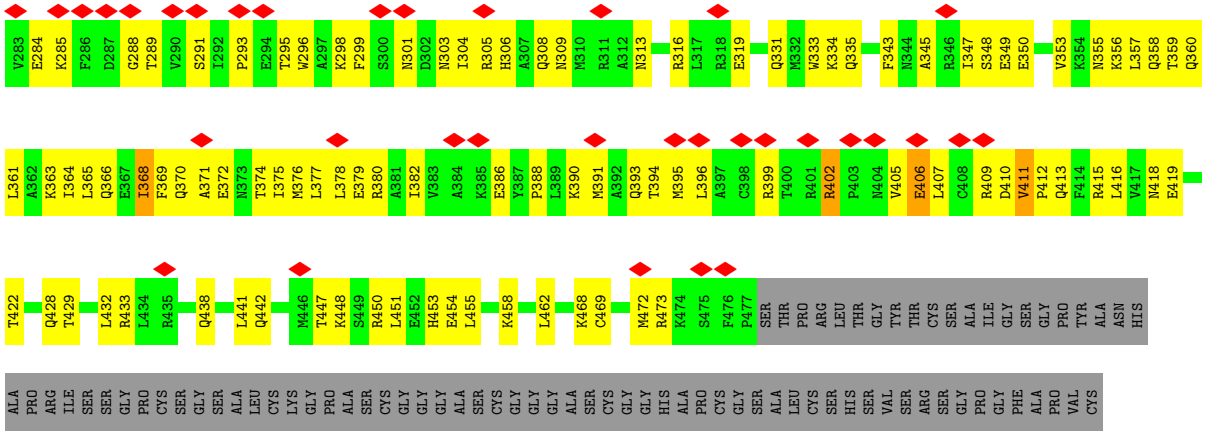
Chain Fa:



• Molecule 11: Tektin-5

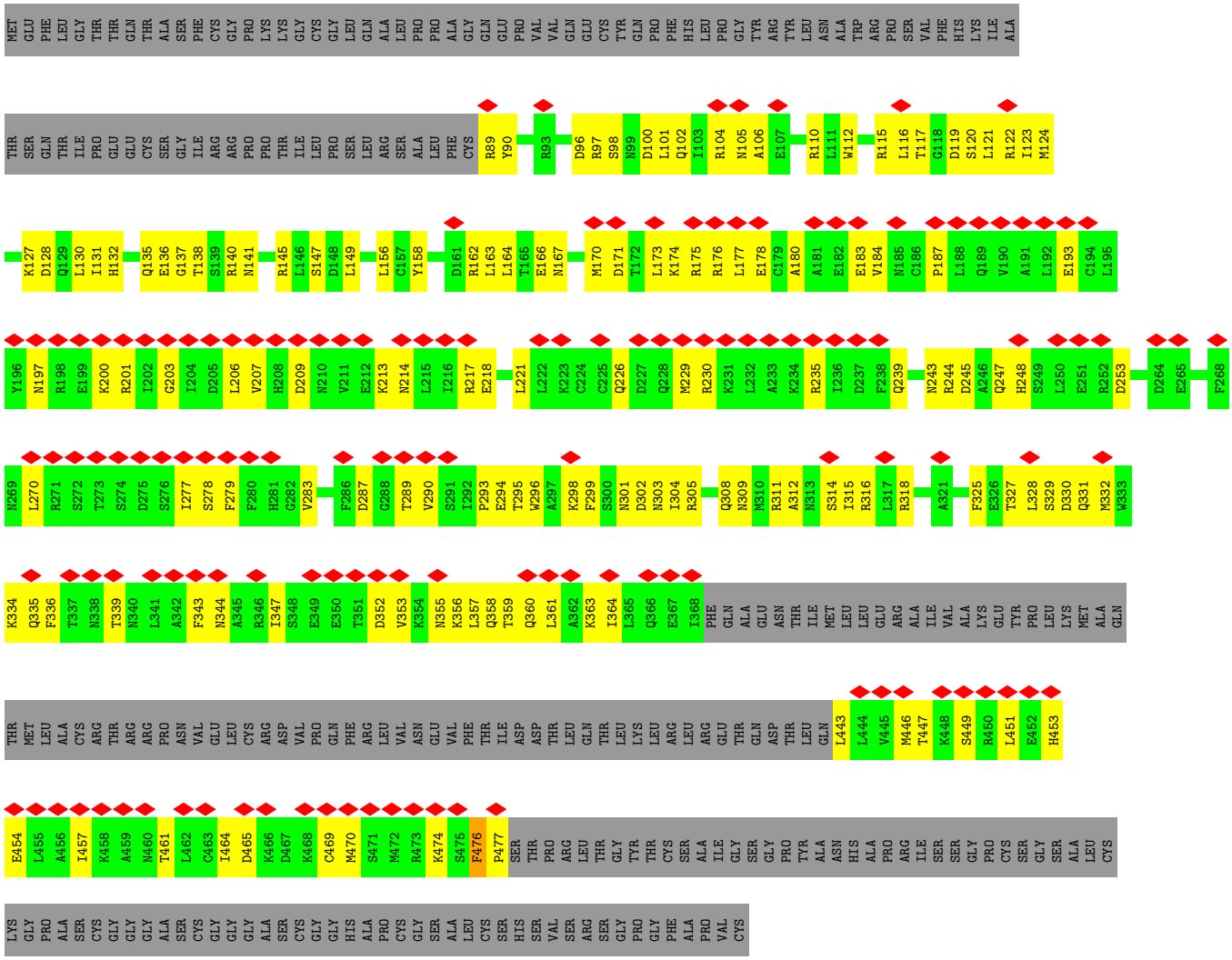
Chain Fb:





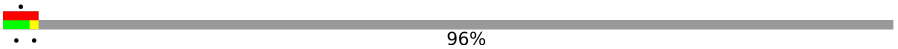
• Molecule 11: Tektin-5

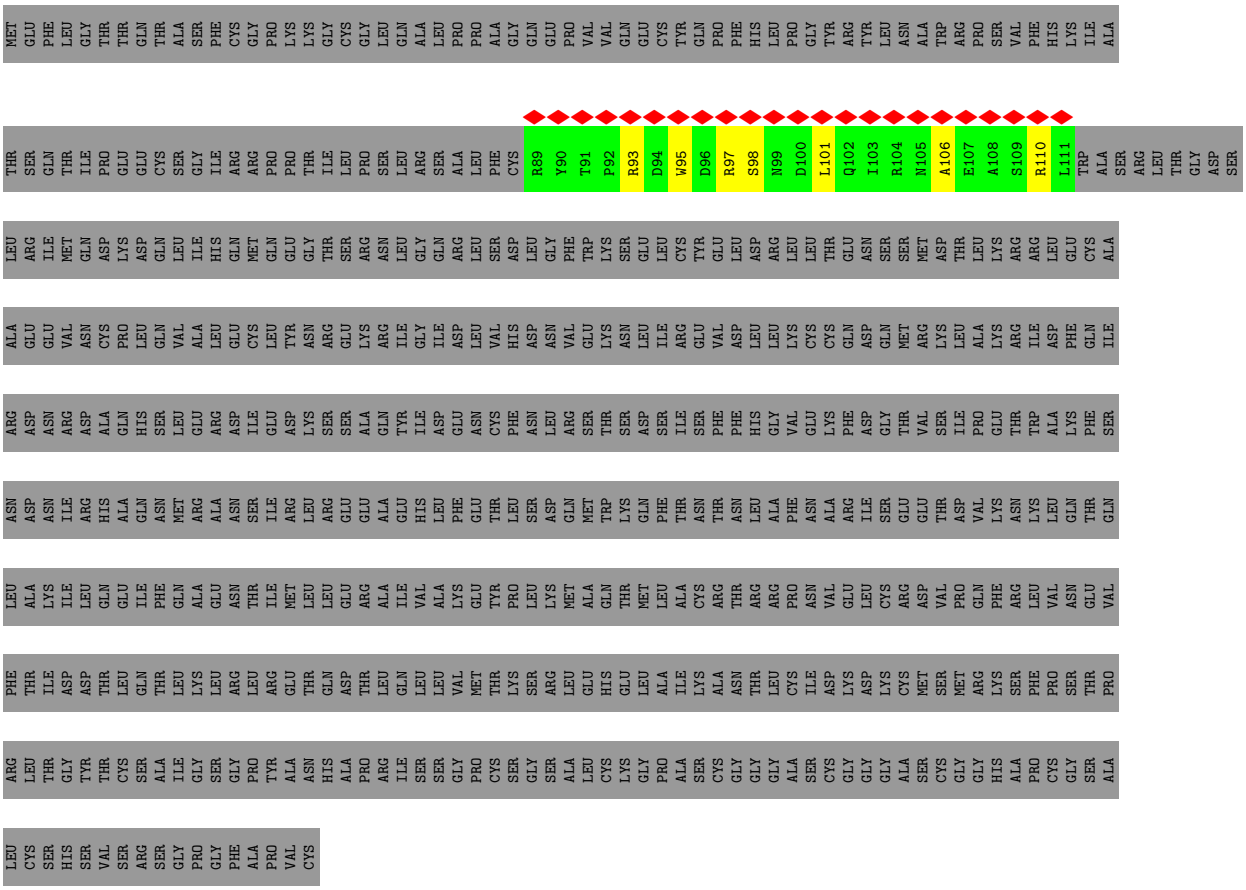
Chain Fc:



• Molecule 11: Tektin-5

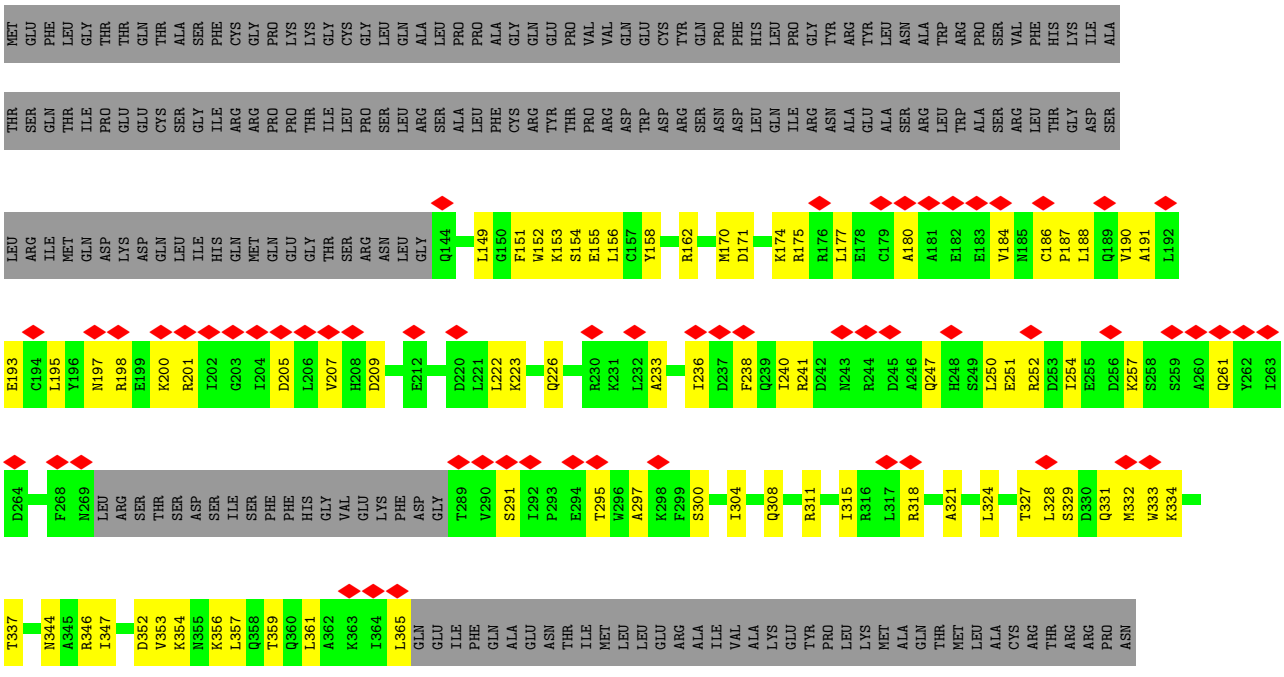
Chain Fd:

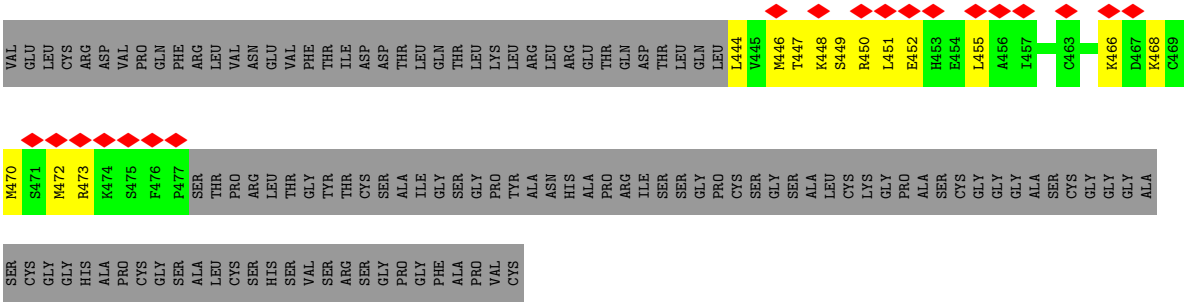




• Molecule 11: Tektin-5

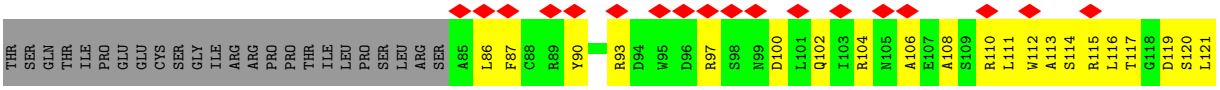
Chain Fe:

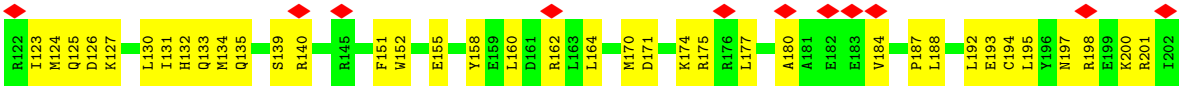


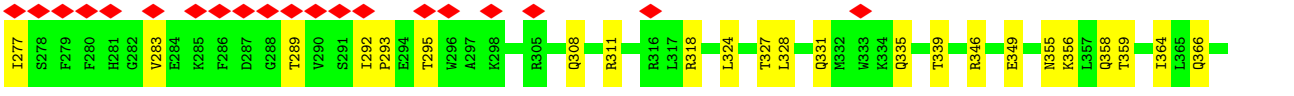


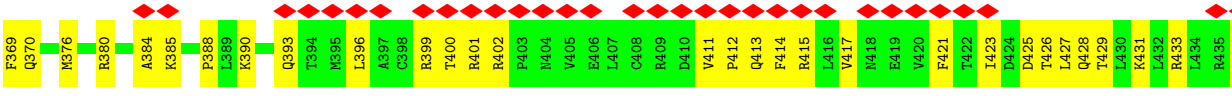
• Molecule 11: Tektin-5

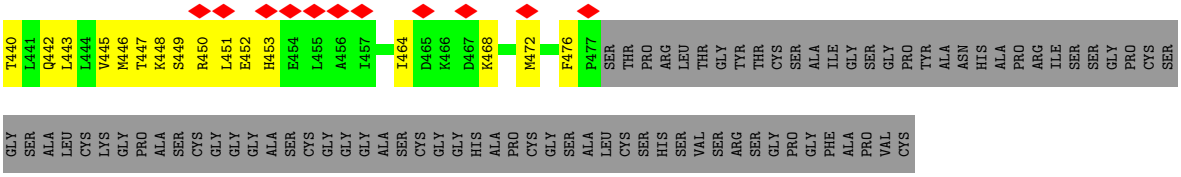
Chain Ff:





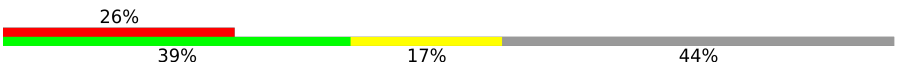


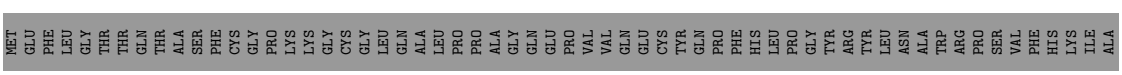


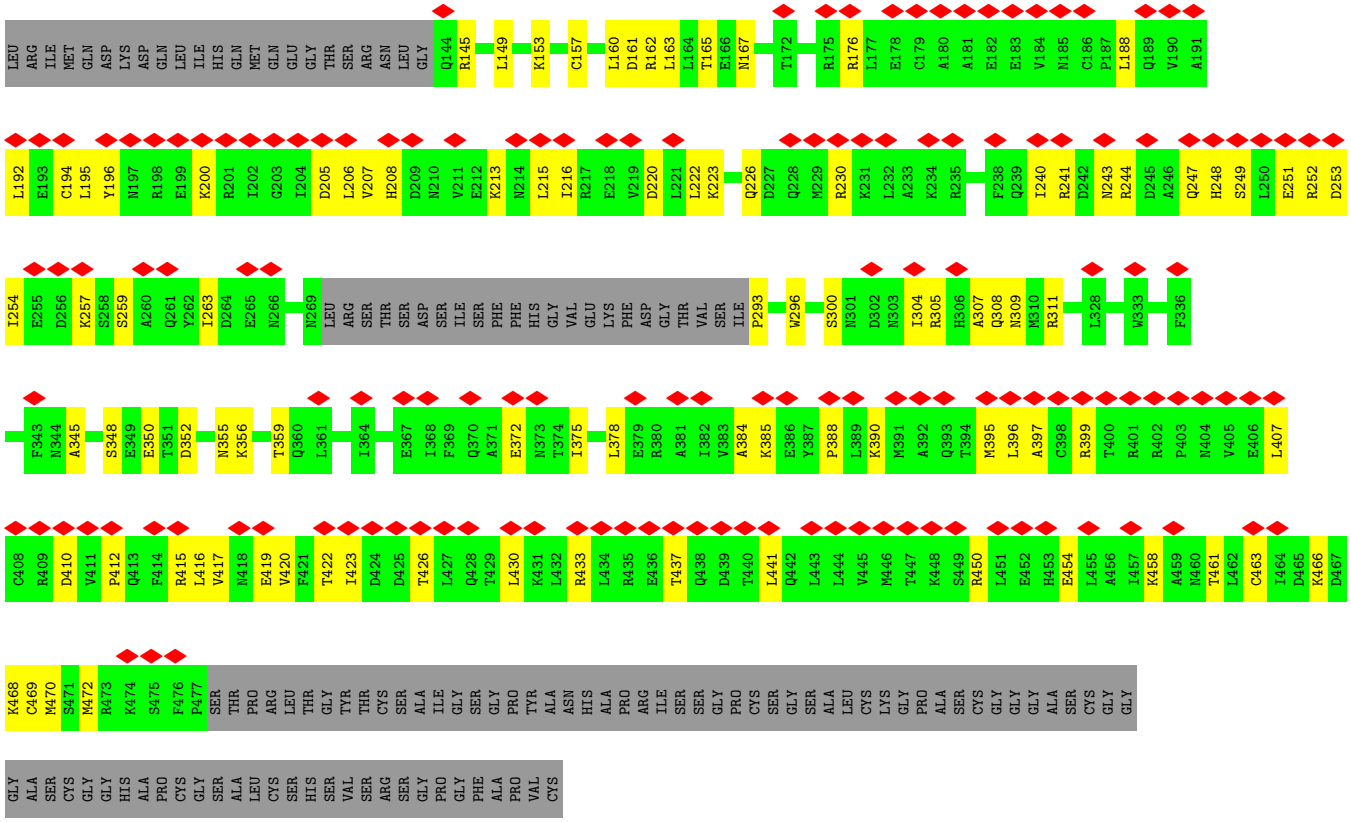


• Molecule 11: Tektin-5

Chain Fg:

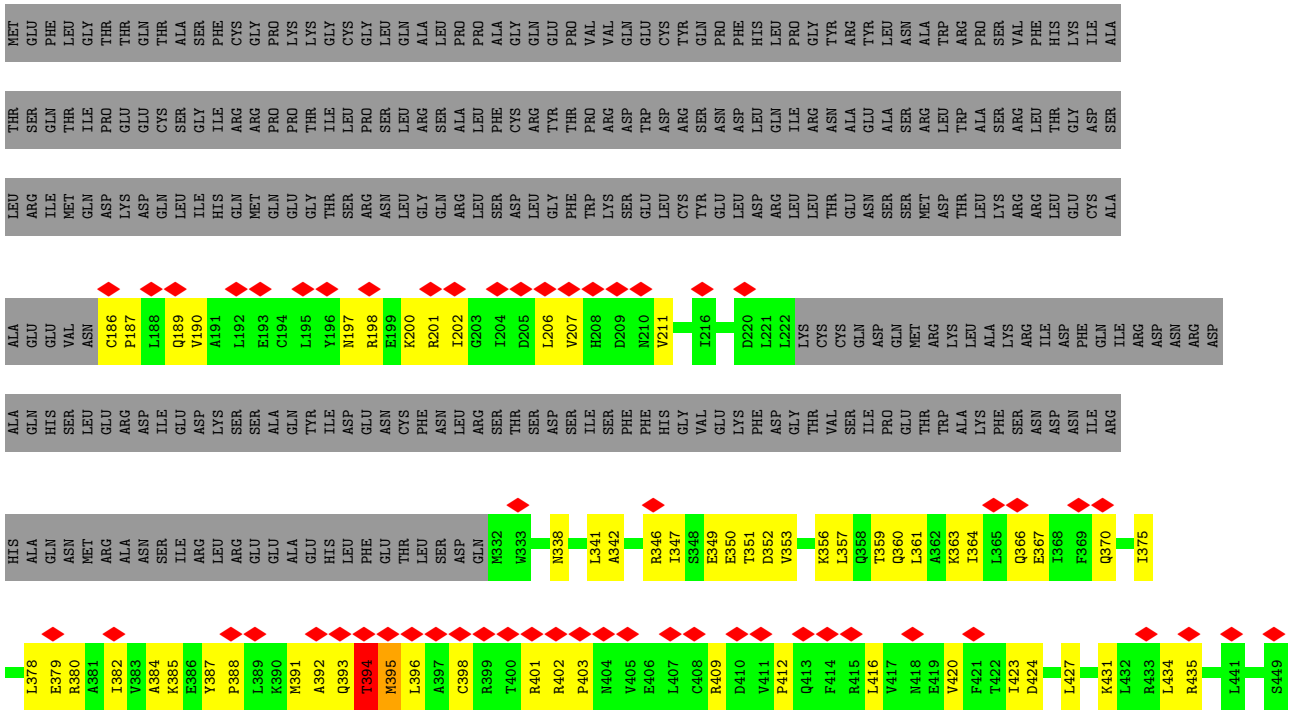


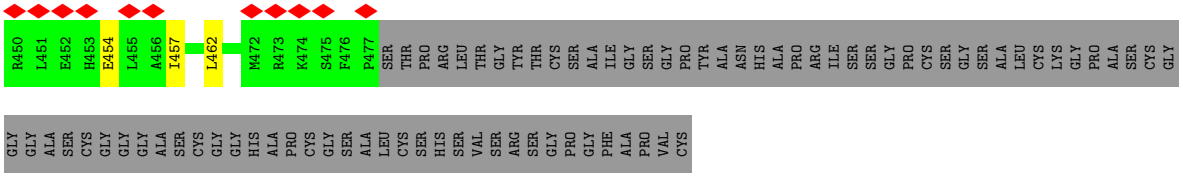




• Molecule 11: Tektin-5

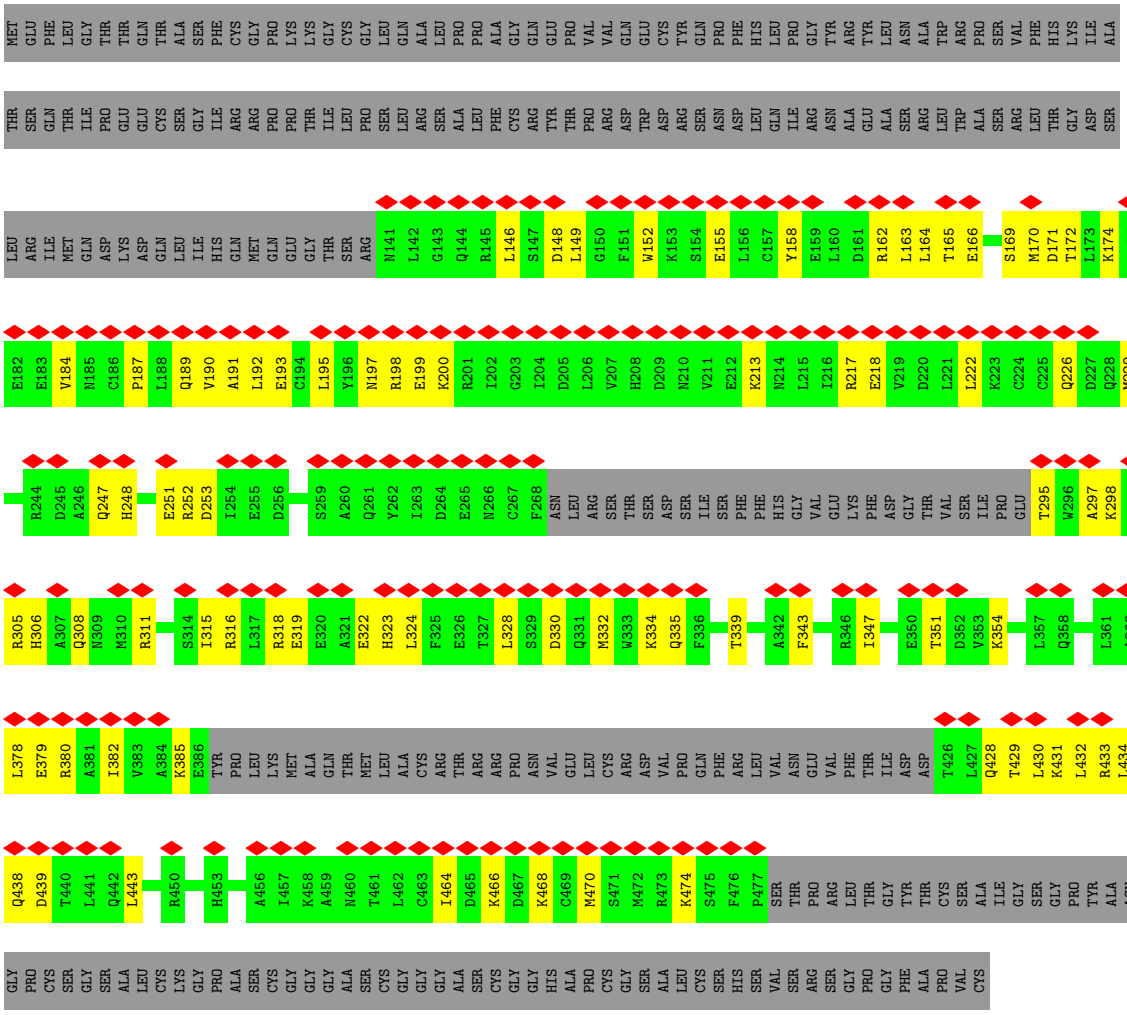
Chain Fh:





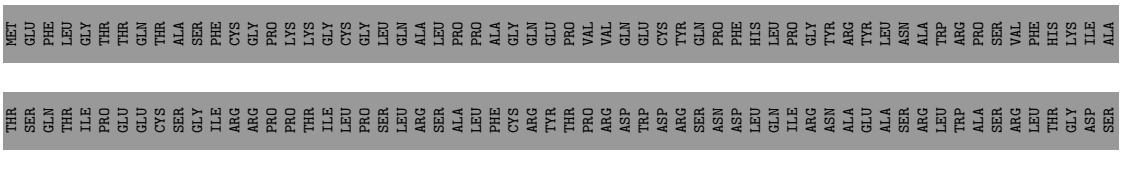
• Molecule 11: Tektin-5

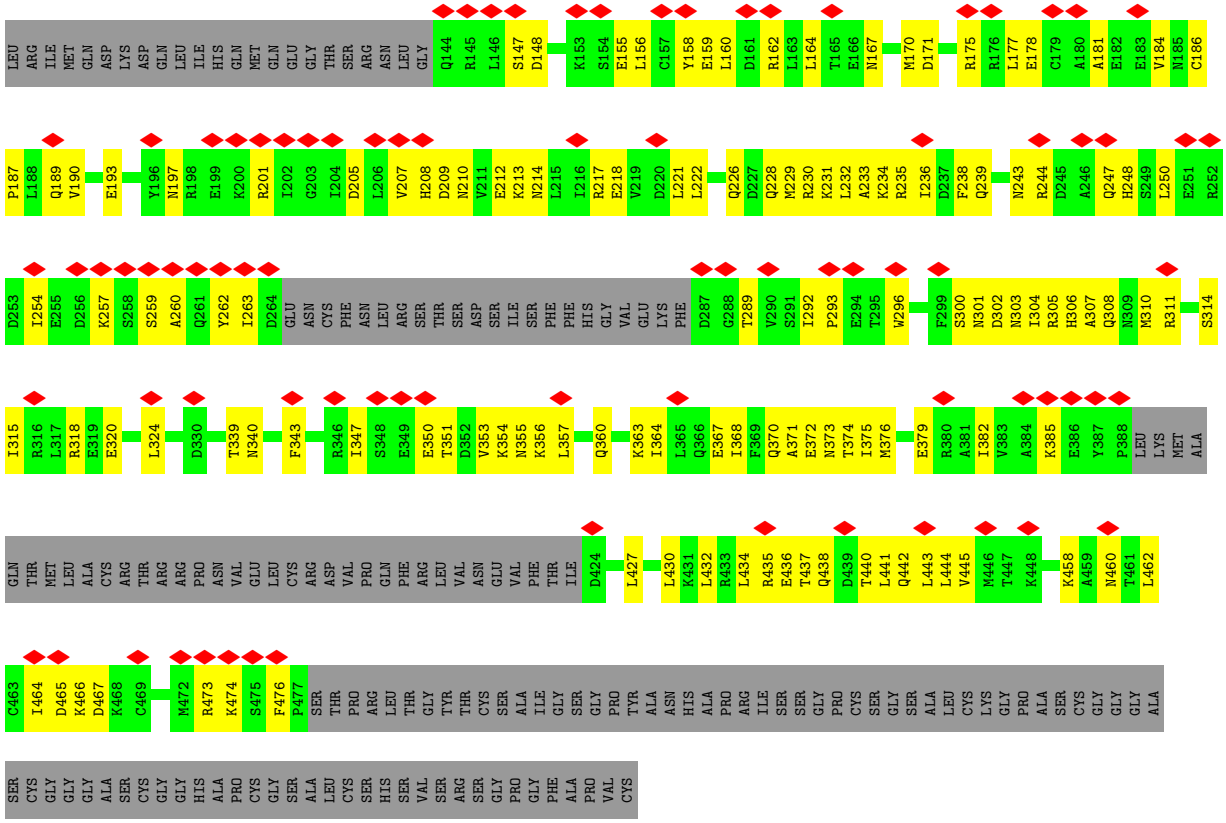
Chain Fi:



• Molecule 11: Tektin-5

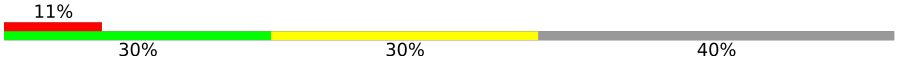
Chain Fj:

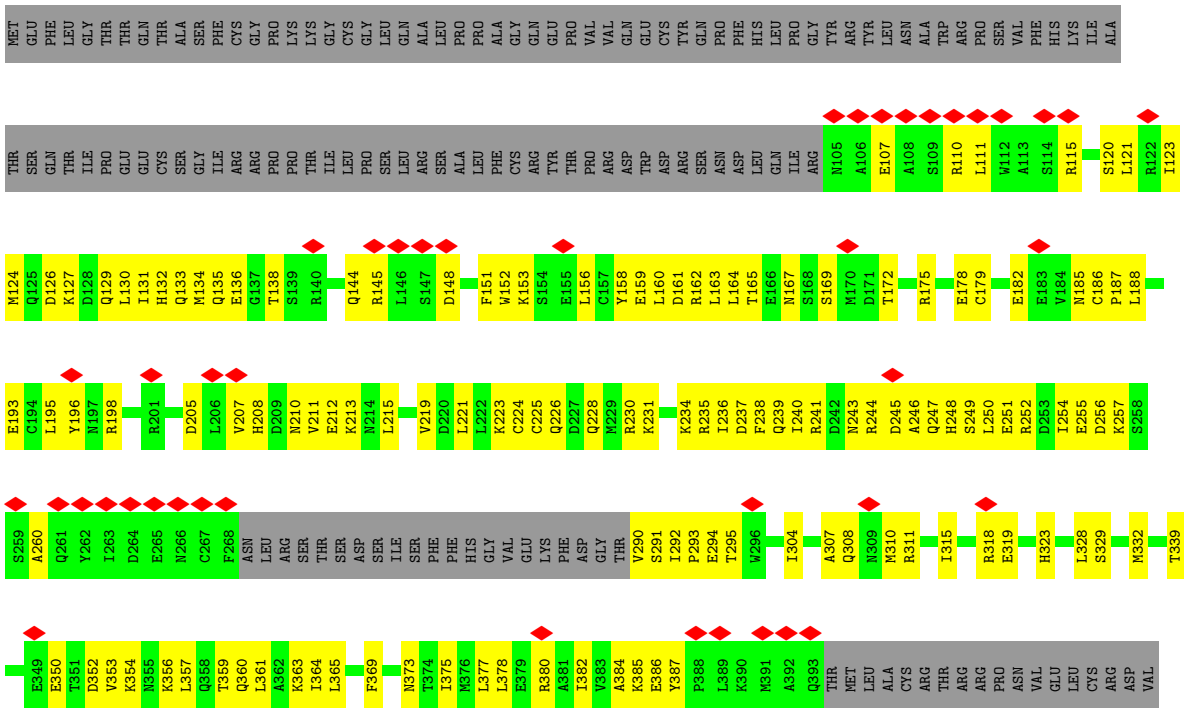


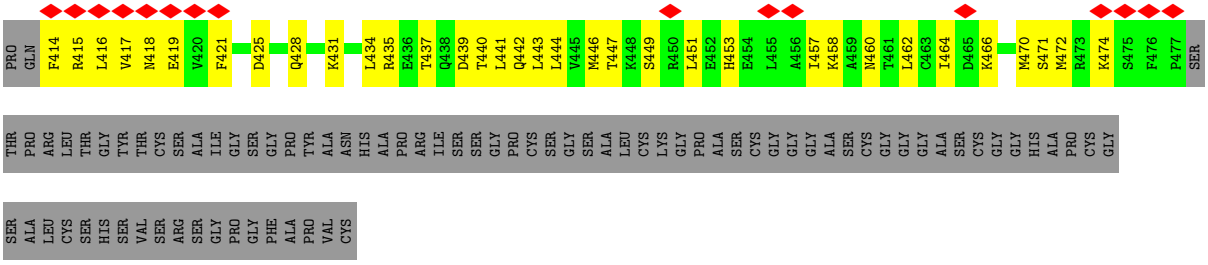


• Molecule 11: Tektin-5

Chain Fk:

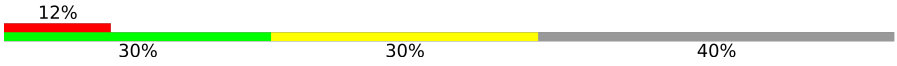


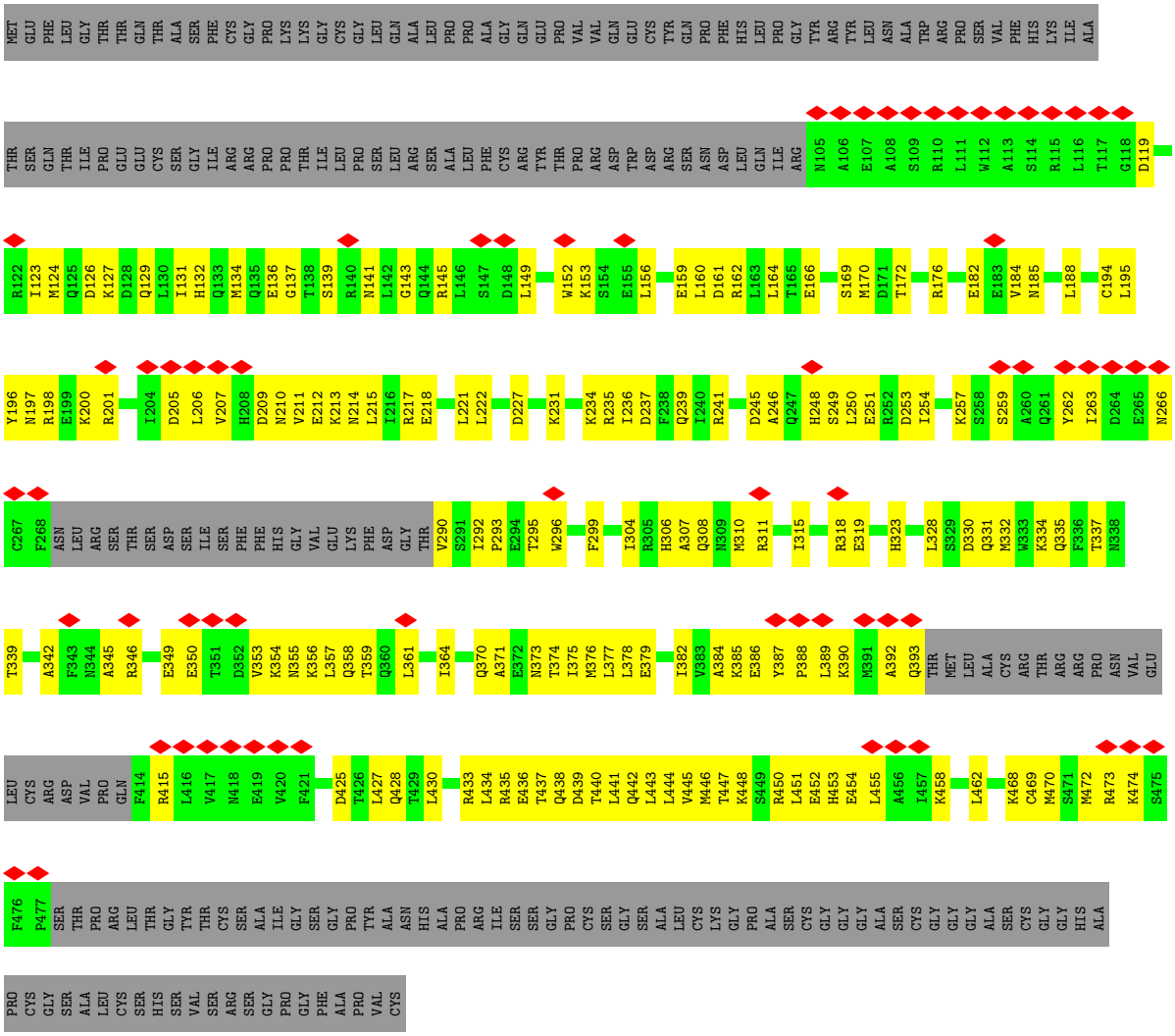




• Molecule 11: Tektin-5

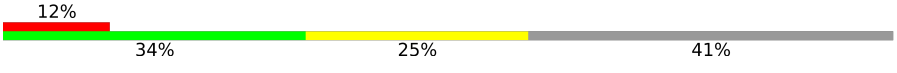
Chain Fl:

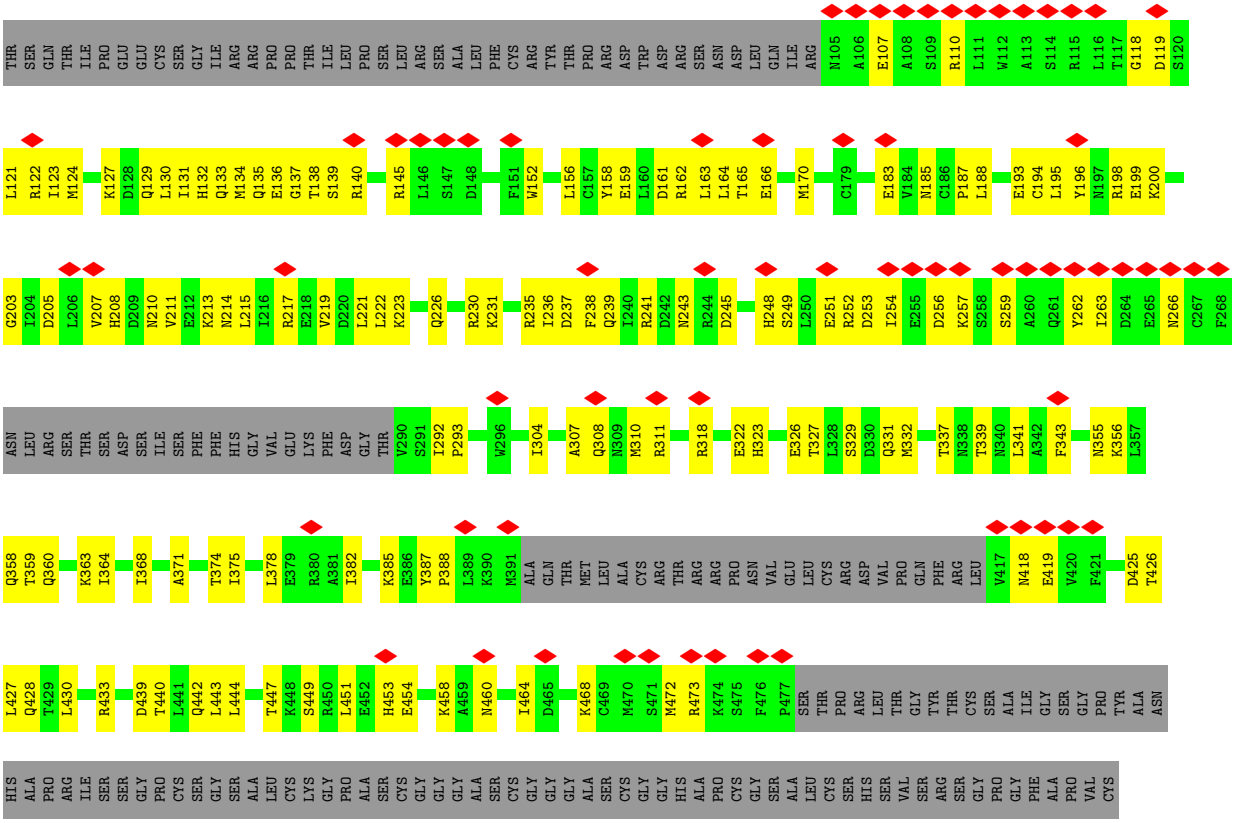




• Molecule 11: Tektin-5

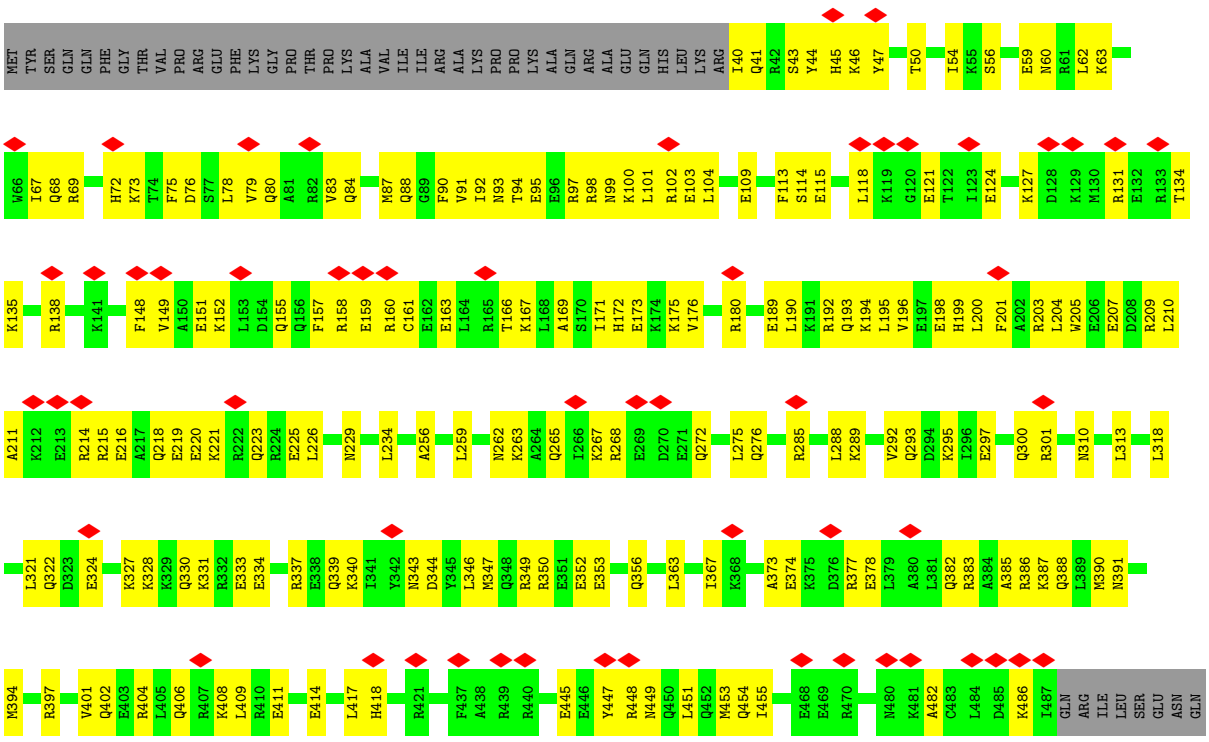
Chain Fm:





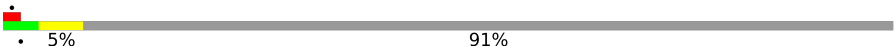
• Molecule 12: Cilia- and flagella-associated protein 53

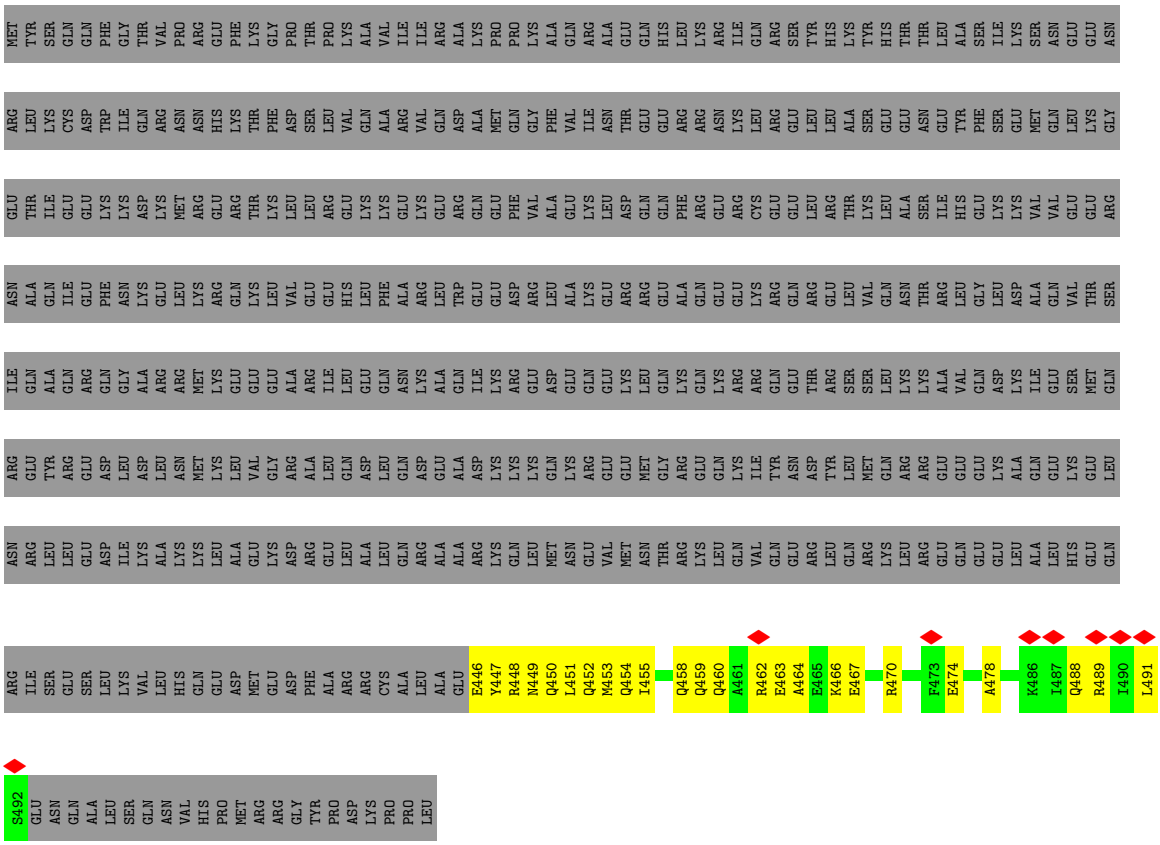
Chain G:



• Molecule 12: Cilia- and flagella-associated protein 53

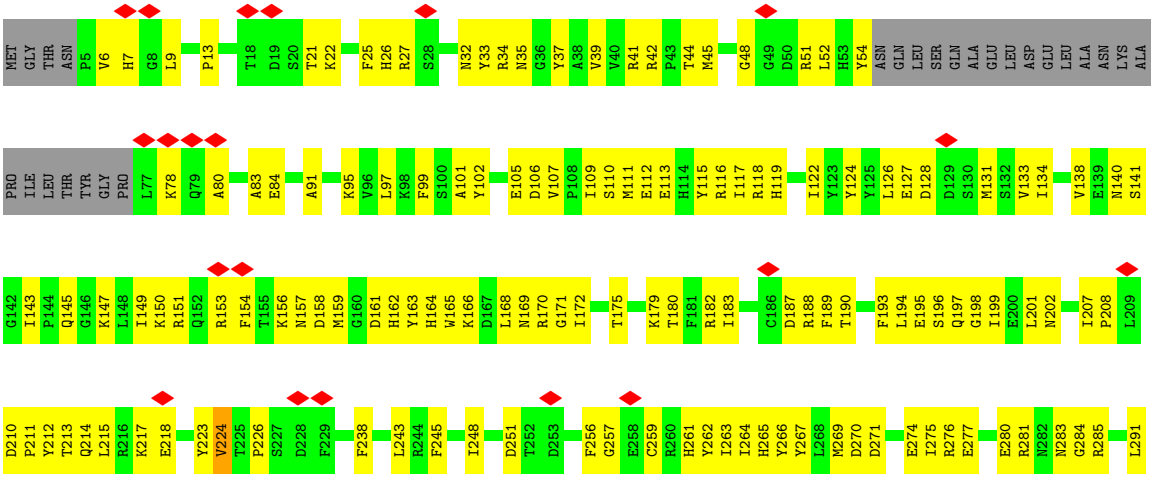
Chain H:

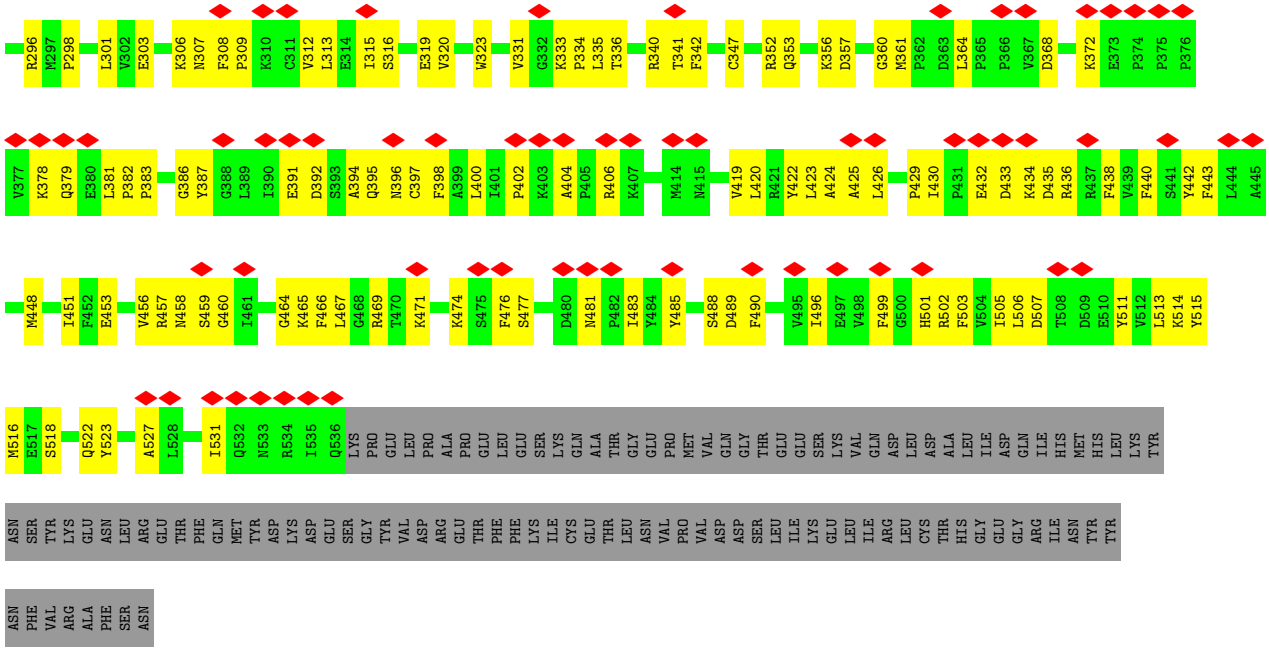




• Molecule 13: EF-hand domain-containing protein 1

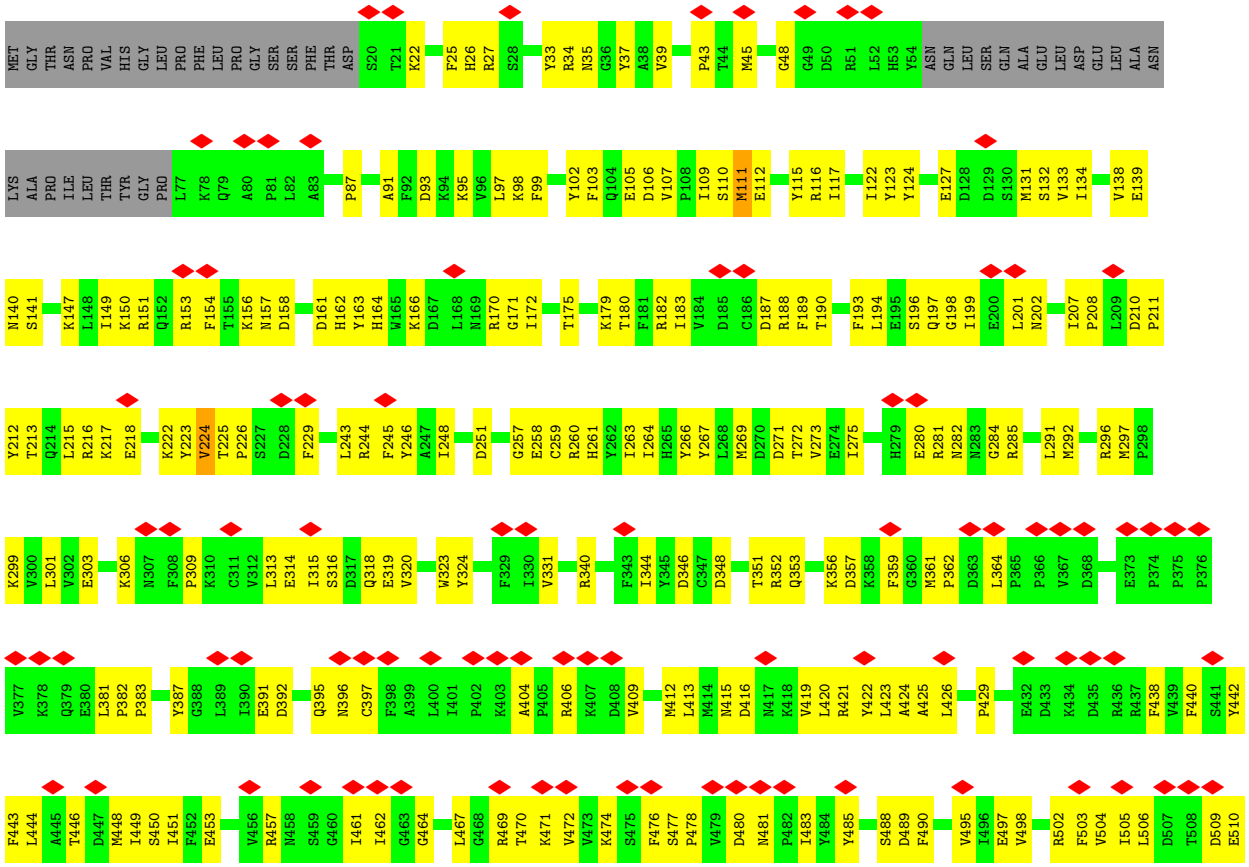
Chain G1:

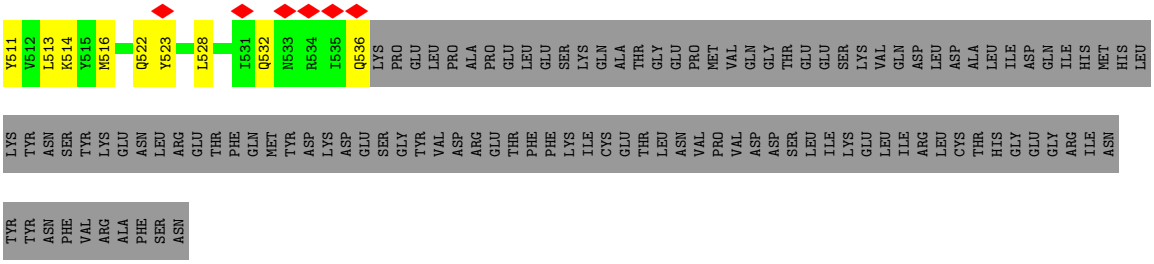




• Molecule 13: EF-hand domain-containing protein 1

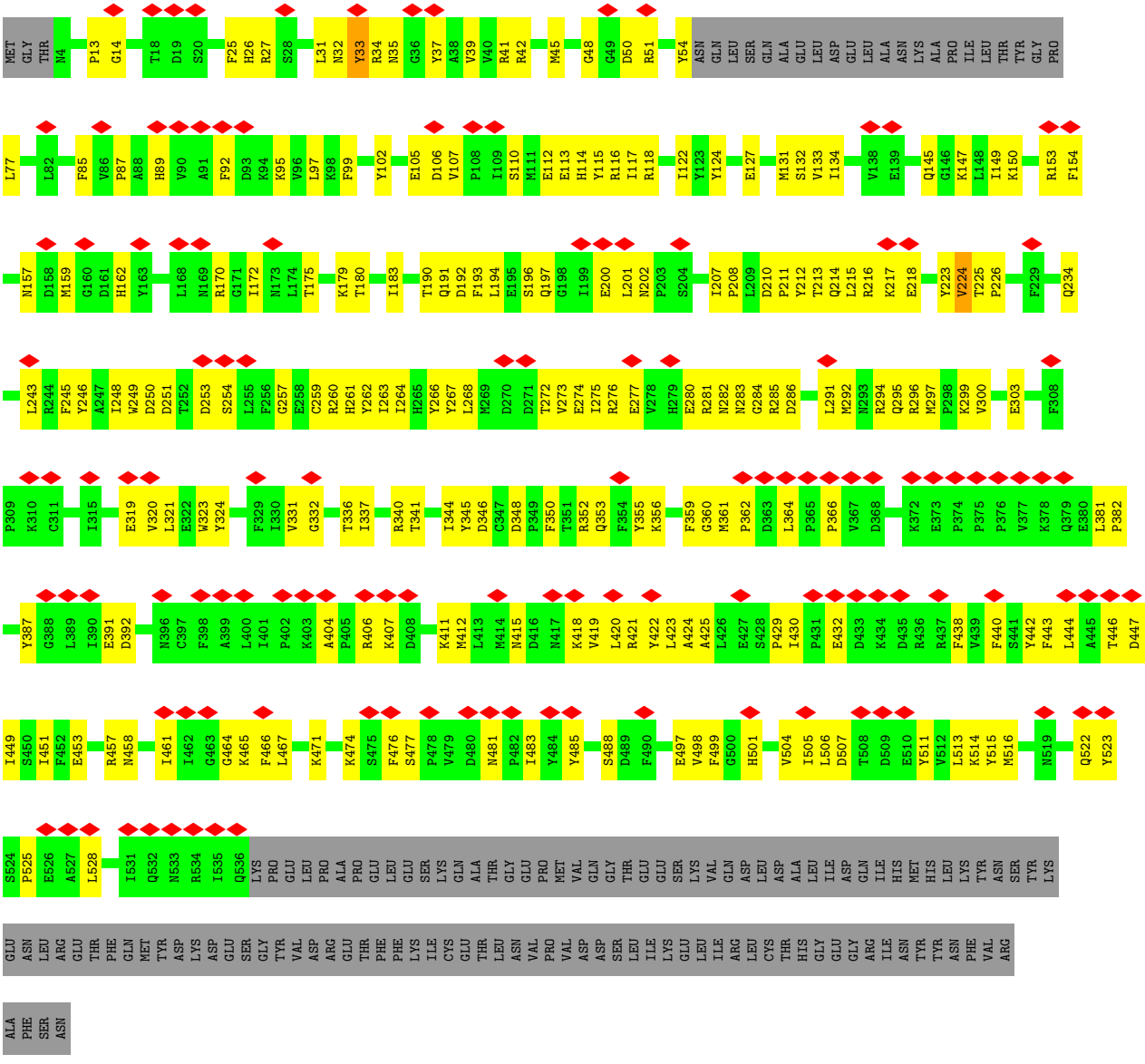
Chain G2:





• Molecule 13: EF-hand domain-containing protein 1

Chain G3:

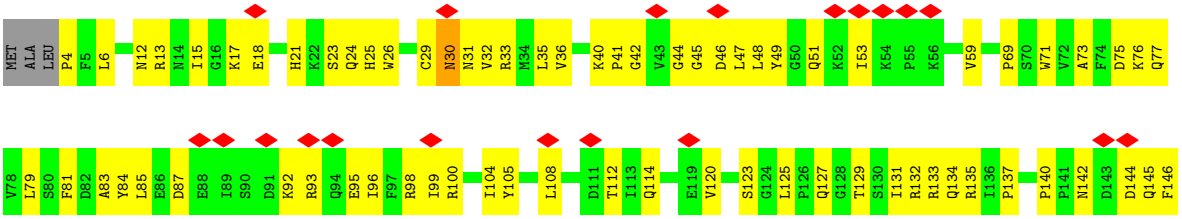


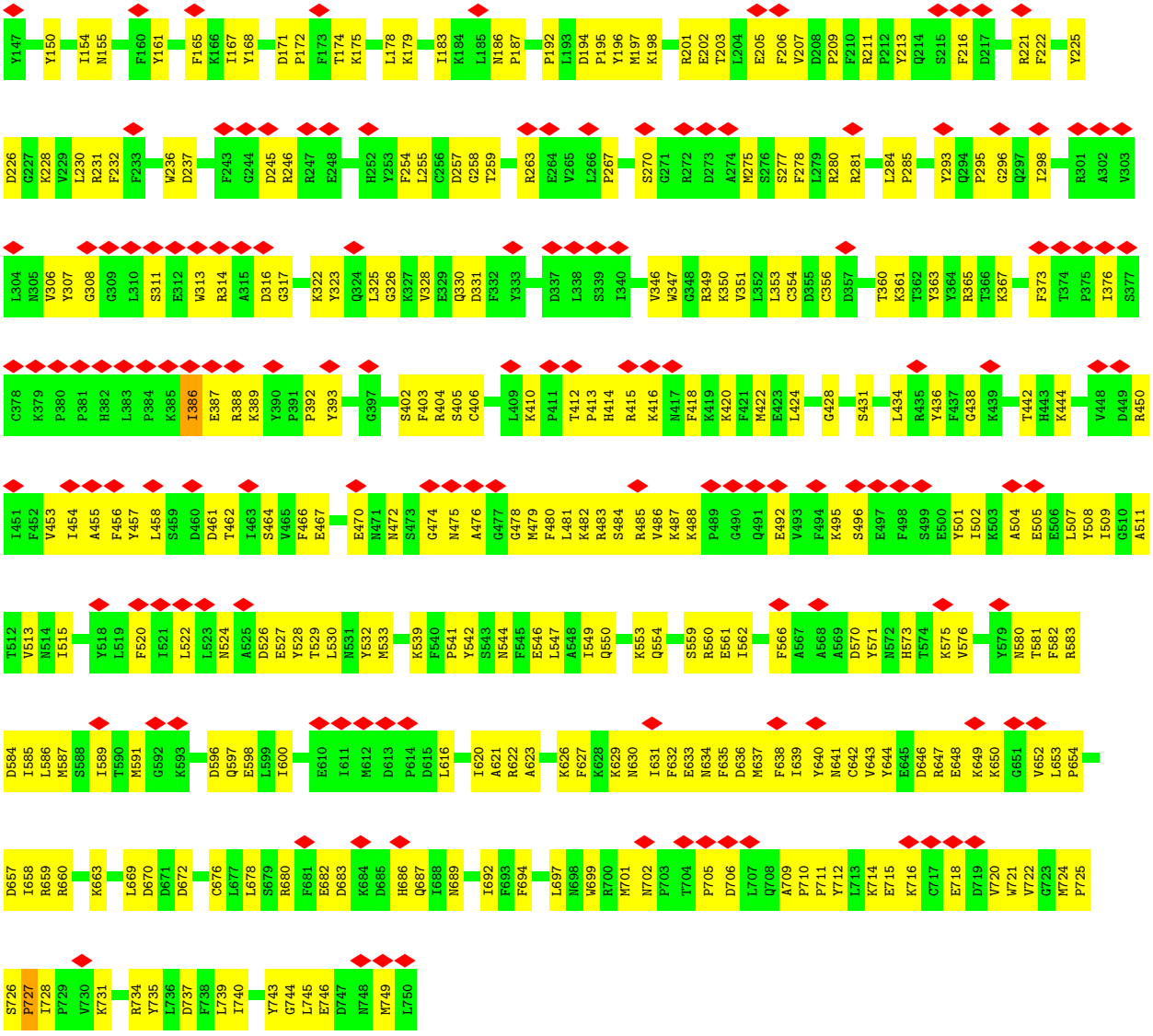
• Molecule 14: EF-hand domain-containing family member C2

Chain G4:

• Molecule 14: EF-hand domain-containing family member C2

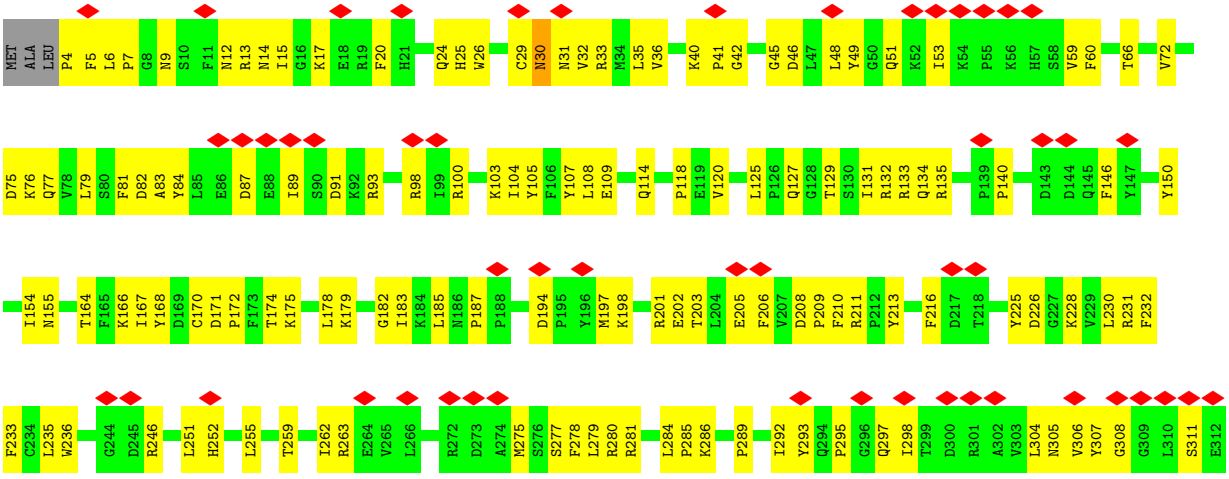
Chain G5:

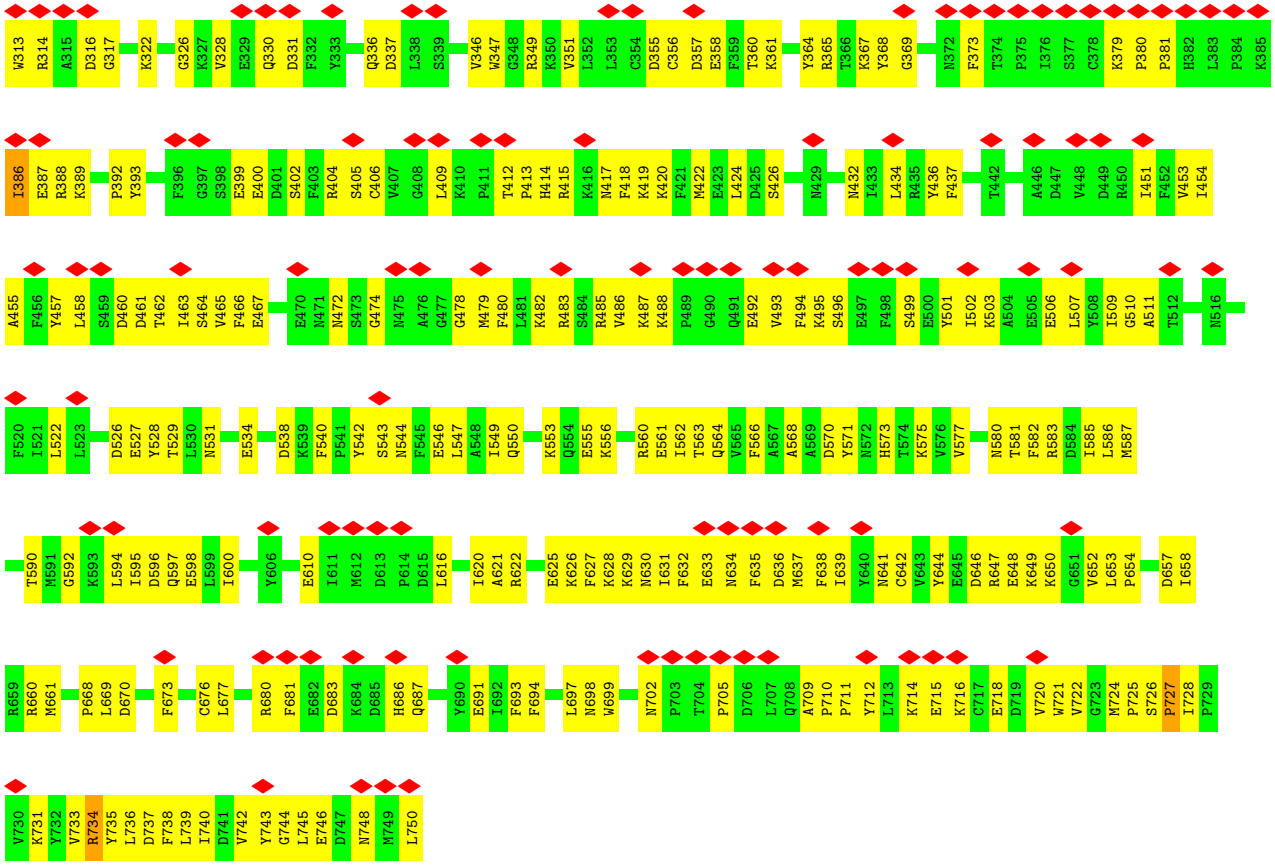




• Molecule 14: EF-hand domain-containing family member C2

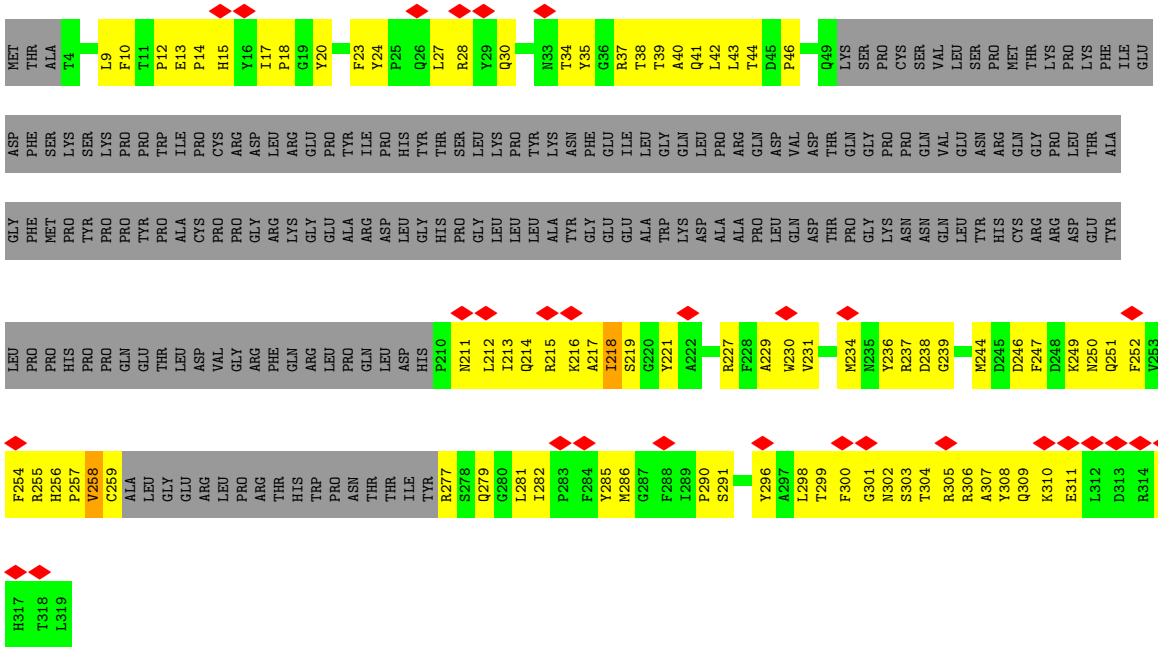
Chain G6:





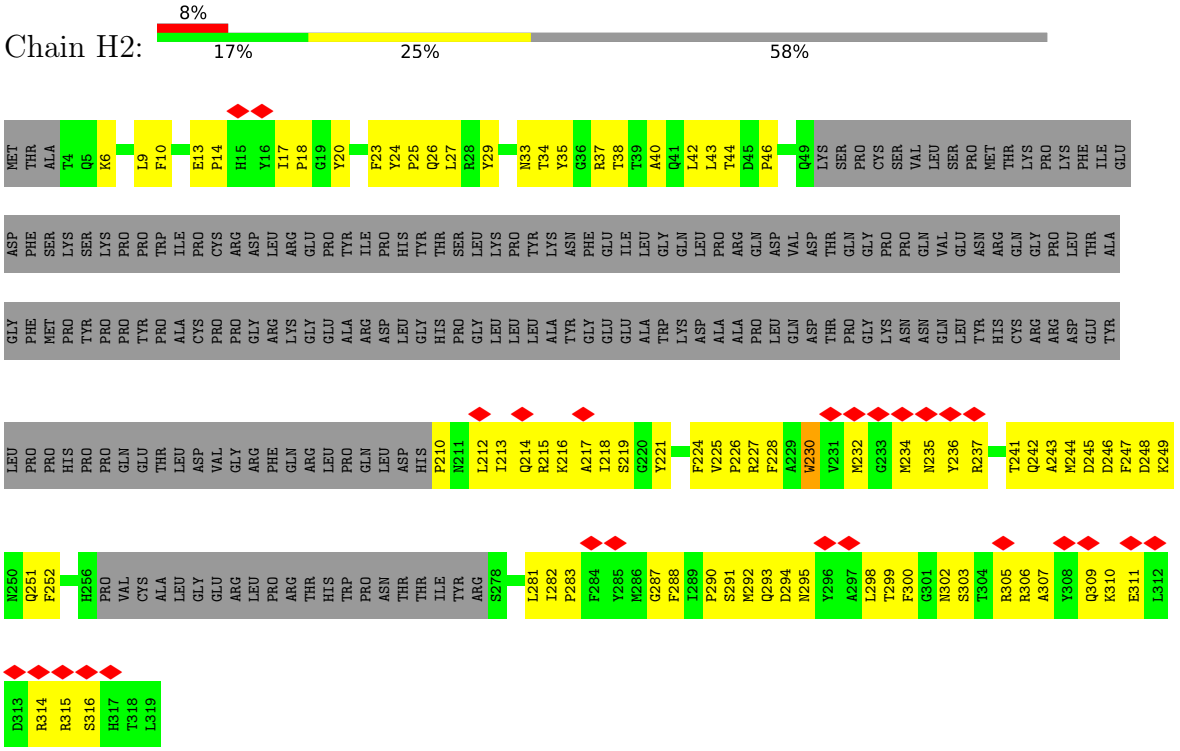
• Molecule 15: Protein FAM166A

Chain H1:



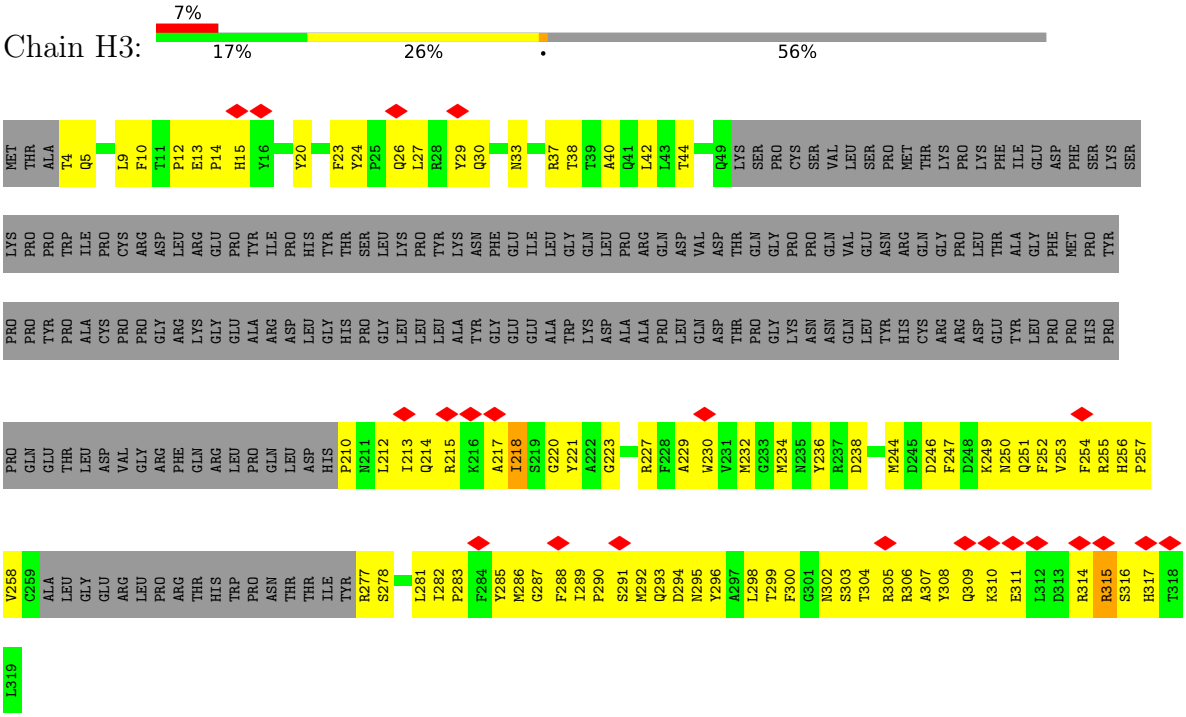
• Molecule 15: Protein FAM166A

Chain H2:



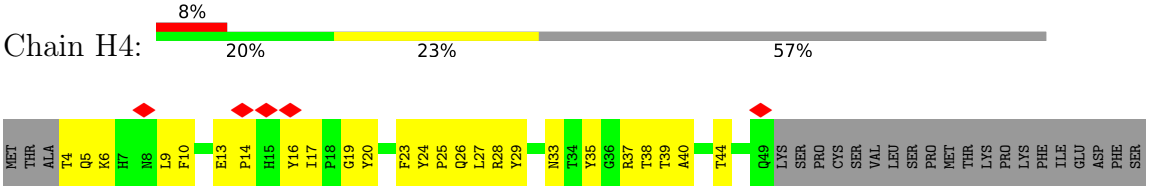
• Molecule 15: Protein FAM166A

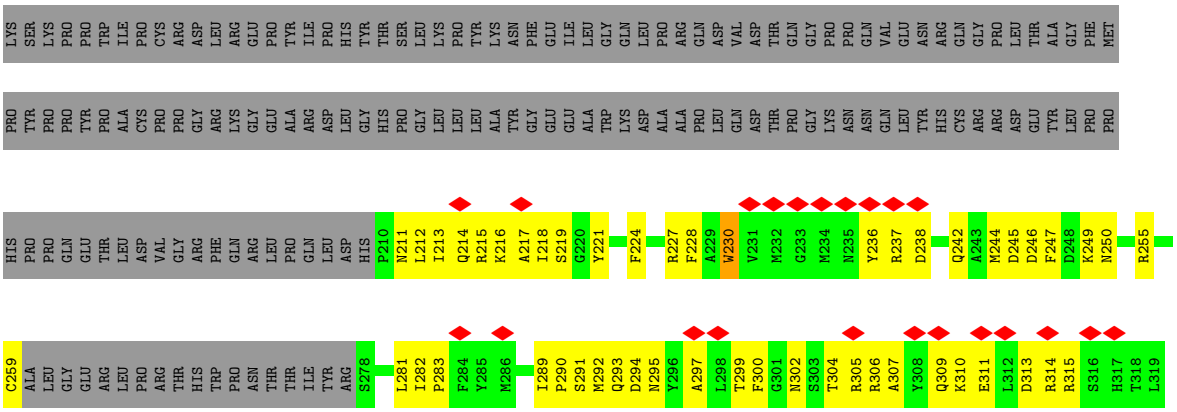
Chain H3:



• Molecule 15: Protein FAM166A

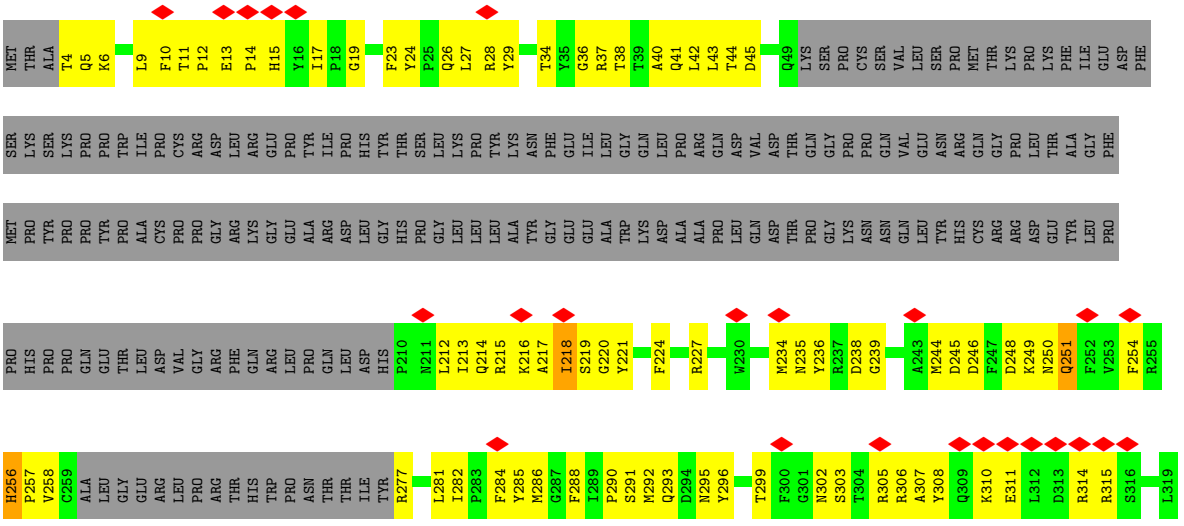
Chain H4:





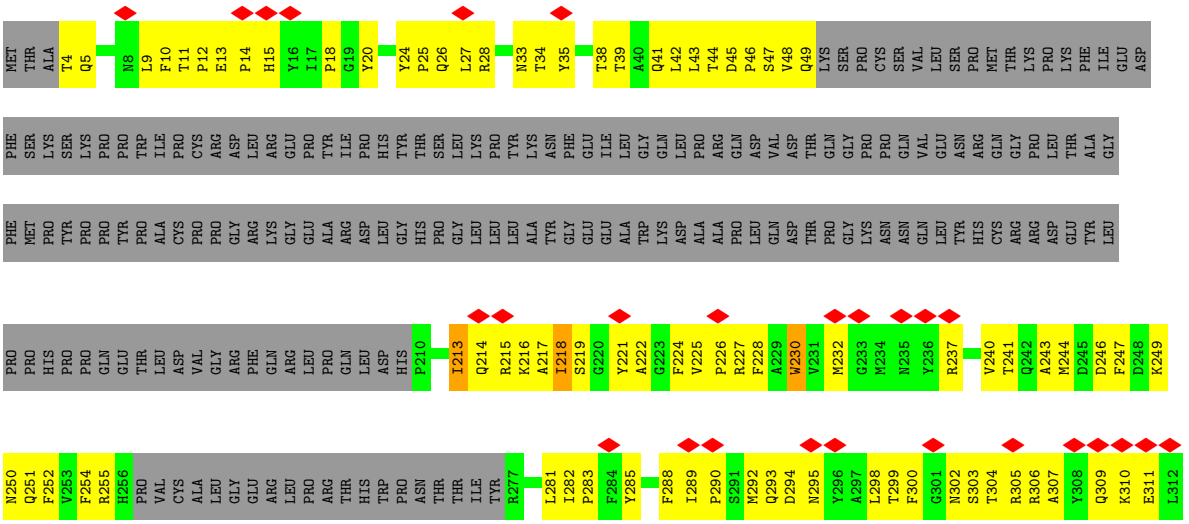
• Molecule 15: Protein FAM166A

Chain H5:



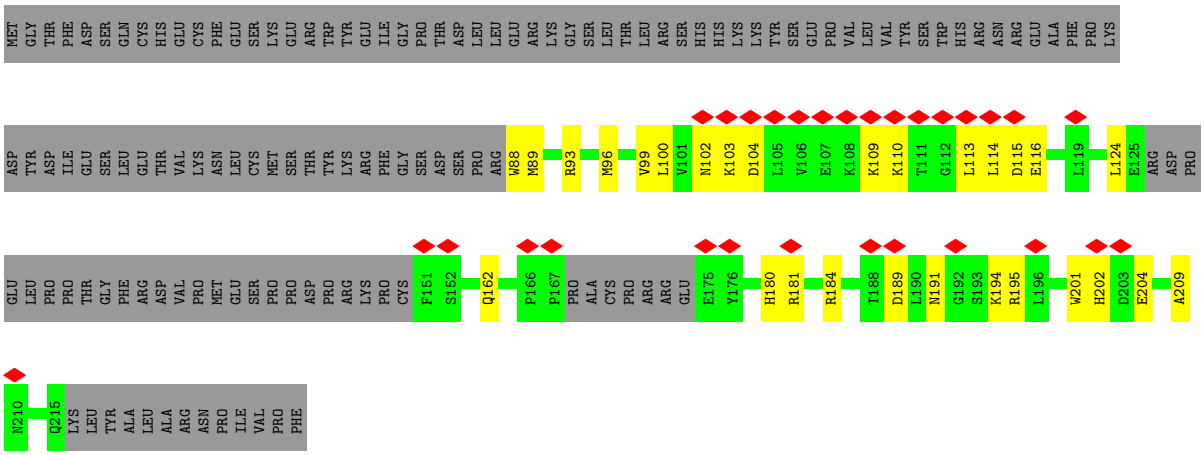
• Molecule 15: Protein FAM166A

Chain H6:



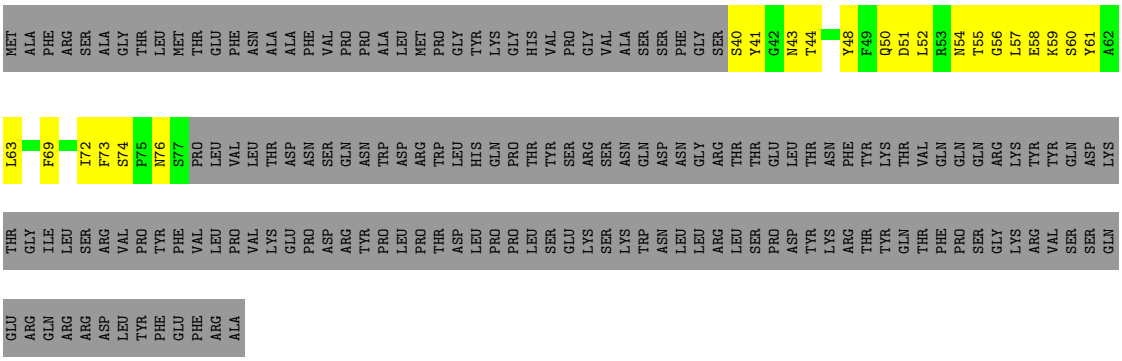
• Molecule 16: Cilia- and flagella-associated protein 95

Chain I:



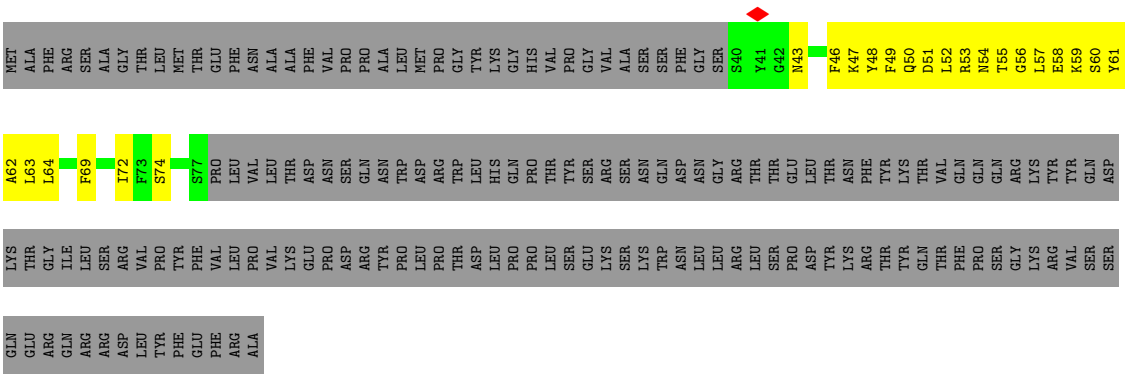
• Molecule 17: Protein FAM166C

Chain I1:



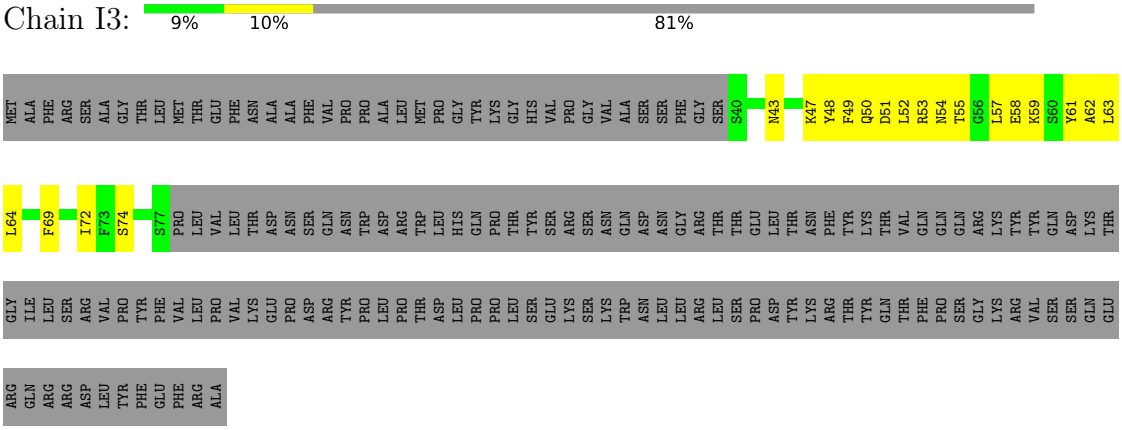
• Molecule 17: Protein FAM166C

Chain I2:



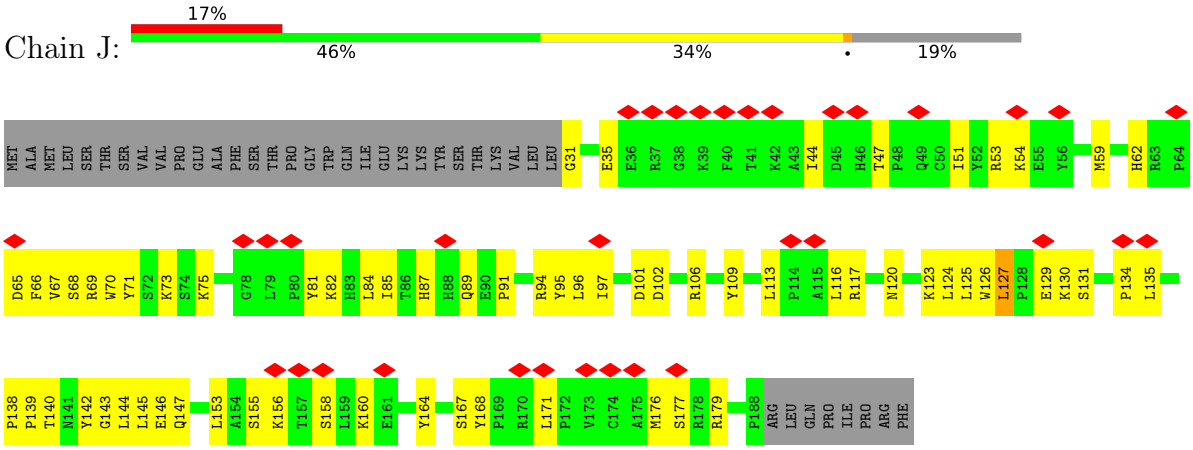
• Molecule 17: Protein FAM166C

Chain I3:



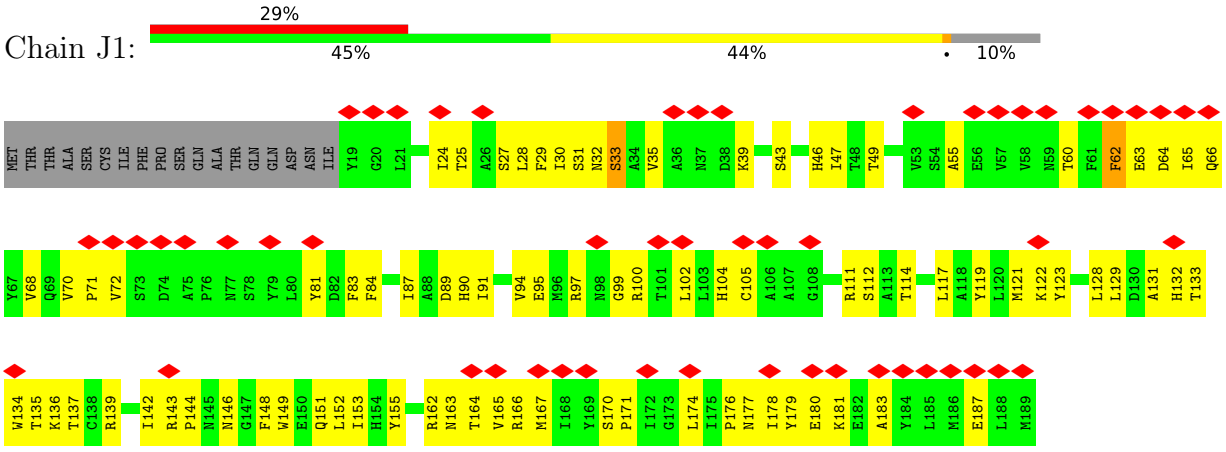
• Molecule 18: Cilia- and flagella-associated protein 107

Chain J:



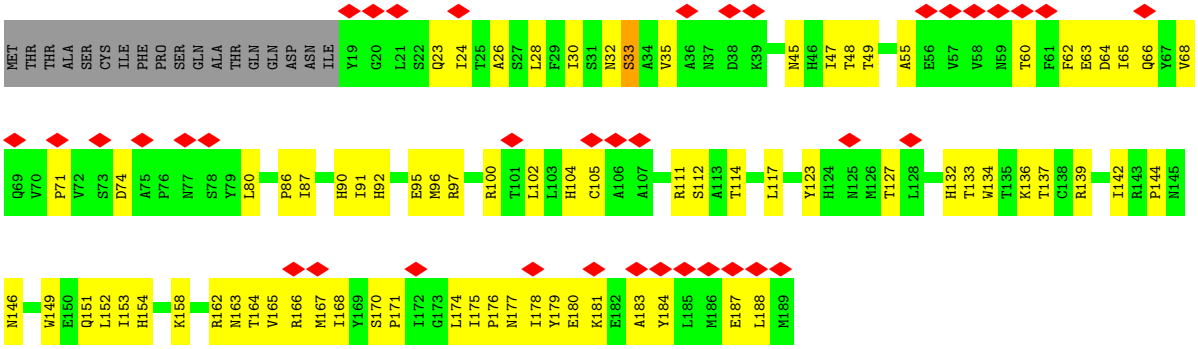
• Molecule 19: Dual specificity phosphatase 21

Chain J1:



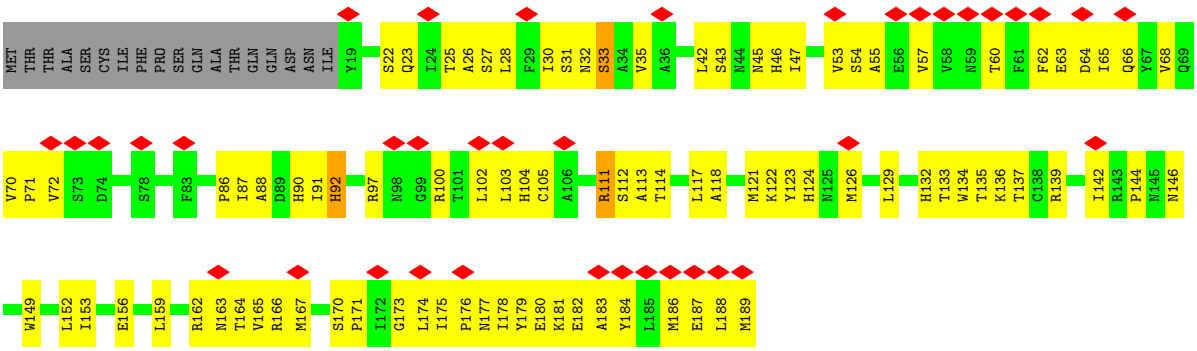
• Molecule 19: Dual specificity phosphatase 21

Chain J2:



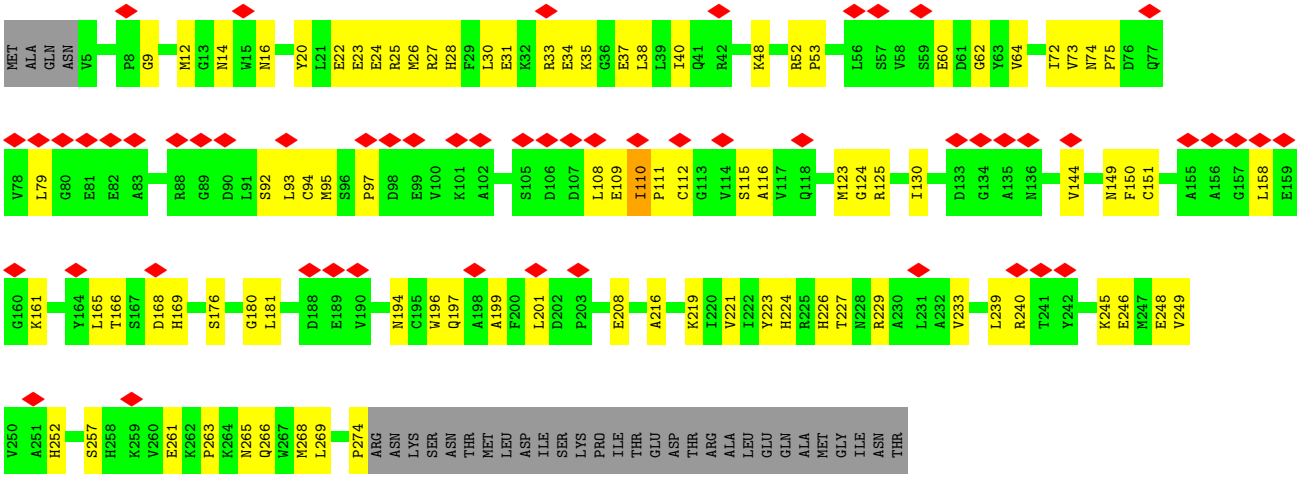
• Molecule 19: Dual specificity phosphatase 21

Chain J3:



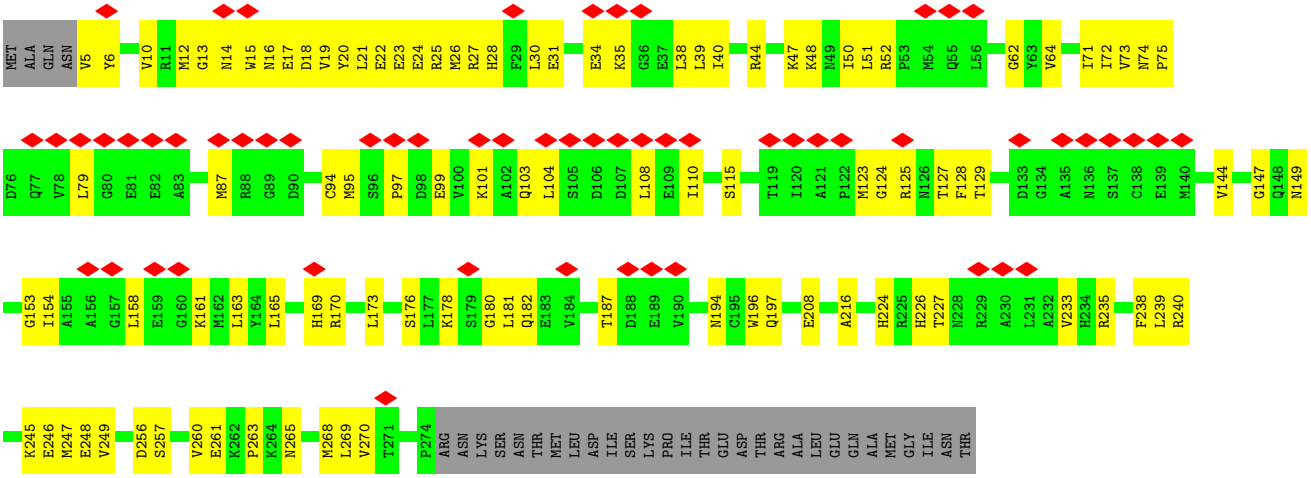
• Molecule 20: Cilia- and flagella-associated protein 161

Chain K:



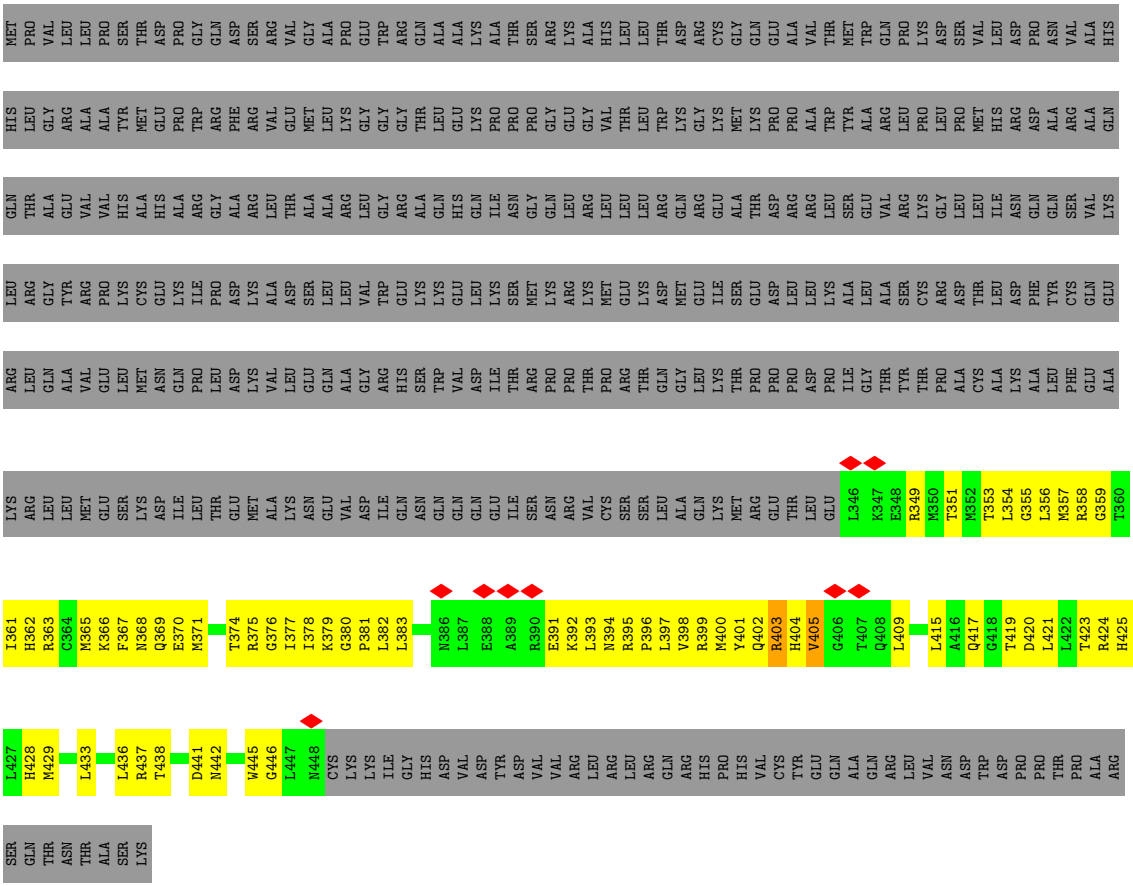
• Molecule 20: Cilia- and flagella-associated protein 161

Chain L:



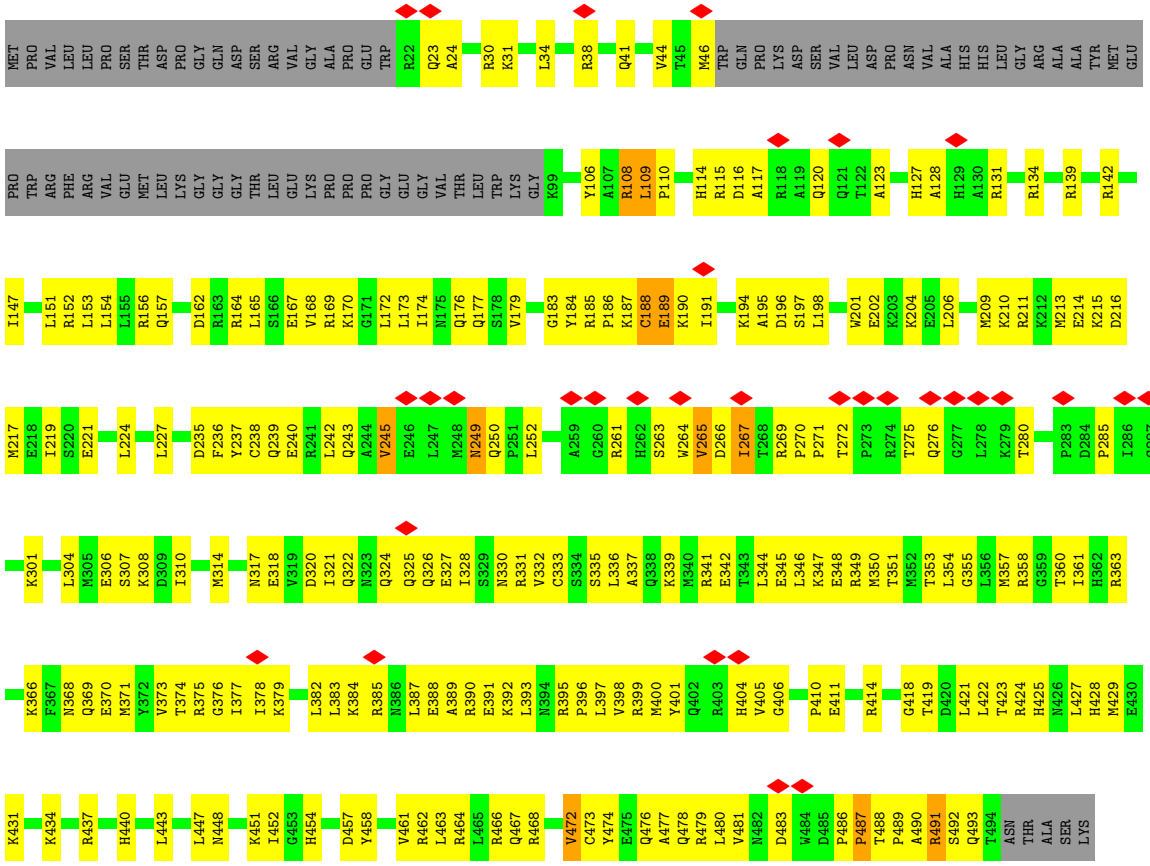
• Molecule 21: Coiled-coil domain-containing protein 105

Chain K1:



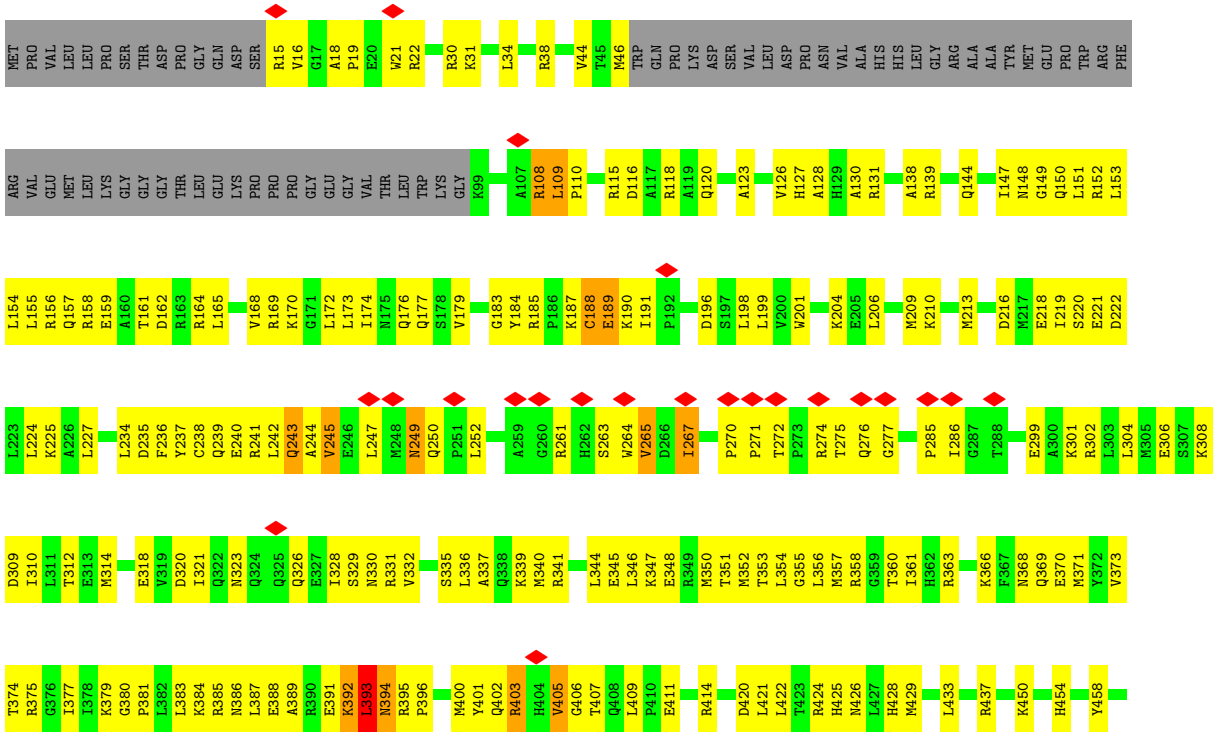
• Molecule 21: Coiled-coil domain-containing protein 105

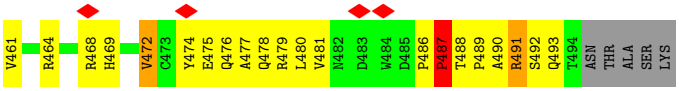
Chain K2:



• Molecule 21: Coiled-coil domain-containing protein 105

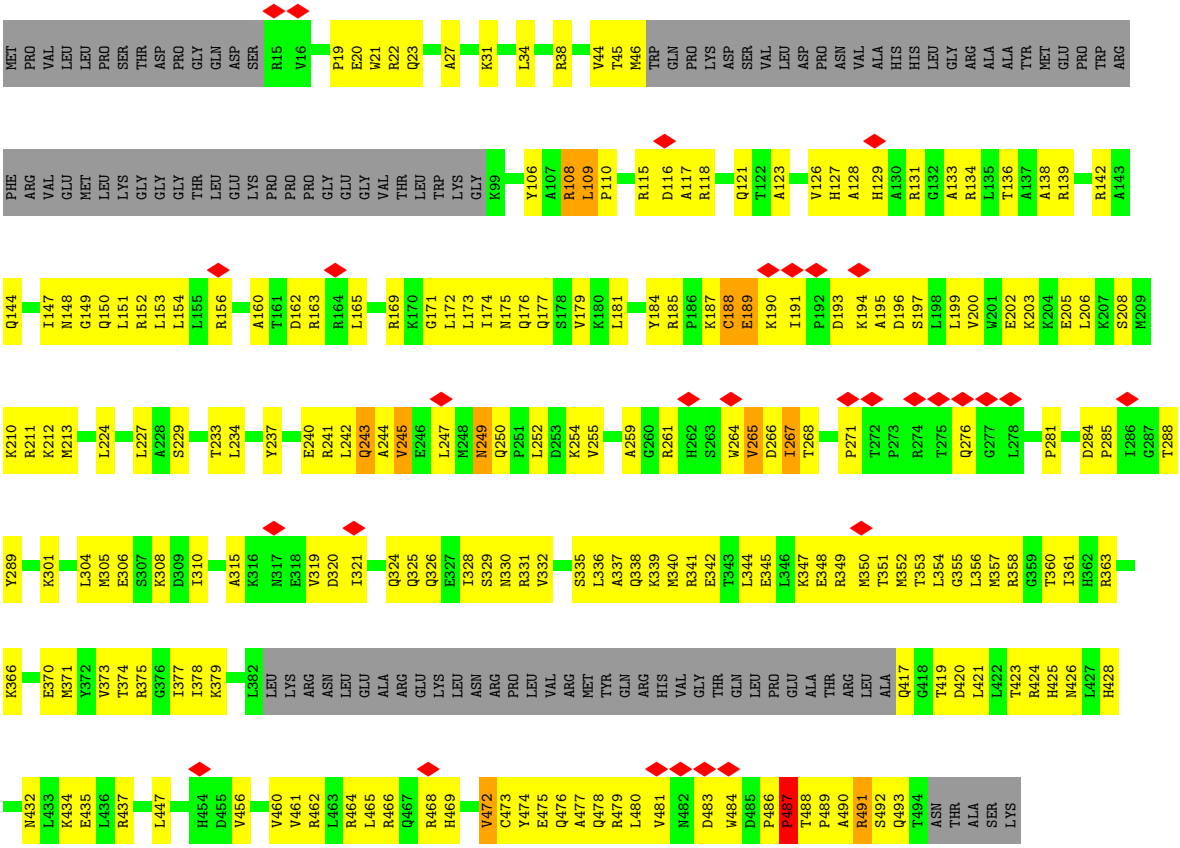
Chain K3:





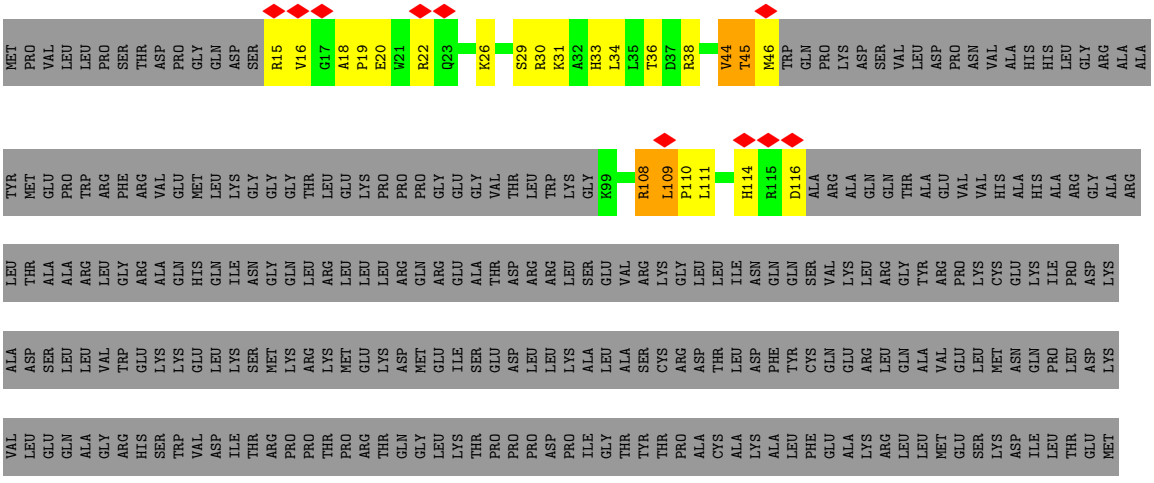
• Molecule 21: Coiled-coil domain-containing protein 105

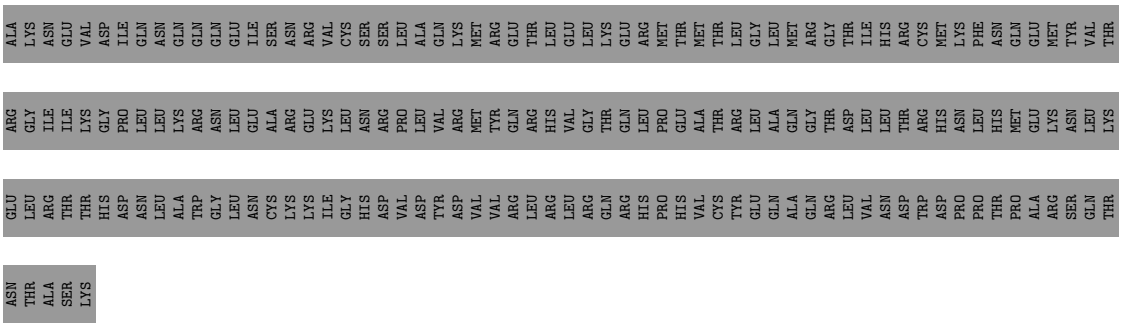
Chain K4:



• Molecule 21: Coiled-coil domain-containing protein 105

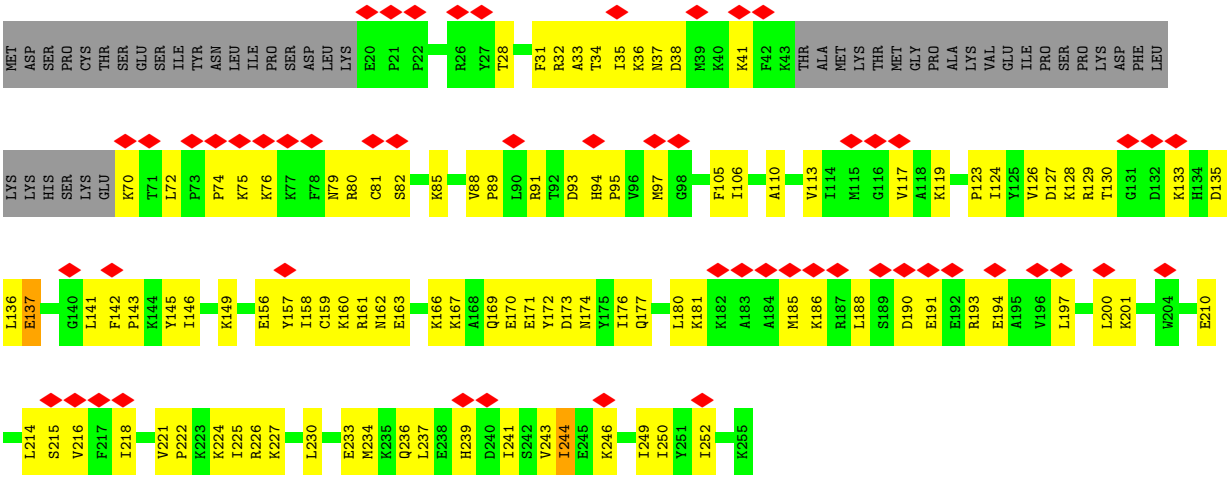
Chain K5:





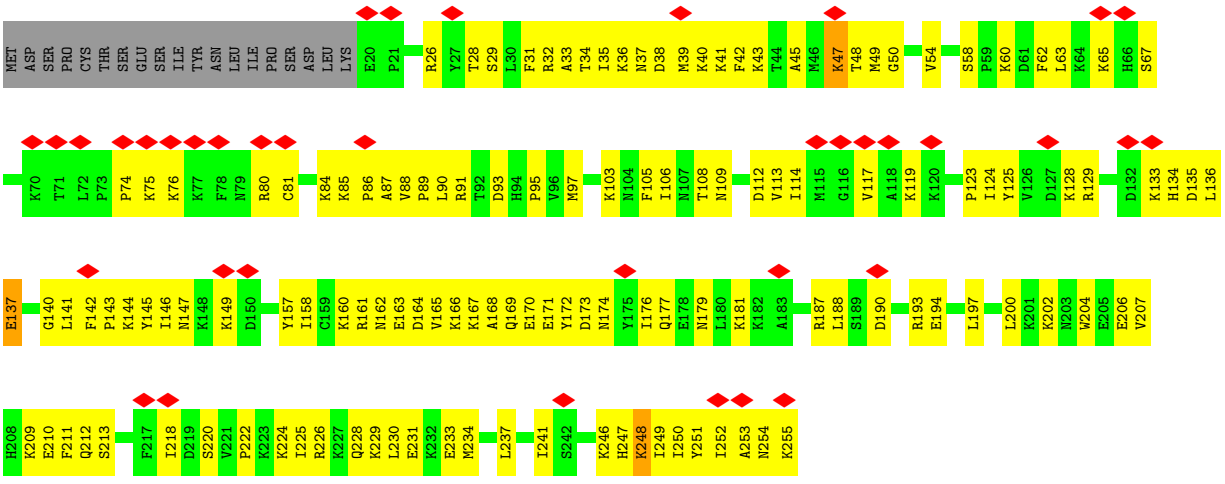
• Molecule 22: Enkurin

Chain L1:



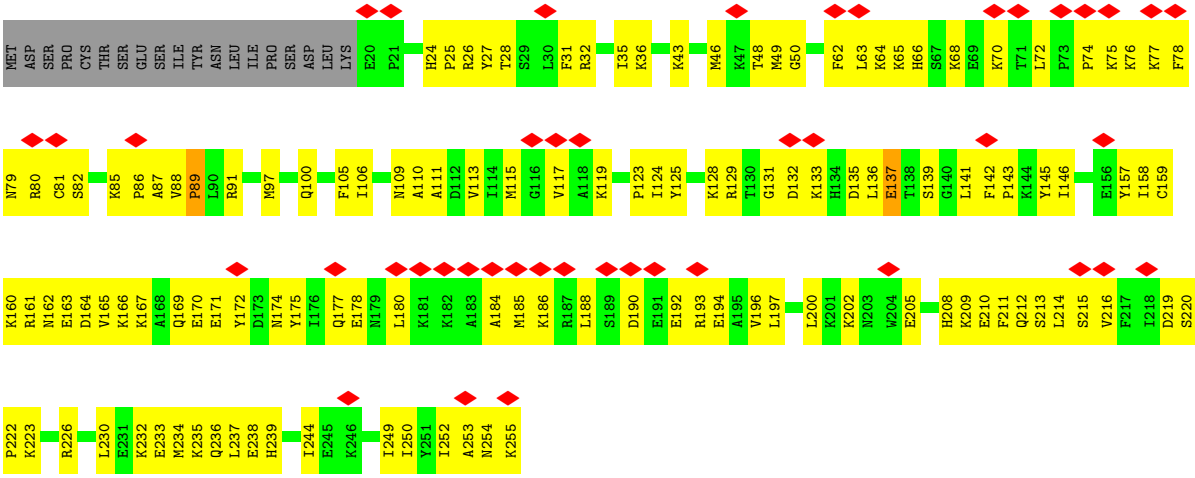
• Molecule 22: Enkurin

Chain L2:



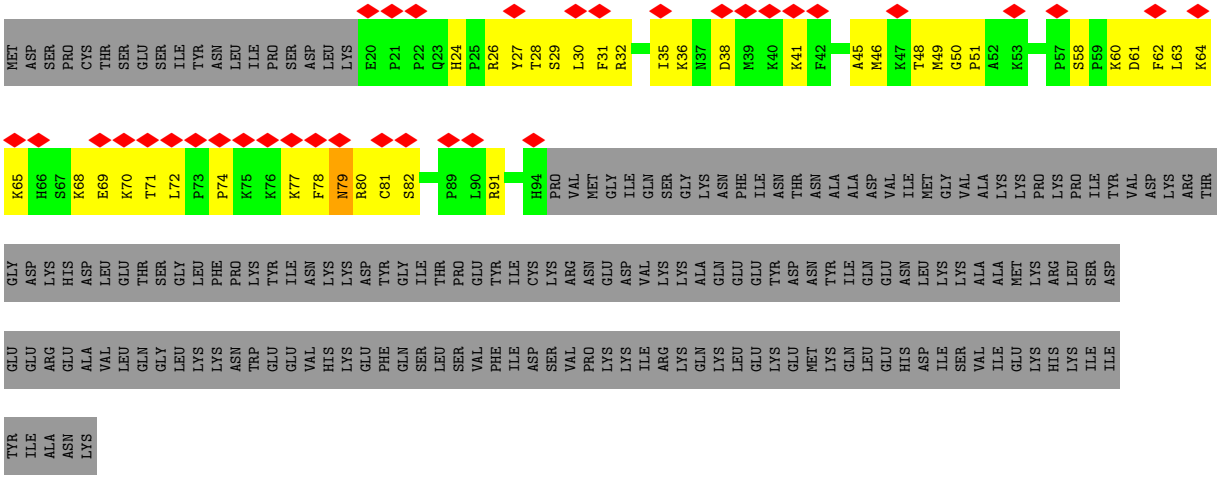
• Molecule 22: Enkurin

Chain L3:



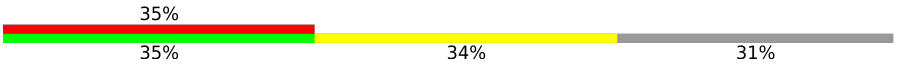
• Molecule 22: Enkurin

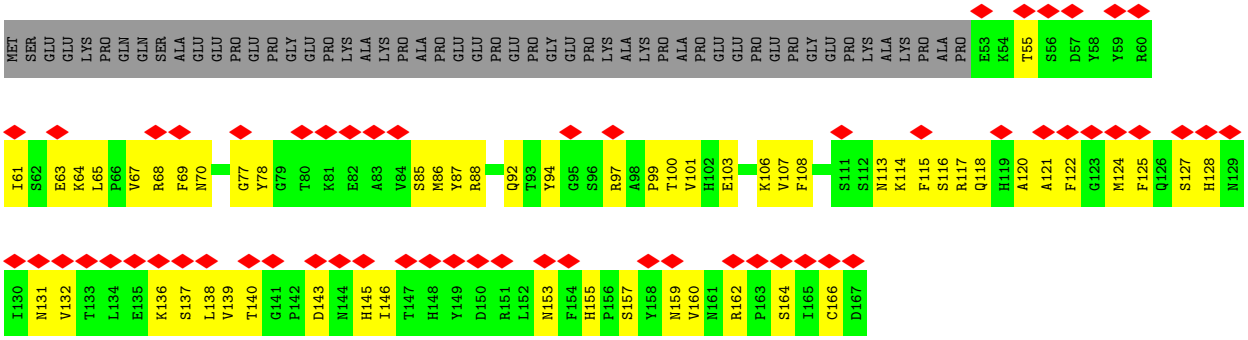
Chain L4:



• Molecule 23: Piercer of microtubule wall 1 protein

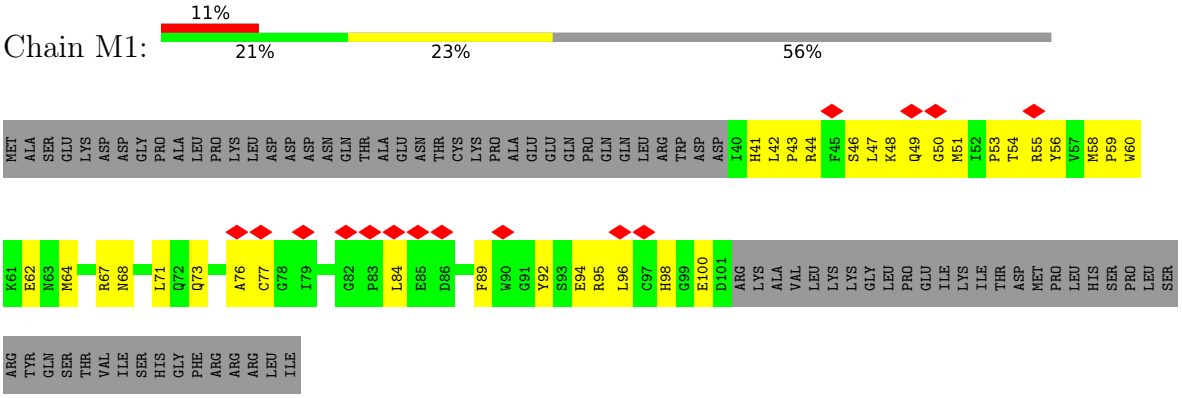
Chain M:





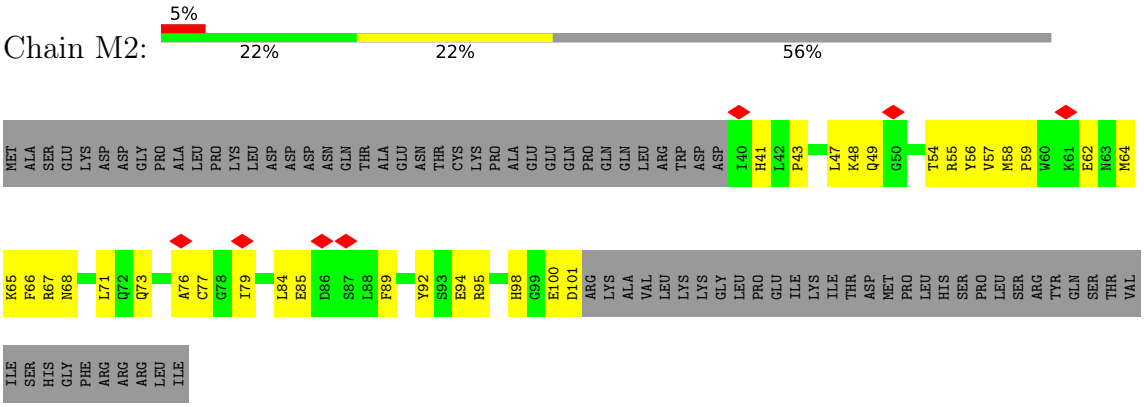
• Molecule 24: Testis-expressed protein 43

Chain M1:



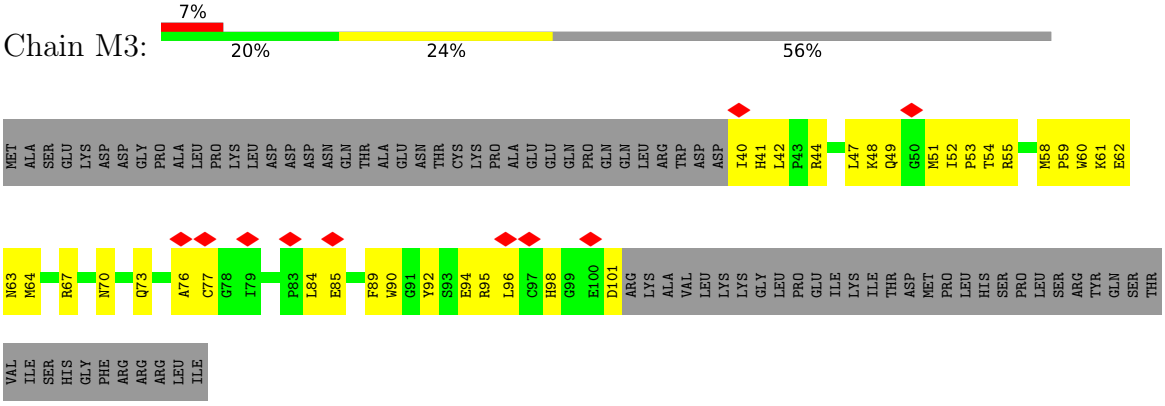
• Molecule 24: Testis-expressed protein 43

Chain M2:



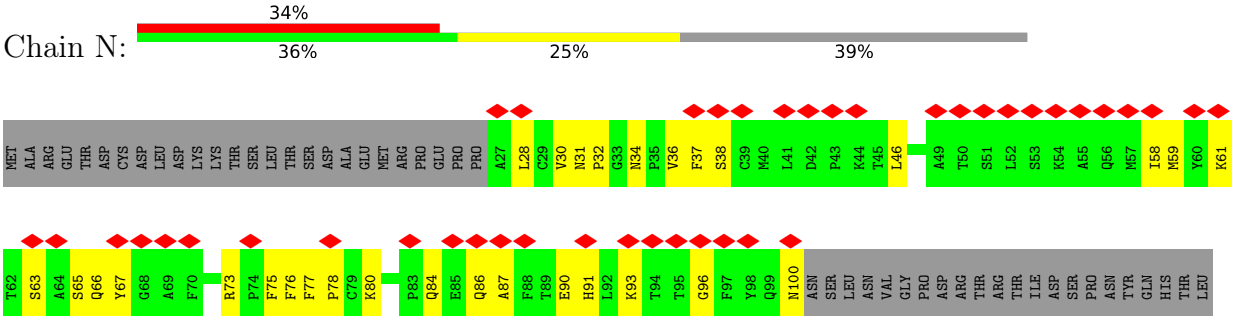
• Molecule 24: Testis-expressed protein 43

Chain M3:



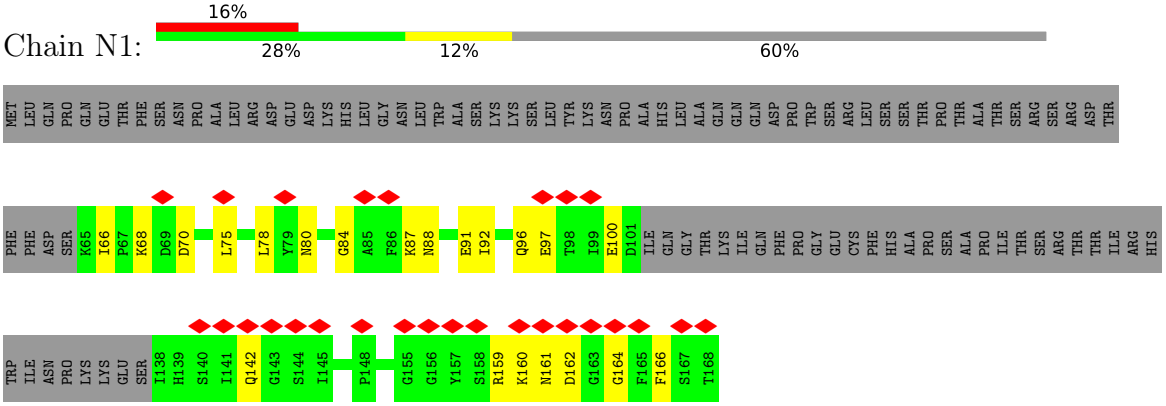
• Molecule 25: Piercer of microtubule wall 2 protein

Chain N:



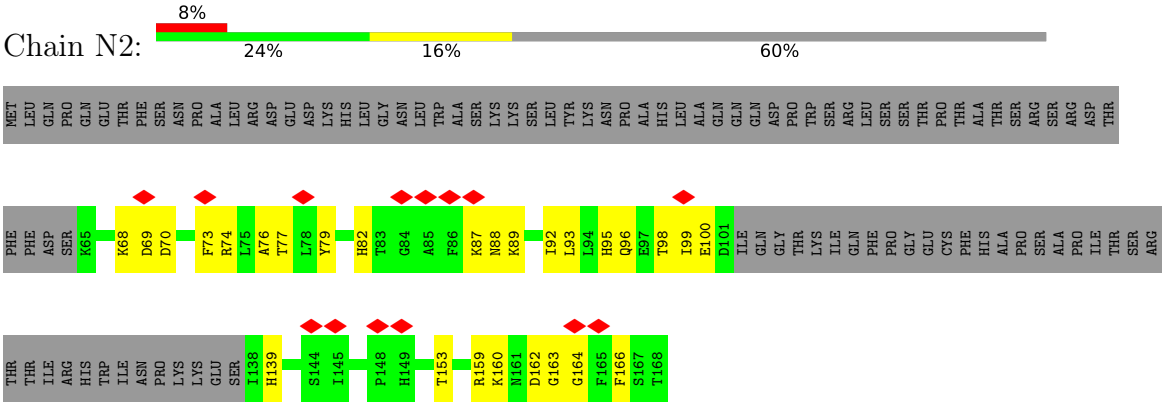
• Molecule 26: Cilia- and flagella-associated protein 276

Chain N1:



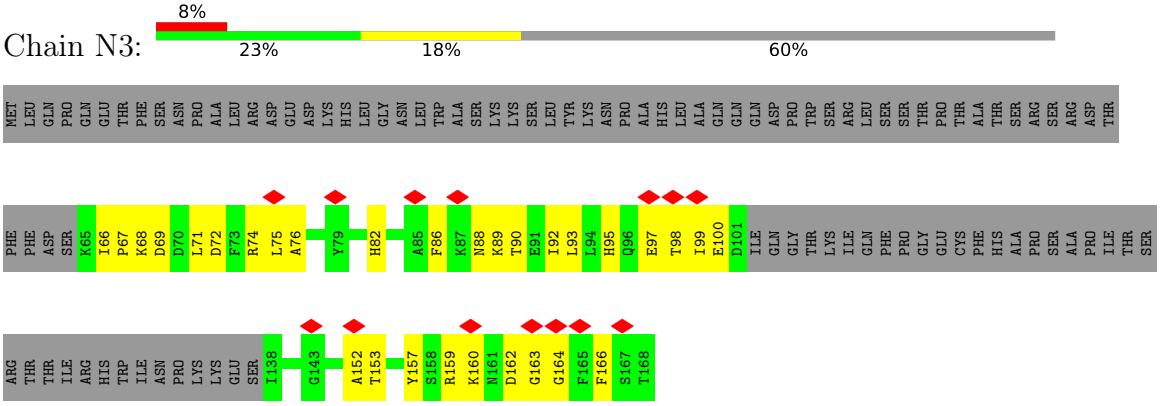
• Molecule 26: Cilia- and flagella-associated protein 276

Chain N2:



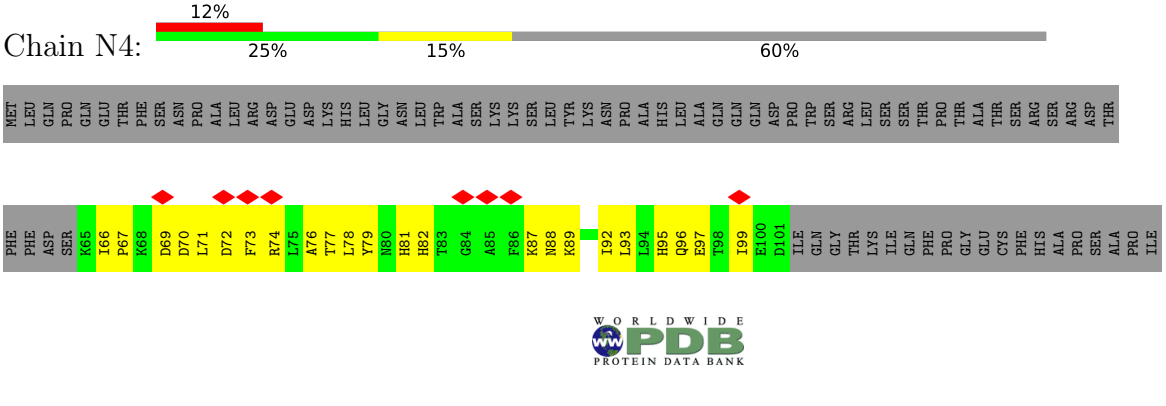
• Molecule 26: Cilia- and flagella-associated protein 276

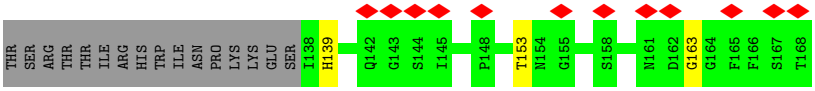
Chain N3:



• Molecule 26: Cilia- and flagella-associated protein 276

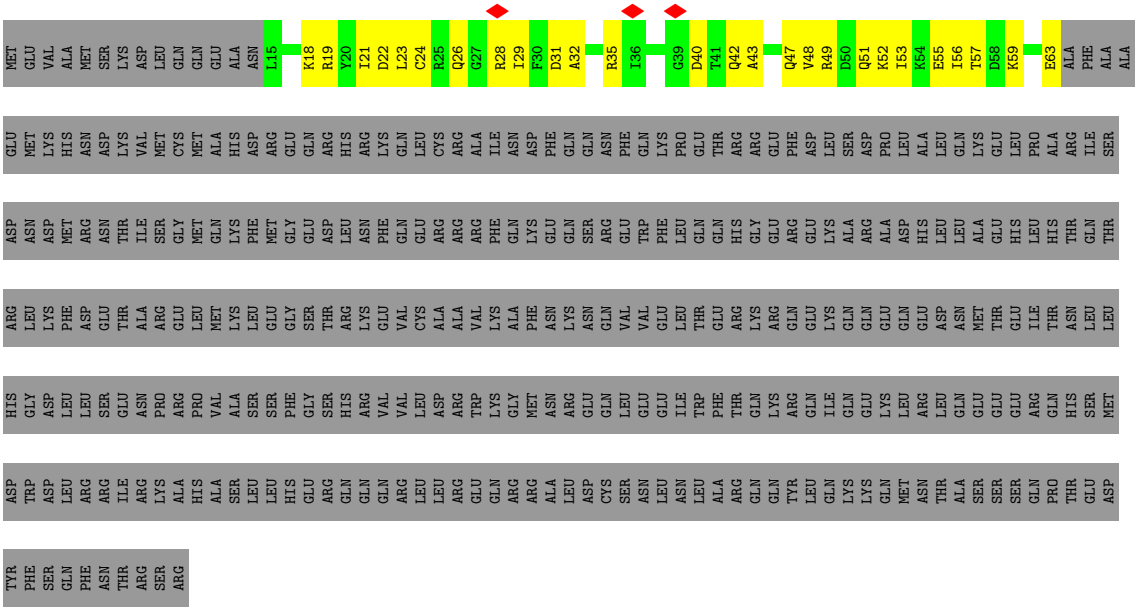
Chain N4:





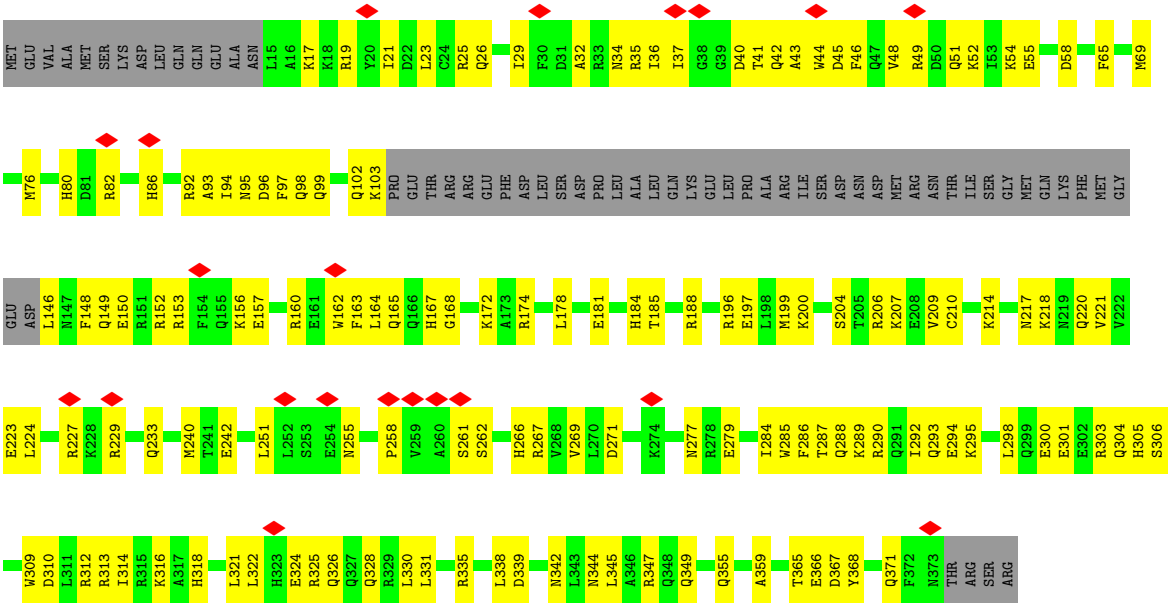
• Molecule 27: RIB43A-like with coiled-coils protein 2

Chain O:



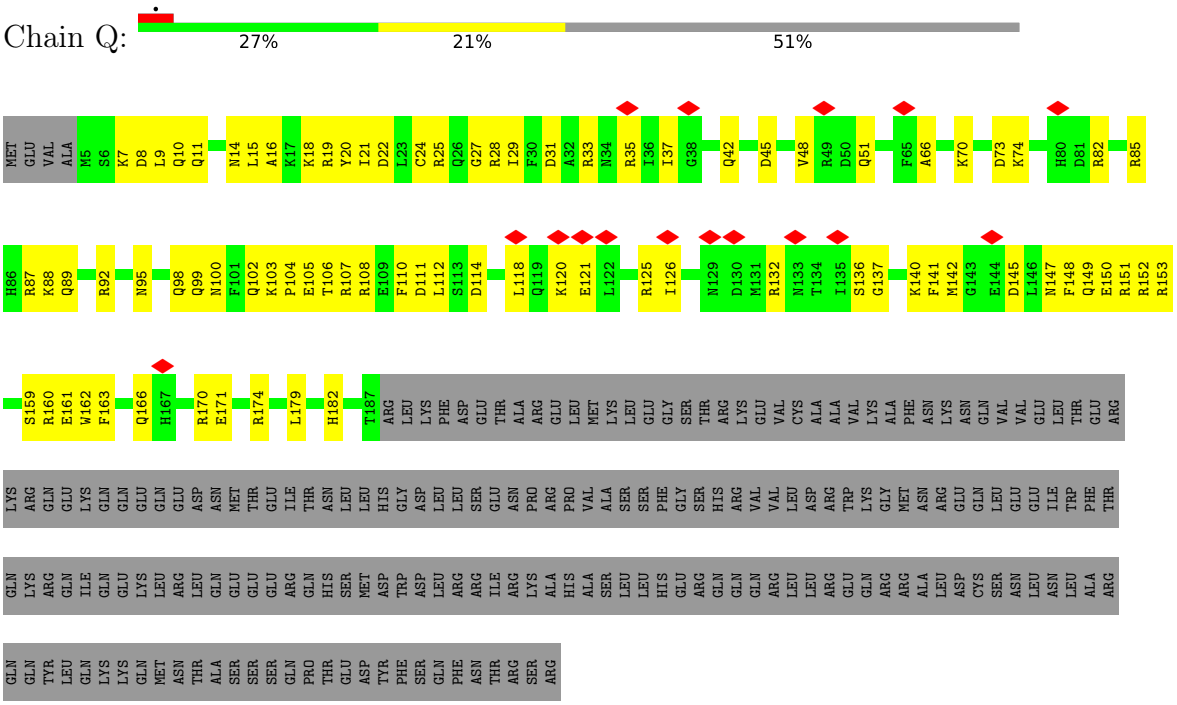
• Molecule 27: RIB43A-like with coiled-coils protein 2

Chain P:



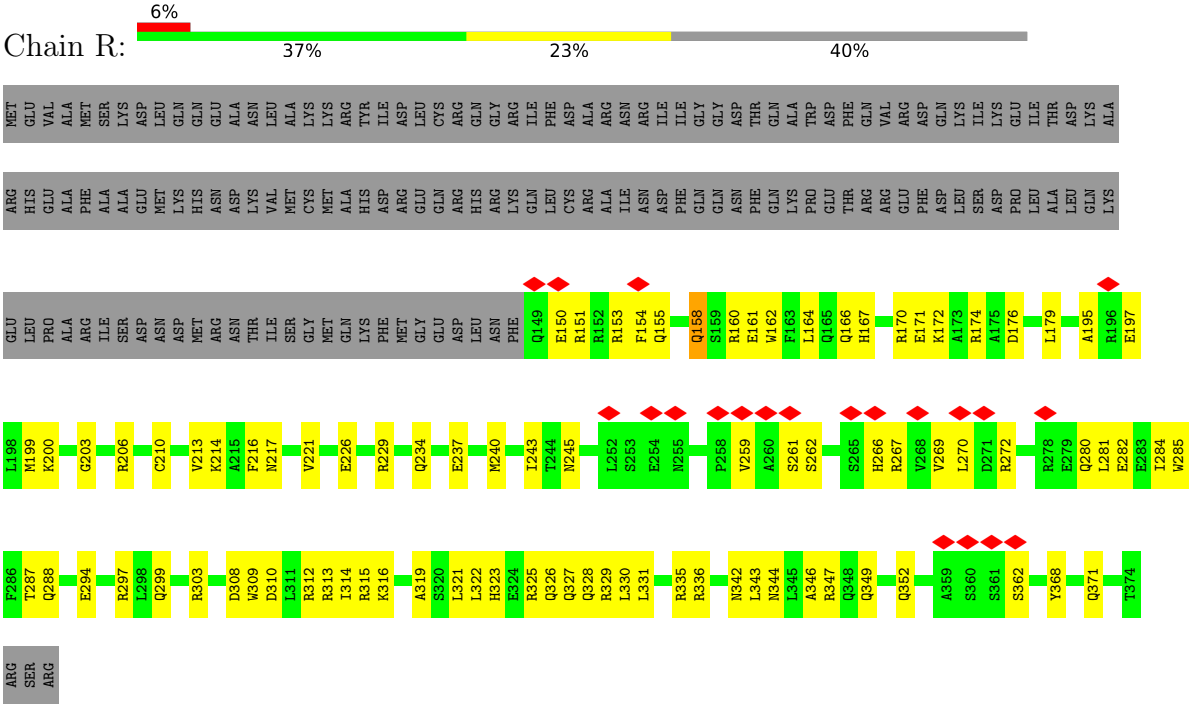
• Molecule 27: RIB43A-like with coiled-coils protein 2

Chain Q:



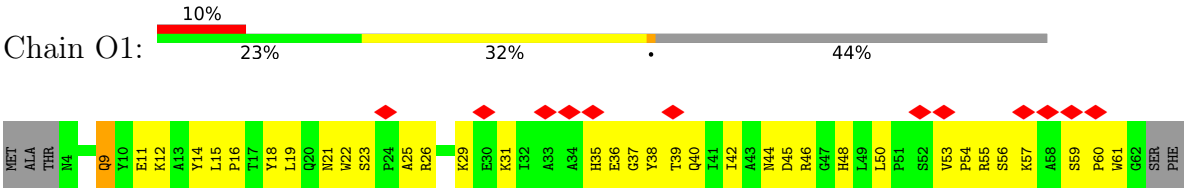
• Molecule 27: RIB43A-like with coiled-coils protein 2

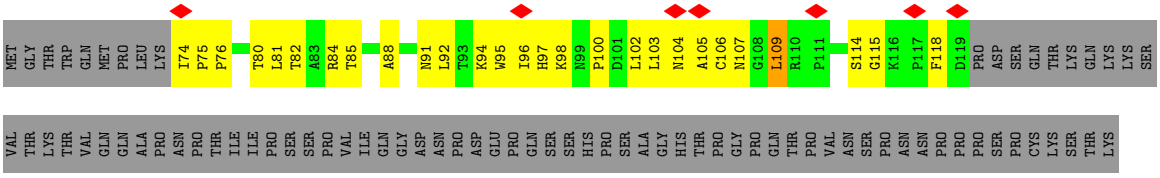
Chain R:



• Molecule 28: Protein Flattop

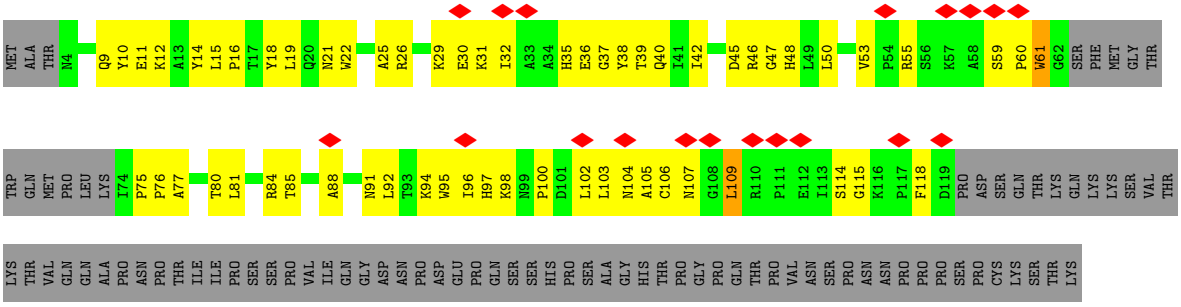
Chain O1:





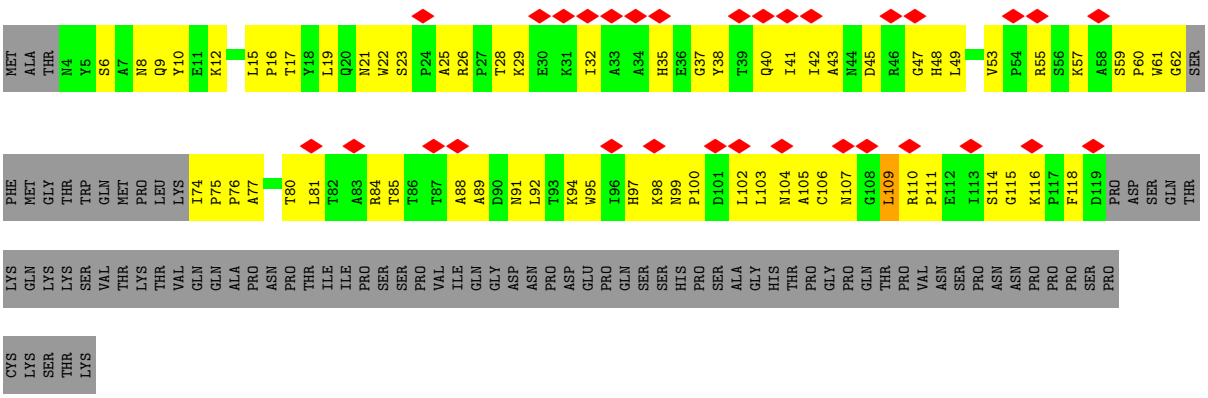
• Molecule 28: Protein Flattop

Chain O2:



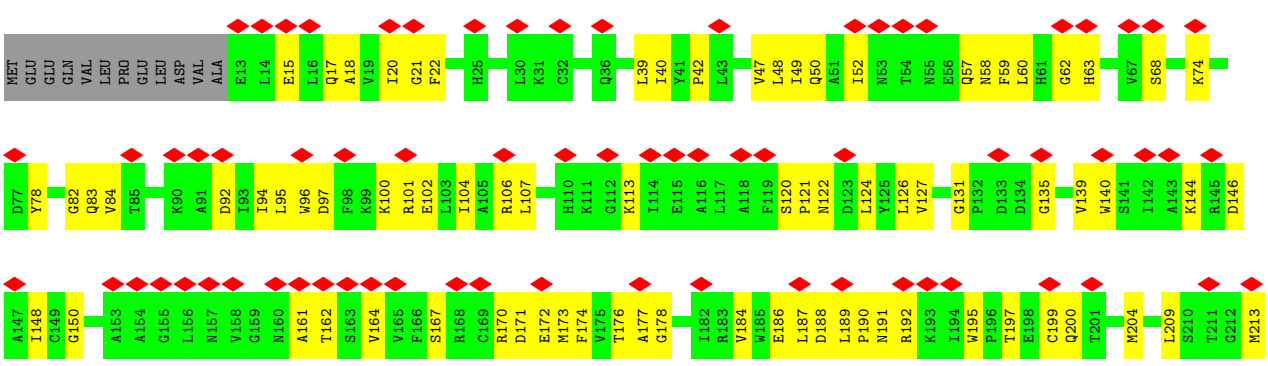
• Molecule 28: Protein Flattop

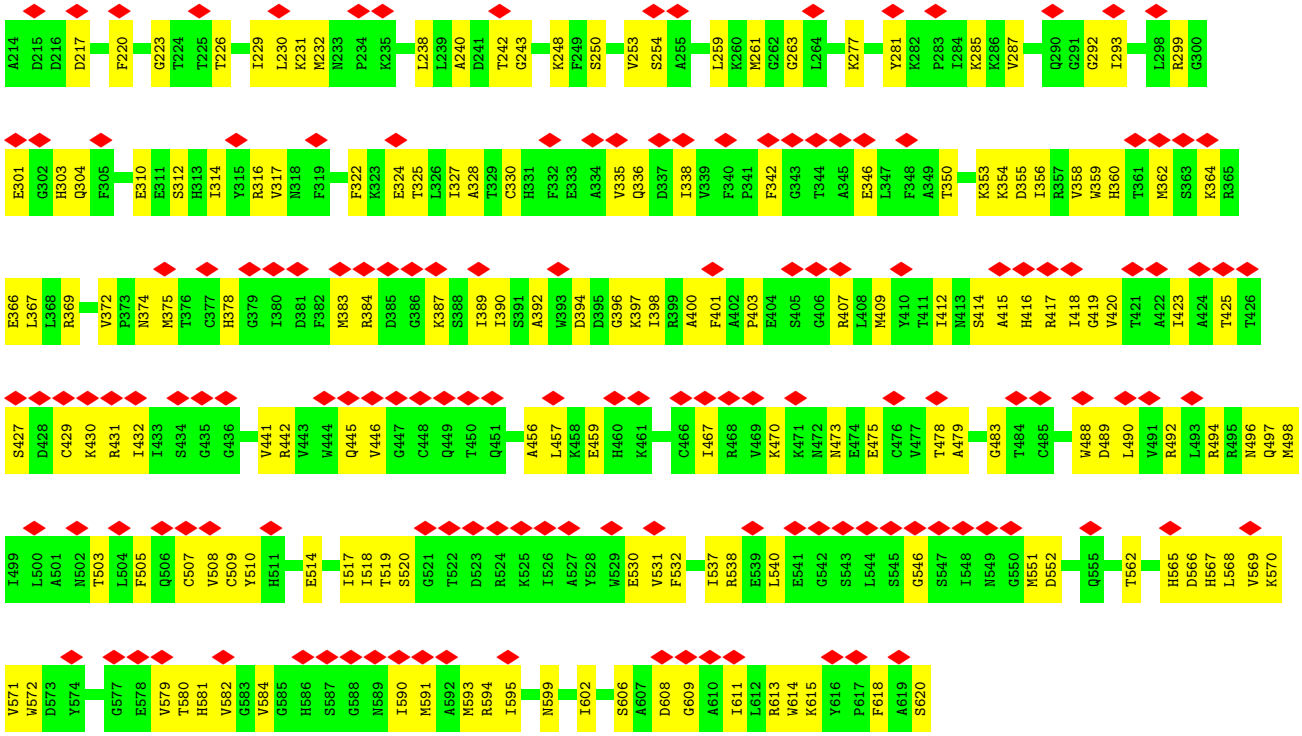
Chain O3:



• Molecule 29: Cilia- and flagella-associated protein 52

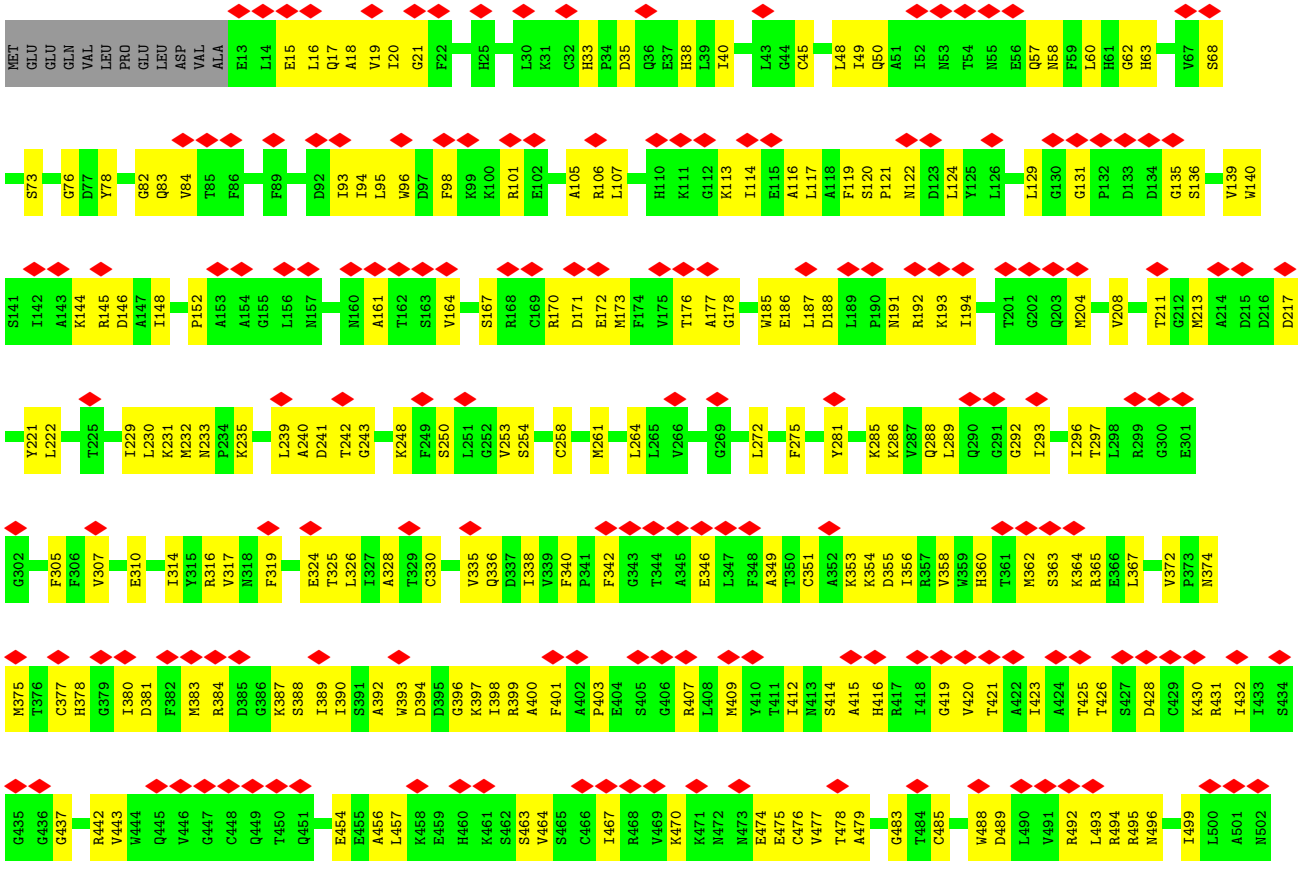
Chain P1:

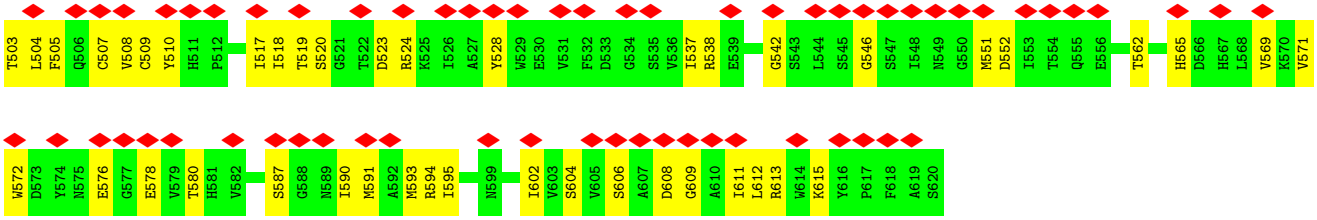




• Molecule 29: Cilia- and flagella-associated protein 52

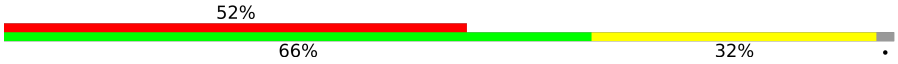
Chain P2:

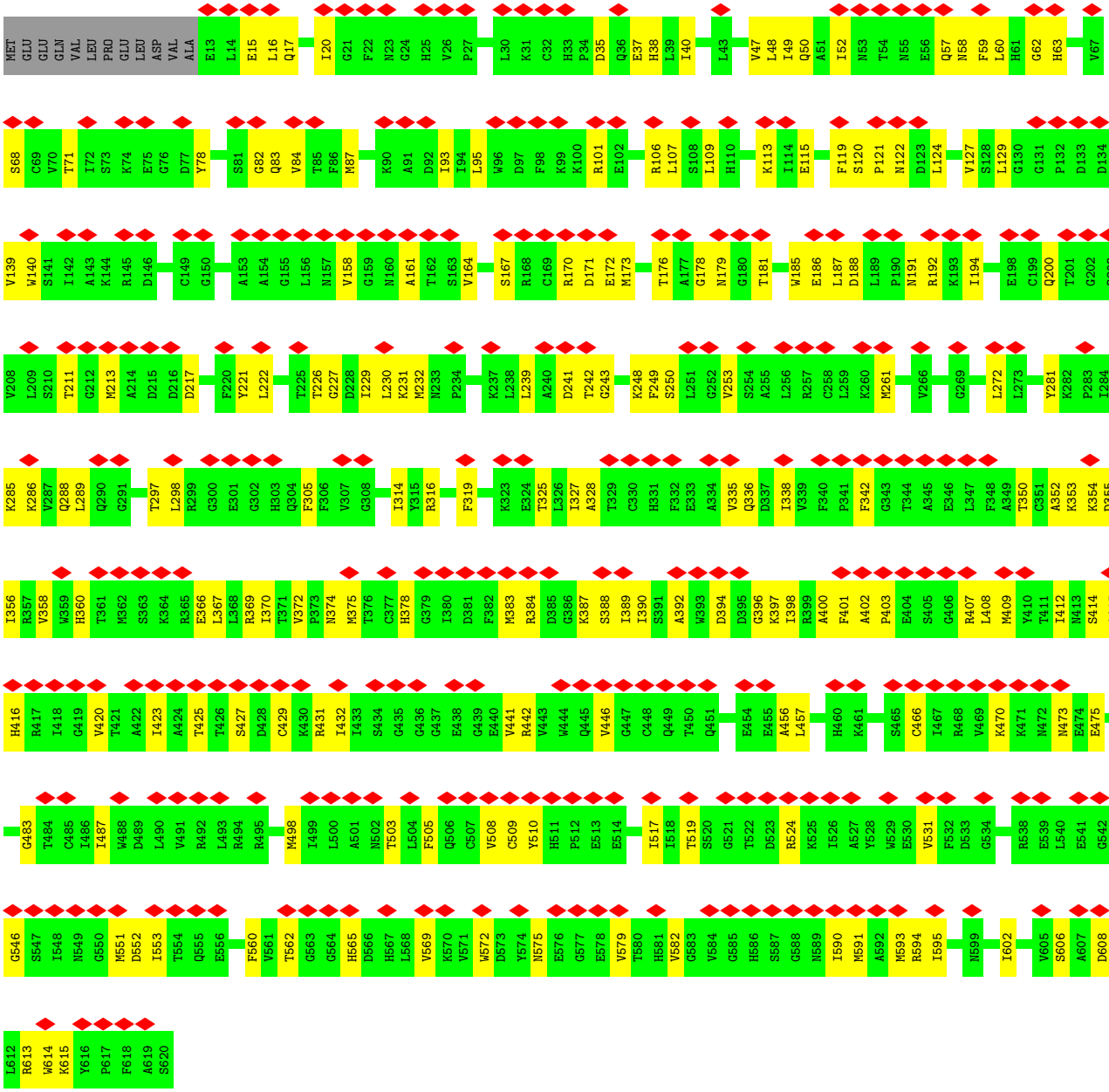




• Molecule 29: Cilia- and flagella-associated protein 52

Chain P3:

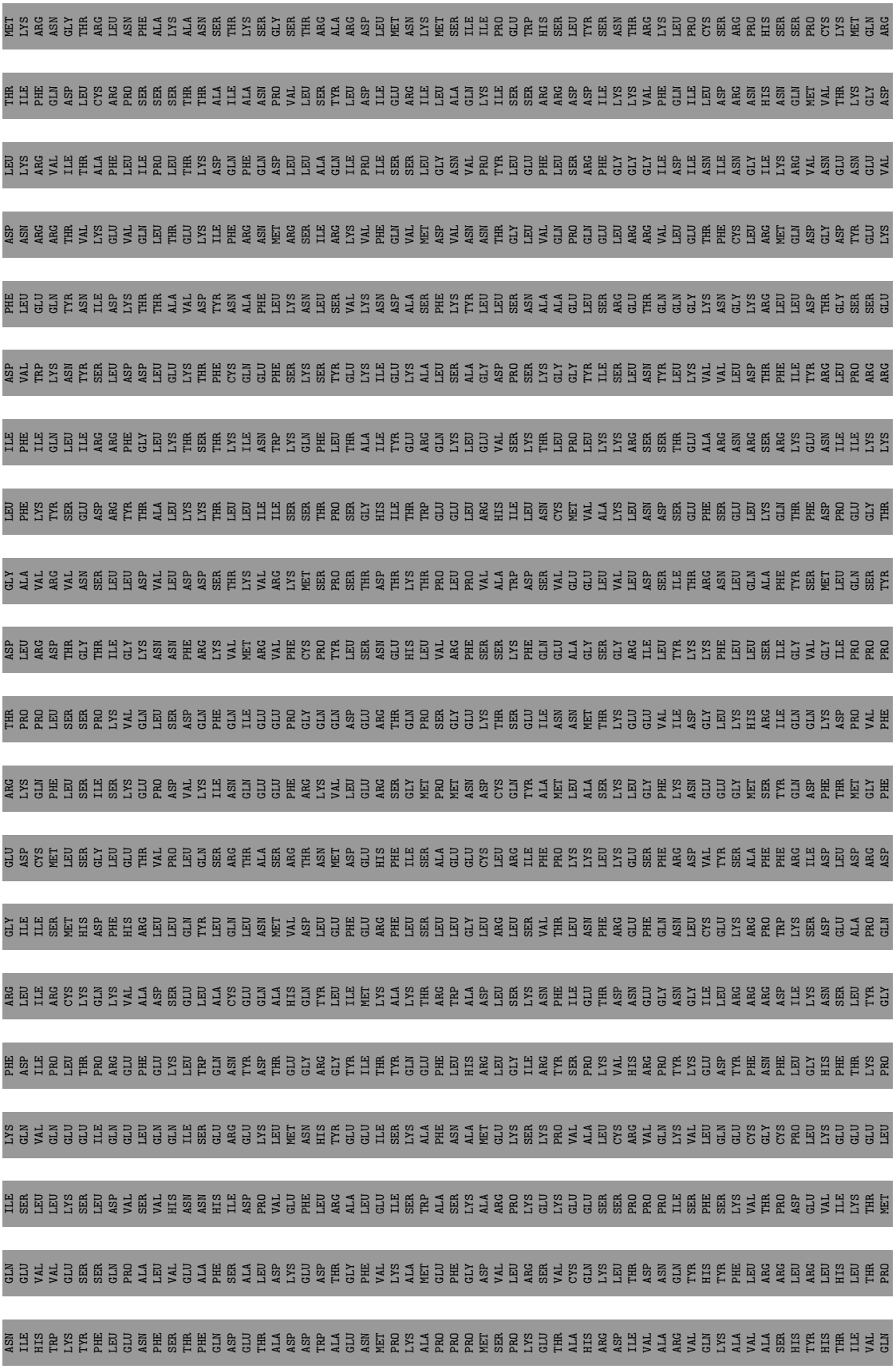


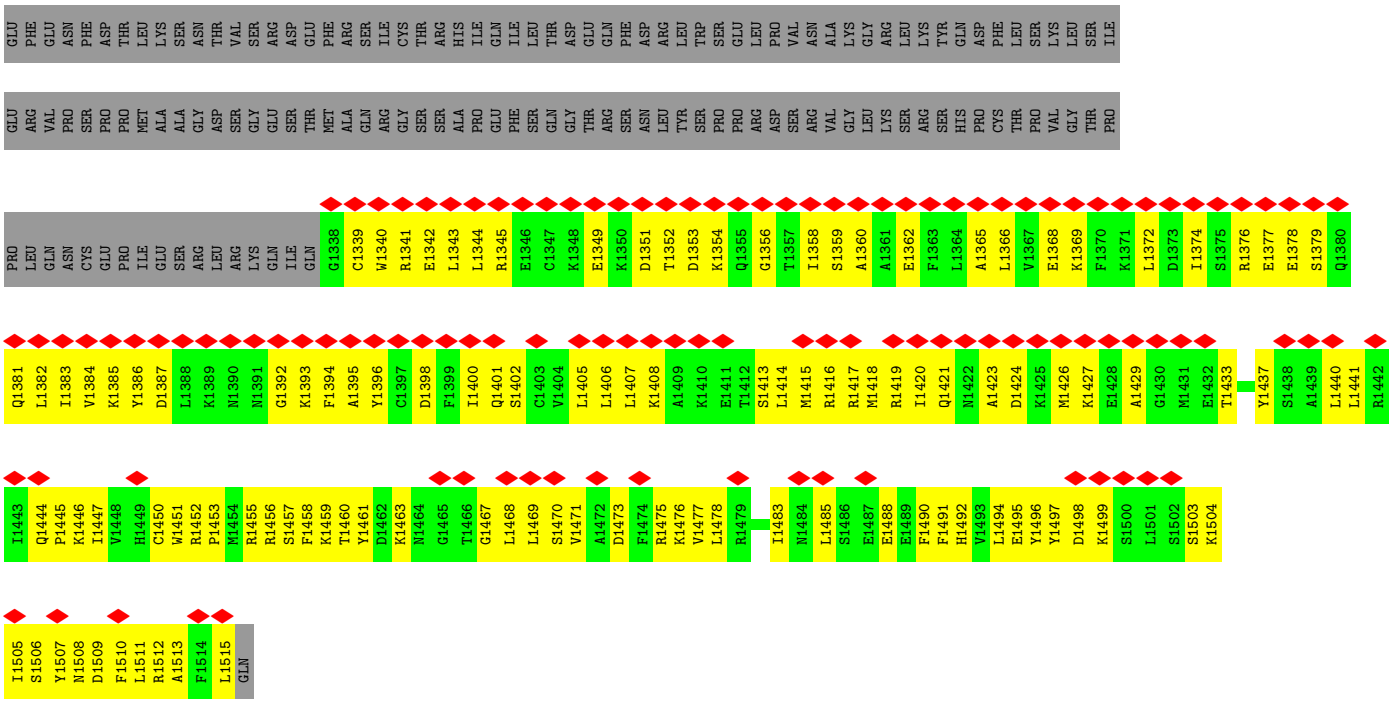


• Molecule 30: EF-hand calcium-binding domain-containing protein 6

Chain Q1:

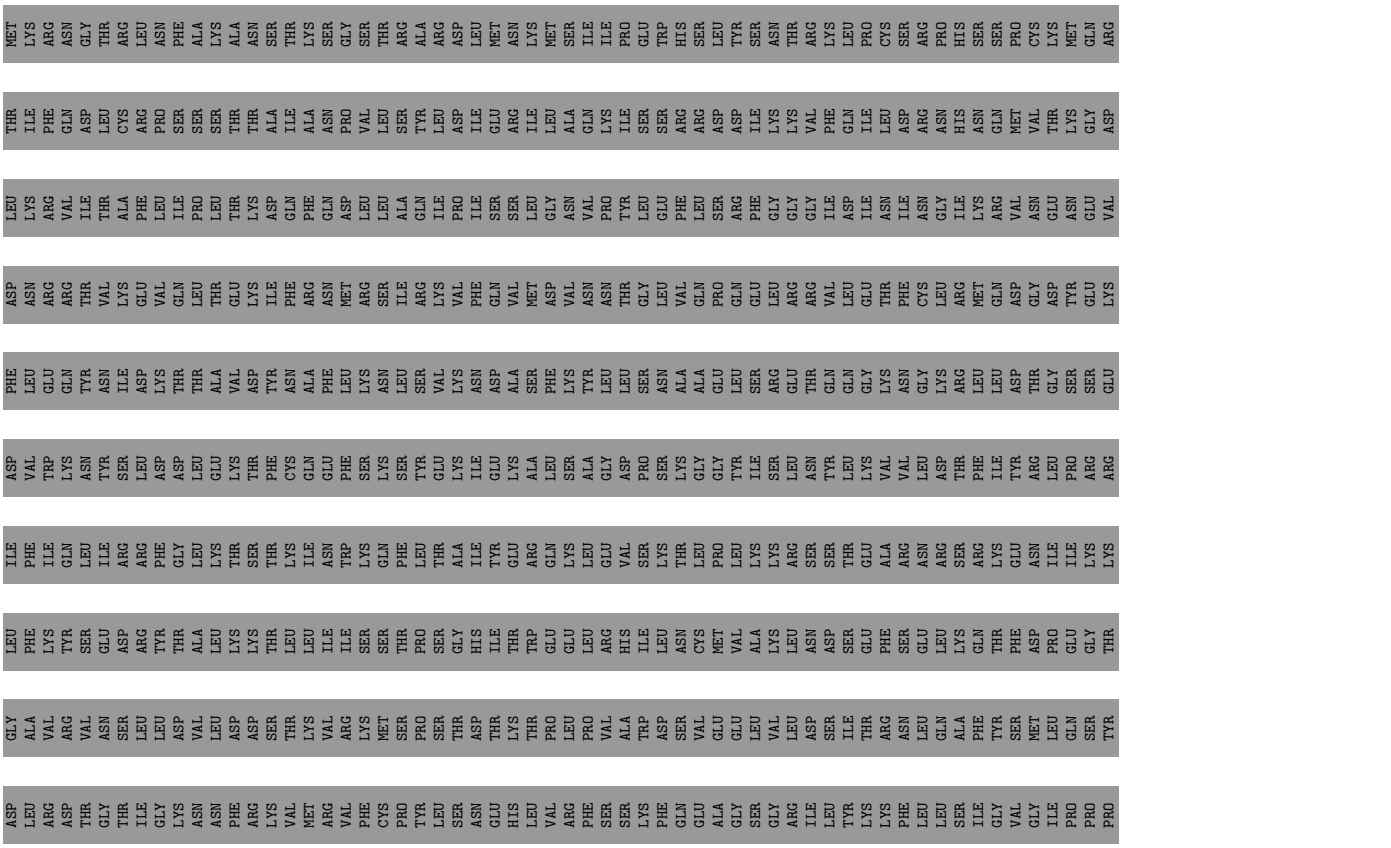
8%
8%
88%

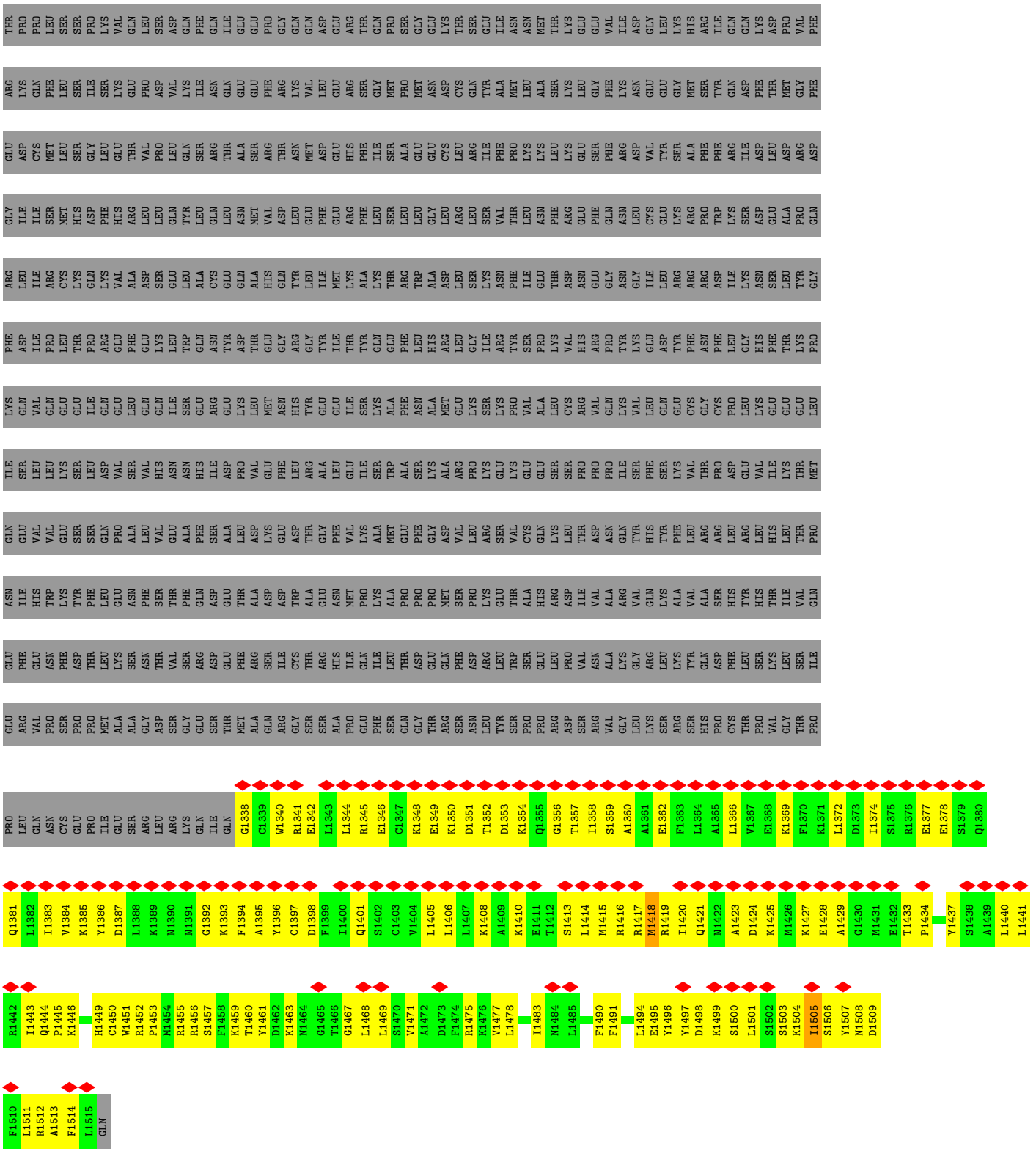

MET LYS ARG ASN GLY THR ARG LEU ASN PHE ALA LYS ALA ASN SER THR LYS SER GLY SER THR ARG ALA ARG ASP LEU MET ASN LYS MET SER ILE ILE PRO GLU TRP HIS SER LEU TYR SER ASN THR ARG LYS LEU PRO CYS SER ARG PRO HIS SER SER PRO CYS LYS MET GLN ARG
THR ILE PHE GLN ASP LEU CYS ARG PRO SER SER SER THR THR ALA ILE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



• Molecule 30: EF-hand calcium-binding domain-containing protein 6

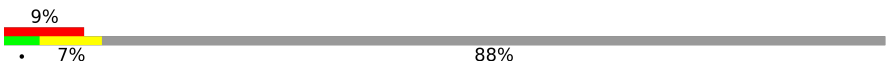
Chain Q2:

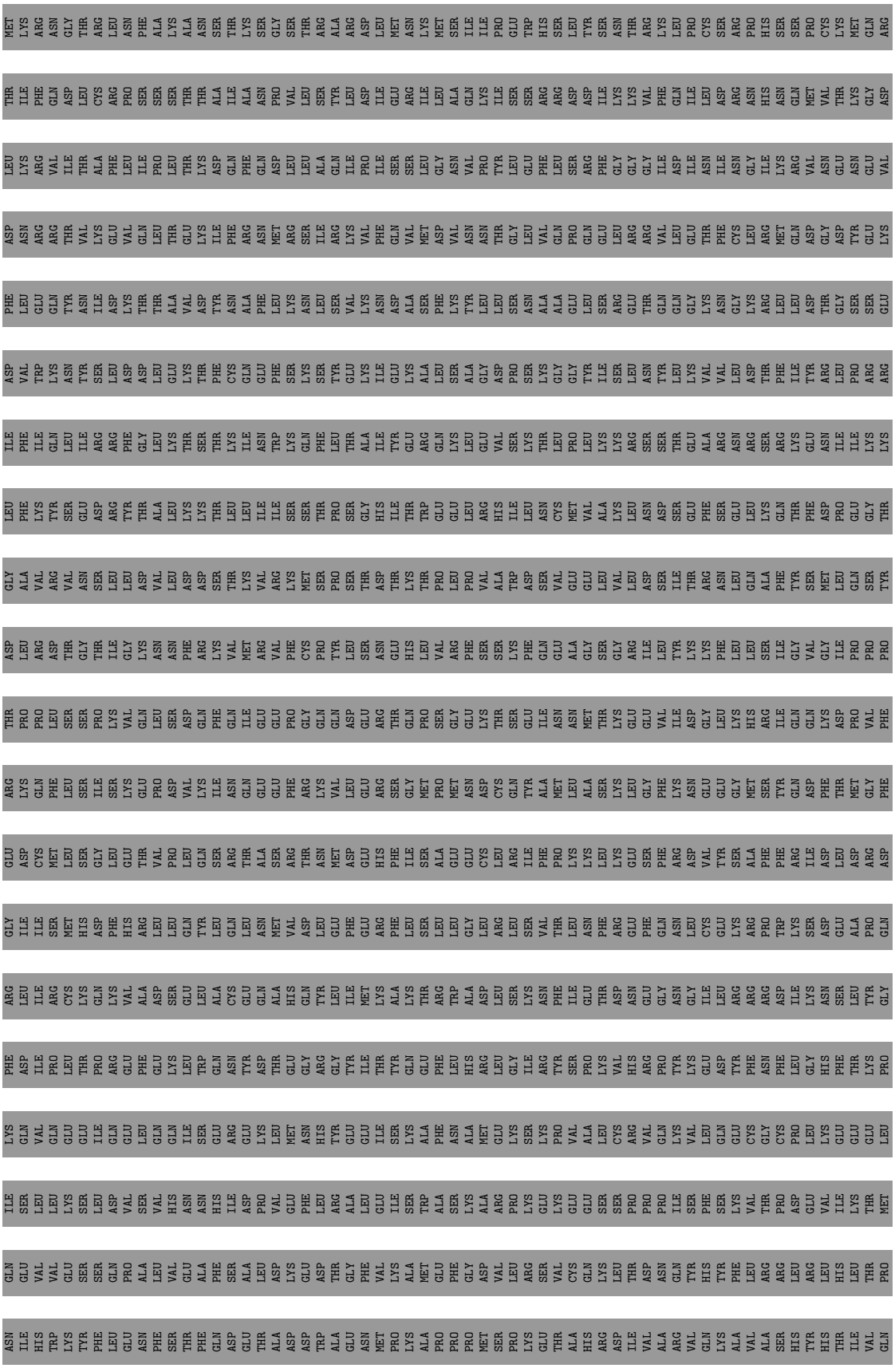




• Molecule 30: EF-hand calcium-binding domain-containing protein 6

Chain Q3:

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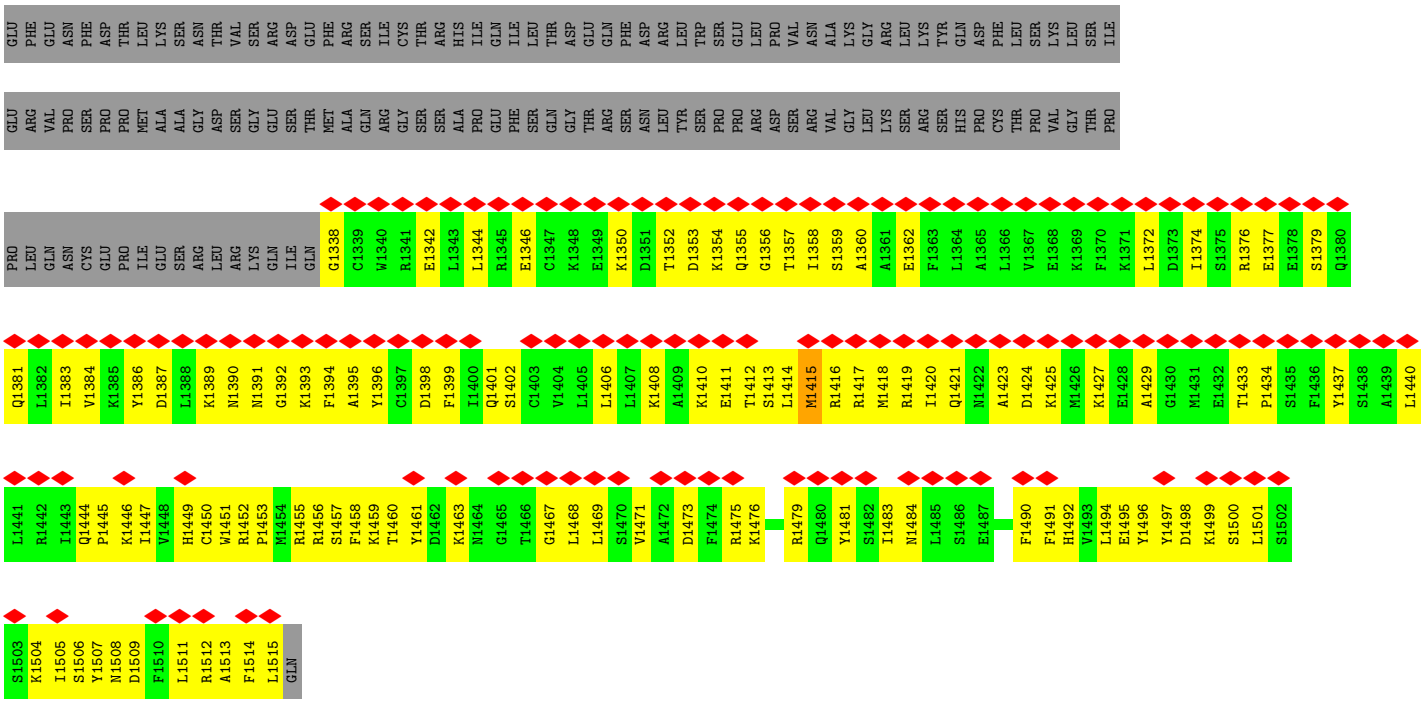
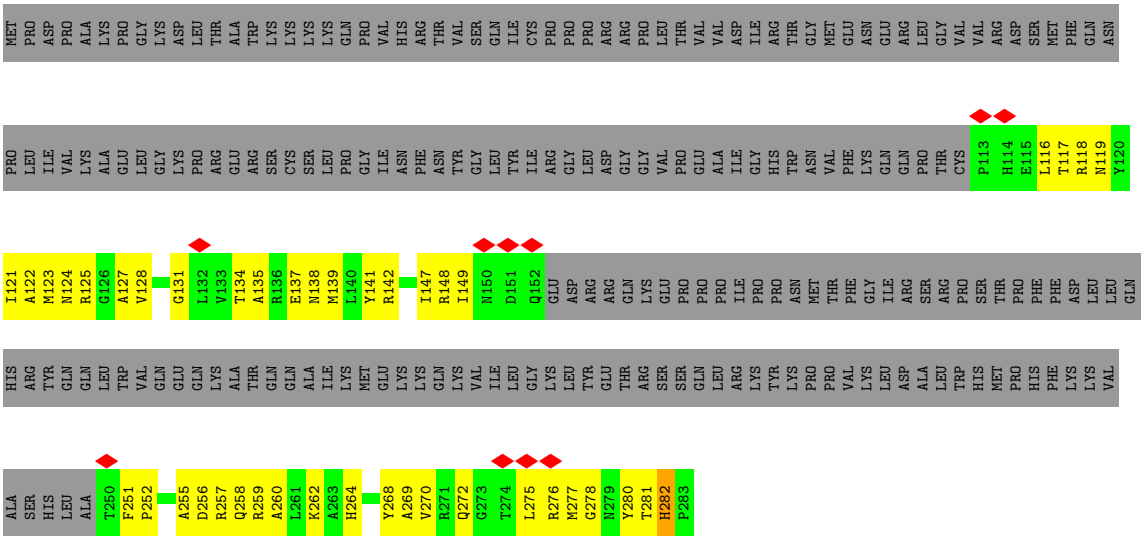
THR ILE PHE GLN ASP LEU CYS ARG PRO SER SER SER THR THR ALA ILE ALA ASN PRO VAL LEU SER TYR LEU ASP ILE GLU ARG ILE LEU LEU ASP ARG ASN GLN LYS ILE SER SER ARG ASP ASP ILE LYS LYS VAL PHE GLN ILE LEU ASP ARG ASN HIS SER ASN GLN MET VAL THR LYS GLY ASP
LEU LYS ARG VAL ILE THR ALA PHE LEU ILE PRO LEU THR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



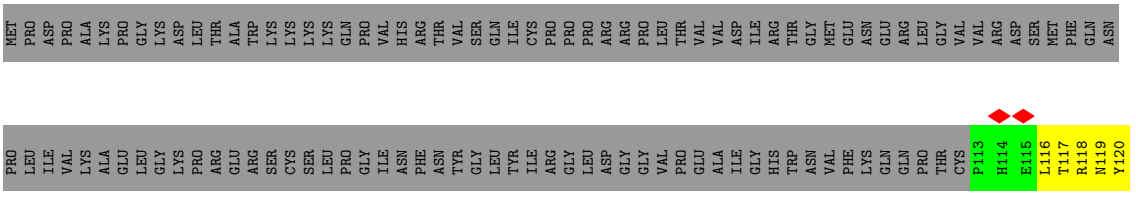
• Molecule 31: Cilia and flagella-associated protein 77

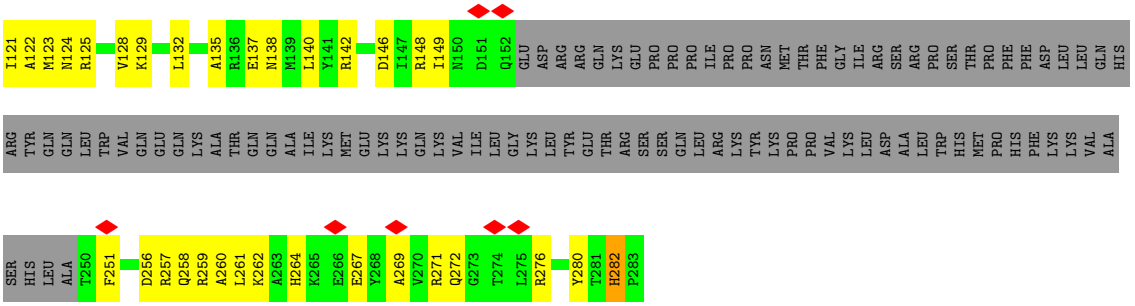
Chain R1:



• Molecule 31: Cilia and flagella-associated protein 77

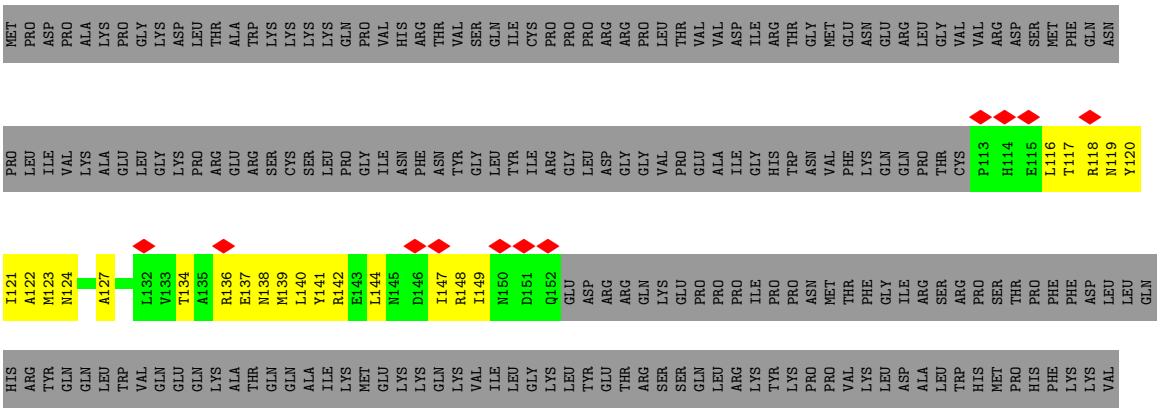
Chain R2:





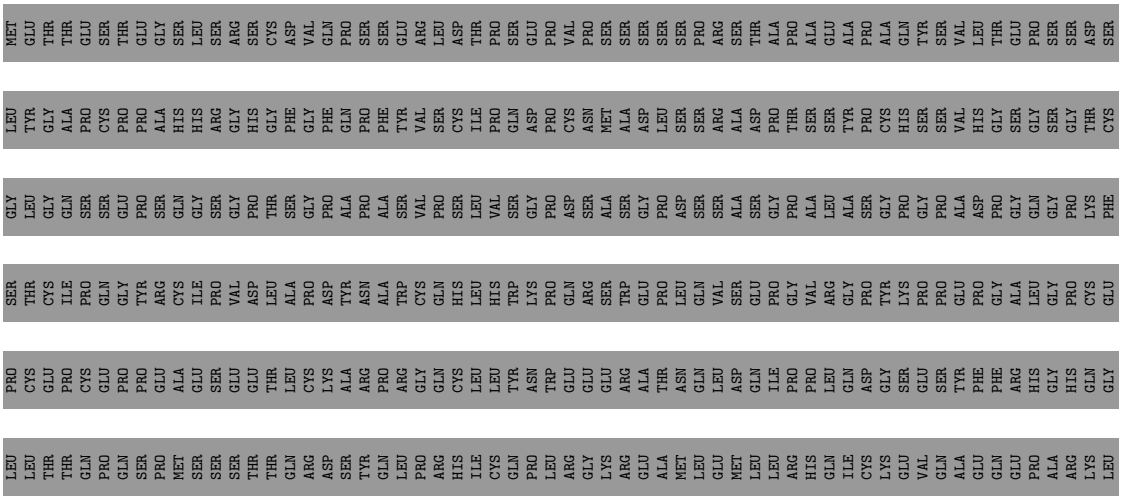
• Molecule 31: Cilia and flagella-associated protein 77

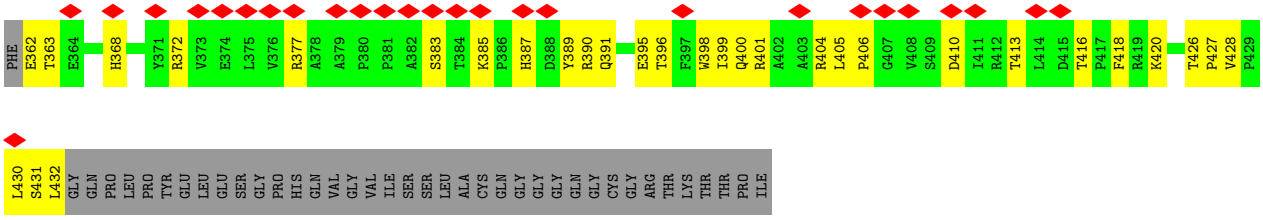
Chain R3:



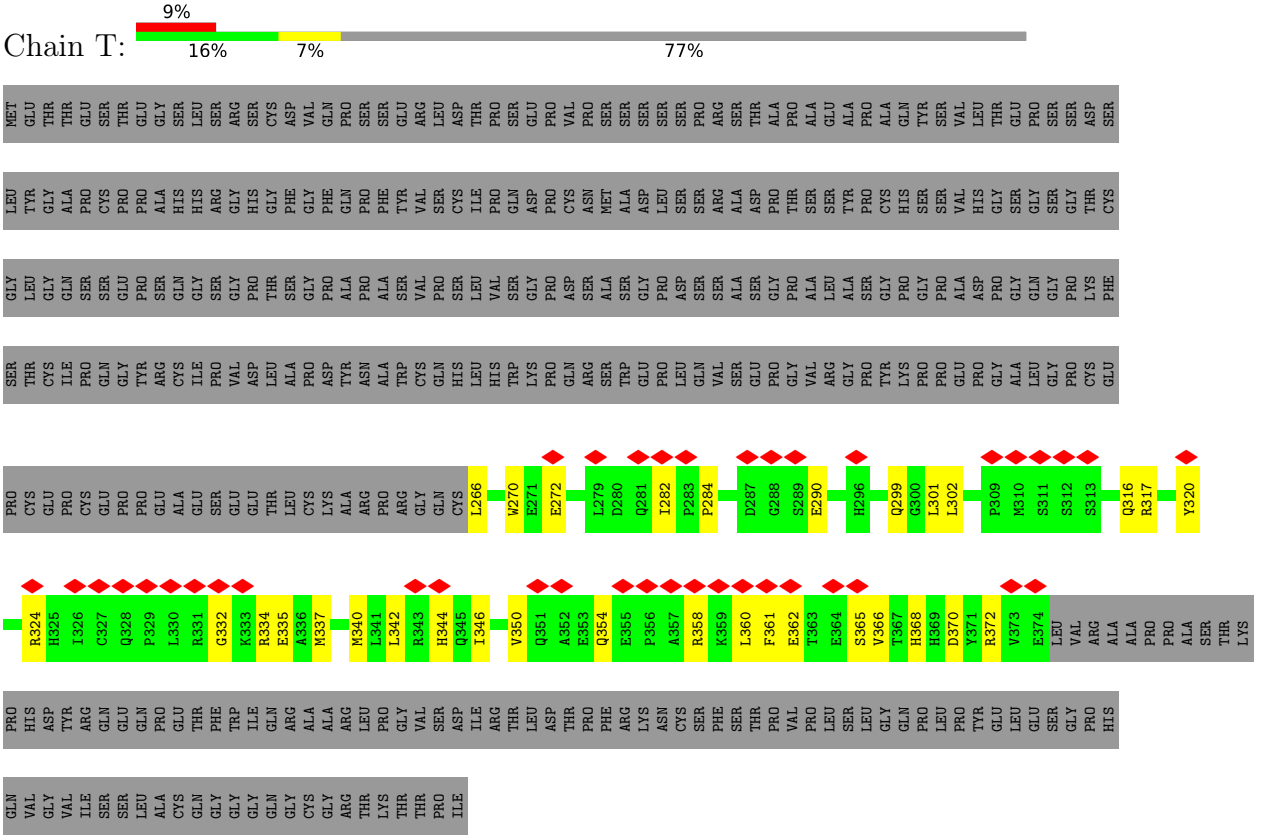
• Molecule 32: Sperm-associated antigen 8

Chain S:

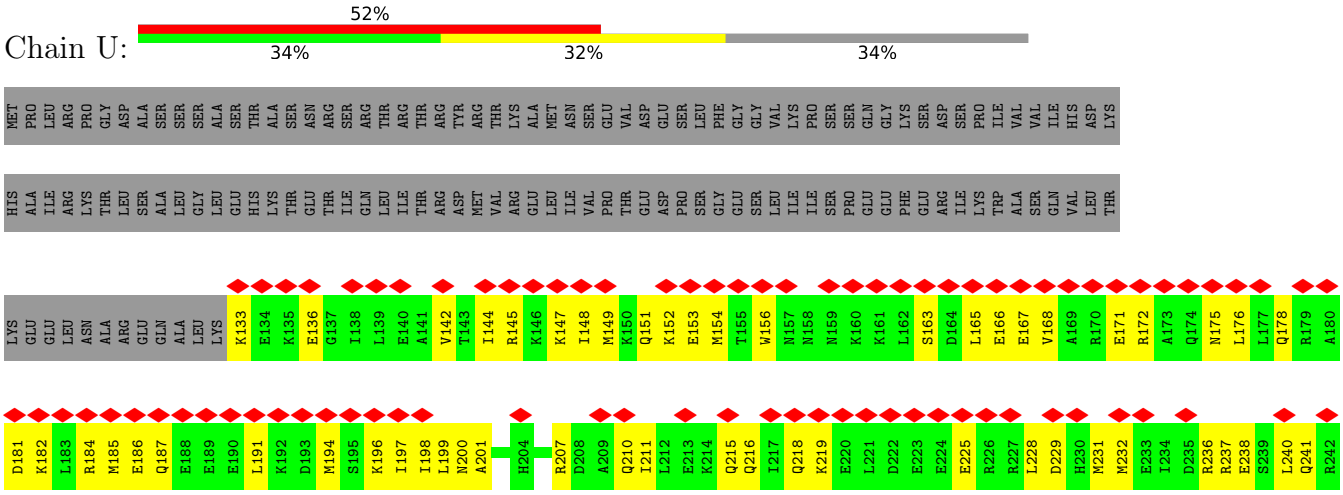


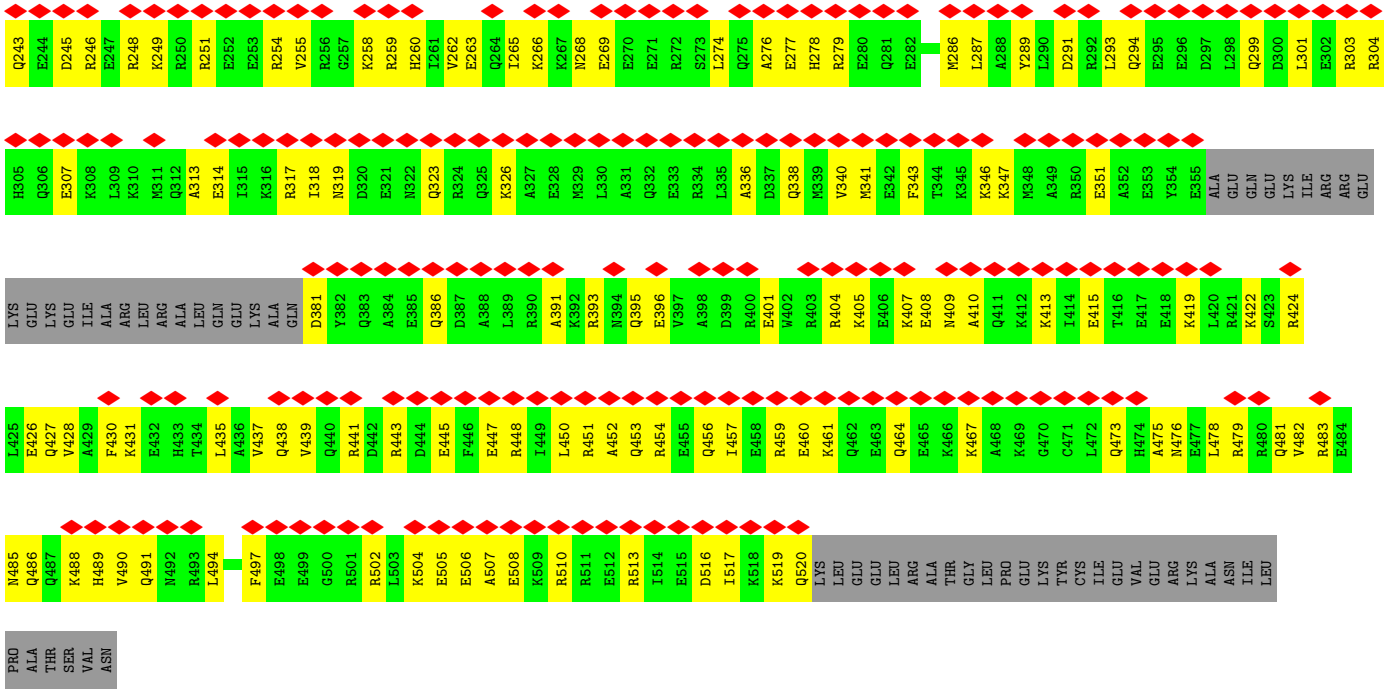


• Molecule 32: Sperm-associated antigen 8

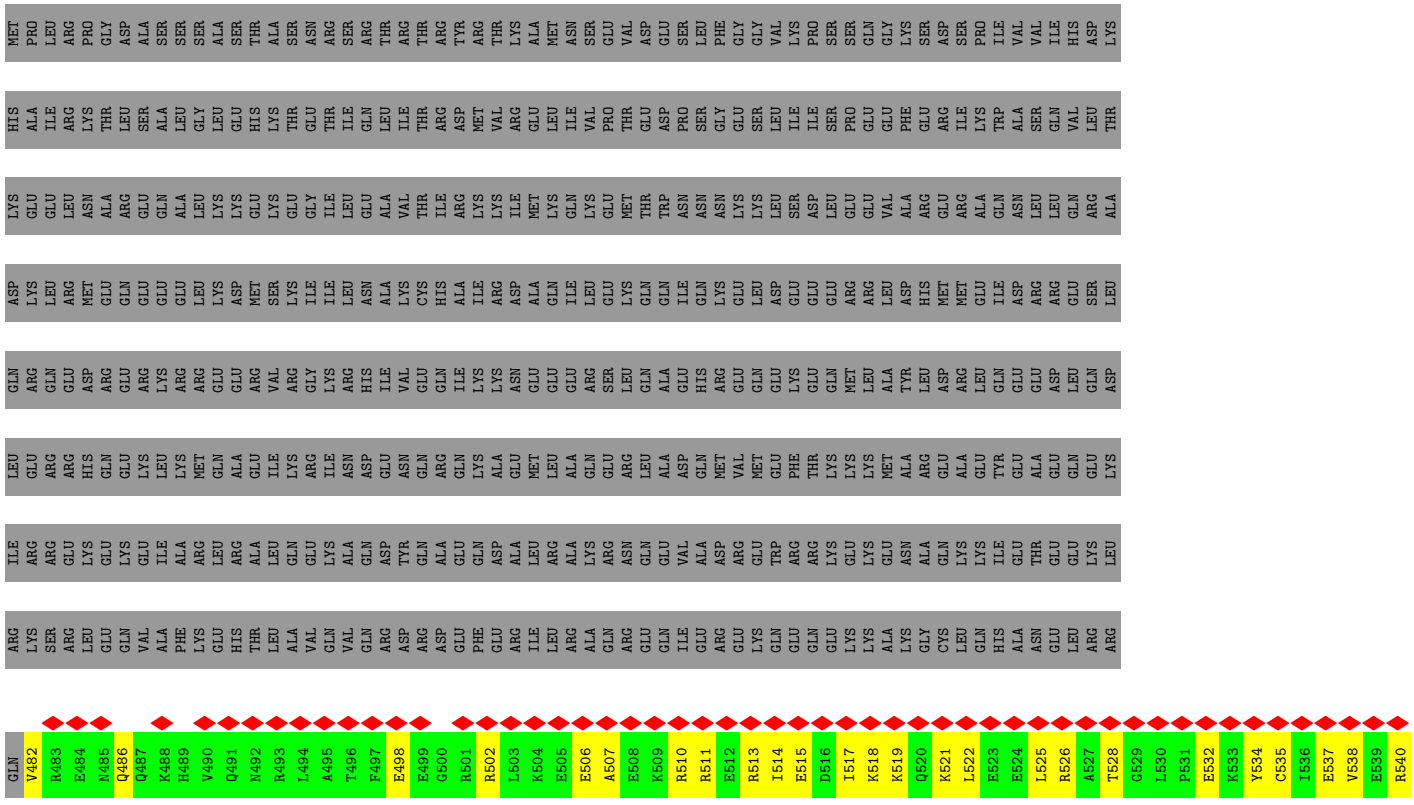


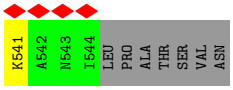
• Molecule 33: Cilia- and flagella-associated protein 45





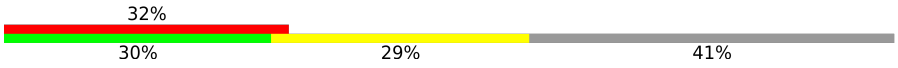
- Molecule 33: Cilia- and flagella-associated protein 45

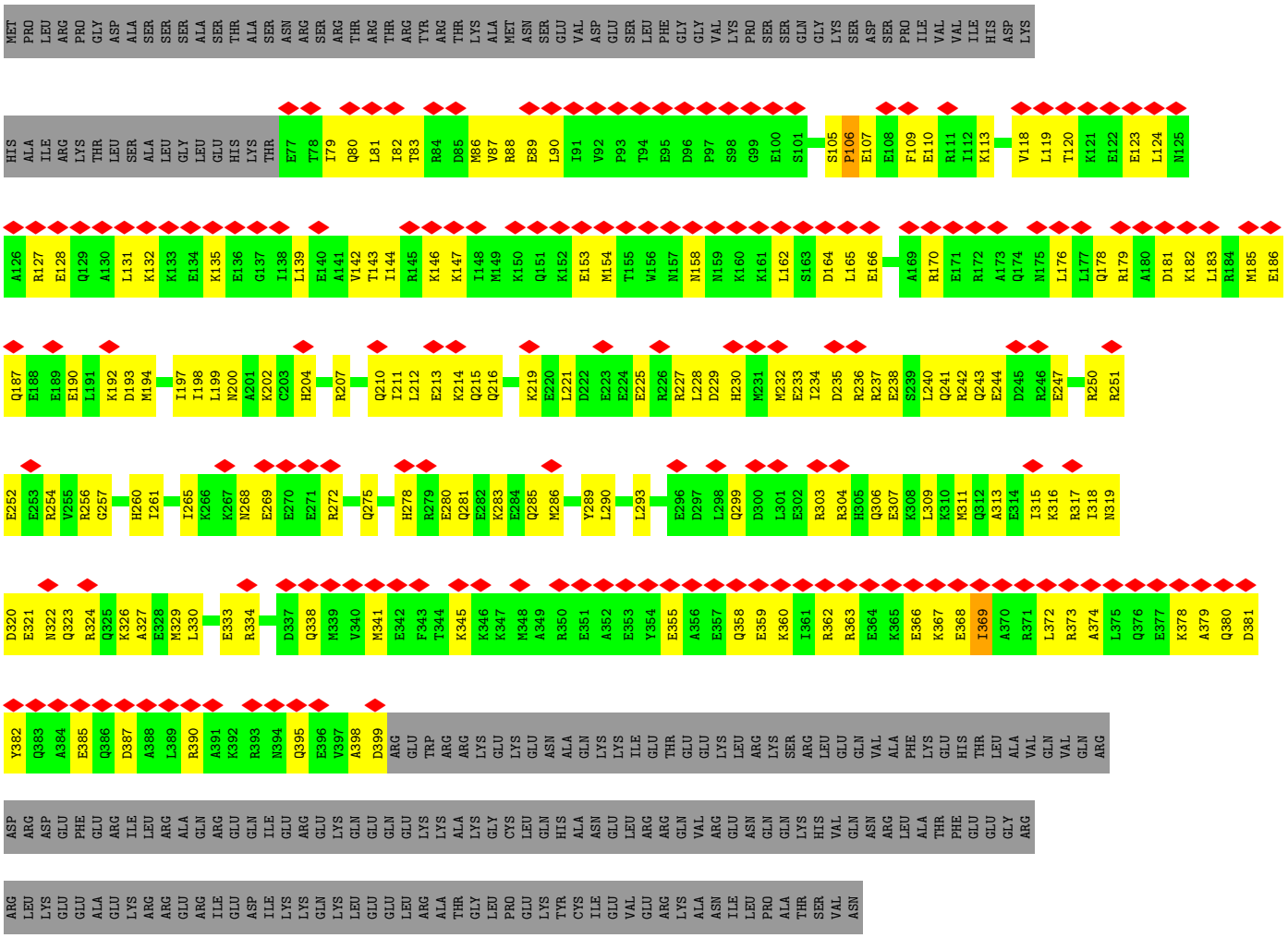




• Molecule 33: Cilia- and flagella-associated protein 45

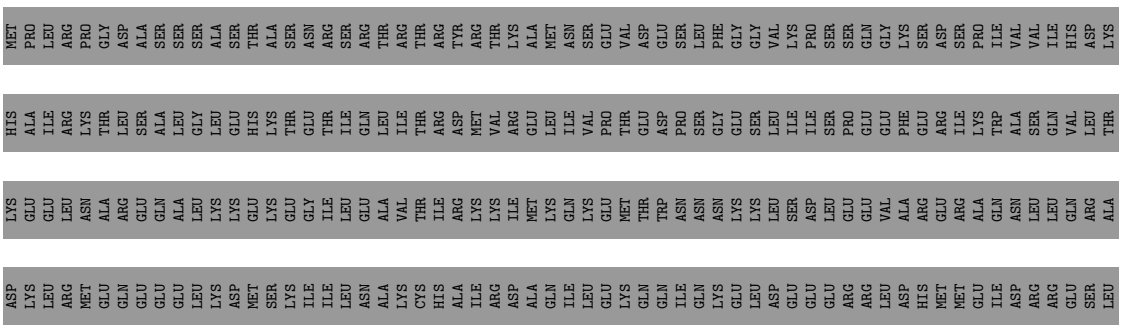
Chain W:

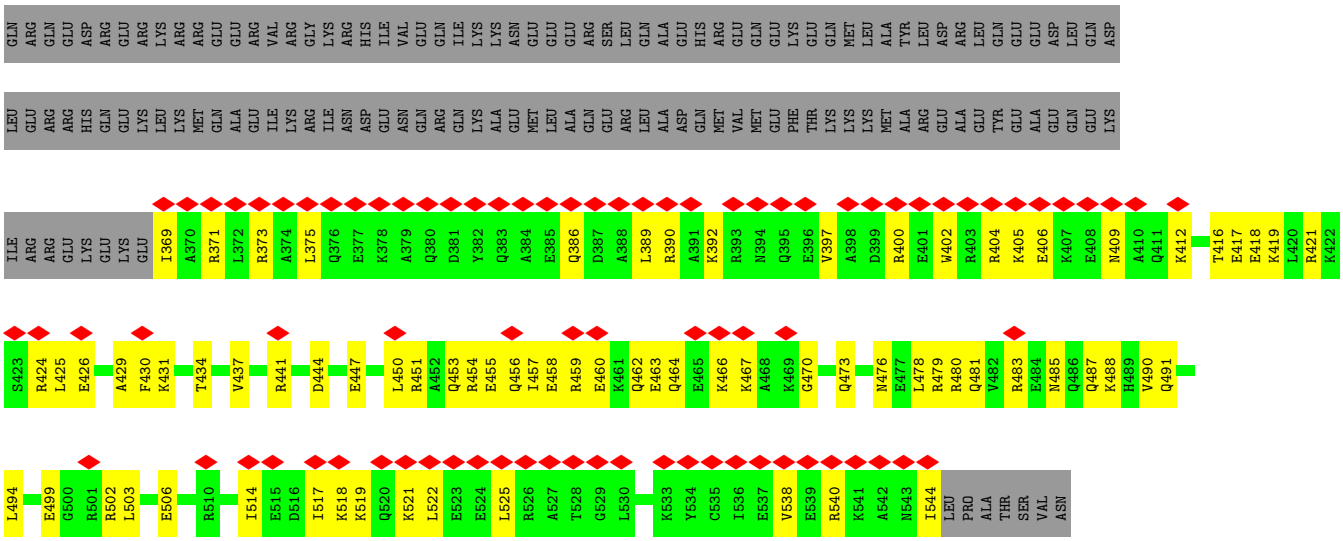




• Molecule 33: Cilia- and flagella-associated protein 45

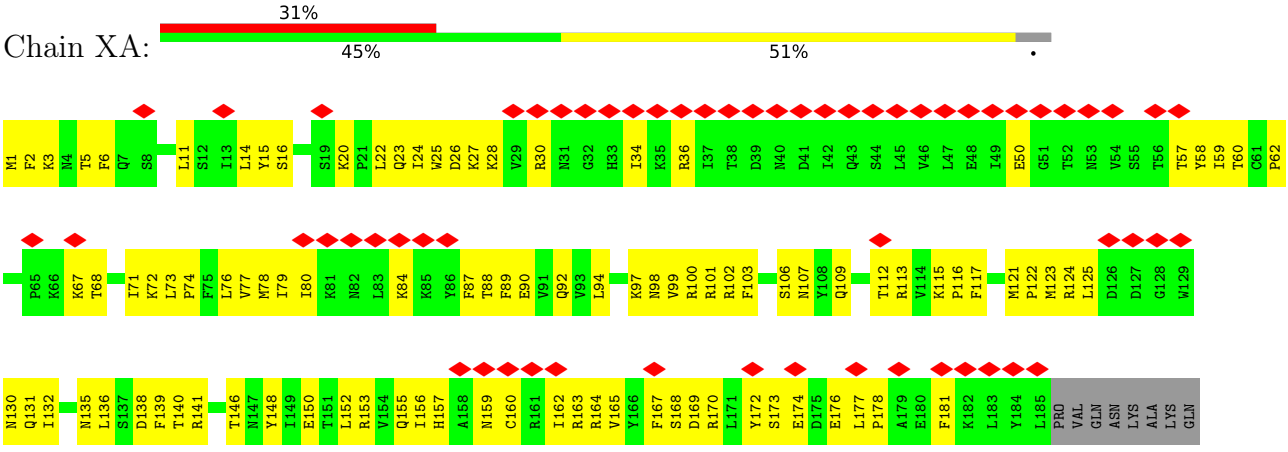
Chain X:





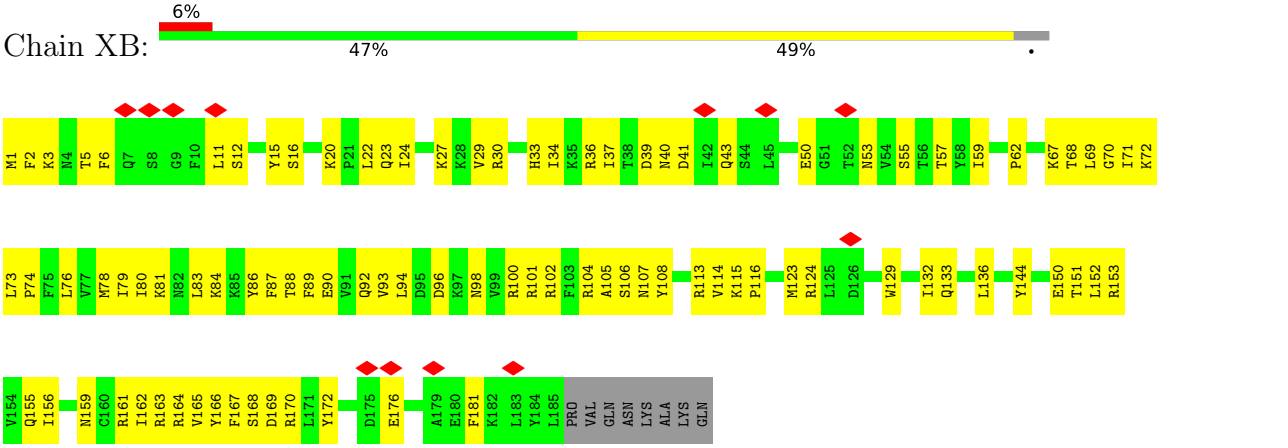
• Molecule 34: Cilia- and flagella-associated protein 20

Chain XA:



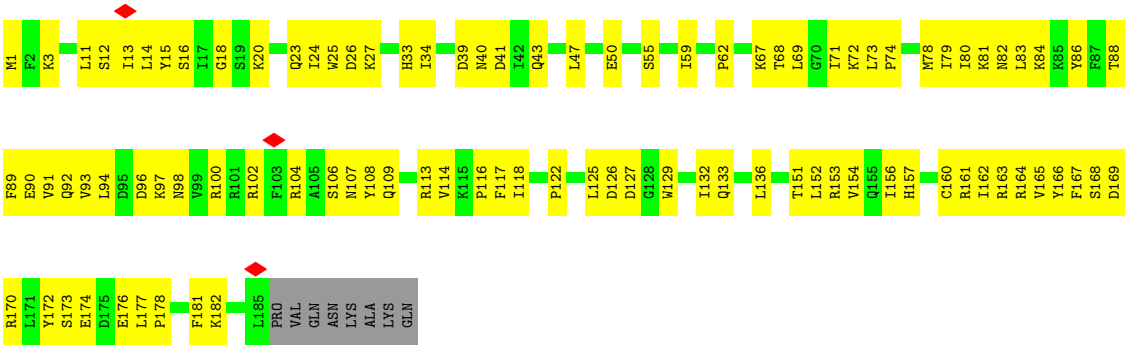
• Molecule 34: Cilia- and flagella-associated protein 20

Chain XB:

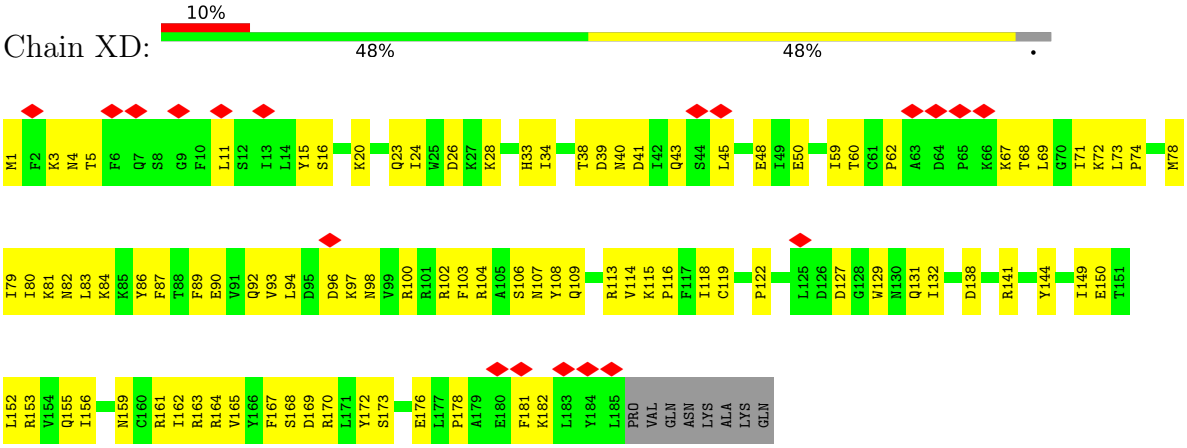


• Molecule 34: Cilia- and flagella-associated protein 20

Chain XC:



• Molecule 34: Cilia- and flagella-associated protein 20



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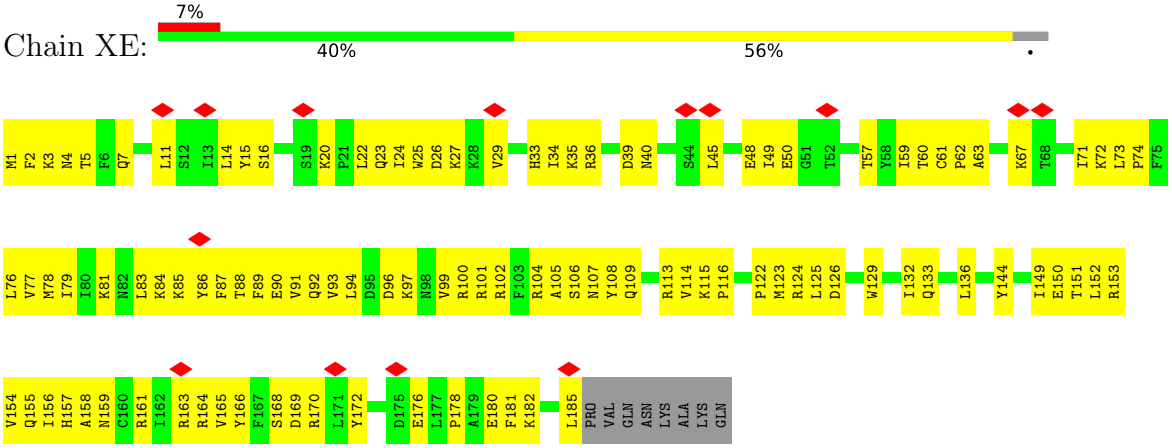
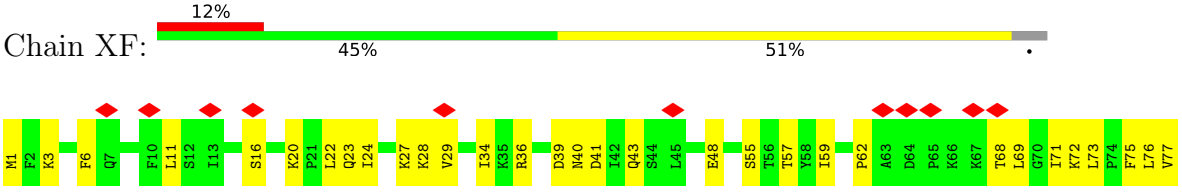
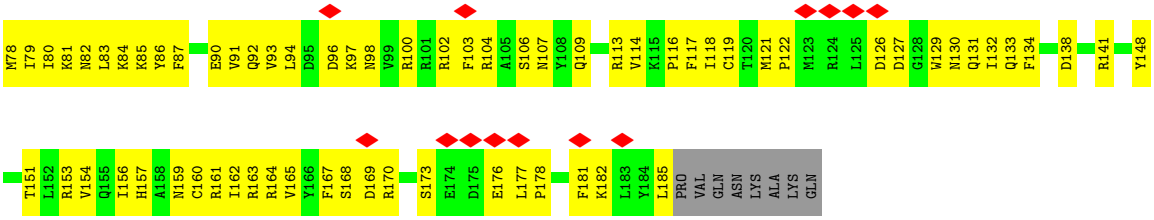
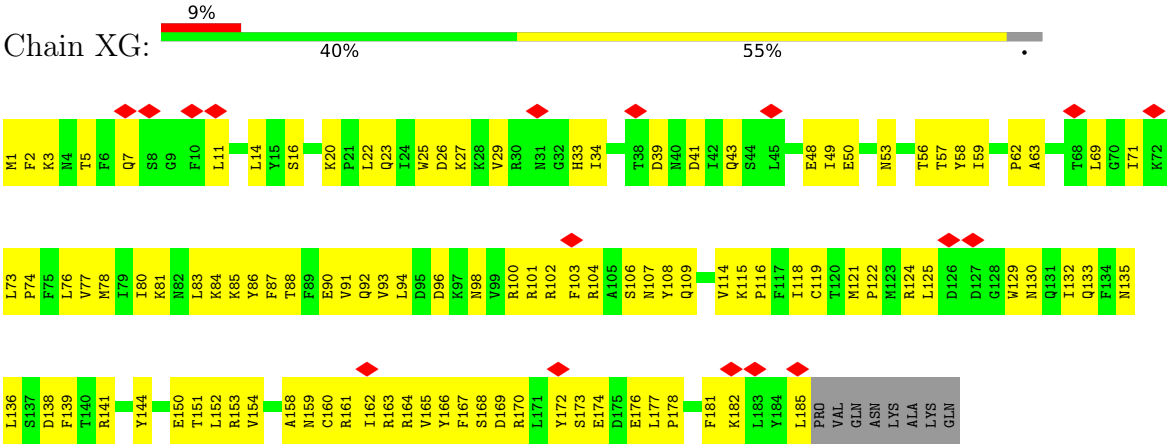


• Molecule 34: Cilia- and flagella-associated protein 20

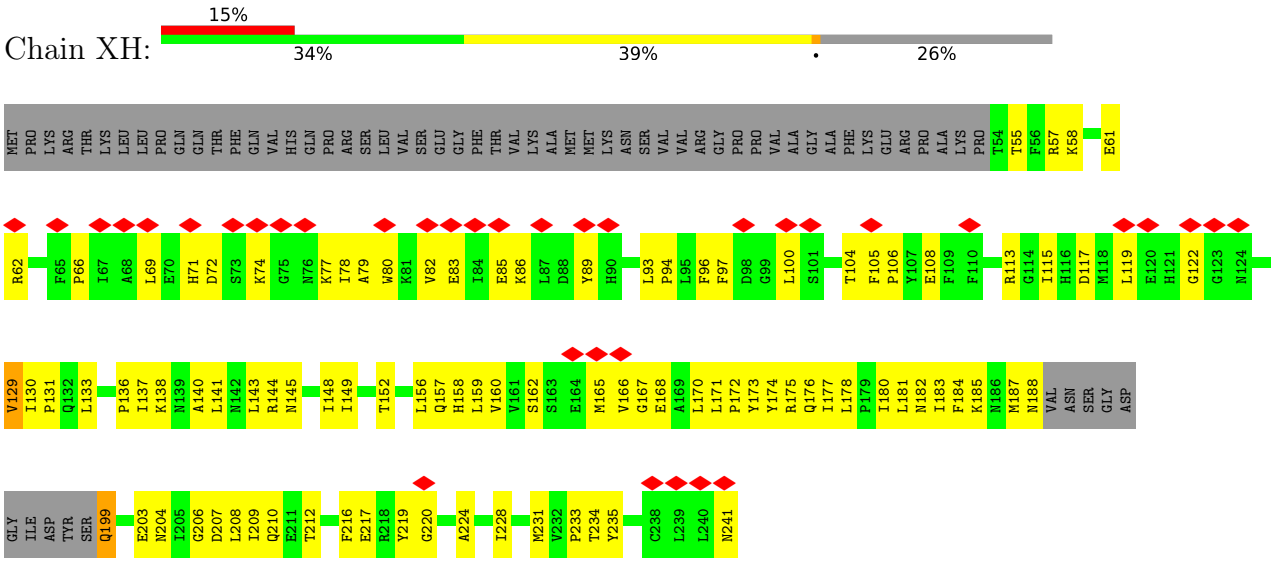




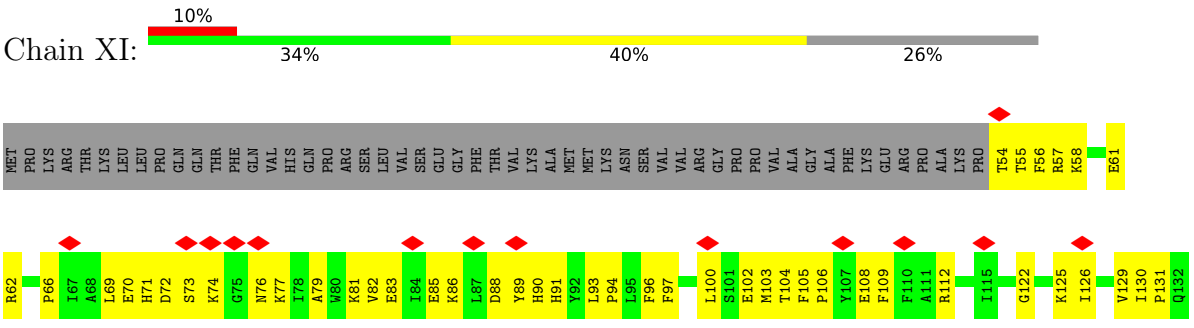
• Molecule 34: Cilia- and flagella-associated protein 20

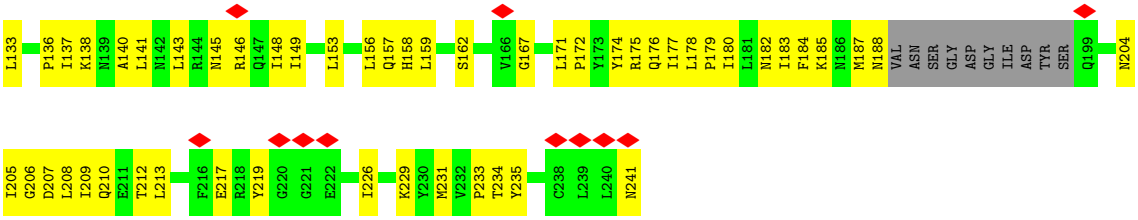


• Molecule 35: Parkin coregulated gene protein homolog

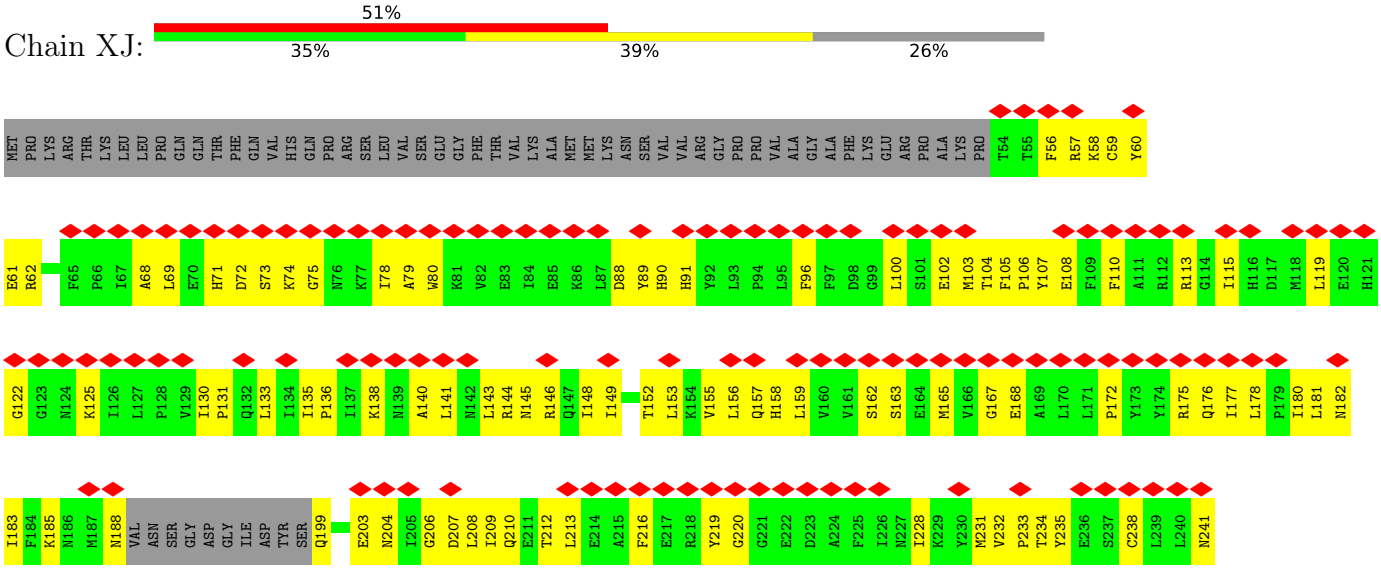


• Molecule 35: Parkin coregulated gene protein homolog

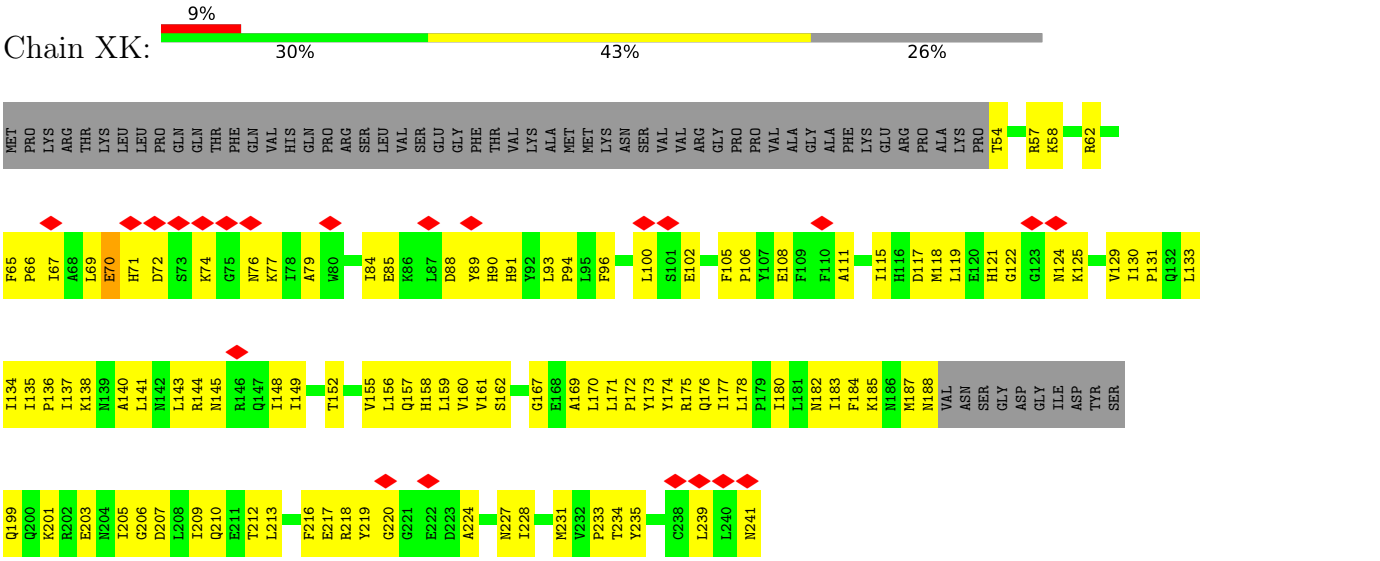




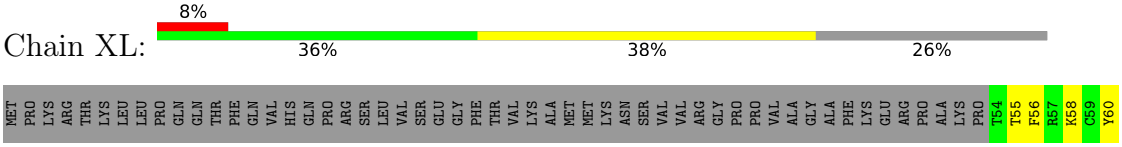
• Molecule 35: Parkin coregulated gene protein homolog

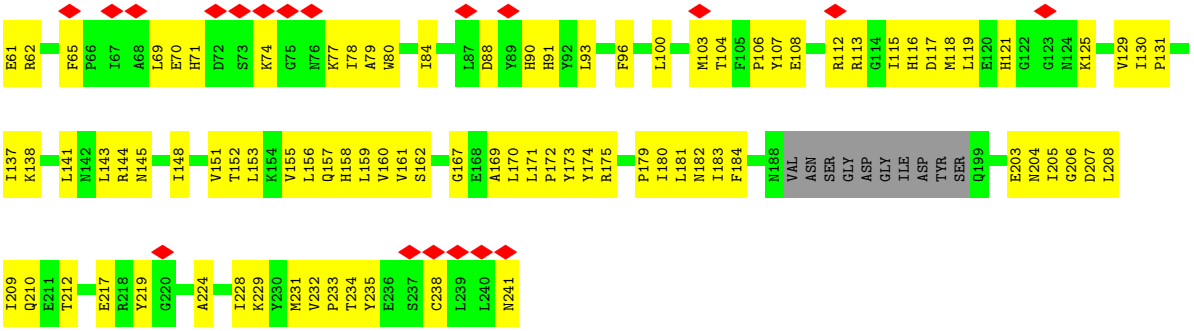


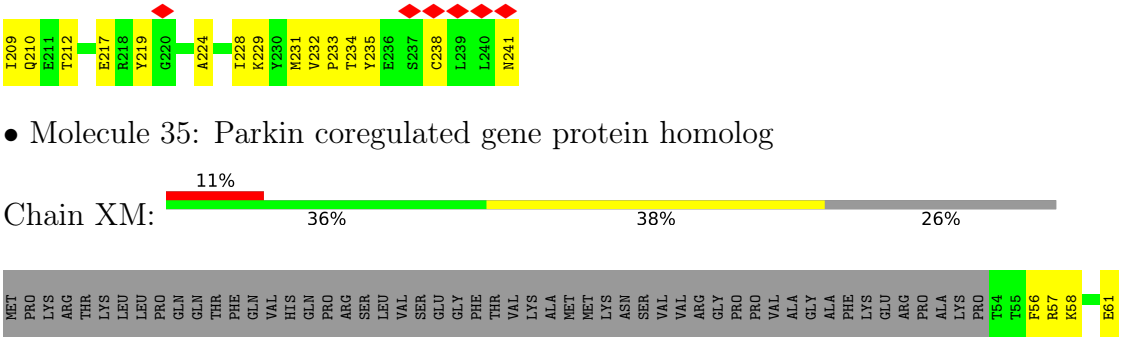
• Molecule 35: Parkin coregulated gene protein homolog



• Molecule 35: Parkin coregulated gene protein homolog

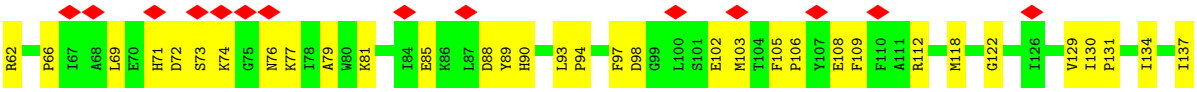


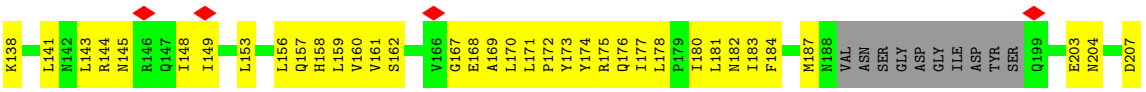


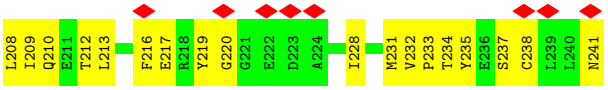


• Molecule 35: Parkin coregulated gene protein homolog

Chain XM:

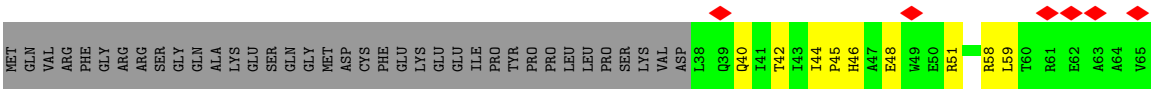


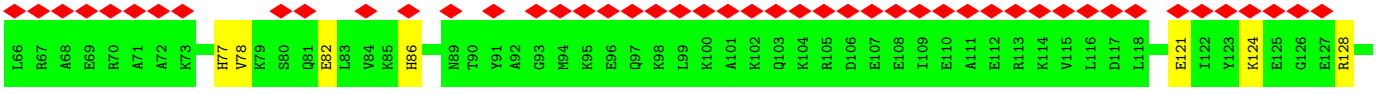


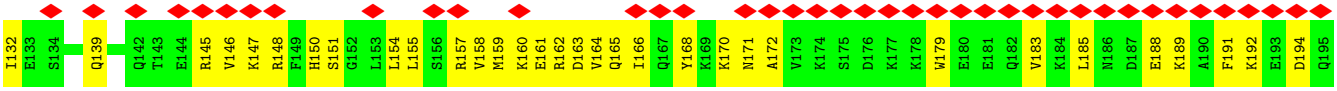


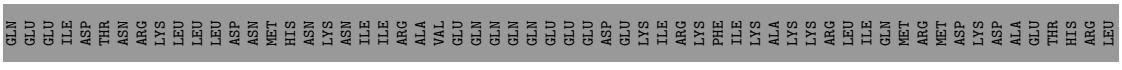
• Molecule 36: Cilia- and flagella-associated protein 210

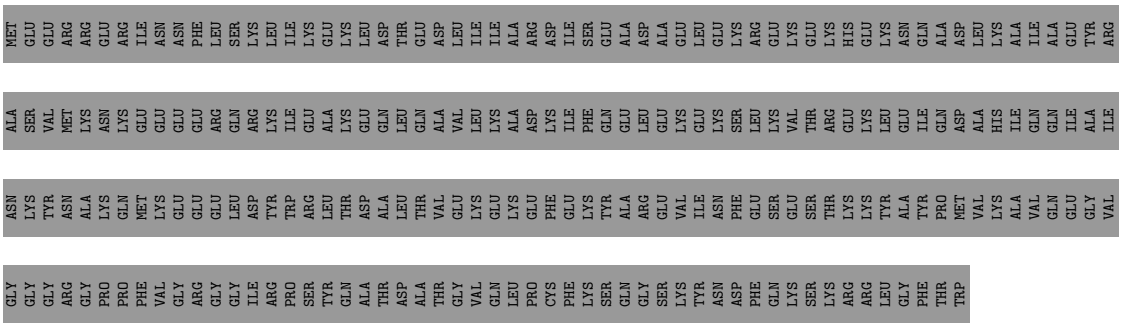
Chain Y:





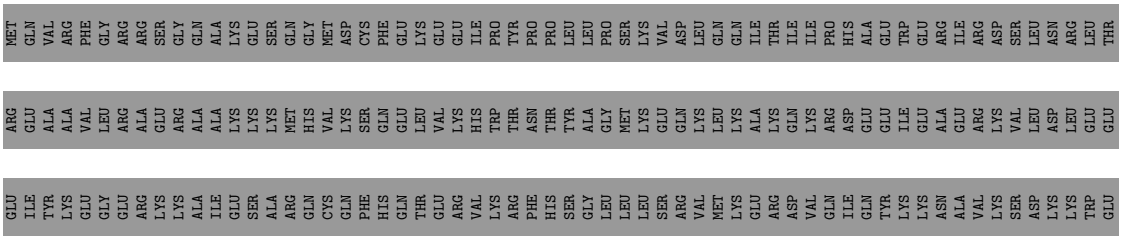


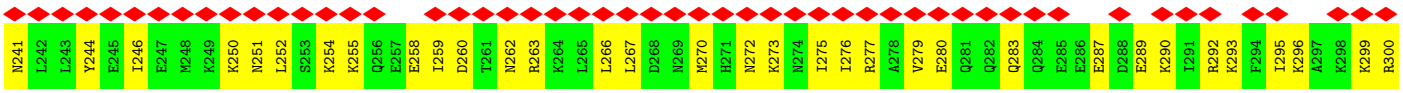


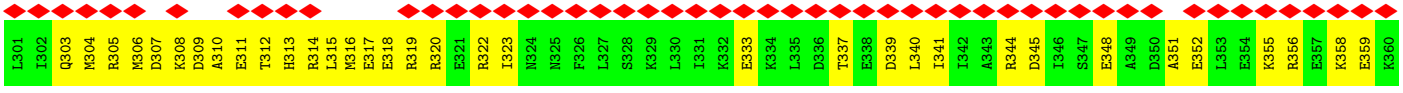


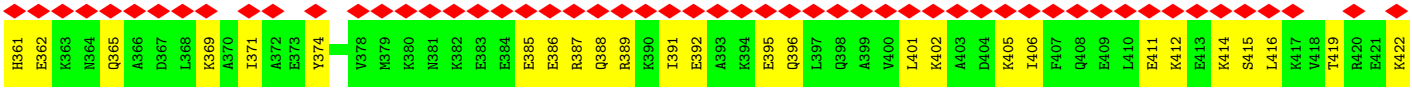
• Molecule 36: Cilia- and flagella-associated protein 210

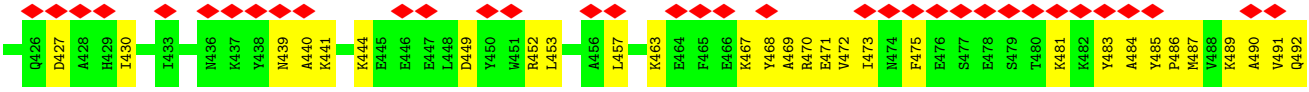
Chain Z:

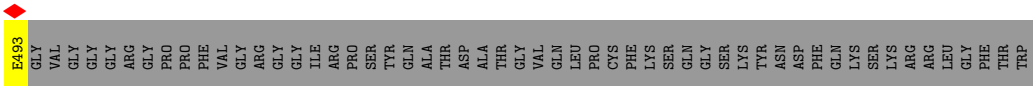






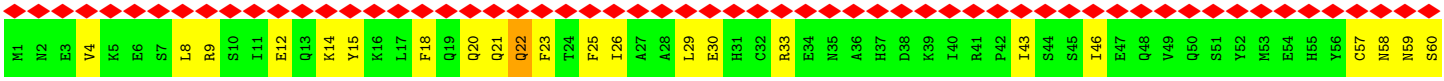


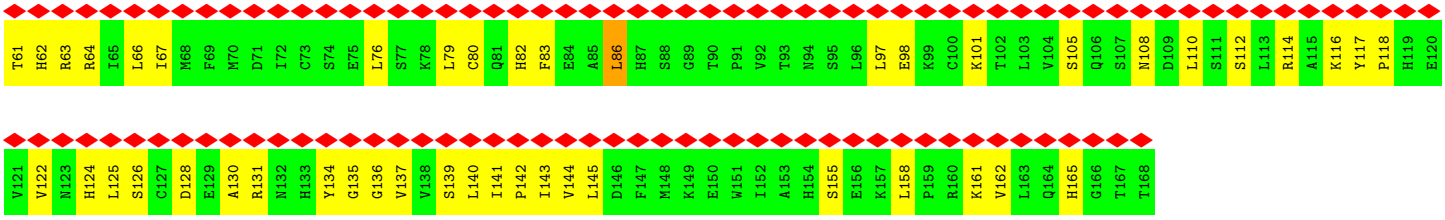




• Molecule 37: Sperm acrosome-associated protein 9

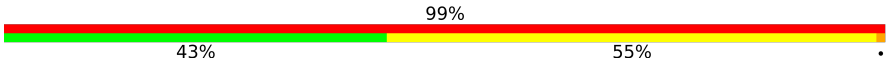
Chain YA:

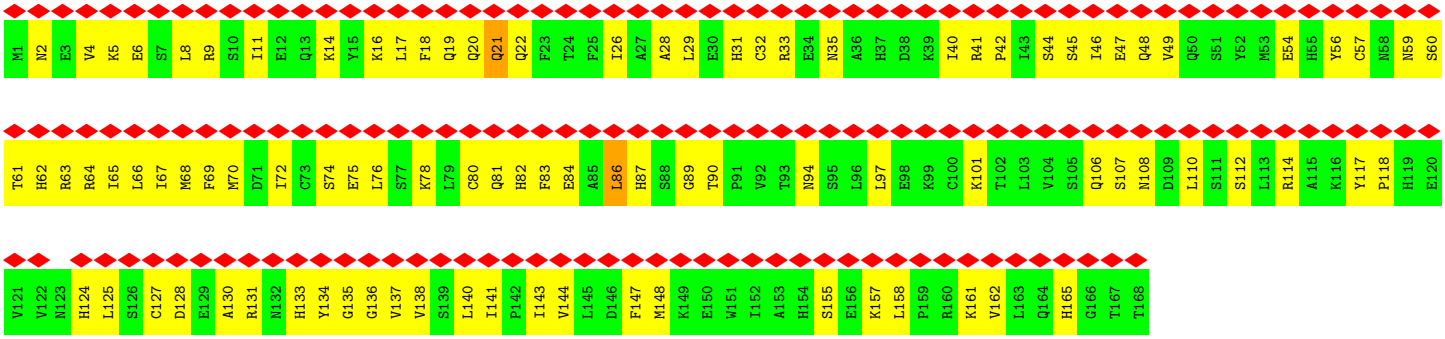




• Molecule 37: Sperm acrosome-associated protein 9

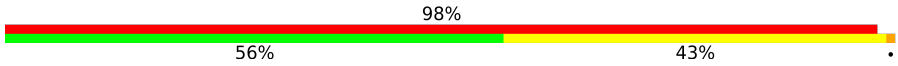
Chain YB:

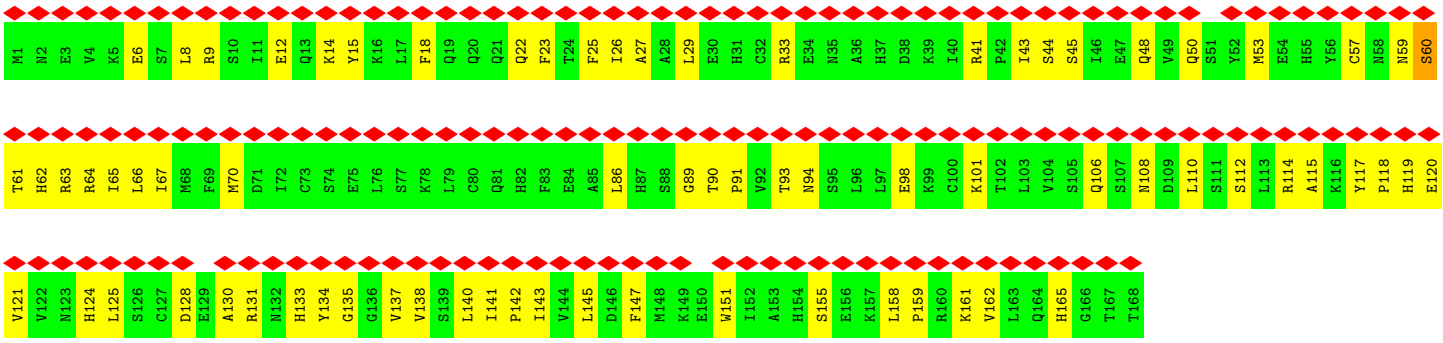




• Molecule 37: Sperm acrosome-associated protein 9

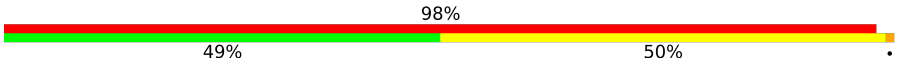
Chain YC:

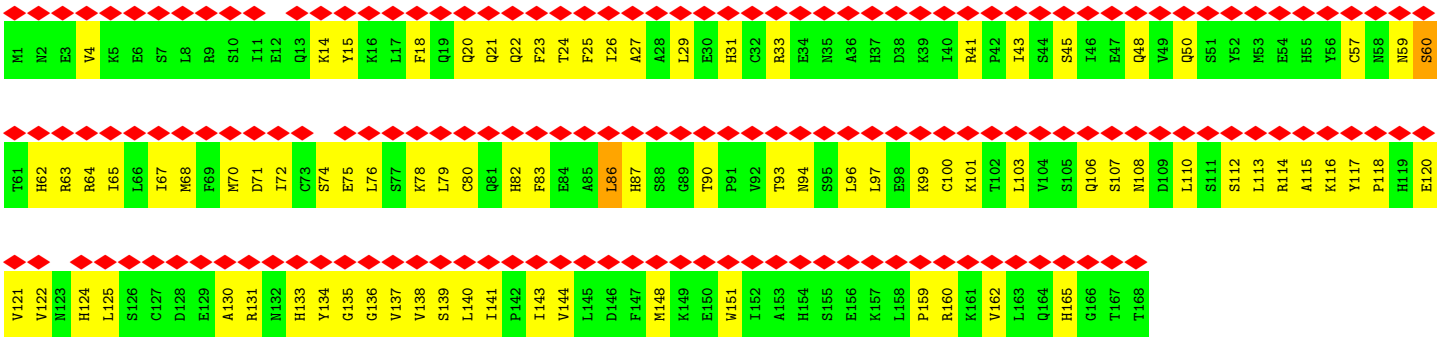




• Molecule 37: Sperm acrosome-associated protein 9

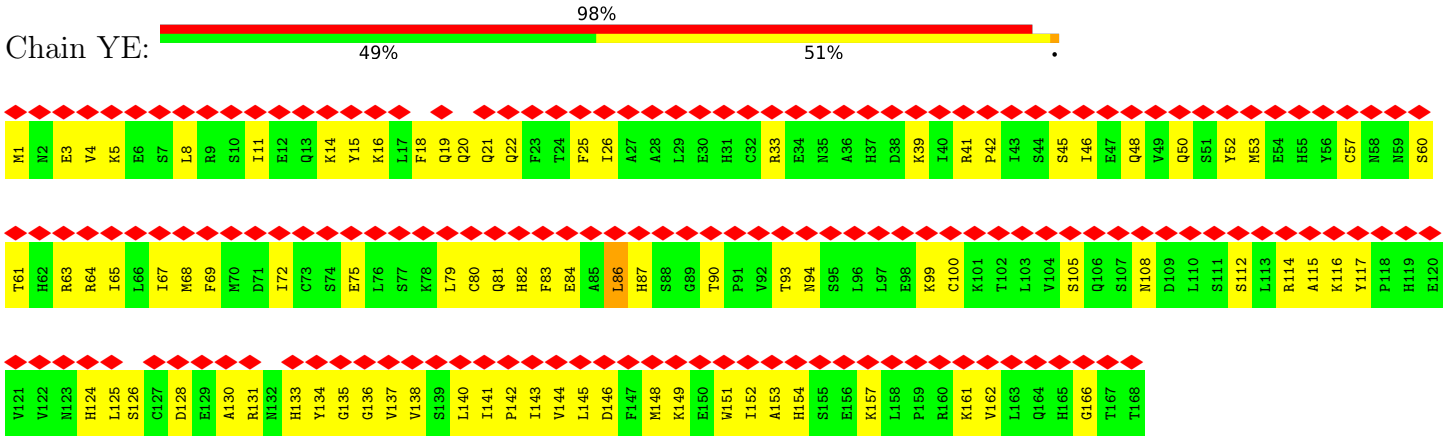
Chain YD:





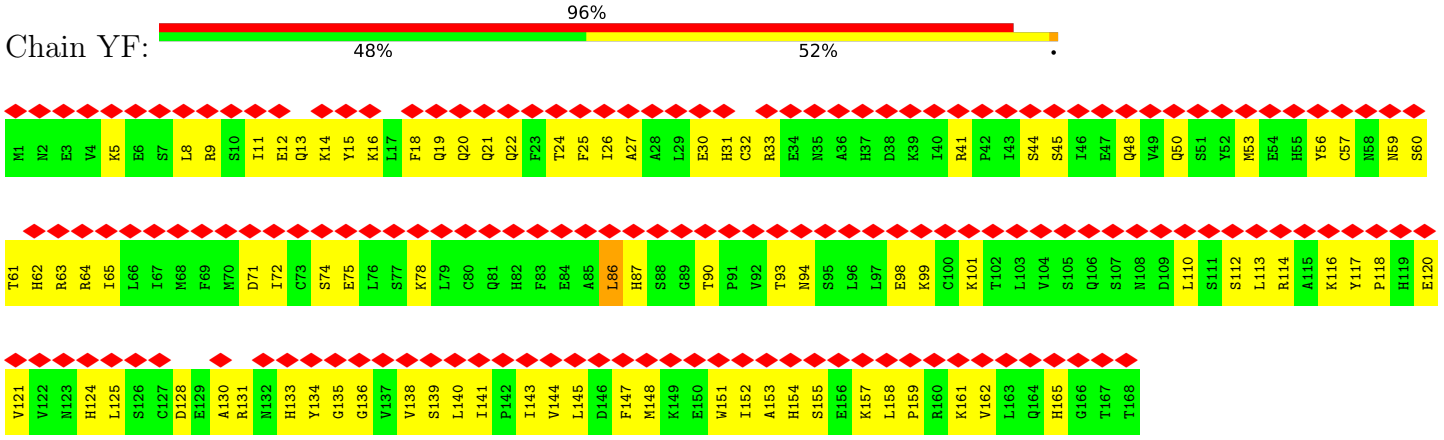
• Molecule 37: Sperm acrosome-associated protein 9

Chain YE:



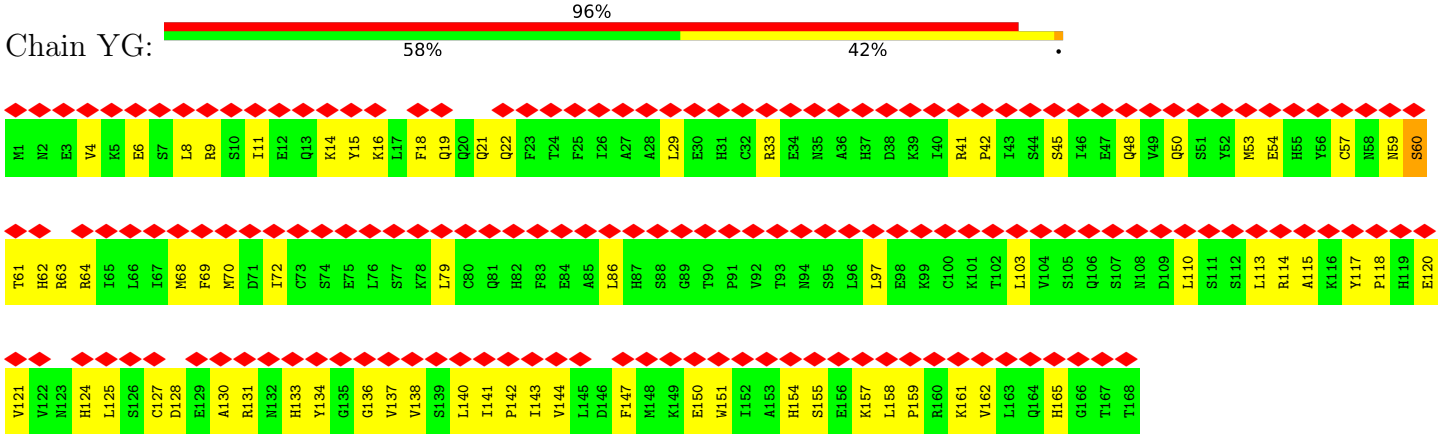
• Molecule 37: Sperm acrosome-associated protein 9

Chain YF:



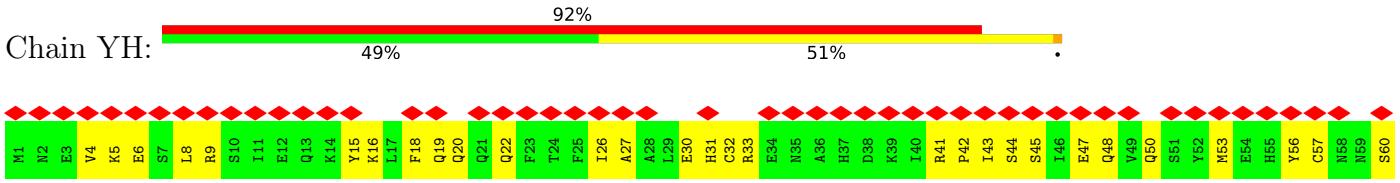
• Molecule 37: Sperm acrosome-associated protein 9

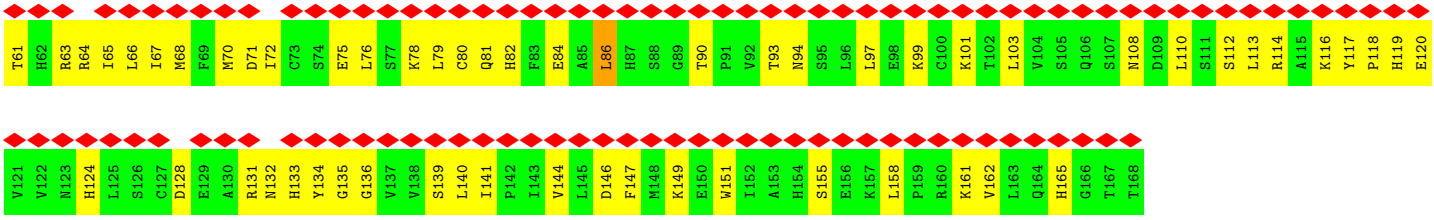
Chain YG:



• Molecule 37: Sperm acrosome-associated protein 9

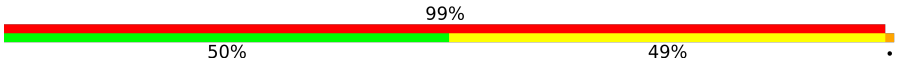
Chain YH:

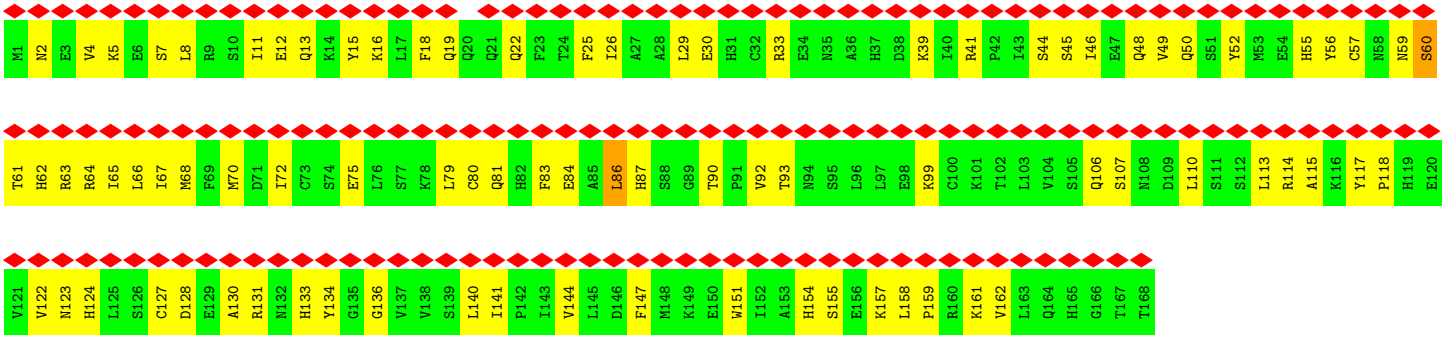




• Molecule 37: Sperm acrosome-associated protein 9

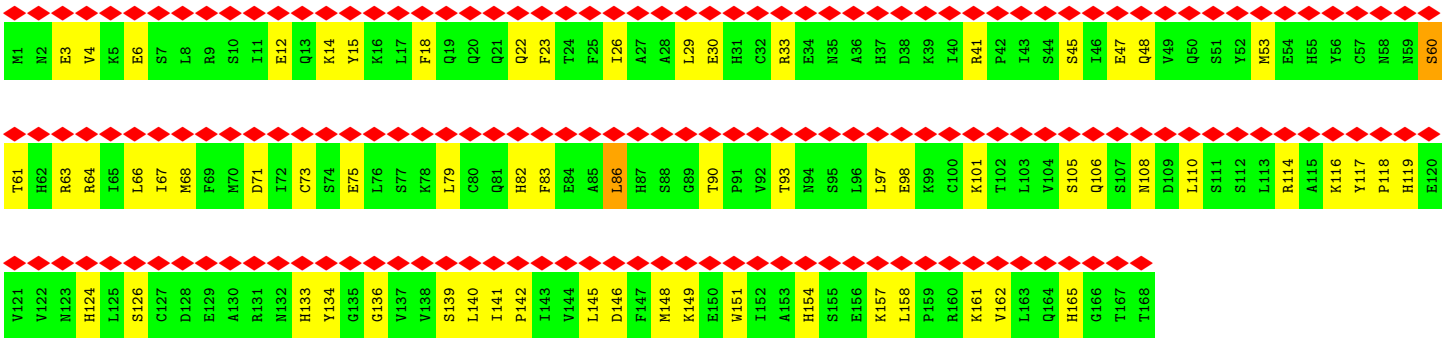
Chain YI:





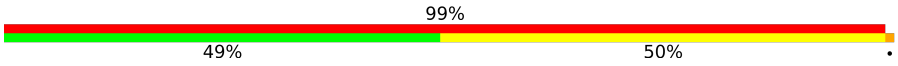
• Molecule 37: Sperm acrosome-associated protein 9

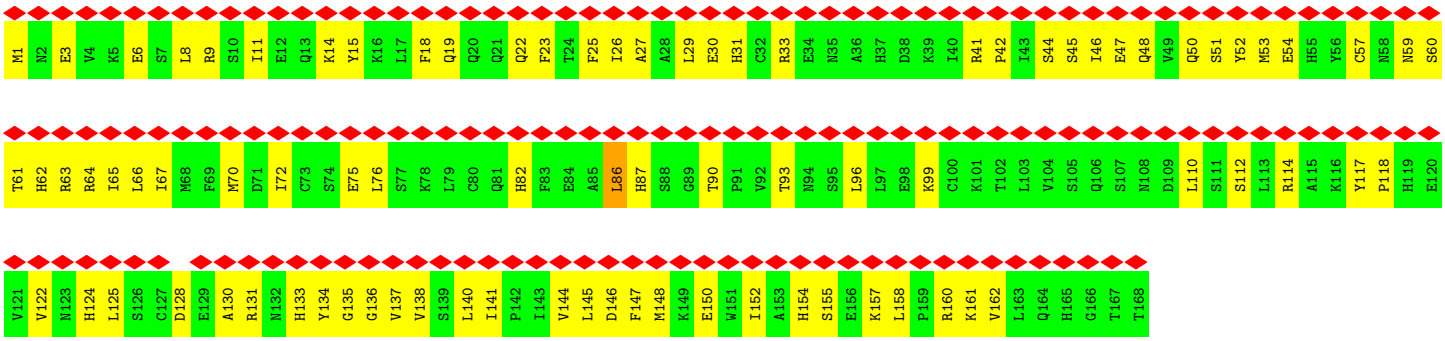
Chain YJ:



• Molecule 37: Sperm acrosome-associated protein 9

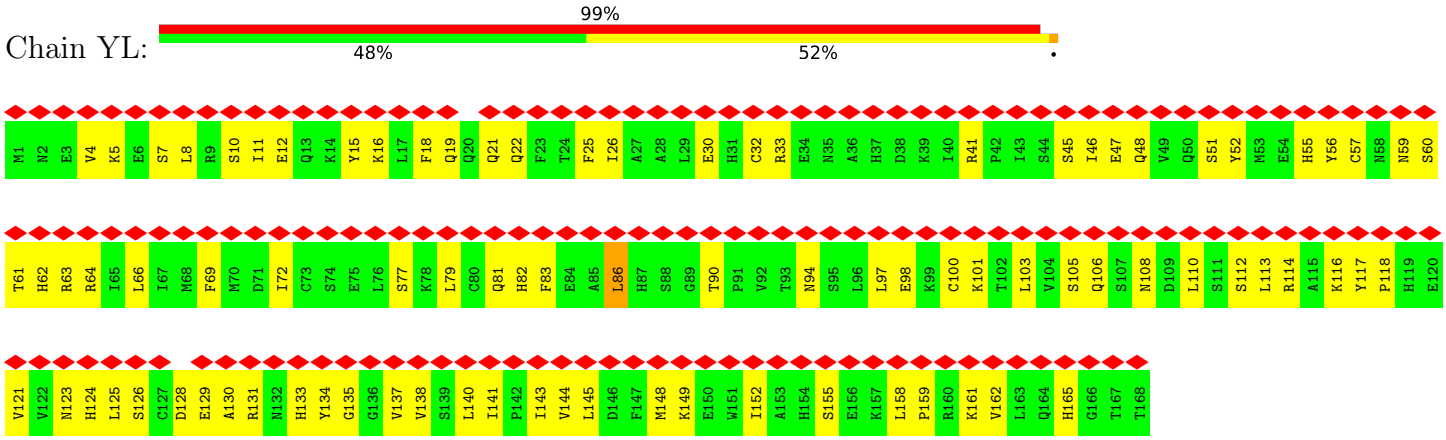
Chain YK:





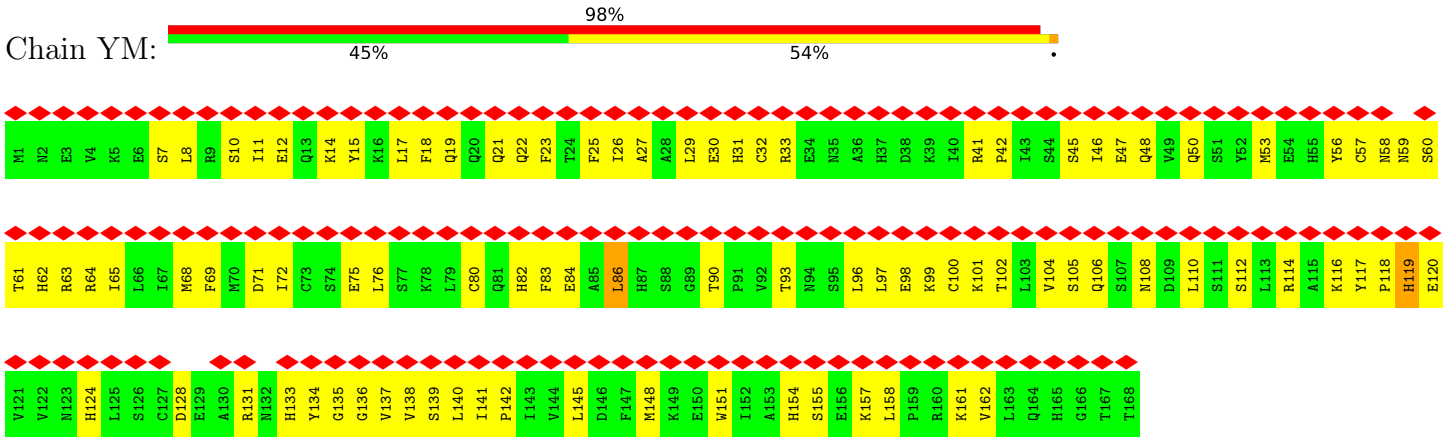
• Molecule 37: Sperm acrosome-associated protein 9

Chain YL:



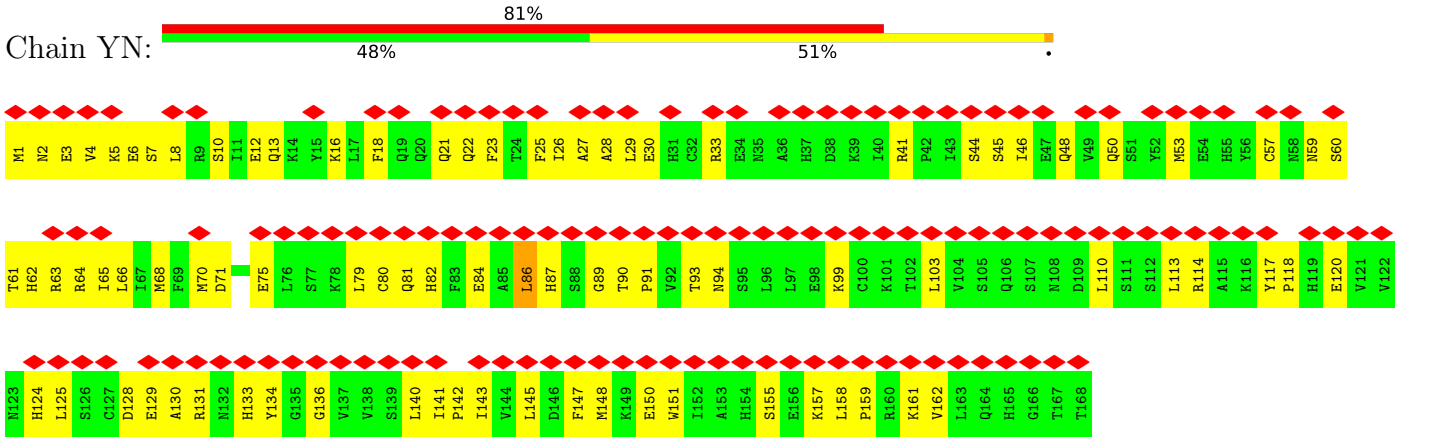
• Molecule 37: Sperm acrosome-associated protein 9

Chain YM:



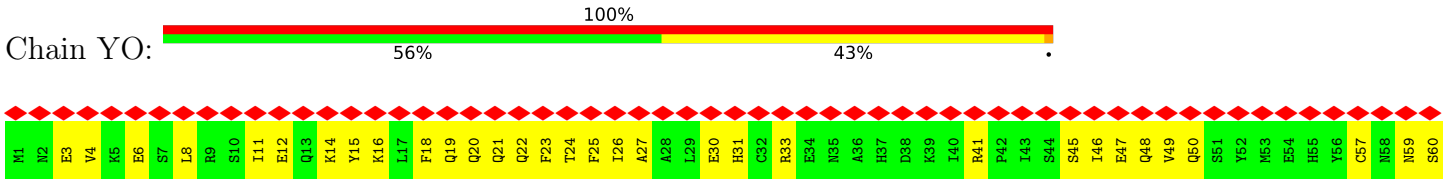
• Molecule 37: Sperm acrosome-associated protein 9

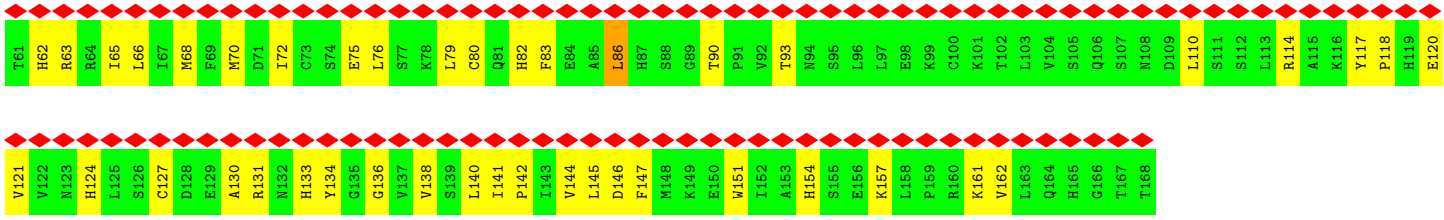
Chain YN:



• Molecule 37: Sperm acrosome-associated protein 9

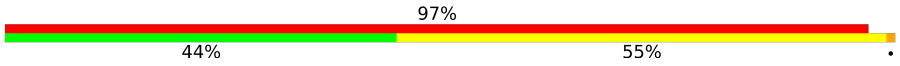
Chain YO:

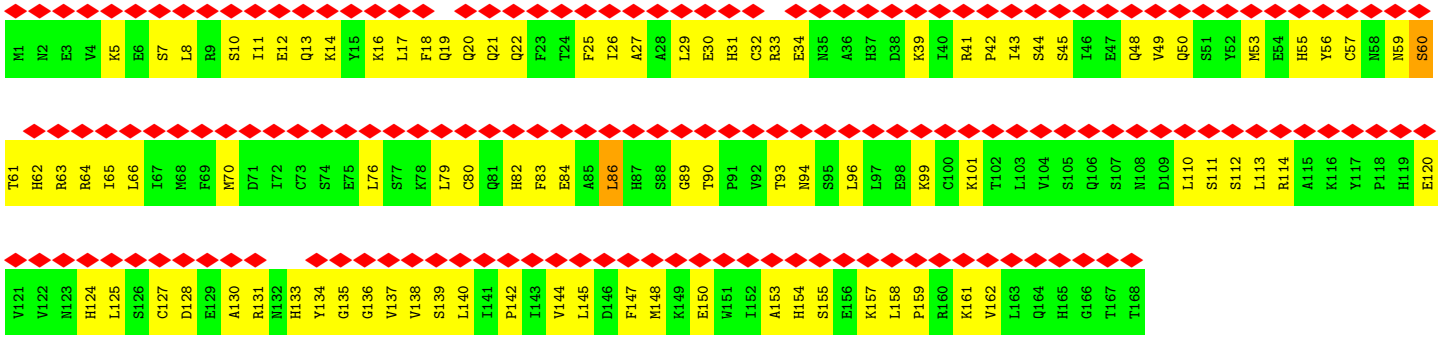




• Molecule 37: Sperm acrosome-associated protein 9

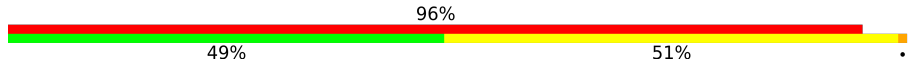
Chain YP:





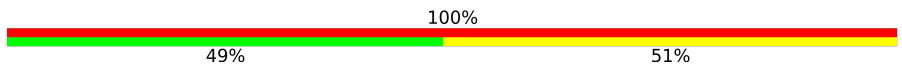
• Molecule 37: Sperm acrosome-associated protein 9

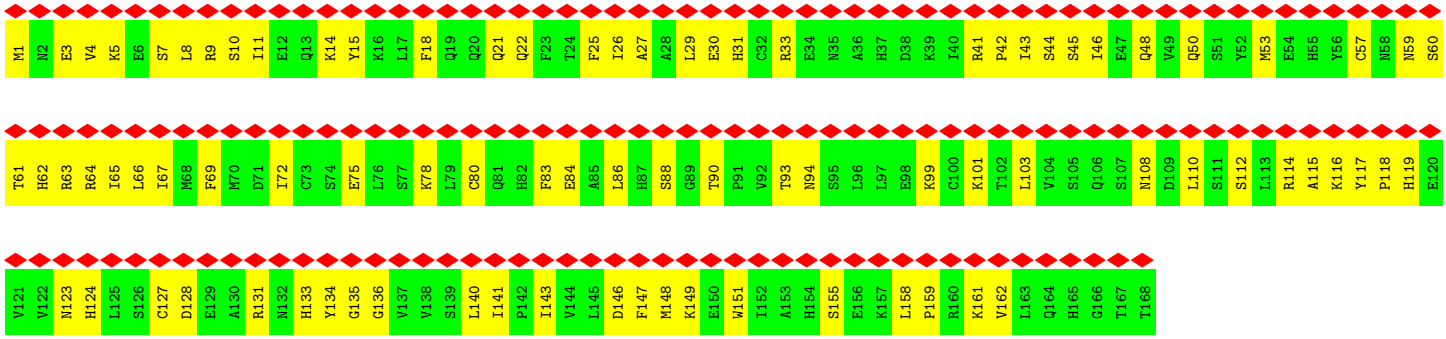
Chain YQ:



• Molecule 37: Sperm acrosome-associated protein 9

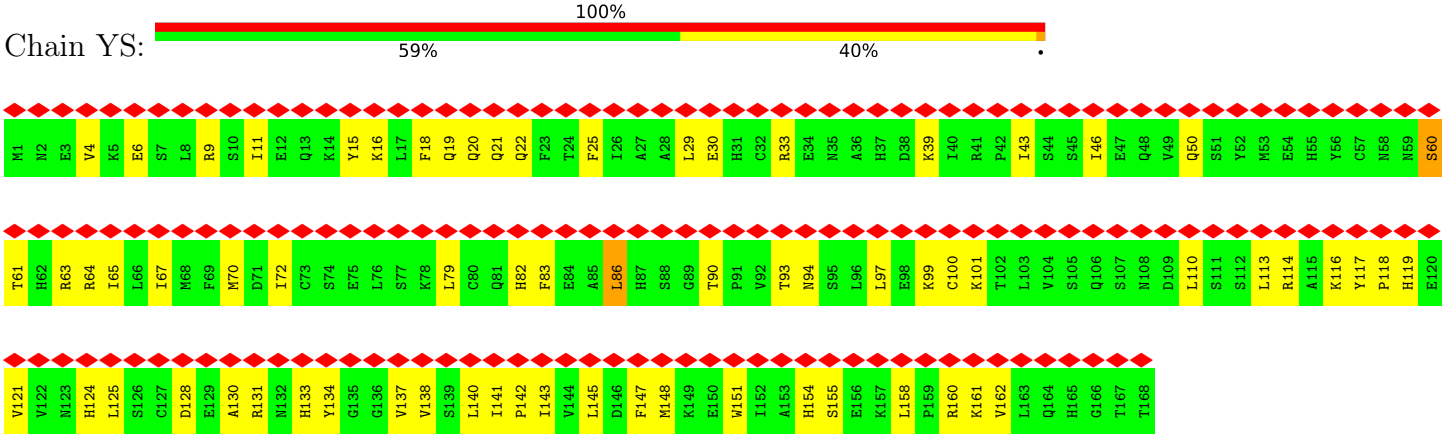
Chain YR:





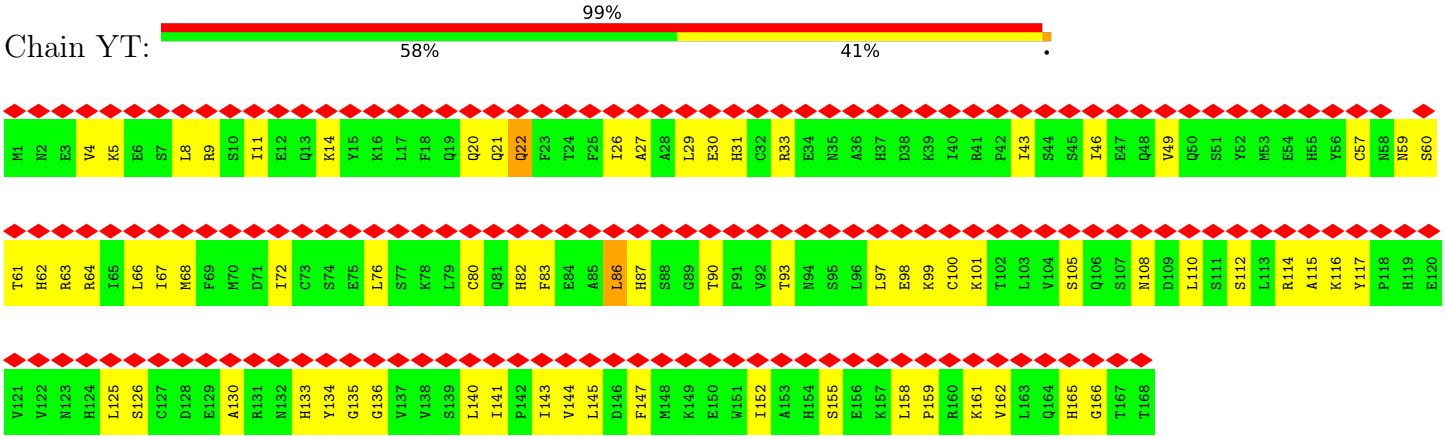
• Molecule 37: Sperm acrosome-associated protein 9

Chain YS:



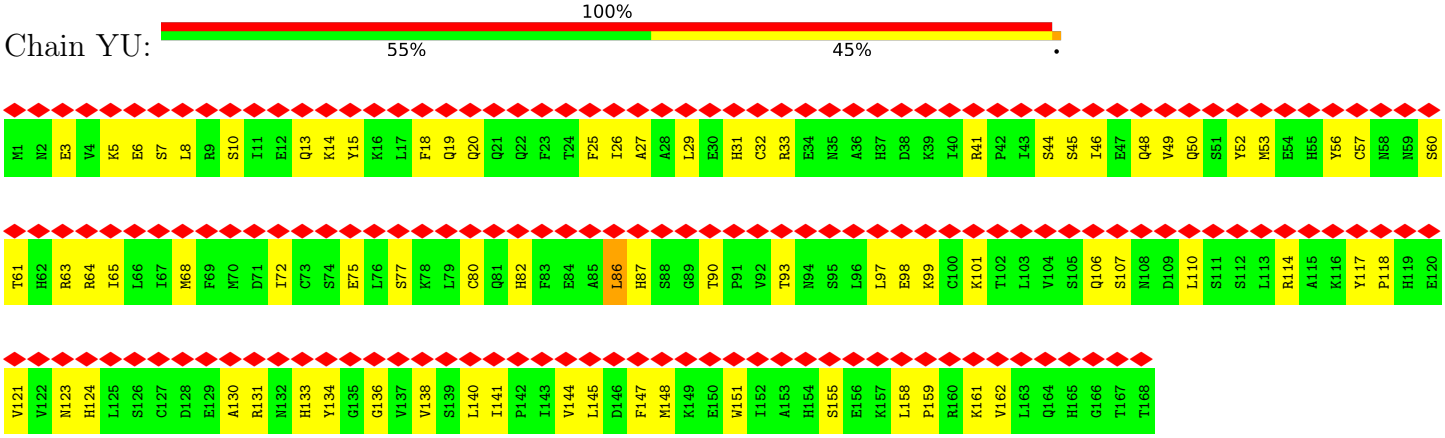
• Molecule 37: Sperm acrosome-associated protein 9

Chain YT:



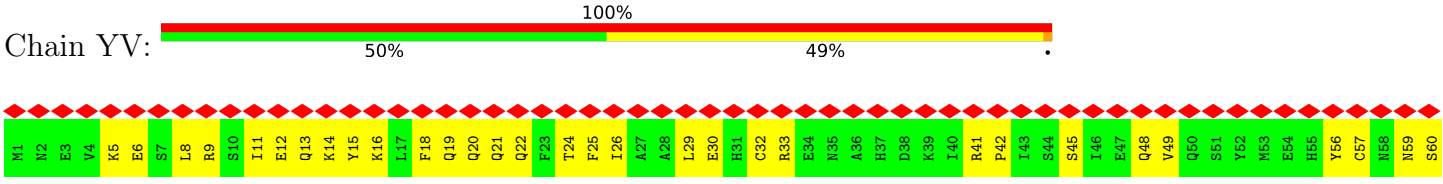
• Molecule 37: Sperm acrosome-associated protein 9

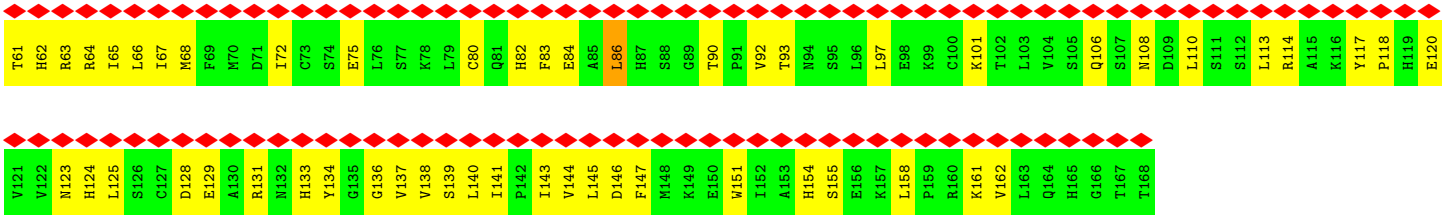
Chain YU:



• Molecule 37: Sperm acrosome-associated protein 9

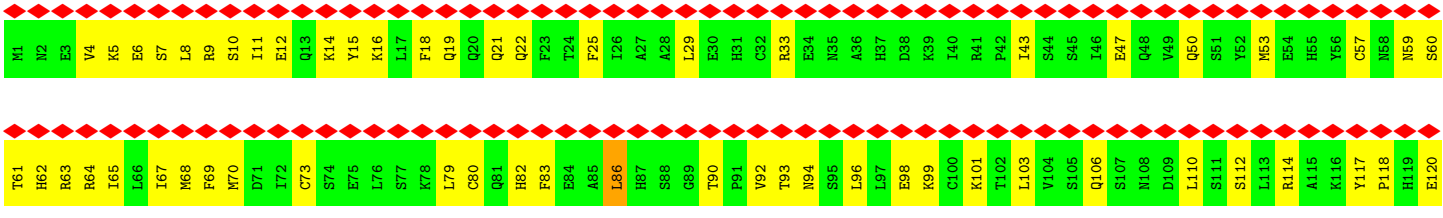
Chain YV:





• Molecule 37: Sperm acrosome-associated protein 9

Chain YW:



• Molecule 38: Cilia- and flagella-associated protein 141

Chain a:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	17450	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	117	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	563.2, 563.2, 563.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.76, 1.76, 1.76	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.12	0/2754	0.40	0/3652
1	B	0.13	0/1684	0.44	0/2233
2	A1	0.23	0/2604	0.53	0/3506
2	A2	0.27	0/3290	0.57	0/4433
2	A3	0.28	0/3290	0.56	0/4433
2	A4	0.24	0/1583	0.47	0/2133
3	AB	0.14	0/3431	0.42	2/4649 (0.0%)
3	AD	0.14	0/3431	0.39	0/4649
3	AF	0.14	0/3431	0.42	2/4649 (0.0%)
3	AH	0.15	0/3431	0.43	0/4649
3	AJ	0.15	0/3431	0.44	0/4649
3	AL	0.15	0/3431	0.43	0/4649
3	BB	0.15	0/3431	0.42	0/4649
3	BD	0.14	0/3431	0.42	2/4649 (0.0%)
3	BF	0.15	0/3431	0.43	0/4649
3	BH	0.14	0/3431	0.43	0/4649
3	BJ	0.21	0/3431	0.48	2/4649 (0.0%)
3	BL	0.14	0/3431	0.42	0/4649
3	CB	0.16	0/3431	0.44	0/4649
3	CD	0.15	0/3431	0.43	0/4649
3	CF	0.14	0/3431	0.44	0/4649
3	CH	0.16	0/3431	0.46	2/4649 (0.0%)
3	CJ	0.15	0/3431	0.44	2/4649 (0.0%)
3	CL	0.22	0/3431	0.46	0/4649
3	DB	0.15	0/3431	0.42	2/4649 (0.0%)
3	DD	0.16	0/3431	0.44	0/4649
3	DF	0.16	0/3431	0.44	0/4649
3	DH	0.14	0/3431	0.39	0/4649
3	DJ	0.16	0/3431	0.47	2/4649 (0.0%)
3	DL	0.15	0/3431	0.43	0/4649
3	EB	0.17	0/3431	0.44	0/4649
3	ED	0.17	0/3431	0.45	1/4649 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	EF	0.16	0/3431	0.45	1/4649 (0.0%)
3	EH	0.14	0/3431	0.43	0/4649
3	EJ	0.14	0/3431	0.42	2/4649 (0.0%)
3	EL	0.17	0/3431	0.48	2/4649 (0.0%)
3	FB	0.15	0/3431	0.44	0/4649
3	FD	0.16	0/3431	0.47	1/4649 (0.0%)
3	FF	0.14	0/3431	0.42	0/4649
3	FH	0.19	0/3431	0.50	1/4649 (0.0%)
3	FJ	0.16	0/3431	0.45	0/4649
3	FL	0.15	0/3431	0.44	0/4649
3	GB	0.16	0/3431	0.47	0/4649
3	GD	0.14	0/3431	0.45	0/4649
3	GF	0.16	0/3431	0.45	0/4649
3	GH	0.15	0/3431	0.43	0/4649
3	GJ	0.15	0/3431	0.43	0/4649
3	GL	0.17	0/3431	0.46	0/4649
3	HB	0.15	0/3431	0.43	0/4649
3	HD	0.16	0/3431	0.44	0/4649
3	HF	0.15	0/3431	0.45	1/4649 (0.0%)
3	HH	0.15	0/3431	0.43	0/4649
3	HJ	0.16	0/3431	0.45	0/4649
3	HL	0.14	0/3431	0.42	0/4649
3	IB	0.15	0/3431	0.45	0/4649
3	ID	0.15	0/3431	0.43	0/4649
3	IF	0.14	0/3431	0.41	0/4649
3	IH	0.14	0/3431	0.43	0/4649
3	IJ	0.15	0/3431	0.44	0/4649
3	IL	0.15	0/3431	0.43	0/4649
3	JB	0.13	0/3431	0.40	0/4649
3	JD	0.14	0/3431	0.42	0/4649
3	JF	0.14	0/3431	0.41	0/4649
3	JH	0.14	0/3431	0.42	0/4649
3	JJ	0.13	0/3431	0.40	0/4649
3	JL	0.13	0/3431	0.38	0/4649
3	KB	0.15	0/3431	0.42	0/4649
3	KD	0.15	0/3431	0.42	0/4649
3	KF	0.15	0/3431	0.39	0/4649
3	KH	0.16	0/3431	0.44	0/4649
3	KJ	0.14	0/3431	0.41	0/4649
3	KL	0.15	0/3431	0.45	0/4649
3	LB	0.15	0/3431	0.43	0/4649
3	LD	0.15	0/3431	0.43	0/4649
3	LF	0.16	0/3431	0.44	0/4649

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	LH	0.16	0/3431	0.43	0/4649
3	LJ	0.16	0/3431	0.43	0/4649
3	LL	0.15	0/3431	0.44	0/4649
3	MB	0.15	0/3431	0.44	0/4649
3	MD	0.17	0/3431	0.46	0/4649
3	MF	0.13	0/3431	0.39	0/4649
3	MH	0.15	0/3431	0.44	0/4649
3	MJ	0.15	0/3431	0.46	2/4649 (0.0%)
3	ML	0.17	0/3431	0.45	0/4649
3	NB	0.13	0/3431	0.41	1/4649 (0.0%)
3	ND	0.14	0/3431	0.42	3/4649 (0.1%)
3	NF	0.13	0/3431	0.40	0/4649
3	NH	0.14	0/3431	0.43	0/4649
3	NJ	0.14	0/3431	0.41	0/4649
3	NL	0.13	0/3431	0.41	3/4649 (0.1%)
3	OB	0.15	0/3431	0.42	1/4649 (0.0%)
3	OD	0.14	0/3431	0.42	1/4649 (0.0%)
3	OF	0.14	0/3431	0.40	0/4649
3	OH	0.14	0/3431	0.41	0/4649
3	OJ	0.13	0/3431	0.40	0/4649
3	OL	0.15	0/3431	0.42	0/4649
3	PB	0.14	0/3431	0.40	0/4649
3	PD	0.15	0/3431	0.44	0/4649
3	PF	0.14	0/3431	0.43	1/4649 (0.0%)
3	PH	0.14	0/3431	0.43	0/4649
3	PJ	0.14	0/3431	0.41	0/4649
3	PL	0.15	0/3431	0.43	1/4649 (0.0%)
3	QB	0.14	0/3431	0.41	0/4649
3	QD	0.14	0/3431	0.41	0/4649
3	QF	0.14	0/3431	0.41	0/4649
3	QH	0.14	0/3431	0.42	0/4649
3	QJ	0.14	0/3431	0.43	0/4649
3	QL	0.14	0/3431	0.43	0/4649
3	RB	0.15	0/3431	0.46	0/4649
3	RD	0.15	0/3431	0.42	0/4649
3	RF	0.14	0/3431	0.41	0/4649
3	RH	0.15	0/3431	0.42	1/4649 (0.0%)
3	RJ	0.15	0/3431	0.44	0/4649
3	RL	0.14	0/3431	0.41	0/4649
3	SB	0.14	0/3431	0.44	0/4649
3	SD	0.13	0/3431	0.40	0/4649
3	SF	0.15	0/3431	0.41	0/4649
3	SH	0.14	0/3431	0.41	0/4649

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	SJ	0.15	0/3431	0.43	2/4649 (0.0%)
3	SL	0.13	0/3431	0.42	0/4649
3	TB	0.14	0/3431	0.42	1/4649 (0.0%)
3	TD	0.14	0/3431	0.42	0/4649
3	TF	0.14	0/3431	0.41	0/4649
3	TH	0.15	0/3431	0.43	1/4649 (0.0%)
3	TJ	0.15	0/3431	0.45	0/4649
3	TL	0.16	0/3431	0.51	6/4649 (0.1%)
3	TN	0.13	0/3431	0.41	1/4649 (0.0%)
3	UB	0.15	0/3431	0.44	0/4649
3	UD	0.13	0/3431	0.40	0/4649
3	UF	0.14	0/3431	0.43	1/4649 (0.0%)
3	UH	0.15	0/3431	0.41	1/4649 (0.0%)
3	UJ	0.14	0/3431	0.39	0/4649
3	UL	0.13	0/3431	0.41	0/4649
3	VB	0.14	0/3431	0.41	0/4649
3	VD	0.14	0/3431	0.40	0/4649
3	VF	0.15	0/3431	0.43	0/4649
3	VH	0.15	0/3431	0.41	0/4649
3	VJ	0.14	0/3431	0.40	0/4649
3	VL	0.14	0/3431	0.41	0/4649
3	WB	0.14	0/3431	0.41	0/4649
3	WD	0.14	0/3431	0.41	0/4649
3	WF	0.14	0/3431	0.41	1/4649 (0.0%)
3	WH	0.14	0/3431	0.40	0/4649
3	WJ	0.14	0/3431	0.40	0/4649
3	WL	0.14	0/3431	0.40	1/4649 (0.0%)
4	AC	0.14	0/3496	0.40	0/4747
4	AE	0.16	0/3496	0.43	1/4747 (0.0%)
4	AG	0.15	0/3496	0.42	0/4747
4	AI	0.15	0/3496	0.43	1/4747 (0.0%)
4	AK	0.16	0/3496	0.44	1/4747 (0.0%)
4	AM	0.15	0/3496	0.42	0/4747
4	BC	0.14	0/3496	0.38	0/4747
4	BE	0.15	0/3496	0.42	0/4747
4	BG	0.14	0/3496	0.40	0/4747
4	BI	0.14	0/3496	0.39	0/4747
4	BK	0.14	0/3496	0.43	0/4747
4	BM	0.17	0/3496	0.45	0/4747
4	CC	0.14	0/3496	0.42	0/4747
4	CE	0.15	0/3496	0.42	0/4747
4	CG	0.16	0/3496	0.46	0/4747
4	CI	0.16	0/3496	0.45	0/4747

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	CK	0.17	0/3496	0.46	0/4747
4	CM	0.15	0/3496	0.45	0/4747
4	DA	0.14	0/3496	0.40	0/4747
4	DC	0.16	0/3496	0.45	0/4747
4	DE	0.16	0/3496	0.44	0/4747
4	DG	0.14	0/3496	0.40	0/4747
4	DI	0.14	0/3496	0.40	0/4747
4	DK	0.16	0/3496	0.47	1/4747 (0.0%)
4	EA	0.14	0/3496	0.41	0/4747
4	EC	0.18	0/3496	0.50	3/4747 (0.1%)
4	EE	0.16	0/3496	0.44	0/4747
4	EG	0.15	0/3496	0.43	0/4747
4	EI	0.16	0/3496	0.43	0/4747
4	EK	0.15	0/3496	0.43	0/4747
4	FA	0.15	0/3496	0.43	1/4747 (0.0%)
4	FC	0.17	0/3496	0.45	1/4747 (0.0%)
4	FE	0.15	0/3496	0.42	0/4747
4	FG	0.16	0/3496	0.43	0/4747
4	FI	0.15	0/3496	0.42	0/4747
4	FK	0.17	0/3496	0.45	0/4747
4	GA	0.16	0/3496	0.48	0/4747
4	GC	0.14	0/3496	0.43	1/4747 (0.0%)
4	GE	0.15	0/3496	0.43	0/4747
4	GG	0.15	0/3496	0.42	0/4747
4	GI	0.16	0/3496	0.43	0/4747
4	GK	0.15	0/3496	0.41	0/4747
4	HA	0.16	0/3496	0.45	1/4747 (0.0%)
4	HC	0.15	0/3496	0.46	1/4747 (0.0%)
4	HE	0.16	0/3496	0.44	0/4747
4	HG	0.17	0/3496	0.46	0/4747
4	HI	0.16	0/3496	0.46	1/4747 (0.0%)
4	HK	0.14	0/3496	0.41	0/4747
4	IA	0.14	0/3496	0.41	0/4747
4	IC	0.15	0/3496	0.43	0/4747
4	IE	0.15	0/3496	0.42	0/4747
4	IG	0.16	0/3496	0.42	1/4747 (0.0%)
4	II	0.15	0/3496	0.41	0/4747
4	IK	0.14	0/3496	0.41	0/4747
4	IM	0.15	0/3496	0.44	0/4747
4	JA	0.14	0/3496	0.40	0/4747
4	JC	0.14	0/3496	0.40	0/4747
4	JE	0.15	0/3496	0.43	1/4747 (0.0%)
4	JG	0.14	0/3496	0.41	0/4747

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	JI	0.14	0/3496	0.40	0/4747
4	JK	0.14	0/3496	0.40	0/4747
4	KA	0.15	0/3496	0.43	0/4747
4	KC	0.15	0/3496	0.41	0/4747
4	KE	0.15	0/3496	0.42	0/4747
4	KG	0.15	0/3496	0.40	0/4747
4	KI	0.15	0/3496	0.41	0/4747
4	KK	0.15	0/3496	0.41	0/4747
4	LA	0.15	0/3496	0.44	2/4747 (0.0%)
4	LC	0.15	0/3496	0.42	0/4747
4	LE	0.15	0/3496	0.42	0/4747
4	LG	0.15	0/3496	0.40	0/4747
4	LI	0.15	0/3496	0.44	0/4747
4	LK	0.15	0/3496	0.42	0/4747
4	MC	0.15	0/3496	0.43	0/4747
4	ME	0.14	0/3496	0.42	0/4747
4	MG	0.15	0/3496	0.44	0/4747
4	MI	0.15	0/3496	0.41	0/4747
4	MK	0.16	0/3496	0.43	0/4747
4	MM	0.14	0/3496	0.41	0/4747
4	NA	0.13	0/3496	0.37	0/4747
4	NC	0.13	0/3496	0.38	0/4747
4	NE	0.14	0/3496	0.39	0/4747
4	NG	0.13	0/3496	0.39	0/4747
4	NI	0.14	0/3496	0.40	0/4747
4	NK	0.13	0/3496	0.39	0/4747
4	OA	0.13	0/3496	0.39	0/4747
4	OC	0.14	0/3496	0.39	0/4747
4	OE	0.15	0/3496	0.43	1/4747 (0.0%)
4	OG	0.13	0/3496	0.40	0/4747
4	OI	0.14	0/3496	0.41	0/4747
4	OK	0.14	0/3496	0.40	0/4747
4	PA	0.13	0/3496	0.40	0/4747
4	PC	0.14	0/3496	0.40	0/4747
4	PE	0.14	0/3496	0.42	0/4747
4	PG	0.14	0/3496	0.41	0/4747
4	PI	0.14	0/3496	0.41	0/4747
4	PK	0.13	0/3496	0.41	0/4747
4	PM	0.18	0/3496	0.47	1/4747 (0.0%)
4	QC	0.13	0/3496	0.41	0/4747
4	QE	0.15	0/3496	0.41	0/4747
4	QG	0.16	0/3496	0.43	0/4747
4	QI	0.15	0/3496	0.40	0/4747

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	QK	0.14	0/3496	0.41	0/4747
4	QM	0.14	0/3496	0.41	0/4747
4	RC	0.16	0/3496	0.42	0/4747
4	RE	0.14	0/3496	0.40	0/4747
4	RG	0.13	0/3496	0.39	0/4747
4	RI	0.14	0/3496	0.40	0/4747
4	RK	0.15	0/3496	0.41	0/4747
4	RM	0.13	0/3496	0.40	0/4747
4	SC	0.14	0/3496	0.38	0/4747
4	SE	0.14	0/3496	0.41	0/4747
4	SG	0.15	0/3496	0.42	0/4747
4	SI	0.15	0/3496	0.42	0/4747
4	SK	0.14	0/3496	0.40	0/4747
4	SM	0.16	0/3496	0.44	2/4747 (0.0%)
4	TC	0.14	0/3496	0.41	1/4747 (0.0%)
4	TE	0.14	0/3496	0.40	0/4747
4	TG	0.15	0/3496	0.40	0/4747
4	TI	0.14	0/3496	0.39	0/4747
4	TK	0.15	0/3496	0.41	0/4747
4	TM	0.14	0/3496	0.39	0/4747
4	UA	0.14	0/3496	0.40	0/4747
4	UC	0.14	0/3496	0.40	0/4747
4	UE	0.15	0/3496	0.42	0/4747
4	UG	0.15	0/3496	0.41	0/4747
4	UI	0.15	0/3496	0.43	0/4747
4	UK	0.14	0/3496	0.39	0/4747
4	VA	0.14	0/3496	0.40	0/4747
4	VC	0.13	0/3496	0.40	0/4747
4	VE	0.14	0/3496	0.42	1/4747 (0.0%)
4	VG	0.15	0/3496	0.42	0/4747
4	VI	0.15	0/3496	0.41	0/4747
4	VK	0.15	0/3496	0.41	0/4747
4	WA	0.13	0/3496	0.38	0/4747
4	WC	0.13	0/3496	0.39	0/4747
4	WE	0.19	0/3496	0.44	2/4747 (0.0%)
4	WG	0.14	0/3496	0.42	0/4747
4	WI	0.16	0/3496	0.43	1/4747 (0.0%)
4	WK	0.15	0/3496	0.42	0/4747
5	B1	0.24	0/1957	0.53	0/2632
5	B2	0.26	0/3456	0.51	0/4659
5	B3	0.25	0/3456	0.51	0/4659
5	B4	0.23	0/2581	0.54	0/3482
5	B5	0.20	0/412	0.48	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	B6	0.27	0/3009	0.56	0/4054
5	B7	0.24	0/3362	0.53	2/4531 (0.0%)
5	B8	0.27	0/3307	0.53	2/4456 (0.0%)
5	B9	0.23	0/961	0.61	0/1288
6	C	0.17	0/3007	0.53	0/4060
6	D	0.16	0/3007	0.47	0/4060
7	C1	0.19	0/814	0.48	0/1097
7	C2	0.23	0/3208	0.53	2/4320 (0.0%)
7	C3	0.24	1/3208 (0.0%)	0.51	0/4320
7	C4	0.25	0/2966	0.56	2/3992 (0.1%)
7	C5	0.23	0/525	0.70	0/703
7	C6	0.13	0/1653	0.38	0/2224
7	C7	0.26	0/3256	0.60	2/4386 (0.0%)
7	C8	0.26	0/3256	0.61	3/4386 (0.1%)
7	C9	0.21	0/2452	0.51	0/3298
7	Ca	0.21	0/1814	0.47	0/2437
7	Cb	0.26	0/3208	0.59	2/4320 (0.0%)
7	Cc	0.24	0/3208	0.56	0/4320
7	Cd	0.13	0/2183	0.38	0/2942
8	D1	0.13	0/479	0.42	0/644
8	D2	0.24	0/3041	0.49	0/4095
8	D3	0.25	0/3538	0.49	0/4763
8	D4	0.25	0/3538	0.51	0/4763
8	D5	0.23	0/1072	0.55	0/1435
8	D6	0.21	0/617	0.55	0/828
8	D7	0.26	0/3068	0.54	1/4129 (0.0%)
8	D8	0.27	0/3337	0.53	1/4491 (0.0%)
8	D9	0.25	0/3304	0.51	0/4443
8	Da	0.18	0/499	0.49	0/669
9	E	0.17	0/2209	0.53	0/2979
9	F	0.21	0/1218	0.62	2/1652 (0.1%)
10	E1	0.20	0/1613	0.53	0/2194
10	E2	0.21	0/1613	0.54	0/2194
10	E3	0.20	0/1613	0.55	0/2194
10	E4	0.18	0/492	0.46	0/673
11	F1	0.23	0/2357	0.53	0/3163
11	F2	0.28	0/3267	0.68	3/4394 (0.1%)
11	F3	0.29	0/3267	0.69	4/4394 (0.1%)
11	F4	0.22	0/1770	0.49	0/2374
11	F5	0.26	0/2147	0.56	0/2885
11	F6	0.25	0/3236	0.58	2/4352 (0.0%)
11	F7	0.27	0/3236	0.64	0/4352
11	F8	0.25	0/1894	0.59	0/2543

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
11	F9	0.19	0/1424	0.50	0/1913
11	Fa	0.24	0/3236	0.54	1/4352 (0.0%)
11	Fb	0.25	0/3236	0.63	3/4352 (0.1%)
11	Fc	0.24	0/2619	0.56	0/3516
11	Fd	0.16	0/202	0.50	0/272
11	Fe	0.18	0/1968	0.44	0/2639
11	Ff	0.19	0/3267	0.43	0/4394
11	Fg	0.17	0/2591	0.46	0/3481
11	Fh	0.18	0/1510	0.50	0/2032
11	Fi	0.19	0/2257	0.46	0/3026
11	Fj	0.20	0/2296	0.51	0/3083
11	Fk	0.15	0/2751	0.44	0/3693
11	Fl	0.16	0/2751	0.46	0/3693
11	Fm	0.15	0/2706	0.44	0/3633
12	G	0.11	0/3831	0.33	0/5084
12	H	0.17	0/389	0.59	0/517
13	G1	0.17	0/4309	0.47	0/5839
13	G2	0.16	0/4192	0.47	0/5678
13	G3	0.17	0/4317	0.47	0/5851
14	G4	0.18	0/6347	0.51	1/8582 (0.0%)
14	G5	0.18	0/6339	0.49	0/8570
14	G6	0.17	0/6339	0.48	1/8570 (0.0%)
15	H1	0.19	0/1171	0.65	0/1582
15	H2	0.22	0/1139	0.68	0/1538
15	H3	0.22	0/1171	0.68	1/1582 (0.1%)
15	H4	0.23	0/1160	0.64	0/1568
15	H5	0.23	0/1171	0.72	0/1582
15	H6	0.22	0/1150	0.71	0/1552
16	I	0.18	0/796	0.48	0/1072
17	I1	0.13	0/306	0.37	0/413
17	I2	0.25	0/306	0.54	0/413
17	I3	0.15	0/306	0.39	0/413
18	J	0.19	0/1373	0.56	1/1872 (0.1%)
19	J1	0.21	0/1413	0.56	0/1923
19	J2	0.18	0/1413	0.50	0/1923
19	J3	0.21	0/1413	0.57	0/1923
20	K	0.16	0/2196	0.41	0/2965
20	L	0.15	0/2196	0.43	0/2965
21	K1	0.17	0/859	0.59	0/1150
21	K2	0.17	0/3463	0.53	0/4658
21	K3	0.16	0/3523	0.53	0/4741
21	K4	0.16	0/3234	0.49	0/4351
21	K5	0.19	0/410	0.58	0/552

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
22	L1	0.19	0/1763	0.59	0/2358
22	L2	0.21	0/1970	0.61	0/2636
22	L3	0.22	0/1970	0.63	2/2636 (0.1%)
22	L4	0.21	0/627	0.63	1/840 (0.1%)
23	M	0.18	0/975	0.49	0/1321
24	M1	0.19	0/525	0.55	0/708
24	M2	0.20	0/525	0.62	0/708
24	M3	0.21	0/525	0.62	0/708
25	N	0.16	0/602	0.52	0/816
26	N1	0.17	0/546	0.52	0/734
26	N2	0.19	0/546	0.59	0/734
26	N3	0.23	0/546	0.66	0/734
26	N4	0.17	0/546	0.53	0/734
27	O	0.13	0/418	0.55	0/556
27	P	0.12	0/2734	0.35	0/3649
27	Q	0.14	0/1566	0.43	0/2088
27	R	0.12	0/1951	0.34	0/2609
28	O1	0.24	0/849	0.82	2/1160 (0.2%)
28	O2	0.24	0/849	0.74	2/1160 (0.2%)
28	O3	0.24	0/849	0.70	2/1160 (0.2%)
29	P1	0.13	0/4793	0.37	1/6480 (0.0%)
29	P2	0.13	0/4793	0.37	0/6480
29	P3	0.13	0/4793	0.36	0/6480
30	Q1	0.20	0/1500	0.61	0/2007
30	Q2	0.20	0/1500	0.63	0/2007
30	Q3	0.19	0/1500	0.62	2/2007 (0.1%)
31	R1	0.14	0/613	0.57	1/823 (0.1%)
31	R2	0.21	0/613	0.53	0/823
31	R3	0.14	0/613	0.49	0/823
32	S	0.16	0/592	0.49	0/809
32	T	0.14	0/925	0.42	0/1250
33	U	0.11	0/3142	0.38	0/4156
33	V	0.11	0/540	0.33	0/715
33	W	0.16	0/2749	0.51	3/3652 (0.1%)
33	X	0.11	0/1516	0.37	0/2010
34	XA	0.15	0/1573	0.40	0/2122
34	XB	0.14	0/1573	0.38	0/2122
34	XC	0.17	0/1573	0.42	0/2122
34	XD	0.16	0/1573	0.42	0/2122
34	XE	0.16	0/1573	0.40	0/2122
34	XF	0.17	0/1573	0.44	0/2122
34	XG	0.16	0/1573	0.40	0/2122
35	XH	0.16	0/1503	0.48	2/2028 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	XI	0.15	0/1503	0.46	0/2028
35	XJ	0.16	0/1503	0.46	0/2028
35	XK	0.18	0/1503	0.51	0/2028
35	XL	0.16	0/1503	0.45	0/2028
35	XM	0.15	0/1503	0.44	0/2028
36	Y	0.10	0/1841	0.35	0/2442
36	Z	0.14	0/2421	0.45	0/3214
37	YA	0.15	0/1393	0.46	0/1876
37	YB	0.20	0/1393	0.58	1/1876 (0.1%)
37	YC	0.17	0/1393	0.51	0/1876
37	YD	0.15	0/1393	0.48	0/1876
37	YE	0.15	0/1393	0.46	0/1876
37	YF	0.15	0/1393	0.48	0/1876
37	YG	0.16	0/1393	0.48	0/1876
37	YH	0.15	0/1393	0.47	0/1876
37	YI	0.16	0/1393	0.50	0/1876
37	YJ	0.15	0/1393	0.47	0/1876
37	YK	0.15	0/1393	0.48	0/1876
37	YL	0.17	0/1393	0.50	0/1876
37	YM	0.15	0/1393	0.48	0/1876
37	YN	0.15	0/1393	0.46	0/1876
37	YO	0.15	0/1393	0.45	0/1876
37	YP	0.16	0/1393	0.48	0/1876
37	YQ	0.16	0/1393	0.49	0/1876
37	YR	0.14	0/1393	0.46	0/1876
37	YS	0.15	0/1393	0.48	0/1876
37	YT	0.16	0/1393	0.48	0/1876
37	YU	0.15	0/1393	0.45	0/1876
37	YV	0.17	0/1393	0.49	0/1876
37	YW	0.16	0/1393	0.48	0/1876
38	a	0.16	0/795	0.48	0/1064
All	All	0.16	1/1301480 (0.0%)	0.45	135/1761933 (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
2	A2	0	1
2	A4	0	1
3	AB	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	AD	0	1
3	AF	0	1
3	AH	0	1
3	AJ	0	1
3	BB	0	1
3	BD	0	1
3	BF	0	2
3	BH	0	1
3	BJ	0	3
3	BL	0	1
3	CB	0	1
3	CD	0	1
3	CF	0	1
3	CH	0	1
3	CJ	0	1
3	CL	0	1
3	DB	0	1
3	DD	0	1
3	DF	0	1
3	DH	0	1
3	DJ	0	1
3	DL	0	1
3	EB	0	1
3	ED	0	1
3	EF	0	1
3	EH	0	1
3	EJ	0	1
3	EL	0	1
3	FB	0	2
3	FD	0	1
3	FF	0	1
3	FH	0	1
3	FJ	0	2
3	FL	0	1
3	GB	0	1
3	GD	0	1
3	GF	0	2
3	GH	0	1
3	GJ	0	1
3	GL	0	1
3	HB	0	1
3	HD	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	HF	0	2
3	HH	0	1
3	HJ	0	1
3	HL	0	1
3	IB	0	1
3	ID	0	1
3	IF	0	2
3	IH	0	1
3	IJ	0	2
3	IL	0	1
3	JB	0	1
3	JD	0	1
3	JF	0	1
3	JH	0	1
3	JJ	0	1
3	JL	0	1
3	KB	0	1
3	KD	0	1
3	KF	0	1
3	KJ	0	1
3	KL	0	1
3	LB	0	1
3	LD	0	1
3	LF	0	1
3	LH	0	1
3	LL	0	1
3	MB	0	1
3	MD	0	1
3	MF	0	1
3	MH	0	1
3	MJ	0	1
3	ML	0	1
3	NB	0	1
3	ND	0	1
3	NF	0	1
3	NH	0	1
3	NJ	0	1
3	NL	0	1
3	OB	0	1
3	OD	0	1
3	OF	0	1
3	OH	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	OJ	0	1
3	PB	0	1
3	PD	0	1
3	PF	0	1
3	PH	0	1
3	PJ	0	1
3	PL	0	1
3	QB	0	1
3	QF	0	1
3	QH	0	1
3	QJ	0	1
3	QL	0	1
3	RD	0	1
3	RF	0	1
3	RJ	0	1
3	RL	0	1
3	SB	0	3
3	SD	0	2
3	SF	0	1
3	SH	0	1
3	TD	0	1
3	TF	0	1
3	TH	0	1
3	TJ	0	1
3	TL	0	3
3	TN	0	1
3	UB	0	1
3	UD	0	1
3	UF	0	1
3	UH	0	1
3	UJ	0	1
3	UL	0	1
3	VB	0	1
3	VD	0	1
3	VF	0	1
3	VH	0	1
3	VJ	0	2
3	VL	0	1
3	WB	0	1
3	WD	0	1
3	WF	0	1
3	WH	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	WJ	0	1
3	WL	0	1
4	AG	0	1
4	BM	0	1
4	CM	0	1
4	DK	0	2
4	EC	0	1
4	FC	0	1
4	HC	0	2
4	HI	0	1
4	HK	0	1
4	IG	0	1
4	OE	0	1
4	WE	0	1
9	E	0	1
10	E1	0	2
10	E2	0	2
10	E3	0	1
11	Fb	0	1
11	Fh	0	1
13	G1	0	1
13	G2	0	2
13	G3	0	1
14	G4	0	1
14	G5	0	1
14	G6	0	2
21	K2	0	2
21	K3	0	2
21	K4	0	1
22	L2	0	1
27	P	0	1
35	XK	0	1
All	All	0	184

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C3	174	LEU	CA-C	5.97	1.62	1.52

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	O1	109	LEU	CA-C-N	-12.36	107.19	122.64
28	O1	109	LEU	C-N-CA	-12.36	107.19	122.64
3	BJ	15	GLN	CA-CB-CG	11.19	136.47	114.10
3	TL	15	GLN	CA-CB-CG	-10.04	94.02	114.10
3	TL	15	GLN	CG-CD-NE2	-8.95	102.97	116.40

There are no chirality outliers.

5 of 184 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A2	206	ARG	Peptide
2	A4	31	ARG	Sidechain
3	AB	271	ALA	Peptide
3	AD	271	ALA	Peptide
3	AF	271	ALA	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	2736	0	2753	149	0
1	B	1673	0	1716	93	0
2	A1	2578	0	2613	148	0
2	A2	3251	0	3274	225	0
2	A3	3251	0	3274	210	0
2	A4	1563	0	1555	99	0
3	AB	3356	0	3237	177	0
3	AD	3356	0	3235	179	0
3	AF	3356	0	3236	177	0
3	AH	3356	0	3236	197	0
3	AJ	3356	0	3235	204	0
3	AL	3356	0	3236	183	0
3	BB	3356	0	3234	168	0
3	BD	3356	0	3235	192	0
3	BF	3356	0	3235	180	0
3	BH	3356	0	3235	183	0
3	BJ	3356	0	3234	197	0
3	BL	3356	0	3235	201	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	CB	3356	0	3238	199	0
3	CD	3356	0	3236	209	0
3	CF	3356	0	3235	188	0
3	CH	3356	0	3237	215	0
3	CJ	3356	0	3236	188	0
3	CL	3356	0	3234	211	0
3	DB	3356	0	3236	183	0
3	DD	3356	0	3235	211	0
3	DF	3356	0	3235	194	0
3	DH	3356	0	3235	172	0
3	DJ	3356	0	3235	197	0
3	DL	3356	0	3238	167	0
3	EB	3356	0	3236	191	0
3	ED	3356	0	3236	220	0
3	EF	3356	0	3236	173	0
3	EH	3356	0	3236	196	0
3	EJ	3356	0	3238	200	0
3	EL	3356	0	3237	184	0
3	FB	3356	0	3236	180	0
3	FD	3356	0	3237	189	0
3	FF	3356	0	3235	189	0
3	FH	3356	0	3236	199	0
3	FJ	3356	0	3237	182	0
3	FL	3356	0	3238	179	0
3	GB	3356	0	3235	195	0
3	GD	3356	0	3238	188	0
3	GF	3356	0	3235	214	0
3	GH	3356	0	3235	179	0
3	GJ	3356	0	3236	209	0
3	GL	3356	0	3237	185	0
3	HB	3356	0	3235	179	0
3	HD	3356	0	3235	176	0
3	HF	3356	0	3235	187	0
3	HH	3356	0	3236	186	0
3	HJ	3356	0	3236	198	0
3	HL	3356	0	3237	204	0
3	IB	3356	0	3235	217	0
3	ID	3356	0	3236	191	0
3	IF	3356	0	3237	186	0
3	IH	3356	0	3236	200	0
3	IJ	3356	0	3237	206	0
3	IL	3356	0	3234	187	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	JB	3356	0	3235	172	0
3	JD	3356	0	3235	181	0
3	JF	3356	0	3235	168	0
3	JH	3356	0	3235	186	0
3	JJ	3356	0	3235	178	0
3	JL	3356	0	3237	164	0
3	KB	3356	0	3237	181	0
3	KD	3356	0	3235	207	0
3	KF	3356	0	3234	182	0
3	KH	3356	0	3236	201	0
3	KJ	3356	0	3235	167	0
3	KL	3356	0	3237	202	0
3	LB	3356	0	3236	235	0
3	LD	3356	0	3232	204	0
3	LF	3356	0	3236	218	0
3	LH	3356	0	3237	198	0
3	LJ	3356	0	3232	228	0
3	LL	3356	0	3238	194	0
3	MB	3356	0	3235	179	0
3	MD	3356	0	3234	231	0
3	MF	3356	0	3236	187	0
3	MH	3356	0	3235	240	0
3	MJ	3356	0	3233	178	0
3	ML	3356	0	3235	239	0
3	NB	3356	0	3236	151	0
3	ND	3356	0	3236	167	0
3	NF	3356	0	3236	165	0
3	NH	3356	0	3236	180	0
3	NJ	3356	0	3235	153	0
3	NL	3356	0	3238	135	0
3	OB	3356	0	3235	181	0
3	OD	3356	0	3236	176	0
3	OF	3356	0	3235	178	0
3	OH	3356	0	3234	167	0
3	OJ	3356	0	3234	170	0
3	OL	3356	0	3237	160	0
3	PB	3356	0	3235	163	0
3	PD	3356	0	3235	180	0
3	PF	3356	0	3235	169	0
3	PH	3356	0	3235	177	0
3	PJ	3356	0	3234	178	0
3	PL	3356	0	3235	181	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	QB	3356	0	3235	185	0
3	QD	3356	0	3236	191	0
3	QF	3356	0	3233	174	0
3	QH	3356	0	3235	173	0
3	QJ	3356	0	3235	178	0
3	QL	3356	0	3234	165	0
3	RB	3356	0	3235	183	0
3	RD	3356	0	3236	184	0
3	RF	3356	0	3235	182	0
3	RH	3356	0	3236	213	0
3	RJ	3356	0	3236	183	0
3	RL	3356	0	3236	166	0
3	SB	3356	0	3235	181	0
3	SD	3356	0	3236	171	0
3	SF	3356	0	3236	187	0
3	SH	3356	0	3234	167	0
3	SJ	3356	0	3235	179	0
3	SL	3356	0	3236	177	0
3	TB	3356	0	3236	157	0
3	TD	3356	0	3235	184	0
3	TF	3356	0	3235	174	0
3	TH	3356	0	3235	196	0
3	TJ	3356	0	3233	185	0
3	TL	3356	0	3235	196	0
3	TN	3356	0	3238	162	0
3	UB	3356	0	3236	169	0
3	UD	3356	0	3234	171	0
3	UF	3356	0	3235	193	0
3	UH	3356	0	3236	178	0
3	UJ	3356	0	3234	183	0
3	UL	3356	0	3237	146	0
3	VB	3356	0	3236	192	0
3	VD	3356	0	3236	186	0
3	VF	3356	0	3235	190	0
3	VH	3356	0	3236	176	0
3	VJ	3356	0	3236	172	0
3	VL	3356	0	3238	151	0
3	WB	3356	0	3236	183	0
3	WD	3356	0	3238	189	0
3	WF	3356	0	3236	196	0
3	WH	3356	0	3234	175	0
3	WJ	3356	0	3236	182	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	WL	3356	0	3238	158	0
4	AC	3418	0	3327	217	0
4	AE	3418	0	3327	226	0
4	AG	3418	0	3328	212	0
4	AI	3418	0	3328	227	0
4	AK	3418	0	3328	205	0
4	AM	3418	0	3328	215	0
4	BC	3418	0	3327	189	0
4	BE	3418	0	3327	219	0
4	BG	3418	0	3329	198	0
4	BI	3418	0	3328	196	0
4	BK	3418	0	3327	218	0
4	BM	3418	0	3329	189	0
4	CC	3418	0	3328	218	0
4	CE	3418	0	3328	204	0
4	CG	3418	0	3328	233	0
4	CI	3418	0	3330	240	0
4	CK	3418	0	3327	240	0
4	CM	3418	0	3327	214	0
4	DA	3418	0	3328	194	0
4	DC	3418	0	3328	207	0
4	DE	3418	0	3328	217	0
4	DG	3418	0	3327	216	0
4	DI	3418	0	3329	201	0
4	DK	3418	0	3329	210	0
4	EA	3418	0	3328	189	0
4	EC	3418	0	3329	215	0
4	EE	3418	0	3329	204	0
4	EG	3418	0	3328	213	0
4	EI	3418	0	3329	256	0
4	EK	3418	0	3328	207	0
4	FA	3418	0	3329	174	0
4	FC	3418	0	3329	207	0
4	FE	3418	0	3328	213	0
4	FG	3418	0	3329	206	0
4	FI	3418	0	3327	210	0
4	FK	3418	0	3328	214	0
4	GA	3418	0	3329	192	0
4	GC	3418	0	3330	230	0
4	GE	3418	0	3329	239	0
4	GG	3418	0	3329	226	0
4	GI	3418	0	3328	234	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	GK	3418	0	3329	204	0
4	HA	3418	0	3328	226	0
4	HC	3418	0	3329	208	0
4	HE	3418	0	3328	215	0
4	HG	3418	0	3328	238	0
4	HI	3418	0	3329	230	0
4	HK	3418	0	3328	197	0
4	IA	3418	0	3328	199	0
4	IC	3418	0	3328	207	0
4	IE	3418	0	3329	208	0
4	IG	3418	0	3328	212	0
4	II	3418	0	3328	203	0
4	IK	3418	0	3329	216	0
4	IM	3418	0	3329	220	0
4	JA	3418	0	3329	160	0
4	JC	3418	0	3328	212	0
4	JE	3418	0	3328	210	0
4	JG	3418	0	3327	188	0
4	JI	3418	0	3327	205	0
4	JK	3418	0	3328	197	0
4	KA	3418	0	3327	193	0
4	KC	3418	0	3329	213	0
4	KE	3418	0	3327	224	0
4	KG	3418	0	3329	206	0
4	KI	3418	0	3328	245	0
4	KK	3418	0	3327	220	0
4	LA	3418	0	3328	208	0
4	LC	3418	0	3329	235	0
4	LE	3418	0	3329	225	0
4	LG	3418	0	3328	220	0
4	LI	3418	0	3329	226	0
4	LK	3418	0	3329	224	0
4	MC	3418	0	3328	247	0
4	ME	3418	0	3328	227	0
4	MG	3418	0	3327	234	0
4	MI	3418	0	3329	209	0
4	MK	3418	0	3330	241	0
4	MM	3418	0	3328	210	0
4	NA	3418	0	3329	149	0
4	NC	3418	0	3327	174	0
4	NE	3418	0	3329	179	0
4	NG	3418	0	3328	190	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	NI	3418	0	3327	191	0
4	NK	3418	0	3329	174	0
4	OA	3418	0	3329	148	0
4	OC	3418	0	3329	177	0
4	OE	3418	0	3329	189	0
4	OG	3418	0	3329	189	0
4	OI	3418	0	3328	184	0
4	OK	3418	0	3328	170	0
4	PA	3418	0	3328	174	0
4	PC	3418	0	3328	170	0
4	PE	3418	0	3329	196	0
4	PG	3418	0	3329	184	0
4	PI	3418	0	3328	221	0
4	PK	3418	0	3329	187	0
4	PM	3418	0	3329	188	0
4	QC	3418	0	3327	203	0
4	QE	3418	0	3328	202	0
4	QG	3418	0	3328	208	0
4	QI	3418	0	3328	197	0
4	QK	3418	0	3328	205	0
4	QM	3418	0	3328	191	0
4	RC	3418	0	3329	211	0
4	RE	3418	0	3328	180	0
4	RG	3418	0	3327	192	0
4	RI	3418	0	3328	208	0
4	RK	3418	0	3329	194	0
4	RM	3418	0	3327	180	0
4	SC	3418	0	3329	199	0
4	SE	3418	0	3327	194	0
4	SG	3418	0	3328	203	0
4	SI	3418	0	3328	221	0
4	SK	3418	0	3328	195	0
4	SM	3418	0	3328	174	0
4	TC	3418	0	3327	200	0
4	TE	3418	0	3328	183	0
4	TG	3418	0	3327	195	0
4	TI	3418	0	3327	179	0
4	TK	3418	0	3328	202	0
4	TM	3418	0	3328	186	0
4	UA	3418	0	3328	167	0
4	UC	3418	0	3328	194	0
4	UE	3418	0	3327	203	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	UG	3418	0	3328	200	0
4	UI	3418	0	3328	179	0
4	UK	3418	0	3327	172	0
4	VA	3418	0	3327	167	0
4	VC	3418	0	3329	189	0
4	VE	3418	0	3328	200	0
4	VG	3418	0	3328	208	0
4	VI	3418	0	3327	199	0
4	VK	3418	0	3328	187	0
4	WA	3418	0	3328	164	0
4	WC	3418	0	3329	178	0
4	WE	3418	0	3329	202	0
4	WG	3418	0	3327	189	0
4	WI	3418	0	3329	205	0
4	WK	3418	0	3329	186	0
5	B1	1941	0	1987	112	0
5	B2	3417	0	3436	189	0
5	B3	3417	0	3436	199	0
5	B4	2553	0	2563	143	0
5	B5	406	0	396	29	0
5	B6	2977	0	2998	181	0
5	B7	3324	0	3346	199	0
5	B8	3271	0	3289	186	0
5	B9	952	0	959	74	0
6	C	2945	0	2916	195	0
6	D	2945	0	2916	172	0
7	C1	803	0	770	65	0
7	C2	3169	0	3138	186	0
7	C3	3169	0	3138	194	0
7	C4	2934	0	2932	181	0
7	C5	523	0	548	47	0
7	C6	1633	0	1587	77	0
7	C7	3216	0	3192	178	0
7	C8	3216	0	3192	167	0
7	C9	2426	0	2435	127	0
7	Ca	1797	0	1822	94	0
7	Cb	3169	0	3138	157	0
7	Cc	3169	0	3138	169	0
7	Cd	2154	0	2095	84	0
8	D1	467	0	427	21	0
8	D2	2997	0	2907	180	0
8	D3	3488	0	3424	199	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D4	3488	0	3424	214	0
8	D5	1063	0	1081	100	0
8	D6	612	0	622	37	0
8	D7	3031	0	3006	189	0
8	D8	3291	0	3235	203	0
8	D9	3260	0	3206	176	0
8	Da	490	0	460	44	0
9	E	2160	0	2083	97	0
9	F	1182	0	1209	71	0
10	E1	1558	0	1502	81	0
10	E2	1558	0	1502	87	0
10	E3	1558	0	1502	71	0
10	E4	472	0	447	22	0
11	F1	2335	0	2379	122	0
11	F2	3224	0	3221	204	0
11	F3	3224	0	3221	230	0
11	F4	1745	0	1676	100	0
11	F5	2116	0	2051	111	0
11	F6	3194	0	3192	189	0
11	F7	3194	0	3192	203	0
11	F8	1877	0	1946	128	0
11	F9	1412	0	1478	71	0
11	Fa	3194	0	3192	166	0
11	Fb	3194	0	3192	194	0
11	Fc	2585	0	2556	163	0
11	Fd	199	0	188	4	0
11	Fe	1946	0	1940	73	0
11	Ff	3224	0	3222	122	0
11	Fg	2561	0	2581	84	0
11	Fh	1495	0	1563	58	0
11	Fi	2235	0	2252	90	0
11	Fj	2272	0	2282	103	0
11	Fk	2721	0	2733	139	0
11	Fl	2721	0	2733	141	0
11	Fm	2677	0	2687	110	0
12	G	3804	0	3850	180	0
12	H	387	0	377	21	0
13	G1	4192	0	4130	238	0
13	G2	4081	0	4025	192	0
13	G3	4200	0	4135	203	0
14	G4	6177	0	6054	349	0
14	G5	6169	0	6044	317	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	G6	6169	0	6044	340	0
15	H1	1138	0	1091	77	0
15	H2	1107	0	1057	96	0
15	H3	1138	0	1091	98	0
15	H4	1127	0	1078	82	0
15	H5	1138	0	1091	83	0
15	H6	1118	0	1070	105	0
16	I	781	0	744	35	0
17	I1	298	0	281	18	0
17	I2	298	0	281	34	0
17	I3	298	0	281	23	0
18	J	1323	0	1287	77	0
19	J1	1378	0	1354	70	0
19	J2	1378	0	1354	56	0
19	J3	1378	0	1354	80	0
20	K	2154	0	2144	77	0
20	L	2154	0	2144	76	0
21	K1	847	0	889	60	0
21	K2	3408	0	3519	216	0
21	K3	3465	0	3572	222	0
21	K4	3181	0	3266	199	0
21	K5	400	0	408	22	0
22	L1	1728	0	1795	119	0
22	L2	1929	0	2013	161	0
22	L3	1929	0	2013	159	0
22	L4	609	0	653	49	0
23	M	944	0	885	64	0
24	M1	510	0	492	40	0
24	M2	510	0	492	36	0
24	M3	510	0	492	39	0
25	N	583	0	568	34	0
26	N1	535	0	512	16	0
26	N2	535	0	512	36	0
26	N3	535	0	512	39	0
26	N4	535	0	512	28	0
27	O	413	0	418	18	0
27	P	2693	0	2656	128	0
27	Q	1541	0	1502	92	0
27	R	1922	0	1892	69	0
28	O1	825	0	817	69	0
28	O2	825	0	817	77	0
28	O3	825	0	817	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	P1	4696	0	4674	178	0
29	P2	4696	0	4674	187	0
29	P3	4696	0	4674	139	0
30	Q1	1473	0	1492	113	0
30	Q2	1473	0	1492	119	0
30	Q3	1473	0	1492	110	0
31	R1	604	0	597	43	0
31	R2	604	0	597	38	0
31	R3	604	0	597	36	0
32	S	575	0	558	30	0
32	T	904	0	865	37	0
33	U	3125	0	3166	137	0
33	V	537	0	555	19	0
33	W	2733	0	2775	134	0
33	X	1506	0	1539	75	0
34	XA	1540	0	1570	86	0
34	XB	1540	0	1570	84	0
34	XC	1540	0	1570	90	0
34	XD	1540	0	1570	87	0
34	XE	1540	0	1570	96	0
34	XF	1540	0	1570	92	0
34	XG	1540	0	1570	96	0
35	XH	1469	0	1477	94	0
35	XI	1469	0	1477	86	0
35	XJ	1469	0	1477	91	0
35	XK	1469	0	1477	95	0
35	XL	1469	0	1477	86	0
35	XM	1469	0	1477	78	0
36	Y	1821	0	1858	78	0
36	Z	2401	0	2444	138	0
37	YA	1365	0	1356	57	0
37	YB	1365	0	1356	87	0
37	YC	1365	0	1356	64	0
37	YD	1365	0	1356	76	0
37	YE	1365	0	1356	61	0
37	YF	1365	0	1356	76	0
37	YG	1365	0	1356	71	0
37	YH	1365	0	1356	65	0
37	YI	1365	0	1356	73	0
37	YJ	1365	0	1356	55	0
37	YK	1365	0	1356	82	0
37	YL	1365	0	1356	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	YM	1365	0	1356	71	0
37	YN	1365	0	1356	65	0
37	YO	1365	0	1356	60	0
37	YP	1365	0	1356	71	0
37	YQ	1365	0	1356	70	0
37	YR	1365	0	1356	76	0
37	YS	1365	0	1356	61	0
37	YT	1365	0	1356	57	0
37	YU	1365	0	1356	60	0
37	YV	1365	0	1356	72	0
37	YW	1365	0	1356	68	0
38	a	782	0	780	52	0
39	AB	32	0	11	7	0
39	AC	32	0	12	4	0
39	AD	32	0	11	6	0
39	AE	32	0	12	5	0
39	AF	32	0	11	10	0
39	AG	32	0	12	6	0
39	AH	32	0	10	6	0
39	AI	32	0	12	4	0
39	AJ	32	0	11	7	0
39	AK	32	0	12	8	0
39	AL	32	0	10	8	0
39	AM	32	0	12	5	0
39	BB	32	0	11	7	0
39	BC	32	0	12	5	0
39	BD	32	0	10	7	0
39	BE	32	0	12	7	0
39	BF	32	0	11	9	0
39	BG	32	0	12	4	0
39	BH	32	0	11	9	0
39	BI	32	0	12	4	0
39	BJ	32	0	11	1	0
39	BK	32	0	12	9	0
39	BL	32	0	11	9	0
39	BM	32	0	12	9	0
39	CB	32	0	11	6	0
39	CC	32	0	12	5	0
39	CD	32	0	11	7	0
39	CE	32	0	12	7	0
39	CF	32	0	11	11	0
39	CG	32	0	12	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	CH	32	0	11	6	0
39	CI	32	0	12	4	0
39	CJ	32	0	10	7	0
39	CK	32	0	12	7	0
39	CL	32	0	11	3	0
39	CM	32	0	12	6	0
39	DA	32	0	12	6	0
39	DB	32	0	11	6	0
39	DC	32	0	12	9	0
39	DD	32	0	11	4	0
39	DE	32	0	12	6	0
39	DF	32	0	11	7	0
39	DG	32	0	12	8	0
39	DH	32	0	11	7	0
39	DI	32	0	12	6	0
39	DJ	32	0	10	6	0
39	DK	32	0	12	6	0
39	DL	32	0	11	7	0
39	EA	32	0	12	4	0
39	EB	32	0	11	9	0
39	EC	32	0	12	8	0
39	ED	32	0	10	4	0
39	EE	32	0	12	10	0
39	EF	32	0	11	3	0
39	EG	32	0	12	2	0
39	EH	32	0	10	8	0
39	EI	32	0	12	10	0
39	EJ	32	0	11	8	0
39	EK	32	0	12	5	0
39	EL	32	0	11	6	0
39	FA	32	0	12	6	0
39	FB	32	0	11	8	0
39	FC	32	0	12	7	0
39	FD	32	0	10	8	0
39	FE	32	0	12	7	0
39	FF	32	0	10	6	0
39	FG	32	0	12	6	0
39	FH	32	0	10	7	0
39	FI	32	0	12	5	0
39	FJ	32	0	10	6	0
39	FK	32	0	12	12	0
39	FL	32	0	10	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	GA	32	0	12	5	0
39	GB	32	0	10	9	0
39	GC	32	0	12	9	0
39	GD	32	0	10	8	0
39	GE	32	0	12	5	0
39	GF	32	0	10	7	0
39	GG	32	0	12	6	0
39	GH	32	0	10	9	0
39	GI	32	0	12	5	0
39	GJ	32	0	11	7	0
39	GK	32	0	12	7	0
39	GL	32	0	10	8	0
39	HA	32	0	12	5	0
39	HB	32	0	11	7	0
39	HC	32	0	12	2	0
39	HD	32	0	10	7	0
39	HE	32	0	12	5	0
39	HF	32	0	11	5	0
39	HG	32	0	12	5	0
39	HH	32	0	11	9	0
39	HI	32	0	12	3	0
39	HJ	32	0	10	7	0
39	HK	32	0	12	6	0
39	HL	32	0	10	6	0
39	IA	32	0	12	6	0
39	IB	32	0	10	5	0
39	IC	32	0	12	7	0
39	ID	32	0	11	8	0
39	IE	32	0	12	7	0
39	IF	32	0	11	8	0
39	IG	32	0	12	9	0
39	IH	32	0	10	6	0
39	II	32	0	12	4	0
39	IJ	32	0	11	10	0
39	IK	32	0	12	3	0
39	IL	32	0	10	4	0
39	IM	32	0	12	8	0
39	JA	32	0	12	3	0
39	JB	32	0	11	7	0
39	JC	32	0	12	4	0
39	JD	32	0	10	7	0
39	JE	32	0	12	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	JF	32	0	10	5	0
39	JG	32	0	12	3	0
39	JH	32	0	11	10	0
39	JI	32	0	12	10	0
39	JJ	32	0	11	8	0
39	JK	32	0	12	5	0
39	JL	32	0	11	8	0
39	KA	32	0	12	5	0
39	KB	32	0	11	6	0
39	KC	32	0	12	6	0
39	KD	32	0	11	9	0
39	KE	32	0	12	8	0
39	KF	32	0	10	6	0
39	KG	32	0	12	7	0
39	KH	32	0	10	5	0
39	KI	32	0	12	5	0
39	KJ	32	0	11	7	0
39	KK	32	0	12	3	0
39	KL	32	0	11	9	0
39	LA	32	0	12	5	0
39	LB	32	0	10	7	0
39	LC	32	0	12	6	0
39	LD	32	0	11	6	0
39	LE	32	0	12	2	0
39	LF	32	0	11	8	0
39	LG	32	0	12	4	0
39	LH	32	0	11	8	0
39	LI	32	0	12	3	0
39	LJ	32	0	11	8	0
39	LK	32	0	12	4	0
39	LL	32	0	11	8	0
39	MB	32	0	11	8	0
39	MC	32	0	12	9	0
39	MD	64	0	23	9	0
39	MF	32	0	11	9	0
39	MG	32	0	12	6	0
39	MH	32	0	11	7	0
39	MI	32	0	12	8	0
39	MJ	32	0	11	10	0
39	MK	32	0	12	5	0
39	ML	32	0	10	9	0
39	MM	32	0	12	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	NA	32	0	12	3	0
39	NB	32	0	11	7	0
39	NC	32	0	12	6	0
39	ND	32	0	10	4	0
39	NE	32	0	12	5	0
39	NF	32	0	11	8	0
39	NG	32	0	12	5	0
39	NH	32	0	10	10	0
39	NI	32	0	12	11	0
39	NJ	32	0	10	6	0
39	NK	32	0	12	5	0
39	NL	32	0	11	5	0
39	OA	32	0	12	5	0
39	OB	32	0	11	8	0
39	OC	32	0	12	4	0
39	OD	32	0	11	6	0
39	OE	32	0	12	4	0
39	OF	32	0	10	7	0
39	OG	32	0	12	6	0
39	OH	32	0	11	7	0
39	OI	32	0	12	6	0
39	OJ	32	0	11	7	0
39	OK	32	0	12	4	0
39	OL	32	0	11	6	0
39	PA	32	0	12	7	0
39	PB	32	0	11	9	0
39	PC	32	0	12	5	0
39	PD	32	0	10	4	0
39	PE	32	0	12	7	0
39	PF	32	0	11	8	0
39	PG	32	0	12	3	0
39	PH	32	0	10	6	0
39	PI	32	0	12	5	0
39	PJ	32	0	11	7	0
39	PK	32	0	12	2	0
39	PL	32	0	10	8	0
39	PM	32	0	12	6	0
39	QB	32	0	11	9	0
39	QC	32	0	12	6	0
39	QD	64	0	23	14	0
39	QF	32	0	10	6	0
39	QG	32	0	12	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	QH	32	0	11	6	0
39	QI	32	0	12	4	0
39	QJ	32	0	11	7	0
39	QK	32	0	12	6	0
39	QL	64	0	23	10	0
39	RB	32	0	10	7	0
39	RC	32	0	12	4	0
39	RD	32	0	11	9	0
39	RE	32	0	12	5	0
39	RF	32	0	11	7	0
39	RG	32	0	12	5	0
39	RH	32	0	11	9	0
39	RI	32	0	12	4	0
39	RJ	32	0	11	8	0
39	RK	32	0	12	8	0
39	RL	32	0	11	7	0
39	RM	32	0	12	5	0
39	SB	32	0	10	7	0
39	SC	32	0	12	5	0
39	SD	32	0	11	7	0
39	SE	32	0	12	5	0
39	SF	32	0	10	6	0
39	SG	32	0	12	7	0
39	SH	32	0	11	9	0
39	SI	32	0	12	7	0
39	SJ	32	0	11	7	0
39	SK	32	0	12	6	0
39	SL	32	0	10	8	0
39	SM	32	0	12	7	0
39	TB	32	0	11	7	0
39	TC	32	0	12	7	0
39	TD	32	0	10	7	0
39	TE	32	0	12	4	0
39	TF	32	0	11	6	0
39	TG	32	0	12	5	0
39	TH	32	0	11	6	0
39	TI	32	0	12	6	0
39	TJ	32	0	10	10	0
39	TK	32	0	12	2	0
39	TL	32	0	11	5	0
39	TM	32	0	12	4	0
39	TN	32	0	11	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	UA	32	0	12	3	0
39	UB	32	0	11	7	0
39	UC	32	0	12	5	0
39	UD	32	0	11	8	0
39	UE	32	0	12	5	0
39	UF	32	0	10	9	0
39	UG	32	0	12	6	0
39	UH	32	0	10	7	0
39	UI	32	0	12	7	0
39	UJ	32	0	11	8	0
39	UK	32	0	12	9	0
39	UL	32	0	10	7	0
39	VA	32	0	12	3	0
39	VB	32	0	10	7	0
39	VC	32	0	12	6	0
39	VD	32	0	11	8	0
39	VE	32	0	12	6	0
39	VF	32	0	11	9	0
39	VG	32	0	12	7	0
39	VH	32	0	10	9	0
39	VI	32	0	12	8	0
39	VJ	32	0	11	7	0
39	VK	32	0	12	2	0
39	VL	32	0	11	8	0
39	WA	32	0	12	5	0
39	WB	32	0	11	7	0
39	WC	32	0	12	6	0
39	WD	32	0	11	10	0
39	WE	32	0	12	7	0
39	WF	32	0	11	8	0
39	WG	32	0	12	7	0
39	WH	32	0	10	4	0
39	WI	32	0	12	5	0
39	WJ	32	0	10	7	0
39	WK	32	0	12	1	0
39	WL	32	0	11	9	0
All	All	1283344	0	1247168	66836	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 26.

The worst 5 of 66836 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)
3:FD:99:ASN:HB2	3:FD:142:GLY:HA3	1.39	1.03
4:GG:30:ILE:HA	4:GG:36:MET:HE1	1.40	1.02
11:Fb:402:ARG:HG2	11:Fb:406:GLU:HG2	1.38	1.01
7:C7:361:ILE:HD12	7:C7:462:LYS:HZ1	1.25	1.01
3:TL:15:GLN:HB3	3:TL:16:ILE:HG13	1.44	1.00

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/491 (64%)	302 (96%)	11 (4%)	0	100	100
1	B	194/491 (40%)	188 (97%)	6 (3%)	0	100	100
2	A1	311/418 (74%)	297 (96%)	14 (4%)	0	100	100
2	A2	394/418 (94%)	366 (93%)	27 (7%)	1 (0%)	36	72
2	A3	394/418 (94%)	374 (95%)	20 (5%)	0	100	100
2	A4	184/418 (44%)	178 (97%)	6 (3%)	0	100	100
3	AB	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	AD	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	AF	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	AH	425/427 (100%)	400 (94%)	24 (6%)	1 (0%)	43	78
3	AJ	425/427 (100%)	391 (92%)	31 (7%)	3 (1%)	18	56
3	AL	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	BB	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	BD	425/427 (100%)	399 (94%)	25 (6%)	1 (0%)	43	78
3	BF	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	BH	425/427 (100%)	391 (92%)	33 (8%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BJ	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	BL	425/427 (100%)	396 (93%)	28 (7%)	1 (0%)	43	78
3	CB	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	CD	425/427 (100%)	403 (95%)	21 (5%)	1 (0%)	43	78
3	CF	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	CH	425/427 (100%)	397 (93%)	26 (6%)	2 (0%)	24	63
3	CJ	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	CL	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	DB	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	DD	425/427 (100%)	395 (93%)	28 (7%)	2 (0%)	24	63
3	DF	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	DH	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	DJ	425/427 (100%)	391 (92%)	32 (8%)	2 (0%)	24	63
3	DL	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	EB	425/427 (100%)	397 (93%)	26 (6%)	2 (0%)	24	63
3	ED	425/427 (100%)	397 (93%)	27 (6%)	1 (0%)	43	78
3	EF	425/427 (100%)	397 (93%)	27 (6%)	1 (0%)	43	78
3	EH	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	EJ	425/427 (100%)	400 (94%)	24 (6%)	1 (0%)	43	78
3	EL	425/427 (100%)	395 (93%)	29 (7%)	1 (0%)	43	78
3	FB	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	FD	425/427 (100%)	397 (93%)	27 (6%)	1 (0%)	43	78
3	FF	425/427 (100%)	395 (93%)	29 (7%)	1 (0%)	43	78
3	FH	425/427 (100%)	401 (94%)	23 (5%)	1 (0%)	43	78
3	FJ	425/427 (100%)	397 (93%)	27 (6%)	1 (0%)	43	78
3	FL	425/427 (100%)	397 (93%)	27 (6%)	1 (0%)	43	78
3	GB	425/427 (100%)	390 (92%)	33 (8%)	2 (0%)	24	63
3	GD	425/427 (100%)	404 (95%)	20 (5%)	1 (0%)	43	78
3	GF	425/427 (100%)	398 (94%)	26 (6%)	1 (0%)	43	78
3	GH	425/427 (100%)	402 (95%)	22 (5%)	1 (0%)	43	78
3	GJ	425/427 (100%)	403 (95%)	21 (5%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	GL	425/427 (100%)	393 (92%)	30 (7%)	2 (0%)	24	63
3	HB	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	HD	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	HF	425/427 (100%)	397 (93%)	26 (6%)	2 (0%)	24	63
3	HH	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	HJ	425/427 (100%)	401 (94%)	23 (5%)	1 (0%)	43	78
3	HL	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	IB	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	ID	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	IF	425/427 (100%)	401 (94%)	23 (5%)	1 (0%)	43	78
3	IH	425/427 (100%)	397 (93%)	26 (6%)	2 (0%)	24	63
3	IJ	425/427 (100%)	395 (93%)	29 (7%)	1 (0%)	43	78
3	IL	425/427 (100%)	407 (96%)	16 (4%)	2 (0%)	24	63
3	JB	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	JD	425/427 (100%)	405 (95%)	18 (4%)	2 (0%)	24	63
3	JF	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	JH	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	JJ	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	JL	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	KB	425/427 (100%)	405 (95%)	18 (4%)	2 (0%)	24	63
3	KD	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	KF	425/427 (100%)	398 (94%)	26 (6%)	1 (0%)	43	78
3	KH	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	KJ	425/427 (100%)	399 (94%)	25 (6%)	1 (0%)	43	78
3	KL	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	LB	425/427 (100%)	401 (94%)	23 (5%)	1 (0%)	43	78
3	LD	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	LF	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	LH	425/427 (100%)	397 (93%)	26 (6%)	2 (0%)	24	63
3	LJ	425/427 (100%)	394 (93%)	29 (7%)	2 (0%)	24	63
3	LL	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	MB	425/427 (100%)	394 (93%)	29 (7%)	2 (0%)	24	63
3	MD	425/427 (100%)	394 (93%)	29 (7%)	2 (0%)	24	63
3	MF	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	MH	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	MJ	425/427 (100%)	394 (93%)	30 (7%)	1 (0%)	43	78
3	ML	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	NB	425/427 (100%)	404 (95%)	19 (4%)	2 (0%)	24	63
3	ND	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	NF	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	NH	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	NJ	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	NL	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	OB	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	OD	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	OF	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	OH	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	OJ	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	OL	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	PB	425/427 (100%)	405 (95%)	18 (4%)	2 (0%)	24	63
3	PD	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	PF	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	PH	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	PJ	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	PL	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	QB	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	QD	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	QF	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	QH	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	QJ	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	QL	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	RB	425/427 (100%)	404 (95%)	19 (4%)	2 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	RD	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	RF	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	RH	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	RJ	425/427 (100%)	399 (94%)	25 (6%)	1 (0%)	43	78
3	RL	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	SB	425/427 (100%)	404 (95%)	19 (4%)	2 (0%)	24	63
3	SD	425/427 (100%)	398 (94%)	25 (6%)	2 (0%)	24	63
3	SF	425/427 (100%)	404 (95%)	19 (4%)	2 (0%)	24	63
3	SH	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	SJ	425/427 (100%)	406 (96%)	17 (4%)	2 (0%)	24	63
3	SL	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	TB	425/427 (100%)	400 (94%)	23 (5%)	2 (0%)	24	63
3	TD	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	TF	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	TH	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	TJ	425/427 (100%)	401 (94%)	23 (5%)	1 (0%)	43	78
3	TL	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	TN	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	UB	425/427 (100%)	406 (96%)	17 (4%)	2 (0%)	24	63
3	UD	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	UF	425/427 (100%)	393 (92%)	30 (7%)	2 (0%)	24	63
3	UH	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	UJ	425/427 (100%)	396 (93%)	27 (6%)	2 (0%)	24	63
3	UL	425/427 (100%)	401 (94%)	23 (5%)	1 (0%)	43	78
3	VB	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	VD	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	VF	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	VH	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	VJ	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	VL	425/427 (100%)	402 (95%)	21 (5%)	2 (0%)	24	63
3	WB	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	WD	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	WF	425/427 (100%)	403 (95%)	20 (5%)	2 (0%)	24	63
3	WH	425/427 (100%)	401 (94%)	22 (5%)	2 (0%)	24	63
3	WJ	425/427 (100%)	399 (94%)	24 (6%)	2 (0%)	24	63
3	WL	425/427 (100%)	396 (93%)	28 (7%)	1 (0%)	43	78
4	AC	436/438 (100%)	411 (94%)	25 (6%)	0	100	100
4	AE	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	AG	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	AI	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	AK	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	AM	436/438 (100%)	410 (94%)	26 (6%)	0	100	100
4	BC	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	BE	436/438 (100%)	402 (92%)	33 (8%)	1 (0%)	43	78
4	BG	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78
4	BI	436/438 (100%)	403 (92%)	32 (7%)	1 (0%)	43	78
4	BK	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	BM	436/438 (100%)	414 (95%)	21 (5%)	1 (0%)	43	78
4	CC	436/438 (100%)	412 (94%)	24 (6%)	0	100	100
4	CE	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	CG	436/438 (100%)	399 (92%)	37 (8%)	0	100	100
4	CI	436/438 (100%)	402 (92%)	33 (8%)	1 (0%)	43	78
4	CK	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	CM	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	DA	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	DC	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	DE	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	DG	436/438 (100%)	403 (92%)	32 (7%)	1 (0%)	43	78
4	DI	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	DK	436/438 (100%)	404 (93%)	30 (7%)	2 (0%)	24	63
4	EA	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	EC	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	EE	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	EG	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	EI	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	EK	436/438 (100%)	403 (92%)	32 (7%)	1 (0%)	43	78
4	FA	436/438 (100%)	414 (95%)	21 (5%)	1 (0%)	43	78
4	FC	436/438 (100%)	408 (94%)	26 (6%)	2 (0%)	24	63
4	FE	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	FG	436/438 (100%)	411 (94%)	25 (6%)	0	100	100
4	FI	436/438 (100%)	403 (92%)	32 (7%)	1 (0%)	43	78
4	FK	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	GA	436/438 (100%)	414 (95%)	21 (5%)	1 (0%)	43	78
4	GC	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	GE	436/438 (100%)	410 (94%)	26 (6%)	0	100	100
4	GG	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	GI	436/438 (100%)	405 (93%)	31 (7%)	0	100	100
4	GK	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78
4	HA	436/438 (100%)	409 (94%)	27 (6%)	0	100	100
4	HC	436/438 (100%)	403 (92%)	32 (7%)	1 (0%)	43	78
4	HE	436/438 (100%)	402 (92%)	33 (8%)	1 (0%)	43	78
4	HG	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	HI	436/438 (100%)	407 (93%)	27 (6%)	2 (0%)	24	63
4	HK	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	IA	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78
4	IC	436/438 (100%)	407 (93%)	29 (7%)	0	100	100
4	IE	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	IG	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	II	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	IK	436/438 (100%)	401 (92%)	34 (8%)	1 (0%)	43	78
4	IM	436/438 (100%)	408 (94%)	28 (6%)	0	100	100
4	JA	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	JC	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	JE	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	JG	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	JI	436/438 (100%)	410 (94%)	26 (6%)	0	100	100
4	JK	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	KA	436/438 (100%)	407 (93%)	29 (7%)	0	100	100
4	KC	436/438 (100%)	401 (92%)	34 (8%)	1 (0%)	43	78
4	KE	436/438 (100%)	407 (93%)	29 (7%)	0	100	100
4	KG	436/438 (100%)	408 (94%)	28 (6%)	0	100	100
4	KI	436/438 (100%)	403 (92%)	33 (8%)	0	100	100
4	KK	436/438 (100%)	407 (93%)	29 (7%)	0	100	100
4	LA	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	LC	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	LE	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	LG	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	LI	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78
4	LK	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	MC	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78
4	ME	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	MG	436/438 (100%)	403 (92%)	32 (7%)	1 (0%)	43	78
4	MI	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	MK	436/438 (100%)	408 (94%)	28 (6%)	0	100	100
4	MM	436/438 (100%)	399 (92%)	36 (8%)	1 (0%)	43	78
4	NA	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	NC	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78
4	NE	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78
4	NG	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	NI	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	NK	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	OA	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	OC	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	OE	436/438 (100%)	409 (94%)	25 (6%)	2 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	OG	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	OI	436/438 (100%)	405 (93%)	30 (7%)	1 (0%)	43	78
4	OK	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	PA	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78
4	PC	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	PE	436/438 (100%)	414 (95%)	22 (5%)	0	100	100
4	PG	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	PI	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	PK	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	PM	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	QC	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	QE	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	QG	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	QI	436/438 (100%)	416 (95%)	19 (4%)	1 (0%)	43	78
4	QK	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	QM	436/438 (100%)	410 (94%)	26 (6%)	0	100	100
4	RC	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	RE	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78
4	RG	436/438 (100%)	412 (94%)	24 (6%)	0	100	100
4	RI	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78
4	RK	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	RM	436/438 (100%)	411 (94%)	25 (6%)	0	100	100
4	SC	436/438 (100%)	415 (95%)	20 (5%)	1 (0%)	43	78
4	SE	436/438 (100%)	414 (95%)	21 (5%)	1 (0%)	43	78
4	SG	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	SI	436/438 (100%)	410 (94%)	26 (6%)	0	100	100
4	SK	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	SM	436/438 (100%)	412 (94%)	23 (5%)	1 (0%)	43	78
4	TC	436/438 (100%)	415 (95%)	20 (5%)	1 (0%)	43	78
4	TE	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	TG	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	TI	436/438 (100%)	408 (94%)	28 (6%)	0	100	100
4	TK	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	TM	436/438 (100%)	409 (94%)	27 (6%)	0	100	100
4	UA	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	UC	436/438 (100%)	408 (94%)	27 (6%)	1 (0%)	43	78
4	UE	436/438 (100%)	410 (94%)	26 (6%)	0	100	100
4	UG	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	UI	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	UK	436/438 (100%)	409 (94%)	26 (6%)	1 (0%)	43	78
4	VA	436/438 (100%)	416 (95%)	20 (5%)	0	100	100
4	VC	436/438 (100%)	406 (93%)	29 (7%)	1 (0%)	43	78
4	VE	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	VG	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	VI	436/438 (100%)	407 (93%)	28 (6%)	1 (0%)	43	78
4	VK	436/438 (100%)	413 (95%)	22 (5%)	1 (0%)	43	78
4	WA	436/438 (100%)	415 (95%)	20 (5%)	1 (0%)	43	78
4	WC	436/438 (100%)	411 (94%)	24 (6%)	1 (0%)	43	78
4	WE	436/438 (100%)	405 (93%)	29 (7%)	2 (0%)	24	63
4	WG	436/438 (100%)	410 (94%)	25 (6%)	1 (0%)	43	78
4	WI	436/438 (100%)	404 (93%)	31 (7%)	1 (0%)	43	78
4	WK	436/438 (100%)	402 (92%)	33 (8%)	1 (0%)	43	78
5	B1	234/430 (54%)	216 (92%)	18 (8%)	0	100	100
5	B2	414/430 (96%)	398 (96%)	15 (4%)	1 (0%)	43	78
5	B3	414/430 (96%)	389 (94%)	24 (6%)	1 (0%)	43	78
5	B4	308/430 (72%)	289 (94%)	18 (6%)	1 (0%)	36	72
5	B5	46/430 (11%)	43 (94%)	3 (6%)	0	100	100
5	B6	359/430 (84%)	344 (96%)	13 (4%)	2 (1%)	21	59
5	B7	403/430 (94%)	383 (95%)	18 (4%)	2 (0%)	24	63
5	B8	396/430 (92%)	378 (96%)	16 (4%)	2 (0%)	24	63
5	B9	113/430 (26%)	109 (96%)	4 (4%)	0	100	100
6	C	370/395 (94%)	313 (85%)	56 (15%)	1 (0%)	36	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	D	370/395 (94%)	328 (89%)	42 (11%)	0	100	100
7	C1	94/490 (19%)	88 (94%)	6 (6%)	0	100	100
7	C2	386/490 (79%)	371 (96%)	15 (4%)	0	100	100
7	C3	386/490 (79%)	368 (95%)	18 (5%)	0	100	100
7	C4	359/490 (73%)	333 (93%)	26 (7%)	0	100	100
7	C5	61/490 (12%)	59 (97%)	2 (3%)	0	100	100
7	C6	196/490 (40%)	187 (95%)	9 (5%)	0	100	100
7	C7	392/490 (80%)	367 (94%)	25 (6%)	0	100	100
7	C8	392/490 (80%)	375 (96%)	17 (4%)	0	100	100
7	C9	294/490 (60%)	279 (95%)	14 (5%)	1 (0%)	36	72
7	Ca	215/490 (44%)	212 (99%)	2 (1%)	1 (0%)	24	63
7	Cb	386/490 (79%)	372 (96%)	14 (4%)	0	100	100
7	Cc	386/490 (79%)	364 (94%)	22 (6%)	0	100	100
7	Cd	262/490 (54%)	257 (98%)	4 (2%)	1 (0%)	30	67
8	D1	54/447 (12%)	53 (98%)	1 (2%)	0	100	100
8	D2	361/447 (81%)	350 (97%)	11 (3%)	0	100	100
8	D3	423/447 (95%)	410 (97%)	13 (3%)	0	100	100
8	D4	423/447 (95%)	402 (95%)	21 (5%)	0	100	100
8	D5	128/447 (29%)	125 (98%)	3 (2%)	0	100	100
8	D6	73/447 (16%)	70 (96%)	2 (3%)	1 (1%)	9	40
8	D7	367/447 (82%)	353 (96%)	13 (4%)	1 (0%)	36	72
8	D8	396/447 (89%)	383 (97%)	12 (3%)	1 (0%)	36	72
8	D9	390/447 (87%)	379 (97%)	10 (3%)	1 (0%)	36	72
8	Da	56/447 (12%)	55 (98%)	1 (2%)	0	100	100
9	E	259/853 (30%)	230 (89%)	26 (10%)	3 (1%)	10	44
9	F	147/853 (17%)	123 (84%)	24 (16%)	0	100	100
10	E1	185/206 (90%)	137 (74%)	48 (26%)	0	100	100
10	E2	185/206 (90%)	143 (77%)	42 (23%)	0	100	100
10	E3	185/206 (90%)	136 (74%)	49 (26%)	0	100	100
10	E4	55/206 (27%)	46 (84%)	9 (16%)	0	100	100
11	F1	280/557 (50%)	271 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	F2	391/557 (70%)	378 (97%)	13 (3%)	0	100	100
11	F3	391/557 (70%)	369 (94%)	22 (6%)	0	100	100
11	F4	208/557 (37%)	203 (98%)	5 (2%)	0	100	100
11	F5	252/557 (45%)	244 (97%)	8 (3%)	0	100	100
11	F6	387/557 (70%)	366 (95%)	20 (5%)	1 (0%)	36	72
11	F7	387/557 (70%)	368 (95%)	18 (5%)	1 (0%)	36	72
11	F8	225/557 (40%)	217 (96%)	8 (4%)	0	100	100
11	F9	169/557 (30%)	160 (95%)	9 (5%)	0	100	100
11	Fa	387/557 (70%)	371 (96%)	16 (4%)	0	100	100
11	Fb	387/557 (70%)	367 (95%)	18 (5%)	2 (0%)	24	63
11	Fc	311/557 (56%)	294 (94%)	15 (5%)	2 (1%)	21	59
11	Fd	21/557 (4%)	20 (95%)	1 (5%)	0	100	100
11	Fe	231/557 (42%)	230 (100%)	0	1 (0%)	30	67
11	Ff	391/557 (70%)	379 (97%)	12 (3%)	0	100	100
11	Fg	307/557 (55%)	293 (95%)	14 (5%)	0	100	100
11	Fh	179/557 (32%)	164 (92%)	12 (7%)	3 (2%)	7	36
11	Fi	266/557 (48%)	261 (98%)	5 (2%)	0	100	100
11	Fj	271/557 (49%)	265 (98%)	6 (2%)	0	100	100
11	Fk	326/557 (58%)	316 (97%)	8 (2%)	2 (1%)	21	59
11	Fl	326/557 (58%)	315 (97%)	9 (3%)	2 (1%)	21	59
11	Fm	321/557 (58%)	309 (96%)	11 (3%)	1 (0%)	36	72
12	G	446/514 (87%)	441 (99%)	5 (1%)	0	100	100
12	H	45/514 (9%)	45 (100%)	0	0	100	100
13	G1	506/648 (78%)	443 (88%)	61 (12%)	2 (0%)	30	67
13	G2	491/648 (76%)	438 (89%)	50 (10%)	3 (1%)	21	59
13	G3	507/648 (78%)	439 (87%)	65 (13%)	3 (1%)	21	59
14	G4	746/750 (100%)	640 (86%)	100 (13%)	6 (1%)	16	54
14	G5	745/750 (99%)	640 (86%)	99 (13%)	6 (1%)	16	54
14	G6	745/750 (99%)	636 (85%)	101 (14%)	8 (1%)	11	46
15	H1	133/319 (42%)	97 (73%)	33 (25%)	3 (2%)	5	28
15	H2	129/319 (40%)	100 (78%)	28 (22%)	1 (1%)	16	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
15	H3	133/319 (42%)	97 (73%)	34 (26%)	2 (2%)	8 40
15	H4	132/319 (41%)	102 (77%)	28 (21%)	2 (2%)	8 40
15	H5	133/319 (42%)	95 (71%)	35 (26%)	3 (2%)	5 28
15	H6	130/319 (41%)	93 (72%)	34 (26%)	3 (2%)	5 28
16	I	90/228 (40%)	80 (89%)	10 (11%)	0	100 100
17	I1	36/200 (18%)	34 (94%)	2 (6%)	0	100 100
17	I2	36/200 (18%)	35 (97%)	1 (3%)	0	100 100
17	I3	36/200 (18%)	35 (97%)	1 (3%)	0	100 100
18	J	156/196 (80%)	122 (78%)	33 (21%)	1 (1%)	21 59
19	J1	169/189 (89%)	131 (78%)	35 (21%)	3 (2%)	6 34
19	J2	169/189 (89%)	135 (80%)	32 (19%)	2 (1%)	10 44
19	J3	169/189 (89%)	127 (75%)	39 (23%)	3 (2%)	6 34
20	K	268/303 (88%)	256 (96%)	12 (4%)	0	100 100
20	L	268/303 (88%)	253 (94%)	15 (6%)	0	100 100
21	K1	101/499 (20%)	92 (91%)	7 (7%)	2 (2%)	6 31
21	K2	417/499 (84%)	366 (88%)	39 (9%)	12 (3%)	3 23
21	K3	424/499 (85%)	364 (86%)	43 (10%)	17 (4%)	2 18
21	K4	388/499 (78%)	340 (88%)	36 (9%)	12 (3%)	3 22
21	K5	46/499 (9%)	36 (78%)	6 (13%)	4 (9%)	0 9
22	L1	206/255 (81%)	166 (81%)	36 (18%)	4 (2%)	6 32
22	L2	234/255 (92%)	181 (77%)	50 (21%)	3 (1%)	9 42
22	L3	234/255 (92%)	187 (80%)	43 (18%)	4 (2%)	7 36
22	L4	73/255 (29%)	55 (75%)	18 (25%)	0	100 100
23	M	113/167 (68%)	102 (90%)	11 (10%)	0	100 100
24	M1	60/141 (43%)	48 (80%)	12 (20%)	0	100 100
24	M2	60/141 (43%)	48 (80%)	12 (20%)	0	100 100
24	M3	60/141 (43%)	52 (87%)	8 (13%)	0	100 100
25	N	72/122 (59%)	68 (94%)	4 (6%)	0	100 100
26	N1	64/168 (38%)	48 (75%)	16 (25%)	0	100 100
26	N2	64/168 (38%)	46 (72%)	18 (28%)	0	100 100
26	N3	64/168 (38%)	51 (80%)	12 (19%)	1 (2%)	7 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
26	N4	64/168 (38%)	47 (73%)	15 (23%)	2 (3%)	3 22
27	O	47/377 (12%)	45 (96%)	2 (4%)	0	100 100
27	P	313/377 (83%)	304 (97%)	9 (3%)	0	100 100
27	Q	181/377 (48%)	167 (92%)	13 (7%)	1 (1%)	21 59
27	R	224/377 (59%)	219 (98%)	5 (2%)	0	100 100
28	O1	101/189 (53%)	77 (76%)	22 (22%)	2 (2%)	6 31
28	O2	101/189 (53%)	72 (71%)	28 (28%)	1 (1%)	12 48
28	O3	101/189 (53%)	74 (73%)	26 (26%)	1 (1%)	12 48
29	P1	606/620 (98%)	593 (98%)	13 (2%)	0	100 100
29	P2	606/620 (98%)	590 (97%)	16 (3%)	0	100 100
29	P3	606/620 (98%)	591 (98%)	15 (2%)	0	100 100
30	Q1	176/1516 (12%)	145 (82%)	29 (16%)	2 (1%)	11 46
30	Q2	176/1516 (12%)	141 (80%)	31 (18%)	4 (2%)	5 28
30	Q3	176/1516 (12%)	144 (82%)	30 (17%)	2 (1%)	11 46
31	R1	70/283 (25%)	62 (89%)	7 (10%)	1 (1%)	9 40
31	R2	70/283 (25%)	61 (87%)	8 (11%)	1 (1%)	9 40
31	R3	70/283 (25%)	63 (90%)	6 (9%)	1 (1%)	9 40
32	S	69/470 (15%)	60 (87%)	9 (13%)	0	100 100
32	T	107/470 (23%)	97 (91%)	10 (9%)	0	100 100
33	U	359/551 (65%)	354 (99%)	5 (1%)	0	100 100
33	V	61/551 (11%)	61 (100%)	0	0	100 100
33	W	321/551 (58%)	303 (94%)	16 (5%)	2 (1%)	21 59
33	X	174/551 (32%)	167 (96%)	7 (4%)	0	100 100
34	XA	183/193 (95%)	174 (95%)	9 (5%)	0	100 100
34	XB	183/193 (95%)	174 (95%)	9 (5%)	0	100 100
34	XC	183/193 (95%)	172 (94%)	11 (6%)	0	100 100
34	XD	183/193 (95%)	176 (96%)	7 (4%)	0	100 100
34	XE	183/193 (95%)	171 (93%)	12 (7%)	0	100 100
34	XF	183/193 (95%)	172 (94%)	11 (6%)	0	100 100
34	XG	183/193 (95%)	174 (95%)	9 (5%)	0	100 100
35	XH	174/241 (72%)	157 (90%)	17 (10%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	XI	174/241 (72%)	160 (92%)	14 (8%)	0	100	100
35	XJ	174/241 (72%)	158 (91%)	16 (9%)	0	100	100
35	XK	174/241 (72%)	152 (87%)	22 (13%)	0	100	100
35	XL	174/241 (72%)	158 (91%)	16 (9%)	0	100	100
35	XM	174/241 (72%)	161 (92%)	13 (8%)	0	100	100
36	Y	212/547 (39%)	207 (98%)	5 (2%)	0	100	100
36	Z	281/547 (51%)	271 (96%)	10 (4%)	0	100	100
37	YA	166/168 (99%)	148 (89%)	15 (9%)	3 (2%)	6	34
37	YB	166/168 (99%)	146 (88%)	19 (11%)	1 (1%)	21	59
37	YC	166/168 (99%)	145 (87%)	19 (11%)	2 (1%)	10	44
37	YD	166/168 (99%)	147 (89%)	17 (10%)	2 (1%)	10	44
37	YE	166/168 (99%)	148 (89%)	16 (10%)	2 (1%)	10	44
37	YF	166/168 (99%)	145 (87%)	18 (11%)	3 (2%)	6	34
37	YG	166/168 (99%)	145 (87%)	19 (11%)	2 (1%)	10	44
37	YH	166/168 (99%)	149 (90%)	15 (9%)	2 (1%)	10	44
37	YI	166/168 (99%)	148 (89%)	16 (10%)	2 (1%)	10	44
37	YJ	166/168 (99%)	145 (87%)	19 (11%)	2 (1%)	10	44
37	YK	166/168 (99%)	146 (88%)	18 (11%)	2 (1%)	10	44
37	YL	166/168 (99%)	147 (89%)	16 (10%)	3 (2%)	6	34
37	YM	166/168 (99%)	145 (87%)	18 (11%)	3 (2%)	6	34
37	YN	166/168 (99%)	147 (89%)	17 (10%)	2 (1%)	10	44
37	YO	166/168 (99%)	145 (87%)	19 (11%)	2 (1%)	10	44
37	YP	166/168 (99%)	149 (90%)	15 (9%)	2 (1%)	10	44
37	YQ	166/168 (99%)	147 (89%)	16 (10%)	3 (2%)	6	34
37	YR	166/168 (99%)	145 (87%)	19 (11%)	2 (1%)	10	44
37	YS	166/168 (99%)	148 (89%)	16 (10%)	2 (1%)	10	44
37	YT	166/168 (99%)	143 (86%)	21 (13%)	2 (1%)	10	44
37	YU	166/168 (99%)	142 (86%)	22 (13%)	2 (1%)	10	44
37	YV	166/168 (99%)	146 (88%)	18 (11%)	2 (1%)	10	44
37	YW	166/168 (99%)	143 (86%)	21 (13%)	2 (1%)	10	44
38	a	89/101 (88%)	81 (91%)	8 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	159844/188175 (85%)	149076 (93%)	10183 (6%)	585 (0%)	31 67

5 of 585 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A2	209	PRO
5	B2	125	ASP
5	B3	125	ASP
5	B6	125	ASP
5	B6	400	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	294/450 (65%)	294 (100%)	0	100 100
1	B	179/450 (40%)	179 (100%)	0	100 100
2	A1	288/380 (76%)	288 (100%)	0	100 100
2	A2	365/380 (96%)	365 (100%)	0	100 100
2	A3	365/380 (96%)	365 (100%)	0	100 100
2	A4	179/380 (47%)	179 (100%)	0	100 100
3	AB	367/367 (100%)	367 (100%)	0	100 100
3	AD	367/367 (100%)	367 (100%)	0	100 100
3	AF	367/367 (100%)	367 (100%)	0	100 100
3	AH	367/367 (100%)	367 (100%)	0	100 100
3	AJ	367/367 (100%)	367 (100%)	0	100 100
3	AL	367/367 (100%)	367 (100%)	0	100 100
3	BB	367/367 (100%)	367 (100%)	0	100 100
3	BD	367/367 (100%)	367 (100%)	0	100 100
3	BF	367/367 (100%)	367 (100%)	0	100 100
3	BH	367/367 (100%)	367 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BJ	367/367 (100%)	367 (100%)	0	100	100
3	BL	367/367 (100%)	367 (100%)	0	100	100
3	CB	367/367 (100%)	367 (100%)	0	100	100
3	CD	367/367 (100%)	367 (100%)	0	100	100
3	CF	367/367 (100%)	367 (100%)	0	100	100
3	CH	367/367 (100%)	367 (100%)	0	100	100
3	CJ	367/367 (100%)	367 (100%)	0	100	100
3	CL	367/367 (100%)	367 (100%)	0	100	100
3	DB	367/367 (100%)	367 (100%)	0	100	100
3	DD	367/367 (100%)	367 (100%)	0	100	100
3	DF	367/367 (100%)	367 (100%)	0	100	100
3	DH	367/367 (100%)	367 (100%)	0	100	100
3	DJ	367/367 (100%)	367 (100%)	0	100	100
3	DL	367/367 (100%)	367 (100%)	0	100	100
3	EB	367/367 (100%)	367 (100%)	0	100	100
3	ED	367/367 (100%)	367 (100%)	0	100	100
3	EF	367/367 (100%)	367 (100%)	0	100	100
3	EH	367/367 (100%)	367 (100%)	0	100	100
3	EJ	367/367 (100%)	367 (100%)	0	100	100
3	EL	367/367 (100%)	367 (100%)	0	100	100
3	FB	367/367 (100%)	366 (100%)	1 (0%)	86	86
3	FD	367/367 (100%)	367 (100%)	0	100	100
3	FF	367/367 (100%)	367 (100%)	0	100	100
3	FH	367/367 (100%)	367 (100%)	0	100	100
3	FJ	367/367 (100%)	367 (100%)	0	100	100
3	FL	367/367 (100%)	367 (100%)	0	100	100
3	GB	367/367 (100%)	367 (100%)	0	100	100
3	GD	367/367 (100%)	367 (100%)	0	100	100
3	GF	367/367 (100%)	367 (100%)	0	100	100
3	GH	367/367 (100%)	367 (100%)	0	100	100
3	GJ	367/367 (100%)	367 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	GL	367/367 (100%)	367 (100%)	0	100	100
3	HB	367/367 (100%)	367 (100%)	0	100	100
3	HD	367/367 (100%)	367 (100%)	0	100	100
3	HF	367/367 (100%)	367 (100%)	0	100	100
3	HH	367/367 (100%)	367 (100%)	0	100	100
3	HJ	367/367 (100%)	367 (100%)	0	100	100
3	HL	367/367 (100%)	367 (100%)	0	100	100
3	IB	367/367 (100%)	367 (100%)	0	100	100
3	ID	367/367 (100%)	367 (100%)	0	100	100
3	IF	367/367 (100%)	367 (100%)	0	100	100
3	IH	367/367 (100%)	367 (100%)	0	100	100
3	IJ	367/367 (100%)	367 (100%)	0	100	100
3	IL	367/367 (100%)	367 (100%)	0	100	100
3	JB	367/367 (100%)	367 (100%)	0	100	100
3	JD	367/367 (100%)	367 (100%)	0	100	100
3	JF	367/367 (100%)	367 (100%)	0	100	100
3	JH	367/367 (100%)	367 (100%)	0	100	100
3	JJ	367/367 (100%)	367 (100%)	0	100	100
3	JL	367/367 (100%)	367 (100%)	0	100	100
3	KB	367/367 (100%)	367 (100%)	0	100	100
3	KD	367/367 (100%)	367 (100%)	0	100	100
3	KF	367/367 (100%)	367 (100%)	0	100	100
3	KH	367/367 (100%)	367 (100%)	0	100	100
3	KJ	367/367 (100%)	367 (100%)	0	100	100
3	KL	367/367 (100%)	367 (100%)	0	100	100
3	LB	367/367 (100%)	367 (100%)	0	100	100
3	LD	367/367 (100%)	367 (100%)	0	100	100
3	LF	367/367 (100%)	367 (100%)	0	100	100
3	LH	367/367 (100%)	367 (100%)	0	100	100
3	LJ	367/367 (100%)	367 (100%)	0	100	100
3	LL	367/367 (100%)	367 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	MB	367/367 (100%)	367 (100%)	0	100	100
3	MD	367/367 (100%)	367 (100%)	0	100	100
3	MF	367/367 (100%)	367 (100%)	0	100	100
3	MH	367/367 (100%)	367 (100%)	0	100	100
3	MJ	367/367 (100%)	367 (100%)	0	100	100
3	ML	367/367 (100%)	367 (100%)	0	100	100
3	NB	367/367 (100%)	367 (100%)	0	100	100
3	ND	367/367 (100%)	367 (100%)	0	100	100
3	NF	367/367 (100%)	367 (100%)	0	100	100
3	NH	367/367 (100%)	367 (100%)	0	100	100
3	NJ	367/367 (100%)	367 (100%)	0	100	100
3	NL	367/367 (100%)	367 (100%)	0	100	100
3	OB	367/367 (100%)	367 (100%)	0	100	100
3	OD	367/367 (100%)	367 (100%)	0	100	100
3	OF	367/367 (100%)	367 (100%)	0	100	100
3	OH	367/367 (100%)	367 (100%)	0	100	100
3	OJ	367/367 (100%)	367 (100%)	0	100	100
3	OL	367/367 (100%)	367 (100%)	0	100	100
3	PB	367/367 (100%)	367 (100%)	0	100	100
3	PD	367/367 (100%)	367 (100%)	0	100	100
3	PF	367/367 (100%)	367 (100%)	0	100	100
3	PH	367/367 (100%)	367 (100%)	0	100	100
3	PJ	367/367 (100%)	367 (100%)	0	100	100
3	PL	367/367 (100%)	367 (100%)	0	100	100
3	QB	367/367 (100%)	367 (100%)	0	100	100
3	QD	367/367 (100%)	367 (100%)	0	100	100
3	QF	367/367 (100%)	367 (100%)	0	100	100
3	QH	367/367 (100%)	367 (100%)	0	100	100
3	QJ	367/367 (100%)	367 (100%)	0	100	100
3	QL	367/367 (100%)	367 (100%)	0	100	100
3	RB	367/367 (100%)	367 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	RD	367/367 (100%)	367 (100%)	0	100	100
3	RF	367/367 (100%)	367 (100%)	0	100	100
3	RH	367/367 (100%)	367 (100%)	0	100	100
3	RJ	367/367 (100%)	367 (100%)	0	100	100
3	RL	367/367 (100%)	367 (100%)	0	100	100
3	SB	367/367 (100%)	367 (100%)	0	100	100
3	SD	367/367 (100%)	367 (100%)	0	100	100
3	SF	367/367 (100%)	367 (100%)	0	100	100
3	SH	367/367 (100%)	367 (100%)	0	100	100
3	SJ	367/367 (100%)	367 (100%)	0	100	100
3	SL	367/367 (100%)	367 (100%)	0	100	100
3	TB	367/367 (100%)	367 (100%)	0	100	100
3	TD	367/367 (100%)	367 (100%)	0	100	100
3	TF	367/367 (100%)	367 (100%)	0	100	100
3	TH	367/367 (100%)	367 (100%)	0	100	100
3	TJ	367/367 (100%)	367 (100%)	0	100	100
3	TL	367/367 (100%)	367 (100%)	0	100	100
3	TN	367/367 (100%)	367 (100%)	0	100	100
3	UB	367/367 (100%)	367 (100%)	0	100	100
3	UD	367/367 (100%)	367 (100%)	0	100	100
3	UF	367/367 (100%)	367 (100%)	0	100	100
3	UH	367/367 (100%)	367 (100%)	0	100	100
3	UJ	367/367 (100%)	367 (100%)	0	100	100
3	UL	367/367 (100%)	367 (100%)	0	100	100
3	VB	367/367 (100%)	367 (100%)	0	100	100
3	VD	367/367 (100%)	367 (100%)	0	100	100
3	VF	367/367 (100%)	367 (100%)	0	100	100
3	VH	367/367 (100%)	367 (100%)	0	100	100
3	VJ	367/367 (100%)	367 (100%)	0	100	100
3	VL	367/367 (100%)	367 (100%)	0	100	100
3	WB	367/367 (100%)	367 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	WD	367/367 (100%)	367 (100%)	0	100	100
3	WF	367/367 (100%)	367 (100%)	0	100	100
3	WH	367/367 (100%)	367 (100%)	0	100	100
3	WJ	367/367 (100%)	367 (100%)	0	100	100
3	WL	367/367 (100%)	367 (100%)	0	100	100
4	AC	366/366 (100%)	366 (100%)	0	100	100
4	AE	366/366 (100%)	366 (100%)	0	100	100
4	AG	366/366 (100%)	366 (100%)	0	100	100
4	AI	366/366 (100%)	366 (100%)	0	100	100
4	AK	366/366 (100%)	366 (100%)	0	100	100
4	AM	366/366 (100%)	366 (100%)	0	100	100
4	BC	366/366 (100%)	366 (100%)	0	100	100
4	BE	366/366 (100%)	366 (100%)	0	100	100
4	BG	366/366 (100%)	366 (100%)	0	100	100
4	BI	366/366 (100%)	366 (100%)	0	100	100
4	BK	366/366 (100%)	366 (100%)	0	100	100
4	BM	366/366 (100%)	366 (100%)	0	100	100
4	CC	366/366 (100%)	366 (100%)	0	100	100
4	CE	366/366 (100%)	366 (100%)	0	100	100
4	CG	366/366 (100%)	366 (100%)	0	100	100
4	CI	366/366 (100%)	366 (100%)	0	100	100
4	CK	366/366 (100%)	366 (100%)	0	100	100
4	CM	366/366 (100%)	366 (100%)	0	100	100
4	DA	366/366 (100%)	366 (100%)	0	100	100
4	DC	366/366 (100%)	366 (100%)	0	100	100
4	DE	366/366 (100%)	366 (100%)	0	100	100
4	DG	366/366 (100%)	366 (100%)	0	100	100
4	DI	366/366 (100%)	366 (100%)	0	100	100
4	DK	366/366 (100%)	366 (100%)	0	100	100
4	EA	366/366 (100%)	366 (100%)	0	100	100
4	EC	366/366 (100%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	EE	366/366 (100%)	366 (100%)	0	100	100
4	EG	366/366 (100%)	366 (100%)	0	100	100
4	EI	366/366 (100%)	366 (100%)	0	100	100
4	EK	366/366 (100%)	366 (100%)	0	100	100
4	FA	366/366 (100%)	366 (100%)	0	100	100
4	FC	366/366 (100%)	366 (100%)	0	100	100
4	FE	366/366 (100%)	366 (100%)	0	100	100
4	FG	366/366 (100%)	366 (100%)	0	100	100
4	FI	366/366 (100%)	366 (100%)	0	100	100
4	FK	366/366 (100%)	366 (100%)	0	100	100
4	GA	366/366 (100%)	366 (100%)	0	100	100
4	GC	366/366 (100%)	366 (100%)	0	100	100
4	GE	366/366 (100%)	366 (100%)	0	100	100
4	GG	366/366 (100%)	366 (100%)	0	100	100
4	GI	366/366 (100%)	366 (100%)	0	100	100
4	GK	366/366 (100%)	366 (100%)	0	100	100
4	HA	366/366 (100%)	366 (100%)	0	100	100
4	HC	366/366 (100%)	366 (100%)	0	100	100
4	HE	366/366 (100%)	366 (100%)	0	100	100
4	HG	366/366 (100%)	366 (100%)	0	100	100
4	HI	366/366 (100%)	366 (100%)	0	100	100
4	HK	366/366 (100%)	366 (100%)	0	100	100
4	IA	366/366 (100%)	366 (100%)	0	100	100
4	IC	366/366 (100%)	366 (100%)	0	100	100
4	IE	366/366 (100%)	366 (100%)	0	100	100
4	IG	366/366 (100%)	366 (100%)	0	100	100
4	II	366/366 (100%)	366 (100%)	0	100	100
4	IK	366/366 (100%)	366 (100%)	0	100	100
4	IM	366/366 (100%)	366 (100%)	0	100	100
4	JA	366/366 (100%)	366 (100%)	0	100	100
4	JC	366/366 (100%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	JE	366/366 (100%)	366 (100%)	0	100	100
4	JG	366/366 (100%)	366 (100%)	0	100	100
4	JI	366/366 (100%)	366 (100%)	0	100	100
4	JK	366/366 (100%)	366 (100%)	0	100	100
4	KA	366/366 (100%)	366 (100%)	0	100	100
4	KC	366/366 (100%)	366 (100%)	0	100	100
4	KE	366/366 (100%)	366 (100%)	0	100	100
4	KG	366/366 (100%)	366 (100%)	0	100	100
4	KI	366/366 (100%)	366 (100%)	0	100	100
4	KK	366/366 (100%)	366 (100%)	0	100	100
4	LA	366/366 (100%)	366 (100%)	0	100	100
4	LC	366/366 (100%)	366 (100%)	0	100	100
4	LE	366/366 (100%)	366 (100%)	0	100	100
4	LG	366/366 (100%)	366 (100%)	0	100	100
4	LI	366/366 (100%)	366 (100%)	0	100	100
4	LK	366/366 (100%)	366 (100%)	0	100	100
4	MC	366/366 (100%)	366 (100%)	0	100	100
4	ME	366/366 (100%)	366 (100%)	0	100	100
4	MG	366/366 (100%)	366 (100%)	0	100	100
4	MI	366/366 (100%)	366 (100%)	0	100	100
4	MK	366/366 (100%)	366 (100%)	0	100	100
4	MM	366/366 (100%)	366 (100%)	0	100	100
4	NA	366/366 (100%)	366 (100%)	0	100	100
4	NC	366/366 (100%)	366 (100%)	0	100	100
4	NE	366/366 (100%)	366 (100%)	0	100	100
4	NG	366/366 (100%)	366 (100%)	0	100	100
4	NI	366/366 (100%)	366 (100%)	0	100	100
4	NK	366/366 (100%)	366 (100%)	0	100	100
4	OA	366/366 (100%)	366 (100%)	0	100	100
4	OC	366/366 (100%)	366 (100%)	0	100	100
4	OE	366/366 (100%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	OG	366/366 (100%)	366 (100%)	0	100	100
4	OI	366/366 (100%)	366 (100%)	0	100	100
4	OK	366/366 (100%)	366 (100%)	0	100	100
4	PA	366/366 (100%)	366 (100%)	0	100	100
4	PC	366/366 (100%)	366 (100%)	0	100	100
4	PE	366/366 (100%)	366 (100%)	0	100	100
4	PG	366/366 (100%)	366 (100%)	0	100	100
4	PI	366/366 (100%)	366 (100%)	0	100	100
4	PK	366/366 (100%)	366 (100%)	0	100	100
4	PM	366/366 (100%)	366 (100%)	0	100	100
4	QC	366/366 (100%)	366 (100%)	0	100	100
4	QE	366/366 (100%)	366 (100%)	0	100	100
4	QG	366/366 (100%)	366 (100%)	0	100	100
4	QI	366/366 (100%)	366 (100%)	0	100	100
4	QK	366/366 (100%)	366 (100%)	0	100	100
4	QM	366/366 (100%)	366 (100%)	0	100	100
4	RC	366/366 (100%)	366 (100%)	0	100	100
4	RE	366/366 (100%)	366 (100%)	0	100	100
4	RG	366/366 (100%)	366 (100%)	0	100	100
4	RI	366/366 (100%)	366 (100%)	0	100	100
4	RK	366/366 (100%)	366 (100%)	0	100	100
4	RM	366/366 (100%)	366 (100%)	0	100	100
4	SC	366/366 (100%)	366 (100%)	0	100	100
4	SE	366/366 (100%)	366 (100%)	0	100	100
4	SG	366/366 (100%)	366 (100%)	0	100	100
4	SI	366/366 (100%)	366 (100%)	0	100	100
4	SK	366/366 (100%)	366 (100%)	0	100	100
4	SM	366/366 (100%)	366 (100%)	0	100	100
4	TC	366/366 (100%)	366 (100%)	0	100	100
4	TE	366/366 (100%)	366 (100%)	0	100	100
4	TG	366/366 (100%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	TI	366/366 (100%)	366 (100%)	0	100	100
4	TK	366/366 (100%)	366 (100%)	0	100	100
4	TM	366/366 (100%)	366 (100%)	0	100	100
4	UA	366/366 (100%)	366 (100%)	0	100	100
4	UC	366/366 (100%)	366 (100%)	0	100	100
4	UE	366/366 (100%)	366 (100%)	0	100	100
4	UG	366/366 (100%)	366 (100%)	0	100	100
4	UI	366/366 (100%)	366 (100%)	0	100	100
4	UK	366/366 (100%)	366 (100%)	0	100	100
4	VA	366/366 (100%)	366 (100%)	0	100	100
4	VC	366/366 (100%)	366 (100%)	0	100	100
4	VE	366/366 (100%)	366 (100%)	0	100	100
4	VG	366/366 (100%)	366 (100%)	0	100	100
4	VI	366/366 (100%)	366 (100%)	0	100	100
4	VK	366/366 (100%)	366 (100%)	0	100	100
4	WA	366/366 (100%)	366 (100%)	0	100	100
4	WC	366/366 (100%)	366 (100%)	0	100	100
4	WE	366/366 (100%)	366 (100%)	0	100	100
4	WG	366/366 (100%)	366 (100%)	0	100	100
4	WI	366/366 (100%)	366 (100%)	0	100	100
4	WK	366/366 (100%)	366 (100%)	0	100	100
5	B1	215/395 (54%)	215 (100%)	0	100	100
5	B2	381/395 (96%)	381 (100%)	0	100	100
5	B3	381/395 (96%)	381 (100%)	0	100	100
5	B4	288/395 (73%)	288 (100%)	0	100	100
5	B5	44/395 (11%)	44 (100%)	0	100	100
5	B6	331/395 (84%)	331 (100%)	0	100	100
5	B7	370/395 (94%)	370 (100%)	0	100	100
5	B8	364/395 (92%)	364 (100%)	0	100	100
5	B9	104/395 (26%)	104 (100%)	0	100	100
6	C	317/337 (94%)	317 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	D	317/337 (94%)	317 (100%)	0	100	100
7	C1	90/445 (20%)	90 (100%)	0	100	100
7	C2	353/445 (79%)	353 (100%)	0	100	100
7	C3	353/445 (79%)	353 (100%)	0	100	100
7	C4	326/445 (73%)	326 (100%)	0	100	100
7	C5	59/445 (13%)	59 (100%)	0	100	100
7	C6	180/445 (40%)	180 (100%)	0	100	100
7	C7	359/445 (81%)	359 (100%)	0	100	100
7	C8	359/445 (81%)	359 (100%)	0	100	100
7	C9	270/445 (61%)	270 (100%)	0	100	100
7	Ca	202/445 (45%)	202 (100%)	0	100	100
7	Cb	353/445 (79%)	353 (100%)	0	100	100
7	Cc	353/445 (79%)	353 (100%)	0	100	100
7	Cd	238/445 (54%)	238 (100%)	0	100	100
8	D1	45/402 (11%)	45 (100%)	0	100	100
8	D2	330/402 (82%)	330 (100%)	0	100	100
8	D3	383/402 (95%)	383 (100%)	0	100	100
8	D4	383/402 (95%)	383 (100%)	0	100	100
8	D5	119/402 (30%)	119 (100%)	0	100	100
8	D6	66/402 (16%)	66 (100%)	0	100	100
8	D7	340/402 (85%)	340 (100%)	0	100	100
8	D8	364/402 (90%)	364 (100%)	0	100	100
8	D9	360/402 (90%)	360 (100%)	0	100	100
8	Da	49/402 (12%)	49 (100%)	0	100	100
9	E	235/745 (32%)	235 (100%)	0	100	100
9	F	130/745 (17%)	130 (100%)	0	100	100
10	E1	159/174 (91%)	159 (100%)	0	100	100
10	E2	159/174 (91%)	159 (100%)	0	100	100
10	E3	159/174 (91%)	159 (100%)	0	100	100
10	E4	45/174 (26%)	45 (100%)	0	100	100
11	F1	265/487 (54%)	265 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	F2	362/487 (74%)	362 (100%)	0	100	100
11	F3	362/487 (74%)	362 (100%)	0	100	100
11	F4	193/487 (40%)	193 (100%)	0	100	100
11	F5	235/487 (48%)	235 (100%)	0	100	100
11	F6	359/487 (74%)	359 (100%)	0	100	100
11	F7	359/487 (74%)	359 (100%)	0	100	100
11	F8	213/487 (44%)	213 (100%)	0	100	100
11	F9	161/487 (33%)	161 (100%)	0	100	100
11	Fa	359/487 (74%)	359 (100%)	0	100	100
11	Fb	359/487 (74%)	359 (100%)	0	100	100
11	Fc	290/487 (60%)	290 (100%)	0	100	100
11	Fd	21/487 (4%)	21 (100%)	0	100	100
11	Fe	220/487 (45%)	220 (100%)	0	100	100
11	Ff	362/487 (74%)	362 (100%)	0	100	100
11	Fg	289/487 (59%)	289 (100%)	0	100	100
11	Fh	171/487 (35%)	171 (100%)	0	100	100
11	Fi	251/487 (52%)	251 (100%)	0	100	100
11	Fj	256/487 (53%)	256 (100%)	0	100	100
11	Fk	305/487 (63%)	305 (100%)	0	100	100
11	Fl	305/487 (63%)	305 (100%)	0	100	100
11	Fm	301/487 (62%)	301 (100%)	0	100	100
12	G	406/464 (88%)	406 (100%)	0	100	100
12	H	39/464 (8%)	39 (100%)	0	100	100
13	G1	465/589 (79%)	465 (100%)	0	100	100
13	G2	452/589 (77%)	452 (100%)	0	100	100
13	G3	466/589 (79%)	465 (100%)	1 (0%)	87	87
14	G4	682/683 (100%)	682 (100%)	0	100	100
14	G5	681/683 (100%)	681 (100%)	0	100	100
14	G6	681/683 (100%)	681 (100%)	0	100	100
15	H1	120/279 (43%)	120 (100%)	0	100	100
15	H2	116/279 (42%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	H3	120/279 (43%)	120 (100%)	0	100 100
15	H4	119/279 (43%)	119 (100%)	0	100 100
15	H5	120/279 (43%)	119 (99%)	1 (1%)	73 80
15	H6	117/279 (42%)	117 (100%)	0	100 100
16	I	87/210 (41%)	87 (100%)	0	100 100
17	I1	33/180 (18%)	33 (100%)	0	100 100
17	I2	33/180 (18%)	33 (100%)	0	100 100
17	I3	33/180 (18%)	33 (100%)	0	100 100
18	J	146/181 (81%)	146 (100%)	0	100 100
19	J1	153/169 (90%)	153 (100%)	0	100 100
19	J2	153/169 (90%)	153 (100%)	0	100 100
19	J3	153/169 (90%)	152 (99%)	1 (1%)	76 81
20	K	236/265 (89%)	235 (100%)	1 (0%)	84 84
20	L	236/265 (89%)	236 (100%)	0	100 100
21	K1	92/434 (21%)	92 (100%)	0	100 100
21	K2	370/434 (85%)	370 (100%)	0	100 100
21	K3	375/434 (86%)	374 (100%)	1 (0%)	86 86
21	K4	345/434 (80%)	345 (100%)	0	100 100
21	K5	40/434 (9%)	40 (100%)	0	100 100
22	L1	193/235 (82%)	193 (100%)	0	100 100
22	L2	216/235 (92%)	216 (100%)	0	100 100
22	L3	216/235 (92%)	216 (100%)	0	100 100
22	L4	70/235 (30%)	70 (100%)	0	100 100
23	M	105/147 (71%)	105 (100%)	0	100 100
24	M1	54/125 (43%)	54 (100%)	0	100 100
24	M2	54/125 (43%)	54 (100%)	0	100 100
24	M3	54/125 (43%)	54 (100%)	0	100 100
25	N	65/110 (59%)	65 (100%)	0	100 100
26	N1	58/148 (39%)	58 (100%)	0	100 100
26	N2	58/148 (39%)	58 (100%)	0	100 100
26	N3	58/148 (39%)	58 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	N4	58/148 (39%)	58 (100%)	0	100	100
27	O	42/341 (12%)	42 (100%)	0	100	100
27	P	287/341 (84%)	287 (100%)	0	100	100
27	Q	162/341 (48%)	162 (100%)	0	100	100
27	R	208/341 (61%)	207 (100%)	1 (0%)	81	83
28	O1	88/165 (53%)	88 (100%)	0	100	100
28	O2	88/165 (53%)	88 (100%)	0	100	100
28	O3	88/165 (53%)	88 (100%)	0	100	100
29	P1	511/522 (98%)	511 (100%)	0	100	100
29	P2	511/522 (98%)	511 (100%)	0	100	100
29	P3	511/522 (98%)	511 (100%)	0	100	100
30	Q1	162/1391 (12%)	162 (100%)	0	100	100
30	Q2	162/1391 (12%)	162 (100%)	0	100	100
30	Q3	162/1391 (12%)	162 (100%)	0	100	100
31	R1	62/250 (25%)	62 (100%)	0	100	100
31	R2	62/250 (25%)	62 (100%)	0	100	100
31	R3	62/250 (25%)	62 (100%)	0	100	100
32	S	65/401 (16%)	65 (100%)	0	100	100
32	T	101/401 (25%)	101 (100%)	0	100	100
33	U	332/497 (67%)	332 (100%)	0	100	100
33	V	57/497 (12%)	57 (100%)	0	100	100
33	W	294/497 (59%)	294 (100%)	0	100	100
33	X	156/497 (31%)	156 (100%)	0	100	100
34	XA	173/180 (96%)	173 (100%)	0	100	100
34	XB	173/180 (96%)	173 (100%)	0	100	100
34	XC	173/180 (96%)	173 (100%)	0	100	100
34	XD	173/180 (96%)	173 (100%)	0	100	100
34	XE	173/180 (96%)	173 (100%)	0	100	100
34	XF	173/180 (96%)	173 (100%)	0	100	100
34	XG	173/180 (96%)	173 (100%)	0	100	100
35	XH	161/215 (75%)	160 (99%)	1 (1%)	78	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	XI	161/215 (75%)	161 (100%)	0	100	100
35	XJ	161/215 (75%)	161 (100%)	0	100	100
35	XK	161/215 (75%)	161 (100%)	0	100	100
35	XL	161/215 (75%)	161 (100%)	0	100	100
35	XM	161/215 (75%)	161 (100%)	0	100	100
36	Y	194/490 (40%)	194 (100%)	0	100	100
36	Z	261/490 (53%)	261 (100%)	0	100	100
37	YA	157/157 (100%)	156 (99%)	1 (1%)	78	83
37	YB	157/157 (100%)	157 (100%)	0	100	100
37	YC	157/157 (100%)	156 (99%)	1 (1%)	78	83
37	YD	157/157 (100%)	157 (100%)	0	100	100
37	YE	157/157 (100%)	157 (100%)	0	100	100
37	YF	157/157 (100%)	157 (100%)	0	100	100
37	YG	157/157 (100%)	157 (100%)	0	100	100
37	YH	157/157 (100%)	157 (100%)	0	100	100
37	YI	157/157 (100%)	157 (100%)	0	100	100
37	YJ	157/157 (100%)	157 (100%)	0	100	100
37	YK	157/157 (100%)	157 (100%)	0	100	100
37	YL	157/157 (100%)	157 (100%)	0	100	100
37	YM	157/157 (100%)	157 (100%)	0	100	100
37	YN	157/157 (100%)	157 (100%)	0	100	100
37	YO	157/157 (100%)	157 (100%)	0	100	100
37	YP	157/157 (100%)	157 (100%)	0	100	100
37	YQ	157/157 (100%)	157 (100%)	0	100	100
37	YR	157/157 (100%)	157 (100%)	0	100	100
37	YS	157/157 (100%)	157 (100%)	0	100	100
37	YT	157/157 (100%)	156 (99%)	1 (1%)	78	83
37	YU	157/157 (100%)	157 (100%)	0	100	100
37	YV	157/157 (100%)	157 (100%)	0	100	100
37	YW	157/157 (100%)	157 (100%)	0	100	100
38	a	82/91 (90%)	82 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	138680/162697 (85%)	138669 (100%)	11 (0%)	100 100

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	XH	199	GLN
37	YA	22	GLN
37	YT	22	GLN
37	YC	119	HIS
20	K	110	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1718 such sidechains are listed below:

Mol	Chain	Res	Type
4	KE	256	GLN
3	OF	424	GLN
3	WH	334	GLN
4	KK	256	GLN
3	KD	426	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

279 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
39	GTP	MB	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.63	9 (18%)
39	GTP	RB	501	-	33,34,34	1.11	5 (15%)	50,54,54	1.84	9 (18%)
39	GTP	QF	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.72	10 (20%)
39	GTP	EA	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.67	12 (24%)
39	GTP	IH	501	-	33,34,34	1.06	4 (12%)	50,54,54	1.74	11 (22%)
39	GTP	JF	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.71	10 (20%)
39	GTP	DB	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.70	9 (18%)
39	GTP	AB	501	-	33,34,34	1.15	4 (12%)	50,54,54	1.75	11 (22%)
39	GTP	FH	501	-	33,34,34	1.26	4 (12%)	50,54,54	1.85	10 (20%)
39	GTP	BB	501	-	33,34,34	1.02	1 (3%)	50,54,54	1.78	11 (22%)
39	GTP	OB	501	-	33,34,34	1.09	4 (12%)	50,54,54	1.69	10 (20%)
39	GTP	OE	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.61	12 (24%)
39	GTP	CB	501	-	33,34,34	1.11	4 (12%)	50,54,54	1.73	11 (22%)
39	GTP	GA	501	-	33,34,34	1.00	4 (12%)	50,54,54	1.61	11 (22%)
39	GTP	HJ	501	-	33,34,34	1.03	3 (9%)	50,54,54	1.67	10 (20%)
39	GTP	HL	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.69	8 (16%)
39	GTP	VI	501	-	33,34,34	1.03	4 (12%)	50,54,54	1.63	12 (24%)
39	GTP	DJ	501	-	33,34,34	1.06	2 (6%)	50,54,54	1.78	11 (22%)
39	GTP	BK	501	-	33,34,34	1.05	3 (9%)	50,54,54	1.65	9 (18%)
39	GTP	FF	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.76	10 (20%)
39	GTP	KK	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.57	10 (20%)
39	GTP	LE	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.61	9 (18%)
39	GTP	JC	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.61	10 (20%)
39	GTP	QJ	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.76	11 (22%)
39	GTP	RK	501	-	33,34,34	0.99	3 (9%)	50,54,54	1.77	14 (28%)
39	GTP	SJ	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.71	9 (18%)
39	GTP	UF	501	-	33,34,34	1.11	4 (12%)	50,54,54	1.81	10 (20%)
39	GTP	LA	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.60	12 (24%)
39	GTP	VA	501	-	33,34,34	1.03	4 (12%)	50,54,54	1.54	10 (20%)
39	GTP	WF	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.66	10 (20%)
39	GTP	RD	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.71	10 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	SK	501	-	33,34,34	1.09	4 (12%)	50,54,54	1.70	10 (20%)
39	GTP	CH	501	-	33,34,34	1.08	3 (9%)	50,54,54	2.00	11 (22%)
39	GTP	KJ	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.65	9 (18%)
39	GTP	TG	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.58	11 (22%)
39	GTP	FC	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.60	13 (26%)
39	GTP	TF	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.67	9 (18%)
39	GTP	FG	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.62	11 (22%)
39	GTP	KA	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.63	13 (26%)
39	GTP	JG	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.73	11 (22%)
39	GTP	SI	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.70	11 (22%)
39	GTP	IL	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.75	9 (18%)
39	GTP	PA	501	-	33,34,34	0.94	3 (9%)	50,54,54	1.65	12 (24%)
39	GTP	TJ	501	-	33,34,34	1.27	4 (12%)	50,54,54	2.09	10 (20%)
39	GTP	TL	501	-	33,34,34	1.50	7 (21%)	50,54,54	2.55	16 (32%)
39	GTP	EL	501	-	33,34,34	1.08	4 (12%)	50,54,54	1.61	9 (18%)
39	GTP	VL	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.67	9 (18%)
39	GTP	KL	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.66	9 (18%)
39	GTP	LD	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.79	11 (22%)
39	GTP	UG	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.61	10 (20%)
39	GTP	CI	501	-	33,34,34	1.01	4 (12%)	50,54,54	1.69	13 (26%)
39	GTP	JJ	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.69	9 (18%)
39	GTP	ND	501	-	33,34,34	1.18	5 (15%)	50,54,54	2.10	14 (28%)
39	GTP	UA	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.66	11 (22%)
39	GTP	TC	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.65	12 (24%)
39	GTP	MK	501	-	33,34,34	1.10	3 (9%)	50,54,54	1.62	10 (20%)
39	GTP	AK	501	-	33,34,34	0.98	3 (9%)	50,54,54	1.56	10 (20%)
39	GTP	IG	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.64	10 (20%)
39	GTP	ML	501	-	33,34,34	1.02	1 (3%)	50,54,54	1.83	11 (22%)
39	GTP	KD	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.63	9 (18%)
39	GTP	GL	501	-	33,34,34	1.13	3 (9%)	50,54,54	1.96	10 (20%)
39	GTP	GJ	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.70	10 (20%)
39	GTP	OH	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.68	9 (18%)
39	GTP	JD	501	-	33,34,34	1.03	3 (9%)	50,54,54	1.73	10 (20%)
39	GTP	CL	501	-	33,34,34	1.31	4 (12%)	50,54,54	2.48	15 (30%)
39	GTP	EE	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.75	15 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	QB	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.71	11 (22%)
39	GTP	SE	501	-	33,34,34	1.00	4 (12%)	50,54,54	1.54	10 (20%)
39	GTP	WJ	501	-	33,34,34	1.01	1 (3%)	50,54,54	1.73	9 (18%)
39	GTP	LF	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.69	10 (20%)
39	GTP	TI	501	-	33,34,34	0.99	3 (9%)	50,54,54	1.67	11 (22%)
39	GTP	DD	501	-	33,34,34	1.05	2 (6%)	50,54,54	1.87	10 (20%)
39	GTP	DE	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.70	11 (22%)
39	GTP	NI	501	-	33,34,34	1.07	3 (9%)	50,54,54	1.74	13 (26%)
39	GTP	PC	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.66	11 (22%)
39	GTP	GH	501	-	33,34,34	1.10	3 (9%)	50,54,54	1.84	11 (22%)
39	GTP	SC	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.60	10 (20%)
39	GTP	LC	501	-	33,34,34	0.99	3 (9%)	50,54,54	1.58	10 (20%)
39	GTP	IA	501	-	33,34,34	0.99	4 (12%)	50,54,54	1.57	11 (22%)
39	GTP	CM	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.65	12 (24%)
39	GTP	PK	501	-	33,34,34	1.21	4 (12%)	50,54,54	1.65	11 (22%)
39	GTP	FK	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.64	12 (24%)
39	GTP	HH	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.65	9 (18%)
39	GTP	LL	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.64	9 (18%)
39	GTP	OA	501	-	33,34,34	0.97	4 (12%)	50,54,54	1.67	13 (26%)
39	GTP	UK	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.65	11 (22%)
39	GTP	PB	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.66	9 (18%)
39	GTP	PE	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.59	11 (22%)
39	GTP	RL	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.73	8 (16%)
39	GTP	BI	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.70	12 (24%)
39	GTP	RH	501	-	33,34,34	0.99	1 (3%)	50,54,54	1.83	10 (20%)
39	GTP	SF	501	-	33,34,34	1.06	4 (12%)	50,54,54	1.77	8 (16%)
39	GTP	CC	501	-	33,34,34	1.08	2 (6%)	50,54,54	1.67	11 (22%)
39	GTP	VG	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.64	14 (28%)
39	GTP	IC	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.83	13 (26%)
39	GTP	GE	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.61	10 (20%)
39	GTP	OL	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.67	9 (18%)
39	GTP	BC	501	-	33,34,34	0.98	3 (9%)	50,54,54	1.68	10 (20%)
39	GTP	UL	501	-	33,34,34	1.02	1 (3%)	50,54,54	1.72	9 (18%)
39	GTP	WK	501	-	33,34,34	1.07	3 (9%)	50,54,54	1.61	12 (24%)
39	GTP	FE	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.65	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
39	GTP	DF	501	-	33,34,34	1.07	4 (12%)	50,54,54	1.75	11 (22%)
39	GTP	JH	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.67	9 (18%)
39	GTP	JE	501	-	33,34,34	0.89	3 (9%)	50,54,54	1.74	12 (24%)
39	GTP	DI	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.74	13 (26%)
39	GTP	OI	501	-	33,34,34	1.14	4 (12%)	50,54,54	1.69	12 (24%)
39	GTP	PH	501	-	33,34,34	1.07	2 (6%)	50,54,54	1.86	13 (26%)
39	GTP	UB	501	-	33,34,34	1.07	5 (15%)	50,54,54	1.75	9 (18%)
39	GTP	WI	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.77	14 (28%)
39	GTP	DH	501	-	33,34,34	1.13	4 (12%)	50,54,54	1.72	11 (22%)
39	GTP	SM	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.55	9 (18%)
39	GTP	NC	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.68	12 (24%)
39	GTP	OJ	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.68	9 (18%)
39	GTP	MG	501	-	33,34,34	1.00	4 (12%)	50,54,54	1.61	12 (24%)
39	GTP	QL	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.71	9 (18%)
39	GTP	PM	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.80	16 (32%)
39	GTP	JB	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.71	9 (18%)
39	GTP	NB	501	-	33,34,34	1.03	4 (12%)	50,54,54	1.69	9 (18%)
39	GTP	QD	502	-	33,34,34	1.04	3 (9%)	50,54,54	1.60	10 (20%)
39	GTP	IE	501	-	33,34,34	0.91	2 (6%)	50,54,54	1.80	13 (26%)
39	GTP	LK	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.57	9 (18%)
39	GTP	HG	501	-	33,34,34	1.09	4 (12%)	50,54,54	1.71	12 (24%)
39	GTP	FD	501	-	33,34,34	1.05	2 (6%)	50,54,54	1.81	10 (20%)
39	GTP	LB	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.75	9 (18%)
39	GTP	NJ	501	-	33,34,34	1.05	1 (3%)	50,54,54	1.87	13 (26%)
39	GTP	WB	501	-	33,34,34	1.13	4 (12%)	50,54,54	1.85	11 (22%)
39	GTP	HK	501	-	33,34,34	1.01	4 (12%)	50,54,54	1.68	12 (24%)
39	GTP	BD	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.71	11 (22%)
39	GTP	JL	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.66	9 (18%)
39	GTP	UI	501	-	33,34,34	1.08	4 (12%)	50,54,54	1.85	13 (26%)
39	GTP	FL	501	-	33,34,34	1.16	5 (15%)	50,54,54	1.88	11 (22%)
39	GTP	EK	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.65	11 (22%)
39	GTP	KI	501	-	33,34,34	0.97	3 (9%)	50,54,54	1.70	11 (22%)
39	GTP	NF	501	-	33,34,34	1.03	3 (9%)	50,54,54	1.72	9 (18%)
39	GTP	QC	501	-	33,34,34	1.03	4 (12%)	50,54,54	1.76	13 (26%)
39	GTP	FB	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.66	10 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	LJ	501	-	33,34,34	1.13	4 (12%)	50,54,54	1.89	12 (24%)
39	GTP	CD	501	-	33,34,34	1.08	4 (12%)	50,54,54	1.70	9 (18%)
39	GTP	TM	501	-	33,34,34	1.06	4 (12%)	50,54,54	1.61	10 (20%)
39	GTP	IB	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.68	7 (14%)
39	GTP	JI	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.59	11 (22%)
39	GTP	OK	501	-	33,34,34	0.97	3 (9%)	50,54,54	1.95	14 (28%)
39	GTP	CJ	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.66	7 (14%)
39	GTP	EF	501	-	33,34,34	1.14	4 (12%)	50,54,54	1.96	13 (26%)
39	GTP	PF	501	-	33,34,34	1.02	1 (3%)	50,54,54	1.84	12 (24%)
39	GTP	BG	501	-	33,34,34	1.01	4 (12%)	50,54,54	1.68	10 (20%)
39	GTP	EH	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.65	9 (18%)
39	GTP	BF	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.67	9 (18%)
39	GTP	AL	501	-	33,34,34	1.11	5 (15%)	50,54,54	1.69	9 (18%)
39	GTP	LI	501	-	33,34,34	0.97	4 (12%)	50,54,54	1.79	13 (26%)
39	GTP	KE	501	-	33,34,34	0.99	3 (9%)	50,54,54	1.63	12 (24%)
39	GTP	MC	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.60	11 (22%)
39	GTP	WE	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.78	14 (28%)
39	GTP	GI	501	-	33,34,34	1.05	2 (6%)	50,54,54	1.58	10 (20%)
39	GTP	TE	501	-	33,34,34	1.07	4 (12%)	50,54,54	1.66	11 (22%)
39	GTP	TN	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.67	9 (18%)
39	GTP	TH	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.70	9 (18%)
39	GTP	GF	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.73	11 (22%)
39	GTP	AI	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.61	11 (22%)
39	GTP	VH	501	-	33,34,34	1.05	3 (9%)	50,54,54	1.75	9 (18%)
39	GTP	EI	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.69	11 (22%)
39	GTP	UC	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.64	11 (22%)
39	GTP	CF	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.65	9 (18%)
39	GTP	IF	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.67	10 (20%)
39	GTP	IJ	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.63	11 (22%)
39	GTP	II	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.81	14 (28%)
39	GTP	TK	501	-	33,34,34	1.11	4 (12%)	50,54,54	1.57	10 (20%)
39	GTP	WD	501	-	33,34,34	1.15	4 (12%)	50,54,54	1.72	10 (20%)
39	GTP	RI	501	-	33,34,34	0.97	3 (9%)	50,54,54	1.74	10 (20%)
39	GTP	BJ	501	-	33,34,34	1.17	3 (9%)	50,54,54	3.10	14 (28%)
39	GTP	QL	502	-	33,34,34	1.14	4 (12%)	50,54,54	1.58	10 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	TB	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.69	9 (18%)
39	GTP	KB	501	-	33,34,34	1.24	4 (12%)	50,54,54	1.91	12 (24%)
39	GTP	RF	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.67	9 (18%)
39	GTP	RJ	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.70	10 (20%)
39	GTP	NA	501	-	33,34,34	0.98	4 (12%)	50,54,54	1.66	11 (22%)
39	GTP	EJ	501	-	33,34,34	1.08	4 (12%)	50,54,54	1.68	9 (18%)
39	GTP	MD	501	-	33,34,34	1.08	4 (12%)	50,54,54	1.59	8 (16%)
39	GTP	OG	501	-	33,34,34	1.00	4 (12%)	50,54,54	1.60	11 (22%)
39	GTP	QD	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.68	9 (18%)
39	GTP	VJ	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.69	9 (18%)
39	GTP	BL	501	-	33,34,34	1.05	3 (9%)	50,54,54	1.68	9 (18%)
39	GTP	DC	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.54	12 (24%)
39	GTP	VD	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.68	9 (18%)
39	GTP	CE	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.65	11 (22%)
39	GTP	FA	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.54	12 (24%)
39	GTP	WL	501	-	33,34,34	1.20	4 (12%)	50,54,54	1.70	11 (22%)
39	GTP	IK	501	-	33,34,34	0.96	3 (9%)	50,54,54	1.67	10 (20%)
39	GTP	VF	501	-	33,34,34	1.14	3 (9%)	50,54,54	1.83	12 (24%)
39	GTP	NG	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.68	11 (22%)
39	GTP	AF	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.65	9 (18%)
39	GTP	SG	501	-	33,34,34	1.06	4 (12%)	50,54,54	1.73	12 (24%)
39	GTP	AE	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.66	11 (22%)
39	GTP	GC	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.53	10 (20%)
39	GTP	NL	501	-	33,34,34	1.08	4 (12%)	50,54,54	1.69	10 (20%)
39	GTP	KF	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.82	11 (22%)
39	GTP	PI	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.62	10 (20%)
39	GTP	MD	502	-	33,34,34	0.98	3 (9%)	50,54,54	1.61	12 (24%)
39	GTP	NH	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.71	8 (16%)
39	GTP	HB	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.70	9 (18%)
39	GTP	BE	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.63	10 (20%)
39	GTP	CK	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.71	12 (24%)
39	GTP	DL	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.73	9 (18%)
39	GTP	EB	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.71	11 (22%)
39	GTP	EC	501	-	33,34,34	1.12	3 (9%)	50,54,54	1.80	13 (26%)
39	GTP	KC	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.54	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	OC	501	-	33,34,34	1.06	4 (12%)	50,54,54	1.75	12 (24%)
39	GTP	QI	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.80	13 (26%)
39	GTP	UH	501	-	33,34,34	1.03	3 (9%)	50,54,54	1.68	7 (14%)
39	GTP	VK	501	-	33,34,34	0.98	4 (12%)	50,54,54	1.66	11 (22%)
39	GTP	WG	501	-	33,34,34	1.05	3 (9%)	50,54,54	1.63	10 (20%)
39	GTP	AH	501	-	33,34,34	0.89	1 (3%)	50,54,54	1.69	9 (18%)
39	GTP	BM	501	-	33,34,34	1.18	3 (9%)	50,54,54	2.24	20 (40%)
39	GTP	WC	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.63	11 (22%)
39	GTP	FJ	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.87	11 (22%)
39	GTP	SL	501	-	33,34,34	1.03	2 (6%)	50,54,54	1.75	9 (18%)
39	GTP	HD	501	-	33,34,34	1.03	2 (6%)	50,54,54	1.68	9 (18%)
39	GTP	HF	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.60	8 (16%)
39	GTP	DK	501	-	33,34,34	1.06	2 (6%)	50,54,54	1.83	16 (32%)
39	GTP	IM	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.72	14 (28%)
39	GTP	UE	501	-	33,34,34	1.05	3 (9%)	50,54,54	1.62	12 (24%)
39	GTP	EG	501	-	33,34,34	0.91	2 (6%)	50,54,54	1.80	12 (24%)
39	GTP	FI	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.57	9 (18%)
39	GTP	OF	501	-	33,34,34	1.16	4 (12%)	50,54,54	1.68	10 (20%)
39	GTP	MJ	501	-	33,34,34	1.07	3 (9%)	50,54,54	1.67	9 (18%)
39	GTP	QK	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.53	10 (20%)
39	GTP	VC	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.83	15 (30%)
39	GTP	SD	501	-	33,34,34	1.09	4 (12%)	50,54,54	1.69	9 (18%)
39	GTP	PD	501	-	33,34,34	1.16	4 (12%)	50,54,54	2.14	12 (24%)
39	GTP	JK	501	-	33,34,34	0.97	3 (9%)	50,54,54	1.59	10 (20%)
39	GTP	GD	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.75	9 (18%)
39	GTP	MI	501	-	33,34,34	0.96	3 (9%)	50,54,54	1.60	11 (22%)
39	GTP	MH	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.70	10 (20%)
39	GTP	ED	501	-	33,34,34	1.01	1 (3%)	50,54,54	1.75	10 (20%)
39	GTP	DA	501	-	33,34,34	0.99	4 (12%)	50,54,54	1.57	10 (20%)
39	GTP	HA	501	-	33,34,34	1.03	3 (9%)	50,54,54	1.61	11 (22%)
39	GTP	LG	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.57	10 (20%)
39	GTP	VE	501	-	33,34,34	1.06	4 (12%)	50,54,54	1.89	14 (28%)
39	GTP	WH	501	-	33,34,34	1.04	1 (3%)	50,54,54	1.77	11 (22%)
39	GTP	AD	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.61	10 (20%)
39	GTP	PL	501	-	33,34,34	1.14	4 (12%)	50,54,54	1.82	12 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	AG	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.61	12 (24%)
39	GTP	WA	501	-	33,34,34	0.99	4 (12%)	50,54,54	1.57	11 (22%)
39	GTP	UJ	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.69	9 (18%)
39	GTP	GK	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.76	13 (26%)
39	GTP	QH	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.72	10 (20%)
39	GTP	MM	501	-	33,34,34	0.96	3 (9%)	50,54,54	1.67	12 (24%)
39	GTP	RC	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.64	11 (22%)
39	GTP	NK	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.58	10 (20%)
39	GTP	SH	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.70	9 (18%)
39	GTP	LH	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.72	9 (18%)
39	GTP	MF	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.65	10 (20%)
39	GTP	HI	501	-	33,34,34	1.11	2 (6%)	50,54,54	1.66	12 (24%)
39	GTP	RG	501	-	33,34,34	1.03	4 (12%)	50,54,54	1.60	11 (22%)
39	GTP	HE	501	-	33,34,34	0.98	4 (12%)	50,54,54	1.79	14 (28%)
39	GTP	AJ	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.77	11 (22%)
39	GTP	ID	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.77	11 (22%)
39	GTP	OD	501	-	33,34,34	1.19	4 (12%)	50,54,54	1.72	11 (22%)
39	GTP	AC	501	-	33,34,34	0.96	3 (9%)	50,54,54	1.67	11 (22%)
39	GTP	HC	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.74	16 (32%)
39	GTP	KG	501	-	33,34,34	1.02	4 (12%)	50,54,54	1.63	11 (22%)
39	GTP	RE	501	-	33,34,34	0.97	3 (9%)	50,54,54	1.55	11 (22%)
39	GTP	NE	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.58	9 (18%)
39	GTP	PJ	501	-	33,34,34	1.04	2 (6%)	50,54,54	1.83	10 (20%)
39	GTP	BH	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.73	10 (20%)
39	GTP	RM	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.59	12 (24%)
39	GTP	TD	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.73	9 (18%)
39	GTP	UD	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.67	9 (18%)
39	GTP	GB	501	-	33,34,34	1.27	6 (18%)	50,54,54	1.96	11 (22%)
39	GTP	QG	501	-	33,34,34	1.16	4 (12%)	50,54,54	1.78	10 (20%)
39	GTP	VB	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.75	10 (20%)
39	GTP	CG	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.65	12 (24%)
39	GTP	JA	501	-	33,34,34	1.04	4 (12%)	50,54,54	1.60	11 (22%)
39	GTP	PG	501	-	33,34,34	1.11	4 (12%)	50,54,54	1.62	11 (22%)
39	GTP	AM	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.65	12 (24%)
39	GTP	DG	501	-	33,34,34	1.00	4 (12%)	50,54,54	1.65	11 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
39	GTP	GG	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.59	11 (22%)
39	GTP	KH	501	-	33,34,34	1.11	3 (9%)	50,54,54	1.85	14 (28%)
39	GTP	SB	501	-	33,34,34	1.11	2 (6%)	50,54,54	1.94	11 (22%)

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
39	GTP	MB	501	-	-	8/22/38/38	0/3/3/3
39	GTP	RB	501	-	-	5/22/38/38	0/3/3/3
39	GTP	QF	501	-	-	8/22/38/38	0/3/3/3
39	GTP	EA	501	-	-	6/22/38/38	0/3/3/3
39	GTP	IH	501	-	-	8/22/38/38	0/3/3/3
39	GTP	JF	501	-	-	6/22/38/38	0/3/3/3
39	GTP	DB	501	-	-	4/22/38/38	0/3/3/3
39	GTP	AB	501	-	-	9/22/38/38	0/3/3/3
39	GTP	FH	501	-	-	5/22/38/38	0/3/3/3
39	GTP	BB	501	-	-	2/22/38/38	0/3/3/3
39	GTP	OB	501	-	-	9/22/38/38	0/3/3/3
39	GTP	OE	501	-	-	6/22/38/38	0/3/3/3
39	GTP	CB	501	-	-	6/22/38/38	0/3/3/3
39	GTP	GA	501	-	-	7/22/38/38	0/3/3/3
39	GTP	HJ	501	-	-	8/22/38/38	0/3/3/3
39	GTP	HL	501	-	-	4/22/38/38	0/3/3/3
39	GTP	VI	501	-	-	9/22/38/38	0/3/3/3
39	GTP	DJ	501	-	-	6/22/38/38	0/3/3/3
39	GTP	BK	501	-	-	4/22/38/38	0/3/3/3
39	GTP	FF	501	-	-	7/22/38/38	0/3/3/3
39	GTP	KK	501	-	-	8/22/38/38	0/3/3/3
39	GTP	LE	501	-	-	6/22/38/38	0/3/3/3
39	GTP	JC	501	-	-	4/22/38/38	0/3/3/3
39	GTP	QJ	501	-	-	3/22/38/38	0/3/3/3
39	GTP	RK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	SJ	501	-	-	2/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	UF	501	-	-	5/22/38/38	0/3/3/3
39	GTP	LA	501	-	-	8/22/38/38	0/3/3/3
39	GTP	VA	501	-	-	8/22/38/38	0/3/3/3
39	GTP	WF	501	-	-	10/22/38/38	0/3/3/3
39	GTP	RD	501	-	-	8/22/38/38	0/3/3/3
39	GTP	SK	501	-	-	10/22/38/38	0/3/3/3
39	GTP	CH	501	-	-	4/22/38/38	0/3/3/3
39	GTP	KJ	501	-	-	10/22/38/38	0/3/3/3
39	GTP	TG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	FC	501	-	-	9/22/38/38	0/3/3/3
39	GTP	TF	501	-	-	5/22/38/38	0/3/3/3
39	GTP	FG	501	-	-	8/22/38/38	0/3/3/3
39	GTP	KA	501	-	-	9/22/38/38	0/3/3/3
39	GTP	JG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	SI	501	-	-	7/22/38/38	0/3/3/3
39	GTP	IL	501	-	-	3/22/38/38	0/3/3/3
39	GTP	PA	501	-	-	5/22/38/38	0/3/3/3
39	GTP	TJ	501	-	-	3/22/38/38	0/3/3/3
39	GTP	TL	501	-	-	6/22/38/38	0/3/3/3
39	GTP	EL	501	-	-	7/22/38/38	0/3/3/3
39	GTP	VL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	KL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	LD	501	-	-	3/22/38/38	0/3/3/3
39	GTP	UG	501	-	-	5/22/38/38	0/3/3/3
39	GTP	CI	501	-	-	12/22/38/38	0/3/3/3
39	GTP	JJ	501	-	-	6/22/38/38	0/3/3/3
39	GTP	ND	501	-	-	3/22/38/38	0/3/3/3
39	GTP	UA	501	-	-	6/22/38/38	0/3/3/3
39	GTP	TC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	MK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	AK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	IG	501	-	-	5/22/38/38	0/3/3/3
39	GTP	ML	501	-	-	4/22/38/38	0/3/3/3
39	GTP	KD	501	-	-	7/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	GL	501	-	-	2/22/38/38	0/3/3/3
39	GTP	GJ	501	-	-	7/22/38/38	0/3/3/3
39	GTP	OH	501	-	-	7/22/38/38	0/3/3/3
39	GTP	JD	501	-	-	11/22/38/38	0/3/3/3
39	GTP	CL	501	-	-	4/22/38/38	0/3/3/3
39	GTP	EE	501	-	-	5/22/38/38	0/3/3/3
39	GTP	QB	501	-	-	6/22/38/38	0/3/3/3
39	GTP	SE	501	-	-	7/22/38/38	0/3/3/3
39	GTP	WJ	501	-	-	7/22/38/38	0/3/3/3
39	GTP	LF	501	-	-	7/22/38/38	0/3/3/3
39	GTP	TI	501	-	-	7/22/38/38	0/3/3/3
39	GTP	DD	501	-	-	4/22/38/38	0/3/3/3
39	GTP	DE	501	-	-	8/22/38/38	0/3/3/3
39	GTP	NI	501	-	-	10/22/38/38	0/3/3/3
39	GTP	PC	501	-	-	9/22/38/38	0/3/3/3
39	GTP	GH	501	-	-	7/22/38/38	0/3/3/3
39	GTP	SC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	LC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	IA	501	-	-	5/22/38/38	0/3/3/3
39	GTP	CM	501	-	-	7/22/38/38	0/3/3/3
39	GTP	PK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	FK	501	-	-	7/22/38/38	0/3/3/3
39	GTP	HH	501	-	-	9/22/38/38	0/3/3/3
39	GTP	LL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	OA	501	-	-	5/22/38/38	0/3/3/3
39	GTP	UK	501	-	-	7/22/38/38	0/3/3/3
39	GTP	PB	501	-	-	9/22/38/38	0/3/3/3
39	GTP	PE	501	-	-	6/22/38/38	0/3/3/3
39	GTP	RL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	BI	501	-	-	6/22/38/38	0/3/3/3
39	GTP	RH	501	-	-	7/22/38/38	0/3/3/3
39	GTP	SF	501	-	-	2/22/38/38	0/3/3/3
39	GTP	CC	501	-	-	12/22/38/38	0/3/3/3
39	GTP	VG	501	-	-	9/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	IC	501	-	-	5/22/38/38	0/3/3/3
39	GTP	GE	501	-	-	7/22/38/38	0/3/3/3
39	GTP	OL	501	-	-	8/22/38/38	0/3/3/3
39	GTP	BC	501	-	-	9/22/38/38	0/3/3/3
39	GTP	UL	501	-	-	7/22/38/38	0/3/3/3
39	GTP	WK	501	-	-	10/22/38/38	0/3/3/3
39	GTP	FE	501	-	-	5/22/38/38	0/3/3/3
39	GTP	DF	501	-	-	10/22/38/38	0/3/3/3
39	GTP	JH	501	-	-	8/22/38/38	0/3/3/3
39	GTP	JE	501	-	-	7/22/38/38	0/3/3/3
39	GTP	DI	501	-	-	7/22/38/38	0/3/3/3
39	GTP	OI	501	-	-	8/22/38/38	0/3/3/3
39	GTP	PH	501	-	-	3/22/38/38	0/3/3/3
39	GTP	UB	501	-	-	9/22/38/38	0/3/3/3
39	GTP	WI	501	-	-	5/22/38/38	0/3/3/3
39	GTP	DH	501	-	-	8/22/38/38	0/3/3/3
39	GTP	SM	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	OJ	501	-	-	7/22/38/38	0/3/3/3
39	GTP	MG	501	-	-	9/22/38/38	0/3/3/3
39	GTP	QL	501	-	-	8/22/38/38	0/3/3/3
39	GTP	PM	501	-	-	7/22/38/38	0/3/3/3
39	GTP	JB	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NB	501	-	-	8/22/38/38	0/3/3/3
39	GTP	QD	502	-	-	7/22/38/38	0/3/3/3
39	GTP	IE	501	-	-	7/22/38/38	0/3/3/3
39	GTP	LK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	HG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	FD	501	-	-	5/22/38/38	0/3/3/3
39	GTP	LB	501	-	-	2/22/38/38	0/3/3/3
39	GTP	NJ	501	-	-	3/22/38/38	0/3/3/3
39	GTP	WB	501	-	-	5/22/38/38	0/3/3/3
39	GTP	HK	501	-	-	7/22/38/38	0/3/3/3
39	GTP	BD	501	-	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	JL	501	-	-	7/22/38/38	0/3/3/3
39	GTP	UI	501	-	-	6/22/38/38	0/3/3/3
39	GTP	FL	501	-	-	7/22/38/38	0/3/3/3
39	GTP	EK	501	-	-	8/22/38/38	0/3/3/3
39	GTP	KI	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NF	501	-	-	8/22/38/38	0/3/3/3
39	GTP	QC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	FB	501	-	-	10/22/38/38	0/3/3/3
39	GTP	LJ	501	-	-	8/22/38/38	0/3/3/3
39	GTP	CD	501	-	-	7/22/38/38	0/3/3/3
39	GTP	TM	501	-	-	6/22/38/38	0/3/3/3
39	GTP	IB	501	-	-	7/22/38/38	0/3/3/3
39	GTP	JI	501	-	-	6/22/38/38	0/3/3/3
39	GTP	OK	501	-	-	6/22/38/38	0/3/3/3
39	GTP	CJ	501	-	-	6/22/38/38	0/3/3/3
39	GTP	EF	501	-	-	4/22/38/38	0/3/3/3
39	GTP	PF	501	-	-	3/22/38/38	0/3/3/3
39	GTP	BG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	EH	501	-	-	8/22/38/38	0/3/3/3
39	GTP	BF	501	-	-	10/22/38/38	0/3/3/3
39	GTP	AL	501	-	-	6/22/38/38	0/3/3/3
39	GTP	LI	501	-	-	7/22/38/38	0/3/3/3
39	GTP	KE	501	-	-	8/22/38/38	0/3/3/3
39	GTP	MC	501	-	-	6/22/38/38	0/3/3/3
39	GTP	WE	501	-	-	10/22/38/38	0/3/3/3
39	GTP	GI	501	-	-	10/22/38/38	0/3/3/3
39	GTP	TE	501	-	-	7/22/38/38	0/3/3/3
39	GTP	TN	501	-	-	10/22/38/38	0/3/3/3
39	GTP	TH	501	-	-	8/22/38/38	0/3/3/3
39	GTP	GF	501	-	-	3/22/38/38	0/3/3/3
39	GTP	AI	501	-	-	7/22/38/38	0/3/3/3
39	GTP	VH	501	-	-	4/22/38/38	0/3/3/3
39	GTP	EI	501	-	-	7/22/38/38	0/3/3/3
39	GTP	UC	501	-	-	8/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	CF	501	-	-	9/22/38/38	0/3/3/3
39	GTP	IF	501	-	-	10/22/38/38	0/3/3/3
39	GTP	IJ	501	-	-	10/22/38/38	0/3/3/3
39	GTP	II	501	-	-	7/22/38/38	0/3/3/3
39	GTP	TK	501	-	-	8/22/38/38	0/3/3/3
39	GTP	WD	501	-	-	7/22/38/38	0/3/3/3
39	GTP	RI	501	-	-	9/22/38/38	0/3/3/3
39	GTP	BJ	501	-	-	5/22/38/38	0/3/3/3
39	GTP	QL	502	-	-	7/22/38/38	0/3/3/3
39	GTP	TB	501	-	-	10/22/38/38	0/3/3/3
39	GTP	KB	501	-	-	7/22/38/38	0/3/3/3
39	GTP	RF	501	-	-	7/22/38/38	0/3/3/3
39	GTP	RJ	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NA	501	-	-	5/22/38/38	0/3/3/3
39	GTP	EJ	501	-	-	6/22/38/38	0/3/3/3
39	GTP	MD	501	-	-	9/22/38/38	0/3/3/3
39	GTP	OG	501	-	-	10/22/38/38	0/3/3/3
39	GTP	QD	501	-	-	5/22/38/38	0/3/3/3
39	GTP	VJ	501	-	-	8/22/38/38	0/3/3/3
39	GTP	BL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	DC	501	-	-	8/22/38/38	0/3/3/3
39	GTP	VD	501	-	-	9/22/38/38	0/3/3/3
39	GTP	CE	501	-	-	5/22/38/38	0/3/3/3
39	GTP	FA	501	-	-	5/22/38/38	0/3/3/3
39	GTP	WL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	IK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	VF	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NG	501	-	-	6/22/38/38	0/3/3/3
39	GTP	AF	501	-	-	9/22/38/38	0/3/3/3
39	GTP	SG	501	-	-	8/22/38/38	0/3/3/3
39	GTP	AE	501	-	-	8/22/38/38	0/3/3/3
39	GTP	GC	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NL	501	-	-	2/22/38/38	0/3/3/3
39	GTP	KF	501	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	PI	501	-	-	8/22/38/38	0/3/3/3
39	GTP	MD	502	-	-	9/22/38/38	0/3/3/3
39	GTP	NH	501	-	-	9/22/38/38	0/3/3/3
39	GTP	HB	501	-	-	8/22/38/38	0/3/3/3
39	GTP	BE	501	-	-	7/22/38/38	0/3/3/3
39	GTP	CK	501	-	-	6/22/38/38	0/3/3/3
39	GTP	DL	501	-	-	6/22/38/38	0/3/3/3
39	GTP	EB	501	-	-	7/22/38/38	0/3/3/3
39	GTP	EC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	KC	501	-	-	8/22/38/38	0/3/3/3
39	GTP	OC	501	-	-	8/22/38/38	0/3/3/3
39	GTP	QI	501	-	-	8/22/38/38	0/3/3/3
39	GTP	UH	501	-	-	7/22/38/38	0/3/3/3
39	GTP	VK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	WG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	AH	501	-	-	6/22/38/38	0/3/3/3
39	GTP	BM	501	-	-	9/22/38/38	0/3/3/3
39	GTP	WC	501	-	-	5/22/38/38	0/3/3/3
39	GTP	FJ	501	-	-	4/22/38/38	0/3/3/3
39	GTP	SL	501	-	-	9/22/38/38	0/3/3/3
39	GTP	HD	501	-	-	8/22/38/38	0/3/3/3
39	GTP	HF	501	-	-	6/22/38/38	0/3/3/3
39	GTP	DK	501	-	-	5/22/38/38	0/3/3/3
39	GTP	IM	501	-	-	8/22/38/38	0/3/3/3
39	GTP	UE	501	-	-	6/22/38/38	0/3/3/3
39	GTP	EG	501	-	-	5/22/38/38	0/3/3/3
39	GTP	FI	501	-	-	6/22/38/38	0/3/3/3
39	GTP	OF	501	-	-	9/22/38/38	0/3/3/3
39	GTP	MJ	501	-	-	9/22/38/38	0/3/3/3
39	GTP	QK	501	-	-	8/22/38/38	0/3/3/3
39	GTP	VC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	SD	501	-	-	7/22/38/38	0/3/3/3
39	GTP	PD	501	-	-	4/22/38/38	0/3/3/3
39	GTP	JK	501	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	GD	501	-	-	8/22/38/38	0/3/3/3
39	GTP	MI	501	-	-	4/22/38/38	0/3/3/3
39	GTP	MH	501	-	-	4/22/38/38	0/3/3/3
39	GTP	ED	501	-	-	9/22/38/38	0/3/3/3
39	GTP	DA	501	-	-	9/22/38/38	0/3/3/3
39	GTP	HA	501	-	-	8/22/38/38	0/3/3/3
39	GTP	LG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	VE	501	-	-	6/22/38/38	0/3/3/3
39	GTP	WH	501	-	-	9/22/38/38	0/3/3/3
39	GTP	AD	501	-	-	4/22/38/38	0/3/3/3
39	GTP	PL	501	-	-	5/22/38/38	0/3/3/3
39	GTP	AG	501	-	-	6/22/38/38	0/3/3/3
39	GTP	WA	501	-	-	8/22/38/38	0/3/3/3
39	GTP	UJ	501	-	-	8/22/38/38	0/3/3/3
39	GTP	GK	501	-	-	6/22/38/38	0/3/3/3
39	GTP	QH	501	-	-	5/22/38/38	0/3/3/3
39	GTP	MM	501	-	-	6/22/38/38	0/3/3/3
39	GTP	RC	501	-	-	7/22/38/38	0/3/3/3
39	GTP	NK	501	-	-	7/22/38/38	0/3/3/3
39	GTP	SH	501	-	-	9/22/38/38	0/3/3/3
39	GTP	LH	501	-	-	7/22/38/38	0/3/3/3
39	GTP	MF	501	-	-	9/22/38/38	0/3/3/3
39	GTP	HI	501	-	-	8/22/38/38	0/3/3/3
39	GTP	RG	501	-	-	8/22/38/38	0/3/3/3
39	GTP	HE	501	-	-	8/22/38/38	0/3/3/3
39	GTP	AJ	501	-	-	4/22/38/38	0/3/3/3
39	GTP	ID	501	-	-	3/22/38/38	0/3/3/3
39	GTP	OD	501	-	-	9/22/38/38	0/3/3/3
39	GTP	AC	501	-	-	10/22/38/38	0/3/3/3
39	GTP	HC	501	-	-	5/22/38/38	0/3/3/3
39	GTP	KG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	RE	501	-	-	5/22/38/38	0/3/3/3
39	GTP	NE	501	-	-	10/22/38/38	0/3/3/3
39	GTP	PJ	501	-	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GTP	BH	501	-	-	4/22/38/38	0/3/3/3
39	GTP	RM	501	-	-	8/22/38/38	0/3/3/3
39	GTP	TD	501	-	-	5/22/38/38	0/3/3/3
39	GTP	UD	501	-	-	8/22/38/38	0/3/3/3
39	GTP	GB	501	-	-	4/22/38/38	0/3/3/3
39	GTP	QG	501	-	-	9/22/38/38	0/3/3/3
39	GTP	VB	501	-	-	6/22/38/38	0/3/3/3
39	GTP	CG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	JA	501	-	-	9/22/38/38	0/3/3/3
39	GTP	PG	501	-	-	8/22/38/38	0/3/3/3
39	GTP	AM	501	-	-	4/22/38/38	0/3/3/3
39	GTP	DG	501	-	-	9/22/38/38	0/3/3/3
39	GTP	GG	501	-	-	7/22/38/38	0/3/3/3
39	GTP	KH	501	-	-	8/22/38/38	0/3/3/3
39	GTP	SB	501	-	-	3/22/38/38	0/3/3/3

The worst 5 of 784 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	TL	501	GTP	C2-N3	4.58	1.44	1.33
39	HI	501	GTP	PB-O3B	3.84	1.63	1.59
39	PK	501	GTP	PB-O3B	3.73	1.63	1.59
39	PD	501	GTP	C2-N3	3.66	1.42	1.33
39	TJ	501	GTP	C2-N3	3.61	1.41	1.33

The worst 5 of 2995 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
39	BJ	501	GTP	O4'-C1'-N9	10.96	133.20	108.36
39	BJ	501	GTP	C2-N3-C4	8.58	127.08	112.30
39	BJ	501	GTP	C5-C4-N3	-8.20	115.33	128.39
39	CL	501	GTP	C5-C4-N3	-7.50	116.45	128.39
39	TL	501	GTP	N9-C4-N3	7.38	140.71	125.95

There are no chirality outliers.

5 of 1884 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	AB	501	GTP	C5'-O5'-PA-O3A
39	AB	501	GTP	C5'-O5'-PA-O1A
39	AB	501	GTP	C5'-O5'-PA-O2A
39	AF	501	GTP	C5'-O5'-PA-O2A
39	AK	501	GTP	PB-O3B-PG-O2G

There are no ring outliers.

279 monomers are involved in 1780 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	MB	501	GTP	8	0
39	RB	501	GTP	7	0
39	QF	501	GTP	6	0
39	EA	501	GTP	4	0
39	IH	501	GTP	6	0
39	JF	501	GTP	5	0
39	DB	501	GTP	6	0
39	AB	501	GTP	7	0
39	FH	501	GTP	7	0
39	BB	501	GTP	7	0
39	OB	501	GTP	8	0
39	OE	501	GTP	4	0
39	CB	501	GTP	6	0
39	GA	501	GTP	5	0
39	HJ	501	GTP	7	0
39	HL	501	GTP	6	0
39	VI	501	GTP	8	0
39	DJ	501	GTP	6	0
39	BK	501	GTP	9	0
39	FF	501	GTP	6	0
39	KK	501	GTP	3	0
39	LE	501	GTP	2	0
39	JC	501	GTP	4	0
39	QJ	501	GTP	7	0
39	RK	501	GTP	8	0
39	SJ	501	GTP	7	0
39	UF	501	GTP	9	0
39	LA	501	GTP	5	0
39	VA	501	GTP	3	0
39	WF	501	GTP	8	0
39	RD	501	GTP	9	0
39	SK	501	GTP	6	0
39	CH	501	GTP	6	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	KJ	501	GTP	7	0
39	TG	501	GTP	5	0
39	FC	501	GTP	7	0
39	TF	501	GTP	6	0
39	FG	501	GTP	6	0
39	KA	501	GTP	5	0
39	JG	501	GTP	3	0
39	SI	501	GTP	7	0
39	IL	501	GTP	4	0
39	PA	501	GTP	7	0
39	TJ	501	GTP	10	0
39	TL	501	GTP	5	0
39	EL	501	GTP	6	0
39	VL	501	GTP	8	0
39	KL	501	GTP	9	0
39	LD	501	GTP	6	0
39	UG	501	GTP	6	0
39	CI	501	GTP	4	0
39	JJ	501	GTP	8	0
39	ND	501	GTP	4	0
39	UA	501	GTP	3	0
39	TC	501	GTP	7	0
39	MK	501	GTP	5	0
39	AK	501	GTP	8	0
39	IG	501	GTP	9	0
39	ML	501	GTP	9	0
39	KD	501	GTP	9	0
39	GL	501	GTP	8	0
39	GJ	501	GTP	7	0
39	OH	501	GTP	7	0
39	JD	501	GTP	7	0
39	CL	501	GTP	3	0
39	EE	501	GTP	10	0
39	QB	501	GTP	9	0
39	SE	501	GTP	5	0
39	WJ	501	GTP	7	0
39	LF	501	GTP	8	0
39	TI	501	GTP	6	0
39	DD	501	GTP	4	0
39	DE	501	GTP	6	0
39	NI	501	GTP	11	0
39	PC	501	GTP	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	GH	501	GTP	9	0
39	SC	501	GTP	5	0
39	LC	501	GTP	6	0
39	IA	501	GTP	6	0
39	CM	501	GTP	6	0
39	PK	501	GTP	2	0
39	FK	501	GTP	12	0
39	HH	501	GTP	9	0
39	LL	501	GTP	8	0
39	OA	501	GTP	5	0
39	UK	501	GTP	9	0
39	PB	501	GTP	9	0
39	PE	501	GTP	7	0
39	RL	501	GTP	7	0
39	BI	501	GTP	4	0
39	RH	501	GTP	9	0
39	SF	501	GTP	6	0
39	CC	501	GTP	5	0
39	VG	501	GTP	7	0
39	IC	501	GTP	7	0
39	GE	501	GTP	5	0
39	OL	501	GTP	6	0
39	BC	501	GTP	5	0
39	UL	501	GTP	7	0
39	WK	501	GTP	1	0
39	FE	501	GTP	7	0
39	DF	501	GTP	7	0
39	JH	501	GTP	10	0
39	JE	501	GTP	4	0
39	DI	501	GTP	6	0
39	OI	501	GTP	6	0
39	PH	501	GTP	6	0
39	UB	501	GTP	7	0
39	WI	501	GTP	5	0
39	DH	501	GTP	7	0
39	SM	501	GTP	7	0
39	NC	501	GTP	6	0
39	OJ	501	GTP	7	0
39	MG	501	GTP	6	0
39	QL	501	GTP	7	0
39	PM	501	GTP	6	0
39	JB	501	GTP	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	NB	501	GTP	7	0
39	QD	502	GTP	6	0
39	IE	501	GTP	7	0
39	LK	501	GTP	4	0
39	HG	501	GTP	5	0
39	FD	501	GTP	8	0
39	LB	501	GTP	7	0
39	NJ	501	GTP	6	0
39	WB	501	GTP	7	0
39	HK	501	GTP	6	0
39	BD	501	GTP	7	0
39	JL	501	GTP	8	0
39	UI	501	GTP	7	0
39	FL	501	GTP	6	0
39	EK	501	GTP	5	0
39	KI	501	GTP	5	0
39	NF	501	GTP	8	0
39	QC	501	GTP	6	0
39	FB	501	GTP	8	0
39	LJ	501	GTP	8	0
39	CD	501	GTP	7	0
39	TM	501	GTP	4	0
39	IB	501	GTP	5	0
39	JI	501	GTP	10	0
39	OK	501	GTP	4	0
39	CJ	501	GTP	7	0
39	EF	501	GTP	3	0
39	PF	501	GTP	8	0
39	BG	501	GTP	4	0
39	EH	501	GTP	8	0
39	BF	501	GTP	9	0
39	AL	501	GTP	8	0
39	LI	501	GTP	3	0
39	KE	501	GTP	8	0
39	MC	501	GTP	9	0
39	WE	501	GTP	7	0
39	GI	501	GTP	5	0
39	TE	501	GTP	4	0
39	TN	501	GTP	7	0
39	TH	501	GTP	6	0
39	GF	501	GTP	7	0
39	AI	501	GTP	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	VH	501	GTP	9	0
39	EI	501	GTP	10	0
39	UC	501	GTP	5	0
39	CF	501	GTP	11	0
39	IF	501	GTP	8	0
39	IJ	501	GTP	10	0
39	II	501	GTP	4	0
39	TK	501	GTP	2	0
39	WD	501	GTP	10	0
39	RI	501	GTP	4	0
39	BJ	501	GTP	1	0
39	QL	502	GTP	3	0
39	TB	501	GTP	7	0
39	KB	501	GTP	6	0
39	RF	501	GTP	7	0
39	RJ	501	GTP	8	0
39	NA	501	GTP	3	0
39	EJ	501	GTP	8	0
39	MD	501	GTP	4	0
39	OG	501	GTP	6	0
39	QD	501	GTP	8	0
39	VJ	501	GTP	7	0
39	BL	501	GTP	9	0
39	DC	501	GTP	9	0
39	VD	501	GTP	8	0
39	CE	501	GTP	7	0
39	FA	501	GTP	6	0
39	WL	501	GTP	9	0
39	IK	501	GTP	3	0
39	VF	501	GTP	9	0
39	NG	501	GTP	5	0
39	AF	501	GTP	10	0
39	SG	501	GTP	7	0
39	AE	501	GTP	5	0
39	GC	501	GTP	9	0
39	NL	501	GTP	5	0
39	KF	501	GTP	6	0
39	PI	501	GTP	5	0
39	MD	502	GTP	5	0
39	NH	501	GTP	10	0
39	HB	501	GTP	7	0
39	BE	501	GTP	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	CK	501	GTP	7	0
39	DL	501	GTP	7	0
39	EB	501	GTP	9	0
39	EC	501	GTP	8	0
39	KC	501	GTP	6	0
39	OC	501	GTP	4	0
39	QI	501	GTP	4	0
39	UH	501	GTP	7	0
39	VK	501	GTP	2	0
39	WG	501	GTP	7	0
39	AH	501	GTP	6	0
39	BM	501	GTP	9	0
39	WC	501	GTP	6	0
39	FJ	501	GTP	6	0
39	SL	501	GTP	8	0
39	HD	501	GTP	7	0
39	HF	501	GTP	5	0
39	DK	501	GTP	6	0
39	IM	501	GTP	8	0
39	UE	501	GTP	5	0
39	EG	501	GTP	2	0
39	FI	501	GTP	5	0
39	OF	501	GTP	7	0
39	MJ	501	GTP	10	0
39	QK	501	GTP	6	0
39	VC	501	GTP	6	0
39	SD	501	GTP	7	0
39	PD	501	GTP	4	0
39	JK	501	GTP	5	0
39	GD	501	GTP	8	0
39	MI	501	GTP	8	0
39	MH	501	GTP	7	0
39	ED	501	GTP	4	0
39	DA	501	GTP	6	0
39	HA	501	GTP	5	0
39	LG	501	GTP	4	0
39	VE	501	GTP	6	0
39	WH	501	GTP	4	0
39	AD	501	GTP	6	0
39	PL	501	GTP	8	0
39	AG	501	GTP	6	0
39	WA	501	GTP	5	0

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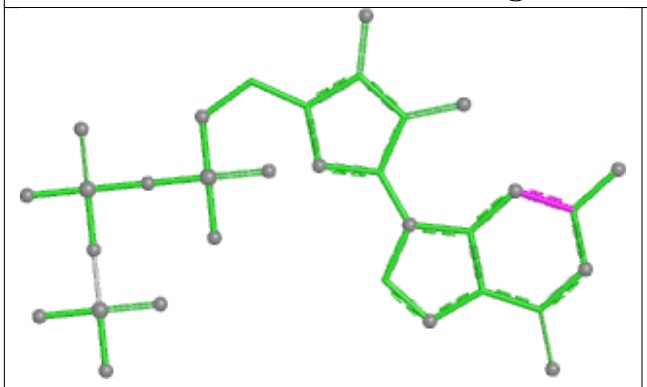
Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	UJ	501	GTP	8	0
39	GK	501	GTP	7	0
39	QH	501	GTP	6	0
39	MM	501	GTP	6	0
39	RC	501	GTP	4	0
39	NK	501	GTP	5	0
39	SH	501	GTP	9	0
39	LH	501	GTP	8	0
39	MF	501	GTP	9	0
39	HI	501	GTP	3	0
39	RG	501	GTP	5	0
39	HE	501	GTP	5	0
39	AJ	501	GTP	7	0
39	ID	501	GTP	8	0
39	OD	501	GTP	6	0
39	AC	501	GTP	4	0
39	HC	501	GTP	2	0
39	KG	501	GTP	7	0
39	RE	501	GTP	5	0
39	NE	501	GTP	5	0
39	PJ	501	GTP	7	0
39	BH	501	GTP	9	0
39	RM	501	GTP	5	0
39	TD	501	GTP	7	0
39	UD	501	GTP	8	0
39	GB	501	GTP	9	0
39	QG	501	GTP	4	0
39	VB	501	GTP	7	0
39	CG	501	GTP	8	0
39	JA	501	GTP	3	0
39	PG	501	GTP	3	0
39	AM	501	GTP	5	0
39	DG	501	GTP	8	0
39	GG	501	GTP	6	0
39	KH	501	GTP	5	0
39	SB	501	GTP	7	0

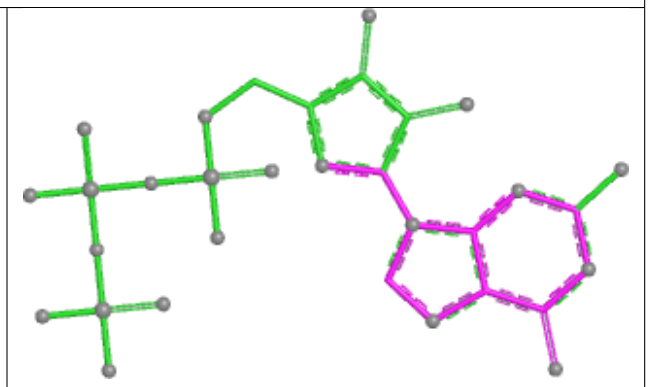
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

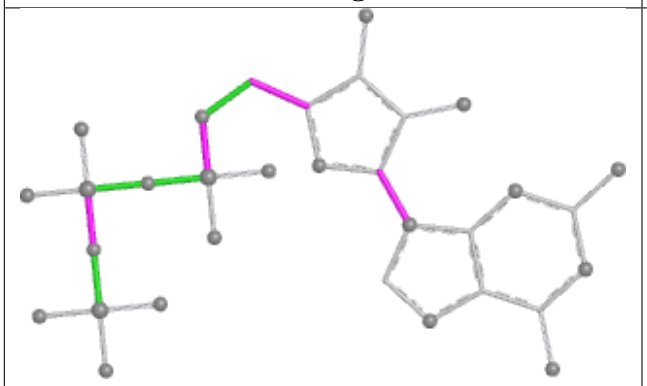
Ligand GTP MB 501



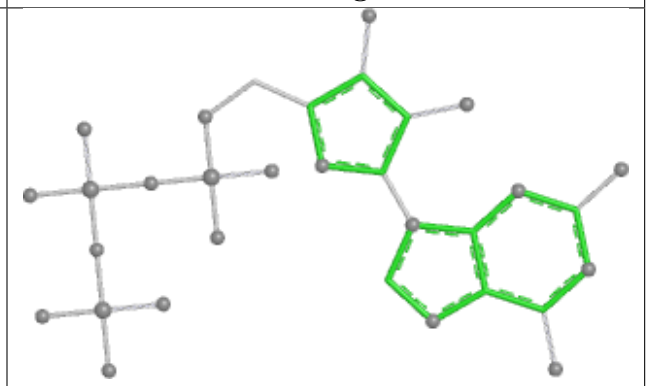
Bond lengths



Bond angles

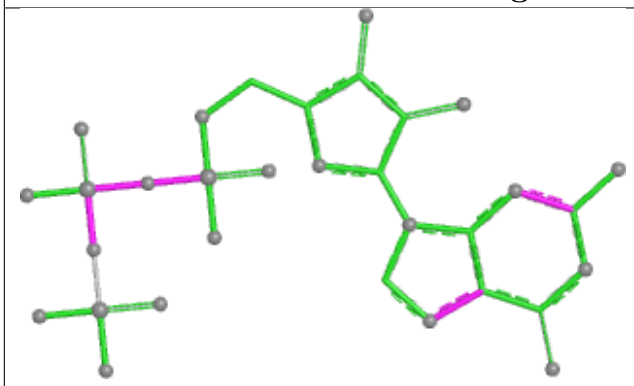


Torsions

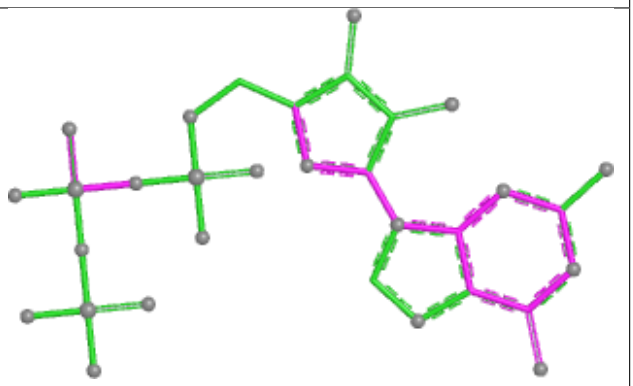


Rings

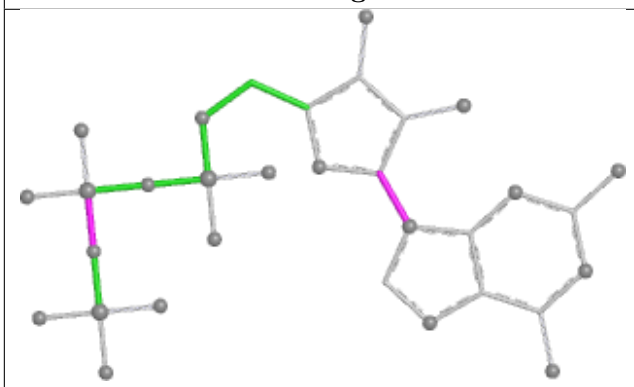
Ligand GTP RB 501



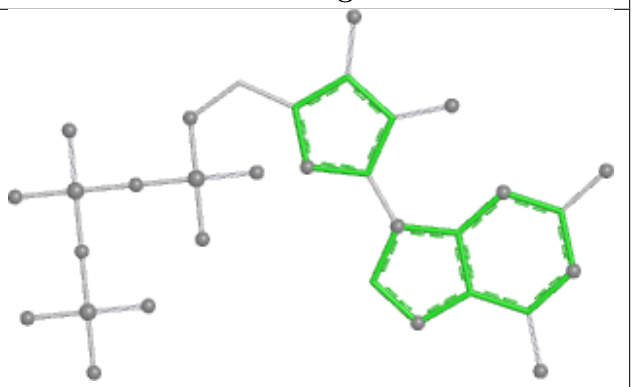
Bond lengths



Bond angles

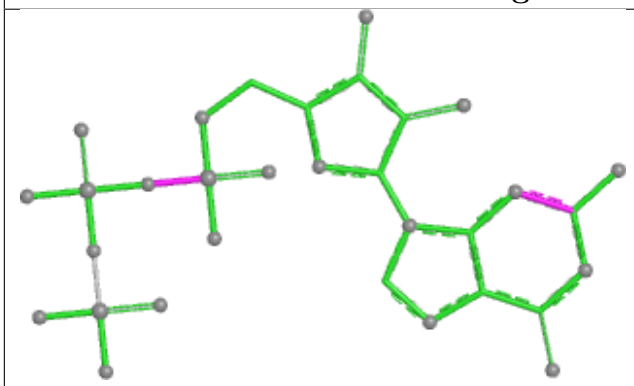


Torsions

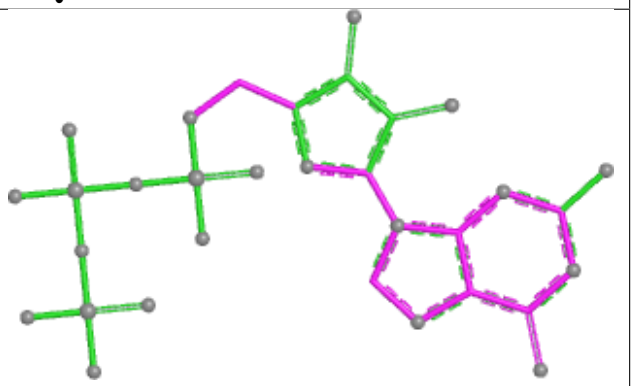


Rings

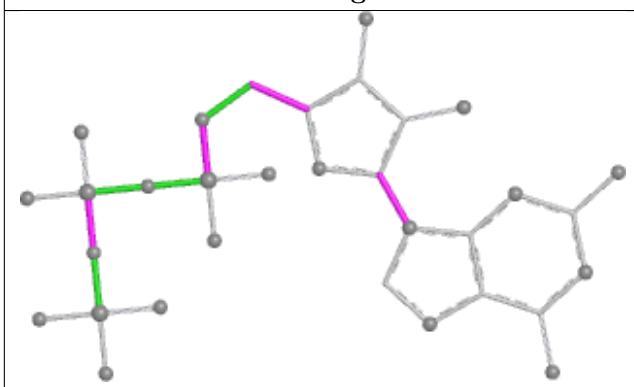
Ligand GTP QF 501



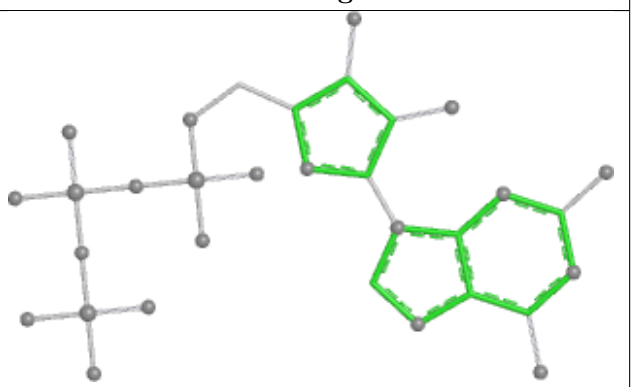
Bond lengths



Bond angles

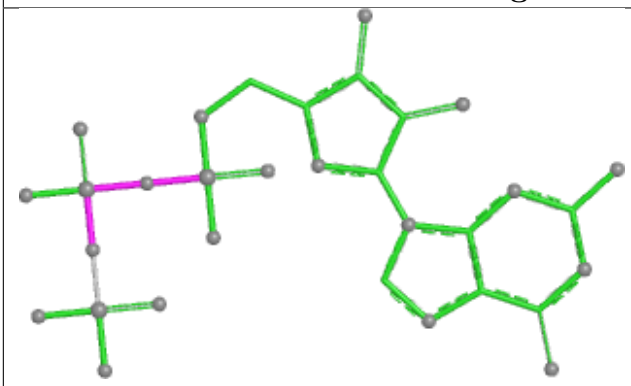


Torsions

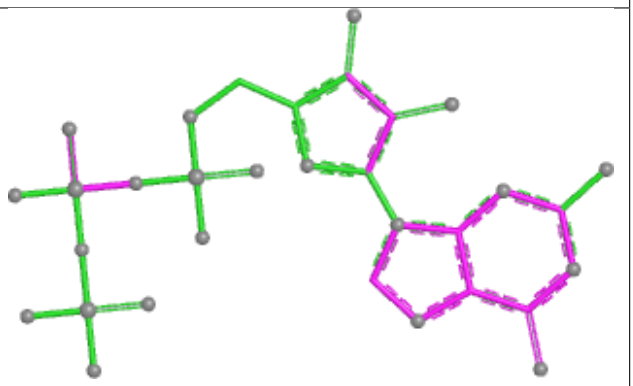


Rings

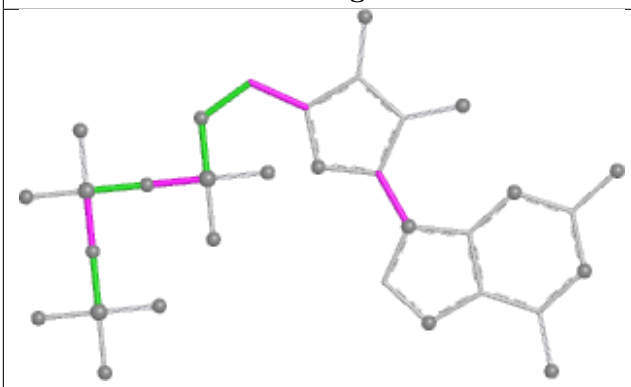
Ligand GTP EA 501



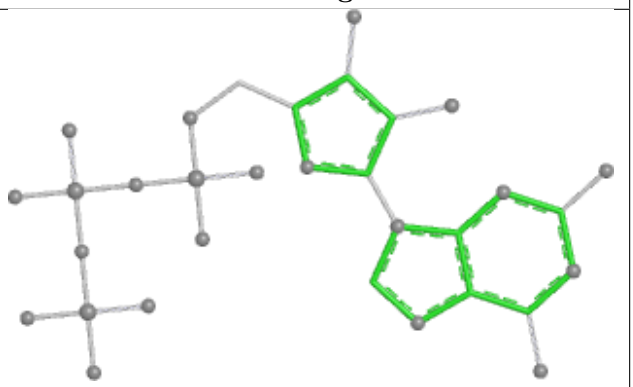
Bond lengths



Bond angles

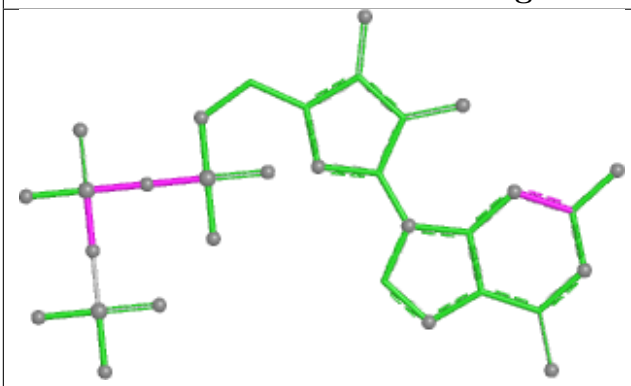


Torsions

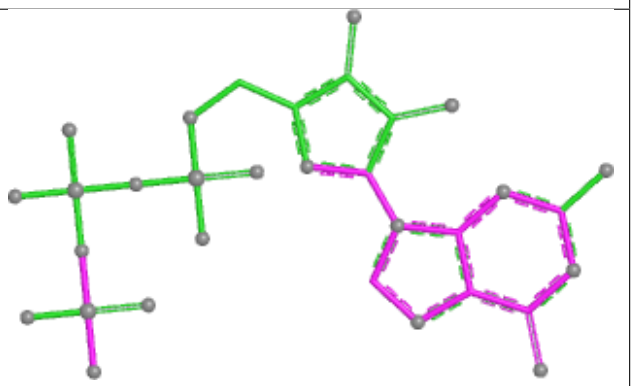


Rings

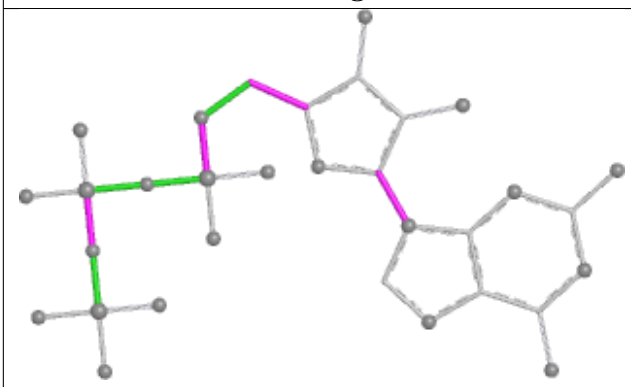
Ligand GTP IH 501



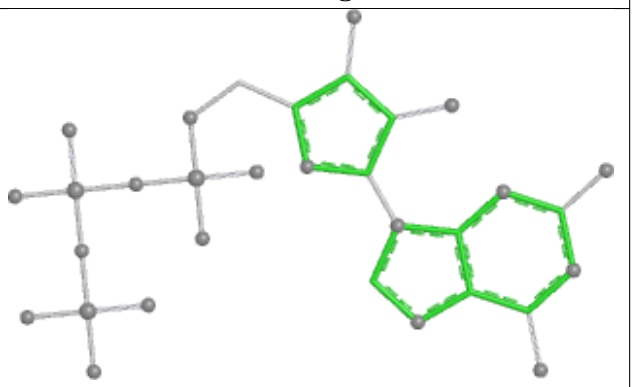
Bond lengths



Bond angles

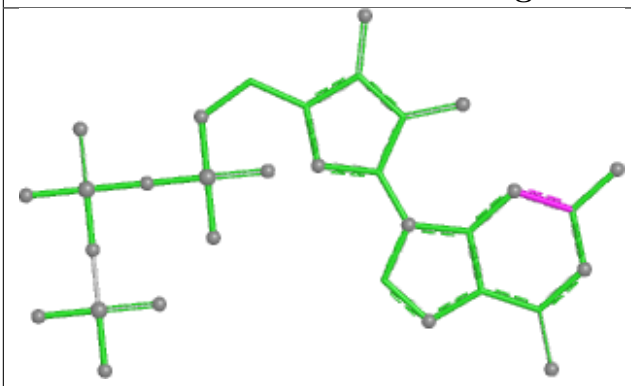


Torsions

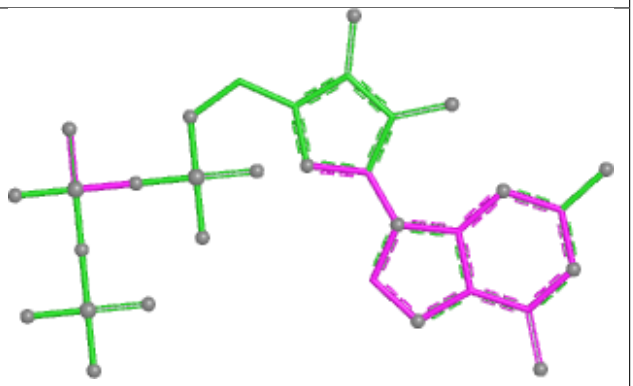


Rings

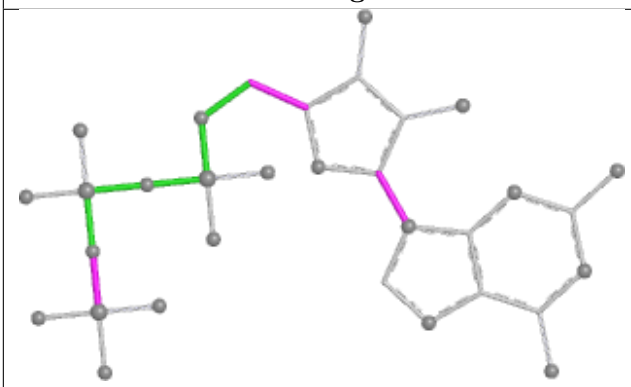
Ligand GTP JF 501



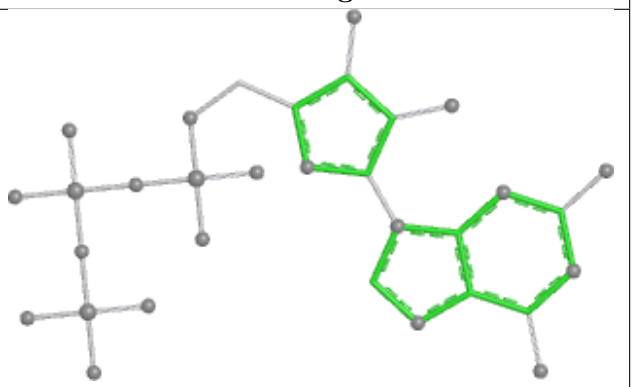
Bond lengths



Bond angles

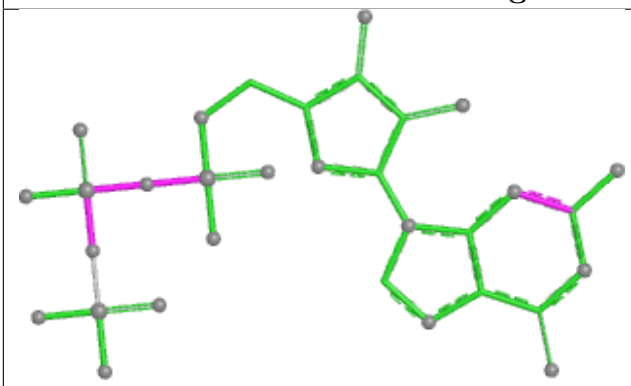


Torsions

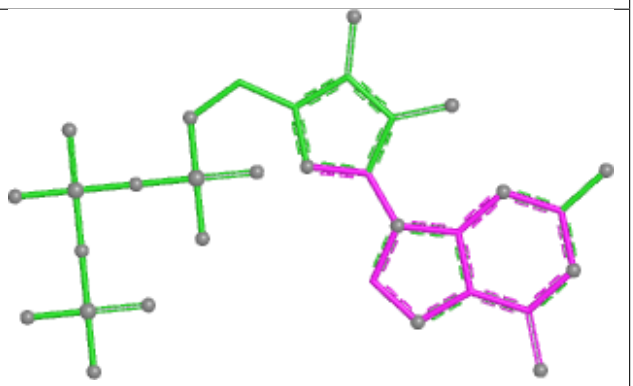


Rings

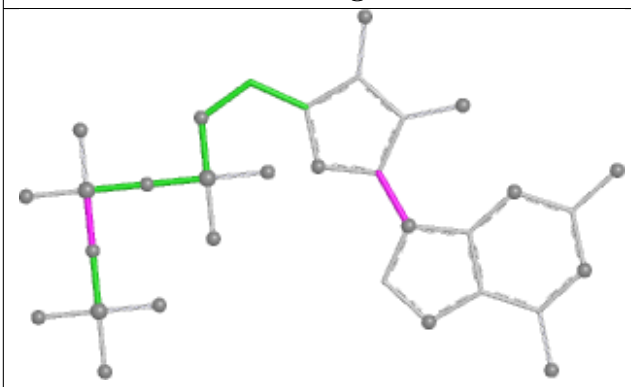
Ligand GTP DB 501



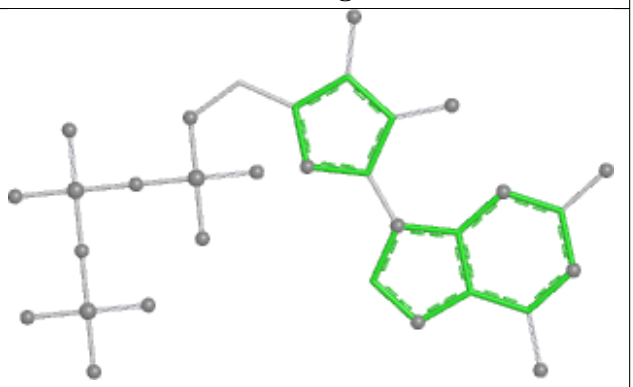
Bond lengths



Bond angles

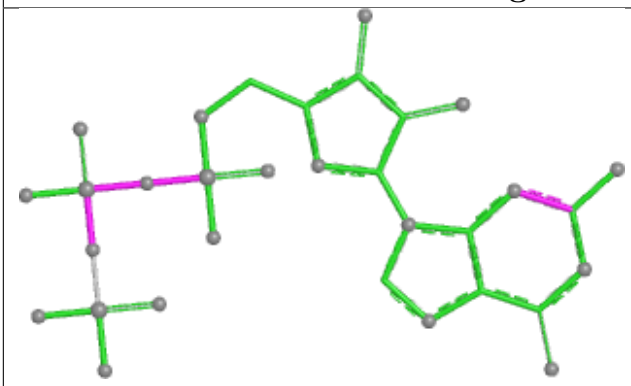


Torsions



Rings

Ligand GTP AB 501



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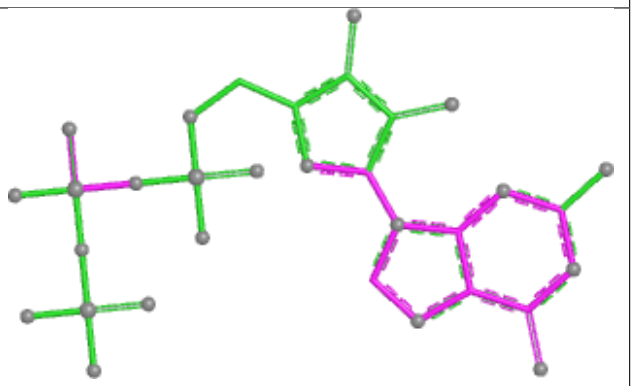

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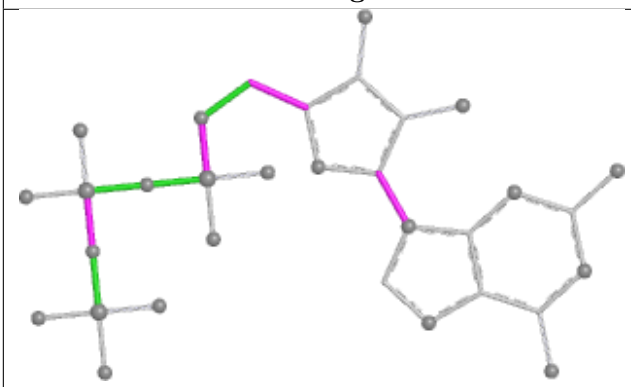

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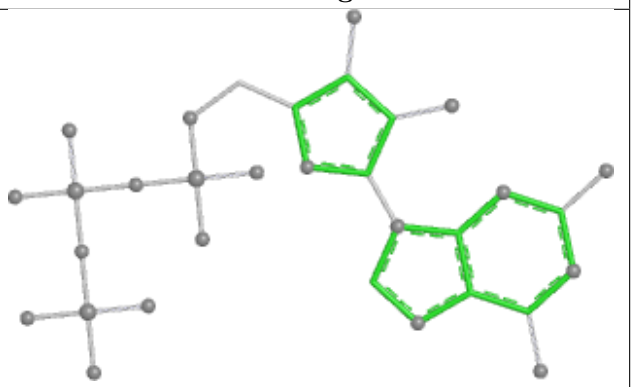
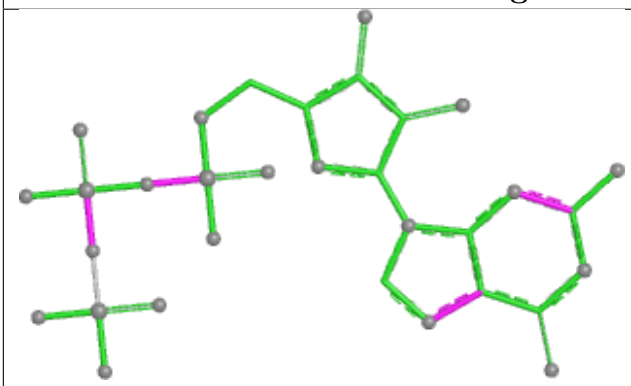


Rings

Ligand GTP FH 501



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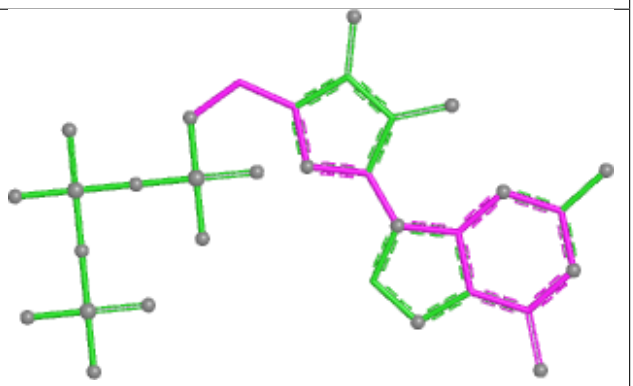

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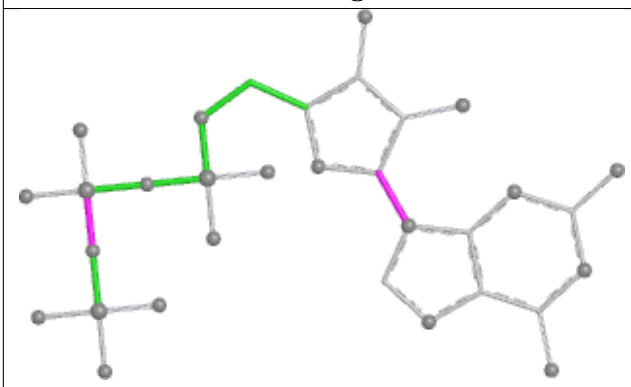

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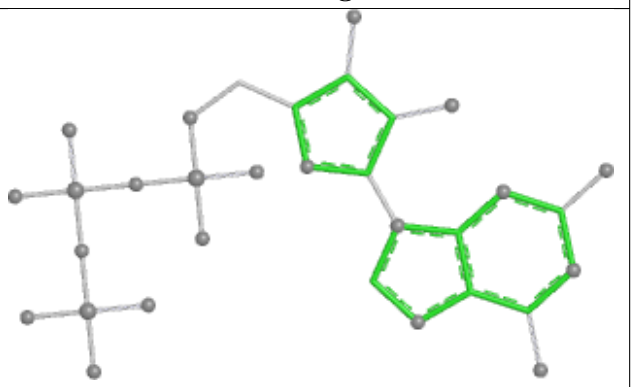
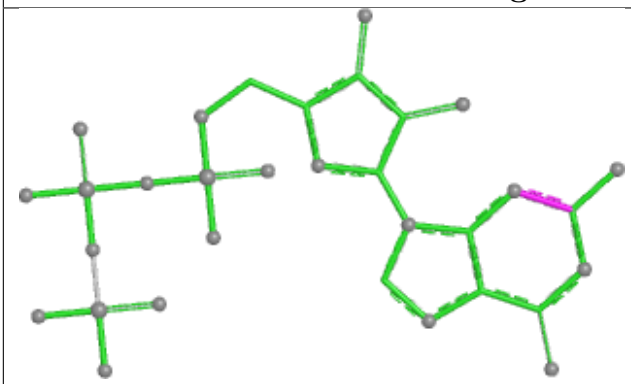


Rings

Ligand GTP BB 501



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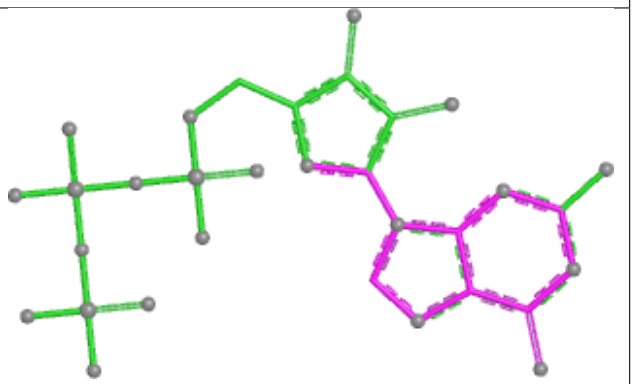

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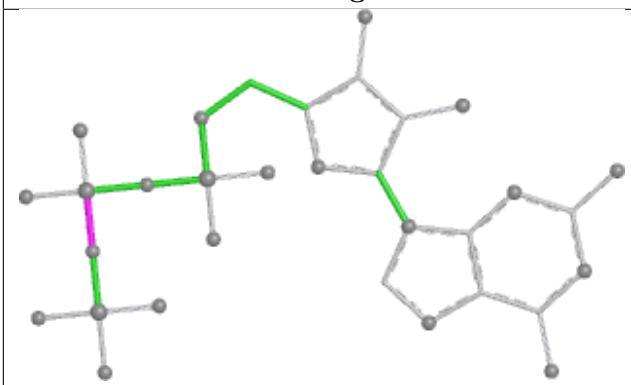

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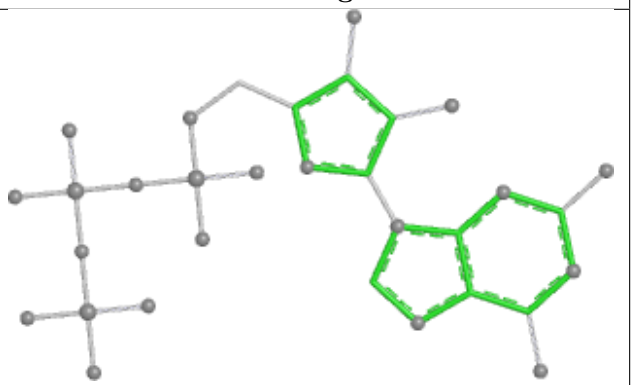
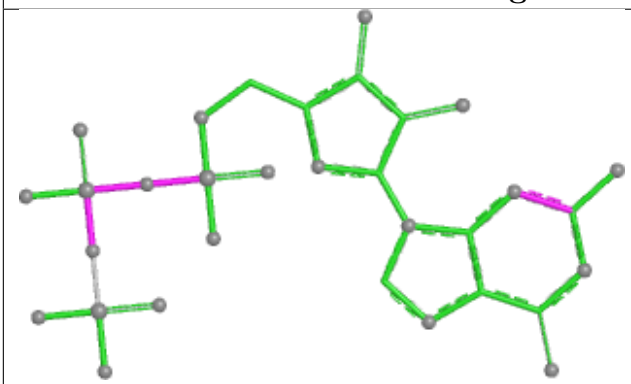


Rings

Ligand GTP OB 501



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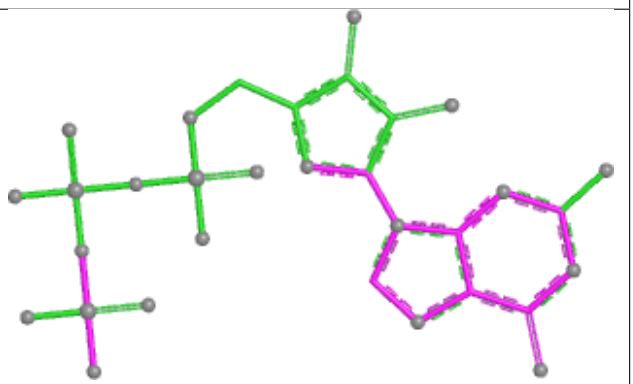

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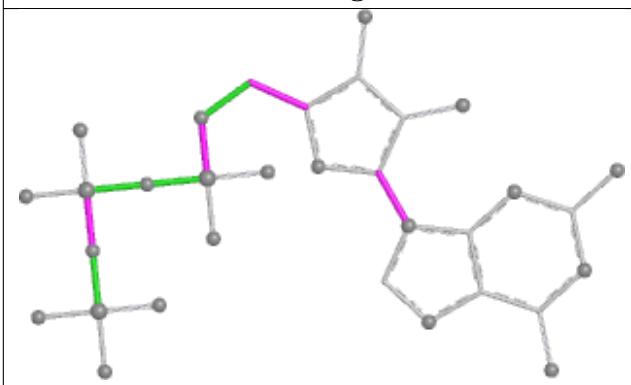

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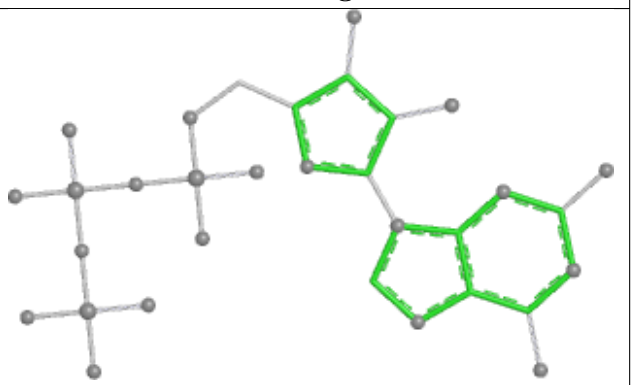
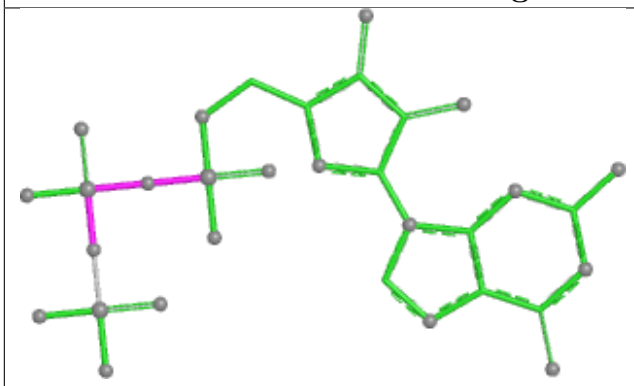


Rings

Ligand GTP OE 501



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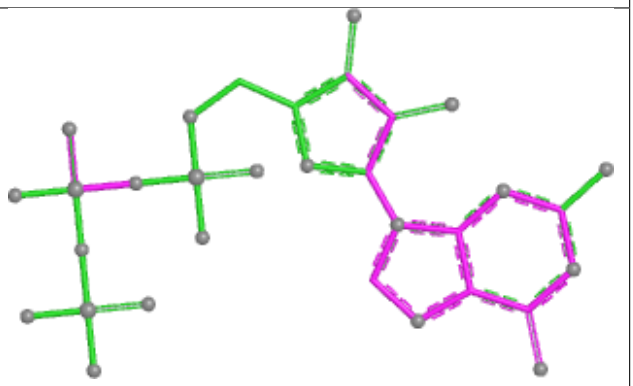

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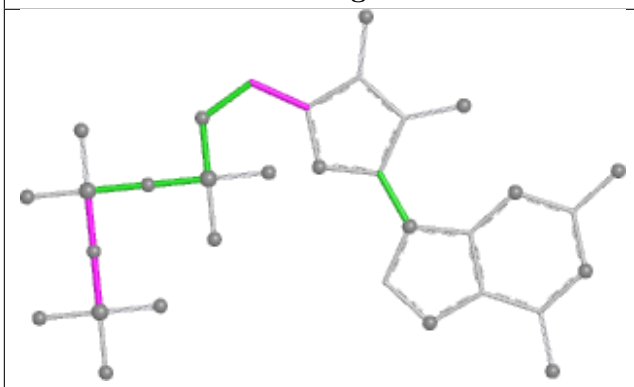

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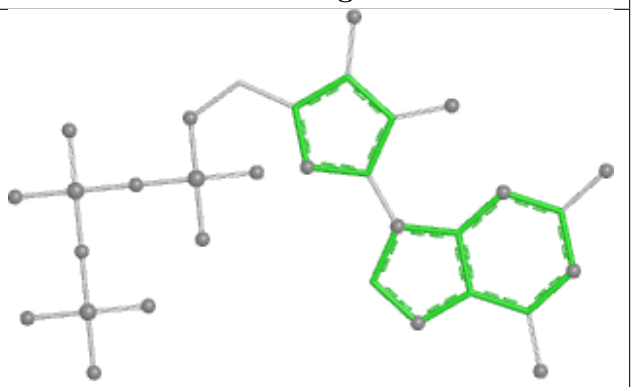
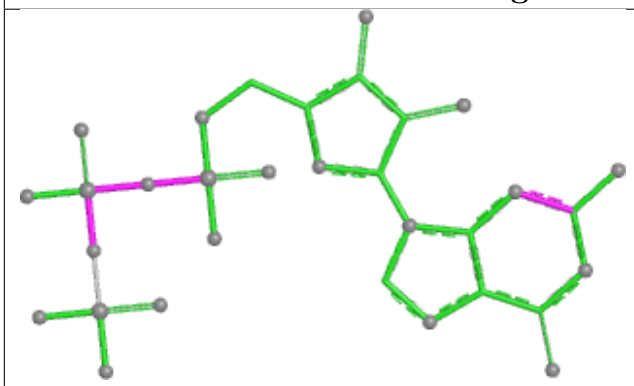


Rings

Ligand GTP CB 501



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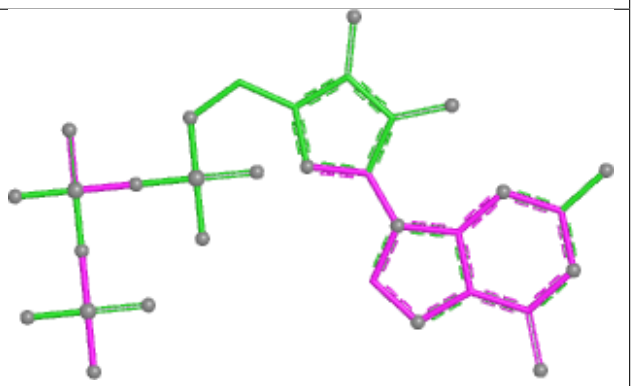

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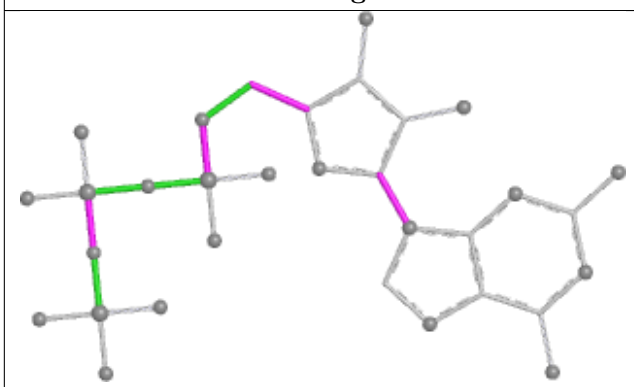

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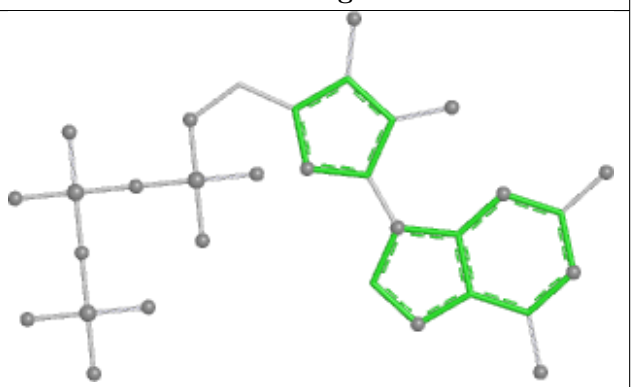
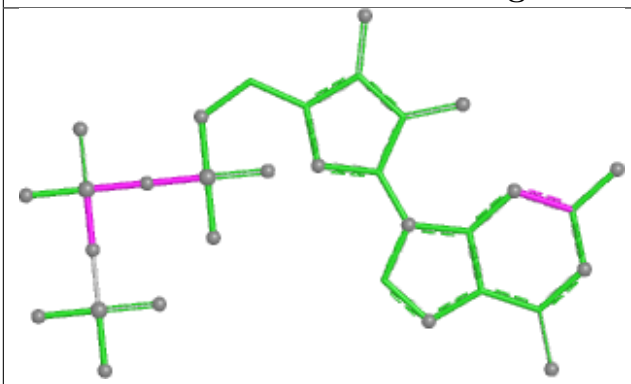


Rings

Ligand GTP GA 501



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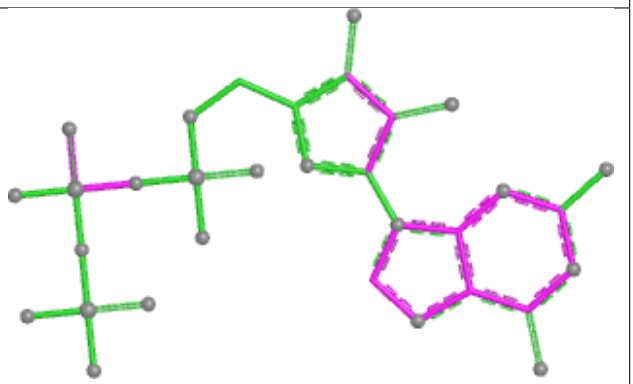

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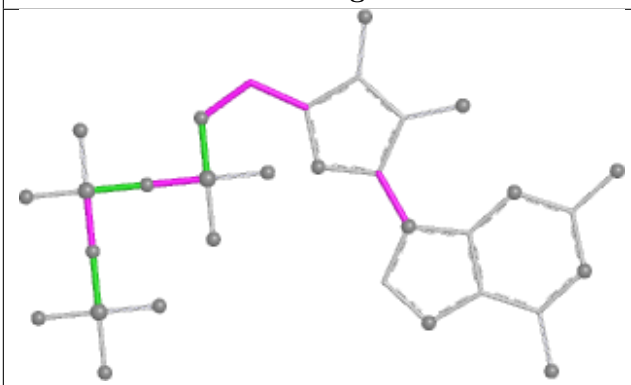

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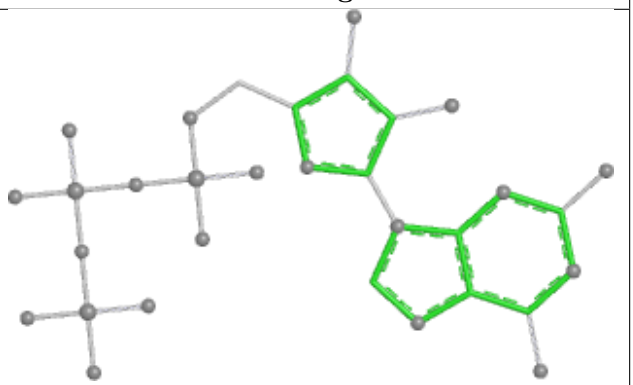
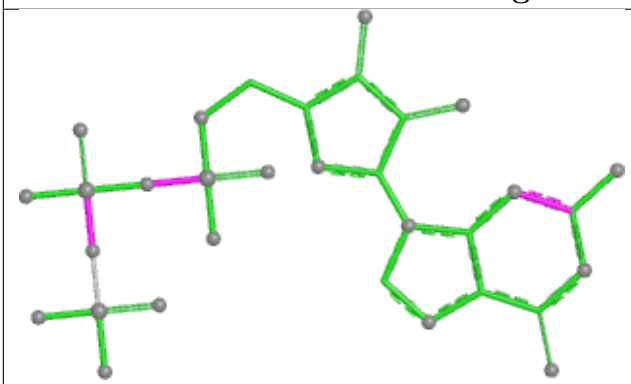


Rings

Ligand GTP HJ 501



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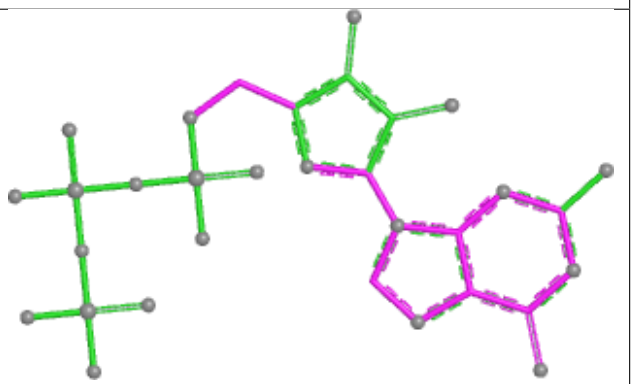

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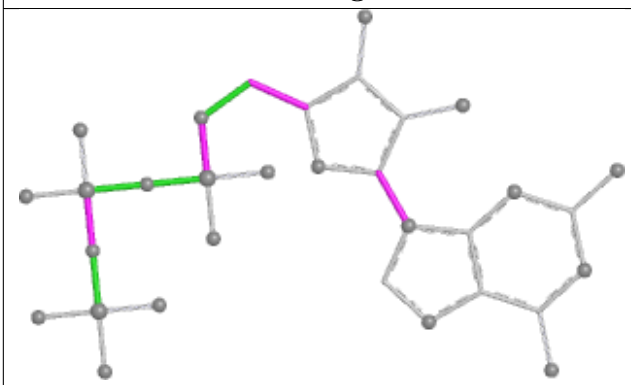

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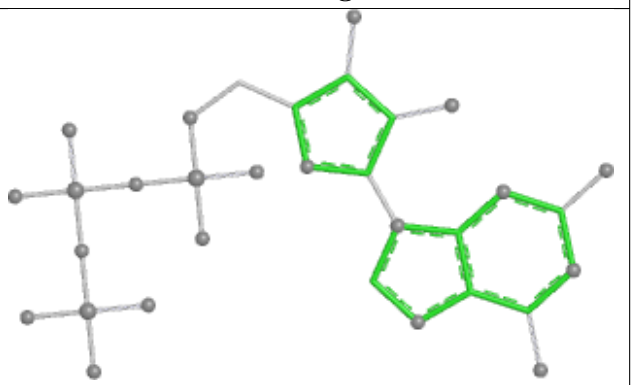
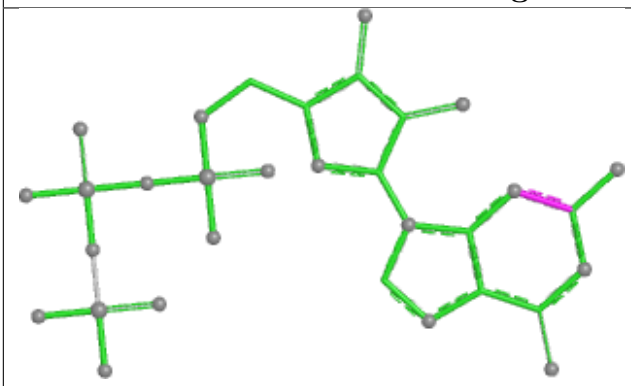


Rings

Ligand GTP HL 501



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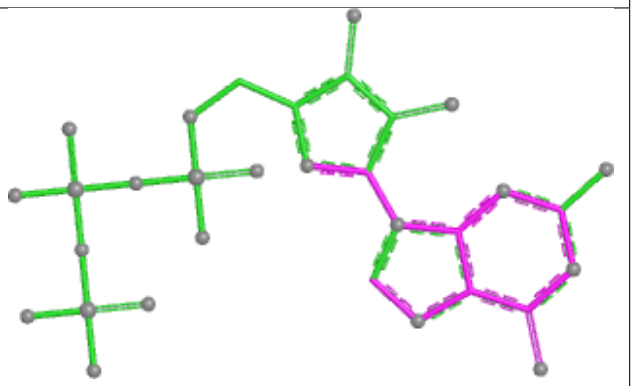

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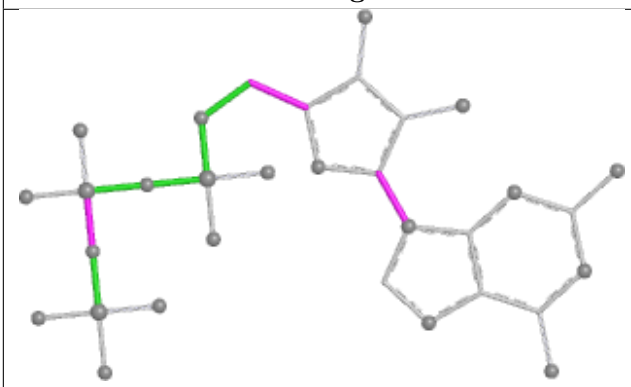

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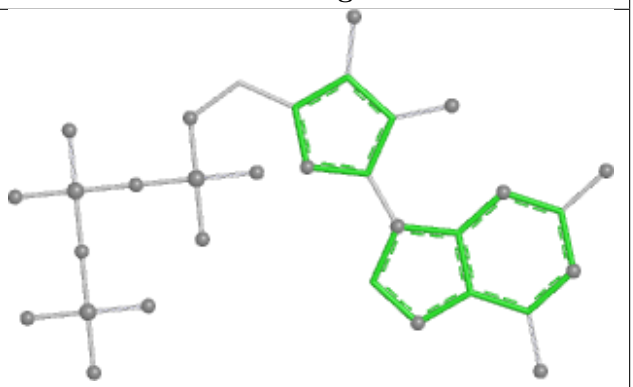
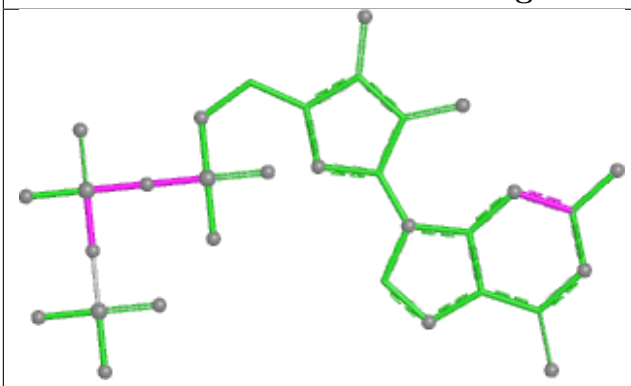


Rings

Ligand GTP VI 501



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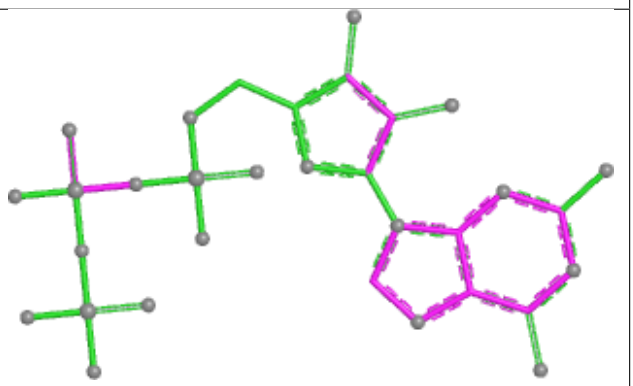

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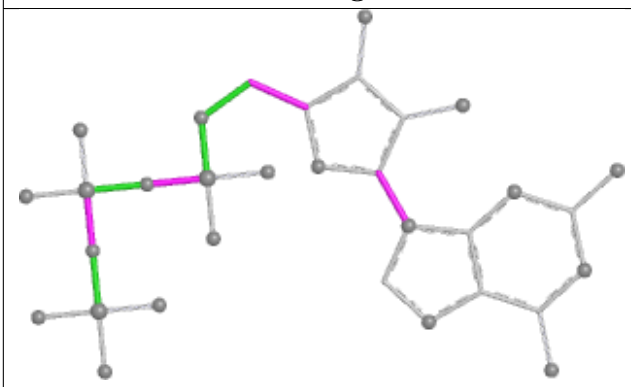

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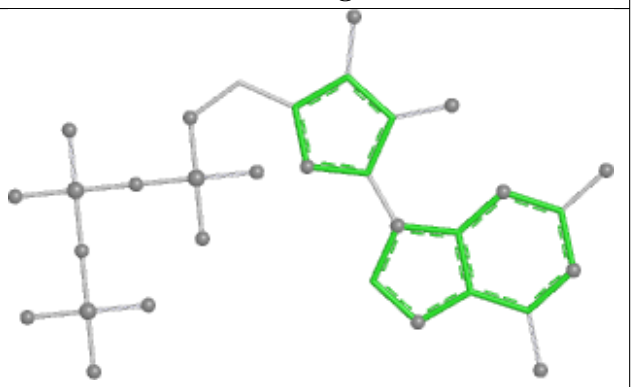
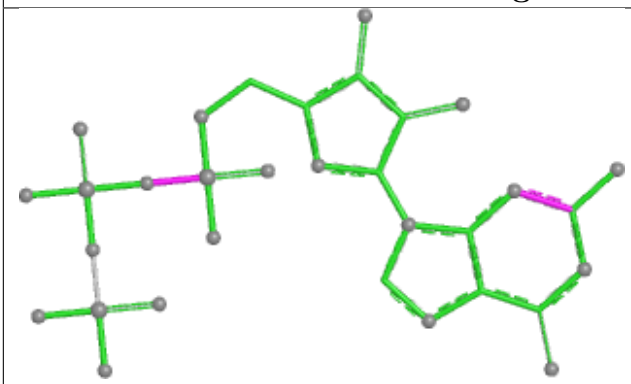


Rings

Ligand GTP DJ 501



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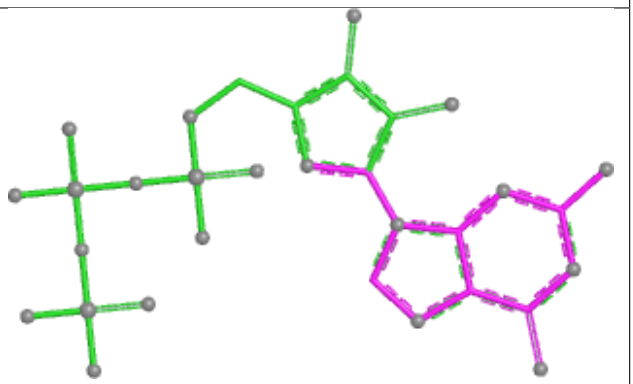

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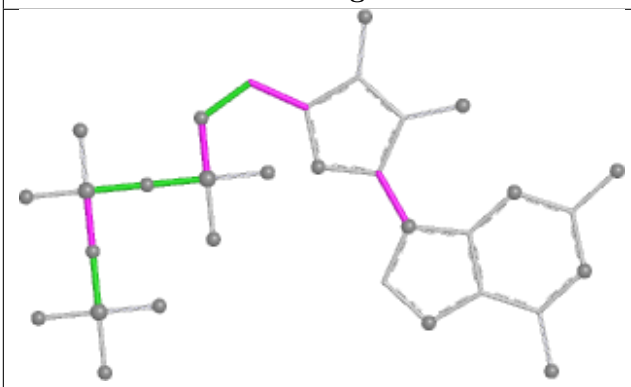

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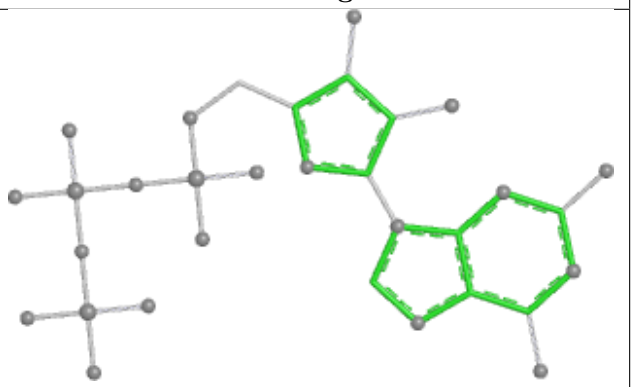
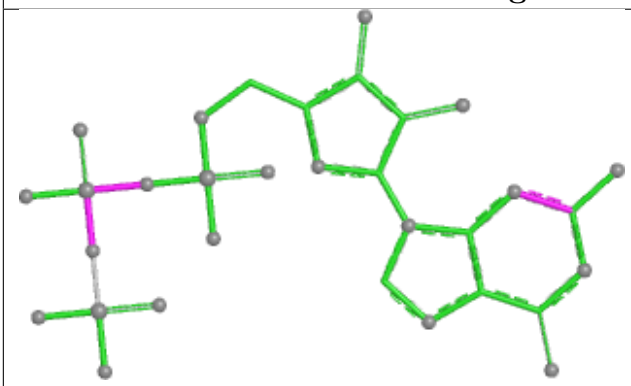


Rings

Ligand GTP BK 501



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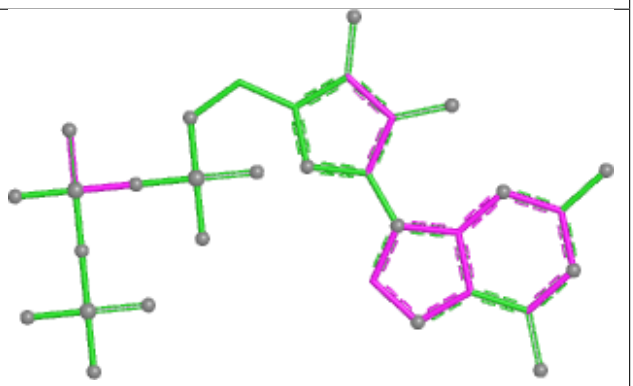

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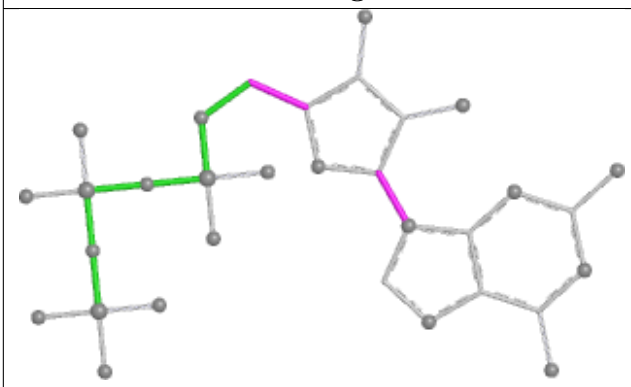

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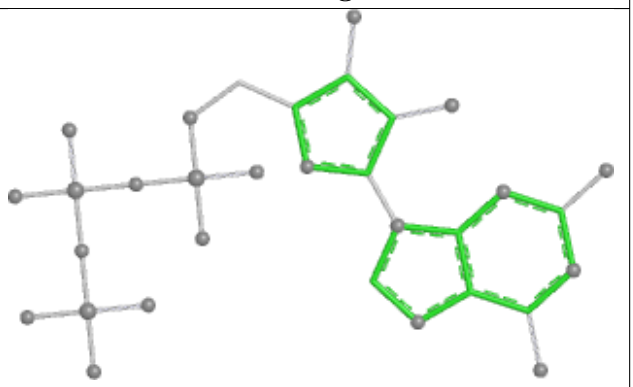
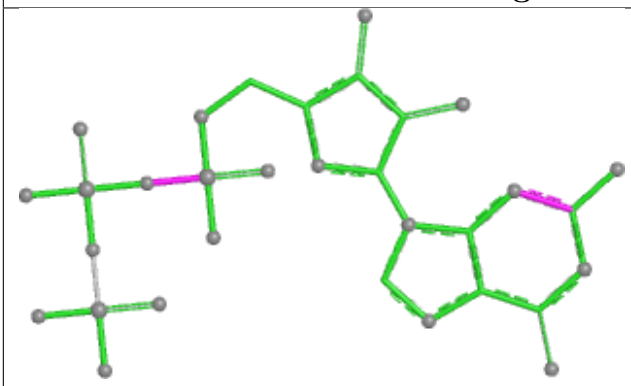


Rings

Ligand GTP FF 501



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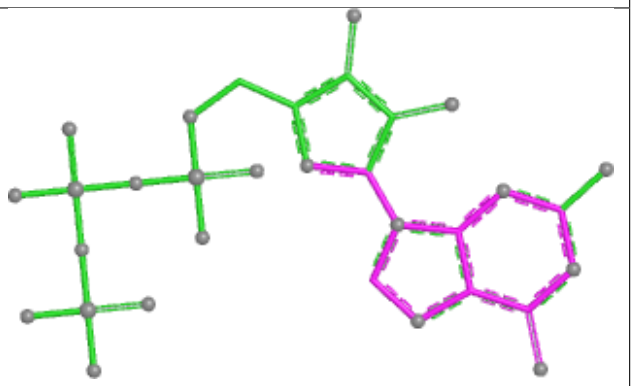
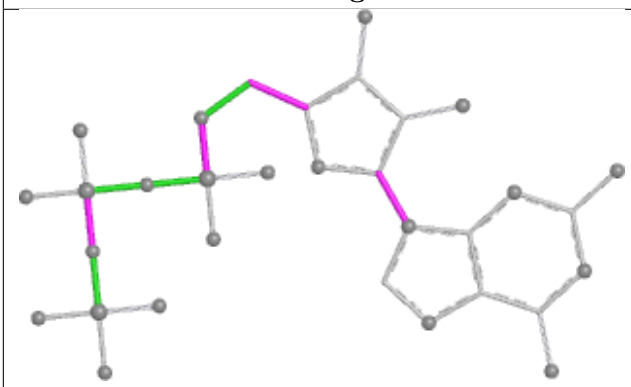


Bond angles



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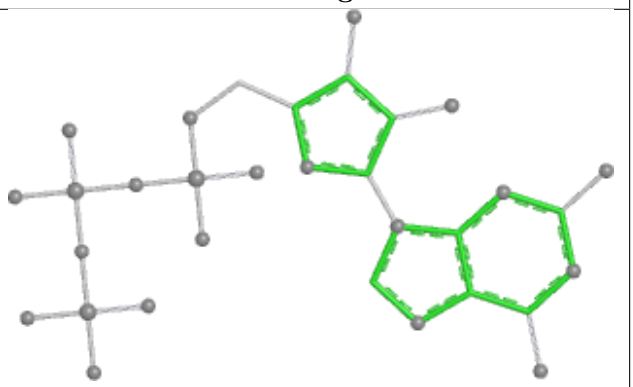
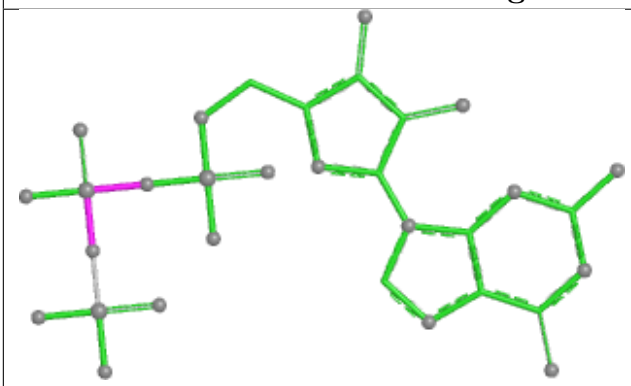
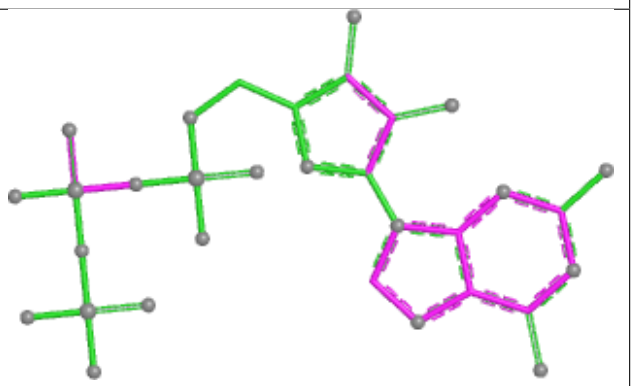


Rings

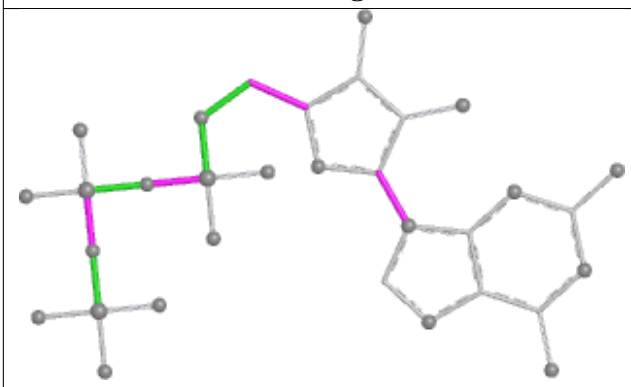
Ligand GTP KK 501



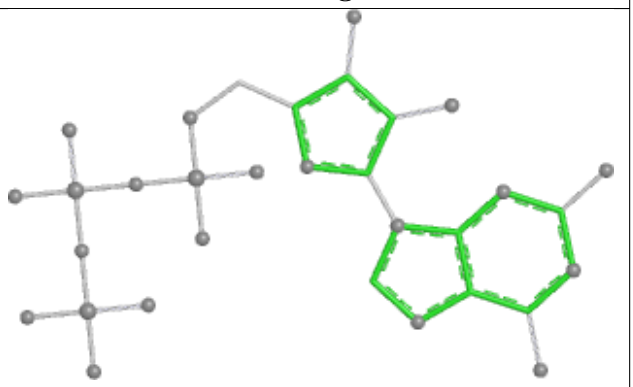
Bond lengths



Bond angles

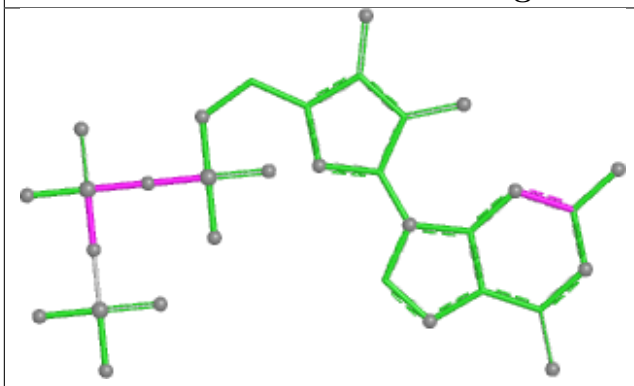


Torsions



Rings

Ligand GTP LE 501



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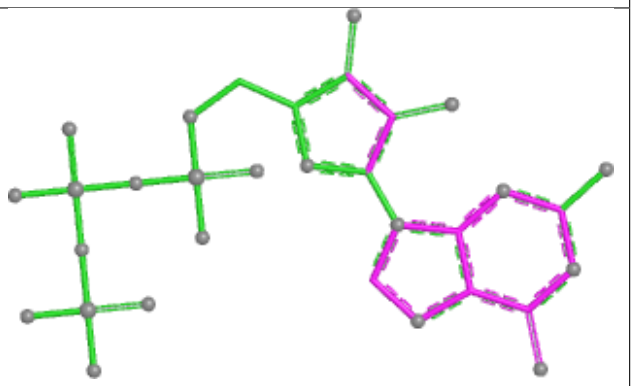

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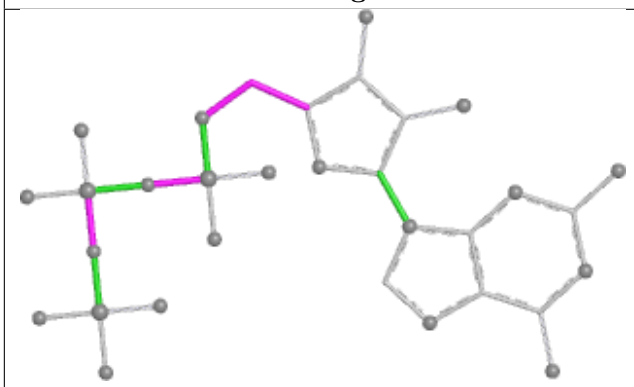

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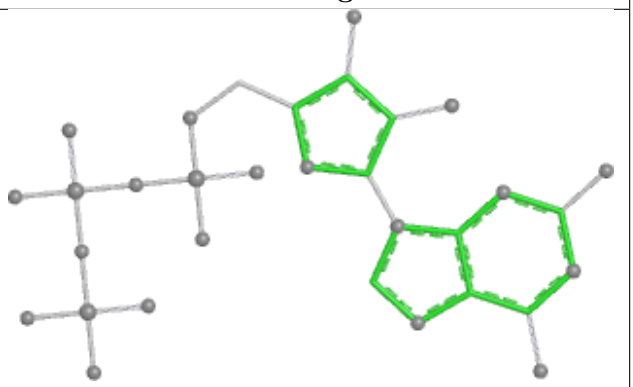
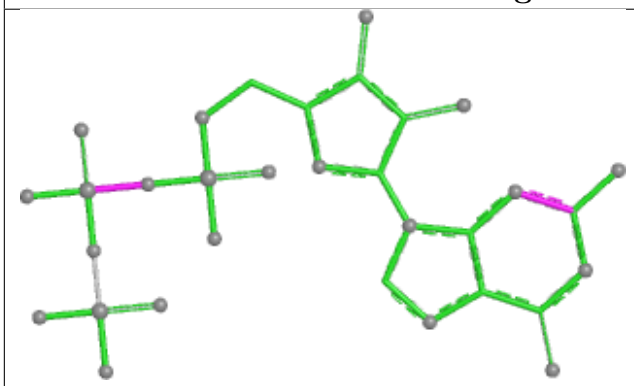


Rings

Ligand GTP JC 501



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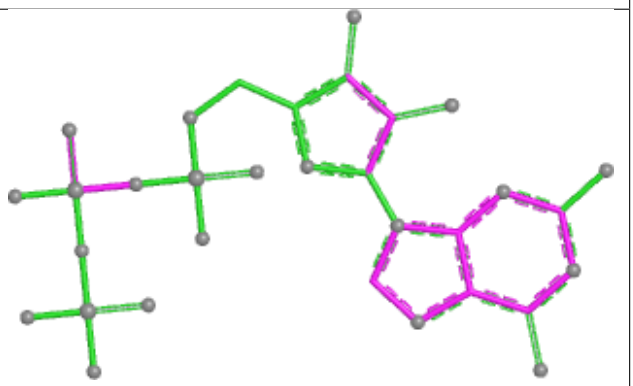

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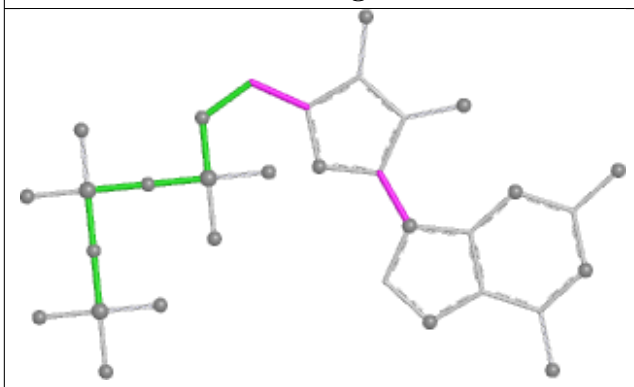

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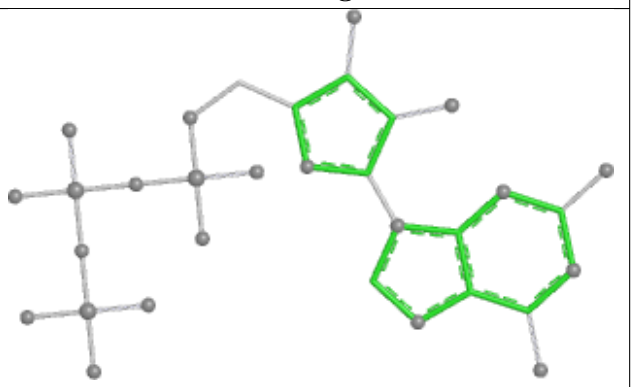
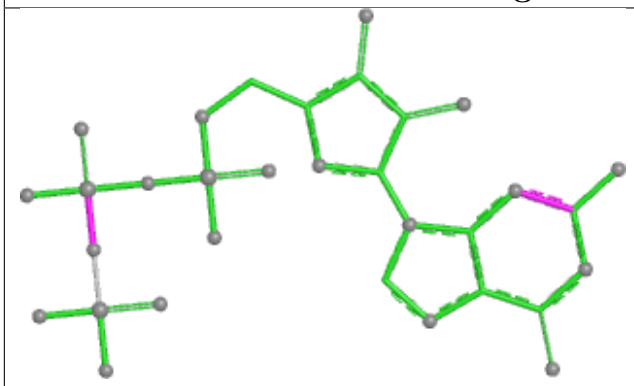


Rings

Ligand GTP QJ 501



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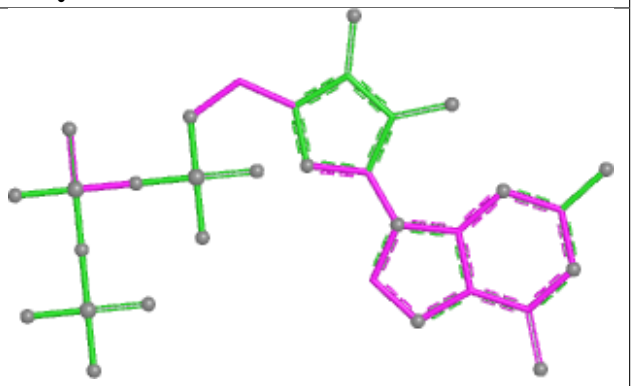

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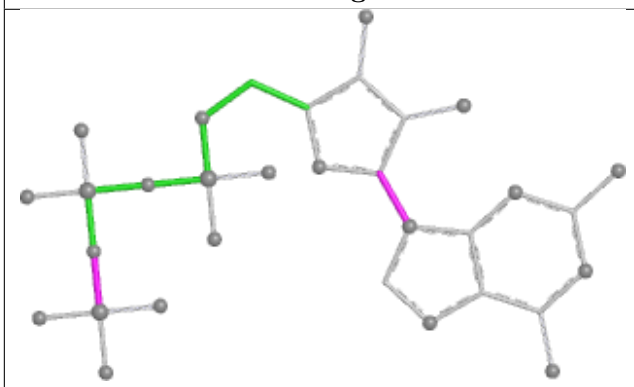

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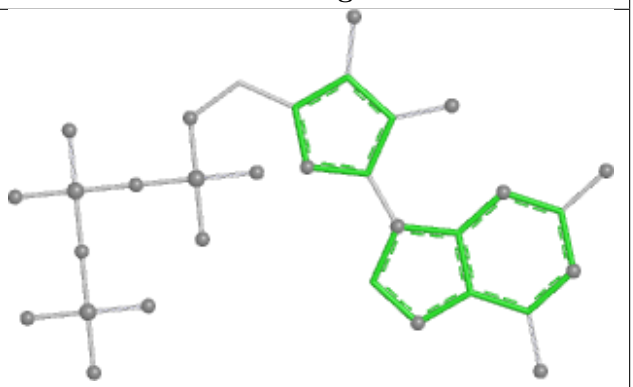
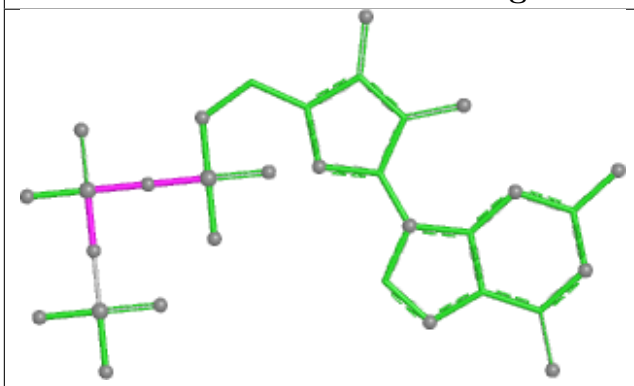


Rings

Ligand GTP RK 501



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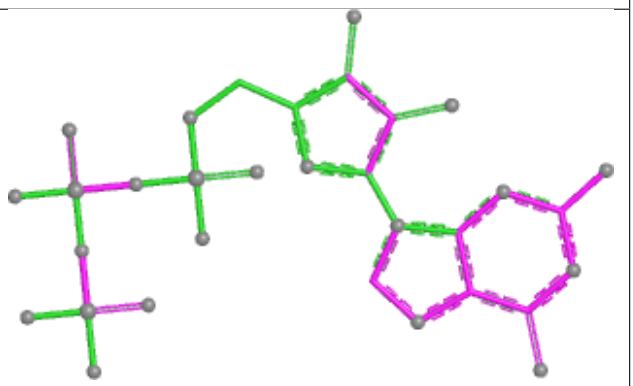

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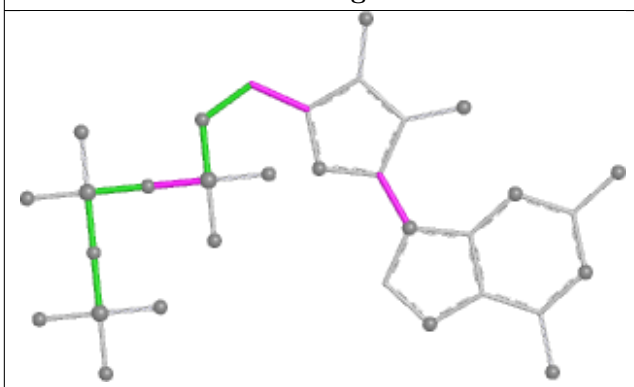

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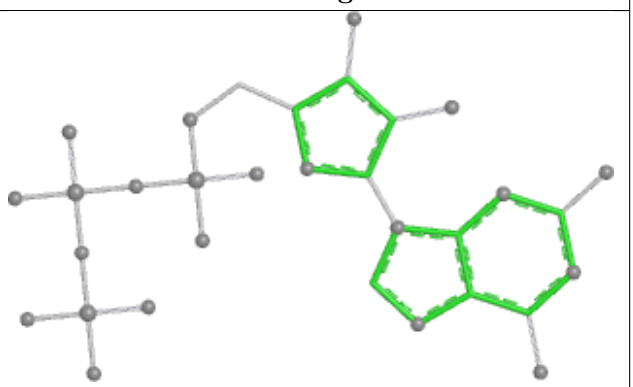
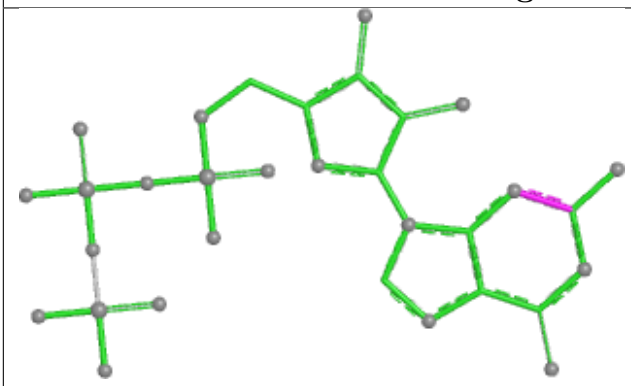


Rings

Ligand GTP SJ 501



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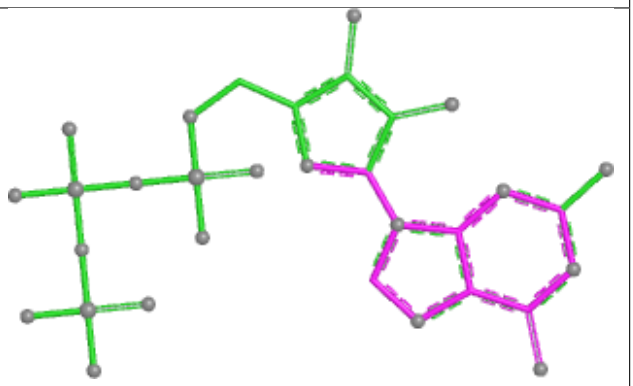

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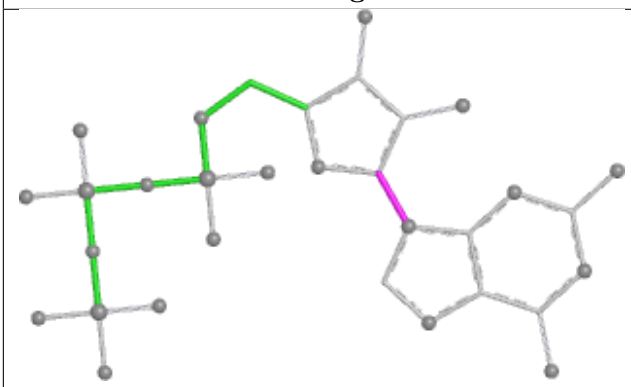

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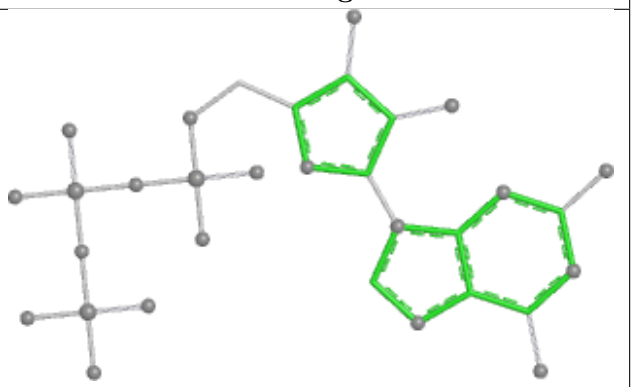
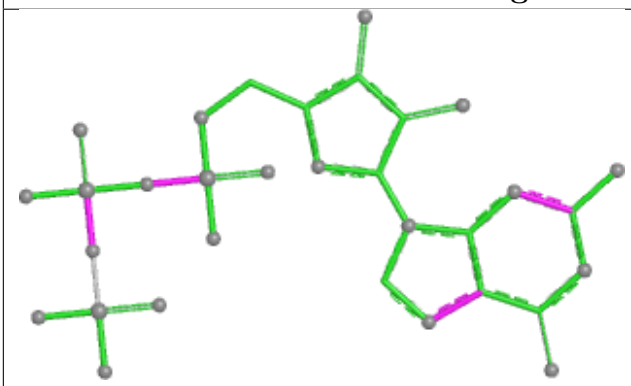


Rings

Ligand GTP UF 501



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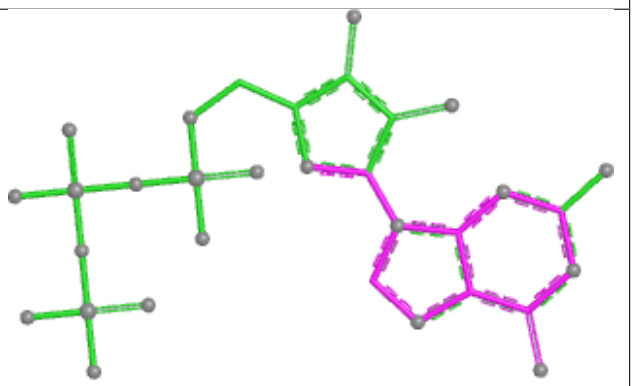

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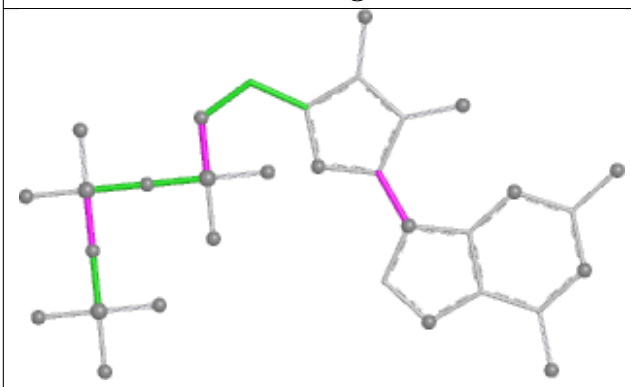

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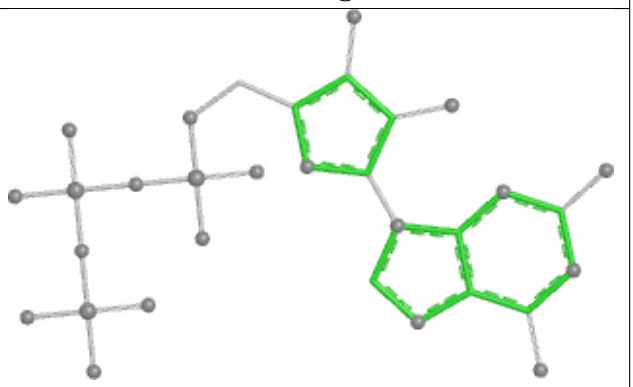
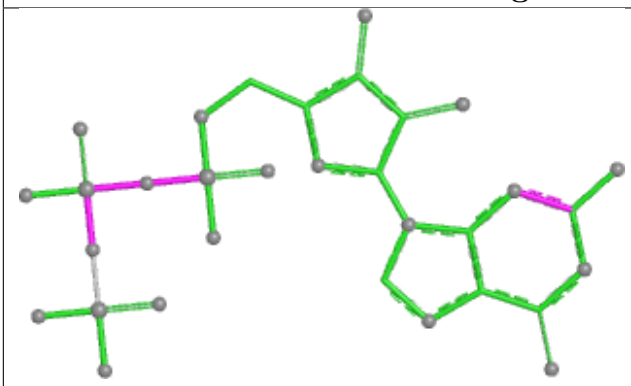


Rings

Ligand GTP LA 501



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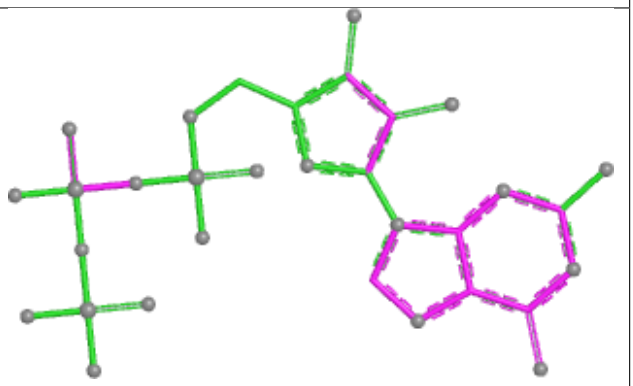

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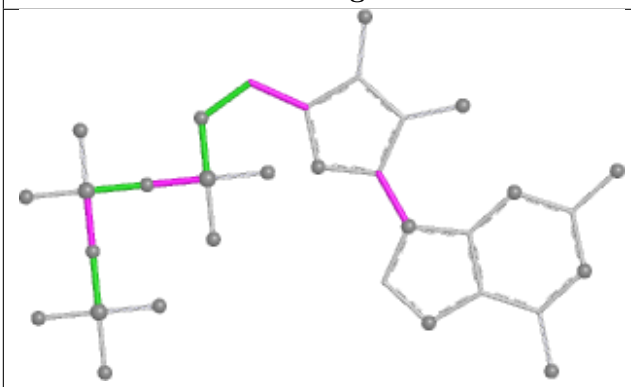

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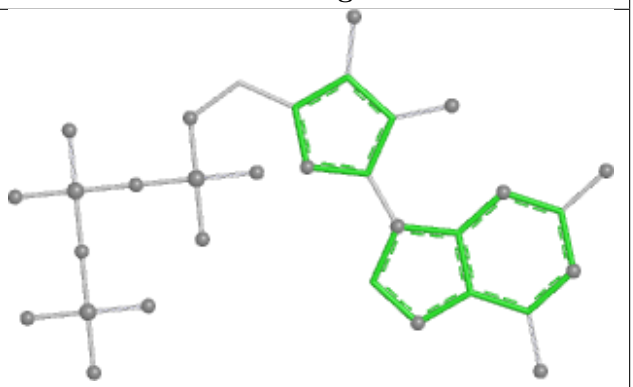
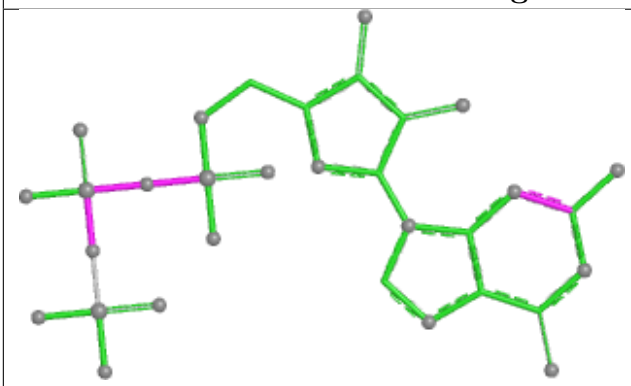


Rings

Ligand GTP VA 501



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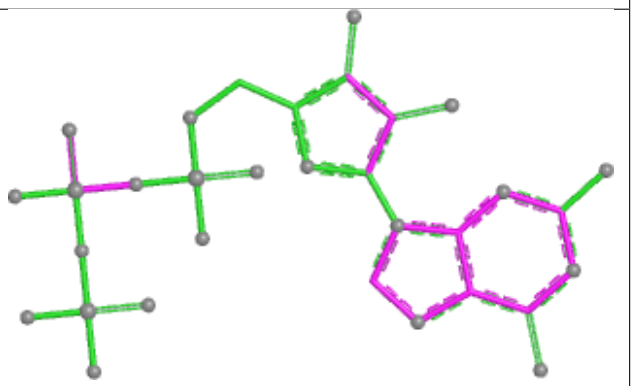

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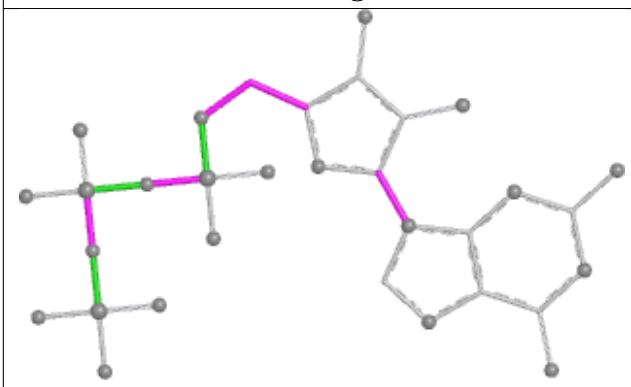

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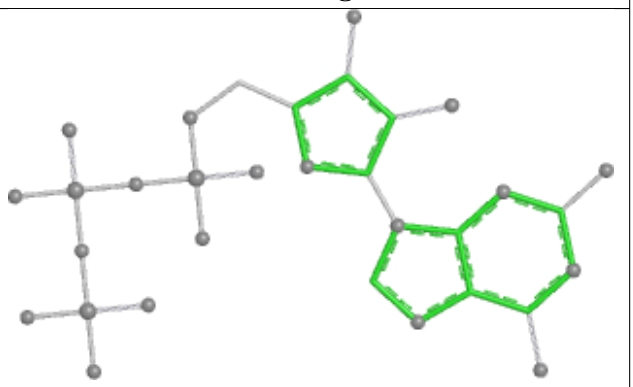
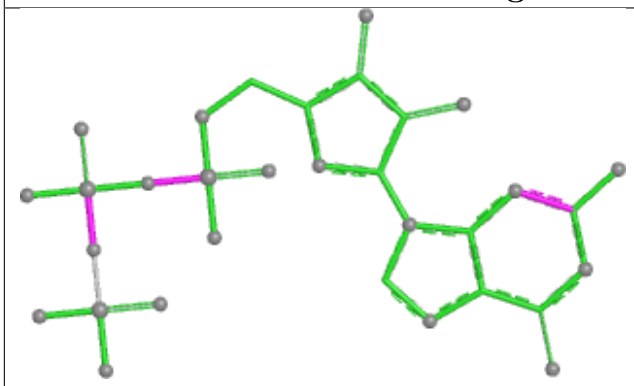


Rings

Ligand GTP WF 501



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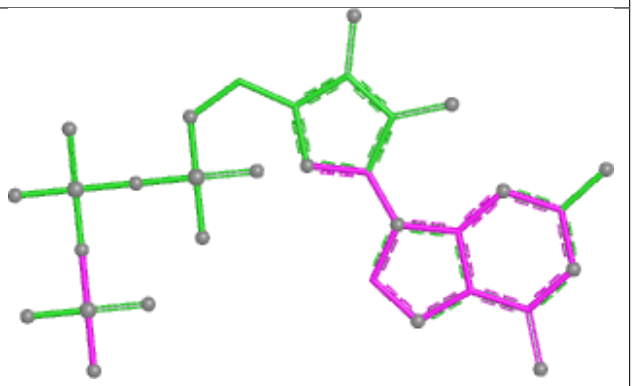

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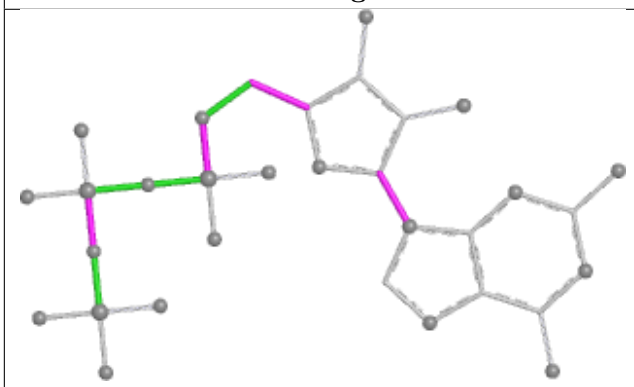

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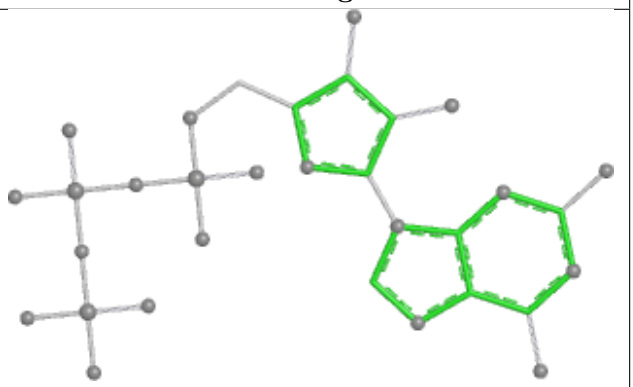
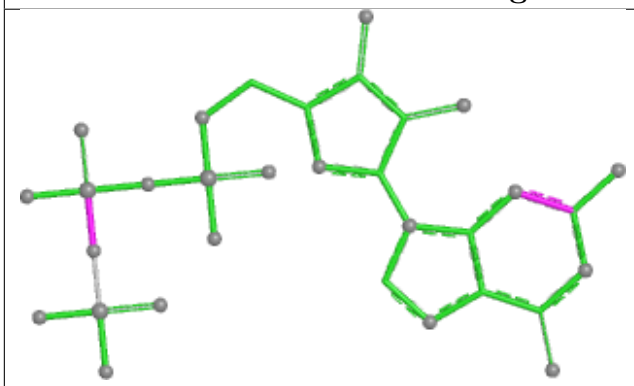


Rings

Ligand GTP RD 501



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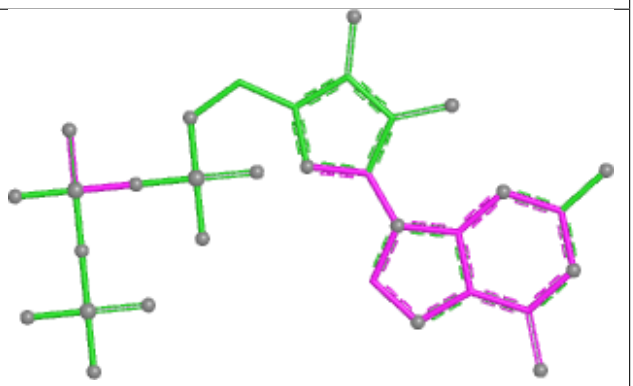

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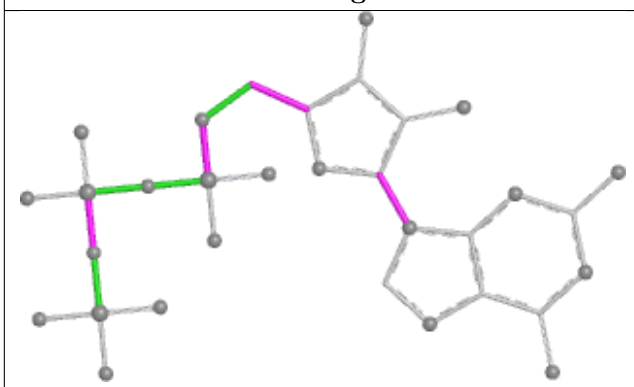

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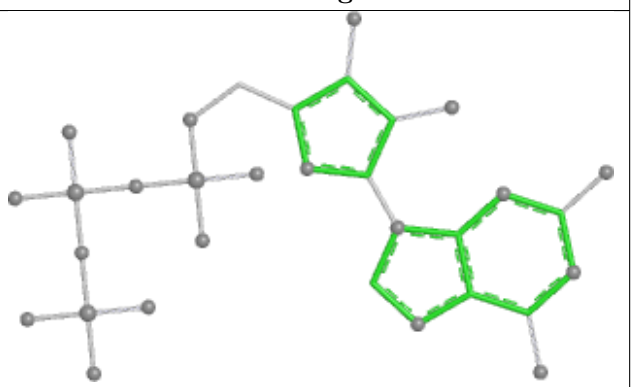
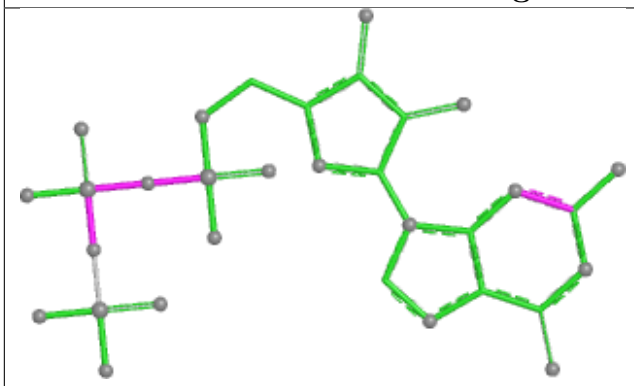


Rings

Ligand GTP SK 501



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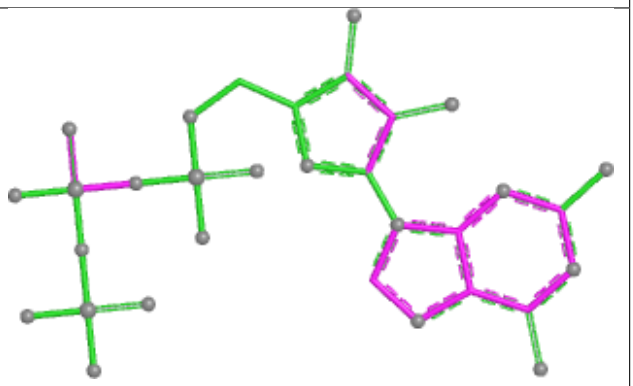

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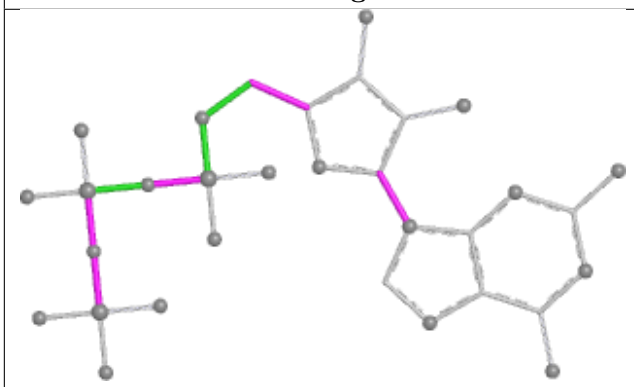

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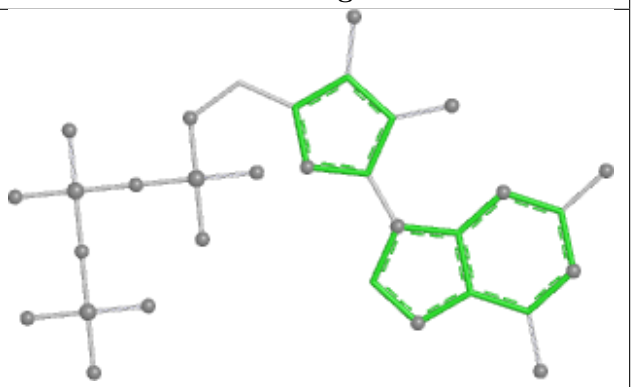
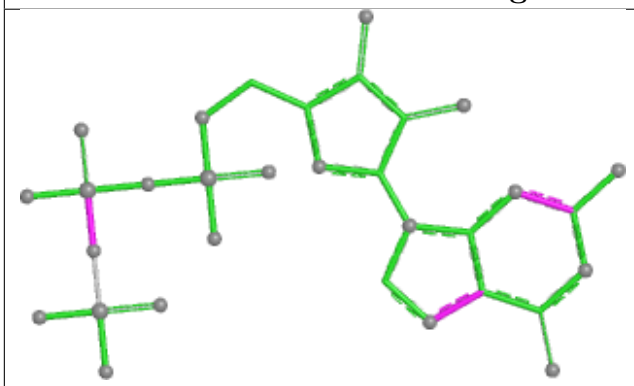


Rings

Ligand GTP CH 501



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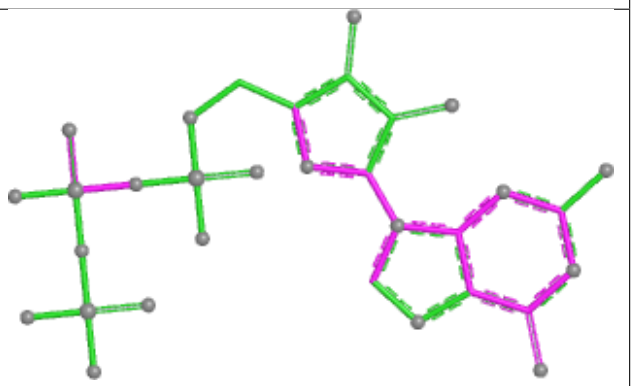
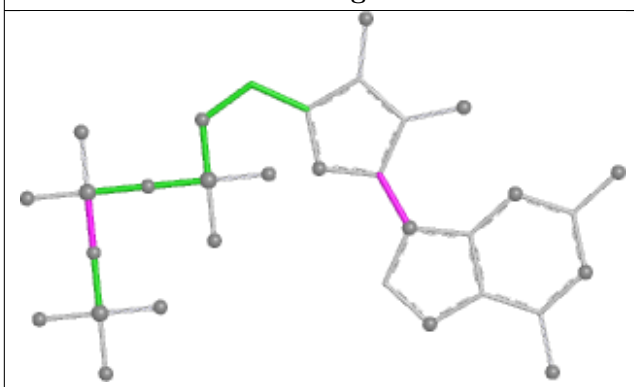


Bond angles



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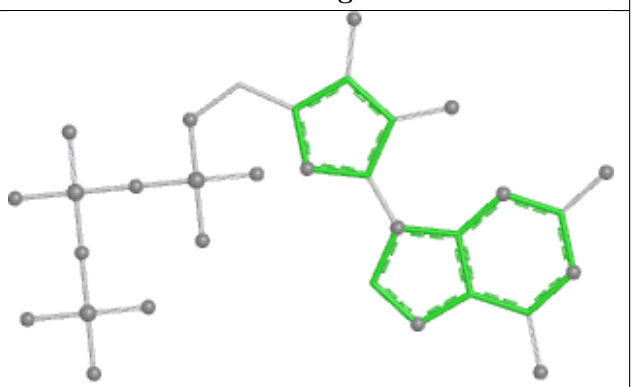
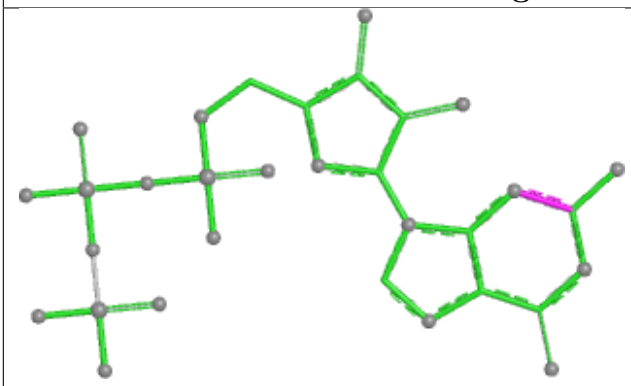


Rings

Ligand GTP KJ 501



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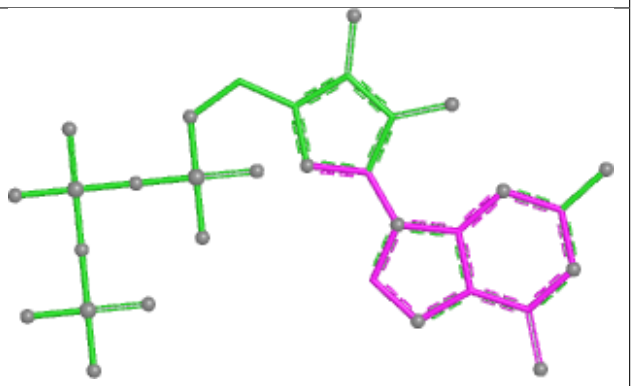
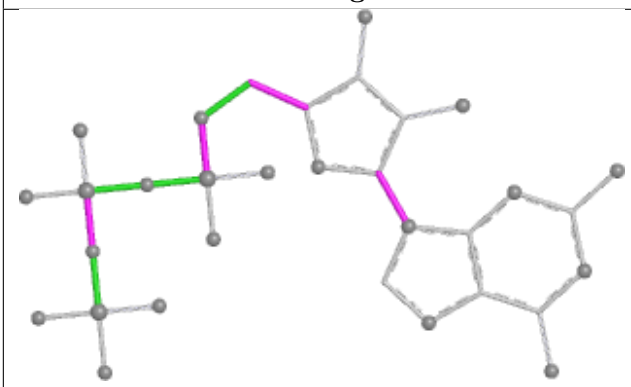


Bond angles



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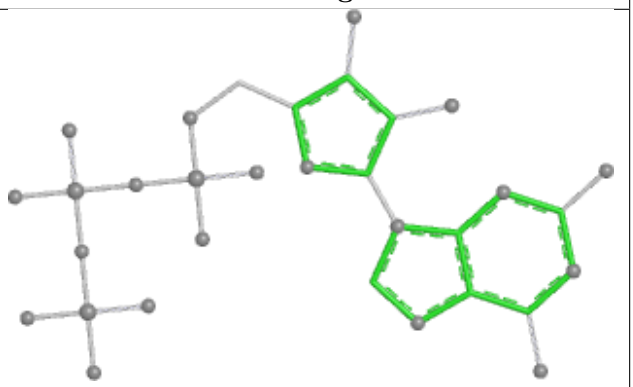
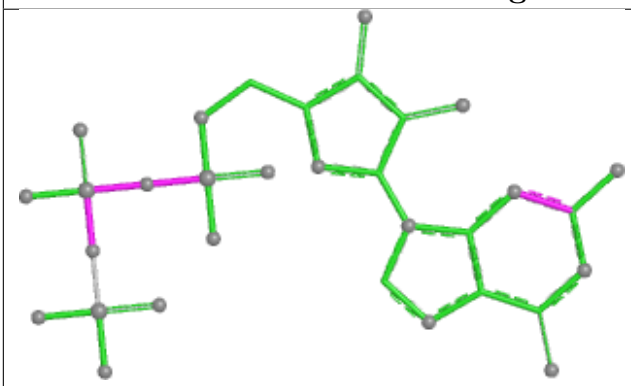


Rings

Ligand GTP TG 501



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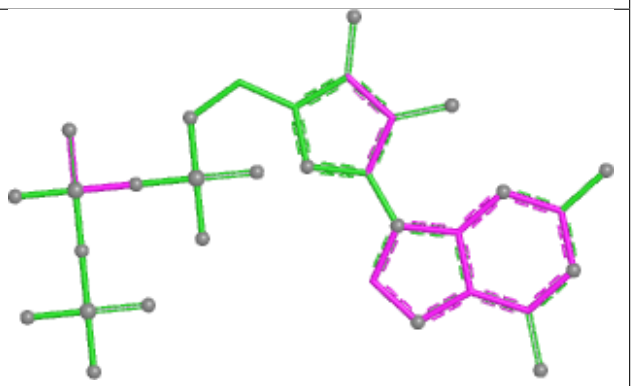

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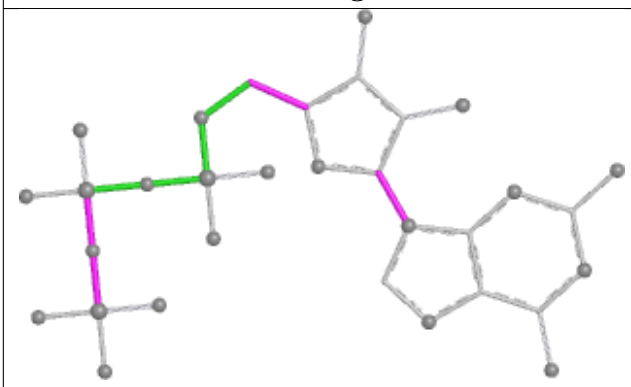
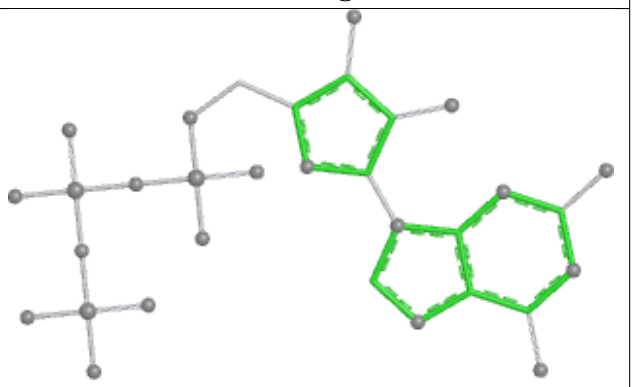
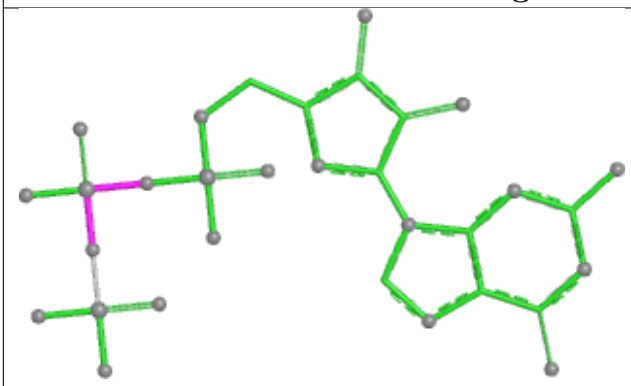


Torsions



Rings

Ligand GTP FC 501



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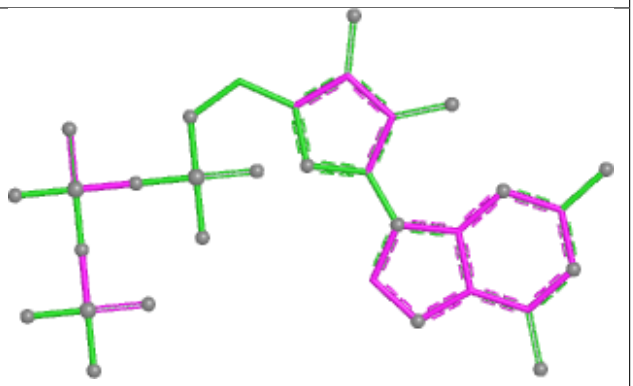

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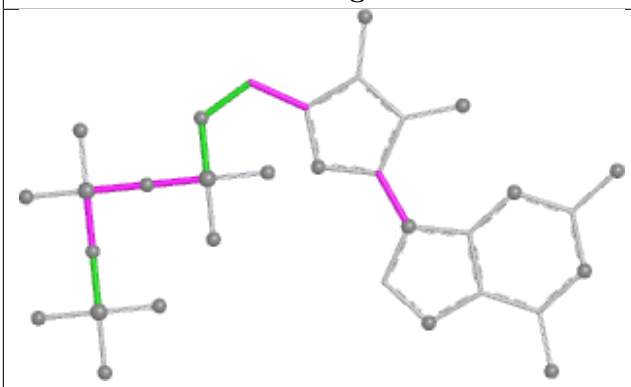

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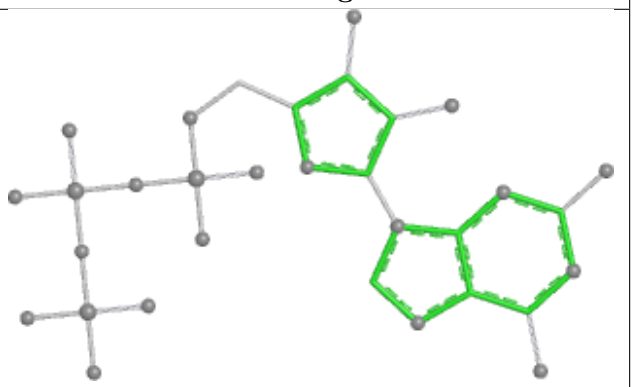
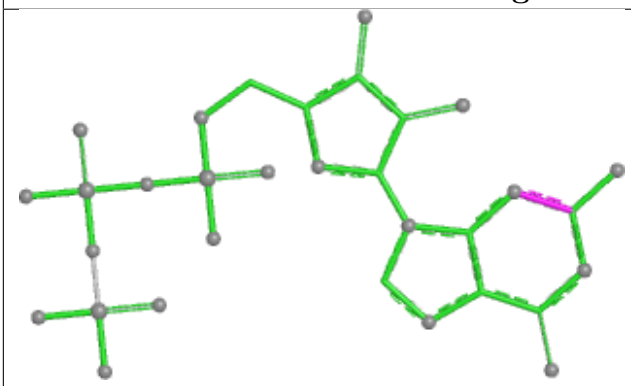


Rings

Ligand GTP TF 501



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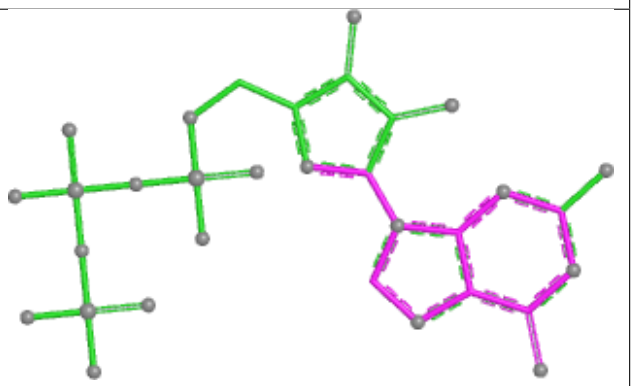

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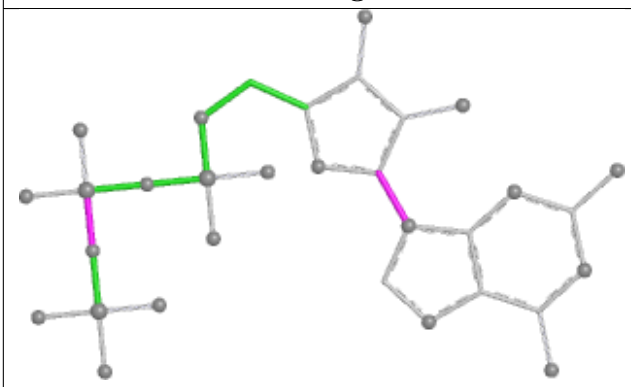

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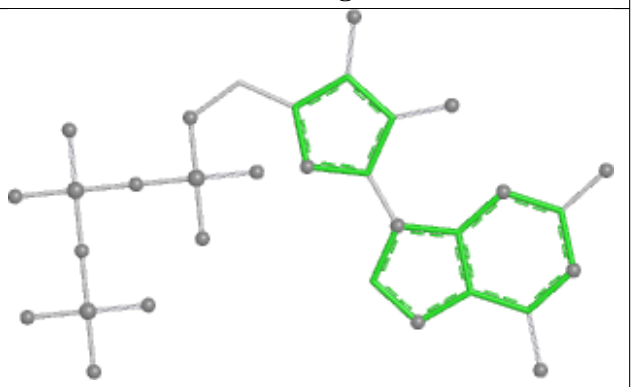

Rings

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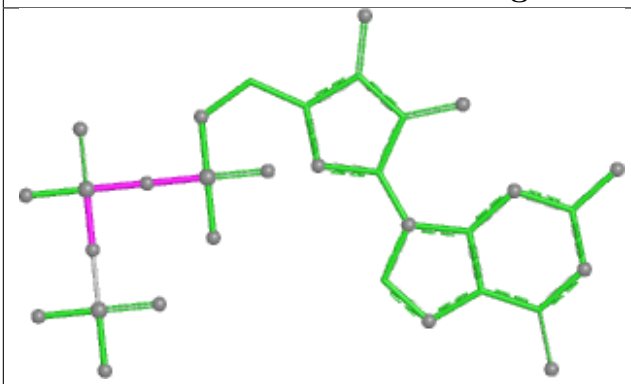

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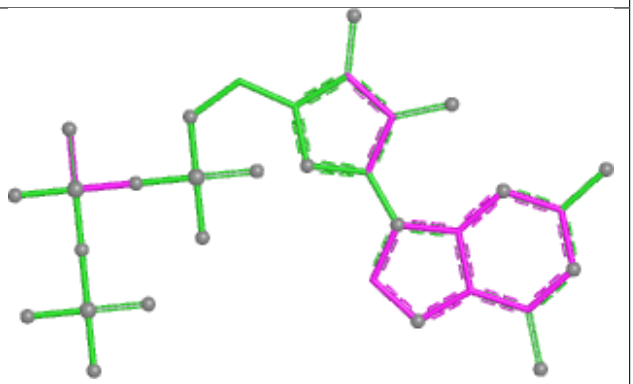

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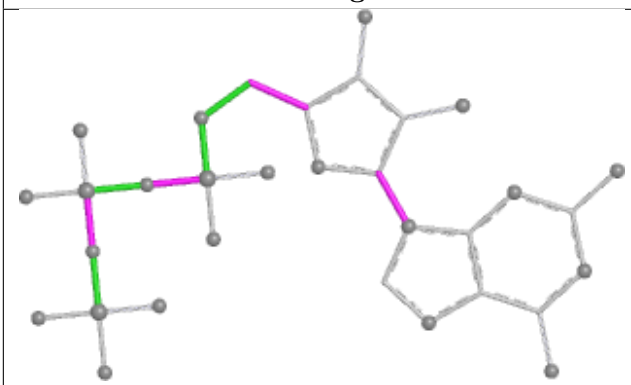

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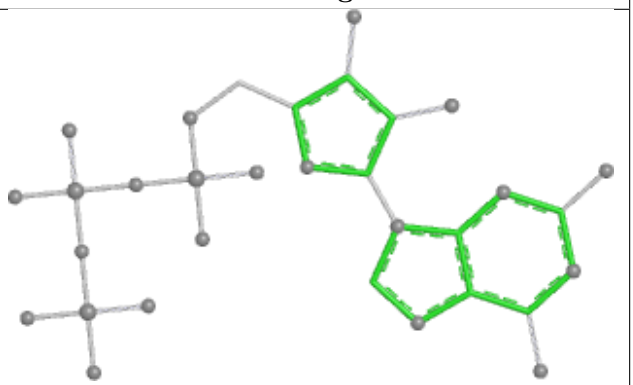
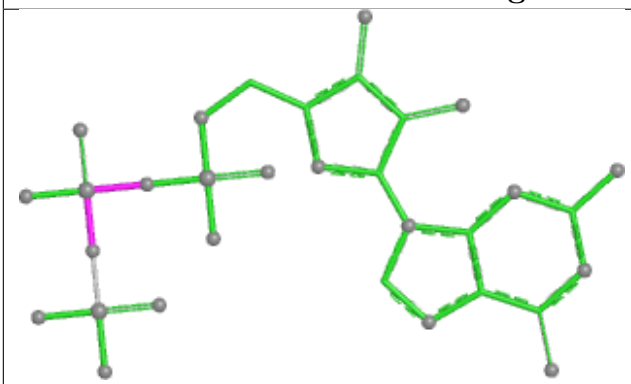


Rings

Ligand GTP KA 501



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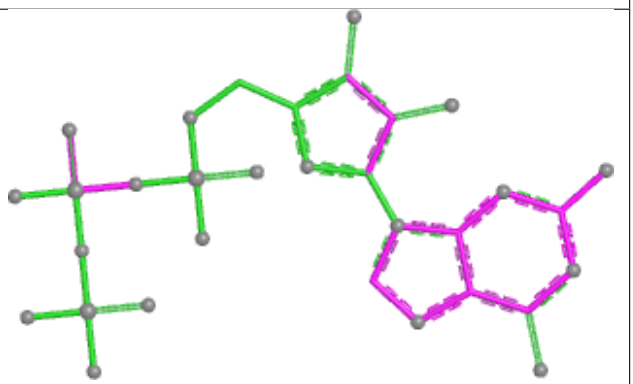

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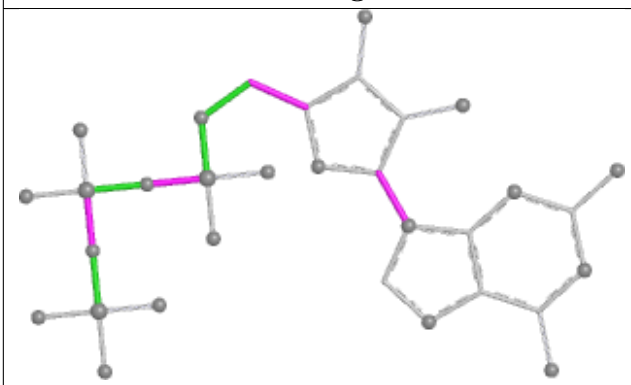

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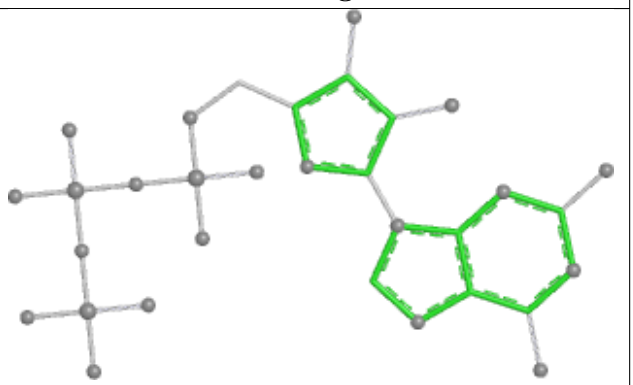

Rings

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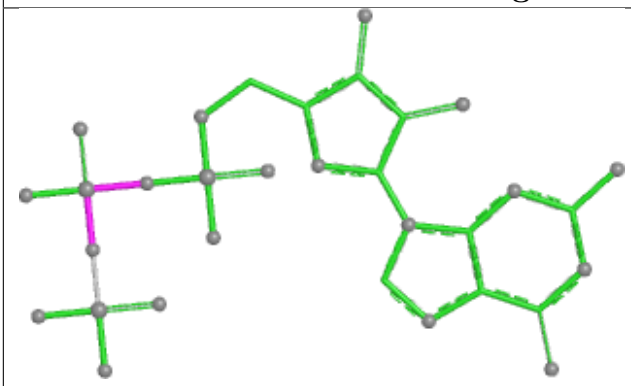

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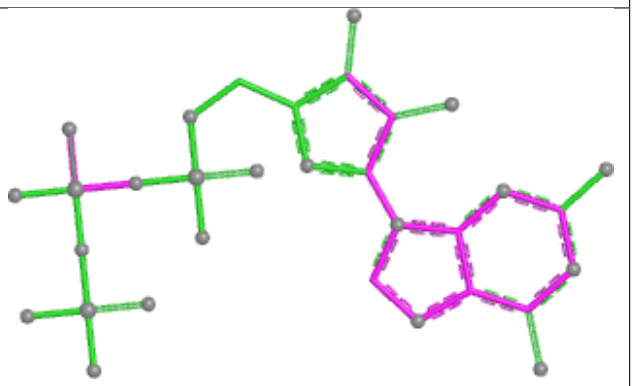

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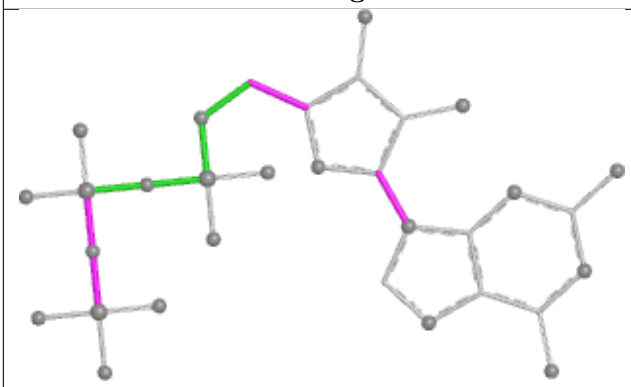

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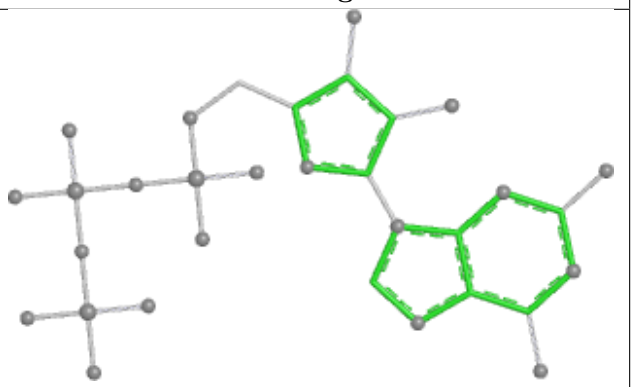

Rings

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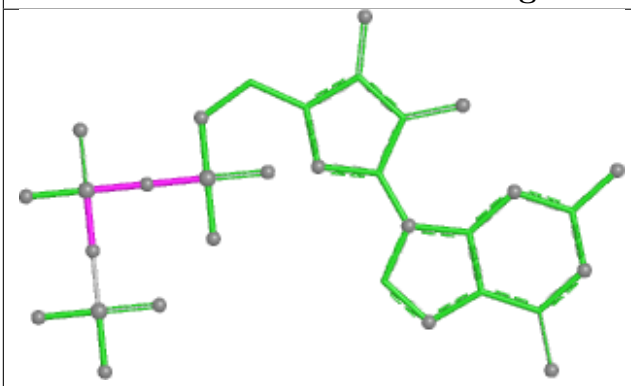

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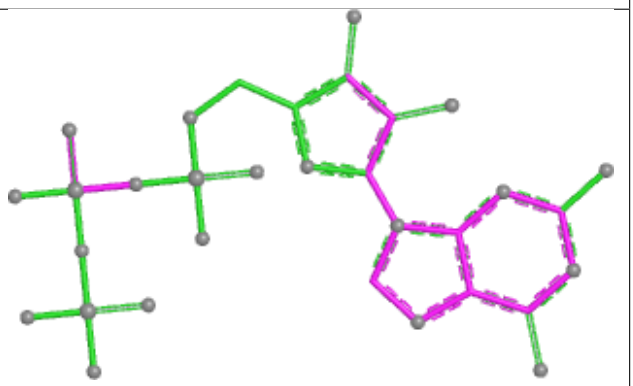

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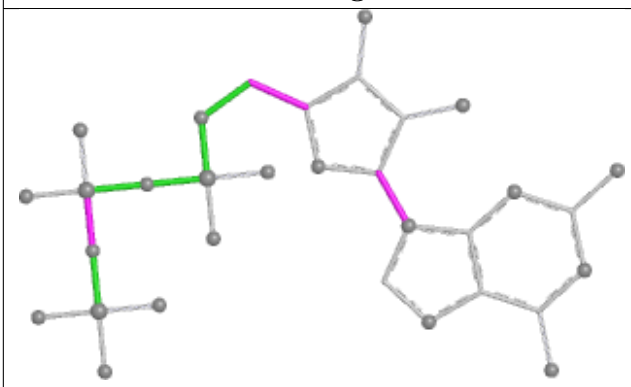

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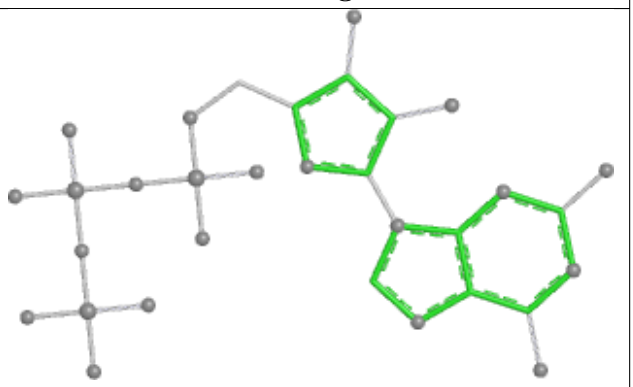

Rings

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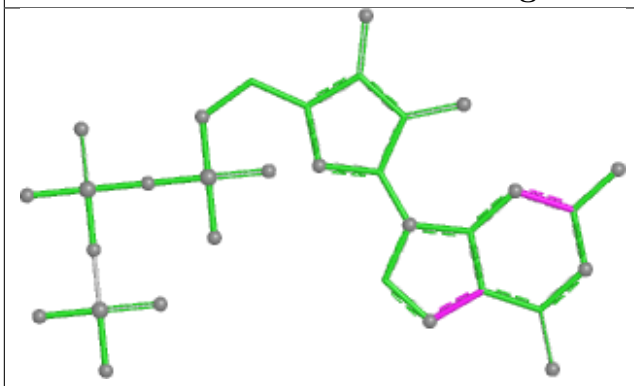

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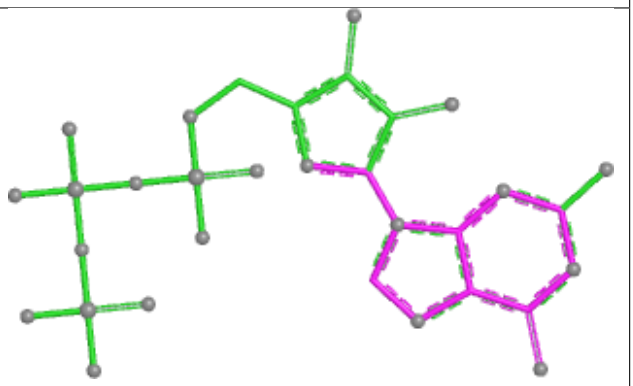

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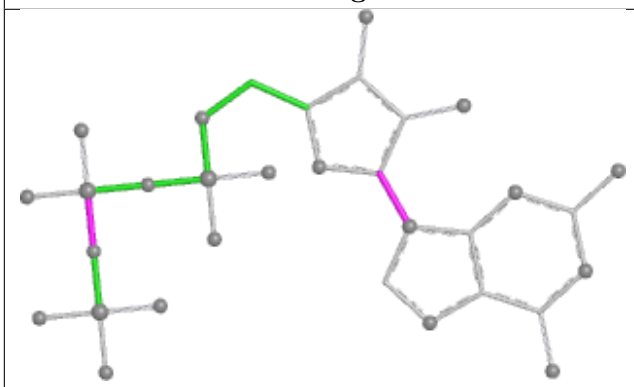

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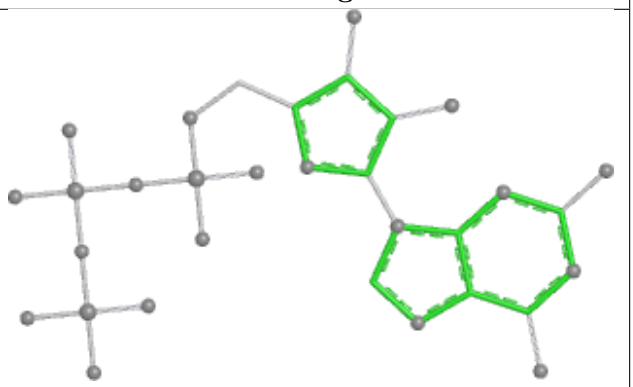

Rings

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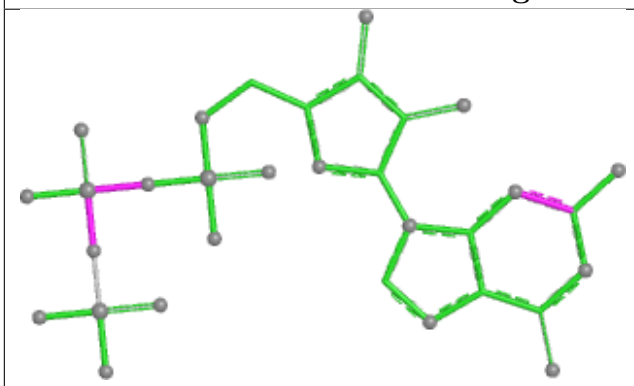

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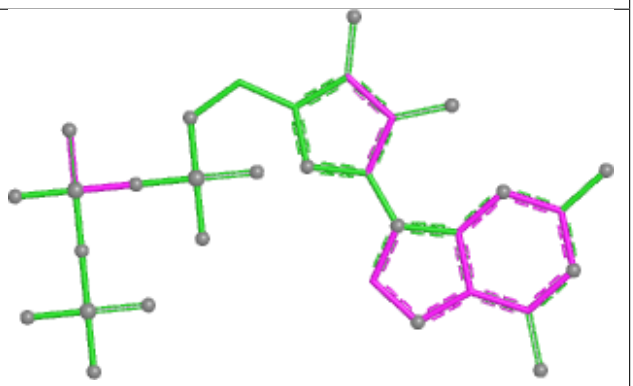

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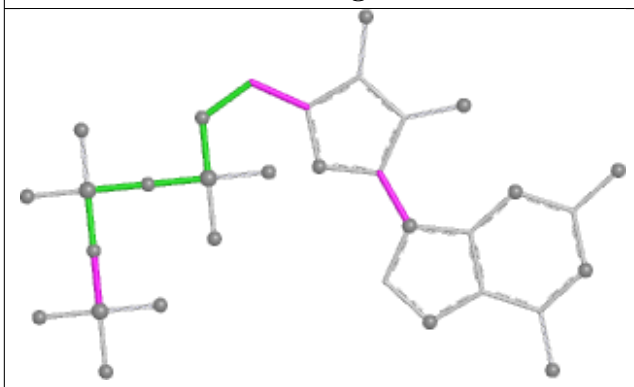

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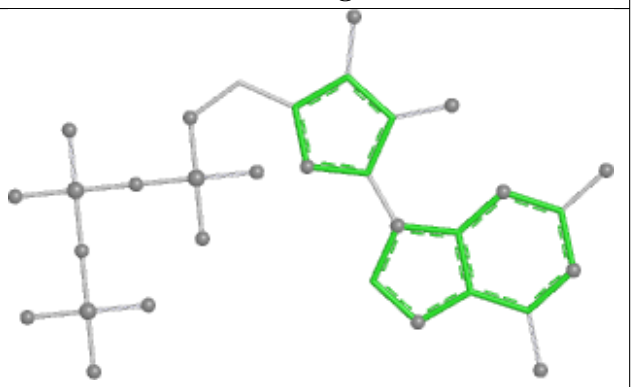

Rings

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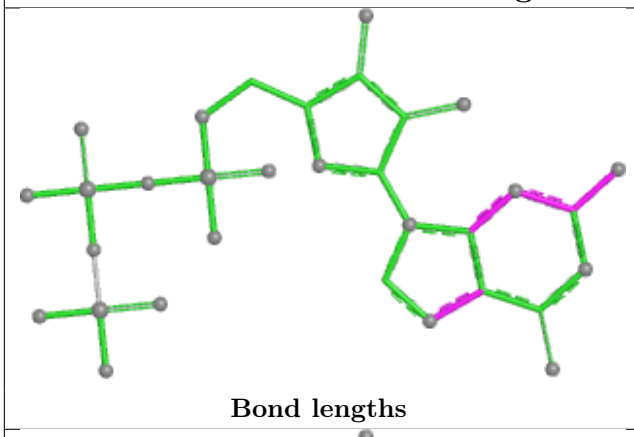

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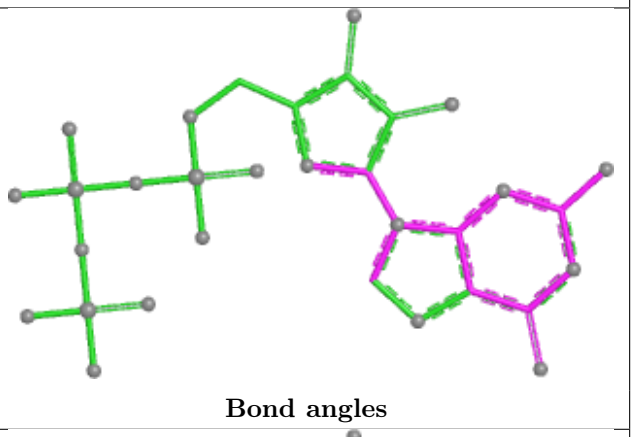

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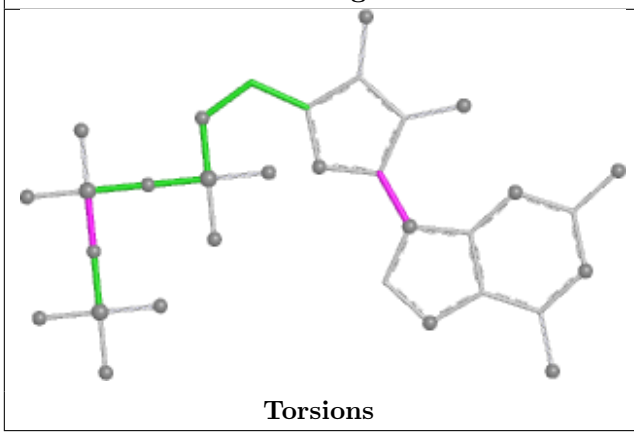

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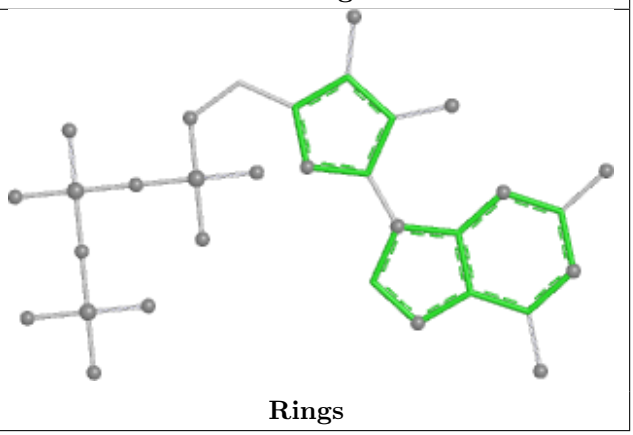
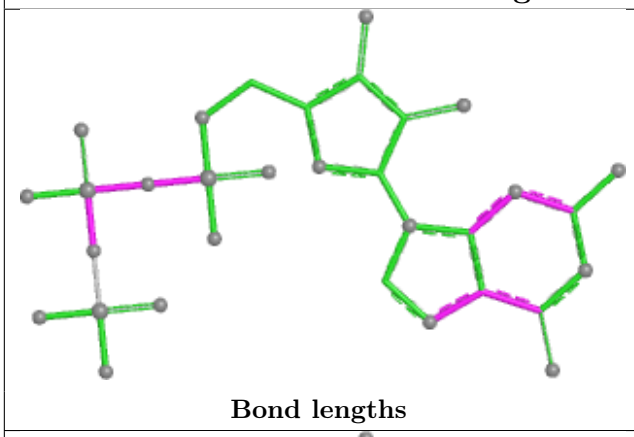


Rings

Ligand GTP TL 501



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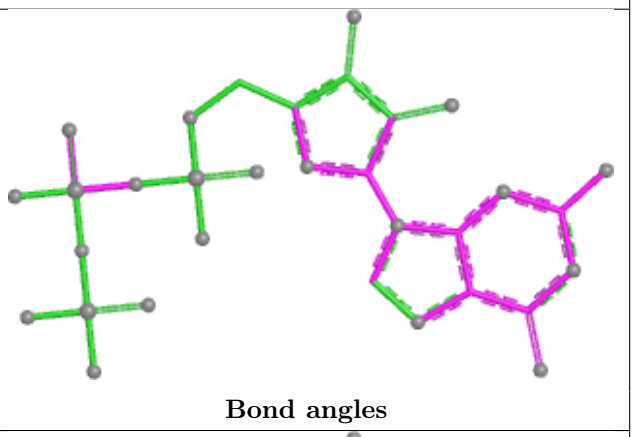

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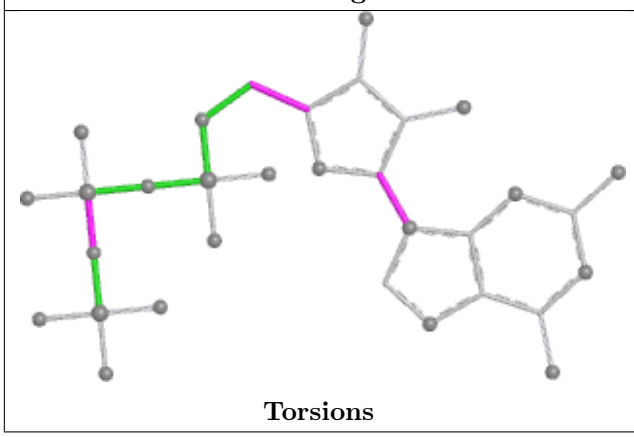

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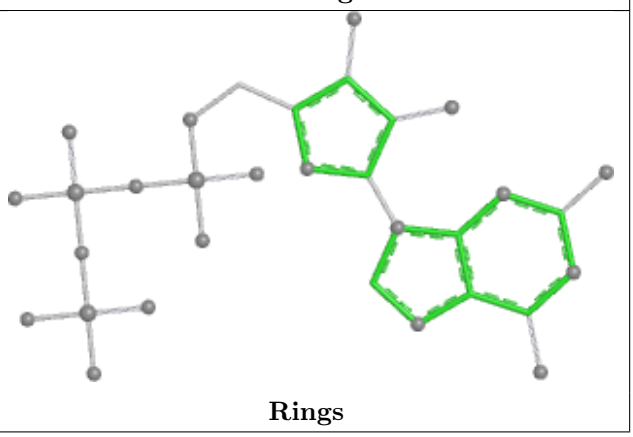

Rings

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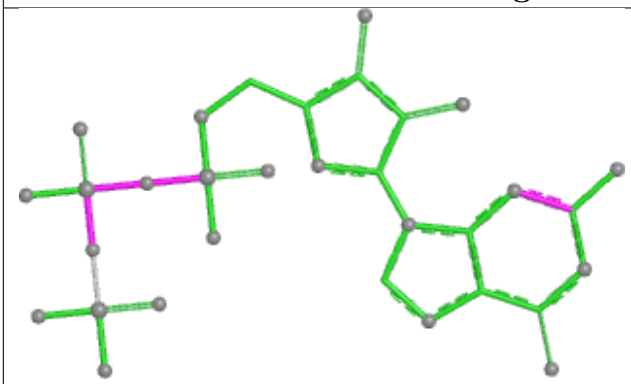

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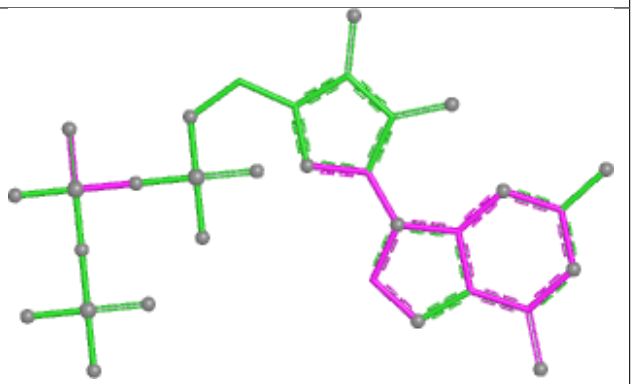
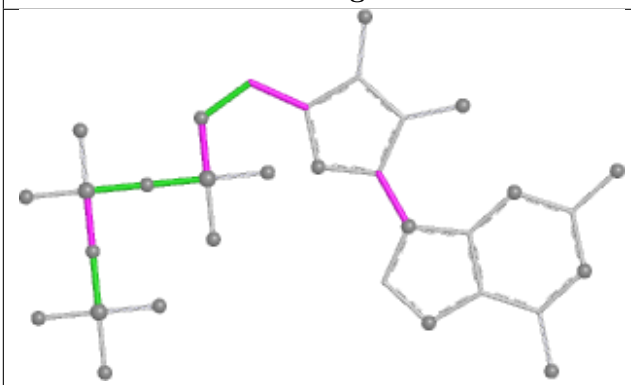
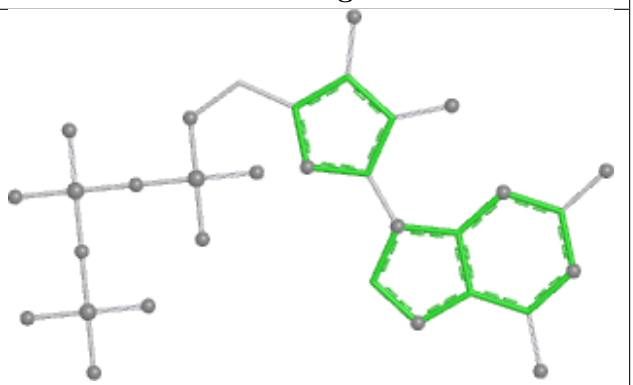


Bond angles



Torsions



Rings

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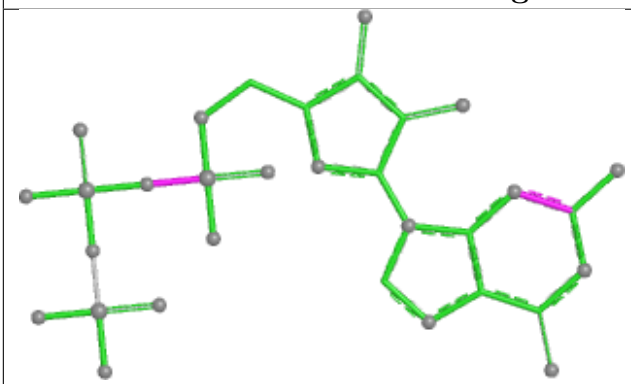

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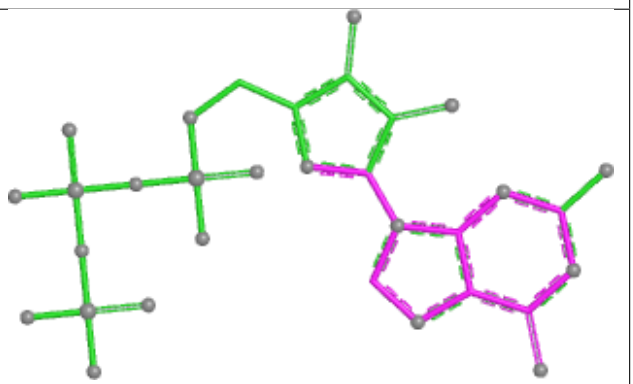
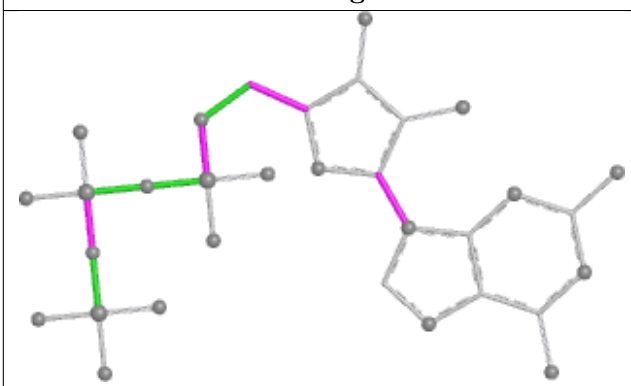


Bond angles



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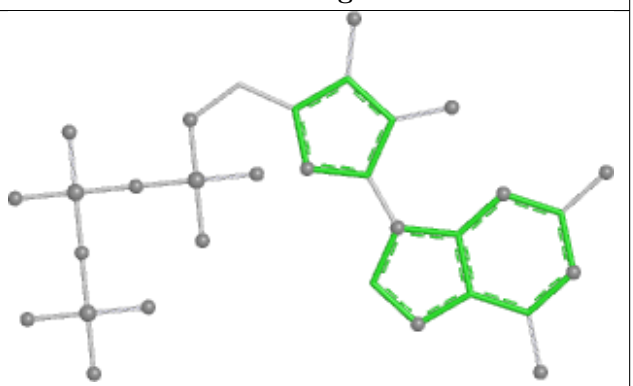
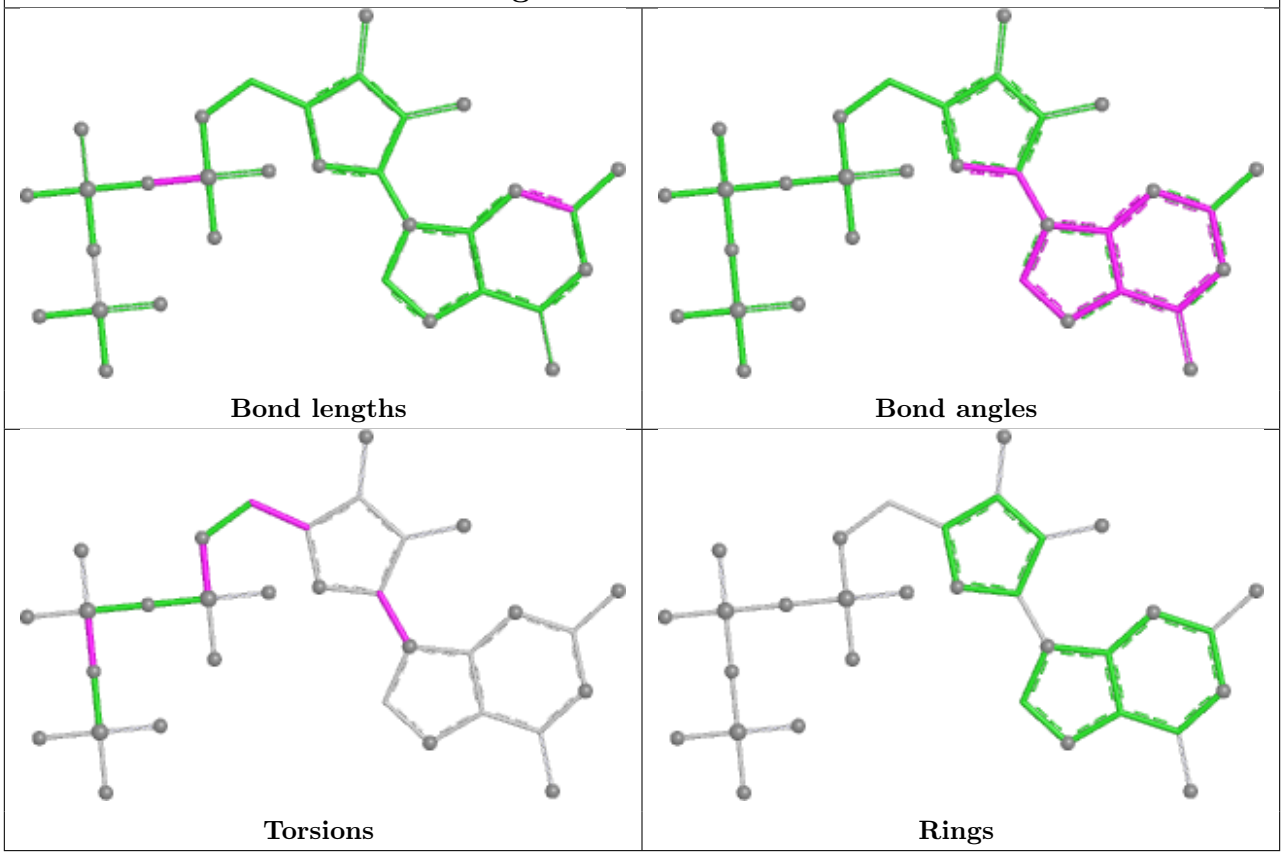


Rings

Ligand GTP KL 501



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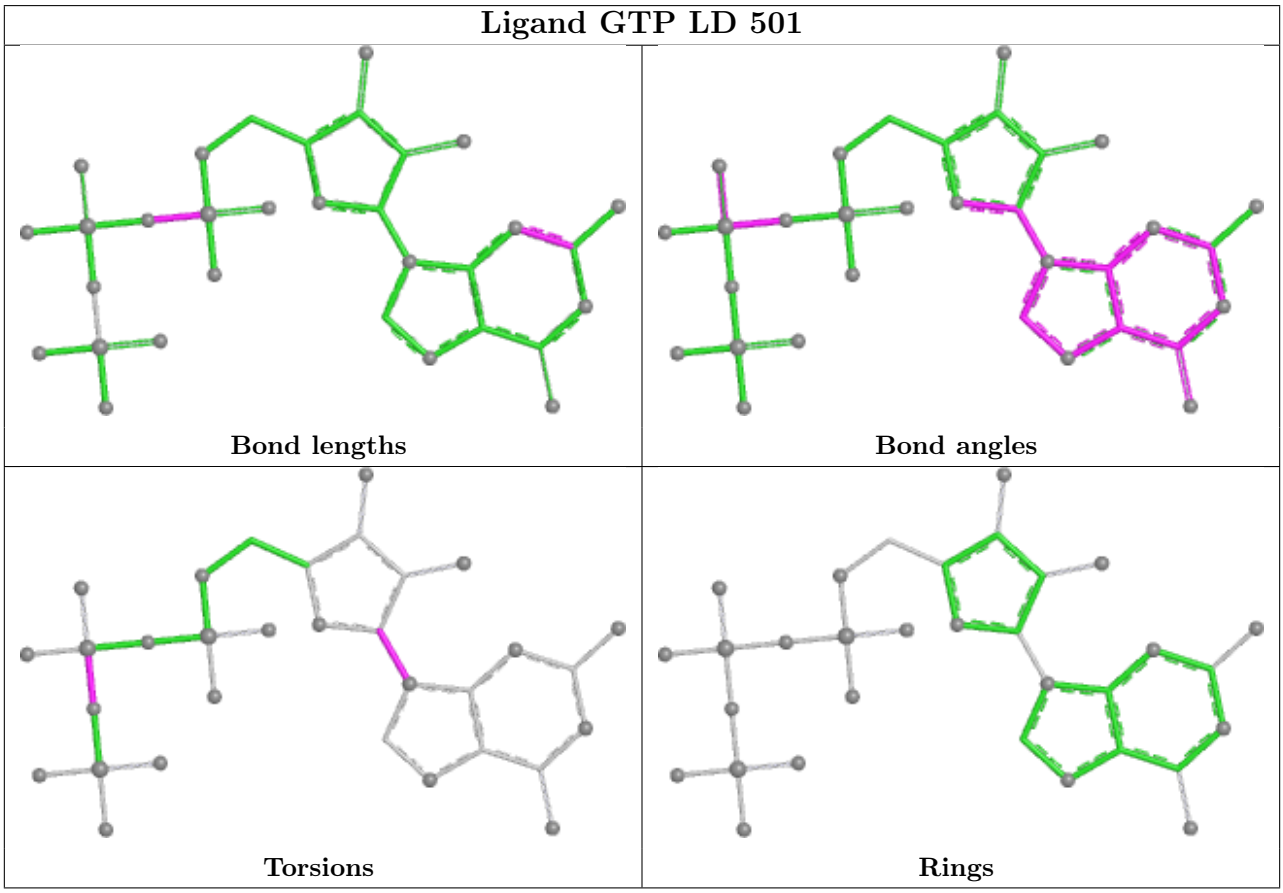

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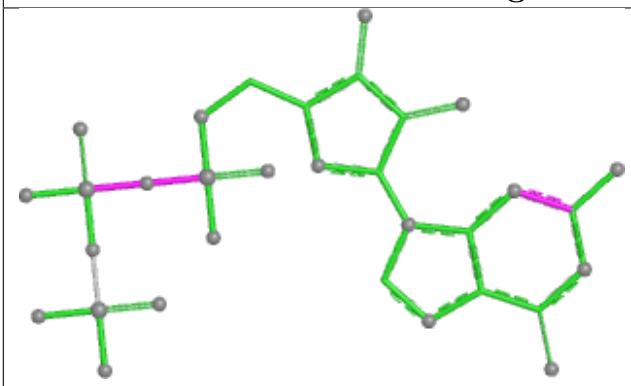

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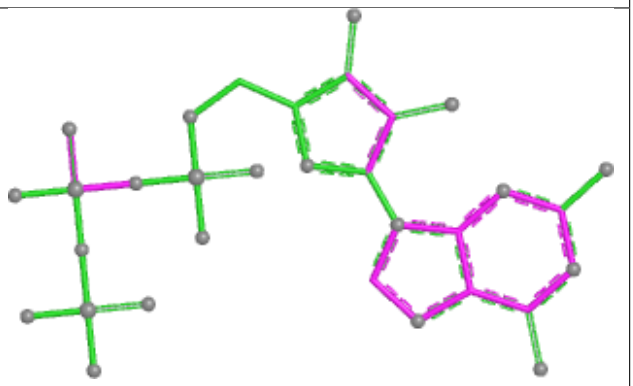
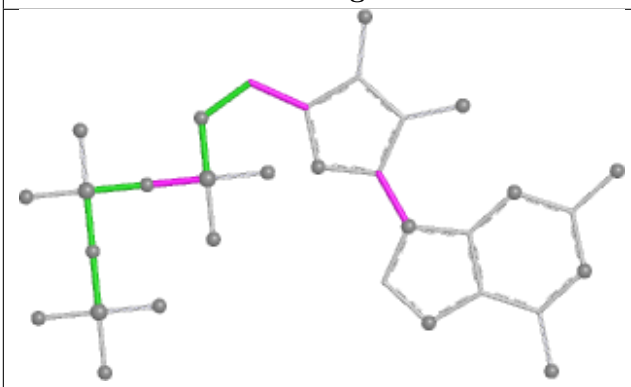
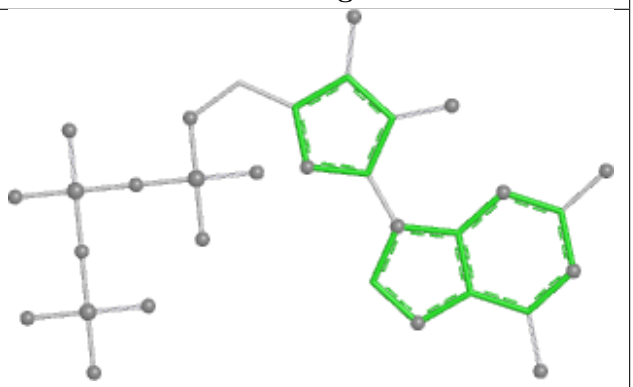


Bond angles

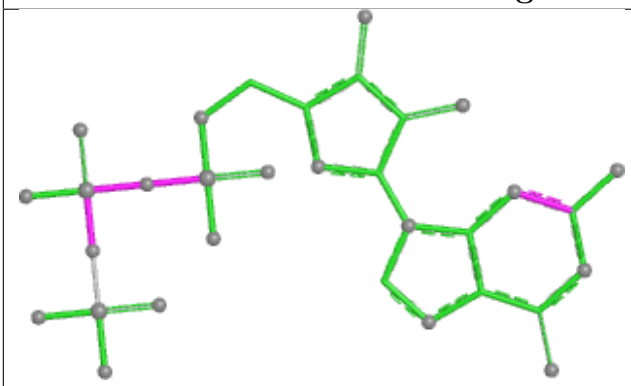


Torsions



Rings

Ligand GTP CI 501



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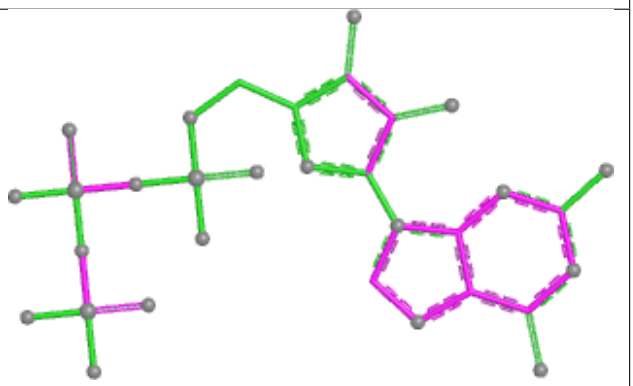

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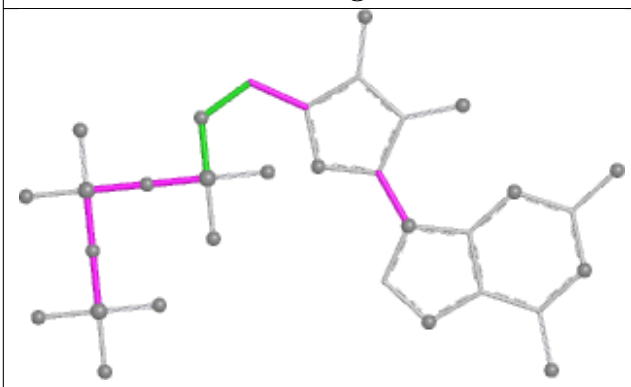

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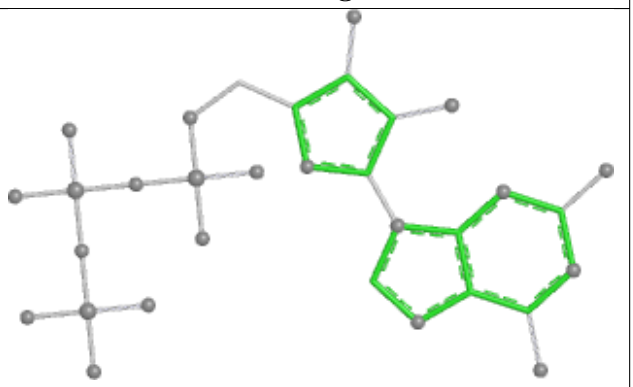
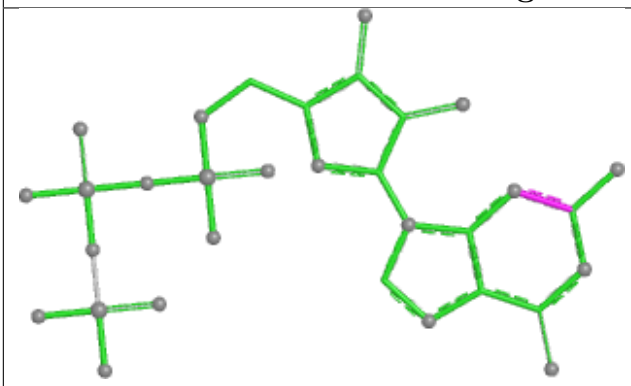


Rings

Ligand GTP JJ 501



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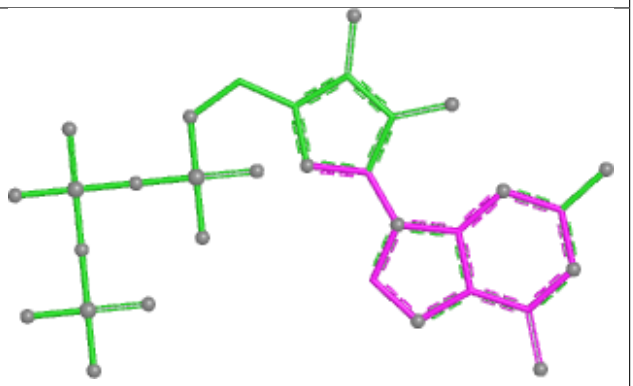

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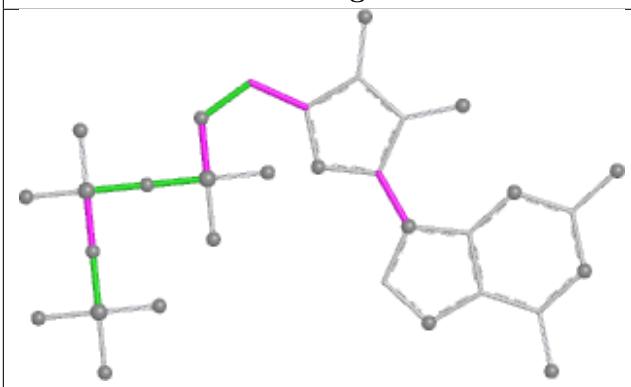

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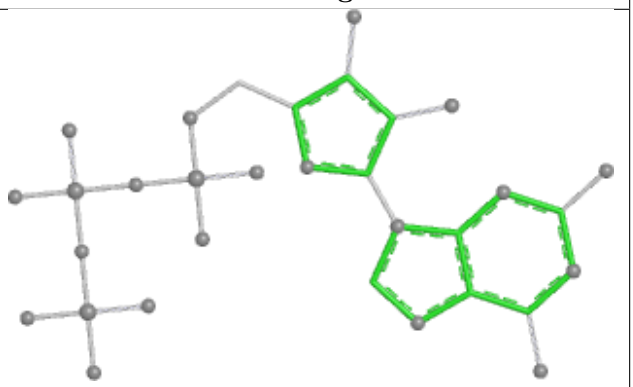
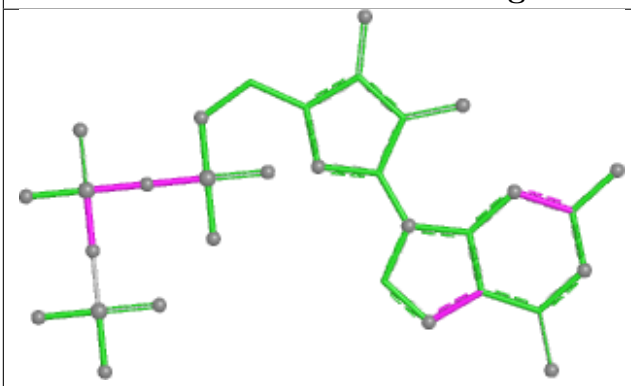


Rings

Ligand GTP ND 501



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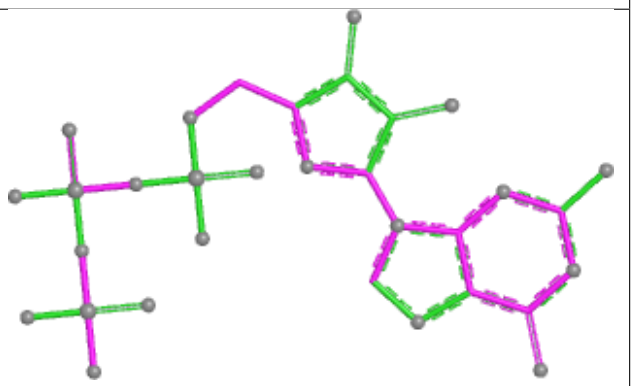

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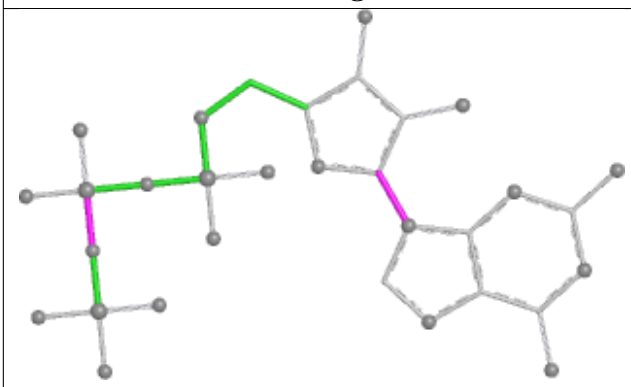

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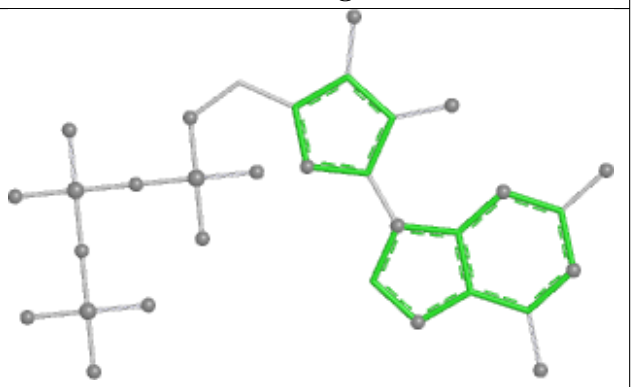
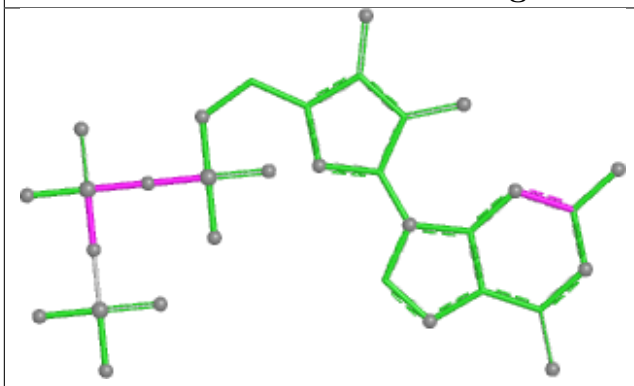


Rings

Ligand GTP UA 501



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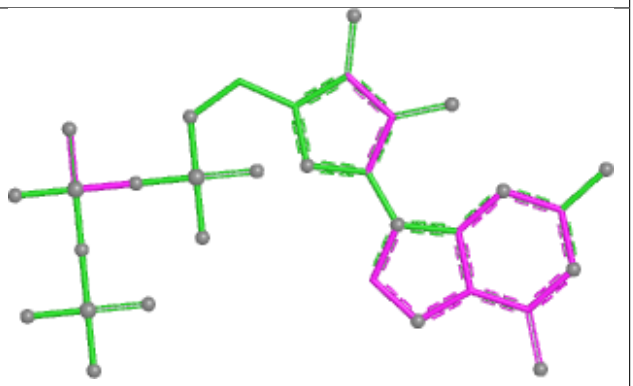

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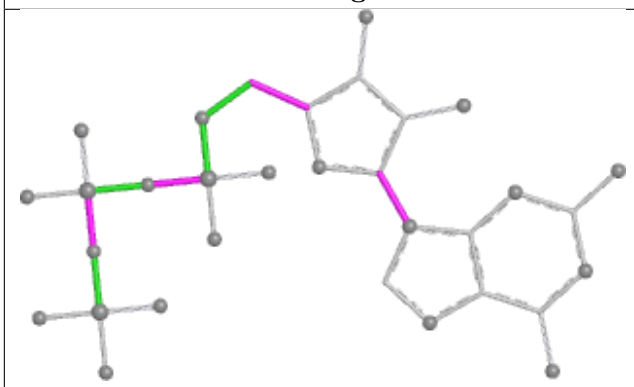

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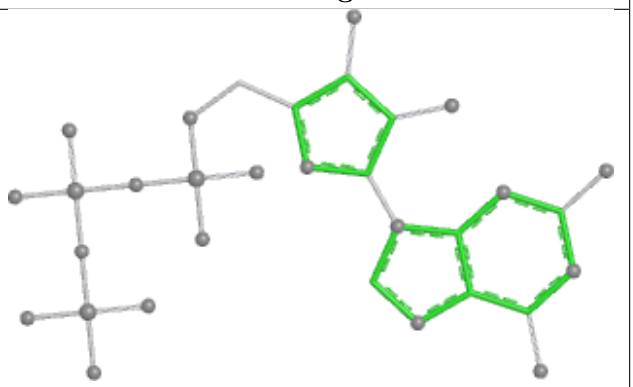
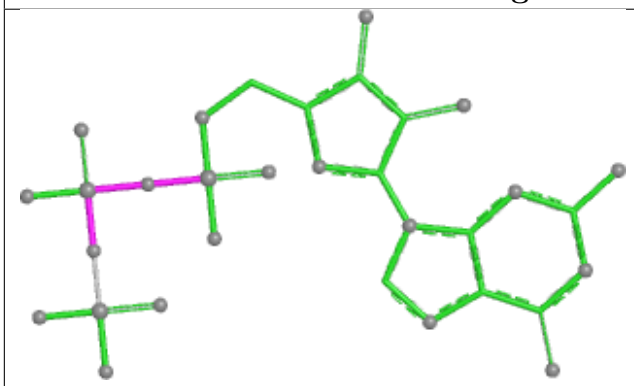


Rings

Ligand GTP TC 501



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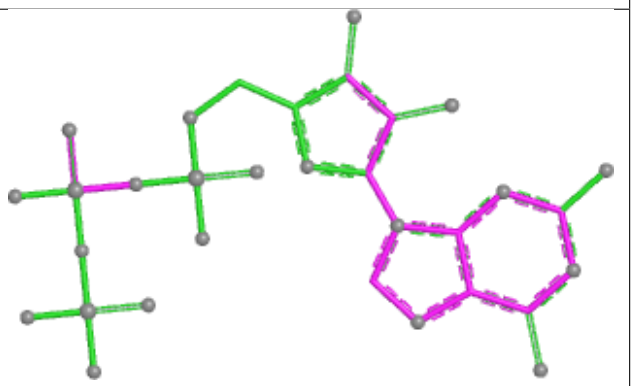

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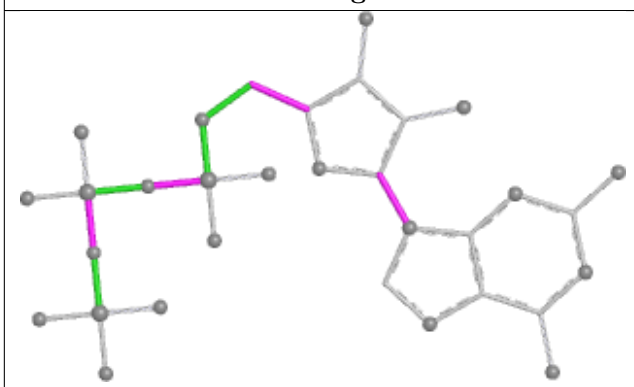

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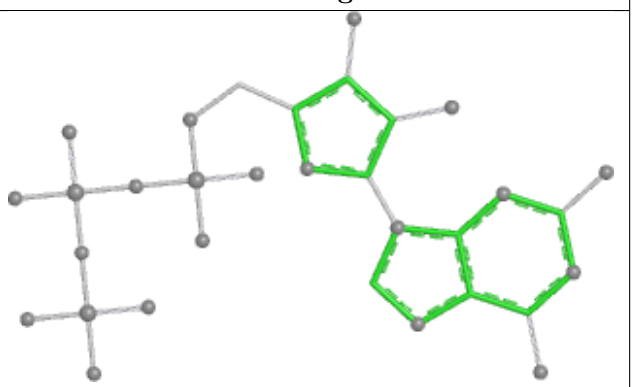

Rings

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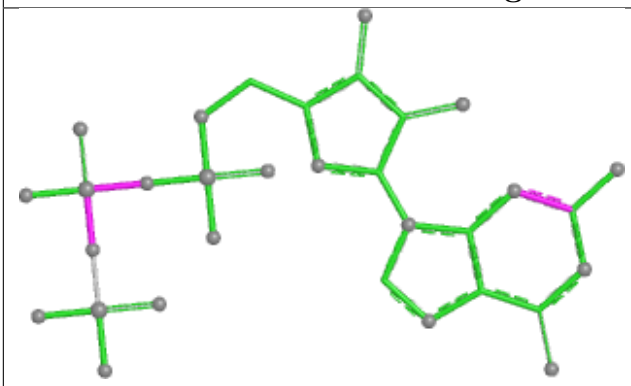

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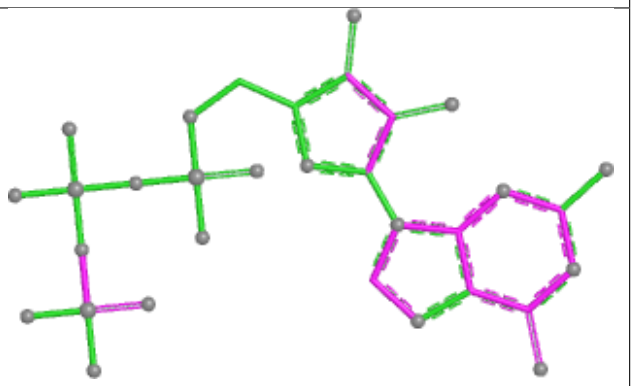

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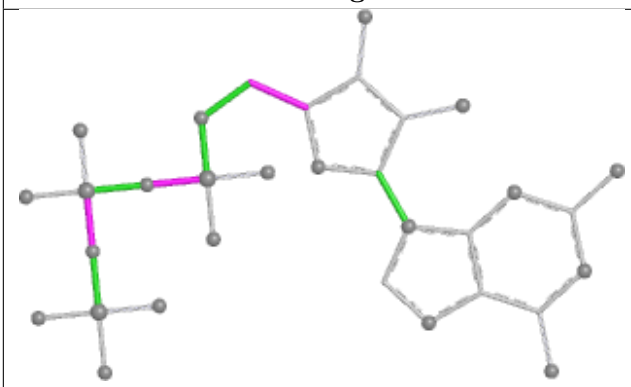

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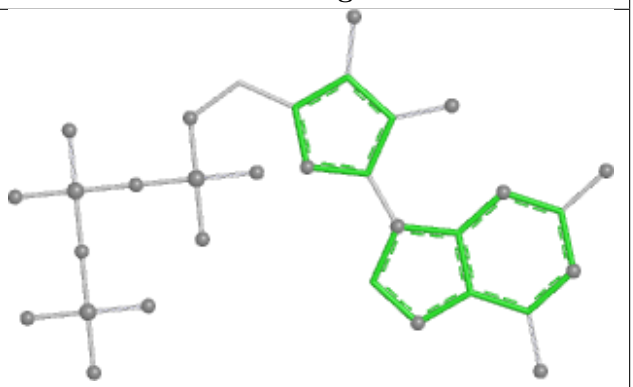
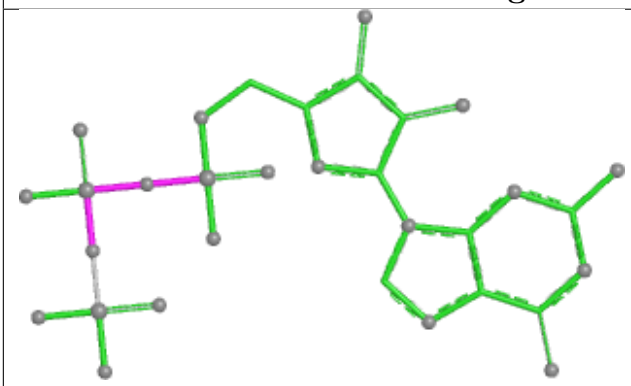


Rings

Ligand GTP AK 501



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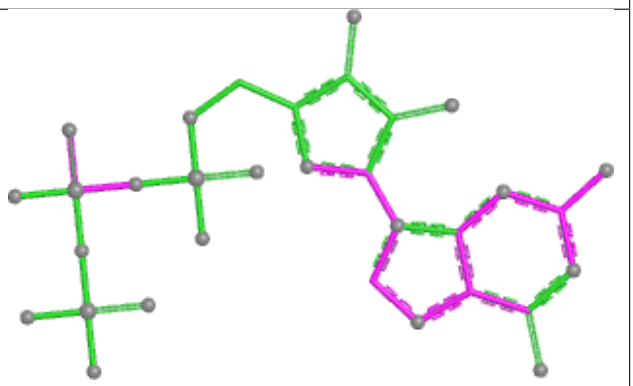

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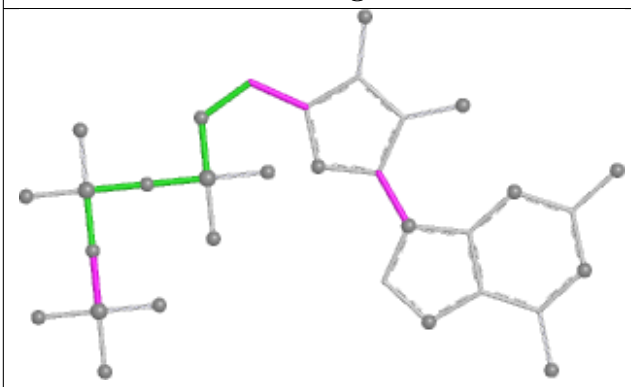

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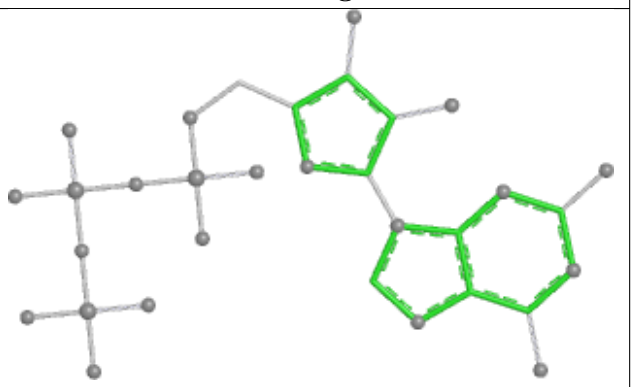
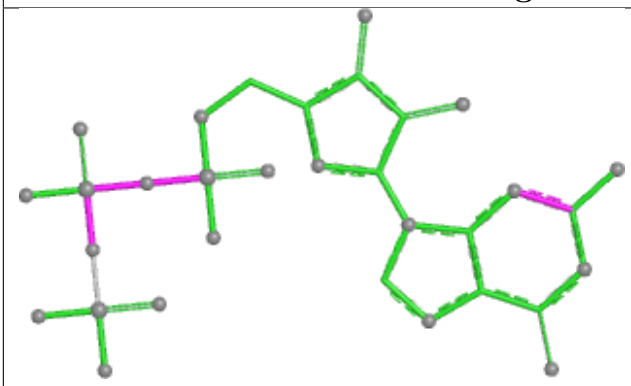


Rings

Ligand GTP IG 501



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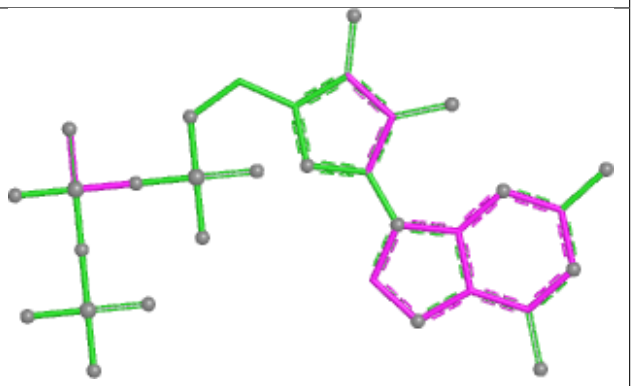

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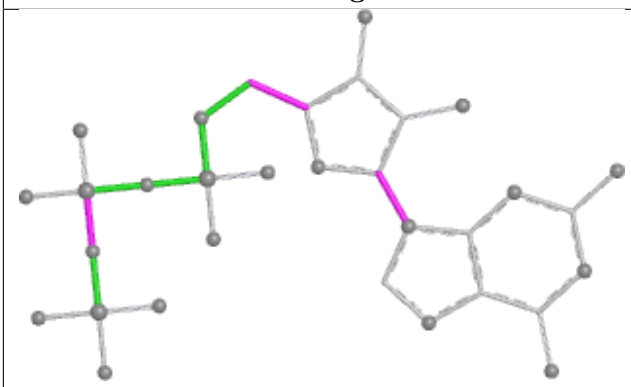

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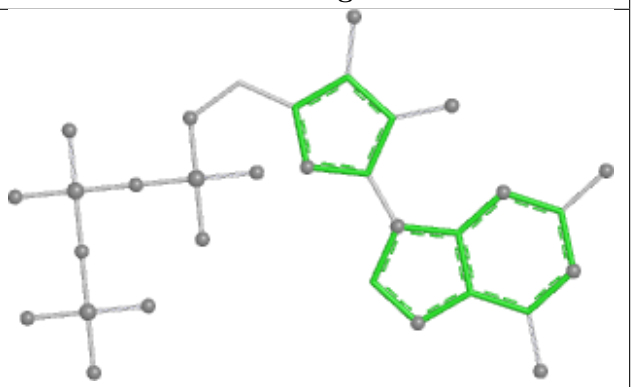
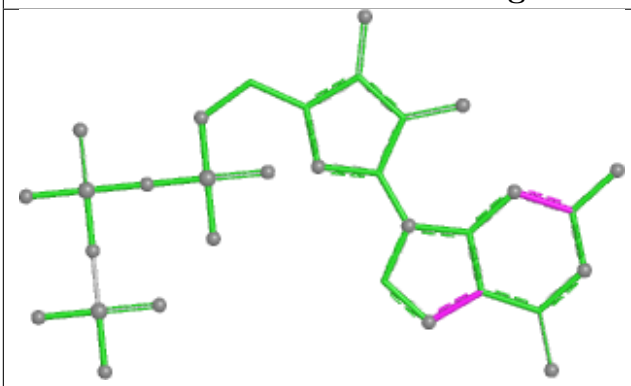


Rings

Ligand GTP ML 501



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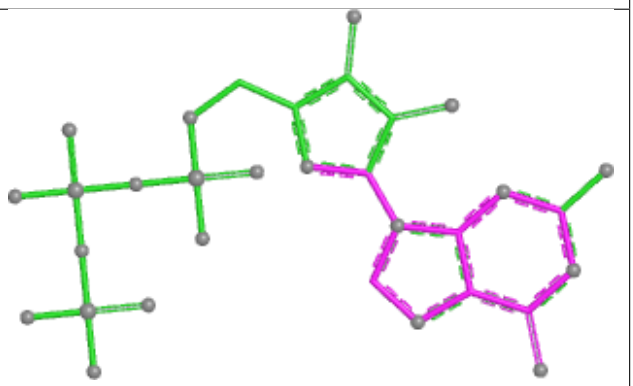

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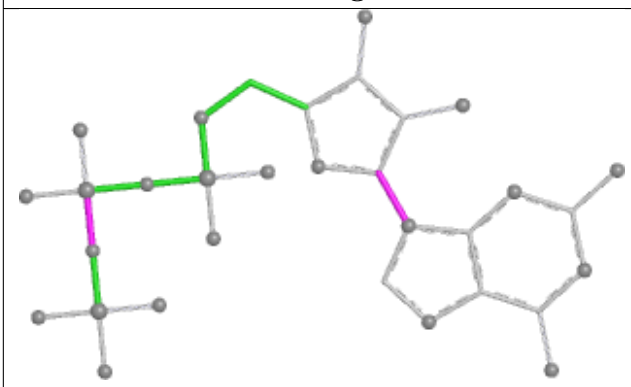

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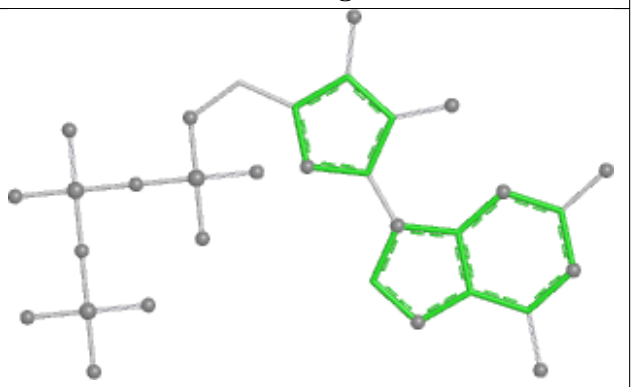

Rings

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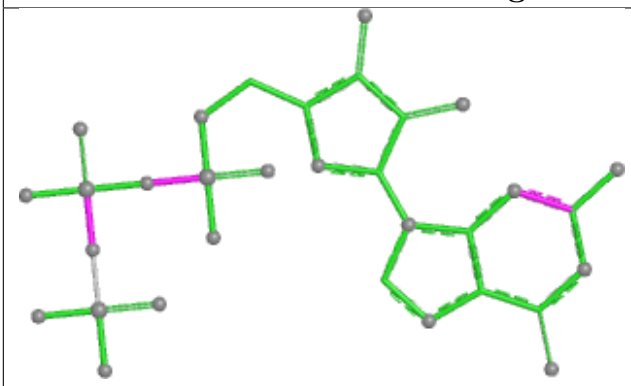

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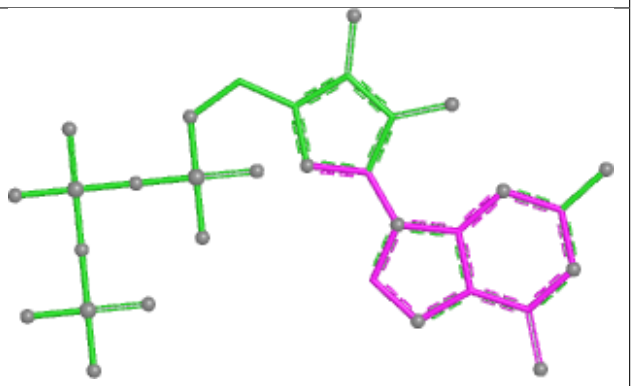

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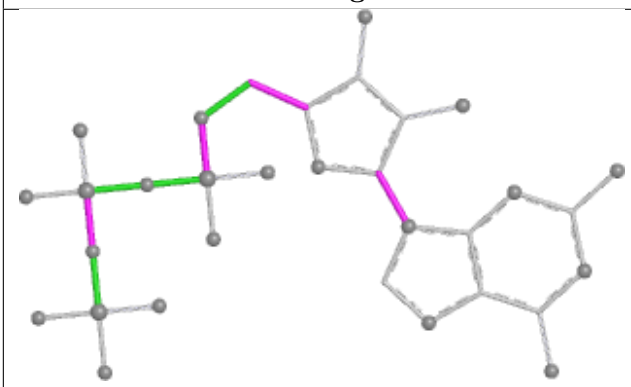

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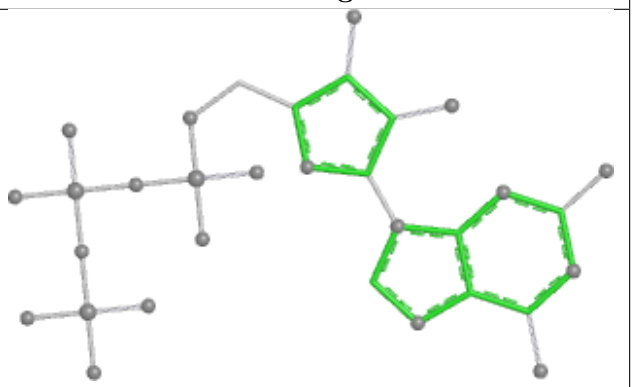
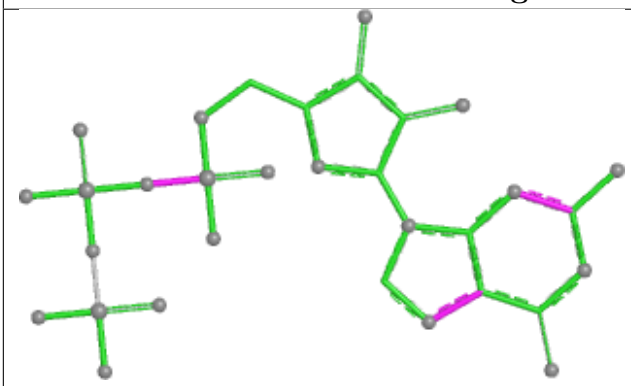


Rings

Ligand GTP GL 501



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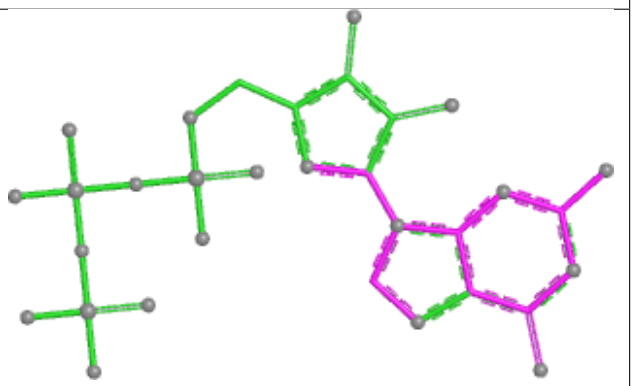

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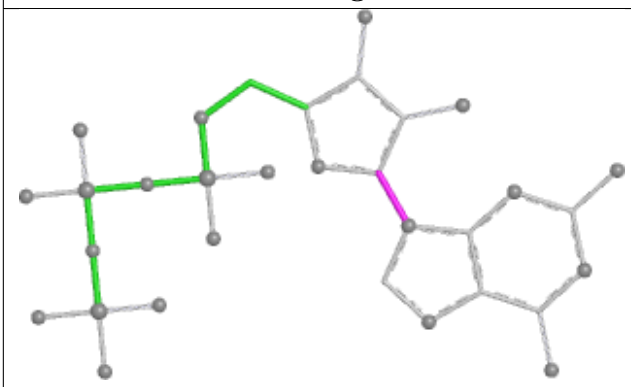

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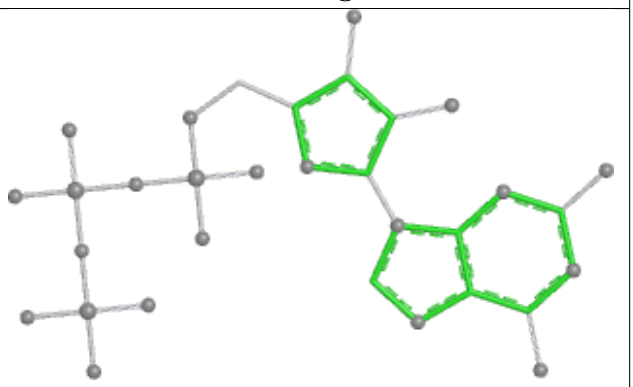
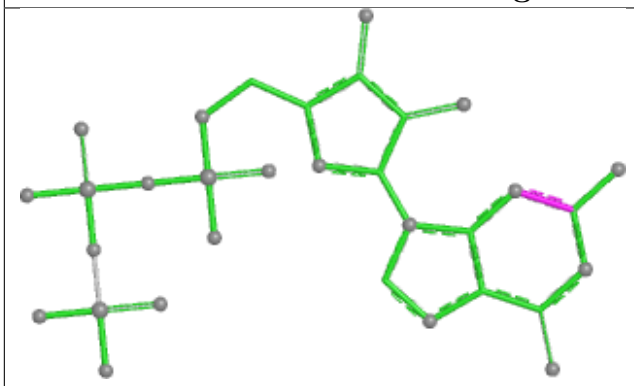


Rings

Ligand GTP GJ 501



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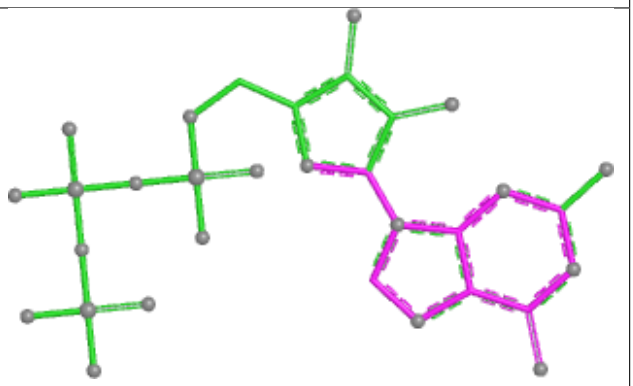

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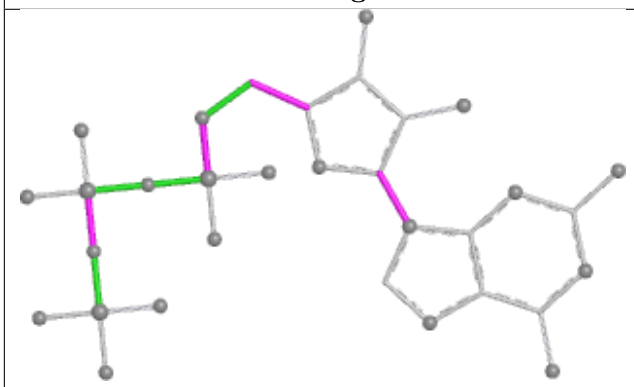

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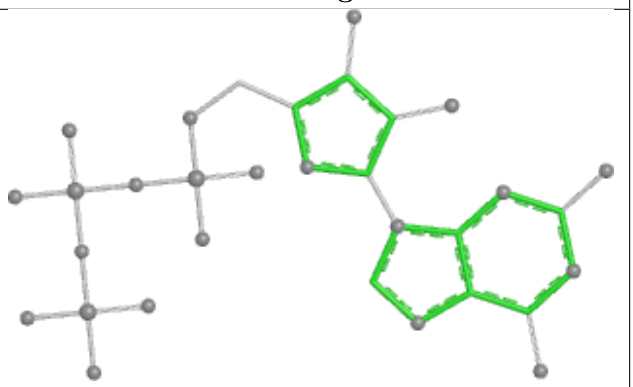
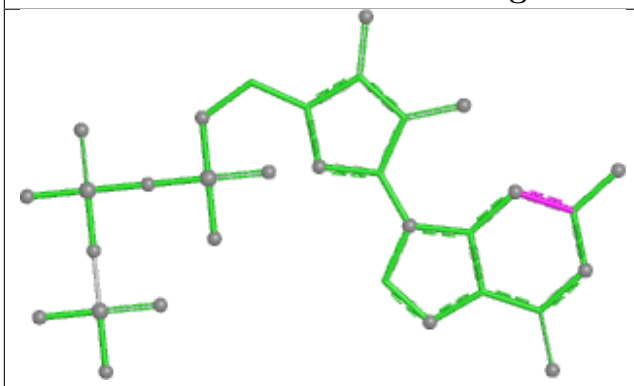


Rings

Ligand GTP OH 501



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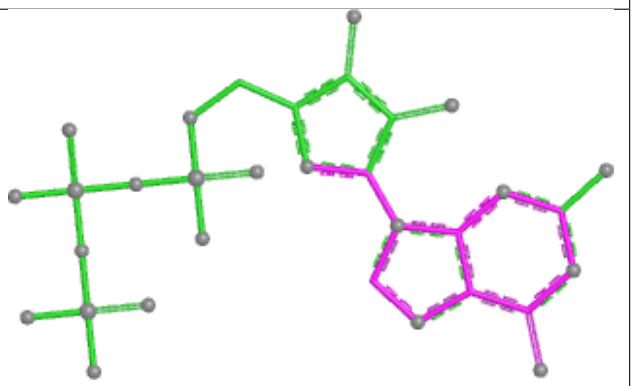
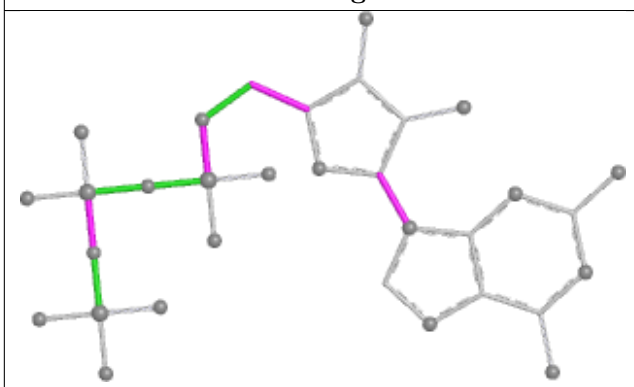


Bond angles



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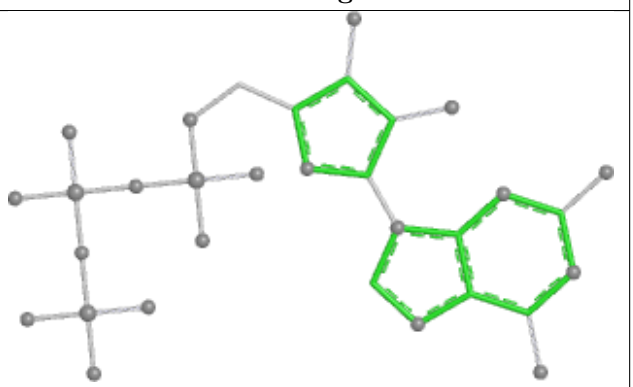

Rings

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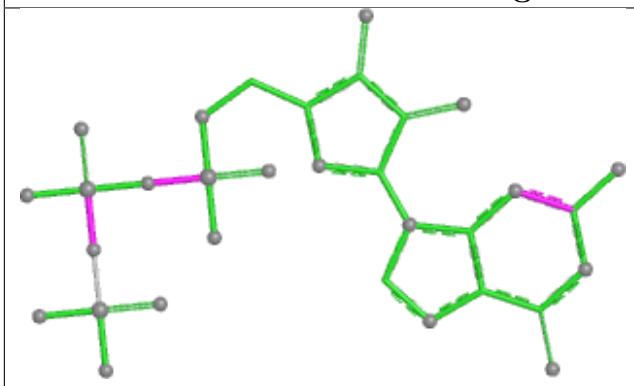
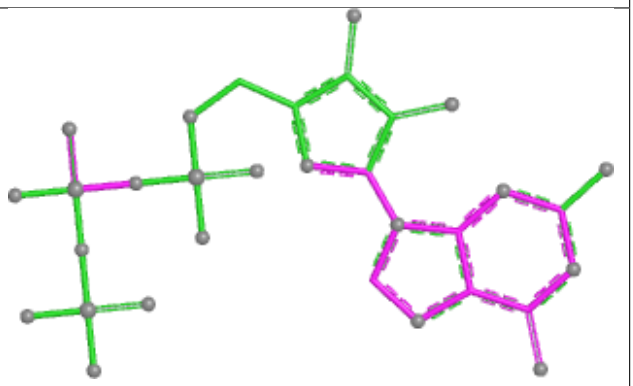


Bond lengths



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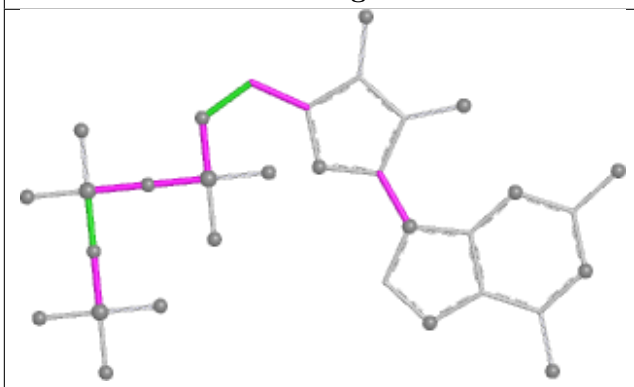
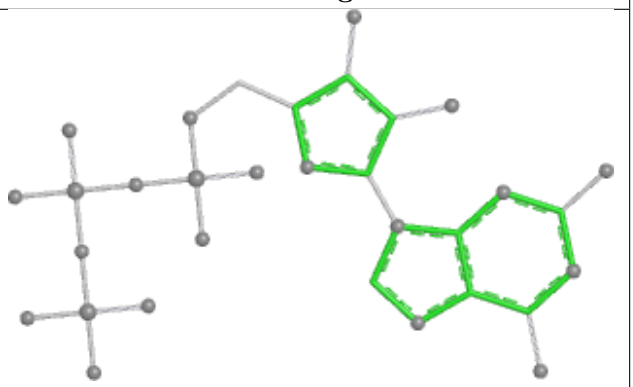
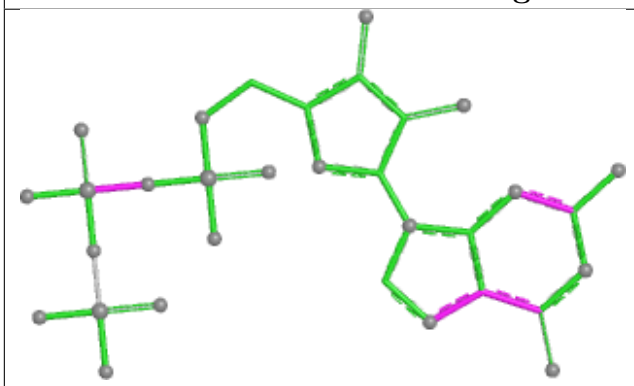


Torsions



Rings

Ligand GTP CL 501



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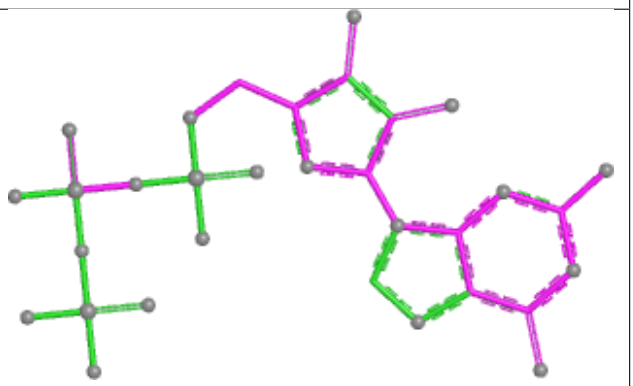

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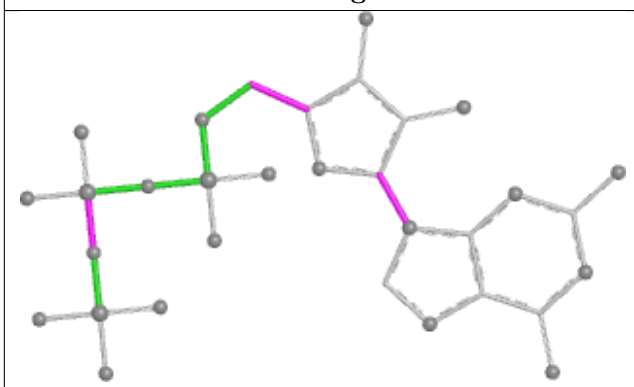

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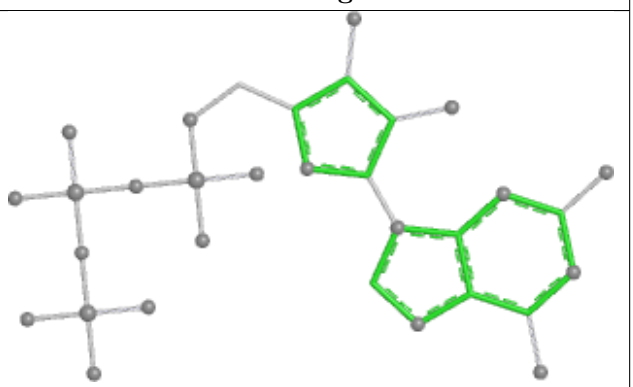
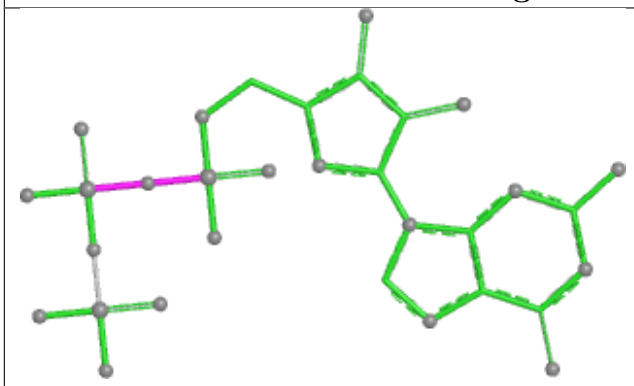


Rings

Ligand GTP EE 501



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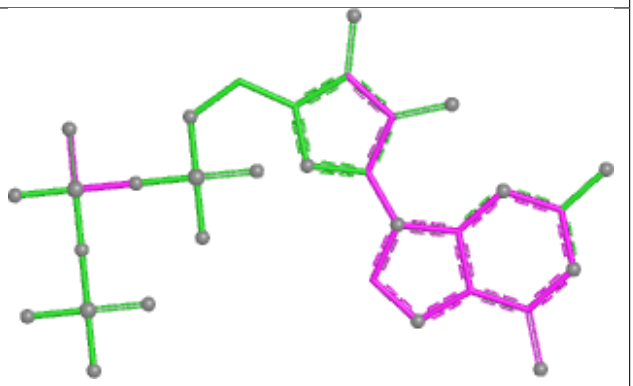

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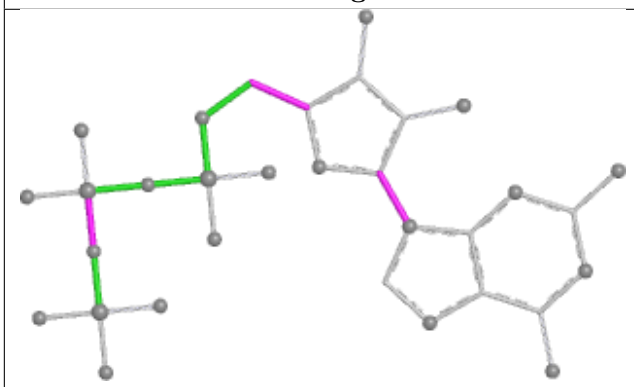

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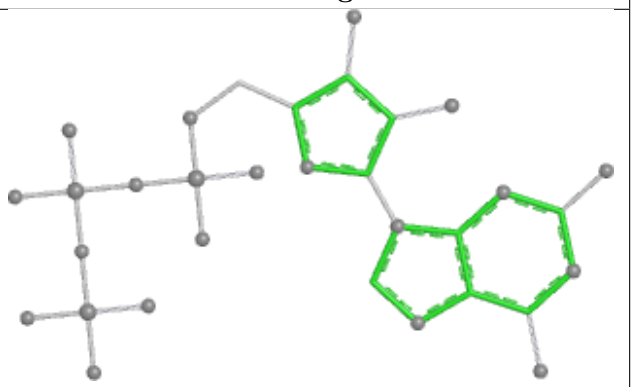
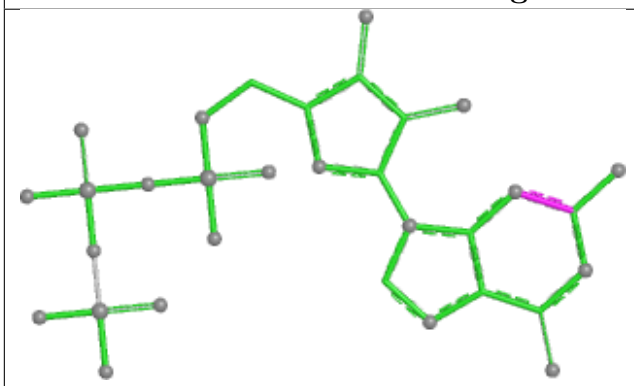


Rings

Ligand GTP QB 501



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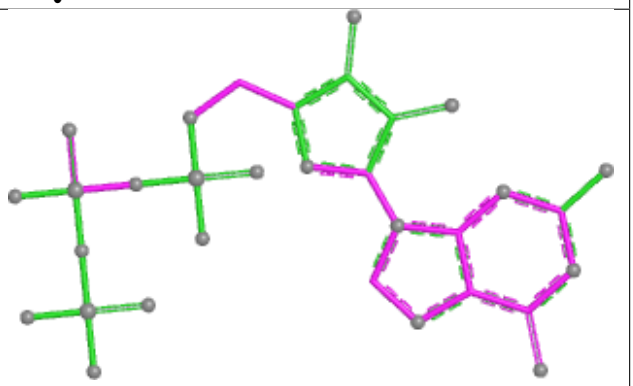

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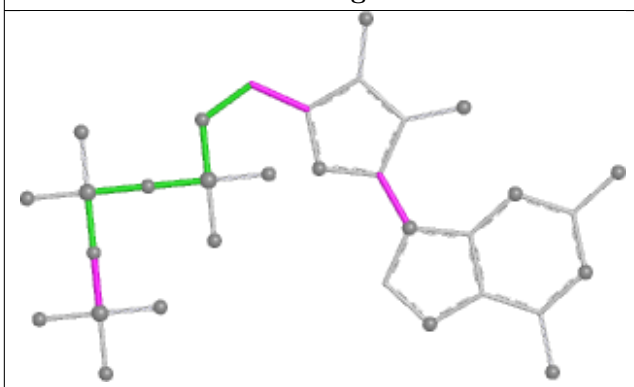

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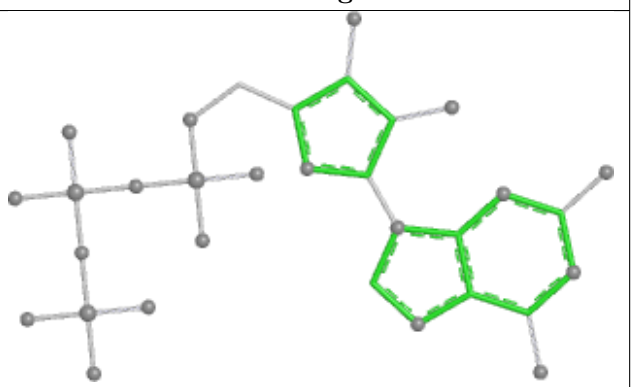
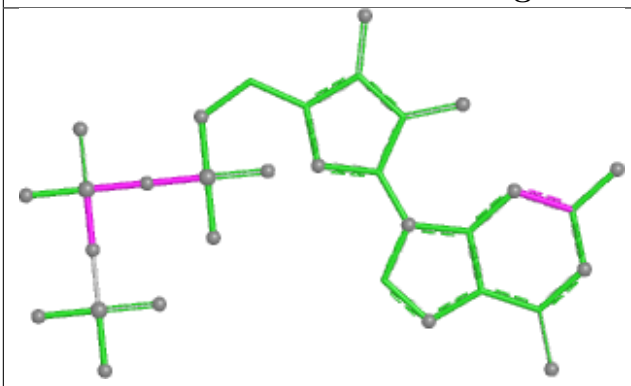


Rings

Ligand GTP SE 501



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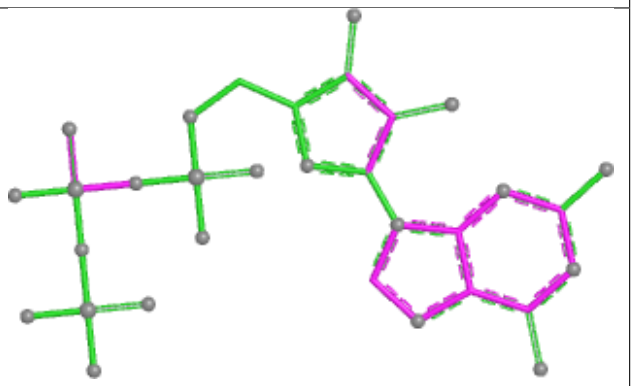

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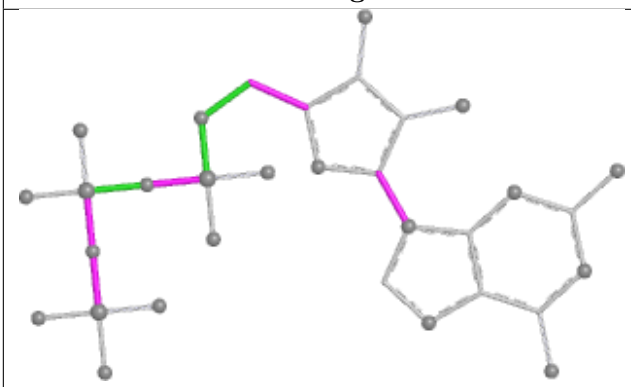

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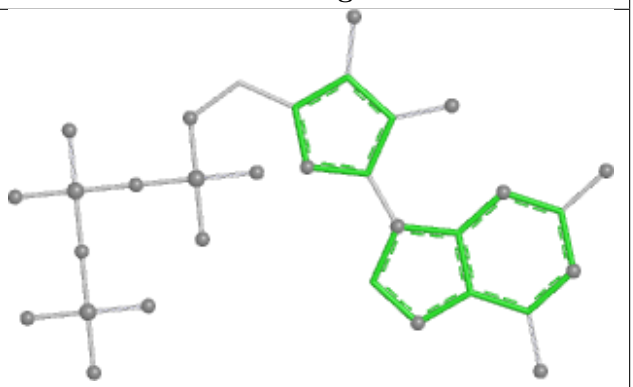
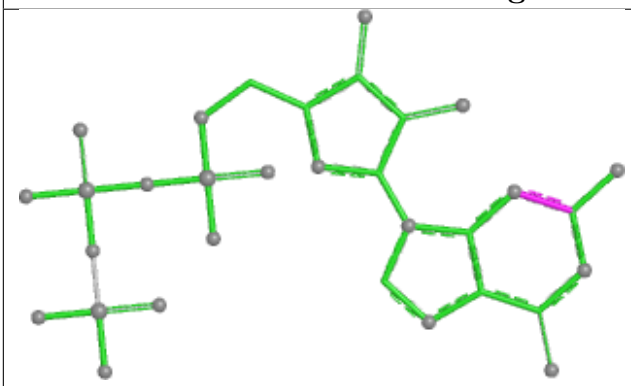


Rings

Ligand GTP WJ 501



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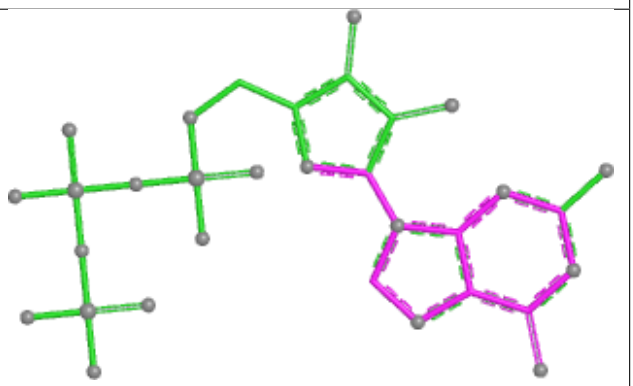

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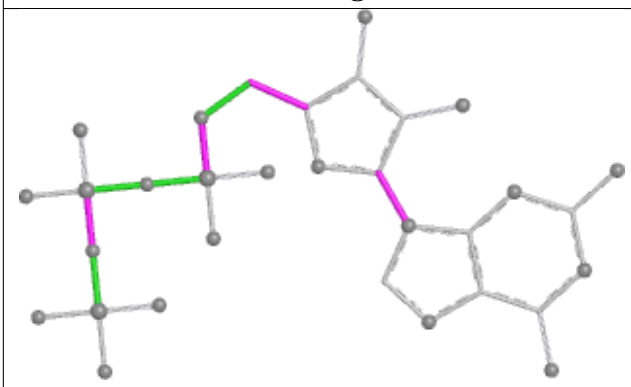

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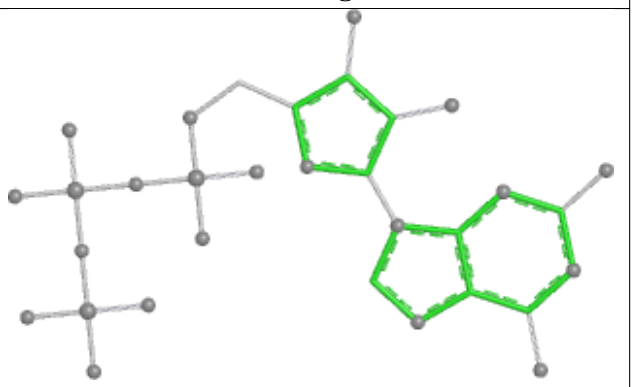
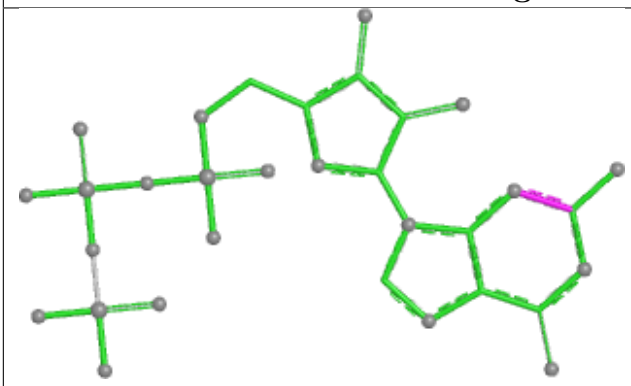


Rings

Ligand GTP LF 501



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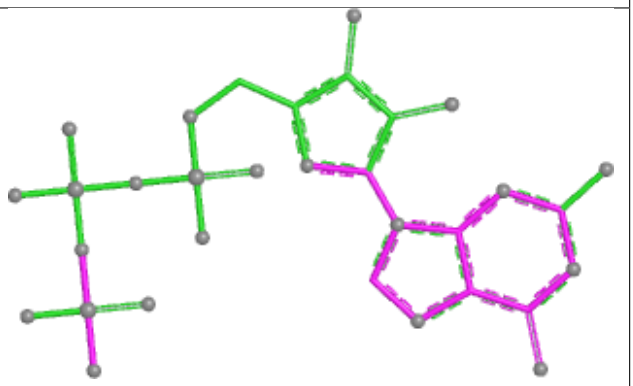

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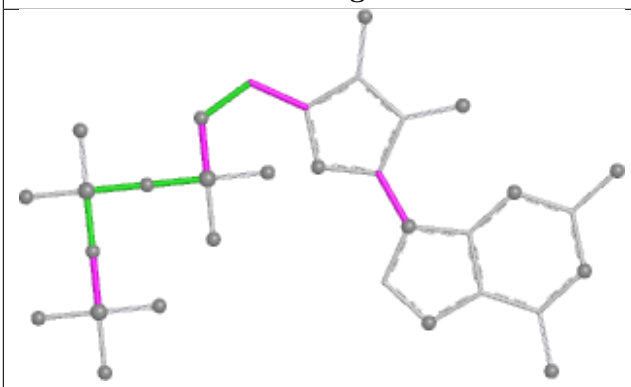

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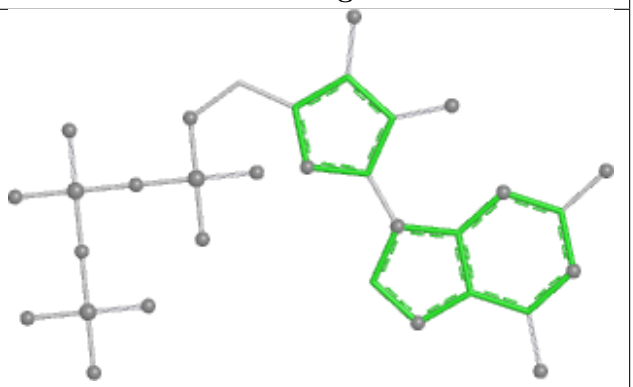
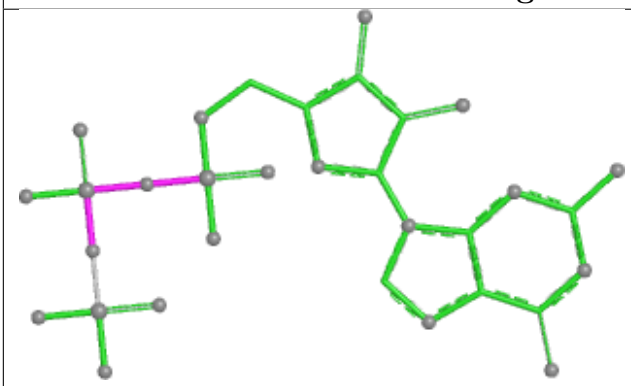


Rings

Ligand GTP TI 501



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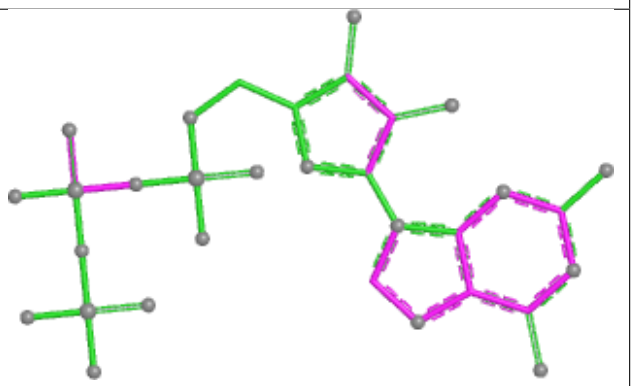

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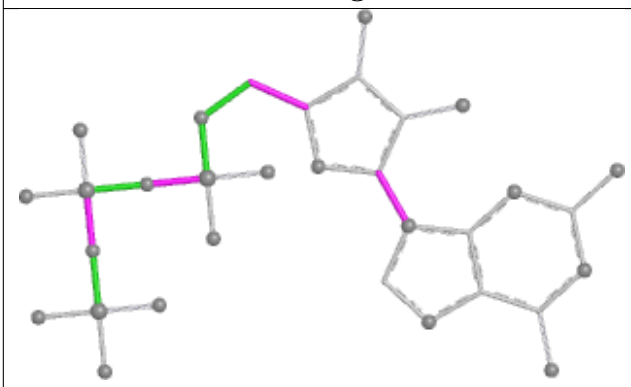

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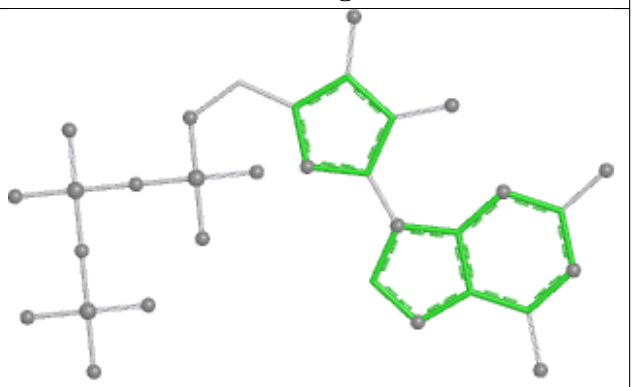
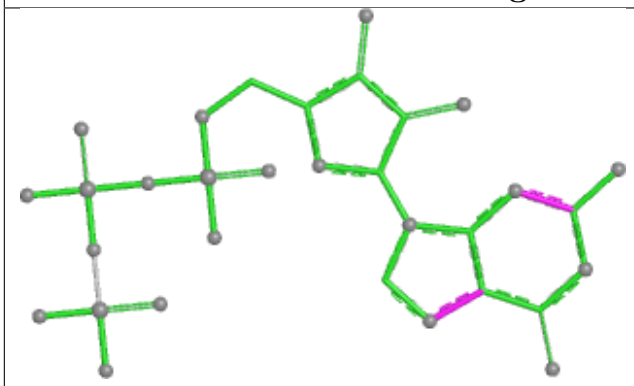


Rings

Ligand GTP DD 501



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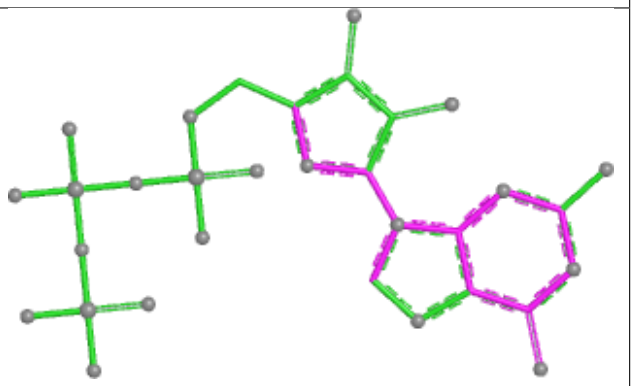

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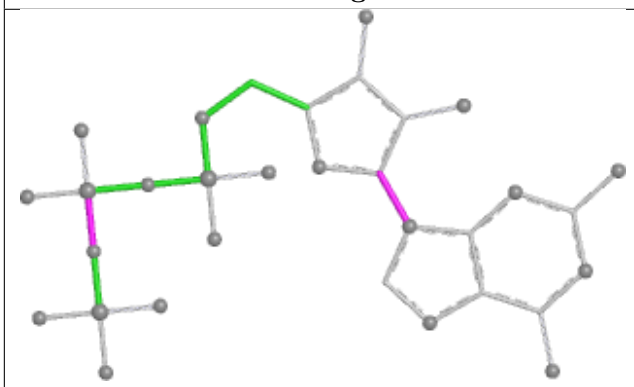

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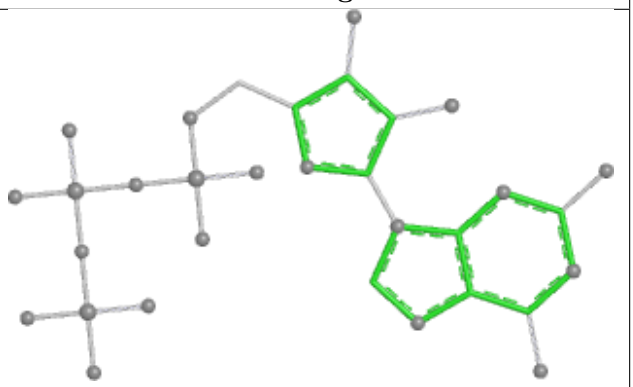

Rings

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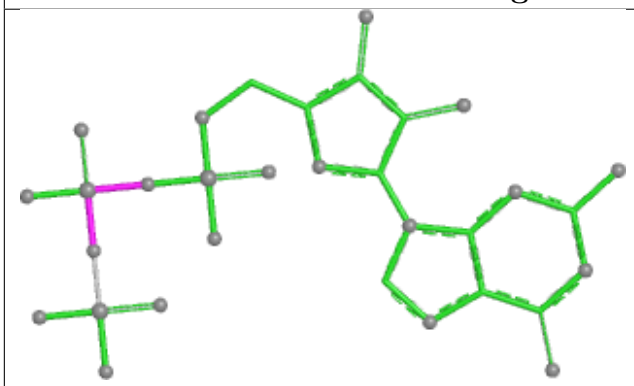

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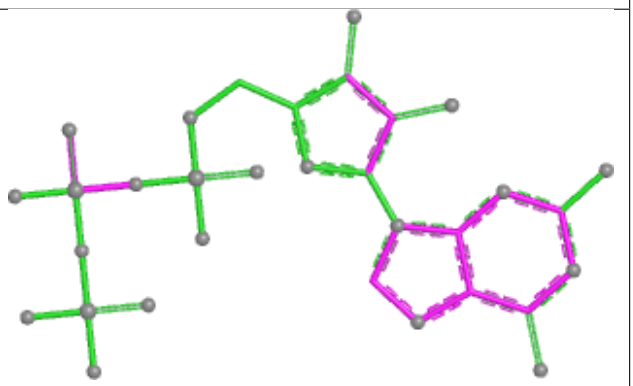

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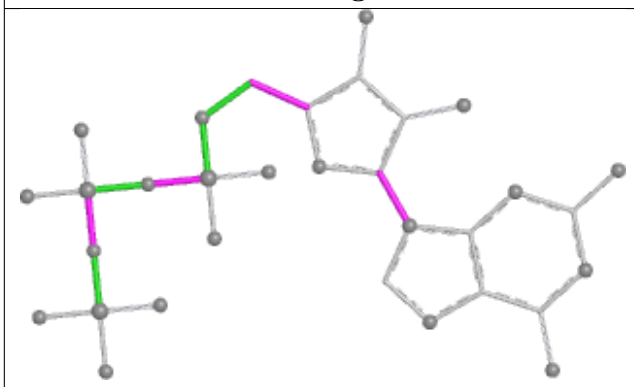

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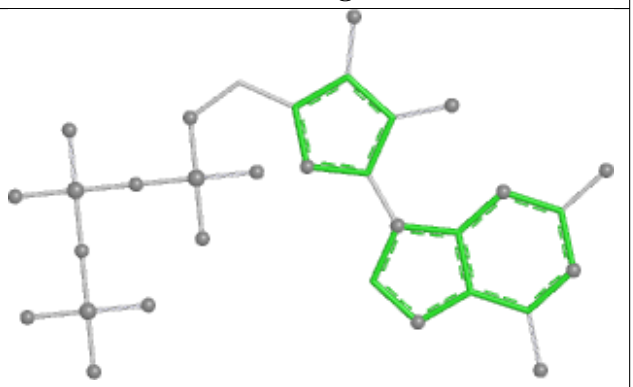
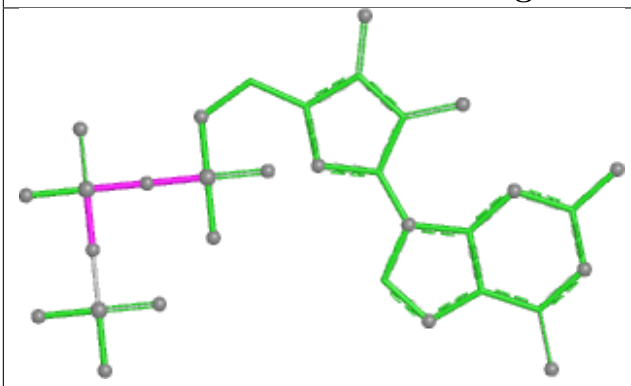


Rings

Ligand GTP NI 501



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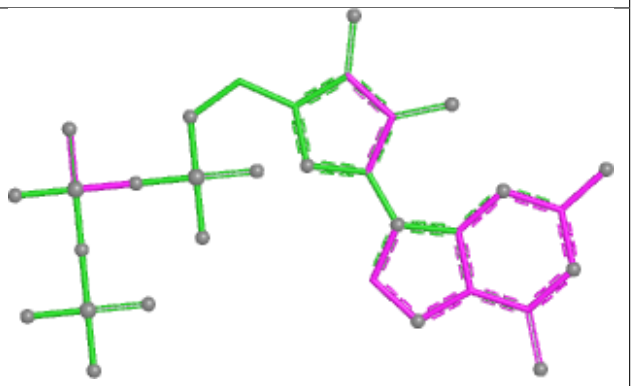

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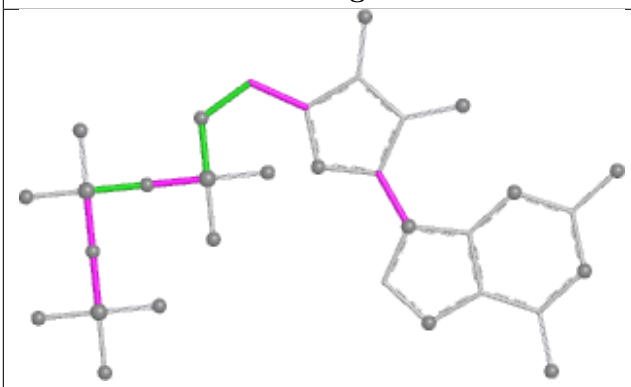

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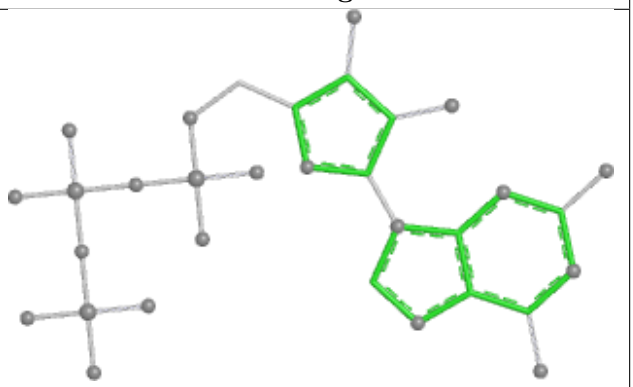
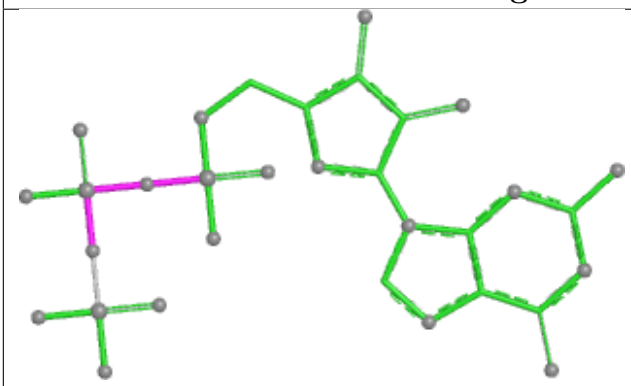


Rings

Ligand GTP PC 501



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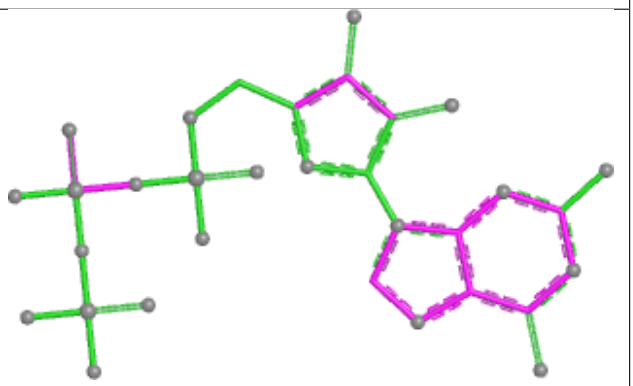

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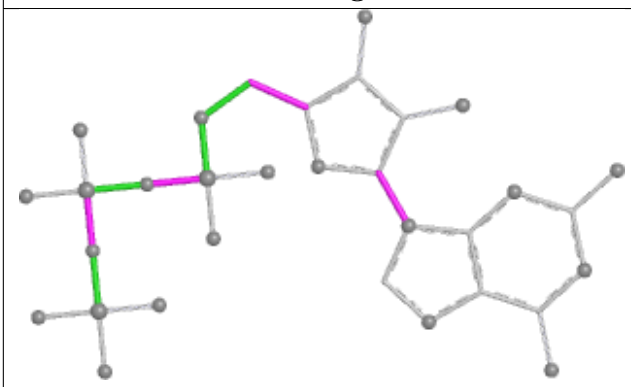

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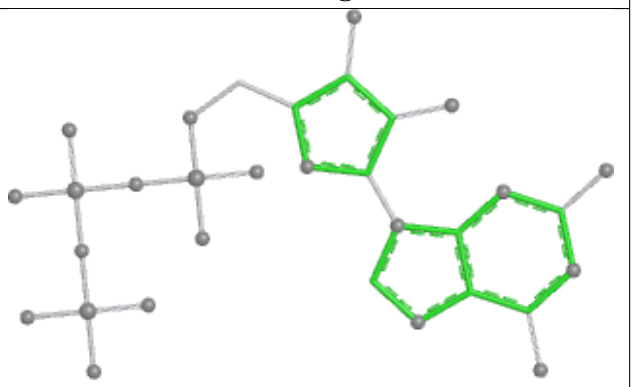
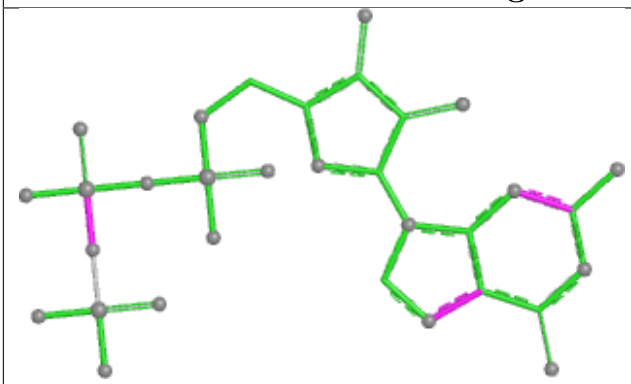


Rings

Ligand GTP GH 501



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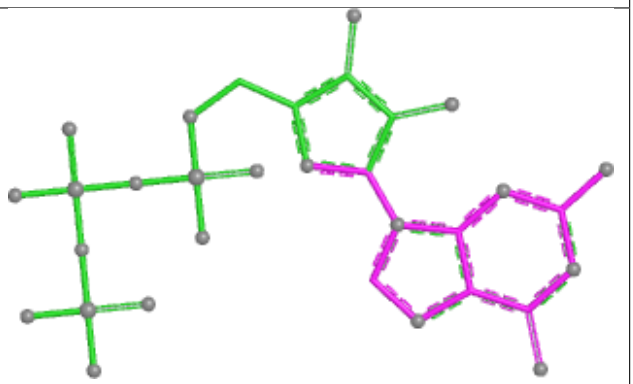
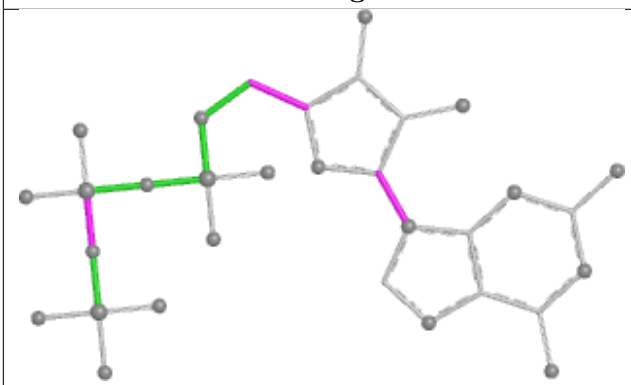


Bond angles



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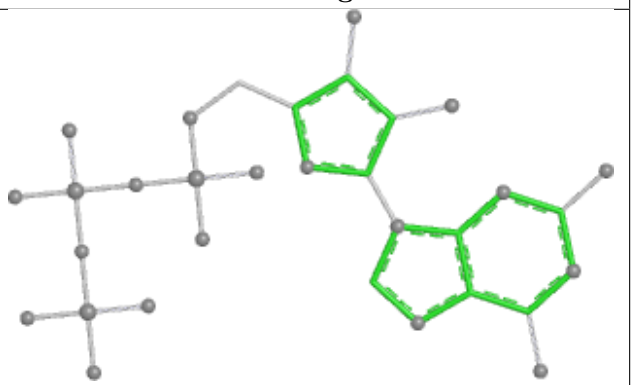
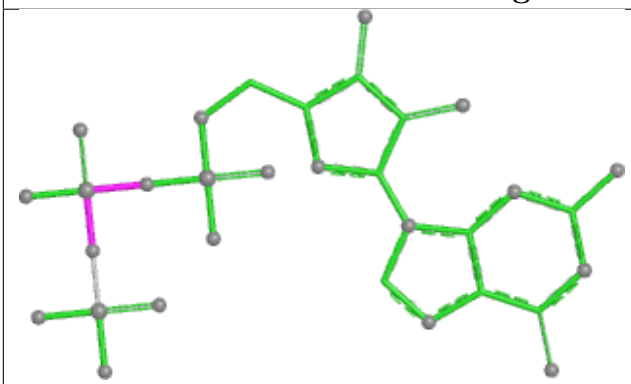


Rings

Ligand GTP SC 501



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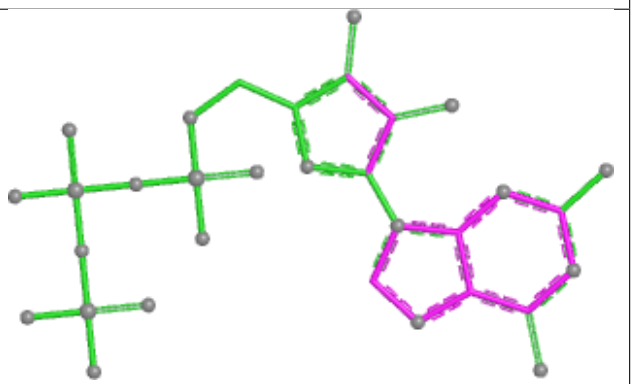
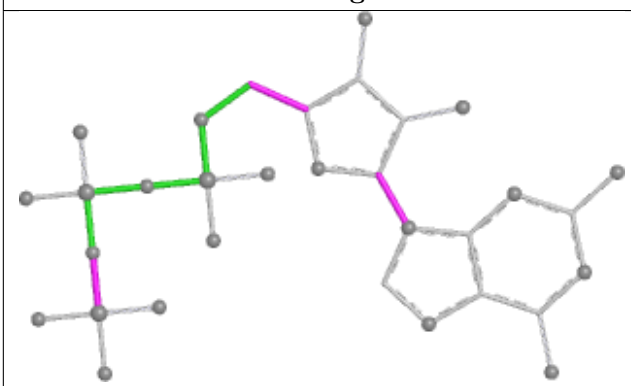


Bond angles



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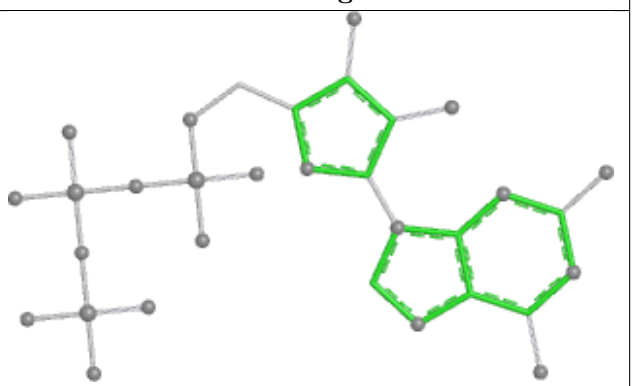
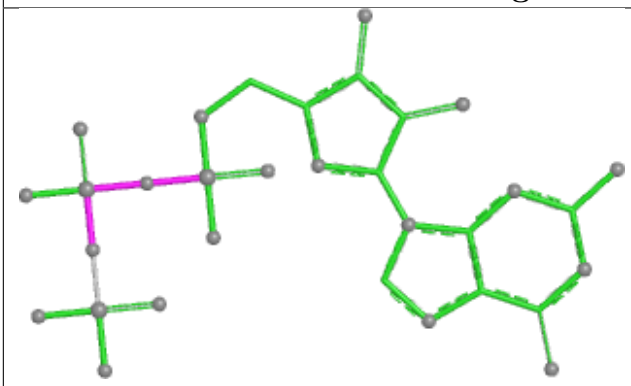


Rings

Ligand GTP LC 501



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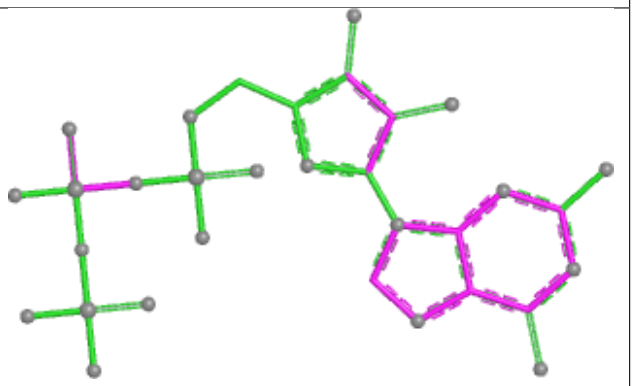

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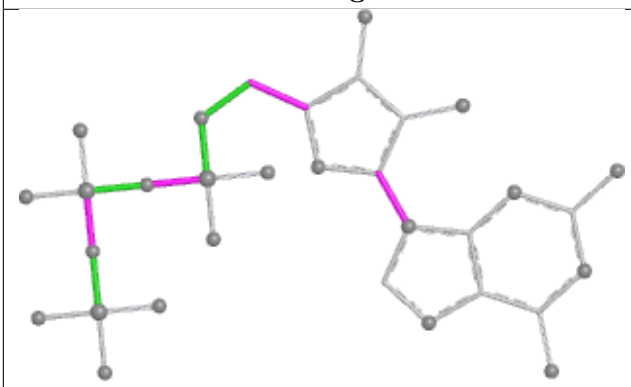
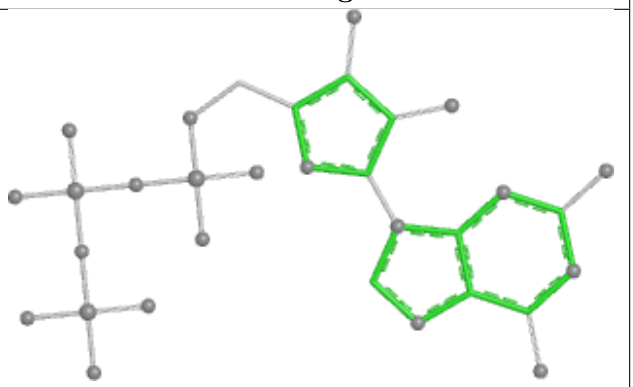
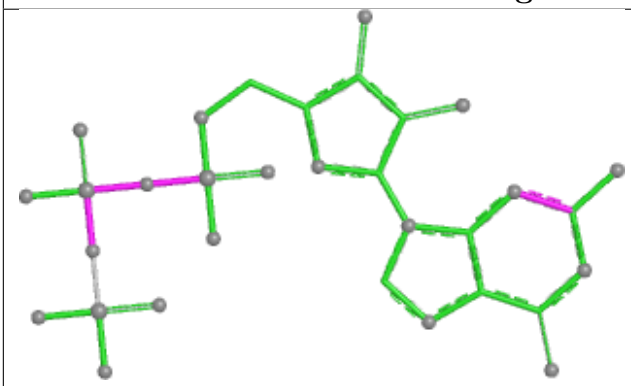


Torsions



Rings

Ligand GTP IA 501



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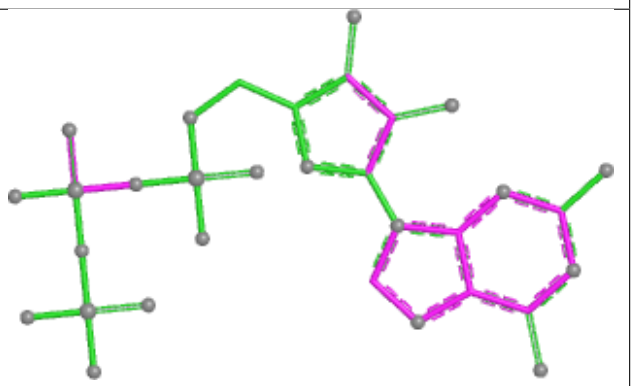

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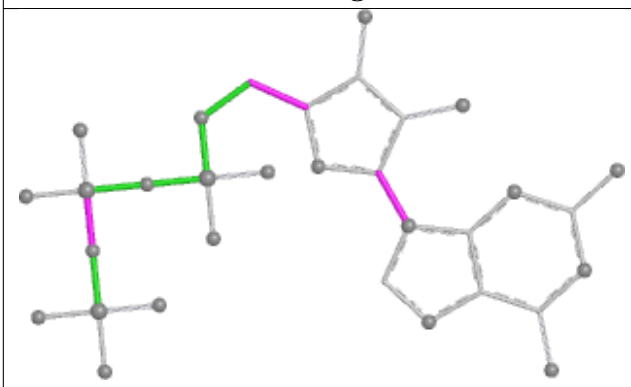

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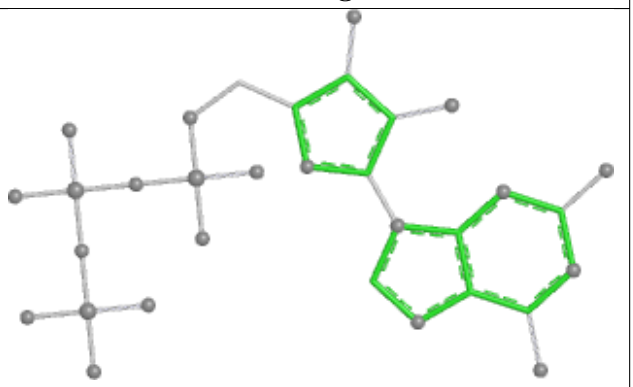
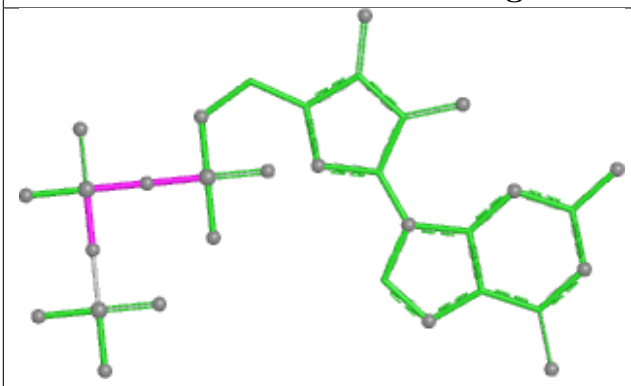


Rings

Ligand GTP CM 501



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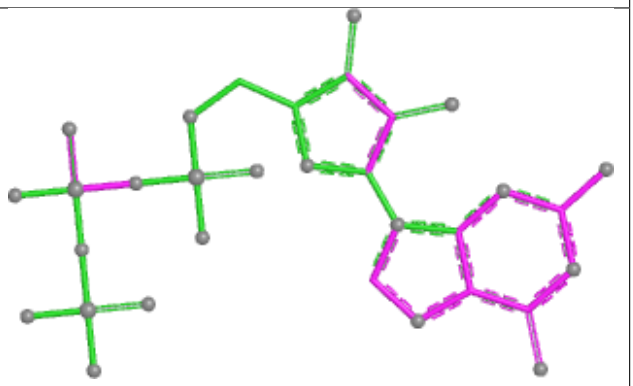

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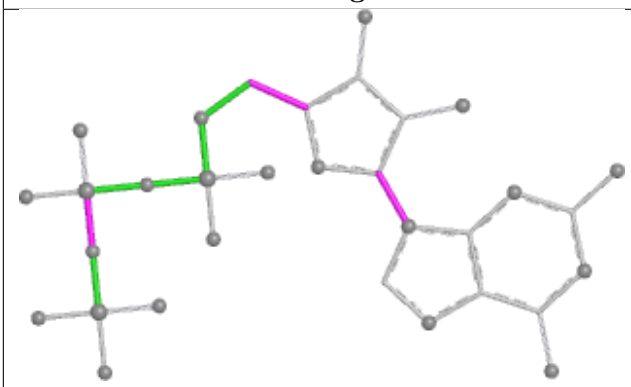

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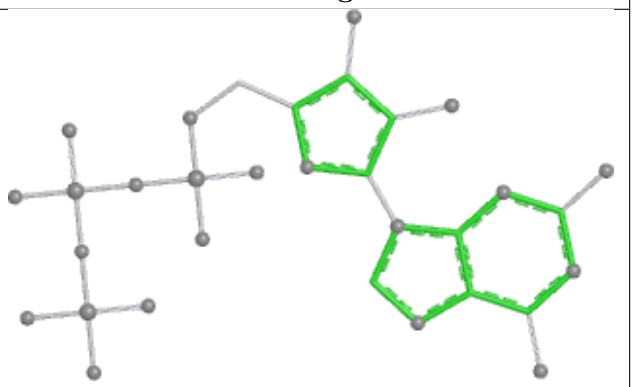
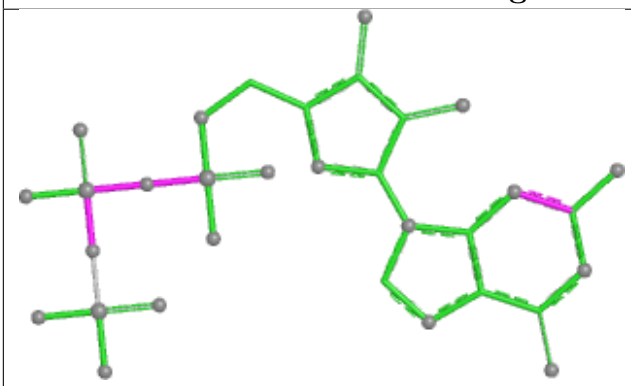


Rings

Ligand GTP PK 501



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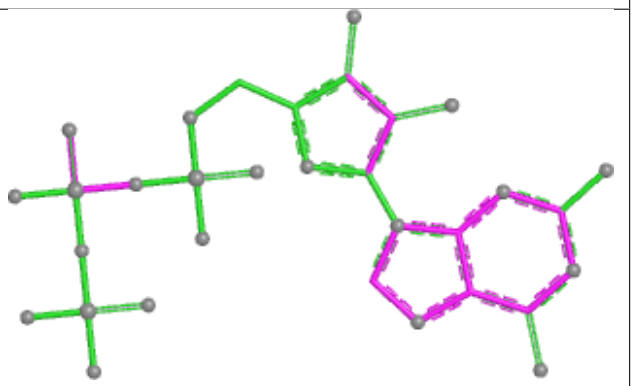

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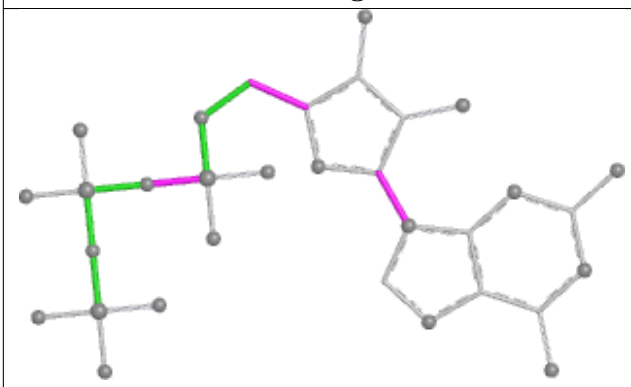

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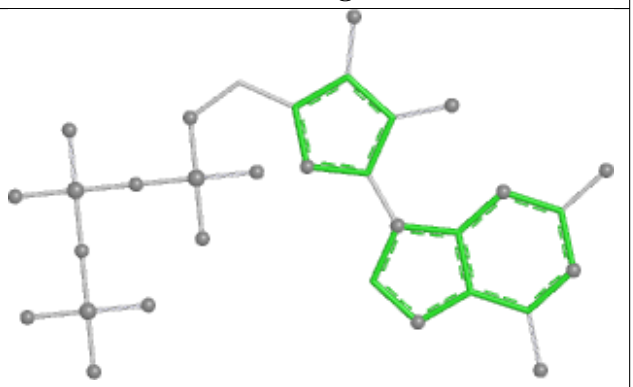
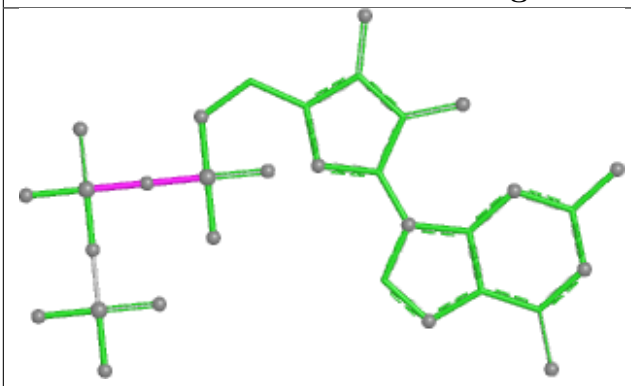


Rings

Ligand GTP FK 501



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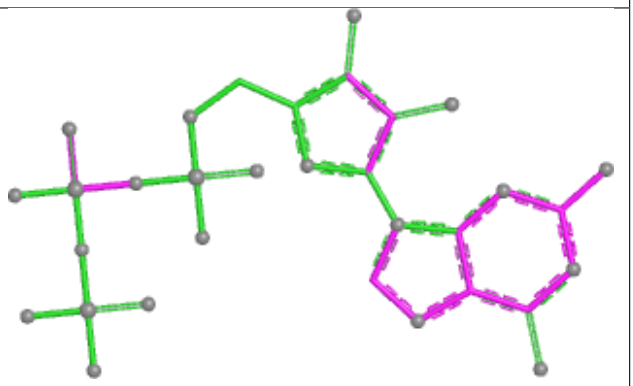

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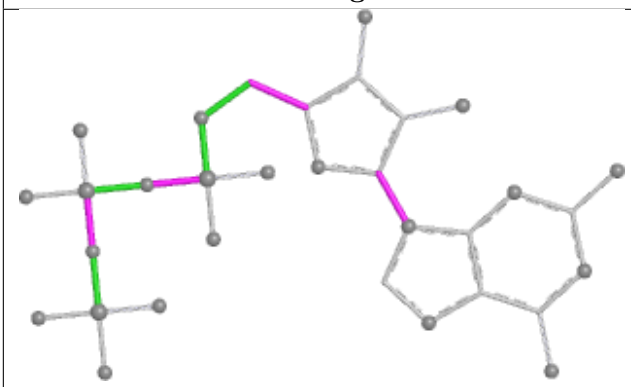

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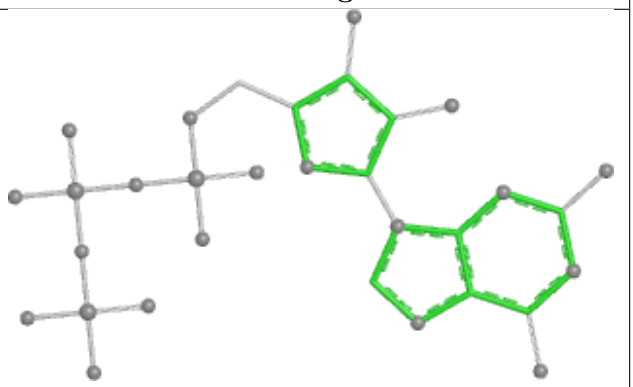
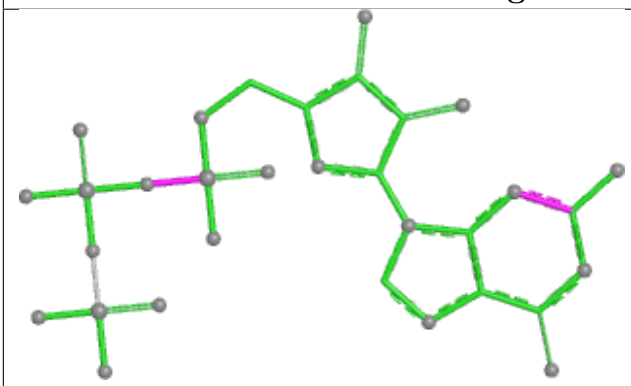


Rings

Ligand GTP HH 501



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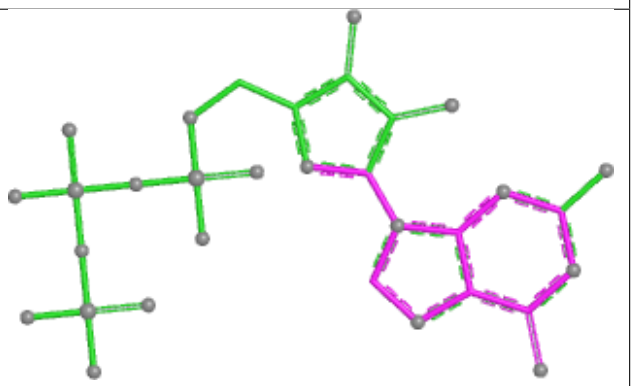

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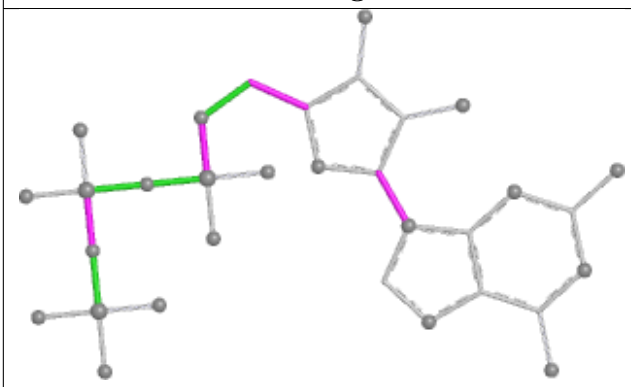

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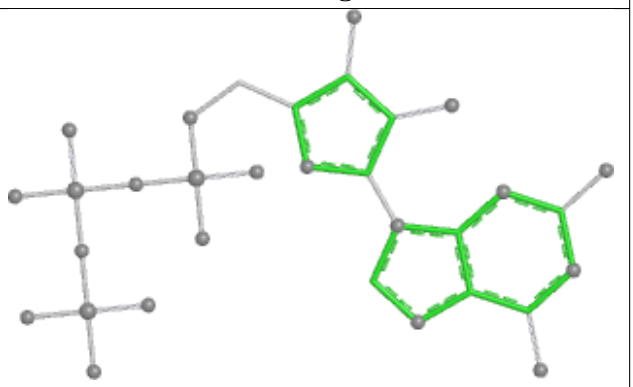
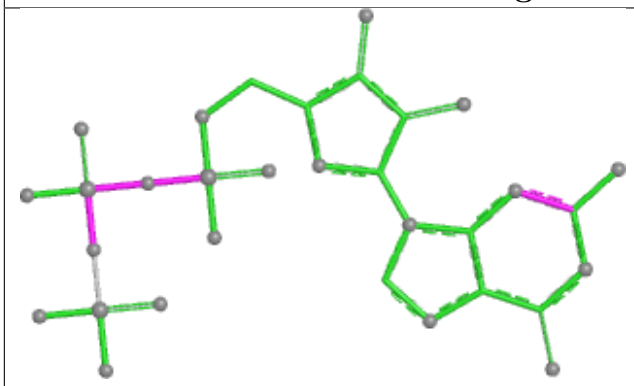


Rings

Ligand GTP LL 501



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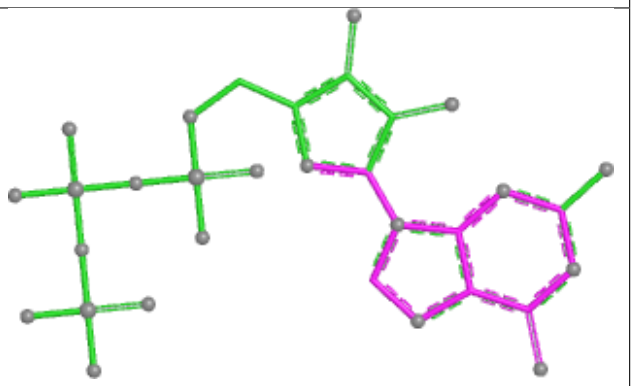

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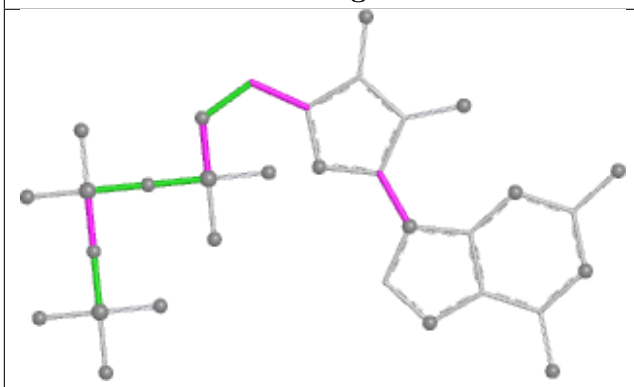

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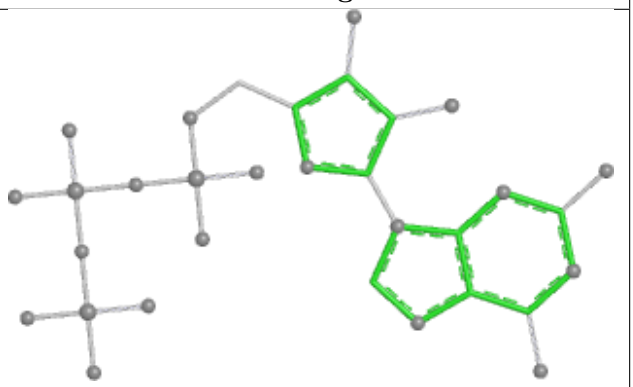

Rings

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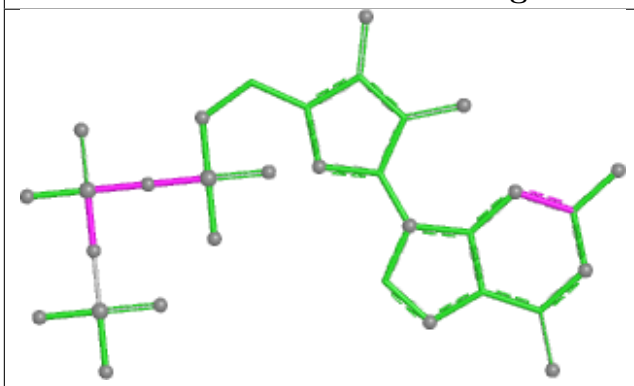

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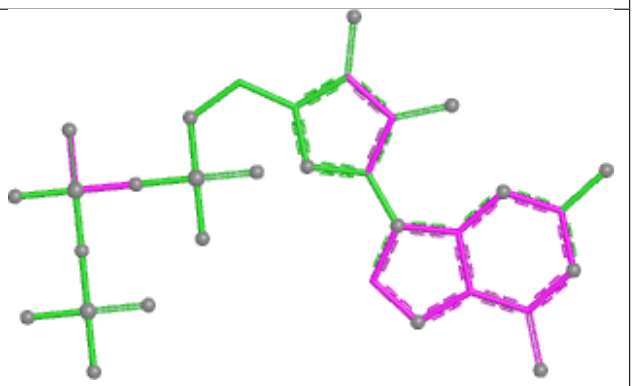

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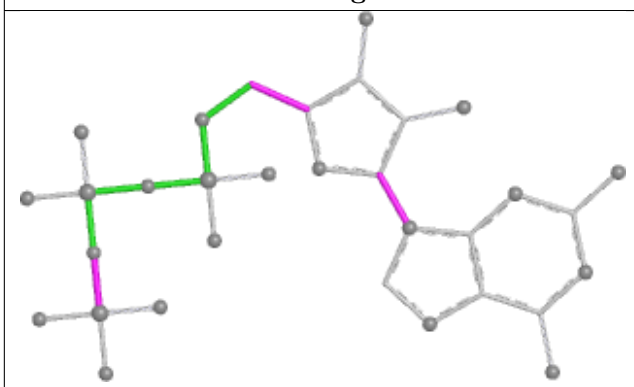

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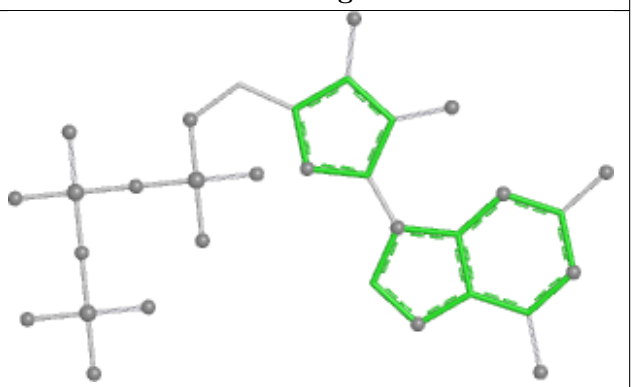

Rings

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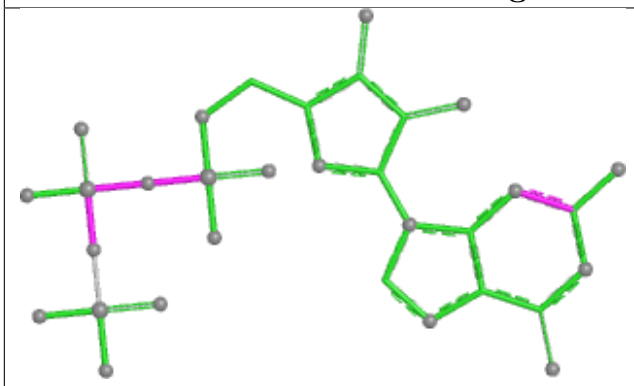

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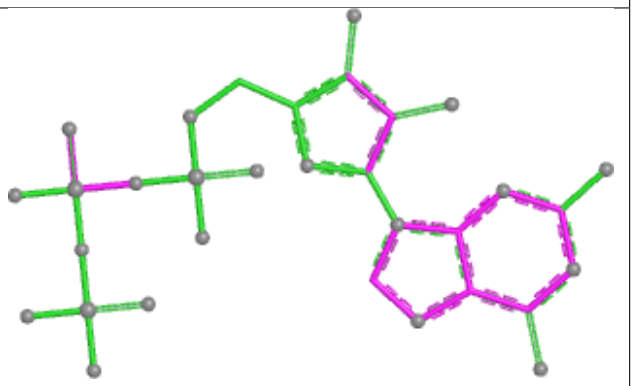

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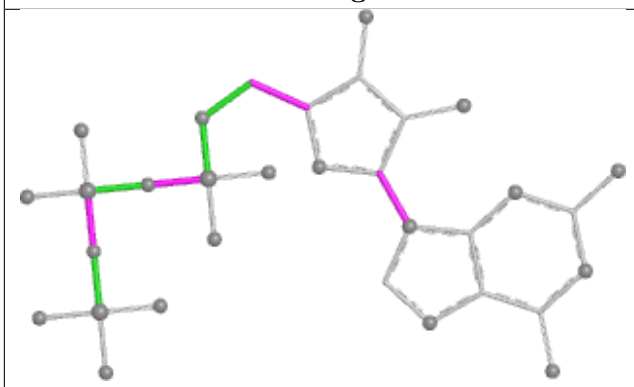

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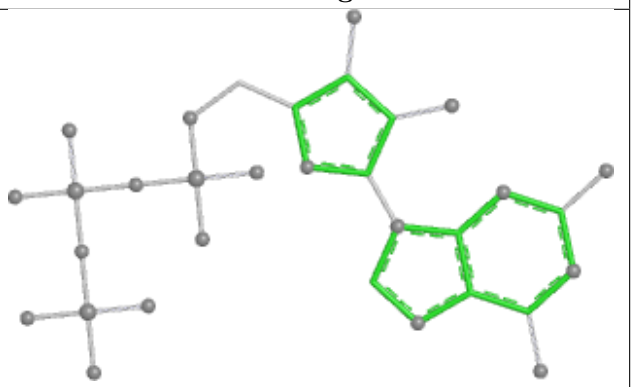

Rings

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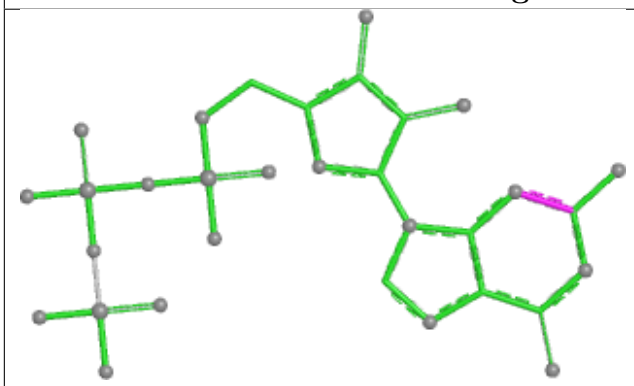

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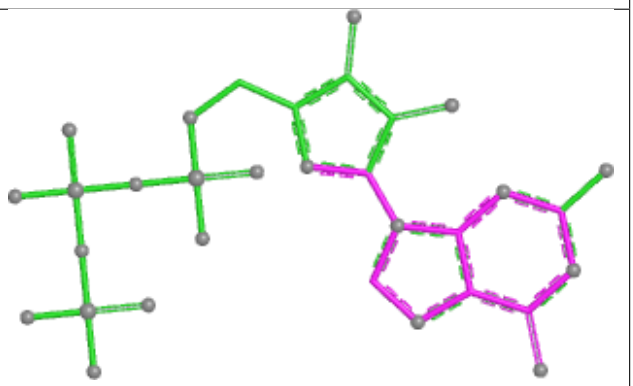

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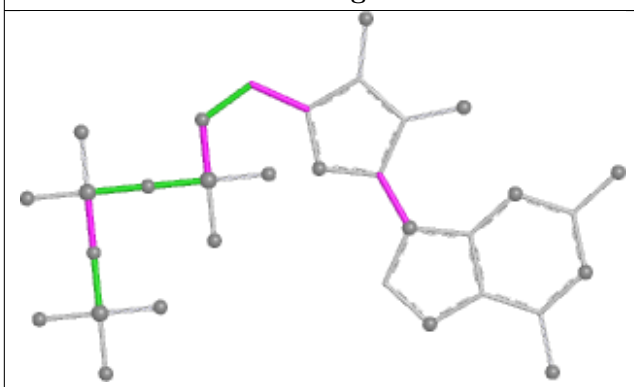

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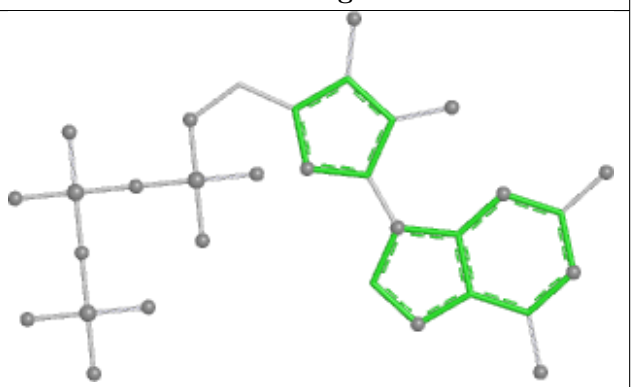
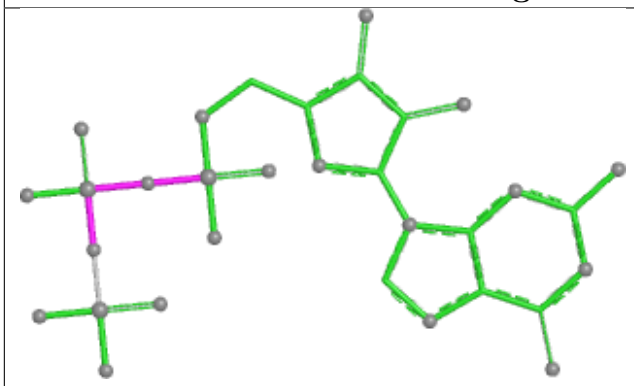


Rings

Ligand GTP PE 501



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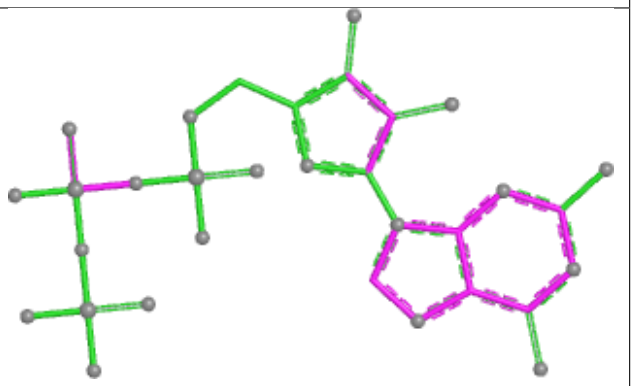

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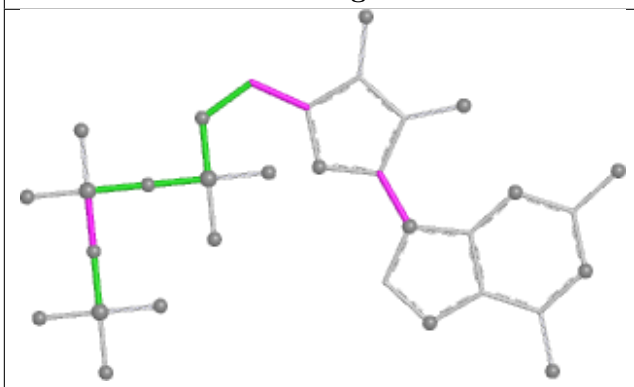

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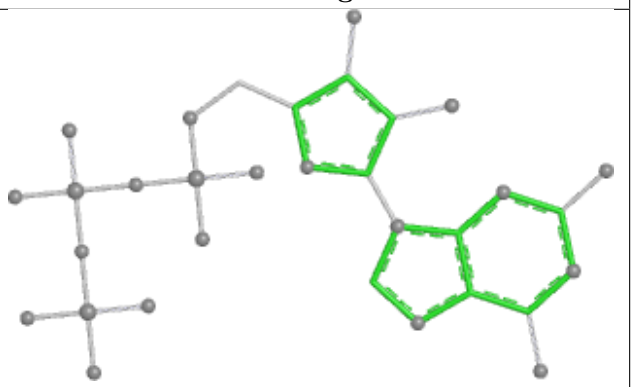
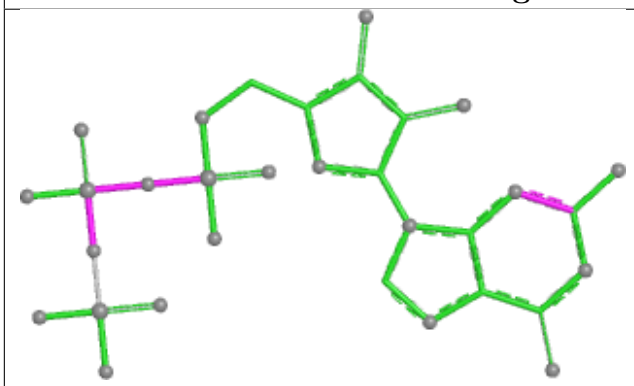


Rings

Ligand GTP RL 501



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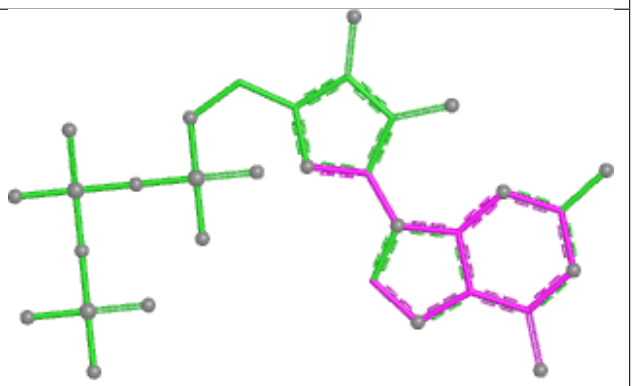

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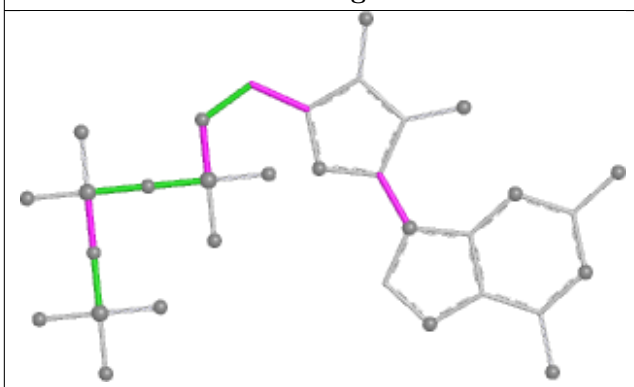

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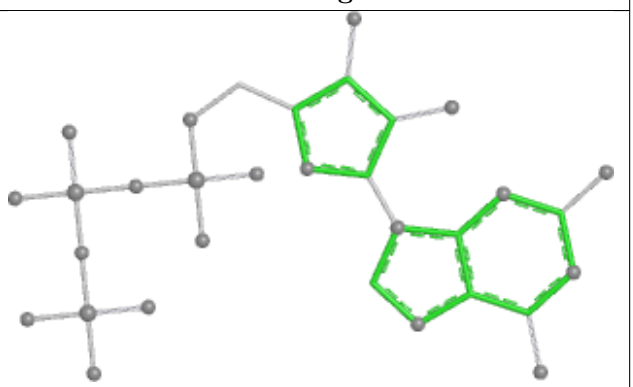
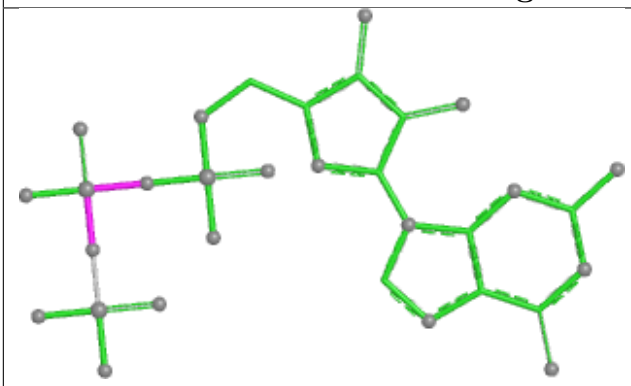


Rings

Ligand GTP BI 501



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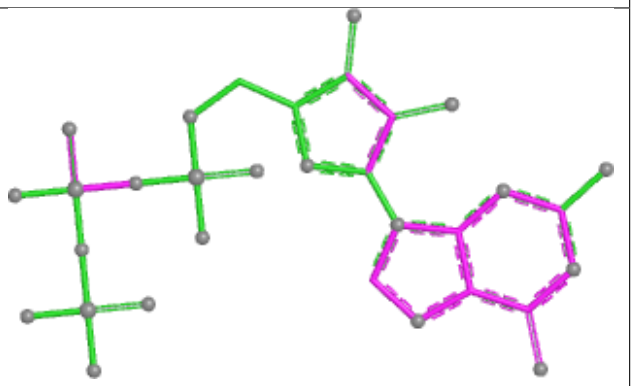
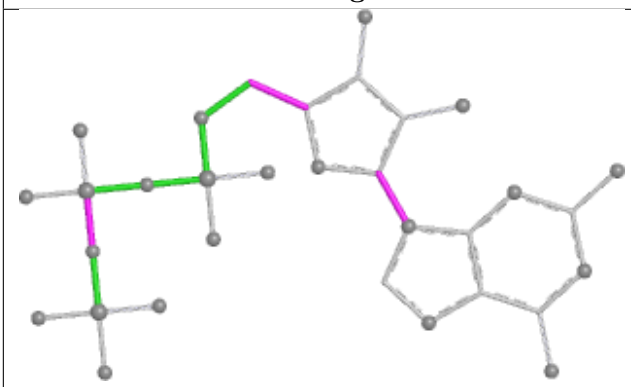


Bond angles



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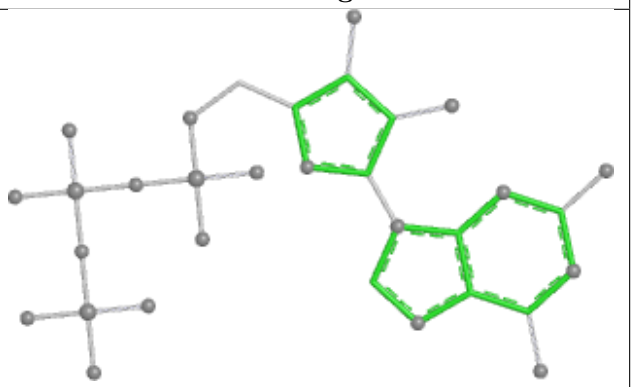
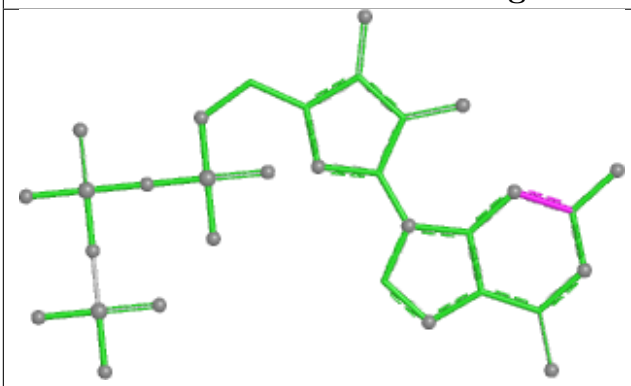


Rings

Ligand GTP RH 501



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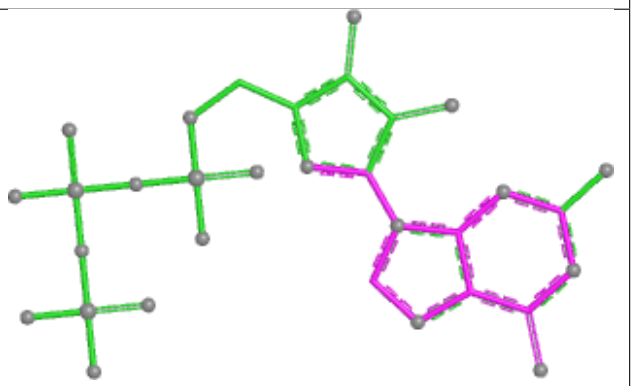

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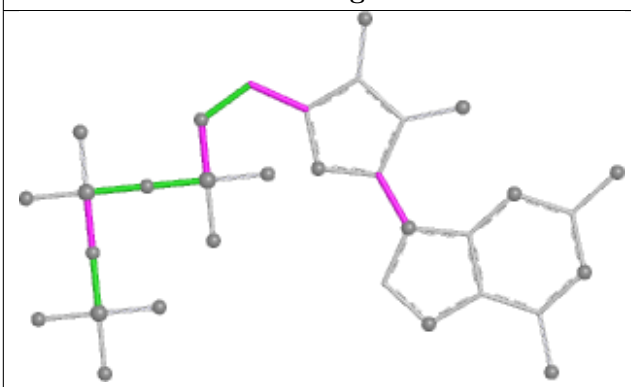

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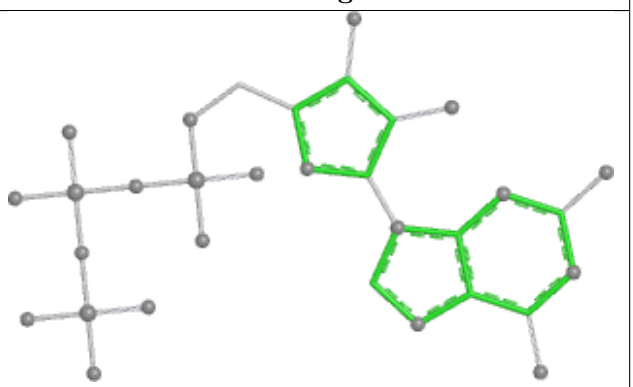
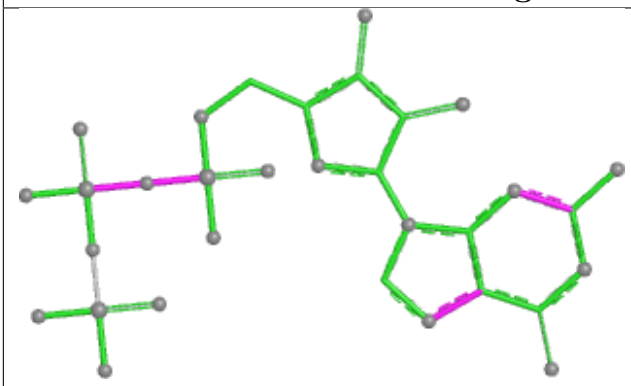


Rings

Ligand GTP SF 501



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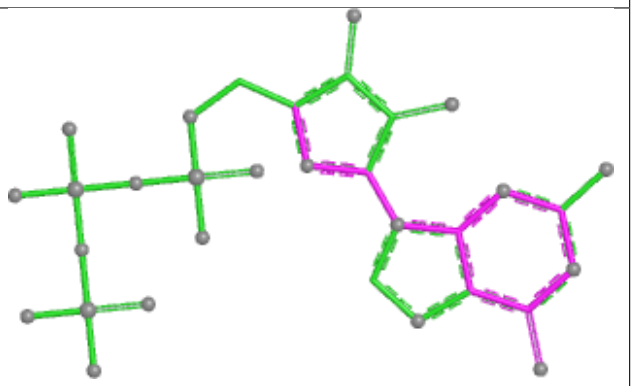

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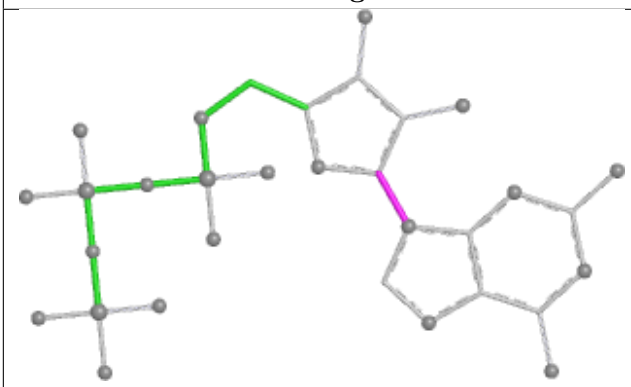
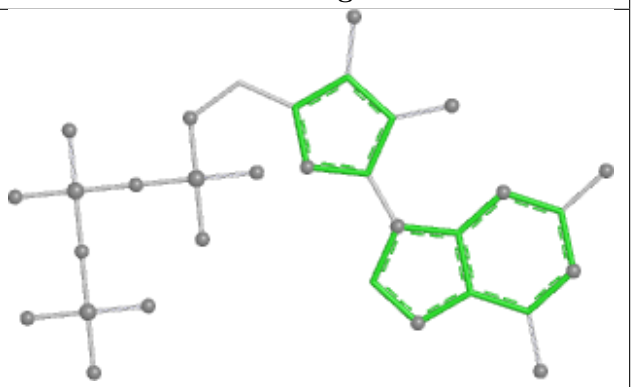
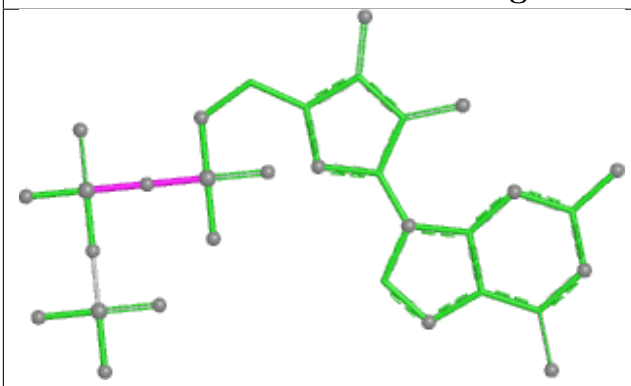


Torsions



Rings

Ligand GTP CC 501



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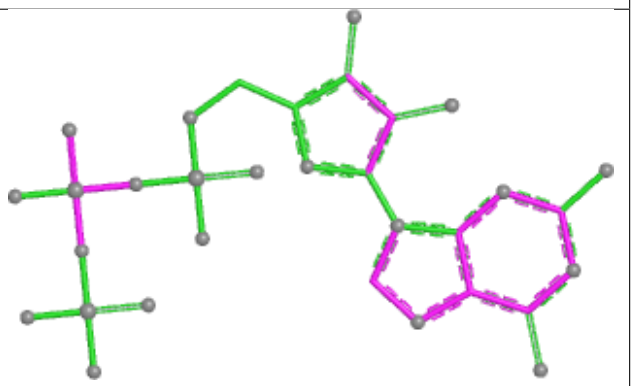

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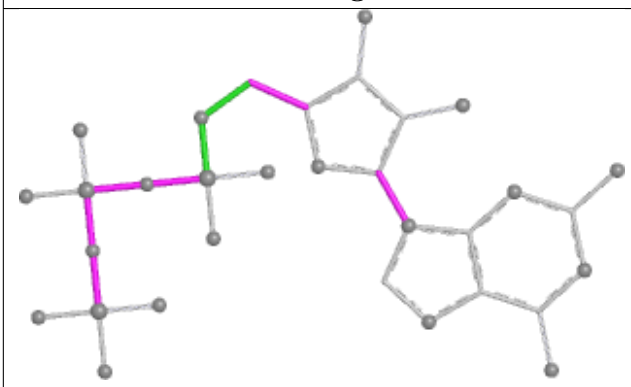

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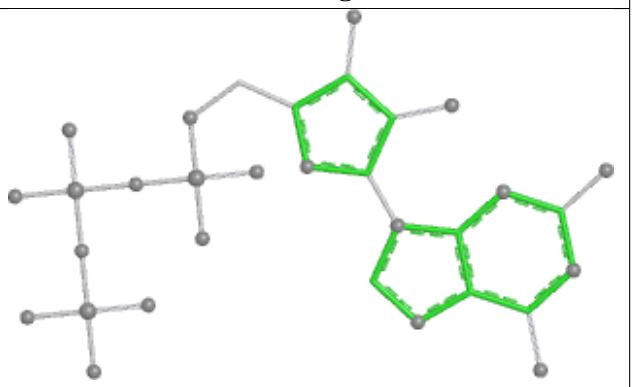
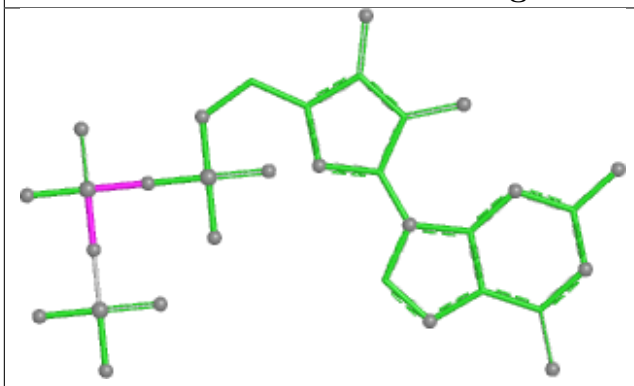


Rings

Ligand GTP VG 501



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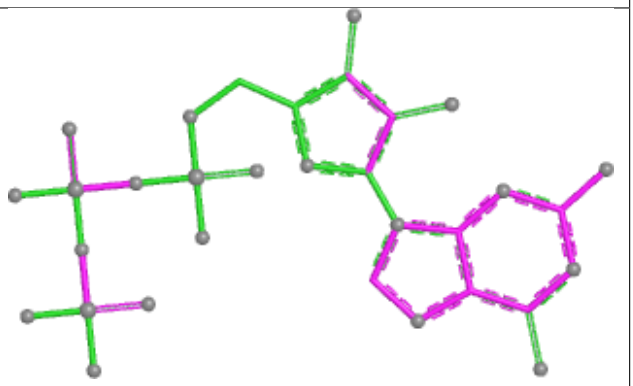

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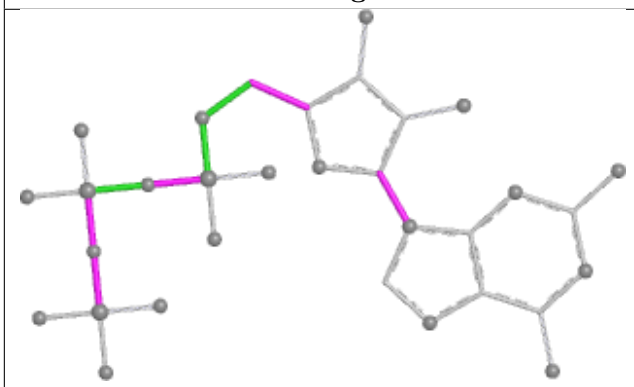

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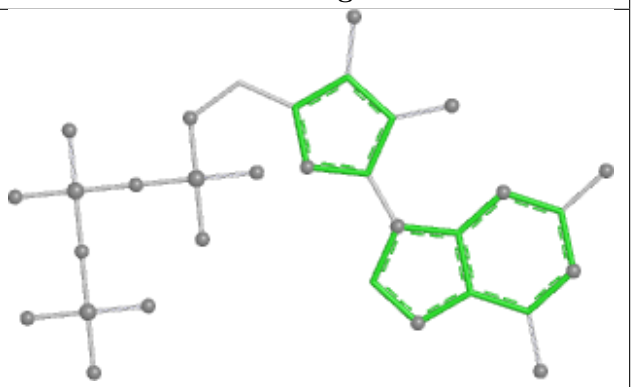
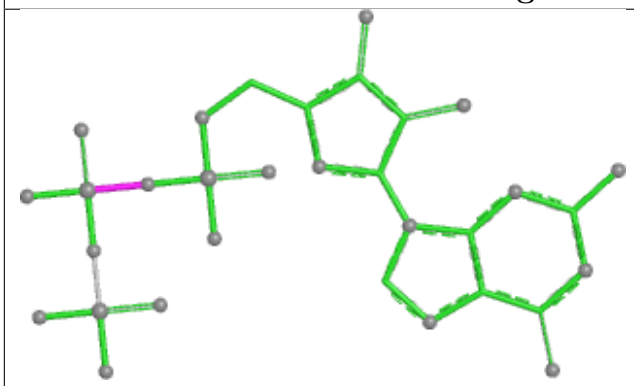


Rings

Ligand GTP IC 501



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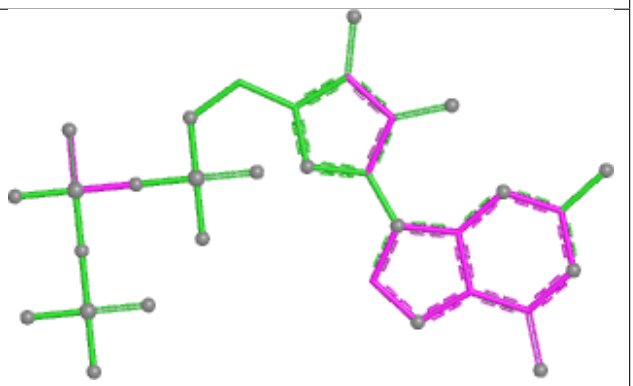

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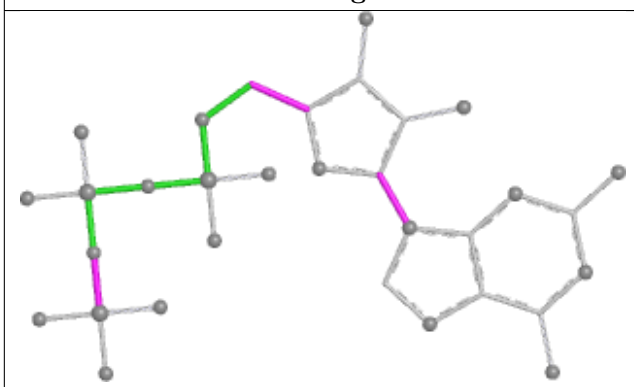

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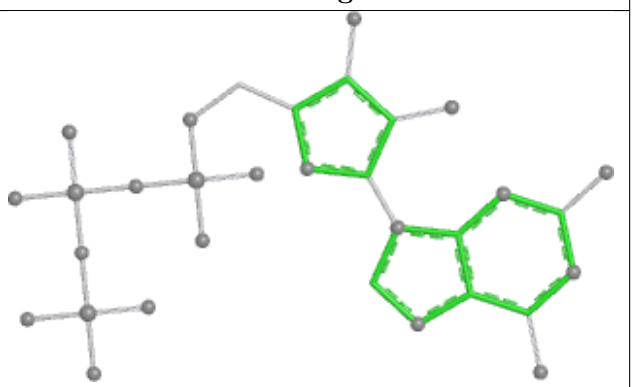

Rings

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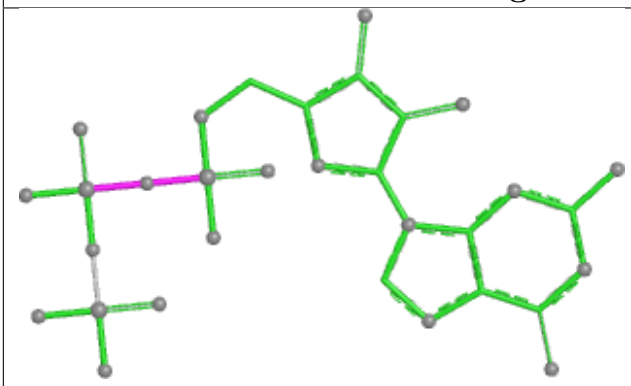

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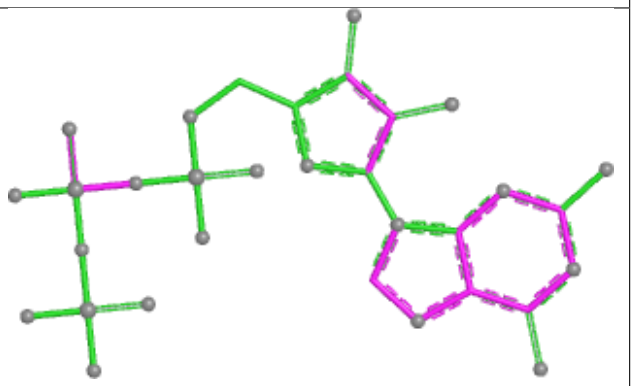

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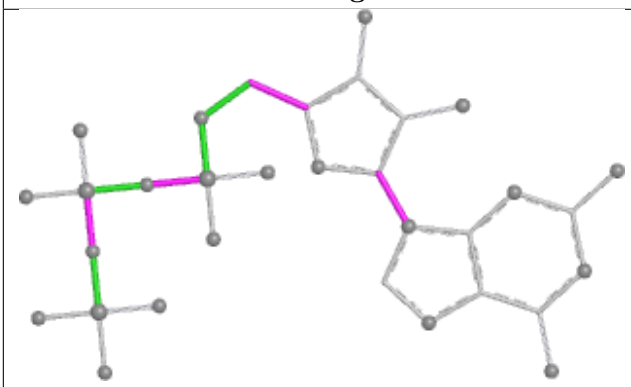

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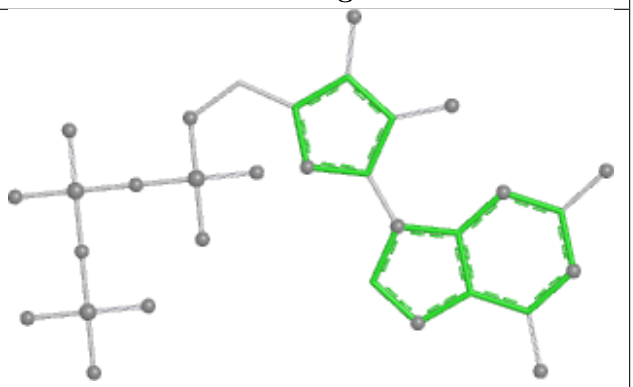

Rings

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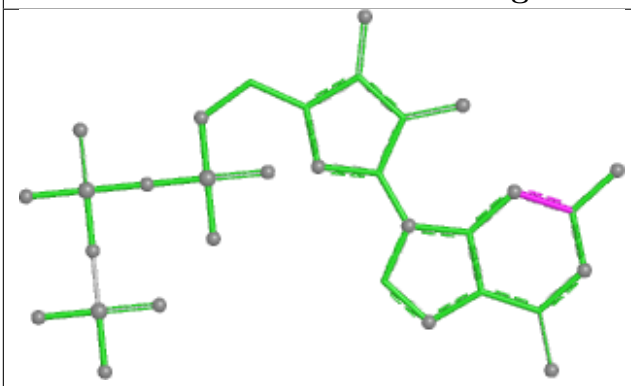

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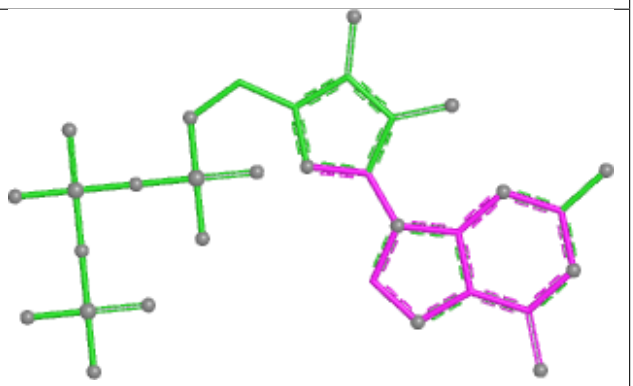

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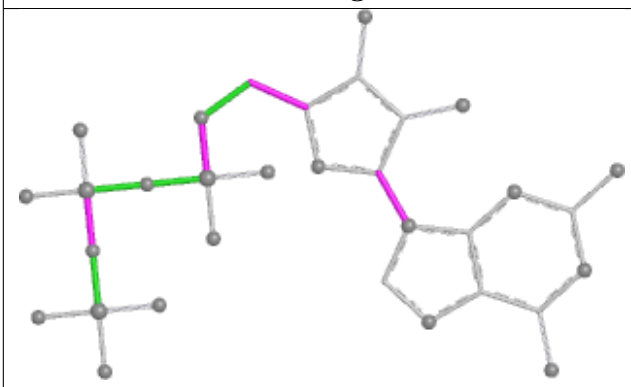

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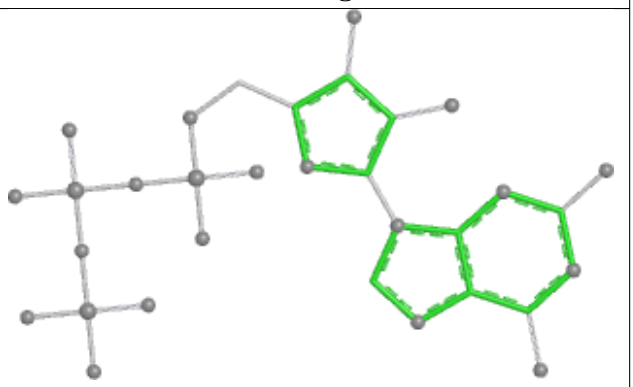
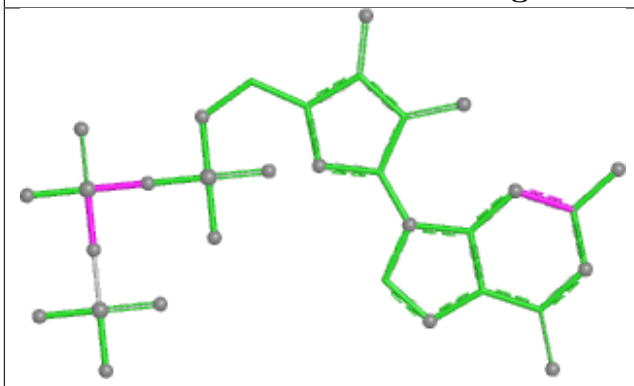


Rings

Ligand GTP BC 501



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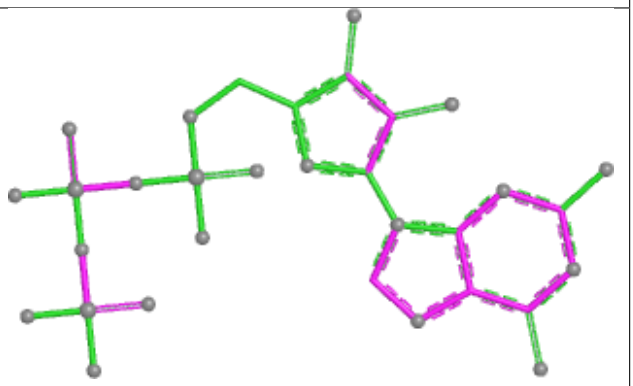

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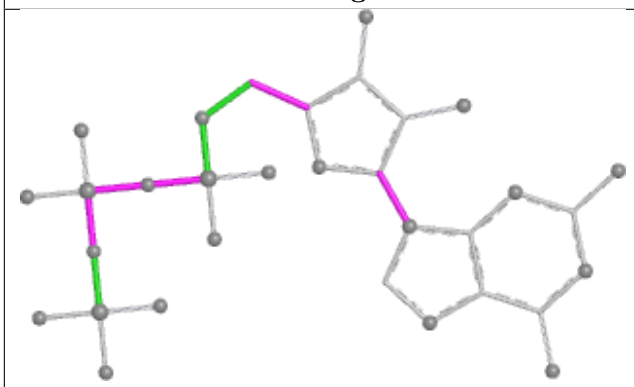

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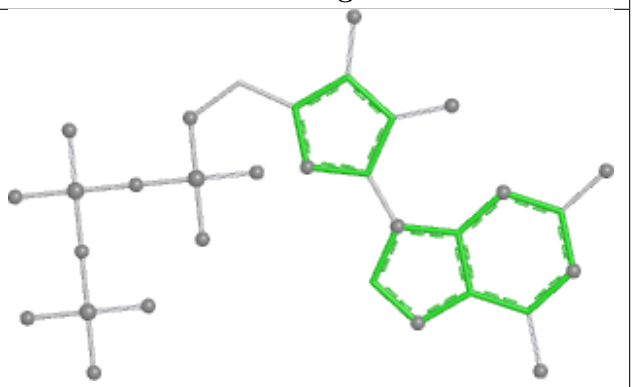

Rings

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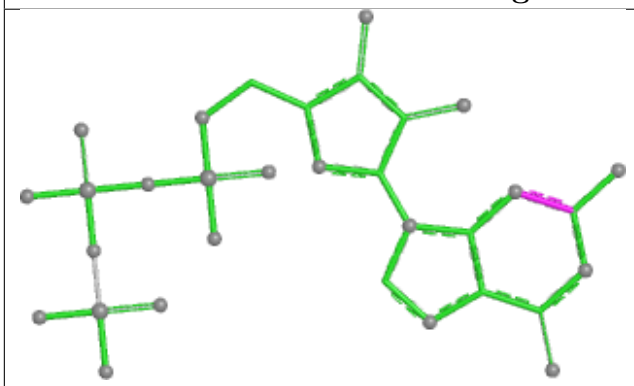

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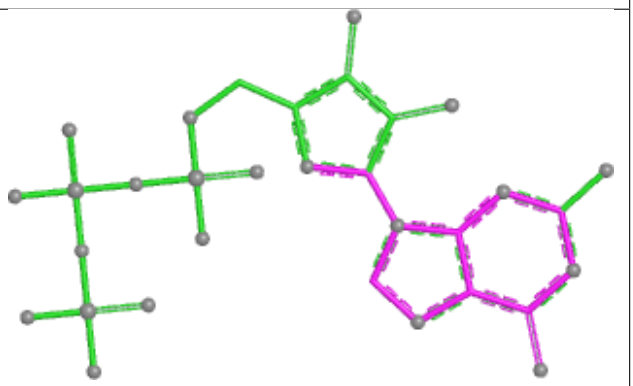

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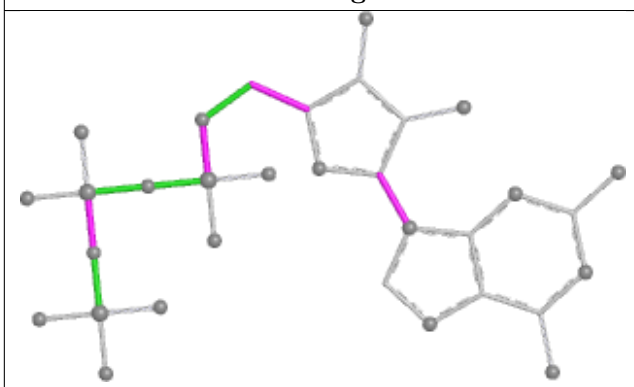

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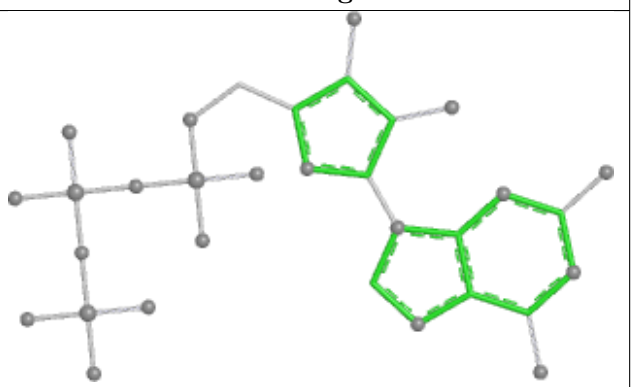
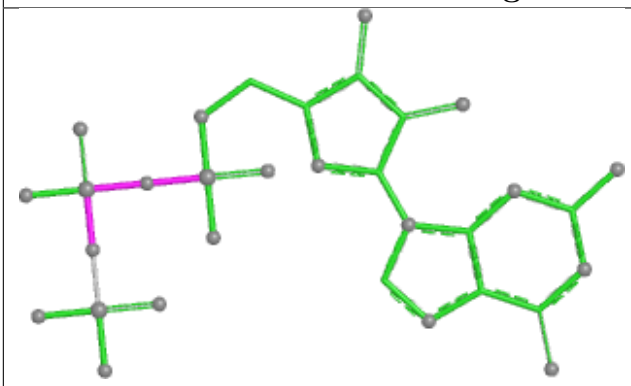


Rings

Ligand GTP WK 501



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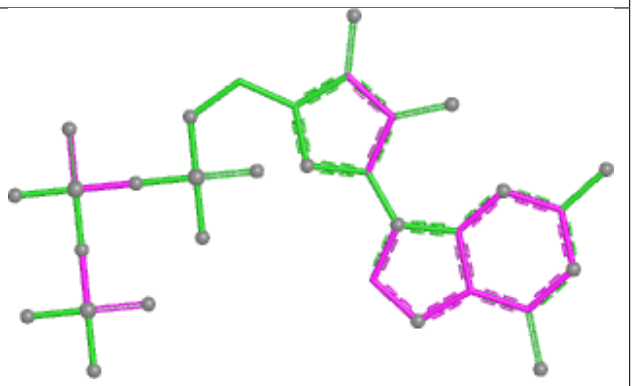

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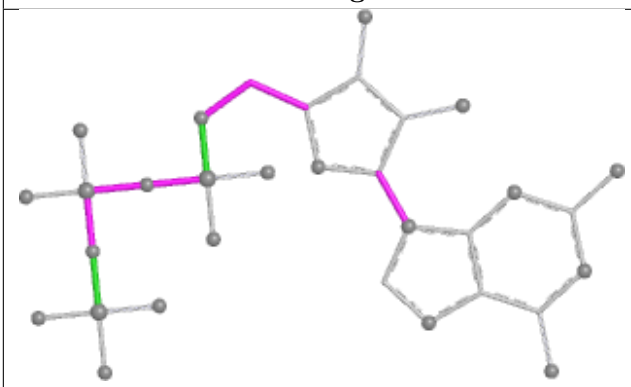

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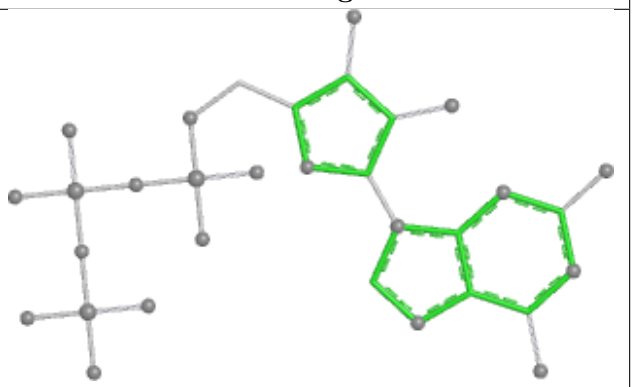

Rings

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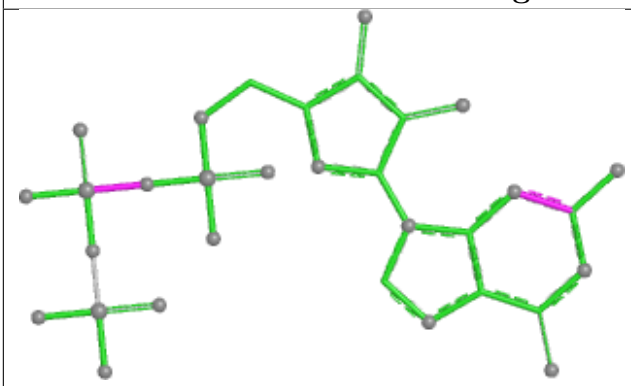

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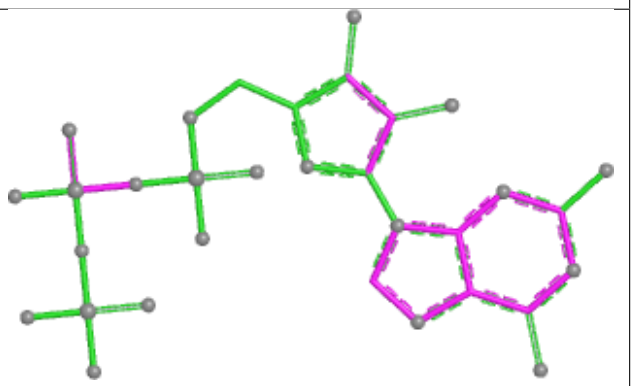

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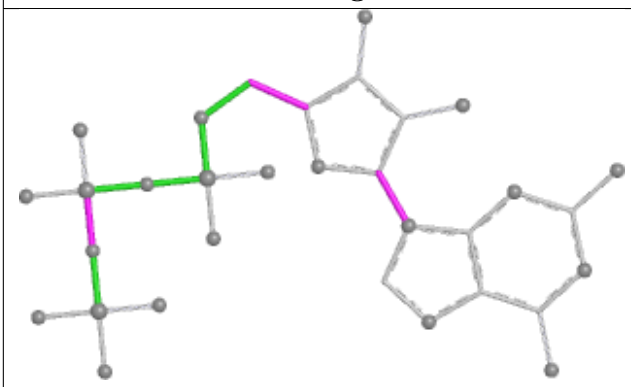

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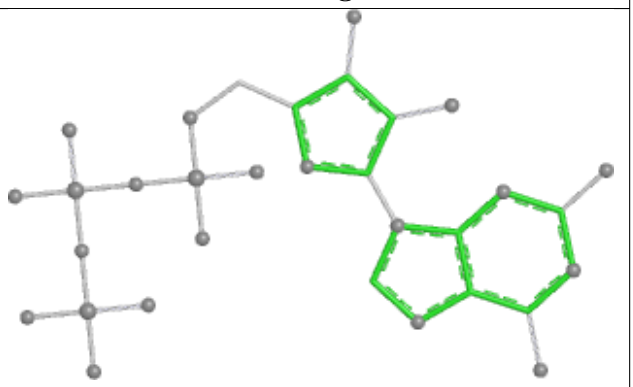

Rings

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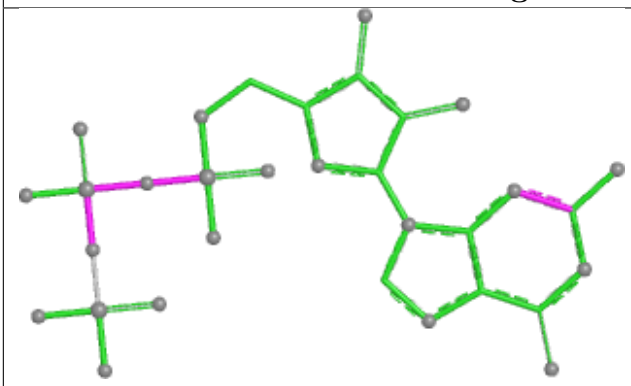

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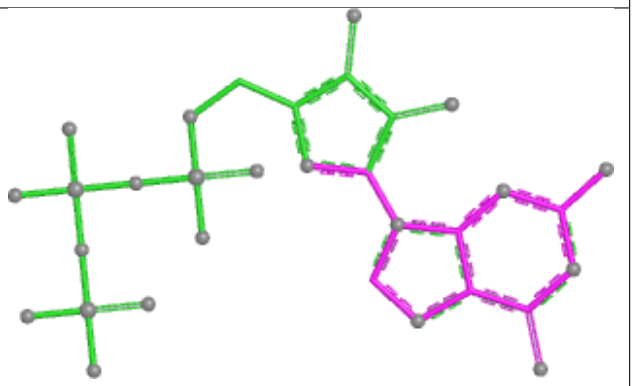

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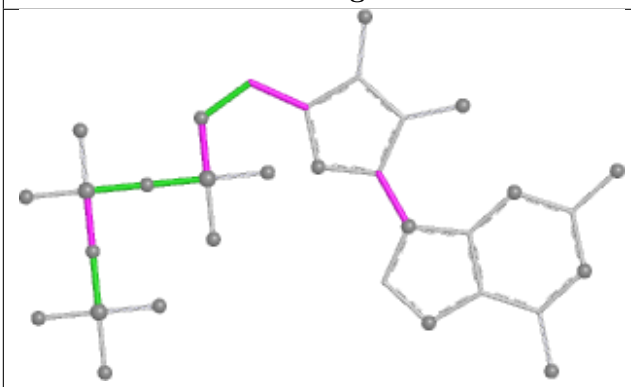

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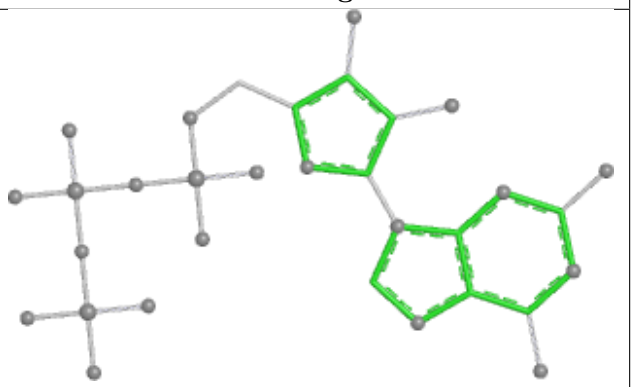
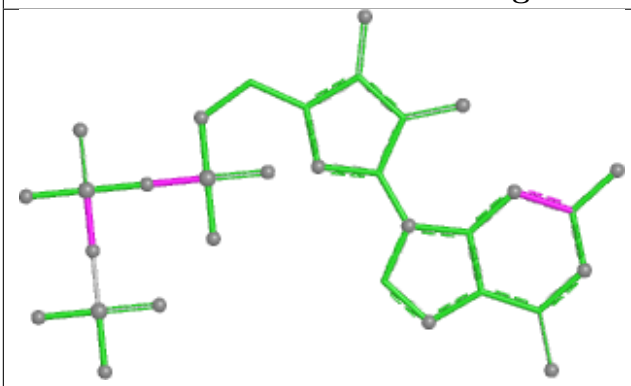


Rings

Ligand GTP JH 501



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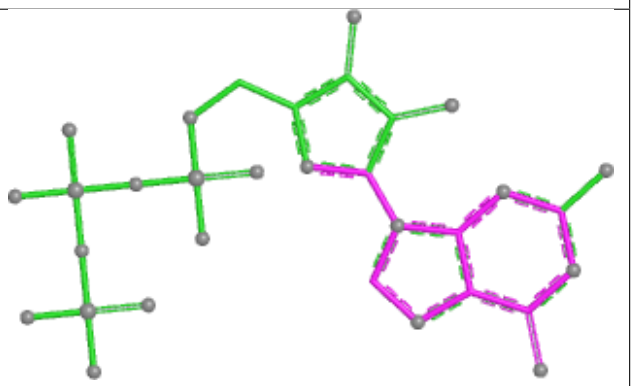

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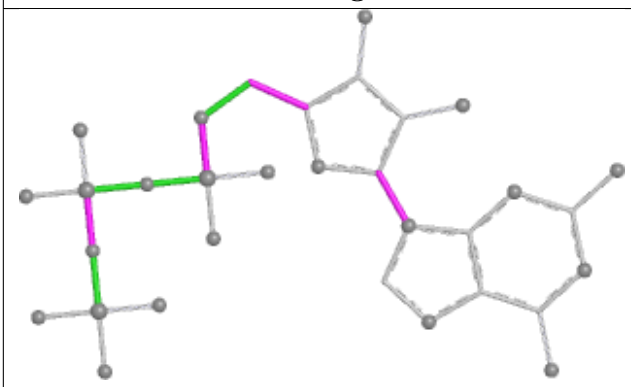

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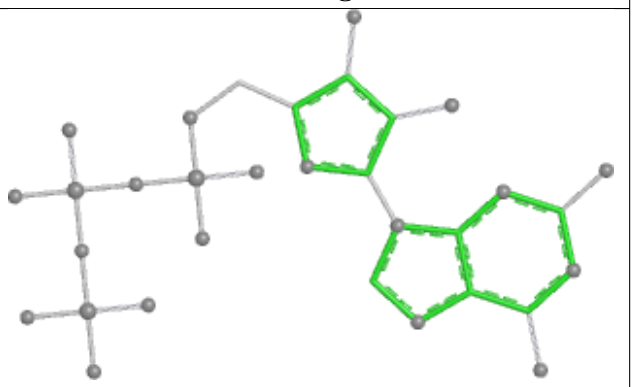
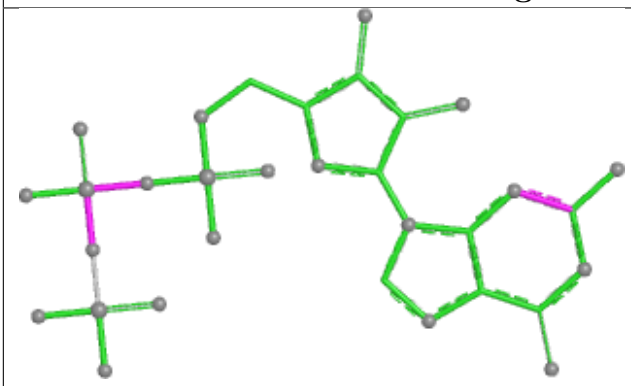


Rings

Ligand GTP JE 501



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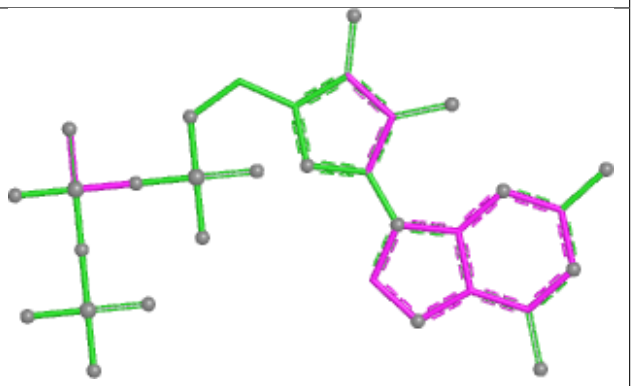

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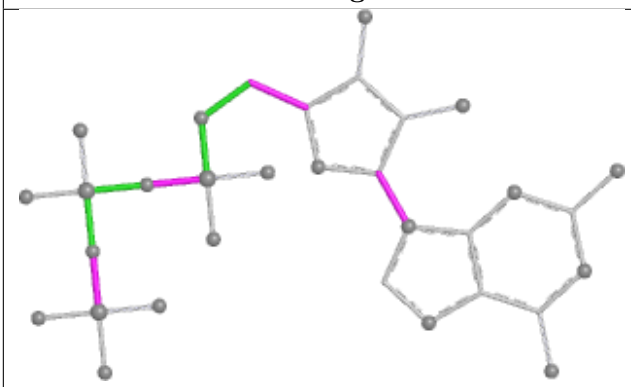

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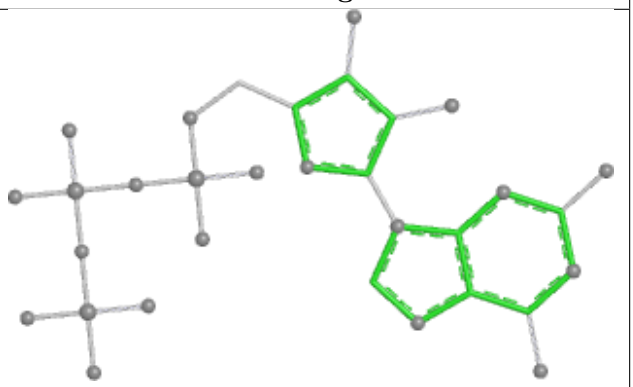
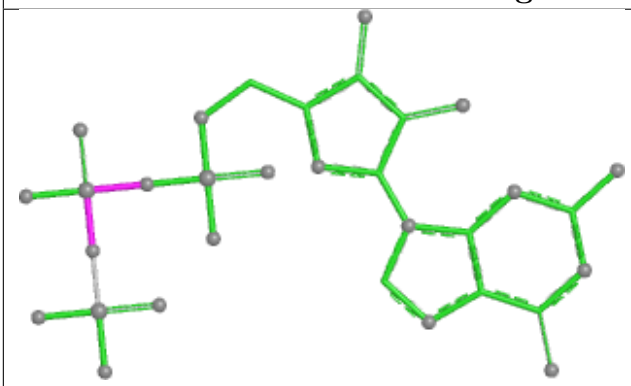


Rings

Ligand GTP DI 501



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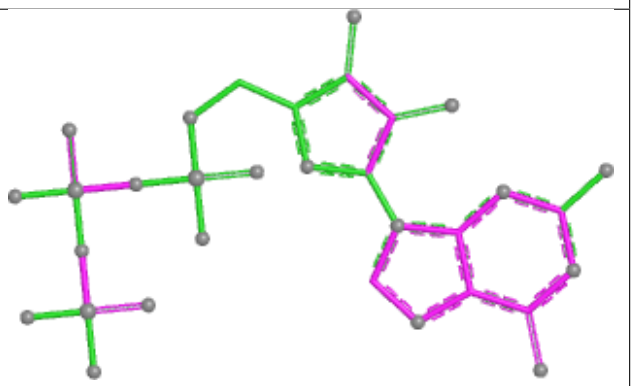

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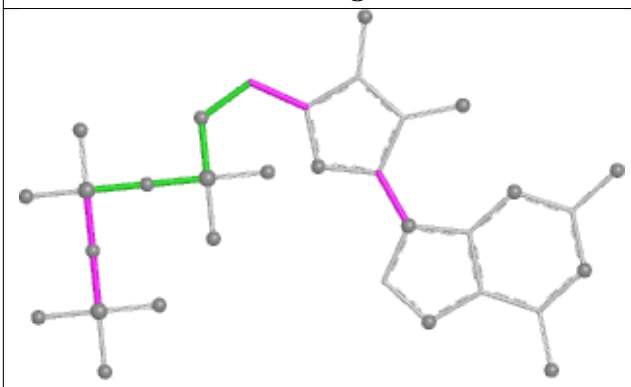

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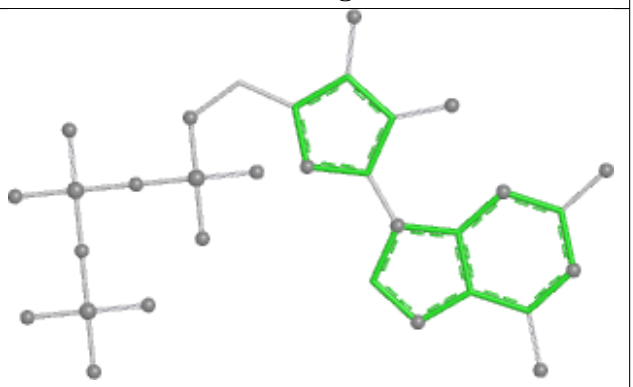
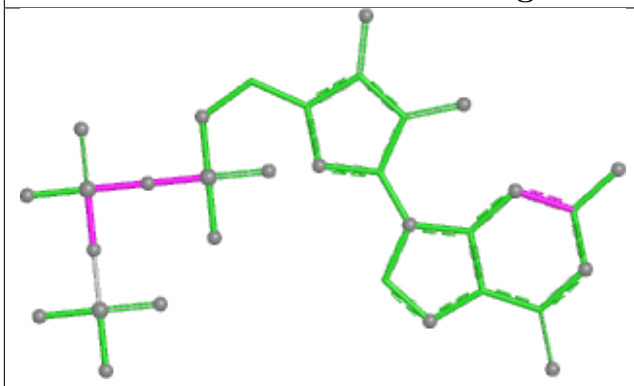


Rings

Ligand GTP OI 501



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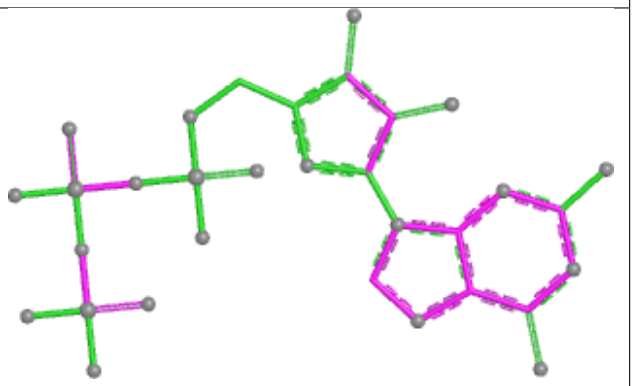

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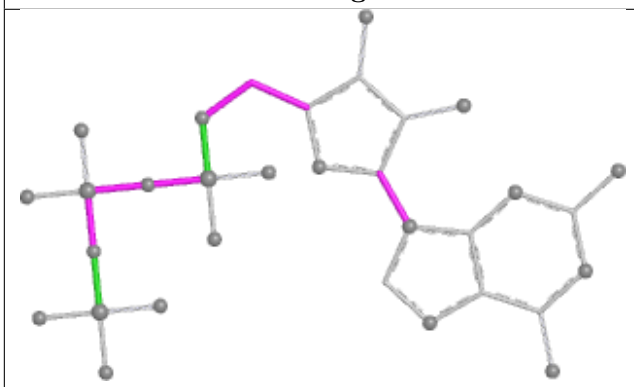
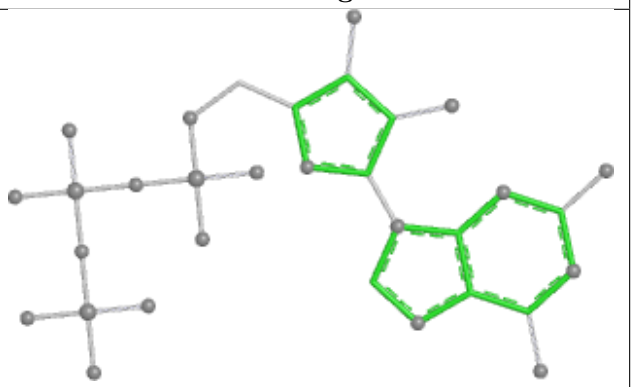
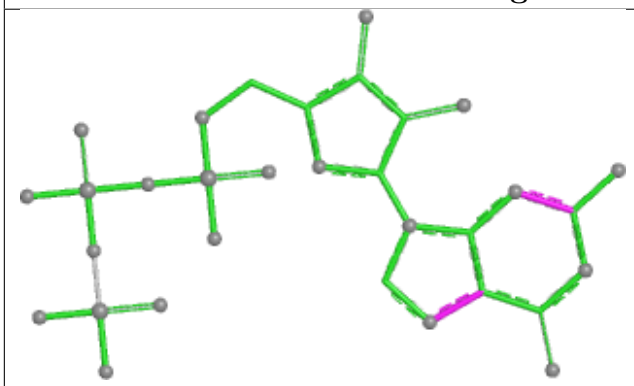


Torsions



Rings

Ligand GTP PH 501



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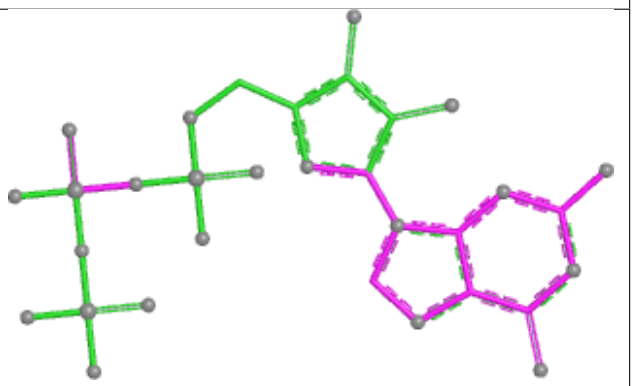

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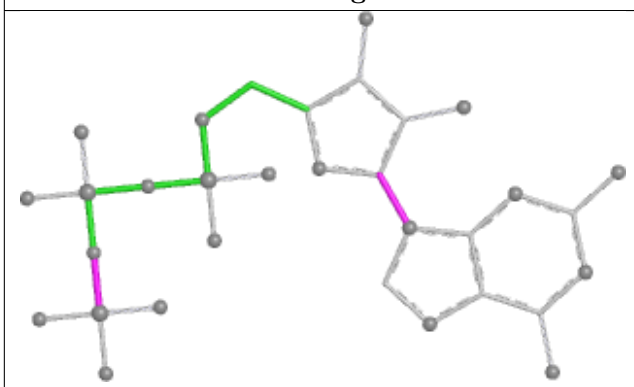

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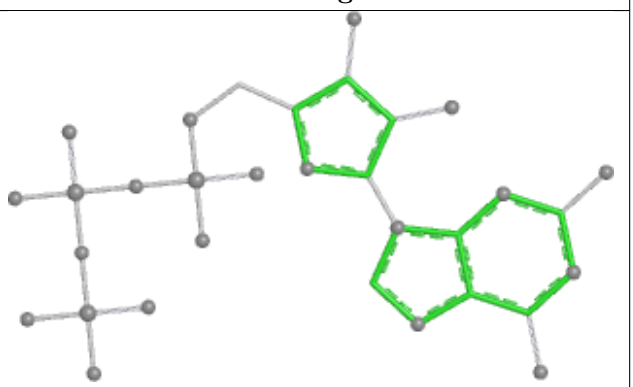
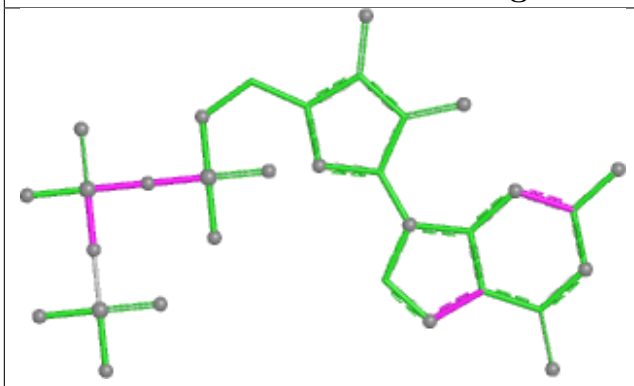


Rings

Ligand GTP UB 501



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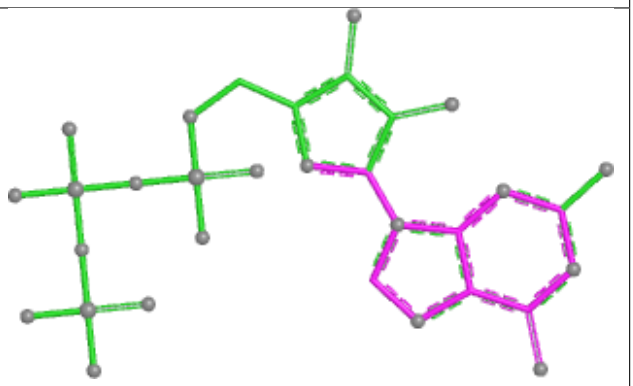

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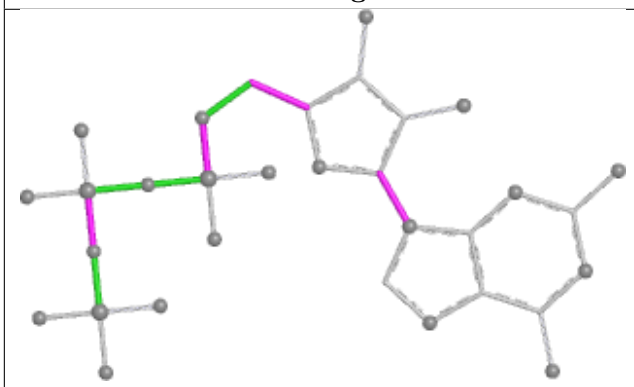

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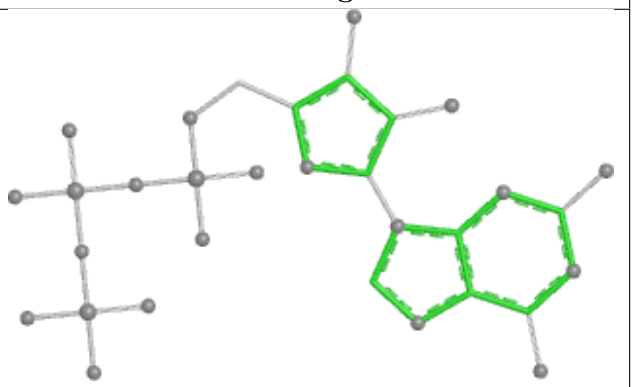

Rings

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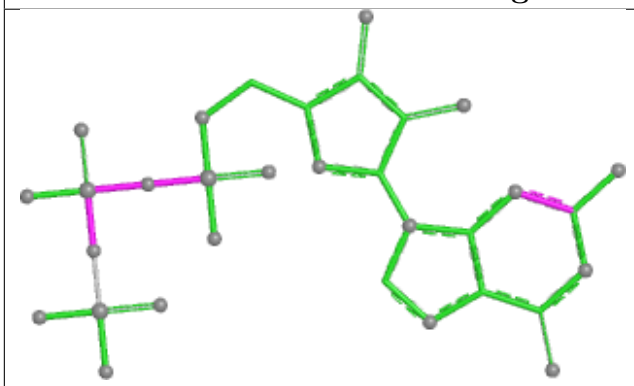

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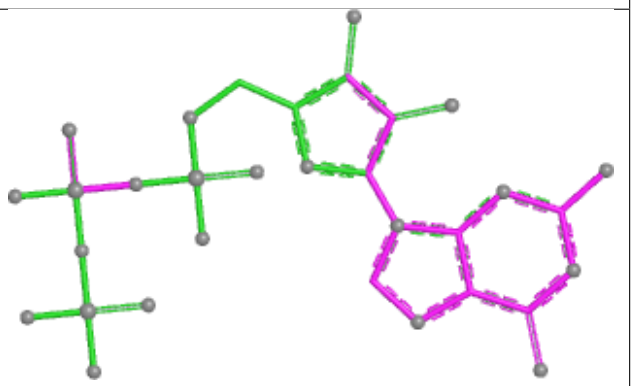

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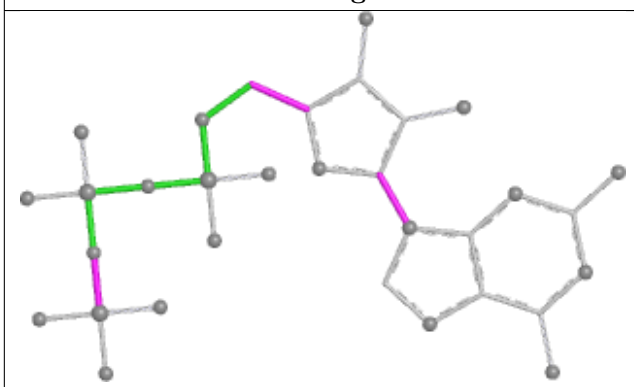

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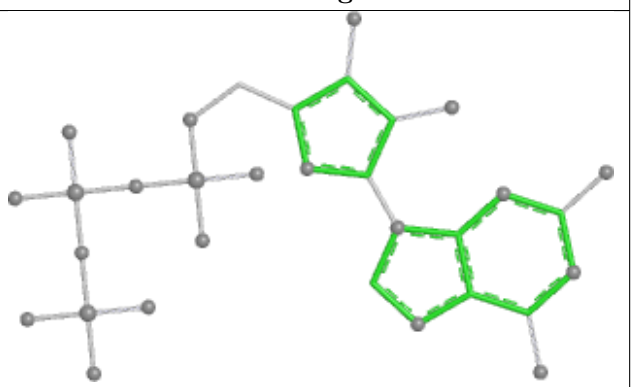

Rings

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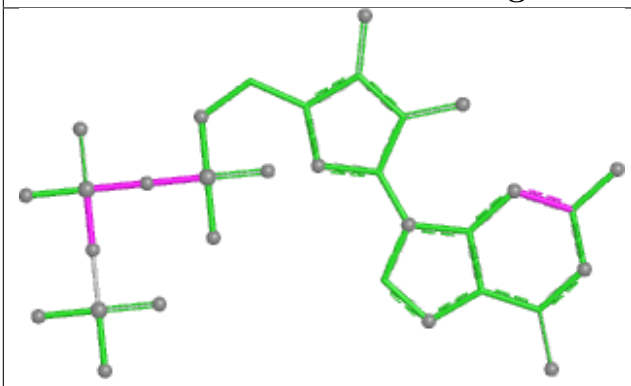

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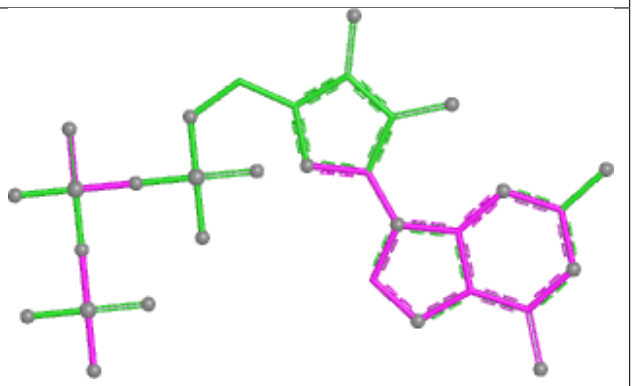

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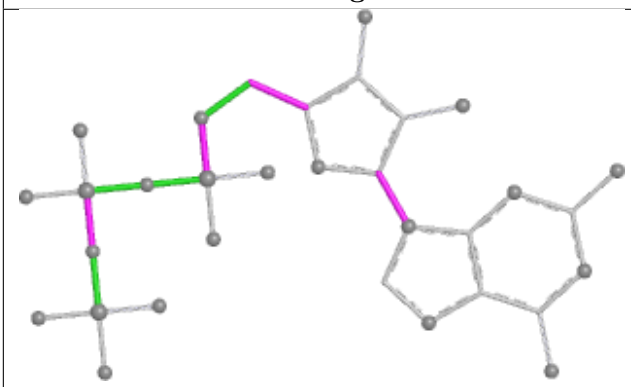

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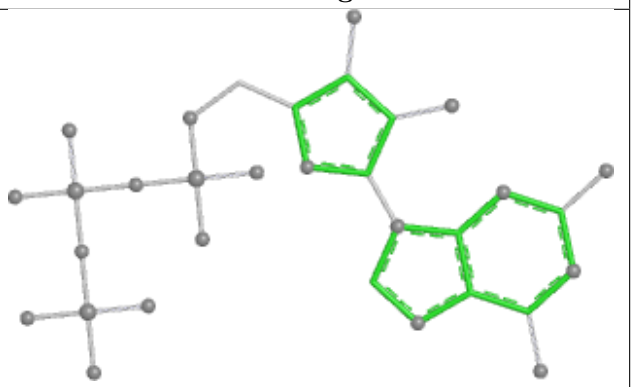
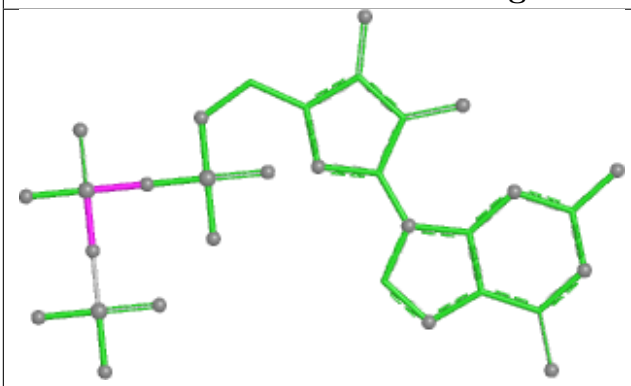


Rings

Ligand GTP SM 501



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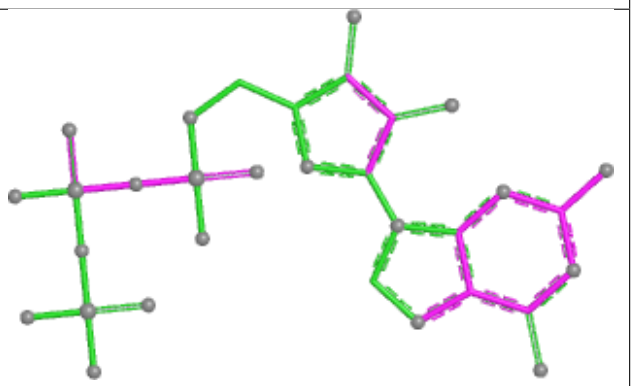

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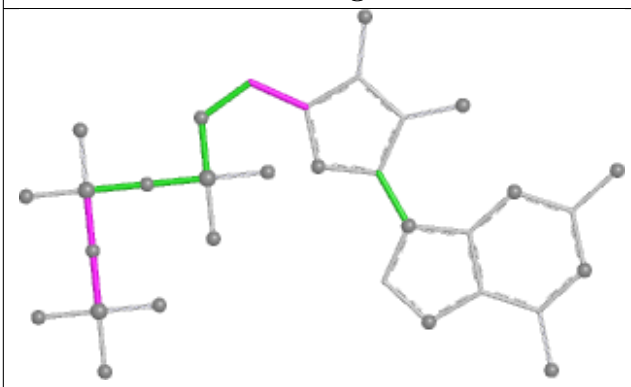

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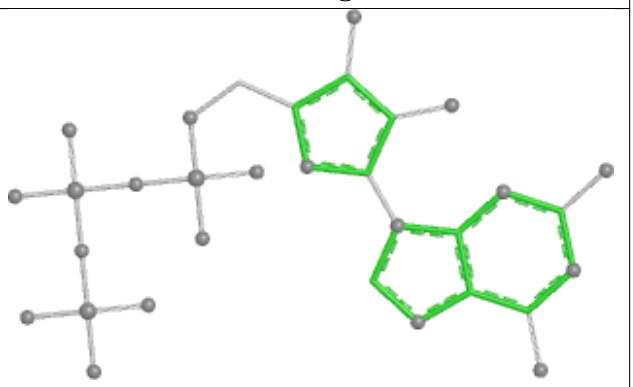

Rings

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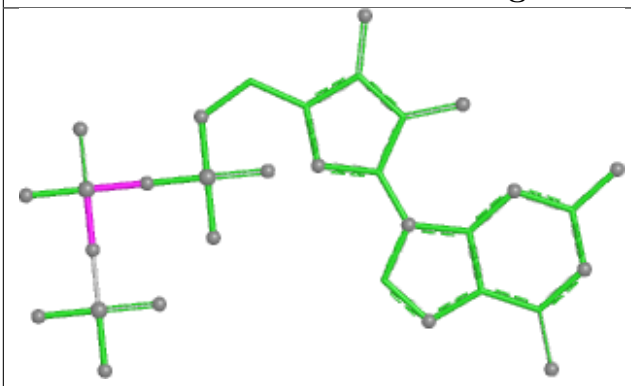

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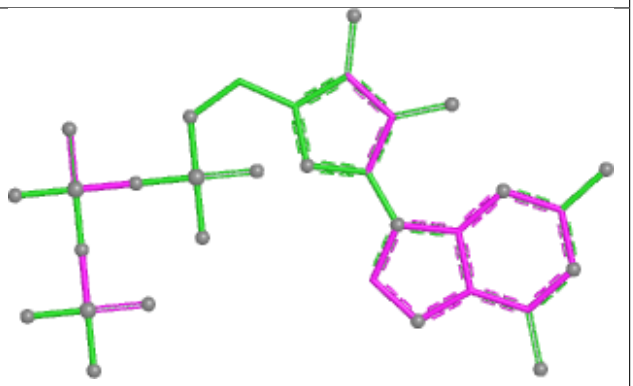

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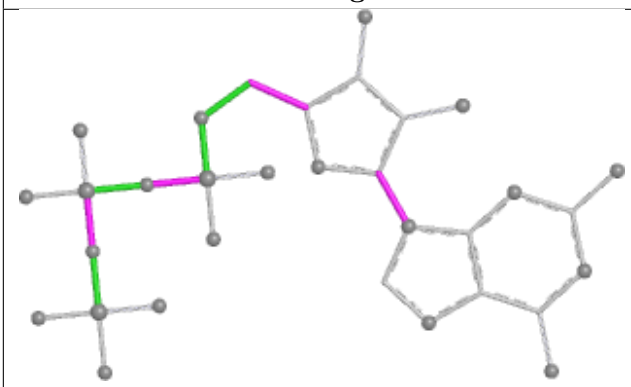

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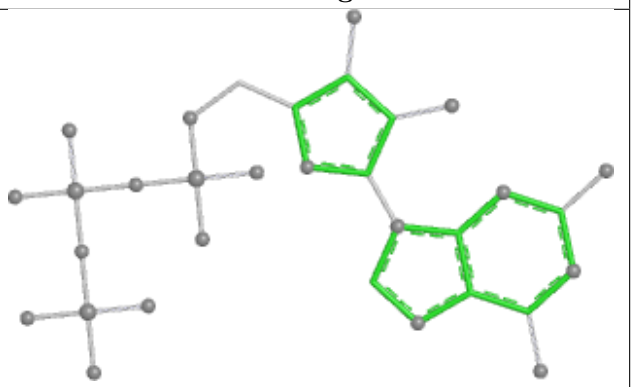
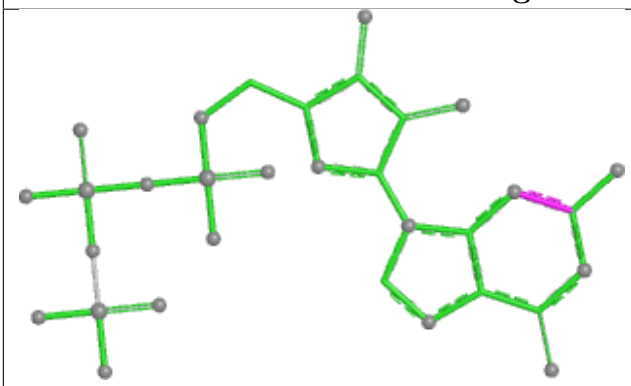


Rings

Ligand GTP OJ 501



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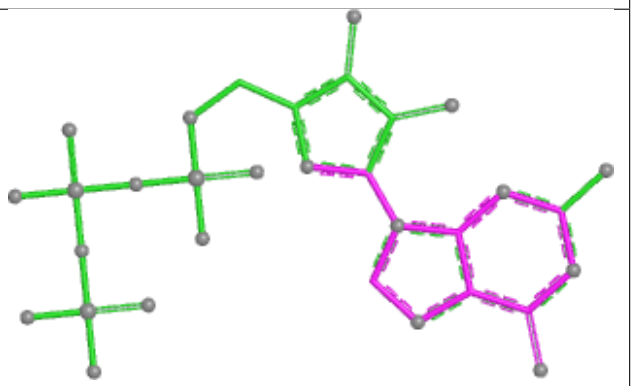

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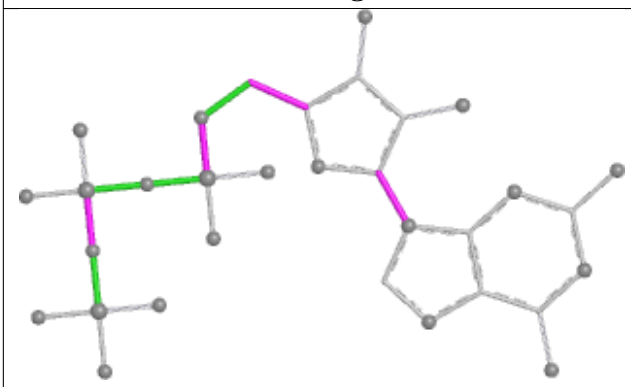

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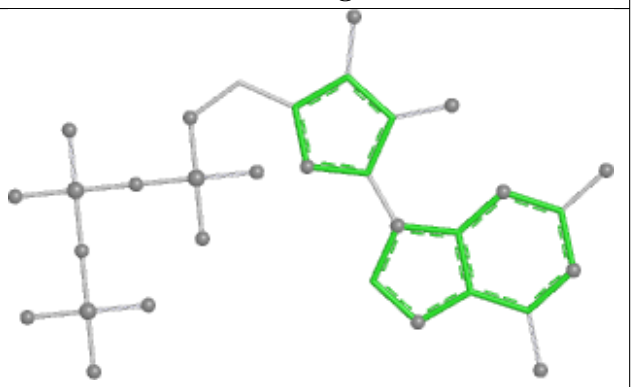
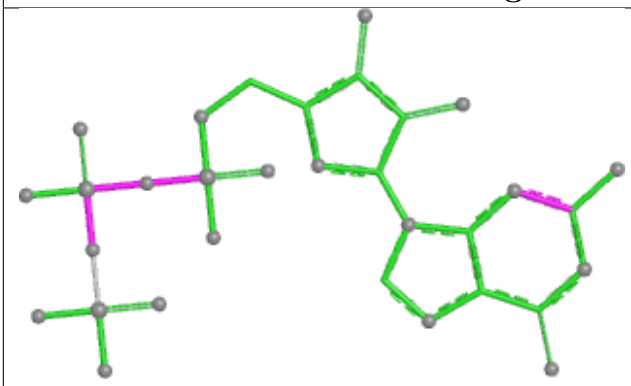


Rings

Ligand GTP MG 501



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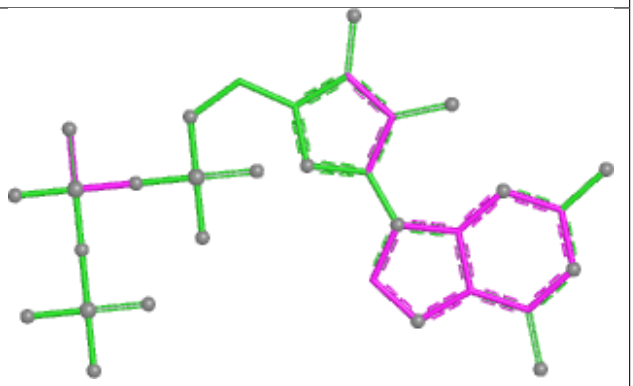

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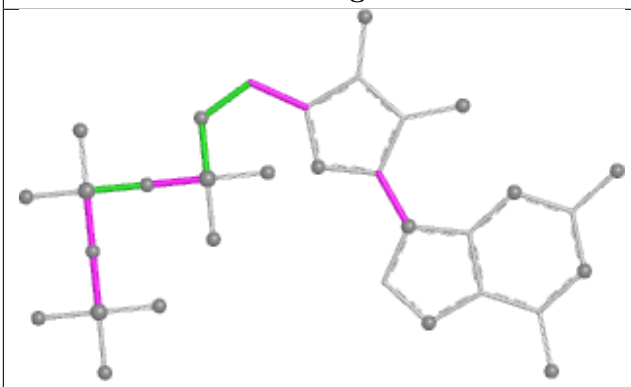

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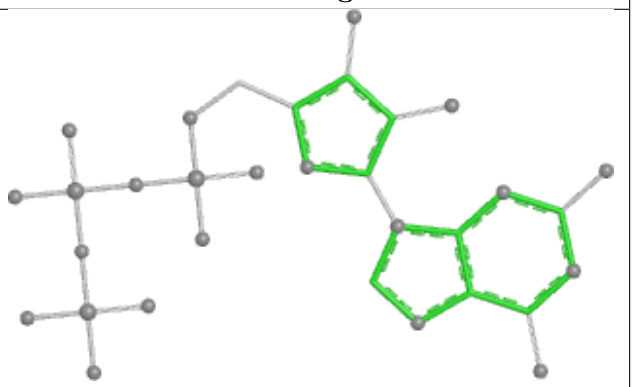
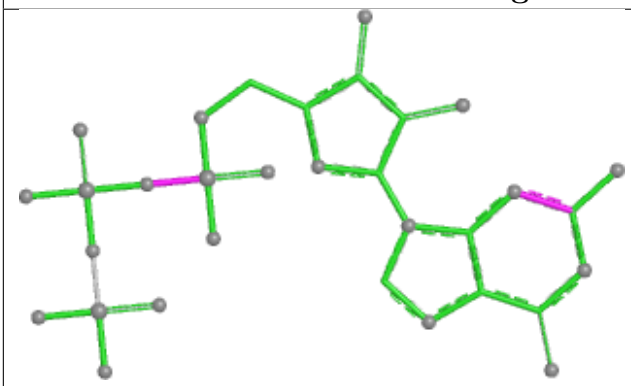


Rings

Ligand GTP QL 501



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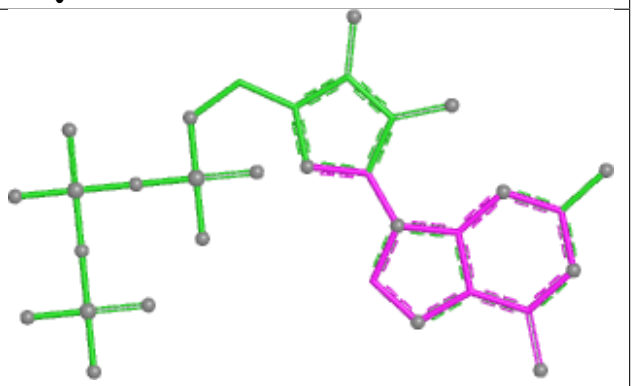

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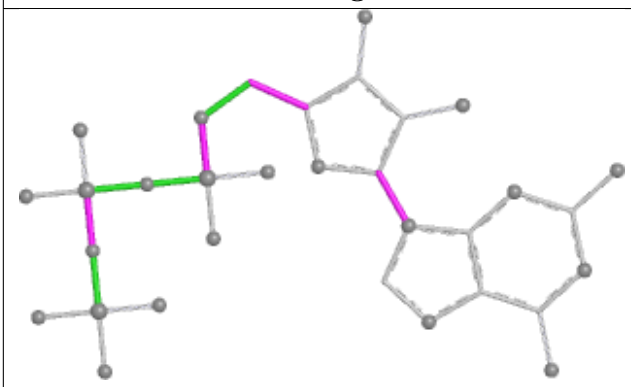

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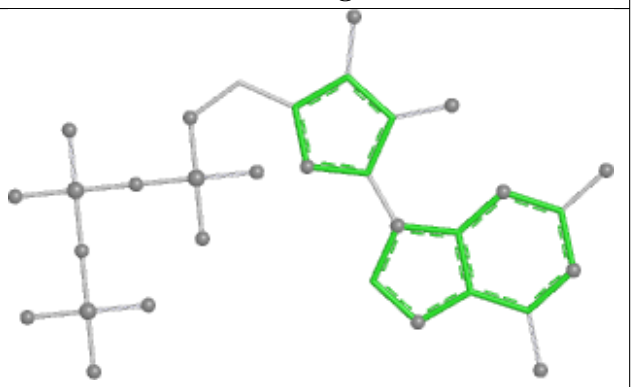

Rings

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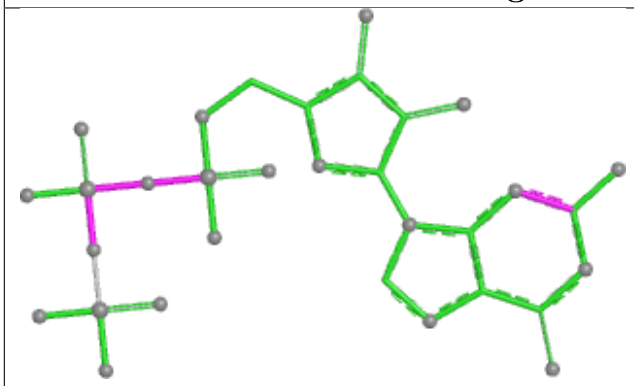

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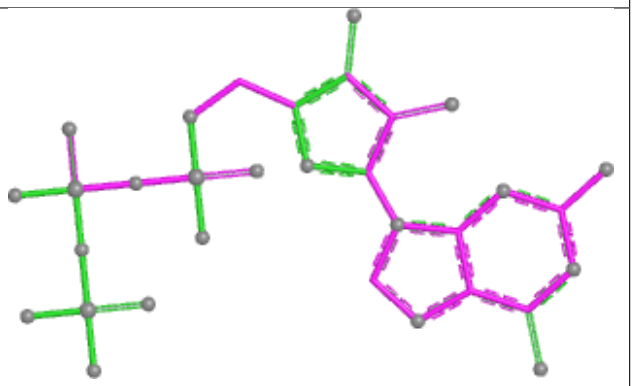

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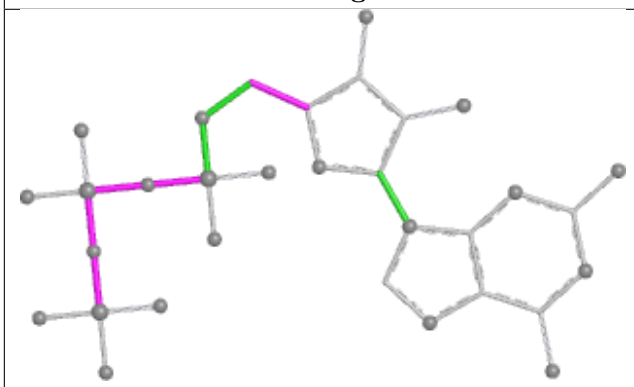

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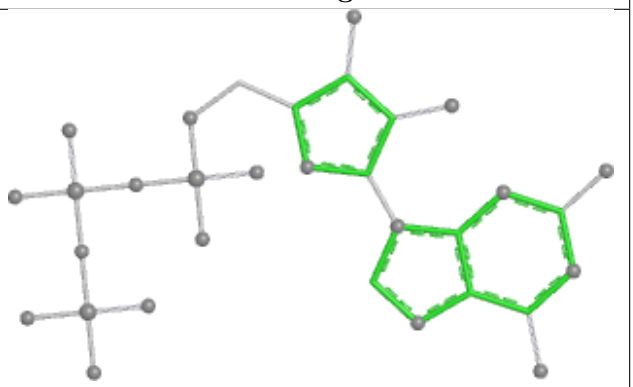
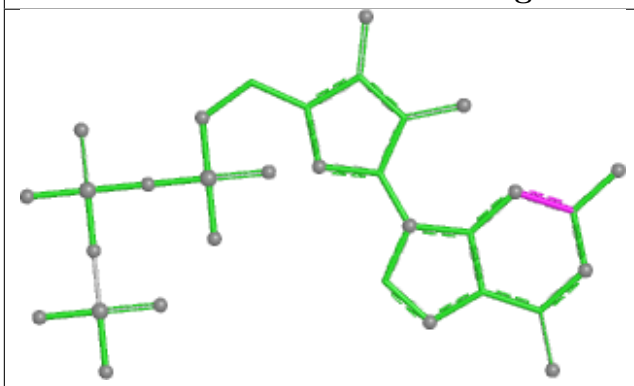


Rings

Ligand GTP JB 501



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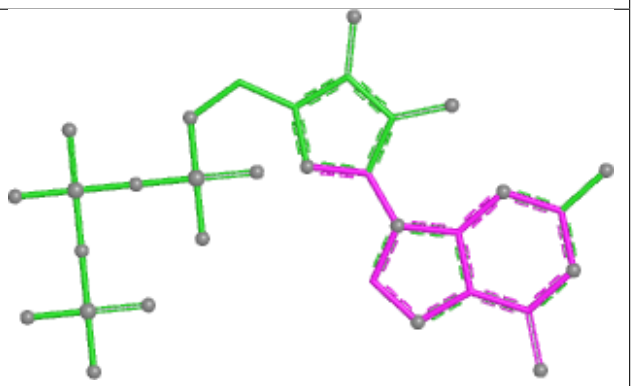

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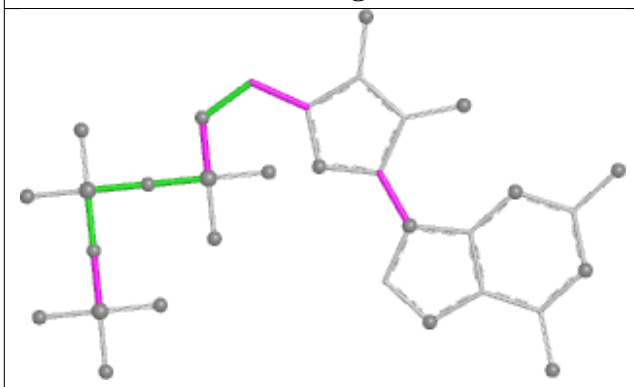

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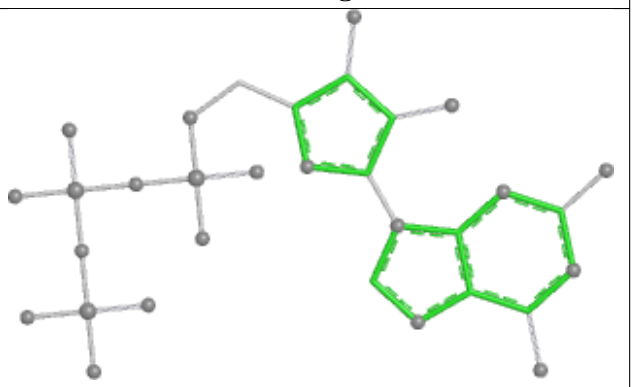
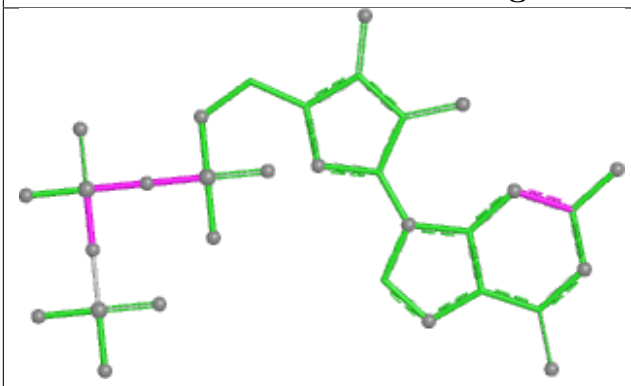


Rings

Ligand GTP NB 501



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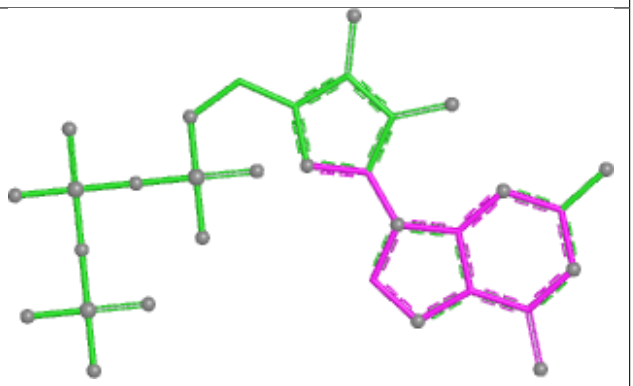

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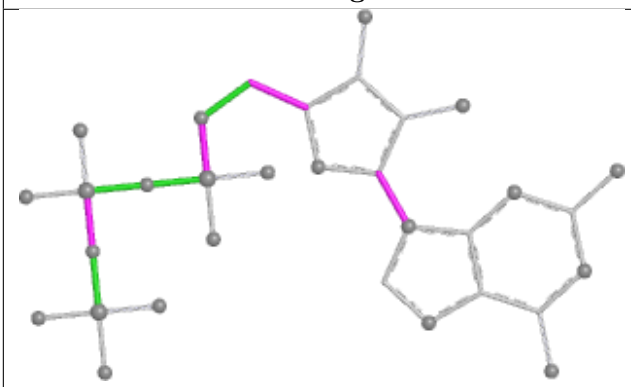

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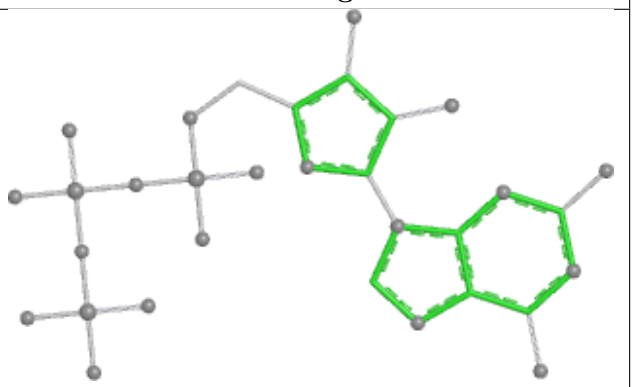
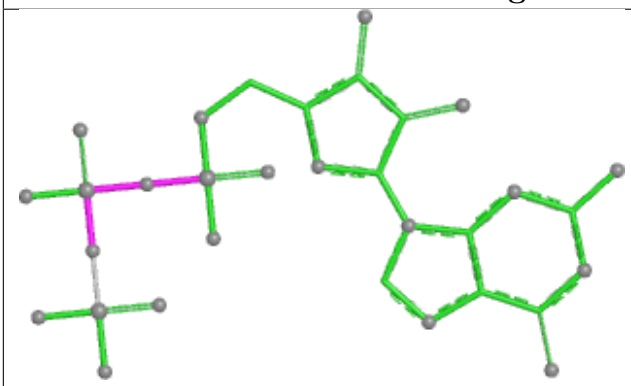


Rings

Ligand GTP QD 502



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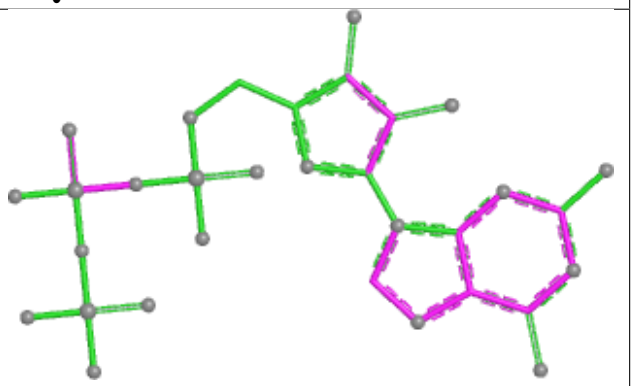

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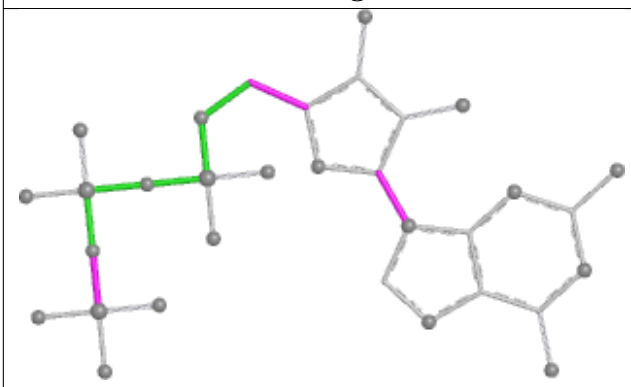

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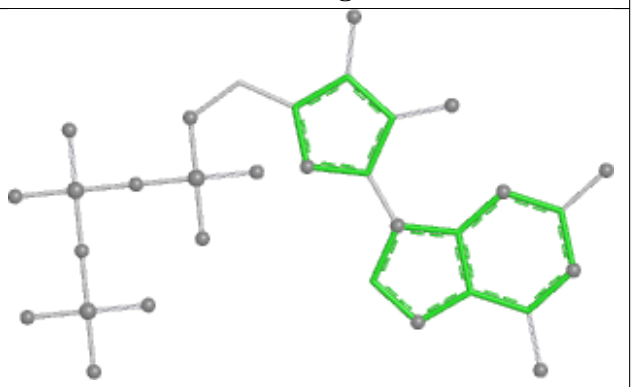
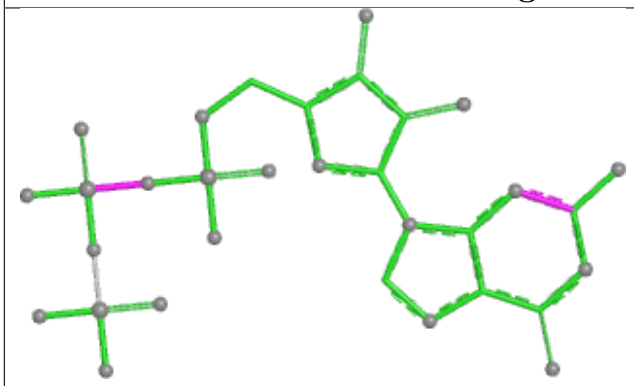


Rings

Ligand GTP IE 501



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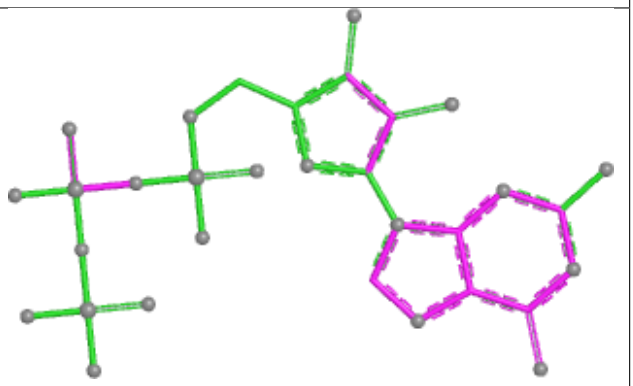

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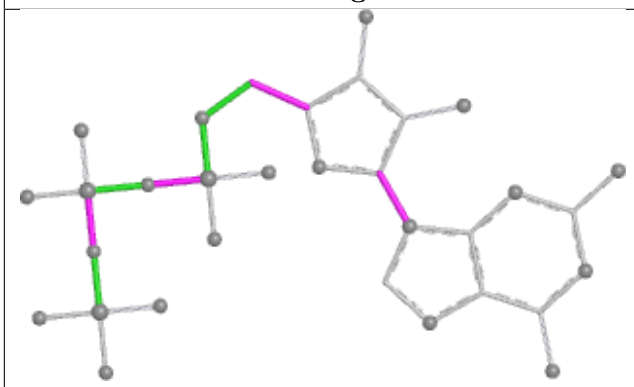
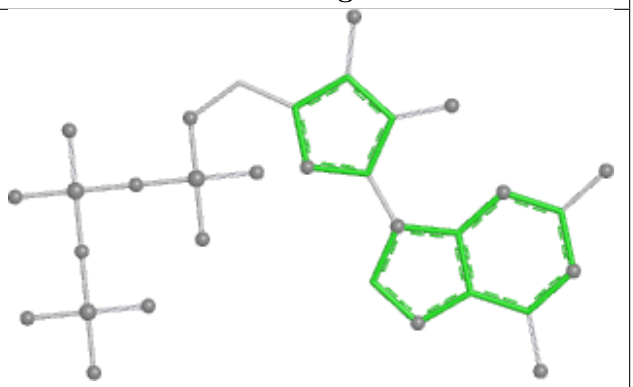
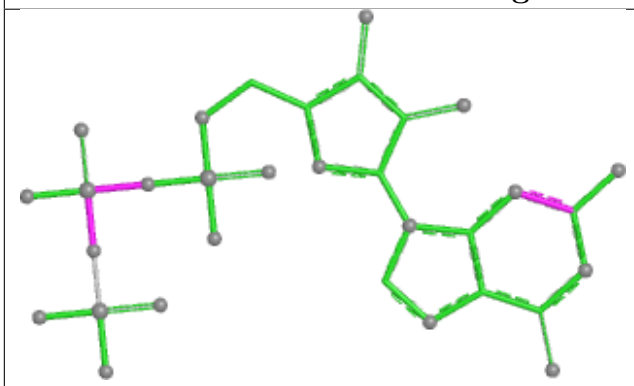


Torsions



Rings

Ligand GTP LK 501



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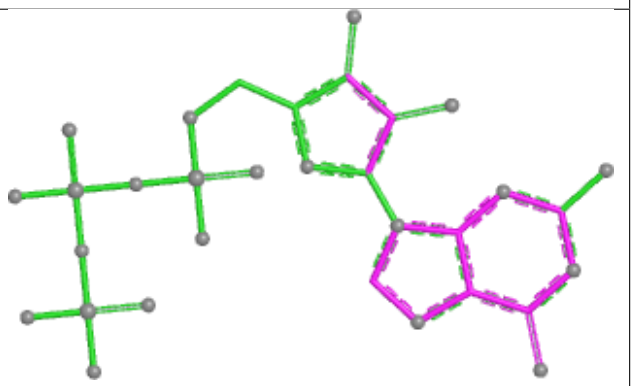

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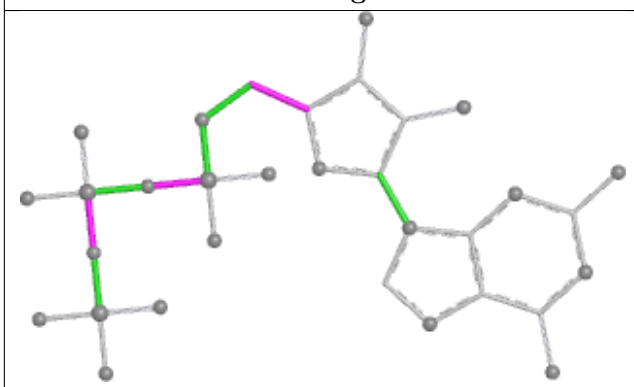

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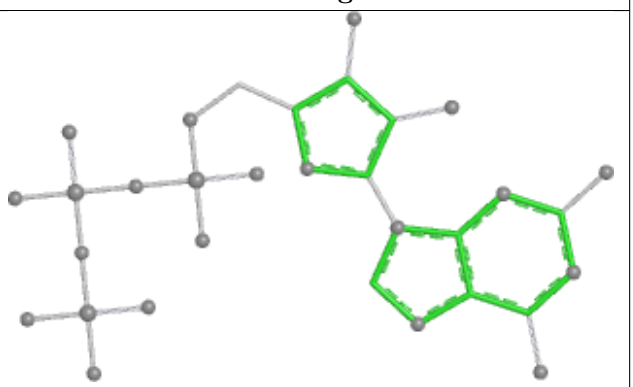
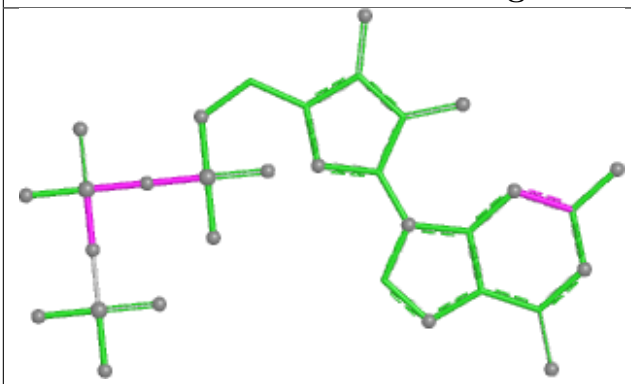


Rings

Ligand GTP HG 501



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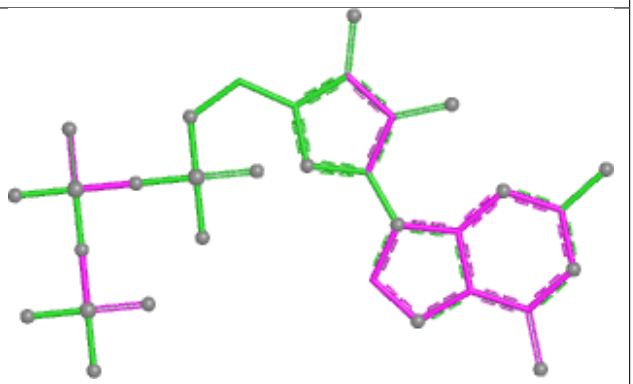

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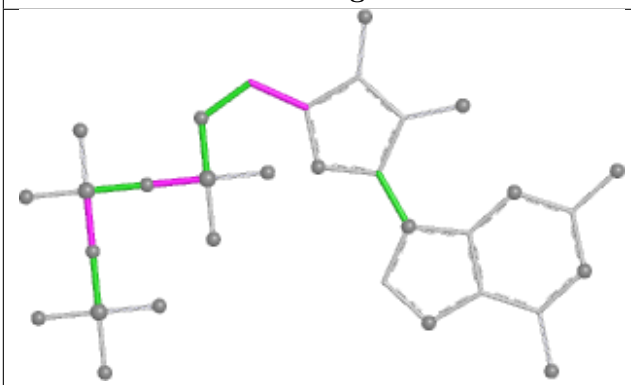

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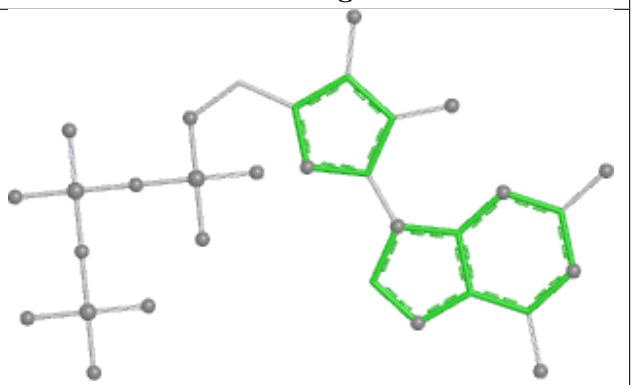
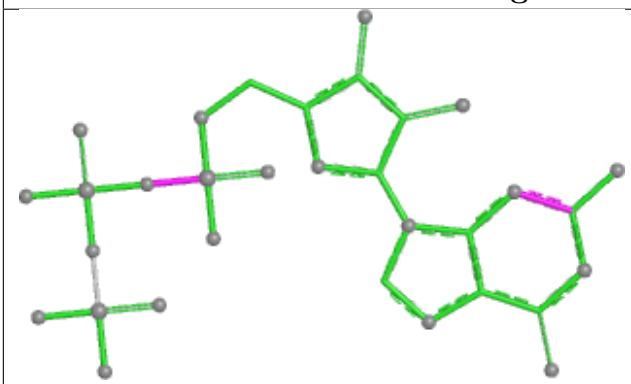


Rings

Ligand GTP FD 501



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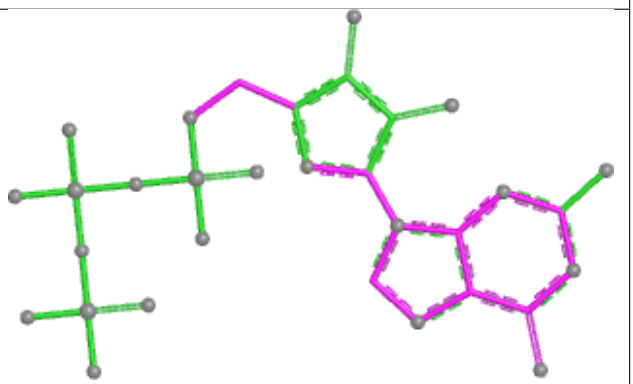

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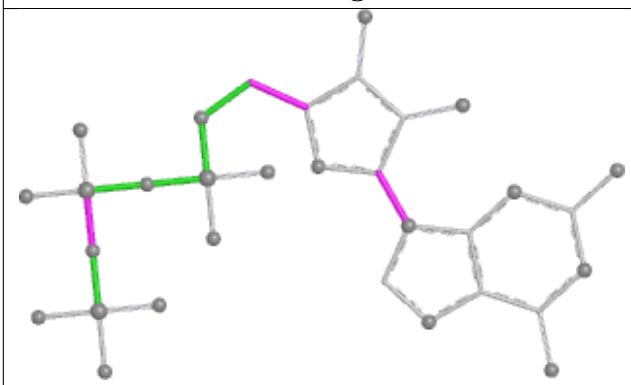

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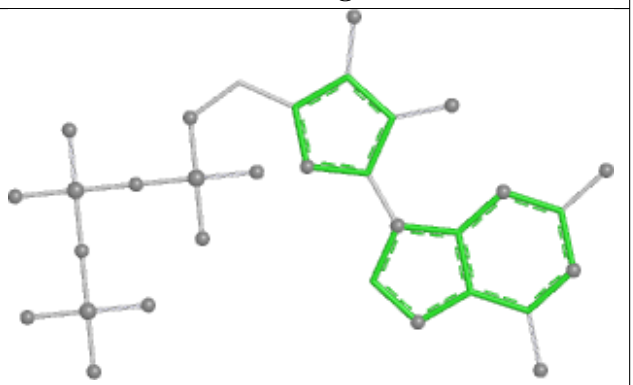

Rings

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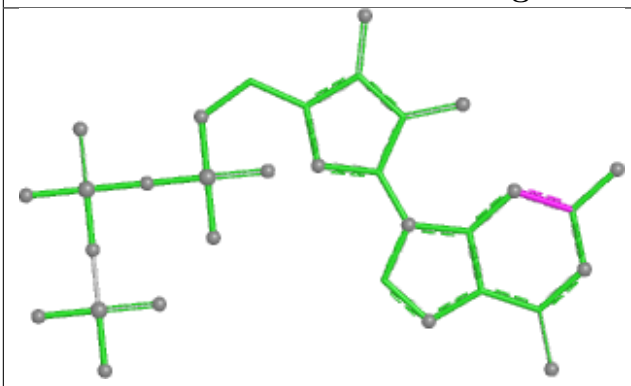

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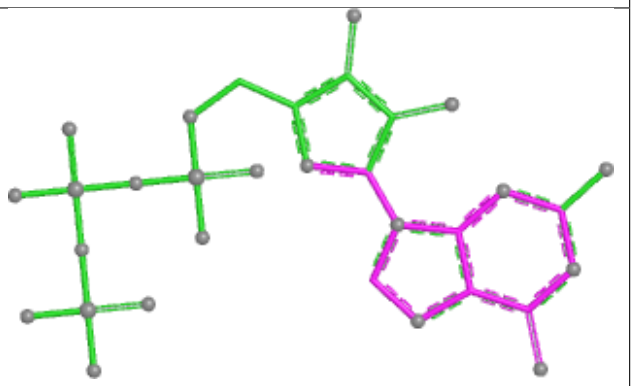

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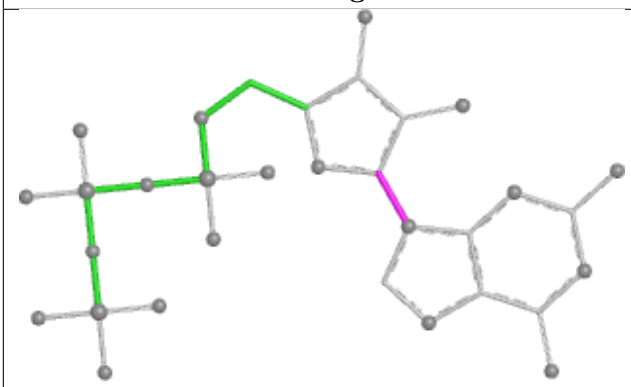

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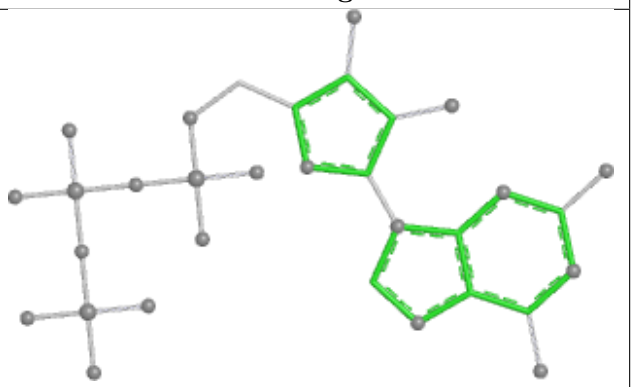

Rings

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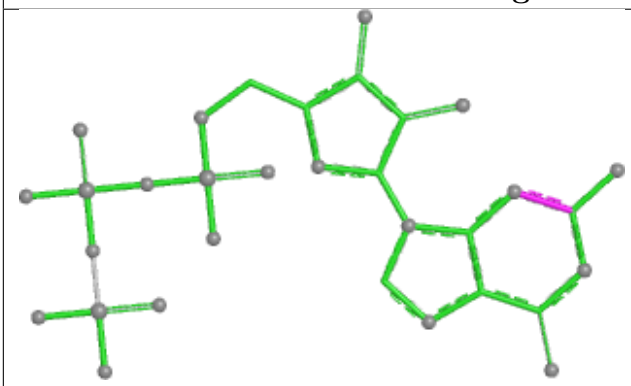

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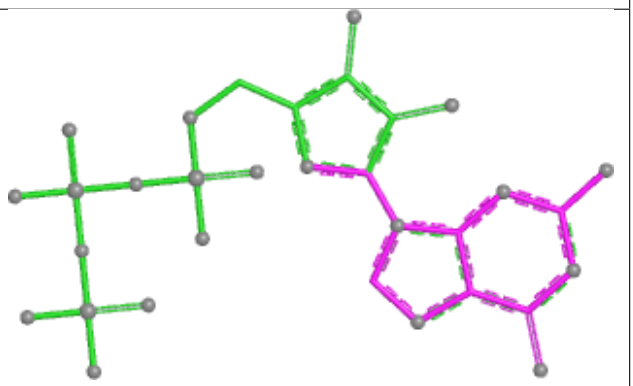

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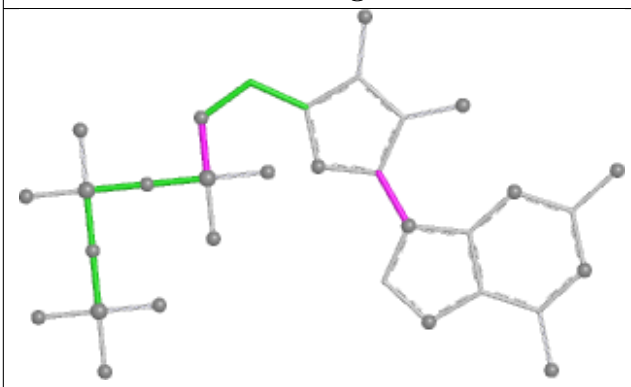

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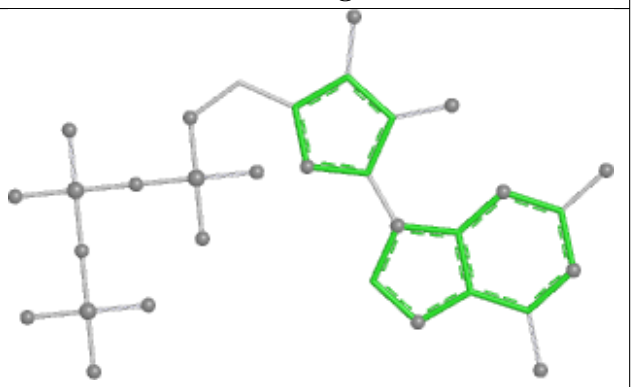
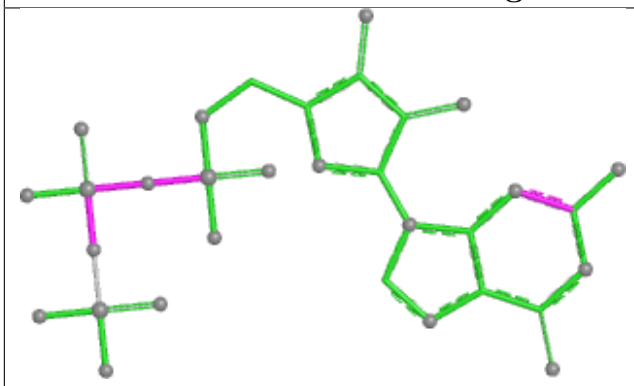


Rings

Ligand GTP WB 501



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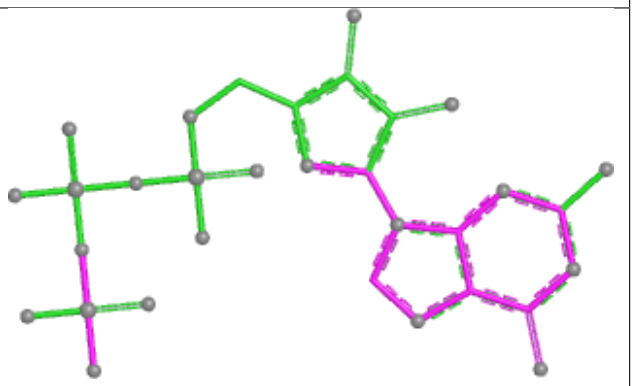

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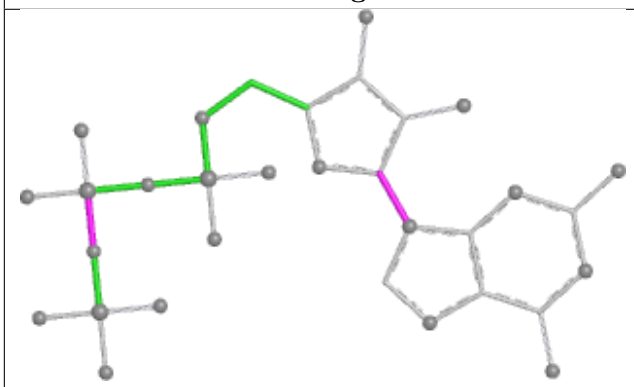

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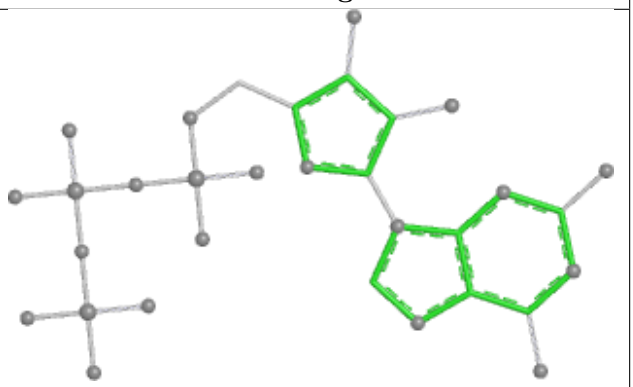
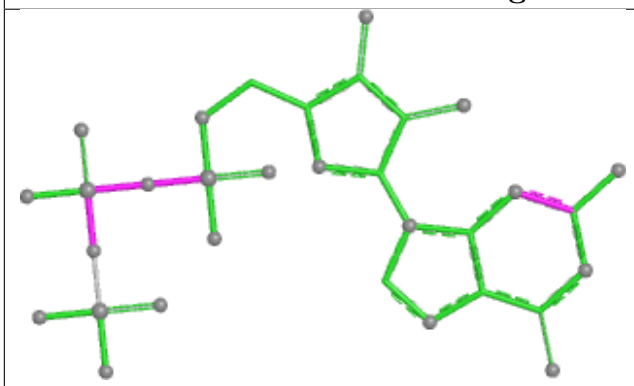


Rings

Ligand GTP HK 501



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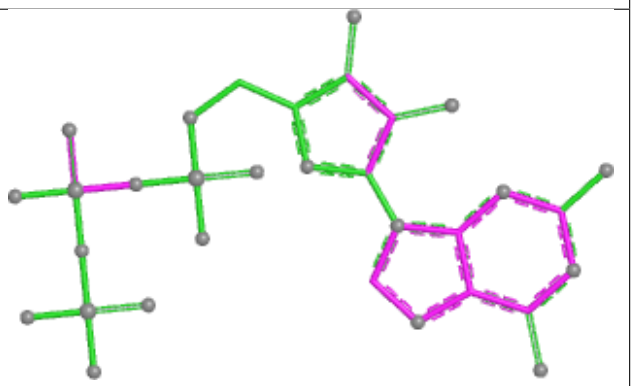

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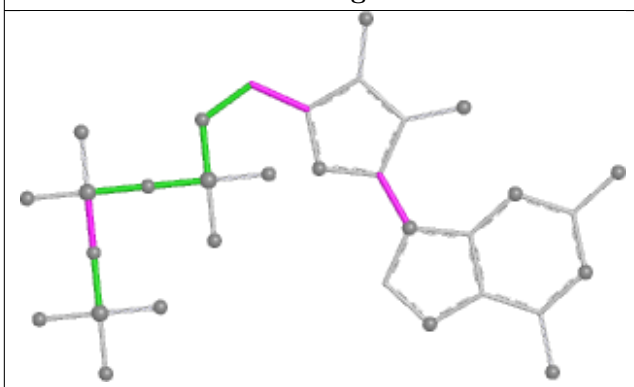

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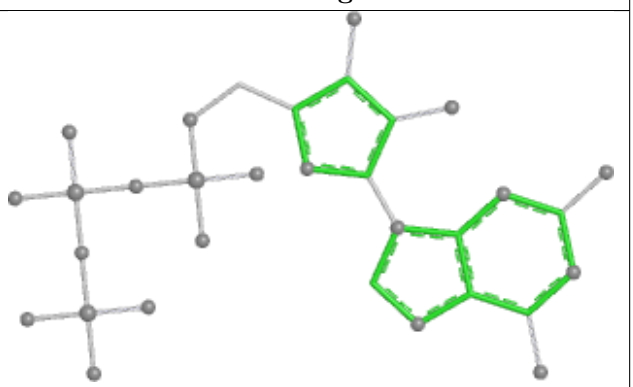

Rings

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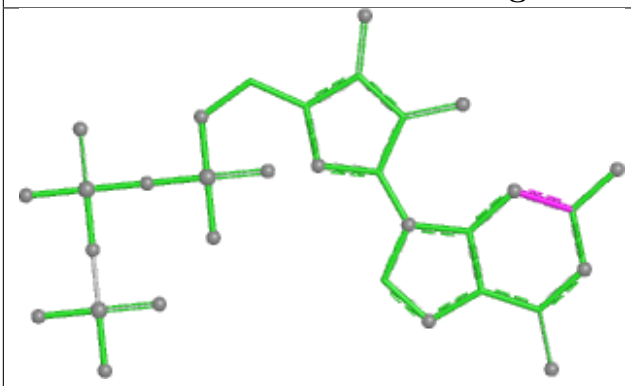

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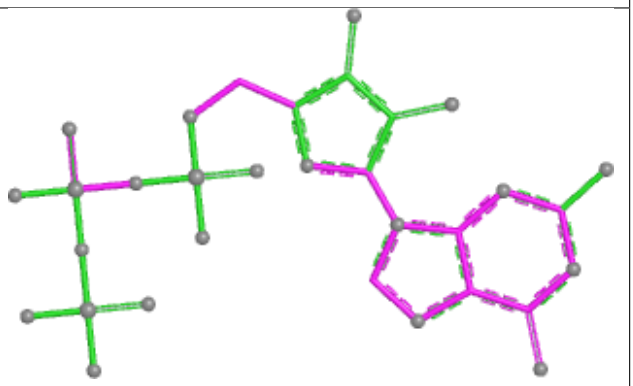

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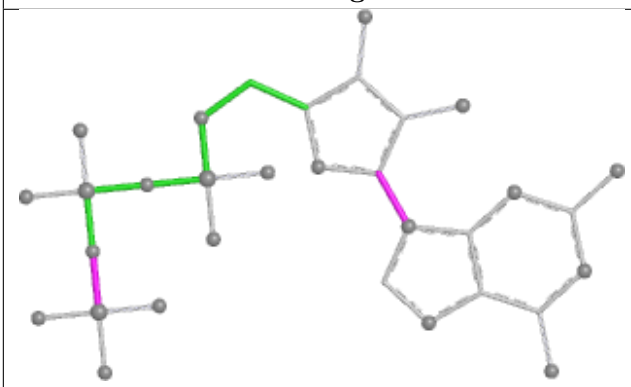

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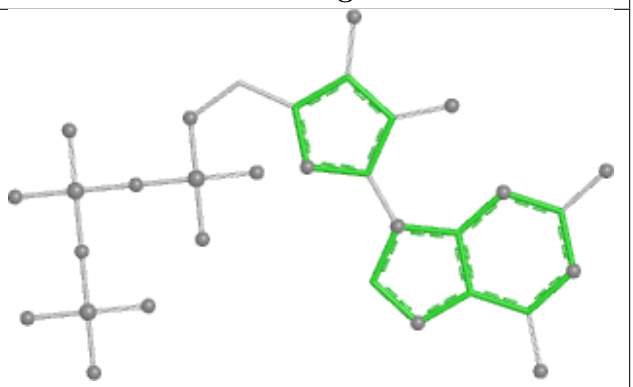

Rings

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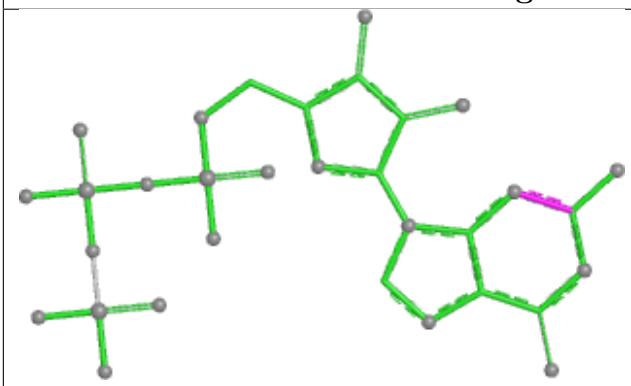

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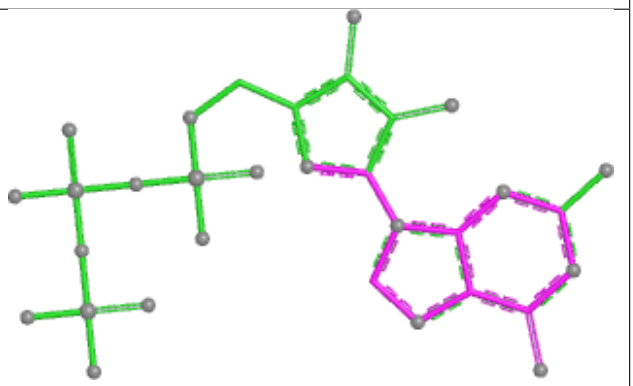

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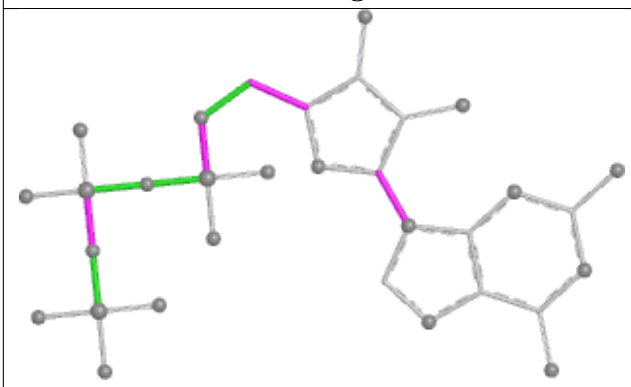

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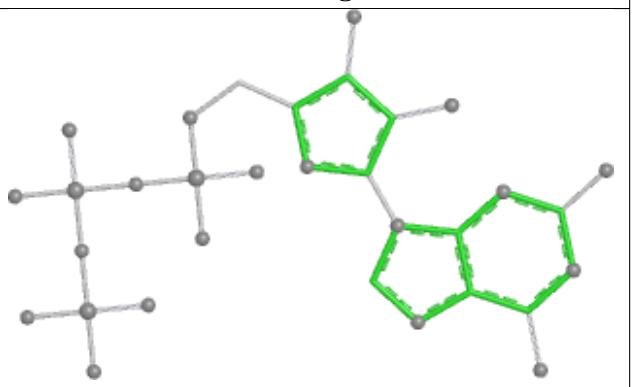
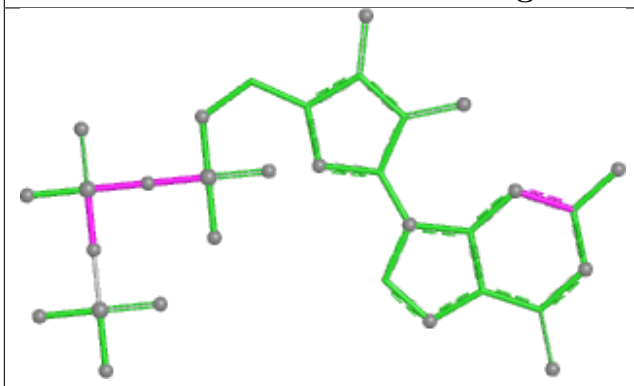


Rings

Ligand GTP UI 501



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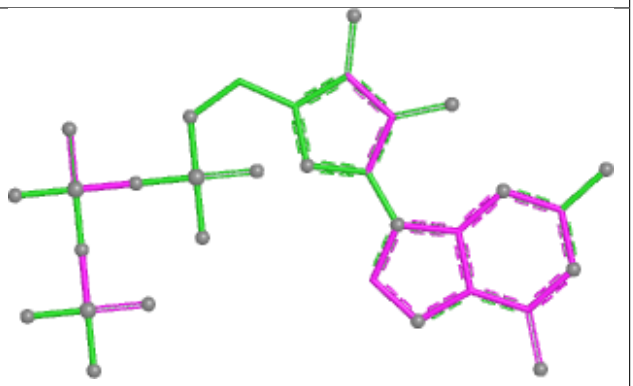

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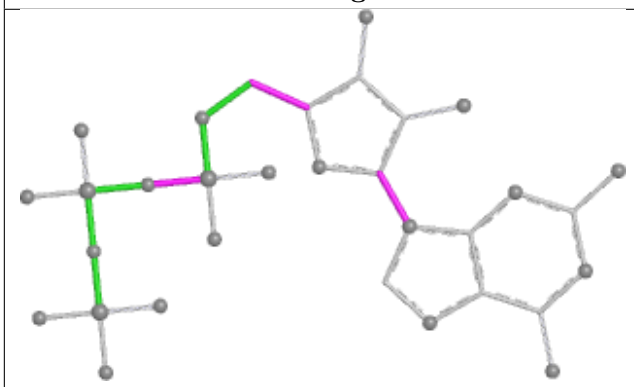

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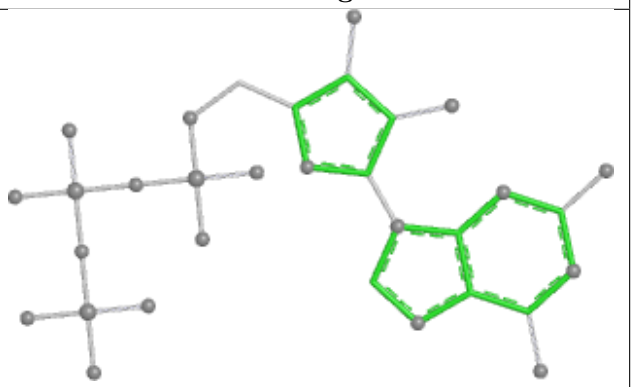
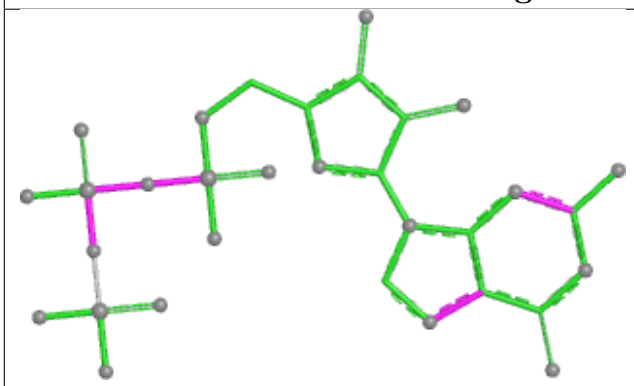


Rings

Ligand GTP FL 501



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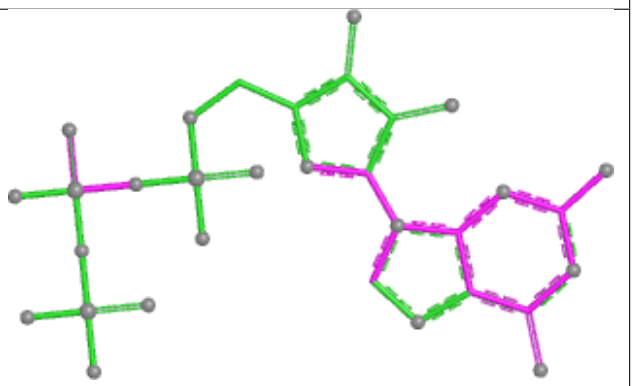

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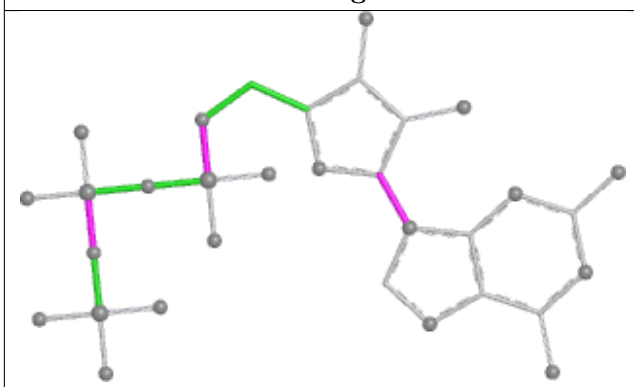

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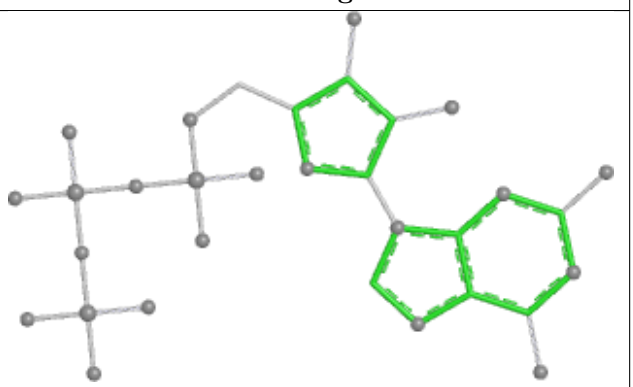
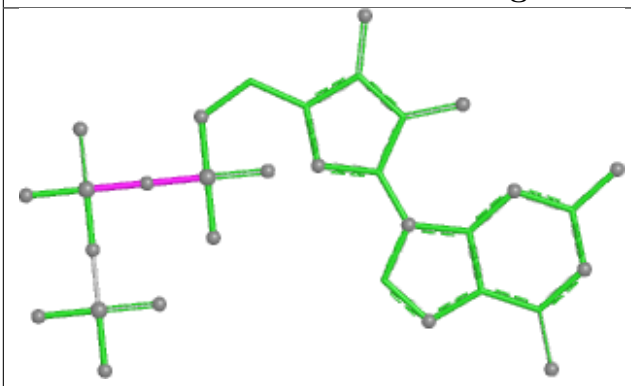


Rings

Ligand GTP EK 501



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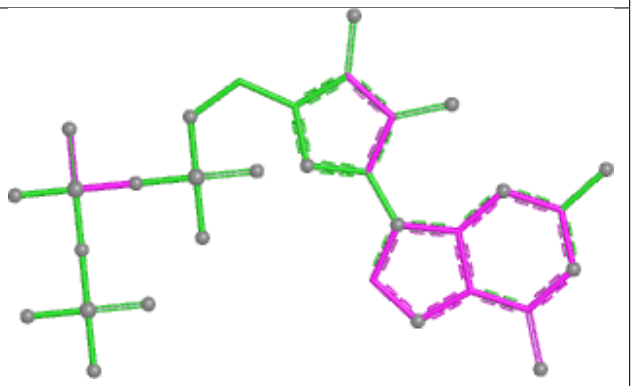

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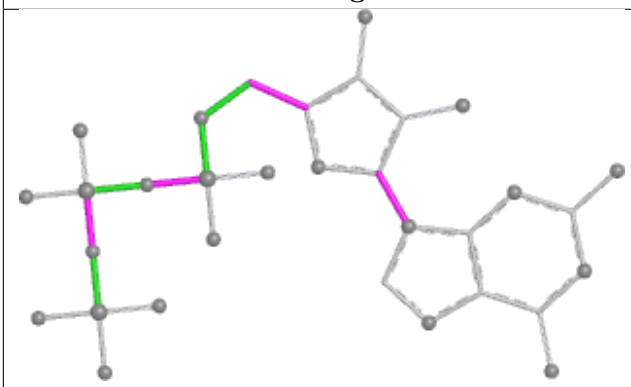

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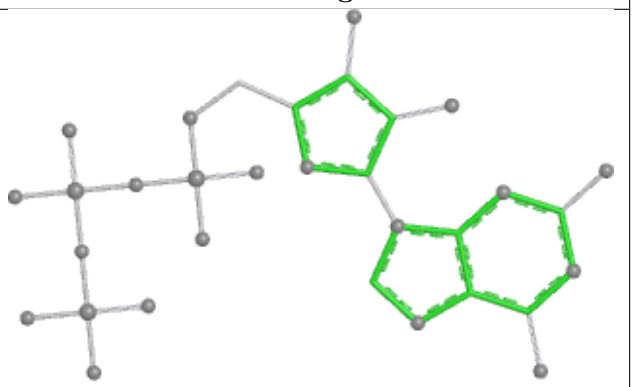
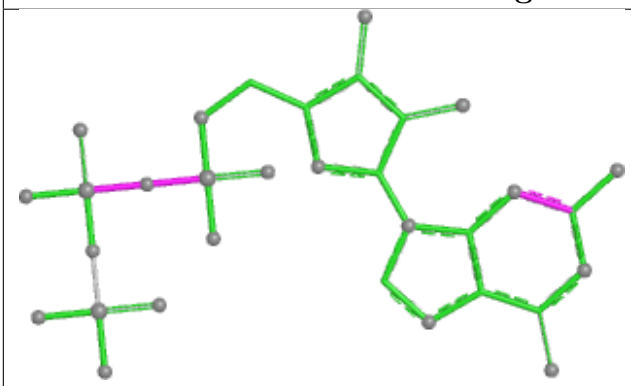


Rings

Ligand GTP KI 501



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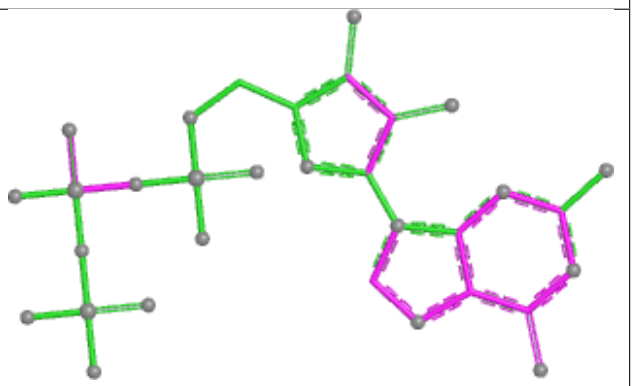

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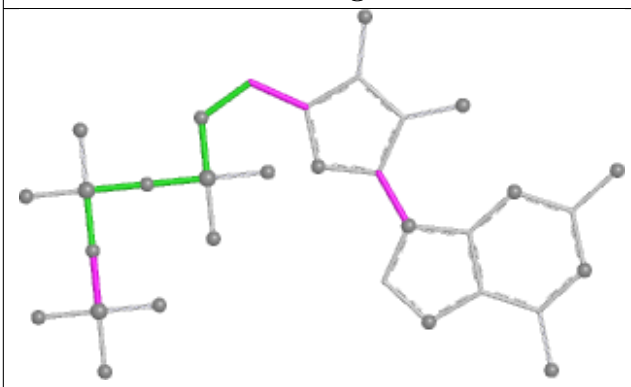

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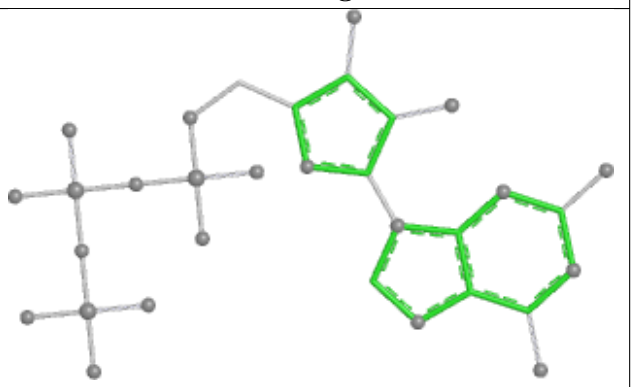
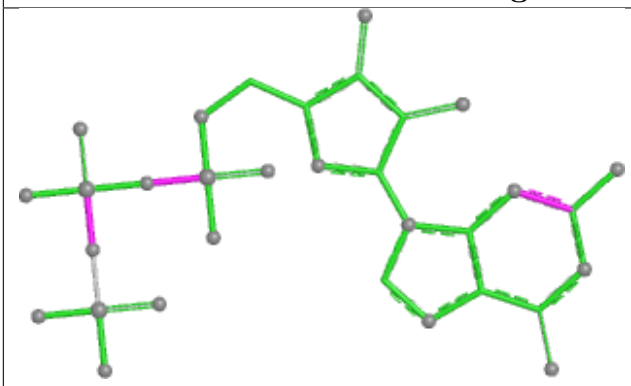


Rings

Ligand GTP NF 501



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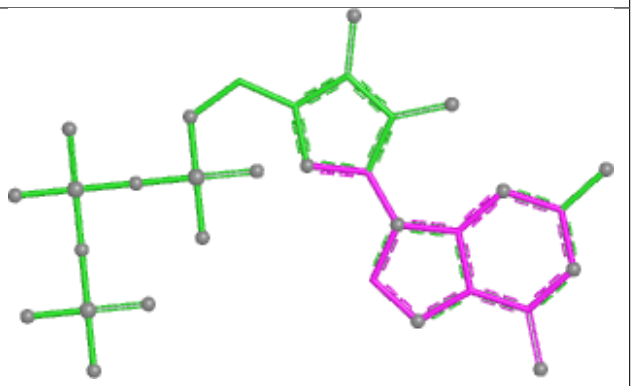

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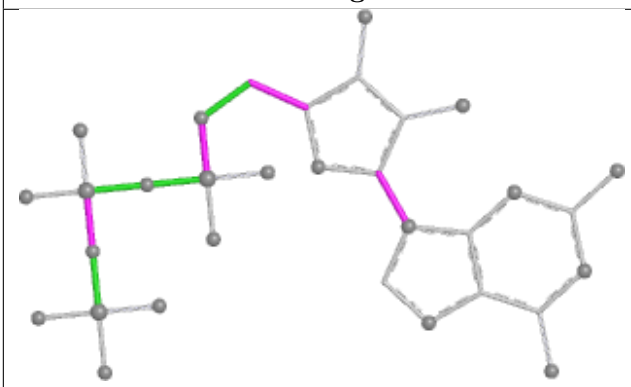
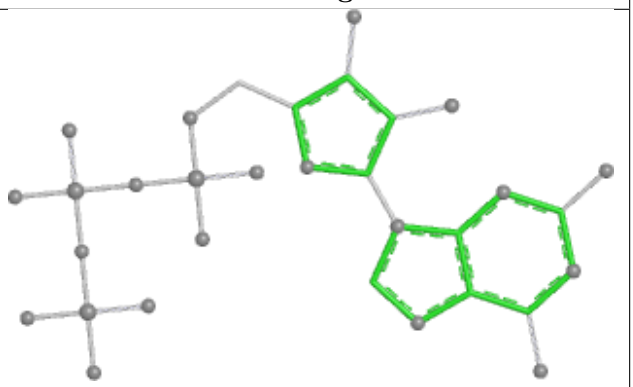
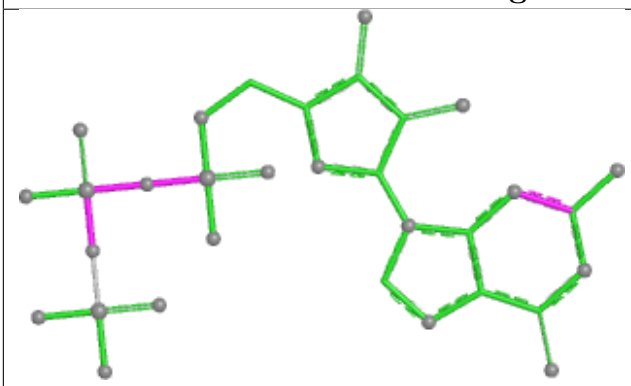


Torsions



Rings

Ligand GTP QC 501



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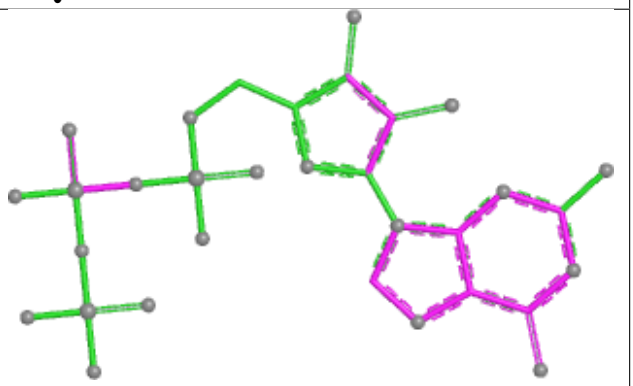

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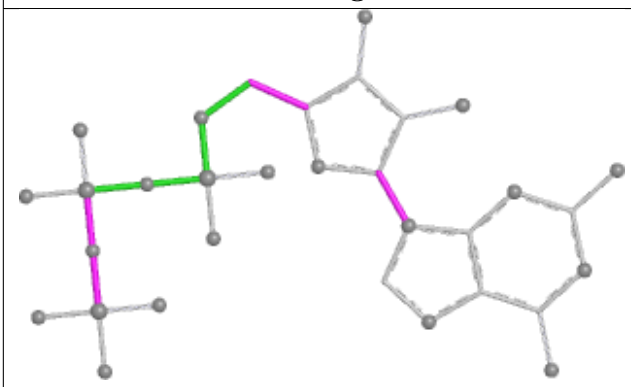

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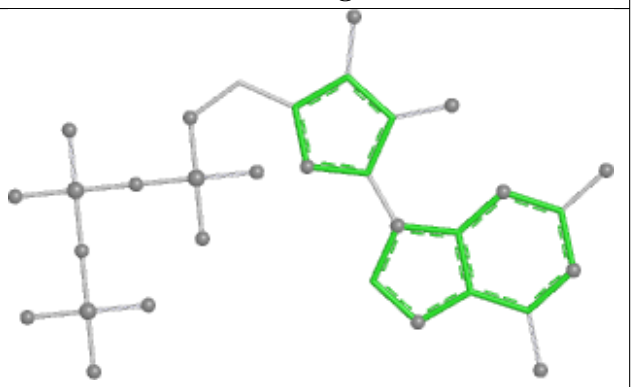
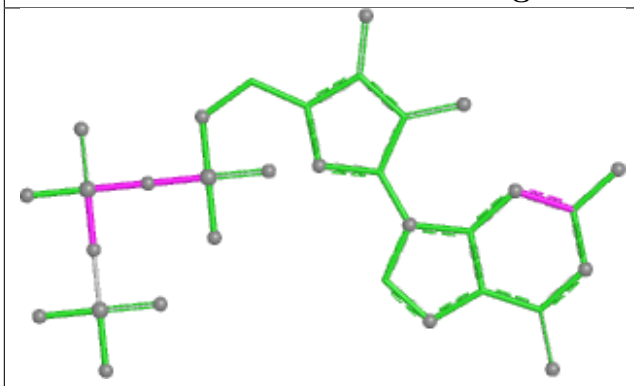


Rings

Ligand GTP FB 501



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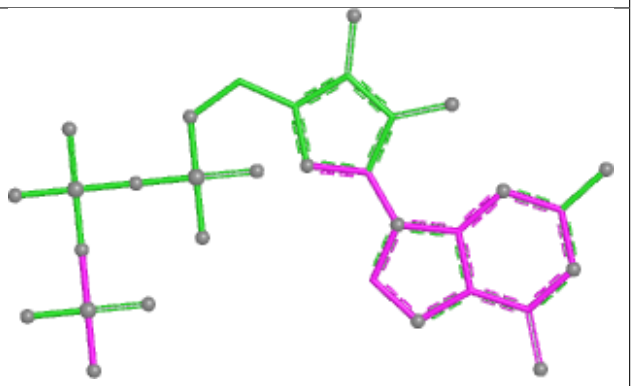

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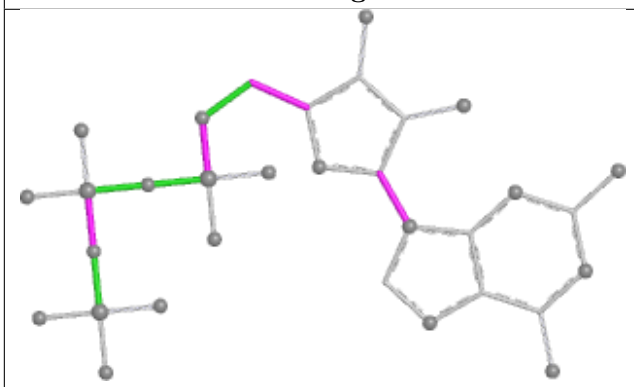

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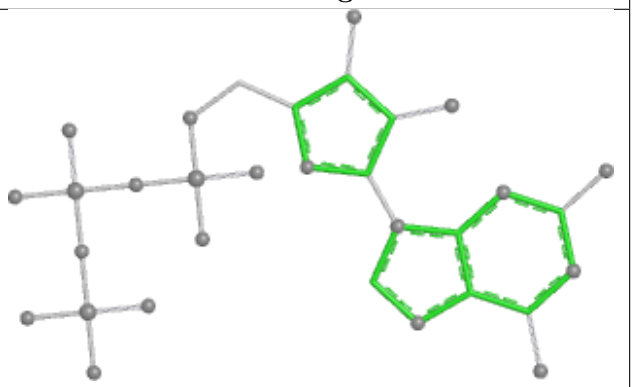
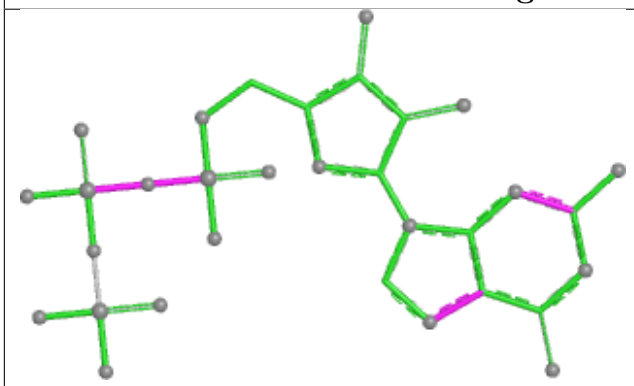


Rings

Ligand GTP LJ 501



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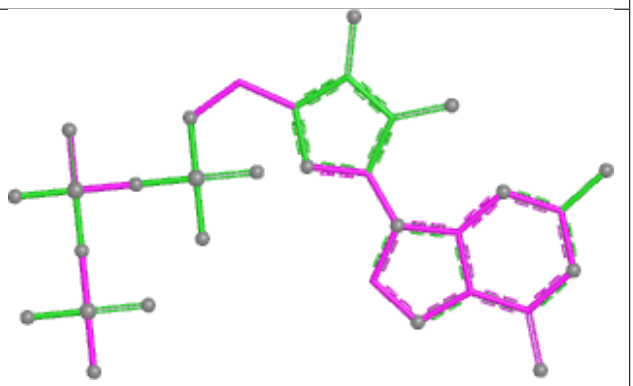

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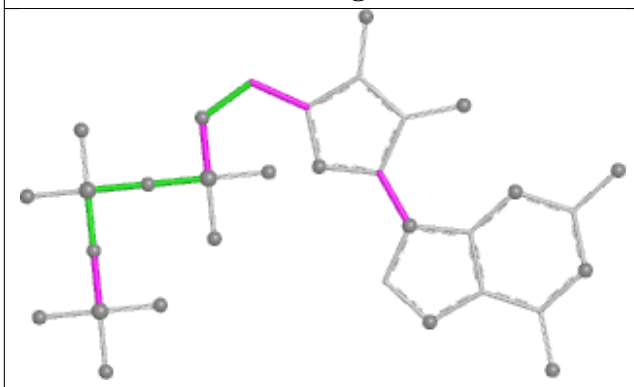

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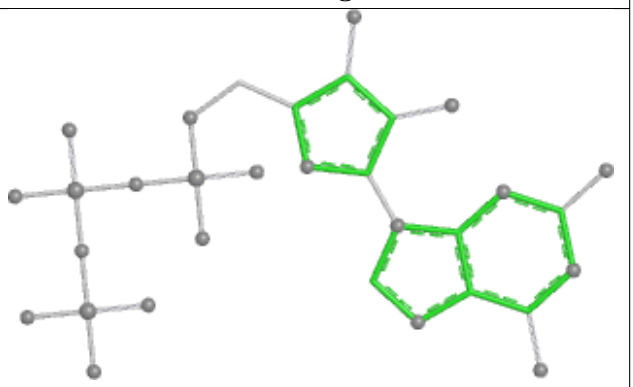

Rings

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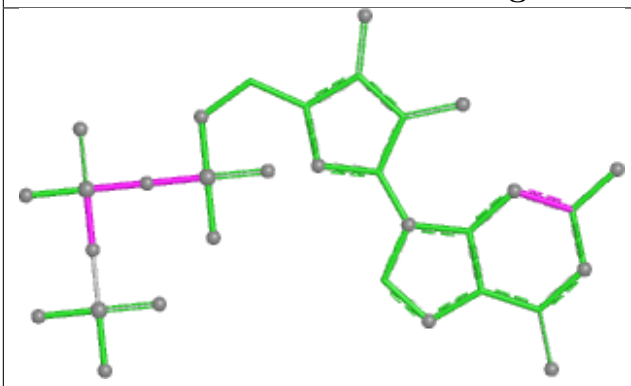

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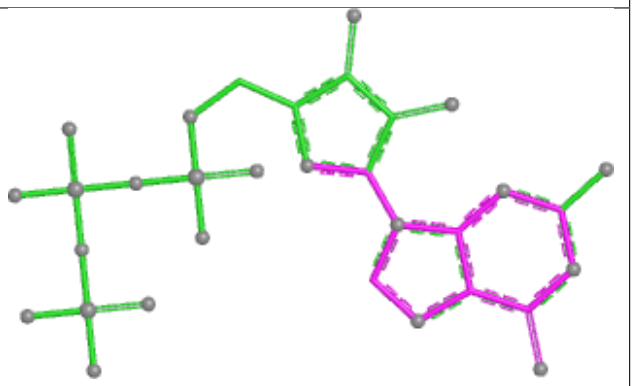

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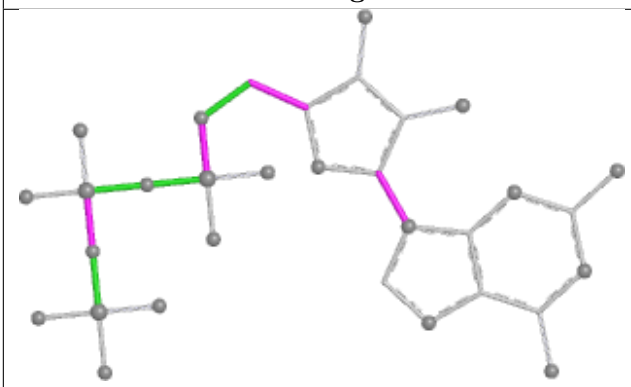

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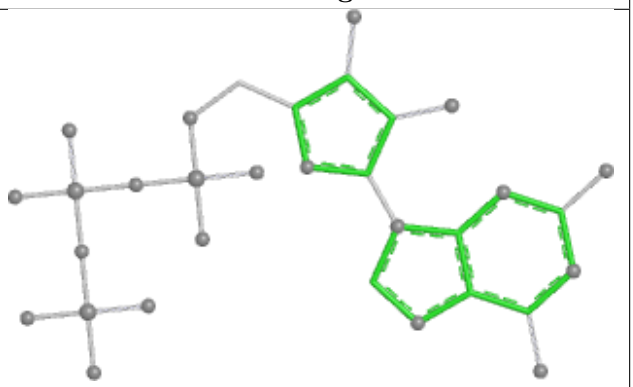
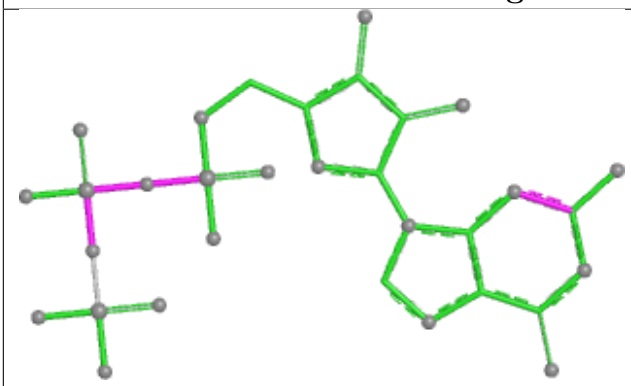


Rings

Ligand GTP TM 501



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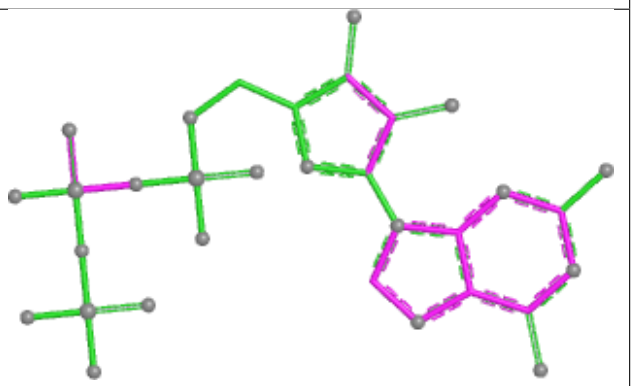

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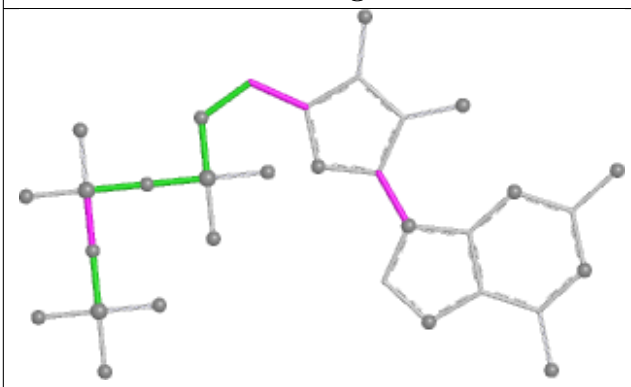

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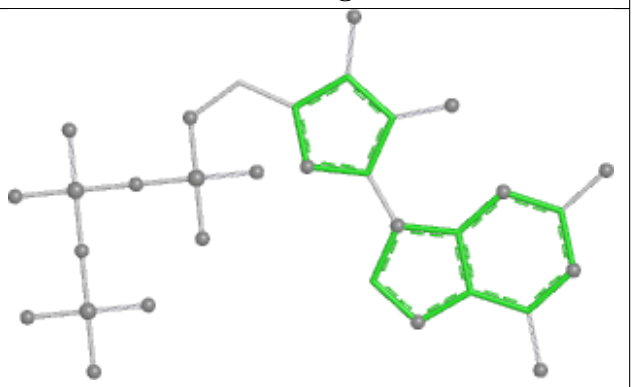
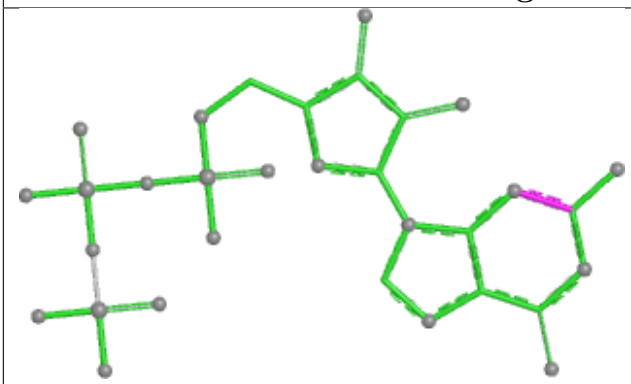


Rings

Ligand GTP IB 501



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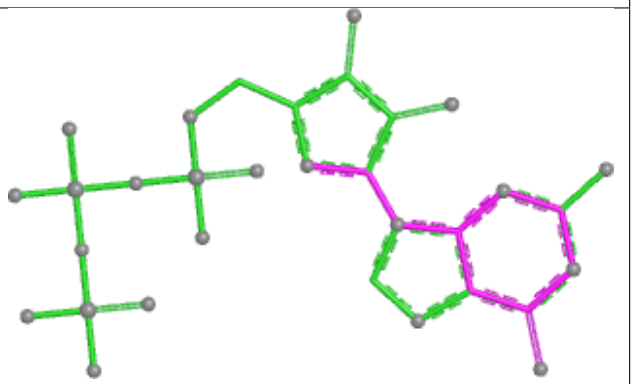

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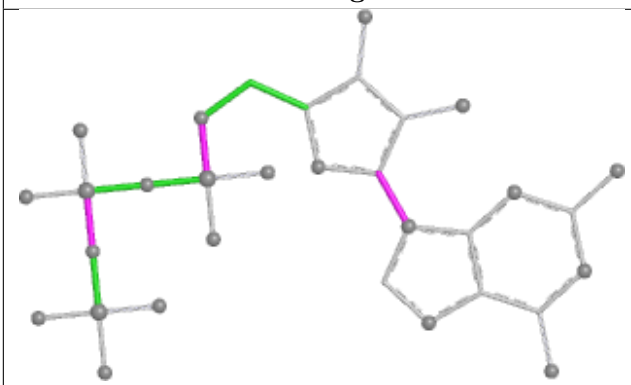

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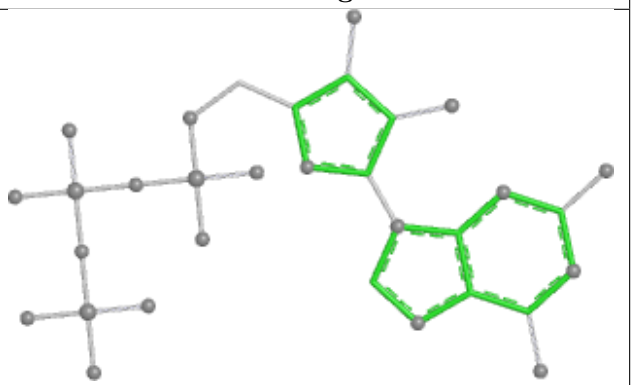
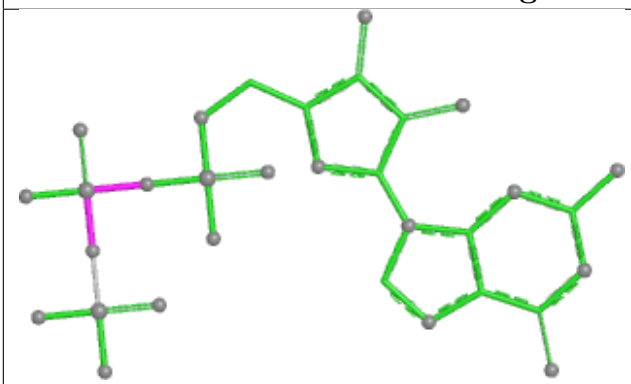


Rings

Ligand GTP JI 501



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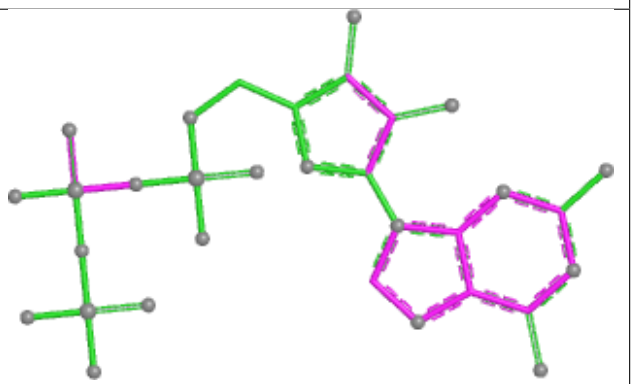

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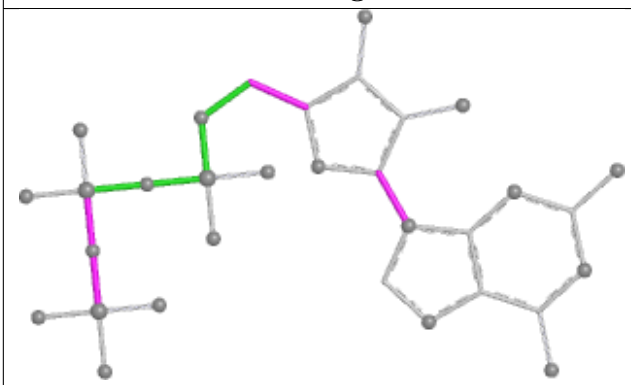

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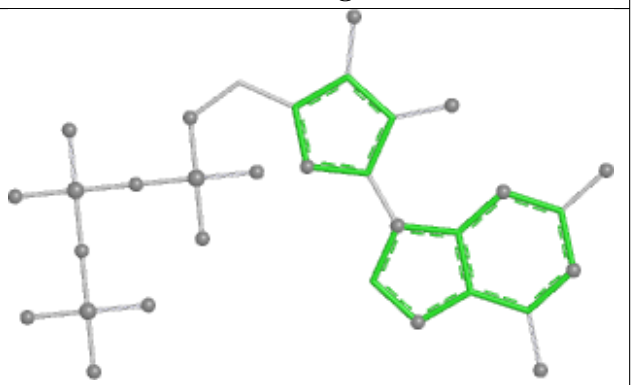
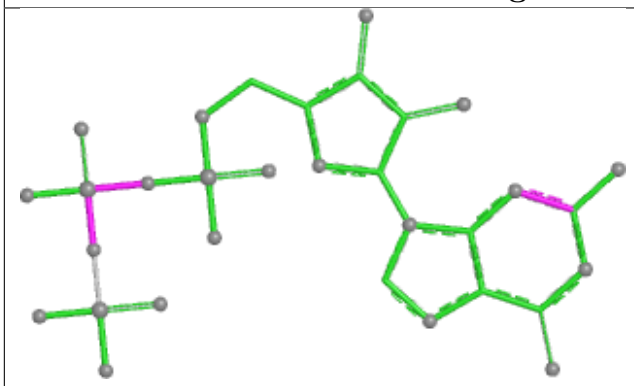


Rings

Ligand GTP OK 501



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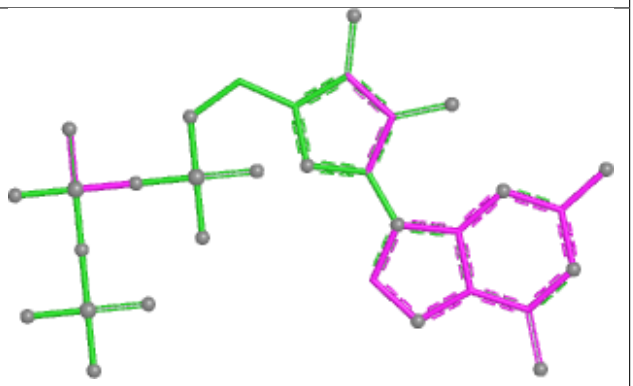

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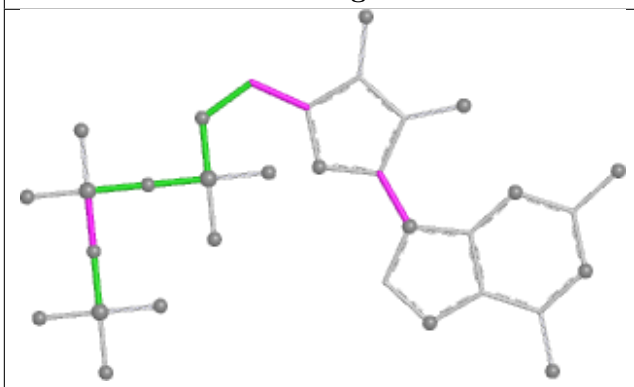

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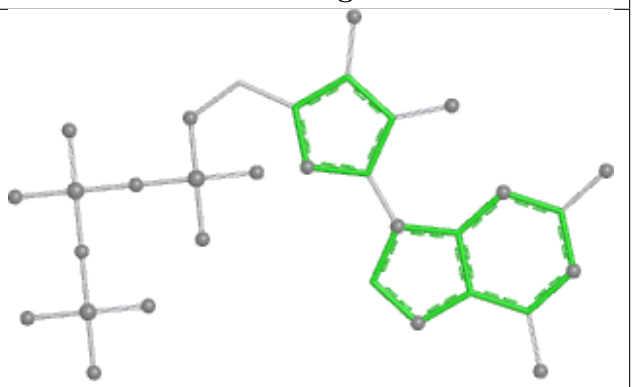
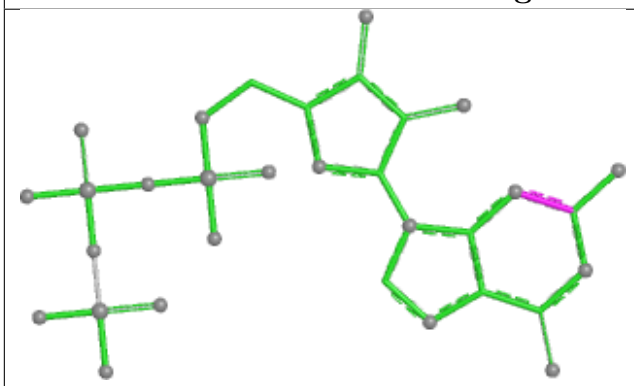


Rings

Ligand GTP CJ 501



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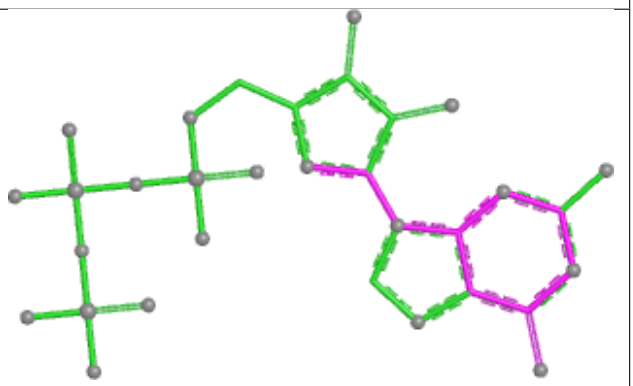

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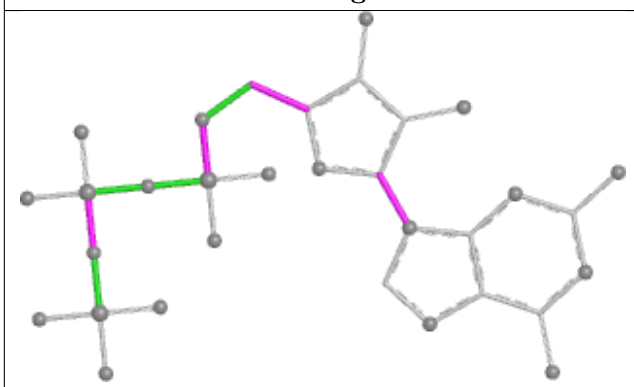

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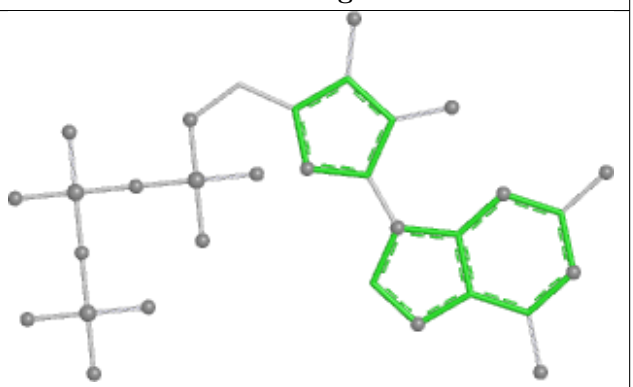
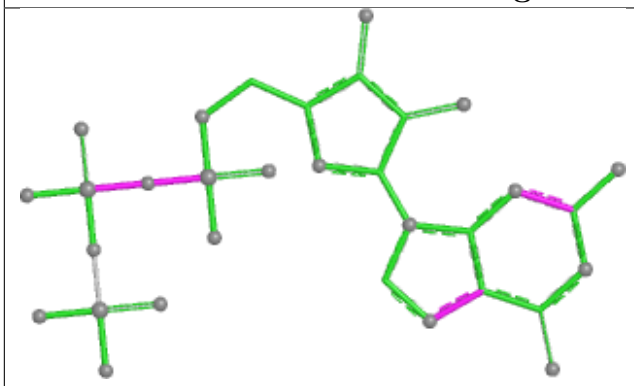


Rings

Ligand GTP EF 501



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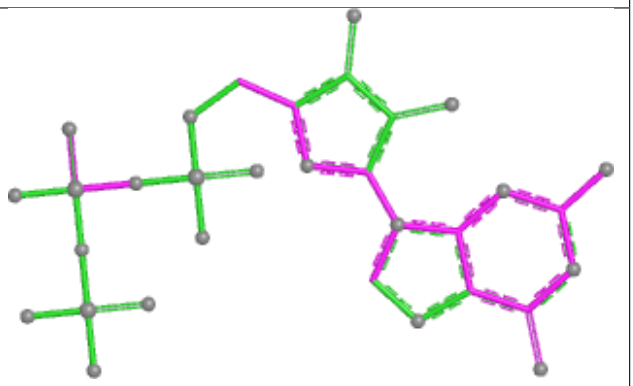

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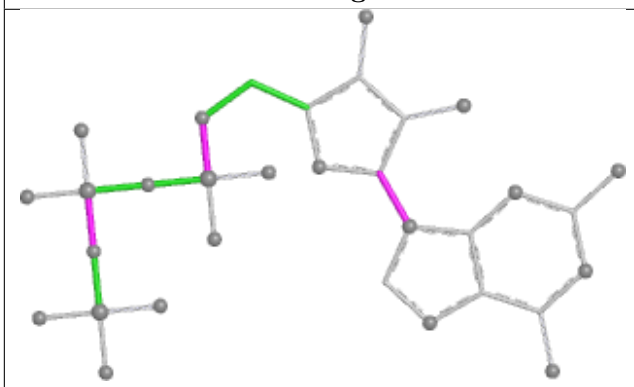

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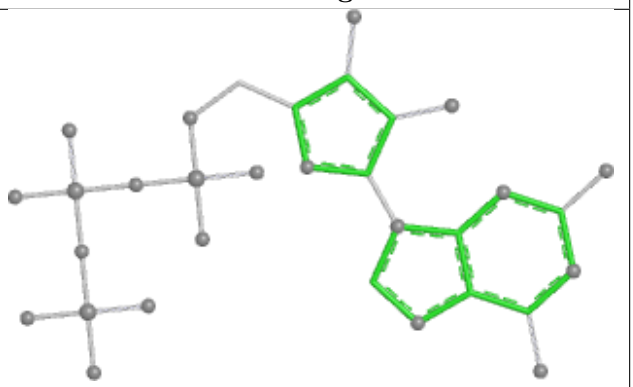
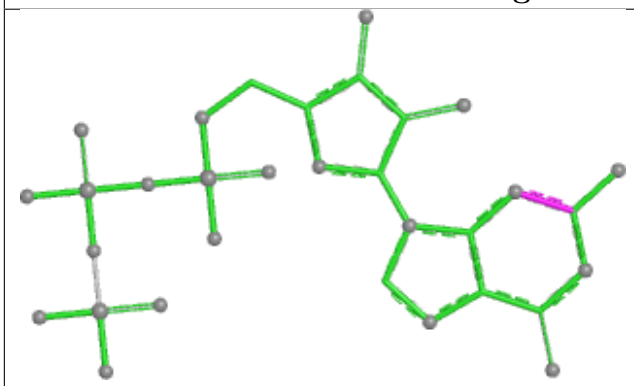


Rings

Ligand GTP PF 501



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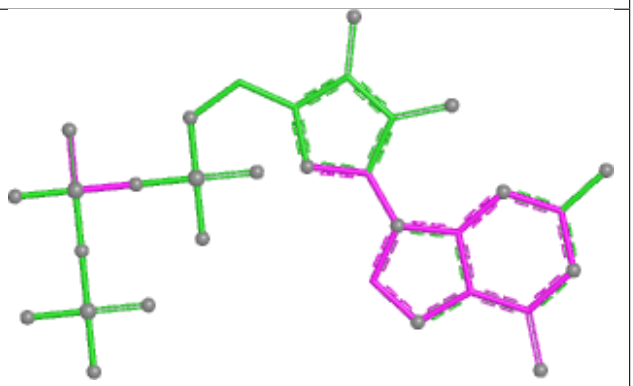

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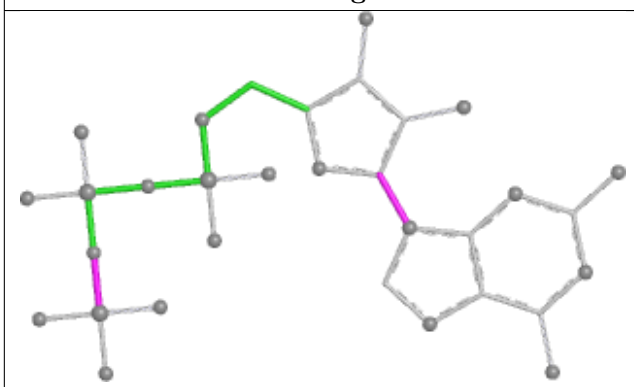

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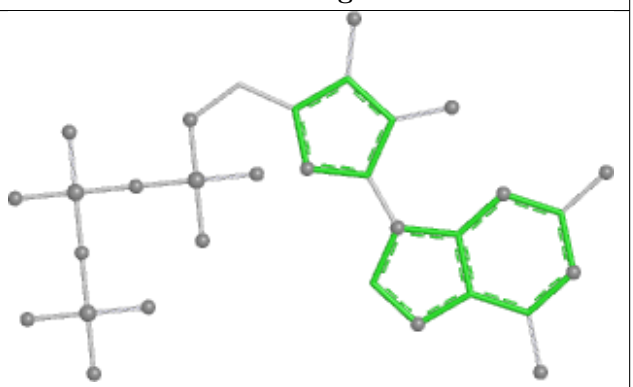
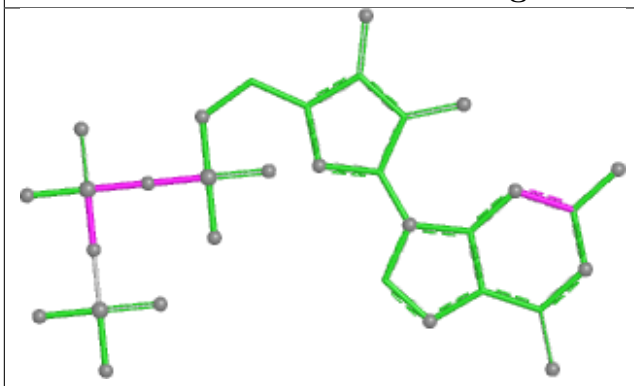


Rings

Ligand GTP BG 501



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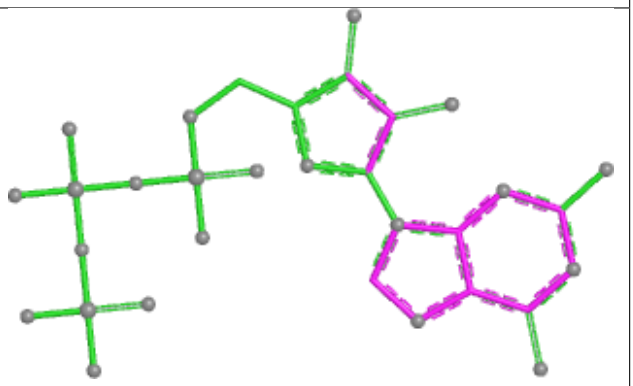

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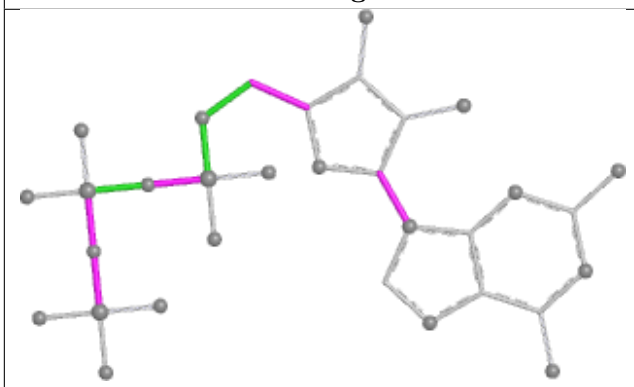

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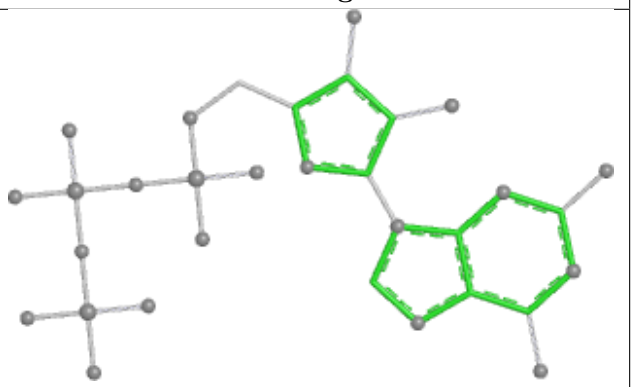
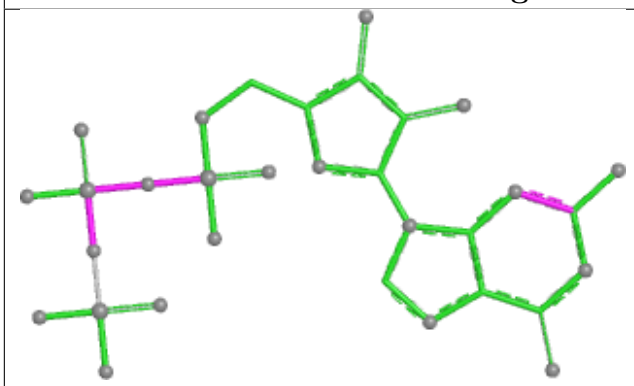


Rings

Ligand GTP EH 501



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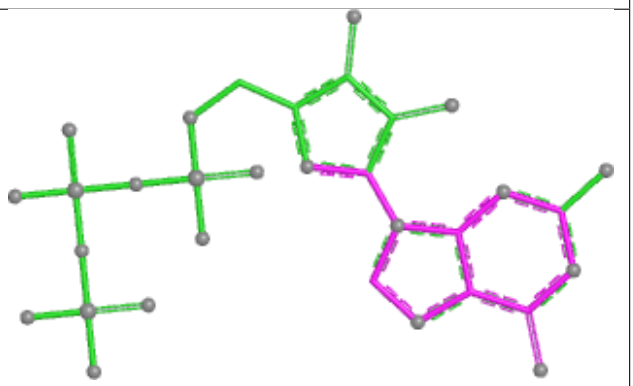

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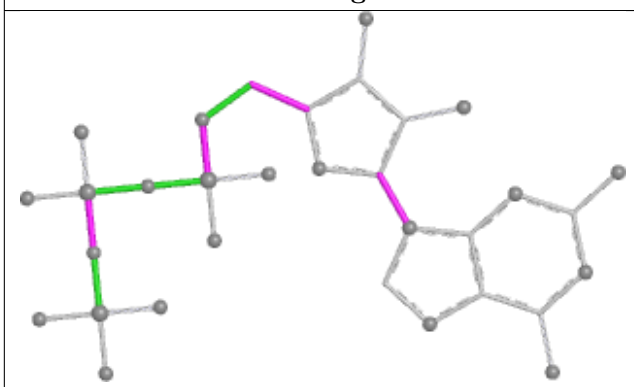

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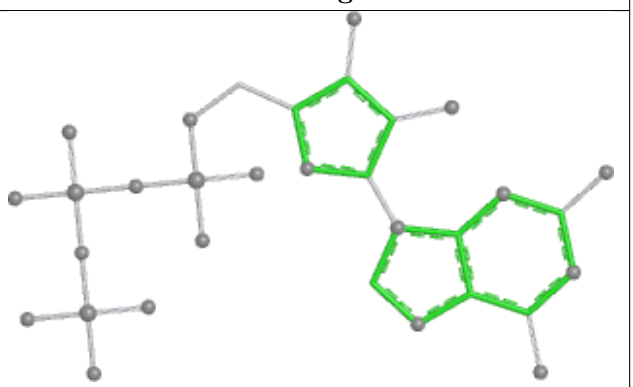
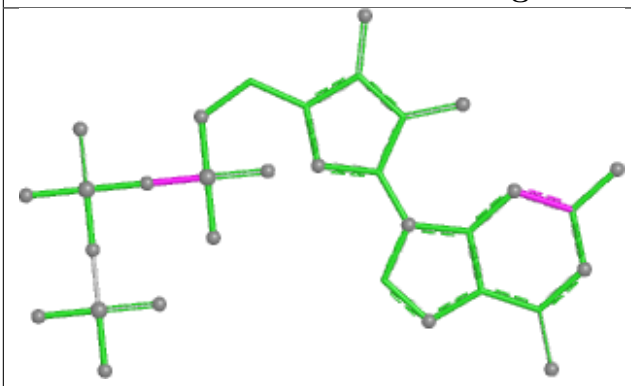


Rings

Ligand GTP BF 501



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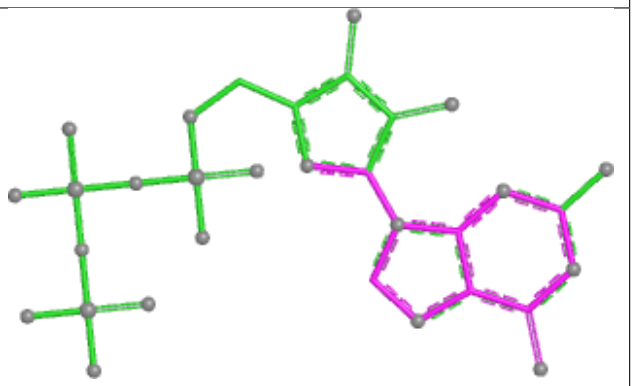

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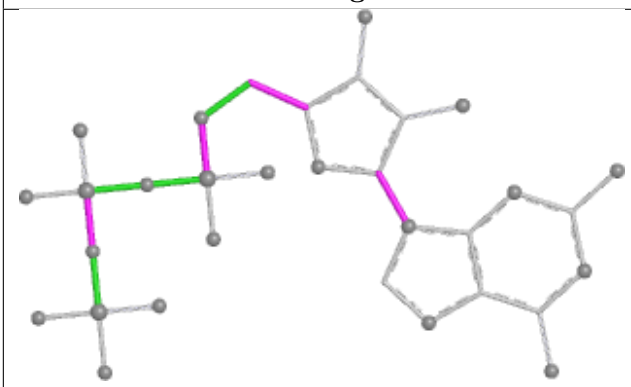
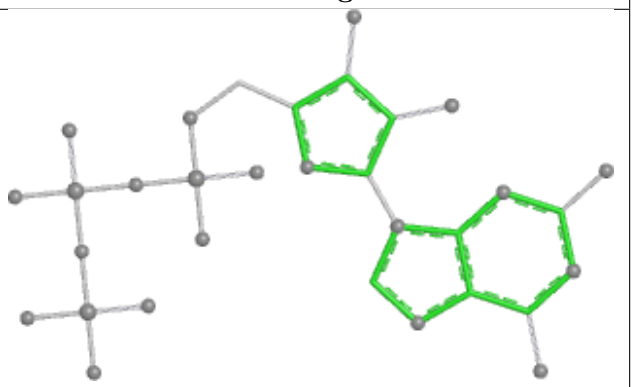
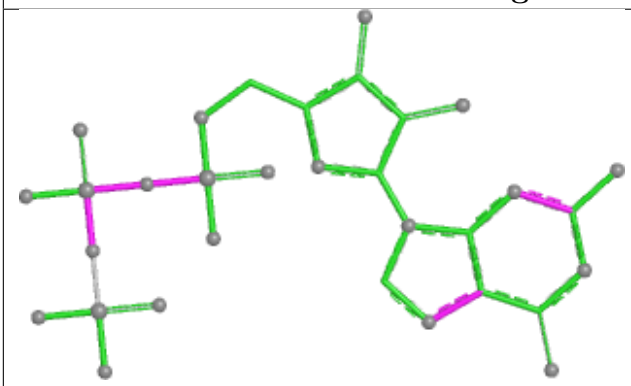


Torsions



Rings

Ligand GTP AL 501



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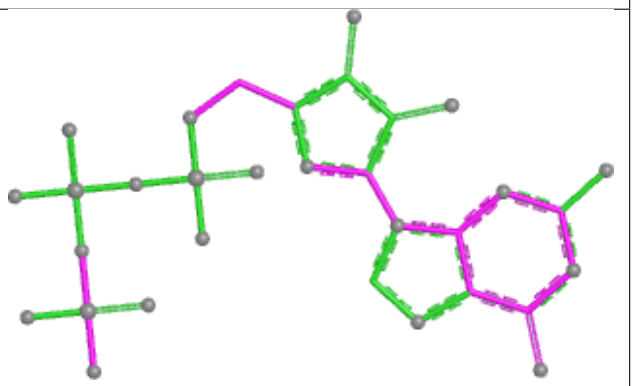

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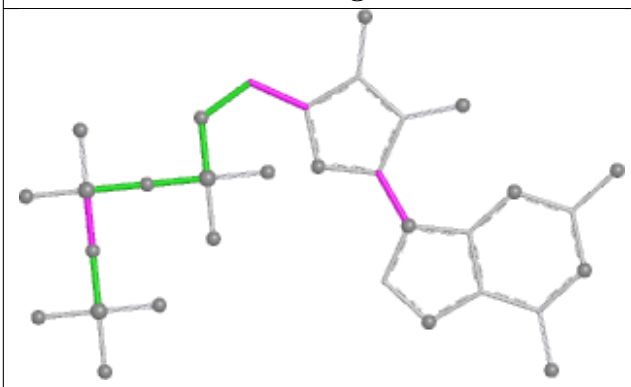

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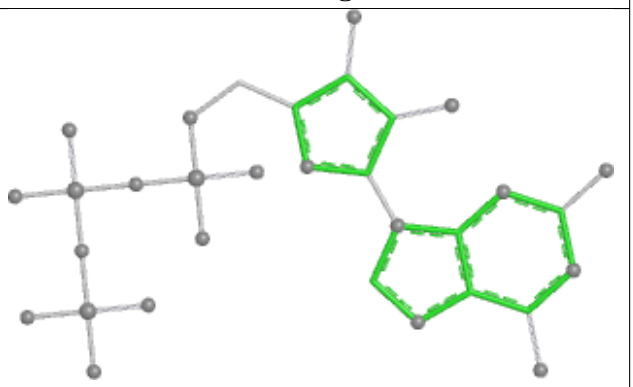
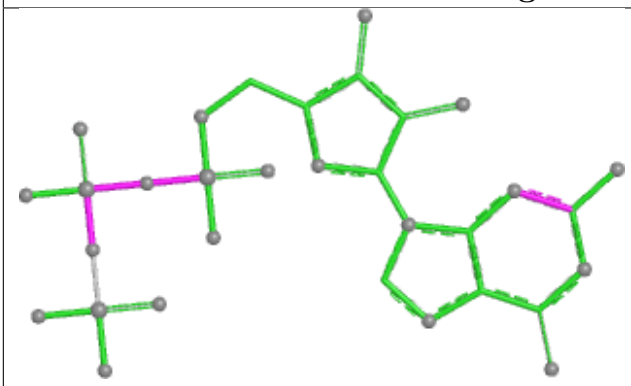


Rings

Ligand GTP LI 501



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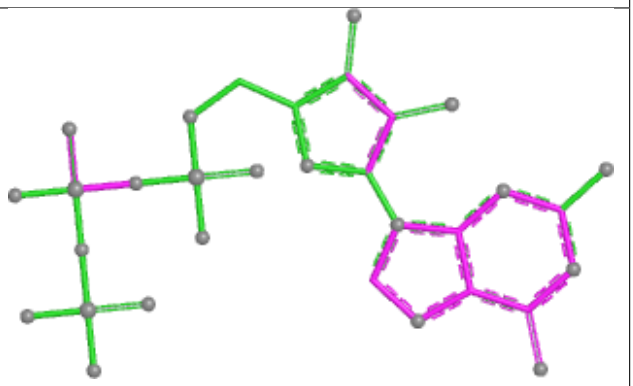

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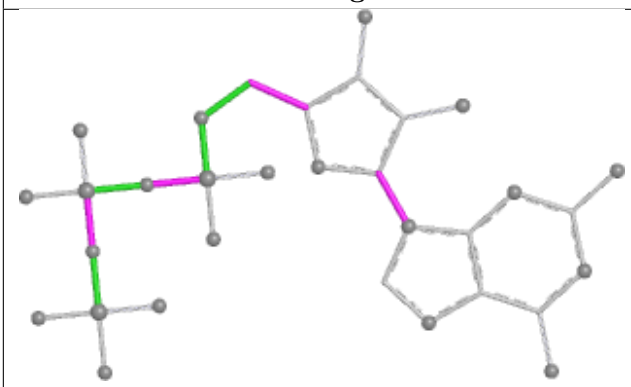

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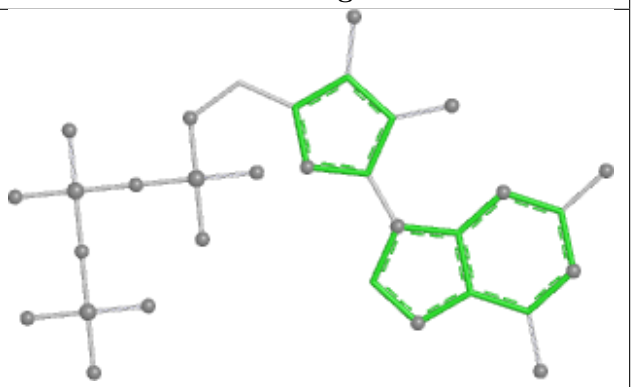
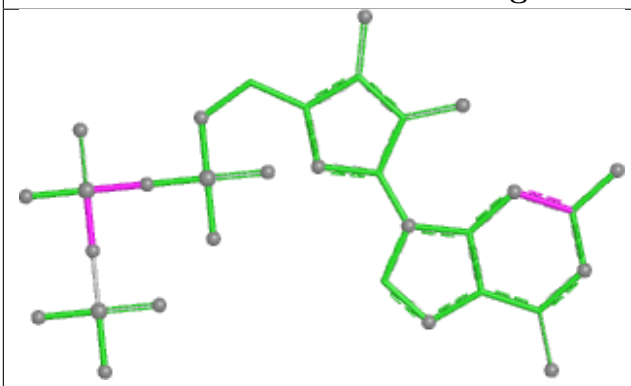


Rings

Ligand GTP KE 501



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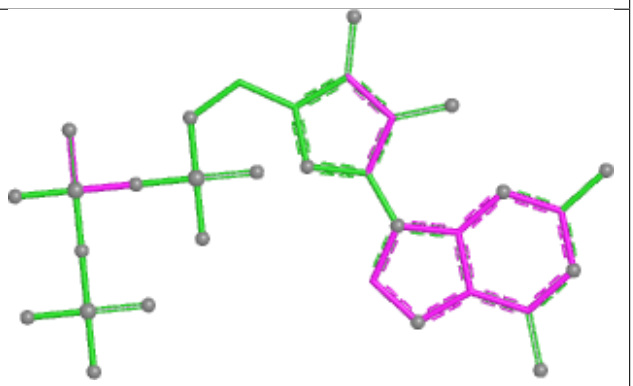

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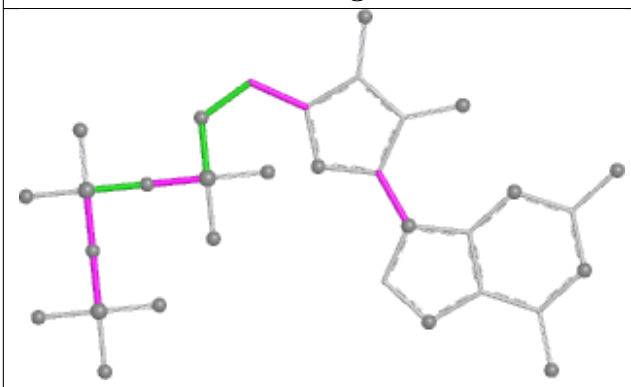

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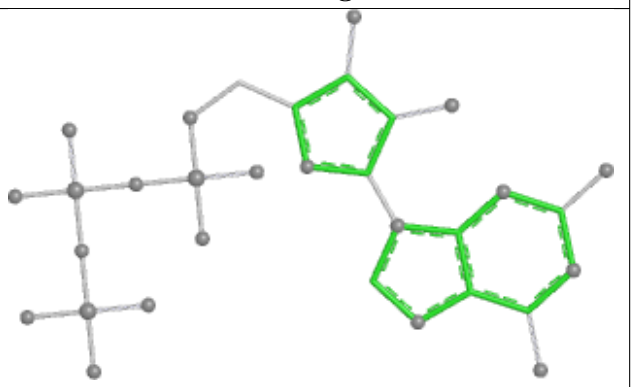

Rings

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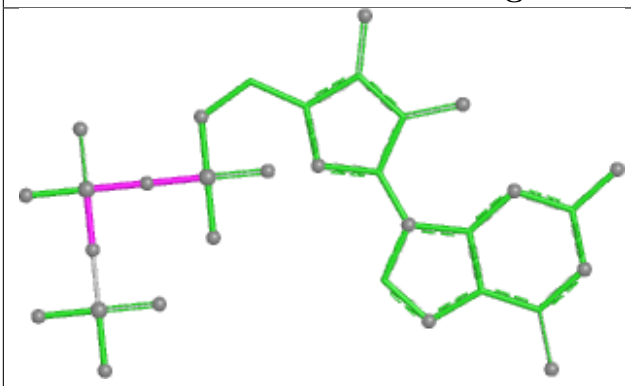

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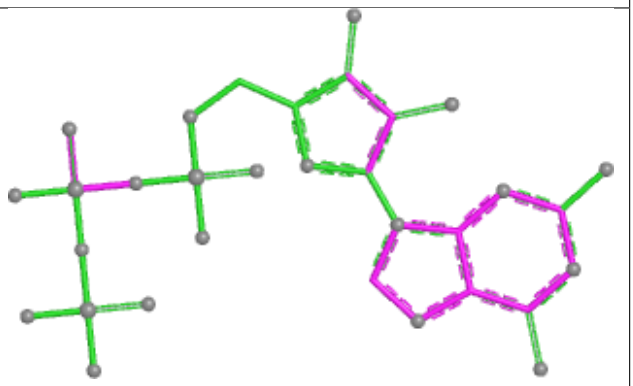

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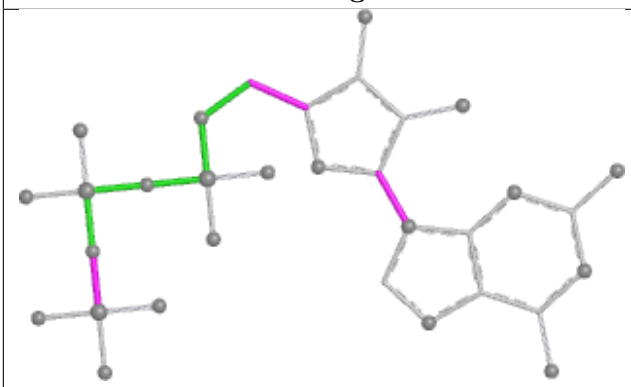

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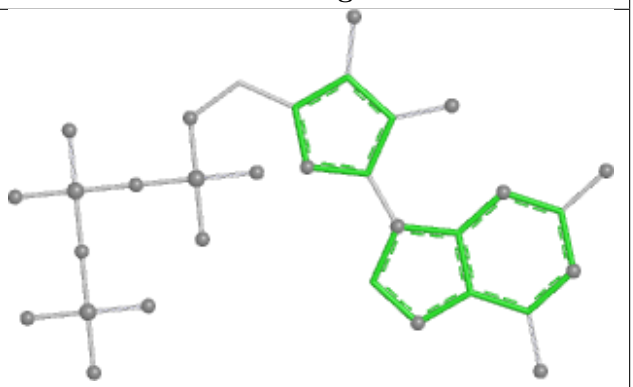

Rings

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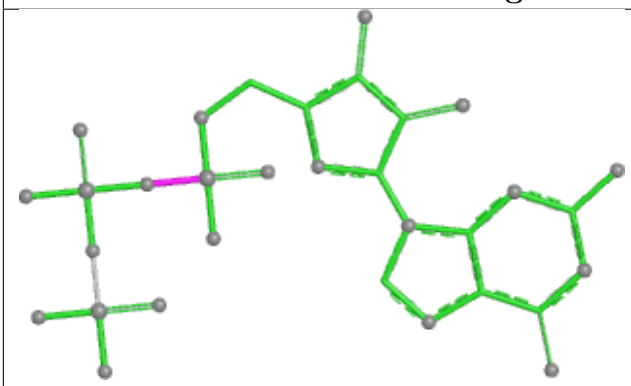

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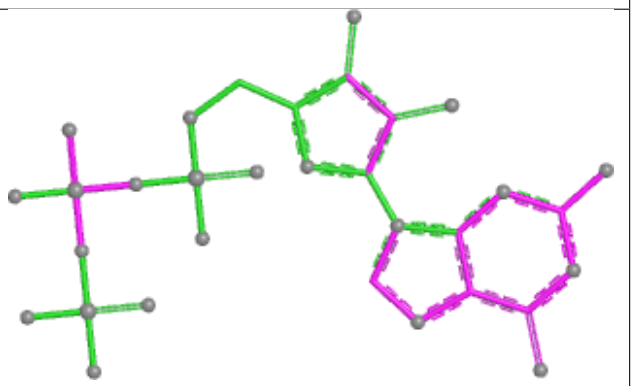

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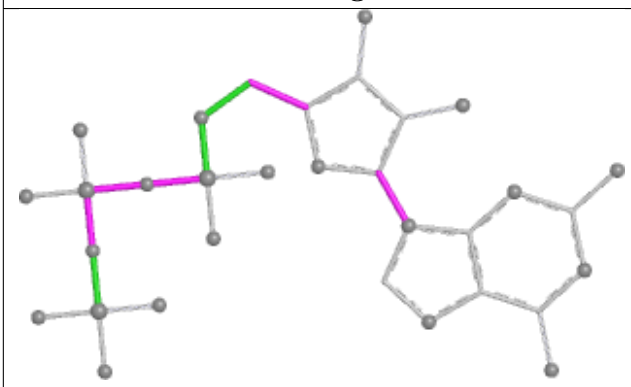

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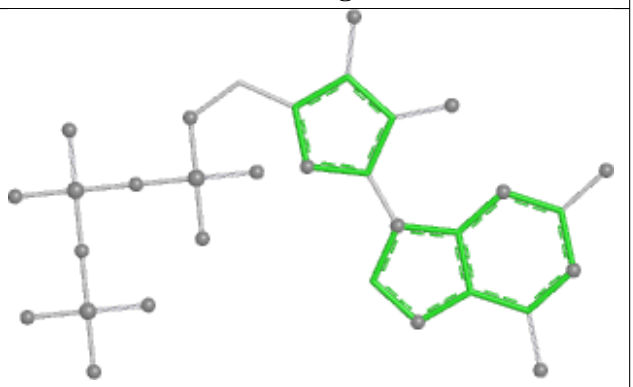

Rings

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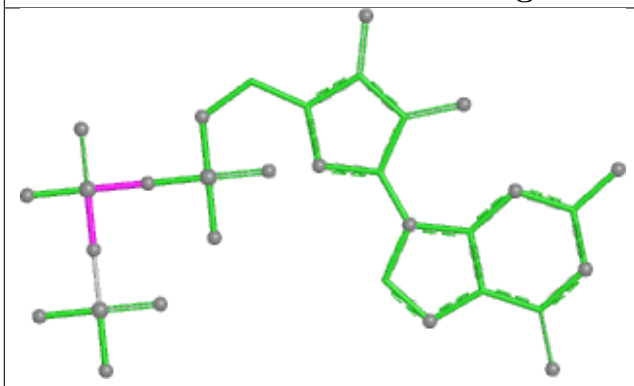

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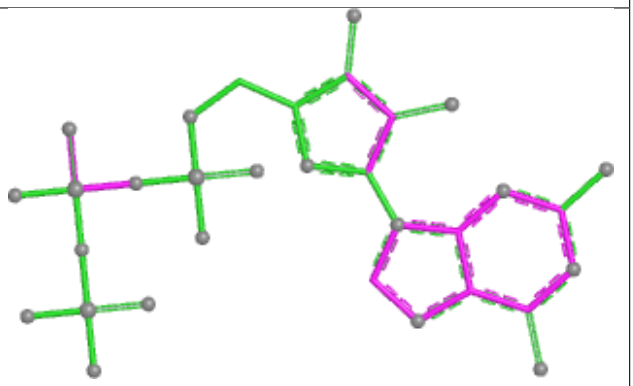

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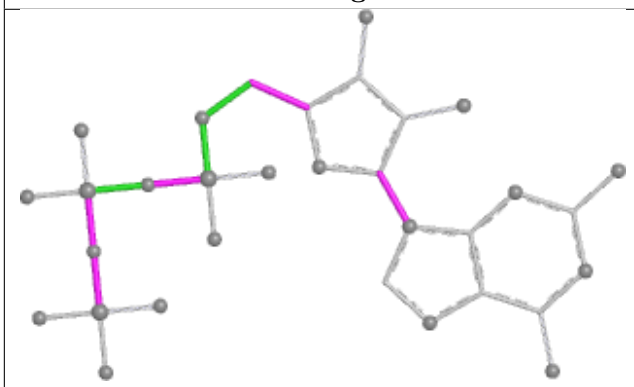

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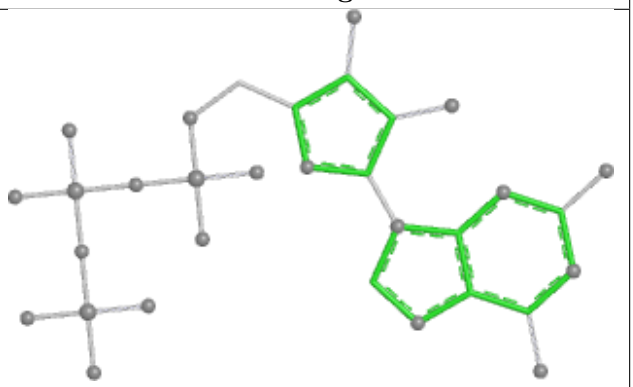
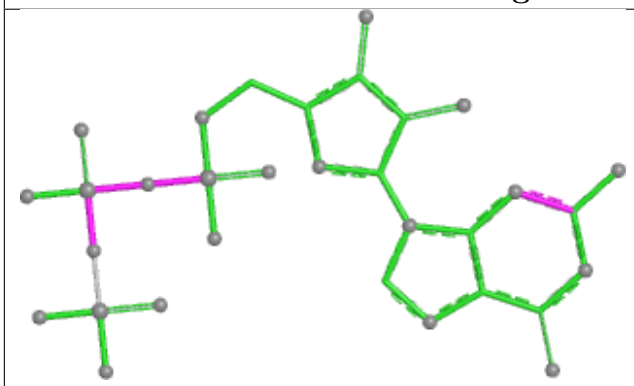


Rings

Ligand GTP TE 501



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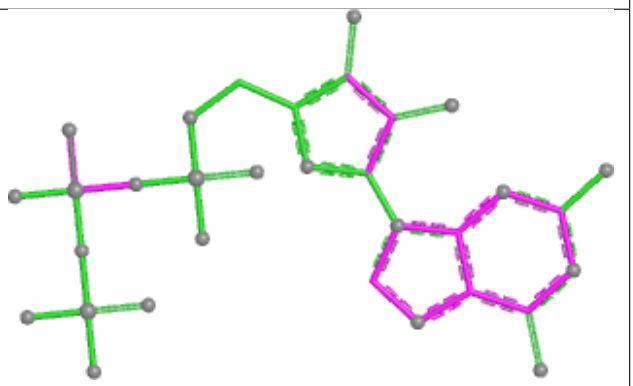

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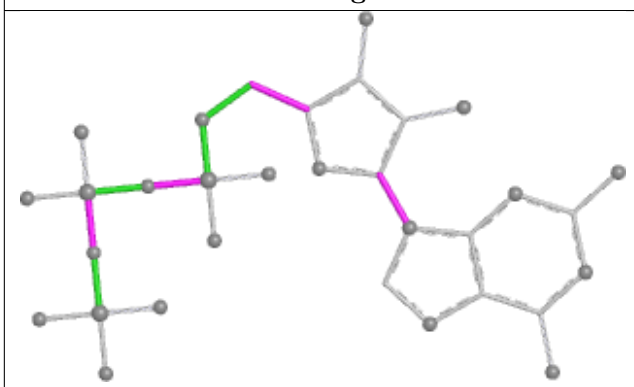

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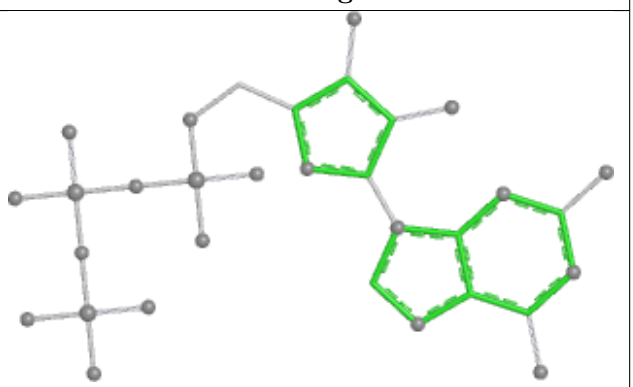
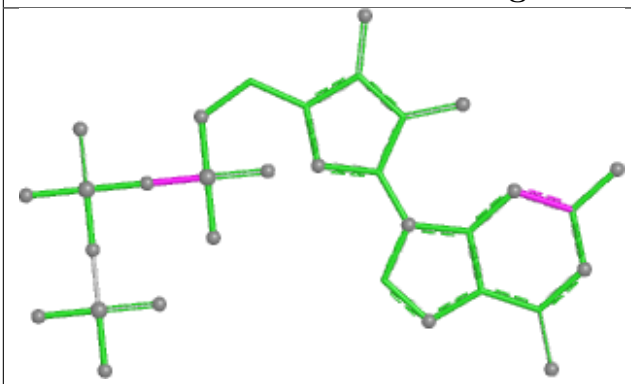


Rings

Ligand GTP TN 501



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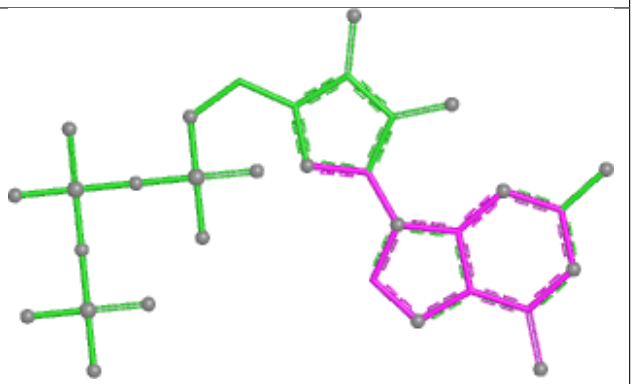

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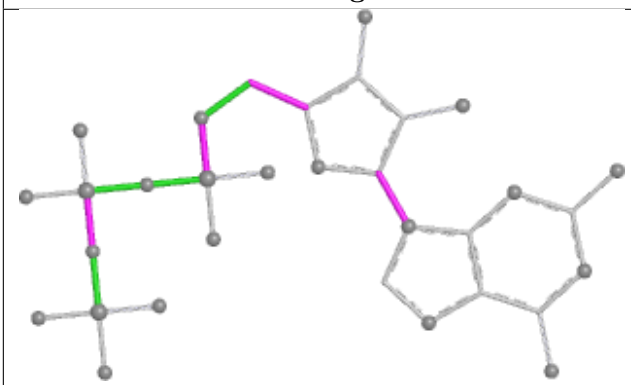

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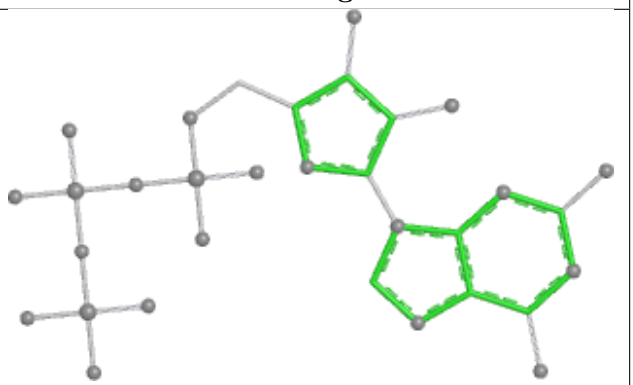

Rings

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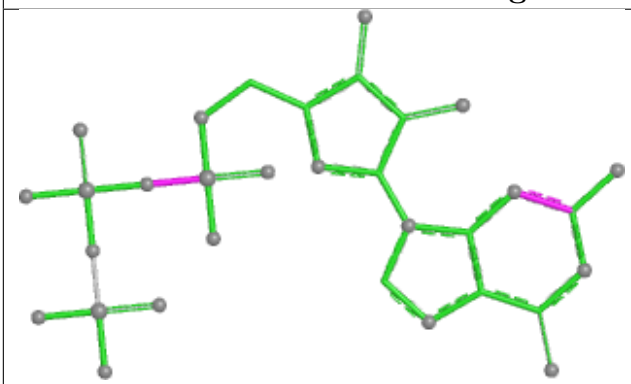

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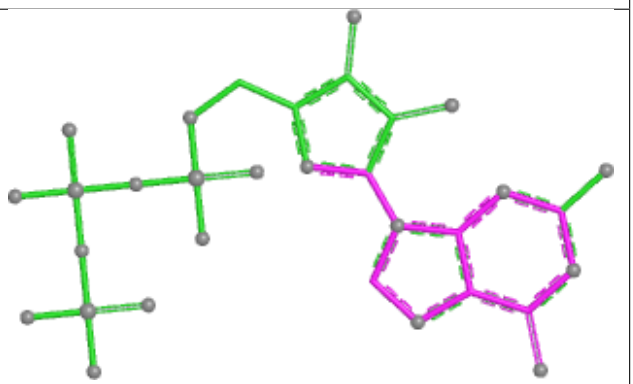

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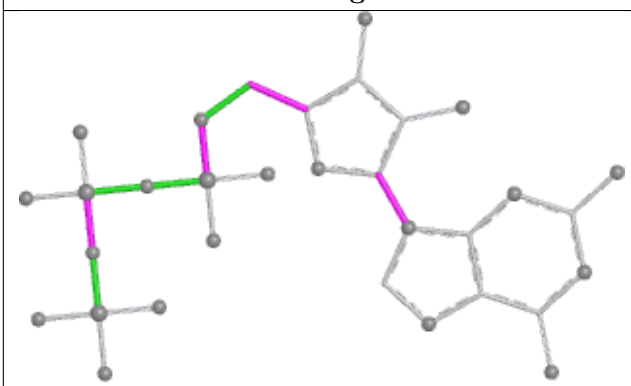

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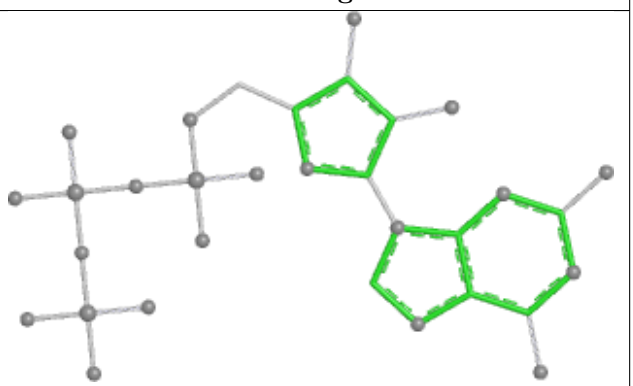

Rings

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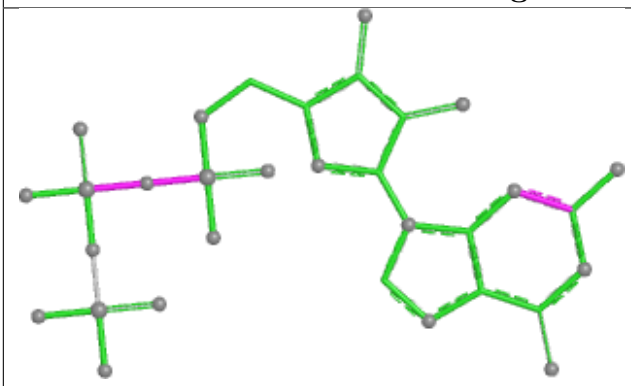

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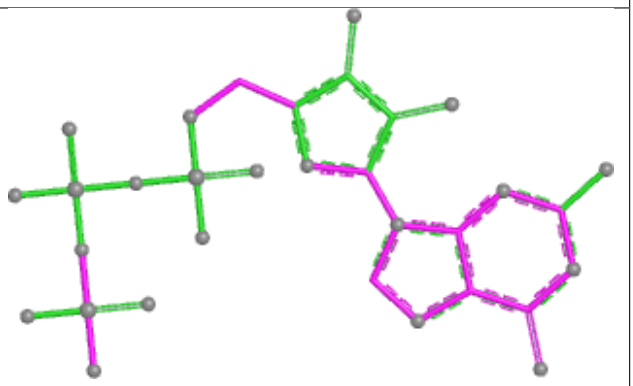

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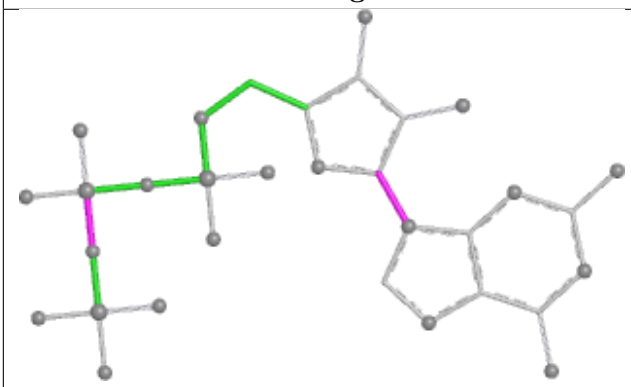

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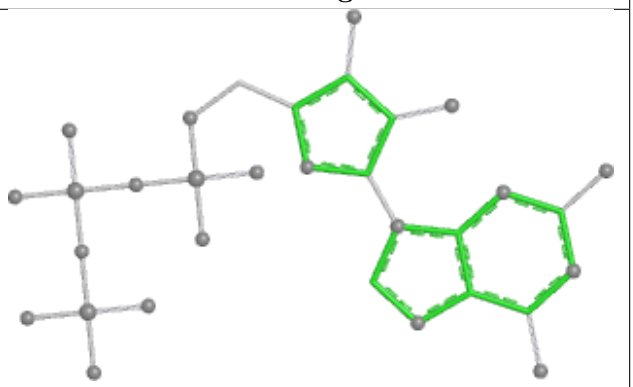
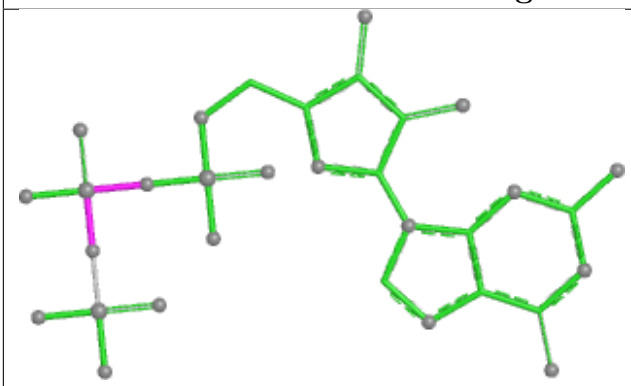


Rings

Ligand GTP AI 501



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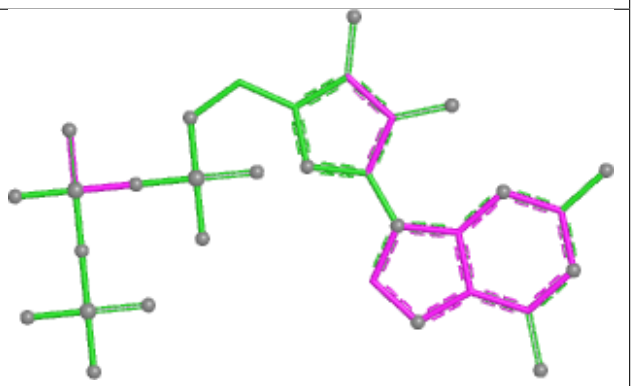

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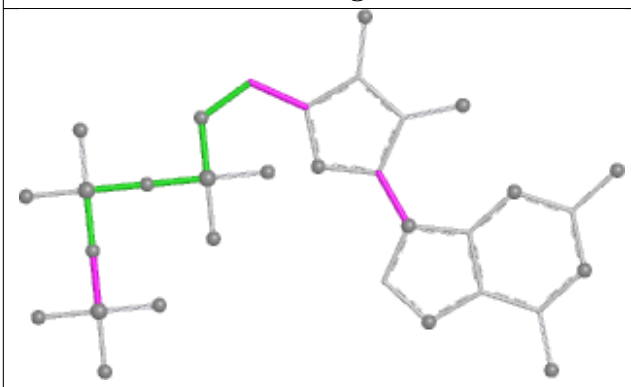

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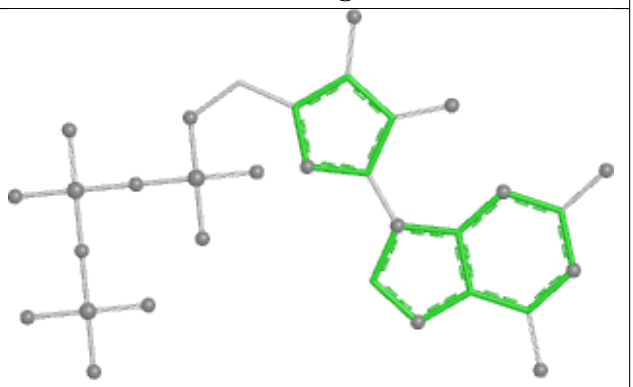
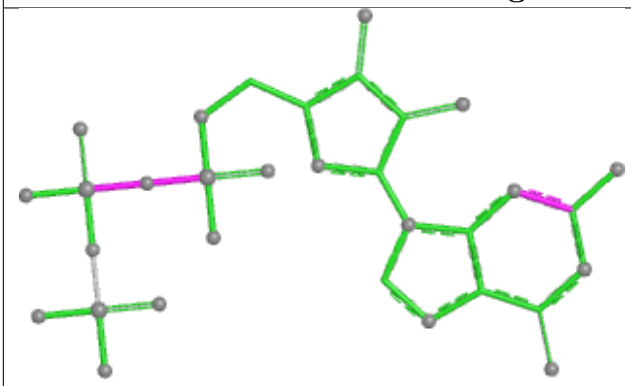


Rings

Ligand GTP VH 501



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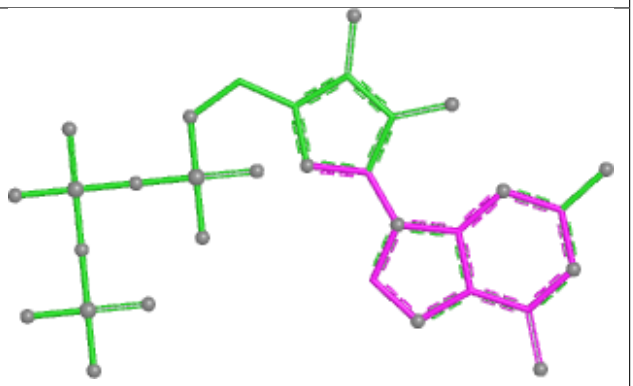
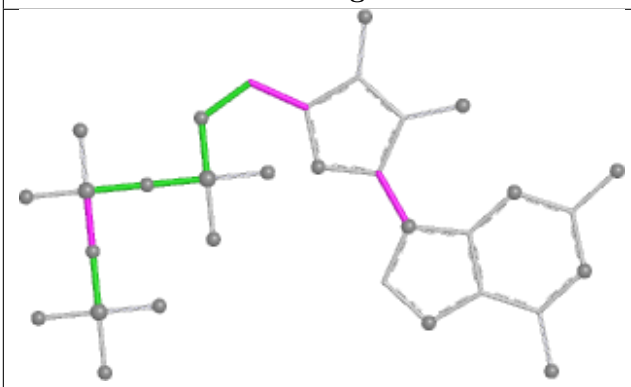


Bond angles



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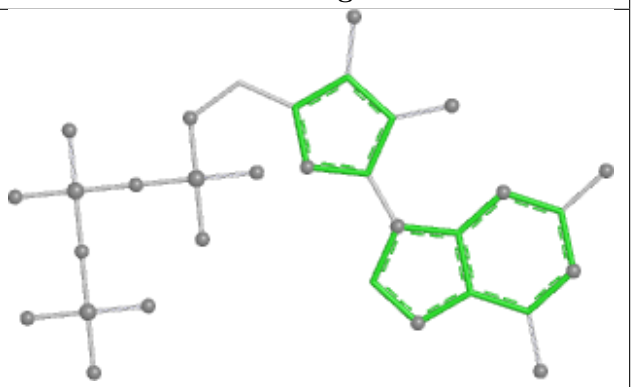
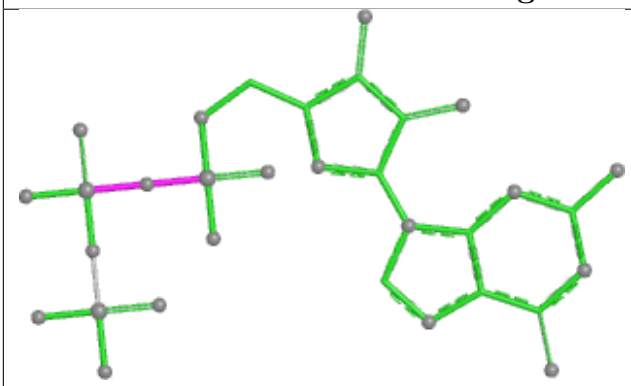


Rings

Ligand GTP EI 501



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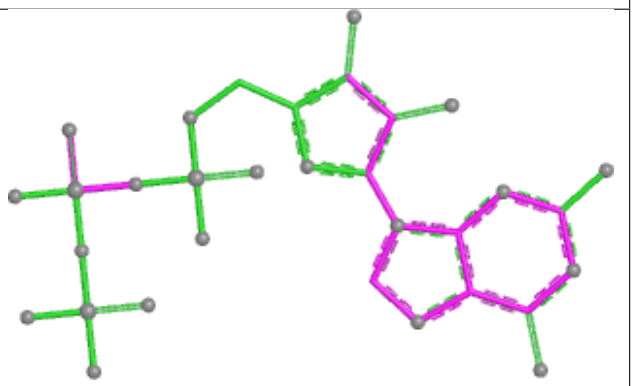

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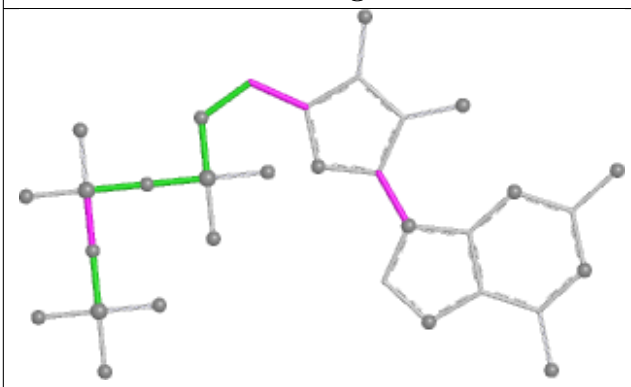

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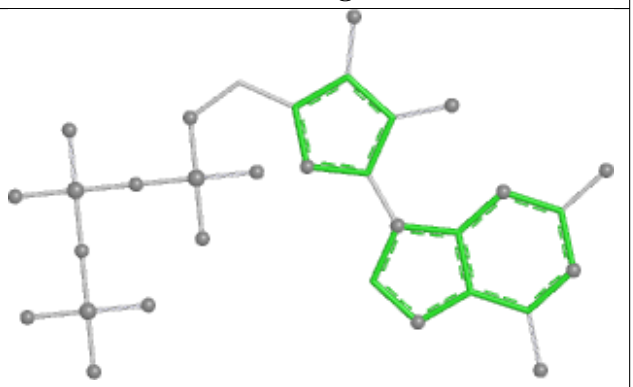
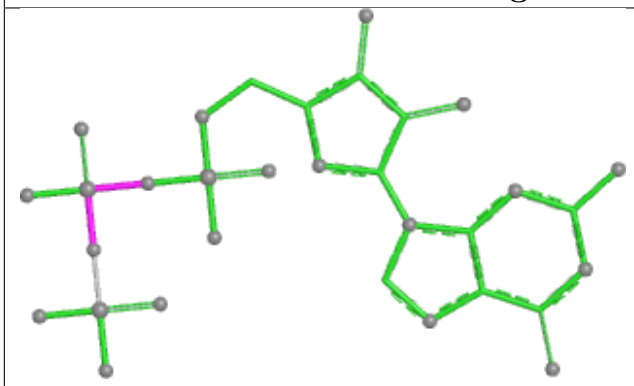


Rings

Ligand GTP UC 501



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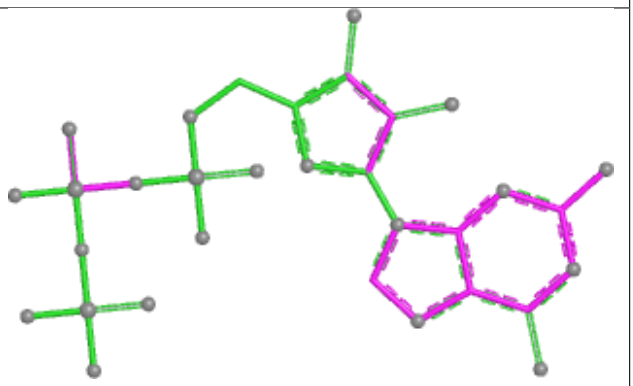

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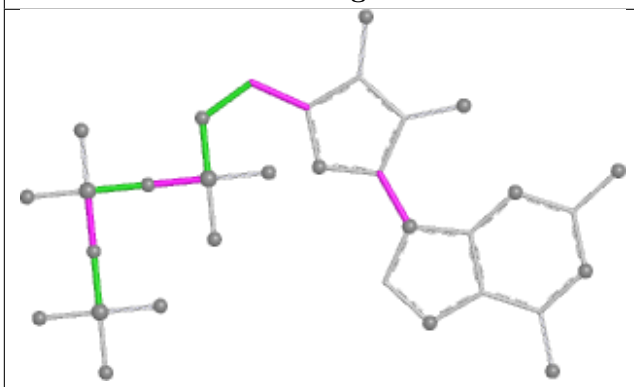
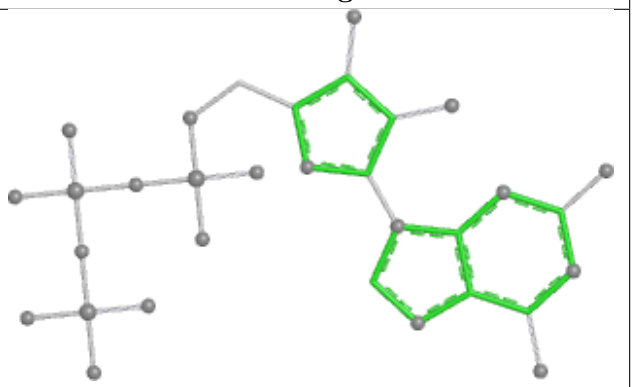
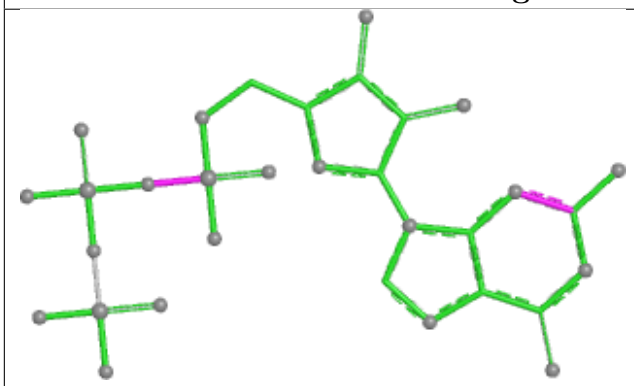


Torsions



Rings

Ligand GTP CF 501



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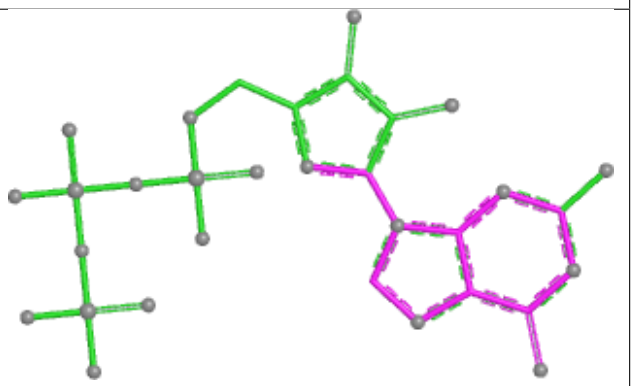

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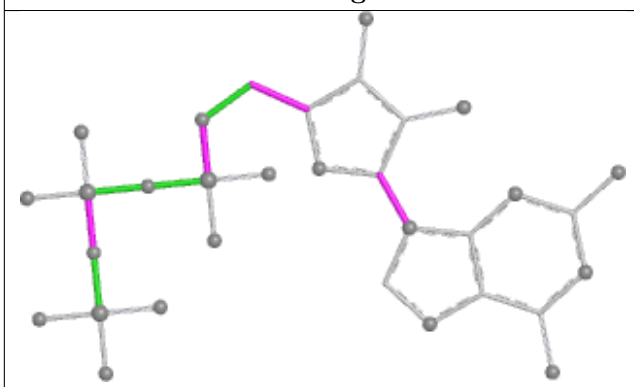

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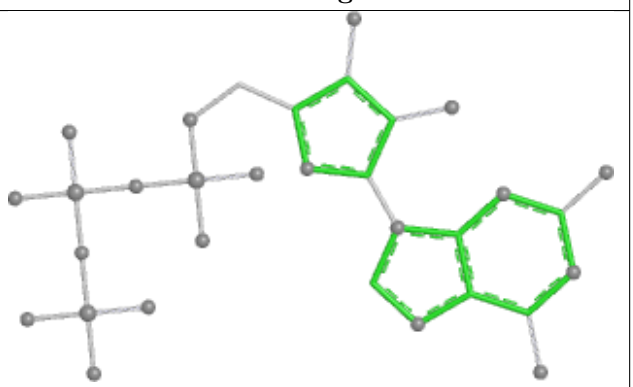
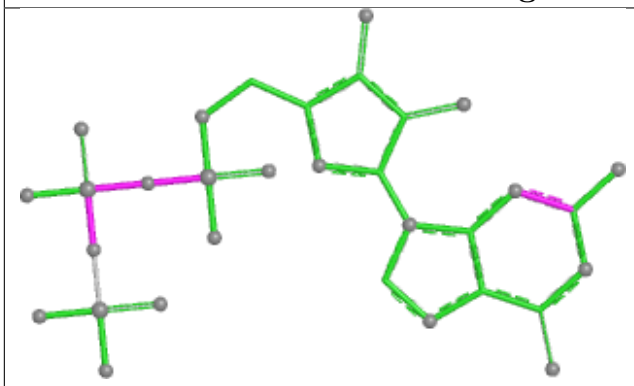


Rings

Ligand GTP IF 501



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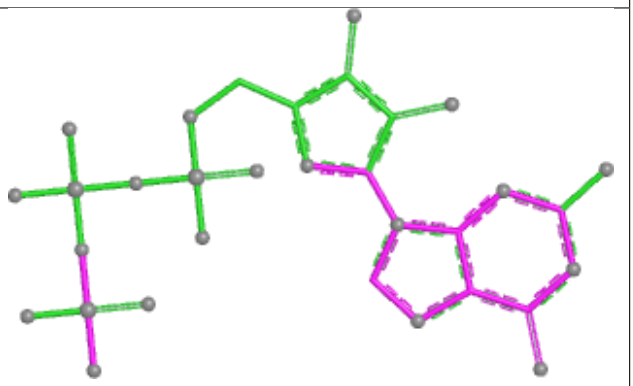

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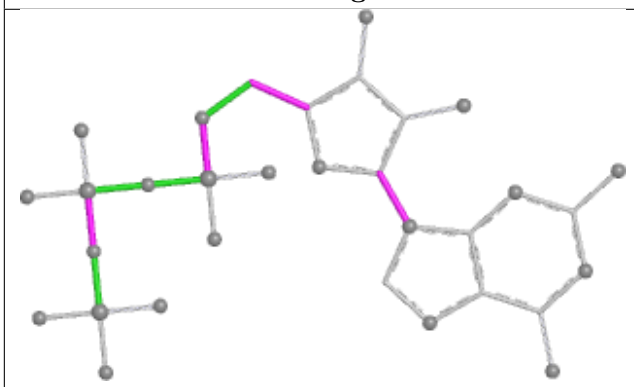

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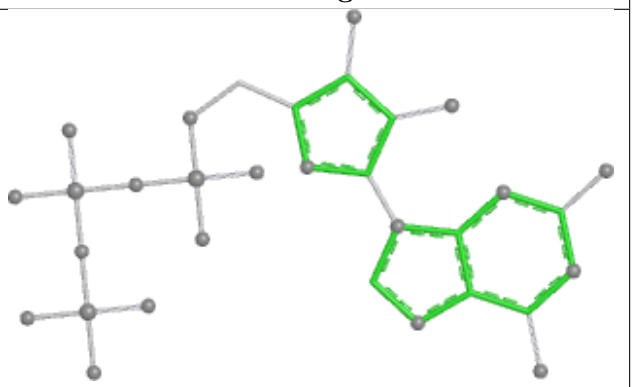
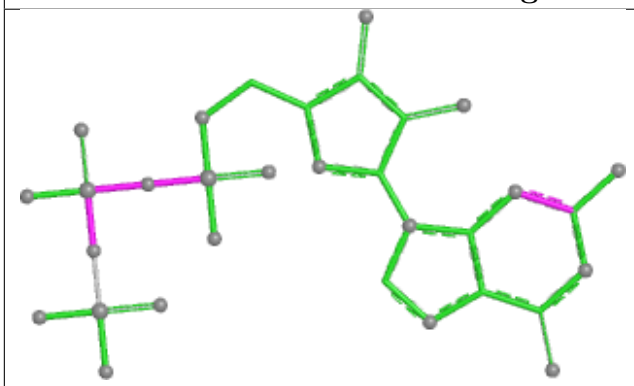


Rings

Ligand GTP IJ 501



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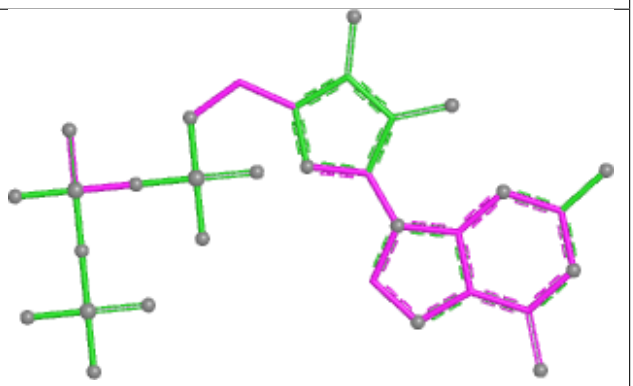

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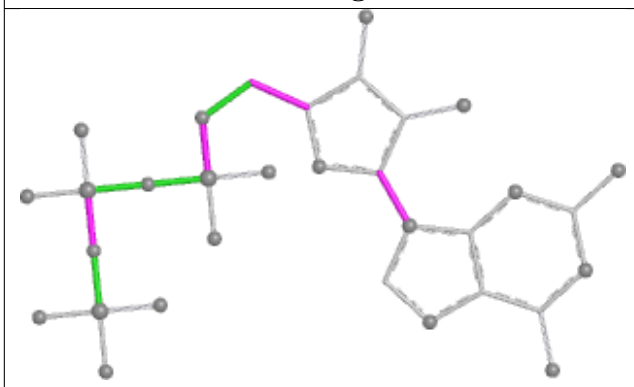

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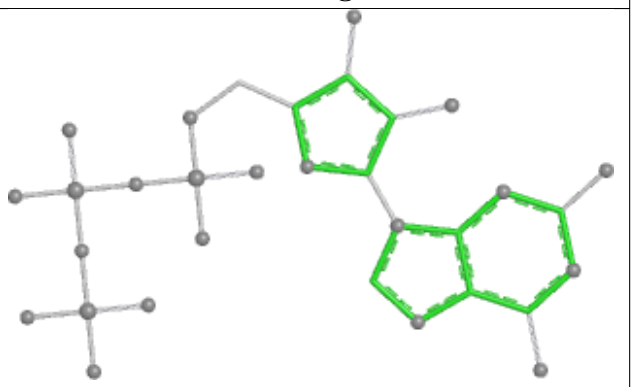
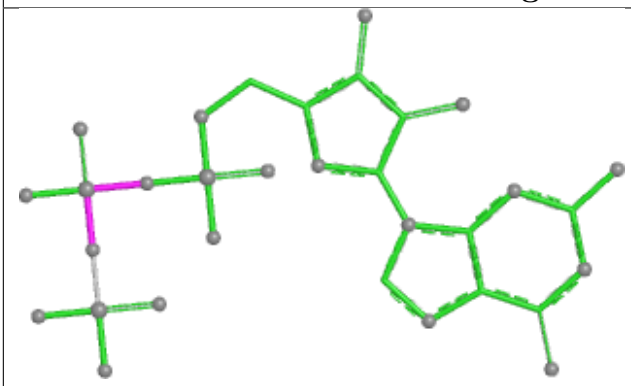


Rings

Ligand GTP II 501



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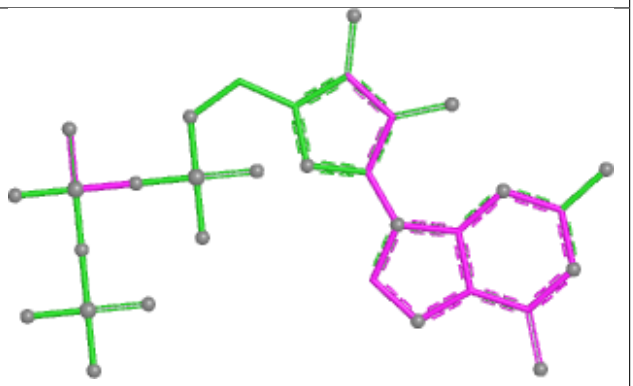

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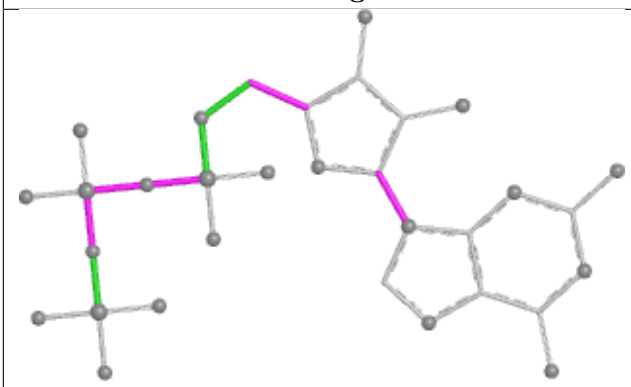

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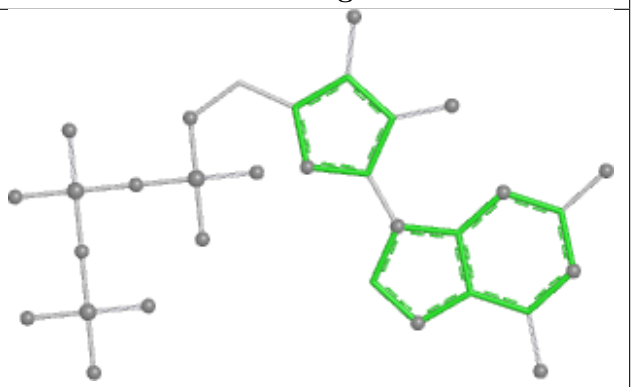
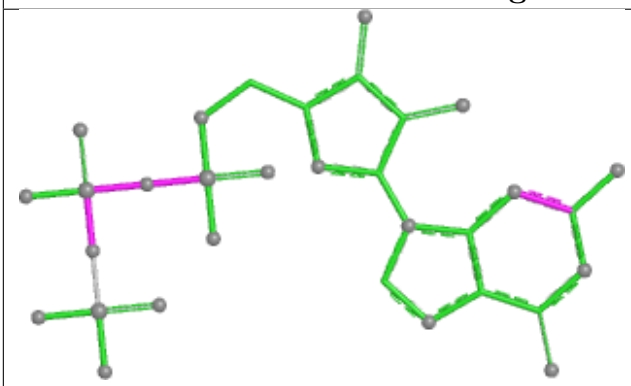


Rings

Ligand GTP TK 501



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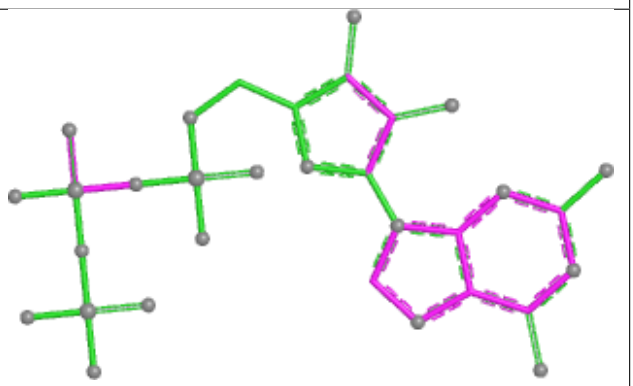

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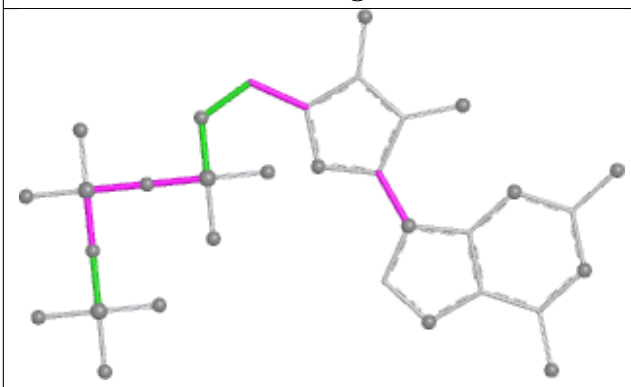

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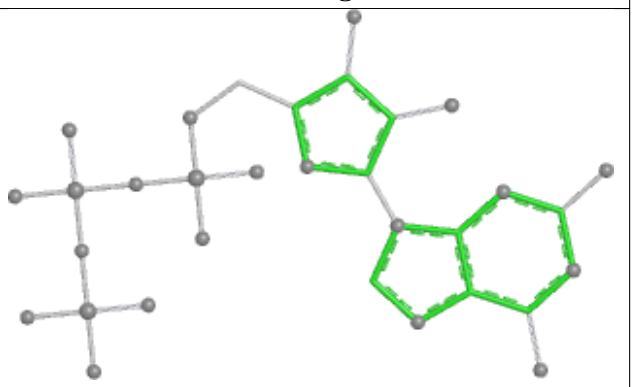

Rings

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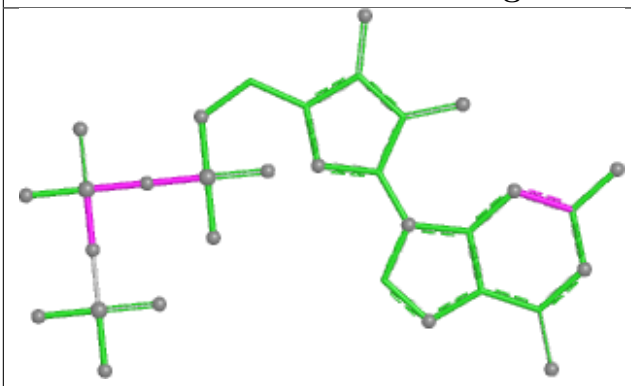

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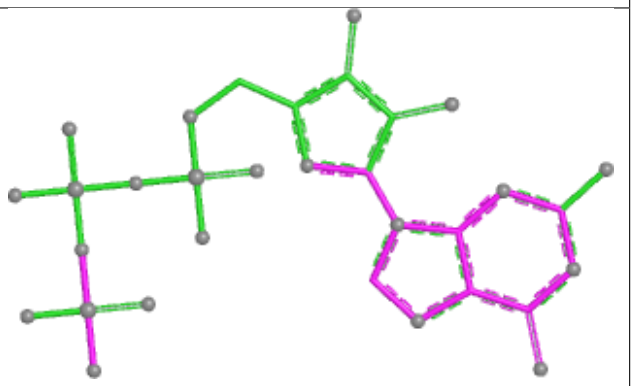

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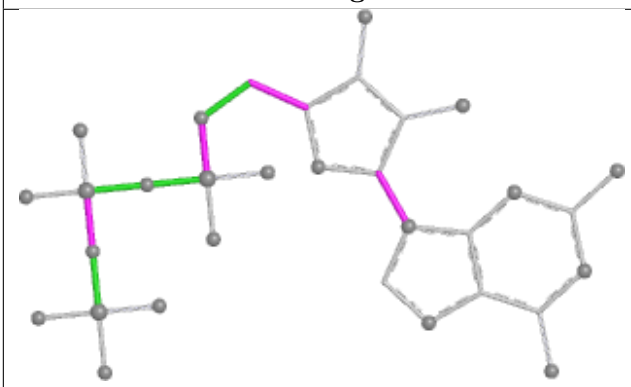

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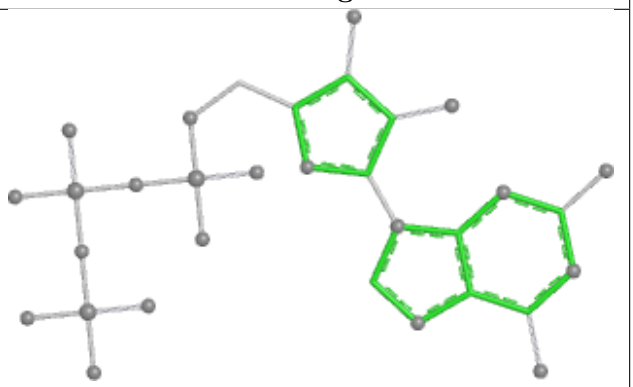
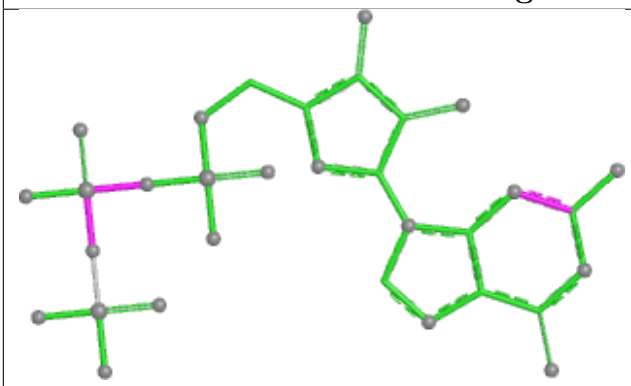


Rings

Ligand GTP RI 501



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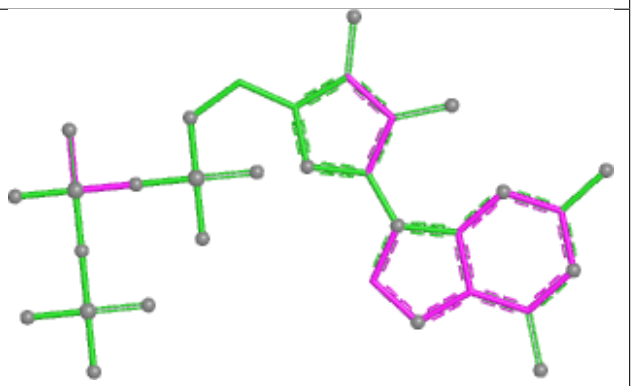

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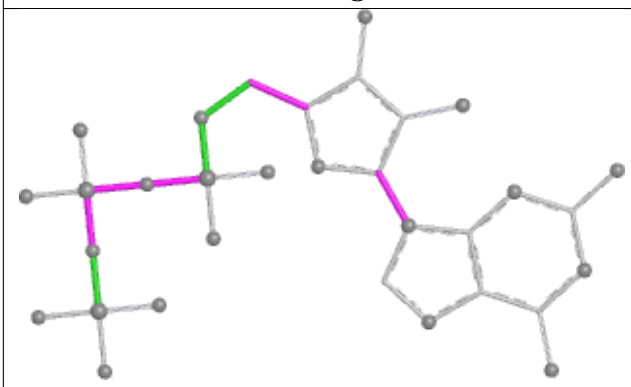

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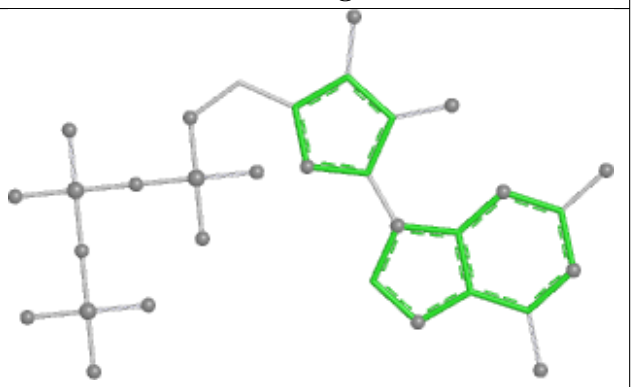
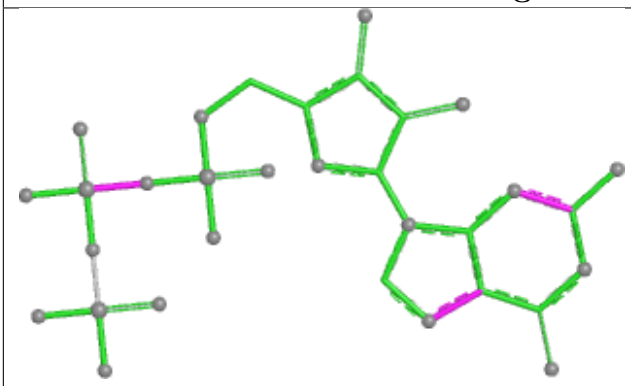


Rings

Ligand GTP BJ 501



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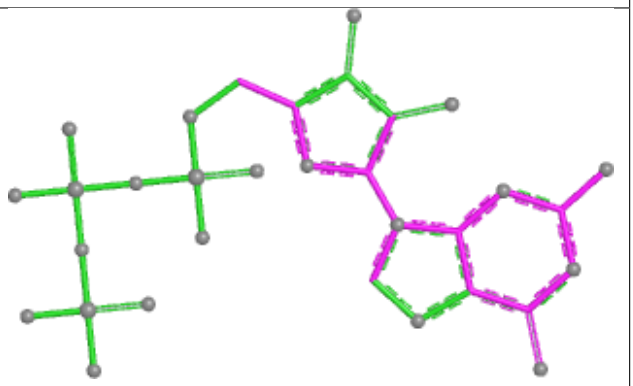

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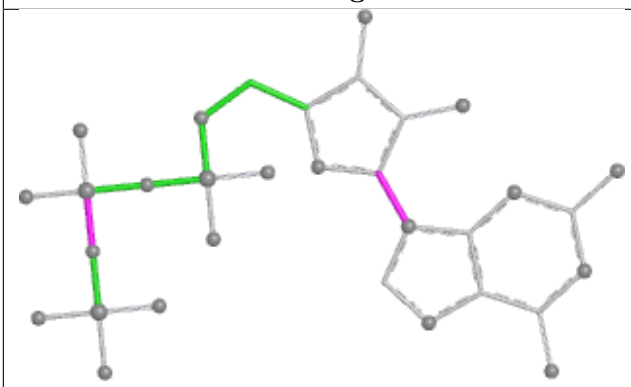

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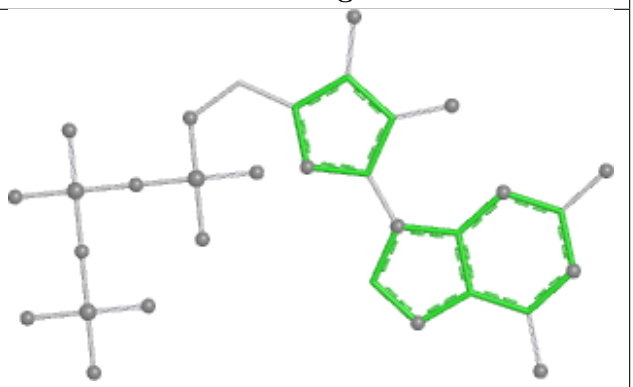
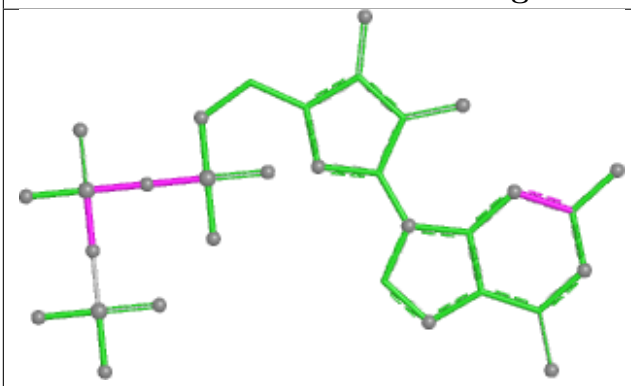


Rings

Ligand GTP QL 502



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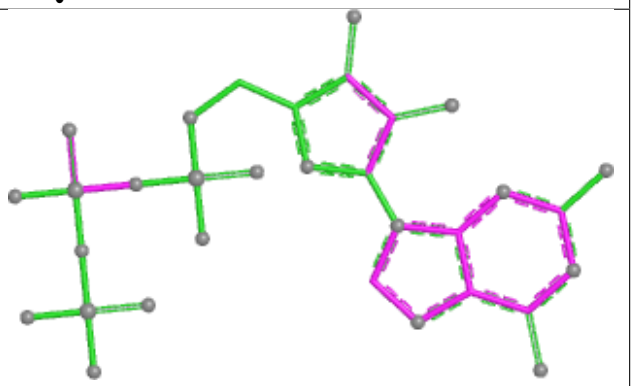

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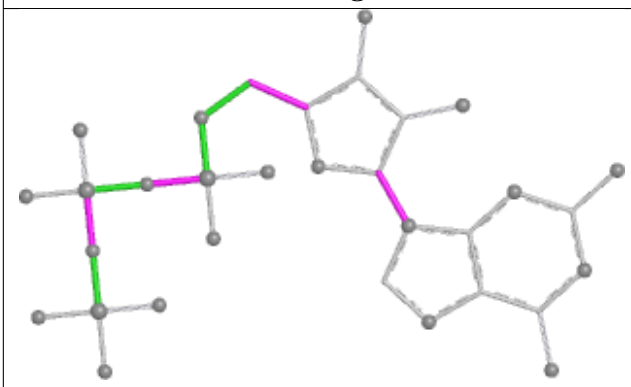

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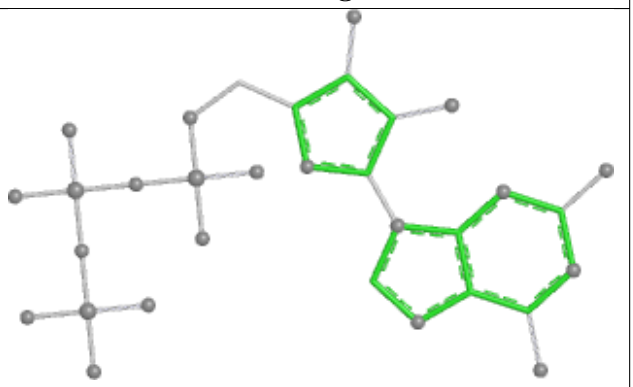

Rings

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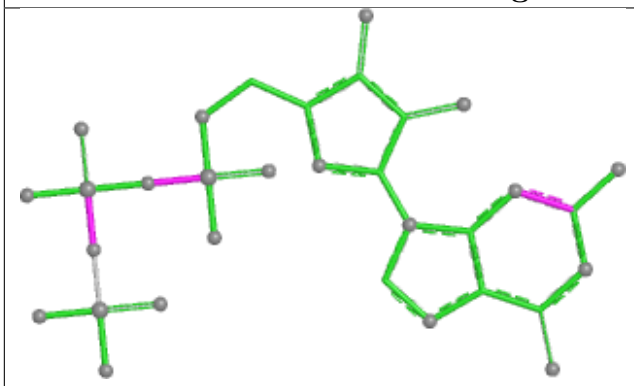

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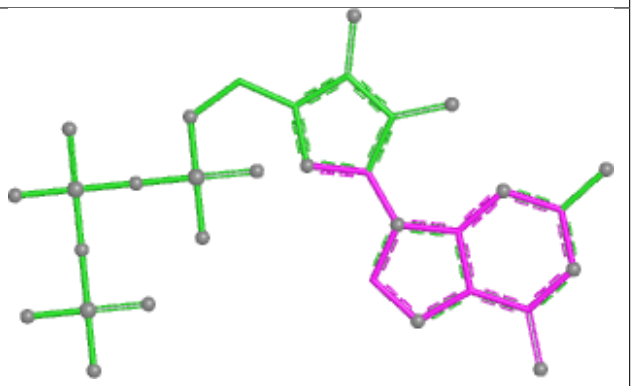

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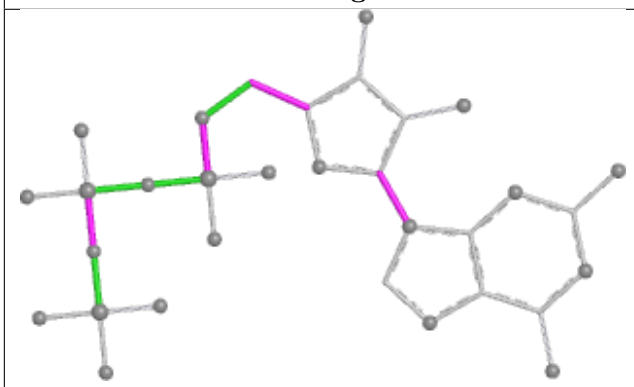

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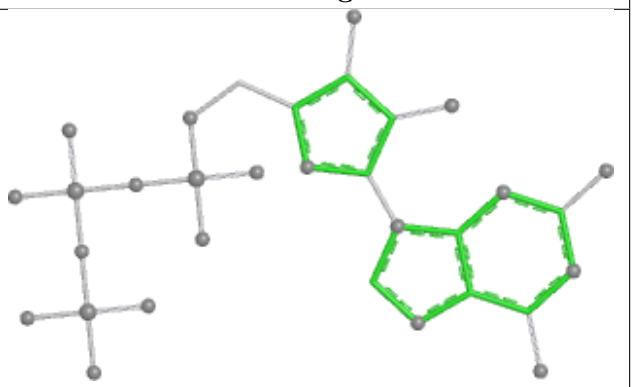
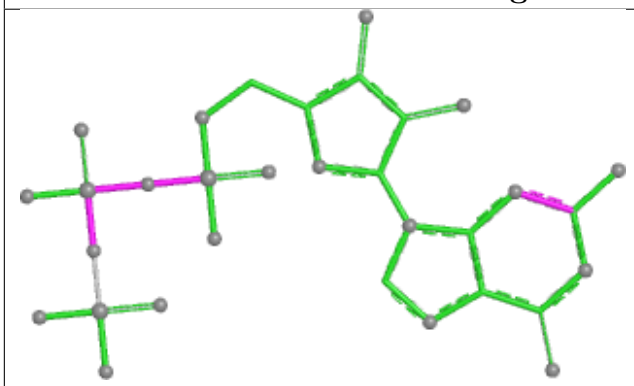


Rings

Ligand GTP KB 501



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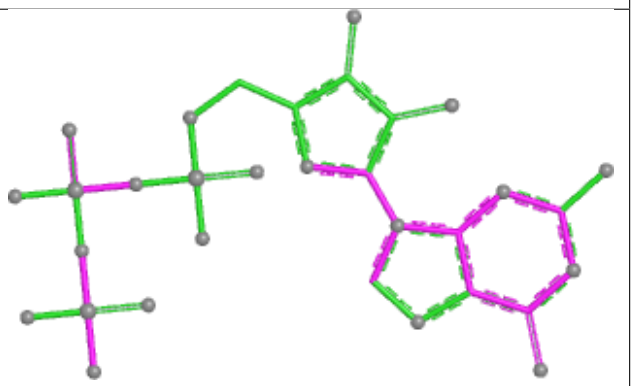

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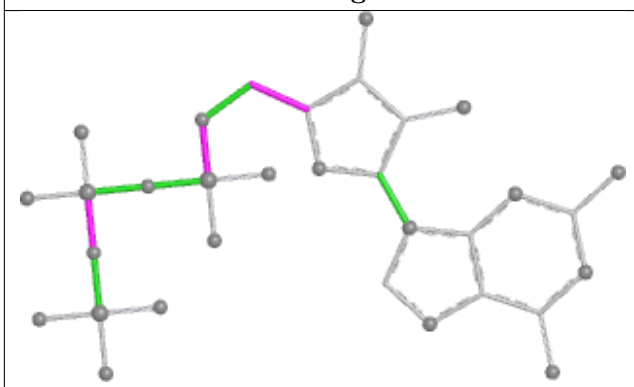

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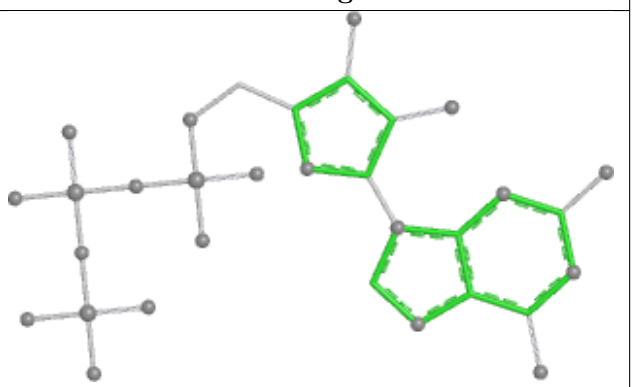
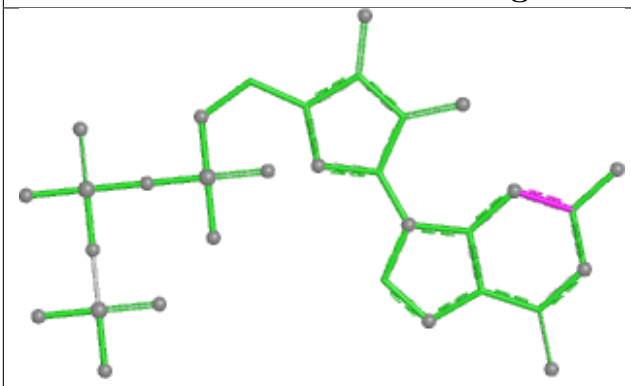


Rings

Ligand GTP RF 501



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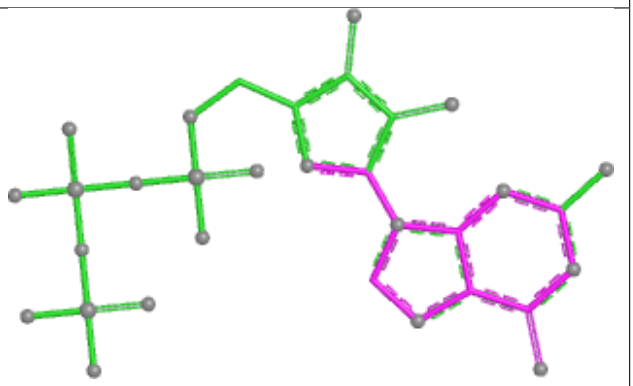

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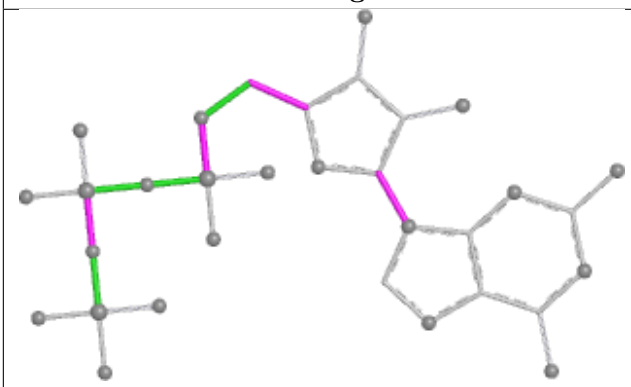

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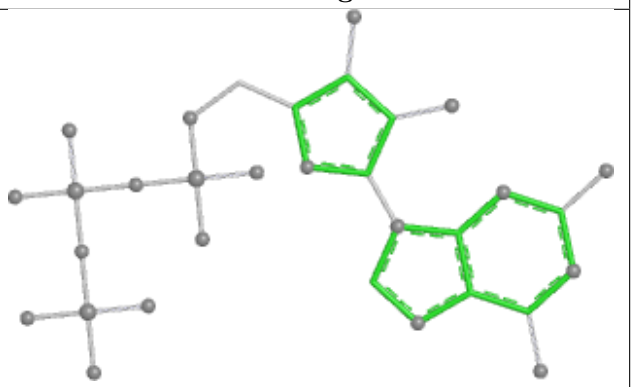
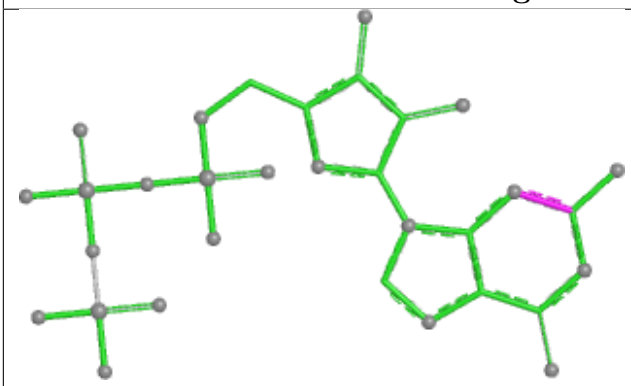


Rings

Ligand GTP RJ 501



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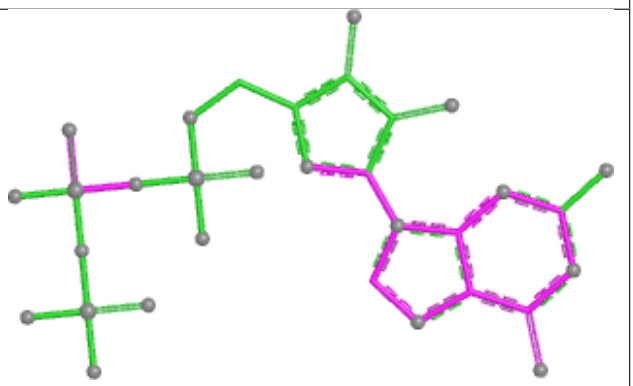

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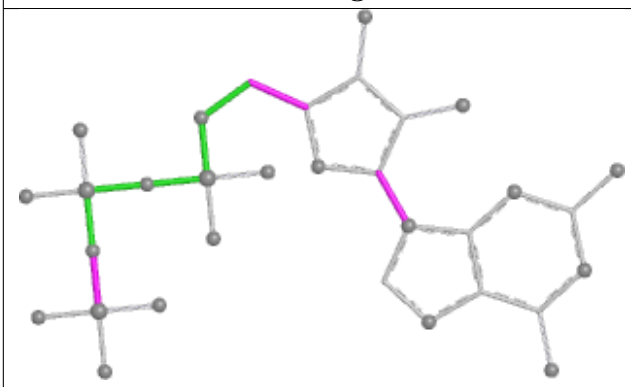

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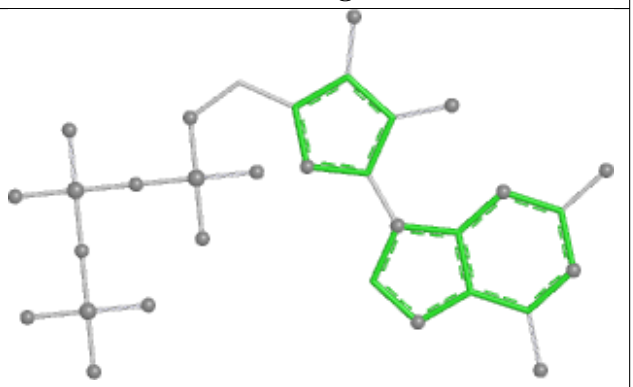
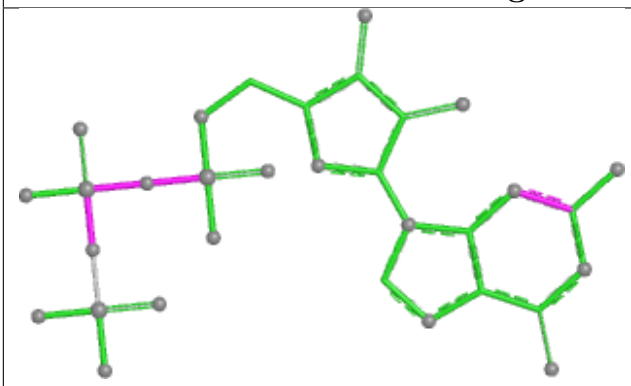


Rings

Ligand GTP NA 501



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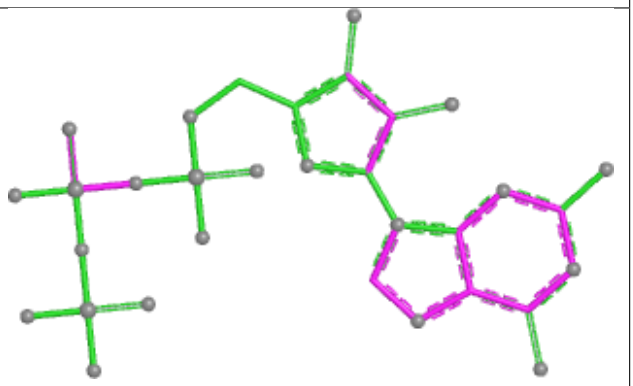

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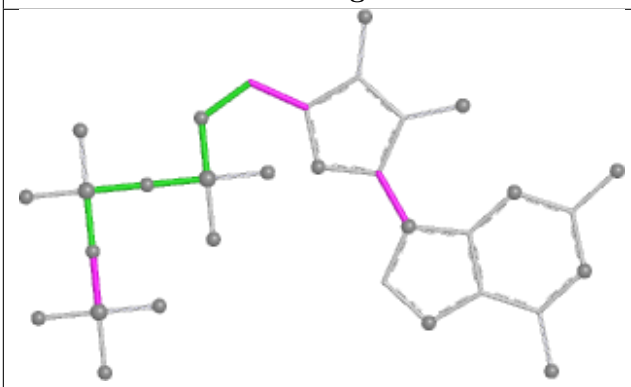
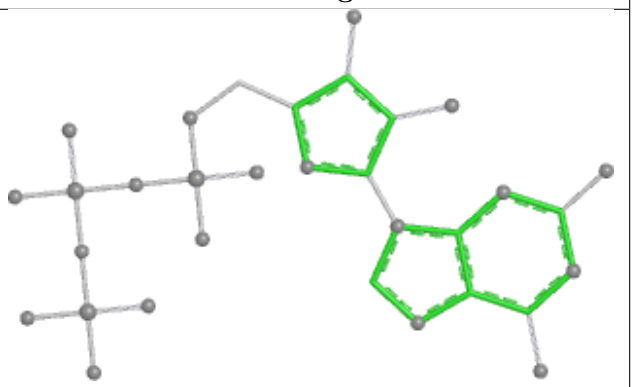
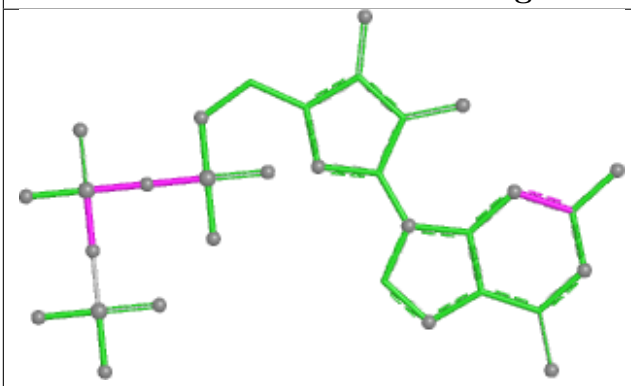


Torsions



Rings

Ligand GTP EJ 501



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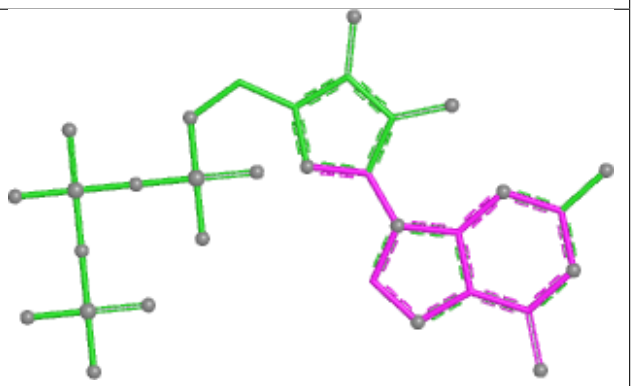

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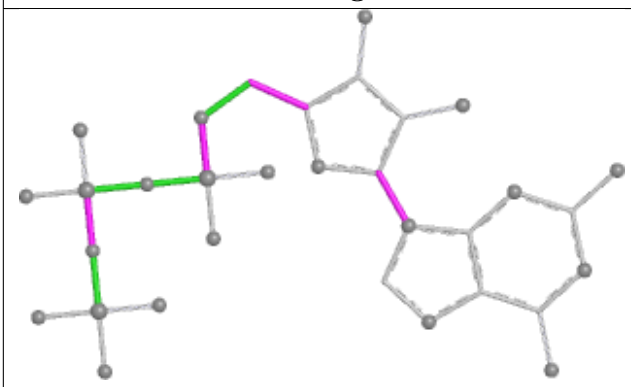

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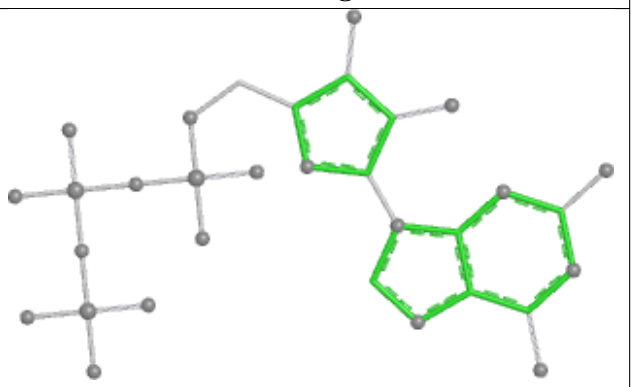
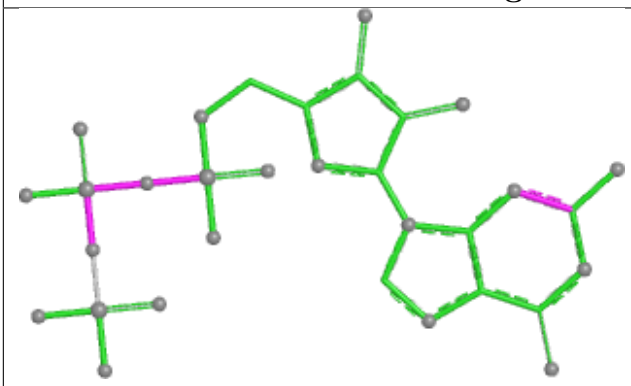


Rings

Ligand GTP MD 501



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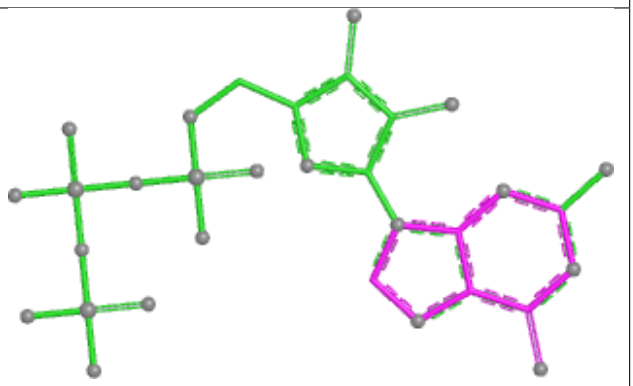

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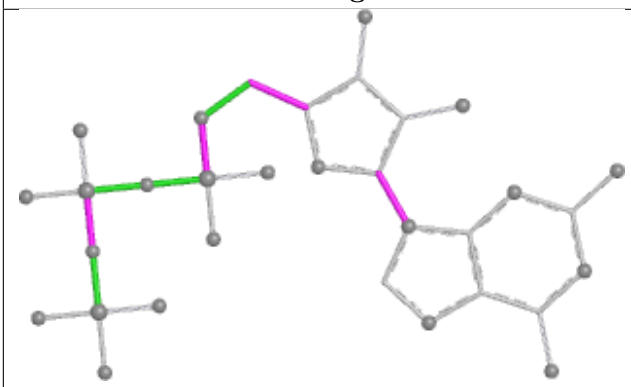

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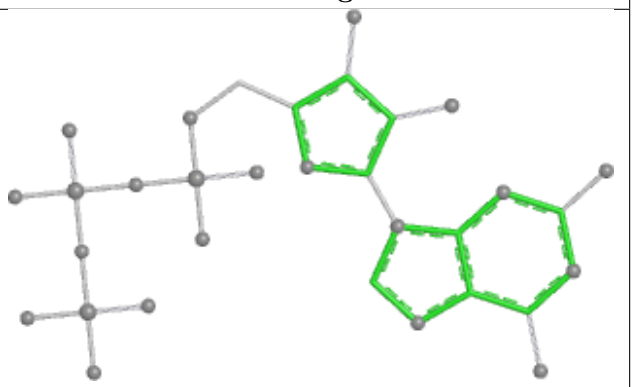
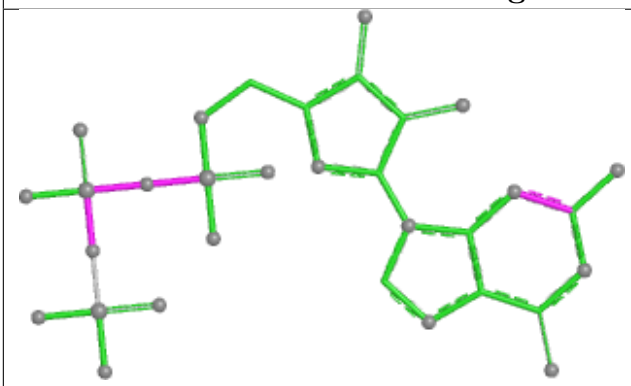


Rings

Ligand GTP OG 501



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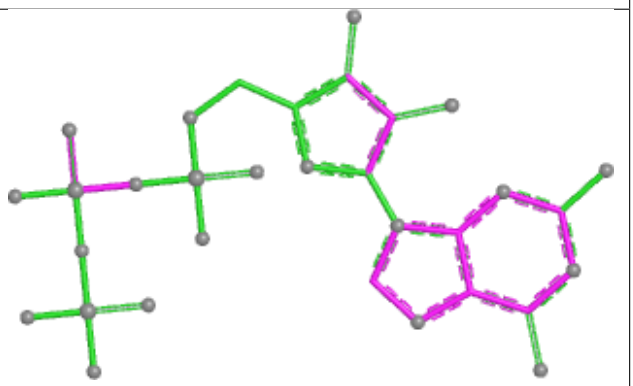

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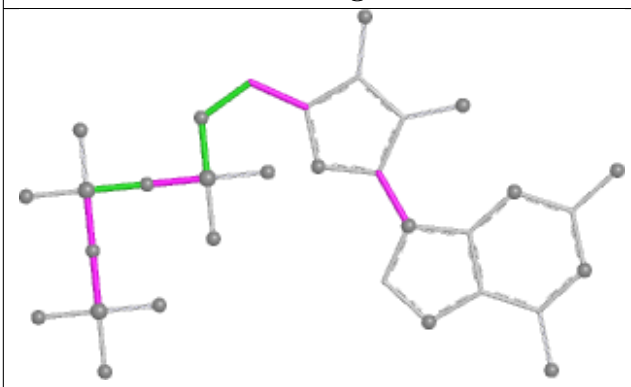

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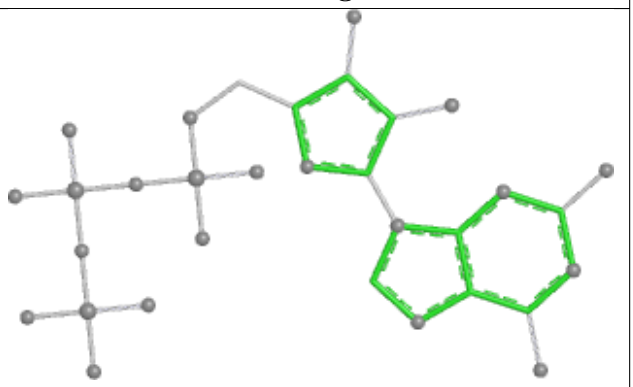

Rings

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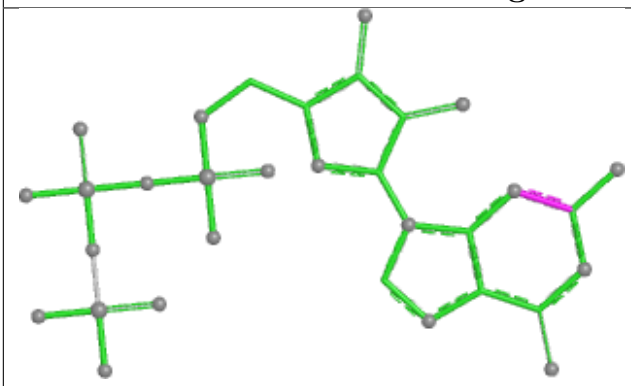

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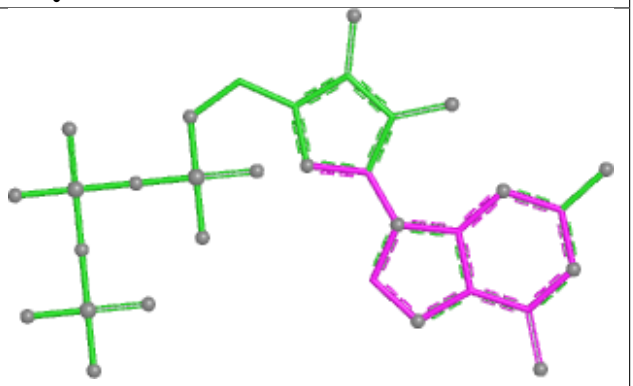

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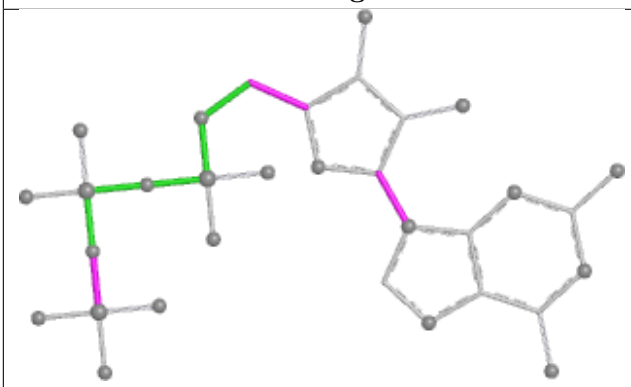

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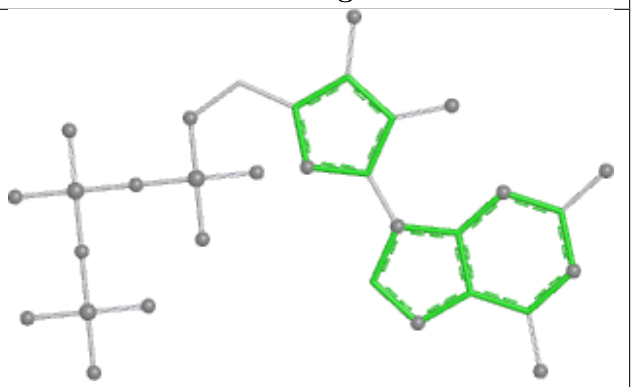
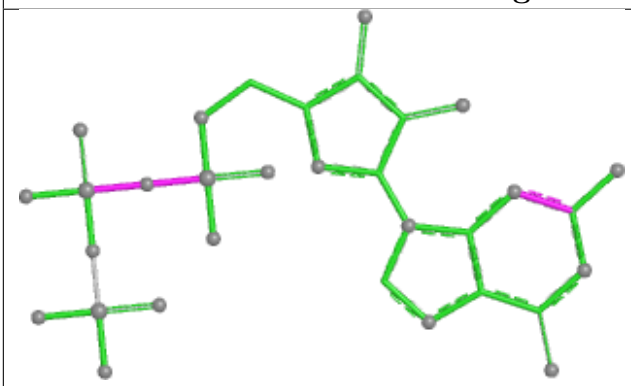


Rings

Ligand GTP VJ 501



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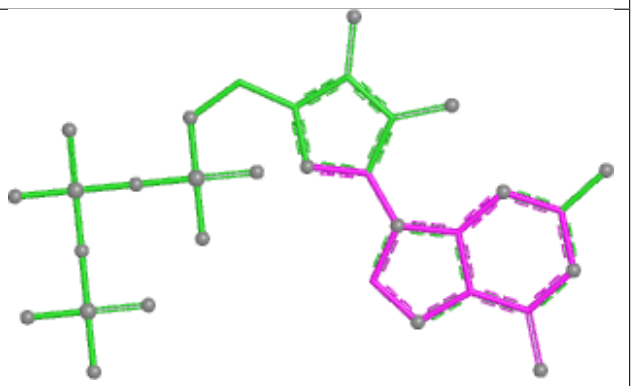

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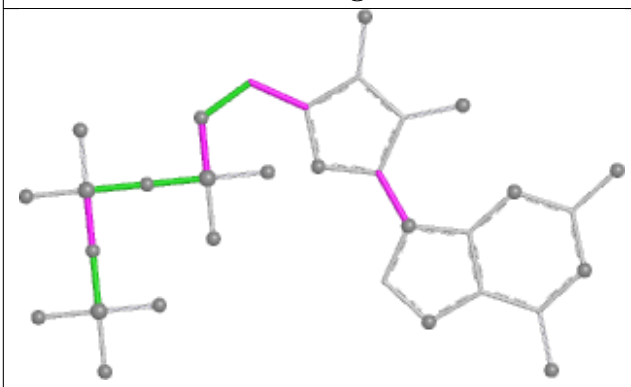

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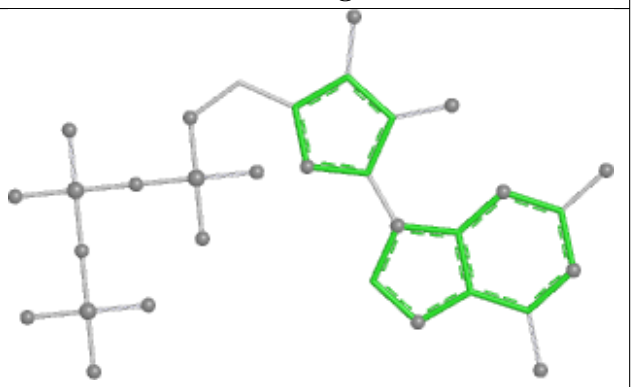
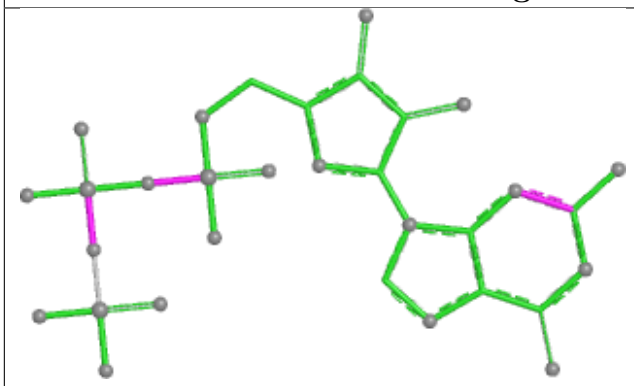


Rings

Ligand GTP BL 501



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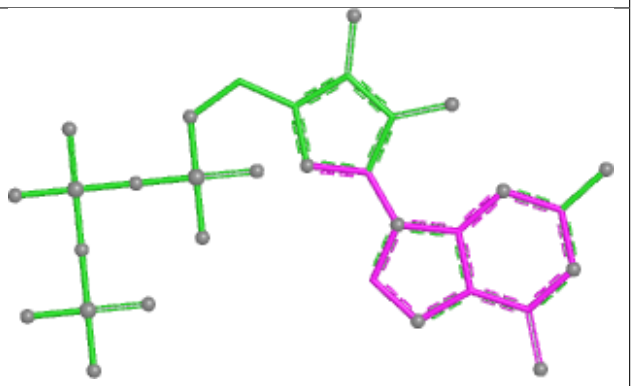

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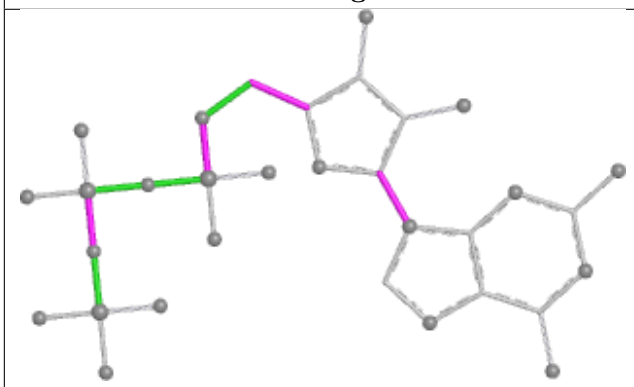

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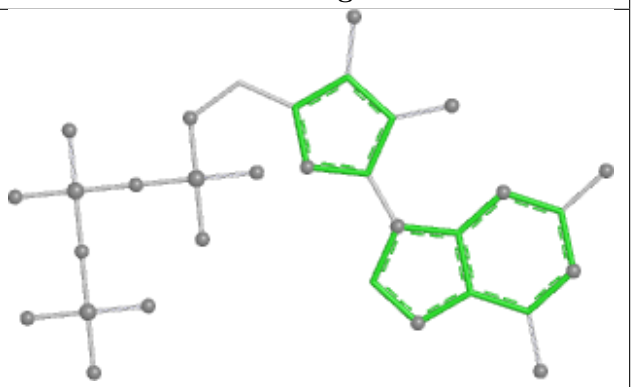
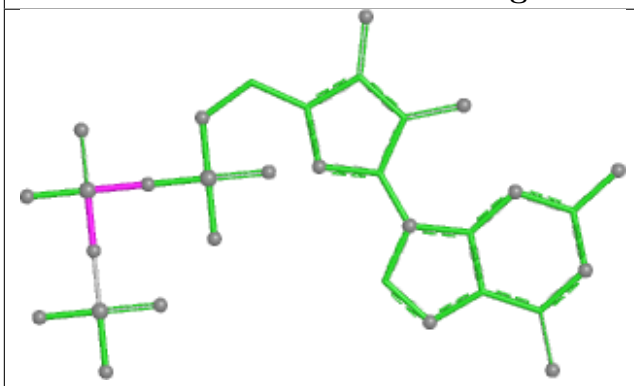


Rings

Ligand GTP DC 501



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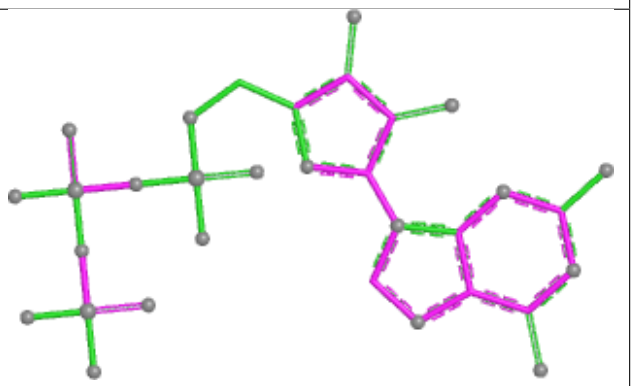

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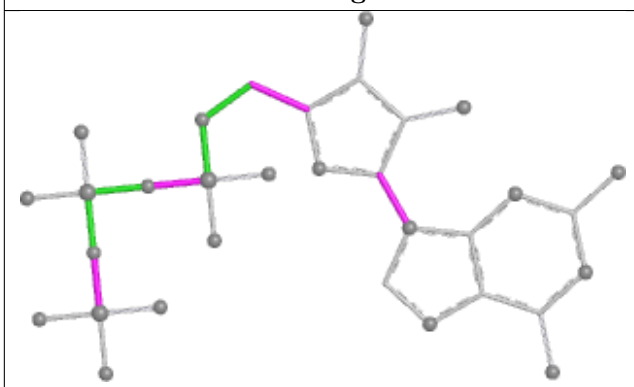

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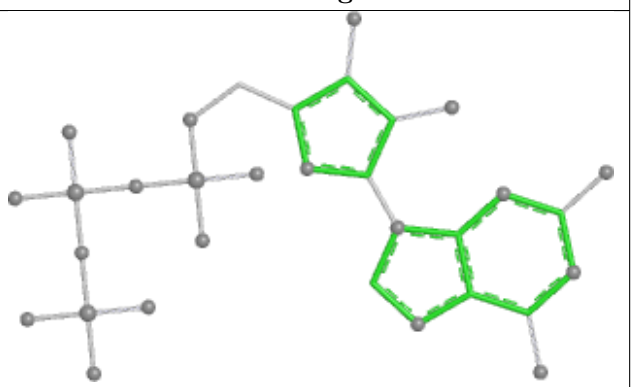

Rings

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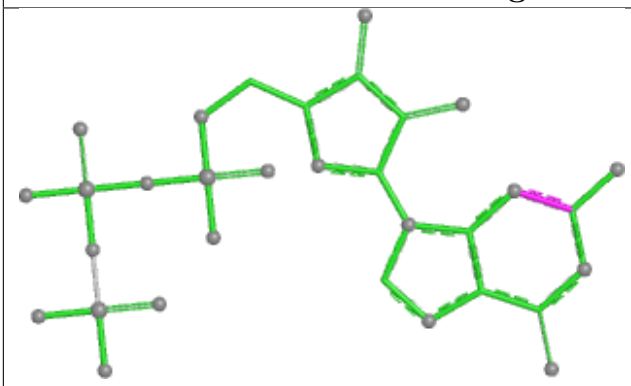

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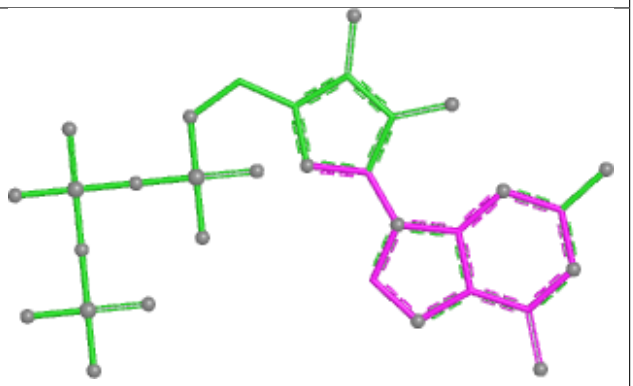

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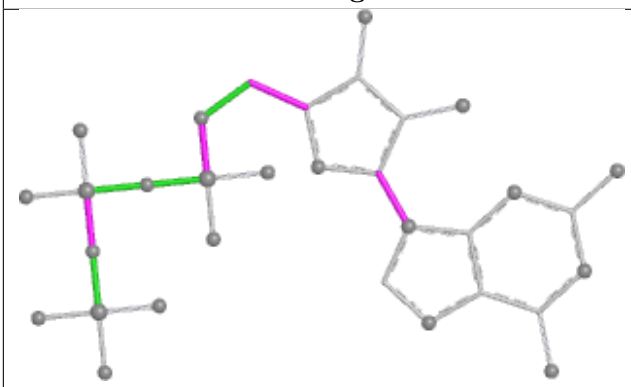

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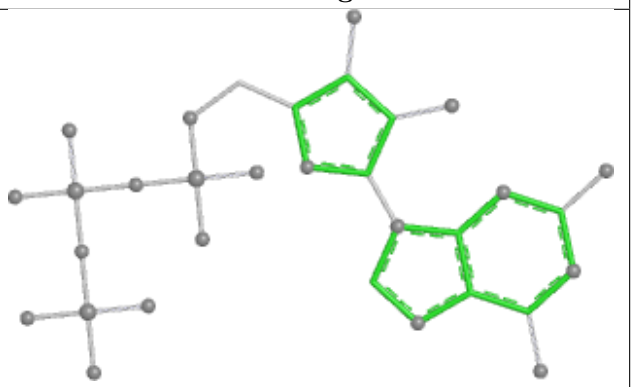

Rings

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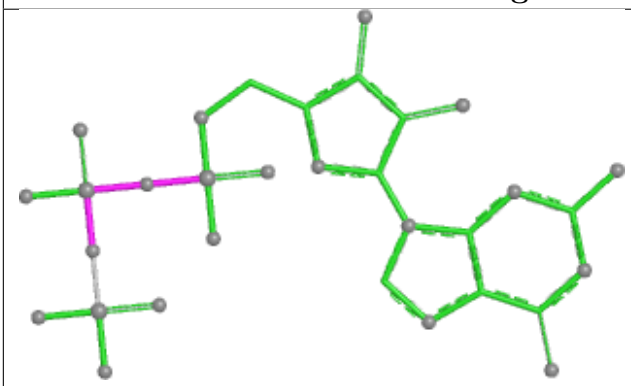

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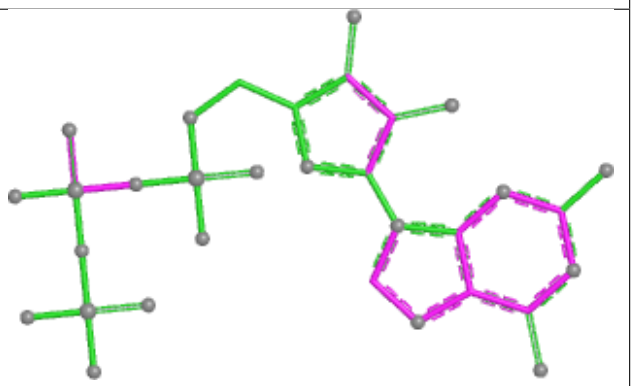

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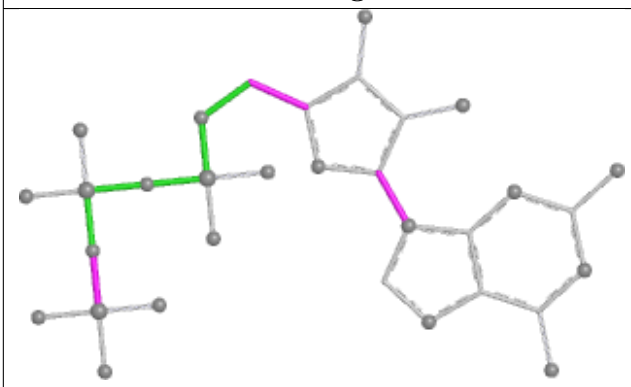

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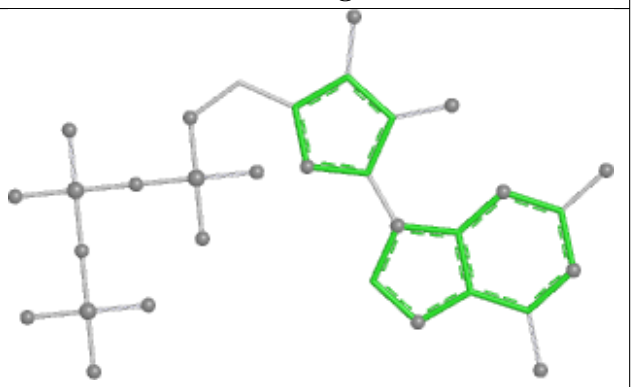
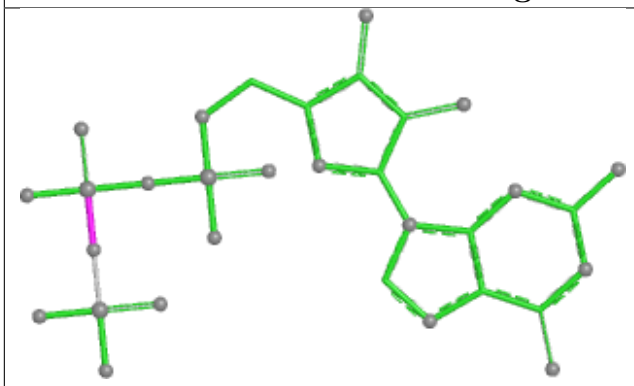


Rings

Ligand GTP FA 501



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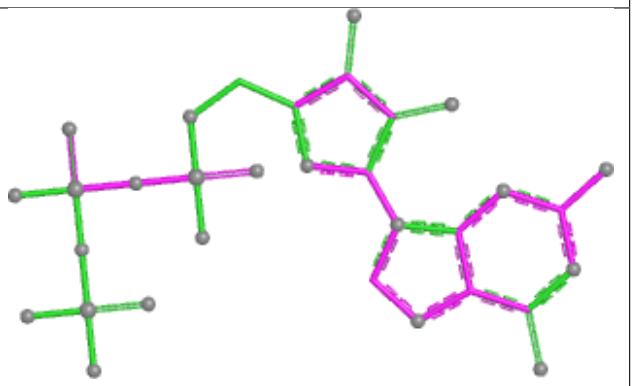

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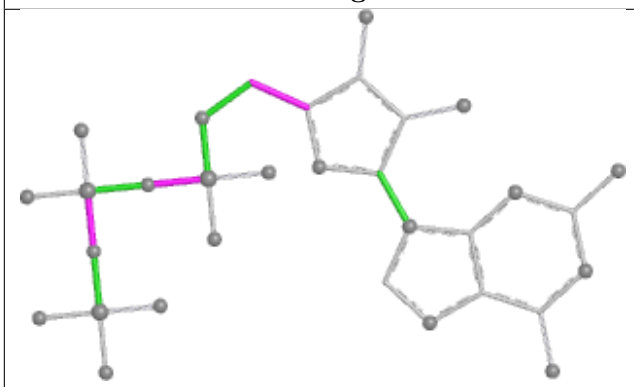

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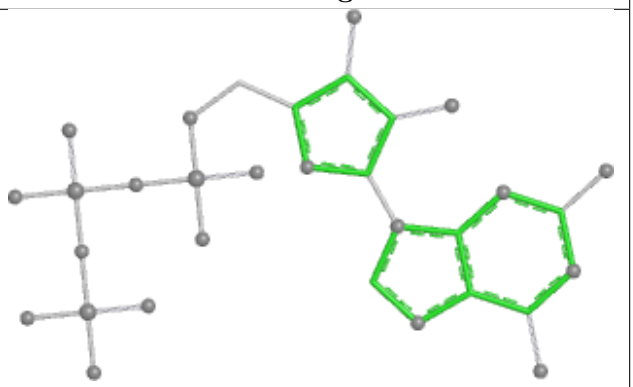
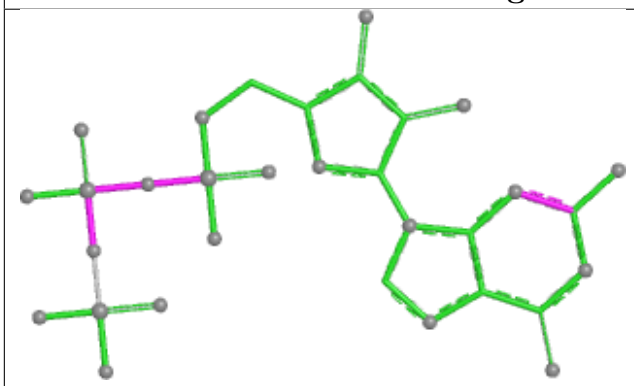


Rings

Ligand GTP WL 501



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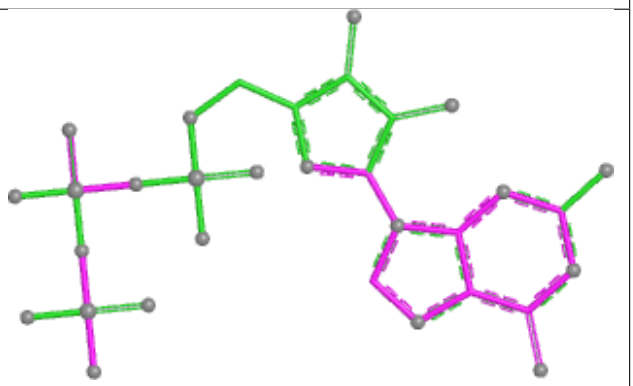

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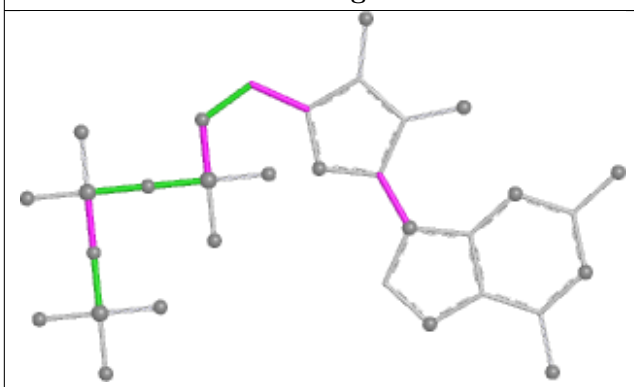

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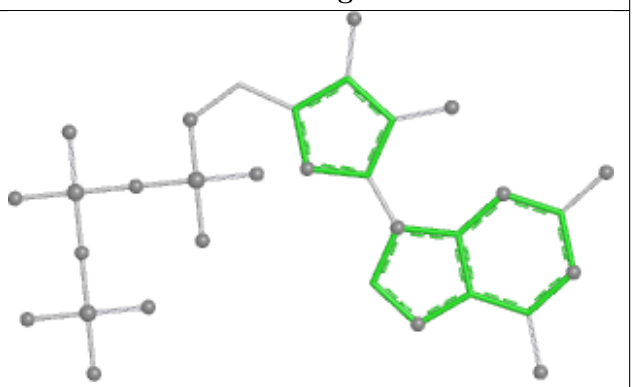
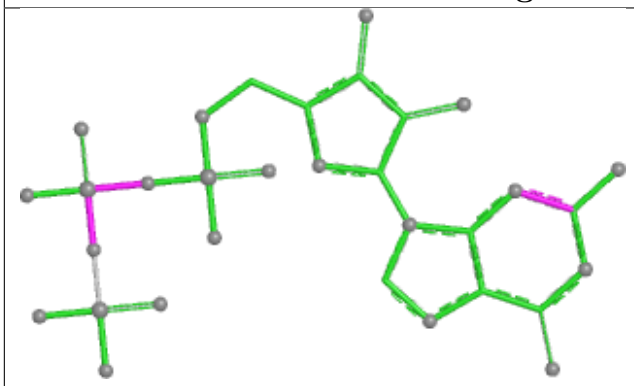


Rings

Ligand GTP IK 501



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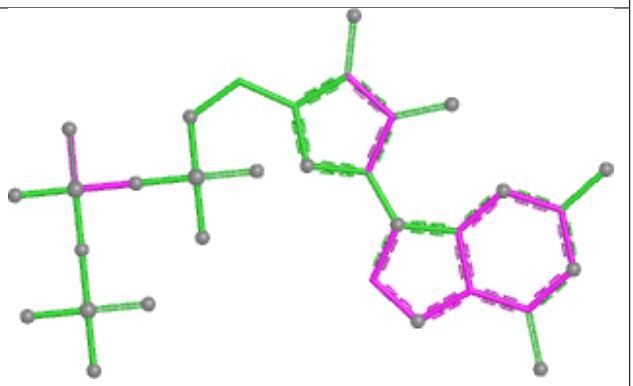

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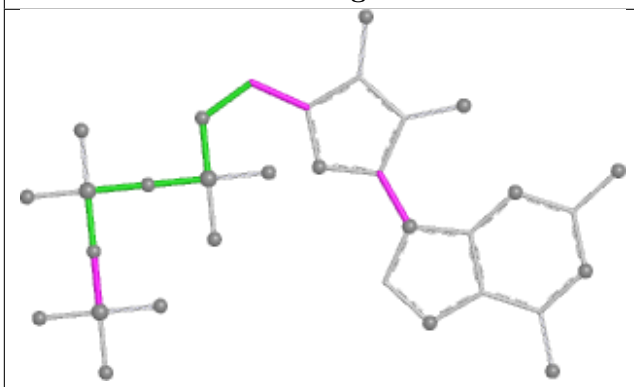

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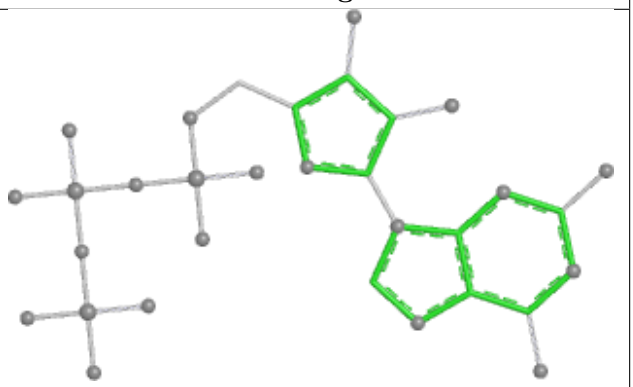
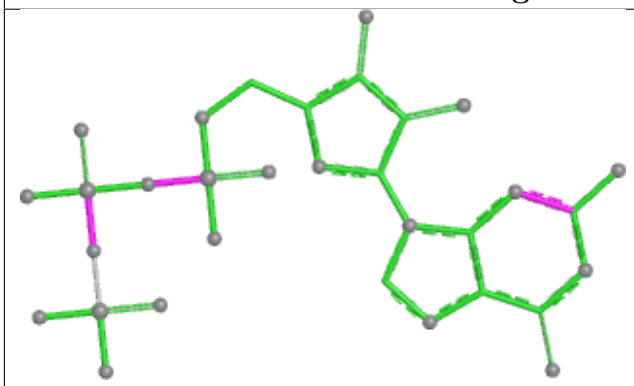


Rings

Ligand GTP VF 501



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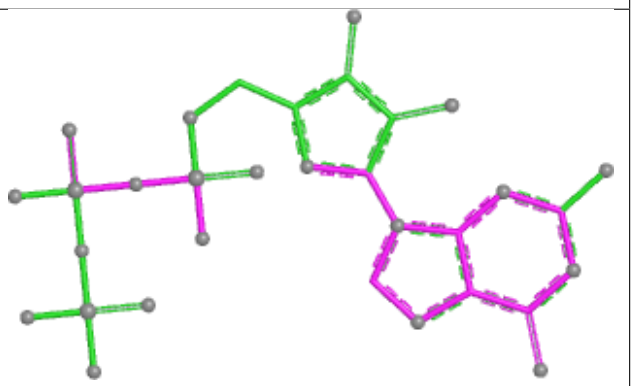
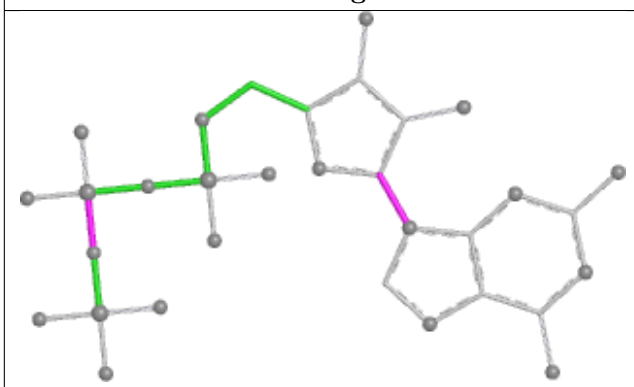


Bond angles



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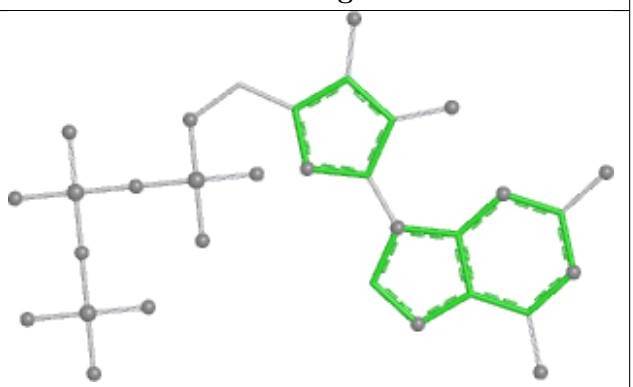
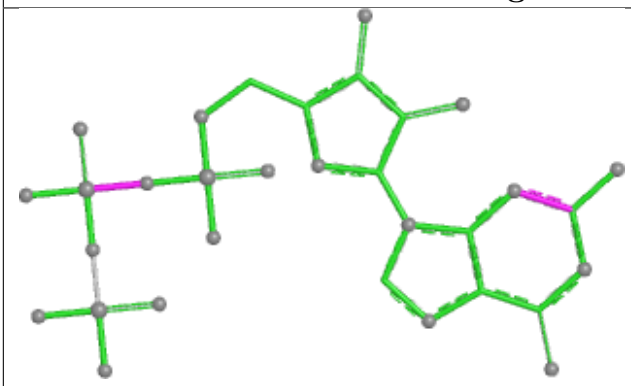


Rings

Ligand GTP NG 501



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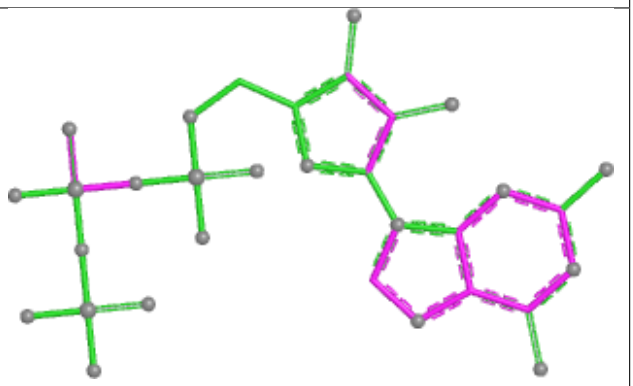

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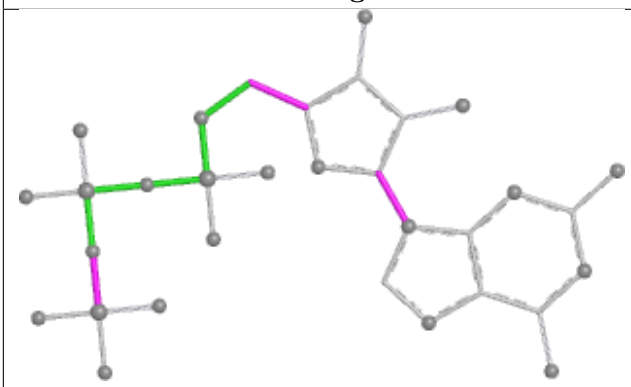
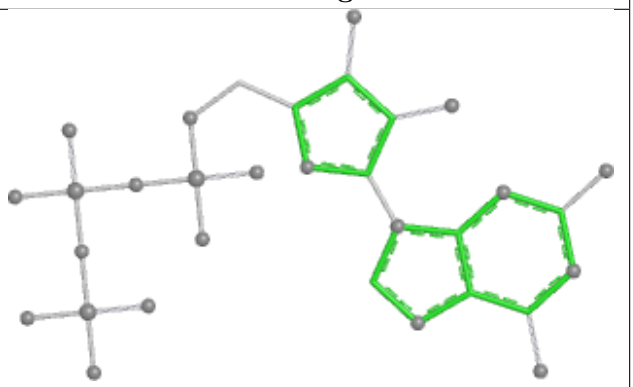
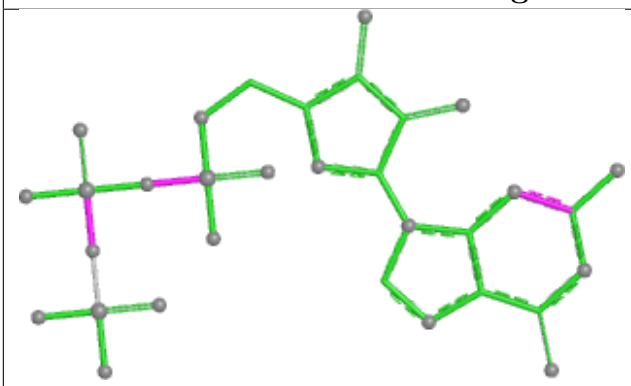


Torsions



Rings

Ligand GTP AF 501



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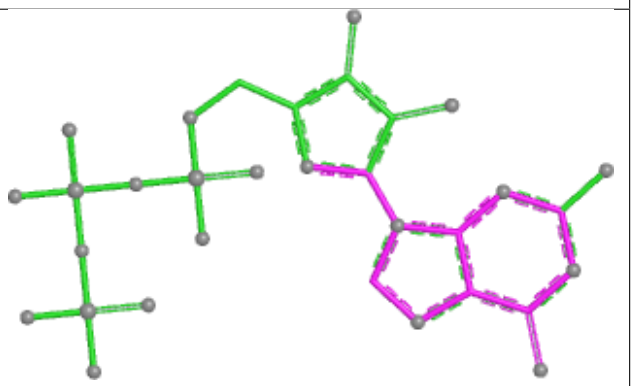

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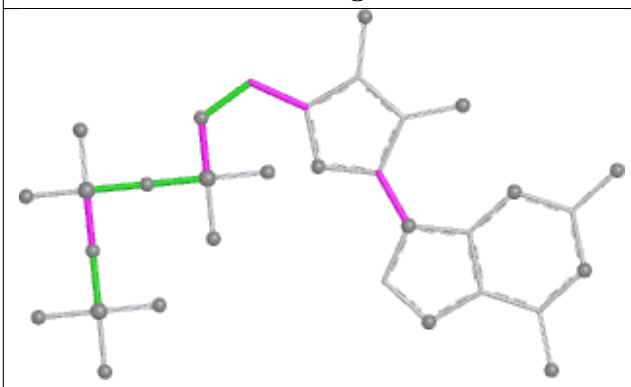

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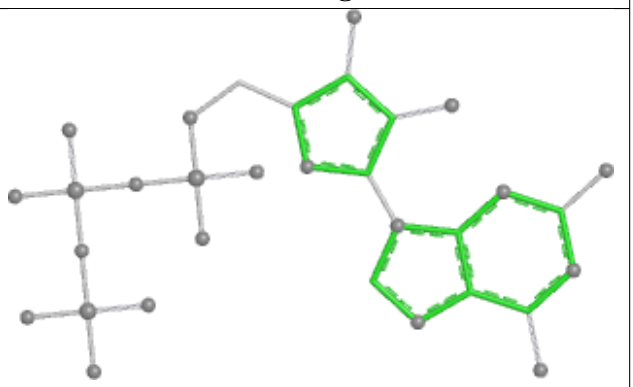
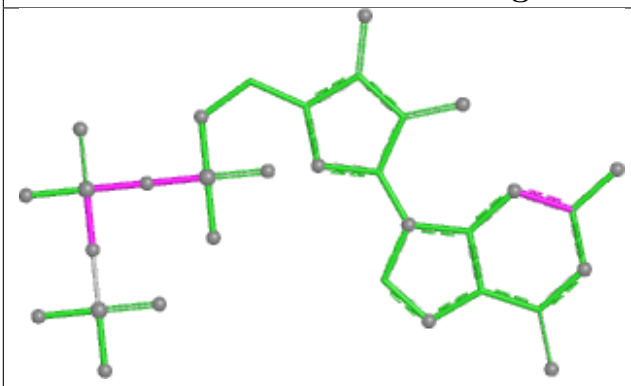


Rings

Ligand GTP SG 501



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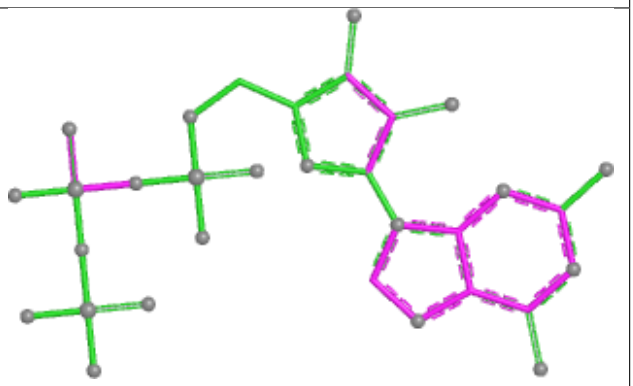

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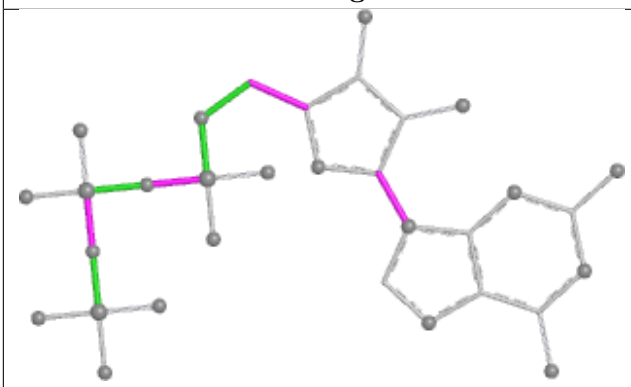

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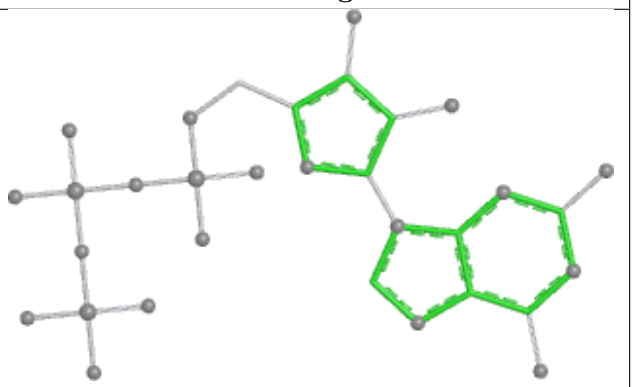

Rings

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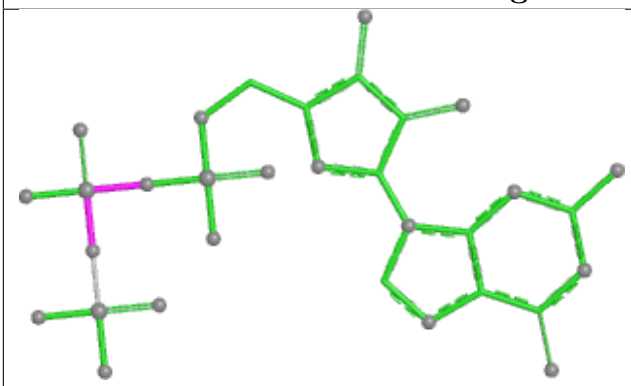

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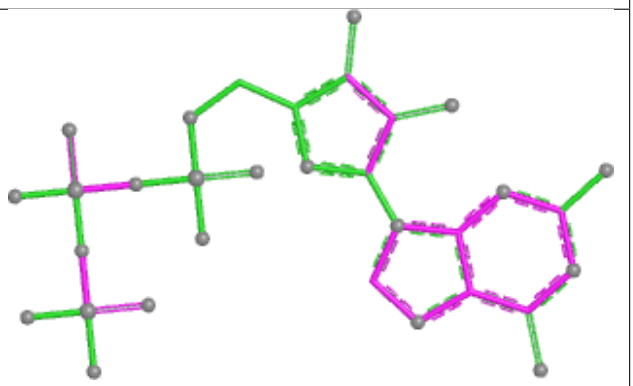

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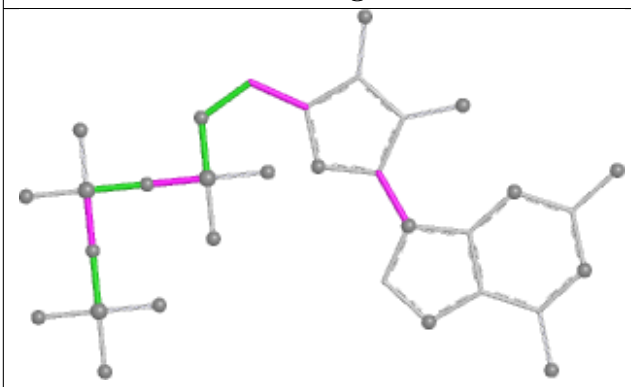

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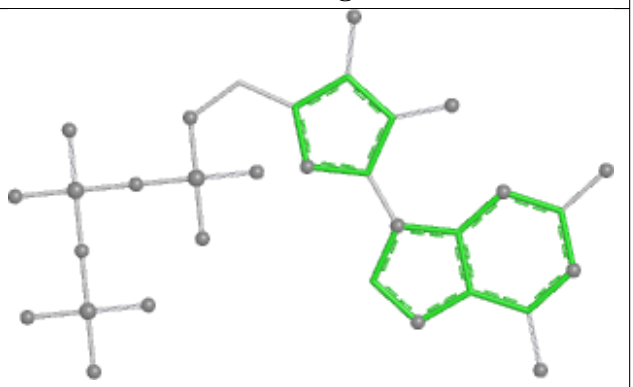
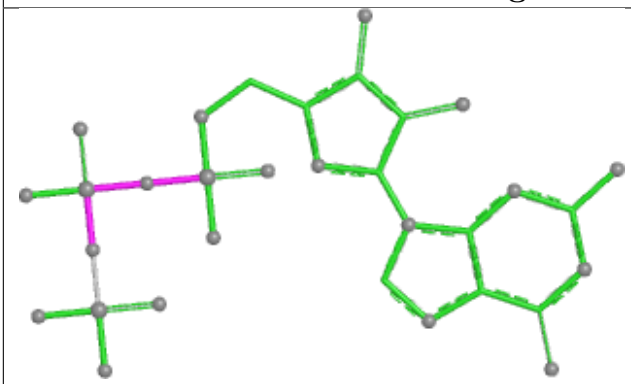


Rings

Ligand GTP GC 501



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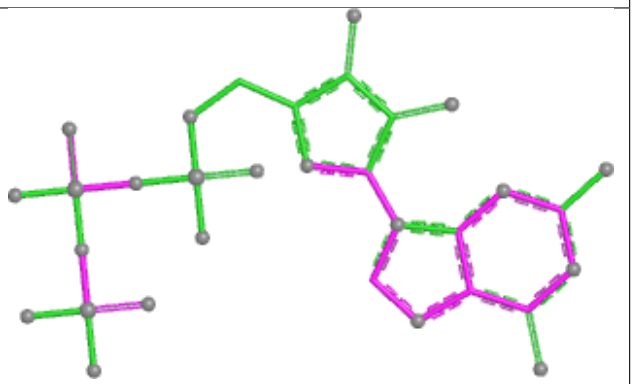

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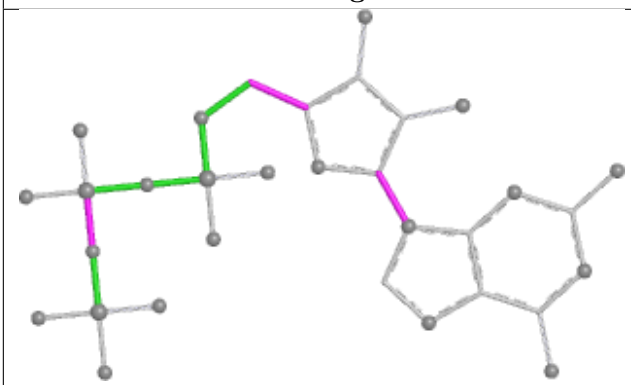

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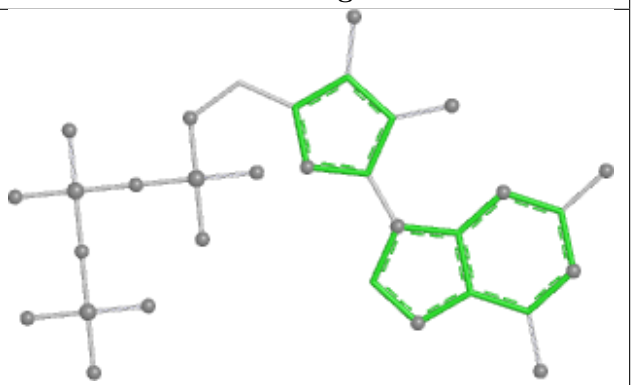

Rings

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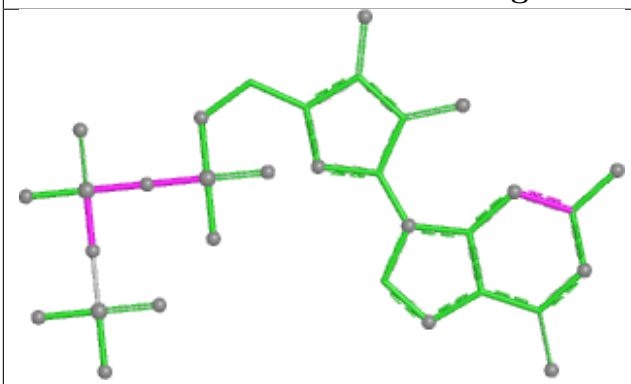

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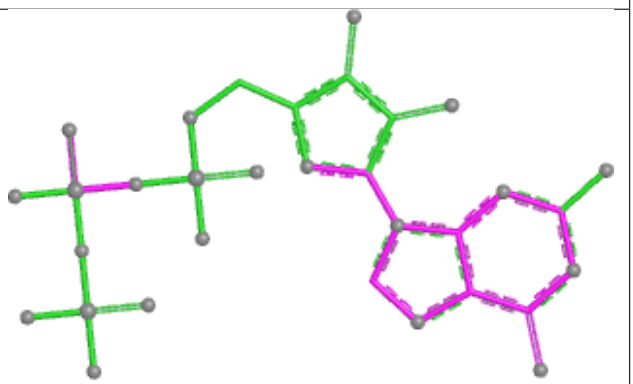

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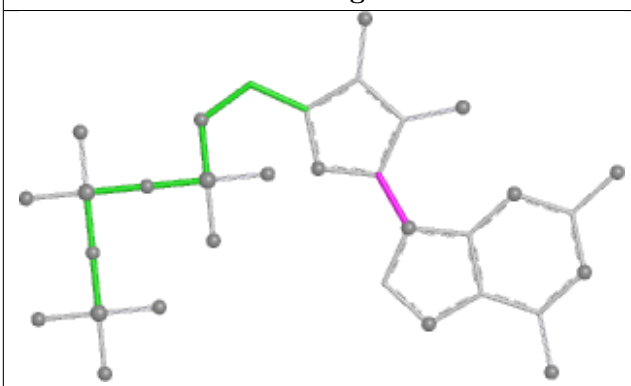

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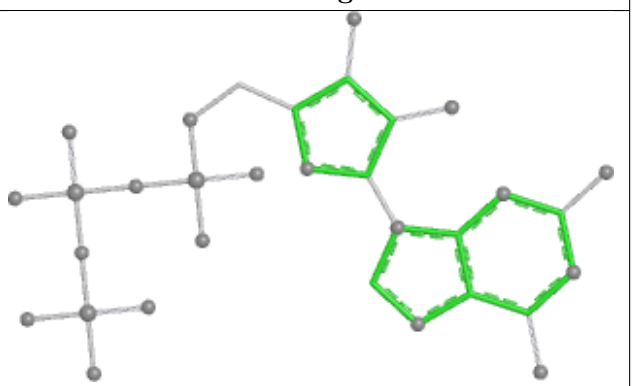
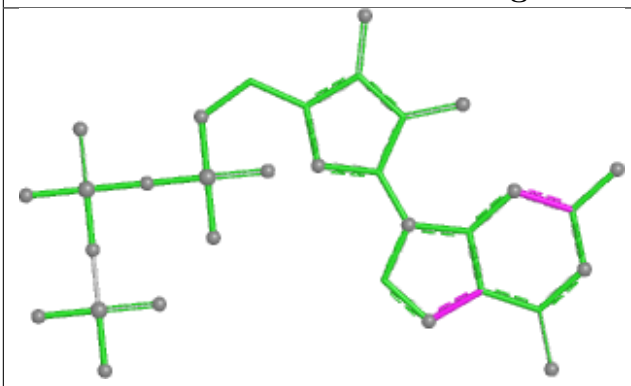


Rings

Ligand GTP KF 501



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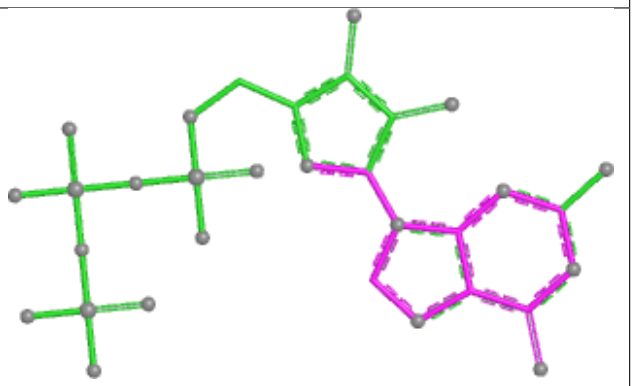

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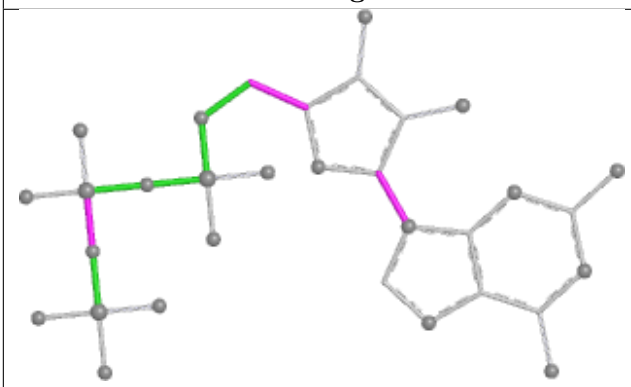

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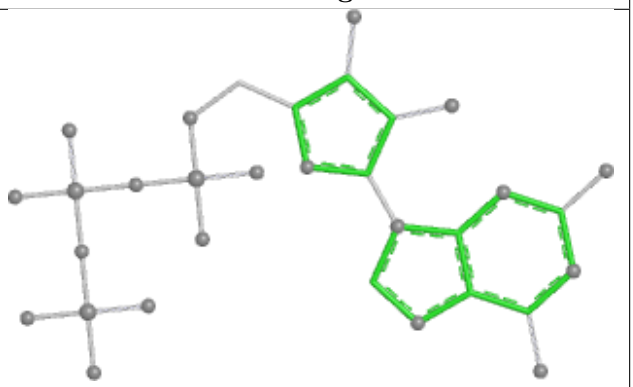
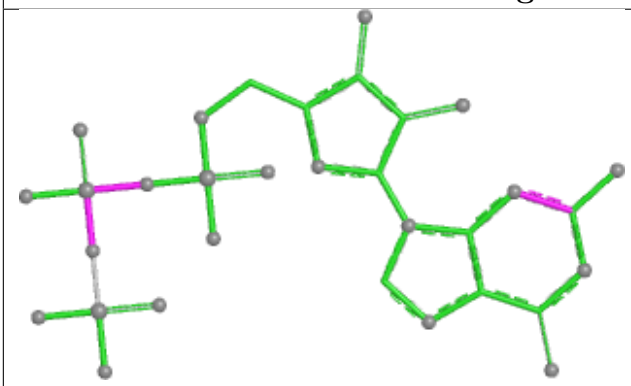


Rings

Ligand GTP PI 501



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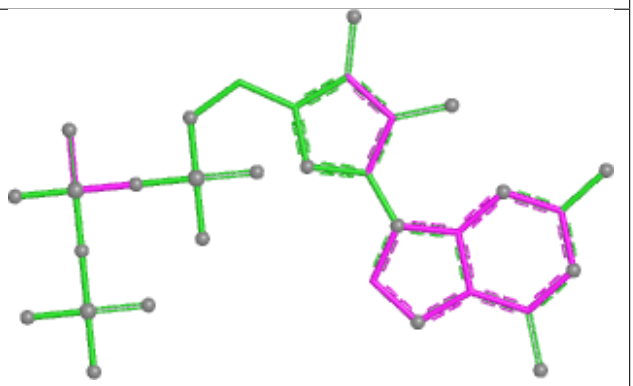

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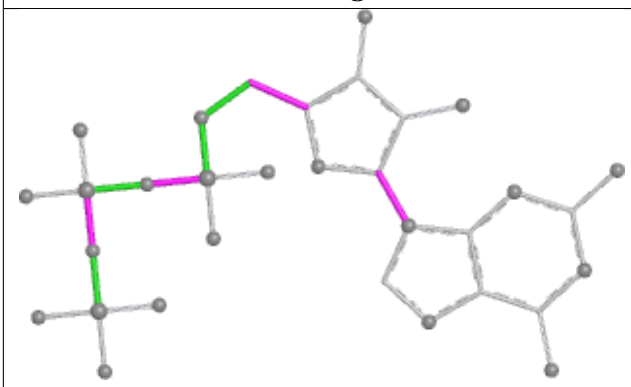

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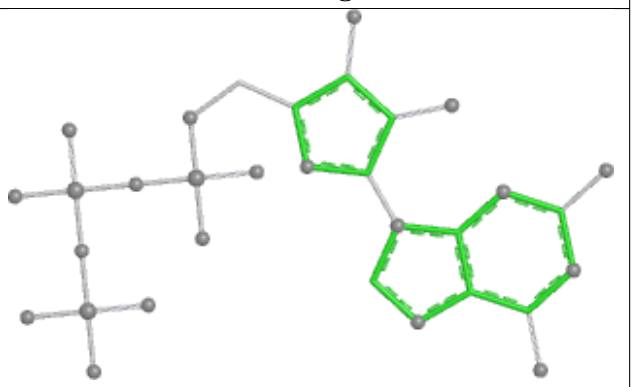
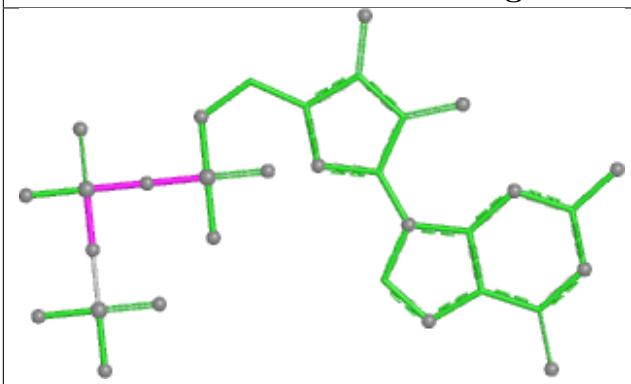


Rings

Ligand GTP MD 502



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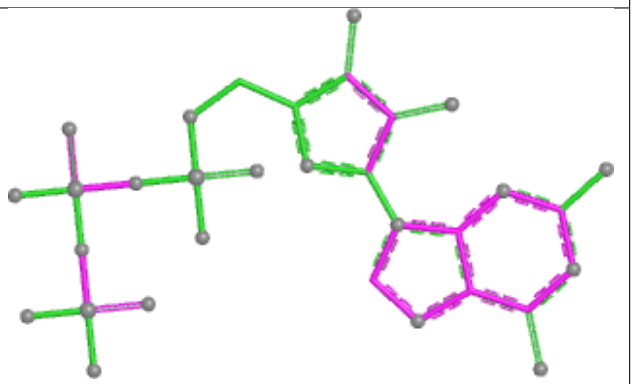

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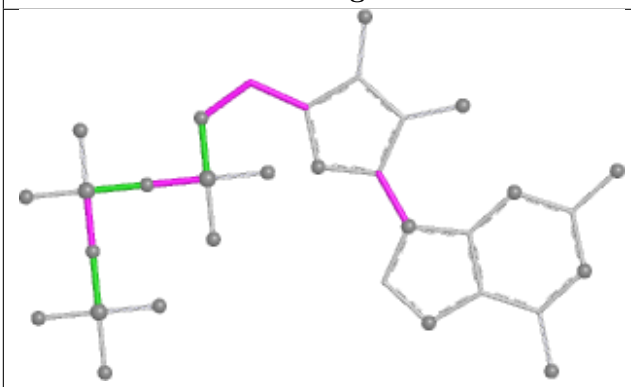

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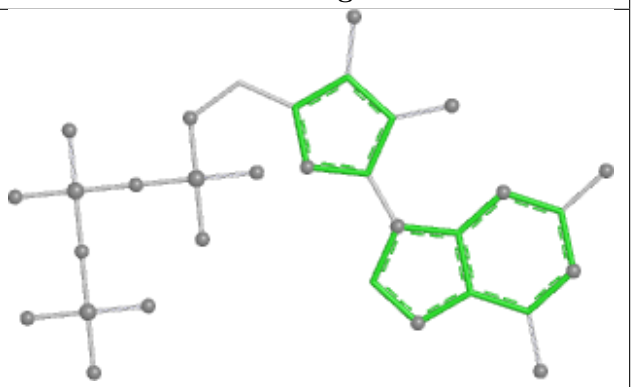

Rings

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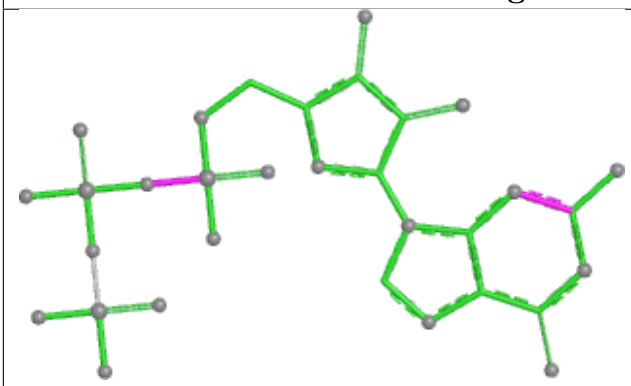

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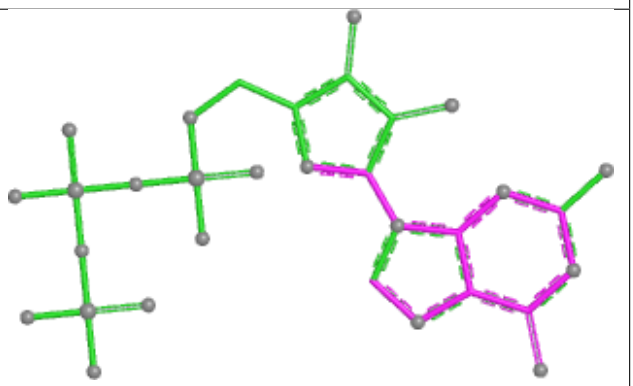

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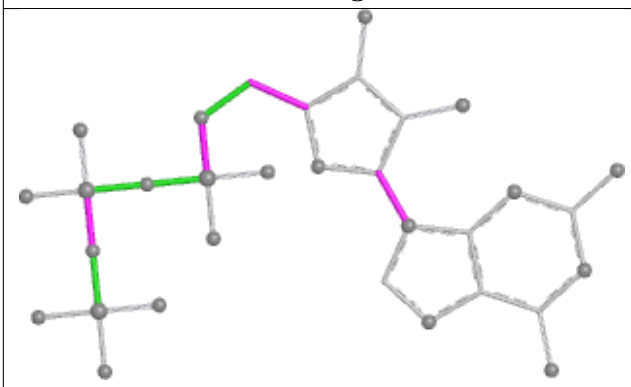

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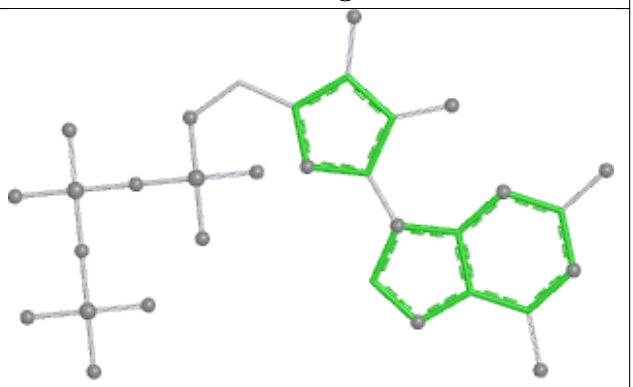

Rings

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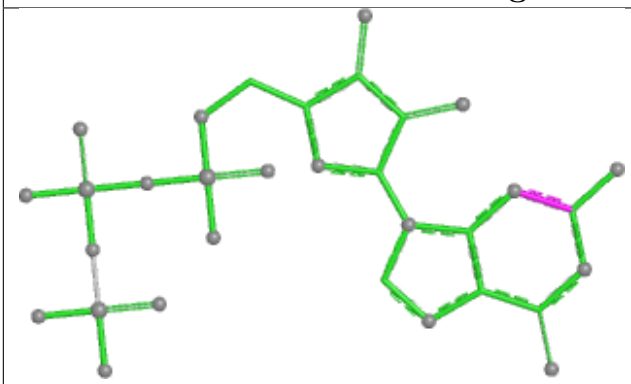

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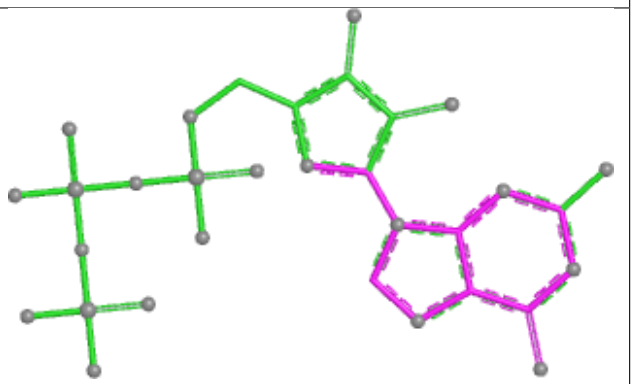

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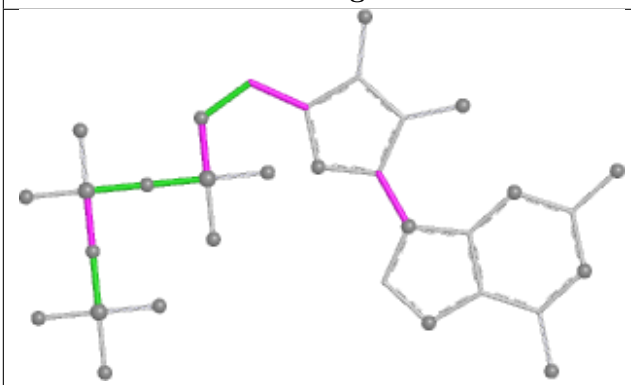

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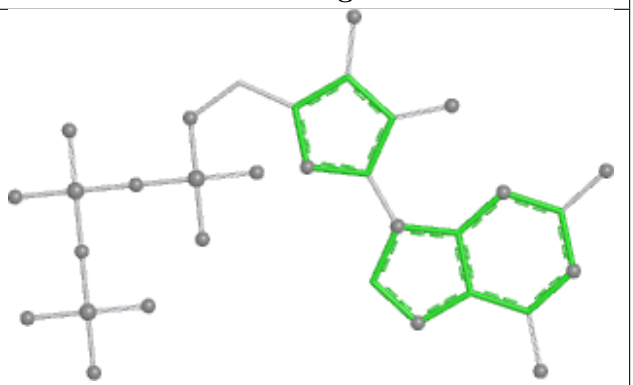
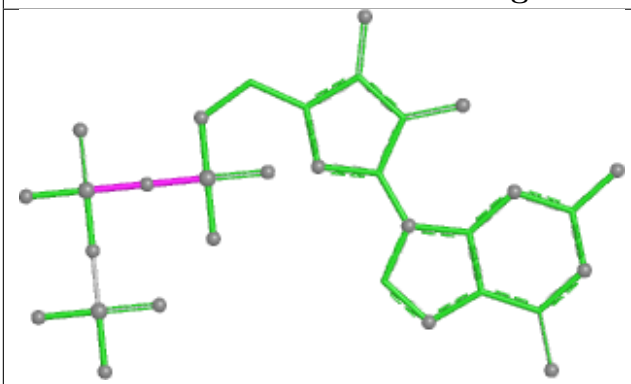


Rings

Ligand GTP BE 501



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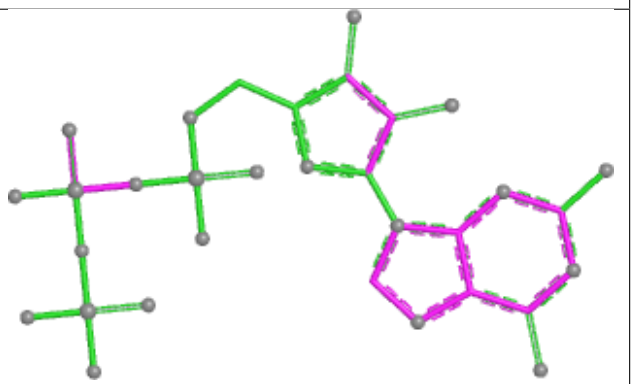
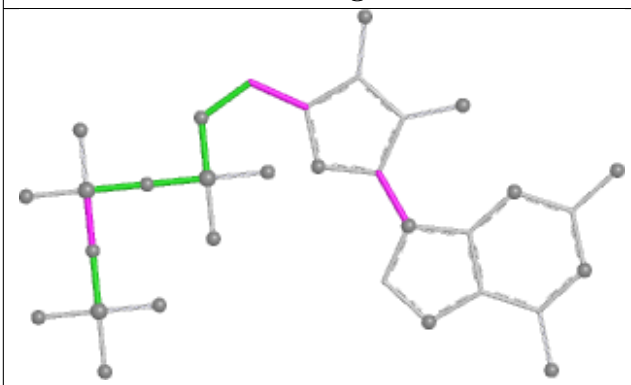
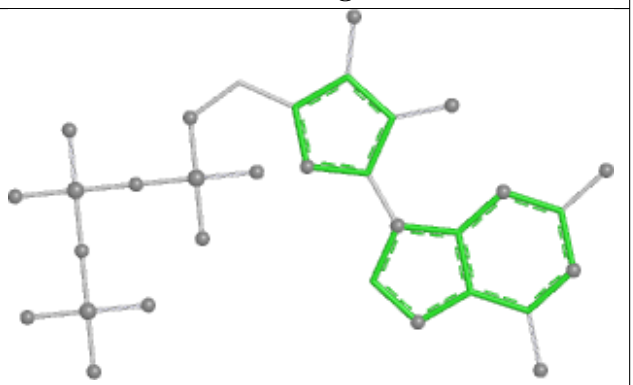


Bond angles

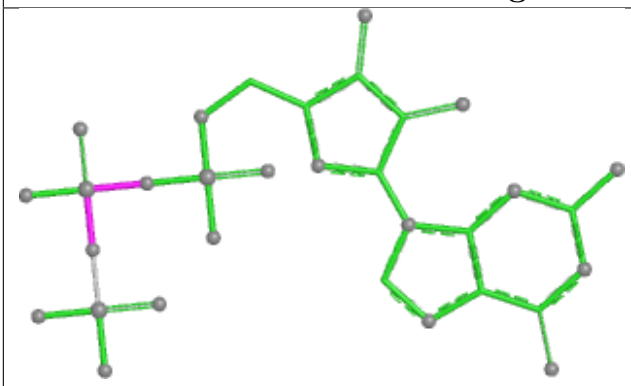


Torsions



Rings

Ligand GTP CK 501



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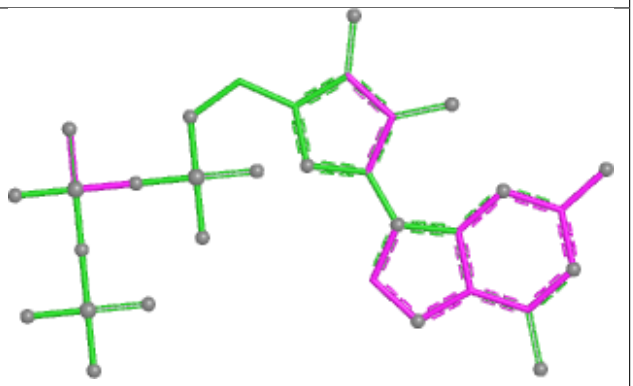

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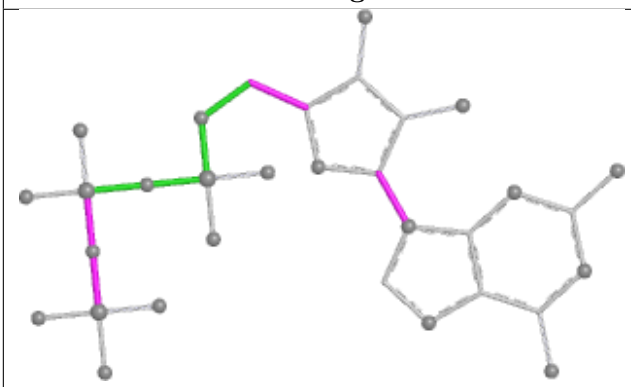

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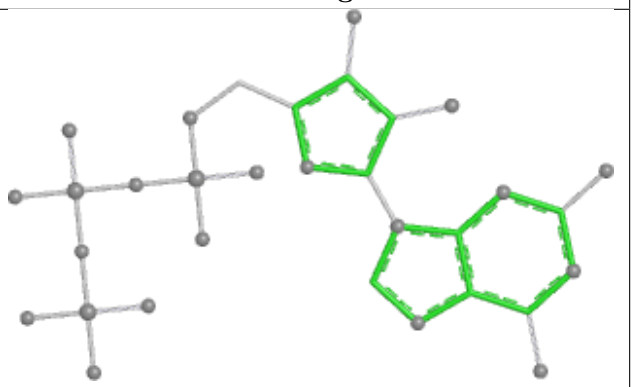
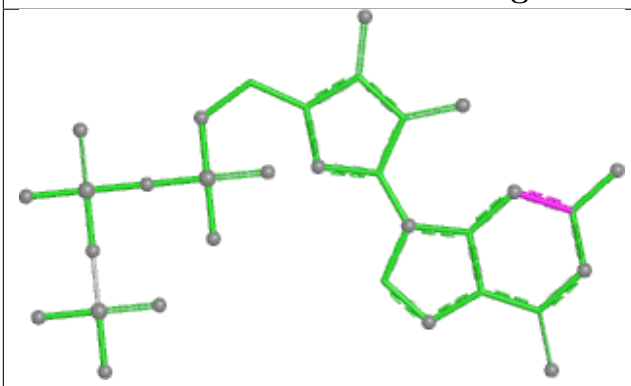


Rings

Ligand GTP DL 501



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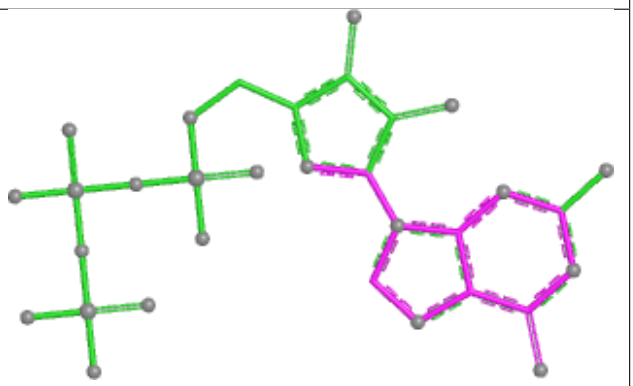

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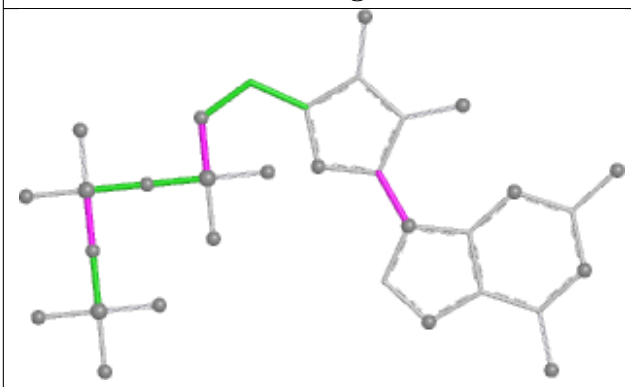

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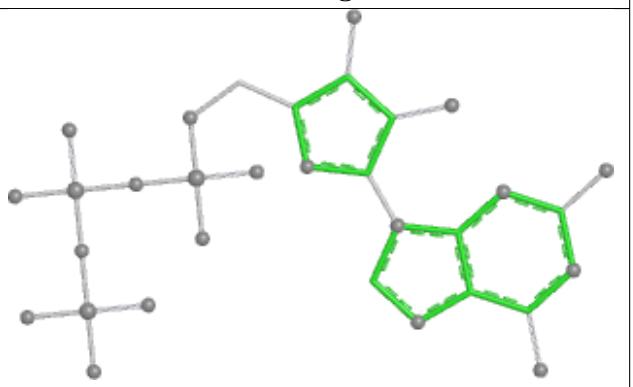
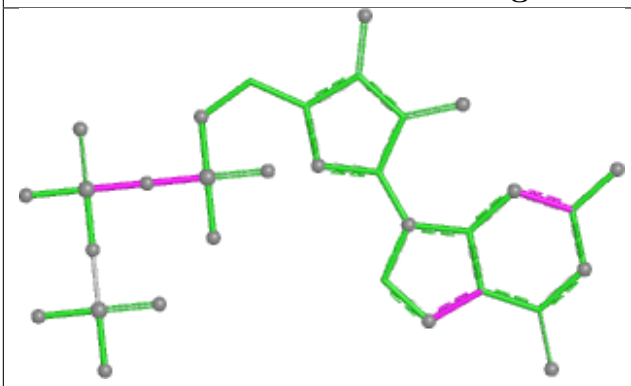


Rings

Ligand GTP EB 501



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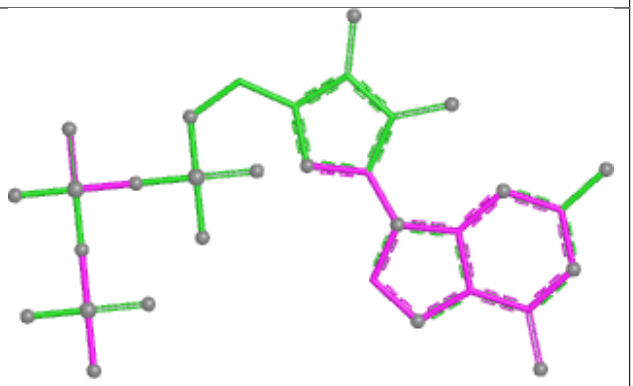

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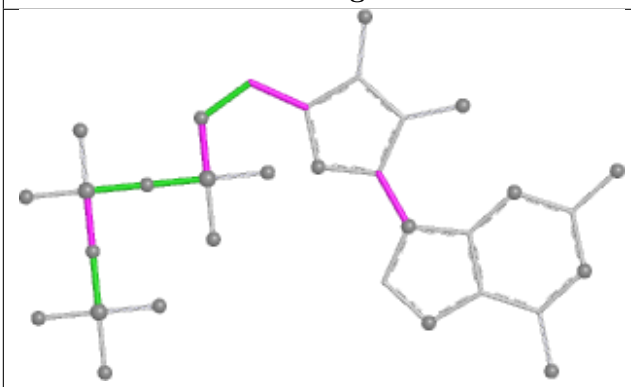
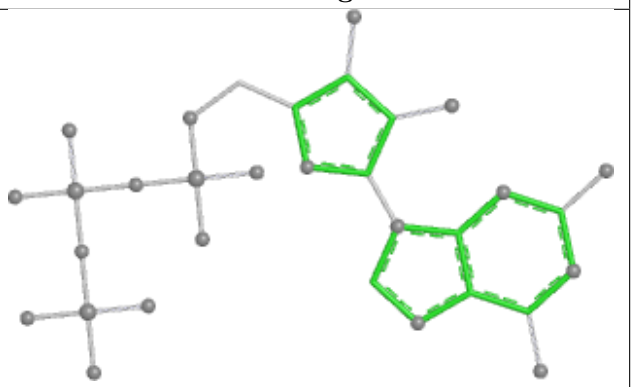
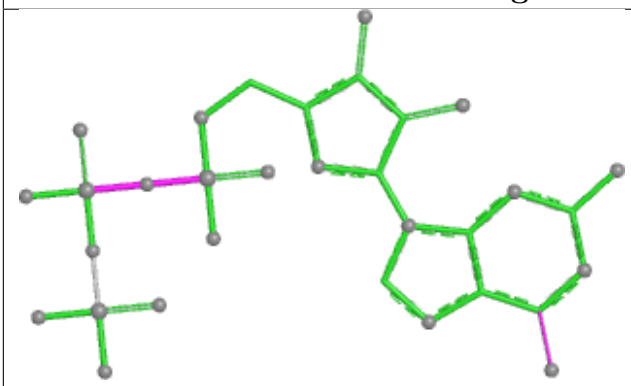


Torsions



Rings

Ligand GTP EC 501



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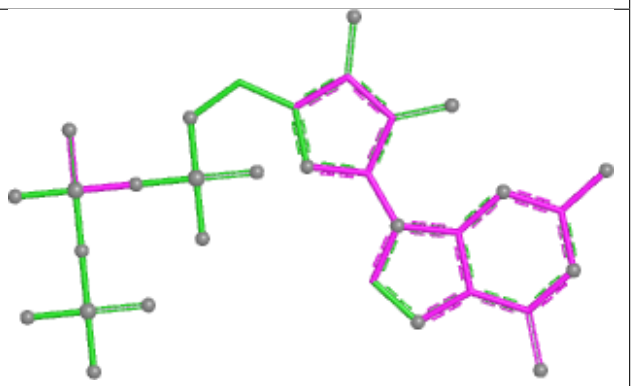

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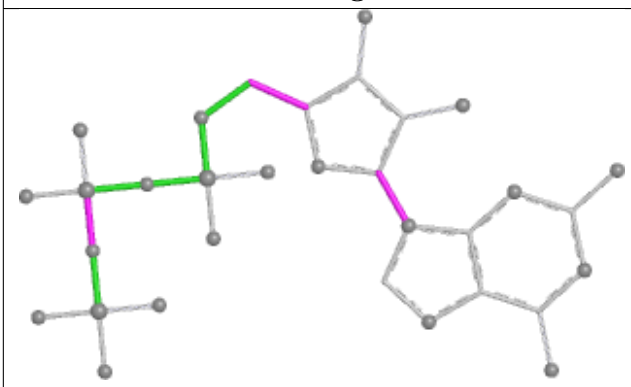

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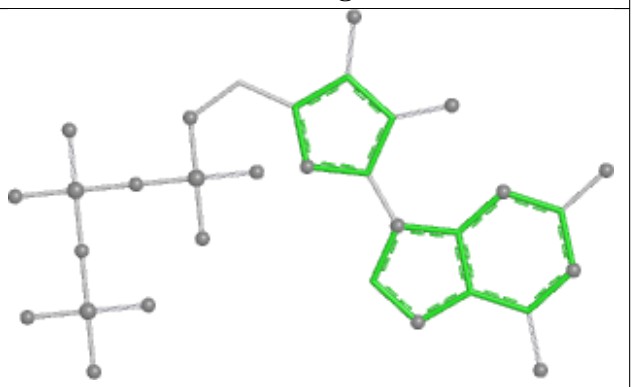
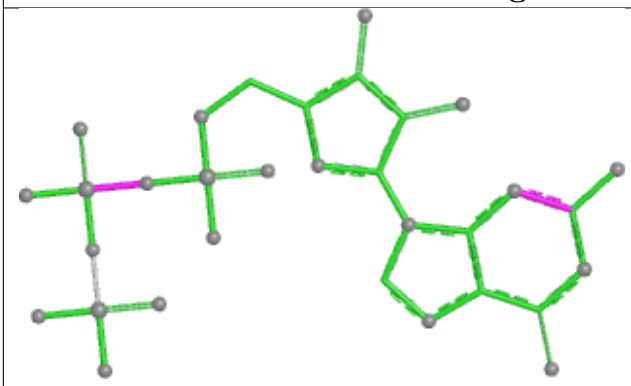


Rings

Ligand GTP KC 501



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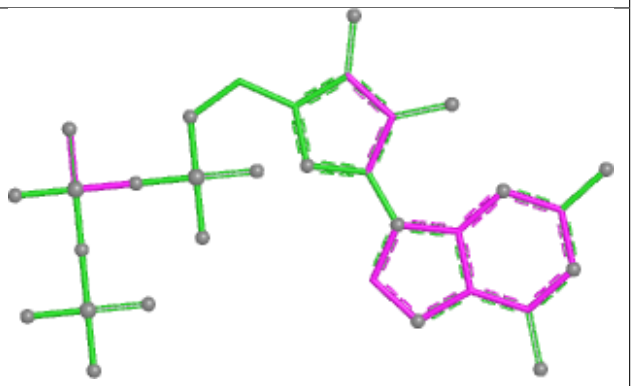

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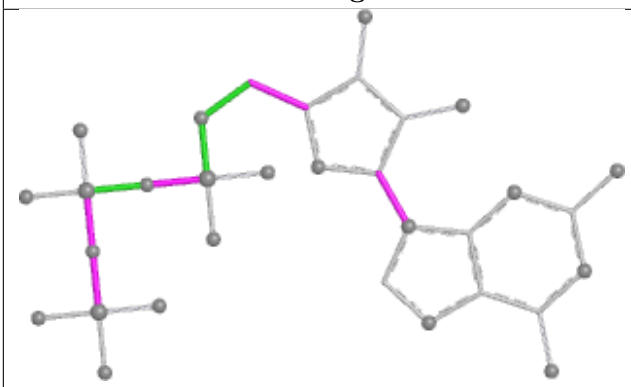

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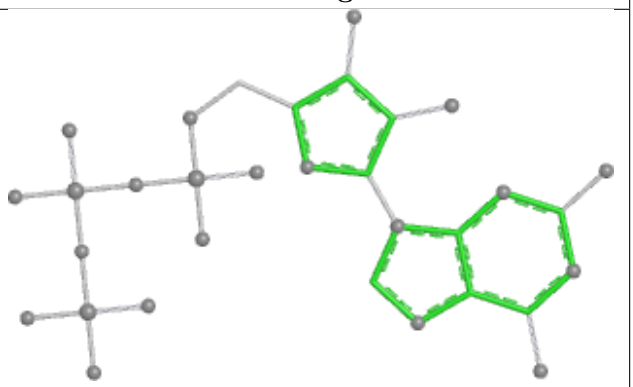

Rings

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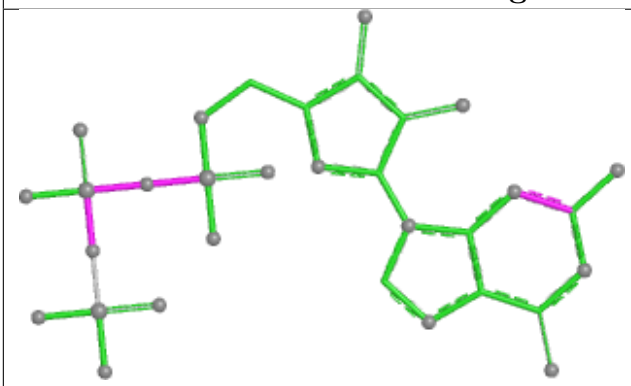

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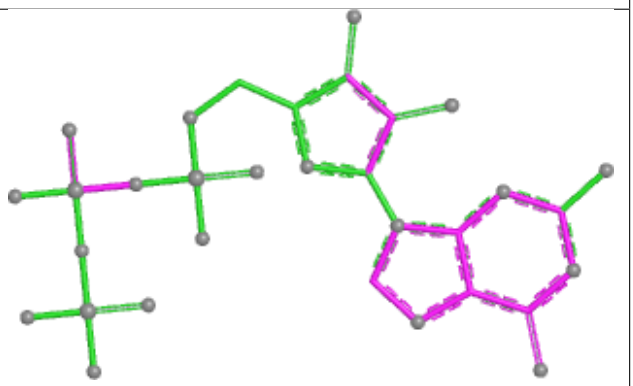

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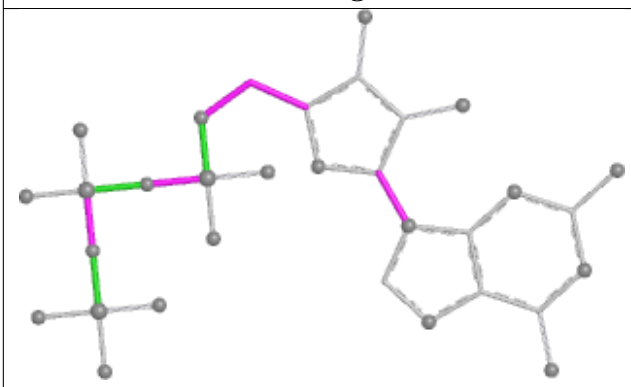

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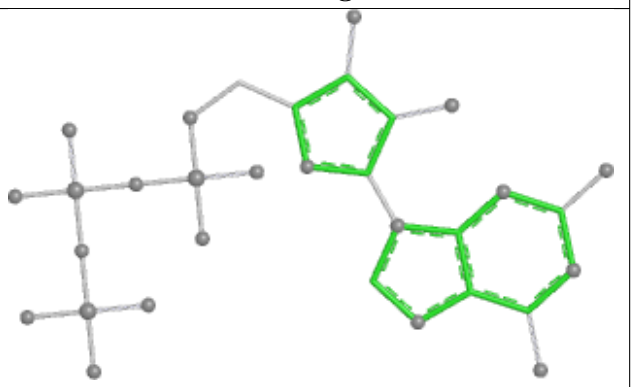

Rings

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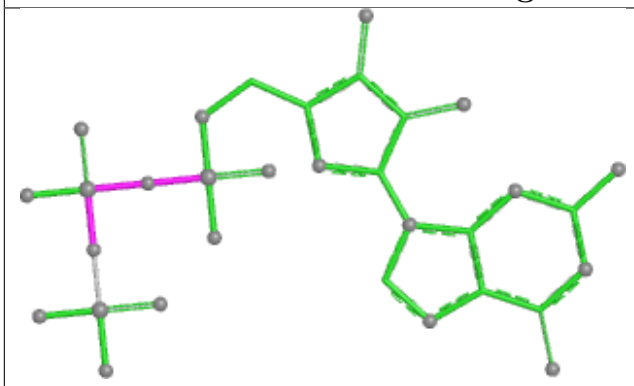

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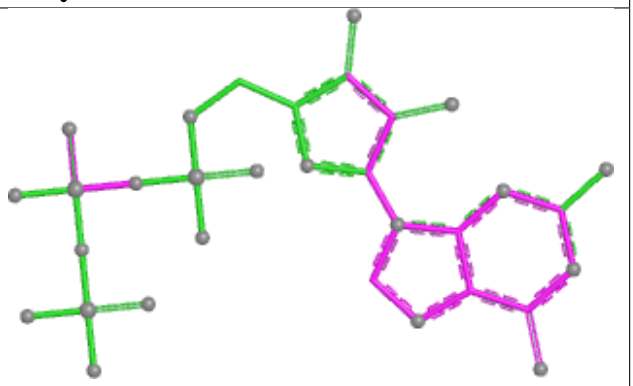

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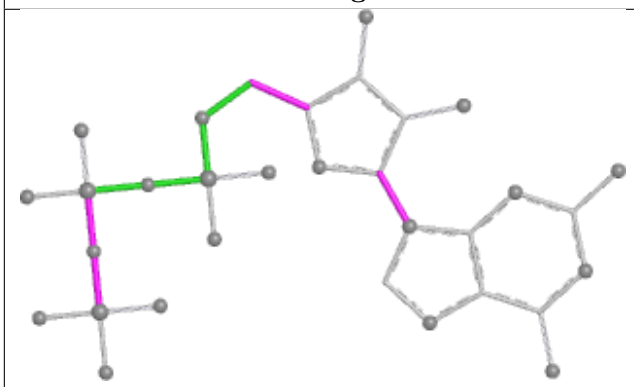

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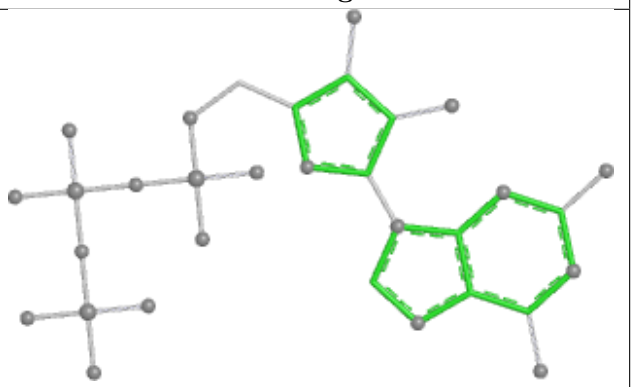
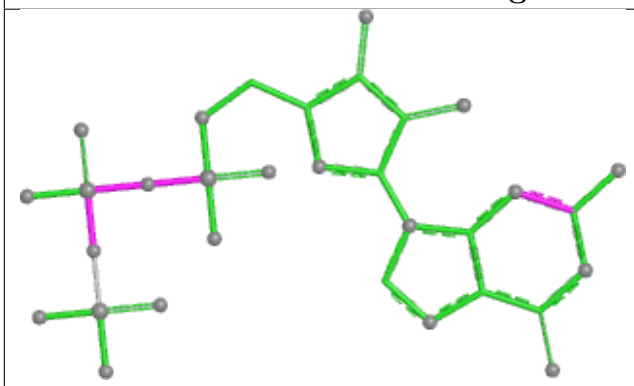


Rings

Ligand GTP UH 501



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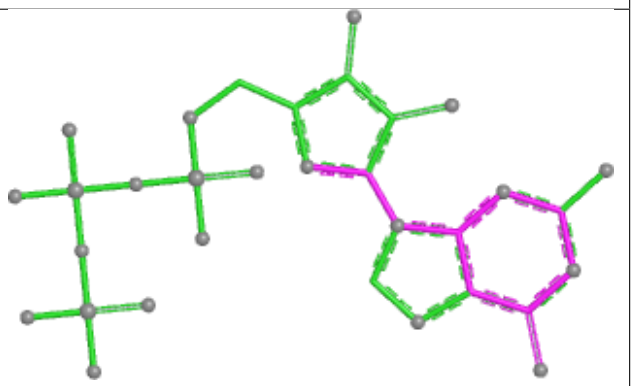

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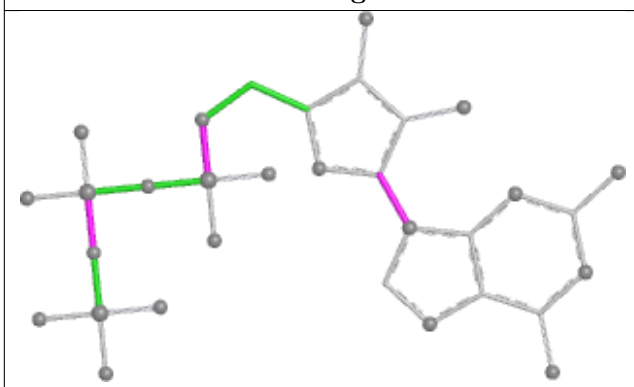

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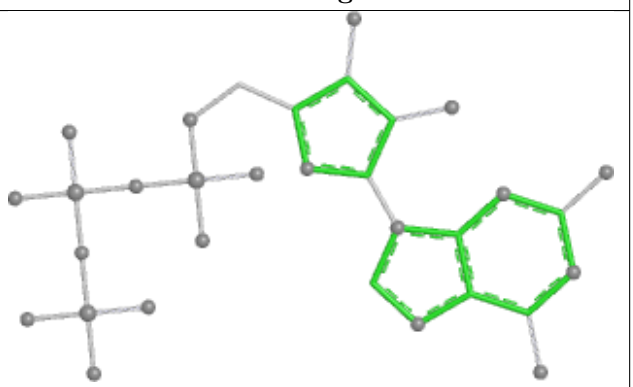
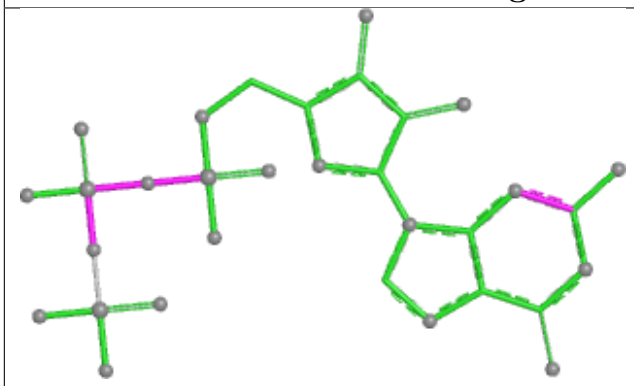


Rings

Ligand GTP VK 501



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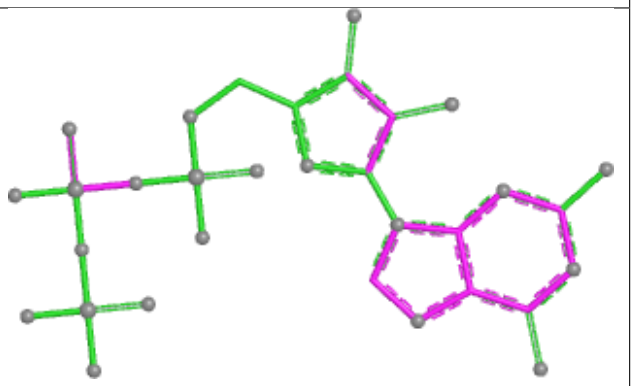

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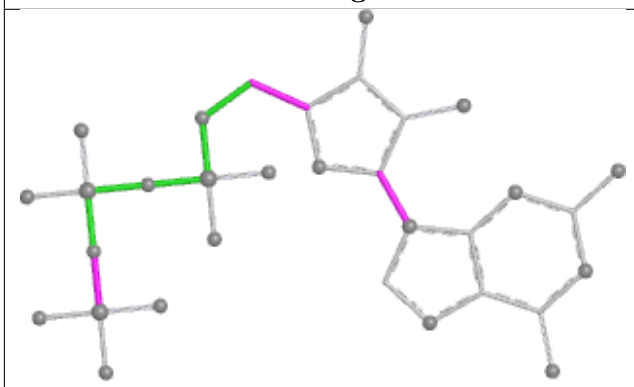

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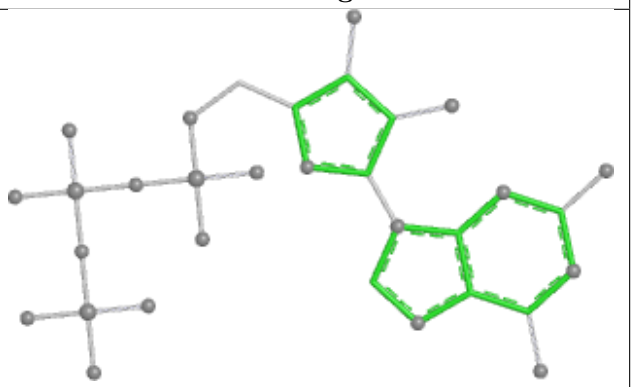
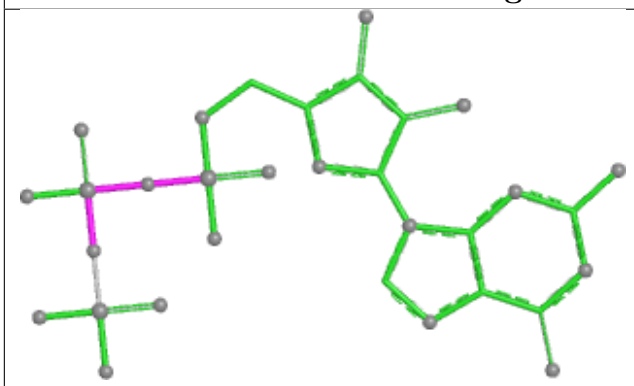


Rings

Ligand GTP WG 501



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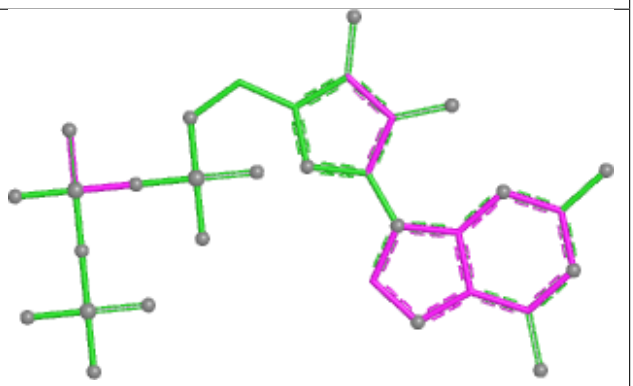

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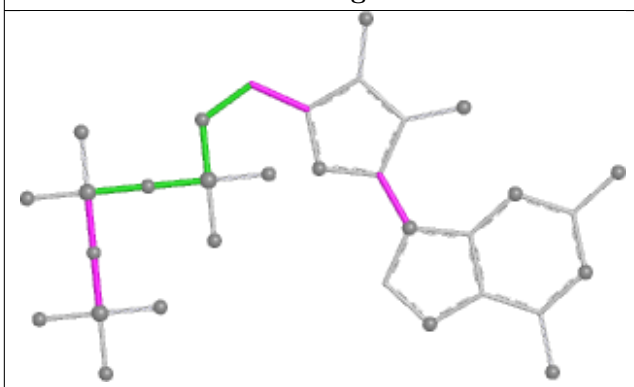

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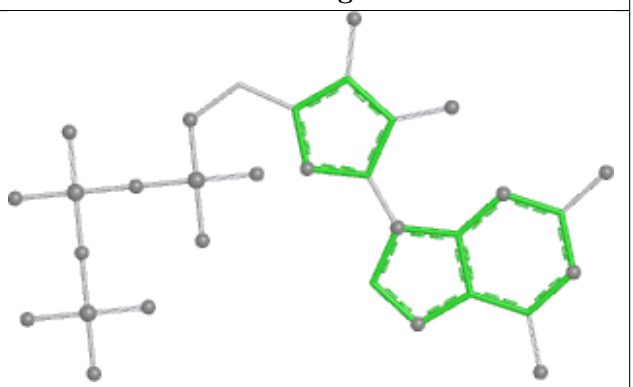
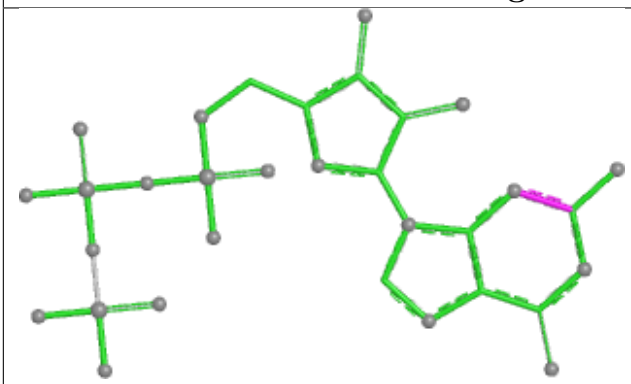


Rings

Ligand GTP AH 501



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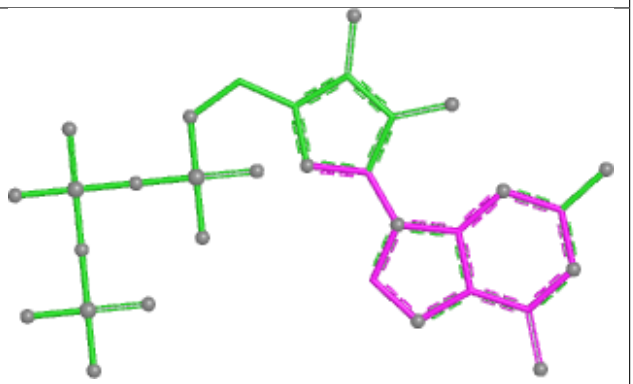

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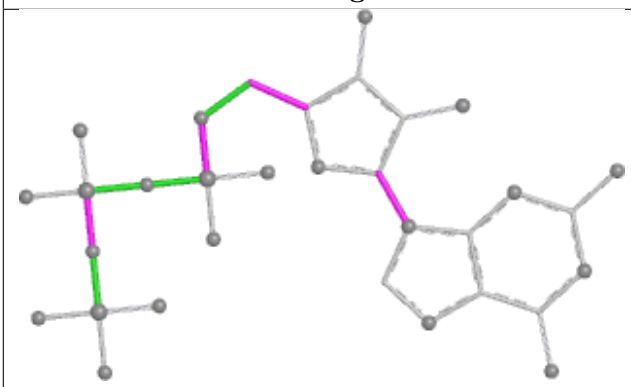

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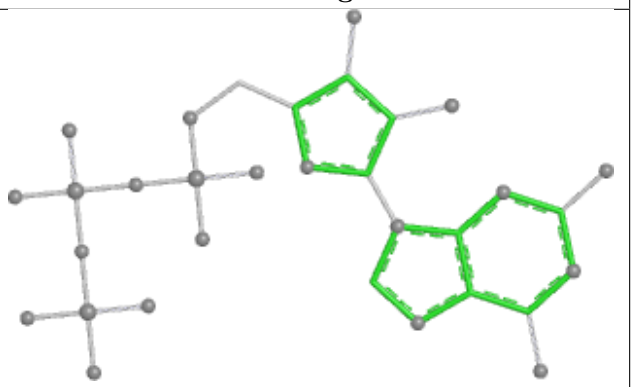

Rings

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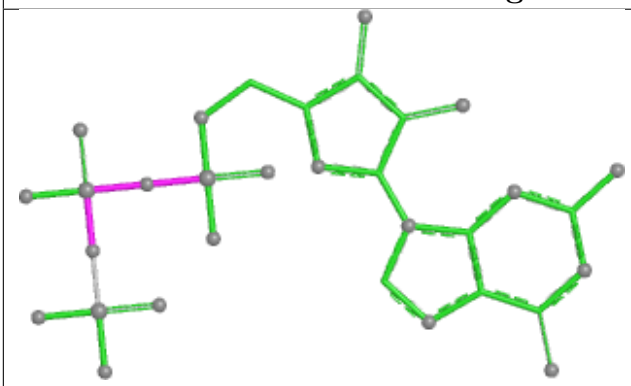

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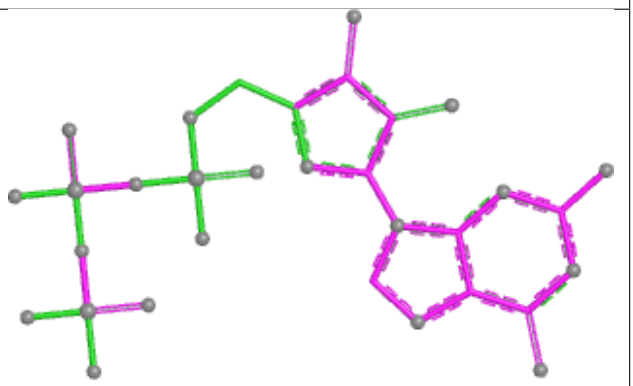

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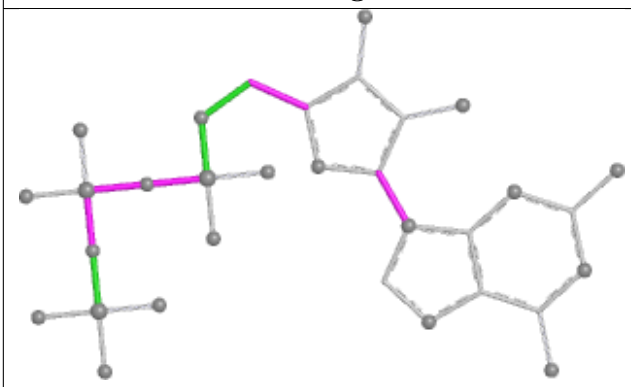

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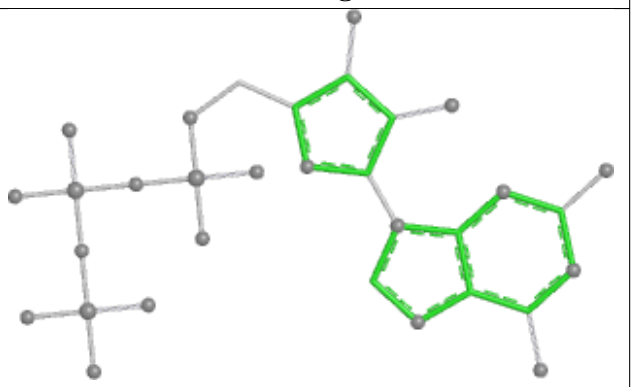

Rings

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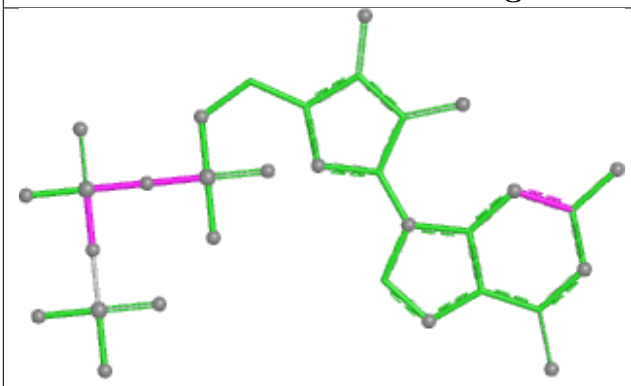

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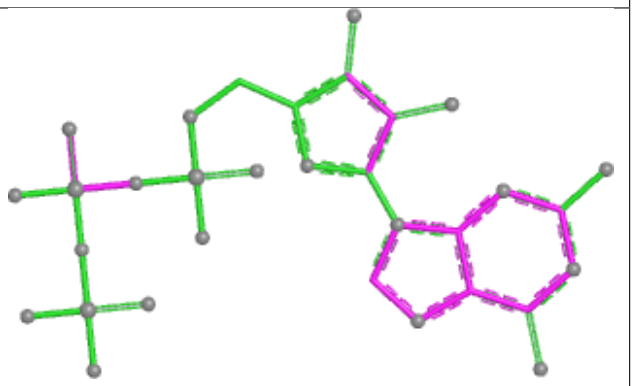

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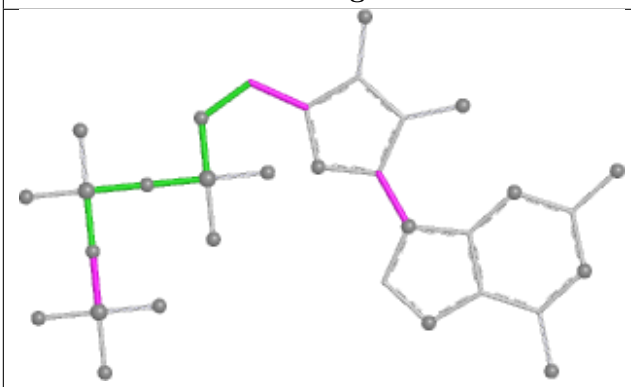

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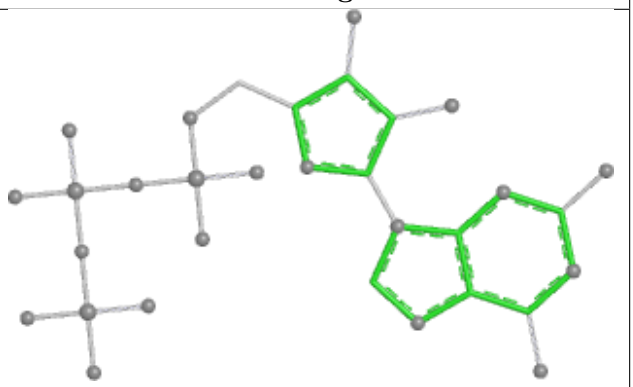
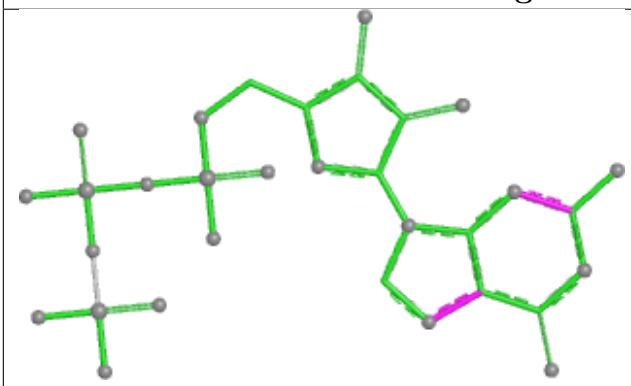


Rings

Ligand GTP FJ 501



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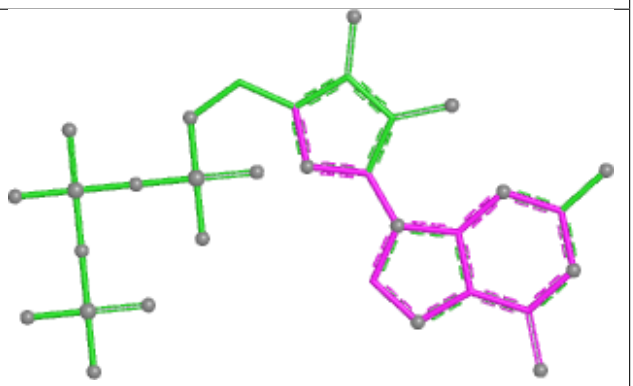
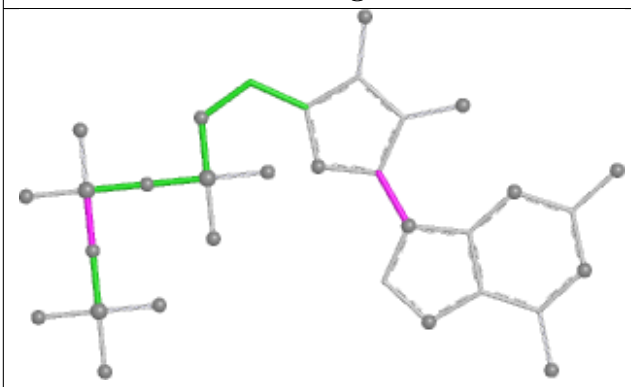


Bond angles



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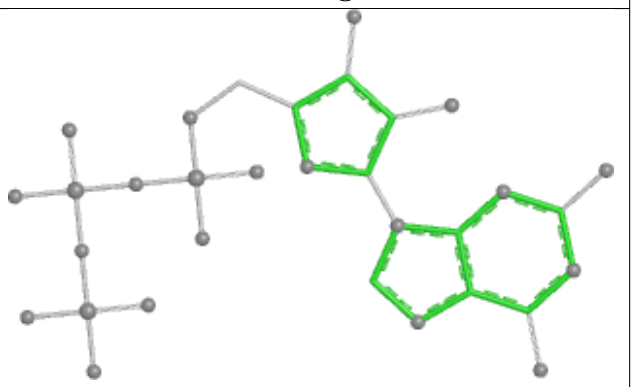
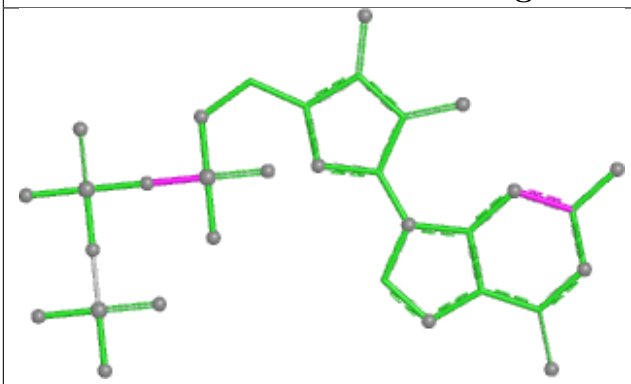


Rings

Ligand GTP SL 501



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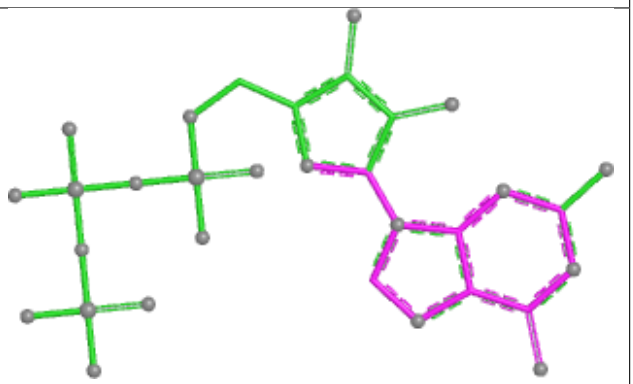
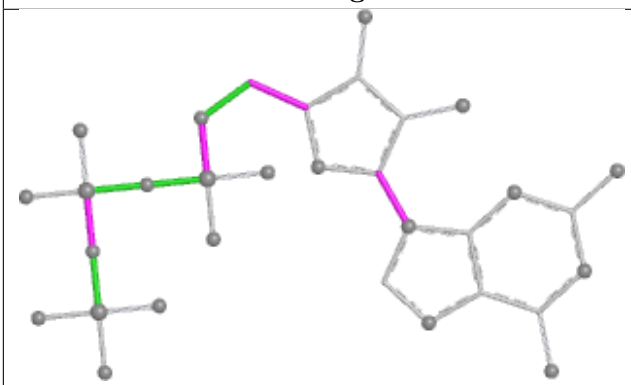


Bond angles



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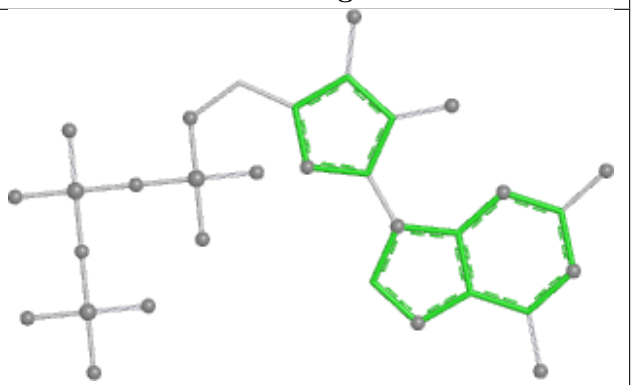
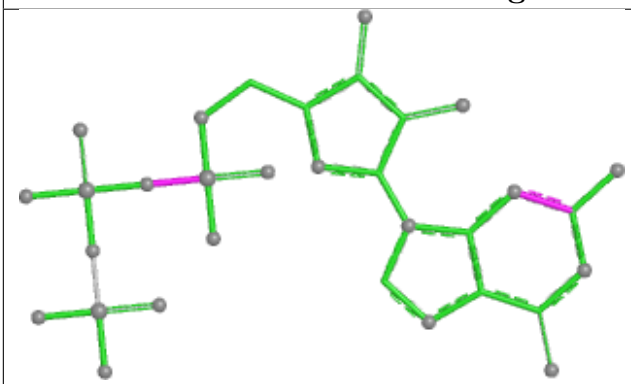


Rings

Ligand GTP HD 501



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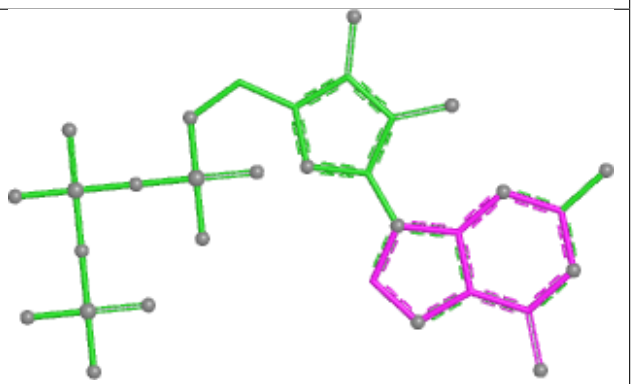

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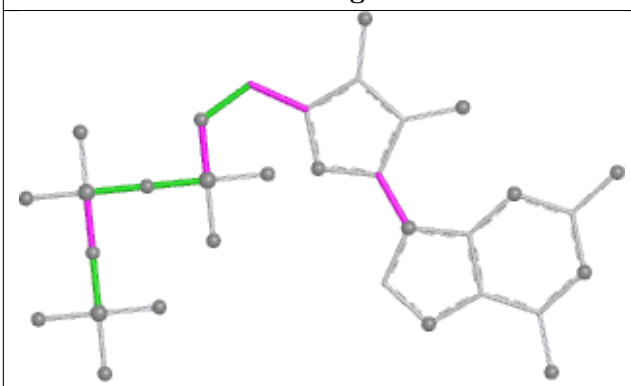

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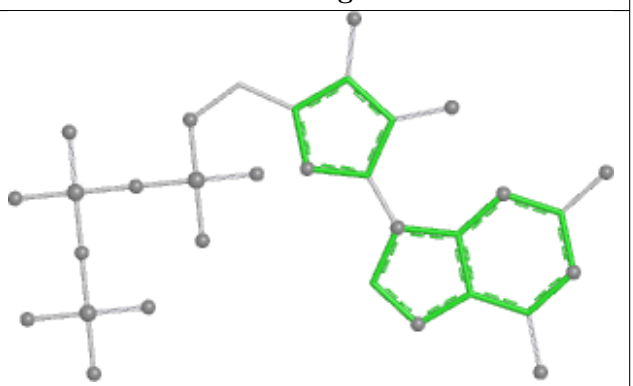
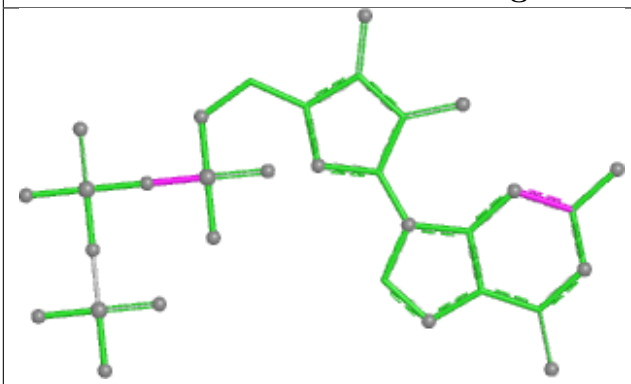


Rings

Ligand GTP HF 501



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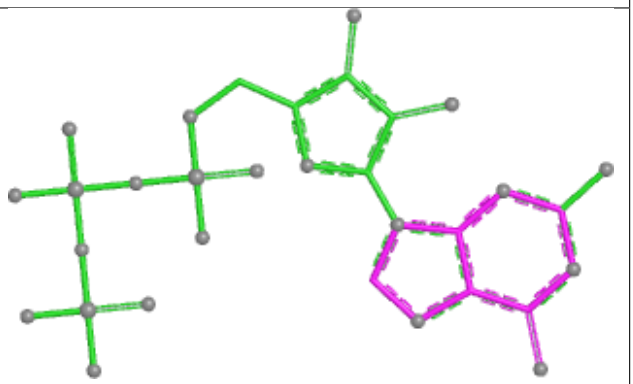

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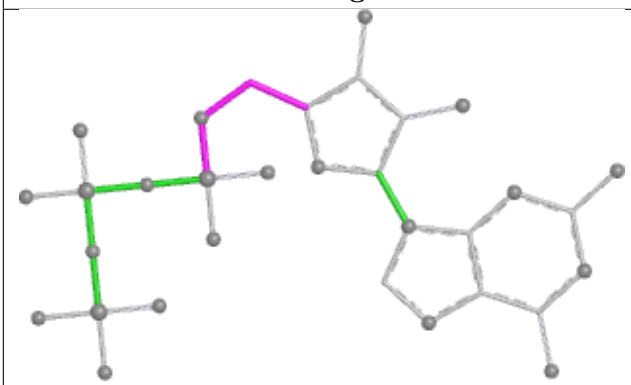
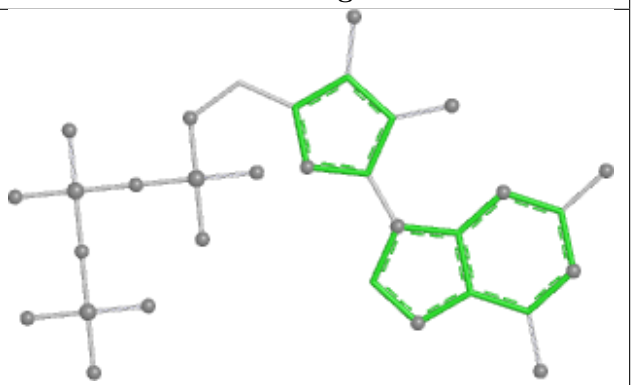
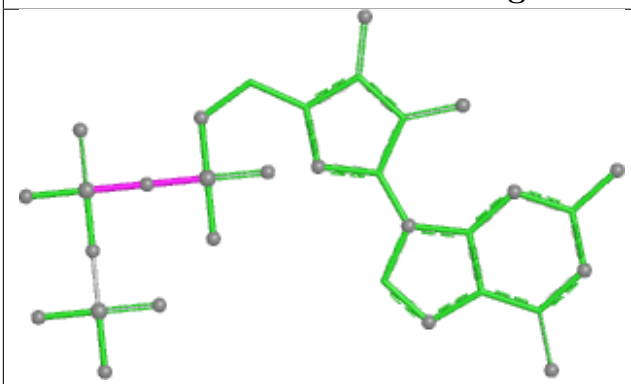


Torsions



Rings

Ligand GTP DK 501



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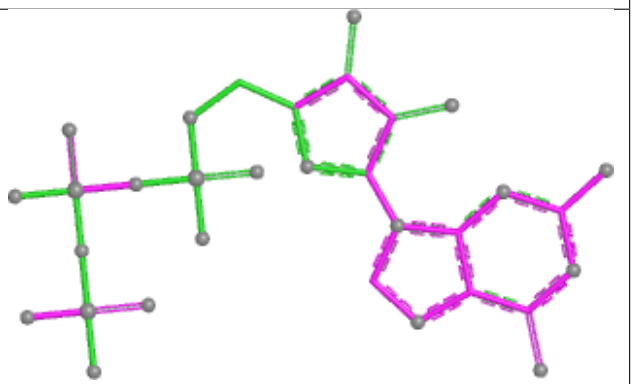

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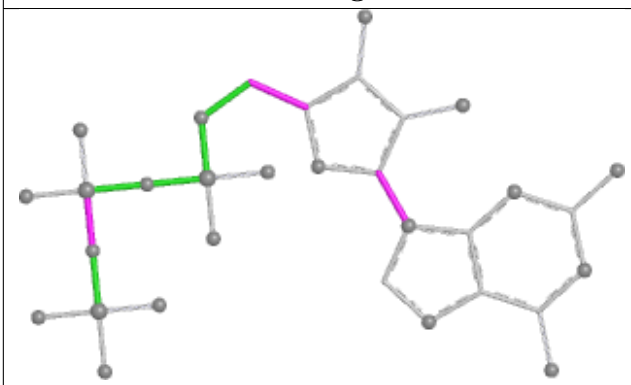

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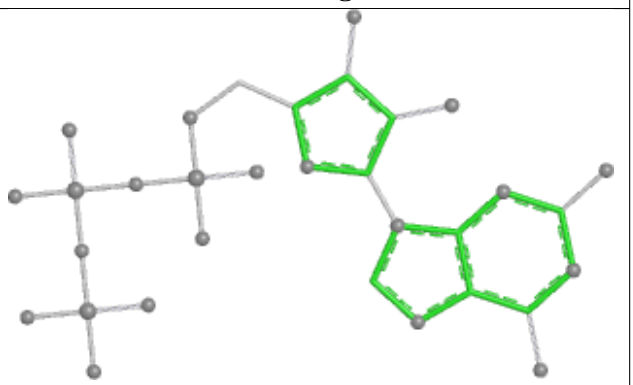
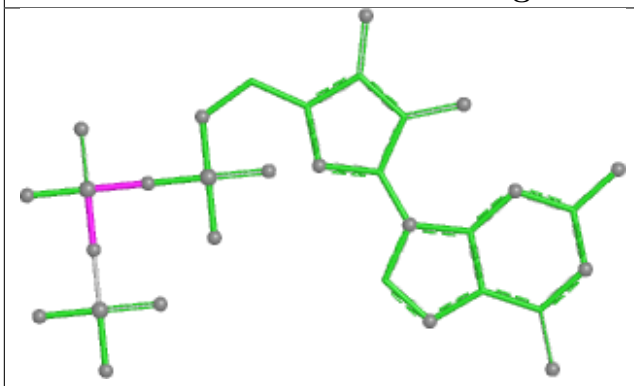


Rings

Ligand GTP IM 501



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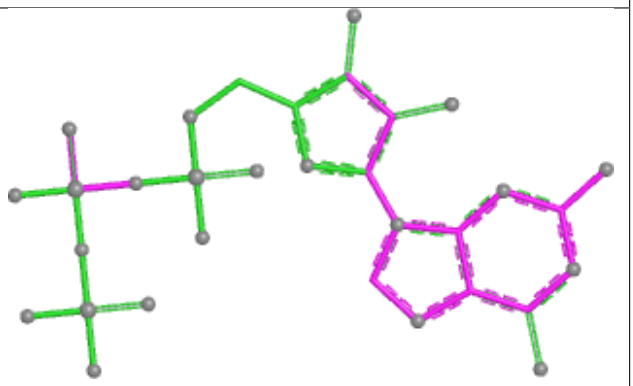

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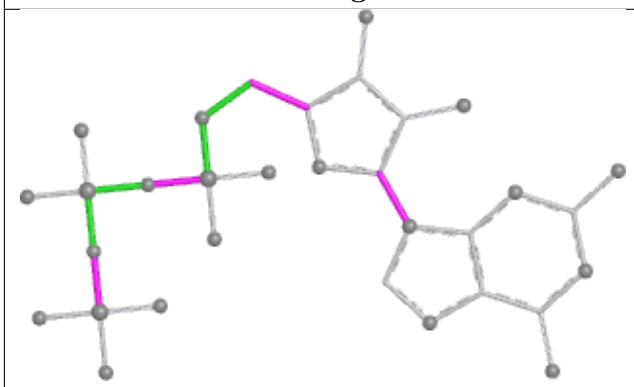

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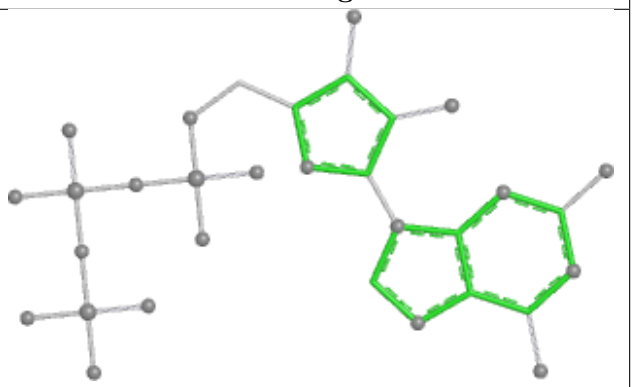
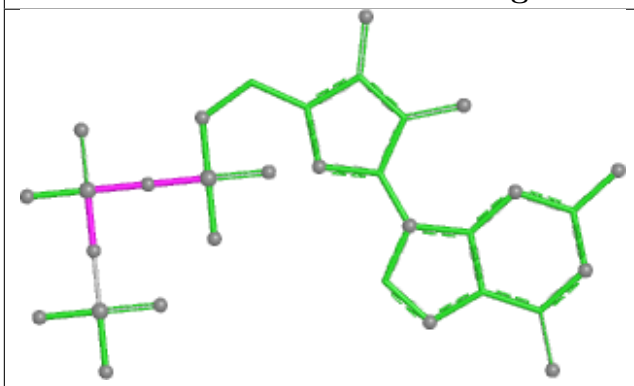


Rings

Ligand GTP UE 501



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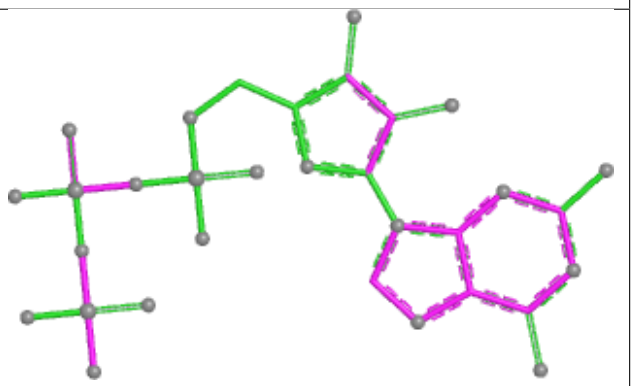

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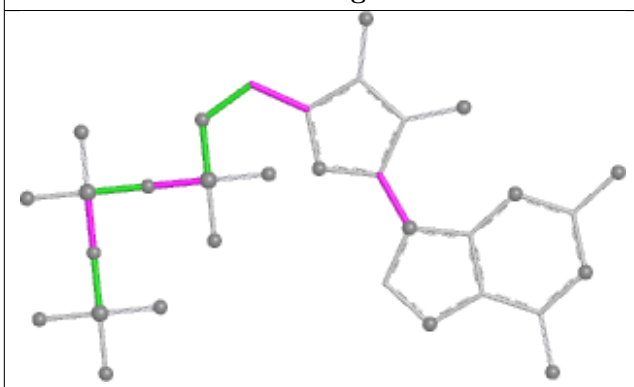

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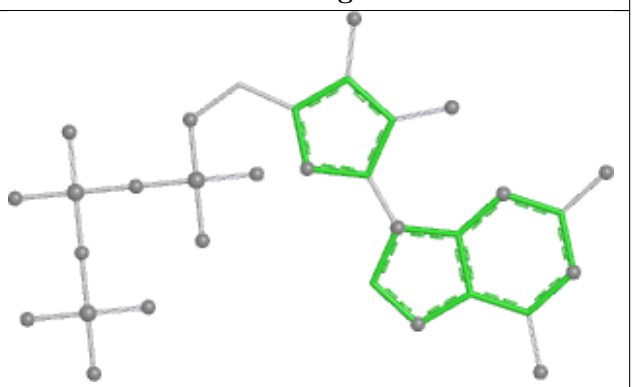

Rings

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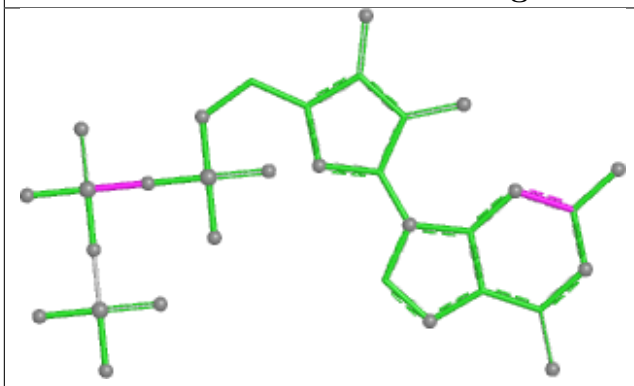

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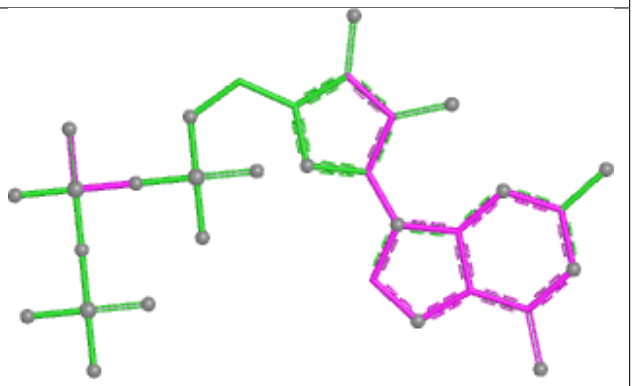

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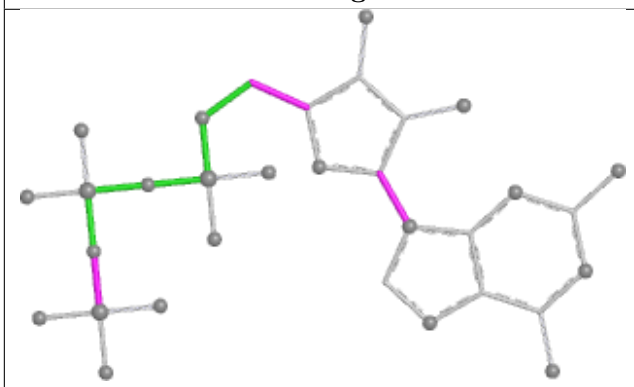

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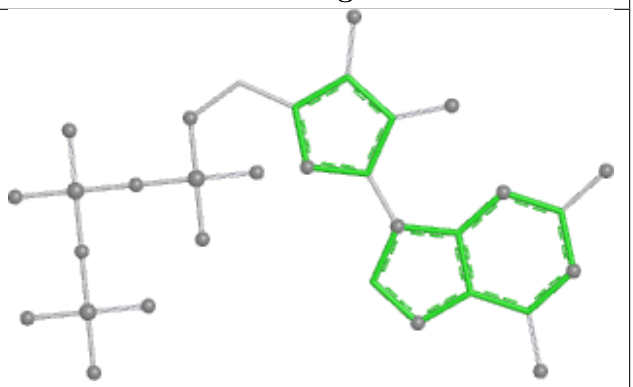

Rings

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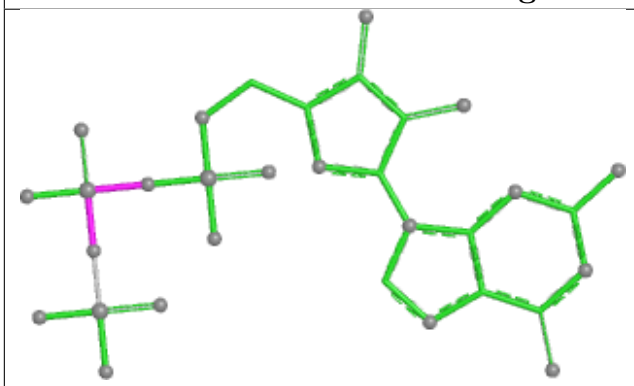

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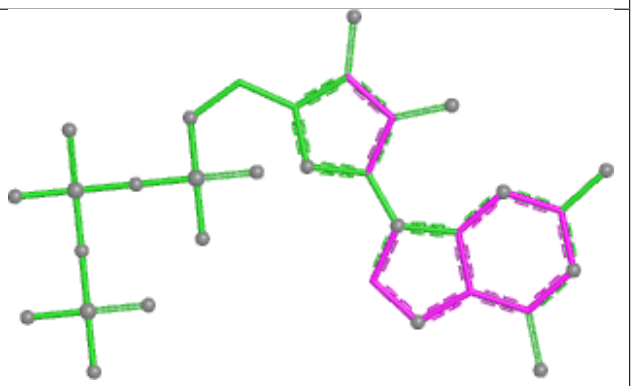

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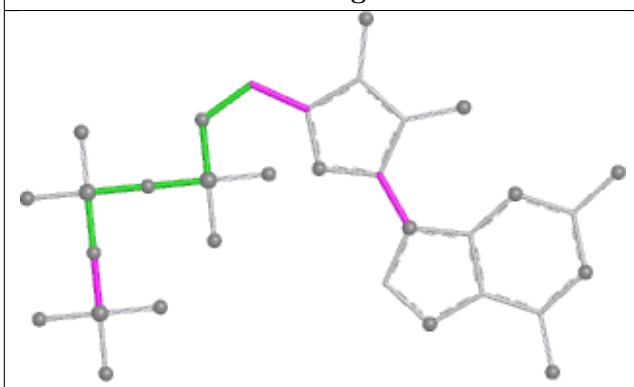

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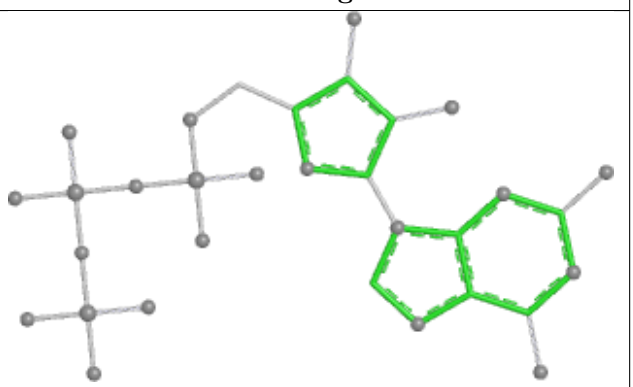
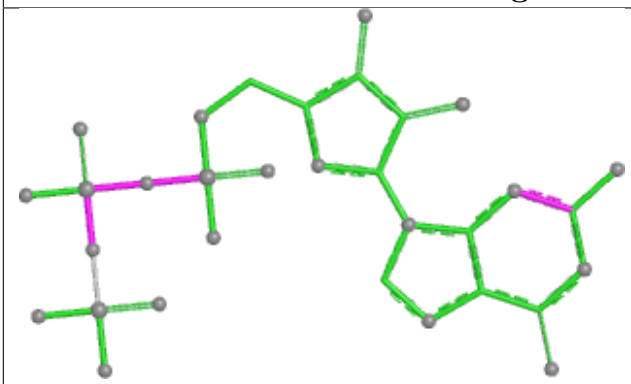


Rings

Ligand GTP OF 501



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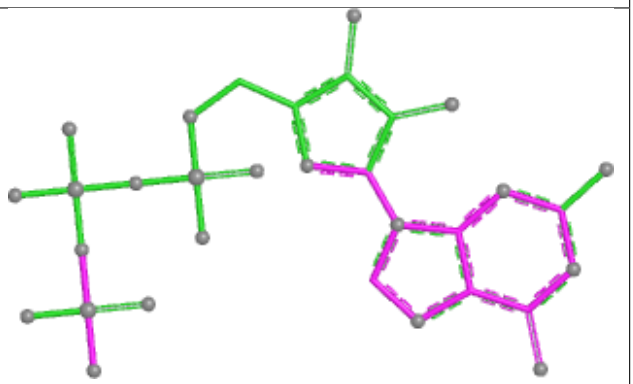

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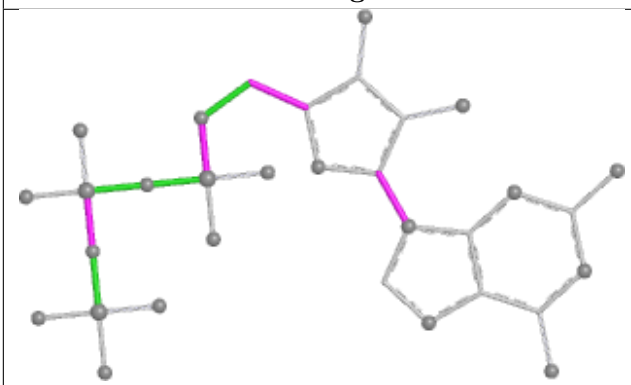

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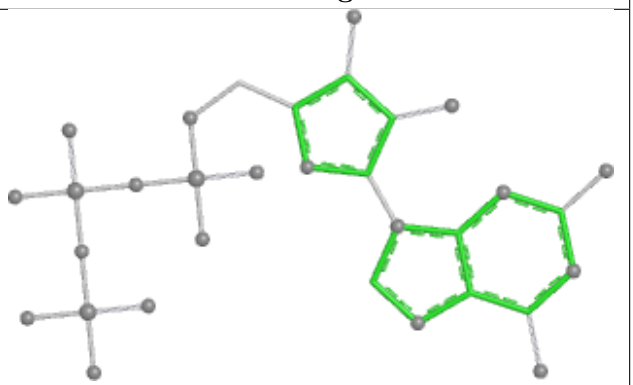
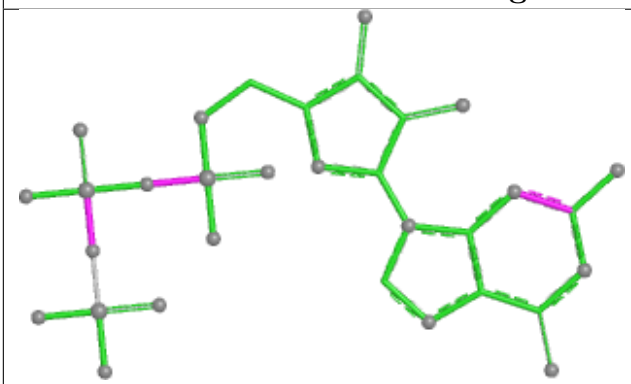


Rings

Ligand GTP MJ 501



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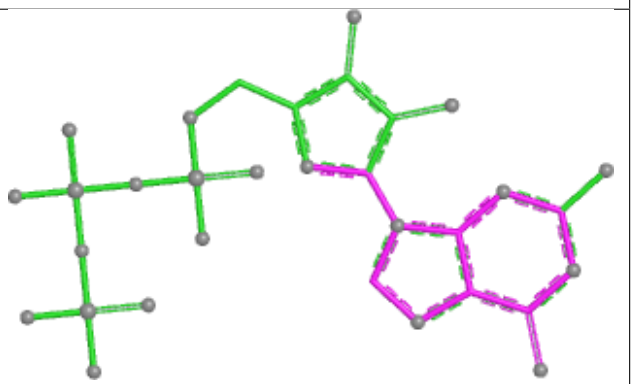

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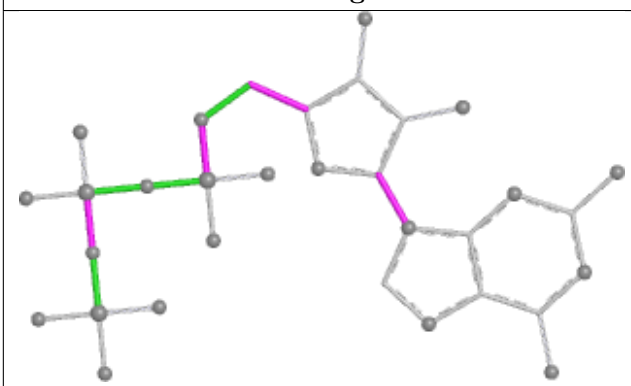

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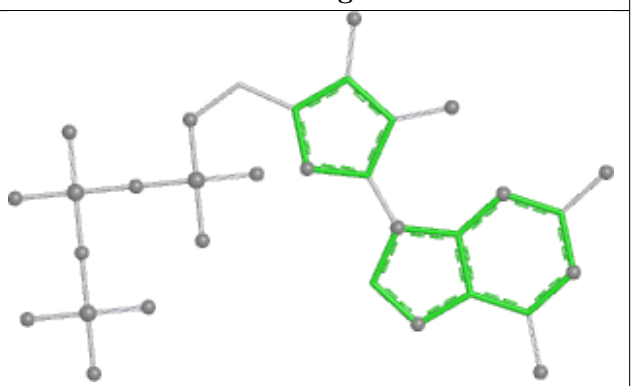
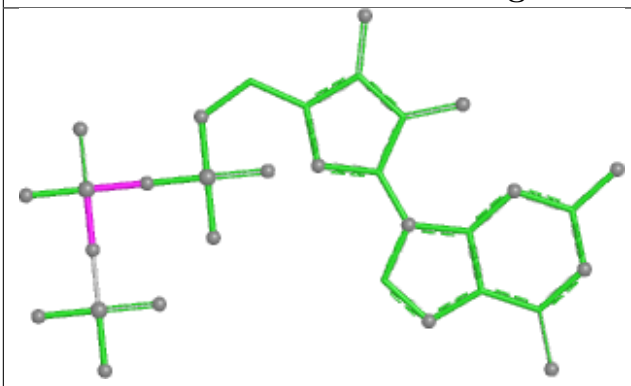


Rings

Ligand GTP QK 501



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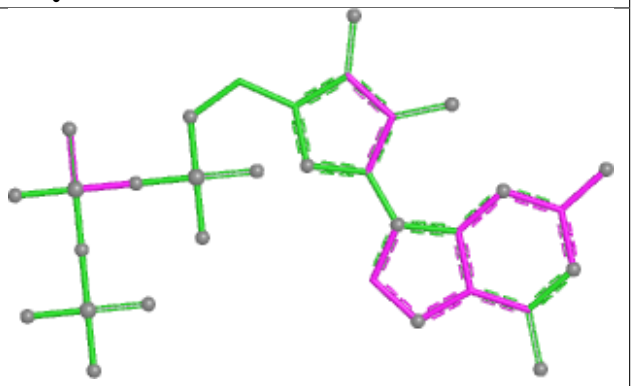

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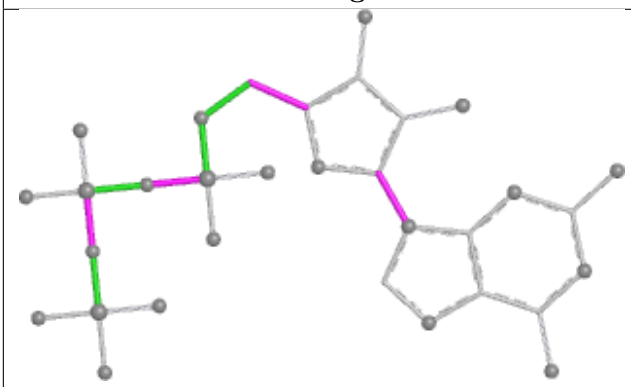

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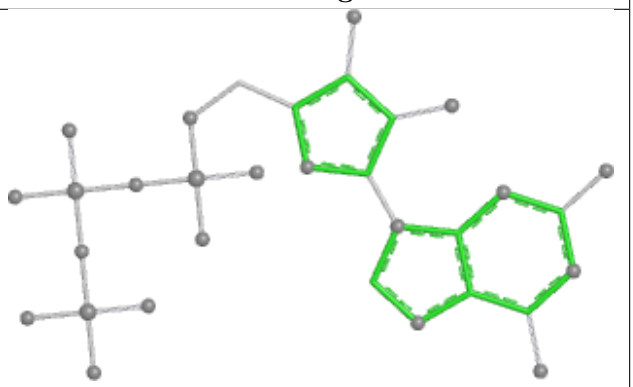

Rings

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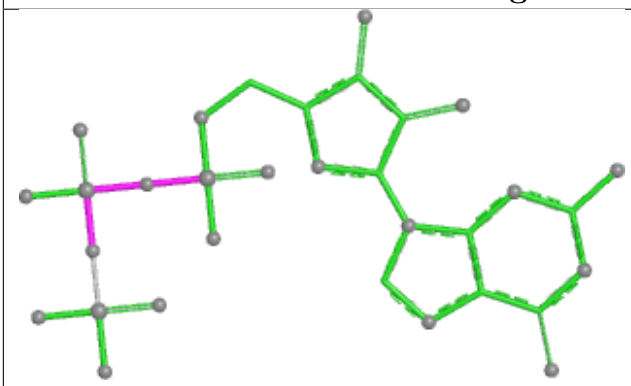

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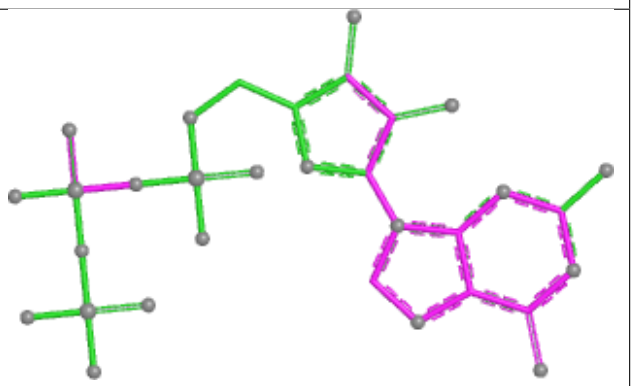

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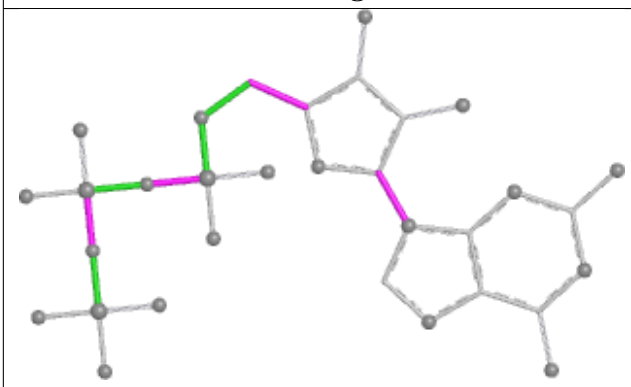

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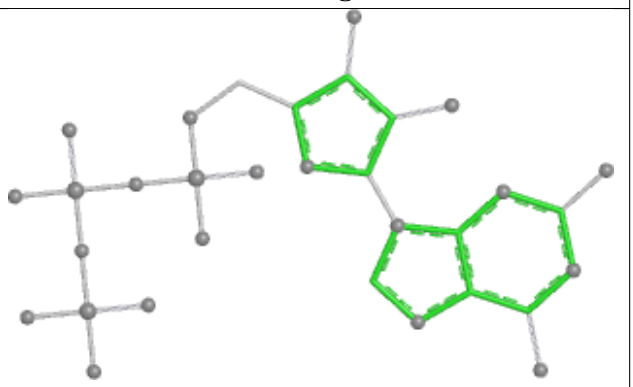

Rings

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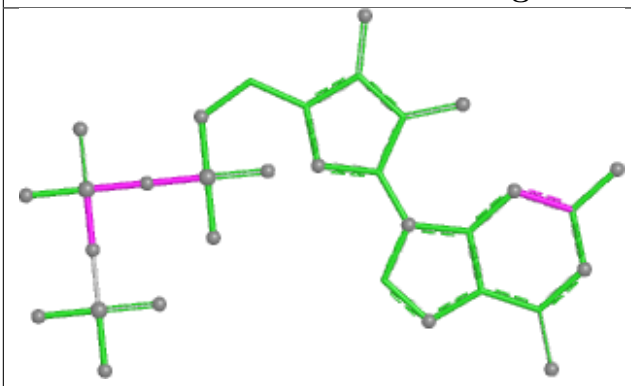

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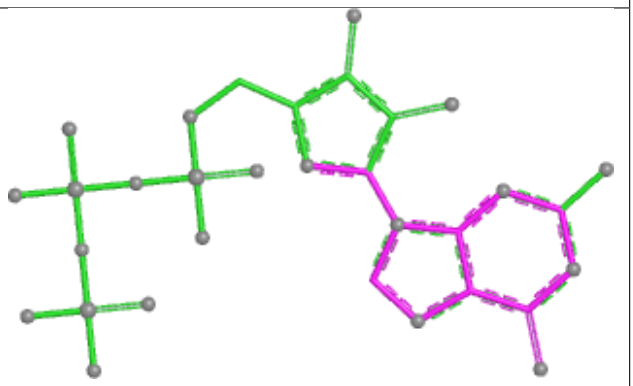

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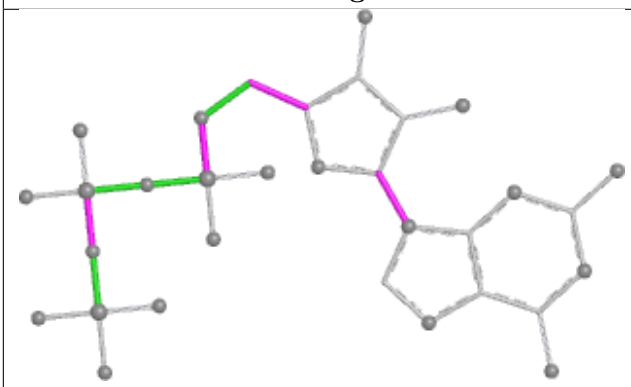

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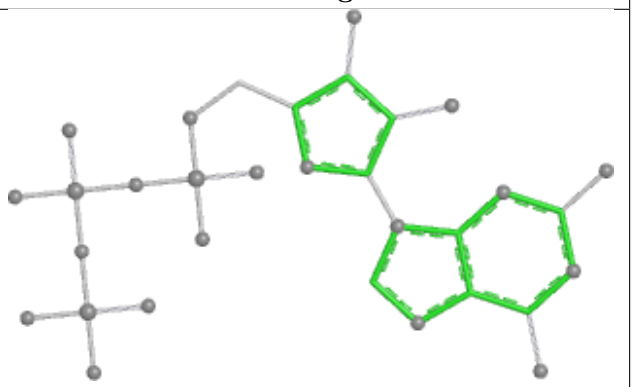

Rings

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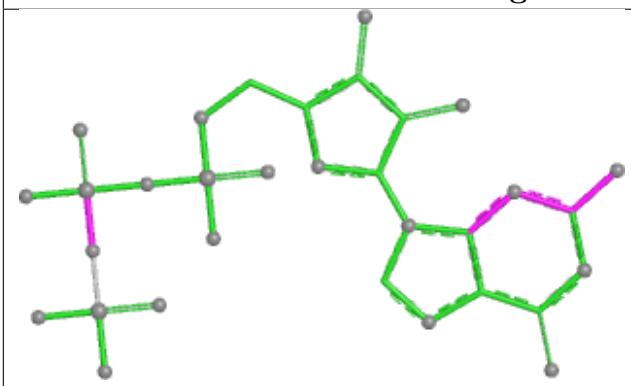

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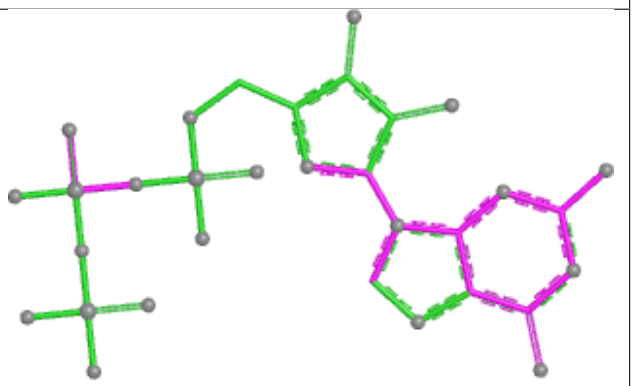

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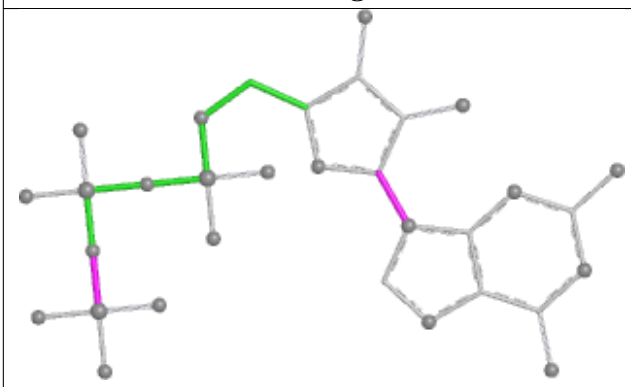

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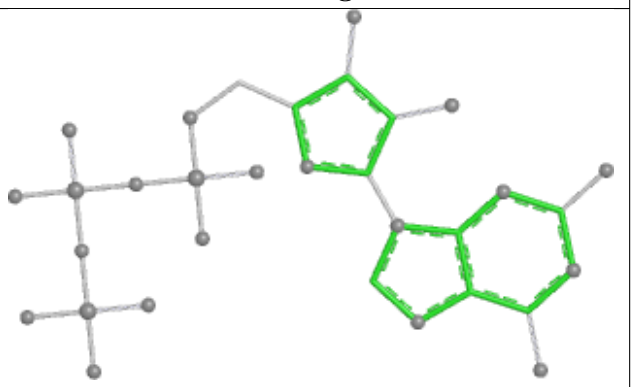
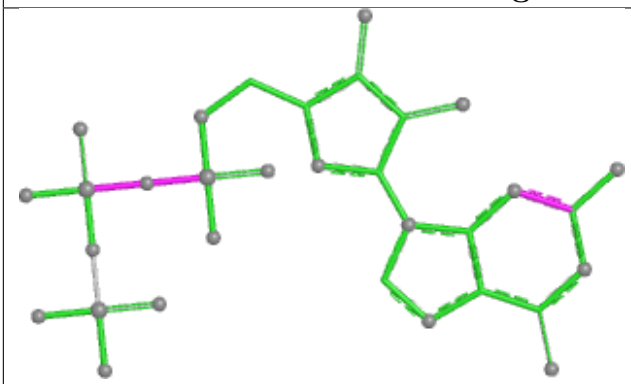


Rings

Ligand GTP JK 501



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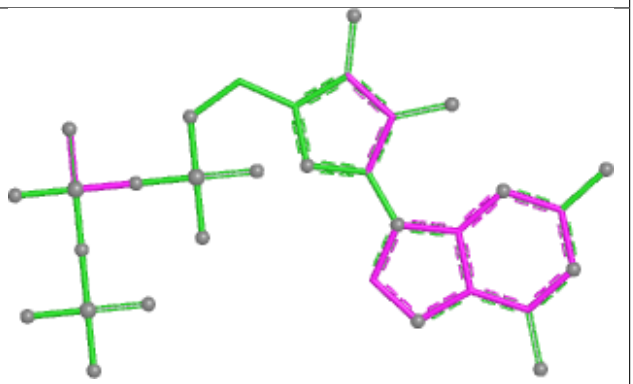

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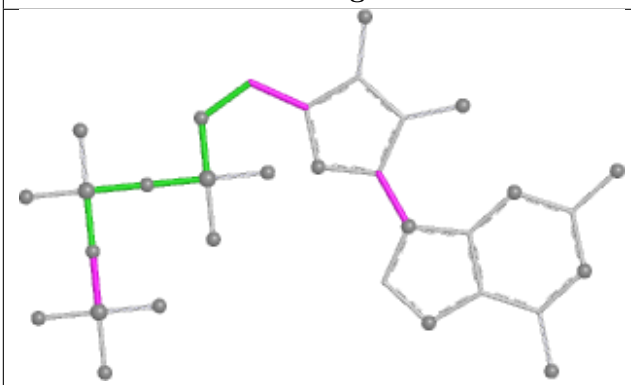

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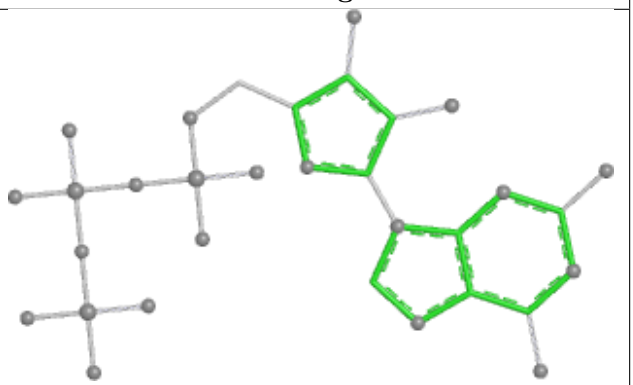
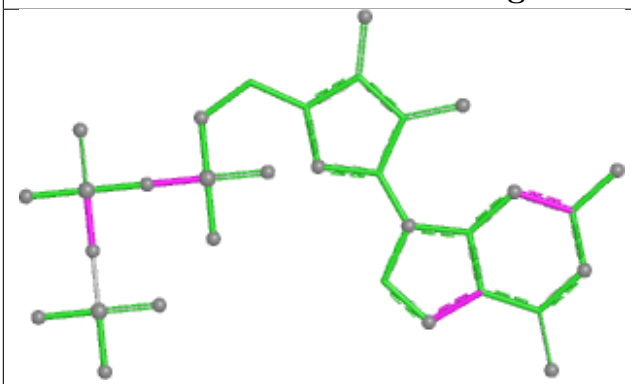


Rings

Ligand GTP GD 501



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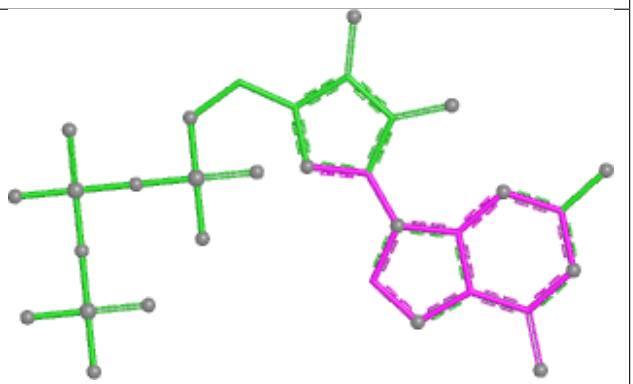

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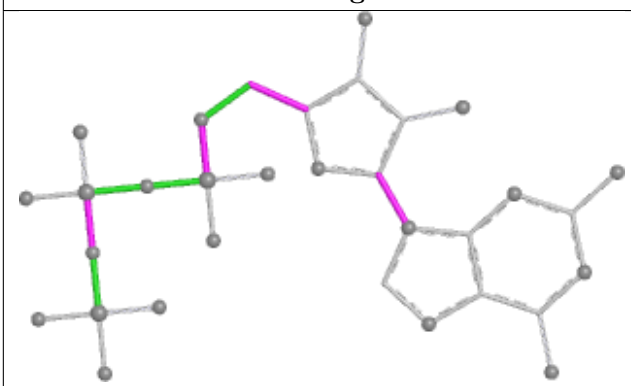

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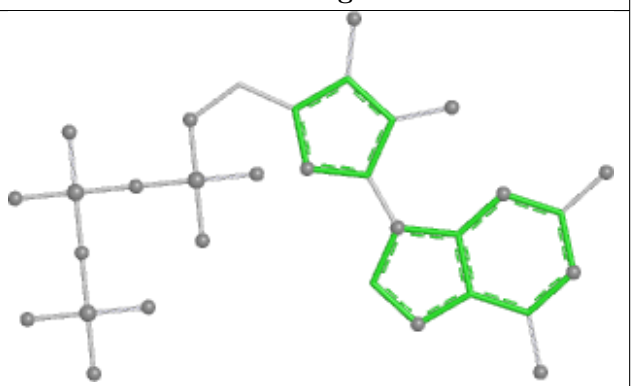
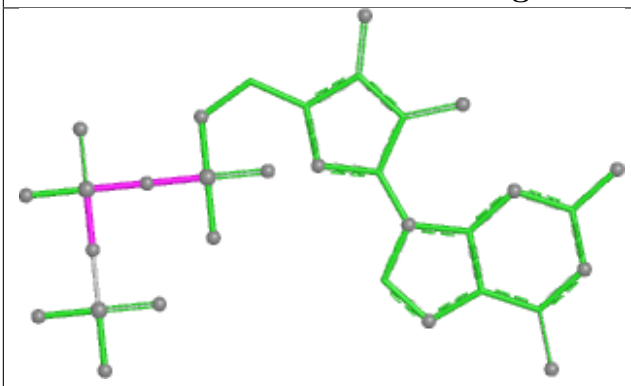


Rings

Ligand GTP MI 501



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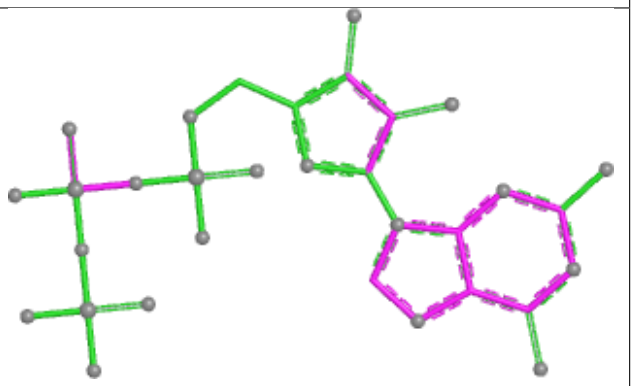

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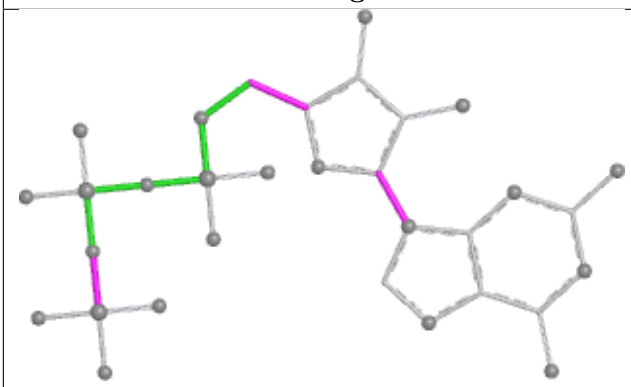
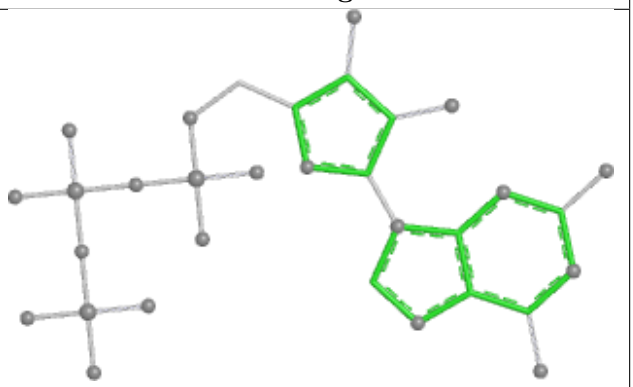
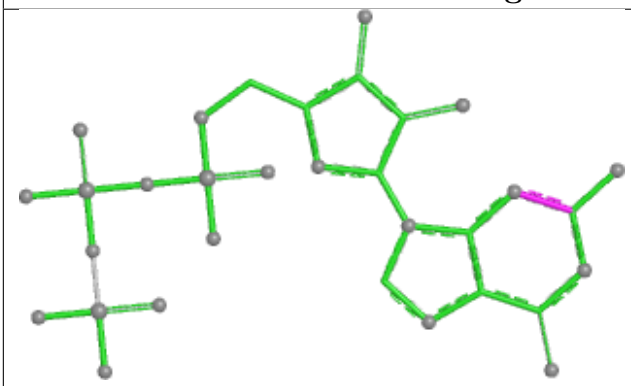


Torsions



Rings

Ligand GTP MH 501



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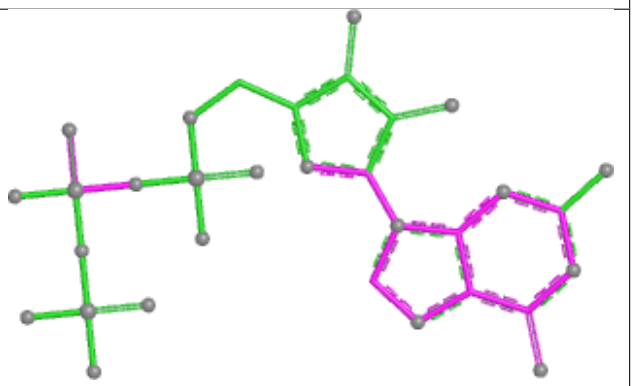

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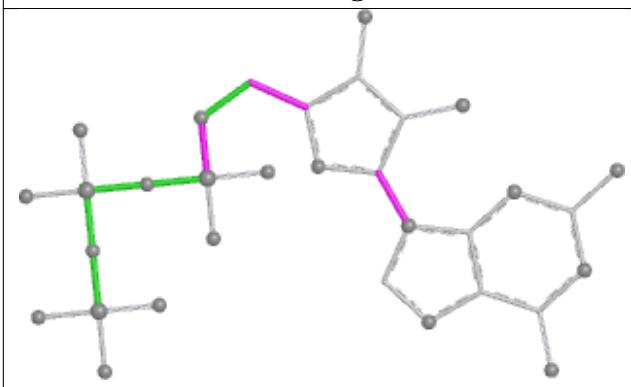

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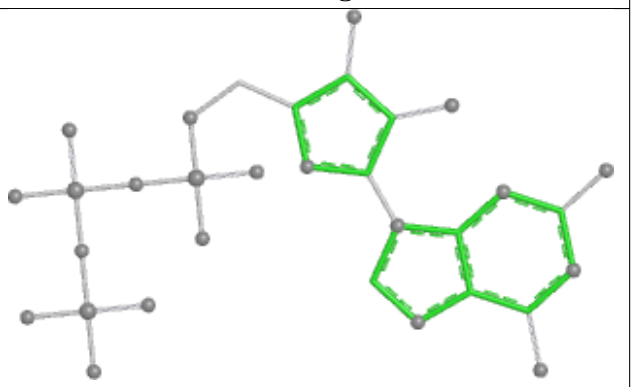

Rings

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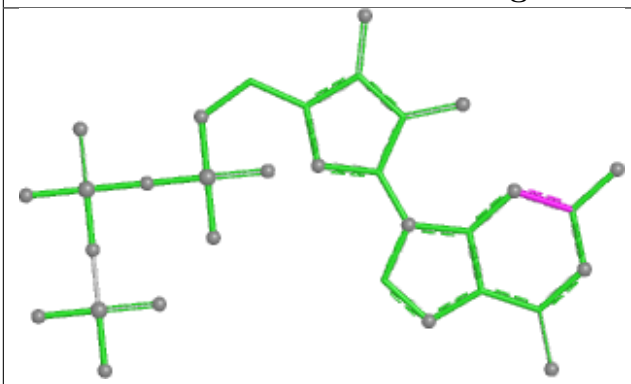

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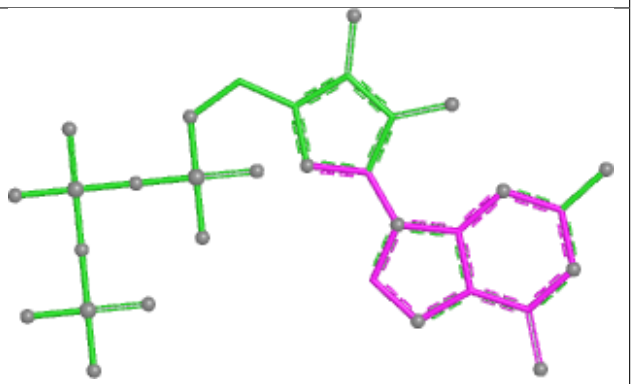

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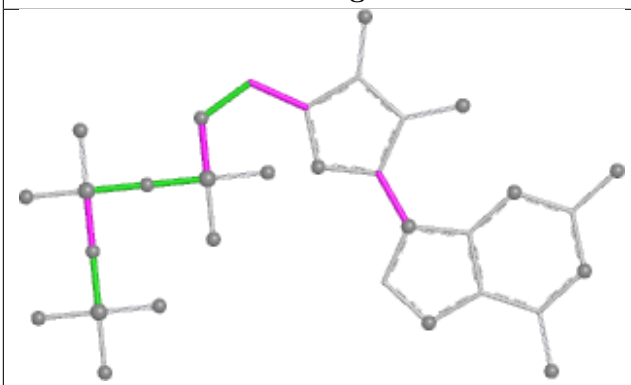

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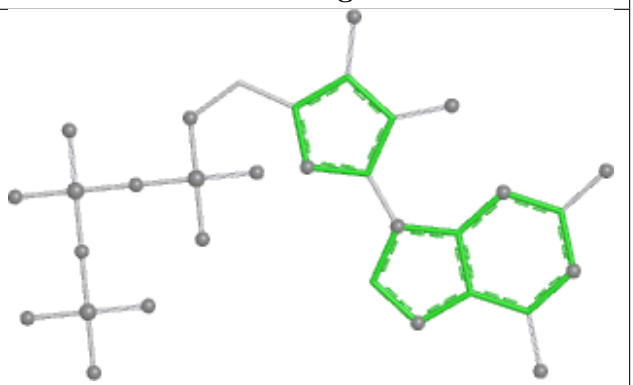

Rings

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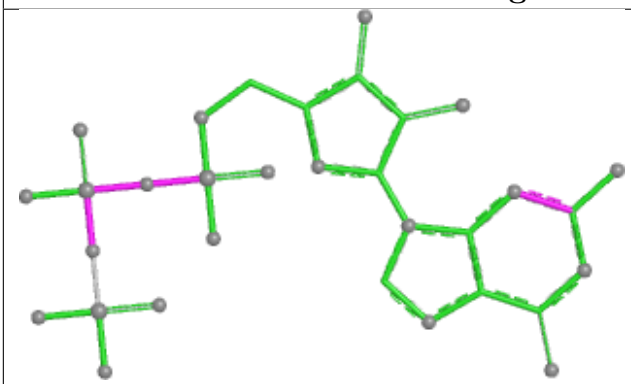

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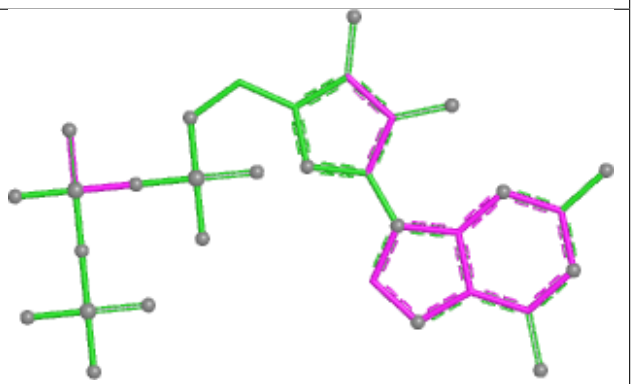

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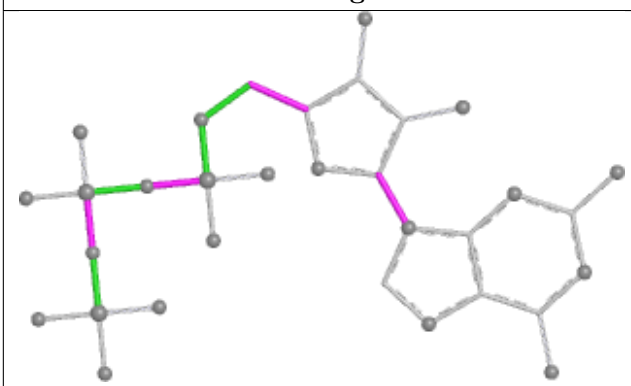

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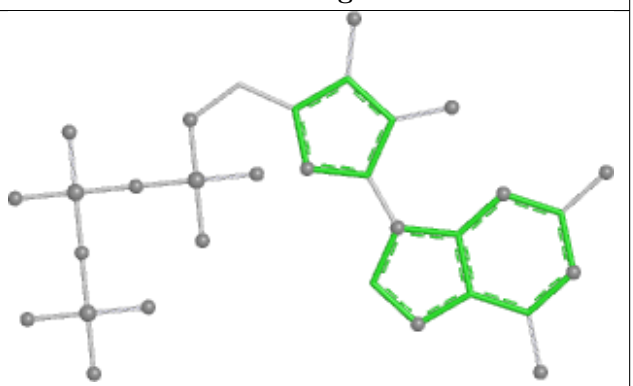

Rings

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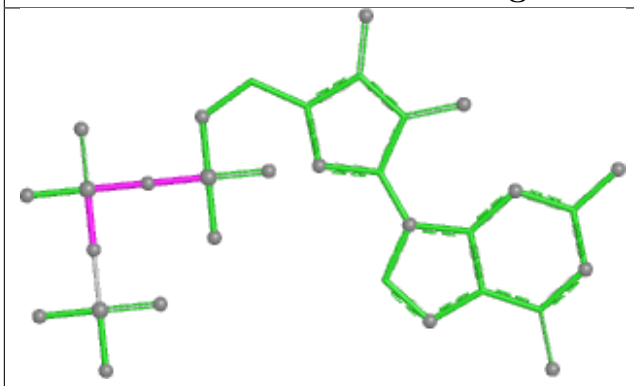

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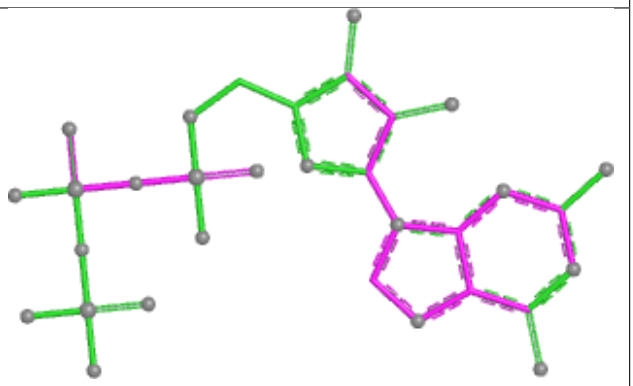

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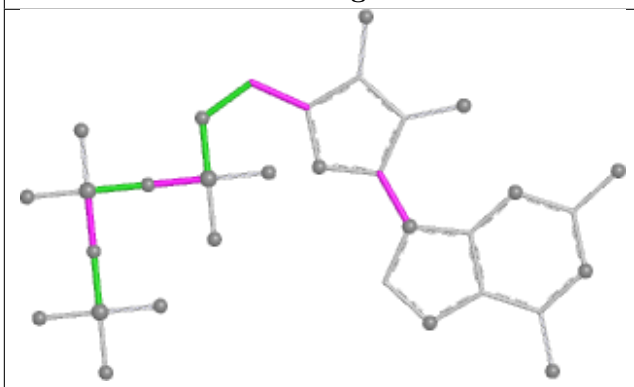

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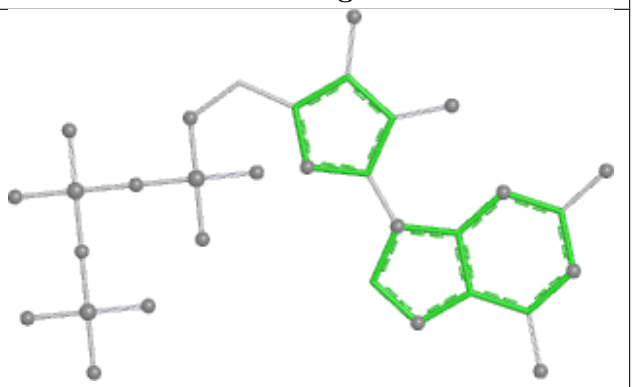

Rings

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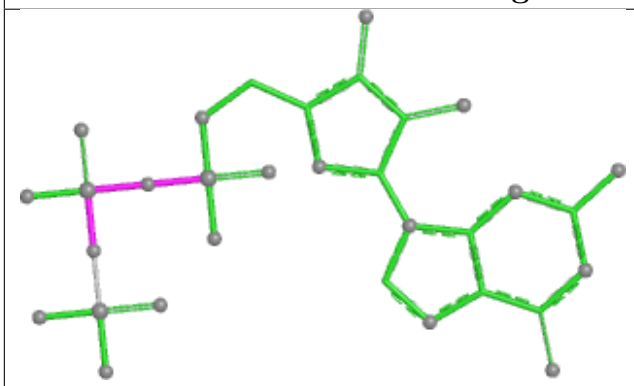

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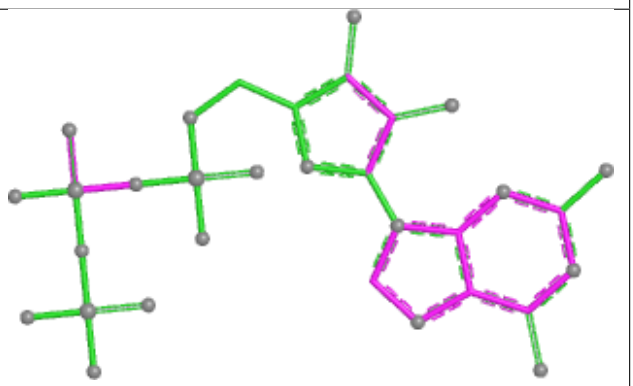

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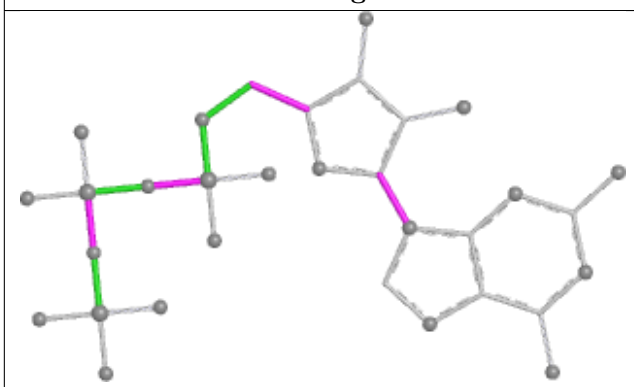

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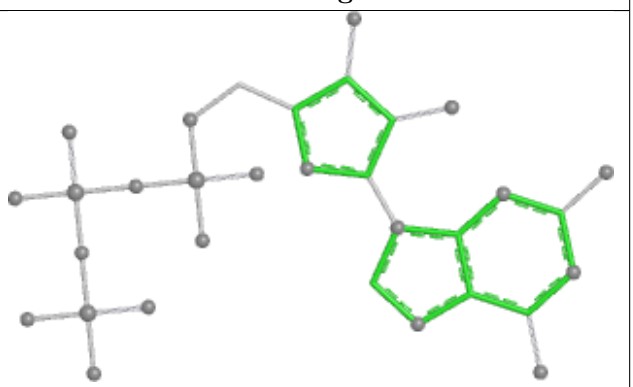

Rings

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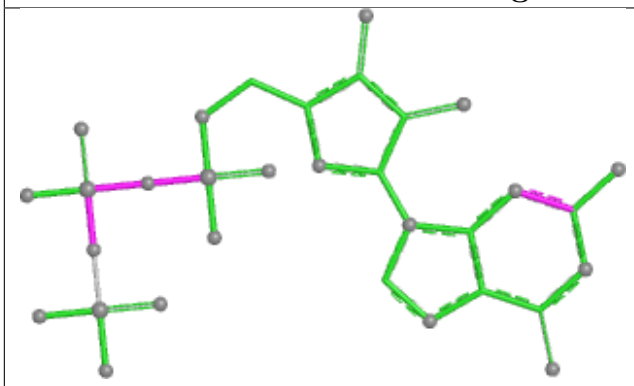

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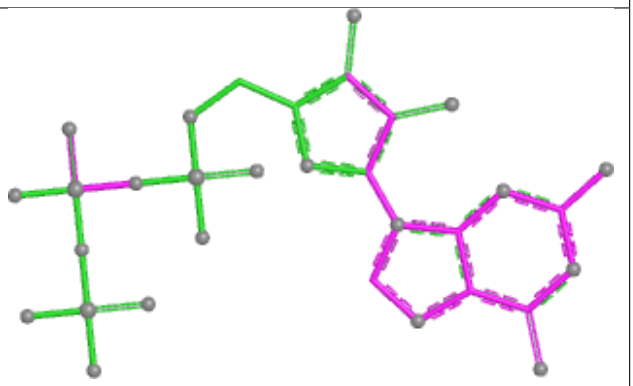

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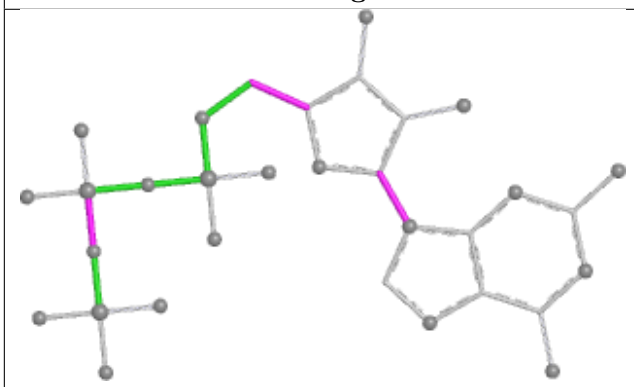

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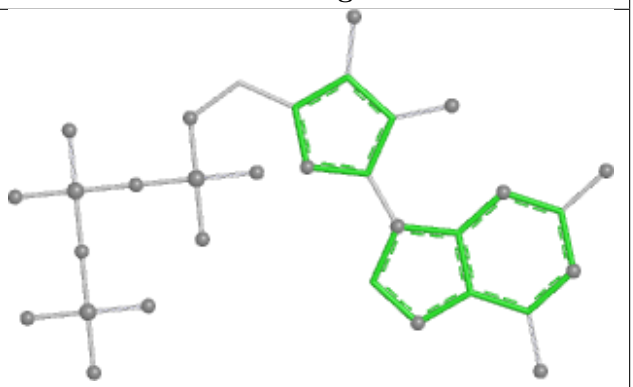
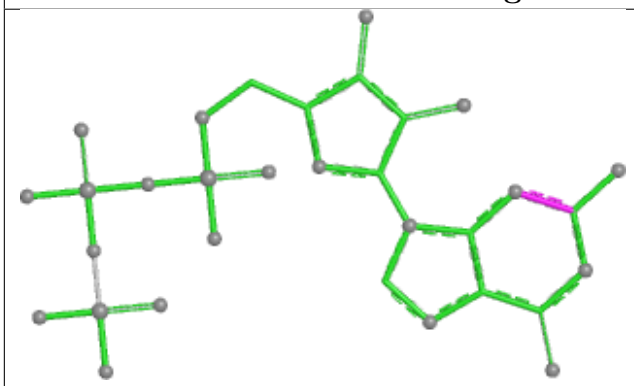


Rings

Ligand GTP WH 501



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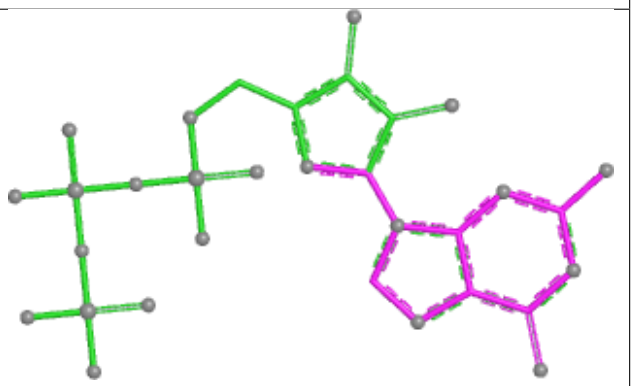

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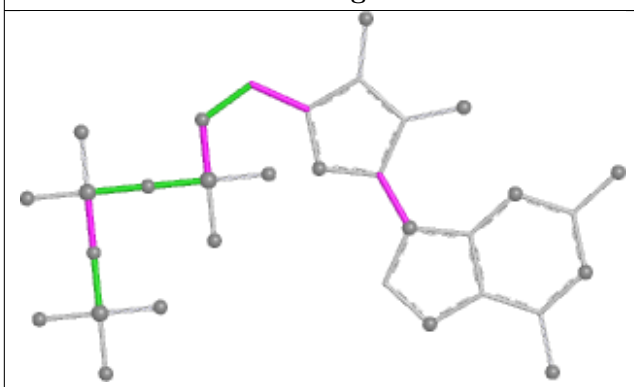

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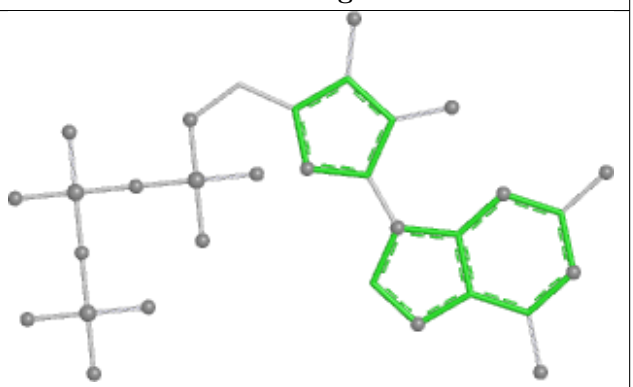
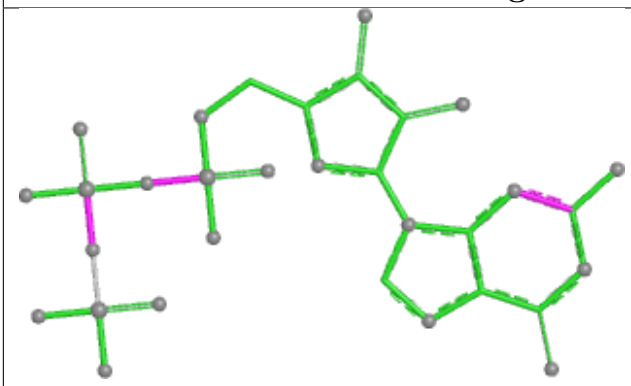


Rings

Ligand GTP AD 501



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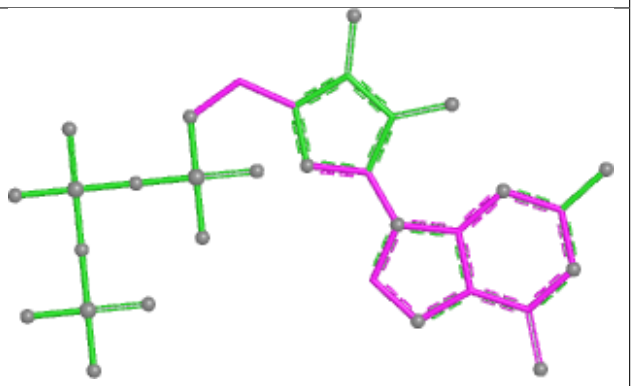

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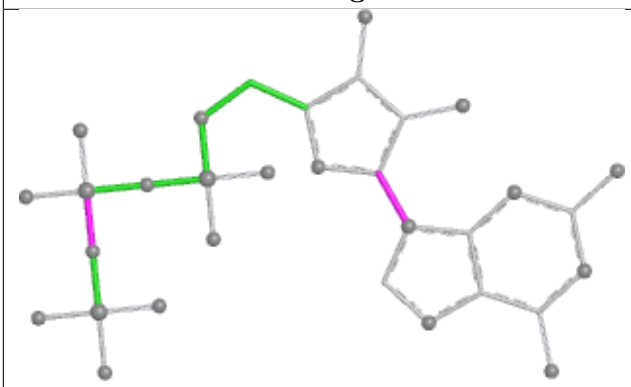

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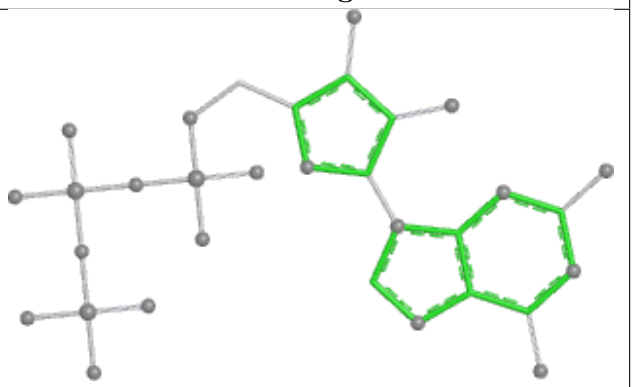

Rings

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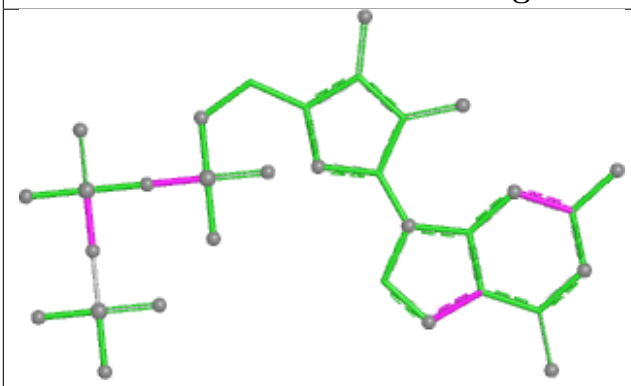

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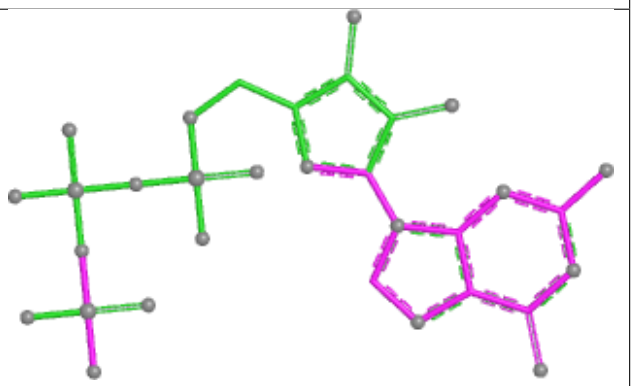

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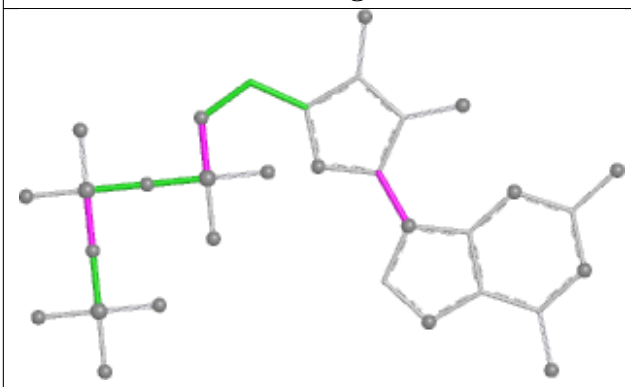

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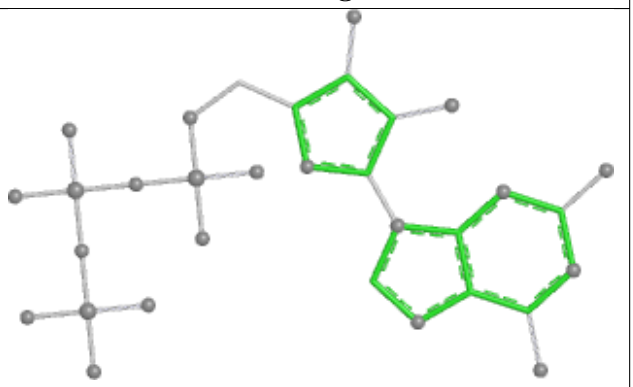

Rings

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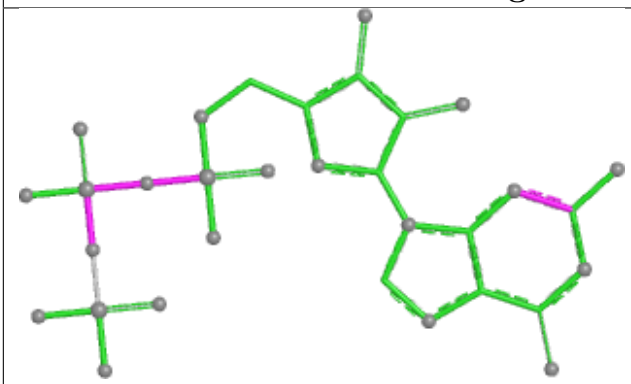

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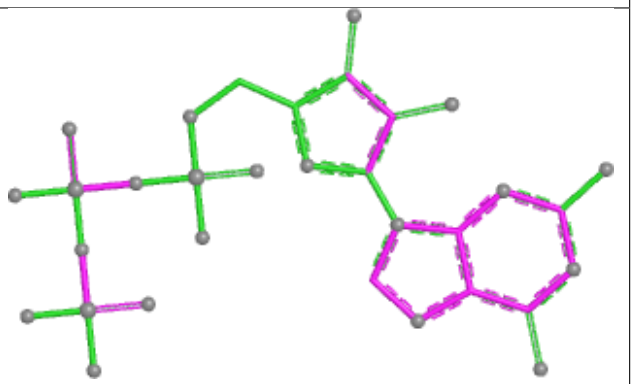

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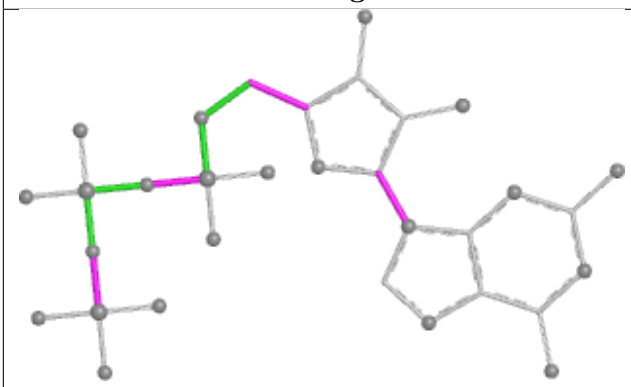

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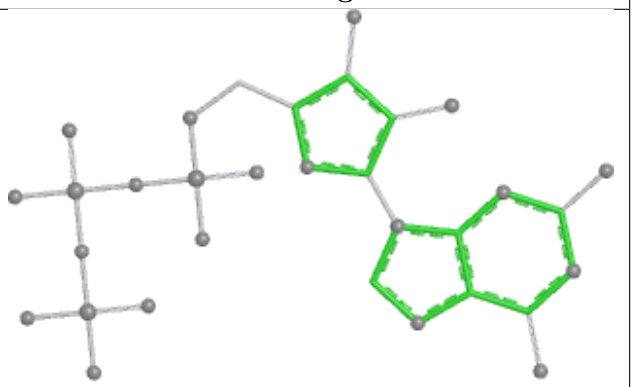
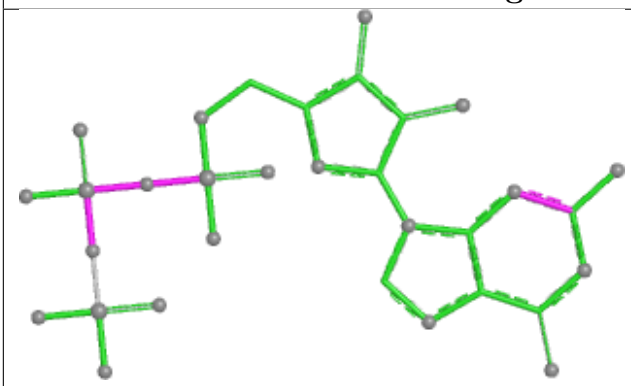


Rings

Ligand GTP WA 501



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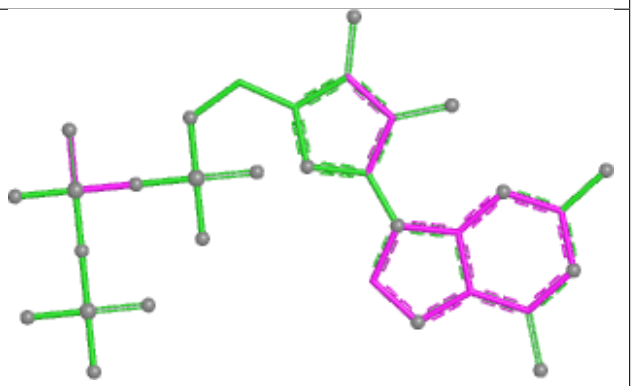
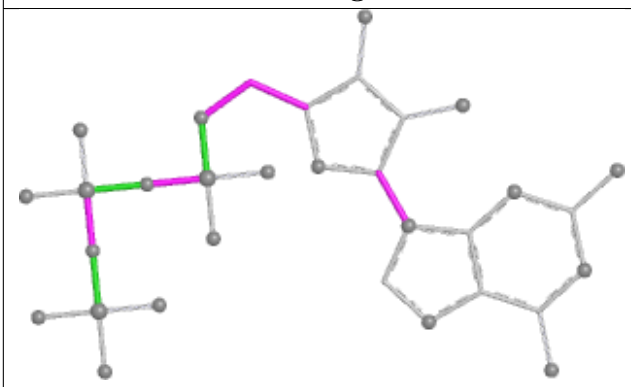


Bond angles



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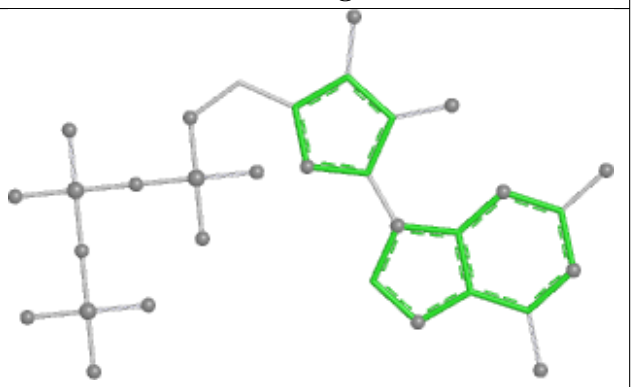

Rings

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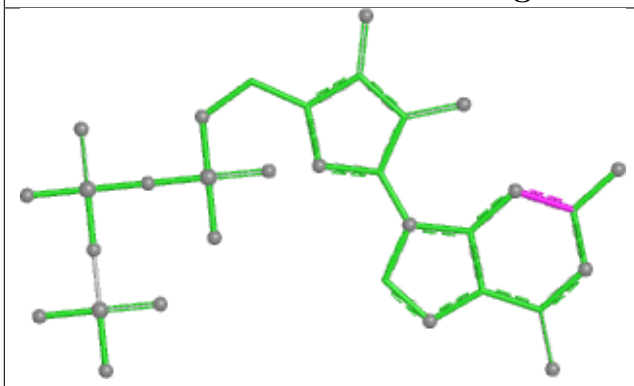

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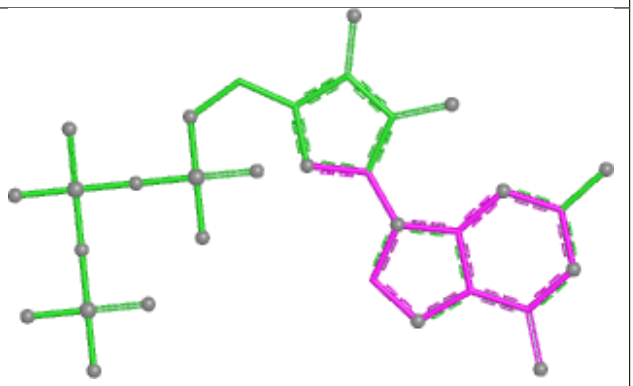

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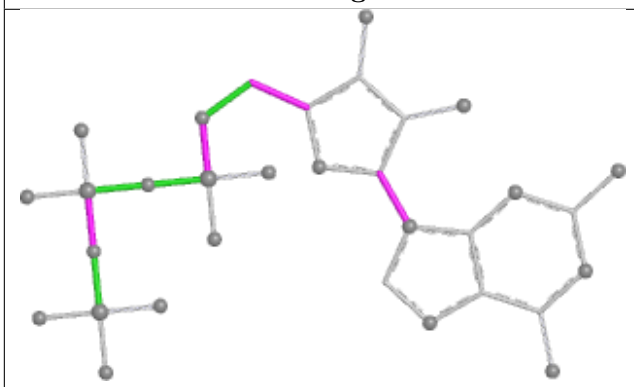

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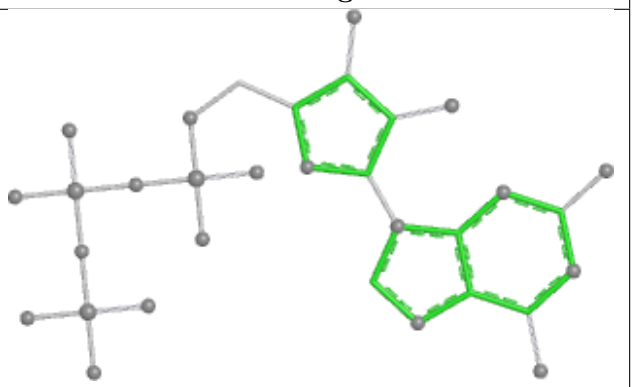
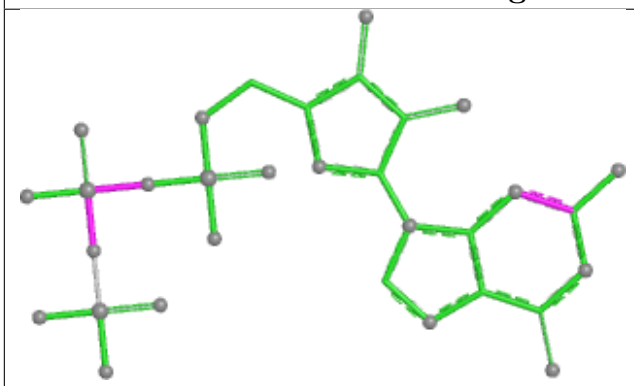


Rings

Ligand GTP GK 501



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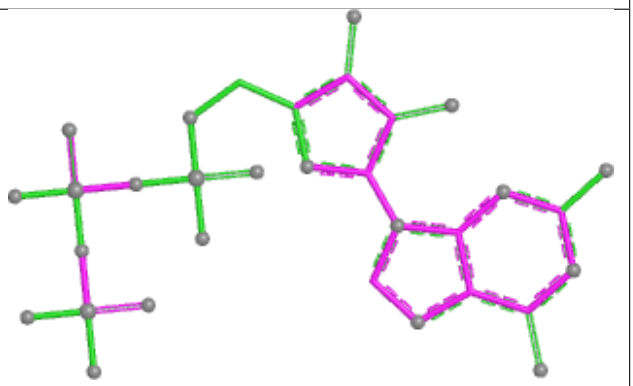

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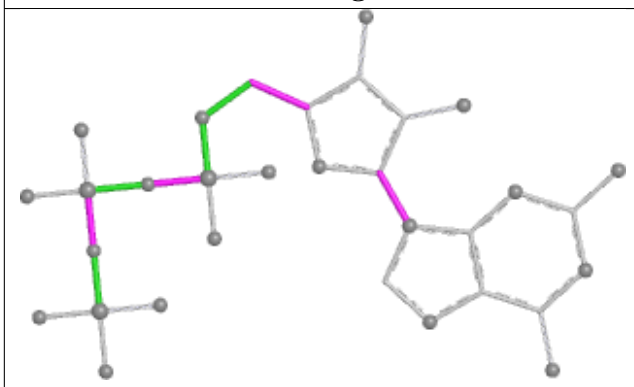

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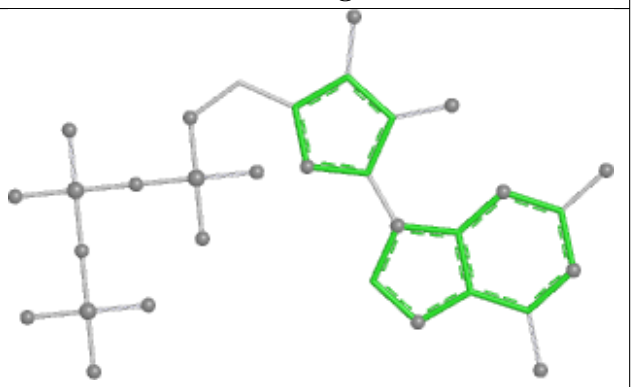
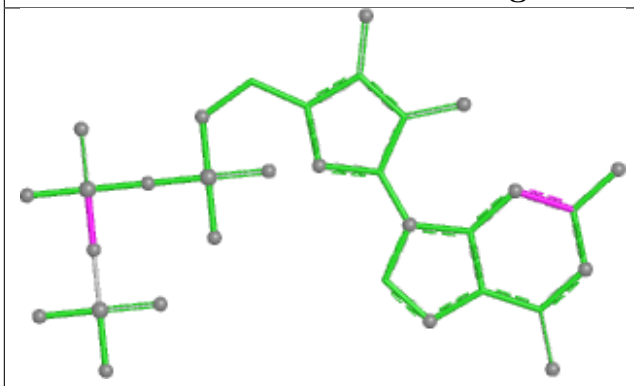


Rings

Ligand GTP QH 501



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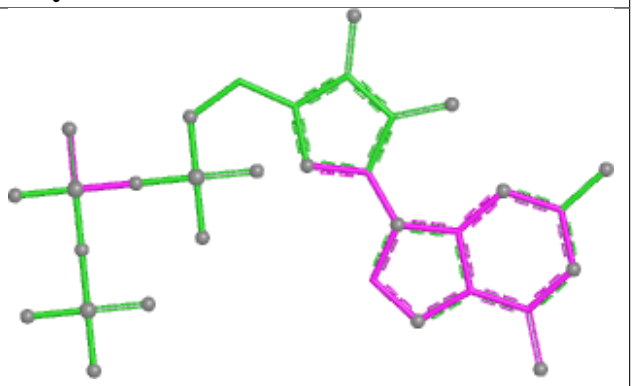

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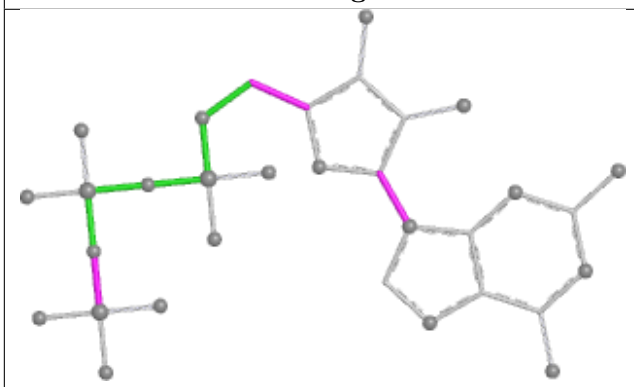
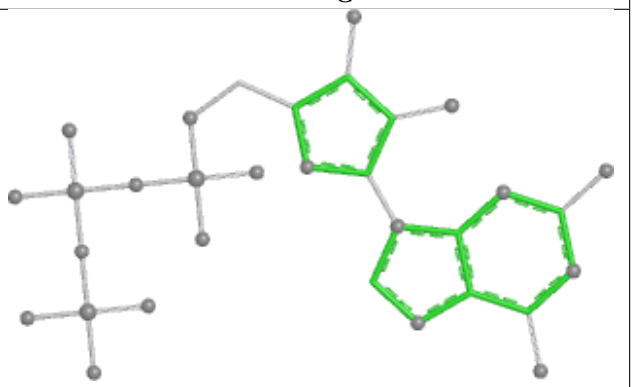
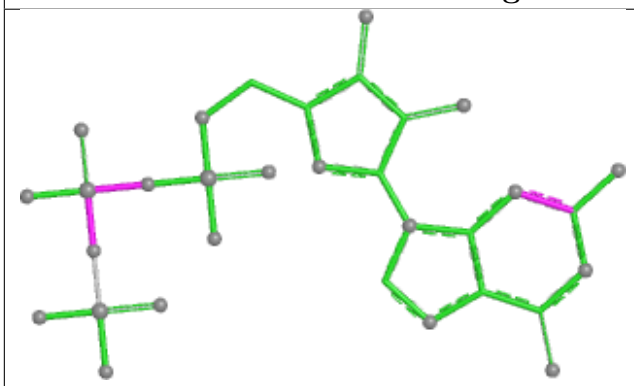


Torsions



Rings

Ligand GTP MM 501



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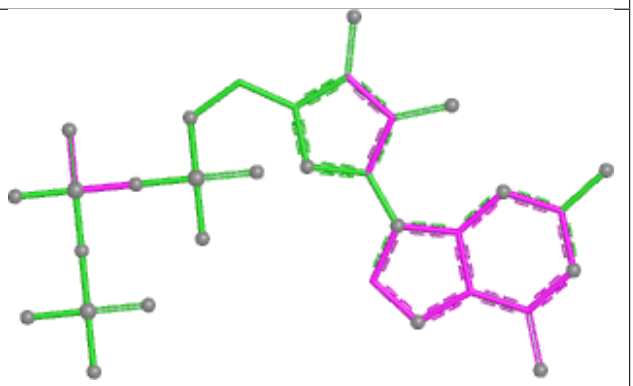

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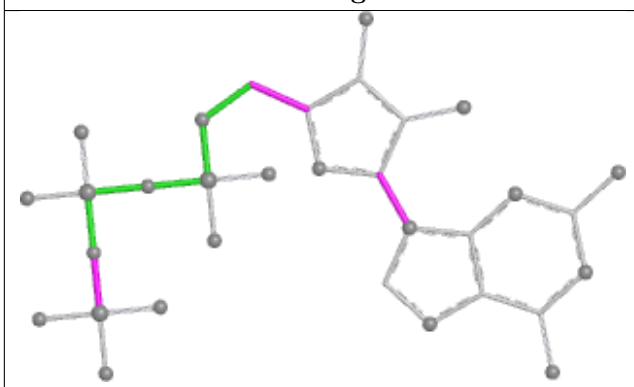

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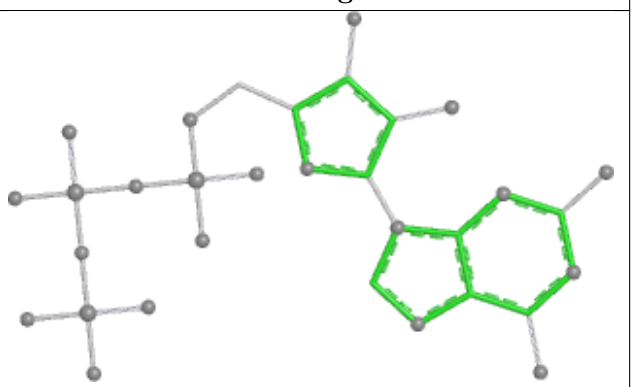
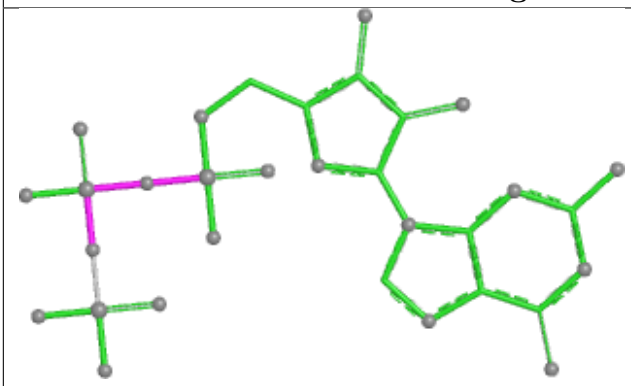


Rings

Ligand GTP RC 501



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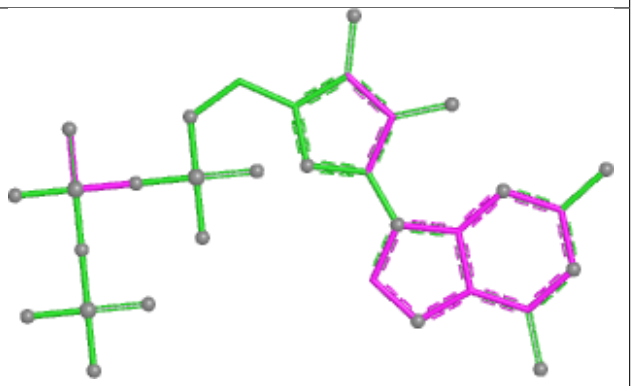

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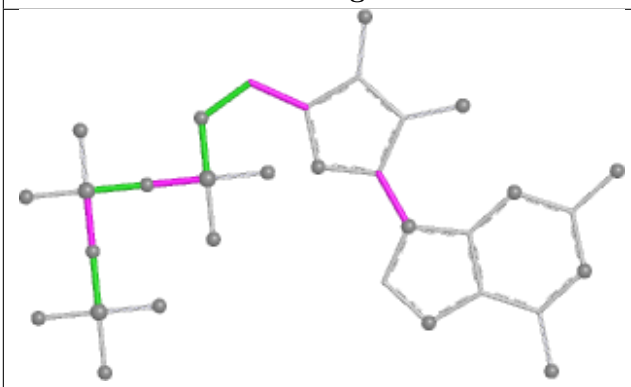

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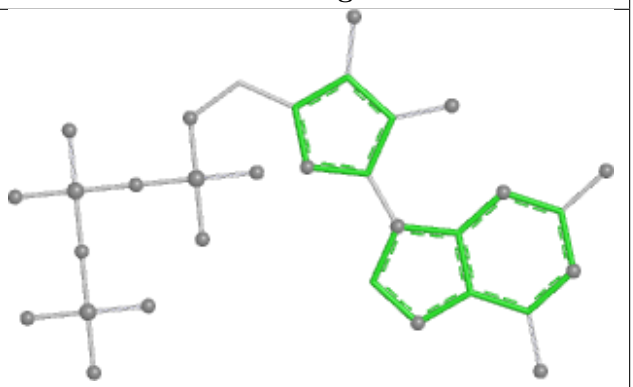
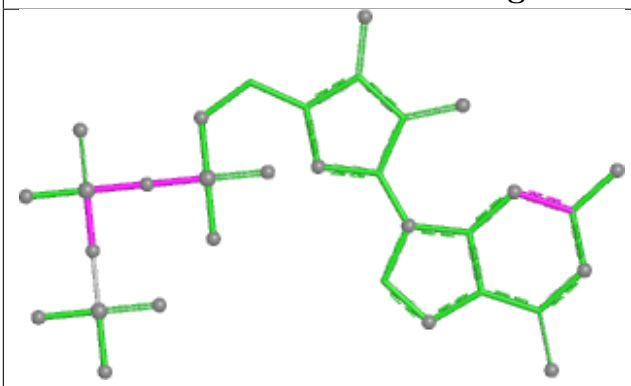


Rings

Ligand GTP NK 501



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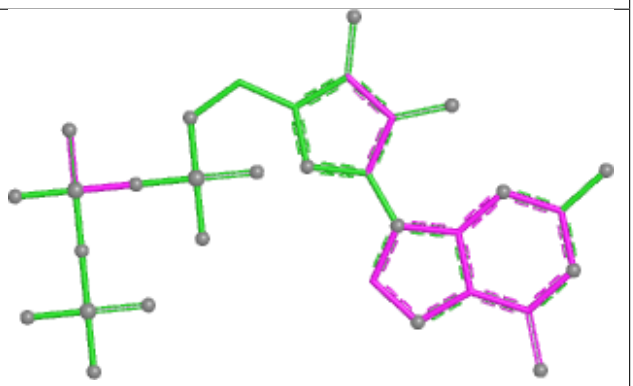

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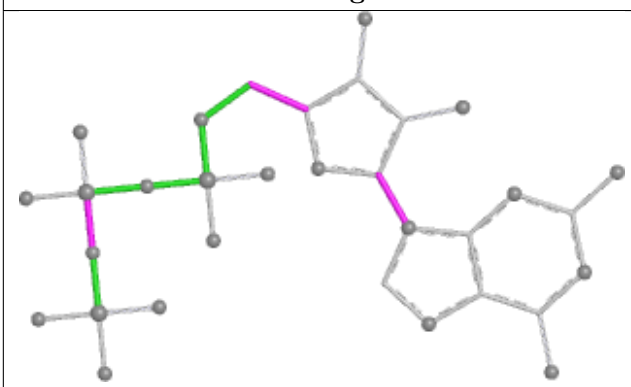

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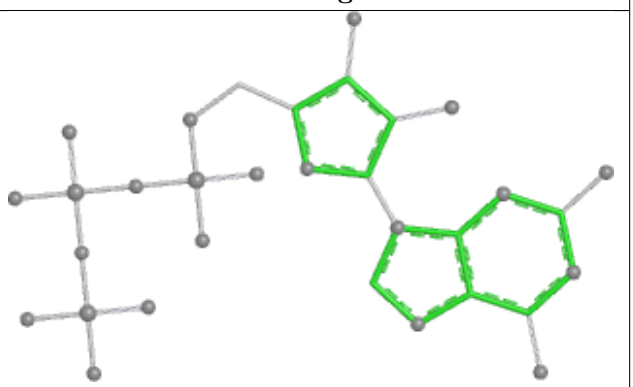
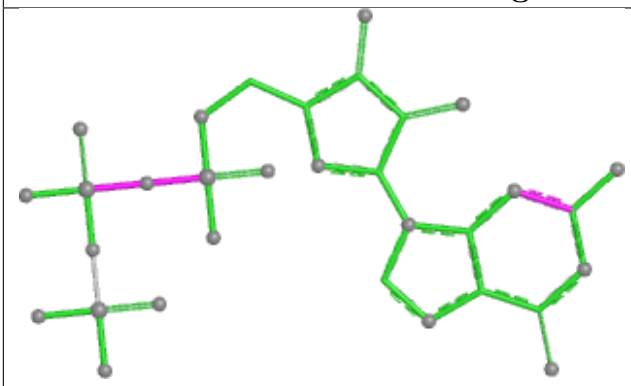


Rings

Ligand GTP SH 501



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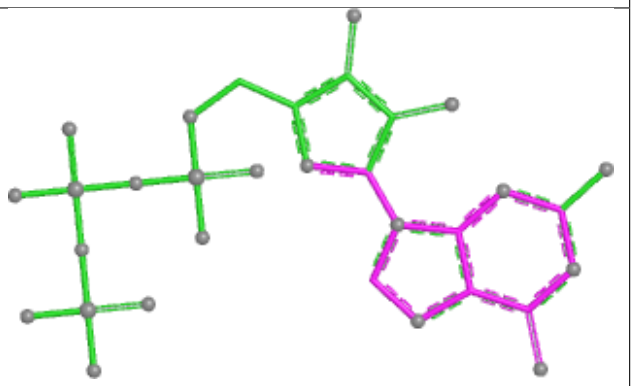

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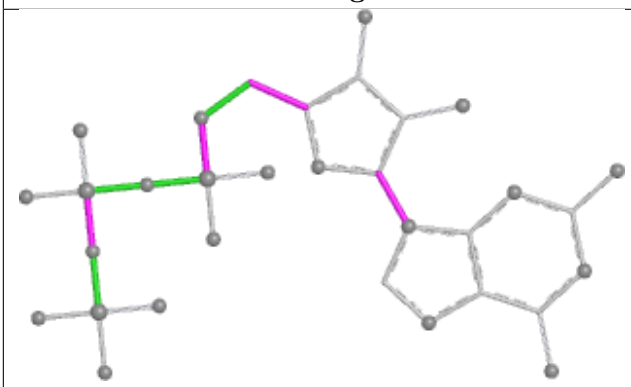

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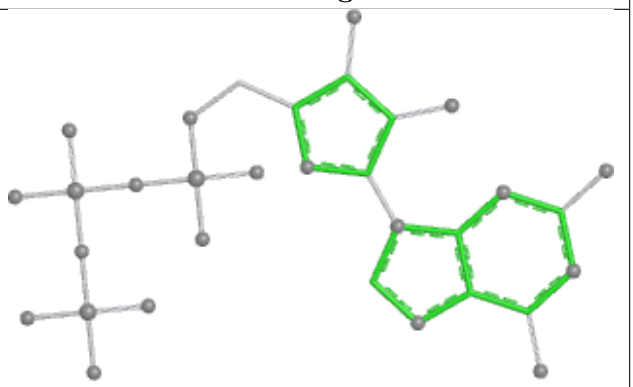
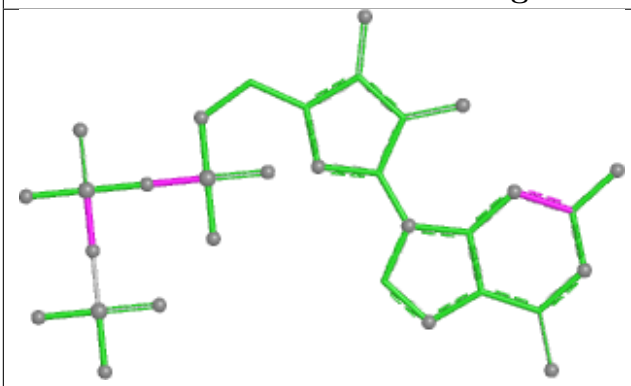


Rings

Ligand GTP LH 501



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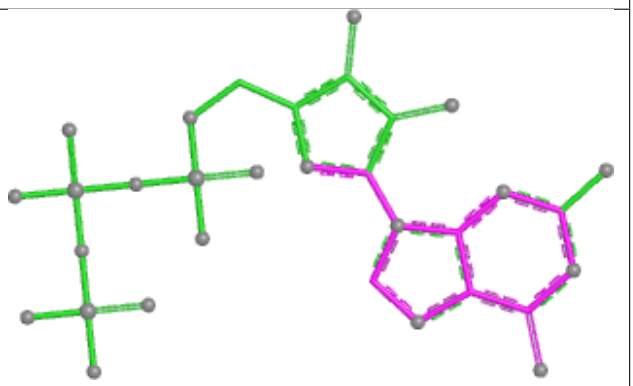

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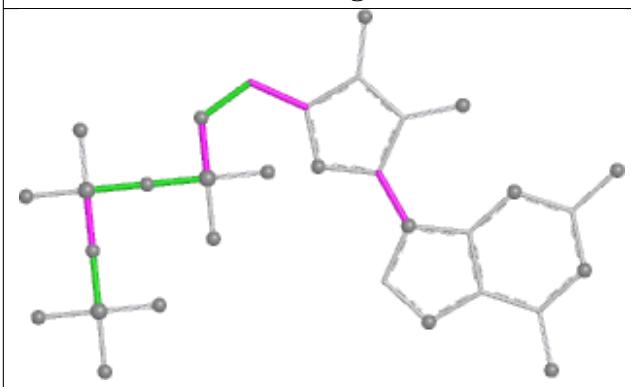

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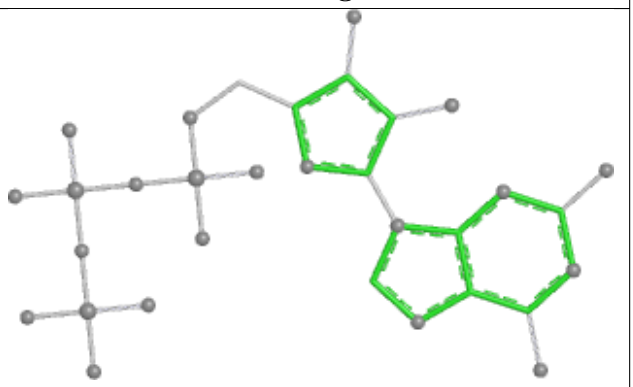

Rings

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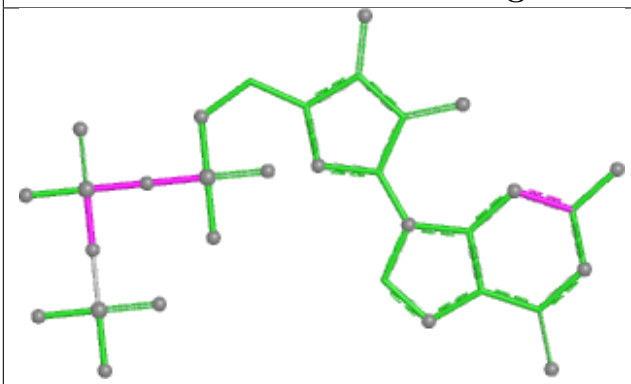

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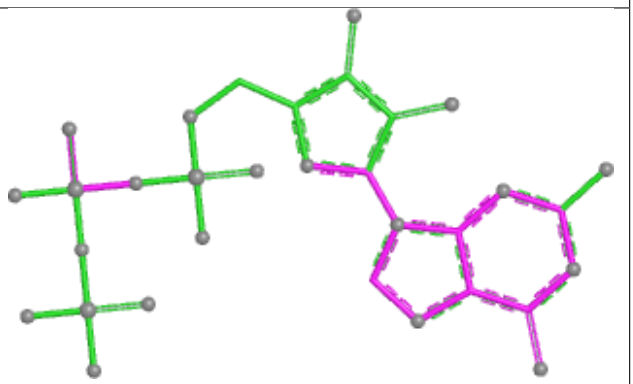

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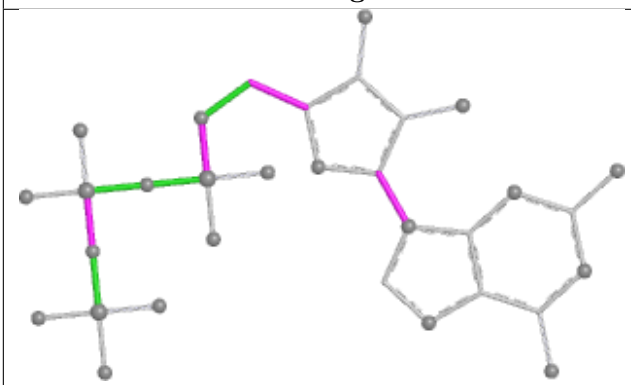

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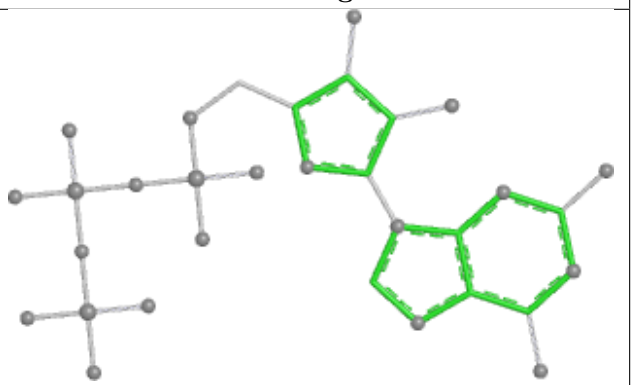
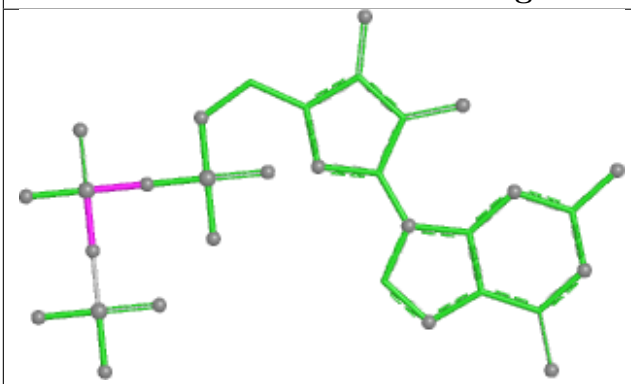


Rings

Ligand GTP HI 501



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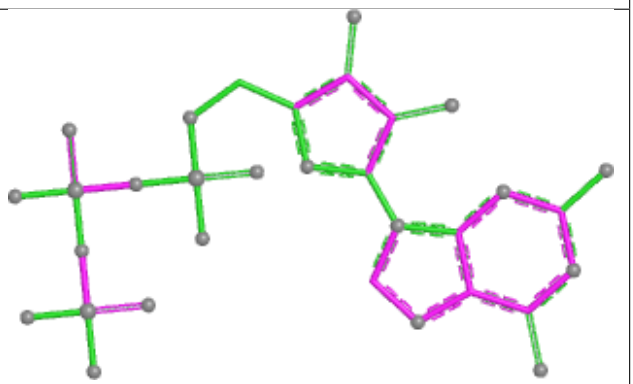

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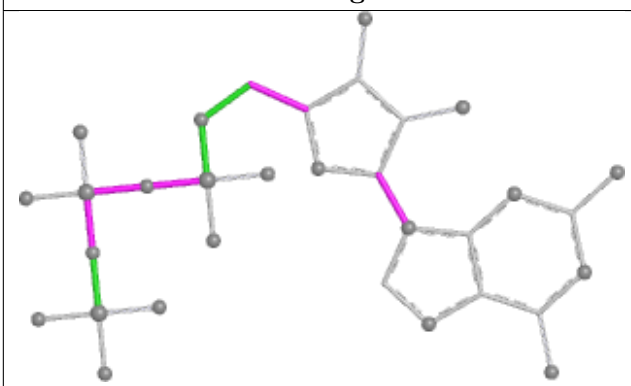

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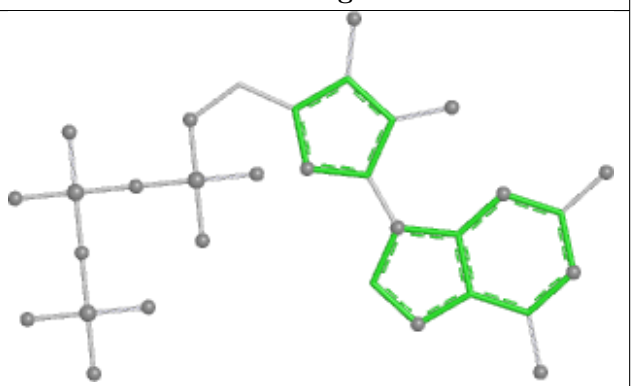

Rings

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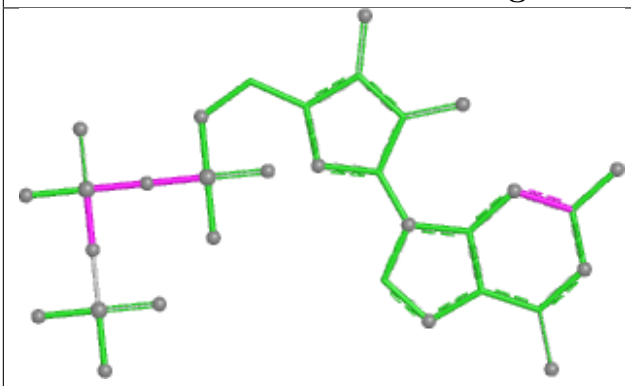

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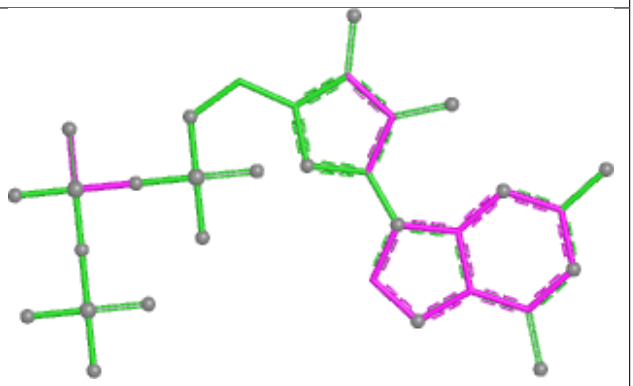

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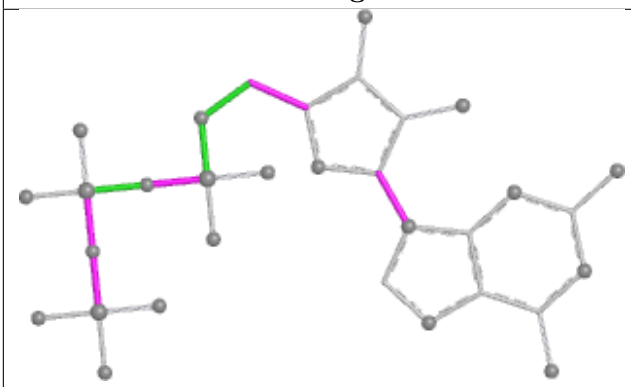

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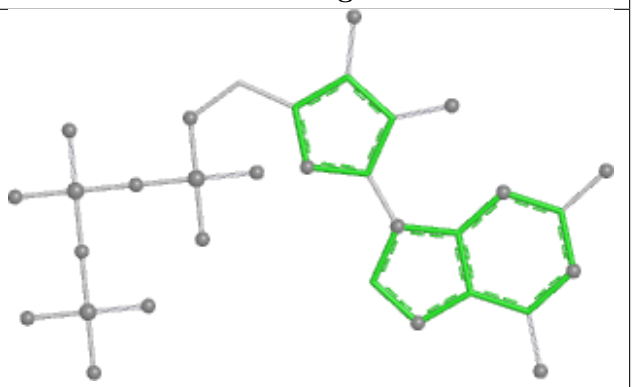

Rings

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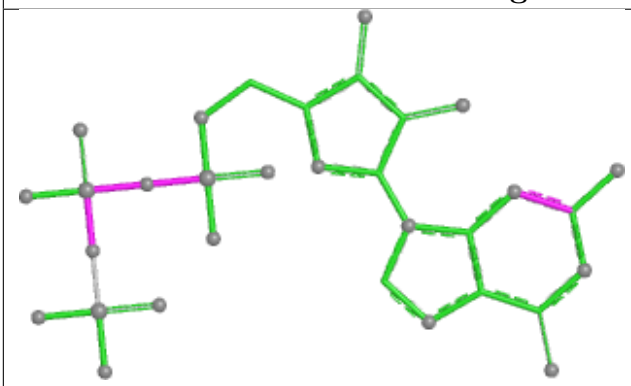

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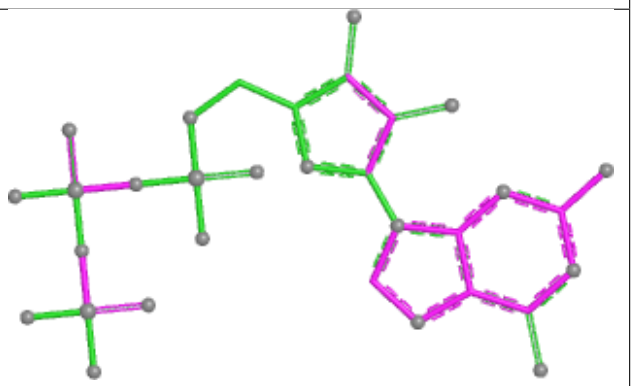

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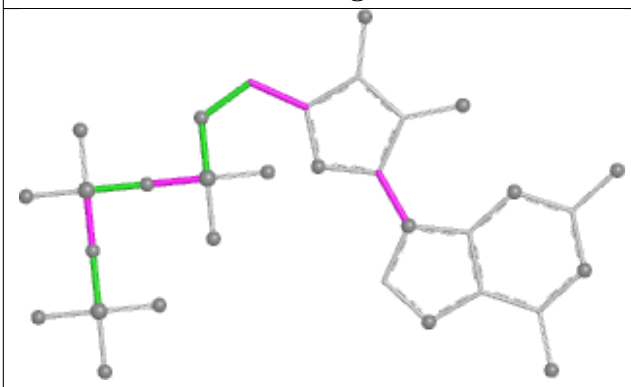

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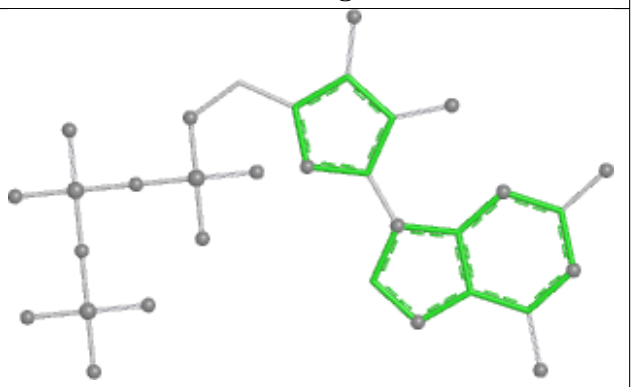
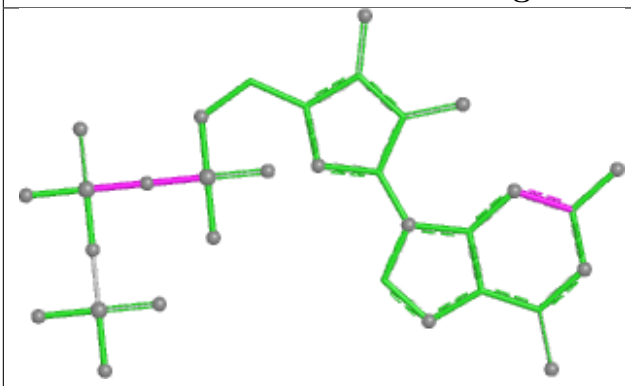


Rings

Ligand GTP AJ 501



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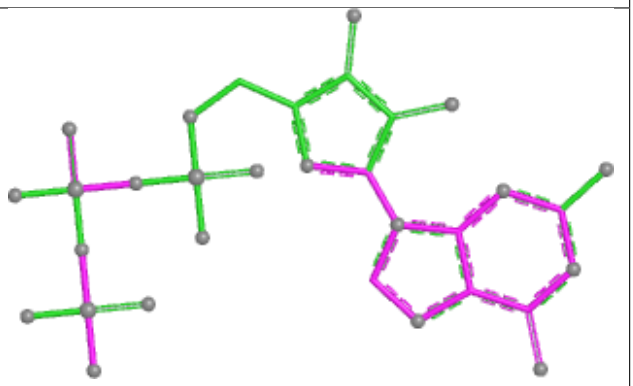

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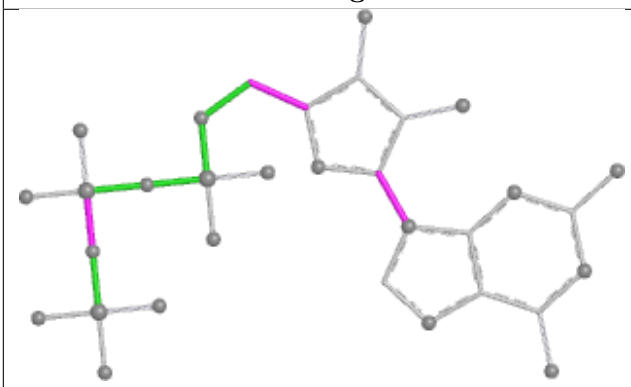

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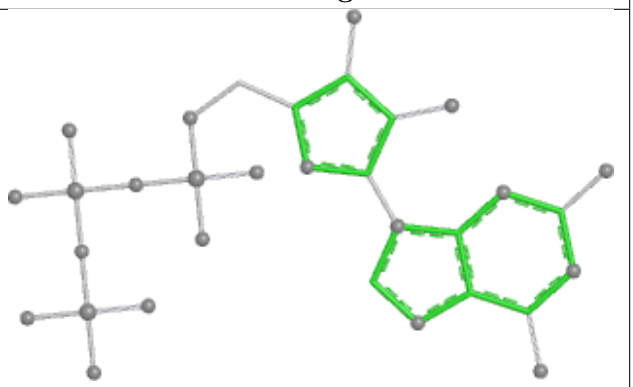
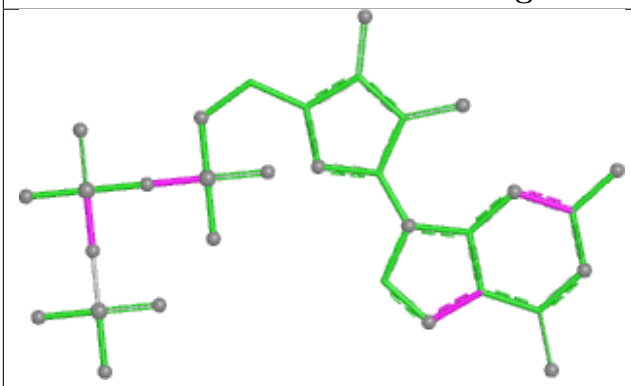


Rings

Ligand GTP ID 501



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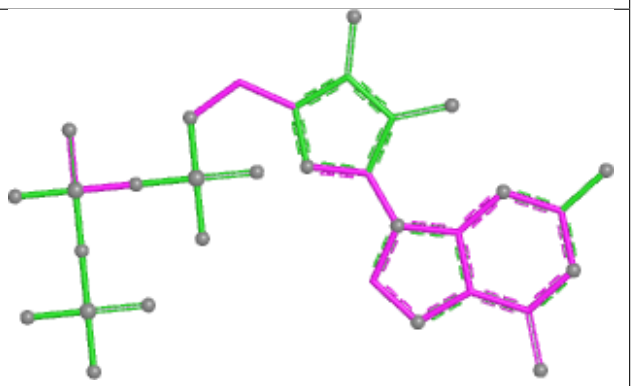

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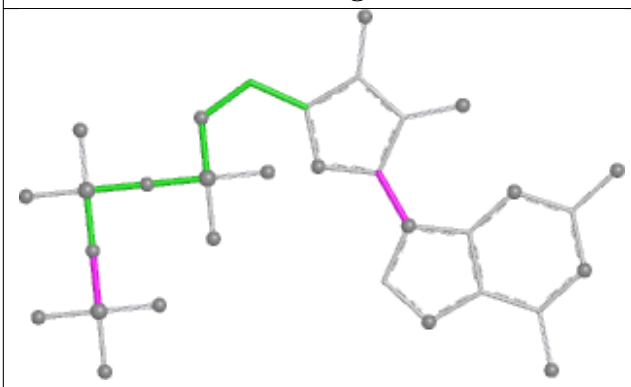

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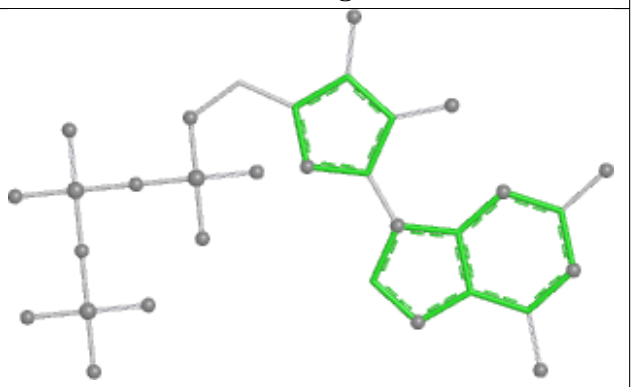
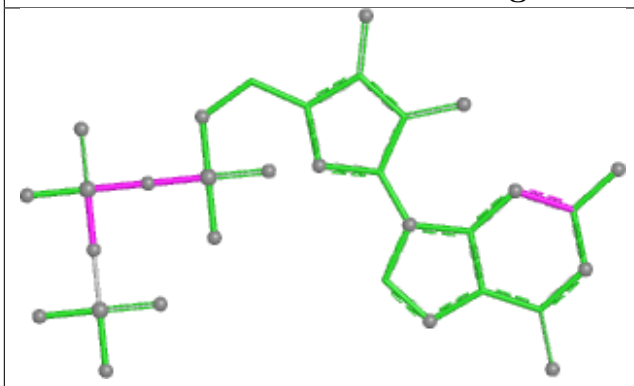


Rings

Ligand GTP OD 501



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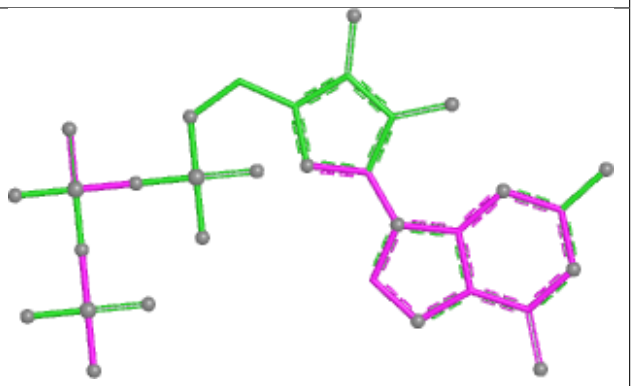

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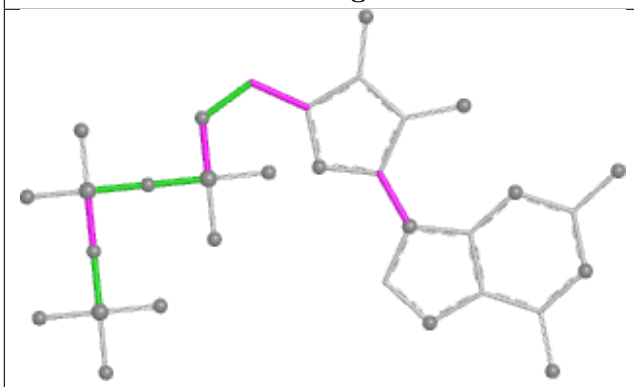

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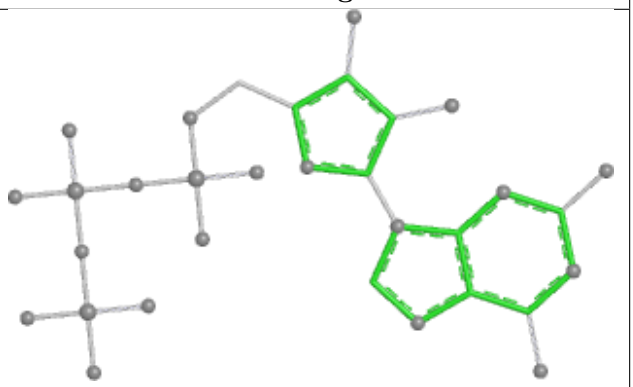
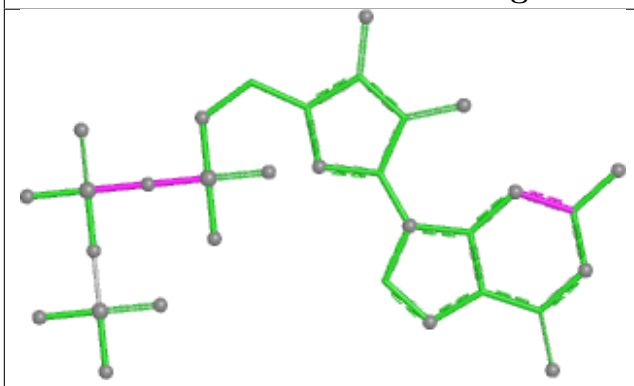


Rings

Ligand GTP AC 501



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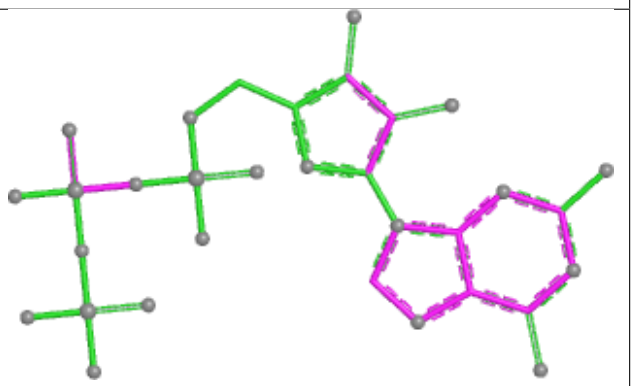
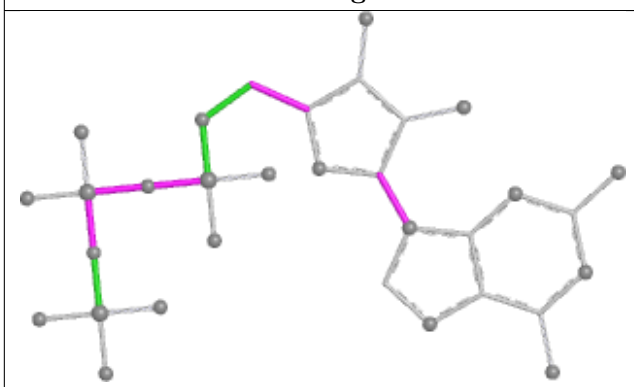


Bond angles



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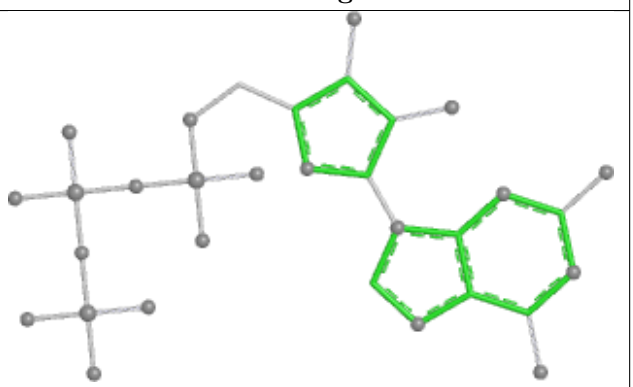
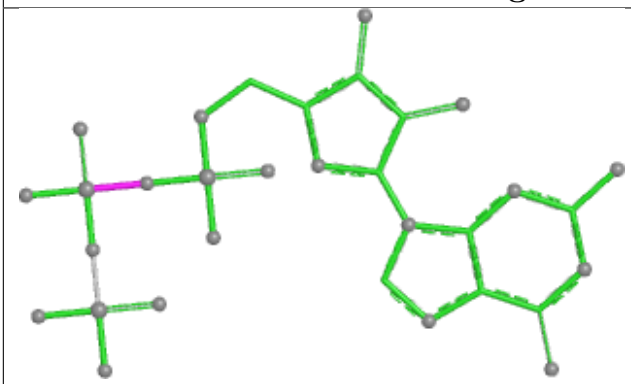


Rings

Ligand GTP HC 501



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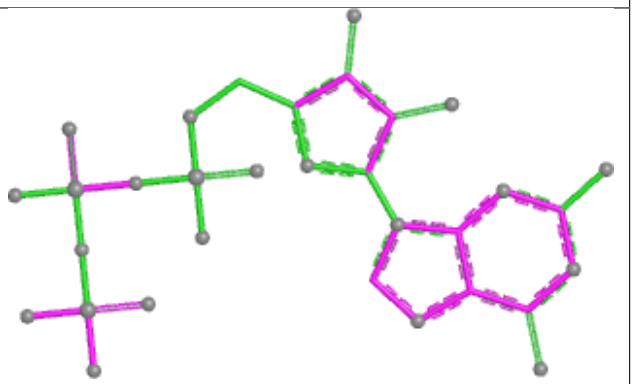

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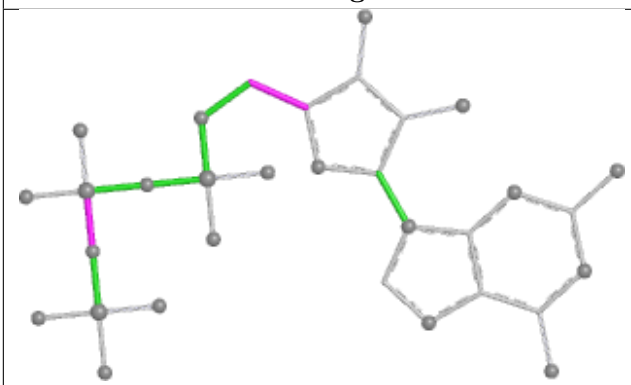
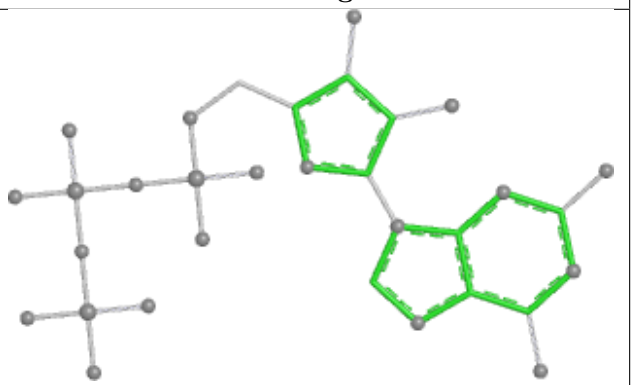
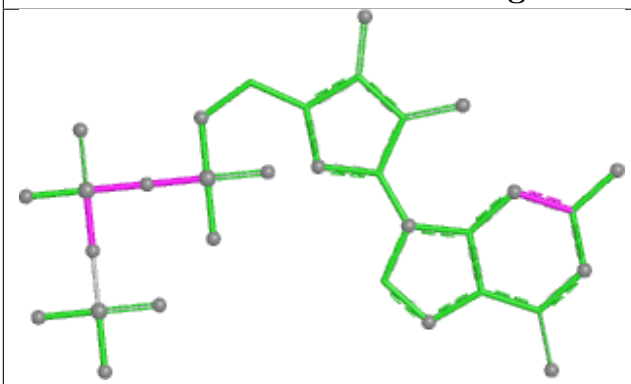


Torsions



Rings

Ligand GTP KG 501



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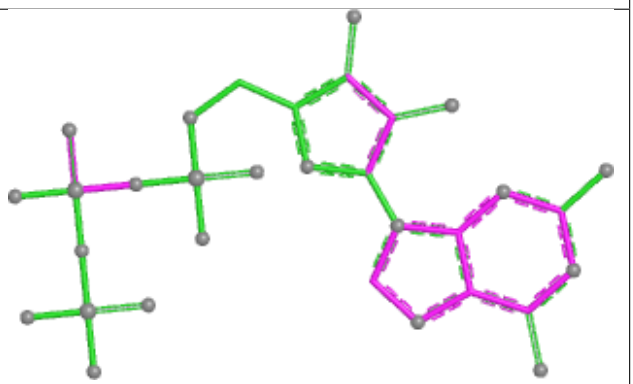

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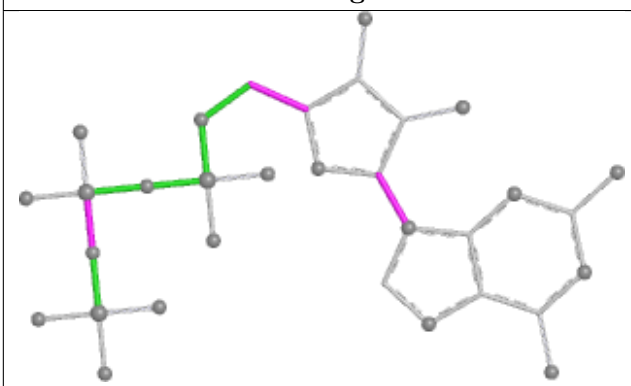

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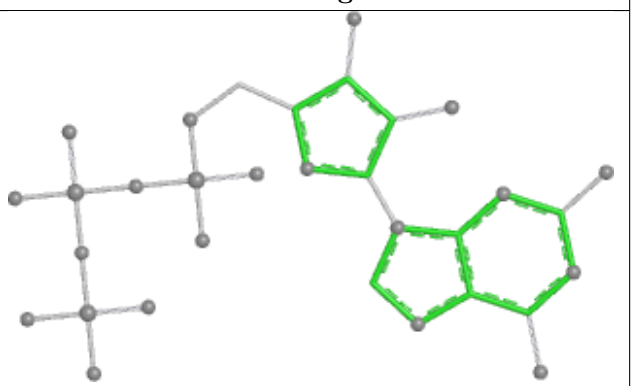
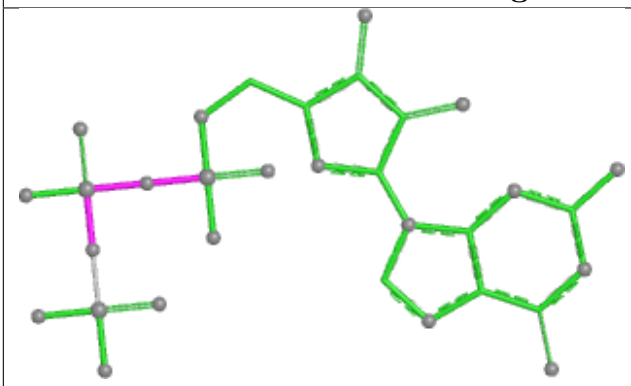


Rings

Ligand GTP RE 501



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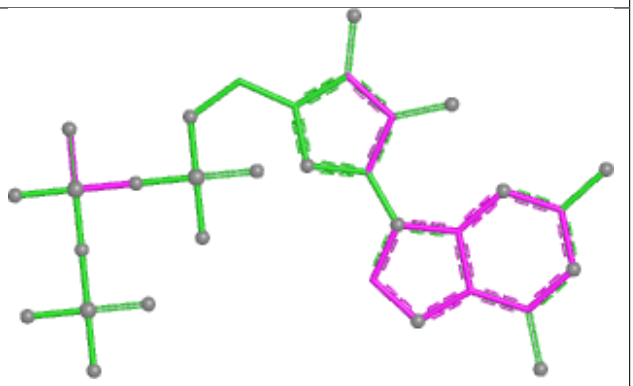

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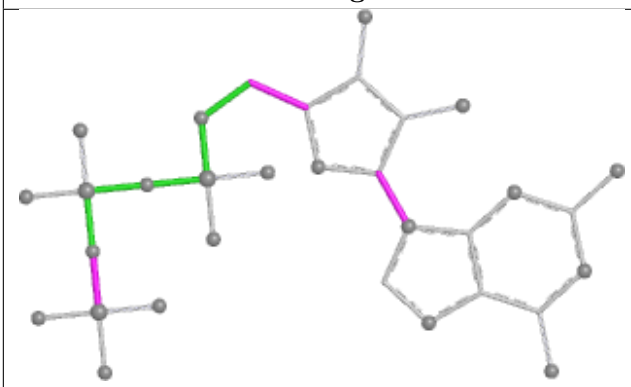

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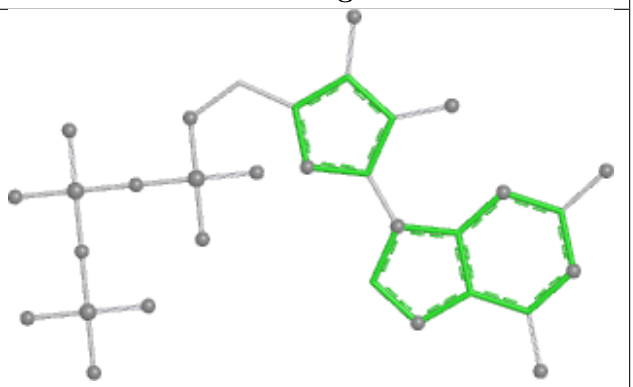
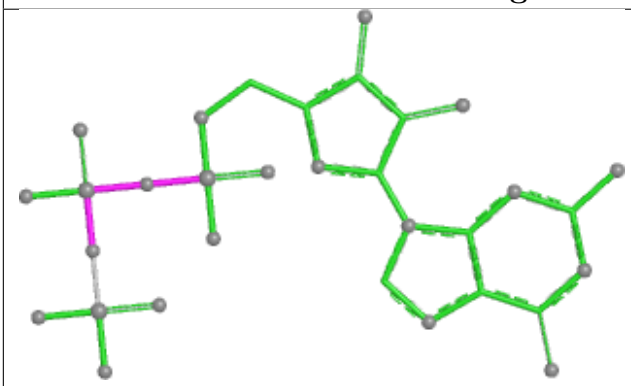


Rings

Ligand GTP NE 501



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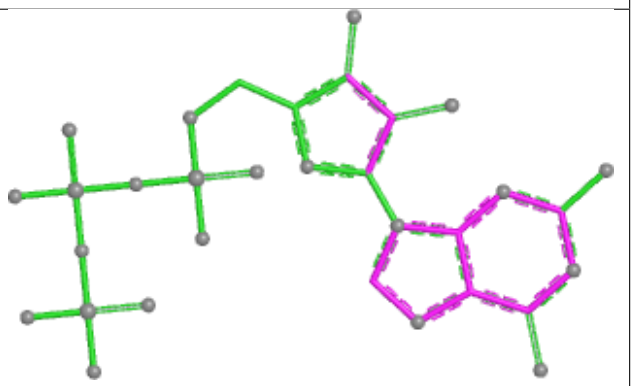

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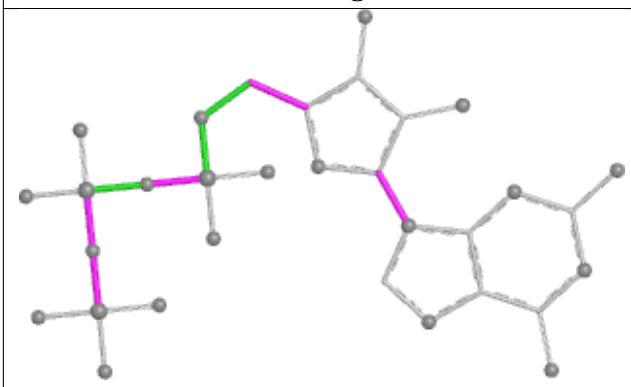

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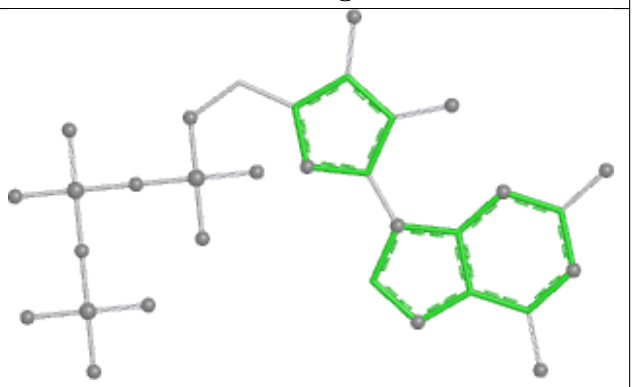
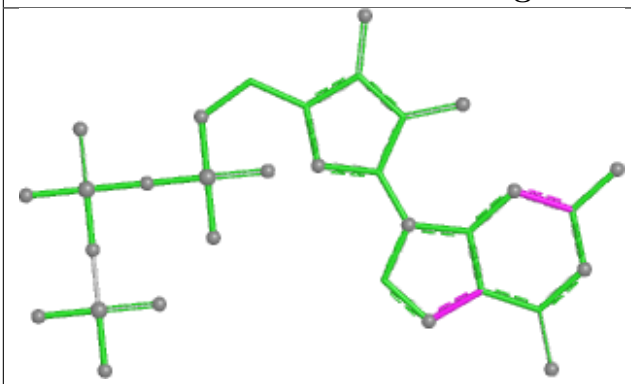


Rings

Ligand GTP PJ 501



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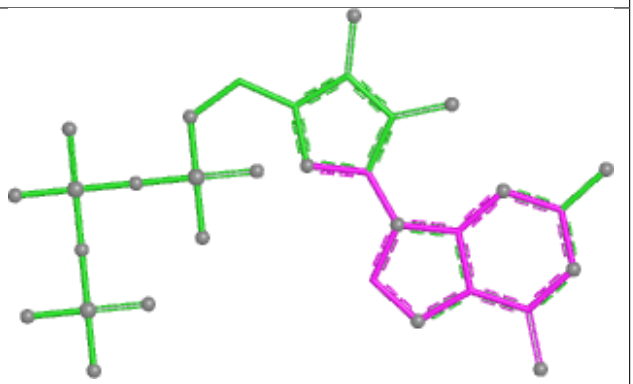

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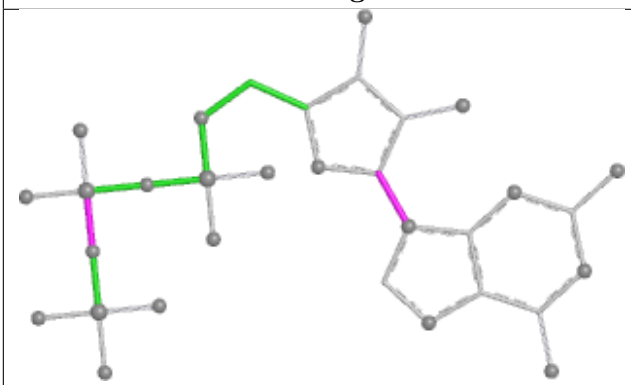

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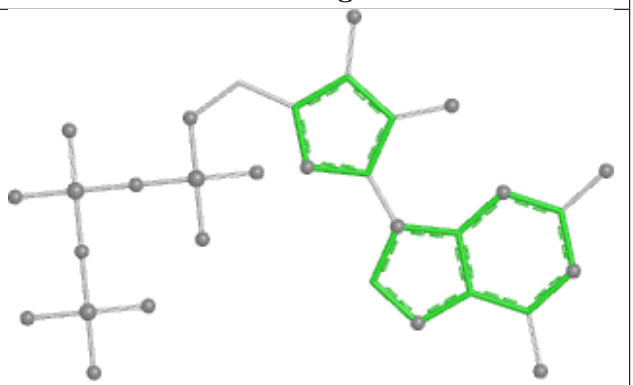
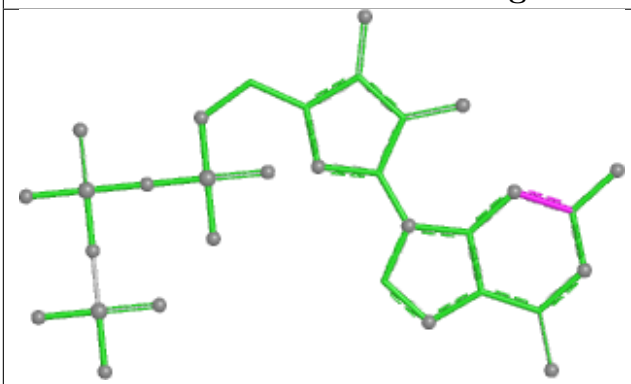


Rings

Ligand GTP BH 501



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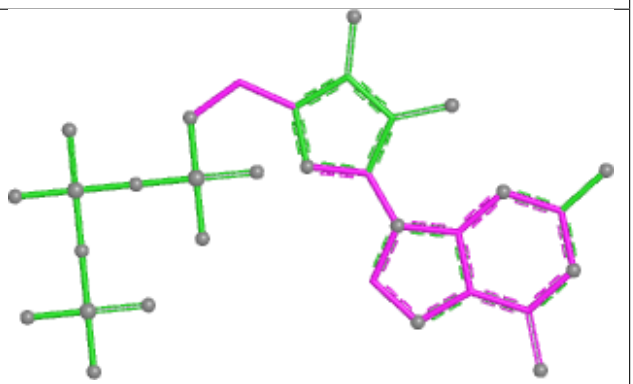

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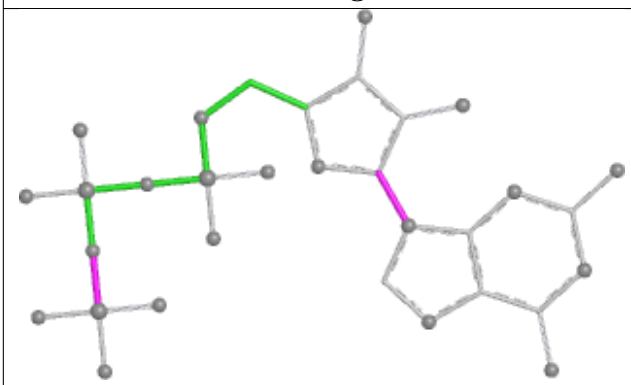

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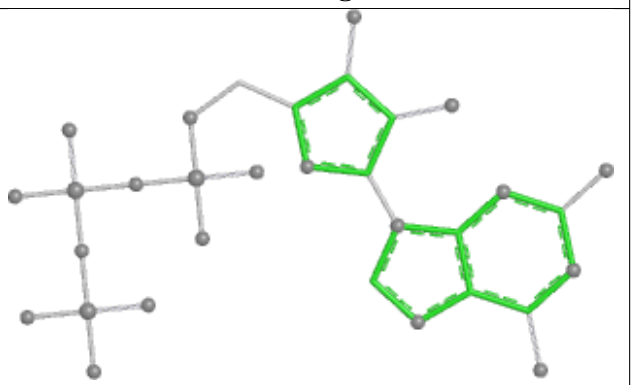

Rings

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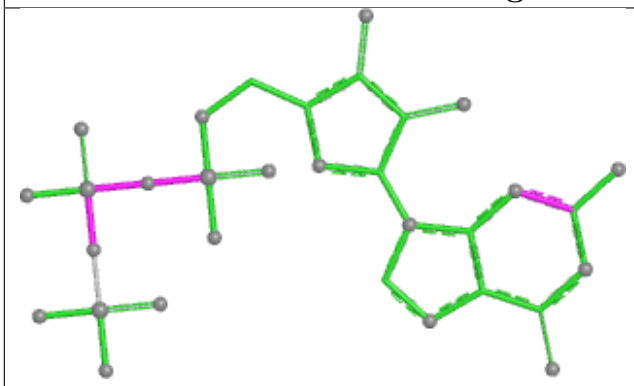

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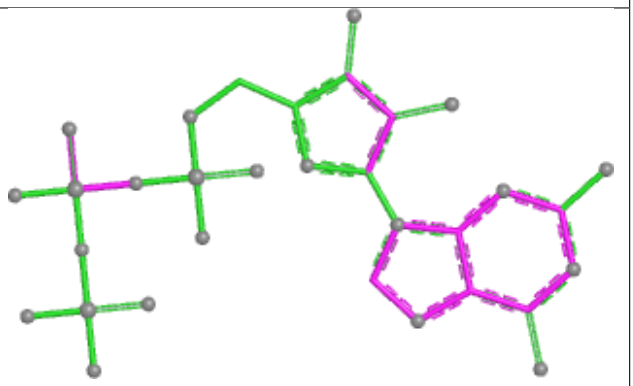

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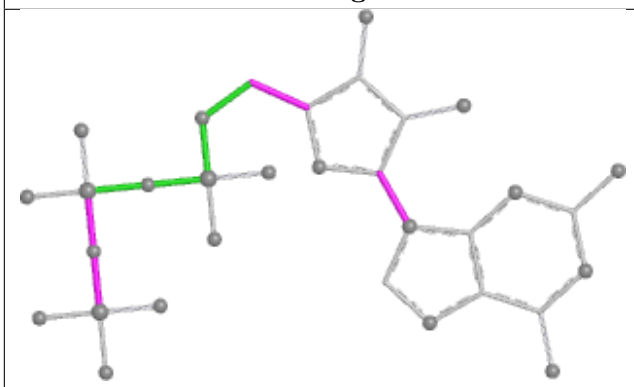

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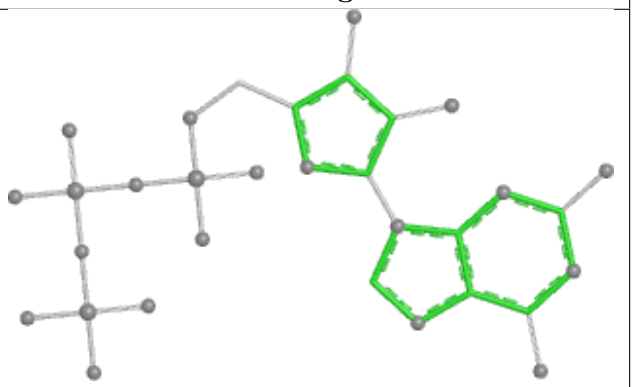

Rings

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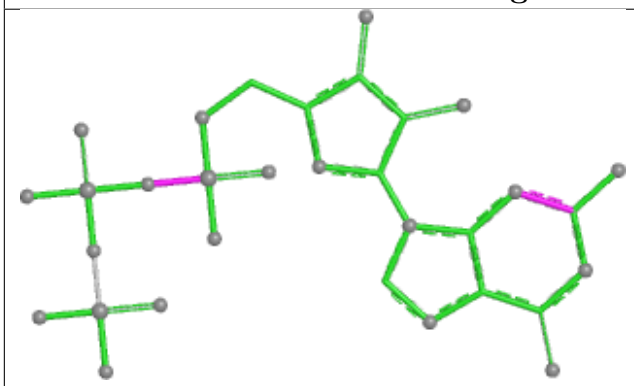

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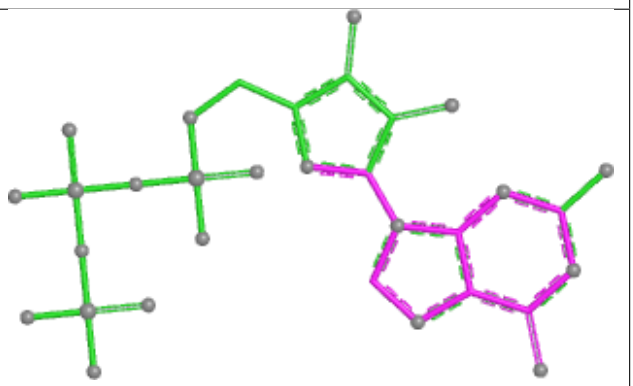

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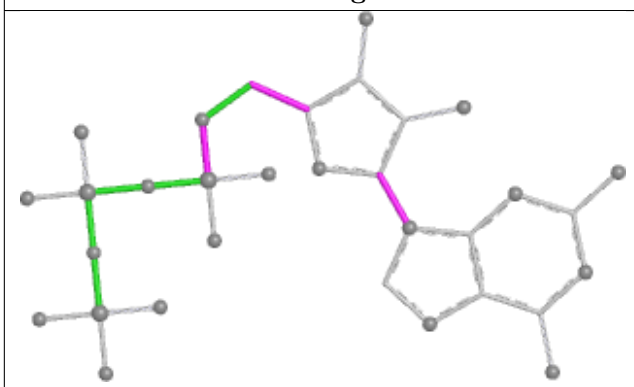

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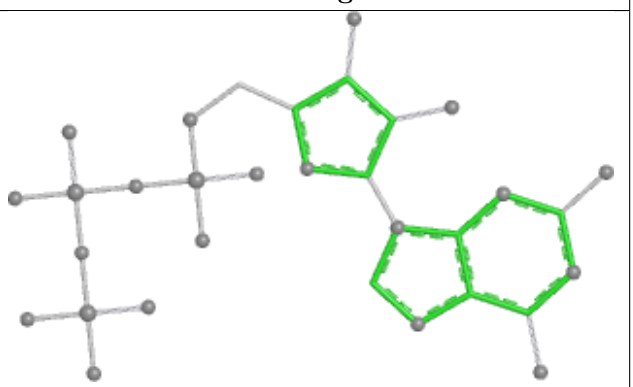

Rings

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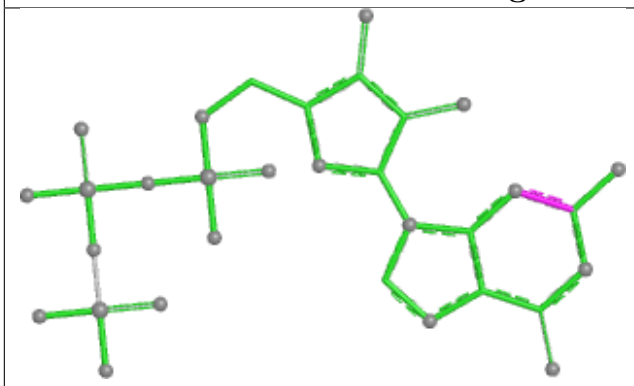

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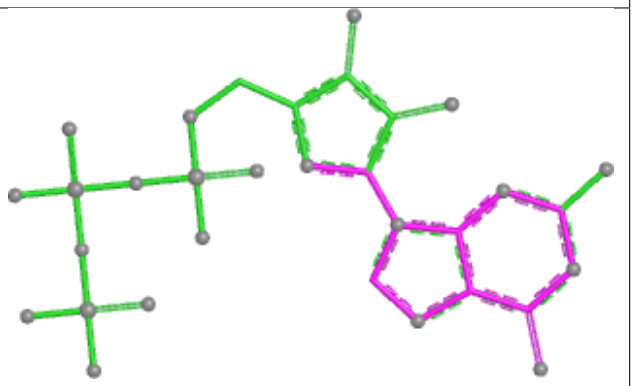

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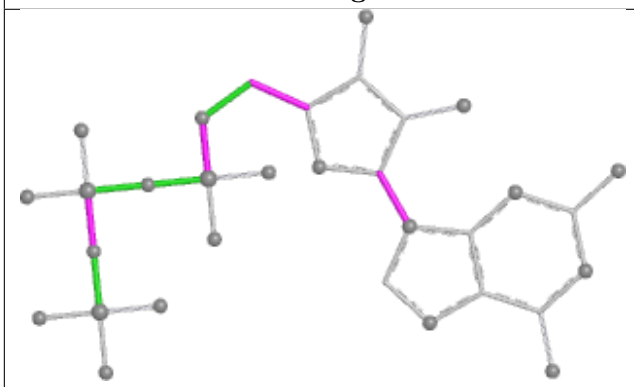

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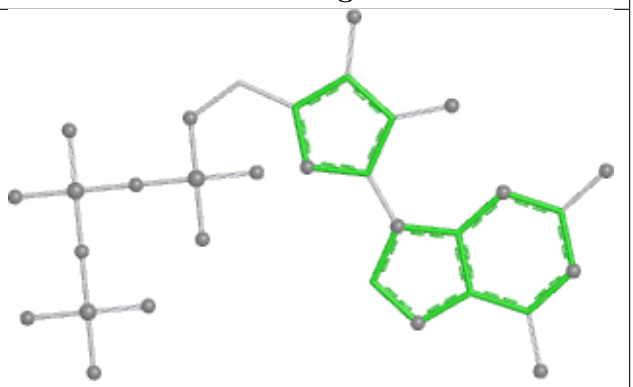

Rings

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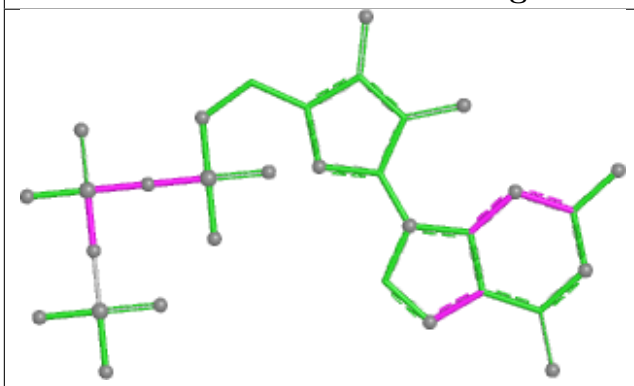

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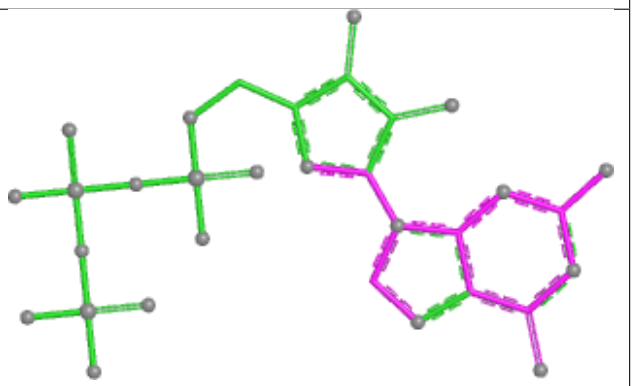

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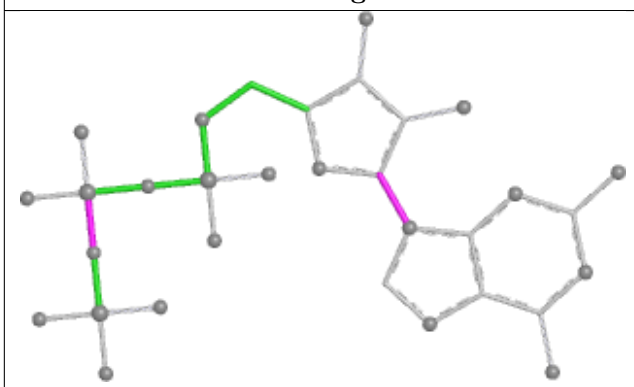

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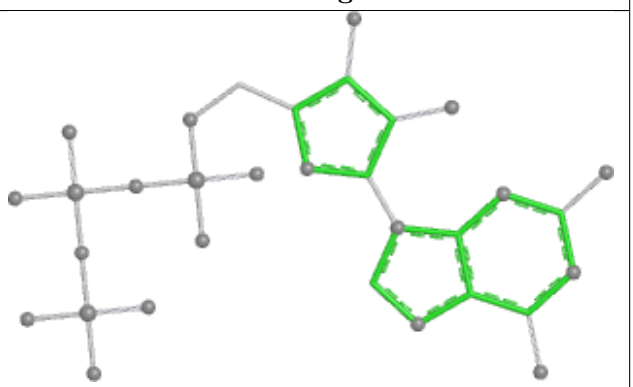

Rings

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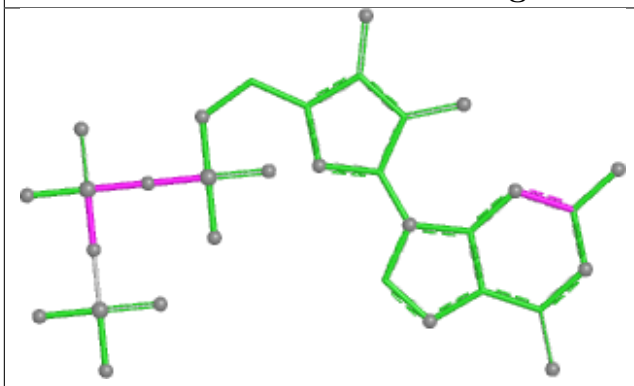

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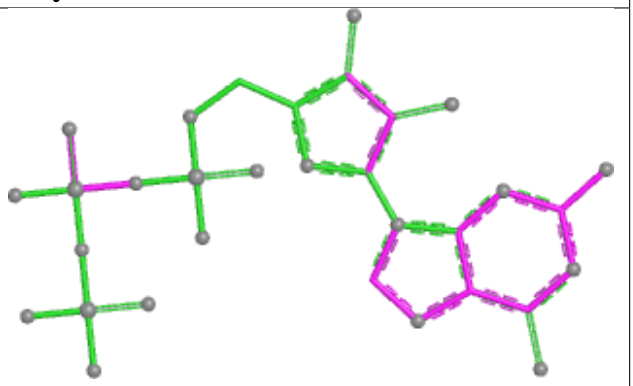

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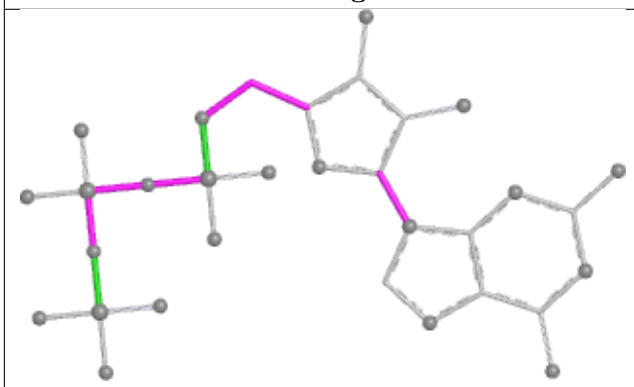

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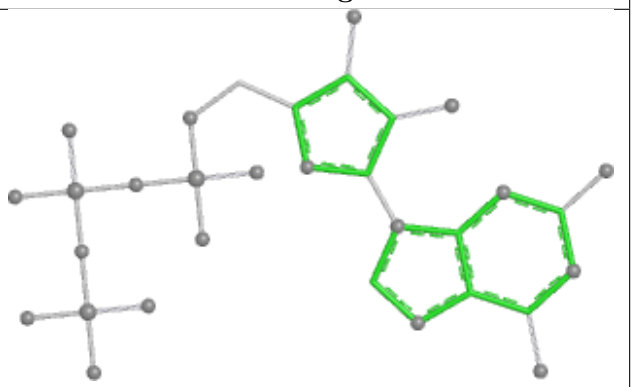
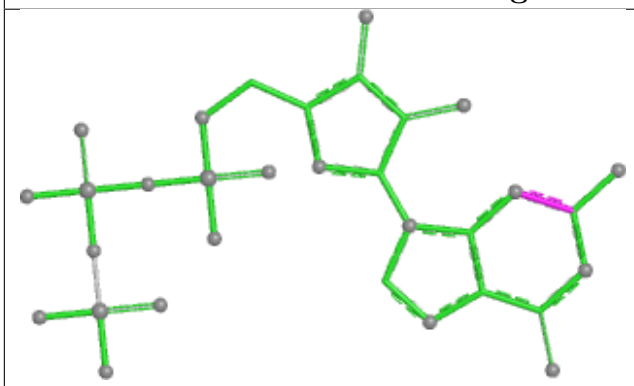


Rings

Ligand GTP VB 501



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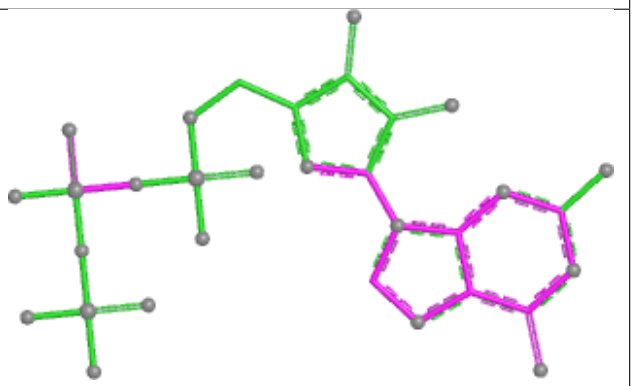

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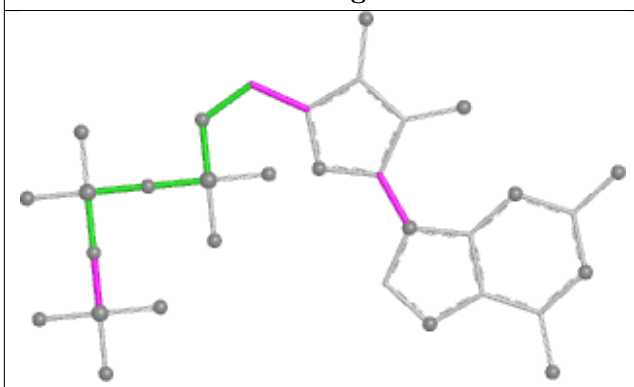
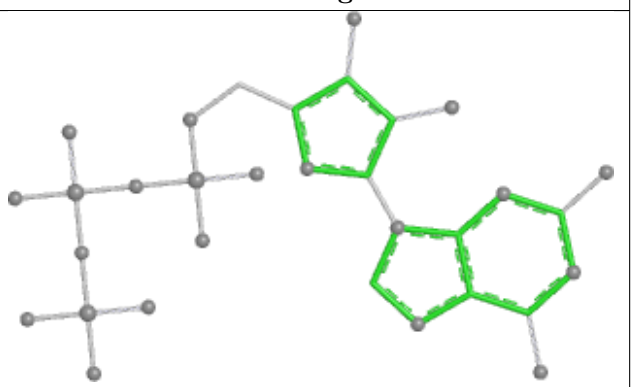
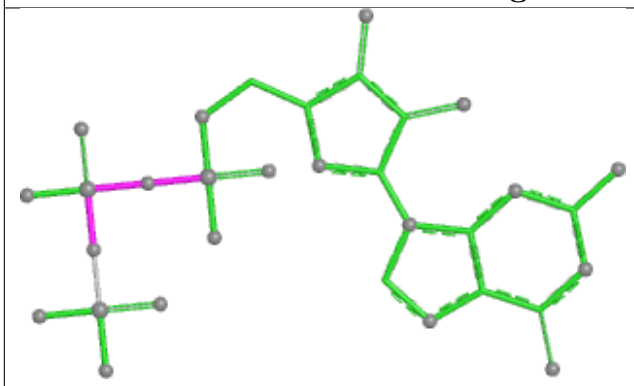


Torsions



Rings

Ligand GTP CG 501



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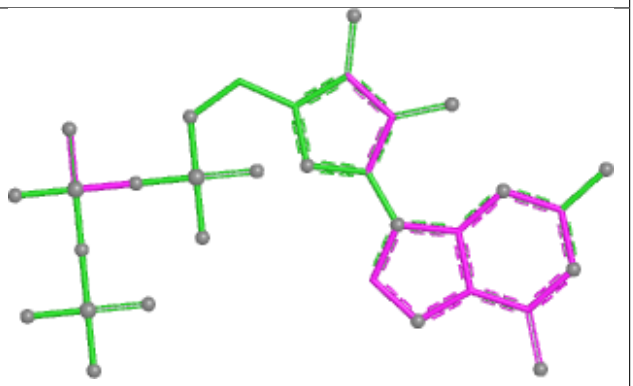
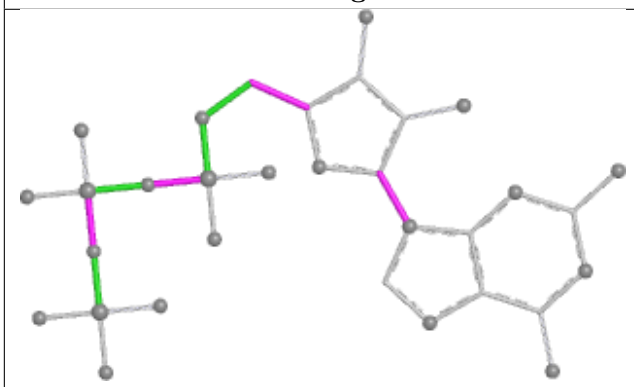


Bond angles



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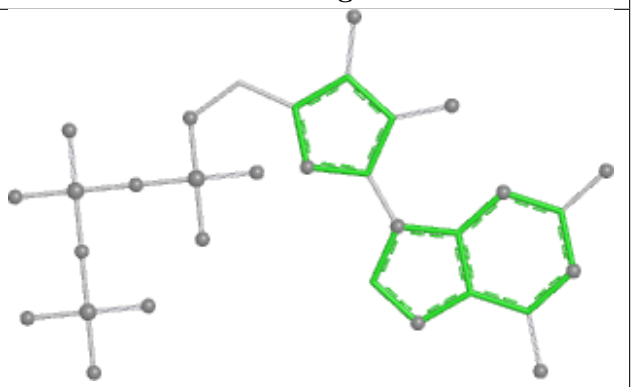
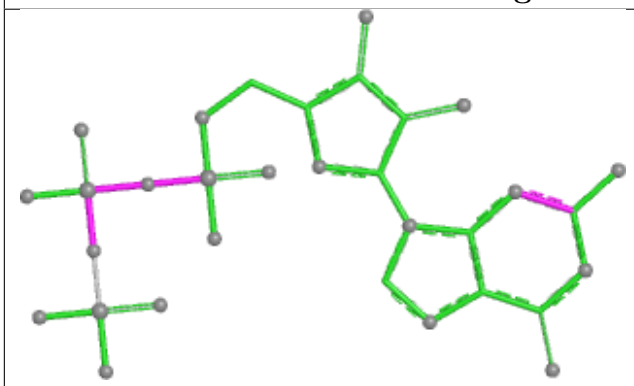


Rings

Ligand GTP JA 501



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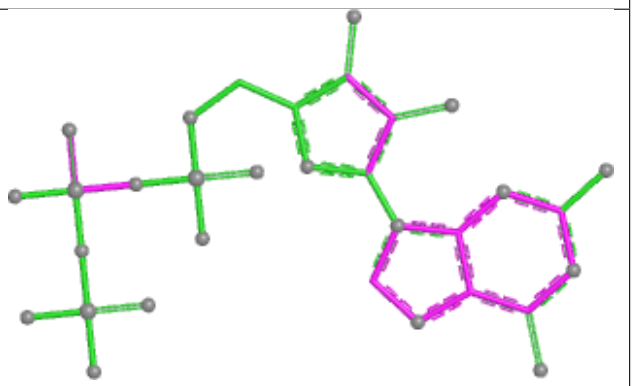

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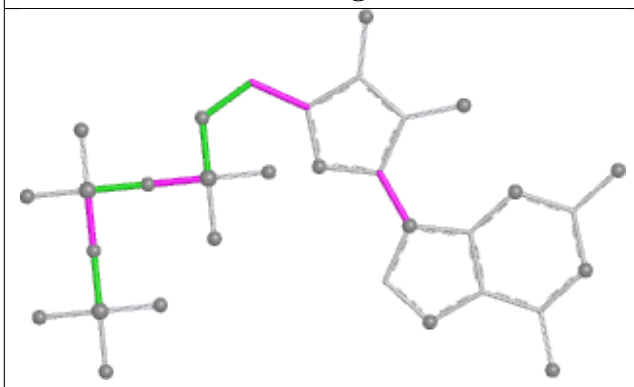

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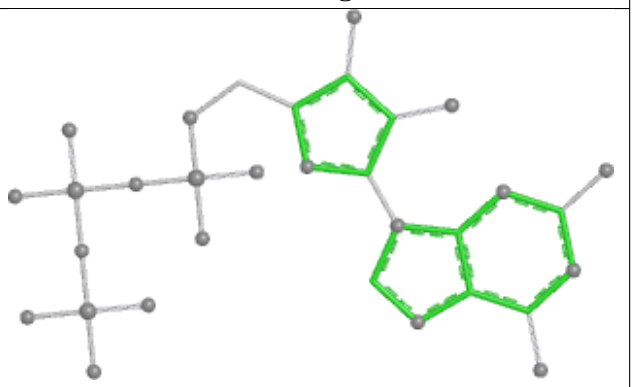
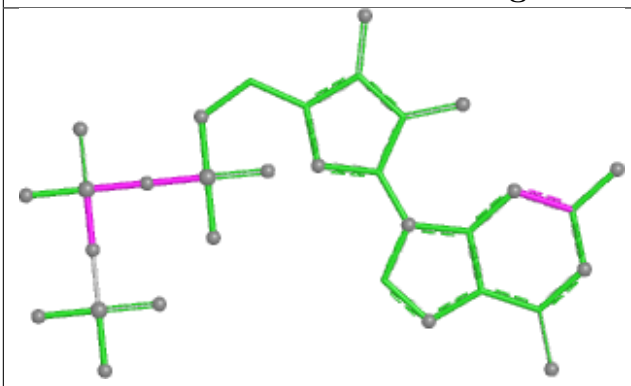
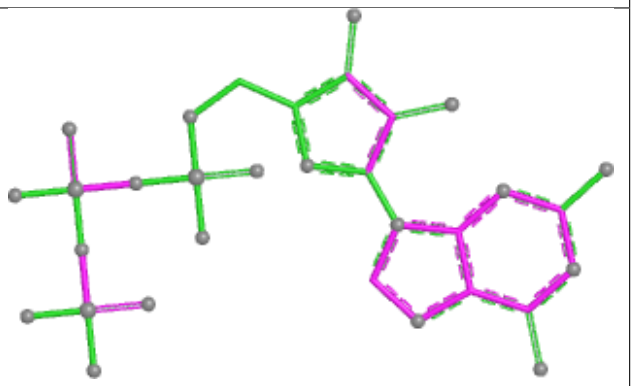


Rings

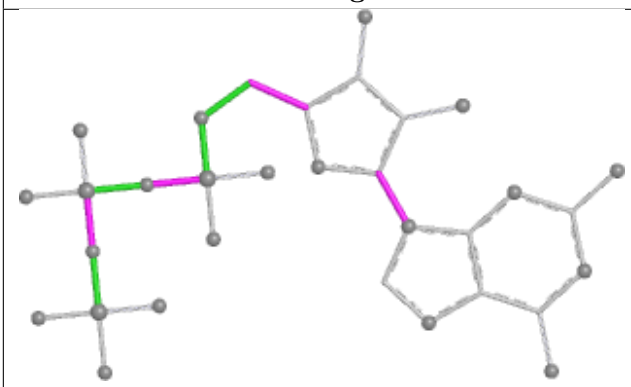
Ligand GTP PG 501



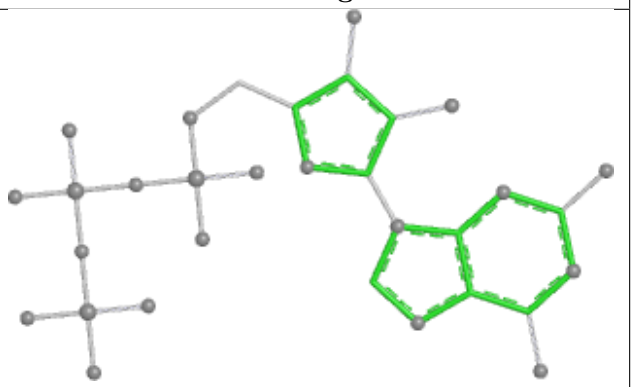
Bond lengths



Bond angles

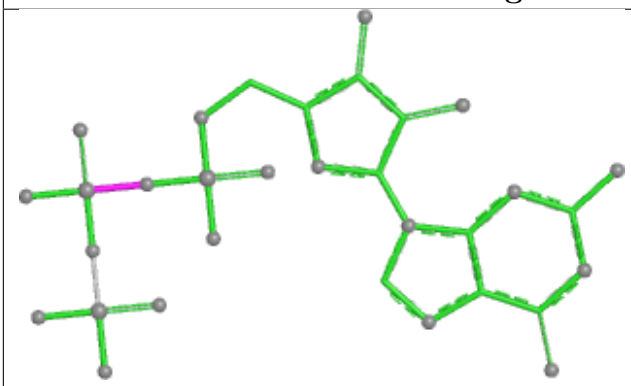


Torsions

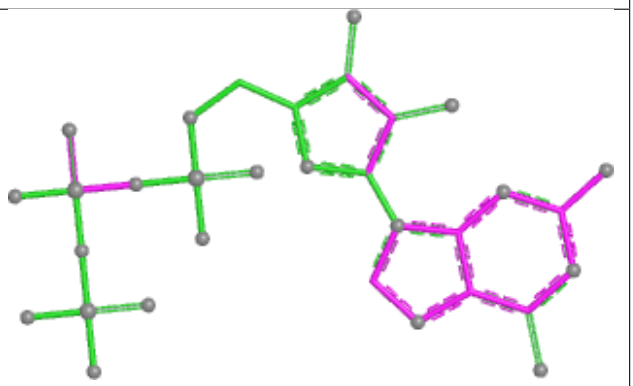


Rings

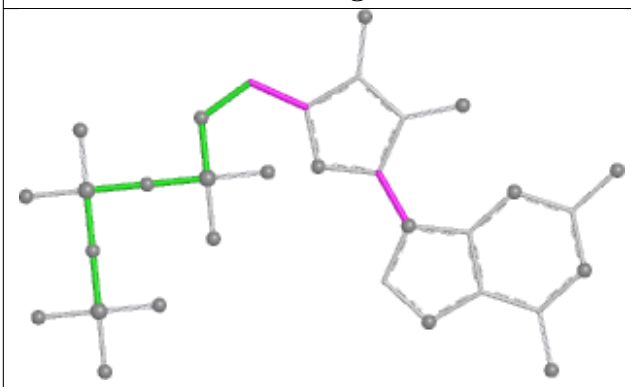
Ligand GTP AM 501



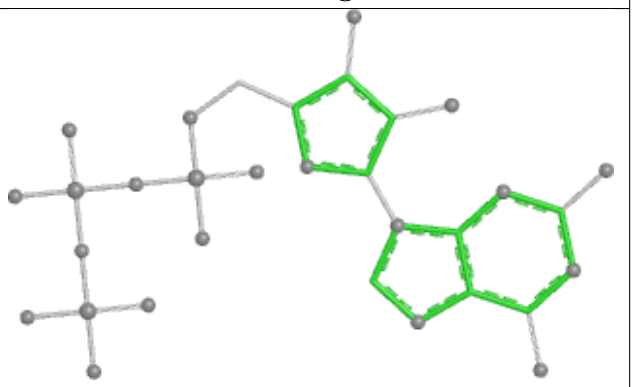
Bond lengths



Bond angles

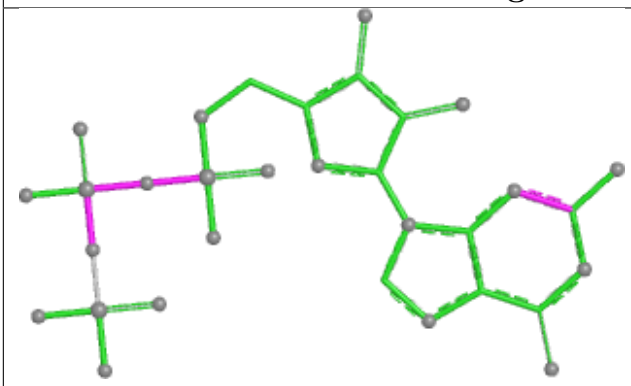


Torsions

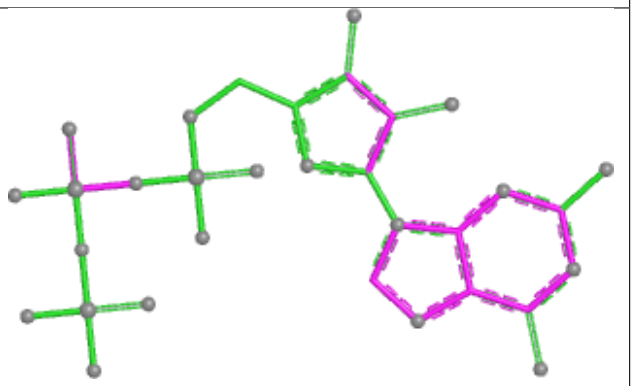


Rings

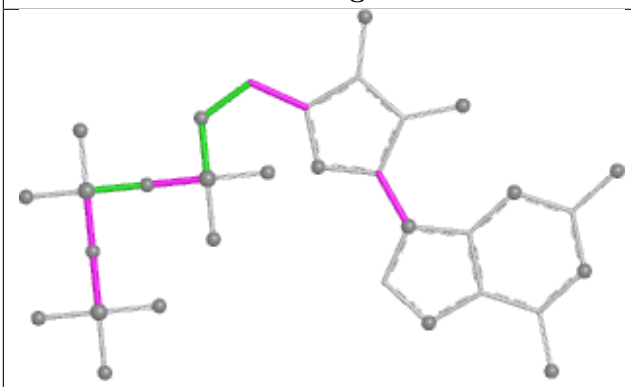
Ligand GTP DG 501



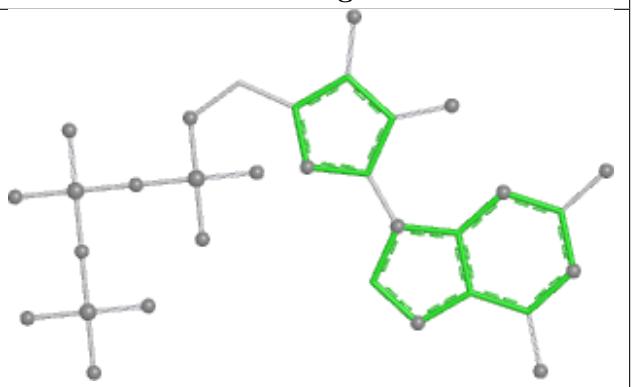
Bond lengths



Bond angles

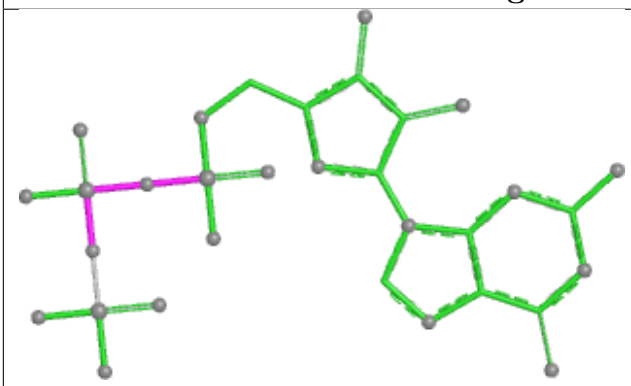


Torsions

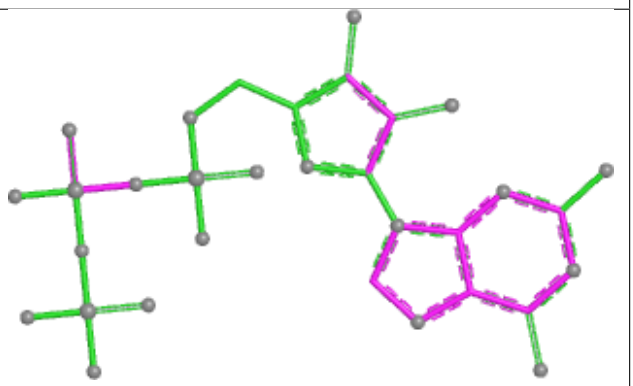


Rings

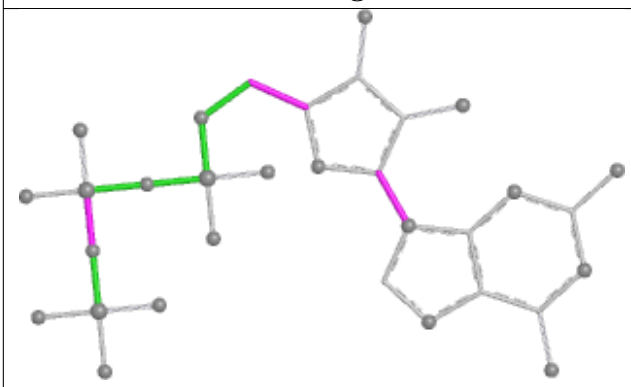
Ligand GTP GG 501



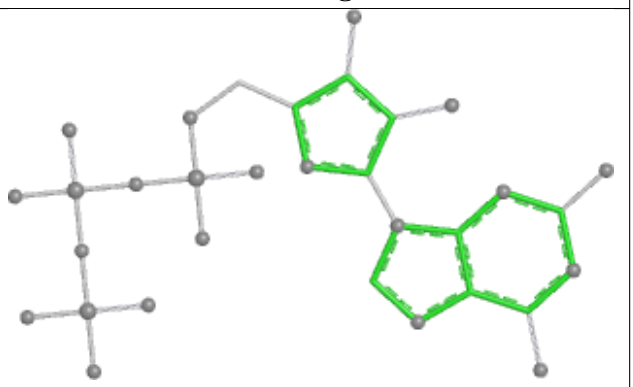
Bond lengths



Bond angles

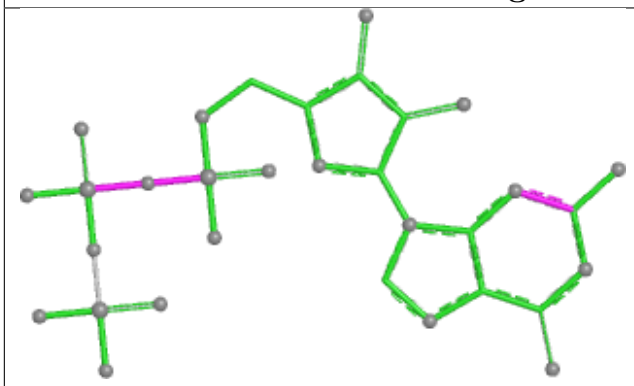


Torsions

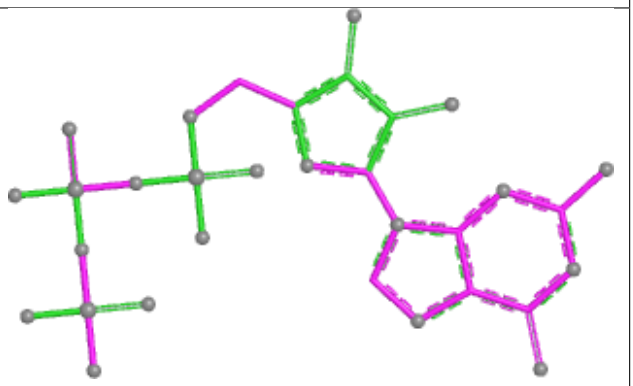


Rings

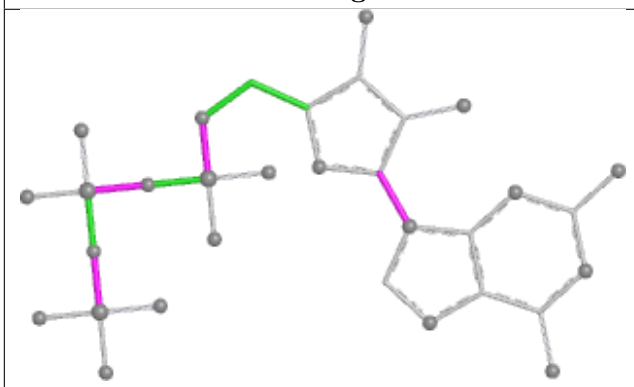
Ligand GTP KH 501



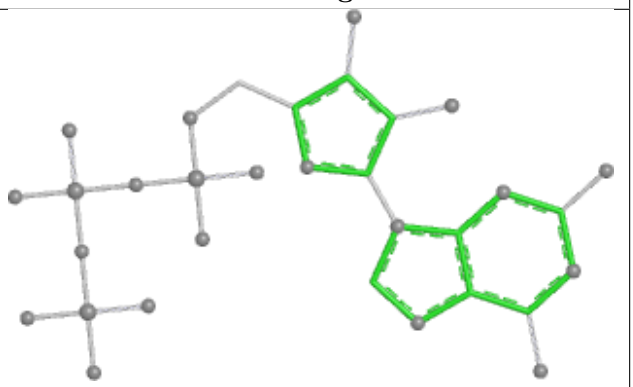
Bond lengths



Bond angles

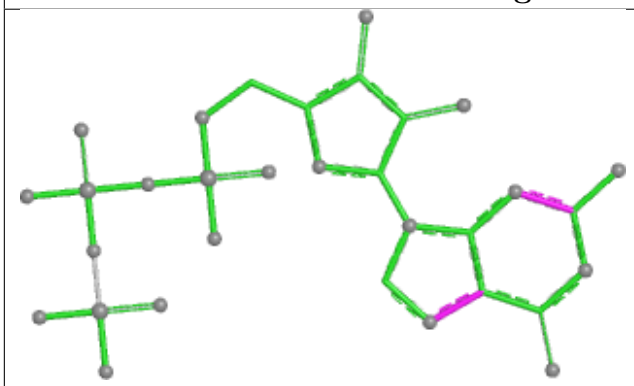


Torsions

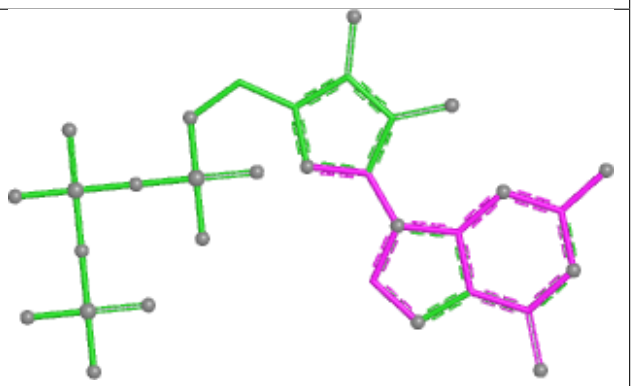


Rings

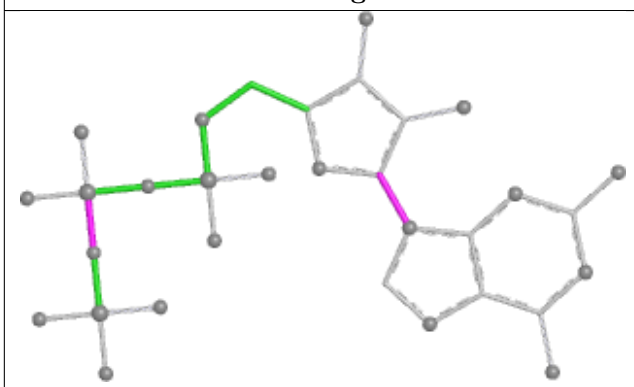
Ligand GTP SB 501



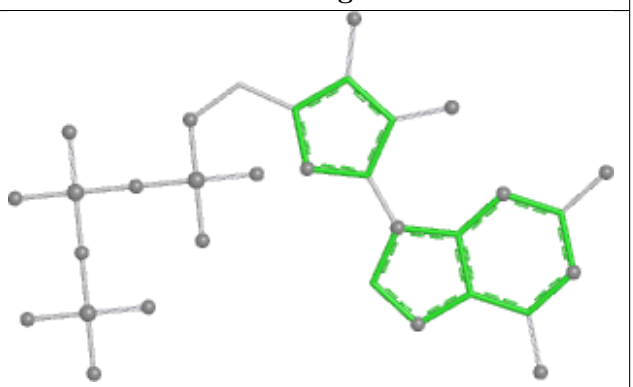
Bond lengths



Bond angles



Torsions



Rings

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.

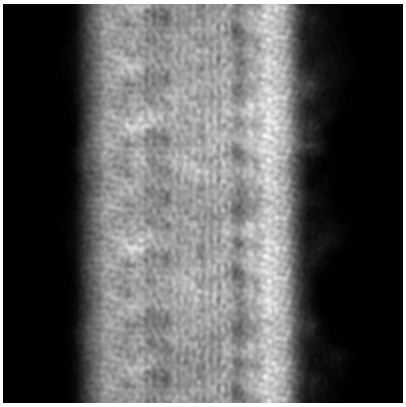
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-35230. These allow visual inspection of the internal detail of the map and identification of artifacts.

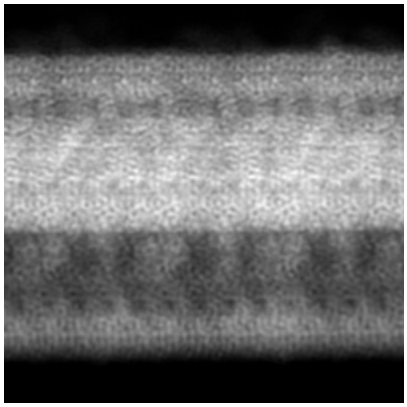
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

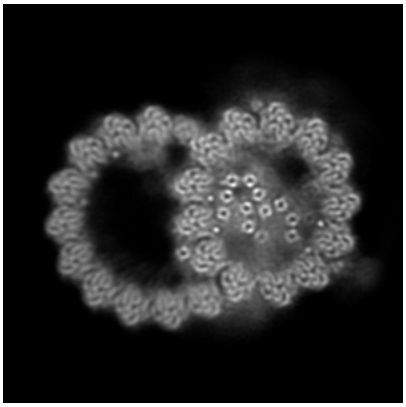
6.1.1 Primary map



X



Y

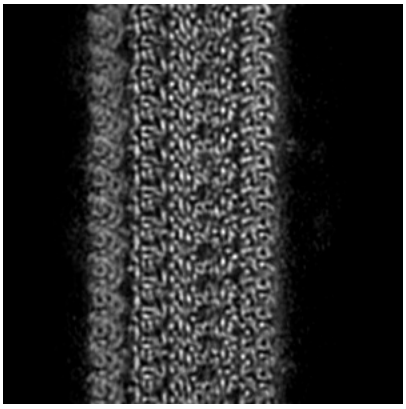


Z

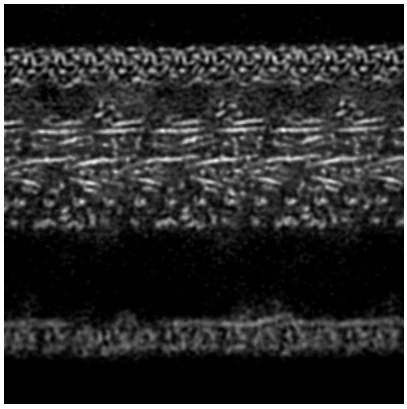
The images above show the map projected in three orthogonal directions.

6.2 Central slices

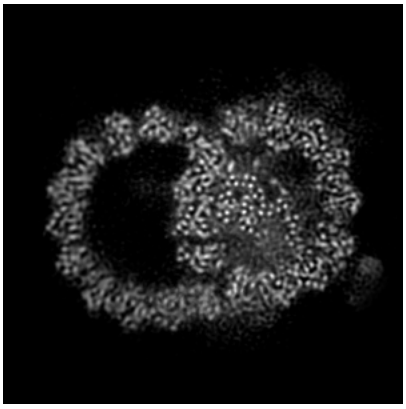
6.2.1 Primary map



X Index: 160



Y Index: 160

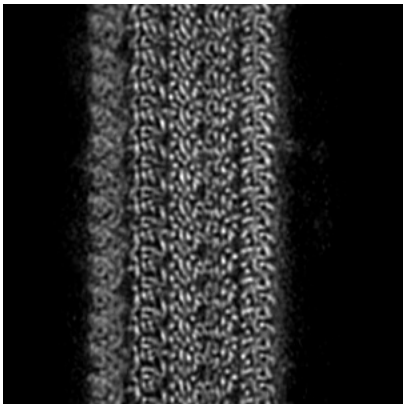


Z Index: 160

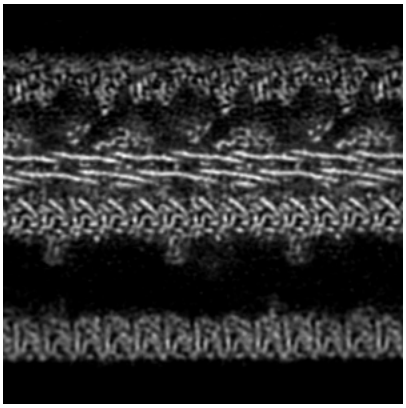
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

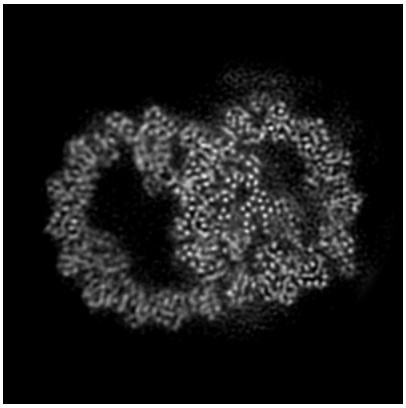
6.3.1 Primary map



X Index: 159



Y Index: 175

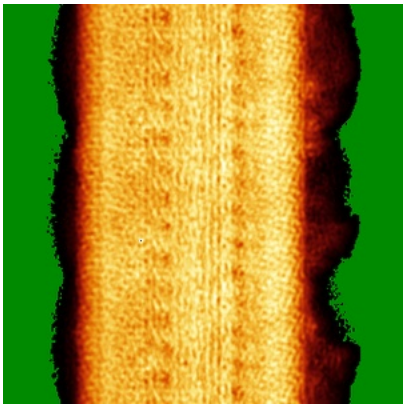


Z Index: 232

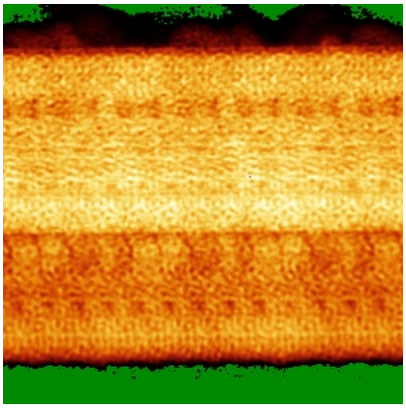
The images above show the largest variance slices of the map in three orthogonal directions.

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

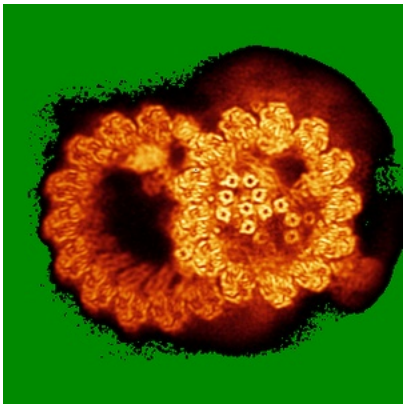
6.4.1 Primary map



X



Y

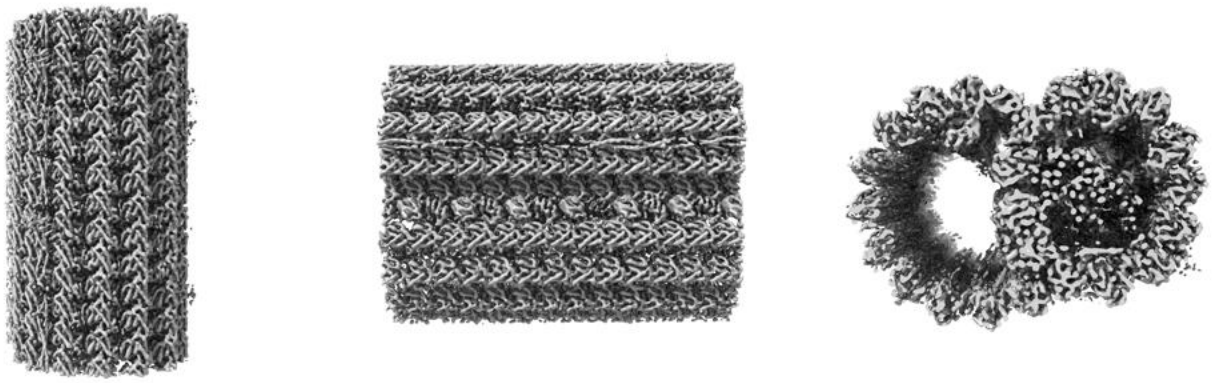


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

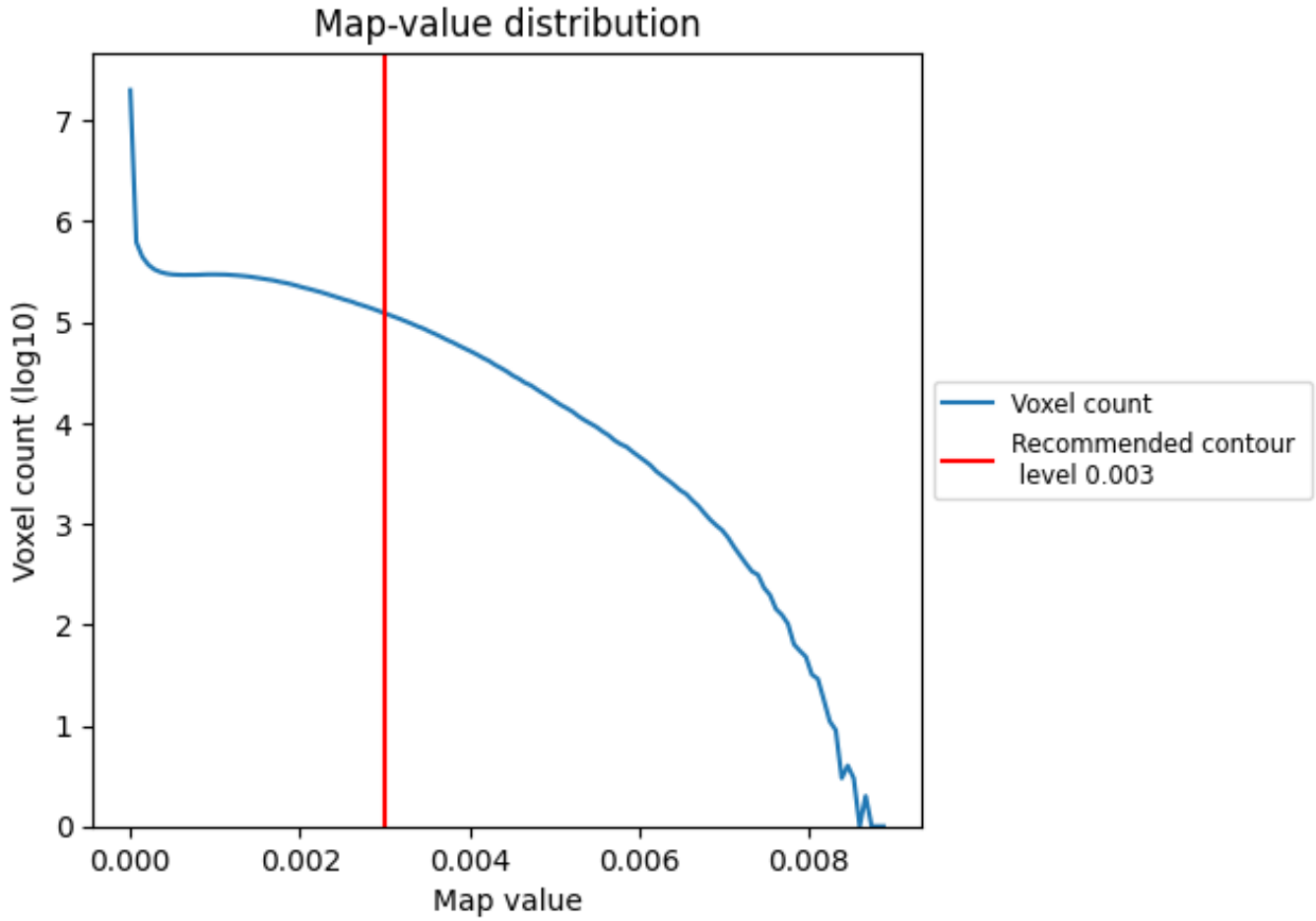
6.6 Mask visualisation (i)

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

7 Map analysis

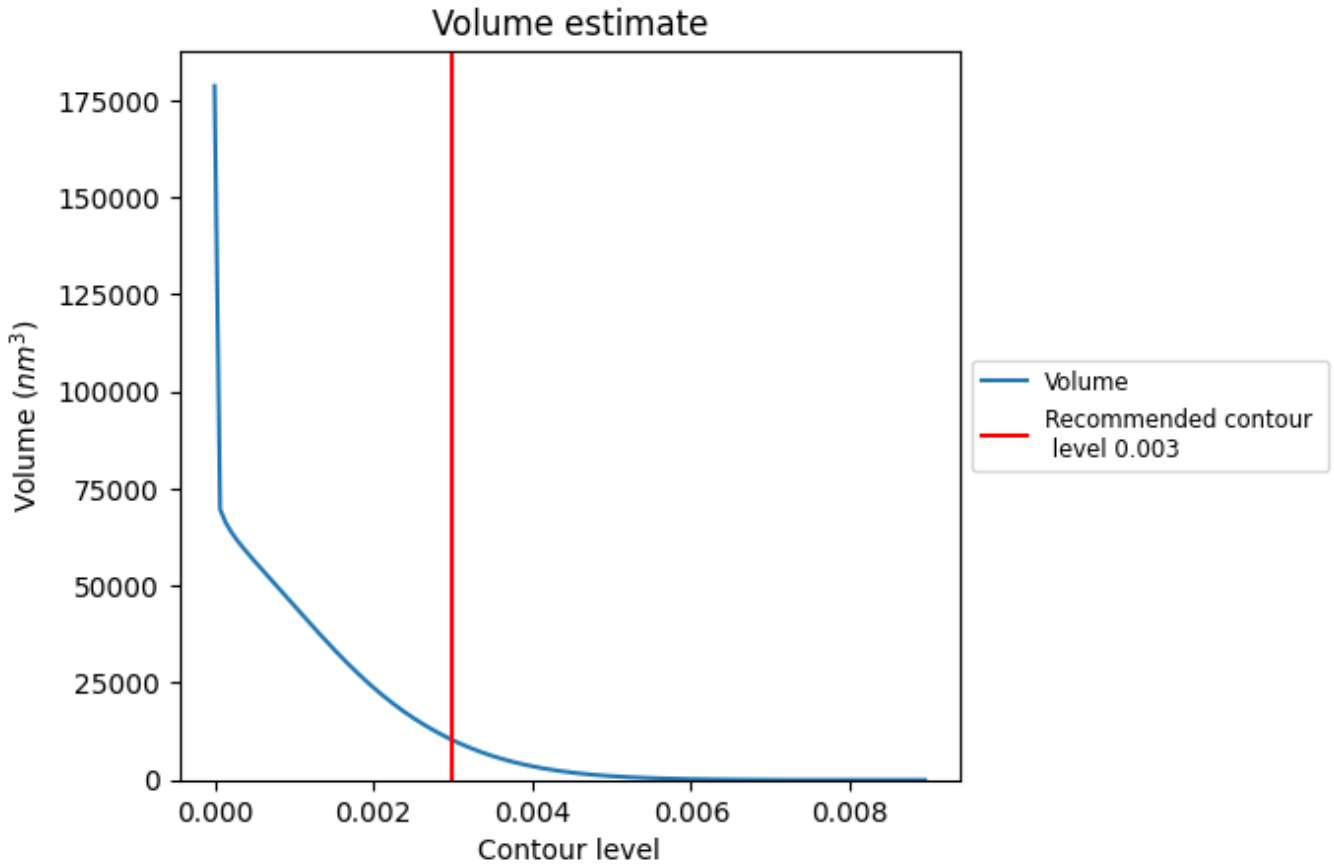
This section contains the results of statistical analysis of the map.

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.

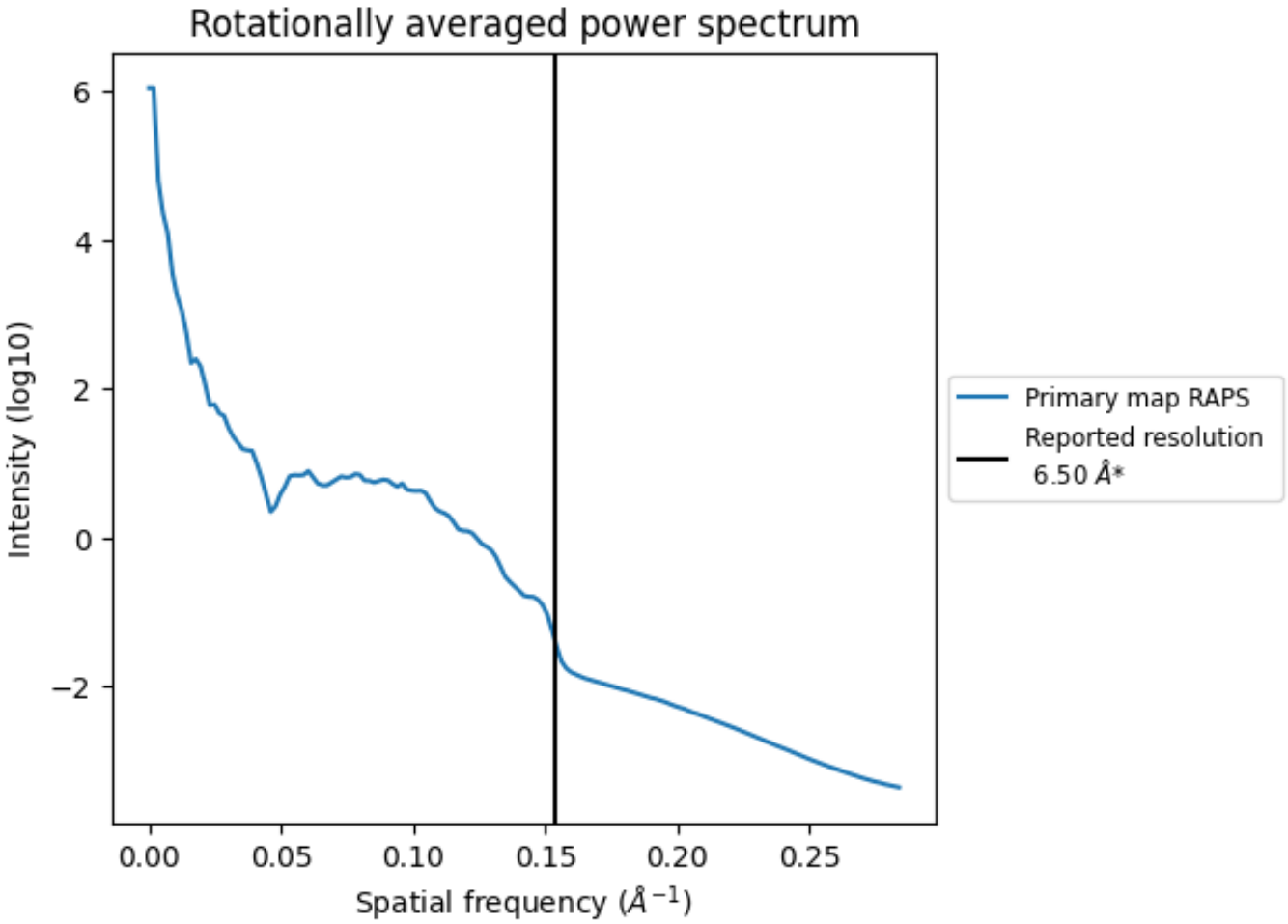
7.2 Volume estimate



The volume at the recommended contour level is 10233 nm^3; this corresponds to an approximate mass of 9243 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 0.154 $Å^{-1}$

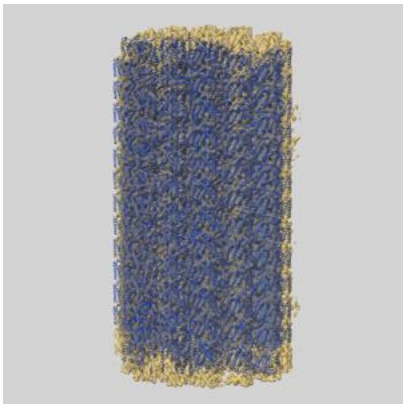
8 Fourier-Shell correlation

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

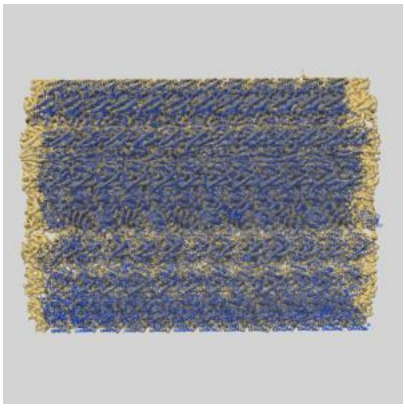
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-35230 and PDB model 8I7R. Per-residue inclusion information can be found in section 3 on page 61.

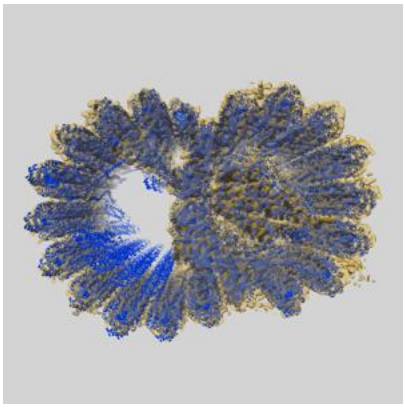
9.1 Map-model overlay



X



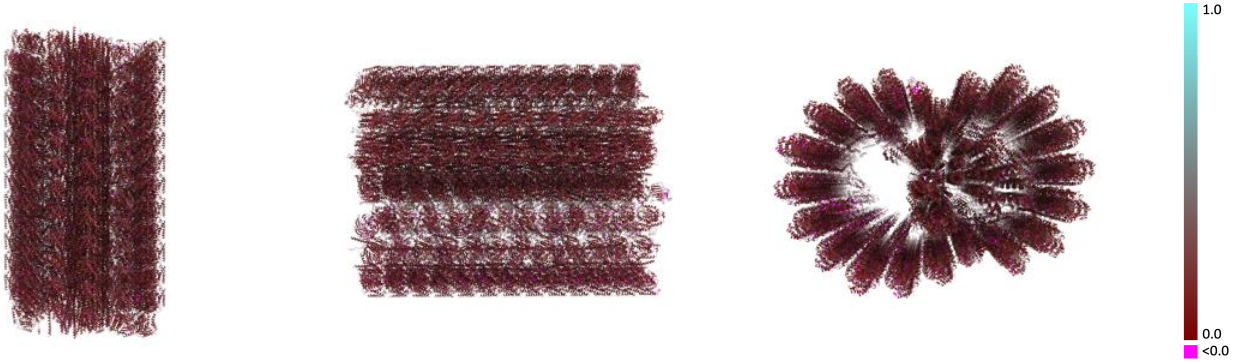
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.003 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.

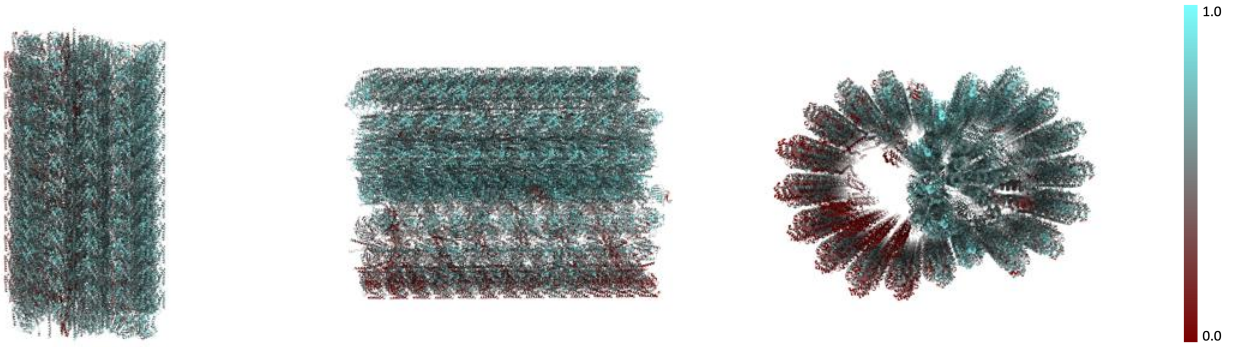
9.2 Q-score mapped to coordinate model



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.

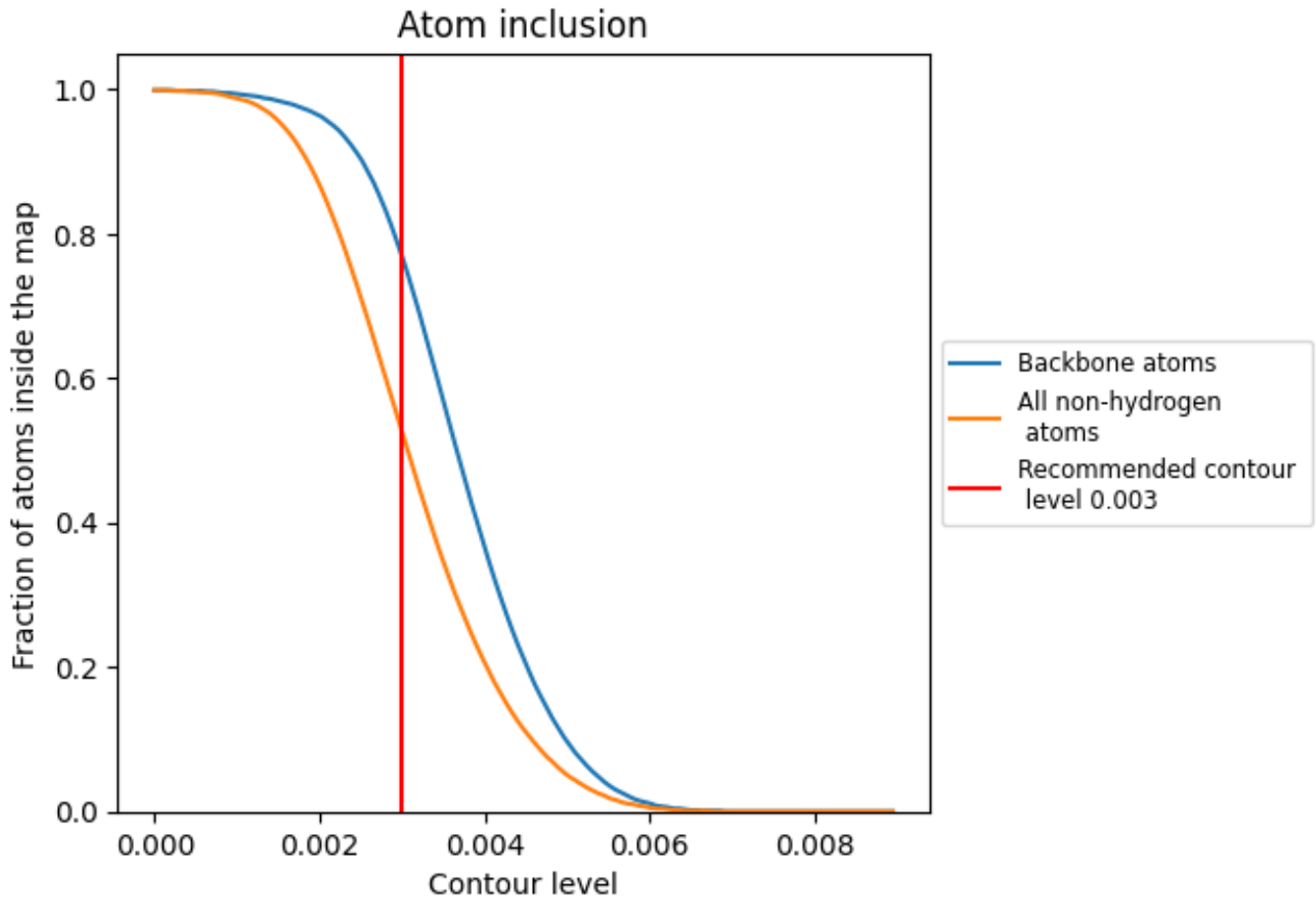
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.003).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 52% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5250	0.1720
A	0.5490	0.1680
A1	0.6650	0.1630
A2	0.6980	0.1740
A3	0.6700	0.1700
A4	0.6350	0.1730
AB	0.6910	0.1760
AC	0.7010	0.1810
AD	0.7540	0.1730
AE	0.7470	0.1790
AF	0.7430	0.1820
AG	0.6680	0.1800
AH	0.6930	0.1800
AI	0.7140	0.1780
AJ	0.7240	0.1800
AK	0.6920	0.1800
AL	0.6800	0.1780
AM	0.6530	0.1730
B	0.4900	0.1850
B1	0.6370	0.1720
B2	0.6750	0.1770
B3	0.6870	0.1750
B4	0.6560	0.1760
B5	0.6100	0.1690
B6	0.6440	0.1620
B7	0.6780	0.1730
B8	0.6710	0.1620
B9	0.6550	0.1620
BB	0.6660	0.1760
BC	0.6590	0.1720
BD	0.6980	0.1720
BE	0.6970	0.1870
BF	0.7070	0.1770
BG	0.6360	0.1720
BH	0.6660	0.1690

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
BI	0.6820	0.1780
BJ	0.6860	0.1790
BK	0.6670	0.1740
BL	0.6500	0.1660
BM	0.6470	0.1670
C	0.5950	0.1670
C1	0.6550	0.1950
C2	0.6970	0.1670
C3	0.7030	0.1730
C4	0.6580	0.1690
C5	0.7060	0.1770
C6	0.6690	0.1710
C7	0.6910	0.1710
C8	0.6840	0.1710
C9	0.6560	0.1580
CB	0.6180	0.1920
CC	0.6180	0.1850
CD	0.6630	0.1890
CE	0.6520	0.1830
CF	0.6750	0.1860
CG	0.6090	0.1850
CH	0.6250	0.1840
CI	0.6380	0.1880
CJ	0.6740	0.1890
CK	0.6310	0.1860
CL	0.6260	0.1870
CM	0.6210	0.1900
Ca	0.6690	0.1670
Cb	0.6920	0.1720
Cc	0.6940	0.1750
Cd	0.6810	0.1720
D	0.5180	0.1540
D1	0.6210	0.1820
D2	0.6660	0.1680
D3	0.6850	0.1690
D4	0.6770	0.1670
D5	0.6550	0.1610
D6	0.6570	0.1680
D7	0.6950	0.1680
D8	0.6860	0.1710
D9	0.6800	0.1650
DA	0.5940	0.1860

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Chain	Atom inclusion	Q-score
DB	0.6360	0.1790
DC	0.6480	0.1860
DD	0.6750	0.1820
DE	0.6000	0.1830
DF	0.6170	0.1820
DG	0.6180	0.1840
DH	0.6680	0.1850
DI	0.6360	0.1850
DJ	0.5980	0.1780
DK	0.5900	0.1810
DL	0.6400	0.1860
Da	0.6590	0.1780
E	0.5590	0.2040
E1	0.6120	0.2100
E2	0.6030	0.2140
E3	0.6140	0.2140
E4	0.5930	0.1820
EA	0.5660	0.1880
EB	0.6000	0.1870
EC	0.6140	0.1870
ED	0.6420	0.1850
EE	0.5850	0.1830
EF	0.5710	0.1860
EG	0.5710	0.1850
EH	0.6240	0.1860
EI	0.6170	0.1860
EJ	0.5490	0.1850
EK	0.5400	0.1830
EL	0.5760	0.1900
F	0.5150	0.2190
F1	0.5880	0.1680
F2	0.6220	0.1820
F3	0.6170	0.1820
F4	0.5840	0.1700
F5	0.4290	0.1820
F6	0.4720	0.1850
F7	0.5710	0.1870
F8	0.5330	0.1720
F9	0.1880	0.1680
FA	0.5110	0.1800
FB	0.5640	0.1820
FC	0.5720	0.1830

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Chain	Atom inclusion	Q-score
FD	0.6130	0.1830
FE	0.5900	0.1830
FF	0.5470	0.1840
FG	0.5380	0.1900
FH	0.6000	0.1880
FI	0.6000	0.1840
FJ	0.5760	0.1890
FK	0.5370	0.1840
FL	0.5600	0.1850
Fa	0.4090	0.1850
Fb	0.5260	0.1830
Fc	0.4060	0.1840
Fd	0.0110	0.2220
Fe	0.4600	0.1520
Ff	0.4680	0.1640
Fg	0.3990	0.1540
Fh	0.4350	0.1530
Fi	0.2630	0.1630
Fj	0.4530	0.1750
Fk	0.5560	0.1680
Fl	0.5210	0.1760
Fm	0.5140	0.1670
G	0.5460	0.1850
G1	0.6430	0.1990
G2	0.6040	0.2020
G3	0.5640	0.2010
G4	0.5780	0.1980
G5	0.5660	0.1980
G6	0.5790	0.1970
GA	0.5070	0.1900
GB	0.5580	0.1840
GC	0.5370	0.1840
GD	0.5880	0.1840
GE	0.5790	0.1840
GF	0.5230	0.1870
GG	0.4960	0.1870
GH	0.5510	0.1850
GI	0.6040	0.1870
GJ	0.5680	0.1820
GK	0.4760	0.1810
GL	0.5250	0.1850
H	0.5480	0.1940

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Chain	Atom inclusion	Q-score
H1	0.5760	0.2130
H2	0.6440	0.1980
H3	0.6840	0.2280
H4	0.6000	0.1920
H5	0.6370	0.2180
H6	0.5550	0.1960
HA	0.4900	0.1790
HB	0.5260	0.1820
HC	0.4910	0.1800
HD	0.5750	0.1780
HE	0.5670	0.1880
HF	0.5150	0.1810
HG	0.5070	0.1790
HH	0.5650	0.1850
HI	0.5910	0.1870
HJ	0.5620	0.1760
HK	0.4680	0.1820
HL	0.5200	0.1880
I	0.5390	0.1960
I1	0.7610	0.2210
I2	0.7750	0.2170
I3	0.7410	0.2250
IA	0.5000	0.1790
IB	0.5590	0.1830
IC	0.5420	0.1760
ID	0.5980	0.1820
IE	0.5900	0.1890
IF	0.5530	0.1830
IG	0.5290	0.1830
IH	0.5730	0.1880
II	0.6050	0.1860
IJ	0.6150	0.1860
IK	0.5290	0.1800
IL	0.5570	0.1800
IM	0.5600	0.1840
J	0.5760	0.2050
J1	0.5120	0.1720
J2	0.5810	0.1740
J3	0.5500	0.1690
JA	0.5940	0.1640
JB	0.6370	0.1660
JC	0.6410	0.1730

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Chain	Atom inclusion	Q-score
JD	0.6650	0.1770
JE	0.6200	0.1750
JF	0.6120	0.1670
JG	0.6080	0.1680
JH	0.6600	0.1700
JI	0.6430	0.1700
JJ	0.6220	0.1690
JK	0.5800	0.1600
JL	0.6180	0.1630
K	0.5880	0.1670
K1	0.6200	0.1900
K2	0.6460	0.1890
K3	0.6550	0.1910
K4	0.6470	0.1930
K5	0.5920	0.2130
KA	0.6330	0.1760
KB	0.6450	0.1710
KC	0.6890	0.1750
KD	0.7190	0.1710
KE	0.7030	0.1760
KF	0.6640	0.1780
KG	0.6480	0.1820
KH	0.7070	0.1770
KI	0.6930	0.1730
KJ	0.7070	0.1820
KK	0.6190	0.1720
KL	0.6420	0.1750
L	0.5800	0.1720
L1	0.5150	0.2060
L2	0.5960	0.2080
L3	0.5960	0.2090
L4	0.4350	0.2200
LA	0.6520	0.1760
LB	0.6510	0.1640
LC	0.7060	0.1660
LD	0.7210	0.1710
LE	0.7110	0.1780
LF	0.7090	0.1740
LG	0.6670	0.1760
LH	0.7210	0.1780
LI	0.7010	0.1780
LJ	0.7210	0.1800

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Chain	Atom inclusion	Q-score
LK	0.6590	0.1660
LL	0.6460	0.1720
M	0.4100	0.2110
M1	0.5530	0.1850
M2	0.6680	0.1940
M3	0.6760	0.1880
MB	0.6540	0.1730
MC	0.6870	0.1710
MD	0.7500	0.1790
ME	0.7300	0.1750
MF	0.7300	0.1790
MG	0.6870	0.1790
MH	0.7190	0.1740
MI	0.6830	0.1750
MJ	0.7060	0.1800
MK	0.6970	0.1740
ML	0.6700	0.1770
MM	0.6300	0.1750
N	0.3720	0.2320
N1	0.4820	0.1840
N2	0.6070	0.1860
N3	0.6160	0.1970
N4	0.5220	0.2040
NA	0.4500	0.1680
NB	0.4700	0.1600
NC	0.4660	0.1620
ND	0.5550	0.1620
NE	0.5160	0.1610
NF	0.5050	0.1650
NG	0.5010	0.1640
NH	0.5560	0.1660
NI	0.5570	0.1680
NJ	0.4830	0.1630
NK	0.4620	0.1570
NL	0.4770	0.1620
O	0.6300	0.1930
O1	0.6540	0.2110
O2	0.6330	0.2200
O3	0.5640	0.2100
OA	0.2650	0.1490
OB	0.3030	0.1570
OC	0.2920	0.1520

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Chain	Atom inclusion	Q-score
OD	0.3710	0.1600
OE	0.3970	0.1570
OF	0.3640	0.1540
OG	0.3690	0.1560
OH	0.3970	0.1590
OI	0.4170	0.1600
OJ	0.3470	0.1580
OK	0.3200	0.1540
OL	0.3420	0.1530
P	0.6400	0.1730
P1	0.5240	0.1350
P2	0.4960	0.1370
P3	0.3900	0.1350
PA	0.2580	0.1360
PB	0.3060	0.1580
PC	0.2720	0.1600
PD	0.3670	0.1630
PE	0.4160	0.1570
PF	0.3680	0.1540
PG	0.3590	0.1630
PH	0.3550	0.1640
PI	0.3730	0.1620
PJ	0.3700	0.1660
PK	0.2750	0.1520
PL	0.2770	0.1570
PM	0.2830	0.1620
Q	0.6760	0.1710
Q1	0.2580	0.1440
Q2	0.2930	0.1390
Q3	0.2010	0.1470
QB	0.2520	0.1570
QC	0.2820	0.1620
QD	0.3490	0.1570
QE	0.4130	0.1630
QF	0.3660	0.1540
QG	0.3480	0.1600
QH	0.3410	0.1650
QI	0.3840	0.1630
QJ	0.3640	0.1620
QK	0.3010	0.1580
QL	0.2780	0.1600
QM	0.2560	0.1580

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Chain	Atom inclusion	Q-score
R	0.6350	0.1630
R1	0.6630	0.2020
R2	0.6440	0.2020
R3	0.5640	0.2040
RB	0.2340	0.1650
RC	0.2270	0.1570
RD	0.2820	0.1640
RE	0.3670	0.1580
RF	0.3650	0.1650
RG	0.3010	0.1600
RH	0.3100	0.1580
RI	0.3410	0.1630
RJ	0.3500	0.1660
RK	0.3200	0.1590
RL	0.2350	0.1580
RM	0.2170	0.1610
S	0.4770	0.1900
SB	0.2760	0.1610
SC	0.2650	0.1610
SD	0.3250	0.1640
SE	0.4180	0.1600
SF	0.4410	0.1640
SG	0.3410	0.1560
SH	0.3410	0.1660
SI	0.3700	0.1650
SJ	0.3740	0.1610
SK	0.3970	0.1580
SL	0.2720	0.1600
SM	0.2470	0.1580
T	0.4340	0.1780
TB	0.2730	0.1490
TC	0.2740	0.1560
TD	0.3210	0.1570
TE	0.4150	0.1560
TF	0.4580	0.1610
TG	0.3950	0.1570
TH	0.3430	0.1650
TI	0.3530	0.1540
TJ	0.4280	0.1660
TK	0.4080	0.1630
TL	0.3390	0.1680
TM	0.2600	0.1630

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Chain	Atom inclusion	Q-score
TN	0.2880	0.1640
U	0.2150	0.1860
UA	0.3580	0.1630
UB	0.3640	0.1620
UC	0.4790	0.1650
UD	0.5280	0.1630
UE	0.4610	0.1600
UF	0.4560	0.1680
UG	0.4310	0.1630
UH	0.4770	0.1670
UI	0.4690	0.1620
UJ	0.4160	0.1650
UK	0.3410	0.1610
UL	0.3740	0.1620
V	0.0950	0.1710
VA	0.4450	0.1700
VB	0.4810	0.1720
VC	0.5070	0.1740
VD	0.5900	0.1710
VE	0.5640	0.1690
VF	0.5370	0.1730
VG	0.4920	0.1750
VH	0.5540	0.1760
VI	0.5520	0.1760
VJ	0.5150	0.1720
VK	0.4450	0.1700
VL	0.4510	0.1660
W	0.3430	0.1870
WA	0.5400	0.1700
WB	0.5970	0.1690
WC	0.5640	0.1710
WD	0.6310	0.1620
WE	0.6210	0.1670
WF	0.6110	0.1670
WG	0.5810	0.1740
WH	0.6200	0.1720
WI	0.5890	0.1680
WJ	0.6070	0.1670
WK	0.5220	0.1720
WL	0.5600	0.1640
X	0.3510	0.1800
XA	0.4960	0.1390

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Chain	Atom inclusion	Q-score
XB	0.6800	0.1950
XC	0.7550	0.1890
XD	0.6600	0.1910
XE	0.7020	0.1900
XF	0.6470	0.1900
XG	0.6660	0.1920
XH	0.5610	0.1750
XI	0.6540	0.1810
XJ	0.2680	0.1580
XK	0.6230	0.1780
XL	0.6780	0.1860
XM	0.6300	0.1800
Y	0.2510	0.1850
YA	0.0010	0.0790
YB	0.0110	0.1200
YC	0.0360	0.1600
YD	0.0330	0.1450
YE	0.0270	0.1190
YF	0.0540	0.1350
YG	0.0590	0.1550
YH	0.1030	0.1720
YI	0.0100	0.1270
YJ	0.0100	0.1240
YK	0.0070	0.1270
YL	0.0070	0.1340
YM	0.0450	0.1520
YN	0.1880	0.1620
YO	0.0040	0.0810
YP	0.0450	0.1060
YQ	0.0410	0.1490
YR	0.0020	0.1310
YS	0.0020	0.1090
YT	0.0060	0.1070
YU	0.0000	0.0980
YV	0.0070	0.1440
YW	0.0070	0.1310
Z	0.1720	0.1840
a	0.6790	0.2020