



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:10 PM UTC

PDB ID : 9MKB / pdb_00009mkb
EMDB ID : EMD-48324
Title : Structure of the bacteriophage T4 portal-neck-tail complex
Authors : Fokine, A.; Zhu, J.; Klose, T.; Vago, F.; Arnaud, C.; Wang, Z.; Khare, B.;
Rossmann, M.G.; Chen, Z.; Sun, L.; Fang, Q.; Kuhn, R.; Rao, V.B.
Deposited on : 2024-12-17
Resolution : 3.80 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
MolProbity : 4-5-2 with Phenix2.0
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

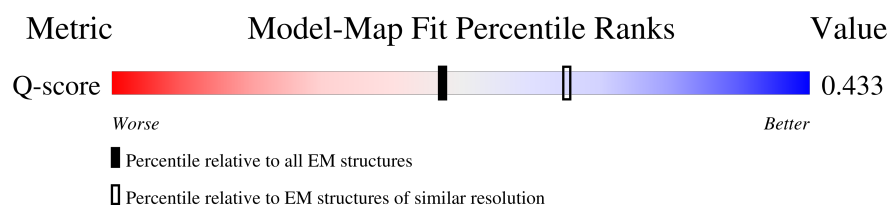
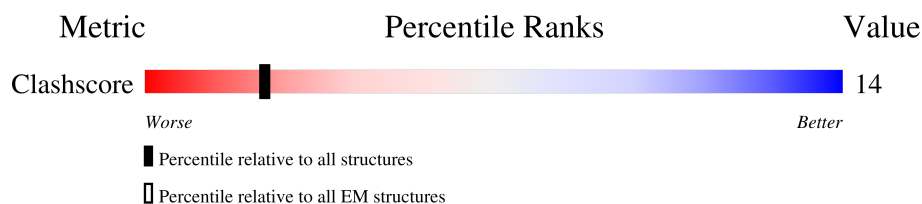
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	0	256	
1	k	256	
1	l	256	
1	m	256	
1	n	256	
1	p	256	

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Mol	Chain	Length	Quality of chain
2	1	659	
2	2	659	
2	3	659	
2	4	659	
2	5	659	
2	AD	659	
2	AK	659	
2	AL	659	
2	AM	659	
2	AN	659	
2	AO	659	
2	AP	659	
2	B1	659	
2	B2	659	
2	B3	659	
2	B4	659	
2	B5	659	
2	B6	659	
2	B7	659	
2	Bp	659	
2	Bq	659	
2	Br	659	
2	Bs	659	
2	Bt	659	
2	Bu	659	













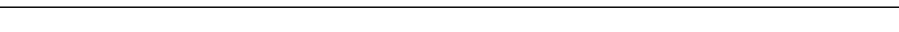

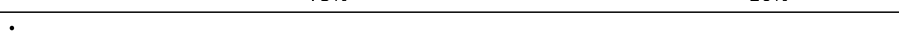

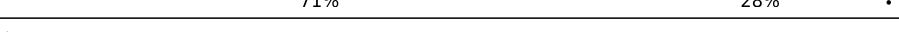








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Mol	Chain	Length	Quality of chain
2	Bv	659	 8% 71% 29%
2	Bw	659	 1% 72% 27%
2	Bx	659	 1% 70% 29%
2	By	659	 6% 75% 25%
2	Bz	659	 1% 71% 29%
2	K0	659	 1% 64% 35%
2	K1	659	 1% 70% 29%
2	K2	659	 1% 76% 24%
2	K3	659	 1% 75% 24%
2	K4	659	 1% 73% 27%
2	K5	659	 1% 73% 26%
2	K6	659	 1% 71% 28%
2	K7	659	 1% 70% 30%
2	K8	659	 1% 68% 32%
2	K9	659	 1% 72% 28%
2	L0	659	 1% 63% 37%
2	L1	659	 1% 70% 29%
2	L2	659	 1% 69% 30%
2	L3	659	 1% 74% 26%
2	L4	659	 1% 72% 27%
2	L5	659	 1% 73% 26%
2	L6	659	 1% 70% 30%
2	L7	659	 1% 71% 29%
2	L8	659	 1% 71% 29%
2	L9	659	 1% 74% 26%







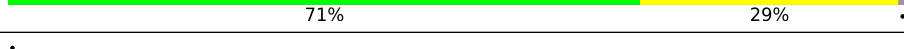
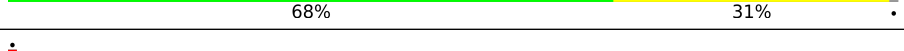
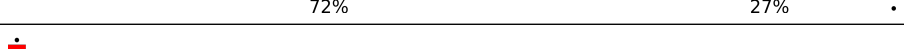
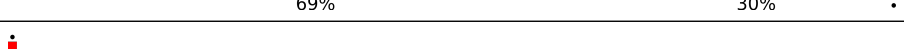
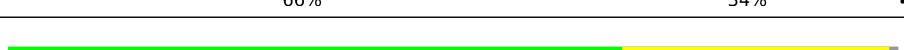

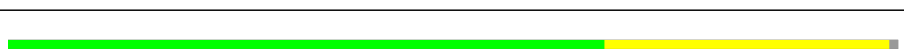

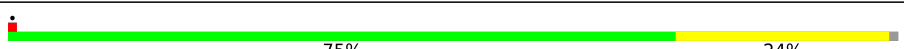





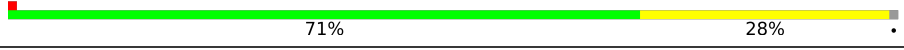
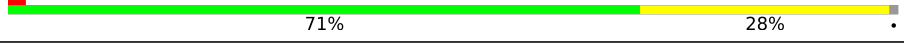



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Mol	Chain	Length	Quality of chain
2	LS	659	 69%30%.
2	LU	659	 68%31%.
2	LV	659	 71%28%.
2	LW	659	 70%30%.
2	LX	659	 72%27%.
2	LY	659	 69%30%.
2	LZ	659	 71%28%.
2	La	659	 68%32%.
2	Lb	659	 73%27%.
2	Lc	659	 71%28%.
2	Ld	659	 69%30%.
2	Le	659	 65%34%.
2	Lx	659	 67%32%.
2	Lz	659	 73%26%.
2	M0	659	 68%32%.
2	M1	659	 71%28%.
2	M2	659	 75%25%.
2	M3	659	 74%25%.
2	M4	659	 72%28%.
2	M5	659	 70%29%.
2	M6	659	 73%26%.
2	M7	659	 70%30%.
2	M8	659	 68%31%.
2	M9	659	 72%27%.
2	MS	659	 68%31%.











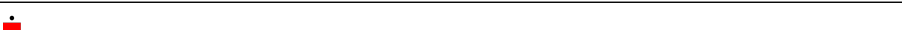

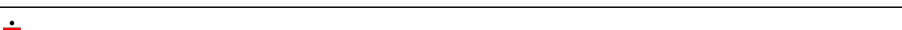
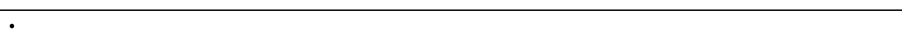











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Mol	Chain	Length	Quality of chain
2	MU	659	
2	MV	659	
2	MW	659	
2	MX	659	
2	MY	659	
2	MZ	659	
2	Ma	659	
2	Mb	659	
2	Mc	659	
2	Md	659	
2	Me	659	
2	Mx	659	
2	Mz	659	
2	NX	659	
2	NZ	659	
2	Na	659	
2	Nb	659	
2	Nc	659	
2	Nd	659	
2	Ne	659	
2	Nf	659	
2	Ng	659	
2	Nh	659	
2	Ni	659	
2	Nj	659	







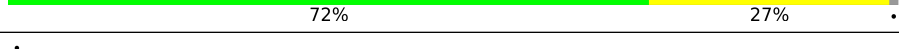
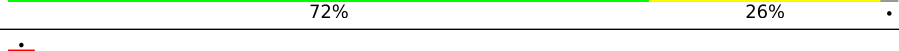
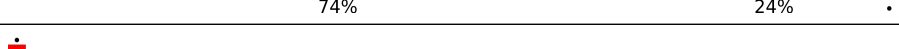
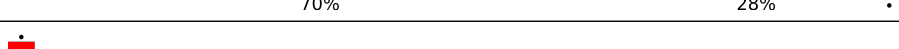
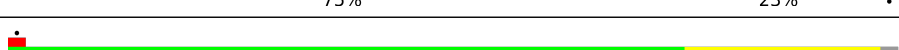

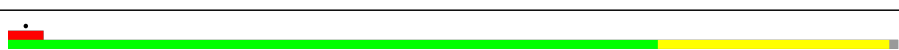

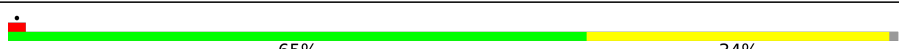





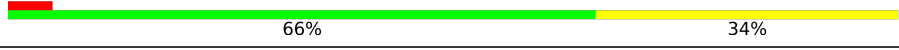
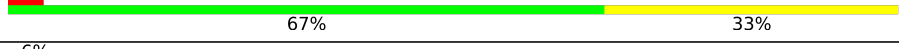



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Mol	Chain	Length	Quality of chain
2	Nx	659	 69% 31%
2	Nz	659	 71% 28%
2	b0	659	 69% 30%
2	b3	659	 70% 29%
2	b4	659	 70% 29%
2	b5	659	 72% 28%
2	b6	659	 71% 29%
2	b7	659	 72% 27%
2	b8	659	 74% 26%
2	b9	659	 71% 28%
2	bN	659	 75% 24%
2	bO	659	 74% 26%
2	bP	659	 74% 25%
2	bQ	659	 75% 25%
2	bR	659	 74% 26%
2	bY	659	 73% 26%
2	cA	659	 69% 30%
2	cB	659	 70% 29%
2	cC	659	 73% 26%
2	cD	659	 72% 28%
2	cE	659	 70% 30%
2	cF	659	 71% 28%
2	cG	659	 76% 24%
2	cH	659	 73% 27%
2	cI	659	 73% 26%



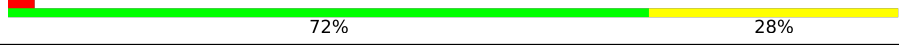

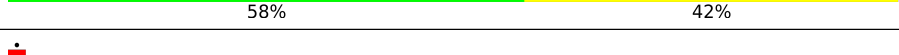
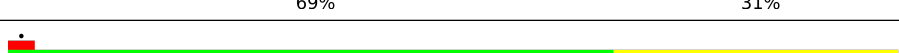
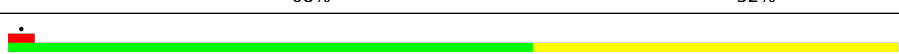
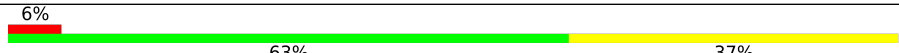


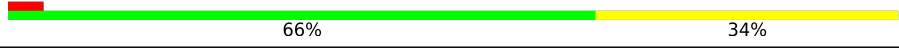




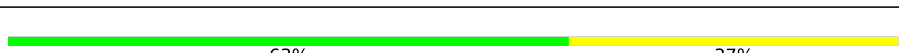


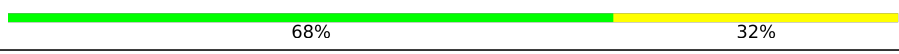


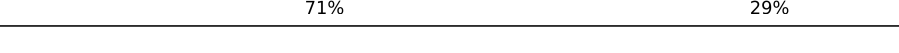



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Mol	Chain	Length	Quality of chain
2	cJ	659	
2	cK	659	
2	cL	659	
2	cM	659	
2	cN	659	
2	cO	659	
2	cP	659	
2	dS	659	
2	dT	659	
2	dU	659	
2	dV	659	
2	dW	659	
2	dZ	659	
3	6	163	
3	7	163	
3	8	163	
3	9	163	
3	AA	163	
3	AE	163	
3	AF	163	
3	AG	163	
3	AH	163	
3	AI	163	
3	AJ	163	
3	BX	163	



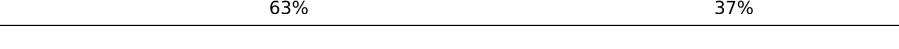
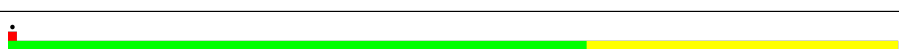



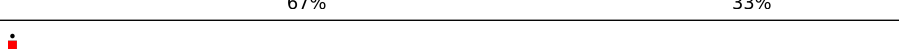



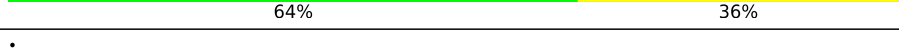

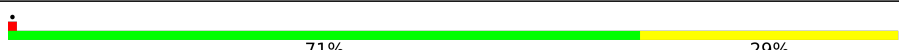


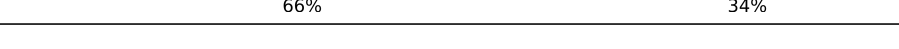







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Mol	Chain	Length	Quality of chain
3	BY	163	 65%35%
3	BZ	163	 62%38%
3	Ba	163	 72%28%
3	Bb	163	 67%33%
3	Bc	163	 58%42%
3	Bd	163	 69%31%
3	Be	163	 68%32%
3	Bf	163	 59%41%
3	Bg	163	 6%63%37%
3	Bh	163	 61%39%
3	Bi	163	 56%44%
3	Bj	163	 66%34%
3	Bk	163	 62%38%
3	Bl	163	 67%33%
3	Bm	163	 74%26%
3	Bn	163	 61%39%
3	Bo	163	 62%38%
3	OE	163	 63%37%
3	OF	163	 69%31%
3	OG	163	 70%29%.
3	OH	163	 68%32%
3	OI	163	 71%29%
3	OJ	163	 64%35%.
3	OK	163	 71%29%
3	OL	163	 77%23%.



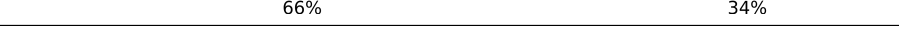
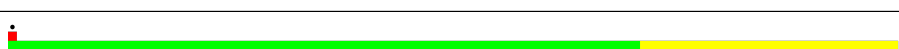



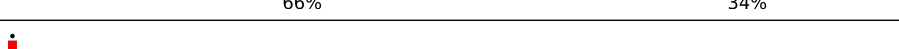



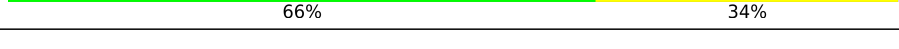

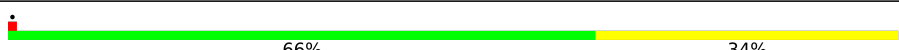


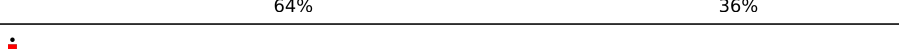







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Mol	Chain	Length	Quality of chain
3	OM	163	
3	ON	163	
3	OO	163	
3	Oj	163	
3	Ok	163	
3	Ol	163	
3	Om	163	
3	On	163	
3	Oo	163	
3	Op	163	
3	Oq	163	
3	Or	163	
3	Os	163	
3	Ot	163	
3	PE	163	
3	PF	163	
3	PG	163	
3	PH	163	
3	PI	163	
3	PJ	163	
3	PK	163	
3	PL	163	
3	PM	163	
3	PN	163	
3	PO	163	







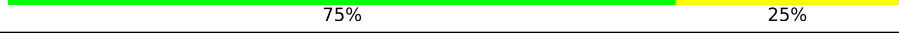
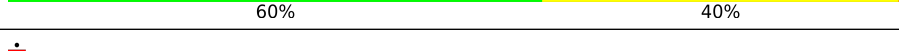
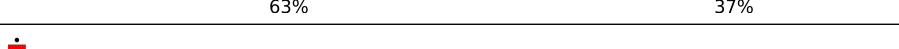
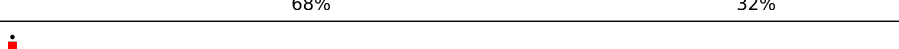
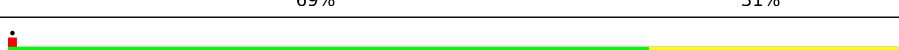

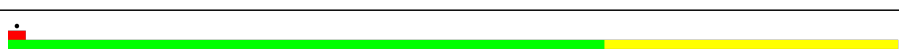

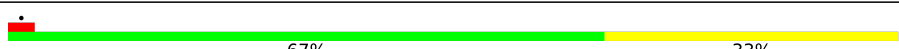





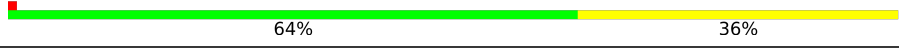
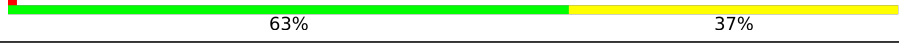



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Mol	Chain	Length	Quality of chain
3	Pj	163	
3	Pk	163	
3	Pl	163	
3	Pm	163	
3	Pn	163	
3	Po	163	
3	Pp	163	
3	Pq	163	
3	Pr	163	
3	Ps	163	
3	Pt	163	
3	RE	163	
3	RF	163	
3	RG	163	
3	RH	163	
3	RI	163	
3	RJ	163	
3	RK	163	
3	RL	163	
3	RM	163	
3	RN	163	
3	RO	163	
3	RT	163	
3	Rk	163	
3	Rl	163	







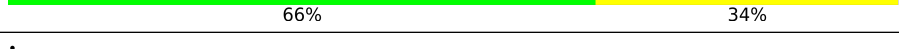
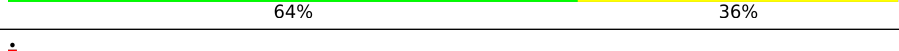
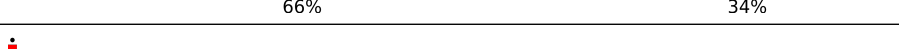
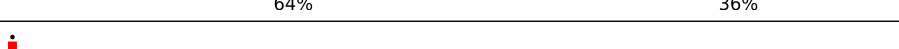
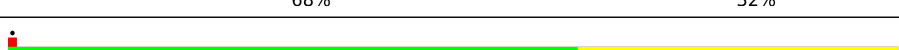

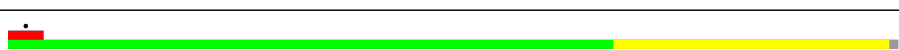












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Mol	Chain	Length	Quality of chain
3	Rm	163	
3	Rn	163	
3	Ro	163	
3	Rp	163	
3	Rq	163	
3	Rr	163	
3	Rs	163	
3	Rt	163	
3	h1	163	
3	h2	163	
3	hI	163	
3	hJ	163	
3	hK	163	
3	hL	163	
3	hM	163	
3	hX	163	
3	he	163	
3	hf	163	
3	hg	163	
3	hh	163	
3	hi	163	
3	hj	163	
3	hk	163	
3	hl	163	
3	hm	163	






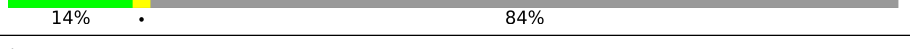

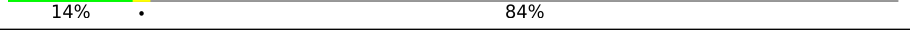
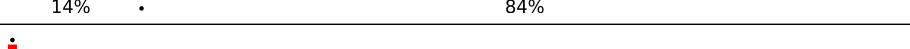
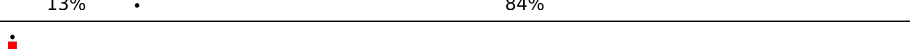















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Mol	Chain	Length	Quality of chain
3	hn	163	
3	ho	163	
3	hp	163	
3	hq	163	
3	hr	163	
3	hs	163	
3	ht	163	
3	hu	163	
3	hv	163	
3	hw	163	
3	hx	163	
3	hy	163	
3	hz	163	
3	o	163	
4	A	487	
4	B	487	
4	C	487	
4	D	487	
4	E	487	
4	F	487	
4	G	487	
4	H	487	
4	I	487	
4	J	487	
4	K	487	

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Mol	Chain	Length	Quality of chain	
4	L	487		
4	M	487		
4	N	487		
4	O	487		
4	P	487		
4	Q	487		
4	R	487		
4	S	487		
4	T	487		
4	U	487		
4	V	487		
4	W	487		
4	X	487		
4	Y	487		
4	Z	487		
4	a	487		
4	b	487		
4	c	487		
4	d	487		
4	e	487		
4	f	487		
4	g	487		
4	h	487		
4	i	487		
4	j	487		

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Mol	Chain	Length	Quality of chain
5	A0	524	
5	A1	524	
5	A2	524	
5	A3	524	
5	Av	524	
5	Ax	524	
5	BA	524	
5	BB	524	
5	BD	524	
5	BF	524	
5	BG	524	
5	BH	524	
6	A4	521	
6	A5	521	
6	A7	521	
6	A8	521	
6	A9	521	
6	AV	521	
6	AW	521	
6	AX	521	
6	AZ	521	
6	Ac	521	
6	Ad	521	
6	Ae	521	
6	Af	521	

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Mol	Chain	Length	Quality of chain
6	Ag	521	
6	Ah	521	
6	Ai	521	
6	Aj	521	
6	Ak	521	
6	Am	521	
6	An	521	
6	Ao	521	
6	Ap	521	
6	Au	521	
6	Aw	521	
6	Ay	521	
6	Az	521	
6	BI	521	
6	BJ	521	
6	BK	521	
6	BM	521	
7	A6	309	
7	AY	309	
7	Aa	309	
7	Ab	309	
7	Al	309	
7	Aq	309	
7	Ar	309	
7	As	309	




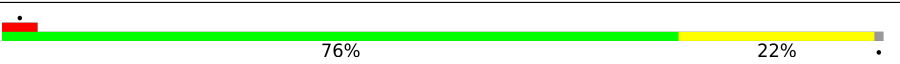
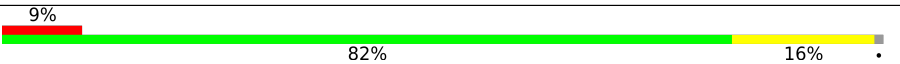

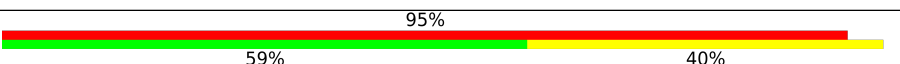
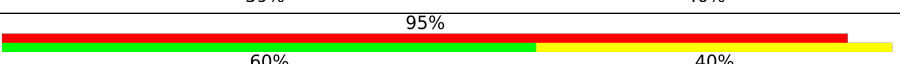
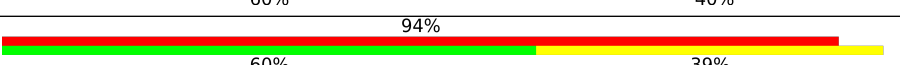
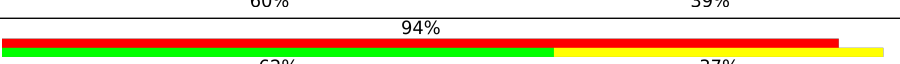
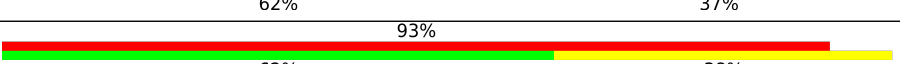
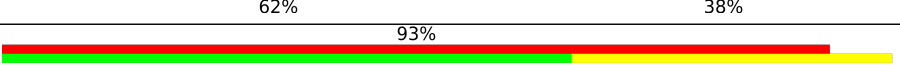
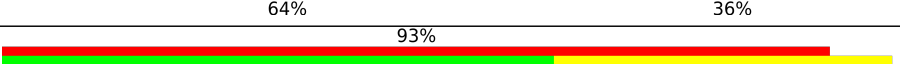
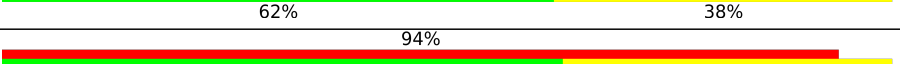
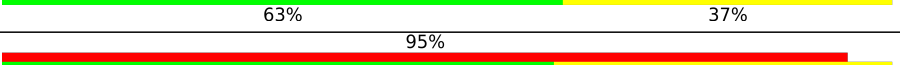
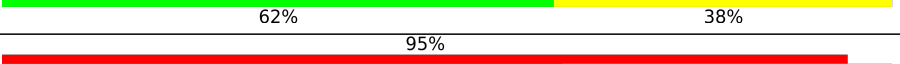
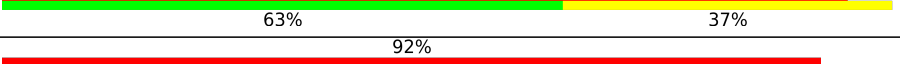
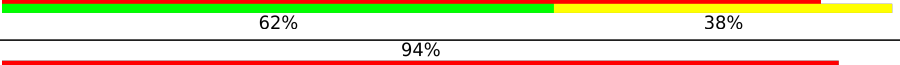
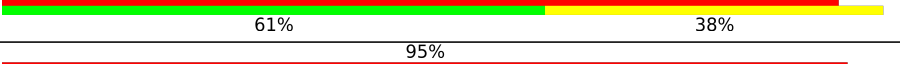
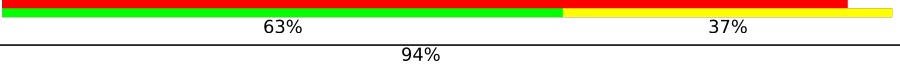
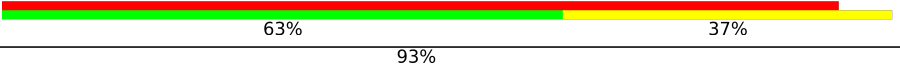

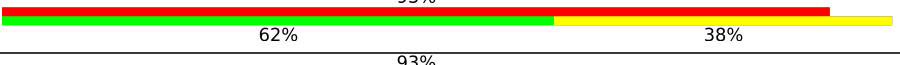
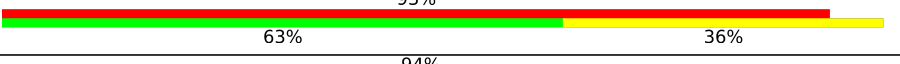
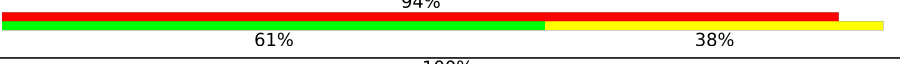
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Mol	Chain	Length	Quality of chain
7	At	309	
7	BC	309	
7	BE	309	
7	BL	309	
8	AB	272	
8	q	272	
8	r	272	
8	s	272	
8	t	272	
8	u	272	
9	AC	176	
9	v	176	
9	w	176	
9	x	176	
9	y	176	
9	z	176	
10	AQ	376	
10	AR	376	
10	AS	376	
10	AT	376	
10	AU	376	
11	BN	80	
11	BO	80	
11	BP	80	
11	BQ	80	

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Mol	Chain	Length	Quality of chain
11	BR	80	
11	BS	80	
11	BT	80	
11	BU	80	
11	BV	80	
11	BW	80	
12	S0	527	
12	S1	527	
12	S2	527	
12	S3	527	
12	S4	527	
12	S5	527	
12	S6	527	
12	S7	527	
12	S8	527	
12	SA	527	
12	SO	527	
12	SP	527	
12	SQ	527	
12	Sv	527	
12	Sw	527	
12	Sx	527	
12	Sy	527	
12	Sz	527	
13	T1	288	

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Mol	Chain	Length	Quality of chain	
13	T2	288	100%	27%
13	T3	288	100%	34%
13	T4	288	100%	32%
13	T5	288	99%	25%
13	T6	288	100%	27%
13	T7	288	100%	31%
13	T8	288	100%	26%
13	T9	288	100%	31%
13	TF	288	99%	32%
13	TG	288	100%	27%
13	TH	288	100%	29%
13	Td	288	100%	35%
13	Te	288	99%	31%
13	Tf	288	100%	26%
13	Tg	288	99%	29%
13	Th	288	100%	27%
13	Ti	288	99%	31%
14	UL	219	98%	35%
14	UM	219	98%	37%
14	UN	219	96%	42%
14	Up	219	98%	36%
14	Uq	219	98%	36%
14	Ur	219	98%	39%
14	Us	219	99%	37%
14	Ut	219	97%	30%

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Mol	Chain	Length	Quality of chain
14	Uu	219	<div>97%</div> <div>64% 35%</div>
14	VL	219	<div>98%</div> <div>62% 37%</div>
14	VM	219	<div>99%</div> <div>61% 39%</div>
14	VN	219	<div>97%</div> <div>69% 31%</div>
14	Vp	219	<div>98%</div> <div>65% 35%</div>
14	Vq	219	<div>100%</div> <div>65% 35%</div>
14	Vr	219	<div>99%</div> <div>62% 37%</div>
14	Vs	219	<div>99%</div> <div>63% 36%</div>
14	Vt	219	<div>96%</div> <div>64% 35%</div>
14	Vu	219	<div>97%</div> <div>61% 38%</div>
15	WI	602	<div>78%</div> <div>59% 41%</div>
15	WJ	602	<div>70%</div> <div>60% 40%</div>
15	WK	602	<div>72%</div> <div>56% 44%</div>
15	Wj	602	<div>77%</div> <div>57% 43%</div>
15	Wk	602	<div>81%</div> <div>60% 40%</div>
15	Wl	602	<div>74%</div> <div>57% 43%</div>
15	Wm	602	<div>73%</div> <div>60% 40%</div>
15	Wn	602	<div>74%</div> <div>58% 42%</div>
15	Wo	602	<div>76%</div> <div>58% 42%</div>
15	XI	602	<div>80%</div> <div>57% 43%</div>
15	XJ	602	<div>75%</div> <div>58% 42%</div>
15	XK	602	<div>76%</div> <div>61% 39%</div>
15	Xj	602	<div>80%</div> <div>59% 41%</div>
15	Xk	602	<div>77%</div> <div>60% 40%</div>
15	Xl	602	<div>76%</div> <div>58% 42%</div>



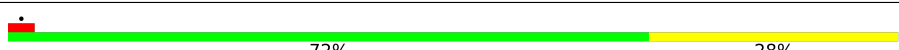
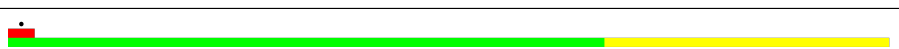

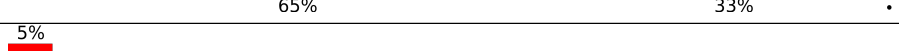
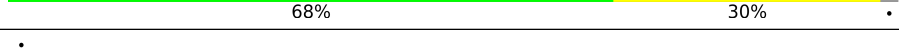





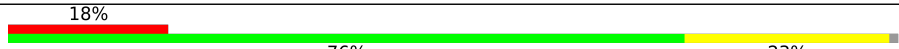


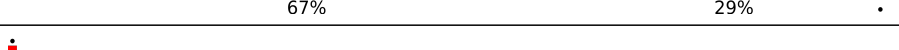

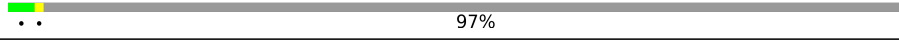
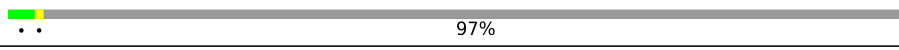
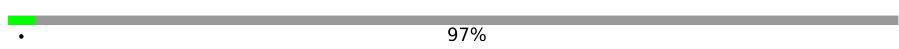




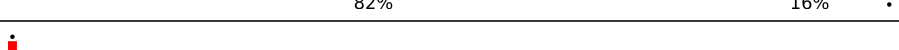
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Mol	Chain	Length	Quality of chain
15	Xm	602	
15	Xn	602	
15	Xo	602	
16	YC	1032	
16	YX	1032	
16	YY	1032	
16	Yc	1032	
16	Yx	1032	
16	Yy	1032	
17	ZD	334	
17	ZE	334	
17	ZZ	334	
17	Za	334	
17	Zb	334	
17	Zc	334	
17	aD	334	
17	aE	334	
17	aZ	334	
17	aa	334	
17	ab	334	
17	ac	334	
18	eB	660	
18	eU	660	
18	eW	660	
18	f9	660	

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Mol	Chain	Length	Quality of chain
18	fA	660	
18	fB	660	
18	fR	660	
18	fS	660	
18	fU	660	
18	fW	660	
18	fr	660	
18	fs	660	
19	gE	575	
19	gG	575	
19	gH	575	
20	gd	97	
21	iC	391	
21	iD	391	
21	iF	391	
22	ja	590	
22	jb	590	
22	jc	590	
23	k3	196	
23	k4	196	
23	k7	196	
23	k8	196	
23	kV	196	
23	lV	196	
24	m1	132	

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Mol	Chain	Length	Quality of chain
24	m2	132	
24	m5	132	
24	m6	132	
24	mT	132	
24	nT	132	
25	o0	364	
25	o1	364	
25	o2	364	
25	o6	364	
25	pA	364	
25	pB	364	
26	q3	320	
26	q4	320	
26	q5	320	
26	q7	320	
26	q8	320	
26	q9	320	
27	rc	25	
27	rd	25	
27	re	25	
27	rf	25	
27	rg	25	
27	rh	25	
28	sQ	18	
28	sT	18	

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Mol	Chain	Length	Quality of chain
28	sU	18	
29	tS	10	
29	tX	10	
29	tY	10	
30	uR	7	
30	uV	7	
30	uW	7	
31	vZ	9	
31	va	9	
31	vb	9	

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 1533268 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 gp14, neck protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	244	Total 1993	C 1279	N 323	O 387	S 4	0	0
1	k	244	Total 1993	C 1279	N 323	O 387	S 4	0	0
1	l	244	Total 1993	C 1279	N 323	O 387	S 4	0	0
1	m	244	Total 1993	C 1279	N 323	O 387	S 4	0	0
1	n	244	Total 1993	C 1279	N 323	O 387	S 4	0	0
1	p	244	Total 1993	C 1279	N 323	O 387	S 4	0	0

- Molecule 2 is a protein called gp18, tail sheath protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	653	Total 4985	C 3142	N 839	O 993	S 11	0	0
2	2	653	Total 4985	C 3142	N 839	O 993	S 11	0	0
2	3	653	Total 4985	C 3142	N 839	O 993	S 11	0	0
2	4	653	Total 4985	C 3142	N 839	O 993	S 11	0	0
2	5	653	Total 4985	C 3142	N 839	O 993	S 11	0	0
2	AD	653	Total 4985	C 3142	N 839	O 993	S 11	0	0
2	AK	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	AL	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	AM	655	Total 5000	C 3152	N 841	O 996	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	AN	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	AO	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	AP	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B1	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B2	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B3	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B4	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B5	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B6	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	B7	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bp	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bq	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Br	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bs	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bt	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bu	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bv	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bw	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bx	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	By	655	Total 5000	C 3152	N 841	O 996	S 11	0	0
2	Bz	655	Total 5000	C 3152	N 841	O 996	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	K0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K1	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K2	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	K9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L1	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L2	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	L9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	LS	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	LU	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	LV	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	LW	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	LX	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	LY	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	LZ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	La	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Lb	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Lc	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Ld	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Le	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Lx	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Lz	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M1	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M2	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	M8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	M9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MS	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MU	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MV	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MW	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MX	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MY	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	MZ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Ma	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Mb	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Mc	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Md	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Me	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Mx	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Mz	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	NX	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	NZ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Na	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nb	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nc	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Nd	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Ne	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nf	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Ng	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nh	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Ni	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nj	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nx	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	Nz	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	b9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	bN	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	bO	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	bP	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	bQ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	bR	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	bY	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cA	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cB	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cC	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cD	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cE	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cF	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cG	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cH	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cI	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cJ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cK	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cL	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cM	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cN	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cO	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	cP	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
2	dS	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
2	dT	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
2	dU	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	dV	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
2	dW	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		
2	dZ	647	Total	C	N	O	S	0	0
			4941	3115	833	982	11		

There are 414 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	109	ASN	SER	conflict	UNP A0A7S9SVW9
1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
2	109	ASN	SER	conflict	UNP A0A7S9SVW9
2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
3	109	ASN	SER	conflict	UNP A0A7S9SVW9
3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
4	109	ASN	SER	conflict	UNP A0A7S9SVW9
4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
5	109	ASN	SER	conflict	UNP A0A7S9SVW9
5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AD	109	ASN	SER	conflict	UNP A0A7S9SVW9
AD	301	GLY	GLU	conflict	UNP A0A7S9SVW9
AD	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AK	109	ASN	SER	conflict	UNP A0A7S9SVW9
AK	301	GLY	GLU	conflict	UNP A0A7S9SVW9
AK	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AL	109	ASN	SER	conflict	UNP A0A7S9SVW9
AL	301	GLY	GLU	conflict	UNP A0A7S9SVW9
AL	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AM	109	ASN	SER	conflict	UNP A0A7S9SVW9
AM	301	GLY	GLU	conflict	UNP A0A7S9SVW9
AM	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AN	109	ASN	SER	conflict	UNP A0A7S9SVW9
AN	301	GLY	GLU	conflict	UNP A0A7S9SVW9
AN	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AO	109	ASN	SER	conflict	UNP A0A7S9SVW9
AO	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
AO	399	VAL	ALA	conflict	UNP A0A7S9SVW9
AP	109	ASN	SER	conflict	UNP A0A7S9SVW9
AP	301	GLY	GLU	conflict	UNP A0A7S9SVW9
AP	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B1	109	ASN	SER	conflict	UNP A0A7S9SVW9
B1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B2	109	ASN	SER	conflict	UNP A0A7S9SVW9
B2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B3	109	ASN	SER	conflict	UNP A0A7S9SVW9
B3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B4	109	ASN	SER	conflict	UNP A0A7S9SVW9
B4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B5	109	ASN	SER	conflict	UNP A0A7S9SVW9
B5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B6	109	ASN	SER	conflict	UNP A0A7S9SVW9
B6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
B7	109	ASN	SER	conflict	UNP A0A7S9SVW9
B7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
B7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bp	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bp	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bp	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bq	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bq	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bq	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Br	109	ASN	SER	conflict	UNP A0A7S9SVW9
Br	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Br	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bs	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bs	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bs	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bt	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bt	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bt	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bu	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bu	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
Bu	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bv	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bv	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bv	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bw	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bw	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bw	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
By	109	ASN	SER	conflict	UNP A0A7S9SVW9
By	301	GLY	GLU	conflict	UNP A0A7S9SVW9
By	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Bz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Bz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Bz	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K0	109	ASN	SER	conflict	UNP A0A7S9SVW9
K0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K1	109	ASN	SER	conflict	UNP A0A7S9SVW9
K1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K2	109	ASN	SER	conflict	UNP A0A7S9SVW9
K2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K3	109	ASN	SER	conflict	UNP A0A7S9SVW9
K3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K4	109	ASN	SER	conflict	UNP A0A7S9SVW9
K4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K5	109	ASN	SER	conflict	UNP A0A7S9SVW9
K5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K6	109	ASN	SER	conflict	UNP A0A7S9SVW9
K6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K7	109	ASN	SER	conflict	UNP A0A7S9SVW9
K7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K8	109	ASN	SER	conflict	UNP A0A7S9SVW9
K8	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
K8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K9	109	ASN	SER	conflict	UNP A0A7S9SVW9
K9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L0	109	ASN	SER	conflict	UNP A0A7S9SVW9
L0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L1	109	ASN	SER	conflict	UNP A0A7S9SVW9
L1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L2	109	ASN	SER	conflict	UNP A0A7S9SVW9
L2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L3	109	ASN	SER	conflict	UNP A0A7S9SVW9
L3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L4	109	ASN	SER	conflict	UNP A0A7S9SVW9
L4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L5	109	ASN	SER	conflict	UNP A0A7S9SVW9
L5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L6	109	ASN	SER	conflict	UNP A0A7S9SVW9
L6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L7	109	ASN	SER	conflict	UNP A0A7S9SVW9
L7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L8	109	ASN	SER	conflict	UNP A0A7S9SVW9
L8	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L9	109	ASN	SER	conflict	UNP A0A7S9SVW9
L9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LS	109	ASN	SER	conflict	UNP A0A7S9SVW9
LS	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LS	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LU	109	ASN	SER	conflict	UNP A0A7S9SVW9
LU	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LU	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LV	109	ASN	SER	conflict	UNP A0A7S9SVW9
LV	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
LV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LW	109	ASN	SER	conflict	UNP A0A7S9SVW9
LW	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LX	109	ASN	SER	conflict	UNP A0A7S9SVW9
LX	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LX	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LY	109	ASN	SER	conflict	UNP A0A7S9SVW9
LY	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LY	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
LZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
La	109	ASN	SER	conflict	UNP A0A7S9SVW9
La	301	GLY	GLU	conflict	UNP A0A7S9SVW9
La	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lb	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lb	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lb	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lc	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lc	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lc	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ld	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ld	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ld	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Le	109	ASN	SER	conflict	UNP A0A7S9SVW9
Le	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Le	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lz	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M0	109	ASN	SER	conflict	UNP A0A7S9SVW9
M0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M1	109	ASN	SER	conflict	UNP A0A7S9SVW9
M1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M2	109	ASN	SER	conflict	UNP A0A7S9SVW9
M2	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
M2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M3	109	ASN	SER	conflict	UNP A0A7S9SVW9
M3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M4	109	ASN	SER	conflict	UNP A0A7S9SVW9
M4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M5	109	ASN	SER	conflict	UNP A0A7S9SVW9
M5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M6	109	ASN	SER	conflict	UNP A0A7S9SVW9
M6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M7	109	ASN	SER	conflict	UNP A0A7S9SVW9
M7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M8	109	ASN	SER	conflict	UNP A0A7S9SVW9
M8	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M9	109	ASN	SER	conflict	UNP A0A7S9SVW9
M9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MS	109	ASN	SER	conflict	UNP A0A7S9SVW9
MS	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MS	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MU	109	ASN	SER	conflict	UNP A0A7S9SVW9
MU	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MU	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MV	109	ASN	SER	conflict	UNP A0A7S9SVW9
MV	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MW	109	ASN	SER	conflict	UNP A0A7S9SVW9
MW	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MX	109	ASN	SER	conflict	UNP A0A7S9SVW9
MX	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MX	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MY	109	ASN	SER	conflict	UNP A0A7S9SVW9
MY	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MY	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
MZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
MZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ma	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ma	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ma	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mb	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mb	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mb	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mc	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mc	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mc	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Md	109	ASN	SER	conflict	UNP A0A7S9SVW9
Md	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Md	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Me	109	ASN	SER	conflict	UNP A0A7S9SVW9
Me	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Me	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mz	399	VAL	ALA	conflict	UNP A0A7S9SVW9
NX	109	ASN	SER	conflict	UNP A0A7S9SVW9
NX	301	GLY	GLU	conflict	UNP A0A7S9SVW9
NX	399	VAL	ALA	conflict	UNP A0A7S9SVW9
NZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
NZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
NZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Na	109	ASN	SER	conflict	UNP A0A7S9SVW9
Na	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Na	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nb	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nb	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nb	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nc	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nc	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nc	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nd	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nd	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nd	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ne	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ne	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
Ne	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nf	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nf	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nf	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ng	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ng	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ng	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nh	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nh	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nh	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ni	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ni	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ni	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nj	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nj	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nj	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nz	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b0	109	ASN	SER	conflict	UNP A0A7S9SVW9
b0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b3	109	ASN	SER	conflict	UNP A0A7S9SVW9
b3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b4	109	ASN	SER	conflict	UNP A0A7S9SVW9
b4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b5	109	ASN	SER	conflict	UNP A0A7S9SVW9
b5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b6	109	ASN	SER	conflict	UNP A0A7S9SVW9
b6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b7	109	ASN	SER	conflict	UNP A0A7S9SVW9
b7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b8	109	ASN	SER	conflict	UNP A0A7S9SVW9
b8	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
b8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
b9	109	ASN	SER	conflict	UNP A0A7S9SVW9
b9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
b9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bN	109	ASN	SER	conflict	UNP A0A7S9SVW9
bN	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bN	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bO	109	ASN	SER	conflict	UNP A0A7S9SVW9
bO	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bO	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bP	109	ASN	SER	conflict	UNP A0A7S9SVW9
bP	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bP	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bQ	109	ASN	SER	conflict	UNP A0A7S9SVW9
bQ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bQ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bR	109	ASN	SER	conflict	UNP A0A7S9SVW9
bR	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bR	399	VAL	ALA	conflict	UNP A0A7S9SVW9
bY	109	ASN	SER	conflict	UNP A0A7S9SVW9
bY	301	GLY	GLU	conflict	UNP A0A7S9SVW9
bY	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cA	109	ASN	SER	conflict	UNP A0A7S9SVW9
cA	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cA	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cB	109	ASN	SER	conflict	UNP A0A7S9SVW9
cB	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cB	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cC	109	ASN	SER	conflict	UNP A0A7S9SVW9
cC	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cC	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cD	109	ASN	SER	conflict	UNP A0A7S9SVW9
cD	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cD	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cE	109	ASN	SER	conflict	UNP A0A7S9SVW9
cE	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cE	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cF	109	ASN	SER	conflict	UNP A0A7S9SVW9
cF	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cF	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cG	109	ASN	SER	conflict	UNP A0A7S9SVW9
cG	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
cG	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cH	109	ASN	SER	conflict	UNP A0A7S9SVW9
cH	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cH	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cI	109	ASN	SER	conflict	UNP A0A7S9SVW9
cI	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cI	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cJ	109	ASN	SER	conflict	UNP A0A7S9SVW9
cJ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cJ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cK	109	ASN	SER	conflict	UNP A0A7S9SVW9
cK	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cK	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cL	109	ASN	SER	conflict	UNP A0A7S9SVW9
cL	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cL	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cM	109	ASN	SER	conflict	UNP A0A7S9SVW9
cM	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cM	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cN	109	ASN	SER	conflict	UNP A0A7S9SVW9
cN	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cN	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cO	109	ASN	SER	conflict	UNP A0A7S9SVW9
cO	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cO	399	VAL	ALA	conflict	UNP A0A7S9SVW9
cP	109	ASN	SER	conflict	UNP A0A7S9SVW9
cP	301	GLY	GLU	conflict	UNP A0A7S9SVW9
cP	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dS	109	ASN	SER	conflict	UNP A0A7S9SVW9
dS	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dS	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dT	109	ASN	SER	conflict	UNP A0A7S9SVW9
dT	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dT	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dU	109	ASN	SER	conflict	UNP A0A7S9SVW9
dU	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dU	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dV	109	ASN	SER	conflict	UNP A0A7S9SVW9
dV	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dW	109	ASN	SER	conflict	UNP A0A7S9SVW9
dW	301	GLY	GLU	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
dW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
dZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
dZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
dZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9

- Molecule 3 is a protein called gp19, tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	162	Total	C	N	O	S	0	0
			1296	823	218	252	3		
3	7	162	Total	C	N	O	S	0	0
			1296	823	218	252	3		
3	8	162	Total	C	N	O	S	0	0
			1296	823	218	252	3		
3	9	162	Total	C	N	O	S	0	0
			1296	823	218	252	3		
3	AA	162	Total	C	N	O	S	0	0
			1296	823	218	252	3		
3	AE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	AF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	AG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	AH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	AI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	AJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	BX	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	BY	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	BZ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Ba	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bb	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bc	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Bd	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Be	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bf	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bg	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bh	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bi	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Bo	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	ON	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	OO	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Oj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Ok	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Ol	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Om	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	On	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Oo	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Op	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Oq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Or	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Os	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Ot	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	PM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PN	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	PO	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Po	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pp	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pr	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Ps	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Pt	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	RL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RN	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RO	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	RT	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Ro	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rp	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rr	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rs	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	Rt	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	h1	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	h2	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	hM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hX	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	he	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hf	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hg	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hh	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hi	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	ho	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hp	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hr	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hs	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	ht	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hu	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hv	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hw	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	hx	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hy	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	hz	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
3	o	162	Total	C	N	O	S	0	0
			1296	823	218	252	3		

- Molecule 4 is a protein called gpwac, fibrinin.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	B	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	C	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	D	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	E	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	F	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	G	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	H	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	I	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	J	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	K	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	L	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	M	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	N	79	Total	C	N	O	S	0	0
			601	373	102	125	1		
4	O	79	Total	C	N	O	S	0	0
			601	373	102	125	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	Q	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	R	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	S	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	T	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	U	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	V	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	W	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	X	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	Y	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	Z	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	a	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	b	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	c	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	d	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	e	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	f	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	g	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	h	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	i	79	Total 601	C 373	N 102	O 125	S 1	0	0
4	j	79	Total 601	C 373	N 102	O 125	S 1	0	0

- Molecule 5 is a protein called gp20, portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A0	507	Total	C	N	O	S	0	0
			4140	2611	717	790	22		
5	A1	507	Total	C	N	O	S	0	0
			4140	2611	717	790	22		
5	A2	506	Total	C	N	O	S	0	0
			4132	2607	715	788	22		
5	A3	506	Total	C	N	O	S	0	0
			4132	2607	715	788	22		
5	Av	506	Total	C	N	O	S	0	0
			4132	2607	715	788	22		
5	Ax	506	Total	C	N	O	S	0	0
			4132	2607	715	788	22		
5	BA	500	Total	C	N	O	S	0	0
			4074	2571	707	776	20		
5	BB	488	Total	C	N	O	S	0	0
			3995	2517	695	761	22		
5	BD	506	Total	C	N	O	S	0	0
			4132	2607	715	788	22		
5	BF	506	Total	C	N	O	S	0	0
			4132	2607	715	788	22		
5	BG	497	Total	C	N	O	S	0	0
			4039	2549	702	768	20		
5	BH	506	Total	C	N	O	S	0	0
			4091	2582	710	779	20		

- Molecule 6 is a protein called gp23, major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A4	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	A5	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	A7	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	A8	440	Total	C	N	O	S	0	0
			3311	2099	564	633	15		
6	A9	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	AV	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	AW	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AX	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	AZ	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ac	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ad	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ae	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Af	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ag	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ah	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ai	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Aj	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ak	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Am	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	An	440	Total	C	N	O	S	0	0
			3311	2099	564	633	15		
6	Ao	437	Total	C	N	O	S	0	0
			3291	2088	560	628	15		
6	Ap	440	Total	C	N	O	S	0	0
			3311	2099	564	633	15		
6	Au	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Aw	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Ay	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	Az	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	BI	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	BJ	437	Total	C	N	O	S	0	0
			3291	2088	560	628	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	BK	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		
6	BM	456	Total	C	N	O	S	0	0
			3425	2167	584	659	15		

- Molecule 7 is a protein called gp13, neck protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A6	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	AY	308	Total	C	N	O	S	0	0
			2435	1550	412	460	13		
7	Aa	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	Ab	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	Al	308	Total	C	N	O	S	0	0
			2435	1550	412	460	13		
7	Aq	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	Ar	290	Total	C	N	O	S	0	0
			2310	1473	389	437	11		
7	As	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	At	298	Total	C	N	O	S	0	0
			2371	1512	402	445	12		
7	BC	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	BE	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		
7	BL	308	Total	C	N	O	S	0	0
			2438	1551	413	461	13		

- Molecule 8 is a protein called gp15, tail terminator protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AB	272	Total	C	N	O	S	0	0
			2227	1424	369	425	9		
8	q	272	Total	C	N	O	S	0	0
			2227	1424	369	425	9		
8	r	272	Total	C	N	O	S	0	0
			2227	1424	369	425	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	s	272	Total	C	N	O	S	0	0
			2227	1424	369	425	9		
8	t	272	Total	C	N	O	S	0	0
			2227	1424	369	425	9		
8	u	272	Total	C	N	O	S	0	0
			2227	1424	369	425	9		

- Molecule 9 is a protein called gp3, tube terminator protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AC	175	Total	C	N	O	S	0	0
			1383	890	215	274	4		
9	v	175	Total	C	N	O	S	0	0
			1383	890	215	274	4		
9	w	175	Total	C	N	O	S	0	0
			1383	890	215	274	4		
9	x	175	Total	C	N	O	S	0	0
			1383	890	215	274	4		
9	y	175	Total	C	N	O	S	0	0
			1383	890	215	274	4		
9	z	175	Total	C	N	O	S	0	0
			1383	890	215	274	4		

- Molecule 10 is a protein called Hoc, highly immunogenic outer capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AQ	96	Total	C	N	O	S	0	0
			805	519	129	152	5		
10	AR	96	Total	C	N	O	S	0	0
			805	519	129	152	5		
10	AS	96	Total	C	N	O	S	0	0
			805	519	129	152	5		
10	AT	96	Total	C	N	O	S	0	0
			805	519	129	152	5		
10	AU	96	Total	C	N	O	S	0	0
			805	519	129	152	5		

- Molecule 11 is a protein called Soc, small outer capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BN	79	Total	C	N	O		0	0
			636	405	106	125			

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Mol	Chain	Residues	Atoms				AltConf	Trace
11	BO	79	Total 636	C 405	N 106	O 125	0	0
11	BP	79	Total 636	C 405	N 106	O 125	0	0
11	BQ	79	Total 636	C 405	N 106	O 125	0	0
11	BR	79	Total 636	C 405	N 106	O 125	0	0
11	BS	79	Total 636	C 405	N 106	O 125	0	0
11	BT	79	Total 636	C 405	N 106	O 125	0	0
11	BU	79	Total 636	C 405	N 106	O 125	0	0
11	BV	79	Total 636	C 405	N 106	O 125	0	0
11	BW	79	Total 636	C 405	N 106	O 125	0	0

- Molecule 12 is a protein called gp12, short tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S0	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S1	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S2	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S3	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S4	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S5	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S6	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S7	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	S8	526	Total 3945	C 2429	N 702	O 803	S 11	0	0
12	SA	526	Total 3945	C 2429	N 702	O 803	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	SO	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	SP	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	SQ	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	Sv	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	Sw	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	Sx	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	Sy	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		
12	Sz	526	Total	C	N	O	S	0	0
			3945	2429	702	803	11		

- Molecule 13 is a protein called gp9, baseplate wedge tail fiber connector.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T1	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T2	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T3	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T4	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T5	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T6	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T7	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T8	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	T9	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	TF	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	TG	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	TH	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	Td	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	Te	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	Tf	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	Tg	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	Th	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		
13	Ti	288	Total	C	N	O	S	0	0
			2175	1354	366	446	9		

- Molecule 14 is a protein called gp11, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UL	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	UM	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	UN	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Up	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Uq	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Ur	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Us	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Ut	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Uu	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	VL	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	VM	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	VN	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	Vp	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Vq	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Vr	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Vs	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Vt	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		
14	Vu	218	Total	C	N	O	S	0	0
			1665	1056	273	334	2		

- Molecule 15 is a protein called gp10, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	WI	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	WJ	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	WK	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Wj	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Wk	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Wl	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Wm	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Wn	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Wo	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	XI	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	XJ	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	XK	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Xj	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	Xk	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Xl	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Xm	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Xn	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		
15	Xo	602	Total	C	N	O	S	0	0
			4675	2933	779	953	10		

- Molecule 16 is a protein called gp7, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	YC	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
16	YX	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
16	YY	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
16	Yc	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
16	Yx	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		
16	Yy	1004	Total	C	N	O	S	0	0
			8199	5247	1347	1578	27		

- Molecule 17 is a protein called gp8, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	ZD	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
17	ZE	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
17	ZZ	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
17	Za	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
17	Zb	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
17	Zc	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	aD	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
17	aE	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
17	aZ	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
17	aa	328	Total	C	N	O	S	0	0
			2631	1677	430	507	17		
17	ab	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		
17	ac	332	Total	C	N	O	S	0	0
			2658	1692	434	515	17		

- Molecule 18 is a protein called gp6, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	eB	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
18	eU	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
18	eW	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
18	f9	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
18	fA	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
18	fB	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
18	fR	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
18	fS	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
18	fU	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
18	fW	648	Total	C	N	O	S	0	0
			5157	3259	854	1034	10		
18	fr	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		
18	fs	658	Total	C	N	O	S	0	0
			5235	3308	867	1050	10		

- Molecule 19 is a protein called gp5, baseplate central spike protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	gE	559	Total	C	N	O	S	0	0
			4321	2681	761	856	23		
19	gG	559	Total	C	N	O	S	0	0
			4321	2681	761	856	23		
19	gH	559	Total	C	N	O	S	0	0
			4321	2681	761	856	23		

- Molecule 20 is a protein called gp5.4, tip of the central spike.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	gd	96	Total	C	N	O	S	0	0
			709	447	120	139	3		

- Molecule 21 is a protein called gp27, baseplate hub protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	iC	375	Total	C	N	O	S	0	0
			3000	1916	491	575	18		
21	iD	375	Total	C	N	O	S	0	0
			3000	1916	491	575	18		
21	iF	375	Total	C	N	O	S	0	0
			3000	1916	491	575	18		

- Molecule 22 is a protein called gp29, tape measure protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	ja	20	Total	C	N	O	S	0	0
			137	84	22	30	1		
22	jb	20	Total	C	N	O	S	0	0
			137	84	22	30	1		
22	jc	20	Total	C	N	O	S	0	0
			137	84	22	30	1		

- Molecule 23 is a protein called gp53, baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	k3	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
23	k4	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
23	k7	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
23	k8	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
23	kV	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		
23	lV	193	Total	C	N	O	S	0	0
			1599	1035	259	299	6		

- Molecule 24 is a protein called gp25, baseplate protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	m1	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
24	m2	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
24	m5	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
24	m6	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
24	mT	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		
24	nT	127	Total	C	N	O	S	0	0
			1019	640	171	204	4		

- Molecule 25 is a protein called gp48, baseplate protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	o0	358	Total	C	N	O	S	0	0
			2749	1714	467	559	9		
25	o1	314	Total	C	N	O	S	0	0
			2436	1523	414	491	8		
25	o2	314	Total	C	N	O	S	0	0
			2436	1523	414	491	8		
25	o6	314	Total	C	N	O	S	0	0
			2436	1523	414	491	8		
25	pA	358	Total	C	N	O	S	0	0
			2749	1714	467	559	9		
25	pB	358	Total	C	N	O	S	0	0
			2749	1714	467	559	9		

- Molecule 26 is a protein called gp54, baseplate protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	q3	207	Total	C	N	O	S	0	0
			1650	1037	280	321	12		
26	q4	207	Total	C	N	O	S	0	0
			1650	1037	280	321	12		
26	q5	213	Total	C	N	O	S	0	0
			1693	1064	287	330	12		
26	q7	213	Total	C	N	O	S	0	0
			1693	1064	287	330	12		
26	q8	207	Total	C	N	O	S	0	0
			1650	1037	280	321	12		
26	q9	213	Total	C	N	O	S	0	0
			1693	1064	287	330	12		

- Molecule 27 is a protein called unassigned peptide A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	rc	25	Total	C	N	O	0	0
			125	75	25	25		
27	rd	25	Total	C	N	O	0	0
			125	75	25	25		
27	re	25	Total	C	N	O	0	0
			125	75	25	25		
27	rf	25	Total	C	N	O	0	0
			125	75	25	25		
27	rg	25	Total	C	N	O	0	0
			125	75	25	25		
27	rh	25	Total	C	N	O	0	0
			125	75	25	25		

- Molecule 28 is a protein called unassigned peptide B.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	sQ	18	Total	C	N	O	0	0
			90	54	18	18		
28	sT	18	Total	C	N	O	0	0
			90	54	18	18		
28	sU	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 29 is a protein called unassigned peptide C.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	tS	10	Total	C	N	O	0	0
			50	30	10	10		
29	tX	10	Total	C	N	O	0	0
			50	30	10	10		
29	tY	10	Total	C	N	O	0	0
			50	30	10	10		

- Molecule 30 is a protein called unassigned peptide D.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	uR	7	Total	C	N	O	0	0
			35	21	7	7		
30	uV	7	Total	C	N	O	0	0
			35	21	7	7		
30	uW	7	Total	C	N	O	0	0
			35	21	7	7		

- Molecule 31 is a protein called unassigned peptide E.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	vZ	9	Total	C	N	O	0	0
			45	27	9	9		
31	va	9	Total	C	N	O	0	0
			45	27	9	9		
31	vb	9	Total	C	N	O	0	0
			45	27	9	9		

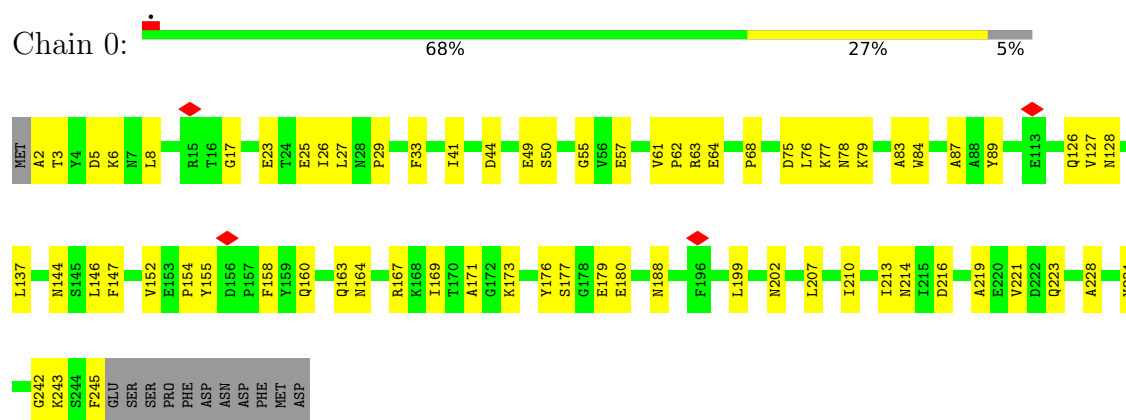
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	S0	1	Total	Zn	0
			1	1	
32	S1	1	Total	Zn	0
			1	1	
32	S4	1	Total	Zn	0
			1	1	
32	SA	1	Total	Zn	0
			1	1	
32	SQ	1	Total	Zn	0
			1	1	
32	Sv	1	Total	Zn	0
			1	1	

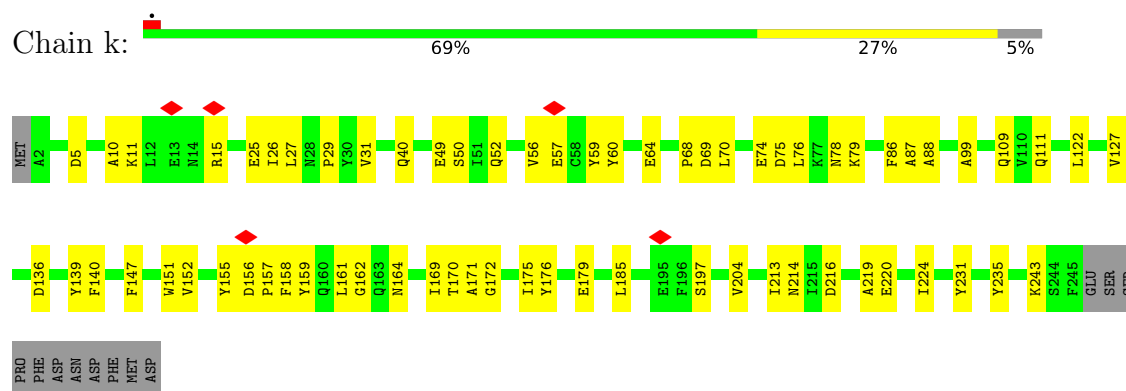
3 Residue-property plots

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.

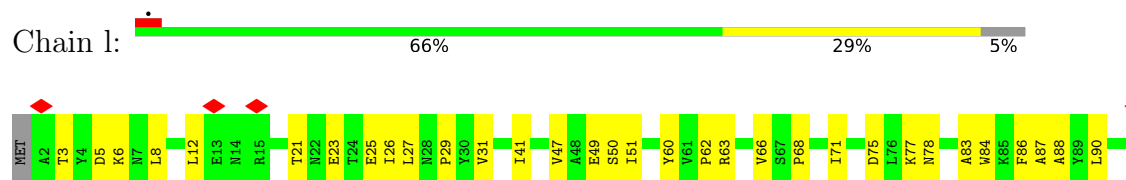
- Molecule 1: gp14, neck protein

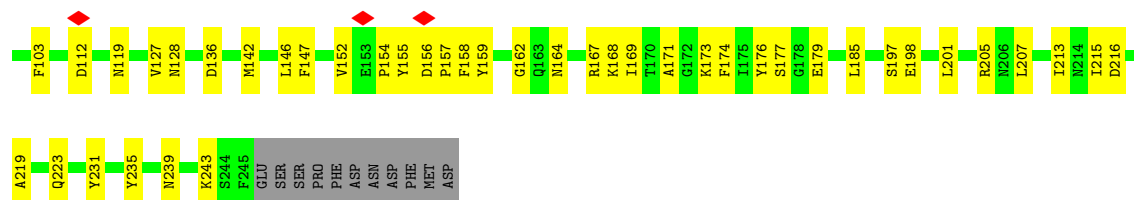


- Molecule 1: gp14, neck protein

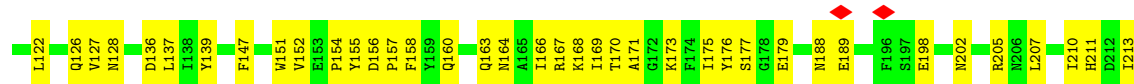
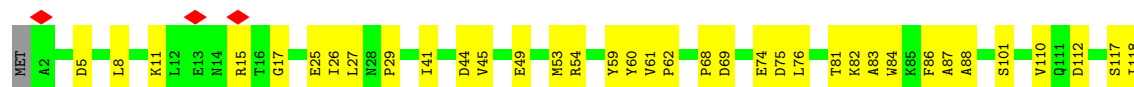


- Molecule 1: gp14, neck protein

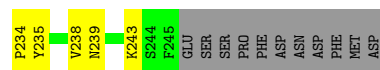




- Molecule 1: gp14, neck protein



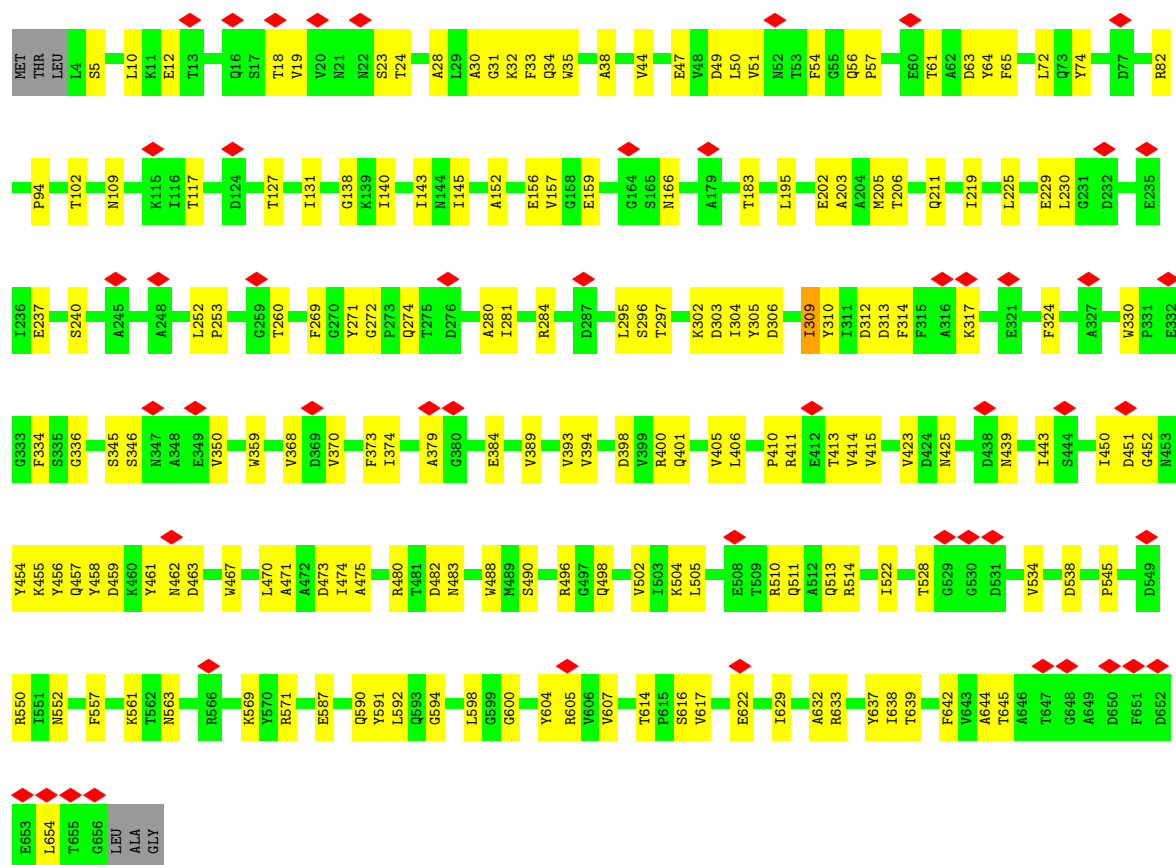
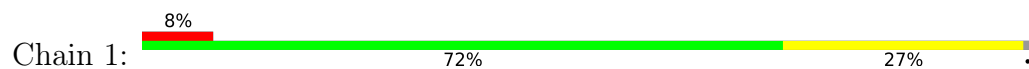
- Molecule 1: gp14, neck protein



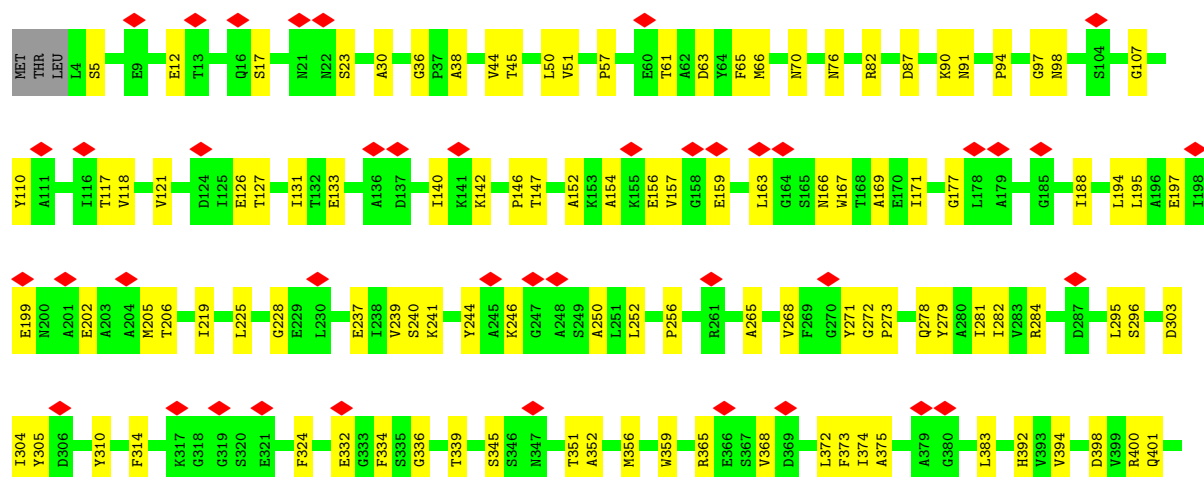
- Molecule 1: gp14, neck protein

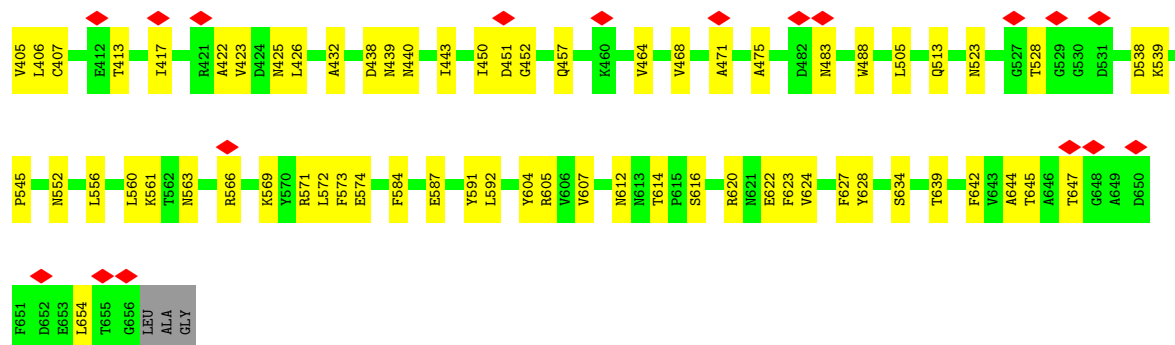


- Molecule 2: gp18, tail sheath protein



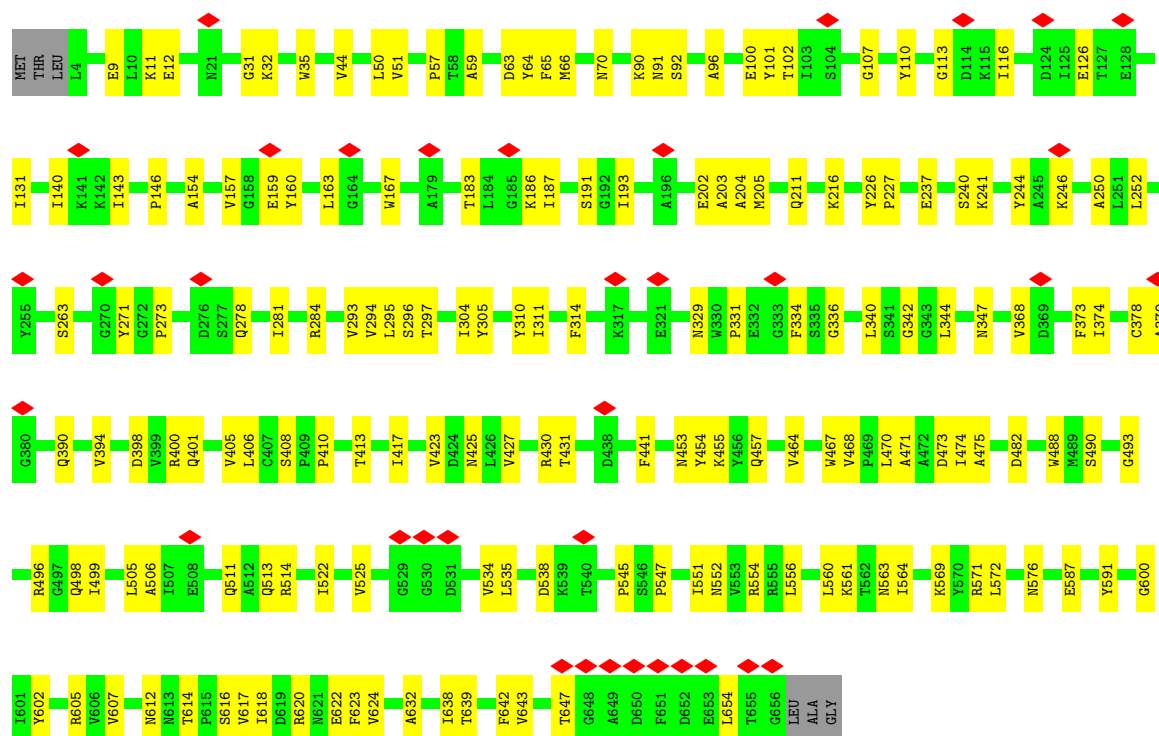
- Molecule 2: gp18, tail sheath protein





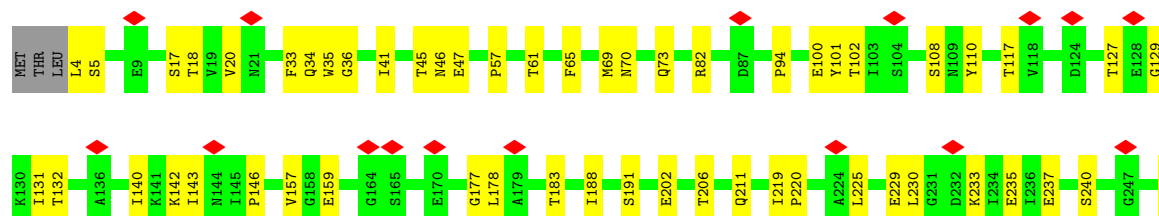
- Molecule 2: gp18, tail sheath protein

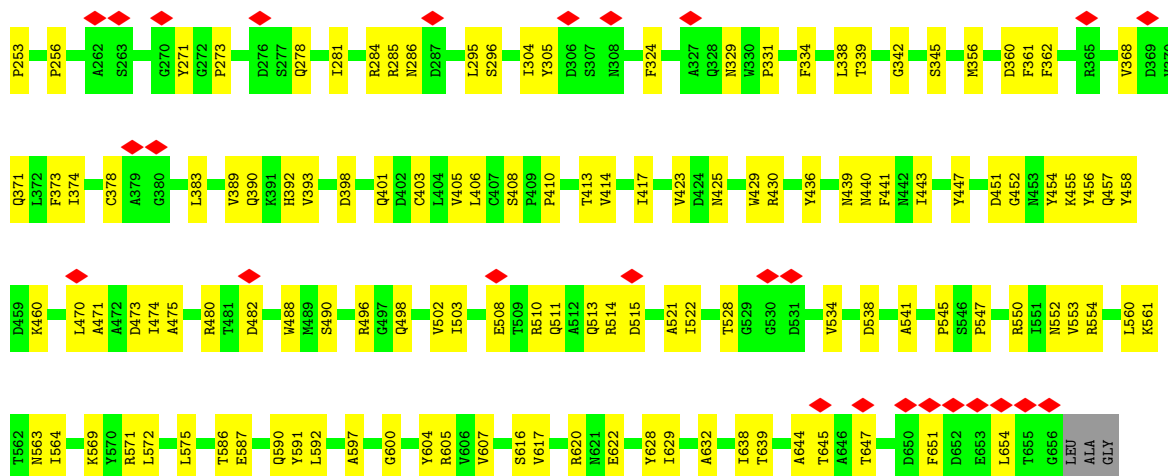
Chain 3: 5% 73% 26%



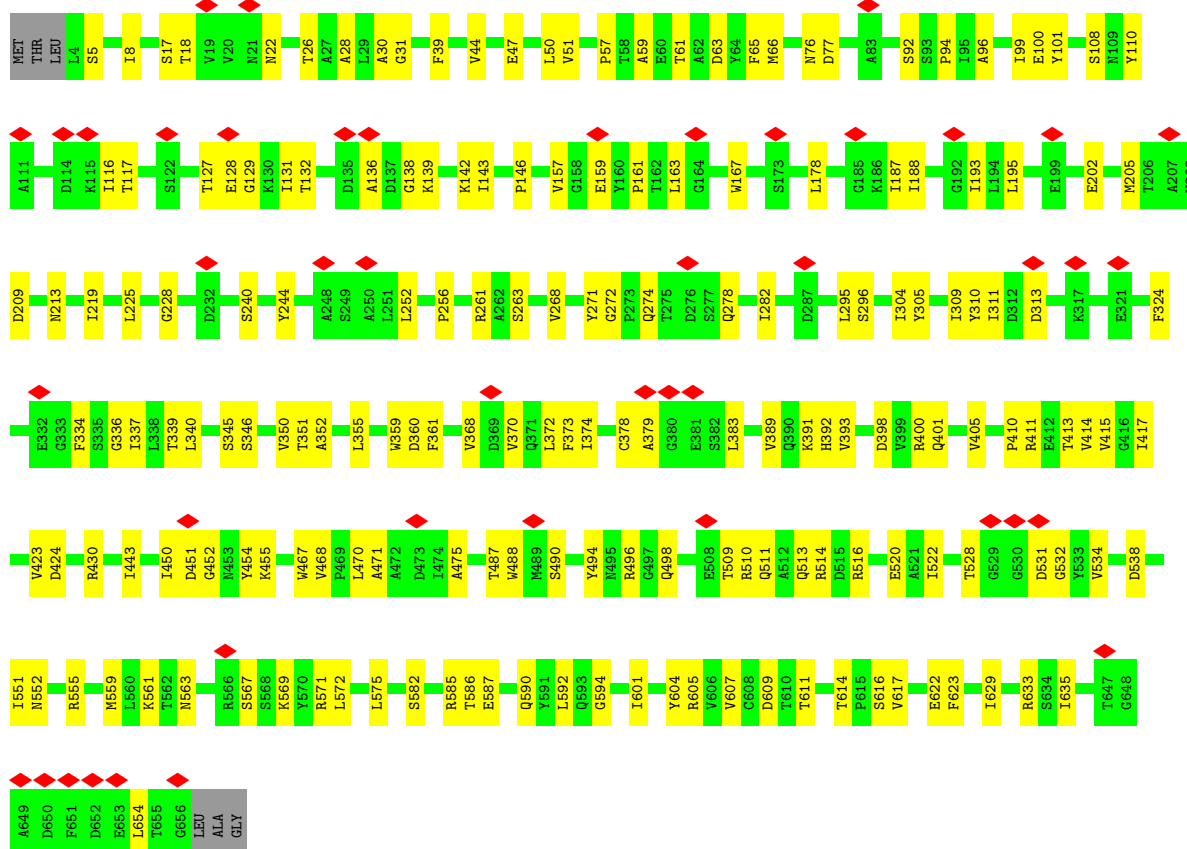
- Molecule 2: gp18, tail sheath protein

Chain 4: 7% 72% 27%



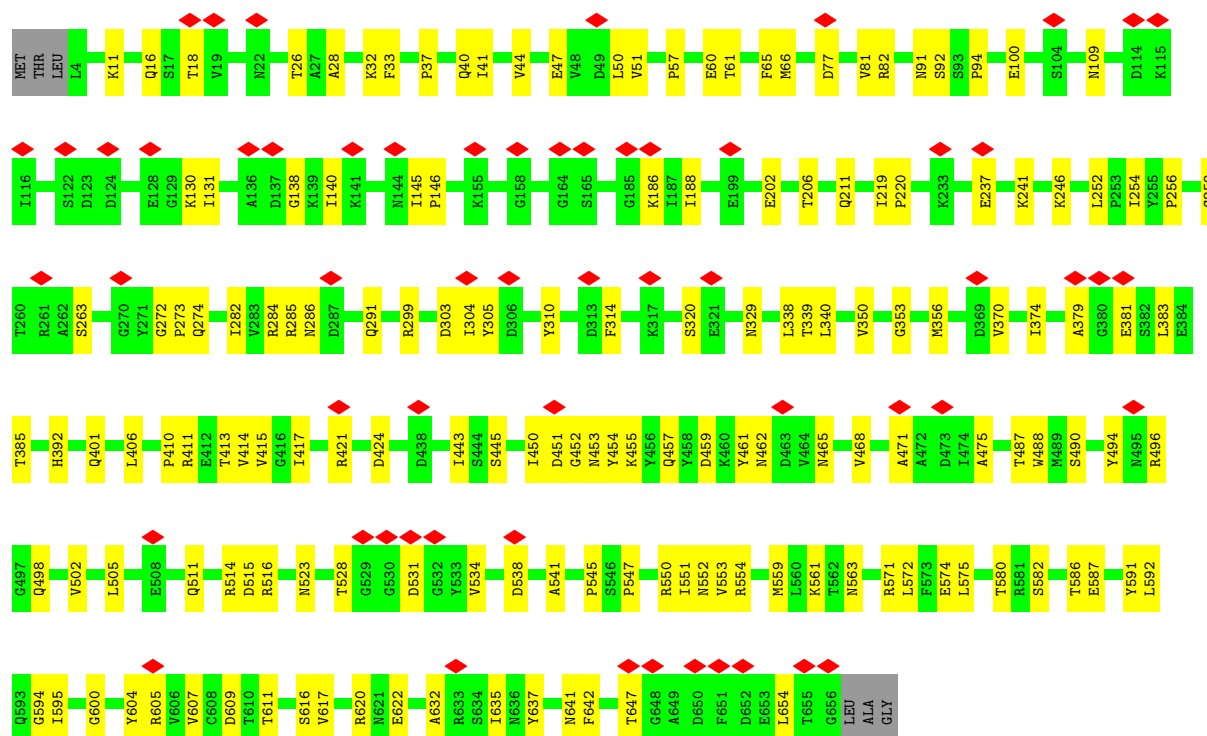


- Molecule 2: gp18, tail sheath protein

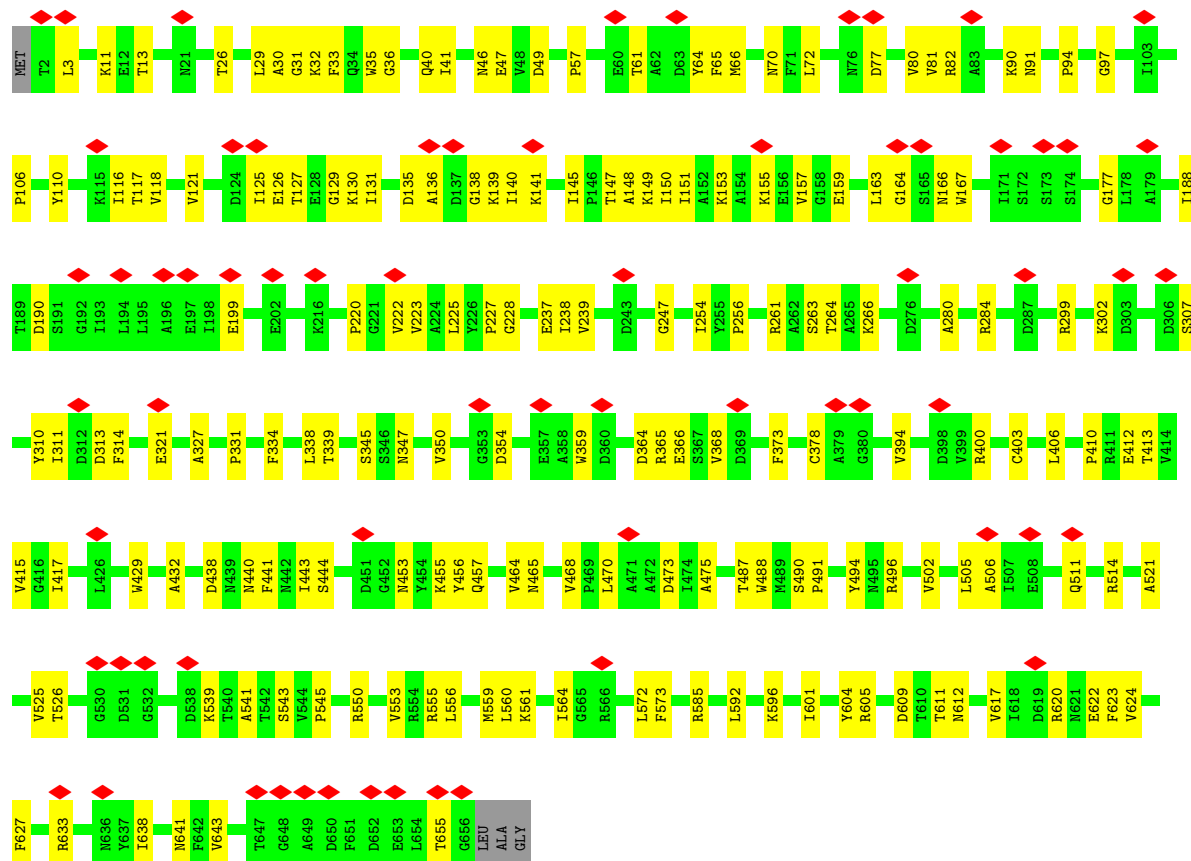
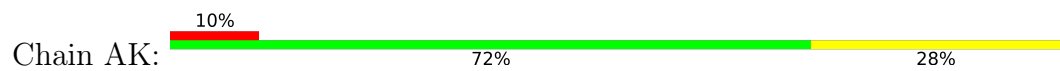


- Molecule 2: gp18, tail sheath protein

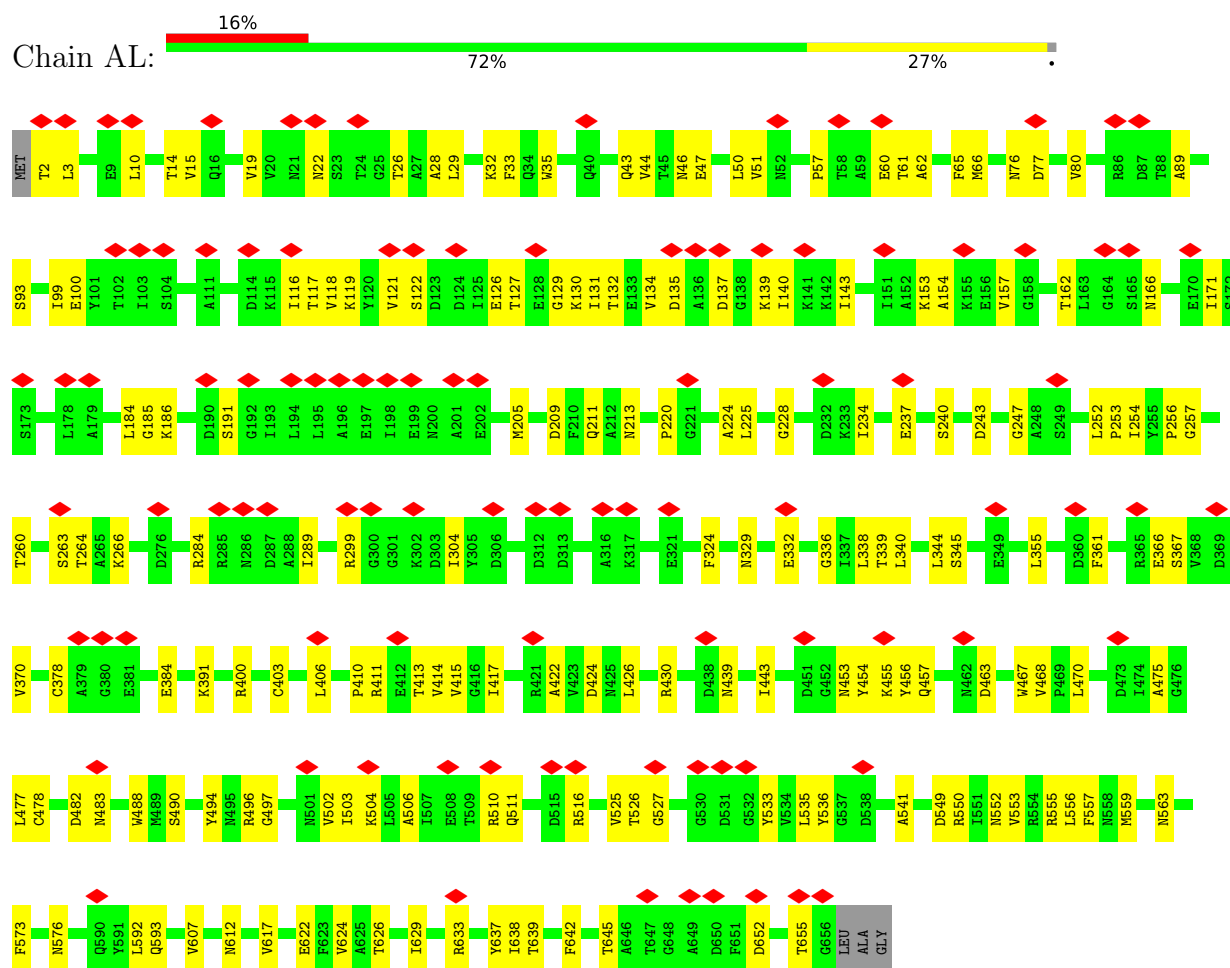




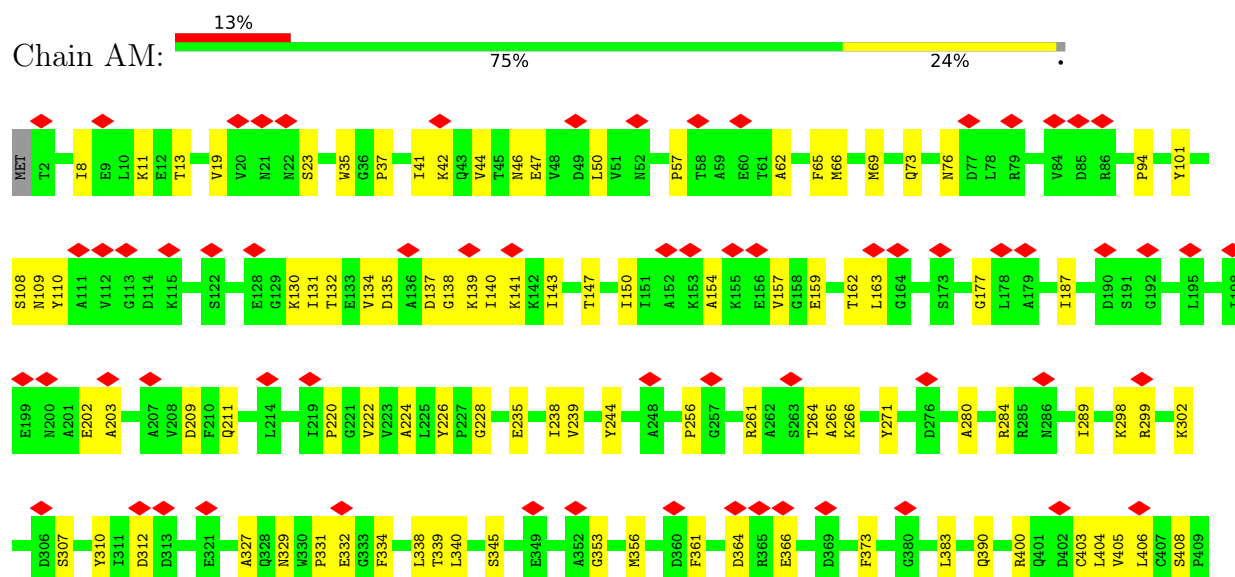
• Molecule 2: gp18, tail sheath protein

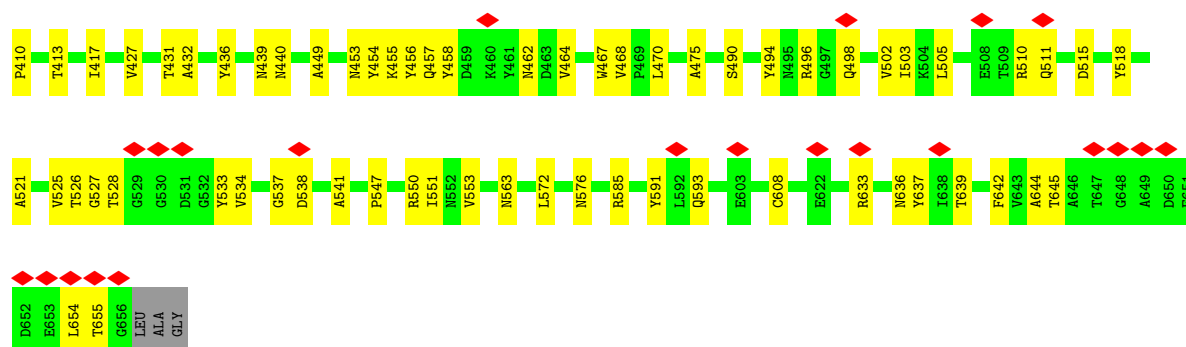


- Molecule 2: gp18, tail sheath protein

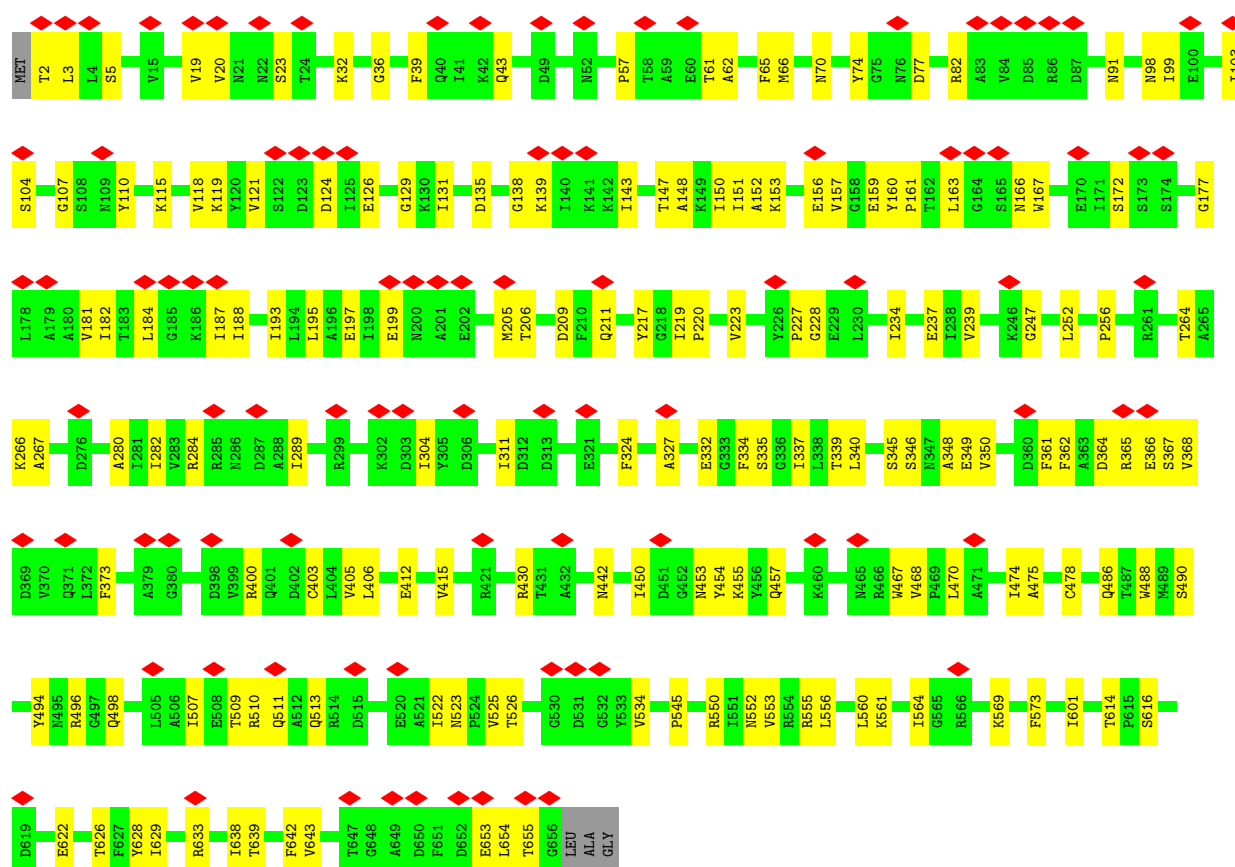
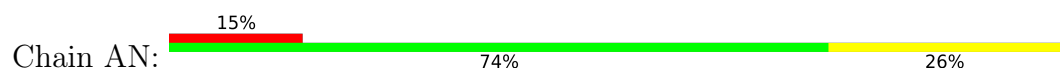


- Molecule 2: gp18, tail sheath protein

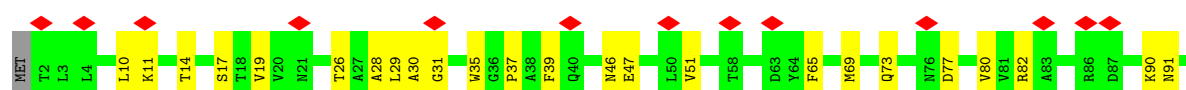
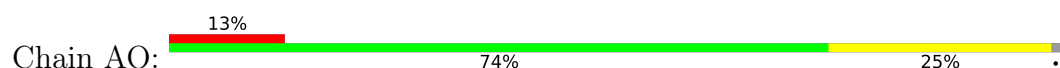


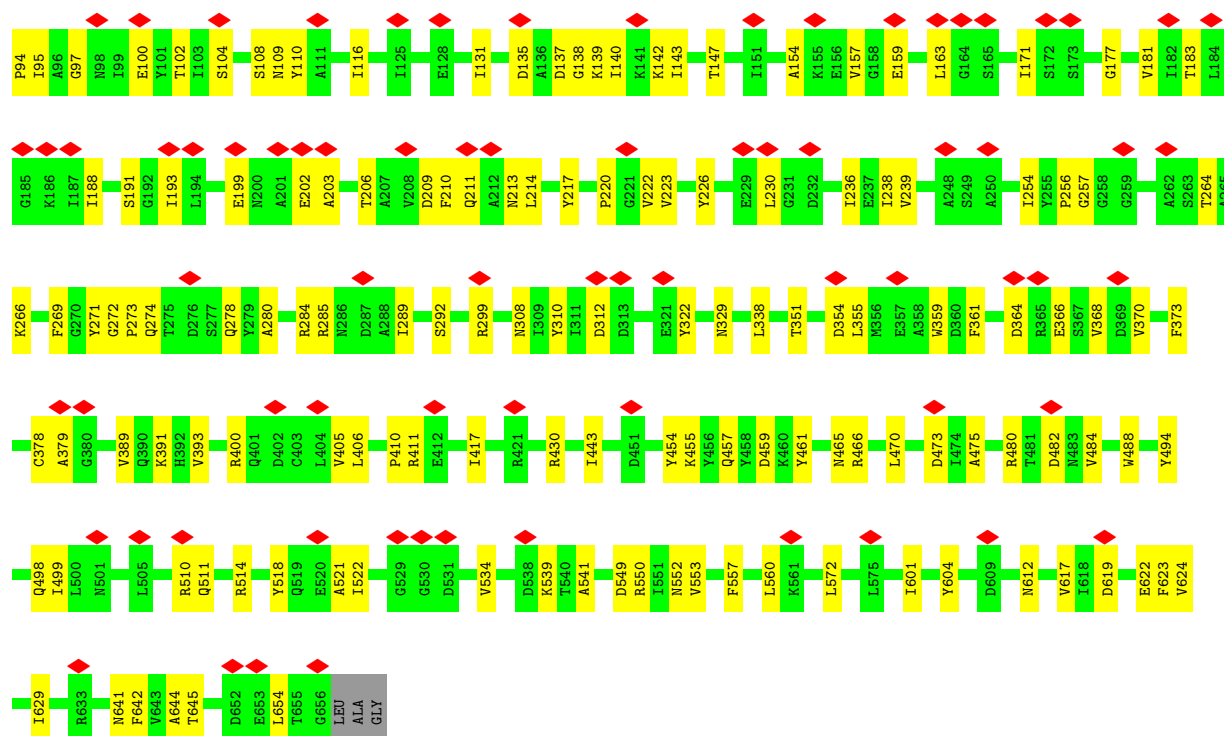


• Molecule 2: gp18, tail sheath protein

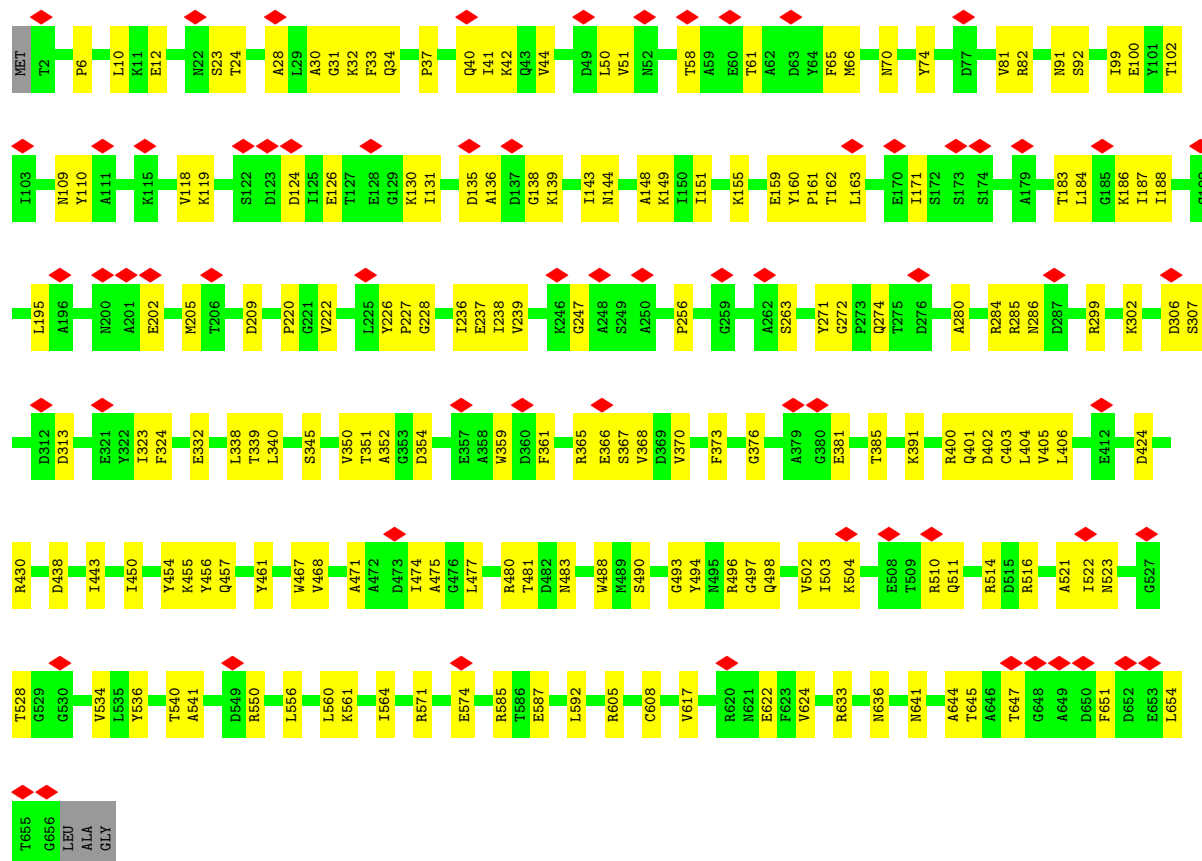
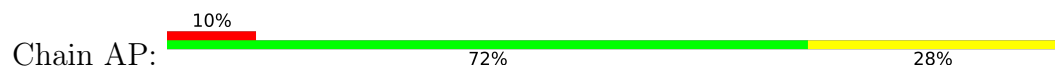


• Molecule 2: gp18, tail sheath protein

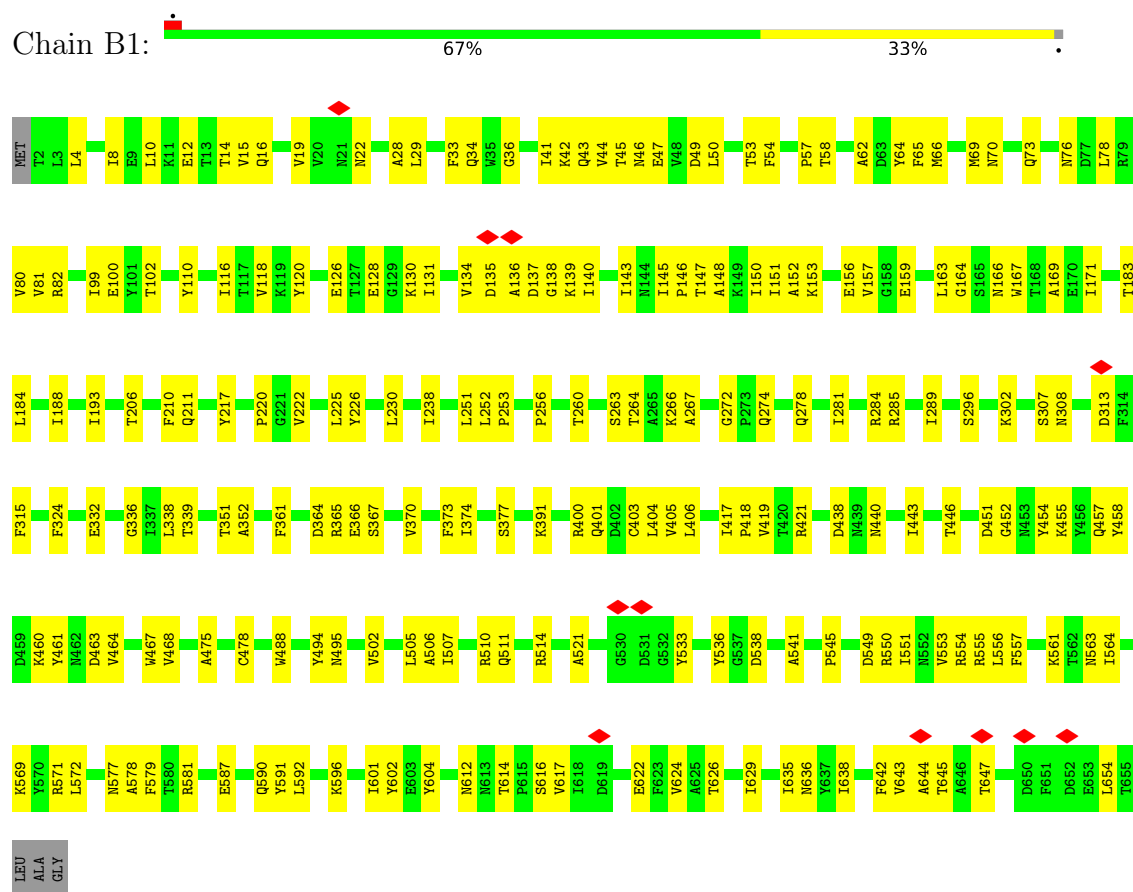




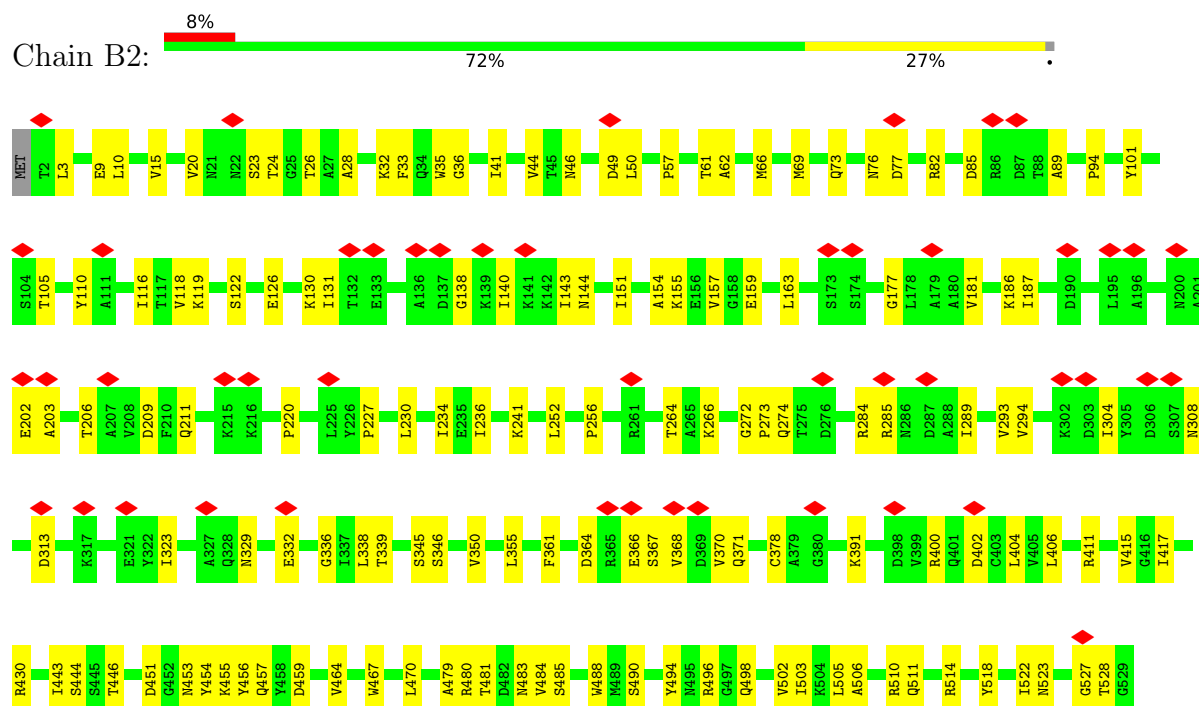
- Molecule 2: gp18, tail sheath protein

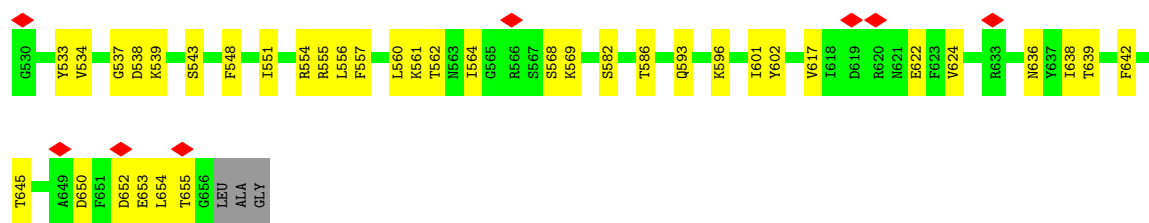


- Molecule 2: gp18, tail sheath protein



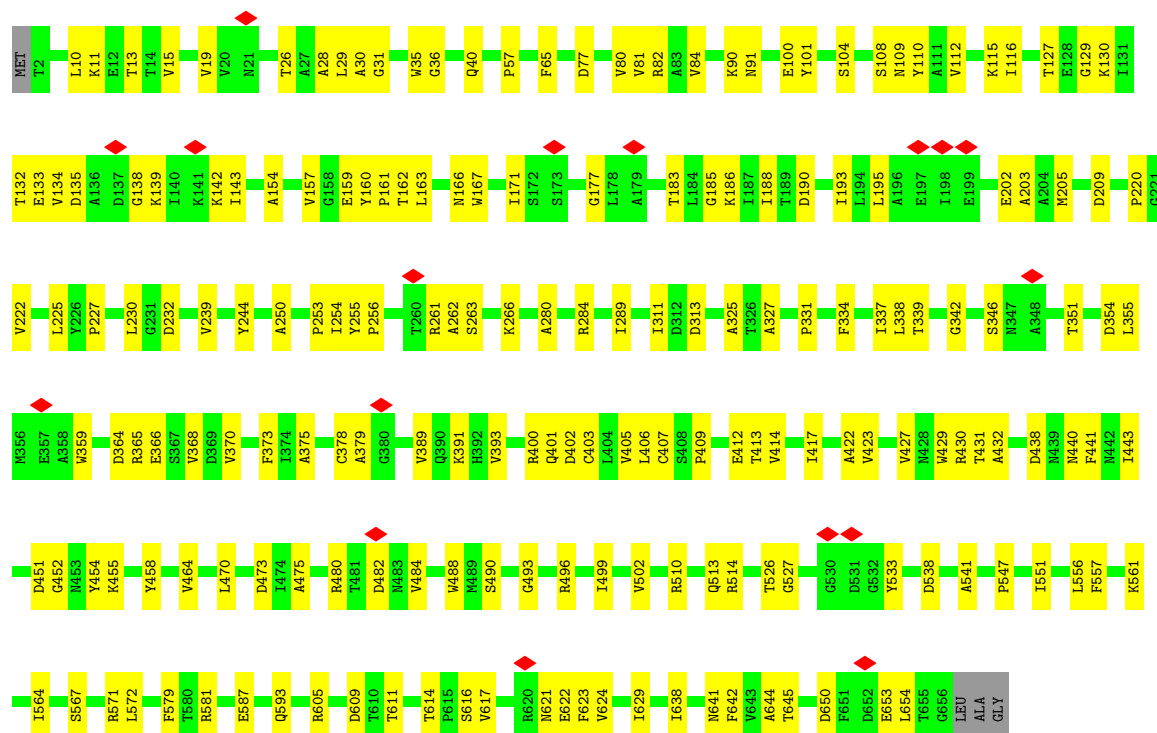
- Molecule 2: gp18, tail sheath protein





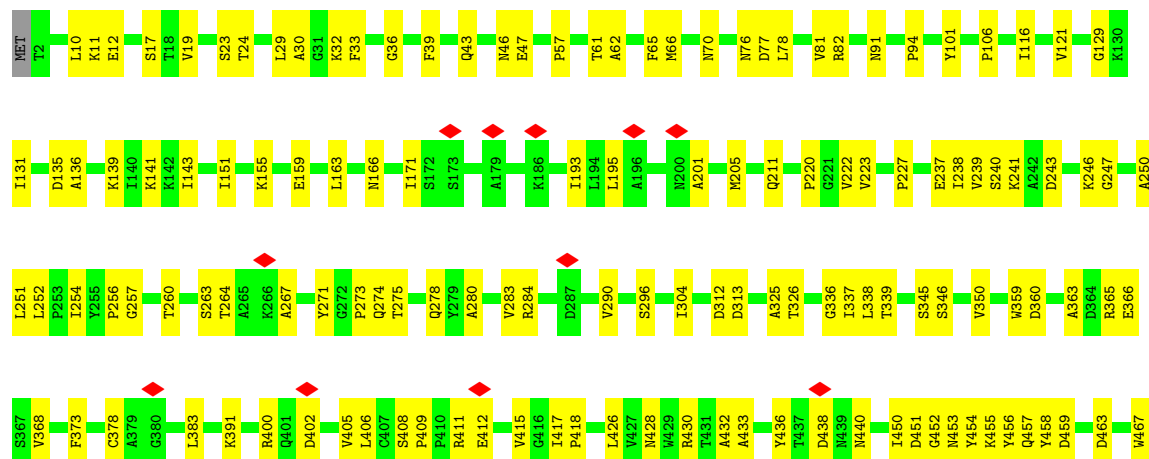
- Molecule 2: gp18, tail sheath protein

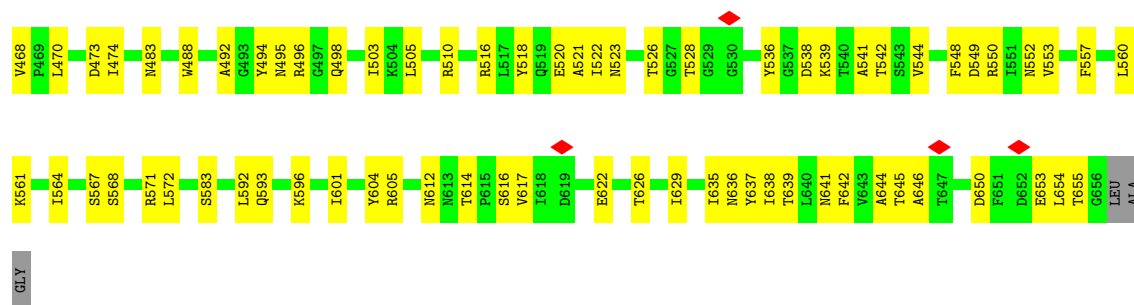
Chain B3: 70% 29%



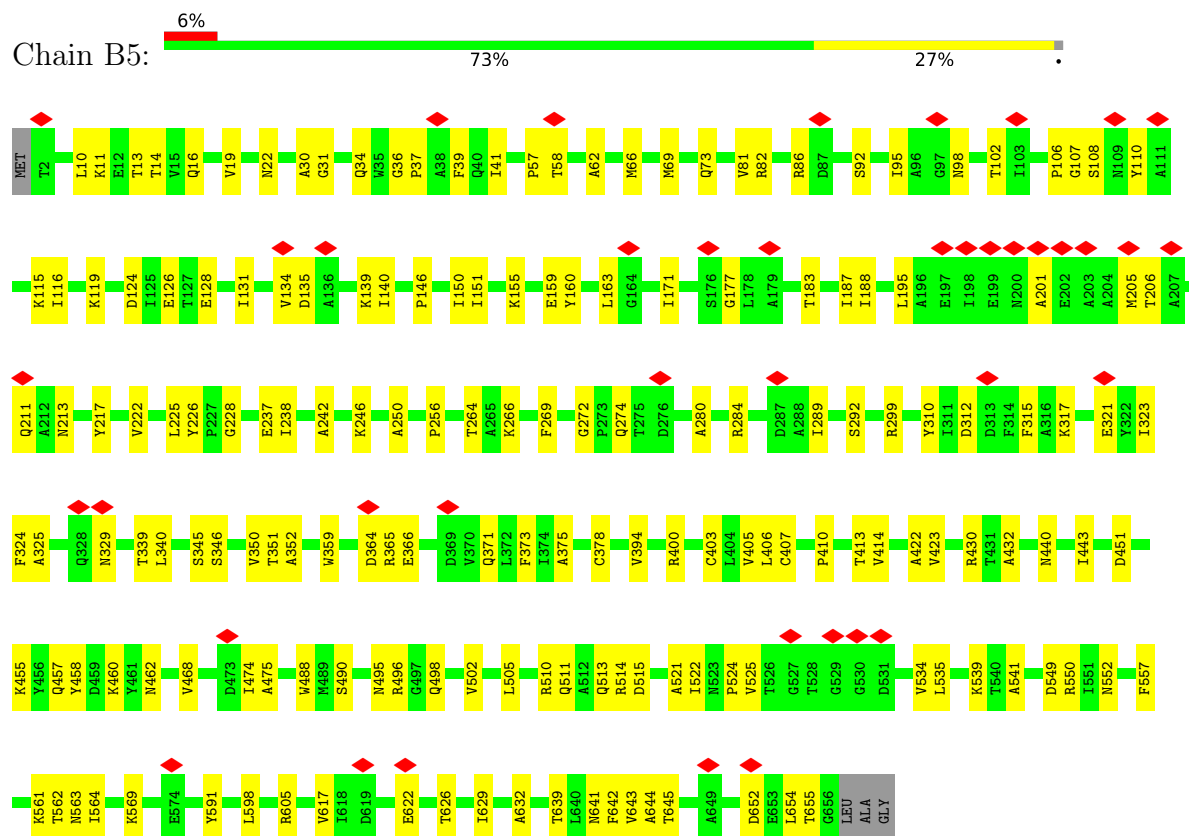
- Molecule 2: gp18, tail sheath protein

Chain B4: 68% 31%

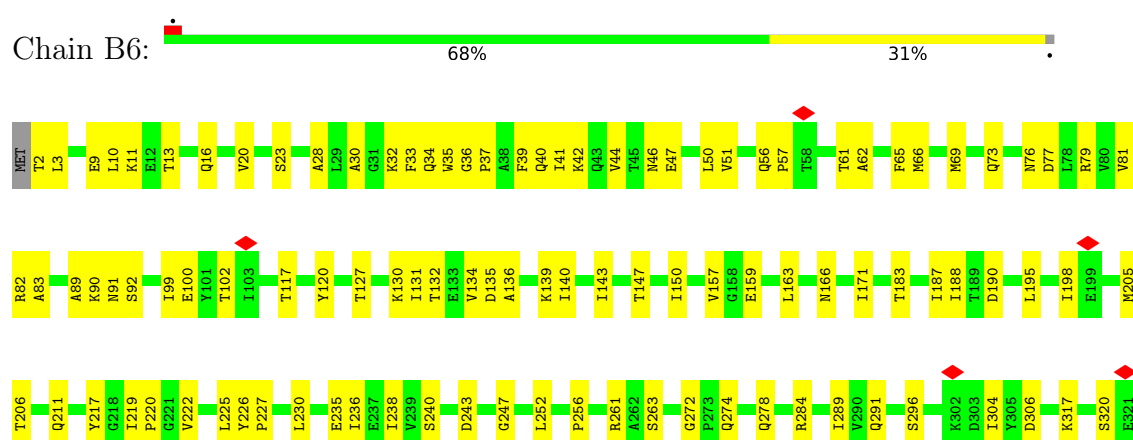




- Molecule 2: gp18, tail sheath protein

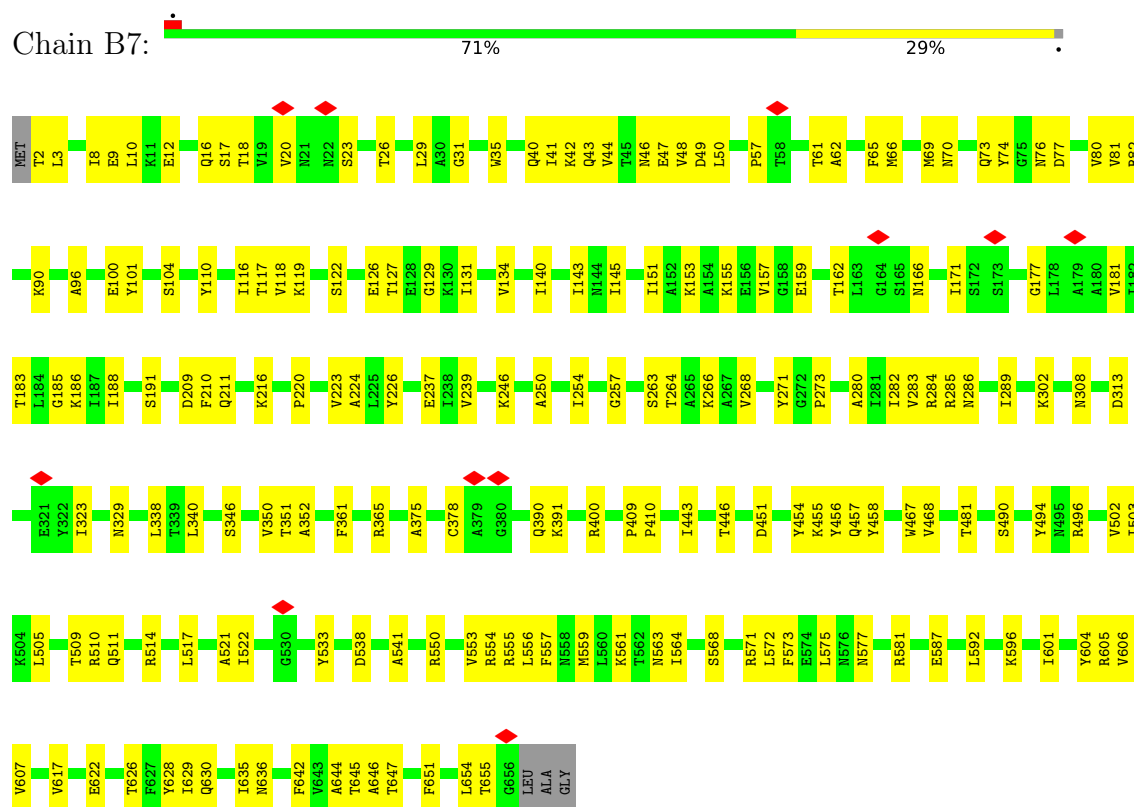


- Molecule 2: gp18, tail sheath protein

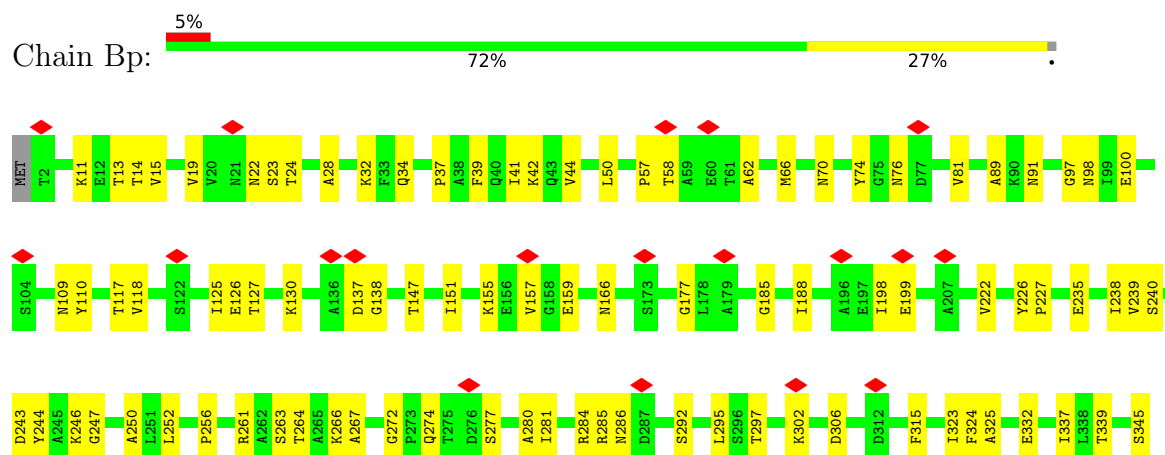


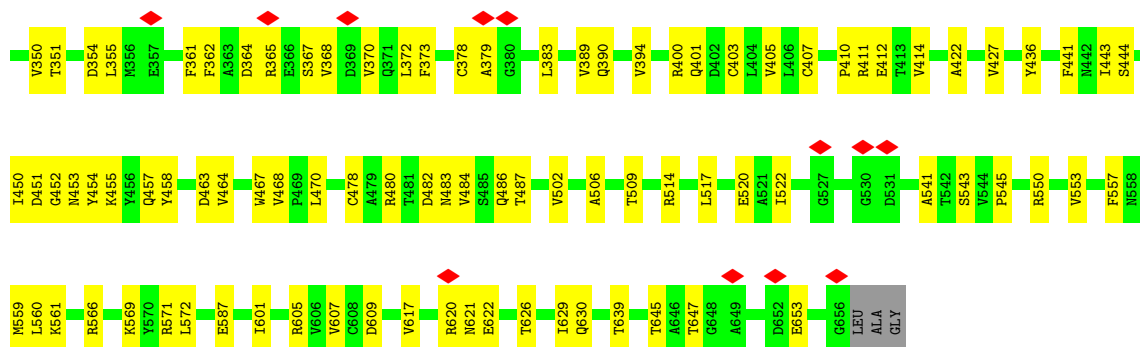


• Molecule 2: gp18, tail sheath protein

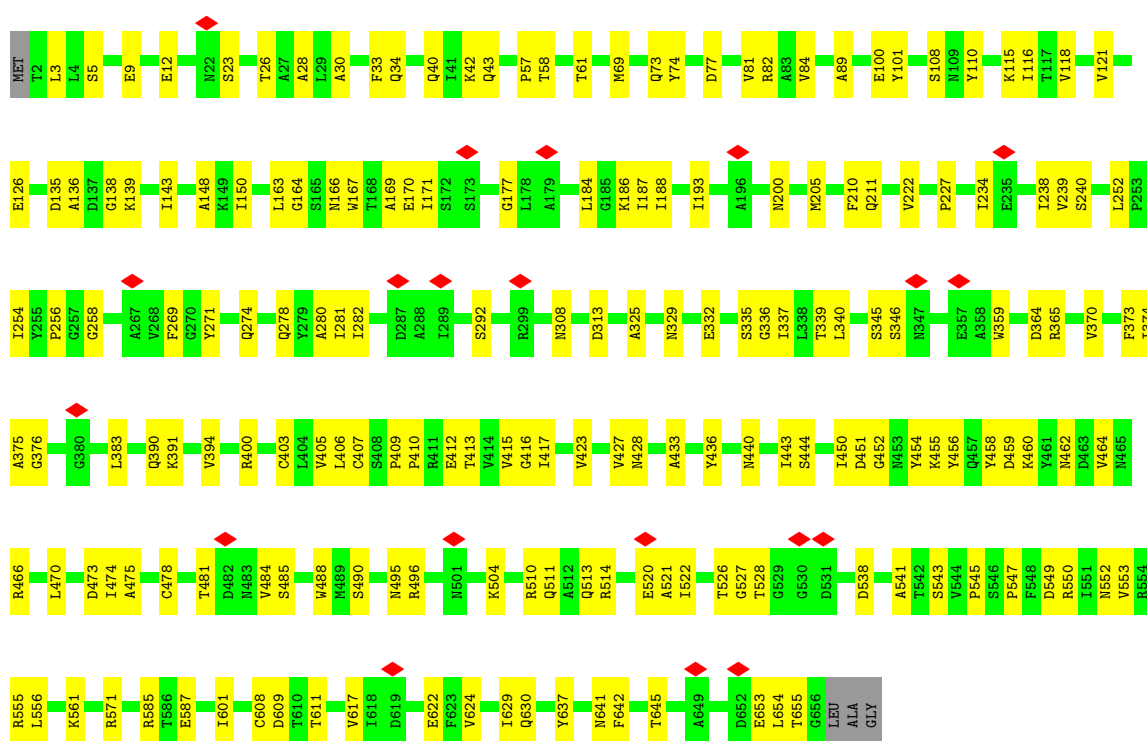


• Molecule 2: gp18, tail sheath protein

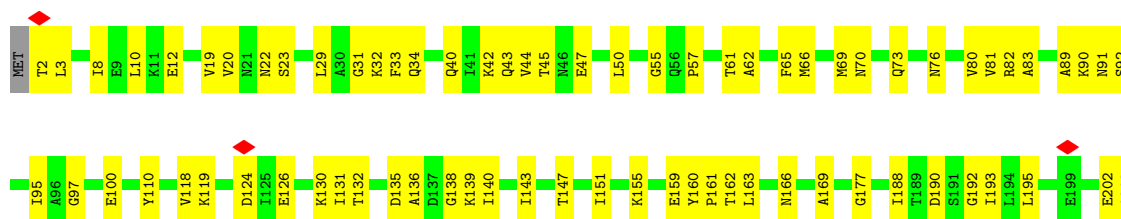


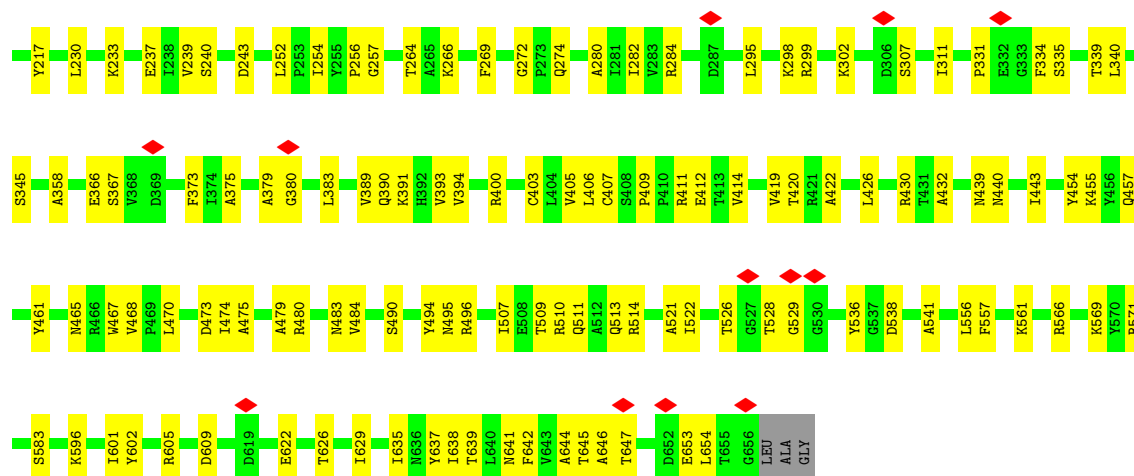


• Molecule 2: gp18, tail sheath protein

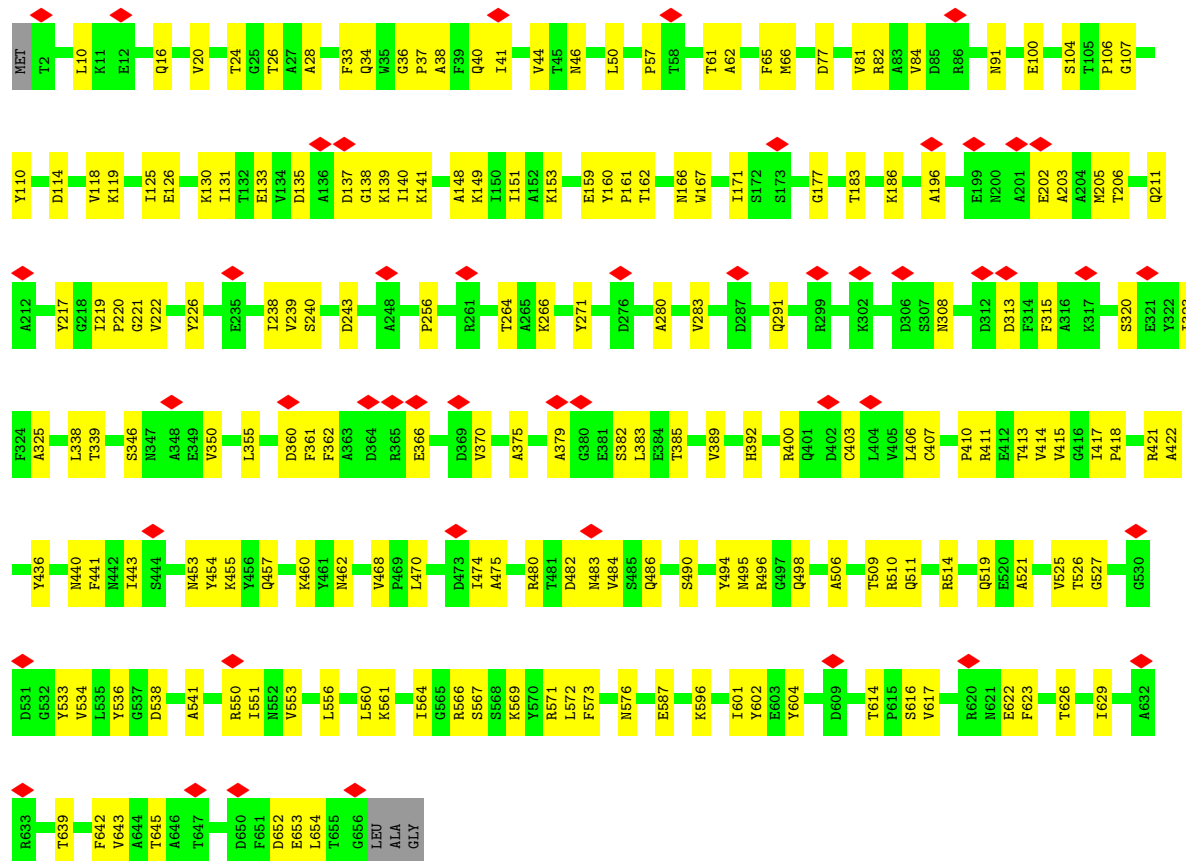


• Molecule 2: gp18, tail sheath protein



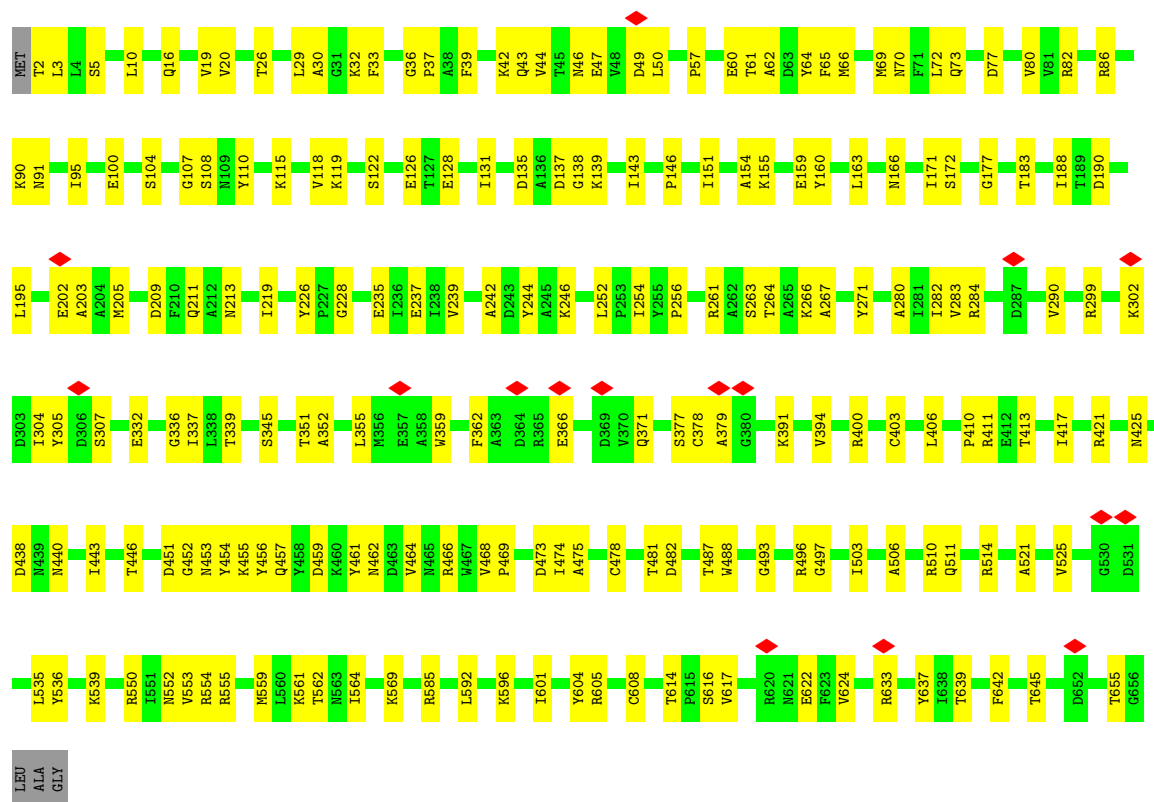


• Molecule 2: gp18, tail sheath protein

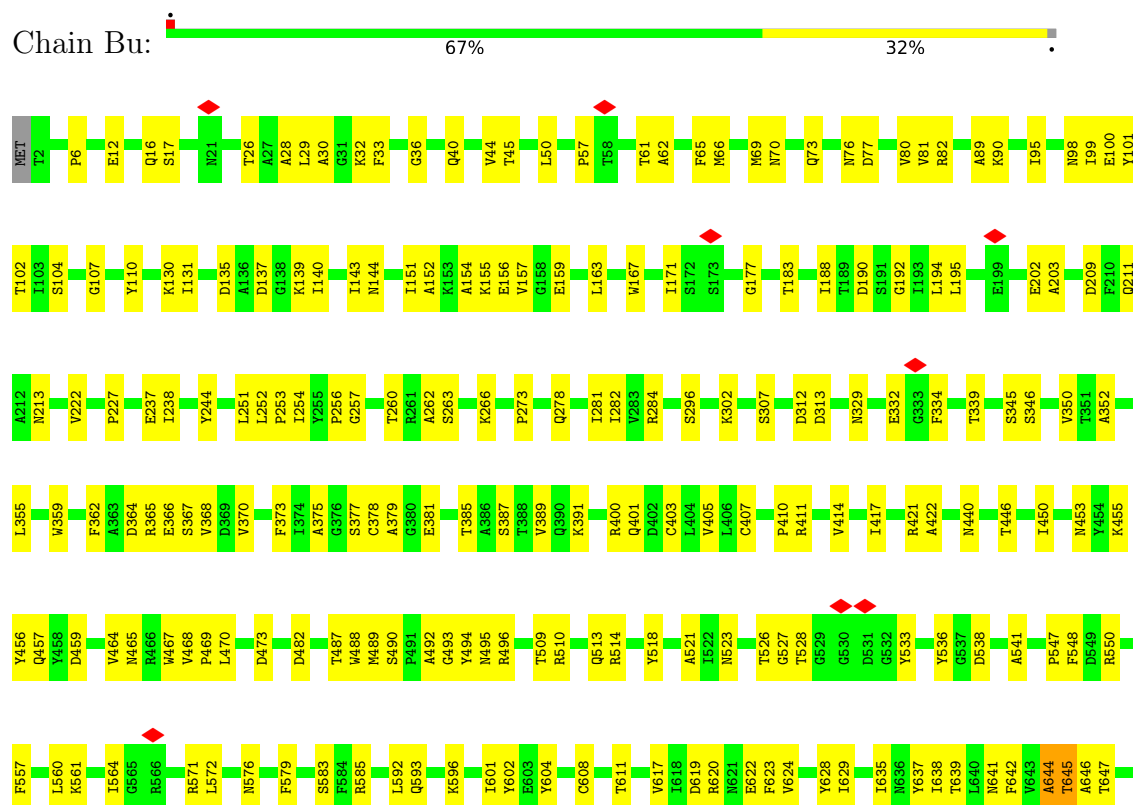


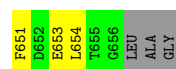
• Molecule 2: gp18, tail sheath protein



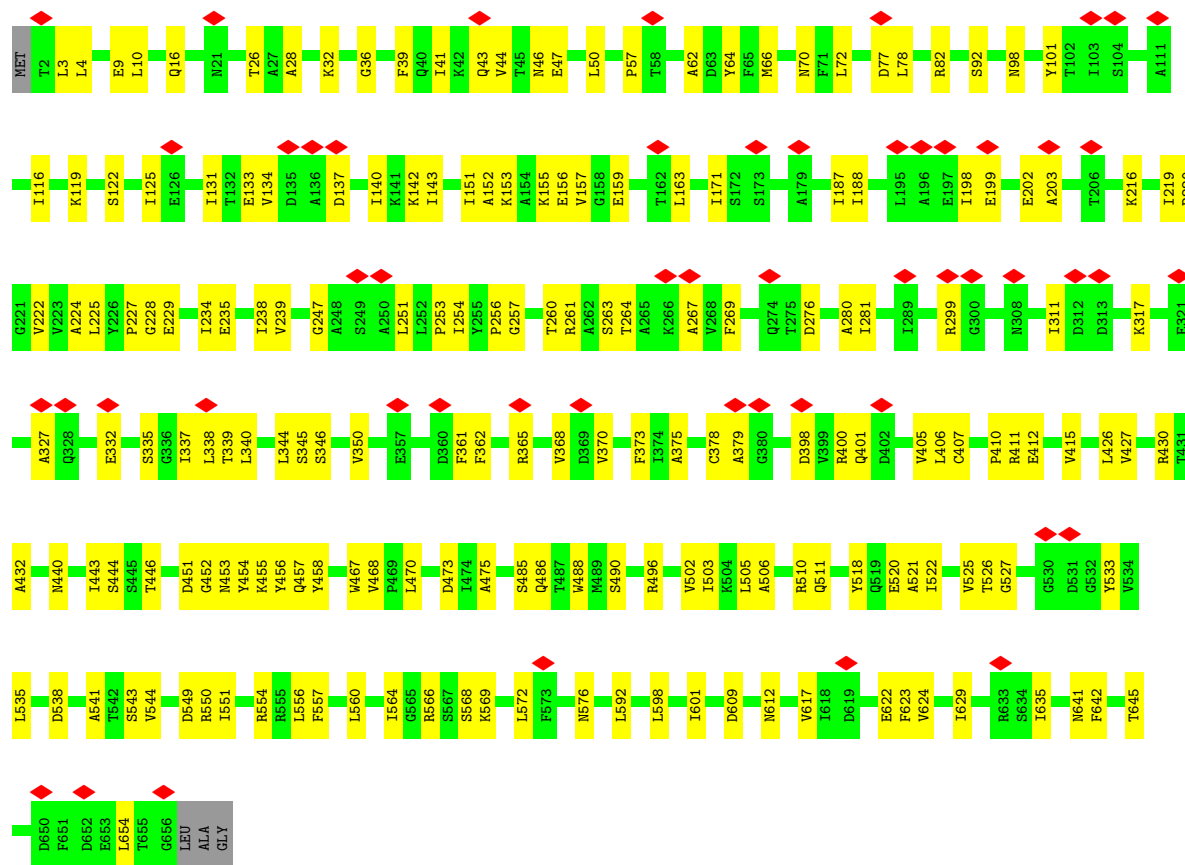
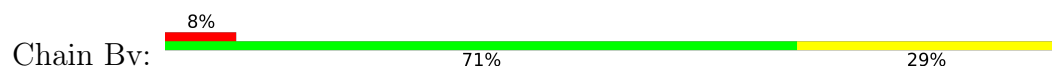


• Molecule 2: gp18, tail sheath protein

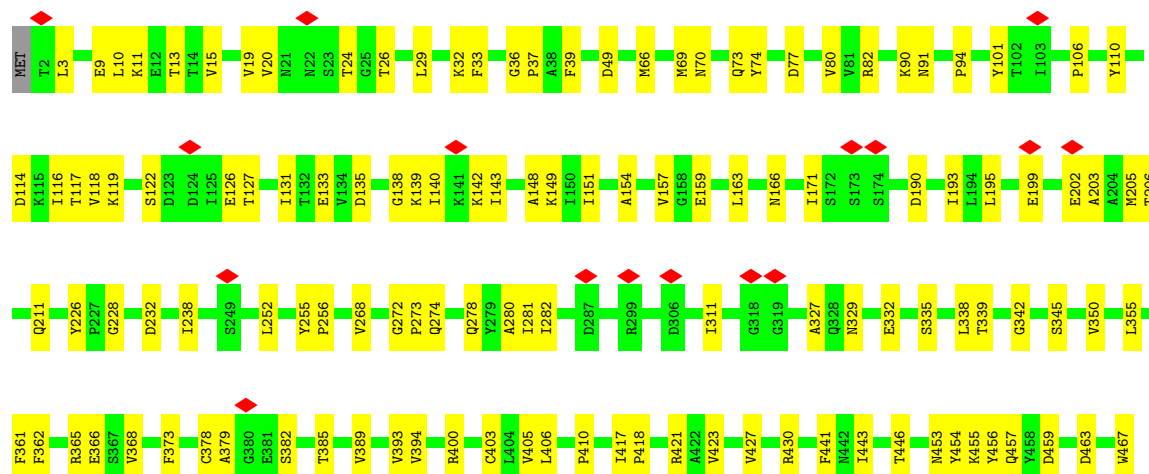
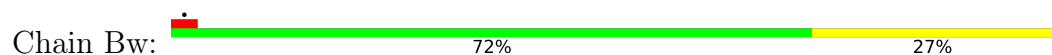


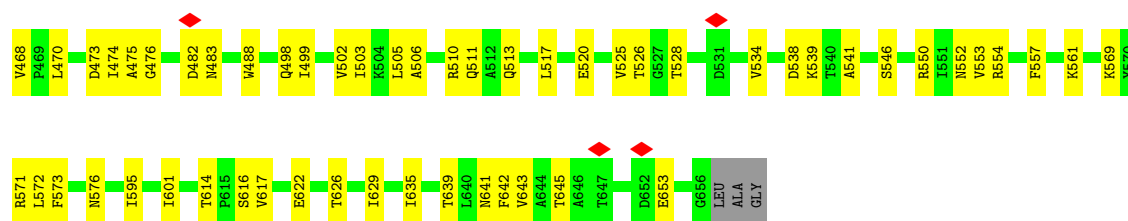


• Molecule 2: gp18, tail sheath protein

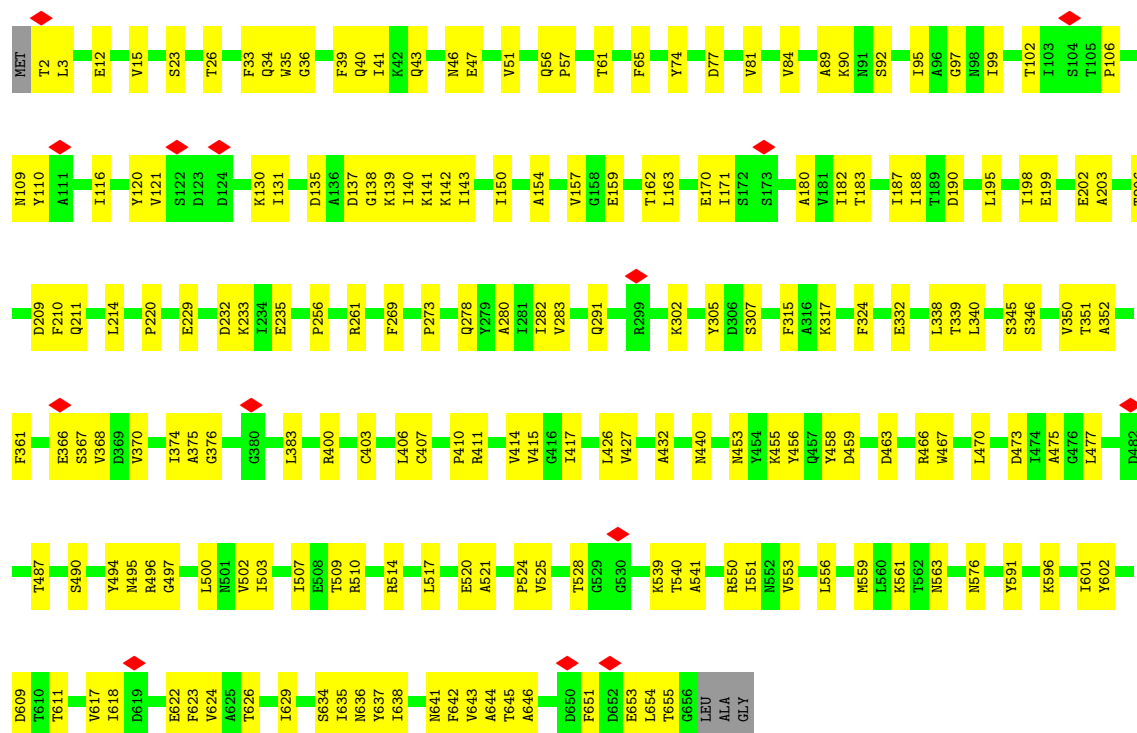


• Molecule 2: gp18, tail sheath protein

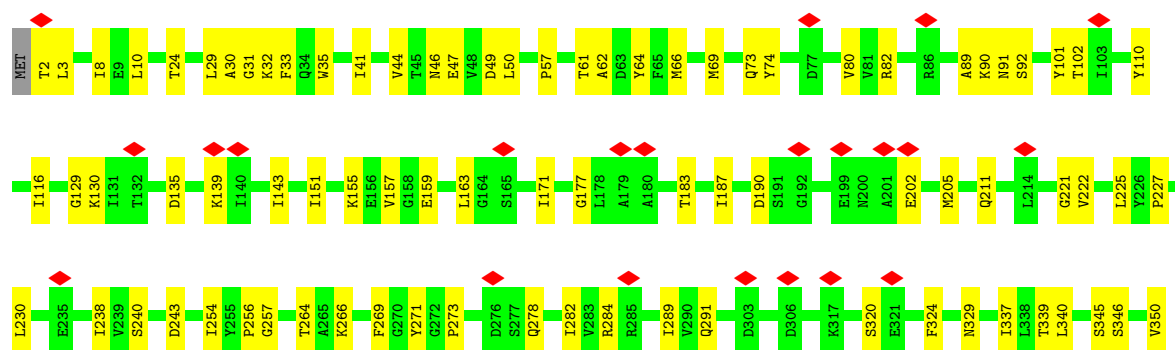
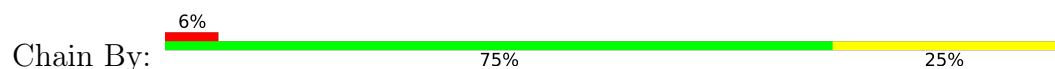


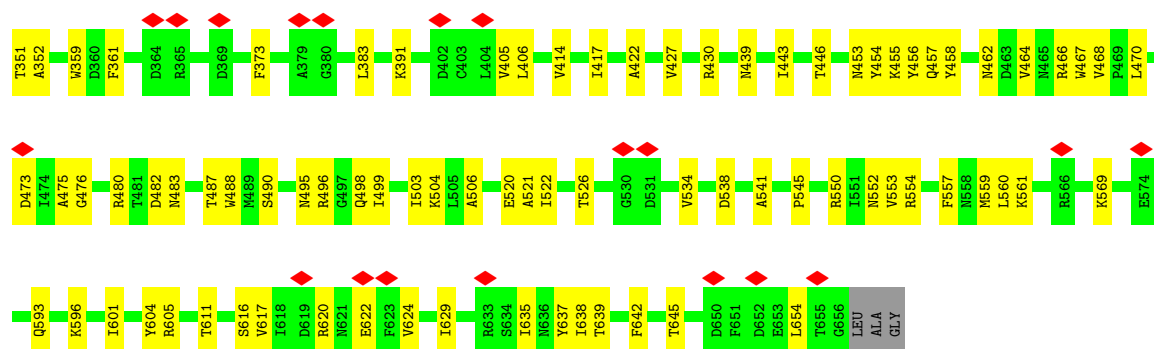


- Molecule 2: gp18, tail sheath protein

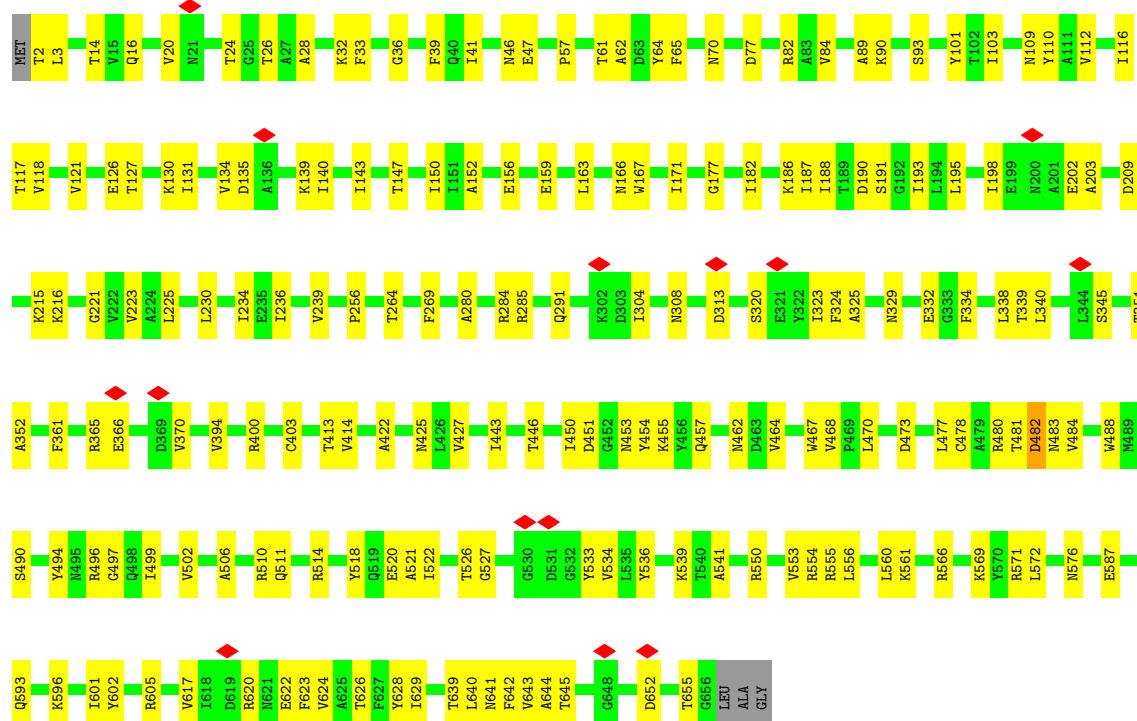


- Molecule 2: gp18, tail sheath protein



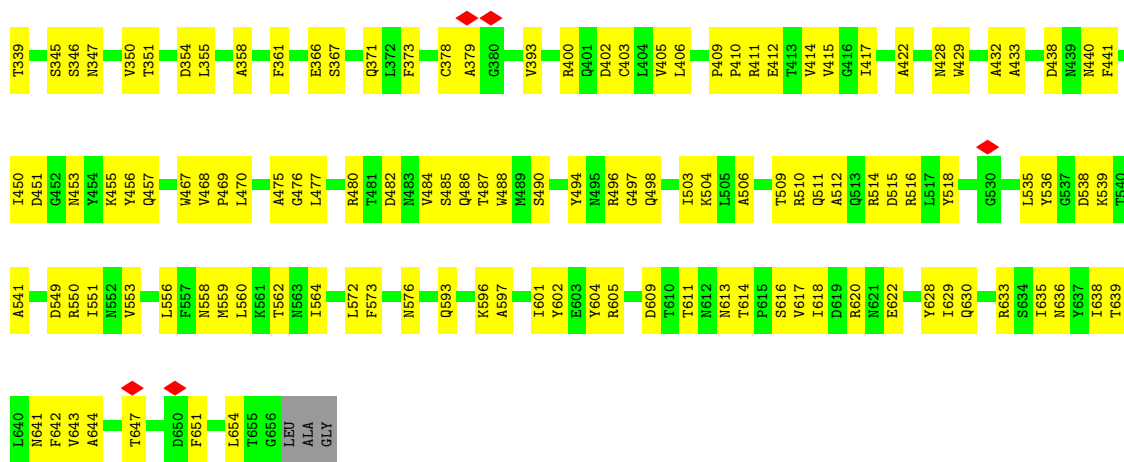


- Molecule 2: gp18, tail sheath protein

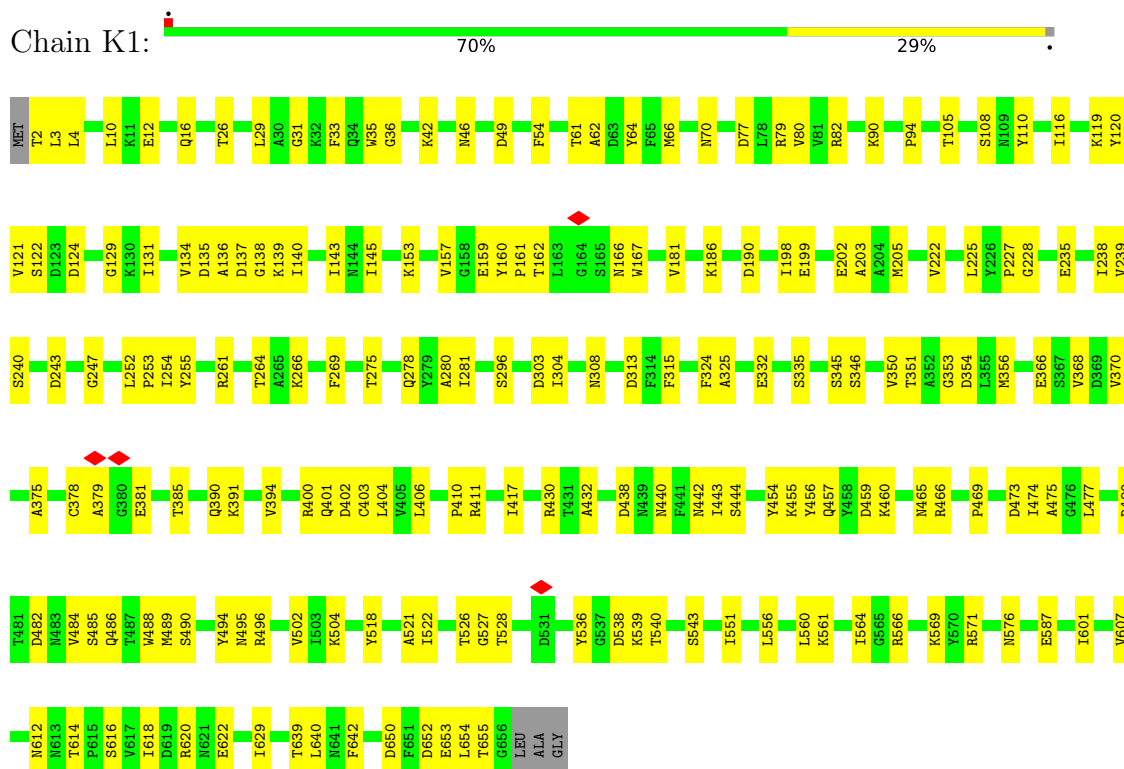


- Molecule 2: gp18, tail sheath protein

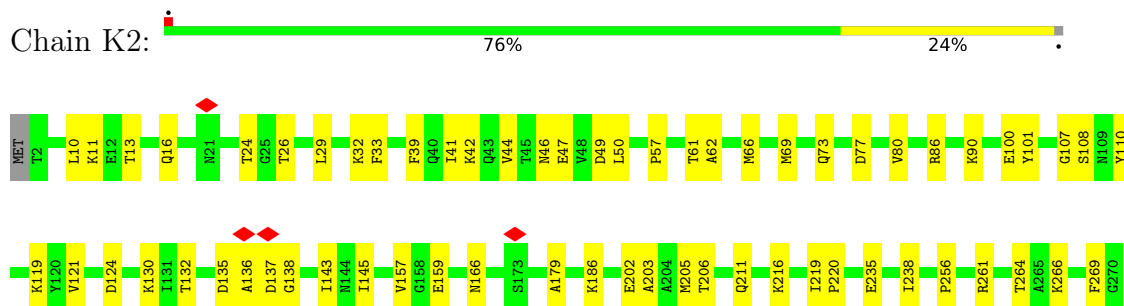


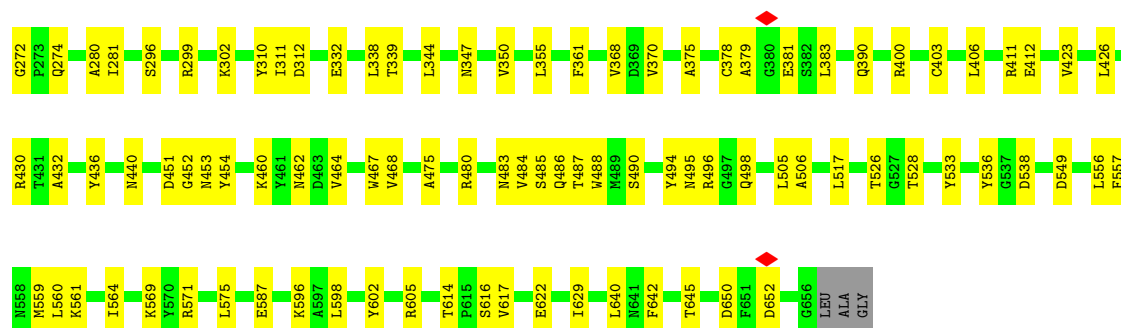


- Molecule 2: gp18, tail sheath protein

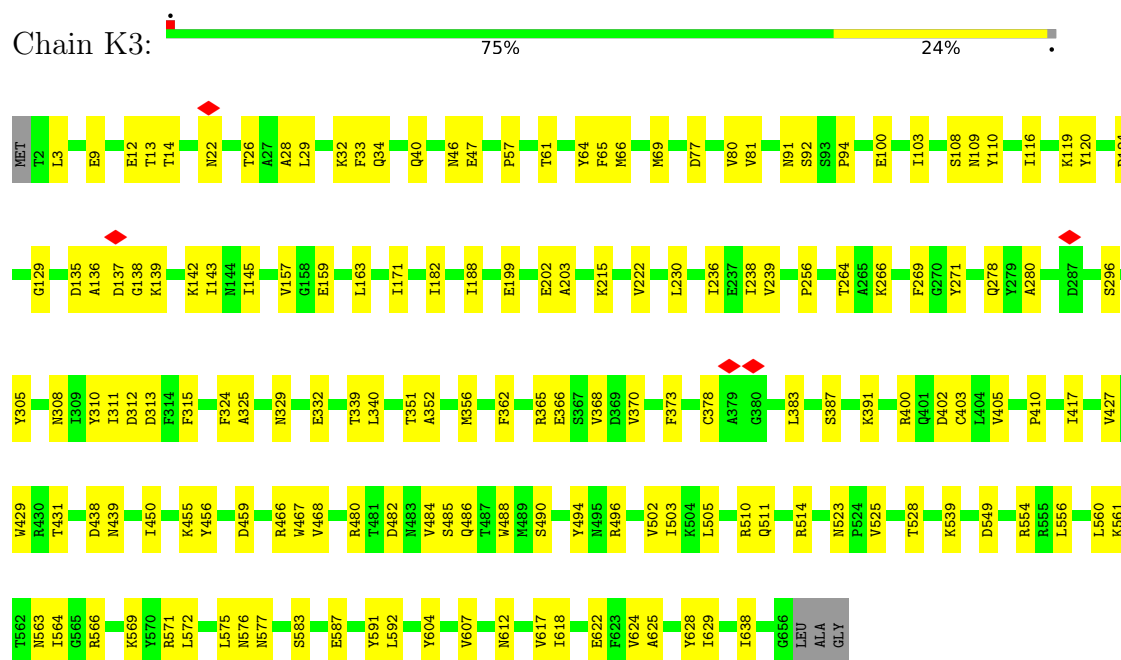


- Molecule 2: gp18, tail sheath protein

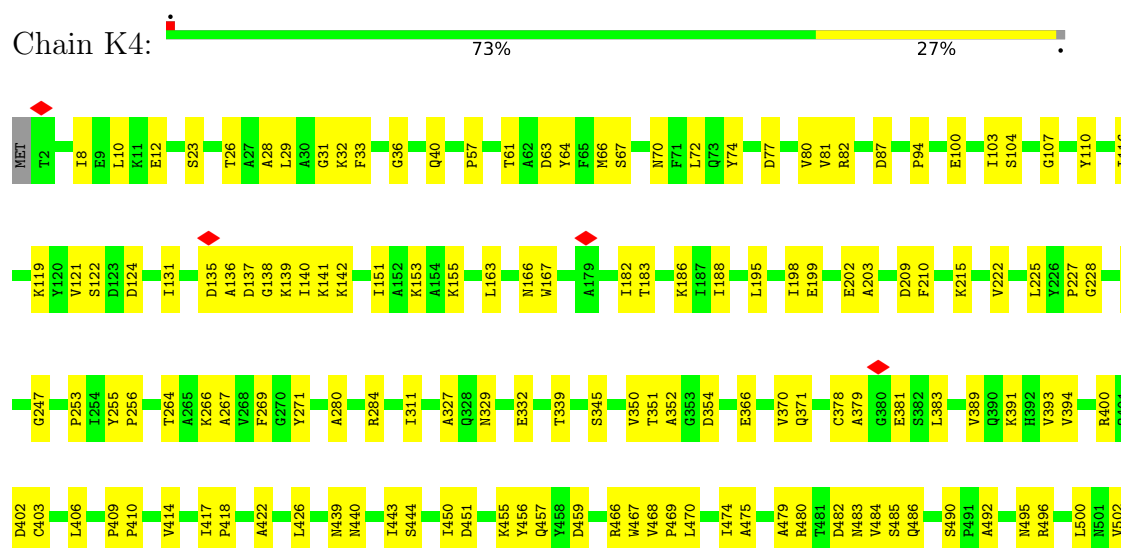


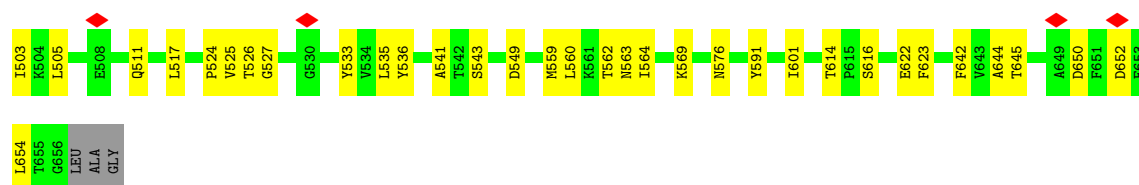


- Molecule 2: gp18, tail sheath protein



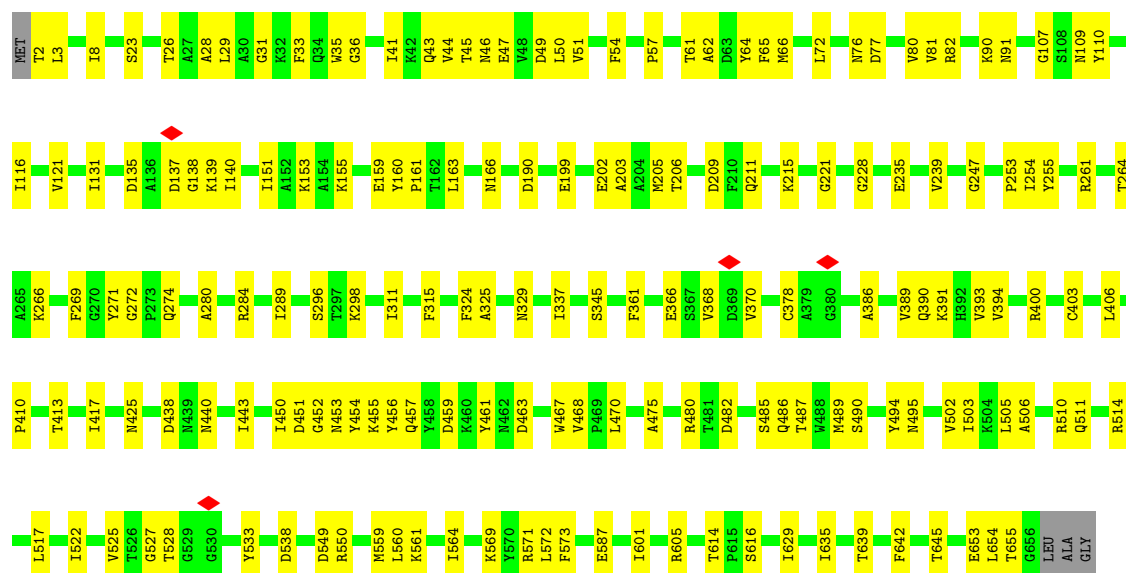
- Molecule 2: gp18, tail sheath protein





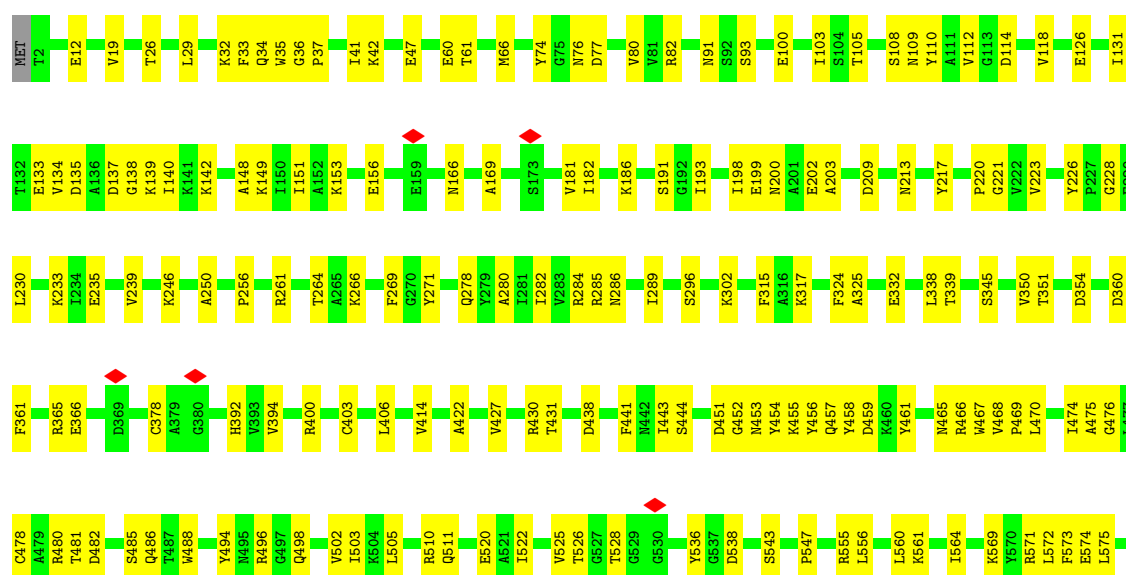
- Molecule 2: gp18, tail sheath protein

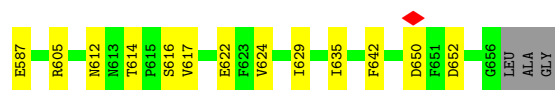
Chain K5: 73% 26%



- Molecule 2: gp18, tail sheath protein

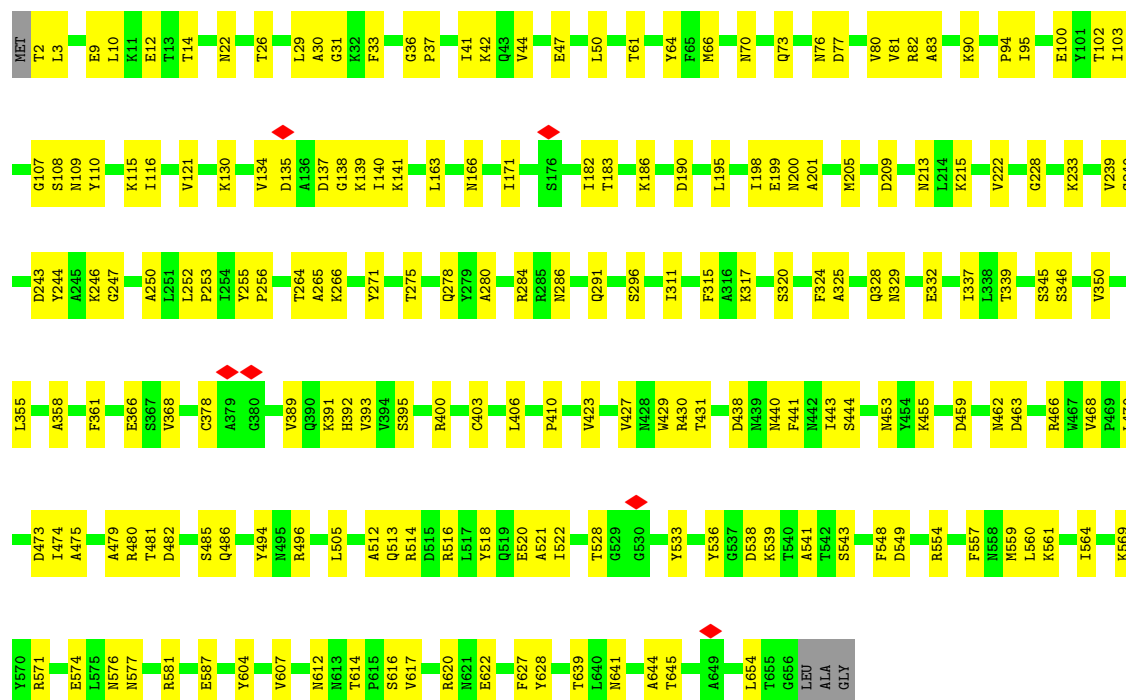
Chain K6: 71% 28%





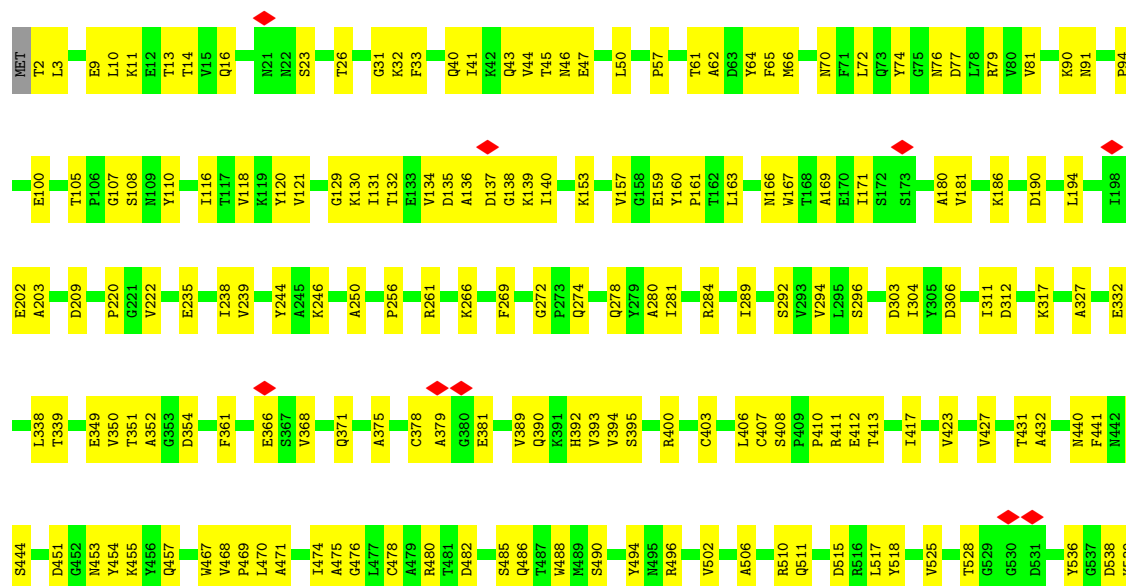
- Molecule 2: gp18, tail sheath protein

Chain K7: 70% 30%



- Molecule 2: gp18, tail sheath protein

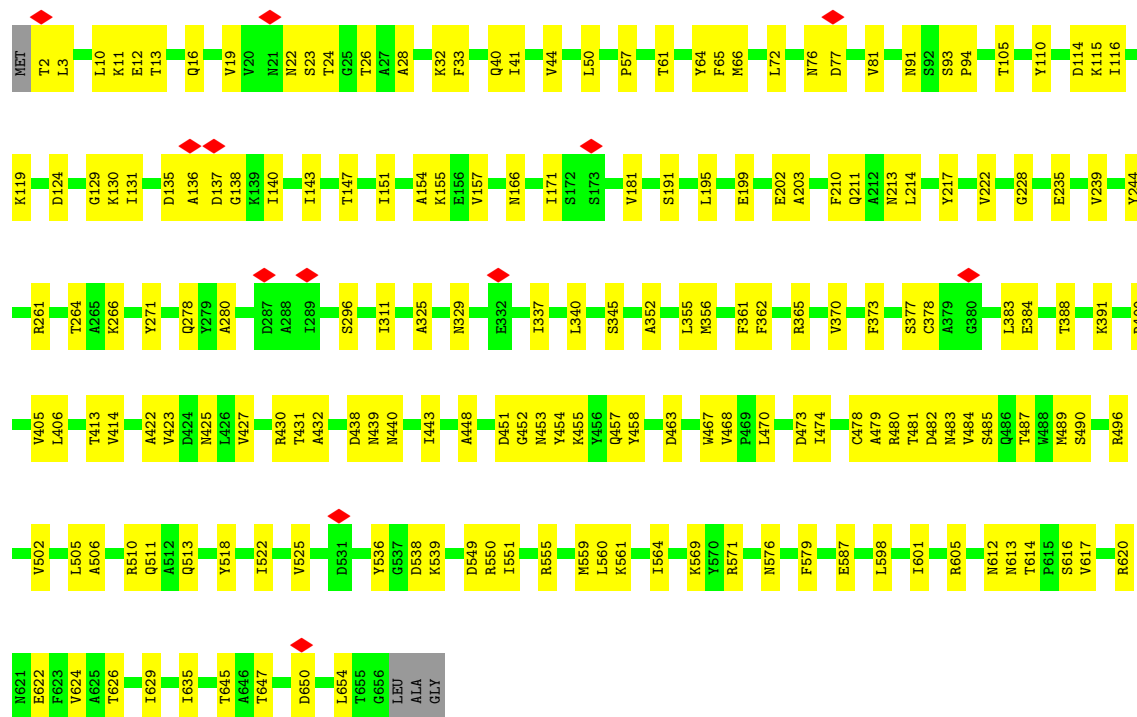
Chain K8: 68% 32%





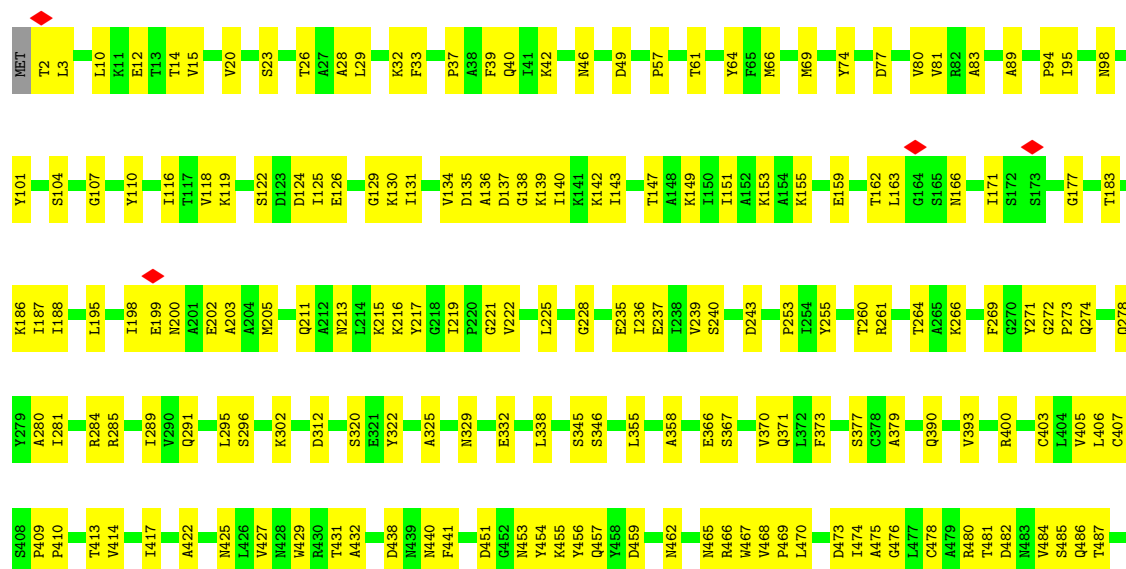
- Molecule 2: gp18, tail sheath protein

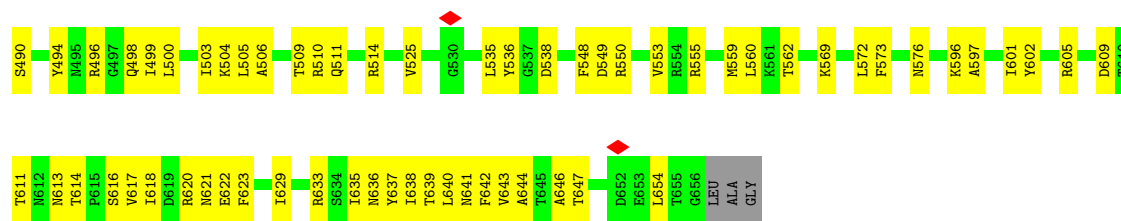
Chain K9: 72% 28%



- Molecule 2: gp18, tail sheath protein

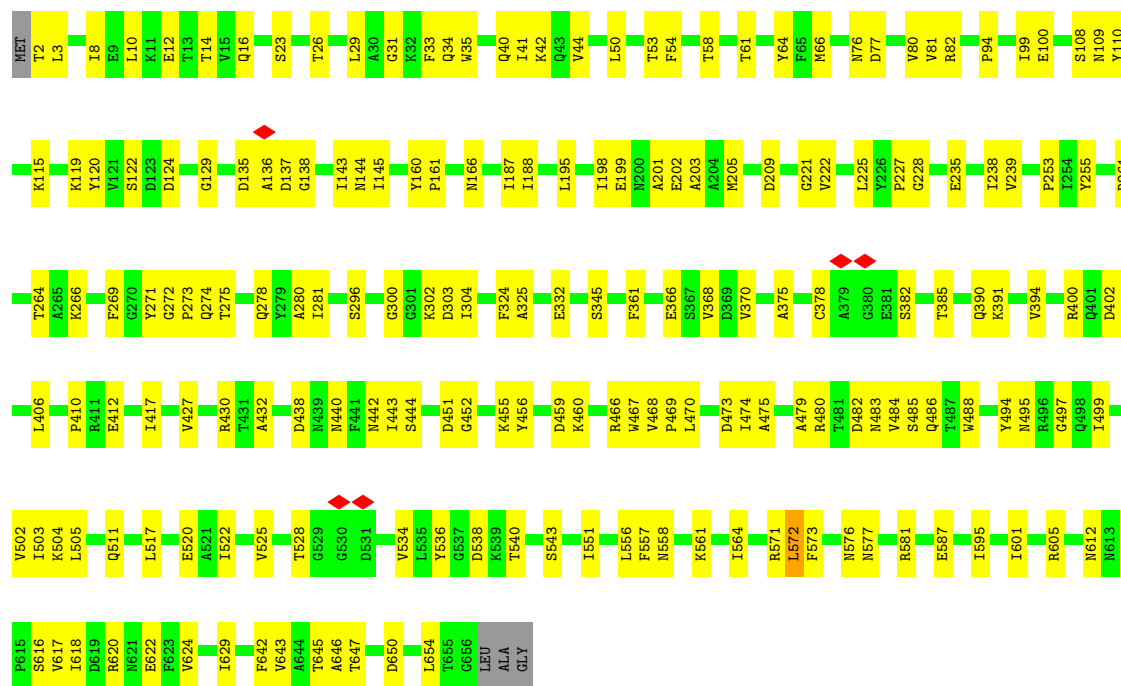
Chain L0: 63% 37%





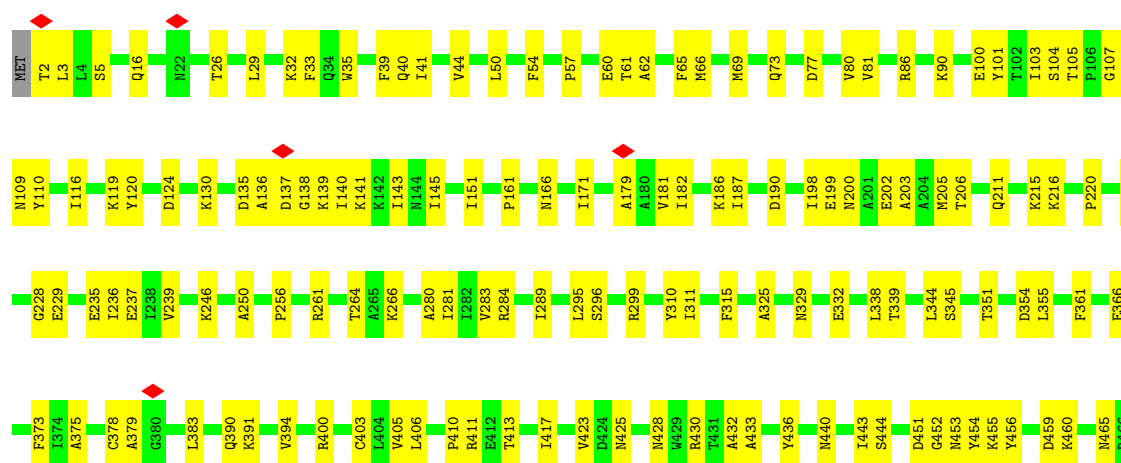
- Molecule 2: gp18, tail sheath protein

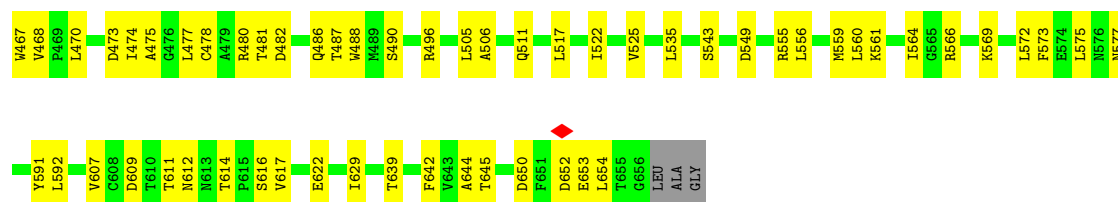
Chain L1: 70% 29%



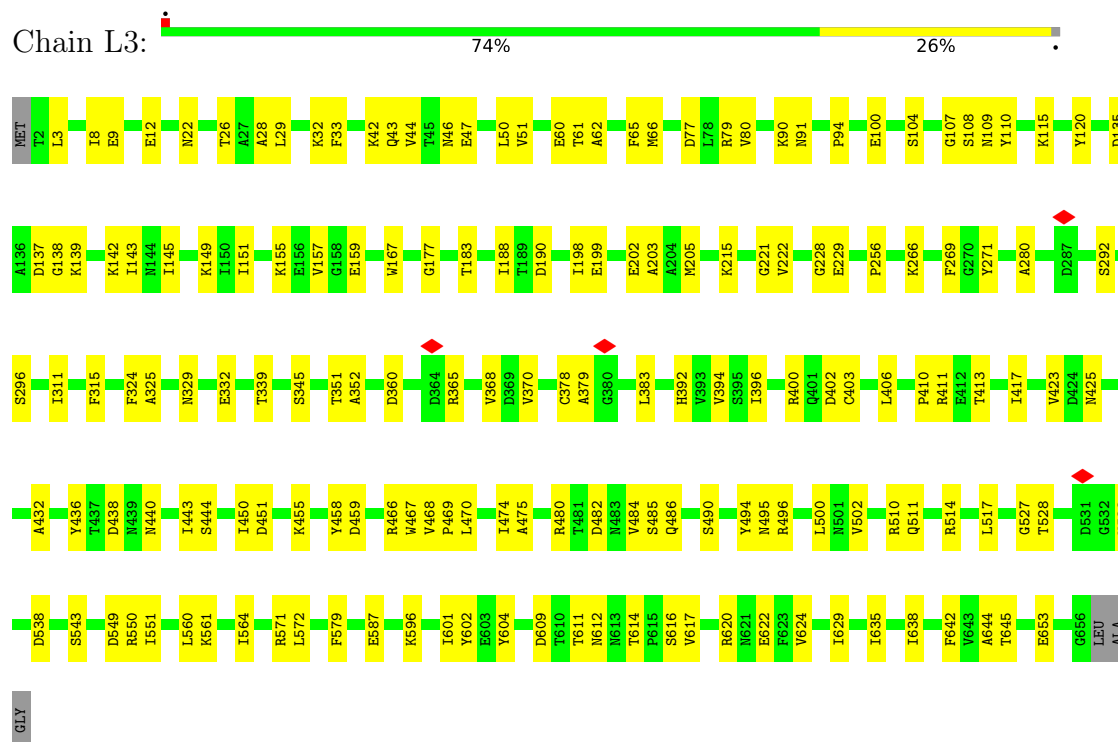
- Molecule 2: gp18, tail sheath protein

Chain L2: 69% 30%

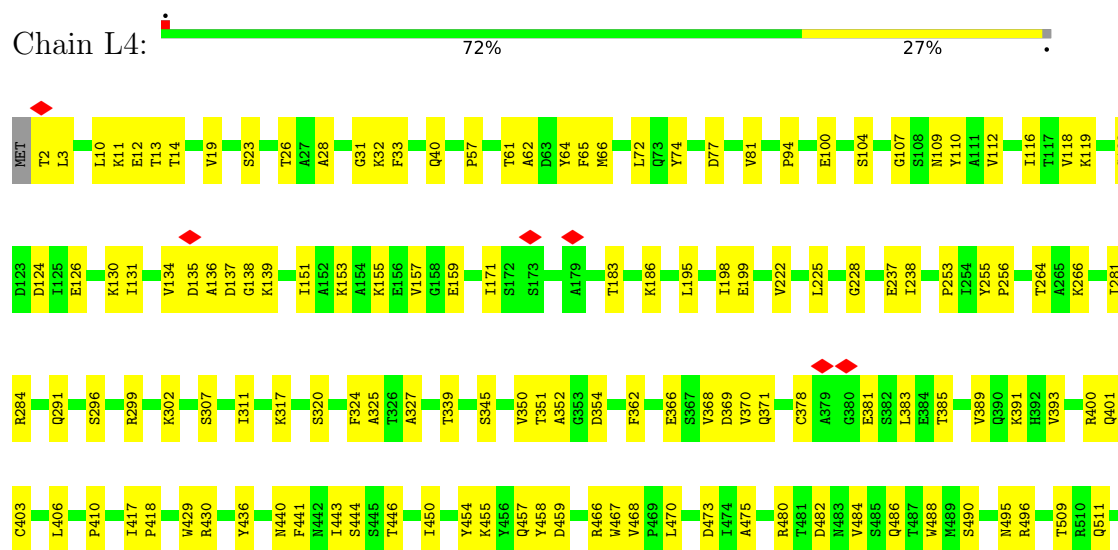




- Molecule 2: gp18, tail sheath protein

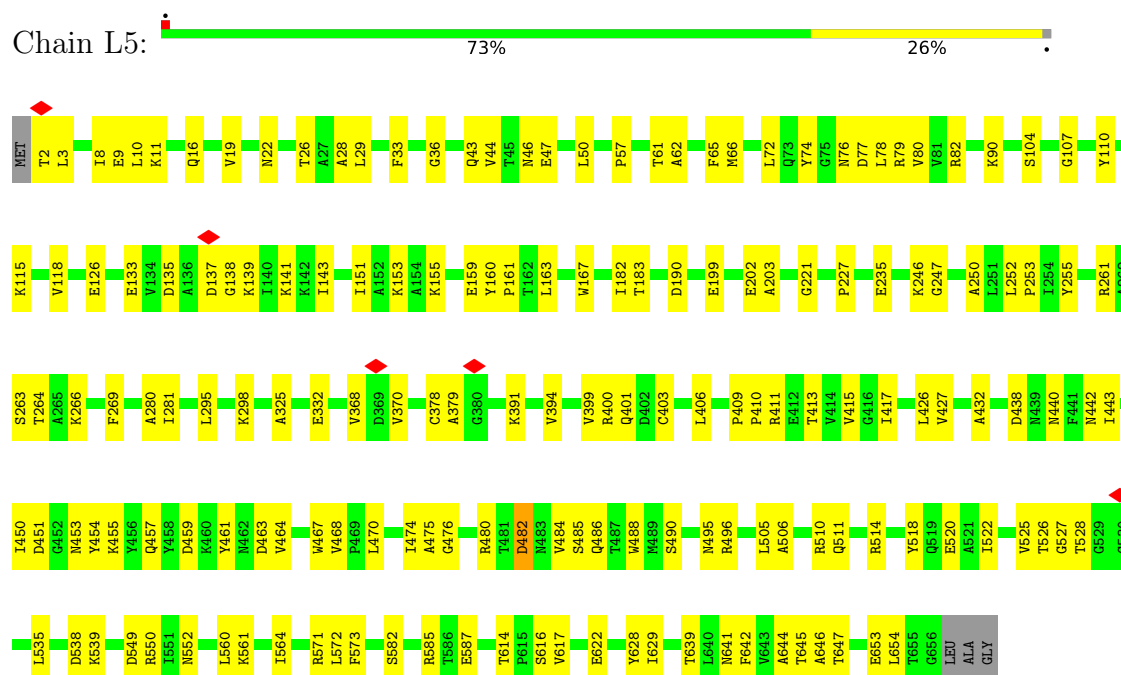


- Molecule 2: gp18, tail sheath protein

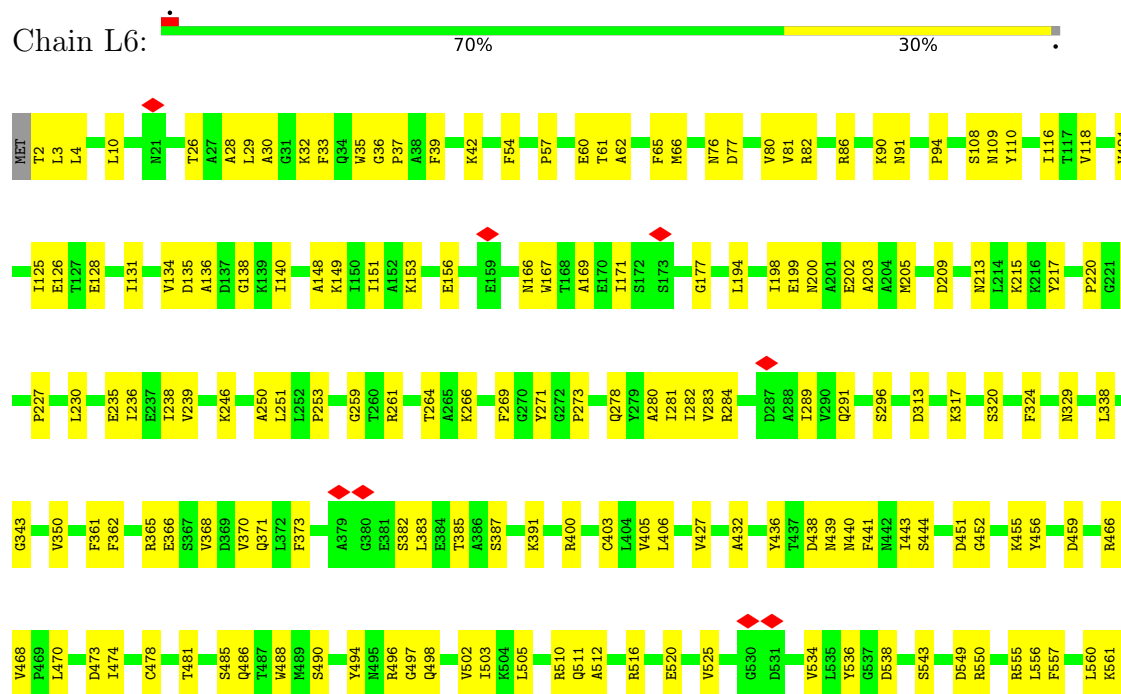


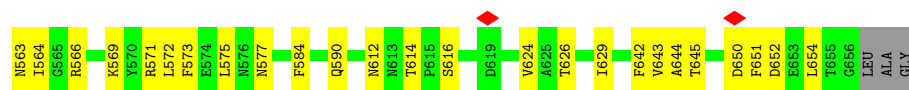


- Molecule 2: gp18, tail sheath protein

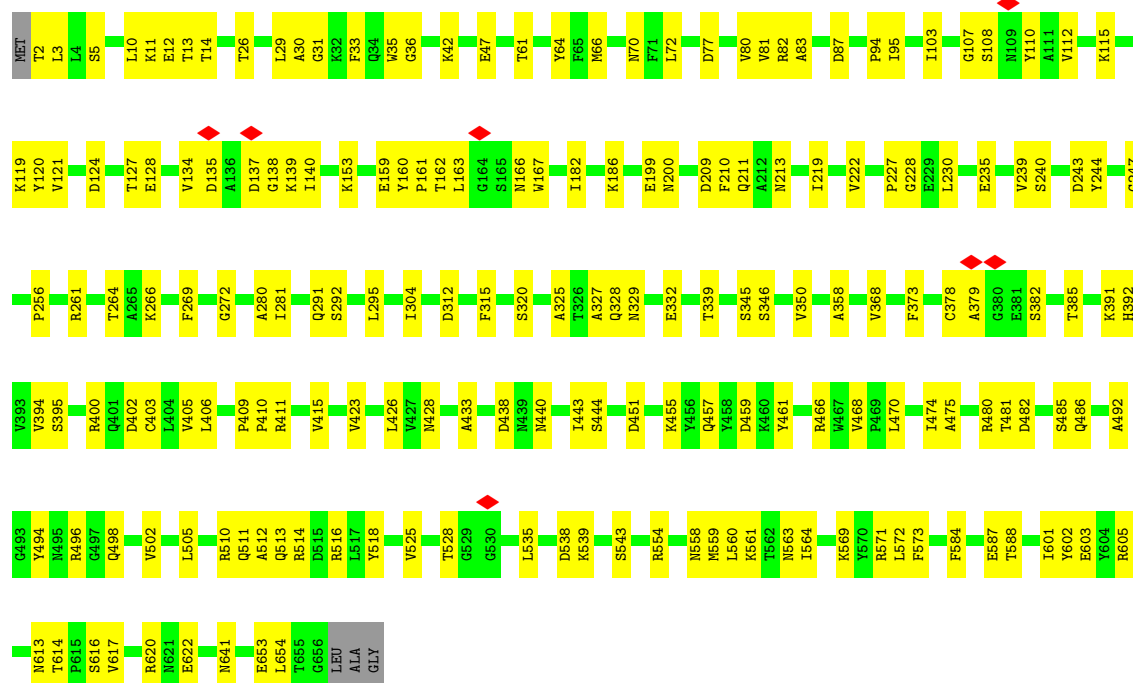


- Molecule 2: gp18, tail sheath protein

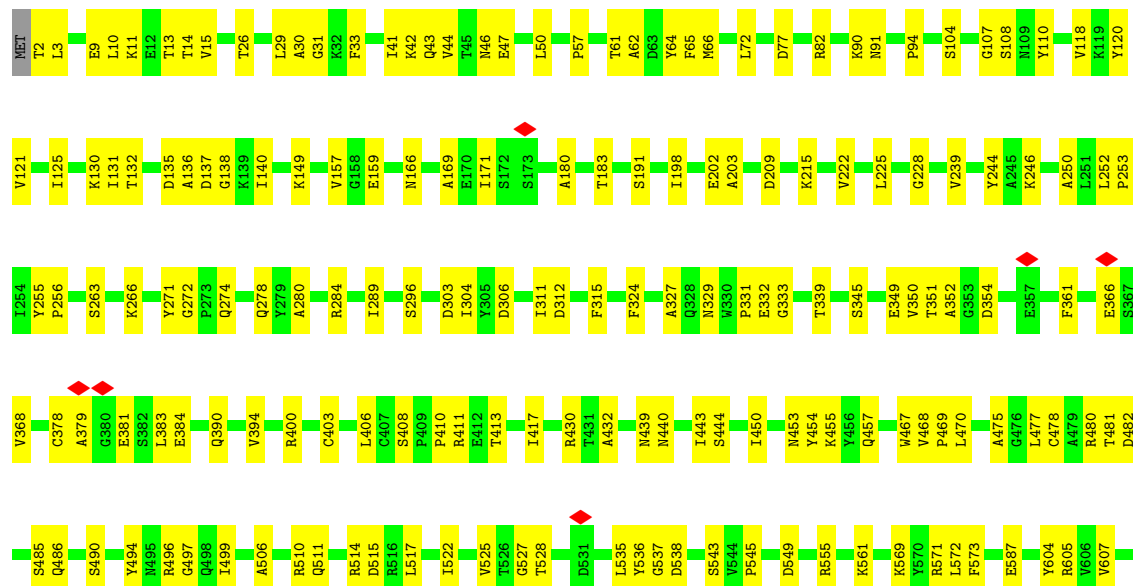




- Molecule 2: gp18, tail sheath protein



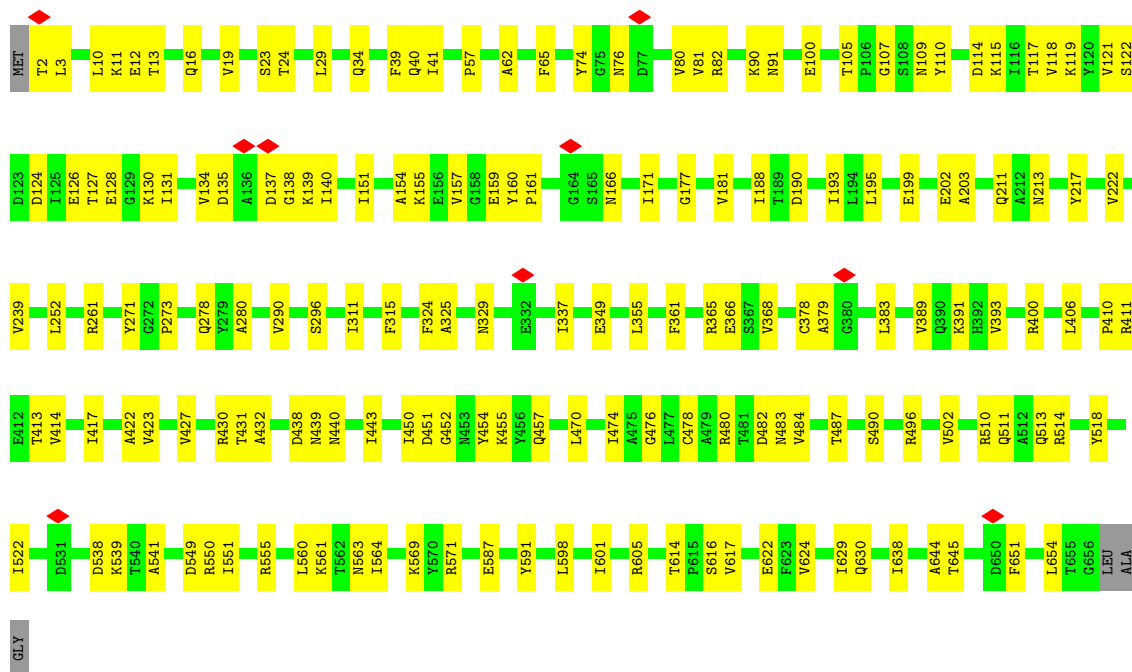
- Molecule 2: gp18, tail sheath protein





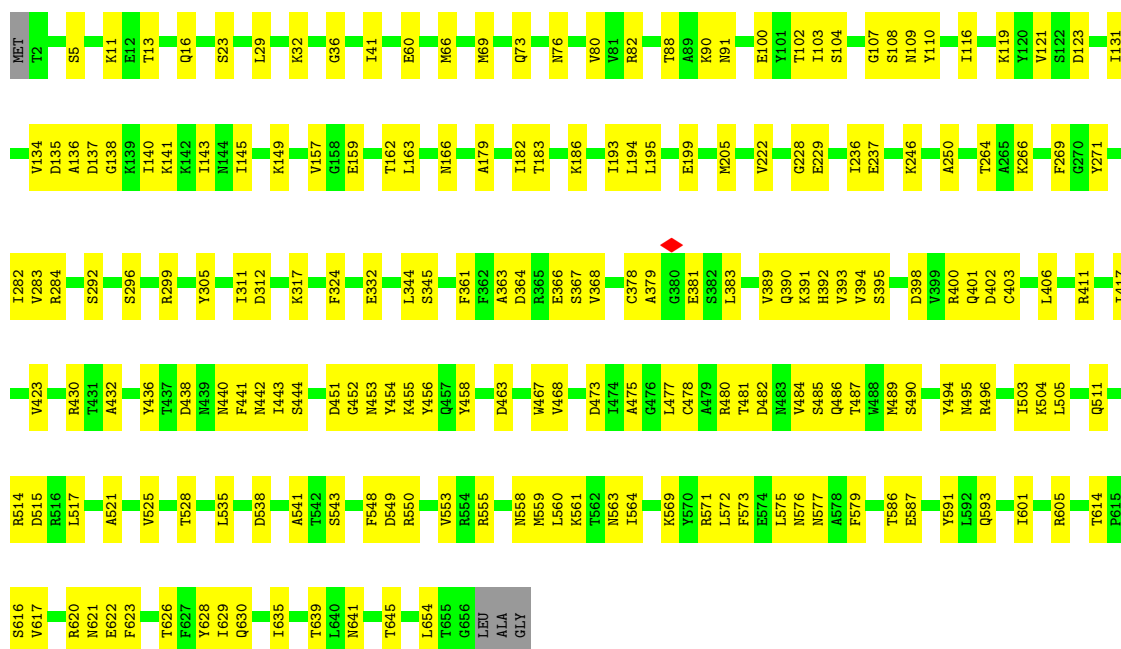
- Molecule 2: gp18, tail sheath protein

Chain L9: 74% 26%

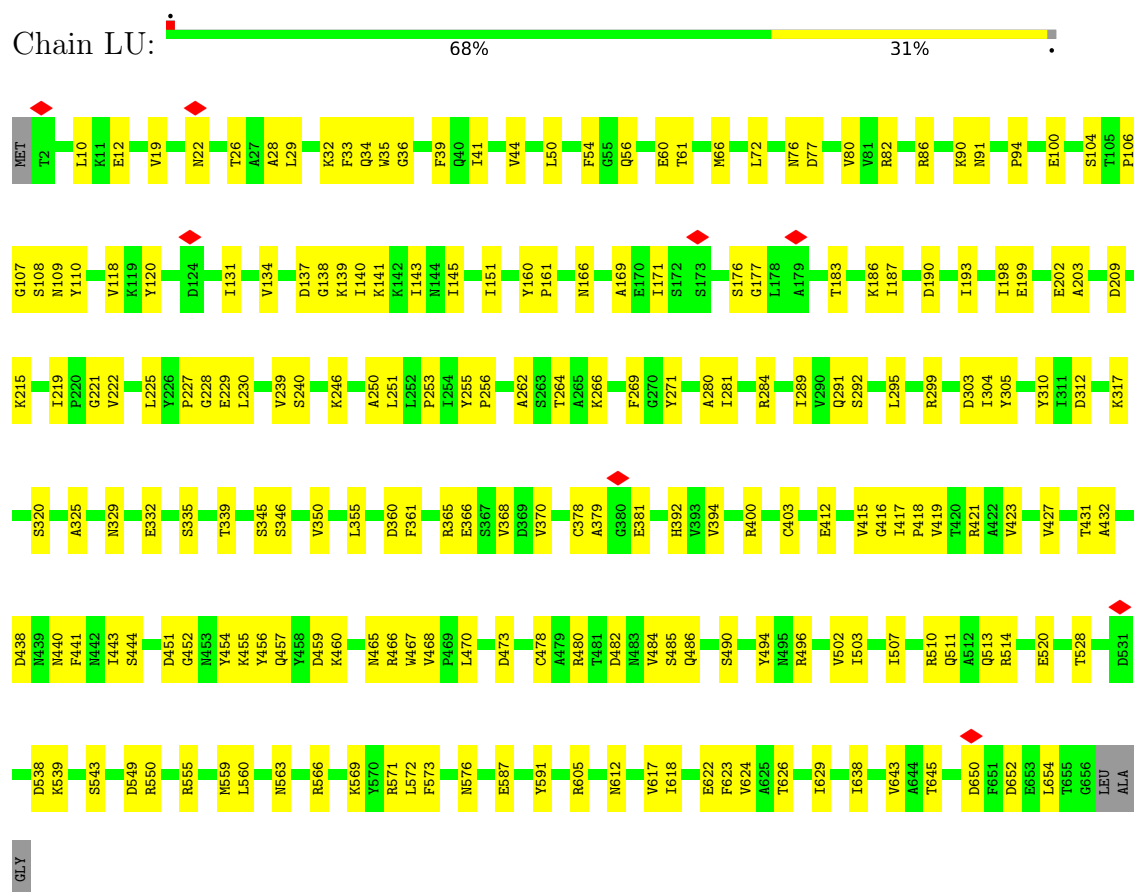


- Molecule 2: gp18, tail sheath protein

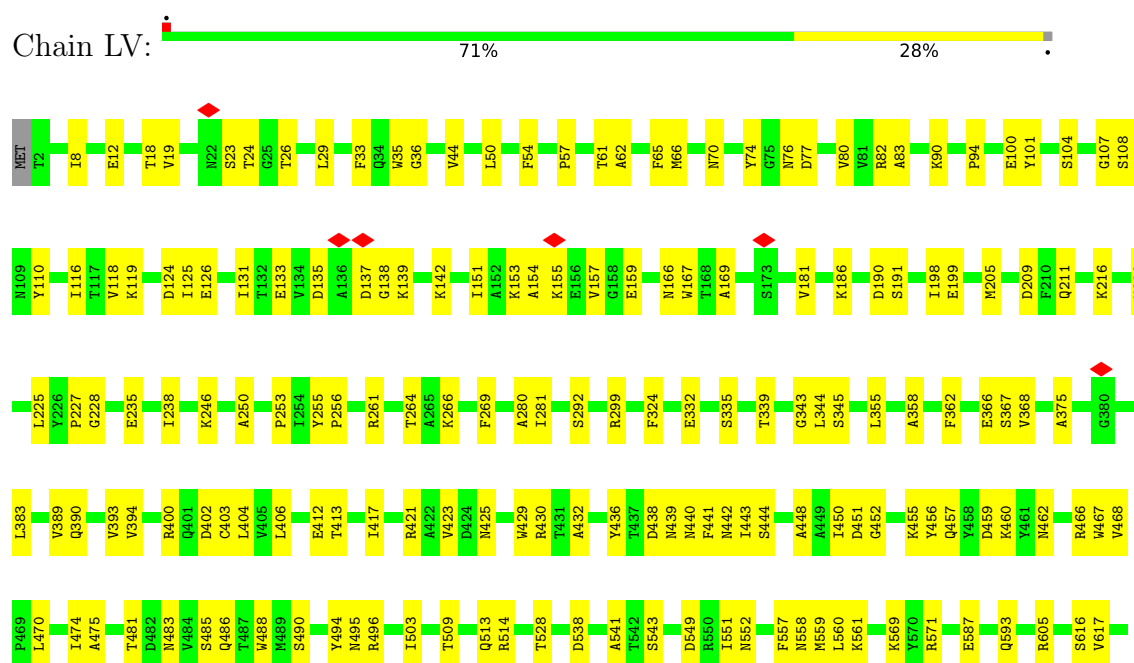
Chain LS: 69% 30%



• Molecule 2: gp18, tail sheath protein

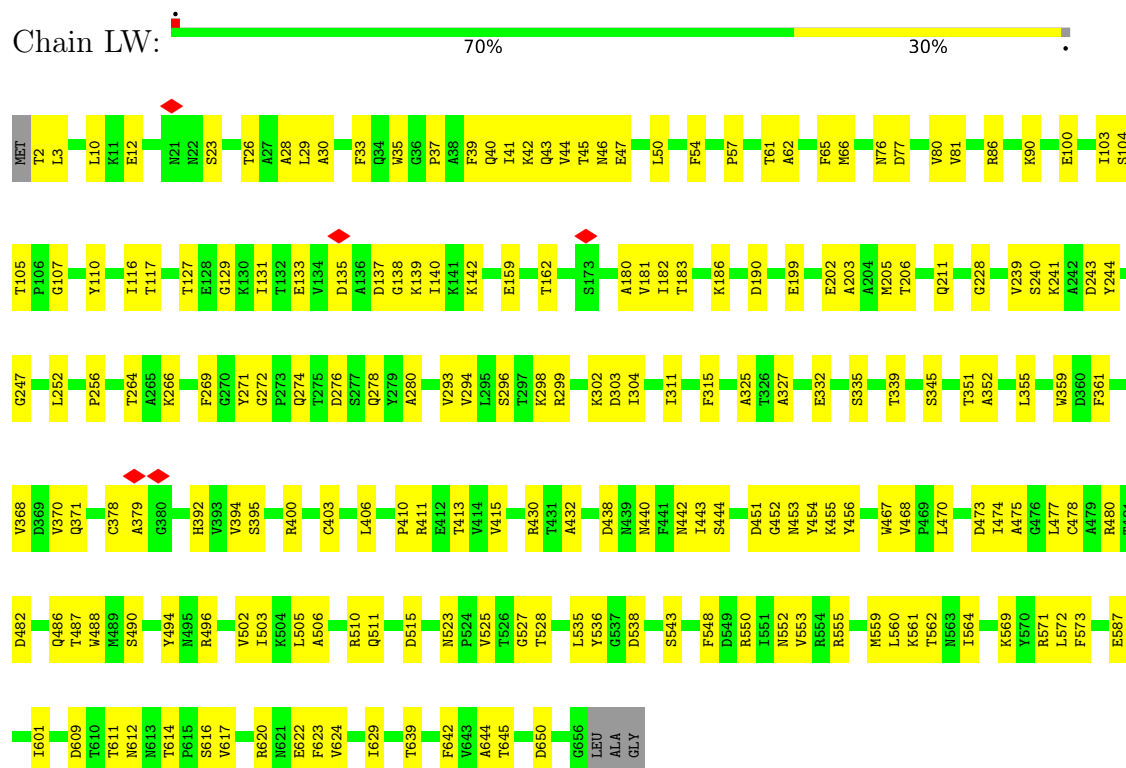


• Molecule 2: gp18, tail sheath protein

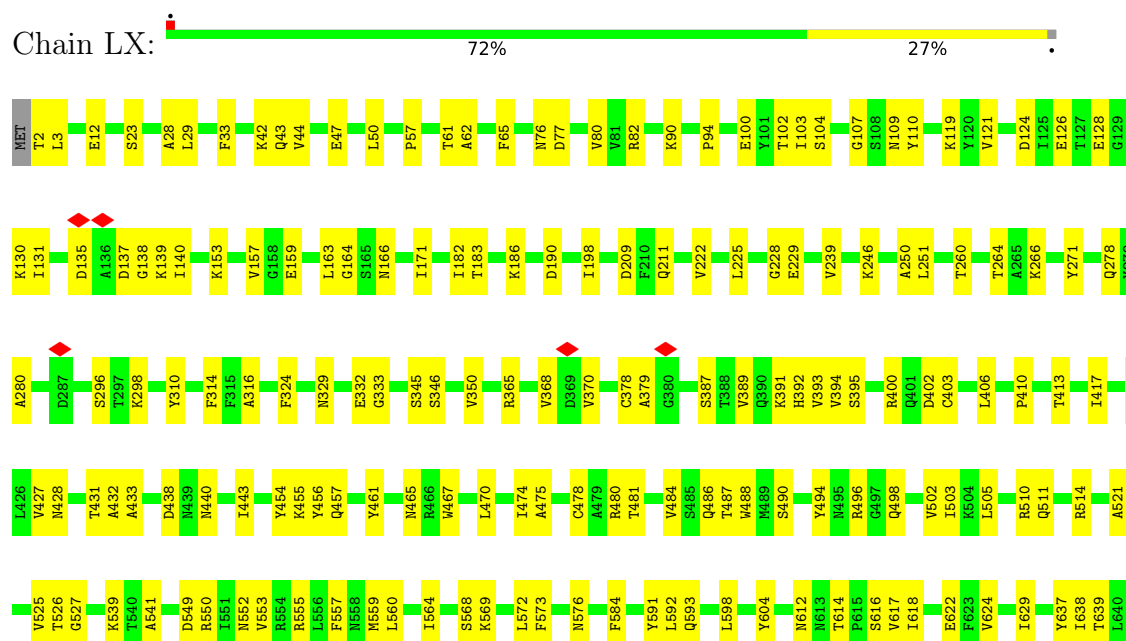




- Molecule 2: gp18, tail sheath protein



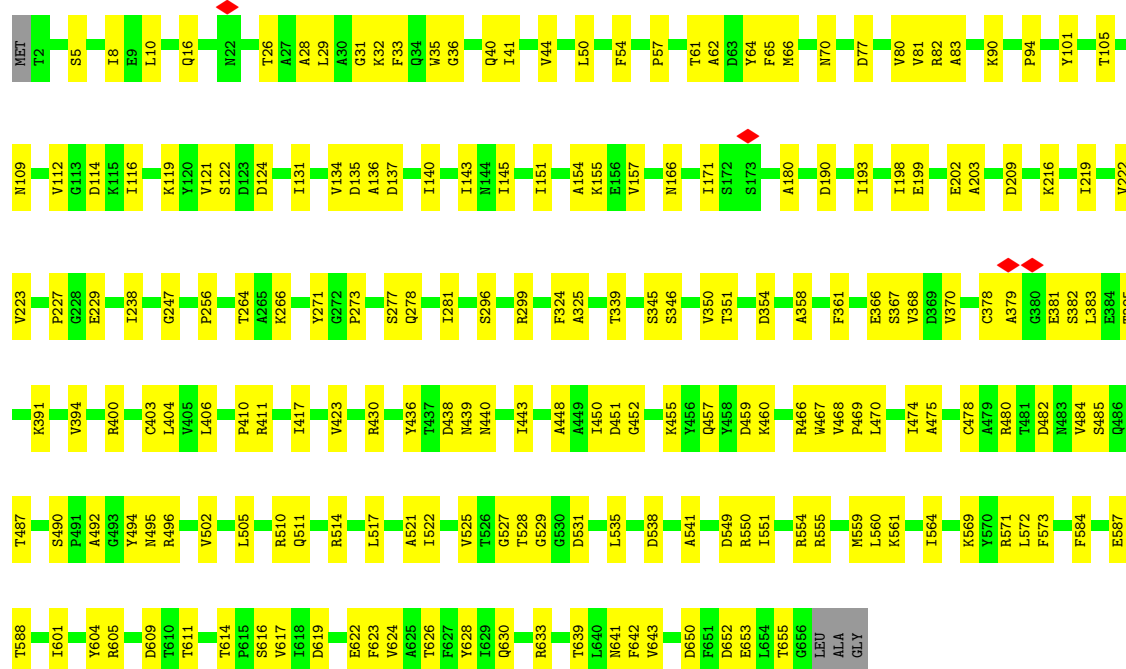
- Molecule 2: gp18, tail sheath protein





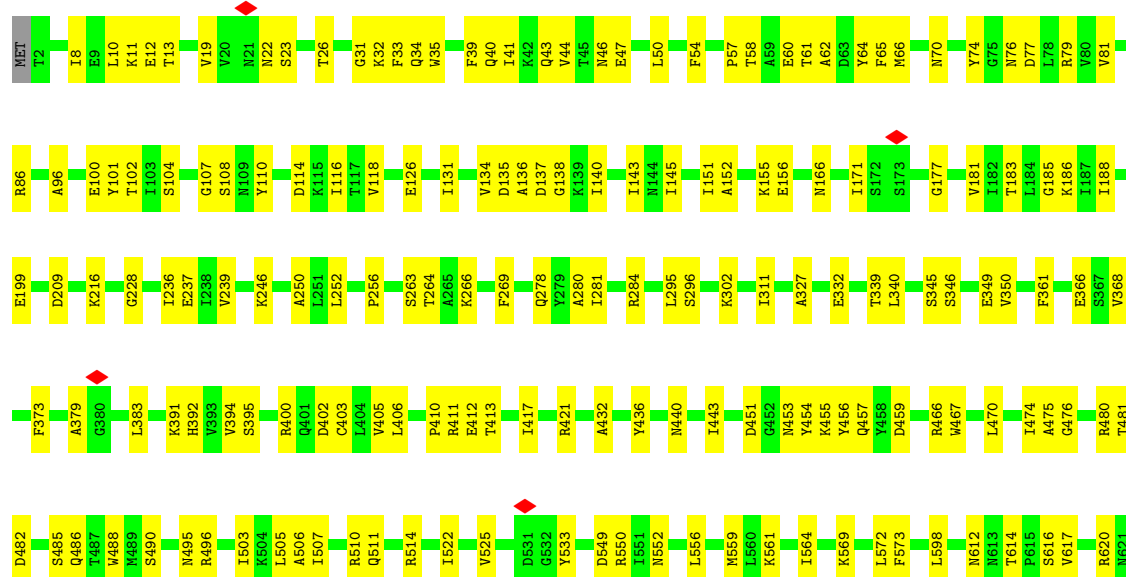
• Molecule 2: gp18, tail sheath protein

Chain LY: 69% 30%



• Molecule 2: gp18, tail sheath protein

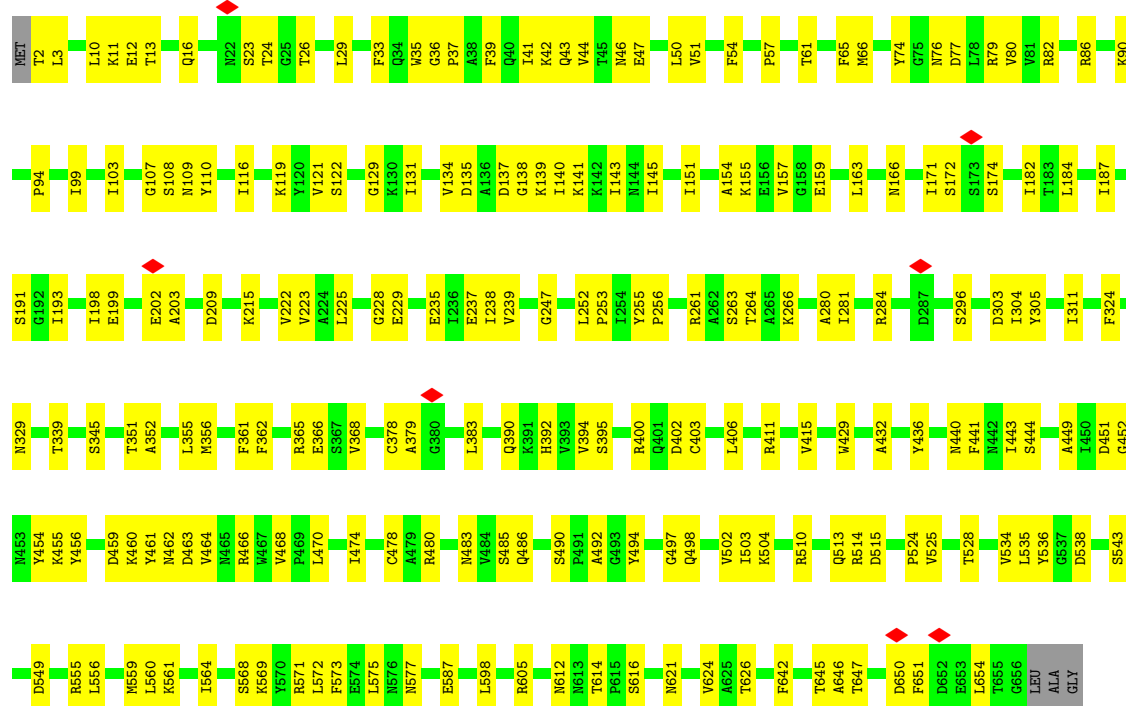
Chain LZ: 71% 28%





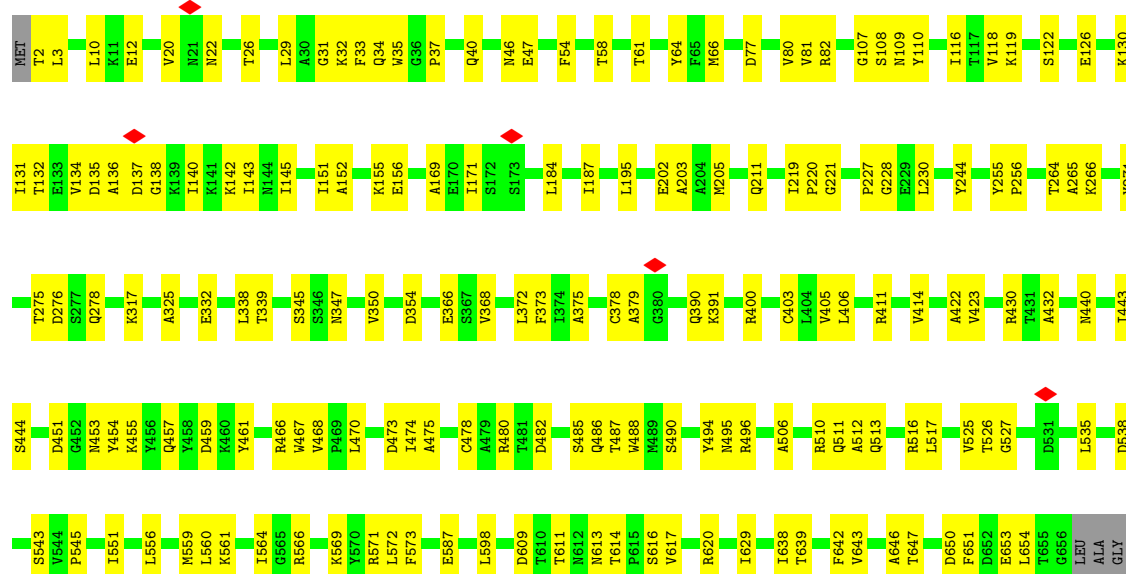
- Molecule 2: gp18, tail sheath protein

Chain La: 68% 32%

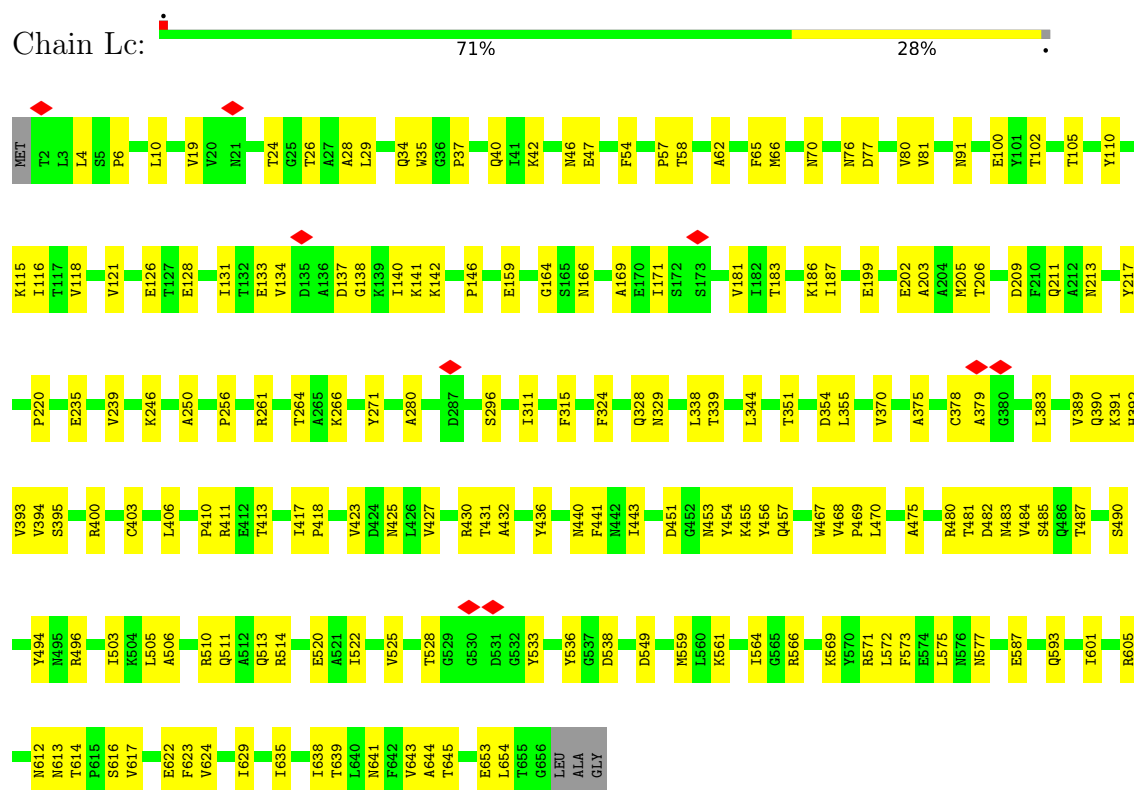


- Molecule 2: gp18, tail sheath protein

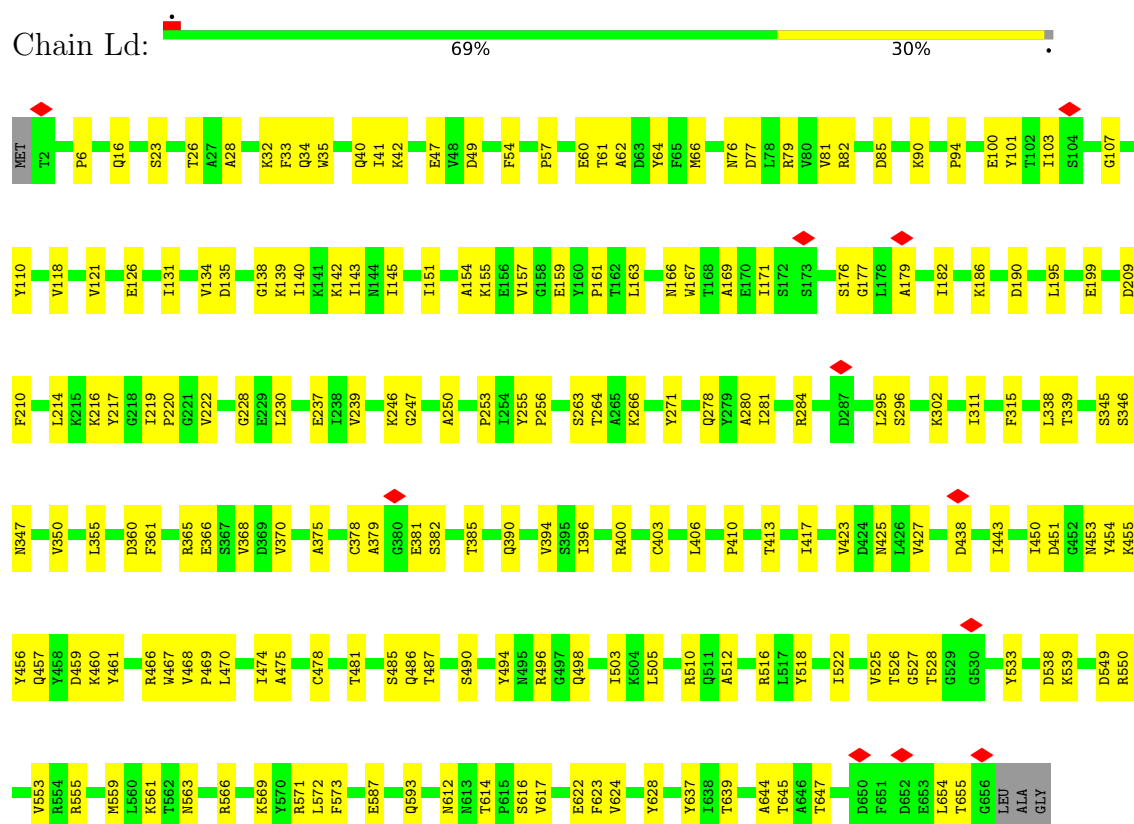
Chain Lb: 73% 27%



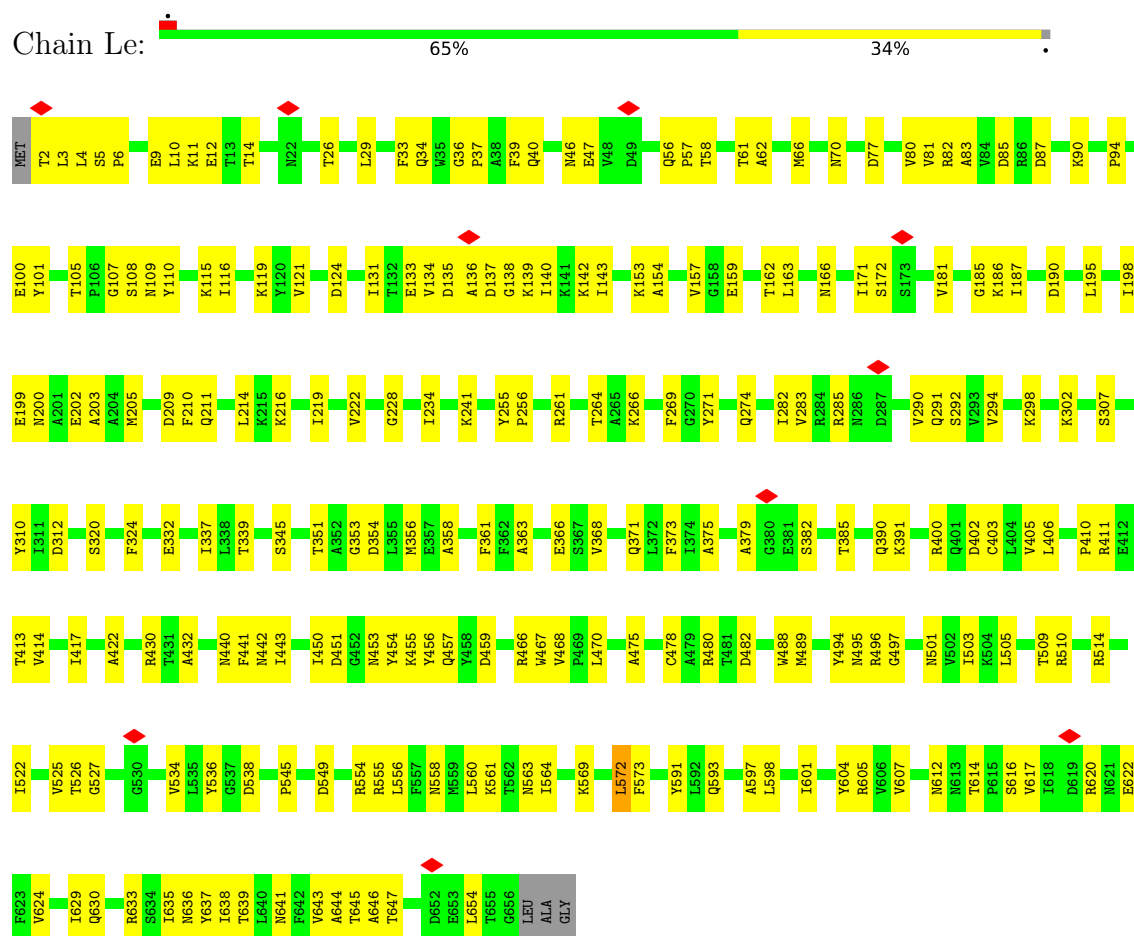
- Molecule 2: gp18, tail sheath protein



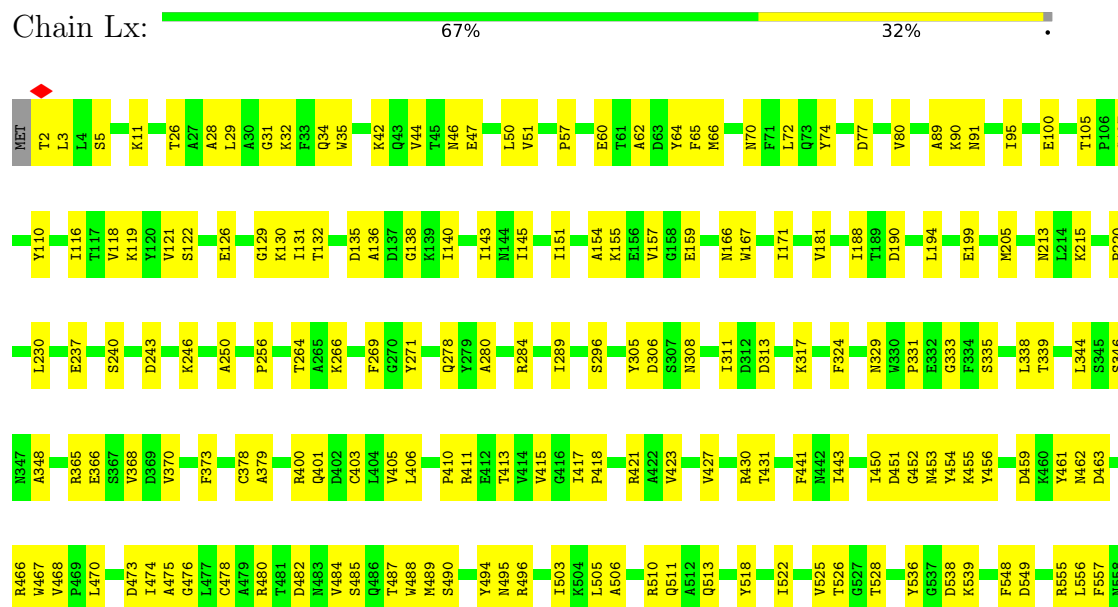
- Molecule 2: gp18, tail sheath protein



- Molecule 2: gp18, tail sheath protein

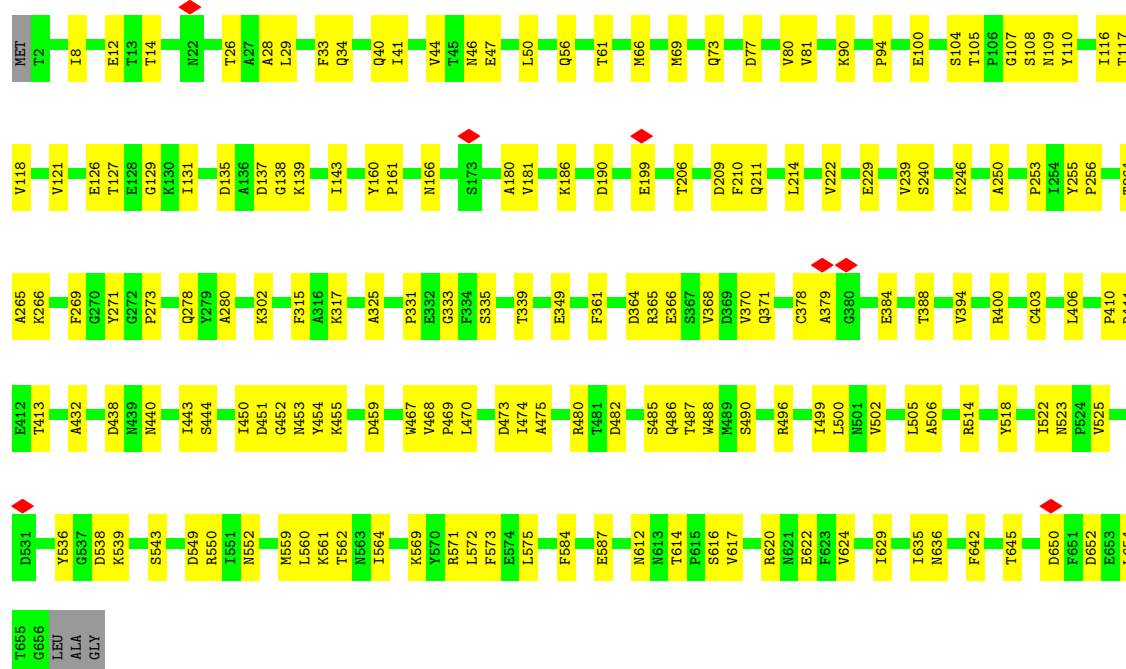
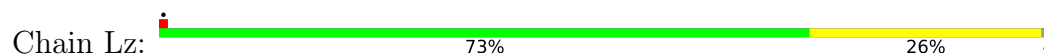


- Molecule 2: gp18, tail sheath protein

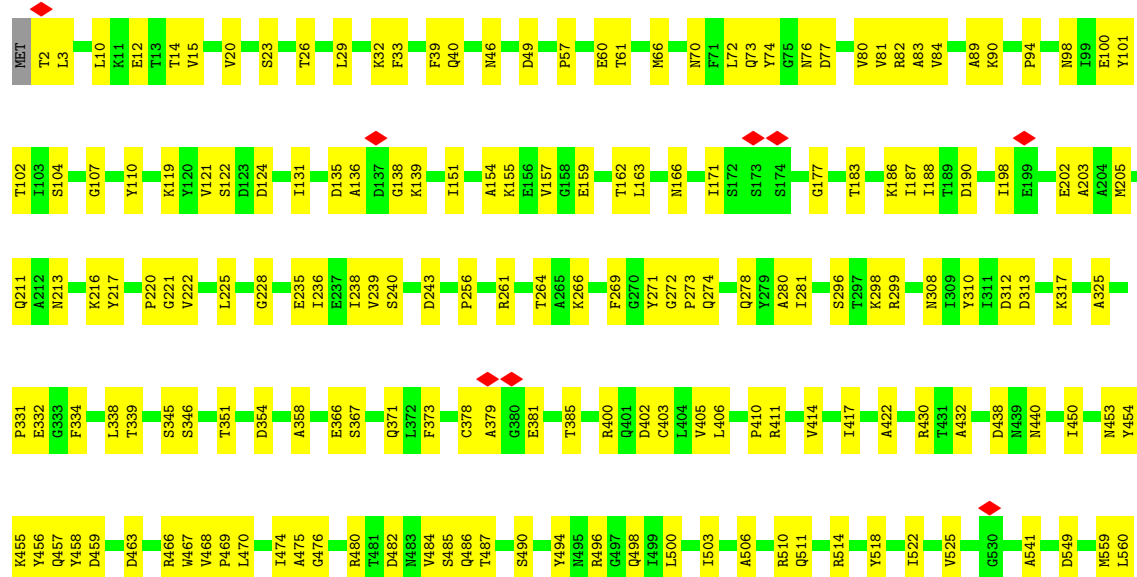




- Molecule 2: gp18, tail sheath protein



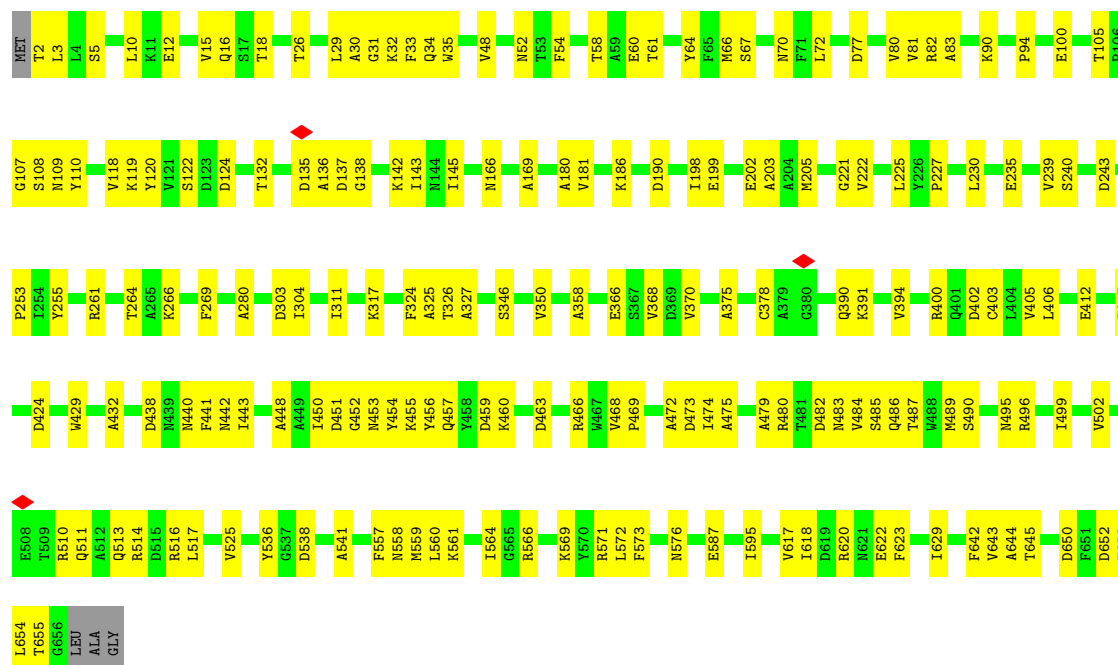
- Molecule 2: gp18, tail sheath protein





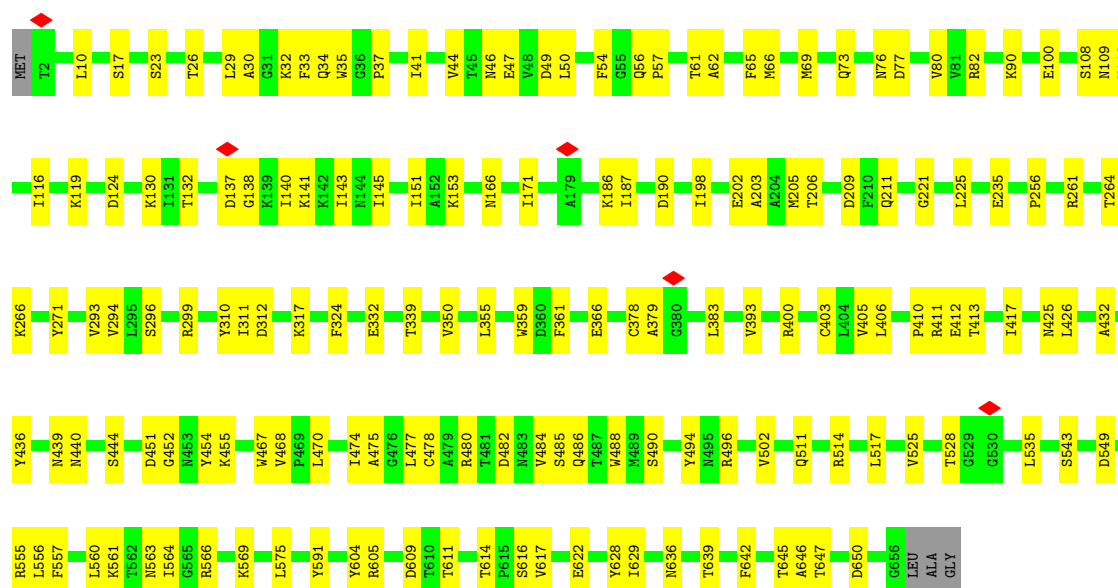
- Molecule 2: gp18, tail sheath protein

Chain M1:

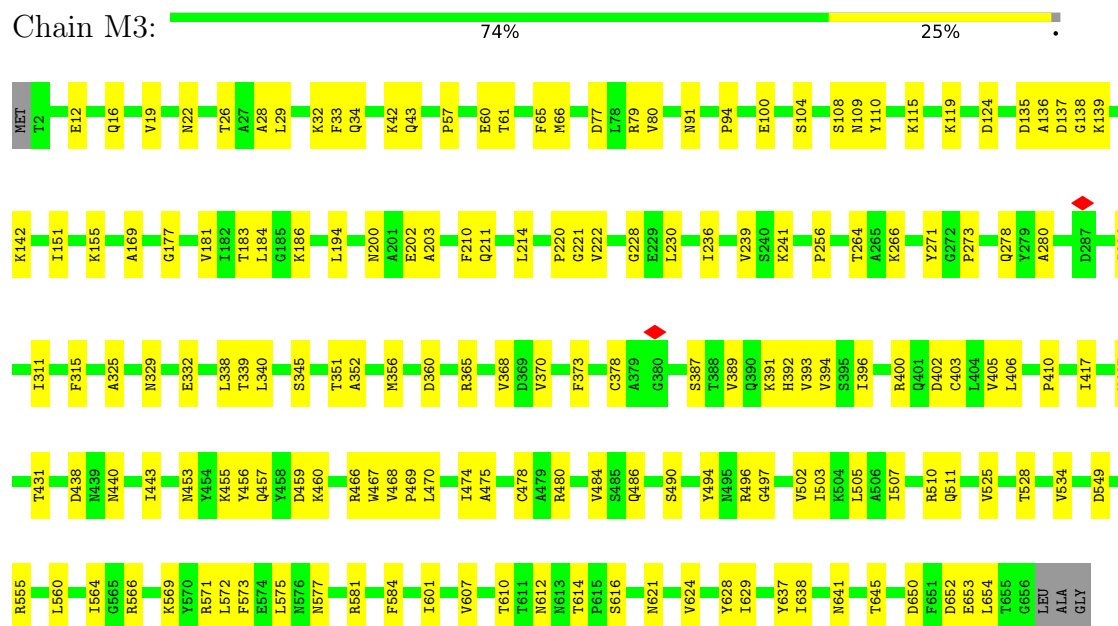


- Molecule 2: gp18, tail sheath protein

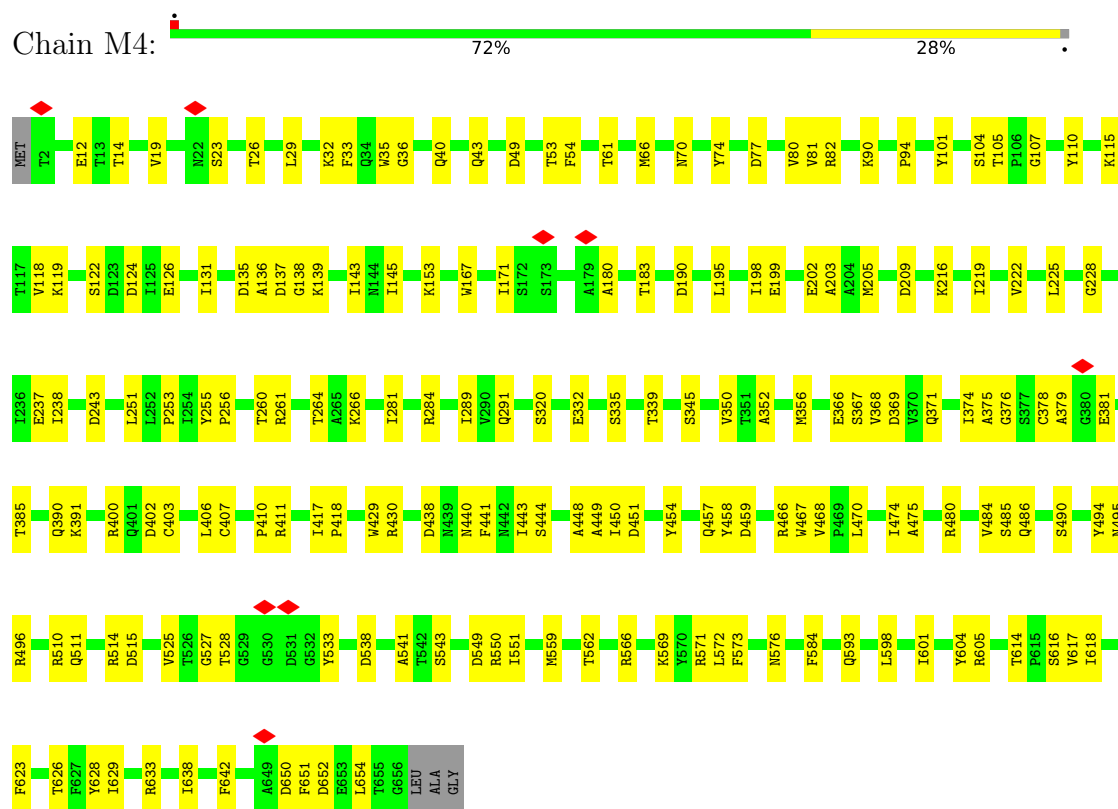
Chain M2:



- Molecule 2: gp18, tail sheath protein

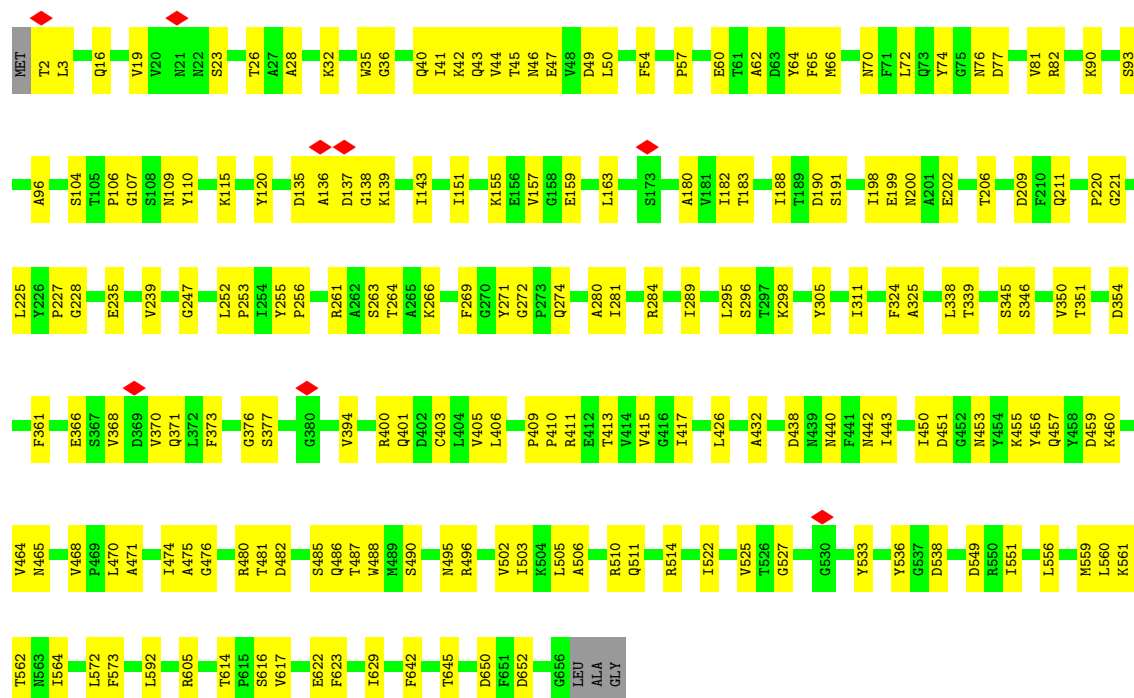


- Molecule 2: gp18, tail sheath protein

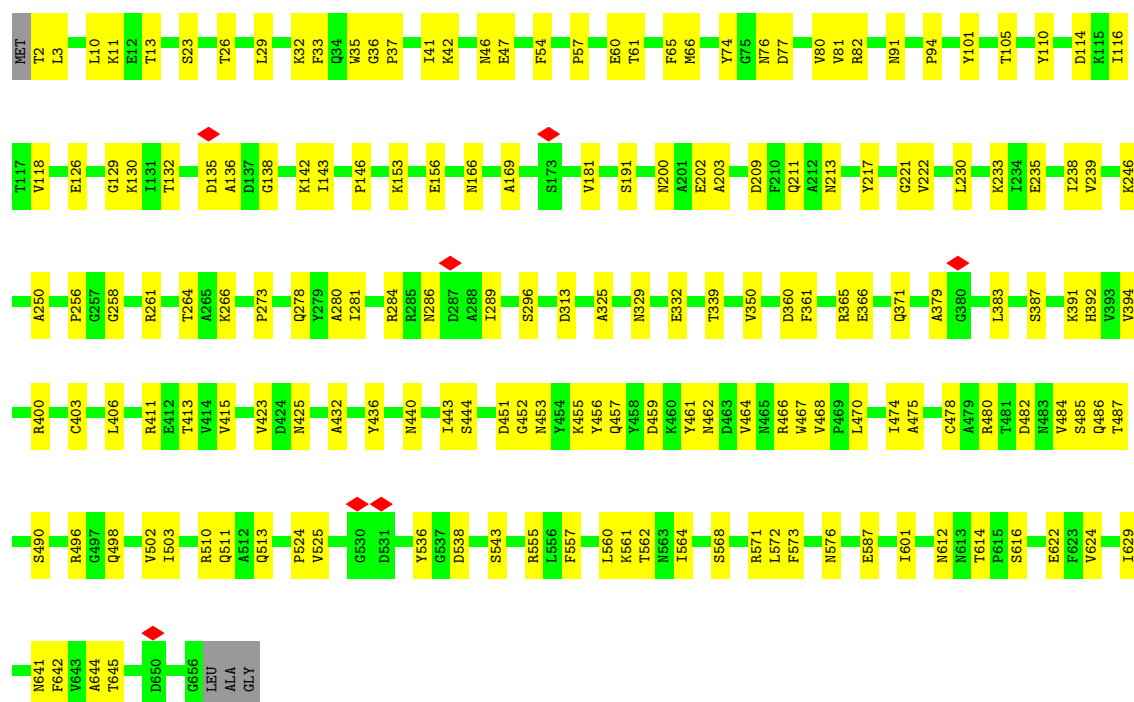
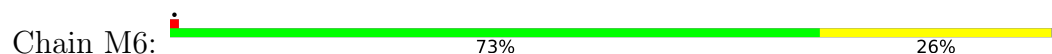


- Molecule 2: gp18, tail sheath protein



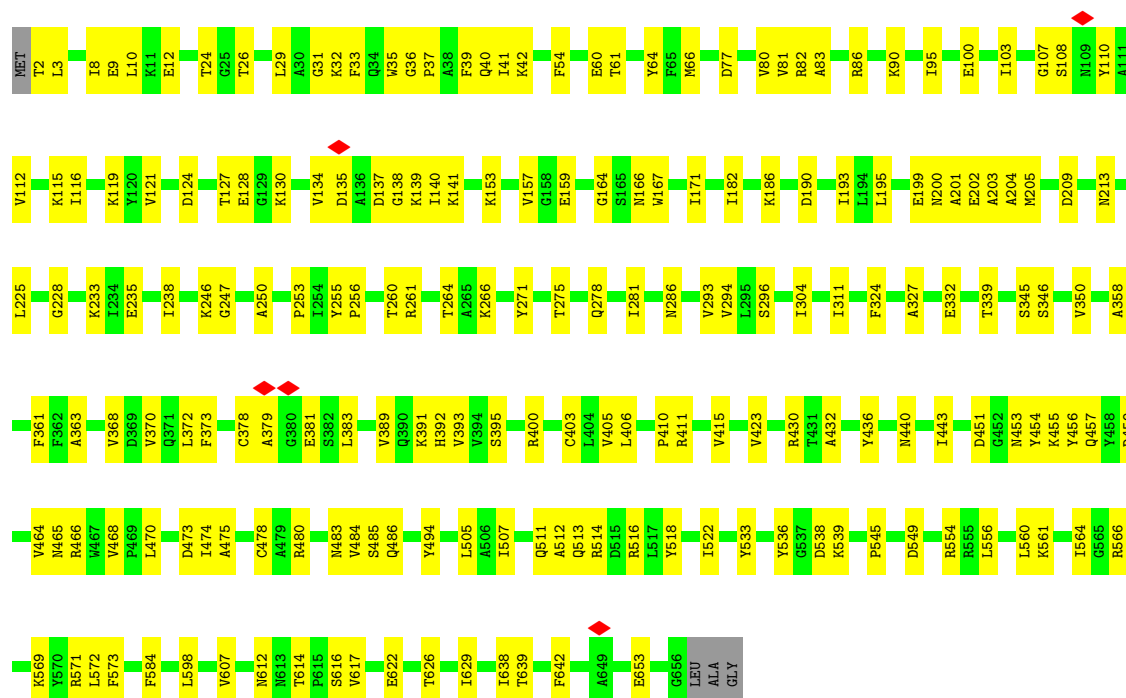


- Molecule 2: gp18, tail sheath protein

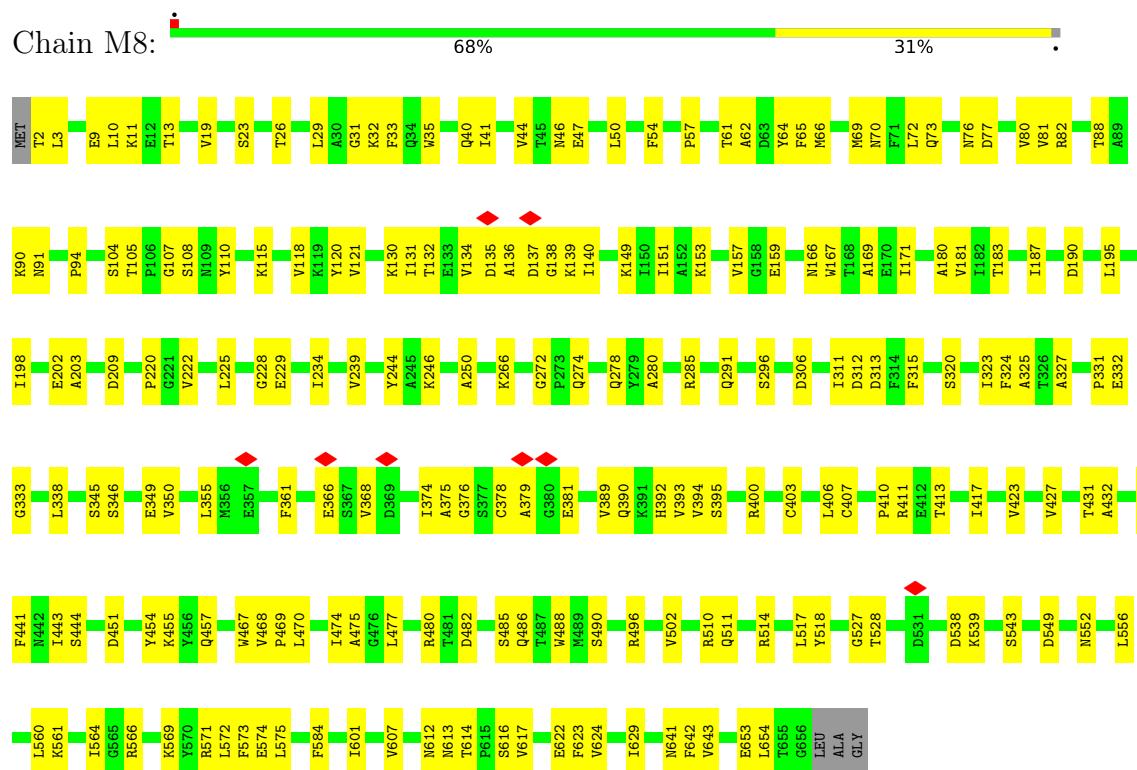


- Molecule 2: gp18, tail sheath protein

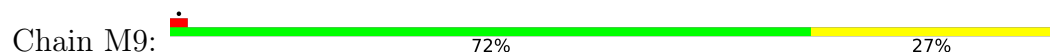


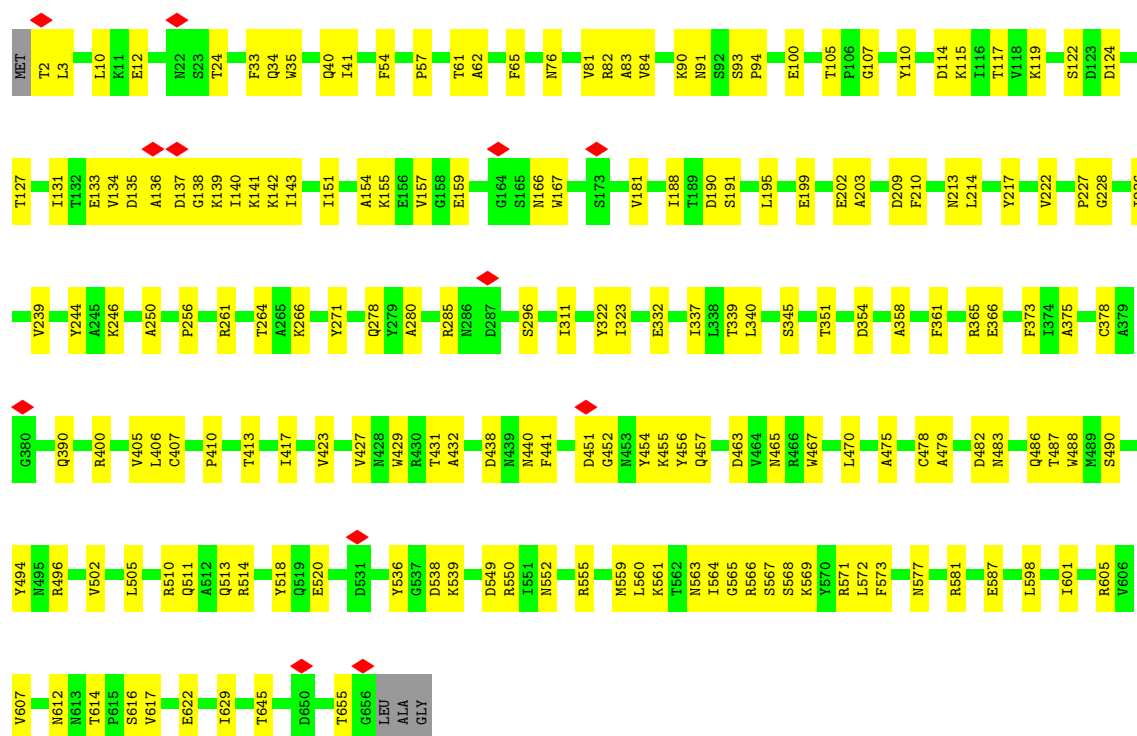


Chain M8:

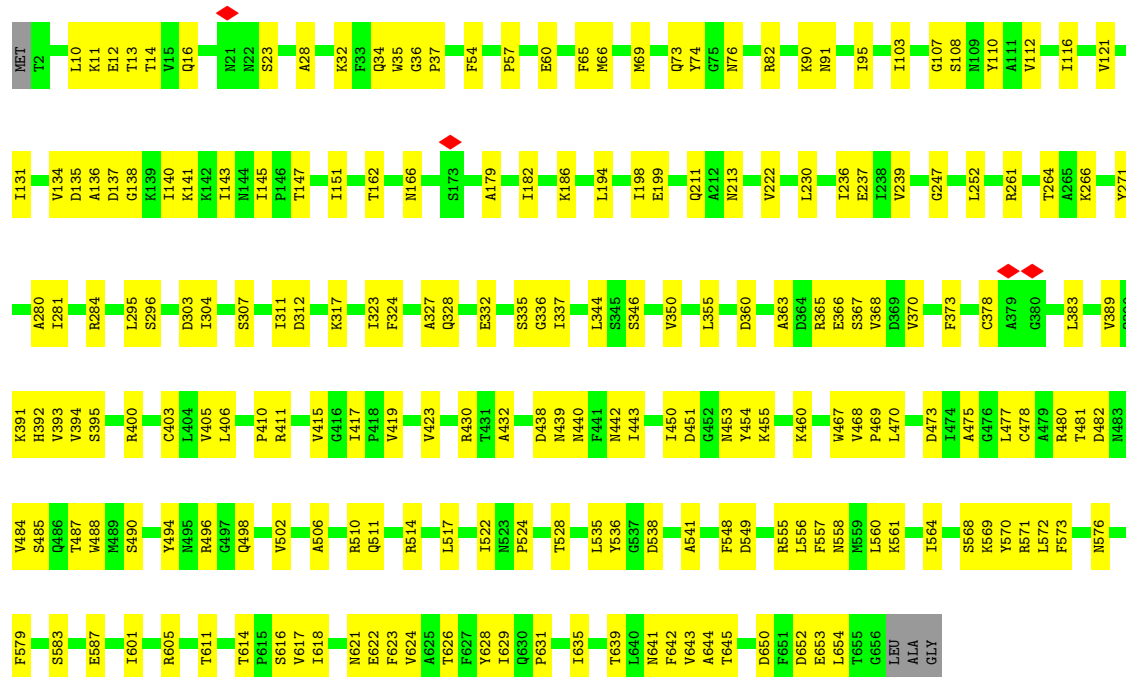


Chain M9:



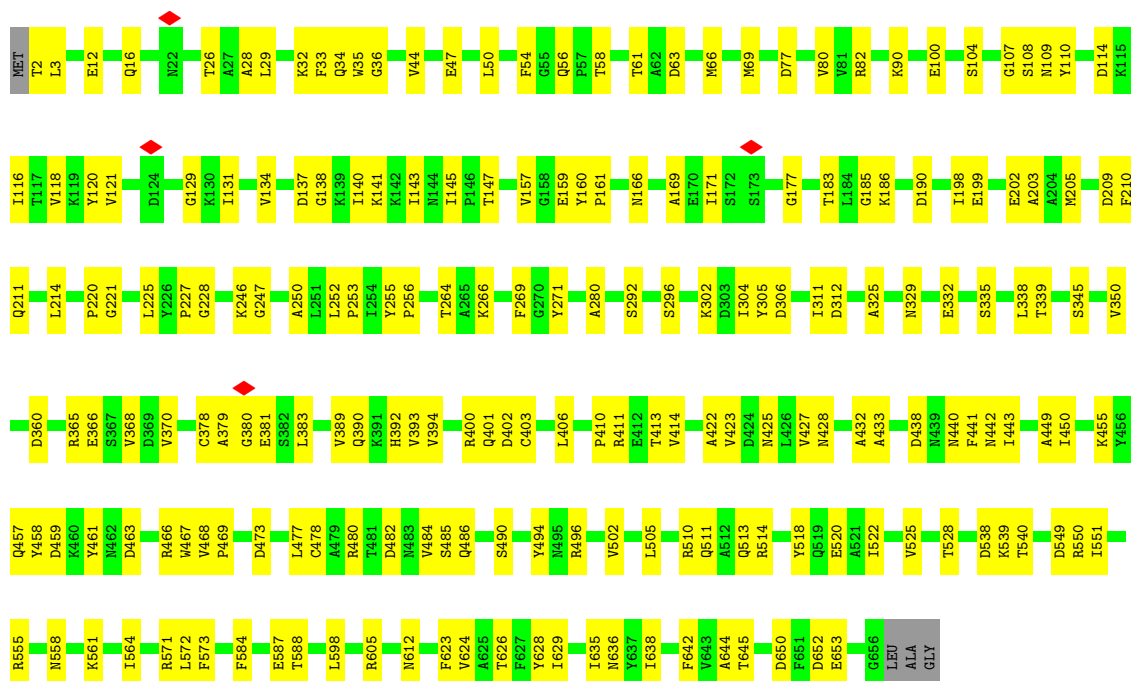


• Molecule 2: gp18, tail sheath protein

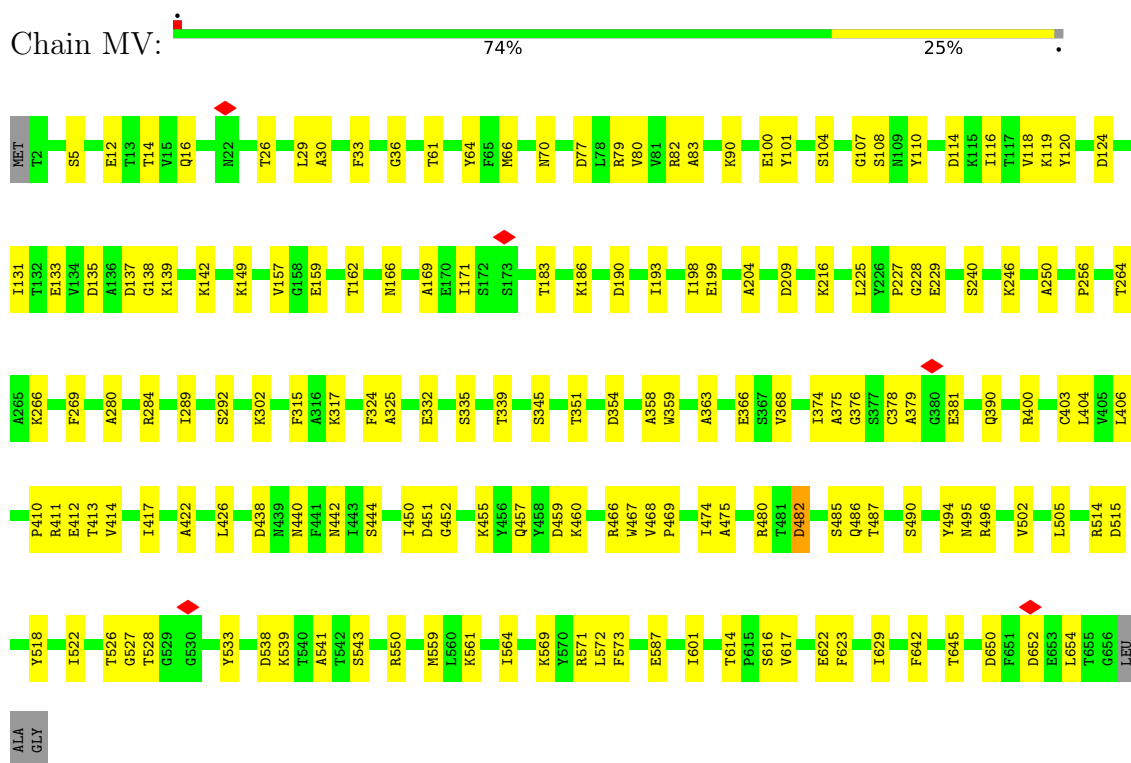


• Molecule 2: gp18, tail sheath protein



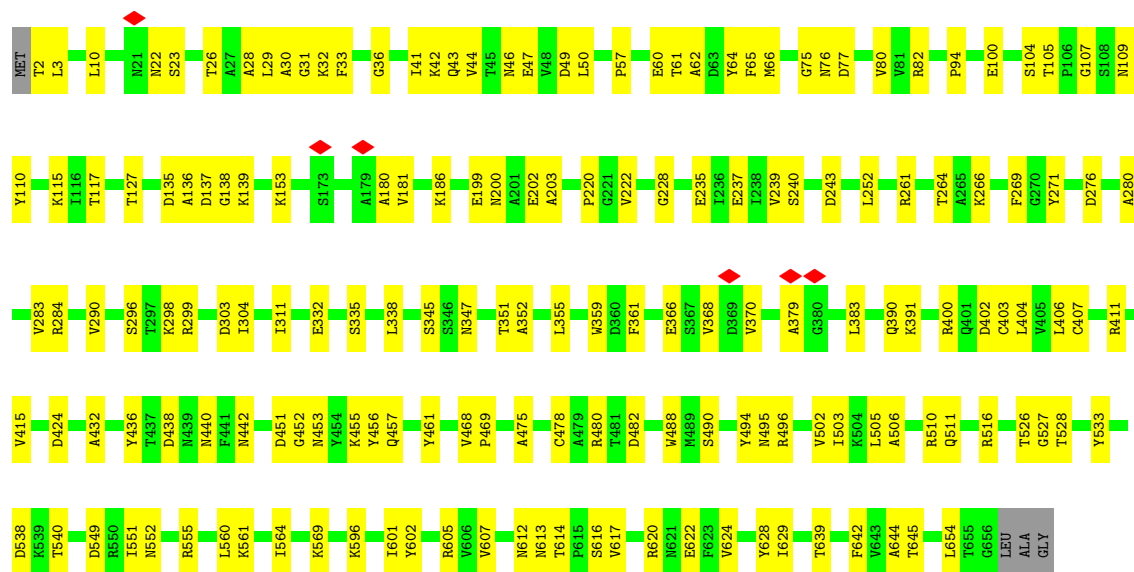


• Molecule 2: gp18, tail sheath protein



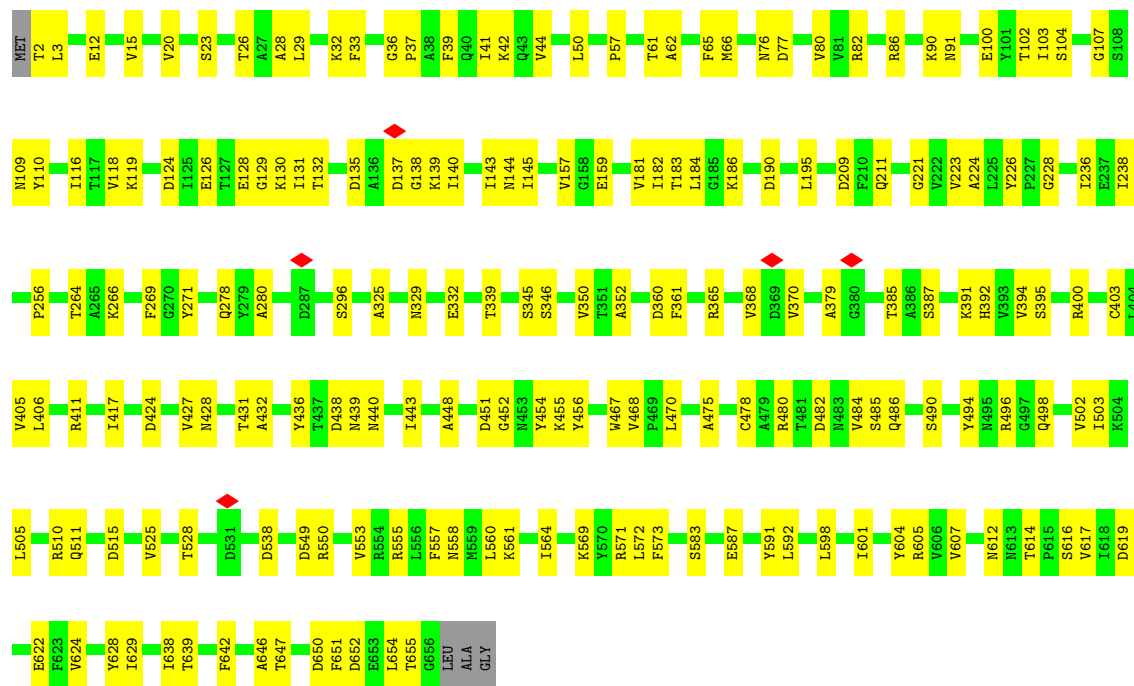
• Molecule 2: gp18, tail sheath protein





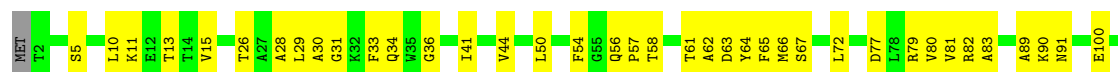
• Molecule 2: gp18, tail sheath protein

Chain MX: 71% 28%



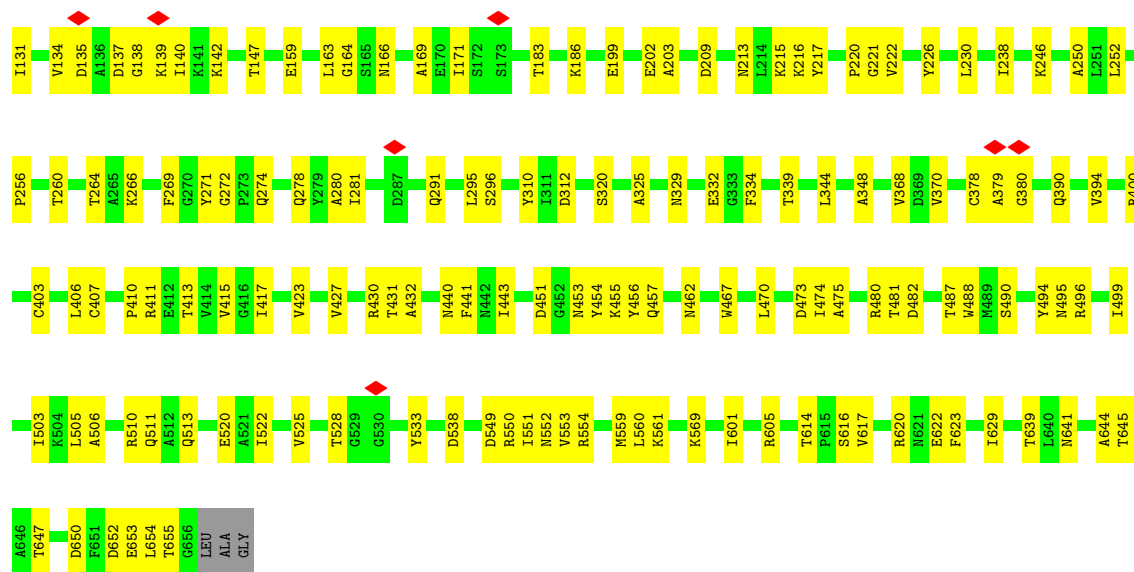
• Molecule 2: gp18, tail sheath protein

Chain MY: 71% 29%

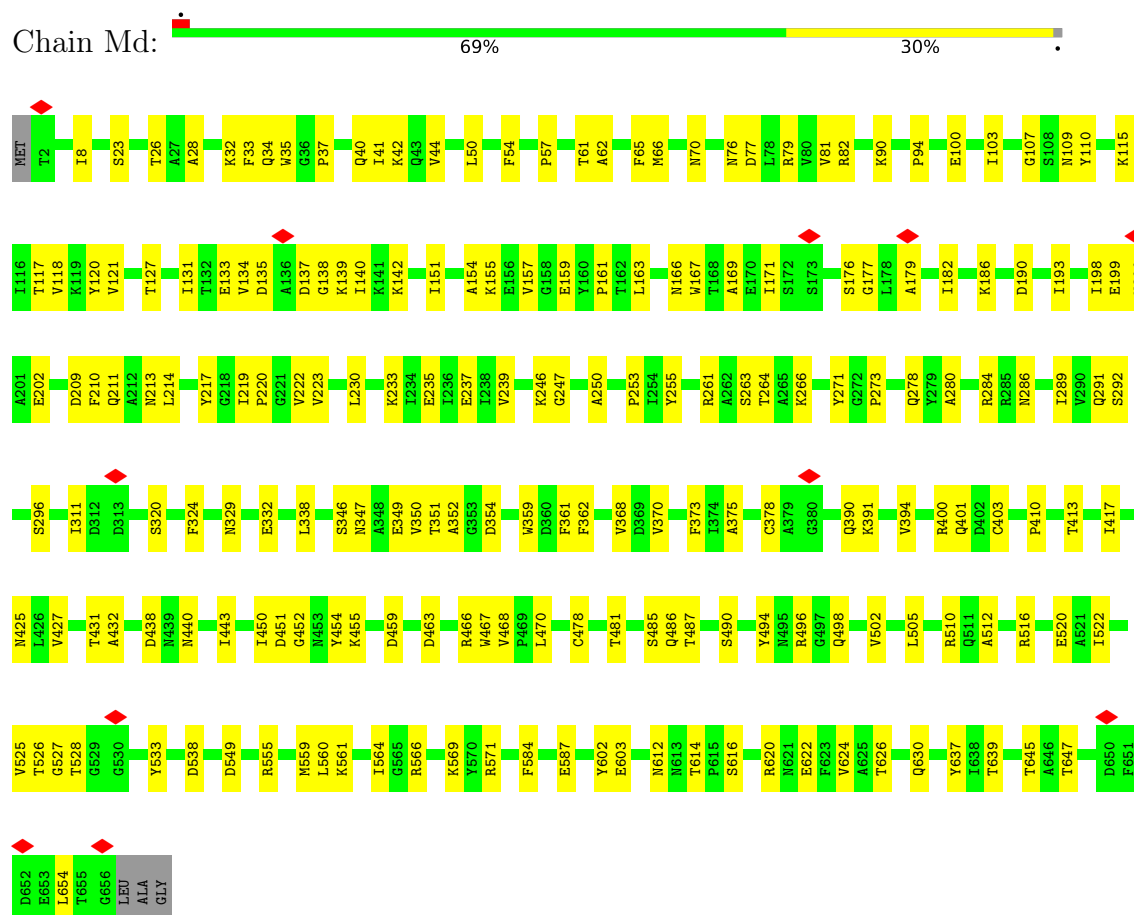






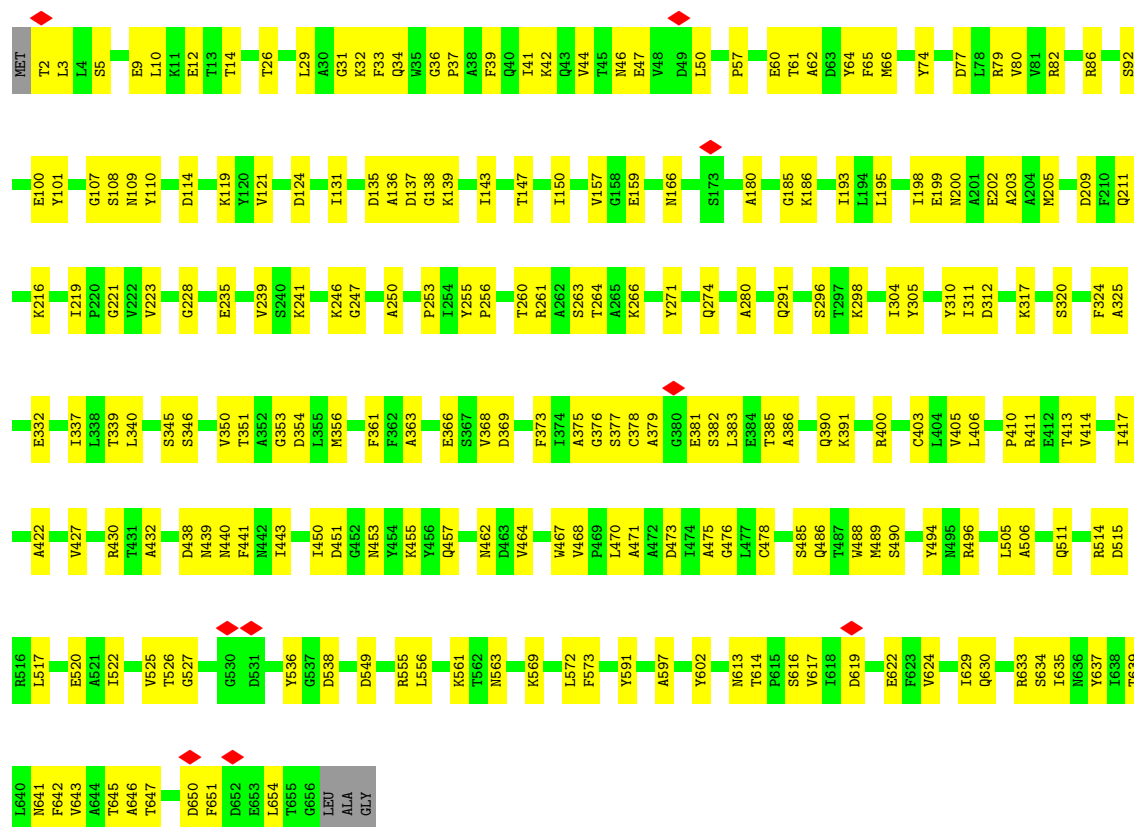


- Molecule 2: gp18, tail sheath protein

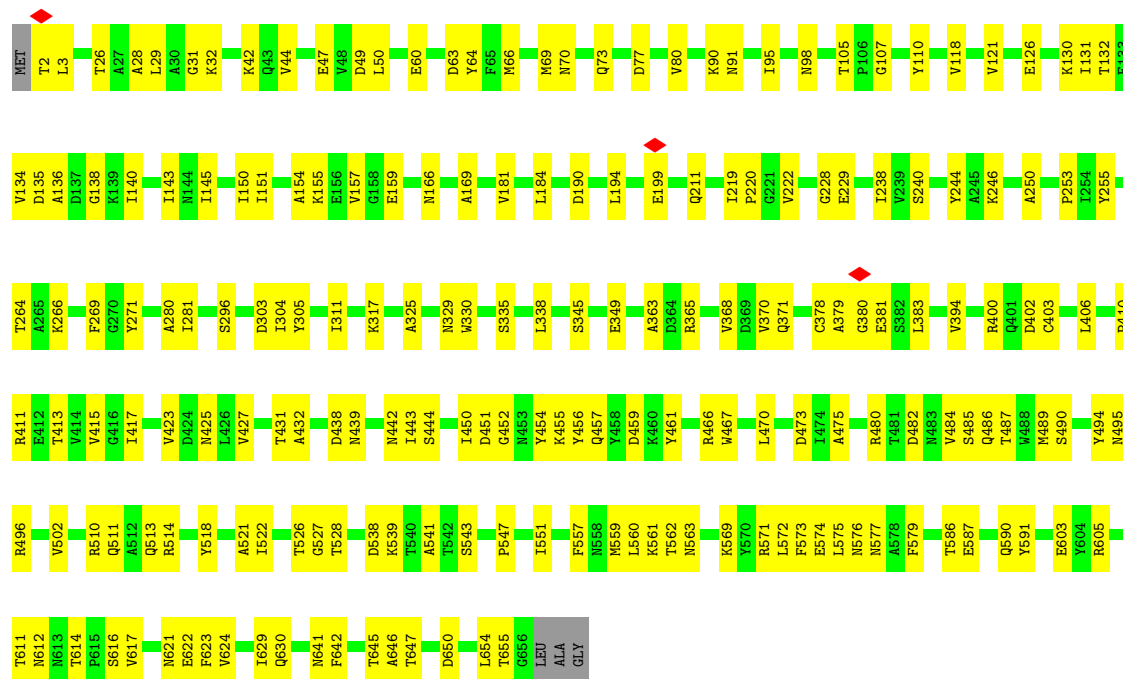


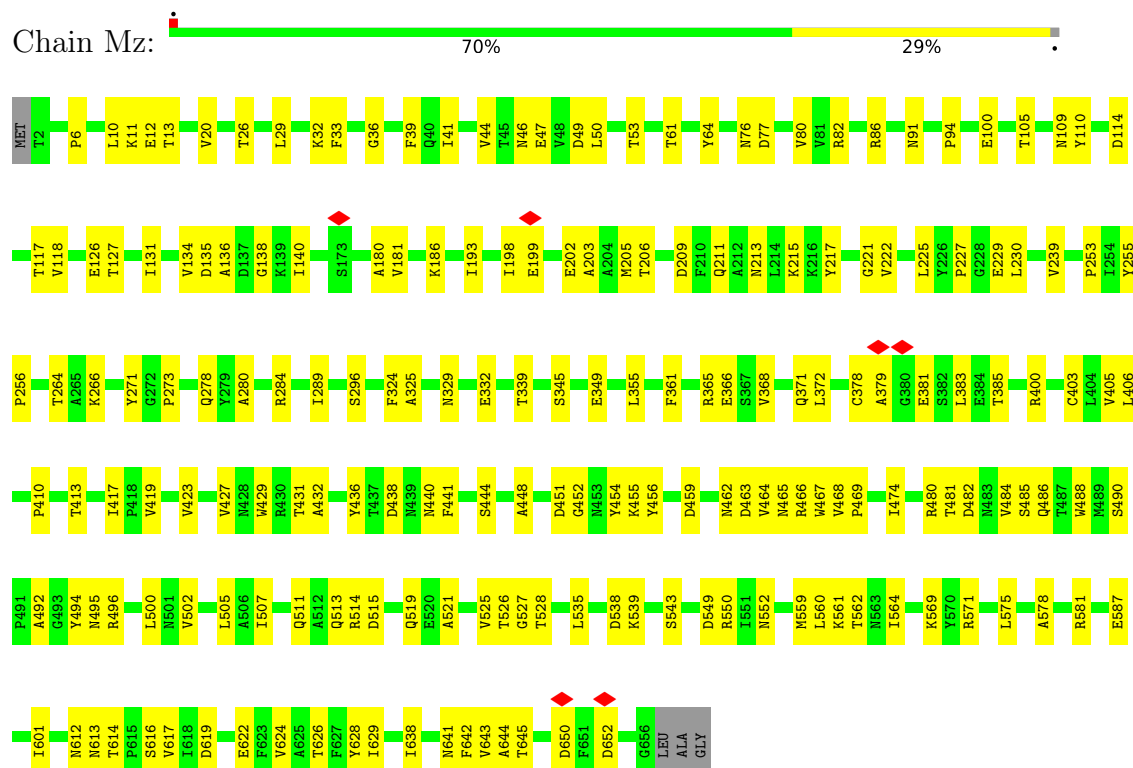
- Molecule 2: gp18, tail sheath protein



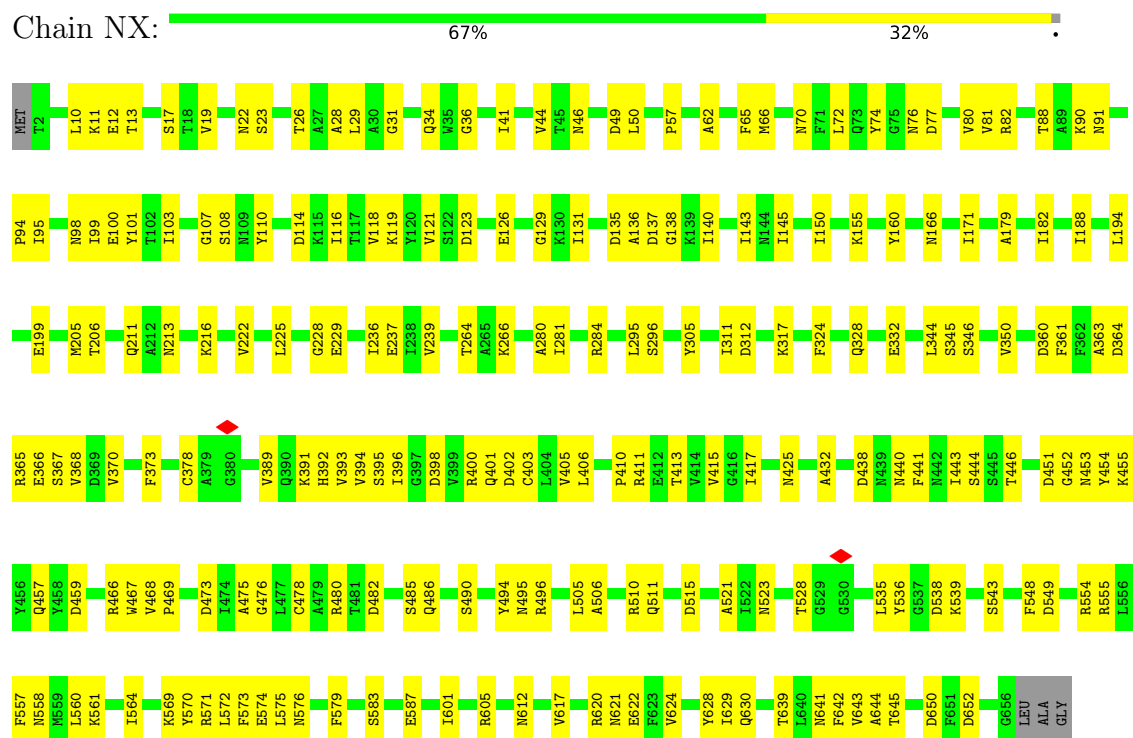


Chain Mx: 69% 30%



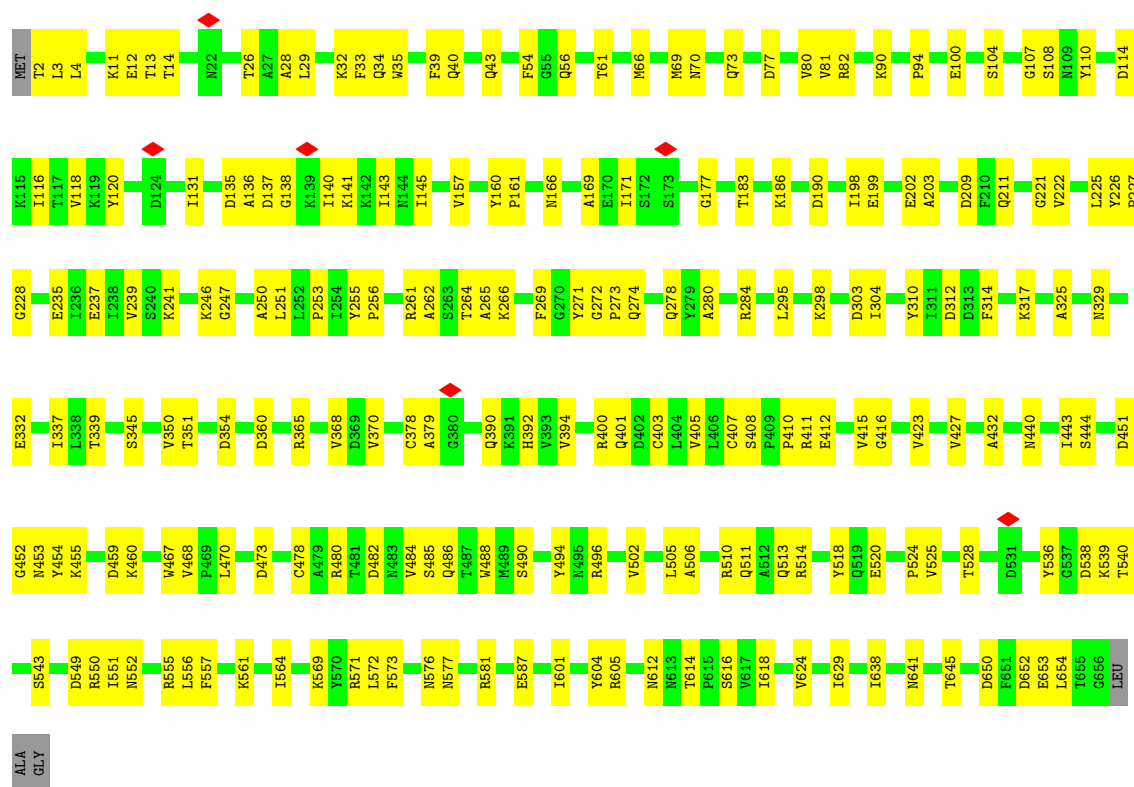


- Molecule 2: gp18, tail sheath protein

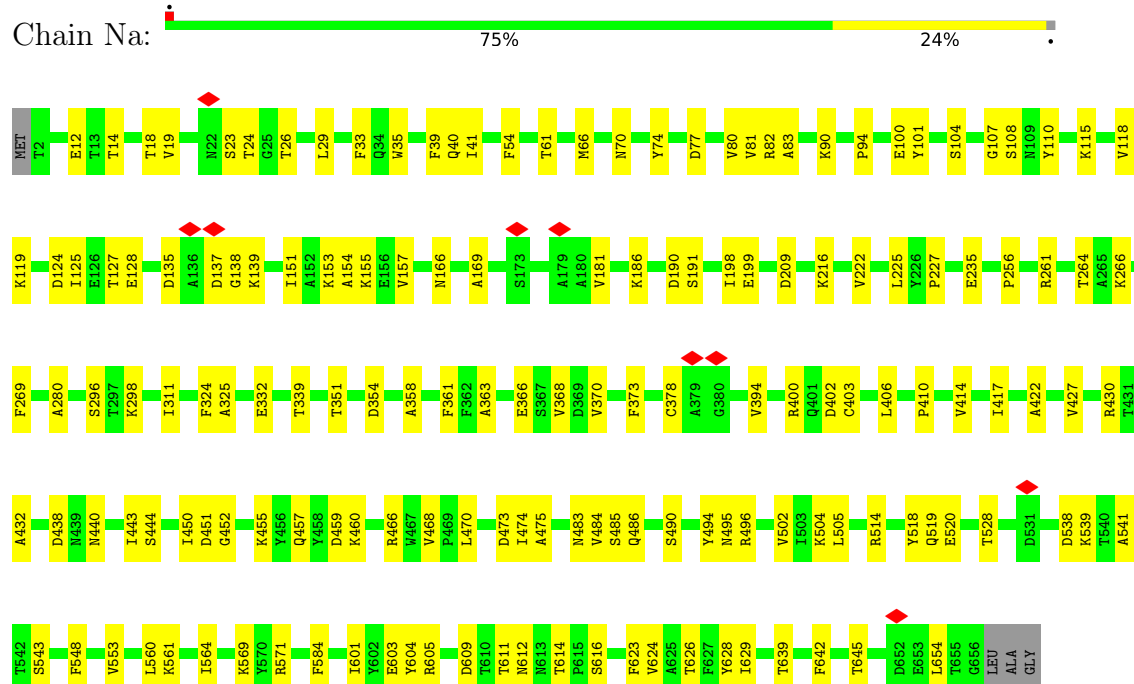


- Molecule 2: gp18, tail sheath protein



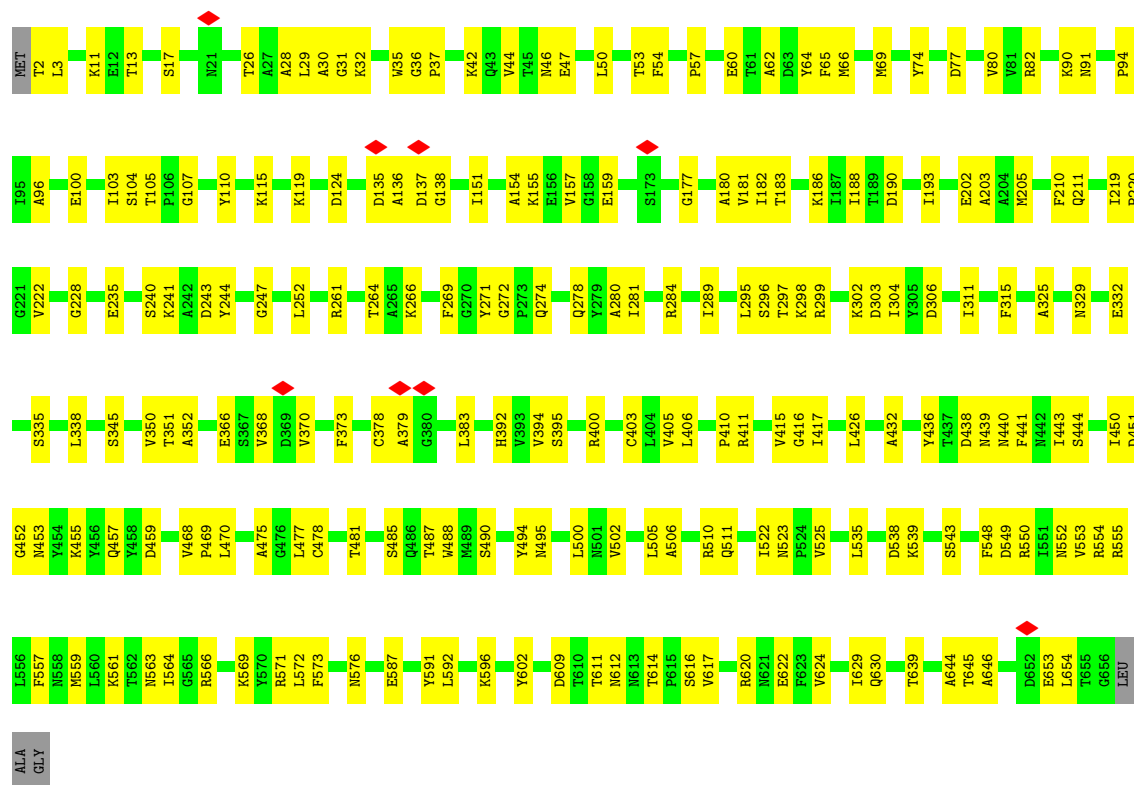


• Molecule 2: gp18, tail sheath protein

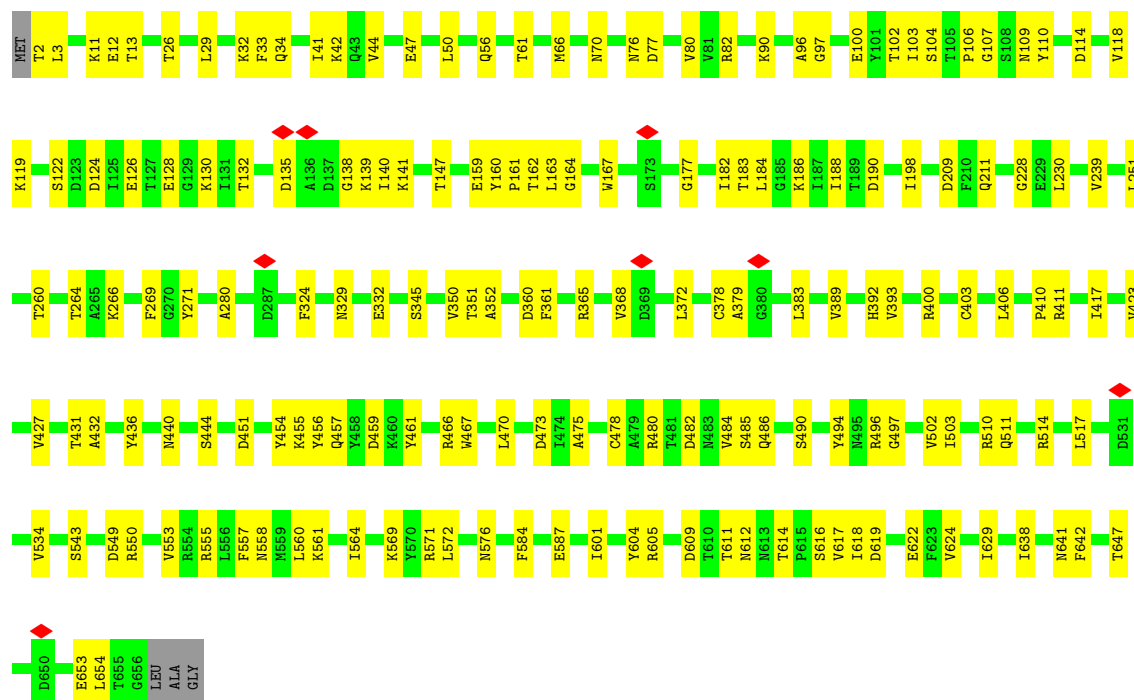
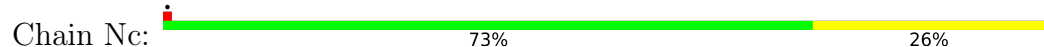


• Molecule 2: gp18, tail sheath protein

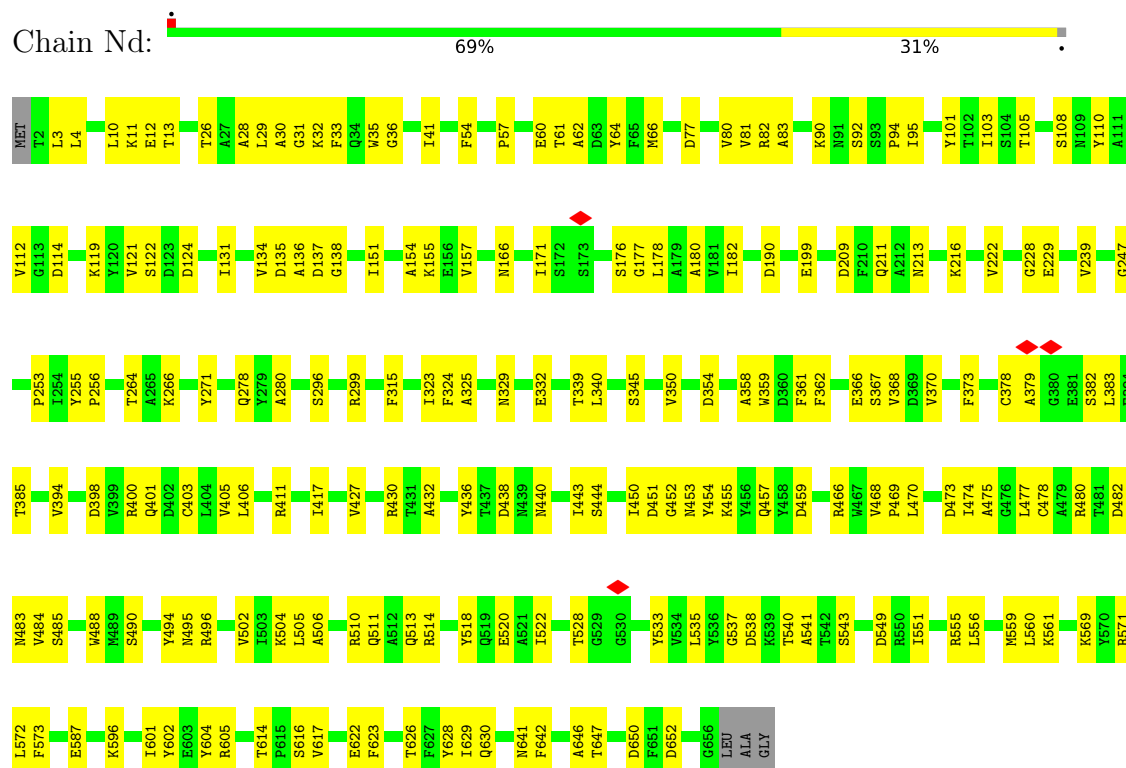




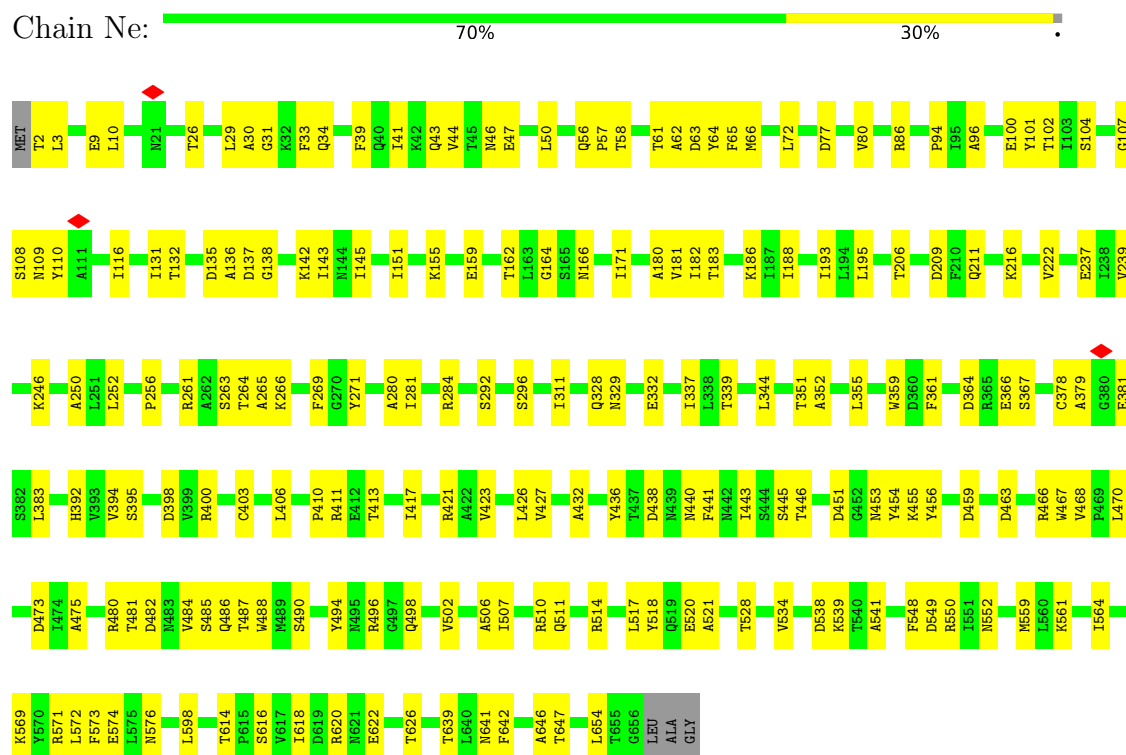
- Molecule 2: gp18, tail sheath protein



- Molecule 2: gp18, tail sheath protein

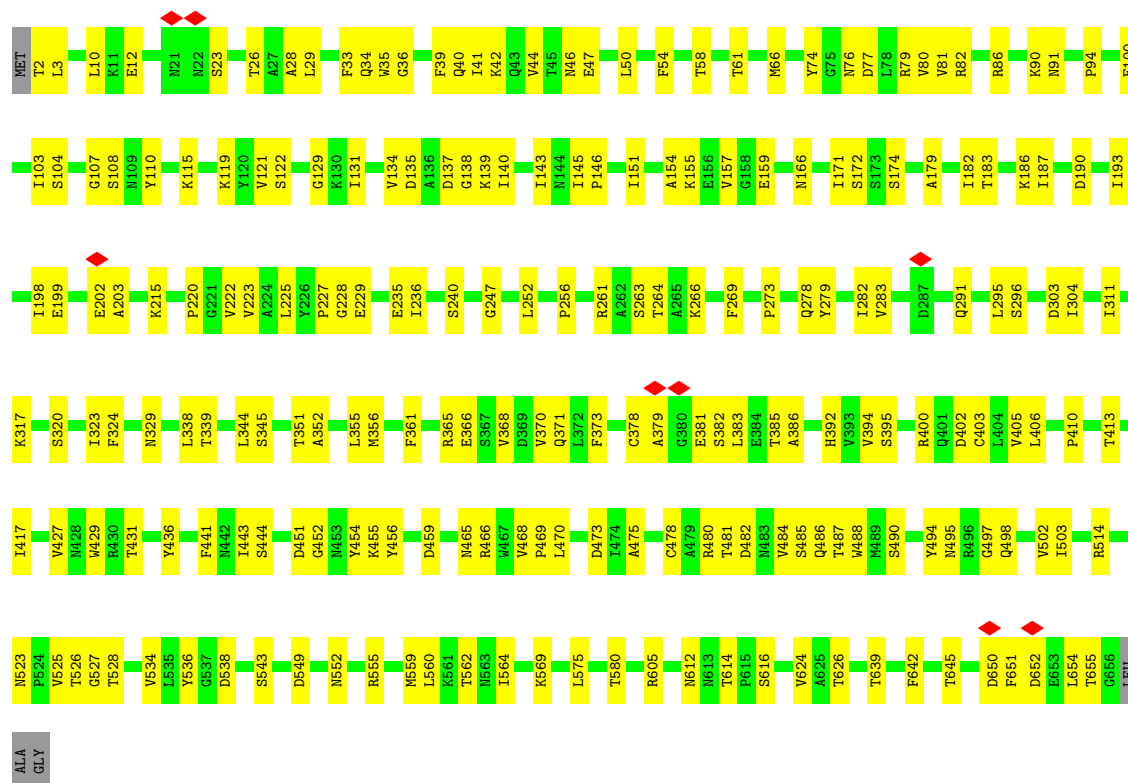


- Molecule 2: gp18, tail sheath protein

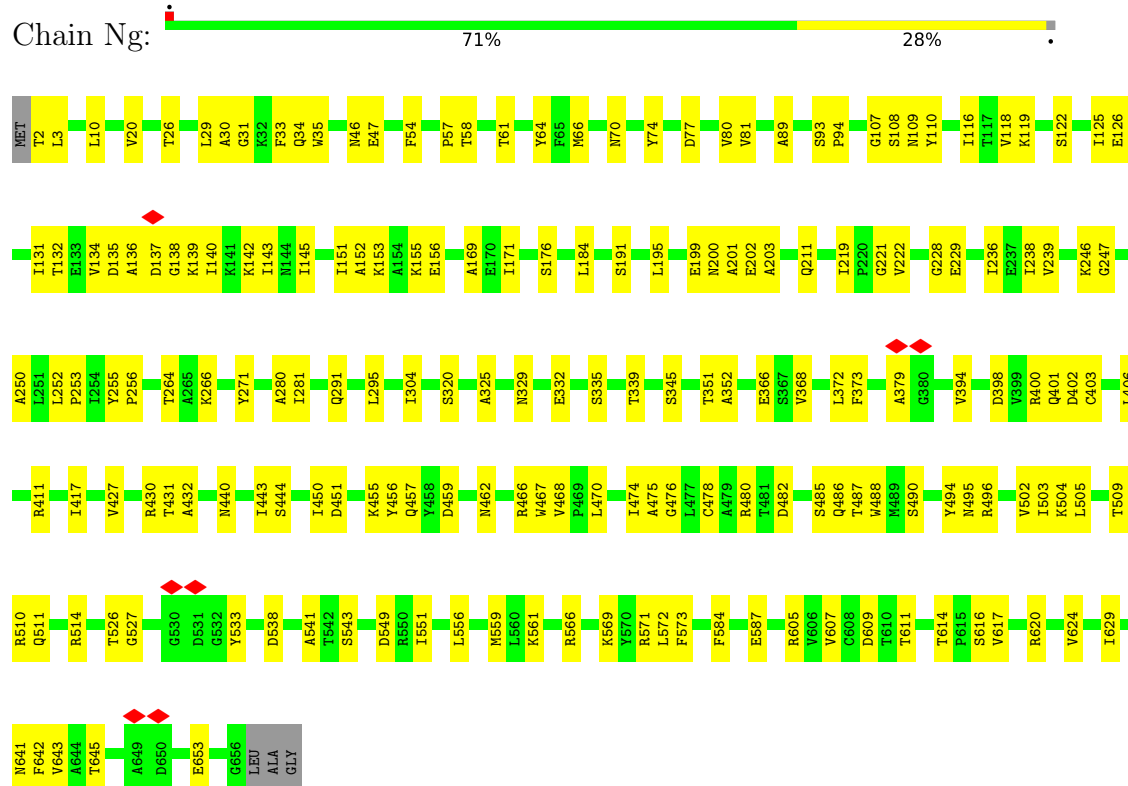


- Molecule 2: gp18, tail sheath protein

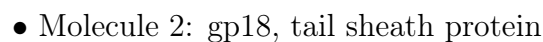
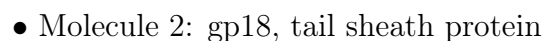


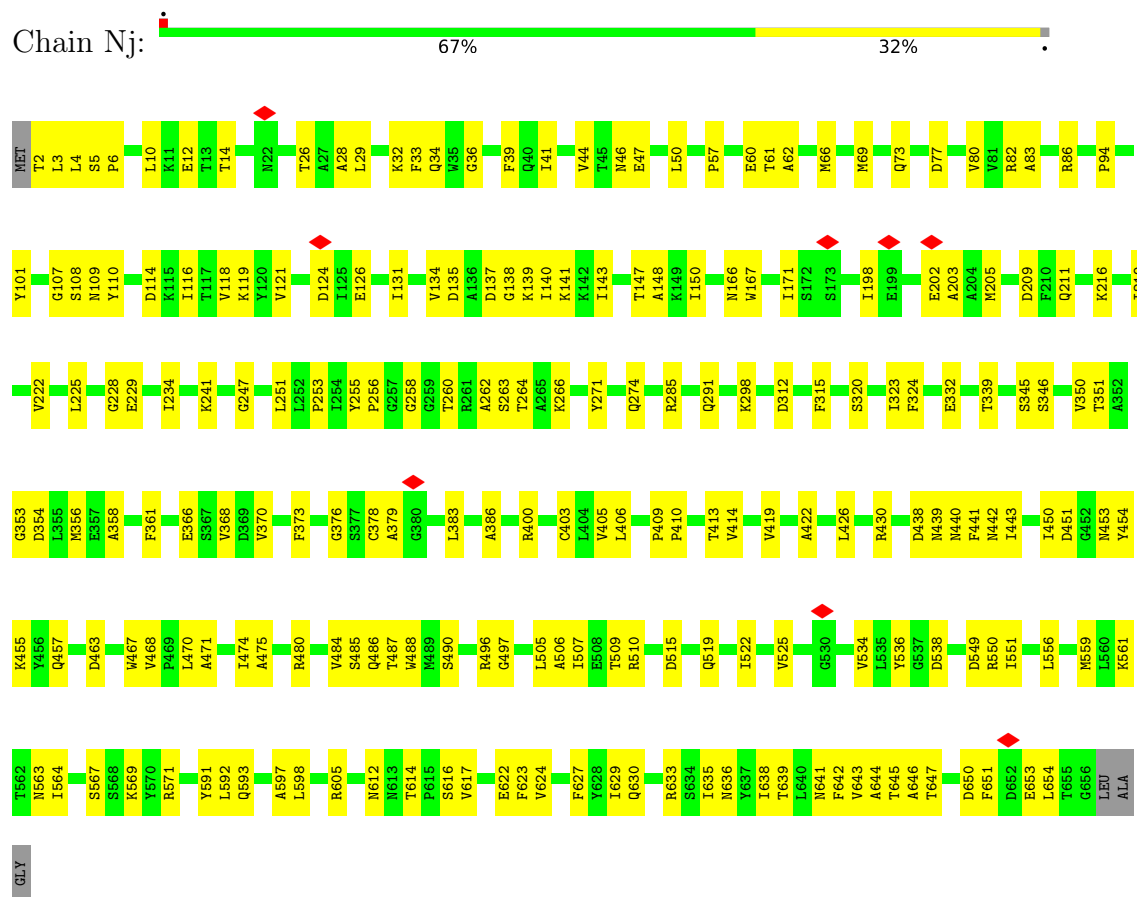


• Molecule 2: gp18, tail sheath protein

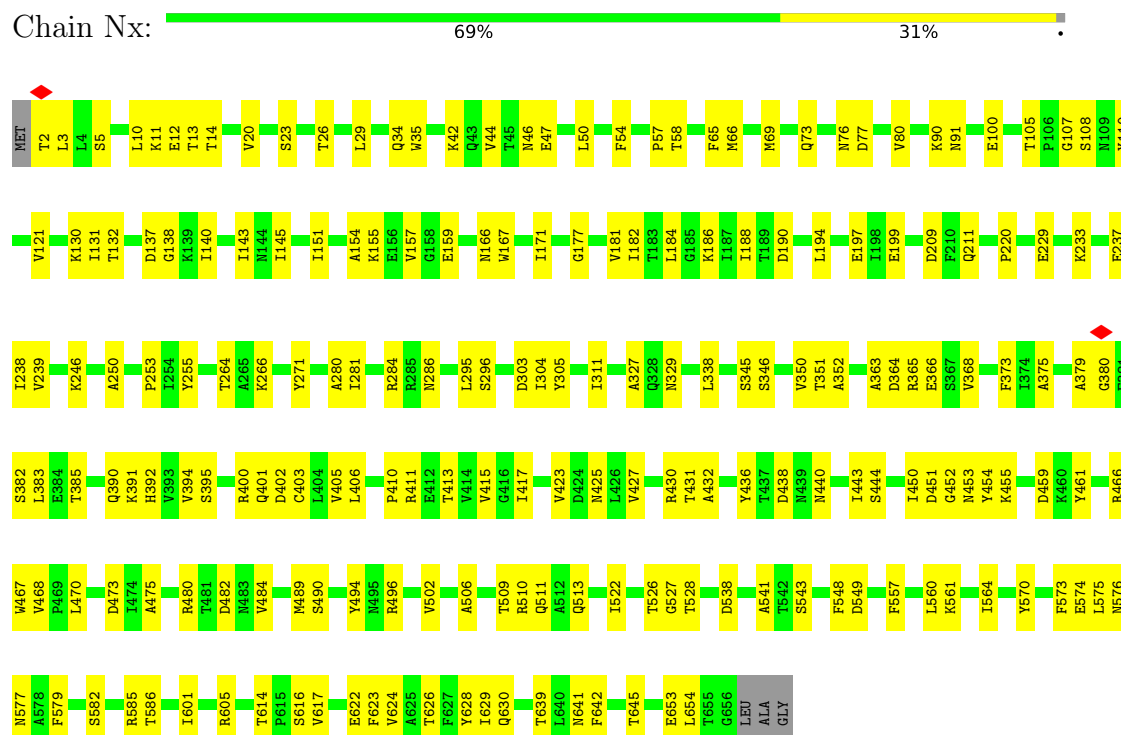


• Molecule 2: gp18, tail sheath protein

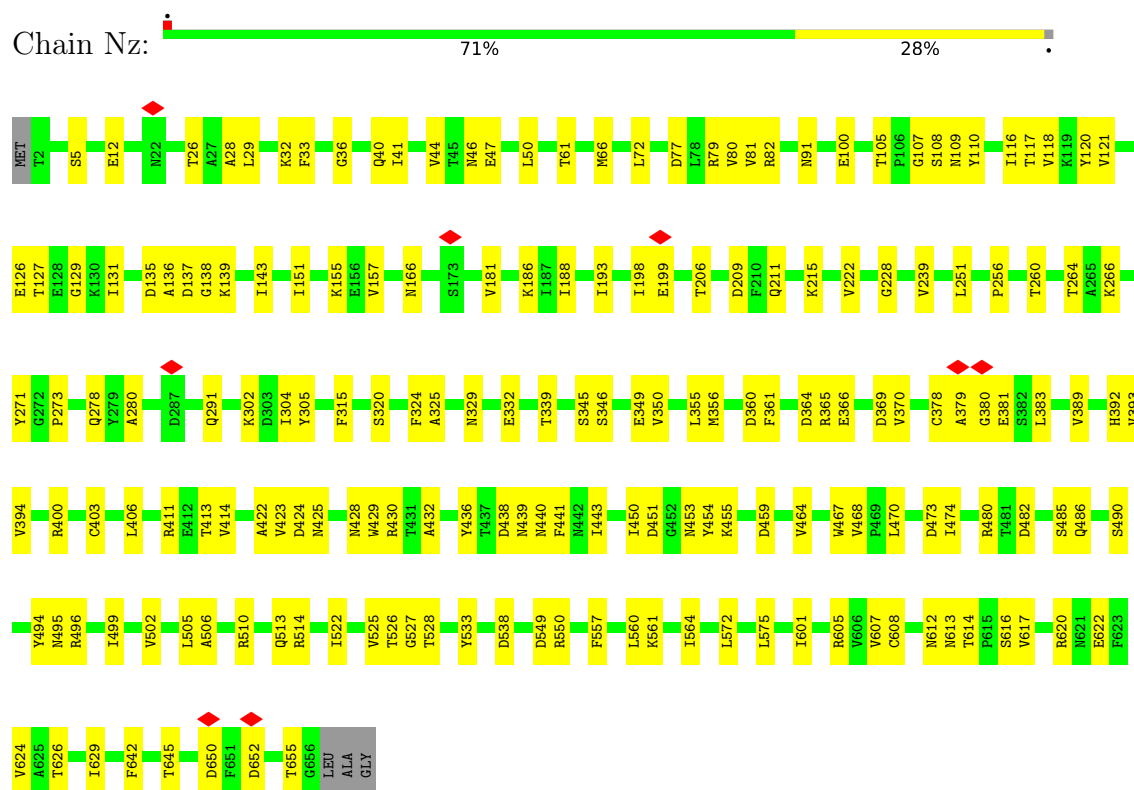




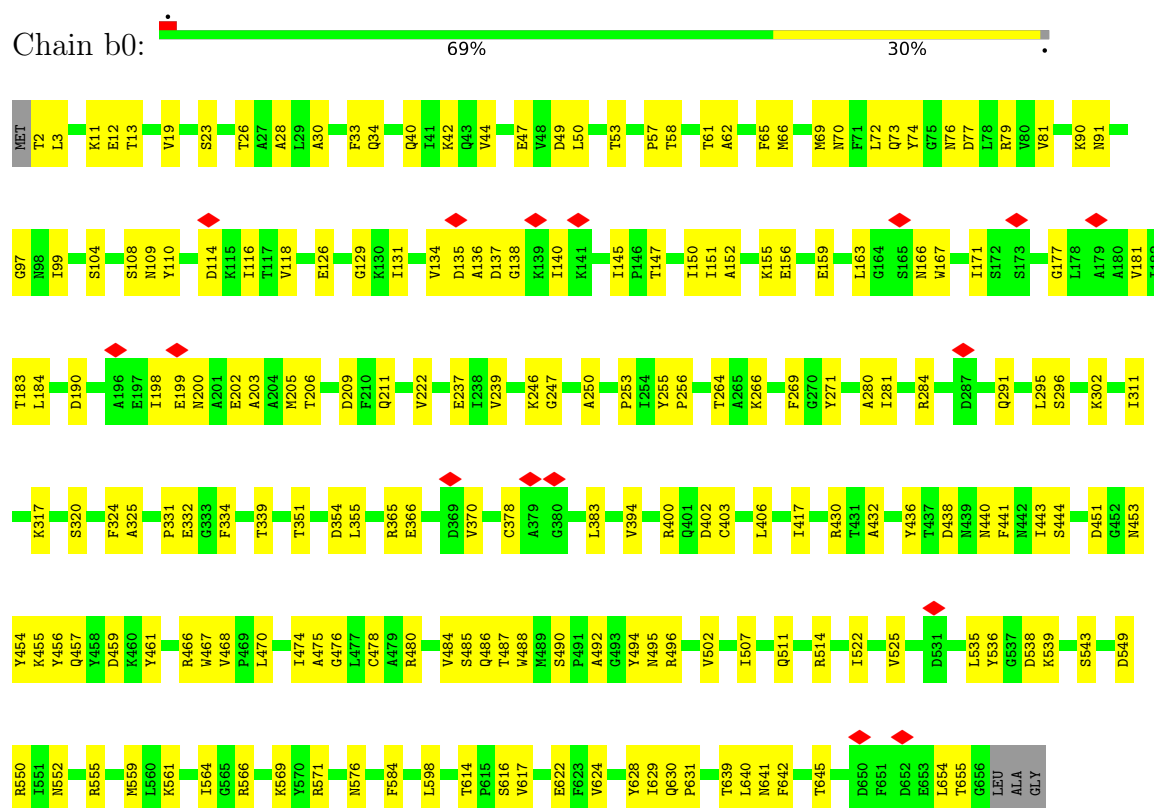
- Molecule 2: gp18, tail sheath protein



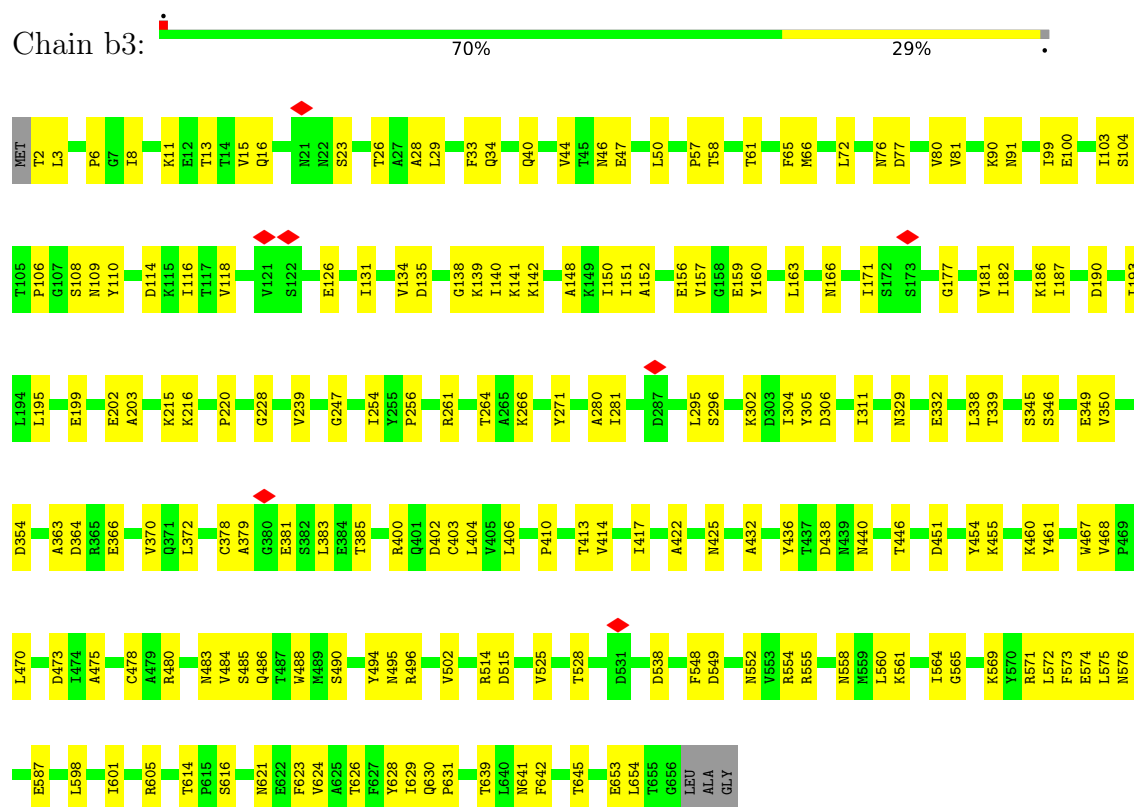
- Molecule 2: gp18, tail sheath protein



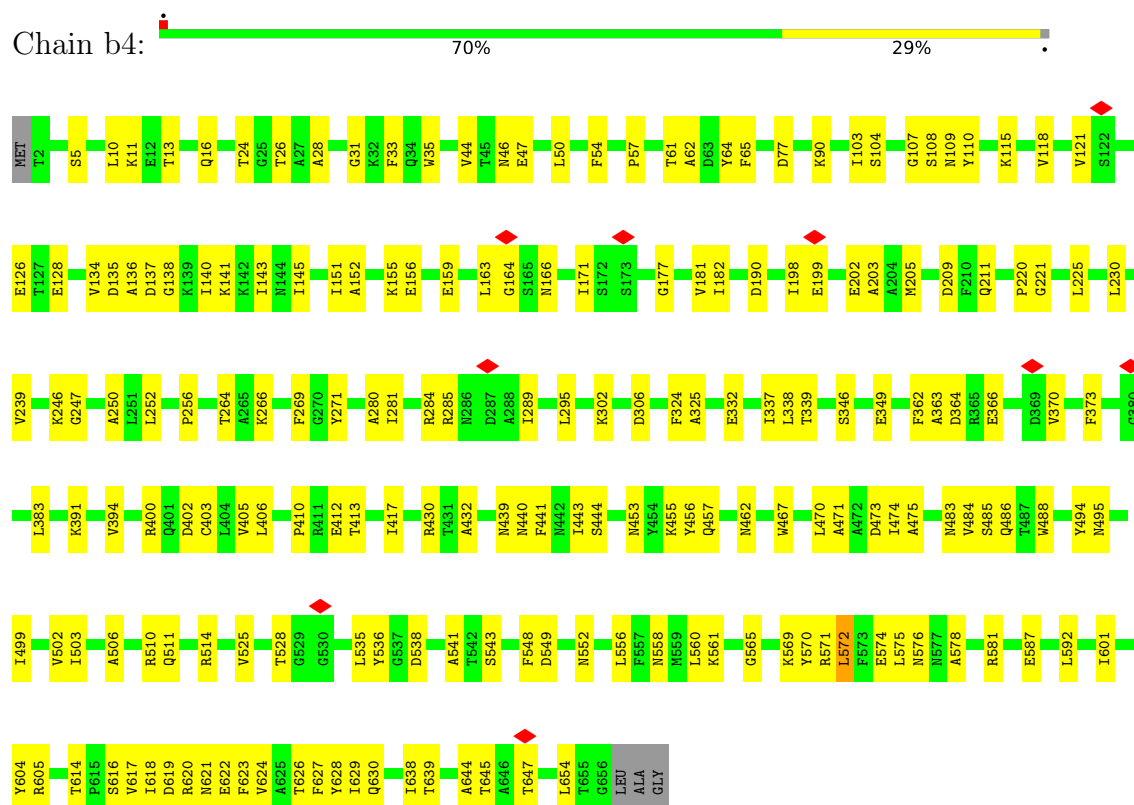
- Molecule 2: gp18, tail sheath protein



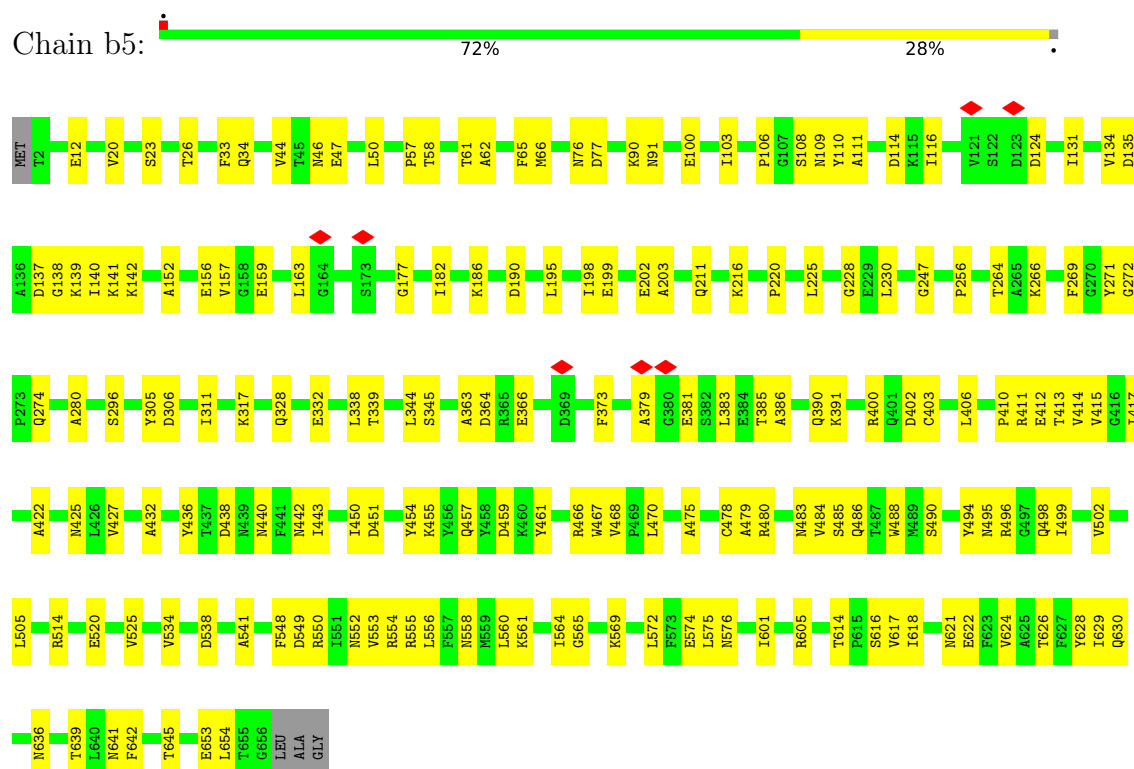
- Molecule 2: gp18, tail sheath protein



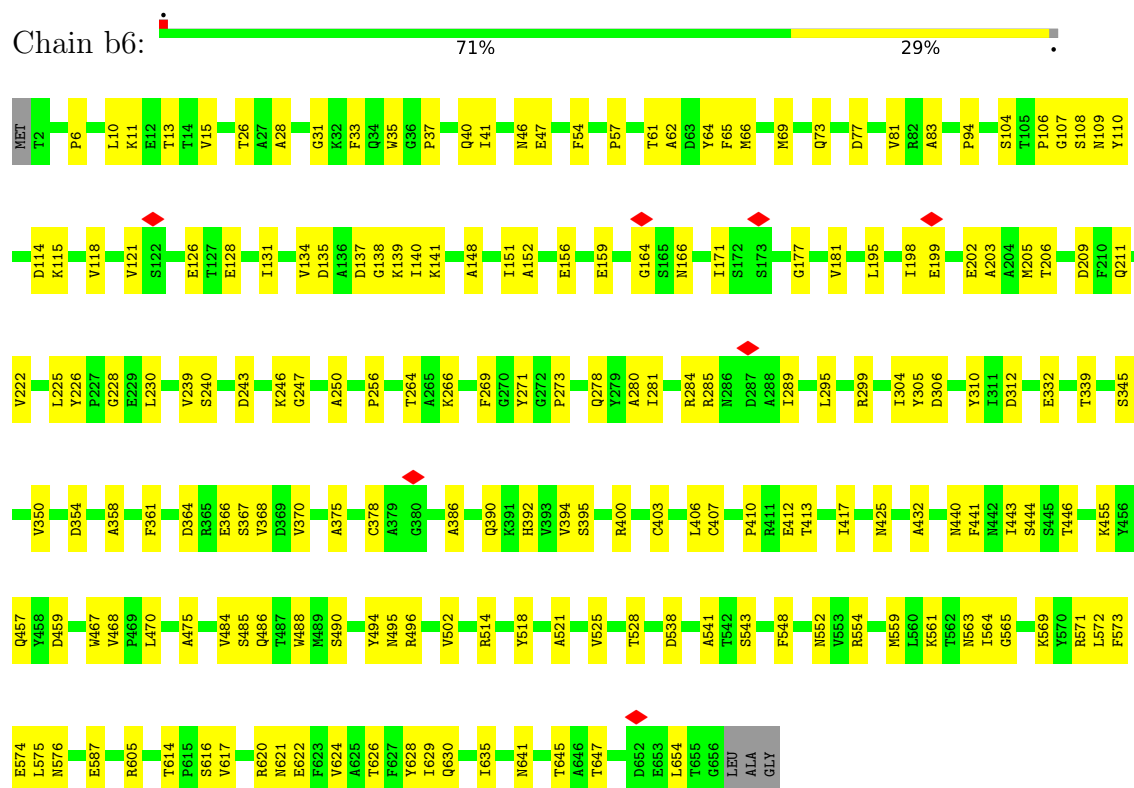
- Molecule 2: gp18, tail sheath protein




- Molecule 2: gp18, tail sheath protein

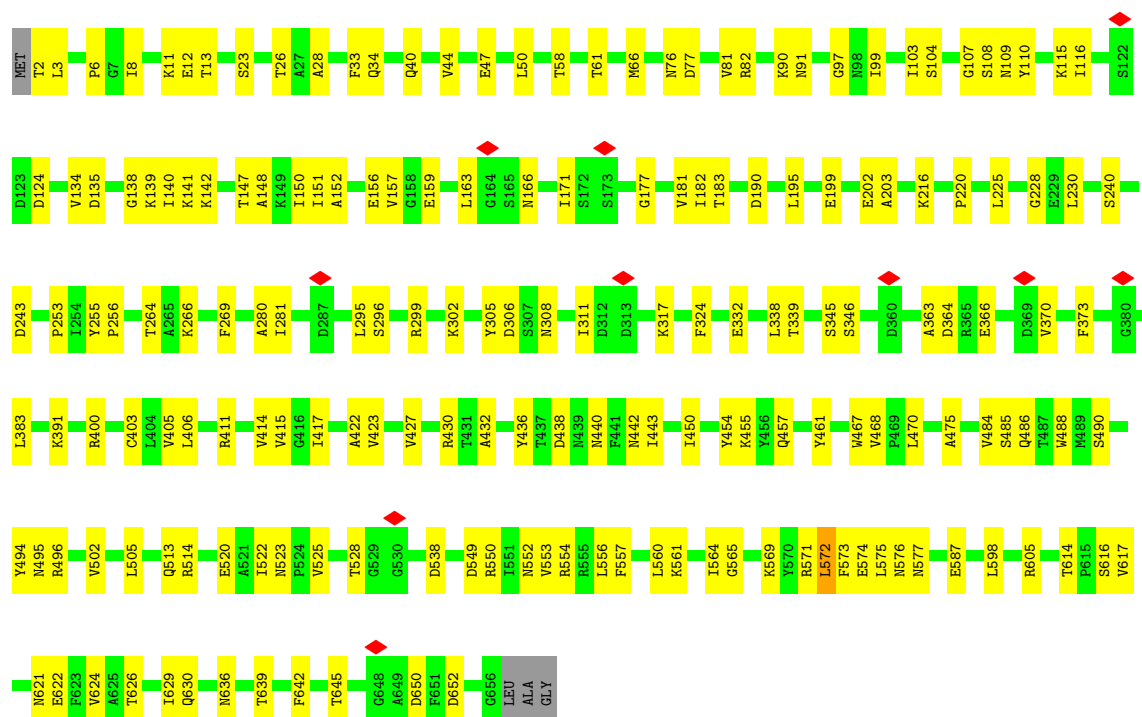


- Molecule 2: gp18, tail sheath protein




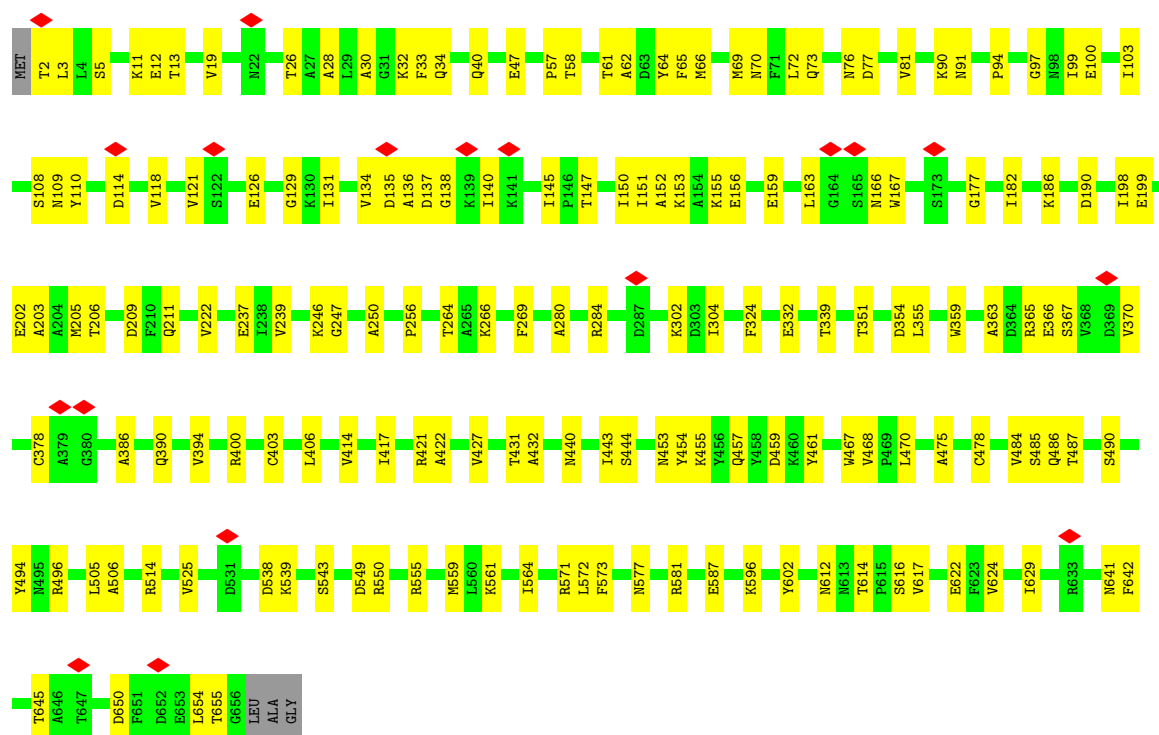
- Molecule 2: gp18, tail sheath protein

Chain b7:  72% 27%

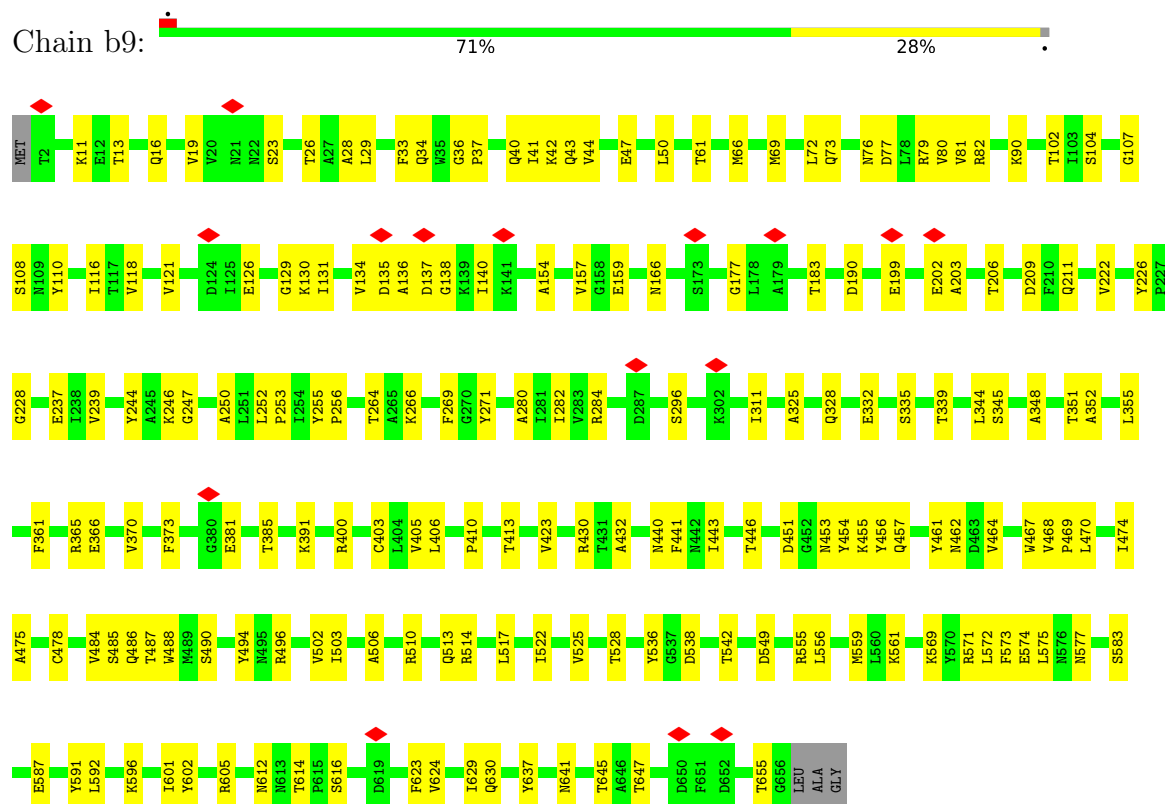


- Molecule 2: gp18, tail sheath protein

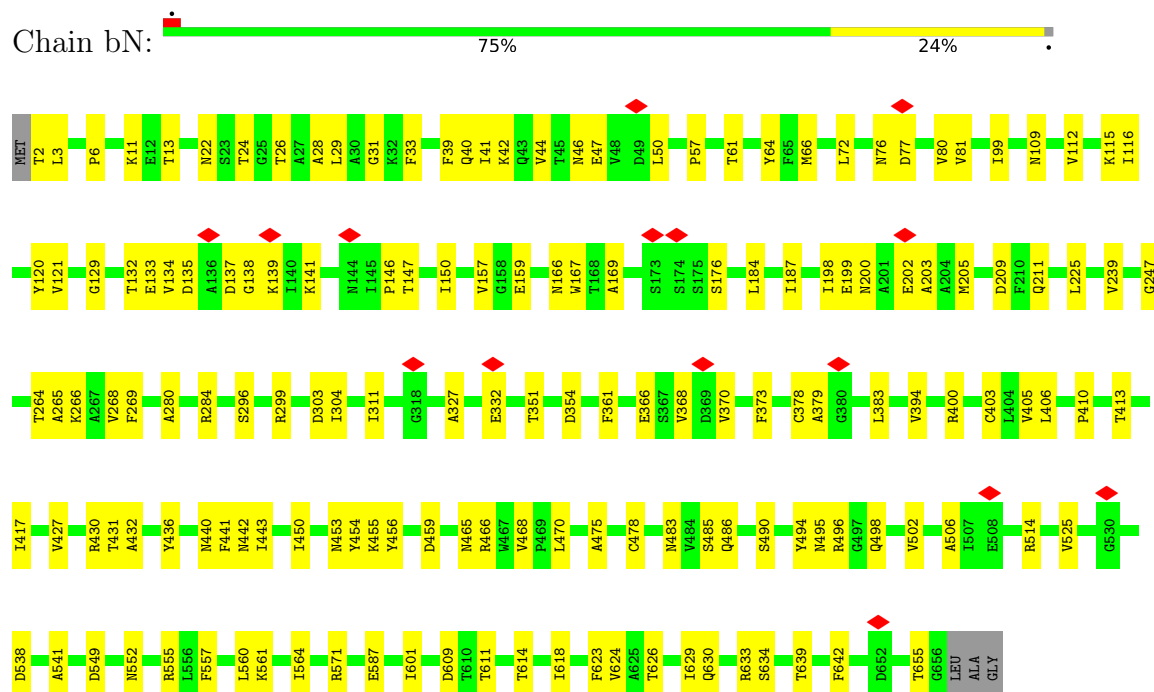
Chain b8:  74% 26%



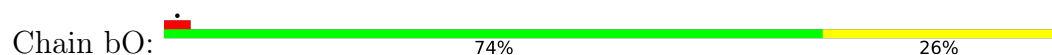
- Molecule 2: gp18, tail sheath protein

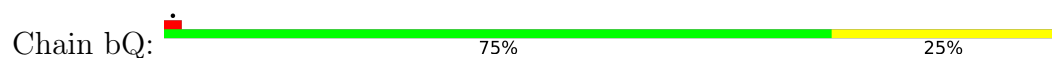
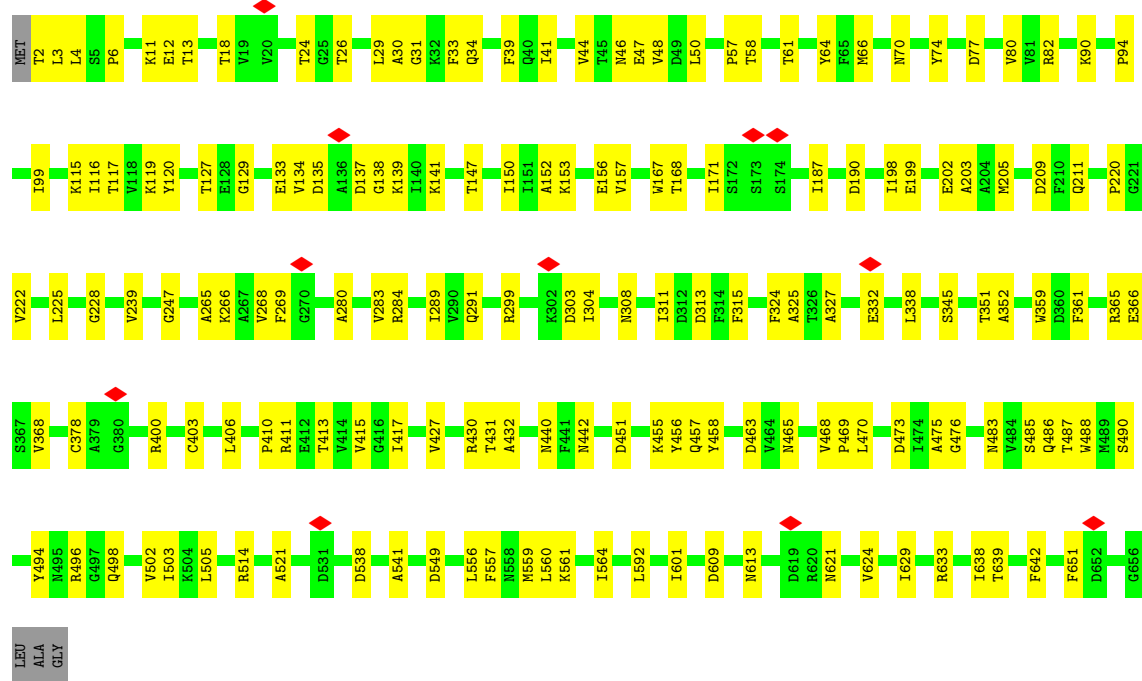
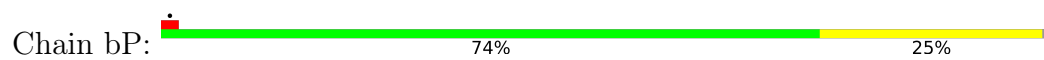
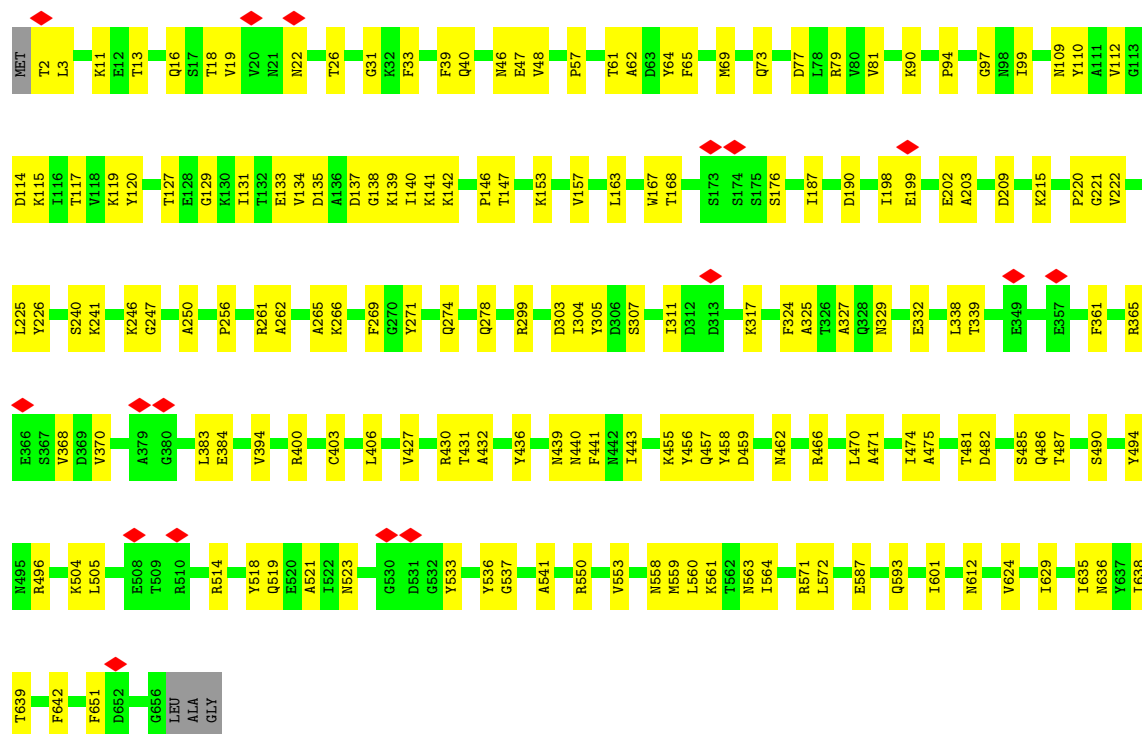


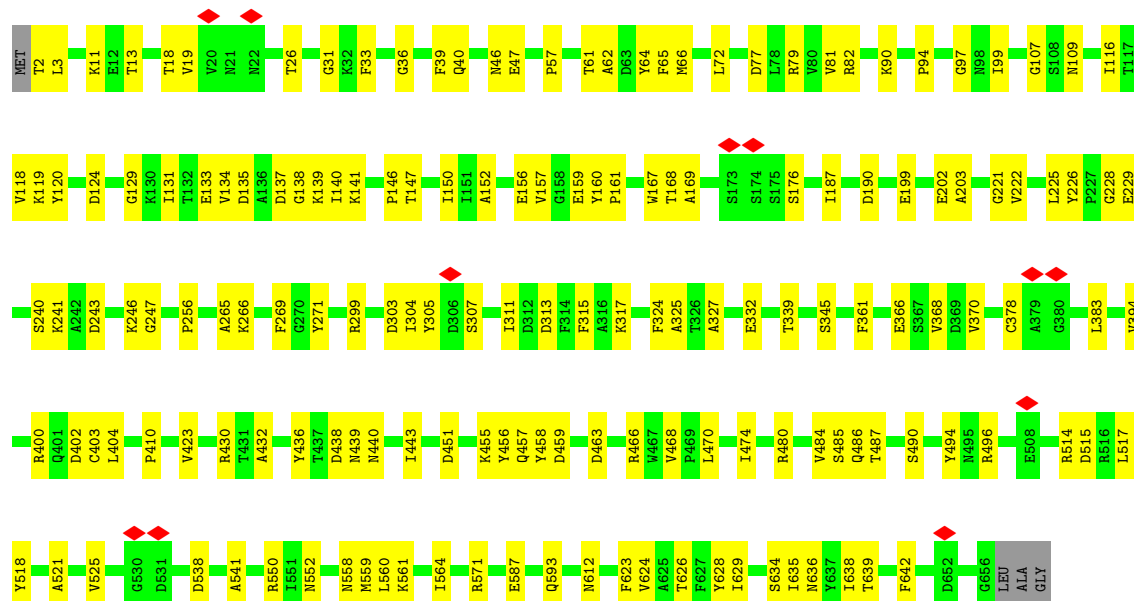
• Molecule 2: gp18, tail sheath protein



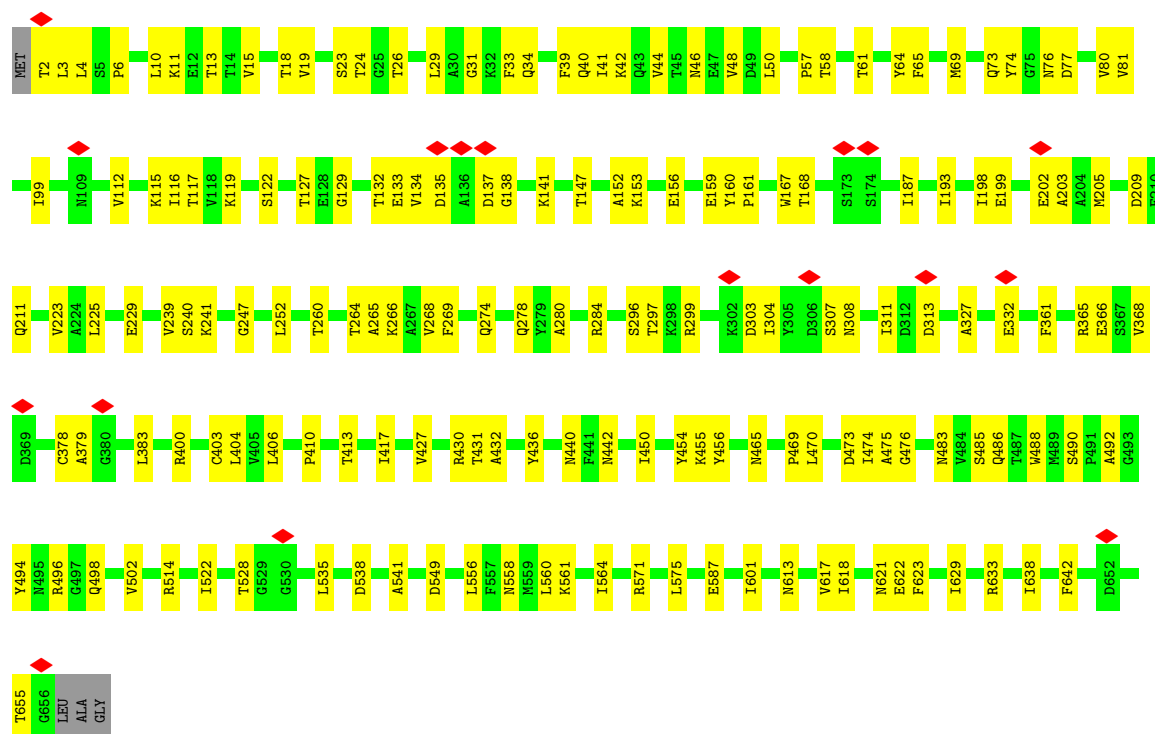
• Molecule 2: gp18, tail sheath protein



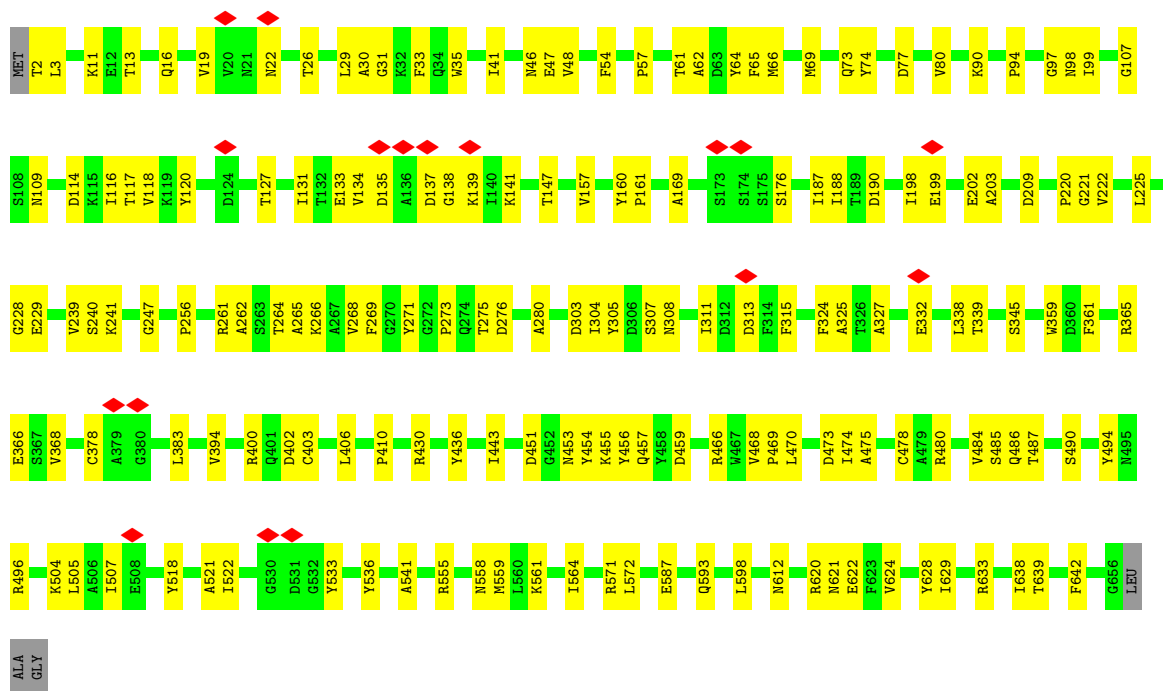




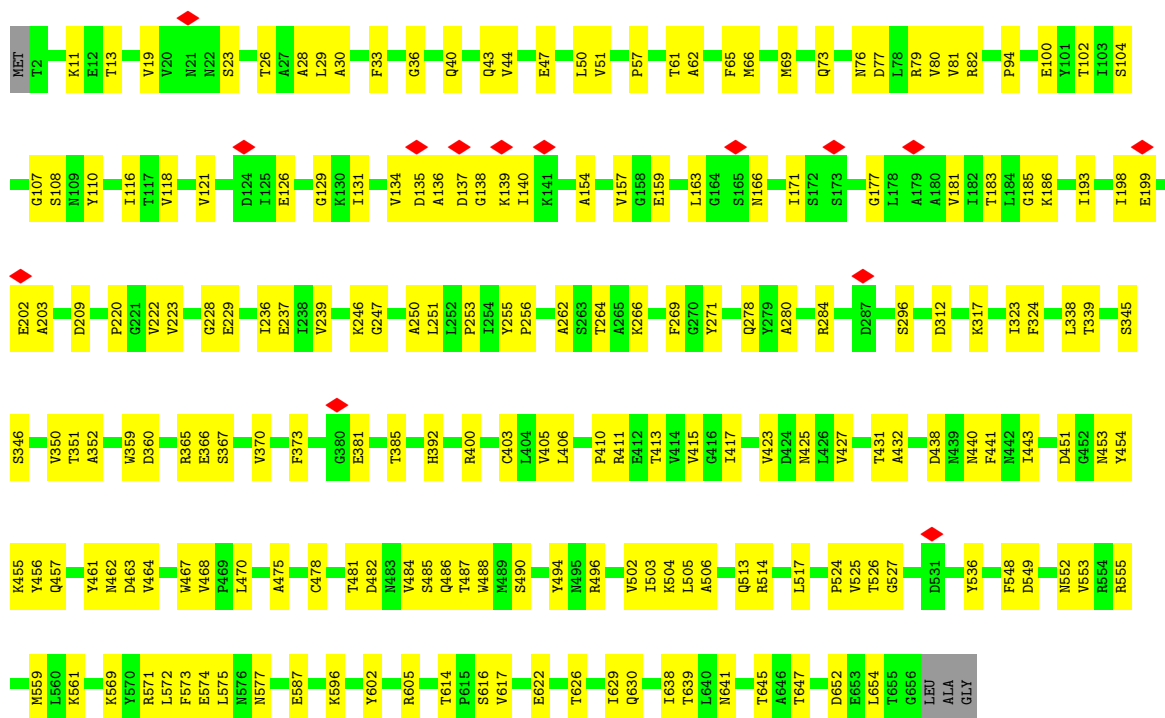
Chain bR: 74% 26%



Chain bY: 73% 26%

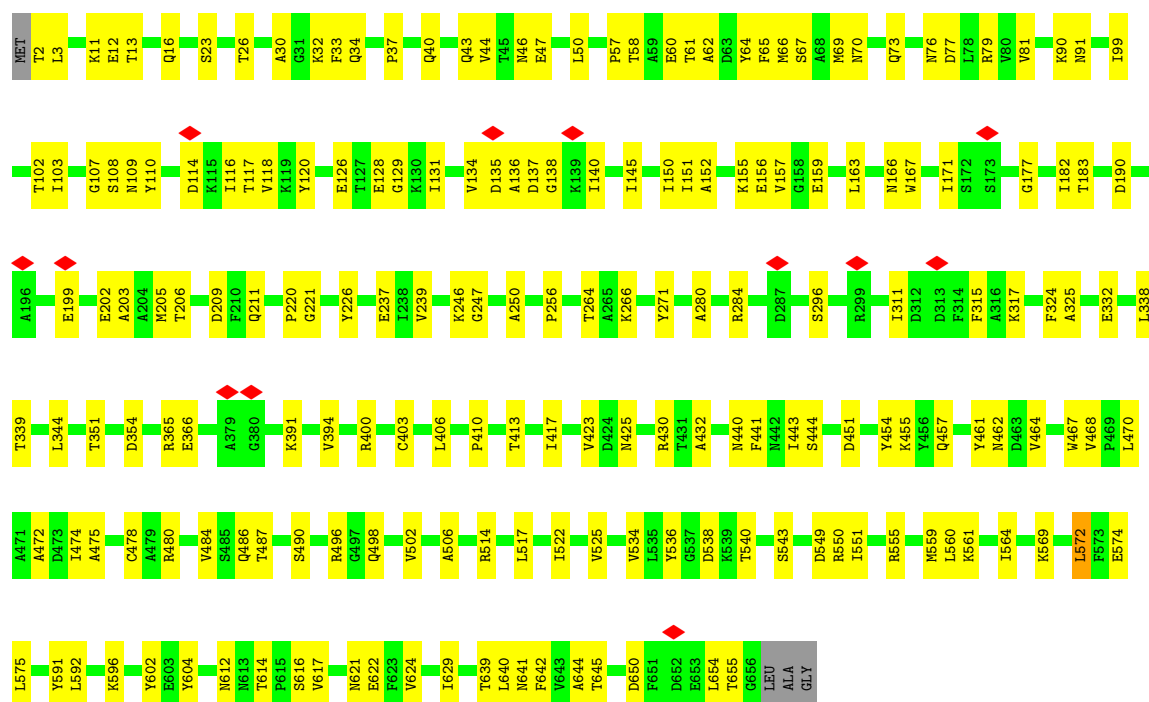


- Molecule 2: gp18, tail sheath protein



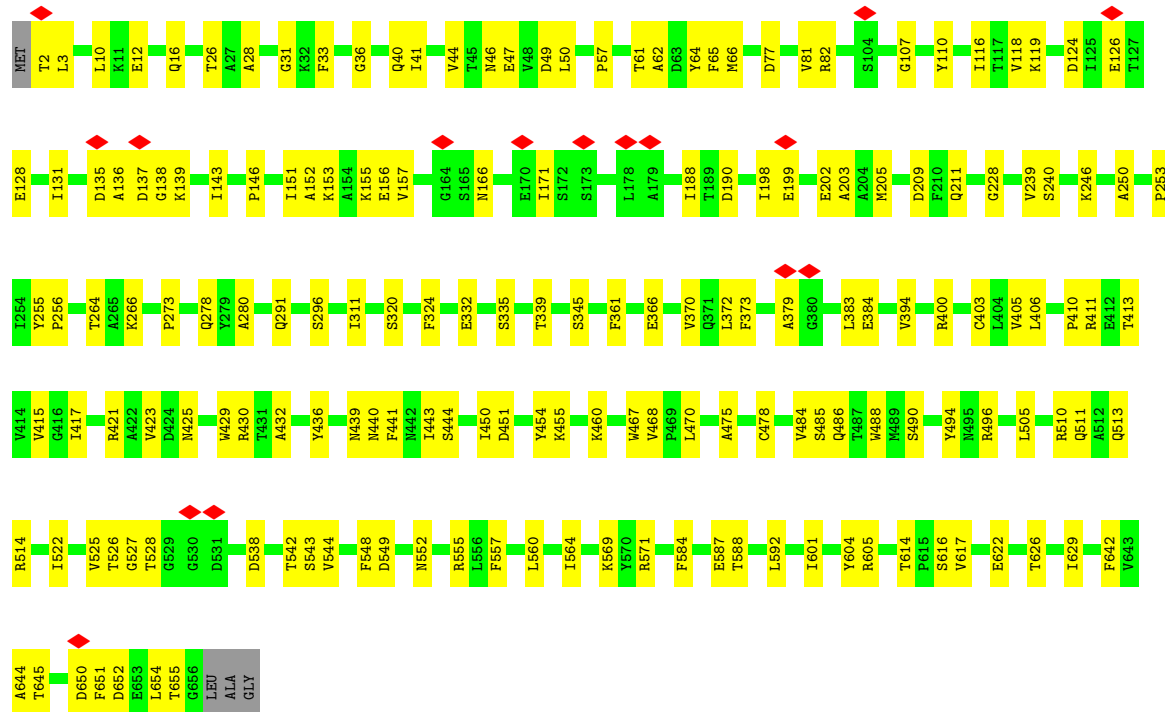
- Molecule 2: gp18, tail sheath protein





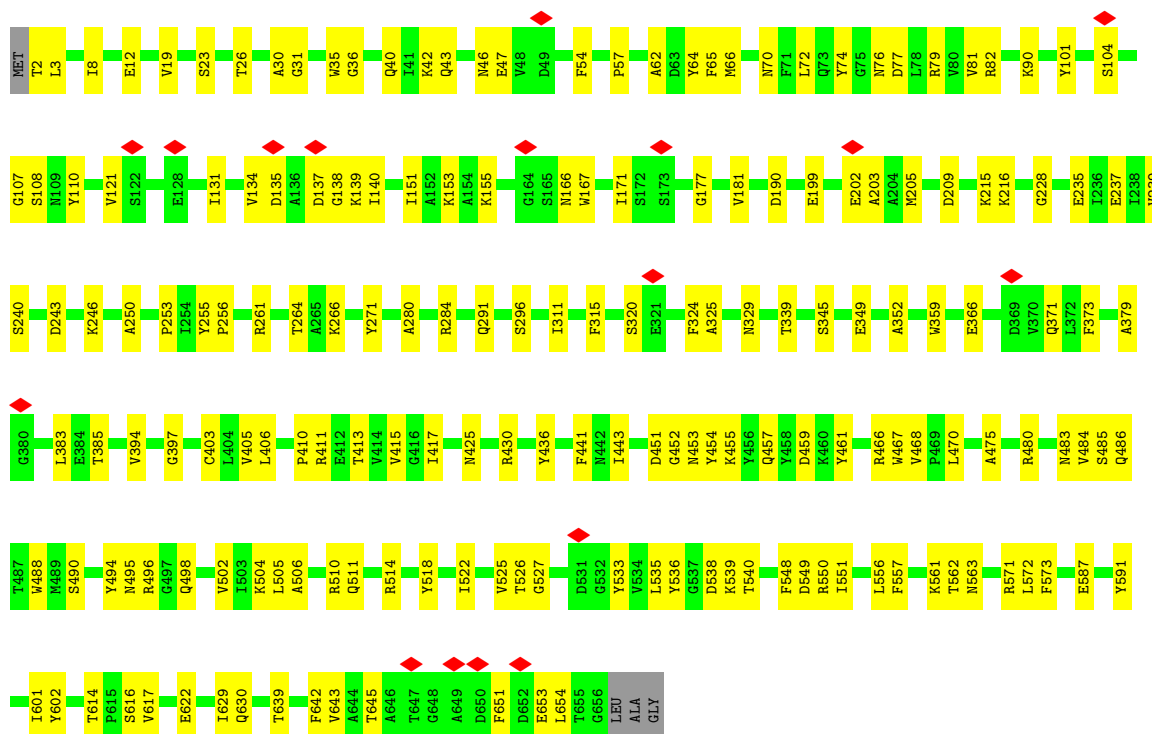
• Molecule 2: gp18, tail sheath protein

Chain cC: 73% 26%

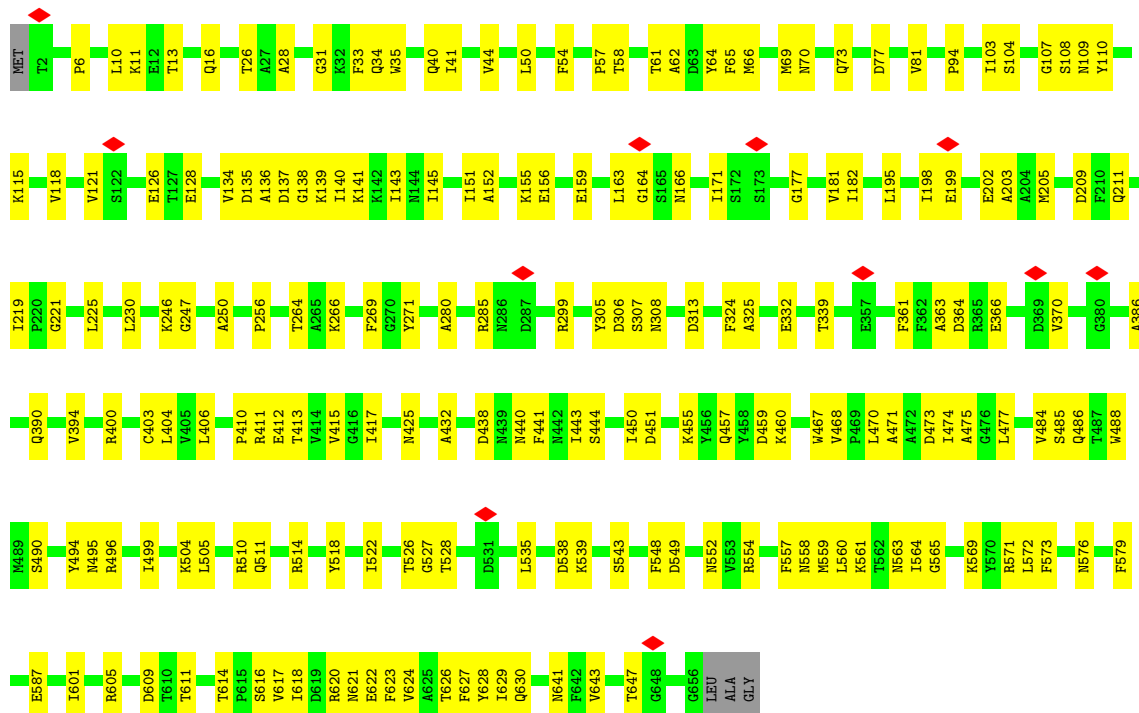


• Molecule 2: gp18, tail sheath protein

Chain cD: 72% 28%

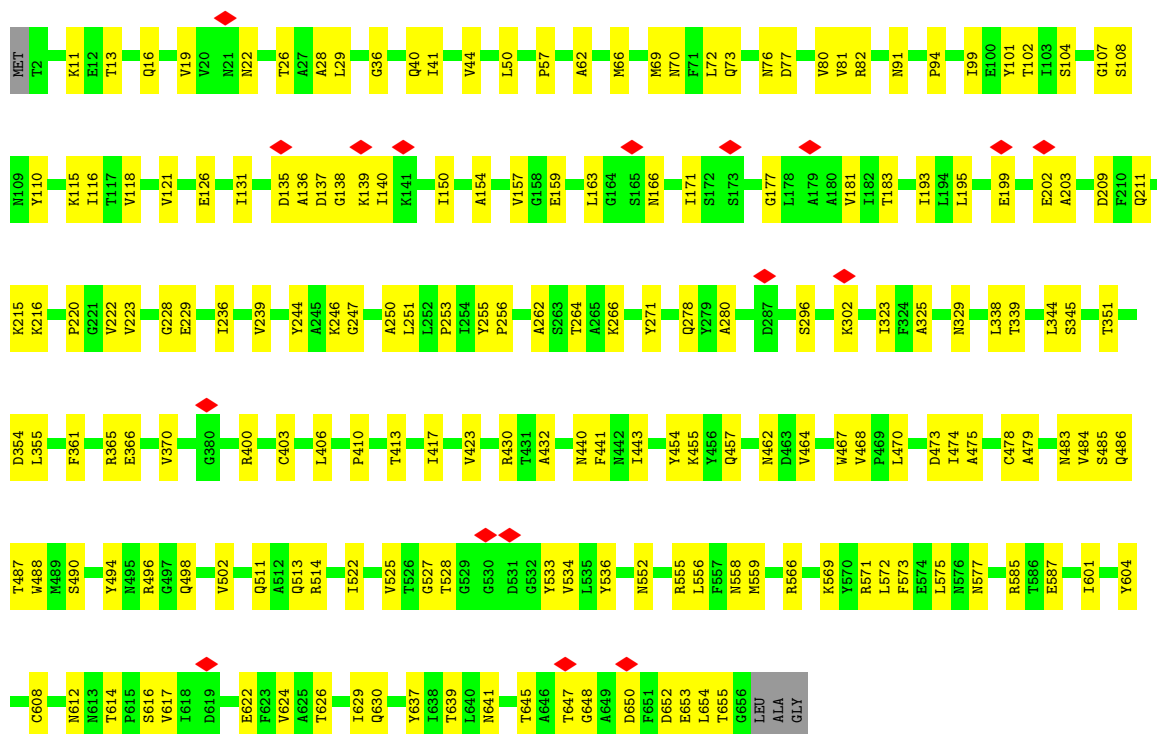


Chain cE:

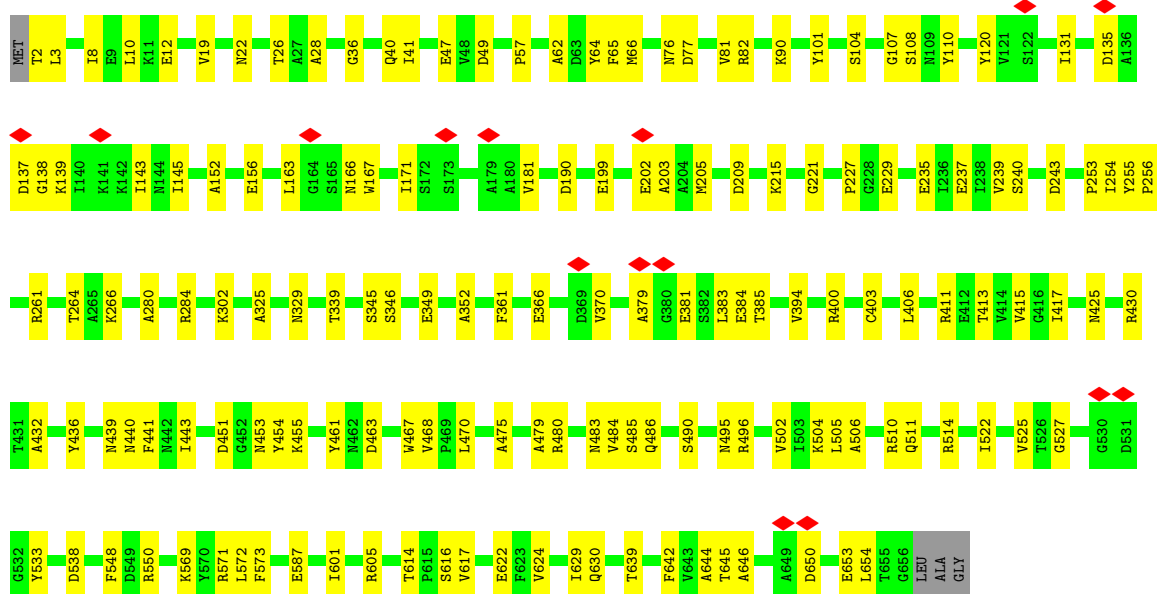
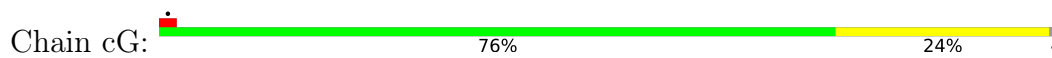


Chain cF:



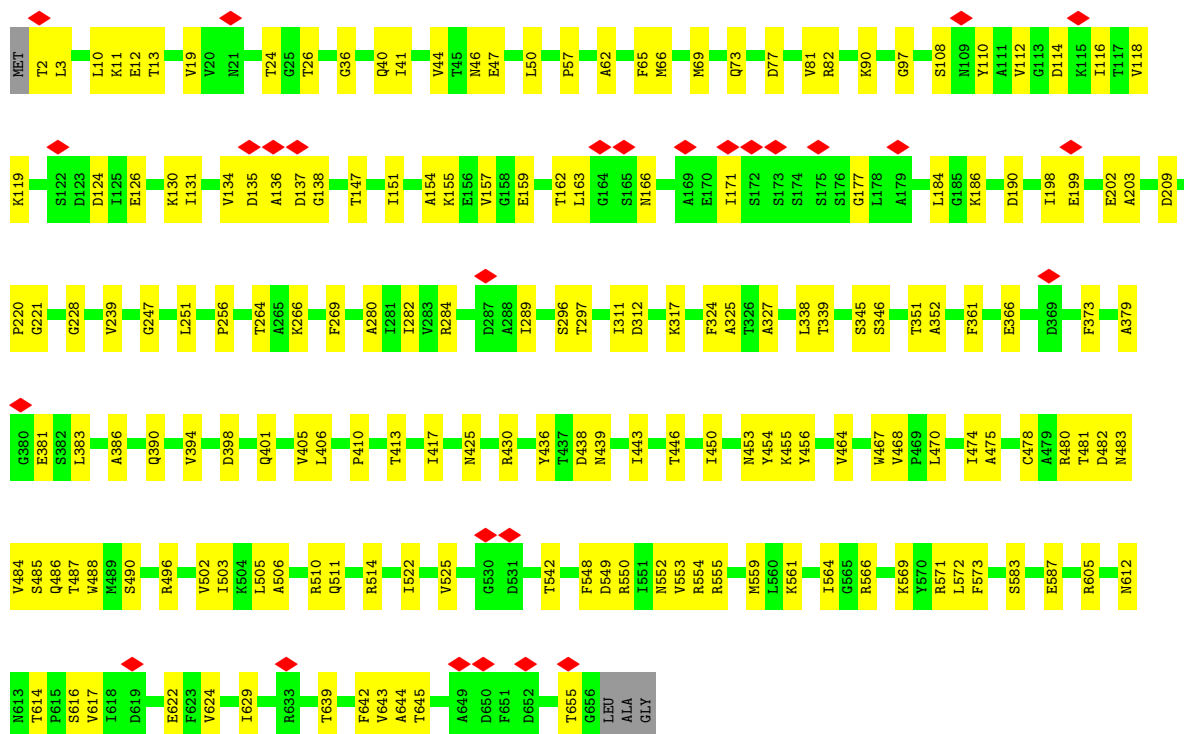


• Molecule 2: gp18, tail sheath protein

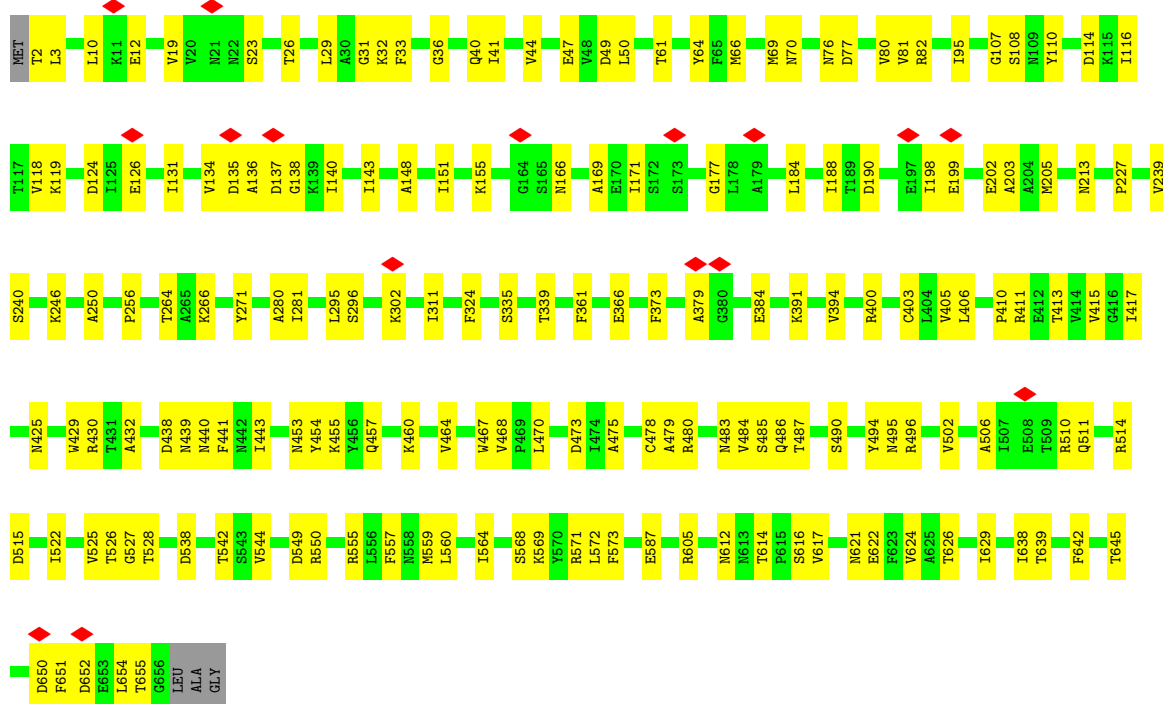


• Molecule 2: gp18, tail sheath protein



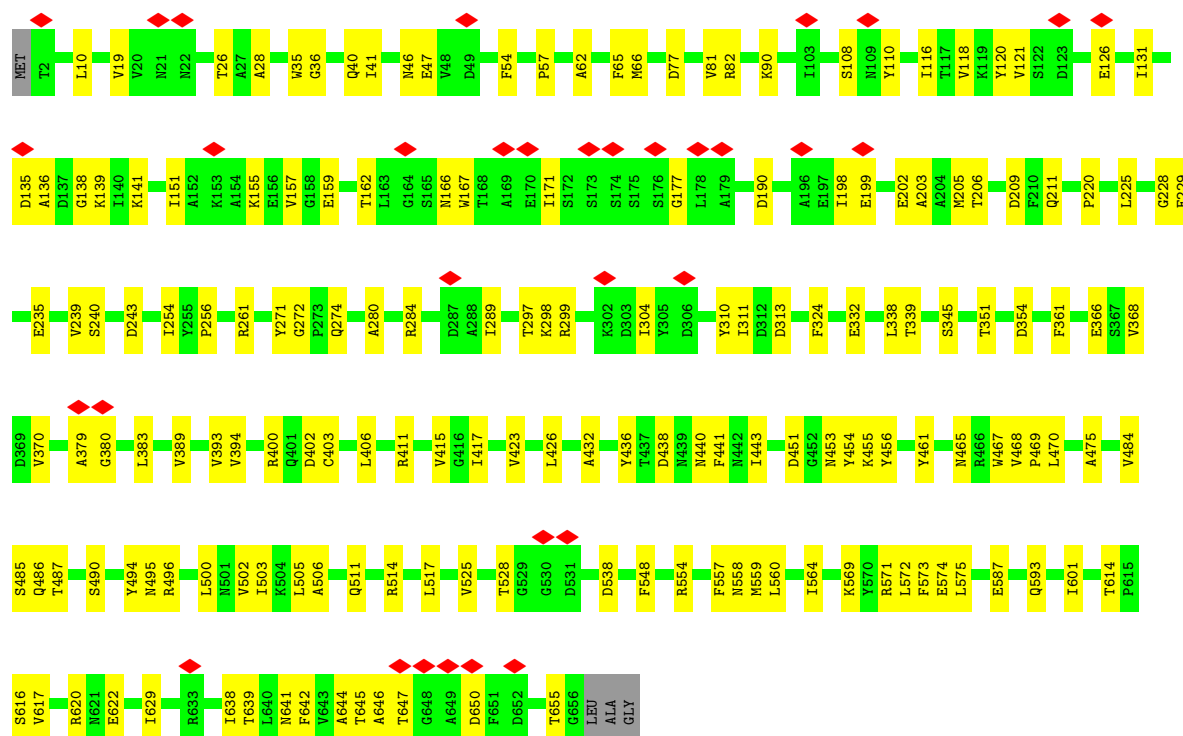


Chain cI:

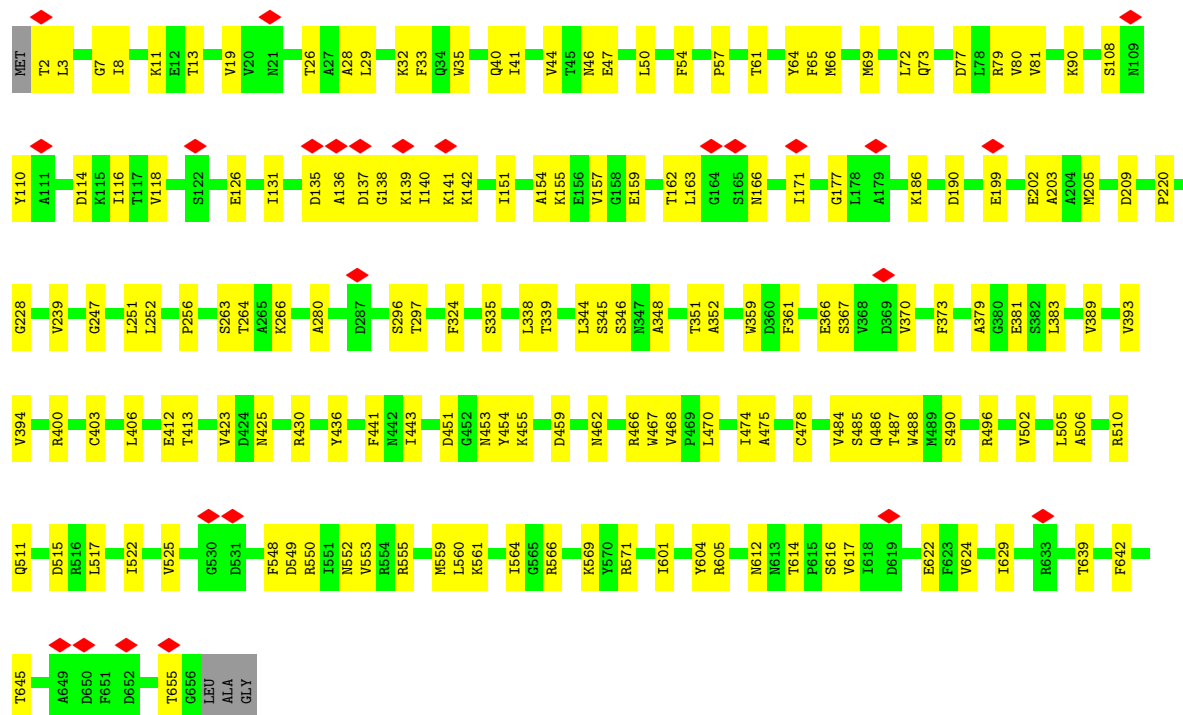
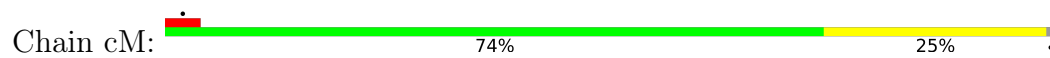


Chain cJ:



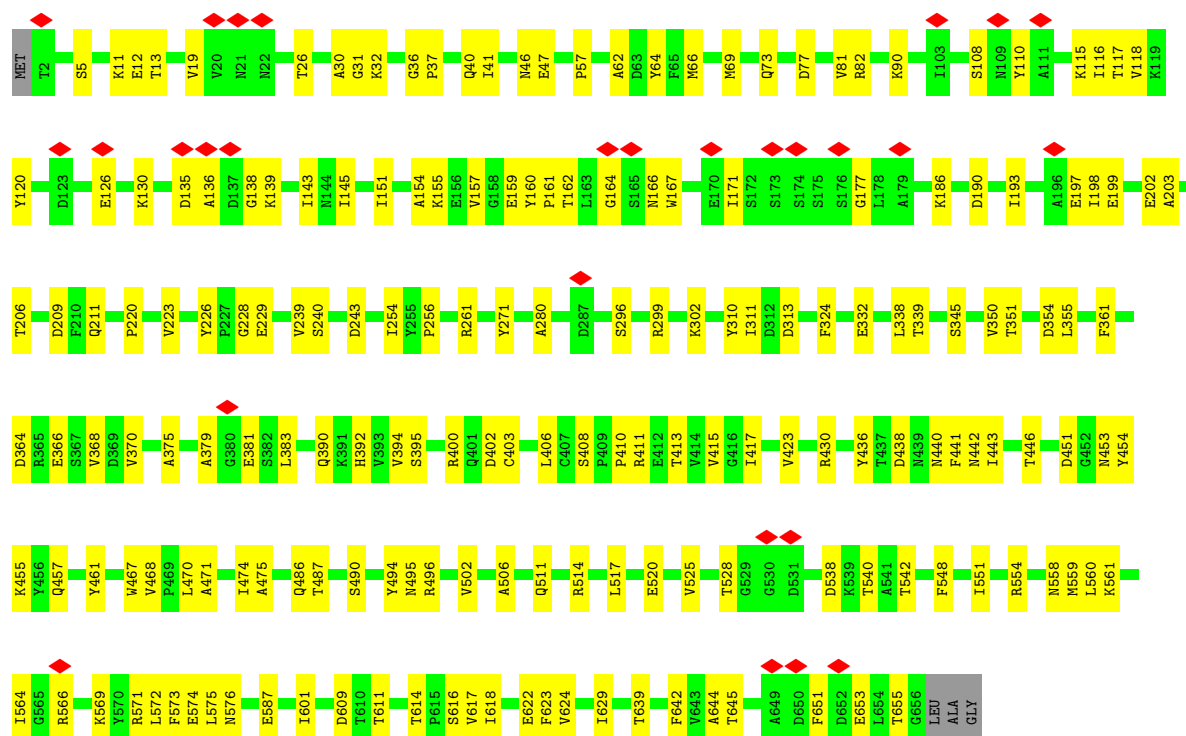


• Molecule 2: gp18, tail sheath protein

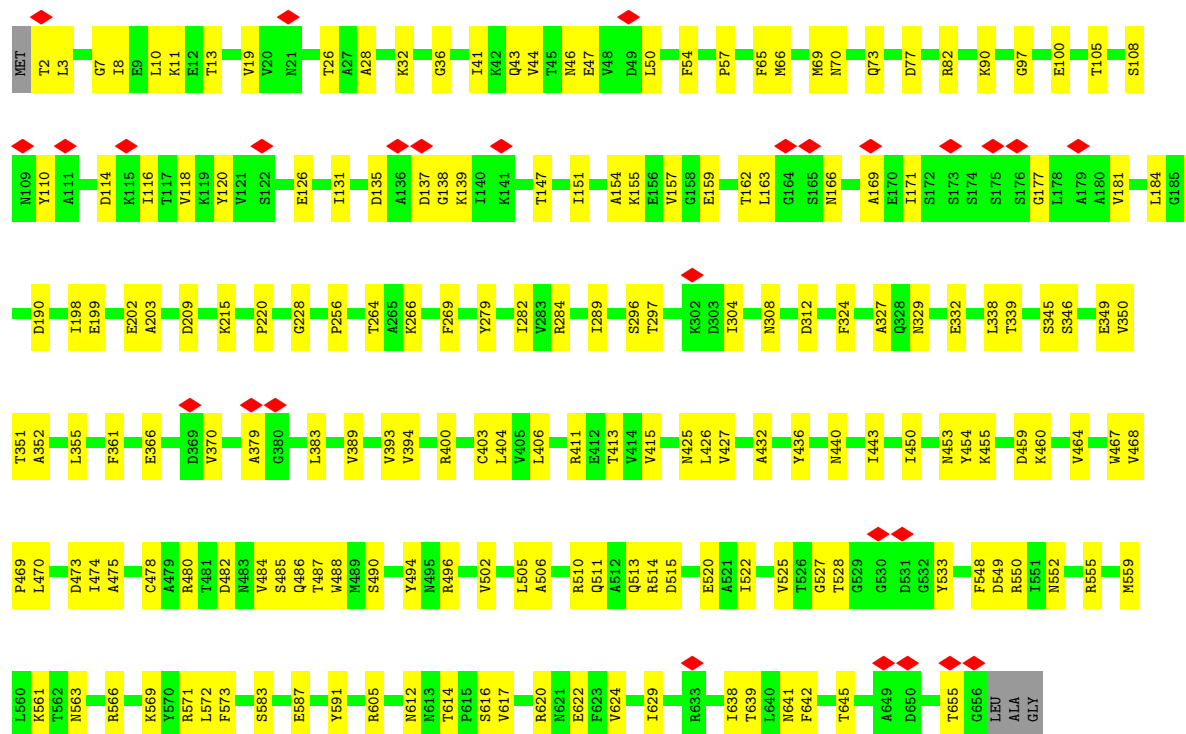


• Molecule 2: gp18, tail sheath protein



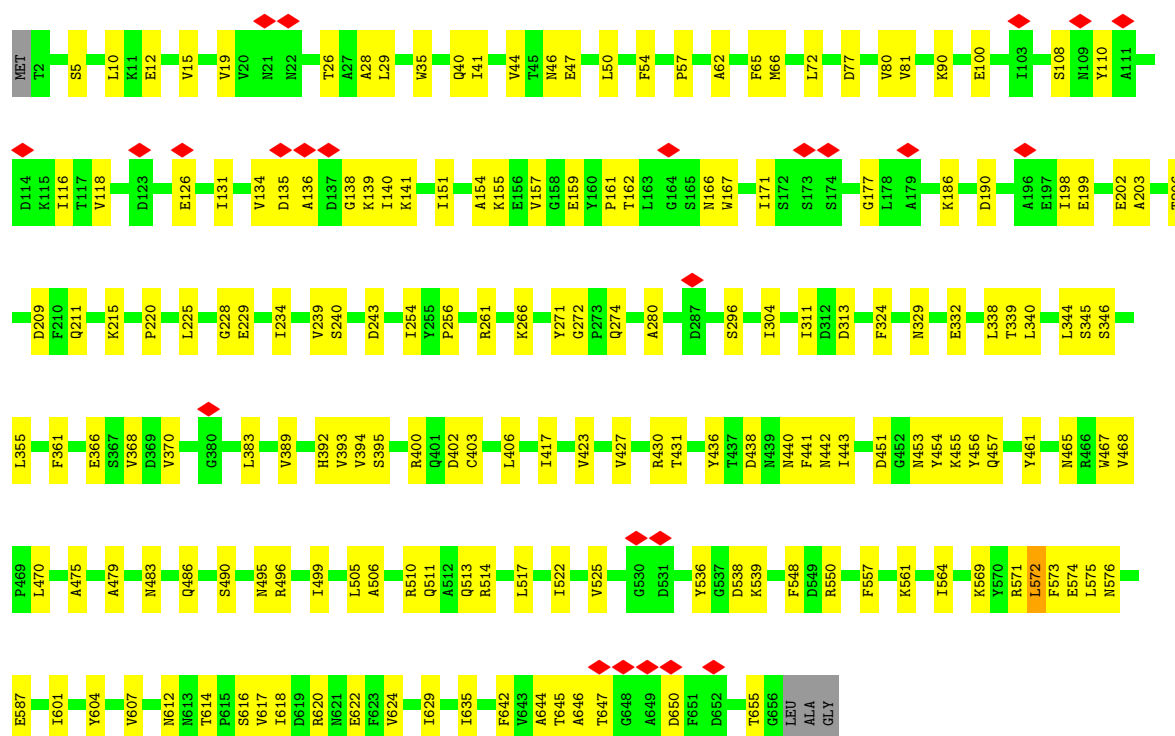


• Molecule 2: gp18, tail sheath protein



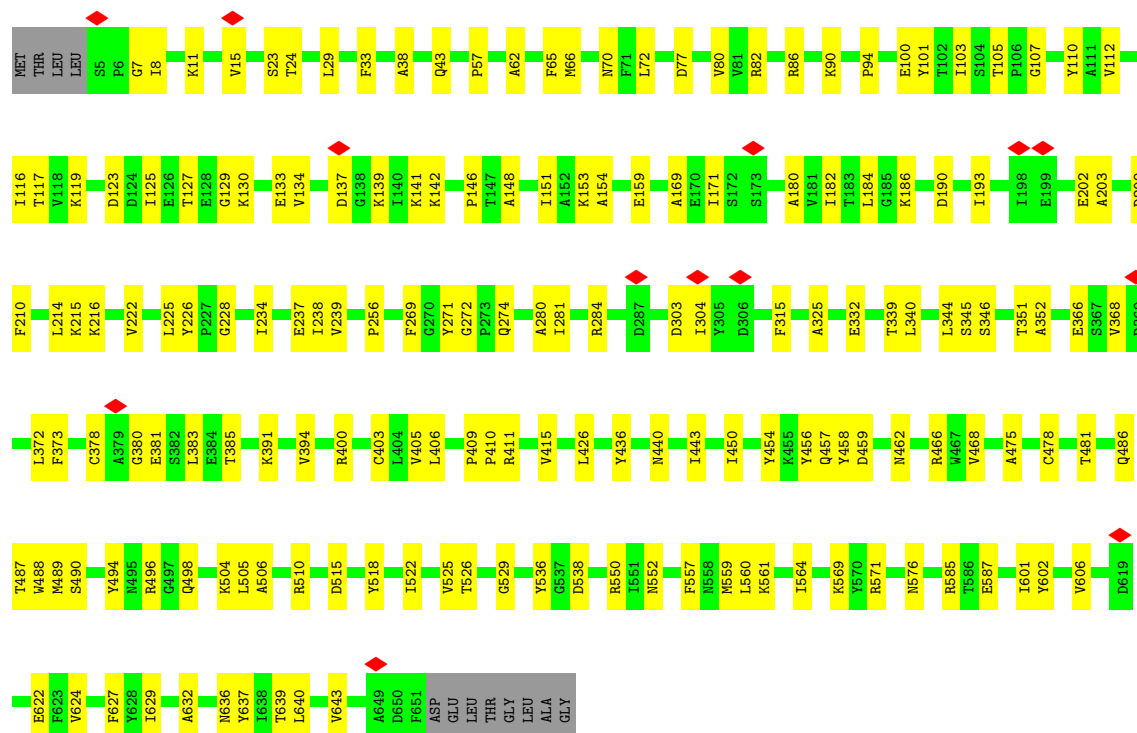
• Molecule 2: gp18, tail sheath protein

Chain cP: 

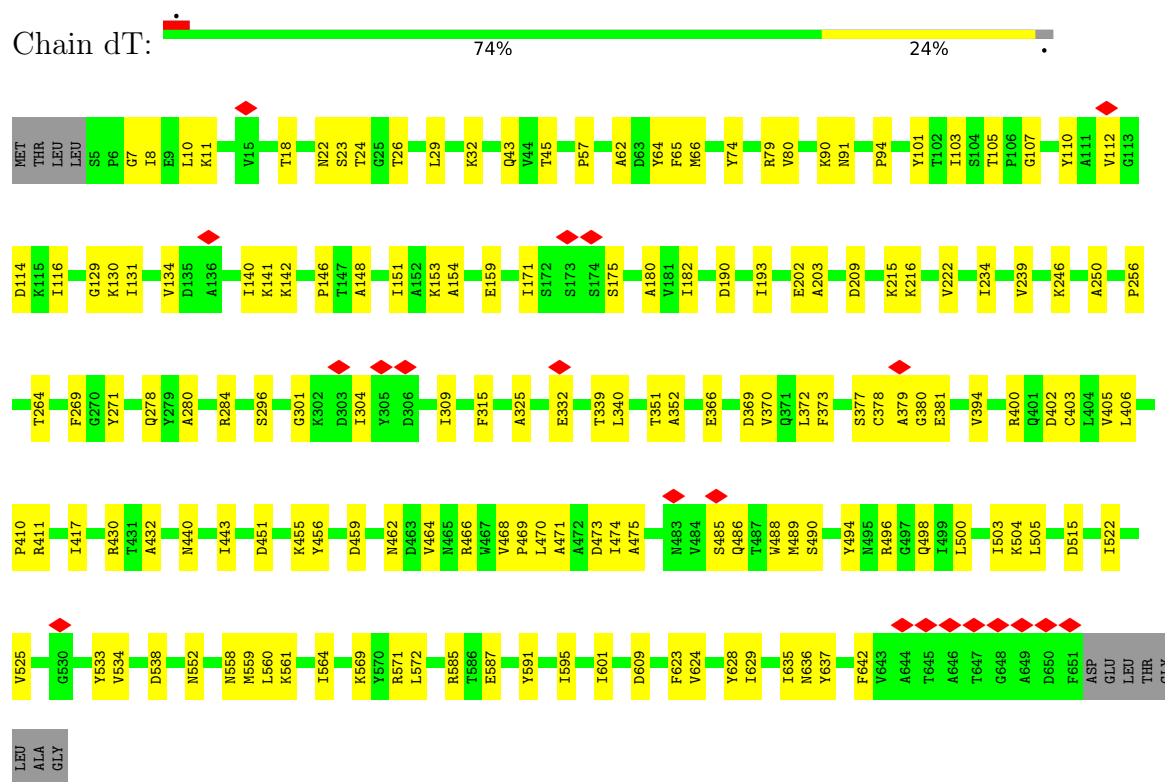


• Molecule 2: gp18, tail sheath protein

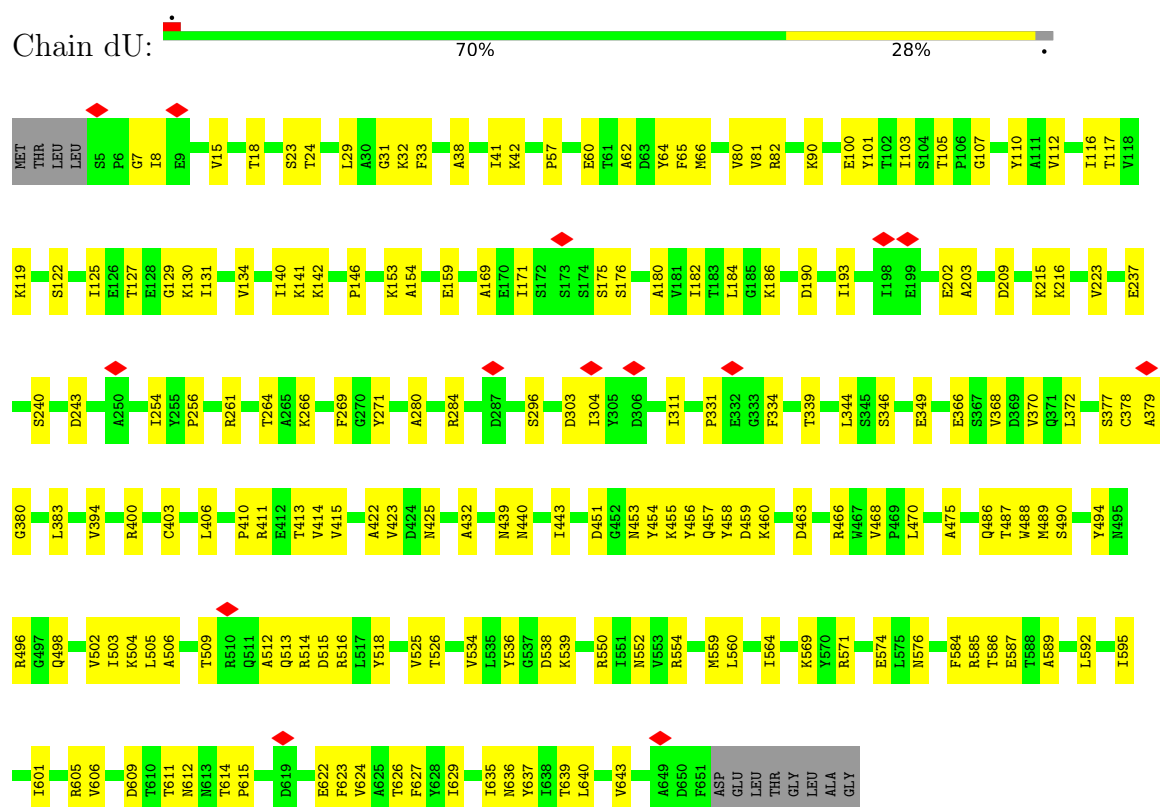
Chain dS: 



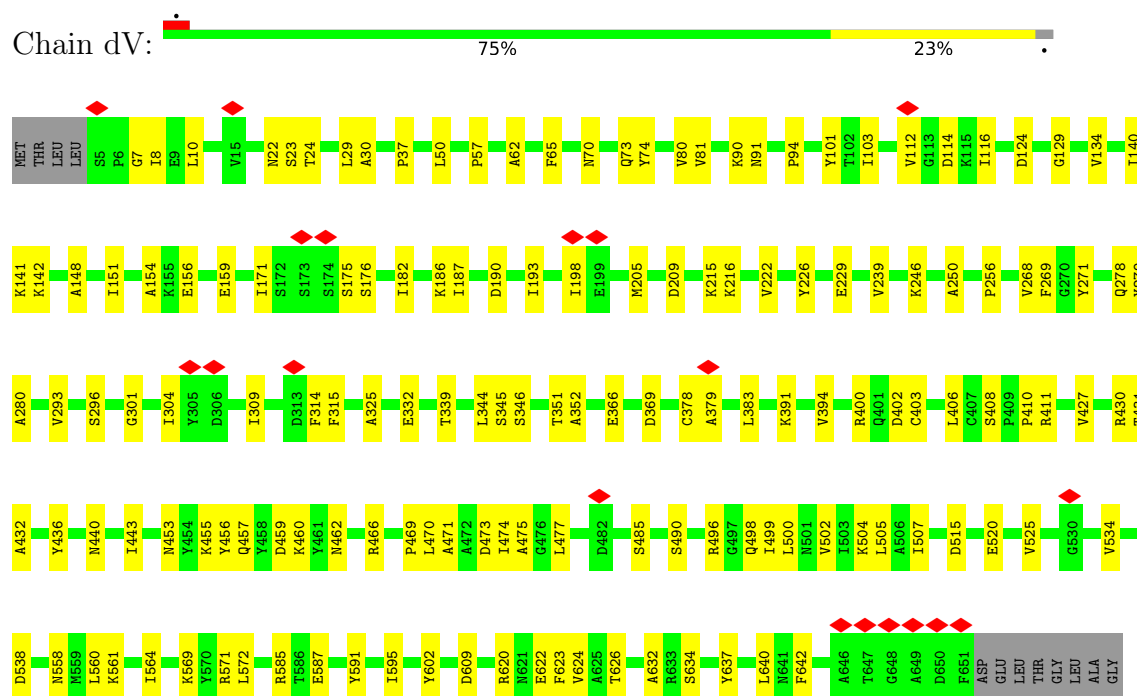
• Molecule 2: gp18, tail sheath protein



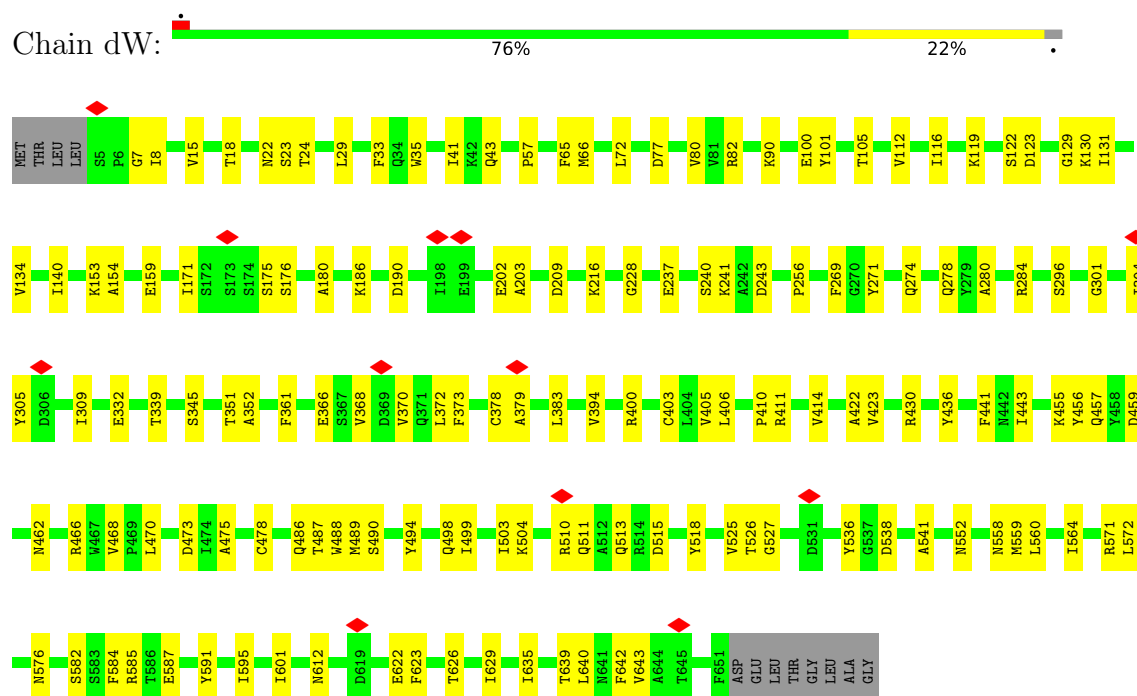
• Molecule 2: gp18, tail sheath protein



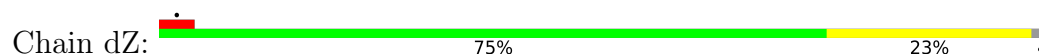
- Molecule 2: gp18, tail sheath protein

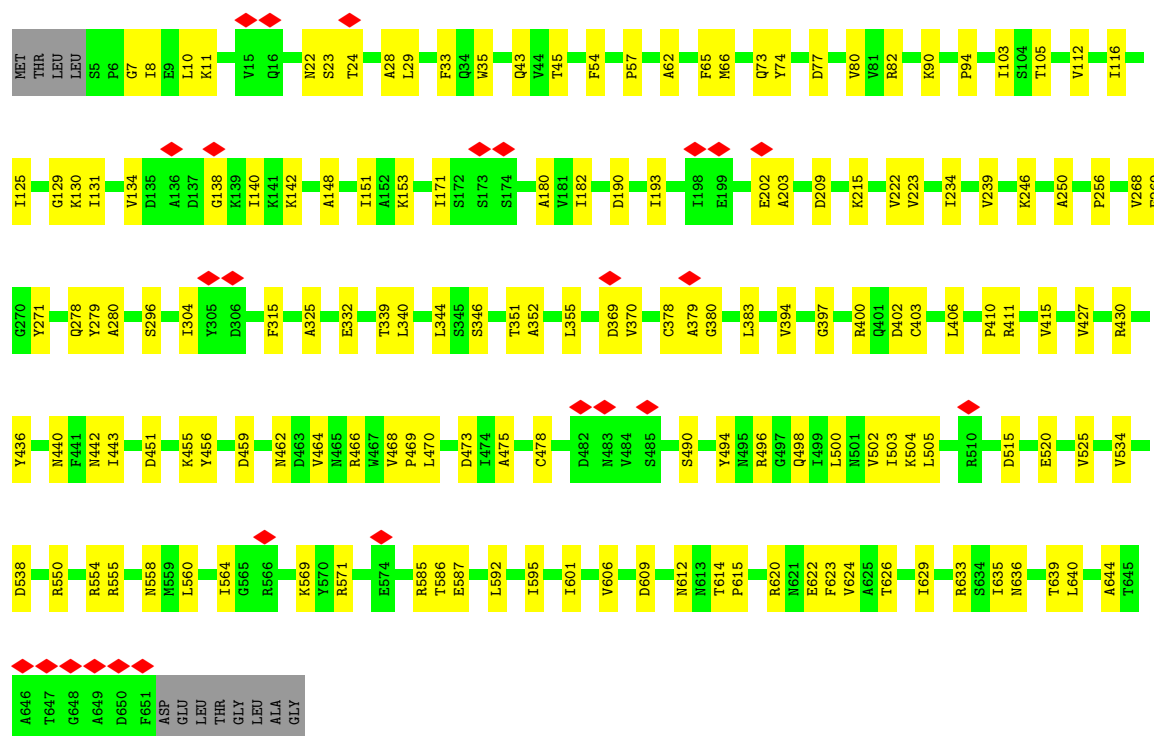


- Molecule 2: gp18, tail sheath protein

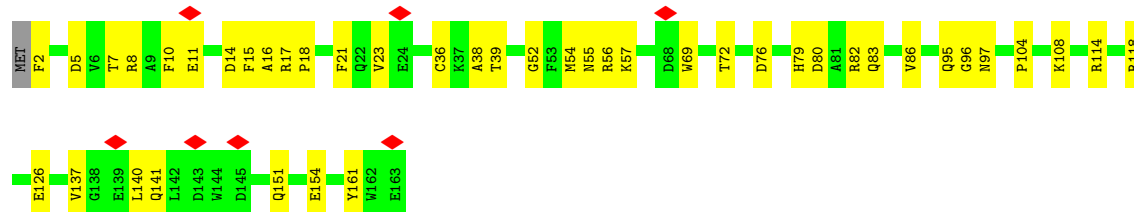


- Molecule 2: gp18, tail sheath protein

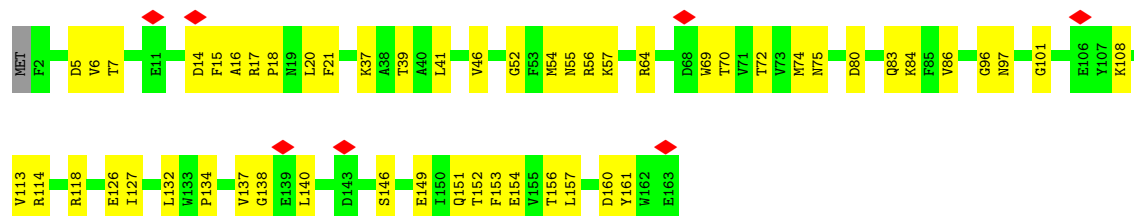




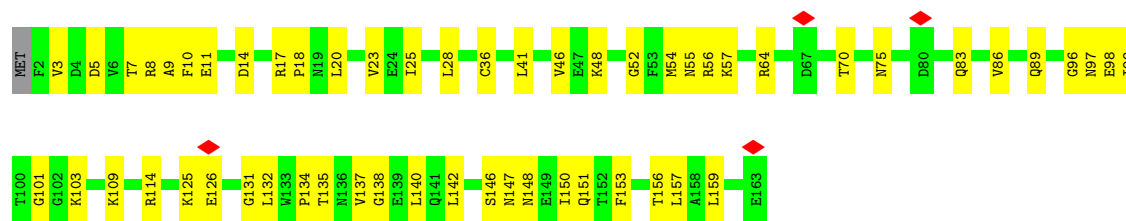
Chain 6: 73% 26%



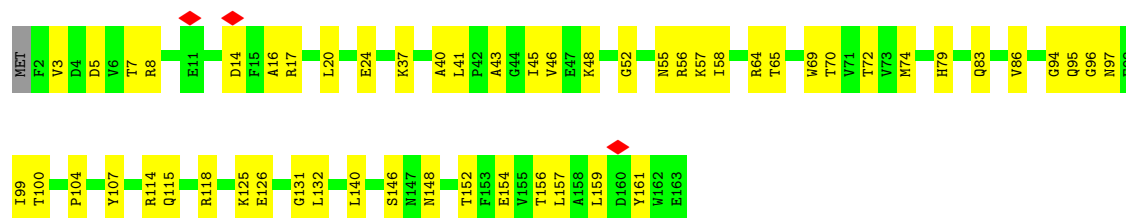
Chain 7: 67% 33%



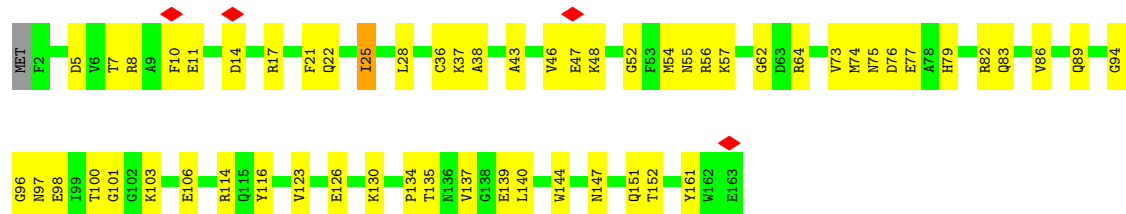
Chain 8: 65% 34%



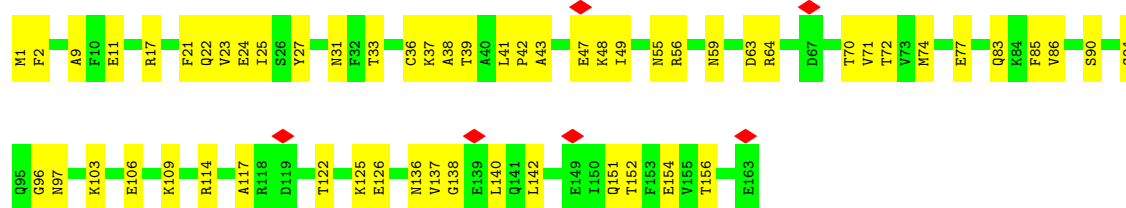
- Molecule 3: gp19, tail tube protein



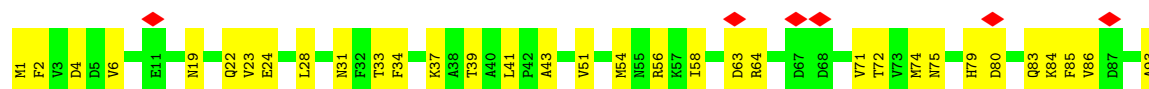
- Molecule 3: gp19, tail tube protein

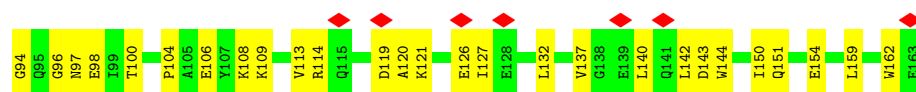


- Molecule 3: gp19, tail tube protein

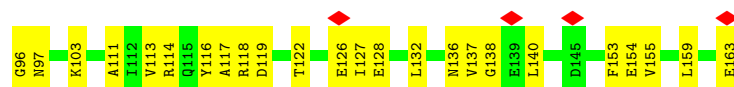


- Molecule 3: gp19, tail tube protein





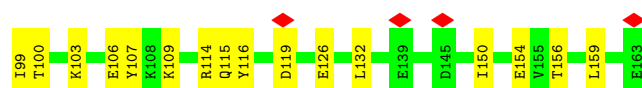
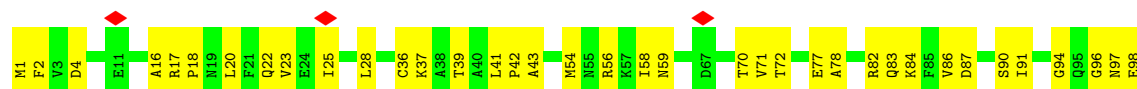
- Molecule 3: gp19, tail tube protein



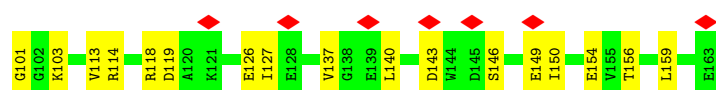
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

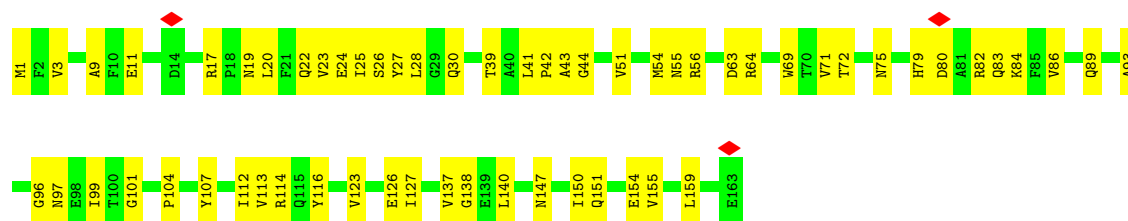


- Molecule 3: gp19, tail tube protein



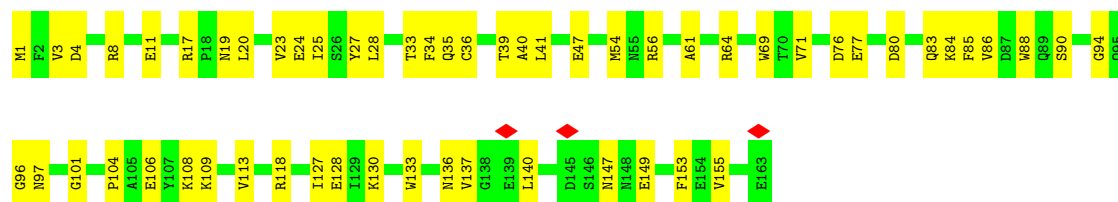
- Molecule 3: gp19, tail tube protein

Chain BX:  63% 37%



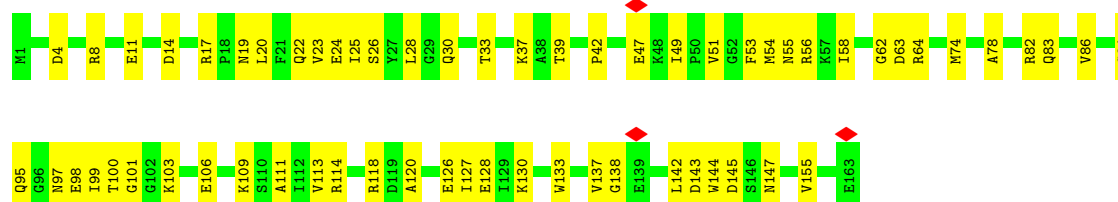
- Molecule 3: gp19, tail tube protein

Chain BY:  65% 35%



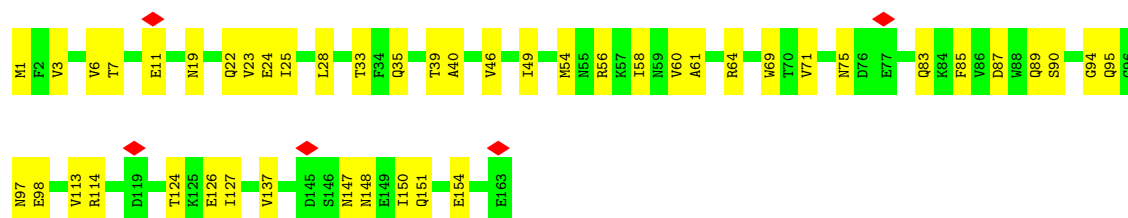
- Molecule 3: gp19, tail tube protein

Chain BZ:  62% 38%



- Molecule 3: gp19, tail tube protein

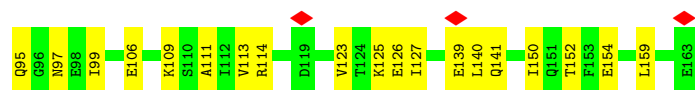
Chain Ba:  72% 28%



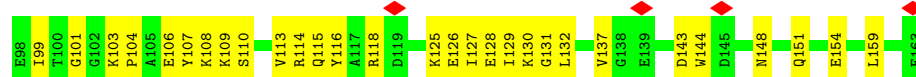
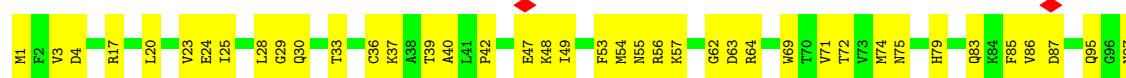
- Molecule 3: gp19, tail tube protein

Chain Bb:  67% 33%

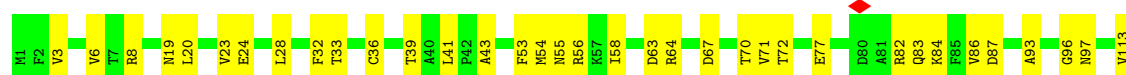




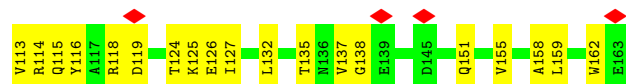
- Molecule 3: gp19, tail tube protein



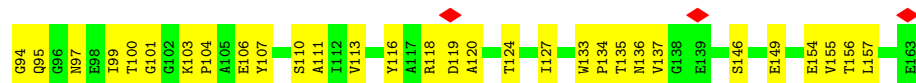
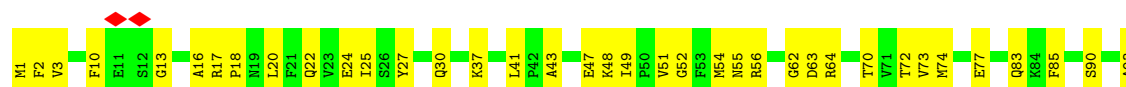
- Molecule 3: gp19, tail tube protein



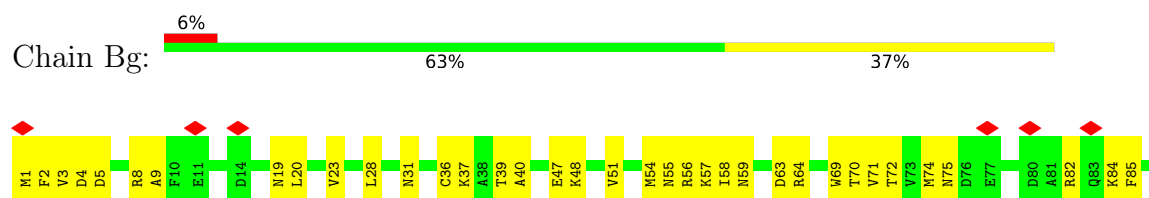
- Molecule 3: gp19, tail tube protein



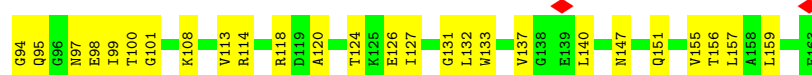
- Molecule 3: gp19, tail tube protein



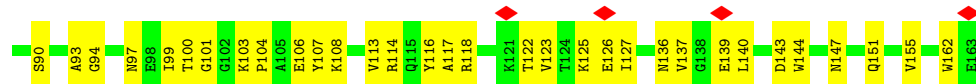
- Molecule 3: gp19, tail tube protein



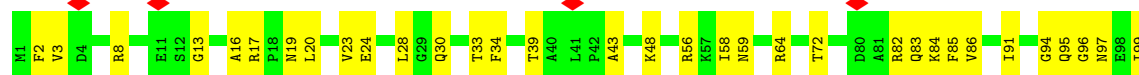
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

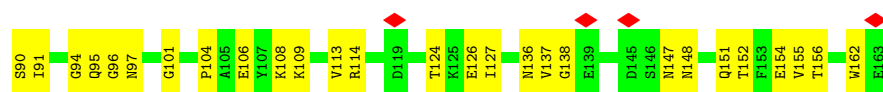


- Molecule 3: gp19, tail tube protein

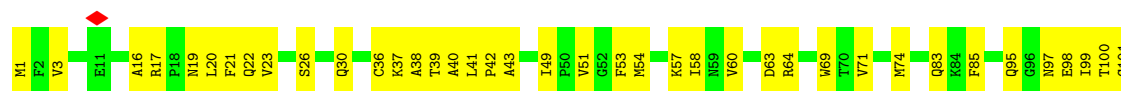


- Molecule 3: gp19, tail tube protein

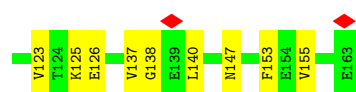
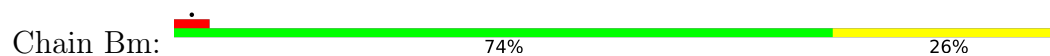




- Molecule 3: gp19, tail tube protein



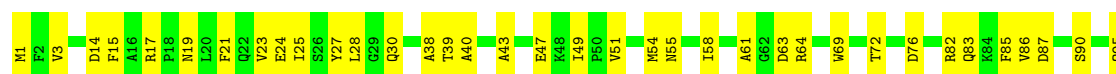
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

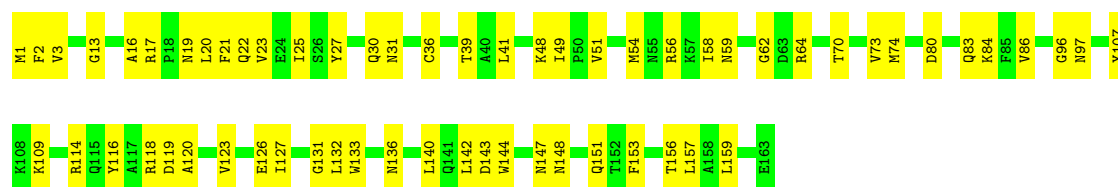


- Molecule 3: gp19, tail tube protein



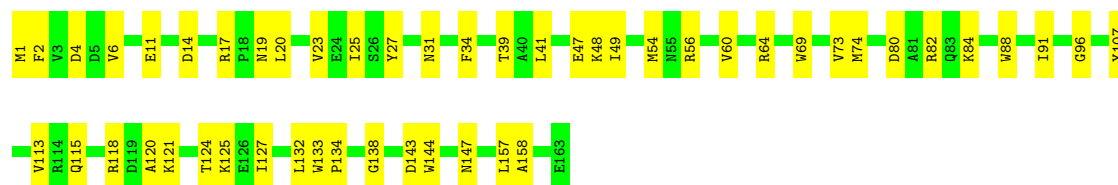
- Molecule 3: gp19, tail tube protein

Chain OE:  63% 37%



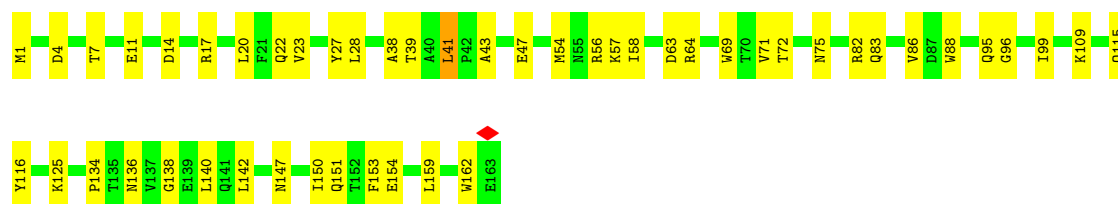
- Molecule 3: gp19, tail tube protein

Chain OF:  69% 31%



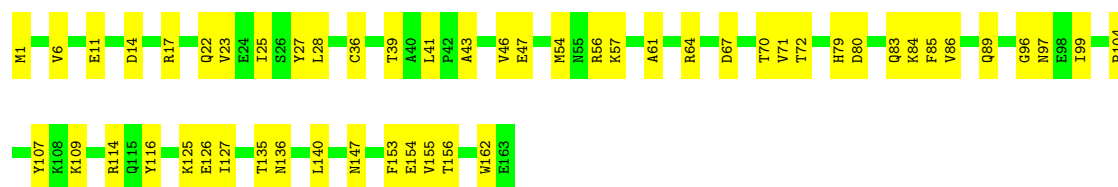
- Molecule 3: gp19, tail tube protein

Chain OG:  70% 29%



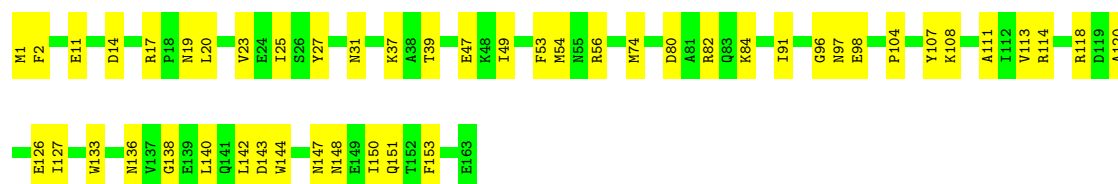
- Molecule 3: gp19, tail tube protein

Chain OH:  68% 32%

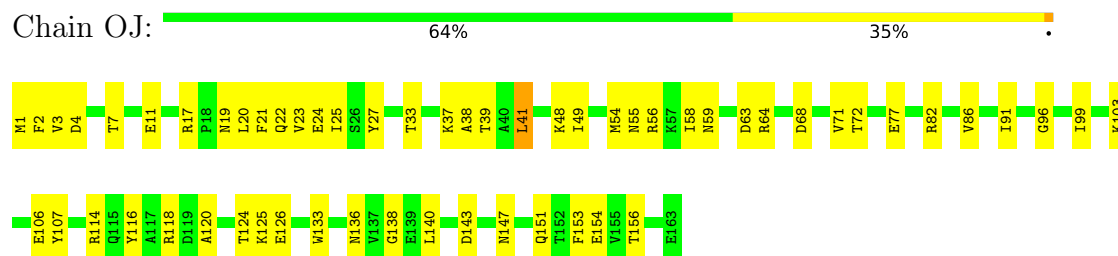


- Molecule 3: gp19, tail tube protein

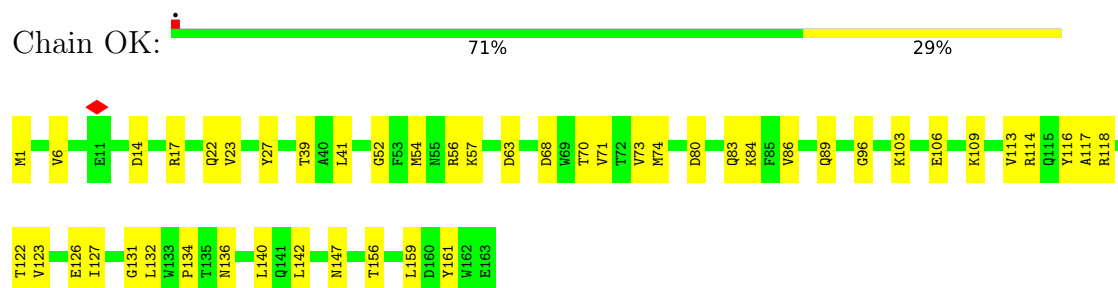
Chain OI:  71% 29%



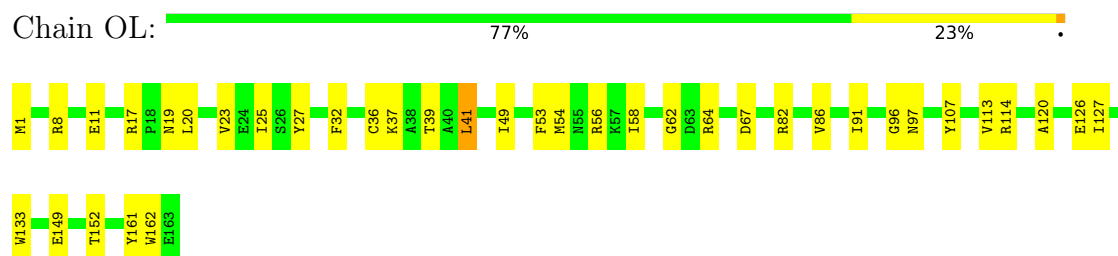
- Molecule 3: gp19, tail tube protein



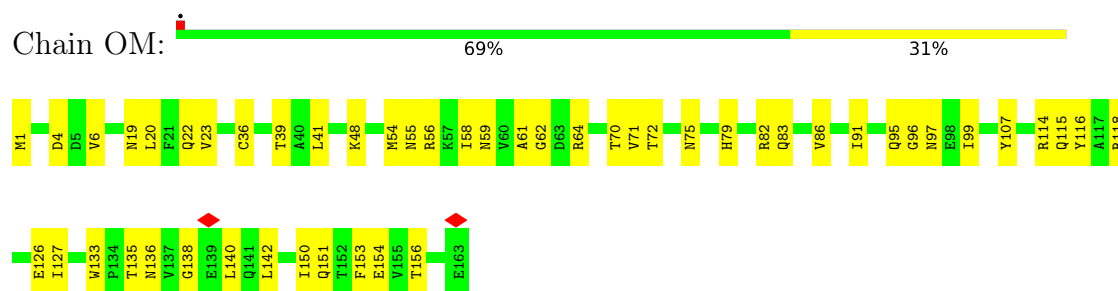
- Molecule 3: gp19, tail tube protein



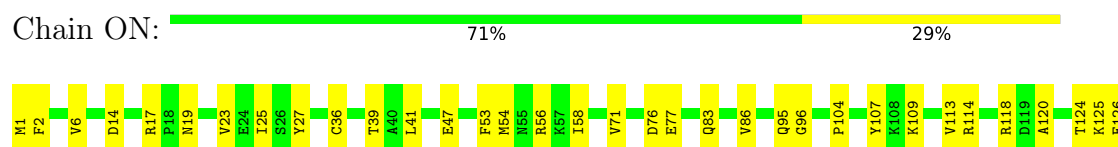
- Molecule 3: gp19, tail tube protein

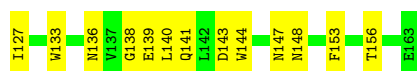


- Molecule 3: gp19, tail tube protein

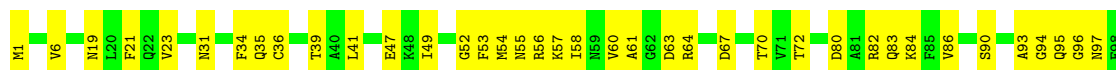


- Molecule 3: gp19, tail tube protein





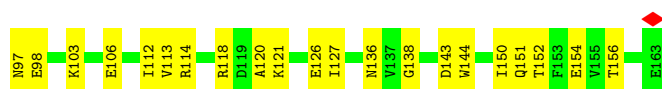
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

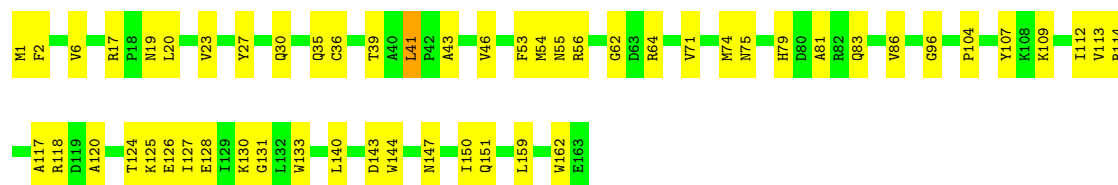


- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein





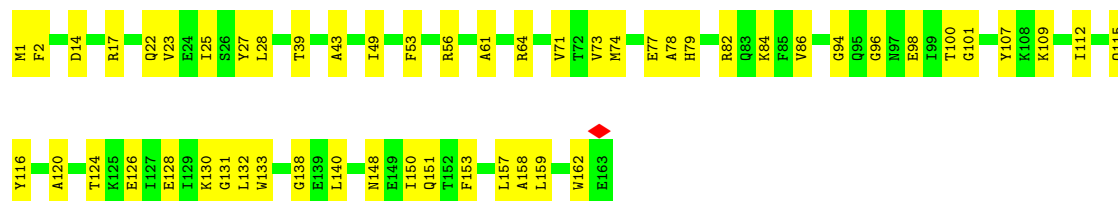
- Molecule 3: gp19, tail tube protein

Chain On: 70%



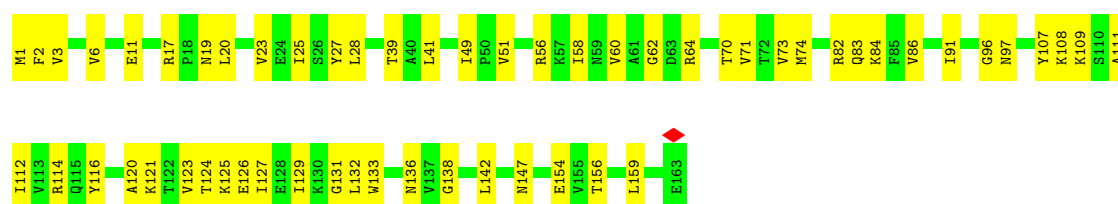
- Molecule 3: gp19, tail tube protein

Chain On: 67%



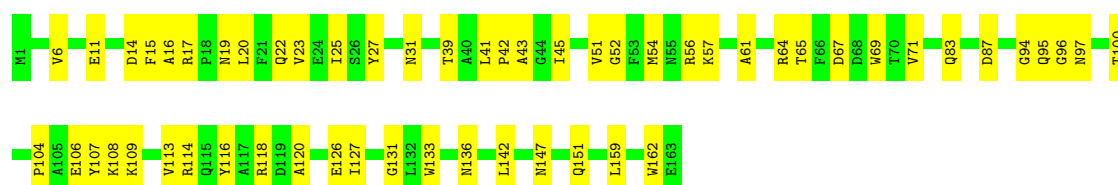
- Molecule 3: gp19, tail tube protein

Chain On: 65%



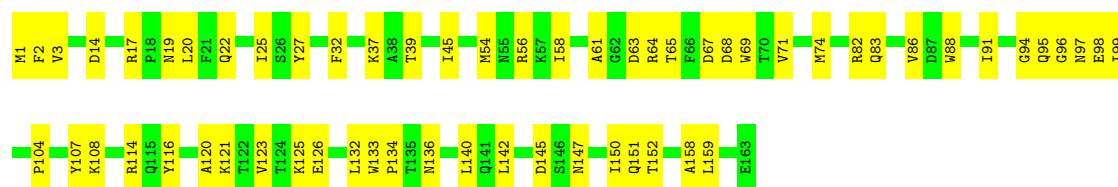
- Molecule 3: gp19, tail tube protein

Chain On: 66%



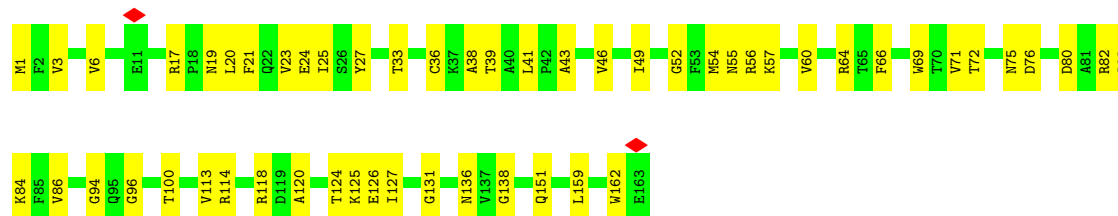
- Molecule 3: gp19, tail tube protein

Chain Or:  63% 37%



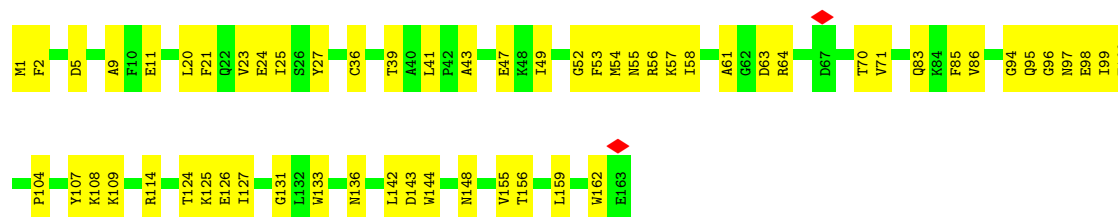
• Molecule 3: gp19, tail tube protein

Chain Os:  67% 33%



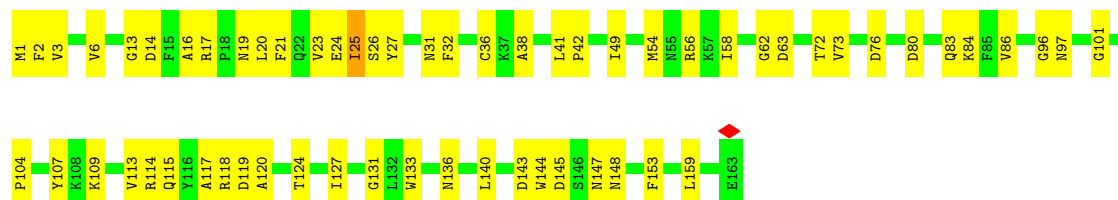
• Molecule 3: gp19, tail tube protein

Chain Ot:  64% 36%



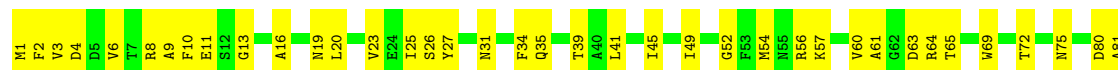
• Molecule 3: gp19, tail tube protein

Chain PE:  63% 37%



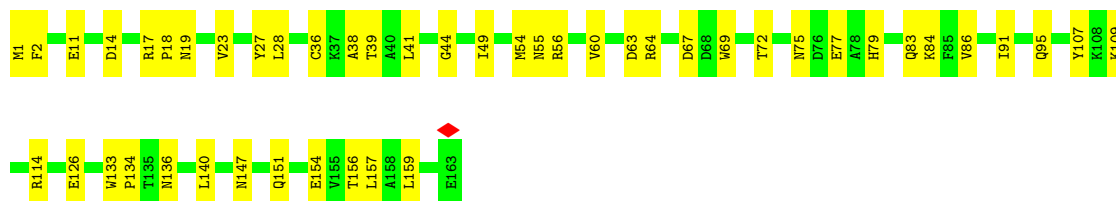
• Molecule 3: gp19, tail tube protein

Chain PF:  61% 39%

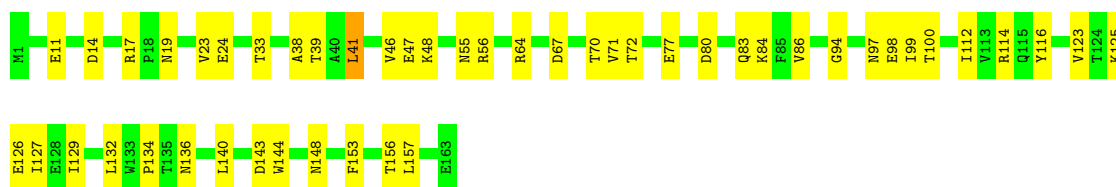




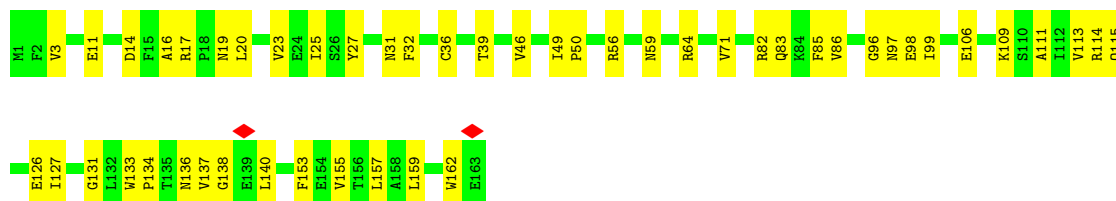
- Molecule 3: gp19, tail tube protein



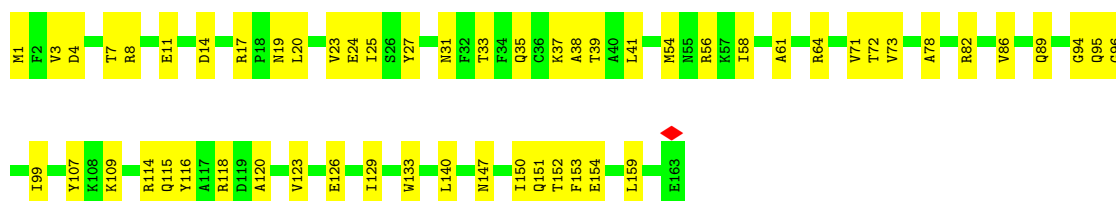
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

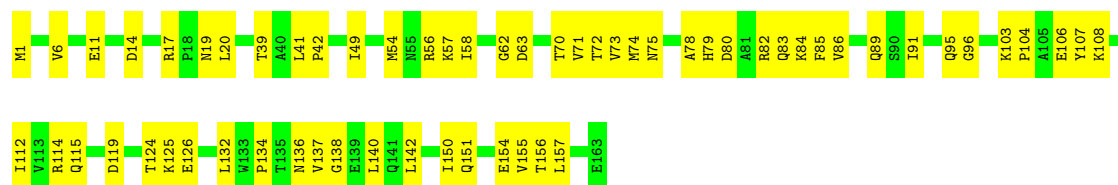


- Molecule 3: gp19, tail tube protein



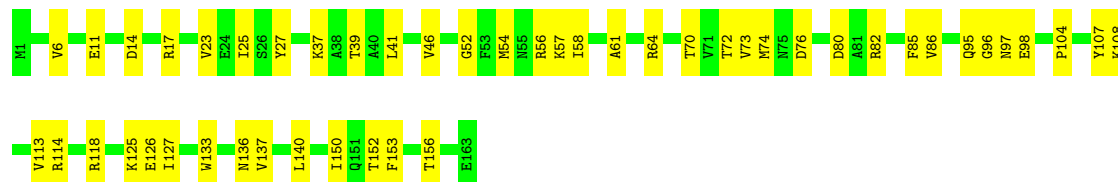
- Molecule 3: gp19, tail tube protein





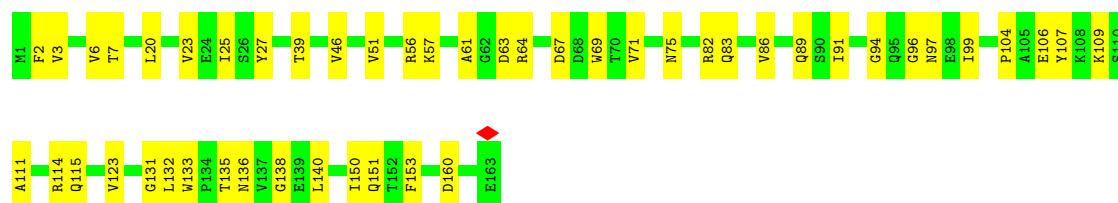
- Molecule 3: gp19, tail tube protein

Chain PL: 71% 29%



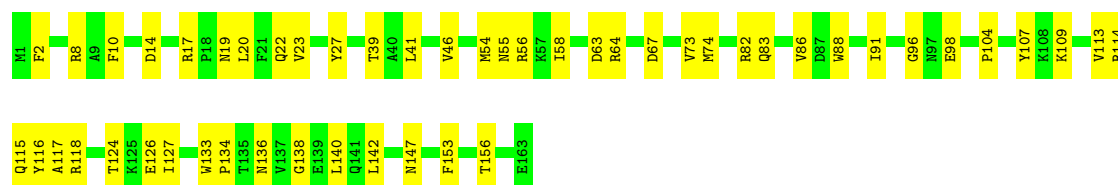
- Molecule 3: gp19, tail tube protein

Chain PM: 71% 29%



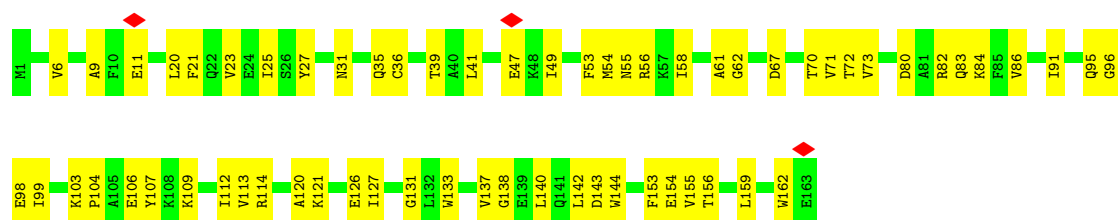
- Molecule 3: gp19, tail tube protein

Chain PN: 69% 31%



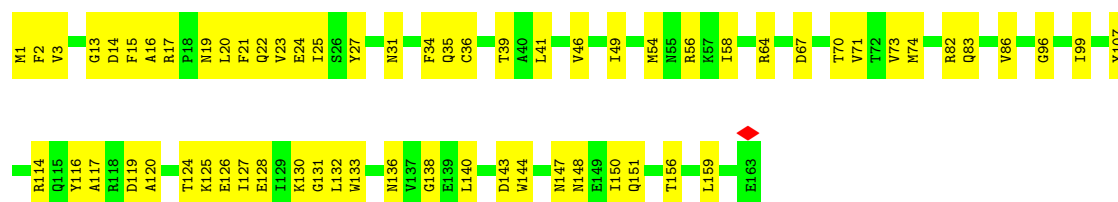
- Molecule 3: gp19, tail tube protein

Chain PO: 61% 39%



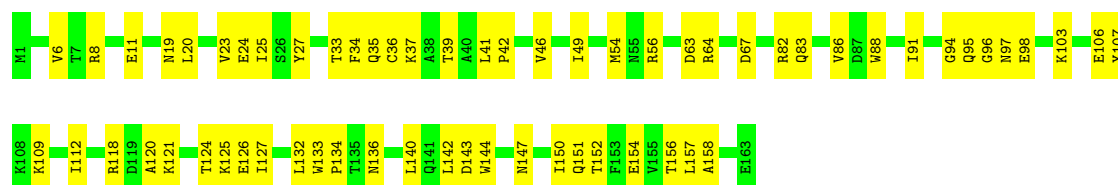
- Molecule 3: gp19, tail tube protein

Chain Pj:  61% 39%



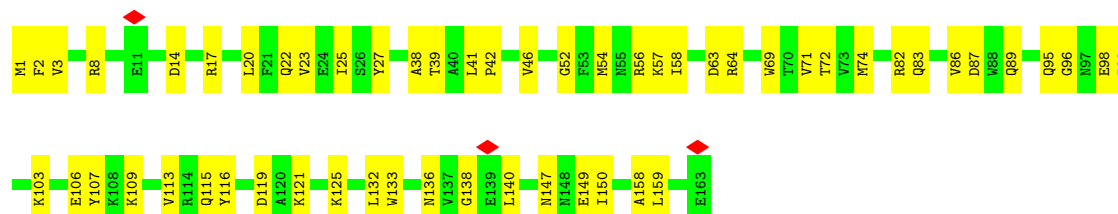
- Molecule 3: gp19, tail tube protein

Chain Pk:  62% 38%




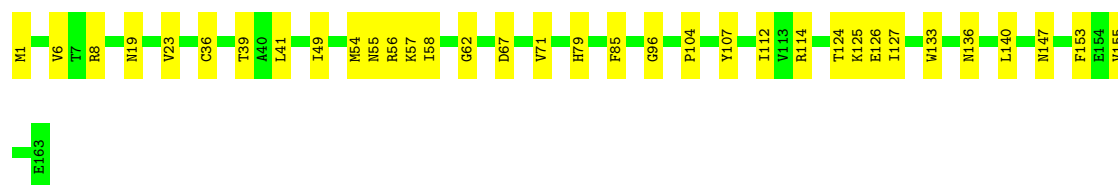
- Molecule 3: gp19, tail tube protein

Chain Pl:  66% 34%



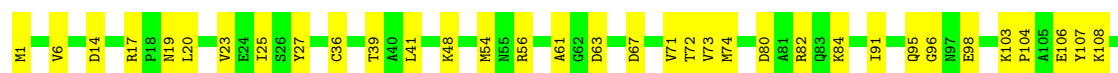
- Molecule 3: gp19, tail tube protein

Chain Pm:  79% 21%



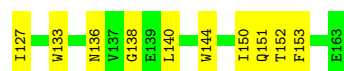
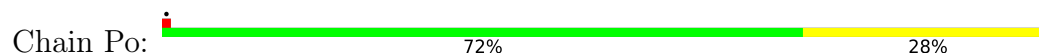
- Molecule 3: gp19, tail tube protein

Chain Pn:  71% 29%

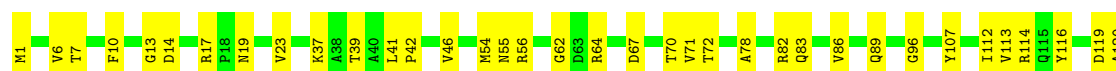




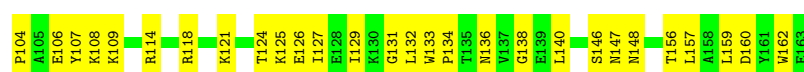
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

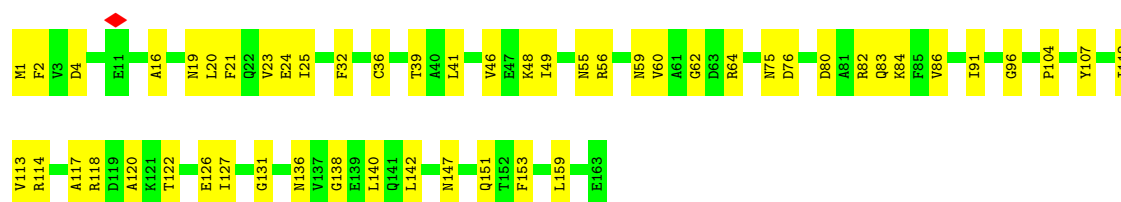


- Molecule 3: gp19, tail tube protein



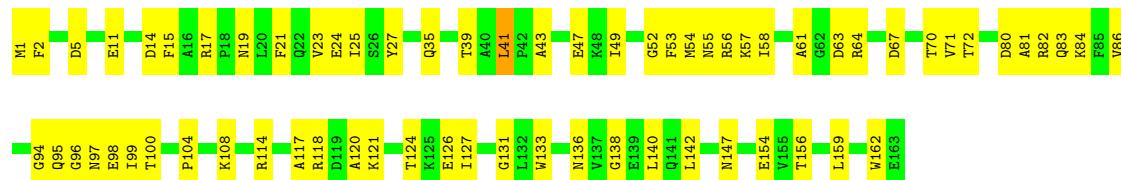
- Molecule 3: gp19, tail tube protein





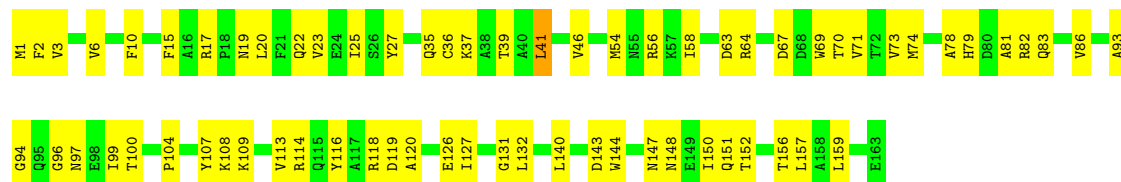
- Molecule 3: gp19, tail tube protein

Chain Pt: 59% 40%



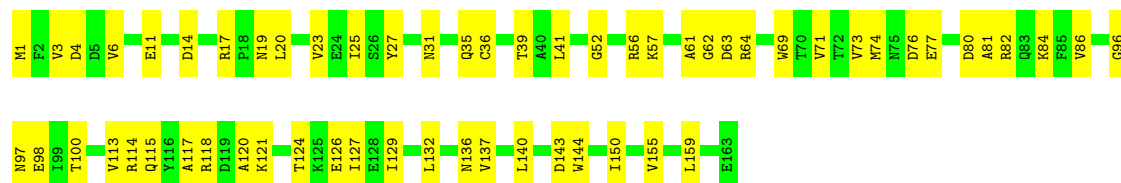
- Molecule 3: gp19, tail tube protein

Chain RE: 59% 40%



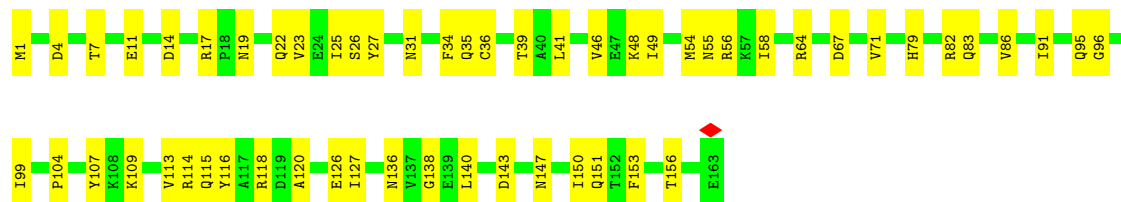
- Molecule 3: gp19, tail tube protein

Chain RF: 64% 36%



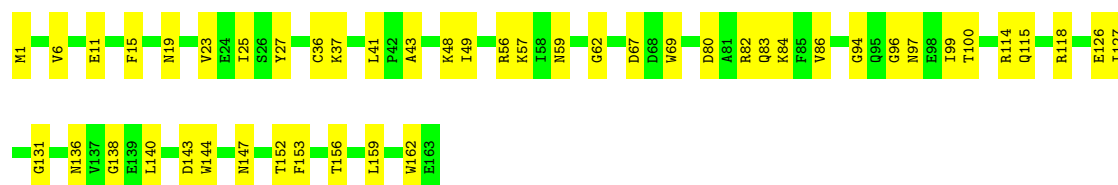
- Molecule 3: gp19, tail tube protein

Chain RG: 66% 34%



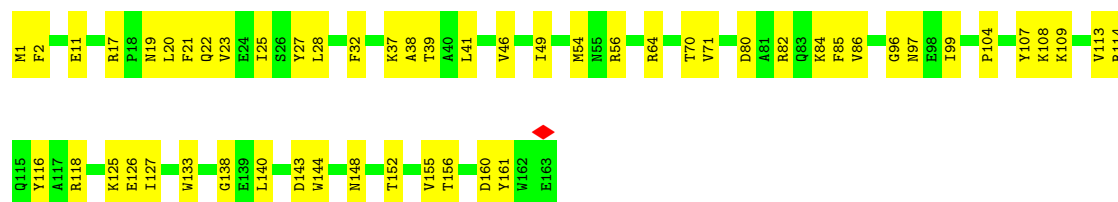
- Molecule 3: gp19, tail tube protein

Chain RH:  71% 29%



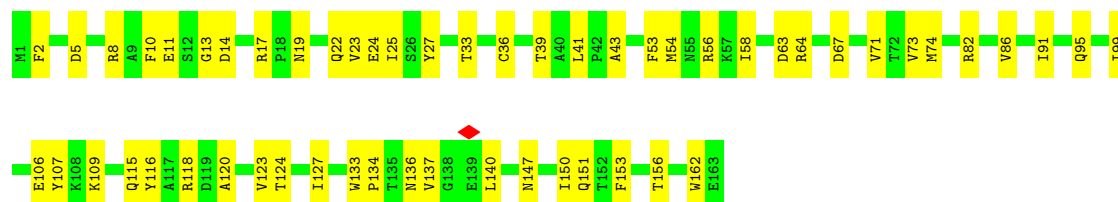
- Molecule 3: gp19, tail tube protein

Chain RI:  67% 33%



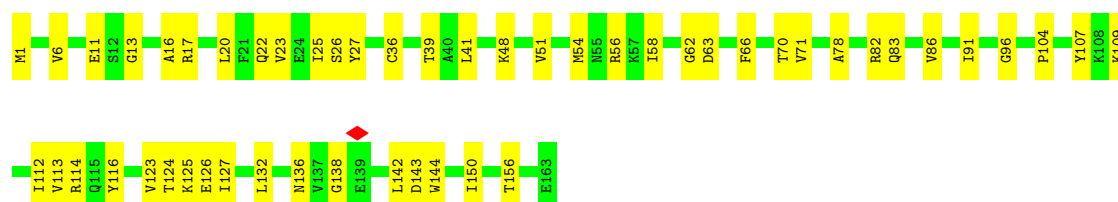
- Molecule 3: gp19, tail tube protein

Chain RJ:  66% 34%



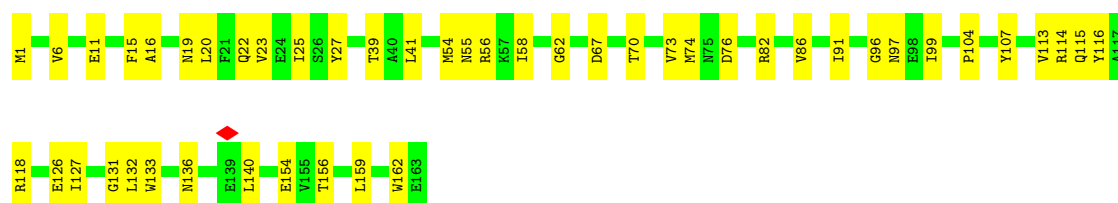
- Molecule 3: gp19, tail tube protein

Chain RK:  69% 31%



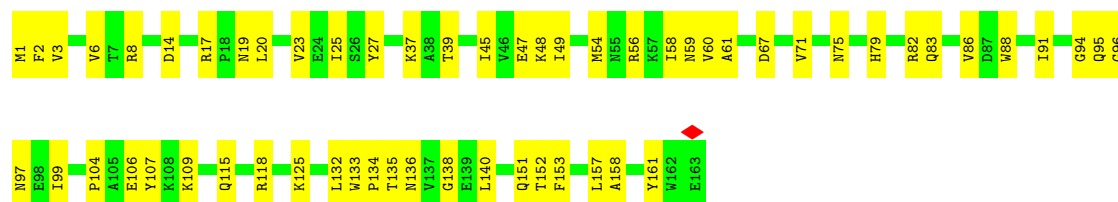
- Molecule 3: gp19, tail tube protein

Chain RL:  71% 29%



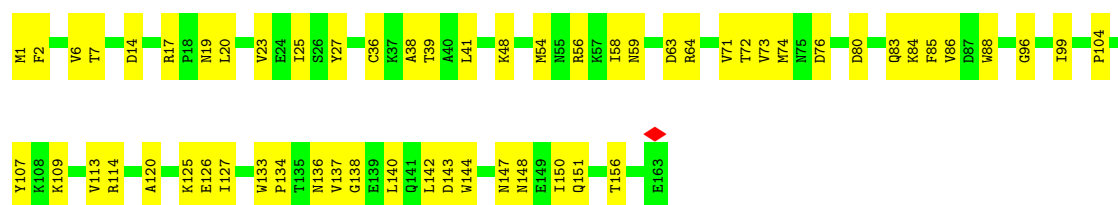
- Molecule 3: gp19, tail tube protein

Chain RM:  64% 36%



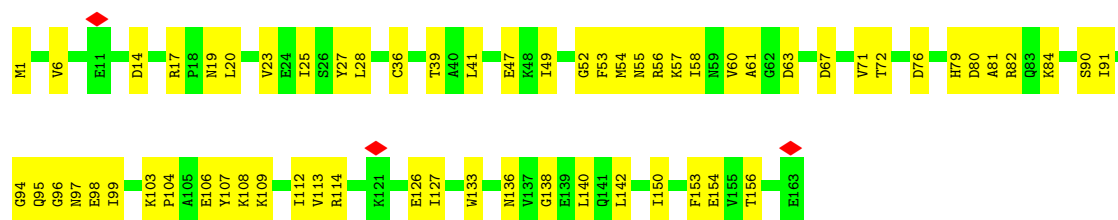
- Molecule 3: gp19, tail tube protein

Chain RN:  64% 36%



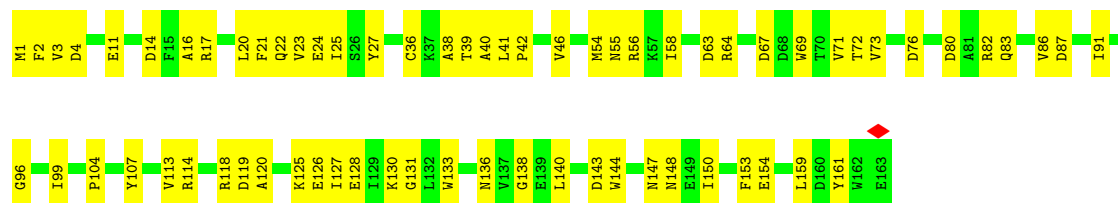
- Molecule 3: gp19, tail tube protein

Chain RO:  62% 38%



- Molecule 3: gp19, tail tube protein

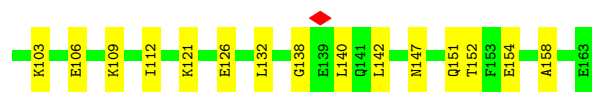
Chain RT:  58% 42%



- Molecule 3: gp19, tail tube protein

Chain Rk:  69% 31%

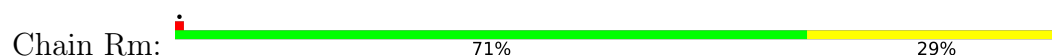




- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

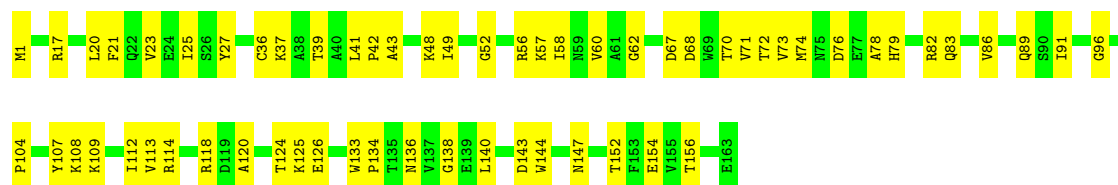


- Molecule 3: gp19, tail tube protein

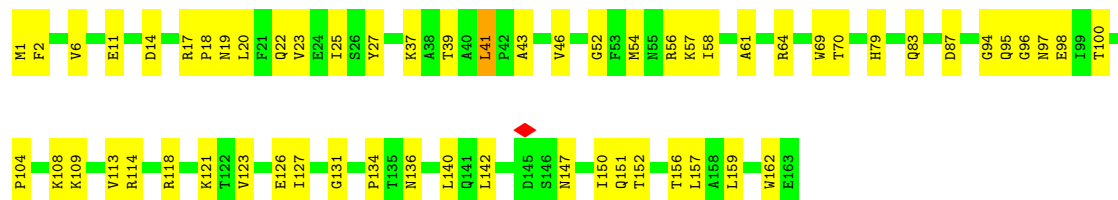


- Molecule 3: gp19, tail tube protein

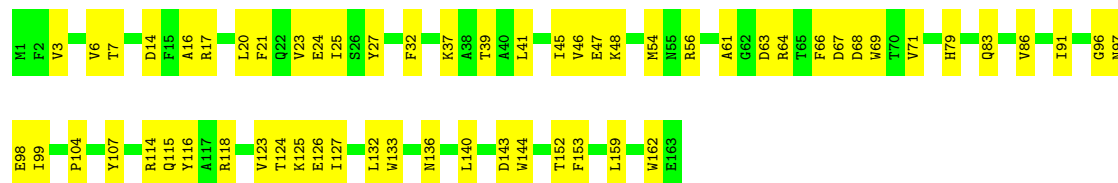




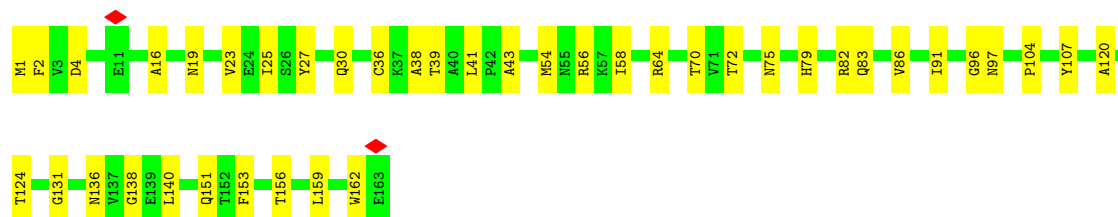
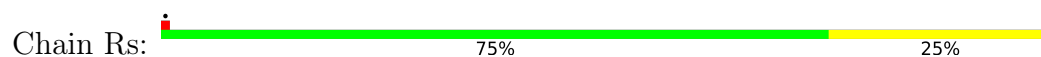
- Molecule 3: gp19, tail tube protein



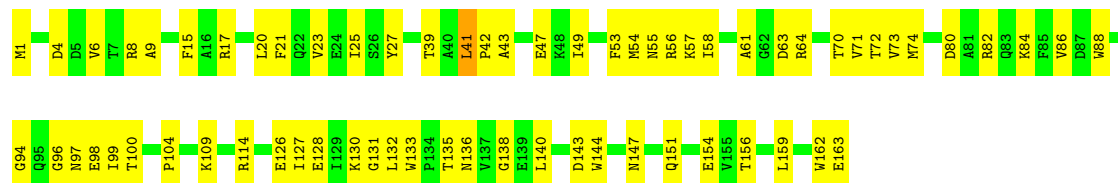
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

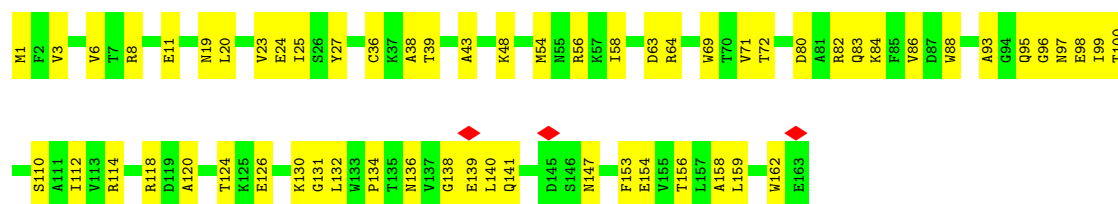


- Molecule 3: gp19, tail tube protein



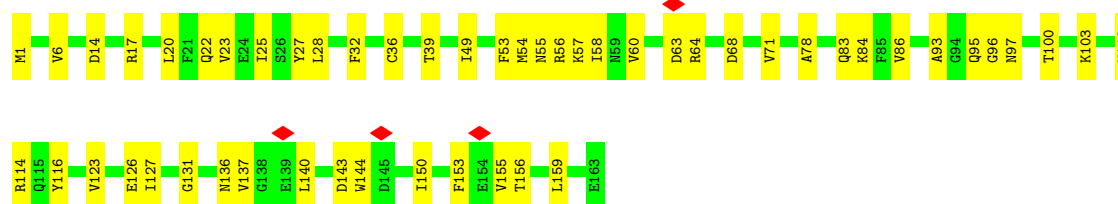
- Molecule 3: gp19, tail tube protein

Chain h1:  63% 37%



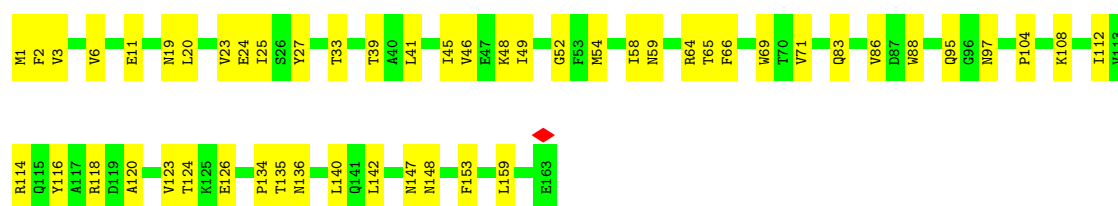
• Molecule 3: gp19, tail tube protein

Chain h2:  68% 32%



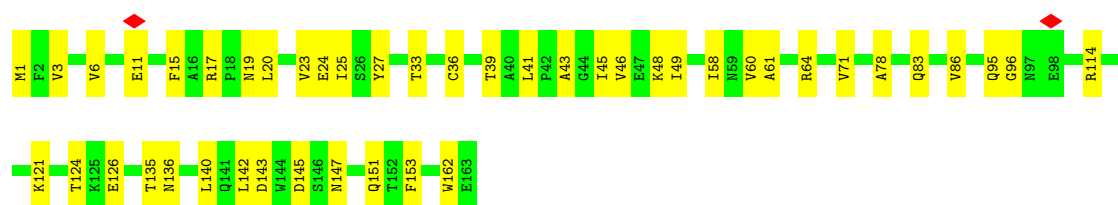
• Molecule 3: gp19, tail tube protein

Chain hI:  69% 31%



• Molecule 3: gp19, tail tube protein

Chain hJ:  72% 28%



• Molecule 3: gp19, tail tube protein

Chain hK:  62% 38%





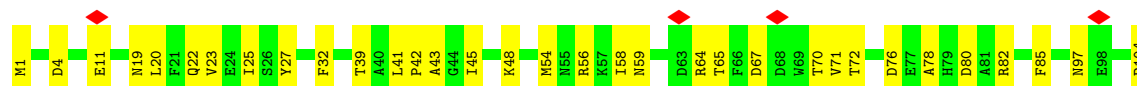
- Molecule 3: gp19, tail tube protein



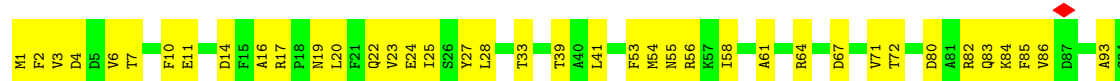
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

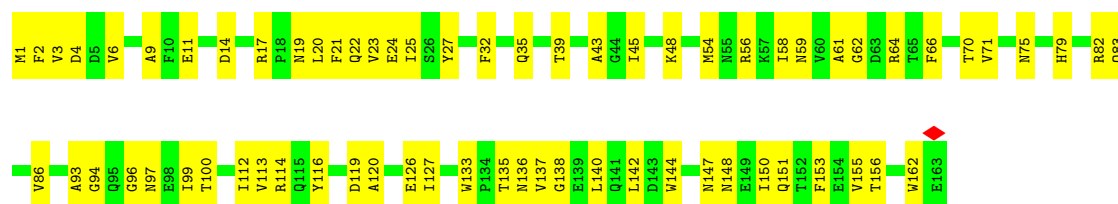


- Molecule 3: gp19, tail tube protein



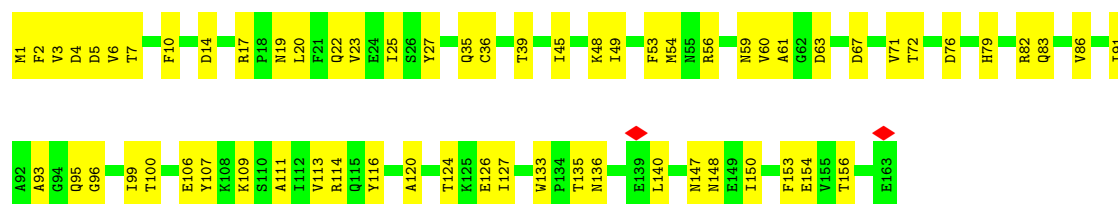
- Molecule 3: gp19, tail tube protein

Chain hf:  58% 42%



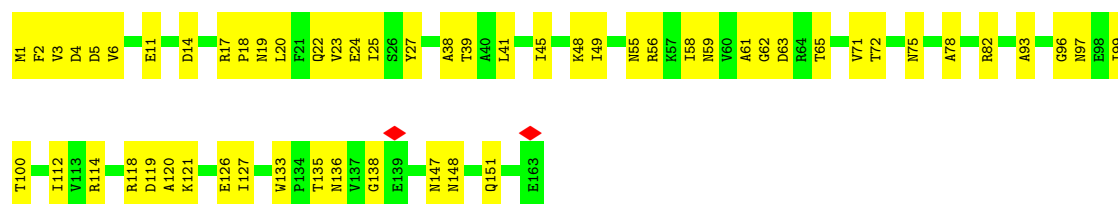
- Molecule 3: gp19, tail tube protein

Chain hg:  61% 39%



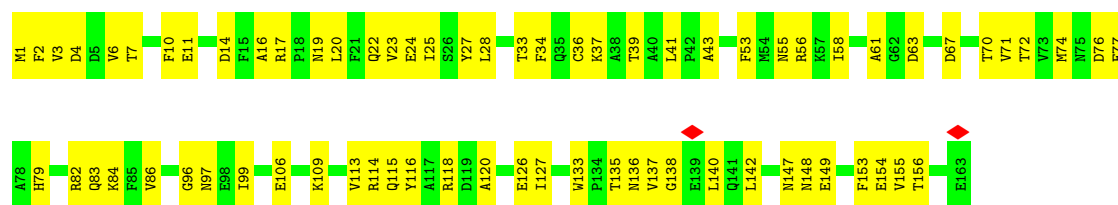
- Molecule 3: gp19, tail tube protein

Chain hh:  66% 34%



- Molecule 3: gp19, tail tube protein

Chain hi:  56% 44%



- Molecule 3: gp19, tail tube protein

Chain hj:  64% 36%

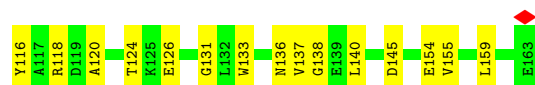




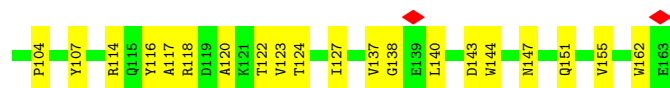
- Molecule 3: gp19, tail tube protein



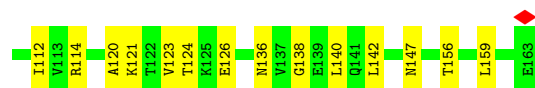
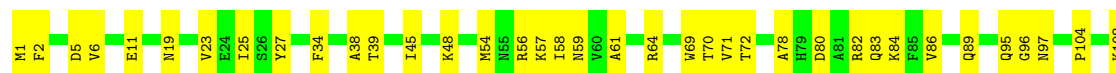
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein

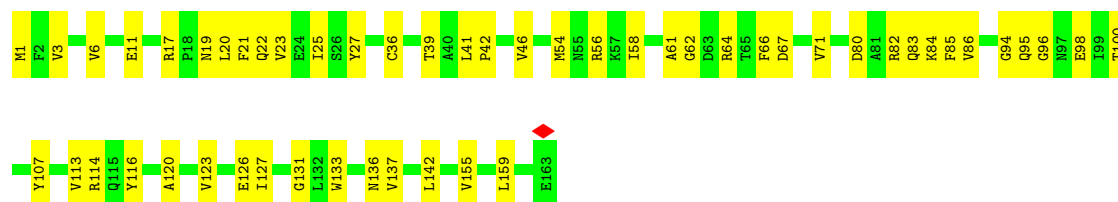


- Molecule 3: gp19, tail tube protein

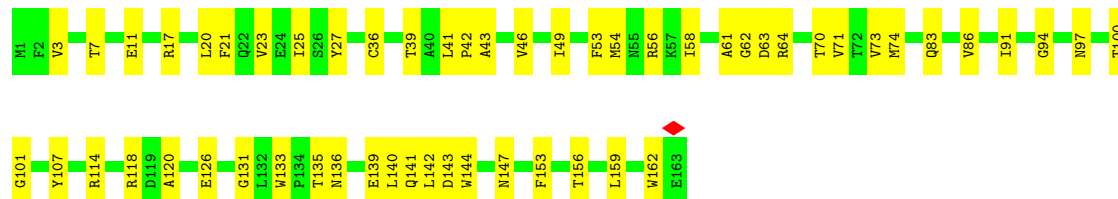


- Molecule 3: gp19, tail tube protein

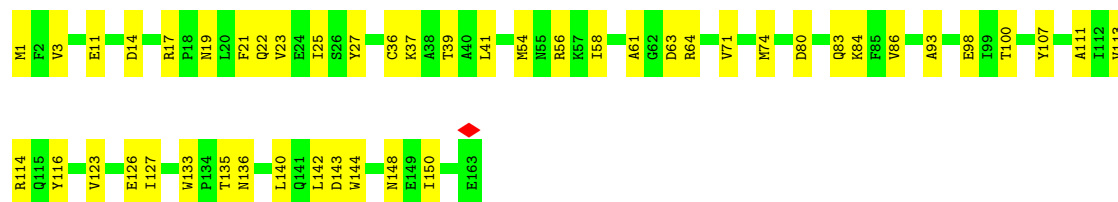




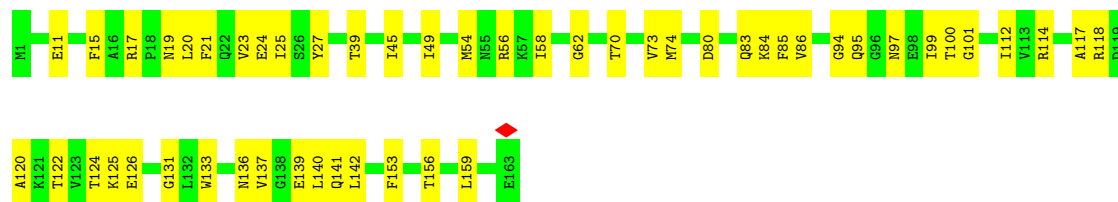
- Molecule 3: gp19, tail tube protein



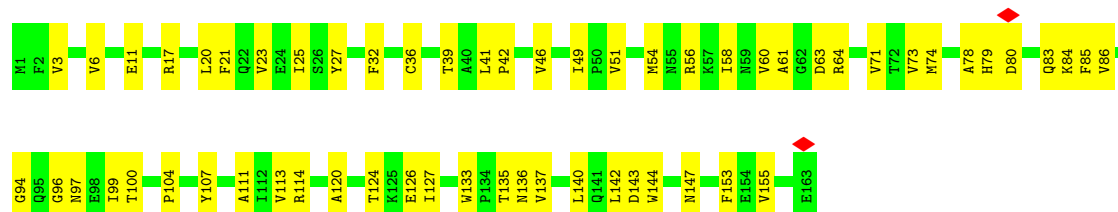
- Molecule 3: gp19, tail tube protein



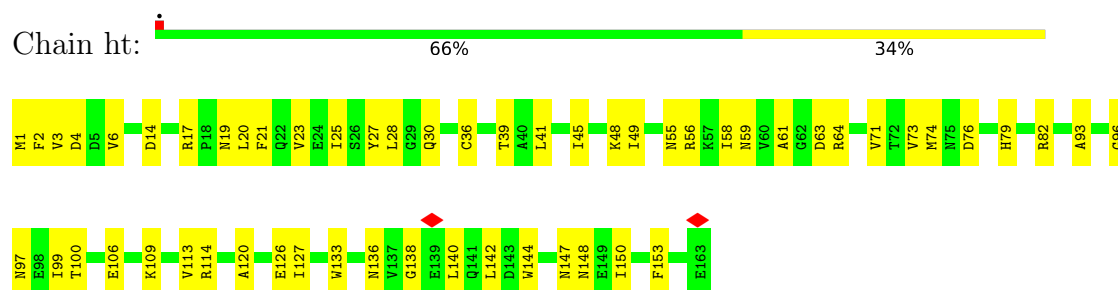
- Molecule 3: gp19, tail tube protein



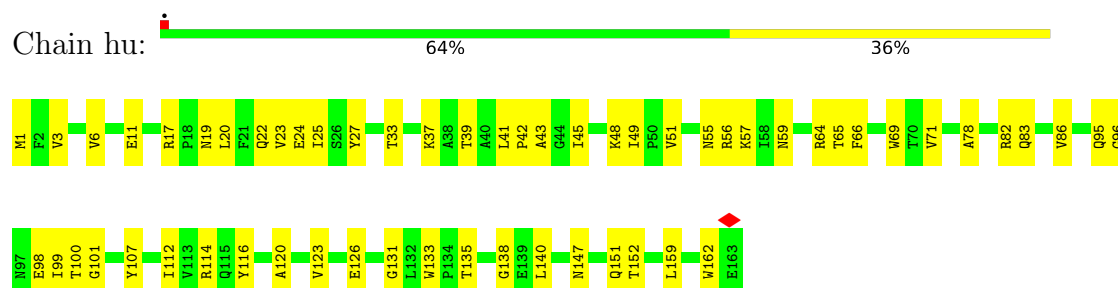
- Molecule 3: gp19, tail tube protein



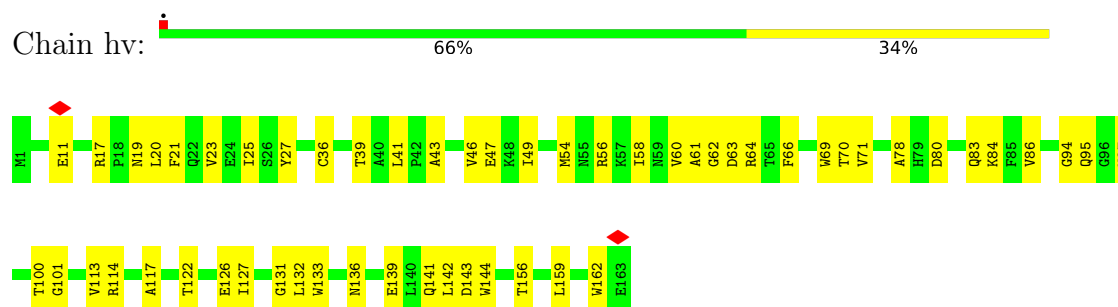
- Molecule 3: gp19, tail tube protein



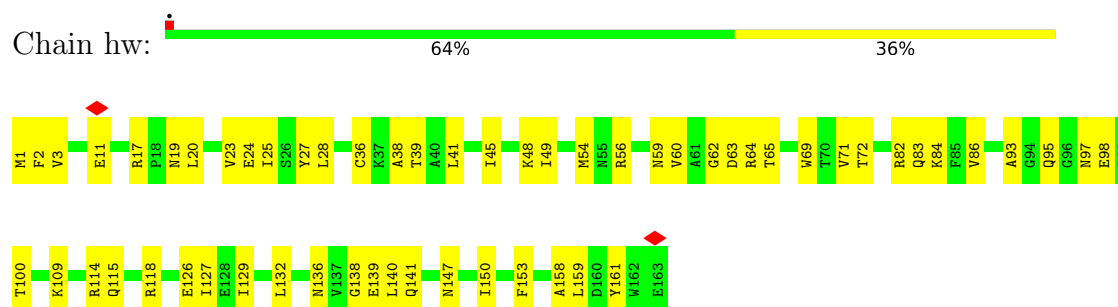
- Molecule 3: gp19, tail tube protein



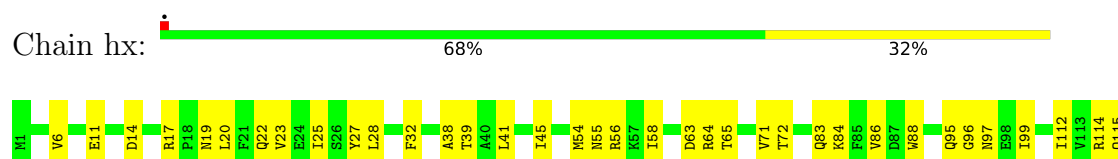
- Molecule 3: gp19, tail tube protein

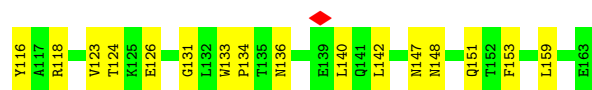


- Molecule 3: gp19, tail tube protein

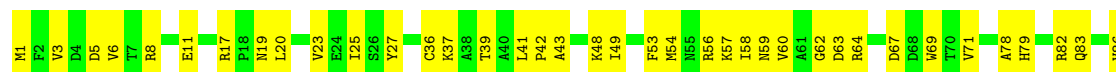


- Molecule 3: gp19, tail tube protein

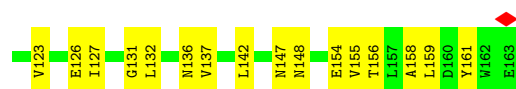




- Molecule 3: gp19, tail tube protein



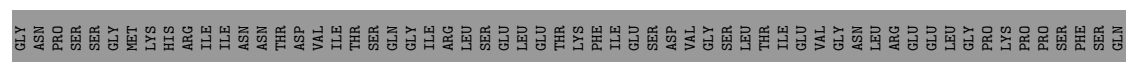
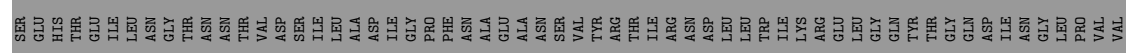
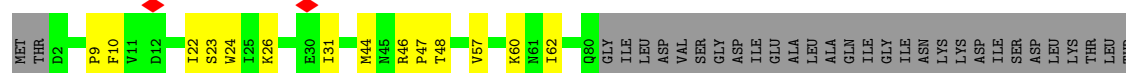
- Molecule 3: gp19, tail tube protein



- Molecule 3: gp19, tail tube protein



- Molecule 4: gpwac, fibrinin





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

- Molecule 4: gpwac, fibrin

[illegible]

- Molecule 4: gpwac, fibrin

[illegible]



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

- Molecule 4: gpwac, fibrinin

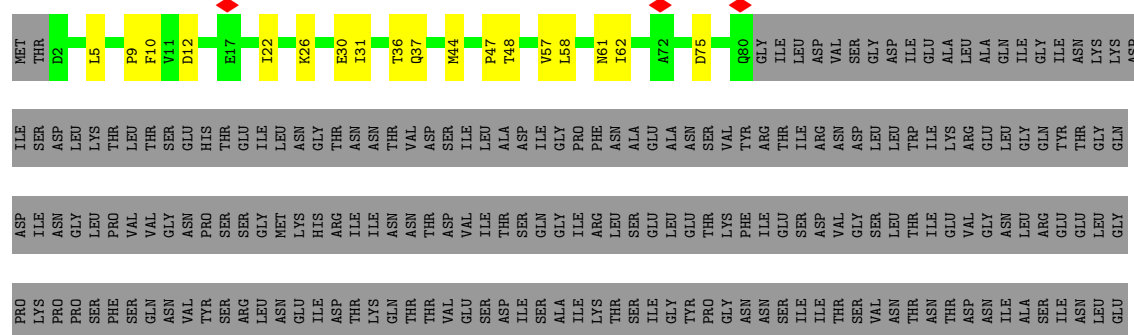
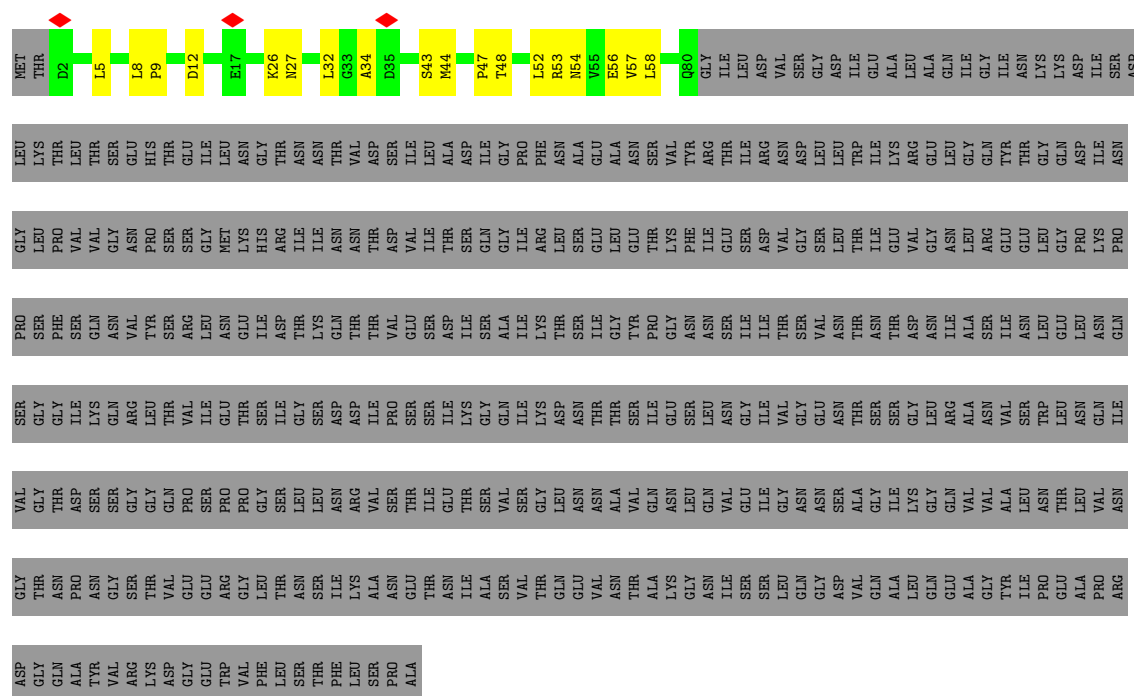
Chain J: 15% 84%

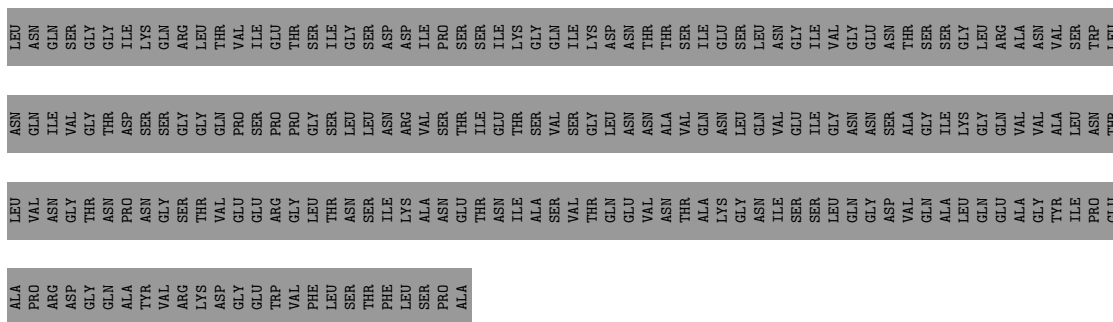
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THR	VAL	THR	LEU	THR	THR	GLY	GLY	GLY	GLY	THR	GLU	LYS	ASN	GLY
THR	LEU	LEU	LEU	THR	THR	ASN	ASN	THR	THR	THR	THR	ARG	THR	THR
THR	THR	THR	THR	THR	THR	ASN	ASN	THR	THR	THR	THR	ILE	ASN	THR
PHE	THR	THR	THR	THR	THR	ASN	ASN	THR	THR	THR	GLN	ASN	ASN	ASN
LEU	THR	THR	THR	THR	THR	ARG	ARG	THR	THR	THR	THR	ASN	VAL	THR
LEU	THR	THR	THR	THR	THR	ALA	ALA	ALA	THR	THR	THR	ASP	ASP	THR
LEU	THR	THR	THR	THR	THR	ASN	ASN	ASN	THR	THR	THR	ASP	ASP	THR
PRO	PRO	PRO	PRO	PRO	PRO	GLU	GLU	GLU	PRO	GLU	VAL	VAL	ILE	ILE
ALA	ALA	ALA	ALA	ALA	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR
						ILE	ILE	ILE	ILE	ILE	ILE	ILE	ALA	ALA
						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
						GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
						THR	THR	THR	THR	THR	THR	THR	THR	THR
						THR	THR	THR	THR	THR	THR	THR	THR	THR
						GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
						GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
						ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
						THR	THR	THR	THR	THR	THR	THR	THR	THR
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						GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
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						GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
						THR	THR	THR	THR	THR	THR	THR	THR	THR
						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
						ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
						THR	THR	THR	THR	THR	THR	THR	THR	THR
						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
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						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
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						THR	THR	THR	THR	THR	THR	THR	THR	THR
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						THR	THR	THR	THR	THR	THR	THR	THR	THR
						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
						GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
						LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
						GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
						THR	THR	THR</						

- Molecule 4: gpwac, fibrinin

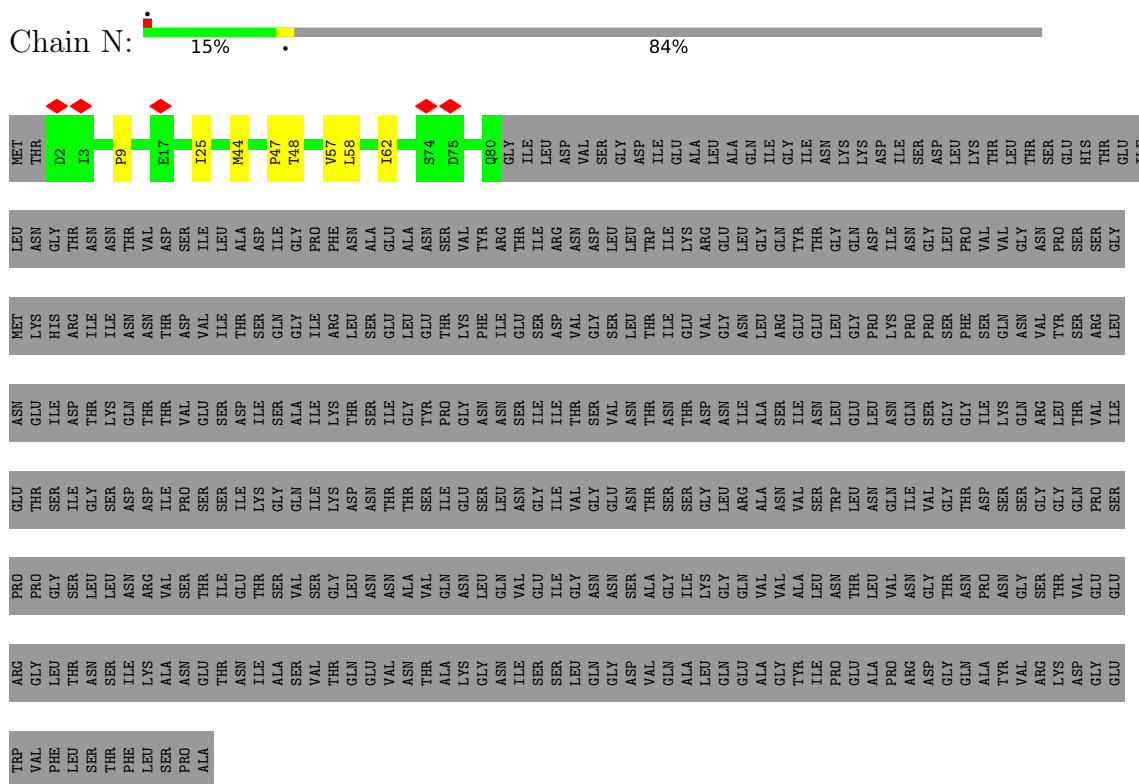
Chain K:  13% . 84%

[illegible]

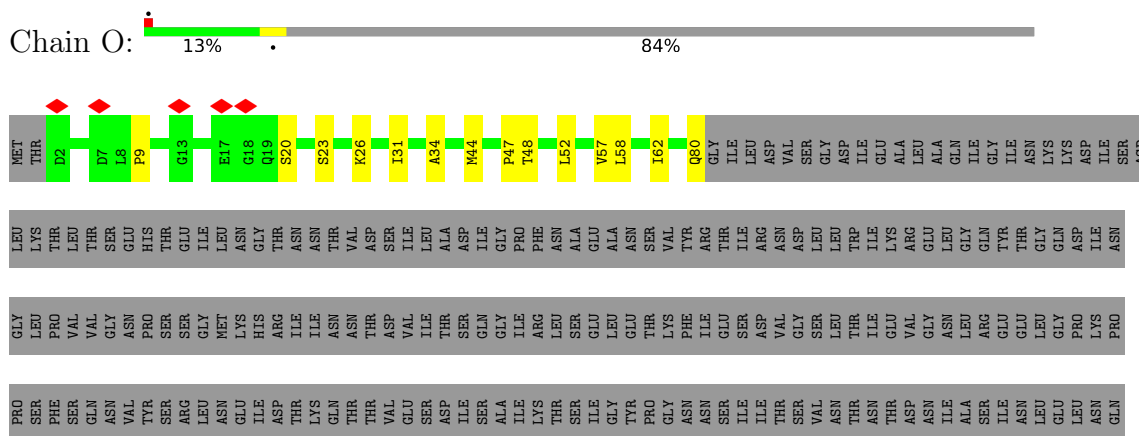




- Molecule 4: gpwac, fibrinin



- Molecule 4: gpwac, fibrinin



[illegible]

- Molecule 4: gpwac, fibrinin

[illegible]

- Molecule 4: gpwac, fibrinin

[illegible]

[illegible]

- Molecule 4: gpwac, fibrin

[illegible]

- Molecule 4: gpwac, fibrinin

[illegible]

[illegible]

- Molecule 4: gpwac, fibrinin

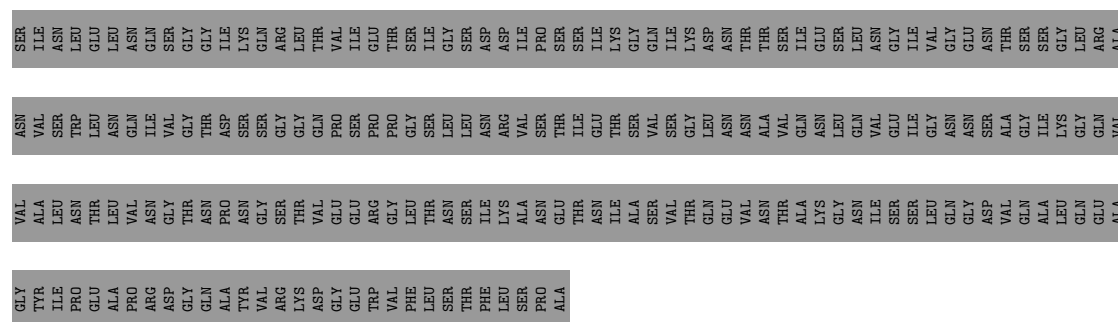
Chain T:  14% . 84%

[illegible]

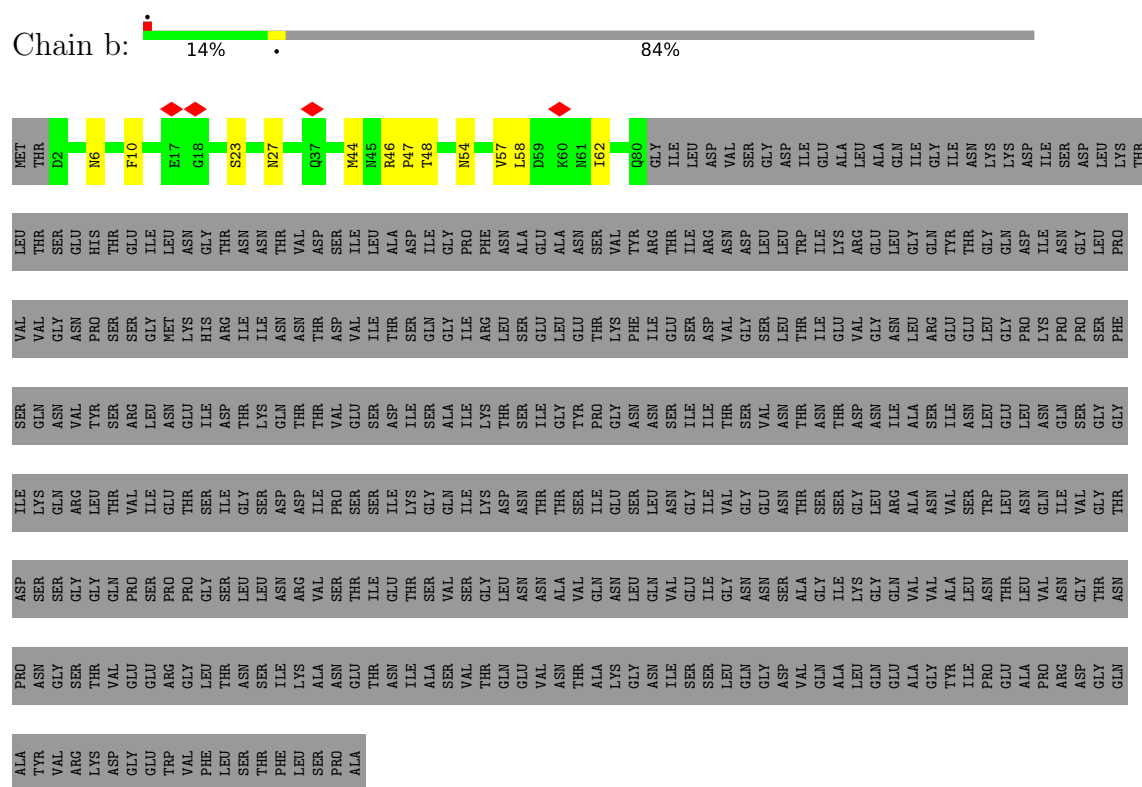
- Molecule 4: gpwac, fibrinin

Chain U:  13% 84%

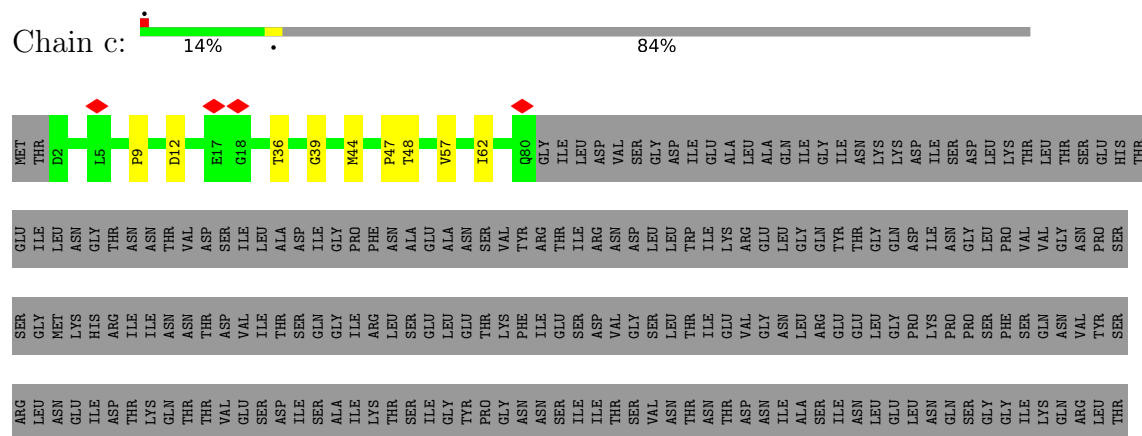
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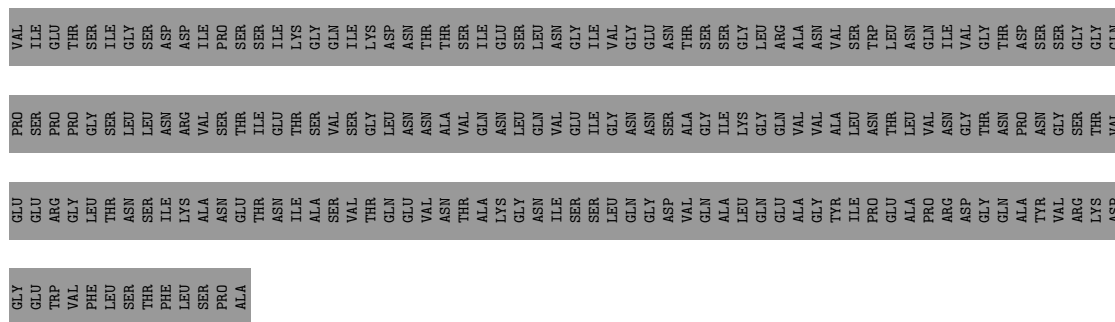


- Molecule 4: gpwac, fibrin

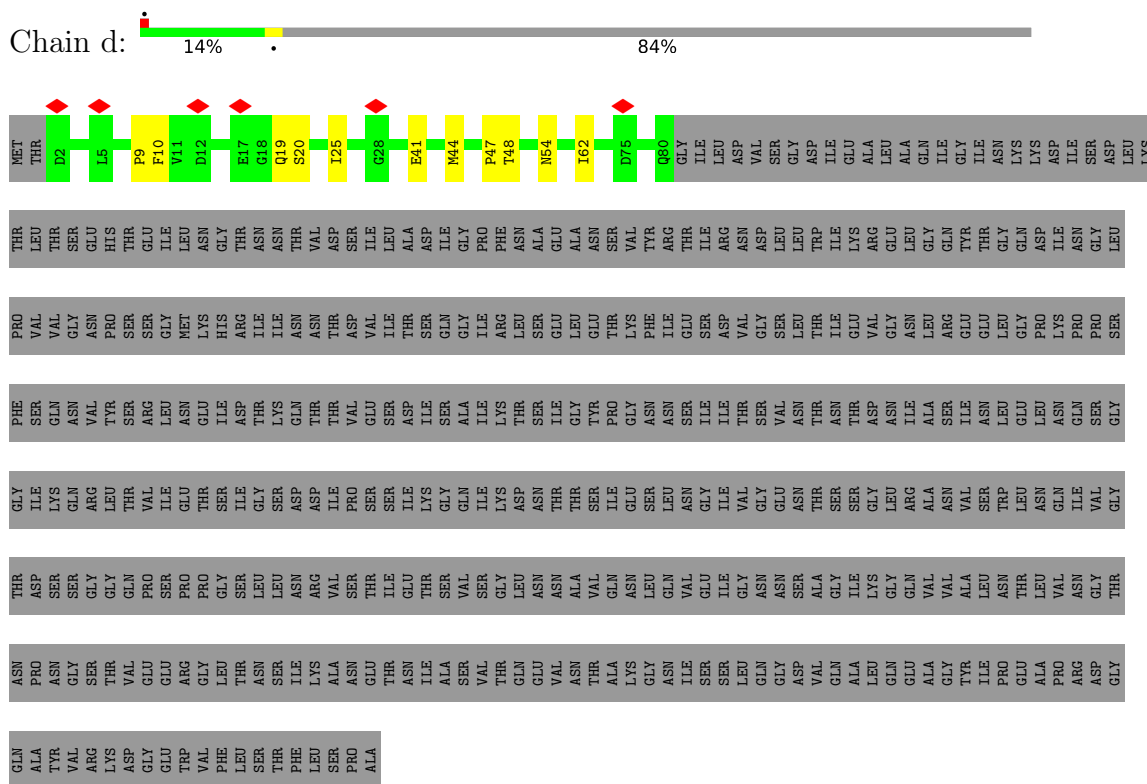


- Molecule 4: gpwac, fibrin

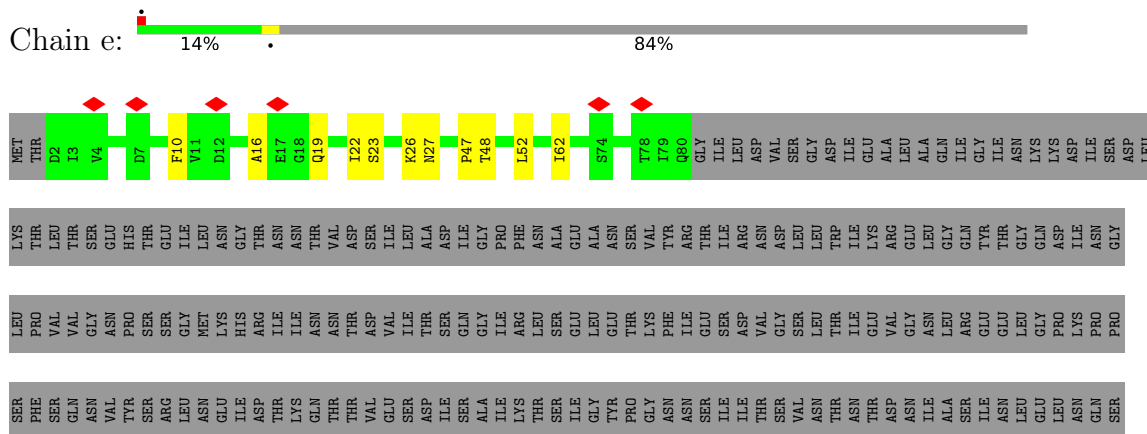


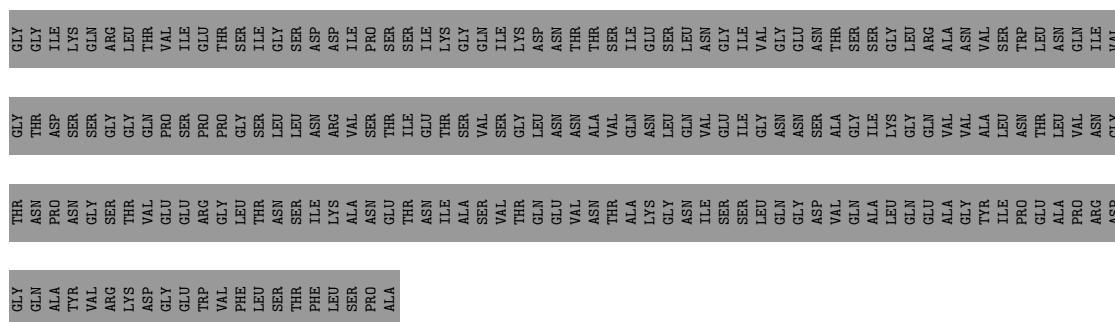


- Molecule 4: gpwac, fibrin

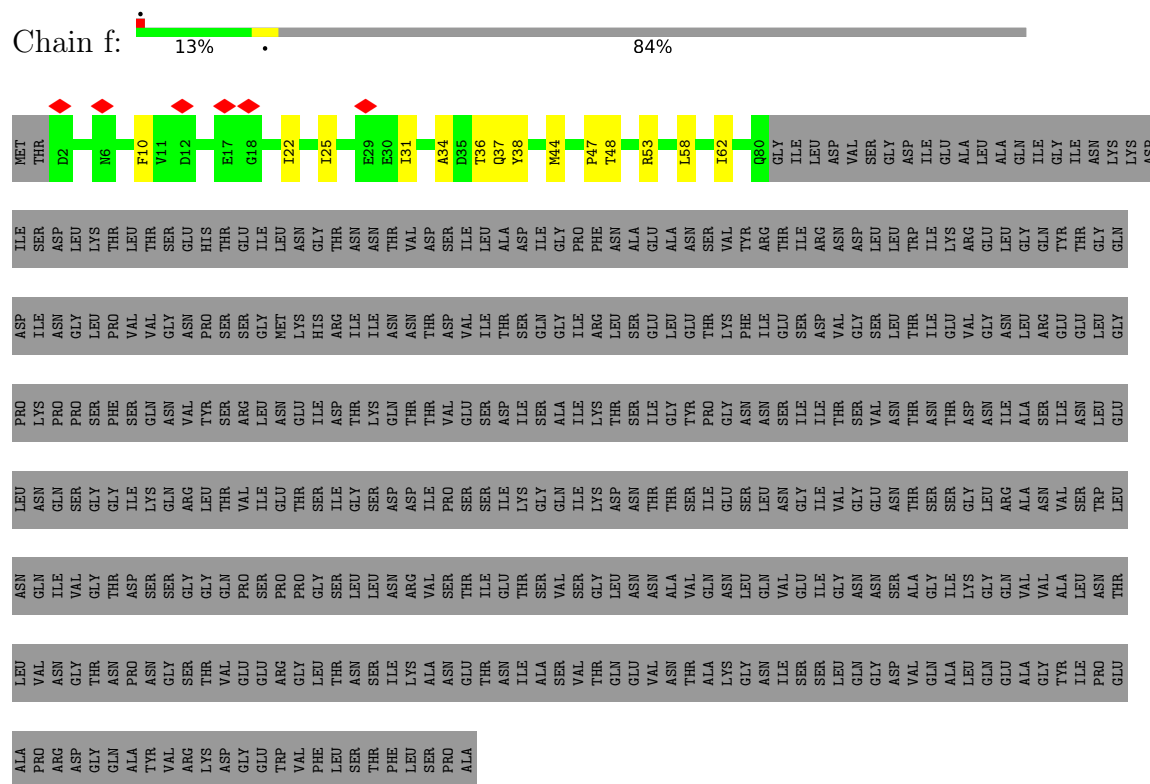


- Molecule 4: gpwac, fibrin

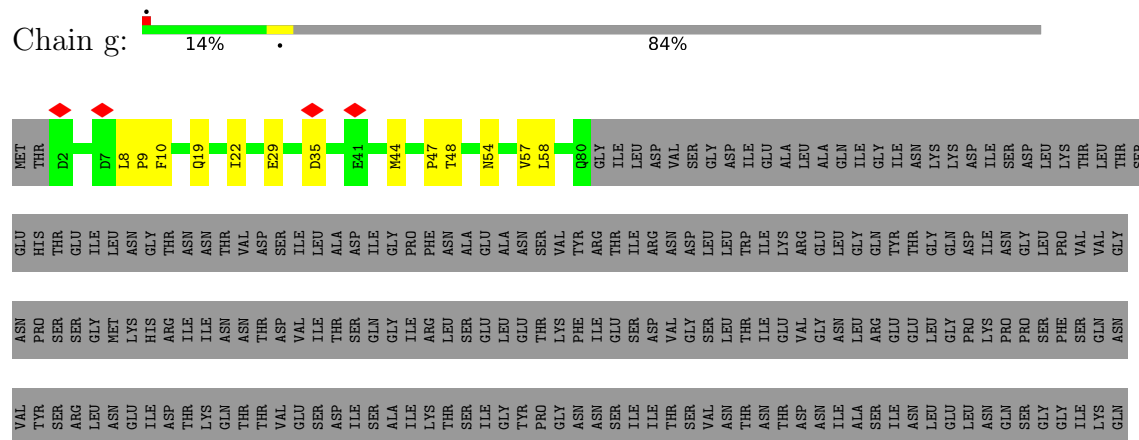


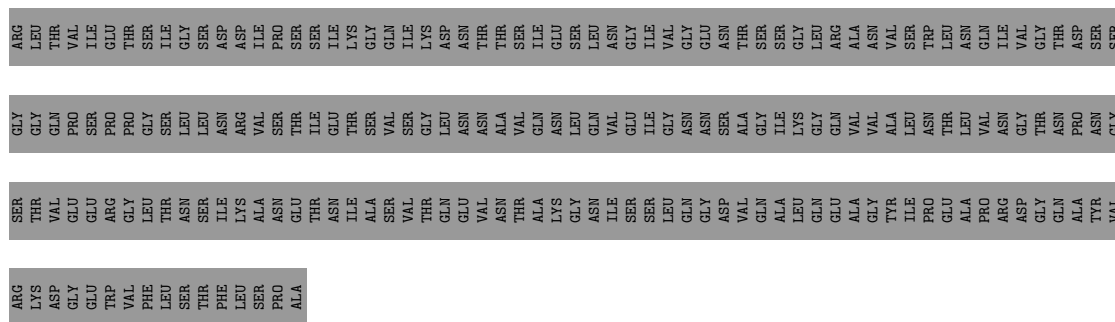


- Molecule 4: gpwac, fibrinin

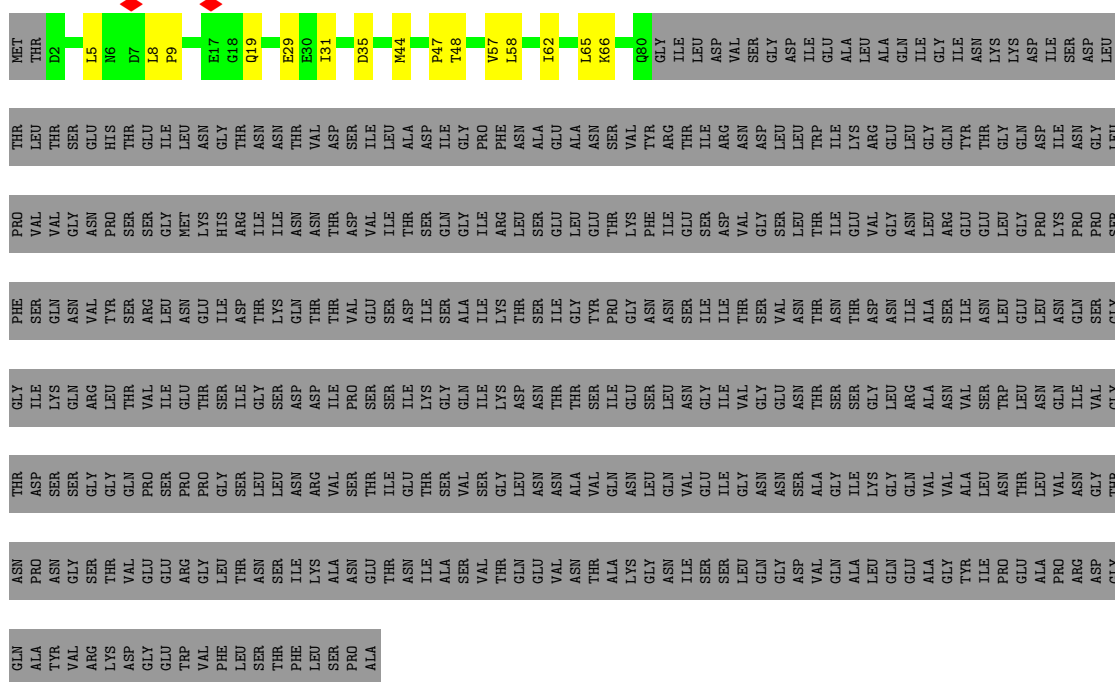


- Molecule 4: gpwac, fibrinin

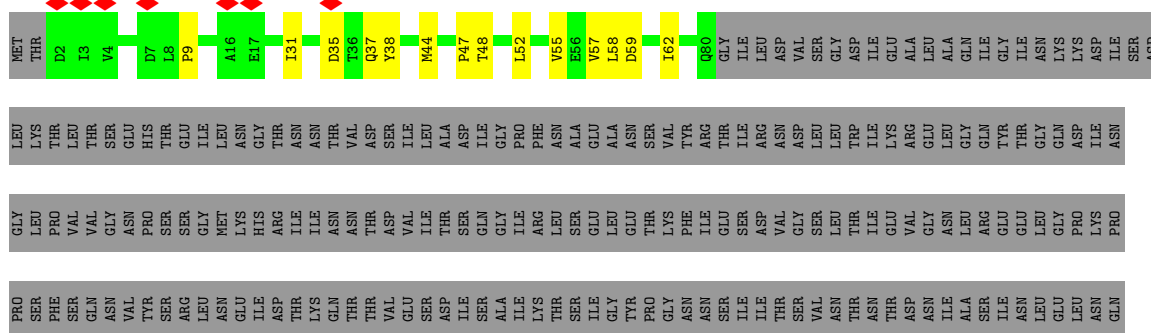




- Molecule 4: gpwac, fibrin



- Molecule 4: gpwac, fibrin

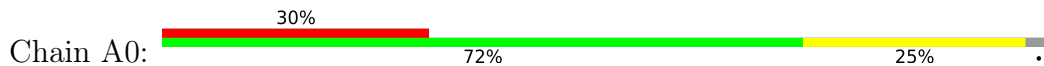


[illegible]

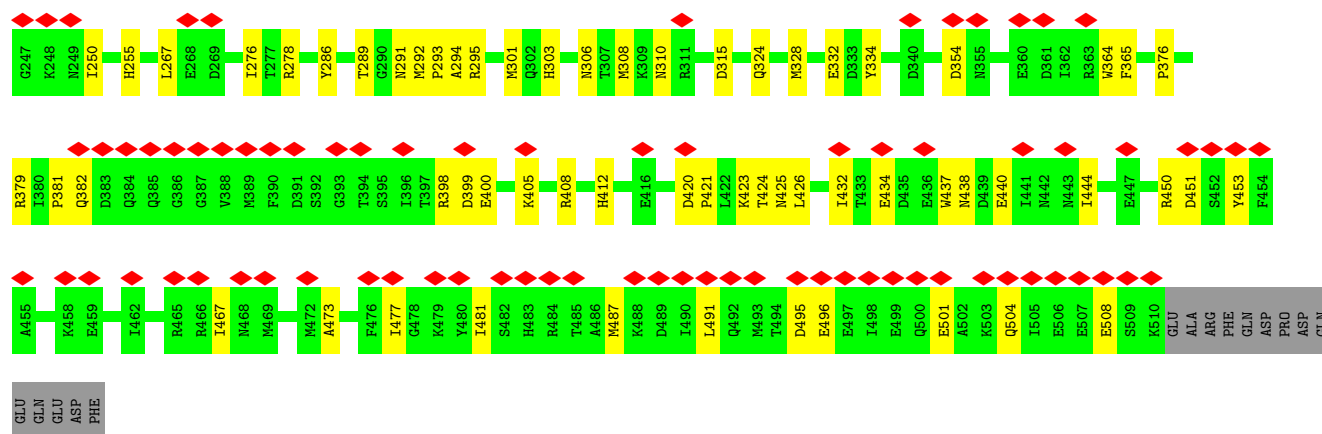
- Molecule 4: gpwac, fibrinin

[illegible]

- Molecule 5: gp20, portal protein

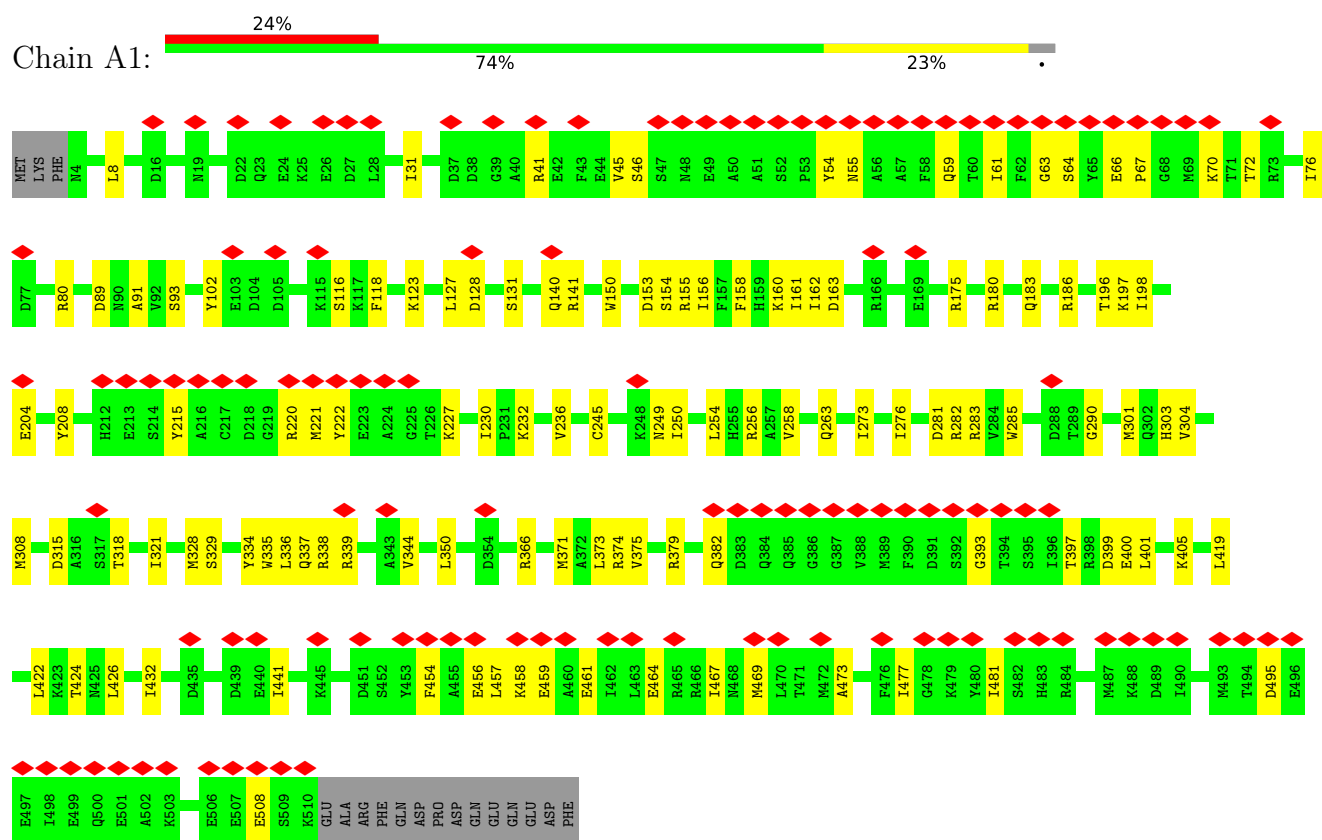


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T72	R73	E74	L75	T76	D77	T78	R79	R80	N81	N84	Y86	S87	D98	E103	D104	D105	T106	E107	L111	D114	K115	S116	K117	F118	S119	P120	K121	I122	M125	M126	L127	D128	E129	L134	L137	R141	F147	R148	D153	S154	R155	I156	K160	I161	I162	K166									
WET	LVS	PHE	M4	V5	L6	S7	L8	F9	R18	M19	D22	Q23	E24	K25	E26	D27	L28	V29	S30	I31	K35	L36	D37	D38	G39	A40	R41	E42	F43	E44	S47	M48	E49	A50	A51	S52	P53	Y54	N55	A56	A57	F58	Q59	T60	I61	F62	G63	S64	Y65	E66	P67	G68	M69	K70	T71



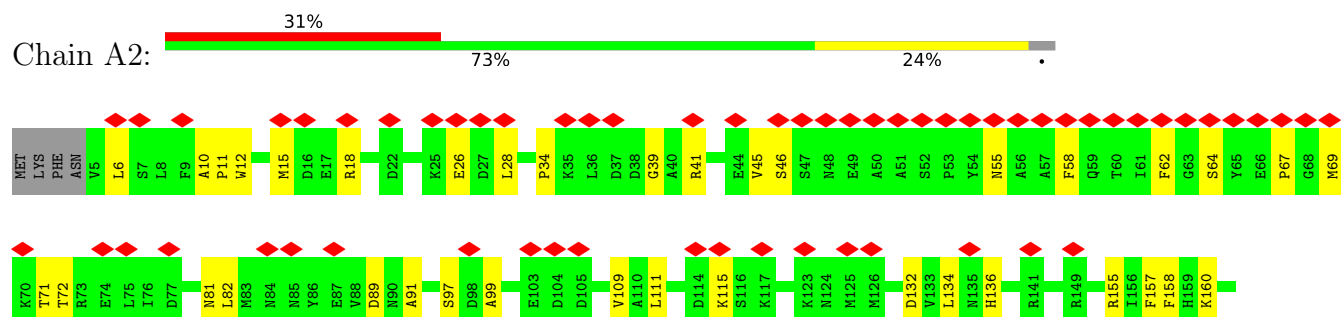
• Molecule 5: gp20, portal protein

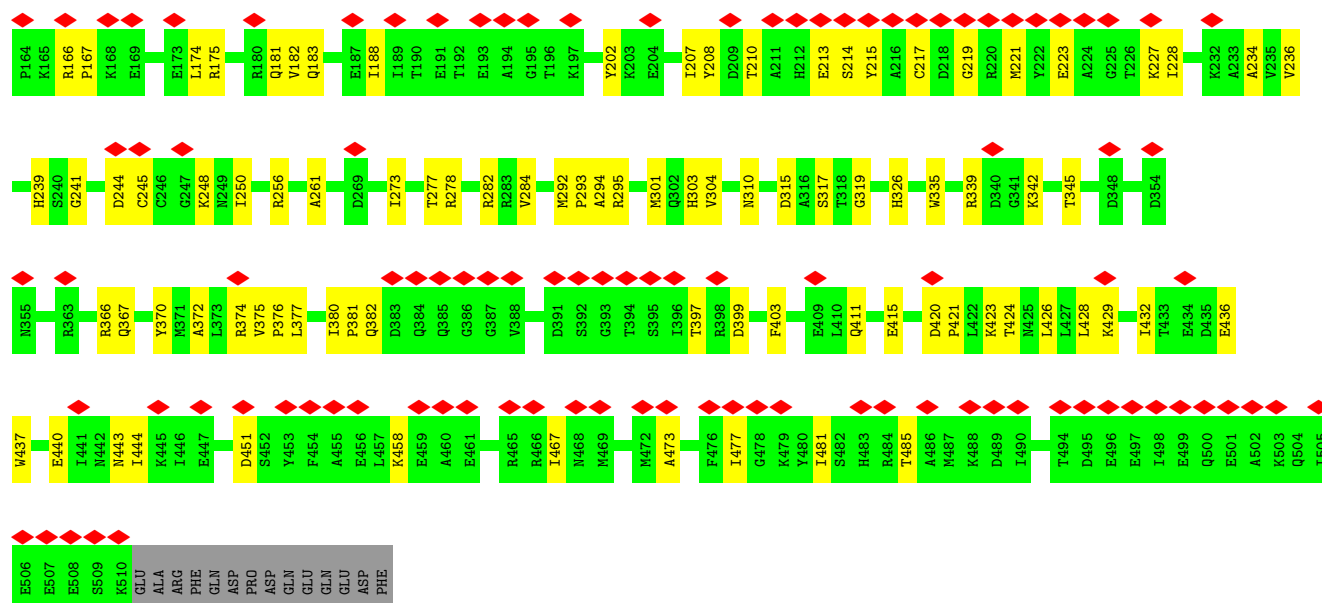
Chain A1:



• Molecule 5: gp20, portal protein

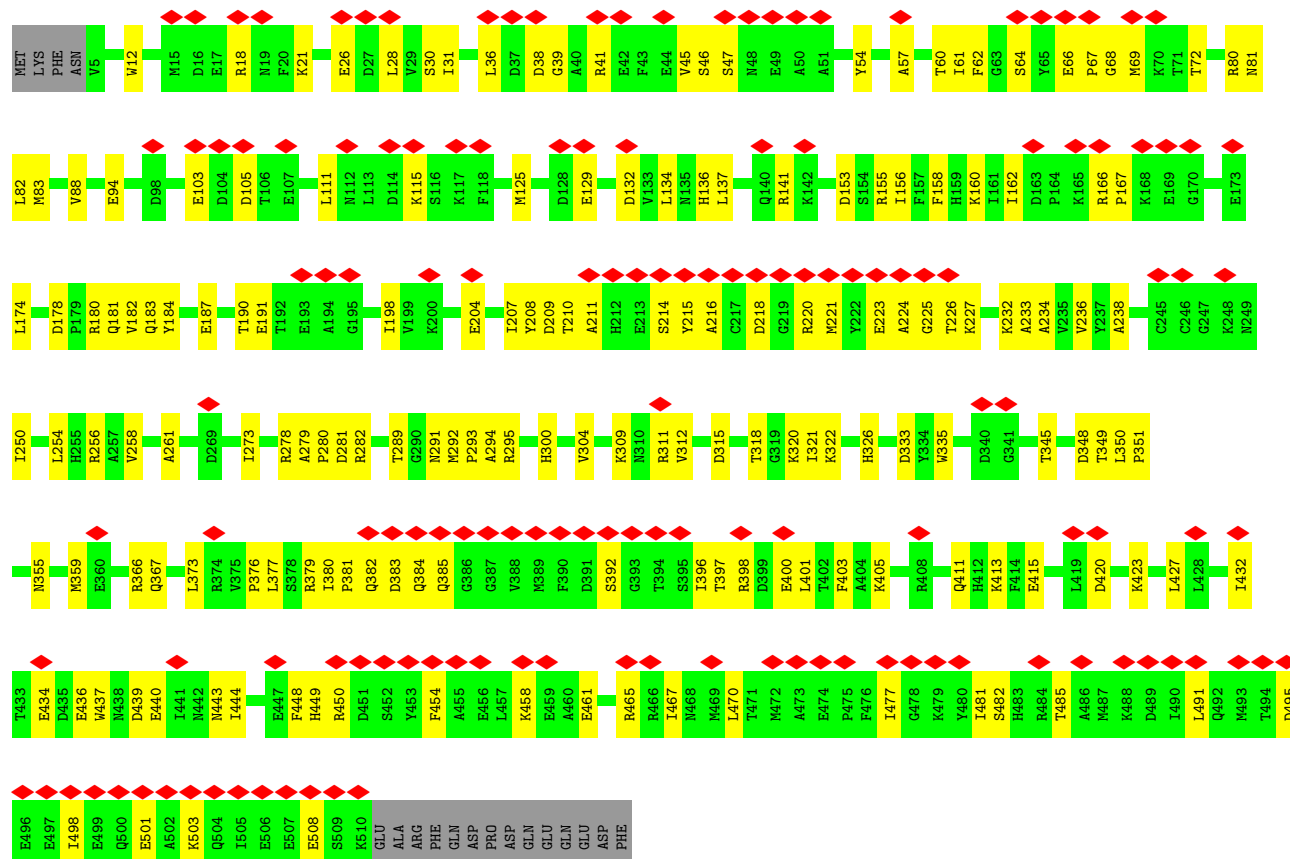
Chain A2:



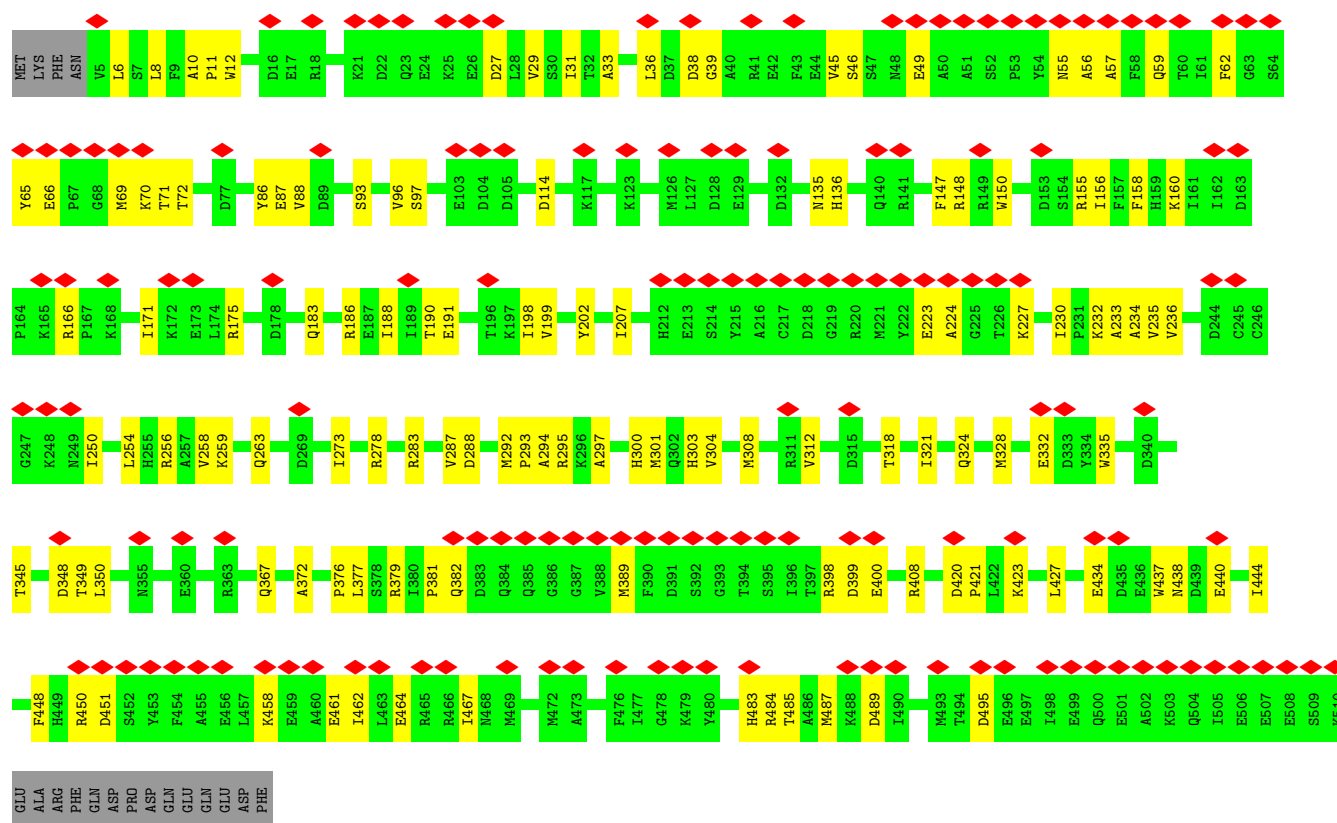
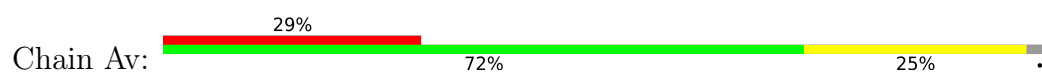


- Molecule 5: gp20, portal protein

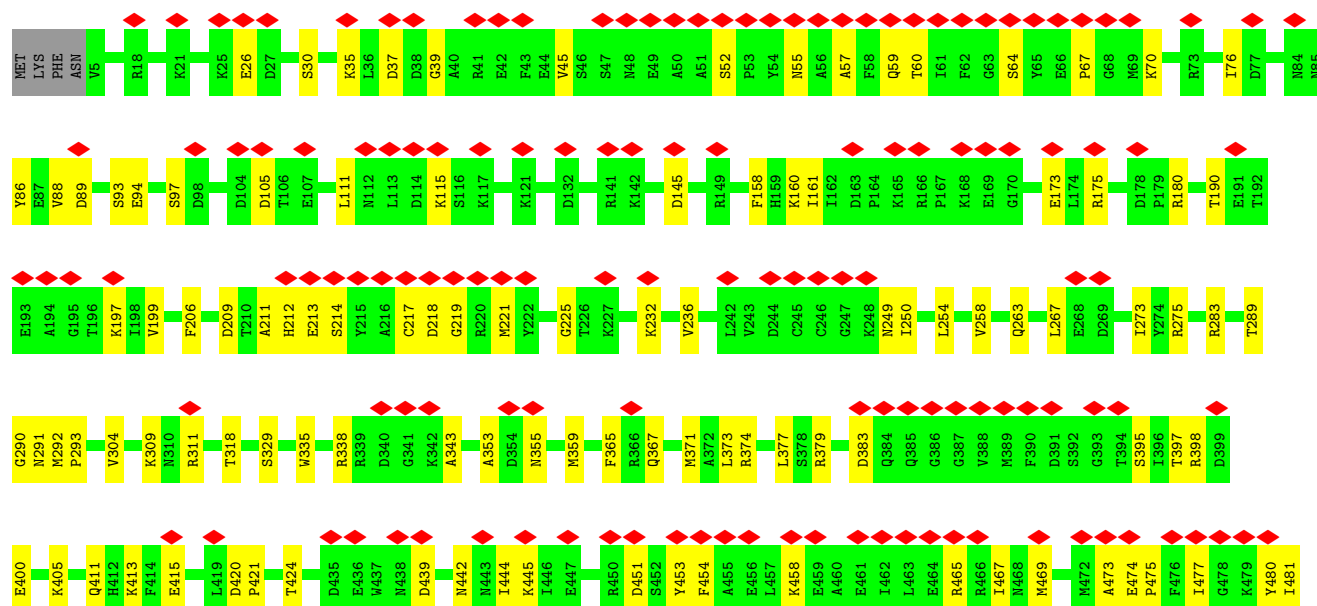
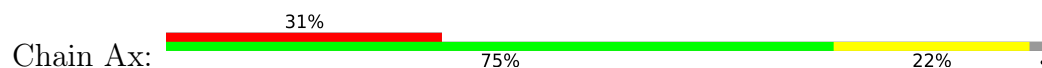
Chain A3: 28% 64% 33%

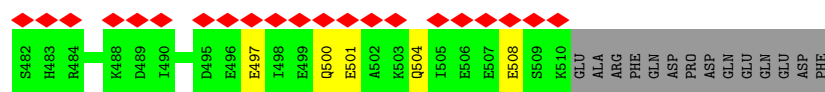


- Molecule 5: gp20, portal protein

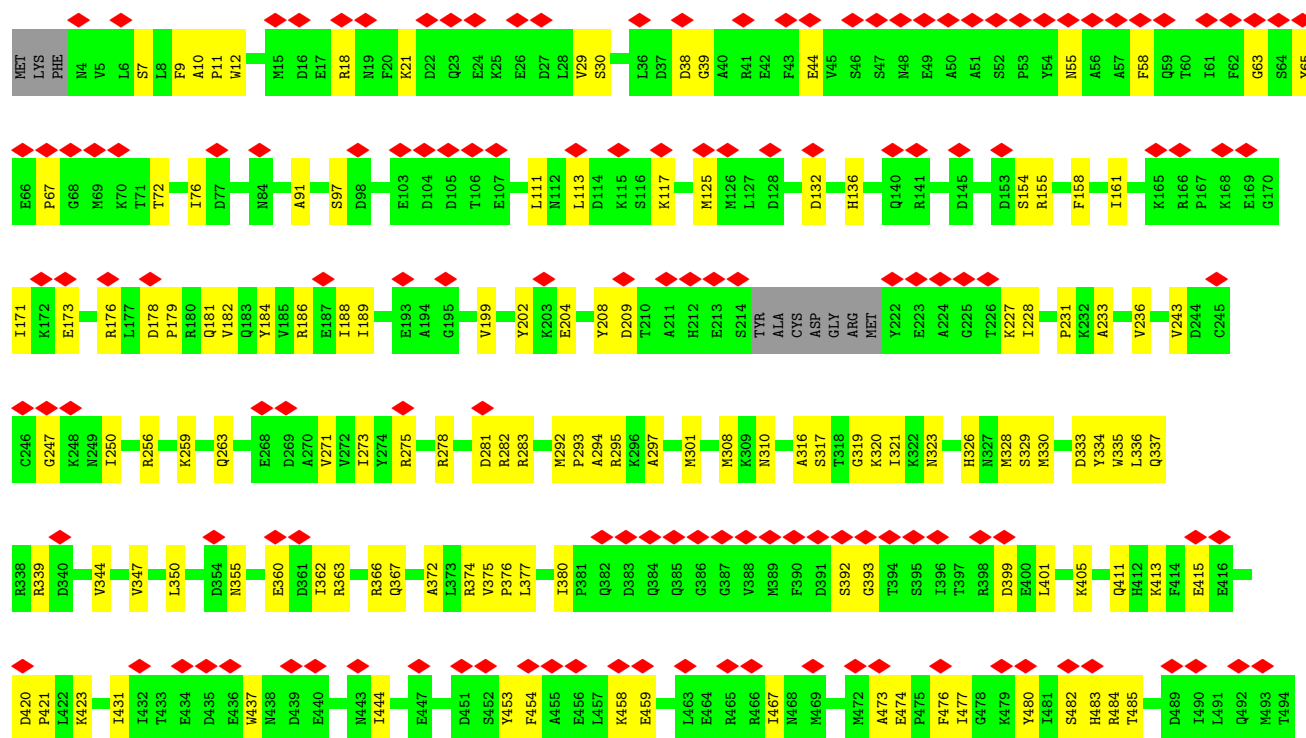


• Molecule 5: gp20, portal protein

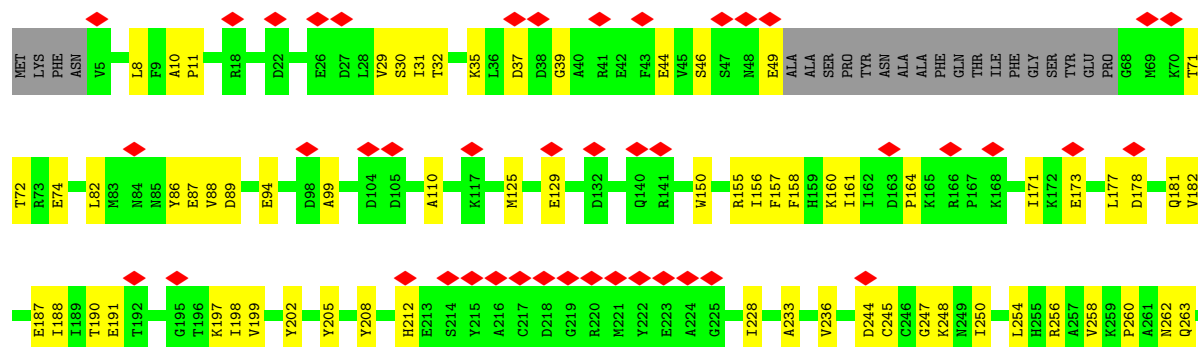


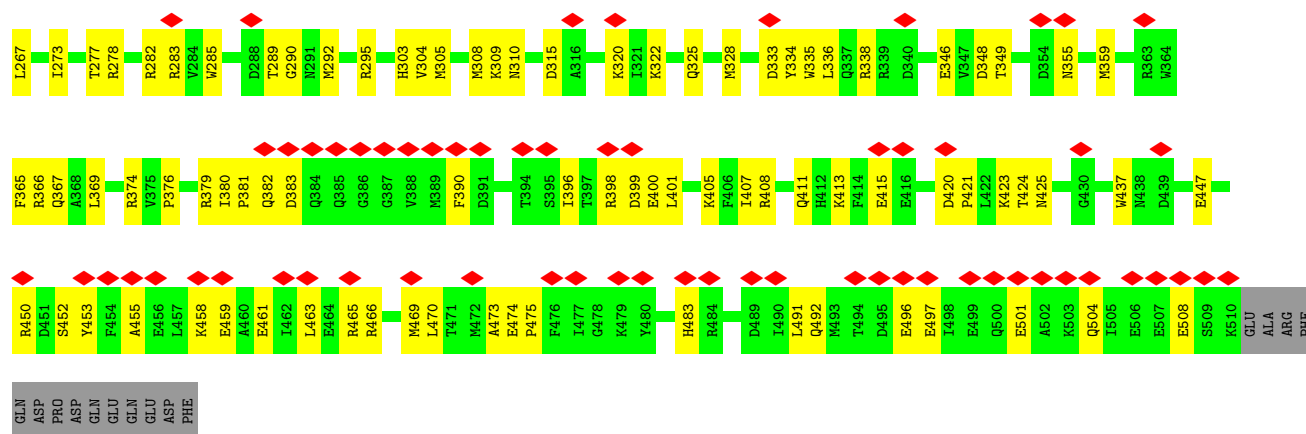


• Molecule 5: gp20, portal protein

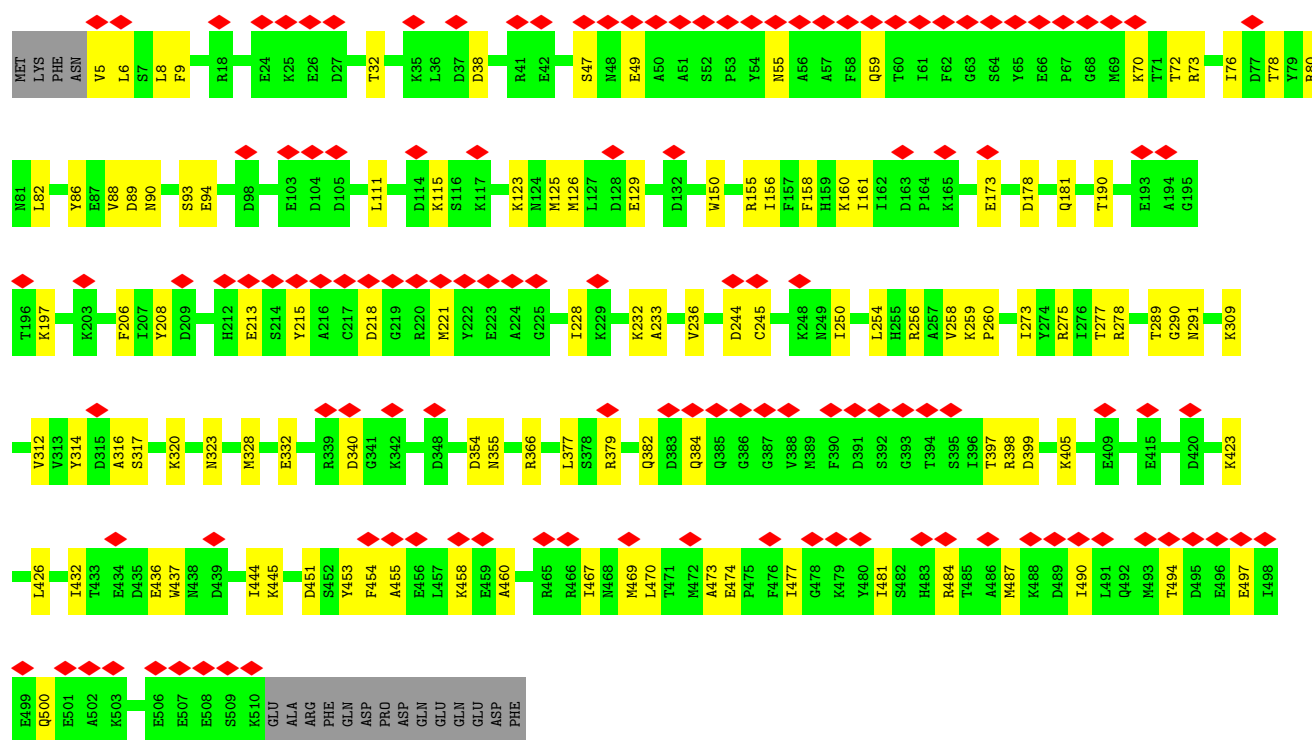
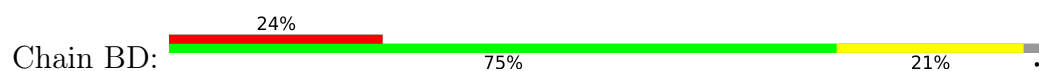


• Molecule 5: gp20, portal protein

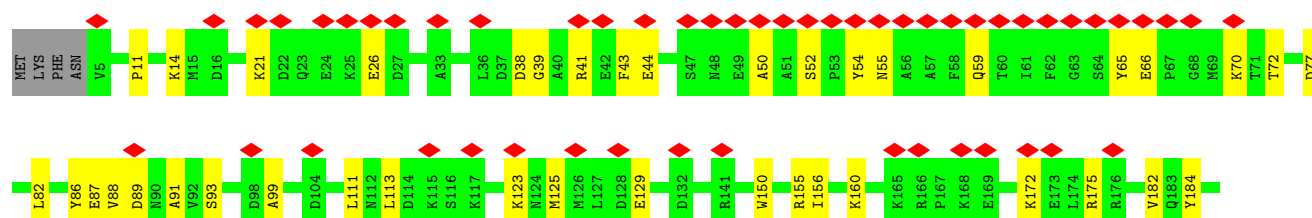
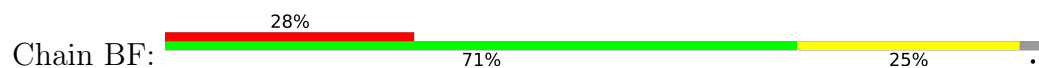


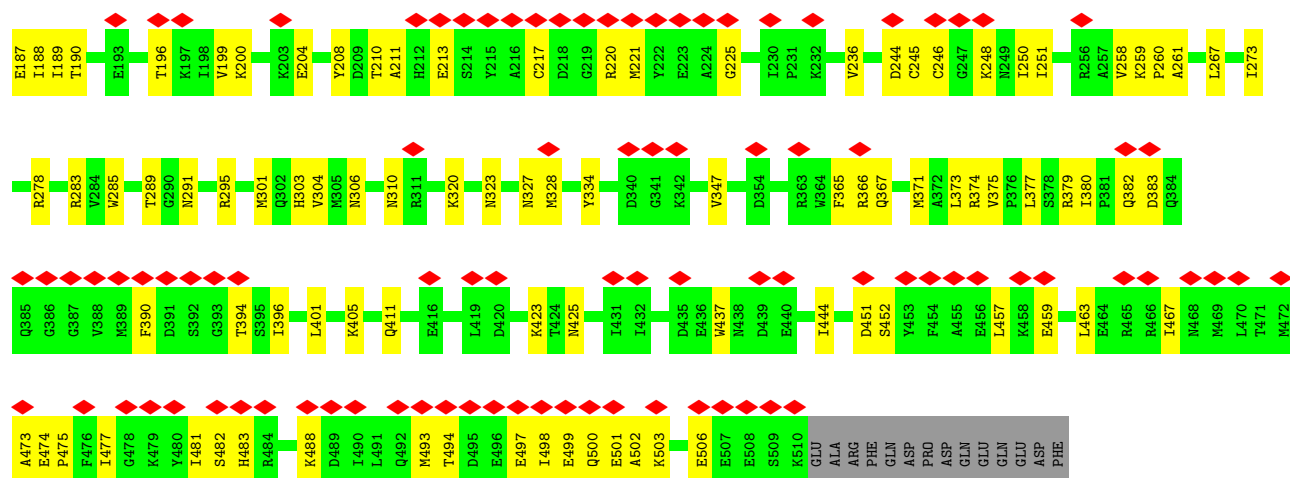


• Molecule 5: gp20, portal protein

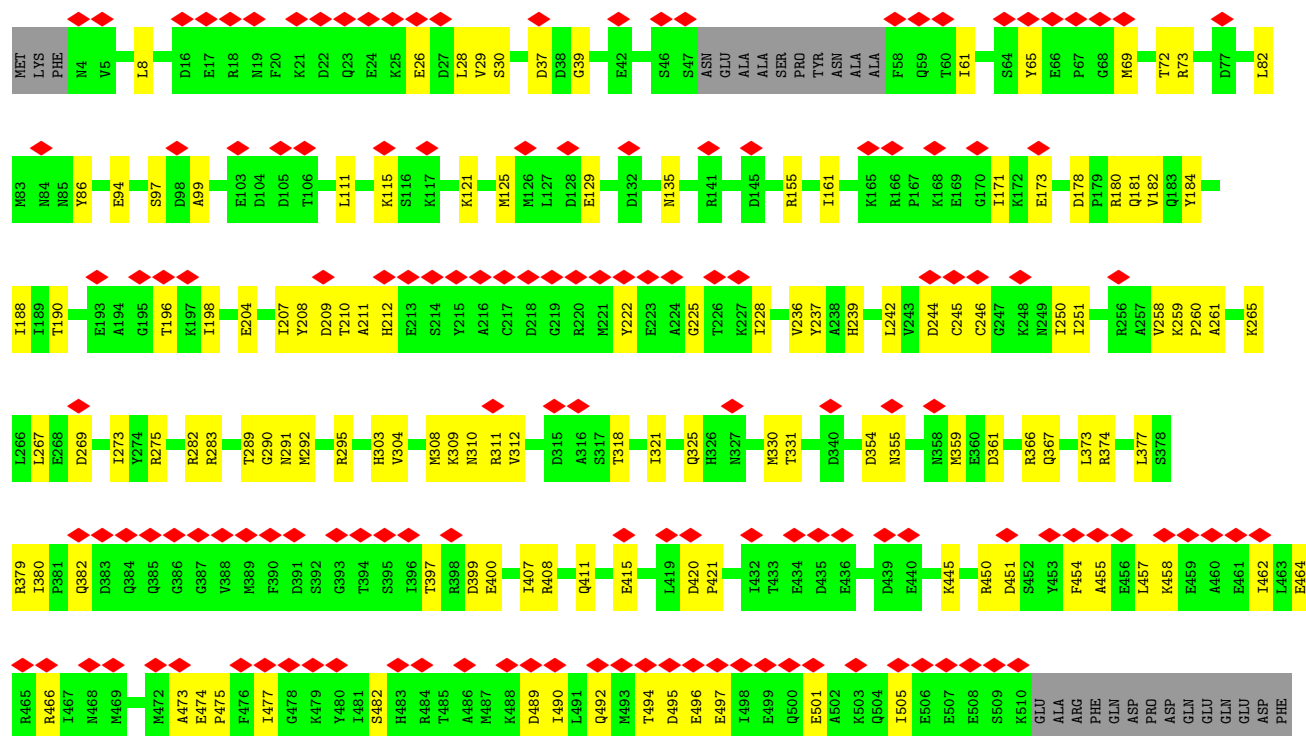
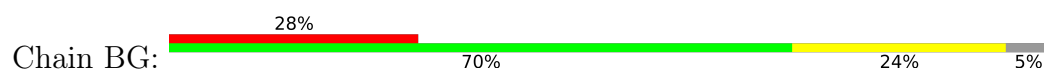


• Molecule 5: gp20, portal protein

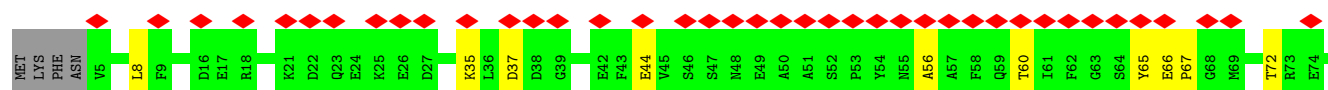
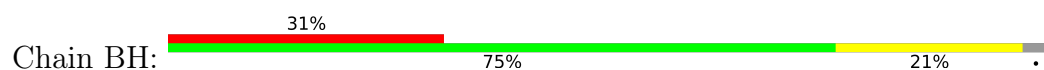


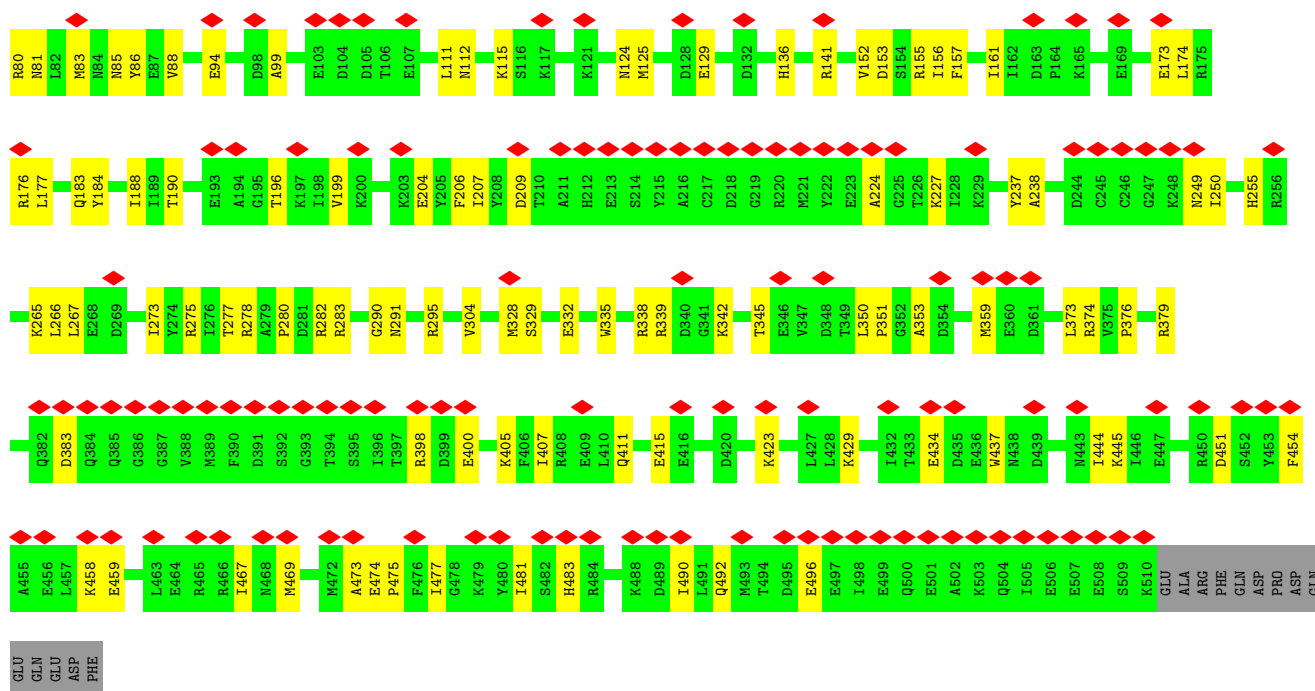


• Molecule 5: gp20, portal protein

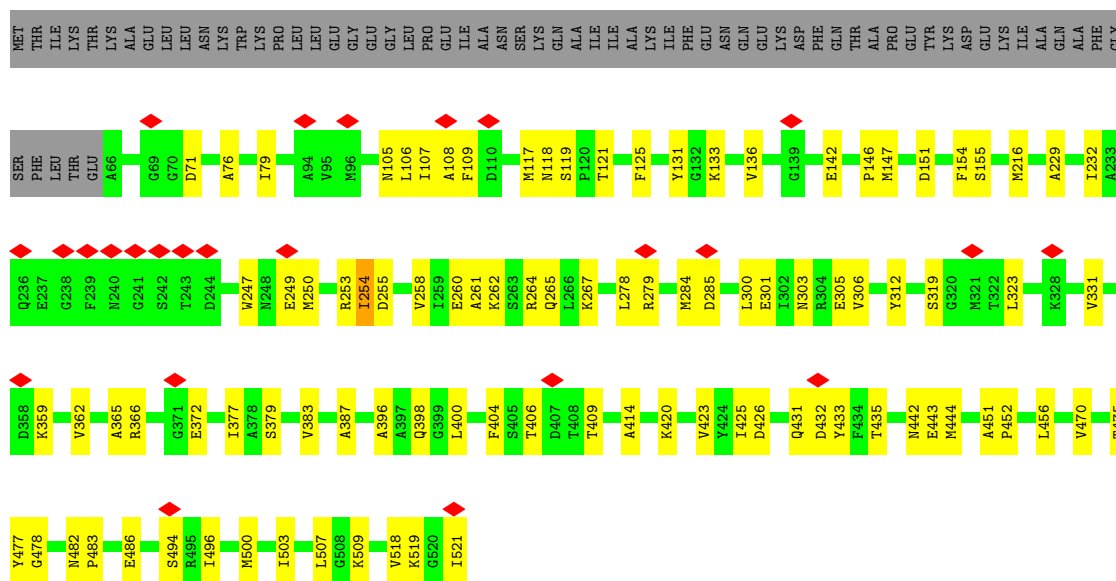


• Molecule 5: gp20, portal protein

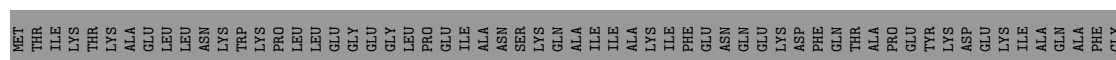


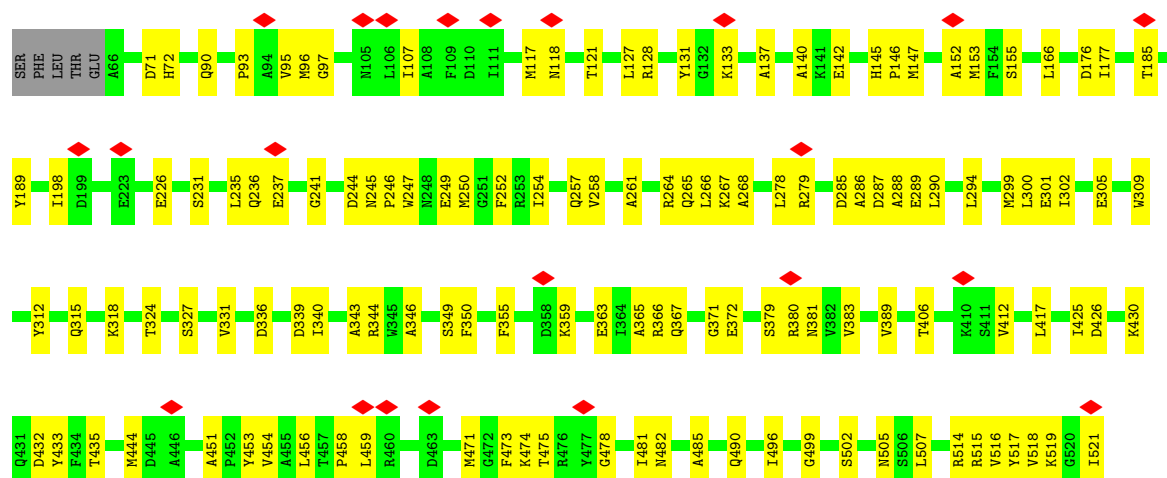


- Molecule 6: gp23, major capsid protein



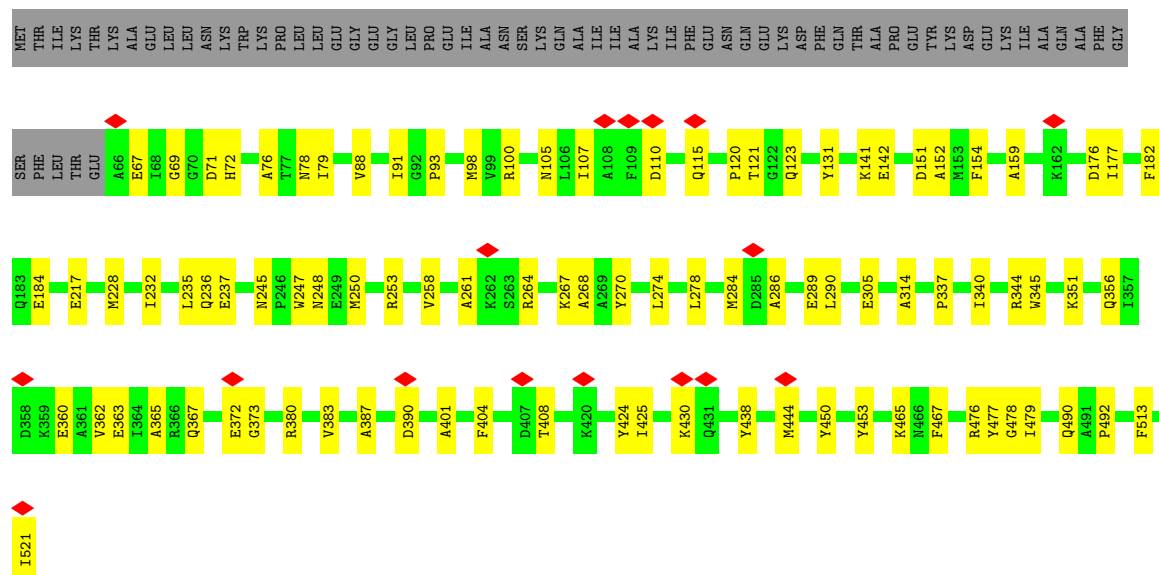
- Molecule 6: gp23, major capsid protein





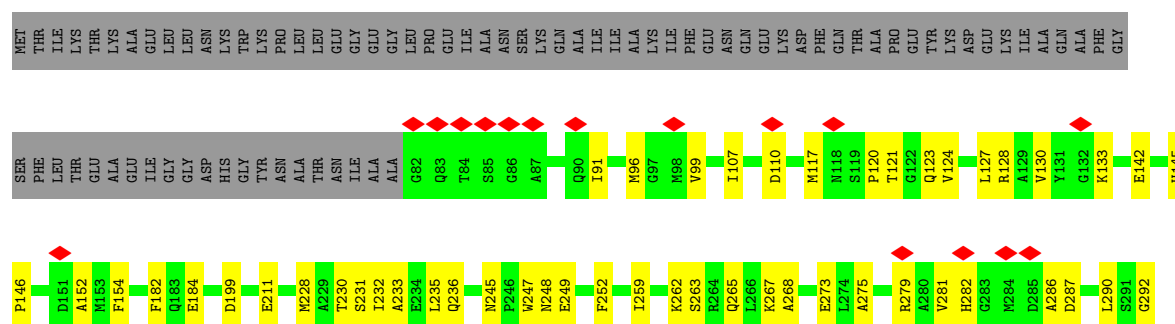
- Molecule 6: gp23, major capsid protein

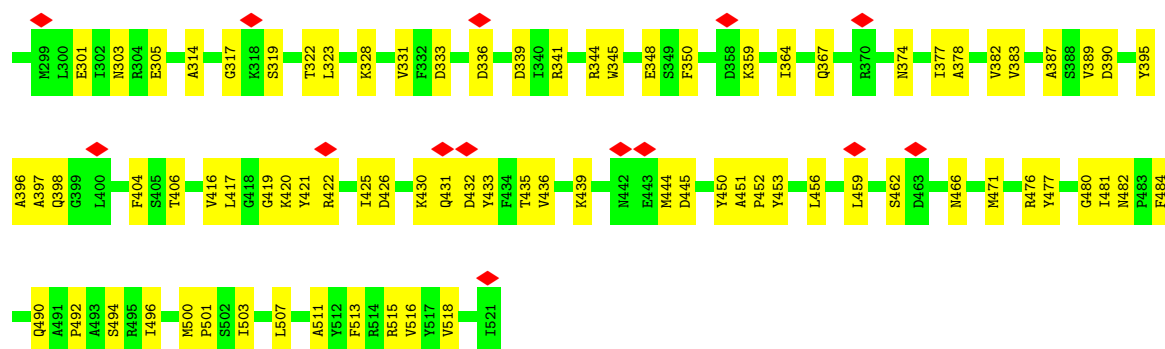
Chain A7: 70% 18% 12%



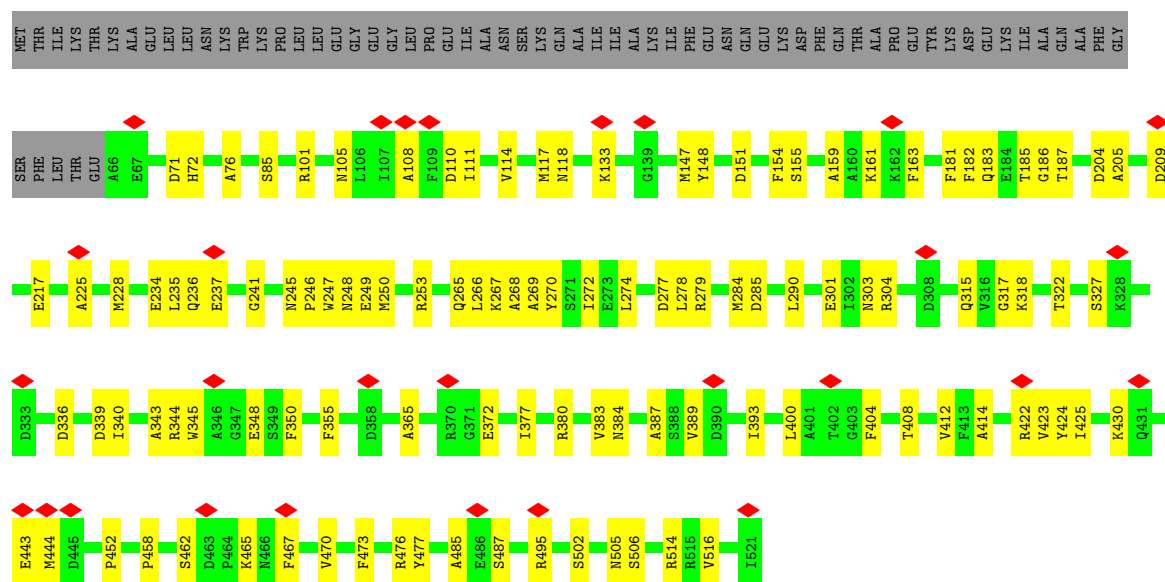
- Molecule 6: gp23, major capsid protein

Chain A8: 6% 60% 25% 16%

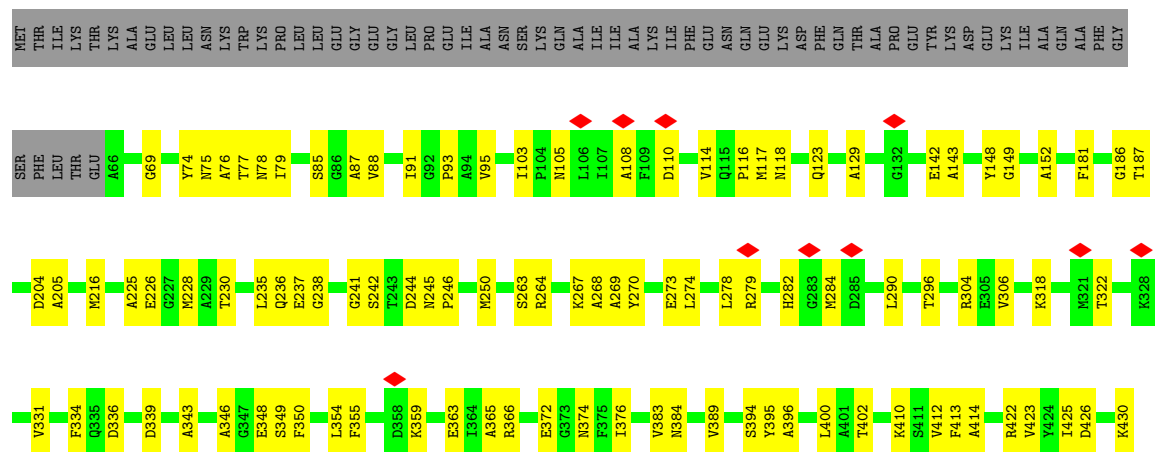




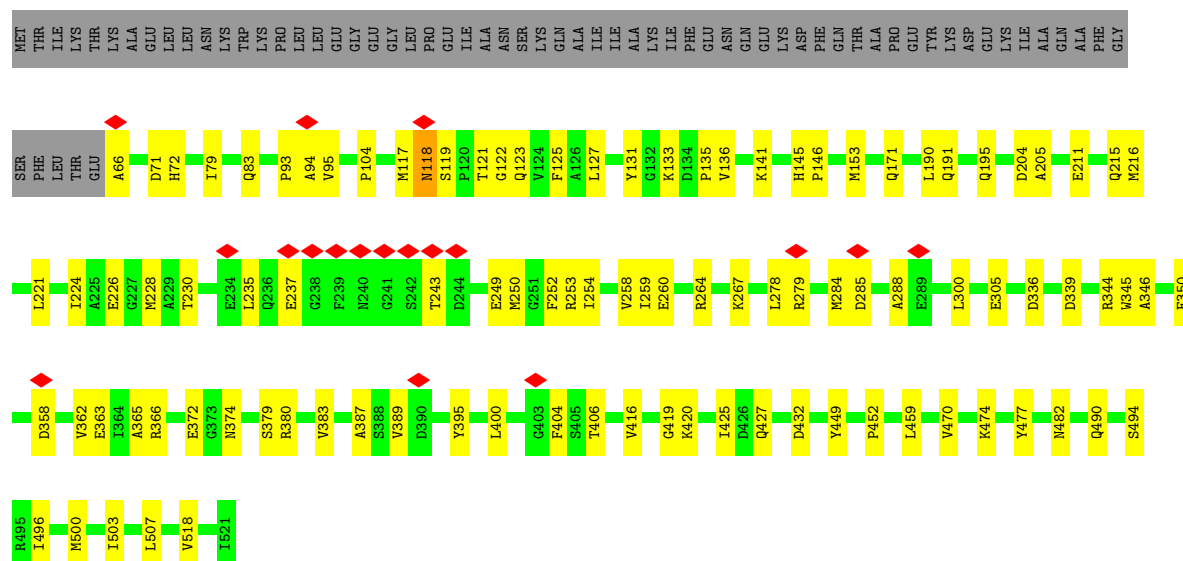
- Molecule 6: gp23, major capsid protein



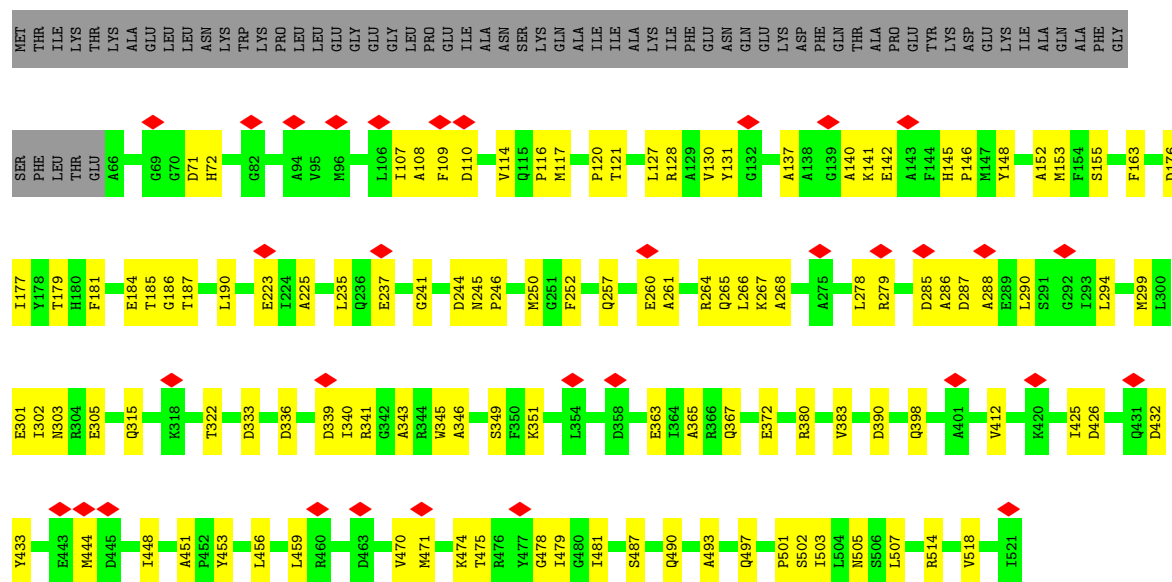
- Molecule 6: gp23, major capsid protein



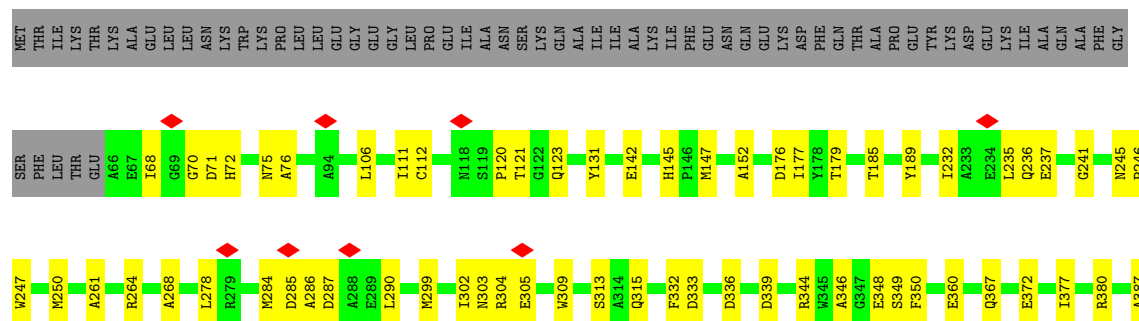


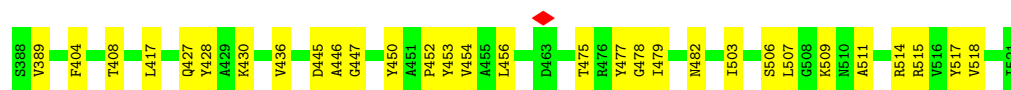


• Molecule 6: gp23, major capsid protein

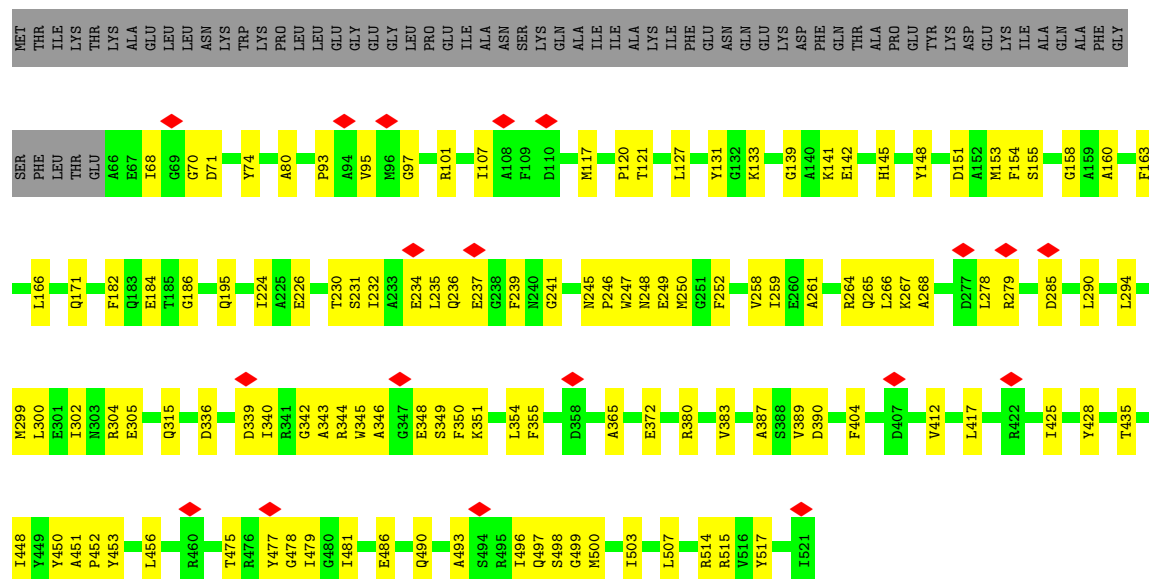


• Molecule 6: gp23, major capsid protein

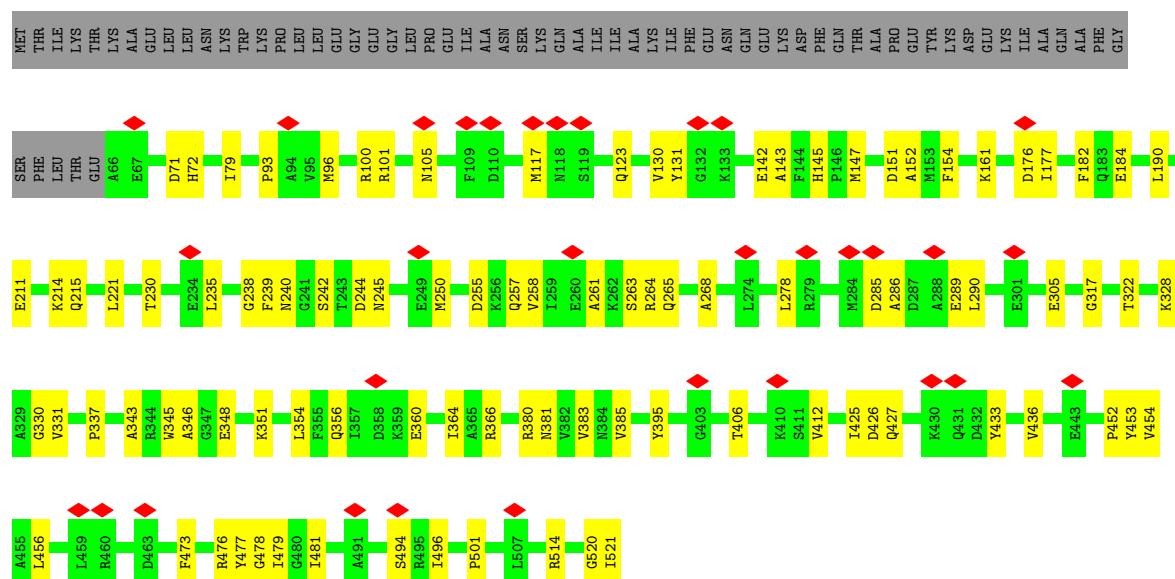




- Molecule 6: gp23, major capsid protein



- Molecule 6: gp23, major capsid protein



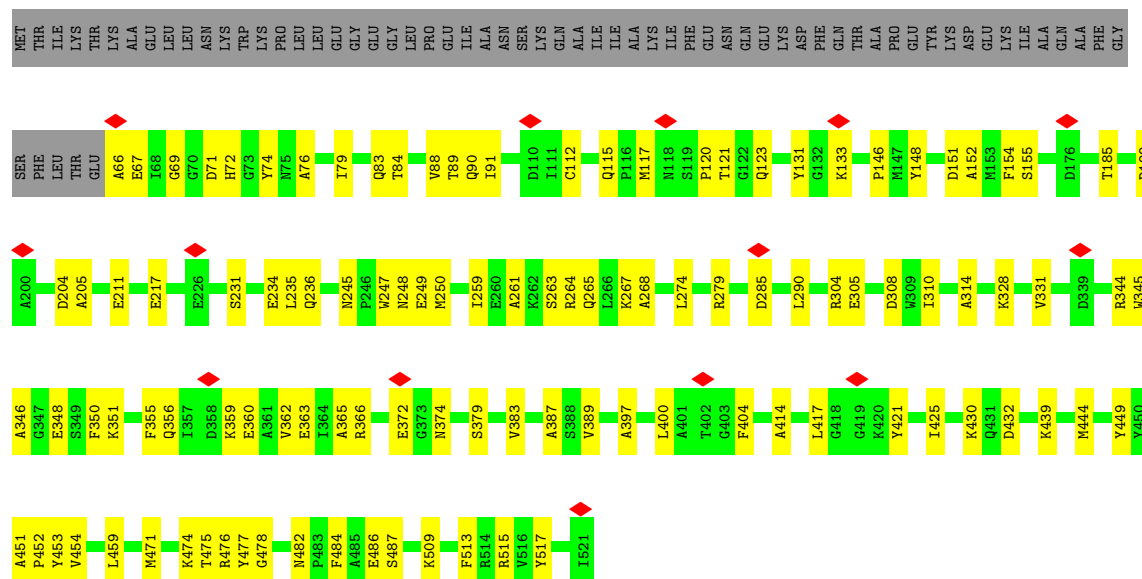
- Molecule 6: gp23, major capsid protein





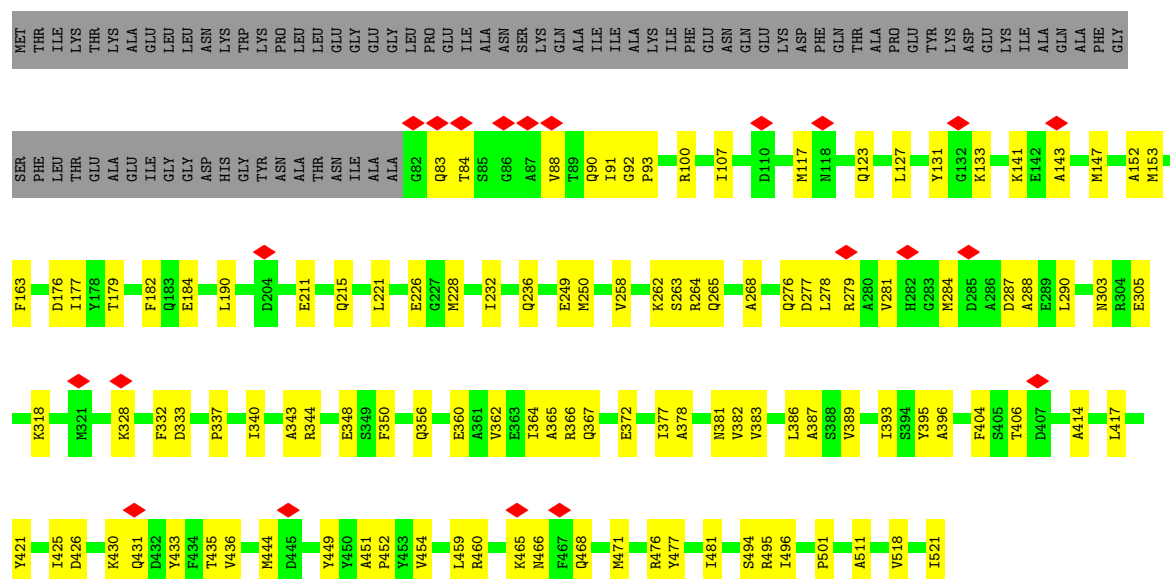
- Molecule 6: gp23, major capsid protein

Chain Am: 66% 21% 12%



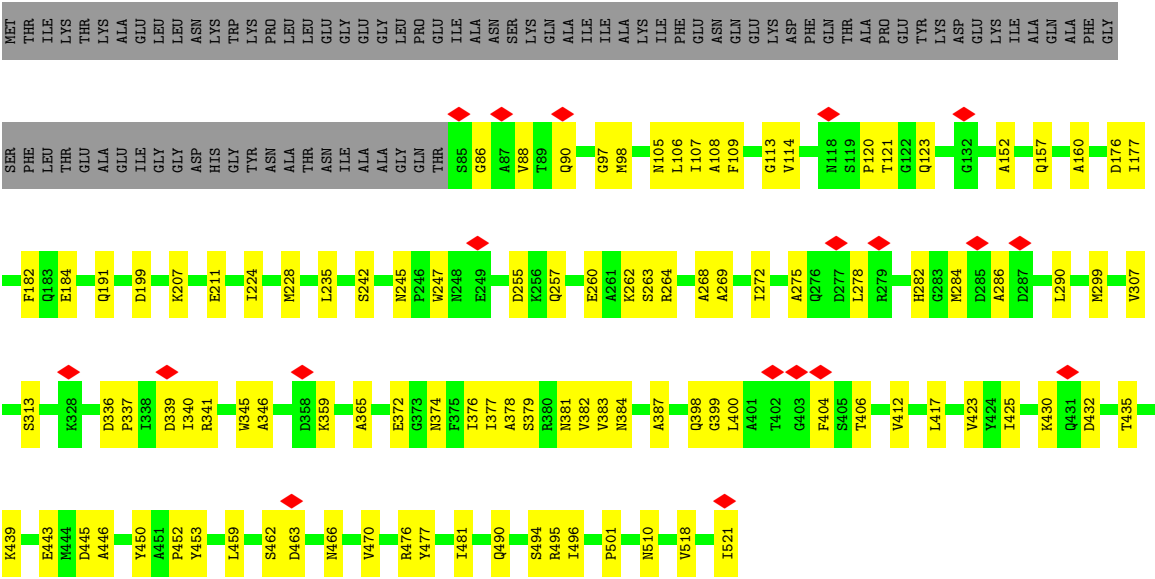
- Molecule 6: gp23, major capsid protein

Chain An: 63% 22% 16%

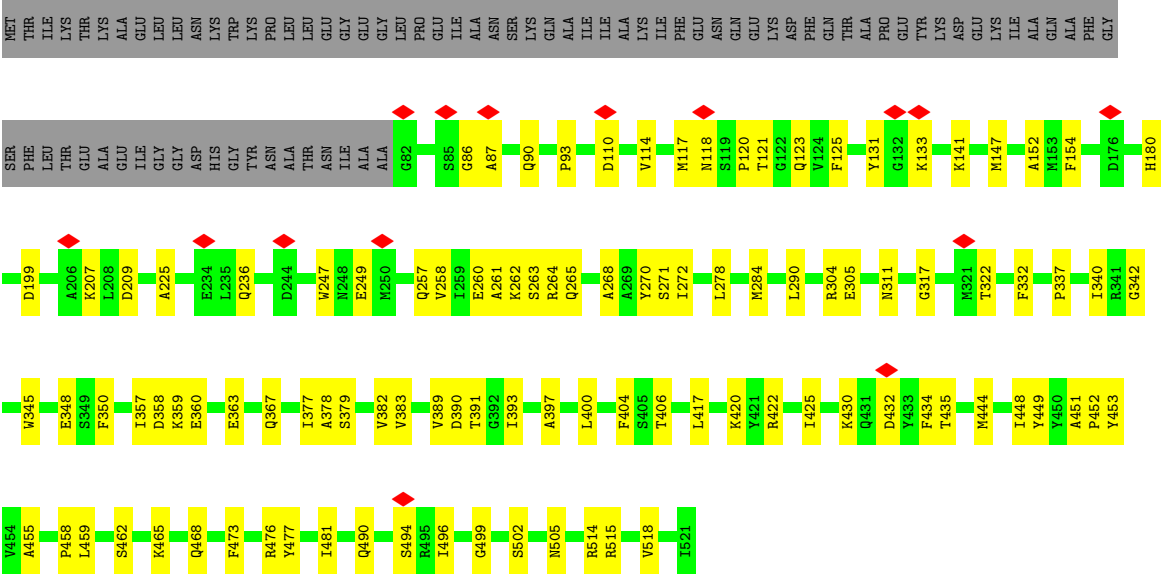


- Molecule 6: gp23, major capsid protein

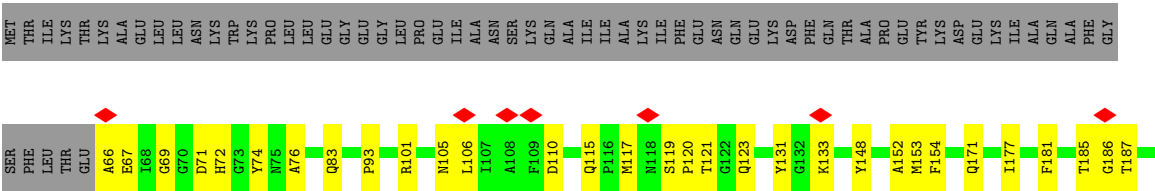
Chain Ao: 64% 20% 16%

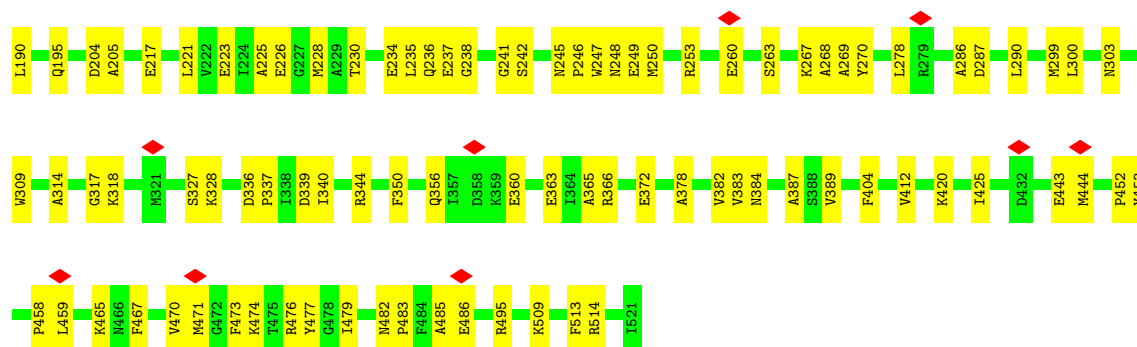


• Molecule 6: gp23, major capsid protein

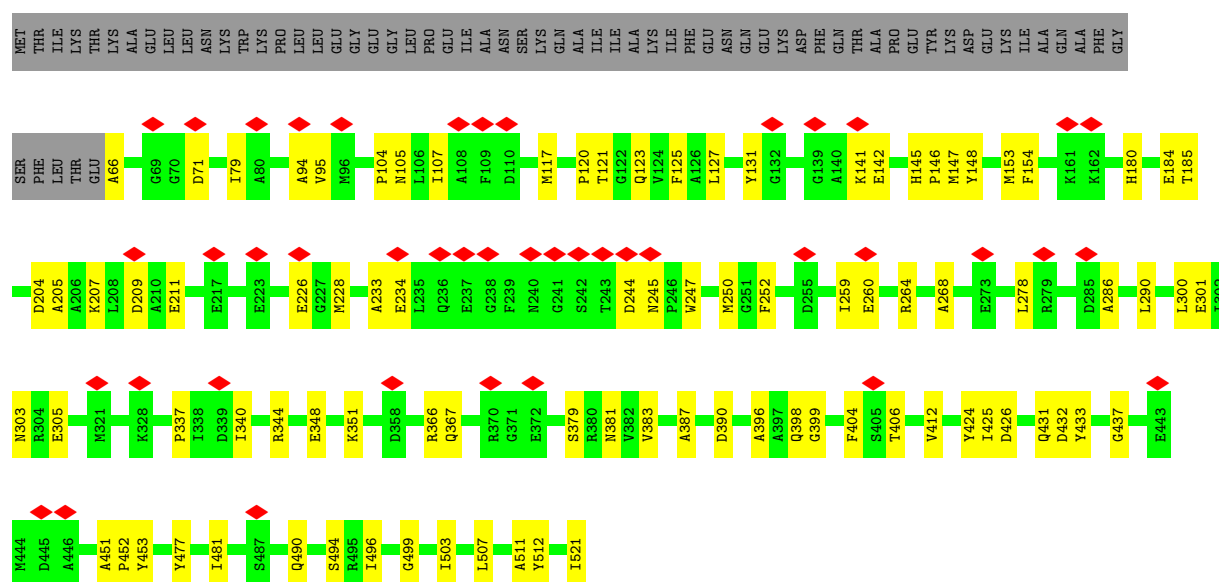
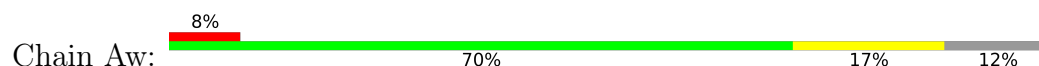


• Molecule 6: gp23, major capsid protein

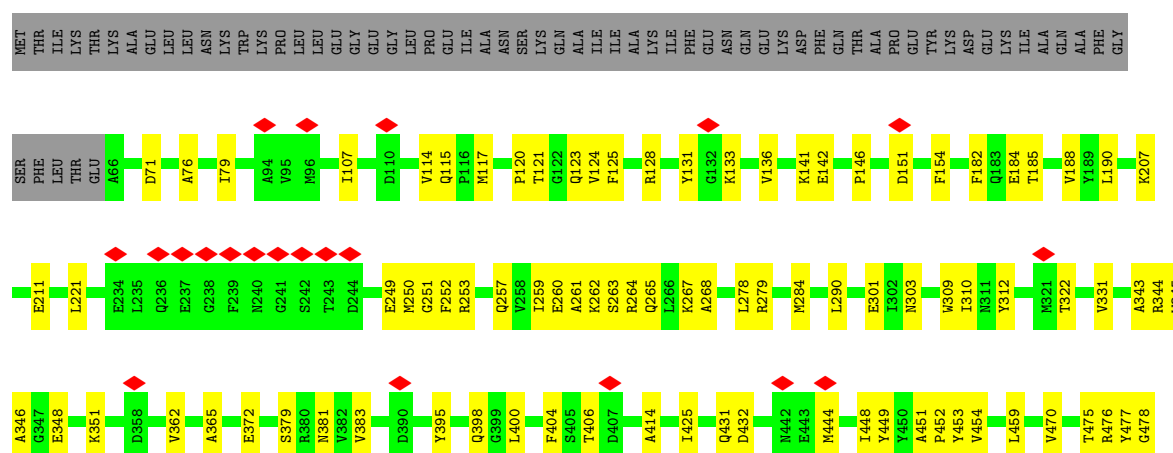




- Molecule 6: gp23, major capsid protein



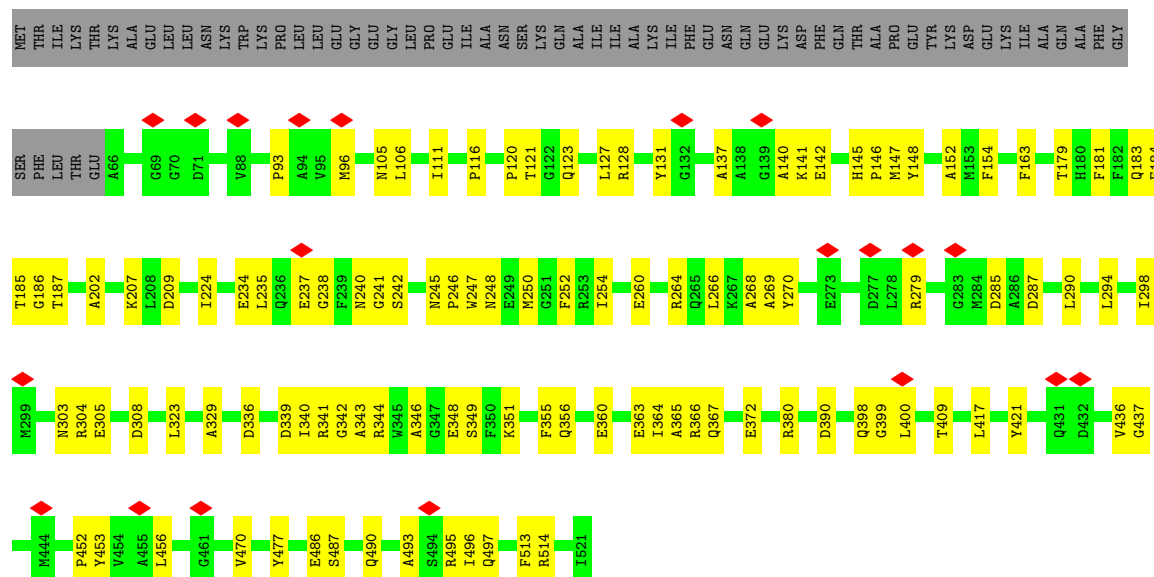
- Molecule 6: gp23, major capsid protein





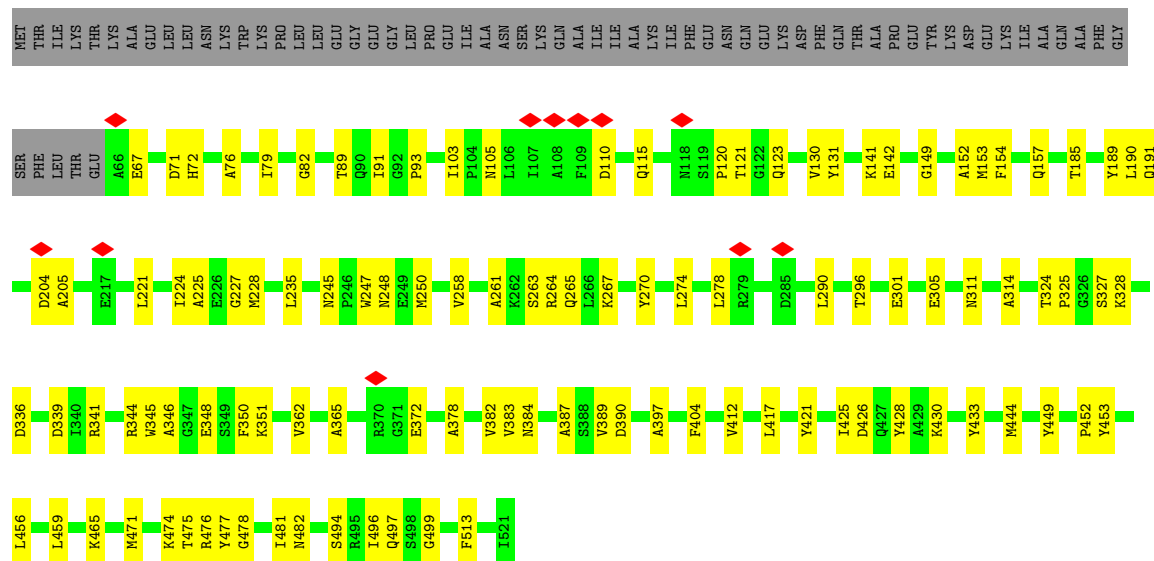
- Molecule 6: gp23, major capsid protein

Chain Az: 66% 21% 12%



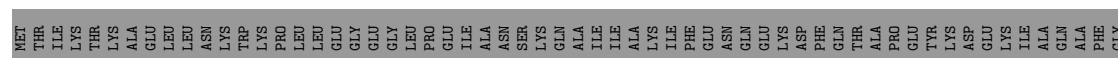
- Molecule 6: gp23, major capsid protein

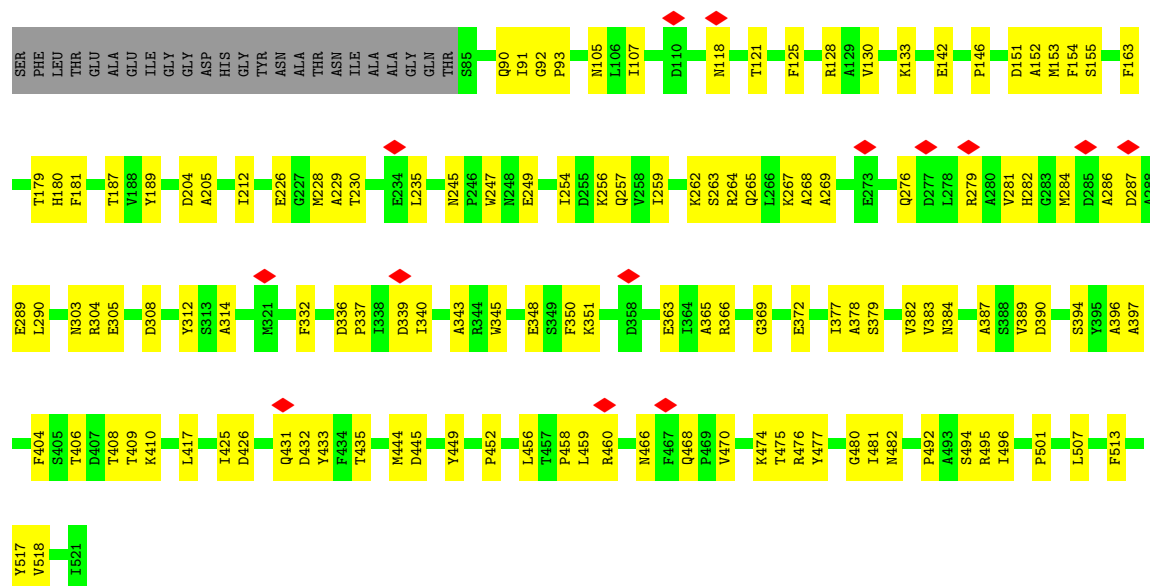
Chain BI: 67% 21% 12%



- Molecule 6: gp23, major capsid protein

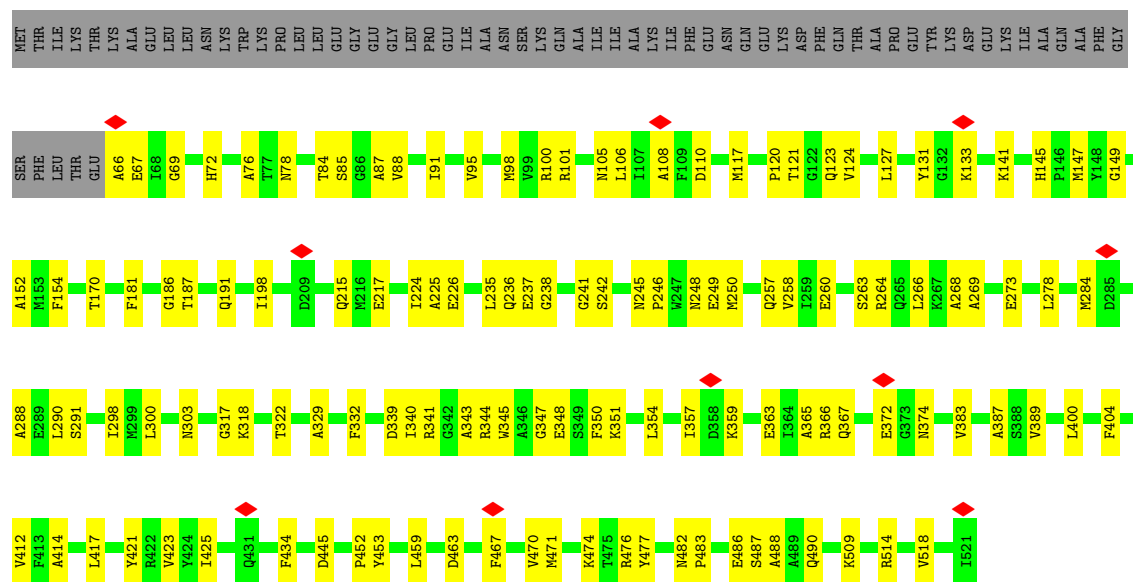
Chain BJ: 59% 25% 16%





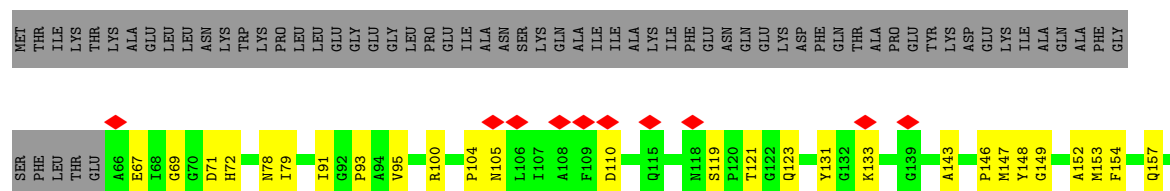
- Molecule 6: gp23, major capsid protein

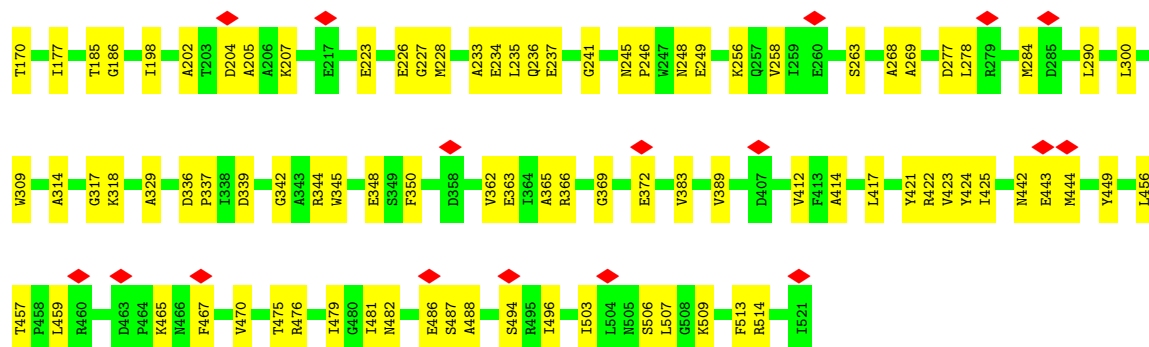
Chain BK: 63% 25% 12%



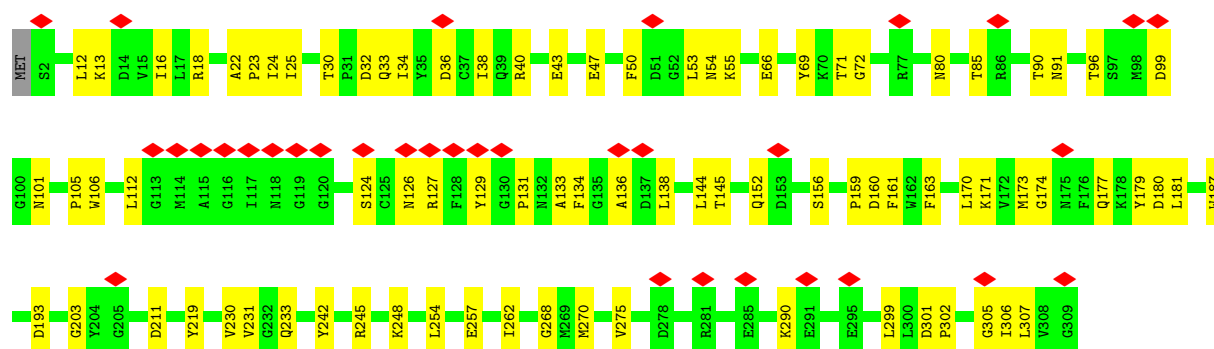
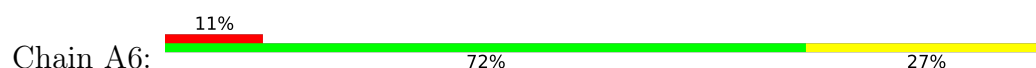
- Molecule 6: gp23, major capsid protein

Chain BM: 5% 65% 22% 12%

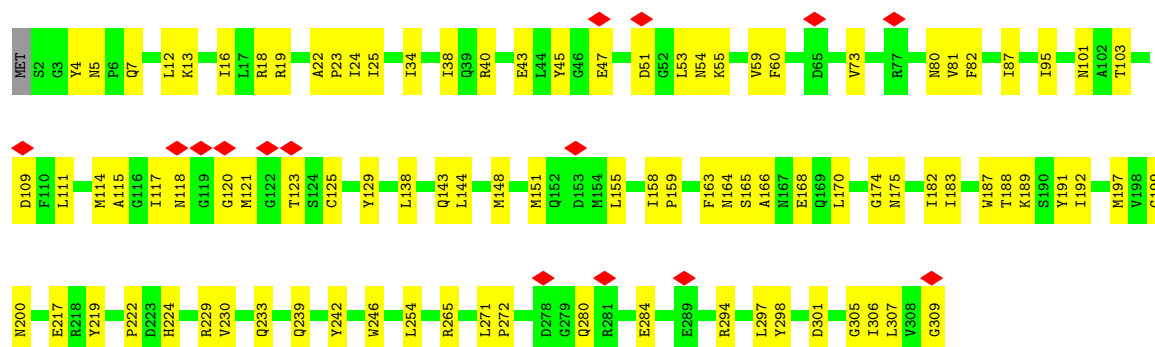
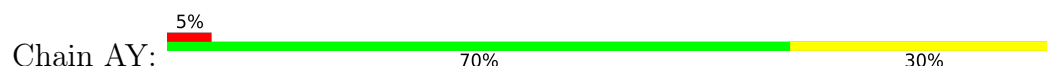




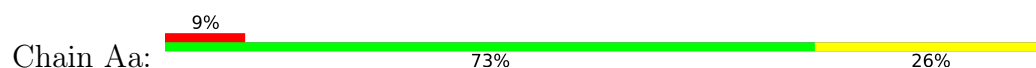
• Molecule 7: gp13, neck protein

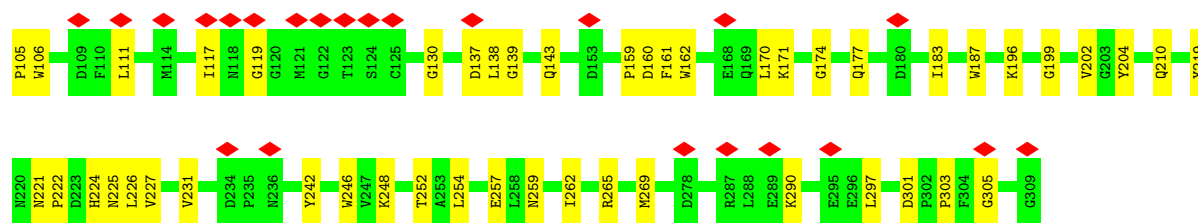


• Molecule 7: gp13, neck protein

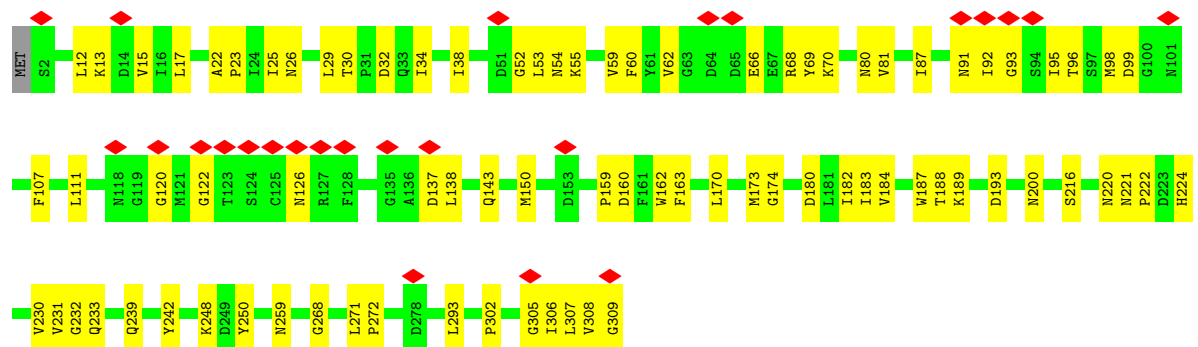
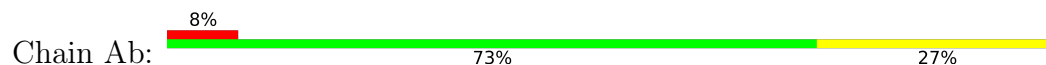


• Molecule 7: gp13, neck protein

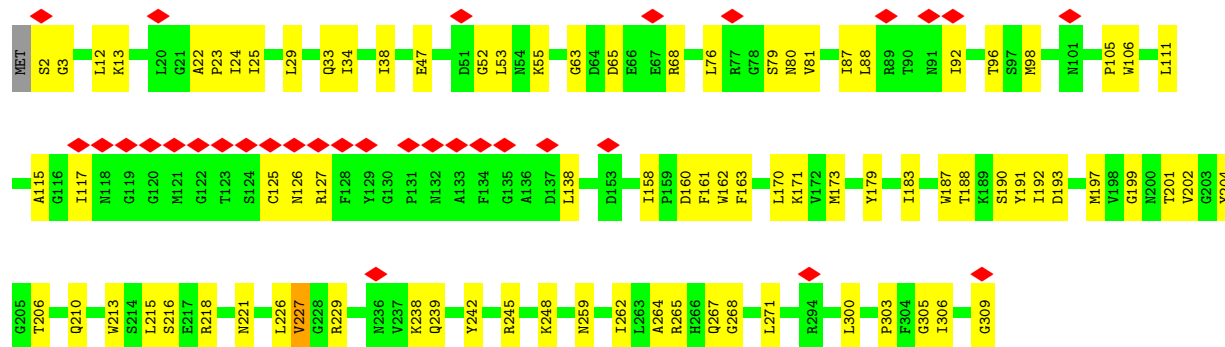
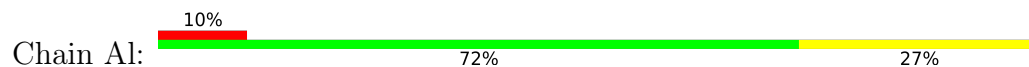




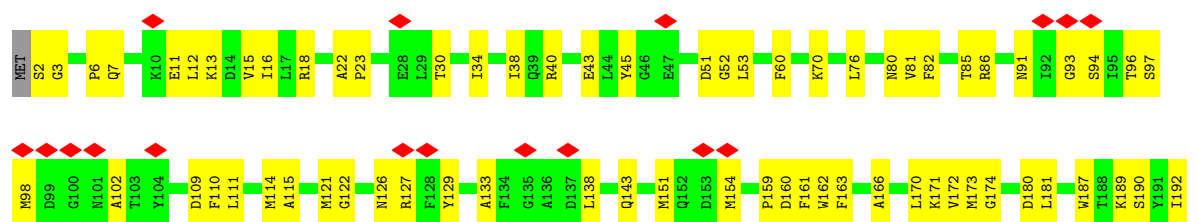
- Molecule 7: gp13, neck protein

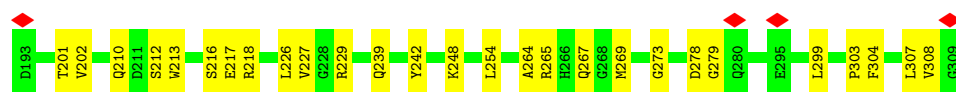


- Molecule 7: gp13, neck protein

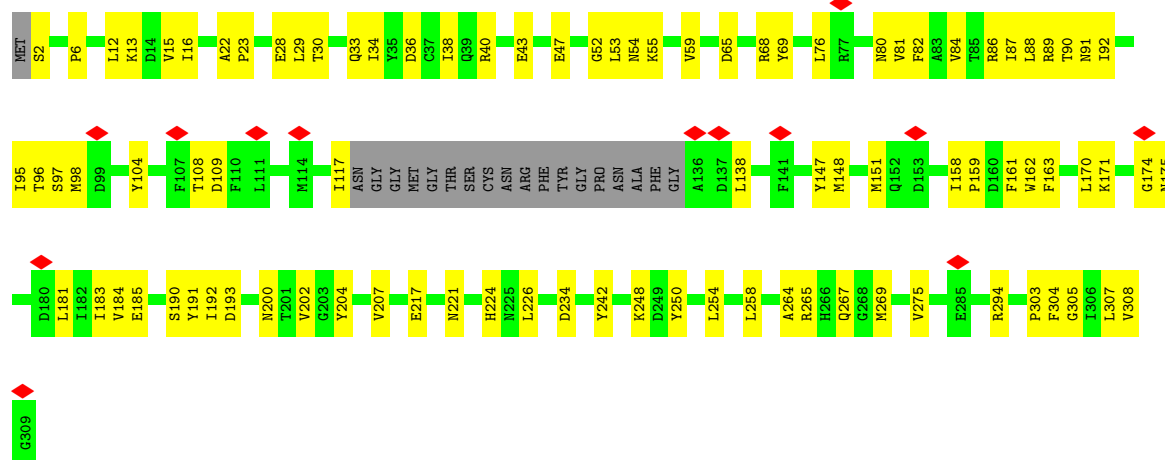


- Molecule 7: gp13, neck protein

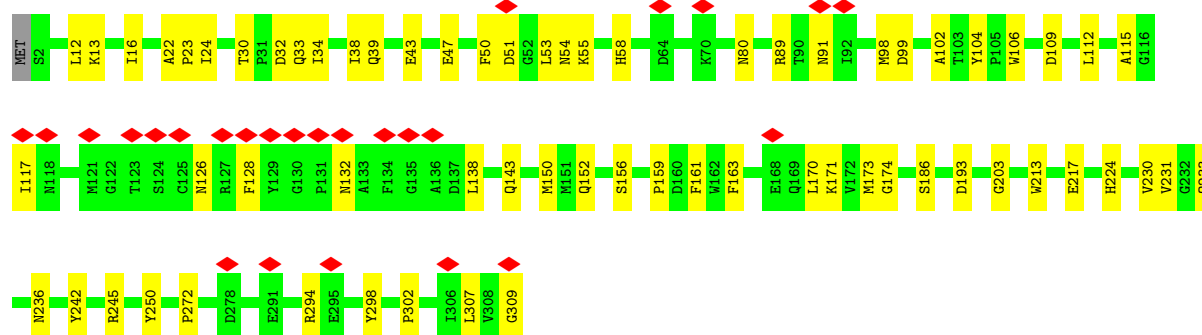
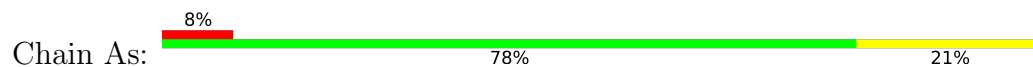




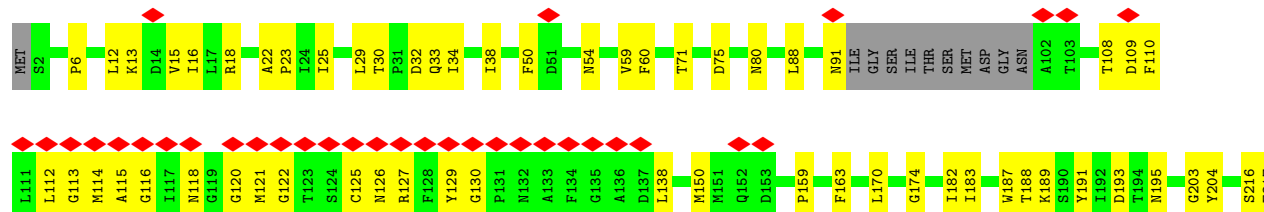
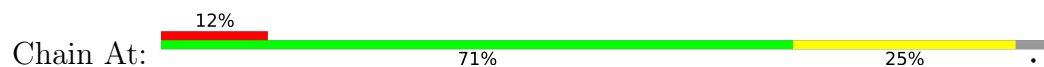
- Molecule 7: gp13, neck protein

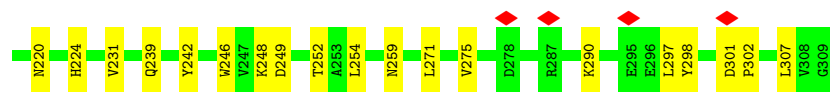


- Molecule 7: gp13, neck protein

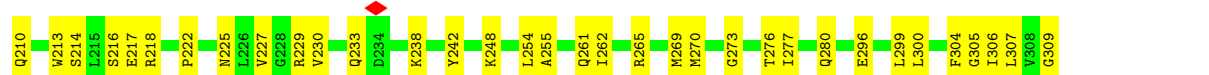
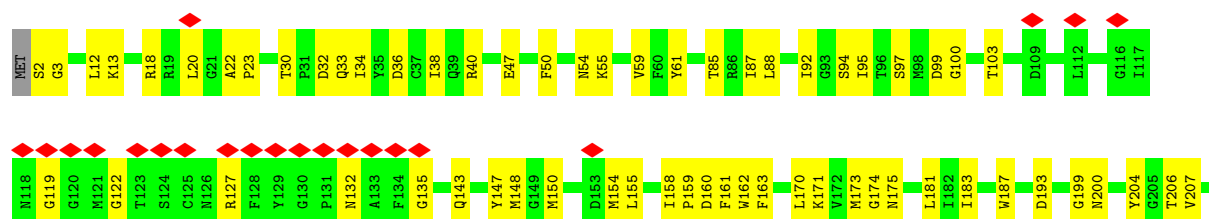
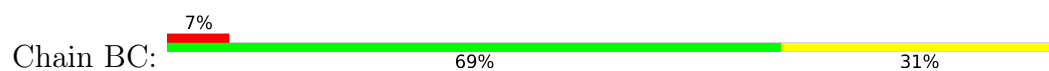


- Molecule 7: gp13, neck protein

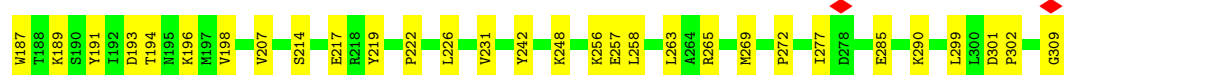
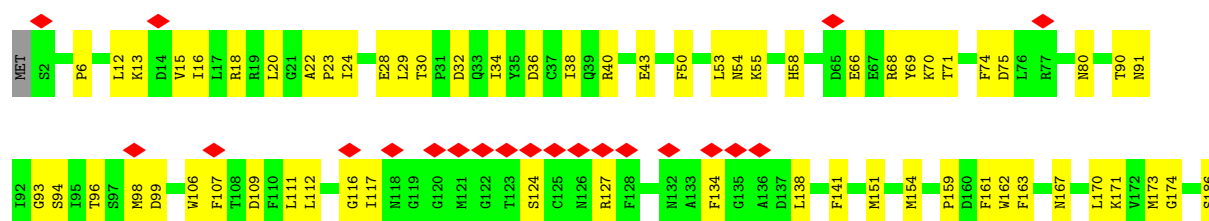
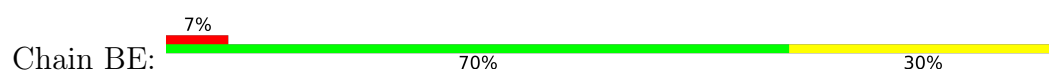




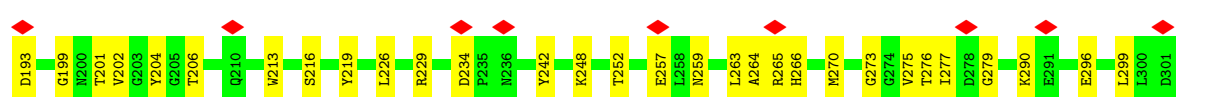
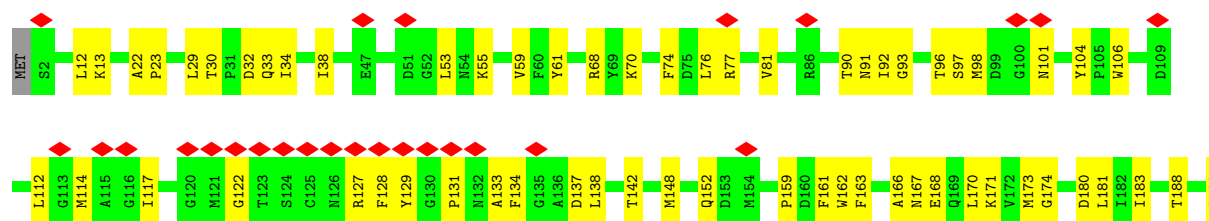
- Molecule 7: gp13, neck protein

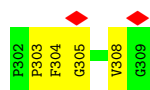


- Molecule 7: gp13, neck protein



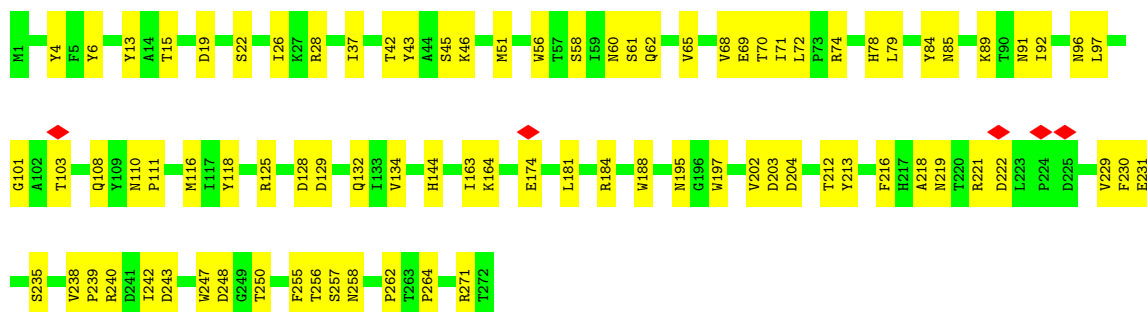
- Molecule 7: gp13, neck protein





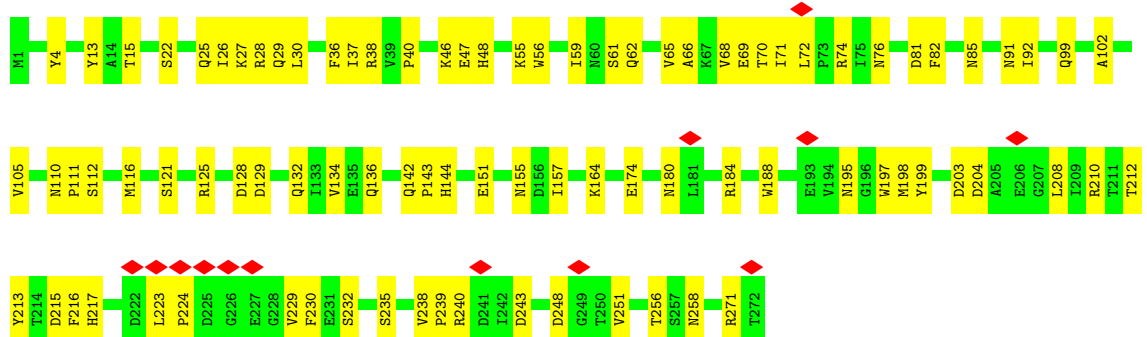
- Molecule 8: gp15, tail terminator protein

Chain AB: 69% 31%



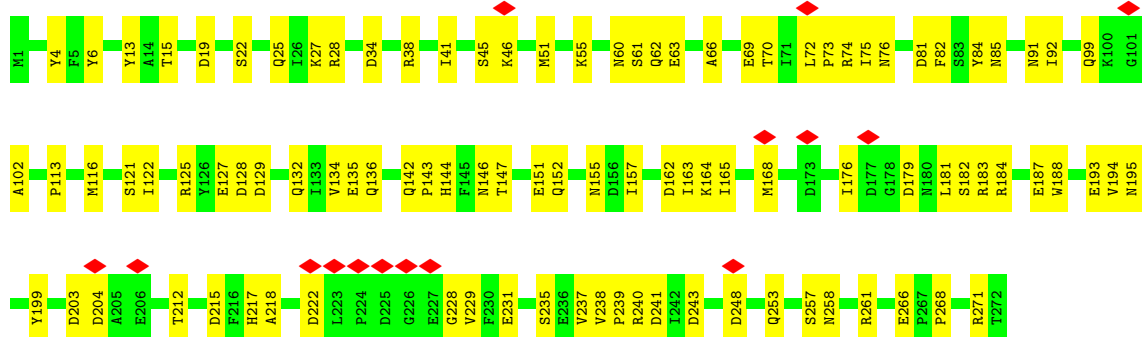
- Molecule 8: gp15, tail terminator protein

Chain q: 5% 67% 33%



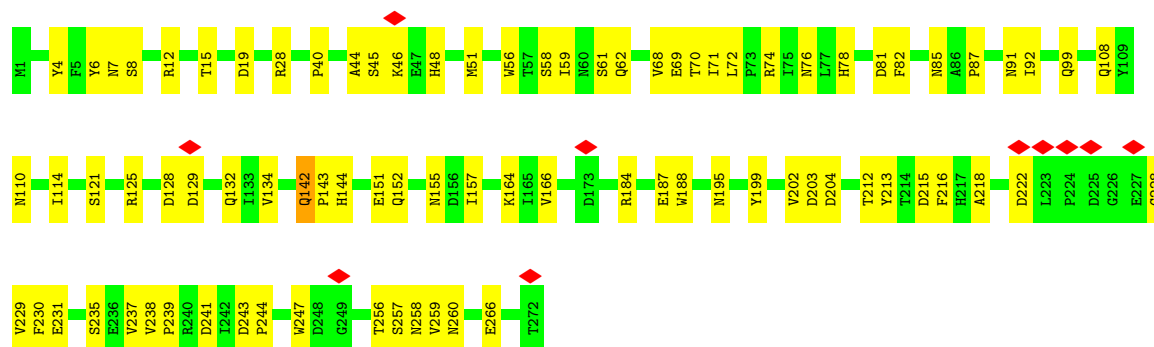
- Molecule 8: gp15, tail terminator protein

Chain r: 6% 64% 36%

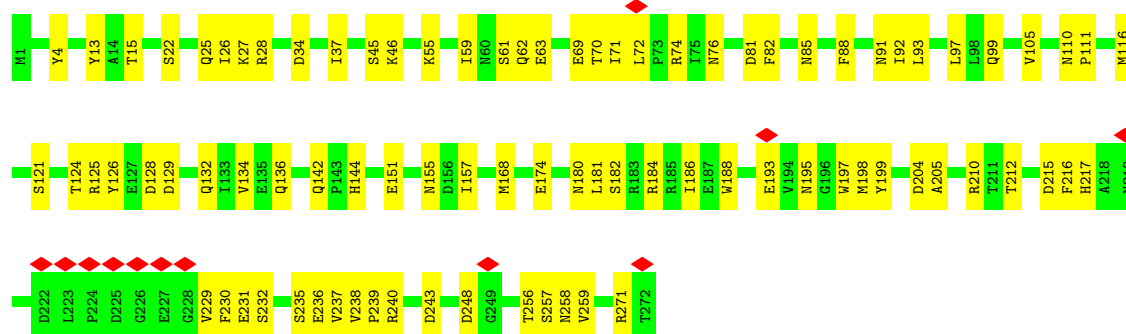


- Molecule 8: gp15, tail terminator protein

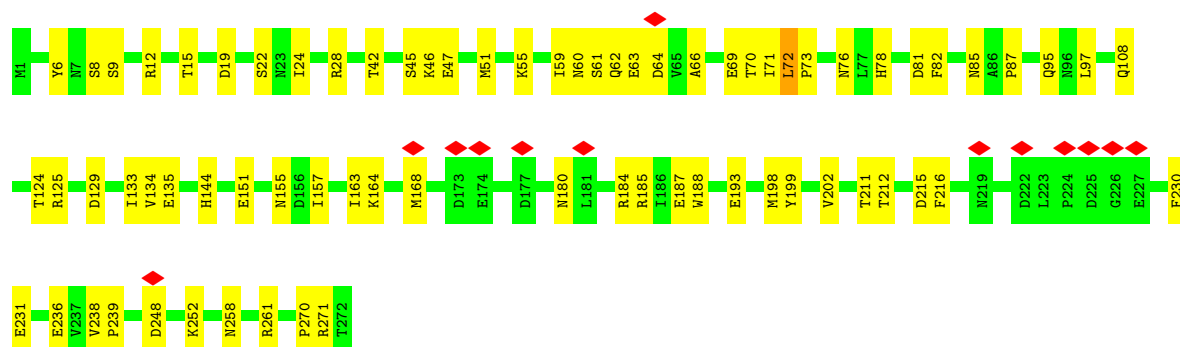
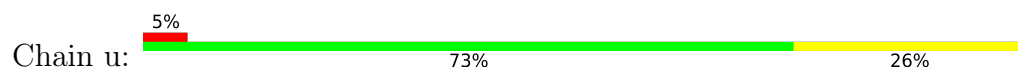
Chain s: 69% 31%



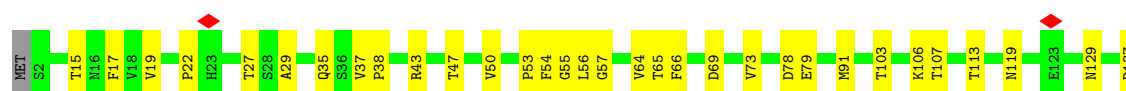
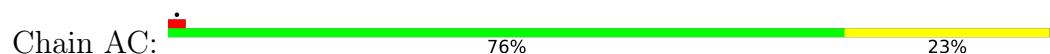
- Molecule 8: gp15, tail terminator protein



- Molecule 8: gp15, tail terminator protein

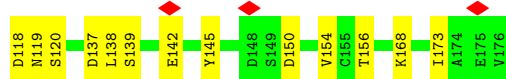
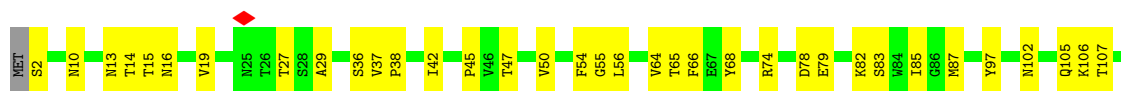


- Molecule 9: gp3, tube terminator protein

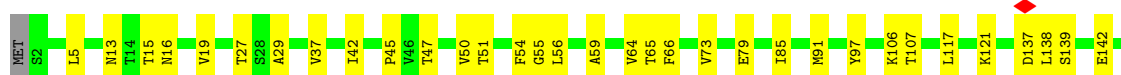
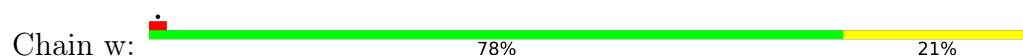




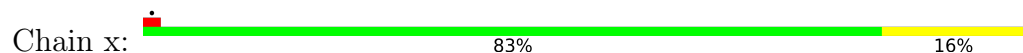
- Molecule 9: gp3, tube terminator protein



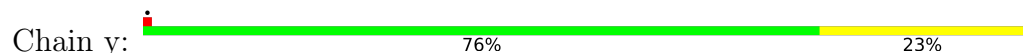
- Molecule 9: gp3, tube terminator protein



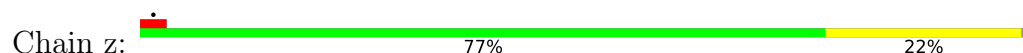
- Molecule 9: gp3, tube terminator protein

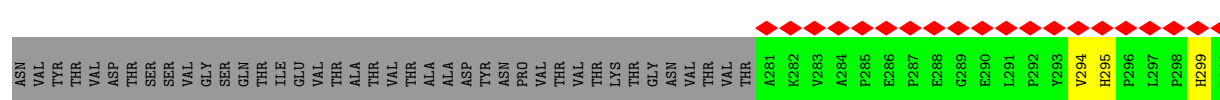


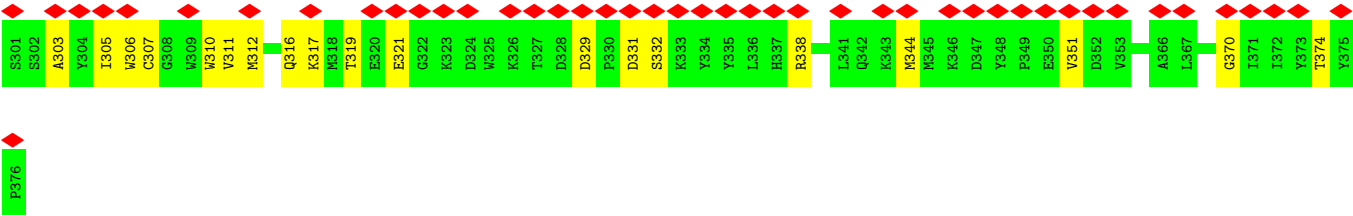
- Molecule 9: gp3, tube terminator protein



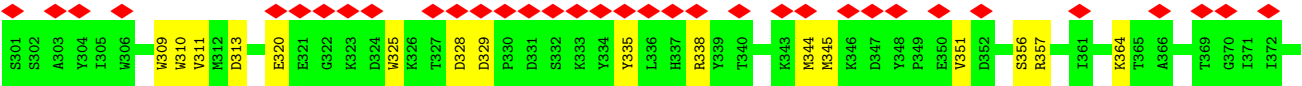
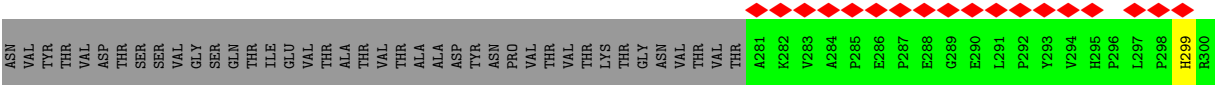
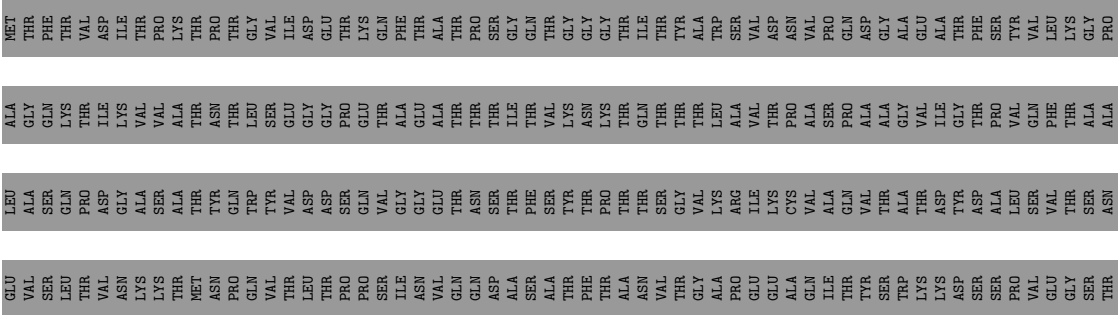
- Molecule 9: gp3, tube terminator protein



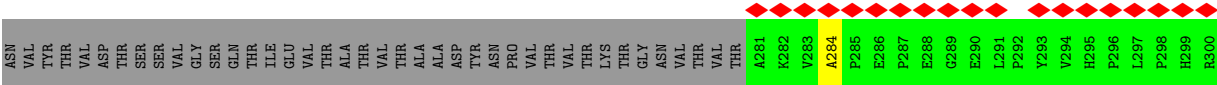
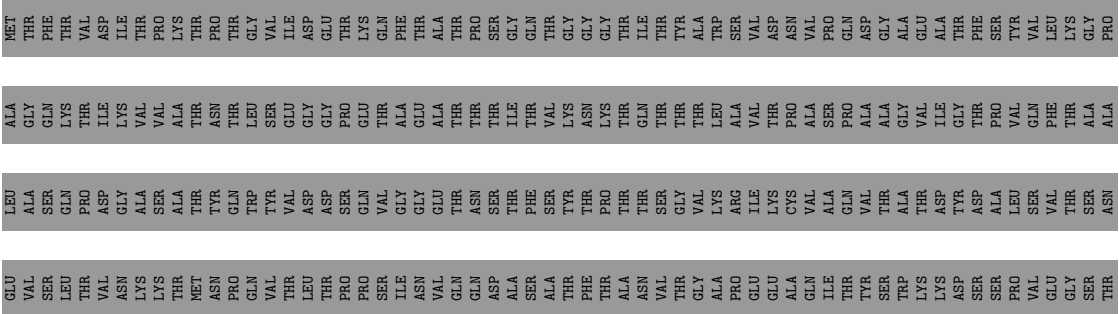




• Molecule 10: Hoc, highly immunogenic outer capsid protein

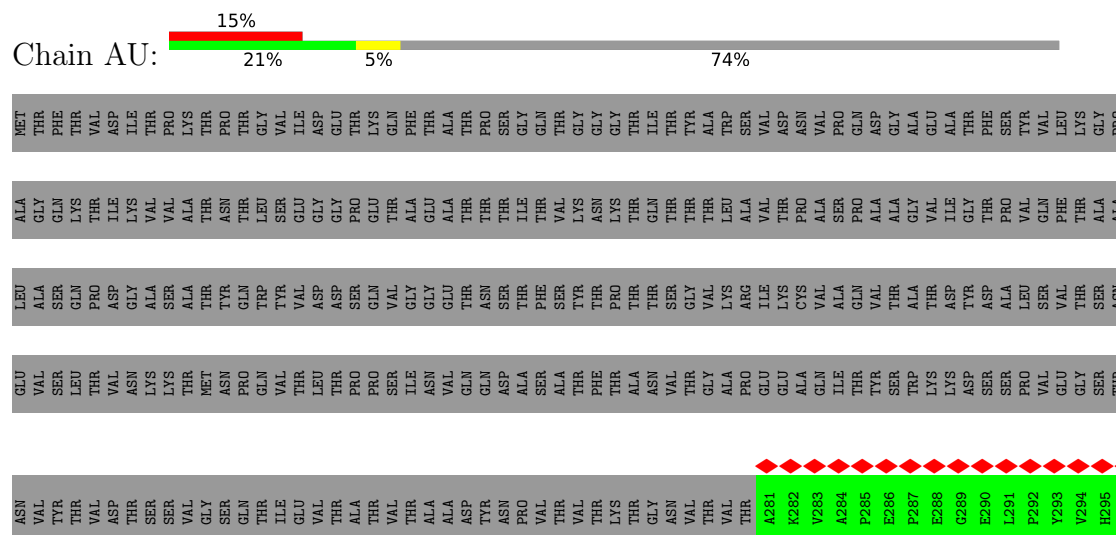


• Molecule 10: Hoc, highly immunogenic outer capsid protein

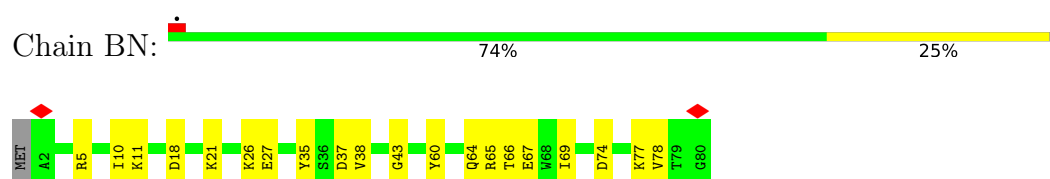




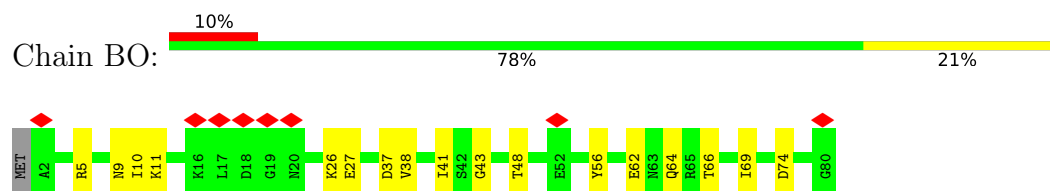
- Molecule 10: Hoc, highly immunogenic outer capsid protein



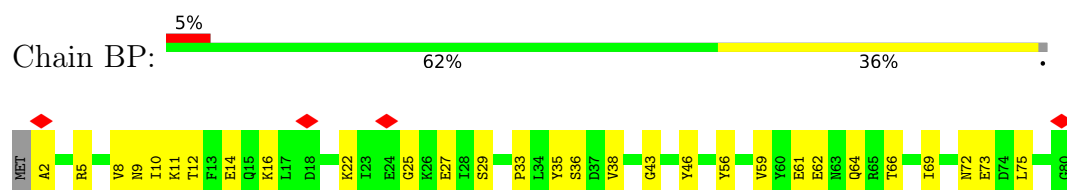
- Molecule 11: Soc, small outer capsid protein



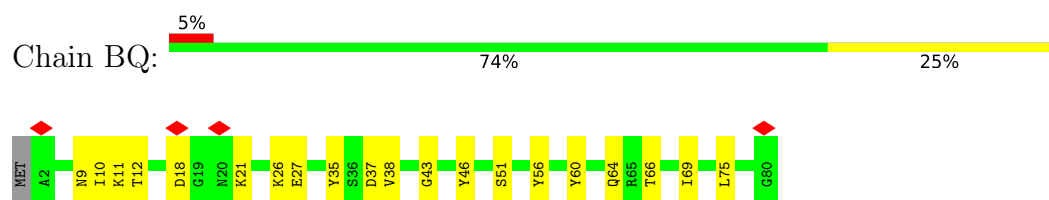
- Molecule 11: Soc, small outer capsid protein



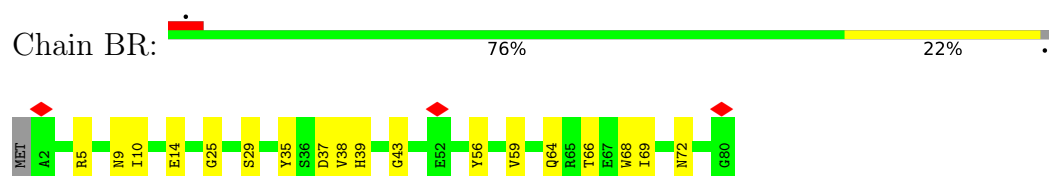
- Molecule 11: Soc, small outer capsid protein



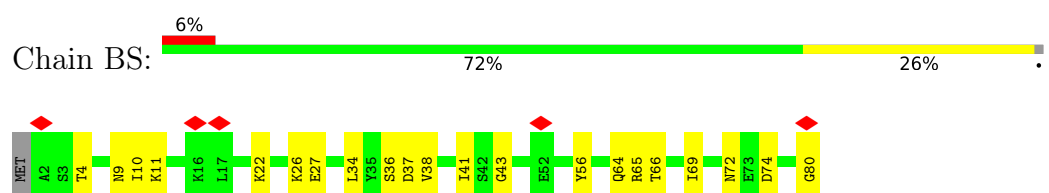
- Molecule 11: Soc, small outer capsid protein



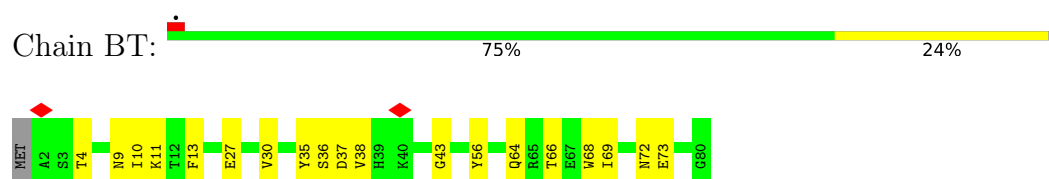
- Molecule 11: Soc, small outer capsid protein



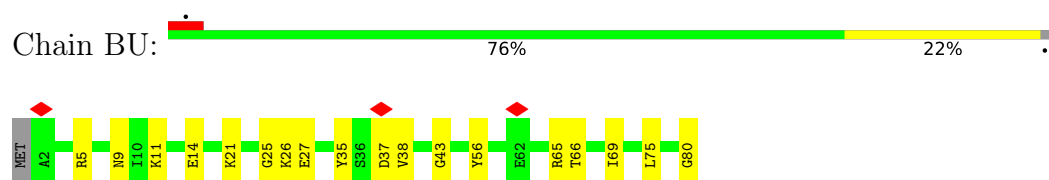
- Molecule 11: Soc, small outer capsid protein



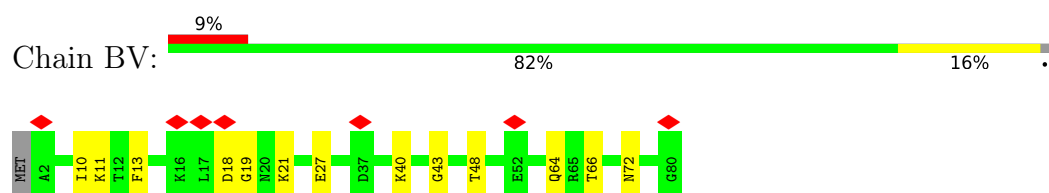
- Molecule 11: Soc, small outer capsid protein



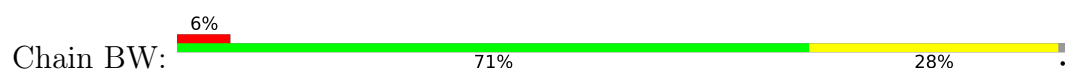
- Molecule 11: Soc, small outer capsid protein

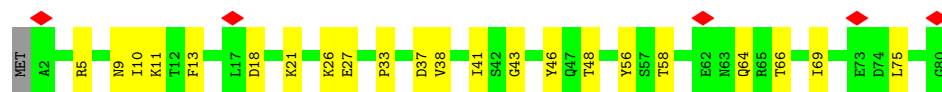


- Molecule 11: Soc, small outer capsid protein

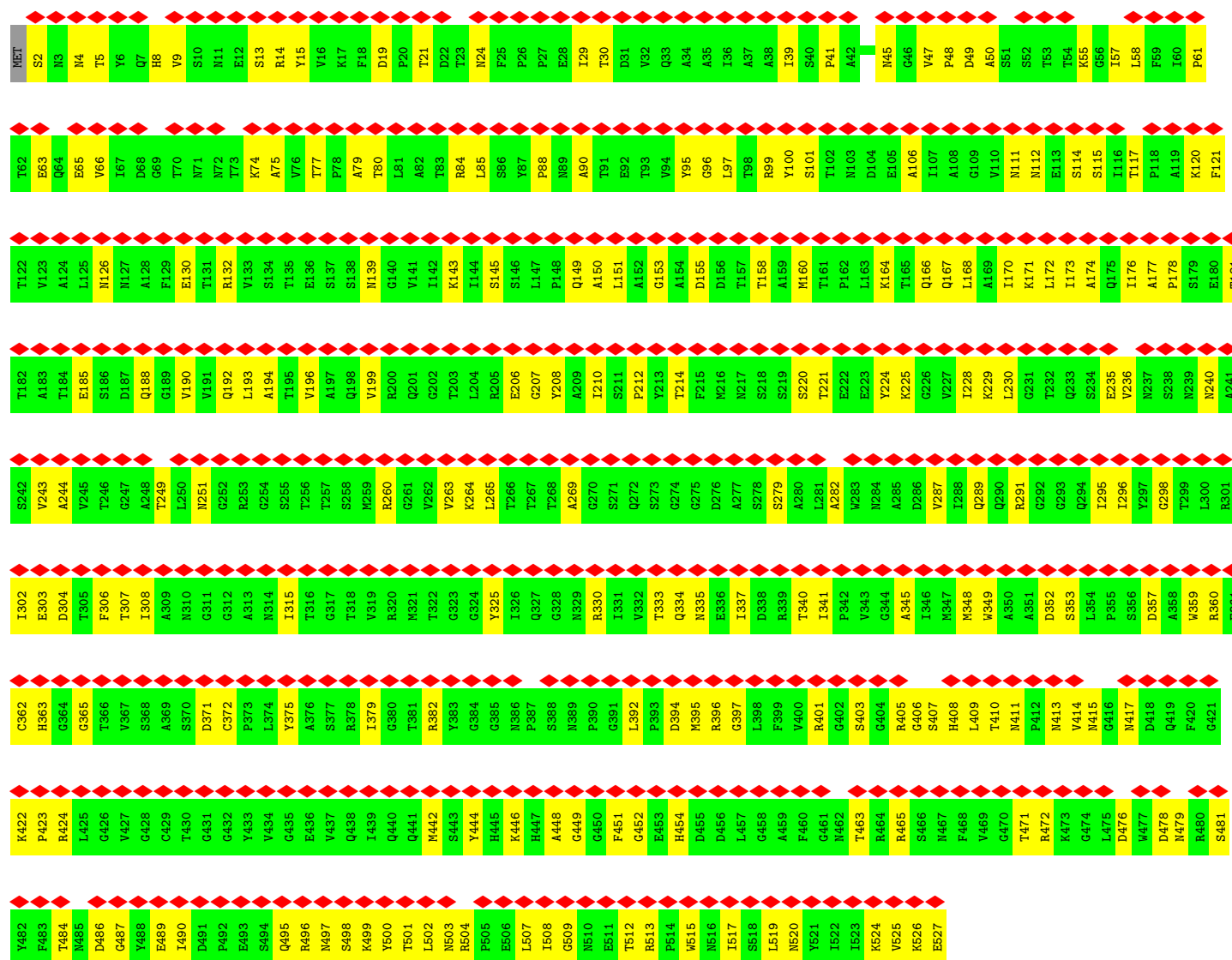


- Molecule 11: Soc, small outer capsid protein





- Molecule 12: gp12, short tail fiber protein



- Molecule 12: gp12, short tail fiber protein

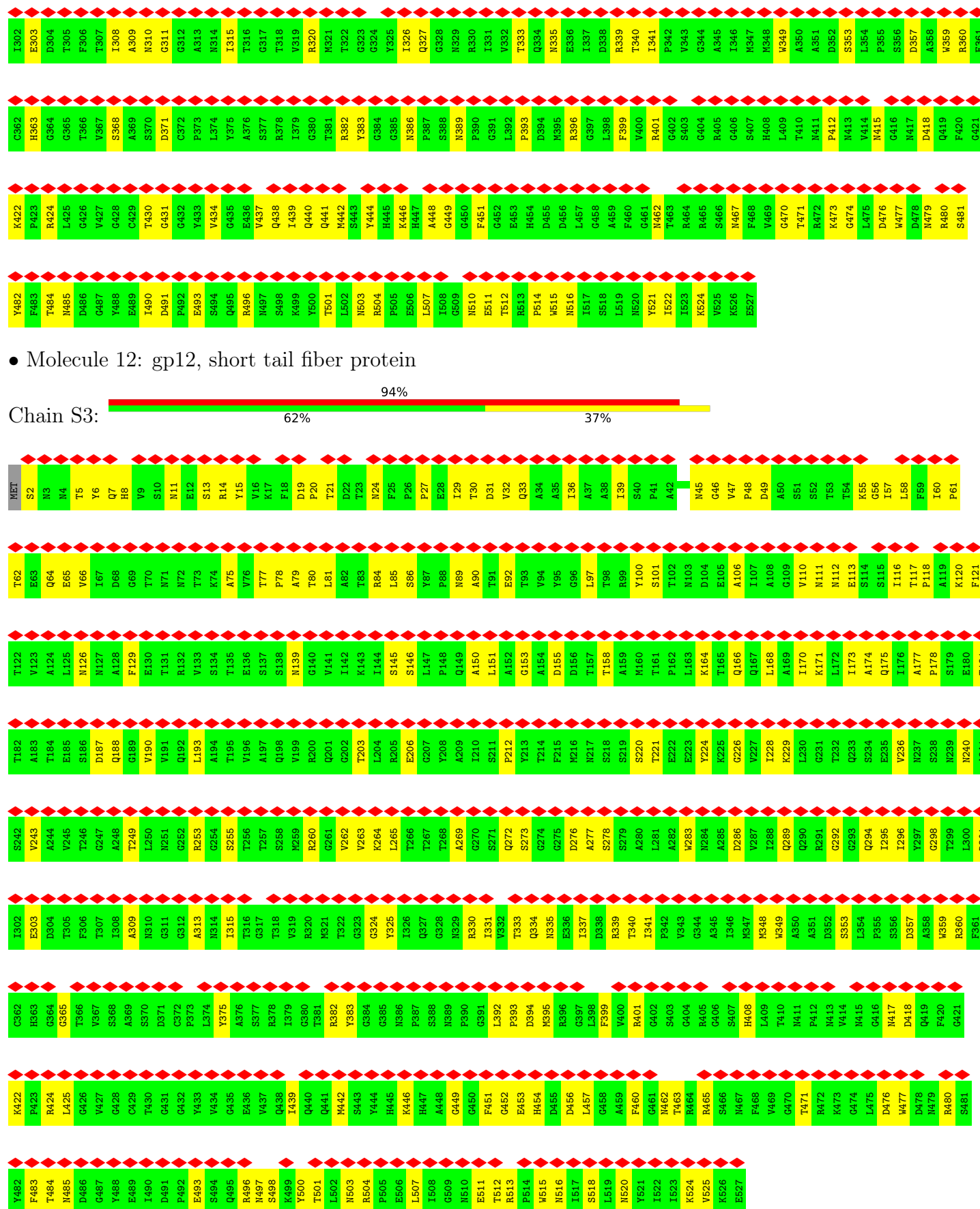


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V66	N126	S186	T246	F306	T366	G426	D486
I67	N127	D187	G247	T307	V367	V427	G487
D68	A128	Q188	A248	I308	S368	G428	Y488
G69	F129	G189	T249	A309	A369	C429	E489
T70	E130	Y190	N250	N310	S370	T430	L490
N71	T131	V191	N251	G311	D371	G431	D491
N72	R132	Q192	G252	G312	G372	G432	P492
T73	V133	L193	R253	A313	P373	G433	E493
K74	S134	A194	G254	N314	L374	Y434	S494
A75	T135	T195	S255	I315	Y375	G435	Q495
V76	E136	V196	T256	T316	A376	E436	R496
T77	S137	A197	T257	G317	S377	V437	N497
P78	S138	Q198	S258	T318	R378	Q438	S498
A79	N139	V199	M259	V319	I379	T439	K499
T80	G140	R200	R260	R320	G380	Q440	Y500
L81	V141	Q201	G261	M321	T381	Q441	T501
A82	I142	G202	V262	T322	R382	M442	L502
T83	K143	T203	L204	G323	Y383	S443	R503
R84	I144	L204	K264	G324	G384	Y444	R504
L85	G145	R205	L265	Y325	G385	H445	P505
S86	S146	E206	T266	I326	N386	K446	E506
Y87	L147	G207	T267	Q327	P387	H447	L507
P88	P148	Y208	T268	G328	S388	A448	L508
N89	Q149	A209	A269	N329	N389	G449	G509
A90	I150	I210	G270	R330	P390	G450	N510
T91	L151	S211	S271	I331	G391	F451	E511
E92	A152	P212	Q272	V332	L392	G452	T512
T93	G153	Y213	S273	T333	P393	E453	R513
V94	A154	T214	G274	Q334	D394	H454	P514
Y95	D155	F215	G275	N335	K395	D455	W515
G96	D156	M216	D276	E336	R396	D456	N516
L97	T157	N217	A277	I337	G397	L457	T517
T98	S158	S218	S278	L338	L398	G458	S518
R99	A159	S219	S279	R339	F399	A459	L519
Y100	M160	S220	A280	T340	V400	F460	N520
S101	T161	T221	L281	I341	R401	G461	Y521
T102	P162	E222	L282	G402	G402	N462	T522
N103	L163	E223	W283	V343	S403	T463	T523
D104	K164	Y224	N284	G344	G404	R464	K524
E105	T165	K225	A285	A345	R405	R465	V525
A106	Q166	G226	D286	I346	G406	S466	K526
I107	Q167	V227	V287	M347	S407	M467	
A108	L168	I228	I288	M348	H408	F468	
G109	A169	K229	I289	W349	L409	V469	
V110	I170	L230	Q290	A350	T410	G470	
N111	K171	G231	Q291	R291	N411	T471	
N112	L172	T232	G292	A351	P412	R472	
E113	A173	Q233	G293	D352	M413	K473	
S114	I174	S234	Q294	S353	V414	G474	
S115	Q175	E235	I295	L354	N415	L475	
I116	I176	V236	I296	P355	G416	D476	
T117	A177	N237	I297	S356	N417	V477	
P118	P178	S238	G298	D357	D418	D478	
K120	S179	N239	T299	A358	Q419	N479	
F121	E180	N240	L300	W359	F420	R480	
V123	T181	A241	R301	R360	G421	S481	
A124	A183	V243	I302	F361	K422	Y482	
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• Molecule 12: gp12, short tail fiber protein

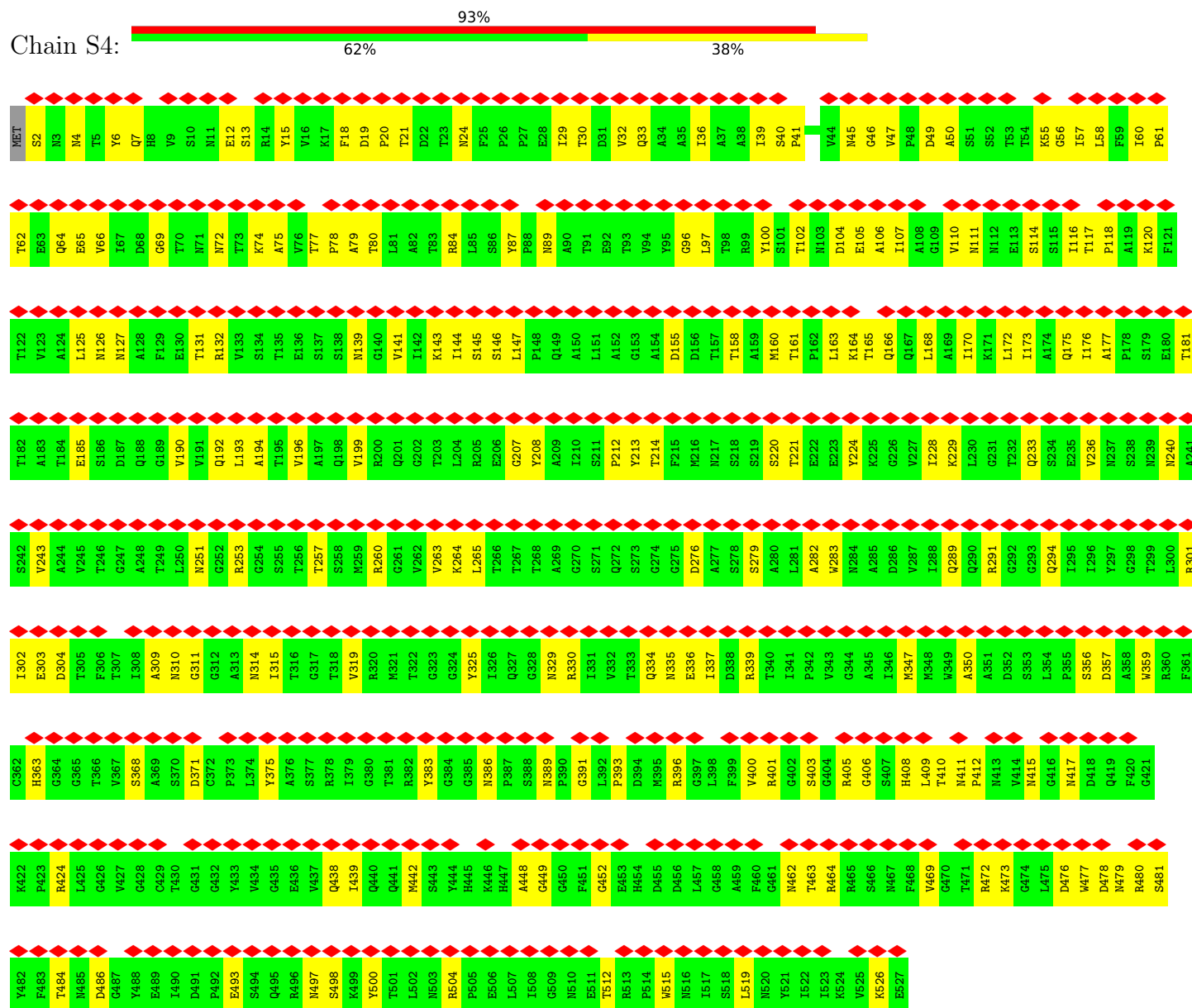


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N3	Q64	A124	T184	A244
N4	E65	L125	E185	V245
Y6	V66	N126	S186	T246
Q7	I67	N127	D187	G247
H8	D68	A128	Q188	A248
V9	G69	F129	G189	T249
S10	T70	E130	V190	L250
N11	N71	T131	V191	N251
E12	N72	R132	Q192	G252
R14	T73	V133	L193	R253
Y15	K74	S134	A194	G254
V16	A75	T135	T195	S255
F17	V76	E136	V196	T256
K18	T77	S137	A197	T257
D19	P78	S138	Q198	S258
P20	T80	N139	V199	M259
T21	L81	G140	R200	R260
D22	A82	V141	Q201	G261
T23	T83	I142	G202	V262
N24	R84	K143	T203	V263
P25	L85	I144	L204	K264
P26	S86	S145	R205	L265
P27	Y87	S146	E206	T266
G28	P88	L147	G207	T267
I29	N89	P148	Y208	T268
T30	A90	Q149	A209	A269
D31	N91	A150	I210	G270
V32	T91	L151	S211	L271
Q33	E92	A152	P212	Q272
A34	T93	G153	Y213	S273
A35	V94	A154	T214	G274
I36	Y95	D155	F215	M216
A37	G96	D156	M217	N218
A38	L97	T157	N219	A277
I39	T98	S158	S218	S278
S40	Y100	A159	S219	S279
P41	S101	M160	S220	A280
V44	T102	T161	E222	L281
G46	N103	P162	E223	A282
V47	E105	K164	Y224	M284
P48	A106	T165	K225	A285
Q49	I107	Q166	G226	D286
A50	A108	L168	V227	T287
S51	G109	L169	I228	T288
S52	V110	A169	K229	Q289
T53	N111	L170	S230	L290
T54	N112	K171	G231	R291
T55	E113	L172	T232	G292
G56	S114	I173	Q233	G293
I57	S115	Q175	S234	E235
L58	I116	T117	V236	T237
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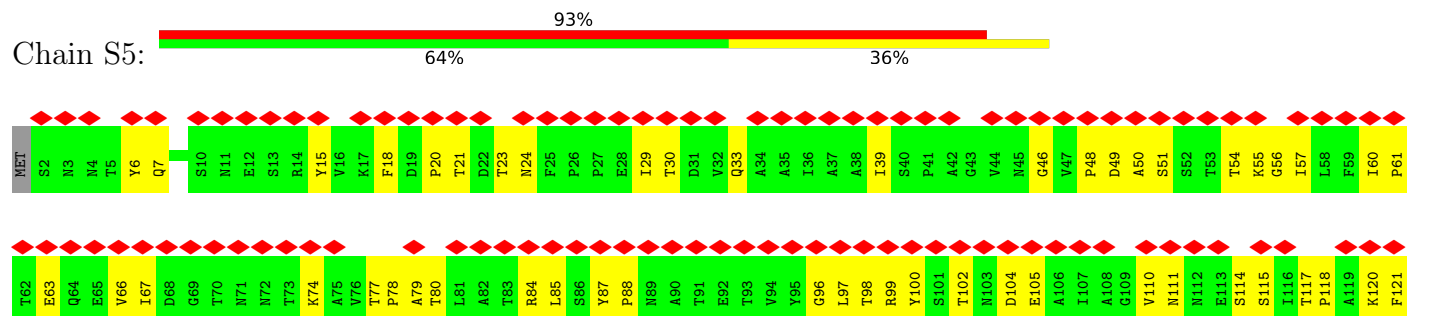
• Molecule 12: gp12, short tail fiber protein

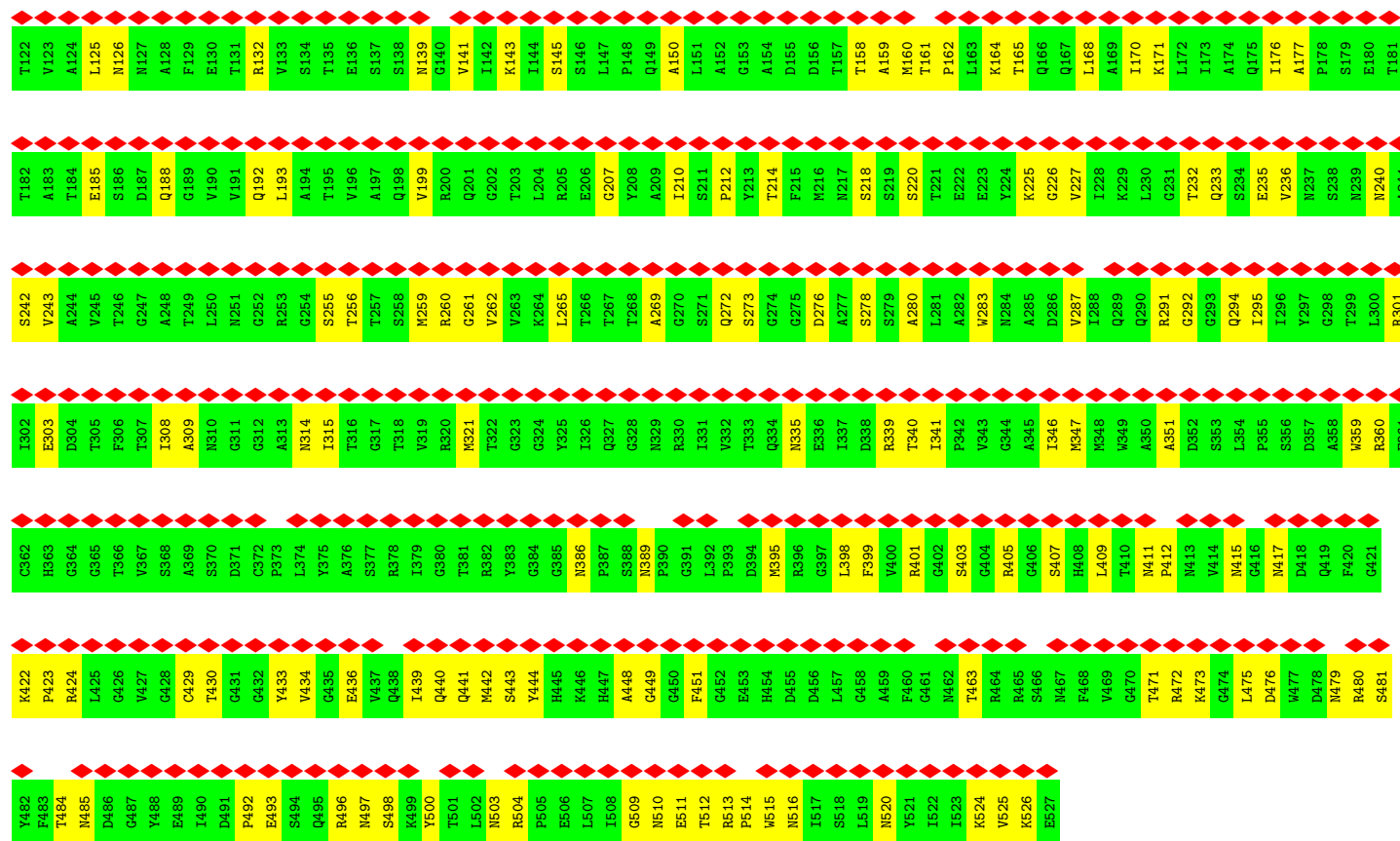
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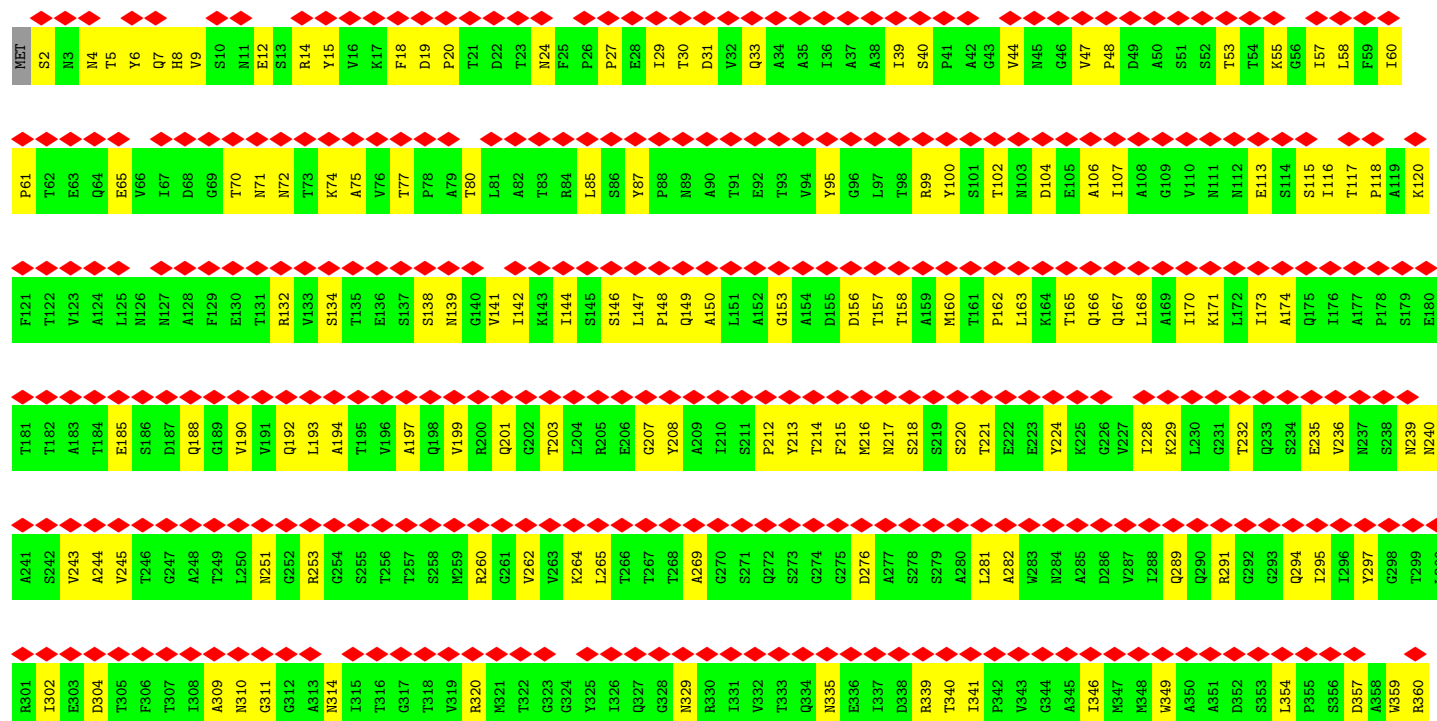
• Molecule 12: gp12, short tail fiber protein

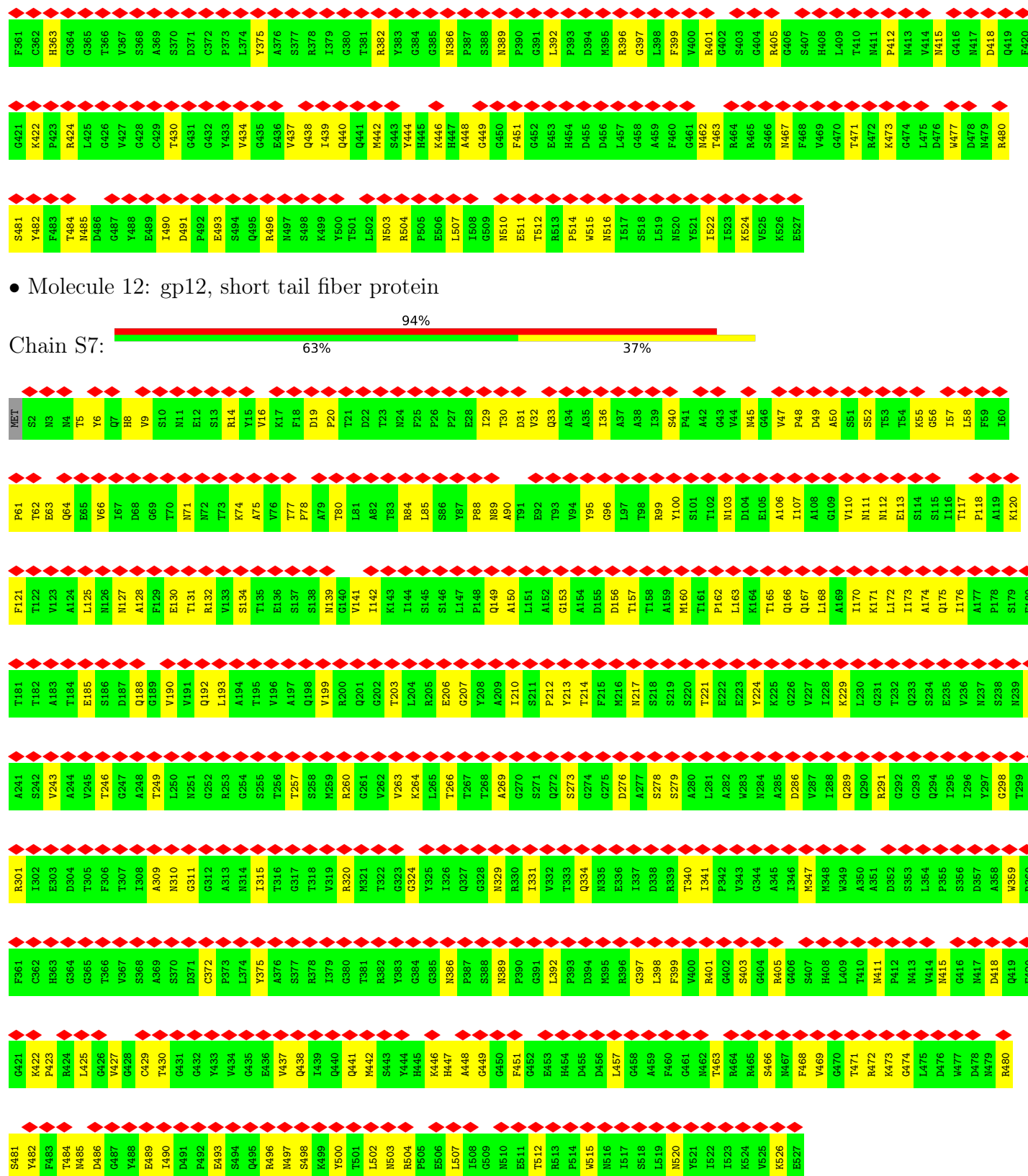
Chain S5:





• Molecule 12: gp12, short tail fiber protein

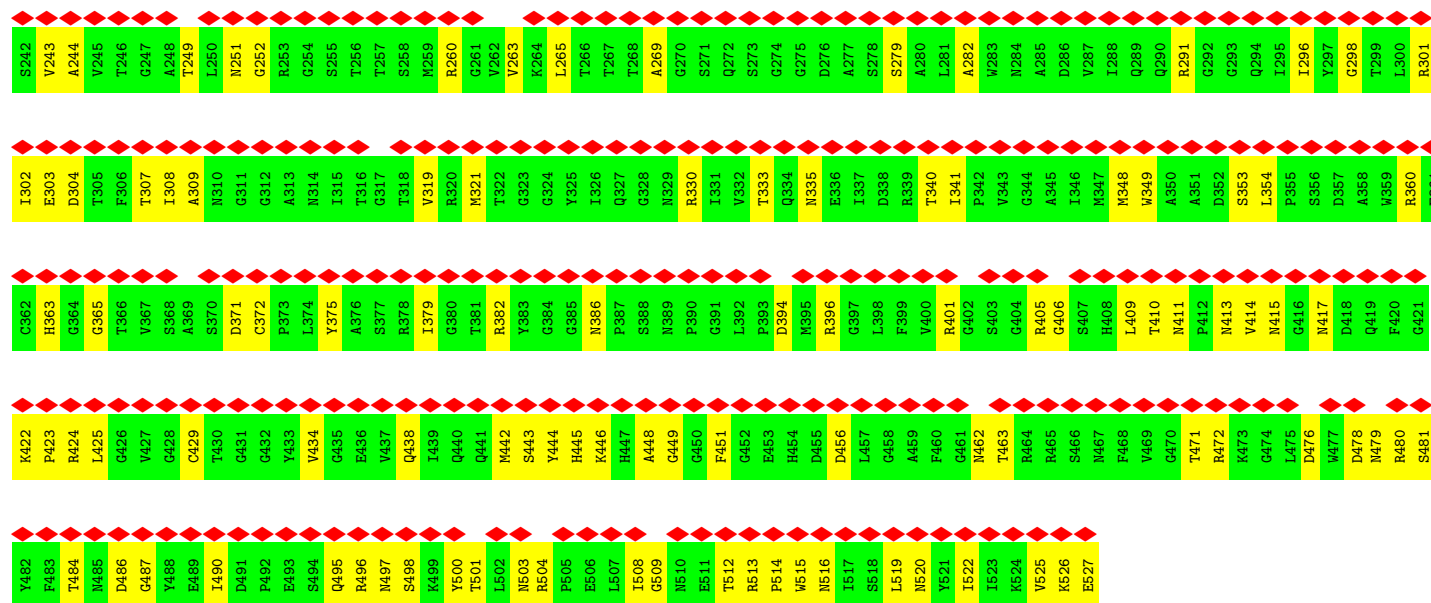




• Molecule 12: gp12, short tail fiber protein

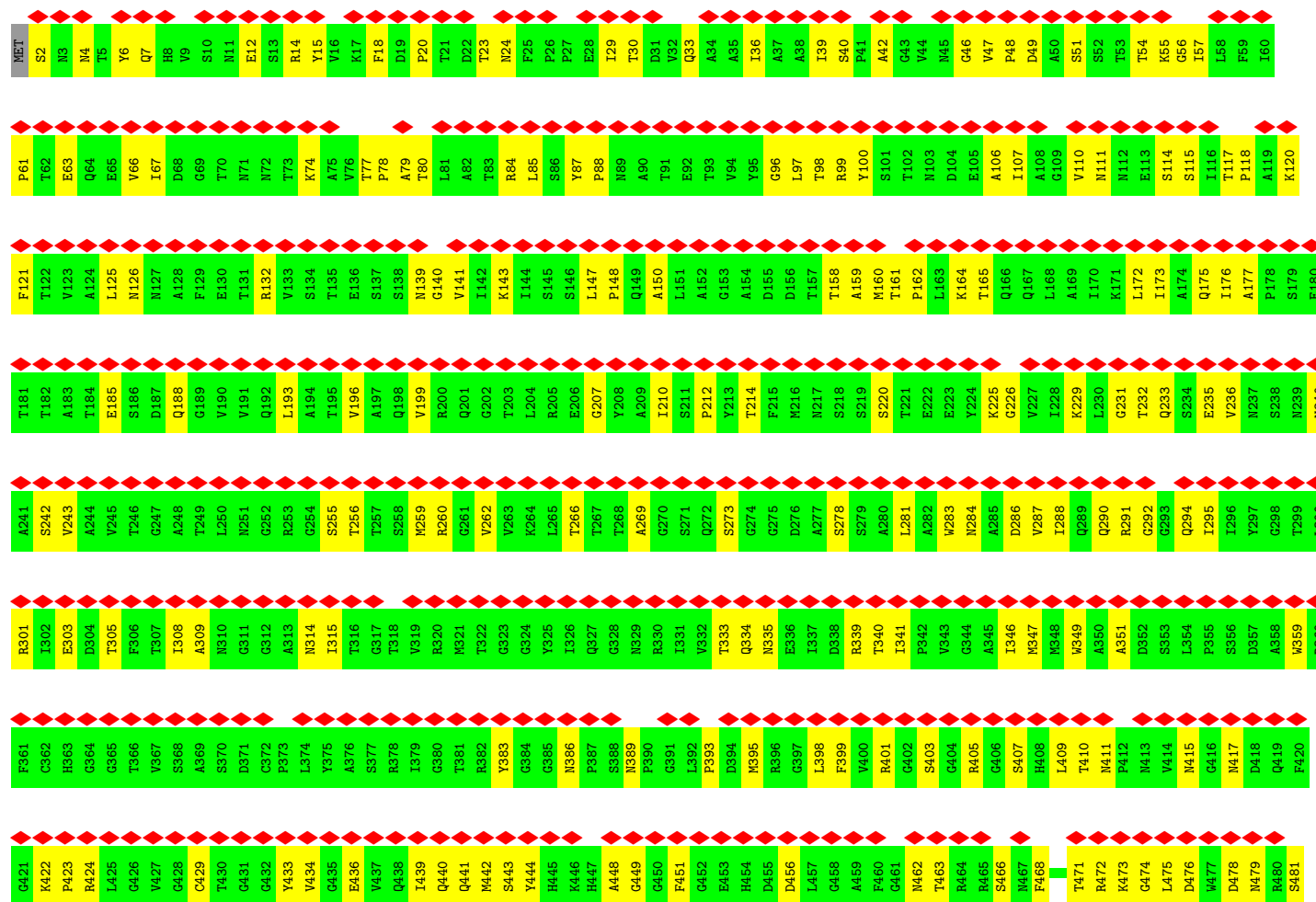


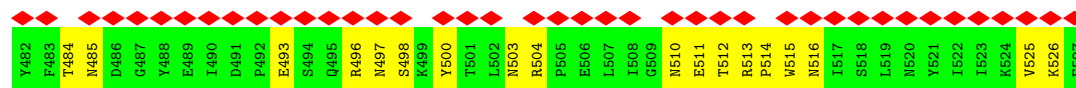




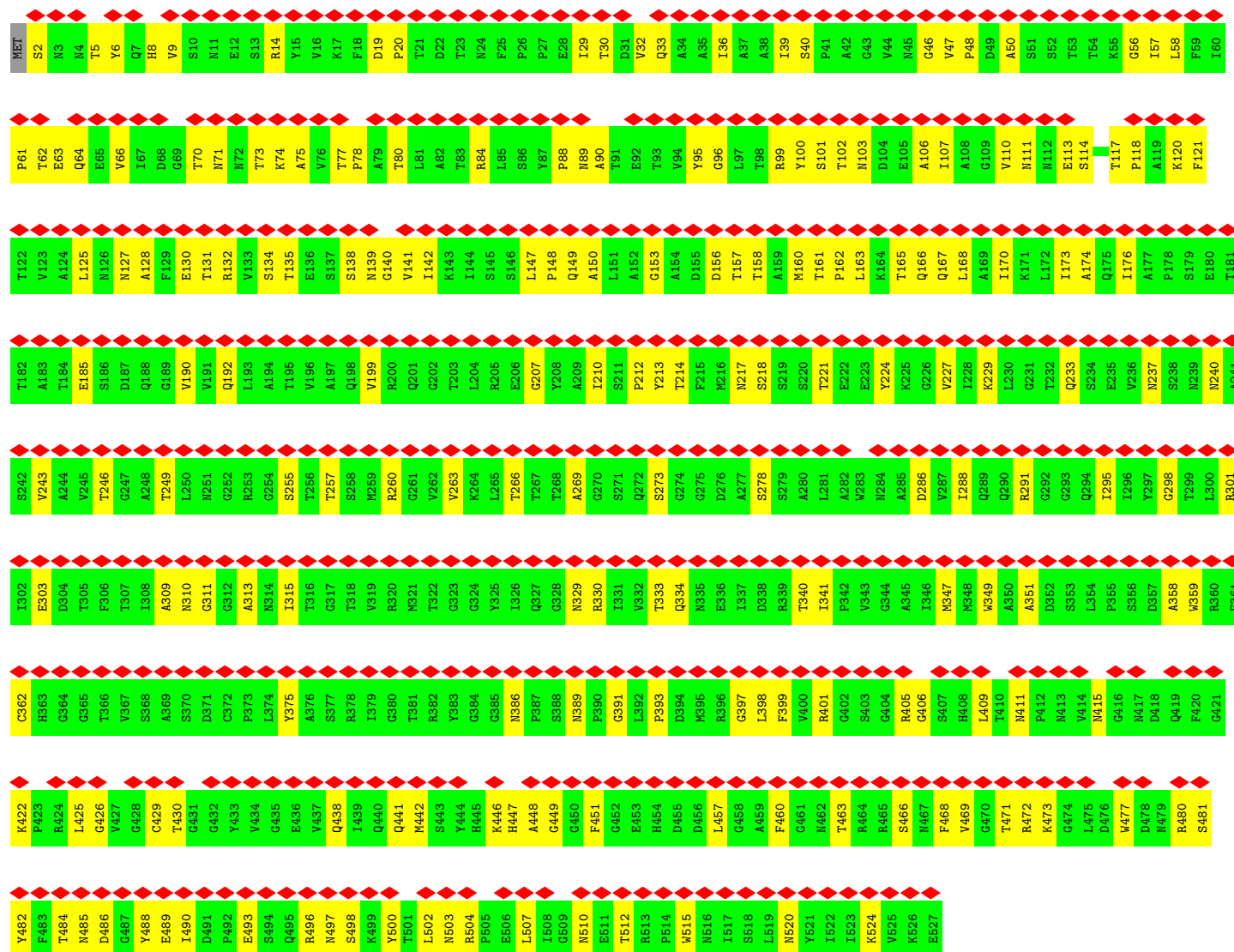
• Molecule 12: gp12, short tail fiber protein

Chain SO:

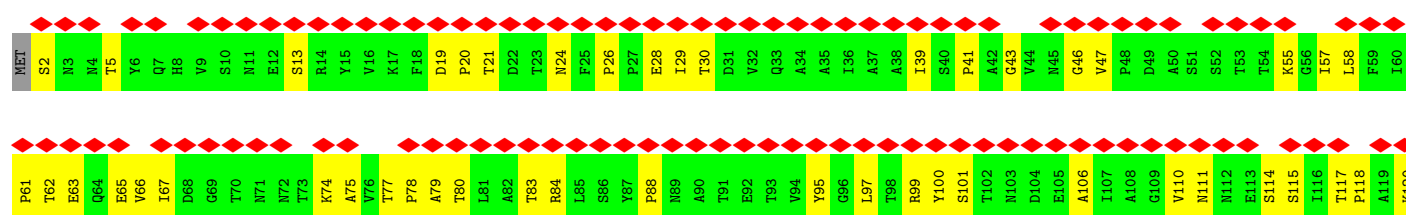


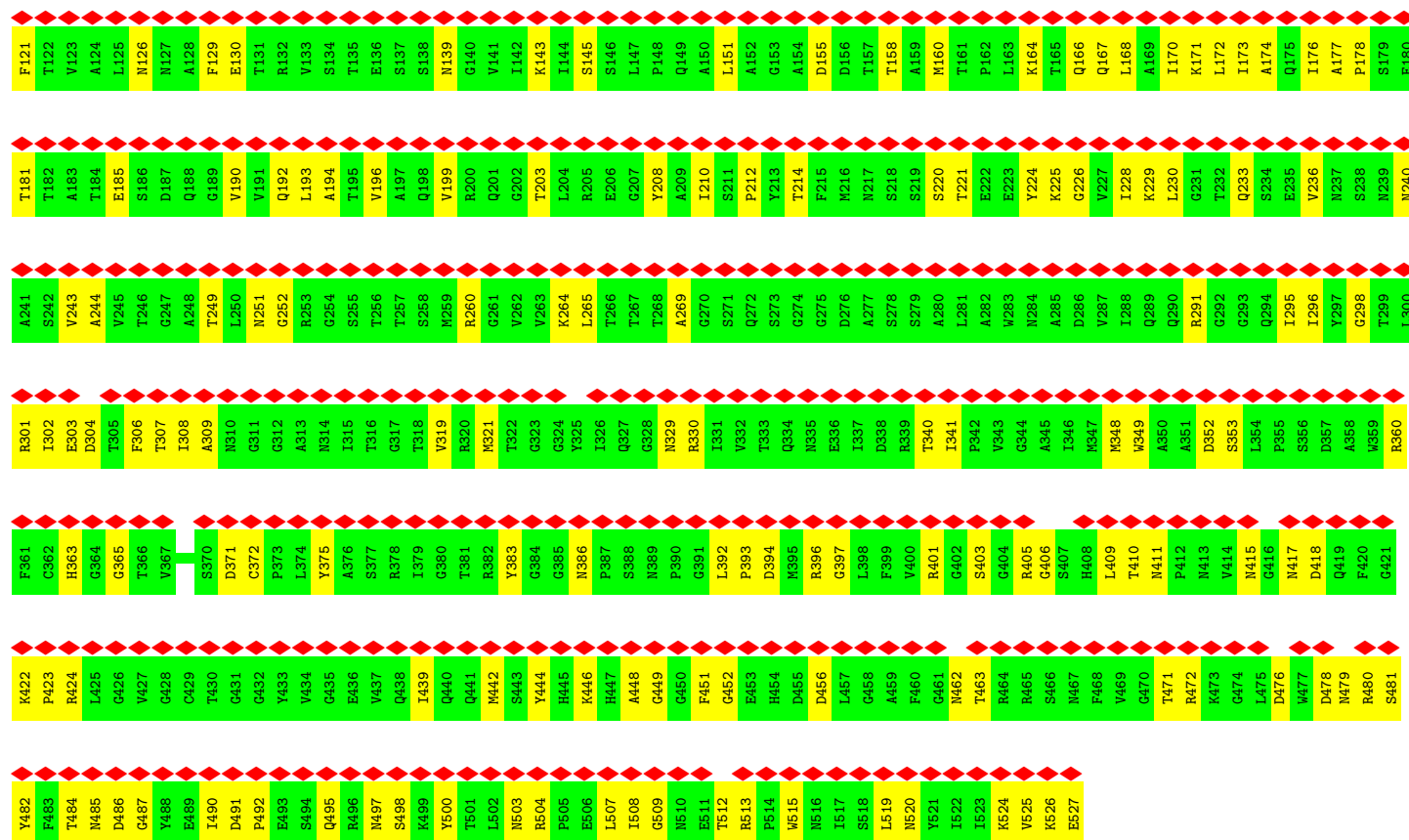


- Molecule 12: gp12, short tail fiber protein

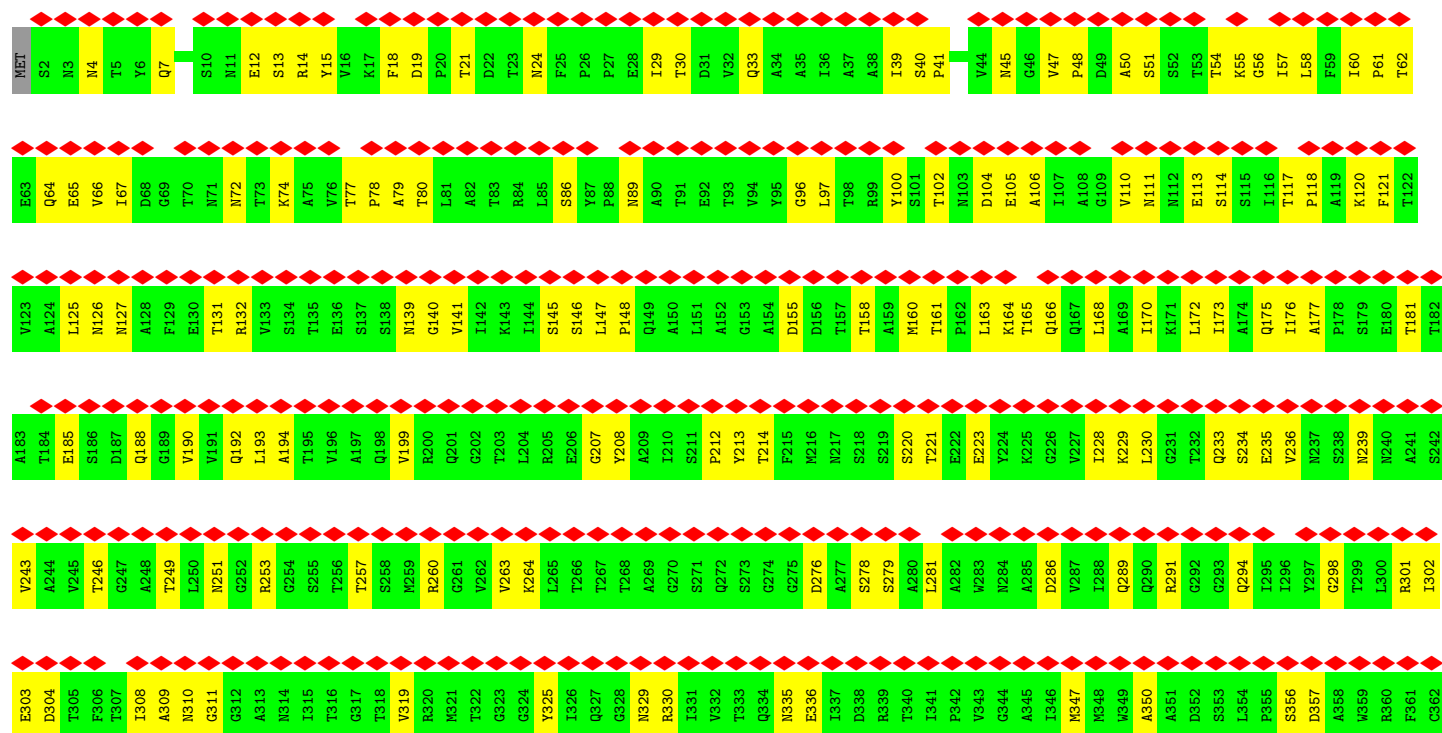


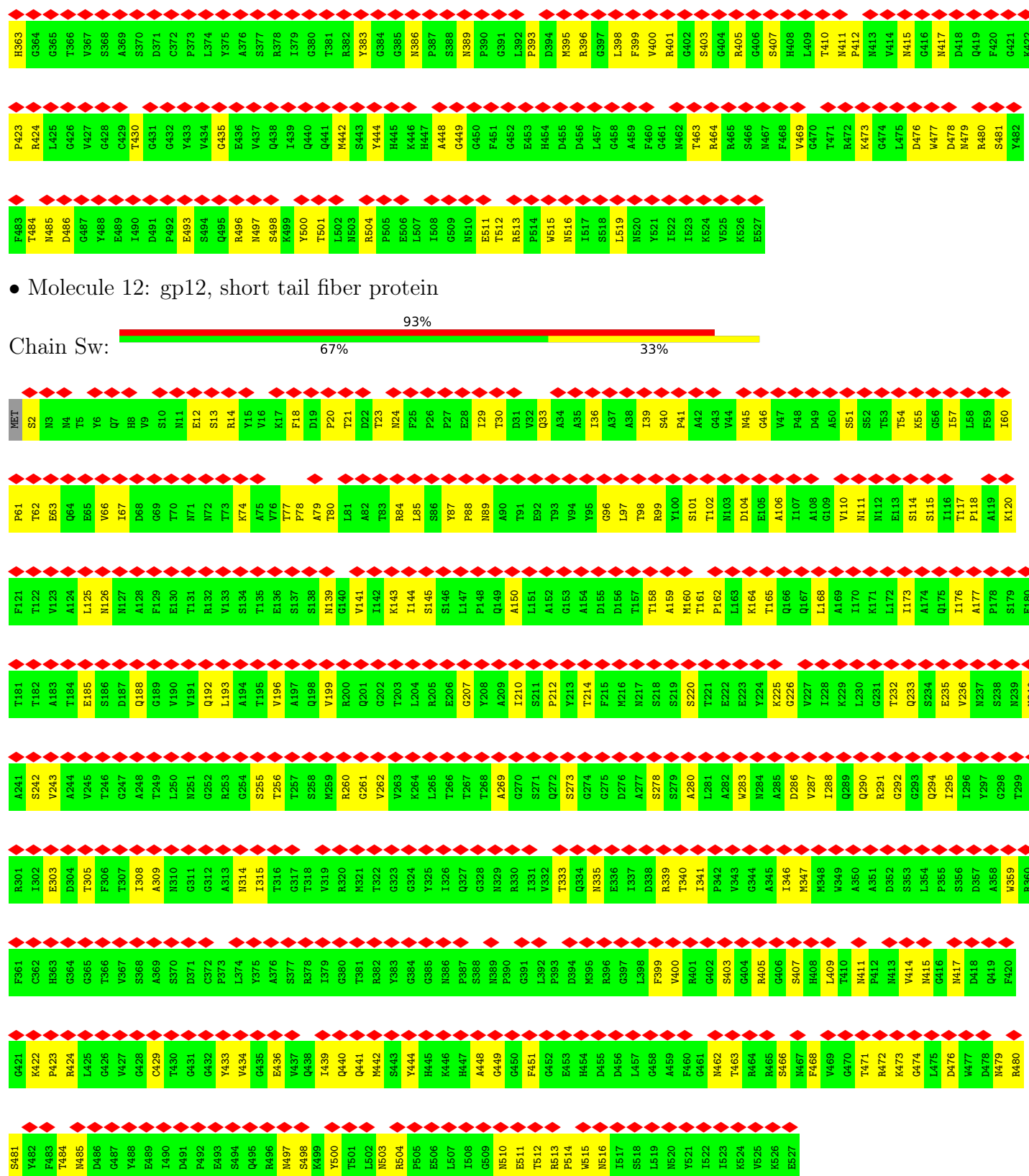
- Molecule 12: gp12, short tail fiber protein



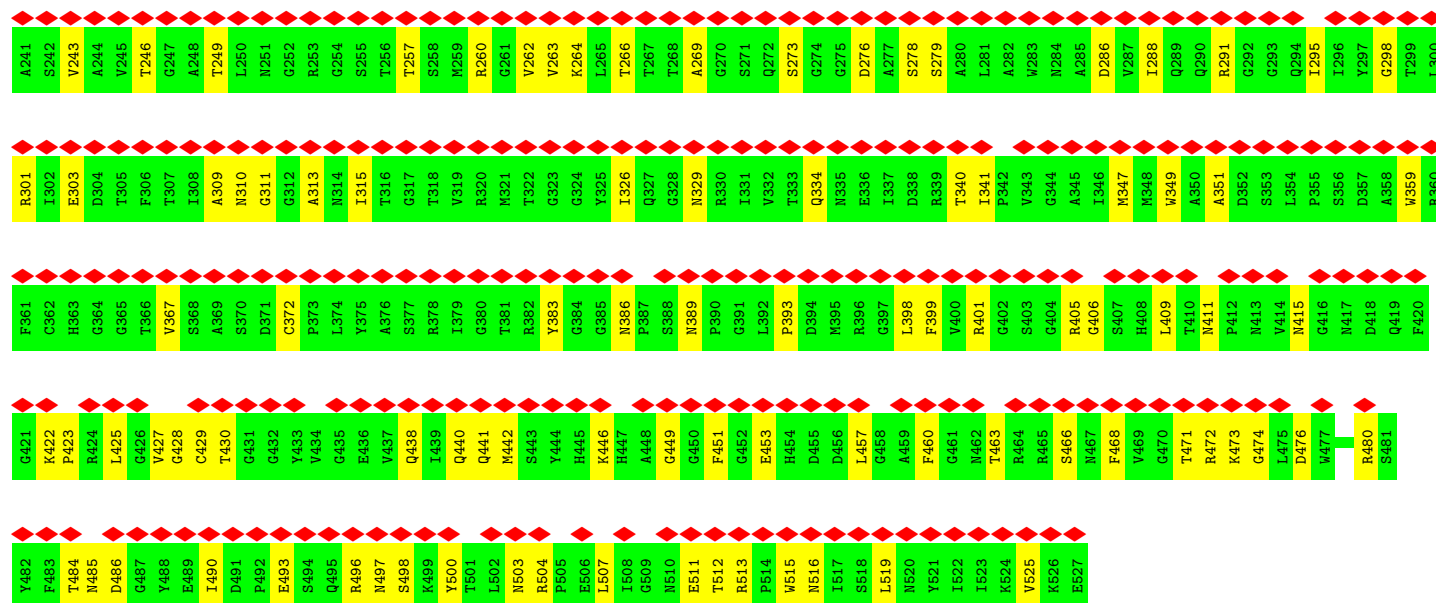


• Molecule 12: gp12, short tail fiber protein

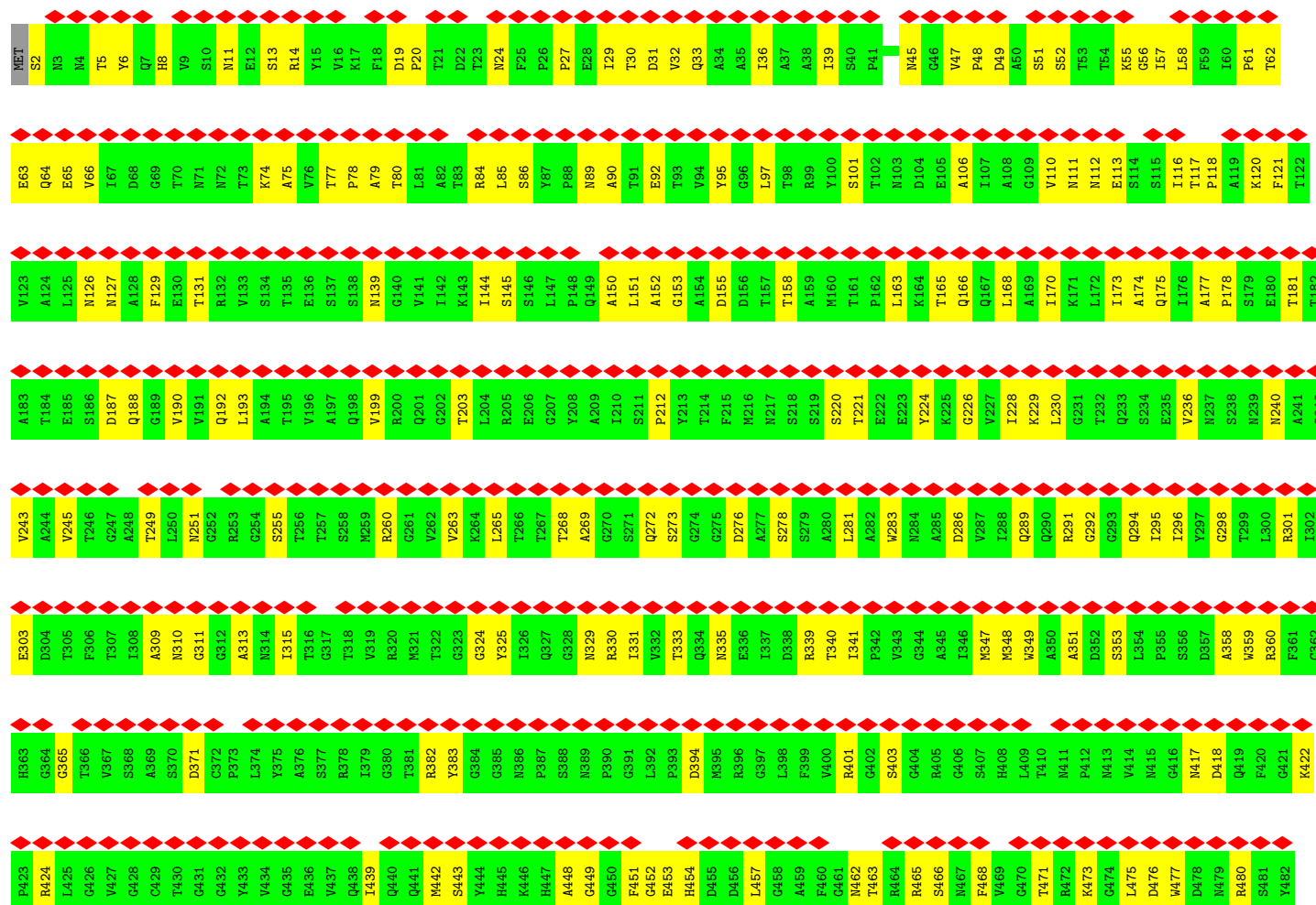


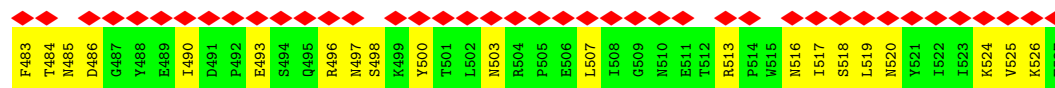


• Molecule 12: gp12, short tail fiber protein

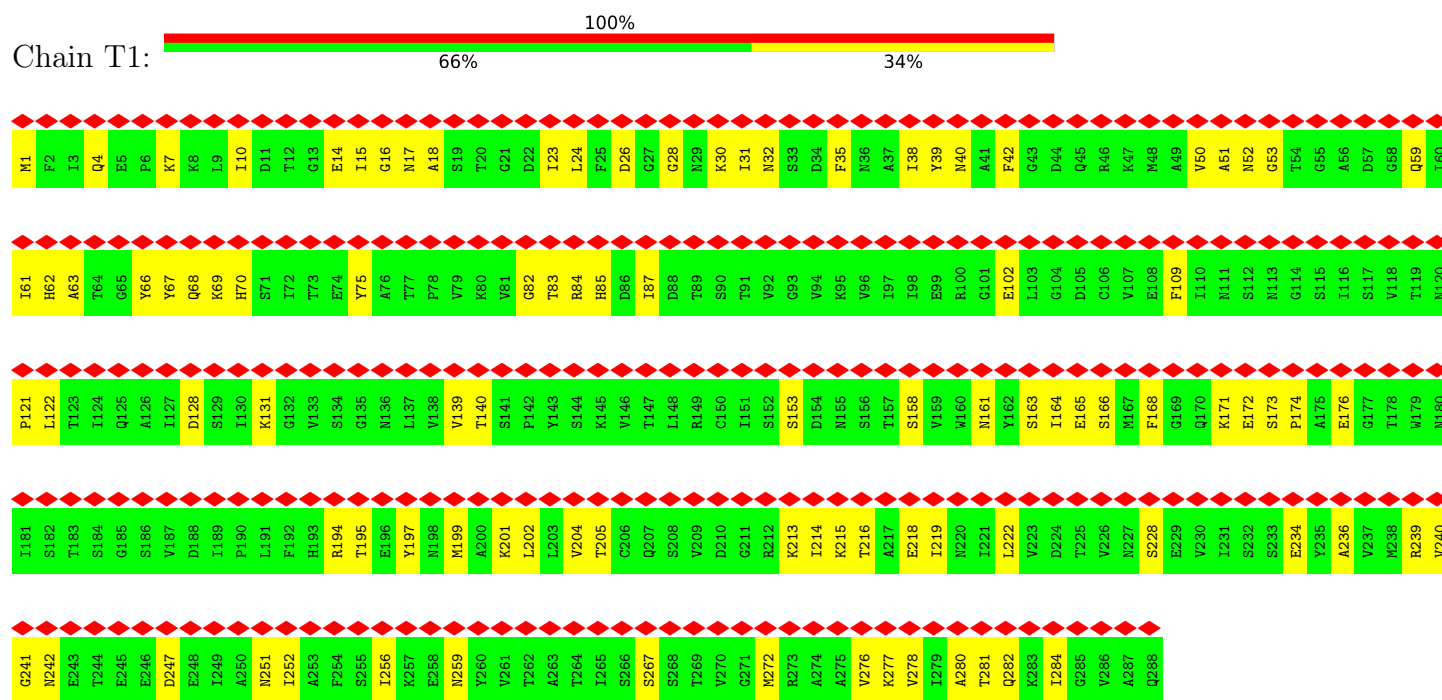


• Molecule 12: gp12, short tail fiber protein

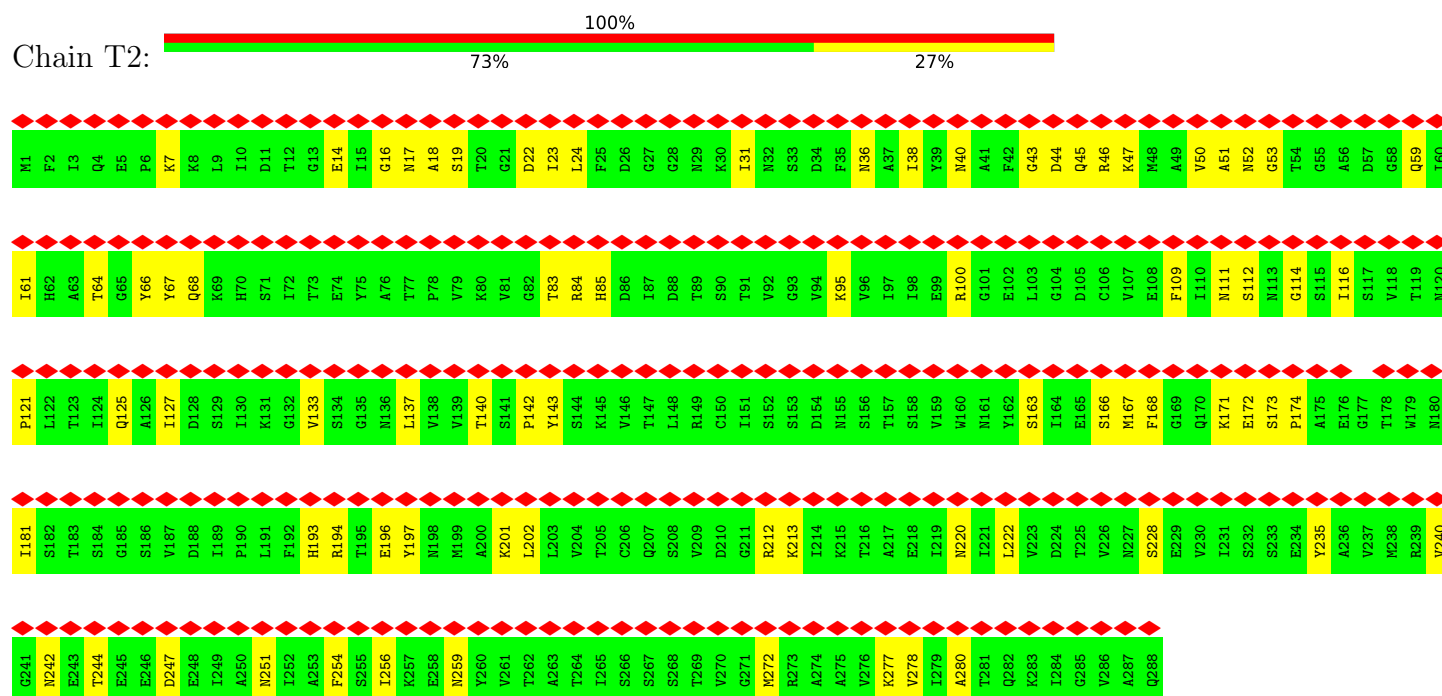




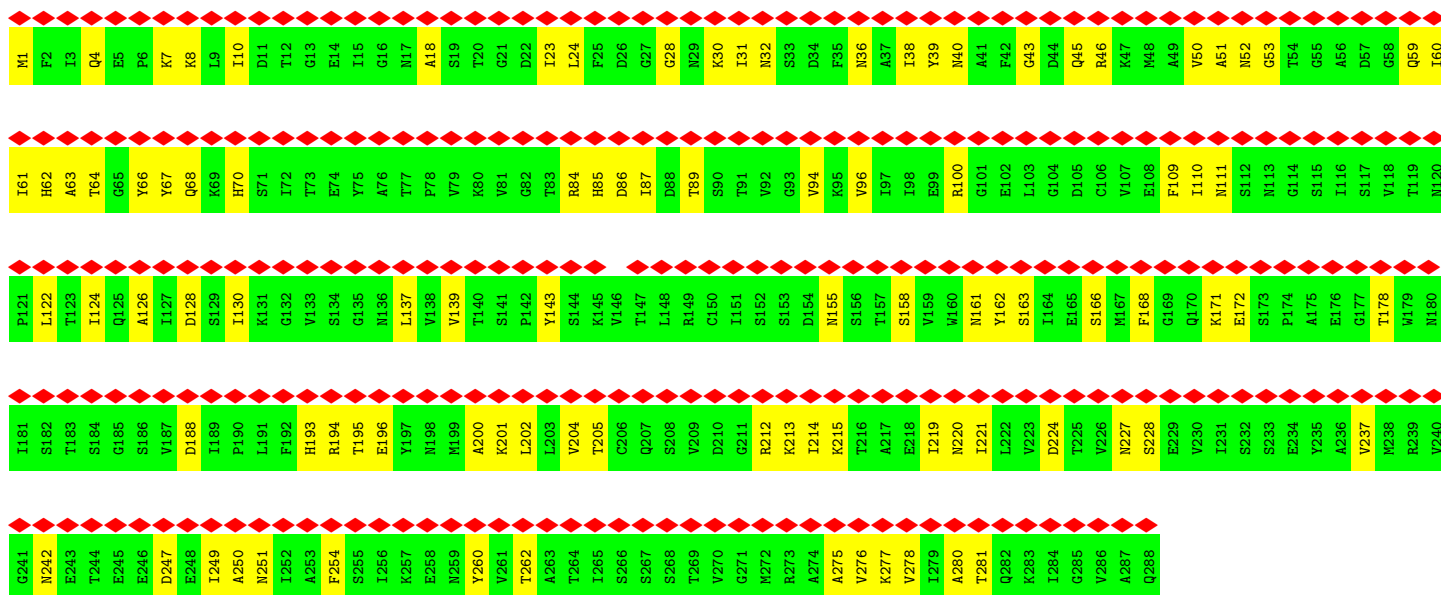
- Molecule 13: gp9, baseplate wedge tail fiber connector



- Molecule 13: gp9, baseplate wedge tail fiber connector

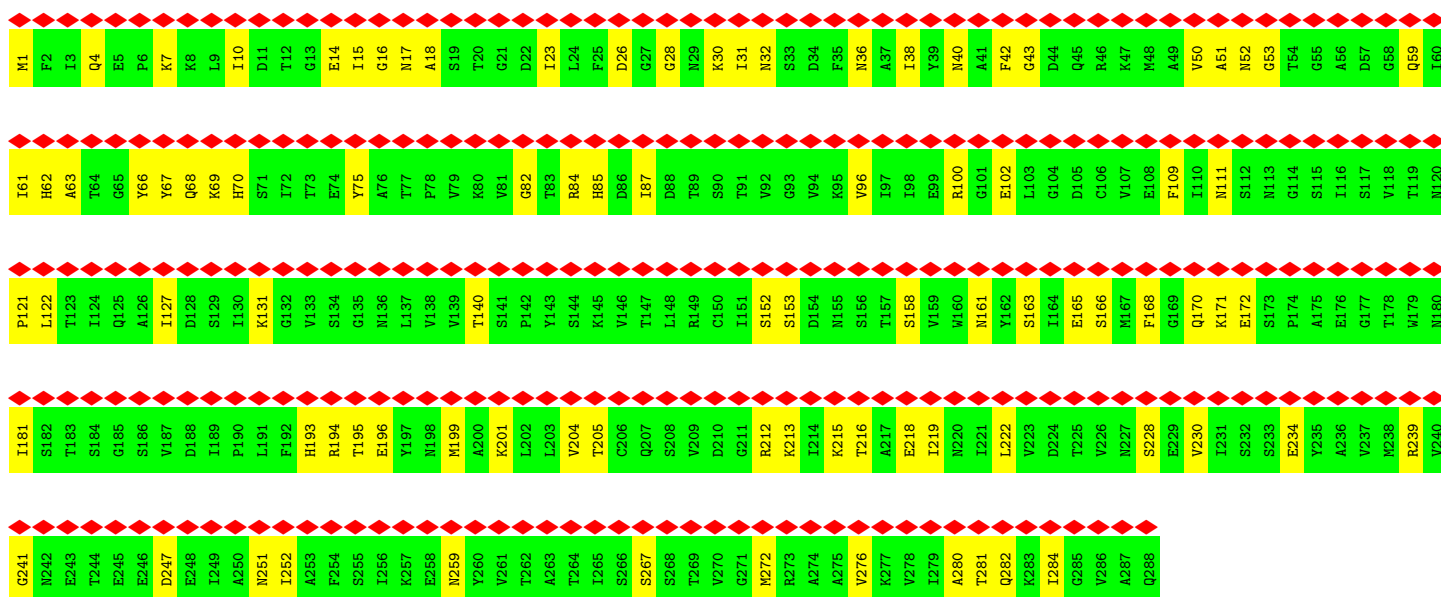


- Molecule 13: gp9, baseplate wedge tail fiber connector



• Molecule 13: gp9, baseplate wedge tail fiber connector

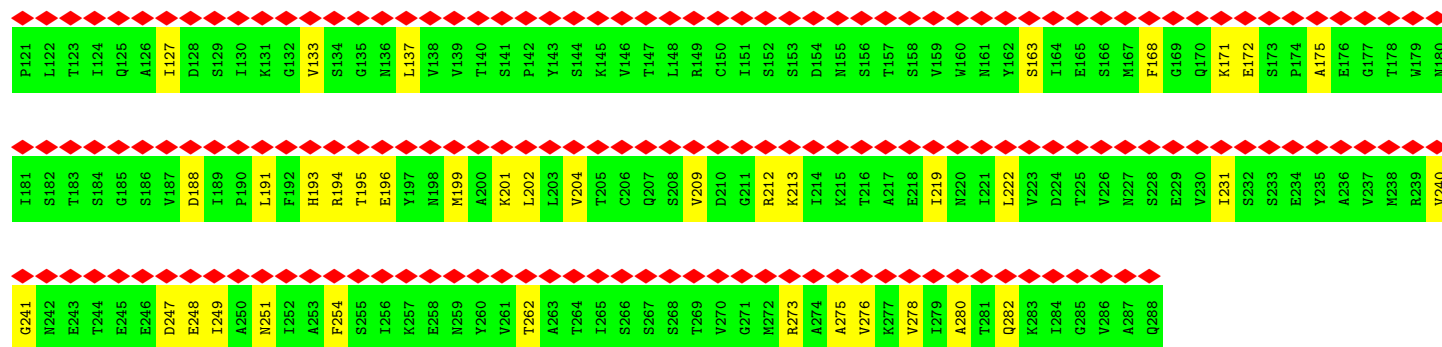
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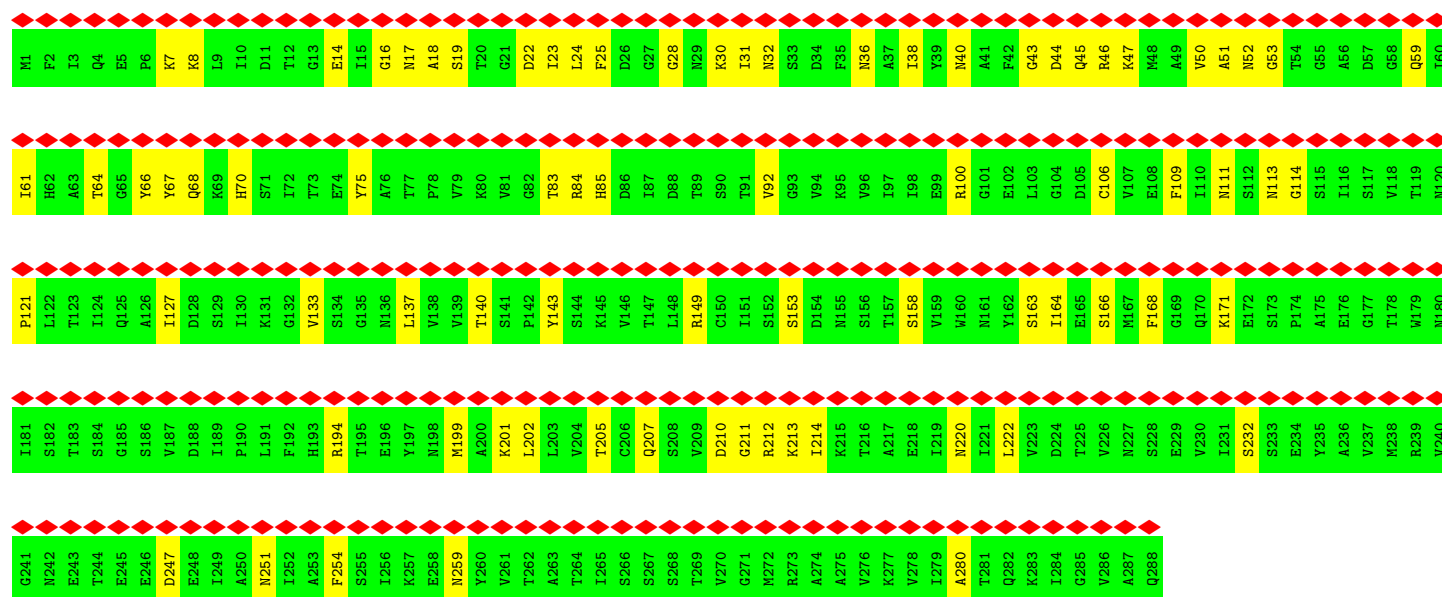
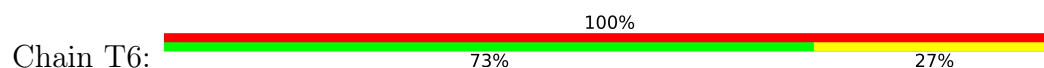
• Molecule 13: gp9, baseplate wedge tail fiber connector

Chain T5:

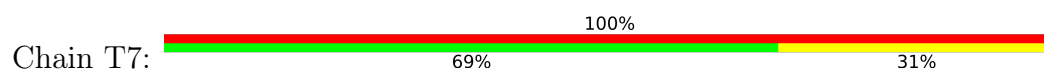




• Molecule 13: gp9, baseplate wedge tail fiber connector

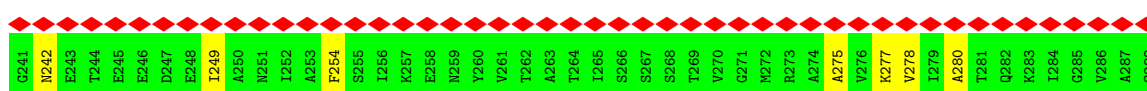
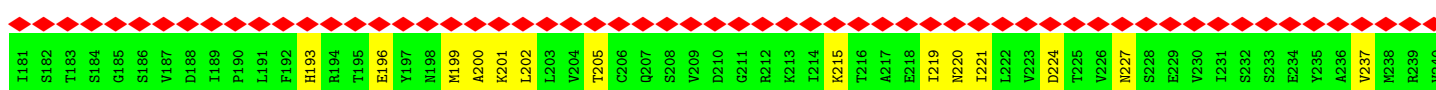
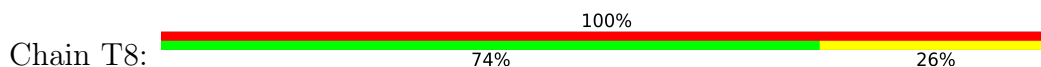


• Molecule 13: gp9, baseplate wedge tail fiber connector

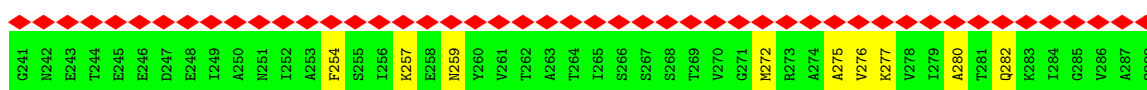
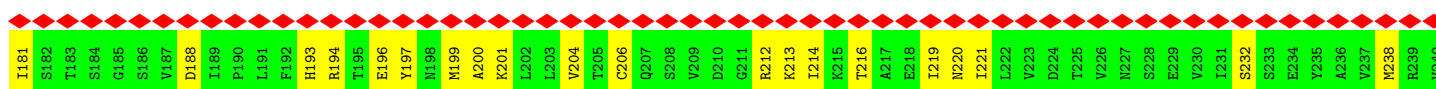
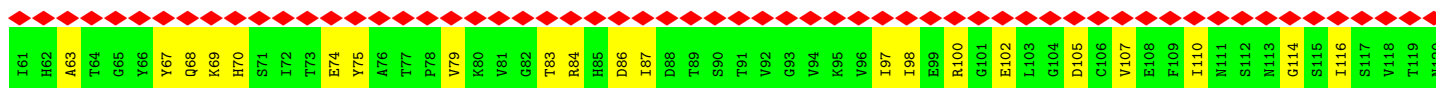
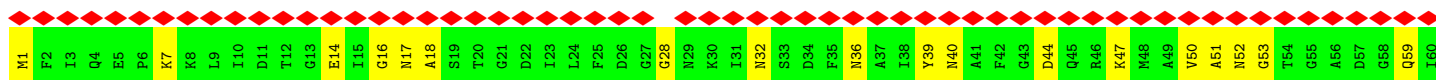




- Molecule 13: gp9, baseplate wedge tail fiber connector

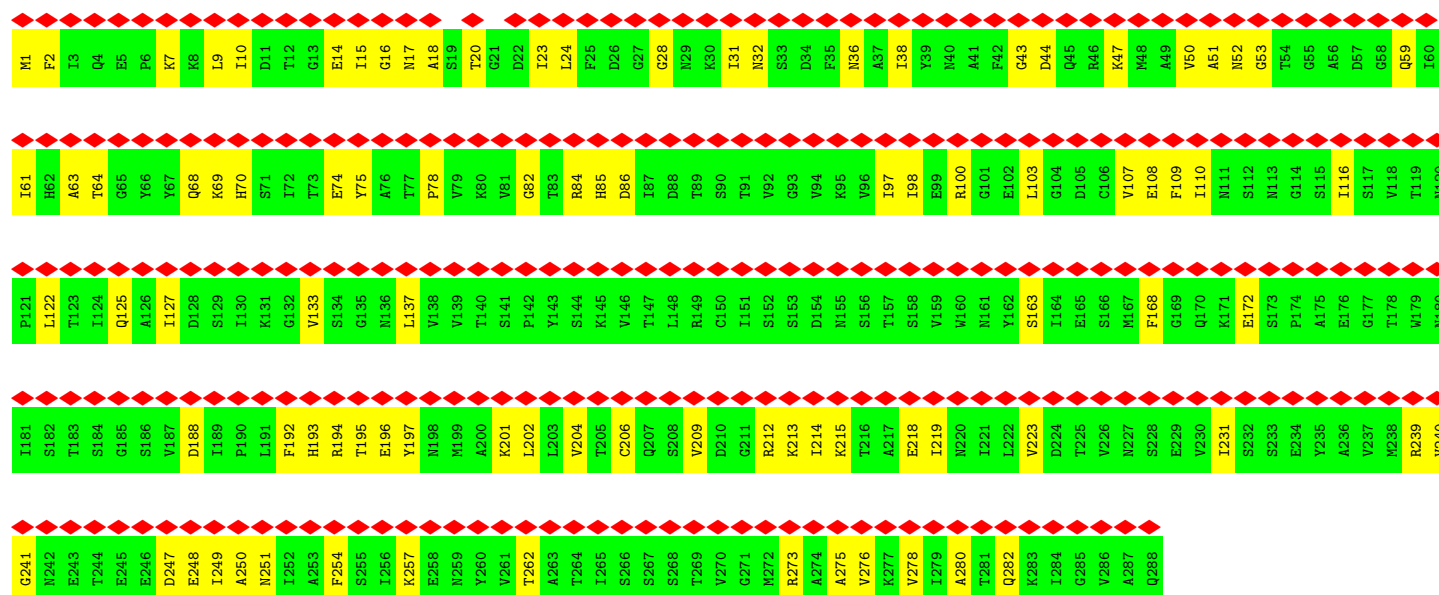


- Molecule 13: gp9, baseplate wedge tail fiber connector

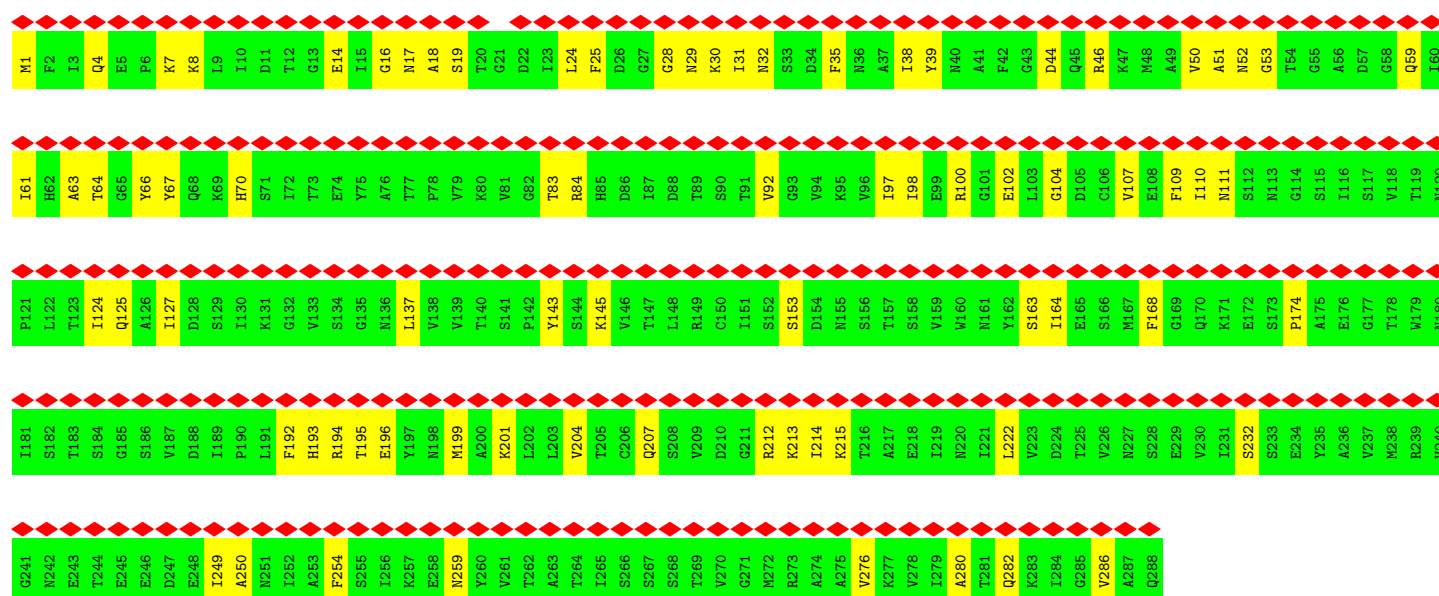
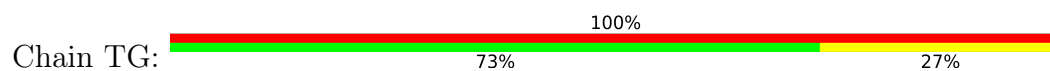


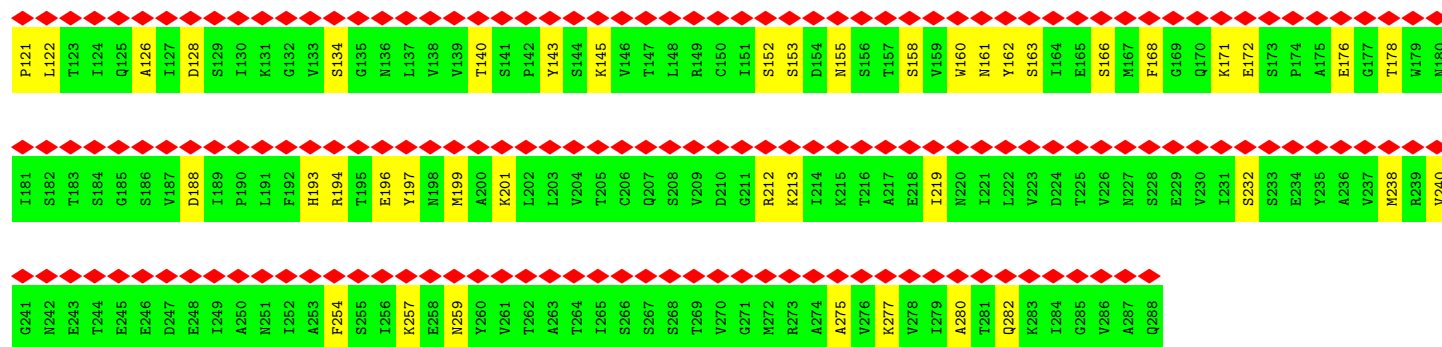
- Molecule 13: gp9, baseplate wedge tail fiber connector



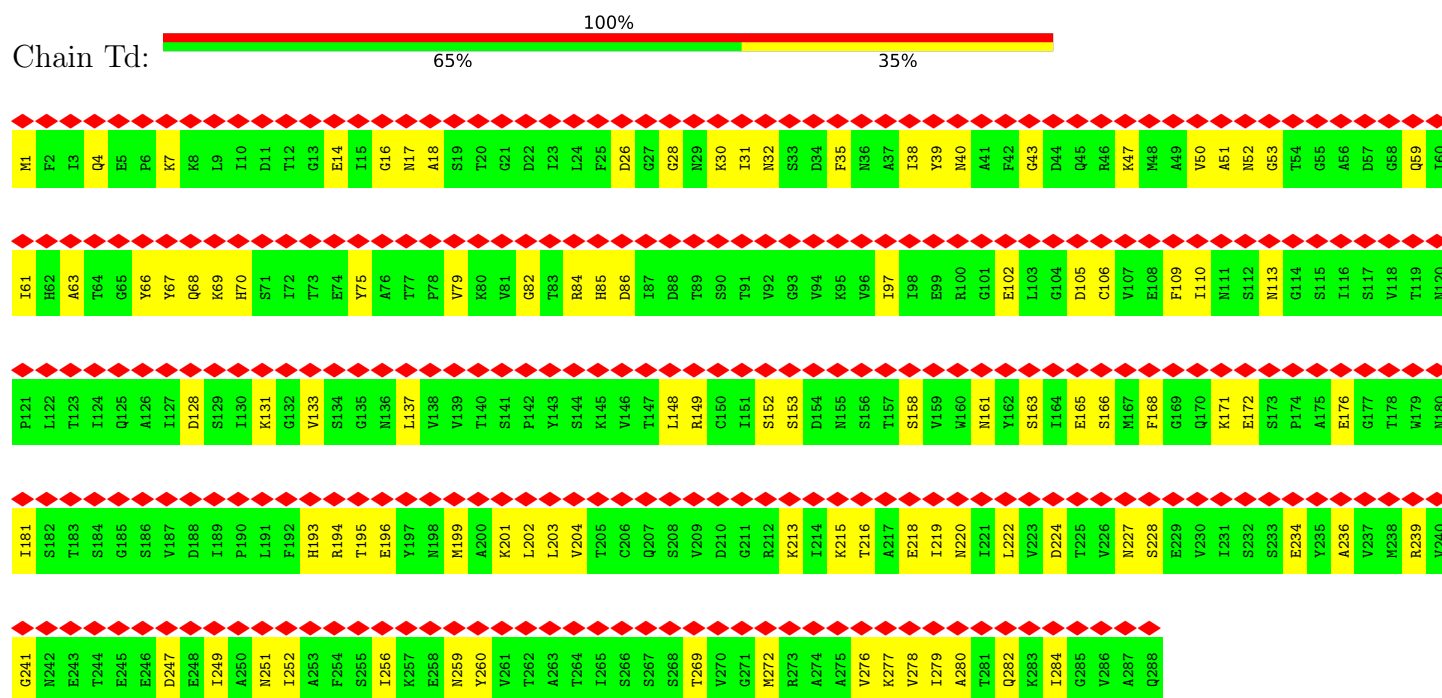


- Molecule 13: gp9, baseplate wedge tail fiber connector

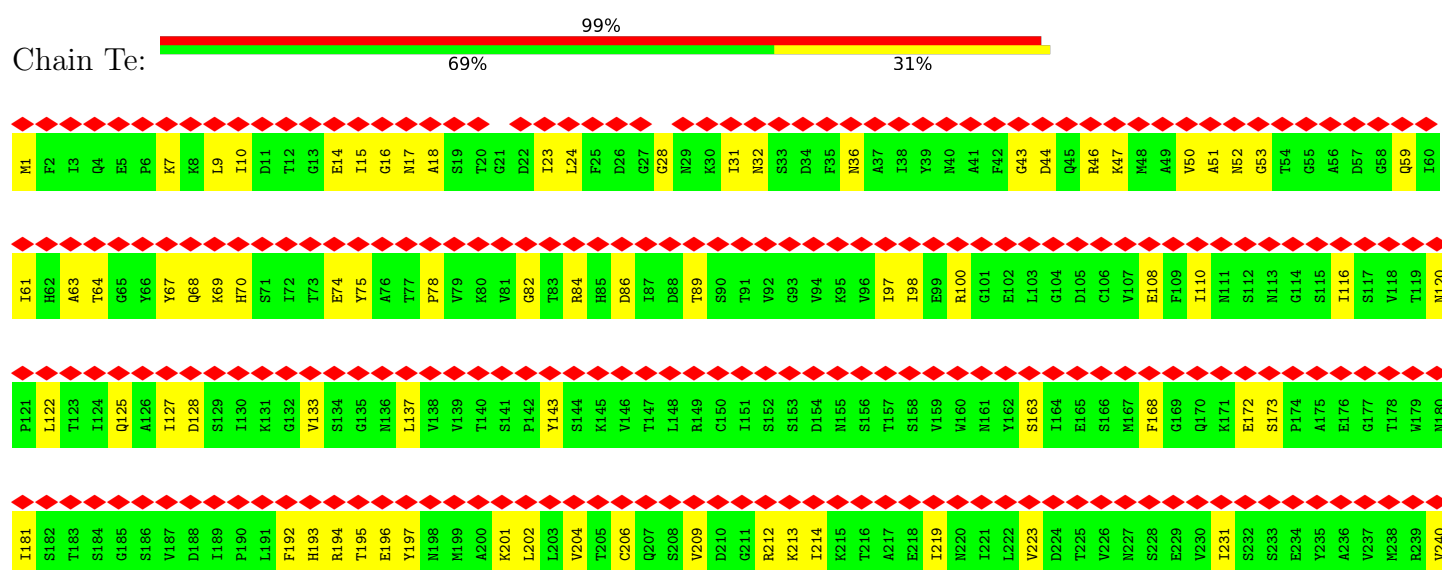




- Molecule 13: gp9, baseplate wedge tail fiber connector

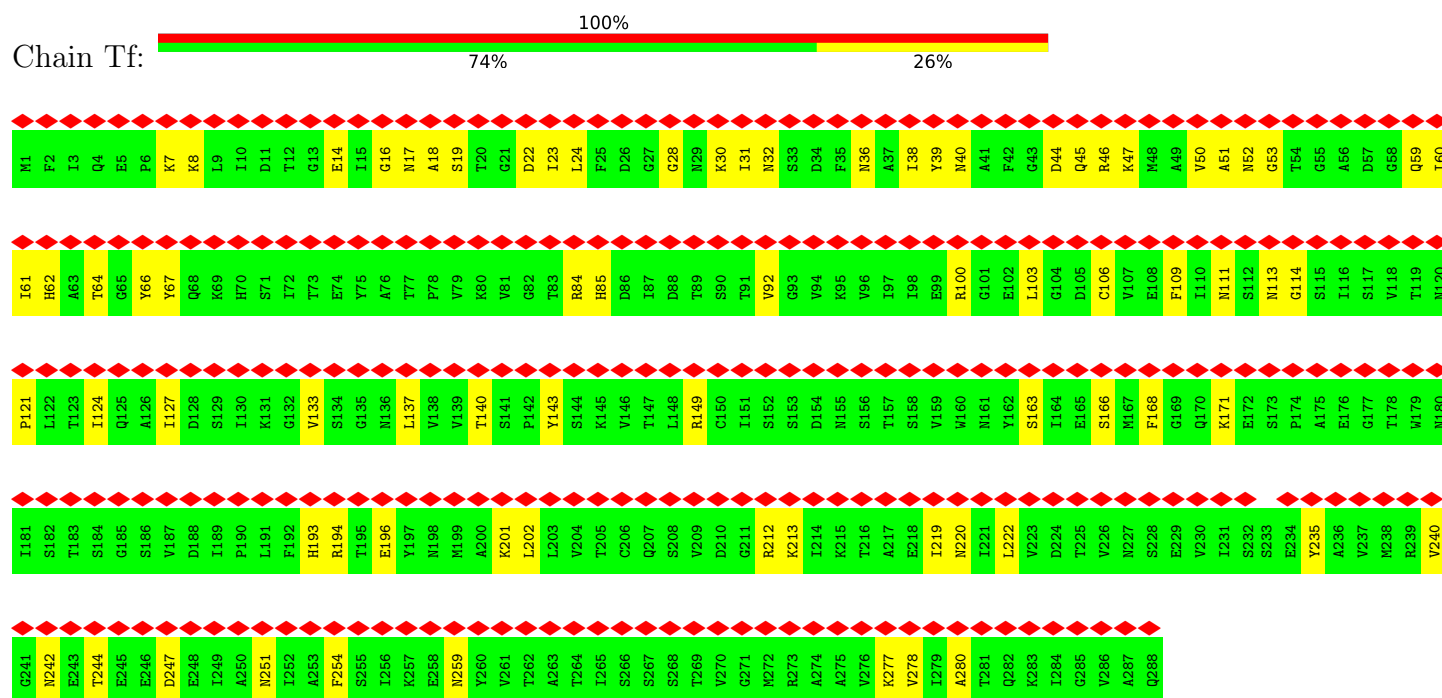


- Molecule 13: gp9, baseplate wedge tail fiber connector

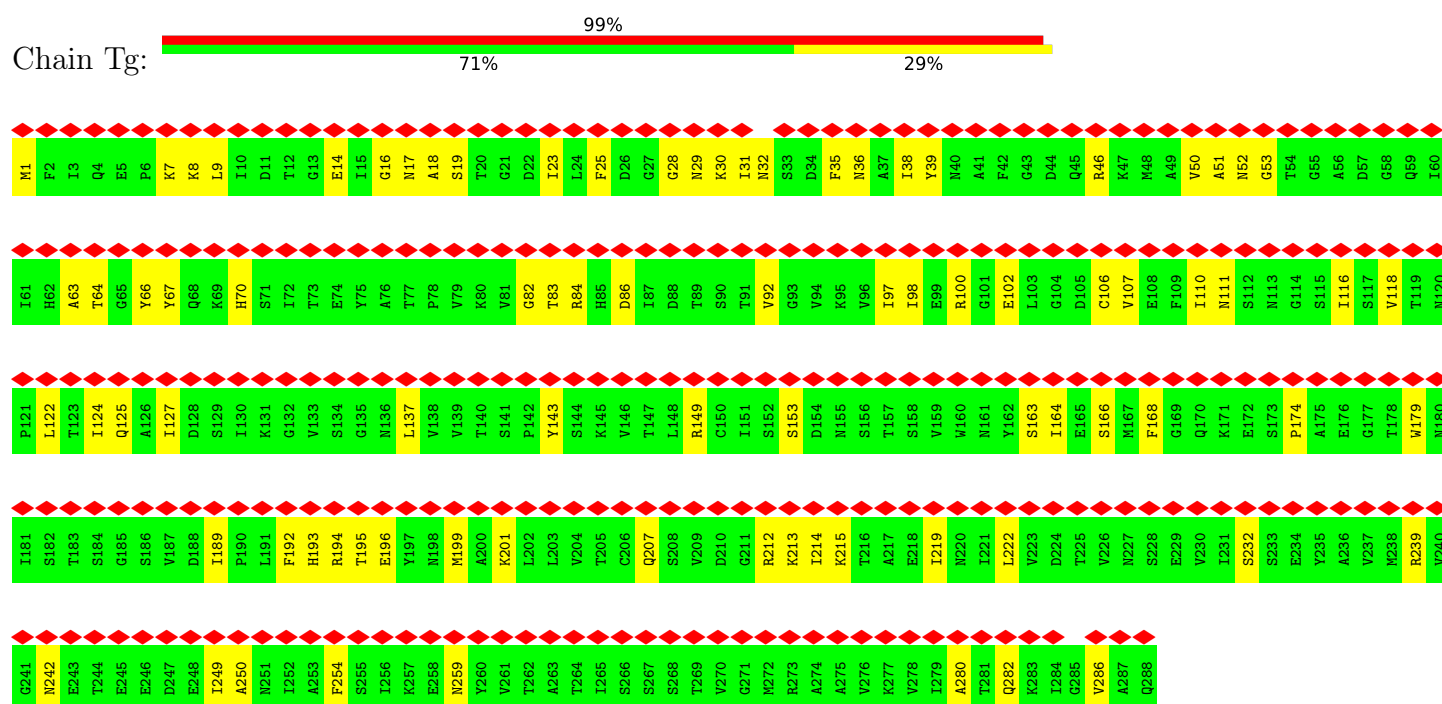




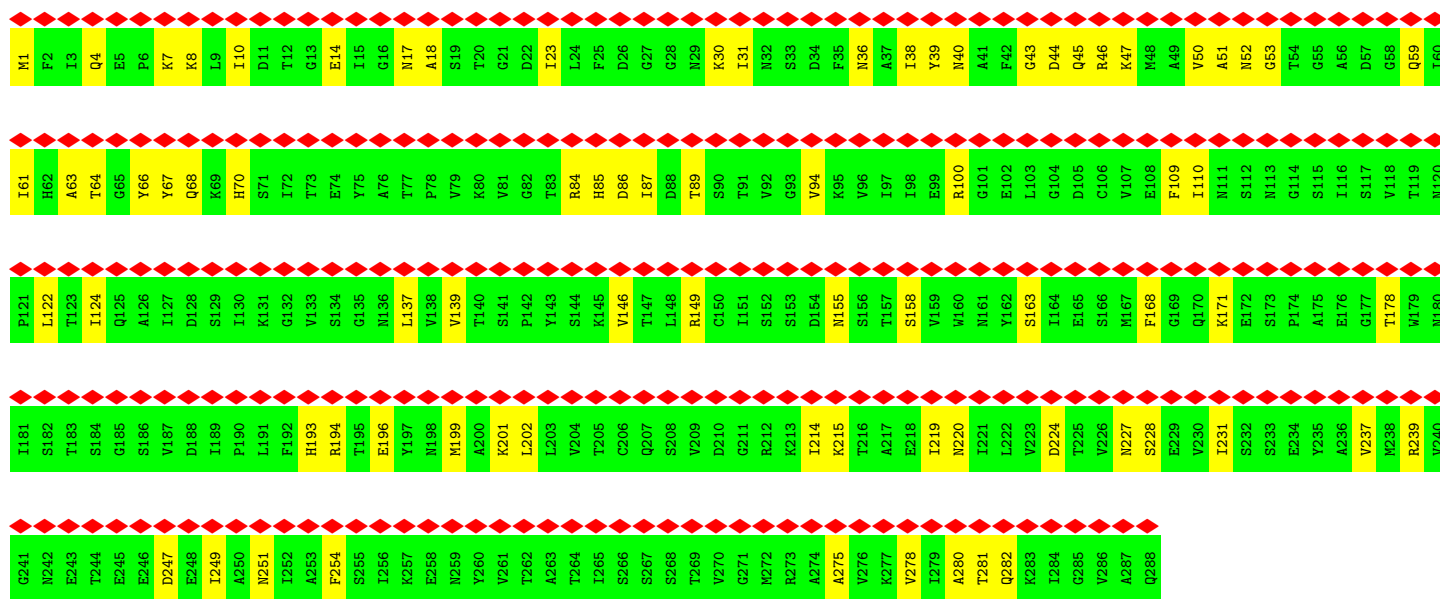
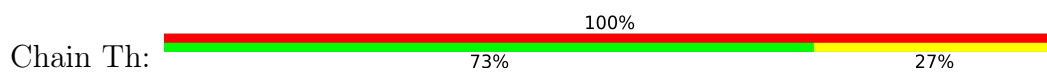
- Molecule 13: gp9, baseplate wedge tail fiber connector



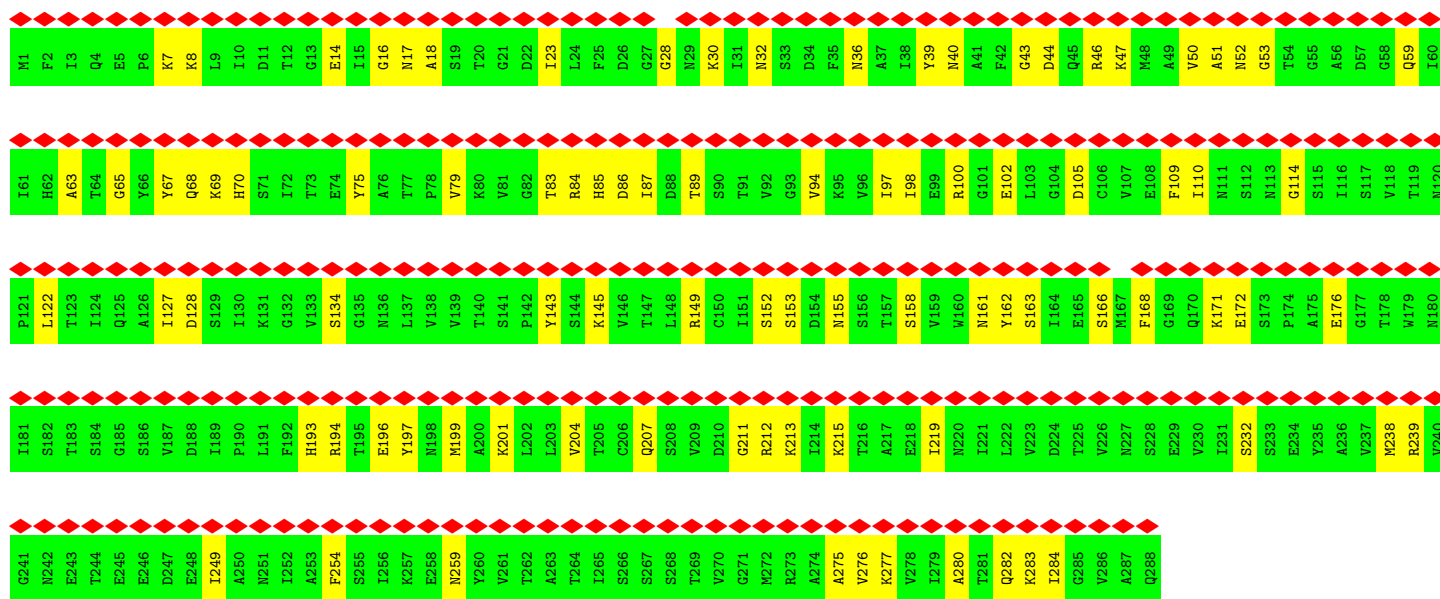
- Molecule 13: gp9, baseplate wedge tail fiber connector



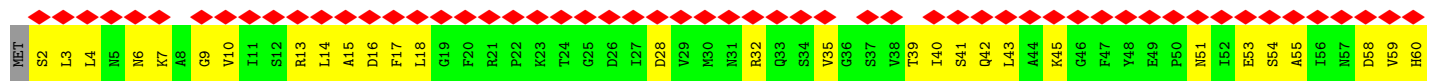
- Molecule 13: gp9, baseplate wedge tail fiber connector

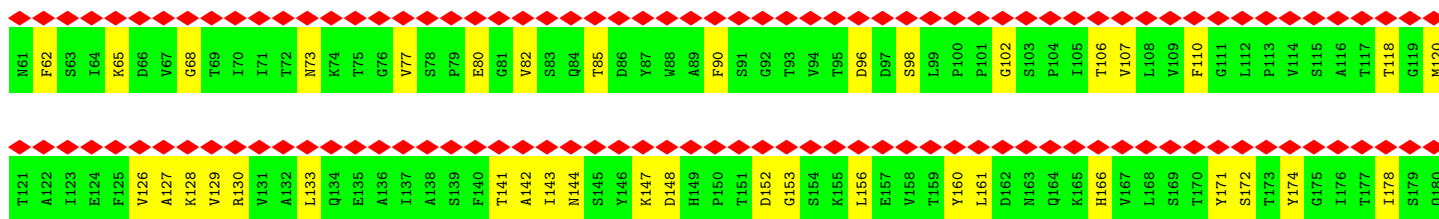


• Molecule 13: gp9, baseplate wedge tail fiber connector

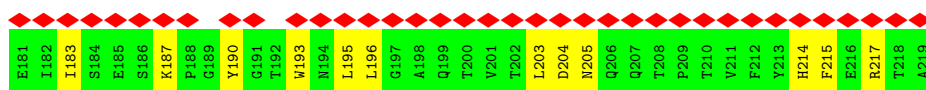
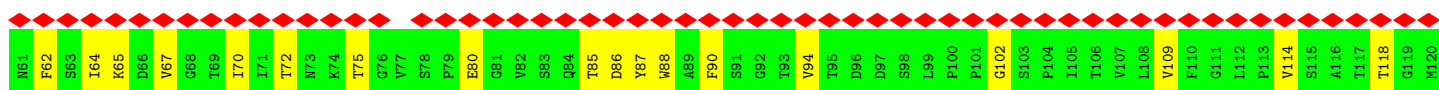
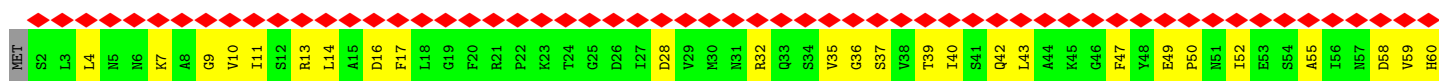


• Molecule 14: gp11, baseplate wedge protein





• Molecule 14: gp11, baseplate wedge protein

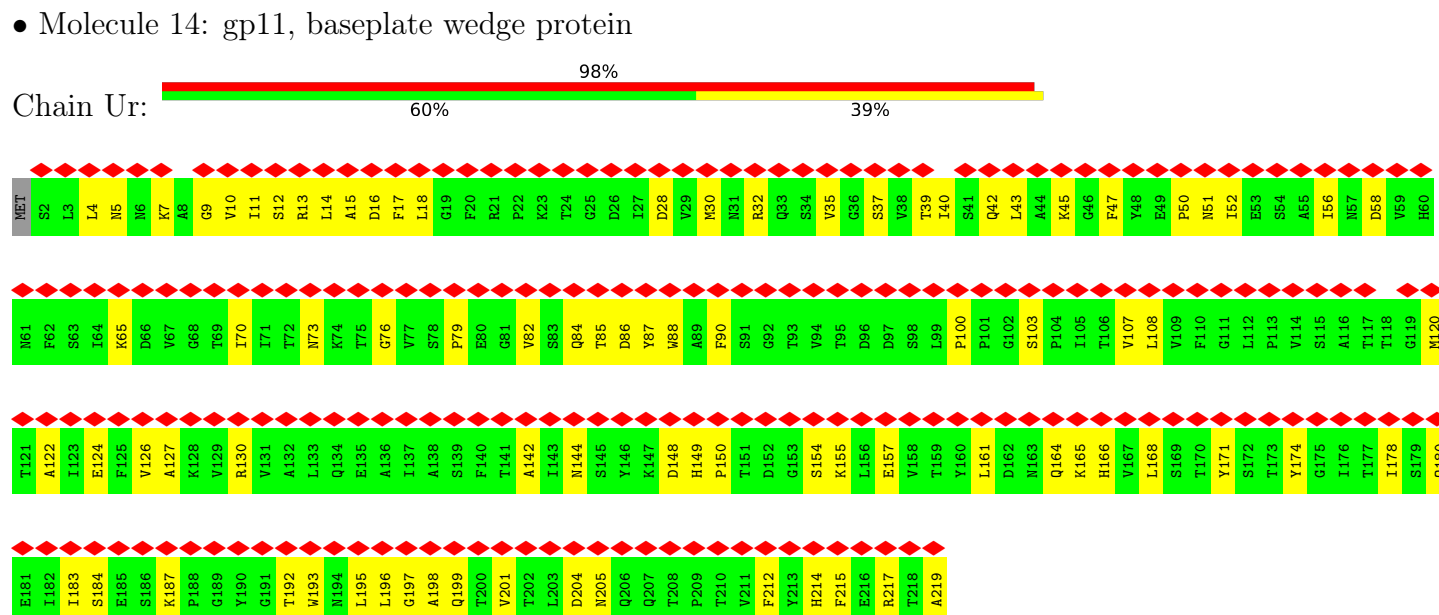
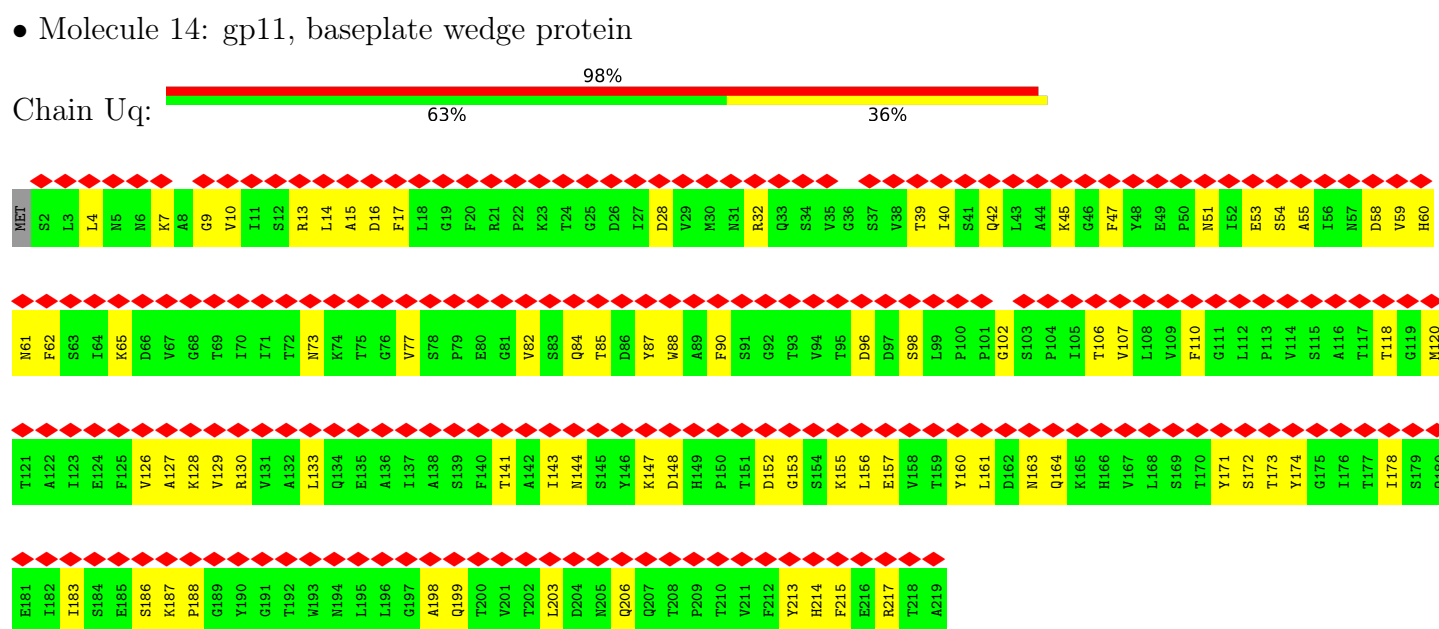
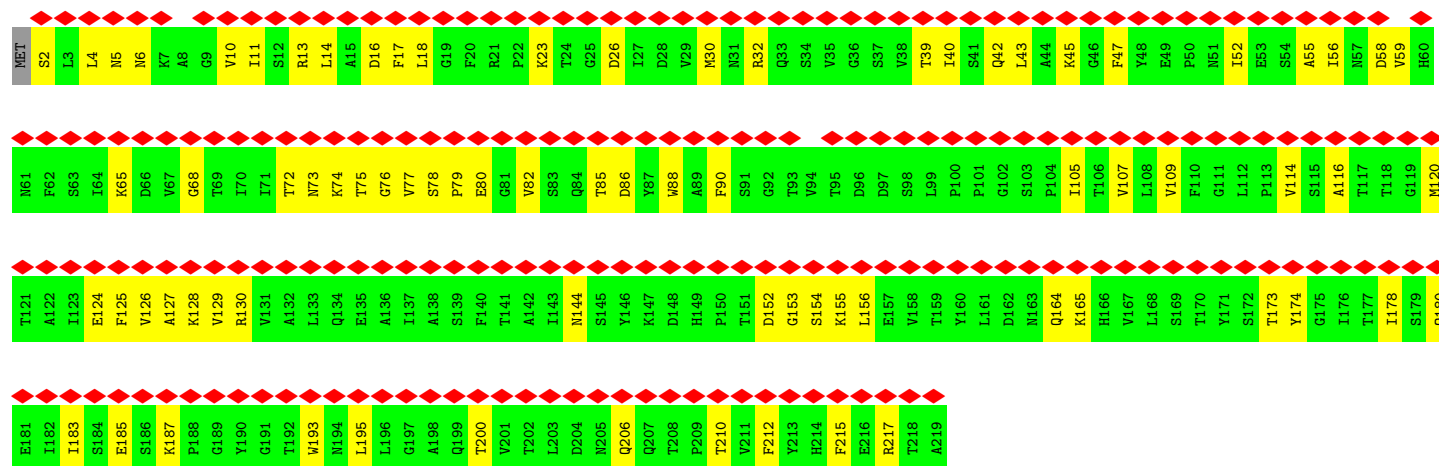


• Molecule 14: gp11, baseplate wedge protein

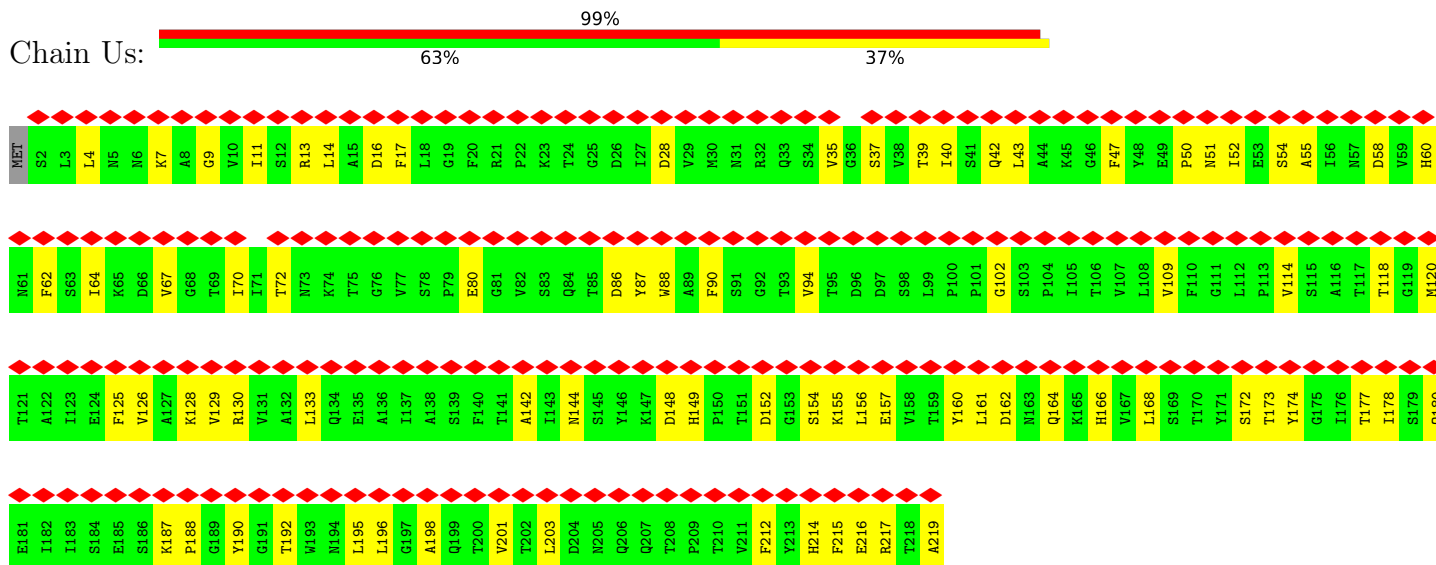


• Molecule 14: gp11, baseplate wedge protein

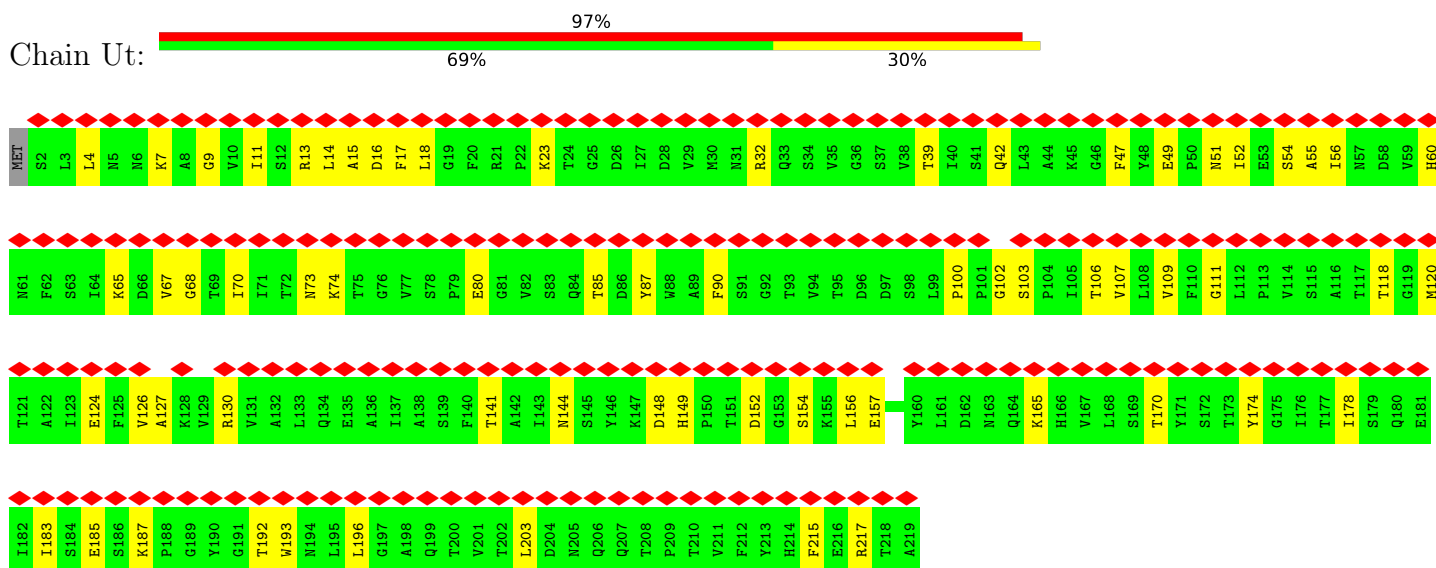




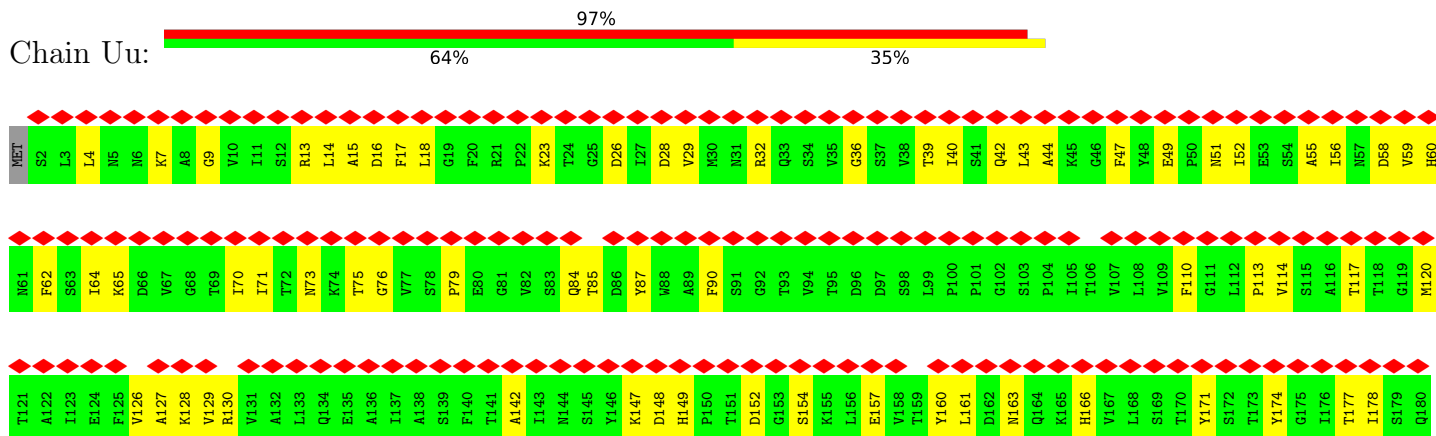
- Molecule 14: gp11, baseplate wedge protein



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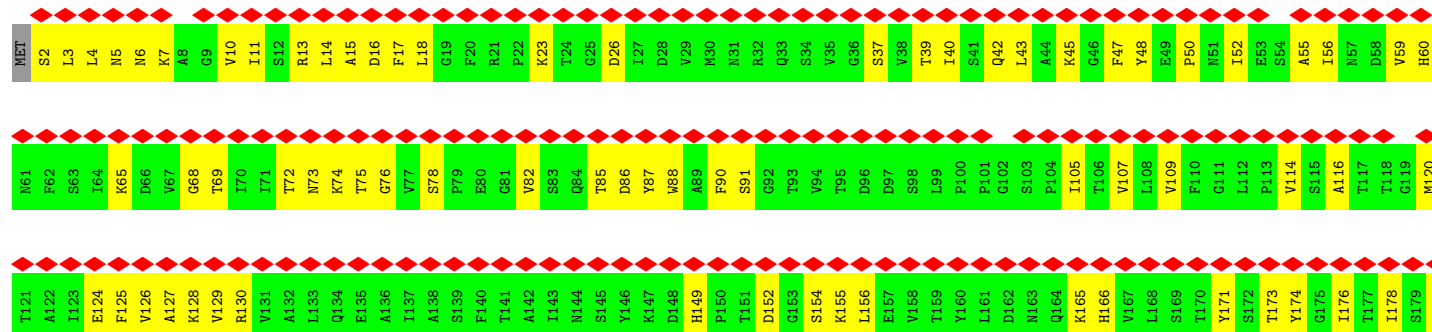


- Molecule 14: gp11, baseplate wedge protein





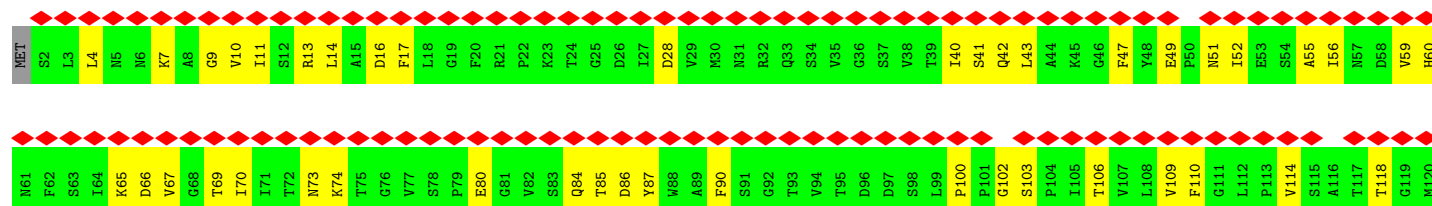
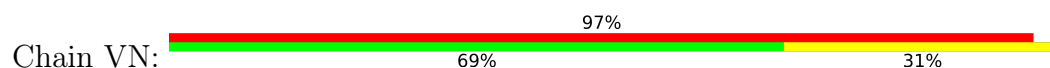
- Molecule 14: gp11, baseplate wedge protein

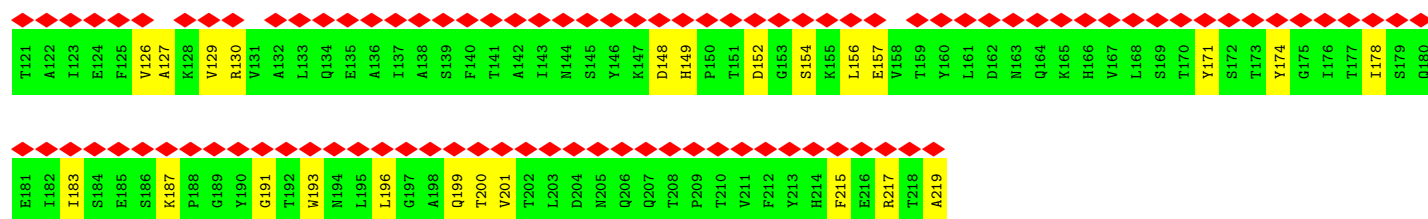


- Molecule 14: gp11, baseplate wedge protein

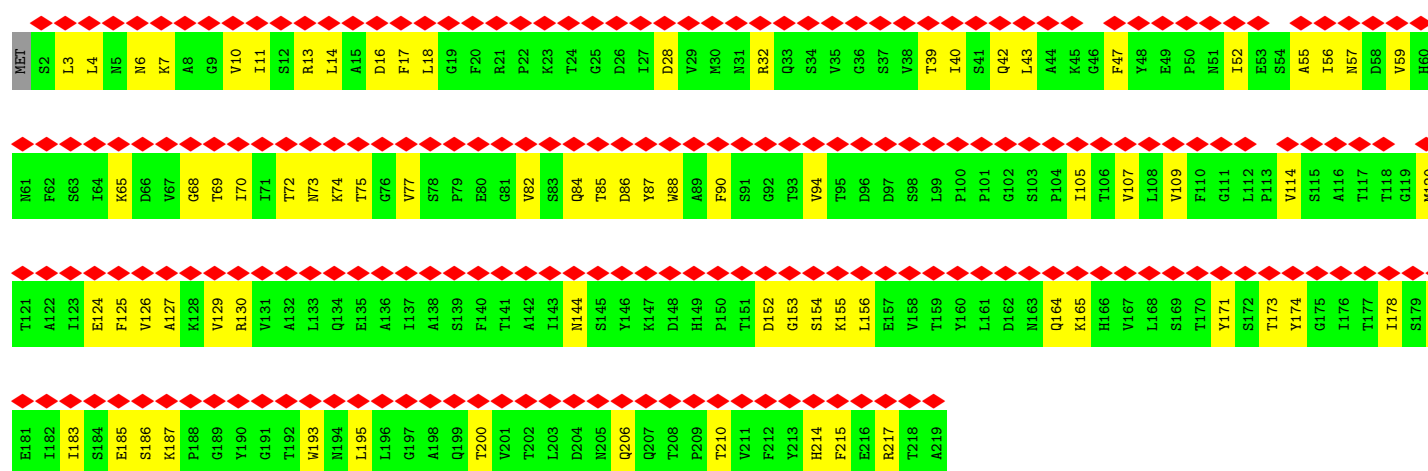


- Molecule 14: gp11, baseplate wedge protein

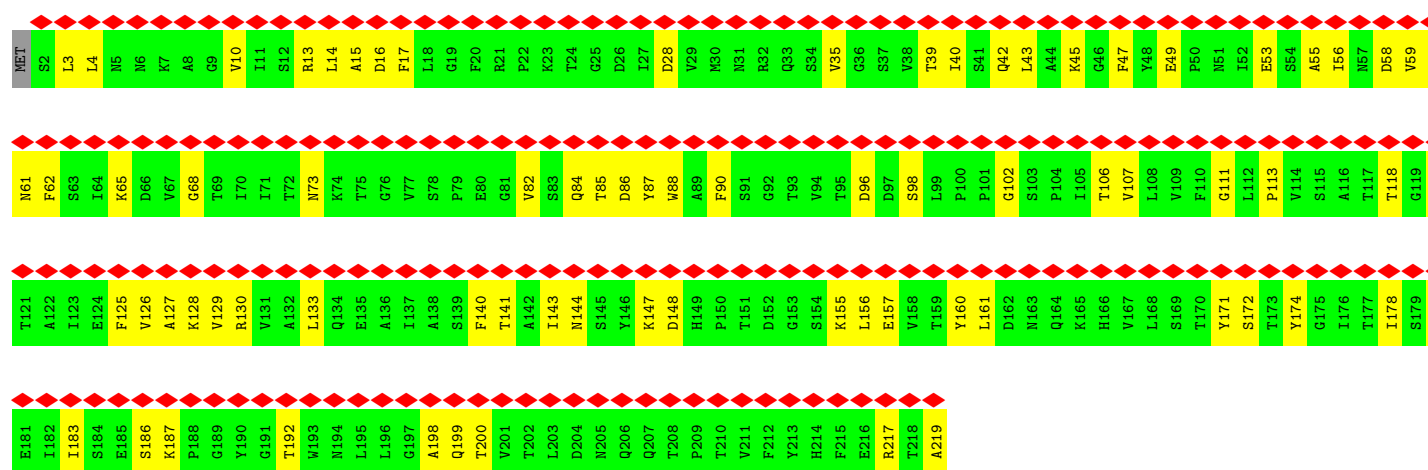




- Molecule 14: gp11, baseplate wedge protein

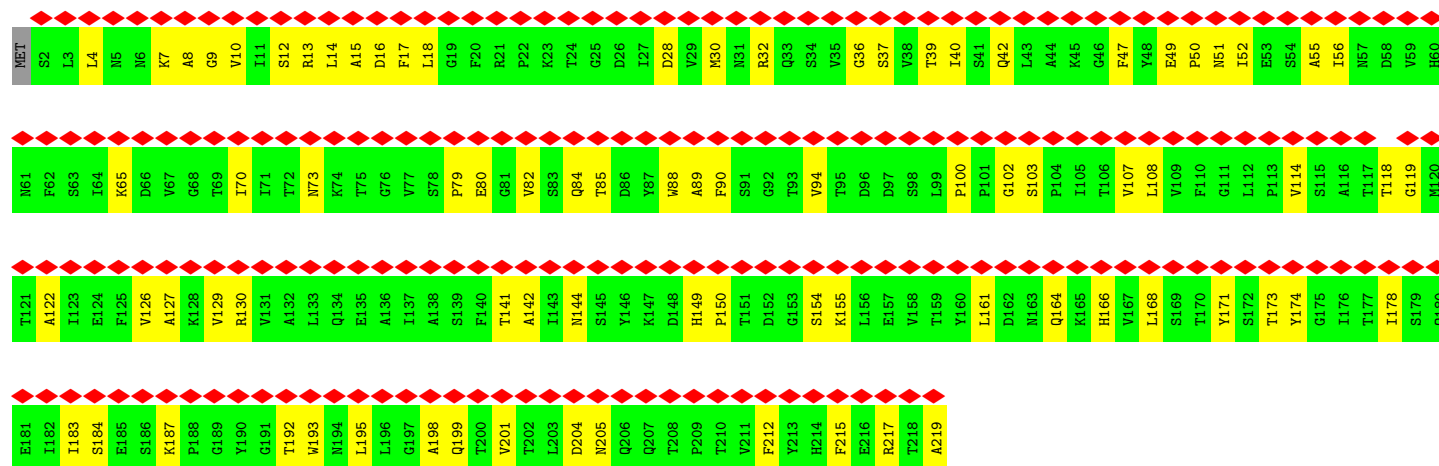


- Molecule 14: gp11, baseplate wedge protein

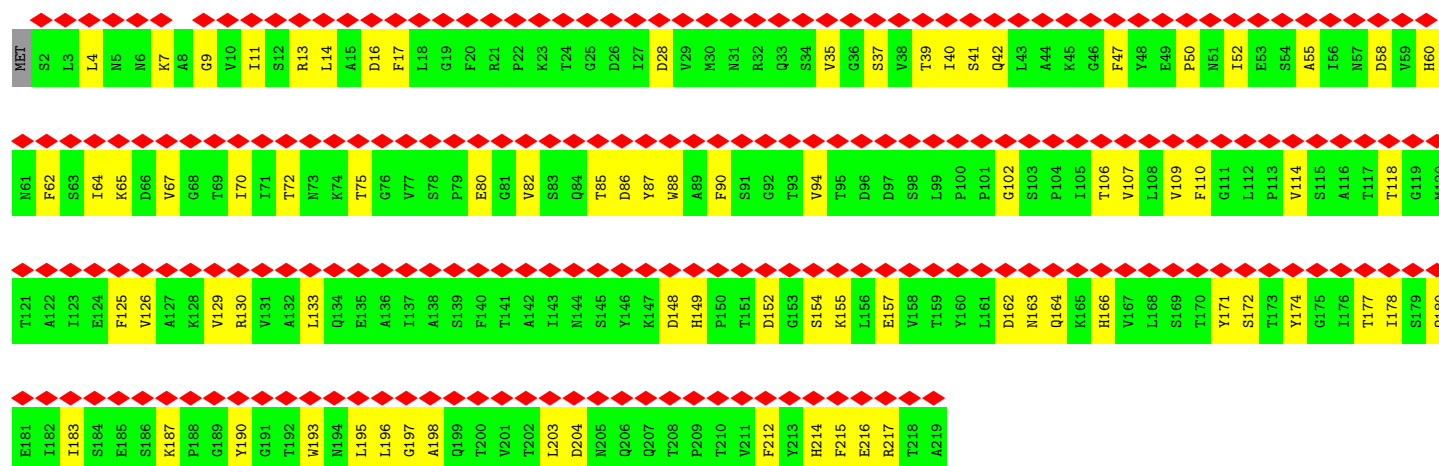


- Molecule 14: gp11, baseplate wedge protein

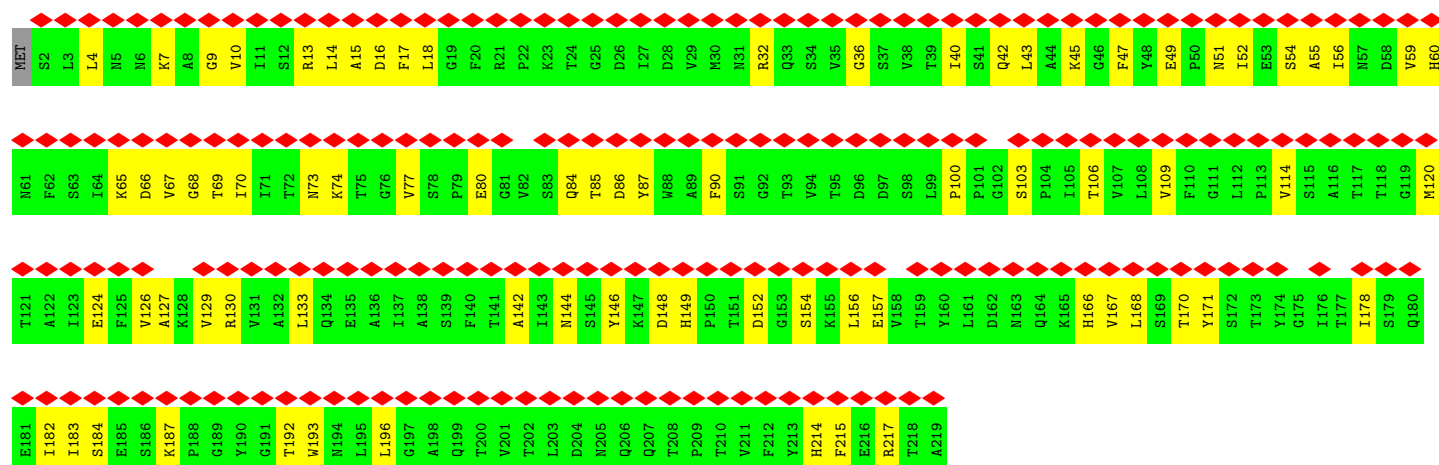




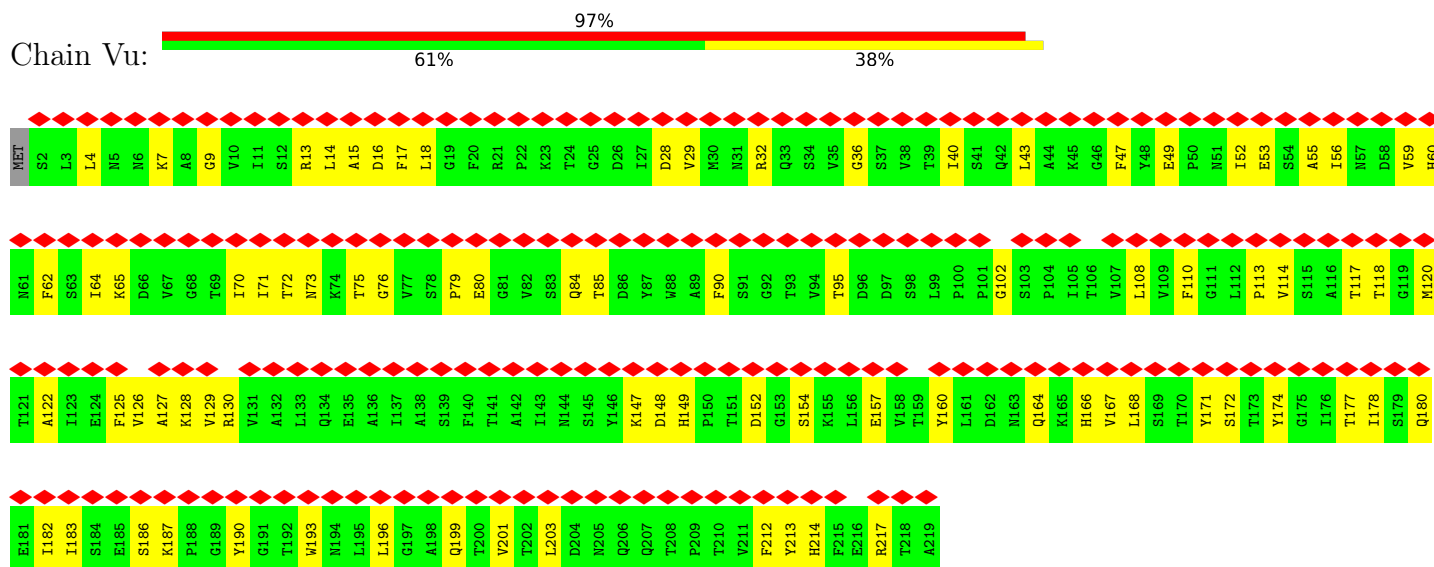
• Molecule 14: gp11, baseplate wedge protein



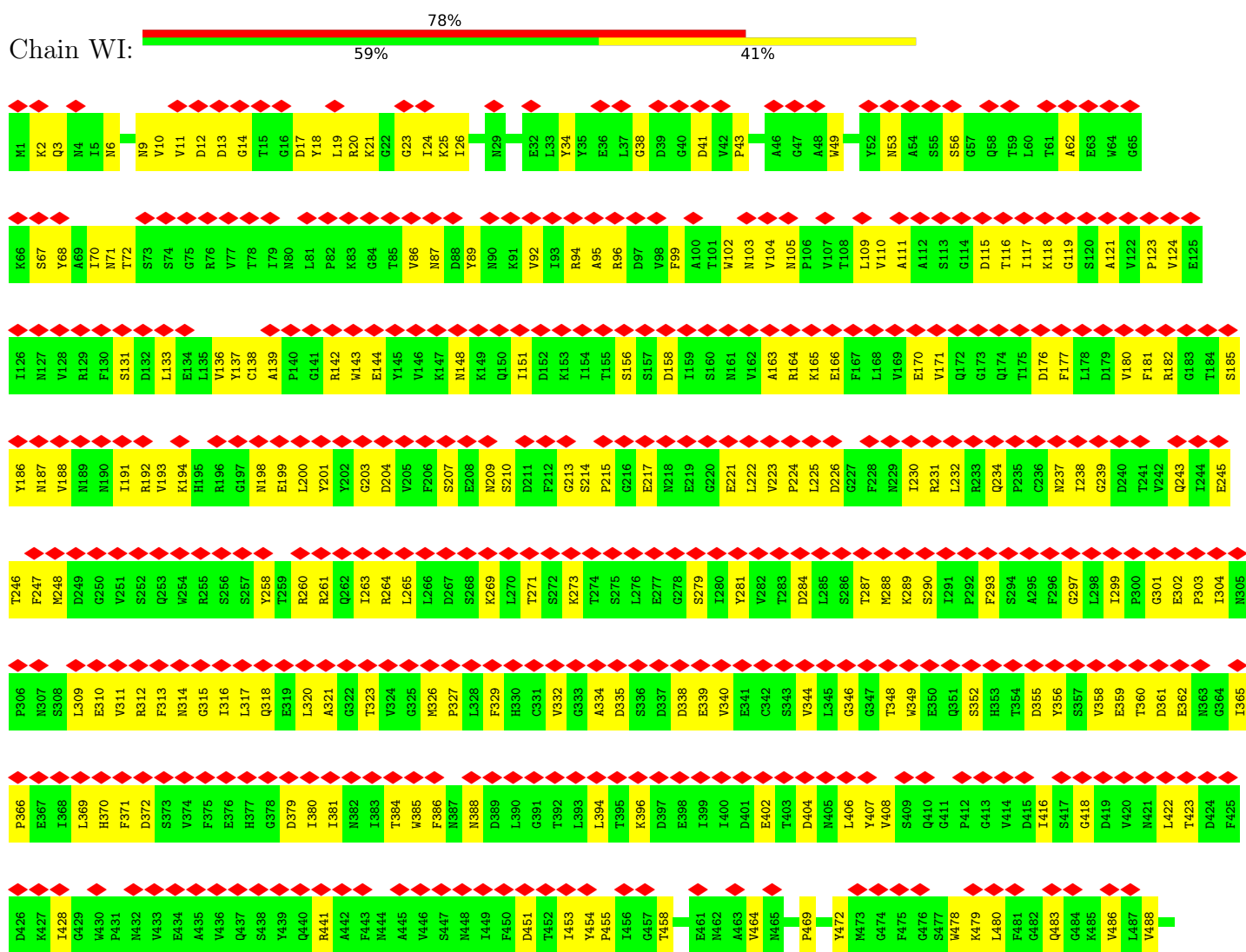
• Molecule 14: gp11, baseplate wedge protein

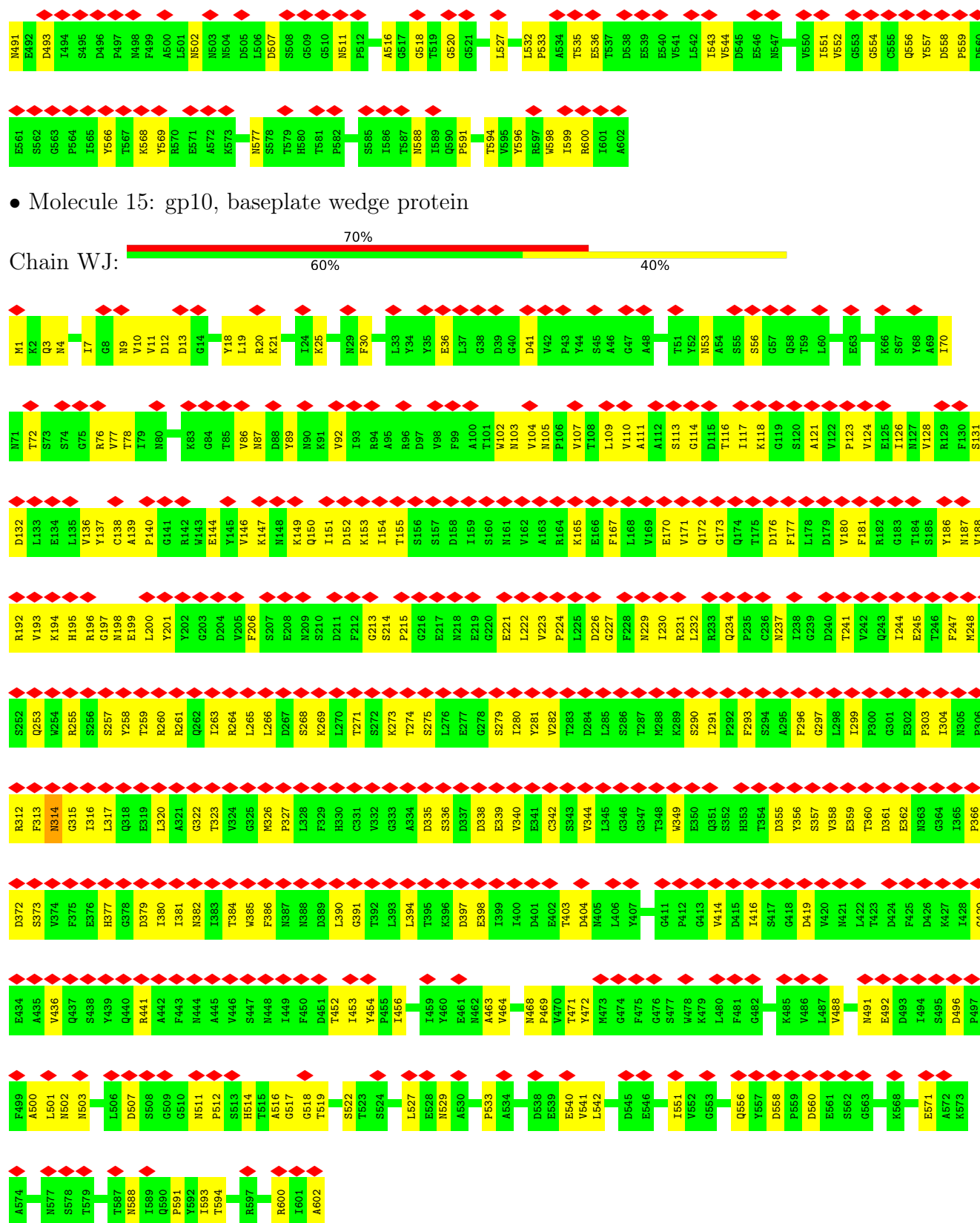


● Molecule 14: gp11, baseplate wedge protein

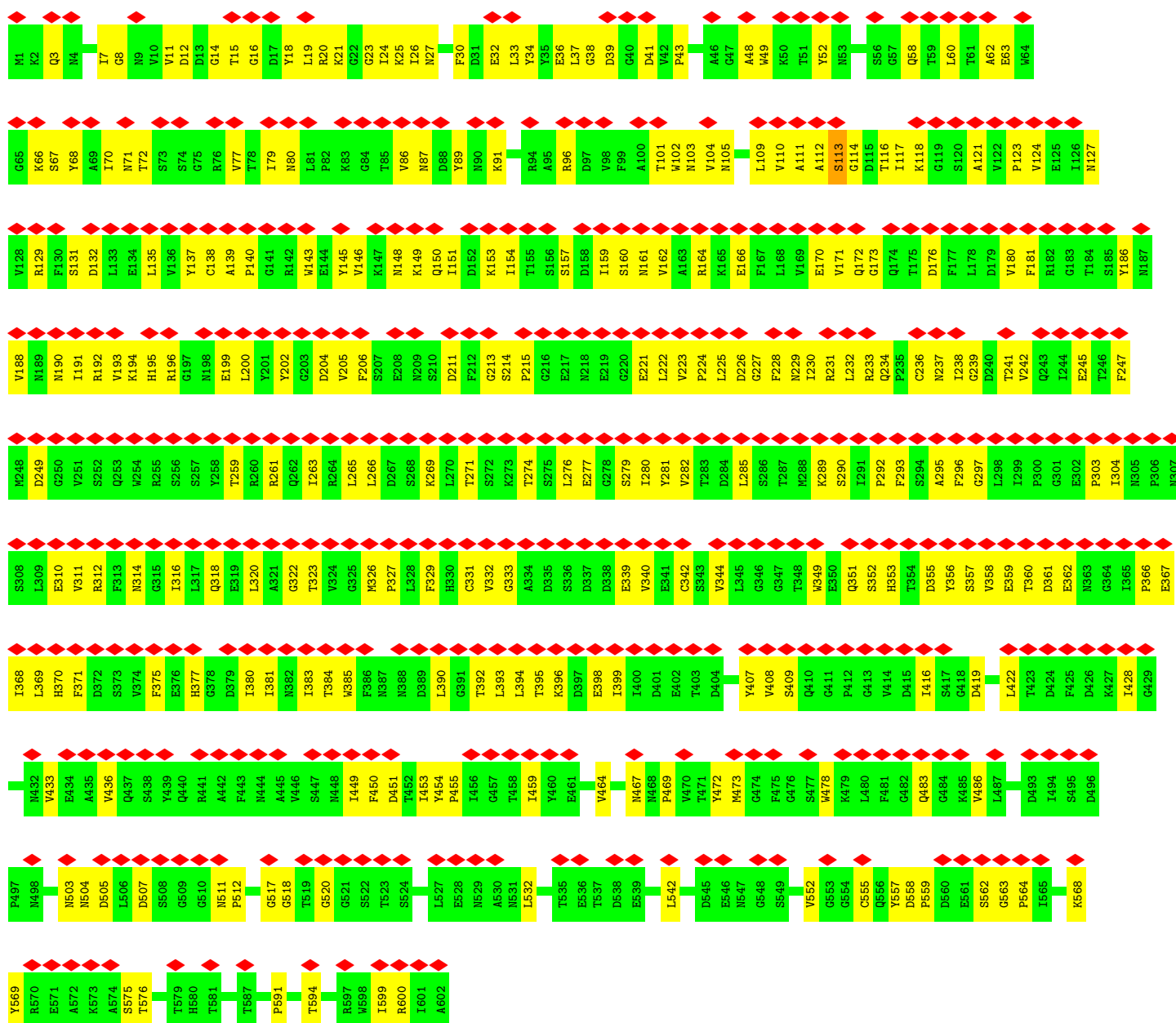
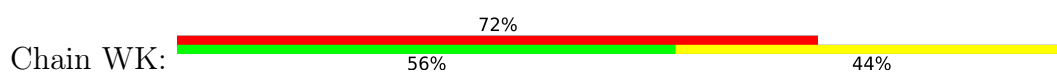


● Molecule 15: gp10, baseplate wedge protein

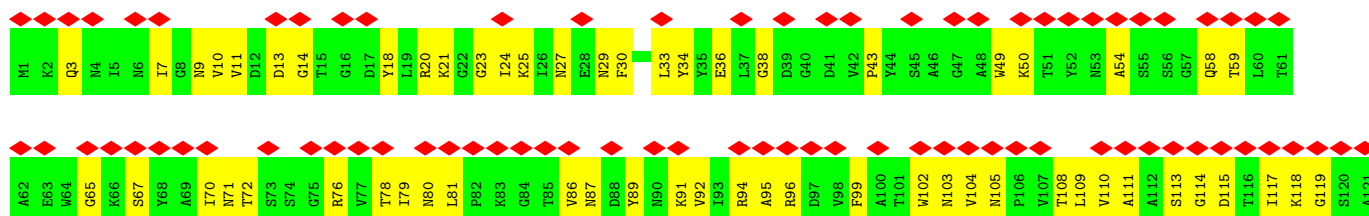
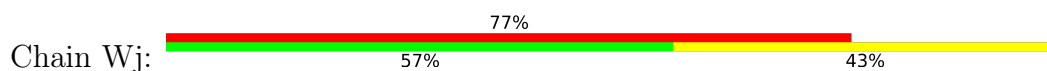


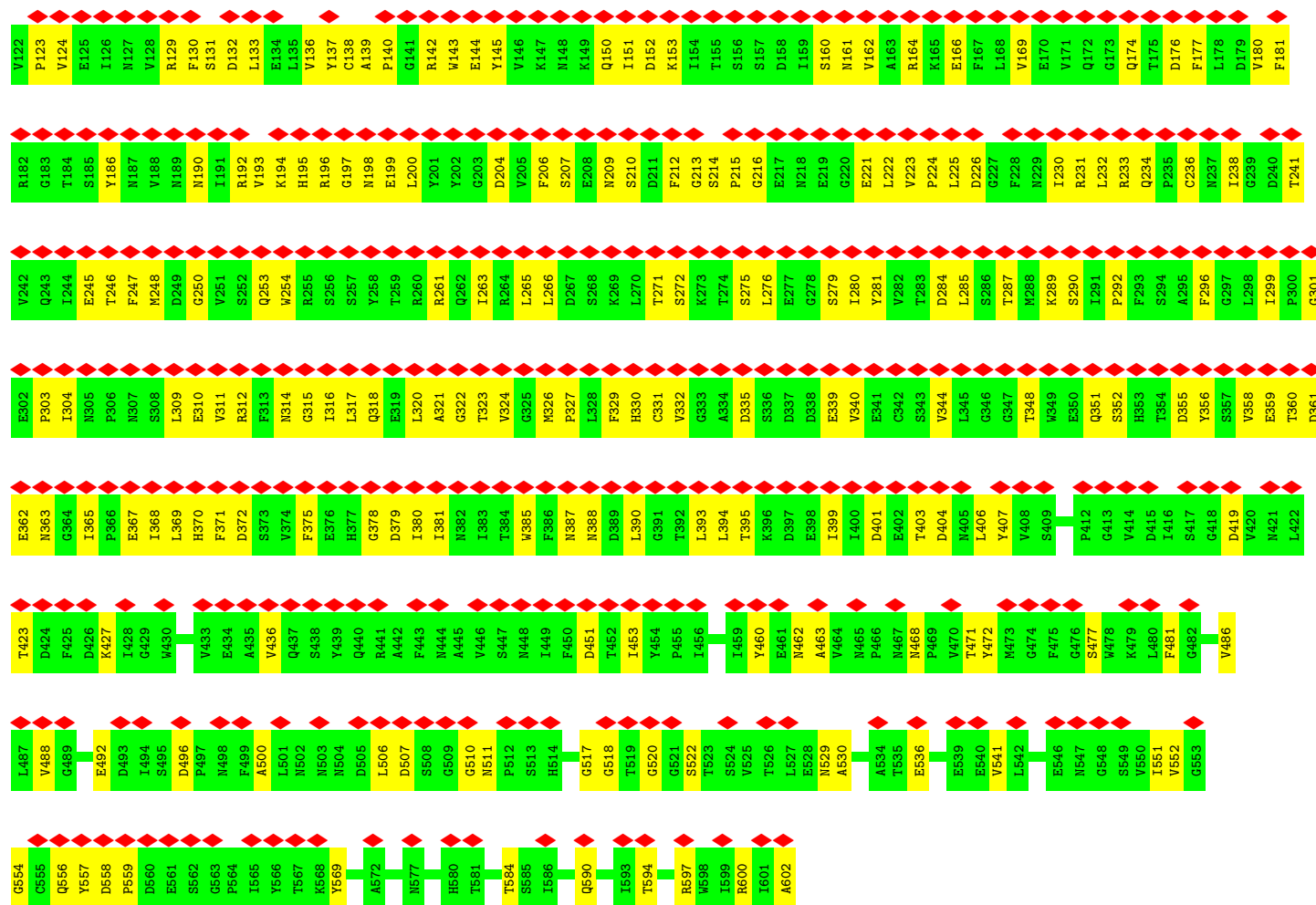


• Molecule 15: gp10, baseplate wedge protein

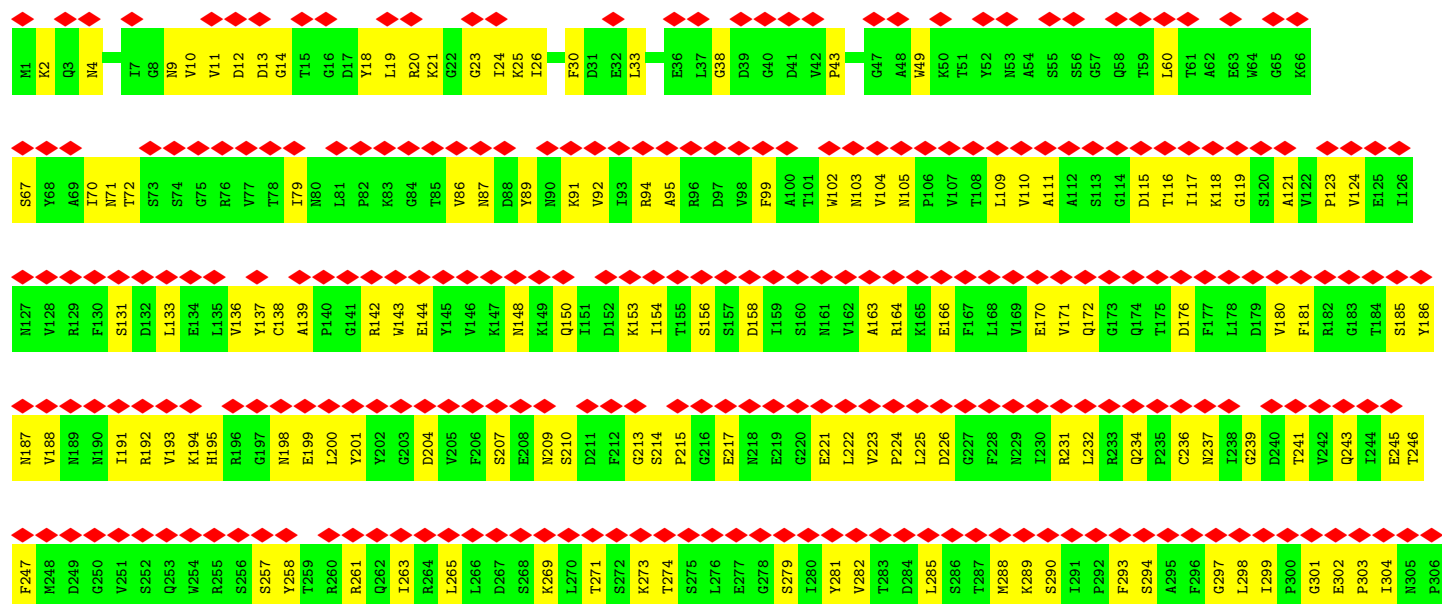
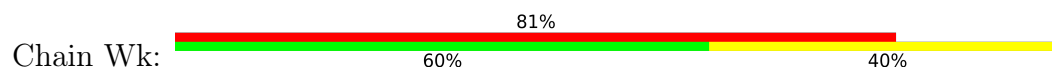


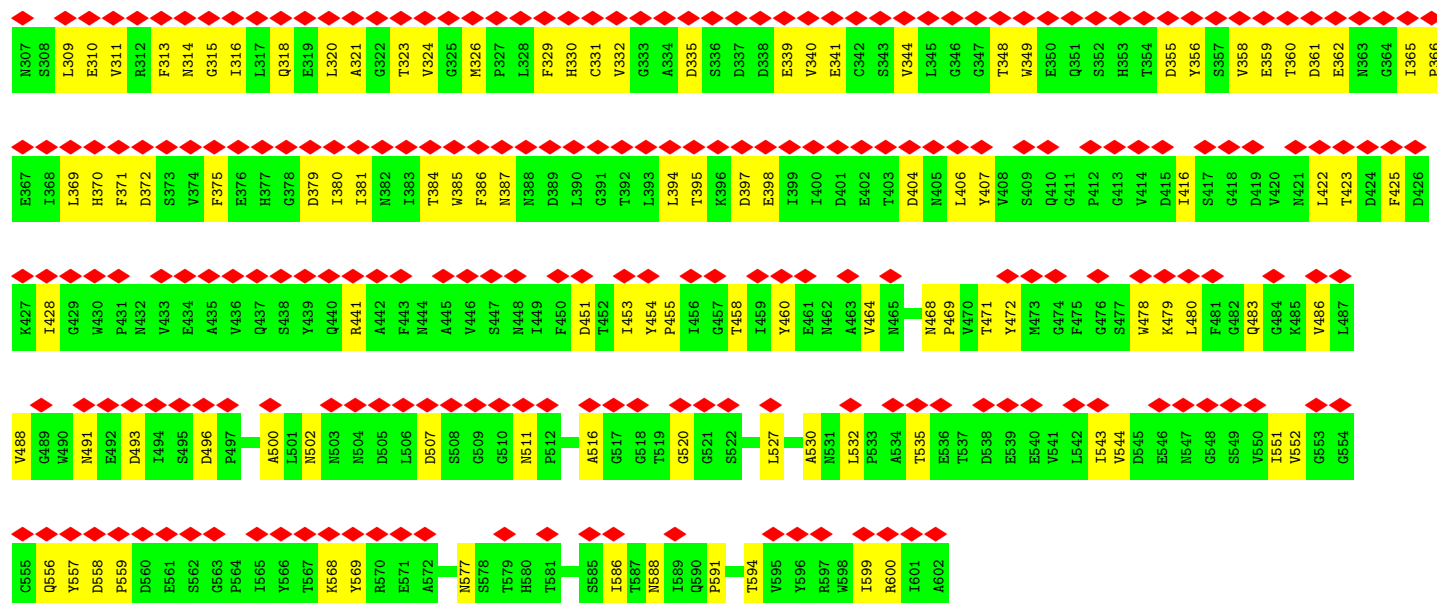
- Molecule 15: gp10, baseplate wedge protein



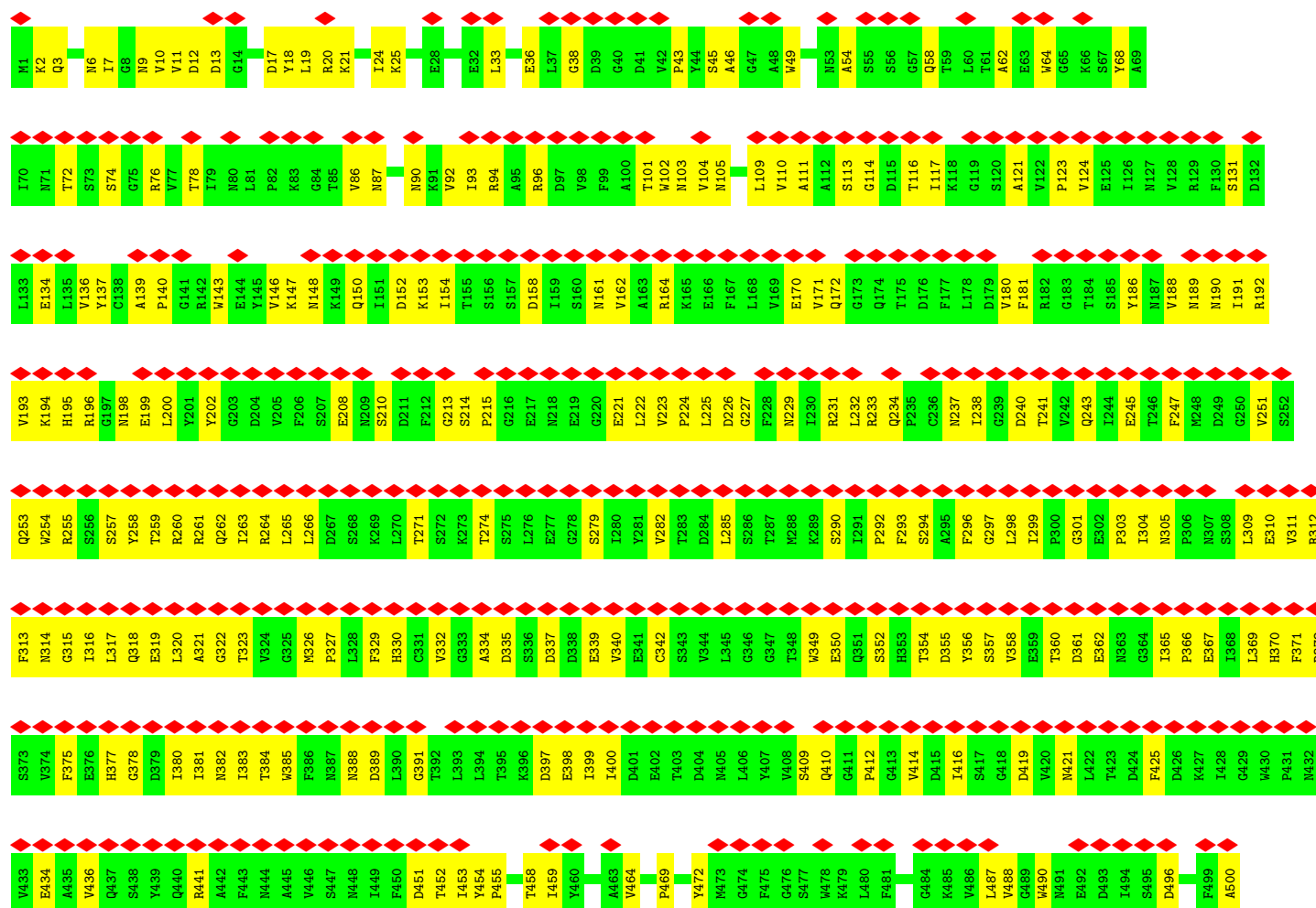
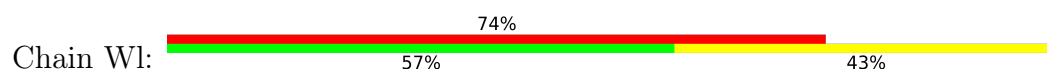


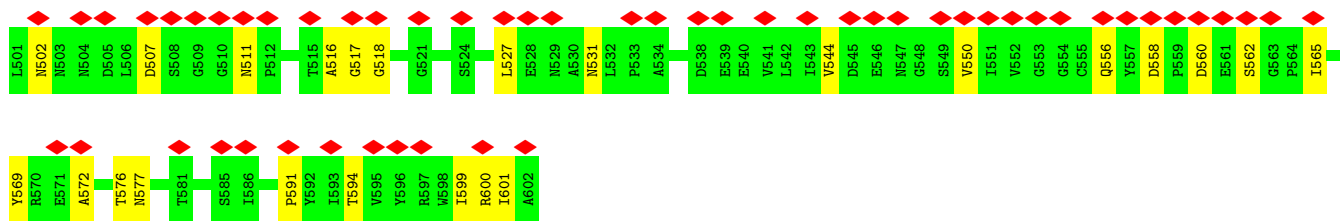
• Molecule 15: gp10, baseplate wedge protein



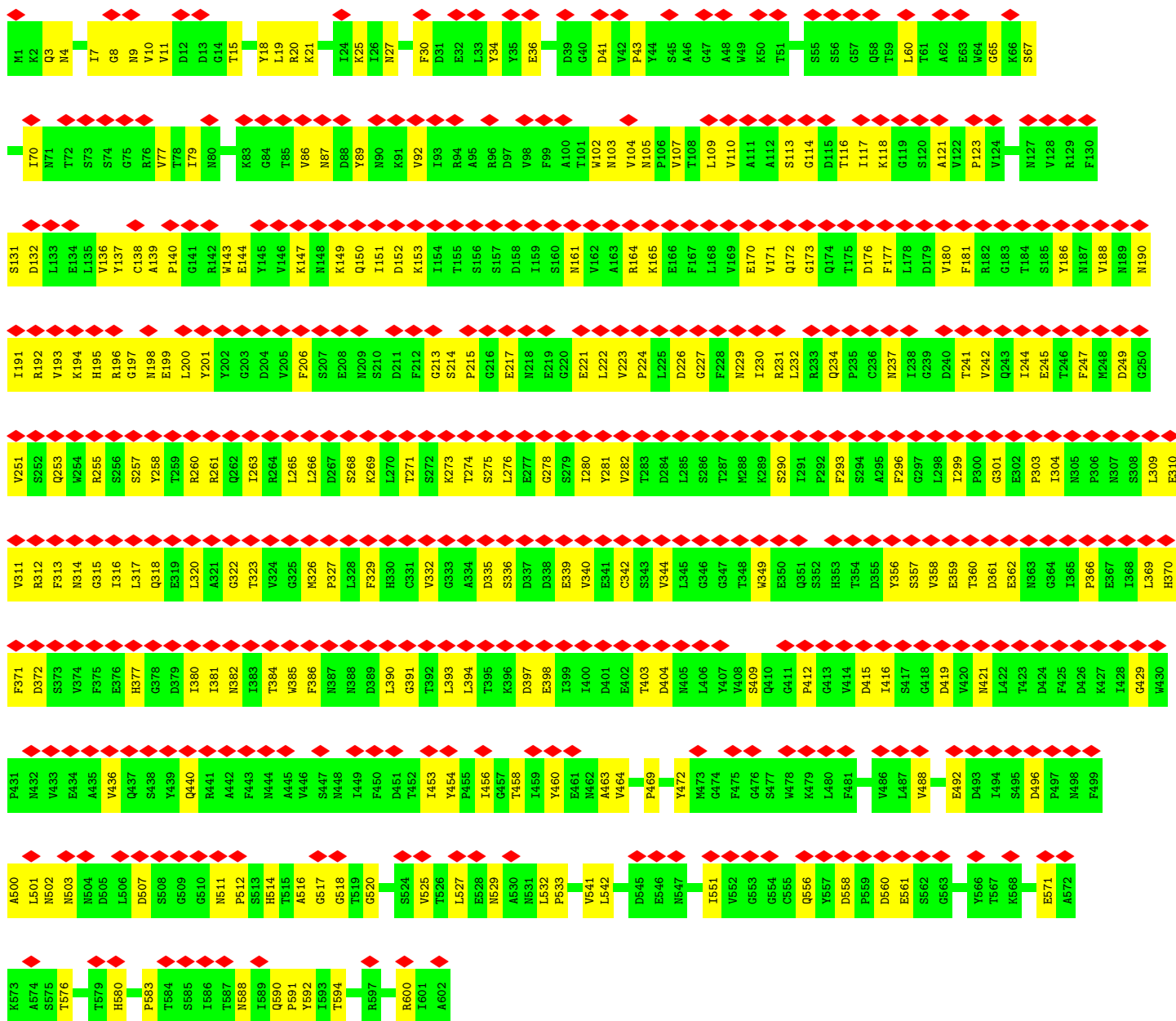
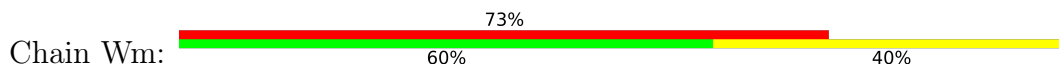


• Molecule 15: gp10, baseplate wedge protein

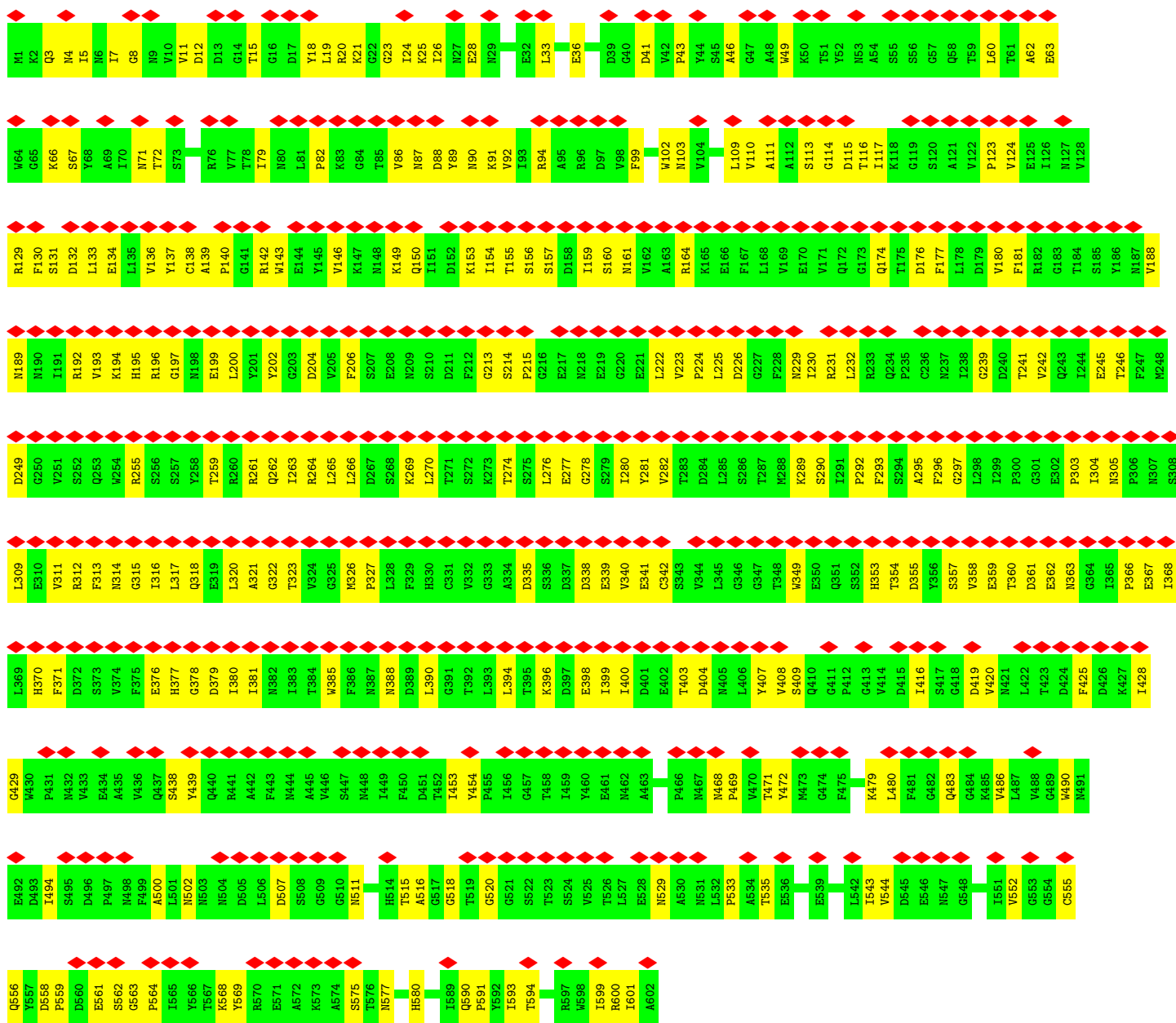
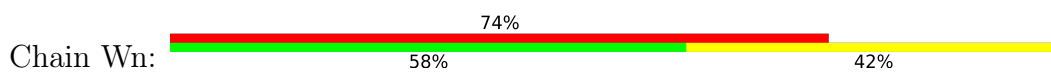




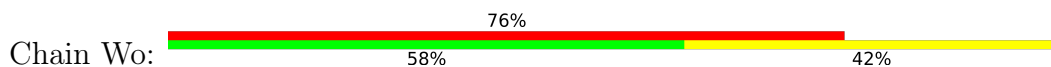
• Molecule 15: gp10, baseplate wedge protein

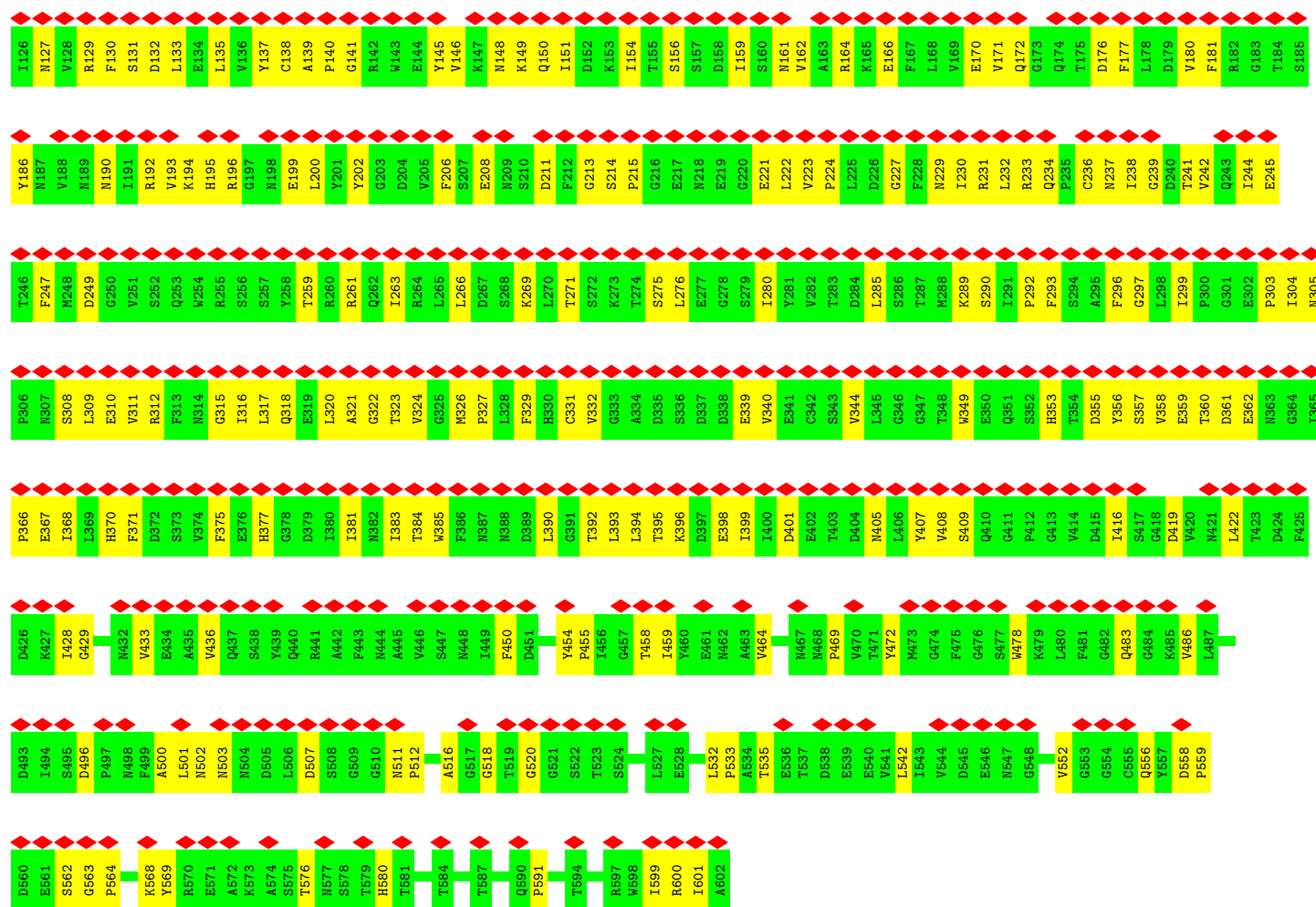


• Molecule 15: gp10, baseplate wedge protein

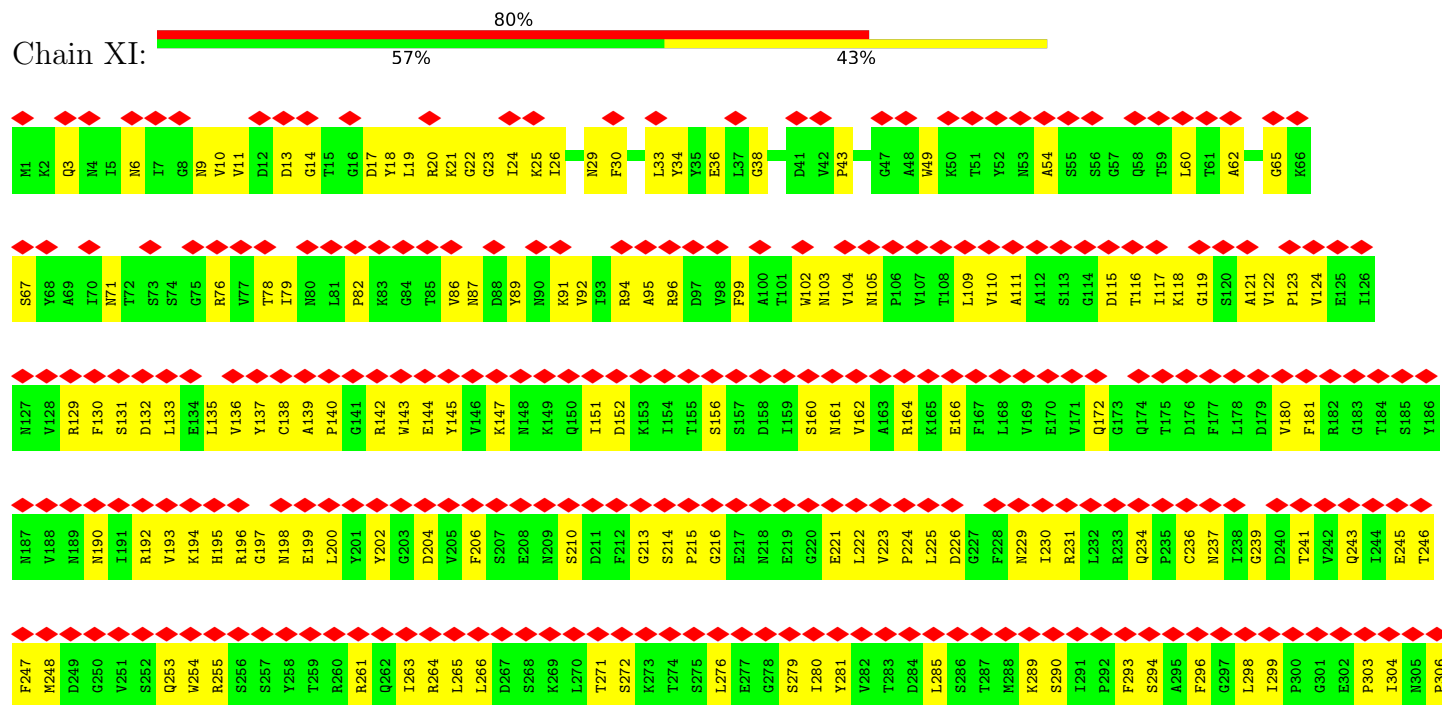


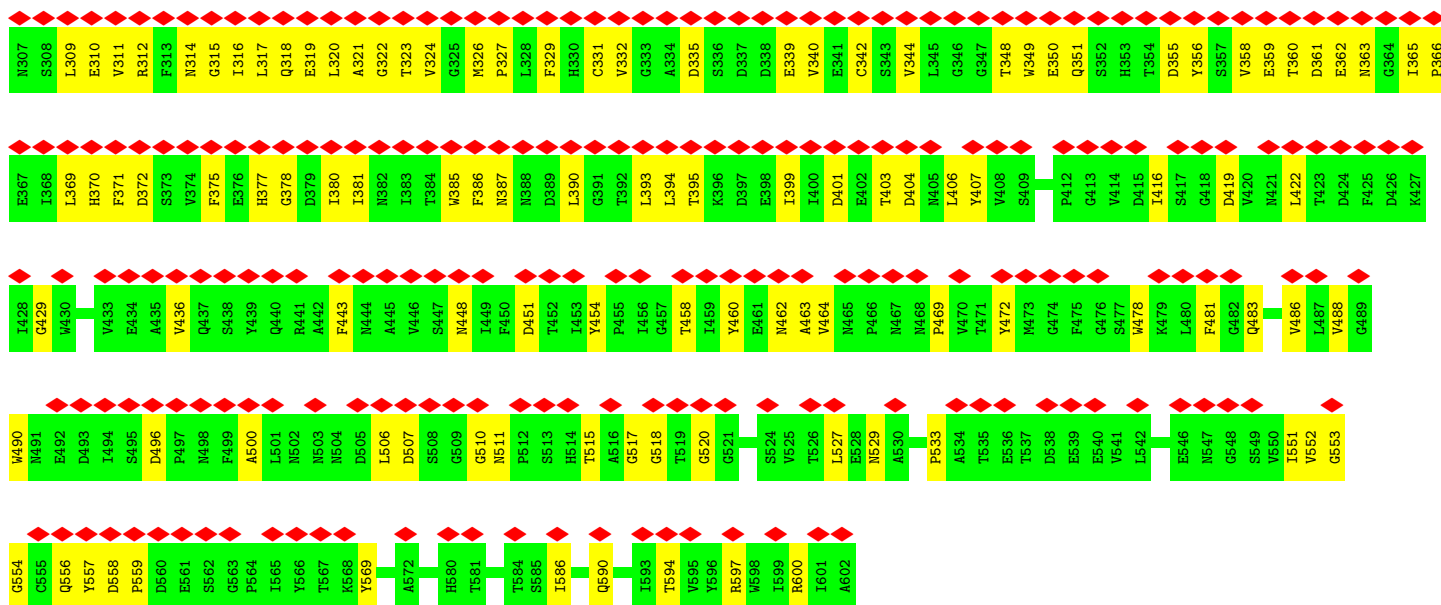
- Molecule 15: gp10, baseplate wedge protein



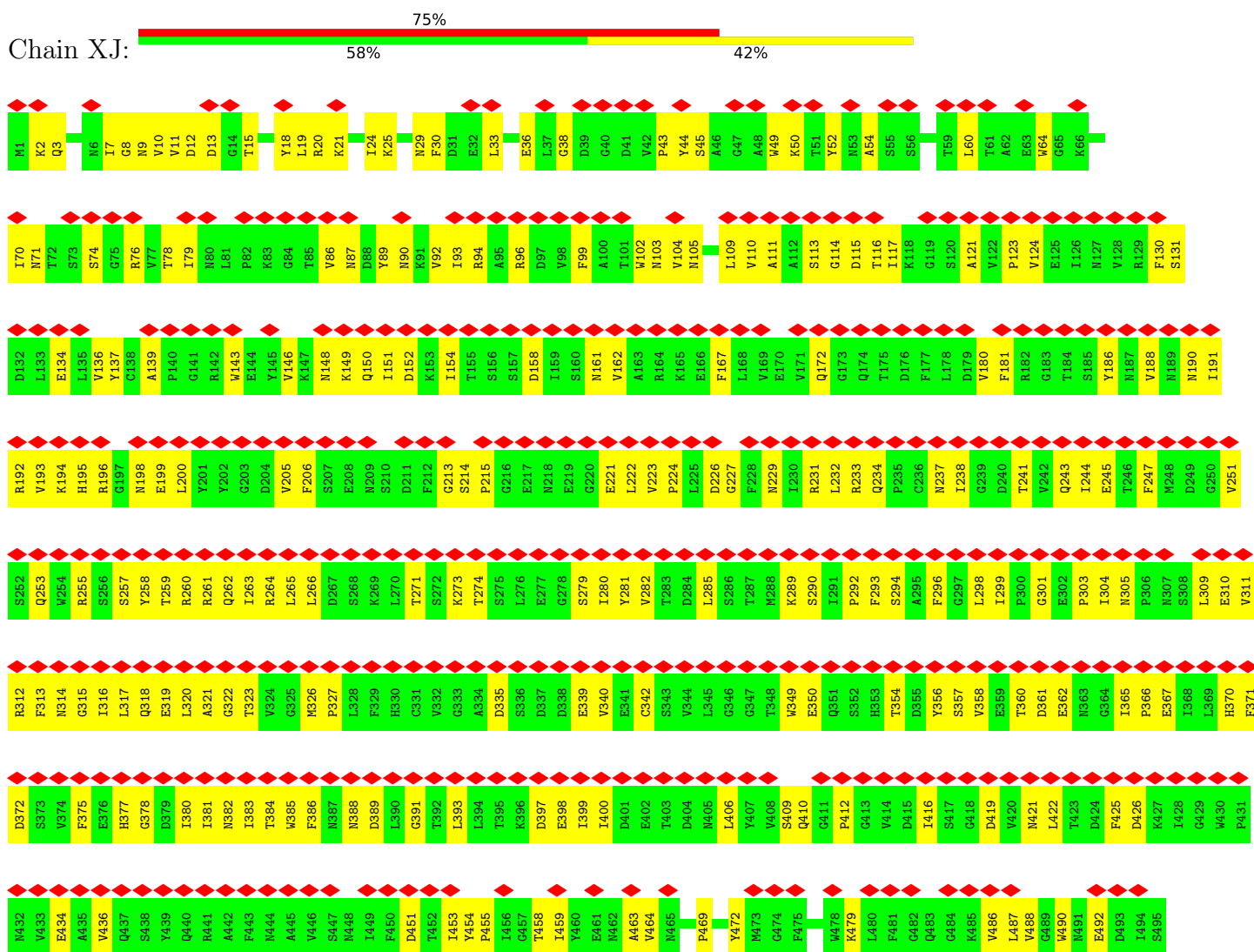


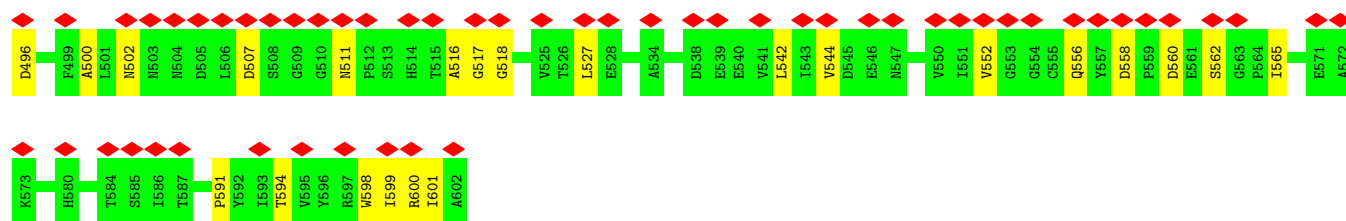
• Molecule 15: gp10, baseplate wedge protein





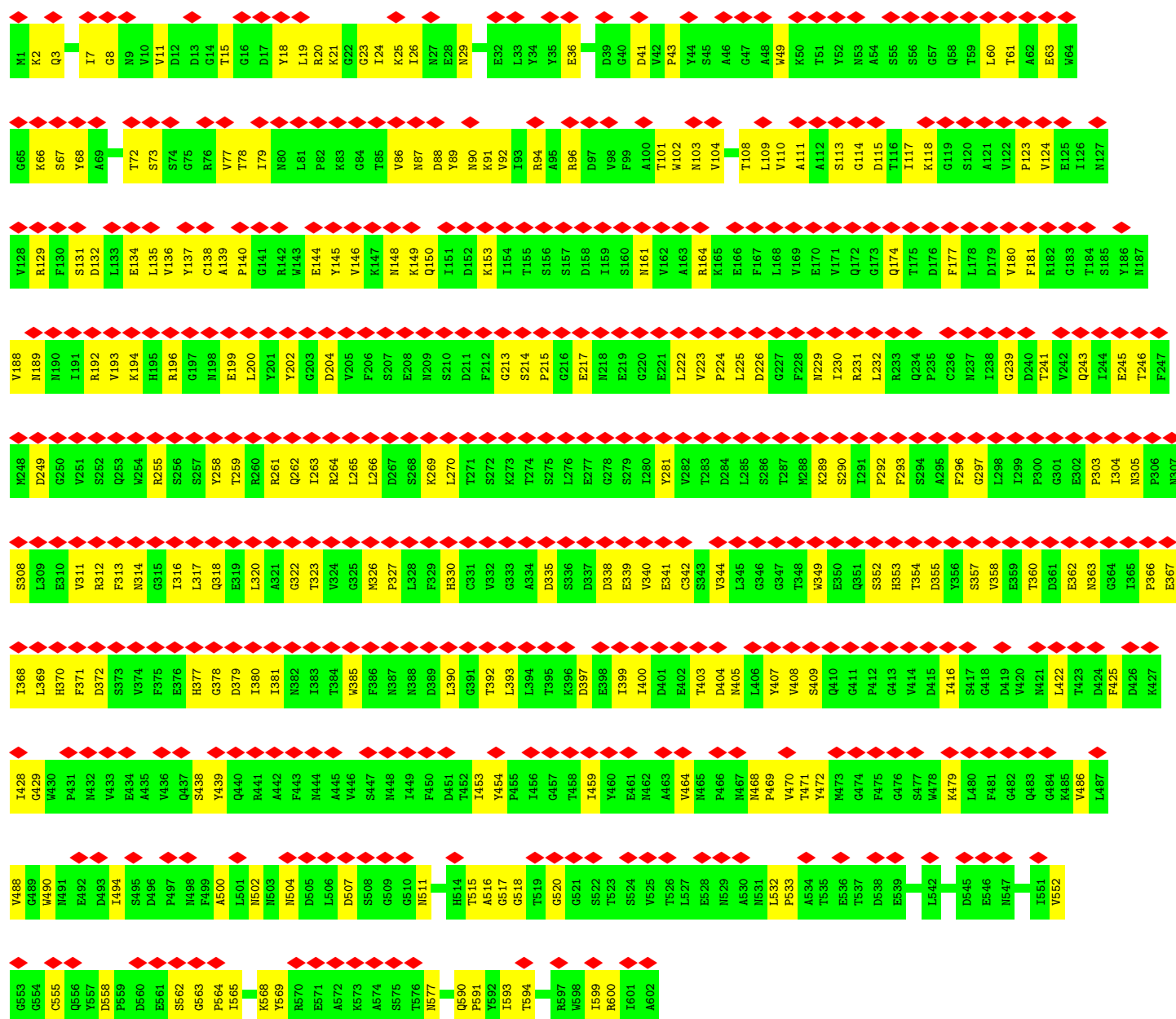
• Molecule 15: gp10, baseplate wedge protein



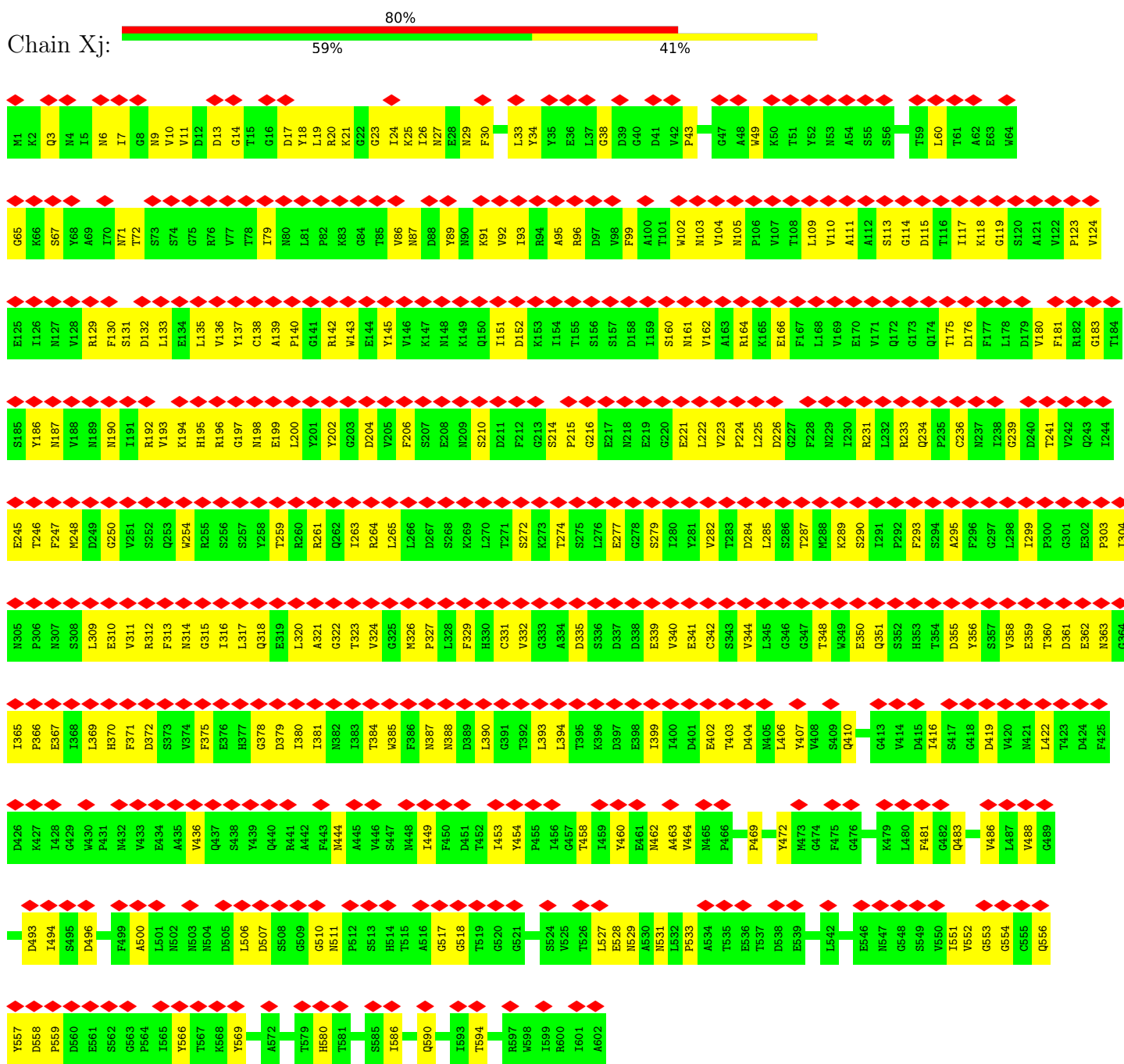


- Molecule 15: gp10, baseplate wedge protein

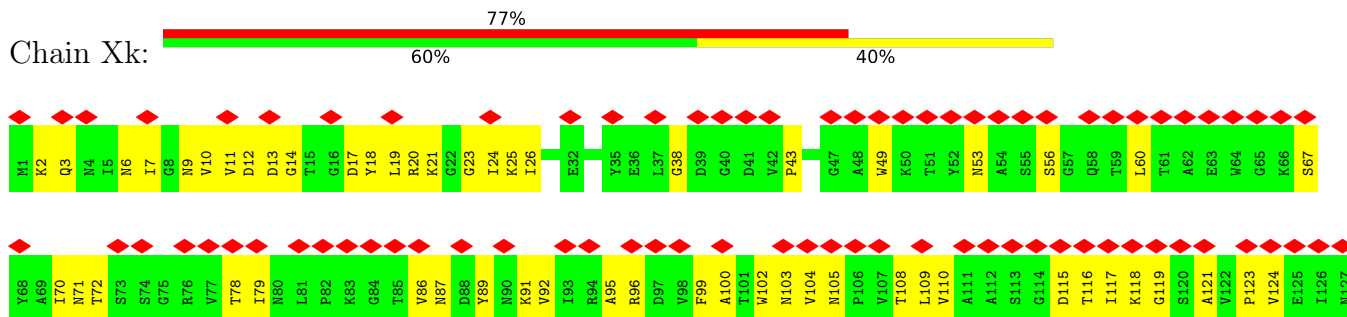
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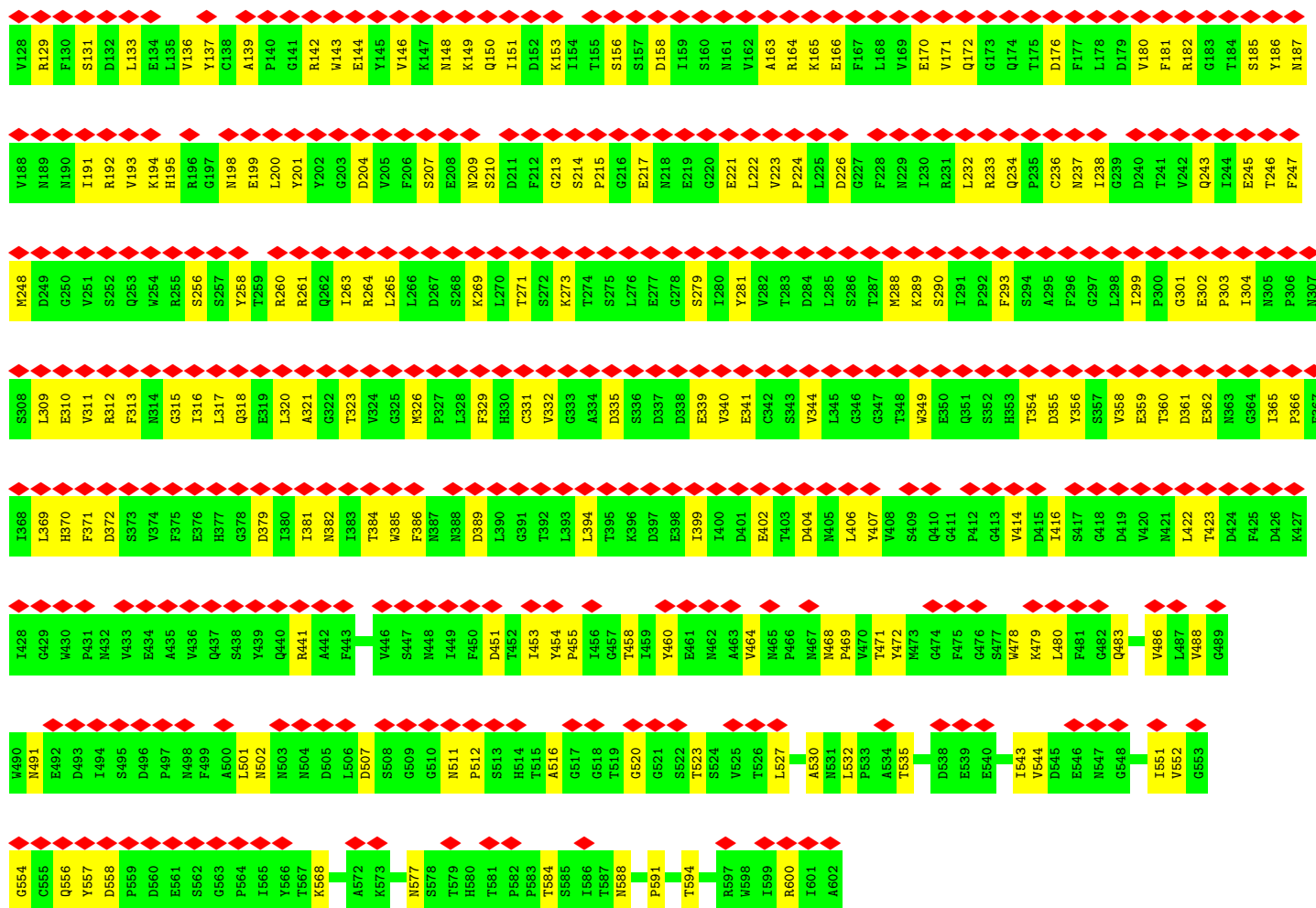


- Molecule 15: gp10, baseplate wedge protein

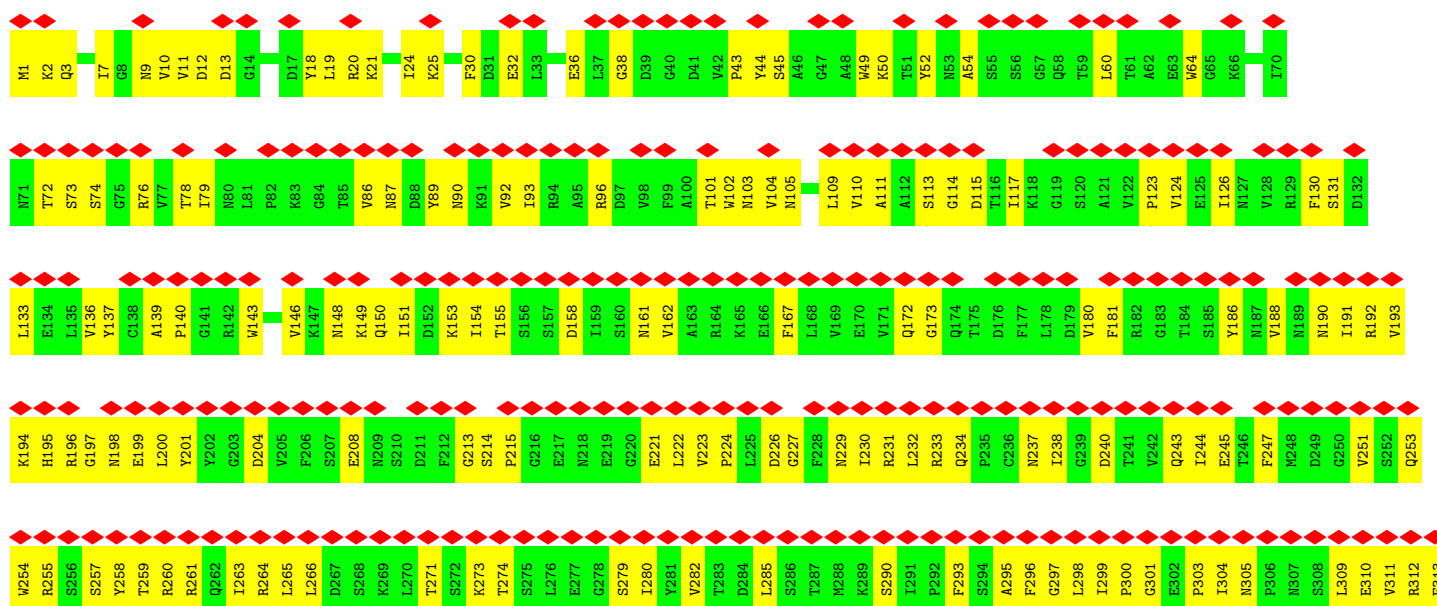
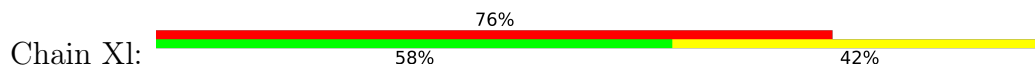


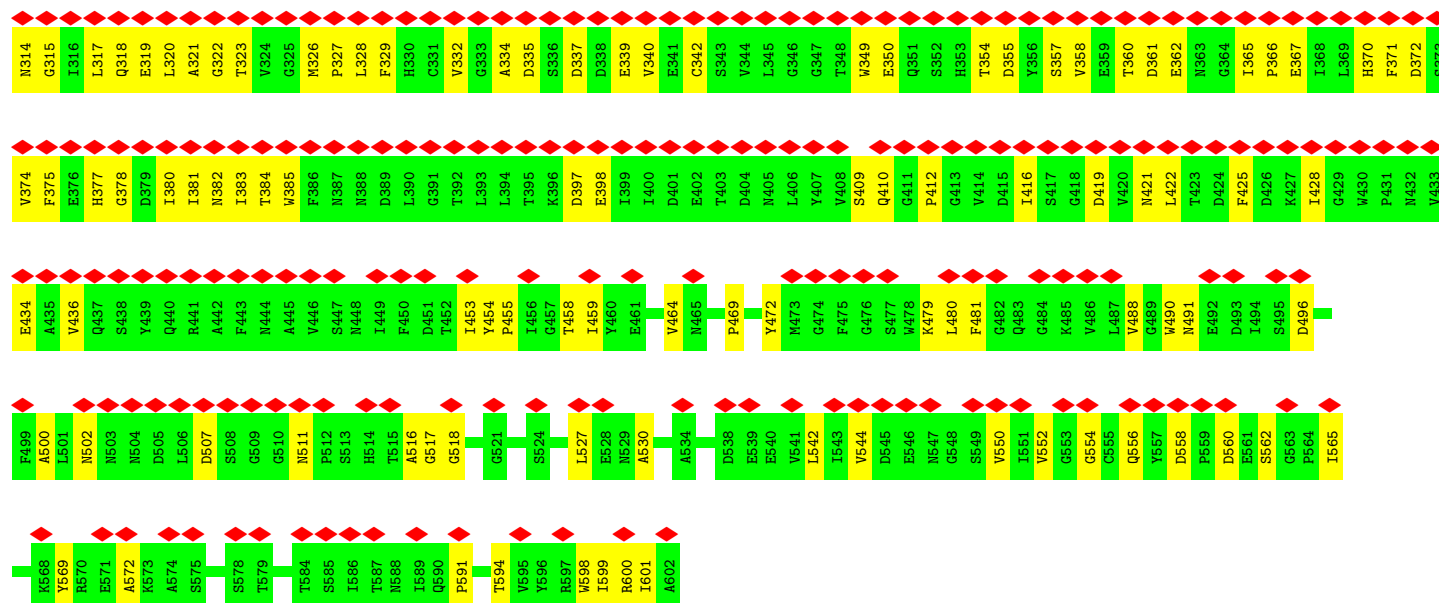
- Molecule 15: gp10, baseplate wedge protein



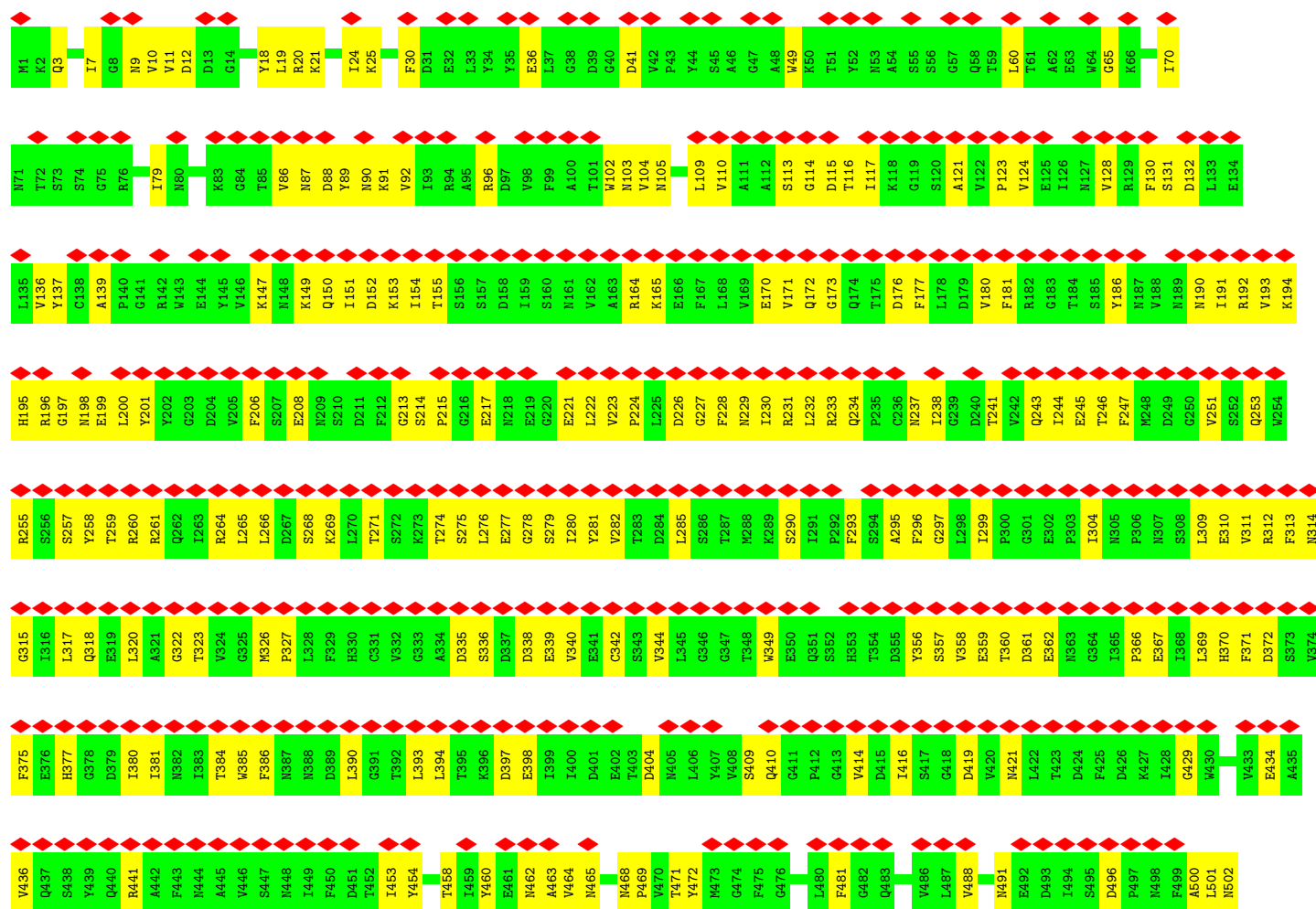
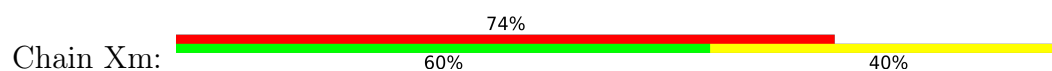


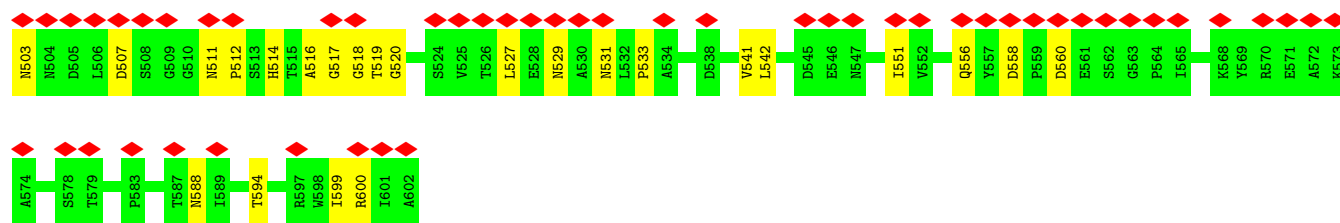
• Molecule 15: gp10, baseplate wedge protein



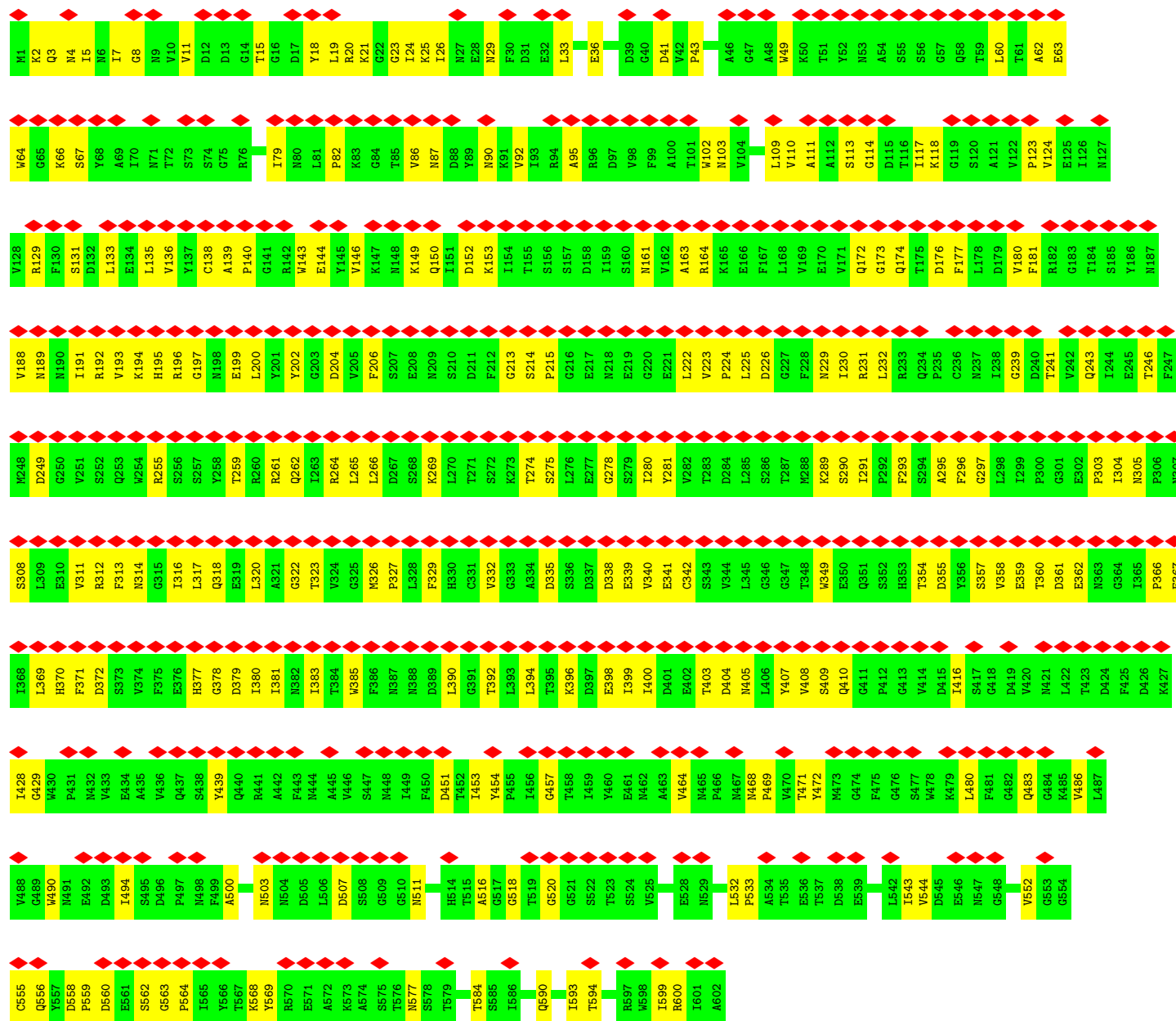
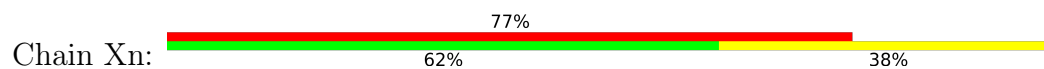


• Molecule 15: gp10, baseplate wedge protein

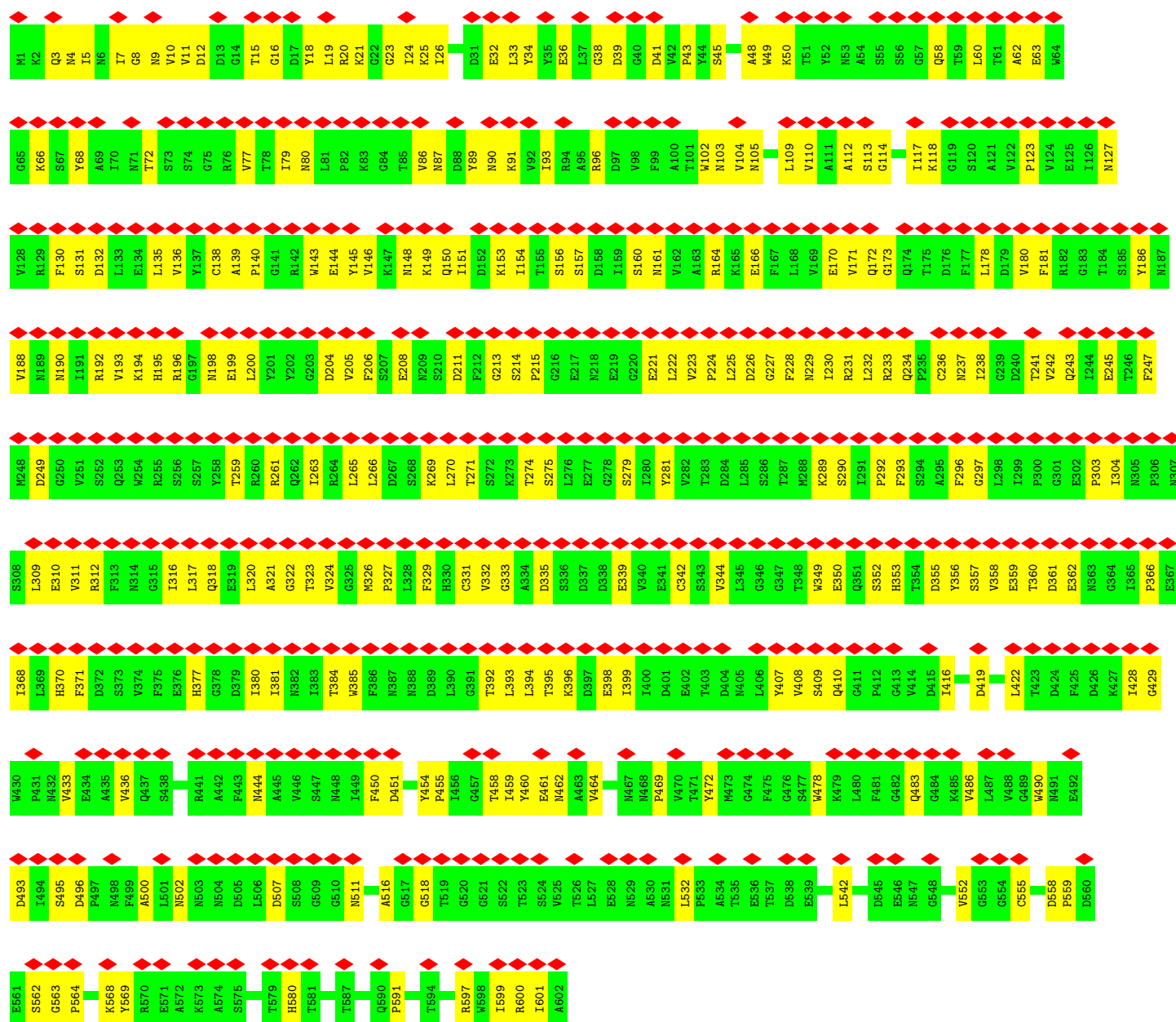
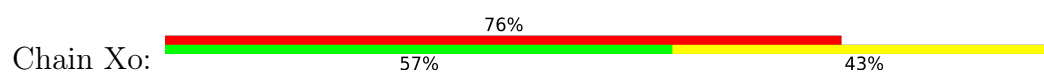




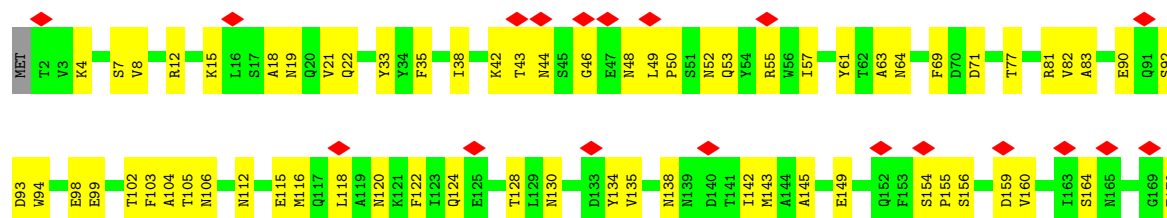
- Molecule 15: gp10, baseplate wedge protein



- Molecule 15: gp10, baseplate wedge protein



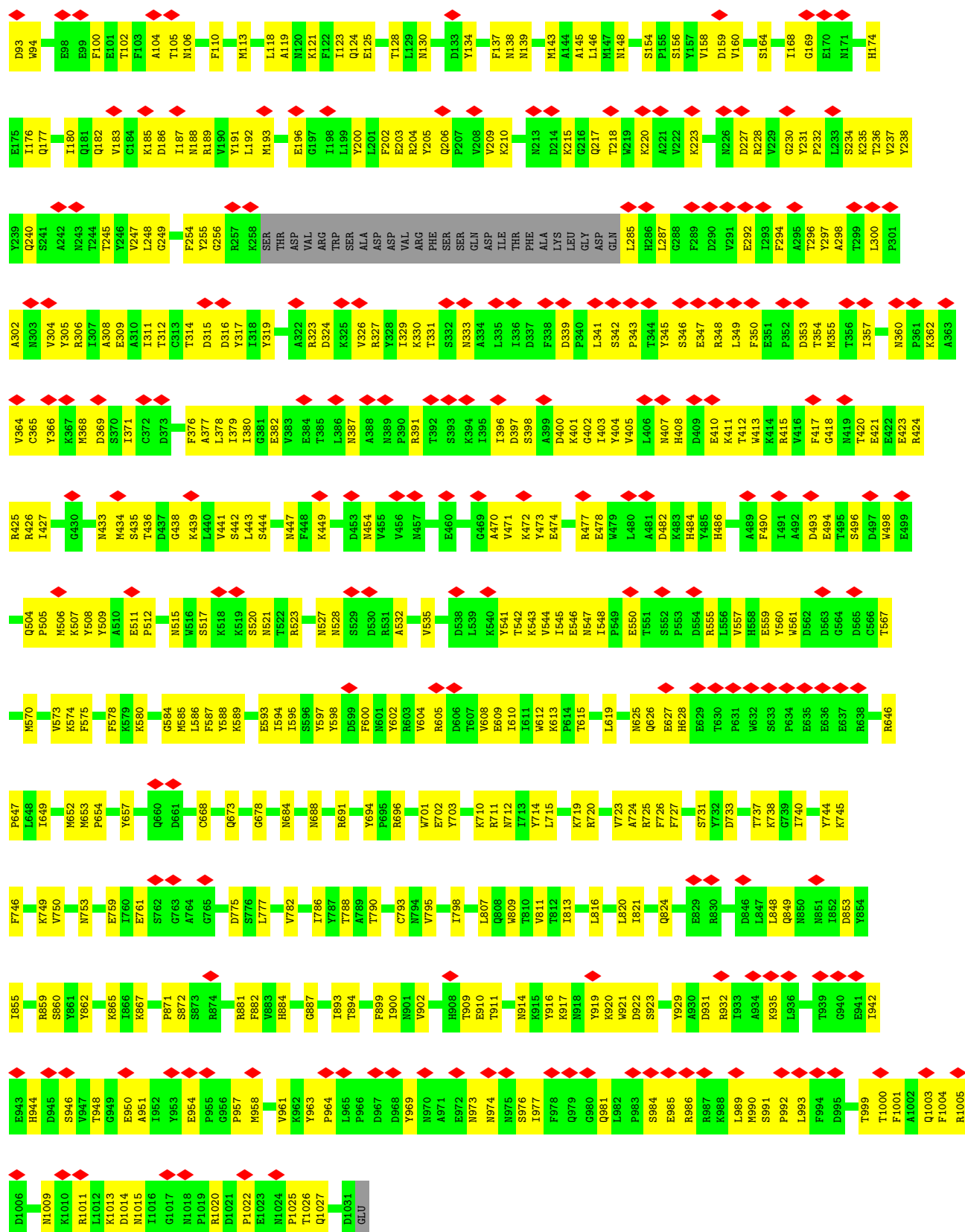
- Molecule 16: gp7, baseplate wedge protein



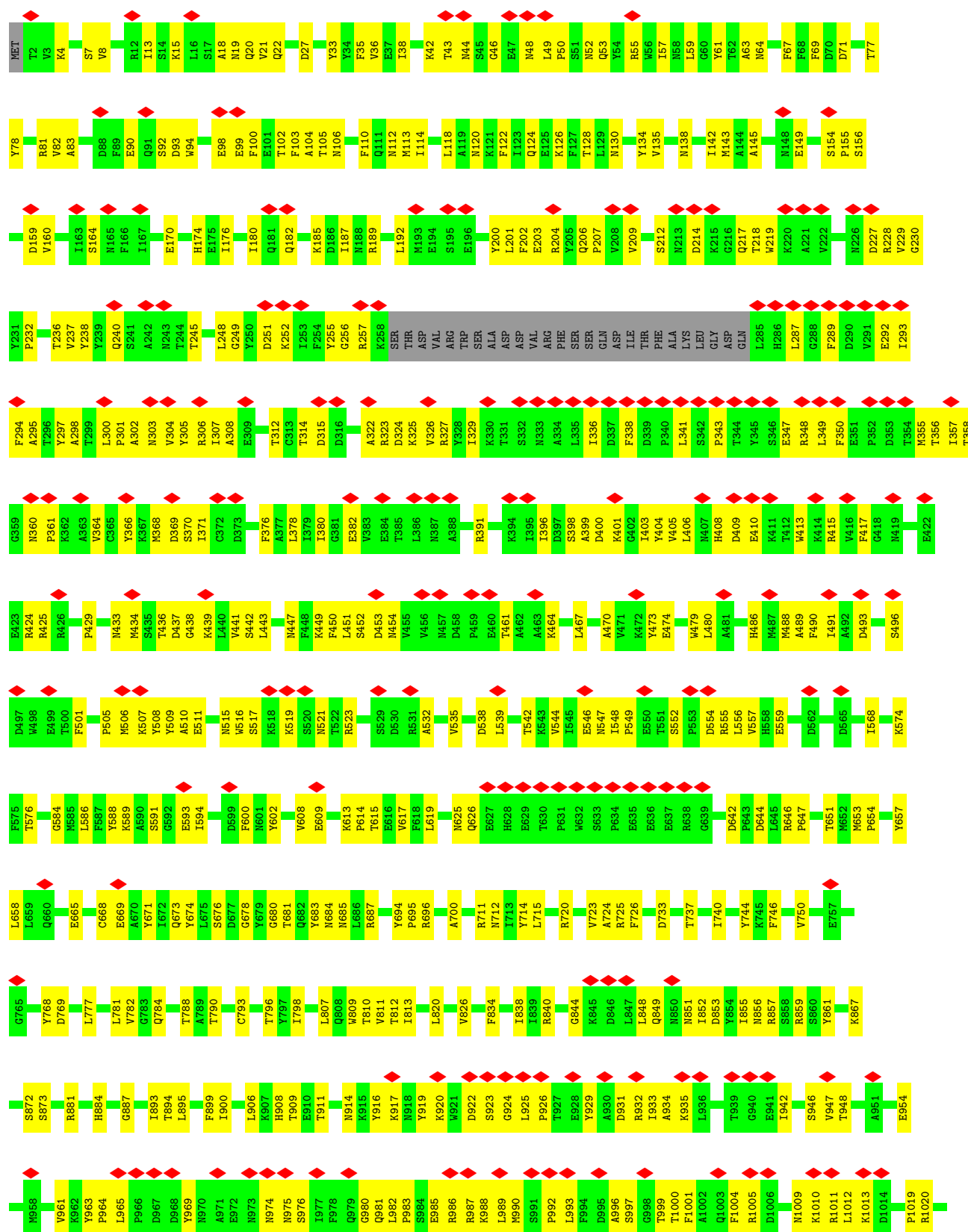


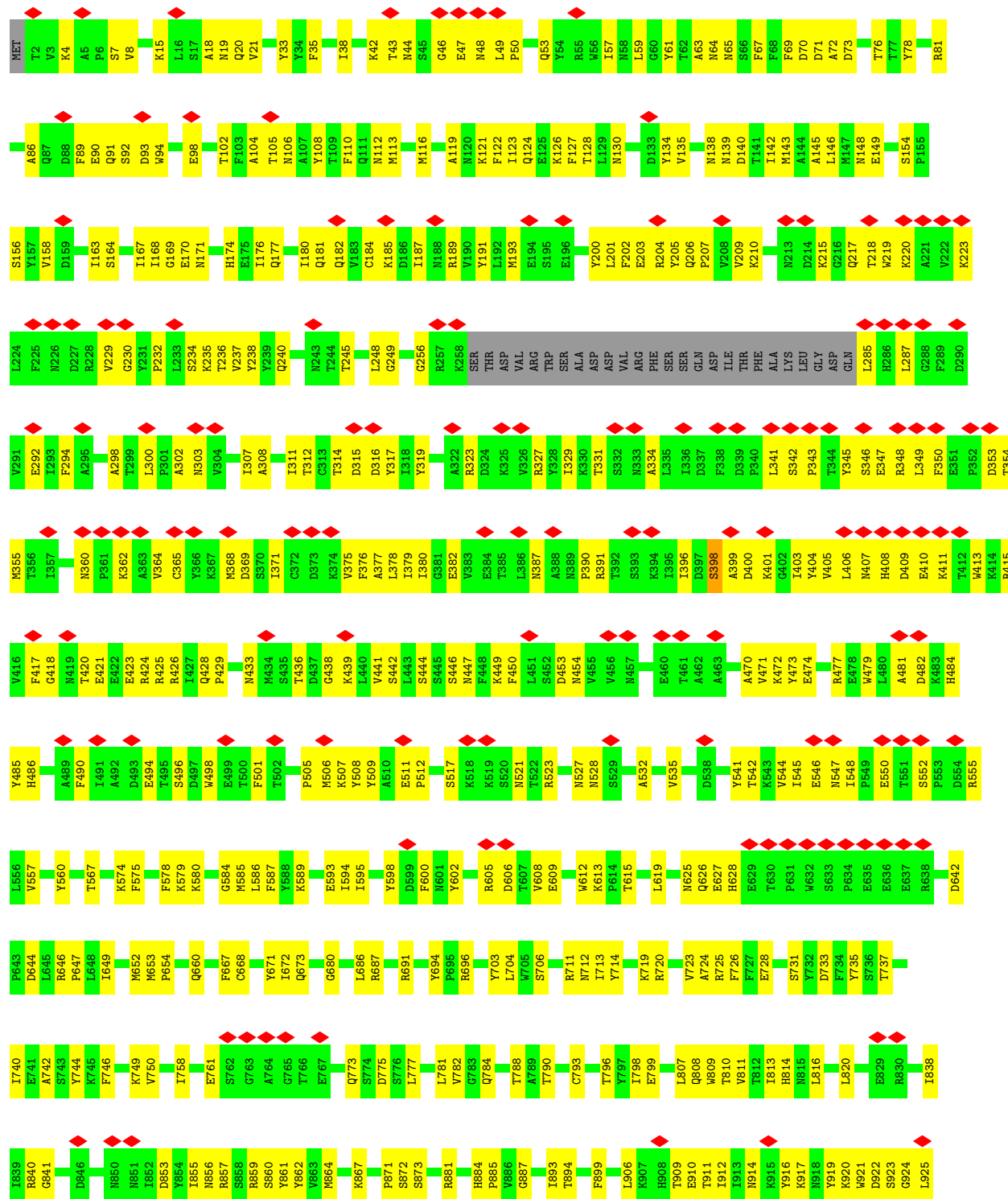
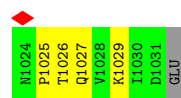
- Molecule 16: gp7, baseplate wedge protein

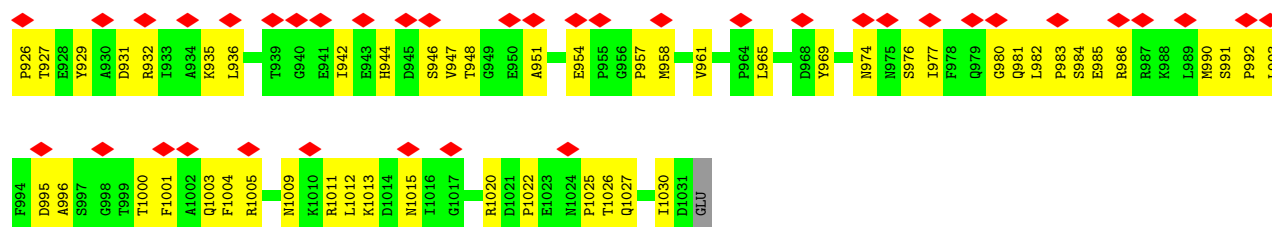




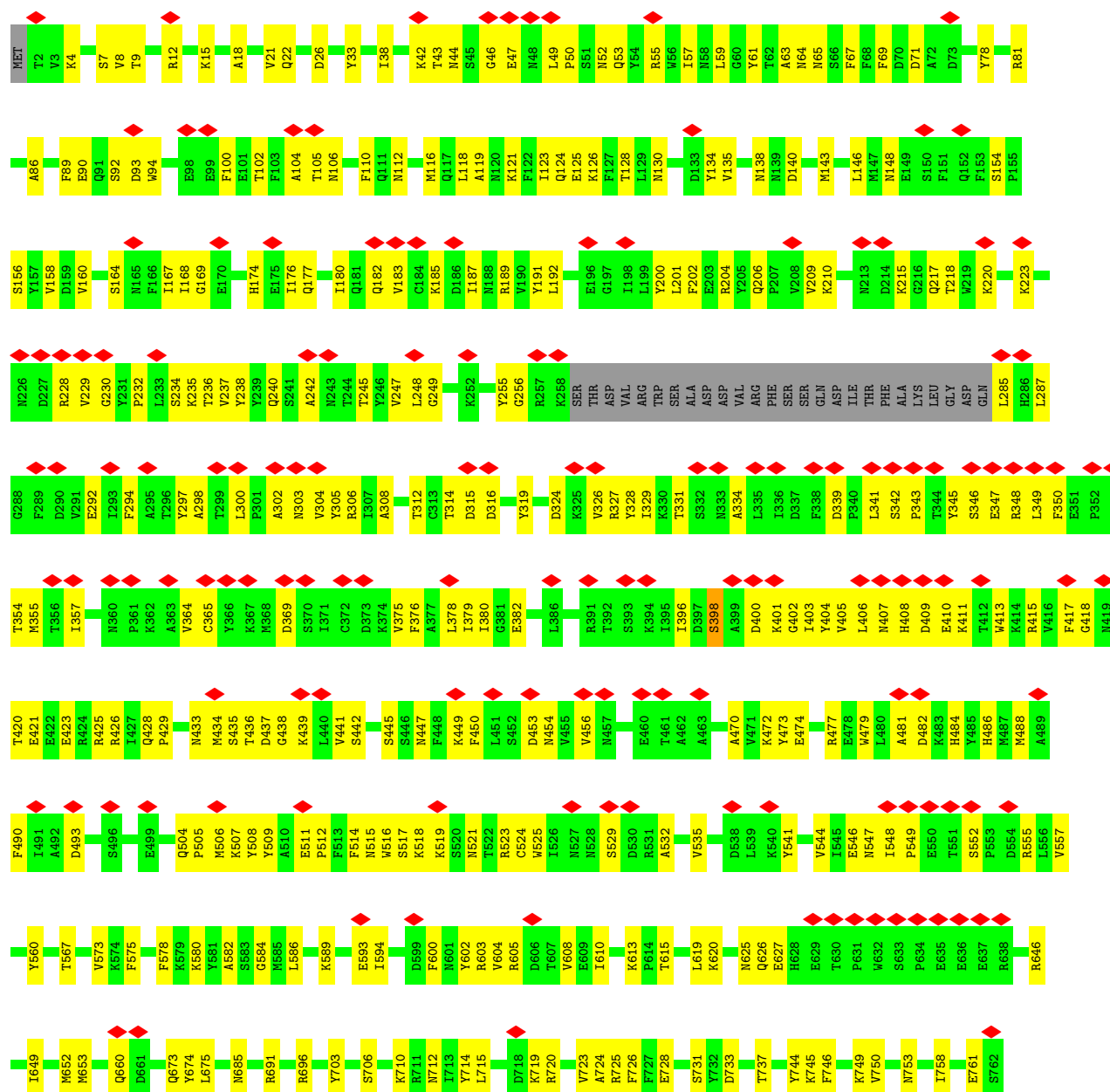
- Molecule 16: gp7, baseplate wedge protein

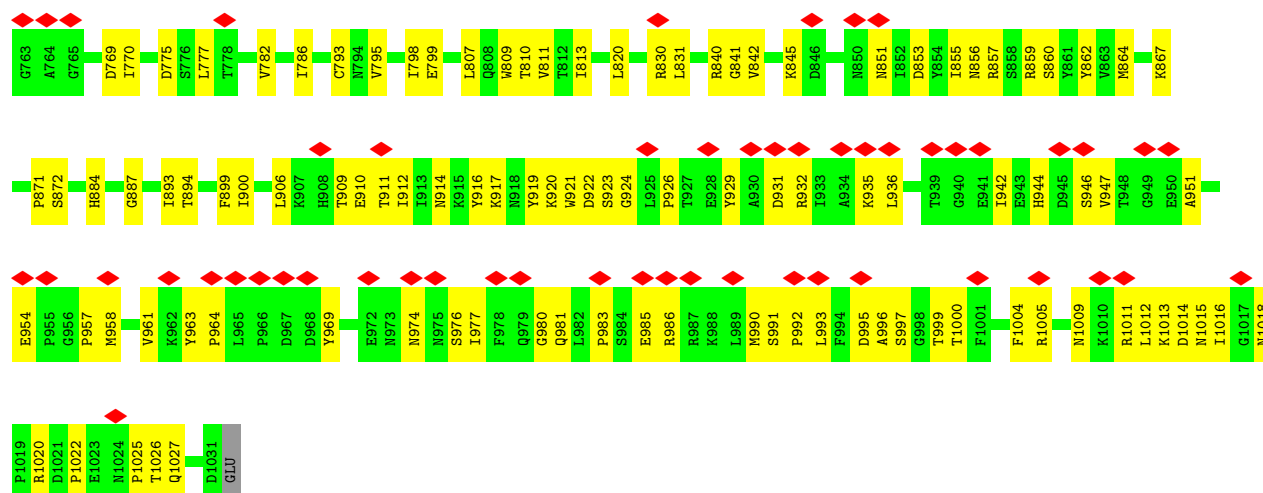




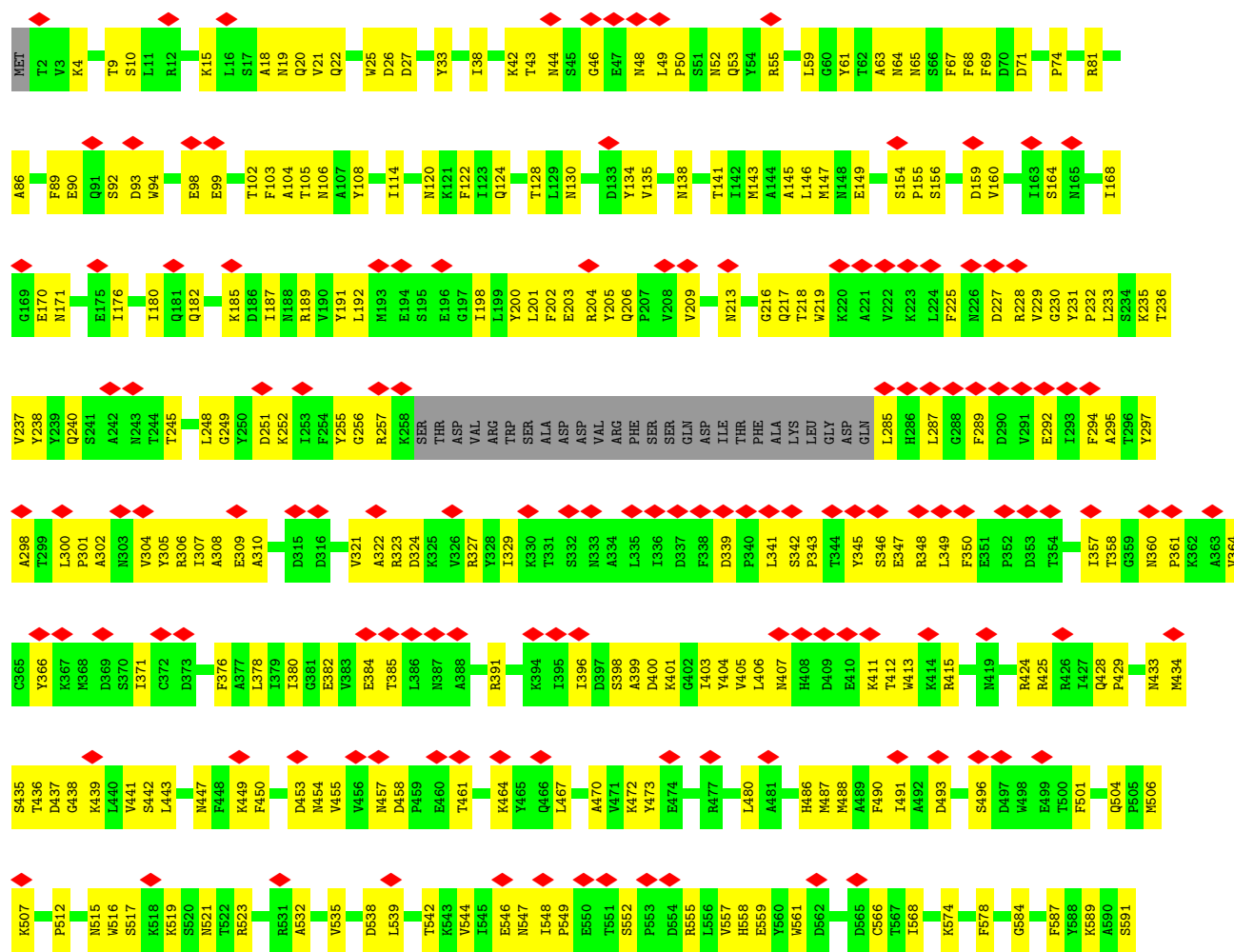


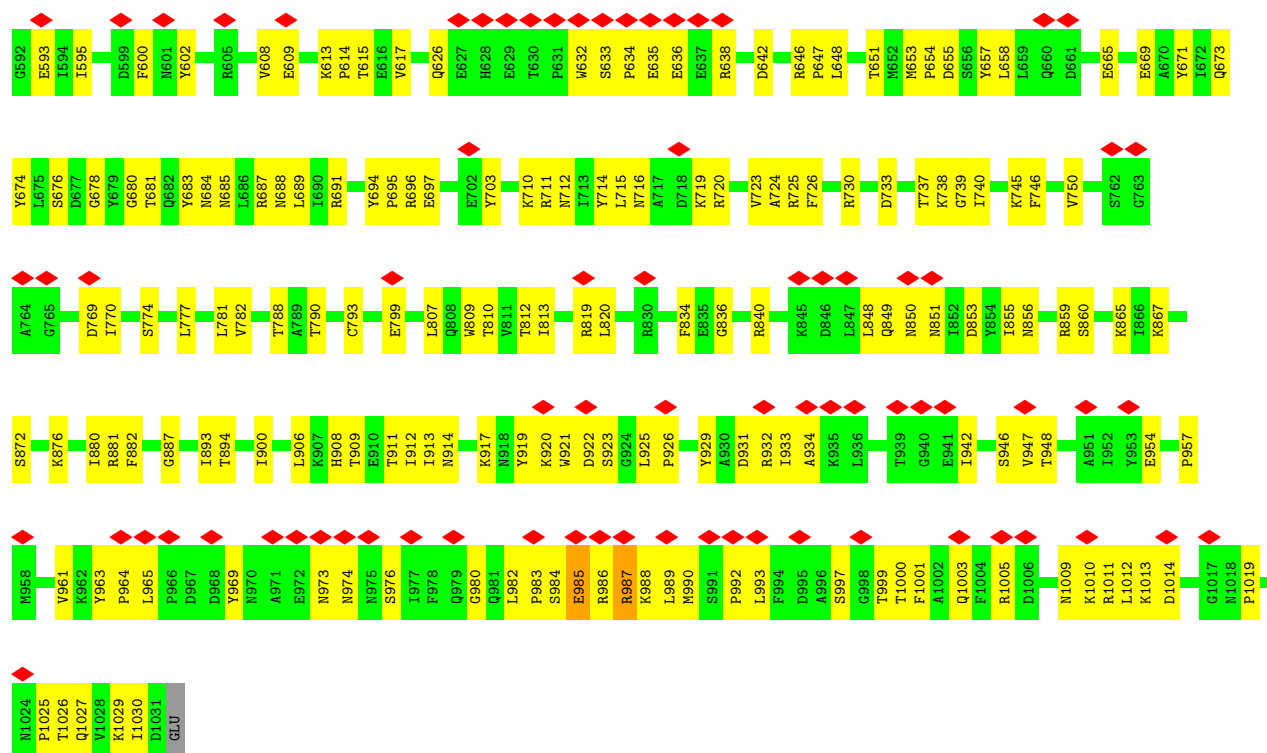
• Molecule 16: gp7, baseplate wedge protein



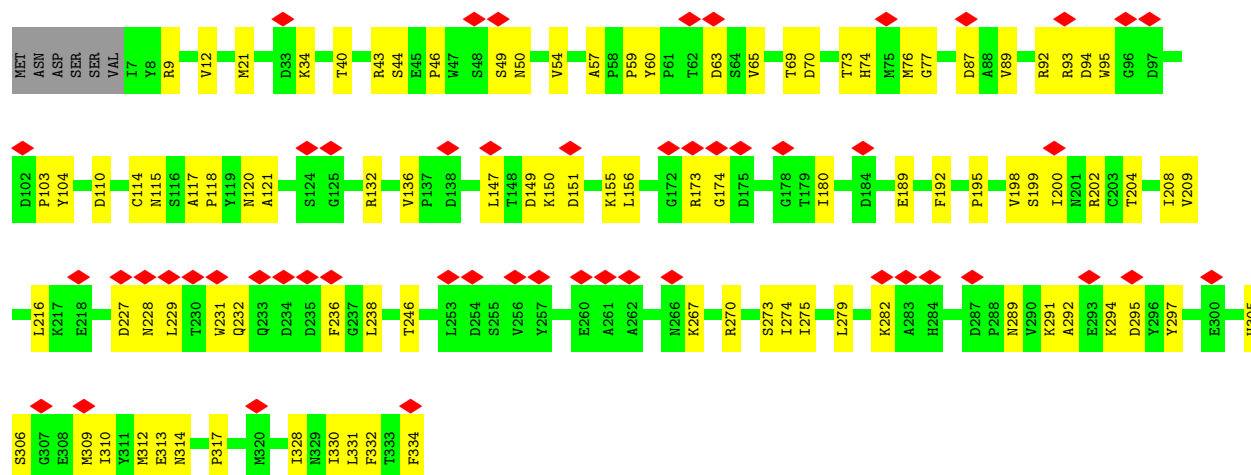


• Molecule 16: gp7, baseplate wedge protein

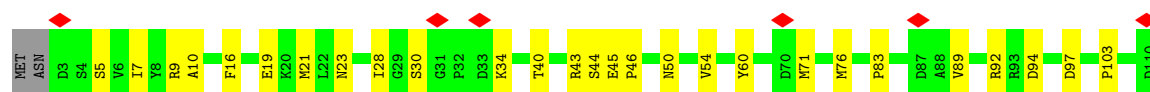
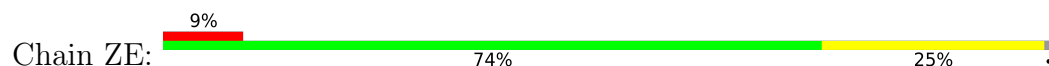


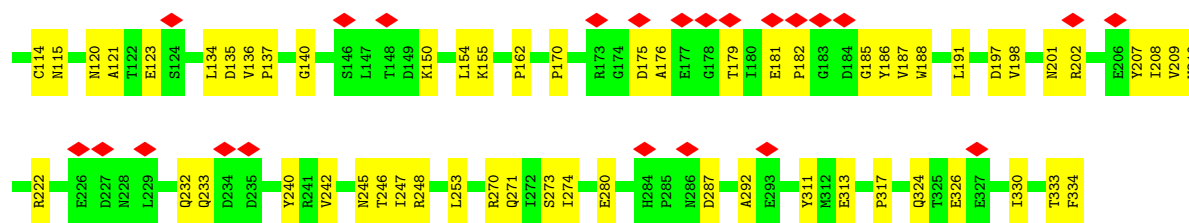


- Molecule 17: gp8, baseplate wedge protein

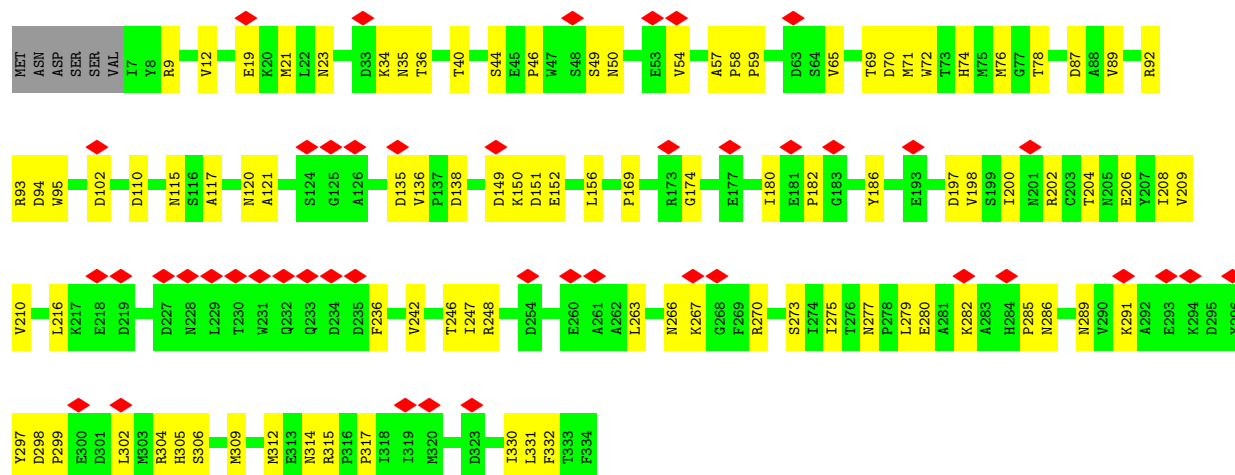
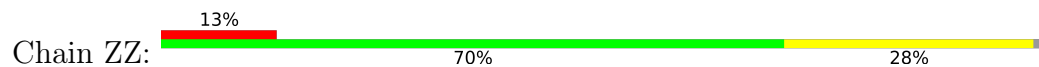


- Molecule 17: gp8, baseplate wedge protein

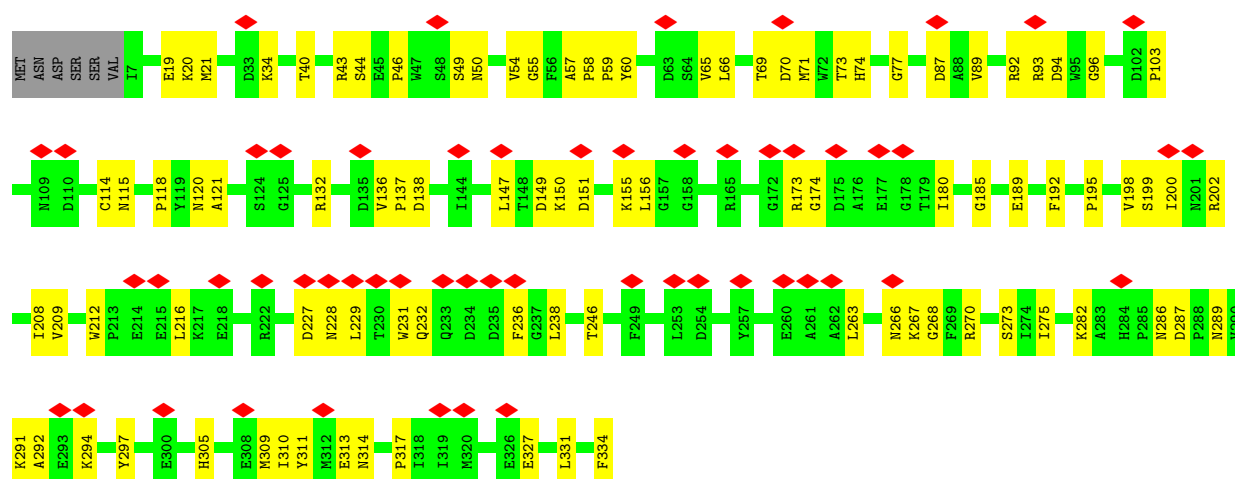




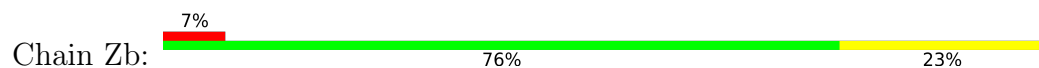
- Molecule 17: gp8, baseplate wedge protein

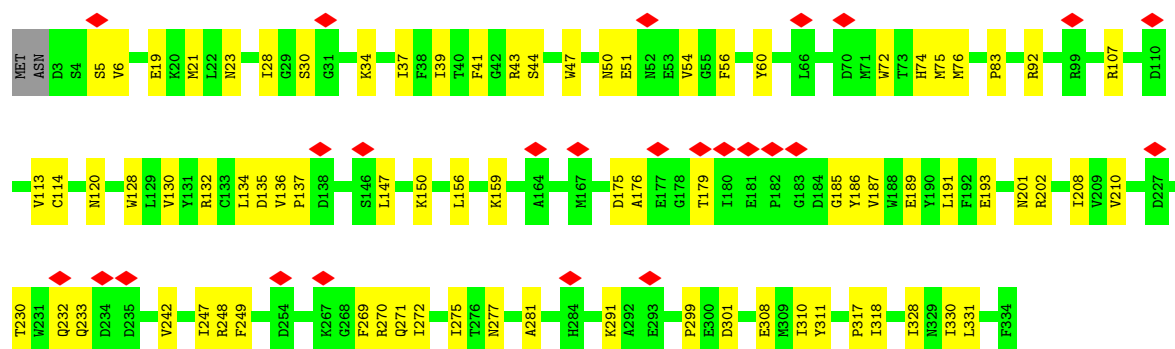


- Molecule 17: gp8, baseplate wedge protein

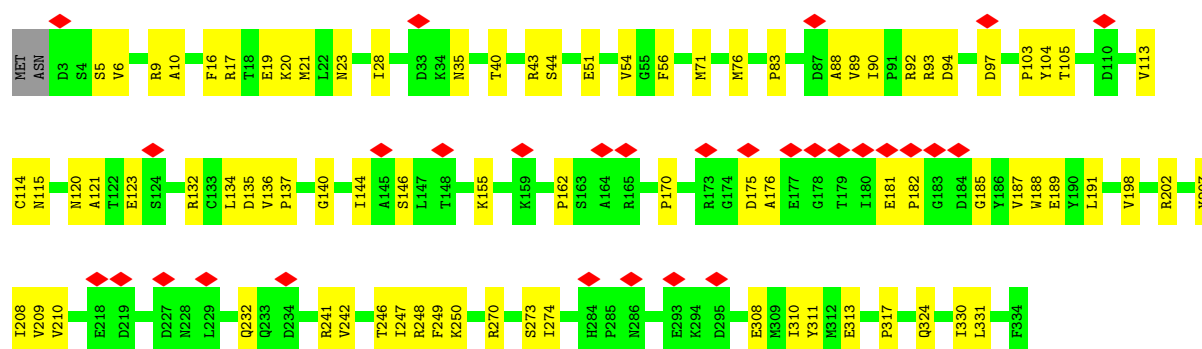
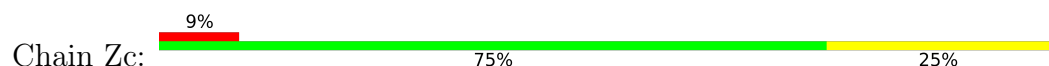


- Molecule 17: gp8, baseplate wedge protein

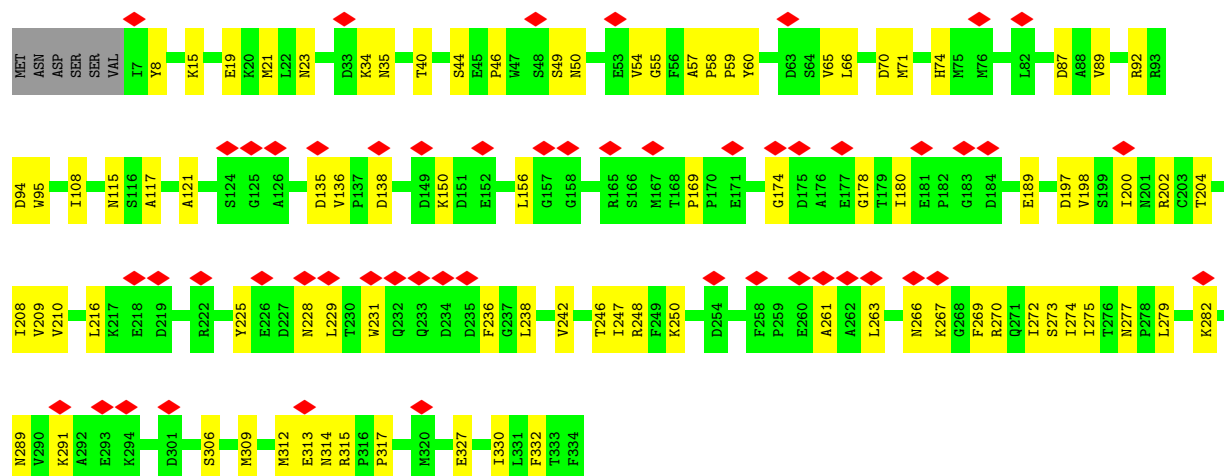
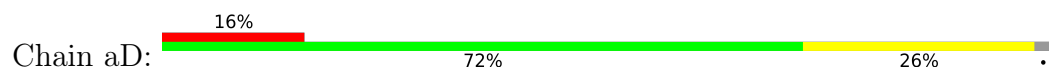




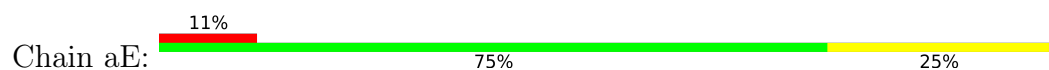
- Molecule 17: gp8, baseplate wedge protein

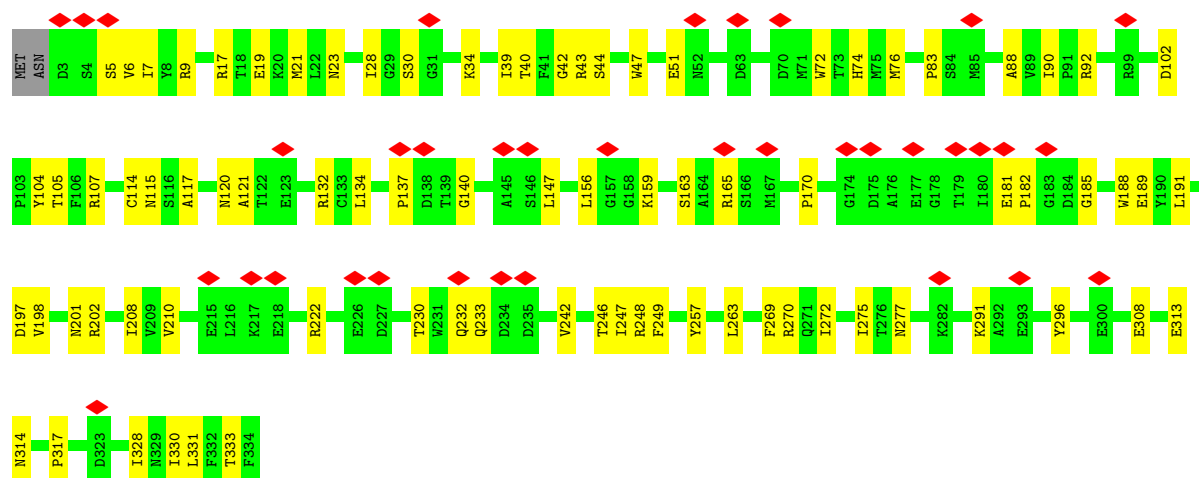


- Molecule 17: gp8, baseplate wedge protein



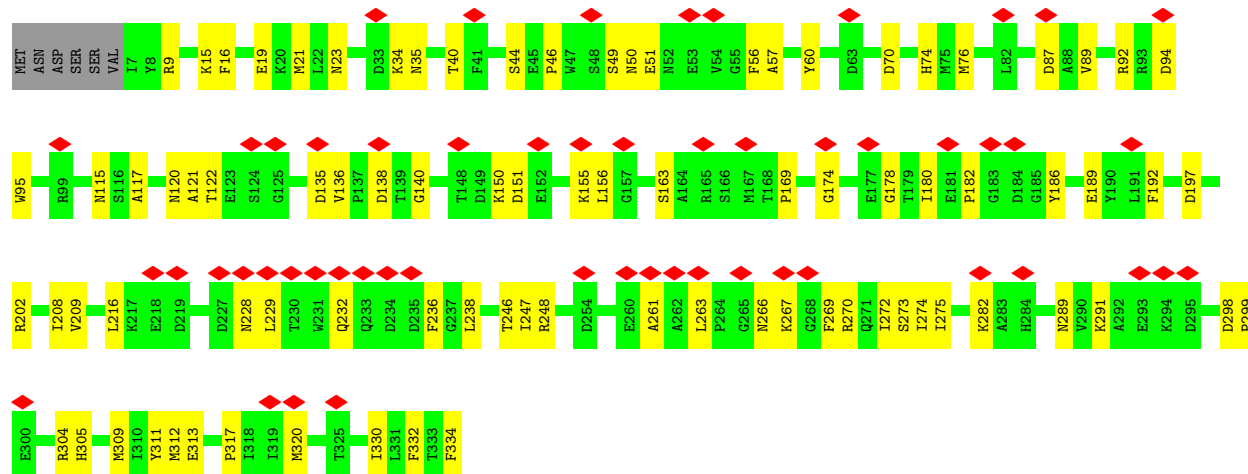
- Molecule 17: gp8, baseplate wedge protein





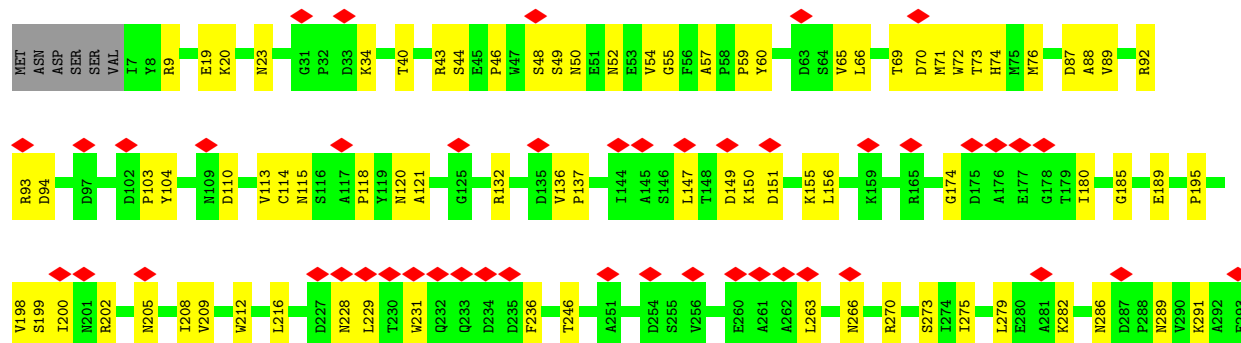
- Molecule 17: gp8, baseplate wedge protein

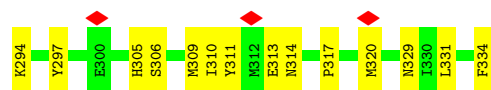
Chain aZ: 16% 72% 26%



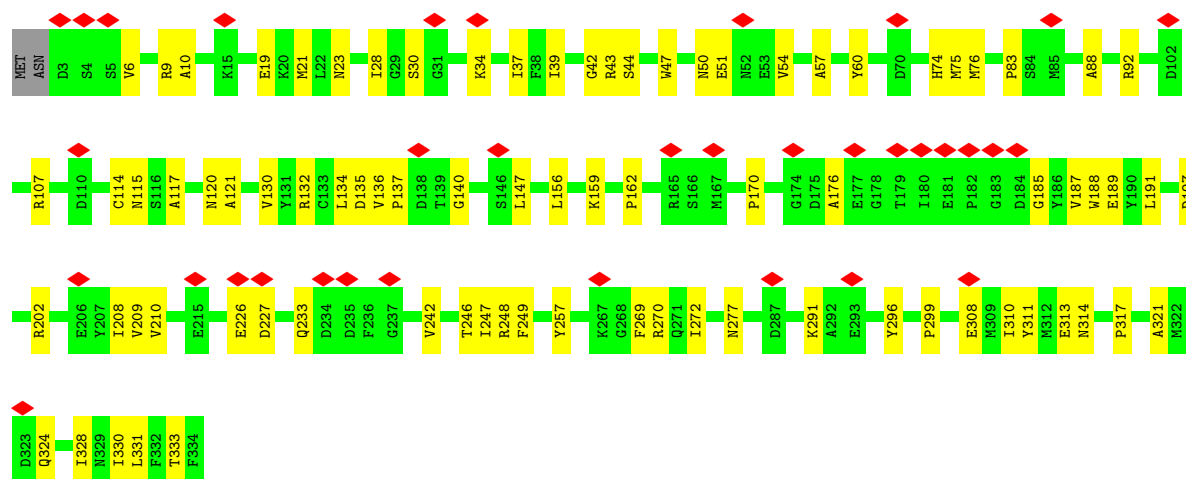
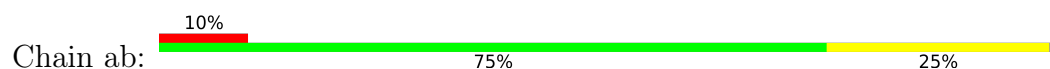
- Molecule 17: gp8, baseplate wedge protein

Chain aa: 15% 70% 28%

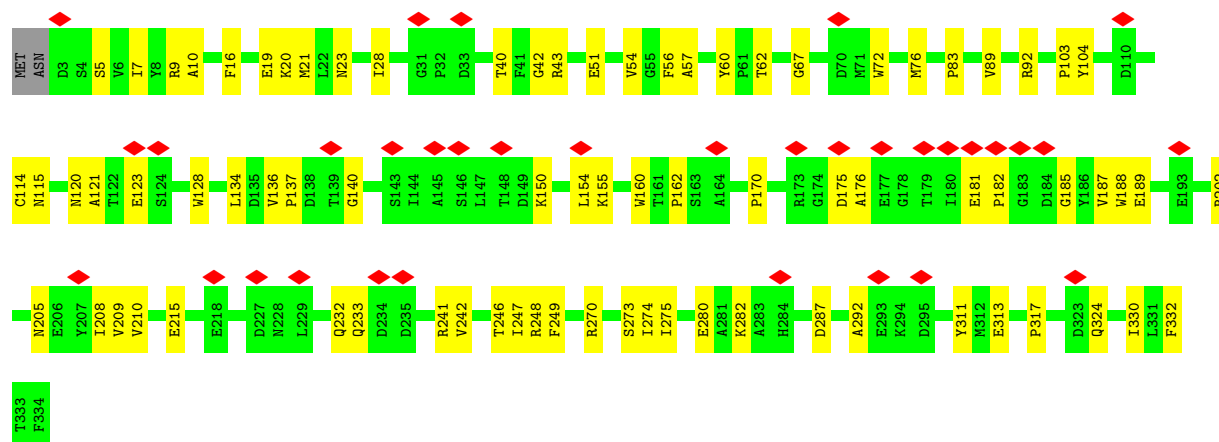
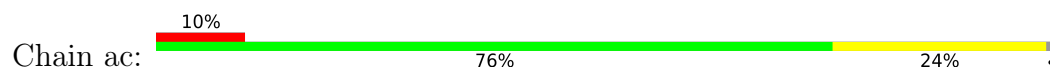




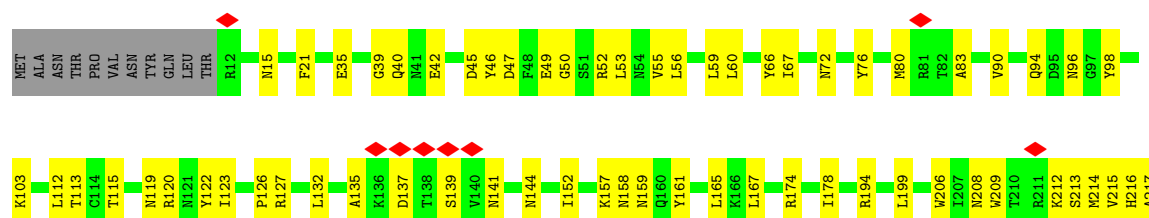
- Molecule 17: gp8, baseplate wedge protein

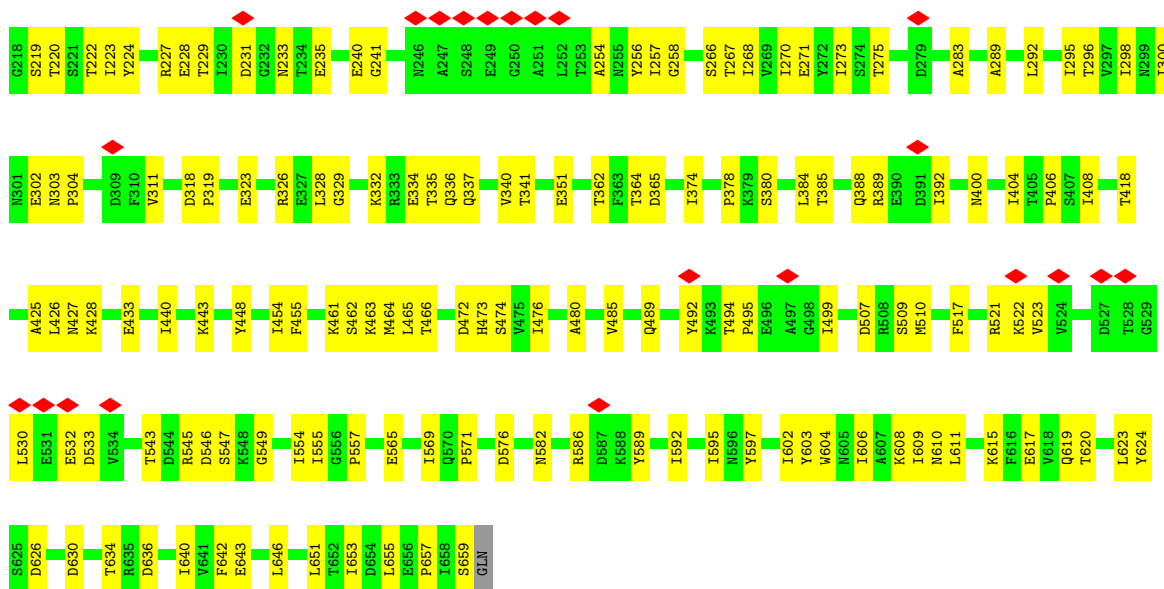


- Molecule 17: gp8, baseplate wedge protein

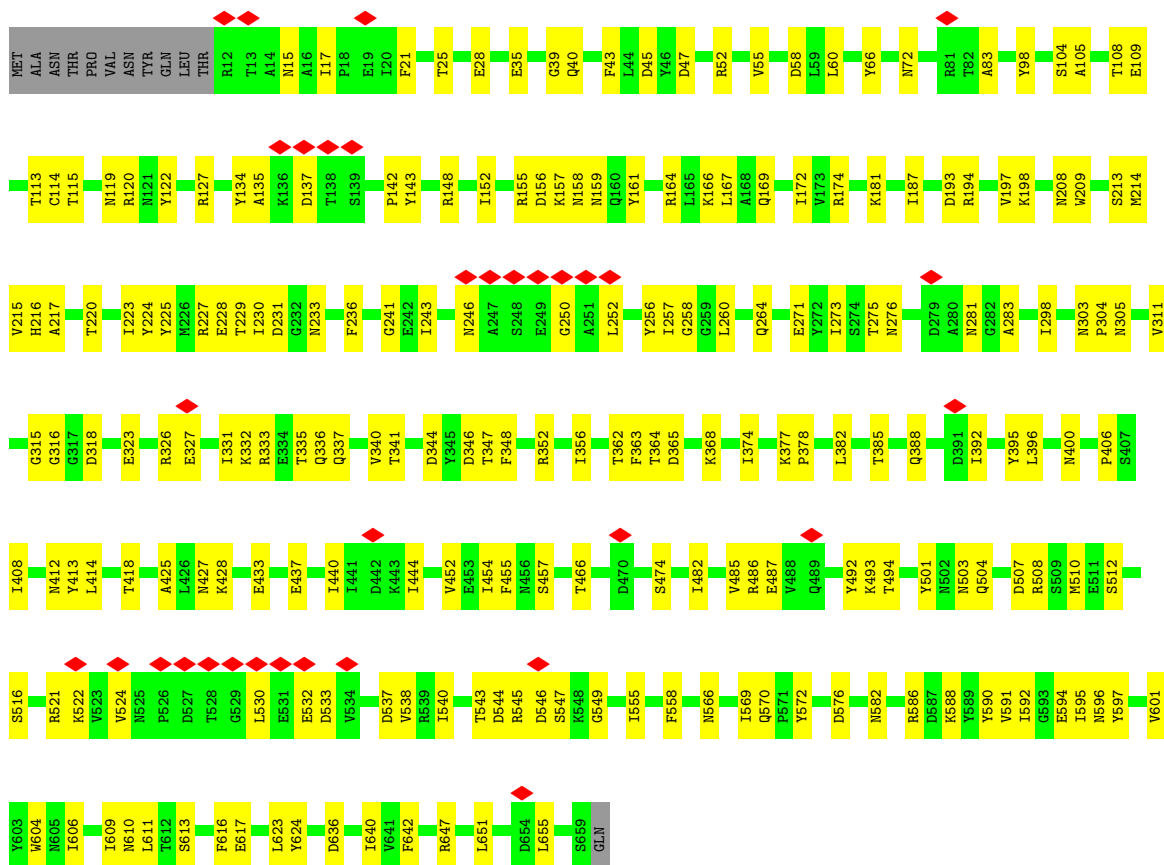


- Molecule 18: gp6, baseplate wedge protein



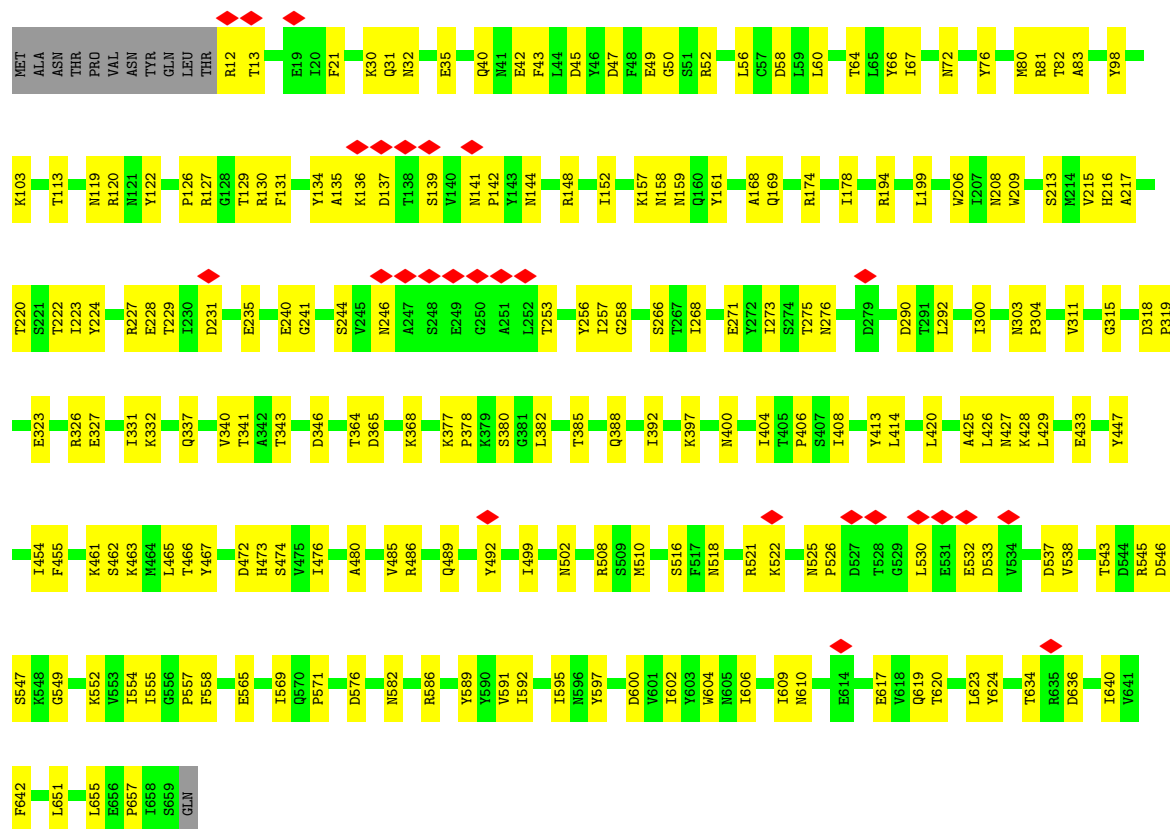


- Molecule 18: gp6, baseplate wedge protein



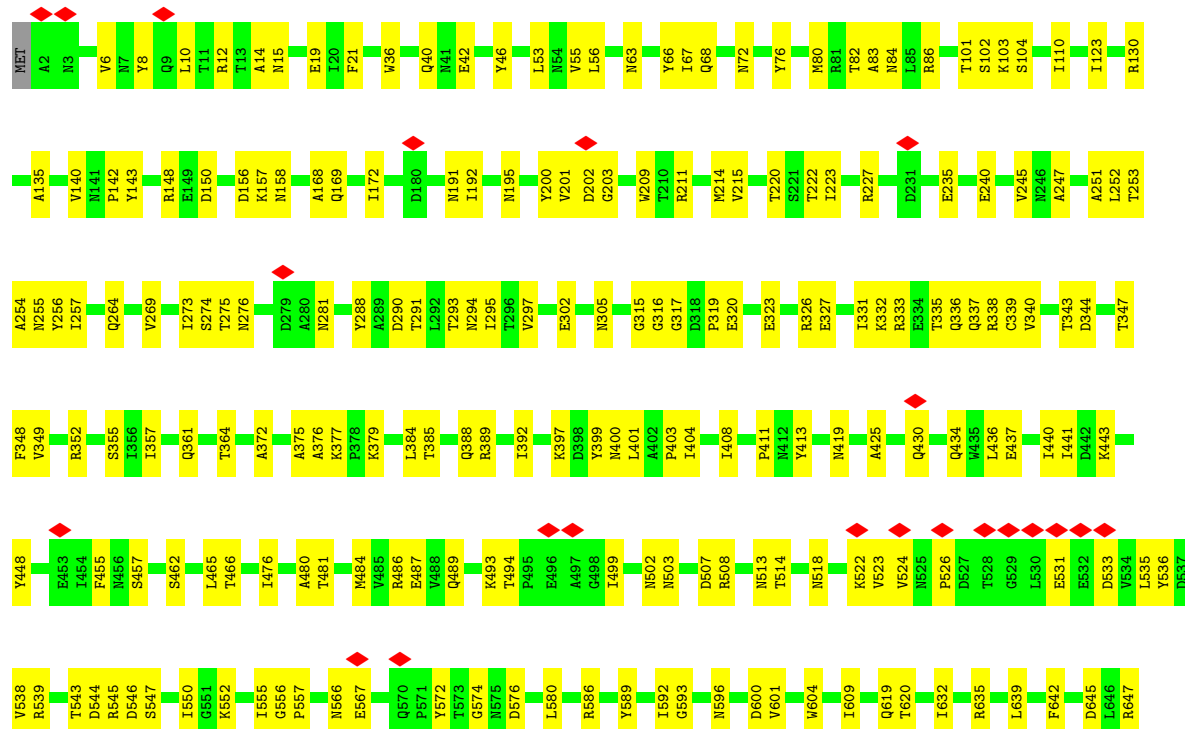
- Molecule 18: gp6, baseplate wedge protein

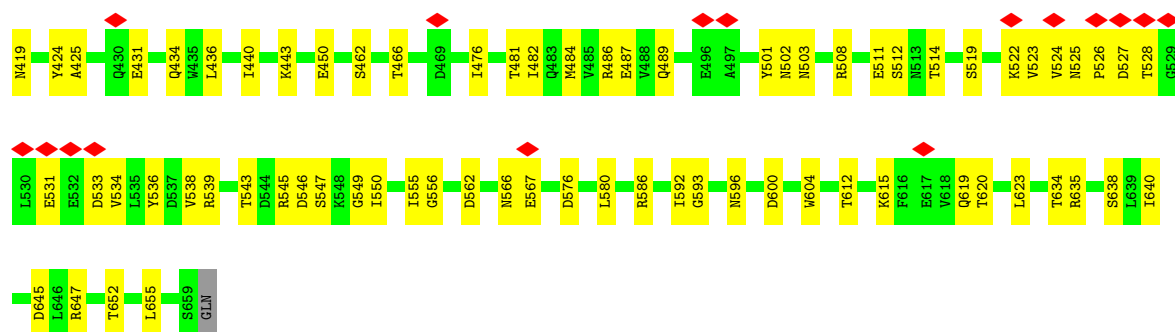




- Molecule 18: gp6, baseplate wedge protein

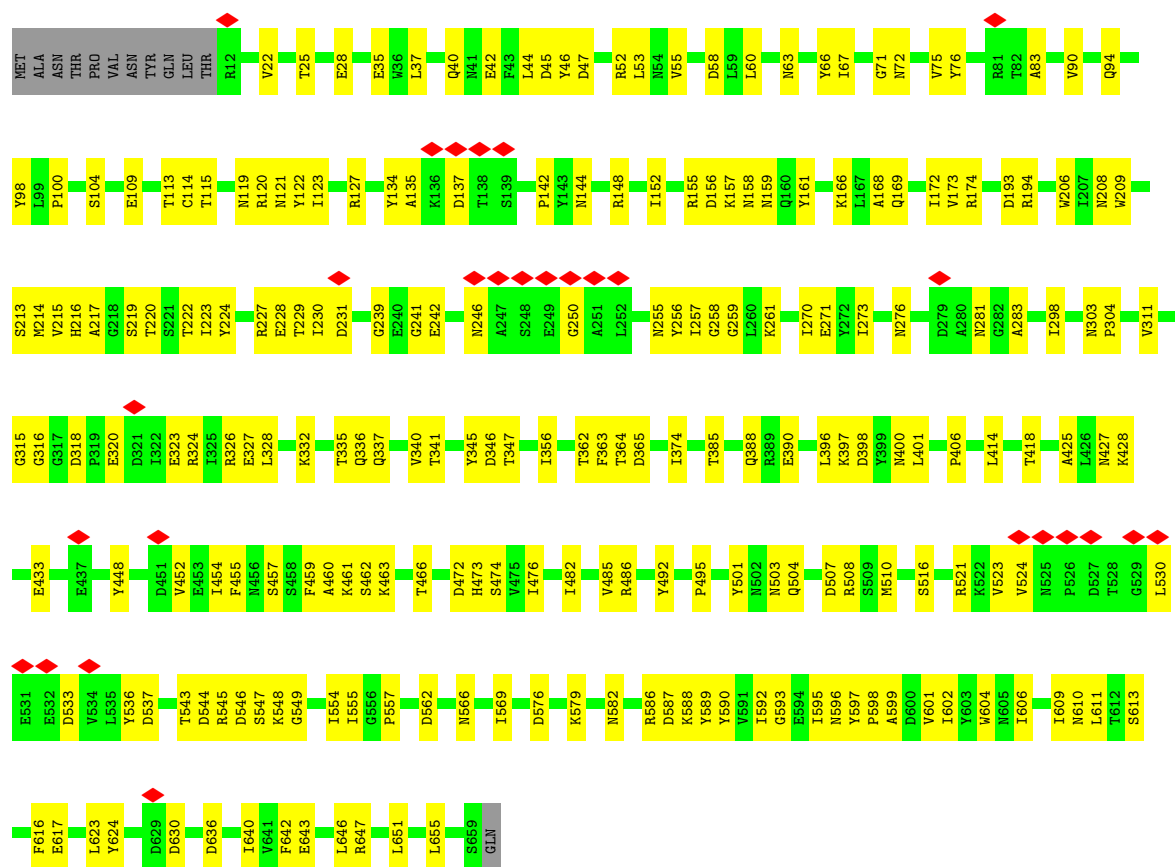
Chain f9: 68% 32%





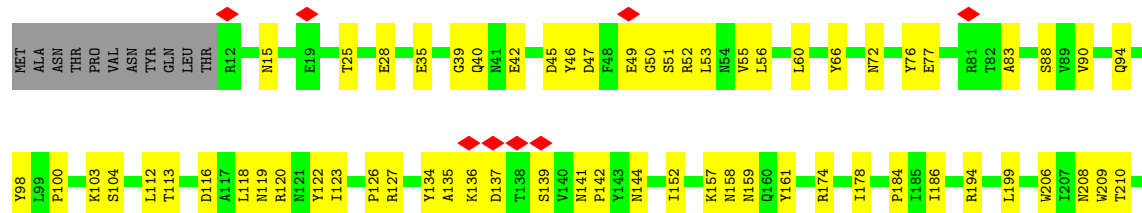
- Molecule 18: gp6, baseplate wedge protein

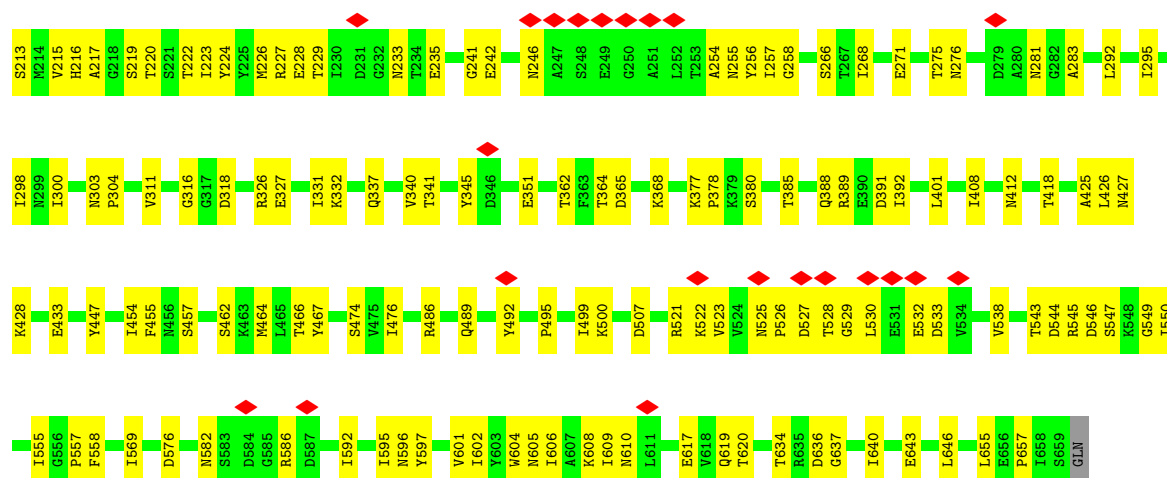
Chain fu: 65% 33%



- Molecule 18: gp6, baseplate wedge protein

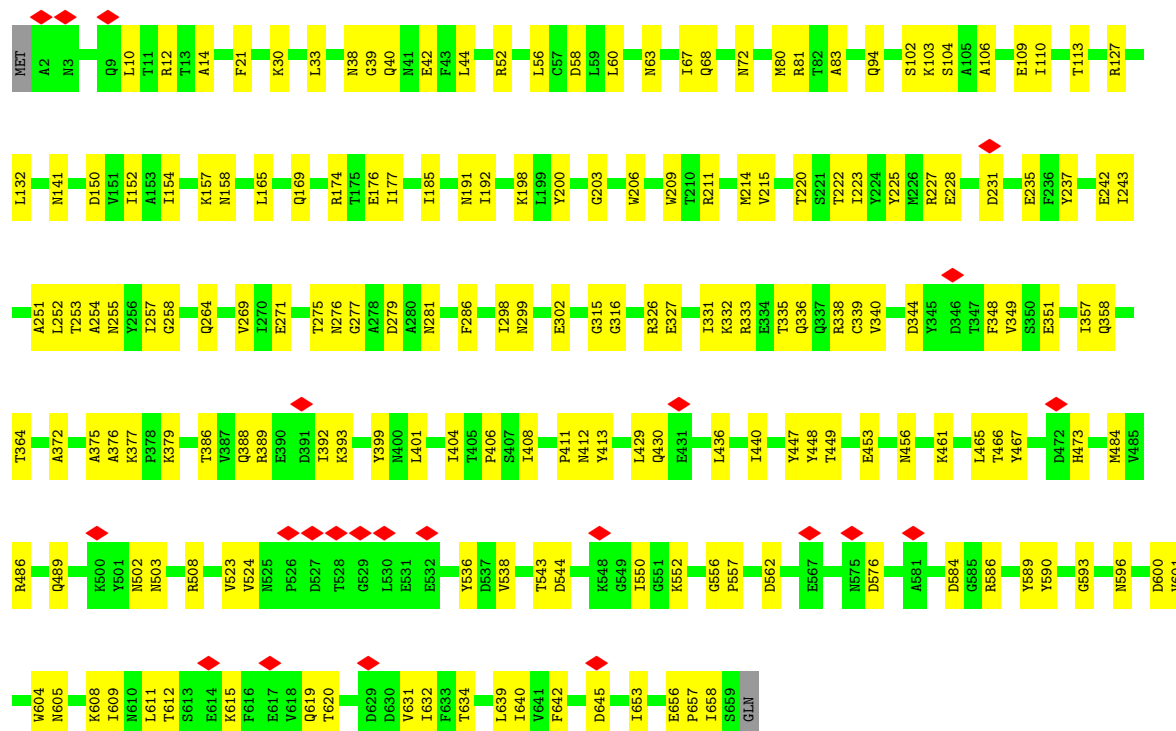
Chain fw: 5% 68% 30%





- Molecule 18: gp6, baseplate wedge protein

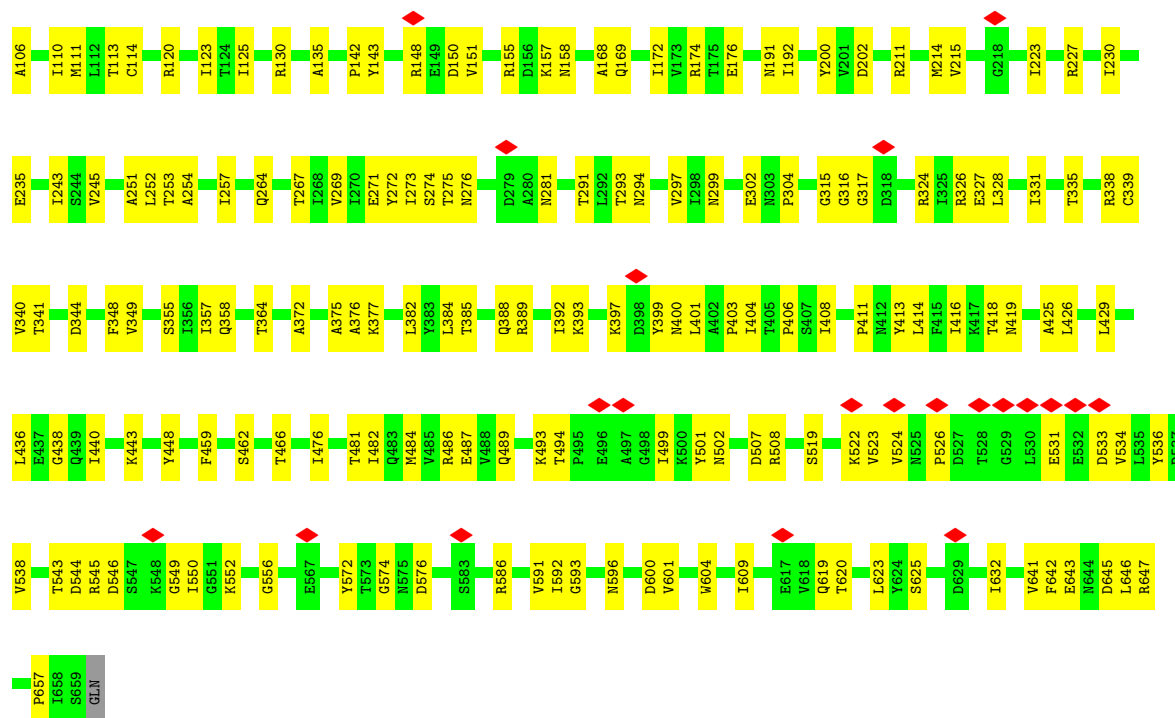
Chain fr: 72% 27%



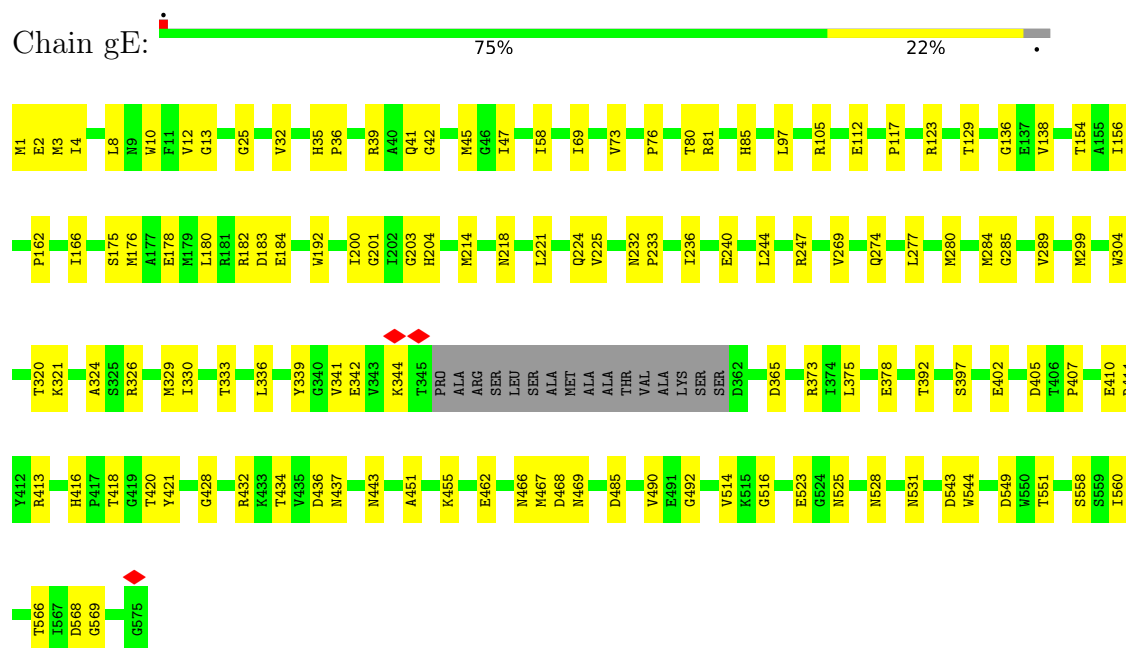
- Molecule 18: gp6, baseplate wedge protein

Chain fs: 69% 31%

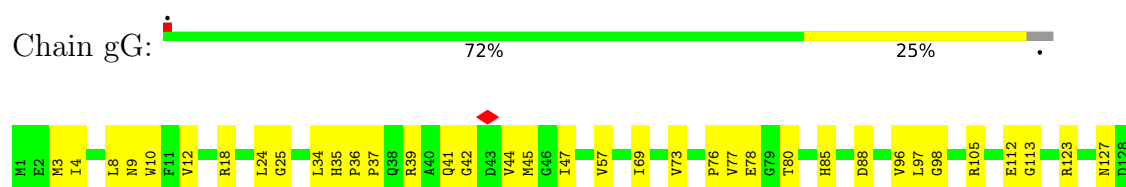


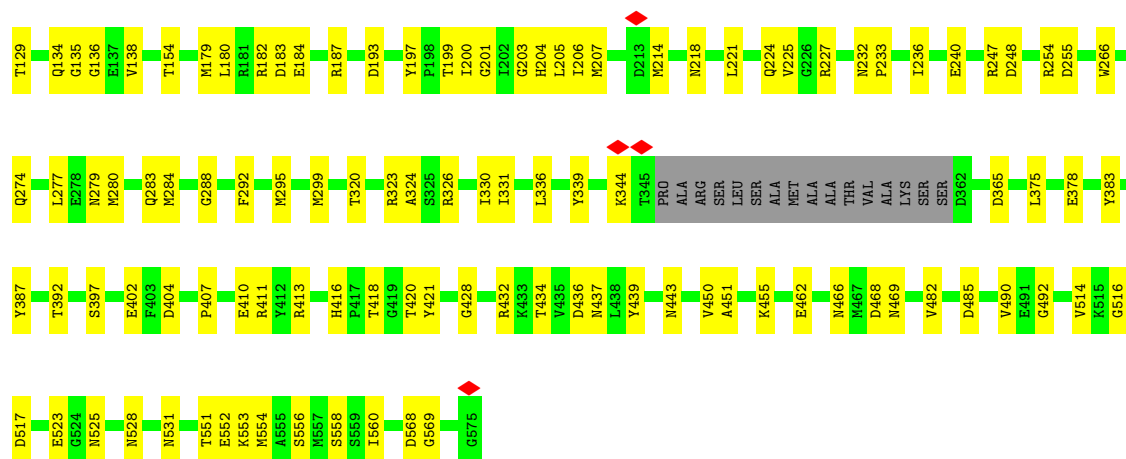


• Molecule 19: gp5, baseplate central spike protein

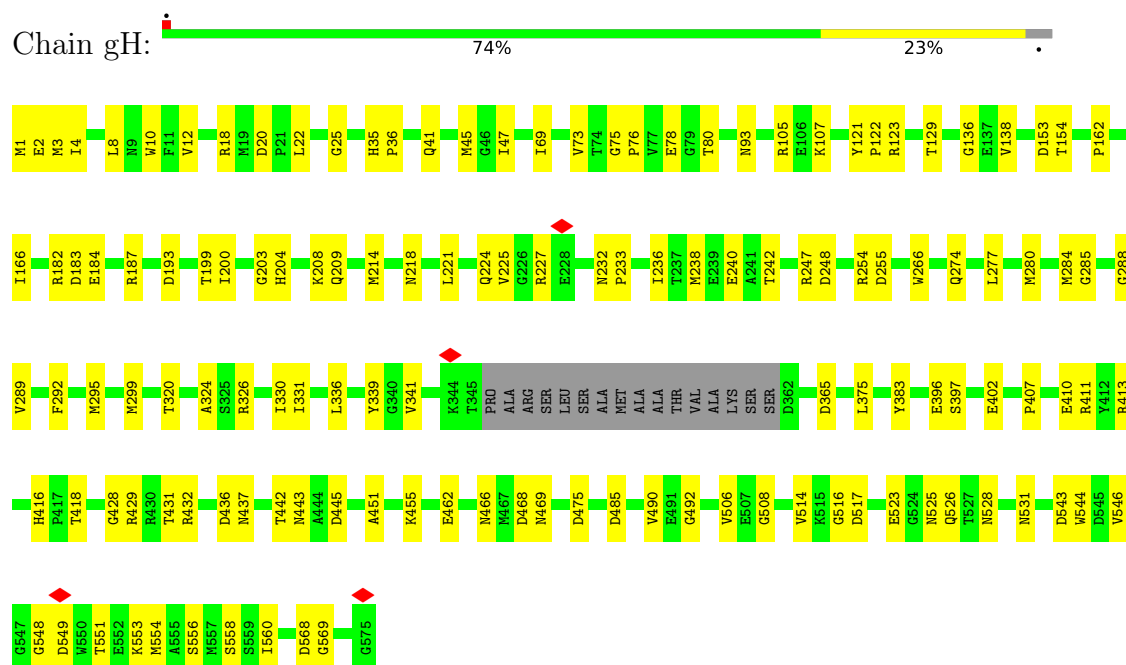


• Molecule 19: gp5, baseplate central spike protein

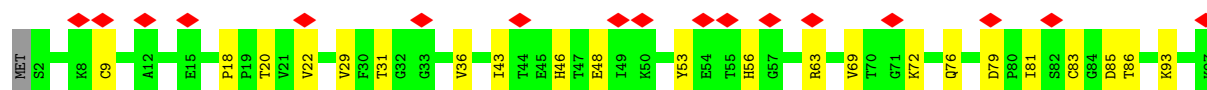
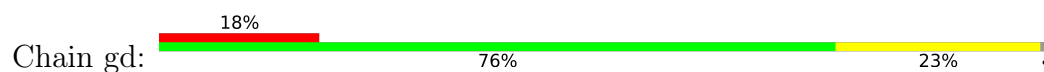




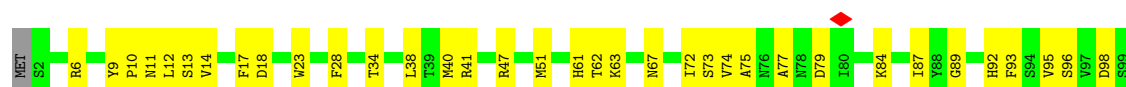
- Molecule 19: gp5, baseplate central spike protein

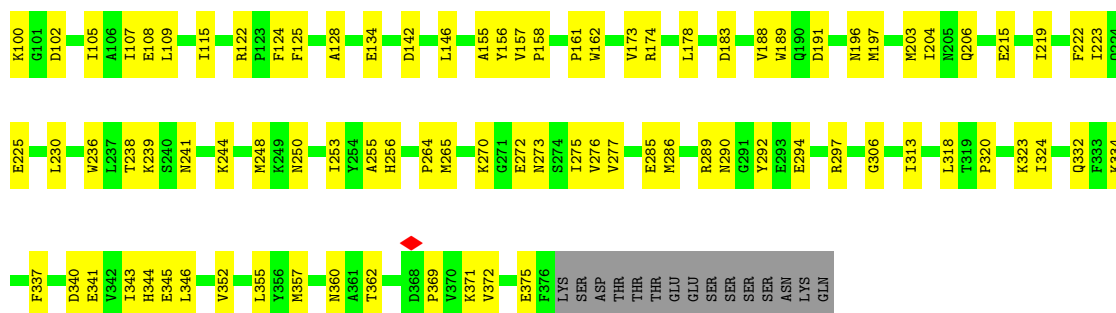


- Molecule 20: gp5.4, tip of the central spike



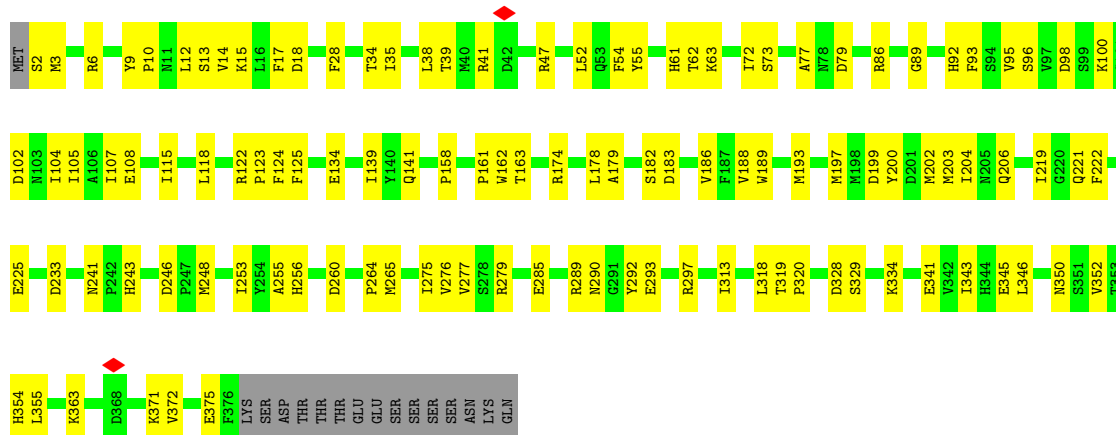
- Molecule 21: gp27, baseplate hub protein





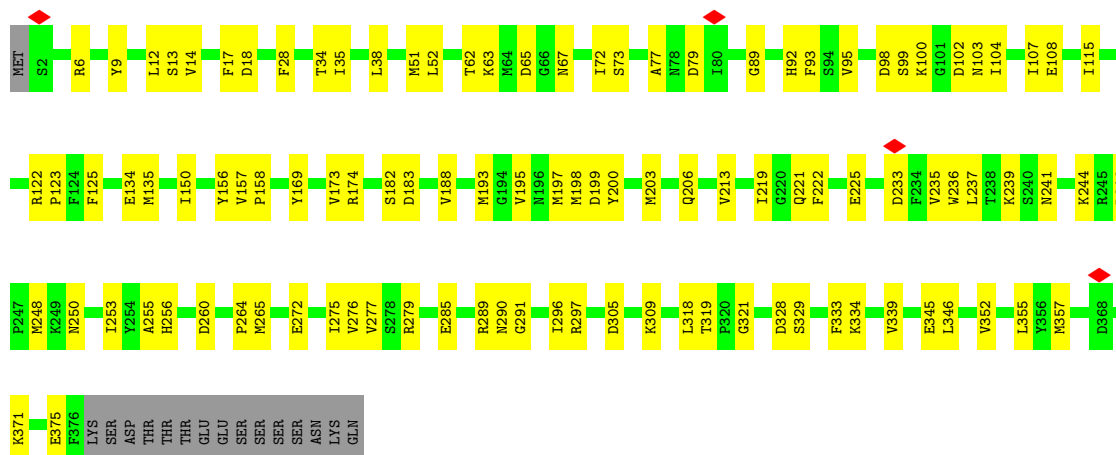
- Molecule 21: gp27, baseplate hub protein

Chain iD: 67% 29% .



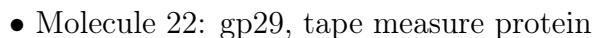
- Molecule 21: gp27, baseplate hub protein

Chain iF: 69% 27% .



- Molecule 22: gp29, tape measure protein

Chain ja: 97%



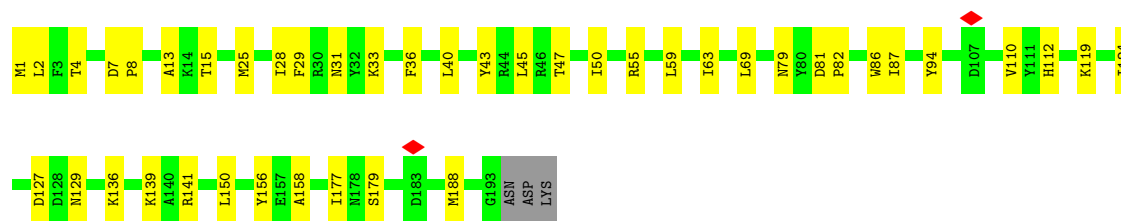
LYS ASN LYS LYS ALA ALA GLN GLN ALA ALA SER PRO PRO VAL GLN GLN GLN ALA ASN ASN THR ASN ASN ASN VAL VAL ILE ILE LYS LYS ASN THR VAL VAL VAL HIS

- Molecule 23: gp53, baseplate wedge protein

D128	M129	Y134	D135	K136	K139	A140	R141	L150	A151	Y156	K170	M188	G193	ASN	ASP	LYS	M1	F2	T4	F5	F6	D7	A13	V16	T28	F29	R30	N31	K33	D34	Y35	F36	L40	A41	G42	Y43	R44	Y48	Y49	P56	L59	I63	W71	V72	L73	L74	P82	W86	Y94	I98	D107	H112	E118	K119	I124	P137
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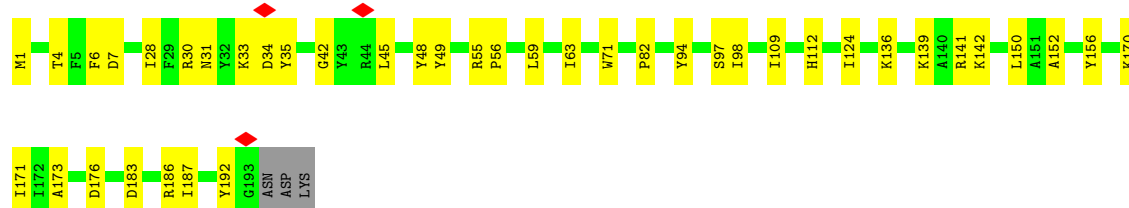
- Molecule 23: gp53, baseplate wedge protein





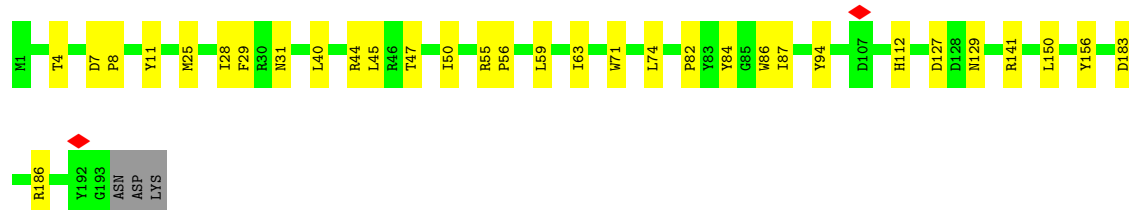
- Molecule 23: gp53, baseplate wedge protein

Chain k7: 78% 21%



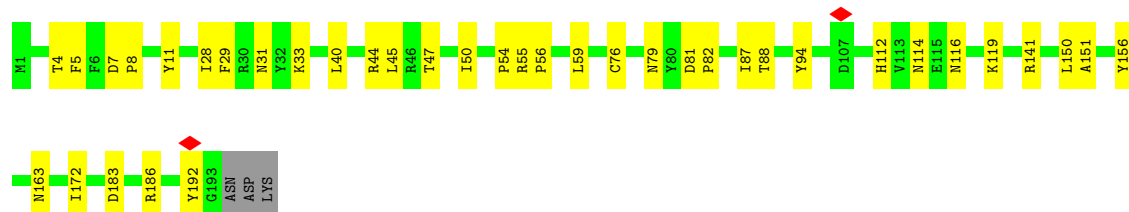
- Molecule 23: gp53, baseplate wedge protein

Chain k8: 82% 16%



- Molecule 23: gp53, baseplate wedge protein

Chain kV: 79% 19%



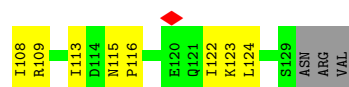
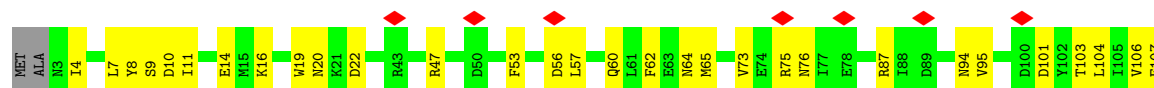
- Molecule 23: gp53, baseplate wedge protein

Chain IV: 74% 24%

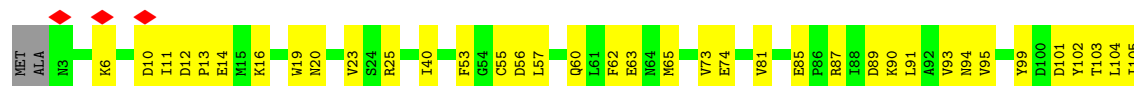




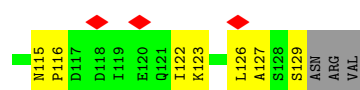
- Molecule 24: gp25, baseplate protein



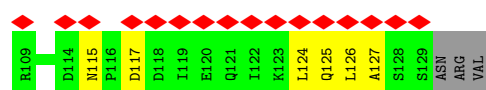
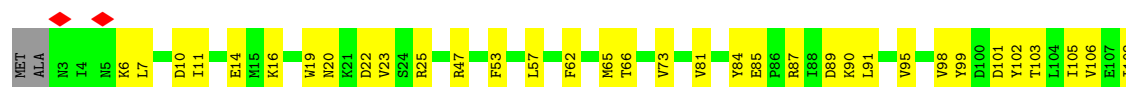
- Molecule 24: gp25, baseplate protein



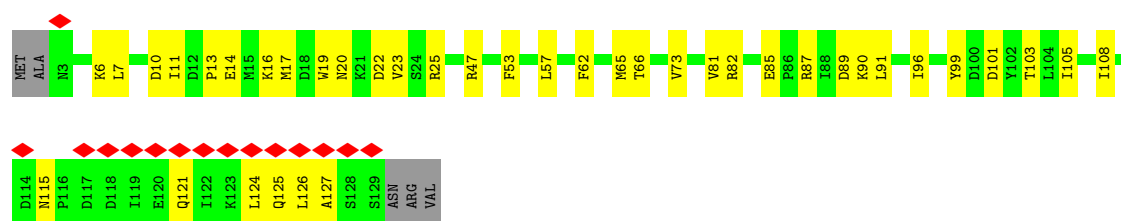
- Molecule 24: gp25, baseplate protein



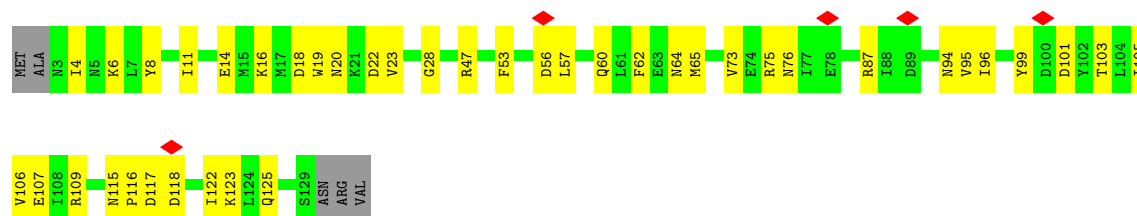
- Molecule 24: gp25, baseplate protein



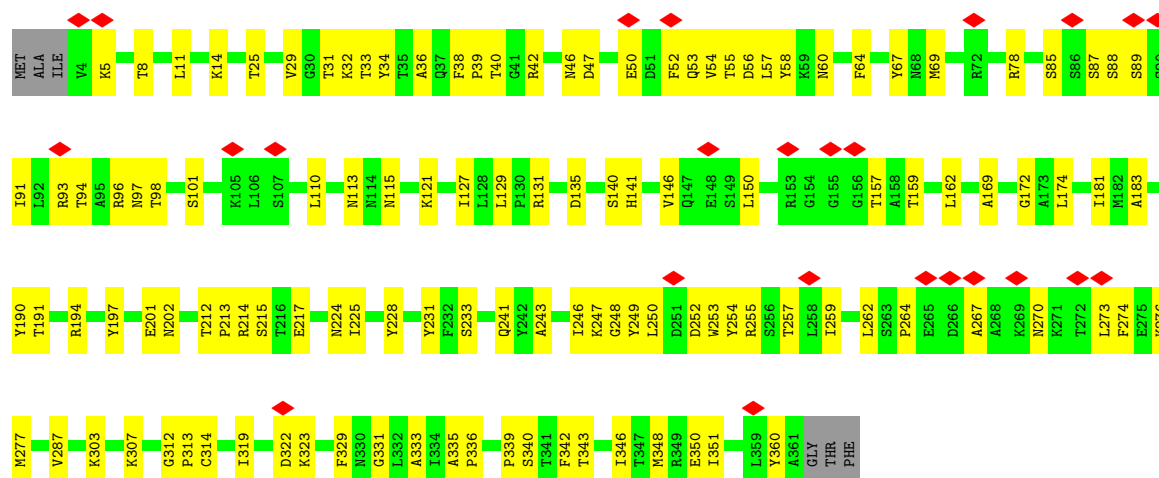
- Molecule 24: gp25, baseplate protein



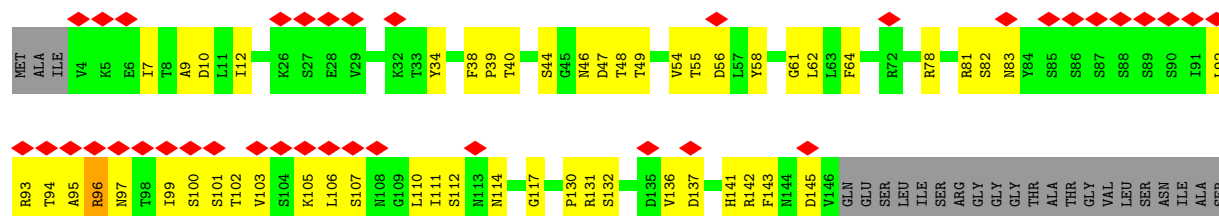
- Molecule 24: gp25, baseplate protein

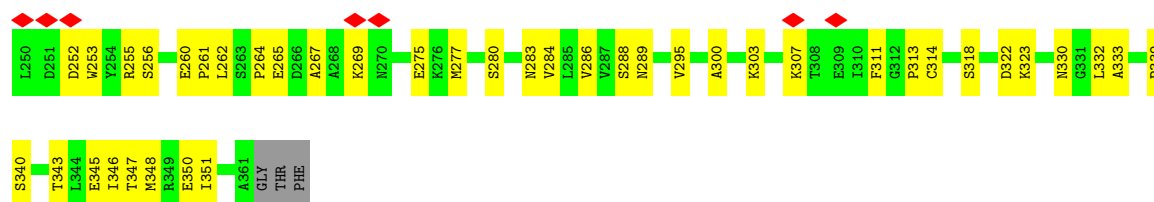


- Molecule 25: gp48, baseplate protein

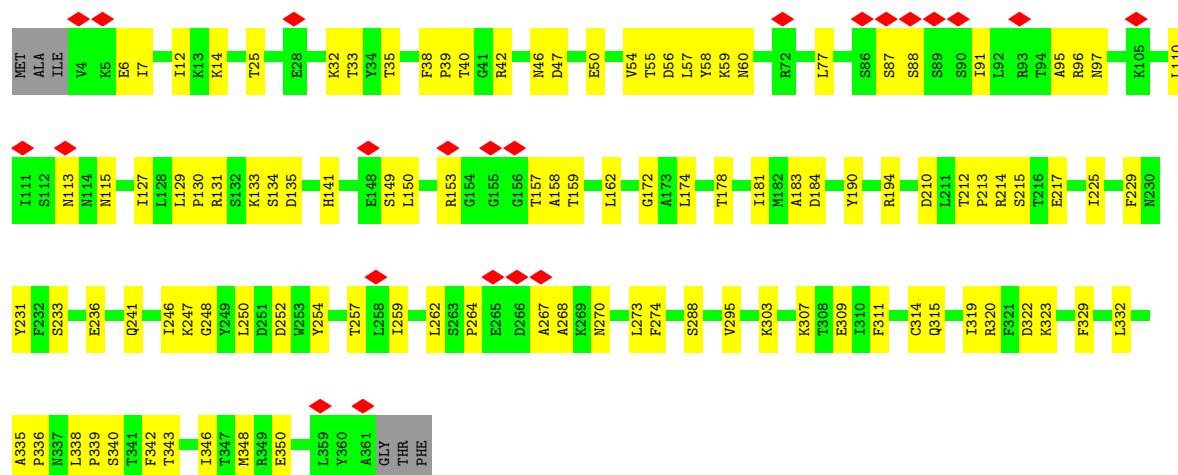


- Molecule 25: gp48, baseplate protein

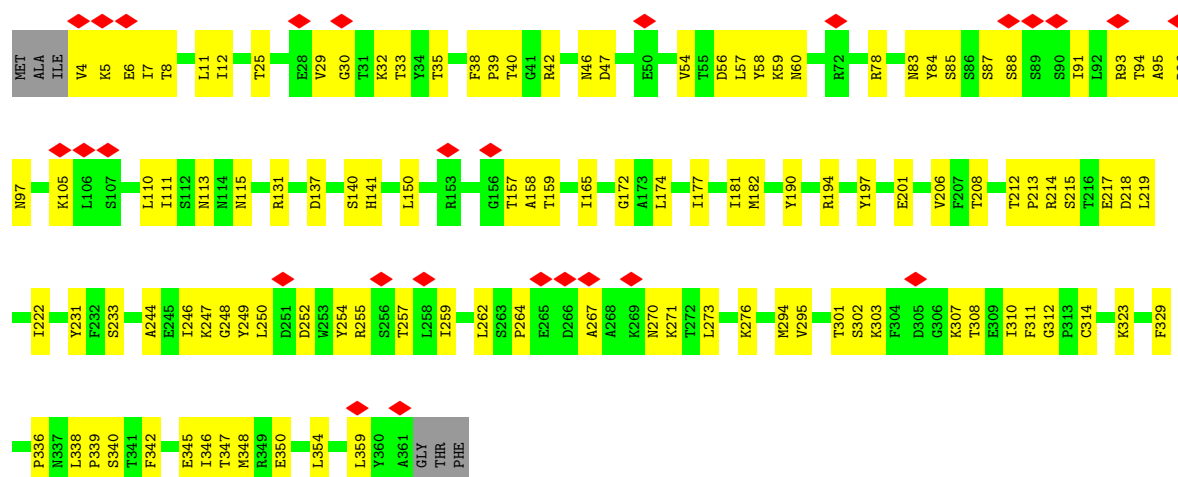




- Molecule 25: gp48, baseplate protein



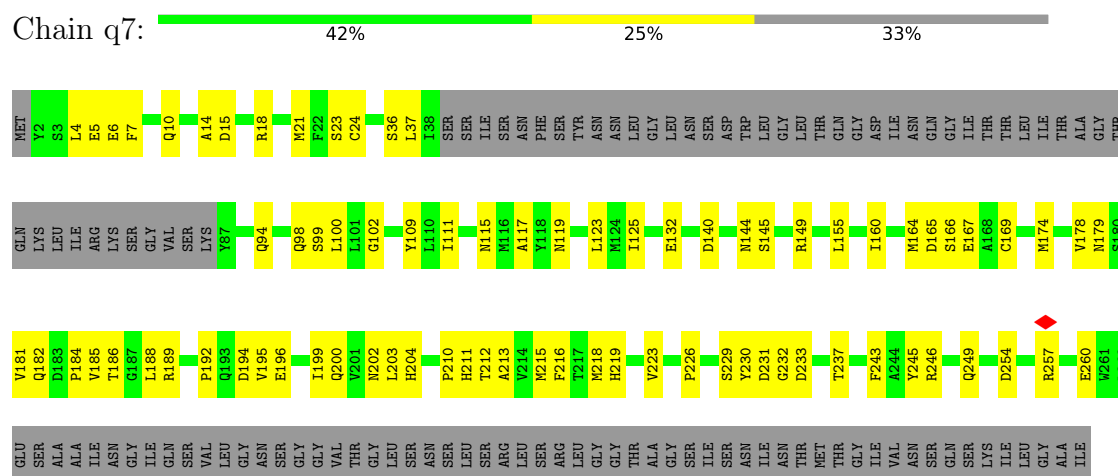
- Molecule 25: gp48, baseplate protein



- Molecule 26: gp54, baseplate protein

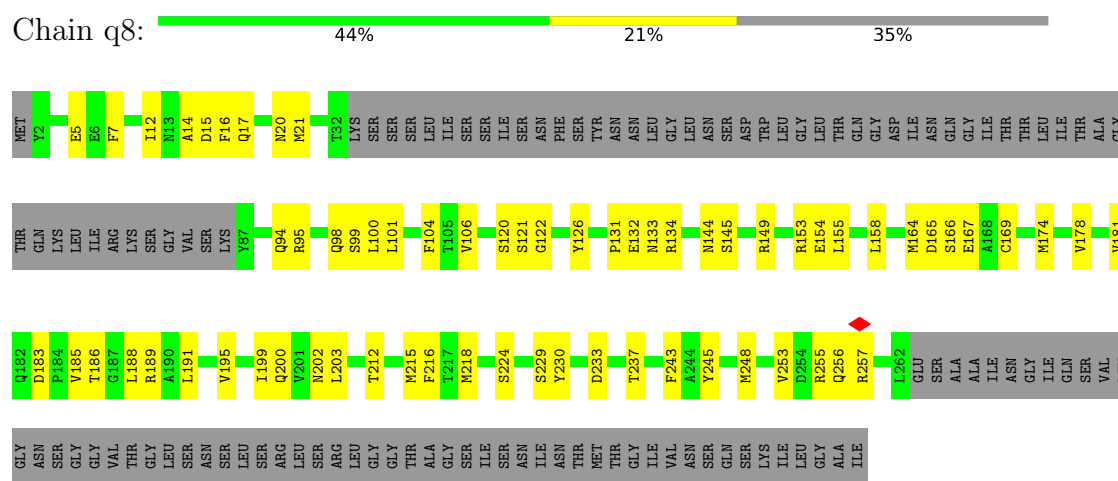


Chain q7:



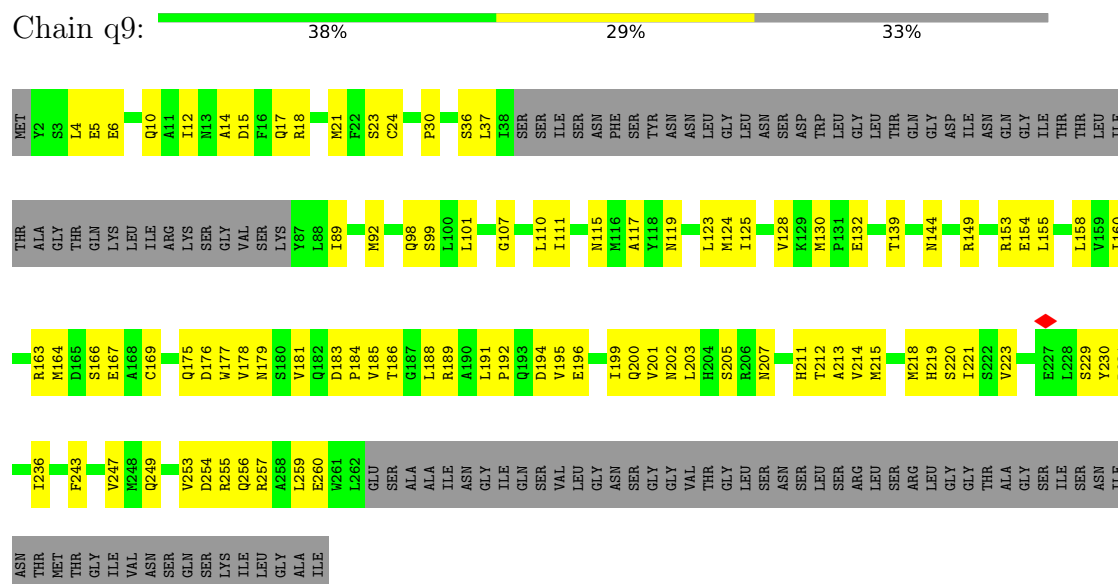
- Molecule 26: gp54, baseplate protein

Chain q8:



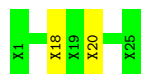
- Molecule 26: gp54, baseplate protein

Chain q9:




- Molecule 27: unassigned peptide A

Chain rc:  92% 8%




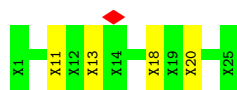
- Molecule 27: unassigned peptide A

Chain rd:  84% 16%




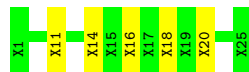
- Molecule 27: unassigned peptide A

Chain re:  84% 16%



- Molecule 27: unassigned peptide A

Chain rf:  80% 20%



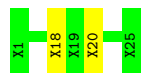
- Molecule 27: unassigned peptide A

Chain rg:  100%

There are no outlier residues recorded for this chain.

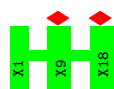
- Molecule 27: unassigned peptide A

Chain rh:  92% 8%

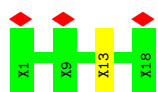


- Molecule 28: unassigned peptide B

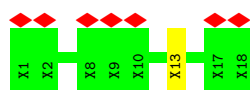
Chain sQ:  11% 100%



- Molecule 28: unassigned peptide B



- Molecule 28: unassigned peptide B



- Molecule 29: unassigned peptide C



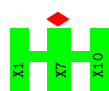
There are no outlier residues recorded for this chain.

- Molecule 29: unassigned peptide C

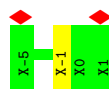
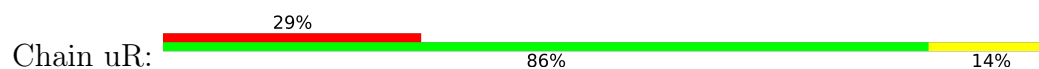


There are no outlier residues recorded for this chain.

- Molecule 29: unassigned peptide C



- Molecule 30: unassigned peptide D



- Molecule 30: unassigned peptide D



- Molecule 30: unassigned peptide D





- Molecule 31: unassigned peptide E

Chain vZ:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: unassigned peptide E

Chain va:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: unassigned peptide E

Chain vb:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	659.328, 657.71204, 1664.4801	wwPDB
Map dimensions	408, 407, 1030	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.616, 1.616, 1.616	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.12	0/2042	0.39	0/2768
1	k	0.13	0/2042	0.40	0/2768
1	l	0.13	0/2042	0.41	0/2768
1	m	0.12	0/2042	0.38	0/2768
1	n	0.13	0/2042	0.38	0/2768
1	p	0.13	0/2042	0.39	0/2768
2	1	0.11	0/5077	0.31	1/6907 (0.0%)
2	2	0.11	0/5077	0.31	0/6907
2	3	0.11	0/5077	0.32	1/6907 (0.0%)
2	4	0.11	0/5077	0.31	0/6907
2	5	0.11	0/5077	0.31	0/6907
2	AD	0.11	0/5077	0.30	0/6907
2	AK	0.10	0/5092	0.30	0/6928
2	AL	0.10	0/5092	0.31	0/6928
2	AM	0.10	0/5092	0.29	0/6928
2	AN	0.10	0/5092	0.31	0/6928
2	AO	0.11	0/5092	0.32	0/6928
2	AP	0.10	0/5092	0.30	0/6928
2	B1	0.10	0/5092	0.32	0/6928
2	B2	0.11	0/5092	0.30	0/6928
2	B3	0.10	0/5092	0.31	0/6928
2	B4	0.10	0/5092	0.32	1/6928 (0.0%)
2	B5	0.10	0/5092	0.30	0/6928
2	B6	0.10	0/5092	0.29	0/6928
2	B7	0.10	0/5092	0.30	0/6928
2	Bp	0.10	0/5092	0.31	0/6928
2	Bq	0.10	0/5092	0.30	0/6928
2	Br	0.10	0/5092	0.30	0/6928
2	Bs	0.10	0/5092	0.31	0/6928
2	Bt	0.10	0/5092	0.29	0/6928
2	Bu	0.10	0/5092	0.39	4/6928 (0.1%)
2	Bv	0.10	0/5092	0.31	0/6928

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Bw	0.10	0/5092	0.32	1/6928 (0.0%)
2	Bx	0.10	0/5092	0.32	0/6928
2	By	0.11	0/5092	0.32	0/6928
2	Bz	0.10	0/5092	0.32	1/6928 (0.0%)
2	K0	0.26	0/5092	0.38	1/6928 (0.0%)
2	K1	0.37	0/5092	0.43	0/6928
2	K2	0.37	0/5092	0.42	0/6928
2	K3	0.36	0/5092	0.42	0/6928
2	K4	0.36	0/5092	0.41	1/6928 (0.0%)
2	K5	0.36	0/5092	0.41	0/6928
2	K6	0.36	0/5092	0.42	0/6928
2	K7	0.35	0/5092	0.40	0/6928
2	K8	0.33	0/5092	0.41	0/6928
2	K9	0.30	0/5092	0.39	0/6928
2	L0	0.26	0/5092	0.38	0/6928
2	L1	0.37	0/5092	0.44	0/6928
2	L2	0.37	0/5092	0.44	0/6928
2	L3	0.37	0/5092	0.43	0/6928
2	L4	0.36	0/5092	0.41	0/6928
2	L5	0.36	0/5092	0.43	1/6928 (0.0%)
2	L6	0.36	0/5092	0.43	0/6928
2	L7	0.35	0/5092	0.42	1/6928 (0.0%)
2	L8	0.33	0/5092	0.41	0/6928
2	L9	0.31	0/5092	0.41	1/6928 (0.0%)
2	LS	0.34	0/5092	0.42	0/6928
2	LU	0.36	0/5092	0.43	0/6928
2	LV	0.37	0/5092	0.42	1/6928 (0.0%)
2	LW	0.37	0/5092	0.43	0/6928
2	LX	0.37	0/5092	0.42	0/6928
2	LY	0.37	0/5092	0.41	0/6928
2	LZ	0.36	0/5092	0.43	0/6928
2	La	0.37	0/5092	0.43	0/6928
2	Lb	0.36	0/5092	0.42	0/6928
2	Lc	0.34	0/5092	0.41	0/6928
2	Ld	0.30	0/5092	0.40	0/6928
2	Le	0.26	0/5092	0.37	0/6928
2	Lx	0.35	0/5092	0.42	0/6928
2	Lz	0.36	0/5092	0.42	0/6928
2	M0	0.26	0/5092	0.37	0/6928
2	M1	0.37	0/5092	0.43	0/6928
2	M2	0.36	0/5092	0.41	0/6928
2	M3	0.37	0/5092	0.42	0/6928
2	M4	0.36	0/5092	0.41	0/6928

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	M5	0.36	0/5092	0.42	0/6928
2	M6	0.37	0/5092	0.43	0/6928
2	M7	0.36	0/5092	0.41	0/6928
2	M8	0.34	0/5092	0.41	0/6928
2	M9	0.30	0/5092	0.40	1/6928 (0.0%)
2	MS	0.34	0/5092	0.42	0/6928
2	MU	0.36	0/5092	0.42	0/6928
2	MV	0.37	0/5092	0.43	1/6928 (0.0%)
2	MW	0.37	0/5092	0.43	0/6928
2	MX	0.36	0/5092	0.42	0/6928
2	MY	0.37	0/5092	0.42	0/6928
2	MZ	0.36	0/5092	0.41	0/6928
2	Ma	0.37	0/5092	0.42	0/6928
2	Mb	0.36	0/5092	0.41	1/6928 (0.0%)
2	Mc	0.34	0/5092	0.40	0/6928
2	Md	0.30	0/5092	0.39	0/6928
2	Me	0.26	0/5092	0.37	0/6928
2	Mx	0.34	0/5092	0.41	0/6928
2	Mz	0.36	0/5092	0.42	0/6928
2	NX	0.34	0/5092	0.42	0/6928
2	NZ	0.36	0/5092	0.42	0/6928
2	Na	0.37	0/5092	0.43	0/6928
2	Nb	0.37	0/5092	0.43	0/6928
2	Nc	0.37	0/5092	0.41	0/6928
2	Nd	0.37	0/5092	0.42	0/6928
2	Ne	0.36	0/5092	0.42	0/6928
2	Nf	0.36	0/5092	0.42	0/6928
2	Ng	0.35	0/5092	0.42	0/6928
2	Nh	0.33	0/5092	0.41	0/6928
2	Ni	0.30	0/5092	0.40	0/6928
2	Nj	0.26	0/5092	0.37	0/6928
2	Nx	0.34	0/5092	0.40	0/6928
2	Nz	0.37	0/5092	0.42	0/6928
2	b0	0.21	0/5092	0.38	0/6928
2	b3	0.19	0/5092	0.37	0/6928
2	b4	0.19	0/5092	0.36	0/6928
2	b5	0.20	0/5092	0.37	0/6928
2	b6	0.19	0/5092	0.37	0/6928
2	b7	0.20	0/5092	0.38	0/6928
2	b8	0.21	0/5092	0.38	0/6928
2	b9	0.21	0/5092	0.38	1/6928 (0.0%)
2	bN	0.22	0/5092	0.36	0/6928
2	bO	0.22	0/5092	0.38	1/6928 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	bP	0.22	0/5092	0.37	0/6928
2	bQ	0.22	0/5092	0.37	0/6928
2	bR	0.22	0/5092	0.37	0/6928
2	bY	0.22	0/5092	0.38	0/6928
2	cA	0.21	0/5092	0.38	0/6928
2	cB	0.21	0/5092	0.37	0/6928
2	cC	0.21	0/5092	0.37	0/6928
2	cD	0.22	0/5092	0.37	0/6928
2	cE	0.19	0/5092	0.36	0/6928
2	cF	0.21	0/5092	0.39	0/6928
2	cG	0.22	0/5092	0.38	0/6928
2	cH	0.22	0/5092	0.38	0/6928
2	cI	0.22	0/5092	0.38	0/6928
2	cJ	0.21	0/5092	0.38	0/6928
2	cK	0.22	0/5092	0.37	0/6928
2	cL	0.22	0/5092	0.38	0/6928
2	cM	0.22	0/5092	0.37	0/6928
2	cN	0.22	0/5092	0.38	0/6928
2	cO	0.22	0/5092	0.37	0/6928
2	cP	0.22	0/5092	0.38	0/6928
2	dS	0.23	0/5033	0.38	0/6847
2	dT	0.23	0/5033	0.38	0/6847
2	dU	0.23	0/5033	0.39	0/6847
2	dV	0.22	0/5033	0.38	0/6847
2	dW	0.23	0/5033	0.39	0/6847
2	dZ	0.23	0/5033	0.38	0/6847
3	6	0.12	0/1325	0.37	0/1797
3	7	0.12	0/1325	0.35	0/1797
3	8	0.12	0/1325	0.36	0/1797
3	9	0.13	0/1325	0.37	0/1797
3	AA	0.12	0/1325	0.38	1/1797 (0.1%)
3	AE	0.15	0/1333	0.39	0/1807
3	AF	0.11	0/1333	0.32	0/1807
3	AG	0.13	0/1333	0.31	0/1807
3	AH	0.12	0/1333	0.31	0/1807
3	AI	0.11	0/1333	0.34	0/1807
3	AJ	0.11	0/1333	0.33	0/1807
3	BX	0.11	0/1333	0.33	0/1807
3	BY	0.11	0/1333	0.32	0/1807
3	BZ	0.10	0/1333	0.32	0/1807
3	Ba	0.11	0/1333	0.34	0/1807
3	Bb	0.10	0/1333	0.33	0/1807
3	Bc	0.10	0/1333	0.32	0/1807

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	Bd	0.11	0/1333	0.32	0/1807
3	Be	0.11	0/1333	0.33	0/1807
3	Bf	0.10	0/1333	0.29	0/1807
3	Bg	0.11	0/1333	0.34	0/1807
3	Bh	0.11	0/1333	0.34	0/1807
3	Bi	0.11	0/1333	0.32	0/1807
3	Bj	0.11	0/1333	0.33	0/1807
3	Bk	0.11	0/1333	0.32	0/1807
3	Bl	0.13	0/1333	0.33	0/1807
3	Bm	0.15	0/1333	0.38	1/1807 (0.1%)
3	Bn	0.17	0/1333	0.38	0/1807
3	Bo	0.10	0/1333	0.31	0/1807
3	OE	0.47	0/1333	0.50	0/1807
3	OF	0.47	0/1333	0.48	0/1807
3	OG	0.46	0/1333	0.52	0/1807
3	OH	0.45	0/1333	0.46	0/1807
3	OI	0.45	0/1333	0.50	0/1807
3	OJ	0.46	0/1333	0.52	0/1807
3	OK	0.45	0/1333	0.46	0/1807
3	OL	0.45	0/1333	0.47	0/1807
3	OM	0.43	0/1333	0.47	0/1807
3	ON	0.41	0/1333	0.50	1/1807 (0.1%)
3	OO	0.38	0/1333	0.43	0/1807
3	Oj	0.46	0/1333	0.48	0/1807
3	Ok	0.48	0/1333	0.52	0/1807
3	Ol	0.45	0/1333	0.48	0/1807
3	Om	0.45	0/1333	0.48	0/1807
3	On	0.45	0/1333	0.48	0/1807
3	Oo	0.44	0/1333	0.46	0/1807
3	Op	0.44	0/1333	0.46	0/1807
3	Oq	0.44	0/1333	0.49	0/1807
3	Or	0.44	0/1333	0.48	0/1807
3	Os	0.42	0/1333	0.48	0/1807
3	Ot	0.38	0/1333	0.43	0/1807
3	PE	0.46	0/1333	0.51	1/1807 (0.1%)
3	PF	0.48	0/1333	0.48	0/1807
3	PG	0.47	0/1333	0.54	0/1807
3	PH	0.45	0/1333	0.49	0/1807
3	PI	0.45	0/1333	0.48	0/1807
3	PJ	0.44	0/1333	0.48	0/1807
3	PK	0.44	0/1333	0.51	0/1807
3	PL	0.45	0/1333	0.48	0/1807
3	PM	0.44	0/1333	0.48	0/1807

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	PN	0.41	0/1333	0.49	0/1807
3	PO	0.38	0/1333	0.43	0/1807
3	Pj	0.46	0/1333	0.47	0/1807
3	Pk	0.47	0/1333	0.50	0/1807
3	Pl	0.46	0/1333	0.49	0/1807
3	Pm	0.45	0/1333	0.47	0/1807
3	Pn	0.44	0/1333	0.47	0/1807
3	Po	0.45	0/1333	0.49	0/1807
3	Pp	0.44	0/1333	0.47	0/1807
3	Pq	0.45	0/1333	0.48	0/1807
3	Pr	0.44	0/1333	0.47	0/1807
3	Ps	0.43	0/1333	0.49	0/1807
3	Pt	0.37	0/1333	0.45	0/1807
3	RE	0.47	0/1333	0.49	0/1807
3	RF	0.47	0/1333	0.48	0/1807
3	RG	0.45	0/1333	0.52	0/1807
3	RH	0.46	0/1333	0.48	0/1807
3	RI	0.45	0/1333	0.48	0/1807
3	RJ	0.44	0/1333	0.48	0/1807
3	RK	0.44	0/1333	0.46	0/1807
3	RL	0.45	0/1333	0.46	0/1807
3	RM	0.44	0/1333	0.45	0/1807
3	RN	0.42	0/1333	0.53	1/1807 (0.1%)
3	RO	0.38	0/1333	0.43	0/1807
3	RT	0.45	0/1333	0.47	0/1807
3	Rk	0.46	0/1333	0.53	0/1807
3	Rl	0.46	0/1333	0.49	0/1807
3	Rm	0.44	0/1333	0.46	0/1807
3	Rn	0.44	0/1333	0.46	0/1807
3	Ro	0.44	0/1333	0.48	0/1807
3	Rp	0.44	0/1333	0.49	0/1807
3	Rq	0.45	0/1333	0.48	0/1807
3	Rr	0.44	0/1333	0.49	0/1807
3	Rs	0.41	0/1333	0.46	0/1807
3	Rt	0.38	0/1333	0.45	0/1807
3	h1	0.28	0/1333	0.42	0/1807
3	h2	0.27	0/1333	0.41	0/1807
3	hI	0.27	0/1333	0.42	0/1807
3	hJ	0.27	0/1333	0.43	0/1807
3	hK	0.27	0/1333	0.41	0/1807
3	hL	0.28	0/1333	0.43	0/1807
3	hM	0.27	0/1333	0.42	0/1807
3	hX	0.27	0/1333	0.41	0/1807

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	he	0.22	0/1333	0.40	0/1807
3	hf	0.22	0/1333	0.40	0/1807
3	hg	0.22	0/1333	0.39	0/1807
3	hh	0.22	0/1333	0.40	0/1807
3	hi	0.22	0/1333	0.40	0/1807
3	hj	0.26	0/1333	0.41	0/1807
3	hk	0.27	0/1333	0.43	0/1807
3	hl	0.26	0/1333	0.43	0/1807
3	hm	0.26	0/1333	0.42	0/1807
3	hn	0.26	0/1333	0.42	0/1807
3	ho	0.27	0/1333	0.43	0/1807
3	hp	0.27	0/1333	0.42	0/1807
3	hq	0.27	0/1333	0.40	0/1807
3	hr	0.27	0/1333	0.45	0/1807
3	hs	0.27	0/1333	0.43	0/1807
3	ht	0.22	0/1333	0.39	0/1807
3	hu	0.26	0/1333	0.42	0/1807
3	hv	0.27	0/1333	0.41	0/1807
3	hw	0.28	0/1333	0.42	0/1807
3	hx	0.28	0/1333	0.41	0/1807
3	hy	0.28	0/1333	0.42	0/1807
3	hz	0.28	0/1333	0.43	0/1807
3	o	0.13	0/1325	0.36	0/1797
4	A	0.11	0/608	0.20	0/825
4	B	0.10	0/608	0.19	0/825
4	C	0.10	0/608	0.21	0/825
4	D	0.09	0/608	0.20	0/825
4	E	0.10	0/608	0.19	0/825
4	F	0.09	0/608	0.19	0/825
4	G	0.09	0/608	0.18	0/825
4	H	0.11	0/608	0.22	0/825
4	I	0.09	0/608	0.21	0/825
4	J	0.10	0/608	0.20	0/825
4	K	0.10	0/608	0.20	0/825
4	L	0.09	0/608	0.19	0/825
4	M	0.09	0/608	0.19	0/825
4	N	0.08	0/608	0.17	0/825
4	O	0.10	0/608	0.20	0/825
4	P	0.10	0/608	0.19	0/825
4	Q	0.09	0/608	0.18	0/825
4	R	0.10	0/608	0.22	0/825
4	S	0.09	0/608	0.20	0/825
4	T	0.10	0/608	0.20	0/825

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	U	0.10	0/608	0.19	0/825
4	V	0.09	0/608	0.20	0/825
4	W	0.10	0/608	0.20	0/825
4	X	0.09	0/608	0.20	0/825
4	Y	0.09	0/608	0.19	0/825
4	Z	0.09	0/608	0.20	0/825
4	a	0.09	0/608	0.19	0/825
4	b	0.10	0/608	0.19	0/825
4	c	0.10	0/608	0.21	0/825
4	d	0.09	0/608	0.19	0/825
4	e	0.09	0/608	0.19	0/825
4	f	0.10	0/608	0.20	0/825
4	g	0.10	0/608	0.20	0/825
4	h	0.08	0/608	0.19	0/825
4	i	0.09	0/608	0.20	0/825
4	j	0.10	0/608	0.20	0/825
5	A0	0.11	0/4222	0.33	0/5693
5	A1	0.12	0/4222	0.31	0/5693
5	A2	0.12	0/4214	0.33	0/5682
5	A3	0.12	0/4214	0.33	0/5682
5	Av	0.11	0/4214	0.31	0/5682
5	Ax	0.11	0/4214	0.29	0/5682
5	BA	0.11	0/4153	0.31	0/5600
5	BB	0.11	0/4070	0.30	0/5482
5	BD	0.13	0/4214	0.33	1/5682 (0.0%)
5	BF	0.11	0/4214	0.30	0/5682
5	BG	0.11	0/4116	0.32	0/5548
5	BH	0.11	0/4170	0.29	0/5626
6	A4	0.12	0/3493	0.34	0/4731
6	A5	0.10	0/3493	0.31	0/4731
6	A7	0.11	0/3493	0.31	0/4731
6	A8	0.11	0/3377	0.31	0/4573
6	A9	0.11	0/3493	0.32	0/4731
6	AV	0.12	0/3493	0.32	0/4731
6	AW	0.11	0/3493	0.31	0/4731
6	AX	0.11	0/3493	0.30	0/4731
6	AZ	0.12	0/3493	0.34	2/4731 (0.0%)
6	Ac	0.11	0/3493	0.32	0/4731
6	Ad	0.11	0/3493	0.31	0/4731
6	Ae	0.11	0/3493	0.31	0/4731
6	Af	0.11	0/3493	0.31	0/4731
6	Ag	0.11	0/3493	0.31	0/4731
6	Ah	0.11	0/3493	0.29	0/4731

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	Ai	0.10	0/3493	0.31	1/4731 (0.0%)
6	Aj	0.11	0/3493	0.32	0/4731
6	Ak	0.12	0/3493	0.29	0/4731
6	Am	0.12	0/3493	0.33	0/4731
6	An	0.12	0/3377	0.31	0/4573
6	Ao	0.11	0/3357	0.31	0/4546
6	Ap	0.12	0/3377	0.31	0/4573
6	Au	0.11	0/3493	0.31	0/4731
6	Aw	0.12	0/3493	0.32	0/4731
6	Ay	0.11	0/3493	0.30	0/4731
6	Az	0.11	0/3493	0.31	0/4731
6	BI	0.11	0/3493	0.29	0/4731
6	BJ	0.12	0/3357	0.32	0/4546
6	BK	0.11	0/3493	0.31	0/4731
6	BM	0.12	0/3493	0.34	0/4731
7	A6	0.11	0/2496	0.29	0/3383
7	AY	0.12	0/2493	0.32	0/3379
7	Aa	0.12	0/2496	0.33	0/3383
7	Ab	0.11	0/2496	0.31	0/3383
7	Al	0.13	0/2493	0.34	1/3379 (0.0%)
7	Aq	0.12	0/2496	0.32	0/3383
7	Ar	0.12	0/2363	0.30	0/3203
7	As	0.11	0/2496	0.31	0/3383
7	At	0.12	0/2428	0.31	0/3290
7	BC	0.12	0/2496	0.30	0/3383
7	BE	0.12	0/2496	0.31	0/3383
7	BL	0.12	0/2496	0.32	0/3383
8	AB	0.15	0/2287	0.37	0/3109
8	q	0.16	0/2287	0.38	0/3109
8	r	0.15	0/2287	0.37	0/3109
8	s	0.15	0/2287	0.37	0/3109
8	t	0.14	0/2287	0.37	0/3109
8	u	0.15	0/2287	0.39	0/3109
9	AC	0.13	0/1418	0.33	0/1939
9	v	0.13	0/1418	0.32	0/1939
9	w	0.13	0/1418	0.32	0/1939
9	x	0.13	0/1418	0.34	0/1939
9	y	0.11	0/1418	0.31	0/1939
9	z	0.12	0/1418	0.31	0/1939
10	AQ	0.09	0/833	0.27	0/1133
10	AR	0.10	0/833	0.29	0/1133
10	AS	0.09	0/833	0.27	0/1133
10	AT	0.10	0/833	0.31	0/1133

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
10	AU	0.10	0/833	0.28	0/1133
11	BN	0.10	0/651	0.29	0/880
11	BO	0.10	0/651	0.27	0/880
11	BP	0.11	0/651	0.32	0/880
11	BQ	0.10	0/651	0.31	0/880
11	BR	0.11	0/651	0.32	0/880
11	BS	0.10	0/651	0.29	0/880
11	BT	0.11	0/651	0.30	0/880
11	BU	0.11	0/651	0.30	0/880
11	BV	0.11	0/651	0.29	0/880
11	BW	0.10	0/651	0.30	0/880
12	S0	0.11	0/4016	0.31	0/5464
12	S1	0.12	0/4016	0.31	0/5464
12	S2	0.11	0/4016	0.32	0/5464
12	S3	0.12	0/4016	0.31	0/5464
12	S4	0.12	0/4016	0.32	0/5464
12	S5	0.11	0/4016	0.31	0/5464
12	S6	0.11	0/4016	0.29	0/5464
12	S7	0.11	0/4016	0.30	0/5464
12	S8	0.13	0/4016	0.32	0/5464
12	SA	0.11	0/4016	0.30	0/5464
12	SO	0.12	0/4016	0.35	2/5464 (0.0%)
12	SP	0.12	0/4016	0.32	0/5464
12	SQ	0.11	0/4016	0.32	0/5464
12	Sv	0.11	0/4016	0.31	0/5464
12	Sw	0.11	0/4016	0.30	0/5464
12	Sx	0.11	0/4016	0.30	0/5464
12	Sy	0.12	0/4016	0.31	0/5464
12	Sz	0.11	0/4016	0.31	0/5464
13	T1	0.11	0/2205	0.32	0/2988
13	T2	0.11	0/2205	0.30	0/2988
13	T3	0.12	0/2205	0.31	0/2988
13	T4	0.12	0/2205	0.32	0/2988
13	T5	0.11	0/2205	0.31	0/2988
13	T6	0.11	0/2205	0.30	0/2988
13	T7	0.11	0/2205	0.29	0/2988
13	T8	0.11	0/2205	0.29	0/2988
13	T9	0.12	0/2205	0.31	0/2988
13	TF	0.11	0/2205	0.30	0/2988
13	TG	0.11	0/2205	0.30	0/2988
13	TH	0.11	0/2205	0.30	0/2988
13	Td	0.11	0/2205	0.30	0/2988
13	Te	0.11	0/2205	0.31	0/2988

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	Tf	0.11	0/2205	0.31	0/2988
13	Tg	0.12	0/2205	0.32	0/2988
13	Th	0.12	0/2205	0.31	0/2988
13	Ti	0.12	0/2205	0.33	0/2988
14	UL	0.11	0/1700	0.28	0/2318
14	UM	0.11	0/1700	0.29	0/2318
14	UN	0.11	0/1700	0.30	0/2318
14	Up	0.12	0/1700	0.31	0/2318
14	Uq	0.11	0/1700	0.29	0/2318
14	Ur	0.11	0/1700	0.31	0/2318
14	Us	0.12	0/1700	0.31	0/2318
14	Ut	0.10	0/1700	0.29	0/2318
14	Uu	0.11	0/1700	0.28	0/2318
14	VL	0.11	0/1700	0.31	0/2318
14	VM	0.12	0/1700	0.31	0/2318
14	VN	0.10	0/1700	0.29	0/2318
14	Vp	0.11	0/1700	0.28	0/2318
14	Vq	0.11	0/1700	0.29	0/2318
14	Vr	0.11	0/1700	0.30	0/2318
14	Vs	0.11	0/1700	0.29	0/2318
14	Vt	0.11	0/1700	0.29	0/2318
14	Vu	0.11	0/1700	0.29	0/2318
15	WI	0.13	0/4778	0.38	0/6513
15	WJ	0.14	0/4778	0.39	1/6513 (0.0%)
15	WK	0.14	0/4778	0.39	1/6513 (0.0%)
15	Wj	0.13	0/4778	0.38	0/6513
15	Wk	0.13	0/4778	0.39	0/6513
15	Wl	0.13	0/4778	0.39	0/6513
15	Wm	0.13	0/4778	0.38	0/6513
15	Wn	0.14	0/4778	0.40	0/6513
15	Wo	0.15	0/4778	0.40	1/6513 (0.0%)
15	XI	0.14	0/4778	0.38	0/6513
15	XJ	0.13	0/4778	0.40	0/6513
15	XK	0.14	0/4778	0.39	0/6513
15	Xj	0.13	0/4778	0.37	0/6513
15	Xk	0.13	0/4778	0.38	0/6513
15	Xl	0.13	0/4778	0.40	0/6513
15	Xm	0.13	0/4778	0.39	0/6513
15	Xn	0.13	0/4778	0.39	0/6513
15	Xo	0.14	0/4778	0.41	1/6513 (0.0%)
16	YC	0.18	0/8405	0.46	1/11412 (0.0%)
16	YX	0.19	0/8405	0.46	0/11412
16	YY	0.19	0/8405	0.45	0/11412

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	Yc	0.19	0/8405	0.46	0/11412
16	Yx	0.19	0/8405	0.46	0/11412
16	Yy	0.19	0/8405	0.45	2/11412 (0.0%)
17	ZD	0.14	0/2709	0.30	0/3694
17	ZE	0.16	0/2736	0.32	0/3731
17	ZZ	0.14	0/2709	0.29	0/3694
17	Za	0.14	0/2709	0.29	0/3694
17	Zb	0.17	0/2736	0.31	0/3731
17	Zc	0.16	0/2736	0.32	0/3731
17	aD	0.14	0/2709	0.29	0/3694
17	aE	0.17	0/2736	0.31	0/3731
17	aZ	0.14	0/2709	0.29	0/3694
17	aa	0.14	0/2709	0.30	0/3694
17	ab	0.17	0/2736	0.31	0/3731
17	ac	0.17	0/2736	0.30	0/3731
18	eB	0.22	0/5257	0.39	0/7144
18	eU	0.23	0/5257	0.40	0/7144
18	eW	0.22	0/5257	0.38	0/7144
18	f9	0.23	0/5337	0.40	0/7256
18	fA	0.22	0/5337	0.39	1/7256 (0.0%)
18	fB	0.24	1/5257 (0.0%)	0.39	0/7144
18	fR	0.22	0/5337	0.39	1/7256 (0.0%)
18	fS	0.23	0/5337	0.41	1/7256 (0.0%)
18	fU	0.23	0/5257	0.38	0/7144
18	fW	0.22	0/5257	0.38	0/7144
18	fr	0.22	0/5337	0.38	0/7256
18	fs	0.23	0/5337	0.40	1/7256 (0.0%)
19	gE	0.21	0/4402	0.32	0/5966
19	gG	0.21	0/4402	0.33	0/5966
19	gH	0.21	0/4402	0.33	0/5966
20	gd	0.11	0/724	0.25	0/984
21	iC	0.27	0/3070	0.41	0/4164
21	iD	0.26	0/3070	0.40	0/4164
21	iF	0.27	0/3070	0.41	0/4164
22	ja	0.22	0/139	0.44	0/192
22	jb	0.23	0/139	0.57	0/192
22	jc	0.23	0/139	0.55	0/192
23	k3	0.24	0/1643	0.38	0/2228
23	k4	0.24	0/1643	0.36	0/2228
23	k7	0.25	0/1643	0.39	0/2228
23	k8	0.24	0/1643	0.35	0/2228
23	kV	0.24	0/1643	0.36	0/2228
23	lV	0.24	0/1643	0.38	0/2228

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
24	m1	0.24	0/1035	0.41	1/1403 (0.1%)
24	m2	0.24	0/1035	0.38	0/1403
24	m5	0.25	0/1035	0.39	0/1403
24	m6	0.23	0/1035	0.40	0/1403
24	mT	0.24	0/1035	0.40	0/1403
24	nT	0.25	0/1035	0.39	0/1403
25	o0	0.24	0/2795	0.45	0/3784
25	o1	0.24	0/2479	0.50	0/3354
25	o2	0.25	0/2479	0.50	0/3354
25	o6	0.24	0/2479	0.50	0/3354
25	pA	0.25	0/2795	0.46	0/3784
25	pB	0.25	0/2795	0.44	0/3784
26	q3	0.28	0/1686	0.44	0/2292
26	q4	0.28	0/1686	0.44	0/2292
26	q5	0.30	0/1729	0.50	0/2349
26	q7	0.29	0/1729	0.49	2/2349 (0.1%)
26	q8	0.28	0/1686	0.48	0/2292
26	q9	0.29	0/1729	0.50	0/2349
All	All	0.24	1/1562297 (0.0%)	0.38	46/2122859 (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	L1	0	2
2	LX	0	1
2	Le	0	1
2	MZ	0	1
2	b4	0	1
2	b7	0	1
2	cB	0	1
2	cJ	0	1
2	cK	0	1
2	cP	0	1
2	dV	0	1
3	OG	0	1
3	OJ	0	1
3	OL	0	1
3	Oj	0	1
3	Om	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	Os	0	1
3	PH	0	1
3	PK	0	1
3	Pq	0	1
3	Pt	0	1
3	RE	0	1
3	Rm	0	1
3	Ro	0	1
3	Rq	0	1
3	Rs	0	1
3	Rt	0	1
6	A4	0	1
8	s	0	1
8	u	0	1
12	S2	0	1
12	Sx	0	1
16	Yc	0	1
16	Yx	0	1
25	o1	0	1
25	o2	0	1
All	All	0	37

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	fB	303	ASN	C-O	6.16	1.26	1.23

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Bu	644	ALA	N-CA-C	-14.61	85.56	109.07
2	Bu	644	ALA	CB-CA-C	-9.94	92.52	109.72
2	M9	482	ASP	N-CA-C	-7.40	105.43	114.75
12	SO	46	GLY	CA-C-N	6.98	124.64	120.24
12	SO	46	GLY	C-N-CA	6.98	124.64	120.24

There are no chirality outliers.

5 of 37 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	A4	254	ILE	Peptide

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Mol	Chain	Res	Type	Group
2	L1	572	LEU	Peptide
2	L1	650	ASP	Peptide
2	LX	333	GLY	Peptide
2	Le	572	LEU	Peptide

5.2 Too-close contacts

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	0	1993	0	1903	60	0
1	k	1993	0	1903	57	0
1	l	1993	0	1903	60	0
1	m	1993	0	1903	80	0
1	n	1993	0	1903	61	0
1	p	1993	0	1903	74	0
2	1	4985	0	4900	126	0
2	2	4985	0	4900	117	0
2	3	4985	0	4900	119	0
2	4	4985	0	4900	125	0
2	5	4985	0	4900	120	0
2	AD	4985	0	4900	117	0
2	AK	5000	0	4918	125	0
2	AL	5000	0	4918	122	0
2	AM	5000	0	4918	116	0
2	AN	5000	0	4918	118	0
2	AO	5000	0	4918	121	0
2	AP	5000	0	4918	128	0
2	B1	5000	0	4918	229	0
2	B2	5000	0	4918	128	0
2	B3	5000	0	4918	134	0
2	B4	5000	0	4918	257	0
2	B5	5000	0	4918	119	0
2	B6	5000	0	4918	143	0
2	B7	5000	0	4918	231	0
2	Bp	5000	0	4918	126	0
2	Bq	5000	0	4918	123	0
2	Br	5000	0	4918	238	0
2	Bs	5000	0	4918	128	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Bt	5000	0	4918	137	0
2	Bu	5000	0	4918	221	0
2	Bv	5000	0	4918	135	0
2	Bw	5000	0	4918	126	0
2	Bx	5000	0	4918	243	0
2	By	5000	0	4918	113	0
2	Bz	5000	0	4918	140	0
2	K0	5000	0	4918	251	0
2	K1	5000	0	4918	138	0
2	K2	5000	0	4918	123	0
2	K3	5000	0	4918	114	0
2	K4	5000	0	4918	122	0
2	K5	5000	0	4918	125	0
2	K6	5000	0	4918	137	0
2	K7	5000	0	4918	139	0
2	K8	5000	0	4918	147	0
2	K9	5000	0	4918	135	0
2	L0	5000	0	4918	235	0
2	L1	5000	0	4918	141	0
2	L2	5000	0	4918	139	0
2	L3	5000	0	4918	133	0
2	L4	5000	0	4918	136	0
2	L5	5000	0	4918	118	0
2	L6	5000	0	4918	144	0
2	L7	5000	0	4918	132	0
2	L8	5000	0	4918	134	0
2	L9	5000	0	4918	124	0
2	LS	5000	0	4918	265	0
2	LU	5000	0	4918	150	0
2	LV	5000	0	4918	135	0
2	LW	5000	0	4918	144	0
2	LX	5000	0	4918	129	0
2	LY	5000	0	4918	143	0
2	LZ	5000	0	4918	141	0
2	La	5000	0	4918	158	0
2	Lb	5000	0	4918	127	0
2	Lc	5000	0	4918	136	0
2	Ld	5000	0	4918	153	0
2	Le	5000	0	4918	234	0
2	Lx	5000	0	4918	246	0
2	Lz	5000	0	4918	129	0
2	M0	5000	0	4918	211	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M1	5000	0	4918	140	0
2	M2	5000	0	4918	112	0
2	M3	5000	0	4918	120	0
2	M4	5000	0	4918	132	0
2	M5	5000	0	4918	132	0
2	M6	5000	0	4918	119	0
2	M7	5000	0	4918	142	0
2	M8	5000	0	4918	153	0
2	M9	5000	0	4918	127	0
2	MS	5000	0	4918	263	0
2	MU	5000	0	4918	149	0
2	MV	5000	0	4918	122	0
2	MW	5000	0	4918	133	0
2	MX	5000	0	4918	139	0
2	MY	5000	0	4918	136	0
2	MZ	5000	0	4918	147	0
2	Ma	5000	0	4918	136	0
2	Mb	5000	0	4918	140	0
2	Mc	5000	0	4918	135	0
2	Md	5000	0	4918	147	0
2	Me	5000	0	4918	204	0
2	Mx	5000	0	4916	242	0
2	Mz	5000	0	4918	145	0
2	NX	5000	0	4918	257	0
2	NZ	5000	0	4918	155	0
2	Na	5000	0	4918	112	0
2	Nb	5000	0	4918	143	0
2	Nc	5000	0	4918	125	0
2	Nd	5000	0	4918	144	0
2	Ne	5000	0	4918	138	0
2	Nf	5000	0	4918	158	0
2	Ng	5000	0	4918	131	0
2	Nh	5000	0	4918	130	0
2	Ni	5000	0	4918	140	0
2	Nj	5000	0	4918	219	0
2	Nx	5000	0	4918	229	0
2	Nz	5000	0	4918	137	0
2	b0	5000	0	4918	149	0
2	b3	5000	0	4918	215	0
2	b4	5000	0	4918	208	0
2	b5	5000	0	4918	190	0
2	b6	5000	0	4918	180	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	b7	5000	0	4918	182	0
2	b8	5000	0	4918	122	0
2	b9	5000	0	4918	128	0
2	bN	5000	0	4918	111	0
2	bO	5000	0	4918	121	0
2	bP	5000	0	4918	119	0
2	bQ	5000	0	4918	119	0
2	bR	5000	0	4918	126	0
2	bY	5000	0	4918	119	0
2	cA	5000	0	4918	143	0
2	cB	5000	0	4918	143	0
2	cC	5000	0	4918	116	0
2	cD	5000	0	4918	127	0
2	cE	5000	0	4918	204	0
2	cF	5000	0	4918	137	0
2	cG	5000	0	4918	116	0
2	cH	5000	0	4918	127	0
2	cI	5000	0	4918	133	0
2	cJ	5000	0	4918	123	0
2	cK	5000	0	4918	123	0
2	cL	5000	0	4918	129	0
2	cM	5000	0	4918	122	0
2	cN	5000	0	4918	138	0
2	cO	5000	0	4918	134	0
2	cP	5000	0	4918	136	0
2	dS	4941	0	4858	118	0
2	dT	4941	0	4858	112	0
2	dU	4941	0	4858	138	0
2	dV	4941	0	4858	104	0
2	dW	4941	0	4858	107	0
2	dZ	4941	0	4858	116	0
3	6	1296	0	1243	42	0
3	7	1296	0	1243	42	0
3	8	1296	0	1243	52	0
3	9	1296	0	1243	48	0
3	AA	1296	0	1243	55	0
3	AE	1304	0	1255	46	0
3	AF	1304	0	1255	50	0
3	AG	1304	0	1255	49	0
3	AH	1304	0	1255	47	0
3	AI	1304	0	1255	45	0
3	AJ	1304	0	1255	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BX	1304	0	1255	52	0
3	BY	1304	0	1255	46	0
3	BZ	1304	0	1255	118	0
3	Ba	1304	0	1255	39	0
3	Bb	1304	0	1255	46	0
3	Bc	1304	0	1255	110	0
3	Bd	1304	0	1255	49	0
3	Be	1304	0	1255	44	0
3	Bf	1304	0	1255	91	0
3	Bg	1304	0	1255	52	0
3	Bh	1304	0	1255	55	0
3	Bi	1304	0	1255	122	0
3	Bj	1304	0	1255	47	0
3	Bk	1304	0	1255	53	0
3	Bl	1304	0	1255	123	0
3	Bm	1304	0	1255	37	0
3	Bn	1304	0	1255	54	0
3	Bo	1304	0	1255	95	0
3	OE	1304	0	1255	118	0
3	OF	1304	0	1255	42	0
3	OG	1304	0	1255	49	0
3	OH	1304	0	1255	39	0
3	OI	1304	0	1255	39	0
3	OJ	1304	0	1255	49	0
3	OK	1304	0	1255	37	0
3	OL	1304	0	1255	34	0
3	OM	1304	0	1255	54	0
3	ON	1304	0	1255	38	0
3	OO	1304	0	1255	86	0
3	Oj	1304	0	1255	80	0
3	Ok	1304	0	1255	56	0
3	Ol	1304	0	1255	60	0
3	Om	1304	0	1255	40	0
3	On	1304	0	1255	41	0
3	Oo	1304	0	1255	47	0
3	Op	1304	0	1255	49	0
3	Oq	1304	0	1255	48	0
3	Or	1304	0	1255	49	0
3	Os	1304	0	1255	42	0
3	Ot	1304	0	1255	87	0
3	PE	1304	0	1255	111	0
3	PF	1304	0	1255	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	PG	1304	0	1255	45	0
3	PH	1304	0	1255	35	0
3	PI	1304	0	1255	40	0
3	PJ	1304	0	1255	52	0
3	PK	1304	0	1255	47	0
3	PL	1304	0	1255	43	0
3	PM	1304	0	1255	42	0
3	PN	1304	0	1255	39	0
3	PO	1304	0	1255	90	0
3	Pj	1304	0	1255	87	0
3	Pk	1304	0	1255	56	0
3	Pl	1304	0	1255	56	0
3	Pm	1304	0	1255	33	0
3	Pn	1304	0	1255	41	0
3	Po	1304	0	1255	42	0
3	Pp	1304	0	1255	44	0
3	Pq	1304	0	1255	53	0
3	Pr	1304	0	1255	50	0
3	Ps	1304	0	1255	41	0
3	Pt	1304	0	1255	106	0
3	RE	1304	0	1255	124	0
3	RF	1304	0	1255	53	0
3	RG	1304	0	1255	52	0
3	RH	1304	0	1255	36	0
3	RI	1304	0	1255	47	0
3	RJ	1304	0	1255	47	0
3	RK	1304	0	1255	43	0
3	RL	1304	0	1255	49	0
3	RM	1304	0	1255	52	0
3	RN	1304	0	1255	48	0
3	RO	1304	0	1255	97	0
3	RT	1304	0	1255	89	0
3	Rk	1304	0	1255	49	0
3	Rl	1304	0	1255	48	0
3	Rm	1304	0	1255	40	0
3	Rn	1304	0	1255	45	0
3	Ro	1304	0	1255	46	0
3	Rp	1304	0	1255	46	0
3	Rq	1304	0	1255	52	0
3	Rr	1304	0	1255	53	0
3	Rs	1304	0	1255	34	0
3	Rt	1304	0	1255	107	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	h1	1304	0	1255	50	0
3	h2	1304	0	1255	43	0
3	hI	1304	0	1255	42	0
3	hJ	1304	0	1255	45	0
3	hK	1304	0	1255	53	0
3	hL	1304	0	1255	49	0
3	hM	1304	0	1255	44	0
3	hX	1304	0	1255	52	0
3	he	1304	0	1255	95	0
3	hf	1304	0	1255	107	0
3	hg	1304	0	1255	97	0
3	hh	1304	0	1255	93	0
3	hi	1304	0	1255	104	0
3	hj	1304	0	1255	48	0
3	hk	1304	0	1255	56	0
3	hl	1304	0	1255	42	0
3	hm	1304	0	1255	49	0
3	hn	1304	0	1255	46	0
3	ho	1304	0	1255	42	0
3	hp	1304	0	1255	48	0
3	hq	1304	0	1255	40	0
3	hr	1304	0	1255	37	0
3	hs	1304	0	1255	54	0
3	ht	1304	0	1255	87	0
3	hu	1304	0	1255	46	0
3	hv	1304	0	1255	40	0
3	hw	1304	0	1255	51	0
3	hx	1304	0	1255	49	0
3	hy	1304	0	1255	49	0
3	hz	1304	0	1255	44	0
3	o	1296	0	1243	49	0
4	A	601	0	600	14	0
4	B	601	0	600	7	0
4	C	601	0	600	7	0
4	D	601	0	600	7	0
4	E	601	0	600	5	0
4	F	601	0	600	10	0
4	G	601	0	600	12	0
4	H	601	0	600	15	0
4	I	601	0	600	9	0
4	J	601	0	600	8	0
4	K	601	0	600	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	601	0	600	17	0
4	M	601	0	600	16	0
4	N	601	0	600	7	0
4	O	601	0	600	12	0
4	P	601	0	600	10	0
4	Q	601	0	600	10	0
4	R	601	0	600	11	0
4	S	601	0	600	8	0
4	T	601	0	600	9	0
4	U	601	0	600	13	0
4	V	601	0	600	11	0
4	W	601	0	600	13	0
4	X	601	0	600	10	0
4	Y	601	0	600	9	0
4	Z	601	0	600	9	0
4	a	601	0	600	11	0
4	b	601	0	600	10	0
4	c	601	0	600	9	0
4	d	601	0	600	9	0
4	e	601	0	600	8	0
4	f	601	0	600	12	0
4	g	601	0	600	12	0
4	h	601	0	600	14	0
4	i	601	0	600	14	0
4	j	601	0	600	12	0
5	A0	4140	0	4075	102	0
5	A1	4140	0	4076	102	0
5	A2	4132	0	4070	93	0
5	A3	4132	0	4070	131	0
5	Av	4132	0	4070	107	0
5	Ax	4132	0	4070	94	0
5	BA	4074	0	4013	102	0
5	BB	3995	0	3948	120	0
5	BD	4132	0	4071	83	0
5	BF	4132	0	4070	108	0
5	BG	4039	0	3976	108	0
5	BH	4091	0	4018	91	0
6	A4	3425	0	3371	79	0
6	A5	3425	0	3371	91	0
6	A7	3425	0	3371	76	0
6	A8	3311	0	3271	95	0
6	A9	3425	0	3371	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	AV	3425	0	3371	104	0
6	AW	3425	0	3371	76	0
6	AX	3425	0	3371	81	0
6	AZ	3425	0	3371	84	0
6	Ac	3425	0	3371	79	0
6	Ad	3425	0	3371	68	0
6	Ae	3425	0	3371	89	0
6	Af	3425	0	3371	77	0
6	Ag	3425	0	3371	87	0
6	Ah	3425	0	3371	82	0
6	Ai	3425	0	3371	72	0
6	Aj	3425	0	3371	77	0
6	Ak	3425	0	3371	91	0
6	Am	3425	0	3371	92	0
6	An	3311	0	3271	86	0
6	Ao	3291	0	3253	89	0
6	Ap	3311	0	3271	85	0
6	Au	3425	0	3371	99	0
6	Aw	3425	0	3371	68	0
6	Ay	3425	0	3371	82	0
6	Az	3425	0	3371	79	0
6	BI	3425	0	3371	88	0
6	BJ	3291	0	3253	94	0
6	BK	3425	0	3371	101	0
6	BM	3425	0	3371	86	0
7	A6	2438	0	2356	79	0
7	AY	2435	0	2352	79	0
7	Aa	2438	0	2356	65	0
7	Ab	2438	0	2356	71	0
7	Al	2435	0	2352	84	0
7	Aq	2438	0	2356	88	0
7	Ar	2310	0	2245	77	0
7	As	2438	0	2356	65	0
7	At	2371	0	2291	66	0
7	BC	2438	0	2356	84	0
7	BE	2438	0	2356	87	0
7	BL	2438	0	2357	78	0
8	AB	2227	0	2152	71	0
8	q	2227	0	2152	75	0
8	r	2227	0	2152	86	0
8	s	2227	0	2152	77	0
8	t	2227	0	2152	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	u	2227	0	2152	60	0
9	AC	1383	0	1344	35	0
9	v	1383	0	1344	39	0
9	w	1383	0	1344	31	0
9	x	1383	0	1344	23	0
9	y	1383	0	1344	38	0
9	z	1383	0	1344	32	0
10	AQ	805	0	763	17	0
10	AR	805	0	763	14	0
10	AS	805	0	763	11	0
10	AT	805	0	763	16	0
10	AU	805	0	763	15	0
11	BN	636	0	612	14	0
11	BO	636	0	612	11	0
11	BP	636	0	612	19	0
11	BQ	636	0	612	12	0
11	BR	636	0	612	13	0
11	BS	636	0	612	14	0
11	BT	636	0	612	13	0
11	BU	636	0	612	13	0
11	BV	636	0	612	8	0
11	BW	636	0	612	16	0
12	S0	3945	0	3828	209	0
12	S1	3945	0	3828	210	0
12	S2	3945	0	3828	206	0
12	S3	3945	0	3828	187	0
12	S4	3945	0	3828	210	0
12	S5	3945	0	3828	188	0
12	S6	3945	0	3828	213	0
12	S7	3945	0	3828	196	0
12	S8	3945	0	3828	198	0
12	SA	3945	0	3828	191	0
12	SO	3945	0	3828	191	0
12	SP	3945	0	3828	196	0
12	SQ	3945	0	3828	195	0
12	Sv	3945	0	3828	202	0
12	Sw	3945	0	3828	184	0
12	Sx	3945	0	3828	208	0
12	Sy	3945	0	3828	199	0
12	Sz	3945	0	3828	202	0
13	T1	2175	0	2157	76	0
13	T2	2175	0	2157	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	T3	2175	0	2157	74	0
13	T4	2175	0	2157	72	0
13	T5	2175	0	2157	54	0
13	T6	2175	0	2157	64	0
13	T7	2175	0	2157	65	0
13	T8	2175	0	2157	59	0
13	T9	2175	0	2157	61	0
13	TF	2175	0	2157	70	0
13	TG	2175	0	2157	62	0
13	TH	2175	0	2157	66	0
13	Td	2175	0	2157	75	0
13	Te	2175	0	2157	66	0
13	Tf	2175	0	2157	60	0
13	Tg	2175	0	2157	61	0
13	Th	2175	0	2157	65	0
13	Ti	2175	0	2157	67	0
14	UL	1665	0	1638	75	0
14	UM	1665	0	1638	79	0
14	UN	1665	0	1638	80	0
14	Up	1665	0	1638	64	0
14	Uq	1665	0	1638	77	0
14	Ur	1665	0	1638	72	0
14	Us	1665	0	1638	74	0
14	Ut	1665	0	1638	57	0
14	Uu	1665	0	1638	65	0
14	VL	1665	0	1638	75	0
14	VM	1665	0	1638	76	0
14	VN	1665	0	1638	63	0
14	Vp	1665	0	1638	69	0
14	Vq	1665	0	1638	72	0
14	Vr	1665	0	1638	74	0
14	Vs	1665	0	1638	79	0
14	Vt	1665	0	1638	71	0
14	Vu	1665	0	1638	77	0
15	WI	4675	0	4446	222	0
15	WJ	4675	0	4447	221	0
15	WK	4675	0	4446	241	0
15	Wj	4675	0	4446	236	0
15	Wk	4675	0	4446	215	0
15	Wl	4675	0	4447	230	0
15	Wm	4675	0	4447	223	0
15	Wn	4675	0	4446	247	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	Wo	4675	0	4446	234	0
15	XI	4675	0	4446	238	0
15	XJ	4675	0	4447	241	0
15	XK	4675	0	4446	250	0
15	Xj	4675	0	4446	250	0
15	Xk	4675	0	4446	222	0
15	Xl	4675	0	4447	234	0
15	Xm	4675	0	4447	227	0
15	Xn	4675	0	4446	239	0
15	Xo	4675	0	4446	231	0
16	YC	8199	0	7914	358	0
16	YX	8199	0	7914	358	0
16	YY	8199	0	7914	341	0
16	Yc	8199	0	7914	376	0
16	Yx	8199	0	7914	342	0
16	Yy	8199	0	7914	349	0
17	ZD	2631	0	2509	82	0
17	ZE	2658	0	2532	64	0
17	ZZ	2631	0	2509	72	0
17	Za	2631	0	2509	79	0
17	Zb	2658	0	2532	61	0
17	Zc	2658	0	2532	59	0
17	aD	2631	0	2509	68	0
17	aE	2658	0	2532	59	0
17	aZ	2631	0	2509	66	0
17	aa	2631	0	2509	77	0
17	ab	2658	0	2532	59	0
17	ac	2658	0	2532	57	0
18	eB	5157	0	5011	172	0
18	eU	5157	0	5011	171	0
18	eW	5157	0	5011	154	0
18	f9	5235	0	5086	150	0
18	fA	5235	0	5086	144	0
18	fB	5157	0	5011	158	0
18	fR	5235	0	5086	130	0
18	fS	5235	0	5086	146	0
18	fU	5157	0	5011	183	0
18	fW	5157	0	5011	151	0
18	fr	5235	0	5086	137	0
18	fs	5235	0	5086	145	0
19	gE	4321	0	4227	108	0
19	gG	4321	0	4227	120	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	gH	4321	0	4227	115	0
20	gd	709	0	713	14	0
21	iC	3000	0	2928	100	0
21	iD	3000	0	2928	101	0
21	iF	3000	0	2928	81	0
22	ja	137	0	130	4	0
22	jb	137	0	130	4	0
22	jc	137	0	130	2	0
23	k3	1599	0	1544	34	0
23	k4	1599	0	1544	33	0
23	k7	1599	0	1544	32	0
23	k8	1599	0	1544	27	0
23	kV	1599	0	1544	28	0
23	lV	1599	0	1544	36	0
24	m1	1019	0	1015	36	0
24	m2	1019	0	1015	35	0
24	m5	1019	0	1015	39	0
24	m6	1019	0	1015	36	0
24	mT	1019	0	1015	36	0
24	nT	1019	0	1015	37	0
25	o0	2749	0	2715	106	0
25	o1	2436	0	2408	89	0
25	o2	2436	0	2408	85	0
25	o6	2436	0	2408	92	0
25	pA	2749	0	2715	97	0
25	pB	2749	0	2715	99	0
26	q3	1650	0	1569	77	0
26	q4	1650	0	1569	72	0
26	q5	1693	0	1619	83	0
26	q7	1693	0	1619	75	0
26	q8	1650	0	1569	71	0
26	q9	1693	0	1619	85	0
27	rc	125	0	27	1	0
27	rd	125	0	27	3	0
27	re	125	0	27	2	0
27	rf	125	0	27	3	0
27	rg	125	0	27	0	0
27	rh	125	0	27	1	0
28	sQ	90	0	22	0	0
28	sT	90	0	22	1	0
28	sU	90	0	22	1	0
29	tS	50	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	tX	50	0	12	0	0
29	tY	50	0	12	0	0
30	uR	35	0	10	1	0
30	uV	35	0	10	0	0
30	uW	35	0	10	0	0
31	vZ	45	0	11	0	0
31	va	45	0	11	0	0
31	vb	45	0	11	0	0
32	S0	1	0	0	0	0
32	S1	1	0	0	0	0
32	S4	1	0	0	0	0
32	SA	1	0	0	0	0
32	SQ	1	0	0	0	0
32	Sv	1	0	0	0	0
All	All	1533268	0	1496153	41794	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 14.

The worst 5 of 41794 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)
2:M0:642:PHE:CZ	2:b7:564:ILE:HD11	1.32	1.63
2:Br:510:ARG:HH21	2:NX:364:ASP:CB	1.12	1.60
2:L0:467:TRP:CH2	2:b5:199:GLU:HB2	1.37	1.59
3:Pt:54:MET:SD	3:hi:1:MET:HE1	1.42	1.58
2:Bx:635:ILE:CD1	2:LS:576:ASN:CB	1.81	1.58

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

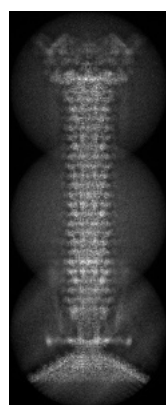
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48324. These allow visual inspection of the internal detail of the map and identification of artifacts.

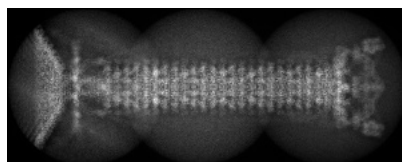
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

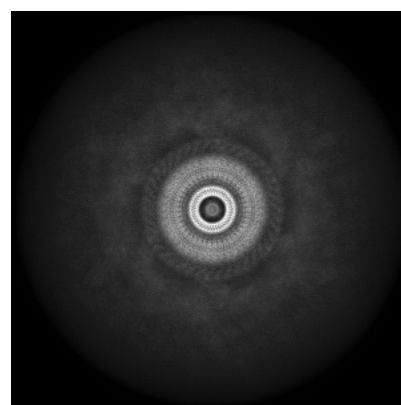
6.1.1 Primary map



X



Y



Z

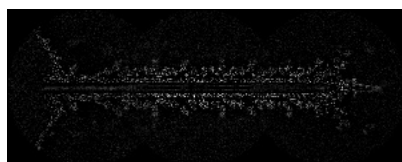
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

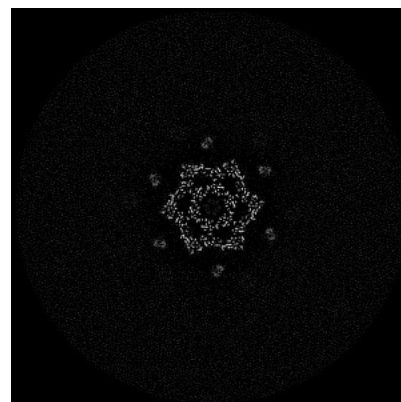
6.2.1 Primary map



X Index: 204



Y Index: 203

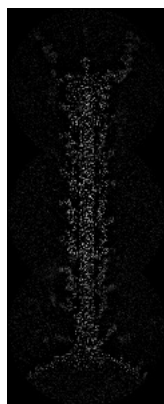


Z Index: 515

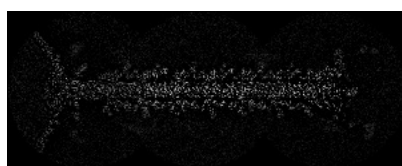
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

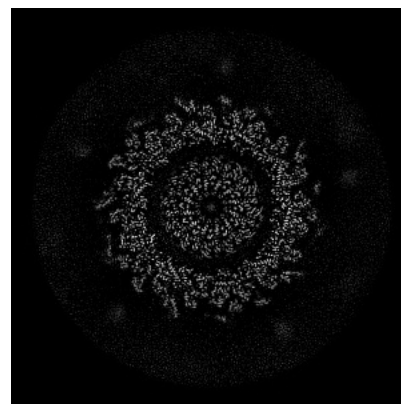
6.3.1 Primary map



X Index: 220



Y Index: 219

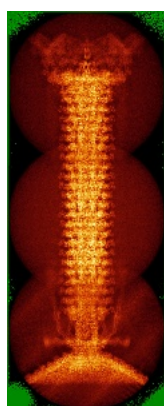


Z Index: 118

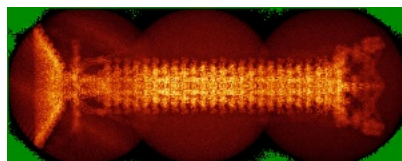
The images above show the largest variance slices of the map in three orthogonal directions.

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

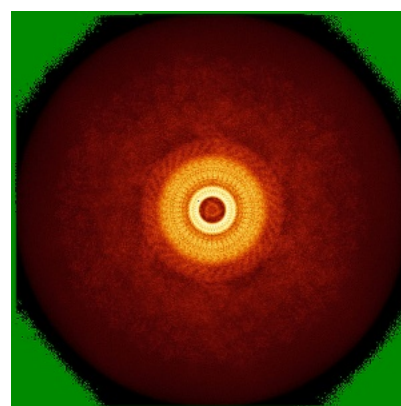
6.4.1 Primary map



X



Y

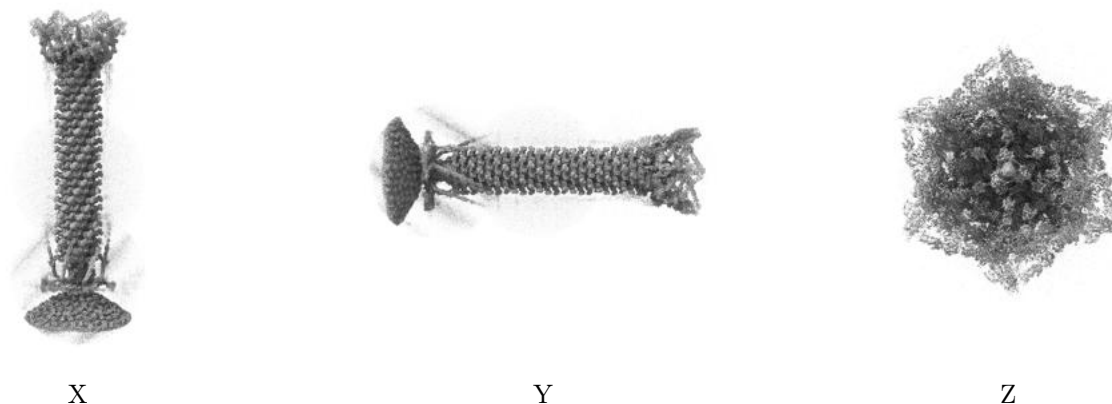


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

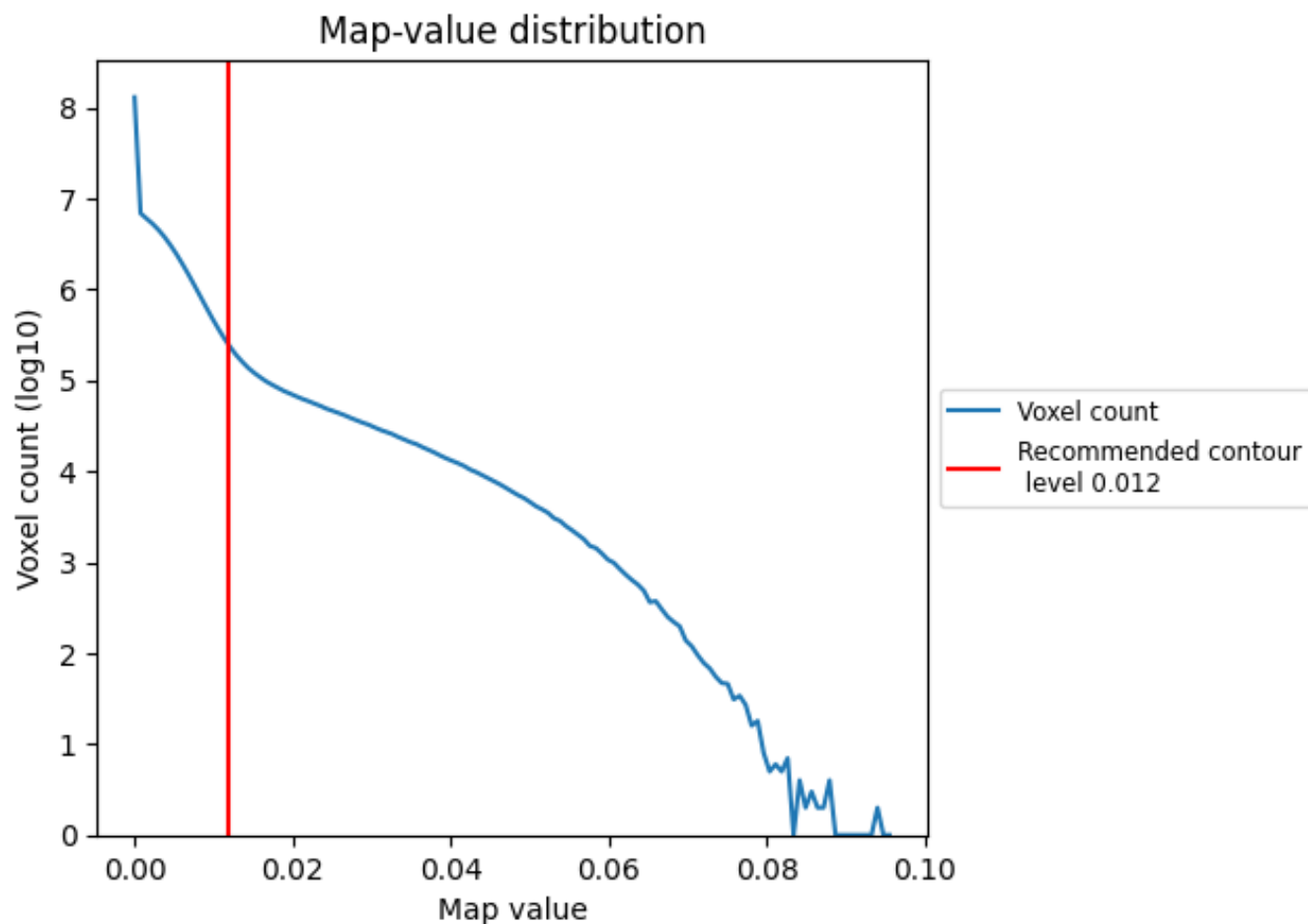
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

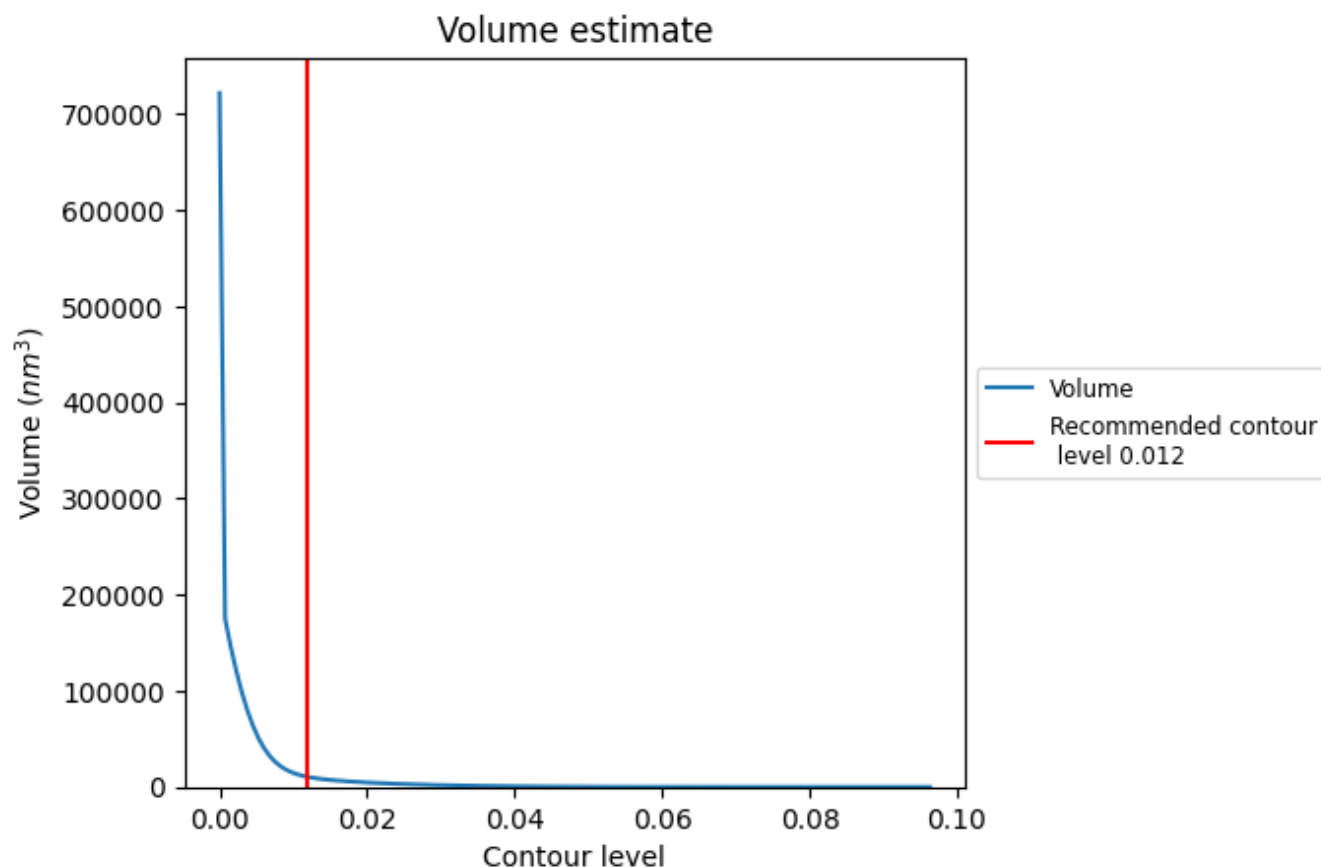
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10391 nm³; this corresponds to an approximate mass of 9387 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

8 Fourier-Shell correlation

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

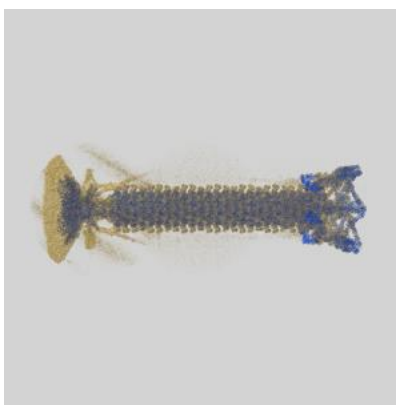
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48324 and PDB model 9MKB. Per-residue inclusion information can be found in [section 3](#) on [page 64](#).

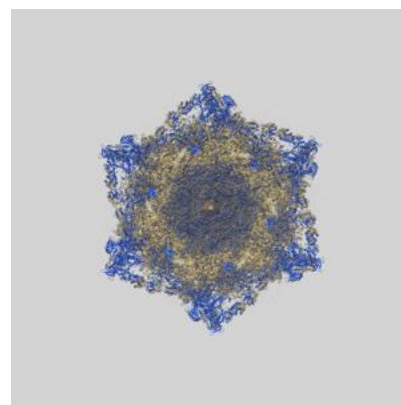
9.1 Map-model overlay [i](#)



X



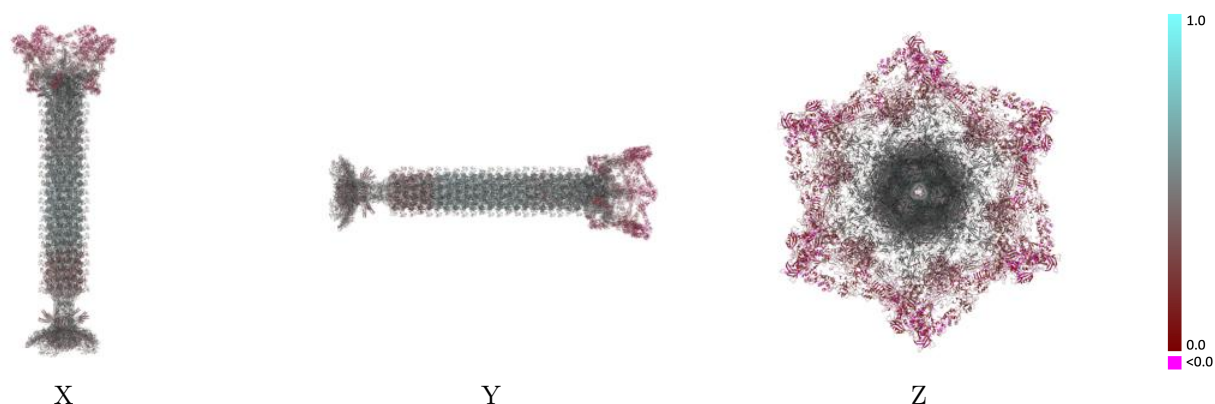
Y



Z

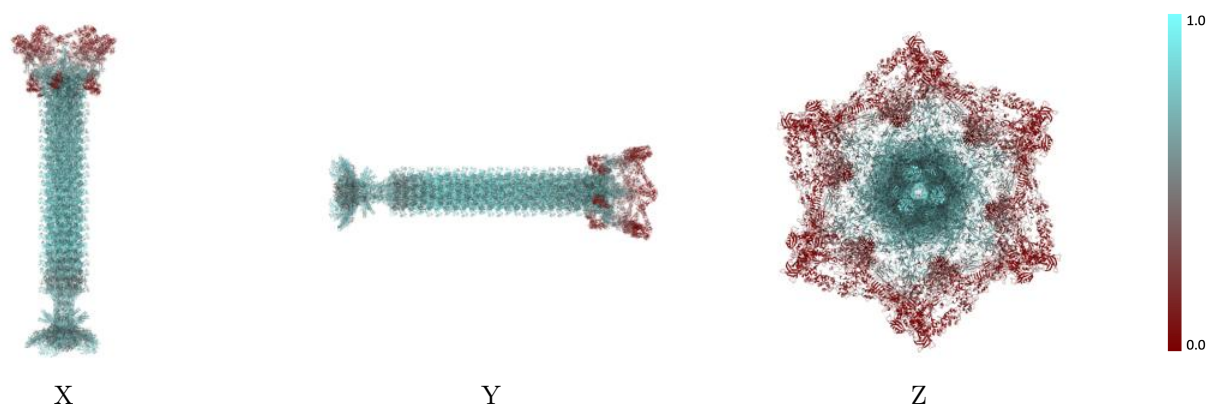
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



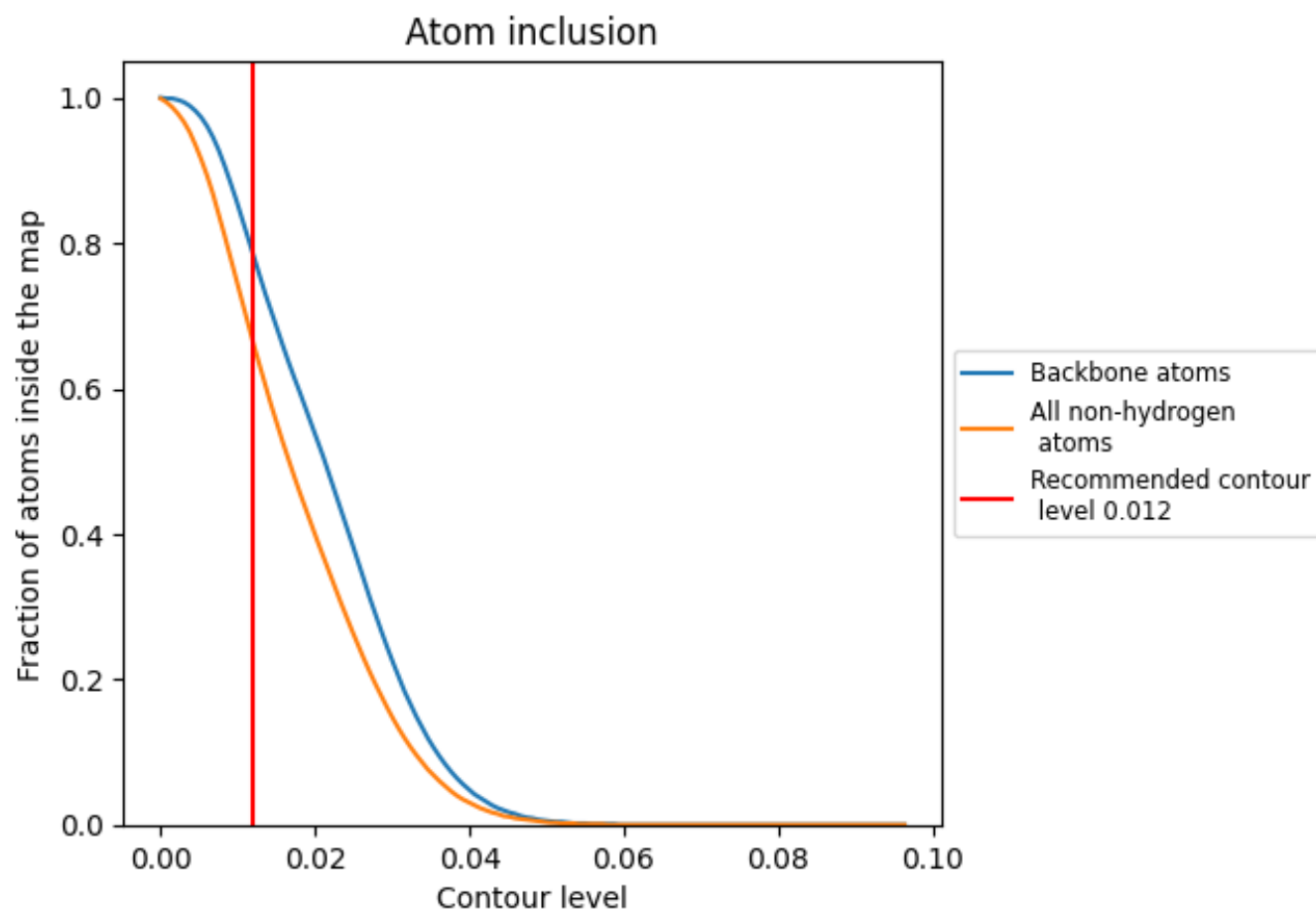
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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 (0.012).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 66% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6630	 0.4330
0	 0.7580	 0.4680
1	 0.6620	 0.3990
2	 0.6610	 0.4030
3	 0.7210	 0.4150
4	 0.7010	 0.4100
5	 0.6770	 0.4050
6	 0.6710	 0.4490
7	 0.6910	 0.4510
8	 0.7240	 0.4560
9	 0.7110	 0.4610
A	 0.7030	 0.4060
A0	 0.4950	 0.4000
A1	 0.5470	 0.4180
A2	 0.5010	 0.3970
A3	 0.5180	 0.4040
A4	 0.6630	 0.4340
A5	 0.6800	 0.4360
A6	 0.6370	 0.4310
A7	 0.6930	 0.4480
A8	 0.6350	 0.4380
A9	 0.6410	 0.4390
AA	 0.6970	 0.4660
AB	 0.7720	 0.4590
AC	 0.7170	 0.4610
AD	 0.6610	 0.3980
AE	 0.7150	 0.4560
AF	 0.6770	 0.4480
AG	 0.6780	 0.4450
AH	 0.6740	 0.4490
AI	 0.6820	 0.4500
AJ	 0.7130	 0.4530
AK	 0.6410	 0.3990
AL	 0.5990	 0.3870
AM	 0.6130	 0.3910























































































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Chain	Atom inclusion	Q-score
AN	 0.5800	 0.3850
AO	 0.6060	 0.3830
AP	 0.6480	 0.3950
AQ	 0.3550	 0.3300
AR	 0.2820	 0.3390
AS	 0.3920	 0.3590
AT	 0.3380	 0.3430
AU	 0.3400	 0.3590
AV	 0.7250	 0.4600
AW	 0.6930	 0.4330
AX	 0.7430	 0.4650
AY	 0.6790	 0.4510
AZ	 0.7460	 0.4680
Aa	 0.6510	 0.4390
Ab	 0.6550	 0.4380
Ac	 0.6220	 0.4320
Ad	 0.7540	 0.4600
Ae	 0.6880	 0.4460
Af	 0.6440	 0.4310
Ag	 0.6480	 0.4320
Ah	 0.7410	 0.4550
Ai	 0.6820	 0.4350
Aj	 0.6730	 0.4380
Ak	 0.6880	 0.4500
Al	 0.6320	 0.4330
Am	 0.6970	 0.4490
An	 0.7210	 0.4540
Ao	 0.6960	 0.4520
Ap	 0.6850	 0.4430
Aq	 0.6710	 0.4470
Ar	 0.6890	 0.4490
As	 0.6560	 0.4430
At	 0.6630	 0.4420
Au	 0.6850	 0.4520
Av	 0.5020	 0.4040
Aw	 0.6240	 0.4340
Ax	 0.4930	 0.4080
Ay	 0.6740	 0.4540
Az	 0.6940	 0.4460
B	 0.7300	 0.4250
B1	 0.7980	 0.3990
B2	 0.6690	 0.3760





















































































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Chain	Atom inclusion	Q-score
B3	 0.7570	 0.3990
B4	 0.7860	 0.3990
B5	 0.7090	 0.3880
B6	 0.7680	 0.4000
B7	 0.7930	 0.4040
BA	 0.4890	 0.3960
BB	 0.5500	 0.4200
BC	 0.6950	 0.4520
BD	 0.5380	 0.4120
BE	 0.6700	 0.4480
BF	 0.5020	 0.3960
BG	 0.5170	 0.4050
BH	 0.4830	 0.3970
BI	 0.6970	 0.4500
BJ	 0.7200	 0.4520
BK	 0.7640	 0.4670
BL	 0.6250	 0.4350
BM	 0.6680	 0.4480
BN	 0.7570	 0.4730
BO	 0.6500	 0.4350
BP	 0.7090	 0.4470
BQ	 0.7070	 0.4480
BR	 0.7440	 0.4680
BS	 0.6820	 0.4390
BT	 0.7170	 0.4530
BU	 0.7070	 0.4360
BV	 0.6580	 0.4400
BW	 0.6610	 0.4400
BX	 0.7140	 0.4420
BY	 0.7680	 0.4310
BZ	 0.8130	 0.4360
Ba	 0.7140	 0.4370
Bb	 0.7640	 0.4370
Bc	 0.8060	 0.4350
Bd	 0.7200	 0.4340
Be	 0.7630	 0.4310
Bf	 0.8060	 0.4240
Bg	 0.7200	 0.4430
Bh	 0.7830	 0.4470
Bi	 0.8030	 0.4390
Bj	 0.7360	 0.4500
Bk	 0.7710	 0.4480





















































































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Chain	Atom inclusion	Q-score
Bl	 0.8130	 0.4260
Bm	 0.7210	 0.4460
Bn	 0.7740	 0.4370
Bo	 0.8090	 0.4310
Bp	 0.7120	 0.3870
Bq	 0.7560	 0.3950
Br	 0.7890	 0.4050
Bs	 0.6750	 0.3760
Bt	 0.7390	 0.3870
Bu	 0.7880	 0.4040
Bv	 0.6740	 0.3770
Bw	 0.7500	 0.3900
Bx	 0.7880	 0.3920
By	 0.6930	 0.3800
Bz	 0.7580	 0.3980
C	 0.7790	 0.4450
D	 0.7590	 0.4200
E	 0.7290	 0.4070
F	 0.7390	 0.4060
G	 0.7660	 0.4080
H	 0.8010	 0.4310
I	 0.7570	 0.4070
J	 0.7230	 0.4110
K	 0.7490	 0.4120
K0	 0.8020	 0.4720
K1	 0.8530	 0.5210
K2	 0.8490	 0.5240
K3	 0.8460	 0.5200
K4	 0.8450	 0.5200
K5	 0.8460	 0.5230
K6	 0.8440	 0.5180
K7	 0.8440	 0.5170
K8	 0.8230	 0.5120
K9	 0.7990	 0.4980
L	 0.6930	 0.4080
L0	 0.8060	 0.4700
L1	 0.8530	 0.5220
L2	 0.8450	 0.5190
L3	 0.8470	 0.5230
L4	 0.8450	 0.5170
L5	 0.8460	 0.5220
L6	 0.8410	 0.5190





















































































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Chain	Atom inclusion	Q-score
L7	 0.8450	 0.5190
L8	 0.8220	 0.5100
L9	 0.7990	 0.4960
LS	 0.8790	 0.4940
LU	 0.8520	 0.5130
LV	 0.8530	 0.5250
LW	 0.8540	 0.5240
LX	 0.8480	 0.5200
LY	 0.8530	 0.5190
LZ	 0.8470	 0.5220
La	 0.8440	 0.5180
Lb	 0.8350	 0.5190
Lc	 0.8270	 0.5140
Ld	 0.7990	 0.4940
Le	 0.7970	 0.4680
Lx	 0.8820	 0.4940
Lz	 0.8530	 0.5140
M	 0.6860	 0.3670
M0	 0.8040	 0.4710
M1	 0.8480	 0.5220
M2	 0.8430	 0.5250
M3	 0.8480	 0.5220
M4	 0.8410	 0.5180
M5	 0.8490	 0.5220
M6	 0.8420	 0.5190
M7	 0.8400	 0.5150
M8	 0.8270	 0.5090
M9	 0.7950	 0.4950
MS	 0.8780	 0.4980
MU	 0.8540	 0.5150
MV	 0.8530	 0.5210
MW	 0.8500	 0.5230
MX	 0.8500	 0.5220
MY	 0.8490	 0.5170
MZ	 0.8520	 0.5220
Ma	 0.8440	 0.5170
Mb	 0.8410	 0.5170
Mc	 0.8210	 0.5140
Md	 0.7960	 0.4960
Me	 0.8030	 0.4680
Mx	 0.8820	 0.4960
Mz	 0.8570	 0.5150





















































































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Chain	Atom inclusion	Q-score
N	 0.6860	 0.3760
NX	 0.8810	 0.4930
NZ	 0.8540	 0.5130
Na	 0.8570	 0.5260
Nb	 0.8490	 0.5230
Nc	 0.8510	 0.5220
Nd	 0.8460	 0.5170
Ne	 0.8510	 0.5230
Nf	 0.8410	 0.5170
Ng	 0.8360	 0.5190
Nh	 0.8290	 0.5130
Ni	 0.8010	 0.4950
Nj	 0.8060	 0.4680
Nx	 0.8820	 0.4920
Nz	 0.8500	 0.5150
O	 0.6880	 0.3940
OE	 0.9030	 0.5370
OF	 0.8790	 0.5420
OG	 0.8730	 0.5400
OH	 0.8700	 0.5450
OI	 0.8700	 0.5380
OJ	 0.8610	 0.5380
OK	 0.8590	 0.5460
OL	 0.8670	 0.5380
OM	 0.8560	 0.5360
ON	 0.8560	 0.5390
OO	 0.8350	 0.5230
Oj	 0.8920	 0.5350
Ok	 0.8760	 0.5410
Ol	 0.8760	 0.5430
Om	 0.8580	 0.5390
On	 0.8700	 0.5420
Oo	 0.8560	 0.5360
Op	 0.8580	 0.5420
Oq	 0.8720	 0.5440
Or	 0.8630	 0.5370
Os	 0.8460	 0.5450
Ot	 0.8310	 0.5180
P	 0.7270	 0.3900
PE	 0.8940	 0.5320
PF	 0.8750	 0.5450
PG	 0.8770	 0.5480





















































































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Chain	Atom inclusion	Q-score
PH	 0.8730	 0.5490
PI	 0.8700	 0.5410
PJ	 0.8560	 0.5300
PK	 0.8580	 0.5400
PL	 0.8670	 0.5440
PM	 0.8590	 0.5380
PN	 0.8580	 0.5370
PO	 0.8280	 0.5150
Pj	 0.8910	 0.5340
Pk	 0.8780	 0.5390
Pl	 0.8770	 0.5430
Pm	 0.8660	 0.5440
Pn	 0.8650	 0.5430
Po	 0.8550	 0.5420
Pp	 0.8600	 0.5440
Pq	 0.8560	 0.5390
Pr	 0.8560	 0.5380
Ps	 0.8570	 0.5420
Pt	 0.8420	 0.5210
Q	 0.7030	 0.4040
R	 0.7180	 0.4050
RE	 0.8950	 0.5340
RF	 0.8840	 0.5460
RG	 0.8780	 0.5410
RH	 0.8720	 0.5490
RI	 0.8660	 0.5370
RJ	 0.8560	 0.5330
RK	 0.8550	 0.5430
RL	 0.8750	 0.5430
RM	 0.8560	 0.5440
RN	 0.8560	 0.5400
RO	 0.8240	 0.5130
RT	 0.8870	 0.5290
Rk	 0.8810	 0.5460
Rl	 0.8770	 0.5460
Rm	 0.8700	 0.5420
Rn	 0.8630	 0.5420
Ro	 0.8580	 0.5330
Rp	 0.8630	 0.5420
Rq	 0.8720	 0.5430
Rr	 0.8490	 0.5370
Rs	 0.8560	 0.5390

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Chain	Atom inclusion	Q-score
Rt	 0.8270	 0.5160
S	 0.7640	 0.4210
S0	 0.0940	 0.1860
S1	 0.1110	 0.2010
S2	 0.1130	 0.1800
S3	 0.1010	 0.1970
S4	 0.1190	 0.1970
S5	 0.1140	 0.1900
S6	 0.1210	 0.1860
S7	 0.1090	 0.1840
S8	 0.1110	 0.1920
SA	 0.1150	 0.1900
SO	 0.1160	 0.1880
SP	 0.1160	 0.1840
SQ	 0.1010	 0.1970
Sv	 0.1200	 0.1980
Sw	 0.1230	 0.1910
Sx	 0.1200	 0.1780
Sy	 0.1280	 0.1780
Sz	 0.1130	 0.1920
T	 0.7370	 0.4110
T1	 0.0230	 0.2310
T2	 0.0330	 0.2410
T3	 0.0360	 0.2440
T4	 0.0200	 0.2320
T5	 0.0260	 0.2260
T6	 0.0210	 0.2490
T7	 0.0330	 0.2460
T8	 0.0230	 0.2520
T9	 0.0310	 0.2610
TF	 0.0300	 0.2370
TG	 0.0390	 0.2410
TH	 0.0410	 0.2630
Td	 0.0250	 0.2210
Te	 0.0280	 0.2300
Tf	 0.0370	 0.2390
Tg	 0.0440	 0.2440
Th	 0.0320	 0.2430
Ti	 0.0440	 0.2640
U	 0.7030	 0.4030
UL	 0.0530	 0.1790
UM	 0.0570	 0.1650





















































































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Chain	Atom inclusion	Q-score
UN	0.0720	0.1620
Up	0.0430	0.1810
Uq	0.0470	0.1720
Ur	0.0580	0.1530
Us	0.0470	0.1630
Ut	0.0670	0.1550
Uu	0.0590	0.1570
V	0.7230	0.4000
VL	0.0350	0.1680
VM	0.0410	0.1580
VN	0.0580	0.1700
Vp	0.0390	0.1750
Vq	0.0430	0.1730
Vr	0.0460	0.1640
Vs	0.0350	0.1700
Vt	0.0630	0.1600
Vu	0.0550	0.1610
W	0.7320	0.3970
WI	0.2280	0.2430
WJ	0.2620	0.2460
WK	0.2650	0.2570
Wj	0.2270	0.2510
Wk	0.2070	0.2420
Wl	0.2560	0.2550
Wm	0.2530	0.2420
Wn	0.2570	0.2500
Wo	0.2460	0.2540
X	0.7370	0.3800
XI	0.2100	0.2360
XJ	0.2410	0.2520
XK	0.2400	0.2490
Xj	0.2070	0.2490
Xk	0.2110	0.2450
Xl	0.2370	0.2570
Xm	0.2440	0.2460
Xn	0.2390	0.2550
Xo	0.2430	0.2490
Y	0.6660	0.3900
YC	0.5930	0.4000
YX	0.5980	0.4010
YY	0.5890	0.3970
Yc	0.5970	0.4030





















































































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Chain	Atom inclusion	Q-score
Yx	 0.5790	 0.4000
Yy	 0.5890	 0.3990
Z	 0.7250	 0.4000
ZD	 0.6040	 0.4090
ZE	 0.6740	 0.4570
ZZ	 0.6090	 0.4120
Za	 0.5970	 0.4000
Zb	 0.6750	 0.4560
Zc	 0.6750	 0.4540
a	 0.6930	 0.3770
aD	 0.6040	 0.4090
aE	 0.6580	 0.4480
aZ	 0.5960	 0.4100
aa	 0.6020	 0.4100
ab	 0.6610	 0.4550
ac	 0.6540	 0.4520
b	 0.7470	 0.3970
b0	 0.7680	 0.4790
b3	 0.7870	 0.4560
b4	 0.7890	 0.4540
b5	 0.7990	 0.4610
b6	 0.7910	 0.4540
b7	 0.7960	 0.4610
b8	 0.7560	 0.4790
b9	 0.7710	 0.4770
bN	 0.7620	 0.4930
bO	 0.7640	 0.4930
bP	 0.7690	 0.4950
bQ	 0.7650	 0.4900
bR	 0.7660	 0.4910
bY	 0.7560	 0.4900
c	 0.7080	 0.3670
cA	 0.7700	 0.4760
cB	 0.7640	 0.4780
cC	 0.7650	 0.4850
cD	 0.7670	 0.4830
cE	 0.7890	 0.4540
cF	 0.7680	 0.4750
cG	 0.7580	 0.4830
cH	 0.7450	 0.4790
cI	 0.7750	 0.4840
cJ	 0.7670	 0.4900





















































































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Chain	Atom inclusion	Q-score
cK	 0.7720	 0.4830
cL	 0.7520	 0.4770
cM	 0.7590	 0.4800
cN	 0.7550	 0.4790
cO	 0.7580	 0.4810
cP	 0.7650	 0.4780
d	 0.6460	 0.3670
dS	 0.7670	 0.4930
dT	 0.7590	 0.4890
dU	 0.7740	 0.4940
dV	 0.7600	 0.4890
dW	 0.7650	 0.4920
dZ	 0.7430	 0.4840
e	 0.6930	 0.3750
eB	 0.7430	 0.4760
eU	 0.7390	 0.4800
eW	 0.7430	 0.4740
f	 0.6640	 0.3940
f9	 0.7430	 0.4780
fA	 0.7390	 0.4720
fB	 0.7260	 0.4720
fR	 0.7500	 0.4760
fS	 0.7330	 0.4760
fU	 0.7320	 0.4760
fW	 0.7230	 0.4680
fr	 0.7310	 0.4760
fs	 0.7350	 0.4770
g	 0.7070	 0.3950
gE	 0.8050	 0.4990
gG	 0.8070	 0.4970
gH	 0.8180	 0.5010
gd	 0.6220	 0.3140
h	 0.7220	 0.4140
h1	 0.8030	 0.5060
h2	 0.8020	 0.5060
hI	 0.7990	 0.5130
hJ	 0.7970	 0.5060
hK	 0.8040	 0.5130
hL	 0.7980	 0.5090
hM	 0.8050	 0.5100
hX	 0.7990	 0.5100
he	 0.7990	 0.4940





















































































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Chain	Atom inclusion	Q-score
hf	 0.8020	 0.5020
hg	 0.8000	 0.4920
hh	 0.7970	 0.4980
hi	 0.8120	 0.4930
hj	 0.8240	 0.5010
hk	 0.8260	 0.4990
hl	 0.8250	 0.5030
hm	 0.8280	 0.4980
hn	 0.8280	 0.4990
ho	 0.8090	 0.5120
hp	 0.8090	 0.5110
hq	 0.8170	 0.5150
hr	 0.8240	 0.5150
hs	 0.8060	 0.5080
ht	 0.8020	 0.4970
hu	 0.8220	 0.4960
hv	 0.8120	 0.5130
hw	 0.8030	 0.5070
hx	 0.8090	 0.5150
hy	 0.8030	 0.5070
hz	 0.8150	 0.5120
i	 0.6420	 0.3840
iC	 0.7800	 0.5100
iD	 0.7800	 0.5130
iF	 0.7840	 0.5110
j	 0.6680	 0.3870
ja	 0.7080	 0.4900
jb	 0.6790	 0.4830
jc	 0.6710	 0.4680
k	 0.7430	 0.4550
k3	 0.7530	 0.4940
k4	 0.7640	 0.4900
k7	 0.7770	 0.4990
k8	 0.7800	 0.4970
kV	 0.7820	 0.4980
l	 0.7210	 0.4480
lV	 0.7730	 0.5020
m	 0.7230	 0.4550
m1	 0.6980	 0.4700
m2	 0.6360	 0.4610
m5	 0.7260	 0.4790
m6	 0.6380	 0.4600







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Chain	Atom inclusion	Q-score
mT	 0.6400	 0.4660
n	 0.7230	 0.4520
nT	 0.7230	 0.4790
o	 0.6850	 0.4580
o0	 0.6930	 0.4940
o1	 0.6390	 0.4710
o2	 0.6380	 0.4700
o6	 0.6470	 0.4720
p	 0.7470	 0.4530
pA	 0.6990	 0.4970
pB	 0.6860	 0.4930
q	 0.7330	 0.4540
q3	 0.7870	 0.5050
q4	 0.7850	 0.5030
q5	 0.7870	 0.5120
q7	 0.7840	 0.5030
q8	 0.7870	 0.5060
q9	 0.7840	 0.5100
r	 0.7240	 0.4490
rc	 0.8480	 0.5240
rd	 0.8720	 0.5270
re	 0.8480	 0.5270
rf	 0.8400	 0.5390
rg	 0.8400	 0.5140
rh	 0.8480	 0.5160
s	 0.7330	 0.4550
sQ	 0.7220	 0.5320
sT	 0.6890	 0.5100
sU	 0.6220	 0.5000
t	 0.7340	 0.4550
tS	 0.8200	 0.5070
tX	 0.8000	 0.4840
tY	 0.7400	 0.4870
u	 0.7440	 0.4520
uR	 0.6000	 0.5020
uV	 0.6860	 0.5050
uW	 0.7430	 0.5190
v	 0.7030	 0.4570
vZ	 0.8890	 0.5880
va	 0.8440	 0.5840
vb	 0.8220	 0.5790
w	 0.7030	 0.4540

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Chain	Atom inclusion	Q-score
x	 0.7290	 0.4610
y	 0.7390	 0.4630
z	 0.7120	 0.4560