wwPDB EM Validation Summary Report (i)

May 26, 2025 – 01:43 AM JST

PDB ID	:	9IJJ / pdb_00009ijj
EMDB ID	:	EMD-60633
Title	:	In situ structure of the central apparatus in mouse sperm axoneme.
Authors	:	Zhu, Y.; Yin, G.; Sun, F.
Deposited on	:	2024-06-23
Resolution	:	7.70 Å(reported)

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

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

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

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

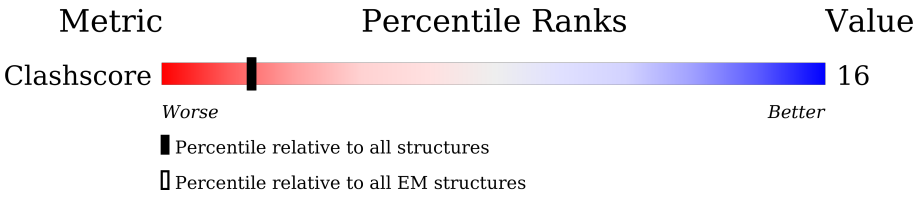
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 7.70 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)
Clashscore	210492	15764

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

Mol	Chain	Length	Quality of chain
1	W	295	44% 18% 38%
1	X	295	46% 16% 38%
1	Y	295	46% 16% 38%
1	Z	295	38% 23% 38%
1	a	295	45% 16% 38%
1	b	295	48% 14% 38%
2	c	790	46% 17% 37%
2	d	790	48% 24% 28%
2	e	790	45% 18% 37%
2	f	790	46% 17% 37%

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Mol	Chain	Length	Quality of chain
2	g	790	49% 23% 28%
3	h	1847	60% 18% 22%
3	i	1847	64% 14% 22%
3	j	1847	60% 18% 22%
4	k	1141	23% 61% 14% 25%
4	l	1141	17% 64% 12% 23%
4	m	1141	23% 61% 15% 25%
4	n	1141	17% 62% 14% 23%
4	o	1141	26% 63% 12% 25%
4	p	1141	18% 62% 14% 23%
5	q	232	55% 33% 12%
5	r	232	57% 31% 12%
5	s	232	57% 30% 12%
6	t	193	69% 26% 5%
6	u	193	68% 27% 5%
7	v	932	10% 7% 83%
7	w	932	9% 8% 83%
8	A	2641	9% 44% 23% 33%
8	B	2641	6% 30% 17% 53%
9	C	1578	6% 39% 22% 38%
9	D	1578	10% 9% 81%
9	E	1578	24% 7% 69%
10	F	1664	5% 43% 20% 37%
10	G	1664	20% 9% 70%
11	H	3106	45% 42% 13%

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Mol	Chain	Length	Quality of chain
11	I	3106	15% 14% 71%
12	L	836	16% 11% 72%
13	M	288	31% 32% 37%
14	O	1741	49% 25% 25%
14	P	1741	25% 9% 66%
15	Q	639	38% 33% 29%
15	R	639	43% 28% 29%
15	S	639	39% 32% 29%
15	T	639	42% 30% 29%
15	U	639	40% 31% 29%
15	V	639	44% 28% 29%
16	x	2320	34% 13% 52%
16	y	2320	6% 35% 13% 52%
16	z	2320	7% 35% 13% 52%
17	Ab	445	71% 26%
17	Ad	445	67% 30%
17	Af	445	68% 29%
17	Ah	445	71% 26%
17	Aj	445	70% 27%
17	An	445	69% 29%
17	Ap	445	67% 30%
17	Ar	445	66% 31%
17	At	445	66% 31%
17	Av	445	69% 29%
17	Bb	445	67% 30%

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Mol	Chain	Length	Quality of chain
17	Bd	445	66% 31%
17	Bf	445	68% 29%
17	Bh	445	67% 30%
17	Bj	445	66% 31%
17	Bn	445	67% 30%
17	Bp	445	63% 34%
17	Br	445	67% 30%
17	Bt	445	67% 30%
17	Bv	445	70% 27%
17	Cb	445	68% 29%
17	Cd	445	66% 31%
17	Cf	445	68% 29%
17	Ch	445	68% 29%
17	Cj	445	67% 30%
17	Cn	445	67% 30%
17	Cp	445	66% 31%
17	Cr	445	64% 32%
17	Ct	445	66% 31%
17	Cv	445	69% 29%
17	Db	445	69% 28%
17	Dd	445	62% 35%
17	Df	445	65% 32%
17	Dh	445	62% 35%
17	Dj	445	65% 32%
17	Dn	445	67% 30%

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Mol	Chain	Length	Quality of chain
17	Dp	445	68% 29%
17	Dr	445	66% 31%
17	Dt	445	68% 29%
17	Dv	445	69% 28%
17	Eb	445	69% 28%
17	Ed	445	67% 30%
17	Ef	445	66% 31%
17	Eh	445	67% 30%
17	Ej	445	68% 29%
17	En	445	64% 33%
17	Ep	445	64% 33%
17	Er	445	67% 30%
17	Et	445	67% 30%
17	Ev	445	69% 29%
17	Fb	445	69% 29%
17	Fd	445	67% 30%
17	Ff	445	69% 28%
17	Fh	445	67% 30%
17	Fj	445	70% 27%
17	Fn	445	70% 27%
17	Fp	445	66% 31%
17	Fr	445	67% 31%
17	Ft	445	64% 33%
17	Fv	445	65% 32%
17	Gb	445	67% 30%

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Mol	Chain	Length	Quality of chain
17	Gd	445	67% 30%
17	Gf	445	64% 33%
17	Gh	445	65% 32%
17	Gj	445	67% 30%
17	Gn	445	71% 26%
17	Gp	445	67% 30%
17	Gr	445	68% 29%
17	Gt	445	68% 29%
17	Gv	445	68% 29%
17	Hb	445	64% 33%
17	Hd	445	66% 31%
17	Hf	445	72% 25%
17	Hh	445	69% 28%
17	Hj	445	66% 31%
17	Hn	445	69% 28%
17	Hp	445	66% 31%
17	Hr	445	67% 30%
17	Ht	445	69% 28%
17	Hv	445	64% 33%
17	Ib	445	68% 29%
17	Id	445	68% 29%
17	If	445	66% 31%
17	Ih	445	69% 28%
17	Ij	445	70% 27%
17	In	445	70% 27%

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Mol	Chain	Length	Quality of chain
17	Ip	445	68% 29%
17	Ir	445	68% 29%
17	It	445	71% 26%
17	Iv	445	69% 28%
17	Jb	445	67% 30%
17	Jd	445	65% 32%
17	Jf	445	64% 33%
17	Jh	445	69% 29%
17	Jj	445	70% 27%
17	Jn	445	69% 28%
17	Jp	445	63% 34%
17	Jr	445	63% 34%
17	Jt	445	67% 31%
17	Jv	445	68% 29%
17	Kb	445	65% 32%
17	Kd	445	66% 31%
17	Kf	445	67% 30%
17	Kh	445	65% 32%
17	Kj	445	68% 29%
17	Kn	445	66% 31%
17	Kp	445	63% 34%
17	Kr	445	63% 34%
17	Kt	445	65% 32%
17	Kv	445	66% 31%
17	Lb	445	68% 29%

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Mol	Chain	Length	Quality of chain
17	Ld	445	67% 30%
17	Lf	445	66% 31%
17	Lh	445	67% 30%
17	Lj	445	68% 29%
17	Ln	445	67% 31%
17	Lp	445	68% 29%
17	Lr	445	66% 31%
17	Lt	445	66% 31%
17	Lv	445	72% 25%
17	Mb	445	73% 24%
17	Md	445	71% 26%
17	Mf	445	69% 28%
17	Mh	445	66% 31%
17	Mj	445	73% 24%
17	Mn	445	67% 30%
17	Mp	445	66% 31%
17	Mr	445	68% 29%
17	Mt	445	67% 31%
17	Mv	445	69% 28%
18	Ac	450	74% 24%
18	Ae	450	73% 24%
18	Ag	450	72% 26%
18	Ai	450	74% 24%
18	Ak	450	72% 26%
18	Ao	450	71% 26%

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Mol	Chain	Length	Quality of chain
18	Aq	450	75% 23%
18	As	450	68% 30%
18	Au	450	74% 24%
18	Aw	450	74% 23%
18	Bc	450	75% 22%
18	Be	450	74% 23%
18	Bg	450	70% 27%
18	Bi	450	71% 26%
18	Bk	450	71% 27%
18	Bm	450	69% 28%
18	Bo	450	68% 30%
18	Bq	450	67% 30%
18	Bs	450	69% 28%
18	Bu	450	72% 25%
18	Cc	450	74% 23%
18	Ce	450	72% 25%
18	Cg	450	70% 28%
18	Ci	450	71% 26%
18	Ck	450	71% 27%
18	Cm	450	71% 27%
18	Co	450	70% 28%
18	Cq	450	69% 29%
18	Cs	450	69% 29%
18	Cu	450	73% 24%
18	Dc	450	74% 24%

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Mol	Chain	Length	Quality of chain
18	De	450	73% 24%
18	Dg	450	70% 27%
18	Di	450	72% 26%
18	Dk	450	72% 26%
18	Dm	450	72% 25%
18	Do	450	70% 27%
18	Dq	450	68% 30%
18	Ds	450	64% 34%
18	Du	450	71% 26%
18	Ec	450	70% 27%
18	Ee	450	74% 24%
18	Eg	450	68% 29%
18	Ei	450	73% 24%
18	Ek	450	69% 28%
18	Em	450	70% 28%
18	Eo	450	76% 22%
18	Eq	450	68% 29%
18	Es	450	73% 25%
18	Eu	450	77% 21%
18	Fa	450	75% 23%
18	Fc	450	70% 27%
18	Fe	450	71% 27%
18	Fg	450	69% 28%
18	Fi	450	72% 25%
18	Fo	450	71% 26%

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Mol	Chain	Length	Quality of chain
18	Fq	450	74% 24%
18	Fs	450	74% 24%
18	Fu	450	74% 23%
18	Fw	450	76% 22%
18	Ga	450	72% 25%
18	Gc	450	70% 28%
18	Ge	450	70% 28%
18	Gg	450	72% 26%
18	Gi	450	71% 27%
18	Go	450	70% 27%
18	Gq	450	66% 31%
18	Gs	450	70% 27%
18	Gu	450	72% 25%
18	Gw	450	70% 28%
18	Ha	450	71% 27%
18	Hc	450	72% 25%
18	He	450	69% 28%
18	Hg	450	68% 29%
18	Hi	450	68% 30%
18	Ho	450	72% 26%
18	Hq	450	66% 32%
18	Hs	450	70% 27%
18	Hu	450	67% 30%
18	Hw	450	69% 28%
18	Ia	450	76% 21%

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Mol	Chain	Length	Quality of chain
18	Ic	450	71% 27%
18	Ie	450	70% 27%
18	Ig	450	70% 28%
18	Ii	450	72% 25%
18	Io	450	66% 31%
18	Iq	450	67% 30%
18	Is	450	65% 33%
18	Iu	450	69% 28%
18	Iw	450	69% 28%
18	Ja	450	75% 22%
18	Jc	450	73% 24%
18	Je	450	69% 28%
18	Jg	450	61% 36%
18	Ji	450	71% 27%
18	Jo	450	67% 31%
18	Jq	450	66% 31%
18	Js	450	67% 30%
18	Ju	450	70% 27%
18	Jw	450	74% 23%
18	Kc	450	72% 26%
18	Ke	450	69% 29%
18	Kg	450	68% 29%
18	Ki	450	70% 28%
18	Kk	450	68% 29%
18	Km	450	74% 23%

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Mol	Chain	Length	Quality of chain
18	Ko	450	66% 32%
18	Kq	450	69% 29%
18	Ks	450	68% 30%
18	Ku	450	69% 29%
18	Lc	450	75% 22%
18	Le	450	74% 24%
18	Lg	450	74% 23%
18	Li	450	74% 24%
18	Lk	450	73% 24%
18	Lm	450	70% 27%
18	Lo	450	70% 28%
18	Lq	450	68% 29%
18	Ls	450	69% 28%
18	Lu	450	74% 24%
18	Mc	450	72% 26%
18	Me	450	73% 24%
18	Mg	450	71% 26%
18	Mi	450	69% 28%
18	Mk	450	76% 22%
18	Mm	450	75% 22%
18	Mo	450	69% 29%
18	Mq	450	71% 26%
18	Ms	450	69% 29%
18	Mu	450	72% 26%
19	A1	507	55% 44%

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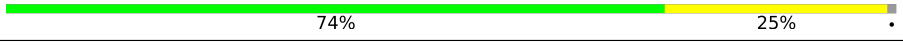
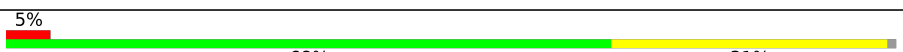
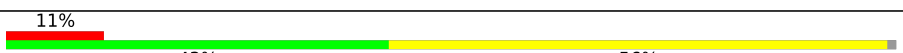
Mol	Chain	Length	Quality of chain
19	AA	507	
19	AB	507	
19	AC	507	
19	AD	507	
19	AE	507	
19	AF	507	
19	AG	507	
19	AH	507	
19	AI	507	
19	AJ	507	
19	AK	507	
19	AL	507	
19	AM	507	
19	AN	507	
19	AO	507	
19	AP	507	
19	AQ	507	
19	AR	507	
19	AS	507	
19	AT	507	
19	AU	507	
19	AV	507	
19	AW	507	
19	AX	507	
19	AY	507	

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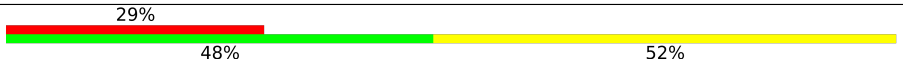
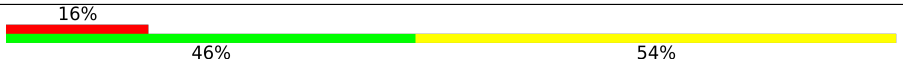
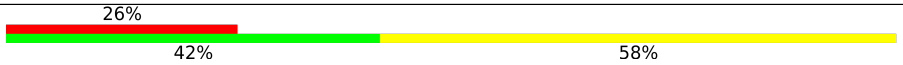
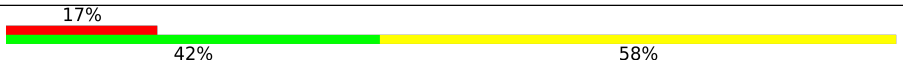
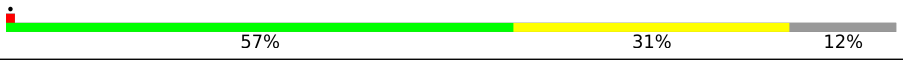
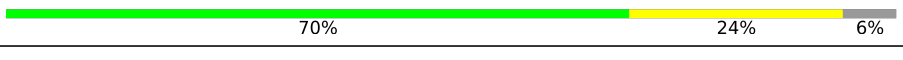
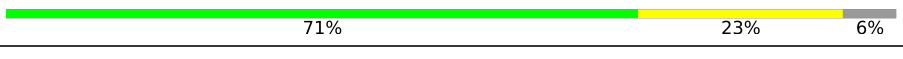
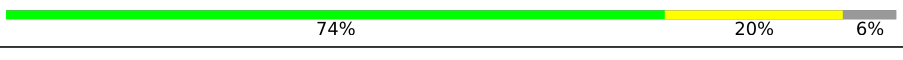
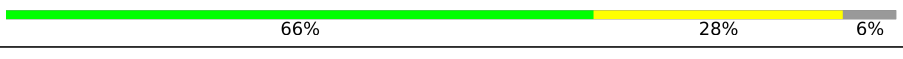
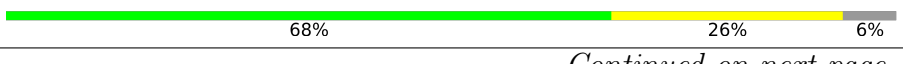
Mol	Chain	Length	Quality of chain
19	AZ	507	
20	3D	149	
20	3E	149	
20	3F	149	
20	3G	149	
20	3H	149	
20	3I	149	
20	3J	149	
21	A2	942	
21	A3	942	
21	A4	942	
22	1A	168	
22	1B	168	
22	1C	168	
22	1D	168	
22	1E	168	
22	1F	168	
22	1G	168	
22	1I	168	
22	1J	168	
22	1K	168	
22	1L	168	
22	1M	168	
22	1N	168	
22	1O	168	

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Mol	Chain	Length	Quality of chain
22	1P	168	30% 65% 29% 6%
22	1Q	168	49% 59% 35% 6%
22	1R	168	43% 60% 33% 6%
22	1S	168	5% 74% 20% 6%
22	1T	168	71% 23% 6%
22	1U	168	71% 23% 6%
22	1V	168	15% 70% 24% 6%
22	1W	168	67% 27% 6%
22	1X	168	8% 63% 31% 6%
22	1Y	168	58% 36% 6%
22	1Z	168	64% 30% 6%
22	1a	168	72% 22% 6%
22	1b	168	63% 31% 6%
22	1c	168	77% 17% 6%
22	1d	168	70% 24% 6%
22	1e	168	33% 71% 23% 6%
22	1f	168	42% 61% 33% 6%
22	1g	168	43% 68% 26% 6%
22	1h	168	40% 71% 22% 6%
22	1i	168	37% 65% 29% 6%
22	1j	168	36% 70% 24% 6%
22	1k	168	57% 71% 23% 6%
22	2A	168	31% 54% 40% 6%
22	2B	168	12% 65% 29% 6%
22	2C	168	25% 58% 35% 6%

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Mol	Chain	Length	Quality of chain
22	2D	168	58% 71% 22% 6%
22	2E	168	63% 31% 6%
22	2F	168	10% 68% 26% 6%
22	2G	168	21% 51% 43% 6%
22	2H	168	11% 64% 30% 6%
22	2I	168	65% 29% 6%
22	2J	168	65% 29% 6%
22	2K	168	8% 57% 37% 6%
22	2L	168	14% 51% 43% 6%
22	2M	168	7% 61% 33% 6%
22	2N	168	61% 33% 6%
22	2O	168	20% 70% 24% 6%
22	2P	168	17% 60% 35% 6%
22	2Q	168	66% 28% 6%
22	2R	168	72% 22% 6%
22	2S	168	10% 64% 30% 6%
22	2T	168	26% 60% 34% 6%
22	2U	168	8% 61% 33% 6%
22	2V	168	68% 26% 6%
23	3T	99	42% 15% 42%
23	3U	99	59% 17% 24%
23	3V	99	14% 49% 10% 40%
23	3W	99	15% 66% 10% 24%
23	3X	99	14% 51% 9% 40%
23	3Y	99	15% 65% 11% 24%

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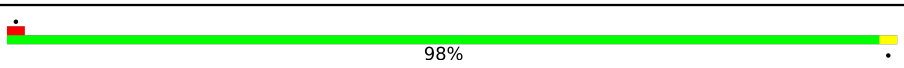
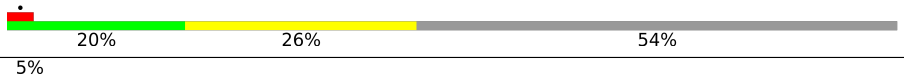
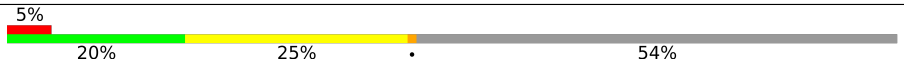
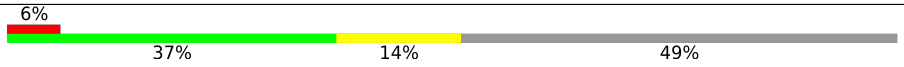
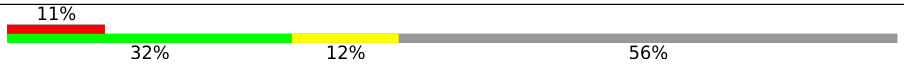
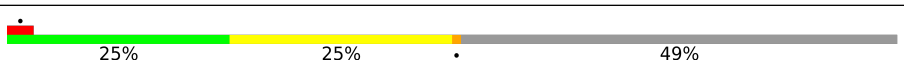
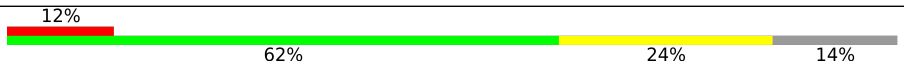
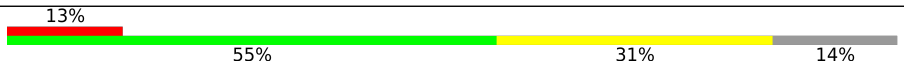
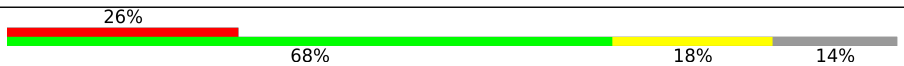
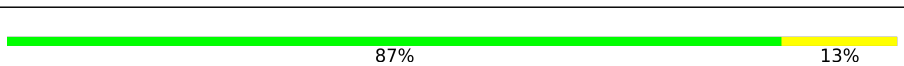
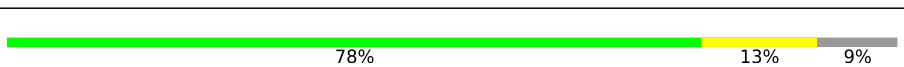
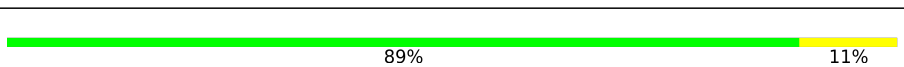
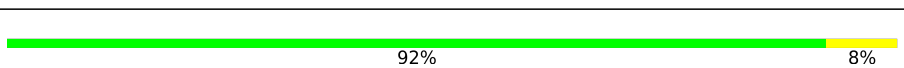
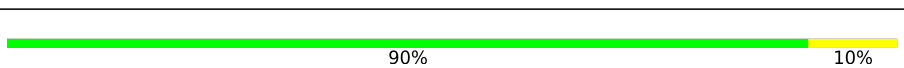
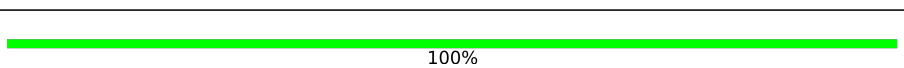
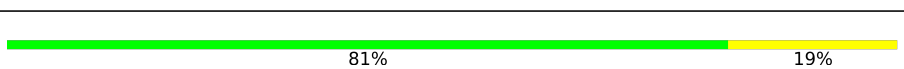
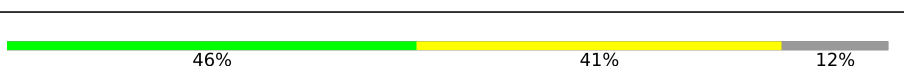
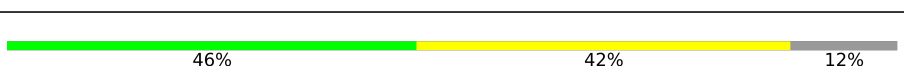
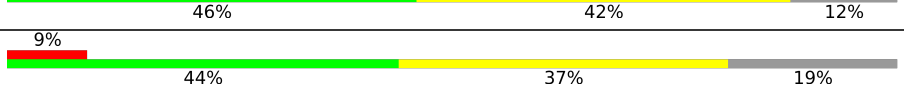
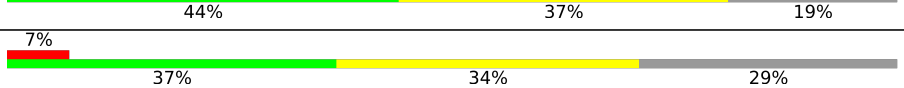
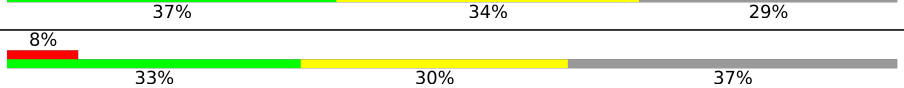
Mol	Chain	Length	Quality of chain
24	3A	57	
25	3B	379	
25	3C	379	
26	3K	333	
26	3L	333	
26	3M	333	
26	3N	333	
26	3O	333	
26	3P	333	
27	3Q	152	
27	3R	152	
27	3S	152	
28	3Z	102	
28	3a	102	
29	3b	143	
29	3c	143	
29	3d	143	
30	3e	54	
31	3f	18	
32	3g	47	
33	4A	3184	
33	4B	3184	
34	4G	5154	
34	4H	5154	
34	4I	5154	

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Mol	Chain	Length	Quality of chain
34	4J	5154	8% 6% 86%
34	4K	5154	5% 92%
35	4C	524	40% 40% 19%
35	4D	524	48% 32% 19%
35	4E	524	39% 41% 19%
35	4F	524	49% 32% 19%
36	4L	1724	5% 38% 41% 21%
36	4M	1724	5% 39% 40% 21%
36	4N	1724	5% 39% 40% 21%
37	4O	820	34% 24% 42%
37	4P	820	36% 22% 42%
37	4Q	820	33% 25% 42%
38	4R	404	53% 43%
38	4S	404	52% 44%
38	4T	404	53% 43%
38	4U	404	51% 45%
38	4V	404	54% 42%
38	4W	404	50% 46%
39	4X	853	13% 32% 52% 16%
39	4Y	853	12% 31% 53% 16%
40	4Z	688	40% 52% 8%
41	4a	323	41% 42% 17%
42	4b	973	22% 35% 43%
42	4c	973	22% 35% 43%
43	5A	648	23% 74%

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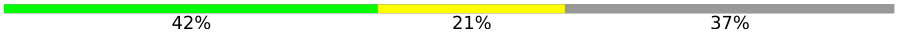
Mol	Chain	Length	Quality of chain
43	J	648	
43	K	648	
44	5B	906	
45	5C	667	

2 Entry composition (i)

There are 45 unique types of molecules in this entry. The entry contains 1637265 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 Spermatogenesis-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	182	Total	C	N	O	S	0	0
			1509	976	264	265	4		
1	a	182	Total	C	N	O	S	0	0
			1509	976	264	265	4		
1	W	182	Total	C	N	O	S	0	0
			1509	976	264	265	4		
1	X	182	Total	C	N	O	S	0	0
			1509	976	264	265	4		
1	Y	182	Total	C	N	O	S	0	0
			1509	976	264	265	4		
1	Z	182	Total	C	N	O	S	0	0
			1509	976	264	265	4		

- Molecule 2 is a protein called Kinesin-like protein KIF9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	497	Total	C	N	O	S	0	0
			4014	2514	707	775	18		
2	d	568	Total	C	N	O	S	0	0
			4578	2866	808	882	22		
2	e	497	Total	C	N	O	S	0	0
			4014	2514	707	775	18		
2	f	497	Total	C	N	O	S	0	0
			4014	2514	707	775	18		
2	g	568	Total	C	N	O	S	0	0
			4578	2866	808	882	22		

- Molecule 3 is a protein called Cilia- and flagella-associated protein 65.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	1444	Total	C	N	O	S	0	0
			11503	7440	1925	2075	63		
3	i	1444	Total	C	N	O	S	0	0
			11503	7440	1925	2075	63		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	j	1444	Total	C	N	O	S	0	0
			11503	7440	1925	2075	63		

- Molecule 4 is a protein called Cilia- and flagella-associated protein 70.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	k	859	Total	C	N	O	S	0	0
			6859	4410	1126	1288	35		
4	n	874	Total	C	N	O	S	0	0
			6979	4486	1145	1313	35		
4	o	859	Total	C	N	O	S	0	0
			6859	4410	1126	1288	35		
4	p	874	Total	C	N	O	S	0	0
			6979	4486	1145	1313	35		
4	m	859	Total	C	N	O	S	0	0
			6859	4410	1126	1288	35		
4	l	874	Total	C	N	O	S	0	0
			6979	4486	1145	1313	35		

- Molecule 5 is a protein called Protein FAM228B.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	q	203	Total	C	N	O	S	0	0
			1723	1096	302	315	10		
5	r	203	Total	C	N	O	S	0	0
			1723	1096	302	315	10		
5	s	203	Total	C	N	O	S	0	0
			1723	1096	302	315	10		

- Molecule 6 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	t	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
6	u	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		

- Molecule 7 is a protein called MYCBP-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	v	157	Total	C	N	O	S	0	0
			1313	837	237	235	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	w	157	Total	C	N	O	S	0	0
			1313	837	237	235	4		

- Molecule 8 is a protein called Cilia and flagella associated protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	1764	Total	C	N	O	S	0	0
			14212	9068	2424	2625	95		
8	B	1246	Total	C	N	O	S	0	0
			10003	6388	1691	1860	64		

- Molecule 9 is a protein called Cilia- and flagella-associated protein 74.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	974	Total	C	N	O	S	0	0
			7752	4956	1335	1426	35		
9	D	304	Total	C	N	O	S	0	0
			2529	1543	505	471	10		
9	E	488	Total	C	N	O	S	0	0
			3814	2471	618	706	19		

- Molecule 10 is a protein called Coiled-coil domain containing 180.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	1048	Total	C	N	O	S	0	0
			8741	5538	1506	1648	49		
10	G	493	Total	C	N	O	S	0	0
			4117	2597	725	770	25		

- Molecule 11 is a protein called Cilia- and flagella-associated protein 54.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	2700	Total	C	N	O	S	0	0
			21709	13992	3633	3951	133		
11	I	895	Total	C	N	O	S	0	0
			7165	4599	1208	1312	46		

- Molecule 12 is a protein called Cilia- and flagella-associated protein 221.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	230	Total	C	N	O	S	0	0
			1866	1212	312	334	8		

- Molecule 13 is a protein called Leucine rich repeat containing 72.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	181	Total	C	N	O	S	0	0
			1507	973	265	264	5		

- Molecule 14 is a protein called Deleted in lung and esophageal cancer 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	1299	Total	C	N	O	S	0	0
			10182	6526	1710	1887	59		
14	P	591	Total	C	N	O	S	0	0
			4660	2960	803	871	26		

- Molecule 15 is a protein called Sperm-associated antigen 16 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	454	Total	C	N	O	S	0	0
			3594	2271	634	666	23		
15	R	456	Total	C	N	O	S	0	0
			3608	2279	636	670	23		
15	S	454	Total	C	N	O	S	0	0
			3594	2271	634	666	23		
15	T	456	Total	C	N	O	S	0	0
			3608	2279	636	670	23		
15	U	454	Total	C	N	O	S	0	0
			3594	2271	634	666	23		
15	V	456	Total	C	N	O	S	0	0
			3608	2279	636	670	23		

- Molecule 16 is a protein called Sperm-associated antigen 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	x	1112	Total	C	N	O	S	0	0
			8949	5724	1486	1694	45		
16	y	1121	Total	C	N	O	S	0	0
			9047	5792	1500	1710	45		
16	z	1121	Total	C	N	O	S	0	0
			9047	5792	1500	1710	45		

- Molecule 17 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ab	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ad	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Af	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ah	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Aj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ch	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Db	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Df	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Eb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ed	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ef	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Eh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ej	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ff	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ib	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Id	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	If	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ih	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ij	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kd	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ld	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mb	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Md	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mf	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mh	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	Mj	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	An	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ap	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ar	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	At	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Av	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Br	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Bv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ct	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Cv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Dv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	En	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ep	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Er	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Et	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ev	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ft	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Fn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Gn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ht	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Hn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ip	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ir	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	It	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Iv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	In	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Jn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kn	432	Total	C	N	O	S	0	0
			3390	2129	579	656	26		
17	Kp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Kv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Ln	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Lv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mn	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mp	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	Mr	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mt	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
17	Mv	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		

- Molecule 18 is a protein called Tubulin alpha-3 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ac	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ae	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ag	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ai	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ak	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Be	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bi	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bk	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Cc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ce	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Cg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ci	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ck	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Dc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	De	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Dg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Di	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Dk	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ec	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ee	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Eg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ei	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ek	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fa	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fe	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fi	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ga	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ge	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gi	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ha	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	He	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hi	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ia	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ic	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ie	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ig	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ii	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ja	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Jc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Je	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Jg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ji	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Kc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ke	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Kg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ki	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Kk	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Lc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Le	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Lg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	Li	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Lk	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mc	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Me	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mg	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mi	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mk	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ao	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Aq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	As	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Au	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Aw	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bo	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bs	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Bm	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Co	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Cq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Cs	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Cu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cm	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Do	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Dq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ds	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Du	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Dm	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Eo	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Eq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Es	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Eu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Em	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fo	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fs	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Fw	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Go	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gs	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Gw	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ho	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hs	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Hw	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Io	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Iq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Is	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Iu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Iw	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Jo	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Jq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Js	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ju	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Jw	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ko	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Kq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ks	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ku	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Km	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Lo	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	Lq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ls	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Lu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Lm	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mo	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mq	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Ms	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mu	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
18	Mm	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		

- Molecule 19 is a protein called Sperm-associated antigen 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AA	461	Total	C	N	O	S	0	0
			3505	2239	597	652	17		
19	AB	501	Total	C	N	O	S	0	0
			3831	2442	658	712	19		
19	AC	477	Total	C	N	O	S	0	0
			3629	2314	625	672	18		
19	AD	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AE	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AF	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AG	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AH	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AI	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AJ	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
19	AK	490	Total	C	N	O	S	0	0
			3744	2387	643	695	19		
19	AL	503	Total	C	N	O	S	0	0
			3845	2449	660	717	19		
19	AM	490	Total	C	N	O	S	0	0
			3744	2387	643	695	19		
19	AN	490	Total	C	N	O	S	0	0
			3744	2387	643	695	19		
19	AO	491	Total	C	N	O	S	0	0
			3751	2392	644	696	19		
19	AP	503	Total	C	N	O	S	0	0
			3845	2449	660	717	19		
19	AQ	502	Total	C	N	O	S	0	0
			3839	2446	659	715	19		
19	AR	501	Total	C	N	O	S	0	0
			3831	2442	658	712	19		
19	AS	503	Total	C	N	O	S	0	0
			3845	2449	660	717	19		
19	AT	490	Total	C	N	O	S	0	0
			3743	2387	643	695	18		
19	AU	491	Total	C	N	O	S	0	0
			3751	2392	644	696	19		
19	AV	503	Total	C	N	O	S	0	0
			3845	2449	660	717	19		
19	AW	507	Total	C	N	O	S	0	0
			3882	2474	665	724	19		
19	AX	501	Total	C	N	O	S	0	0
			3831	2442	658	712	19		
19	AY	501	Total	C	N	O	S	0	0
			3831	2442	658	712	19		
19	AZ	501	Total	C	N	O	S	0	0
			3831	2442	658	712	19		
19	A1	501	Total	C	N	O	S	0	0
			3831	2442	658	712	19		

- Molecule 20 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3D	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		
20	3E	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
20	3F	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		
20	3G	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		
20	3H	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		
20	3I	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		
20	3J	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		

- Molecule 21 is a protein called Cilia- and flagella-associated protein 69.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	A2	825	Total	C	N	O	S	0	0
			6600	4231	1108	1219	42		
21	A3	825	Total	C	N	O	S	0	0
			6600	4231	1108	1219	42		
21	A4	825	Total	C	N	O	S	0	0
			6600	4231	1108	1219	42		

- Molecule 22 is a protein called Sperm acrosome-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1A	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1B	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1C	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1D	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1G	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1I	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1E	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1F	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1J	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
22	1K	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1L	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1M	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1N	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1O	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1P	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1Q	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1R	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1S	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1T	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1U	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1V	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1W	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1X	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1Y	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1Z	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1a	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1b	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1c	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1d	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2A	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
22	2D	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2B	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2C	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2F	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2E	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2G	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2H	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2I	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2J	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2K	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2L	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2M	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2N	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2O	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2P	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2Q	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2R	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2S	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2T	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2U	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	2V	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
22	1e	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1f	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1g	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1h	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1i	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1j	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		
22	1k	158	Total	C	N	O	S	0	0
			1285	807	227	240	11		

- Molecule 23 is a protein called Protein dpy-30 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	3X	59	Total	C	N	O	0	0
			471	302	81	88		
23	3Y	75	Total	C	N	O	0	0
			601	380	104	117		
23	3V	59	Total	C	N	O	0	0
			471	302	81	88		
23	3W	75	Total	C	N	O	0	0
			601	380	104	117		
23	3T	57	Total	C	N	O	0	0
			459	296	79	84		
23	3U	75	Total	C	N	O	0	0
			601	380	104	117		

- Molecule 24 is a protein called Unknown1.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	3A	57	Total	C	N	O	0	0
			285	171	57	57		

- Molecule 25 is a protein called Spermatogenesis-associated protein 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3B	173	Total	C	N	O	S	0	0
			1516	972	277	258	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
25	3C	173	Total	C	N	O	S	0	0
			1516	972	277	258	9		

- Molecule 26 is a protein called Cilia- and flagella-associated protein 119.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3K	169	Total	C	N	O	S	0	0
			1389	904	231	244	10		
26	3L	147	Total	C	N	O	S	0	0
			1208	785	203	210	10		
26	3M	169	Total	C	N	O	S	0	0
			1389	904	231	244	10		
26	3N	147	Total	C	N	O	S	0	0
			1208	785	203	210	10		
26	3O	169	Total	C	N	O	S	0	0
			1389	904	231	244	10		
26	3P	147	Total	C	N	O	S	0	0
			1208	785	203	210	10		

- Molecule 27 is a protein called MORN repeat containing 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	3Q	131	Total	C	N	O	S	0	0
			1031	651	173	201	6		
27	3R	131	Total	C	N	O	S	0	0
			1031	651	173	201	6		
27	3S	131	Total	C	N	O	S	0	0
			1031	651	173	201	6		

- Molecule 28 is a protein called Unknown2.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	3Z	102	Total	C	N	O	0	0
			510	306	102	102		
28	3a	93	Total	C	N	O	0	0
			465	279	93	93		

- Molecule 29 is a protein called Unknown3.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	3b	143	Total	C	N	O	0	0
			716	429	143	144		

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Mol	Chain	Residues	Atoms				AltConf	Trace
29	3c	143	Total 716	C 429	N 143	O 144	0	0
29	3d	143	Total 716	C 429	N 143	O 144	0	0

- Molecule 30 is a protein called Unknown4.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	3e	54	Total 270	C 162	N 54	O 54	0	0

- Molecule 31 is a protein called Unknown5.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	3f	18	Total 90	C 54	N 18	O 18	0	0

- Molecule 32 is a protein called Unknown6.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	3g	47	Total 235	C 141	N 47	O 47	0	0

- Molecule 33 is a protein called Cilia and flagella-associated protein 47.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	4A	2796	Total 22307	C 14458	N 3681	O 4057	S 111	0	0
33	4B	2796	Total 22307	C 14458	N 3681	O 4057	S 111	0	0

- Molecule 34 is a protein called Hydrocephalus-inducing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	4G	4178	Total 33109	C 21318	N 5466	O 6166	S 159	0	0
34	4H	3685	Total 29186	C 18773	N 4822	O 5443	S 148	0	0
34	4I	3245	Total 25730	C 16541	N 4261	O 4803	S 125	0	0
34	4J	709	Total 5614	C 3645	N 923	O 1024	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
34	4K	394	Total	C	N	O	S	0	0
			3102	2021	497	575	9		

- Molecule 35 is a protein called Germ cell-less protein-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4C	422	Total	C	N	O	S	0	0
			3403	2187	561	631	24		
35	4D	422	Total	C	N	O	S	0	0
			3403	2187	561	631	24		
35	4E	422	Total	C	N	O	S	0	0
			3403	2187	561	631	24		
35	4F	422	Total	C	N	O	S	0	0
			3403	2187	561	631	24		

- Molecule 36 is a protein called Sperm flagellar protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4M	1361	Total	C	N	O	S	0	0
			11139	7067	1921	2113	38		
36	4N	1361	Total	C	N	O	S	0	0
			11139	7067	1921	2113	38		
36	4L	1361	Total	C	N	O	S	0	0
			11139	7067	1921	2113	38		

- Molecule 37 is a protein called Leucine-rich repeat and guanylate kinase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	4P	475	Total	C	N	O	S	0	0
			3840	2459	637	723	21		
37	4Q	475	Total	C	N	O	S	0	0
			3840	2459	637	723	21		
37	4O	475	Total	C	N	O	S	0	0
			3840	2459	637	723	21		

- Molecule 38 is a protein called Putative aspartate aminotransferase, cytoplasmic 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	4R	389	Total	C	N	O	S	0	0
			3082	1997	505	561	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
38	4S	388	Total	C	N	O	S	0	0
			3074	1991	504	560	19		
38	4T	389	Total	C	N	O	S	0	0
			3082	1997	505	561	19		
38	4U	388	Total	C	N	O	S	0	0
			3074	1991	504	560	19		
38	4V	389	Total	C	N	O	S	0	0
			3082	1997	505	561	19		
38	4W	389	Total	C	N	O	S	0	0
			3082	1997	505	561	19		

- Molecule 39 is a protein called Leucine-rich repeat and death domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	4X	720	Total	C	N	O	S	0	0
			5789	3698	979	1082	30		
39	4Y	720	Total	C	N	O	S	0	0
			5789	3698	979	1082	30		

- Molecule 40 is a protein called G protein-coupled receptor kinase 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4Z	636	Total	C	N	O	S	0	0
			5203	3311	904	948	40		

- Molecule 41 is a protein called Serine/threonine-protein phosphatase PP1-gamma catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	4a	268	Total	C	N	O	S	0	0
			2170	1396	359	397	18		

- Molecule 42 is a protein called Microtubule-associated protein 1S.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	4b	558	Total	C	N	O	S	0	0
			4236	2697	753	768	18		
42	4c	558	Total	C	N	O	S	0	0
			4236	2697	753	768	18		

- Molecule 43 is a protein called Cilia and flagella associated protein 99.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	J	158	Total	C	N	O	S	0	0
			1303	789	257	249	8		
43	K	411	Total	C	N	O	S	0	0
			3381	2136	590	633	22		
43	5A	171	Total	C	N	O	S	0	0
			1430	947	222	252	9		

- Molecule 44 is a protein called Ankyrin repeat and MYND domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5B	652	Total	C	N	O	S	0	0
			5147	3295	887	932	33		

- Molecule 45 is a protein called Leucine-rich repeat-containing protein 43.

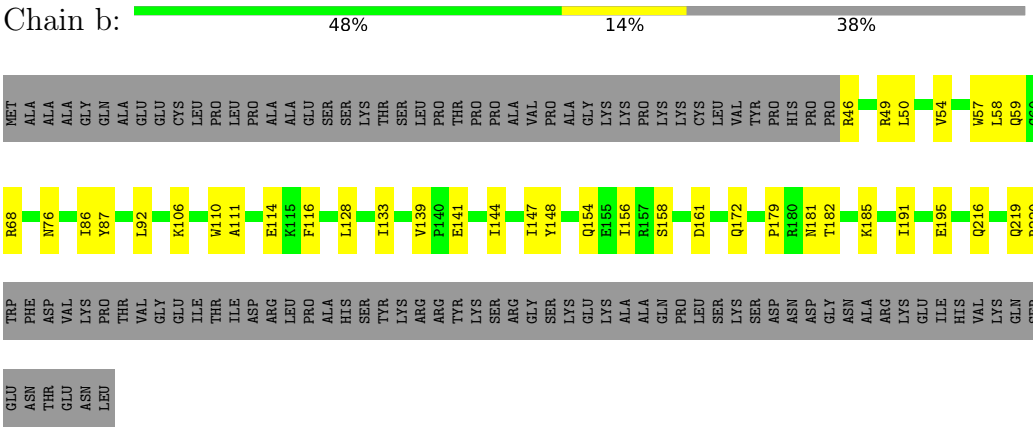
Mol	Chain	Residues	Atoms					AltConf	Trace
45	5C	463	Total	C	N	O	S	0	0
			3669	2365	615	675	14		

3 Residue-property plots (i)

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

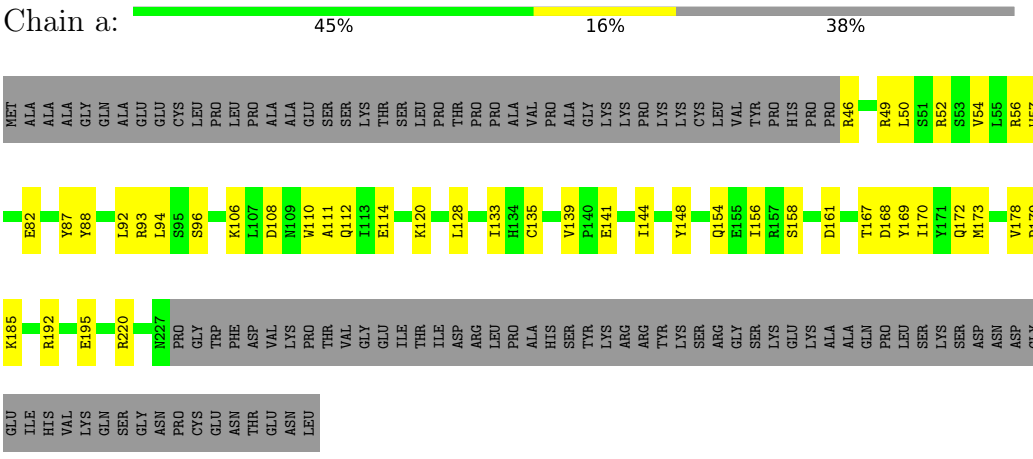
• Molecule 1: Spermatogenesis-associated protein 4

Chain b:



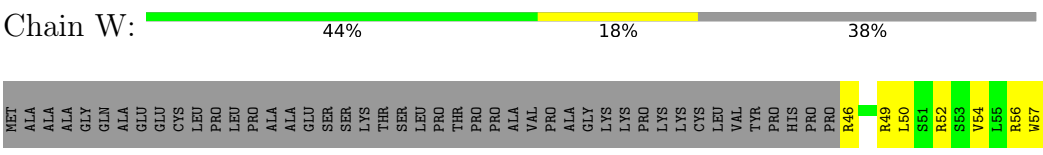
• Molecule 1: Spermatogenesis-associated protein 4

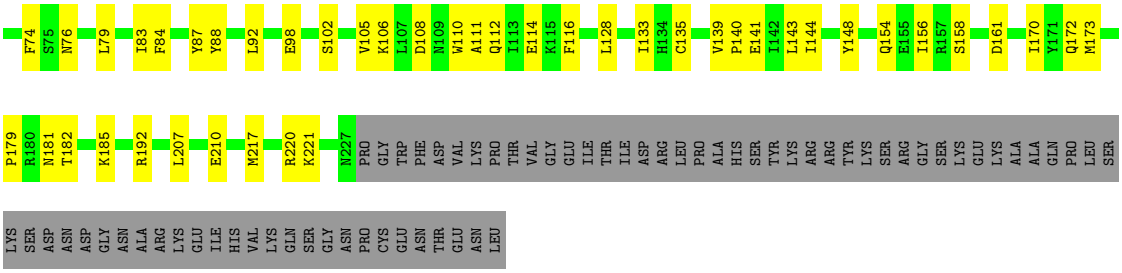
Chain a:



• Molecule 1: Spermatogenesis-associated protein 4

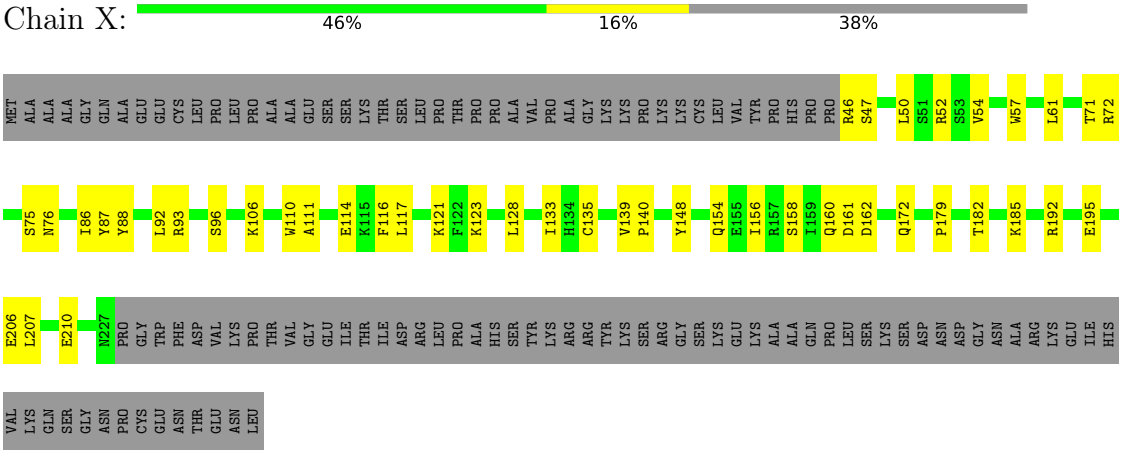
Chain W:





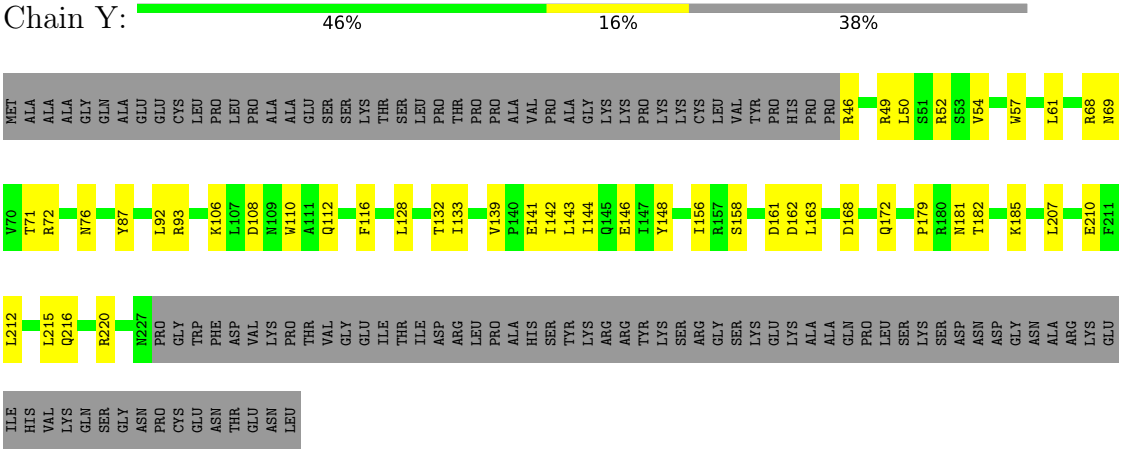
• Molecule 1: Spermatogenesis-associated protein 4

Chain X:



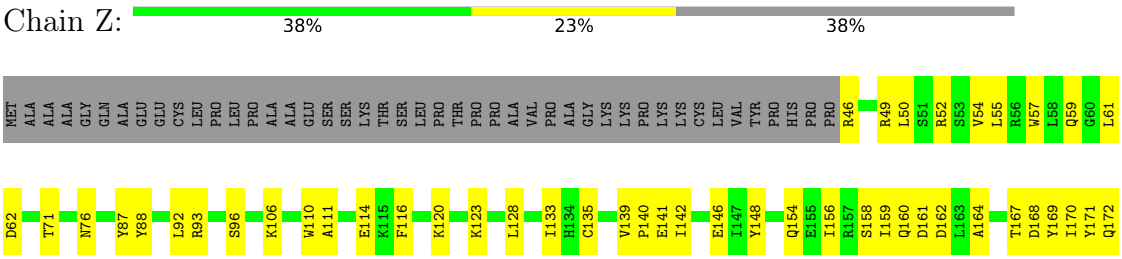
• Molecule 1: Spermatogenesis-associated protein 4

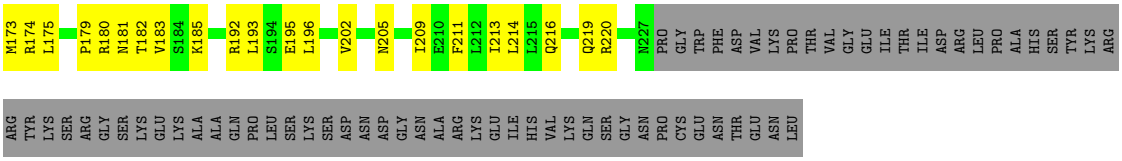
Chain Y:



• Molecule 1: Spermatogenesis-associated protein 4

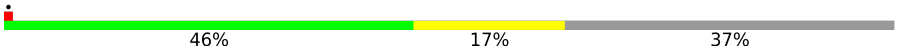
Chain Z:

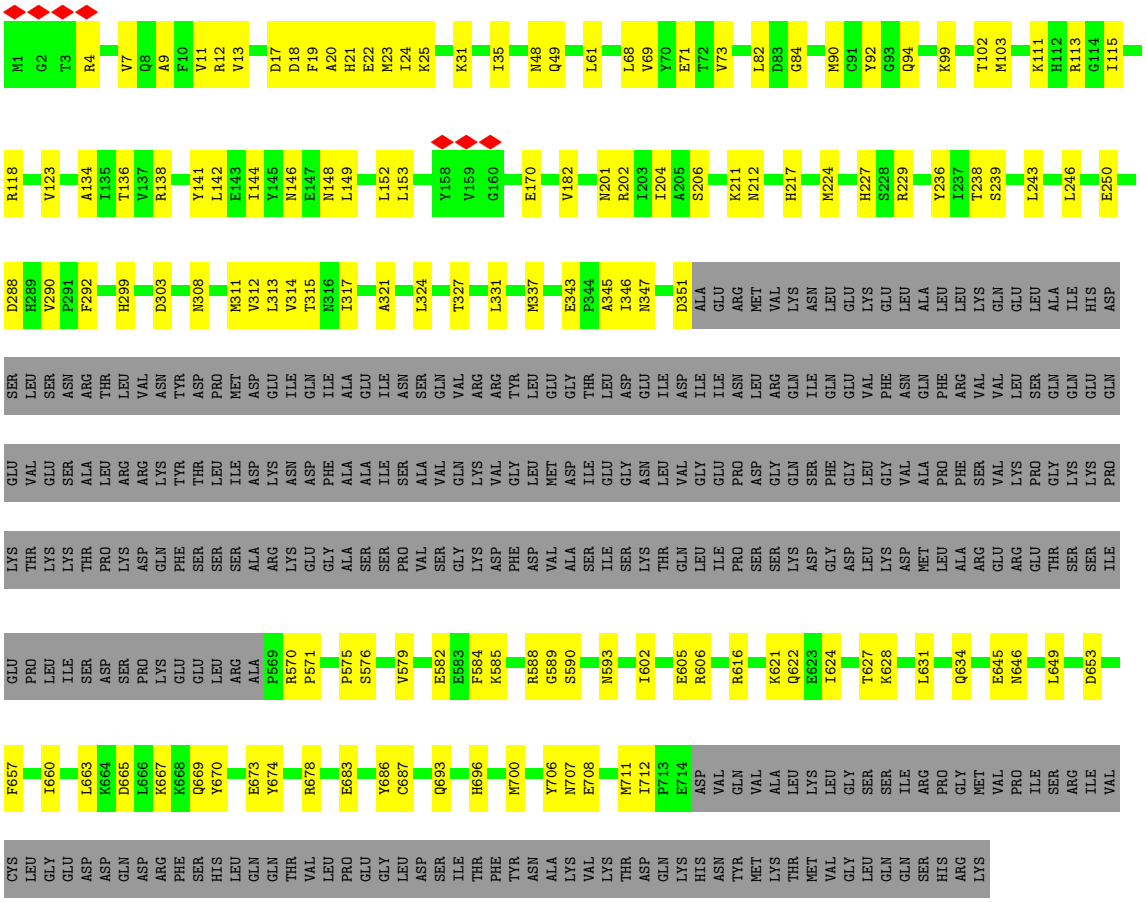




• Molecule 2: Kinesin-like protein KIF9

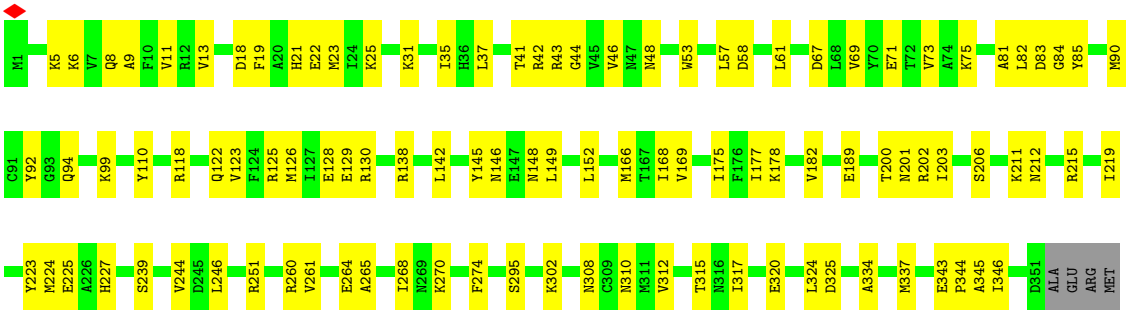
Chain c:

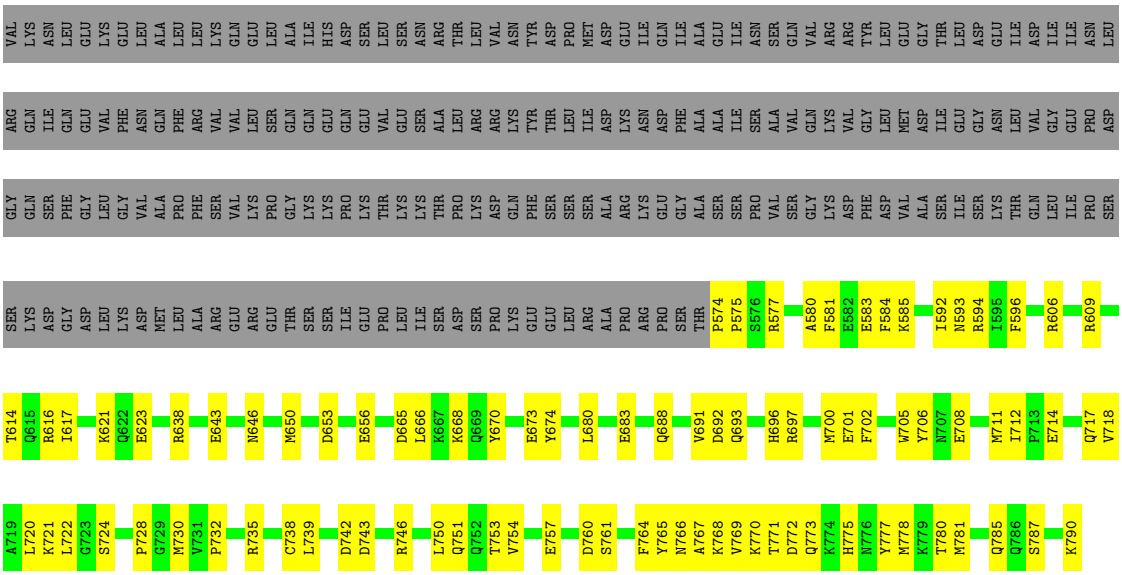




• Molecule 2: Kinesin-like protein KIF9

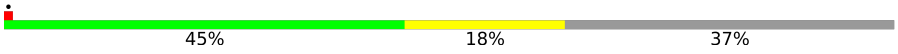
Chain d:

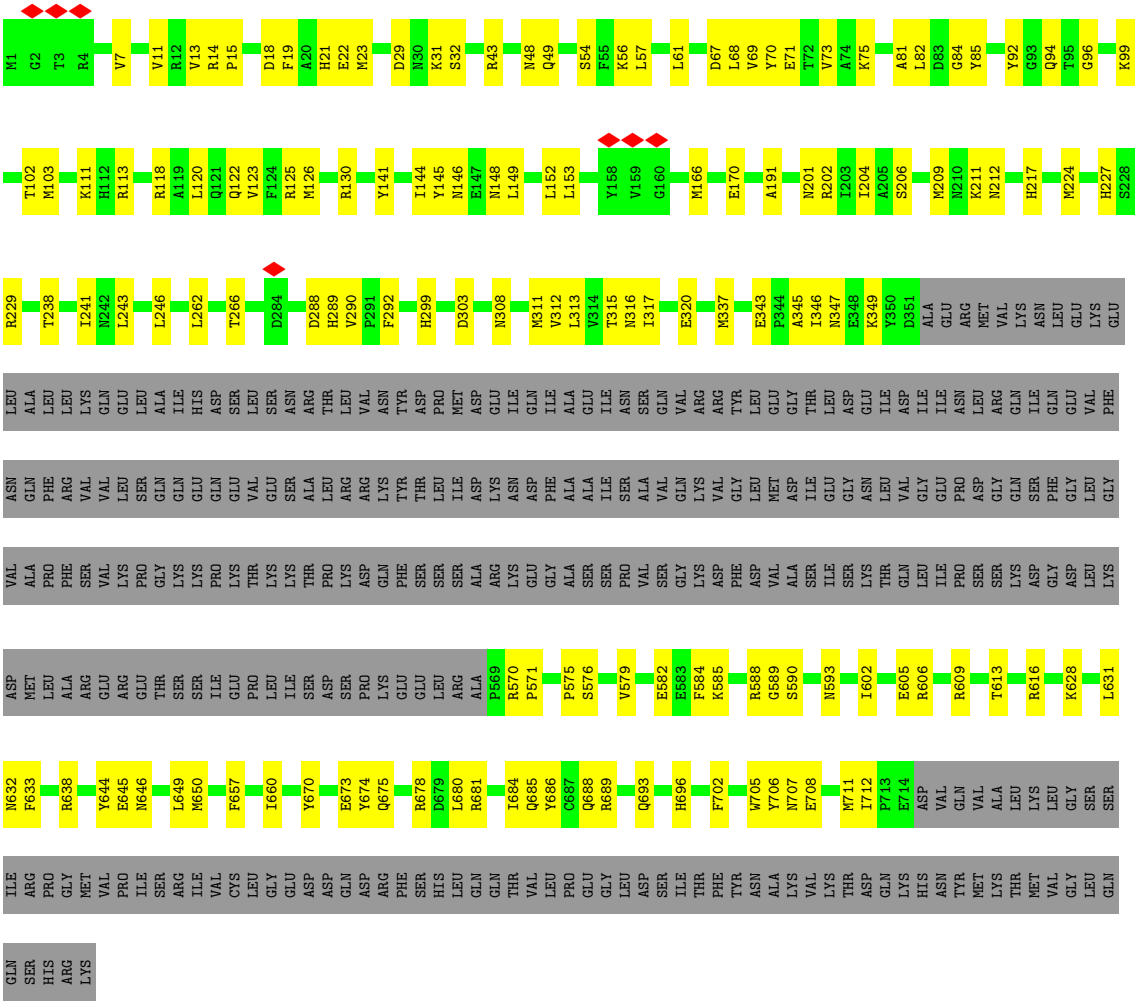




• Molecule 2: Kinesin-like protein KIF9

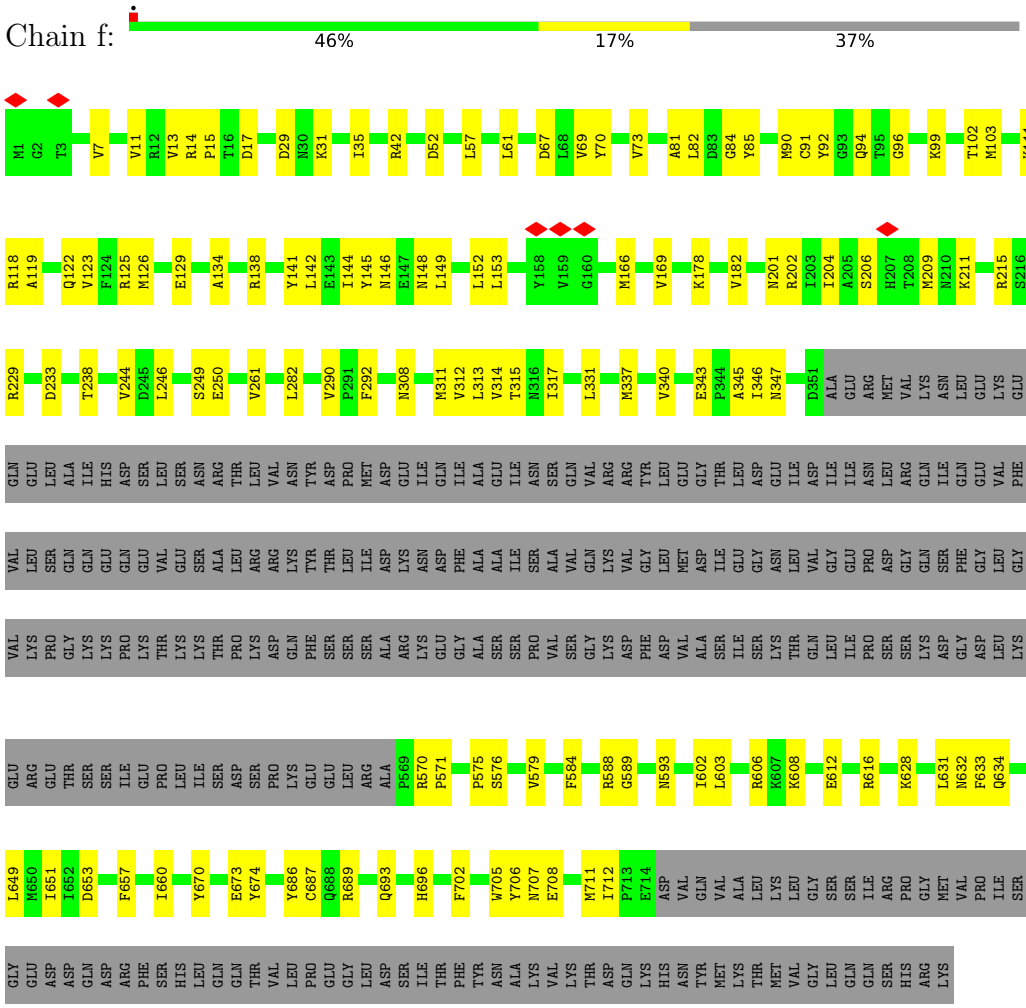
Chain e:





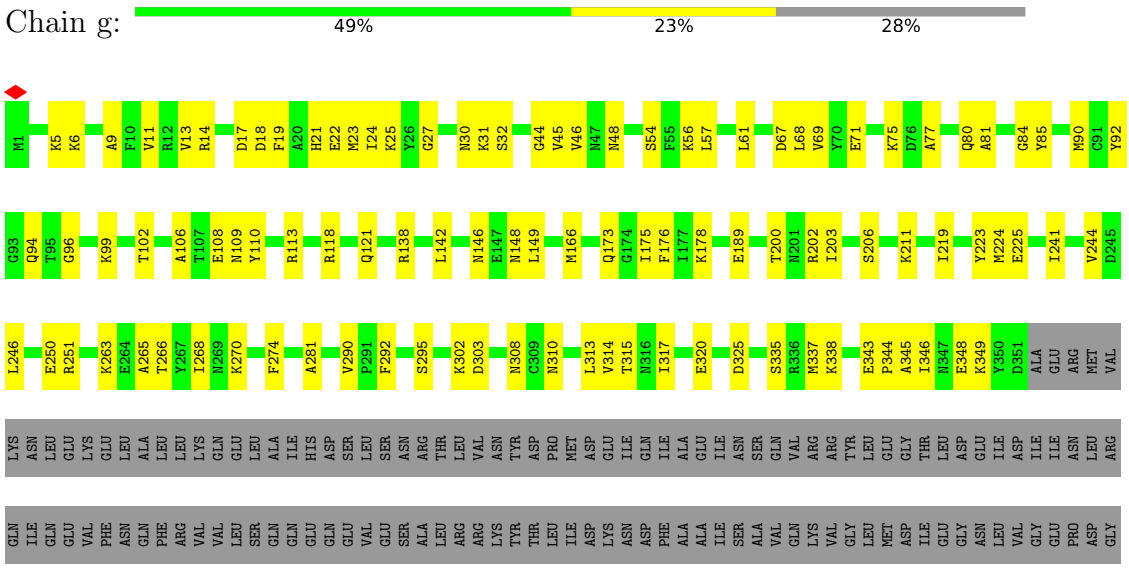
• Molecule 2: Kinesin-like protein KIF9

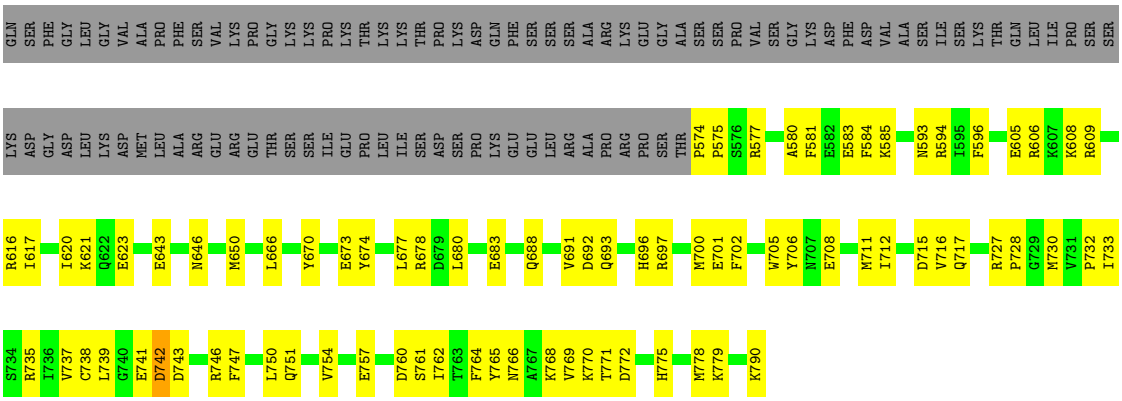
Chain f:



• Molecule 2: Kinesin-like protein KIF9

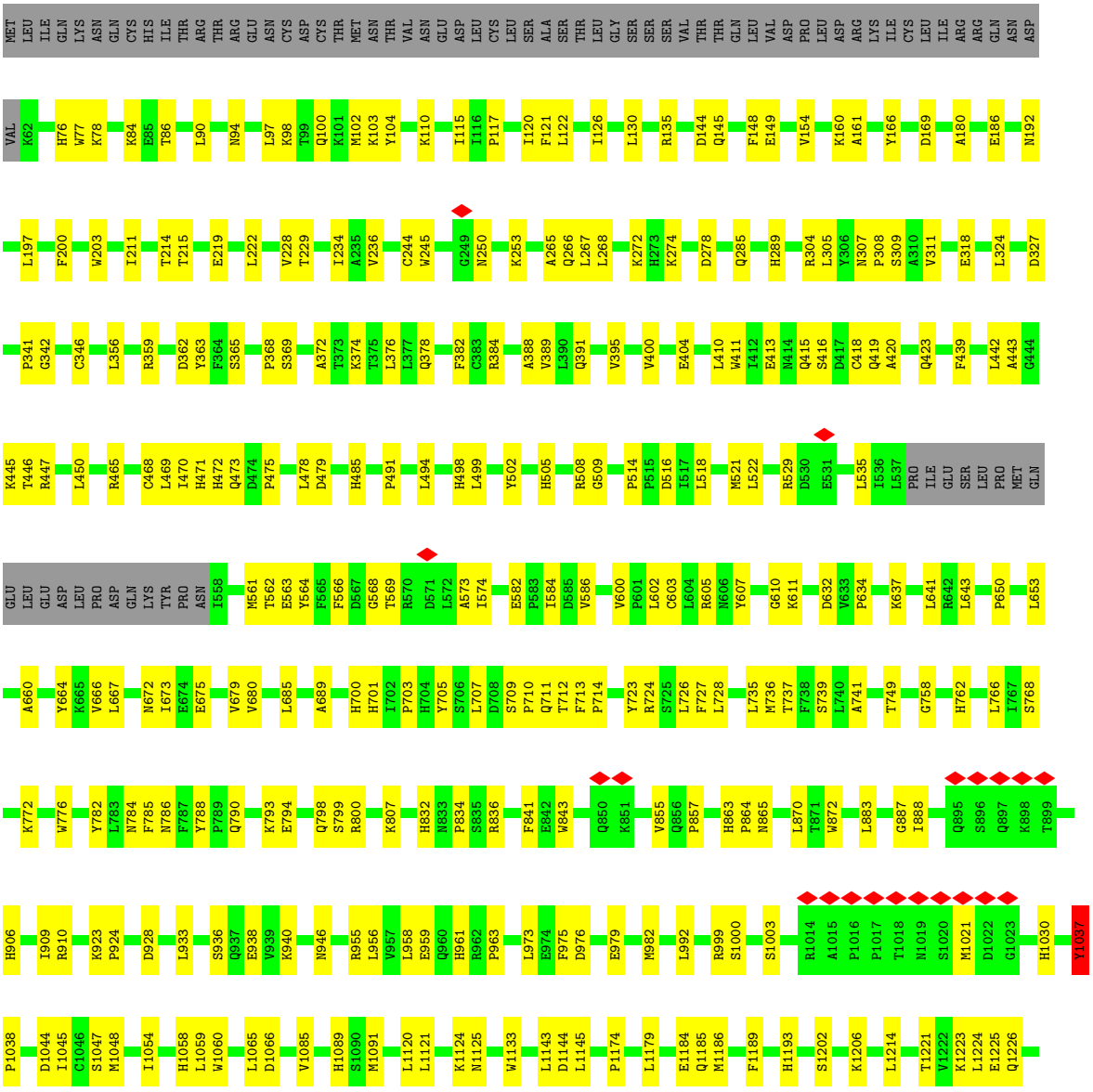
Chain g:

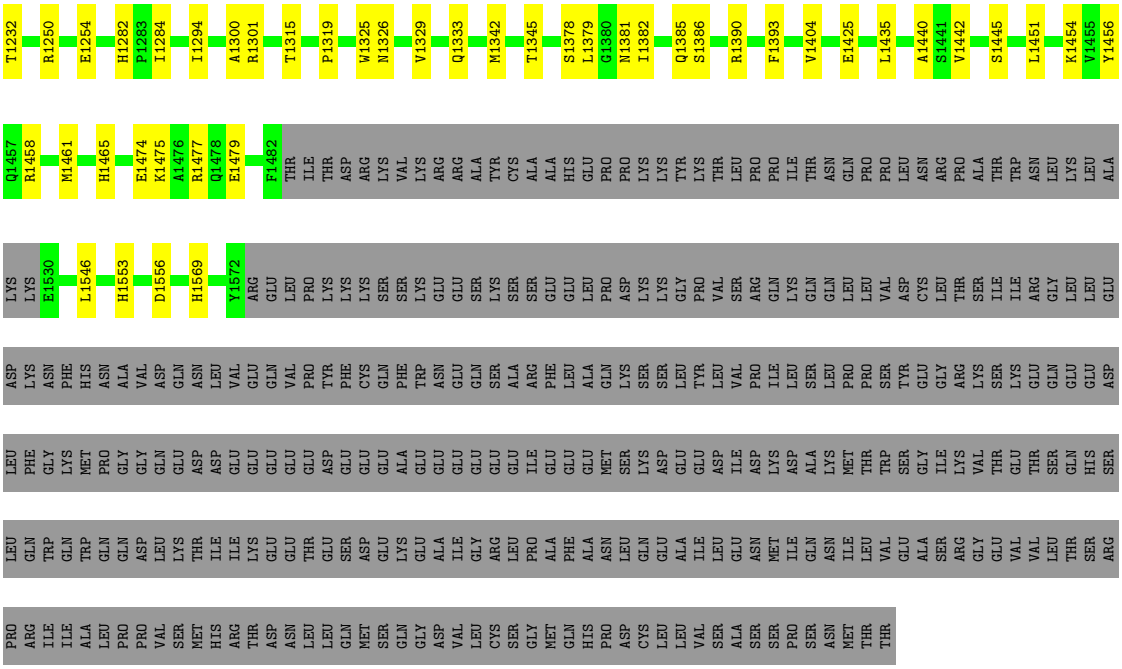




• Molecule 3: Cilia- and flagella-associated protein 65

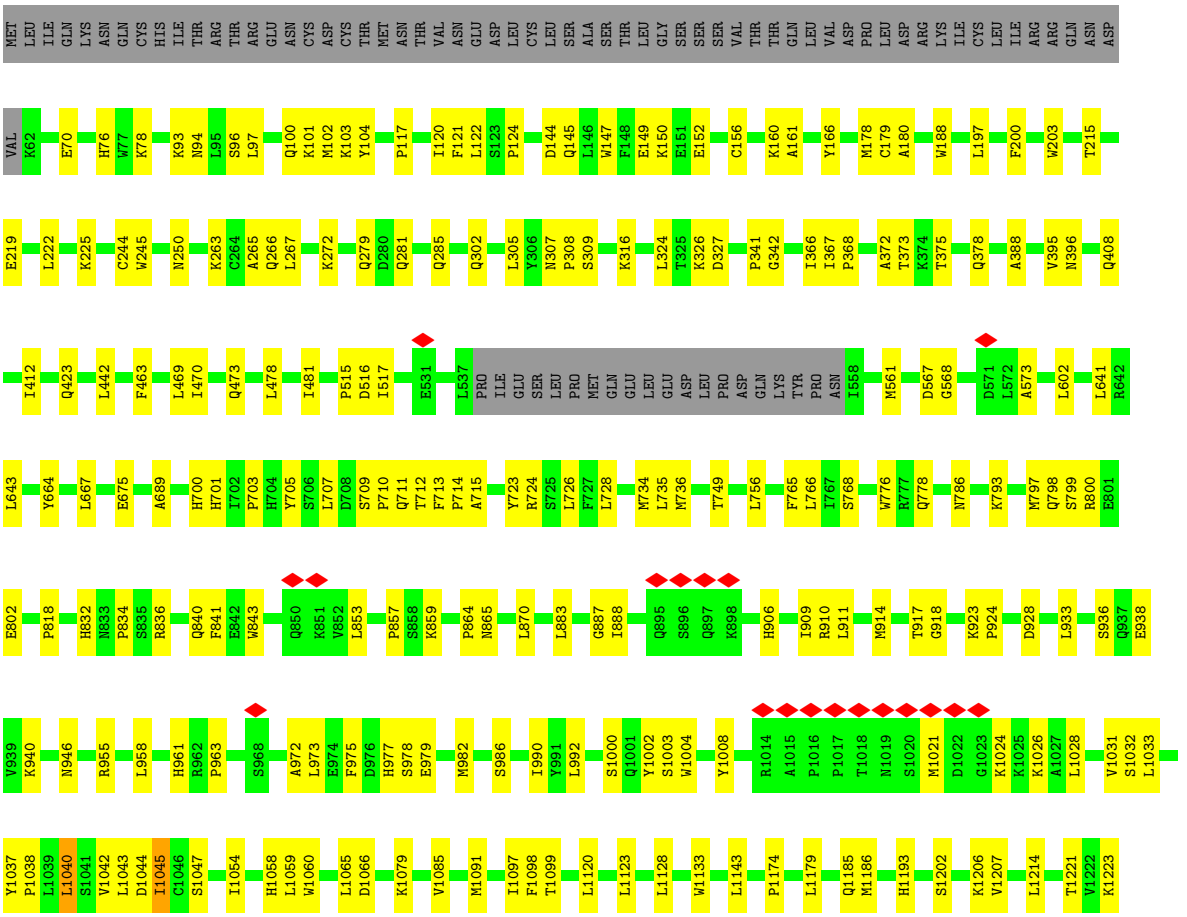
Chain h:

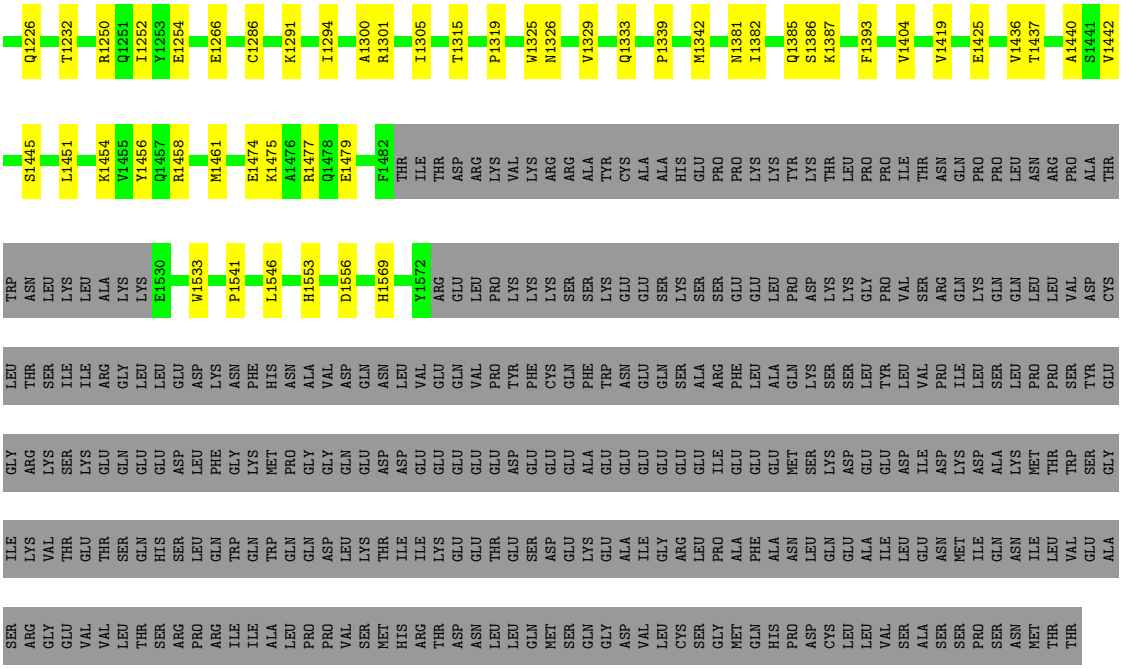




• Molecule 3: Cilia- and flagella-associated protein 65

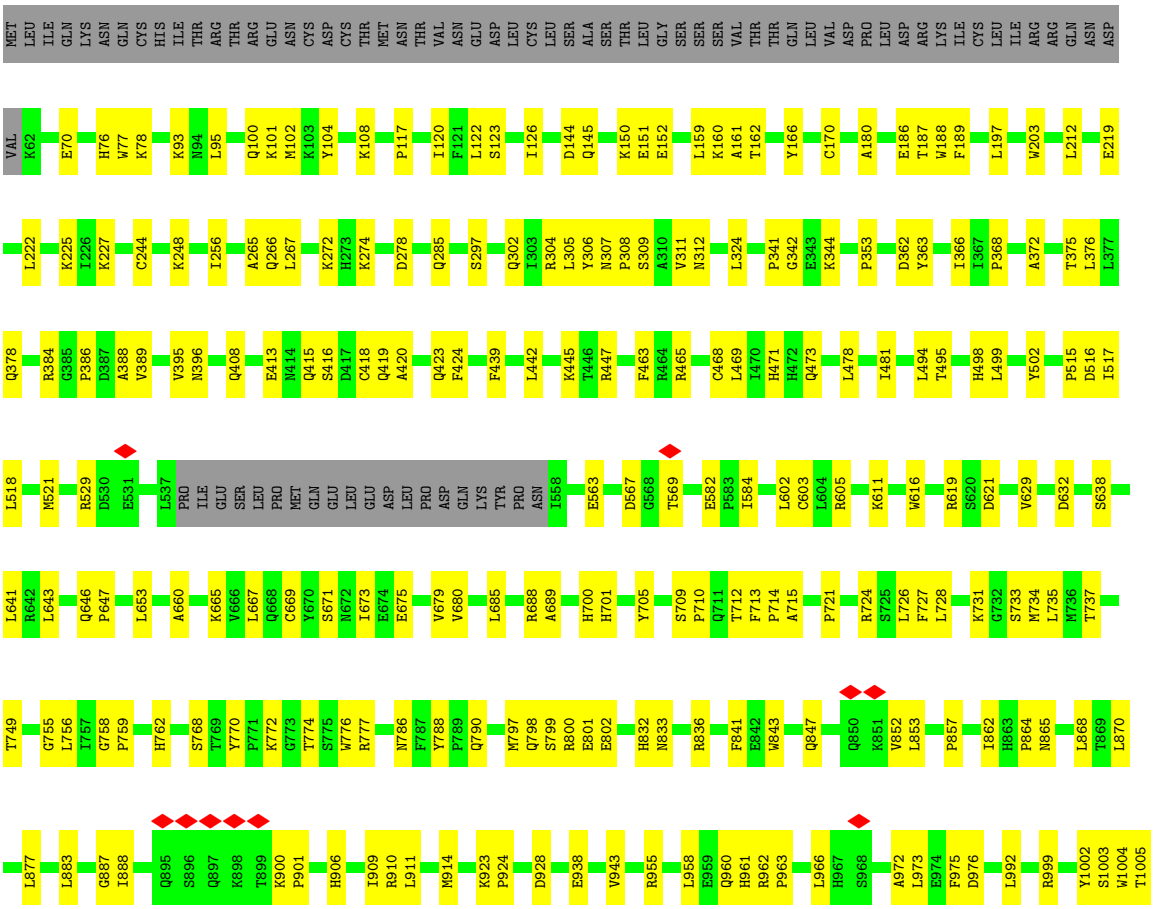
Chain i:

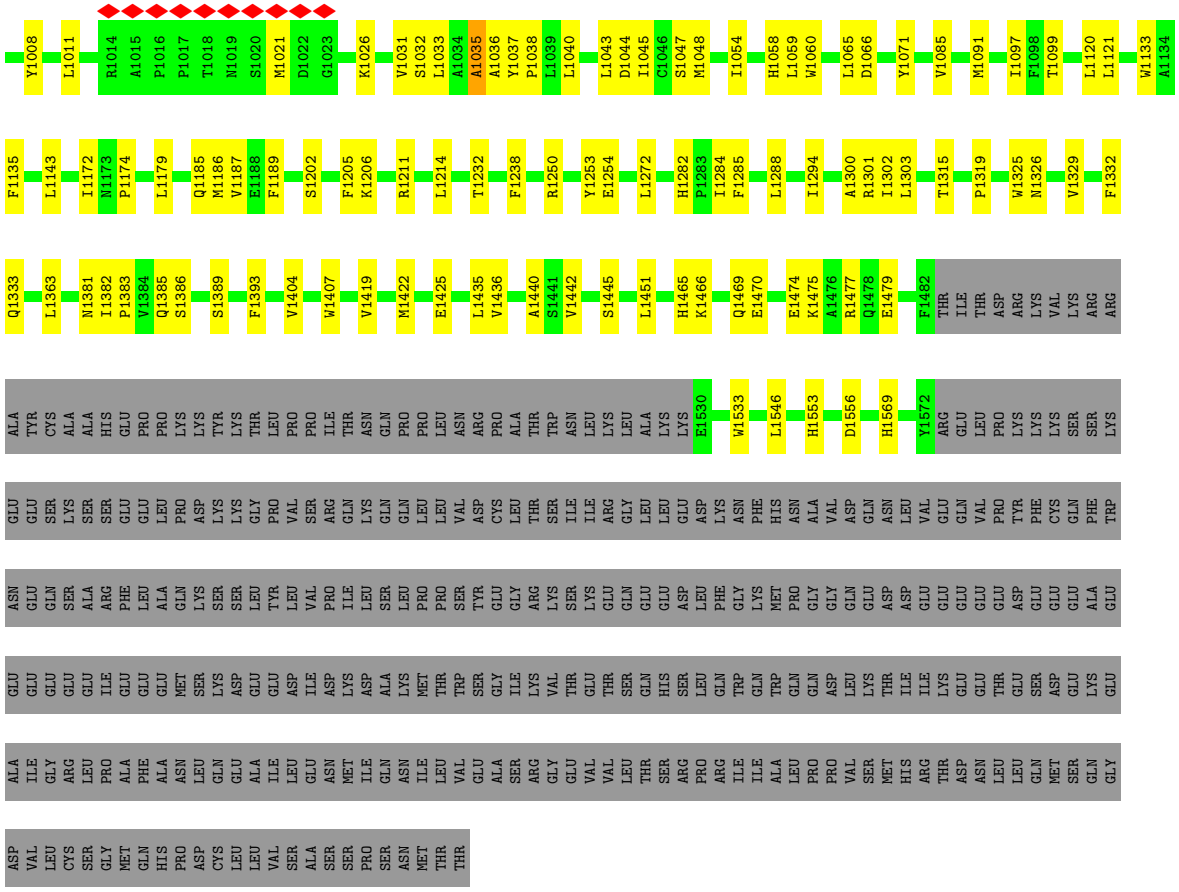




• Molecule 3: Cilia- and flagella-associated protein 65

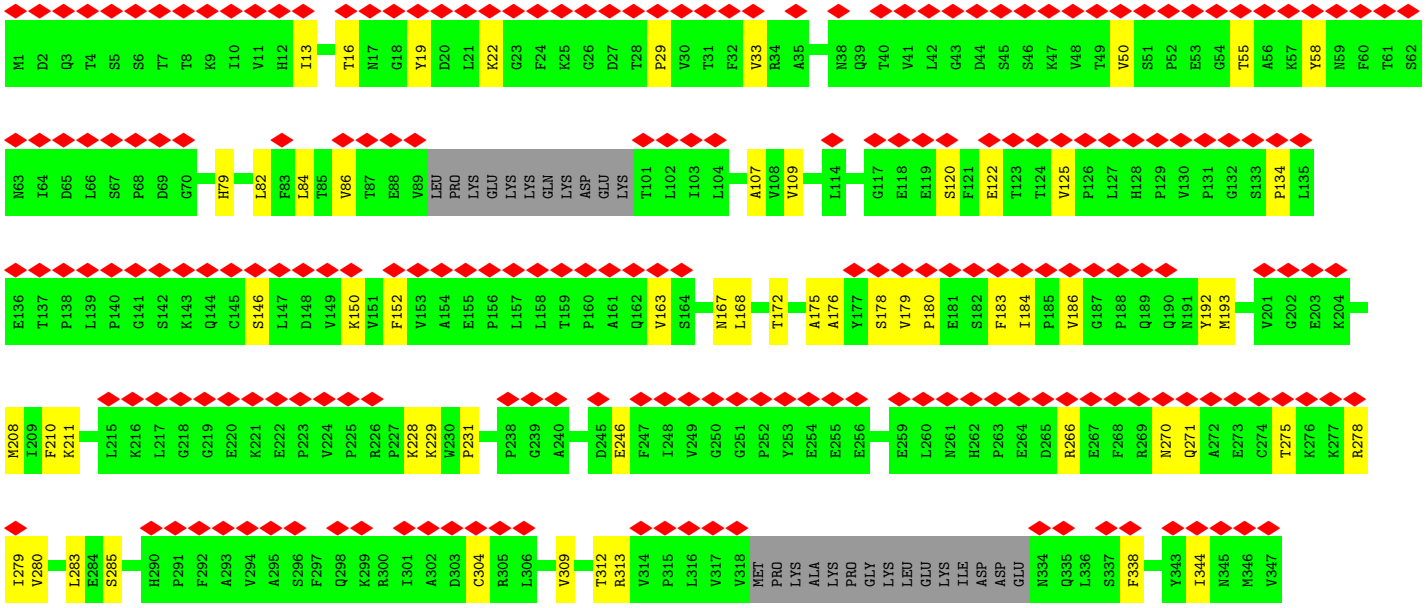
Chain j:

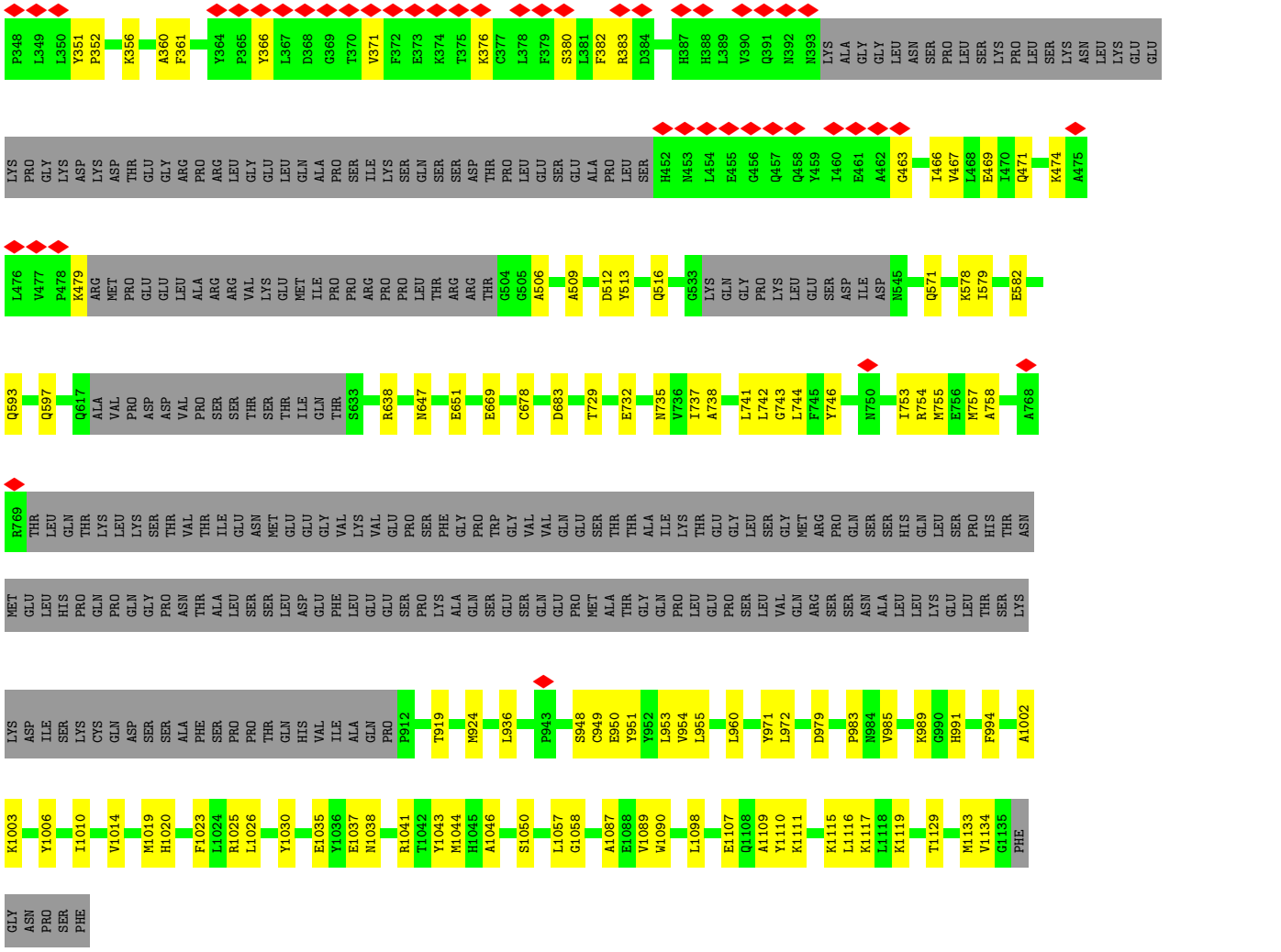




• Molecule 4: Cilia- and flagella-associated protein 70

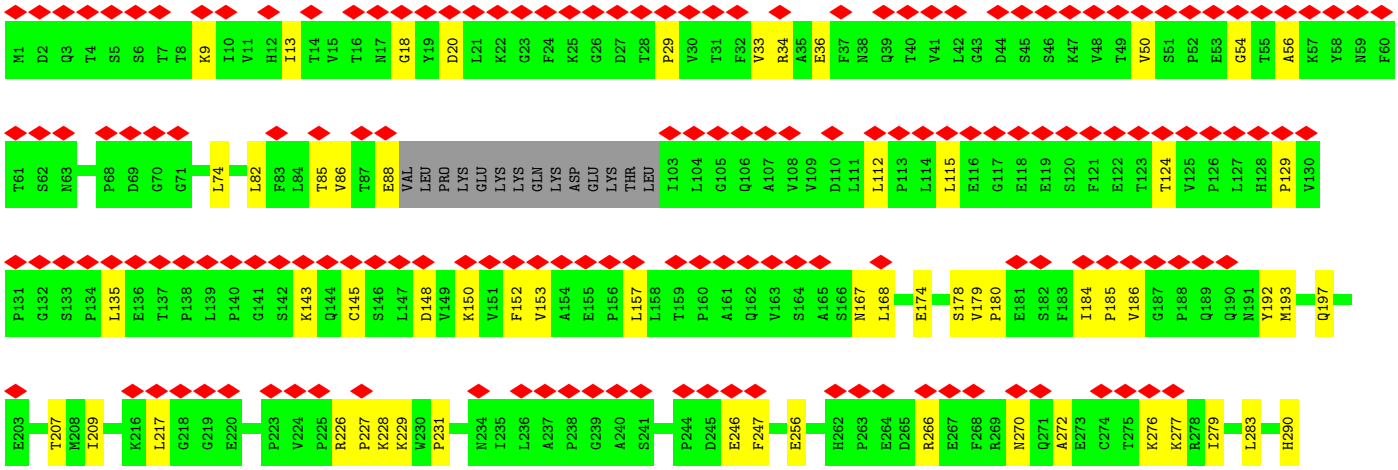
Chain k:

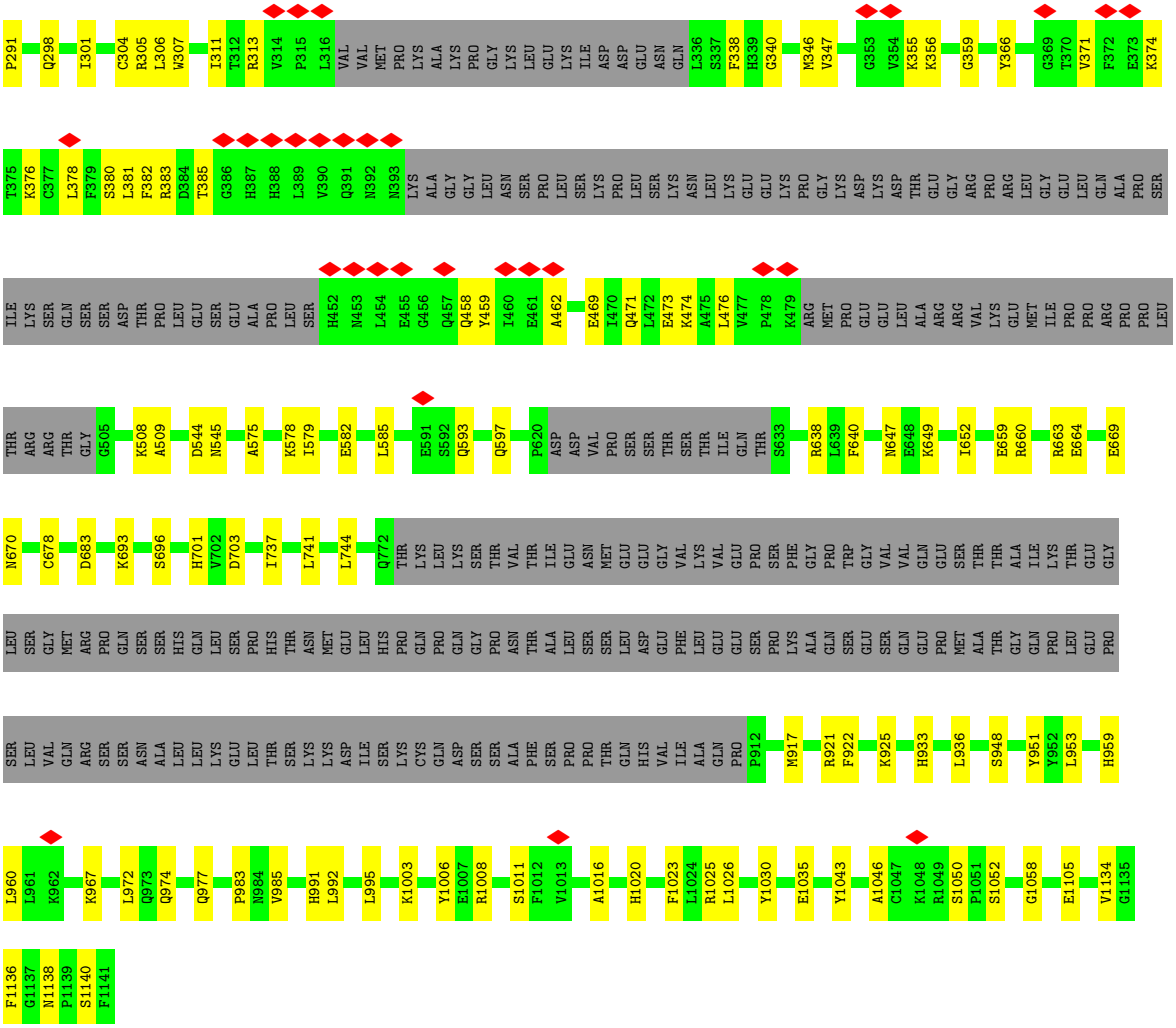




• Molecule 4: Cilia- and flagella-associated protein 70

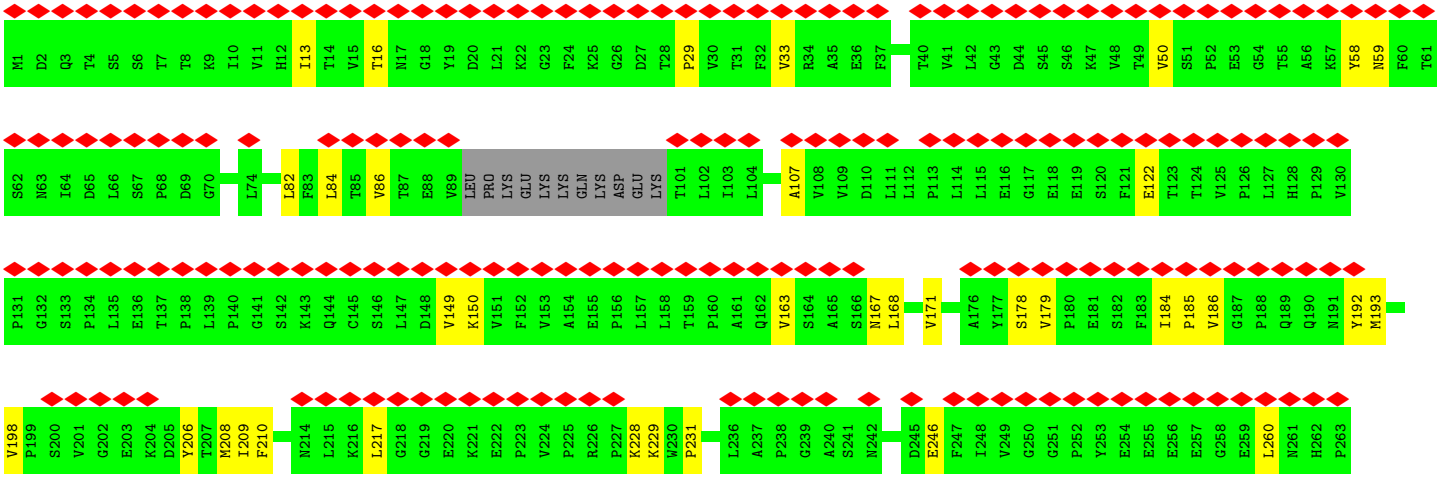
Chain n:

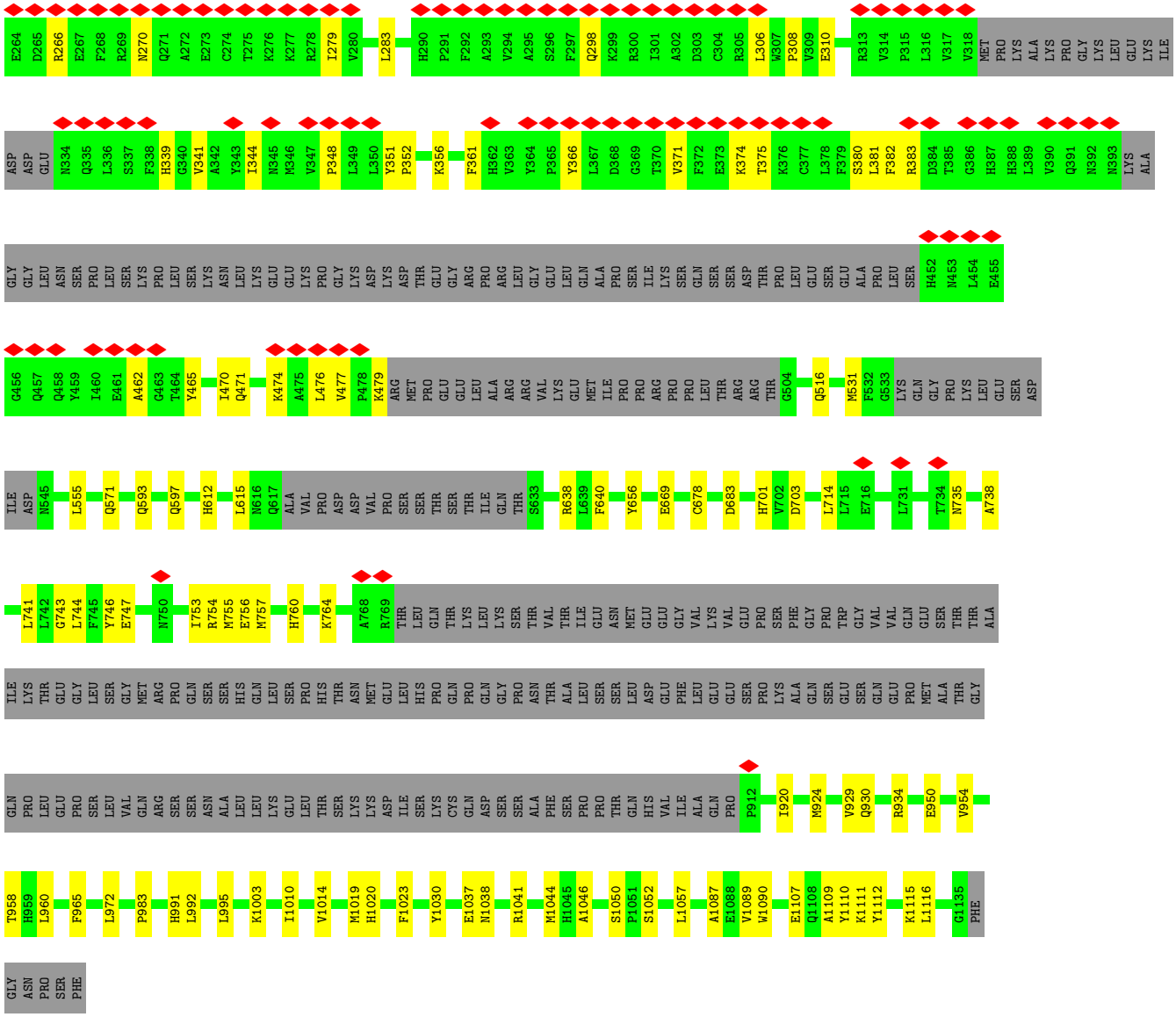




• Molecule 4: Cilia- and flagella-associated protein 70

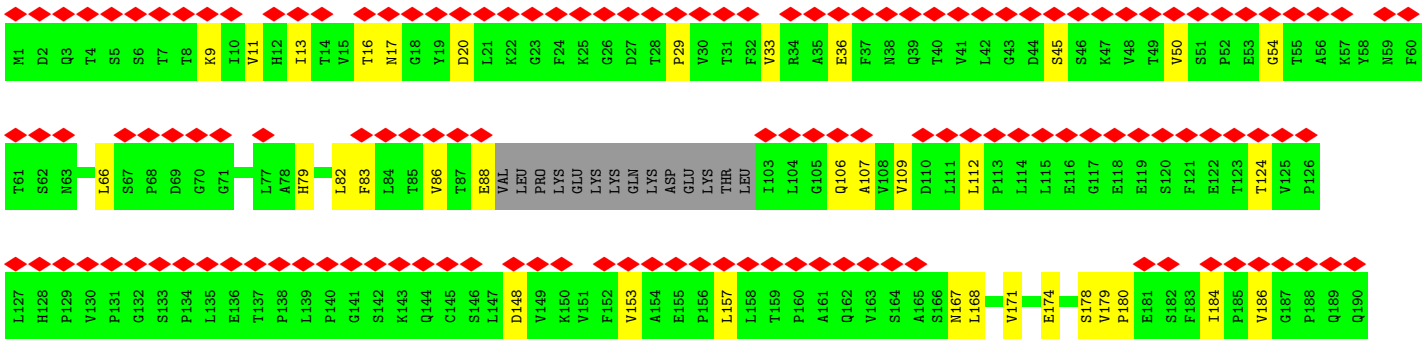
Chain o:

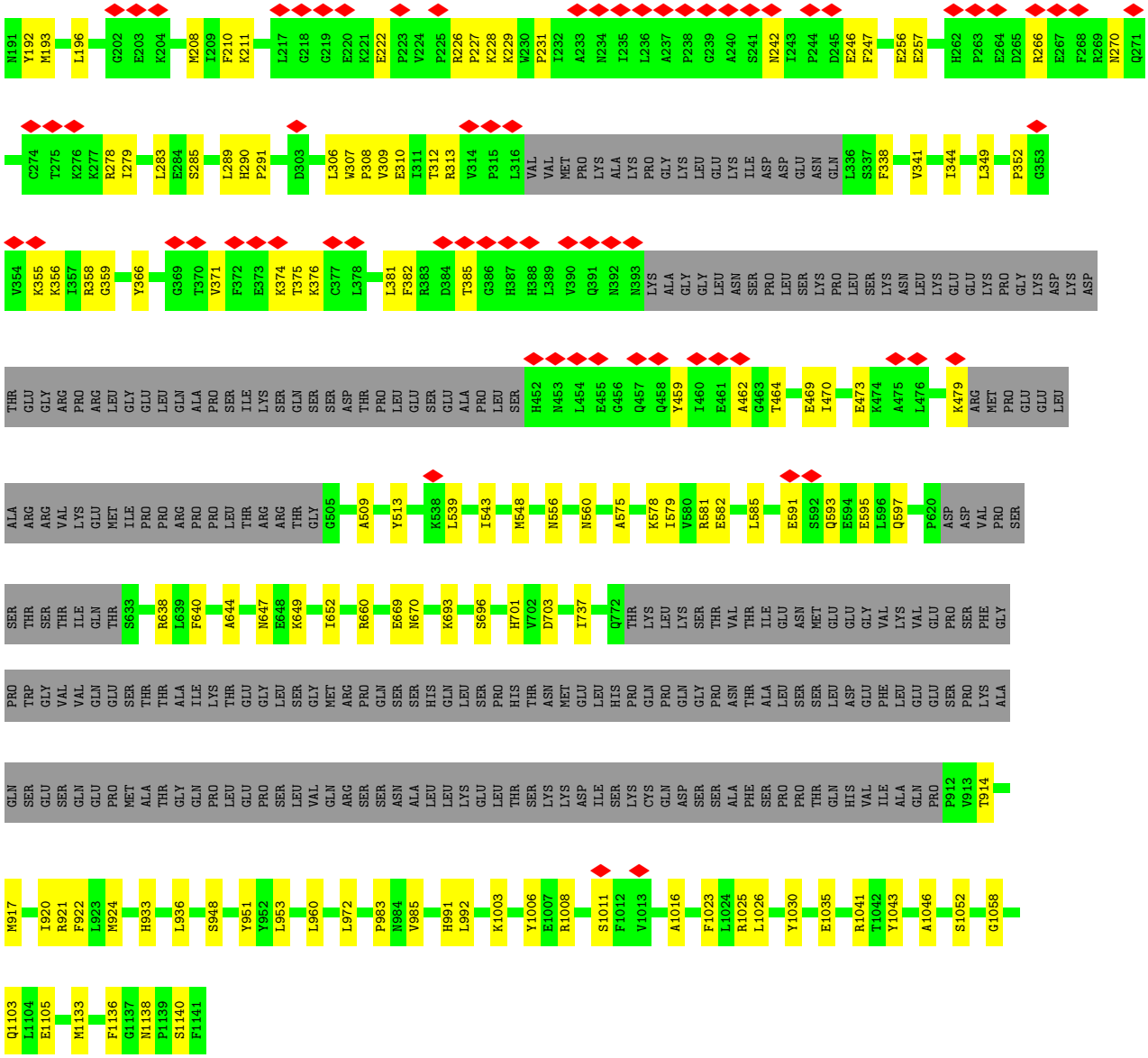




• Molecule 4: Cilia- and flagella-associated protein 70

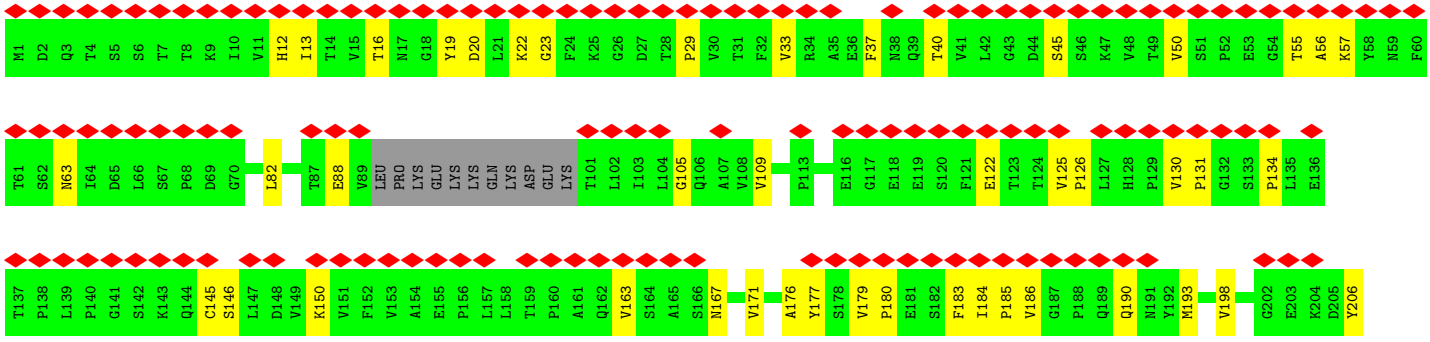
Chain p:

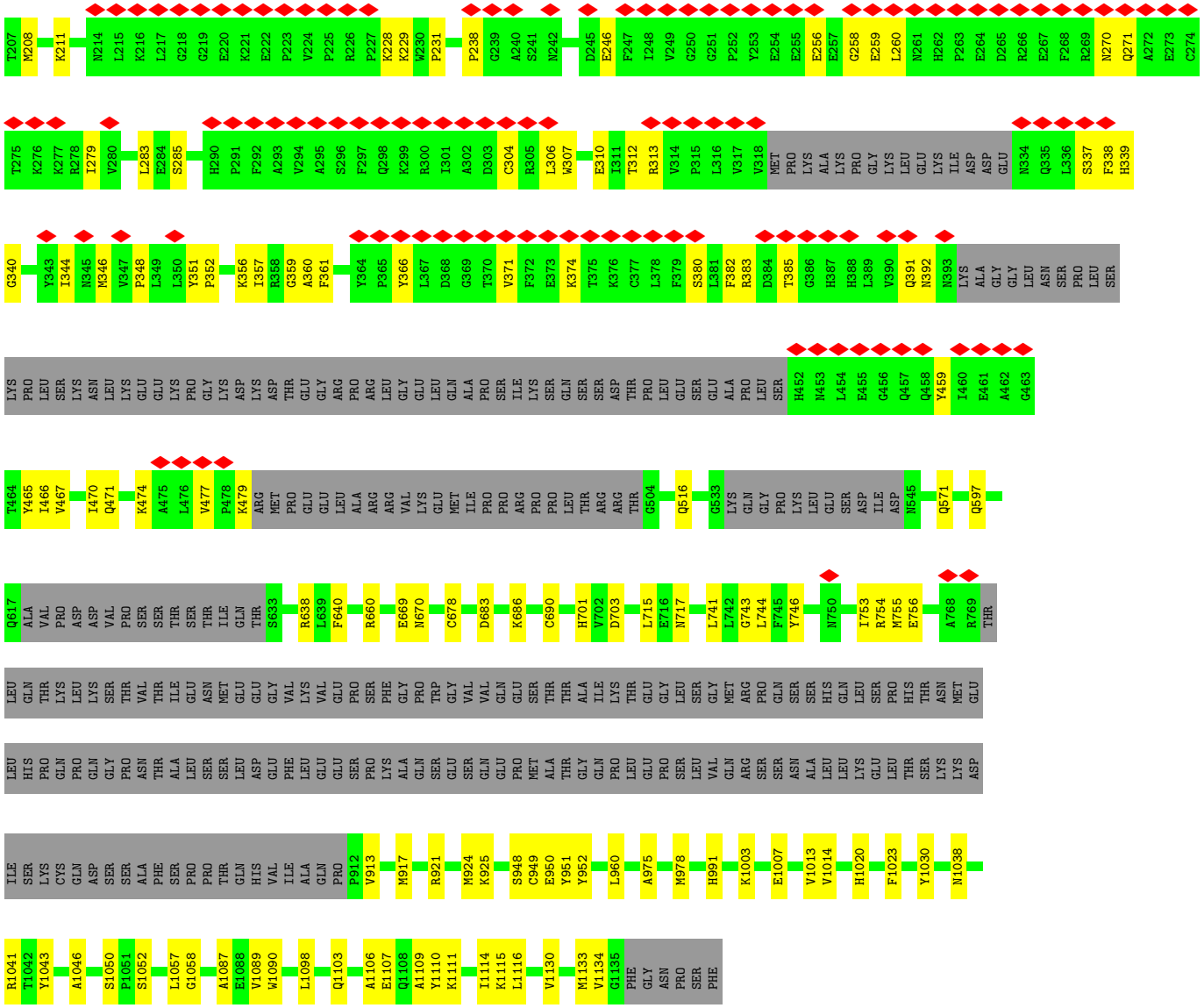




• Molecule 4: Cilia- and flagella-associated protein 70

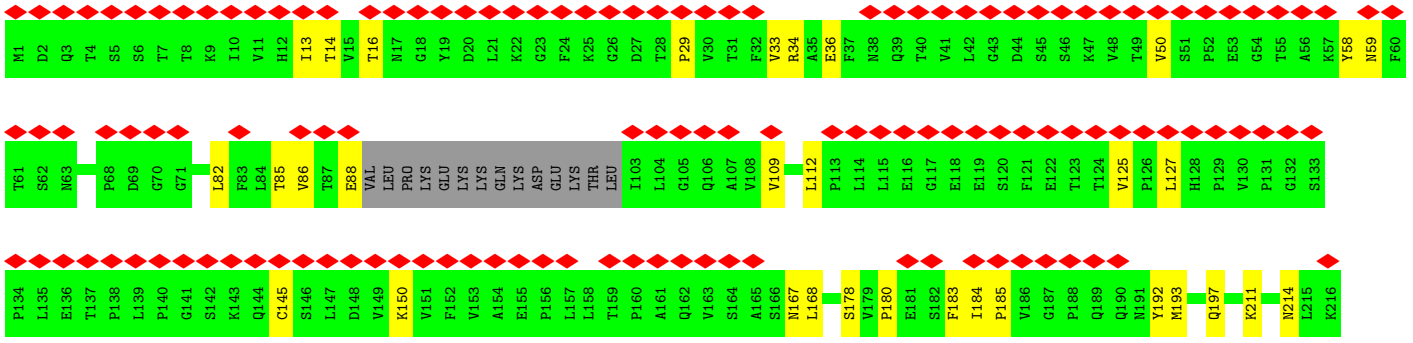
Chain m:

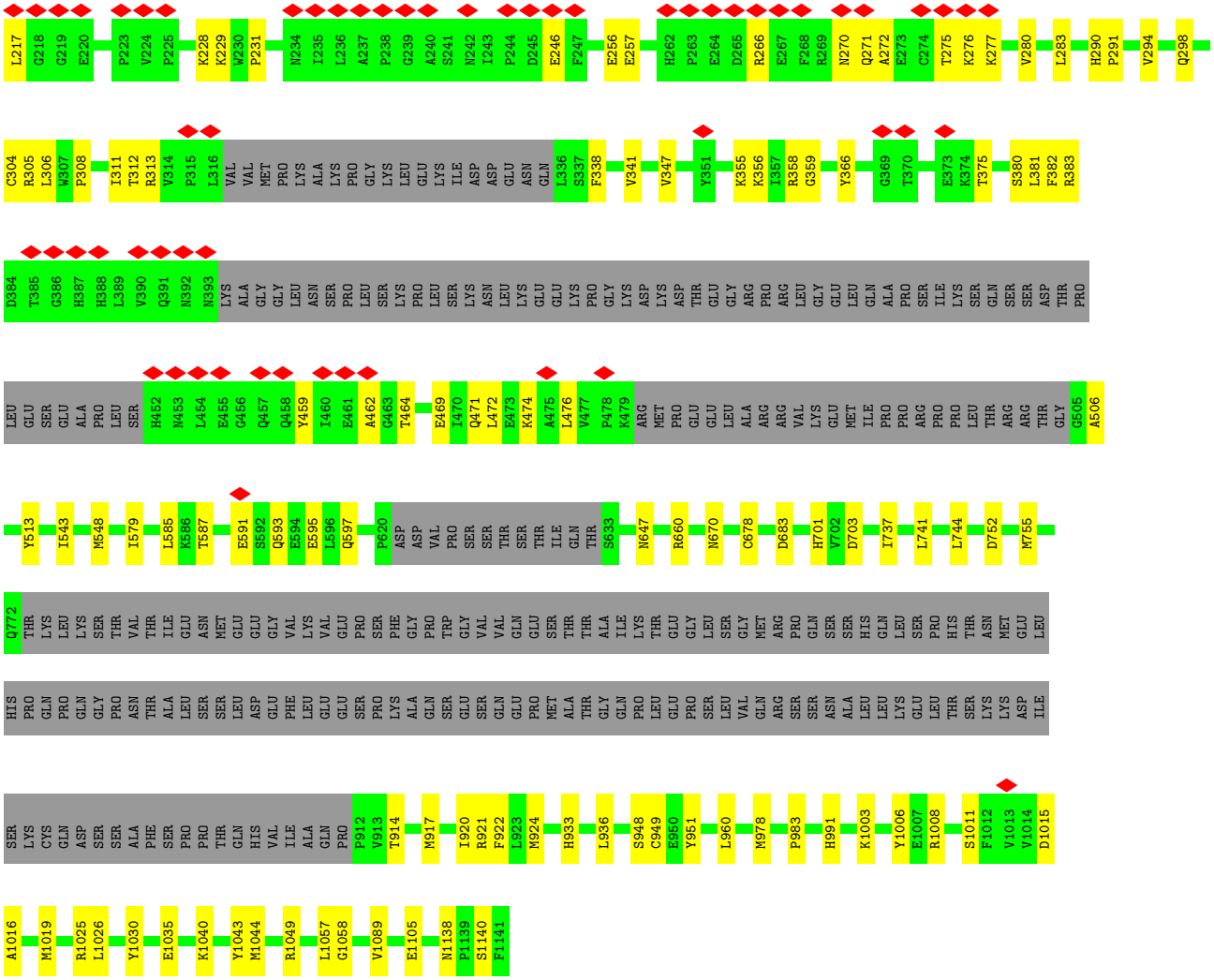




• Molecule 4: Cilia- and flagella-associated protein 70

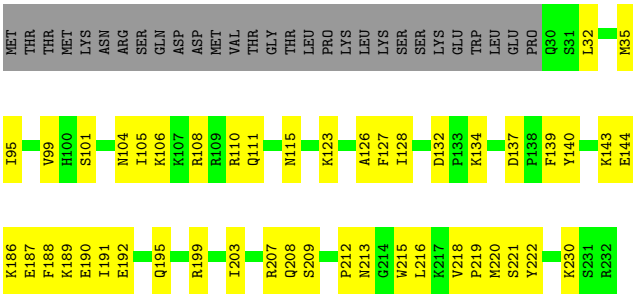
Chain l:





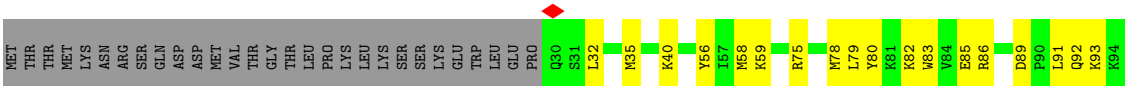
• Molecule 5: Protein FAM228B

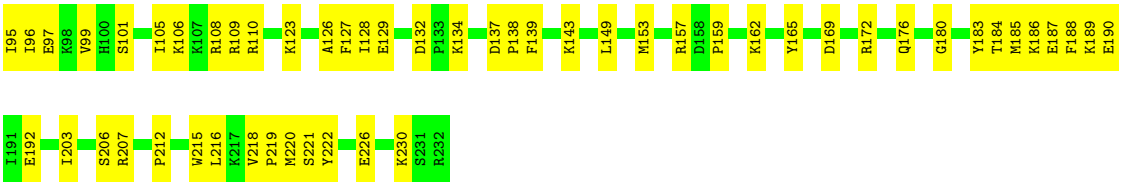
Chain q:



• Molecule 5: Protein FAM228B

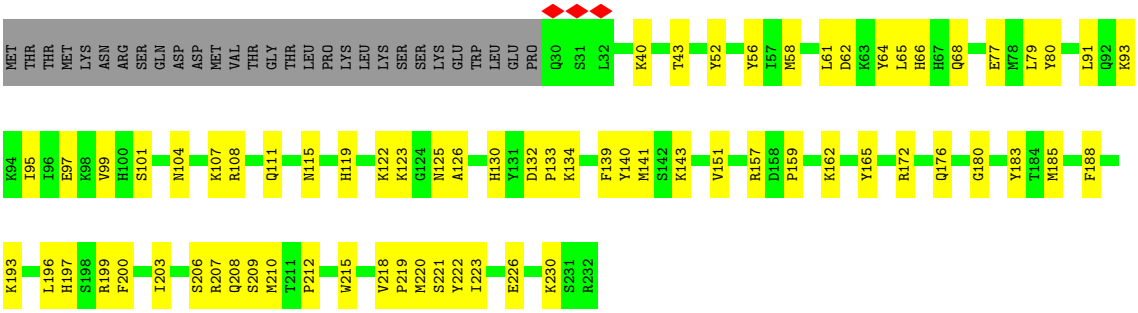
Chain r:





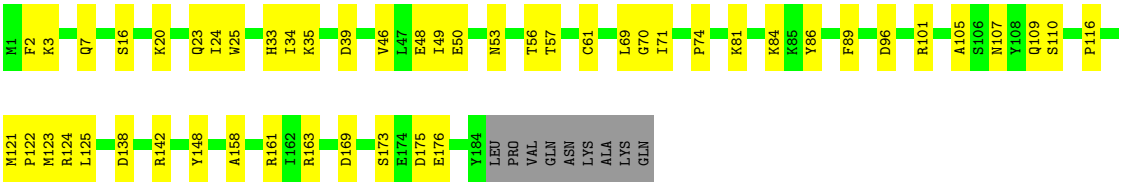
• Molecule 5: Protein FAM228B

Chain s:



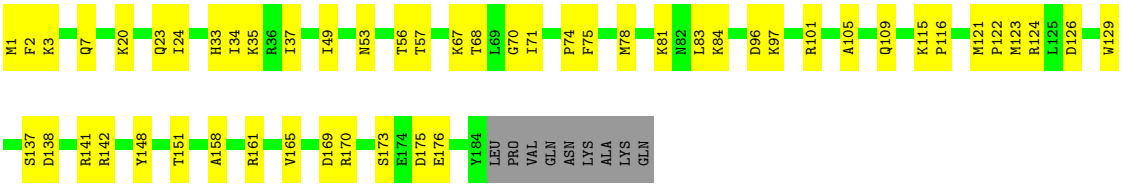
• Molecule 6: Cilia- and flagella-associated protein 20

Chain t:



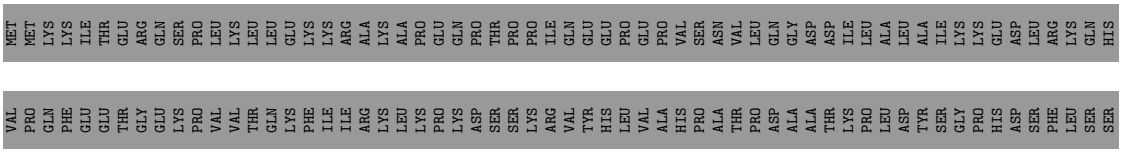
• Molecule 6: Cilia- and flagella-associated protein 20

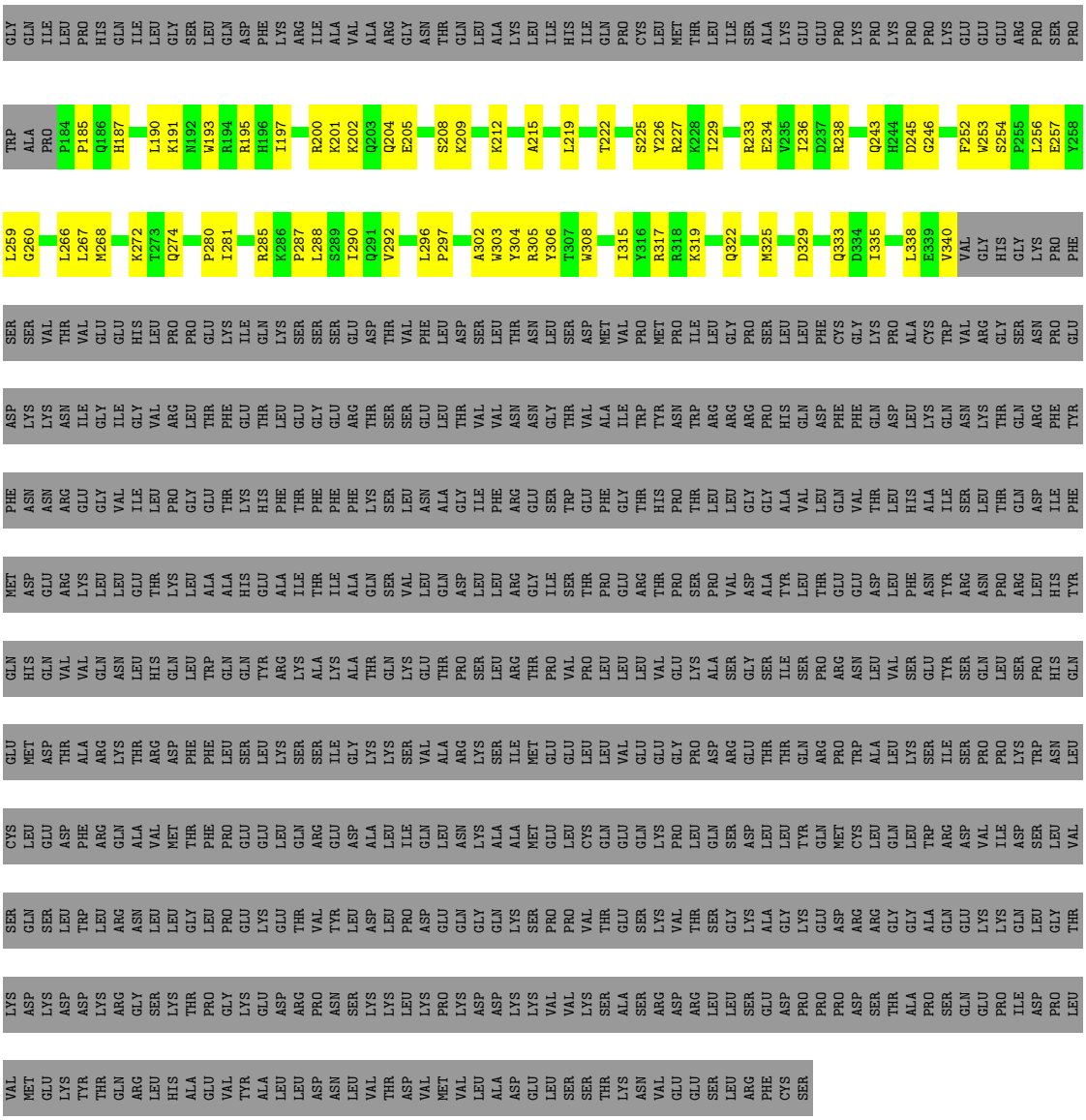
Chain u:



• Molecule 7: MYCBP-associated protein

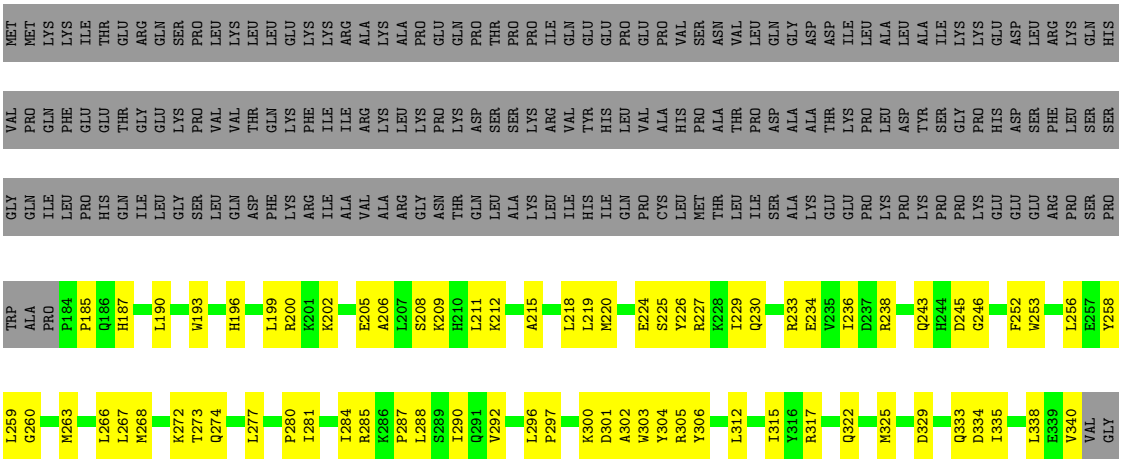
Chain v:

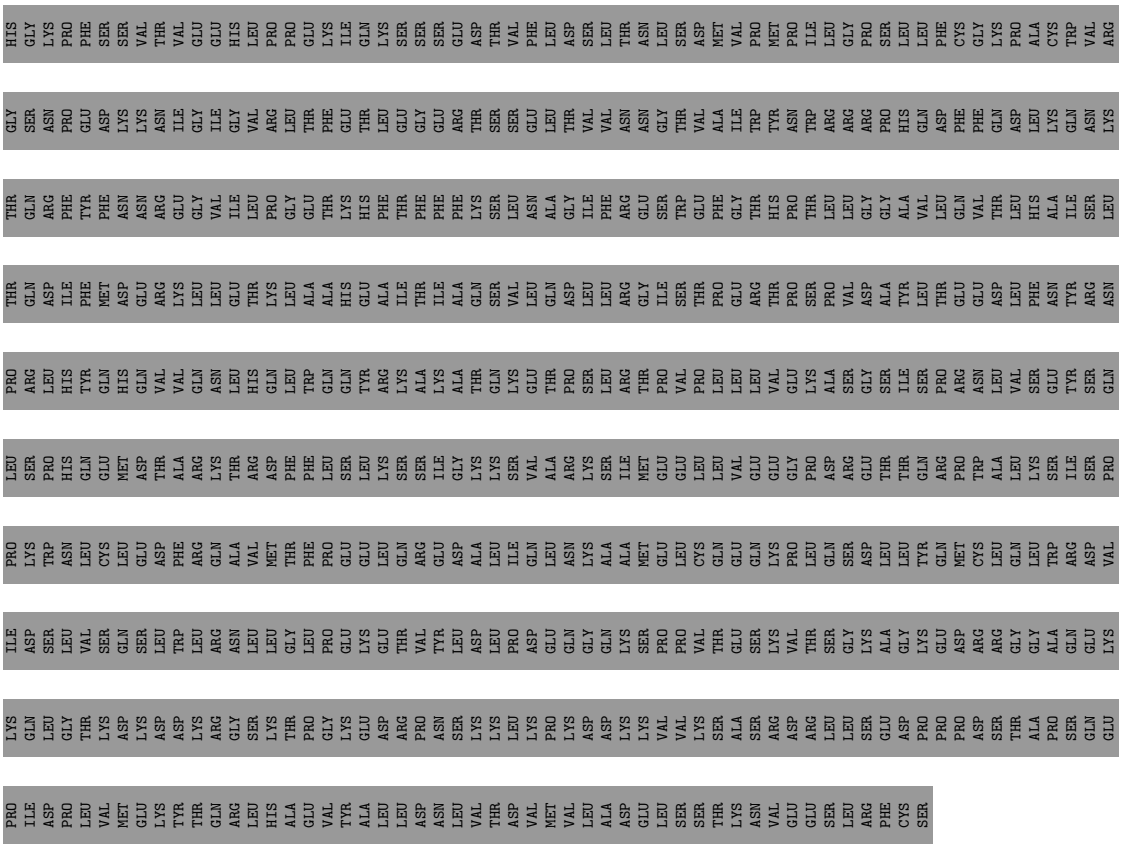




• Molecule 7: MYCBP-associated protein

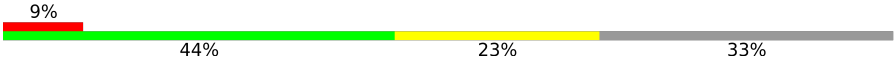
Chain w:

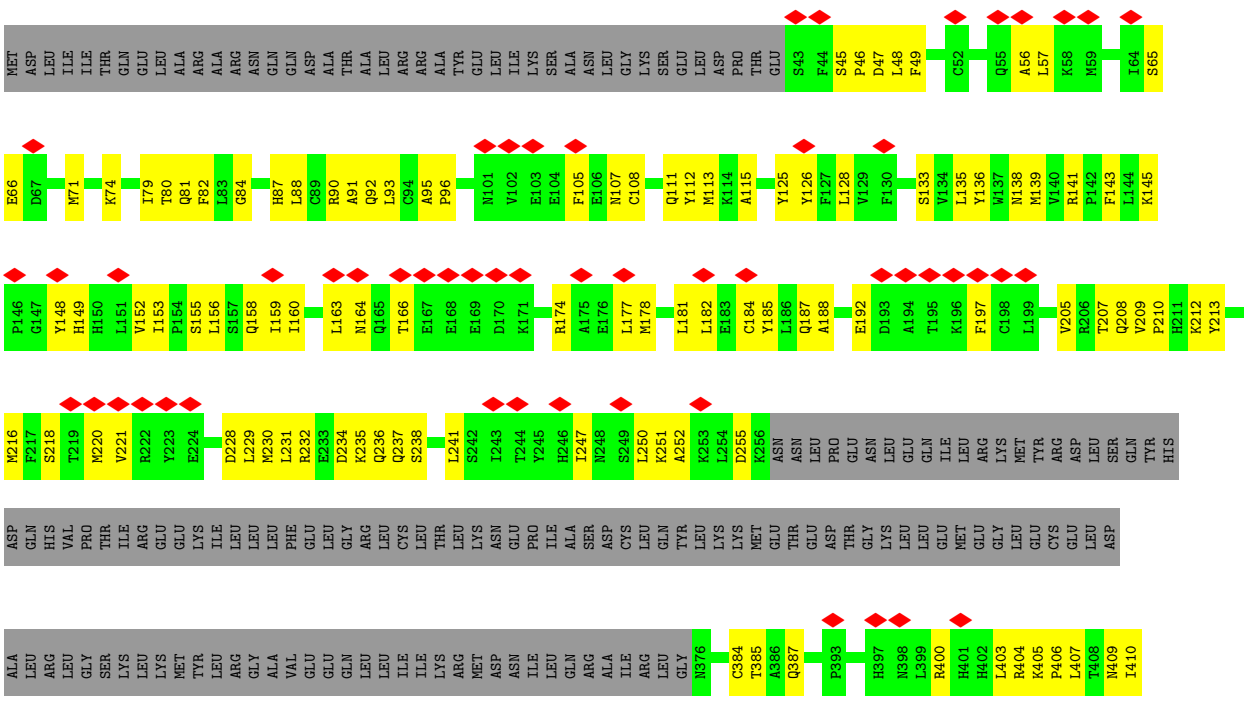


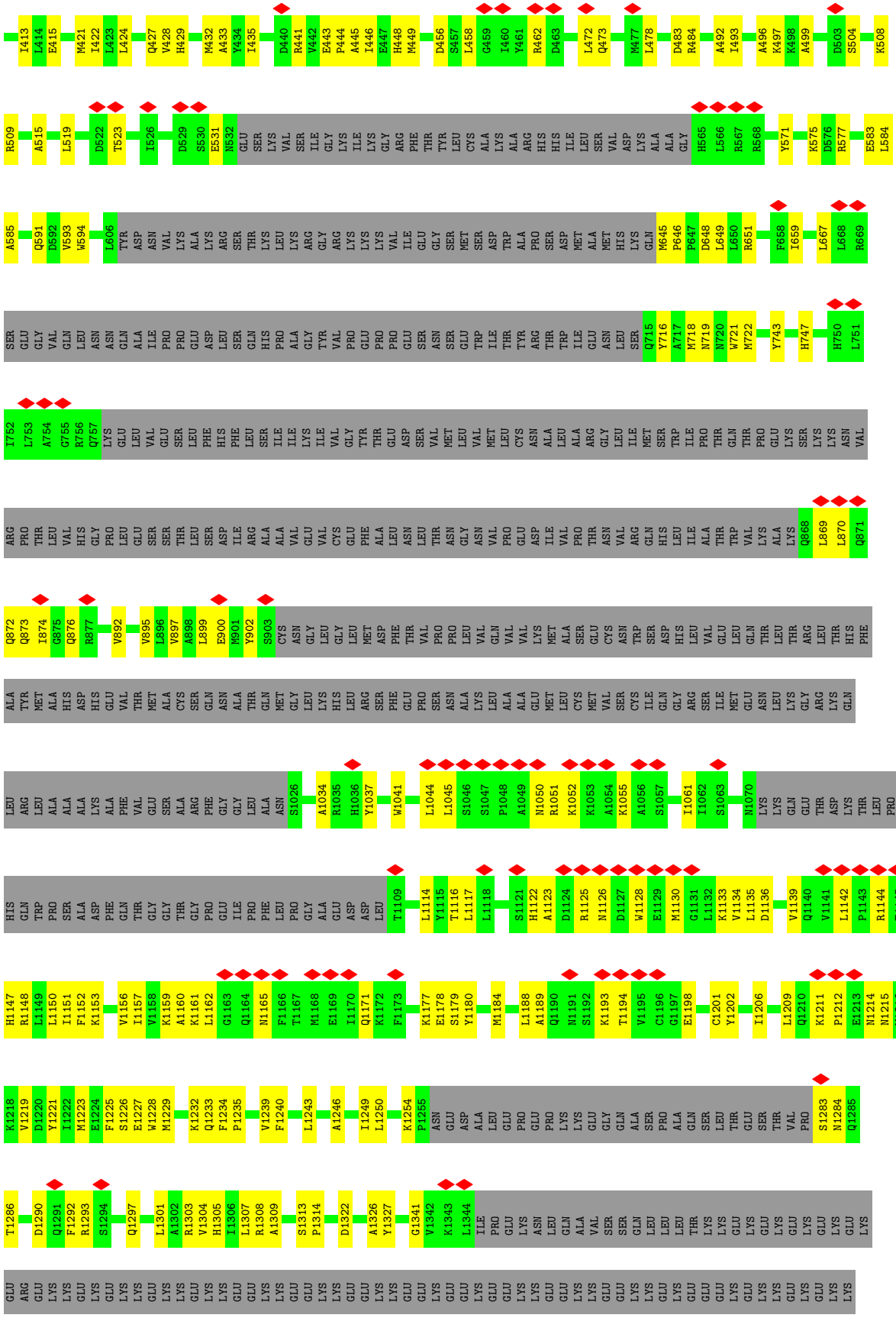


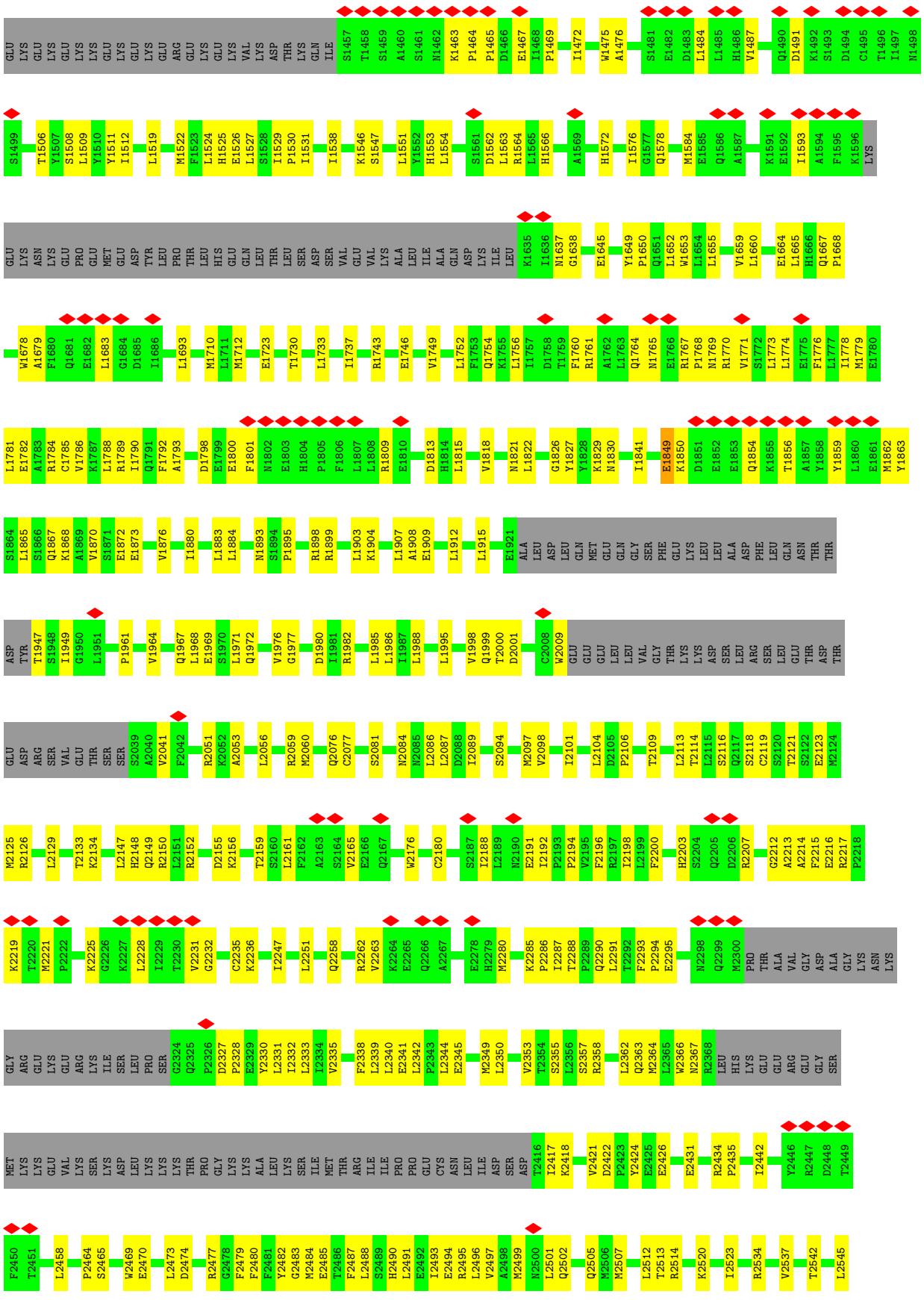
• Molecule 8: Cilia and flagella associated protein 46

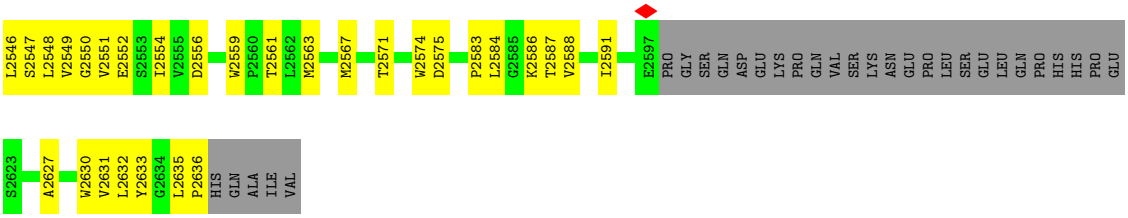
Chain A:





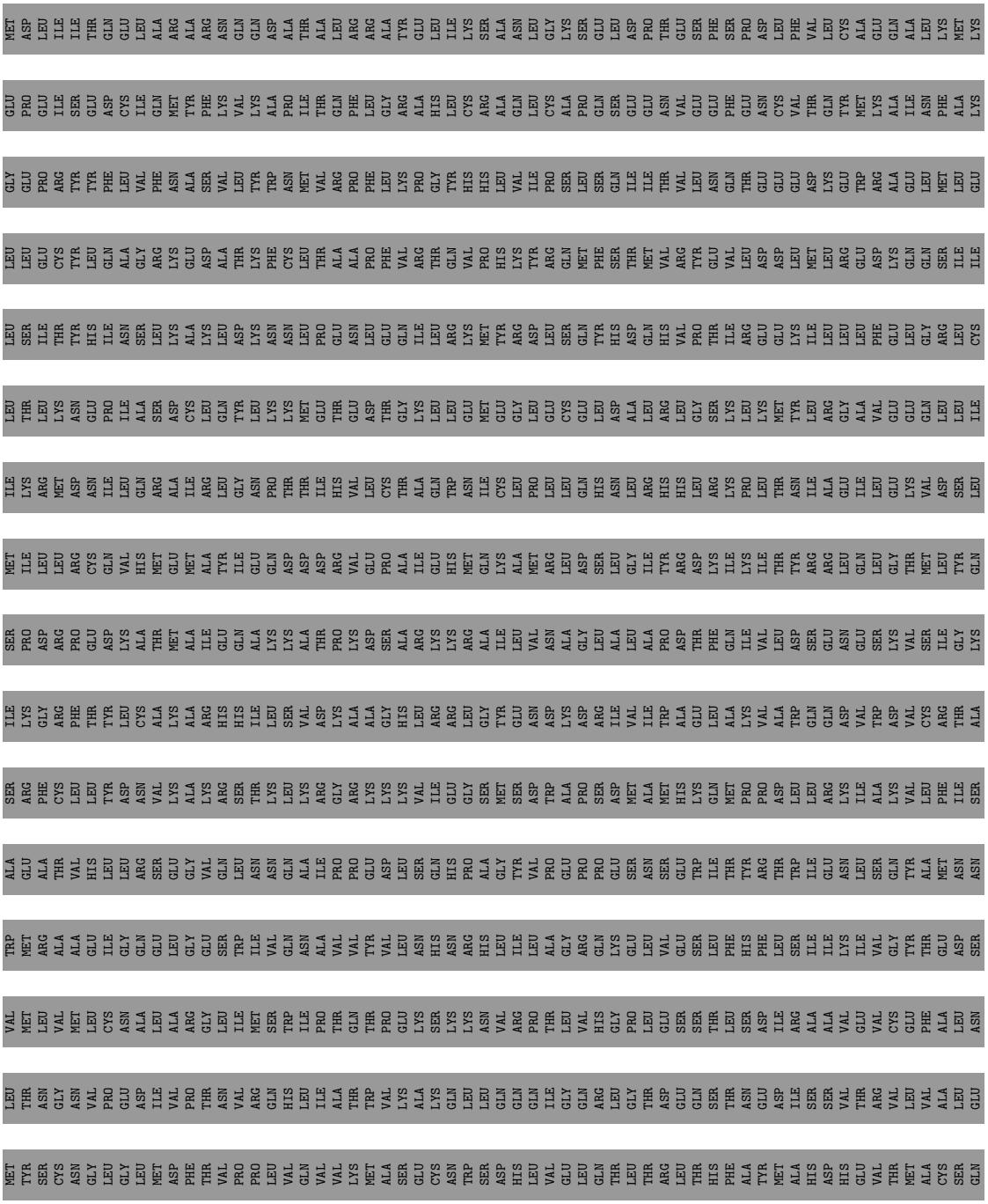


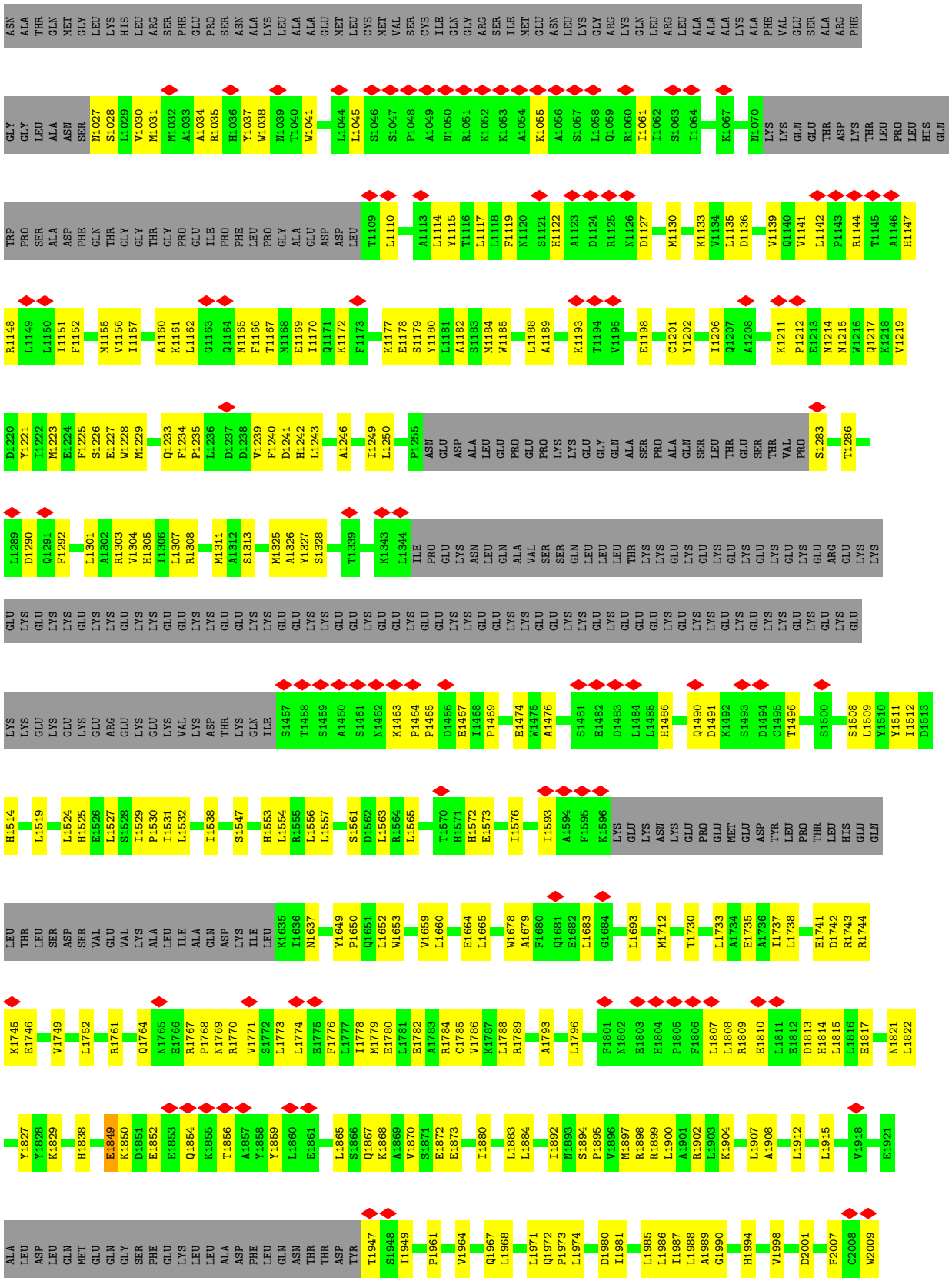


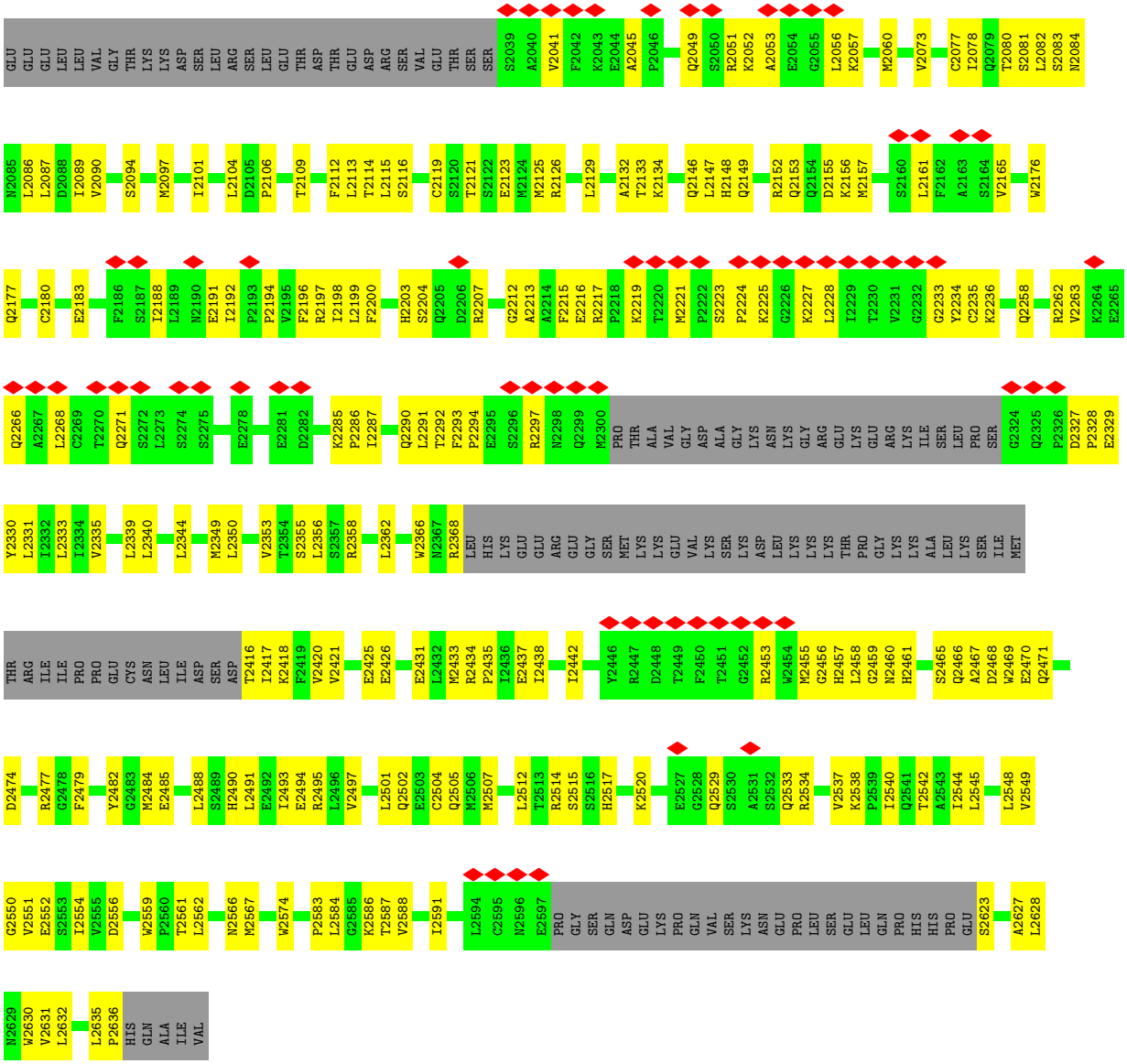


• Molecule 8: Cilia and flagella associated protein 46

Chain B:

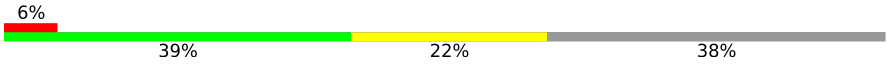


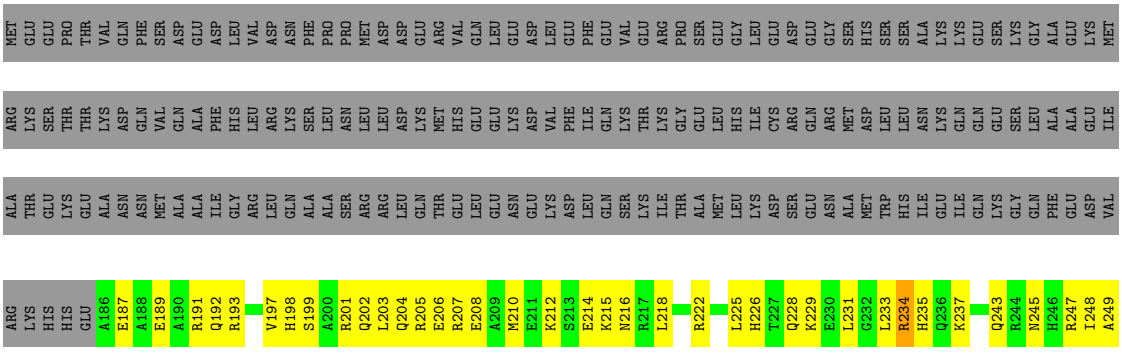


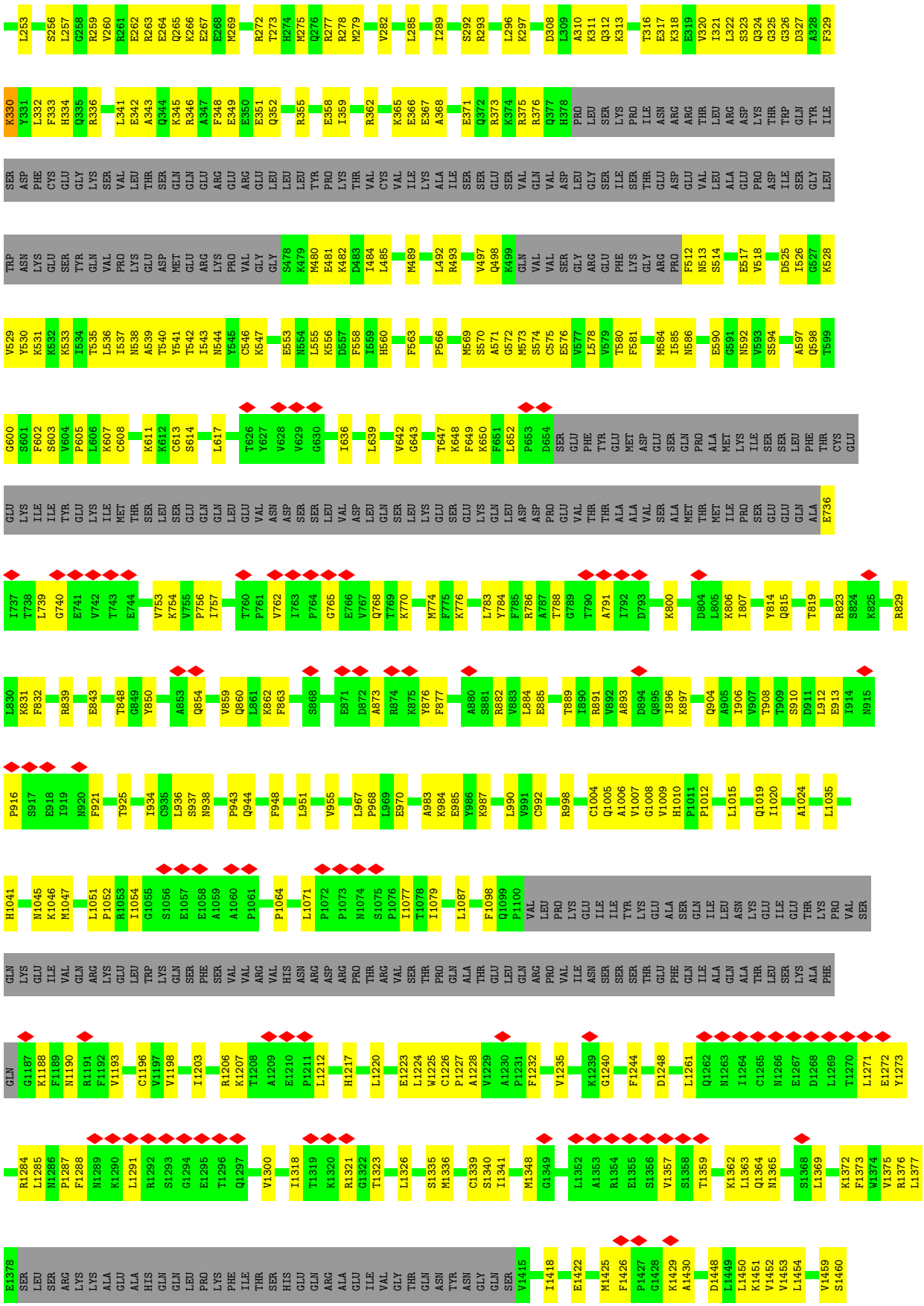


• Molecule 9: Cilia- and flagella-associated protein 74

Chain C:



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SER ASP PHE CYS GLU GLY LYS SER VAL LEU THR SER GLN GLN GLU ARG GLU GLU ARG GLU LEU LEU LEU TYR PRO LYS THR VAL CYS VAL ILE LYS ALA ILE SER SER GLU SER VAL GLN VAL ASP LEU GLY SER ILE SER THR GLU ASP GLU VAL LEU ALA GLU PRO ASP ILE SER GLY LEU
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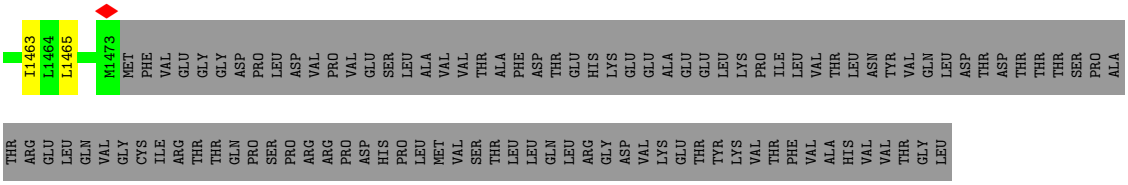
E1378 SER LEU SER ARG LYS LYS ALA GLU ALA HIS GLN GLN LEU PRO LYS PHE ILE THR SER HIS GLU GLN ARG ALA GLU ILE VAL GLY THR GLN ASN TYR ASN GLY GLN SER V1415 I1418 E1422 M1425 F1426 P1427 G1428 K1429 A1430 D1448 L1449 L1450 K1451 V1452 V1453 L1454 V1459 S1460



• Molecule 9: Cilia- and flagella-associated protein 74

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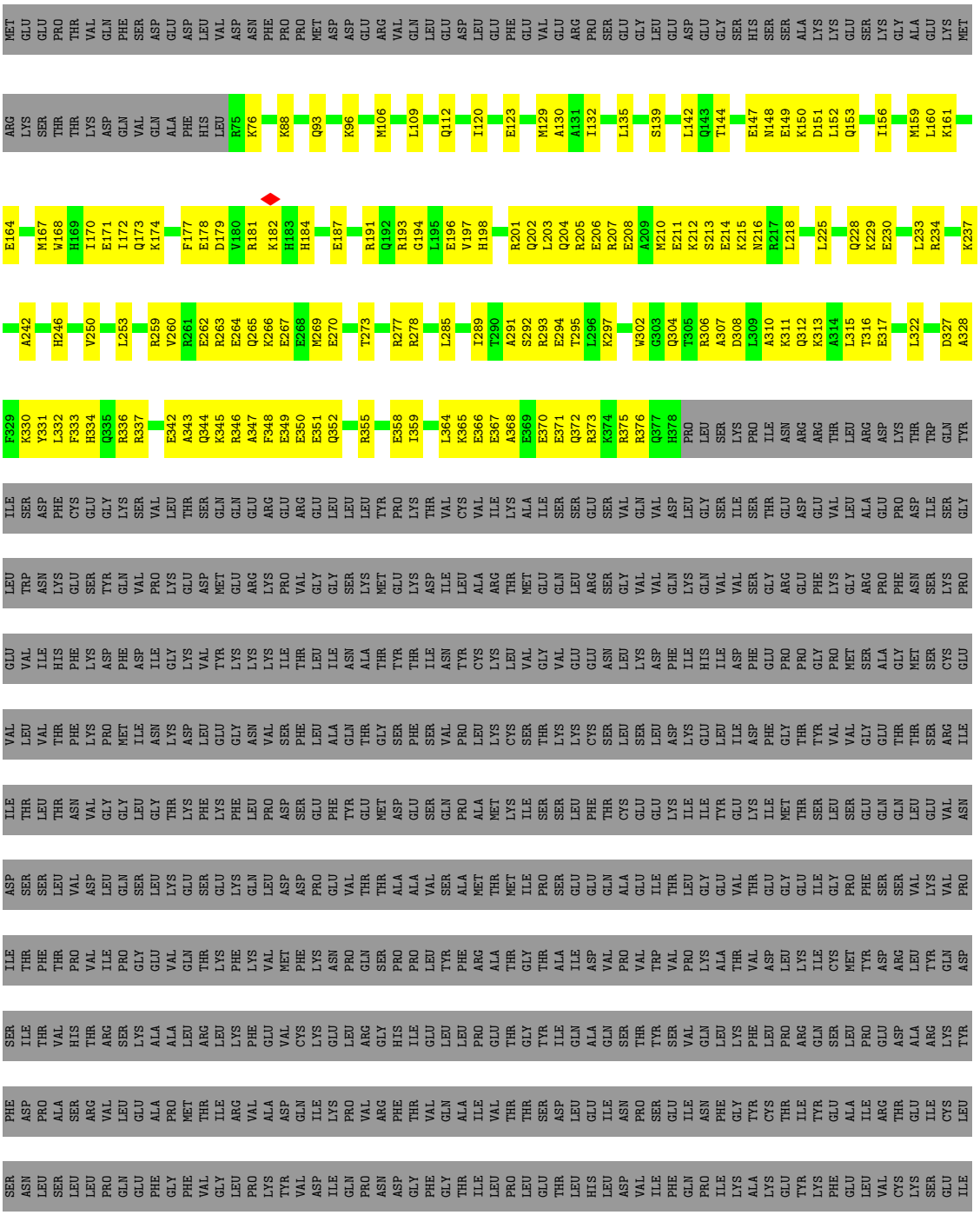

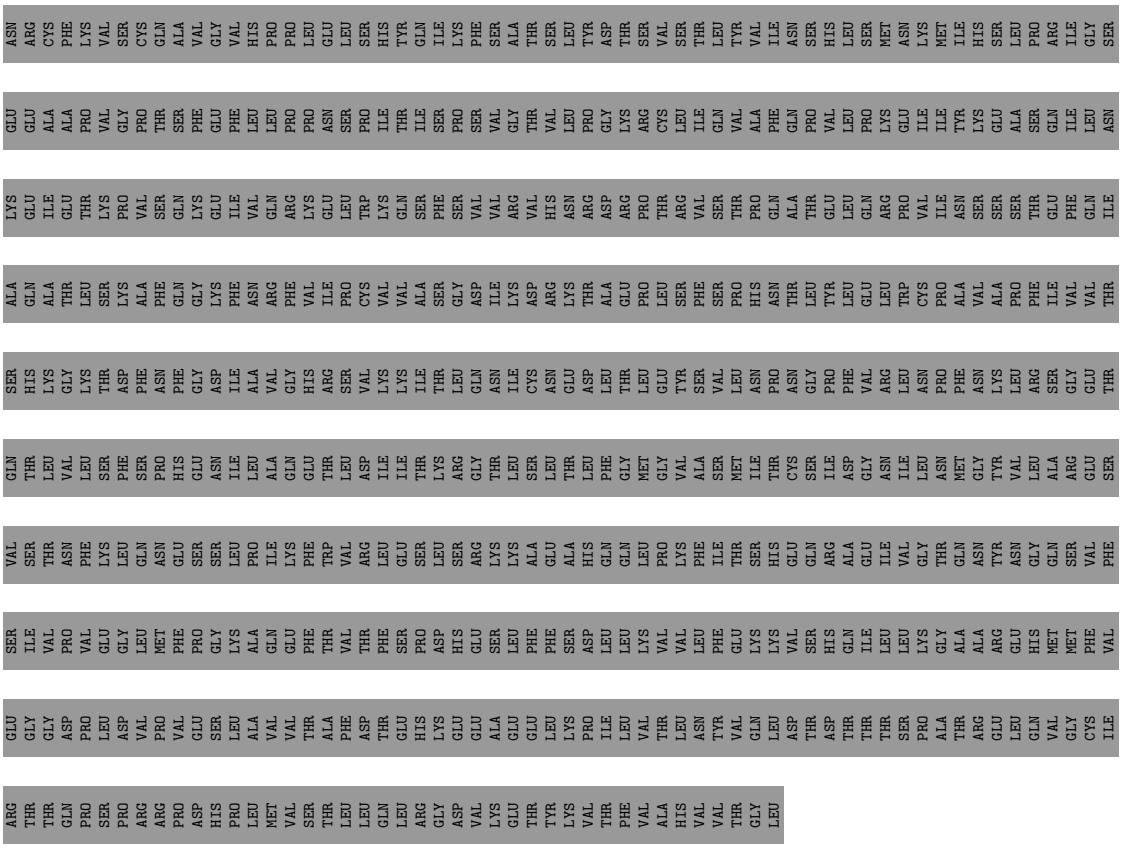

• Molecule 9: Cilia- and flagella-associated protein 74

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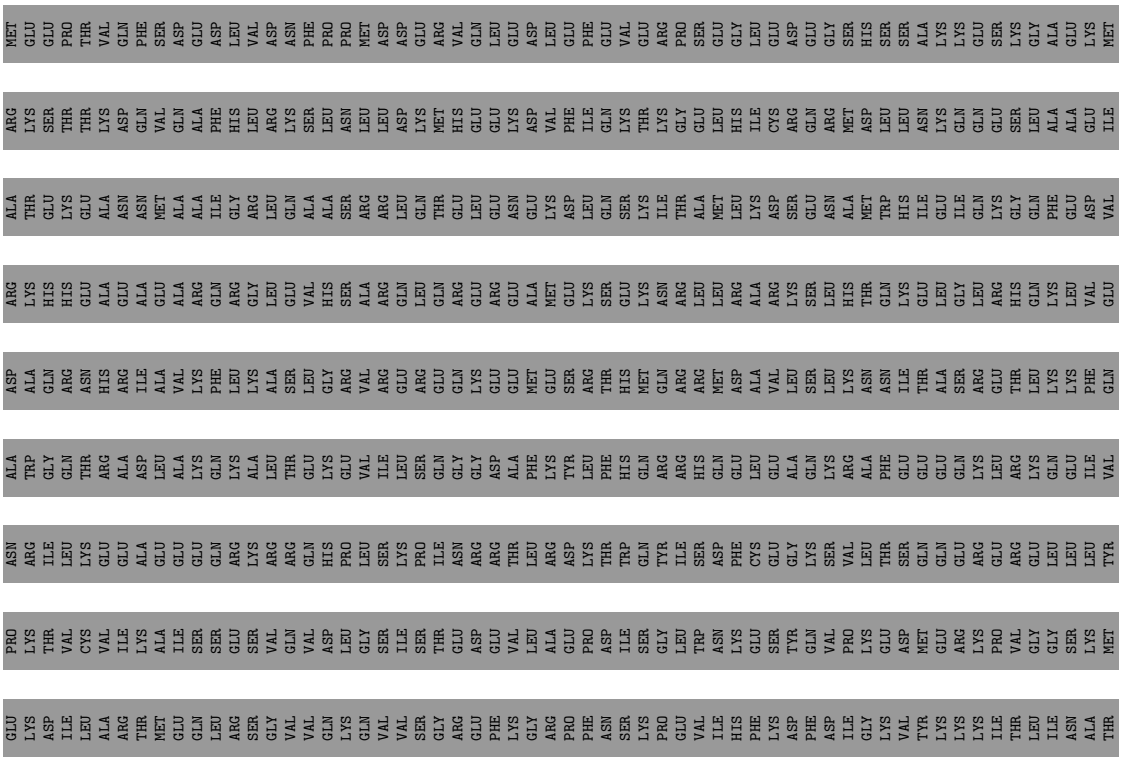

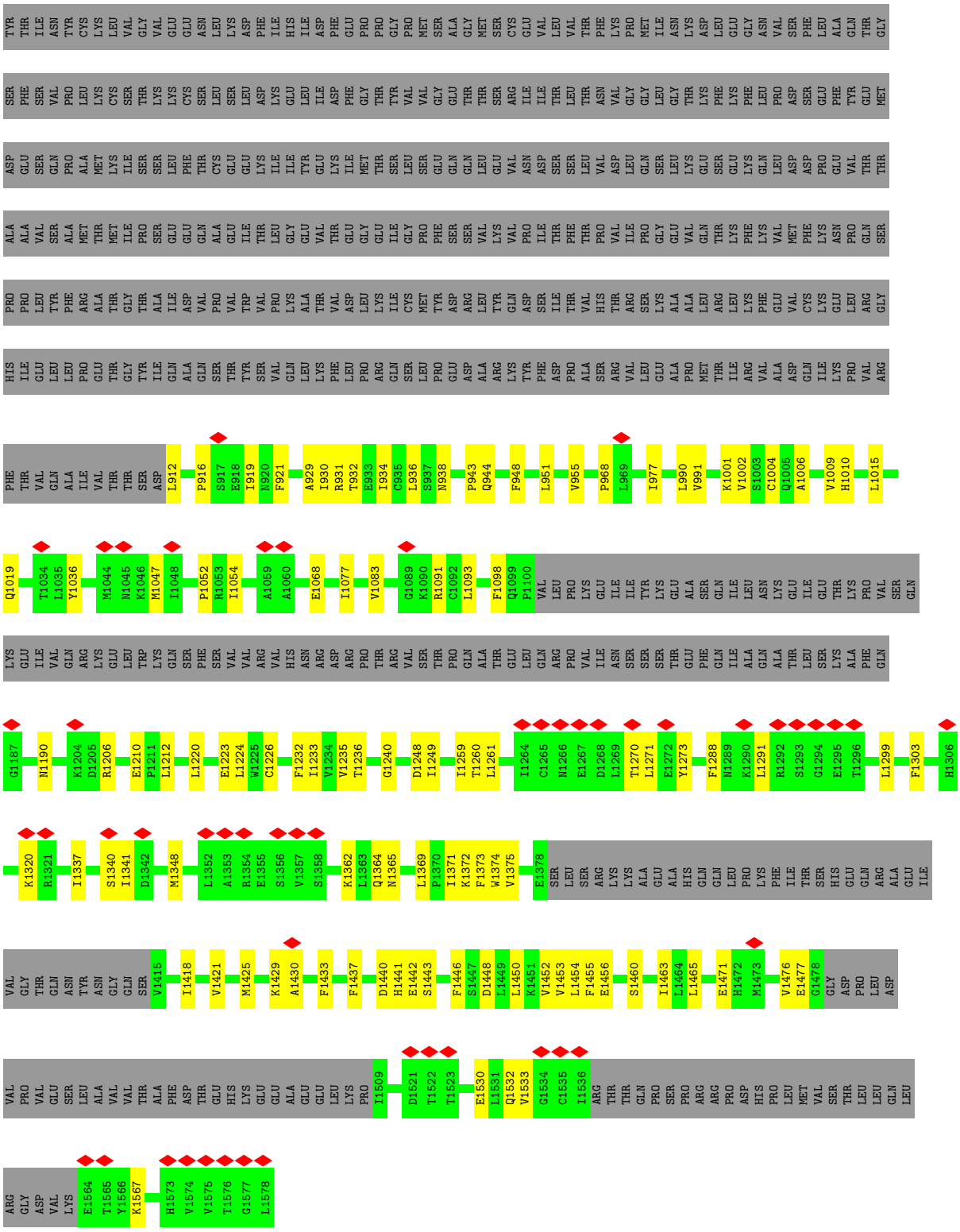

• Molecule 10: Coiled-coil domain containing 180

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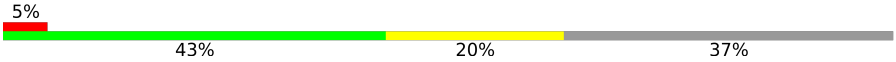

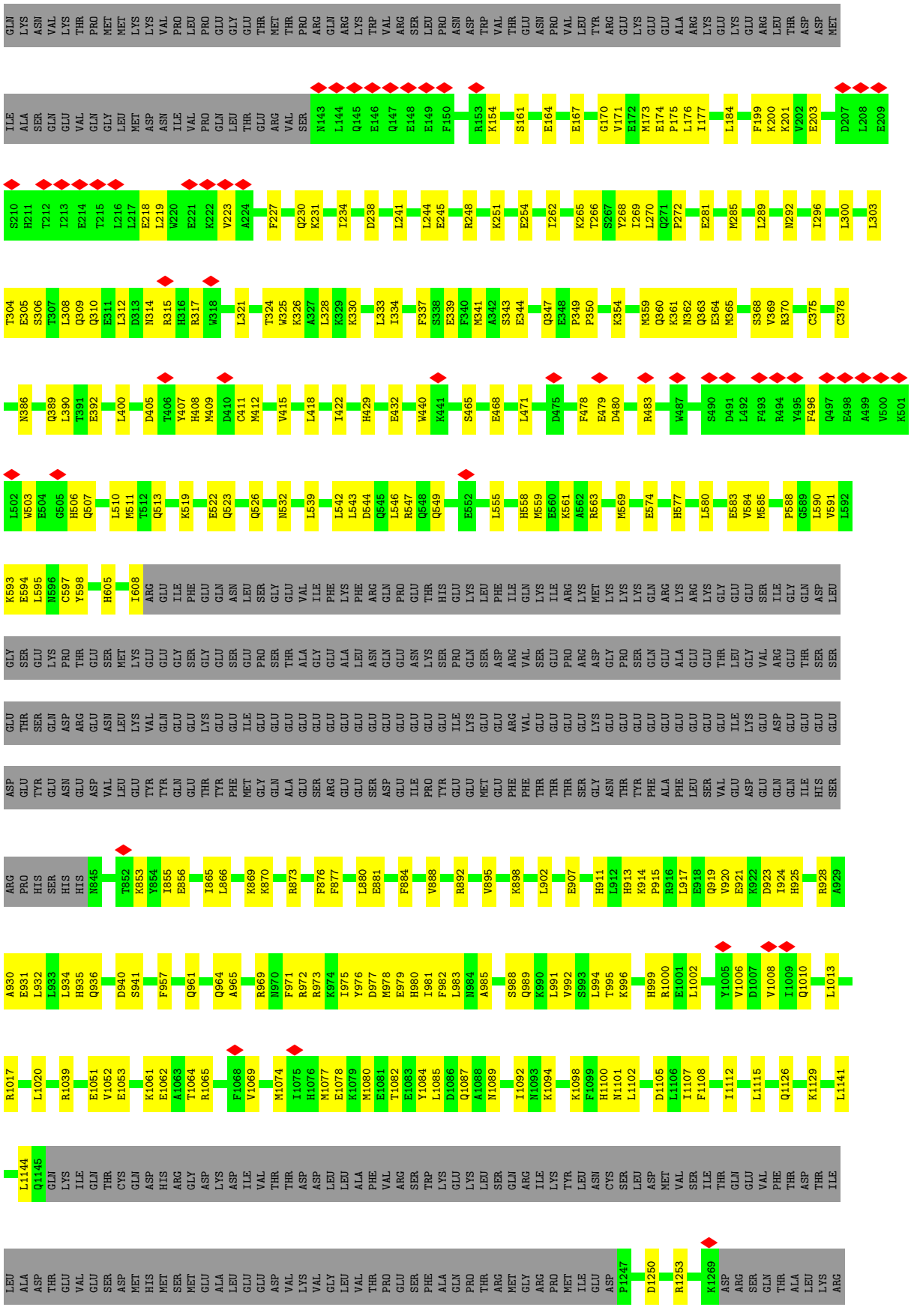

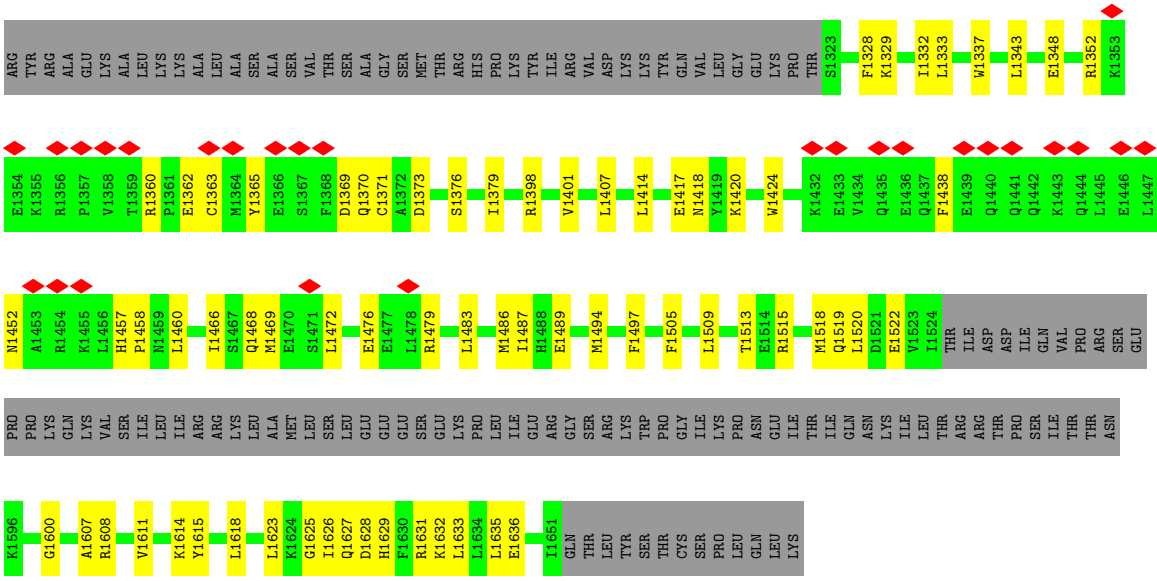

• Molecule 10: Coiled-coil domain containing 180

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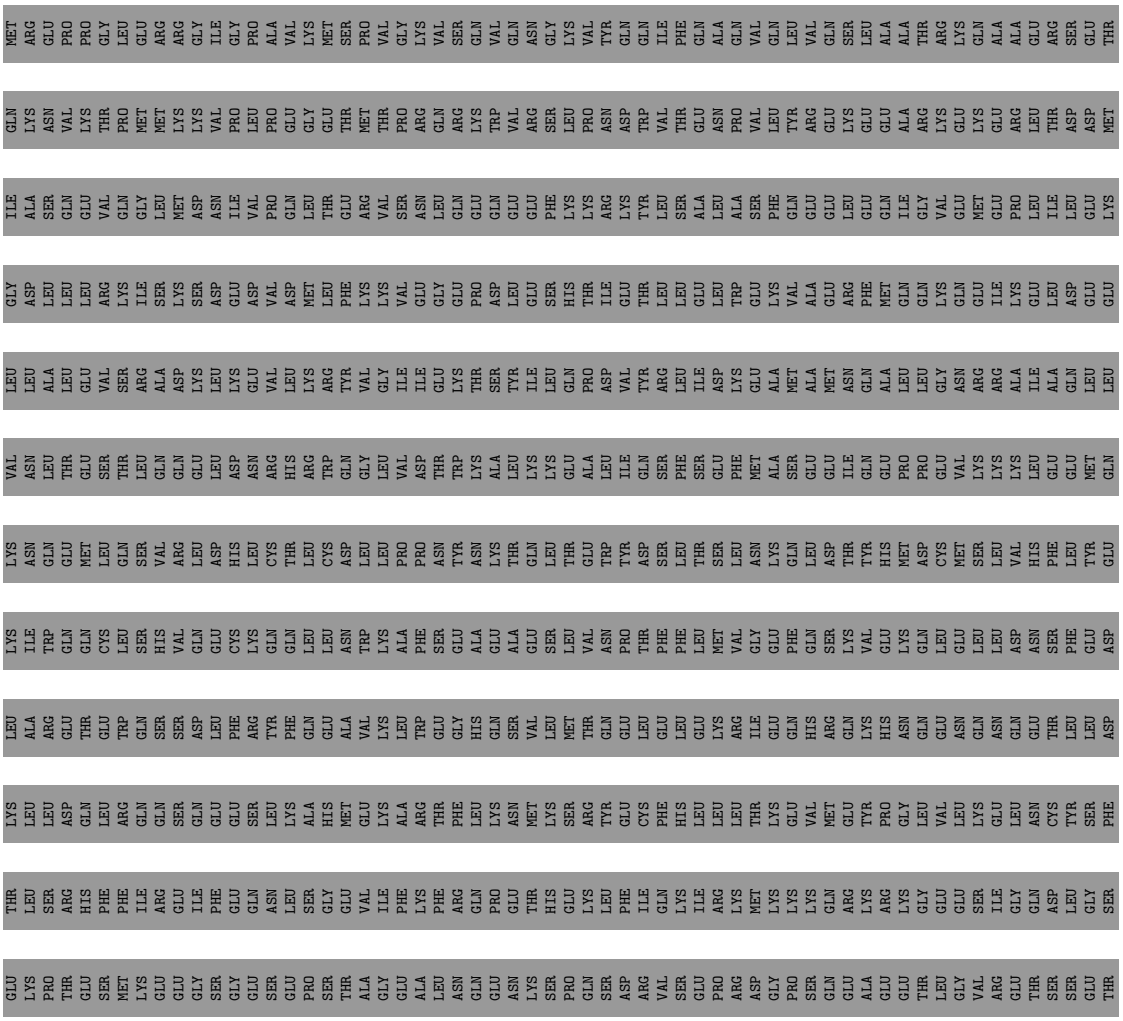

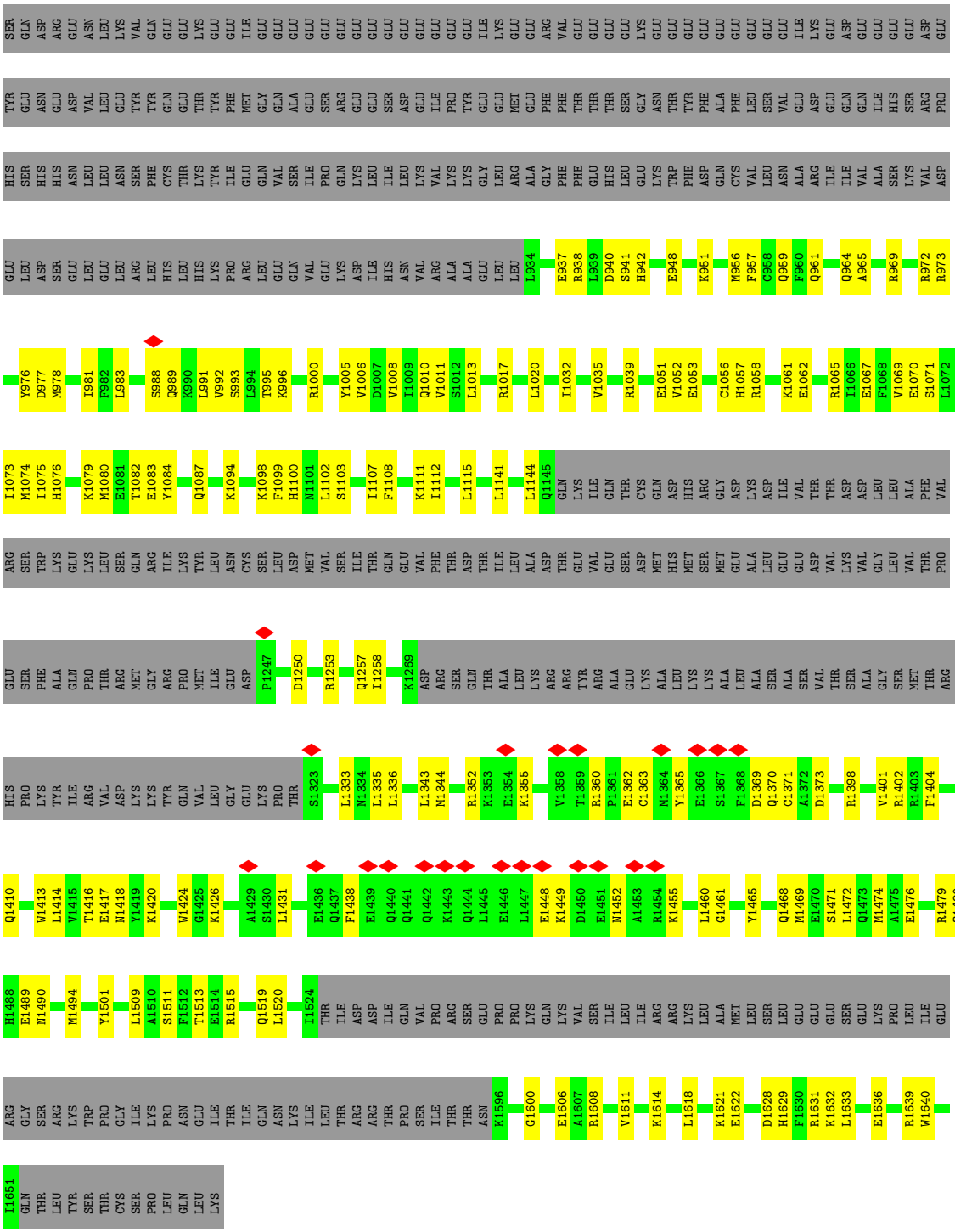

• Molecule 11: Cilia- and flagella-associated protein 54

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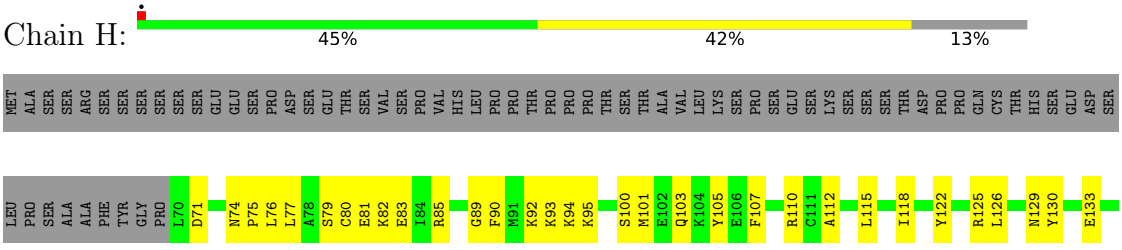

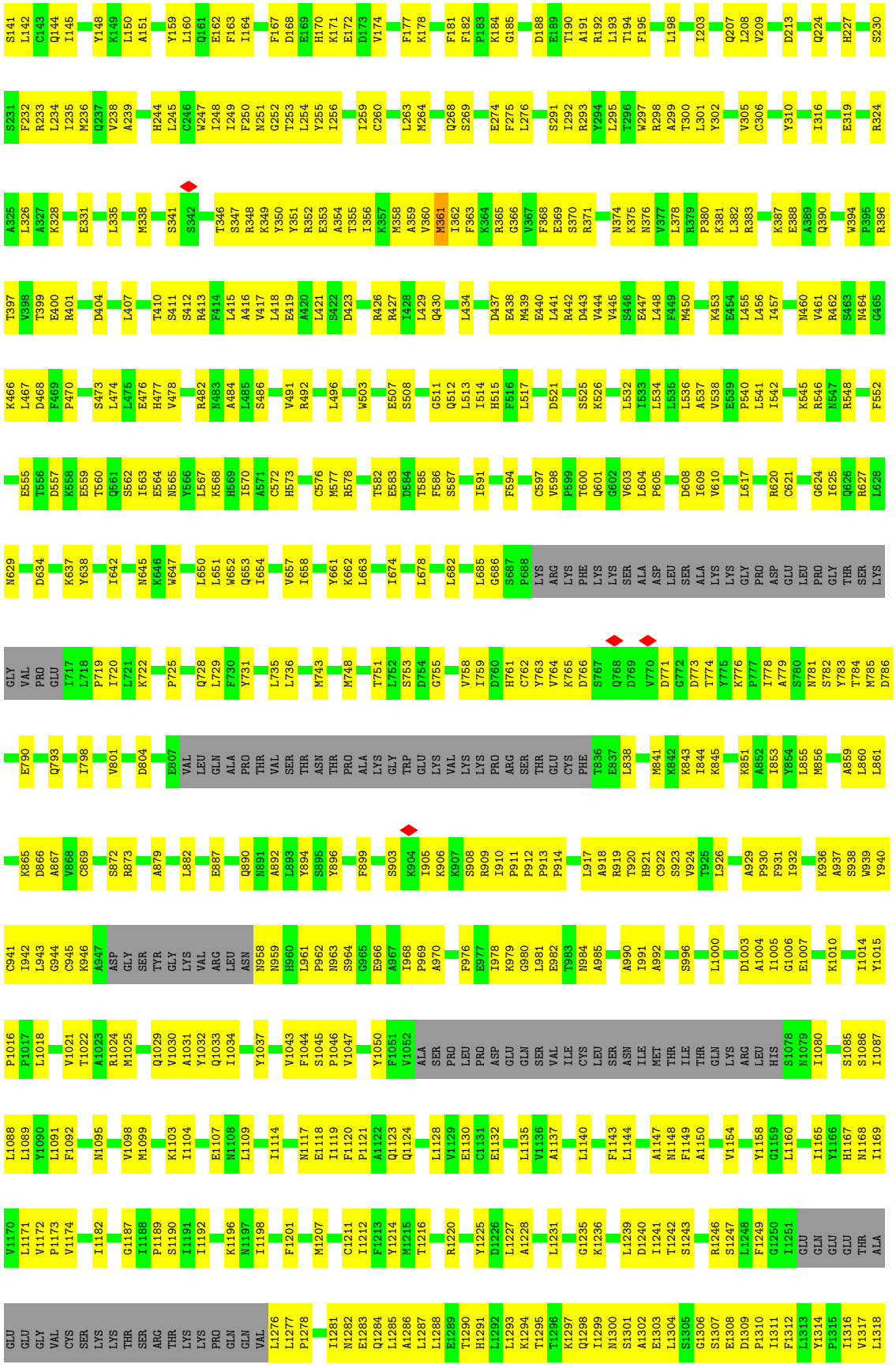

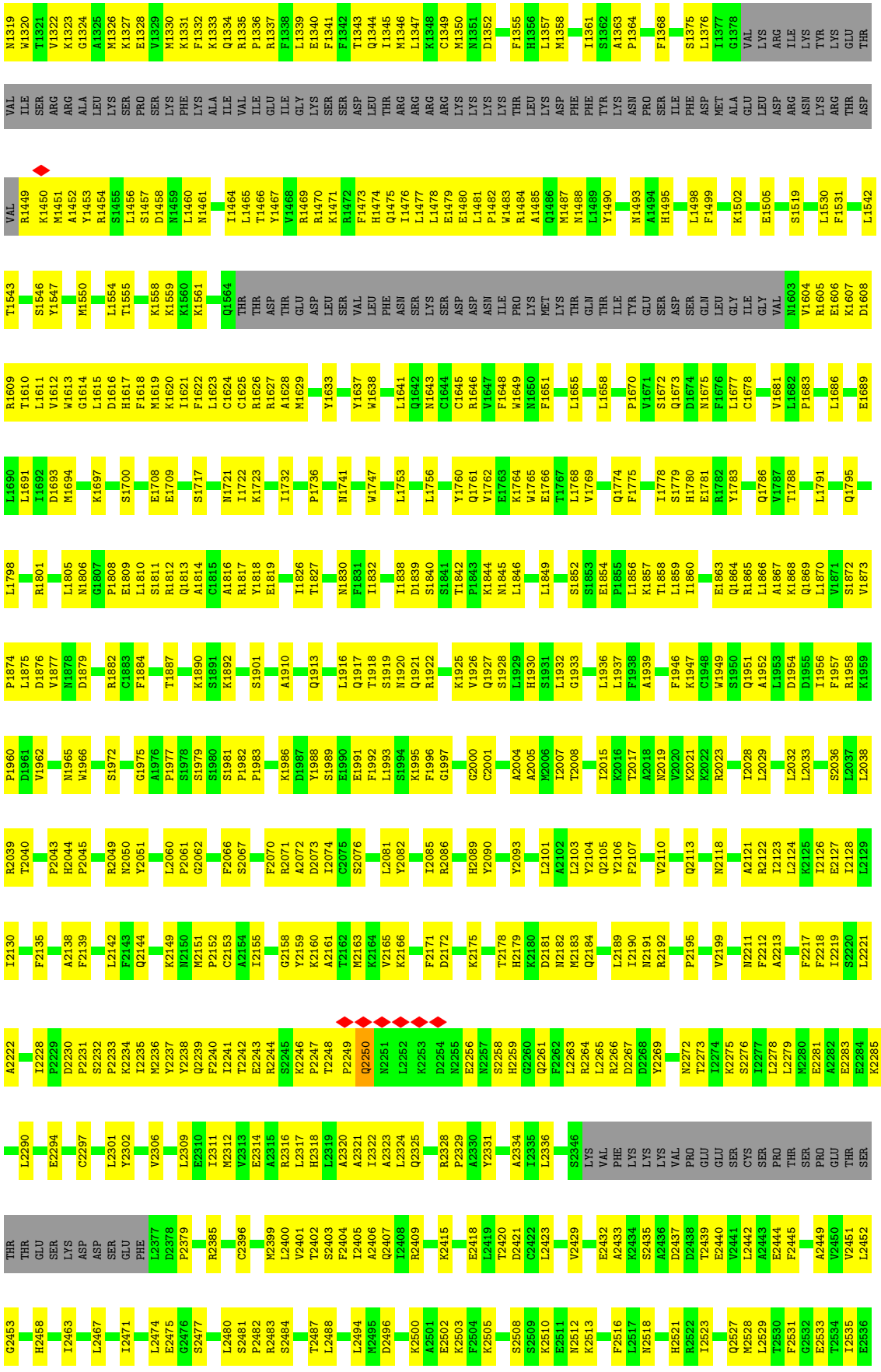

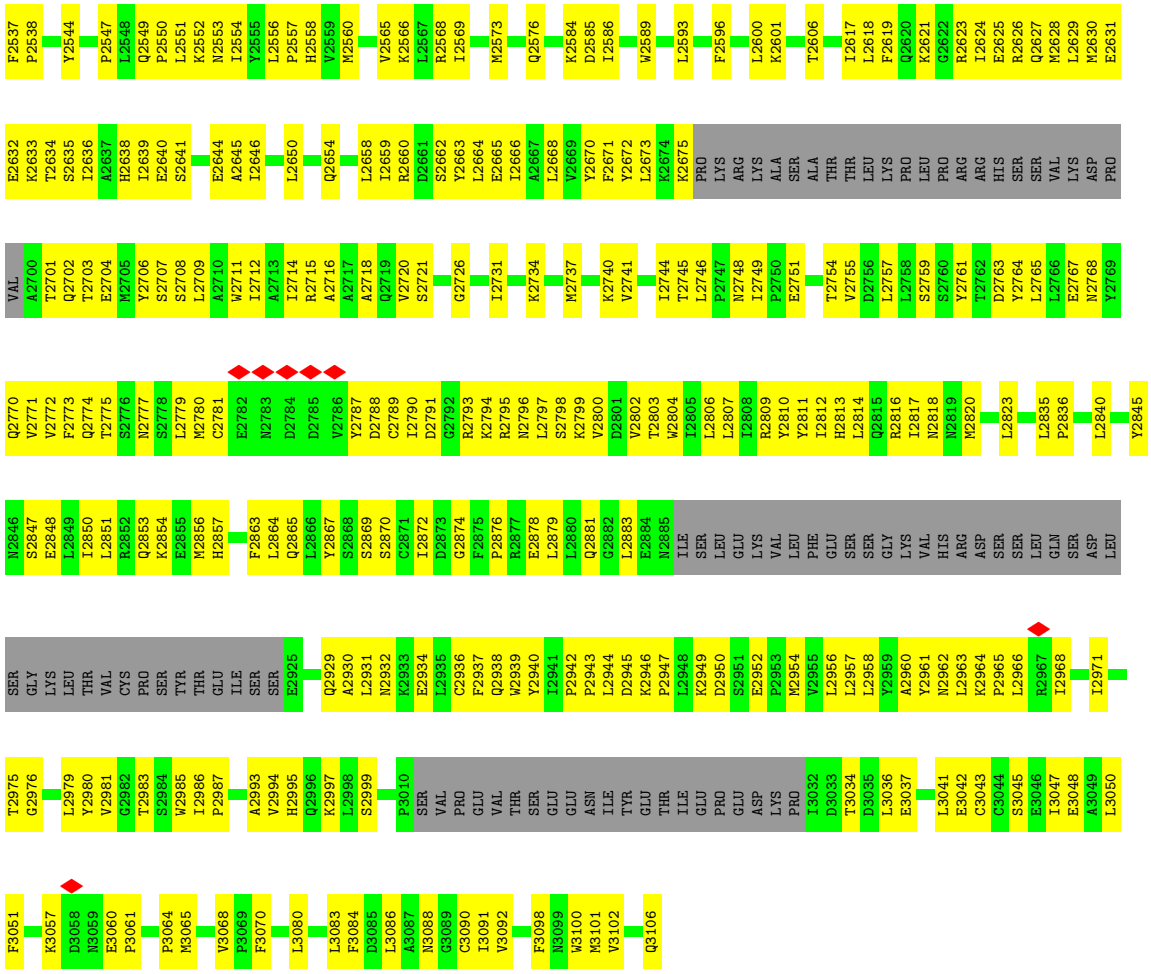

• Molecule 11: Cilia- and flagella-associated protein 54

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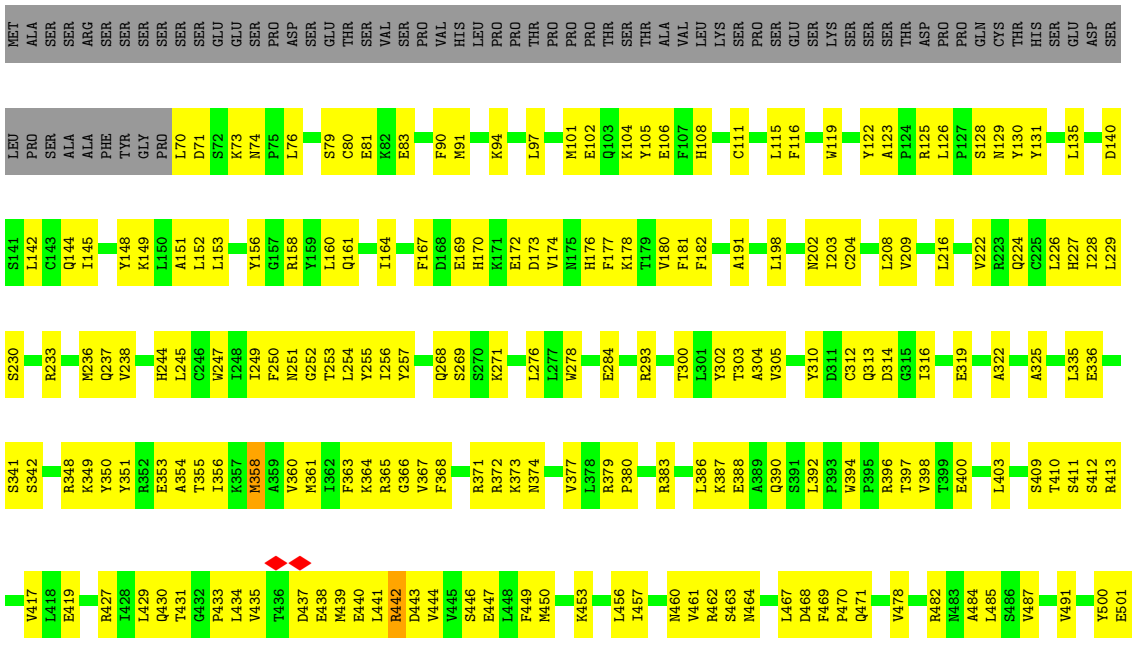

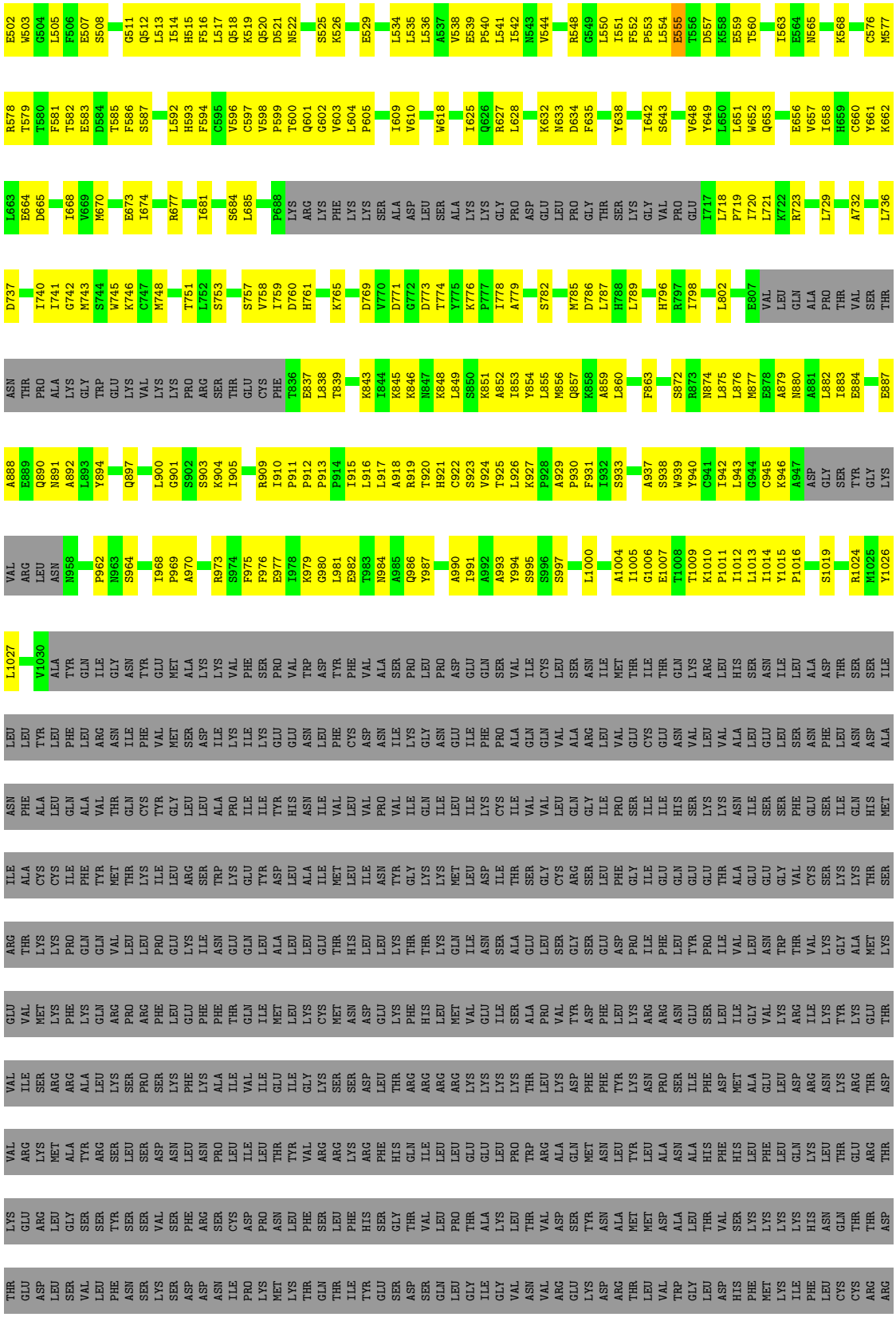
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A888 E889 Q890 N891 A892 L893 Y894 Q897 L900 G901 S902 S903 K904 I905 R909 I910 P911 P912 P913 P914 I915 L916 L917 A918 R919 T920 H921 C922 S923 V924 T925 L926 K927 P928 A929 P930 F931 I932 S933 A937 S938 W939 Y940 C941 I942 L943 G944 C945 K946 A947 A S P G L Y S E R T Y R G L Y L Y S
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L E U L E U T Y R L E U P H E L E U P H E A R G A S N I L E P H E V A L M E T S E R A S P I L E L Y S G L U G L U I L E P H E P R O V A L A L A G L N L E U A R G L E U V A L C Y S C Y S G L U C Y S A S P A S N I L E T H R L E U L E U A S P G L Y A S N I L E S E R L E U G L U L E U A S P
A S N P H E A L A L E U G L N A L A V A L T H R G L N C Y S T Y R G L Y L E U L E U P R O I L E I L E T Y R H I S A S N I L E V A L L E U V A L P R O V A L I L E I L E L Y S C Y S I L E V A L L E U G L N G L Y I L E P R O S E R I L E I L E H I S S E R L Y S L Y S A S N I L E S E R L E U G L U P H E M E T L E U H I S A S N L E U
I L E A L A C Y S C Y S I L E P H E T Y R M E T T H R L Y S I L E L E U A R G S E R T R P L Y S G L U G L N T Y R A S P L E U A L A I L E M E T L E U L E U A S N I L E T Y R G L Y I L E P H E L E U L Y S A R G A S P T H R G L U G L U T H R L E U G L U T H R A L A G L U G L U S E R L E U I L E L Y S L Y S T H R S E R
A R G T H R L Y S L Y S P R O G L N G L N V A L L E U L E U P R O G L U L E U A L A L E U L E U L Y S T H R T H R L Y S G L N I L E A S N S E R A L A G L U L E U S E R A L A G L U G L U T H R I L E V A L L E U A S N S E R L E U T Y R G L U
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L Y S G L U A R G L E U G L Y S E R S E R S E R V A L L E U S E R A S N L E U P H E A R G S E R C Y S A S P P R O L E U A S N L E U T H R V A L A S P S E R T Y R A S N A L A M E T M E T A S P A L A L E U T H R V A L S E R L Y S L Y S L Y S L Y S H I S A S N G L N T H R T H R A S P
T H R G L U A S P L E U S E R A S P A S N A S N I L E P R O L Y S A S P A R G T H R L E U V A L A R G G L U S E R T R P G L Y L E U A S P H I S P H E M E T I L E L Y S I L E P H E L E U C Y S C Y S A R G
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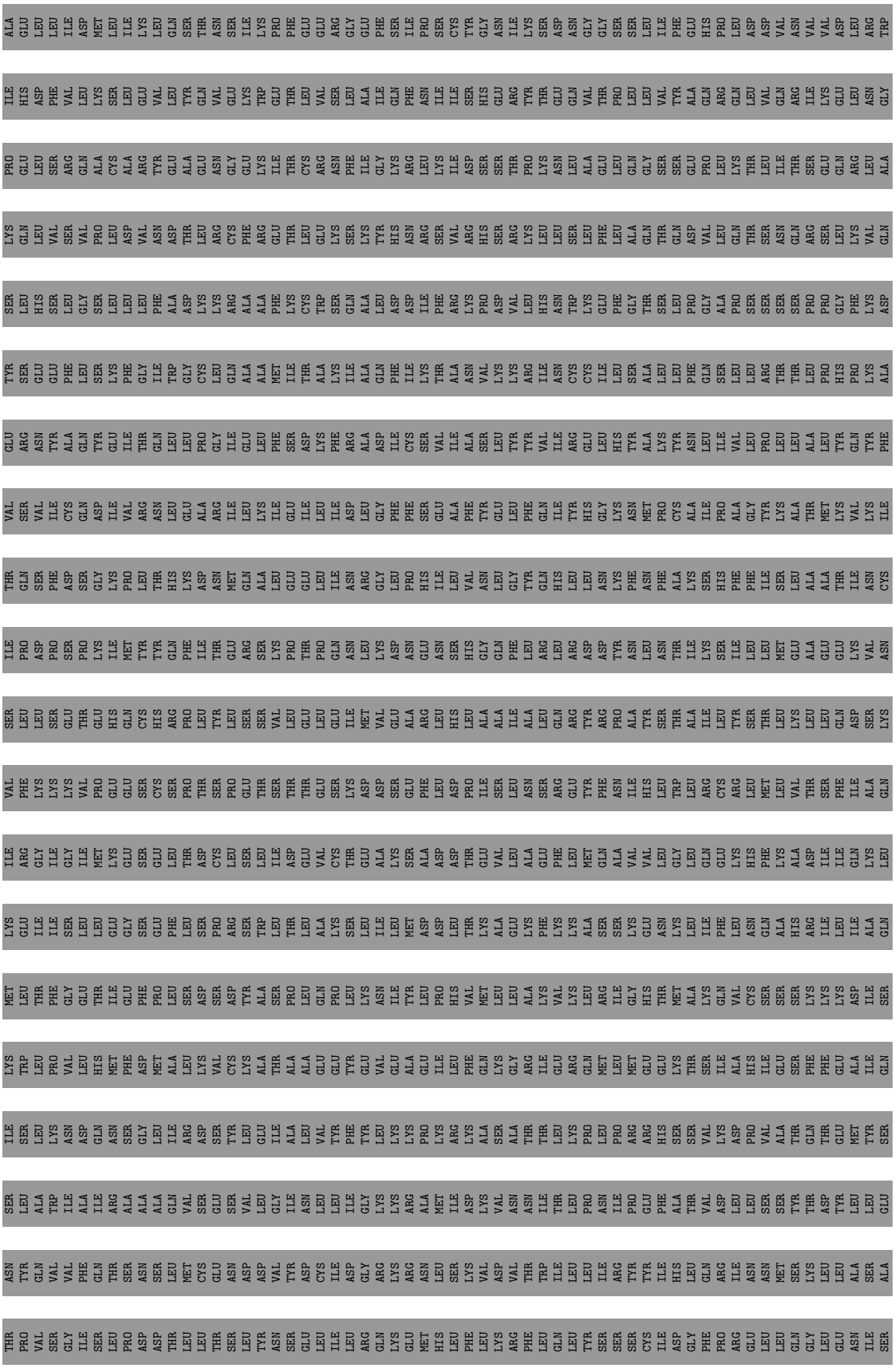
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ILE HIS ASP PHE VAL LEU LYS SER LEU GLU VAL LEU TYR GLN VAL GLU LYS TRP GLU THR LEU VAL SER LEU ALA ILE GLN PHE ASN ILE ILE SER HIS GLU ARG TYR THR GLU GLN VAL THR PRO LEU LEU VAL TYR ALA GLN ARG GLN LEU VAL GLN ARG ILE LYS GLU LEU ASN GLY
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VAL PHE LYS LYS VAL PRO GLU GLU GLU SER CYS SER PRO THR SER PRO GLU THR SER THR THR GLU SER LYS ASP ASP SER GLU PHE LEU ASP PRO ILE SER LEU ASN SER ARG GLU TYR PHE ASN ILE HIS LEU TRP LEU ARG CYS ARG LEU GLN ALA SER LYS GLU ASN LYS LEU ILE PHE LEU GLU GLN GLU LYS HIS PHE LYS ALA HIS ARG ILE LEU LEU ILE ALA GLN
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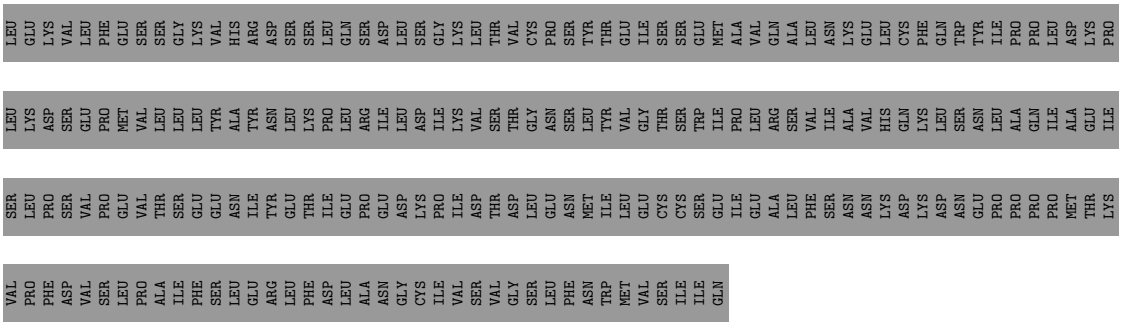
LYS GLU ILE ILE SER LEU GLU GLY SER GLU PHE LEU SER PRO ARG SER TRP LEU THR LEU ALA LYS SER LEU ILE LEU MET ASP ASP LEU THR LYS ALA GLU LYS PHE LYS LYS ALA ALA SER SER LYS GLU ASN GLN ALA HIS ARG ILE LEU LEU ILE ALA GLN
MET LEU THR PHE GLY GLU PHE PRO LEU SER ASP SER ASP TYR ALA SER PRO LEU GLN PRO LEU LYS ASN ILE TYR LEU PRO HIS VAL MET LEU LEU ALA LYS VAL LYS LEU ARG ILE GLY HIS THR MET ALA LYS GLN LEU VAL CYS SER SER SER LYS LYS ASP ILE LEU
LYS TRP LEU PRO VAL LEU HIS MET PHE ASP MET ALA LEU ALA ALA GLU GLU TYR GLU VAL GLU ILE LEU PHE ILE ALA LYS THR ALA ALA GLU GLU ARG GLN MET LEU ARG ILE PHE SER THR SER ILE GLU GLY ARG ILE GLU ARG GLN MET LEU MET GLU GLU HIS THR LYS SER ILE GLU ALA PHE PHE GLU ILE LEU
ILE SER LEU LYS ASN ASP SER TYR LEU GLU ILE LEU ALA ALA LEU VAL TYR PHE TYR LEU LYS LYS PRO ALA SER GLU ALA THR LYS ARG LYS ASP ARG HIS SER SER VAL LYS ASP PRO ARG GLN THR GLU MET TYR SER
SER LEU ALA TRP ILE ILE ARG ALA ALA GLN VAL SER GLU SER VAL LEU GLY ILE ASN LEU GLU LEU LEU ILE GLY LYS LYS ARG ALA MET ILE ASP LYS VAL ASN ASN ILE PRO GLU PHE ALA THR VAL ASP LEU ASP LEU GLU SER SER TYR THR ASP TYR LEU GLU
ASN TYR GLN VAL VAL PHE GLN THR SER ASN SER ASP ASP VAL TYR ASP CYS ILE ASP GLY ARG LYS ARG ASN LEU SER LYS VAL ASP THR TRP ILE LEU LEU LEU ILE ARG TYR TYR ILE HIS LEU GLN ARG ILE ASN ASN MET SER LYS LEU LEU ALA SER ALA
THR PRO VAL SER GLY ILE SER LEU PRO ASP THR LEU SER LEU TYR ASN SER GLU LEU ILE LEU ARG GLN LYS GLU MET HIS LEU PHE LEU LYS ARG PHE LEU GLN LEU TYR SER SER CYS ILE ASP GLY PHE PRO ARG GLU LEU LEU GLN GLY LEU GLU LEU ASN ILE SER



• Molecule 12: Cilia- and flagella-associated protein 221

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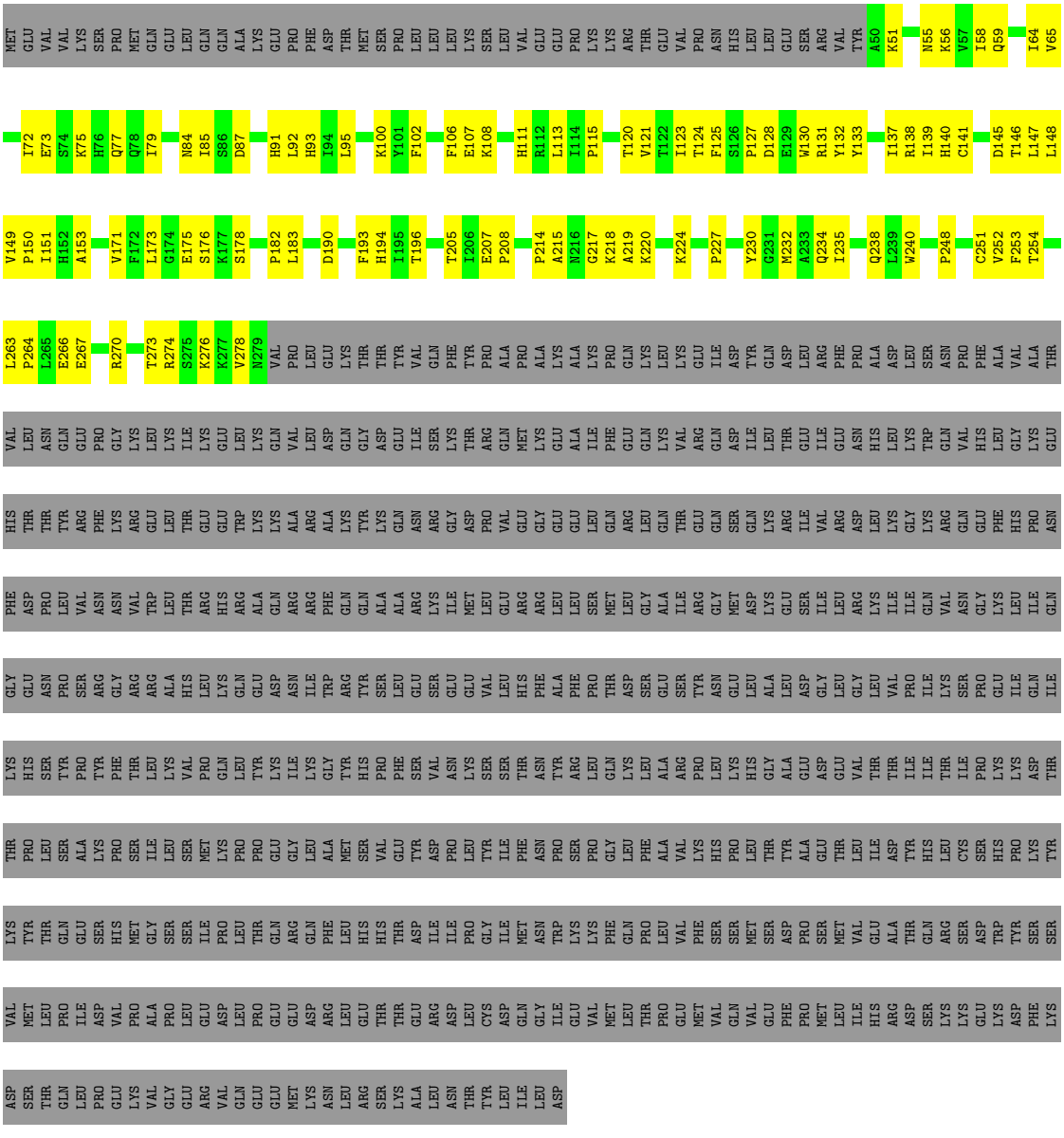
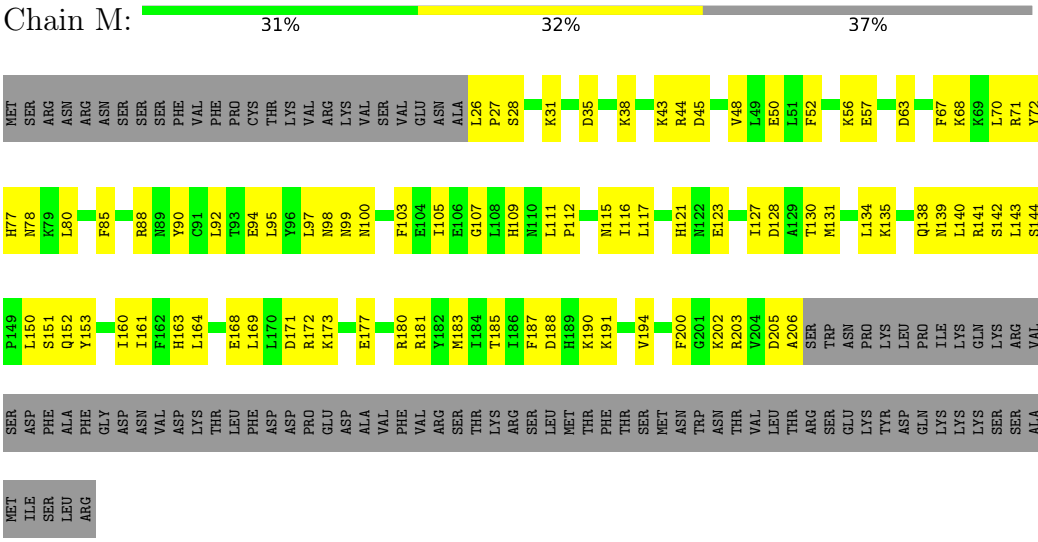


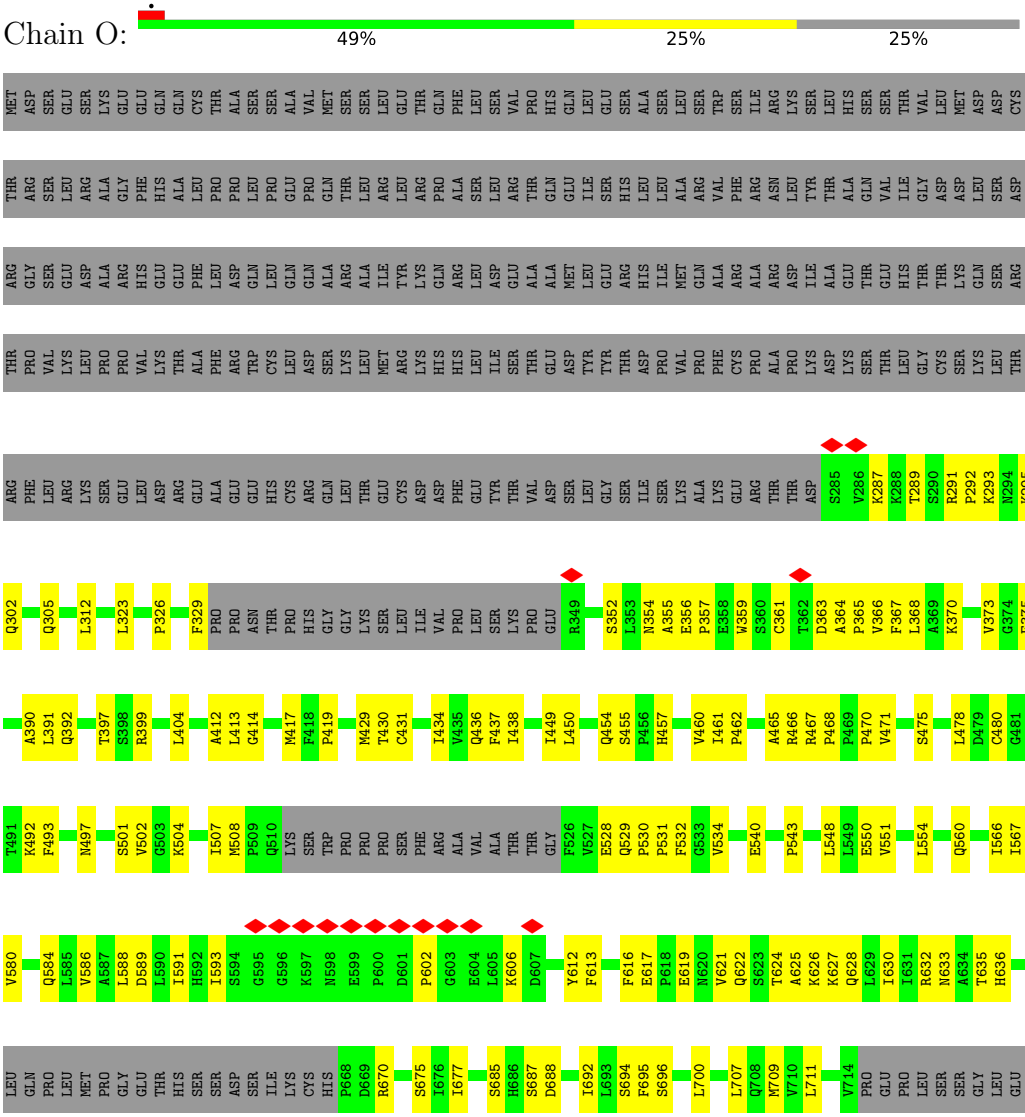
• Molecule 13: Leucine rich repeat containing 72

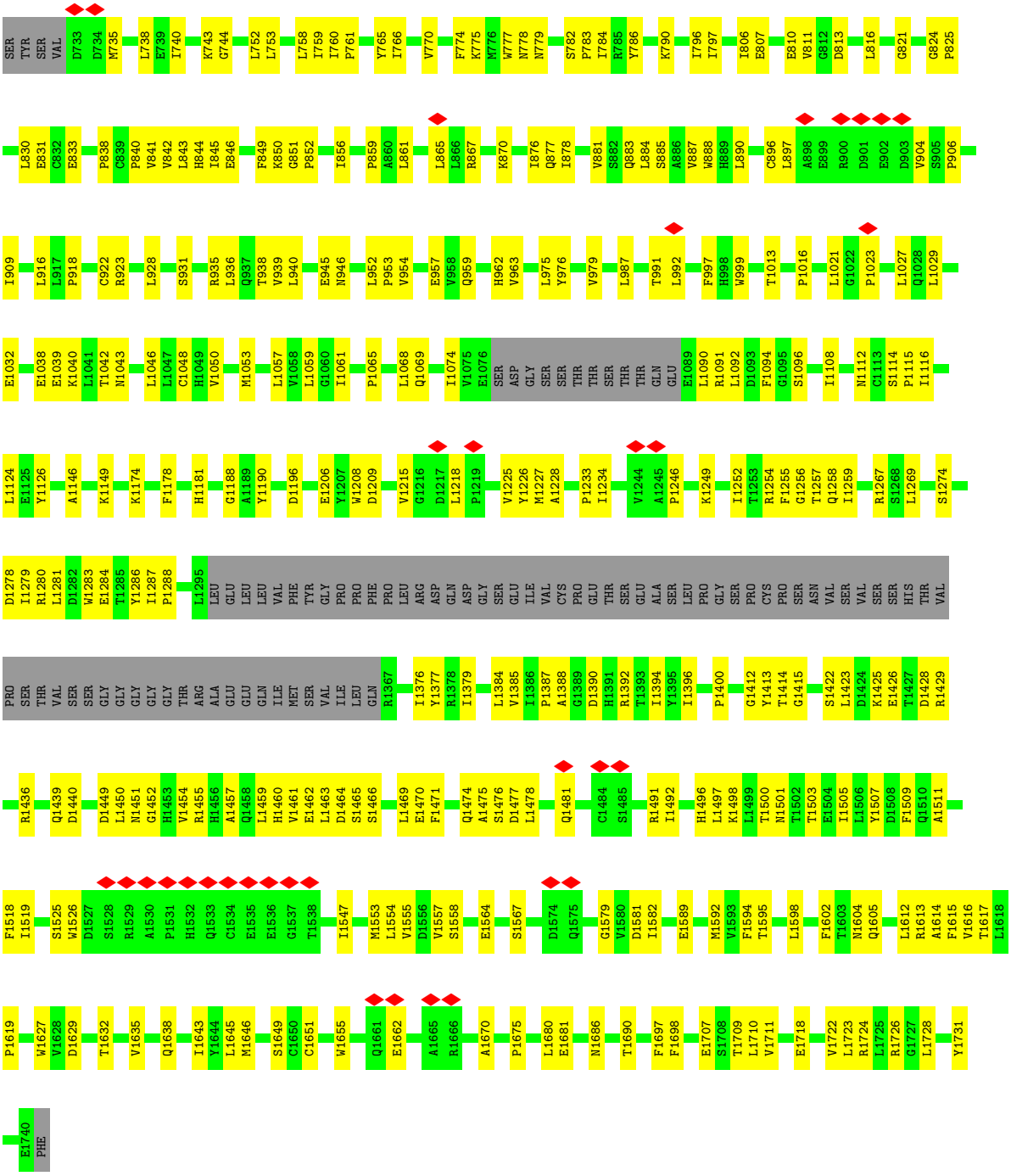
Chain M:



• Molecule 14: Deleted in lung and esophageal cancer 1

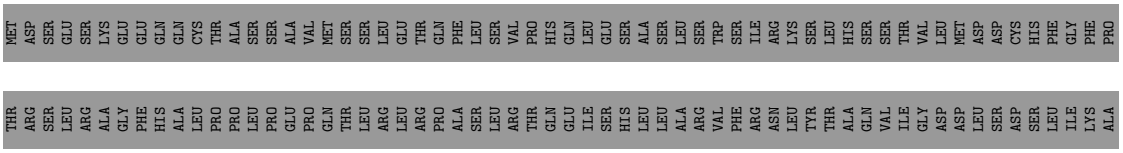
Chain O:

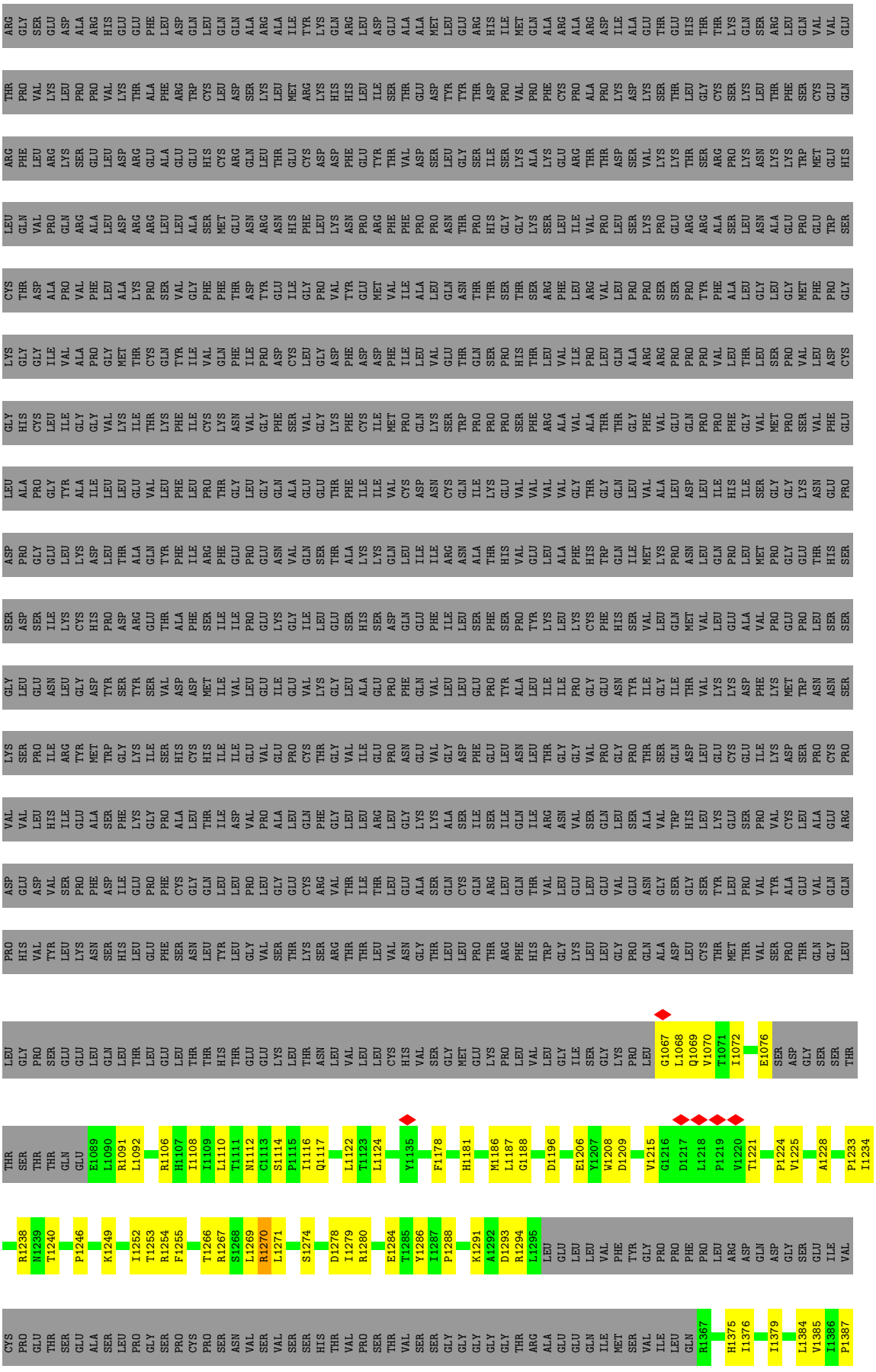




• Molecule 14: Deleted in lung and esophageal cancer 1

Chain P:

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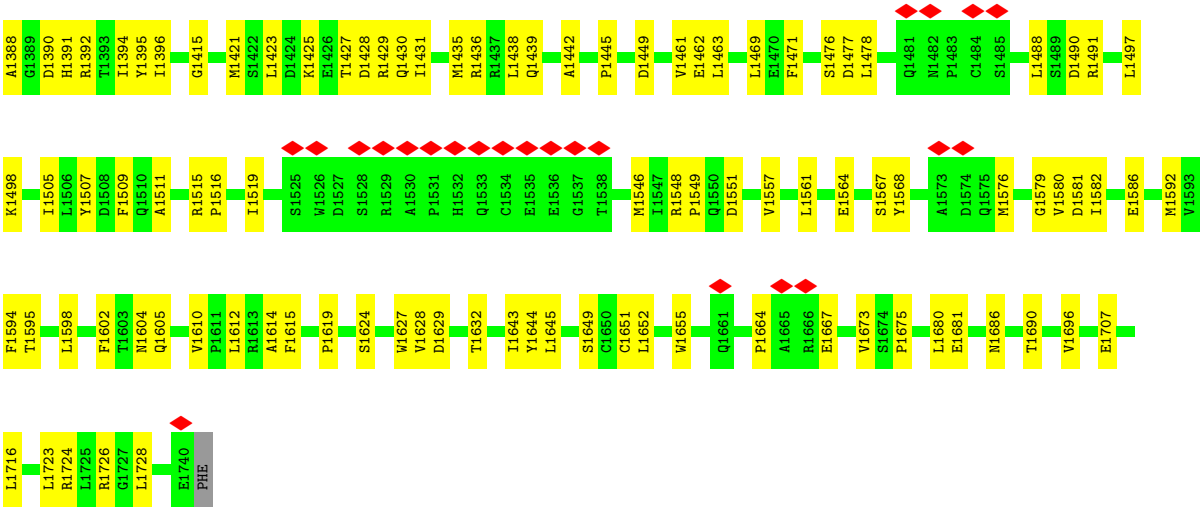
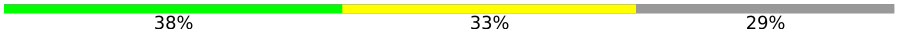
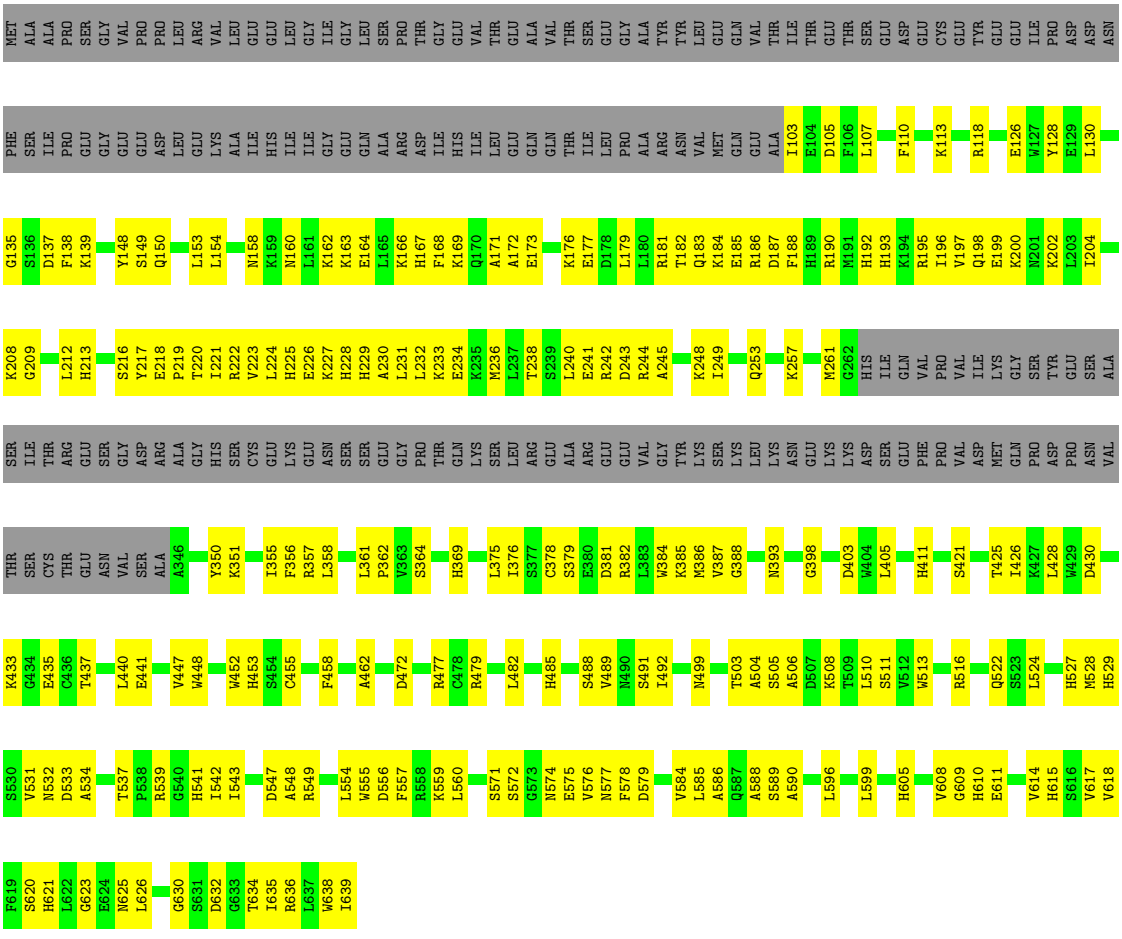
THR PRO VAL LYS LEU PRO PRO VAL LYS THR ALA PHE ARG TRP CYS LEU ASP SER LYS LEU THR GLU CYS ASP PRO ALA PRO LYS ASP LYS SER THR LEU GLY CYS SER LYS LEU THR PHE SER CYS GLU GLN
ARG PHE LEU ARG LYS SER GLU LEU ASP ARG GLU GLU ALA GLU GLU HIS CYS ARG GLN LEU THR GLU CYS ASP ASP PHE GLU TYR THR ASP SER LEU GLY SER ILE SER LYS ALA LYS GLU ARG THR ASP SER ARG GLN LYS LYS TRP MET GLU HIS
LEU GLN VAL PRO GLN ARG ALA LEU ASP ARG ARG LEU LEU ALA SER MET GLU GLY ASN ARG ASN HIS PHE LEU LYS ASN PRO LEU ASP PHE PHE PRO PRO ASN THR PRO HIS GLY GLY LYS SER LEU ILE LEU VAL PRO LEU SER LYS PRO GLU ARG ARG ALA SER LEU ASN ALA GLU PRO GLU TRP SER
CYS THR ASP PRO ALA PHE LEU LYS ALA PRO VAL PHE GLY PHE PHE THR ASP TYR GLU ILE GLY PRO VAL TYR LEU ILE ALA LYS PRO SER VAL LEU ASP ALA MET VAL ILE ALA LEU GLY PRO PRO SER ARG PHE LEU ILE ARG VAL LEU PRO PRO SER SER PRO TYR PHE LEU THR LEU SER GLY MET PHE PRO GLY
LYS GLY GLY ILE VAL ALA PRO GLY MET THR CYS GLN TYR ILE VAL GLN PHE ILE PRO ASP CYS LEU GLY ASP PHE ASP ASP PHE ILE ILE LEU VAL GLU THR GLN GLN SER PRO HIS THR LEU VAL LEU THR LEU SER PRO VAL LEU ASP CYS
GLY HIS CYS LEU ILE GLY GLY VAL LYS ILE THR LYS PHE ILE CYS LYS ASN VAL GLY PHE SER VAL GLY LYS PHE CYS ILE MET PRO GLN LYS SER TRP PRO PRO SER PHE ARG ALA VAL VAL GLY THR PHE VAL GLU GLN PRO PRO PHE GLY VAL MET PRO SER VAL PHE GLU
LEU ALA PRO GLY TYR ALA ILE LEU LEU GLU VAL LEU PHE LEU PRO THR GLY LEU GLY GLN ALA GLU GLU THR PHE ILE ILE VAL CYS ASP ASN CYS GLN ILE LYS GLU VAL VAL VAL GLY THR GLY GLN LEU VAL ALA ILE ASP LEU GLN GLU GLU ASN
ASP PRO GLY GLU LEU LYS ASP LEU THR ALA ALA GLN TYR PHE ILE ARG PHE GLU PRO GLU ASN VAL GLN SER THR ALA LYS LYS GLN LEU ILE ILE ARG ASN ALA THR HIS VAL GLU LEU ALA PHE HIS TRP GLN ILE MET LYS PRO ASN LEU GLN PRO LEU MET PRO GLY GLU THR HIS SER
SER ASP SER ILE LYS CYS HIS PRO ASP ARG GLU THR ALA PHE SER ILE ILE PRO GLU LYS GLY ILE LEU GLU SER HIS SER ASP GLN GLU PHE ILE LEU SER PHE SER PRO TYR LYS LEU LYS CYS PHE HIS SER VAL LEU GLN MET VAL LEU GLU ALA VAL PRO GLU PRO GLY SER SER
GLY LEU GLU ASN LEU GLY ASP TYR SER TYR SER VAL ASP ASP MET ILE VAL LEU GLU ILE GLU VAL LYS GLY LEU ALA GLU PRO PHE GLN GLU VAL LEU LEU LEU GLU PRO PHE TYR ALA LEU LEU ILE PRO GLY GLU ASN TYR ILE GLY ILE THR VAL LYS LYS ASP PHE LYS MET TRP ASN ASN SER
LYS SER PRO ILE ARG TYR MET TRP GLY LYS ILE SER HIS CYS HIS ILE ILE GLU VAL GLU PRO CYS THR GLY VAL ILE GLU PRO ASN GLU VAL GLY ASP PHE GLU LEU ASN LEU THR GLY GLY VAL PRO GLY PRO THR SER GLN ASP LEU GLU GLU LYS PRO LEU VAL LEU GLY ILE SER GLY LYS PRO LEU G1067 L1068 Q1069 V1070 T1071 I1072 E1076 SER ASP GLY SER SER THR
VAL VAL LEU HIS ILE GLU ALA SER PHE LYS GLY PRO ALA LEU THR ILE ASP VAL PRO ALA LEU GLN PHE GLY LEU LEU ARG LEU GLY LYS LYS ALA SER ILE SER ILE LEU GLN ILE ARG ASN VAL SER GLN LEU SER ALA SER VAL TRP HIS LEU LYS GLU SER PRO VAL CYS LEU ALA GLU GLN ARG
ASP GLU ASP VAL SER PRO ILE GLU PRO PHE CYS GLY GLN LEU GLU PRO LEU GLY ALA SER GLN CYS GLN ARG LEU GLN THR VAL LEU GLU GLU LEU GLU VAL GLU ASN GLY SER GLY SER TYR LEU PRO VAL TYR ALA GLU GLN GLN
PRO HIS VAL TYR LEU LYS ASN SER HIS LEU GLU PHE SER ASN LEU TYR LEU GLY VAL SER THR LYS SER ARG THR THR LEU VAL ASN GLY THR LEU LEU PRO THR ARG PHE HIS TRP GLY LYS LEU LEU GLY PRO GLN ALA ASP LEU CYS THR HIS MET THR VAL ALA SER PRO THR GLN GLY LEU
R1238 N1239 T1240 P1246 K1249 I1252 T1253 R1254 F1255 T1266 R1267 S1268 L1269 R1270 L1271 S1274 D1278 I1279 R1280 E1284 T1285 Y1286 I1287 P1288 K1291 A1292 D1293 R1294 L1295 LEU GLU LEU LEU VAL PHE TYR GLY PRO PRO PHE PRO LEU ARG ASP GLN ASP GLY SER GLU ILE VAL
CYS PRO GLU THR SER GLU ALA SER LEU PRO GLY SER PRO CYS PRO SER ASN VAL SER VAL SER SER HIS THR VAL PRO SER THR VAL SER SER GLY GLY GLY GLY THR ARG ALA GLU GLU GLN ILE MET SER VAL ILE LEU GLN R1367 H1375 I1376 I1379 L1384 V1385 I1386 P1387
WORLDWIDE PDB PROTEIN DATA BANK



• Molecule 15: Sperm-associated antigen 16 protein

Chain Q:





• Molecule 15: Sperm-associated antigen 16 protein

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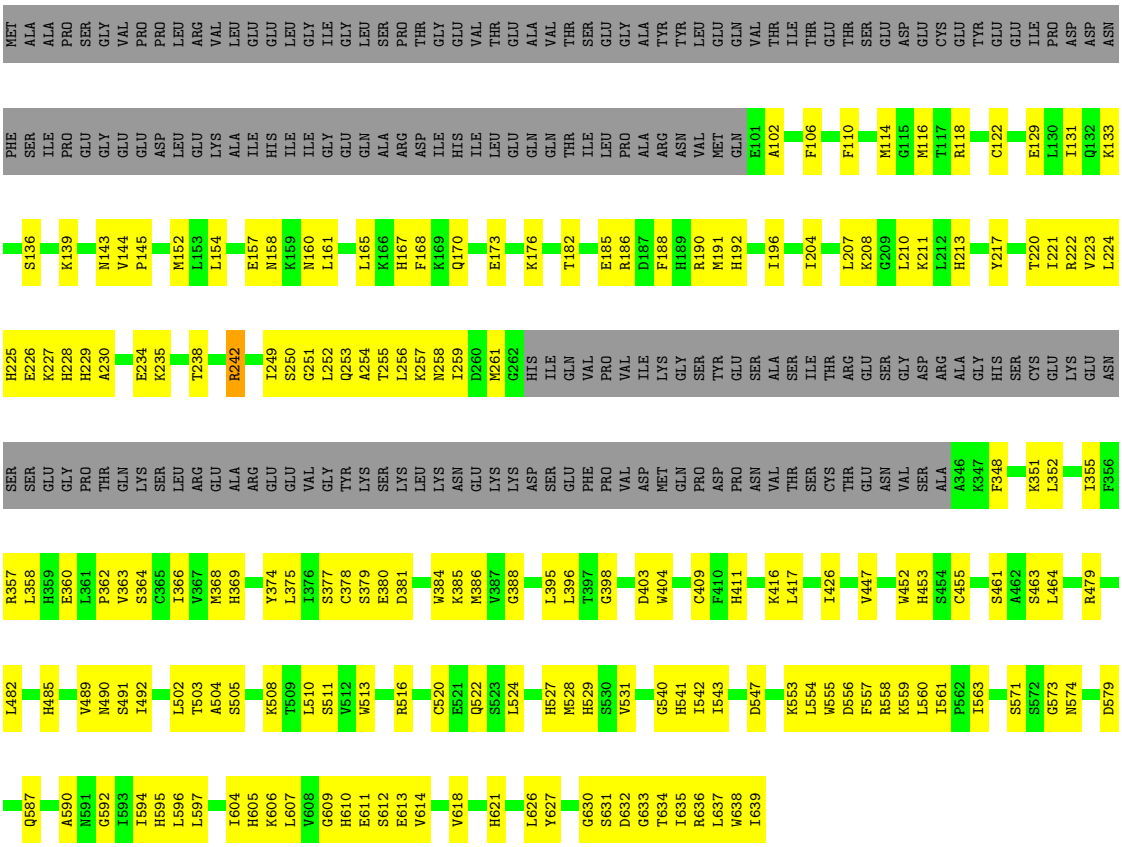
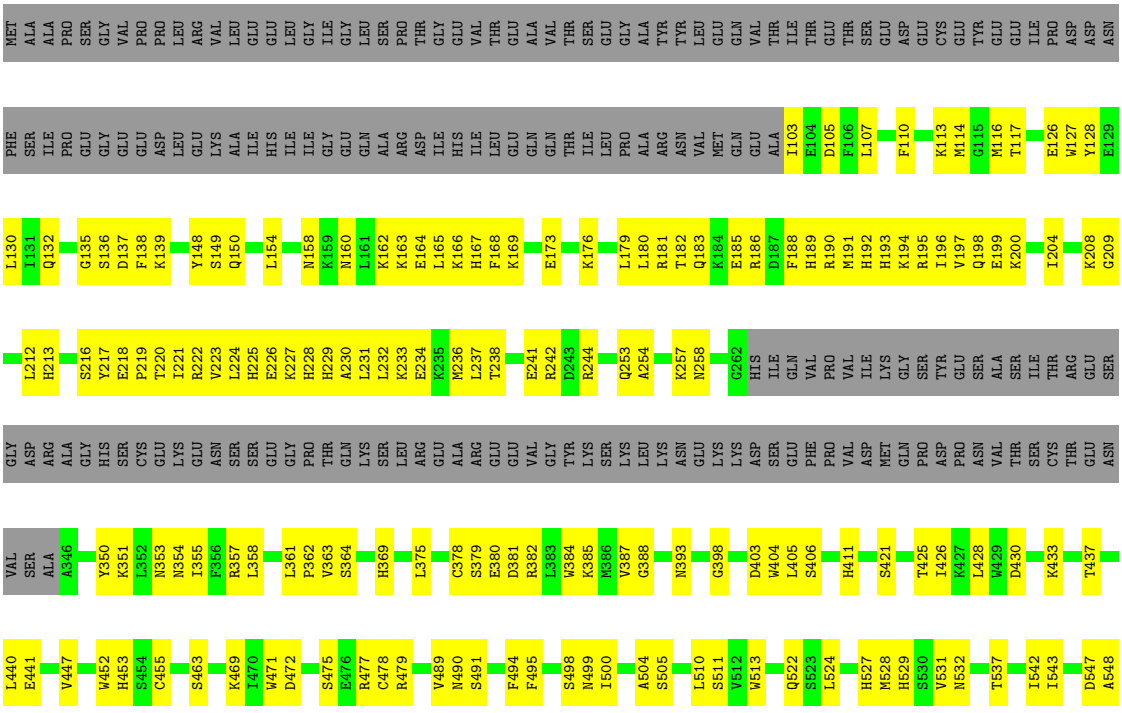
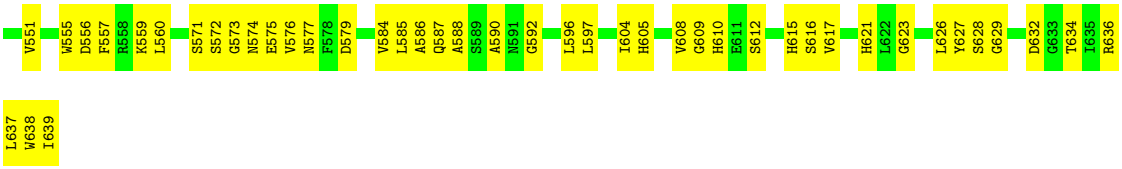


• Molecule 15: Sperm-associated antigen 16 protein

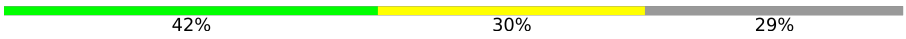
Chain S: 39% 32% 29%

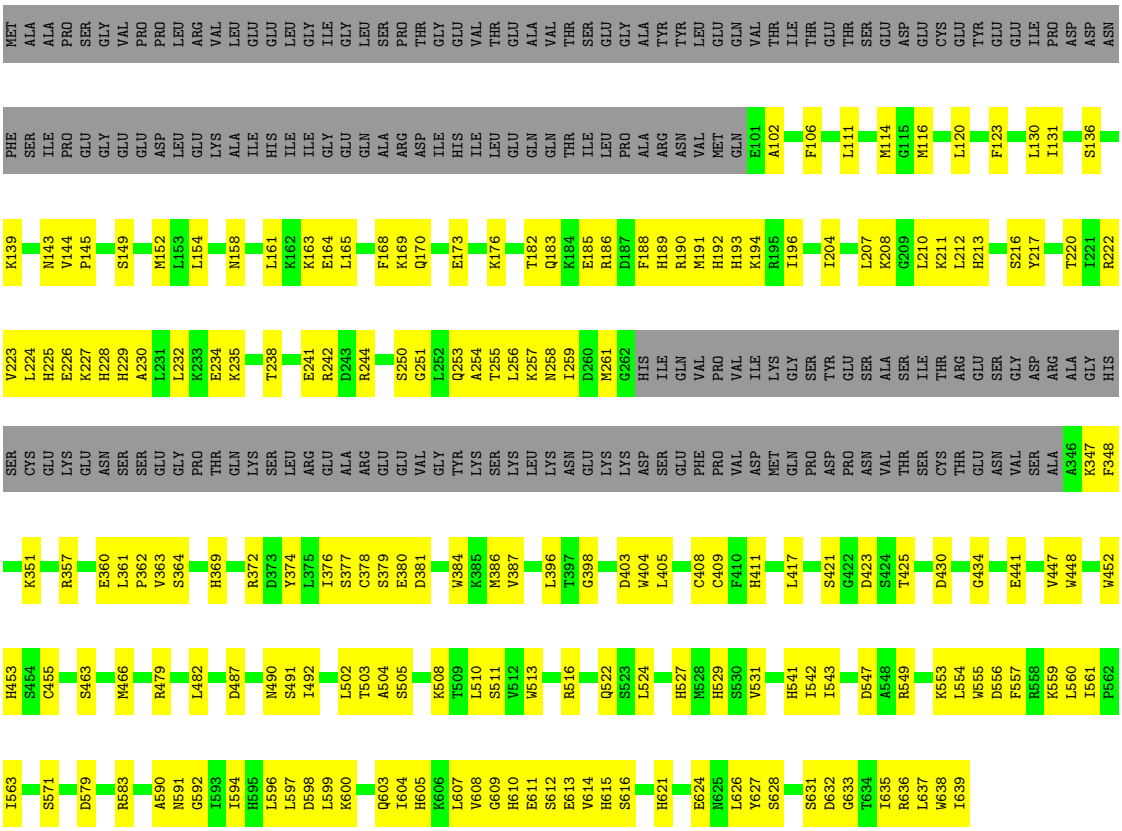




• Molecule 15: Sperm-associated antigen 16 protein

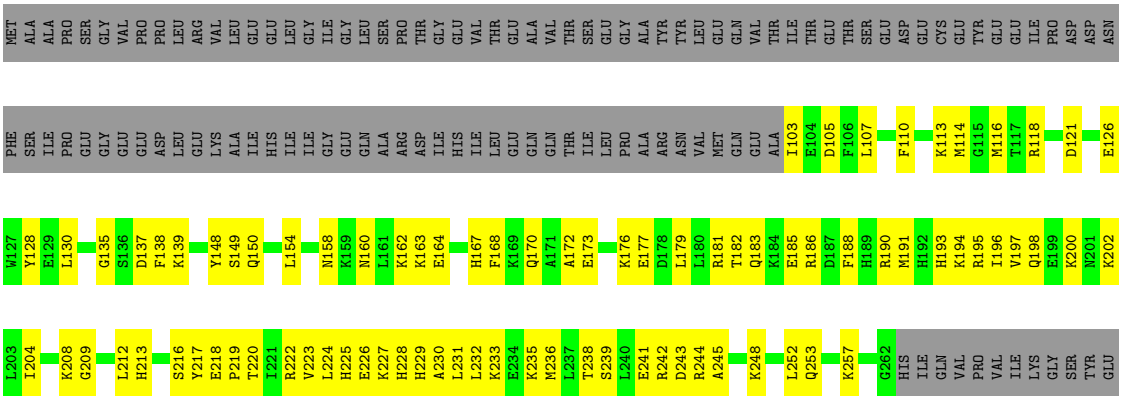
Chain T:

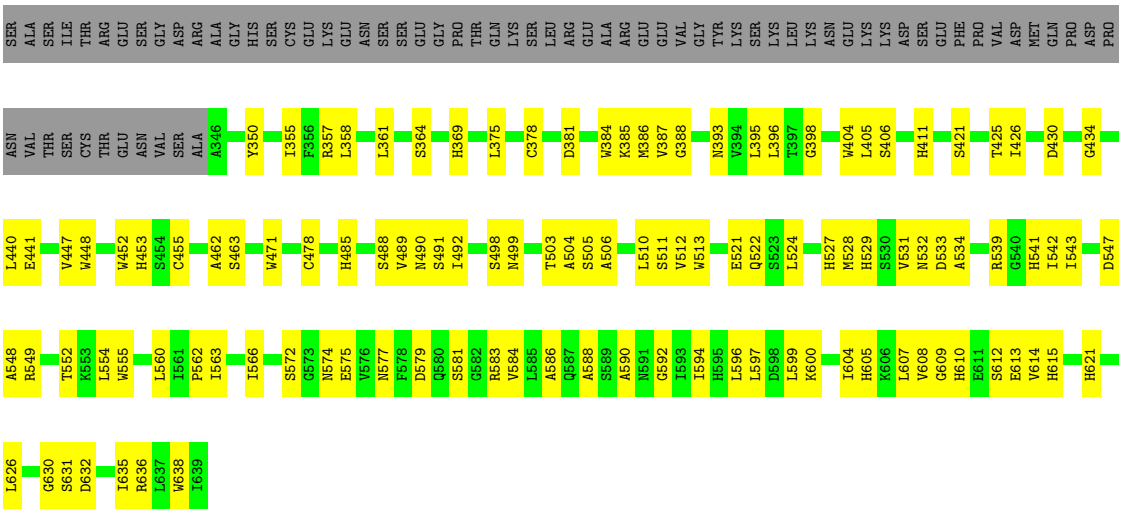




• Molecule 15: Sperm-associated antigen 16 protein

Chain U:





• Molecule 15: Sperm-associated antigen 16 protein

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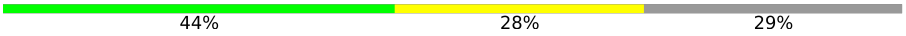

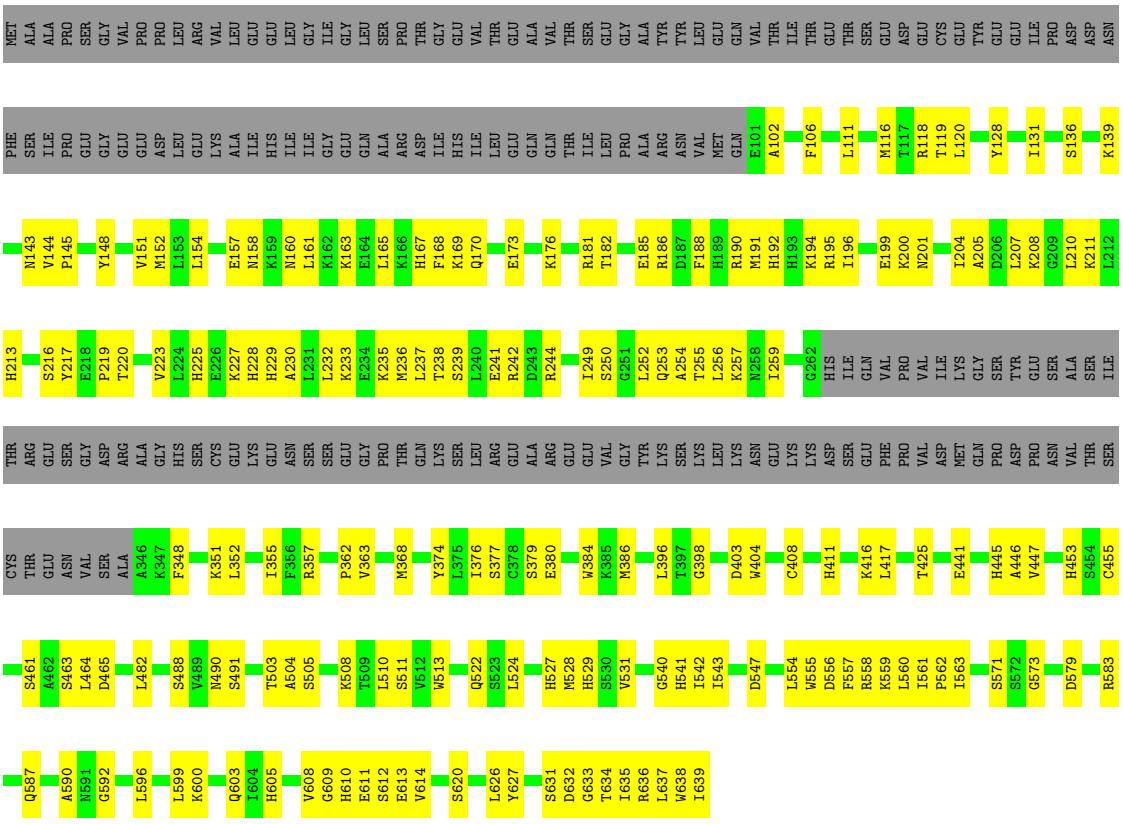

• Molecule 16: Sperm-associated antigen 17

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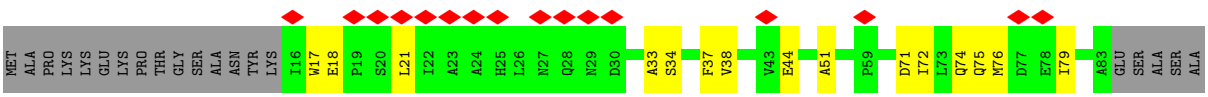
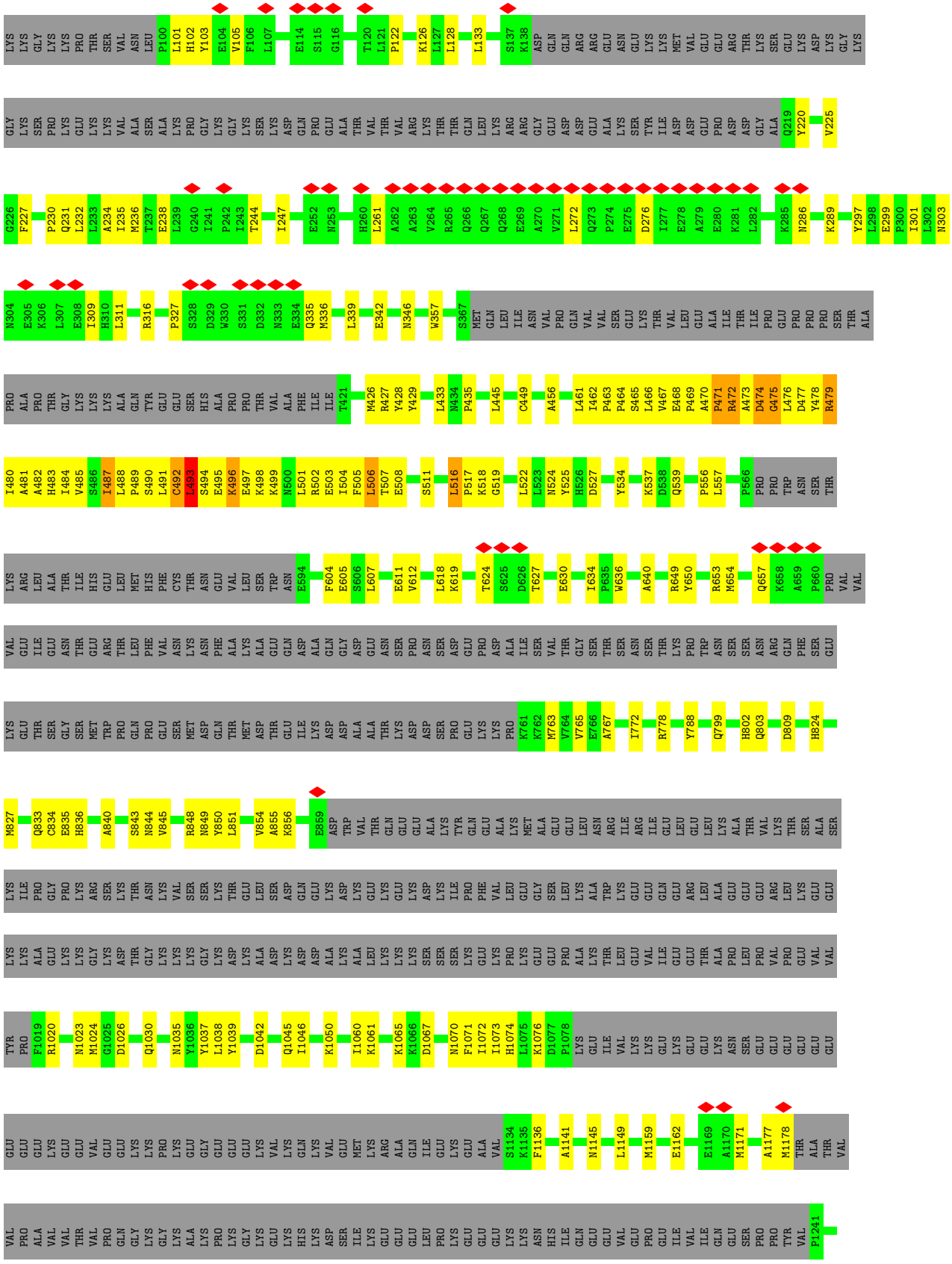
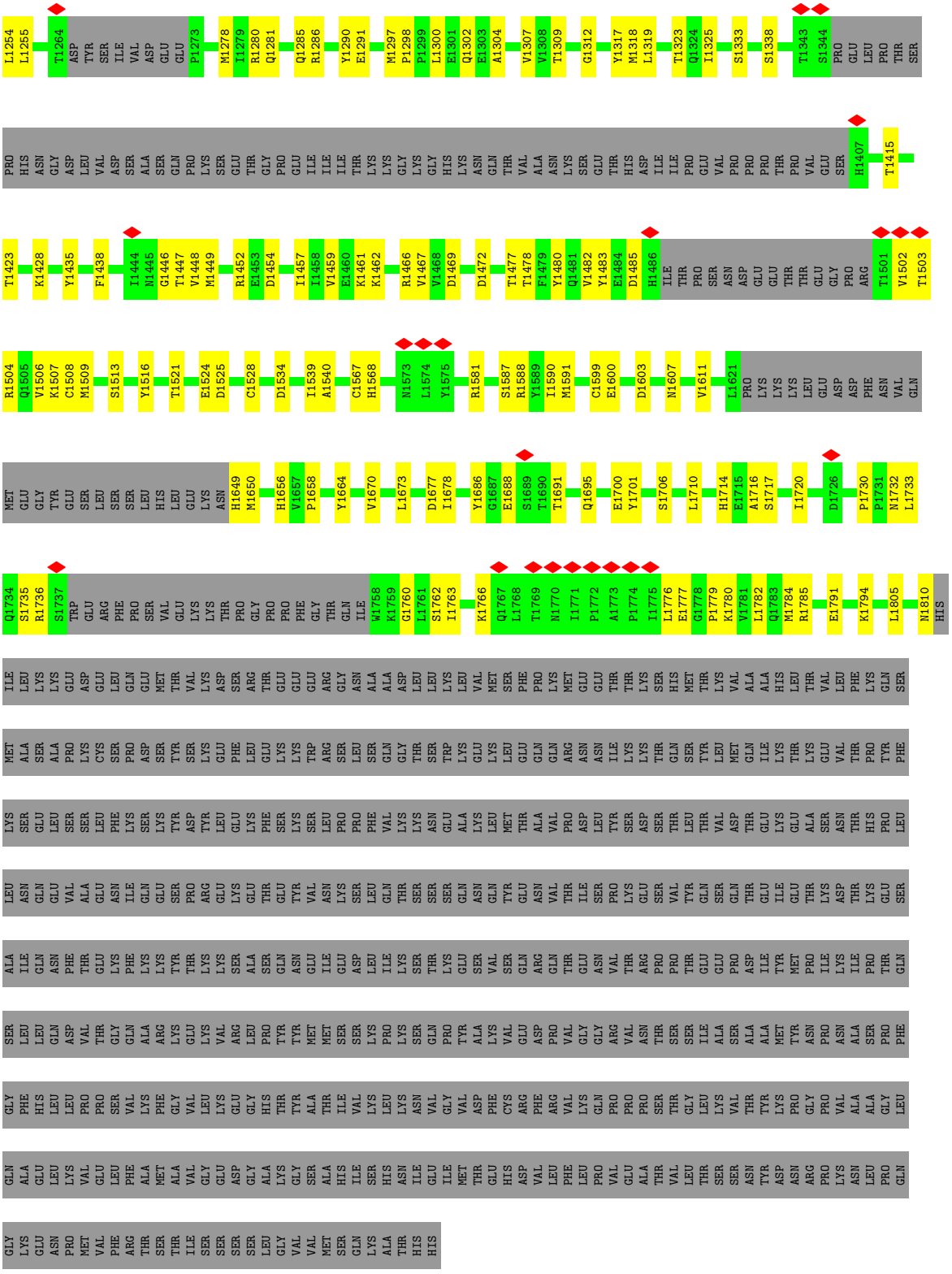
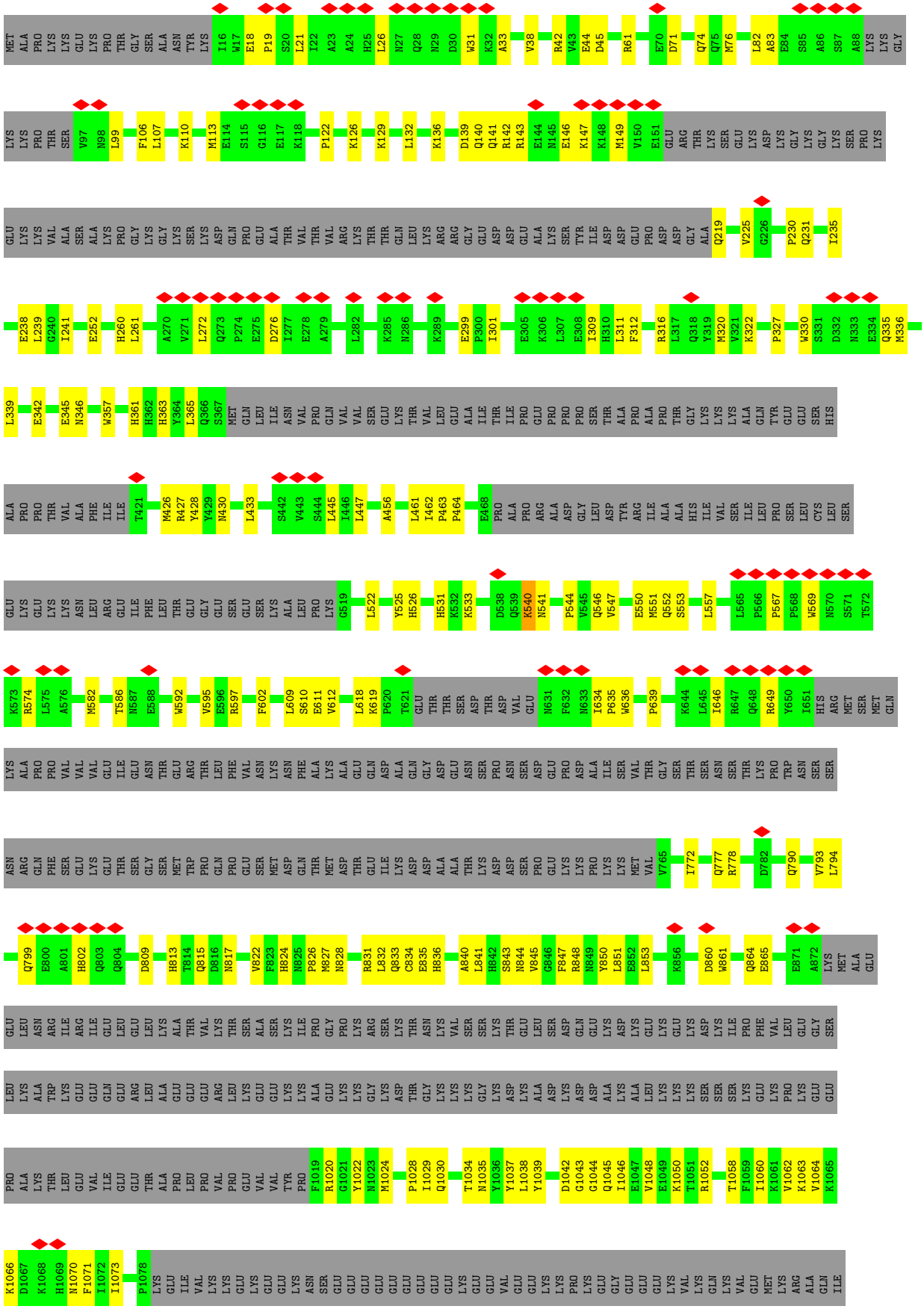


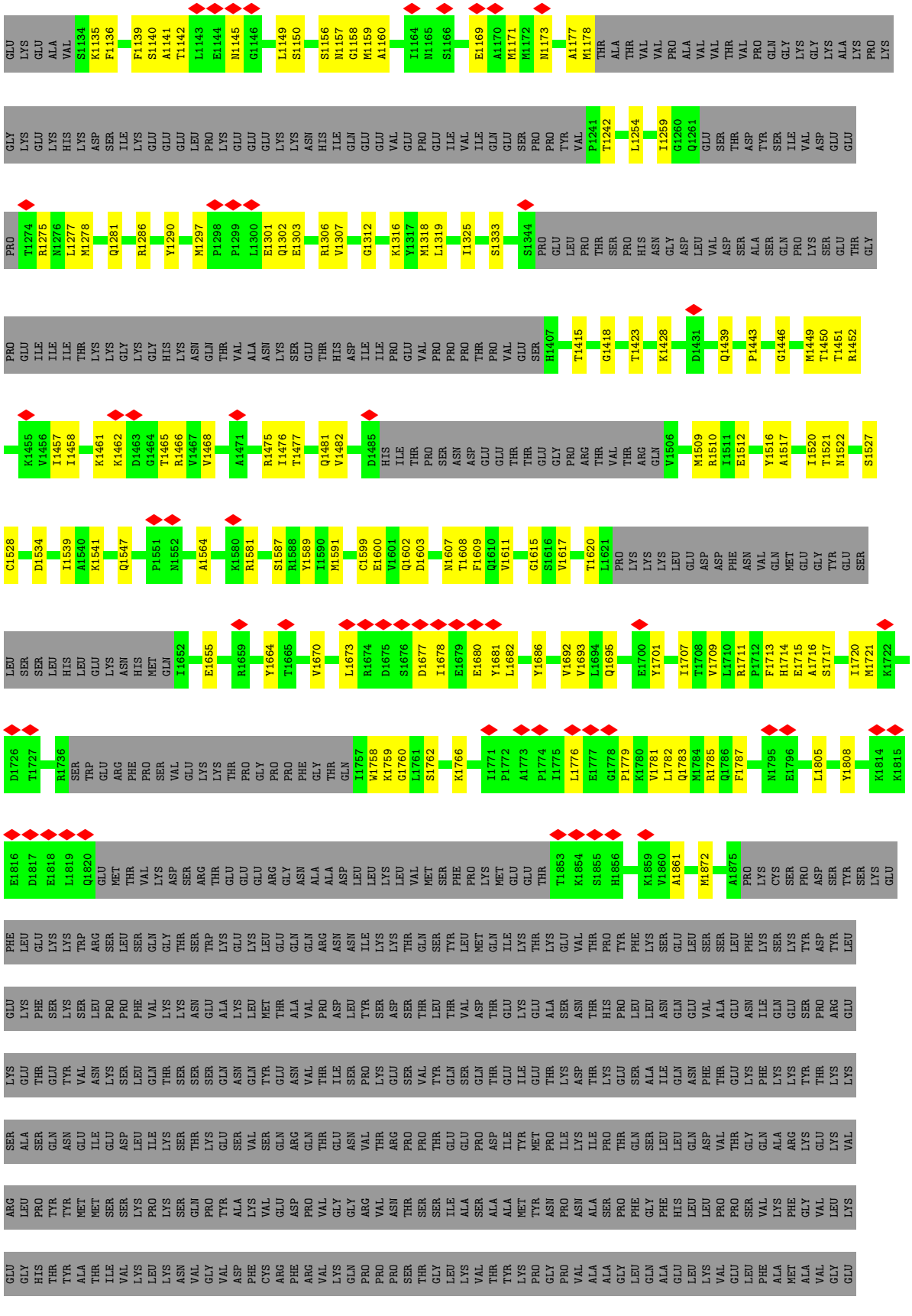


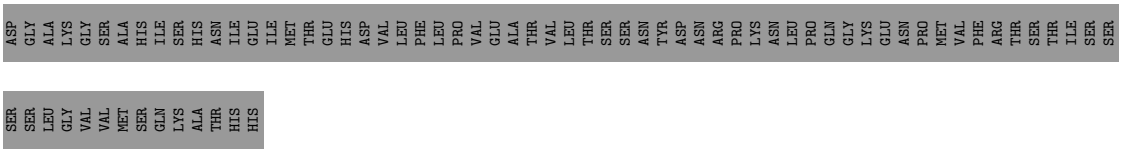


• Molecule 16: Sperm-associated antigen 17

Chain y:

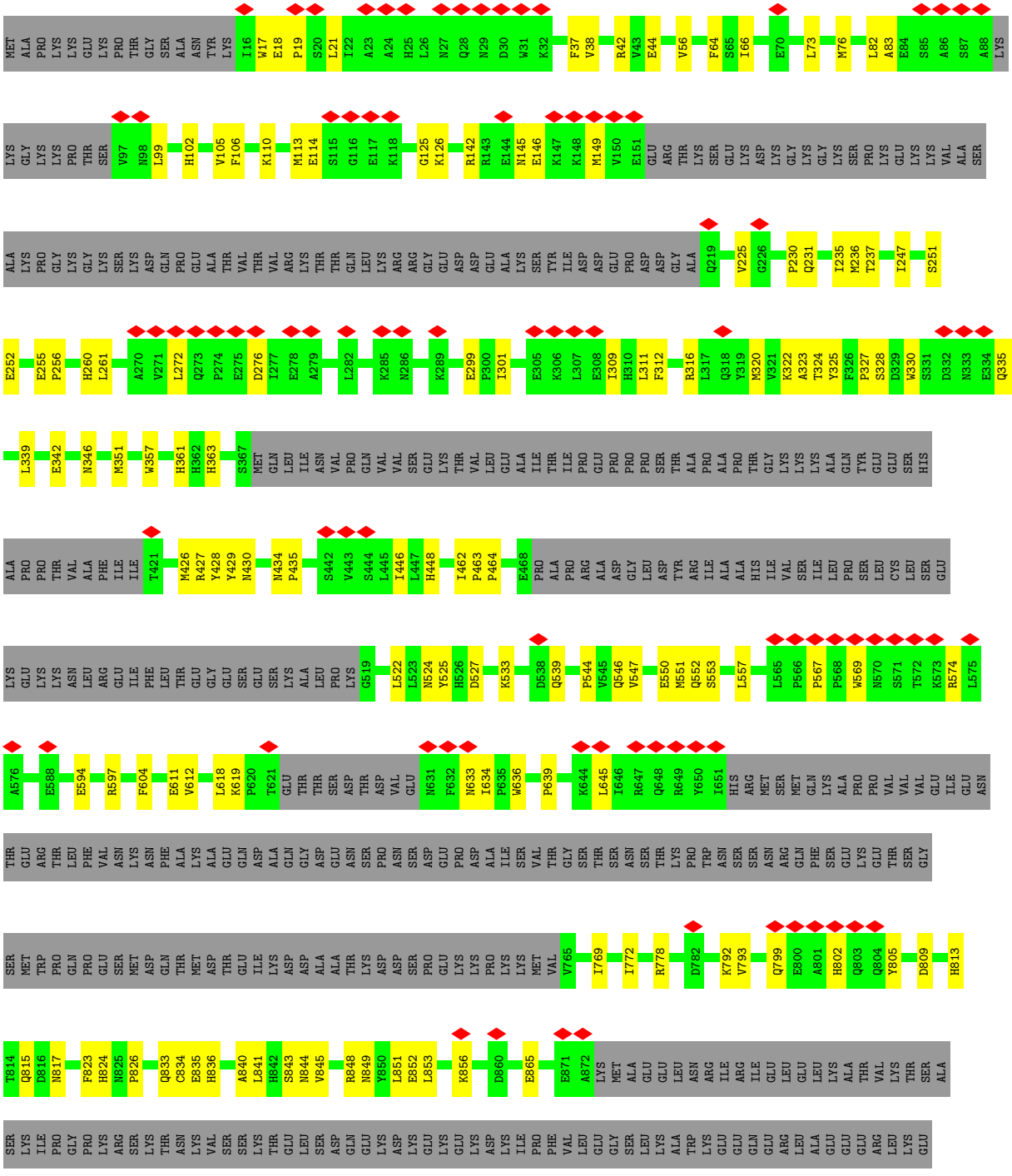


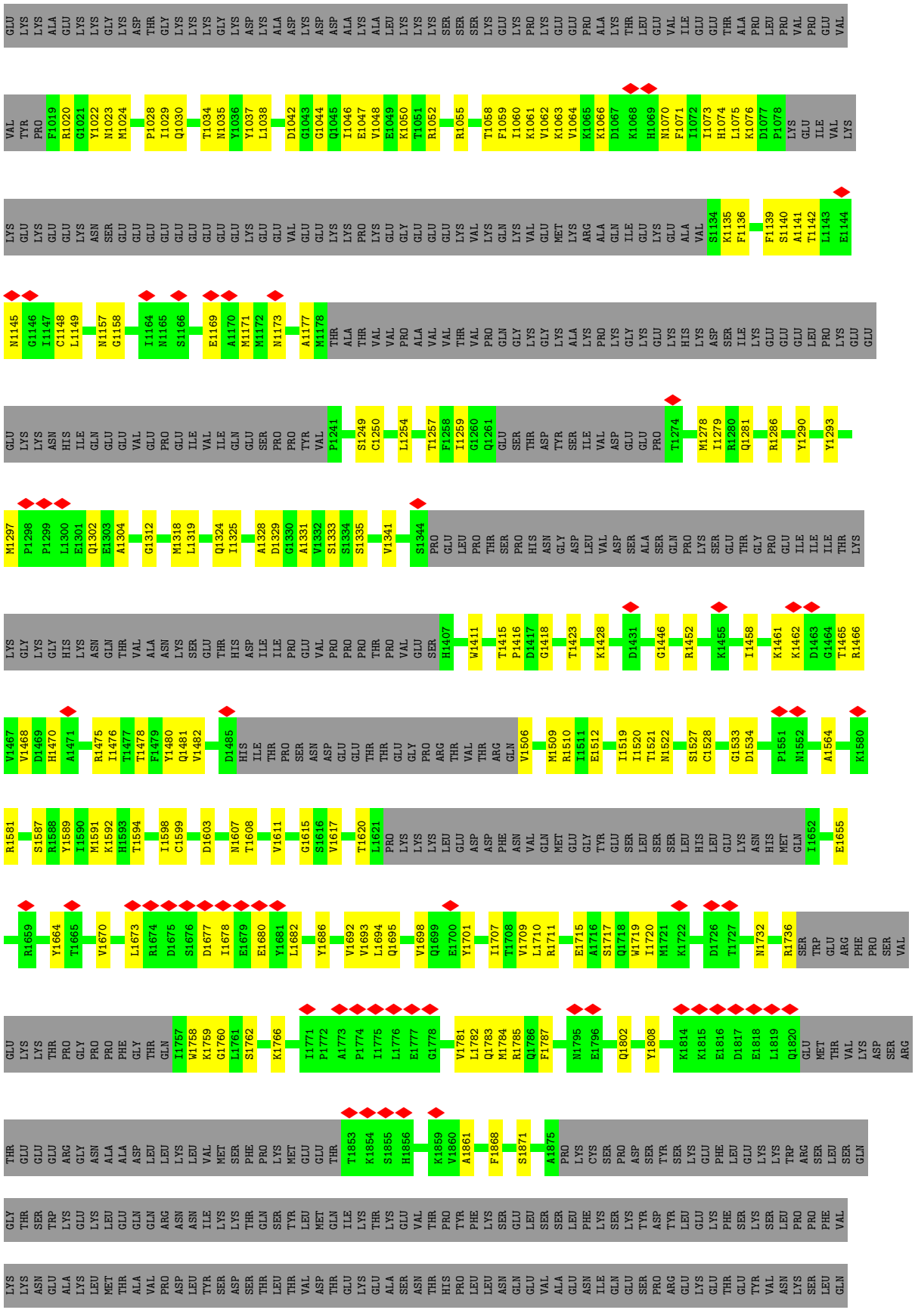


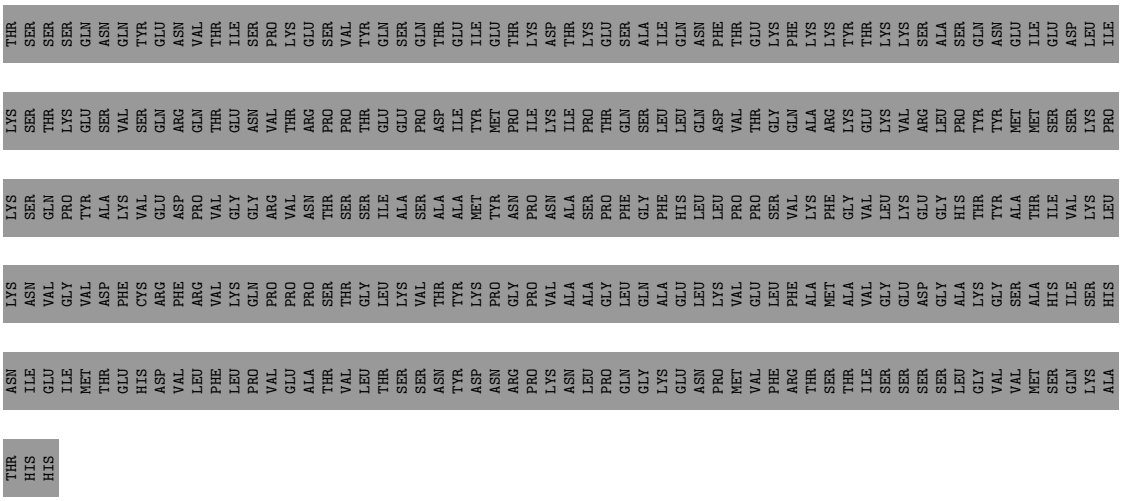


• Molecule 16: Sperm-associated antigen 17

Chain z:

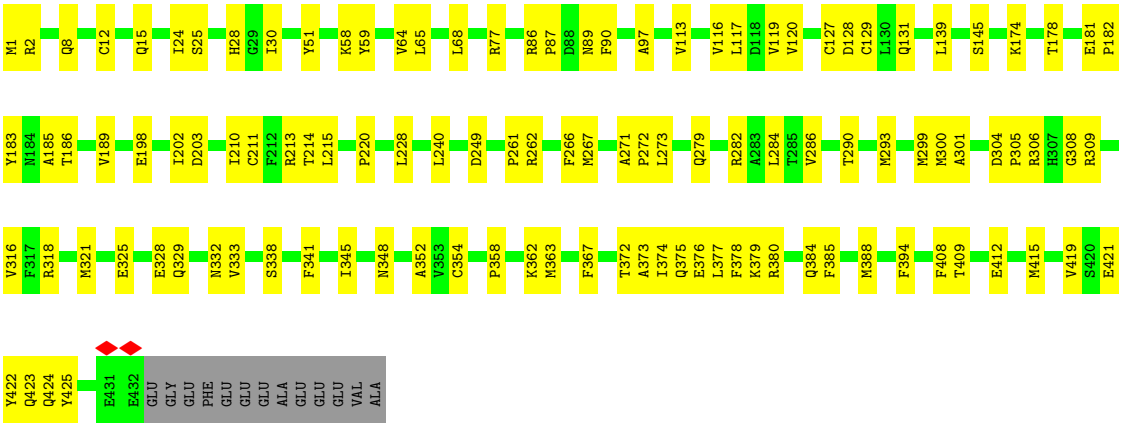






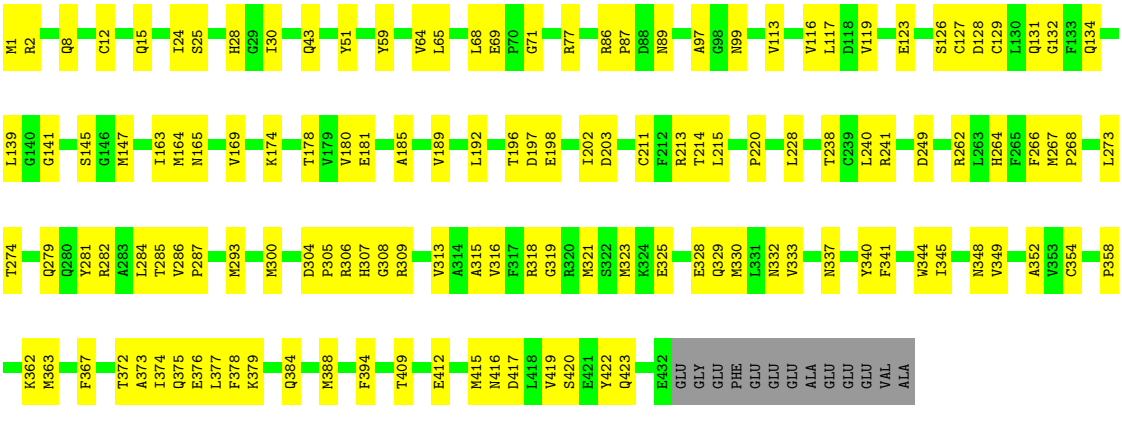
• Molecule 17: Tubulin beta-4B chain

Chain Ab:



• Molecule 17: Tubulin beta-4B chain

Chain Ad:



• Molecule 17: Tubulin beta-4B chain

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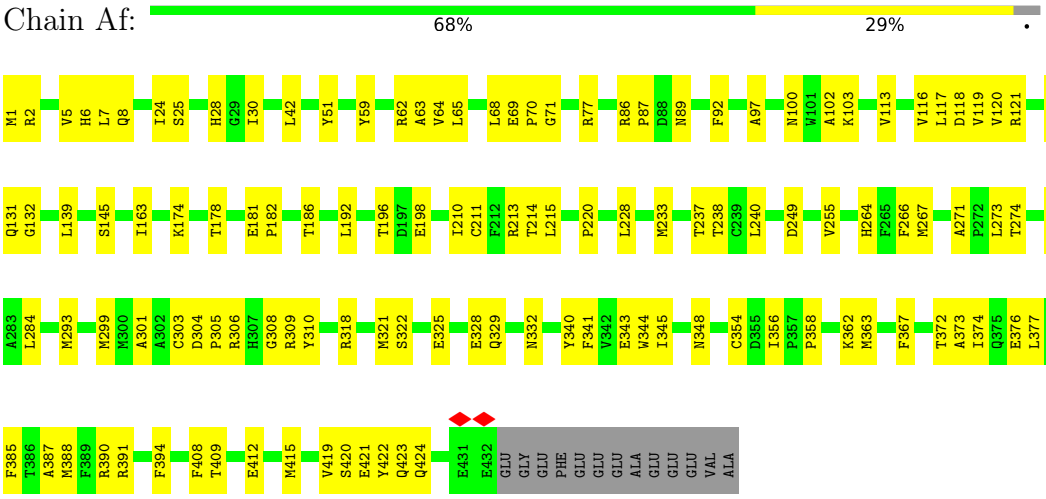
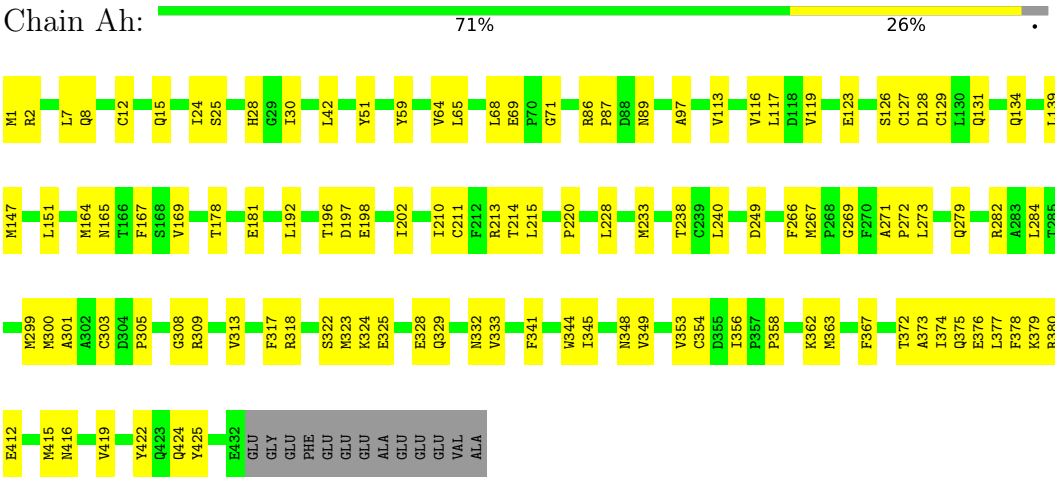


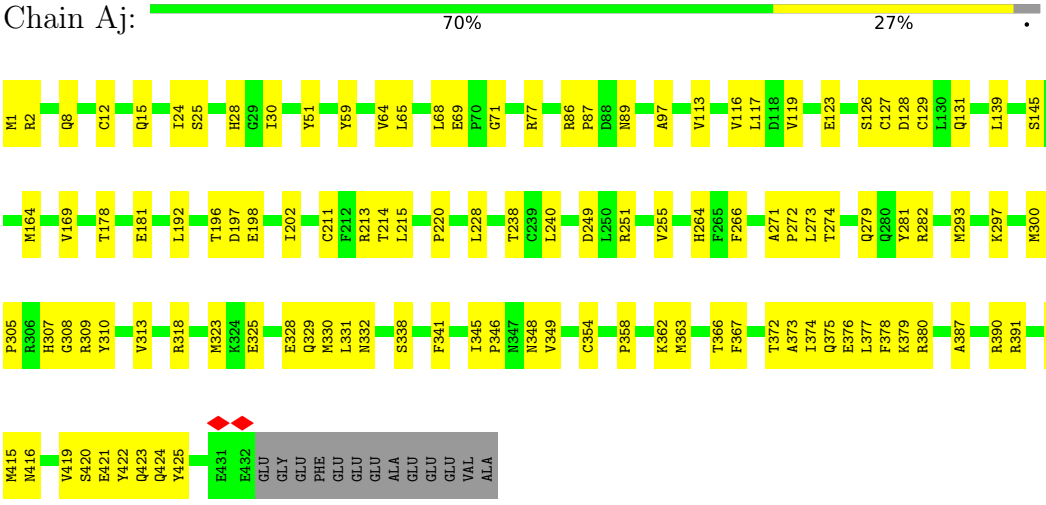
- Molecule 17: Tubulin beta-4B chain

Chain Ah:



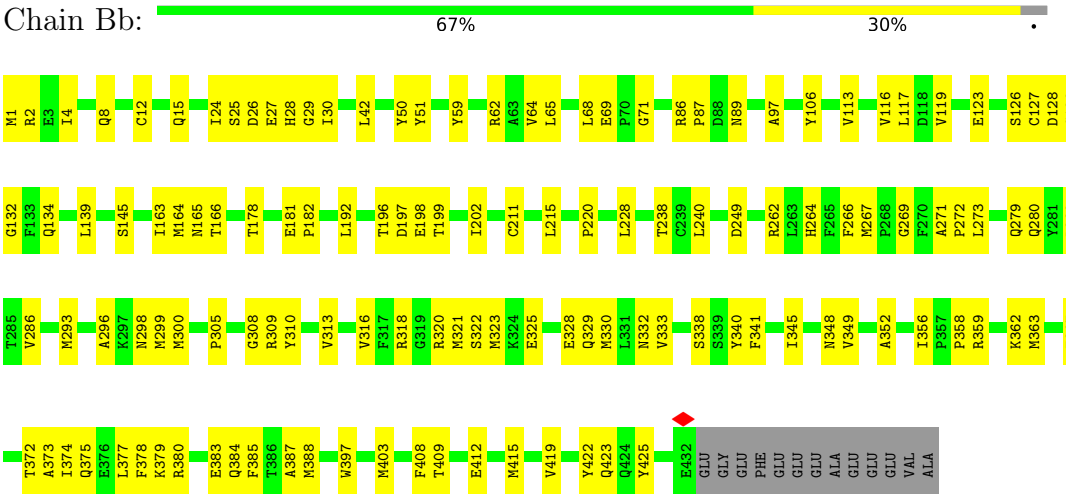
- Molecule 17: Tubulin beta-4B chain

Chain Aj:



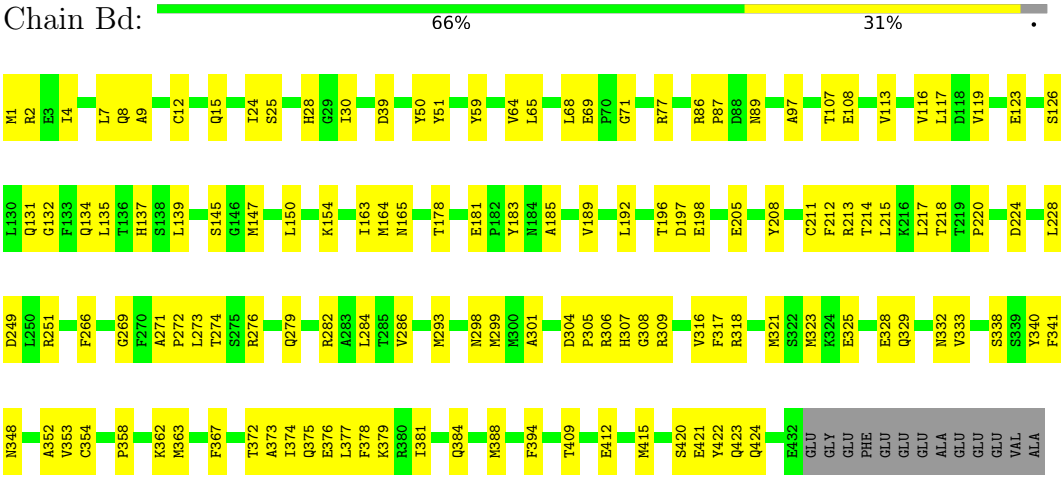
- Molecule 17: Tubulin beta-4B chain

Chain Bb:



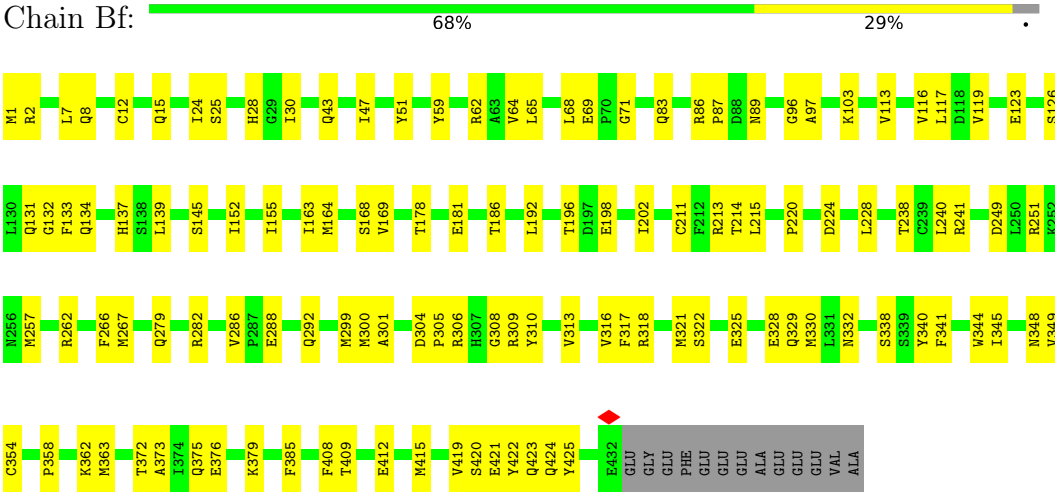
• Molecule 17: Tubulin beta-4B chain

Chain Bd:



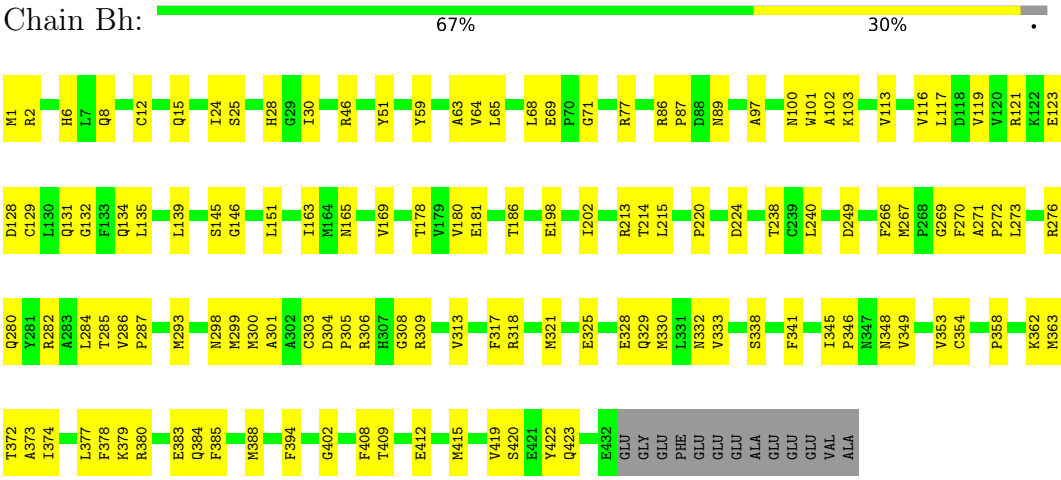
• Molecule 17: Tubulin beta-4B chain

Chain Bf:



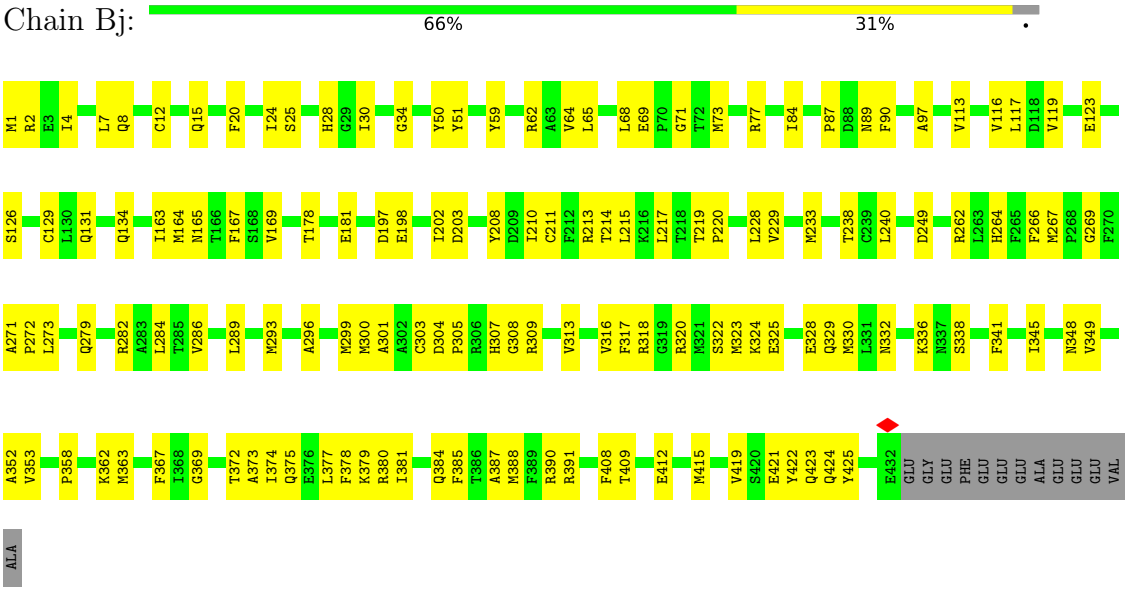
• Molecule 17: Tubulin beta-4B chain

Chain Bh:



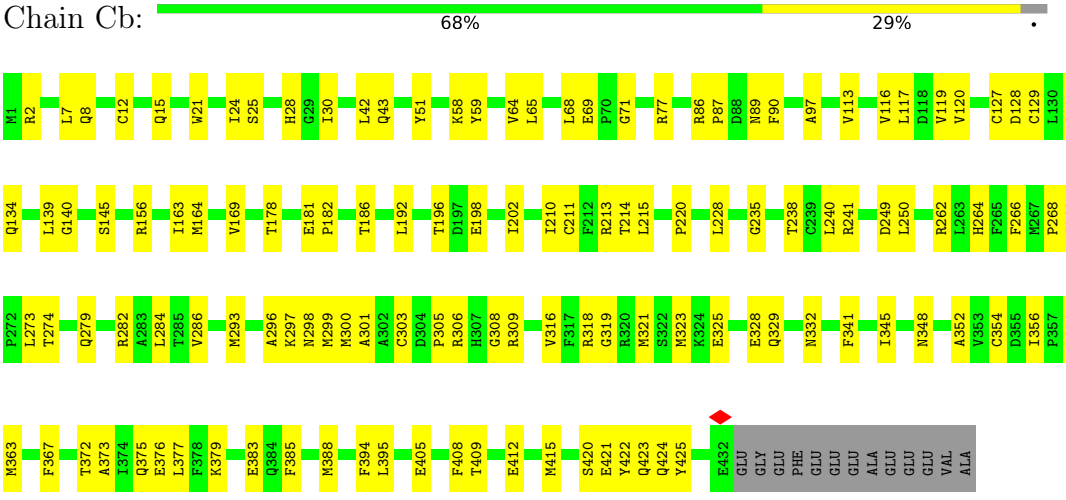
• Molecule 17: Tubulin beta-4B chain

Chain Bj:



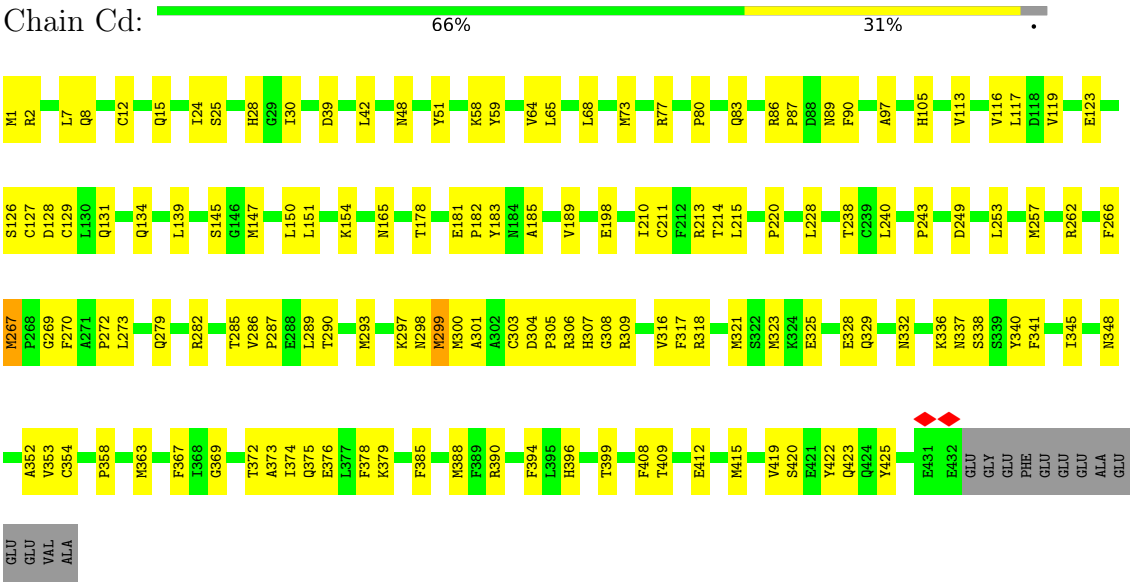
• Molecule 17: Tubulin beta-4B chain

Chain Cb:



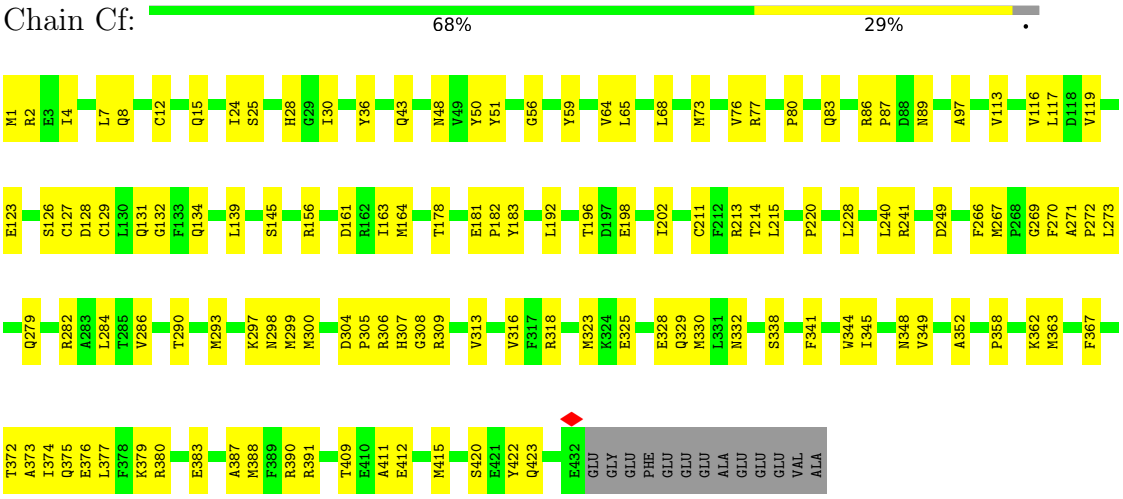
• Molecule 17: Tubulin beta-4B chain

Chain Cd:



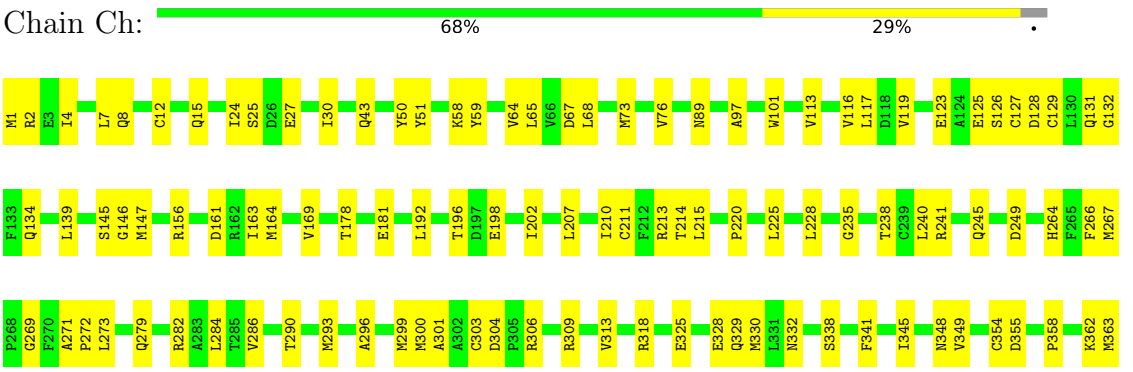
• Molecule 17: Tubulin beta-4B chain

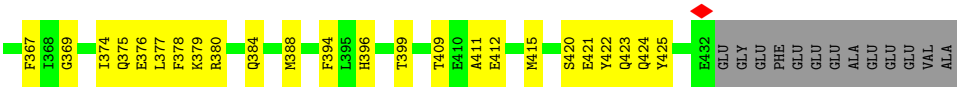
Chain Cf:



• Molecule 17: Tubulin beta-4B chain

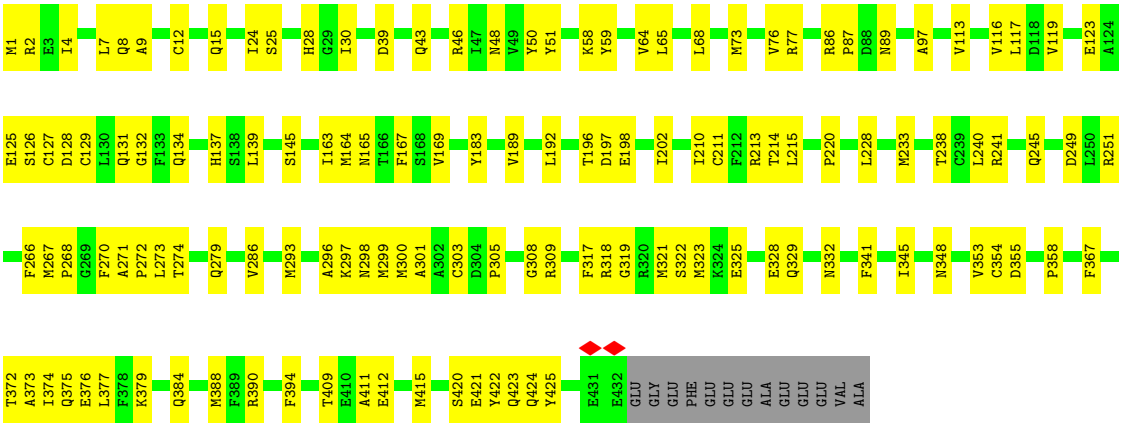
Chain Ch:





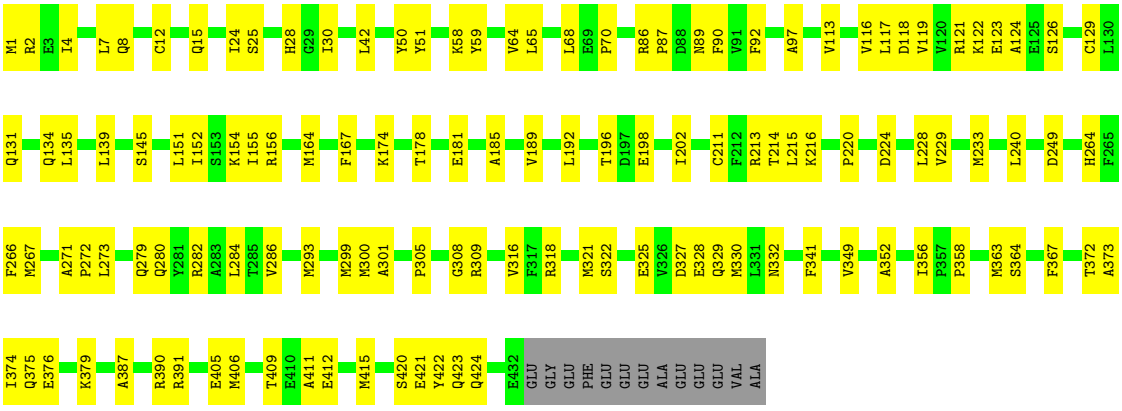
• Molecule 17: Tubulin beta-4B chain

Chain Cj:



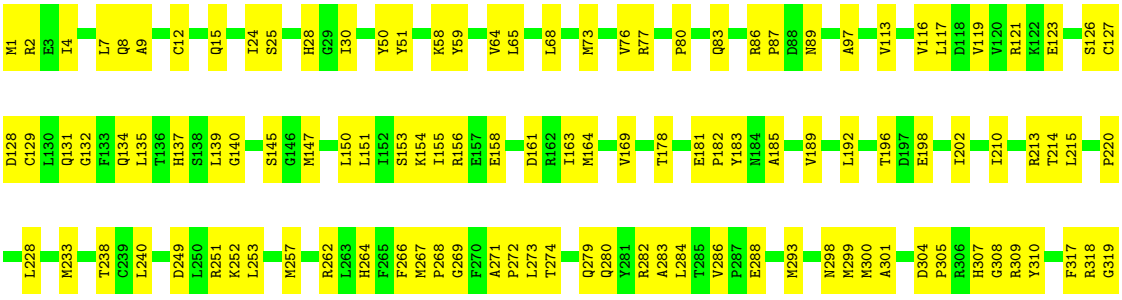
• Molecule 17: Tubulin beta-4B chain

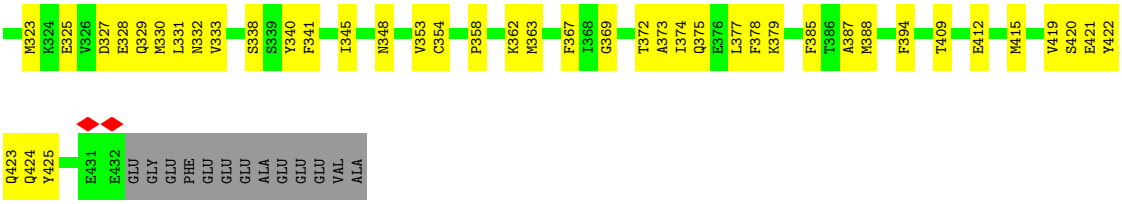
Chain Db:



• Molecule 17: Tubulin beta-4B chain

Chain Dd:





• Molecule 17: Tubulin beta-4B chain

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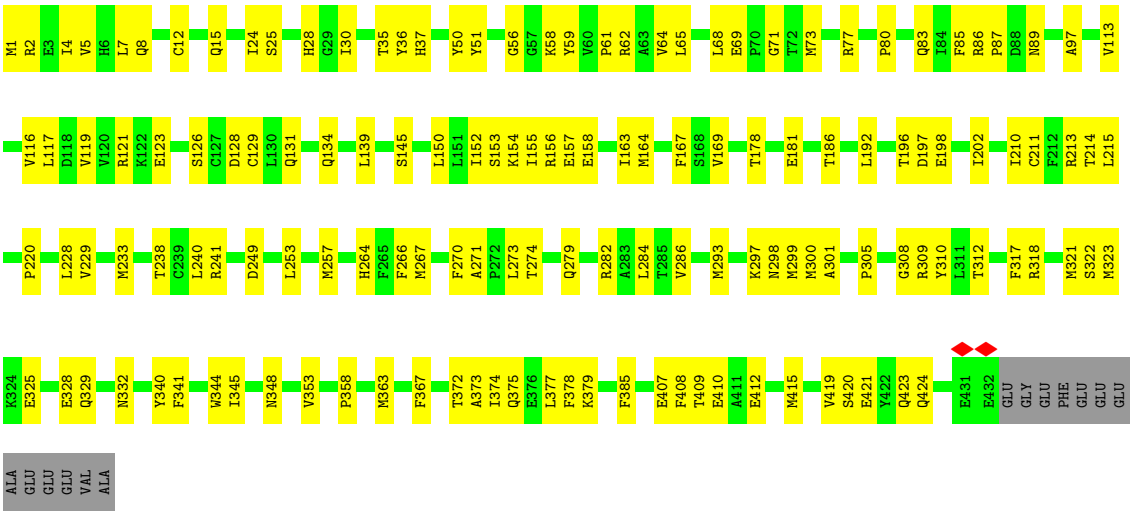

• Molecule 17: Tubulin beta-4B chain

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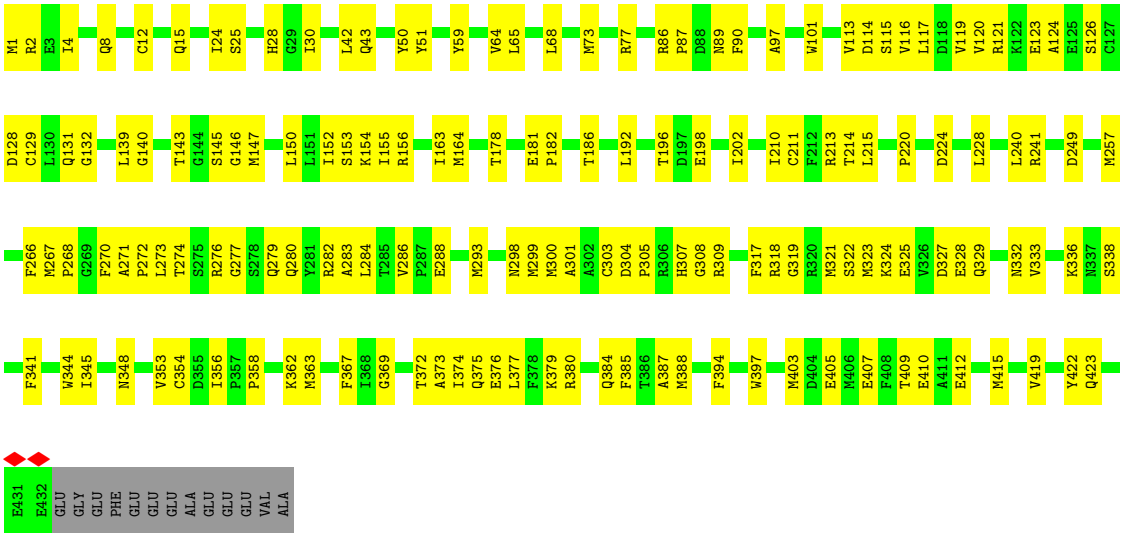

• Molecule 17: Tubulin beta-4B chain

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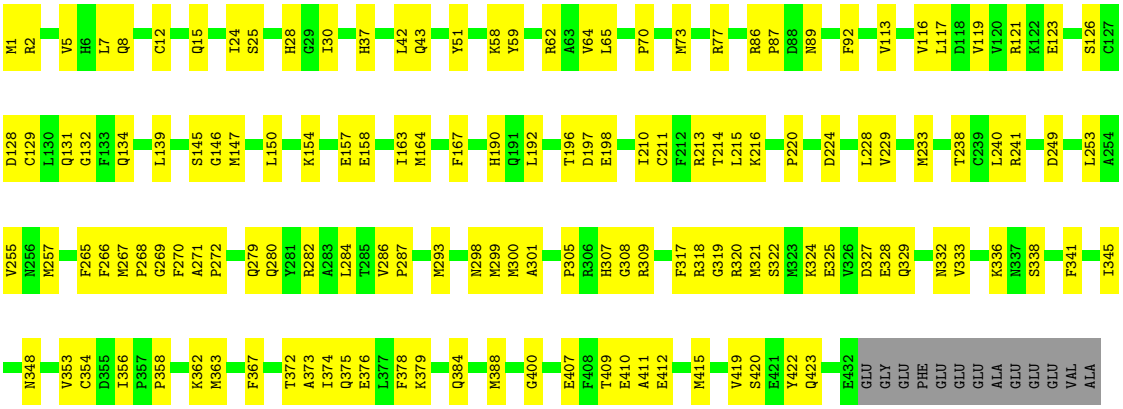

• Molecule 17: Tubulin beta-4B chain

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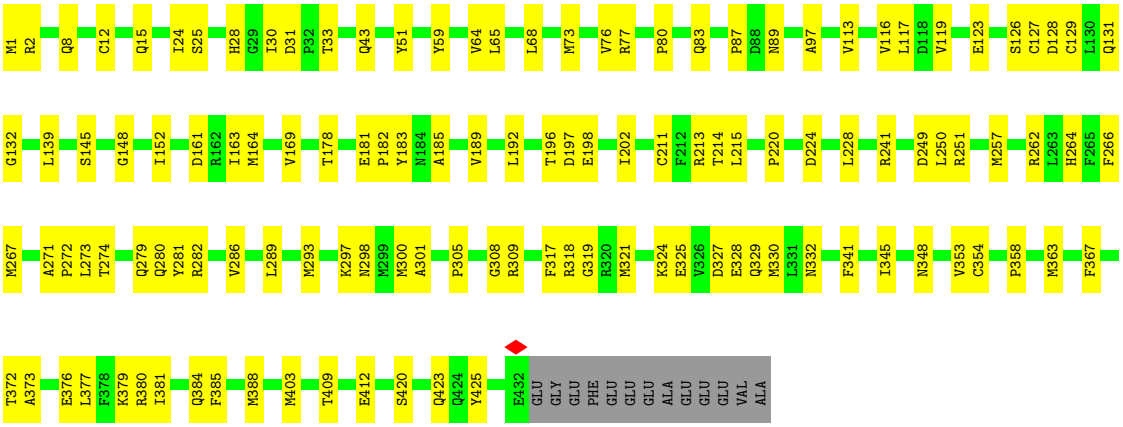

• Molecule 17: Tubulin beta-4B chain

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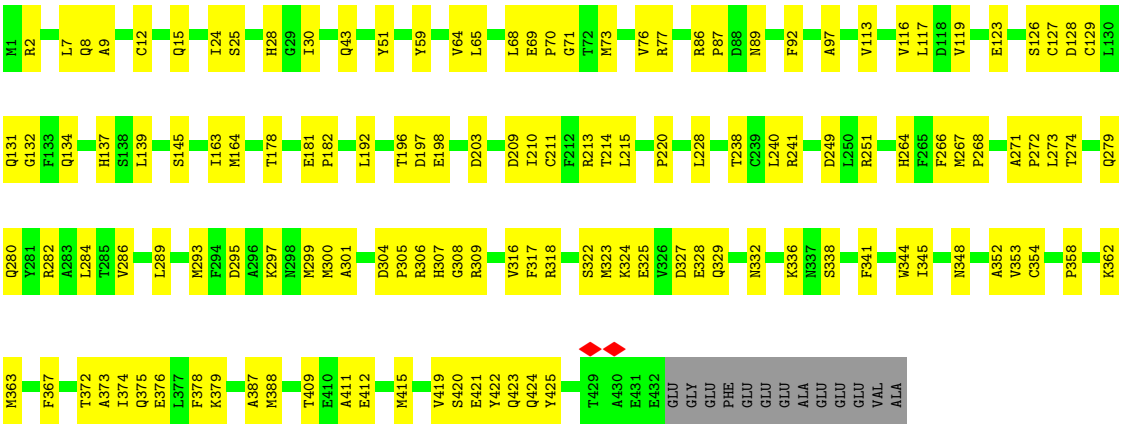
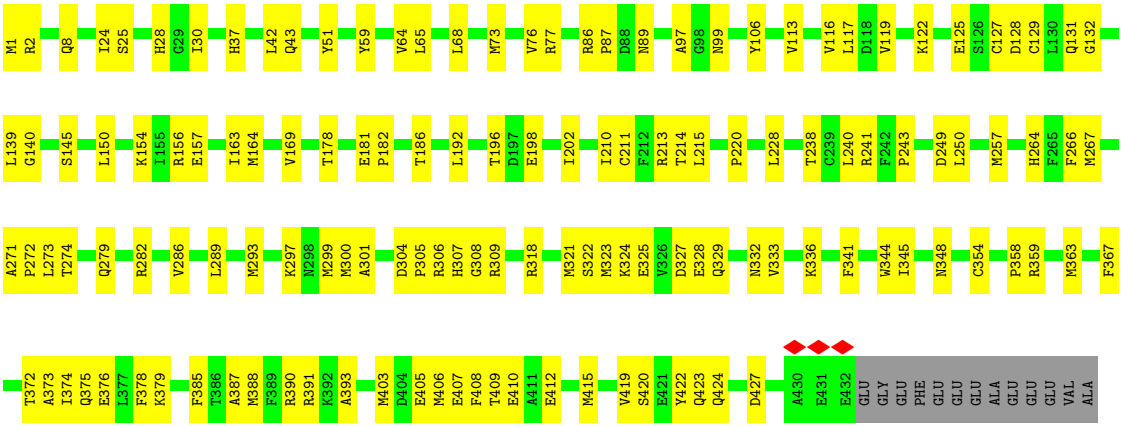


• Molecule 17: Tubulin beta-4B chain

Chain Ef:



• Molecule 17: Tubulin beta-4B chain

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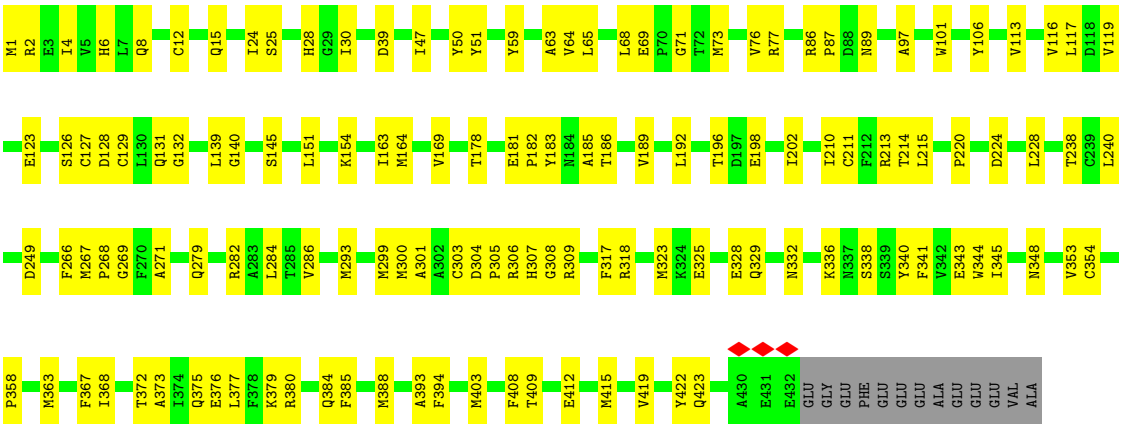

• Molecule 17: Tubulin beta-4B chain

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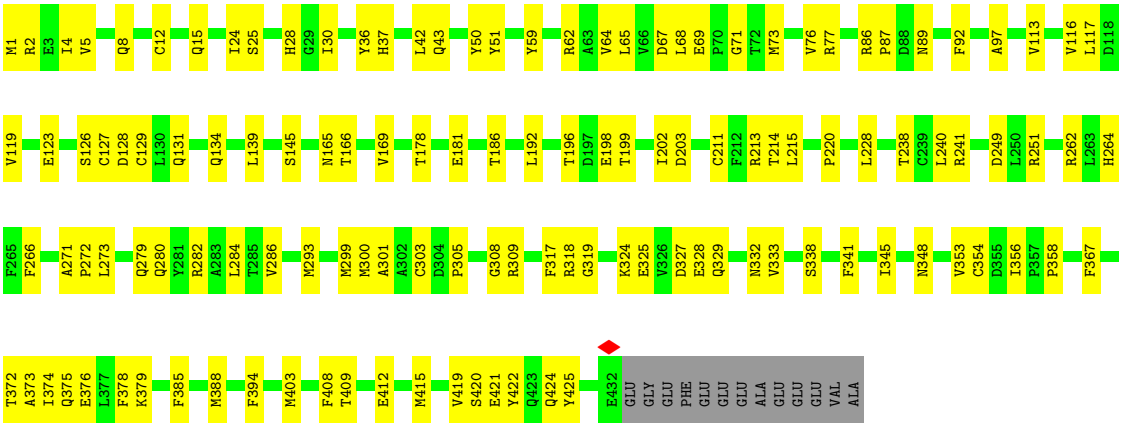
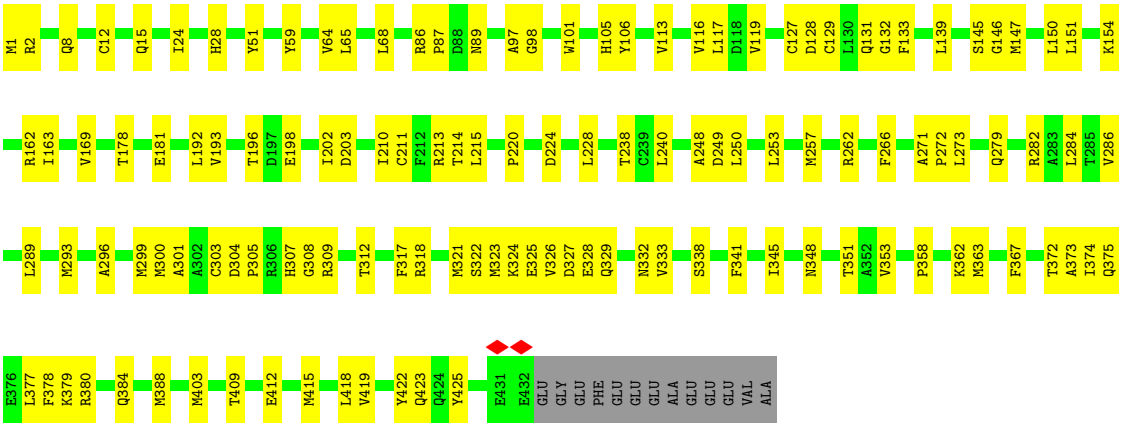


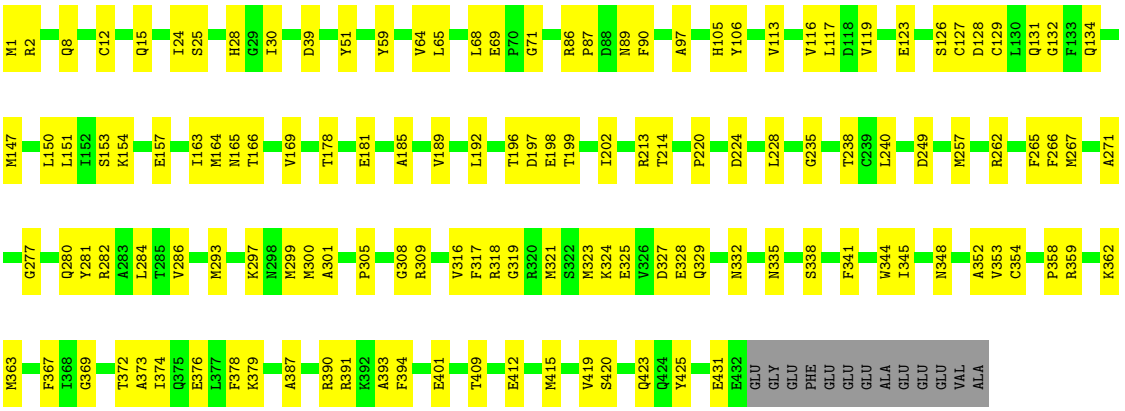
• Molecule 17: Tubulin beta-4B chain

Chain Fb:



• Molecule 17: Tubulin beta-4B chain

Chain Fd:



• Molecule 17: Tubulin beta-4B chain

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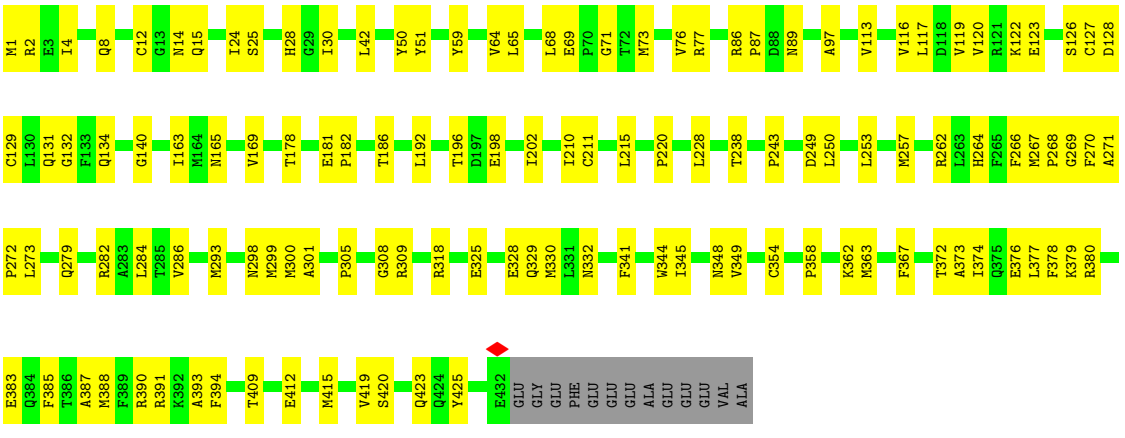
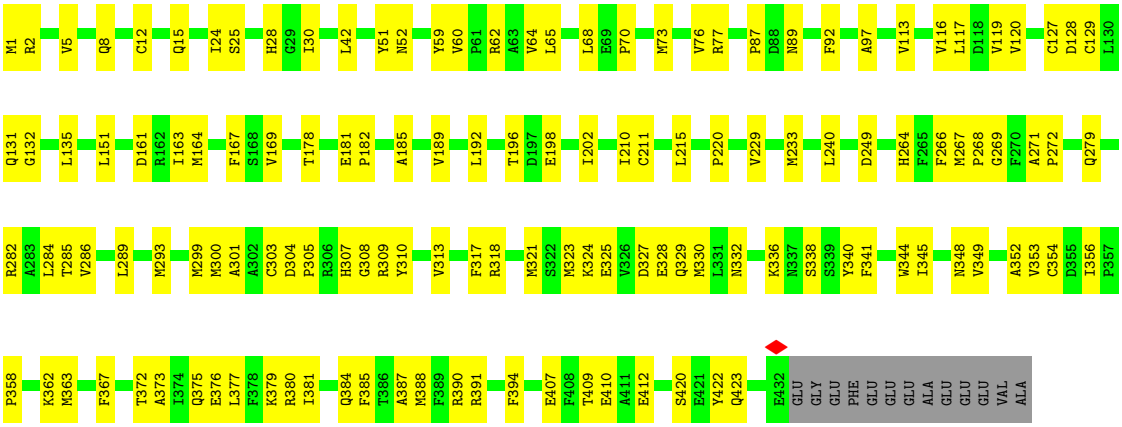


• Molecule 17: Tubulin beta-4B chain

Chain Fh:



• Molecule 17: Tubulin beta-4B chain

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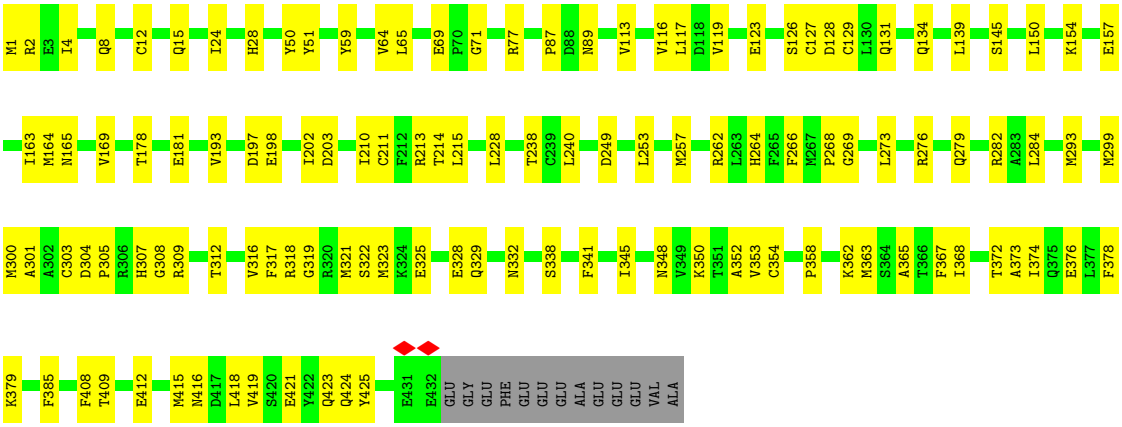
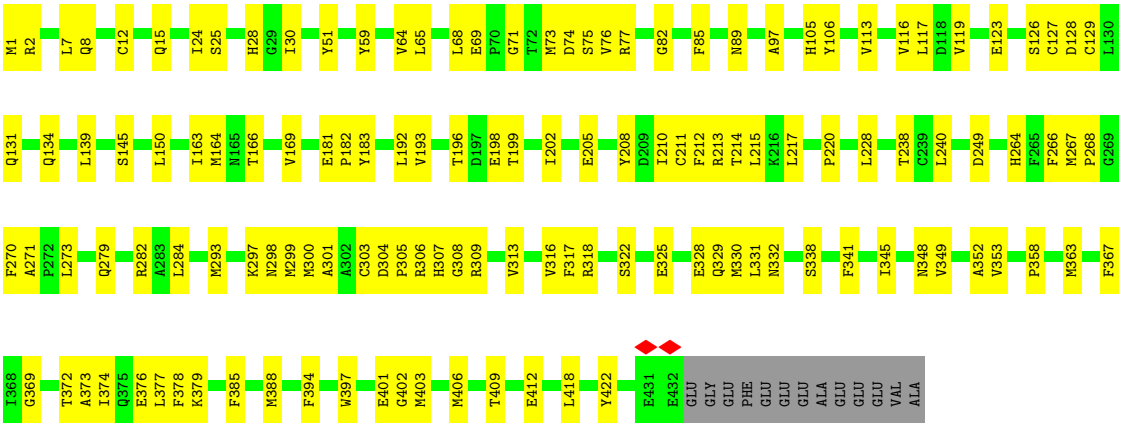


• Molecule 17: Tubulin beta-4B chain

Chain Gb:



• Molecule 17: Tubulin beta-4B chain

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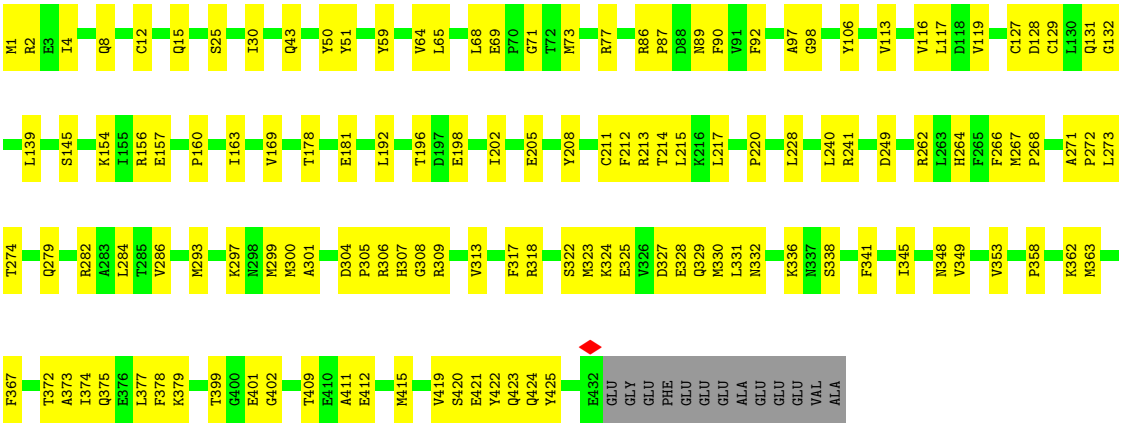

• Molecule 17: Tubulin beta-4B chain

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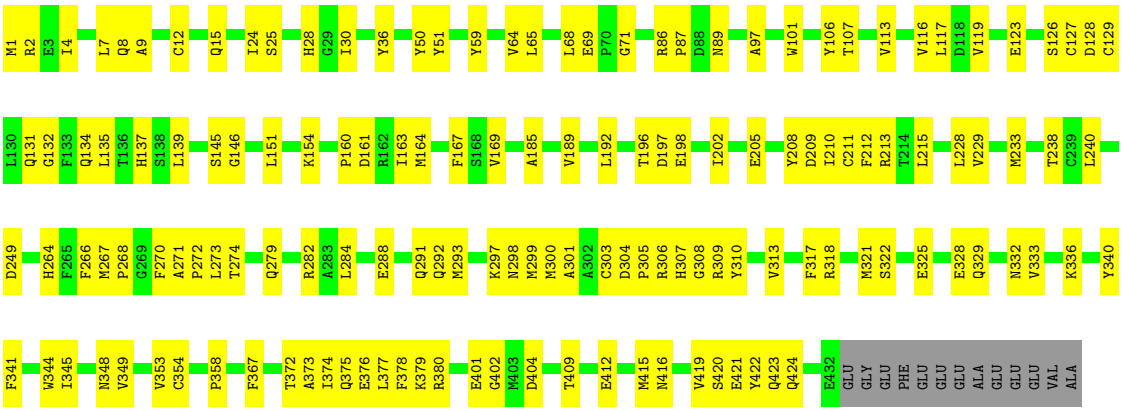

• Molecule 17: Tubulin beta-4B chain

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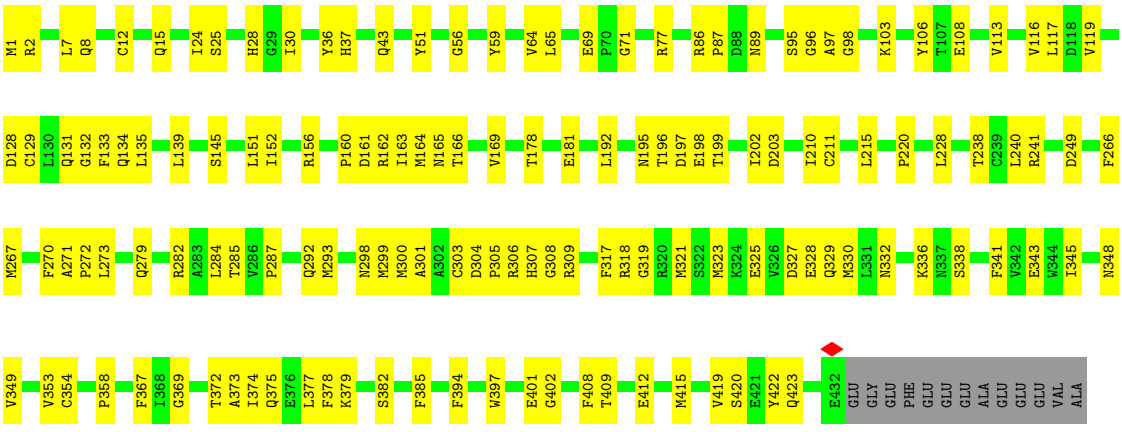

• Molecule 17: Tubulin beta-4B chain

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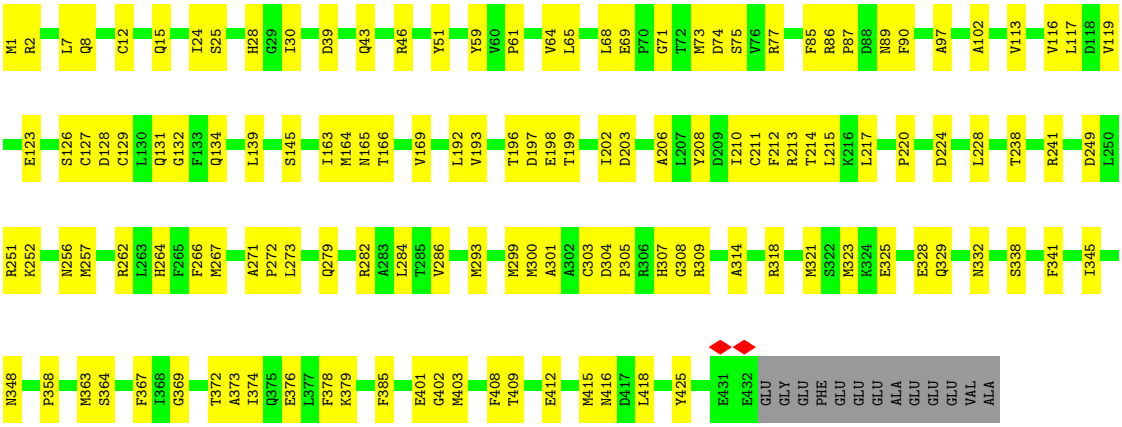

• Molecule 17: Tubulin beta-4B chain

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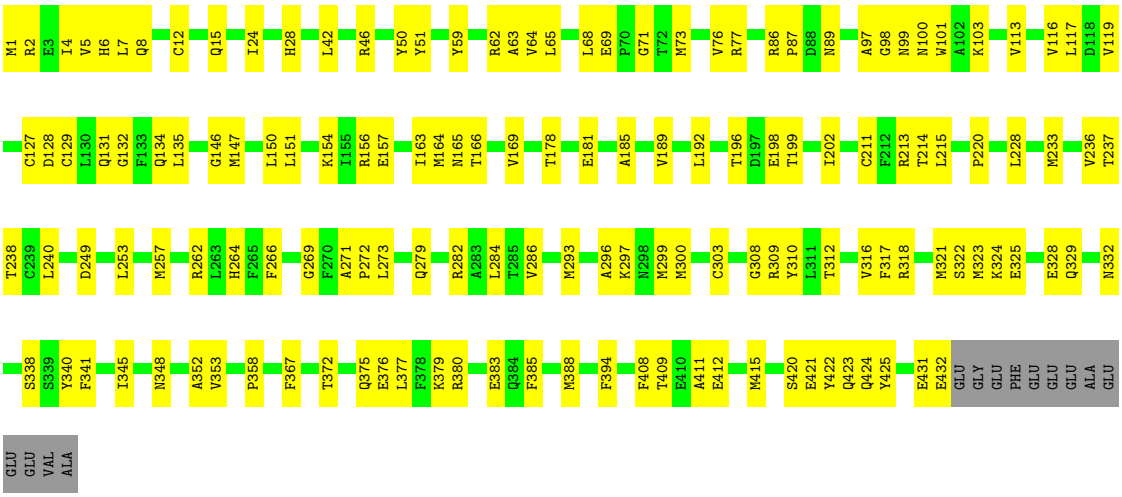

• Molecule 17: Tubulin beta-4B chain

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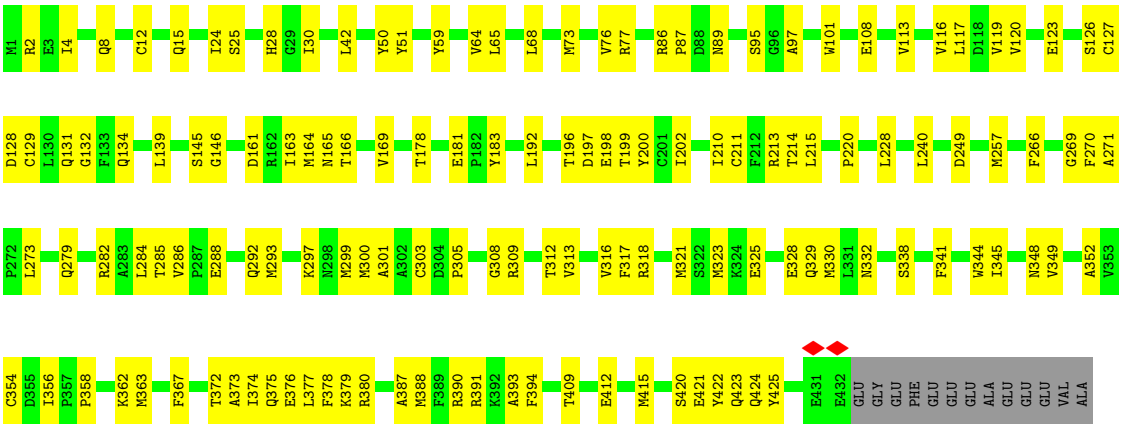

• Molecule 17: Tubulin beta-4B chain

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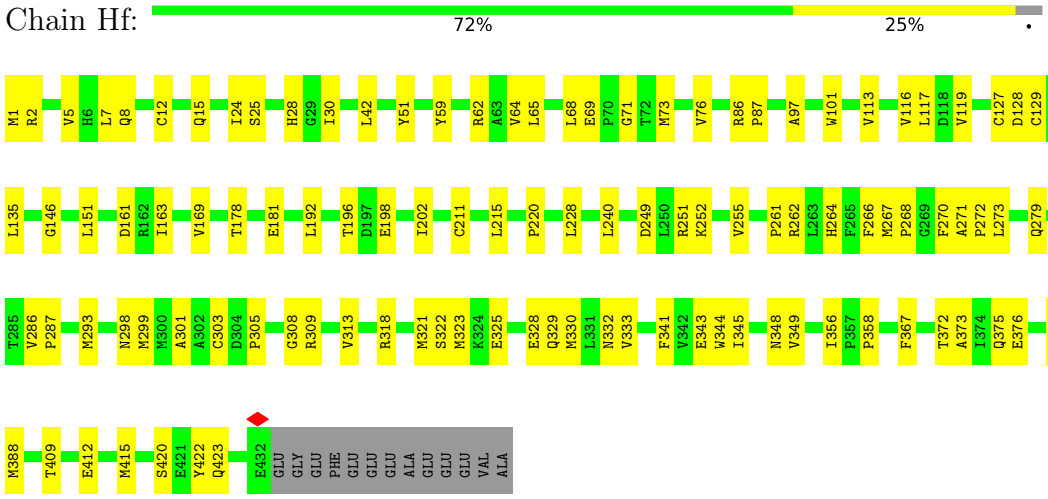
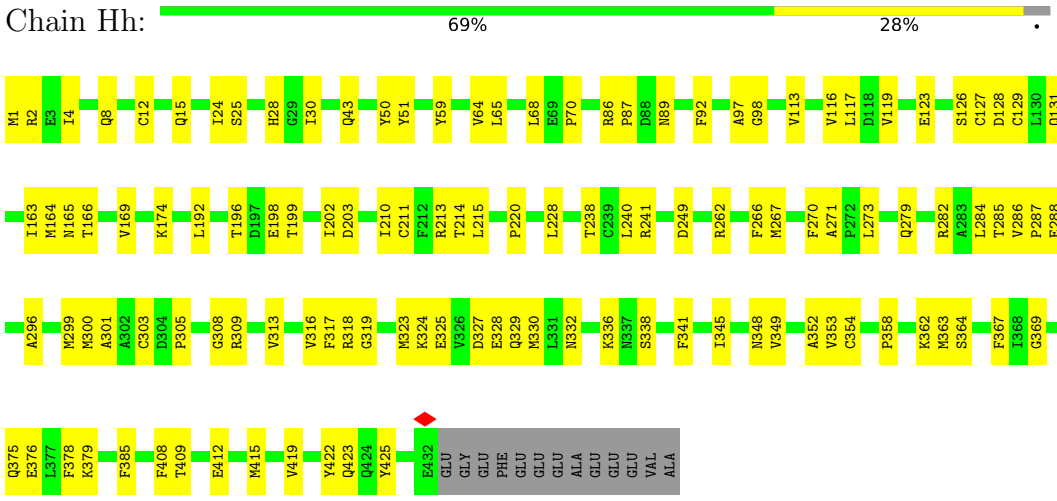


• Molecule 17: Tubulin beta-4B chain

Chain Hh:



• Molecule 17: Tubulin beta-4B chain

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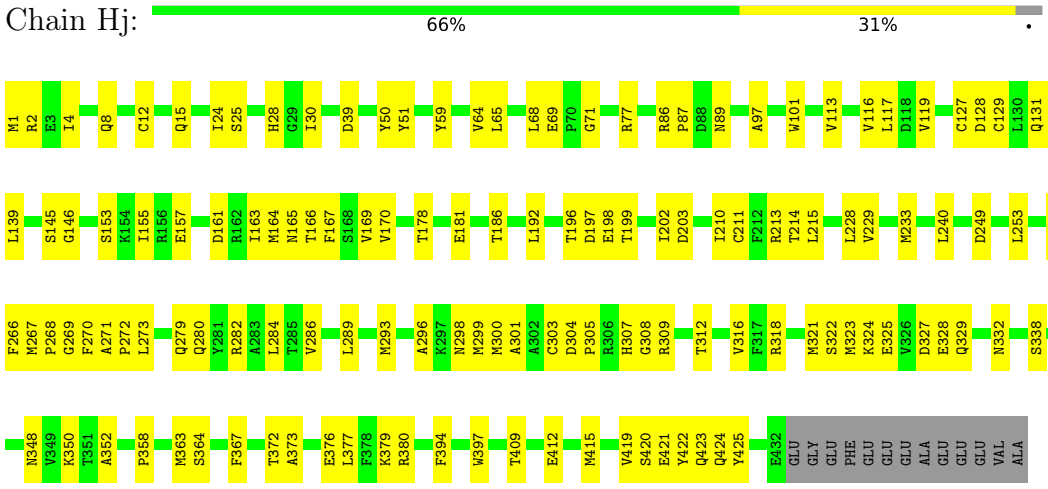

• Molecule 17: Tubulin beta-4B chain

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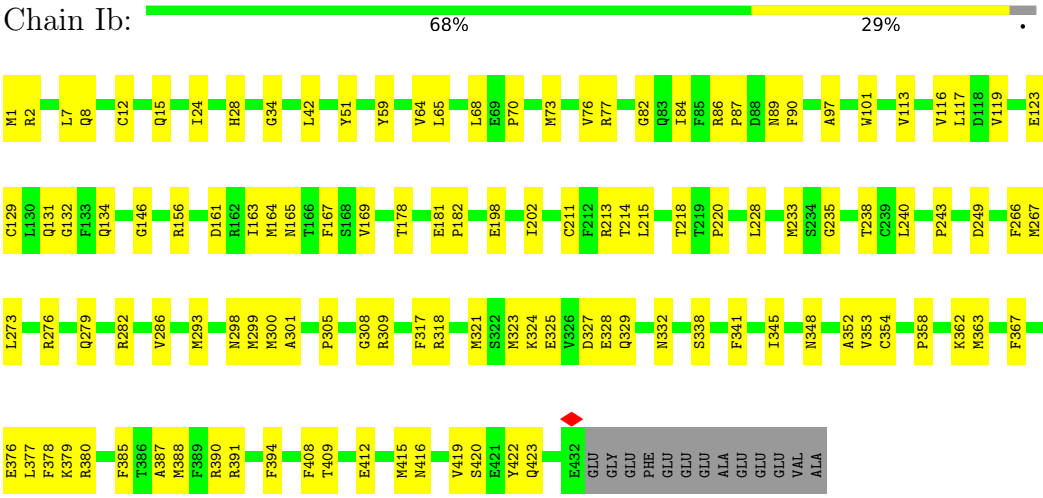

• Molecule 17: Tubulin beta-4B chain

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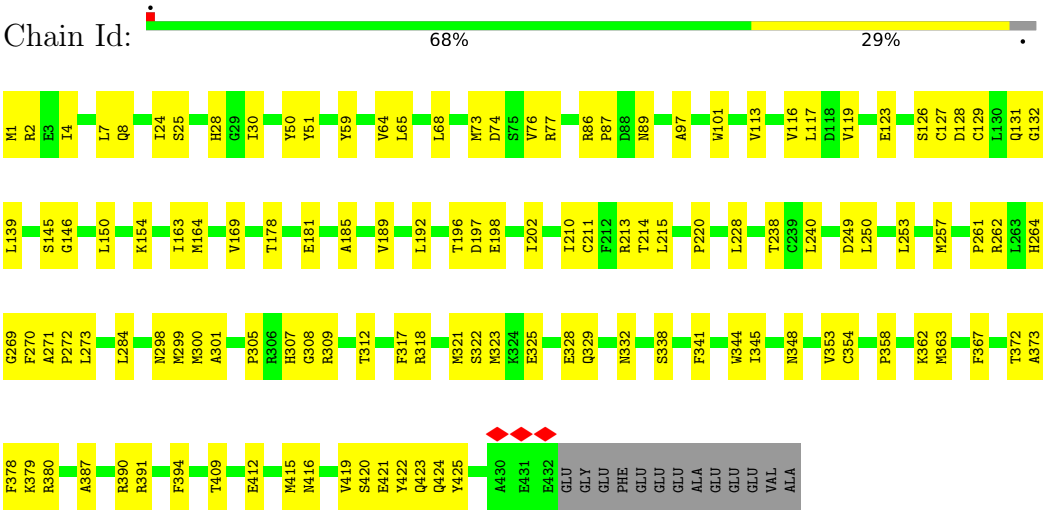

• Molecule 17: Tubulin beta-4B chain

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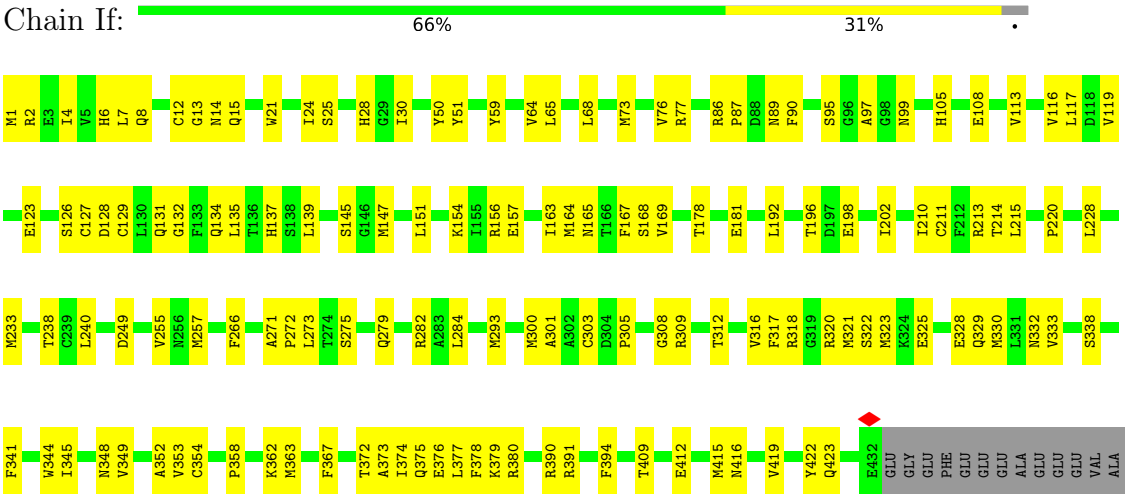

• Molecule 17: Tubulin beta-4B chain

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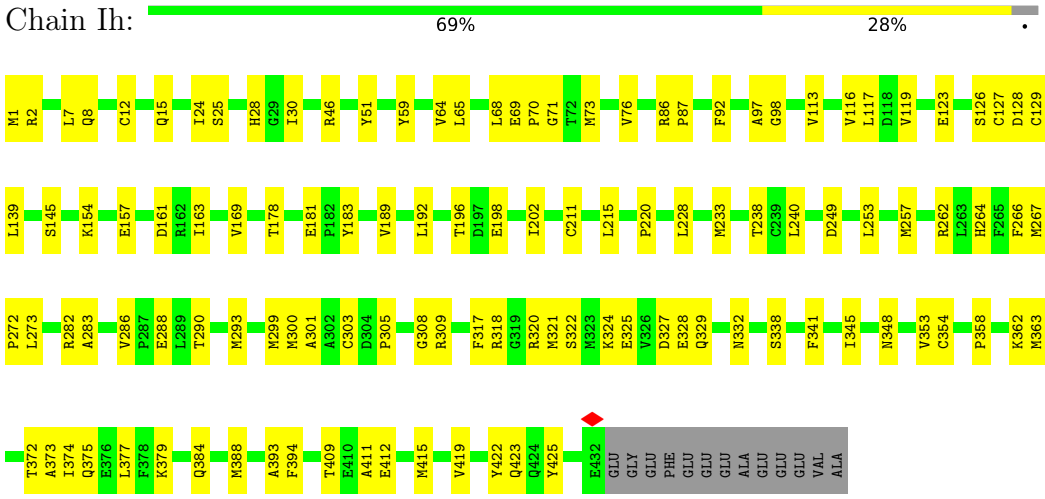

• Molecule 17: Tubulin beta-4B chain

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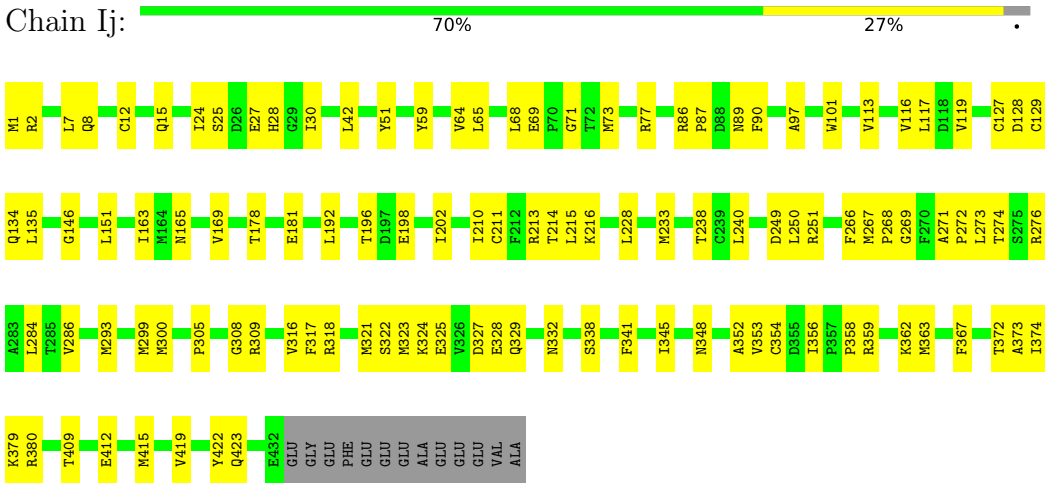

• Molecule 17: Tubulin beta-4B chain

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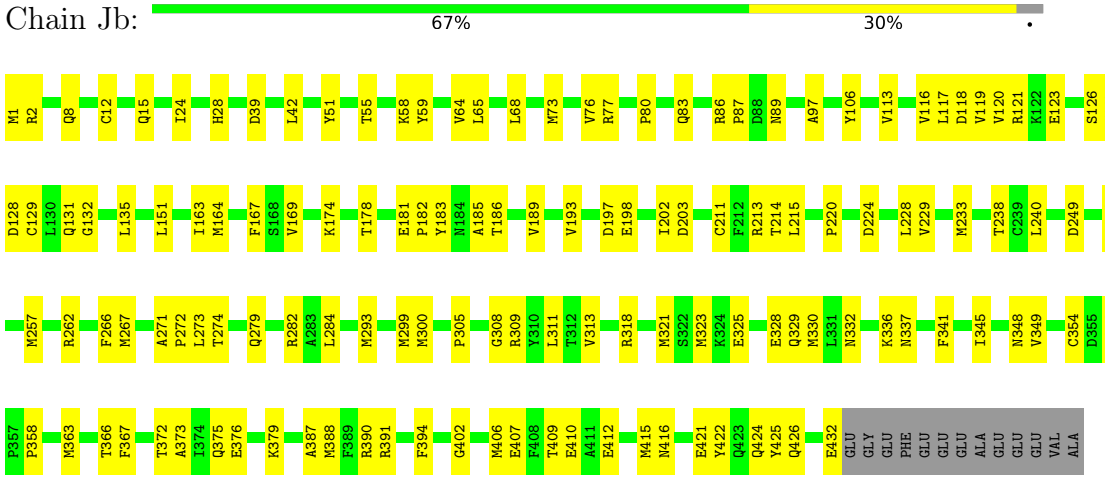

• Molecule 17: Tubulin beta-4B chain

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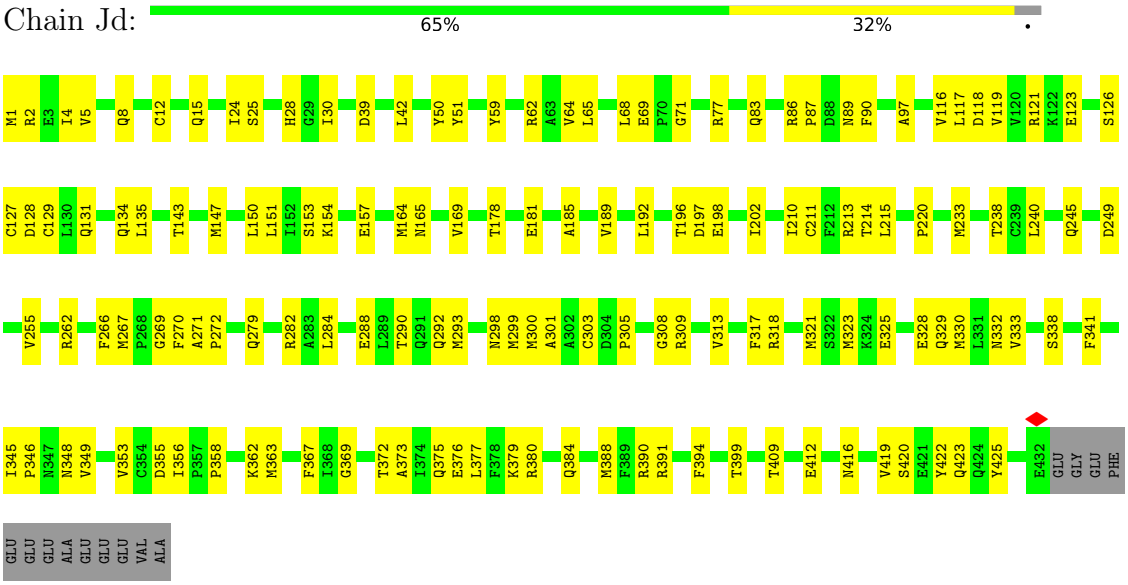

• Molecule 17: Tubulin beta-4B chain

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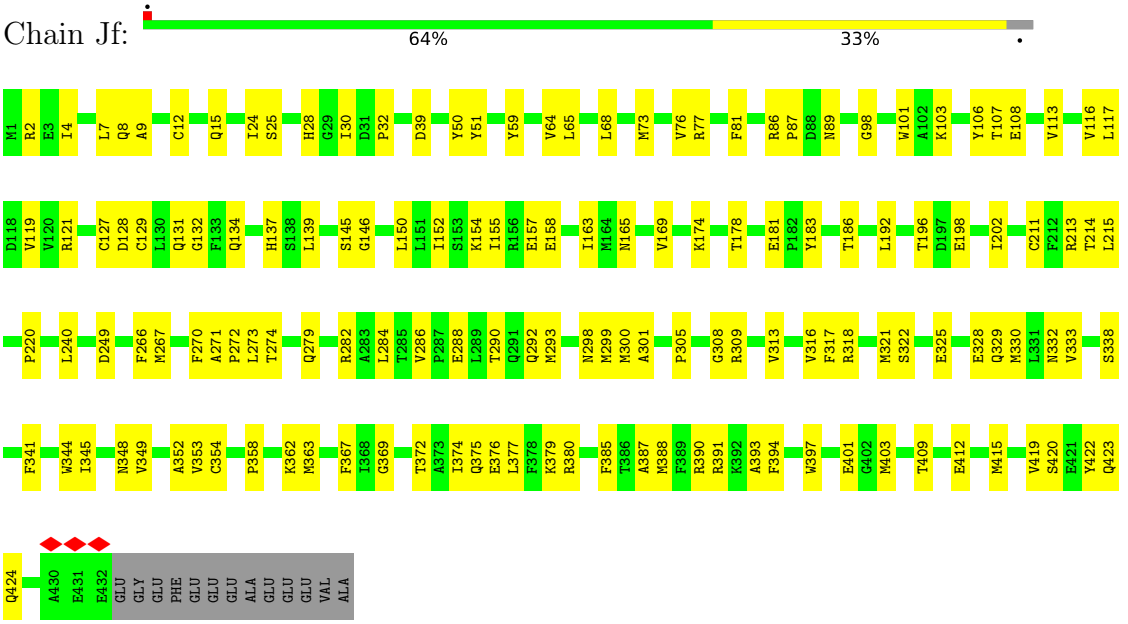

• Molecule 17: Tubulin beta-4B chain

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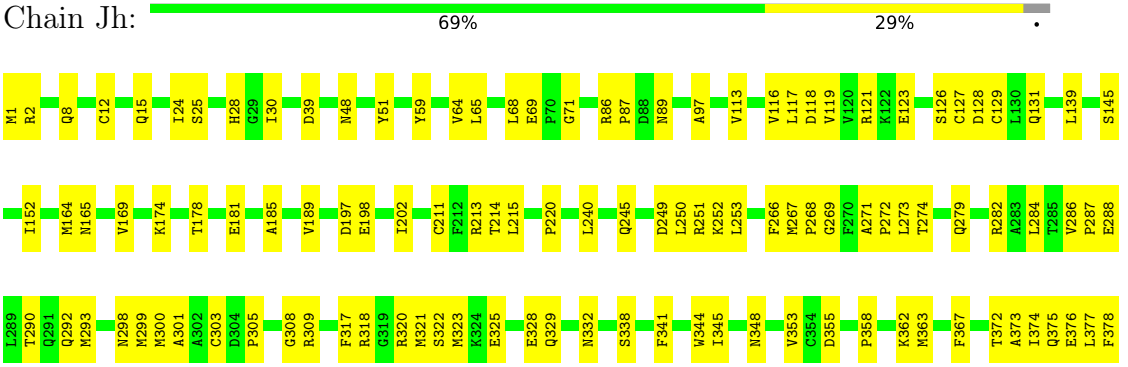

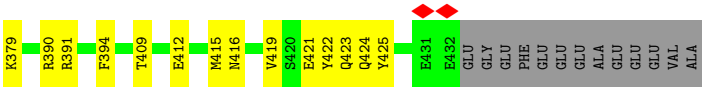

• Molecule 17: Tubulin beta-4B chain

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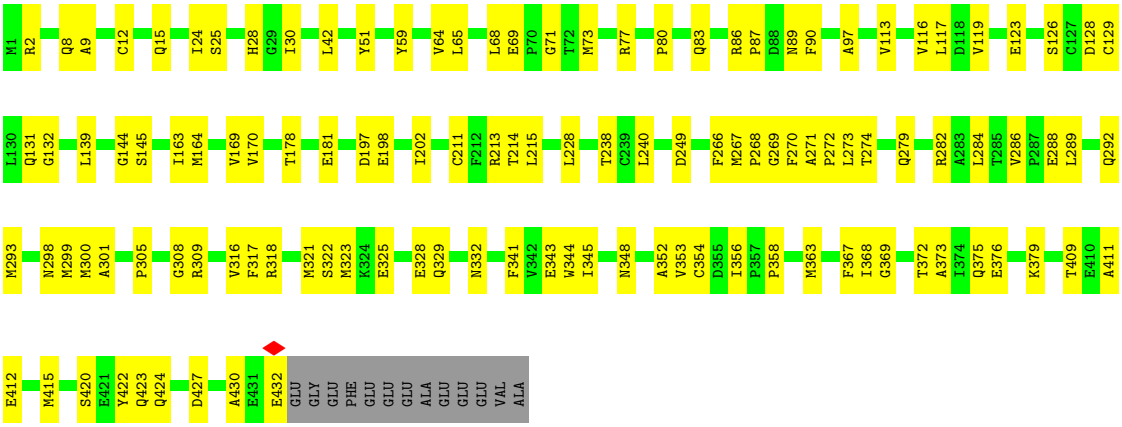
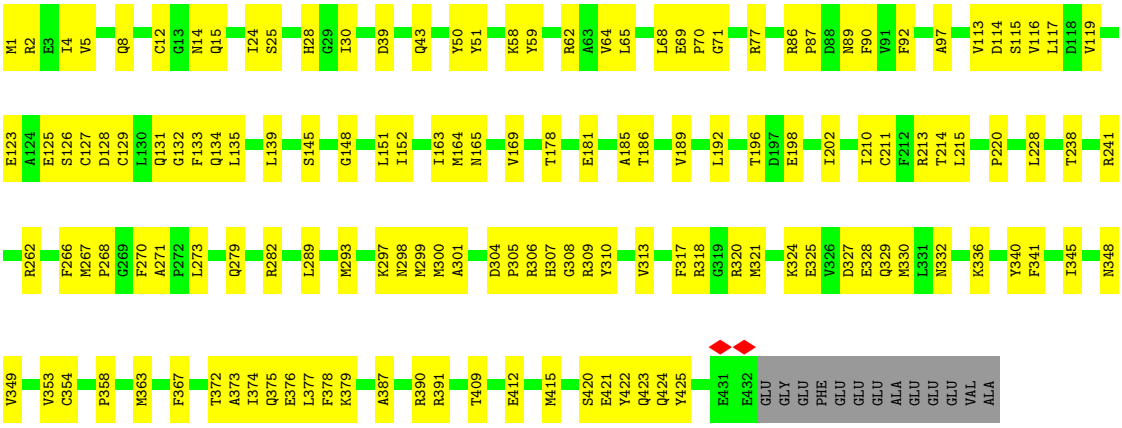


• Molecule 17: Tubulin beta-4B chain

Chain Kb:



• Molecule 17: Tubulin beta-4B chain

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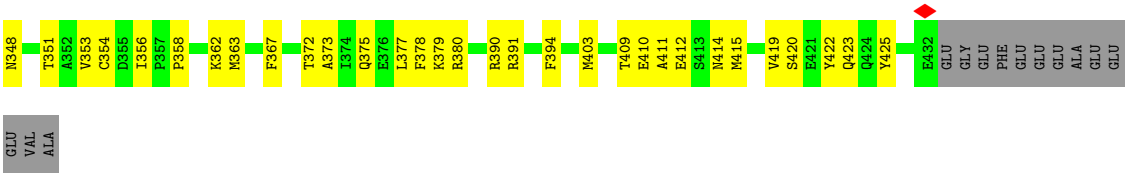

• Molecule 17: Tubulin beta-4B chain

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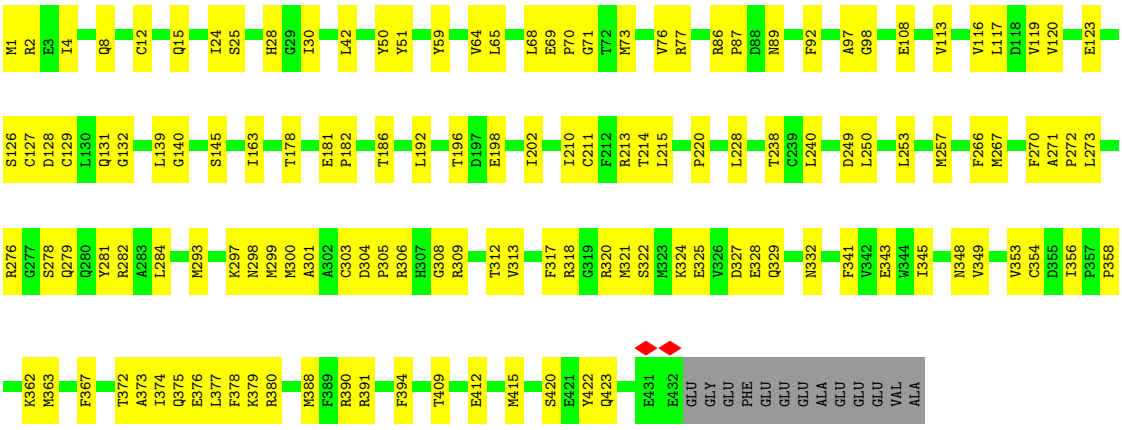

• Molecule 17: Tubulin beta-4B chain

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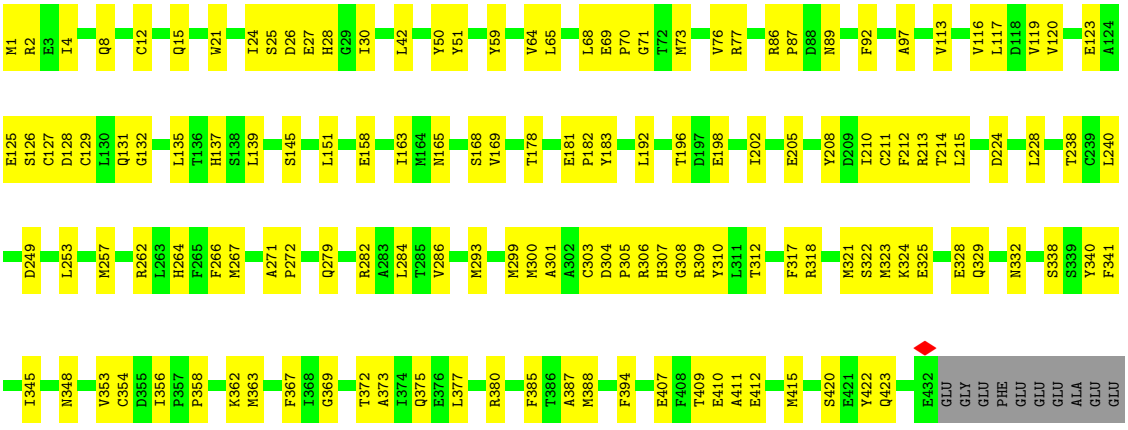

• Molecule 17: Tubulin beta-4B chain

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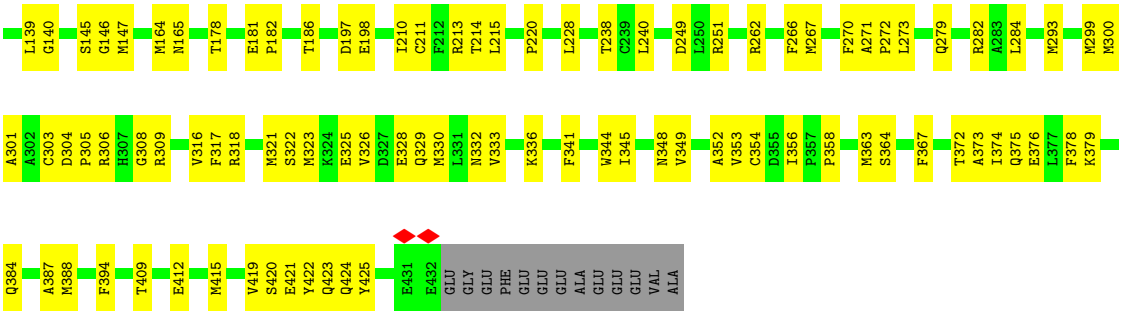

• Molecule 17: Tubulin beta-4B chain

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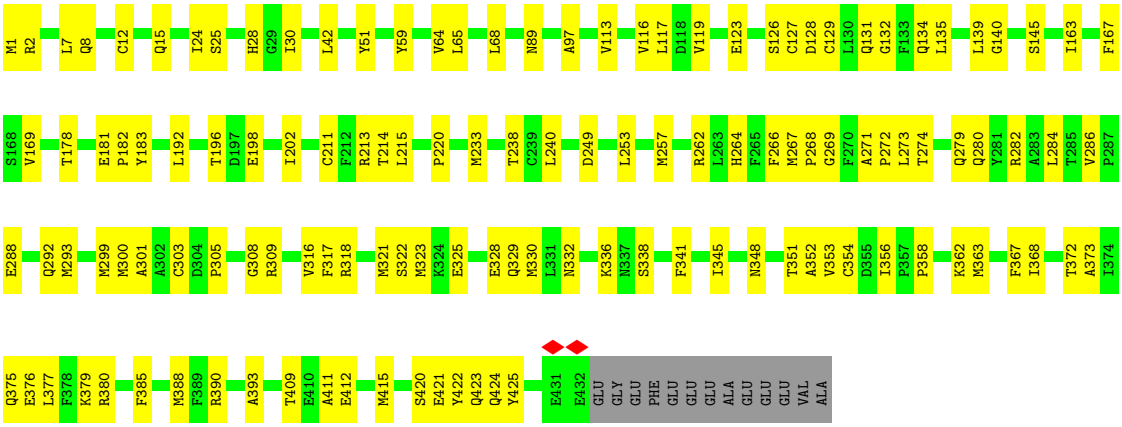

• Molecule 17: Tubulin beta-4B chain

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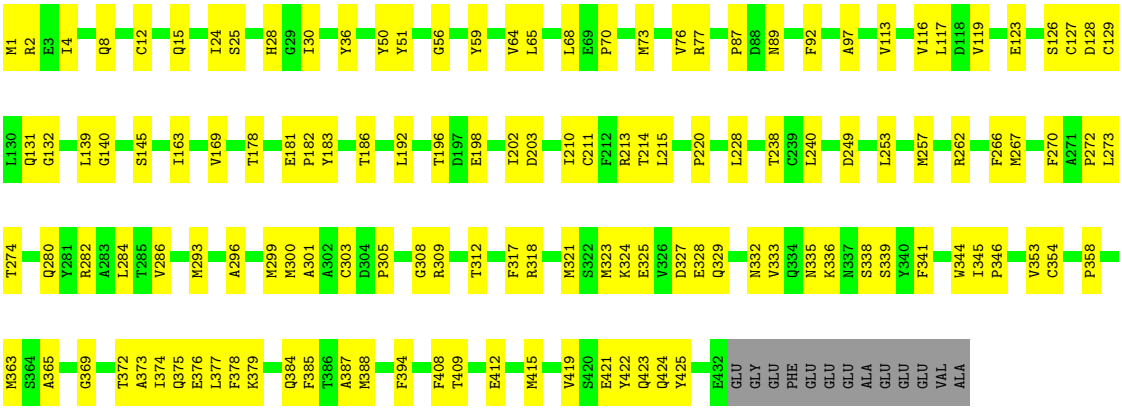

• Molecule 17: Tubulin beta-4B chain

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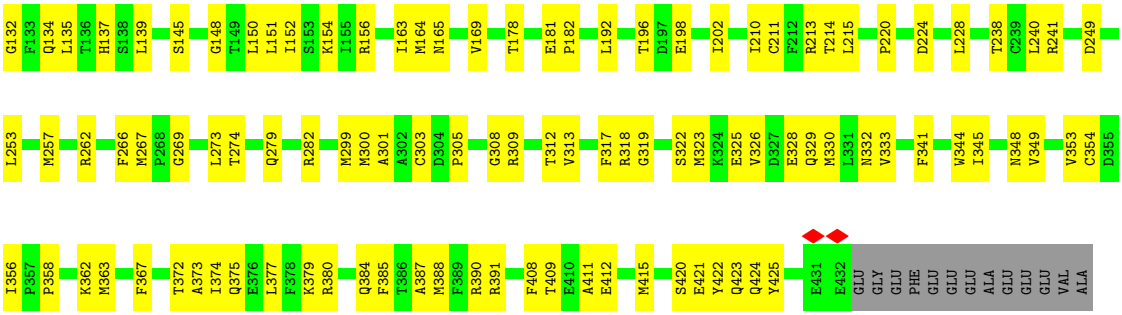

• Molecule 17: Tubulin beta-4B chain

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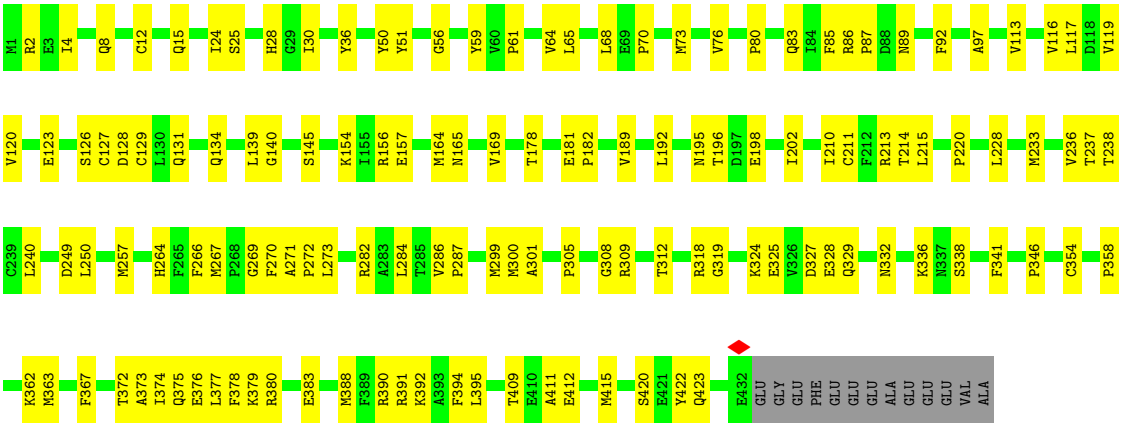

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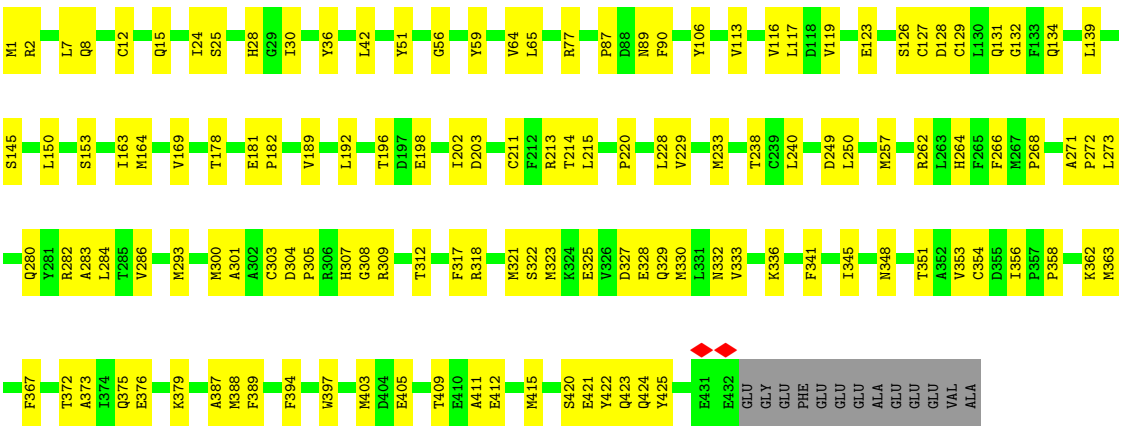

• Molecule 17: Tubulin beta-4B chain

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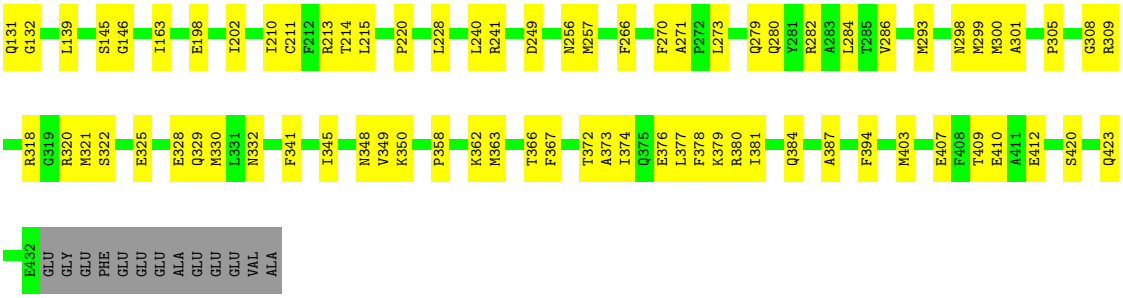

• Molecule 17: Tubulin beta-4B chain

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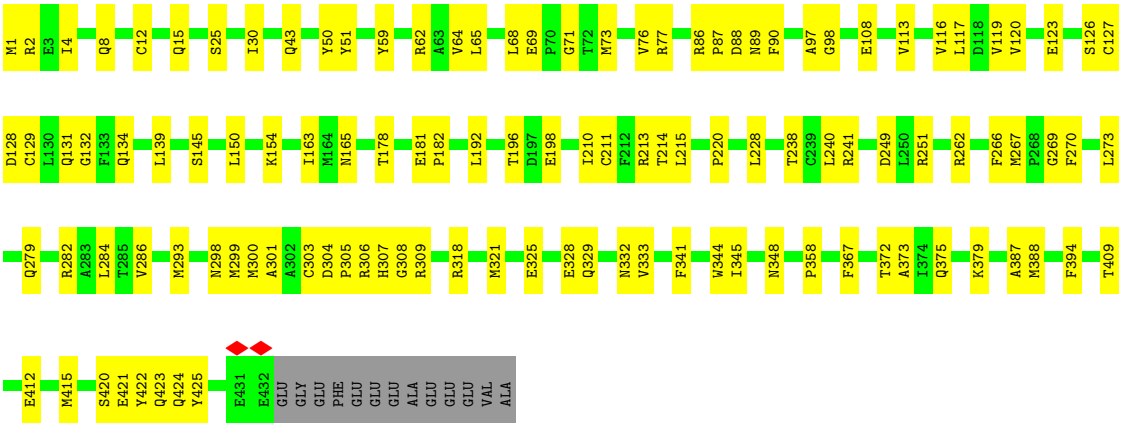

• Molecule 17: Tubulin beta-4B chain

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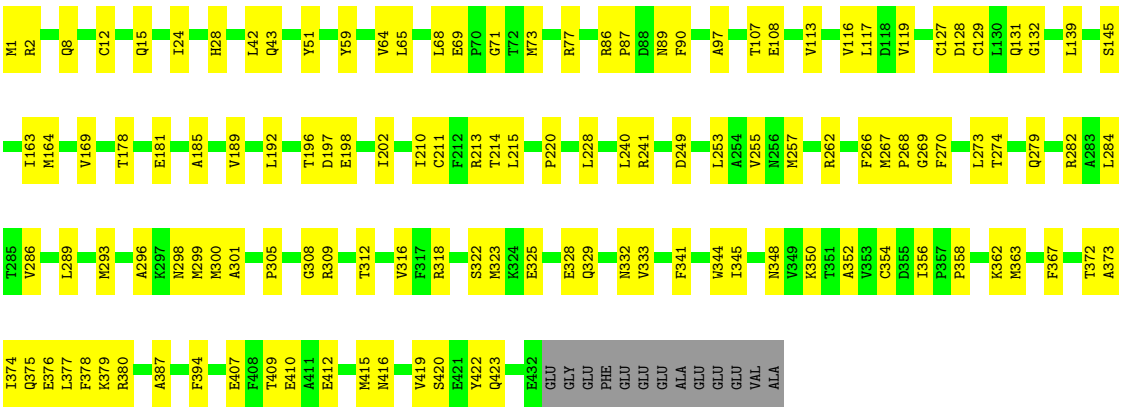

• Molecule 17: Tubulin beta-4B chain

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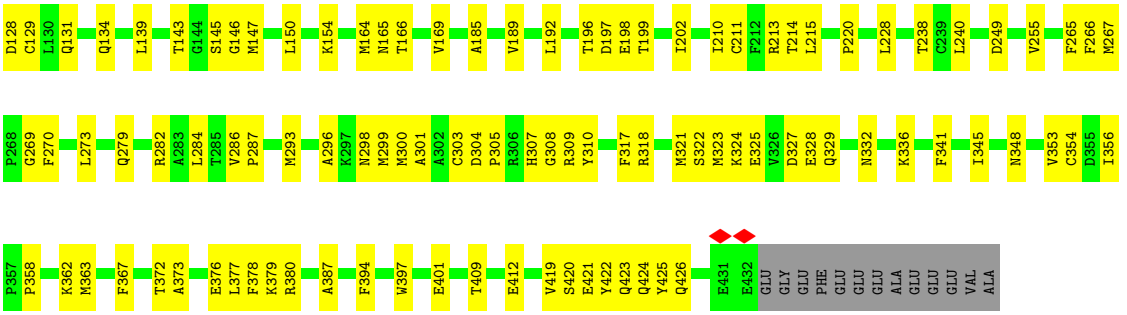

• Molecule 17: Tubulin beta-4B chain

Chain Mj:

• Molecule 17: Tubulin beta-4B chain

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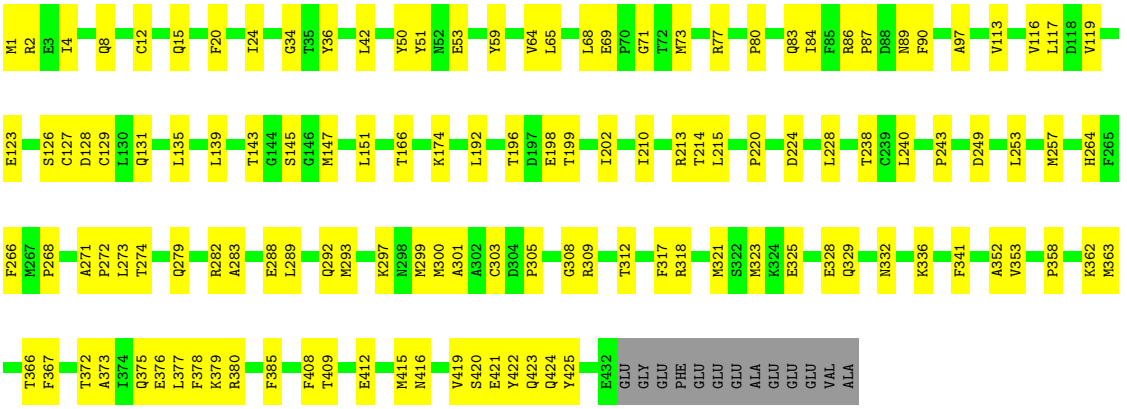

• Molecule 17: Tubulin beta-4B chain

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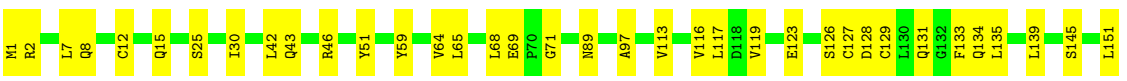

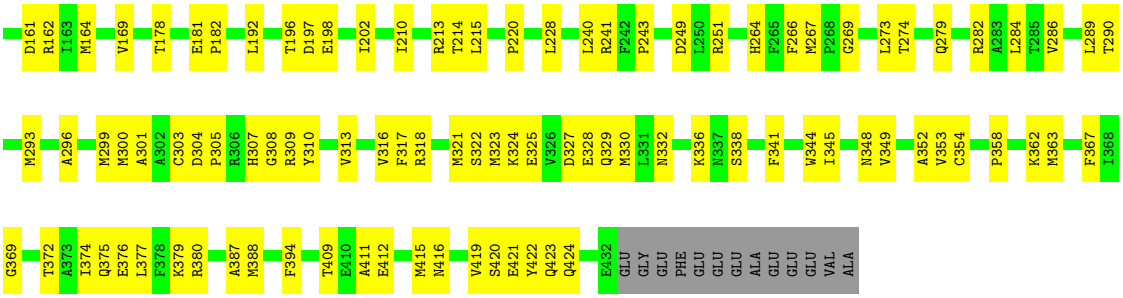

• Molecule 17: Tubulin beta-4B chain

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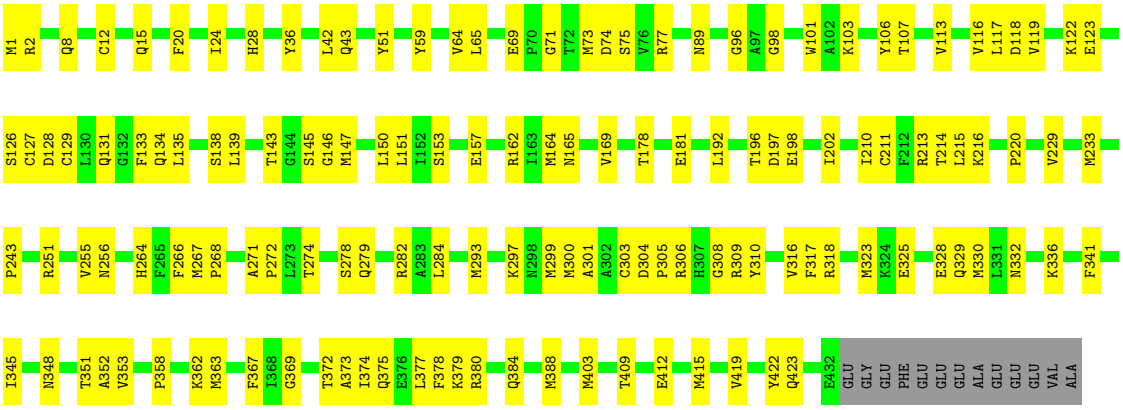

• Molecule 17: Tubulin beta-4B chain

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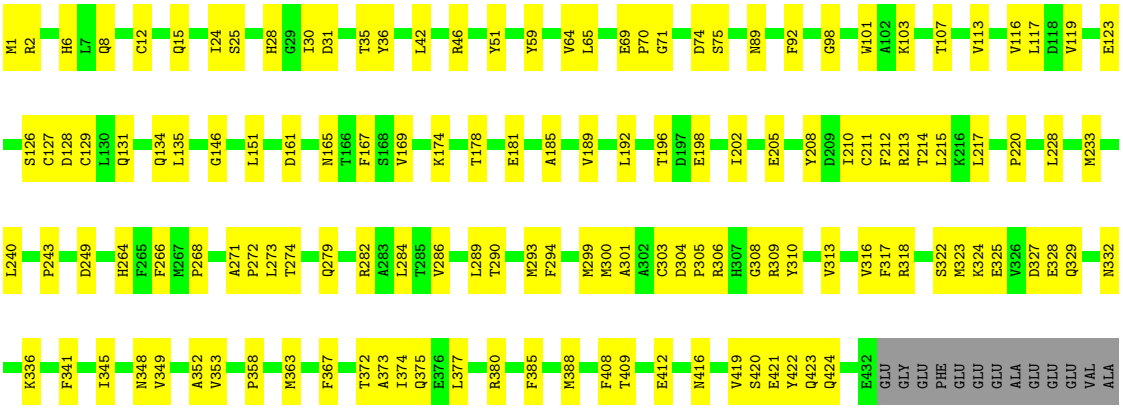

• Molecule 17: Tubulin beta-4B chain

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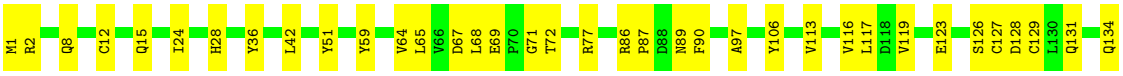

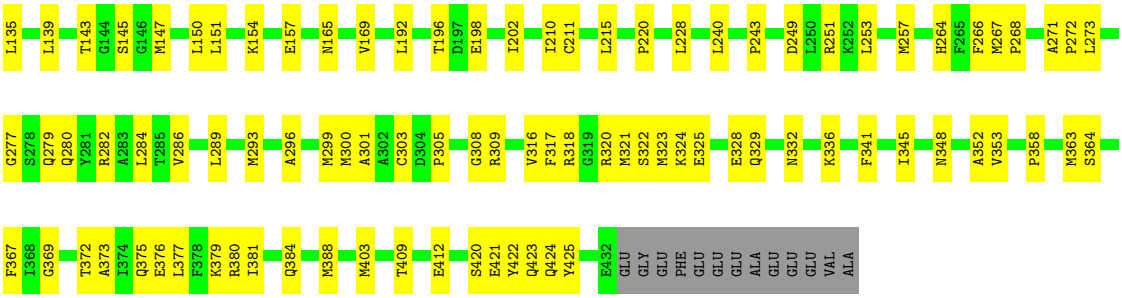

• Molecule 17: Tubulin beta-4B chain

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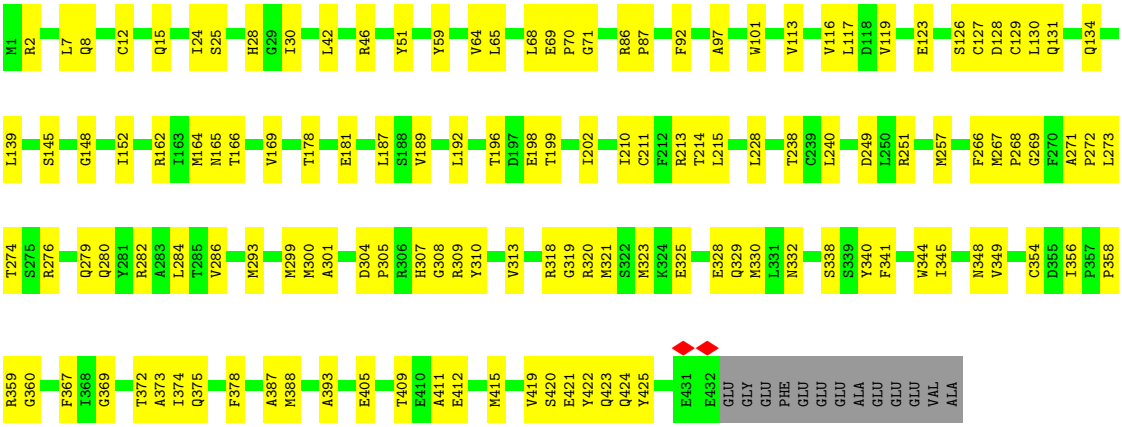

• Molecule 17: Tubulin beta-4B chain

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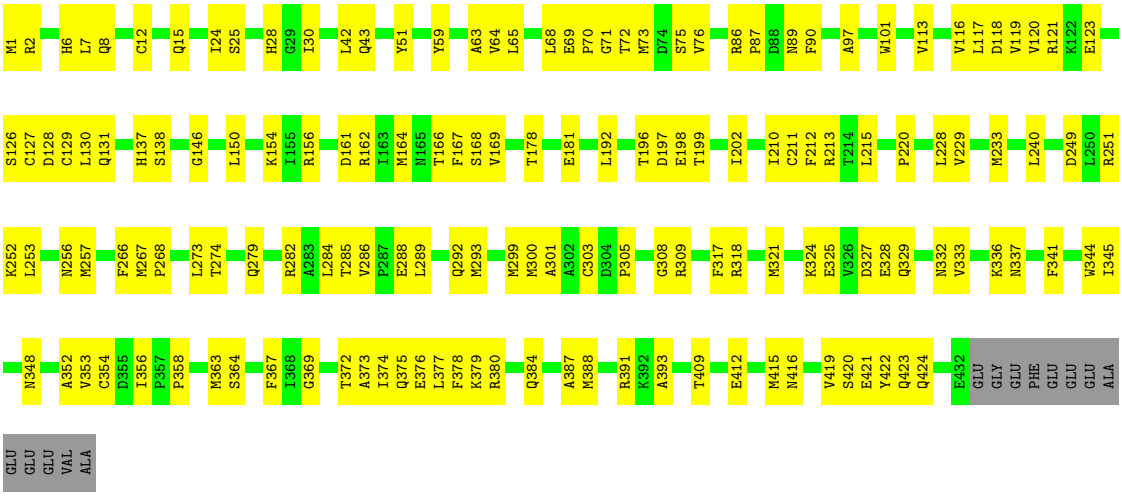

• Molecule 17: Tubulin beta-4B chain

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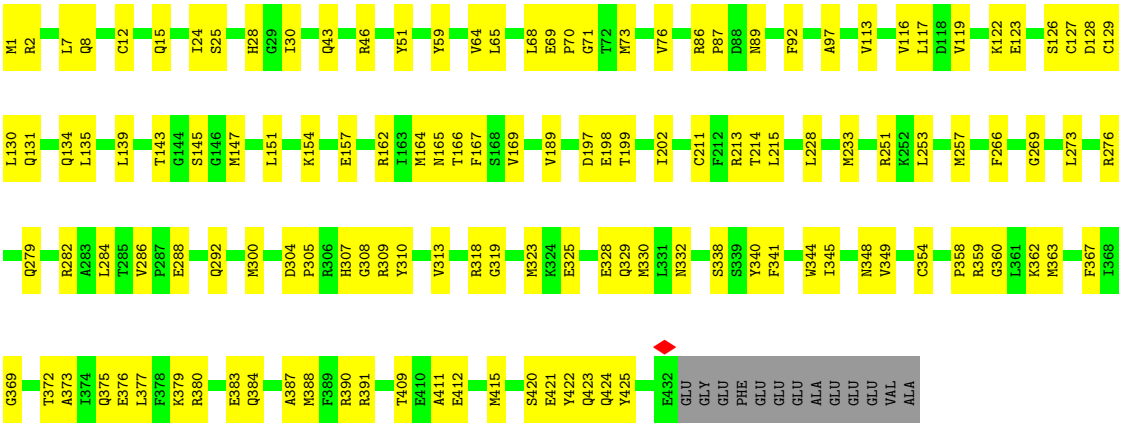

• Molecule 17: Tubulin beta-4B chain

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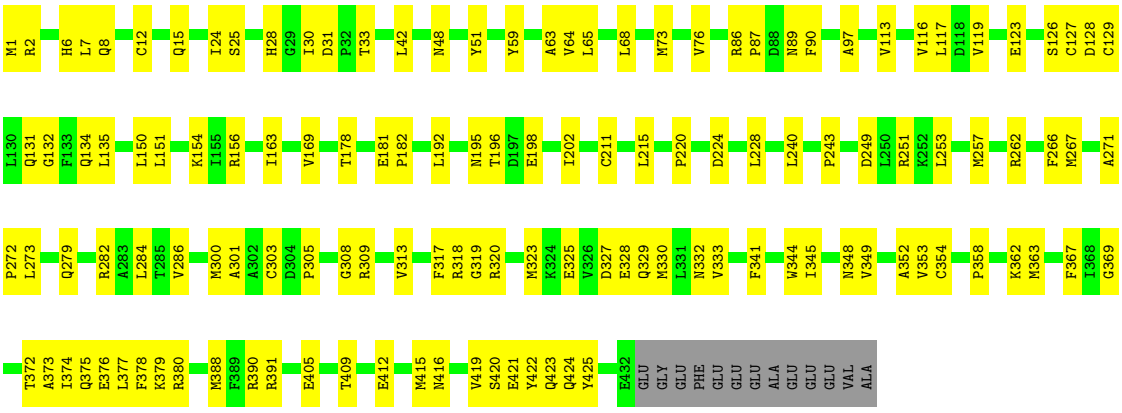

• Molecule 17: Tubulin beta-4B chain

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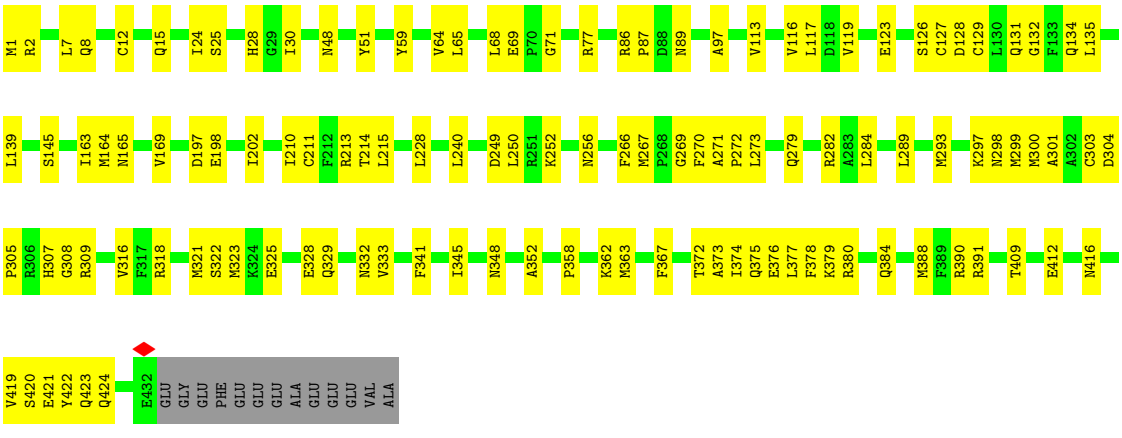

• Molecule 17: Tubulin beta-4B chain

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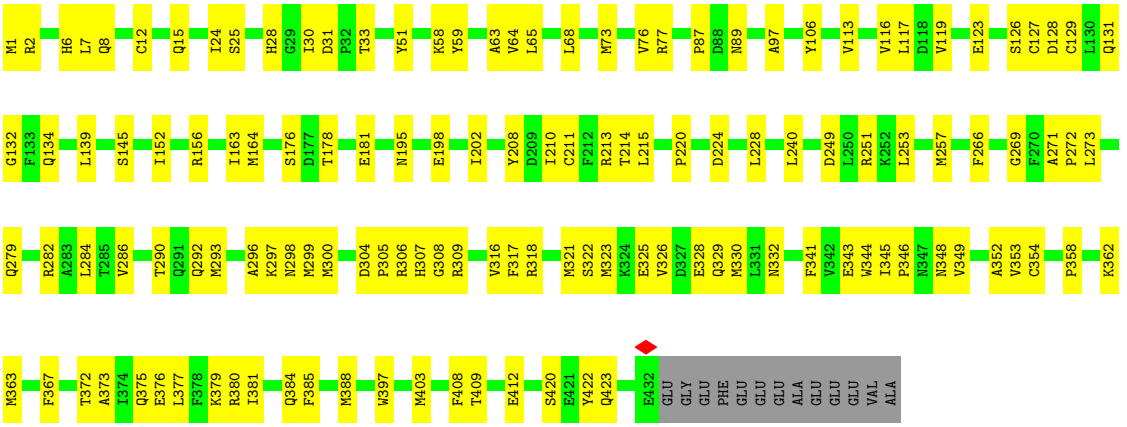

• Molecule 17: Tubulin beta-4B chain

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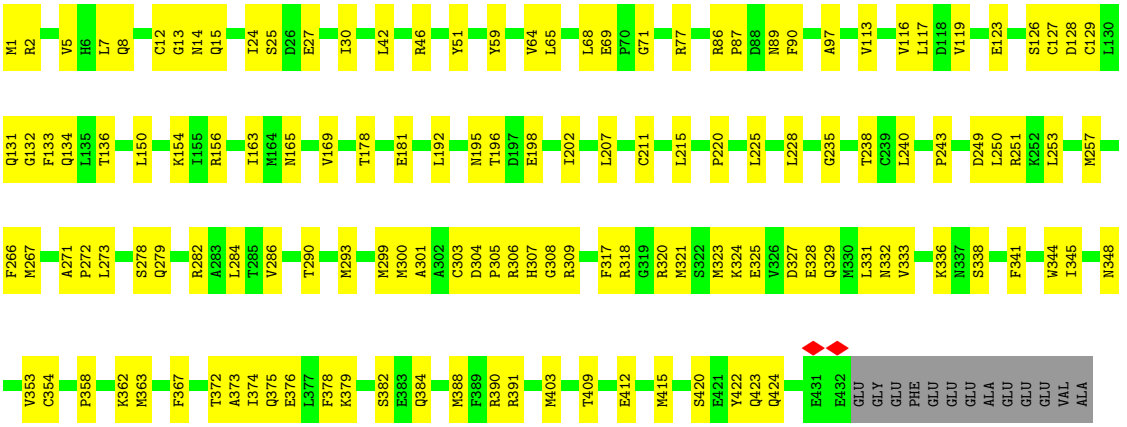

• Molecule 17: Tubulin beta-4B chain

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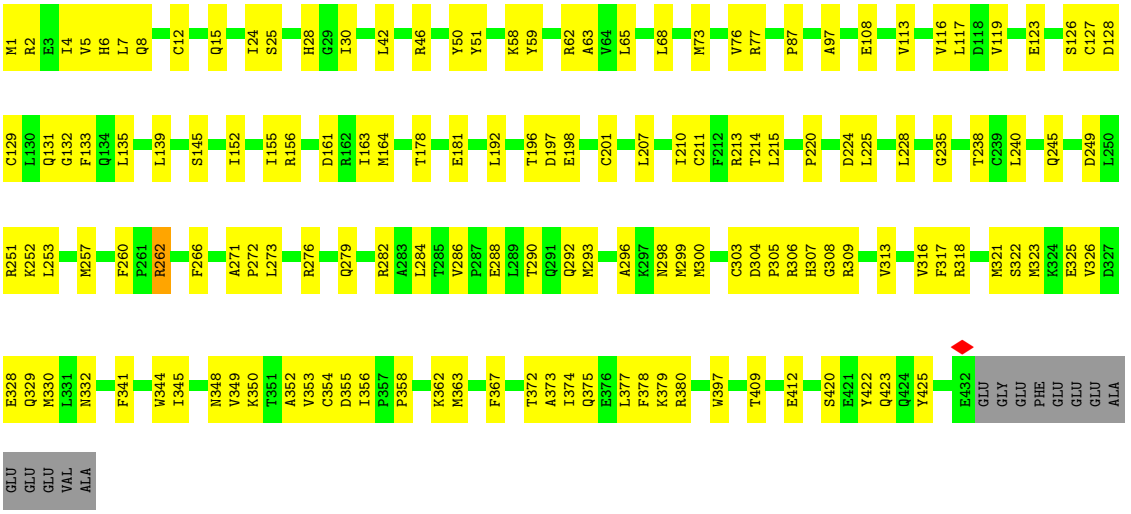

• Molecule 17: Tubulin beta-4B chain

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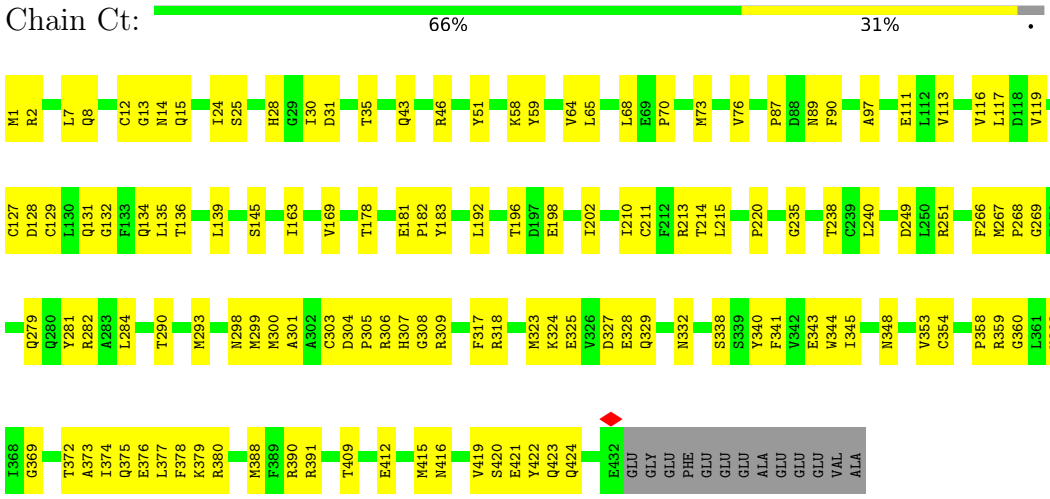

• Molecule 17: Tubulin beta-4B chain

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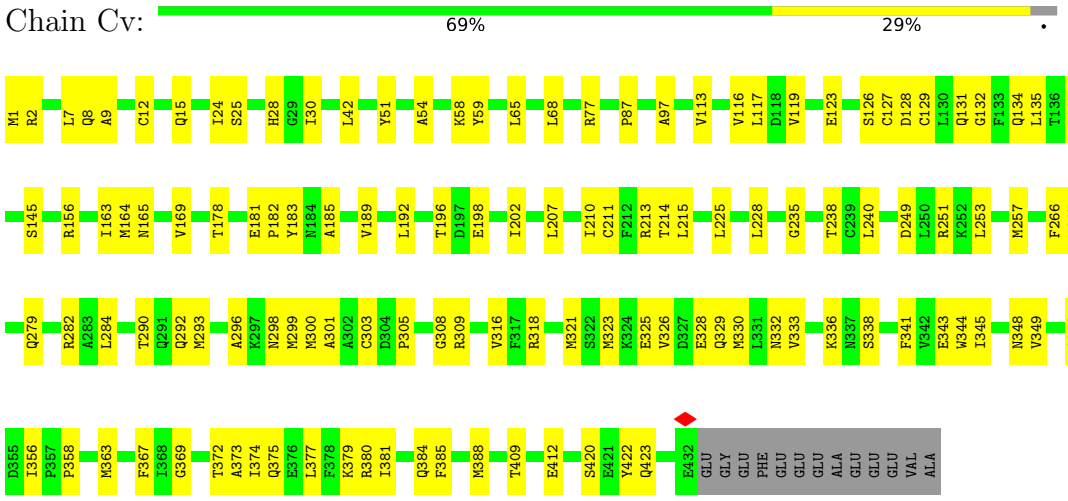

• Molecule 17: Tubulin beta-4B chain

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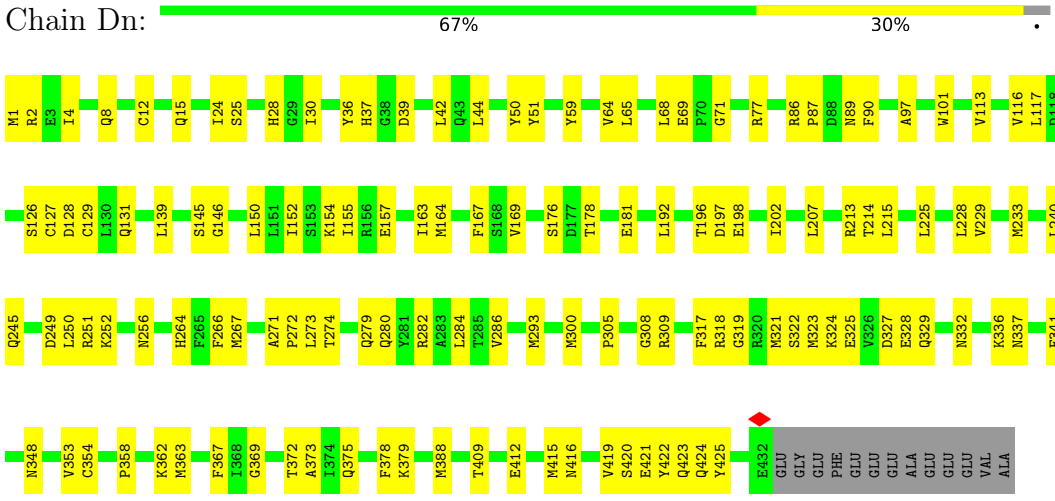

• Molecule 17: Tubulin beta-4B chain

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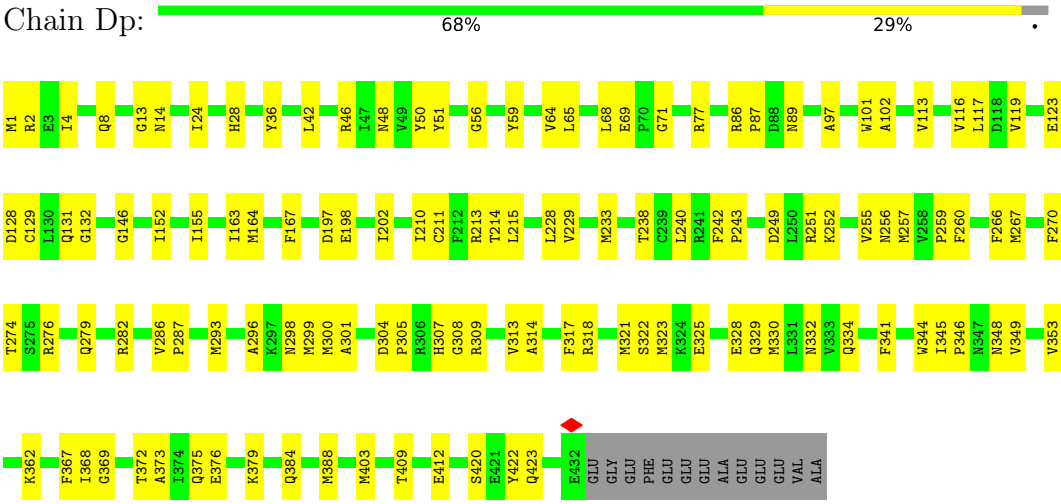

• Molecule 17: Tubulin beta-4B chain

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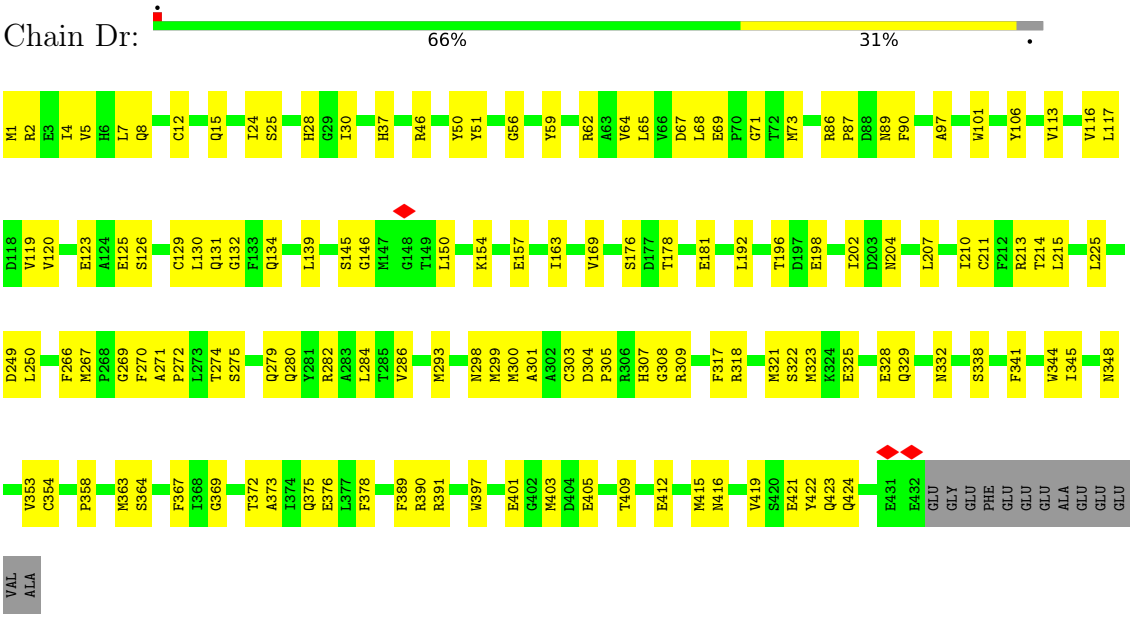

• Molecule 17: Tubulin beta-4B chain

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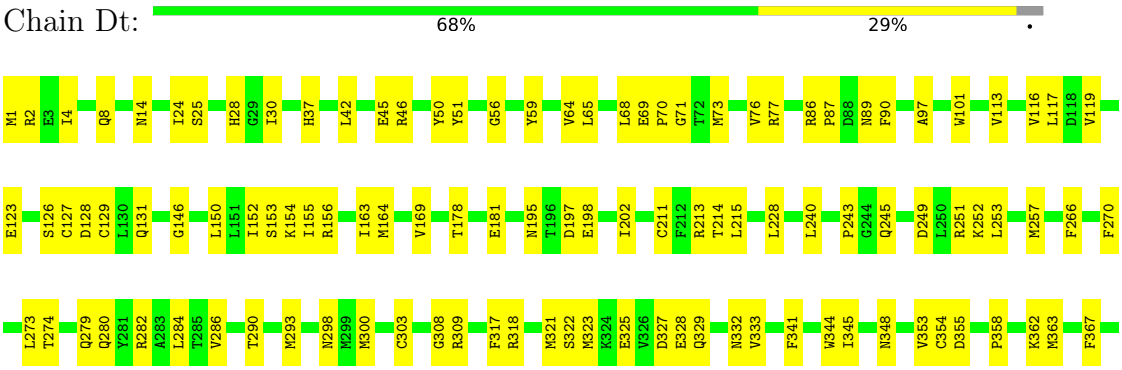

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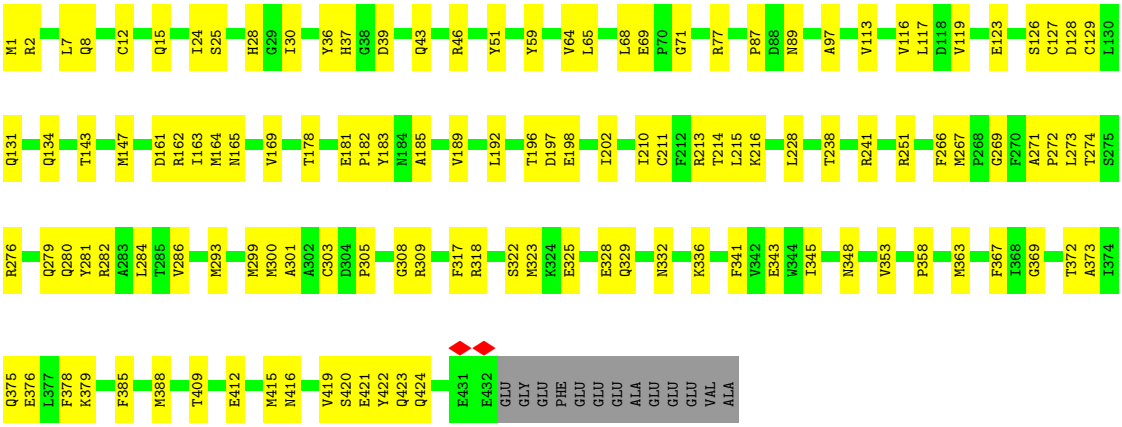

• Molecule 17: Tubulin beta-4B chain

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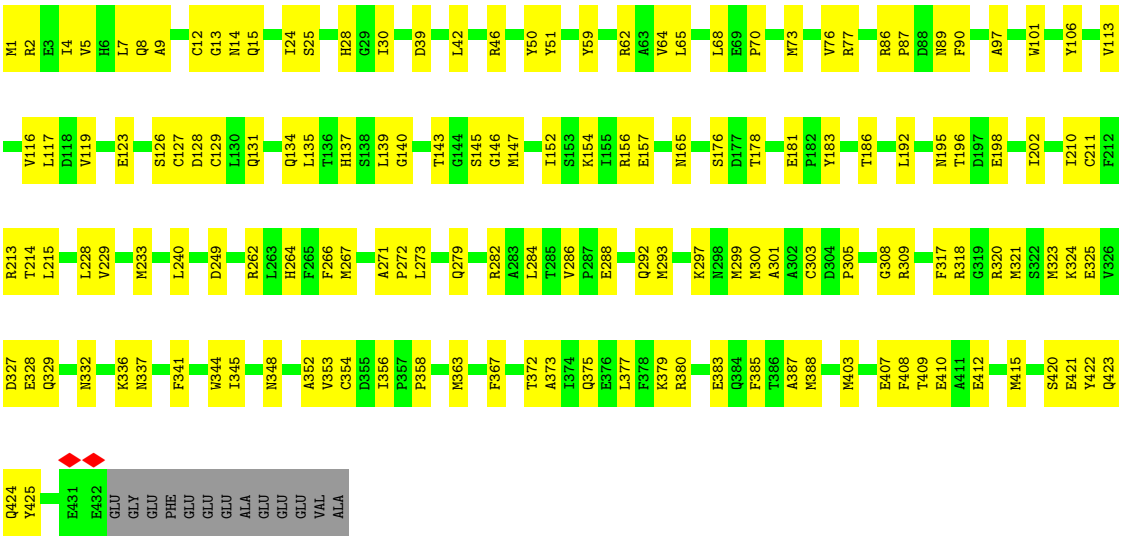

• Molecule 17: Tubulin beta-4B chain

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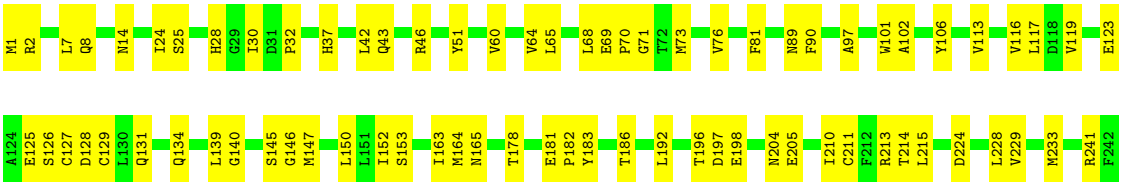

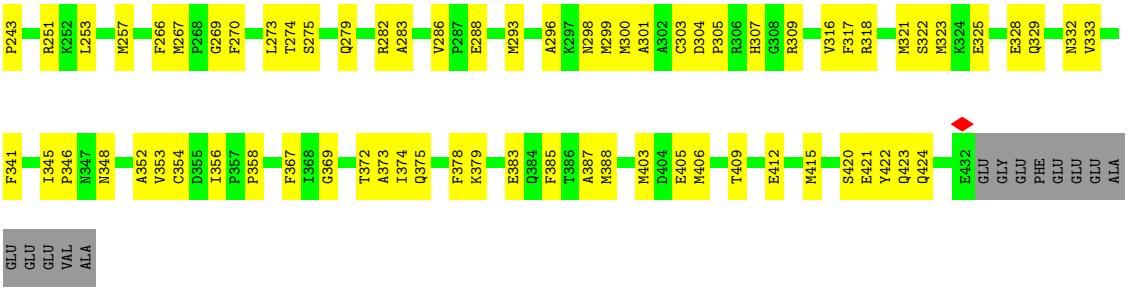

• Molecule 17: Tubulin beta-4B chain

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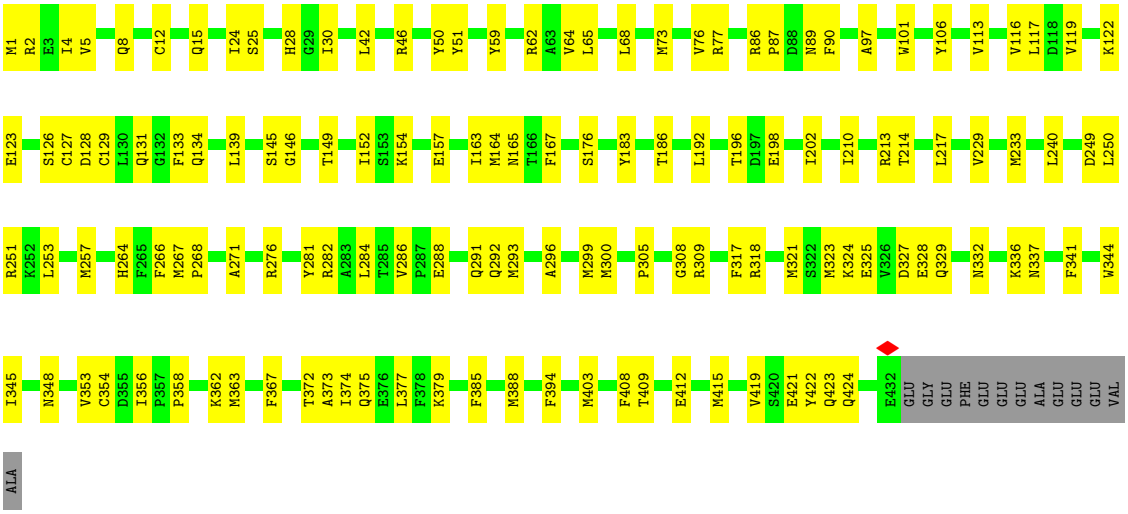

• Molecule 17: Tubulin beta-4B chain

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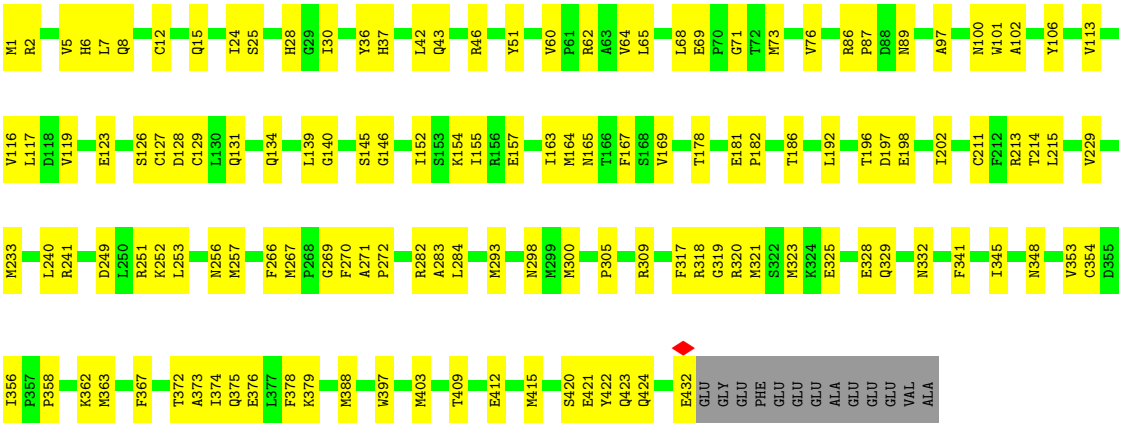

• Molecule 17: Tubulin beta-4B chain

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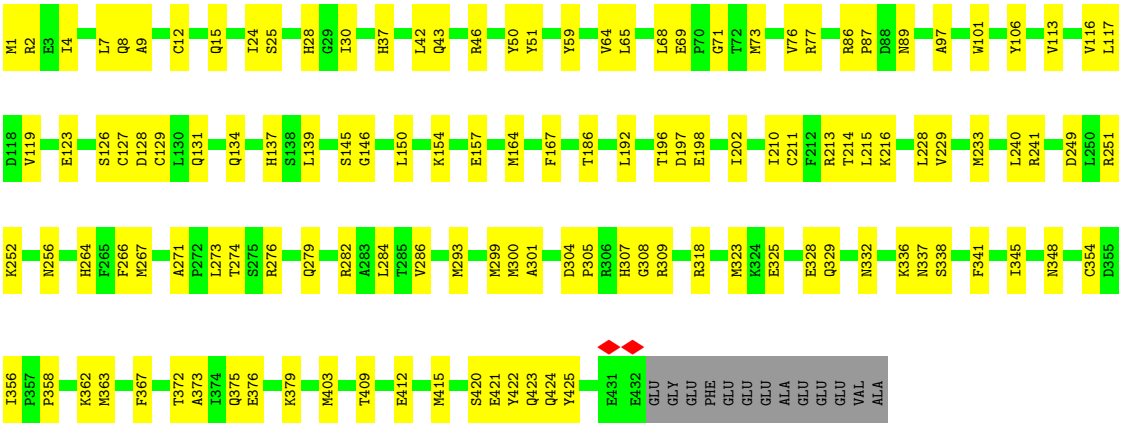

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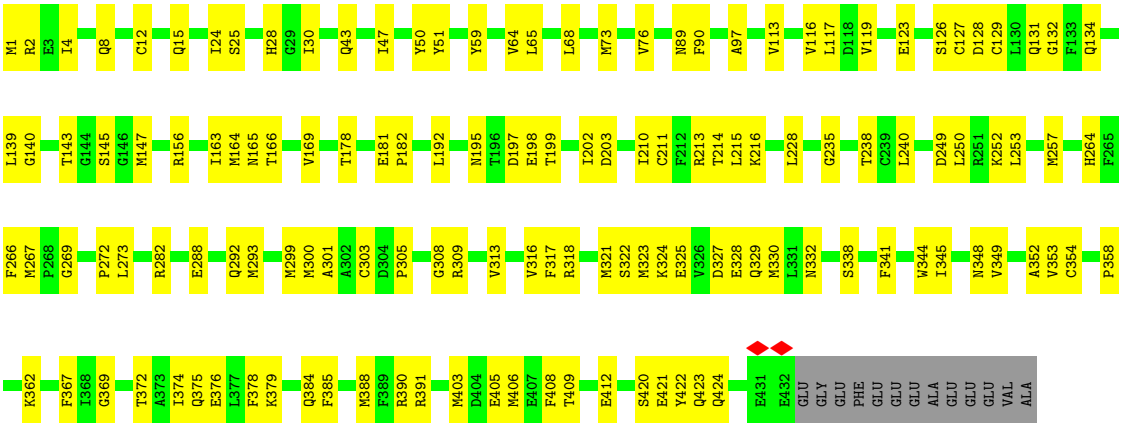

• Molecule 17: Tubulin beta-4B chain

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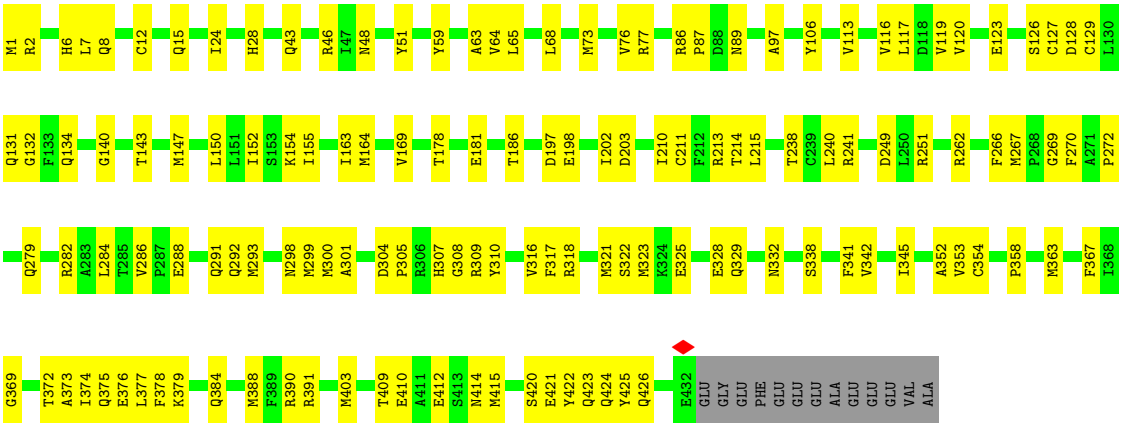

• Molecule 17: Tubulin beta-4B chain

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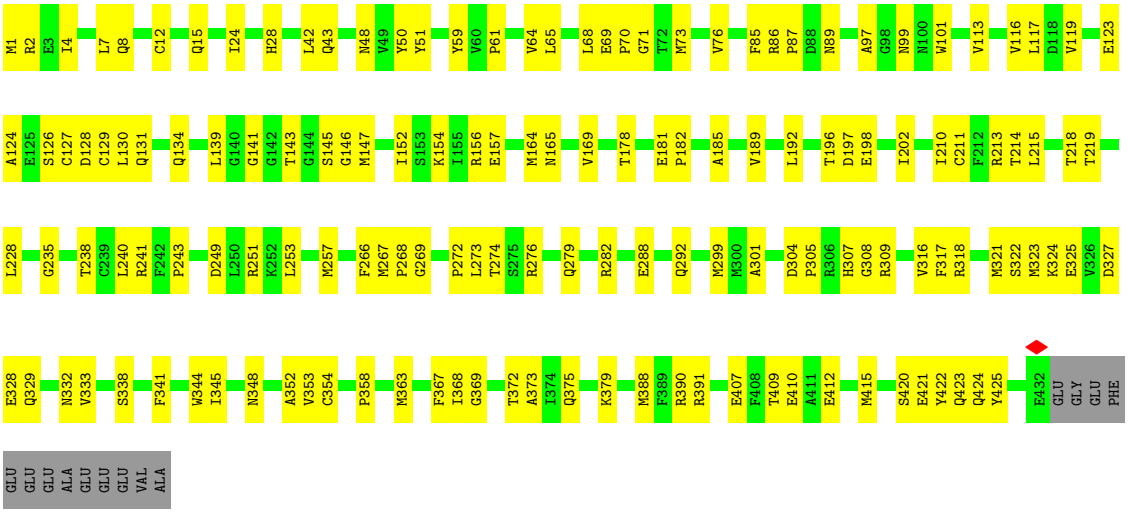

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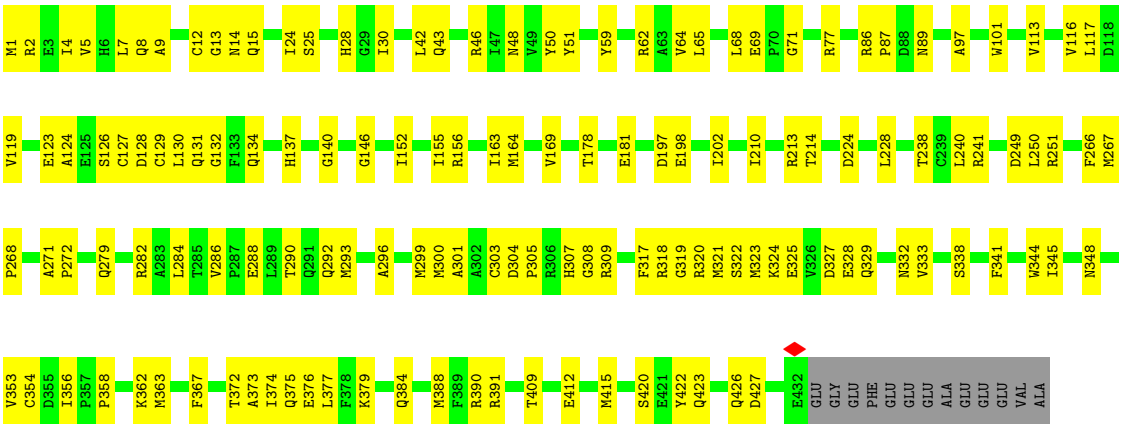

• Molecule 17: Tubulin beta-4B chain

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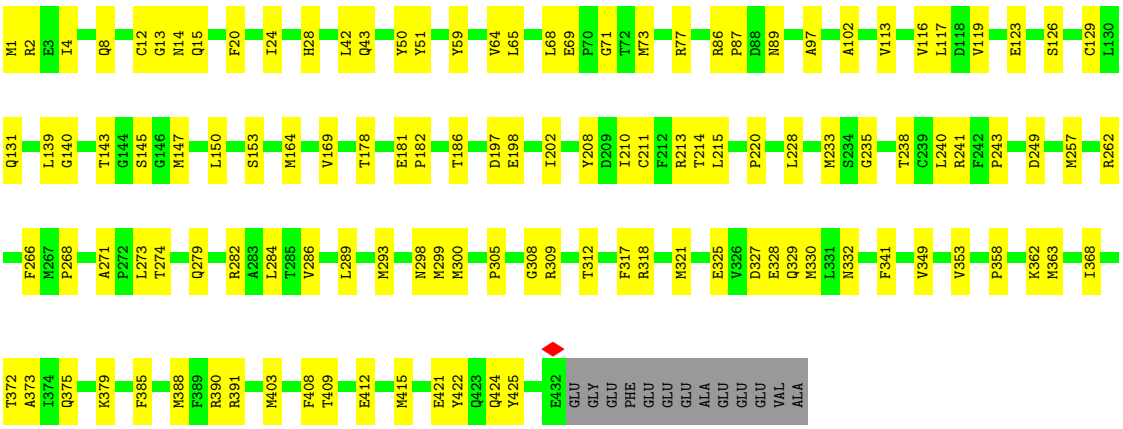

• Molecule 17: Tubulin beta-4B chain

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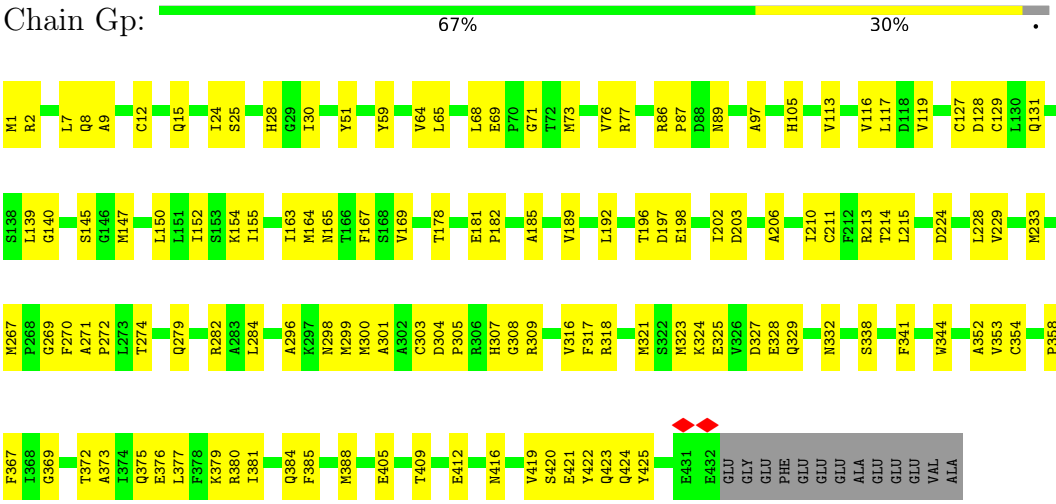

- Molecule 17: Tubulin beta-4B chain

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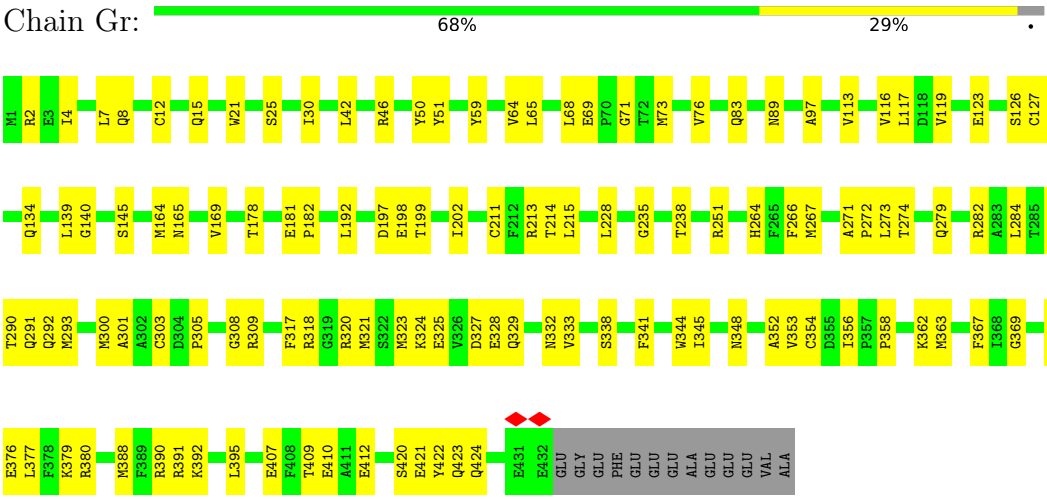

- Molecule 17: Tubulin beta-4B chain

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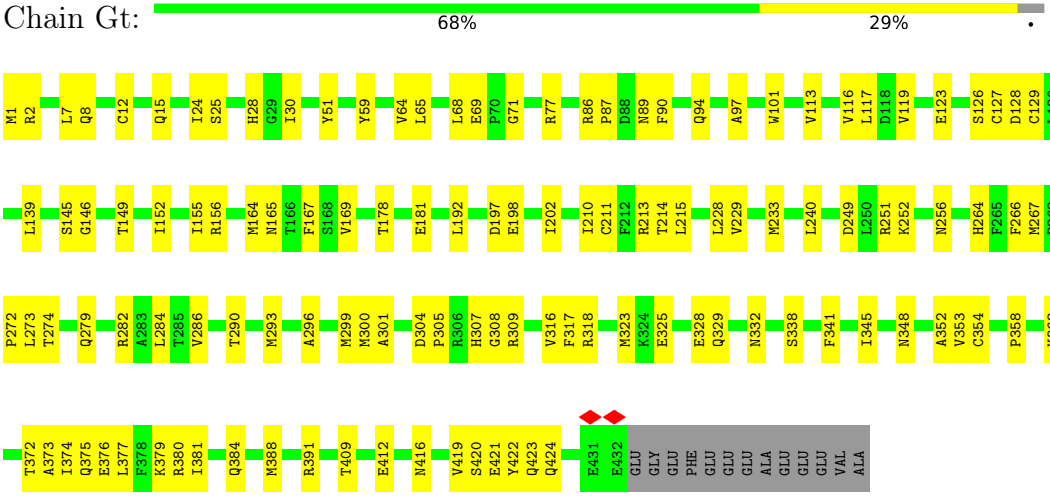

- Molecule 17: Tubulin beta-4B chain

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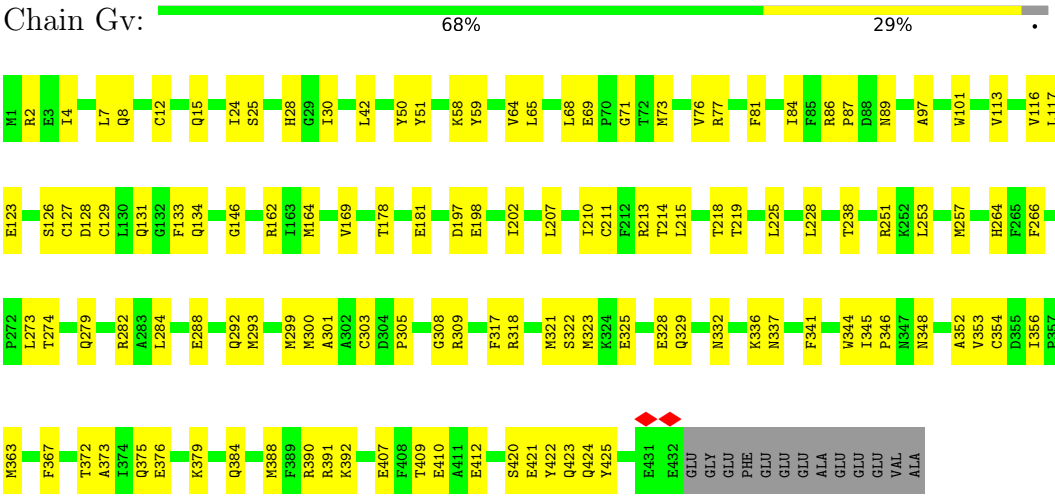

• Molecule 17: Tubulin beta-4B chain

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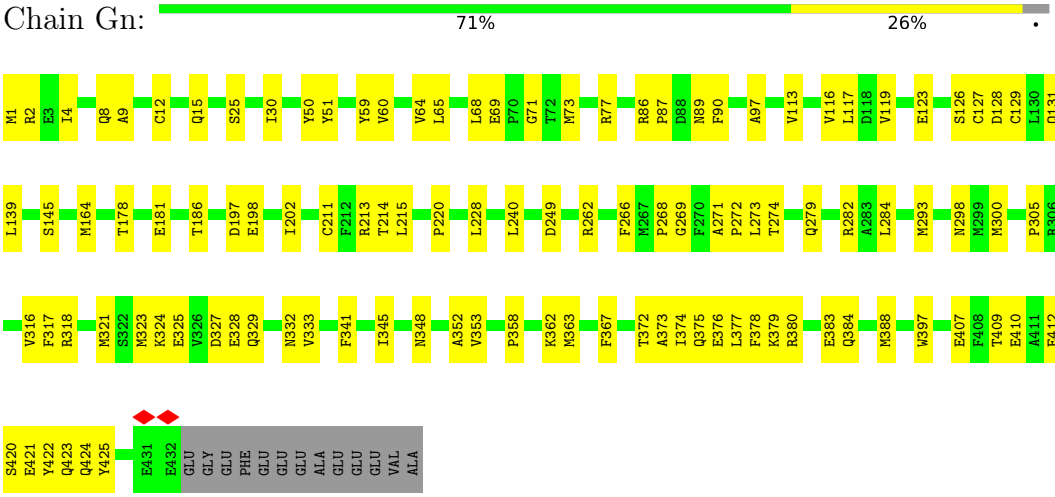

• Molecule 17: Tubulin beta-4B chain

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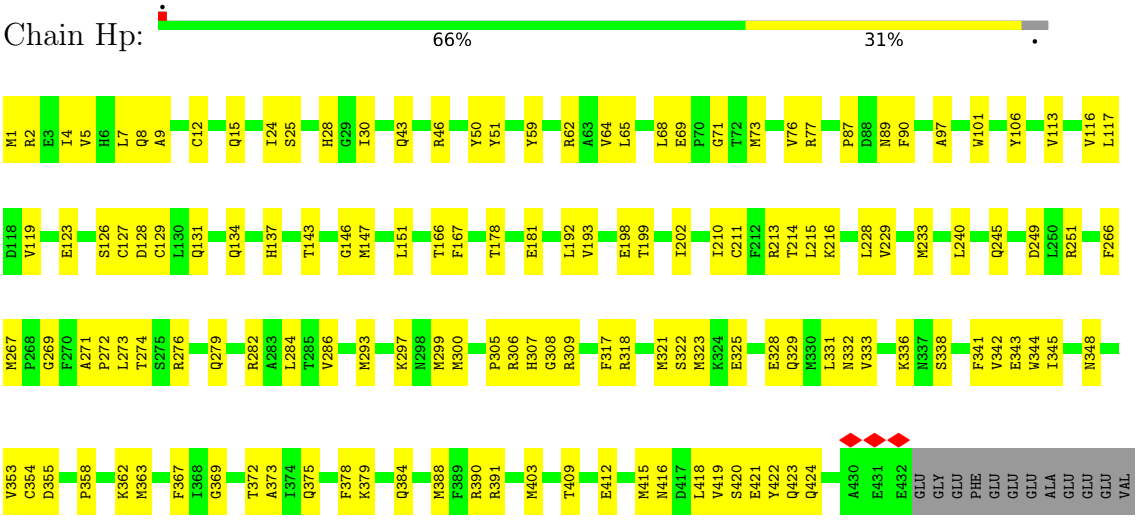

ALA

• Molecule 17: Tubulin beta-4B chain

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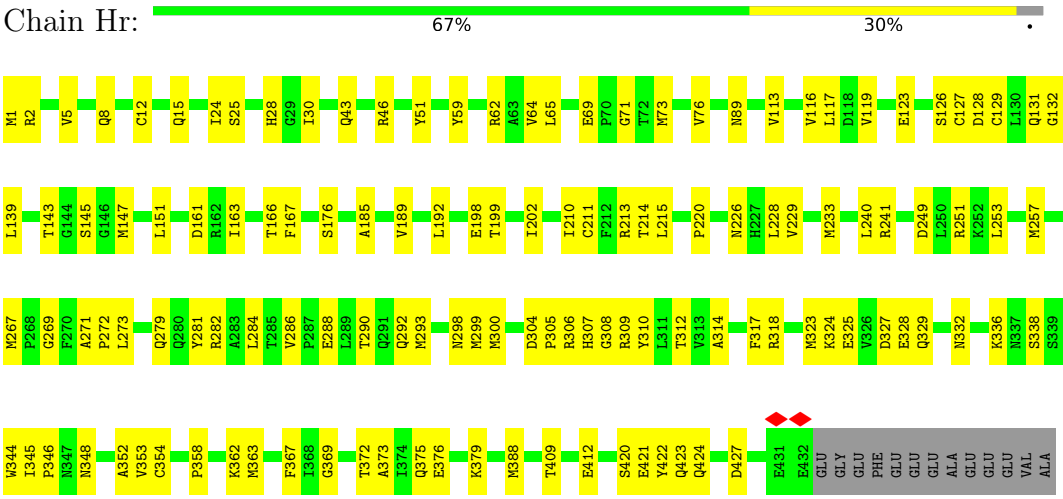

• Molecule 17: Tubulin beta-4B chain

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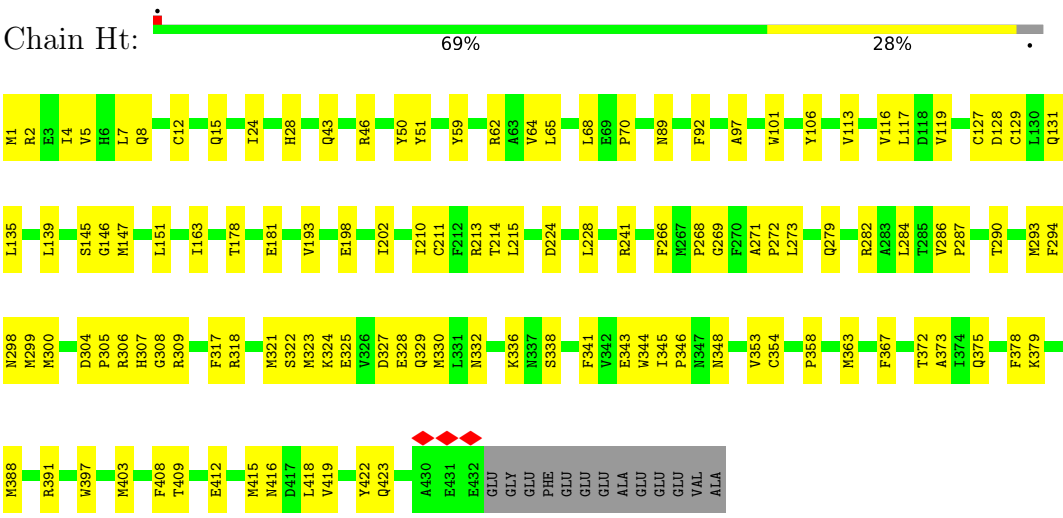

• Molecule 17: Tubulin beta-4B chain

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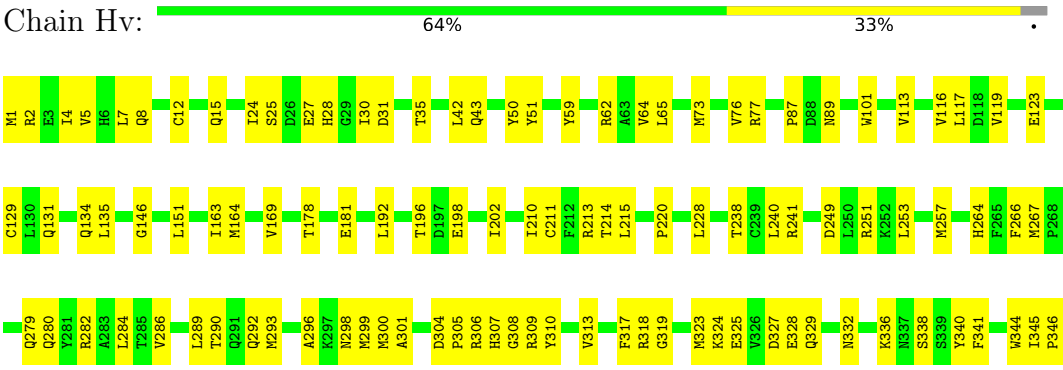

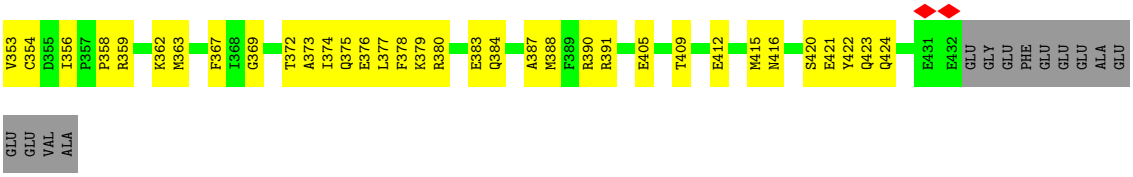

• Molecule 17: Tubulin beta-4B chain

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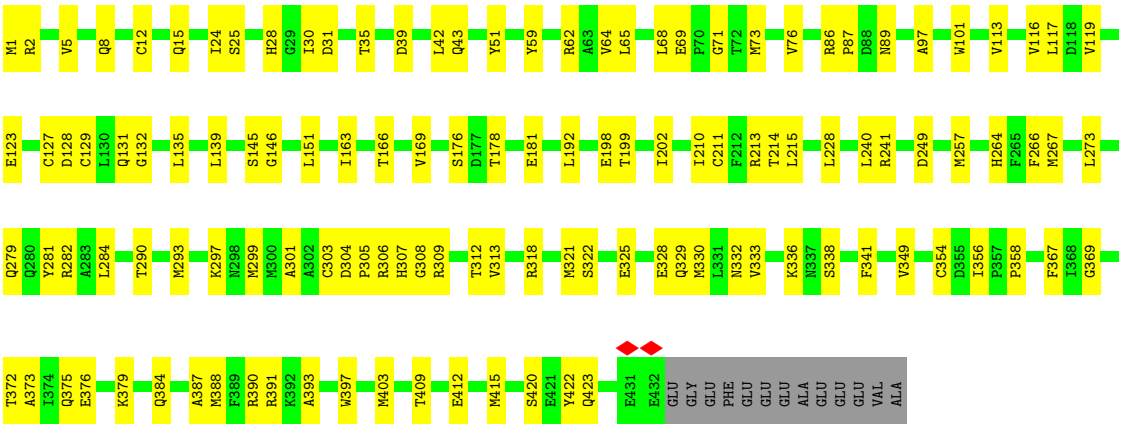
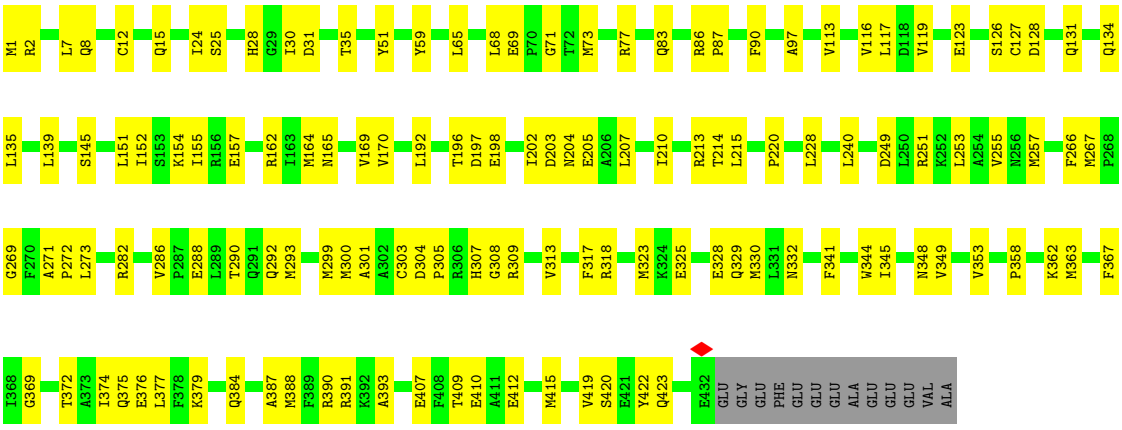


• Molecule 17: Tubulin beta-4B chain

Chain Ip:



• Molecule 17: Tubulin beta-4B chain

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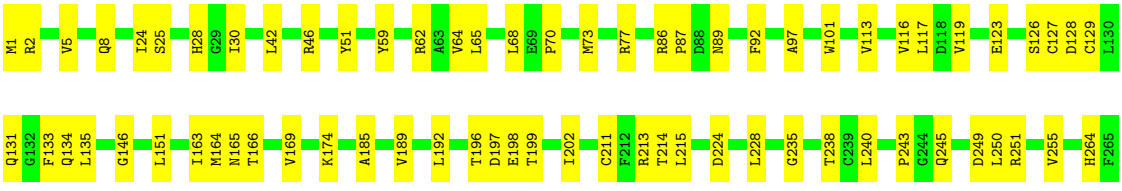

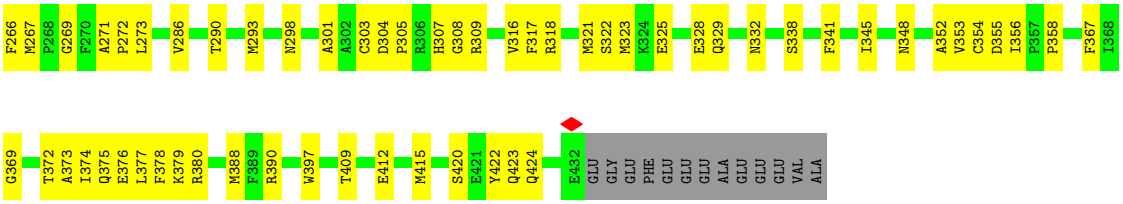

• Molecule 17: Tubulin beta-4B chain

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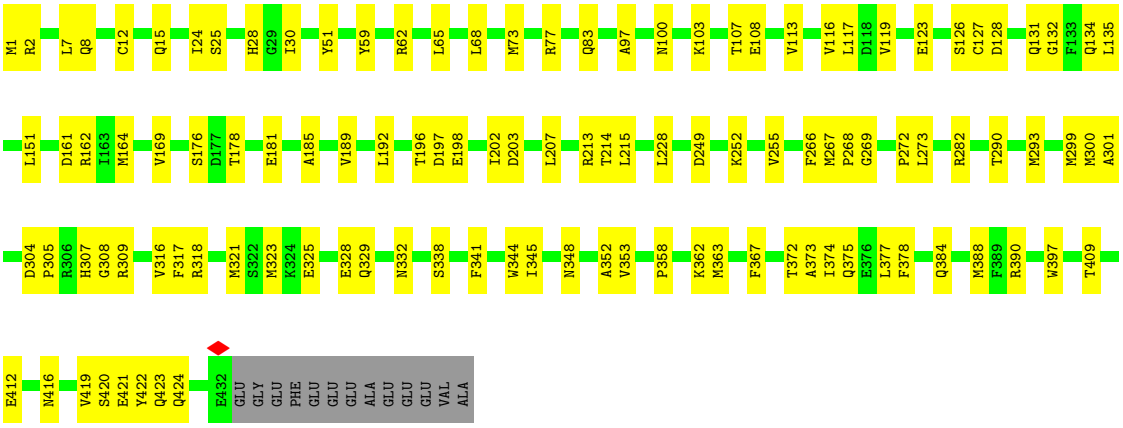

• Molecule 17: Tubulin beta-4B chain

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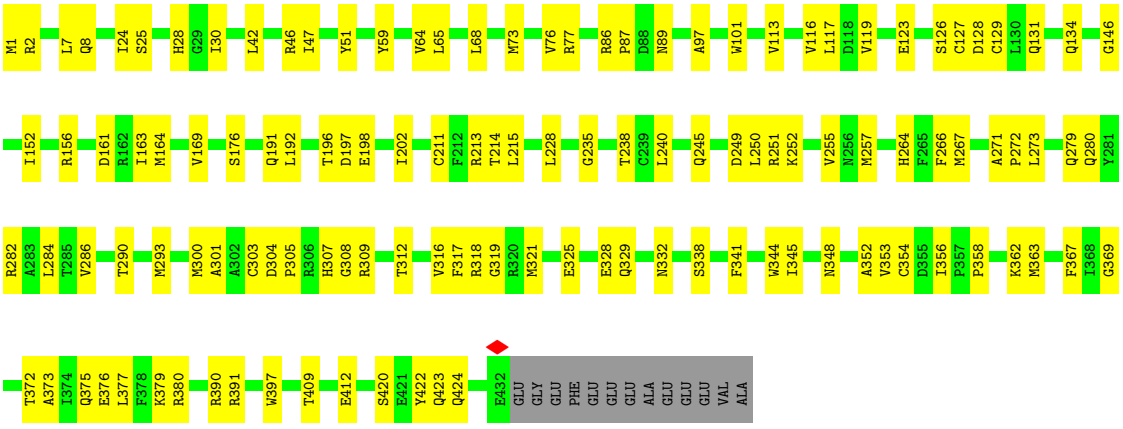
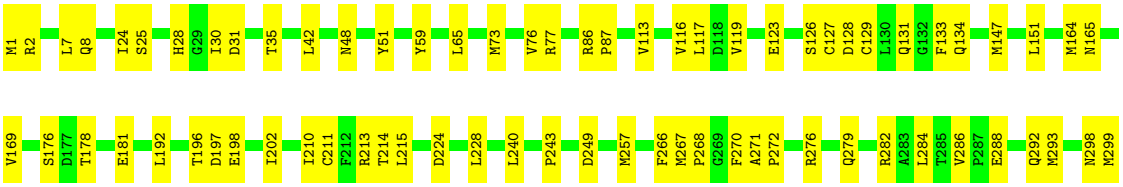
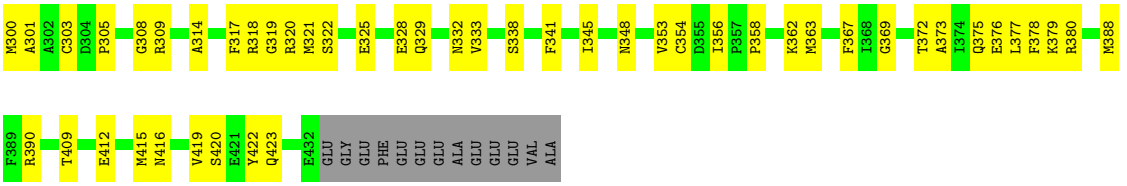


• Molecule 17: Tubulin beta-4B chain

Chain In:





• Molecule 17: Tubulin beta-4B chain

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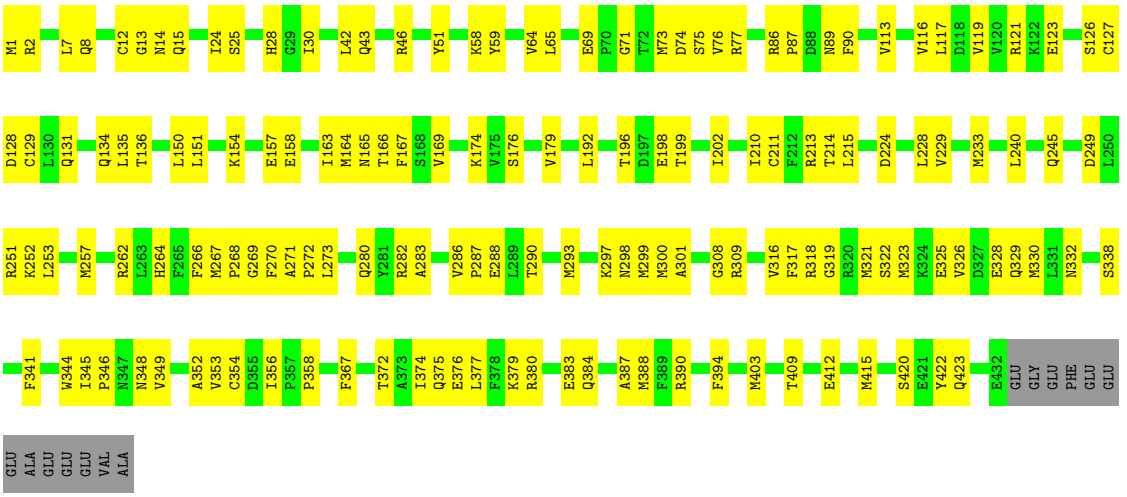

• Molecule 17: Tubulin beta-4B chain

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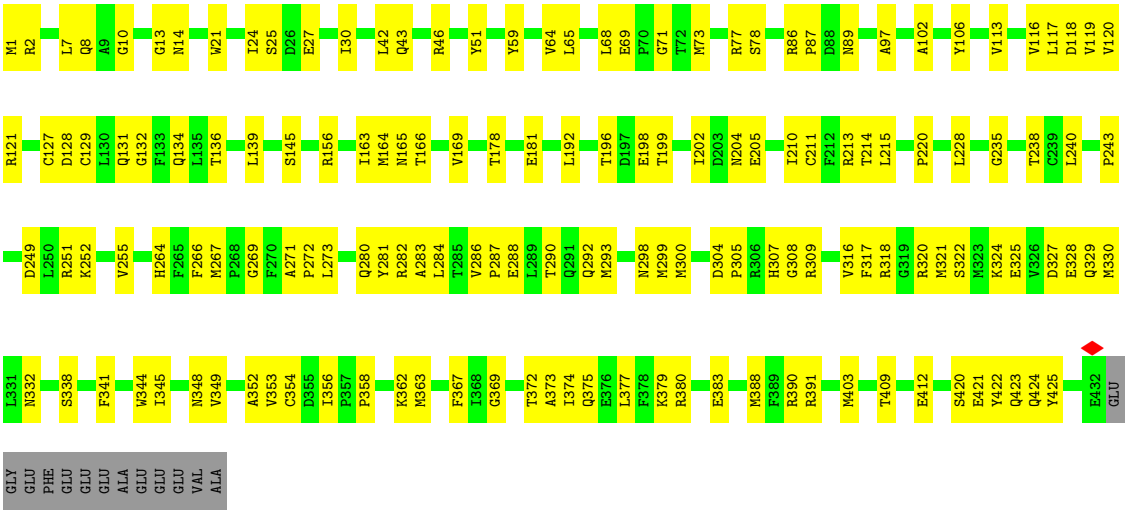
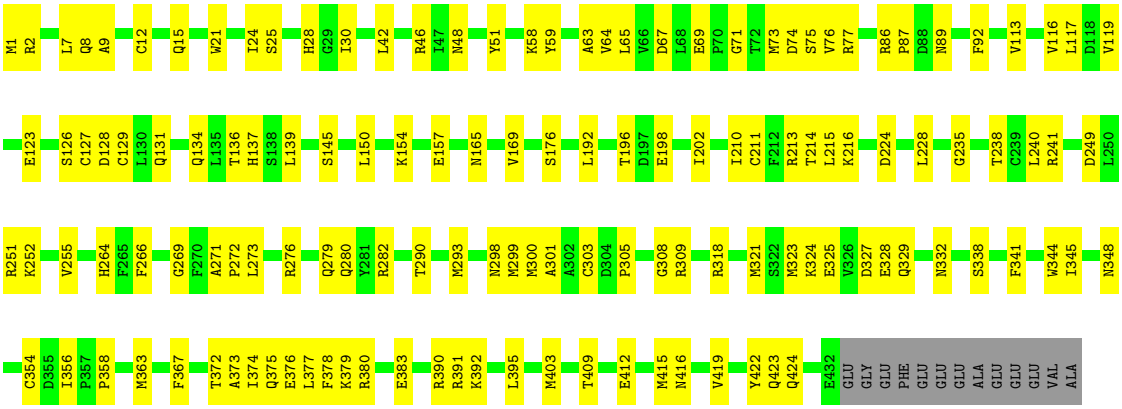


• Molecule 17: Tubulin beta-4B chain

Chain Jt:



• Molecule 17: Tubulin beta-4B chain

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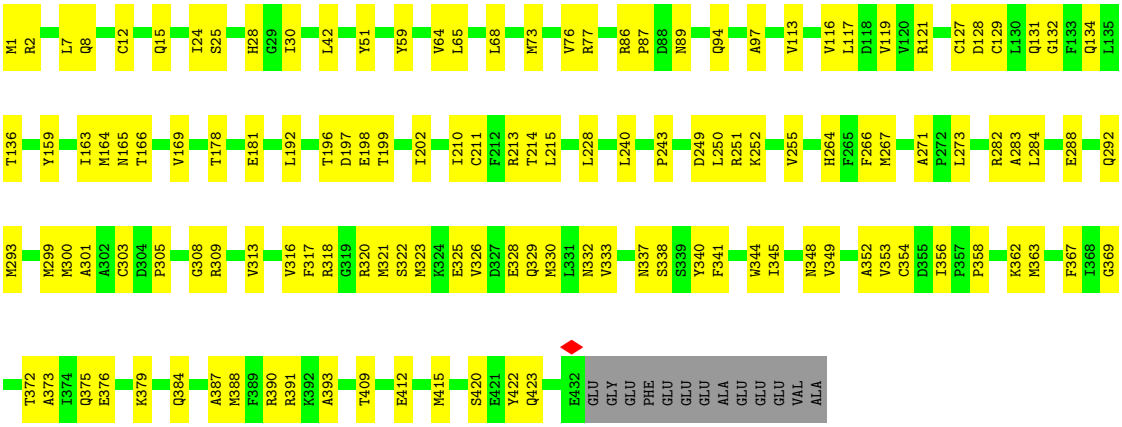

• Molecule 17: Tubulin beta-4B chain

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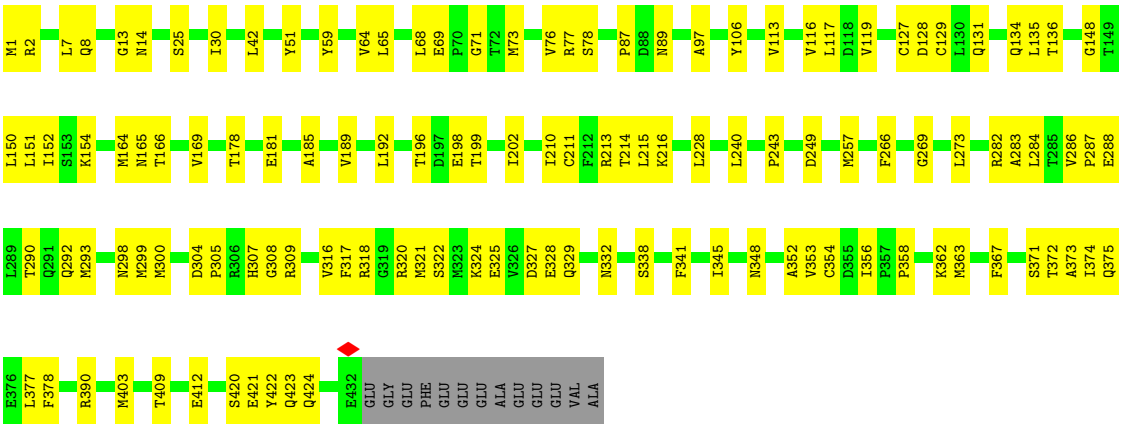

• Molecule 17: Tubulin beta-4B chain

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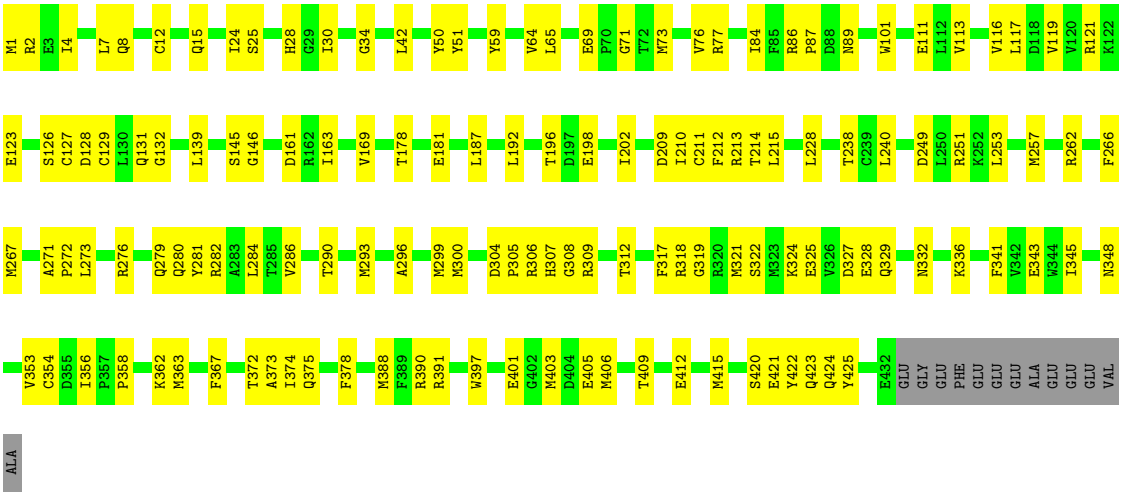

- Molecule 17: Tubulin beta-4B chain

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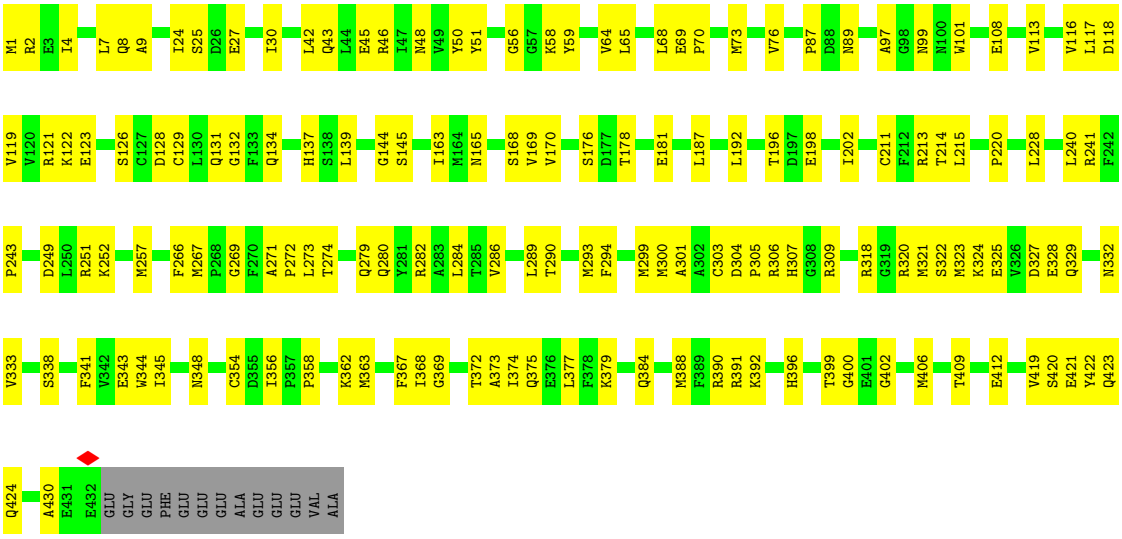
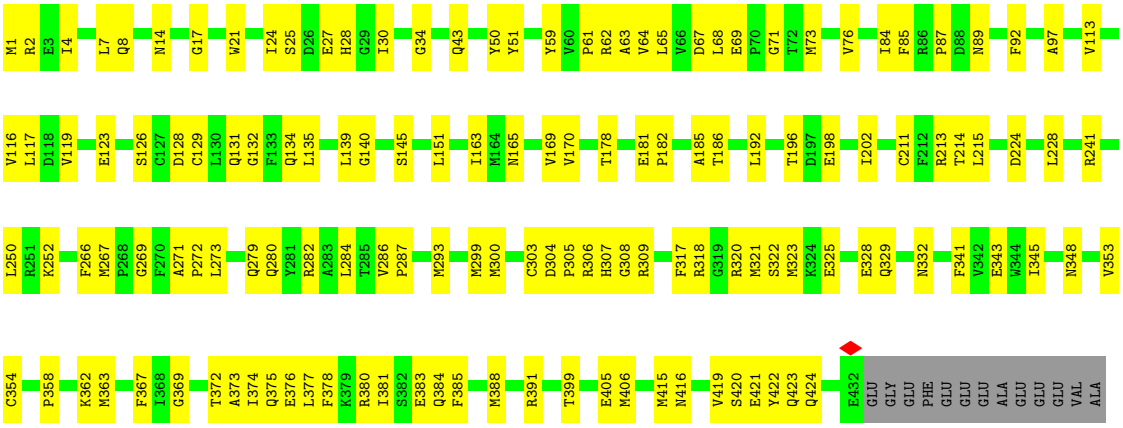


- Molecule 17: Tubulin beta-4B chain

Chain Kr:

• Molecule 17: Tubulin beta-4B chain

Chain Kt:



• Molecule 17: Tubulin beta-4B chain

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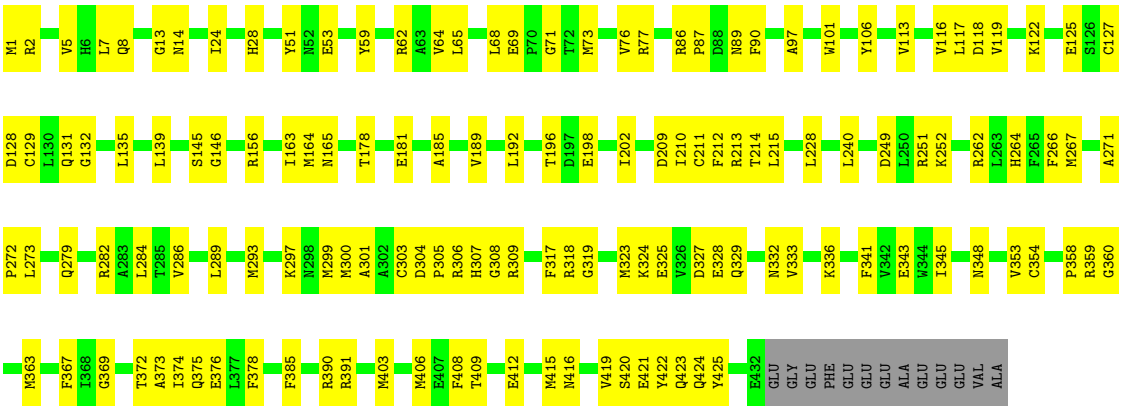
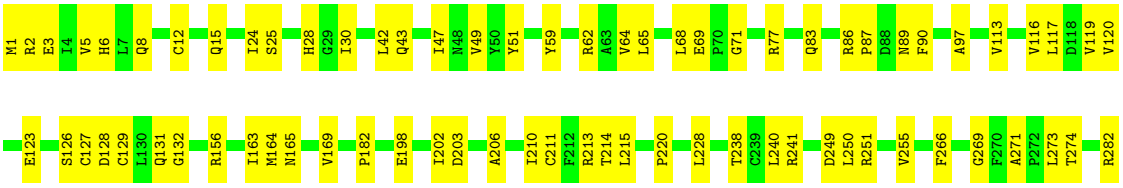
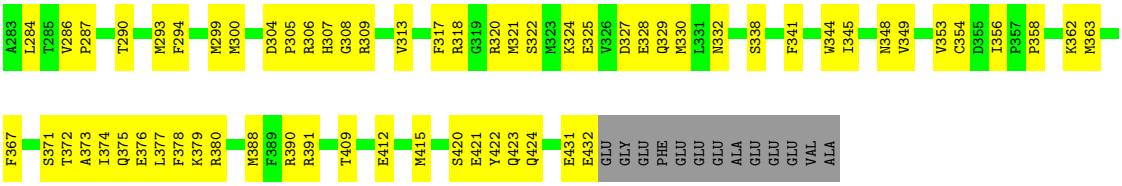


• Molecule 17: Tubulin beta-4B chain

Chain Ln:





• Molecule 17: Tubulin beta-4B chain

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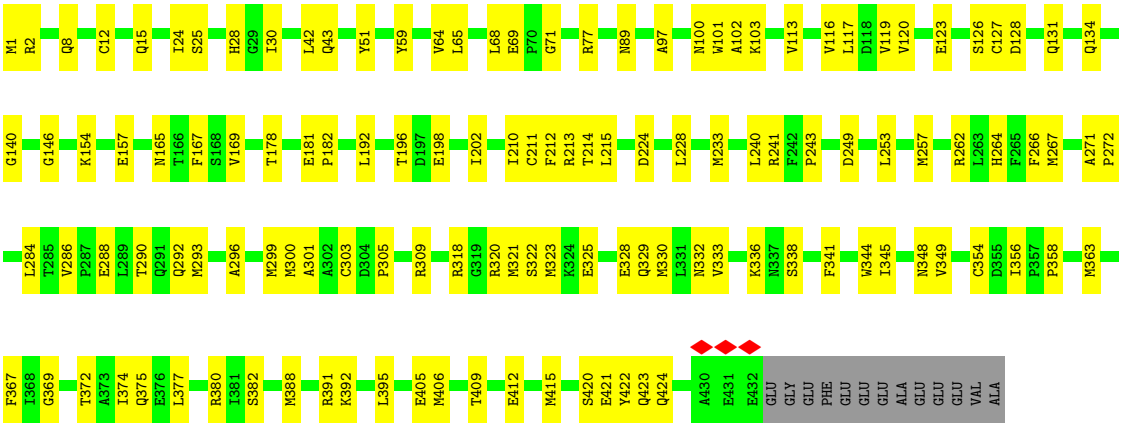

• Molecule 17: Tubulin beta-4B chain

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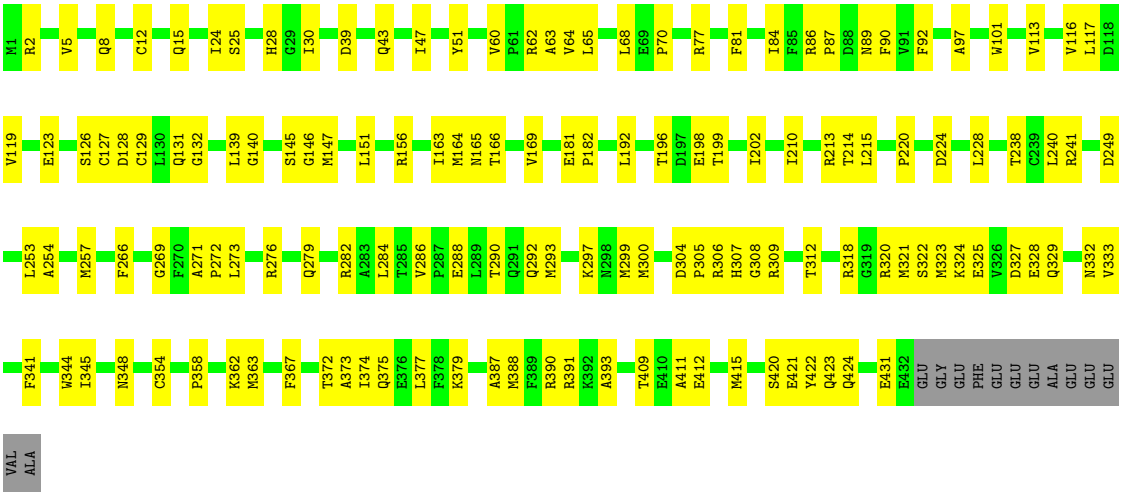

• Molecule 17: Tubulin beta-4B chain

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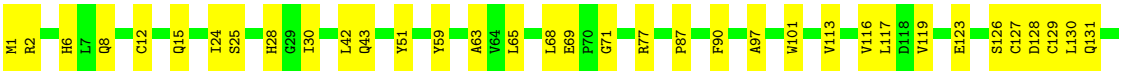
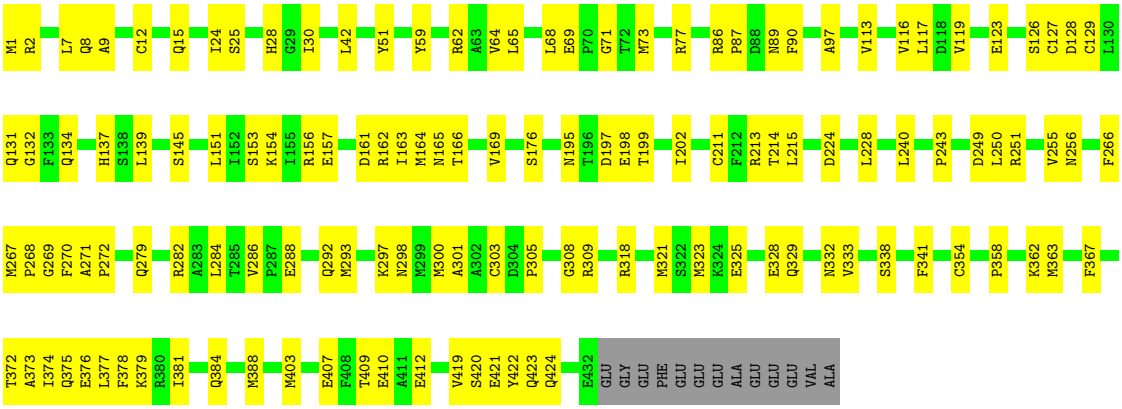


• Molecule 17: Tubulin beta-4B chain

Chain Lv:

• Molecule 17: Tubulin beta-4B chain

Chain Mn:



• Molecule 17: Tubulin beta-4B chain

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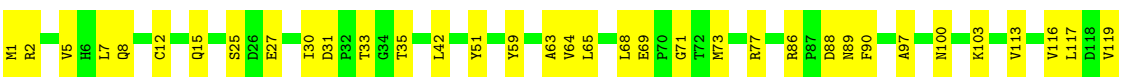

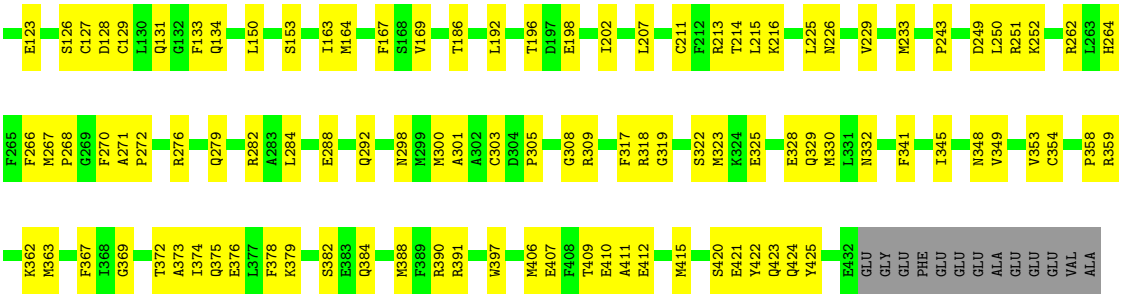

• Molecule 17: Tubulin beta-4B chain

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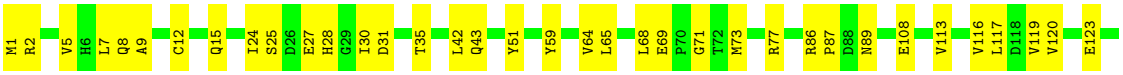
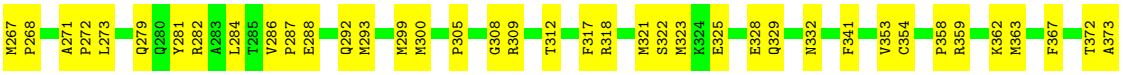
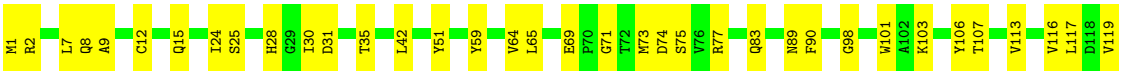
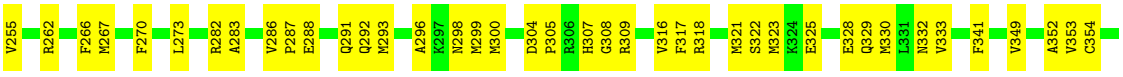




• Molecule 17: Tubulin beta-4B chain

Chain Mt:





• Molecule 17: Tubulin beta-4B chain

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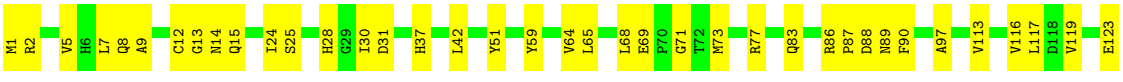

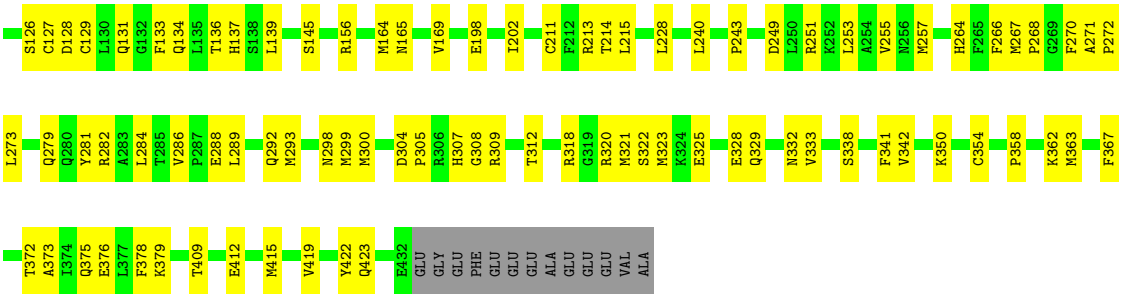

• Molecule 18: Tubulin alpha-3 chain

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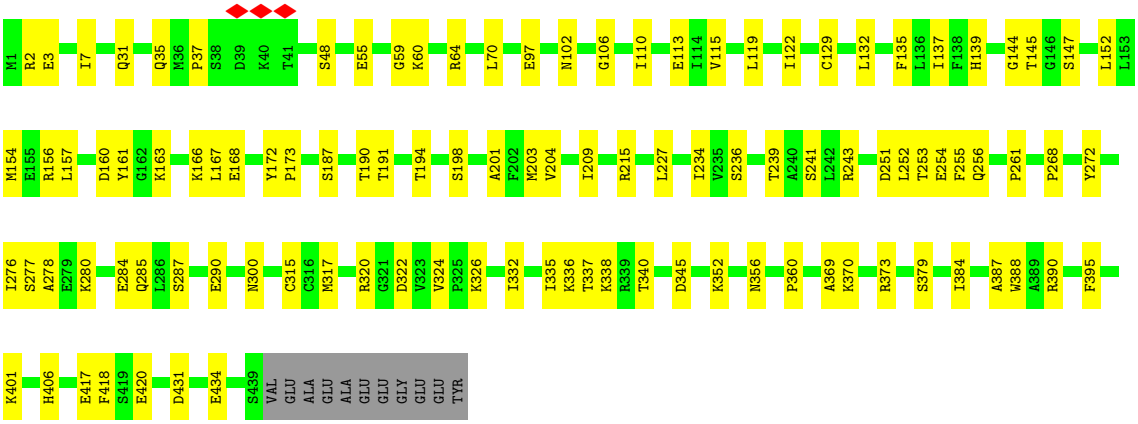

• Molecule 18: Tubulin alpha-3 chain

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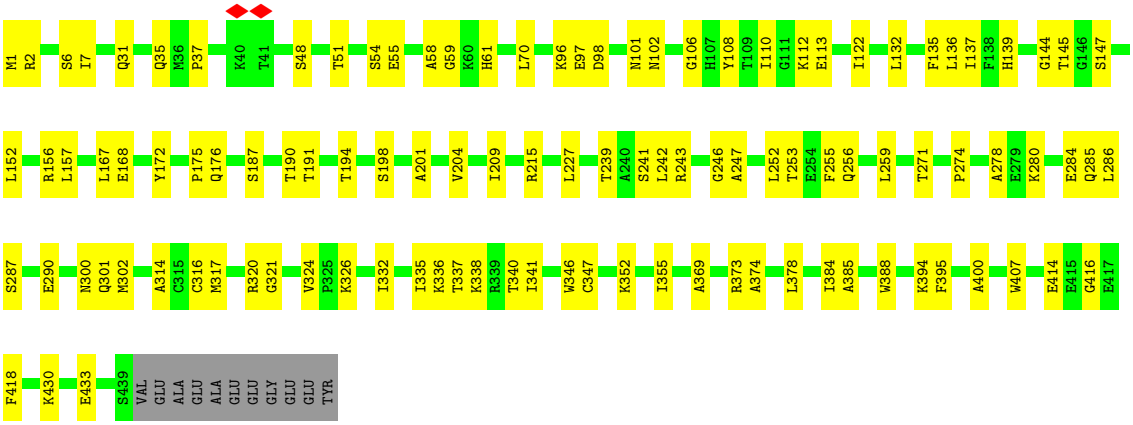

• Molecule 18: Tubulin alpha-3 chain

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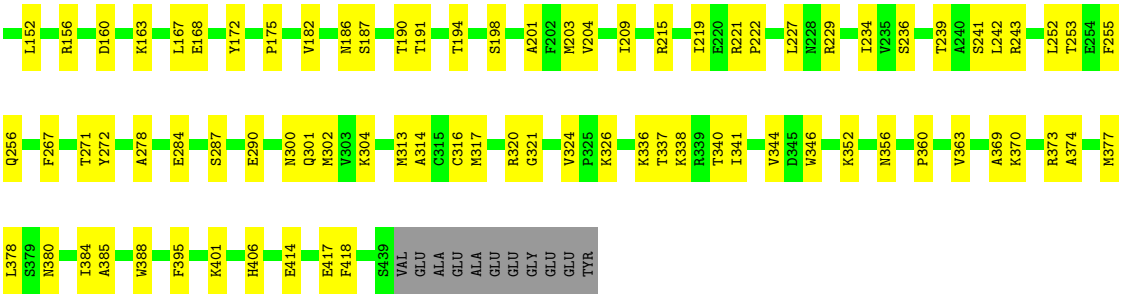

• Molecule 18: Tubulin alpha-3 chain

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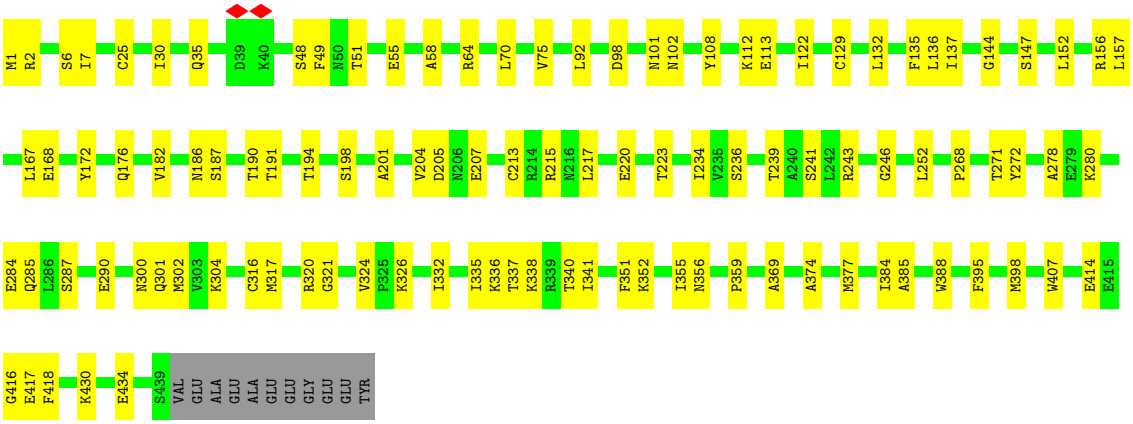

• Molecule 18: Tubulin alpha-3 chain

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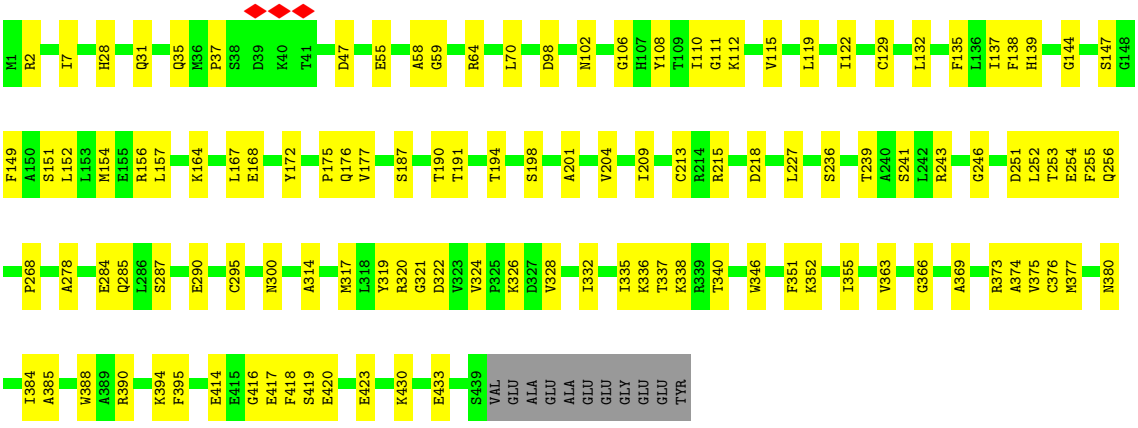

• Molecule 18: Tubulin alpha-3 chain

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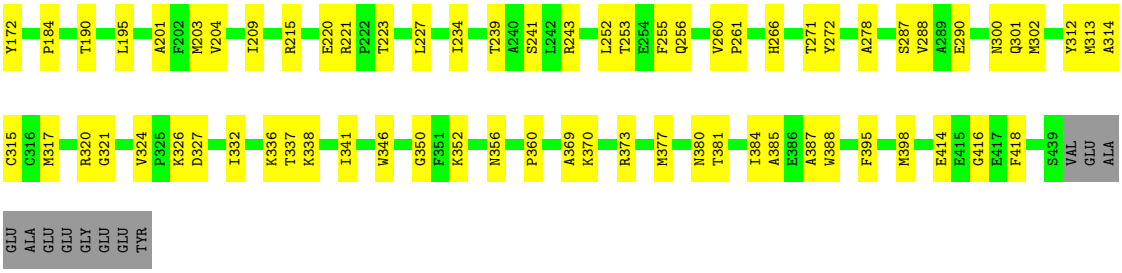
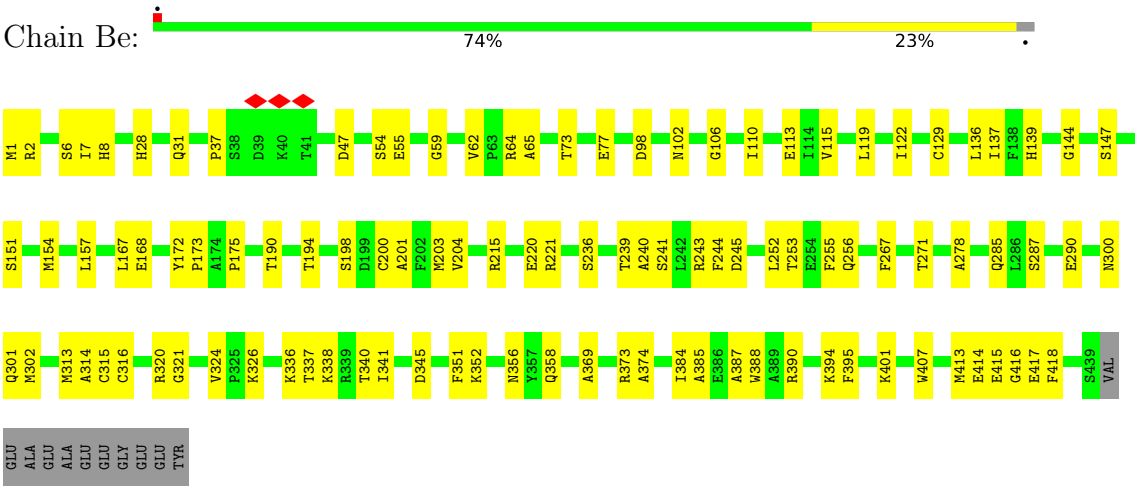
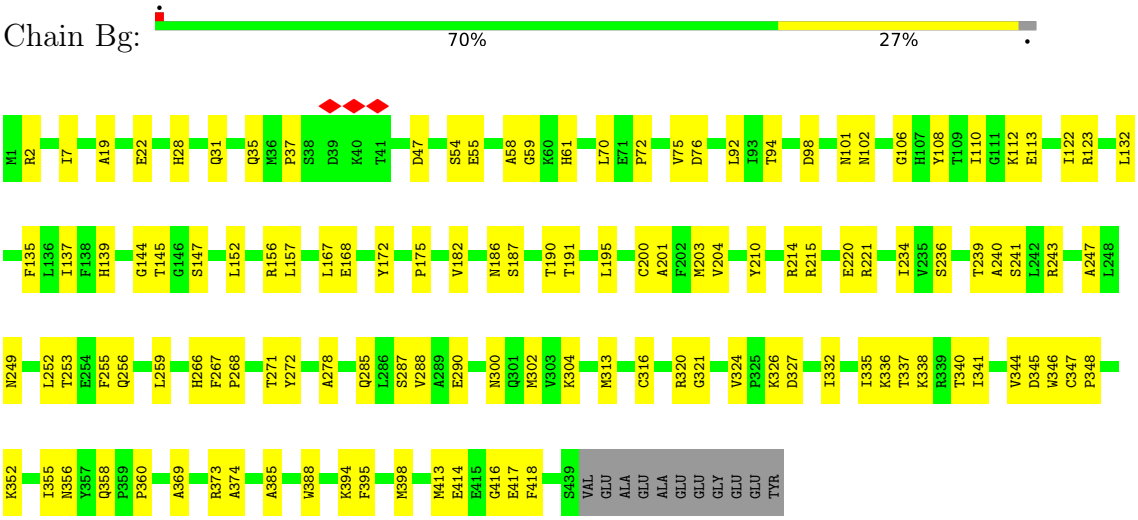


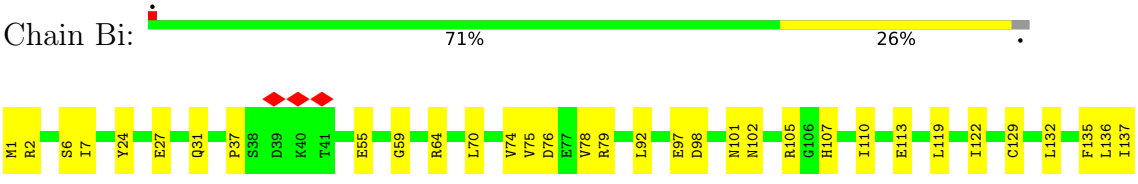
• Molecule 18: Tubulin alpha-3 chain

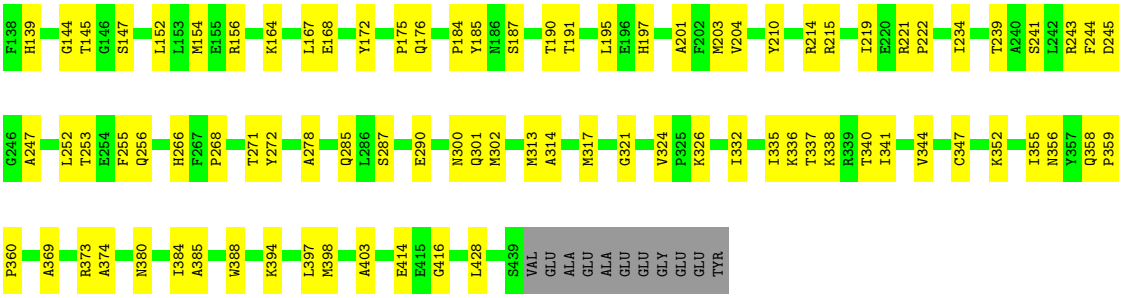


• Molecule 18: Tubulin alpha-3 chain



• Molecule 18: Tubulin alpha-3 chain





• Molecule 18: Tubulin alpha-3 chain

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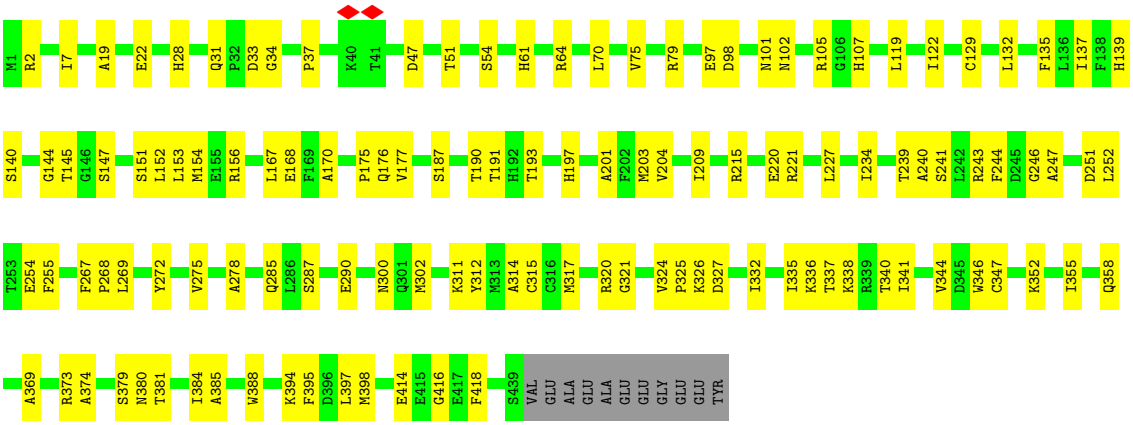

• Molecule 18: Tubulin alpha-3 chain

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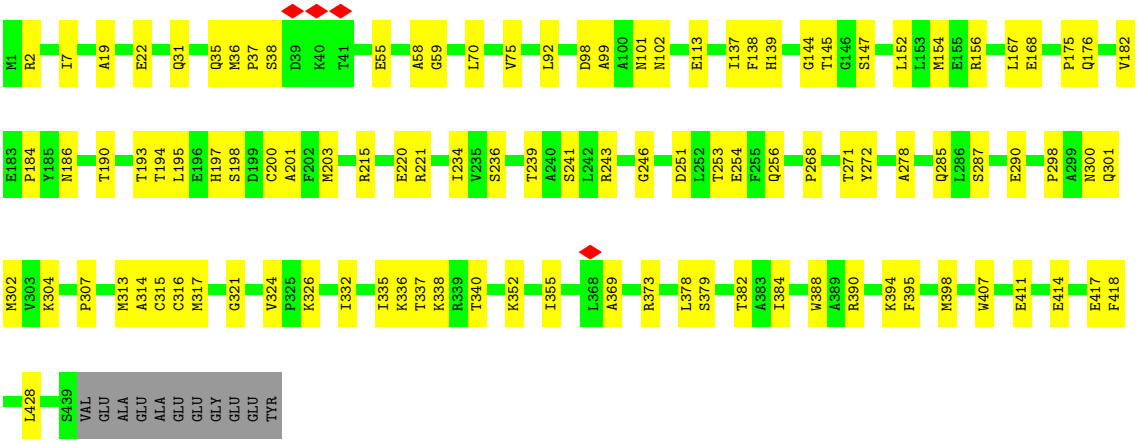

• Molecule 18: Tubulin alpha-3 chain

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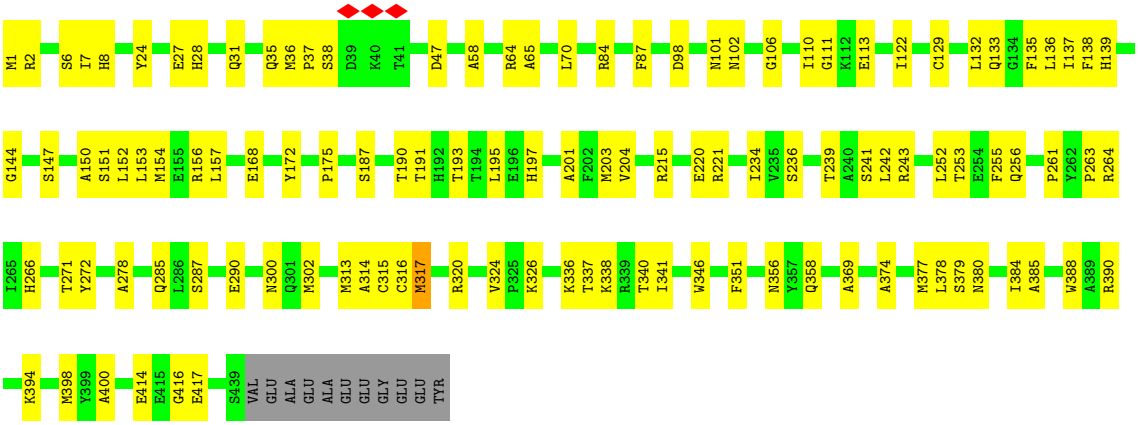

• Molecule 18: Tubulin alpha-3 chain

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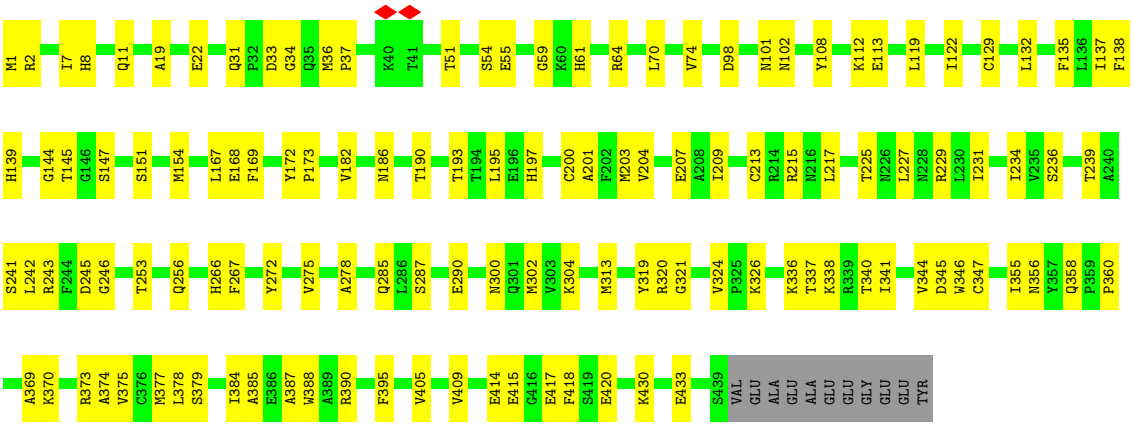

• Molecule 18: Tubulin alpha-3 chain

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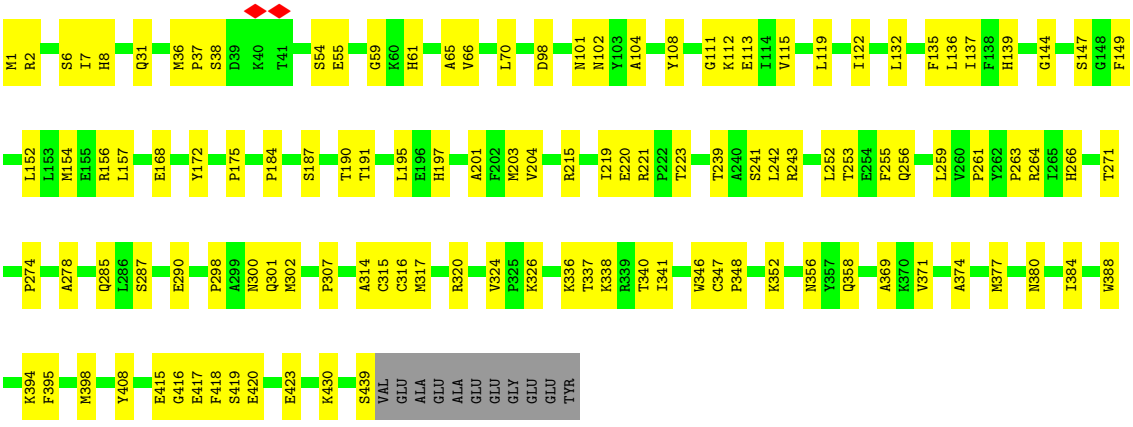

• Molecule 18: Tubulin alpha-3 chain

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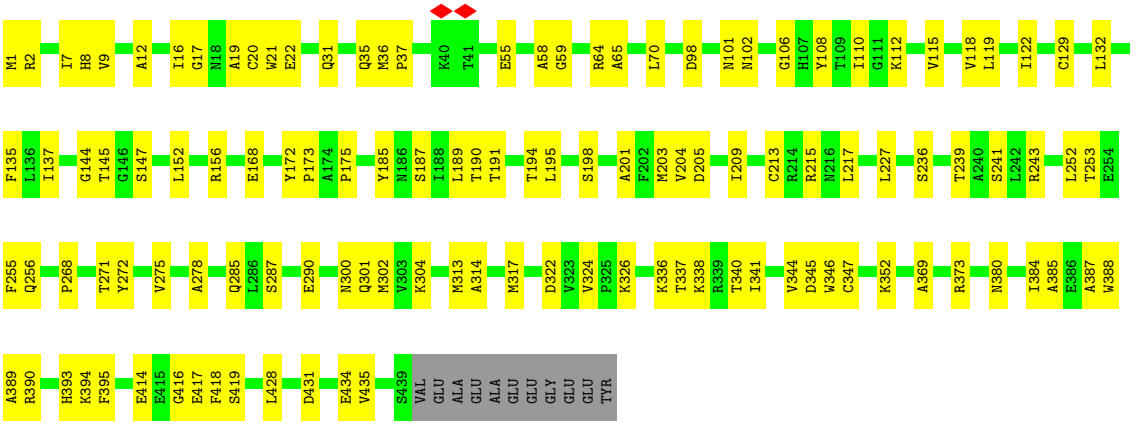

• Molecule 18: Tubulin alpha-3 chain

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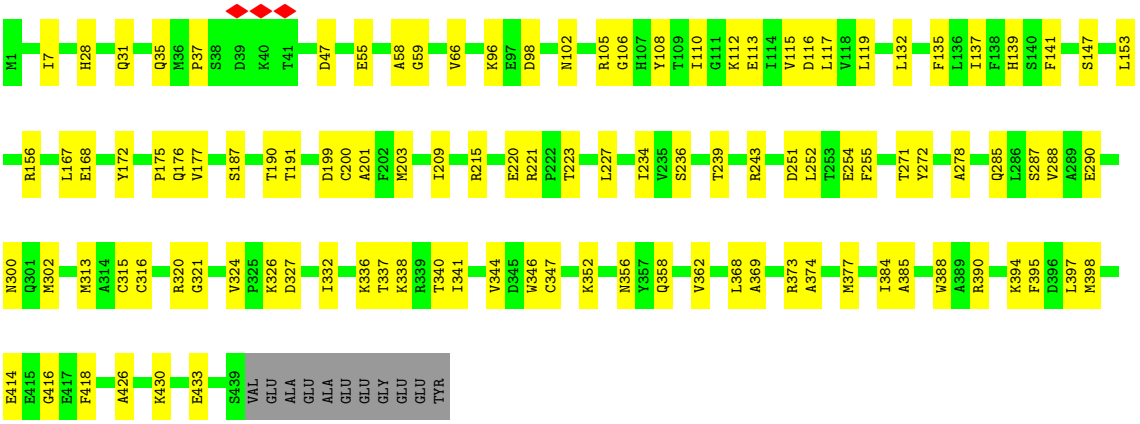

• Molecule 18: Tubulin alpha-3 chain

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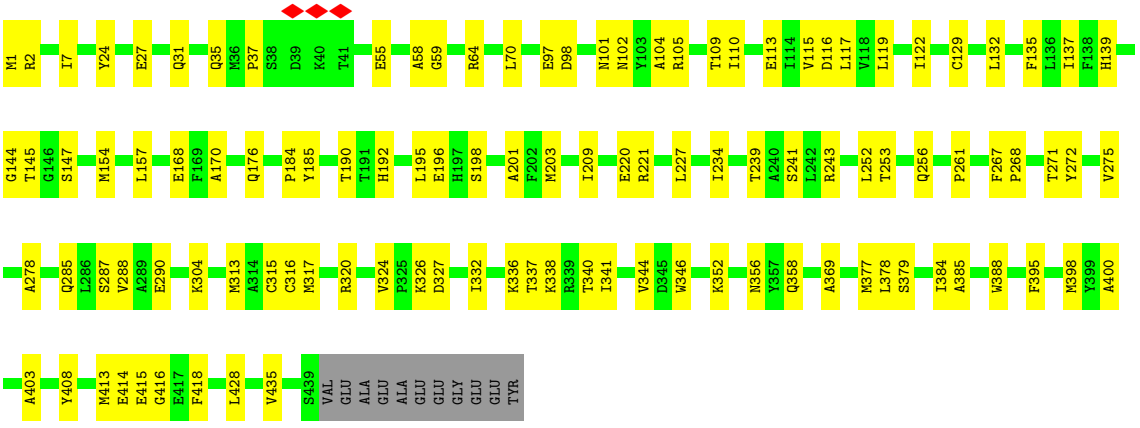

• Molecule 18: Tubulin alpha-3 chain

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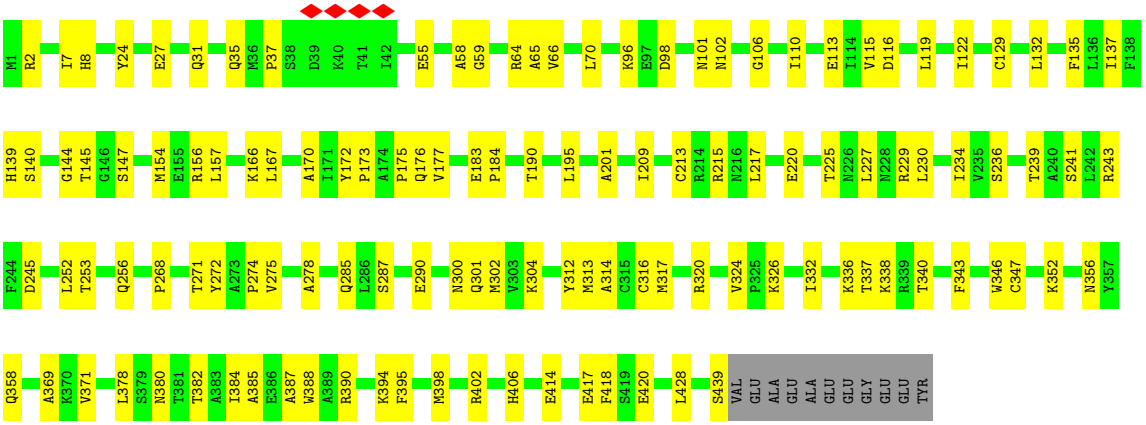
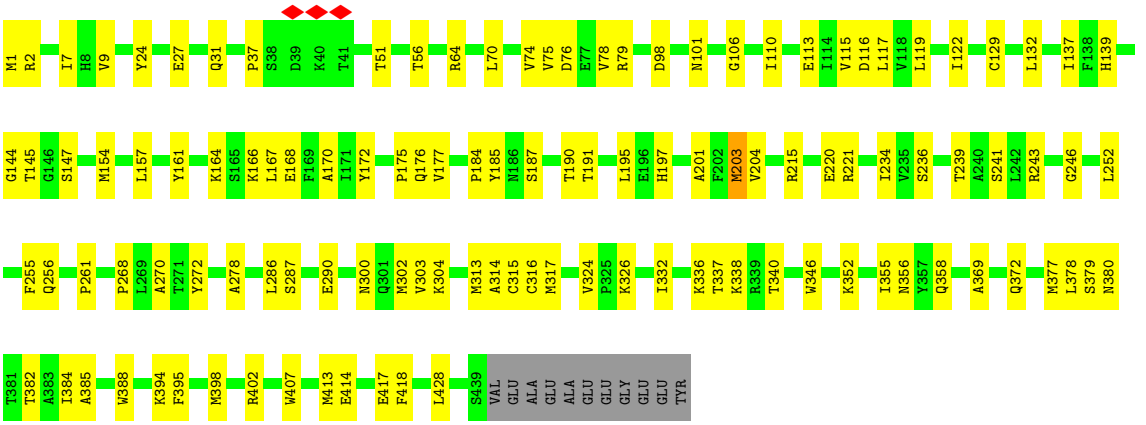
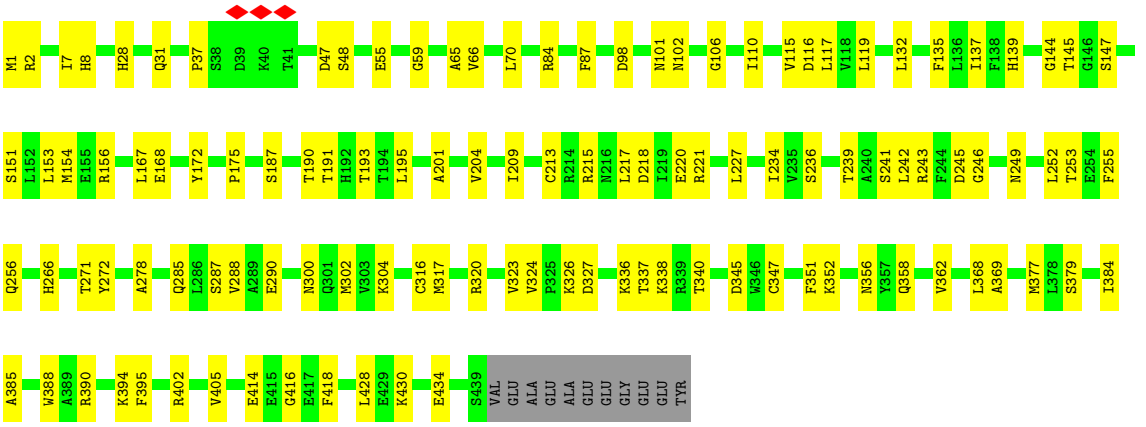


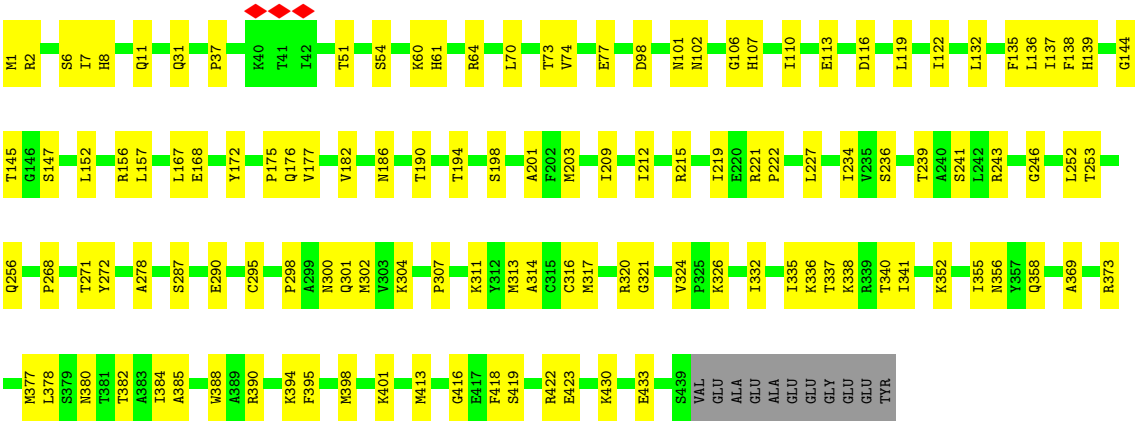
• Molecule 18: Tubulin alpha-3 chain



• Molecule 18: Tubulin alpha-3 chain

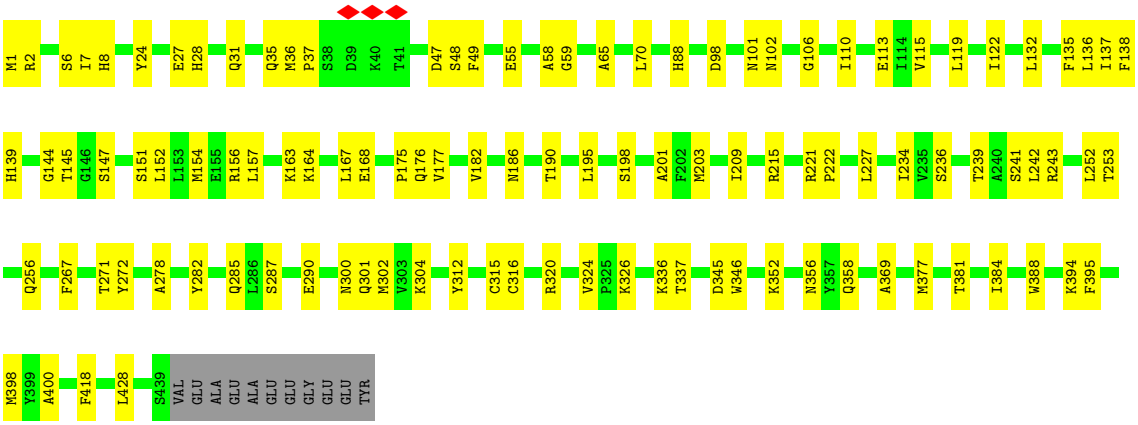


• Molecule 18: Tubulin alpha-3 chain



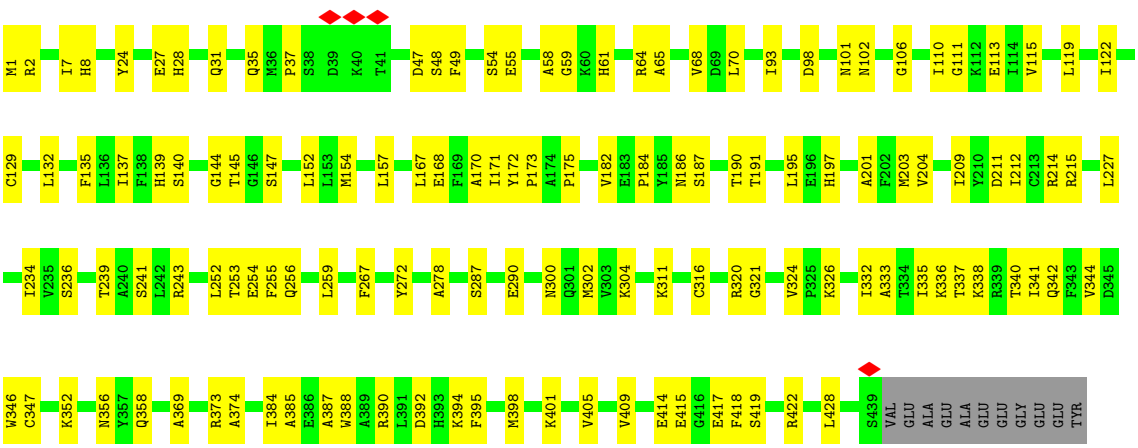
• Molecule 18: Tubulin alpha-3 chain

Chain Ee:



• Molecule 18: Tubulin alpha-3 chain

Chain Eg:



• Molecule 18: Tubulin alpha-3 chain

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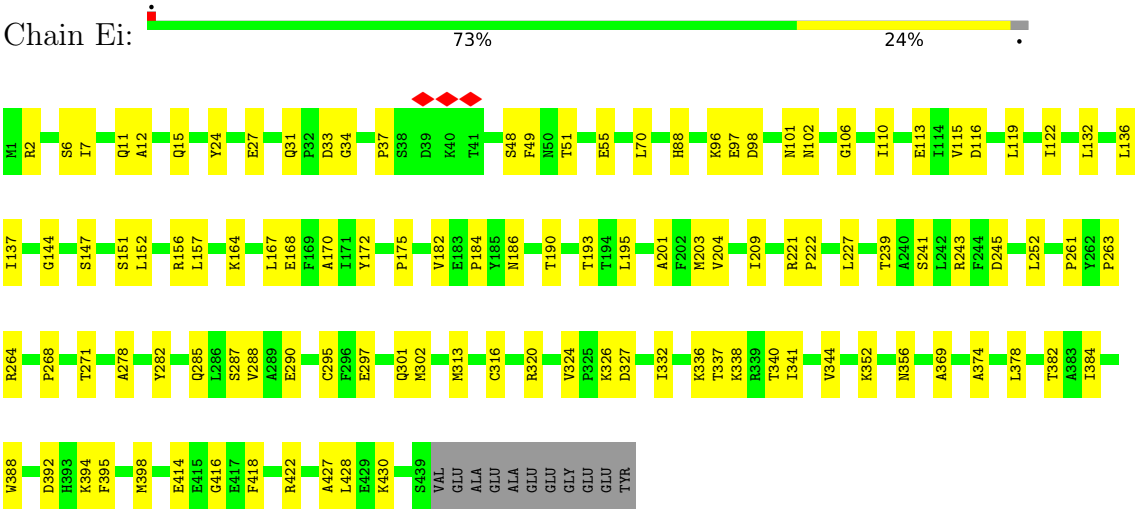

• Molecule 18: Tubulin alpha-3 chain

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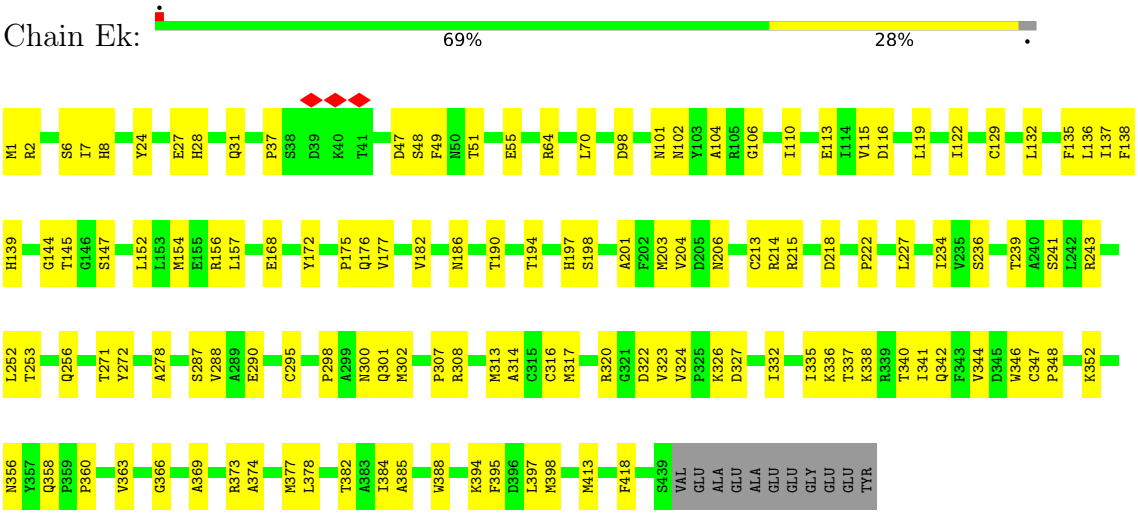
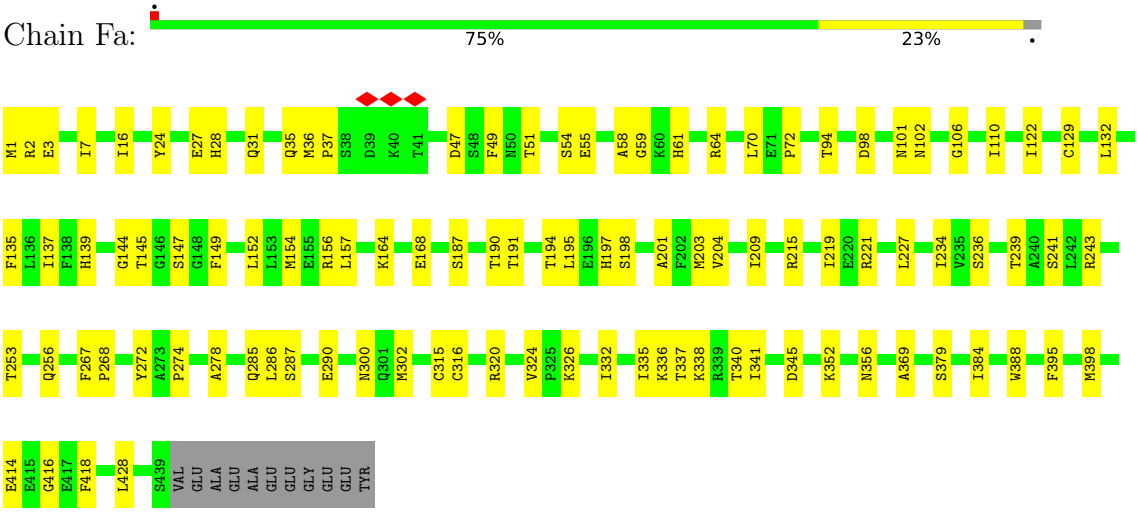


• Molecule 18: Tubulin alpha-3 chain

Chain Fa:



• Molecule 18: Tubulin alpha-3 chain

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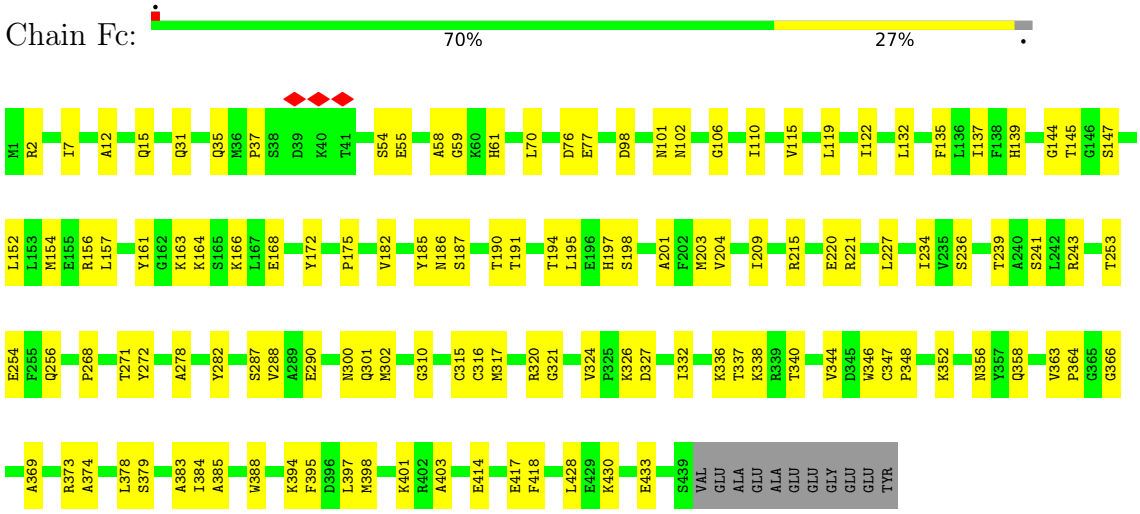
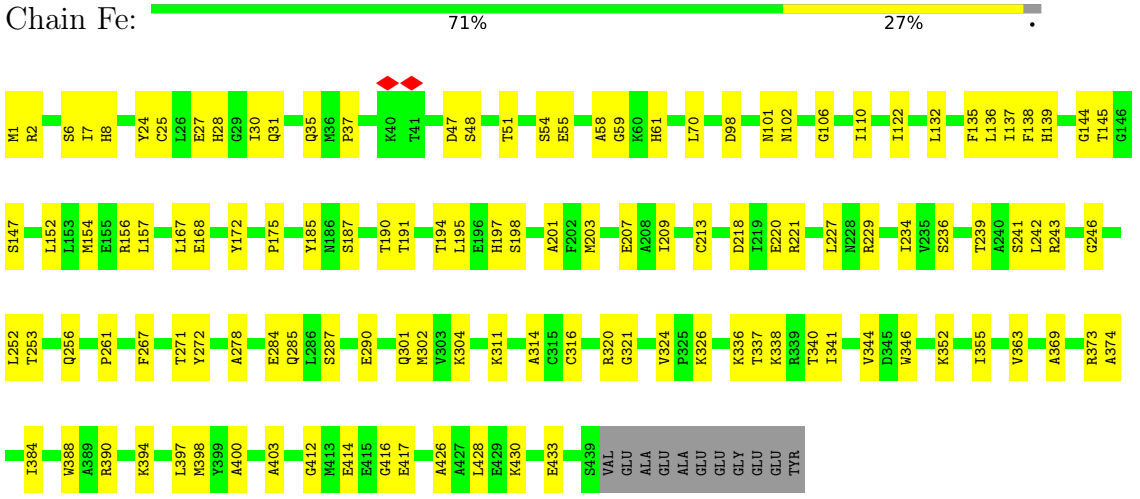


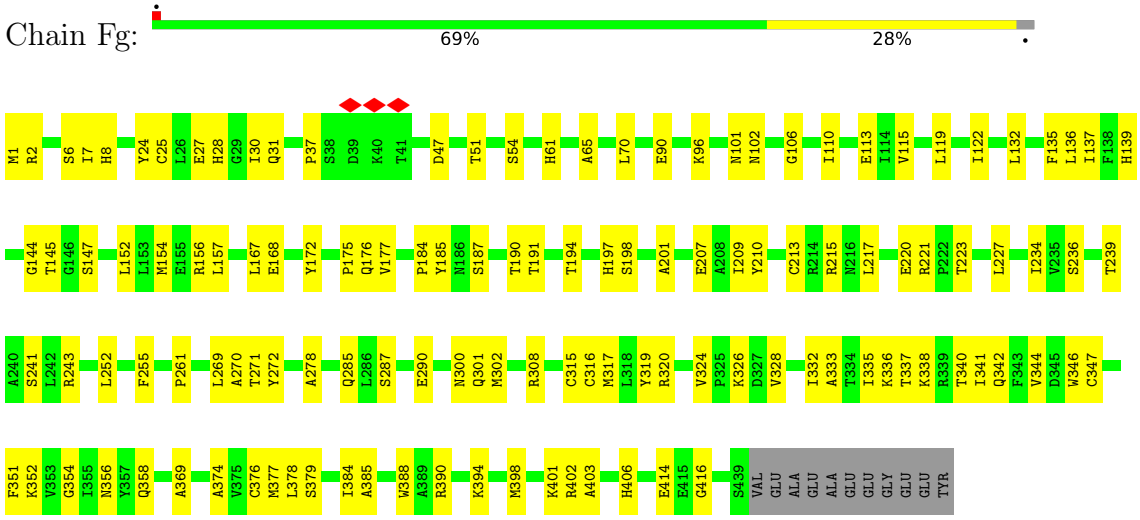
• Molecule 18: Tubulin alpha-3 chain

Chain Fe:



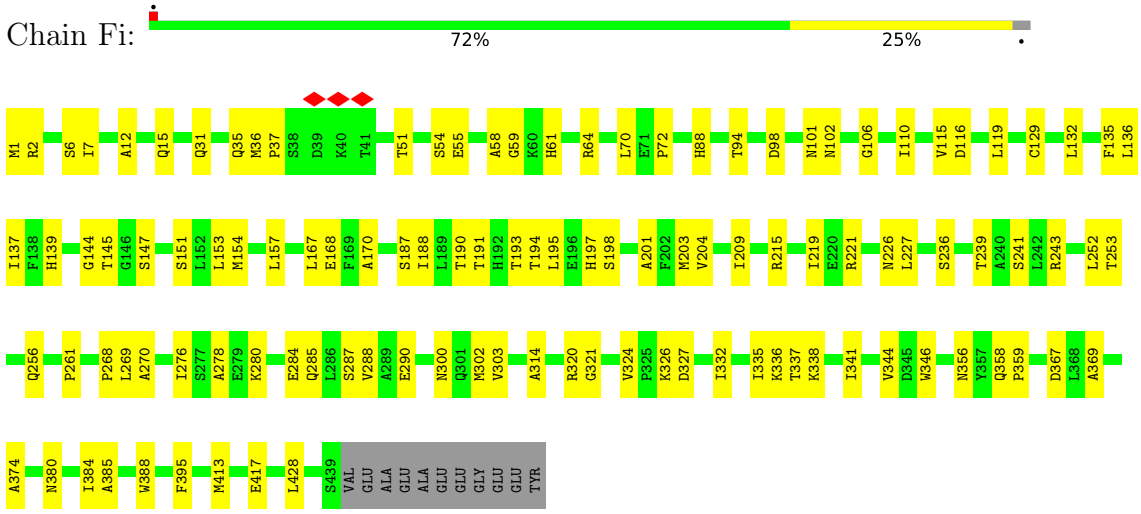
• Molecule 18: Tubulin alpha-3 chain

Chain Fg:



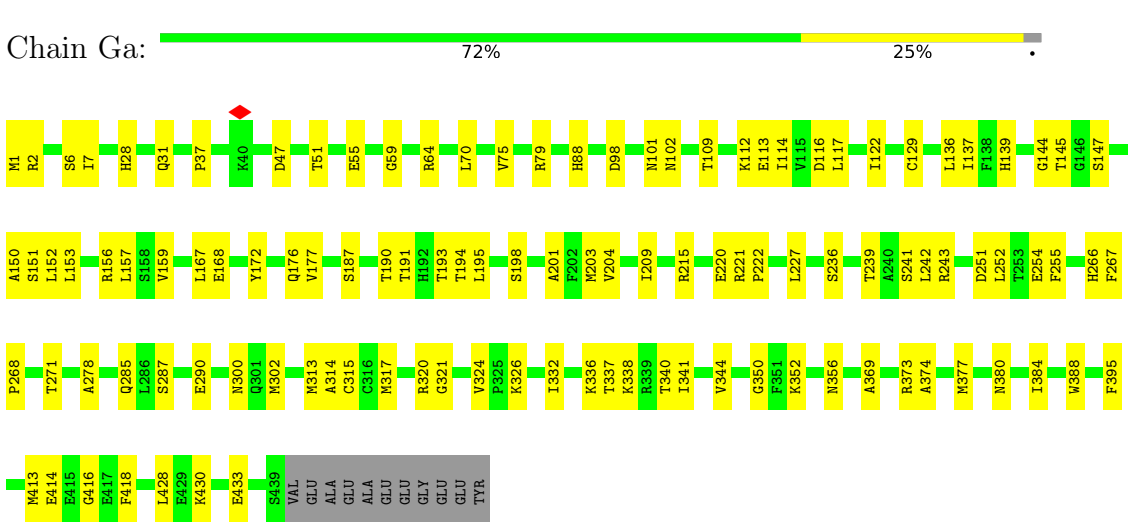
• Molecule 18: Tubulin alpha-3 chain

Chain Fi:



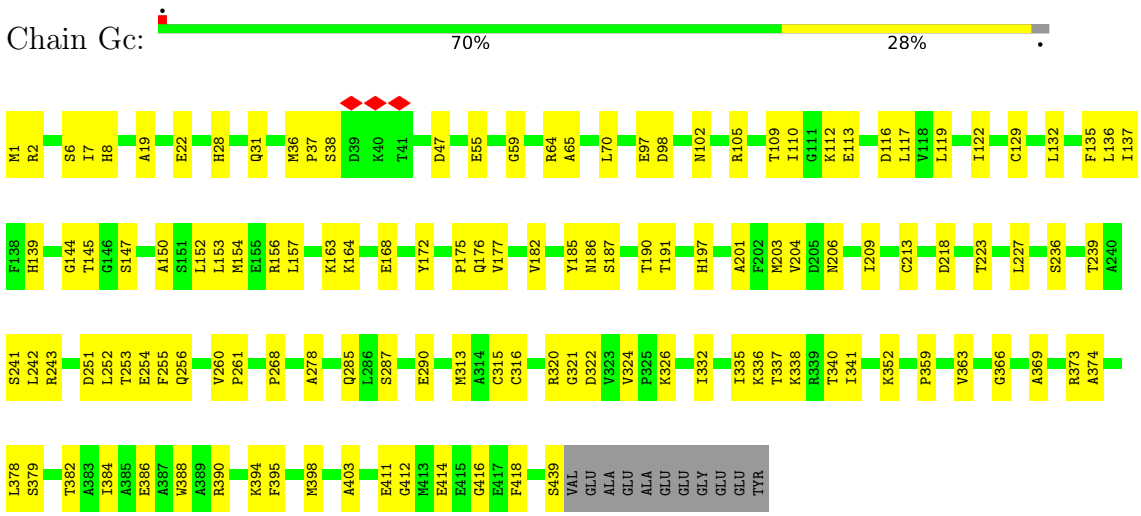
• Molecule 18: Tubulin alpha-3 chain

Chain Ga:



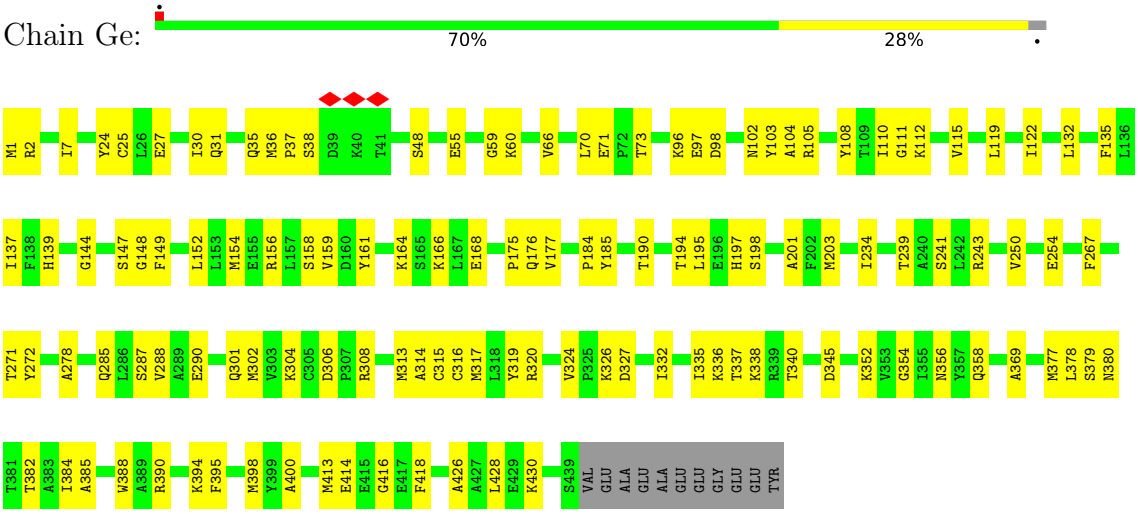
• Molecule 18: Tubulin alpha-3 chain

Chain Gc:



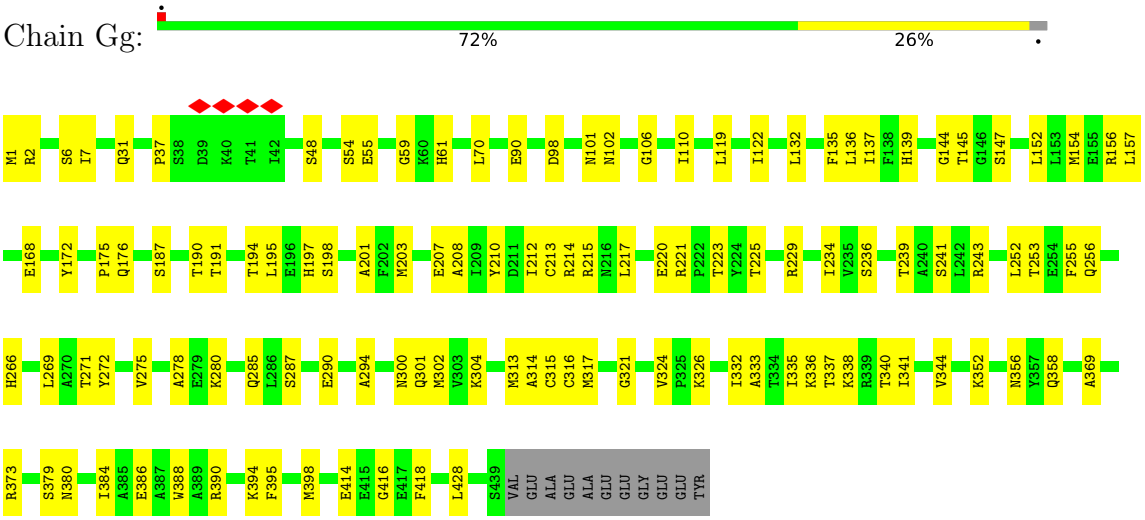
• Molecule 18: Tubulin alpha-3 chain

Chain Ge:



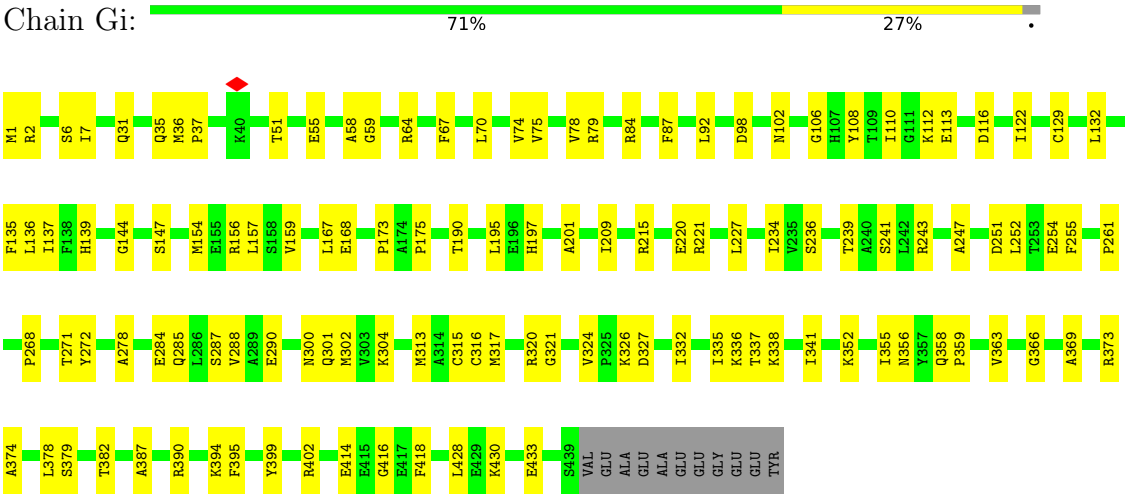
• Molecule 18: Tubulin alpha-3 chain

Chain Gg:



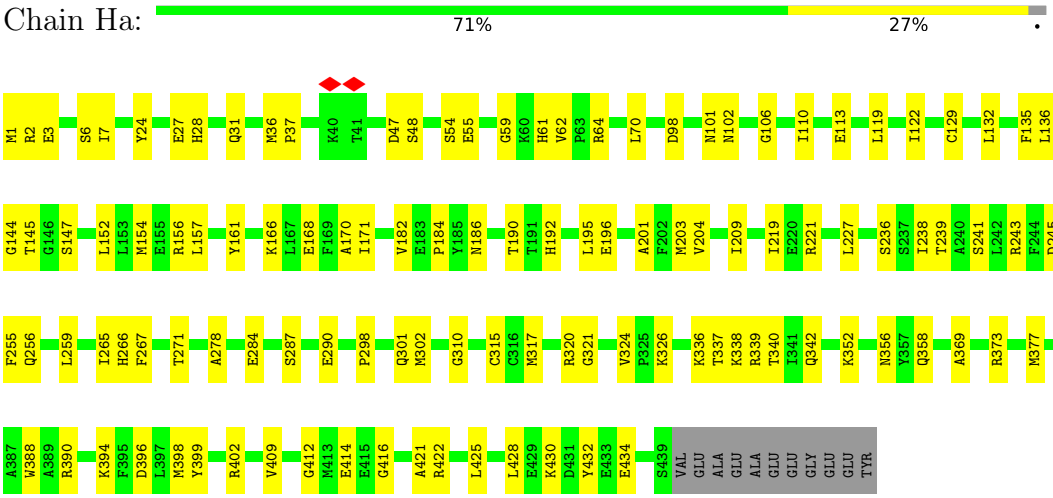
• Molecule 18: Tubulin alpha-3 chain

Chain Gi:



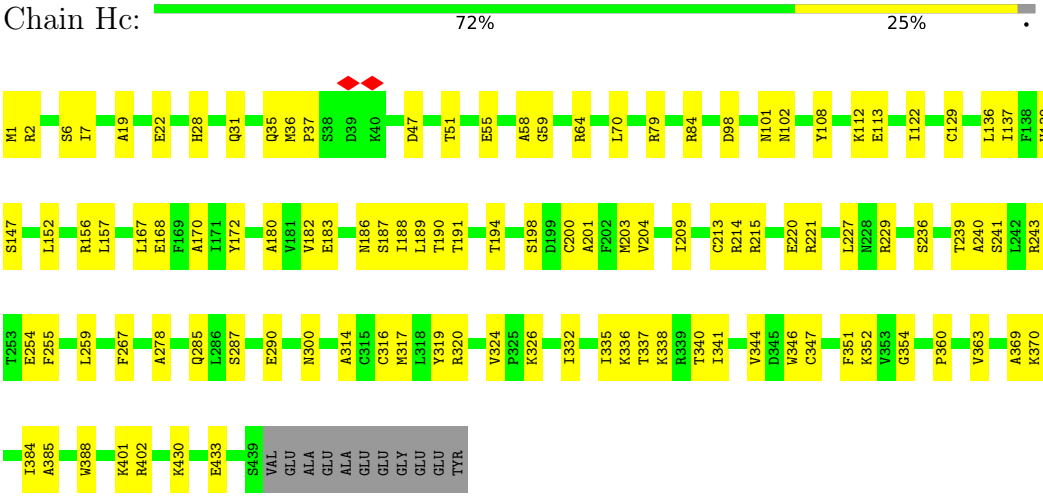
• Molecule 18: Tubulin alpha-3 chain

Chain Ha:



• Molecule 18: Tubulin alpha-3 chain

Chain Hc:



• Molecule 18: Tubulin alpha-3 chain

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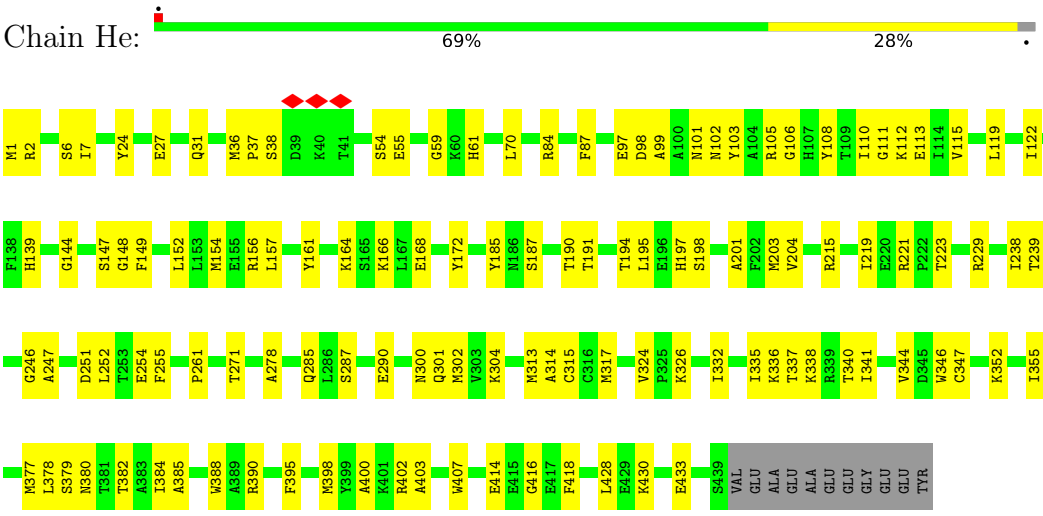
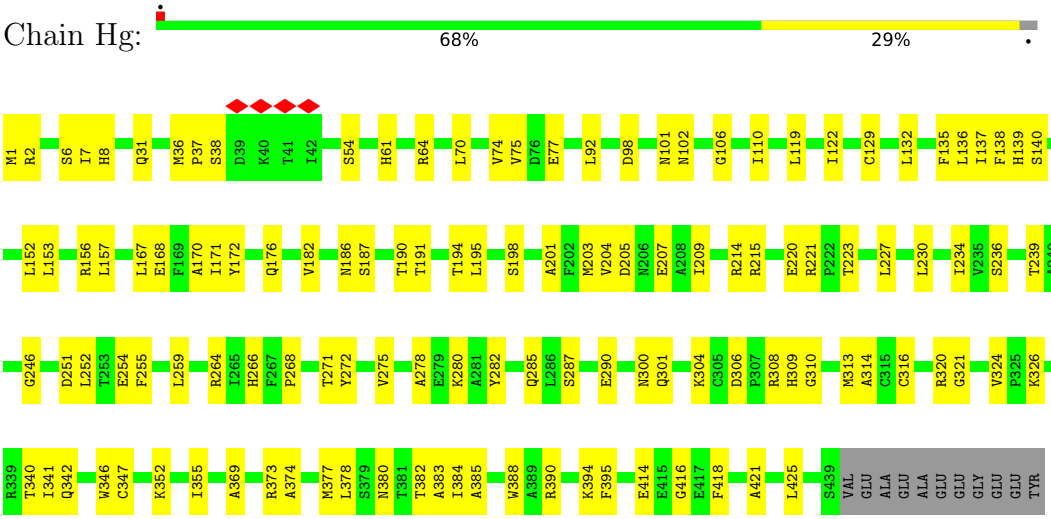


• Molecule 18: Tubulin alpha-3 chain

Chain Hg:



• Molecule 18: Tubulin alpha-3 chain

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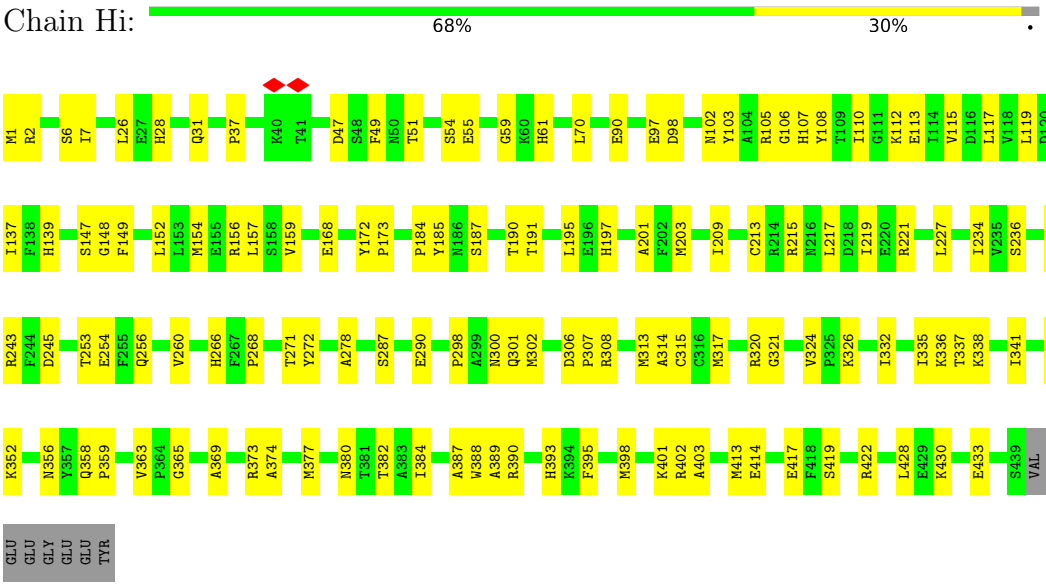
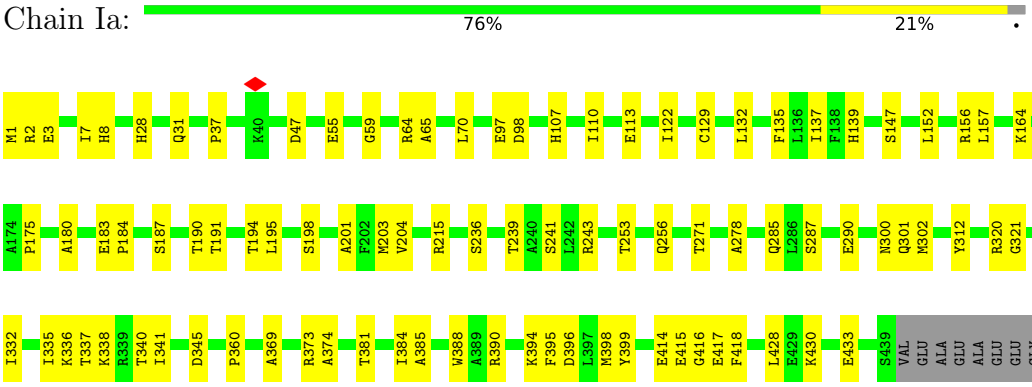


• Molecule 18: Tubulin alpha-3 chain

Chain Ia:



• Molecule 18: Tubulin alpha-3 chain

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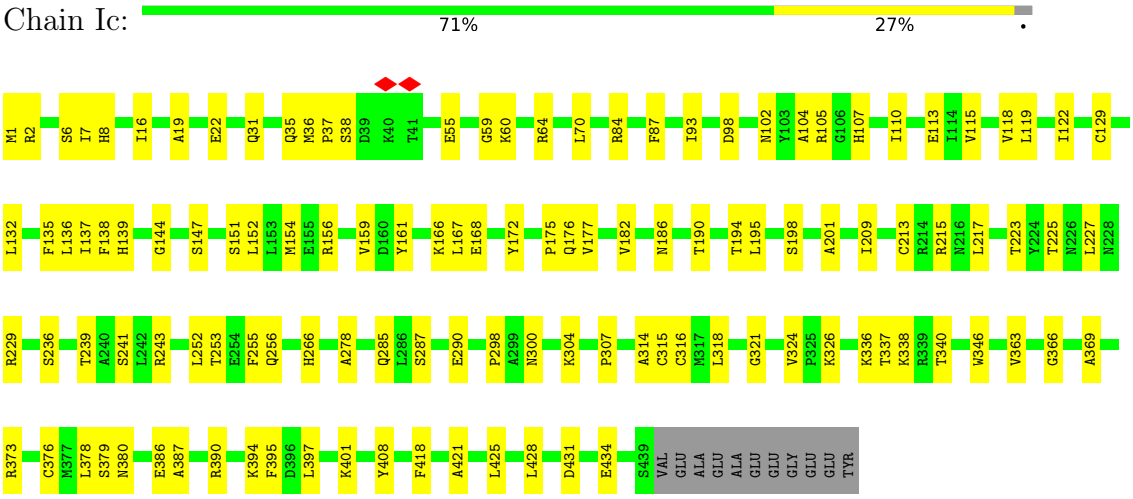

• Molecule 18: Tubulin alpha-3 chain

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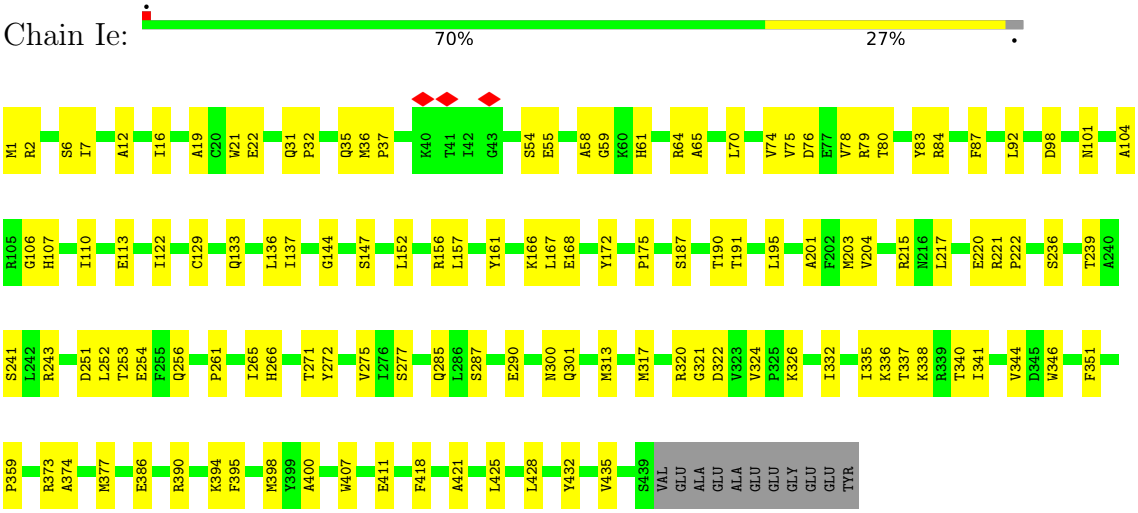

• Molecule 18: Tubulin alpha-3 chain

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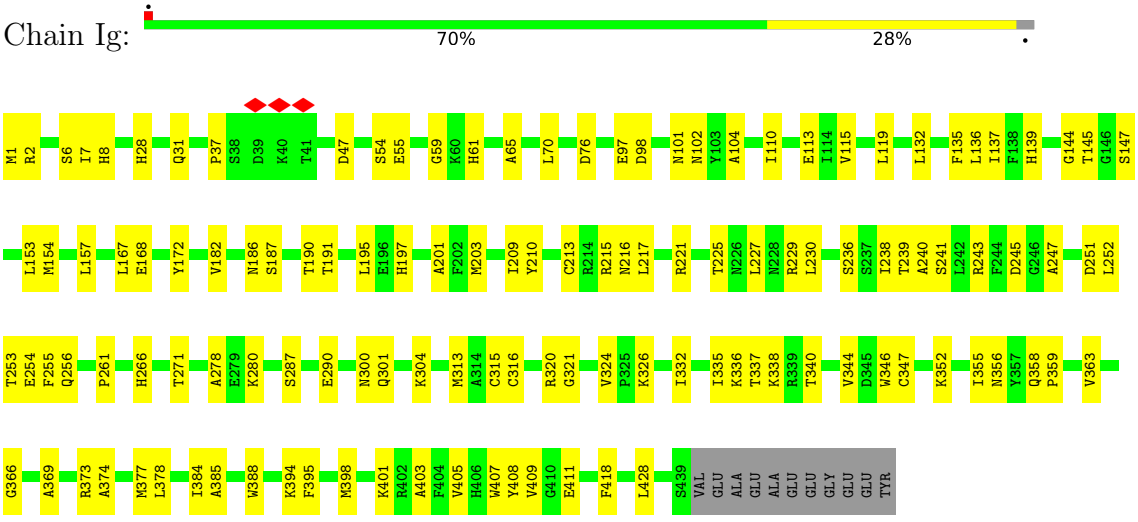

• Molecule 18: Tubulin alpha-3 chain

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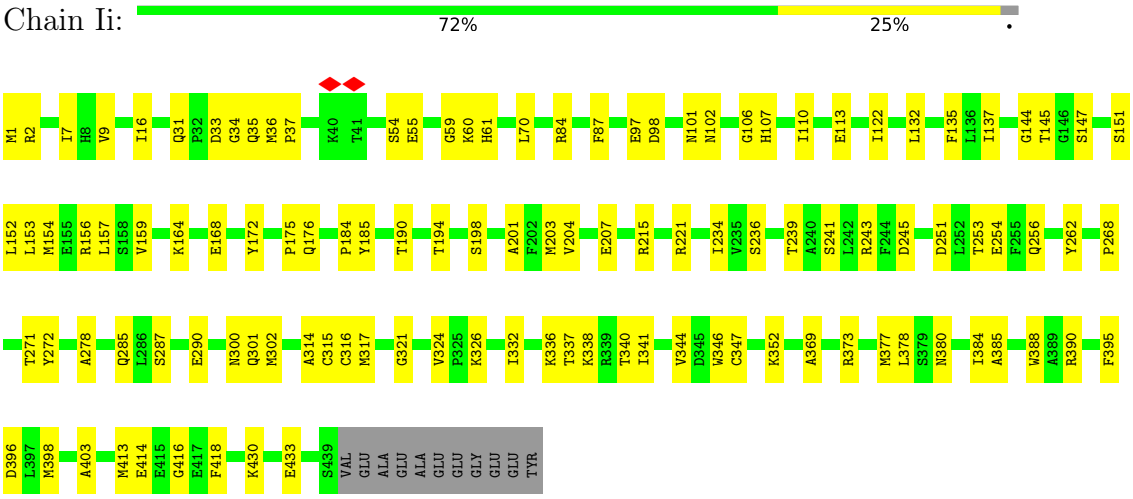

• Molecule 18: Tubulin alpha-3 chain

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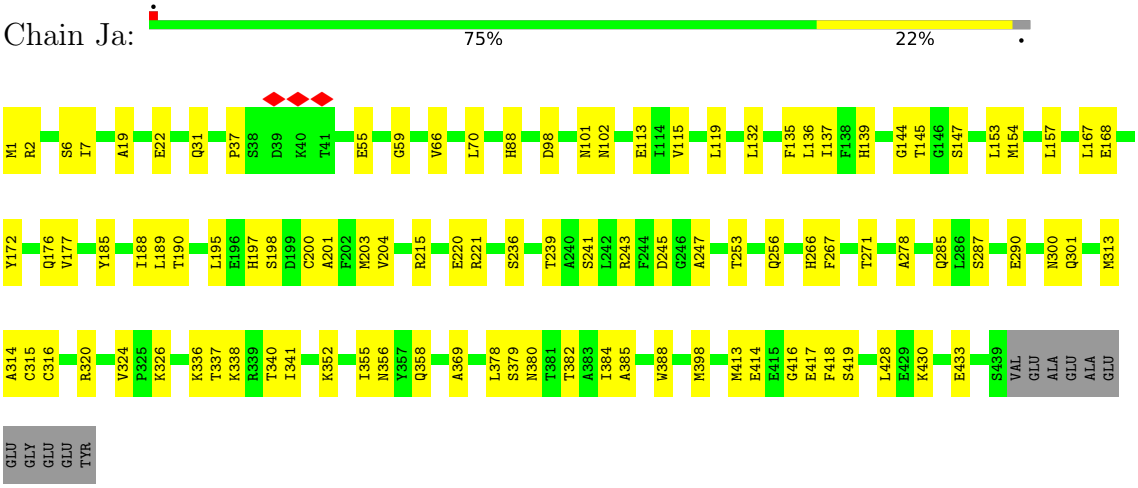

• Molecule 18: Tubulin alpha-3 chain

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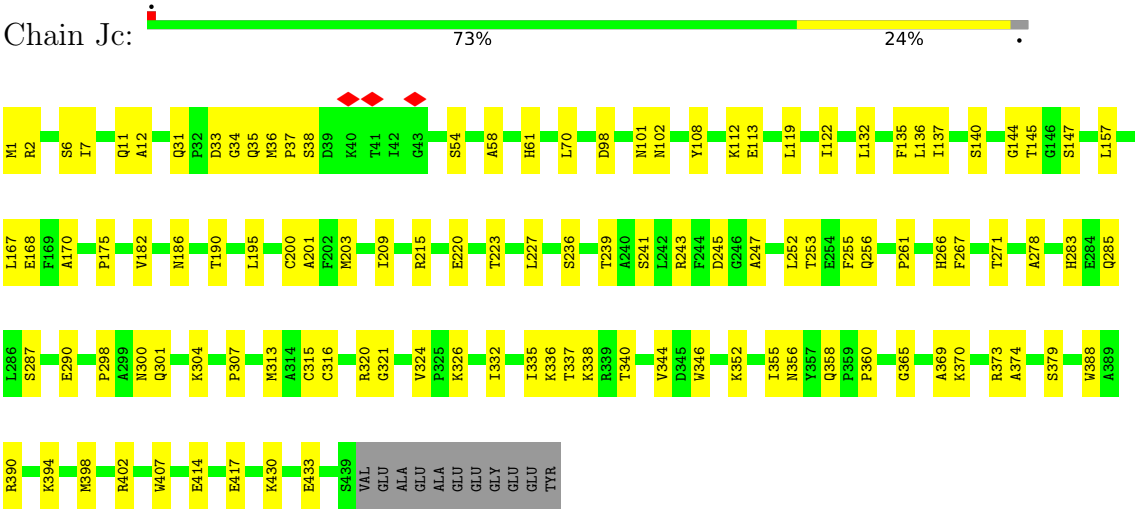

• Molecule 18: Tubulin alpha-3 chain

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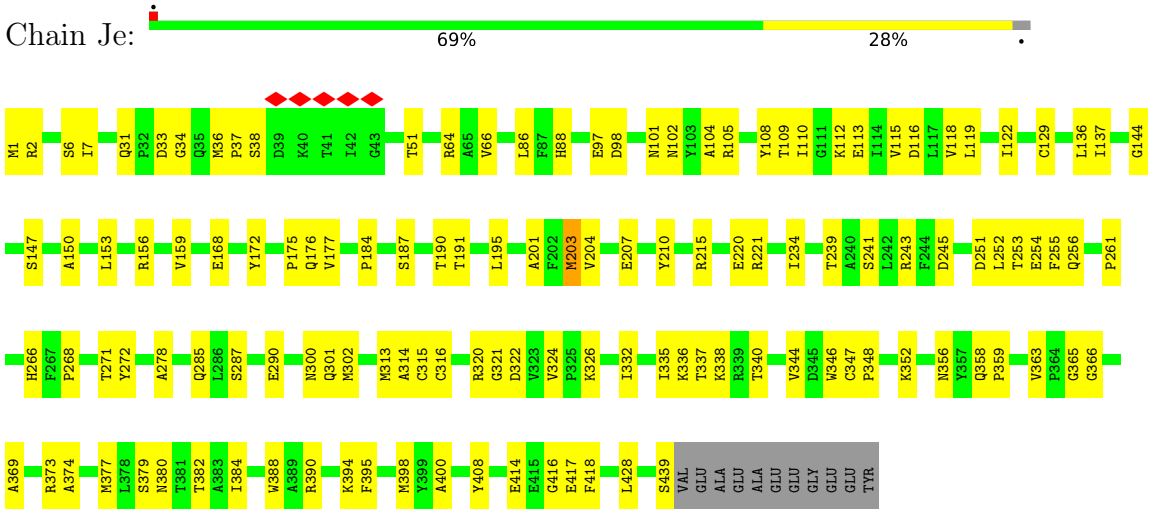

• Molecule 18: Tubulin alpha-3 chain

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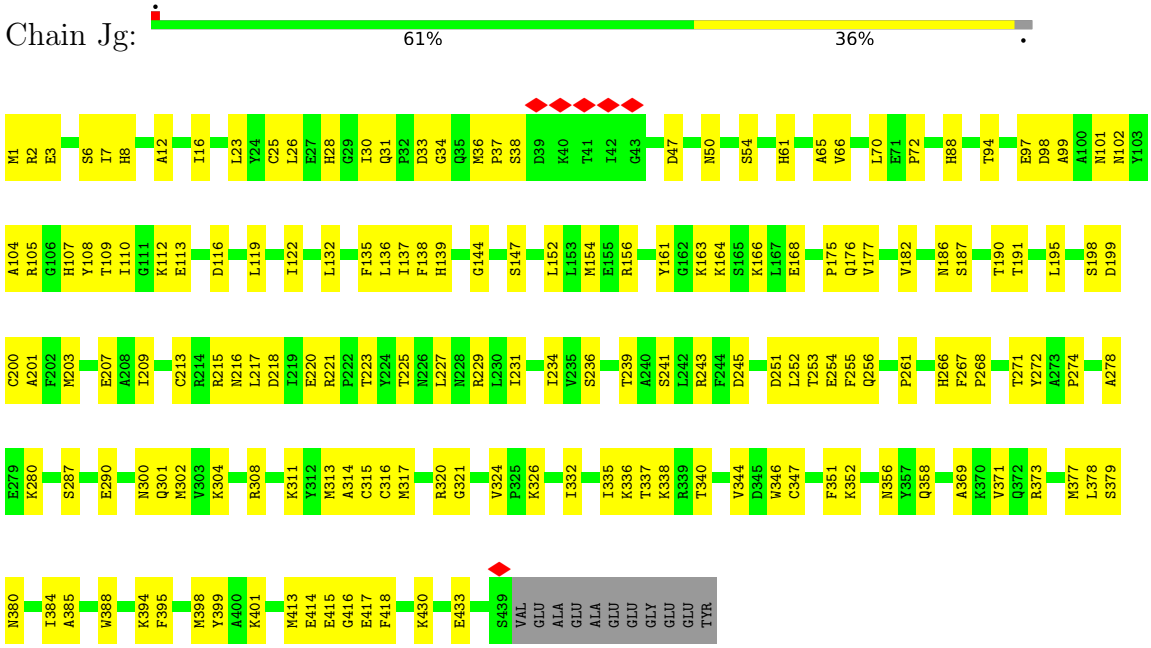

• Molecule 18: Tubulin alpha-3 chain

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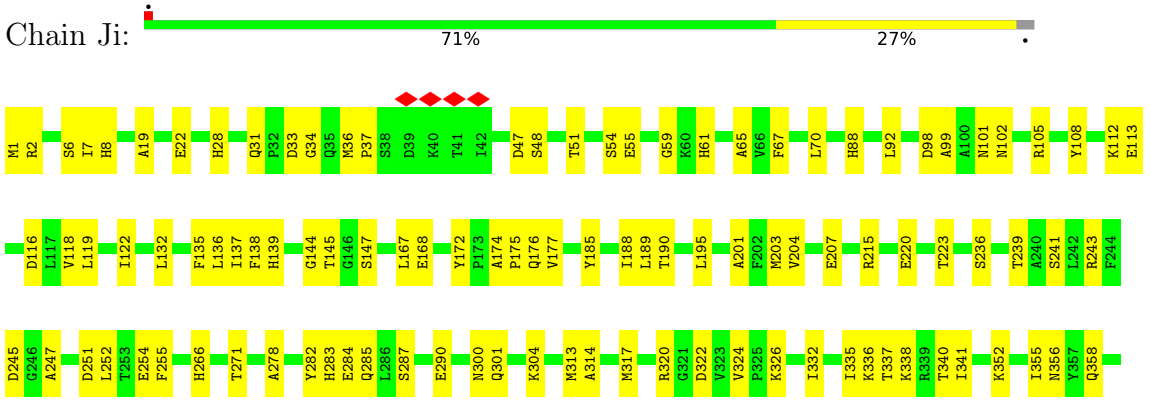

• Molecule 18: Tubulin alpha-3 chain

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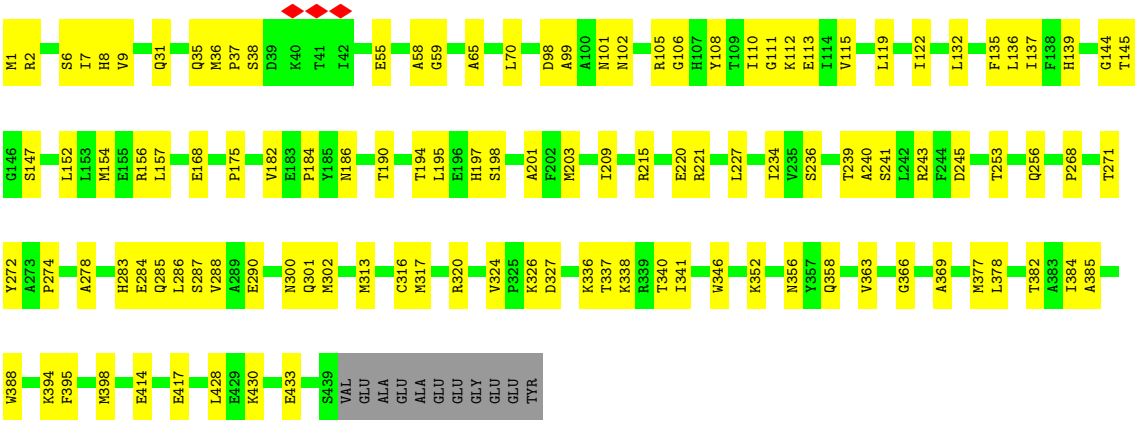

• Molecule 18: Tubulin alpha-3 chain

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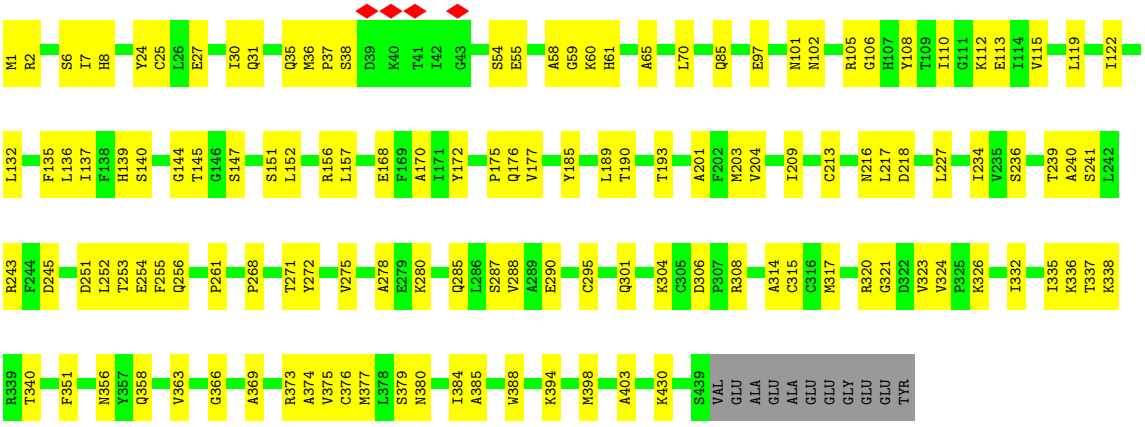

• Molecule 18: Tubulin alpha-3 chain

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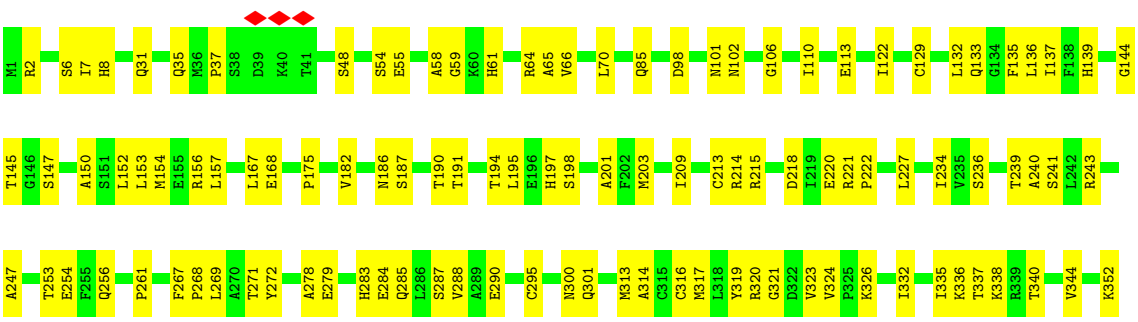

• Molecule 18: Tubulin alpha-3 chain

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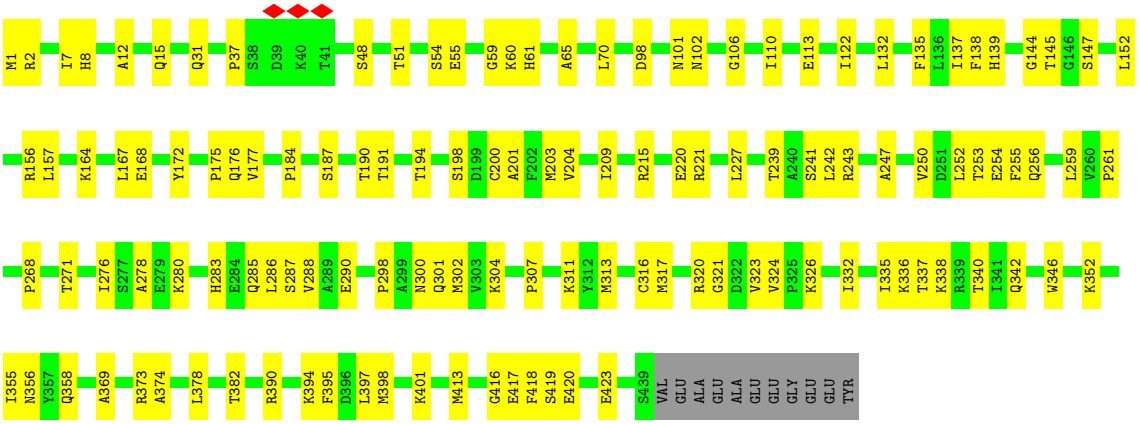

• Molecule 18: Tubulin alpha-3 chain

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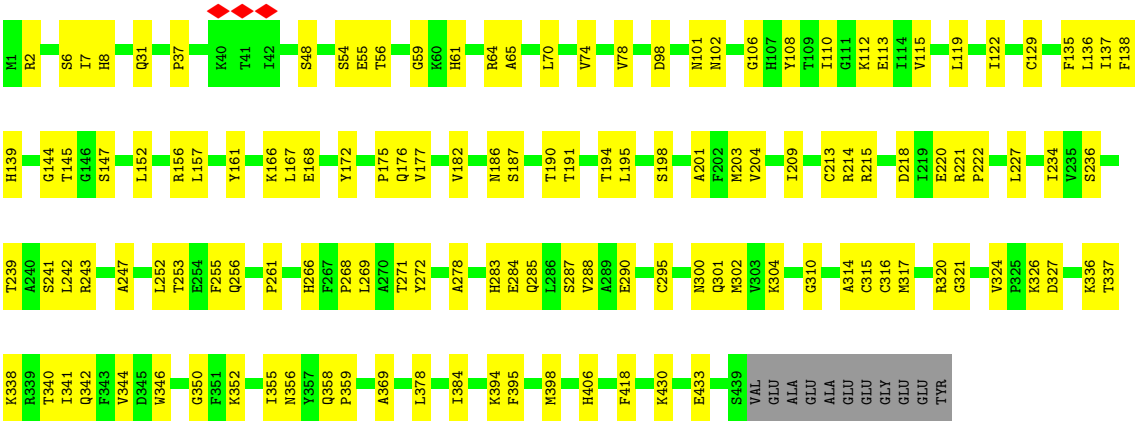

• Molecule 18: Tubulin alpha-3 chain

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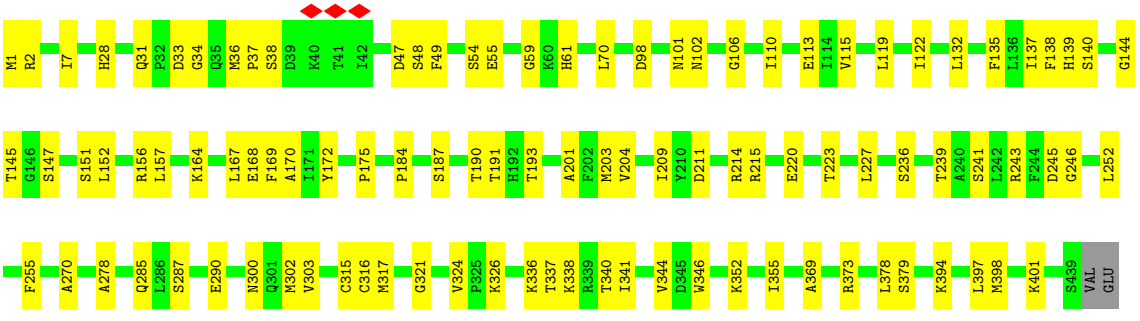

• Molecule 18: Tubulin alpha-3 chain

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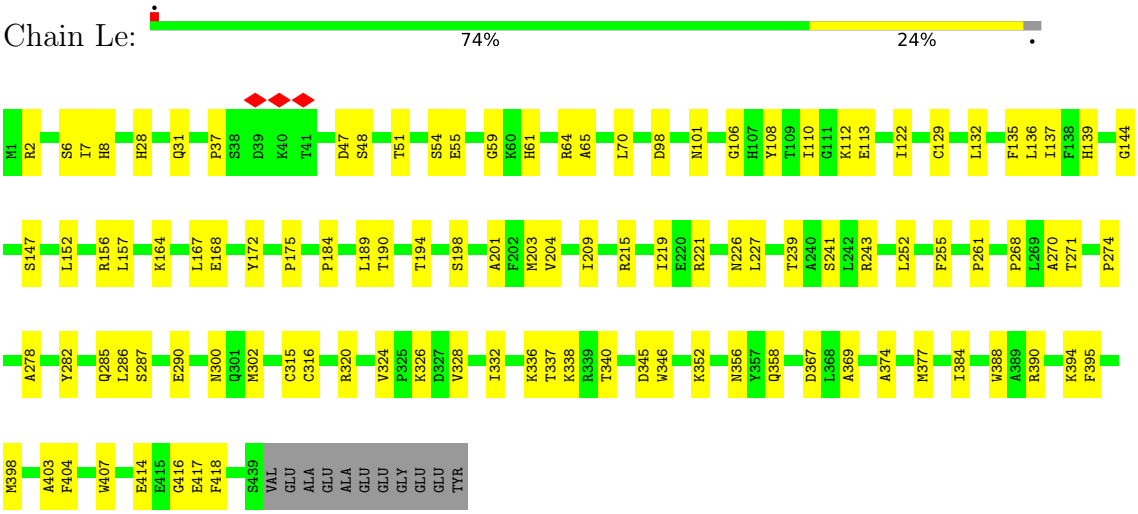

• Molecule 18: Tubulin alpha-3 chain

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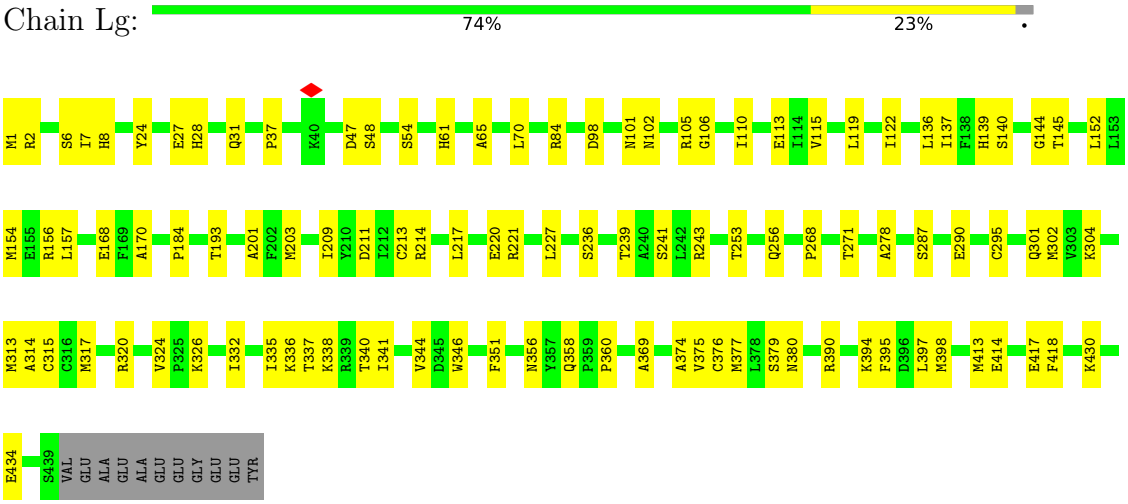

• Molecule 18: Tubulin alpha-3 chain

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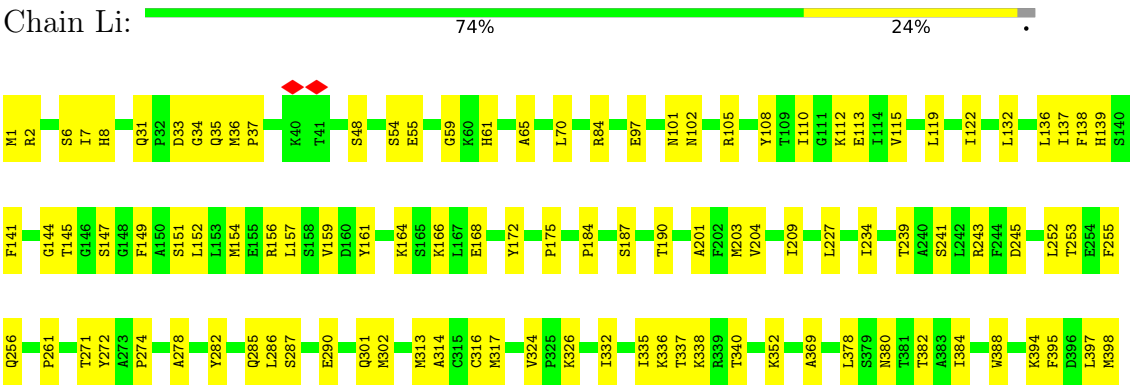
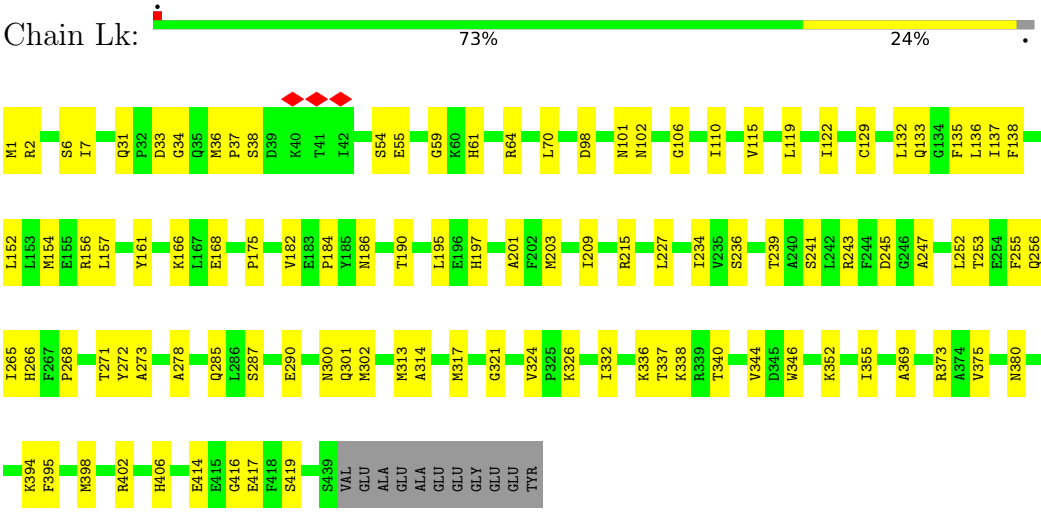
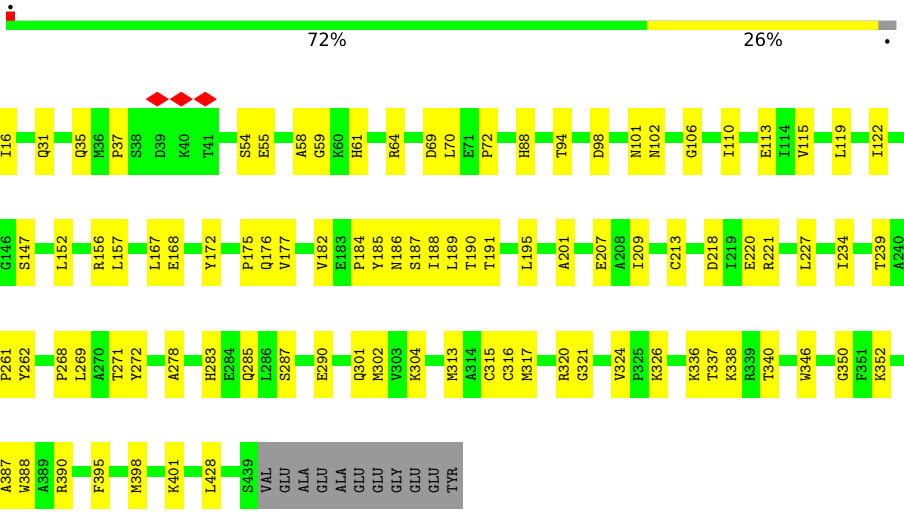


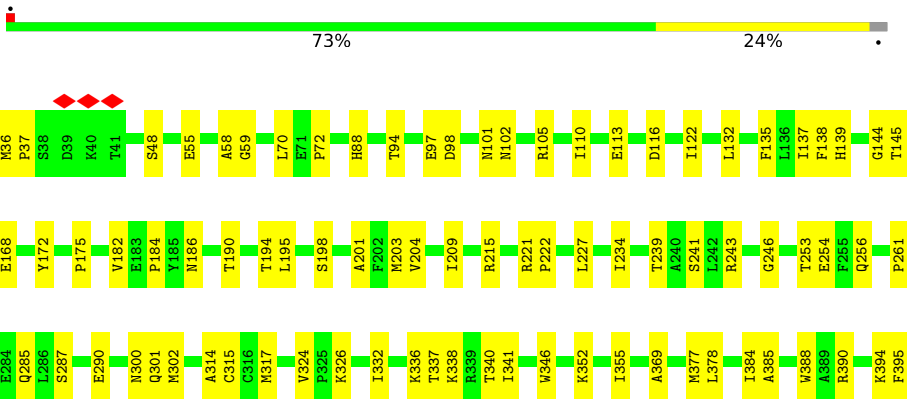
• Molecule 18: Tubulin alpha-3 chain

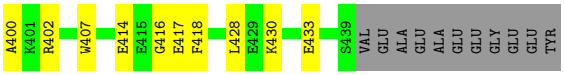


• Molecule 18: Tubulin alpha-3 chain



• Molecule 18: Tubulin alpha-3 chain





• Molecule 18: Tubulin alpha-3 chain

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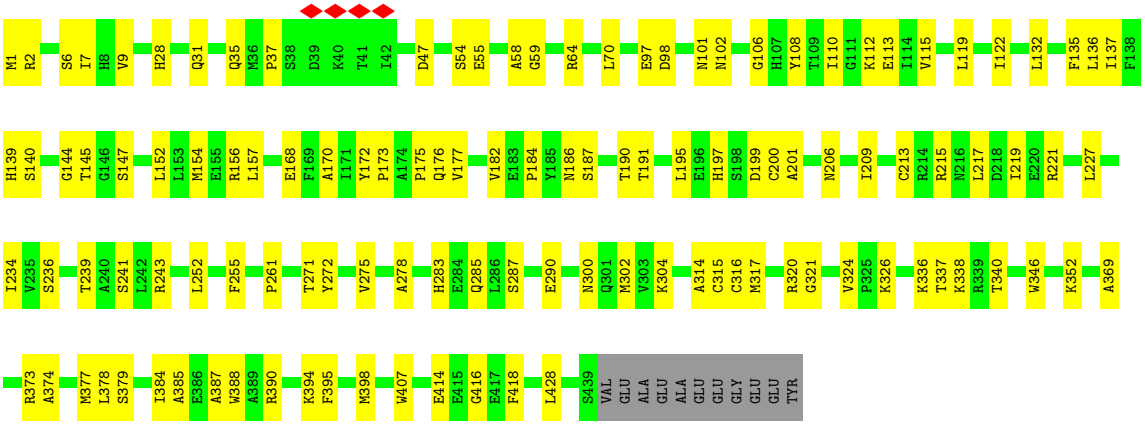

• Molecule 18: Tubulin alpha-3 chain

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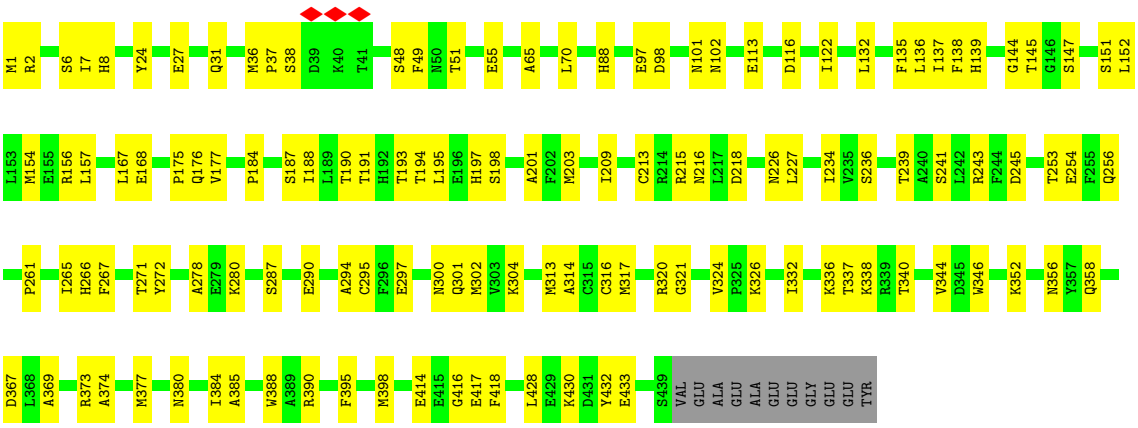

• Molecule 18: Tubulin alpha-3 chain

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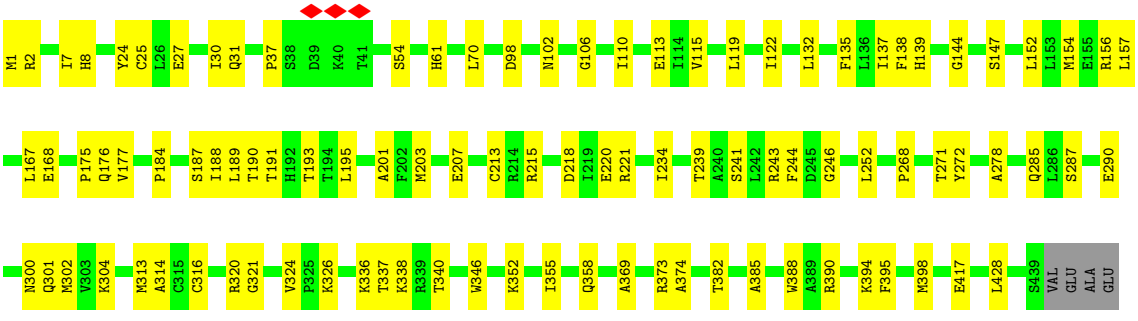
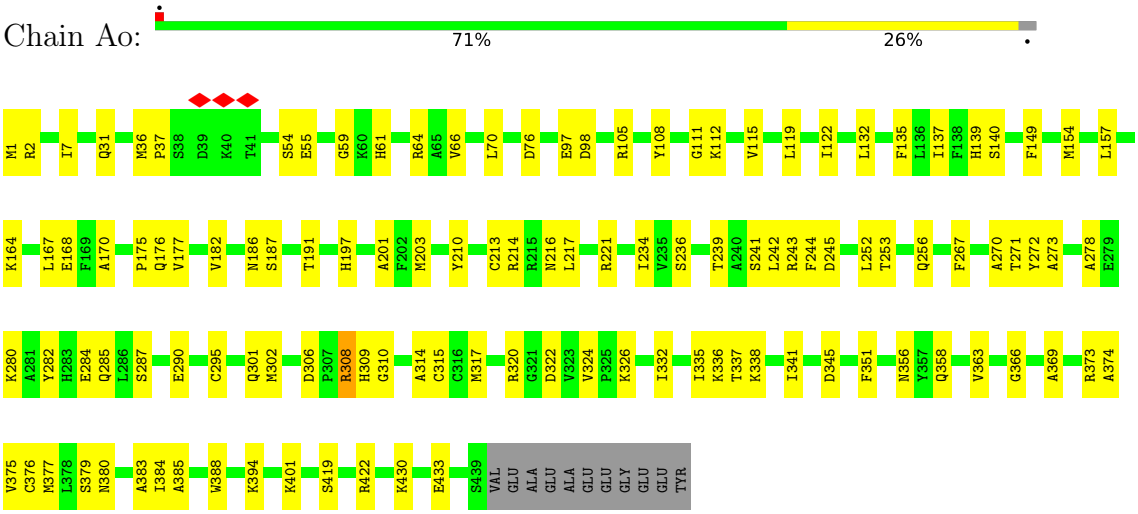


• Molecule 18: Tubulin alpha-3 chain

Chain Ao:



• Molecule 18: Tubulin alpha-3 chain

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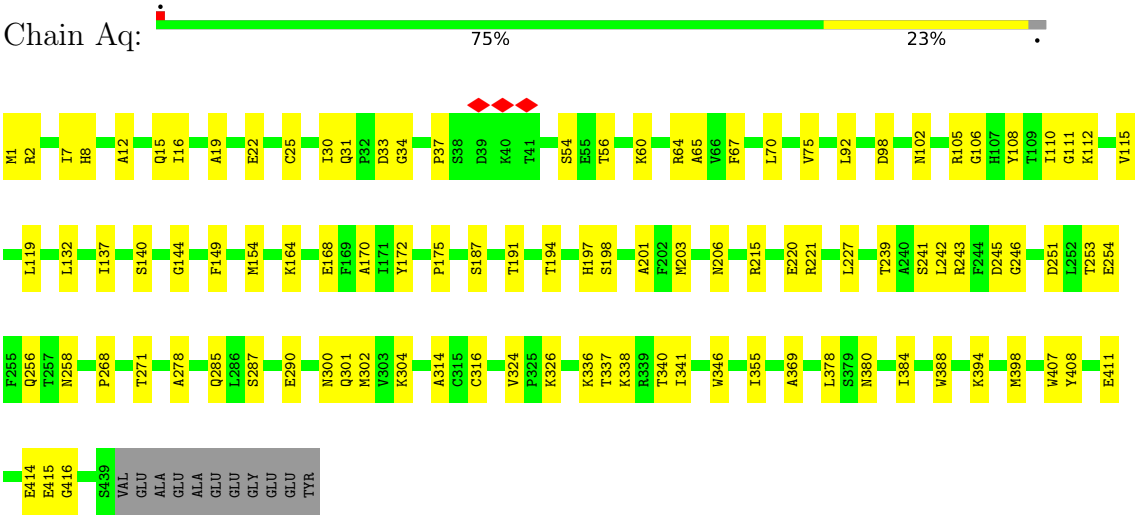

• Molecule 18: Tubulin alpha-3 chain

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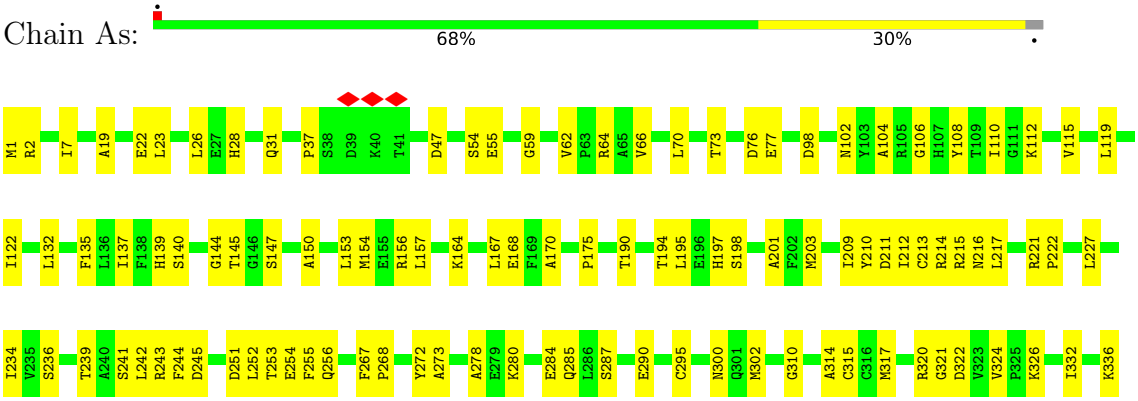

• Molecule 18: Tubulin alpha-3 chain

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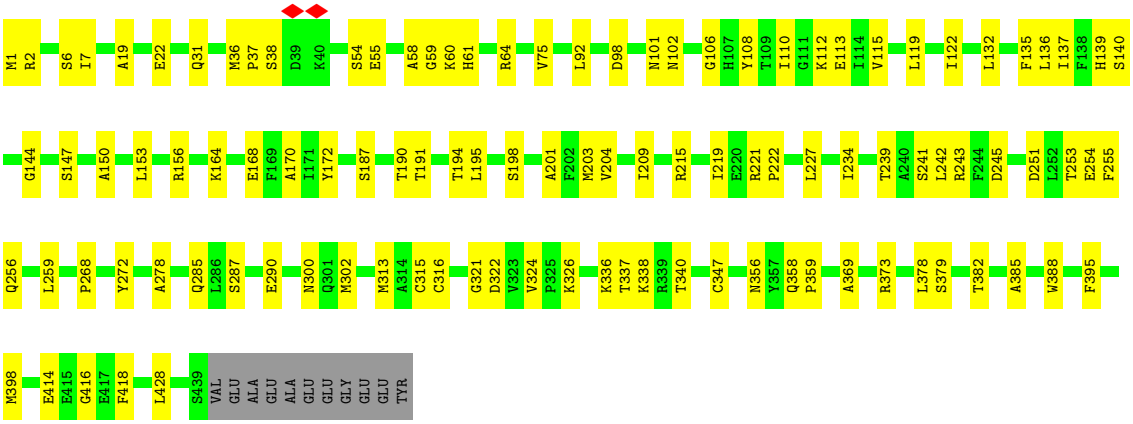

• Molecule 18: Tubulin alpha-3 chain

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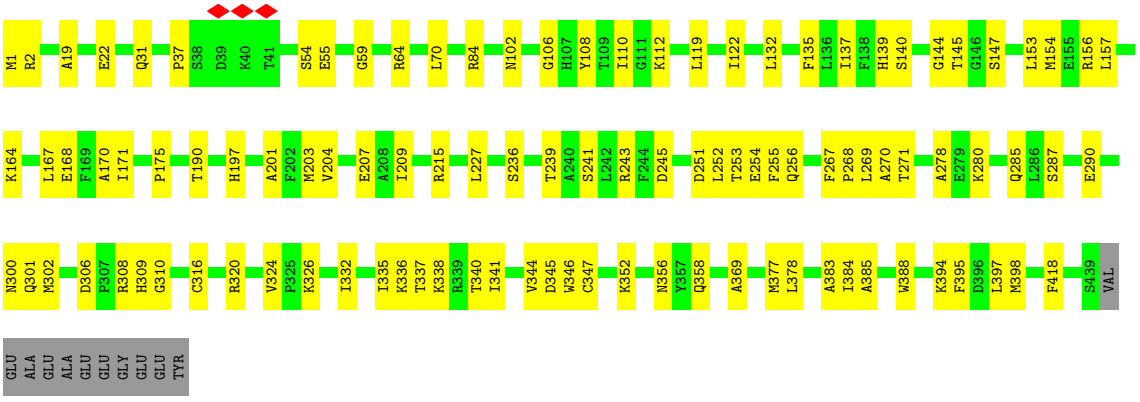
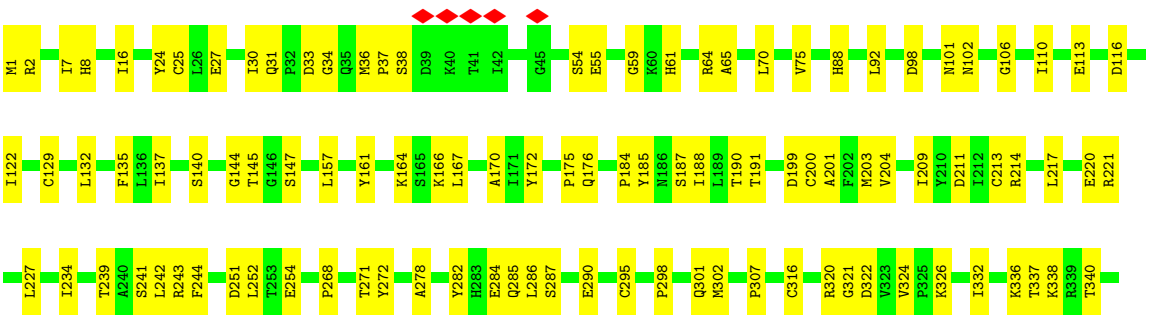
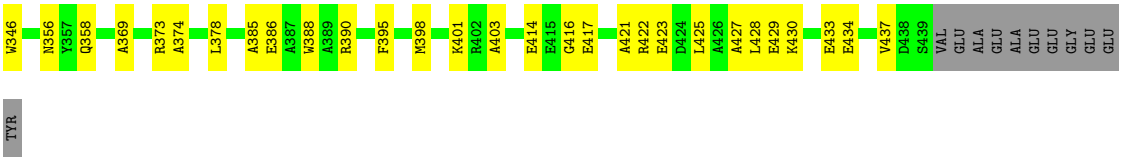


• Molecule 18: Tubulin alpha-3 chain

Chain Bo:





• Molecule 18: Tubulin alpha-3 chain

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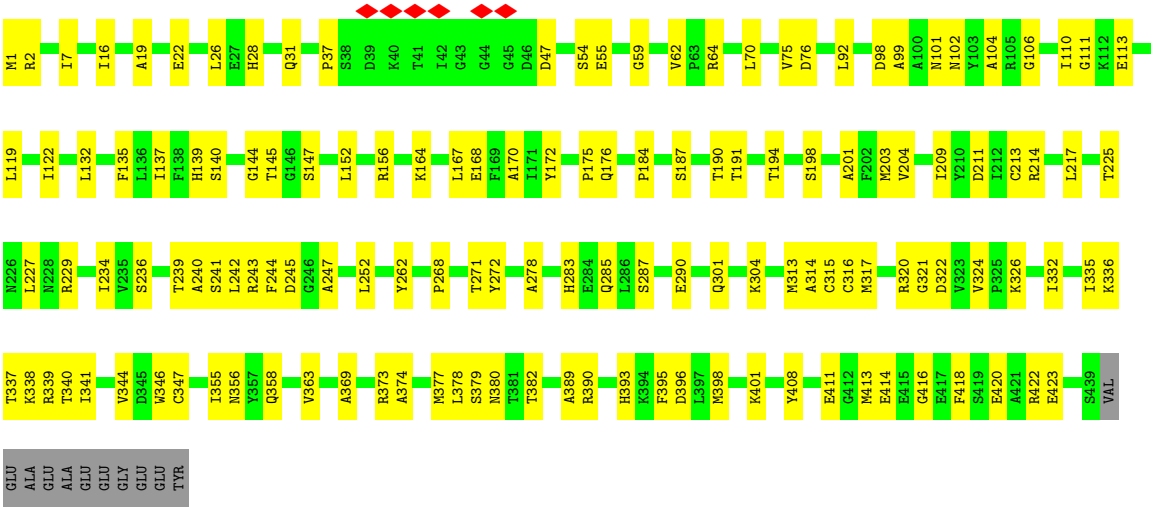

• Molecule 18: Tubulin alpha-3 chain

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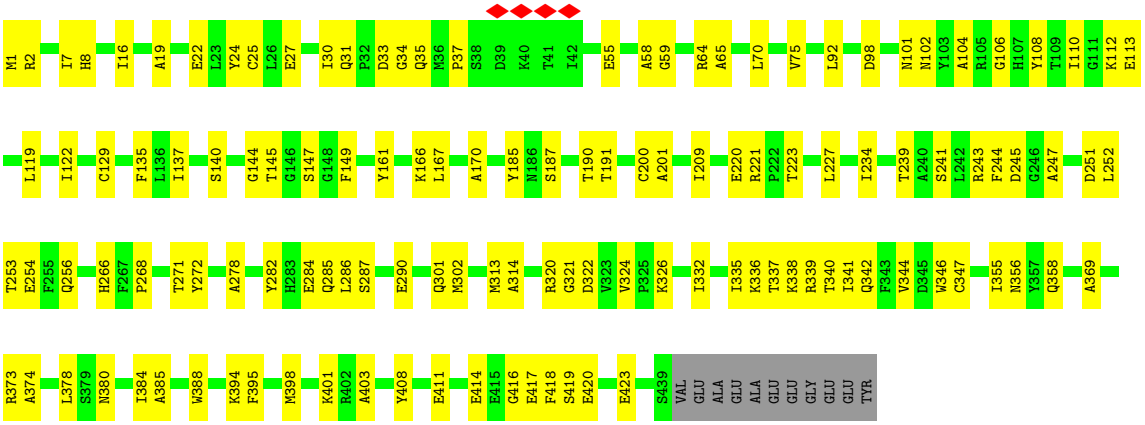

• Molecule 18: Tubulin alpha-3 chain

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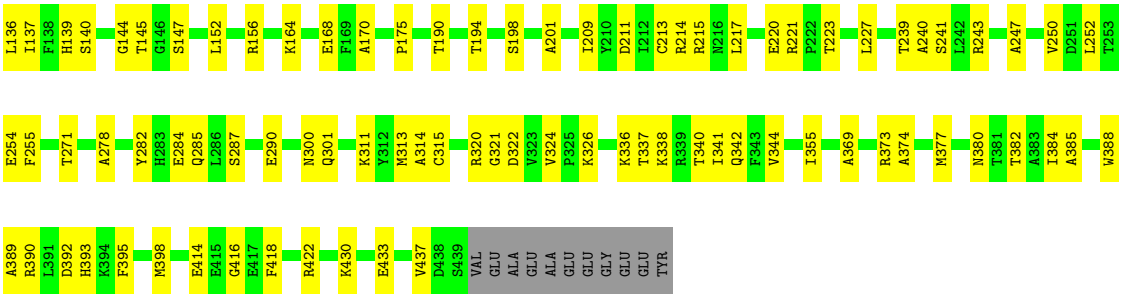

• Molecule 18: Tubulin alpha-3 chain

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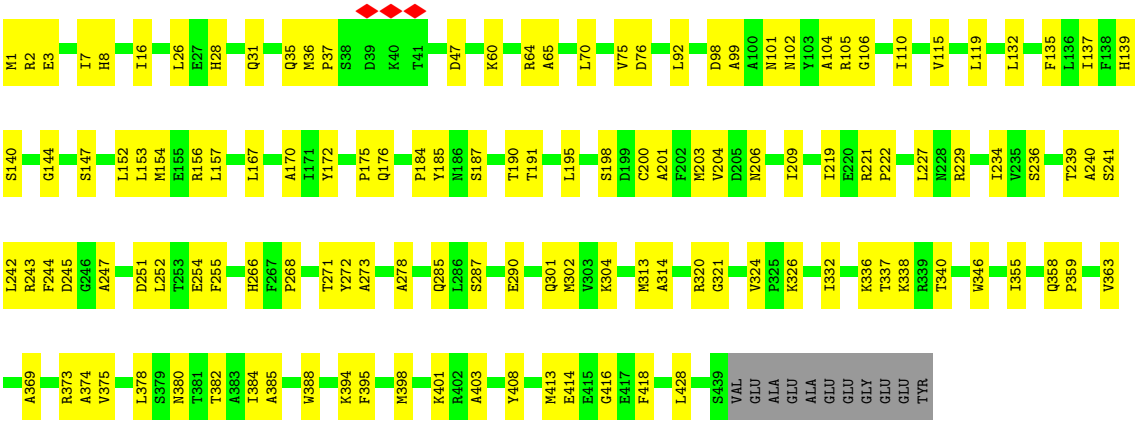

• Molecule 18: Tubulin alpha-3 chain

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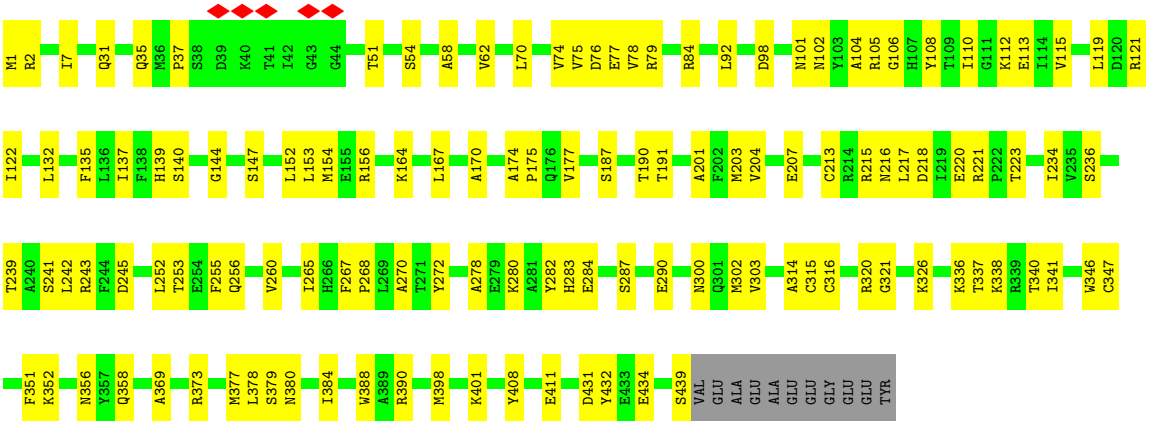

• Molecule 18: Tubulin alpha-3 chain

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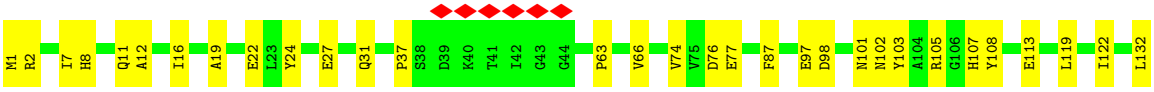

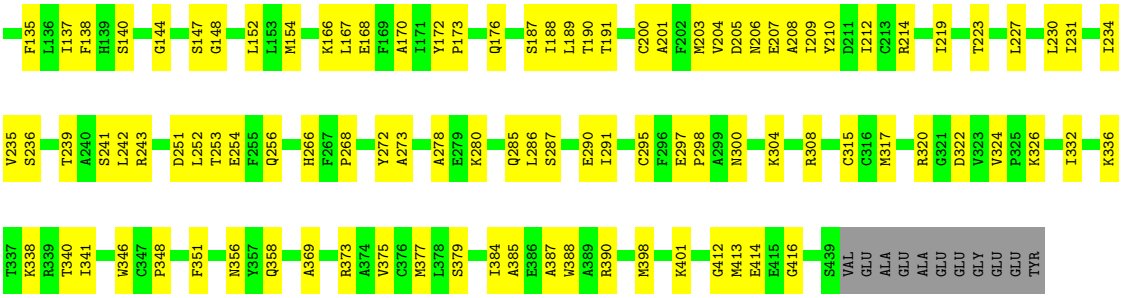

• Molecule 18: Tubulin alpha-3 chain

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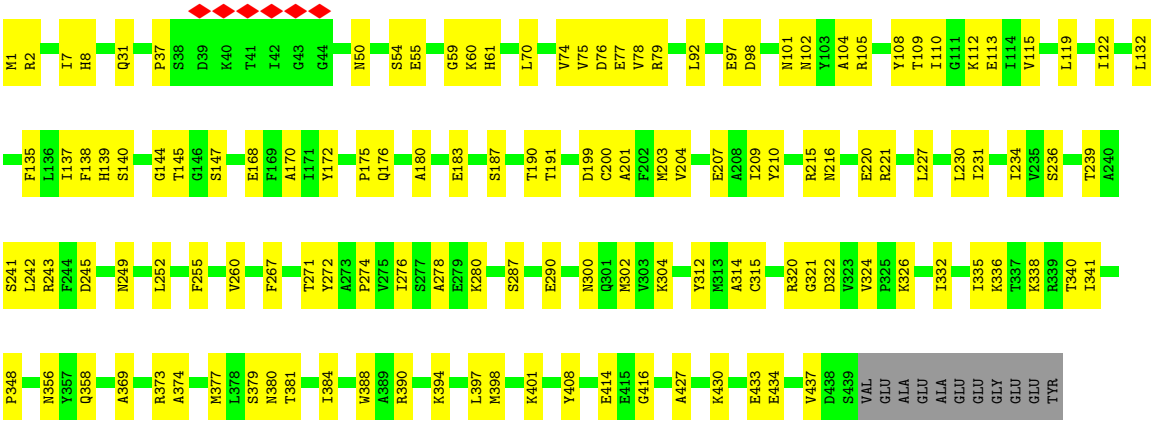

• Molecule 18: Tubulin alpha-3 chain

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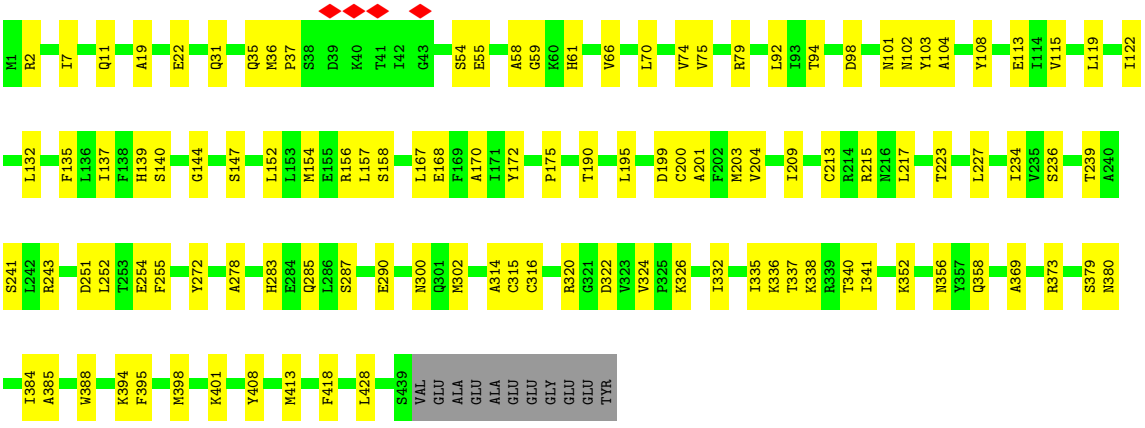

• Molecule 18: Tubulin alpha-3 chain

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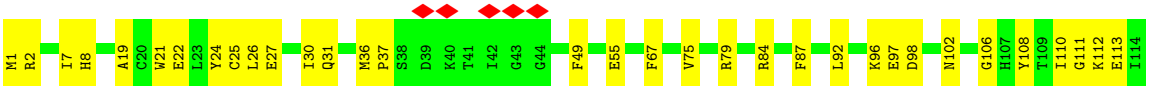

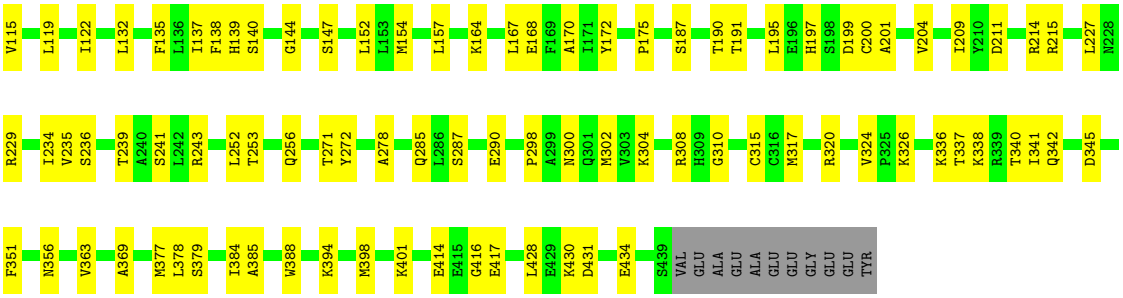

• Molecule 18: Tubulin alpha-3 chain

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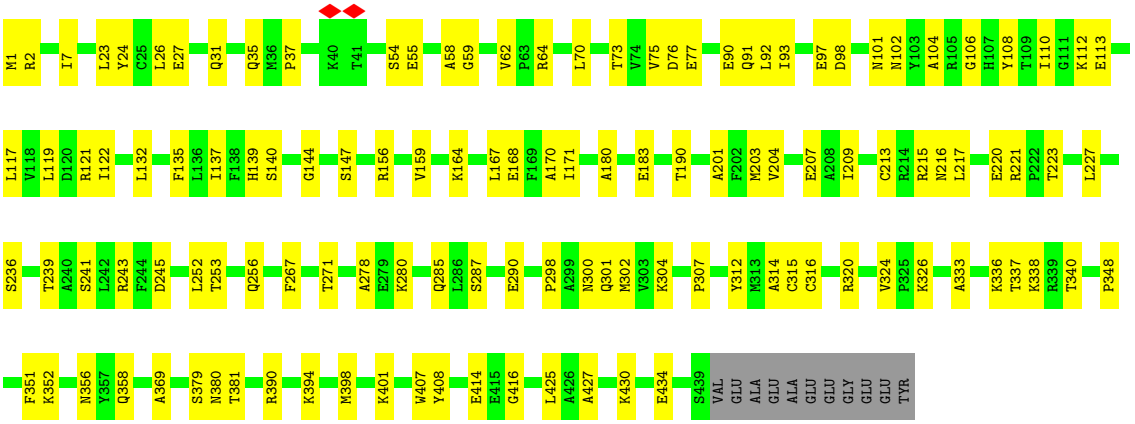

• Molecule 18: Tubulin alpha-3 chain

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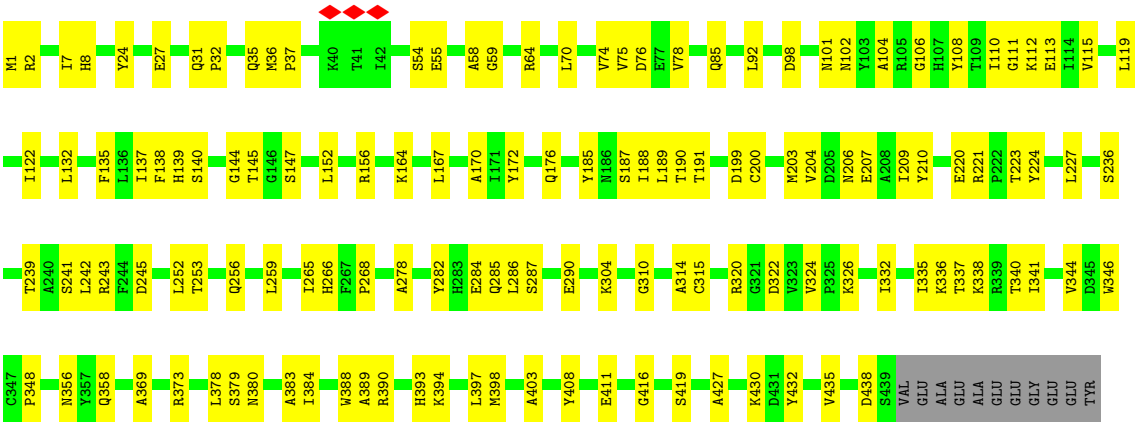

• Molecule 18: Tubulin alpha-3 chain

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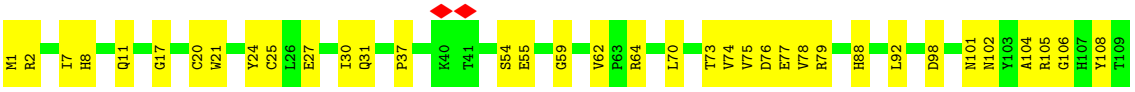

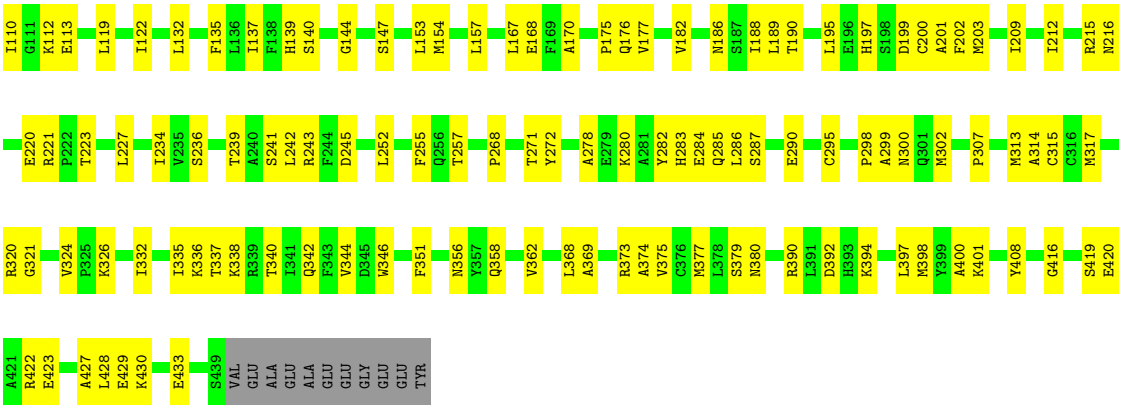

• Molecule 18: Tubulin alpha-3 chain

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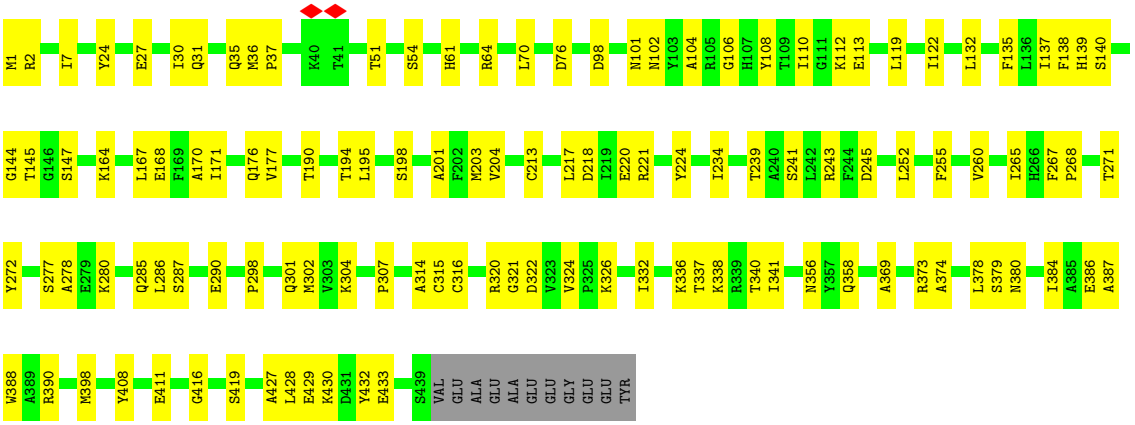

• Molecule 18: Tubulin alpha-3 chain

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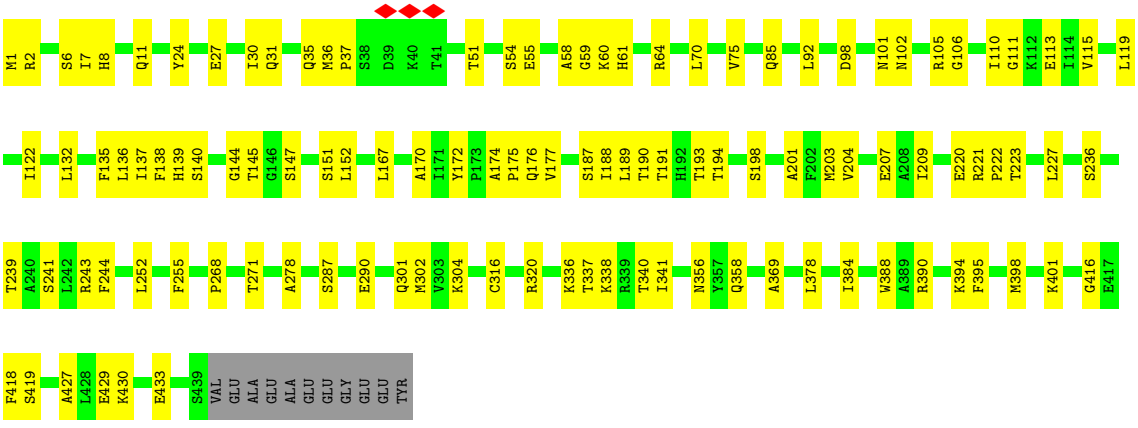

• Molecule 18: Tubulin alpha-3 chain

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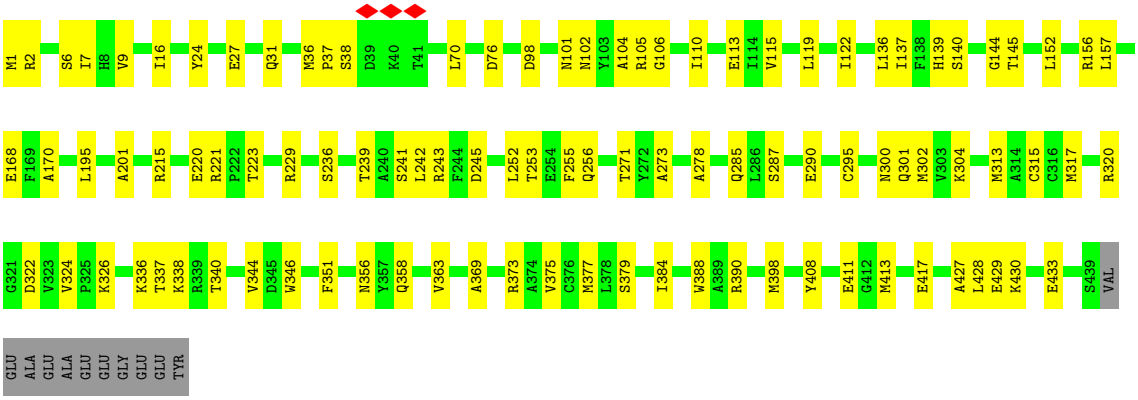

• Molecule 18: Tubulin alpha-3 chain

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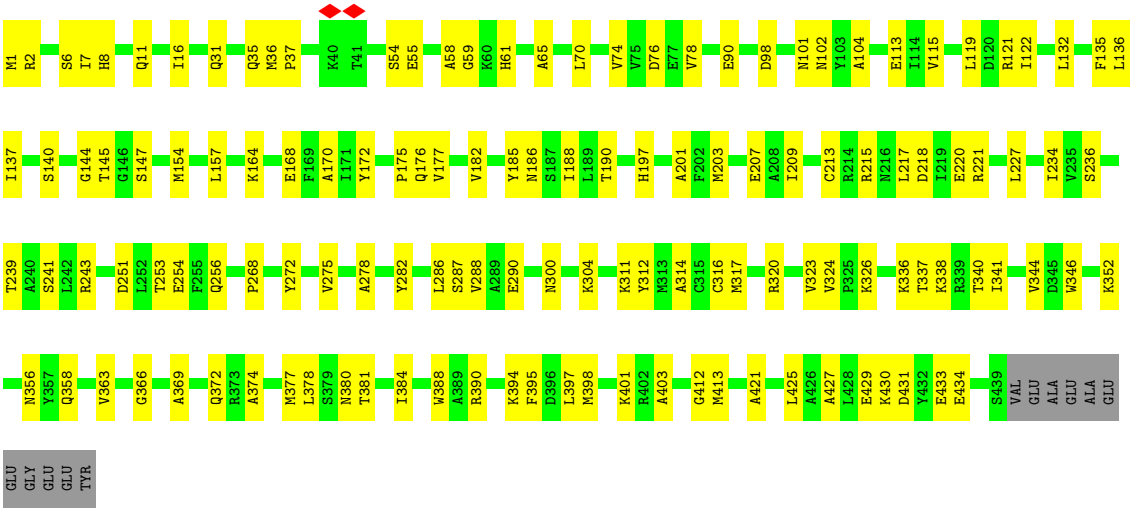

• Molecule 18: Tubulin alpha-3 chain

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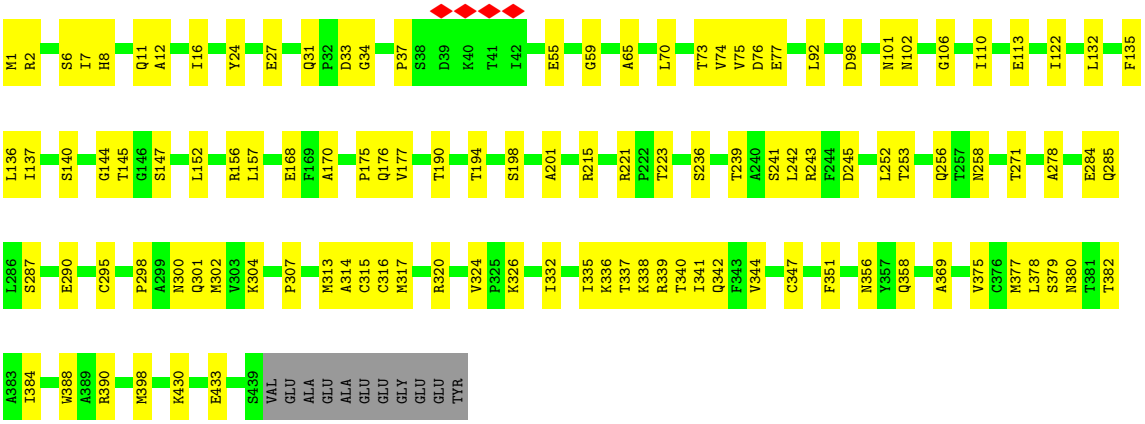

• Molecule 18: Tubulin alpha-3 chain

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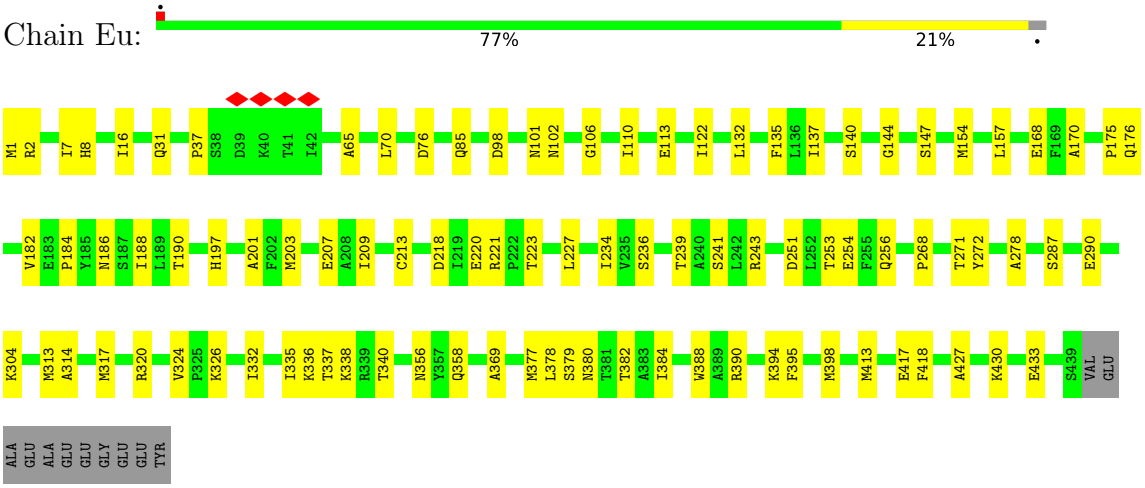

• Molecule 18: Tubulin alpha-3 chain

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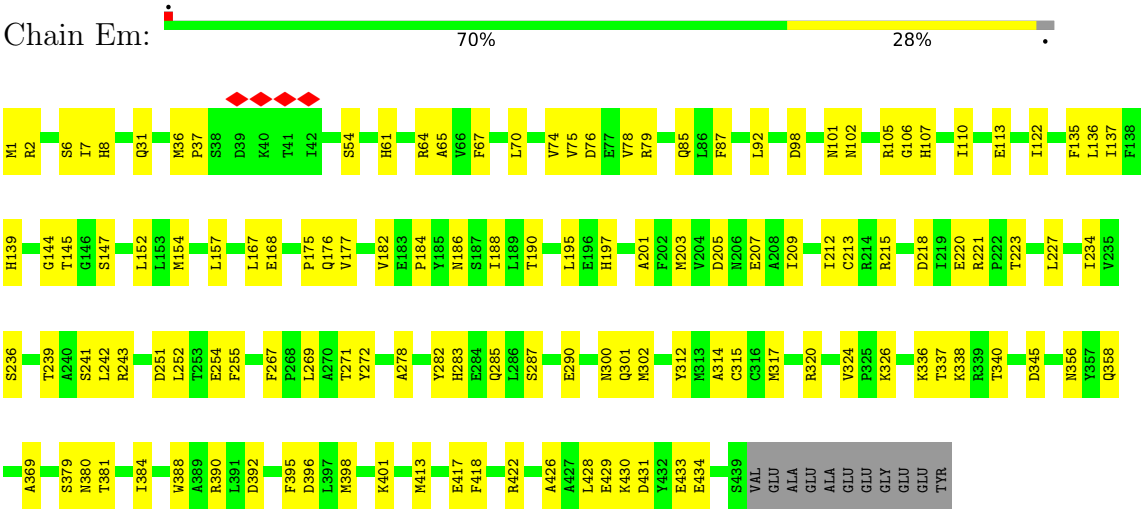

• Molecule 18: Tubulin alpha-3 chain

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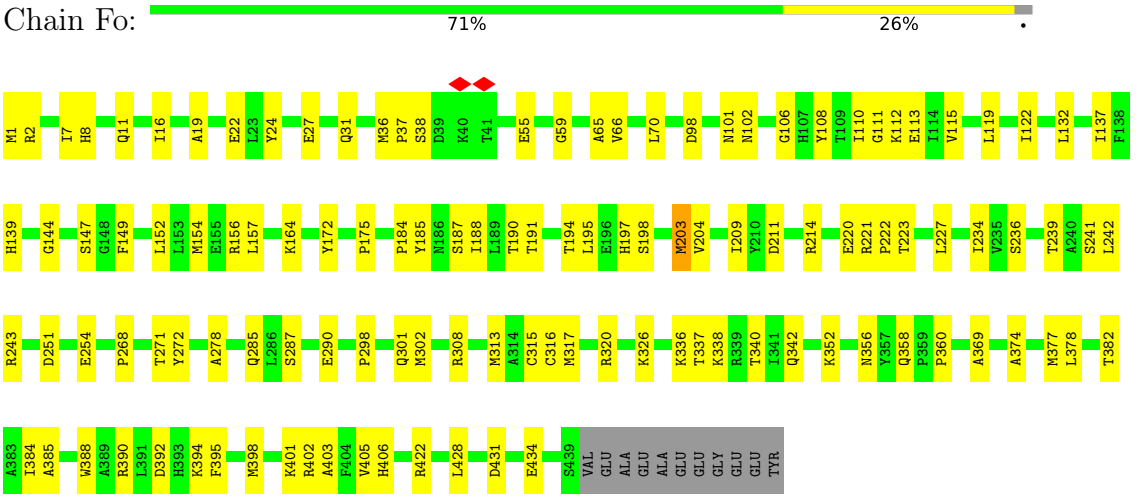

• Molecule 18: Tubulin alpha-3 chain

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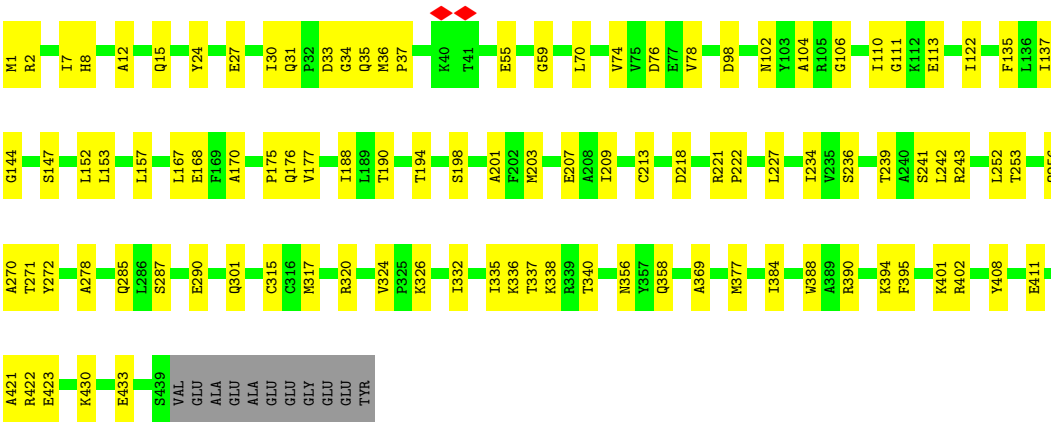

• Molecule 18: Tubulin alpha-3 chain

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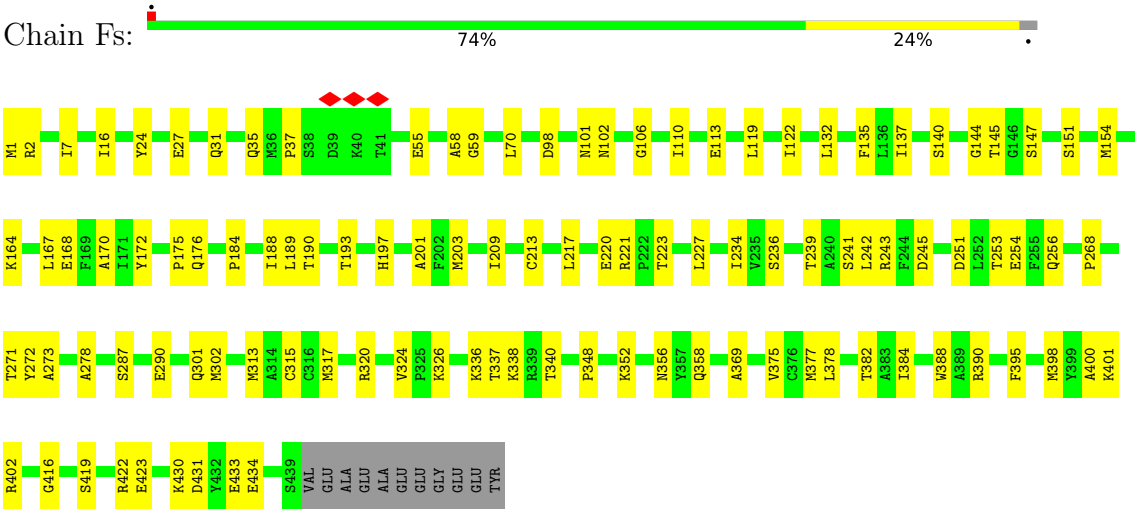

• Molecule 18: Tubulin alpha-3 chain

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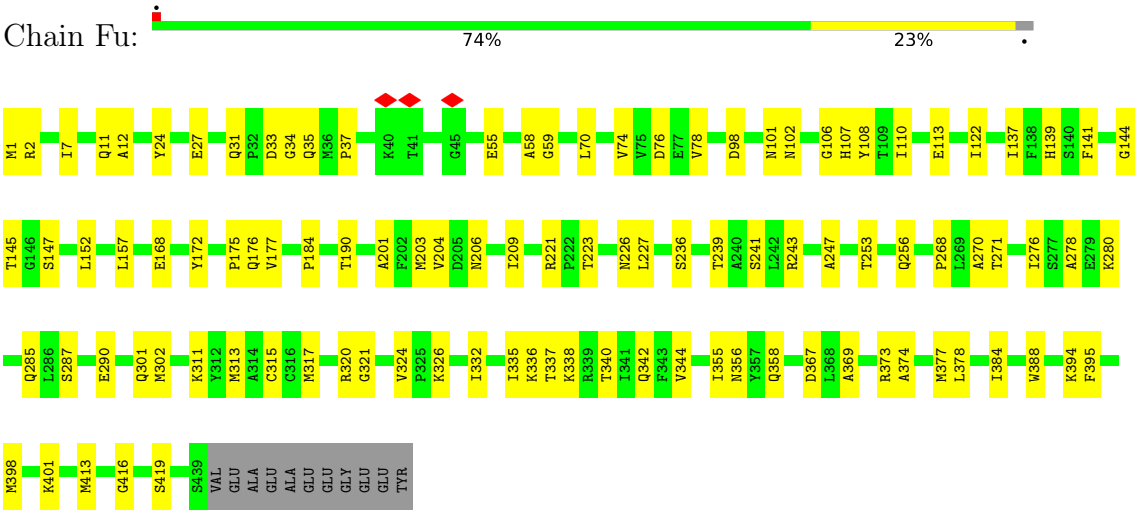

• Molecule 18: Tubulin alpha-3 chain

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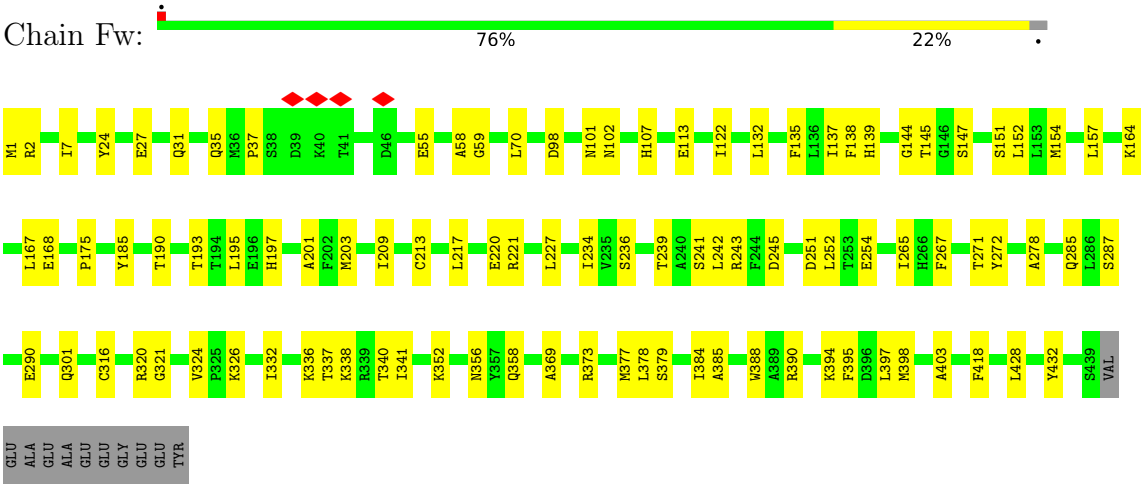

• Molecule 18: Tubulin alpha-3 chain

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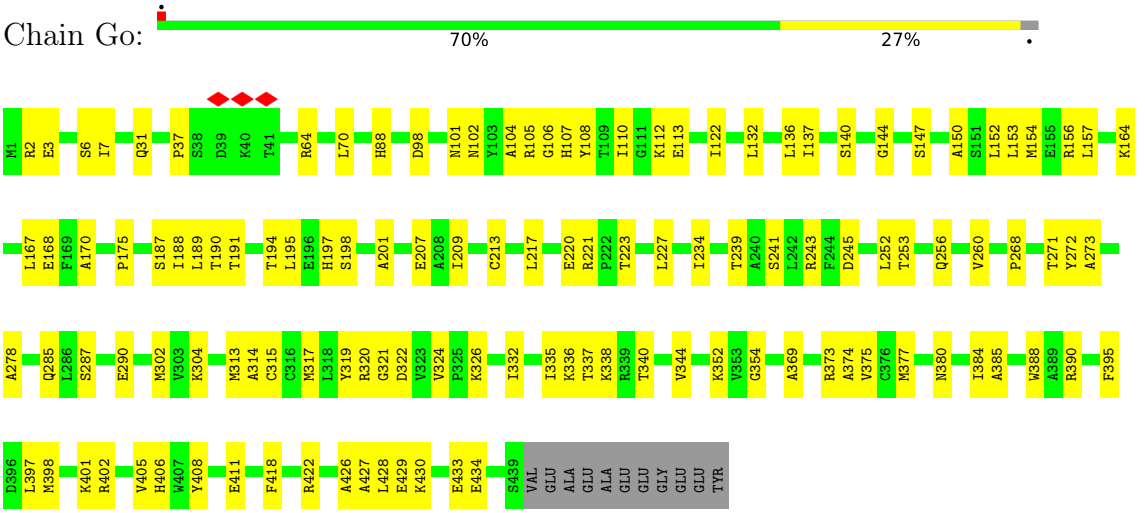

• Molecule 18: Tubulin alpha-3 chain

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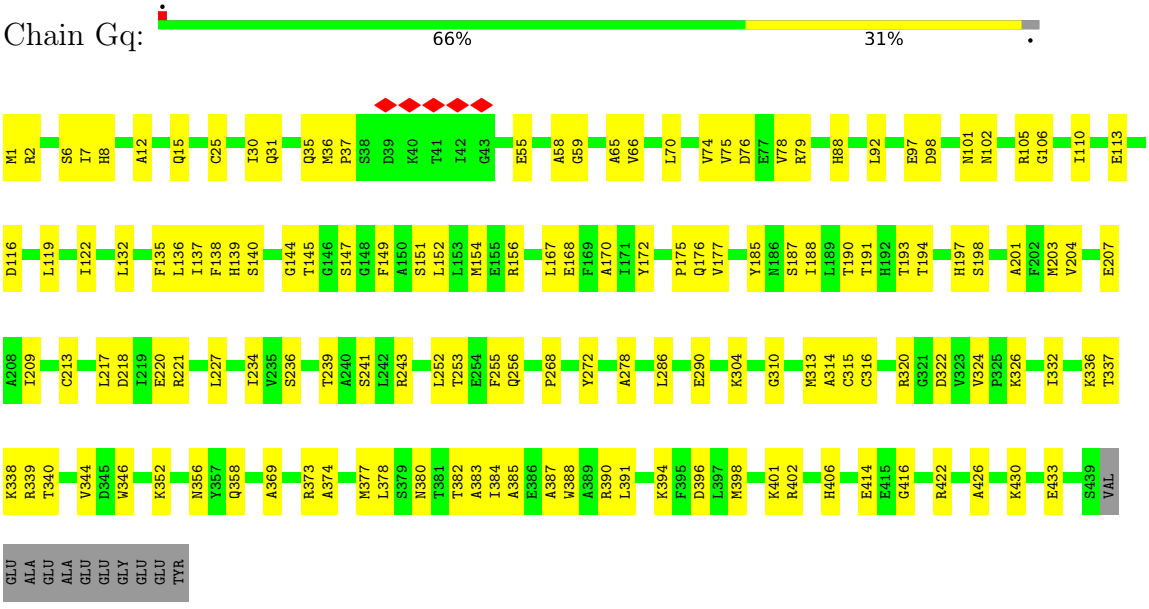

• Molecule 18: Tubulin alpha-3 chain

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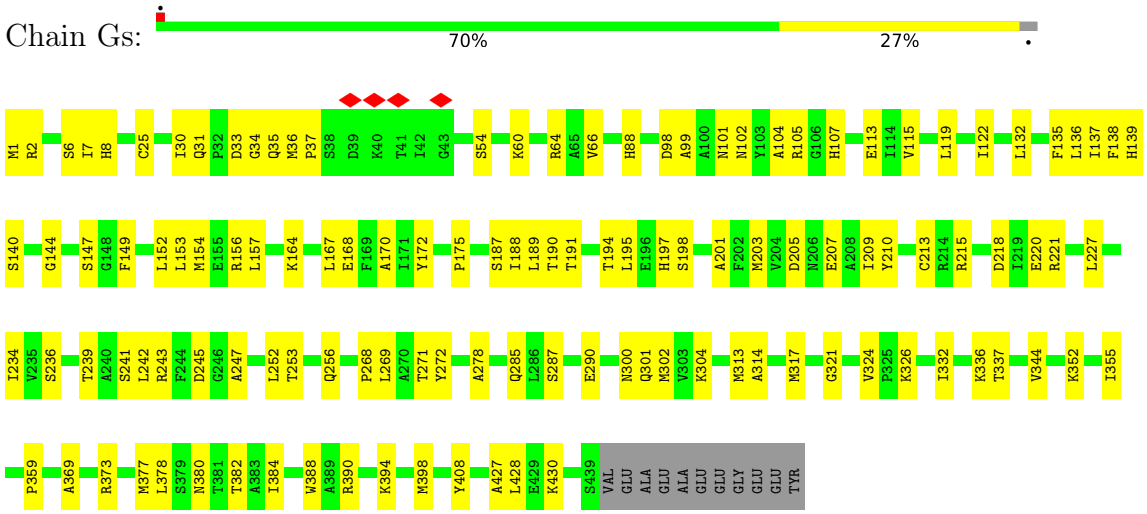

• Molecule 18: Tubulin alpha-3 chain

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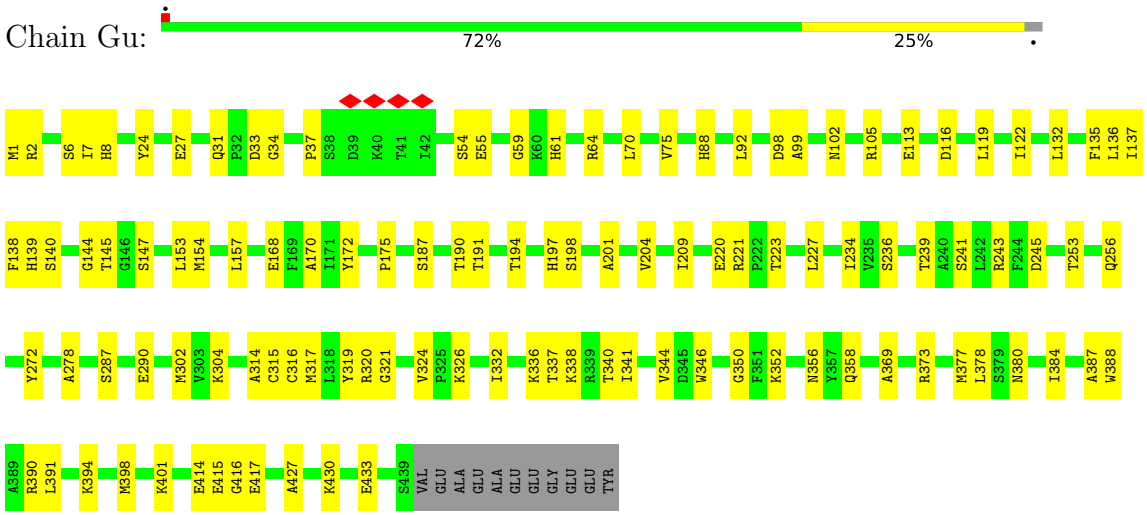

• Molecule 18: Tubulin alpha-3 chain

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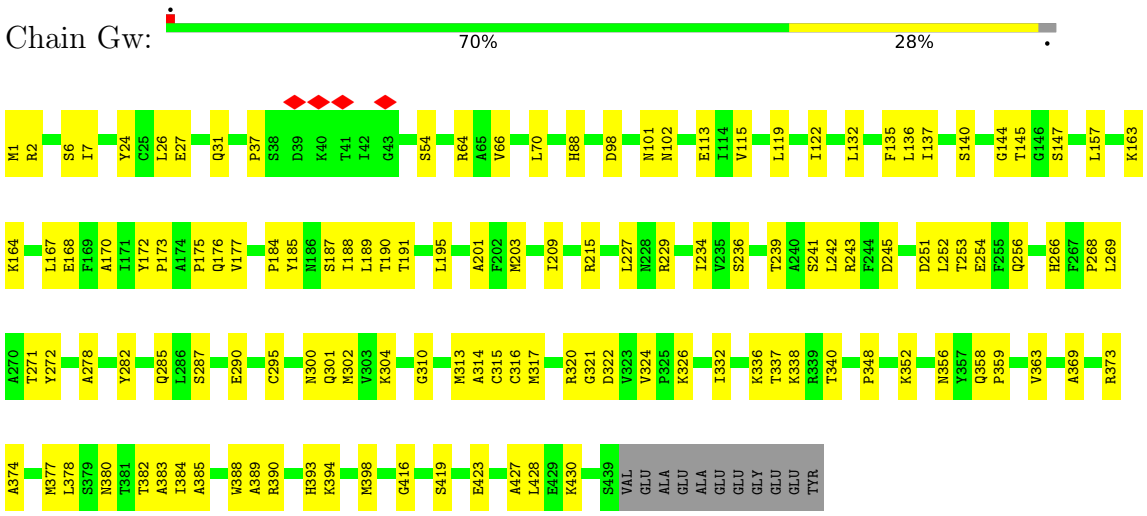

• Molecule 18: Tubulin alpha-3 chain

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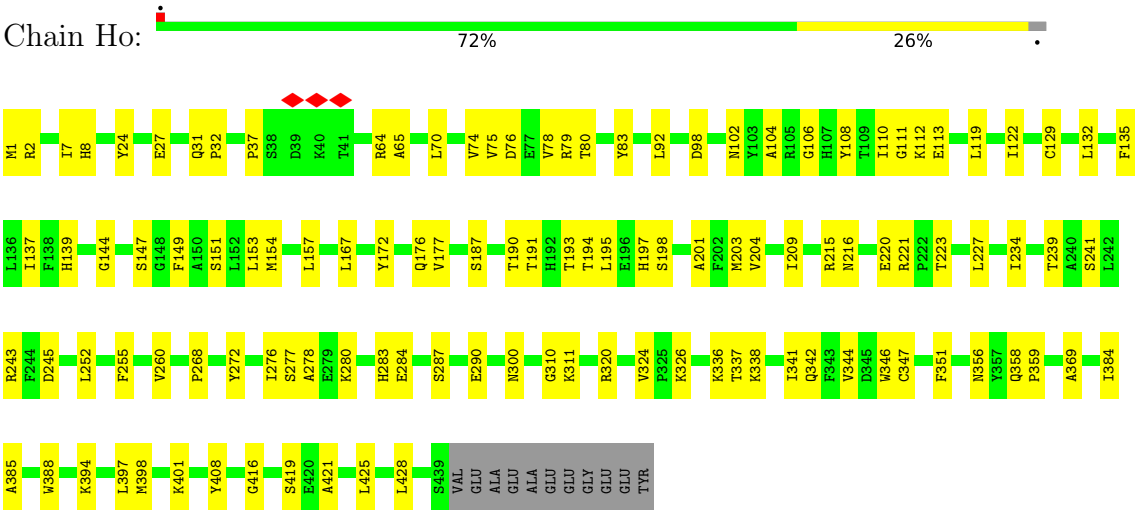

• Molecule 18: Tubulin alpha-3 chain

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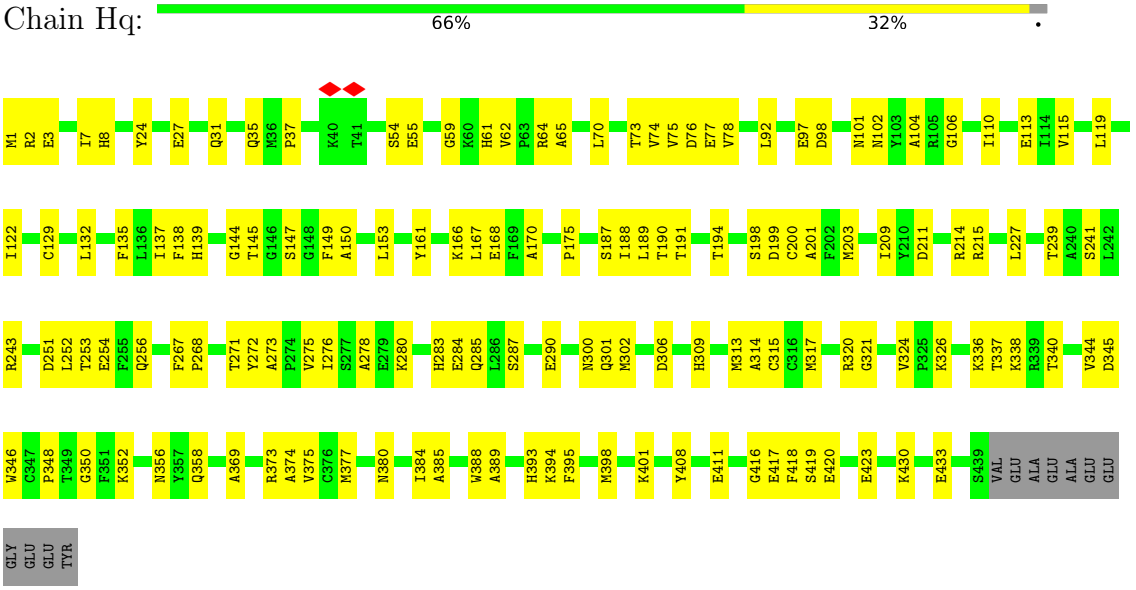

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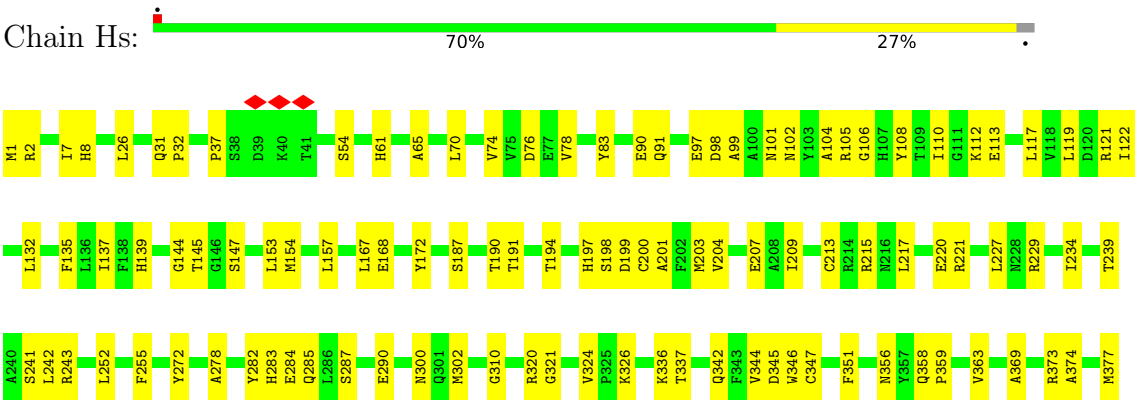

• Molecule 18: Tubulin alpha-3 chain

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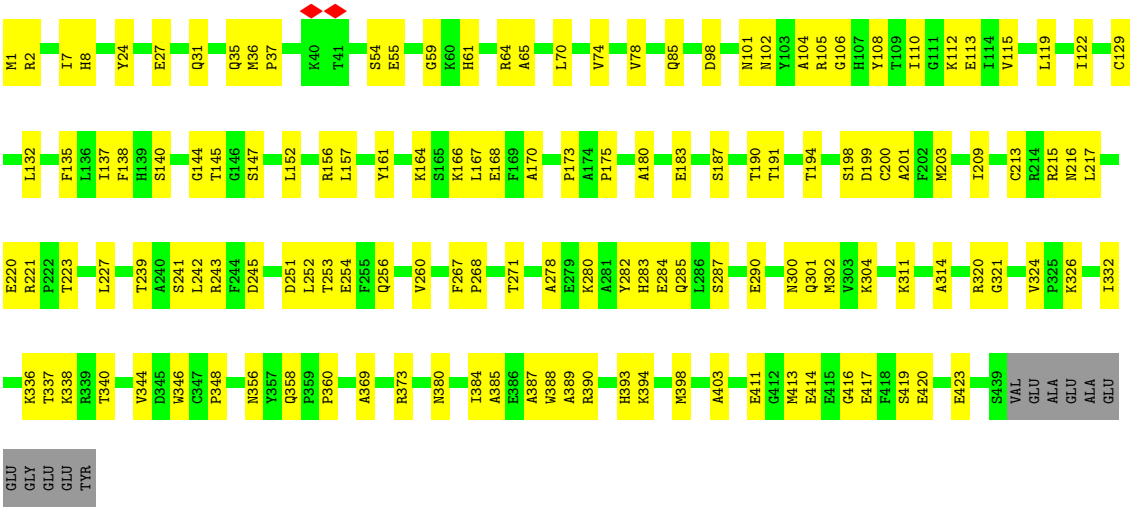

• Molecule 18: Tubulin alpha-3 chain

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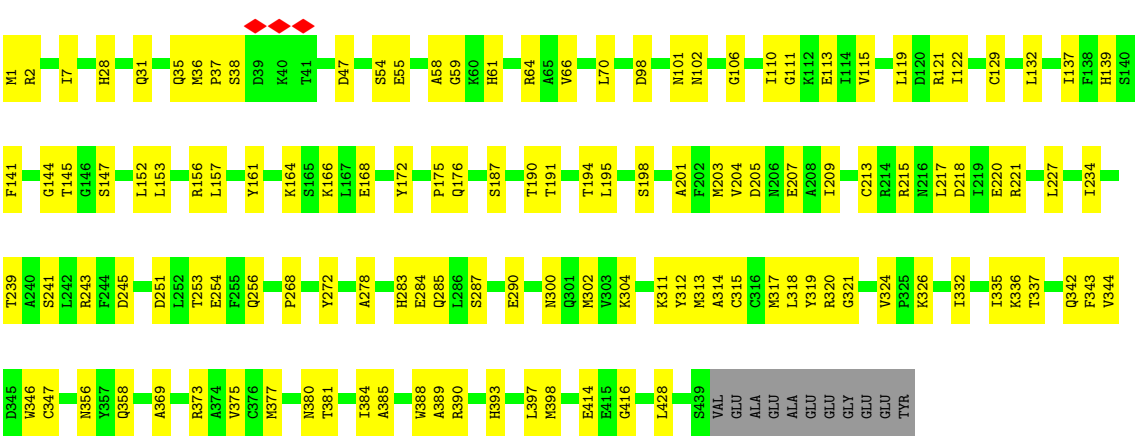

• Molecule 18: Tubulin alpha-3 chain

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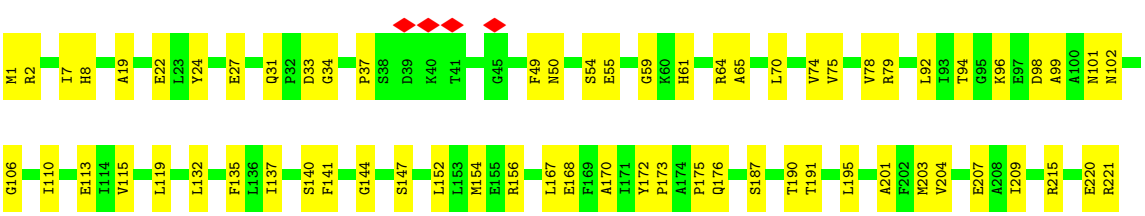

• Molecule 18: Tubulin alpha-3 chain

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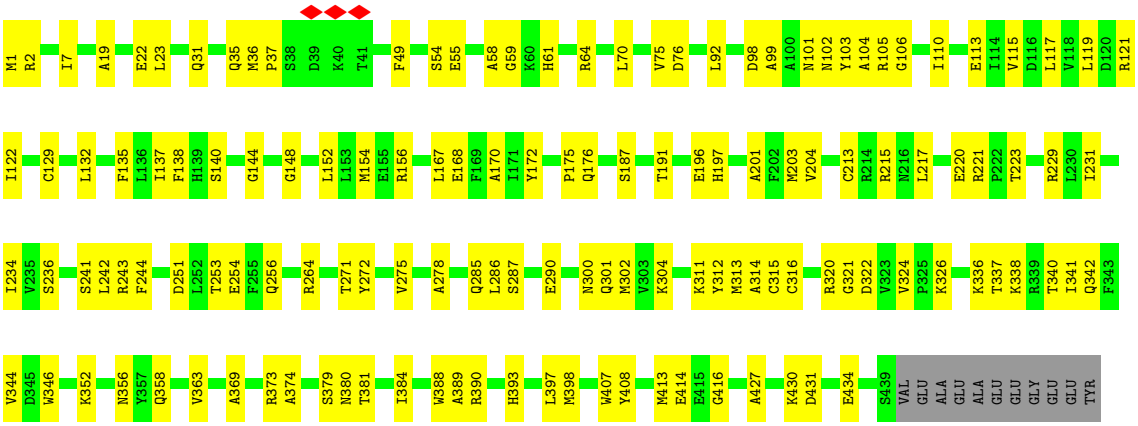

• Molecule 18: Tubulin alpha-3 chain

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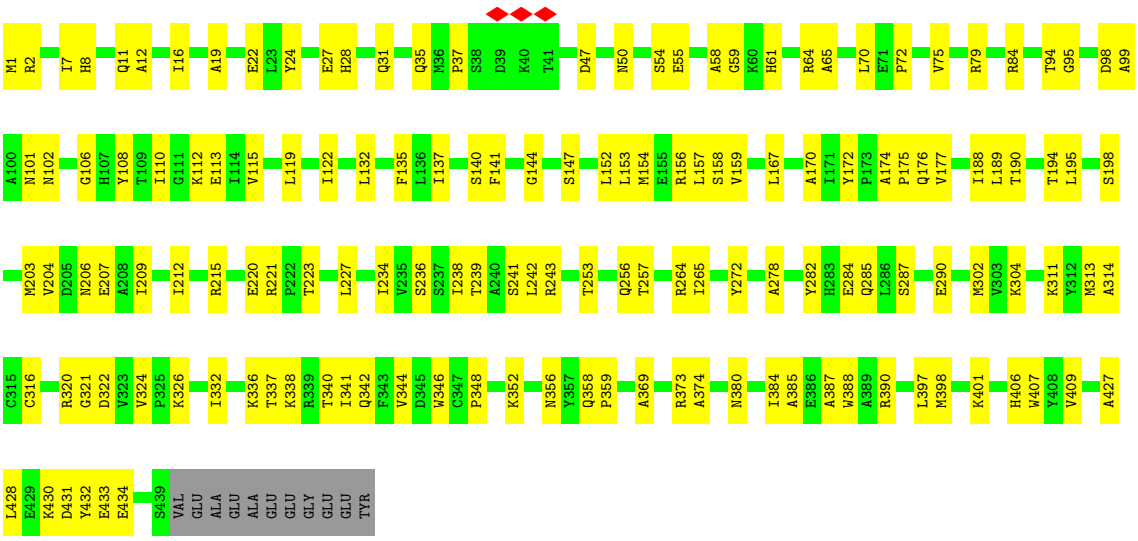

• Molecule 18: Tubulin alpha-3 chain

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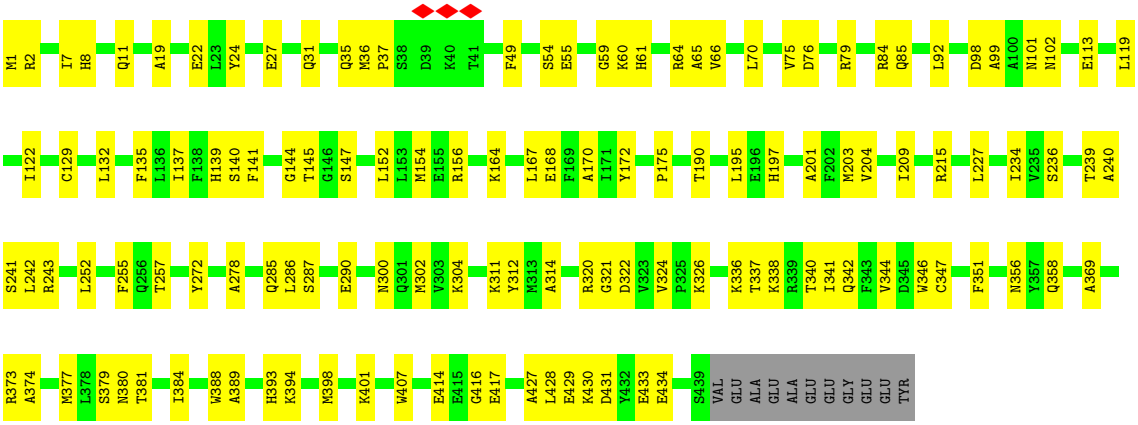

• Molecule 18: Tubulin alpha-3 chain

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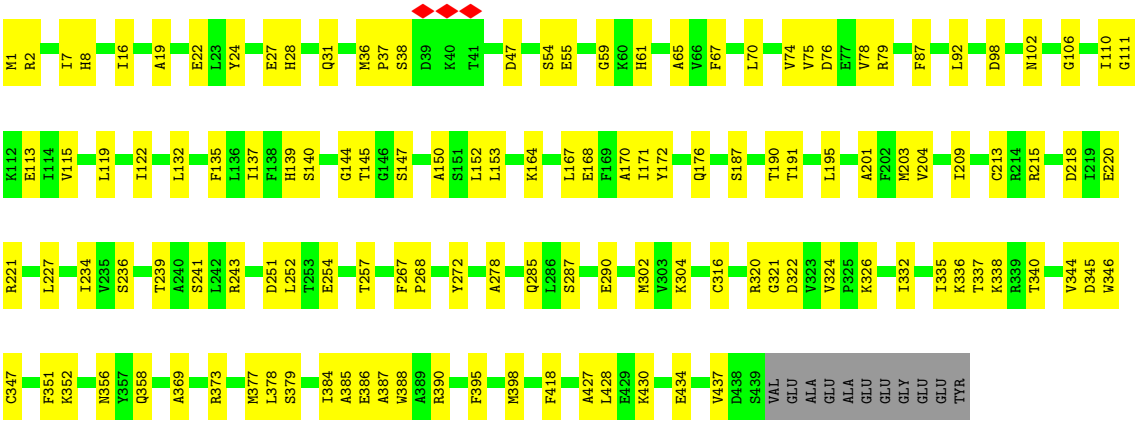

• Molecule 18: Tubulin alpha-3 chain

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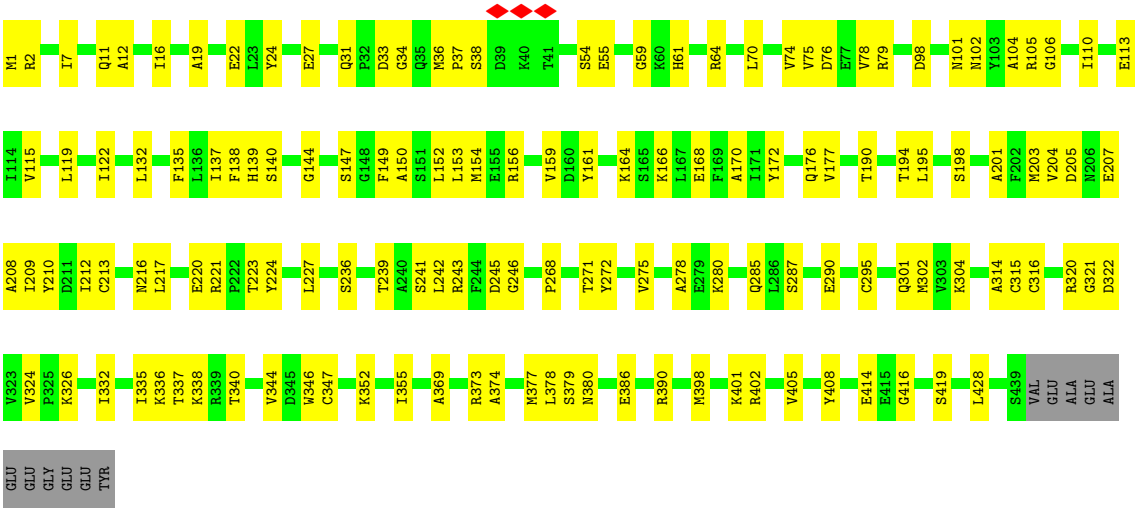

• Molecule 18: Tubulin alpha-3 chain

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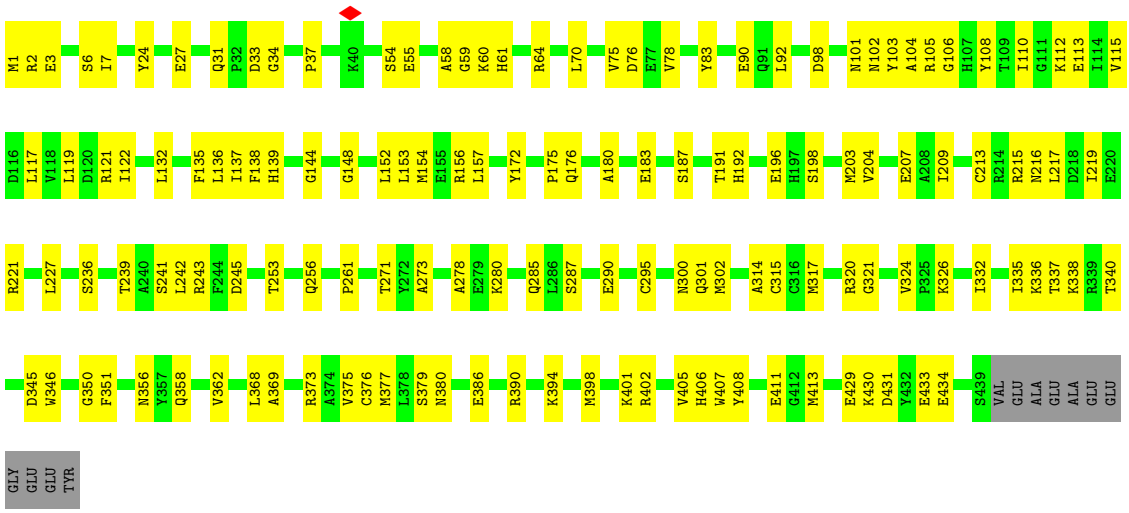

• Molecule 18: Tubulin alpha-3 chain

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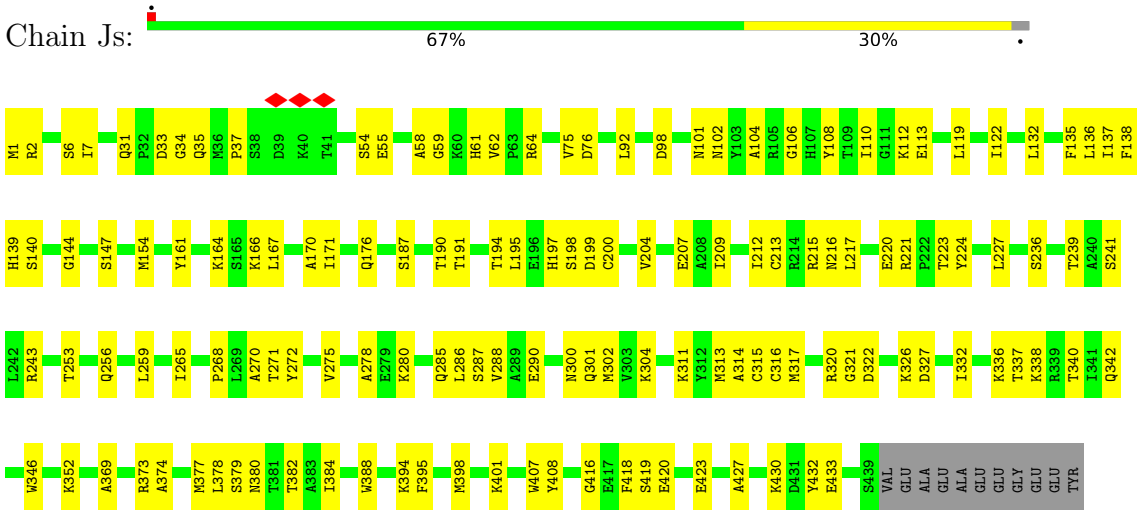

• Molecule 18: Tubulin alpha-3 chain

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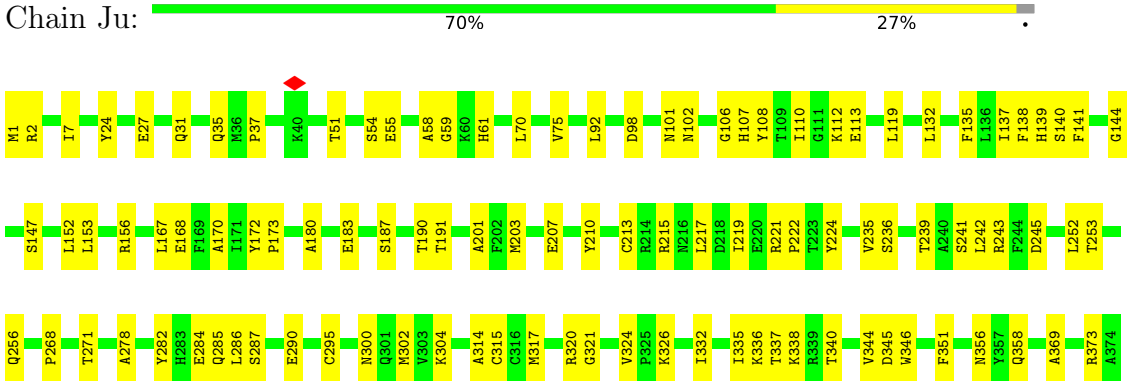

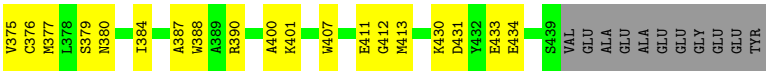

• Molecule 18: Tubulin alpha-3 chain

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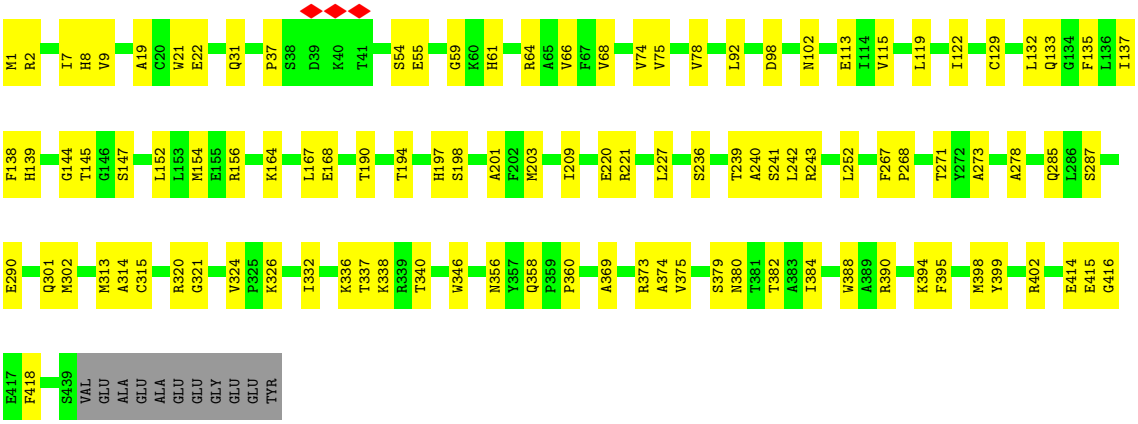

• Molecule 18: Tubulin alpha-3 chain

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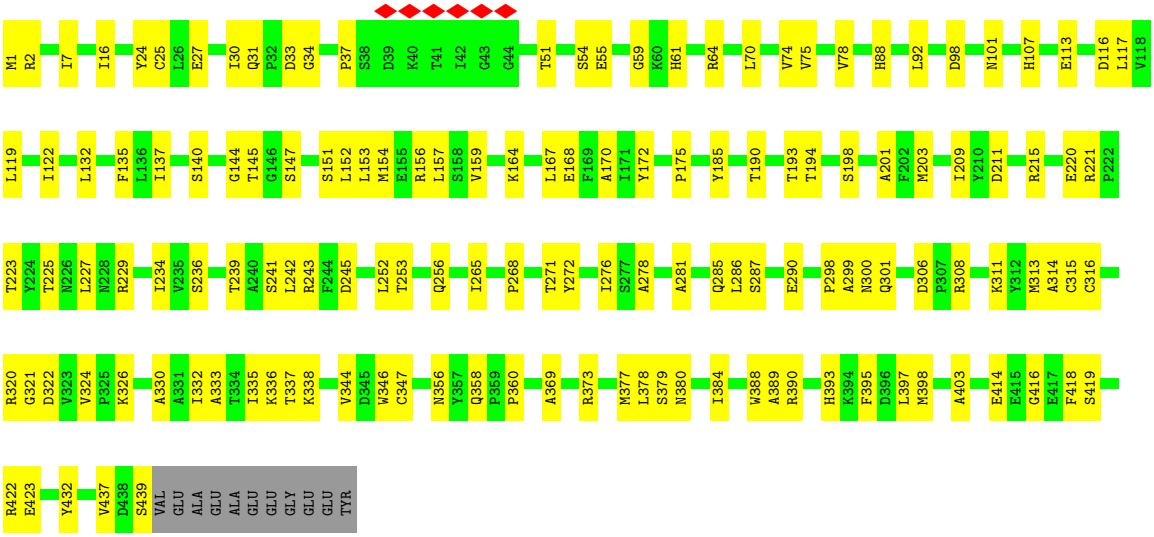

• Molecule 18: Tubulin alpha-3 chain

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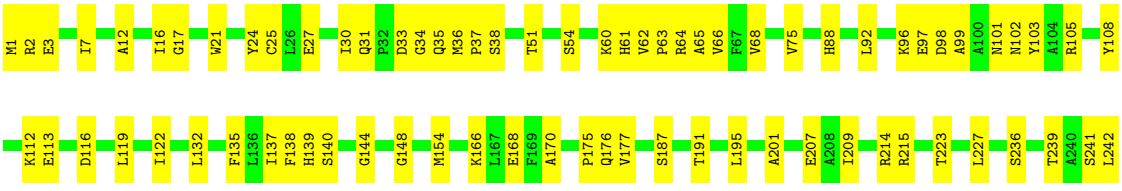
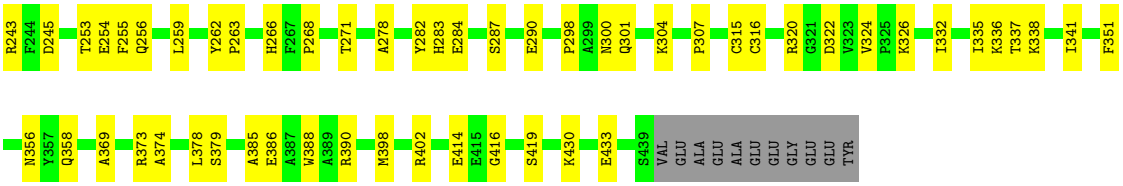
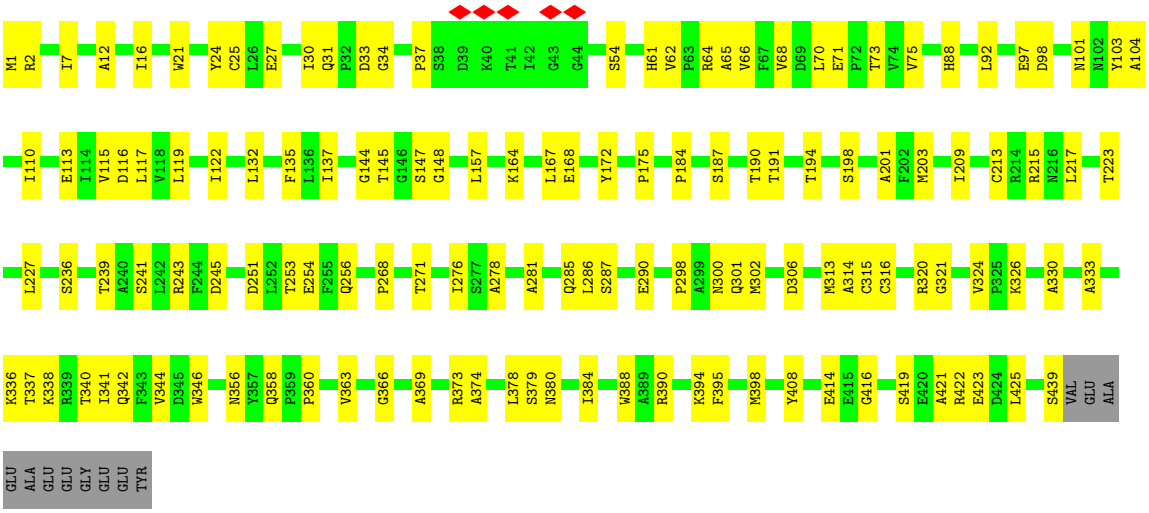




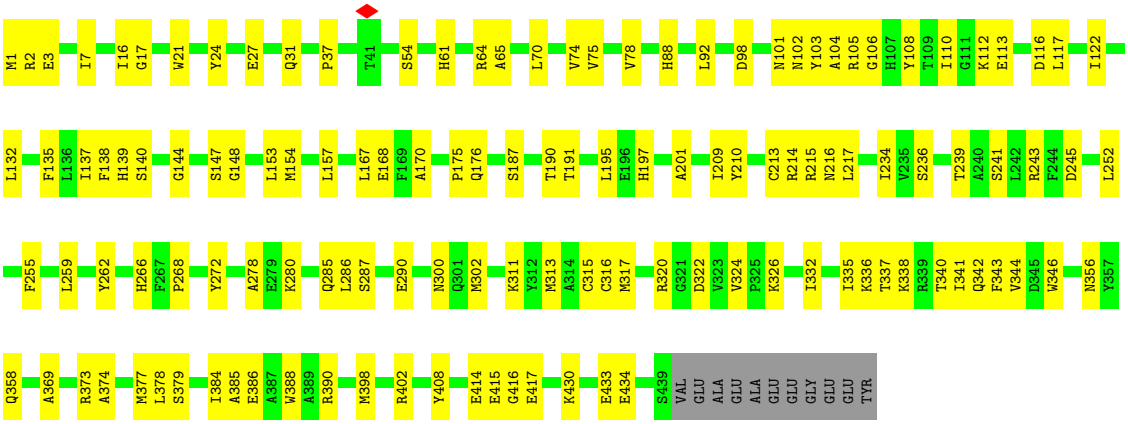
• Molecule 18: Tubulin alpha-3 chain

Chain Ks:



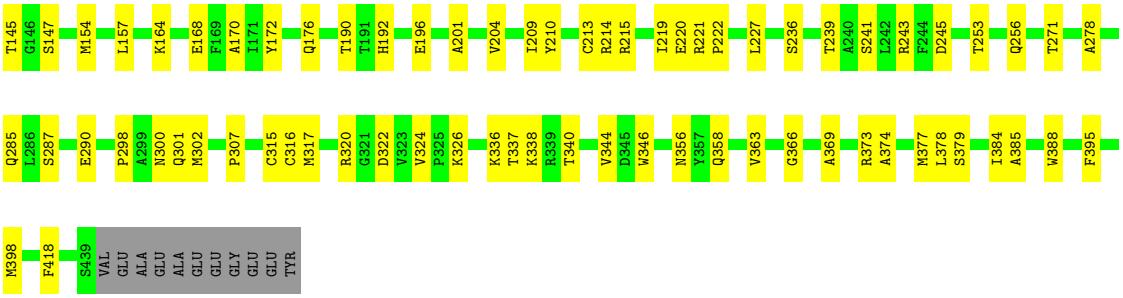
• Molecule 18: Tubulin alpha-3 chain

Chain Ku:

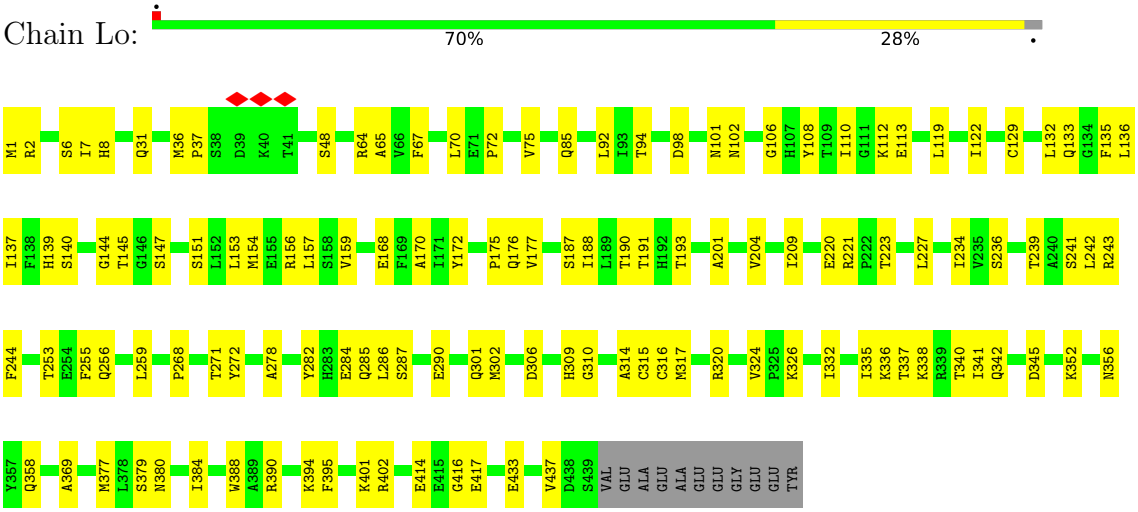


• Molecule 18: Tubulin alpha-3 chain

Chain Km:



• Molecule 18: Tubulin alpha-3 chain



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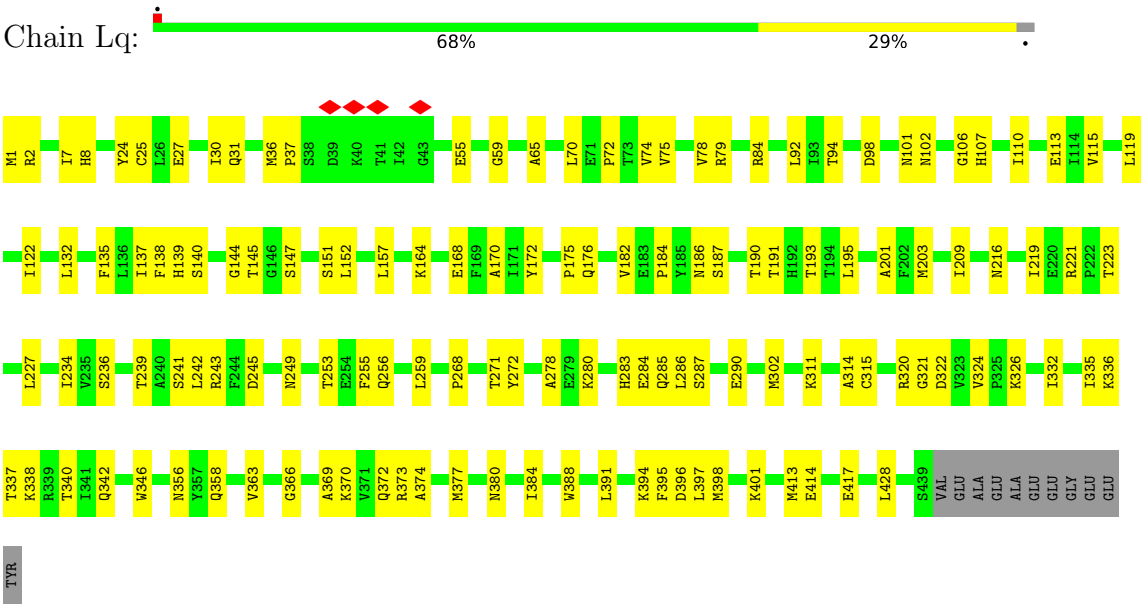

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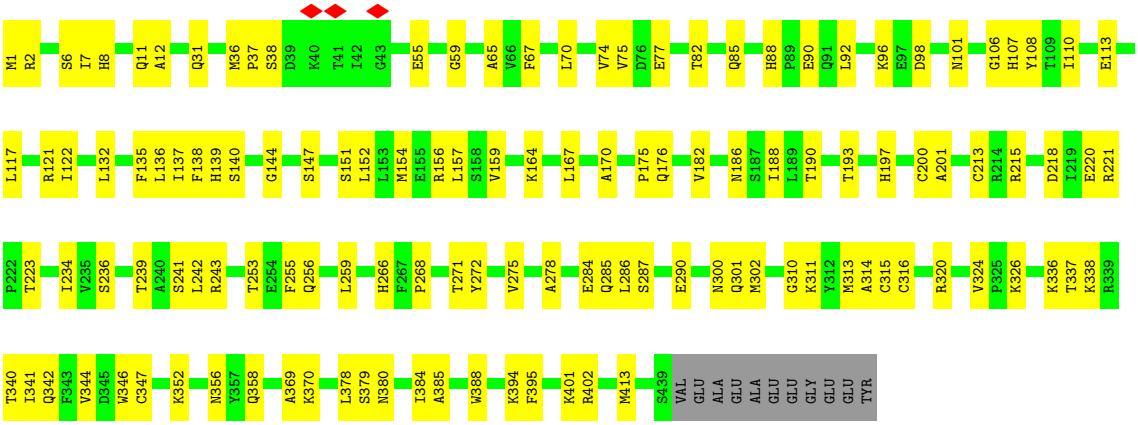
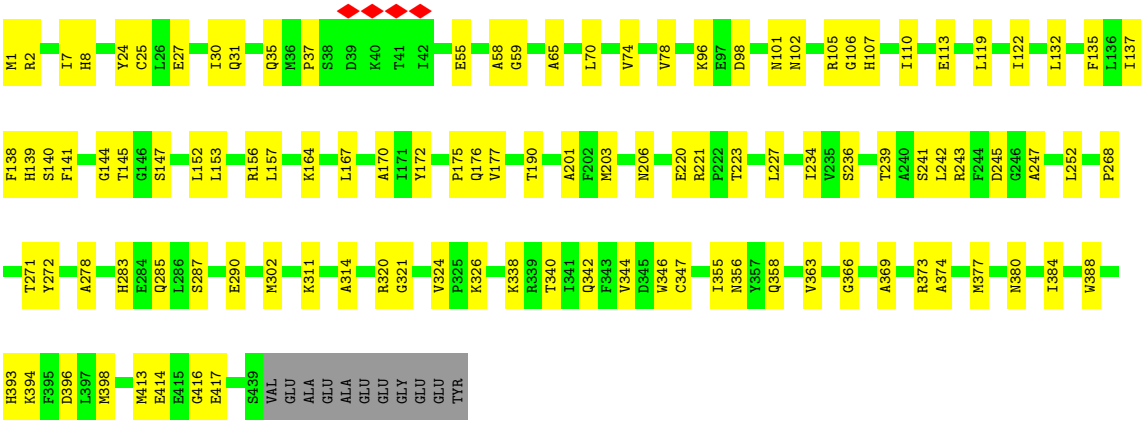


• Molecule 18: Tubulin alpha-3 chain

Chain Lu:



• Molecule 18: Tubulin alpha-3 chain

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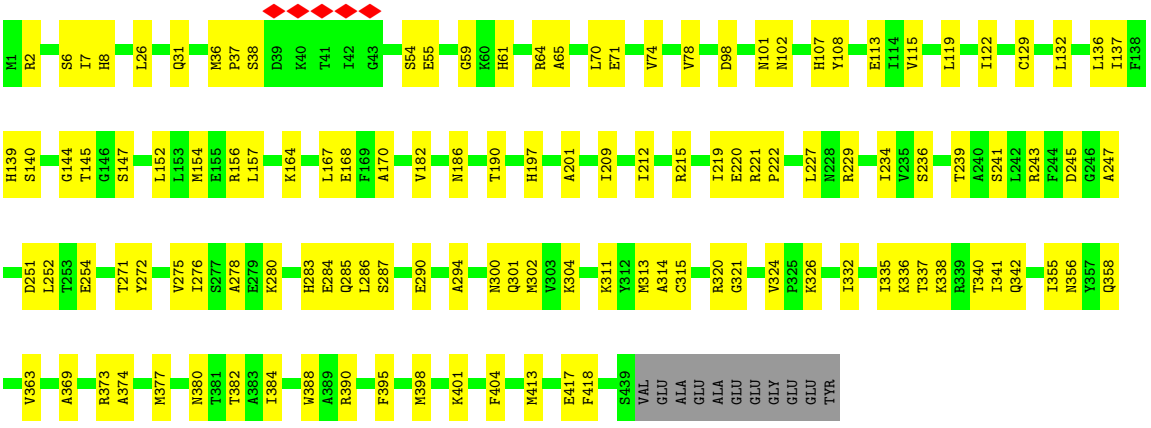

• Molecule 18: Tubulin alpha-3 chain

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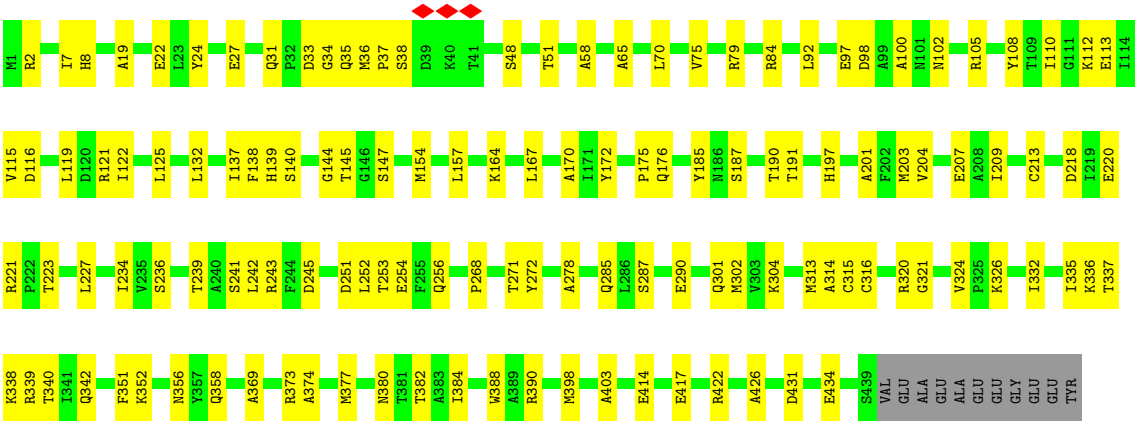
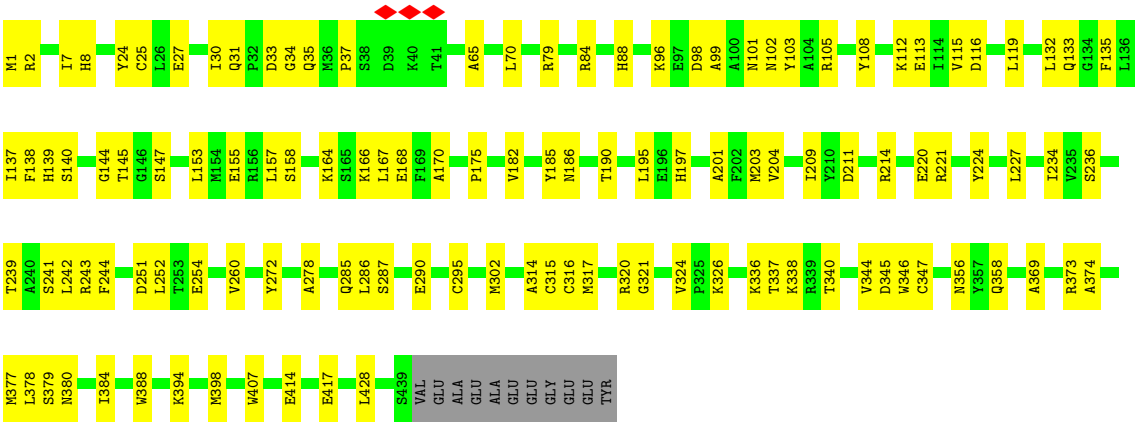


• Molecule 18: Tubulin alpha-3 chain

Chain Mq:



• Molecule 18: Tubulin alpha-3 chain

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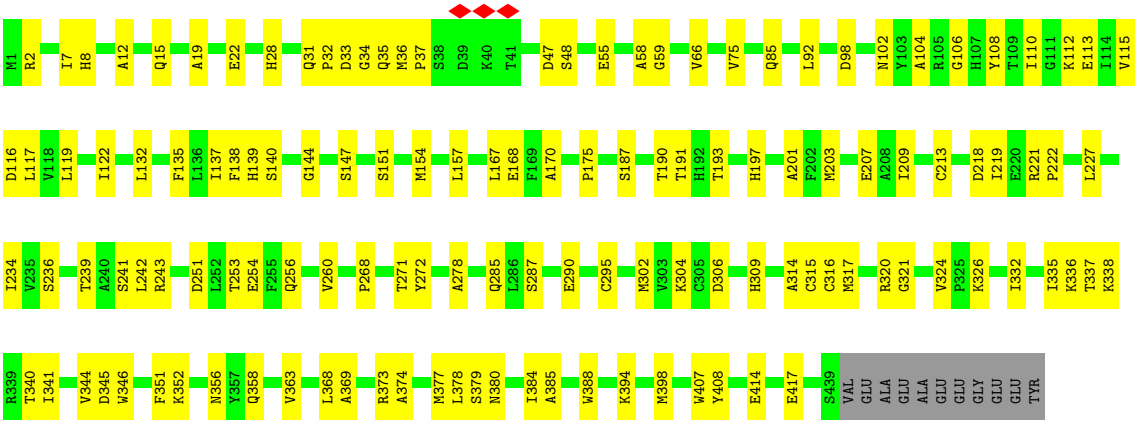

• Molecule 18: Tubulin alpha-3 chain

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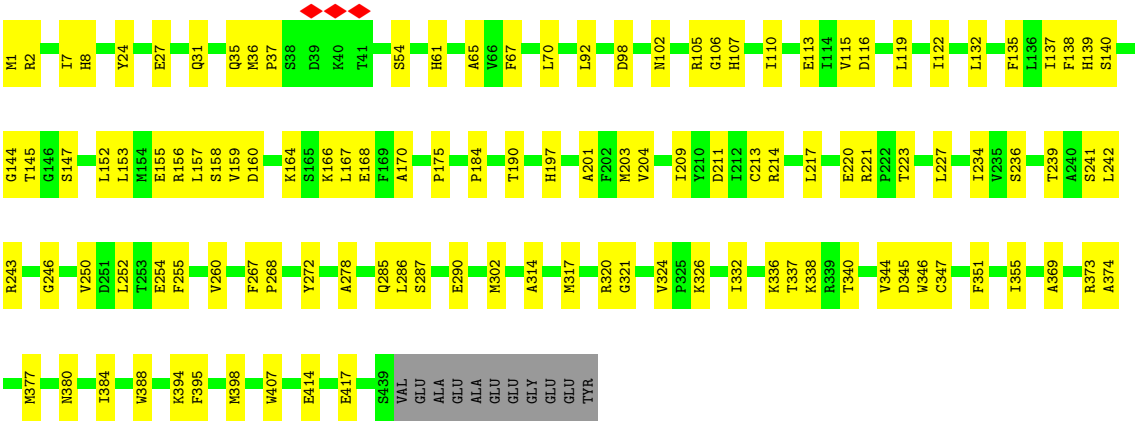

• Molecule 18: Tubulin alpha-3 chain

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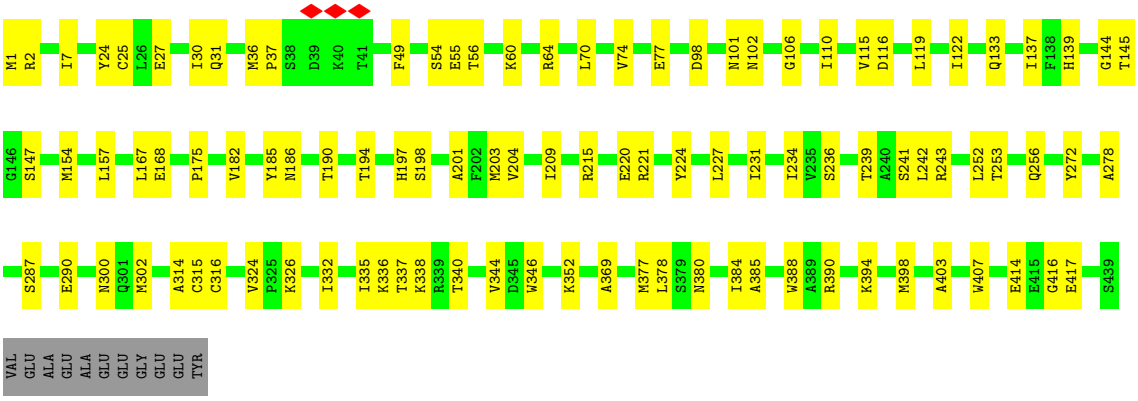
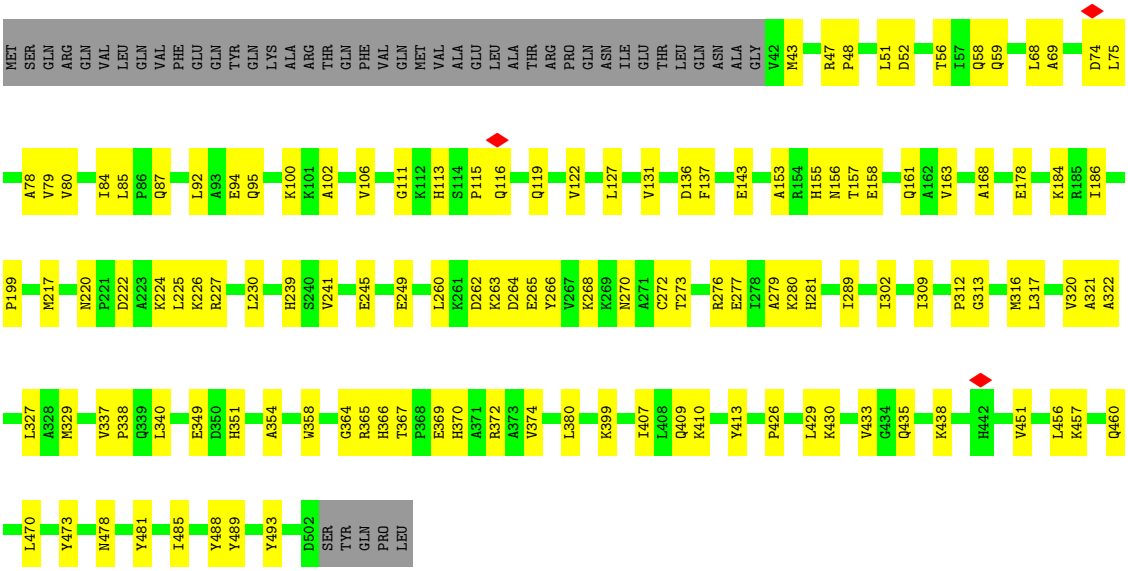


• Molecule 19: Sperm-associated antigen 6

Chain AA:



• Molecule 19: Sperm-associated antigen 6

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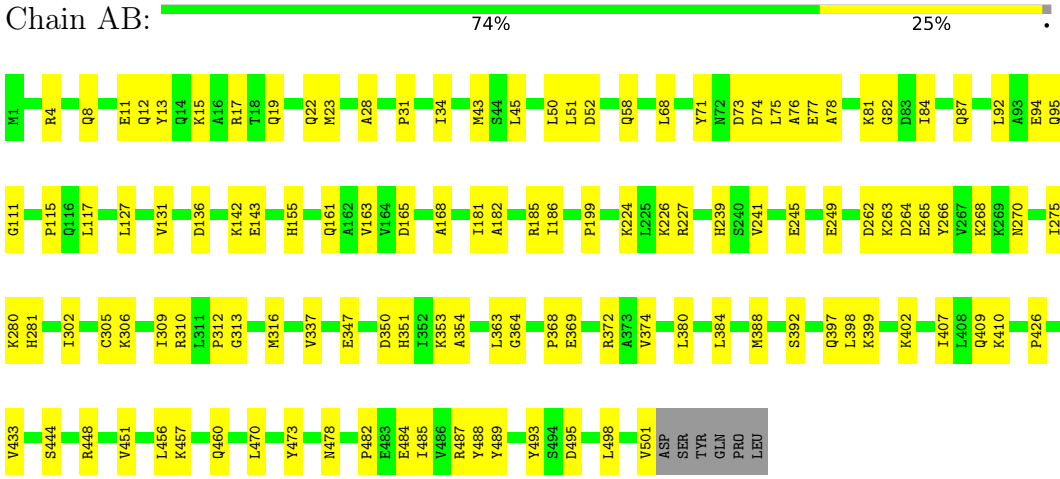
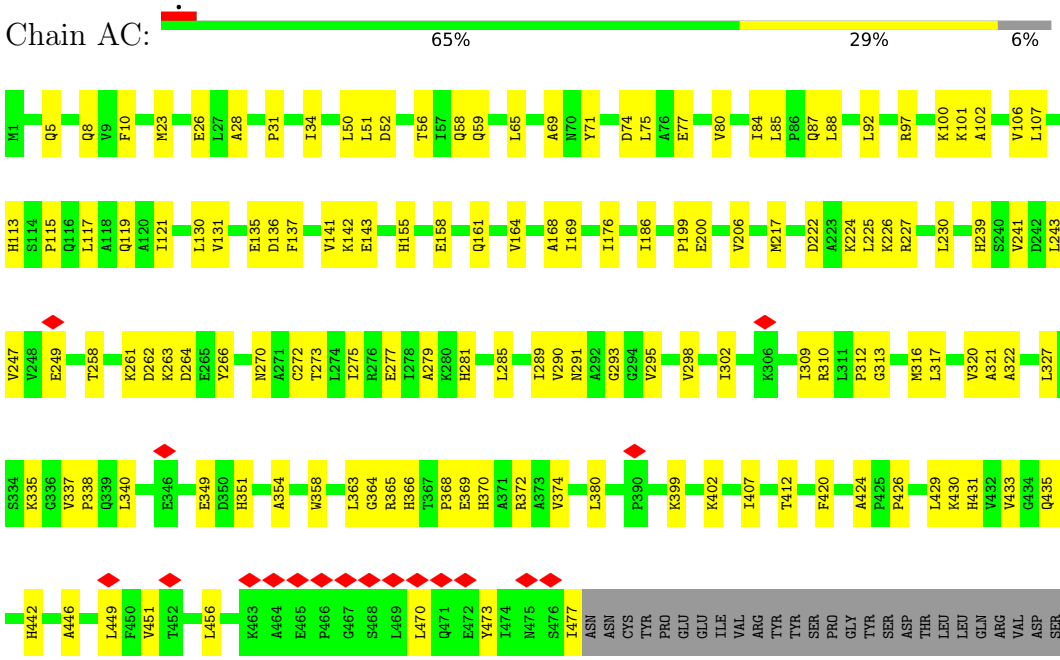


• Molecule 19: Sperm-associated antigen 6

Chain AC:



• Molecule 19: Sperm-associated antigen 6

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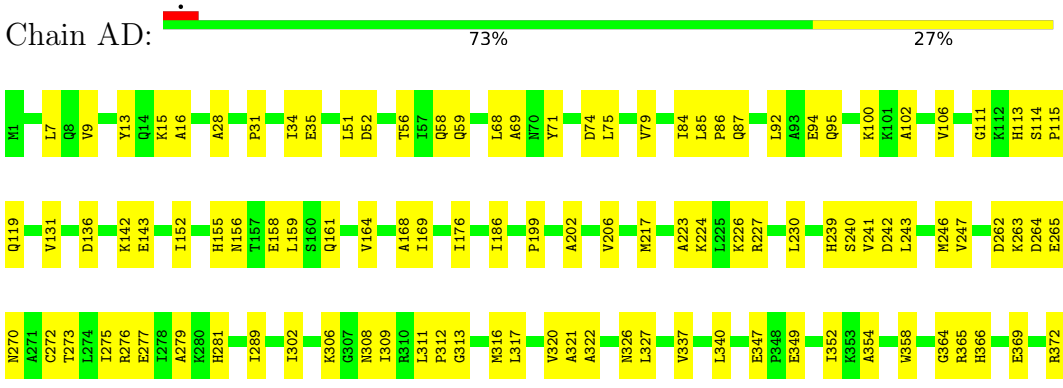

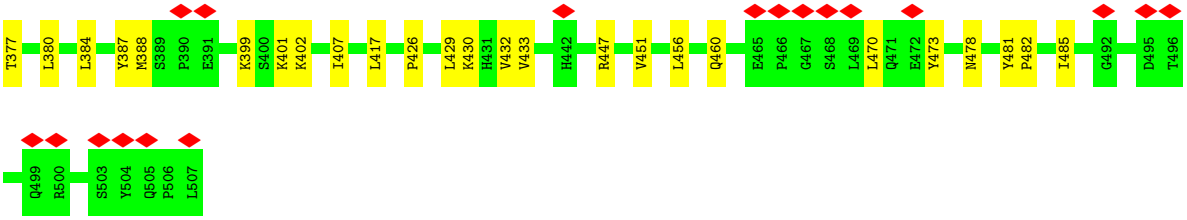

• Molecule 19: Sperm-associated antigen 6

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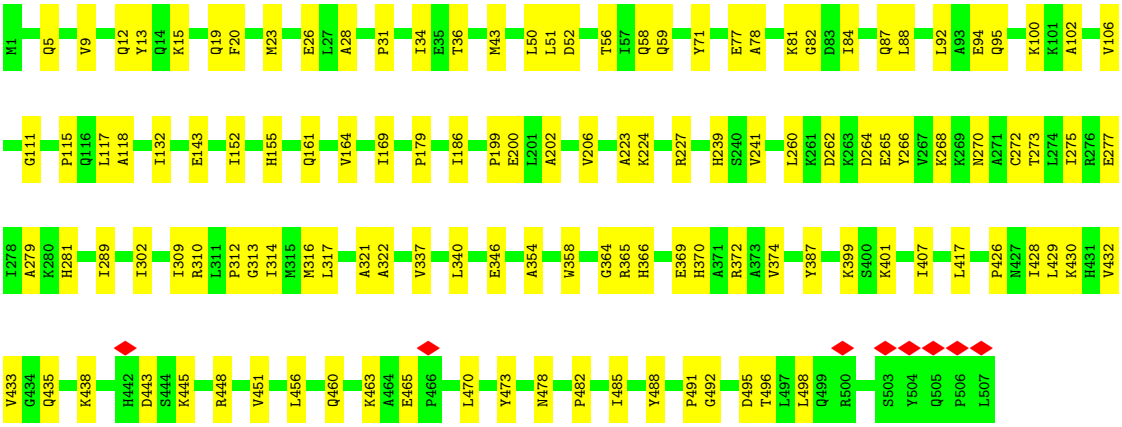

• Molecule 19: Sperm-associated antigen 6

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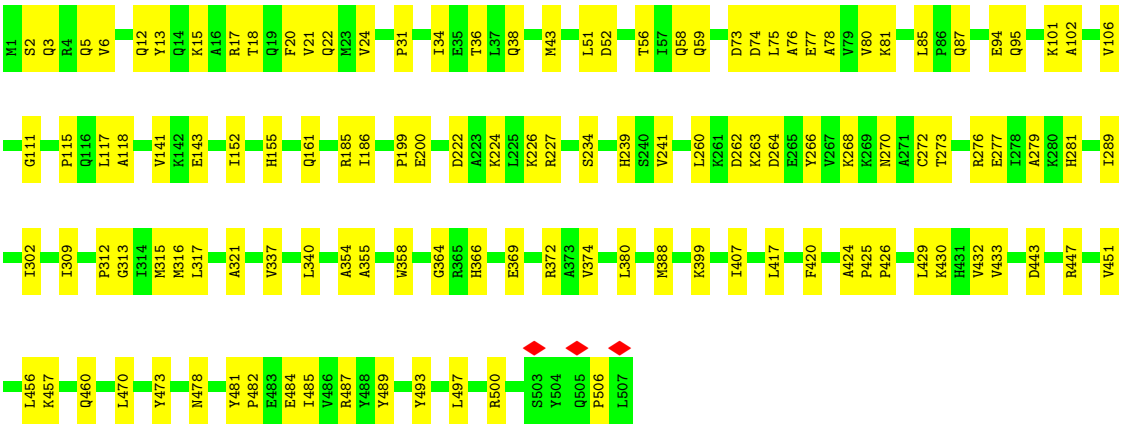

• Molecule 19: Sperm-associated antigen 6

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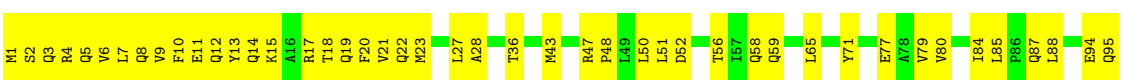

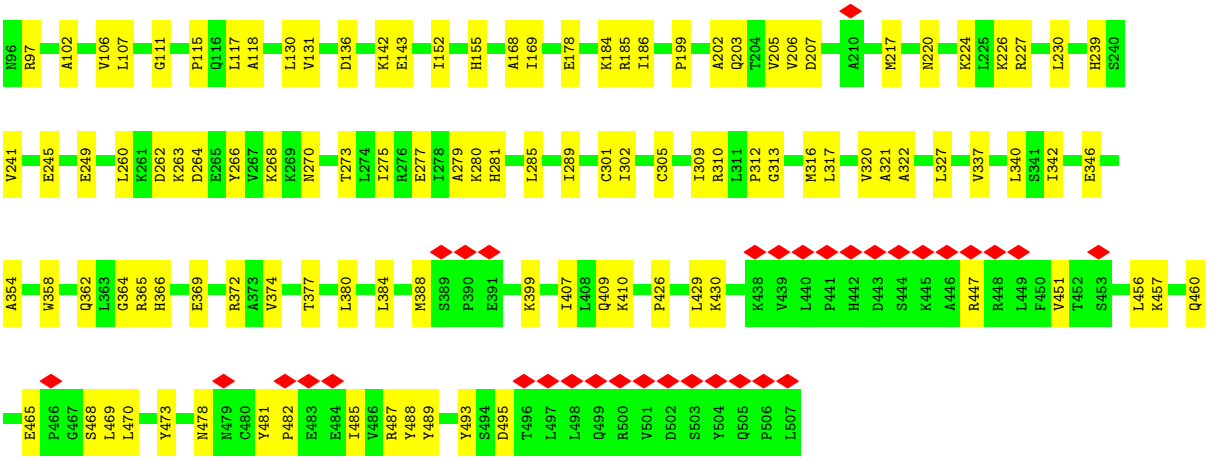

• Molecule 19: Sperm-associated antigen 6

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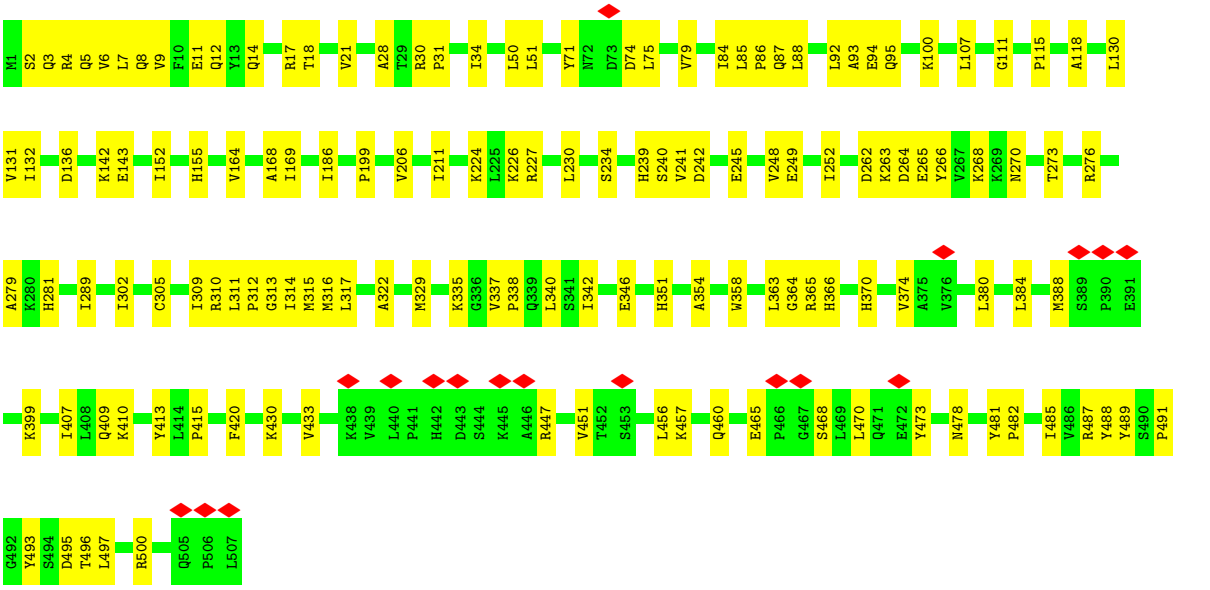

• Molecule 19: Sperm-associated antigen 6

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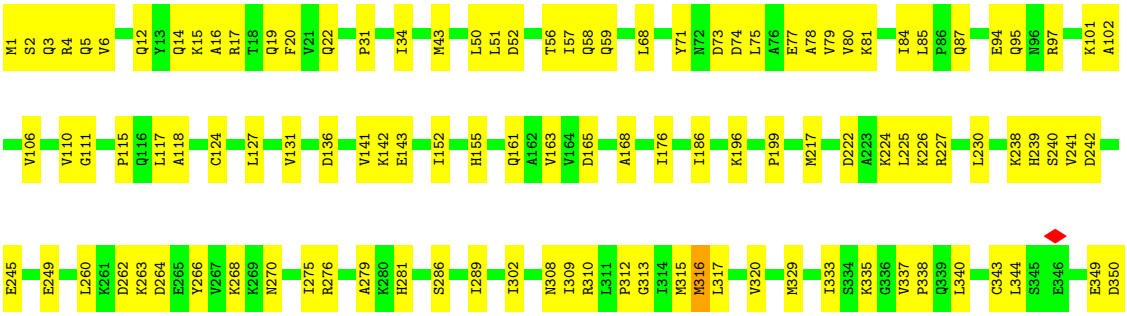

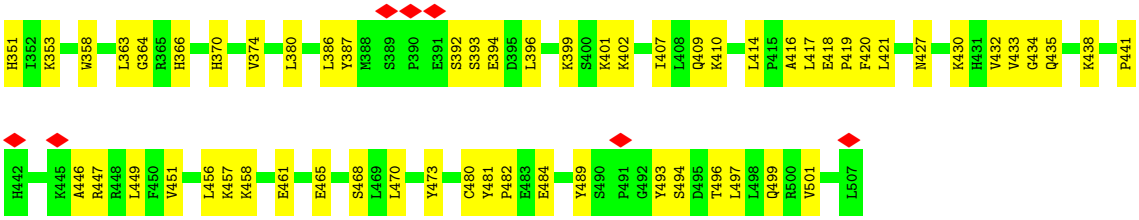

• Molecule 19: Sperm-associated antigen 6

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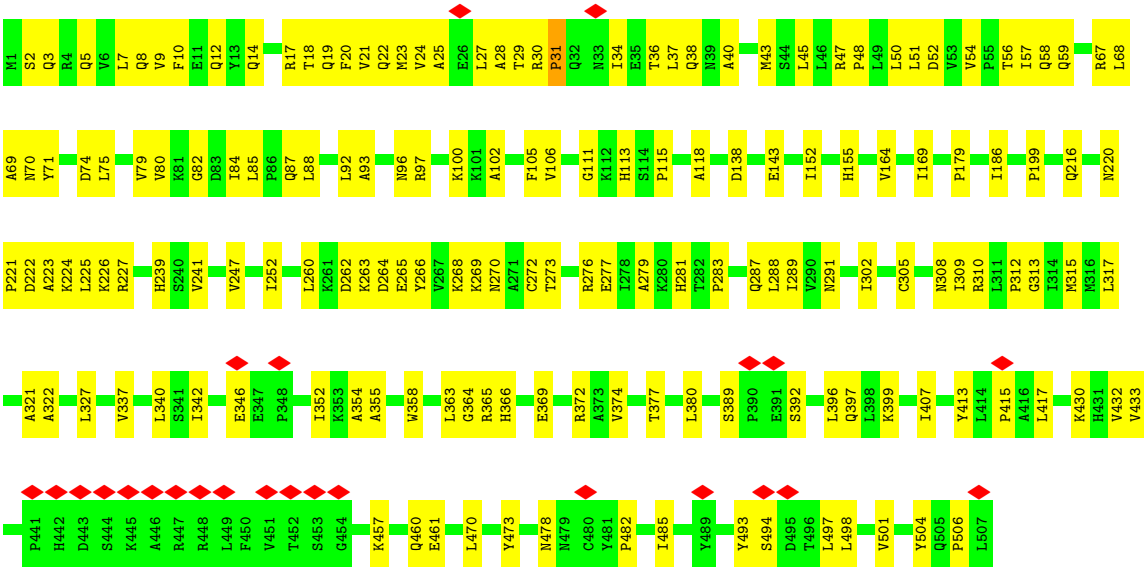

• Molecule 19: Sperm-associated antigen 6

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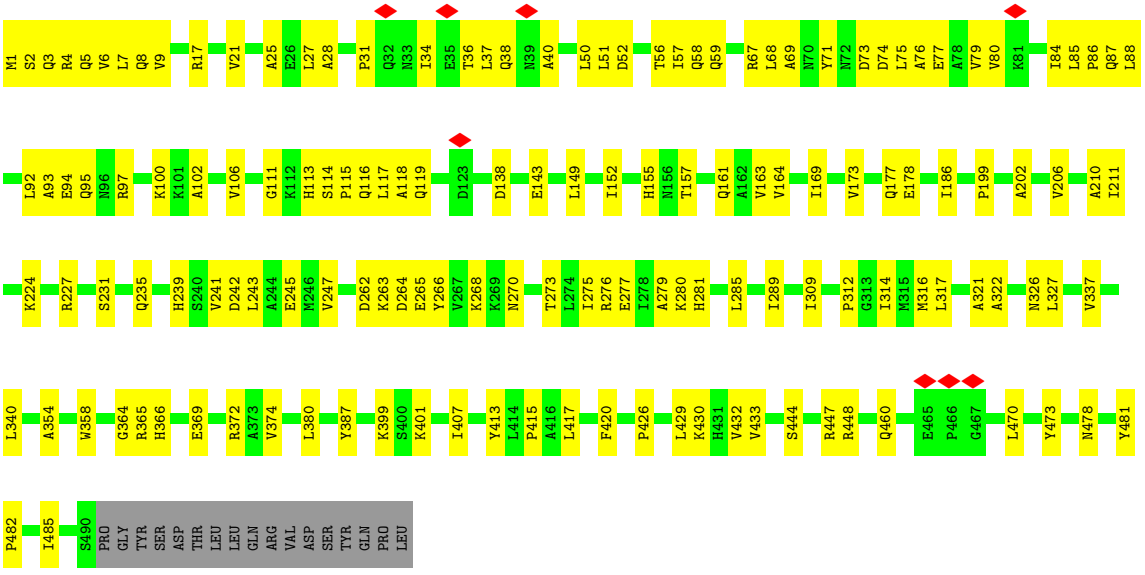

• Molecule 19: Sperm-associated antigen 6

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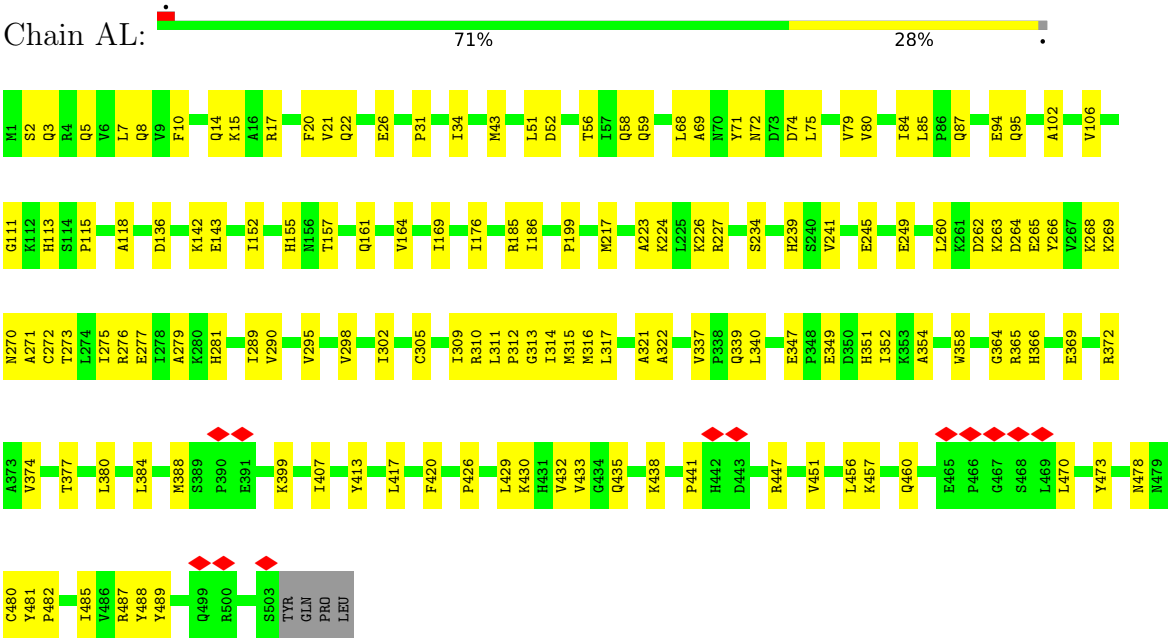

• Molecule 19: Sperm-associated antigen 6

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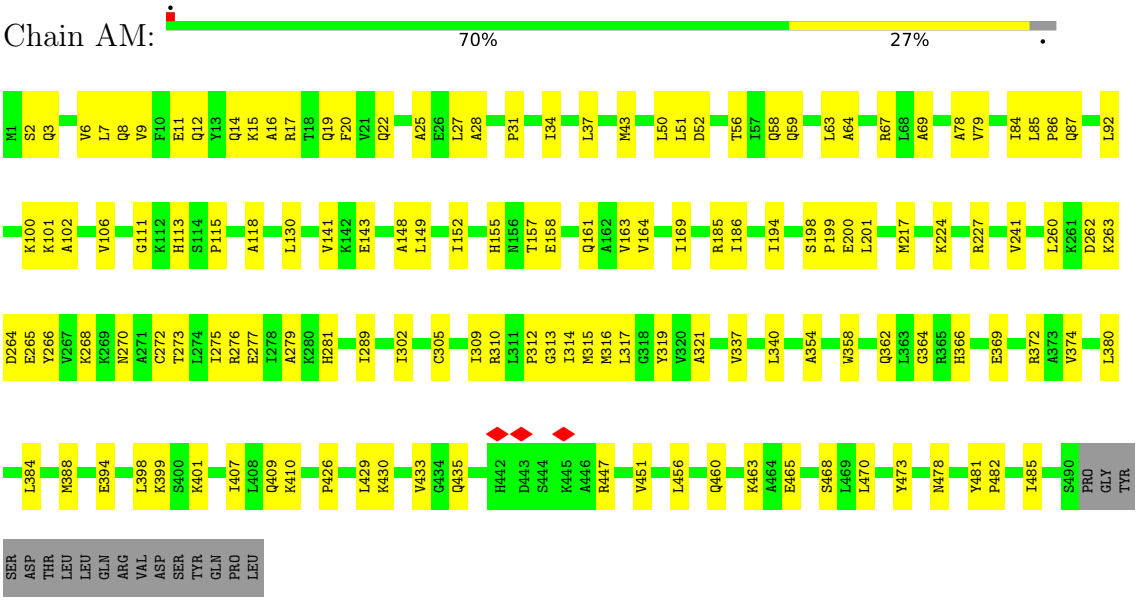

• Molecule 19: Sperm-associated antigen 6

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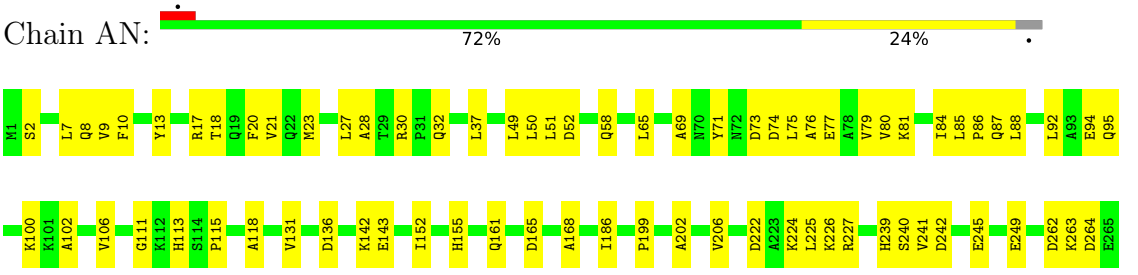

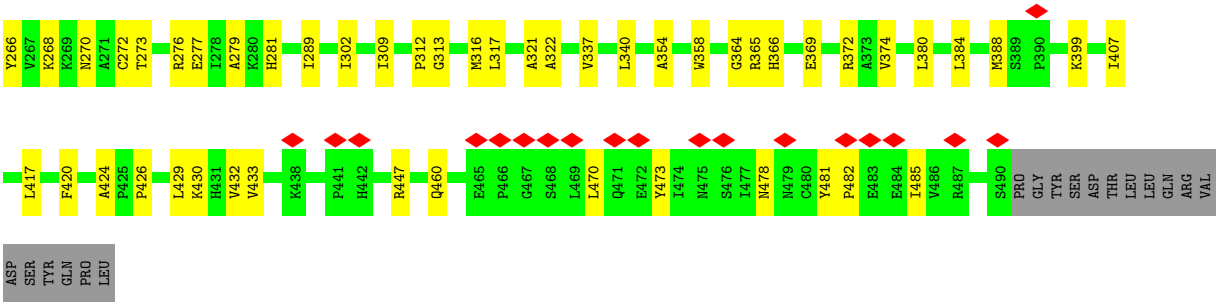

• Molecule 19: Sperm-associated antigen 6

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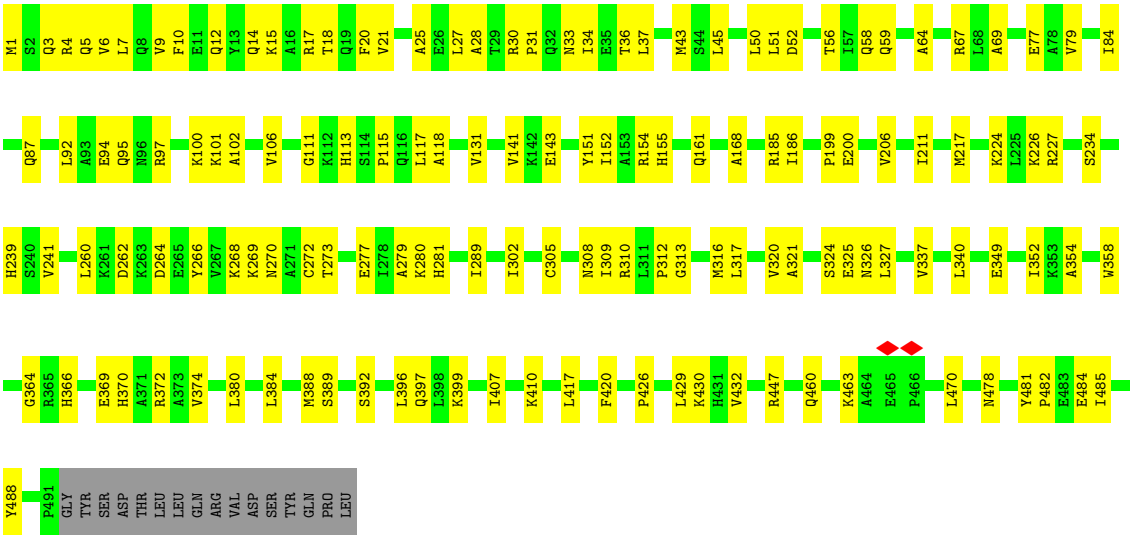

• Molecule 19: Sperm-associated antigen 6

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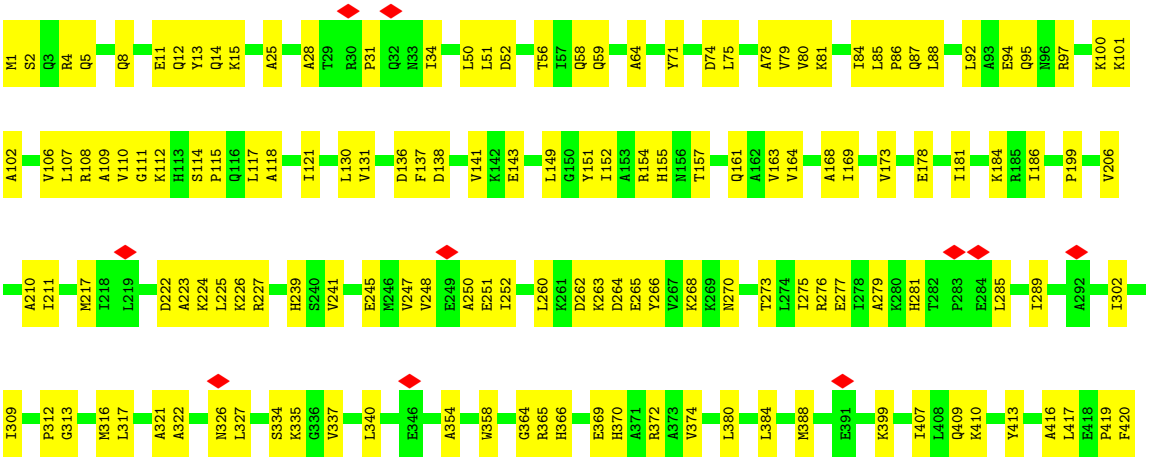

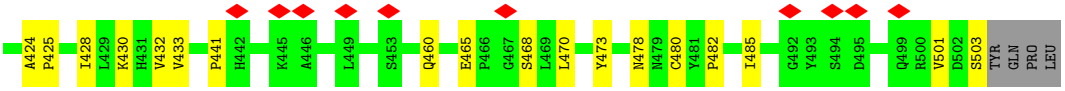

• Molecule 19: Sperm-associated antigen 6

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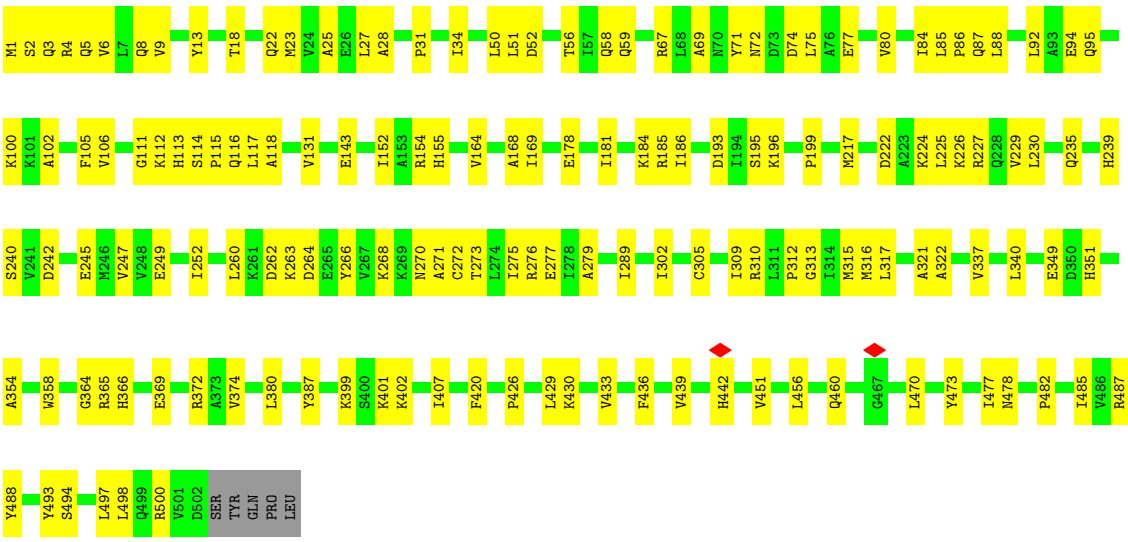

• Molecule 19: Sperm-associated antigen 6

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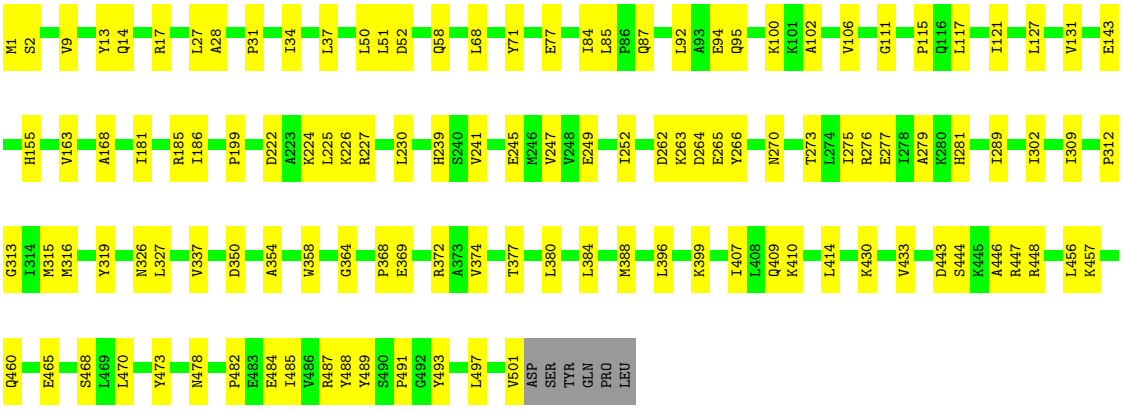

• Molecule 19: Sperm-associated antigen 6

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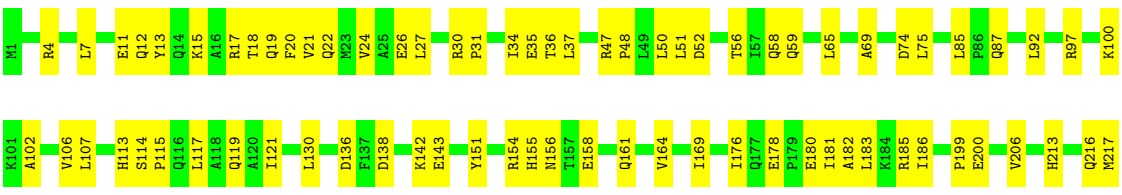

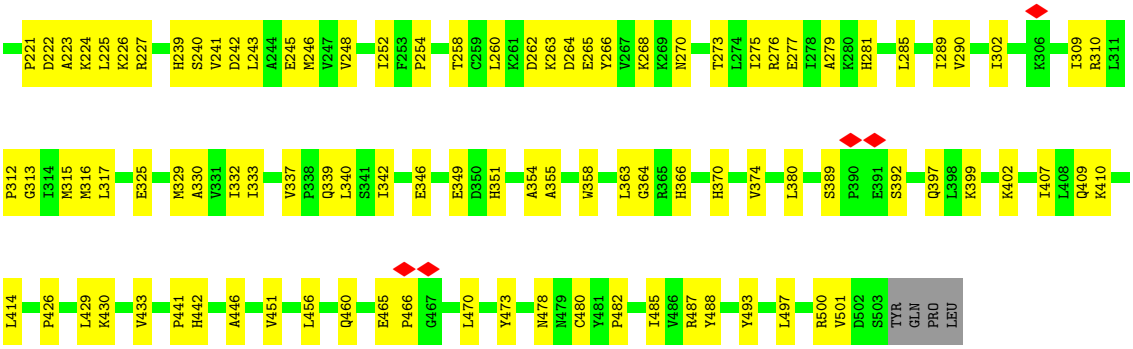

• Molecule 19: Sperm-associated antigen 6

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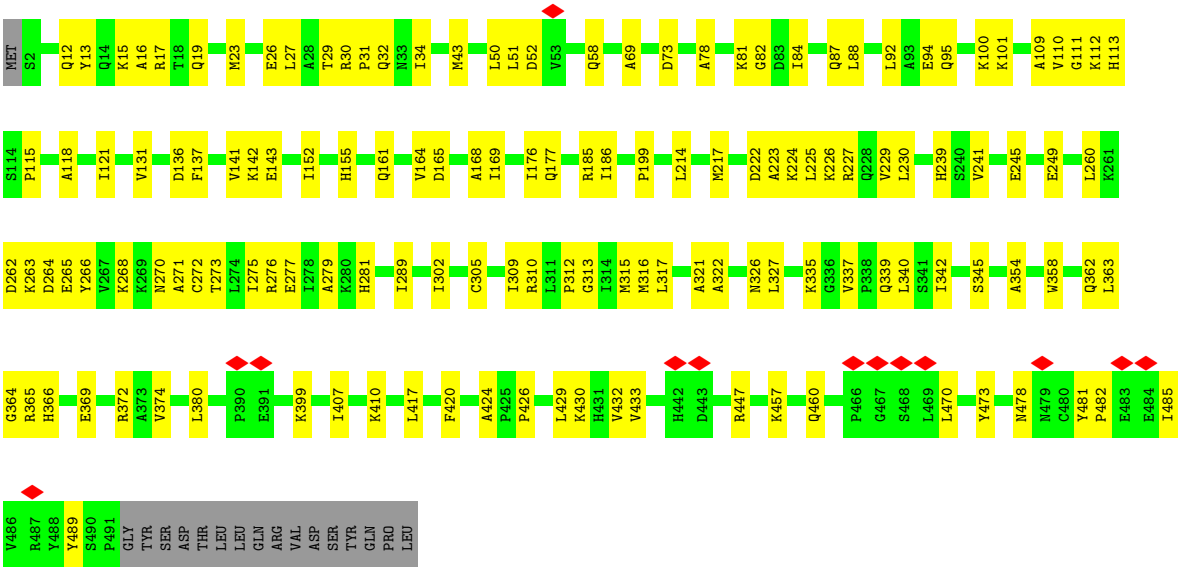

• Molecule 19: Sperm-associated antigen 6

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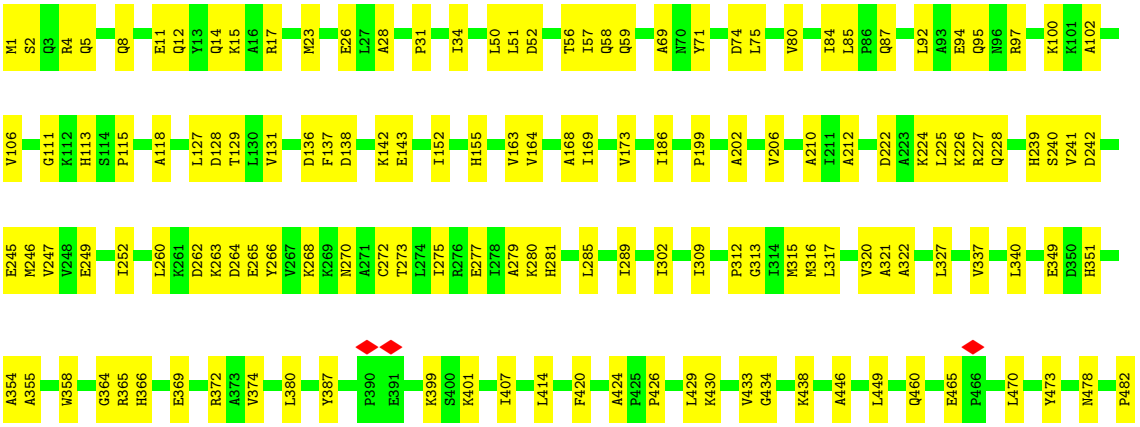

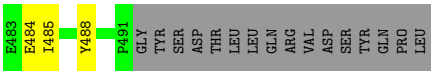

• Molecule 19: Sperm-associated antigen 6

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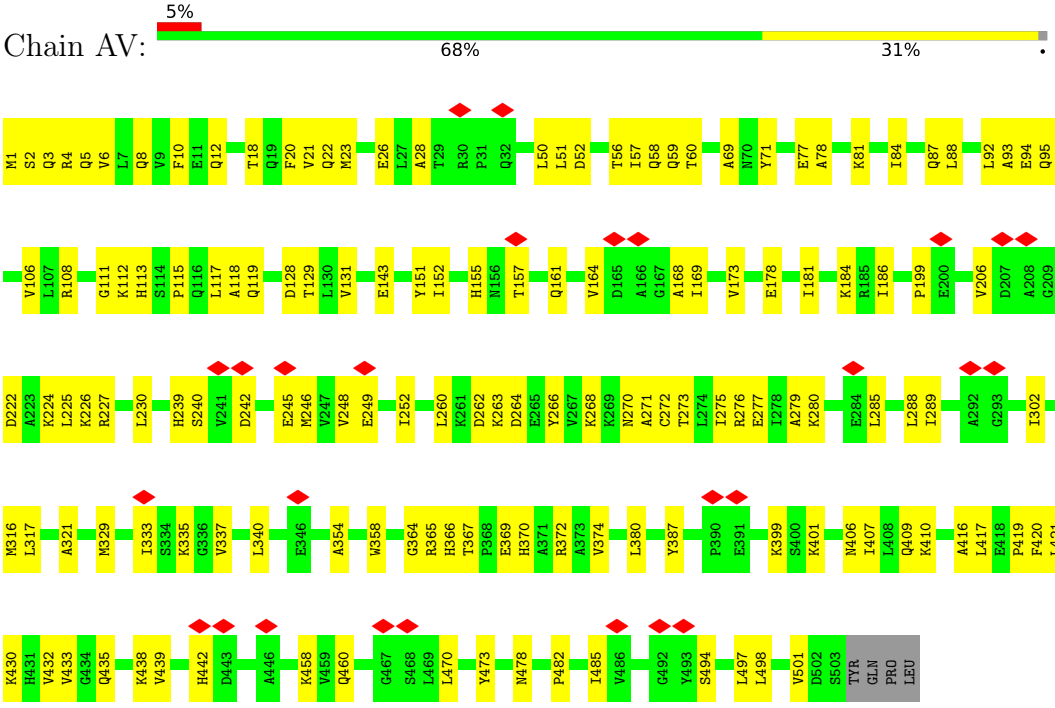

• Molecule 19: Sperm-associated antigen 6

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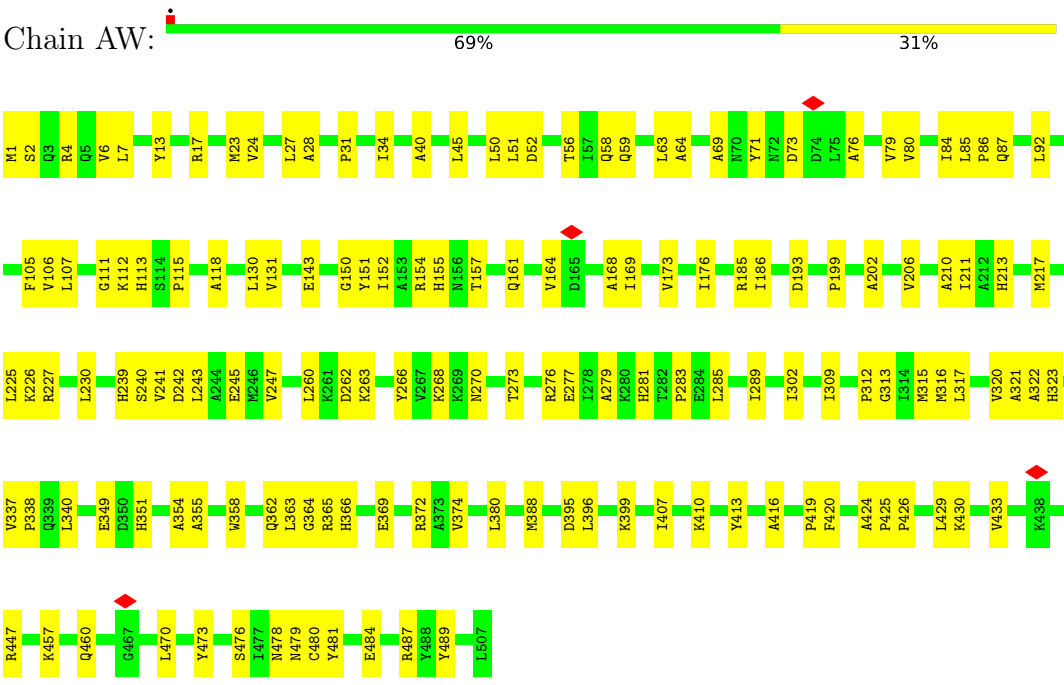

• Molecule 19: Sperm-associated antigen 6

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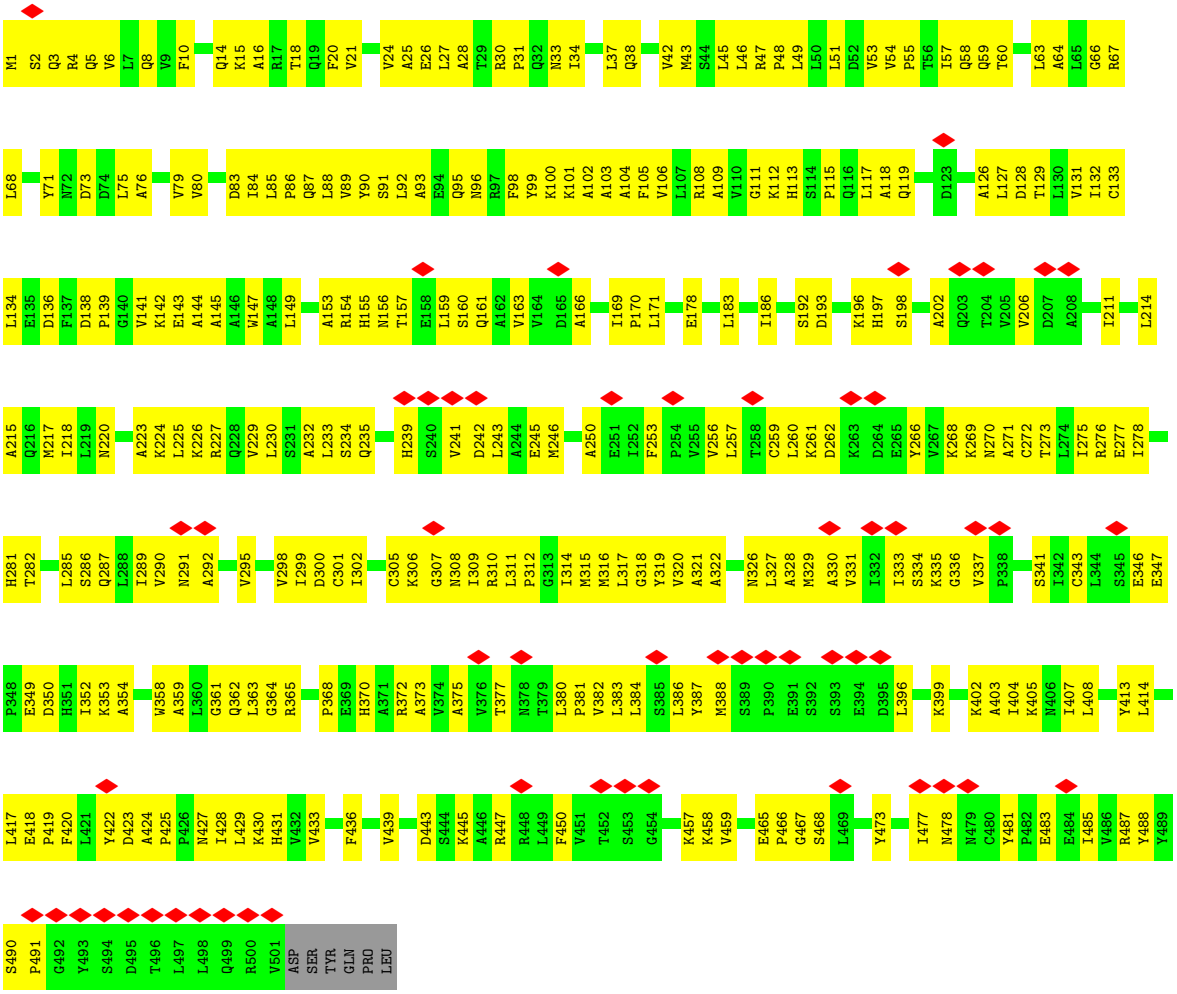
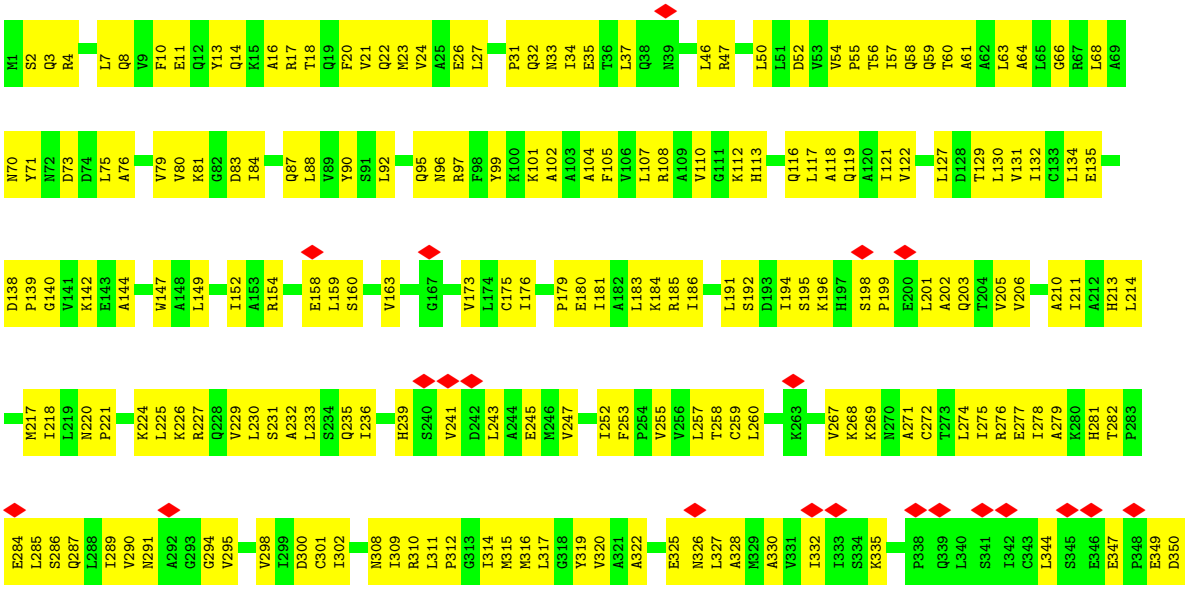
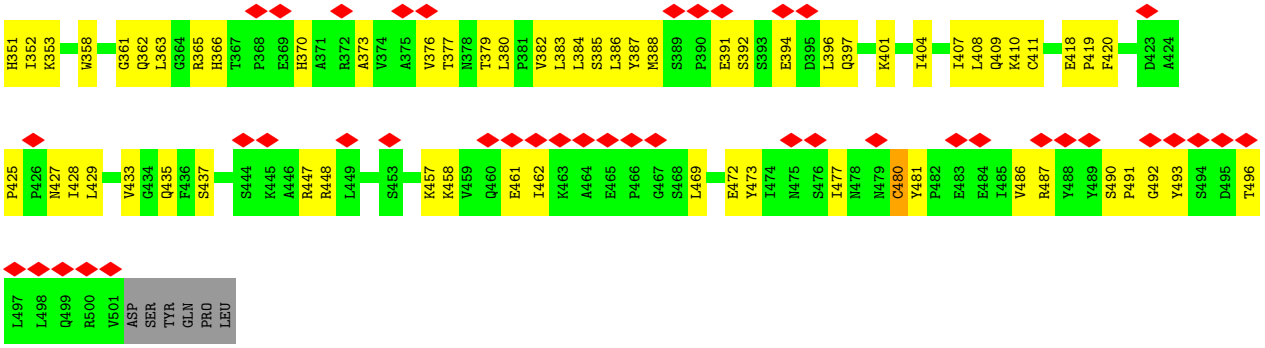


• Molecule 19: Sperm-associated antigen 6

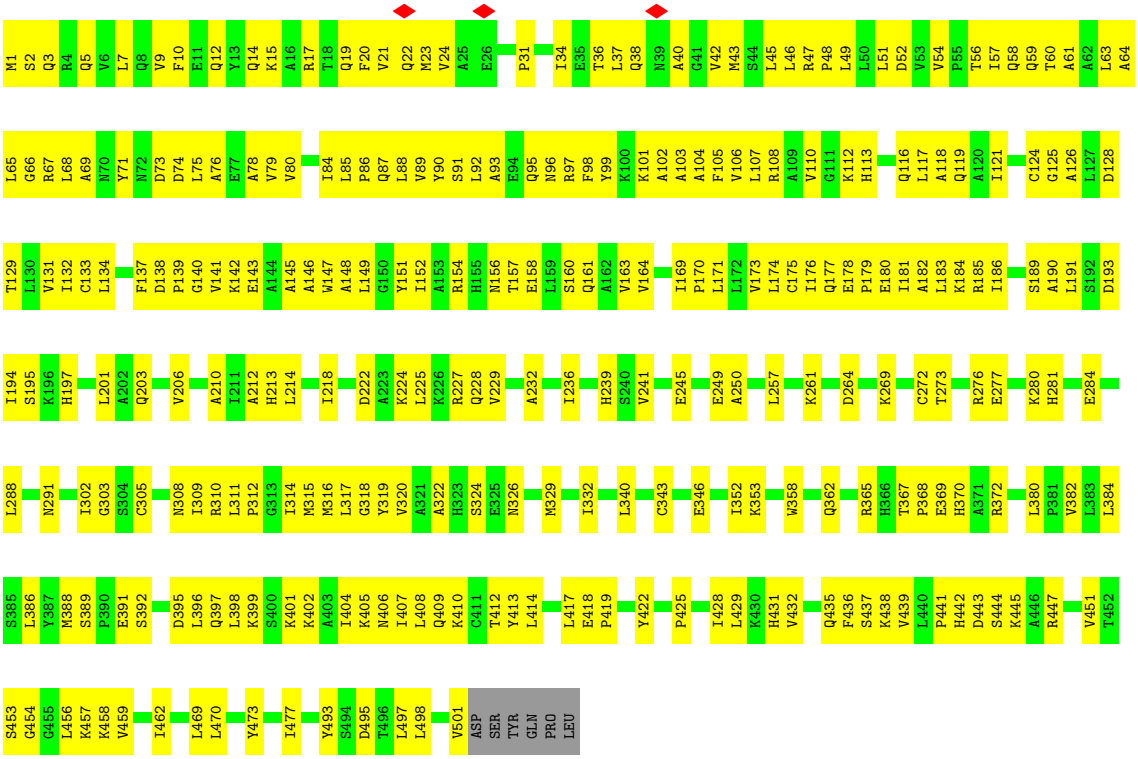
Chain AY:





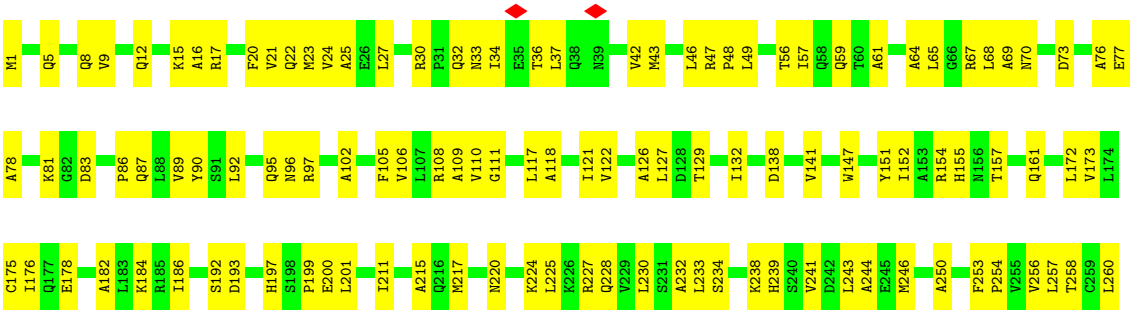
• Molecule 19: Sperm-associated antigen 6

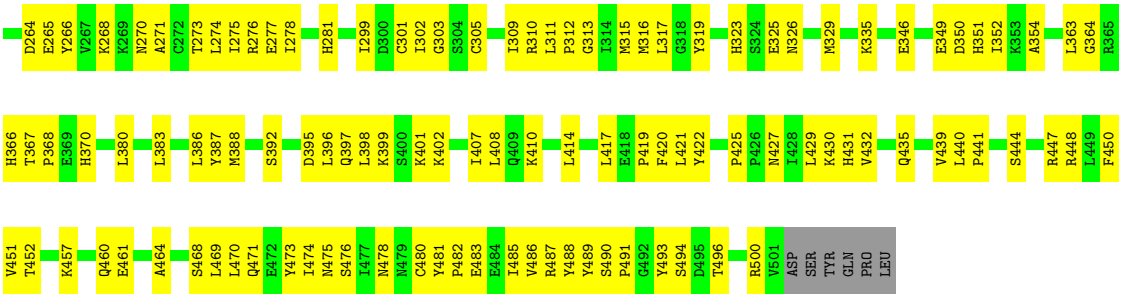
Chain AZ:



• Molecule 19: Sperm-associated antigen 6

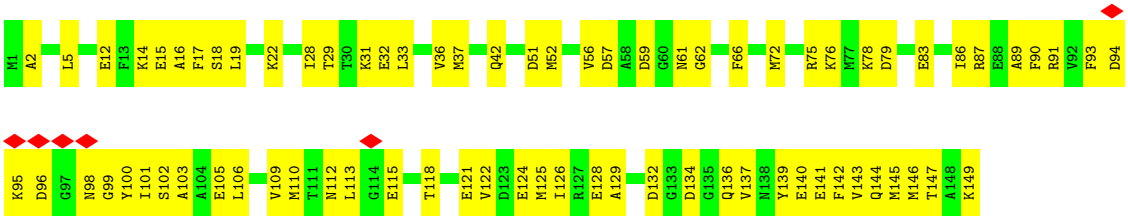
Chain A1:





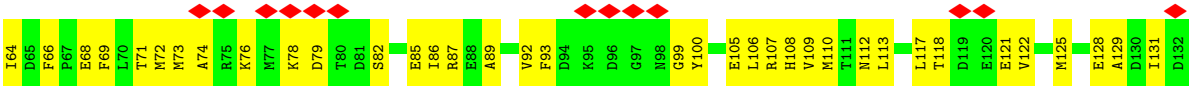
• Molecule 20: Calmodulin-1

Chain 3D:



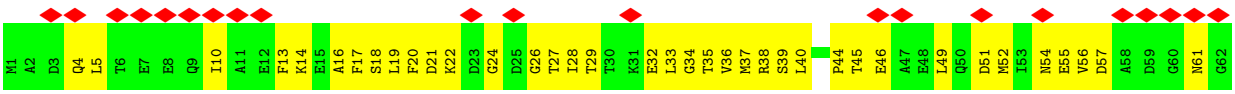
• Molecule 20: Calmodulin-1

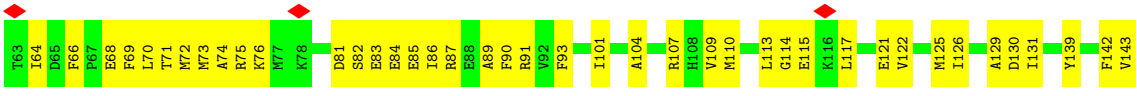
Chain 3E:



• Molecule 20: Calmodulin-1

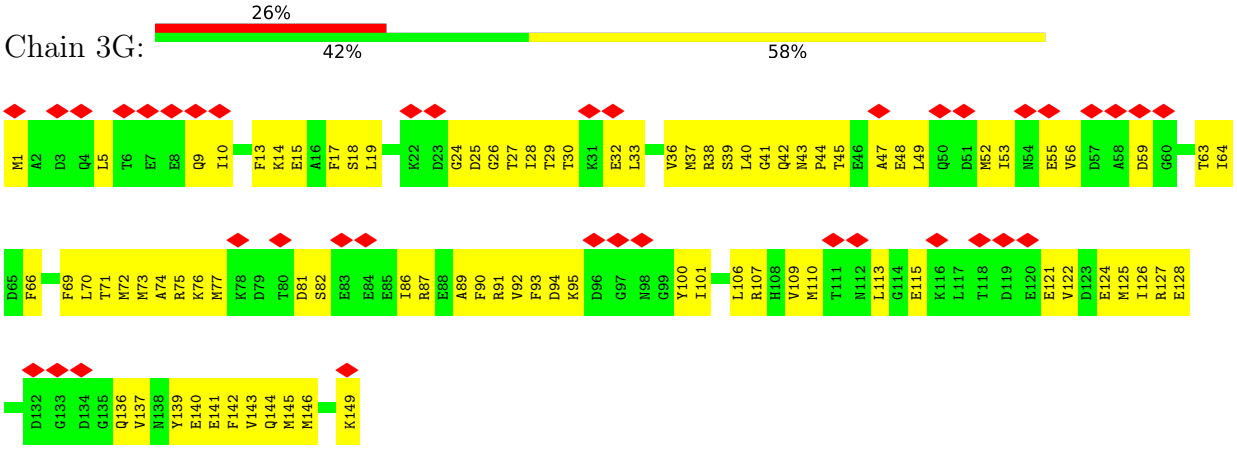
Chain 3F:





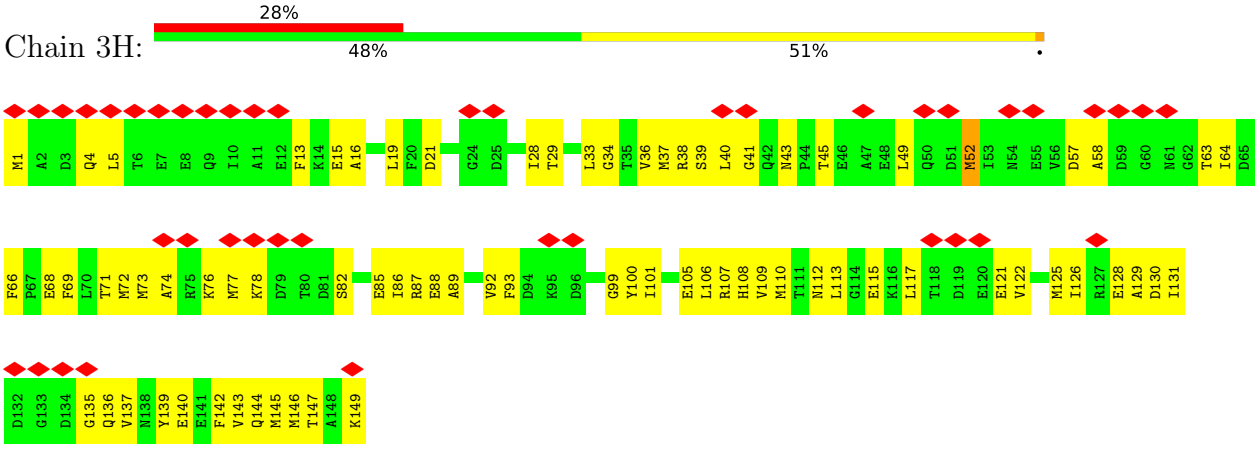
• Molecule 20: Calmodulin-1

Chain 3G:



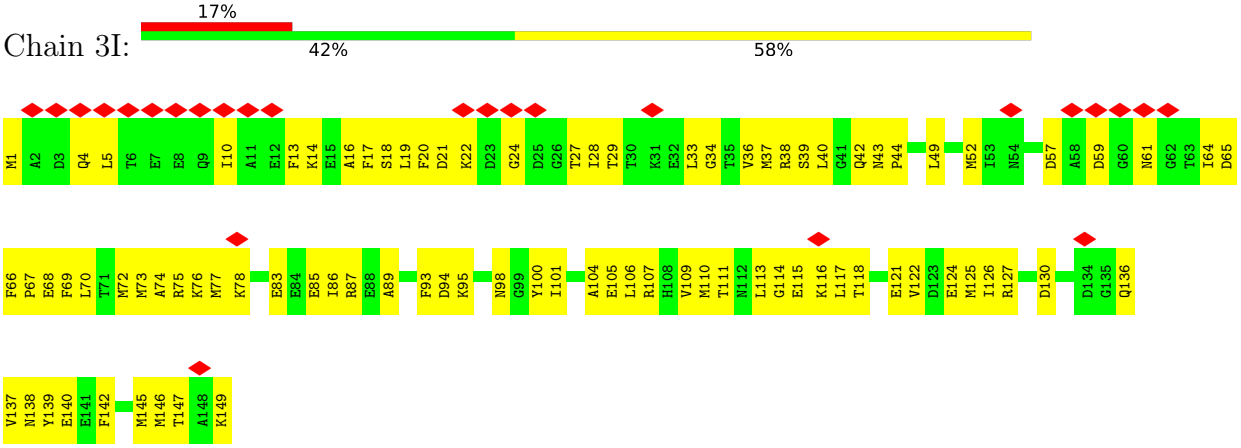
• Molecule 20: Calmodulin-1

Chain 3H:



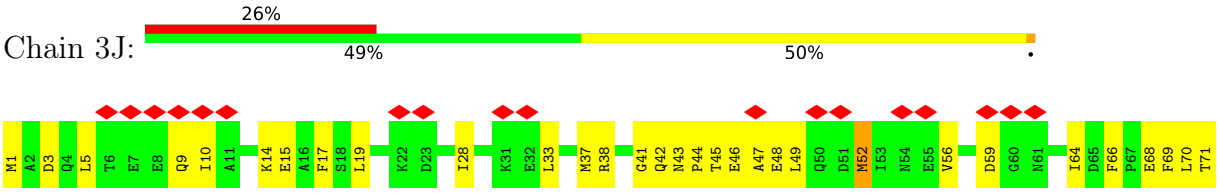
• Molecule 20: Calmodulin-1

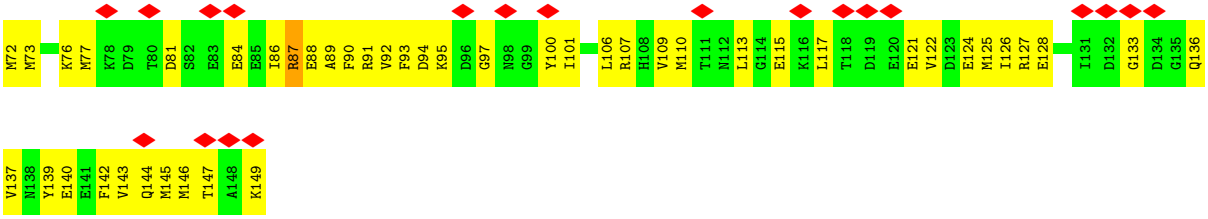
Chain 3I:



• Molecule 20: Calmodulin-1

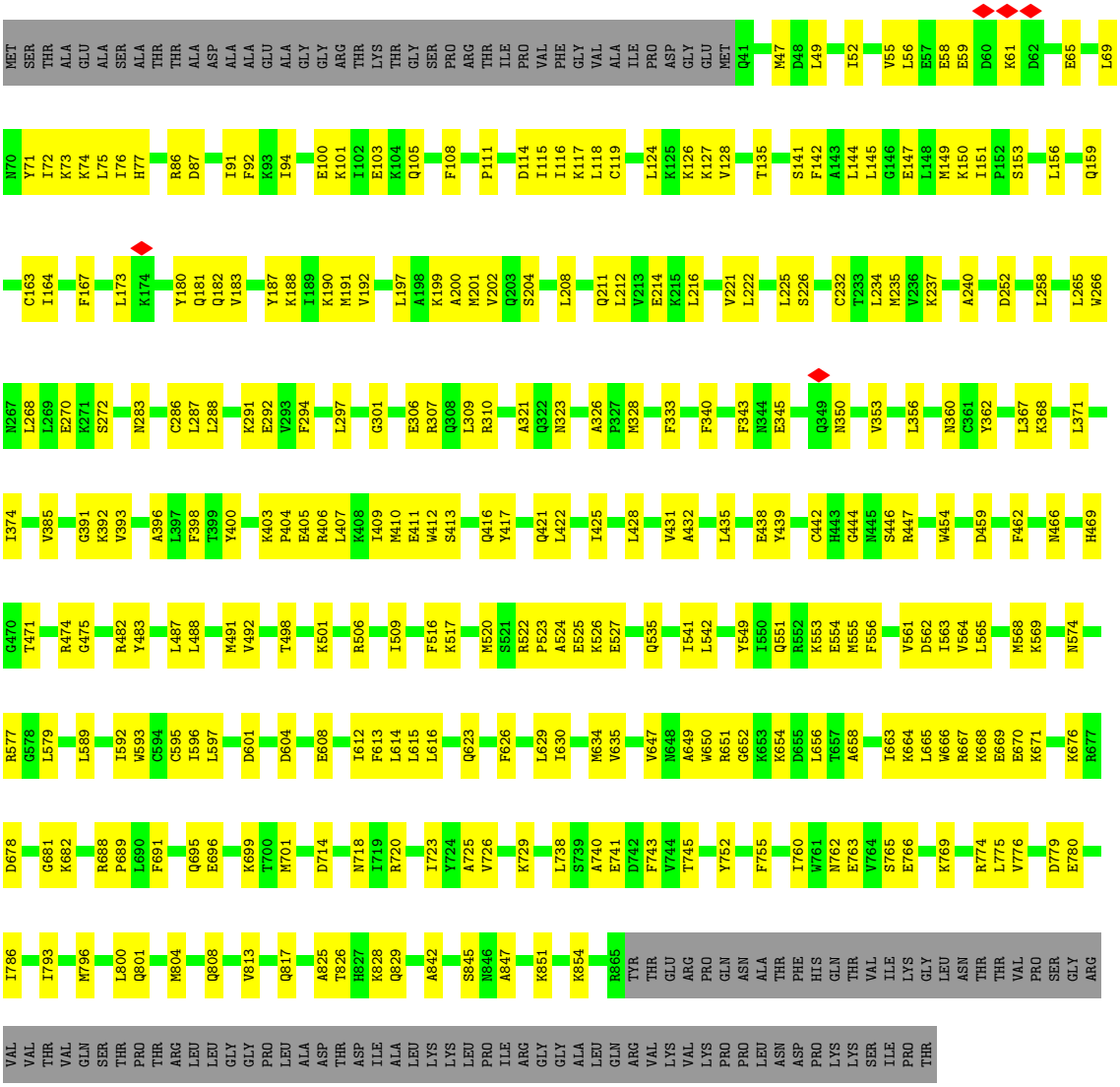
Chain 3J:





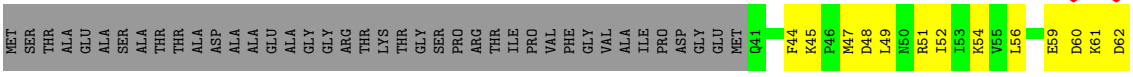
• Molecule 21: Cilia- and flagella-associated protein 69

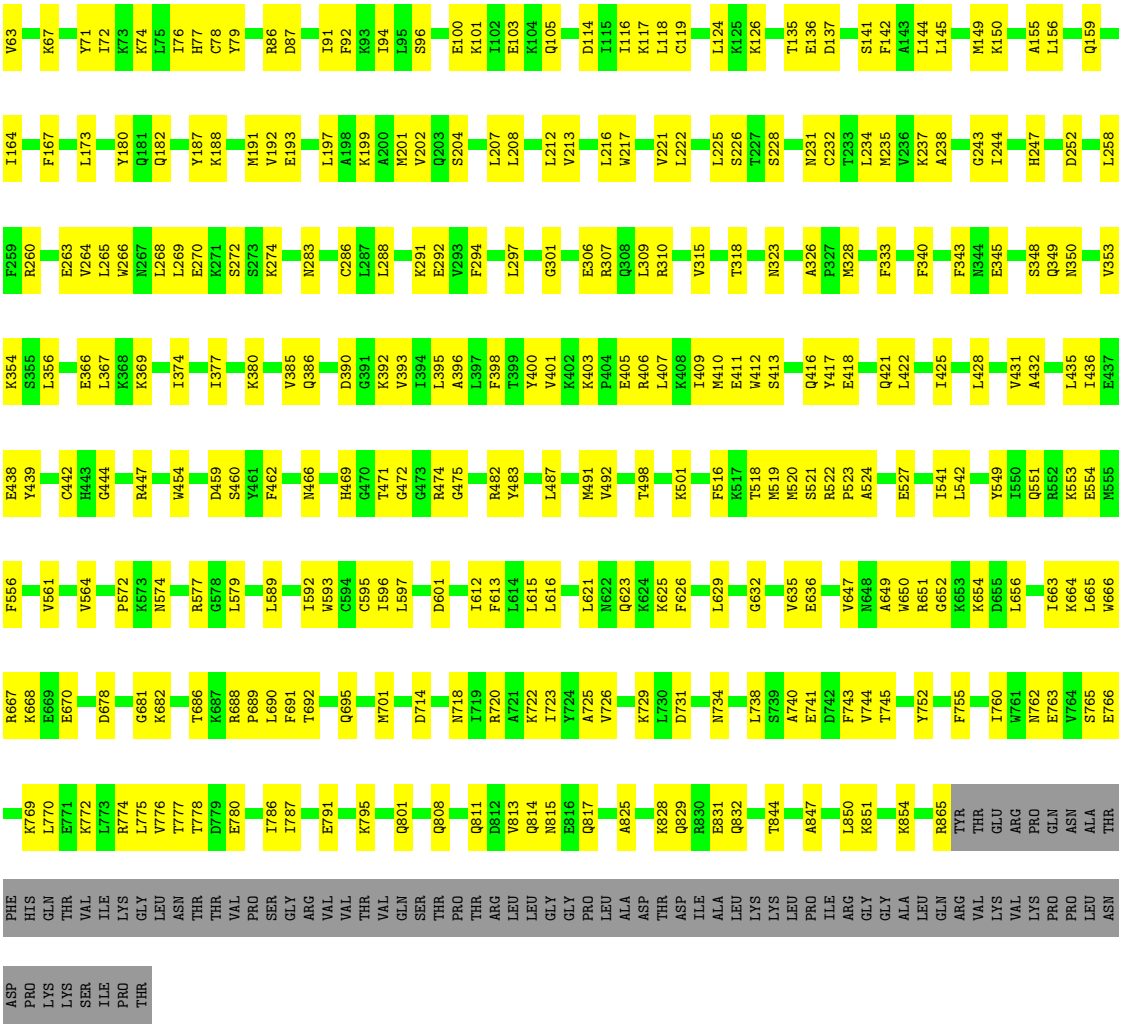
Chain A2:



• Molecule 21: Cilia- and flagella-associated protein 69

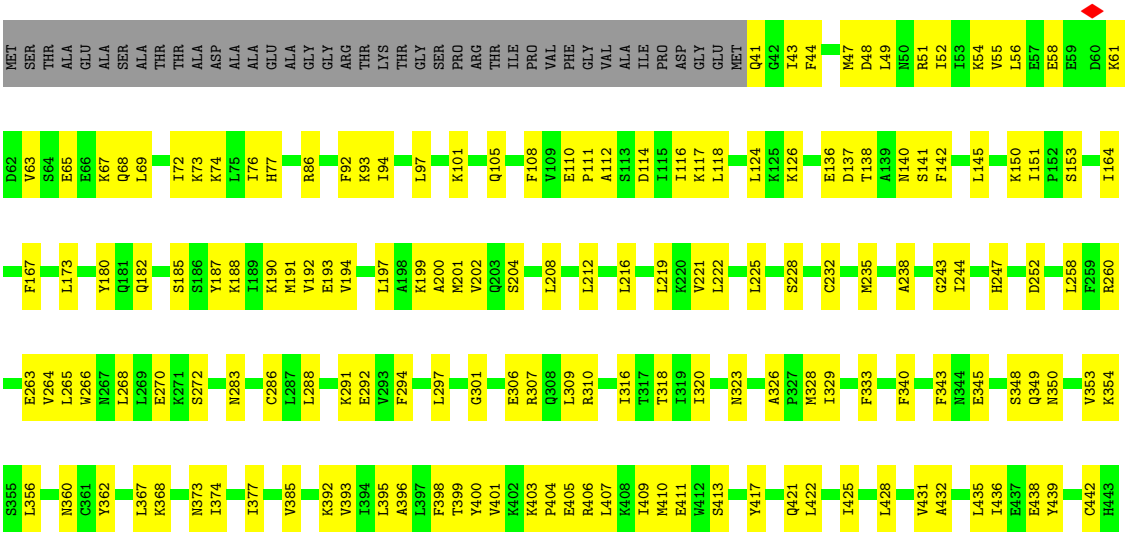
Chain A3:

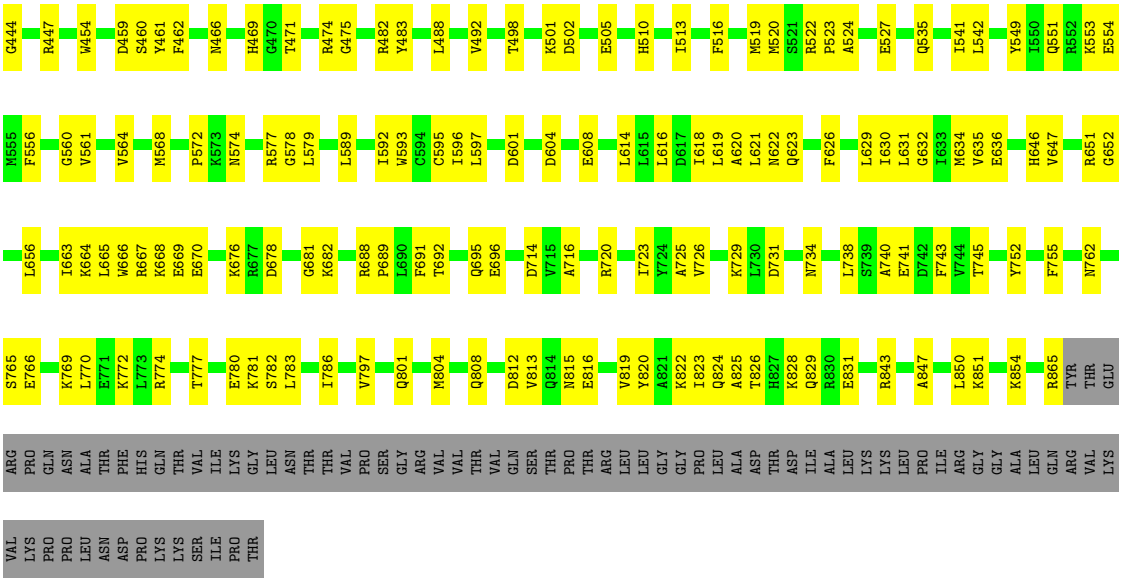




• Molecule 21: Cilia- and flagella-associated protein 69

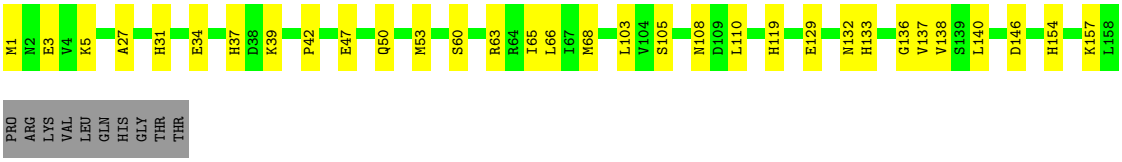
Chain A4:





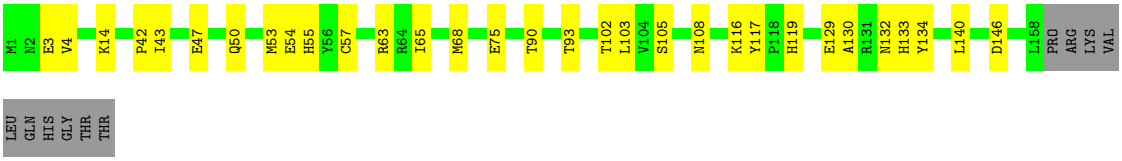
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1A:



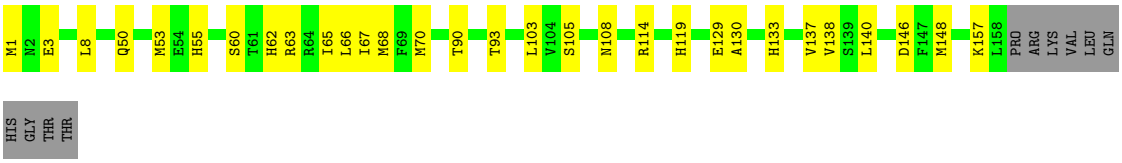
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1B:



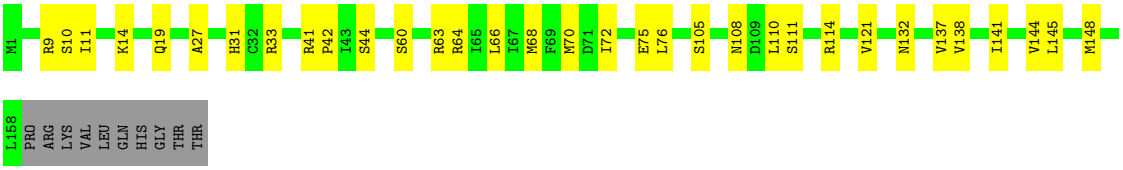
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1C:



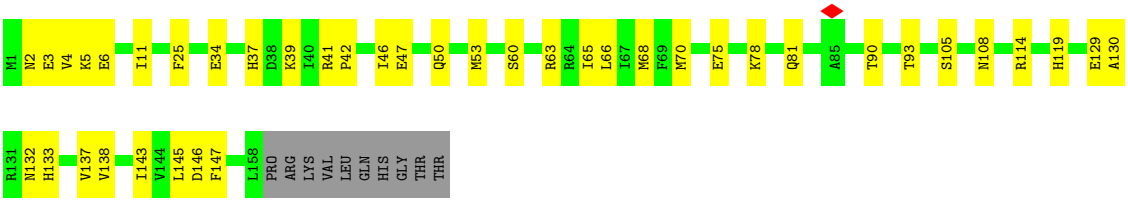
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1D:



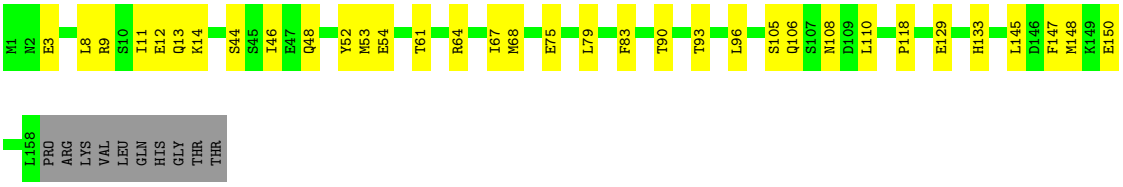
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1G:



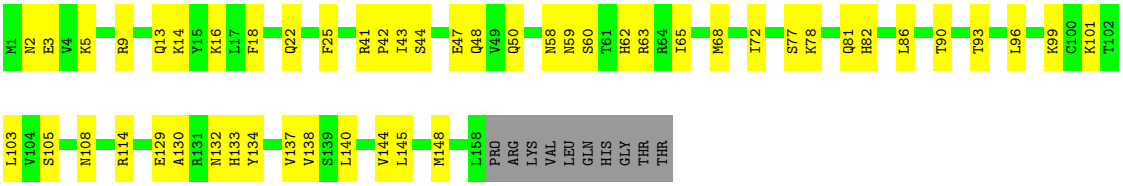
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1I:



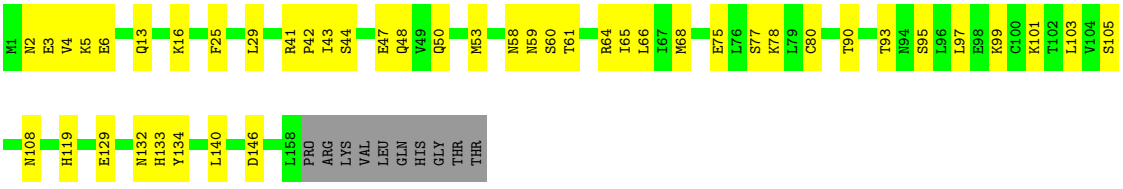
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1E:



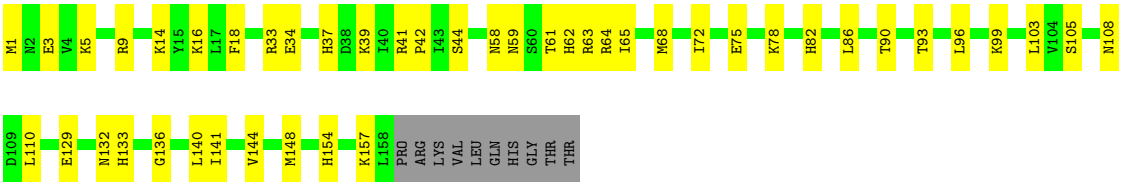
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1F:



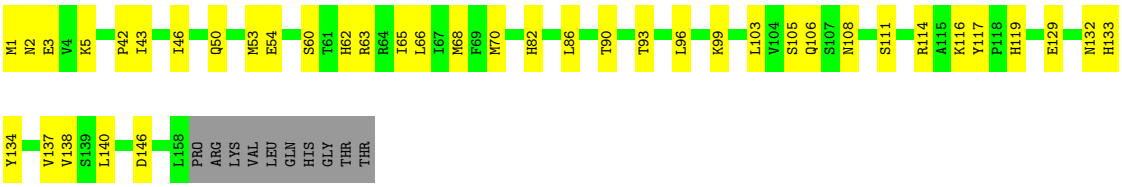
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1J:



• Molecule 22: Sperm acrosome-associated protein 9

Chain 1K:

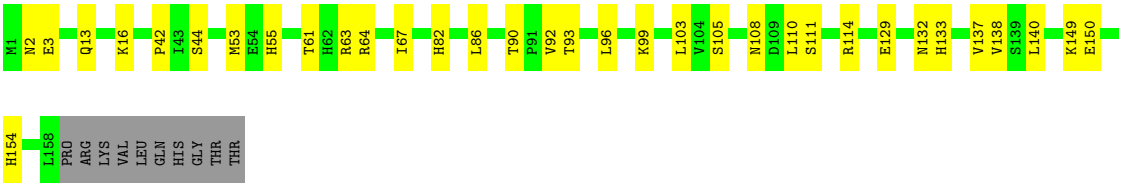


• Molecule 22: Sperm acrosome-associated protein 9

Chain 1L:

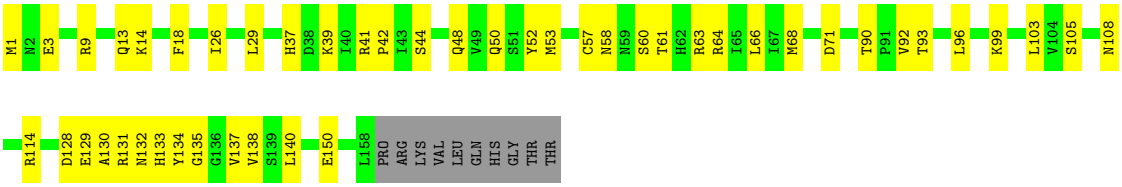
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1M:



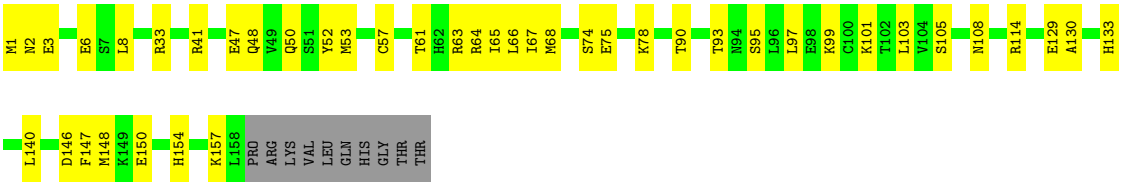
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1N:



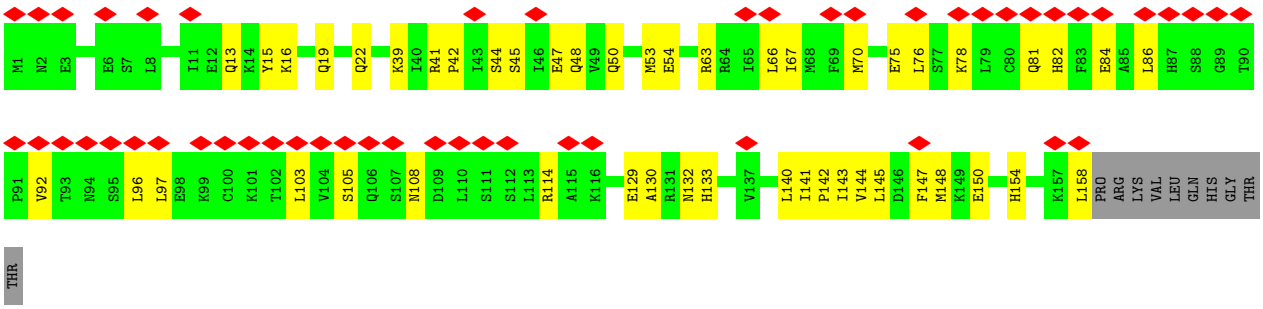
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1O:



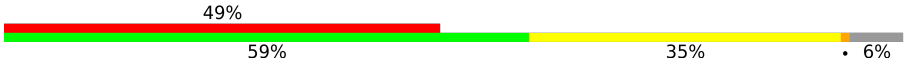
• Molecule 22: Sperm acrosome-associated protein 9

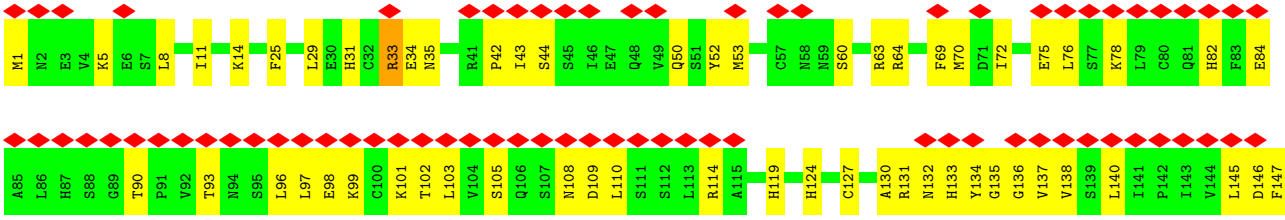
Chain 1P:



• Molecule 22: Sperm acrosome-associated protein 9

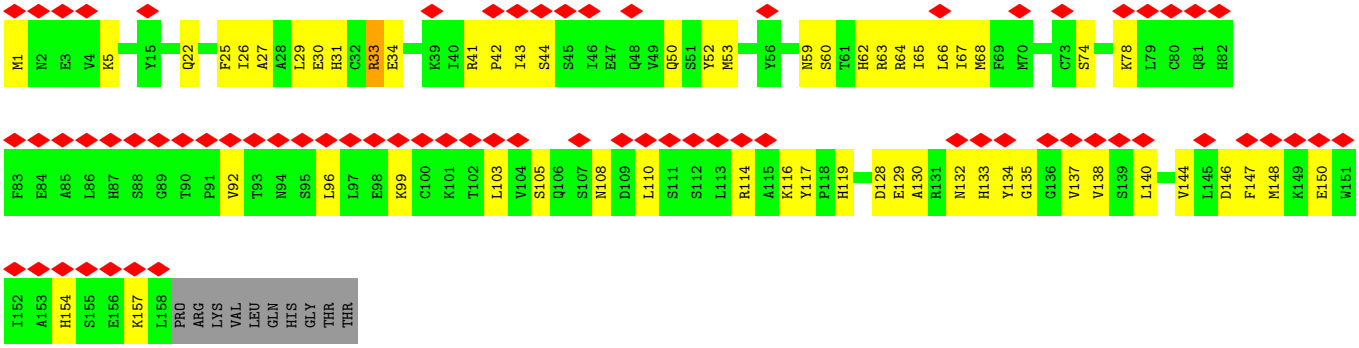
Chain 1Q:





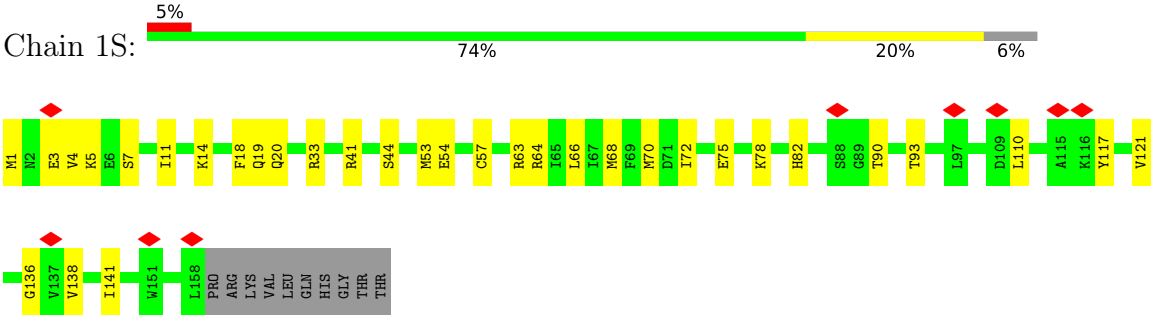
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1R:



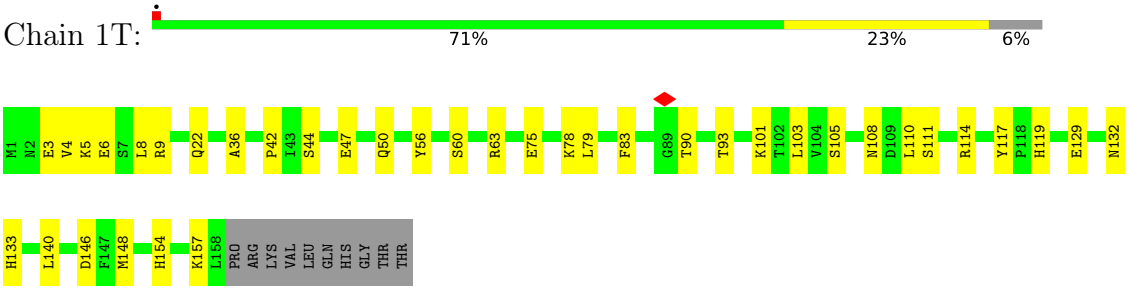
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1S:



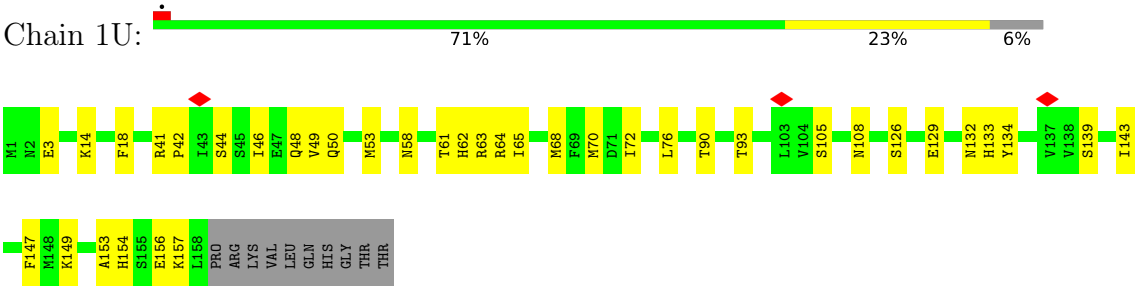
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1T:



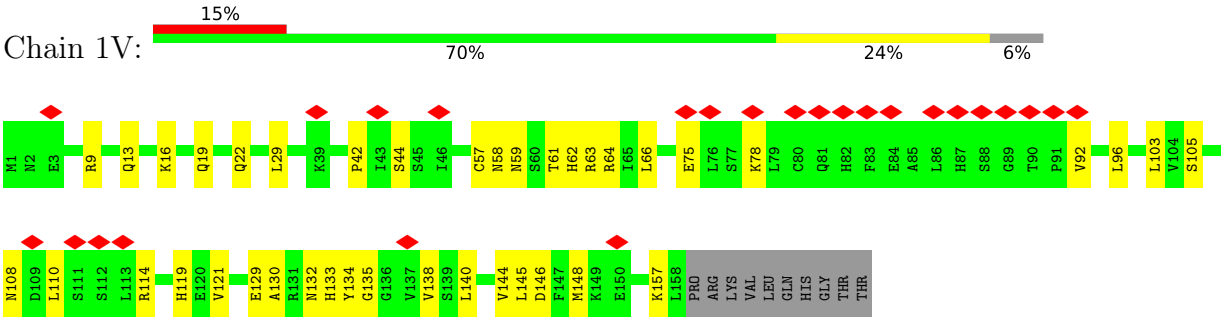
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1U:



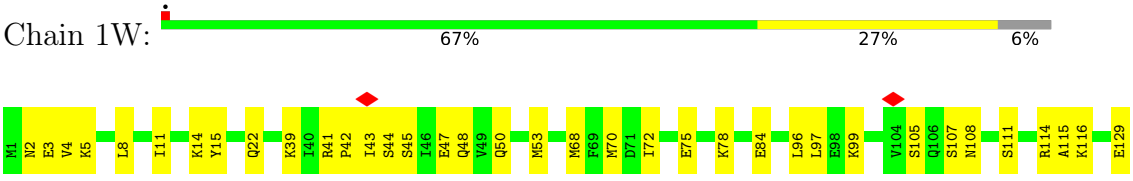
• Molecule 22: Sperm acrosome-associated protein 9

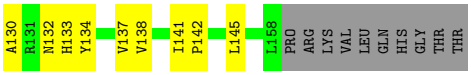
Chain 1V:



• Molecule 22: Sperm acrosome-associated protein 9

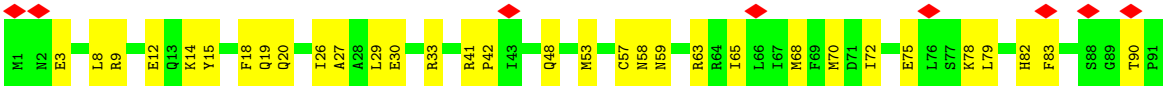
Chain 1W:

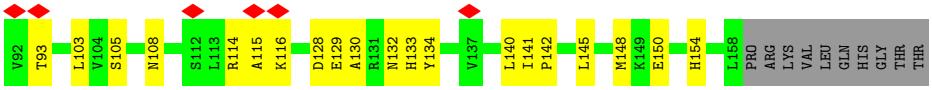




• Molecule 22: Sperm acrosome-associated protein 9

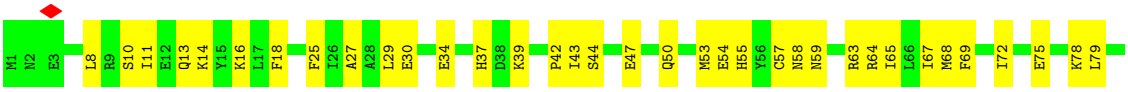
Chain 1X:

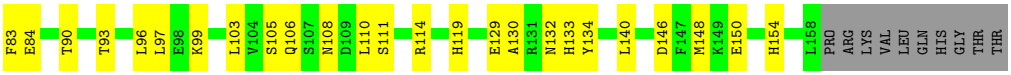




• Molecule 22: Sperm acrosome-associated protein 9

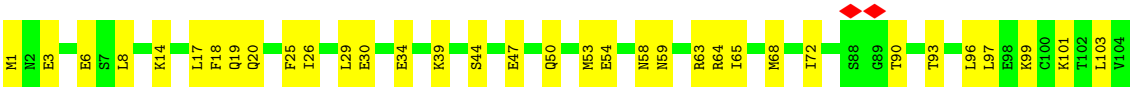
Chain 1Y:





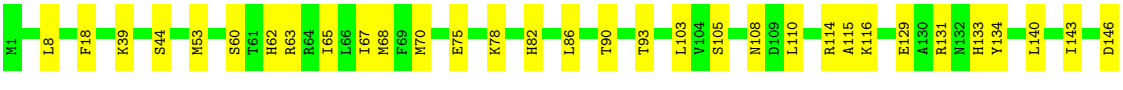
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1Z:



• Molecule 22: Sperm acrosome-associated protein 9

Chain 1a:

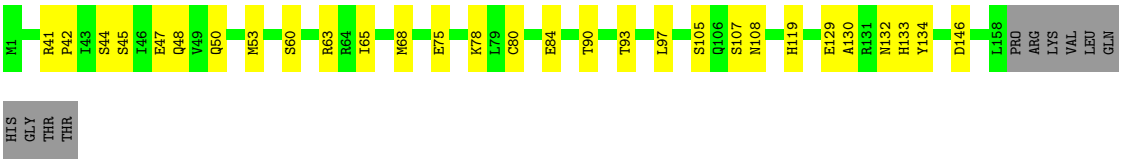


• Molecule 22: Sperm acrosome-associated protein 9

Chain 1b:

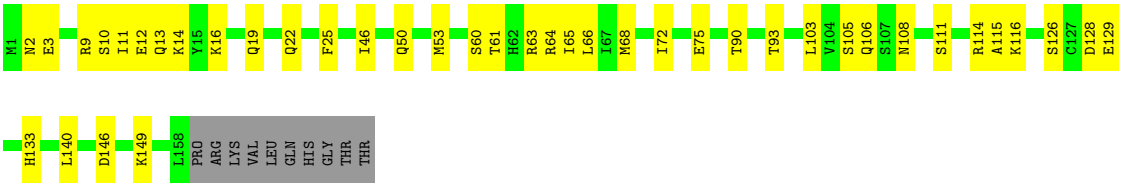
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1c:



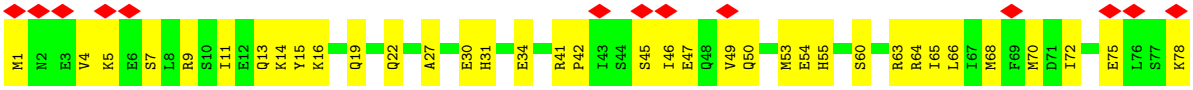
• Molecule 22: Sperm acrosome-associated protein 9

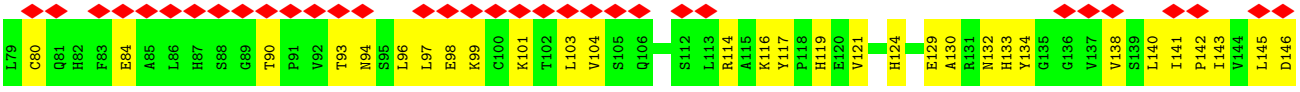
Chain 1d:

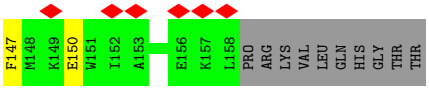


• Molecule 22: Sperm acrosome-associated protein 9

Chain 2A:

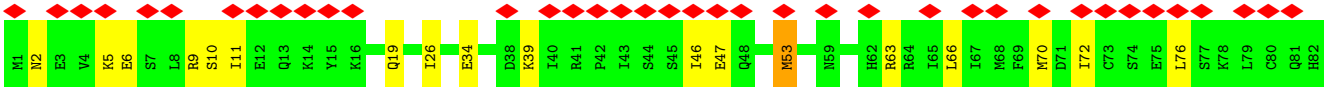


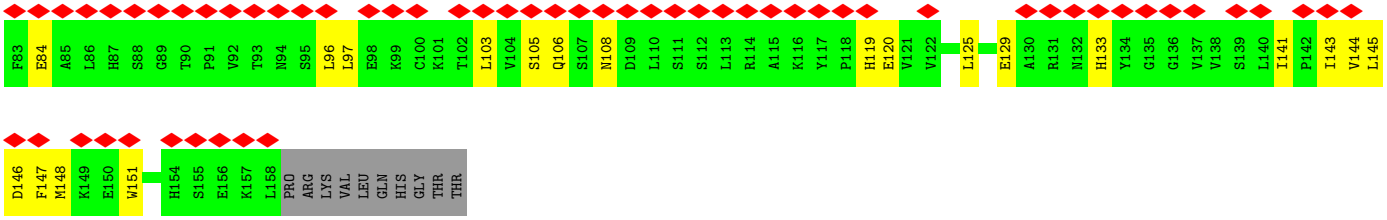




• Molecule 22: Sperm acrosome-associated protein 9

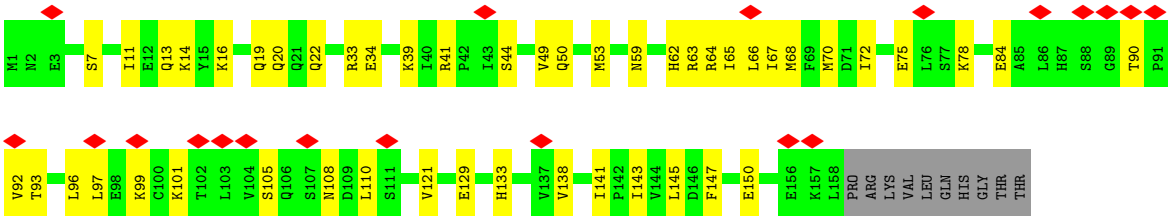
Chain 2D:





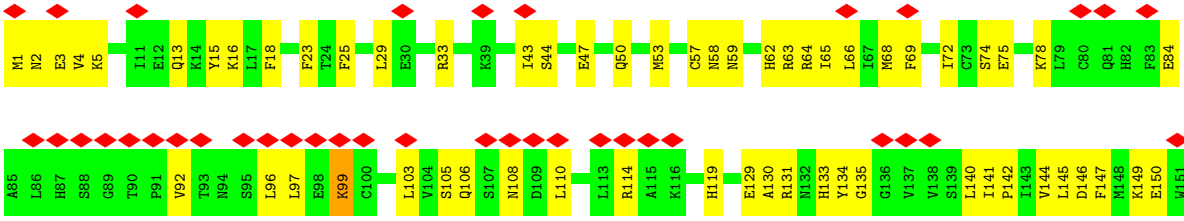
• Molecule 22: Sperm acrosome-associated protein 9

Chain 2B:



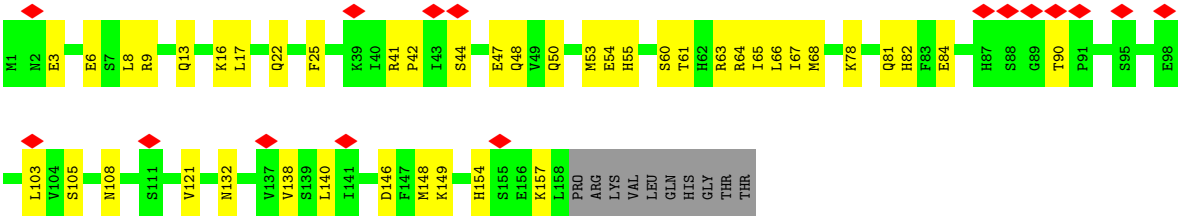
• Molecule 22: Sperm acrosome-associated protein 9

Chain 2C:



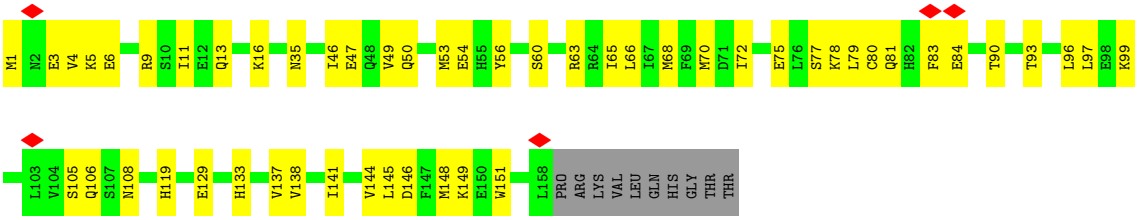
• Molecule 22: Sperm acrosome-associated protein 9

Chain 2F:



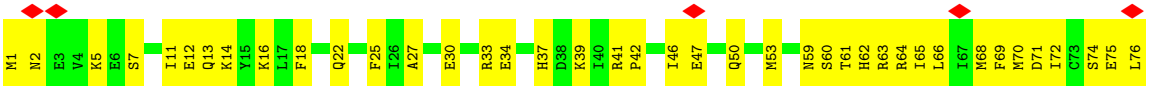
• Molecule 22: Sperm acrosome-associated protein 9

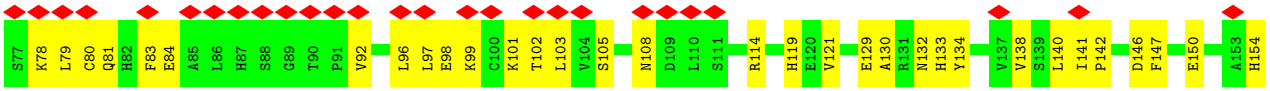
Chain 2E:

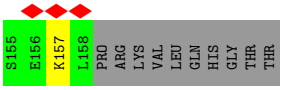


• Molecule 22: Sperm acrosome-associated protein 9

Chain 2G:

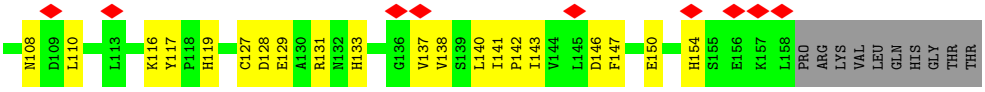






• Molecule 22: Sperm acrosome-associated protein 9

Chain 2H:

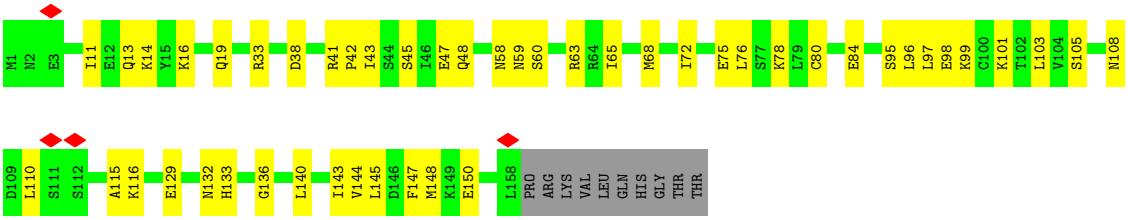


• Molecule 22: Sperm acrosome-associated protein 9

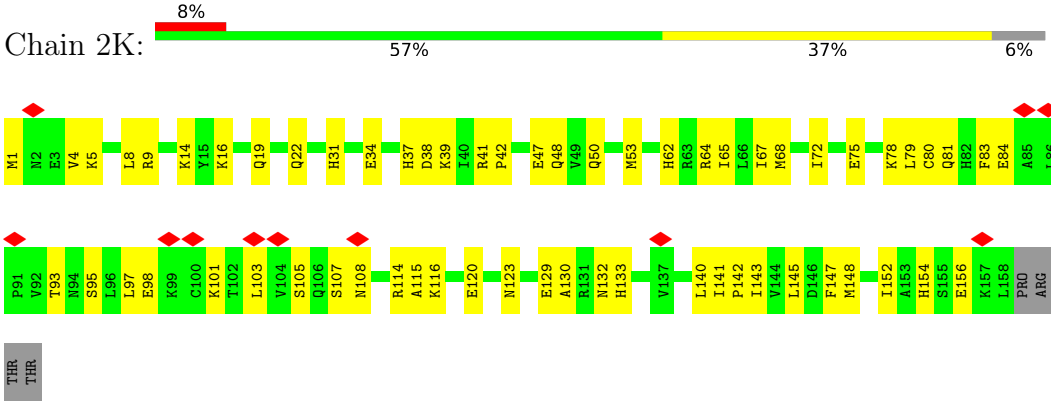
Chain 2I:

• Molecule 22: Sperm acrosome-associated protein 9

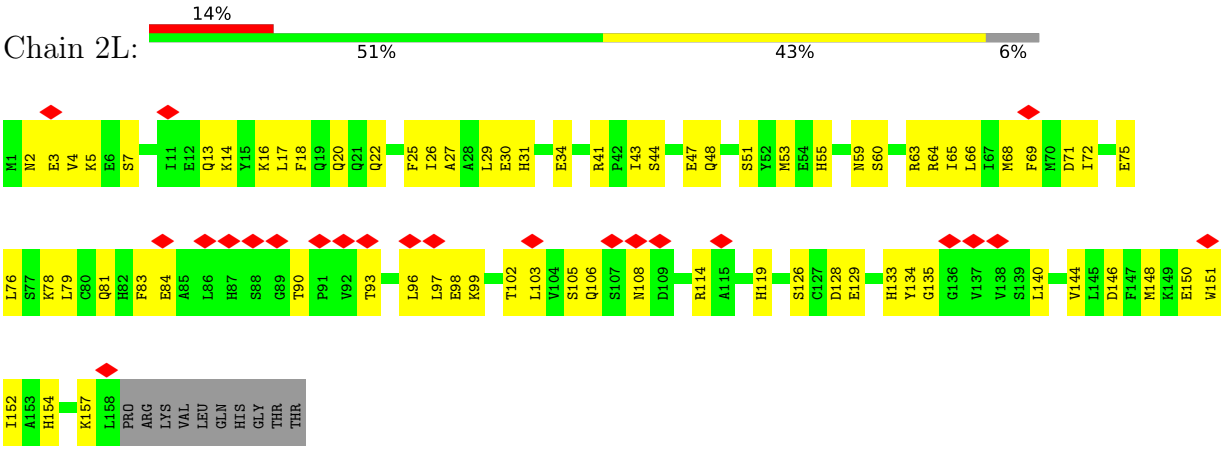
Chain 2J:



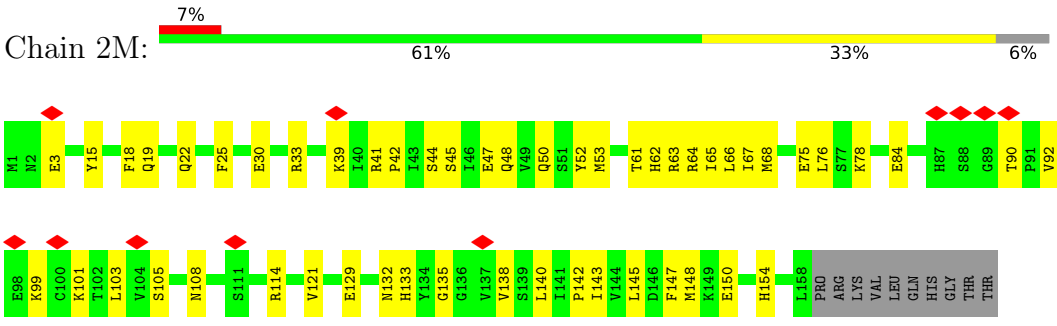
• Molecule 22: Sperm acrosome-associated protein 9



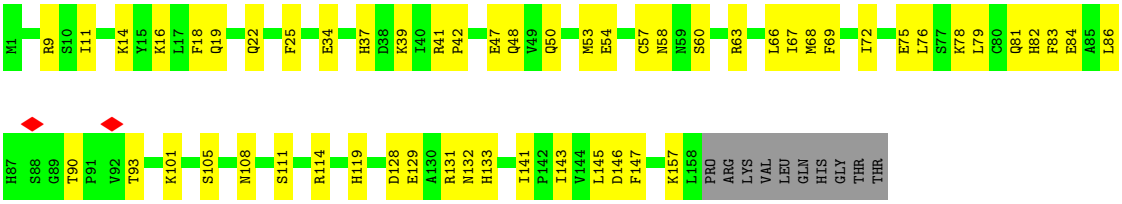
• Molecule 22: Sperm acrosome-associated protein 9



• Molecule 22: Sperm acrosome-associated protein 9

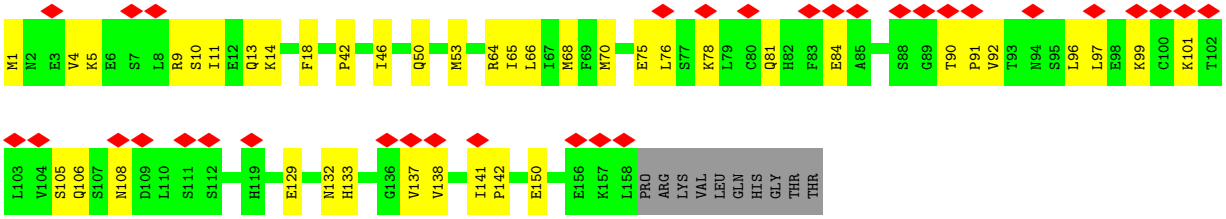


• Molecule 22: Sperm acrosome-associated protein 9



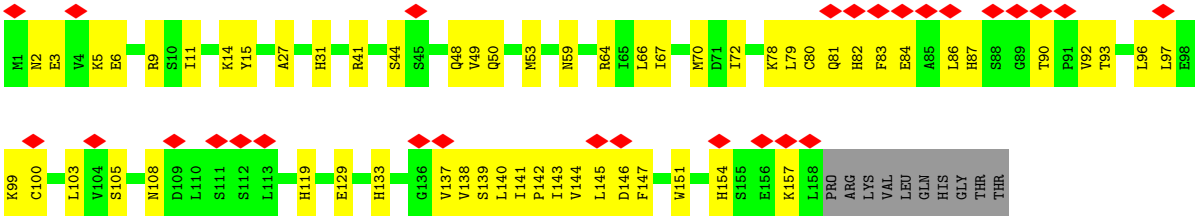
• Molecule 22: Sperm acrosome-associated protein 9

Chain 2O:



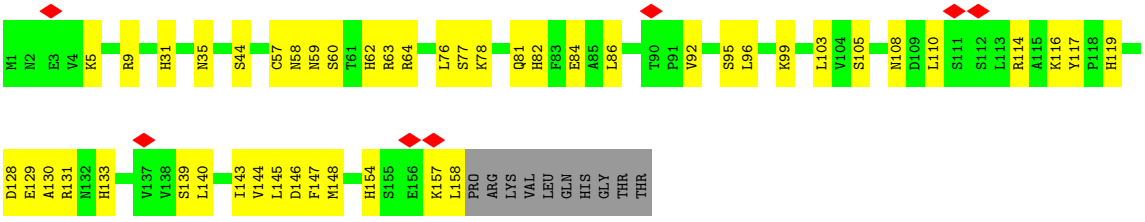
• Molecule 22: Sperm acrosome-associated protein 9

Chain 2P:



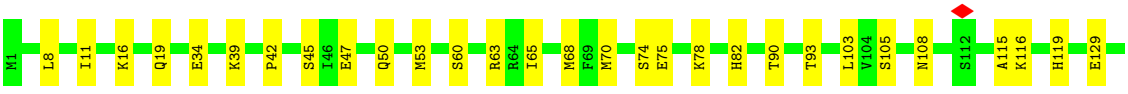
• Molecule 22: Sperm acrosome-associated protein 9

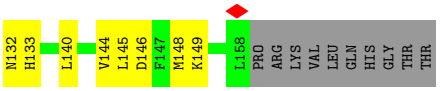
Chain 2Q:



• Molecule 22: Sperm acrosome-associated protein 9

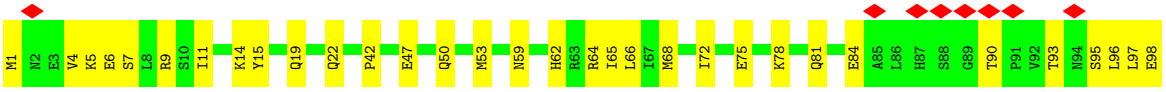
Chain 2R:

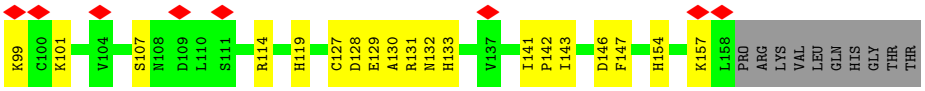




• Molecule 22: Sperm acrosome-associated protein 9

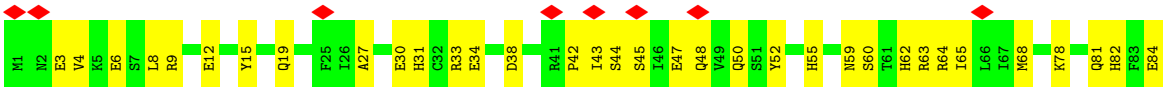
Chain 2S:

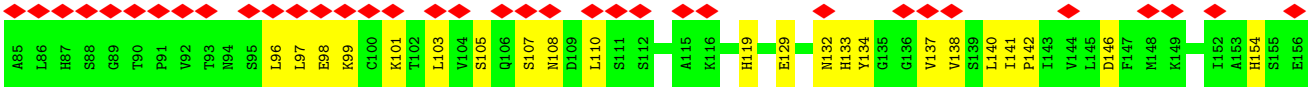


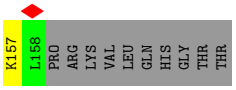


• Molecule 22: Sperm acrosome-associated protein 9

Chain 2T:

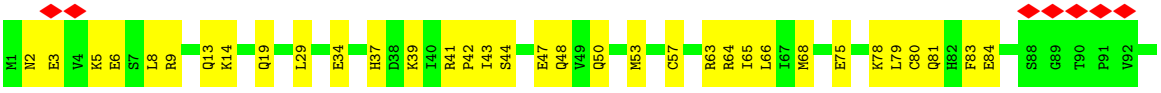


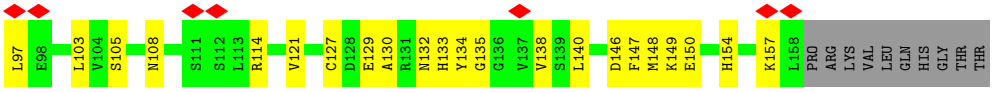




• Molecule 22: Sperm acrosome-associated protein 9

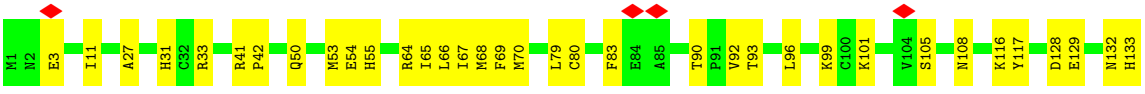
Chain 2U:

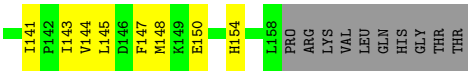




• Molecule 22: Sperm acrosome-associated protein 9

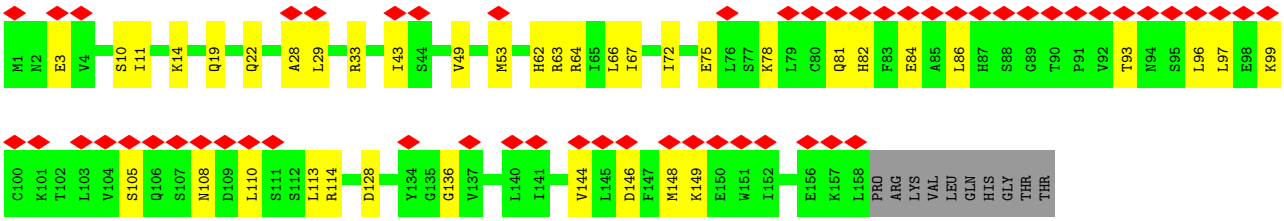
Chain 2V:





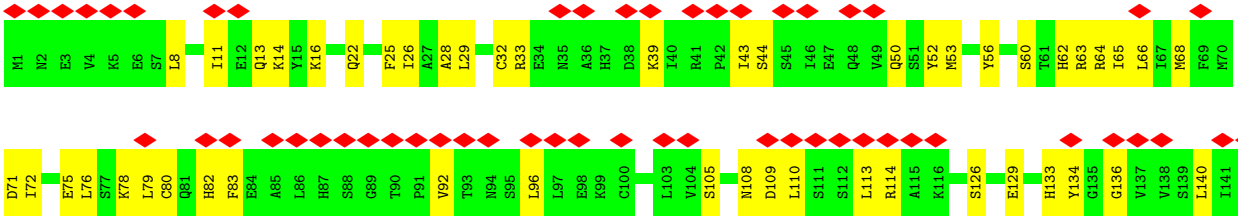
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1e:



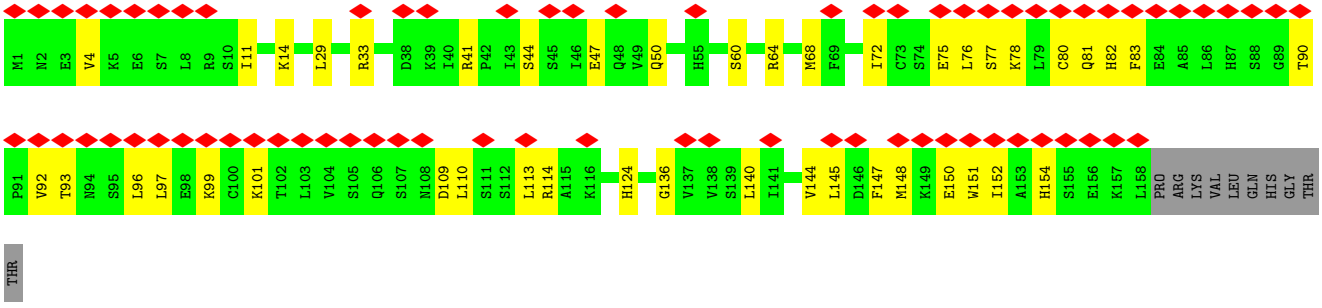
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1f:



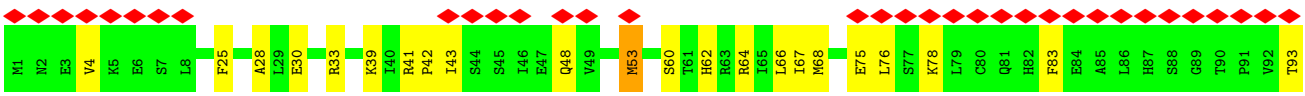
• Molecule 22: Sperm acrosome-associated protein 9

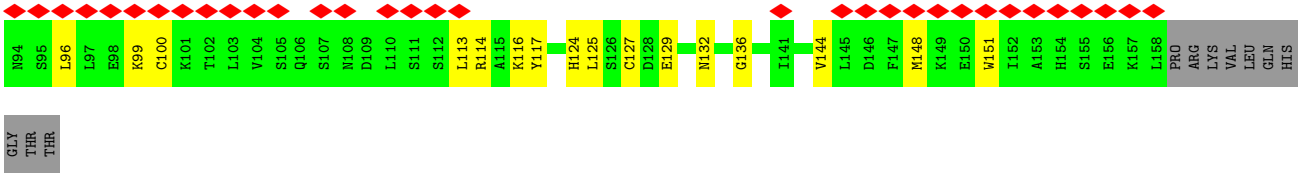
Chain 1g:



• Molecule 22: Sperm acrosome-associated protein 9

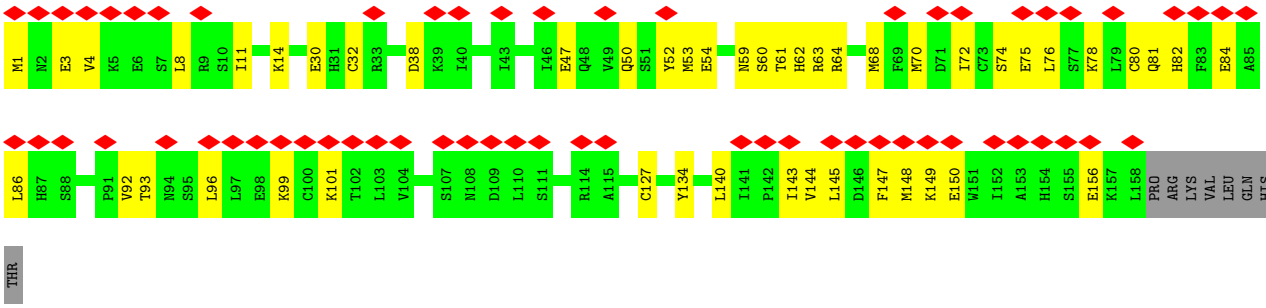
Chain 1h:





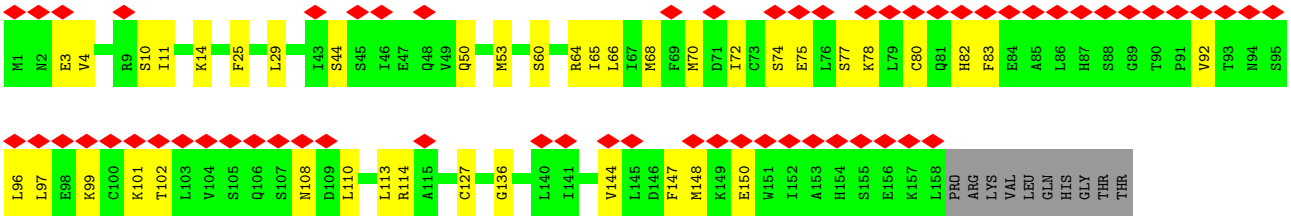
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1i:



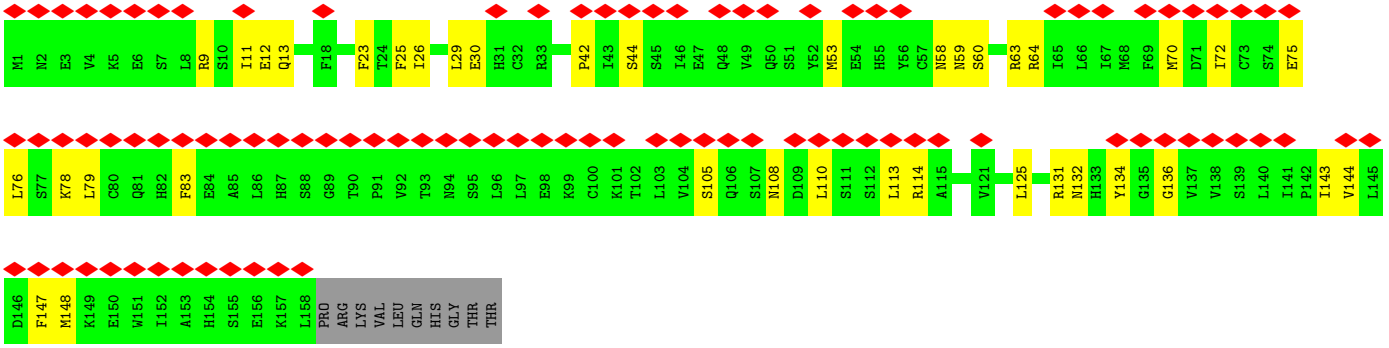
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1j:



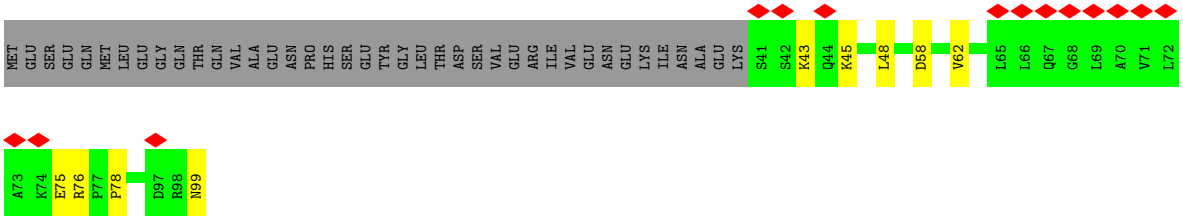
• Molecule 22: Sperm acrosome-associated protein 9

Chain 1k:

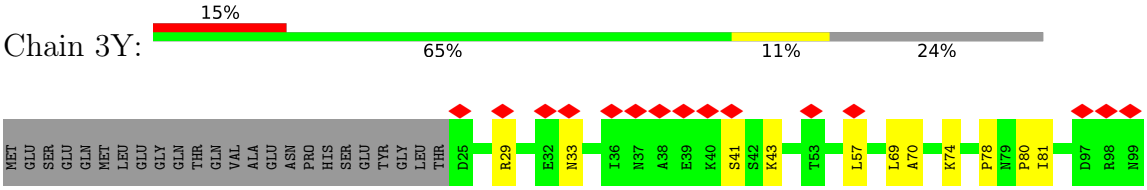


• Molecule 23: Protein dpy-30 homolog

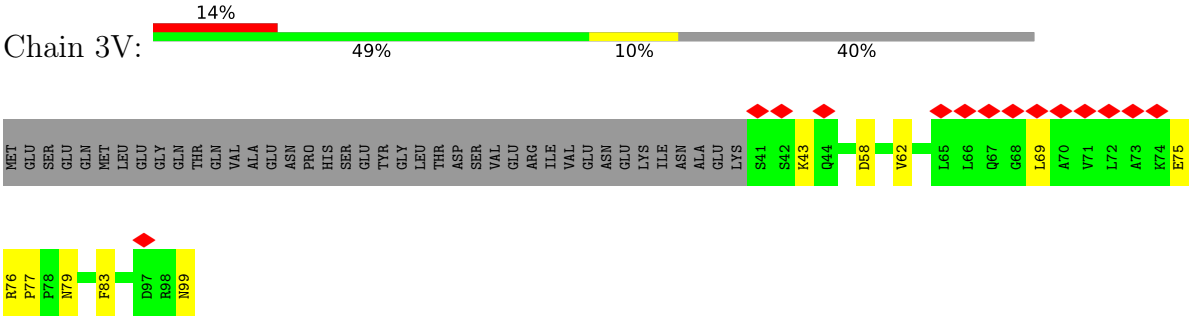
Chain 3X:



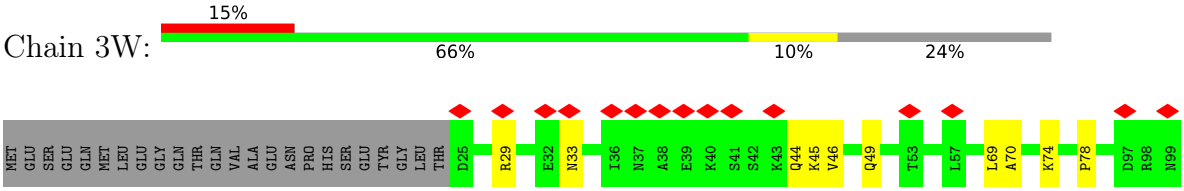
• Molecule 23: Protein dpy-30 homolog



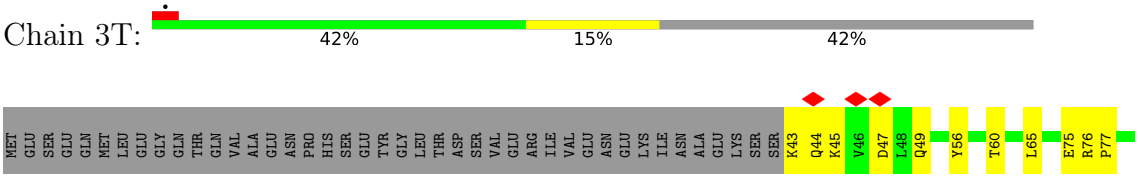
• Molecule 23: Protein dpy-30 homolog



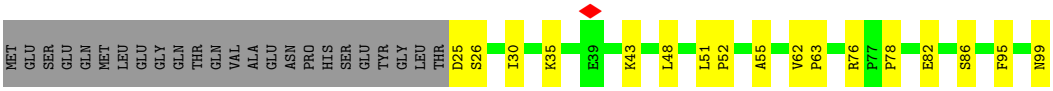
• Molecule 23: Protein dpy-30 homolog



• Molecule 23: Protein dpy-30 homolog

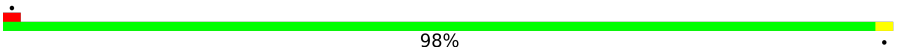


• Molecule 23: Protein dpy-30 homolog



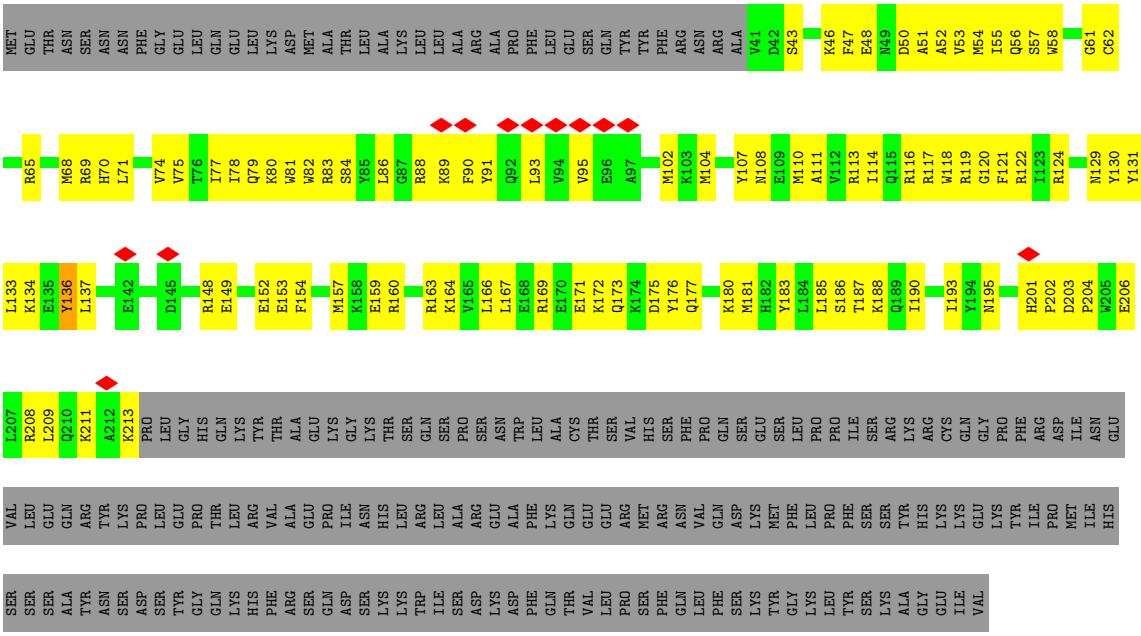
• Molecule 24: Unknown1

Chain 3A:



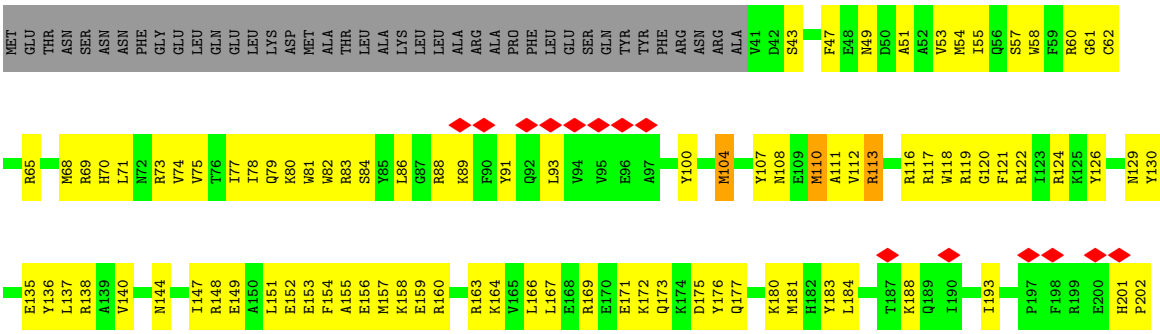
• Molecule 25: Spermatogenesis-associated protein 17

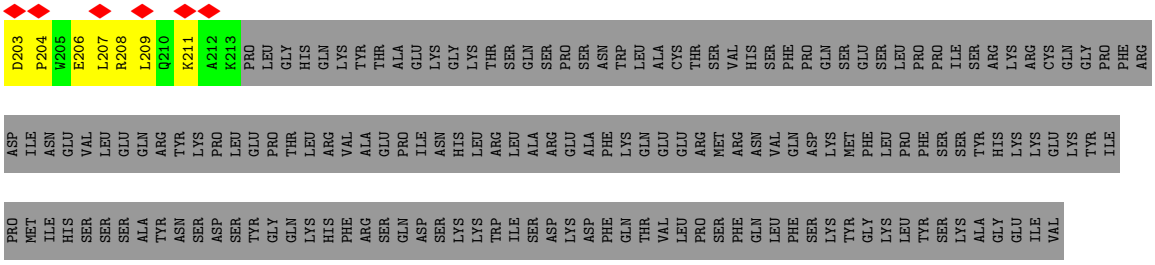
Chain 3B:



• Molecule 25: Spermatogenesis-associated protein 17

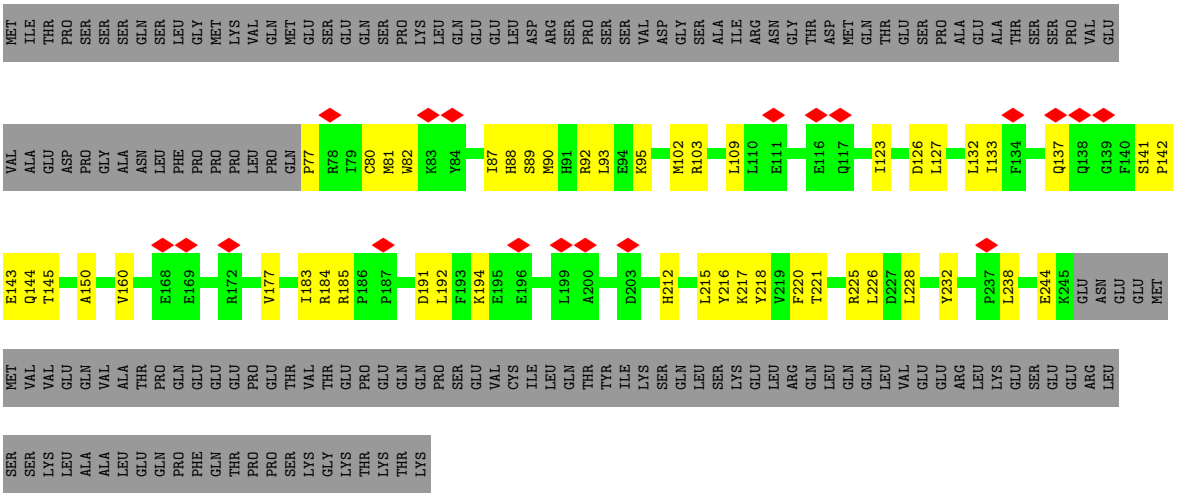
Chain 3C:





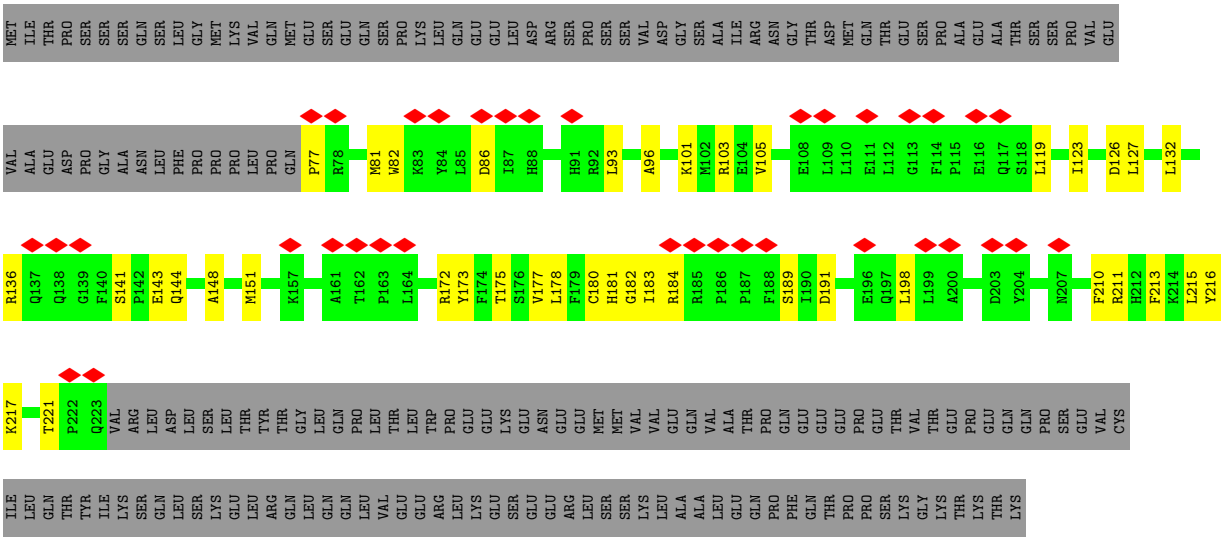
• Molecule 26: Cilia- and flagella-associated protein 119

Chain 3K:



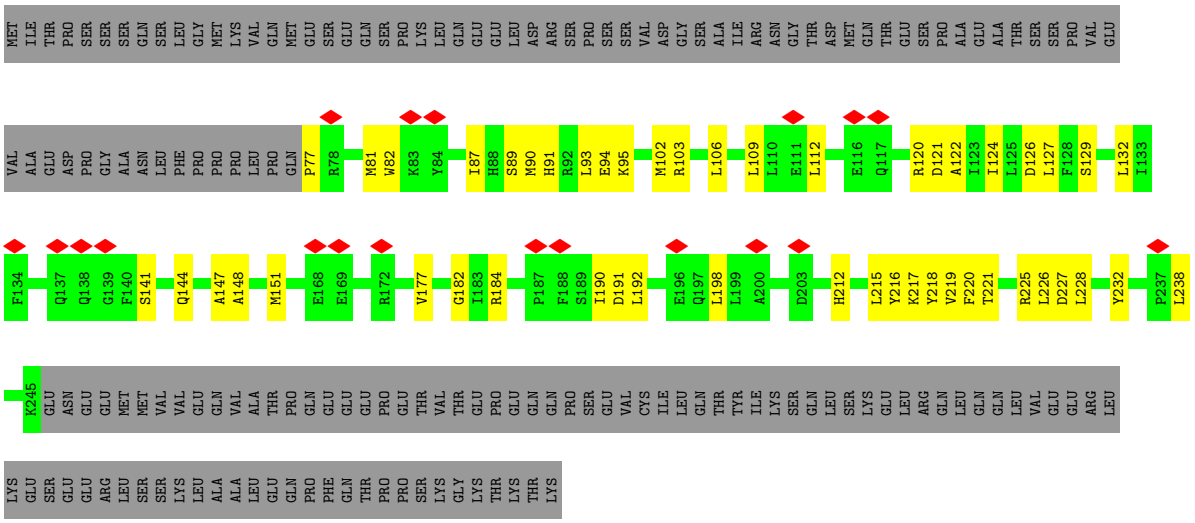
• Molecule 26: Cilia- and flagella-associated protein 119

Chain 3L:



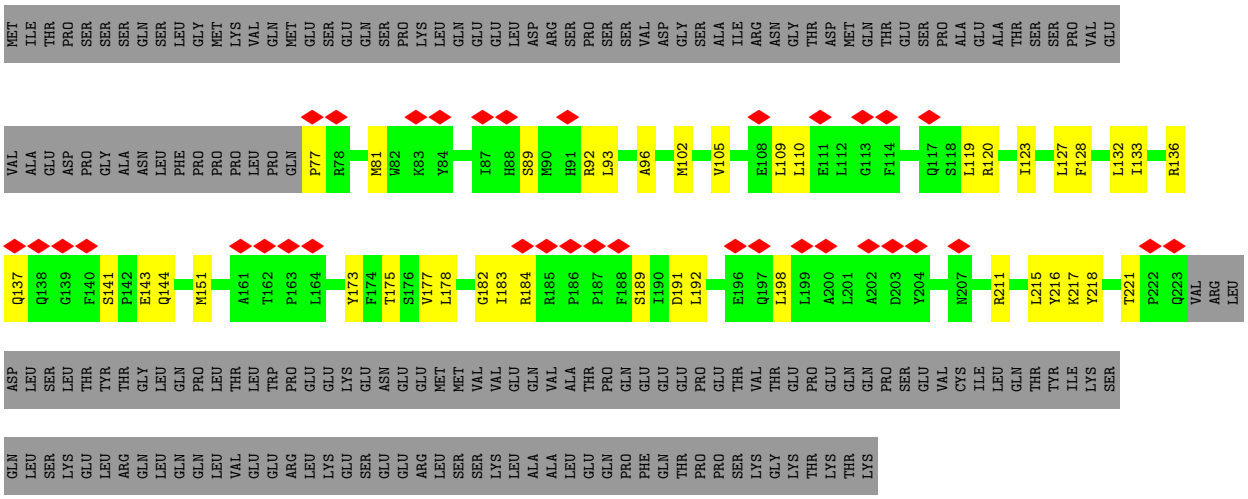
• Molecule 26: Cilia- and flagella-associated protein 119

Chain 3M:



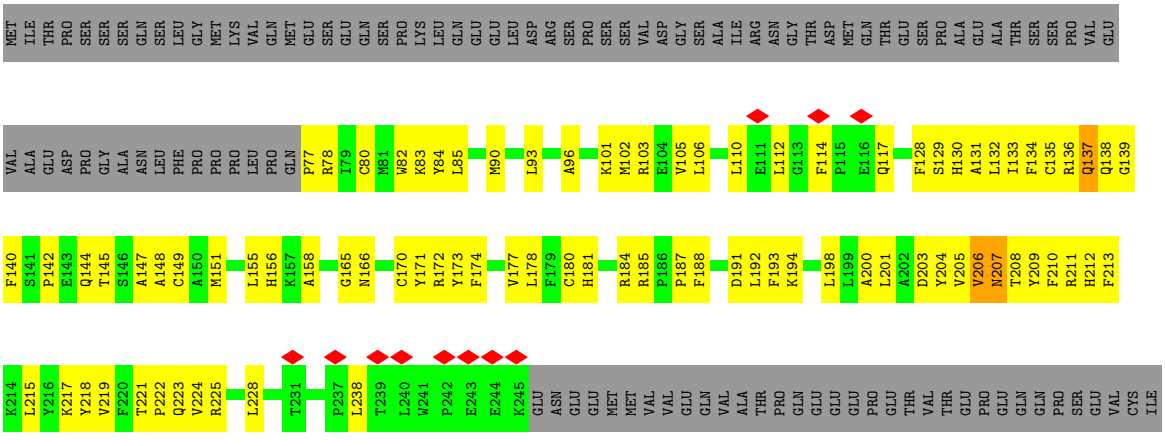
• Molecule 26: Cilia- and flagella-associated protein 119

Chain 3N:



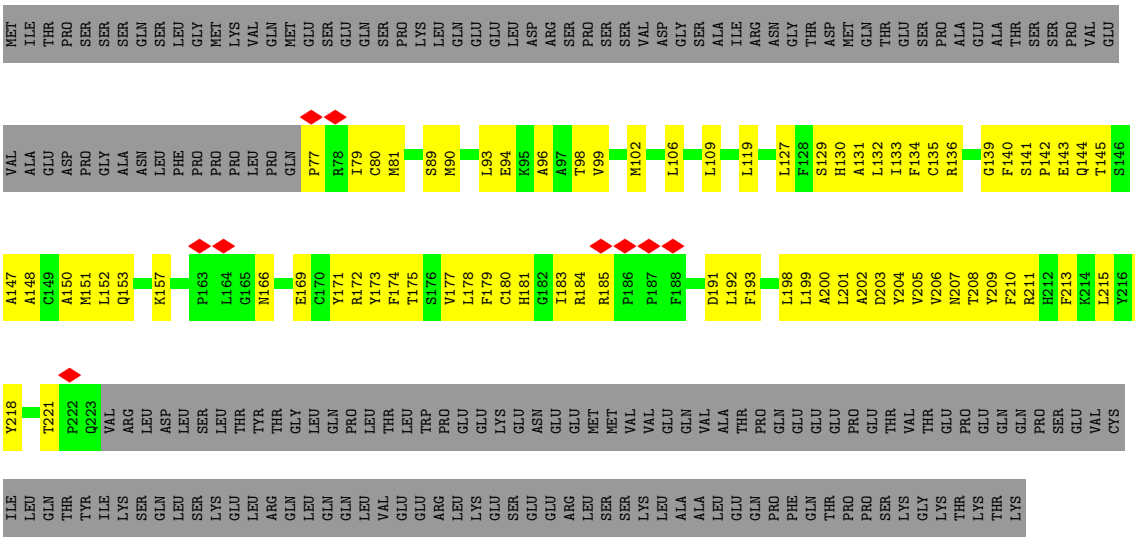
• Molecule 26: Cilia- and flagella-associated protein 119

Chain 3O:



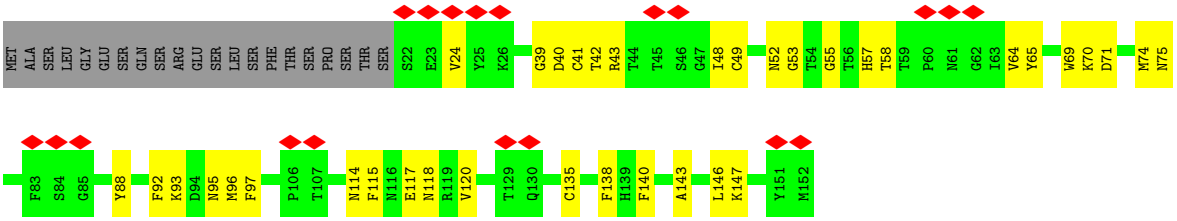
• Molecule 26: Cilia- and flagella-associated protein 119

Chain 3P:



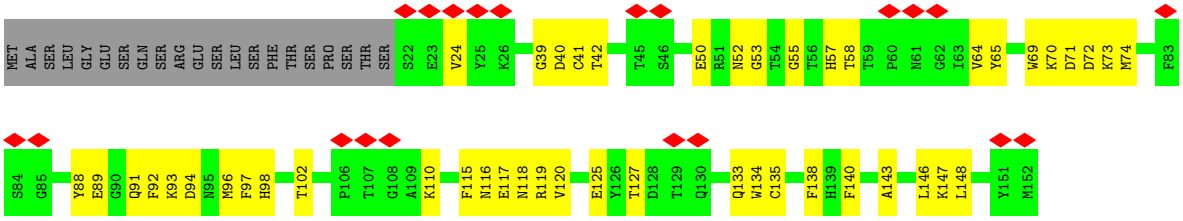
• Molecule 27: MORN repeat containing 2

Chain 3Q:



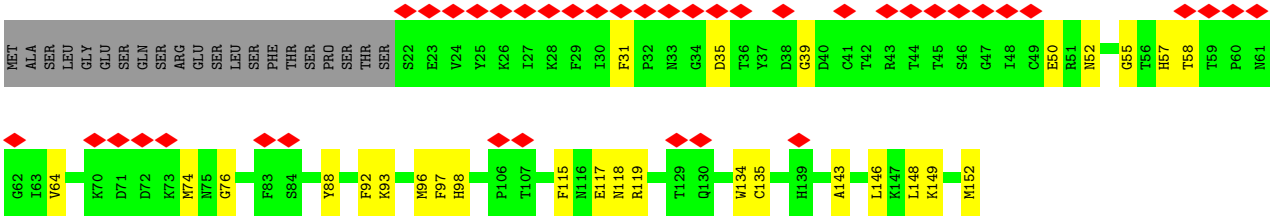
• Molecule 27: MORN repeat containing 2

Chain 3R:



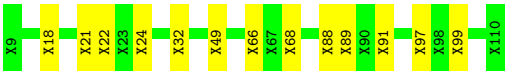
• Molecule 27: MORN repeat containing 2

Chain 3S:



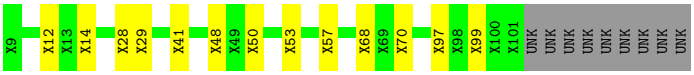
• Molecule 28: Unknown2

Chain 3Z:



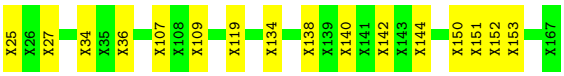
• Molecule 28: Unknown2

Chain 3a:



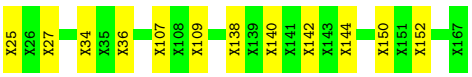
• Molecule 29: Unknown3

Chain 3b:



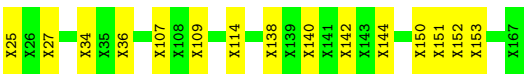
• Molecule 29: Unknown3

Chain 3c:



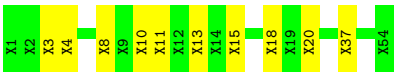
• Molecule 29: Unknown3

Chain 3d:



• Molecule 30: Unknown4

Chain 3e:



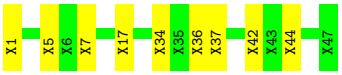
• Molecule 31: Unknown5

Chain 3f:

There are no outlier residues recorded for this chain.

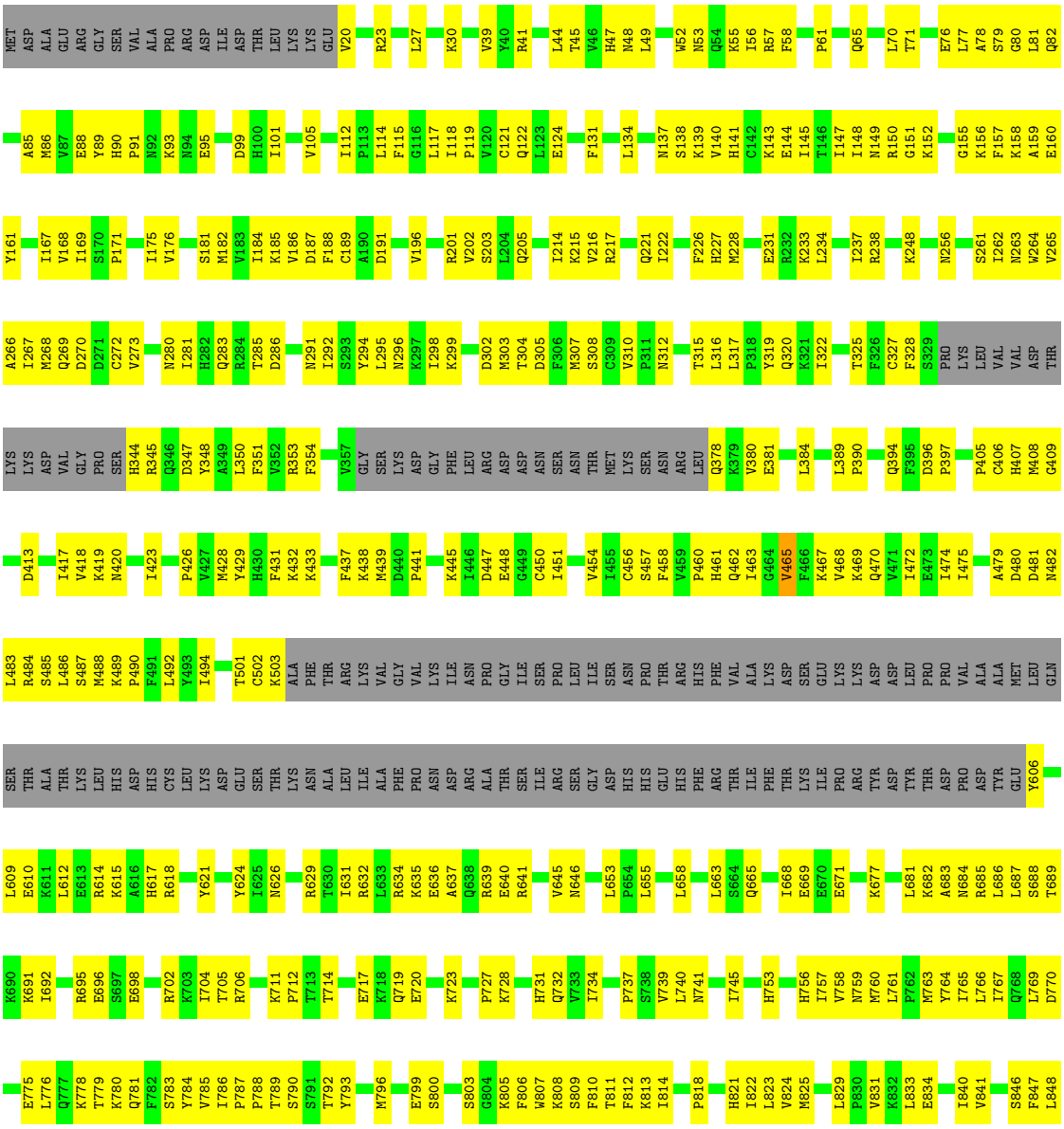
• Molecule 32: Unknown6

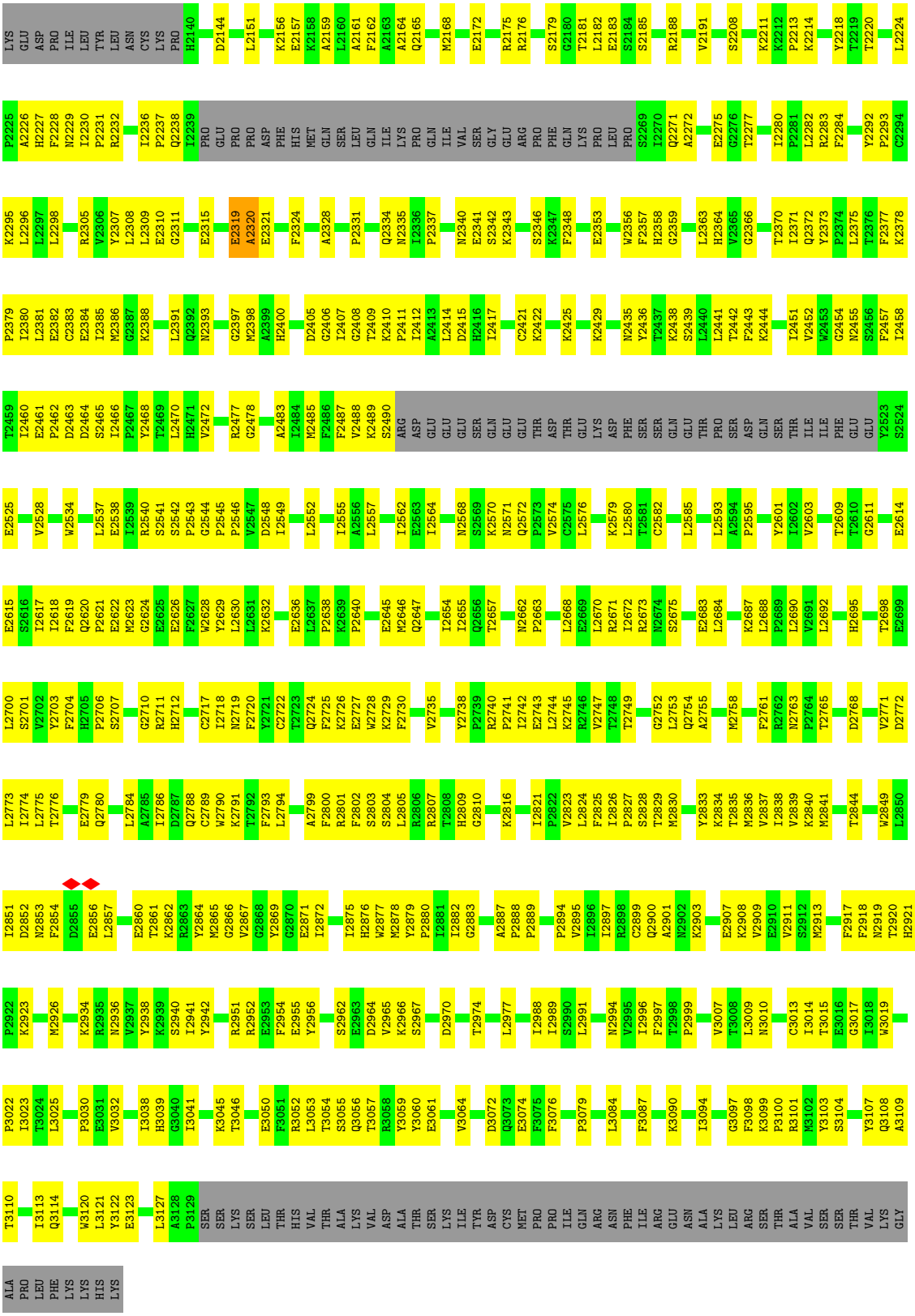
Chain 3g:



• Molecule 33: Cilia and flagella-associated protein 47

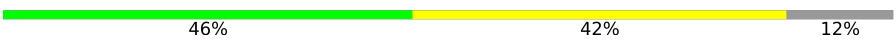
Chain 4A:

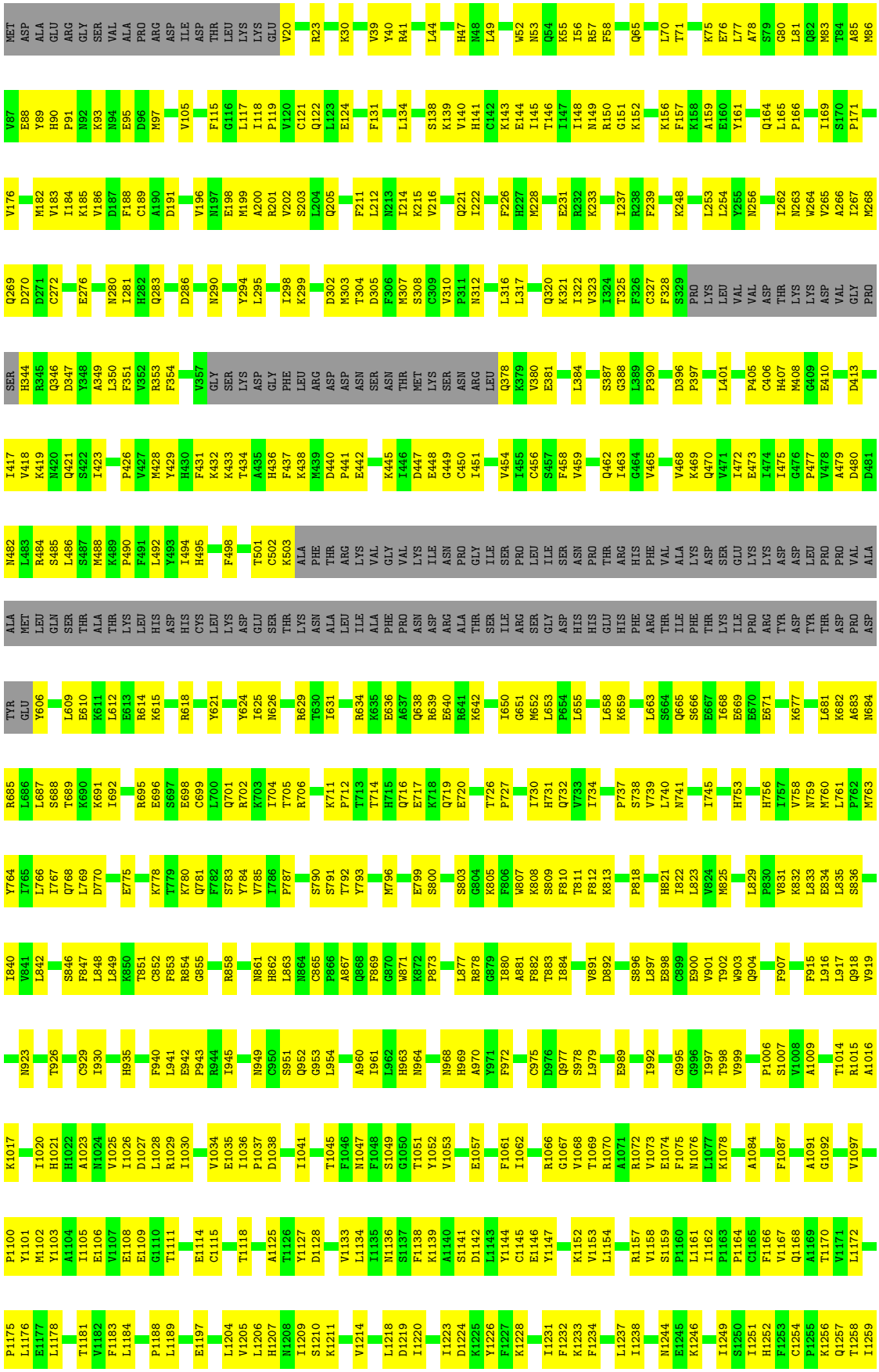


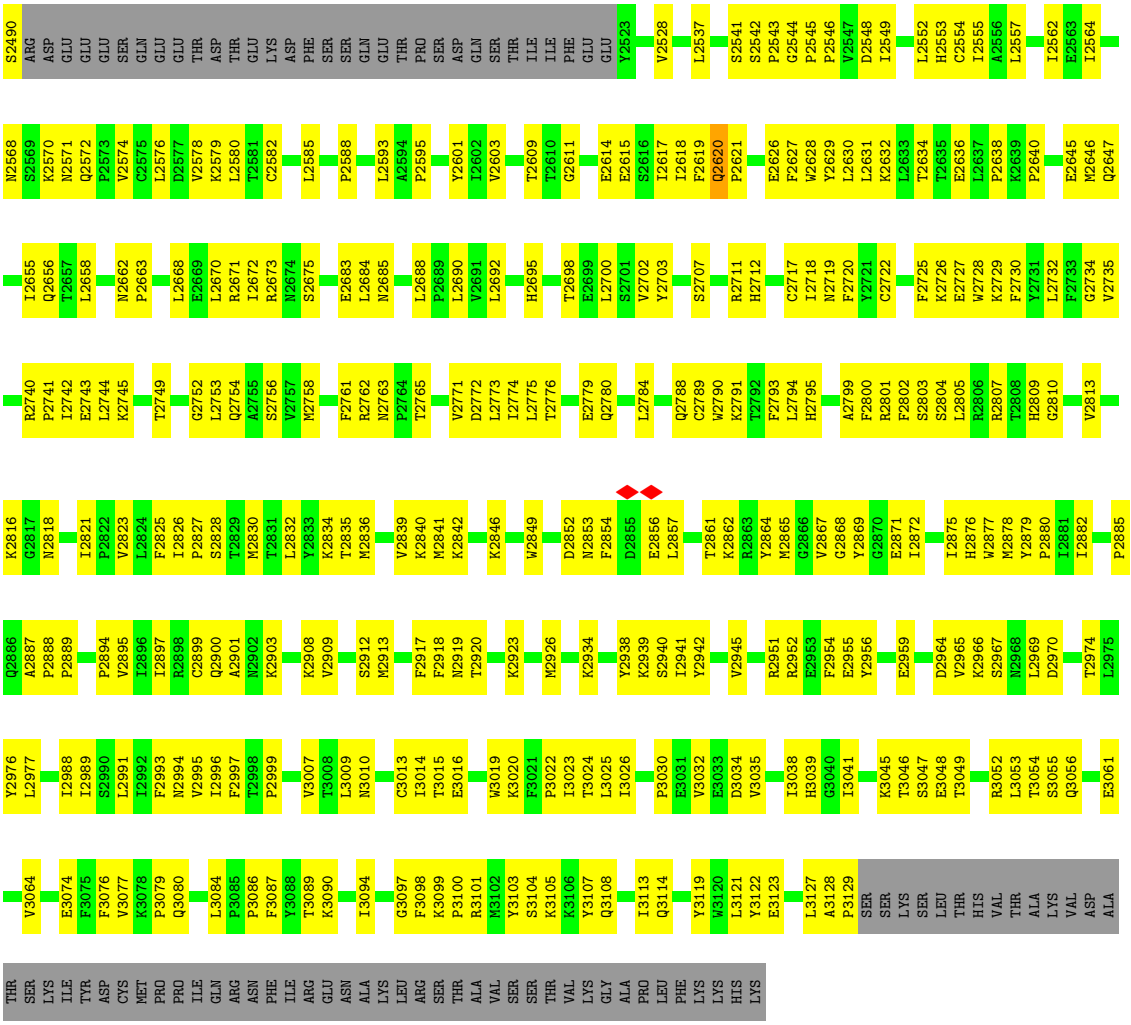


• Molecule 33: Cilia and flagella-associated protein 47

Chain 4B:

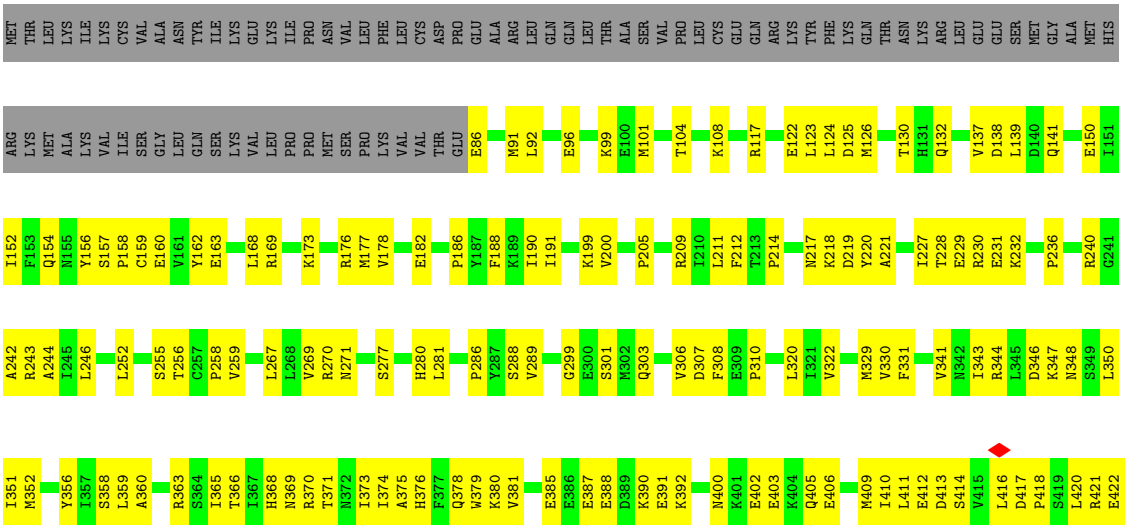


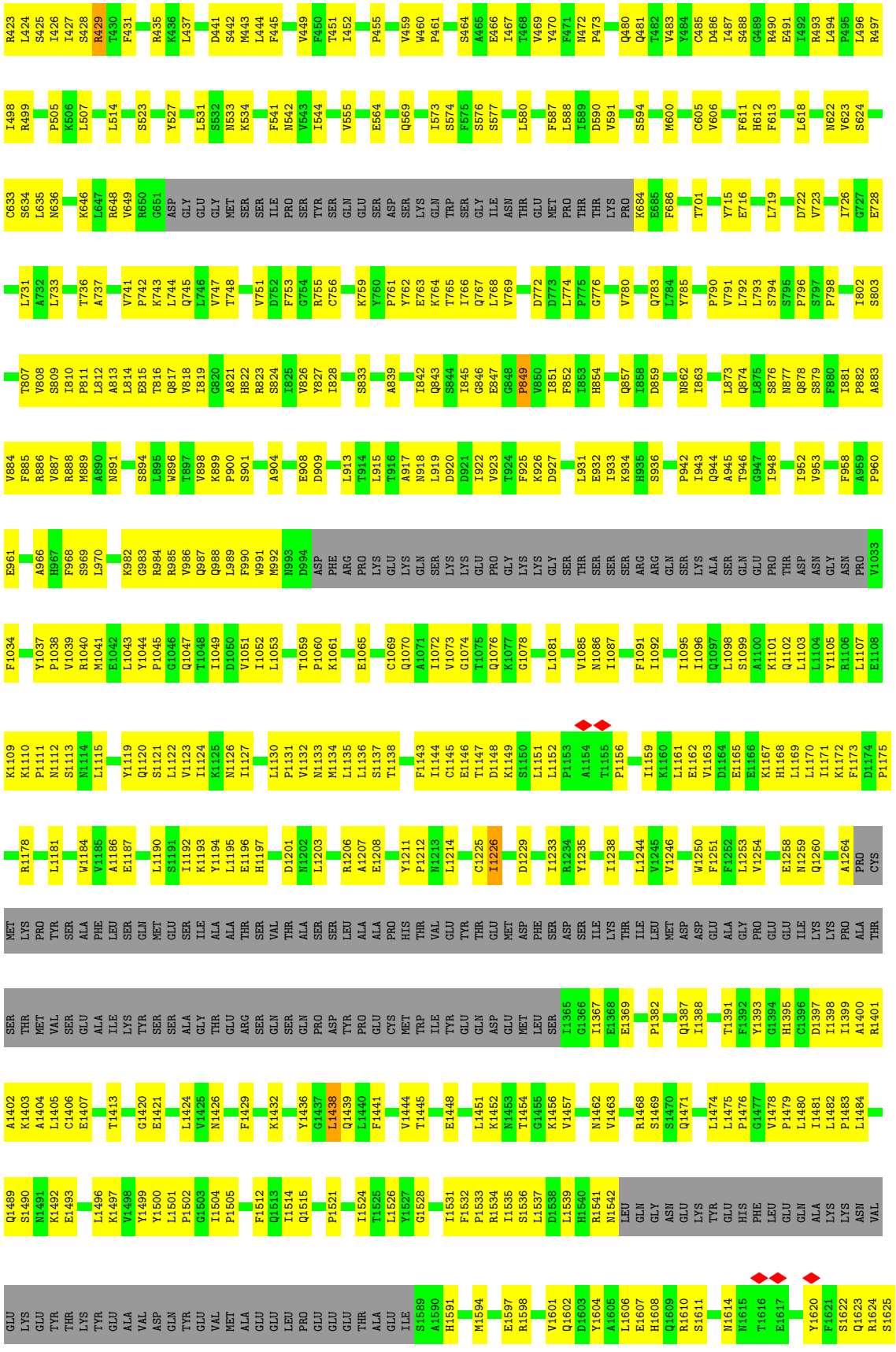


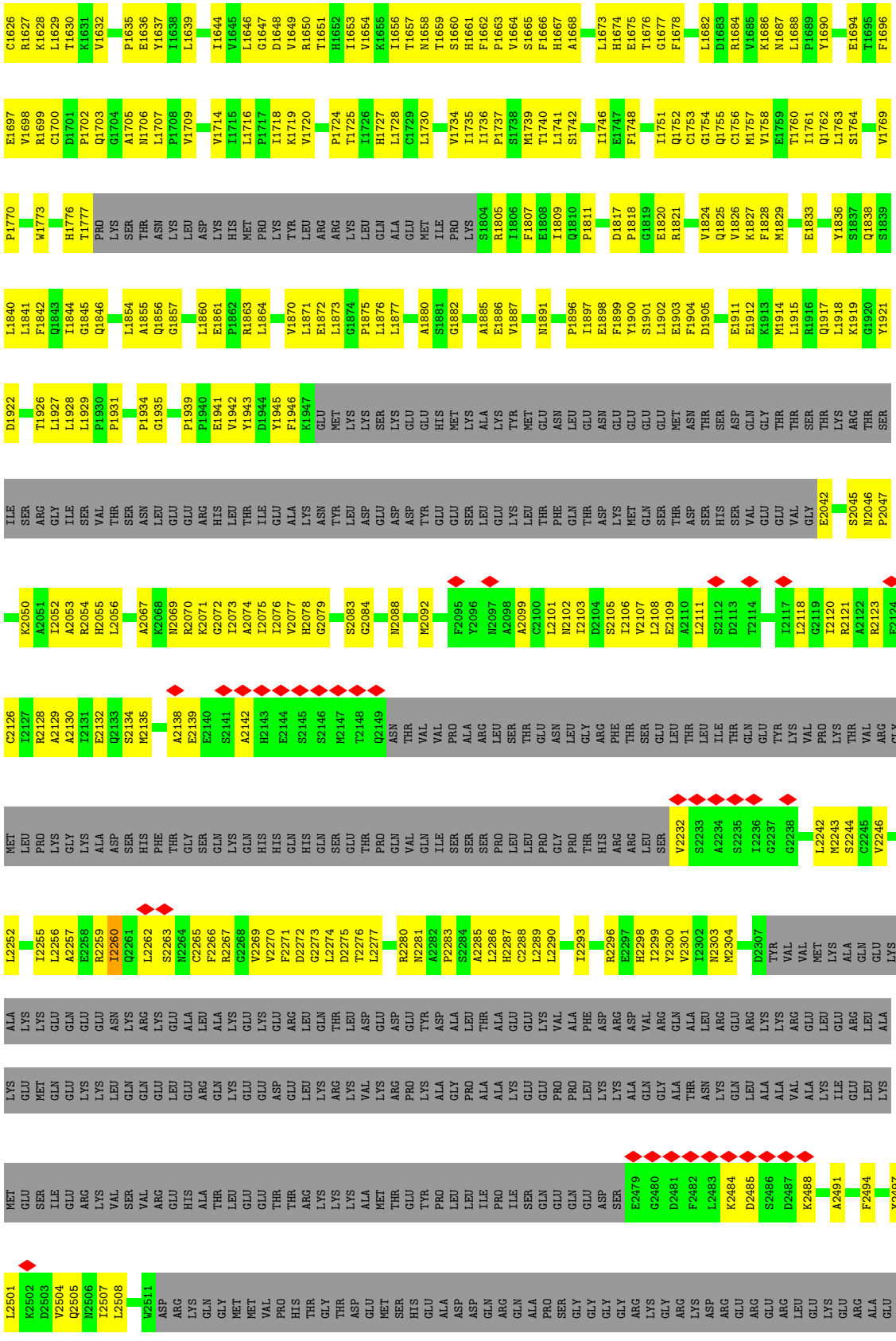


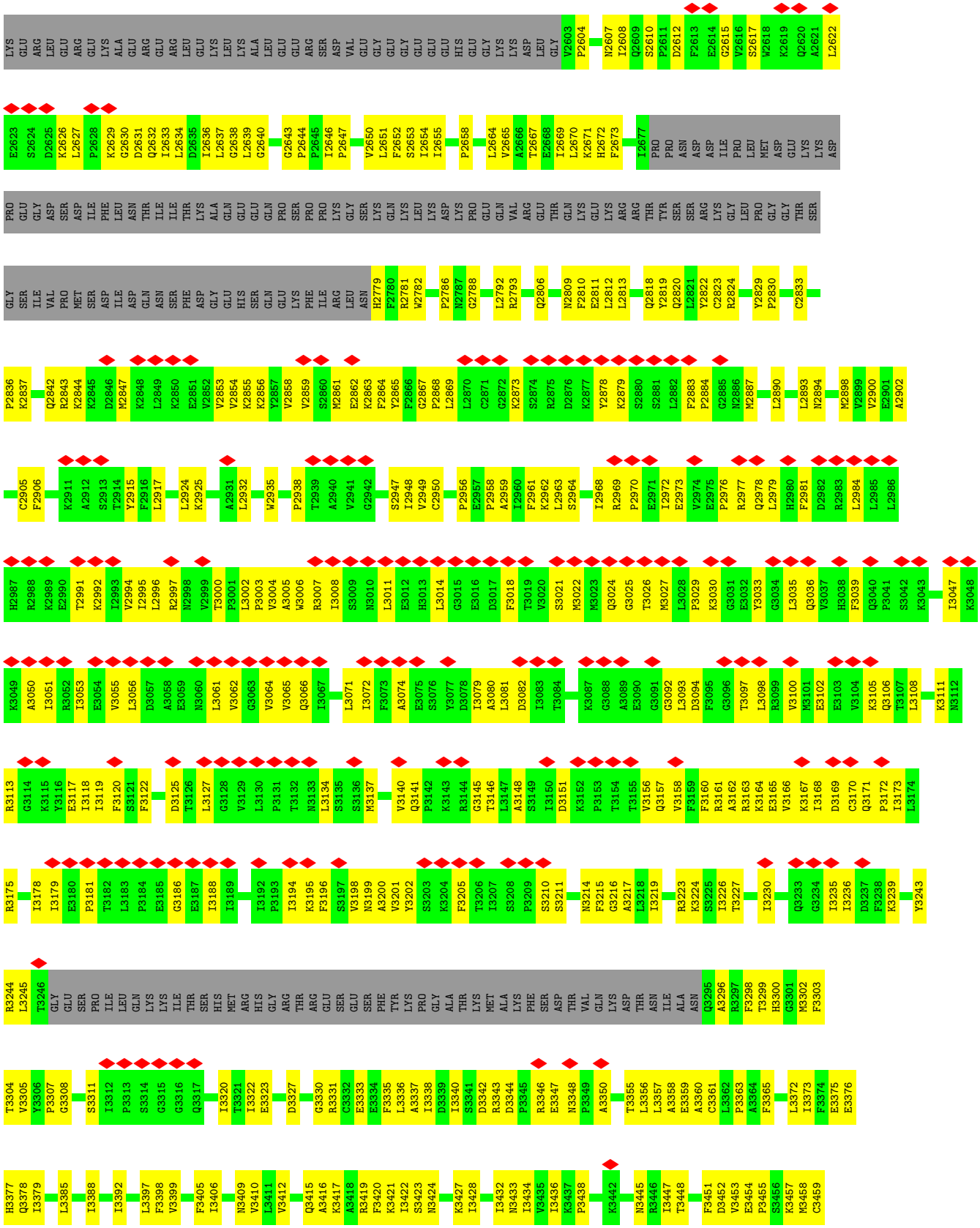
• Molecule 34: Hydrocephalus-inducing protein

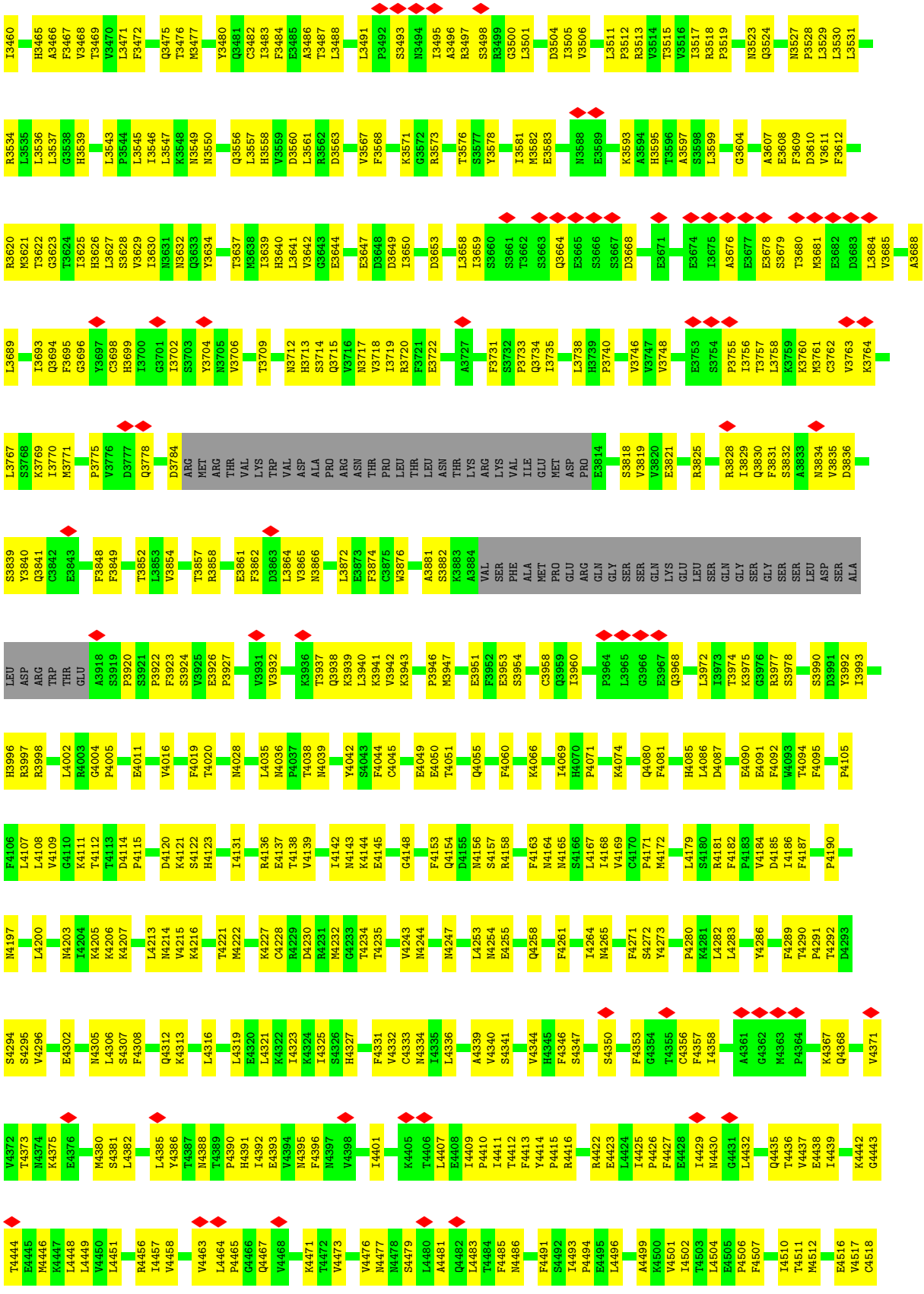
Chain 4G:

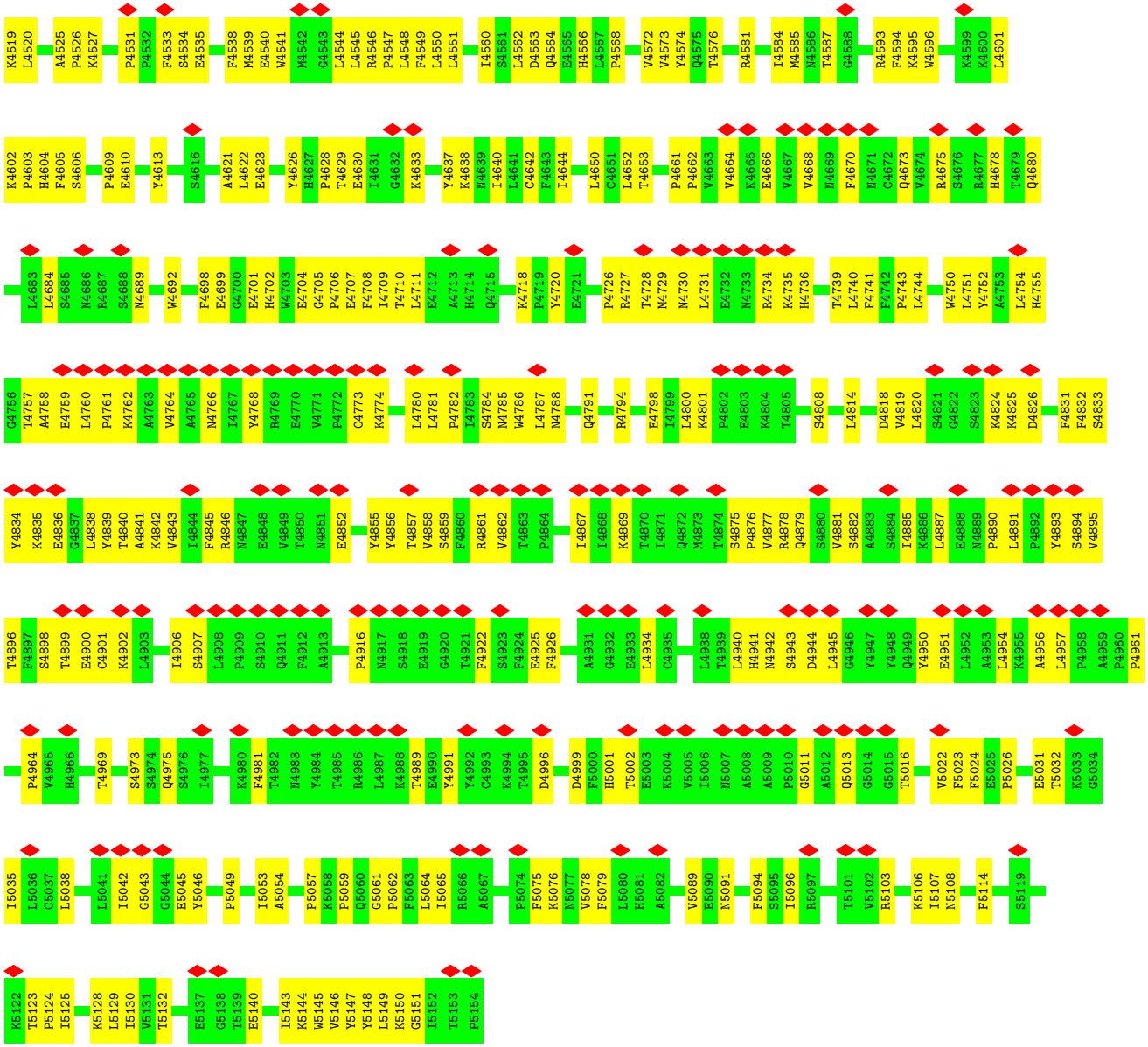





C1626 R1627 K1628 L1629 T1630 K1631 V1632 P1635 E1636 Y1637 I1638 L1639 I1644 V1645 L1646 G1647 D1648 V1649 R1650 T1651 H1652 I1653 V1654 K1655 I1656 T1657 N1658 T1659 S1660 H1661 F1662 P1663 V1664 S1665 F1666 H1667 A1668 L1673 H1674 E1675 T1676 G1677 F1678 L1682 D1683 R1684 V1685 K1686 N1687 L1688 P1689 Y1690 E1694 T1695 F1696
E1697 V1698 R1699 C1700 D1701 P1702 Q1703 G1704 A1705 N1706 L1707 P1708 V1709 V1714 I1715 L1716 P1717 I1718 K1719 V1720 P1724 T1725 I1726 H1727 L1728 C1729 L1730 V1734 I1735 I1736 P1737 S1738 M1739 T1740 L1741 S1742 I1746 E1747 F1748 I1751 Q1752 C1753 G1754 Q1755 C1756 M1757 V1758 E1759 T1760 I1761 Q1762 L1763 S1764 V1769
P1770 W1773 H1776 T1777 PRO LYS SER THR ASN LYS LEU ASP LYS HIS MET PRO LYS TYR LEU ARG ARG LYS LEU GLN ALA GLU MET ILE PRO LYS S1804 R1805 I1806 F1807 E1808 I1809 Q1810 P1811 D1817 P1818 G1819 E1820 R1821 V1824 Q1825 V1826 K1827 F1828 M1829 E1833 Y1836 S1837 Q1838 S1839
L1840 L1841 F1842 Q1843 I1844 G1845 Q1846 L1854 A1855 Q1856 G1857 L1860 E1861 P1862 R1863 L1864 V1870 L1871 E1872 L1873 G1874 P1875 L1876 L1877 A1880 S1881 G1882 A1885 E1886 V1887 N1891 P1896 I1897 E1898 F1899 Y1900 S1901 L1902 E1903 F1904 D1905 E1911 E1912 K1913 M1914 L1915 R1916 Q1917 L1918 K1919 G1920 Y1921
D1922 T1926 L1927 L1928 L1929 P1930 P1931 P1934 G1935 P1939 P1940 E1941 V1942 Y1943 D1944 Y1945 F1946 K1947 GLU MET LYS LYS SER LYS GLU GLU HIS MET LYS ALA LYS TYR MET GLU ASN LEU GLU ASN GLU GLU GLU GLU MET ASN THR SER ASP GLN GLY THR THR SER THR LYS ARG THR SER
ILE SER ARG GLY ILE SER VAL THR SER ASN LEU GLU GLU ARG HIS LEU THR ILE GLU ALA LYS ASN TYR LEU ASP GLU ASP ASP TYR GLU GLU SER LEU GLU LYS LEU THR PHE GLN THR ASP LYS MET GLN SER THR ASP SER HIS SER VAL GLU GLU VAL GLY E2042 S2045 N2046 P2047
K2050 A2051 I2052 A2053 R2054 H2055 L2056 A2067 K2068 N2069 R2070 K2071 G2072 I2073 A2074 I2075 I2076 V2077 H2078 G2079 S2083 G2084 N2088 M2092 F2095 Y2096 N2097 A2098 A2099 C2100 L2101 N2102 I2103 D2104 S2105 I2106 V2107 L2108 E2109 A2110 L2111 S2112 D2113 T2114 I2117 L2118 G2119 I2120 R2121 A2122 R2123 E2124 L2125
C2126 I2127 R2128 A2129 A2130 I2131 E2132 Q2133 S2134 M2135 A2138 E2139 E2140 S2141 A2142 H2143 E2144 S2145 S2146 M2147 T2148 Q2149 ASN THR VAL VAL PRO ALA ARG LEU SER THR GLU ASN LEU GLY ARG PHE THR SER GLU LEU THR LEU ILE THR GLN GLU TYR LYS VAL PRO LYS THR VAL ARG GLY SER VAL
MET LEU PRO LYS GLY LYS ALA ASP SER HIS PHE THR GLY SER GLN LYS GLN HIS HIS GLN HIS GLN SER GLU THR PRO GLN VAL GLN ILE SER SER SER PRO LEU LEU LEU PRO GLY PRO THR HIS ARG ARG LEU SER V2232 S2233 A2234 S2235 I2236 G2237 G2238 L2242 M2243 S2244 C2245 V2246 L2251
L2252 I2255 L2256 A2257 E2258 R2259 I2260 Q2261 L2262 S2263 N2264 C2265 F2266 R2267 G2268 V2269 V2270 F2271 D2272 G2273 L2274 D2275 T2276 L2277 R2280 N2281 A2282 P2283 S2284 A2285 L2286 H2287 C2288 L2289 L2290 I2293 R2296 E2297 H2298 I2299 Y2300 V2301 I2302 N2303 M2304 D2307 TYR VAL VAL MET LYS ALA GLN GLU LYS
ALA LYS LYS GLU GLN GLU GLU ASN LYS GLU ARG LYS GLU ALA LEU ALA ALA LYS GLU LYS GLU GLU LEU ASP GLU ARG LEU GLN THR LEU ASP GLU ASP ARG LYS VAL LYS ARG PRO LYS ALA GLU TYR ASP ALA LYS GLU GLU LYS LYS ARG ASP ALA LEU THR ALA ALA GLU LYS GLU GLU LYS LYS VAL ALA PHE ASP ARG ASP VAL ARG GLN ALA LEU ARG GLU ARG LYS LYS GLU LEU GLU ARG GLU LEU ALA
LYS GLU MET GLN GLU LYS LYS LEU GLN GLN GLU LEU GLU GLU ASP GLU LEU LYS ARG PRO LYS ALA GLY PRO ALA ALA LYS GLU GLU PRO PRO LEU LYS LYS ALA GLN GLY ALA THR ASN LYS GLN LEU ARG LYS LYS ARG LEU GLU LEU ILE GLU LEU LYS
MET GLU SER ILE GLU ARG LYS VAL SER VAL ARG GLU HIS ALA THR LEU GLU GLU GLU THR THR ARG LYS LYS LYS ALA MET THR GLU TYR PRO LEU LEU ILE PRO ILE SER GLN GLU GLN GLU ASP SER E2479 G2480 D2481 F2482 L2483 K2484 D2485 S2486 D2487 K2488 A2491 F2494 Y2497 C2500
L2501 K2502 D2503 V2504 Q2505 N2506 I2507 L2508 W2511 ASP ARG LYS GLN GLY MET MET VAL PRO HIS THR GLY THR ASP GLU MET SER HIS GLU ALA ASP ASP GLN ARG ILE GLN ALA PRO SER GLY GLY GLY GLY ARG LYS GLY ARG LYS ASP ARG GLU ARG GLU ARG LEU GLU LYS GLU ARG ALA GLU

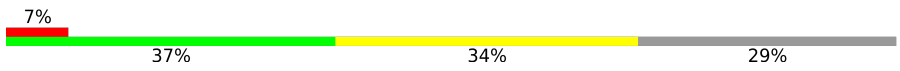


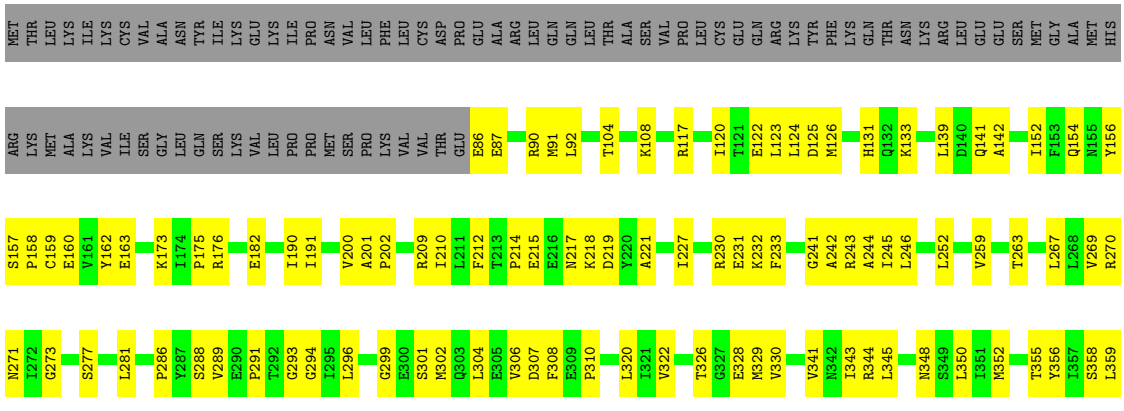


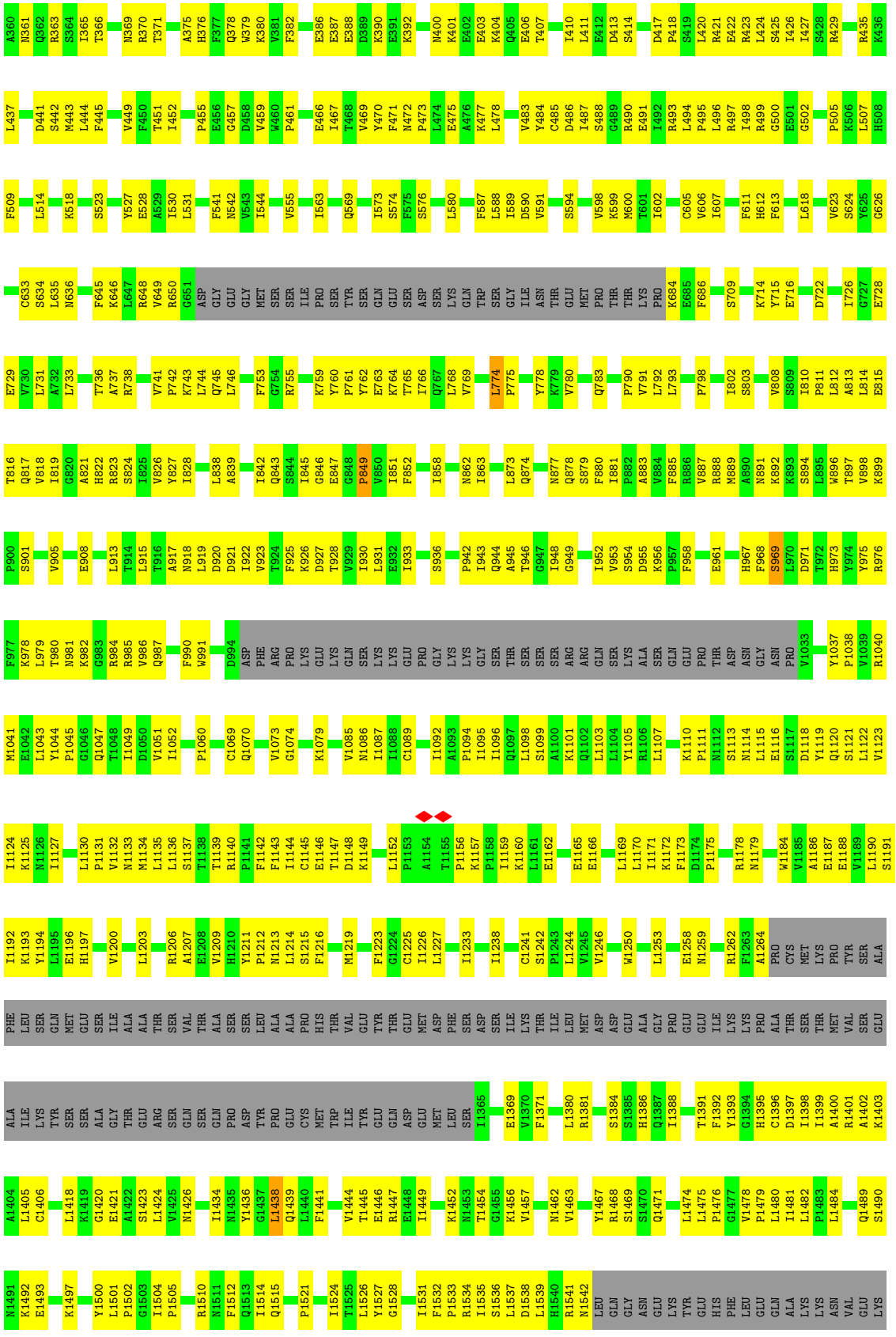


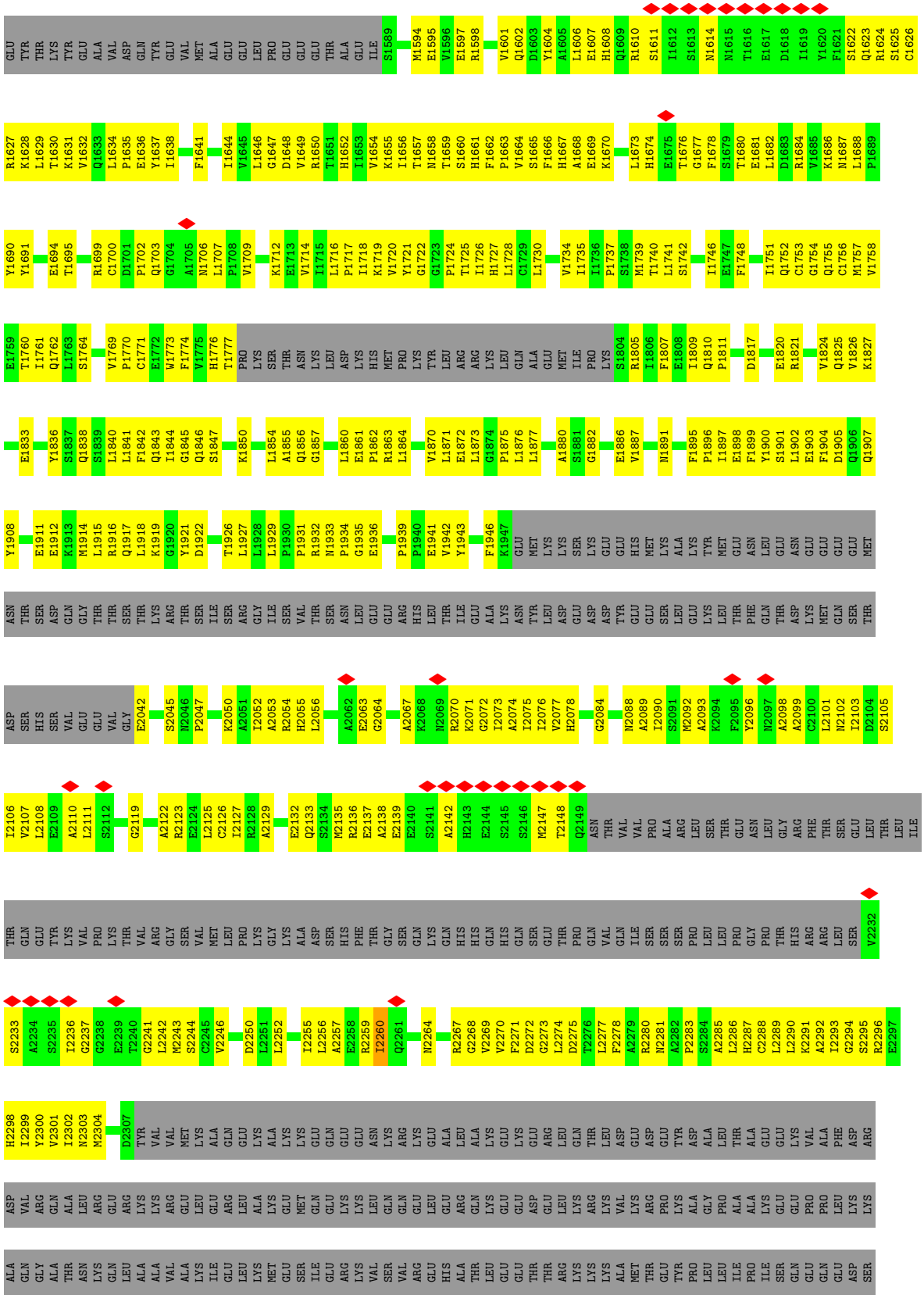
• Molecule 34: Hydrocephalus-inducing protein

Chain 4H:





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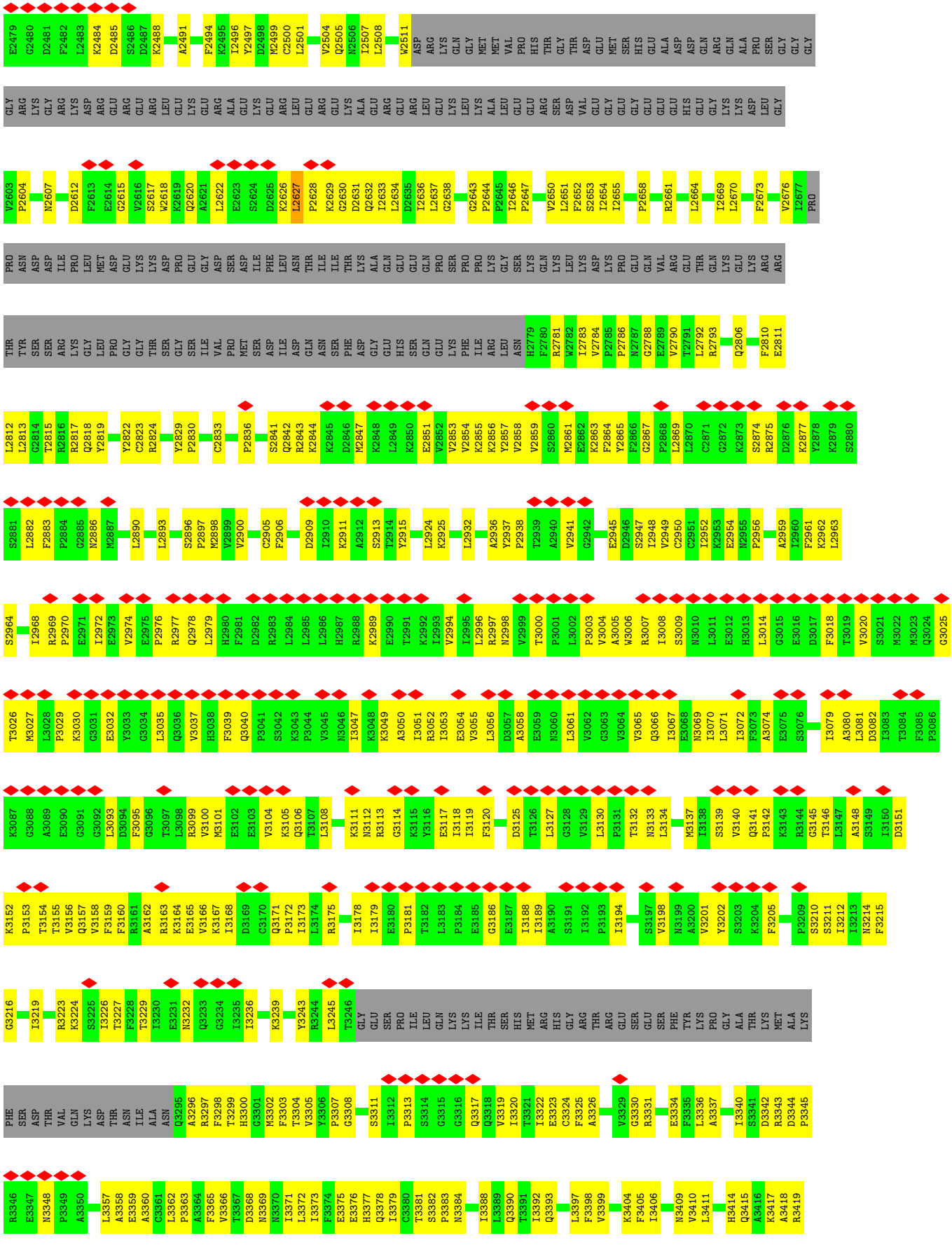
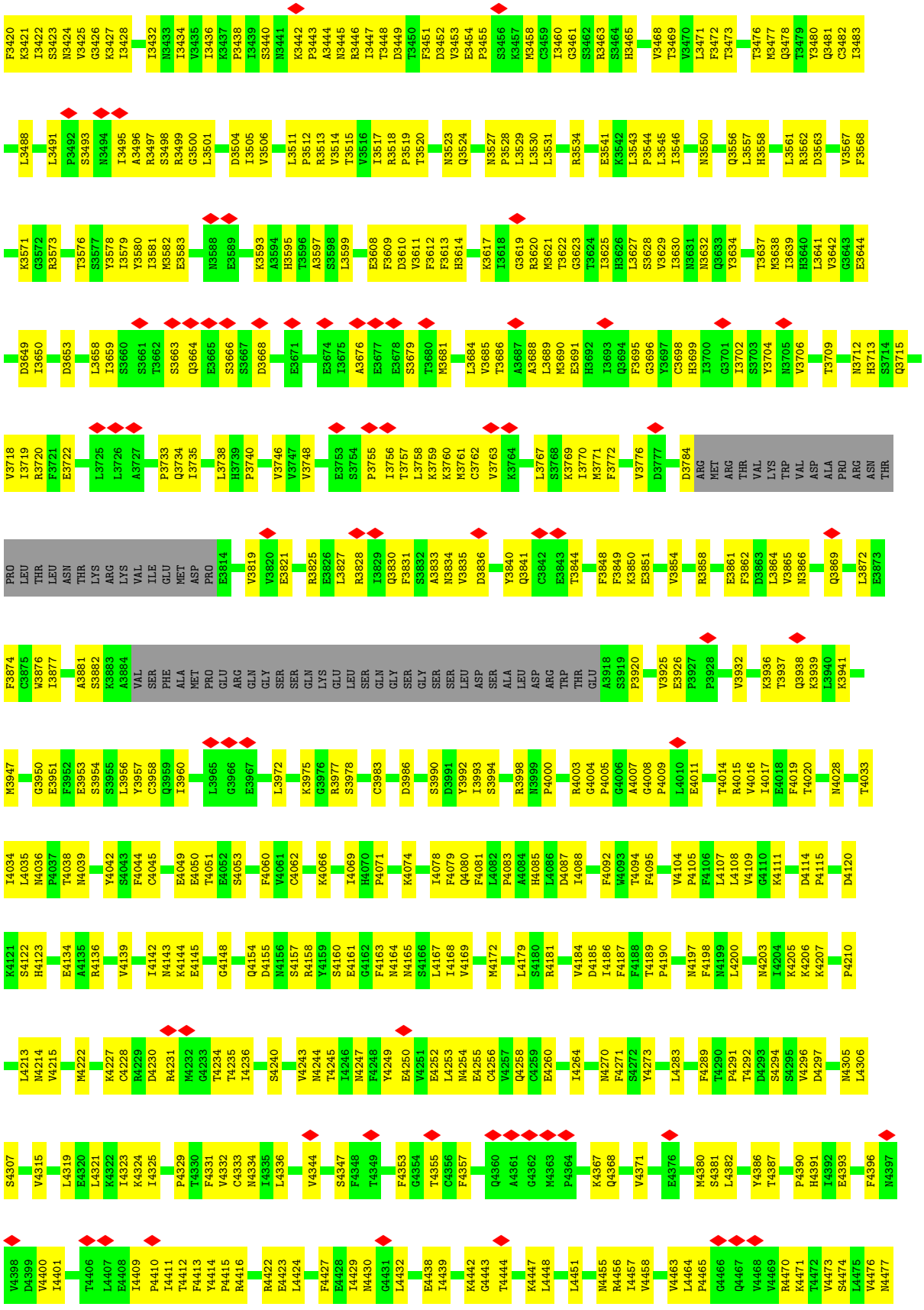
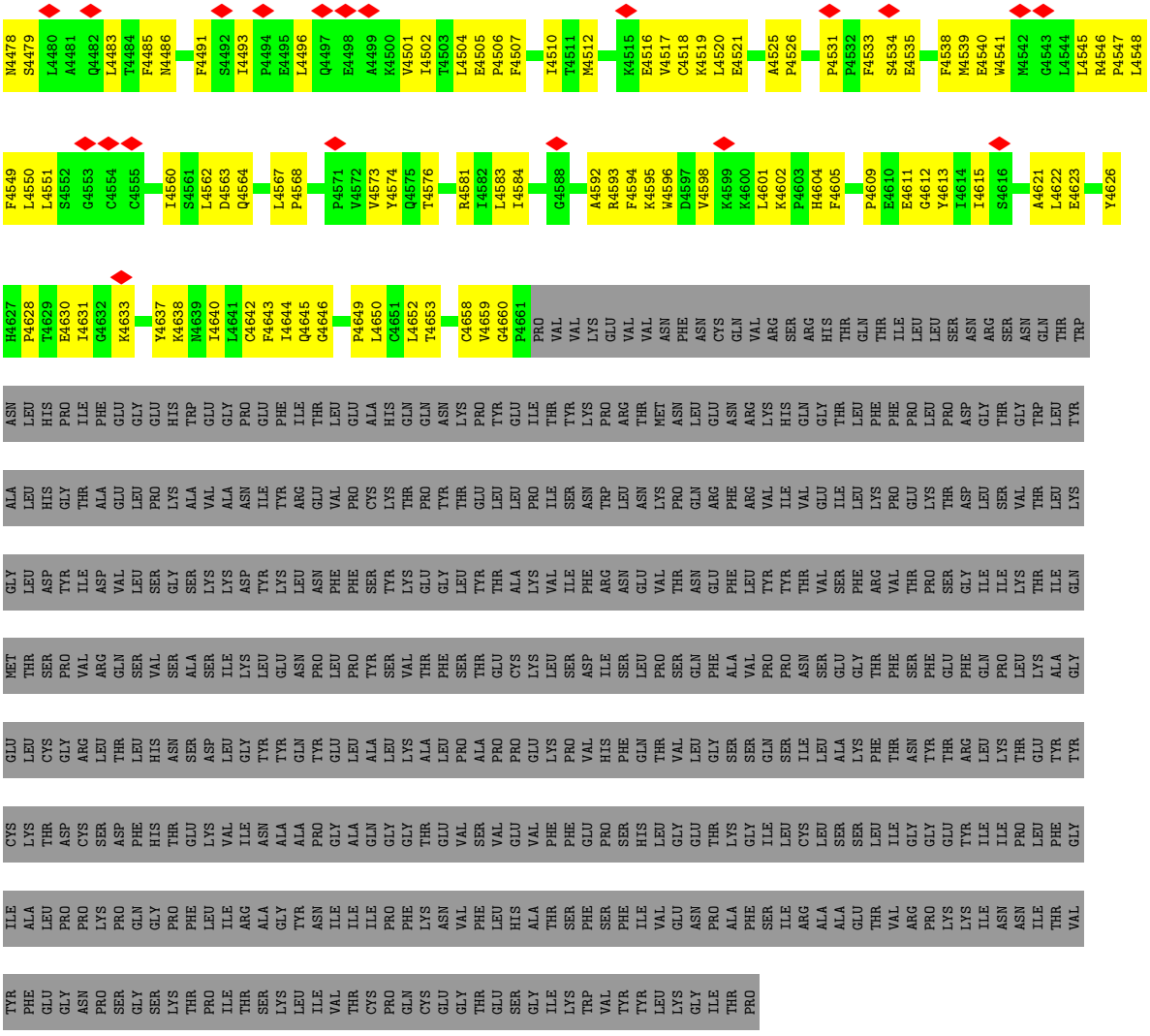
R1627 K1628 L1629 T1630 K1631 V1632 Q1633 L1634 P1635 E1636 Y1637 I1638 F1641 I1644 V1645 L1646 G1647 D1648 V1649 R1650 T1651 H1652 I1653 V1654 K1655 I1656 T1657 N1658 T1659 S1660 H1661 F1662 P1663 V1664 S1665 F1666 H1667 A1668 E1669 K1670 L1673 H1674 E1675 T1676 G1677 F1678 S1679 T1680 E1681 L1682 D1683 R1684 V1685 K1686 N1687 L1688 P1689
Y1690 Y1691 E1694 T1695 R1699 C1700 D1701 P1702 Q1703 G1704 A1705 M1706 L1707 P1708 V1709 K1712 E1713 V1714 I1715 L1716 P1717 I1718 K1719 V1720 Y1721 G1722 G1723 P1724 T1725 I1726 H1727 L1728 C1729 L1730 V1734 I1735 I1736 P1737 S1738 M1739 T1740 L1741 S1742 I1746 E1747 F1748 I1751 Q1752 C1753 G1754 Q1755 C1756 M1757 V1758
E1759 T1760 I1761 Q1762 L1763 S1764 V1769 P1770 C1771 E1772 W1773 F1774 V1775 H1776 T1777 PRO LYS SER THR ASN LYS LEU ASP LYS HIS MET PRO LYS TYR LEU ARG ARG LYS LEU GLN ALA GLU MET ILE PRO LYS S1804 R1805 I1806 F1807 E1808 I1809 Q1810 P1811 D1817 E1820 R1821 V1824 Q1825 V1826 K1827
E1833 Y1836 S1837 Q1838 S1839 L1840 L1841 F1842 Q1843 I1844 G1845 Q1846 S1847 K1850 L1854 A1855 Q1856 G1857 L1860 E1861 P1862 R1863 L1864 V1870 L1871 E1872 L1873 G1874 P1875 L1876 L1877 A1880 S1881 G1882 E1886 V1887 N1891 F1895 P1896 I1897 E1898 F1899 Y1900 S1901 L1902 E1903 F1904 D1905 Q1906 Q1907
Y1908 E1911 E1912 K1913 M1914 L1915 R1916 Q1917 L1918 K1919 G1920 Y1921 D1922 T1926 L1927 L1928 L1929 P1930 P1931 R1932 N1933 P1934 G1935 E1936 P1939 P1940 E1941 V1942 Y1943 F1946 K1947 GLU MET LYS LYS SER LYS GLU GLU HIS MET LYS ALA LYS TYR MET GLU ASN LEU GLU GLU ASN GLU GLU GLU GLU MET
ASN THR SER ASP GLN GLY THR THR SER THR LYS ARG THR SER ILE SER ARG GLY ILE SER VAL THR SER SER ASN LEU GLU GLU ARG HIS LEU THR ILE GLU ALA LYS ASN TYR LEU ASP GLU ASP ASP TYR GLU GLU HIS MET GLU SER LEU GLU LYS LEU LEU THR PHE GLN THR ASP LYS MET GLN SER THR
ASP SER HIS SER VAL GLU GLU VAL GLY E2042 S2045 N2046 P2047 K2050 A2051 I2052 A2053 R2054 H2055 L2056 A2062 E2063 G2064 A2067 K2068 N2069 R2070 K2071 G2072 I2073 A2074 I2075 I2076 V2077 H2078 G2084 N2088 A2089 I2090 S2091 M2092 A2093 K2094 F2095 Y2096 N2097 A2098 A2099 C2100 L2101 N2102 I2103 D2104 S2105
I2106 V2107 L2108 E2109 A2110 L2111 S2112 G2119 A2122 R2123 E2124 L2125 C2126 I2127 R2128 A2129 E2132 Q2133 S2134 M2135 R2136 E2137 A2138 E2139 E2140 S2141 A2142 H2143 E2144 S2145 S2146 M2147 T2148 Q2149 ASN THR VAL VAL PRO ALA ARG LEU SER THR GLU ASN LEU GLY ARG PHE THR SER GLU LEU THR LEU ILE
THR GLN GLU TYR LYS VAL PRO LYS THR VAL ARG GLY SER VAL MET LEU PRO LYS GLY LYS ALA ASP SER HIS PHE THR GLY SER GLN LYS GLN HIS HIS GLN HIS GLN HIS GLN SER GLU THR PRO GLN VAL GLN ILE SER SER SER PRO LEU LEU LEU PRO GLY PRO THR HIS ARG ARG ARG LEU SER V2232
S2233 A2234 S2235 I2236 G2237 G2238 E2239 T2240 G2241 L2242 M2243 S2244 C2245 V2246 D2250 L2251 L2252 I2255 L2256 A2257 E2258 R2259 I2260 G2261 N2264 R2267 G2268 Y2269 V2270 F2271 D2272 G2273 L2274 D2275 T2276 L2277 F2278 A2279 R2280 N2281 A2282 P2283 S2284 A2285 L2286 H2287 C2288 L2289 L2290 K2291 A2292 I2293 G2294 S2295 R2296 E2297
H2298 I2299 Y2300 V2301 I2302 N2303 M2304 D2307 TYR VAL VAL MET LYS ALA GLN GLU LYS ALA LYS LYS GLU GLN GLU GLU ASN LYS ARG GLU ALA LEU LYS GLU GLU LYS GLU ARG GLU ASP GLU LEU LYS ARG LYS VAL LYS ARG PRO LYS ALA LEU GLU GLU LYS VAL ALA PHE ASP ARG
ASP VAL ARG GLN ALA LEU ARG GLU ARG LYS LYS ARG GLU LEU ALA LYS GLU MET GLN GLU GLU LYS LYS LEU GLN GLN GLU LEU GLU GLU GLU ARG GLU GLU ASP GLU LEU LYS ARG LYS VAL LYS ARG PRO LYS ALA LEU GLY PRO ALA ALA LYS GLU GLU LYS VAL PRO PRO LEU LYS
ALA GLN GLY ALA THR ASN LYS GLN LEU ALA ALA VAL ALA LYS ILE GLU LEU LYS MET GLU SER ILE GLU ARG LYS VAL SER VAL ARG GLU HIS ALA THR LEU GLU GLU GLU THR THR ARG LYS LYS LYS ALA MET THR GLU TYR PRO LEU LEU ILE PRO ILE SER GLN GLU GLN GLU ASP SER

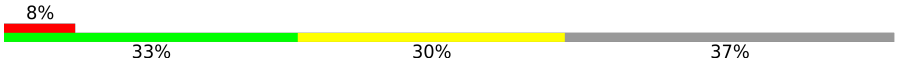

E2479 G2480 D2481 F2482 L2483 K2484 D2485 S2486 D2487 K2488 A2491 F2494 K2495 I2496 Y2497 D2498 M2499 C2500 L2501 V2504 Q2505 N2506 I2507 L2508 W2511 ASP ARG LYS GLN GLY MET MET VAL PRO HIS THR GLY THR ASP GLU MET SER HIS GLU ALA ASP ASP GLN ARG GLN ALA PRO SER GLY GLY GLY
GLY ARG LYS GLY ARG LYS ASP ARG GLU ARG GLU LEU GLU LYS GLU ARG ALA GLU LYS GLU ARG LEU GLU GLU LEU GLU ARG GLU ARG GLU LYS ALA GLY GLU ARG GLU ARG GLU ARG SER ASP VAL GLU GLY GLU GLY GLU GLU GLU HIS GLU GLY LYS LYS ASP LEU GLY
V2603 P2604 N2607 D2612 F2613 E2614 G2615 V2616 S2617 W2618 K2619 Q2620 A2621 L2622 E2623 S2624 D2625 K2626 L2627 P2628 K2629 G2630 D2631 Q2632 I2633 L2634 D2635 I2636 L2637 G2638 G2643 P2644 P2645 I2646 P2647 V2650 L2651 F2652 S2653 I2654 I2665 P2658 R2661 L2664 I2669 L2670 F2673 V2676 I2677 PRO
PRO ASN ASP ASP ILE PRO LEU MET ASP GLU LYS LYS ASP PRO GLU GLY ASP SER ASP ILE PHE LEU ASN THR ILE ILE THR LYS ALA GLN GLU GLU GLN PRO SER PRO PRO LYS GLY SER LYS GLN LYS LEU LYS ASP LYS GLU GLN VAL ARG GLU THR GLN LYS GLU LYS ARG ARG
THR TYR SER SER ARG LYS GLY LEU PRO GLY GLY GLY THR SER GLY SER ILE VAL PRO MET SER ASP ILE ASP GLN ASN SER PHE ASP GLY GLU GLU HIS SER GLN GLU LYS PHE ILE ARG LEU ASN H2779 F2780 R2781 W2782 I2783 V2784 P2785 P2786 N2787 G2788 E2789 V2790 T2791 L2792 R2793 Q2806 F2810 E2811
L2812 L2813 G2814 T2815 R2816 R2817 Q2818 Y2819 Y2822 C2823 R2824 Y2829 P2830 C2833 P2836 S2841 Q2842 R2843 K2844 K2845 D2846 M2847 K2848 L2849 K2850 E2851 V2852 Y2853 V2854 K2855 K2856 K2857 V2858 V2859 S2860 M2861 E2862 K2863 F2864 Y2865 F2866 G2867 P2868 L2869 L2870 C2871 G2872 K2873 S2874 R2875 D2876 K2877 Y2878 K2879 S2880
S2881 L2882 F2883 P2884 G2885 N2886 M2887 L2890 L2893 S2896 P2897 M2898 V2899 V2900 C2905 F2906 D2909 I2910 K2911 A2912 S2913 T2914 Y2915 L2924 K2925 L2932 A2936 Y2937 P2938 T2939 A2940 V2941 G2942 E2945 D2946 S2947 I2948 V2949 C2950 C2951 I2952 K2953 E2954 N2955 P2956 A2959 I2960 F2961 K2962 L2963
S2964 I2968 R2969 P2970 E2971 I2972 E2973 V2974 E2975 P2976 R2977 Q2978 L2979 H2980 F2981 D2982 R2983 L2984 L2985 L2986 H2987 R2988 K2989 E2990 T2991 K2992 I2993 V2994 I2995 L2996 R2997 N2998 V2999 T3000 P3001 L3002 P3003 V3004 A3005 W3006 R3007 I3008 S3009 N3010 L3011 E3012 H3013 L3014 G3015 E3016 D3017 F3018 T3019 V3020 S3021 M3022 M3023 Q3024 G3025
T3026 M3027 L3028 P3029 K3030 G3031 E3032 Y3033 G3034 L3035 Q3036 V3037 H3038 F3039 Q3040 P3041 S3042 K3043 P3044 V3045 N3046 I3047 K3048 K3049 A3050 I3051 R3052 I3053 E3054 V3055 L3056 D3057 A3058 E3059 N3060 L3061 V3062 G3063 V3064 V3065 Q3066 I3067 E3068 N3069 I3070 L3071 I3072 F3073 A3074 E3075 S3076 I3079 A3080 L3081 D3082 I3083 T3084 F3085 P3086
K3087 G3088 A3089 E3090 G3091 G3092 L3093 D3094 F3095 G3096 T3097 L3098 R3099 V3100 M3101 E3102 E3103 V3104 K3105 Q3106 T3107 L3108 K3111 N3112 R3113 G3114 K3115 Y3116 E3117 I3118 I3119 F3120 D3125 T3126 L3127 G3128 V3129 L3130 P3131 T3132 N3133 L3134 M3137 I3138 S3139 V3140 Q3141 P3142 K3143 R3144 G3145 T3146 L3147 A3148 S3149 I3150 D3151
K3152 P3153 T3154 T3155 V3156 Q3157 V3158 F3159 F3160 R3161 A3162 R3163 K3164 E3165 V3166 K3167 I3168 D3169 C3170 Q3171 P3172 I3173 L3174 R3175 I3178 I3179 E3180 P3181 T3182 L3183 P3184 E3185 G3186 E3187 I3188 I3189 A3190 S3191 I3192 P3193 I3194 S3197 V3198 N3199 A3200 V3201 Y3202 S3203 K3204 F3205 F3209 S3210 S3211 T3212 I3213 N3214 F3215
G3216 I3219 R3223 K3224 S3225 I3226 T3227 F3228 T3229 I3230 E3231 N3232 Q3233 G3234 I3235 I3236 K3239 Y3243 R3244 L3245 T3246 GLY GLU SER PRO ILE LEU GLN LYS LYS ILE THR SER HIS MET ARG HIS GLY ARG THR ARG GLU SER GLU SER PHE TYR LYS PRO GLY ALA THR LYS MET ALA LYS
PHE SER ASP THR VAL GLN LYS ASP THR ASN ILE ALA ASN Q3295 A3296 R3297 F3298 T3299 H3300 G3301 M3302 F3303 T3304 V3305 Y3306 P3307 G3308 S3311 I3312 P3313 S3314 G3315 G3316 Q3317 Q3318 V3319 I3320 T3321 I3322 E3323 C3324 F3325 A3326 V3329 G3330 R3331 E3334 F3335 L3336 A3337 I3340 S3341 D3342 R3343 D3344 P3345
R3346 E3347 N3348 P3349 A3350 L3357 A3358 E3359 A3360 C3361 L3362 P3363 A3364 F3365 V3366 T3367 D3368 N3369 N3370 I3371 L3372 I3373 F3374 E3375 E3376 H3377 Q3378 I3379 C3380 T3381 S3382 P3383 N3384 I3388 L3389 Q3390 T3391 I3392 Q3393 L3397 F3398 V3399 K3404 F3405 I3406 N3409 V3410 L3411 H3414 Q3415 A3416 K3417 A3418 R3419

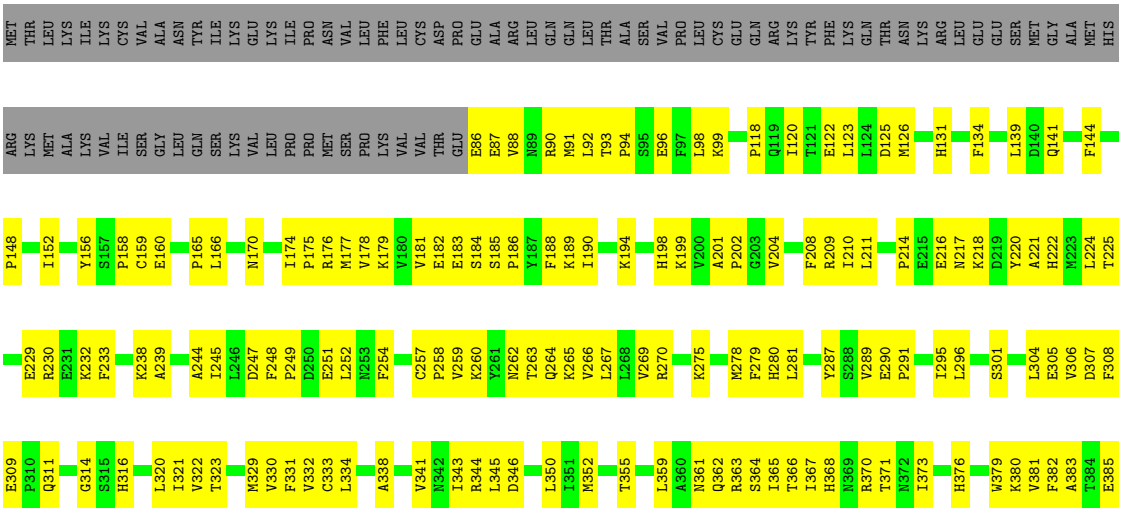


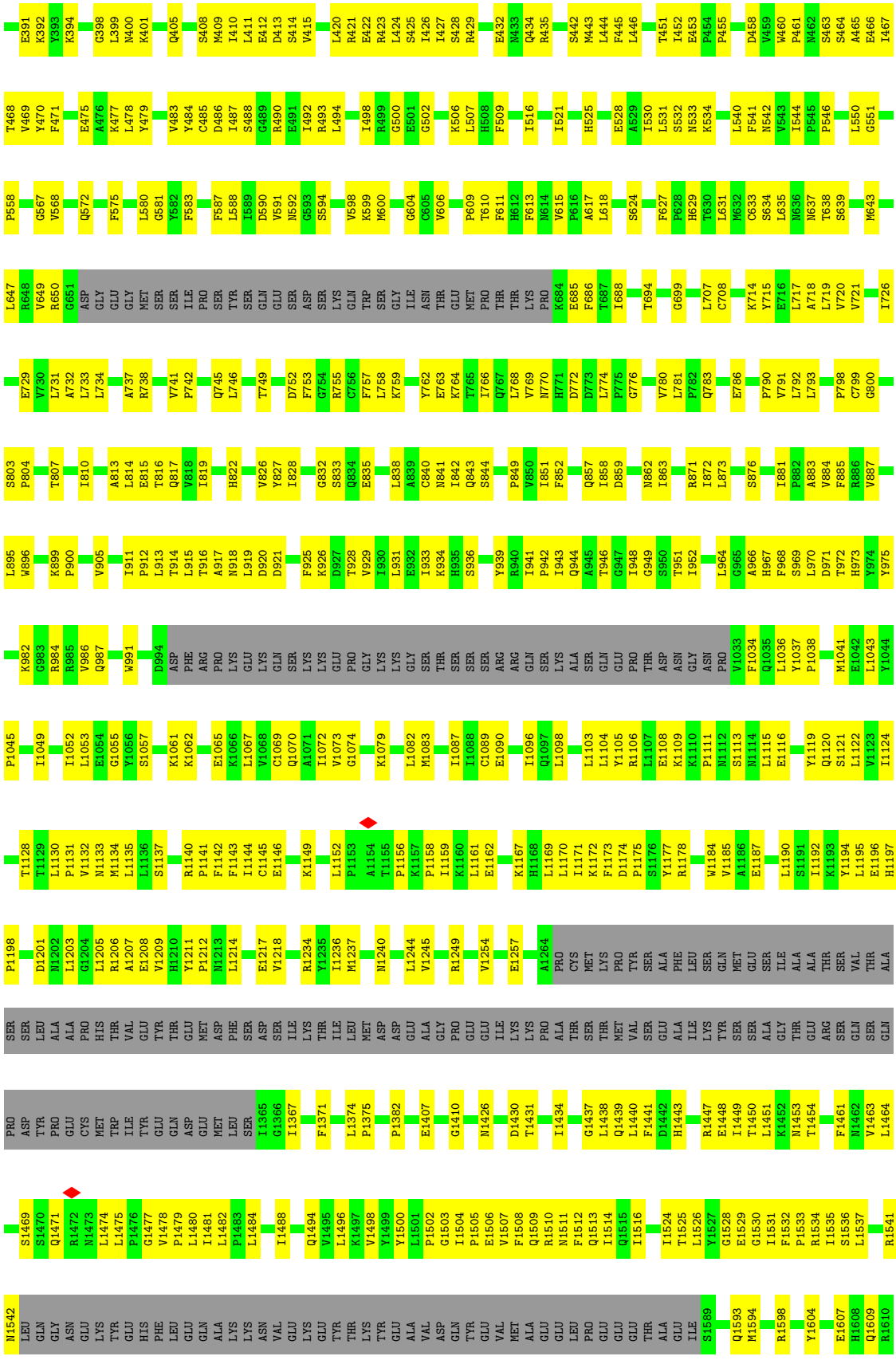


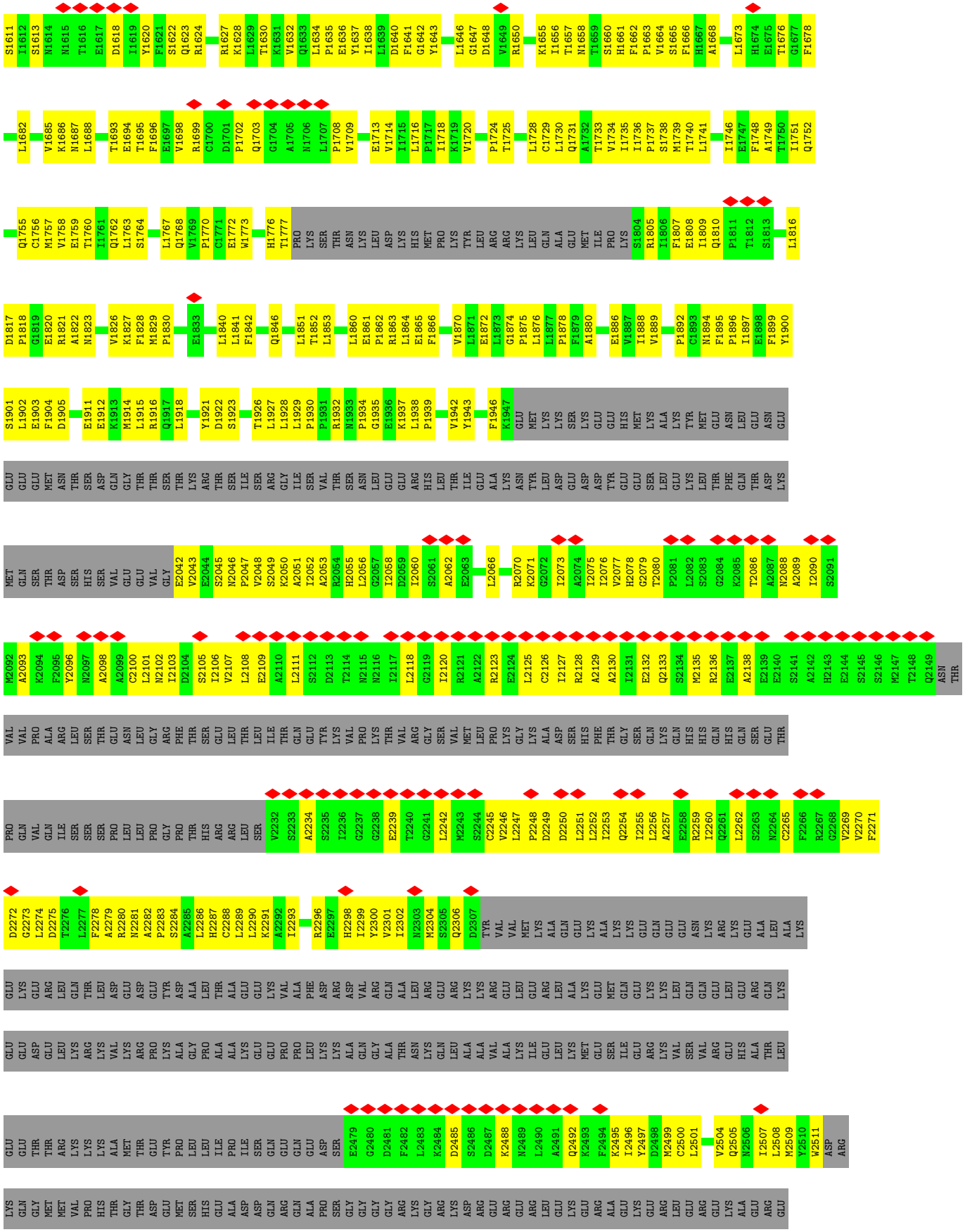
• Molecule 34: Hydrocephalus-inducing protein

Chain 4I:





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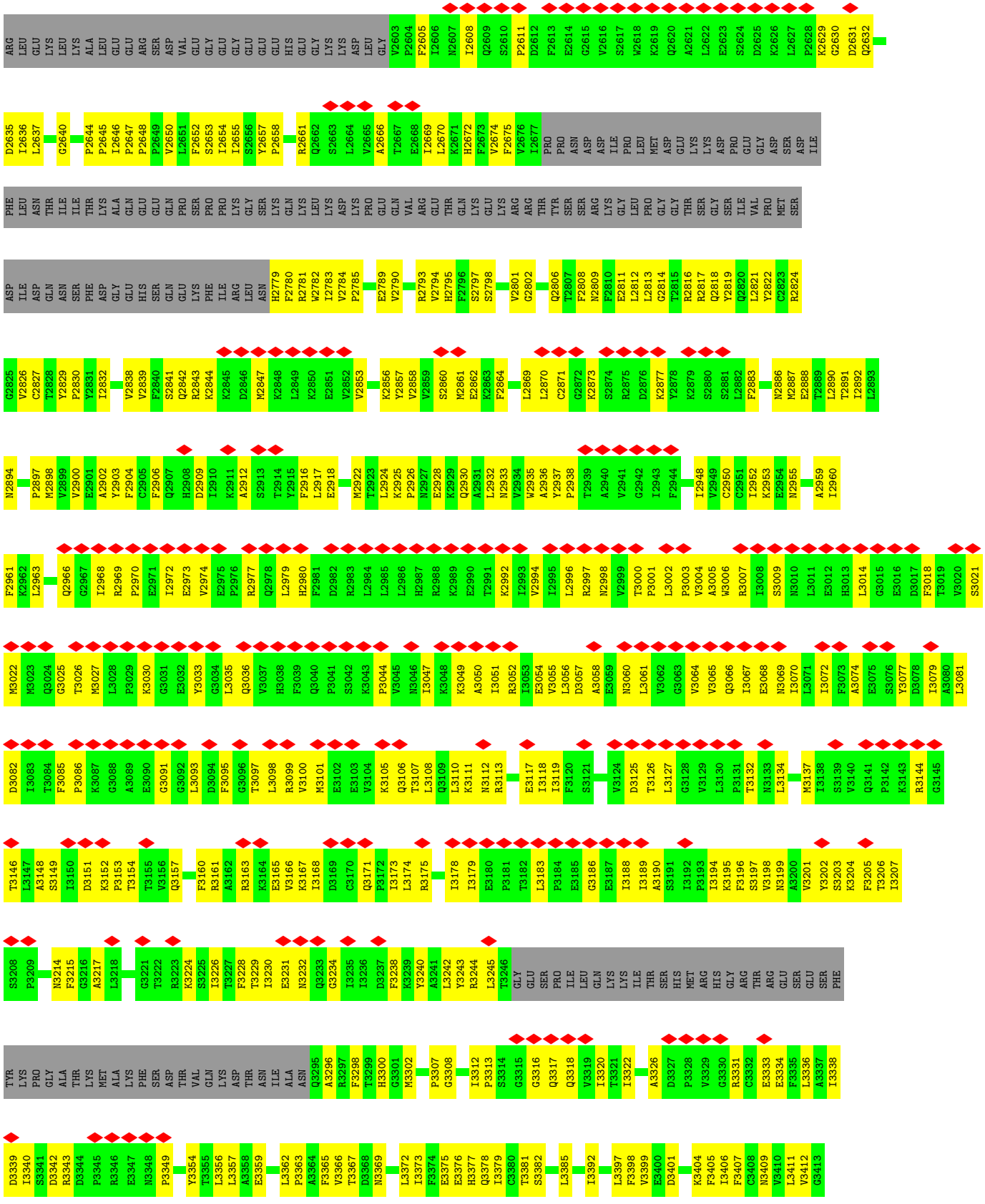
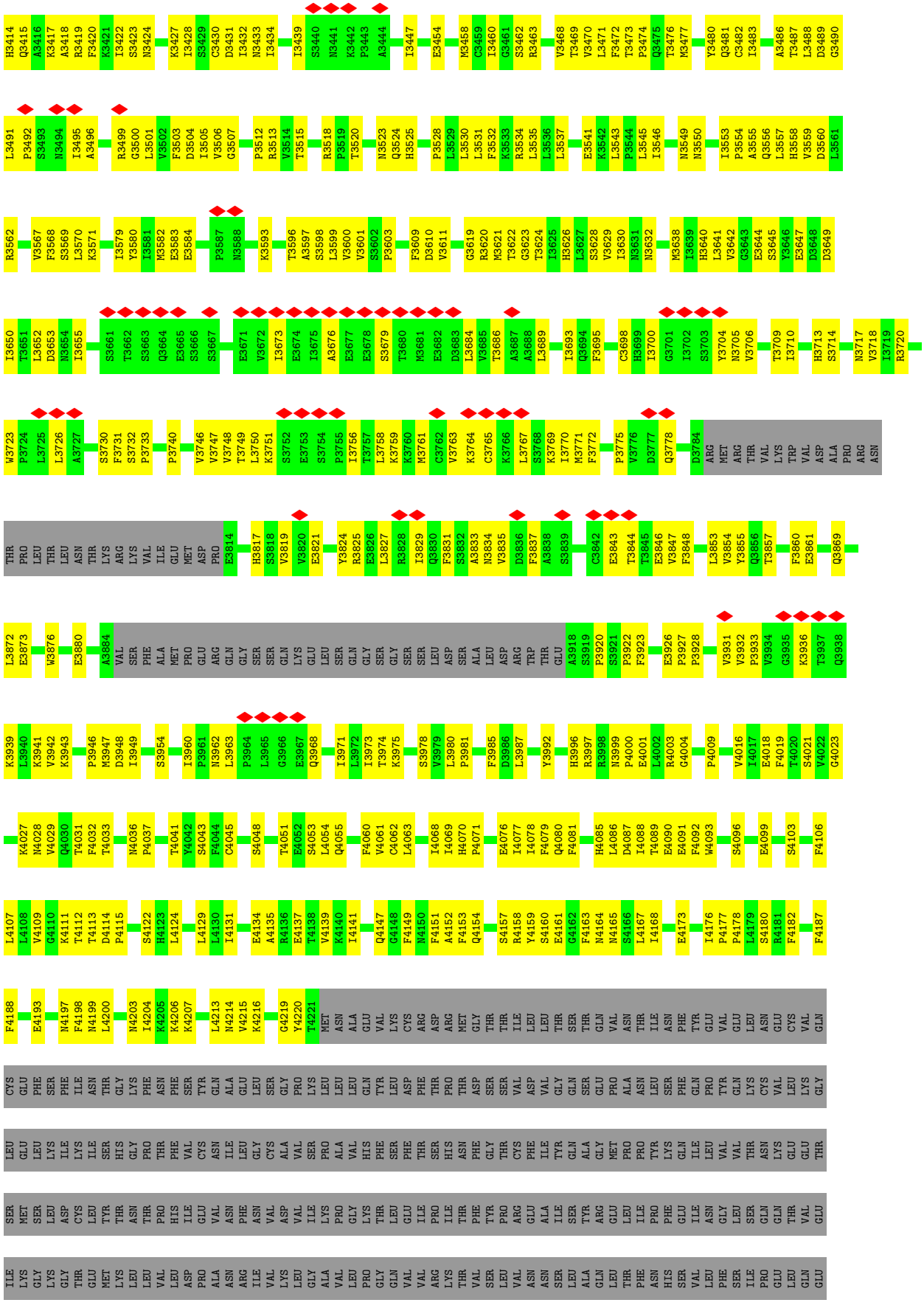
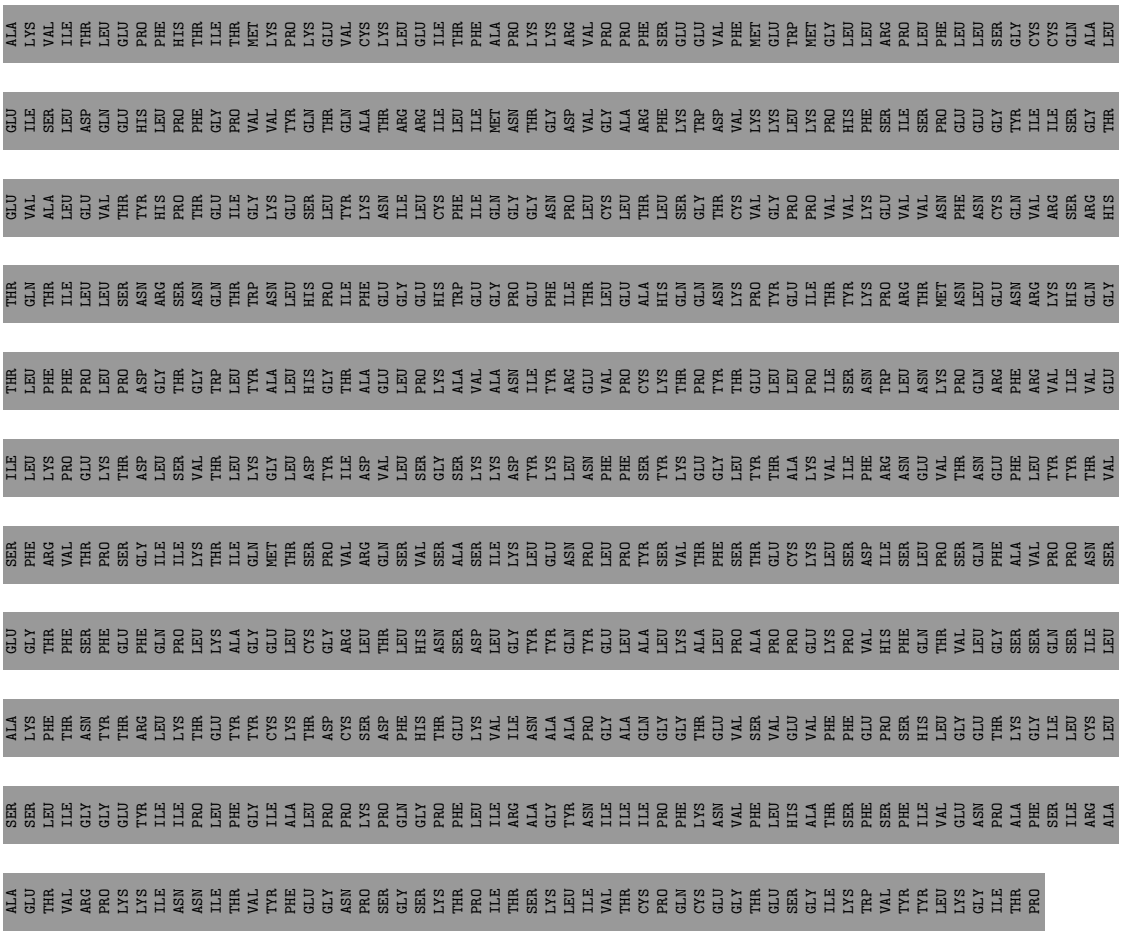
L1682 V1685 K1686 N1687 L1688 T1693 E1694 T1695 F1696 E1697 V1698 R1699 C1700 D1701 P1702 Q1703 G1704 A1705 N1706 L1707 P1708 V1709 E1713 V1714 I1715 L1716 P1717 I1718 K1719 V1720 P1724 T1725 L1728 C1729 L1730 Q1731 A1732 T1733 V1734 I1735 I1736 P1737 S1738 M1739 T1740 L1741 I1746 E1747 F1748 A1749 T1750 I1751 Q1752
Q1755 C1756 M1757 V1758 E1759 T1760 I1761 Q1762 L1763 S1764 L1767 Q1768 V1769 P1770 C1771 E1772 W1773 H1776 T1777 PRO LYS SER THR ASN LYS LEU ASP LYS HIS MET PRO LYS TYR LEU ARG ARG LYS LEU GLN ALA GLU MET ILE PRO LYS S1804 R1805 I1806 F1807 E1808 I1809 Q1810 P1811 T1812 S1813 L1816
D1817 P1818 G1819 E1820 R1821 A1822 N1823 V1826 K1827 F1828 M1829 P1830 E1833 L1840 L1841 F1842 Q1846 L1851 T1852 L1853 L1860 E1861 P1862 R1863 L1864 E1865 F1866 V1870 L1871 E1872 L1873 G1874 P1875 L1876 L1877 P1878 F1879 A1880 E1886 V1887 I1888 V1889 P1892 C1893 N1894 F1895 P1896 I1897 E1898 F1899 Y1900
S1901 L1902 E1903 F1904 D1905 E1911 E1912 K1913 M1914 L1915 R1916 Q1917 L1918 Y1921 D1922 S1923 T1926 L1927 L1928 L1929 P1930 P1931 R1932 N1933 P1934 G1935 E1936 K1937 L1938 P1939 V1942 Y1943 F1946 K1947 GLU MET LYS LYS SER LYS GLU GLU HIS MET LYS ALA LYS TYR MET GLU ASN LEU GLU ASN GLU
GLU GLU GLU MET ASN THR SER ASP GLN GLY THR THR SER THR LYS ARG THR SER ILE SER ARG GLY ILE SER VAL THR SER ASN LEU GLU GLU ARG HIS LEU THR ILE GLU ALA LYS ASN TYR LEU ASP GLU ASP ASP TYR GLU GLU SER LEU GLU LYS LEU THR PHE GLN THR ASP LYS
MET GLN SER THR ASP SER HIS SER VAL GLU GLU VAL GLY E2042 V2043 E2044 S2045 N2046 P2047 V2048 S2049 K2050 A2051 I2052 A2053 R2054 H2055 L2056 G2057 I2058 D2059 I2060 S2061 A2062 E2063 L2066 R2070 K2071 G2072 I2073 A2074 I2075 I2076 V2077 H2078 G2079 T2080 P2081 L2082 S2083 G2084 K2085 T2086 A2087 N2088 A2089 I2090 S2091
M2092 A2093 K2094 F2095 Y2096 N2097 A2098 A2099 C2100 L2101 N2102 I2103 D2104 S2105 I2106 V2107 L2108 E2109 A2110 L2111 S2112 D2113 T2114 N2115 N2116 I2117 L2118 G2119 I2120 R2121 A2122 R2123 E2124 L2125 C2126 I2127 R2128 A2129 A2130 I2131 E2132 Q2133 S2134 M2135 R2136 E2137 A2138 E2139 E2140 S2141 A2142 H2143 E2144 S2145 S2146 M2147 T2148 Q2149 ASN THR
VAL VAL PRO ALA ARG LEU SER THR GLU ASN LEU GLY ARG PHE THR SER GLU LEU THR LEU ILE THR GLN GLU TYR LYS VAL PRO LYS THR VAL ARG GLY SER VAL MET LEU PRO LYS GLY LYS ALA ASP SER HIS PHE THR GLY SER GLN LYS GLN HIS HIS GLN HIS GLN SER GLU THR
PRO GLN VAL GLN ILE SER SER SER PRO LEU LEU PRO GLY PRO THR HIS ARG ARG LEU SER V2232 S2233 A2234 S2235 I2236 G2237 G2238 E2239 T2240 G2241 L2242 M2243 S2244 C2245 V2246 L2247 P2248 D2249 D2250 L2251 L2252 I2253 Q2254 I2255 L2256 A2257 E2258 R2259 I2260 Q2261 L2262 S2263 N2264 C2265 F2266 R2267 G2268 V2269 V2270 F2271
D2272 G2273 L2274 D2275 T2276 L2277 F2278 A2279 R2280 N2281 A2282 P2283 S2284 A2285 L2286 H2287 C2288 L2289 L2290 K2291 A2292 I2293 R2296 E2297 H2298 I2299 Y2300 V2301 I2302 N2303 M2304 S2305 Q2306 D2307 TYR VAL VAL MET LYS ALA GLN GLU LYS ALA LYS GLU GLN GLU GLU ASN LYS ARG LYS ALA LEU ALA LYS
GLU LYS GLU ARG LEU GLN THR LEU ASP GLU ASP GLU TYR ASP ALA LEU THR ALA GLU GLU LYS VAL ALA PHE ASP ARG ASP VAL ARG GLN ALA LEU ARG GLU ARG LYS LYS ARG GLU LEU ALA LYS GLU MET GLN GLU LYS LYS LEU GLN GLN GLU GLN LEU GLU ARG GLN
GLU GLU ASP GLU LEU LYS ARG LYS VAL LYS ARG PRO LYS ALA GLY PRO ALA ALA LYS GLU GLU PRO PRO LEU LYS LYS ALA GLN GLY ALA THR ASN LYS GLN LEU ALA ALA LYS ILE GLU LEU LYS MET GLU SER ILE GLU ARG LYS VAL SER VAL ARG GLU HIS ALA THR LEU
GLU GLU THR THR ARG LYS LYS ALA MET THR GLU TYR PRO LEU LEU ILE PRO ILE SER GLN GLU GLN GLU ASP SER E2479 G2480 D2481 F2482 L2483 K2484 D2485 S2486 D2487 K2488 N2489 L2490 A2491 Q2492 K2493 F2494 K2495 I2496 Y2497 D2498 M2499 C2500 L2501 V2504 Q2505 N2506 I2507 L2508 M2509 Y2510 W2511 ASP ARG
LYS GLN GLY MET MET VAL PRO HIS THR GLY THR ASP GLU MET SER HIS GLU ALA ASP ASP GLN ARG GLN ALA PRO SER GLY GLY GLY ARG LYS GLY ARG LYS ASP ARG GLU ARG GLU ARG LEU GLU LYS GLU ARG ALA ALA GLU LYS GLU ARG LEU GLU ARG GLU LYS ALA GLU ARG GLU

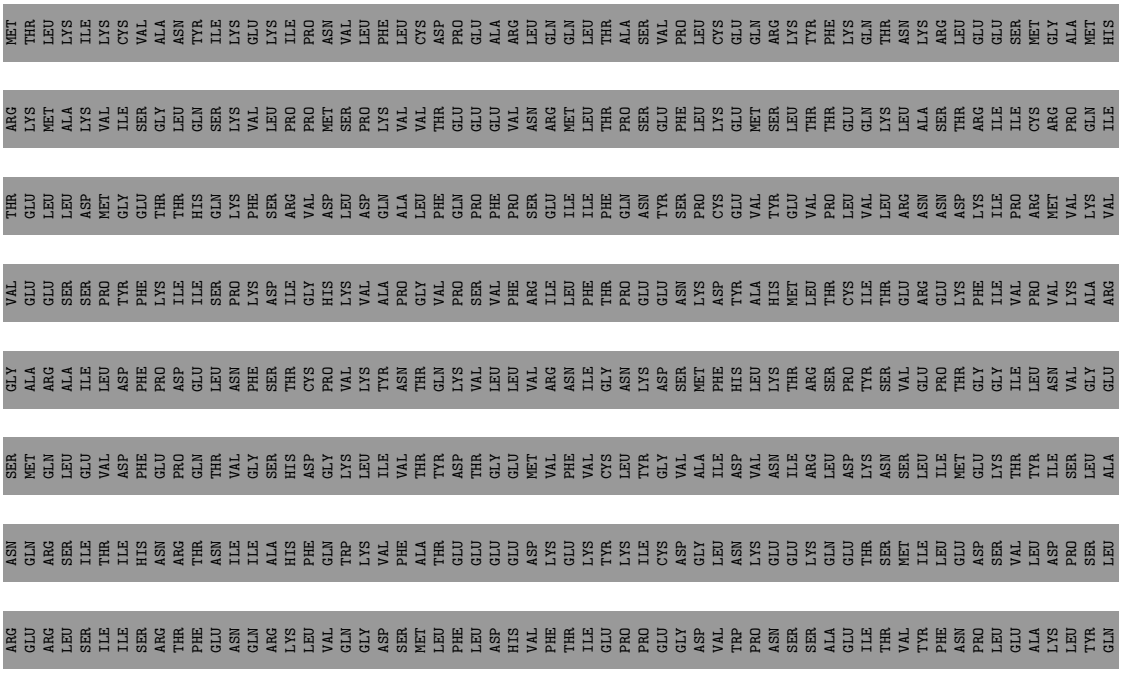


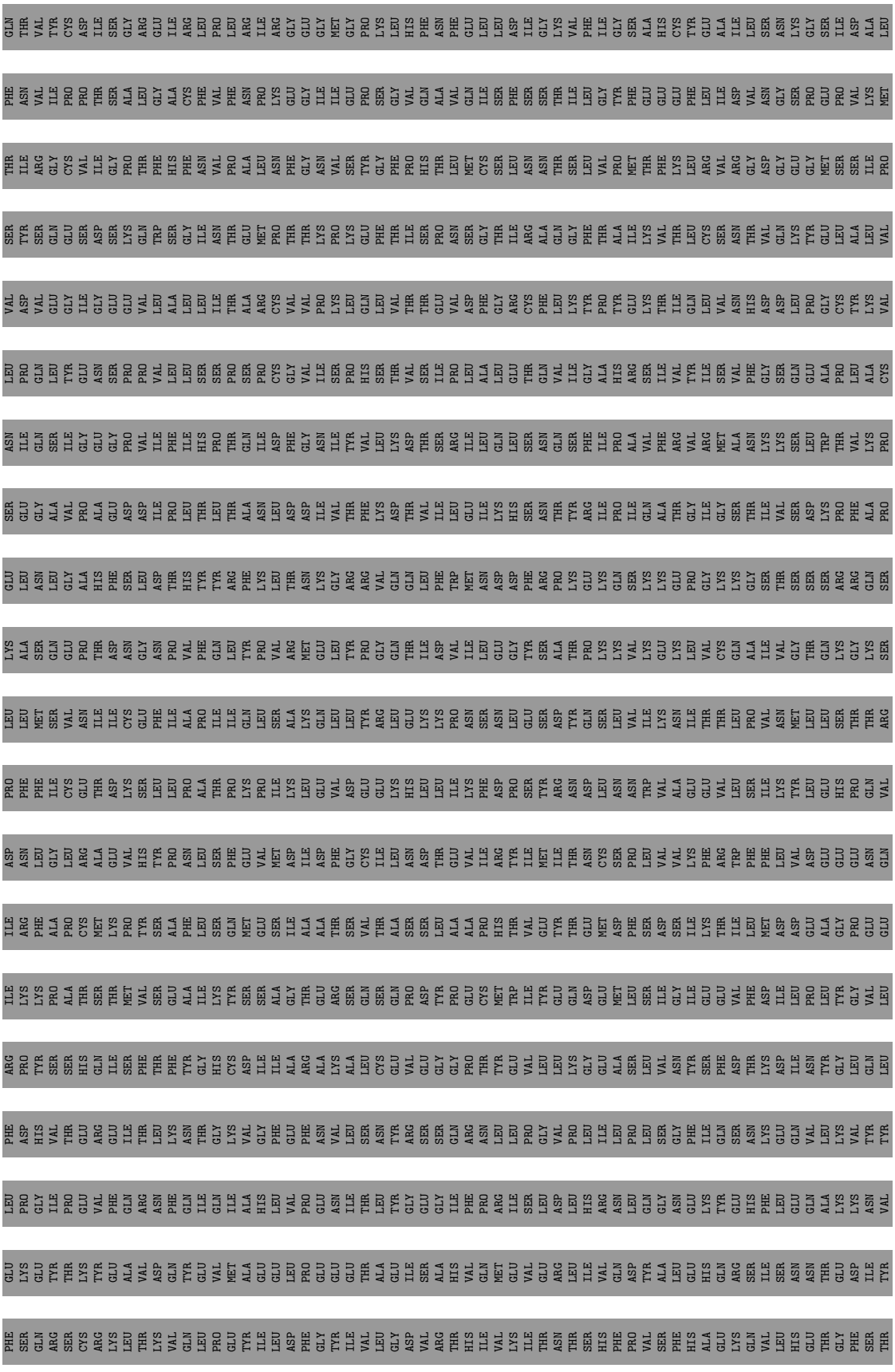




• Molecule 34: Hydrocephalus-inducing protein

Chain 4J:




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

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

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

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

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

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

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

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

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

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

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

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

ASP GLU ASP GLU TYR ASP ALA LEU THR LEU GLU GLU LYS VAL ALA VAL ARG GLN ALA LEU ARG GLU ARG LYS LYS ARG GLU LEU ALA LYS GLU MET GLN GLU LYS LYS LEU GLU LEU GLN LEU GLU ASP GLU LEU LYS LYS

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

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

HIS THR GLY THR ASP GLU MET SER HIS GLU ALA ASP ASP GLN ARG GLN ALA PRO SER GLY GLY GLY GLY ARG LYS GLY GLU ARG GLU ARG GLU ARG LEU LYS GLU ARG LYS ASP ARG ARG GLU GLU LYS LYS GLU LYS GLU ARG ALA GLU ARG GLU LYS ALA GLU ARG GLU ARG LEU GLU LYS LEU LYS ALA

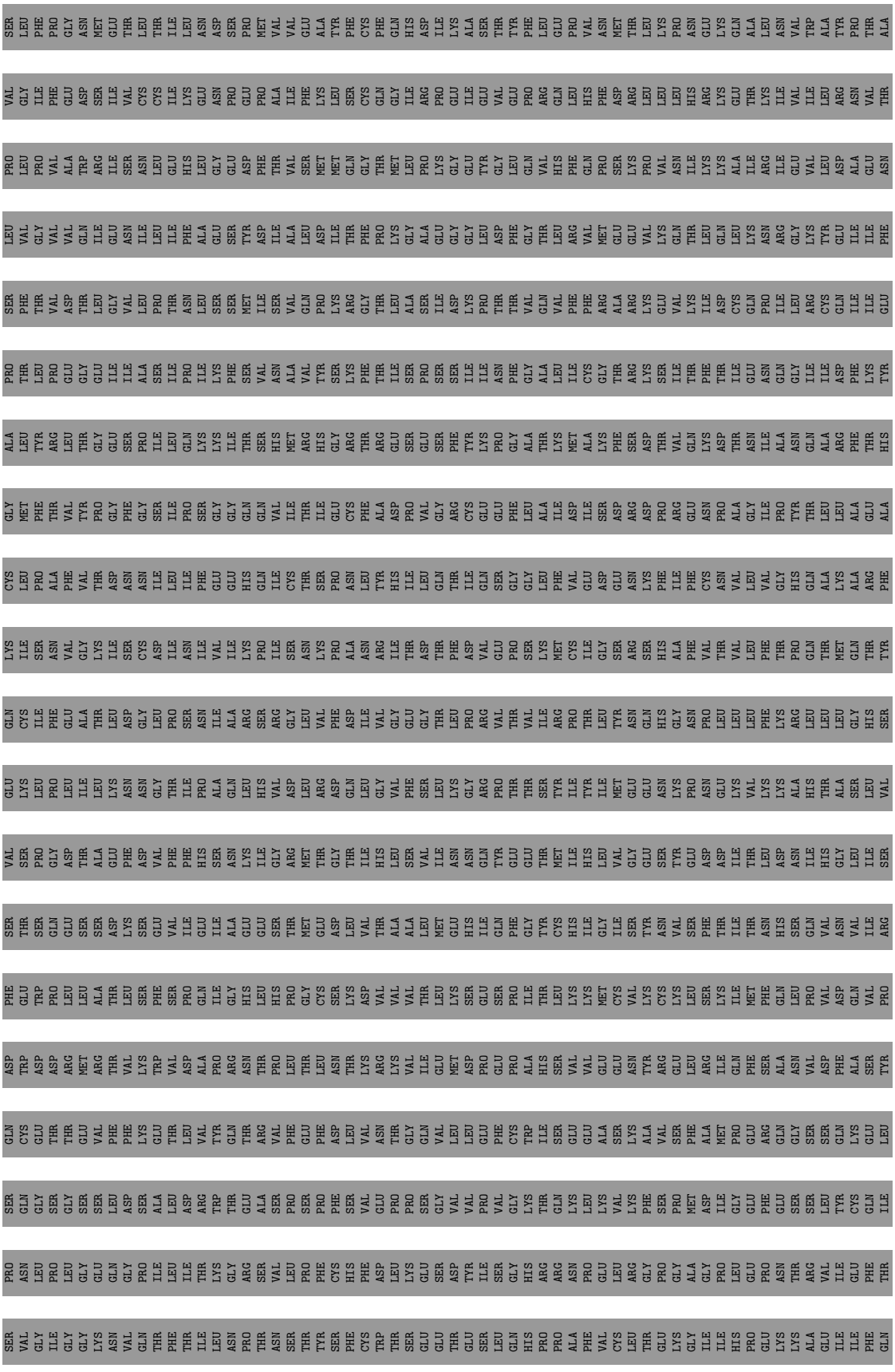
LEU GLU GLU ARG SER ASP VAL GLU GLY GLU GLY GLU GLY LYS LYS ASP ALA GLY VAL PRO PHE ILE ASN ILE GLN SER PRO ASP PHE GLU GLY VAL SER TRP LYS GLN ALA LEU GLU SER GLU LEU PRO LYS GLY ASP PRO ILE LEU LEU GLY LEU GLY

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

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

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

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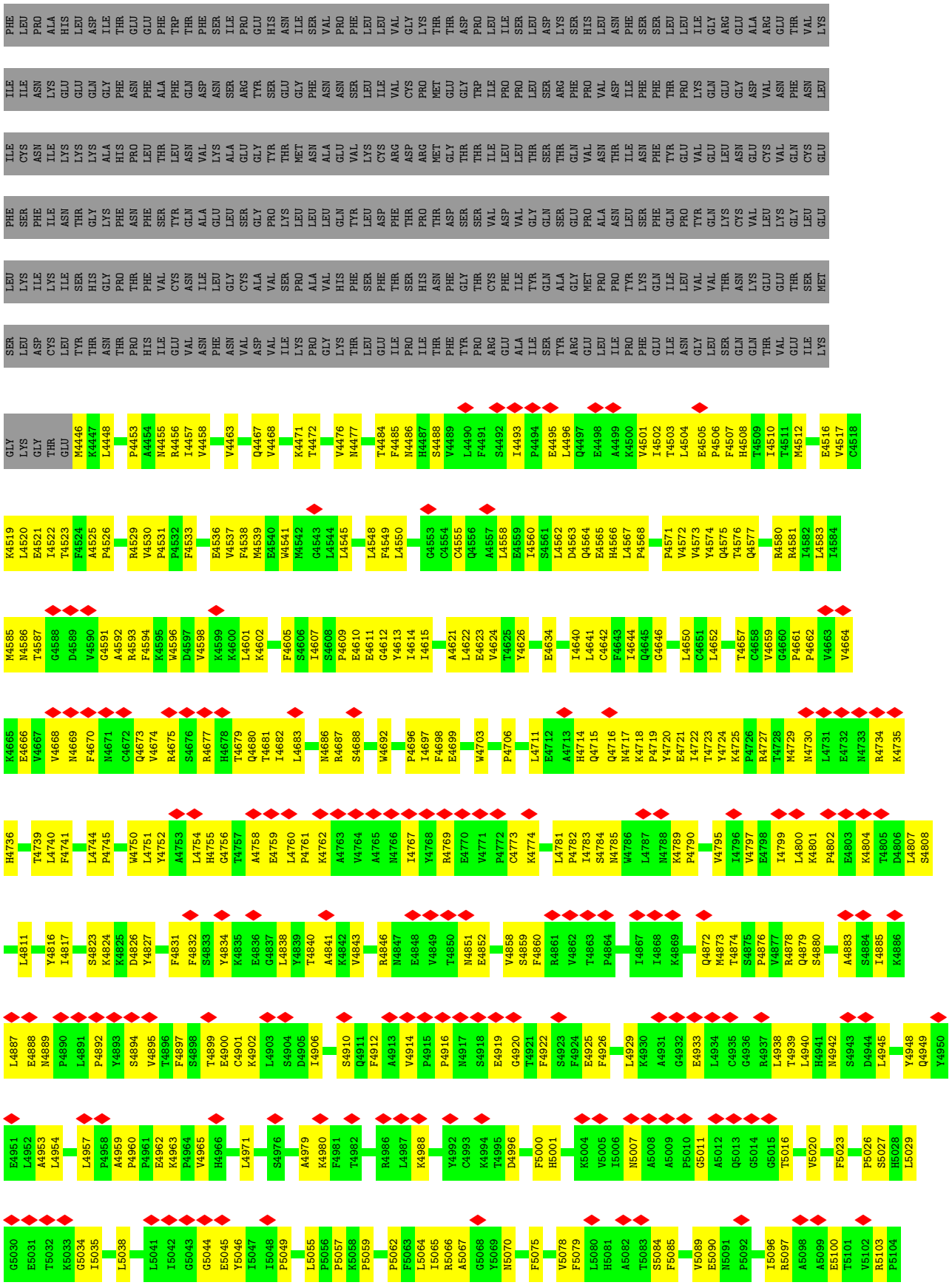
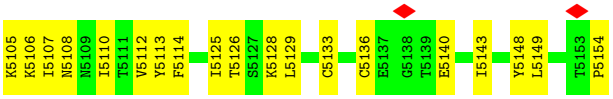
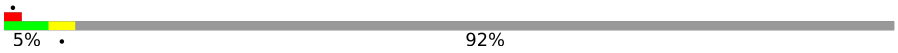
VAL GLY ILE PHE GLU ASP SER ILE VAL CYS CYS ILE LYS GLU ASN PRO GLU PRO ALA ILE PHE LYS LEU SER CYS GLN GLY ILE ARG PRO GLU ILE GLU VAL GLU PRO ARG GLN LEU HIS PHE GLN PRO SER LYS PRO VAL ASN ILE LYS LYS GLY GLU ILE LEU GLN LEU LEU LEU HIS ARG LYS GLU THR LYS ILE VAL ILE LEU ARG ASN VAL THR
PRO LEU PRO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


PHE LEU PRO ALA HIS LEU ASP ILE THR GLU GLU PHE TRP THR PHE SER ILE PRO GLU HIS ASN ILE SER LEU ASP LYS SER LEU LEU ILE SER GLU PRO LEU ASP PRO LEU LEU GLY LYS THR THR ASP PRO LEU LEU ILE GLY ARG GLU ALA ARG GLU THR VAL LYS
ILE ILE ASN LYS GLU GLN GLY PHE ASN PHE PHE ALA PHE GLN ASP ASN SER ARG TYR SER GLU GLY PHE ASN ASN SER LEU ILE VAL CYS PRO MET GLU GLY TRP ILE PRO PRO LEU SER ARG PHE PRO VAL ASP ILE PHE PHE THR PRO LYS GLN GLU GLY ASP VAL ASN PHE ASN LEU
ILE CYS ASN ILE LYS LYS LYS LYS ALA HIS PRO LEU THR LEU ASN VAL LYS ALA GLU GLY TYR THR MET ASN ALA GLU VAL LYS CYS ARG ASP ARG MET GLY THR THR ILE LEU LEU THR SER THR GLN VAL ASN THR ILE ASN PHE TYR GLU VAL GLU LEU ASN ASN GLU CYS VAL ASN GLU CYS VAL GLN GLU
PHE SER PHE ILE ASN THR GLY LYS PHE ASN PHE SER TYR GLN ALA GLU LEU SER GLY PRO LYS LEU LEU LEU ASP PHE THR PRO THR ASP SER SER VAL ASP VAL GLY GLN SER THR GLU PRO ALA ASN LEU SER PHE GLN PRO TYR GLN LYS CYS VAL LEU LYS GLY LEU GLU
LEU LYS ILE LYS ILE SER HIS GLY PRO THR PHE VAL CYS ASN ILE LEU GLY CYS ALA VAL SER PRO ALA ALA VAL HIS PHE SER TYR SER HIS CYS THR ASN LYS GLU GLU THR SER MET
SER LEU ASP CYS LEU TYR THR ASN THR PRO HIS ILE GLU VAL ASN PHE ASN VAL ASP VAL ILE LYS PRO ALA ILE SER TYR ARG GLU LEU ILE PRO GLY LYS THR LEU GLU PHE TYR PRO ARG GLU ALA ILE SER GLN GLN THR VAL GLU ILE LYS
GLY LYS GLY THR GLU M4446 K4447 L4448 P4453 A4454 N4455 R4456 I4457 V4458 V4463 Q4467 V4468 K4471 T4472 V4476 N4477 T4484 F4485 N4486 H4487 S4488 V4489 L4490 F4491 S4492 I4493 P4494 E4495 L4496 Q4497 E4498 A4499 K4500 V4501 I4502 T4503 L4504 E4505 P4506 F4507 H4508 T4509 I4510 T4511 M4512 E4516 V4517 C4518
K4519 L4520 E4521 I4522 T4523 F4524 A4525 P4526 R4529 V4530 P4531 P4532 F4533 E4536 V4537 F4538 M4539 E4540 W4541 M4542 G4543 L4544 L4545 L4548 F4549 L4550 G4553 C4554 C4555 Q4556 A4557 L4558 E4559 I4560 S4561 L4562 D4563 Q4564 E4565 H4566 L4567 P4568 P4571 V4572 V4573 Y4574 Q4575 T4576 Q4577 R4580 R4581 I4582 L4583 I4584
M4585 N4586 T4587 G4588 D4589 V4590 G4591 A4592 R4593 F4594 K4595 W4596 D4597 V4598 K4599 K4600 L4601 K4602 F4605 S4606 I4607 S4608 P4609 E4610 E4611 G4612 Y4613 I4614 I4615 A4621 L4622 E4623 V4624 T4625 Y4626 E4634 I4640 L4641 C4642 F4643 I4644 Q4645 G4646 L4650 C4651 L4652 T4657 C4658 V4659 G4660 P4661 P4662 V4663 V4664
K4665 E4666 Y4667 V4668 N4669 F4670 N4671 C4672 Q4673 V4674 R4675 S4676 R4677 H4678 T4679 Q4680 T4681 I4682 L4683 N4686 R4687 S4688 W4692 P4696 I4697 F4698 E4699 W4703 P4706 L4711 E4712 A4713 H4714 Q4715 Q4716 N4717 K4718 P4719 Y4720 E4721 I4722 T4723 Y4724 K4725 P4726 R4727 T4728 M4729 N4730 L4731 E4732 N4733 R4734 K4735
H4736 T4739 L4740 F4741 L4744 P4745 W4750 L4751 Y4752 A4753 L4754 H4755 G4756 T4757 A4758 E4759 L4760 P4761 K4762 A4763 V4764 A4765 N4766 I4767 Y4768 R4769 E4770 V4771 P4772 C4773 K4774 L4781 P4782 I4783 S4784 N4785 W4786 L4787 N4788 K4789 P4790 V4795 I4796 V4797 E4798 I4799 L4800 K4801 P4802 E4803 K4804 T4805 D4806 L4807 S4808
L4811 Y4816 I4817 S4823 K4824 K4825 D4826 Y4827 F4831 F4832 S4833 Y4834 K4835 E4836 G4837 L4838 Y4839 T4840 A4841 K4842 V4843 R4846 N4847 E4848 V4849 T4850 N4851 E4852 V4858 S4859 F4860 R4861 V4862 T4863 P4864 I4867 I4868 K4869 Q4872 M4873 T4874 S4875 P4876 V4877 R4878 Q4879 S4880 A4883 S4884 I4885 K4886
L4887 E4888 N4889 P4890 L4891 P4892 Y4893 S4894 V4895 T4896 F4897 S4898 T4899 E4900 C4901 K4902 L4903 S4904 D4905 I4906 S4910 Q4911 F4912 A4913 V4914 P4915 P4916 N4917 S4918 E4919 G4920 T4921 F4922 S4923 F4924 E4925 F4926 L4929 K4930 A4931 G4932 E4933 L4934 C4935 G4936 R4937 L4938 T4939 L4940 H4941 N4942 S4943 D4944 L4945 Y4948 Q4949 Y4950
E4951 L4952 A4953 L4954 L4957 P4958 A4959 P4960 P4961 E4962 K4963 P4964 V4965 H4966 L4971 S4976 A4979 K4980 F4981 T4982 R4986 L4987 K4988 Y4992 C4993 K4994 T4995 D4996 P5000 H5001 K5004 V5005 I5006 N5007 A5008 A5009 P5010 G5011 A5012 Q5013 G5014 G5015 T5016 V5020 F5023 P5026 S5027 H5028 L5029
G5030 E5031 T5032 K5033 G5034 I5035 L5038 L5041 I5042 G5043 G5044 E5045 Y5046 I5047 I5048 P5049 L5055 P5056 P5057 K5058 P5059 P5062 F5063 L5064 I5065 R5066 A5067 G5068 Y5069 N5070 F5075 V5078 F5079 L5080 H5081 A5082 T5083 S5084 F5085 V5089 E5090 N5091 P5092 I5096 R5097 A5098 A5099 E5100 T5101 V5102 R5103 P5104



• Molecule 34: Hydrocephalus-inducing protein

Chain 4K:



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

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

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

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

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

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

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

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

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

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

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

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

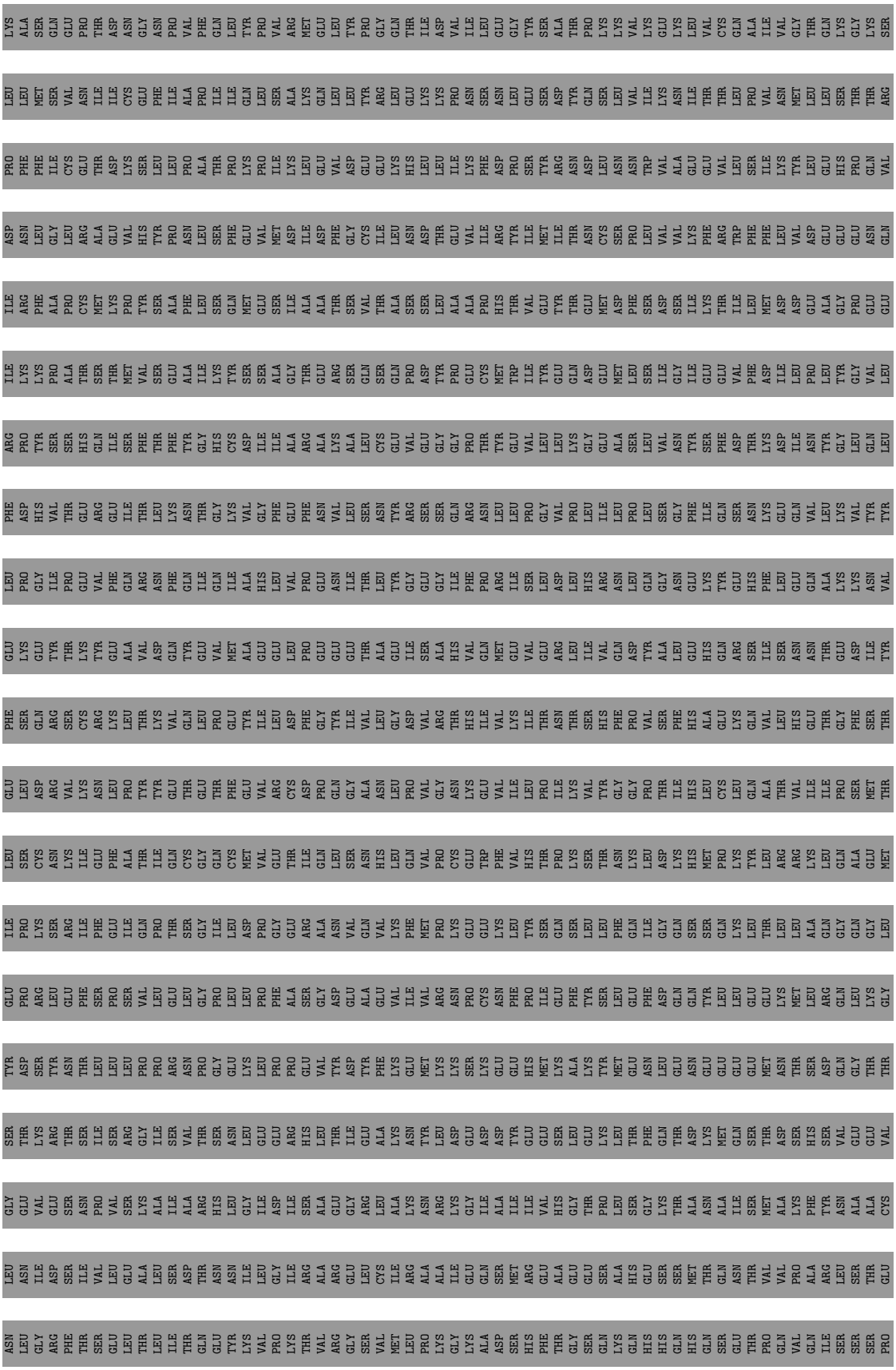
VAL ASP VAL GLU GLY GLU GLU VAL LEU ALA LEU LEU SER ILE THR ALA ARG CYS VAL VAL PRO LYS LEU GLN LEU VAL ASP PHE GLY ARG CYS PHE LEU LYS TYR PRO TYR PRO ALA GLU LYS THR ILE GLN LEU VAL ASN HIS ASP ASP LEU PRO GLY CYS TYR LYS VAL

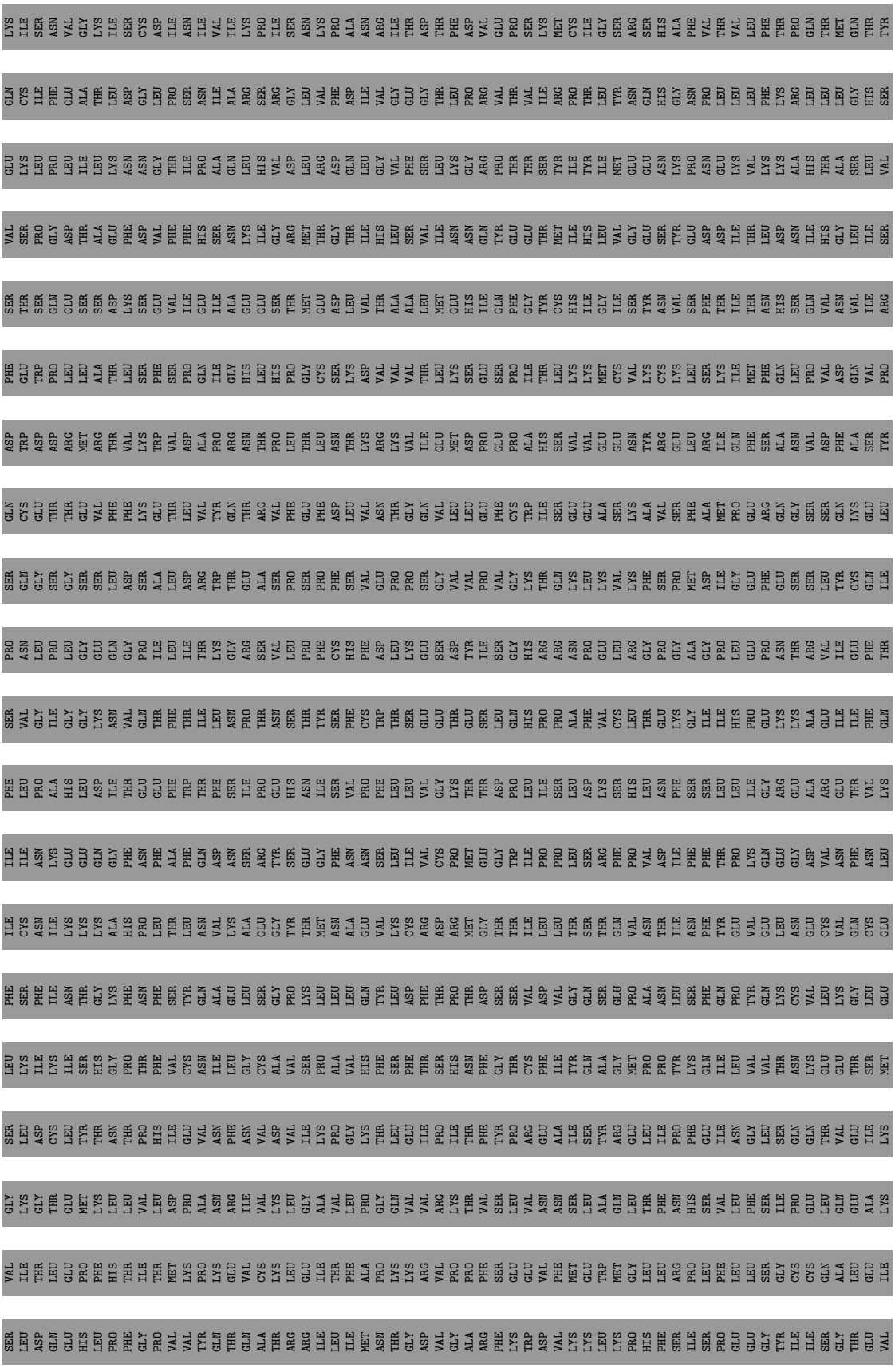
LEU PRO GLN LEU TYR GLU ASN SER PRO PRO VAL LEU LEU LEU SER SER PRO SER PRO CYS GLY VAL ILE SER PRO HIS SER THR VAL SER ILE PRO LEU ALA LEU GLU VAL ALA HIS ARG SER ILE VAL TYR ILE SER VAL PHE GLY SER GLN GLU LEU LEU ALA CYS

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

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

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


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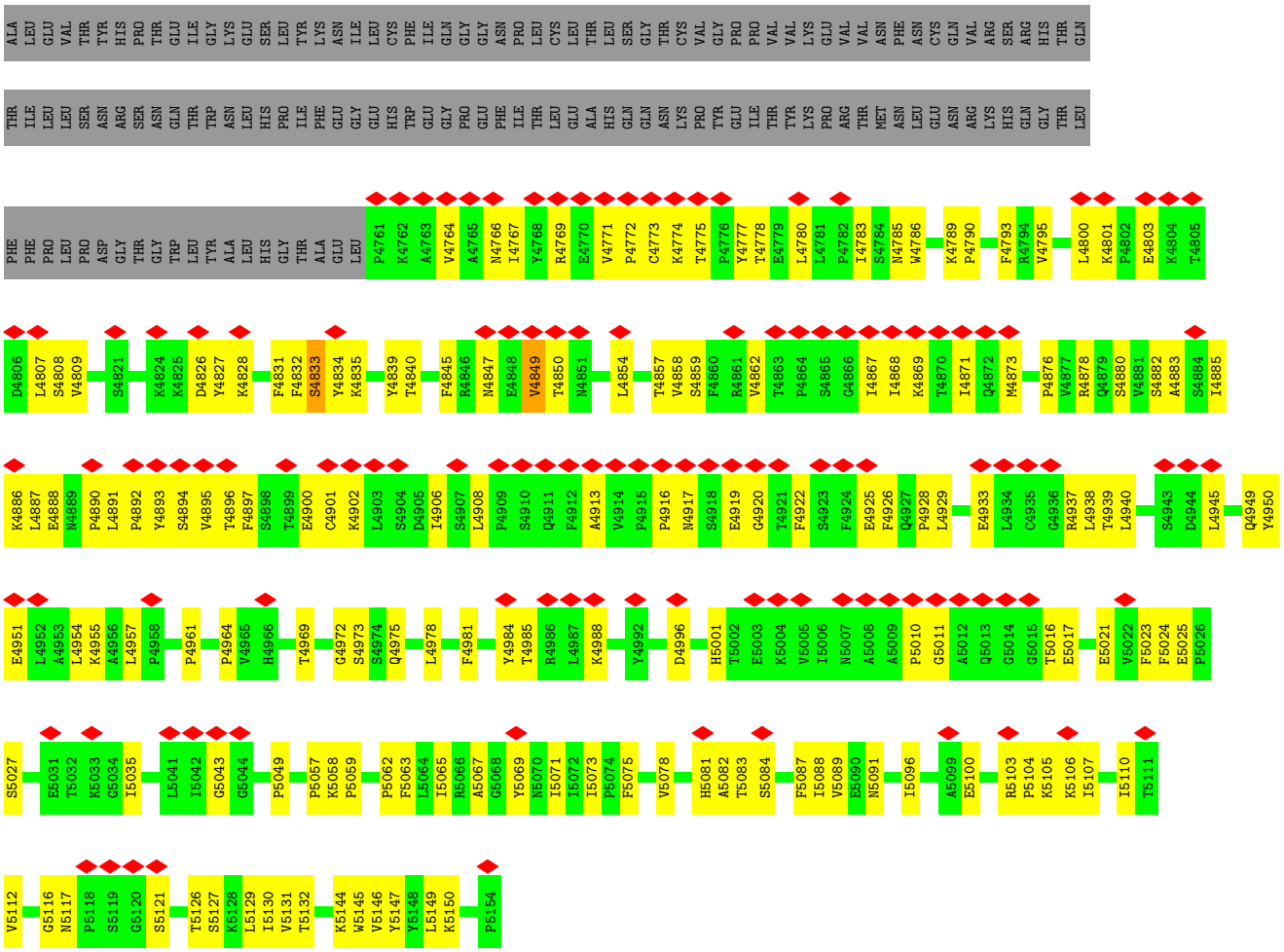
GLN CYS ILE PHE GLU ALA THR LEU ASP GLY LEU PRO SER ASN ILE ALA ARG SER ARG GLY LEU VAL PHE ASP ILE VAL GLY GLU GLY THR LEU PRO ARG VAL THR VAL ILE ARG LEU PRO SER ARG LEU LEU LEU PHE LYS ARG LEU LEU LEU GLY HIS SER
GLU LYS LEU PRO LEU ILE LEU LYS ASN ASN GLY THR ILE PRO ALA GLN LEU HIS VAL ASP LEU ARG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



• Molecule 35: Germ cell-less protein-like 1

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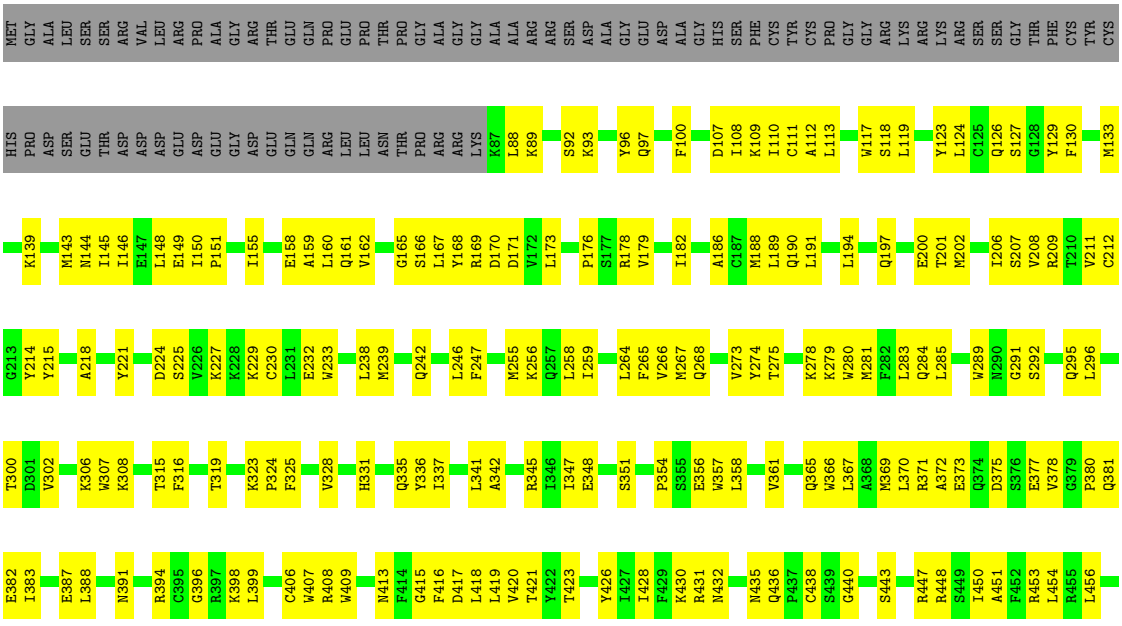

• Molecule 35: Germ cell-less protein-like 1

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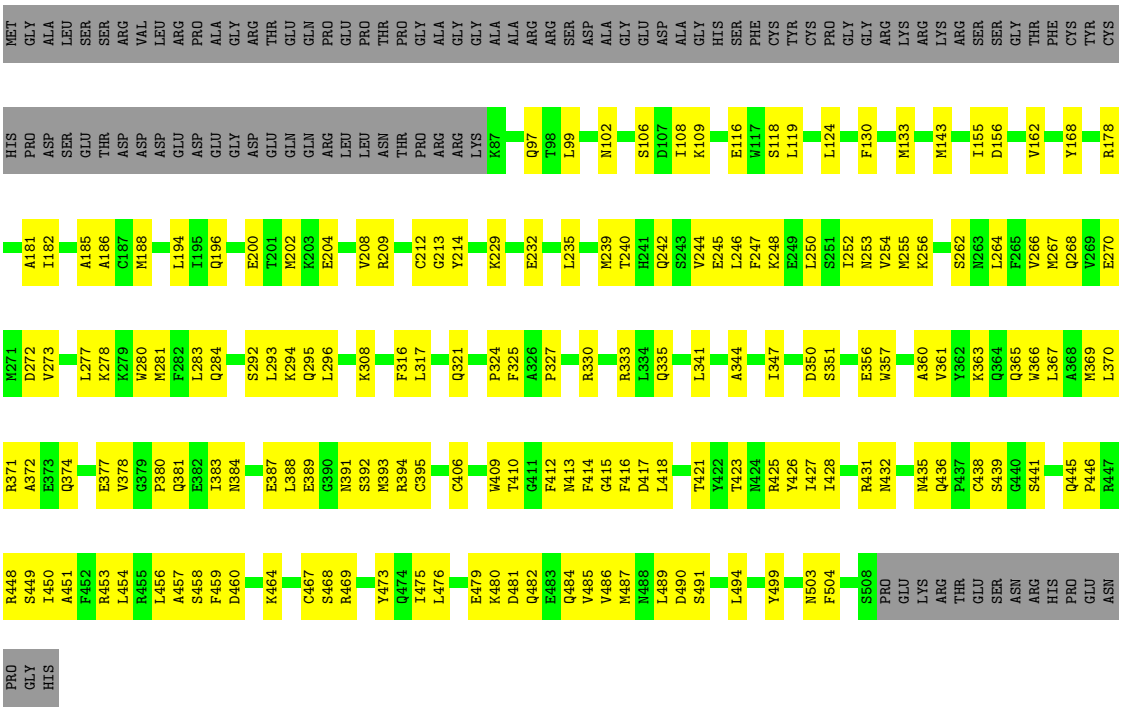

• Molecule 35: Germ cell-less protein-like 1

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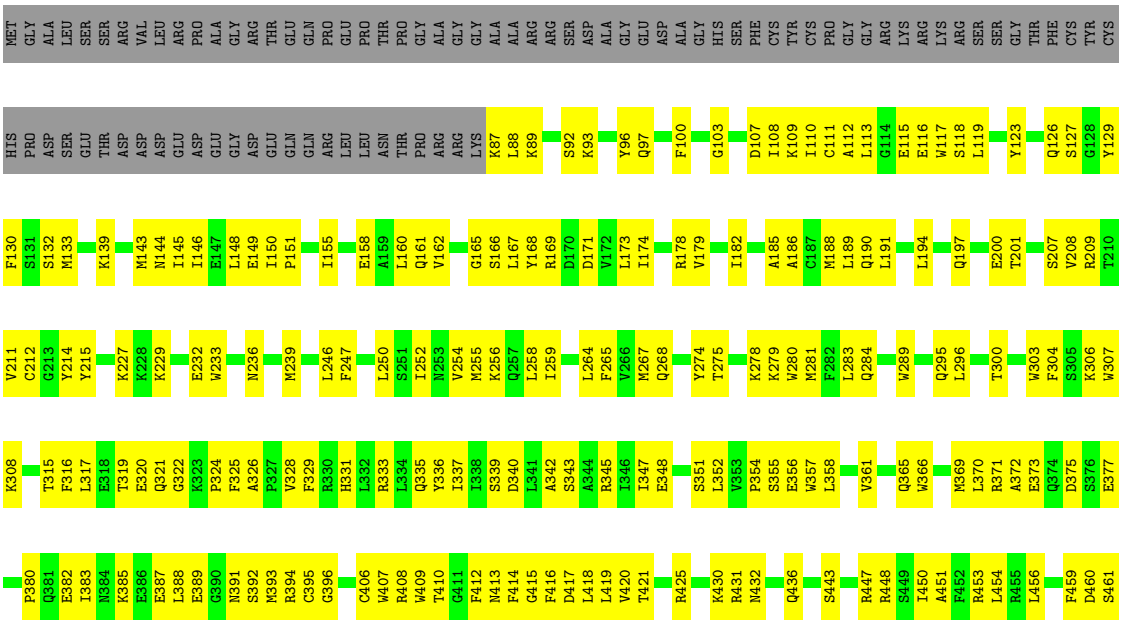

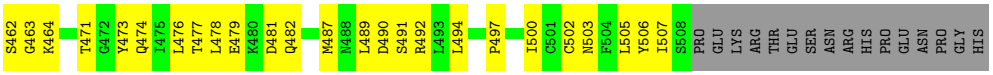

• Molecule 35: Germ cell-less protein-like 1

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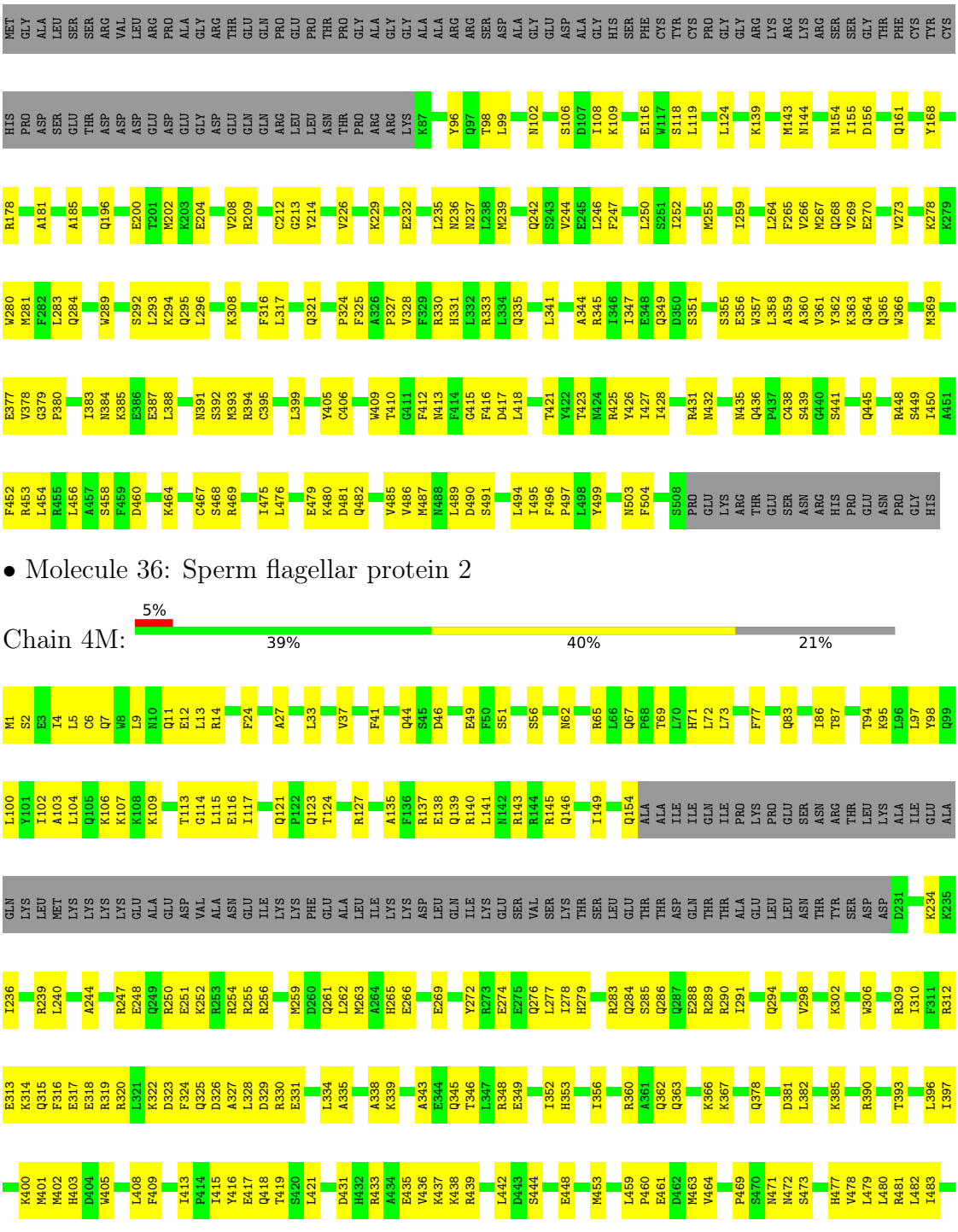
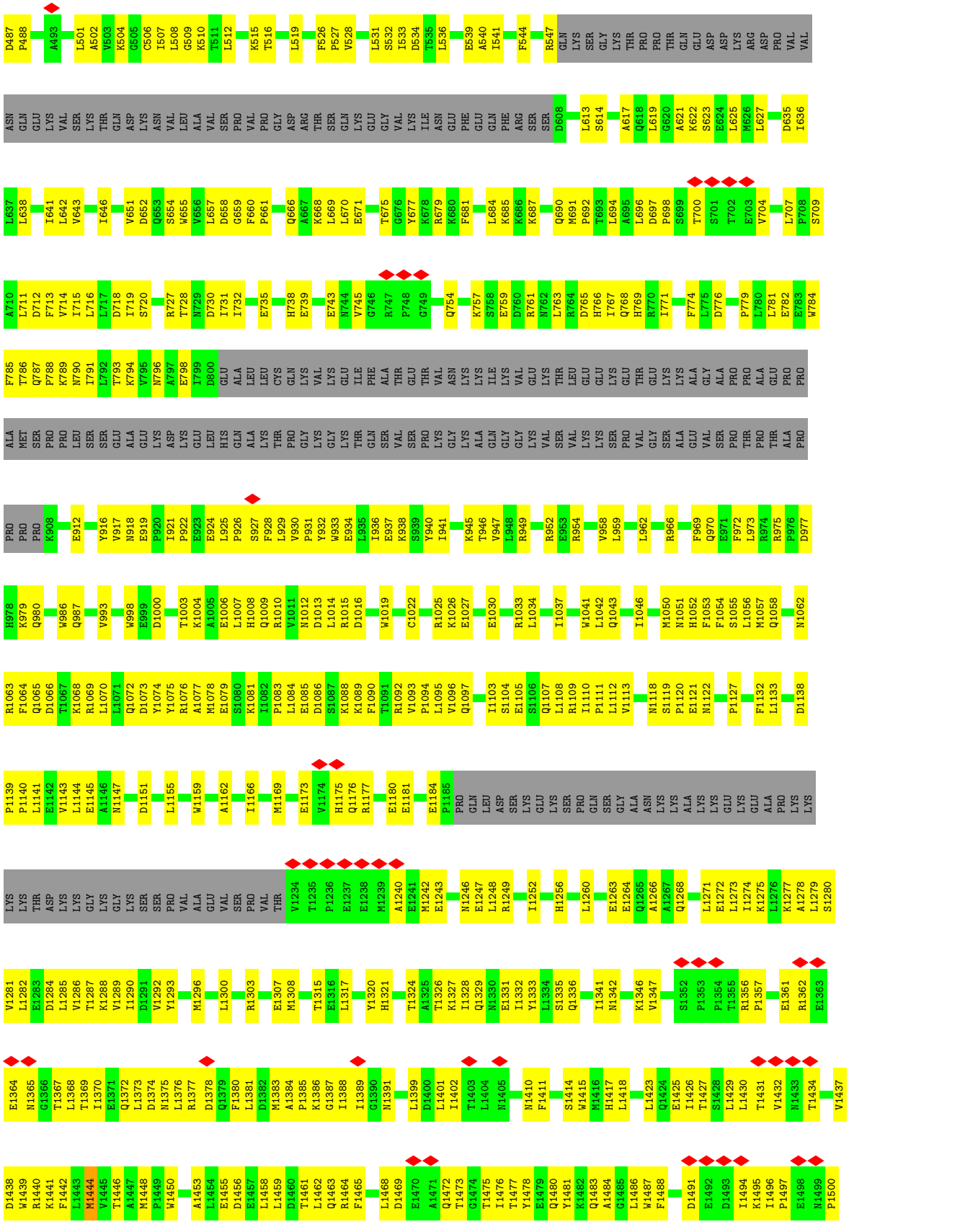


• Molecule 36: Sperm flagellar protein 2

Chain 4M: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ASN GLN GLU LYS VAL SER LYS THR GLN ASP LYS ASN VAL LEU ALA VAL SER PRO VAL PRO GLY ASP ARG THR SER GLN LYS GLU GLY VAL LYS ILE ASN GLU PHE GLU GLN PHE ARG SER SER D608 L613 S614 A617 Q618 L619 G620 A621 K622 S623 E624 L625 M626 L627 D635 I636
L637 L638 I641 L642 V643 I646 V651 D652 Q653 S654 W655 V656 L657 D658 G659 F660 P661 Q666 A667 K668 L669 L670 E671 T675 G676 Y677 K678 R679 K680 F681 L684 K685 K686 K687 Q690 M691 P692 T693 L694 A695 L696 D697 P698 S699 T700 S701 T702 E703 V704 L707 P708 S709
A710 L711 D712 F713 V714 I715 L716 L717 D718 I719 S720 R727 T728 N729 D730 I731 I732 E735 H738 E739 E743 N744 V745 G746 R747 P748 G749 Q754 K757 S758 E759 D760 R761 N762 L763 R764 D765 H766 I767 Q768 H769 R770 I771 F774 L775 D776 P779 L780 L781 E782 E783 W784
F785 T786 Q787 P788 K789 N790 I791 L792 T793 K794 V795 N796 A797 E798 T799 D800 GLU ALA LEU LEU CYS GLN LYS VAL LYS GLU ILE PHE ALA THR GLU THR VAL ASN LYS LYS ILE LYS VAL GLU LYS THR LEU GLU GLU LYS GLU THR GLU LYS LYS LYS ALA GLY ALA PRO PRO ALA GLU PRO PRO
ALA MET SER PRO PRO LEU SER SER GLU ALA GLU LYS ASP LYS GLU LEU HIS GLN ALA LEU LYS THR PRO GLY LYS GLY LYS THR GLN SER VAL SER PRO LYS GLY LYS ALA GLN GLY GLY GLY LYS VAL SER VAL LYS LYS SER PRO VAL GLY SER ALA GLU VAL SER PRO PRO THR PRO THR ALA PRO
PRO PRO PRO K908 E912 Y916 V917 N918 E919 P920 I921 P922 E923 E924 L925 P926 S927 F928 L929 V930 P931 Y932 W933 E934 L935 I936 E937 K938 S939 Y940 I941 K945 T946 V947 L948 R949 R952 E953 R954 V958 L959 L962 R966 F969 Q970 E971 F972 L973 R974 R975 P976 D977
H978 K979 Q980 W986 Q987 V993 W998 E999 D1000 T1003 K1004 A1005 E1006 L1007 H1008 Q1009 R1010 V1011 N1012 D1013 L1014 R1015 D1016 W1019 C1022 R1025 K1026 E1027 E1030 R1033 L1034 I1037 W1041 L1042 Q1043 I1046 M1050 N1051 H1052 F1053 F1054 S1055 L1056 M1057 Q1058 N1062
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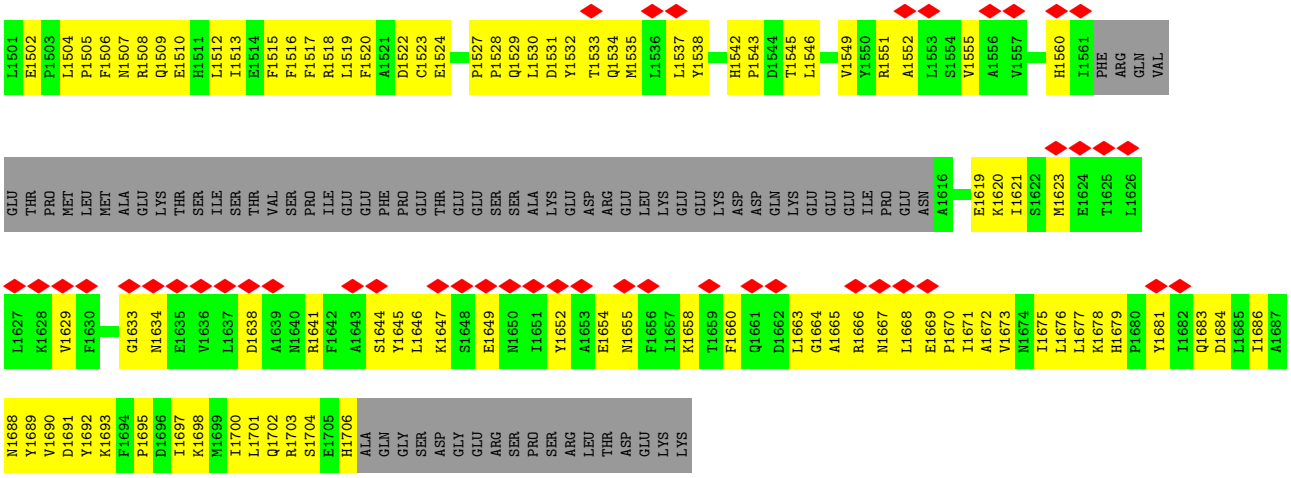
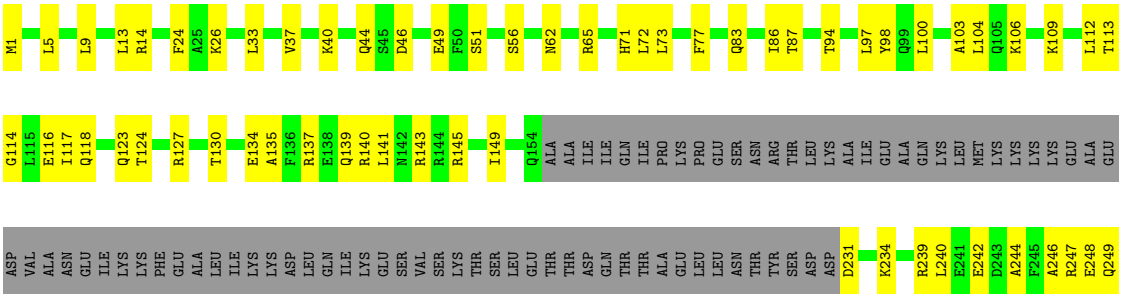
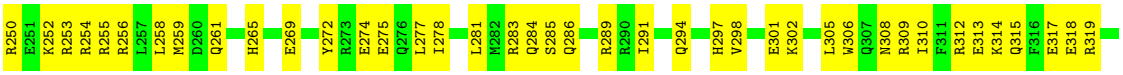
P1139 P1140 L1141 E1142 V1143 L1144 E1145 A1146 N1147 D1151 L1155 W1159 A1162 I1166 M1169 E1173 V1174 H1175 Q1176 R1177 E1180 E1181 E1184 P1185 PRO GLN LEU ASP SER LYS GLU LYS SER PRO GLN SER GLY ALA ASN LYS LYS ALA LYS LYS GLU LYS GLU ALA PRO LYS LYS
LYS THR ASP LYS LYS GLY LYS SER SER PRO VAL ALA GLU VAL SER PRO VAL THR V1234 T1235 P1236 E1237 E1238 M1239 A1240 E1241 M1242 E1243 N1246 E1247 L1248 R1249 I1252 H1256 L1260 E1263 E1264 Q1265 A1266 A1267 Q1268 L1271 E1272 L1273 I1274 K1275 L1276 K1277 A1278 L1279 S1280
V1281 L1282 E1283 D1284 L1285 V1286 T1287 K1288 V1289 I1290 D1291 V1292 Y1293 M1296 L1300 R1303 E1307 M1308 T1315 E1316 L1317 Y1320 H1321 T1324 A1325 T1326 K1327 I1328 Q1329 N1330 E1331 I1332 Y1333 L1334 S1335 Q1336 I1341 N1342 K1346 V1347 S1352 P1353 P1354 T1355 R1356 P1357 E1361 R1362 E1363
E1364 N1365 G1366 T1367 L1368 T1369 I1370 E1371 Q1372 L1373 D1374 N1375 L1376 R1377 D1378 Q1379 F1380 L1381 D1382 M1383 A1384 P1385 K1386 G1387 I1388 I1389 G1390 N1391 L1399 D1400 L1401 I1402 T1403 L1404 N1405 N1410 F1411 S1414 W1415 M1416 H1417 L1418 L1423 Q1424 E1425 I1426 T1427 S1428 L1429 L1430 T1431 V1432 N1433 T1434 V1437
D1438 W1439 R1440 K1441 F1442 L1443 M1444 V1445 T1446 A1447 M1448 P1449 W1450 A1453 L1454 E1455 D1456 E1457 L1458 L1459 D1460 T1461 L1462 Q1463 R1464 F1465 L1468 D1469 E1470 A1471 Q1472 T1473 G1474 T1475 I1476 T1477 Y1478 E1479 Q1480 Y1481 K1482 Q1483 A1484 G1485 L1486 W1487 F1488 D1491 E1492 D1493 I1494 K1495 I1496 P1497 E1498 N1499 P1500

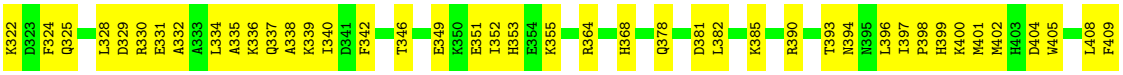


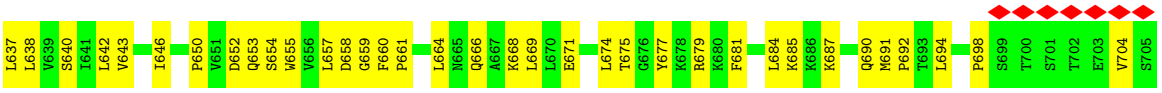
• Molecule 36: Sperm flagellar protein 2

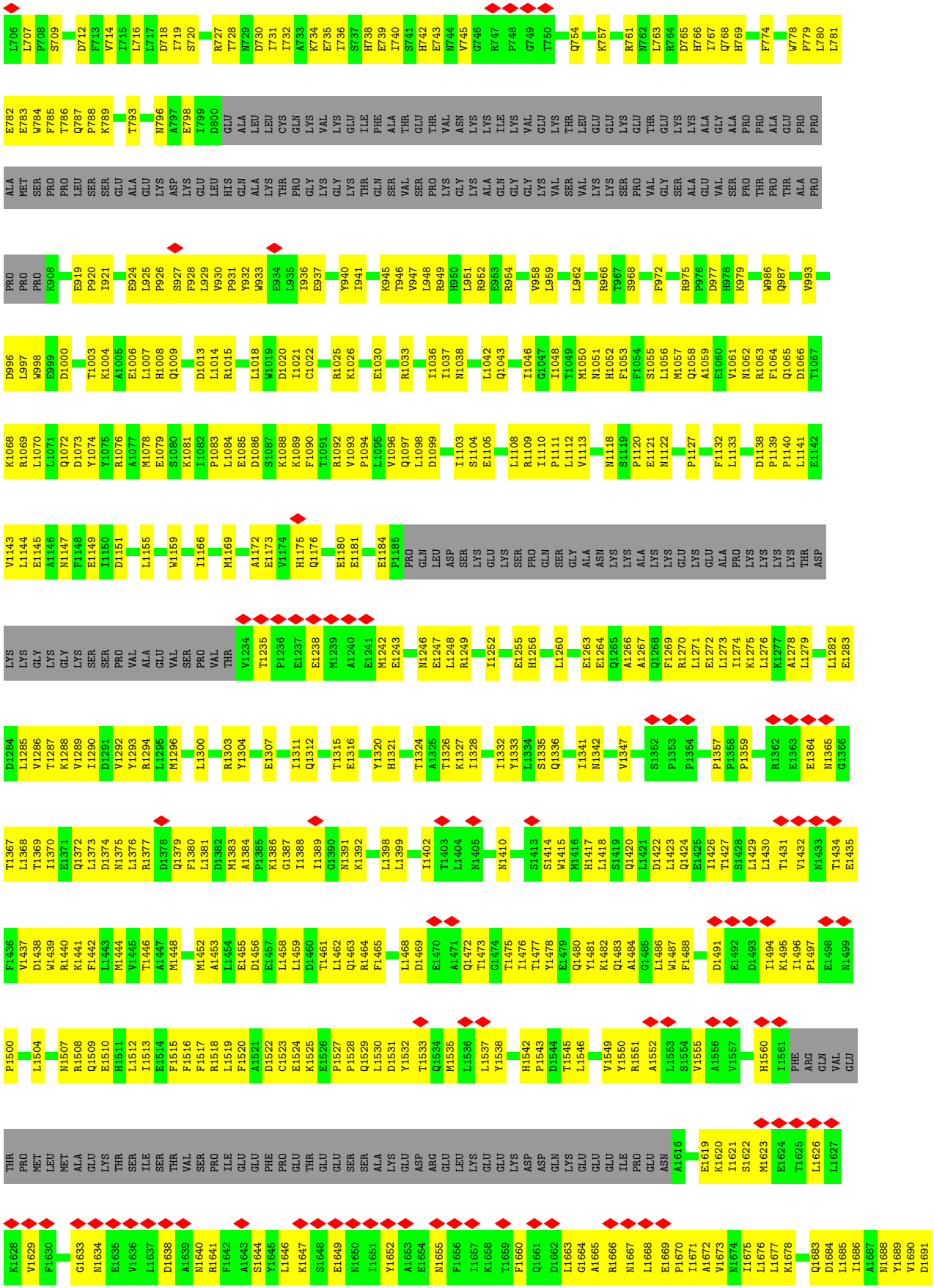
Chain 4N:







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E782 E783 W784 F785 T786 Q787 P788 K789 T793 N796 A797 E798 I799 D800 GLU ALA LEU LEU CYS GLN LYS VAL LYS GLU ILE PHE ALA THR GLU LYS LYS ASN LYS LYS ILE LYS VAL GLU LYS THR LEU GLU GLU LYS LYS GLU ALA GLY ALA PRO PRO ALA GLU PRO PRO
ALA MET SER PRO PRO LEU SER SER GLU ALA GLU LYS ASP LYS GLU LEU HIS GLN ALA LYS THR PRO GLY LYS GLY LYS THR GLN SER PRO LYS GLY LYS ALA GLN GLY GLY LYS VAL SER VAL LYS LYS SER PRO VAL GLY SER ALA GLU VAL SER PRO THR PRO THR ALA PRO
PRO PRO PRO K908 E919 P920 I921 E924 L925 P926 S927 F928 L929 V930 P931 Y932 W933 E934 L935 I936 E937 Y940 I941 K945 T946 V947 L948 R949 H950 L951 R952 E953 R954 V958 L959 L962 R966 T967 S968 F972 R975 P976 D977 H978 K979 W986 Q987 V993
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K1068 R1069 L1070 L1071 Q1072 D1073 Y1074 Y1075 R1076 A1077 M1078 E1079 S1080 K1081 I1082 P1083 L1084 E1085 D1086 S1087 K1088 K1089 F1090 T1091 R1092 V1093 P1094 L1095 V1096 Q1097 L1098 D1099 I1103 S1104 E1105 L1108 R1109 I1110 P1111 L1112 V1113 N1118 S1119 P1120 E1121 N1122 P1127 F1132 L1133 D1138 P1139 P1140 L1141 E1142
V1143 L1144 E1145 A1146 N1147 F1148 E1149 I1150 D1151 L1155 W1159 I1166 M1169 A1172 E1173 V1174 H1175 Q1176 E1180 E1181 E1184 P1185 PRO GLN LEU ASP SER LYS GLU LYS SER PRO GLN SER GLY ALA ASN LYS LYS ALA LYS LYS GLU LYS GLU ALA PRO LYS LYS LYS LYS THR ASP
LYS LYS GLY LYS GLY LYS SER SER PRO VAL ALA GLU VAL SER PRO VAL THR V1234 T1235 P1236 E1237 E1238 M1239 A1240 E1241 M1242 E1243 N1246 E1247 L1248 R1249 I1252 E1255 H1256 L1260 E1263 E1264 Q1265 A1266 A1267 Q1268 F1269 R1270 L1271 E1272 L1273 I1274 K1275 L1276 K1277 A1278 L1279 L1282 E1283
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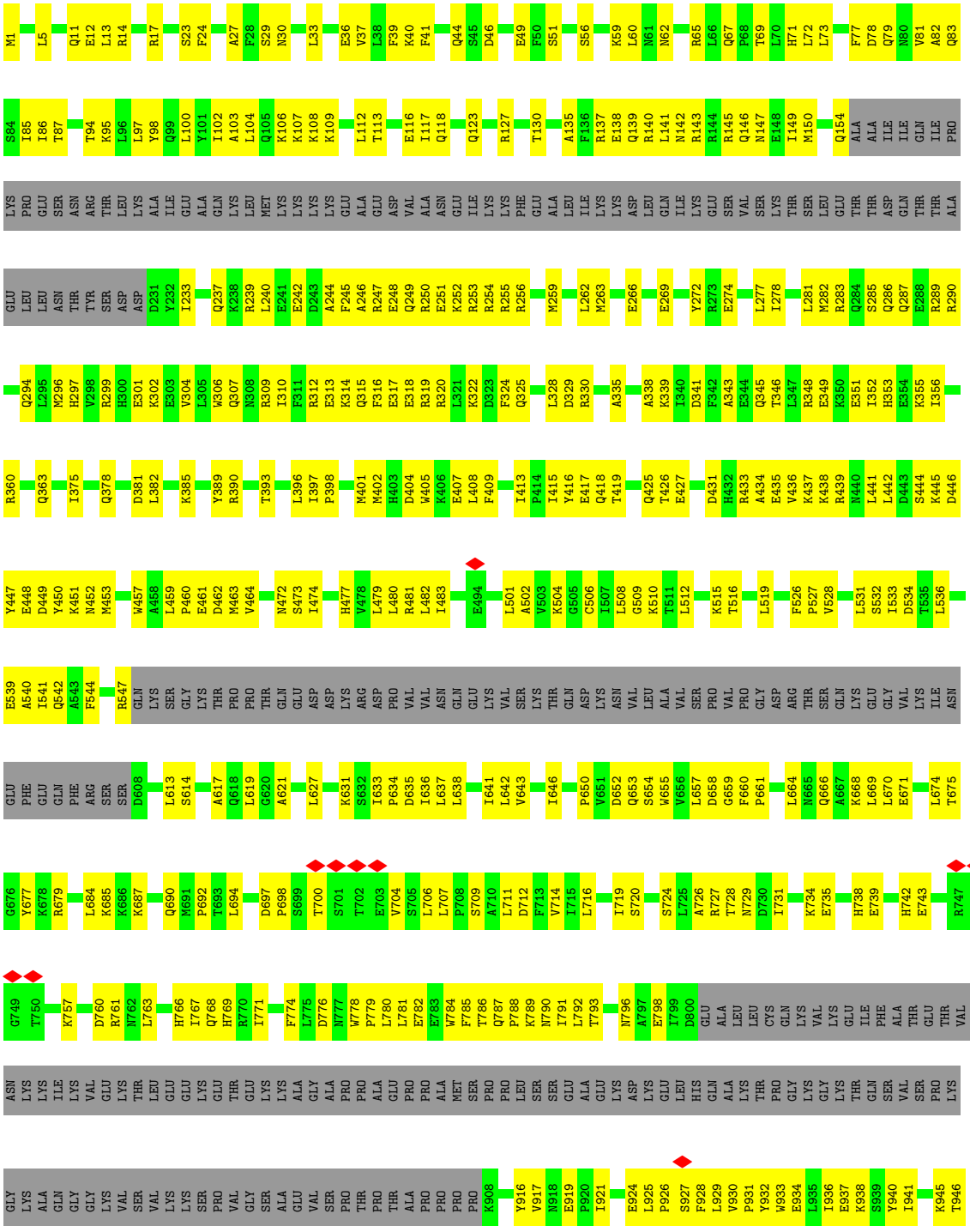
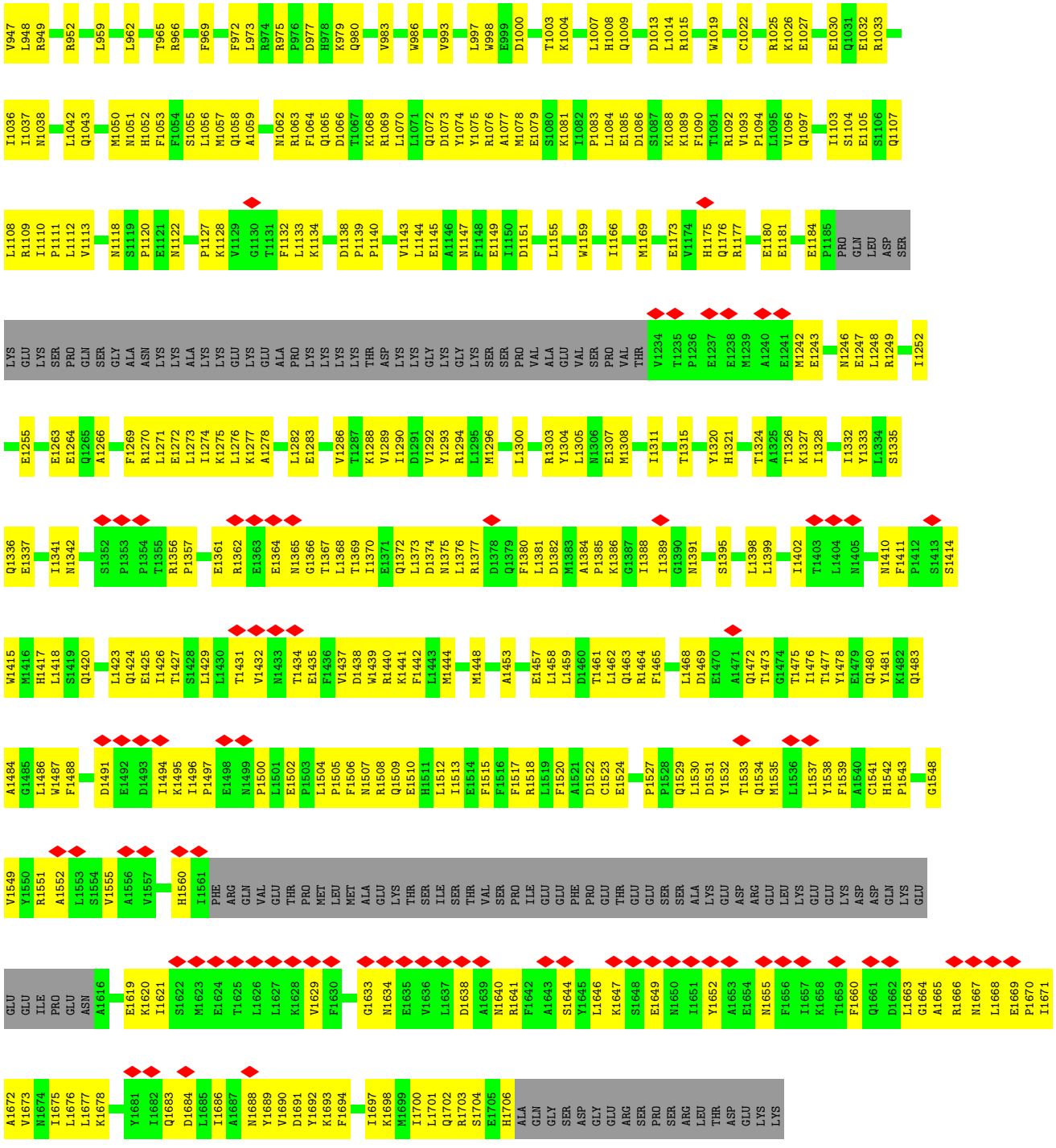
T1367 L1368 T1369 I1370 E1371 Q1372 L1373 D1374 N1375 L1376 R1377 D1378 Q1379 F1380 L1381 D1382 M1383 A1384 P1385 K1386 G1387 I1388 I1389 G1390 N1391 K1392 L1398 L1399 I1402 T1403 L1404 N1405 N1410 S1413 S1414 W1415 M1416 H1417 L1418 S1419 Q1420 L1421 D1422 L1423 Q1424 E1425 I1426 T1427 S1428 L1429 L1430 T1431 V1432 N1433 T1434 E1435
F1436 V1437 D1438 W1439 R1440 K1441 F1442 L1443 M1444 V1445 T1446 A1447 M1448 M1452 A1453 L1454 E1455 D1456 E1457 L1458 L1459 D1460 T1461 L1462 Q1463 R1464 F1465 L1468 D1469 E1470 A1471 Q1472 T1473 G1474 T1475 I1476 T1477 Y1478 E1479 Q1480 Y1481 K1482 Q1483 A1484 G1485 L1486 W1487 F1488 D1491 E1492 D1493 I1494 K1495 I1496 P1497 E1498 N1499
P1500 L1504 N1507 R1508 Q1509 E1510 H1511 L1512 I1513 E1514 F1515 F1516 F1517 R1518 L1519 F1520 A1521 D1522 C1523 E1524 K1525 E1526 P1527 P1528 Q1529 L1530 D1531 Y1532 T1533 Q1534 M1535 L1536 L1537 Y1538 H1542 P1543 D1544 T1545 L1546 V1549 Y1550 R1551 A1552 L1553 S1554 V1555 A1556 V1557 H1560 I1561 PHE ARG GLN VAL GLU
THR PRO MET LEU MET ALA GLU LYS THR SER ILE SER THR VAL SER PRO ILE GLU GLU PHE PRO GLU THR GLU GLU SER SER ALA LYS GLU ASP ARG GLU LEU LYS GLU GLU LYS ASP ASP GLN LEU ASN GLU ILE PRO GLU ASN A1616 E1619 K1620 I1621 S1622 M1623 E1624 T1625 L1626 L1627
K1628 V1629 F1630 G1633 N1634 E1635 V1636 L1637 D1638 A1639 N1640 R1641 F1642 A1643 S1644 Y1645 L1646 K1647 S1648 E1649 N1650 I1651 Y1652 A1653 E1654 N1655 F1656 I1657 K1658 T1659 F1660 Q1661 D1662 L1663 G1664 A1665 R1666 N1667 L1668 E1669 P1670 I1671 A1672 V1673 W1674 I1675 L1676 L1677 K1678 Q1683 D1684 L1685 I1686 A1687 N1688 Y1689 V1690 D1691

• Molecule 36: Sperm flagellar protein 2

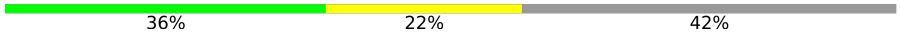
Chain 4L:

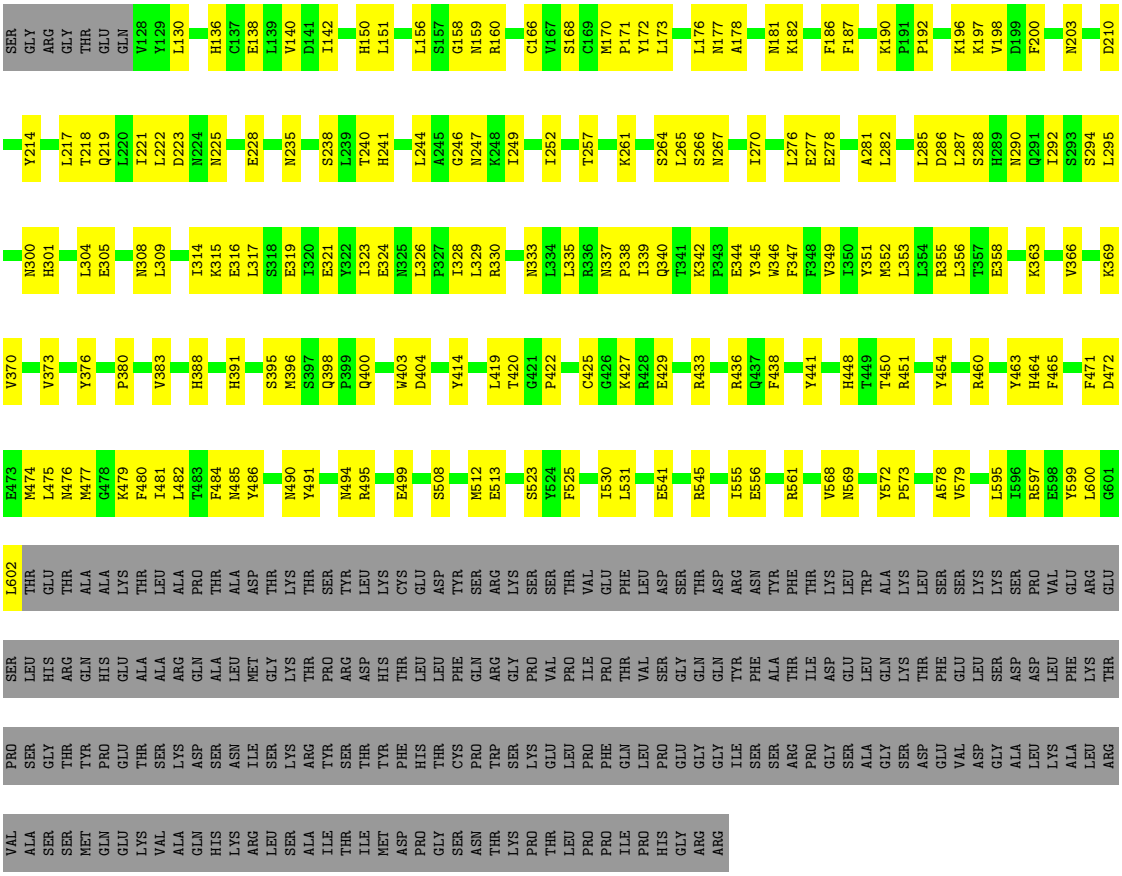




• Molecule 37: Leucine-rich repeat and guanylate kinase domain-containing protein

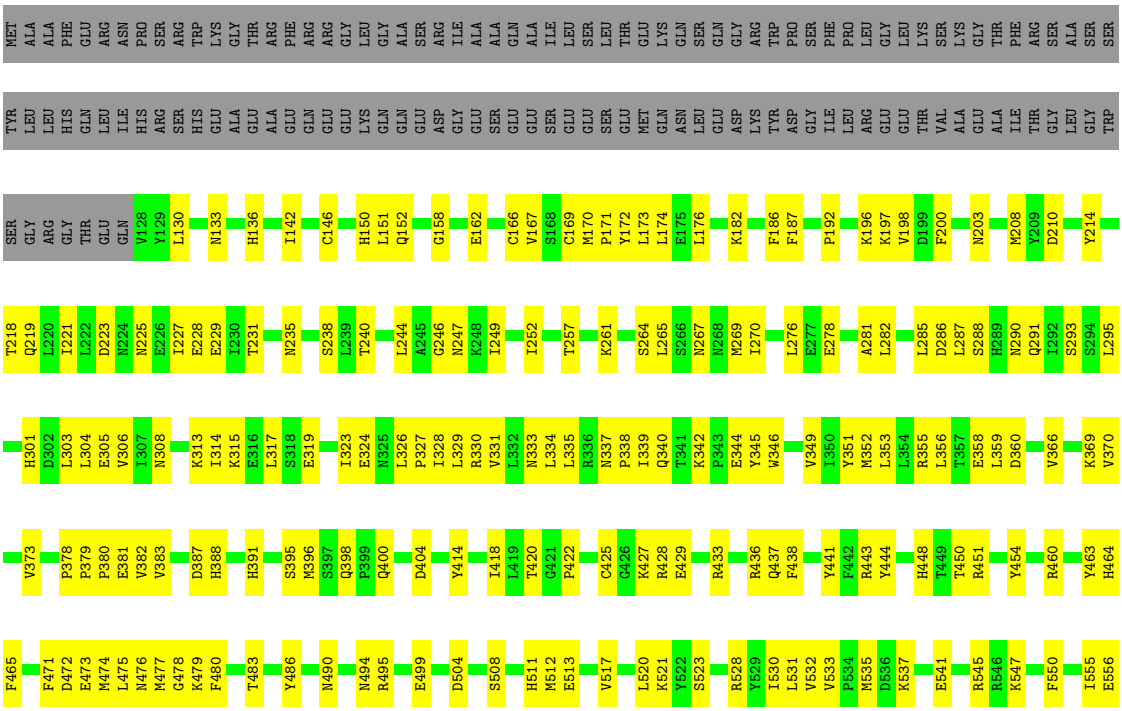
Chain 4P:

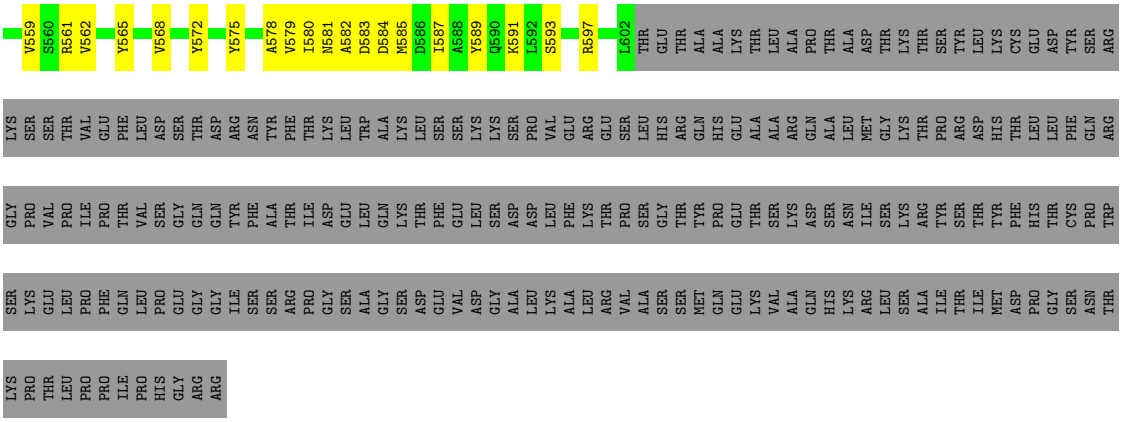




• Molecule 37: Leucine-rich repeat and guanylate kinase domain-containing protein

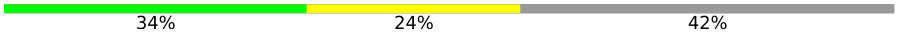
Chain 4Q: 33% 25% 42%

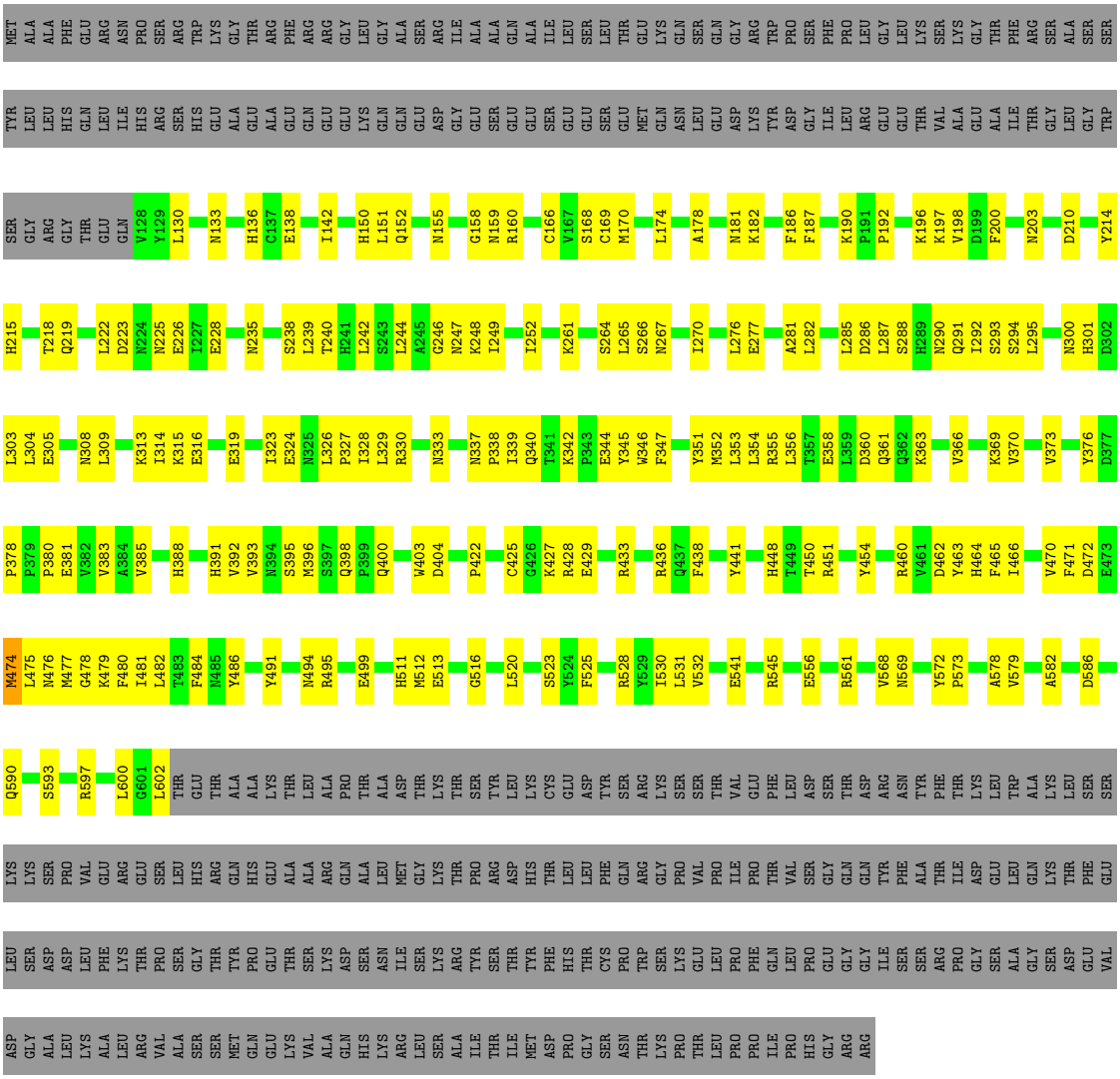




• Molecule 37: Leucine-rich repeat and guanylate kinase domain-containing protein

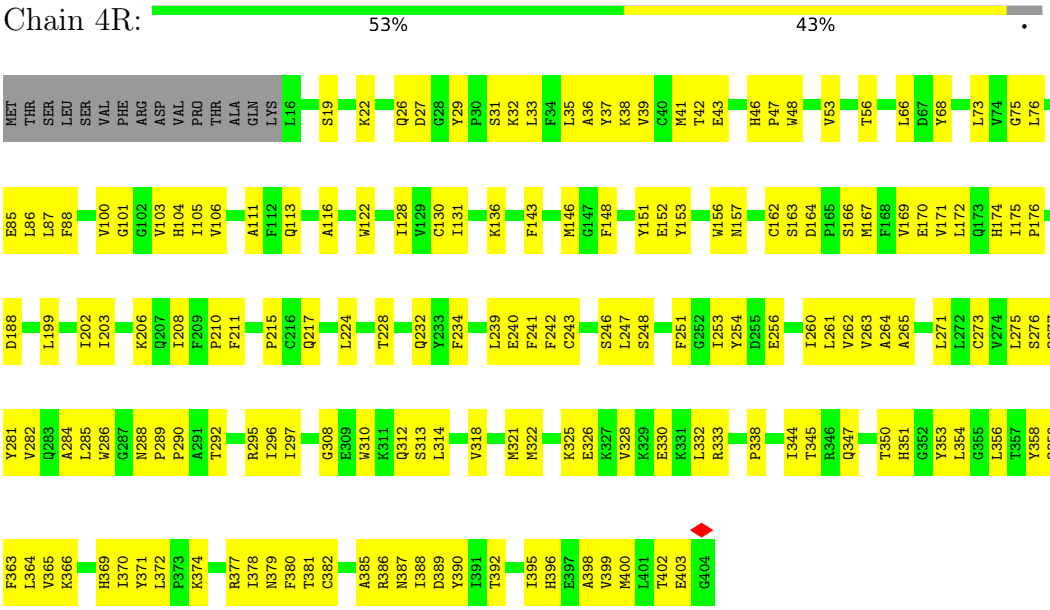
Chain 4O:





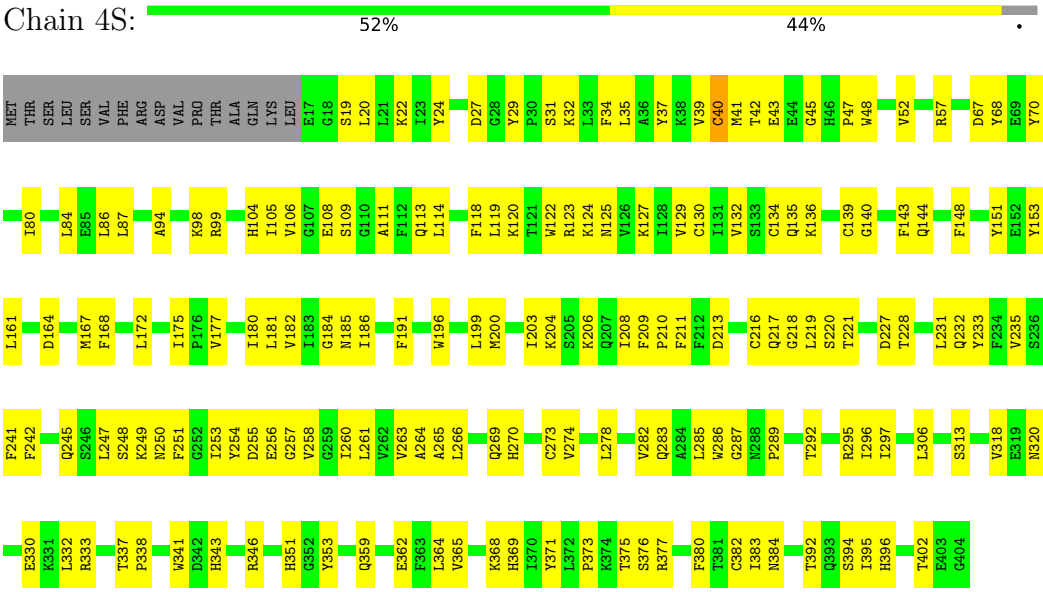
• Molecule 38: Putative aspartate aminotransferase, cytoplasmic 2

Chain 4R:



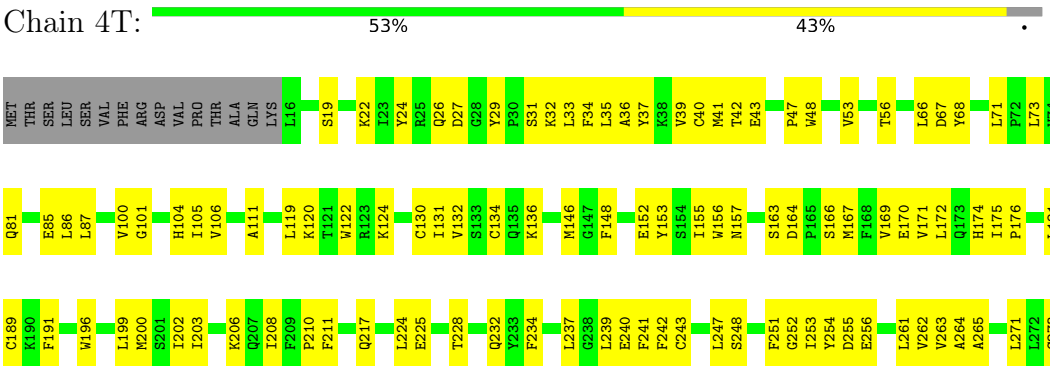
• Molecule 38: Putative aspartate aminotransferase, cytoplasmic 2

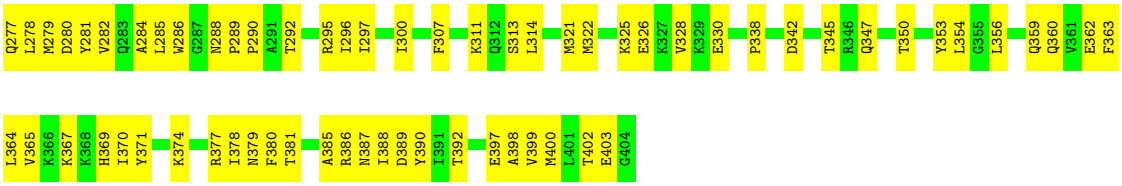
Chain 4S:



• Molecule 38: Putative aspartate aminotransferase, cytoplasmic 2

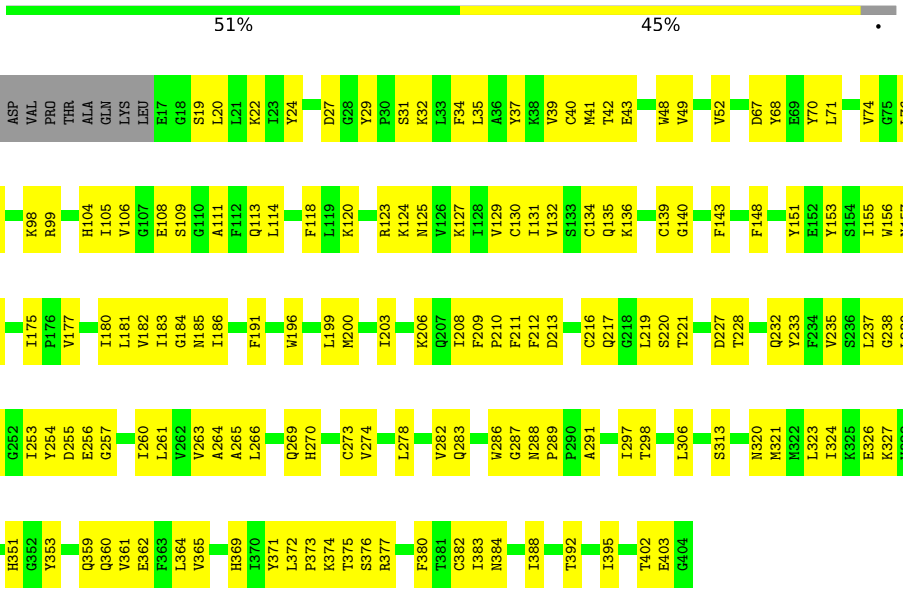
Chain 4T:





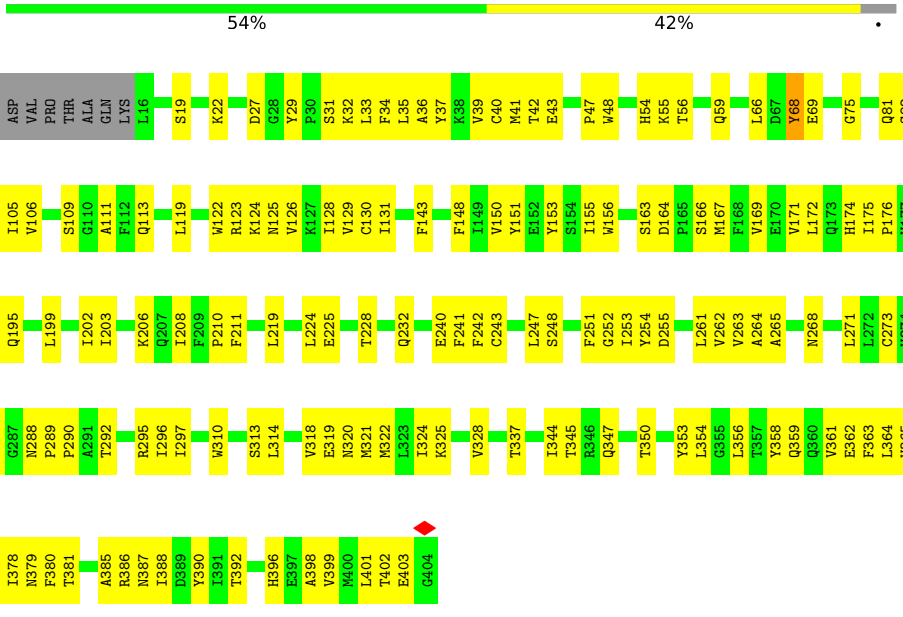
• Molecule 38: Putative aspartate aminotransferase, cytoplasmic 2

Chain 4U:



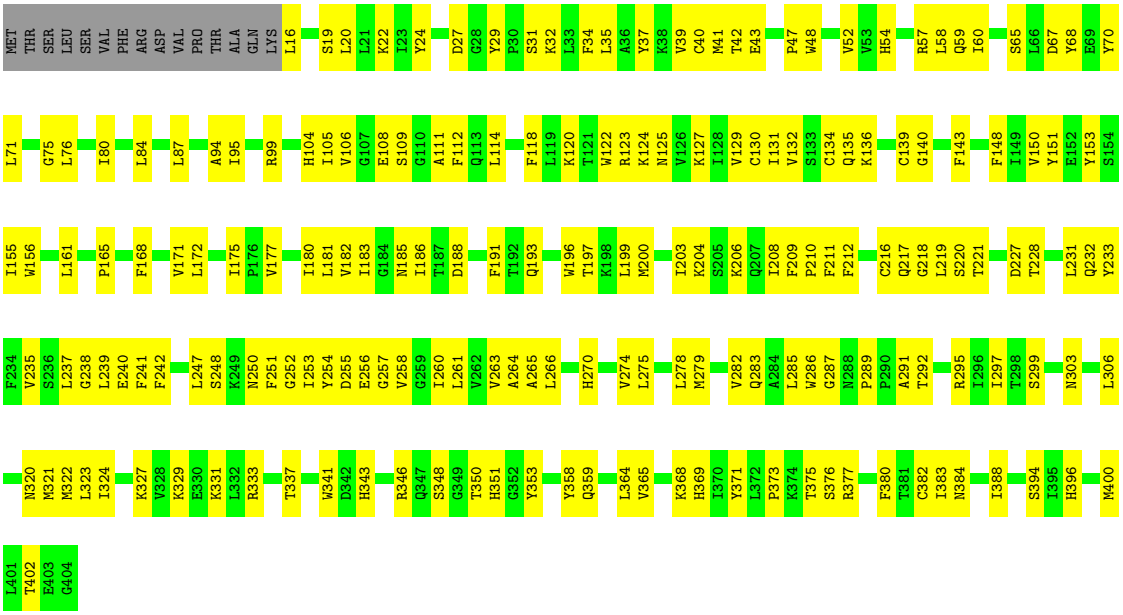
• Molecule 38: Putative aspartate aminotransferase, cytoplasmic 2

Chain 4V:



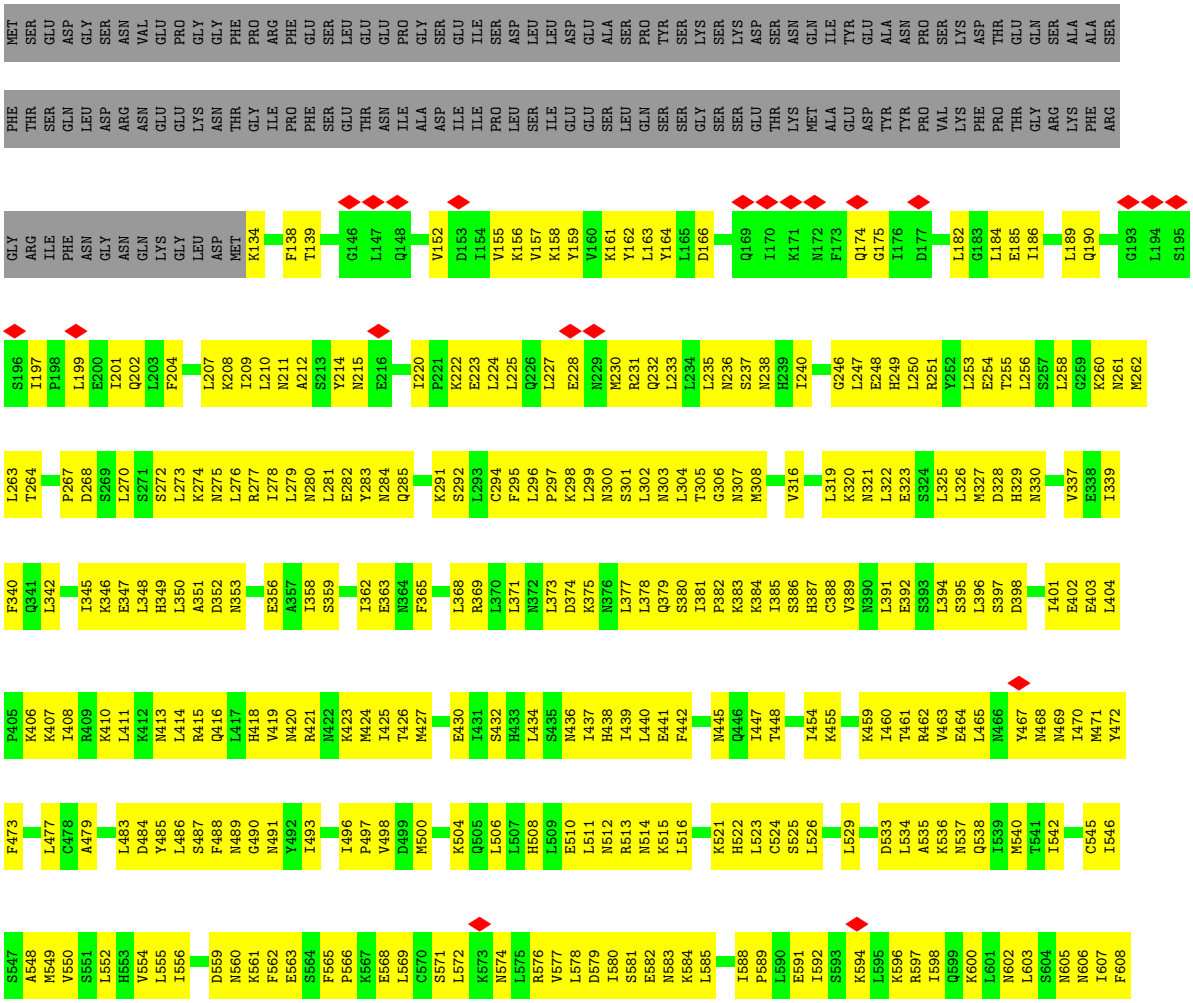
• Molecule 38: Putative aspartate aminotransferase, cytoplasmic 2

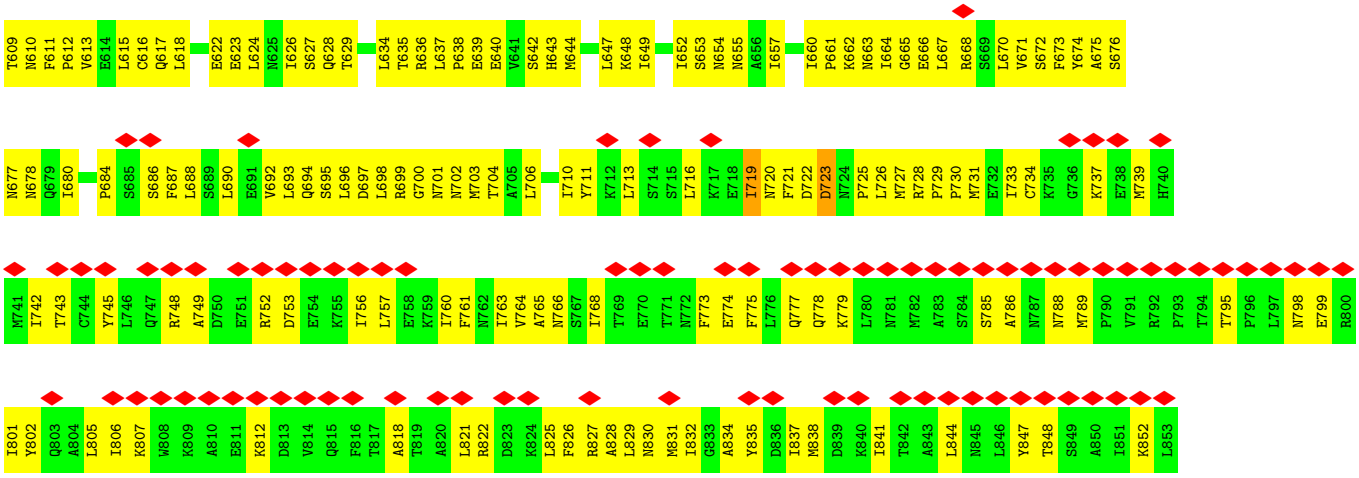
Chain 4W:



• Molecule 39: Leucine-rich repeat and death domain-containing protein 1

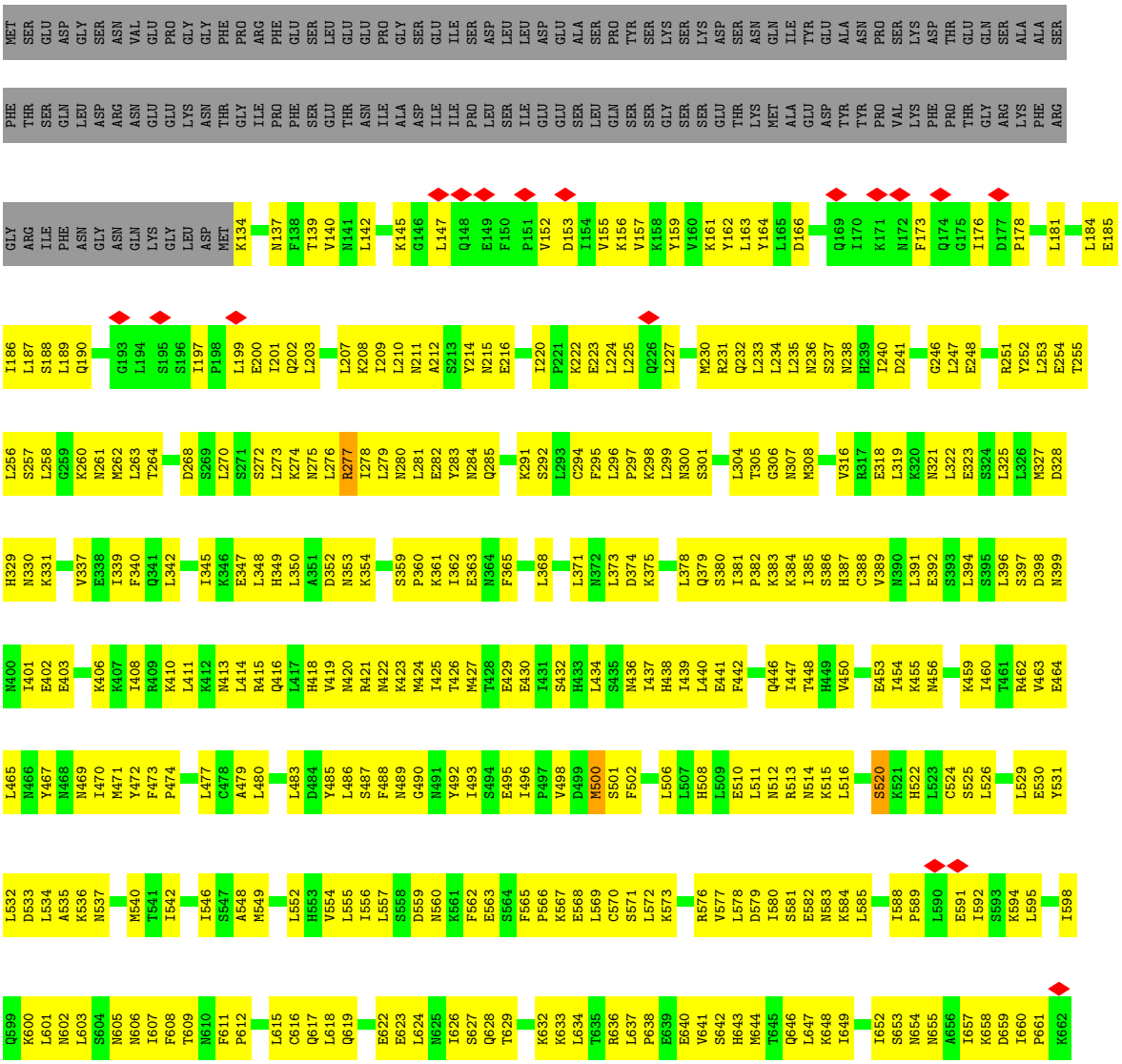
Chain 4X:

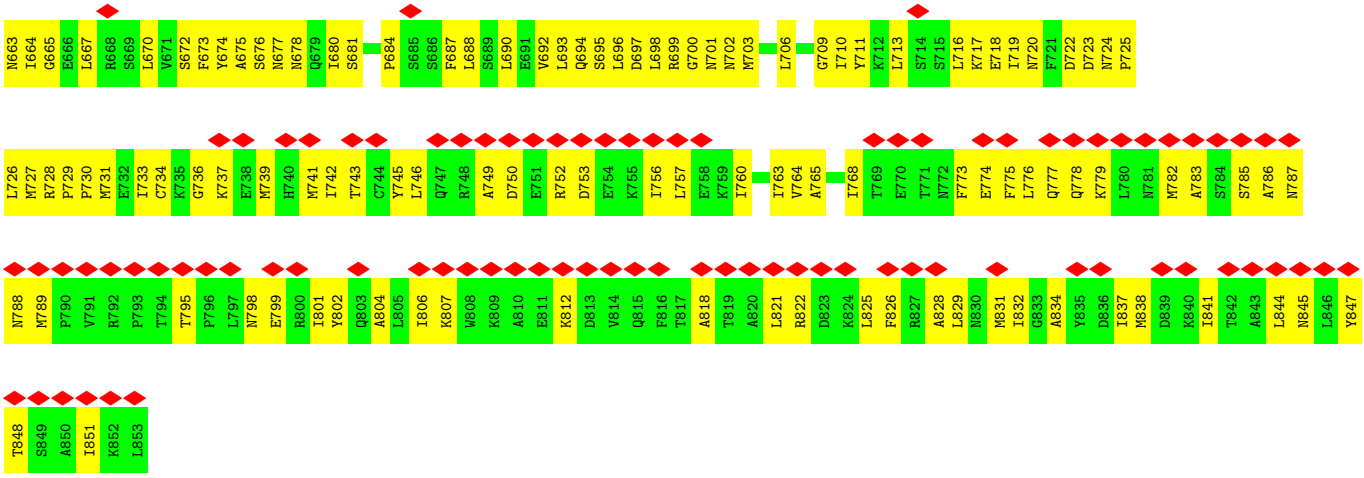




• Molecule 39: Leucine-rich repeat and death domain-containing protein 1

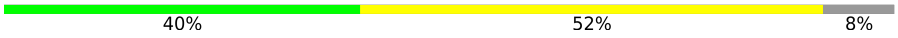
Chain 4Y:

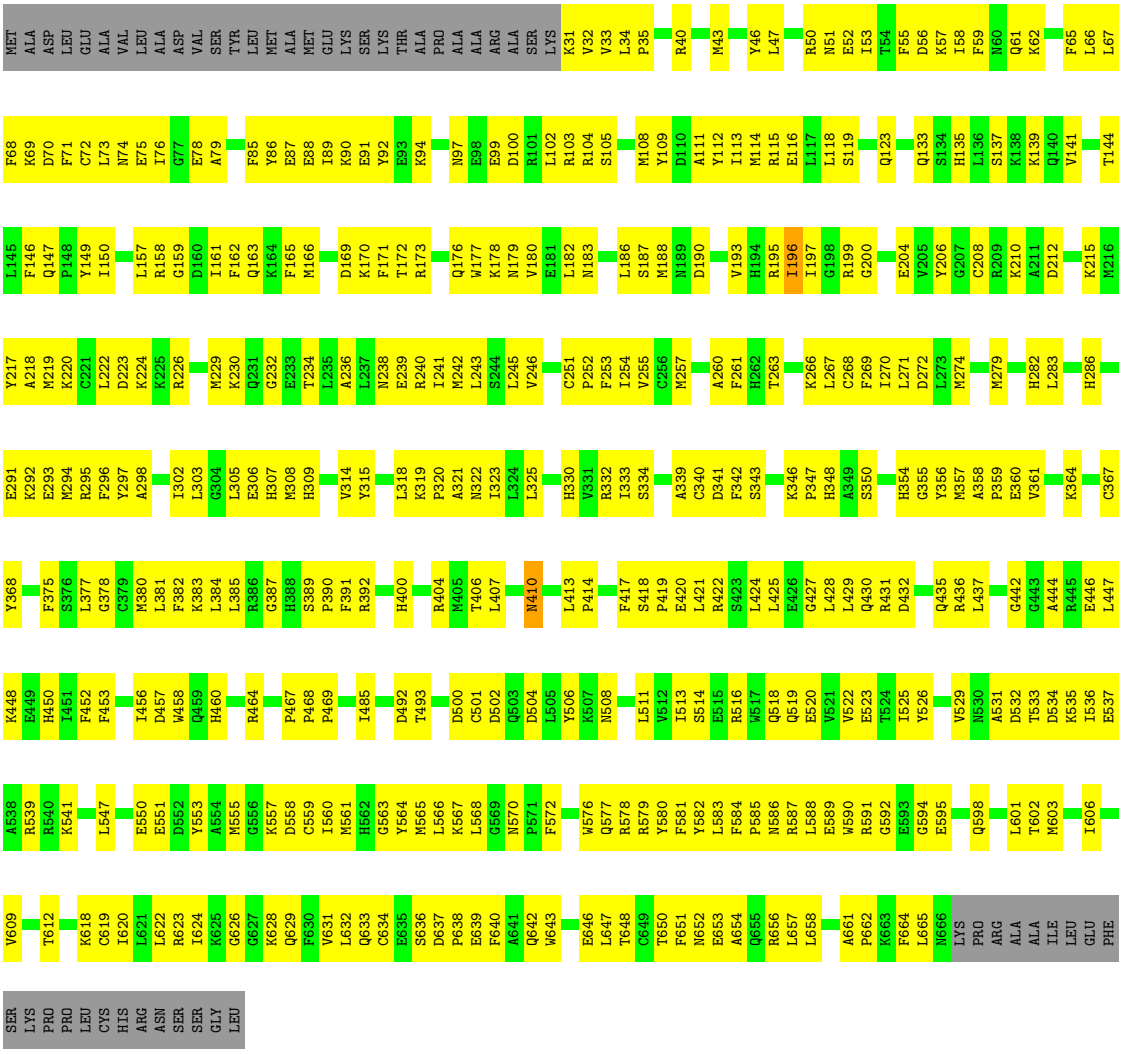




• Molecule 40: G protein-coupled receptor kinase 3

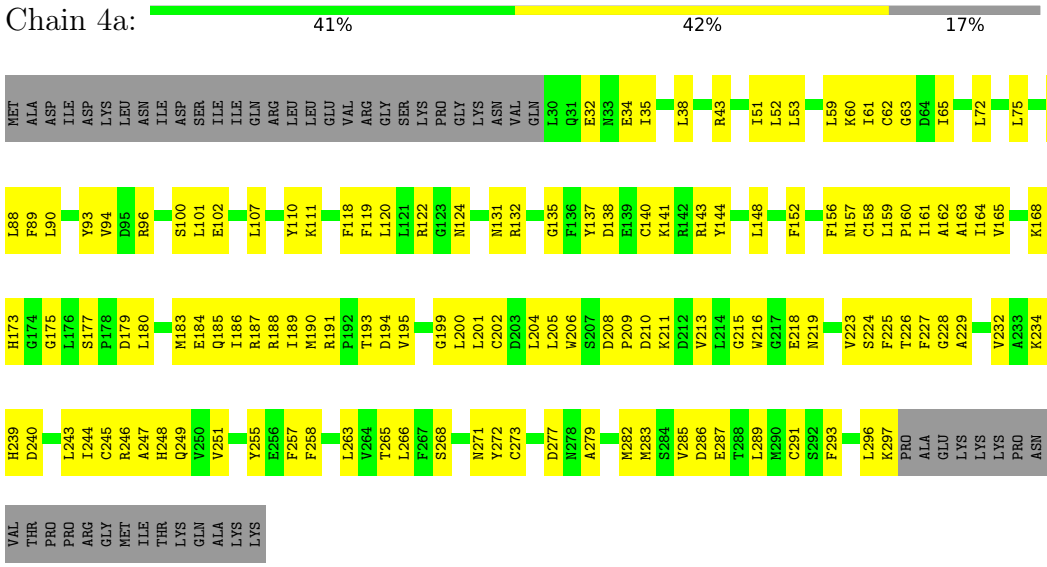
Chain 4Z:





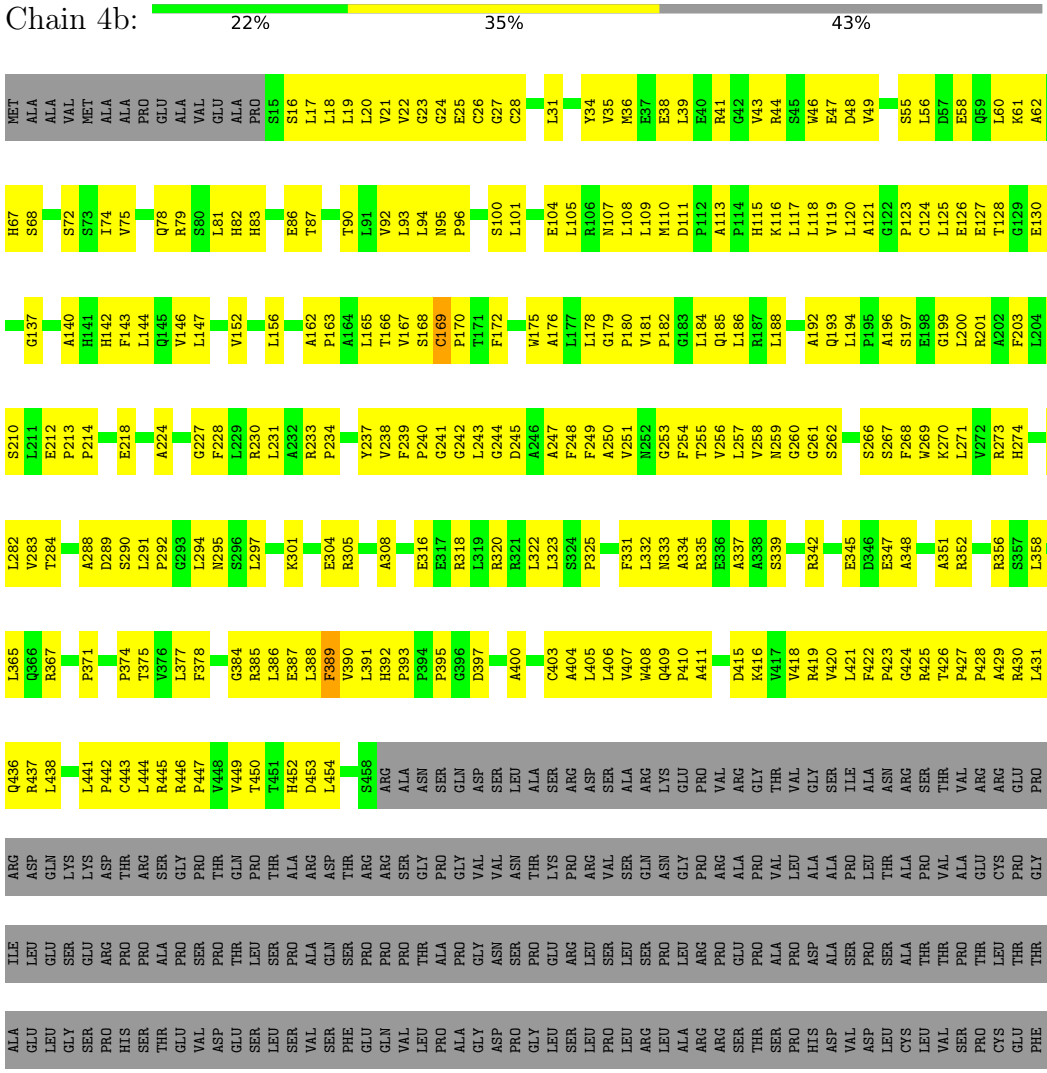
• Molecule 41: Serine/threonine-protein phosphatase PP1-gamma catalytic subunit

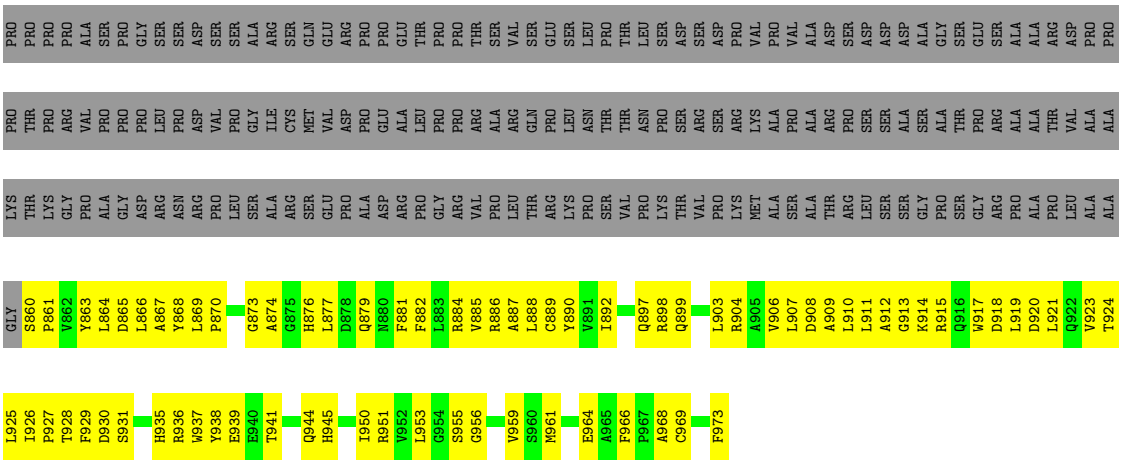
Chain 4a:



• Molecule 42: Microtubule-associated protein 1S

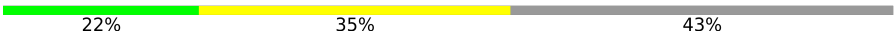
Chain 4b:

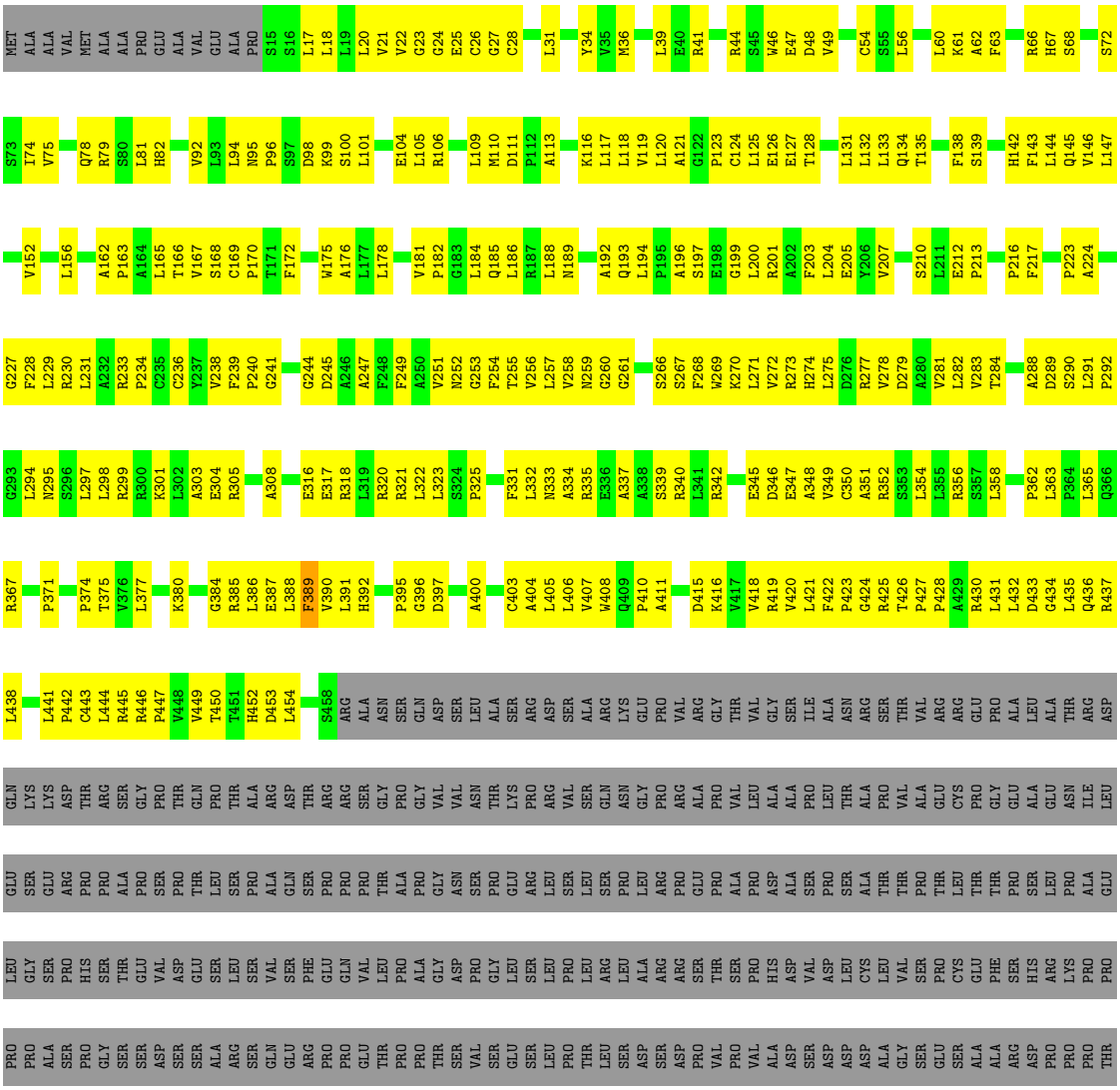


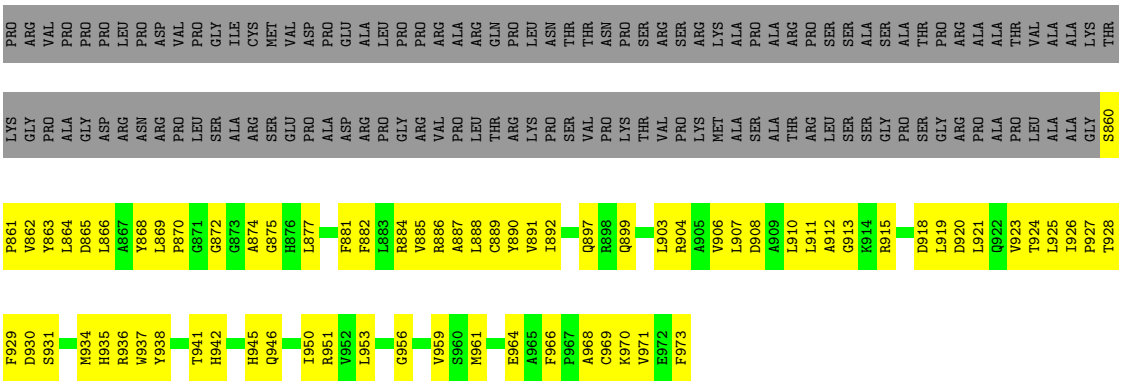


• Molecule 42: Microtubule-associated protein 1S

Chain 4c:

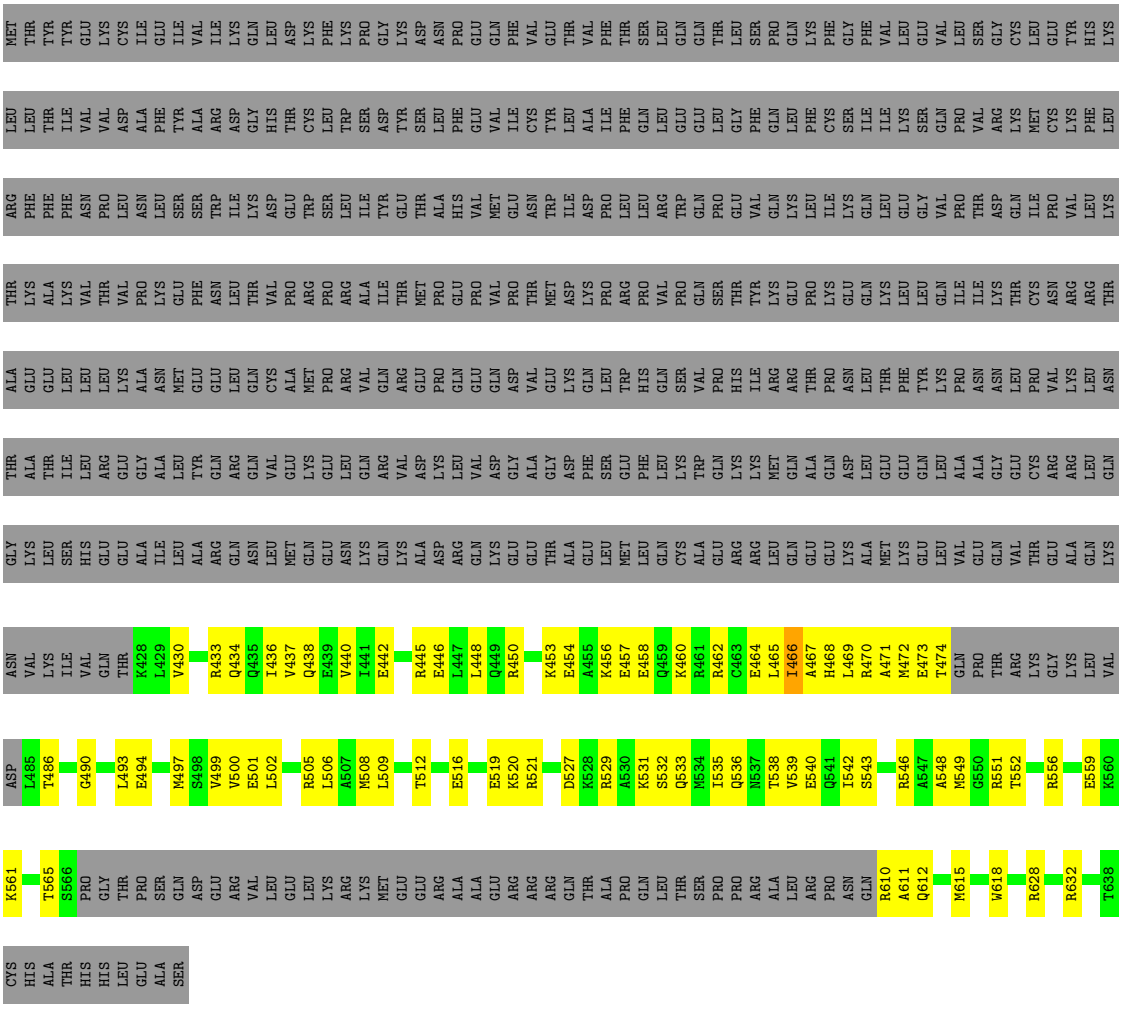






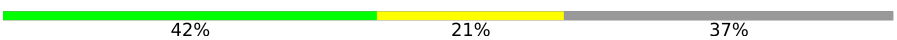
• Molecule 43: Cilia and flagella associated protein 99

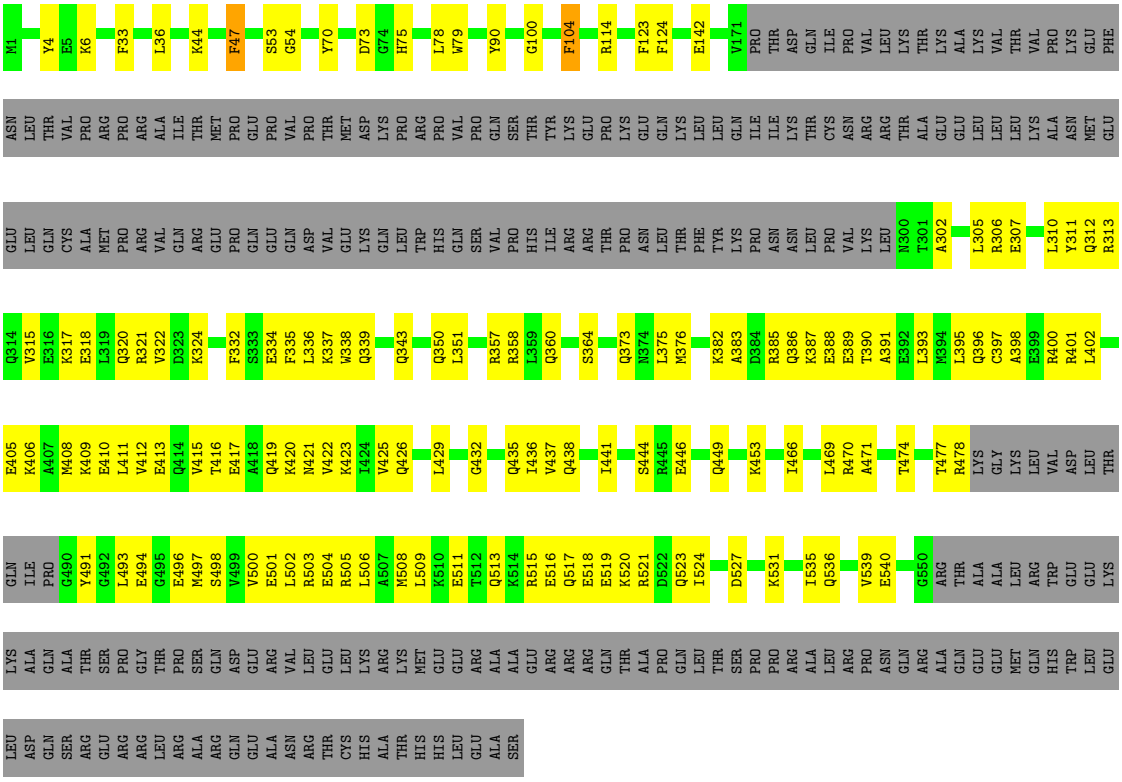
Chain J:



• Molecule 43: Cilia and flagella associated protein 99

Chain K:



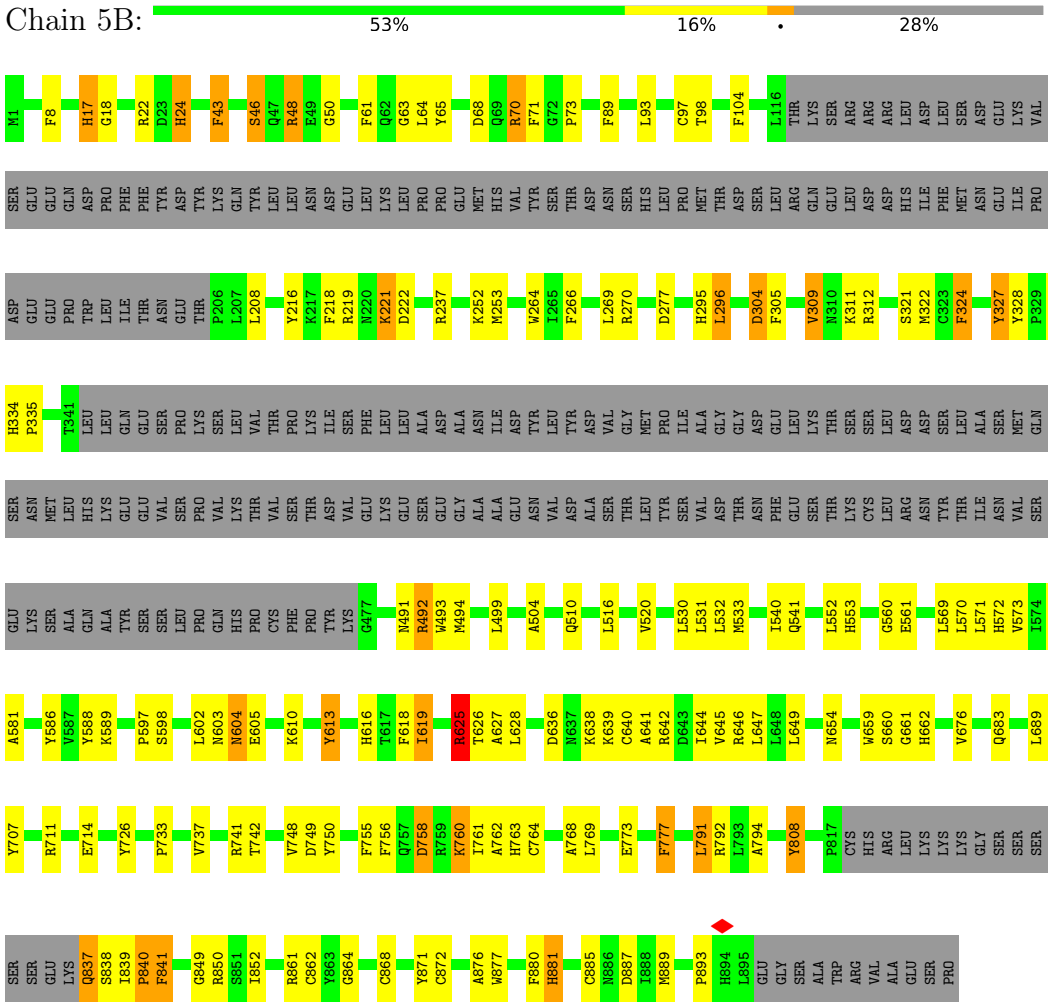


• Molecule 43: Cilia and flagella associated protein 99

Chain 5A:

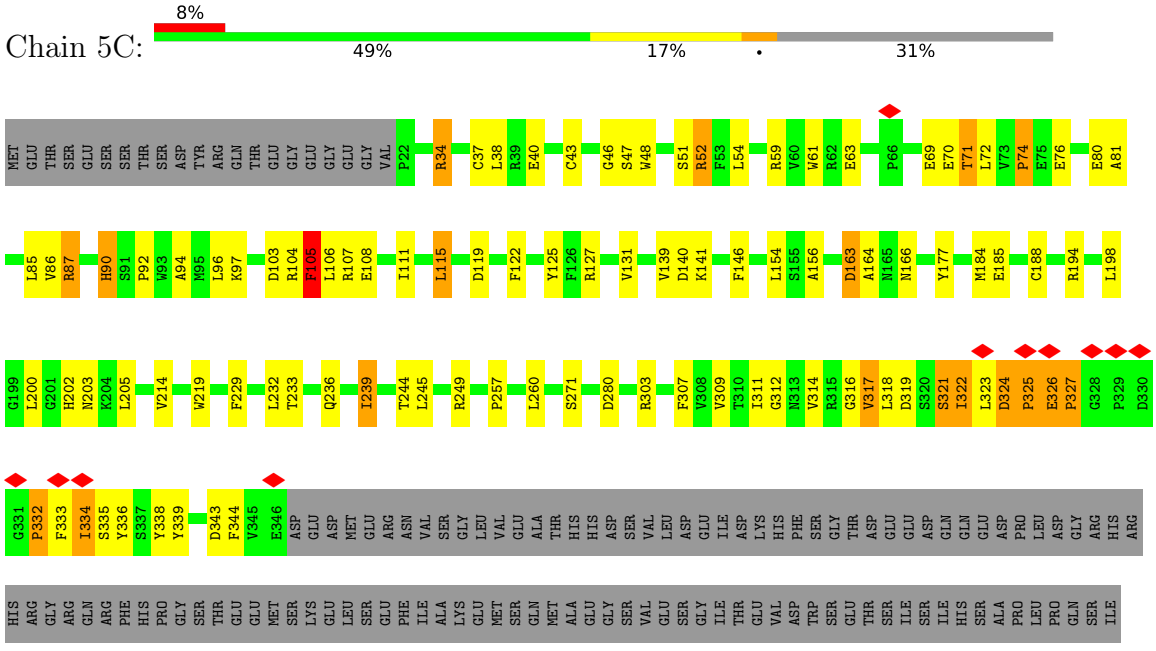
• Molecule 44: Ankyrin repeat and MYND domain-containing protein 1

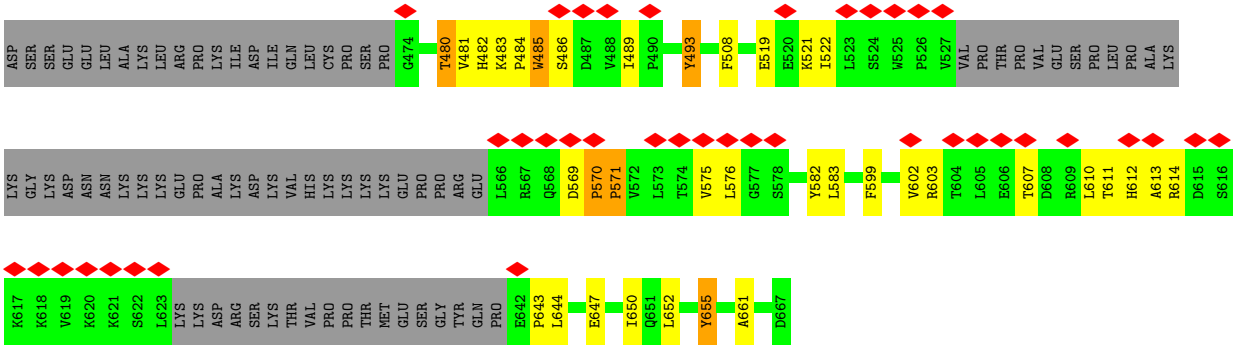
Chain 5B:



• Molecule 45: Leucine-rich repeat-containing protein 43

Chain 5C:




ASP SER SER GLU GLU LEU ALA LYS LEU ARG PRO LYS ILE ASP ILE GLN LEU CYS PRO SER PRO
G474 T480 V481 H482 K483 P484 W485 S486 D487 V488 I489 P490 Y493 F508 E519 E520 K521 I522 L523 S524 W525 P526 V527
VAL PRO THR PRO VAL GLU SER PRO LEU PRO ALA LYS
LYS GLY LYS ASP ASN ASN LYS LYS LYS GLU PRO ALA LYS ASP LYS VAL HIS LYS LYS LYS LYS GLU PRO PRO ARG GLU
L566 R567 Q568 D569 P570 P571 V572 L573 T574 V575 L576 G577 S578 V582 L583 F599 V602 R603 T604 L605 E606 T607 D608 R609 L610 T611 H612 A613 R614 D615 S616
K617 K618 V619 K620 K621 S622 L623
LYS LYS ASP ARG SER LYS THR VAL PRO PRO THR MET GLU SER GLY TYR GLN PRO
E642 P643 L644 E647 I650 G651 L652 Y655 A661 D667

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	19000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	117	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.019	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	950.4, 950.4, 950.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.64, 2.64, 2.64	Depositor

5 Model quality

5.1 Standard geometry

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	W	0.15	0/1539	0.31	0/2077
1	X	0.15	0/1539	0.35	0/2077
1	Y	0.15	0/1539	0.37	0/2077
1	Z	0.16	0/1539	0.39	0/2077
1	a	0.15	0/1539	0.35	0/2077
1	b	0.13	0/1539	0.34	0/2077
2	c	0.11	0/4079	0.29	0/5490
2	d	0.13	0/4651	0.36	0/6257
2	e	0.13	0/4079	0.32	0/5490
2	f	0.11	0/4079	0.31	0/5490
2	g	0.14	0/4651	0.36	0/6257
3	h	0.15	0/11845	0.34	3/16142 (0.0%)
3	i	0.14	0/11845	0.34	7/16142 (0.0%)
3	j	0.16	0/11845	0.33	7/16142 (0.0%)
4	k	0.10	0/7009	0.28	0/9493
4	l	0.10	0/7135	0.26	0/9664
4	m	0.10	0/7009	0.27	0/9493
4	n	0.11	0/7135	0.27	0/9664
4	o	0.10	0/7009	0.27	0/9493
4	p	0.09	0/7135	0.26	0/9664
5	q	0.16	0/1763	0.41	0/2358
5	r	0.16	0/1763	0.45	0/2358
5	s	0.18	0/1763	0.41	0/2358
6	t	0.10	0/1565	0.28	0/2111
6	u	0.10	0/1565	0.28	0/2111
7	v	0.15	0/1345	0.43	0/1812
7	w	0.15	0/1345	0.42	0/1812
8	A	0.14	0/14479	0.37	0/19556
8	B	0.14	0/10192	0.39	2/13768 (0.0%)
9	C	0.14	0/7906	0.38	0/10669
9	D	0.19	0/2553	0.43	0/3391
9	E	0.09	0/3901	0.27	0/5298
10	F	0.12	0/8891	0.32	0/11939
10	G	0.12	0/4187	0.35	0/5613

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
11	H	0.16	0/22139	0.44	1/29914 (0.0%)
11	I	0.18	0/7303	0.49	1/9863 (0.0%)
12	L	0.12	0/1918	0.33	0/2607
13	M	0.14	0/1537	0.41	0/2071
14	O	0.13	0/10424	0.34	1/14171 (0.0%)
14	P	0.11	0/4770	0.29	0/6486
15	Q	0.16	0/3673	0.39	0/4953
15	R	0.15	0/3687	0.39	0/4972
15	S	0.15	0/3673	0.39	0/4953
15	T	0.16	0/3687	0.39	0/4972
15	U	0.17	0/3673	0.39	0/4953
15	V	0.16	0/3687	0.40	0/4972
16	x	0.19	1/9140 (0.0%)	0.39	3/12363 (0.0%)
16	y	0.13	0/9242	0.32	2/12503 (0.0%)
16	z	0.14	0/9242	0.33	0/12503
17	Ab	0.12	0/3466	0.31	0/4697
17	Ad	0.12	0/3466	0.31	0/4697
17	Af	0.12	0/3466	0.31	0/4697
17	Ah	0.12	0/3466	0.32	0/4697
17	Aj	0.12	0/3466	0.31	0/4697
17	An	0.12	0/3466	0.32	0/4697
17	Ap	0.12	0/3466	0.33	0/4697
17	Ar	0.15	0/3466	0.35	0/4697
17	At	0.12	0/3466	0.32	0/4697
17	Av	0.12	0/3466	0.32	0/4697
17	Bb	0.12	0/3466	0.31	0/4697
17	Bd	0.13	0/3466	0.32	0/4697
17	Bf	0.12	0/3466	0.33	0/4697
17	Bh	0.11	0/3466	0.31	0/4697
17	Bj	0.14	0/3466	0.33	0/4697
17	Bn	0.13	0/3466	0.32	0/4697
17	Bp	0.14	0/3466	0.35	0/4697
17	Br	0.13	0/3466	0.33	0/4697
17	Bt	0.11	0/3466	0.32	2/4697 (0.0%)
17	Bv	0.12	0/3466	0.31	0/4697
17	Cb	0.12	0/3466	0.34	0/4697
17	Cd	0.15	0/3466	0.34	2/4697 (0.0%)
17	Cf	0.11	0/3466	0.29	0/4697
17	Ch	0.11	0/3466	0.30	0/4697
17	Cj	0.12	0/3466	0.31	0/4697
17	Cn	0.12	0/3466	0.31	0/4697
17	Cp	0.12	0/3466	0.33	0/4697
17	Cr	0.12	0/3466	0.32	0/4697

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	Ct	0.13	0/3466	0.33	0/4697
17	Cv	0.13	0/3466	0.33	0/4697
17	Db	0.12	0/3466	0.31	0/4697
17	Dd	0.12	0/3466	0.32	0/4697
17	Df	0.11	0/3466	0.30	0/4697
17	Dh	0.13	0/3466	0.33	0/4697
17	Dj	0.12	0/3466	0.31	0/4697
17	Dn	0.12	0/3466	0.31	0/4697
17	Dp	0.15	0/3466	0.35	0/4697
17	Dr	0.15	0/3466	0.34	0/4697
17	Dt	0.13	0/3466	0.33	0/4697
17	Dv	0.12	0/3466	0.31	0/4697
17	Eb	0.11	0/3466	0.30	0/4697
17	Ed	0.11	0/3466	0.30	0/4697
17	Ef	0.12	0/3466	0.30	0/4697
17	Eh	0.12	0/3466	0.32	0/4697
17	Ej	0.12	0/3466	0.31	0/4697
17	En	0.12	0/3466	0.32	0/4697
17	Ep	0.14	0/3466	0.34	0/4697
17	Er	0.12	0/3466	0.32	0/4697
17	Et	0.12	0/3466	0.31	0/4697
17	Ev	0.11	0/3466	0.29	0/4697
17	Fb	0.13	0/3466	0.33	0/4697
17	Fd	0.11	0/3466	0.29	0/4697
17	Ff	0.12	0/3466	0.31	0/4697
17	Fh	0.11	0/3466	0.30	0/4697
17	Fj	0.12	0/3466	0.29	0/4697
17	Fn	0.12	0/3466	0.34	0/4697
17	Fp	0.13	0/3466	0.33	0/4697
17	Fr	0.12	0/3466	0.32	0/4697
17	Ft	0.12	0/3466	0.31	0/4697
17	Fv	0.12	0/3466	0.31	0/4697
17	Gb	0.15	0/3466	0.34	0/4697
17	Gd	0.12	0/3466	0.30	0/4697
17	Gf	0.13	0/3466	0.32	0/4697
17	Gh	0.16	0/3466	0.34	0/4697
17	Gj	0.12	0/3466	0.31	0/4697
17	Gn	0.13	0/3466	0.31	0/4697
17	Gp	0.13	0/3466	0.32	0/4697
17	Gr	0.13	0/3466	0.33	2/4697 (0.0%)
17	Gt	0.11	0/3466	0.31	0/4697
17	Gv	0.12	0/3466	0.30	0/4697
17	Hb	0.13	0/3466	0.33	0/4697

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	Hd	0.12	0/3466	0.31	0/4697
17	Hf	0.12	0/3466	0.31	0/4697
17	Hh	0.12	0/3466	0.33	0/4697
17	Hj	0.12	0/3466	0.32	0/4697
17	Hn	0.12	0/3466	0.30	0/4697
17	Hp	0.14	0/3466	0.34	0/4697
17	Hr	0.12	0/3466	0.33	0/4697
17	Ht	0.13	0/3466	0.33	0/4697
17	Hv	0.13	0/3466	0.34	0/4697
17	Ib	0.12	0/3466	0.30	0/4697
17	Id	0.13	0/3466	0.34	0/4697
17	If	0.13	0/3466	0.32	0/4697
17	Ih	0.11	0/3466	0.30	0/4697
17	Ij	0.11	0/3466	0.30	0/4697
17	In	0.12	0/3466	0.30	0/4697
17	Ip	0.13	0/3466	0.32	0/4697
17	Ir	0.12	0/3466	0.31	0/4697
17	It	0.13	0/3466	0.35	0/4697
17	Iv	0.12	0/3466	0.32	0/4697
17	Jb	0.13	0/3466	0.34	0/4697
17	Jd	0.12	0/3466	0.32	0/4697
17	Jf	0.13	0/3466	0.34	0/4697
17	Jh	0.13	0/3466	0.31	0/4697
17	Jj	0.11	0/3466	0.29	0/4697
17	Jn	0.12	0/3466	0.32	0/4697
17	Jp	0.13	0/3466	0.34	0/4697
17	Jr	0.13	0/3466	0.32	0/4697
17	Jt	0.12	0/3466	0.32	0/4697
17	Jv	0.12	0/3466	0.32	0/4697
17	Kb	0.13	0/3466	0.32	0/4697
17	Kd	0.12	0/3466	0.31	0/4697
17	Kf	0.12	0/3466	0.30	0/4697
17	Kh	0.13	0/3466	0.30	0/4697
17	Kj	0.13	0/3466	0.32	0/4697
17	Kn	0.12	0/3465	0.31	0/4695
17	Kp	0.13	0/3466	0.33	0/4697
17	Kr	0.12	0/3466	0.31	0/4697
17	Kt	0.14	0/3466	0.32	0/4697
17	Kv	0.13	0/3466	0.33	0/4697
17	Lb	0.12	0/3466	0.32	0/4697
17	Ld	0.12	0/3466	0.32	0/4697
17	Lf	0.13	0/3466	0.32	0/4697
17	Lh	0.12	0/3466	0.32	0/4697

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	Lj	0.12	0/3466	0.31	0/4697
17	Ln	0.12	0/3466	0.30	0/4697
17	Lp	0.13	0/3466	0.33	0/4697
17	Lr	0.13	0/3466	0.32	0/4697
17	Lt	0.13	0/3466	0.32	0/4697
17	Lv	0.12	0/3466	0.31	0/4697
17	Mb	0.11	0/3466	0.29	0/4697
17	Md	0.11	0/3466	0.29	0/4697
17	Mf	0.11	0/3466	0.31	0/4697
17	Mh	0.12	0/3466	0.30	0/4697
17	Mj	0.11	0/3466	0.29	0/4697
17	Mn	0.12	0/3466	0.33	0/4697
17	Mp	0.13	0/3466	0.32	0/4697
17	Mr	0.14	0/3466	0.35	0/4697
17	Mt	0.14	0/3466	0.34	0/4697
17	Mv	0.12	0/3466	0.31	0/4697
18	Ac	0.10	0/3502	0.29	0/4755
18	Ae	0.09	0/3502	0.26	0/4755
18	Ag	0.10	0/3502	0.28	0/4755
18	Ai	0.09	0/3502	0.26	0/4755
18	Ak	0.11	0/3502	0.28	0/4755
18	Ao	0.13	0/3502	0.31	0/4755
18	Aq	0.11	0/3502	0.30	0/4755
18	As	0.11	0/3502	0.30	0/4755
18	Au	0.11	0/3502	0.28	0/4755
18	Aw	0.11	0/3502	0.28	0/4755
18	Bc	0.10	0/3502	0.26	0/4755
18	Be	0.10	0/3502	0.28	0/4755
18	Bg	0.10	0/3502	0.28	0/4755
18	Bi	0.10	0/3502	0.29	0/4755
18	Bk	0.11	0/3502	0.30	0/4755
18	Bm	0.11	0/3502	0.28	0/4755
18	Bo	0.11	0/3502	0.31	0/4755
18	Bq	0.13	0/3502	0.30	0/4755
18	Bs	0.11	0/3502	0.29	0/4755
18	Bu	0.11	0/3502	0.28	0/4755
18	Cc	0.09	0/3502	0.26	0/4755
18	Ce	0.11	0/3502	0.29	1/4755 (0.0%)
18	Cg	0.11	0/3502	0.31	0/4755
18	Ci	0.12	0/3502	0.30	0/4755
18	Ck	0.11	0/3502	0.30	0/4755
18	Cm	0.12	0/3502	0.31	0/4755
18	Co	0.11	0/3502	0.29	0/4755

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	Cq	0.13	0/3502	0.32	0/4755
18	Cs	0.14	0/3502	0.35	0/4755
18	Cu	0.10	0/3502	0.27	0/4755
18	Dc	0.11	0/3502	0.29	0/4755
18	De	0.11	0/3502	0.29	0/4755
18	Dg	0.11	0/3502	0.29	0/4755
18	Di	0.22	1/3502 (0.0%)	0.32	1/4755 (0.0%)
18	Dk	0.11	0/3502	0.30	0/4755
18	Dm	0.11	0/3502	0.28	0/4755
18	Do	0.14	0/3502	0.31	0/4755
18	Dq	0.12	0/3502	0.31	0/4755
18	Ds	0.14	0/3502	0.34	0/4755
18	Du	0.11	0/3502	0.30	0/4755
18	Ec	0.10	0/3502	0.27	0/4755
18	Ee	0.10	0/3502	0.27	0/4755
18	Eg	0.11	0/3502	0.29	0/4755
18	Ei	0.11	0/3502	0.29	0/4755
18	Ek	0.10	0/3502	0.28	0/4755
18	Em	0.13	0/3502	0.32	0/4755
18	Eo	0.13	0/3502	0.32	0/4755
18	Eq	0.11	0/3502	0.31	0/4755
18	Es	0.11	0/3502	0.31	0/4755
18	Eu	0.10	0/3502	0.28	0/4755
18	Fa	0.09	0/3502	0.27	0/4755
18	Fc	0.10	0/3502	0.28	0/4755
18	Fe	0.10	0/3502	0.28	0/4755
18	Fg	0.10	0/3502	0.28	0/4755
18	Fi	0.10	0/3502	0.27	0/4755
18	Fo	0.12	0/3502	0.31	1/4755 (0.0%)
18	Fq	0.11	0/3502	0.28	0/4755
18	Fs	0.11	0/3502	0.28	0/4755
18	Fu	0.11	0/3502	0.29	0/4755
18	Fw	0.11	0/3502	0.28	0/4755
18	Ga	0.09	0/3502	0.26	0/4755
18	Gc	0.10	0/3502	0.28	0/4755
18	Ge	0.13	0/3502	0.31	0/4755
18	Gg	0.10	0/3502	0.28	0/4755
18	Gi	0.10	0/3502	0.27	0/4755
18	Go	0.12	0/3502	0.31	0/4755
18	Gq	0.12	0/3502	0.33	0/4755
18	Gs	0.13	0/3502	0.32	0/4755
18	Gu	0.11	0/3502	0.28	0/4755
18	Gw	0.12	0/3502	0.32	0/4755

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	Ha	0.10	0/3502	0.27	0/4755
18	Hc	0.10	0/3502	0.29	0/4755
18	He	0.12	0/3502	0.30	0/4755
18	Hg	0.11	0/3502	0.28	0/4755
18	Hi	0.11	0/3502	0.29	0/4755
18	Ho	0.12	0/3502	0.32	0/4755
18	Hq	0.12	0/3502	0.32	0/4755
18	Hs	0.11	0/3502	0.29	0/4755
18	Hu	0.11	0/3502	0.29	0/4755
18	Hw	0.10	0/3502	0.27	0/4755
18	Ia	0.10	0/3502	0.28	0/4755
18	Ic	0.11	0/3502	0.28	0/4755
18	Ie	0.12	0/3502	0.30	0/4755
18	Ig	0.11	0/3502	0.31	0/4755
18	Ii	0.10	0/3502	0.27	0/4755
18	Io	0.13	0/3502	0.30	0/4755
18	Iq	0.12	0/3502	0.31	0/4755
18	Is	0.12	0/3502	0.31	0/4755
18	Iu	0.13	0/3502	0.33	0/4755
18	Iw	0.12	0/3502	0.31	0/4755
18	Ja	0.09	0/3502	0.25	0/4755
18	Jc	0.11	0/3502	0.29	0/4755
18	Je	0.12	0/3502	0.31	1/4755 (0.0%)
18	Jg	0.11	0/3502	0.31	0/4755
18	Ji	0.10	0/3502	0.28	0/4755
18	Jo	0.13	0/3502	0.33	0/4755
18	Jq	0.13	0/3502	0.34	0/4755
18	Js	0.12	0/3502	0.31	0/4755
18	Ju	0.14	0/3502	0.32	0/4755
18	Jw	0.12	0/3502	0.30	0/4755
18	Kc	0.10	0/3502	0.26	0/4755
18	Ke	0.10	0/3502	0.28	0/4755
18	Kg	0.10	0/3502	0.27	0/4755
18	Ki	0.10	0/3502	0.27	0/4755
18	Kk	0.10	0/3502	0.27	0/4755
18	Km	0.10	0/3502	0.28	0/4755
18	Ko	0.12	0/3502	0.32	0/4755
18	Kq	0.12	0/3502	0.31	0/4755
18	Ks	0.11	0/3502	0.30	0/4755
18	Ku	0.11	0/3502	0.31	0/4755
18	Lc	0.12	0/3502	0.28	0/4755
18	Le	0.10	0/3502	0.27	0/4755
18	Lg	0.14	0/3502	0.30	0/4755

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	Li	0.10	0/3502	0.28	0/4755
18	Lk	0.10	0/3502	0.28	0/4755
18	Lm	0.11	0/3502	0.29	0/4755
18	Lo	0.11	0/3502	0.30	0/4755
18	Lq	0.12	0/3502	0.31	0/4755
18	Ls	0.14	0/3502	0.31	0/4755
18	Lu	0.11	0/3502	0.28	0/4755
18	Mc	0.10	0/3502	0.26	0/4755
18	Me	0.10	0/3502	0.27	0/4755
18	Mg	0.10	0/3502	0.28	0/4755
18	Mi	0.10	0/3502	0.29	0/4755
18	Mk	0.09	0/3502	0.26	0/4755
18	Mm	0.10	0/3502	0.27	0/4755
18	Mo	0.11	0/3502	0.29	0/4755
18	Mq	0.11	0/3502	0.29	0/4755
18	Ms	0.11	0/3502	0.29	0/4755
18	Mu	0.11	0/3502	0.27	0/4755
19	A1	0.17	0/3896	0.46	0/5295
19	AA	0.11	0/3566	0.29	0/4850
19	AB	0.10	0/3896	0.27	0/5295
19	AC	0.13	0/3688	0.32	0/5010
19	AD	0.11	0/3949	0.30	0/5367
19	AE	0.11	0/3949	0.29	0/5367
19	AF	0.11	0/3949	0.28	0/5367
19	AG	0.11	0/3949	0.31	0/5367
19	AH	0.12	0/3949	0.32	0/5367
19	AI	0.14	0/3949	0.35	1/5367 (0.0%)
19	AJ	0.13	0/3949	0.32	0/5367
19	AK	0.12	0/3807	0.32	0/5173
19	AL	0.11	0/3910	0.29	0/5314
19	AM	0.11	0/3807	0.28	0/5173
19	AN	0.11	0/3807	0.33	0/5173
19	AO	0.14	0/3815	0.36	0/5185
19	AP	0.11	0/3910	0.31	0/5314
19	AQ	0.11	0/3904	0.30	0/5306
19	AR	0.10	0/3896	0.27	0/5295
19	AS	0.12	0/3910	0.32	0/5314
19	AT	0.11	0/3807	0.29	0/5175
19	AU	0.11	0/3815	0.30	0/5185
19	AV	0.12	0/3910	0.37	0/5314
19	AW	0.12	0/3949	0.32	0/5367
19	AX	0.22	0/3896	0.51	0/5295
19	AY	0.18	0/3896	0.48	2/5295 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
19	AZ	0.17	0/3896	0.44	0/5295
20	3D	0.22	0/1186	0.55	0/1590
20	3E	0.21	0/1186	0.49	0/1590
20	3F	0.25	0/1186	0.60	0/1590
20	3G	0.24	0/1186	0.58	1/1590 (0.1%)
20	3H	0.19	0/1186	0.53	1/1590 (0.1%)
20	3I	0.22	0/1186	0.56	0/1590
20	3J	0.28	0/1186	0.62	1/1590 (0.1%)
21	A2	0.13	0/6713	0.35	0/9049
21	A3	0.13	0/6713	0.35	1/9049 (0.0%)
21	A4	0.13	0/6713	0.36	0/9049
22	1A	0.10	0/1311	0.30	0/1766
22	1B	0.14	0/1311	0.34	0/1766
22	1C	0.09	0/1311	0.28	0/1766
22	1D	0.13	0/1311	0.35	0/1766
22	1E	0.13	0/1311	0.37	0/1766
22	1F	0.14	0/1311	0.33	0/1766
22	1G	0.12	0/1311	0.31	0/1766
22	1I	0.17	0/1311	0.38	0/1766
22	1J	0.15	0/1311	0.37	0/1766
22	1K	0.10	0/1311	0.27	0/1766
22	1L	0.10	0/1311	0.28	0/1766
22	1M	0.11	0/1311	0.30	0/1766
22	1N	0.13	0/1311	0.31	0/1766
22	1O	0.13	0/1311	0.36	0/1766
22	1P	0.18	0/1311	0.39	0/1766
22	1Q	0.21	0/1311	0.35	0/1766
22	1R	0.21	0/1311	0.38	0/1766
22	1S	0.10	0/1311	0.28	0/1766
22	1T	0.11	0/1311	0.32	0/1766
22	1U	0.13	0/1311	0.35	0/1766
22	1V	0.14	0/1311	0.39	0/1766
22	1W	0.11	0/1311	0.30	0/1766
22	1X	0.15	0/1311	0.35	0/1766
22	1Y	0.11	0/1311	0.29	0/1766
22	1Z	0.12	0/1311	0.31	0/1766
22	1a	0.14	0/1311	0.35	0/1766
22	1b	0.16	0/1311	0.41	0/1766
22	1c	0.11	0/1311	0.31	0/1766
22	1d	0.12	0/1311	0.31	0/1766
22	1e	0.19	0/1311	0.42	0/1766
22	1f	0.16	0/1311	0.40	0/1766
22	1g	0.18	0/1311	0.43	0/1766

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
22	1h	0.15	0/1311	0.38	1/1766 (0.1%)
22	1i	0.22	0/1311	0.48	0/1766
22	1j	0.14	0/1311	0.38	0/1766
22	1k	0.13	0/1311	0.37	0/1766
22	2A	0.26	0/1311	0.48	0/1766
22	2B	0.12	0/1311	0.30	0/1766
22	2C	0.19	0/1311	0.42	1/1766 (0.1%)
22	2D	0.15	0/1311	0.35	1/1766 (0.1%)
22	2E	0.27	0/1311	0.49	0/1766
22	2F	0.12	0/1311	0.37	0/1766
22	2G	0.20	0/1311	0.49	0/1766
22	2H	0.11	0/1311	0.31	0/1766
22	2I	0.14	0/1311	0.38	0/1766
22	2J	0.12	0/1311	0.32	0/1766
22	2K	0.13	0/1311	0.38	0/1766
22	2L	0.19	0/1311	0.42	0/1766
22	2M	0.12	0/1311	0.34	0/1766
22	2N	0.21	0/1311	0.45	0/1766
22	2O	0.12	0/1311	0.33	0/1766
22	2P	0.18	0/1311	0.45	0/1766
22	2Q	0.14	0/1311	0.37	0/1766
22	2R	0.11	0/1311	0.32	0/1766
22	2S	0.13	0/1311	0.35	0/1766
22	2T	0.12	0/1311	0.35	0/1766
22	2U	0.16	0/1311	0.44	0/1766
22	2V	0.12	0/1311	0.35	0/1766
23	3T	0.10	0/467	0.27	0/632
23	3U	0.10	0/609	0.28	0/822
23	3V	0.10	0/479	0.24	0/648
23	3W	0.11	0/609	0.27	0/822
23	3X	0.13	0/479	0.29	0/648
23	3Y	0.10	0/609	0.29	0/822
25	3B	0.26	0/1553	0.58	1/2082 (0.0%)
25	3C	0.25	0/1553	0.60	3/2082 (0.1%)
26	3K	0.11	0/1426	0.29	0/1932
26	3L	0.11	0/1240	0.28	0/1676
26	3M	0.12	0/1426	0.32	0/1932
26	3N	0.12	0/1240	0.33	0/1676
26	3O	0.22	0/1426	0.54	0/1932
26	3P	0.28	0/1240	0.51	0/1676
27	3Q	0.14	0/1060	0.36	0/1431
27	3R	0.16	0/1060	0.34	0/1431
27	3S	0.14	0/1060	0.33	0/1431

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	4A	0.15	0/22852	0.41	4/31018 (0.0%)
33	4B	0.15	0/22852	0.42	0/31018
34	4G	0.16	0/33882	0.41	1/45995 (0.0%)
34	4H	0.16	0/29847	0.42	3/40501 (0.0%)
34	4I	0.17	0/26310	0.44	1/35695 (0.0%)
34	4J	0.16	0/5765	0.42	1/7843 (0.0%)
34	4K	0.17	0/3186	0.43	3/4333 (0.1%)
35	4C	0.16	0/3474	0.43	0/4693
35	4D	0.16	0/3474	0.40	0/4693
35	4E	0.18	0/3474	0.47	0/4693
35	4F	0.14	0/3474	0.37	0/4693
36	4L	0.15	0/11353	0.41	0/15333
36	4M	0.16	0/11353	0.43	2/15333 (0.0%)
36	4N	0.15	0/11353	0.41	0/15333
37	4O	0.12	0/3919	0.32	0/5312
37	4P	0.13	0/3919	0.33	0/5312
37	4Q	0.13	0/3919	0.35	0/5312
38	4R	0.14	0/3151	0.39	0/4262
38	4S	0.13	0/3143	0.38	0/4251
38	4T	0.14	0/3151	0.38	0/4262
38	4U	0.13	0/3143	0.34	0/4251
38	4V	0.15	0/3151	0.43	3/4262 (0.1%)
38	4W	0.13	0/3151	0.36	0/4262
39	4X	0.17	0/5878	0.47	2/7933 (0.0%)
39	4Y	0.21	0/5878	0.52	3/7933 (0.0%)
40	4Z	0.18	0/5318	0.50	1/7147 (0.0%)
41	4a	0.19	0/2222	0.52	0/3001
42	4b	0.18	0/4338	0.51	0/5908
42	4c	0.20	0/4338	0.50	0/5908
43	5A	0.78	0/1470	1.46	6/1991 (0.3%)
43	J	0.31	0/1308	0.65	1/1735 (0.1%)
43	K	0.54	0/3428	1.05	6/4594 (0.1%)
44	5B	0.90	0/5269	1.74	90/7127 (1.3%)
45	5C	0.87	0/3748	1.84	83/5094 (1.6%)
All	All	0.15	2/1668722 (0.0%)	0.37	261/2261114 (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	d	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	g	0	1
3	h	0	1
8	A	0	1
8	B	0	1
9	C	0	2
11	H	0	7
11	I	0	4
14	P	0	1
15	R	0	1
16	x	0	9
17	Cr	0	1
18	Ao	0	1
19	AJ	0	1
20	3J	0	1
22	1Q	0	1
22	1R	0	1
26	3O	0	3
28	3a	0	1
33	4A	0	2
33	4B	0	7
34	4G	0	4
34	4H	0	4
37	4O	0	1
38	4S	0	1
39	4X	0	1
39	4Y	0	1
40	4Z	0	1
41	4a	0	1
42	4b	0	2
42	4c	0	1
43	5A	0	2
43	K	0	2
44	5B	0	14
45	5C	0	13
All	All	0	96

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	x	516	LEU	C-O	7.81	1.27	1.23
18	Di	203	MET	CG-SD	5.40	1.94	1.80

The worst 5 of 261 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	5B	881	HIS	CA-CB-CG	14.66	128.46	113.80
45	5C	571	PRO	CA-C-N	13.17	139.60	121.96
45	5C	571	PRO	C-N-CA	13.17	139.60	121.96
3	i	1044	ASP	N-CA-C	12.93	126.23	110.19
43	5A	104	PHE	CA-CB-CG	11.61	125.41	113.80

There are no chirality outliers.

5 of 96 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	A	1849	GLU	Peptide
8	B	1849	GLU	Peptide
2	d	742	ASP	Peptide
2	g	742	ASP	Peptide
3	h	1037	TYR	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	W	1509	0	1573	42	0
1	X	1509	0	1573	39	0
1	Y	1509	0	1573	41	0
1	Z	1509	0	1573	68	0
1	a	1509	0	1573	44	0
1	b	1509	0	1573	36	0
2	c	4014	0	4003	90	0
2	d	4578	0	4575	165	0
2	e	4014	0	4003	109	0
2	f	4014	0	4003	93	0
2	g	4578	0	4575	157	0
3	h	11503	0	11441	248	0
3	i	11503	0	11441	190	0
3	j	11503	0	11441	239	0
4	k	6859	0	6783	115	0
4	l	6979	0	6894	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	m	6859	0	6783	115	0
4	n	6979	0	6894	113	0
4	o	6859	0	6783	95	0
4	p	6979	0	6894	107	0
5	q	1723	0	1726	70	0
5	r	1723	0	1726	68	0
5	s	1723	0	1726	65	0
6	t	1532	0	1559	36	0
6	u	1532	0	1559	45	0
7	v	1313	0	1326	56	0
7	w	1313	0	1326	61	0
8	A	14212	0	14365	517	0
8	B	10003	0	10107	358	0
9	C	7752	0	7920	317	0
9	D	2529	0	2580	177	0
9	E	3814	0	3860	70	0
10	F	8741	0	8730	259	0
10	G	4117	0	4088	126	0
11	H	21709	0	22235	1092	0
11	I	7165	0	7333	412	0
12	L	1866	0	1869	72	0
13	M	1507	0	1557	89	0
14	O	10182	0	10209	337	0
14	P	4660	0	4623	122	0
15	Q	3594	0	3558	208	0
15	R	3608	0	3569	175	0
15	S	3594	0	3558	201	0
15	T	3608	0	3569	214	0
15	U	3594	0	3558	200	0
15	V	3608	0	3569	178	0
16	x	8949	0	8883	392	0
16	y	9047	0	8959	233	0
16	z	9047	0	8959	243	0
17	Ab	3391	0	3269	82	0
17	Ad	3391	0	3269	95	0
17	Af	3391	0	3269	90	0
17	Ah	3391	0	3269	89	0
17	Aj	3391	0	3269	82	0
17	An	3391	0	3269	88	0
17	Ap	3391	0	3269	101	0
17	Ar	3391	0	3269	100	0
17	At	3391	0	3269	97	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Av	3391	0	3269	90	0
17	Bb	3391	0	3269	99	0
17	Bd	3391	0	3269	99	0
17	Bf	3391	0	3269	85	0
17	Bh	3391	0	3269	98	0
17	Bj	3391	0	3269	121	0
17	Bn	3391	0	3269	107	0
17	Bp	3391	0	3269	122	0
17	Br	3391	0	3269	96	0
17	Bt	3391	0	3269	90	0
17	Bv	3391	0	3269	82	0
17	Cb	3391	0	3269	94	0
17	Cd	3391	0	3269	110	0
17	Cf	3391	0	3269	87	0
17	Ch	3391	0	3269	89	0
17	Cj	3391	0	3269	99	0
17	Cn	3391	0	3269	95	0
17	Cp	3391	0	3269	105	0
17	Cr	3391	0	3269	102	0
17	Ct	3391	0	3269	109	0
17	Cv	3391	0	3269	93	0
17	Db	3391	0	3269	84	0
17	Dd	3391	0	3269	127	0
17	Df	3391	0	3269	95	0
17	Dh	3391	0	3269	115	0
17	Dj	3391	0	3269	105	0
17	Dn	3391	0	3269	102	0
17	Dp	3391	0	3269	103	0
17	Dr	3391	0	3269	101	0
17	Dt	3391	0	3269	103	0
17	Dv	3391	0	3269	86	0
17	Eb	3391	0	3269	82	0
17	Ed	3391	0	3269	90	0
17	Ef	3391	0	3269	101	0
17	Eh	3391	0	3269	101	0
17	Ej	3391	0	3269	93	0
17	En	3391	0	3269	105	0
17	Ep	3391	0	3269	110	0
17	Er	3391	0	3269	98	0
17	Et	3391	0	3269	102	0
17	Ev	3391	0	3269	89	0
17	Fb	3391	0	3269	101	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Fd	3391	0	3269	104	0
17	Ff	3391	0	3269	92	0
17	Fh	3391	0	3269	93	0
17	Fj	3391	0	3269	84	0
17	Fn	3391	0	3269	81	0
17	Fp	3391	0	3269	100	0
17	Fr	3391	0	3269	95	0
17	Ft	3391	0	3269	106	0
17	Fv	3391	0	3269	99	0
17	Gb	3391	0	3269	99	0
17	Gd	3391	0	3268	142	0
17	Gf	3391	0	3269	127	0
17	Gh	3391	0	3269	117	0
17	Gj	3391	0	3269	93	0
17	Gn	3391	0	3269	82	0
17	Gp	3391	0	3269	96	0
17	Gr	3391	0	3269	96	0
17	Gt	3391	0	3269	100	0
17	Gv	3391	0	3269	87	0
17	Hb	3391	0	3269	105	0
17	Hd	3391	0	3269	94	0
17	Hf	3391	0	3269	83	0
17	Hh	3391	0	3269	88	0
17	Hj	3391	0	3269	96	0
17	Hn	3391	0	3269	83	0
17	Hp	3391	0	3269	112	0
17	Hr	3391	0	3269	98	0
17	Ht	3391	0	3269	88	0
17	Hv	3391	0	3269	99	0
17	Ib	3391	0	3269	91	0
17	Id	3391	0	3269	92	0
17	If	3391	0	3269	106	0
17	Ih	3391	0	3269	87	0
17	Ij	3391	0	3269	83	0
17	In	3391	0	3269	79	0
17	Ip	3391	0	3269	93	0
17	Ir	3391	0	3269	95	0
17	It	3391	0	3269	85	0
17	Iv	3391	0	3269	100	0
17	Jb	3391	0	3269	100	0
17	Jd	3391	0	3269	103	0
17	Jf	3391	0	3269	103	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Jh	3391	0	3269	97	0
17	Jj	3391	0	3269	89	0
17	Jn	3391	0	3269	92	0
17	Jp	3391	0	3269	124	0
17	Jr	3391	0	3269	114	0
17	Jt	3391	0	3269	106	0
17	Jv	3391	0	3269	100	0
17	Kb	3391	0	3269	94	0
17	Kd	3391	0	3269	104	0
17	Kf	3391	0	3269	92	0
17	Kh	3391	0	3269	98	0
17	Kj	3391	0	3269	95	0
17	Kn	3390	0	3265	101	0
17	Kp	3391	0	3269	120	0
17	Kr	3391	0	3269	115	0
17	Kt	3391	0	3269	102	0
17	Kv	3391	0	3269	104	0
17	Lb	3391	0	3269	92	0
17	Ld	3391	0	3269	105	0
17	Lf	3391	0	3269	94	0
17	Lh	3391	0	3269	97	0
17	Lj	3391	0	3269	93	0
17	Ln	3391	0	3269	104	0
17	Lp	3391	0	3269	86	0
17	Lr	3391	0	3269	112	0
17	Lt	3391	0	3269	108	0
17	Lv	3391	0	3269	82	0
17	Mb	3391	0	3269	72	0
17	Md	3391	0	3269	84	0
17	Mf	3391	0	3269	91	0
17	Mh	3391	0	3269	104	0
17	Mj	3391	0	3269	76	0
17	Mn	3391	0	3269	98	0
17	Mp	3391	0	3269	94	0
17	Mr	3391	0	3269	99	0
17	Mt	3391	0	3269	101	0
17	Mv	3391	0	3269	91	0
18	Ac	3424	0	3339	76	0
18	Ae	3424	0	3339	72	0
18	Ag	3424	0	3339	79	0
18	Ai	3424	0	3339	72	0
18	Ak	3424	0	3339	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Ao	3424	0	3339	102	0
18	Aq	3424	0	3339	68	0
18	As	3424	0	3339	99	0
18	Au	3424	0	3339	81	0
18	Aw	3424	0	3339	71	0
18	Bc	3424	0	3339	63	0
18	Be	3424	0	3339	71	0
18	Bg	3424	0	3339	80	0
18	Bi	3424	0	3339	88	0
18	Bk	3424	0	3339	86	0
18	Bm	3424	0	3339	90	0
18	Bo	3424	0	3339	93	0
18	Bq	3424	0	3339	108	0
18	Bs	3424	0	3339	81	0
18	Bu	3424	0	3339	75	0
18	Cc	3424	0	3339	68	0
18	Ce	3424	0	3339	86	0
18	Cg	3424	0	3339	89	0
18	Ci	3424	0	3339	88	0
18	Ck	3424	0	3339	87	0
18	Cm	3424	0	3339	91	0
18	Co	3424	0	3339	86	0
18	Cq	3424	0	3339	104	0
18	Cs	3424	0	3339	96	0
18	Cu	3424	0	3339	75	0
18	Dc	3424	0	3339	73	0
18	De	3424	0	3339	73	0
18	Dg	3424	0	3339	83	0
18	Di	3424	0	3339	89	0
18	Dk	3424	0	3339	76	0
18	Dm	3424	0	3339	86	0
18	Do	3424	0	3339	83	0
18	Dq	3424	0	3339	94	0
18	Ds	3424	0	3339	115	0
18	Du	3424	0	3339	79	0
18	Ec	3424	0	3339	93	0
18	Ee	3424	0	3339	72	0
18	Eg	3424	0	3339	95	0
18	Ei	3424	0	3339	76	0
18	Ek	3424	0	3339	83	0
18	Em	3424	0	3339	95	0
18	Eo	3424	0	3339	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Eq	3424	0	3339	92	0
18	Es	3424	0	3339	77	0
18	Eu	3424	0	3339	66	0
18	Fa	3424	0	3339	66	0
18	Fc	3424	0	3339	78	0
18	Fe	3424	0	3339	81	0
18	Fg	3424	0	3339	96	0
18	Fi	3424	0	3339	76	0
18	Fo	3424	0	3339	87	0
18	Fq	3424	0	3339	71	0
18	Fs	3424	0	3339	67	0
18	Fu	3424	0	3339	73	0
18	Fw	3424	0	3339	60	0
18	Ga	3424	0	3339	115	0
18	Gc	3424	0	3339	96	0
18	Ge	3424	0	3339	125	0
18	Gg	3424	0	3339	85	0
18	Gi	3424	0	3339	106	0
18	Go	3424	0	3339	79	0
18	Gq	3424	0	3339	103	0
18	Gs	3424	0	3339	84	0
18	Gu	3424	0	3339	82	0
18	Gw	3424	0	3339	83	0
18	Ha	3424	0	3339	86	0
18	Hc	3424	0	3339	75	0
18	He	3424	0	3339	95	0
18	Hg	3424	0	3339	103	0
18	Hi	3424	0	3338	108	0
18	Ho	3424	0	3339	86	0
18	Hq	3424	0	3339	101	0
18	Hs	3424	0	3339	86	0
18	Hu	3424	0	3339	97	0
18	Hw	3424	0	3339	85	0
18	Ia	3424	0	3339	65	0
18	Ic	3424	0	3339	83	0
18	Ie	3424	0	3339	85	0
18	Ig	3424	0	3339	87	0
18	Ii	3424	0	3339	87	0
18	Io	3424	0	3339	107	0
18	Iq	3424	0	3339	94	0
18	Is	3424	0	3339	110	0
18	Iu	3424	0	3339	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Iw	3424	0	3339	87	0
18	Ja	3424	0	3339	67	0
18	Jc	3424	0	3339	71	0
18	Je	3424	0	3339	101	0
18	Jg	3424	0	3339	128	0
18	Ji	3424	0	3339	88	0
18	Jo	3424	0	3339	100	0
18	Jq	3424	0	3339	111	0
18	Js	3424	0	3339	87	0
18	Ju	3424	0	3339	97	0
18	Jw	3424	0	3339	72	0
18	Kc	3424	0	3339	78	0
18	Ke	3424	0	3339	88	0
18	Kg	3424	0	3339	87	0
18	Ki	3424	0	3339	85	0
18	Kk	3424	0	3339	88	0
18	Km	3424	0	3339	67	0
18	Ko	3424	0	3339	111	0
18	Kq	3424	0	3339	98	0
18	Ks	3424	0	3339	93	0
18	Ku	3424	0	3339	95	0
18	Lc	3424	0	3339	73	0
18	Le	3424	0	3339	73	0
18	Lg	3424	0	3339	72	0
18	Li	3424	0	3339	74	0
18	Lk	3424	0	3339	68	0
18	Lm	3424	0	3339	85	0
18	Lo	3424	0	3339	90	0
18	Lq	3424	0	3339	94	0
18	Ls	3424	0	3339	101	0
18	Lu	3424	0	3339	85	0
18	Mc	3424	0	3339	78	0
18	Me	3424	0	3339	81	0
18	Mg	3424	0	3339	83	0
18	Mi	3424	0	3339	90	0
18	Mk	3424	0	3339	61	0
18	Mm	3424	0	3339	67	0
18	Mo	3424	0	3339	90	0
18	Mq	3424	0	3339	89	0
18	Ms	3424	0	3339	86	0
18	Mu	3424	0	3339	86	0
19	A1	3831	0	3967	189	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	AA	3505	0	3633	85	0
19	AB	3831	0	3967	80	0
19	AC	3629	0	3779	111	0
19	AD	3882	0	4011	96	0
19	AE	3882	0	4011	90	0
19	AF	3882	0	4011	87	0
19	AG	3882	0	4011	108	0
19	AH	3882	0	4011	107	0
19	AI	3882	0	4011	164	0
19	AJ	3882	0	4011	139	0
19	AK	3744	0	3880	111	0
19	AL	3845	0	3976	99	0
19	AM	3744	0	3880	102	0
19	AN	3744	0	3880	81	0
19	AO	3751	0	3887	104	0
19	AP	3845	0	3976	114	0
19	AQ	3839	0	3971	112	0
19	AR	3831	0	3967	77	0
19	AS	3845	0	3976	121	0
19	AT	3743	0	3875	100	0
19	AU	3751	0	3887	90	0
19	AV	3845	0	3976	113	0
19	AW	3882	0	4011	113	0
19	AX	3831	0	3967	259	0
19	AY	3831	0	3967	220	0
19	AZ	3831	0	3967	250	0
20	3D	1174	0	1105	102	0
20	3E	1174	0	1105	103	0
20	3F	1174	0	1105	116	0
20	3G	1174	0	1105	107	0
20	3H	1174	0	1105	114	0
20	3I	1174	0	1105	96	0
20	3J	1174	0	1105	119	0
21	A2	6600	0	6783	226	0
21	A3	6600	0	6783	246	0
21	A4	6600	0	6783	267	0
22	1A	1285	0	1271	23	0
22	1B	1285	0	1271	19	0
22	1C	1285	0	1271	23	0
22	1D	1285	0	1271	24	0
22	1E	1285	0	1271	39	0
22	1F	1285	0	1271	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	1G	1285	0	1271	30	0
22	1I	1285	0	1271	29	0
22	1J	1285	0	1271	31	0
22	1K	1285	0	1271	27	0
22	1L	1285	0	1271	26	0
22	1M	1285	0	1271	26	0
22	1N	1285	0	1271	42	0
22	1O	1285	0	1271	33	0
22	1P	1285	0	1271	42	0
22	1Q	1285	0	1271	53	0
22	1R	1285	0	1271	55	0
22	1S	1285	0	1271	25	0
22	1T	1285	0	1271	23	0
22	1U	1285	0	1271	33	0
22	1V	1285	0	1271	26	0
22	1W	1285	0	1271	33	0
22	1X	1285	0	1271	36	0
22	1Y	1285	0	1271	40	0
22	1Z	1285	0	1271	35	0
22	1a	1285	0	1271	23	0
22	1b	1285	0	1271	39	0
22	1c	1285	0	1271	19	0
22	1d	1285	0	1271	32	0
22	1e	1285	0	1271	33	0
22	1f	1285	0	1271	49	0
22	1g	1285	0	1271	48	0
22	1h	1285	0	1271	31	0
22	1i	1285	0	1271	54	0
22	1j	1285	0	1271	34	0
22	1k	1285	0	1271	32	0
22	2A	1285	0	1271	55	0
22	2B	1285	0	1271	47	0
22	2C	1285	0	1271	53	0
22	2D	1285	0	1271	28	0
22	2E	1285	0	1271	48	0
22	2F	1285	0	1271	30	0
22	2G	1285	0	1271	68	0
22	2H	1285	0	1271	36	0
22	2I	1285	0	1271	39	0
22	2J	1285	0	1271	42	0
22	2K	1285	0	1271	48	0
22	2L	1285	0	1271	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	2M	1285	0	1271	42	0
22	2N	1285	0	1271	50	0
22	2O	1285	0	1271	31	0
22	2P	1285	0	1271	54	0
22	2Q	1285	0	1271	38	0
22	2R	1285	0	1271	25	0
22	2S	1285	0	1271	47	0
22	2T	1285	0	1271	43	0
22	2U	1285	0	1271	51	0
22	2V	1285	0	1271	28	0
23	3T	459	0	482	16	0
23	3U	601	0	621	21	0
23	3V	471	0	492	8	0
23	3W	601	0	621	12	0
23	3X	471	0	492	16	0
23	3Y	601	0	621	9	0
24	3A	285	0	59	1	0
25	3B	1516	0	1509	171	0
25	3C	1516	0	1509	176	0
26	3K	1389	0	1389	43	0
26	3L	1208	0	1202	27	0
26	3M	1389	0	1389	41	0
26	3N	1208	0	1202	30	0
26	3O	1389	0	1388	138	0
26	3P	1208	0	1202	131	0
27	3Q	1031	0	947	33	0
27	3R	1031	0	947	41	0
27	3S	1031	0	947	24	0
28	3Z	510	0	124	9	0
28	3a	465	0	105	10	0
29	3b	716	0	172	8	0
29	3c	716	0	171	6	0
29	3d	716	0	170	8	0
30	3e	270	0	71	6	0
31	3f	90	0	22	0	0
32	3g	235	0	59	6	0
33	4A	22307	0	22673	1090	0
33	4B	22307	0	22673	1100	0
34	4G	33109	0	33286	1682	0
34	4H	29186	0	29358	1552	0
34	4I	25730	0	25853	1407	0
34	4J	5614	0	5686	251	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	4K	3102	0	3140	133	0
35	4C	3403	0	3413	190	0
35	4D	3403	0	3413	146	0
35	4E	3403	0	3413	201	0
35	4F	3403	0	3413	134	0
36	4L	11139	0	11144	627	0
36	4M	11139	0	11144	645	0
36	4N	11139	0	11144	597	0
37	4O	3840	0	3842	153	0
37	4P	3840	0	3842	149	0
37	4Q	3840	0	3842	172	0
38	4R	3082	0	3123	147	0
38	4S	3074	0	3112	166	0
38	4T	3082	0	3123	148	0
38	4U	3074	0	3112	143	0
38	4V	3082	0	3123	144	0
38	4W	3082	0	3123	161	0
39	4X	5789	0	6031	419	0
39	4Y	5789	0	6031	474	0
40	4Z	5203	0	5160	375	0
41	4a	2170	0	2123	129	0
42	4b	4236	0	4265	328	0
42	4c	4236	0	4265	334	0
43	5A	1430	0	1432	13	0
43	J	1303	0	1335	148	0
43	K	3381	0	3429	328	0
44	5B	5147	0	5149	130	0
45	5C	3669	0	3742	95	0
All	All	1637265	0	1612729	51347	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 16.

The worst 5 of 51347 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)
40:4Z:118:LEU:HD21	44:5B:569:LEU:CD2	1.24	1.63
40:4Z:109:TYR:CE2	44:5B:573:VAL:HG12	1.29	1.61
18:Gi:159:VAL:CG1	43:J:506:LEU:HD22	1.27	1.59
9:D:334:HIS:CE1	43:K:478:ARG:HG3	1.36	1.55
18:Gi:159:VAL:CG2	43:J:506:LEU:CD2	1.82	1.55

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

5.3.2 Protein sidechains

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

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

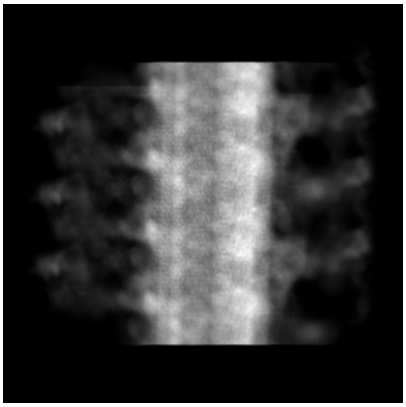
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-60633. These allow visual inspection of the internal detail of the map and identification of artifacts.

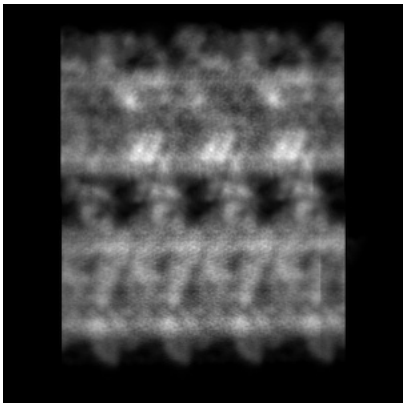
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

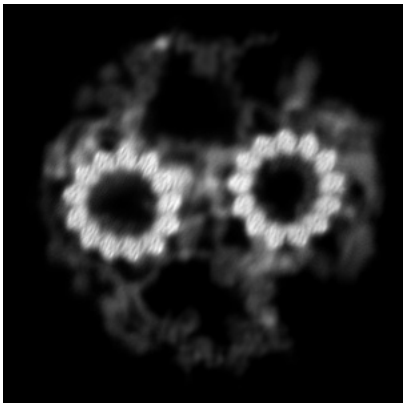
6.1.1 Primary map



X



Y

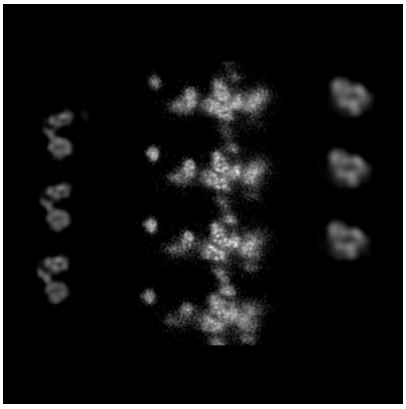


Z

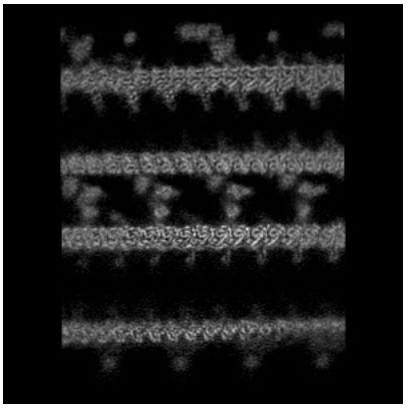
The images above show the map projected in three orthogonal directions.

6.2 Central slices

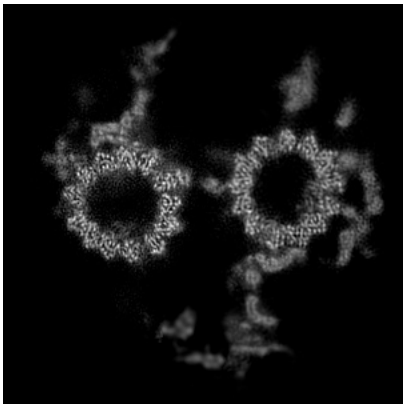
6.2.1 Primary map



X Index: 180



Y Index: 180

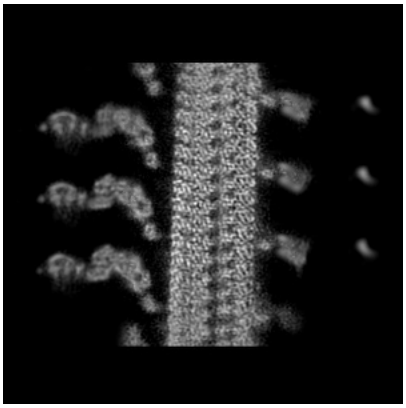


Z Index: 180

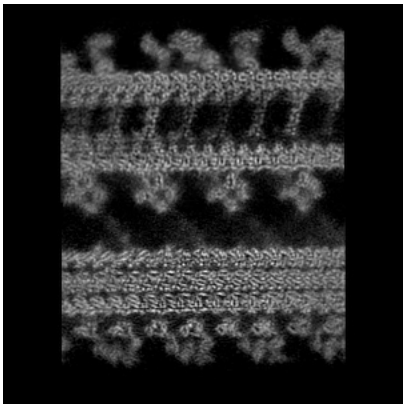
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

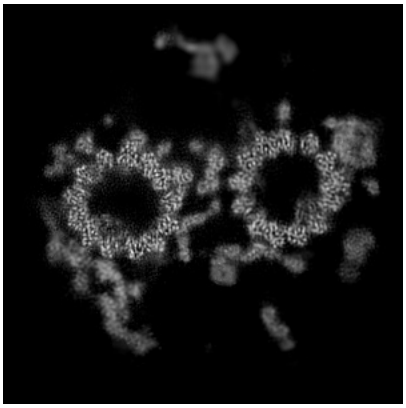
6.3.1 Primary map



X Index: 221



Y Index: 220

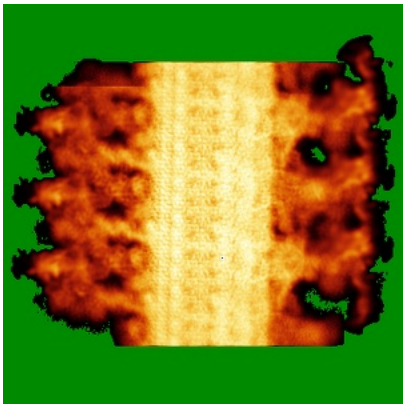


Z Index: 217

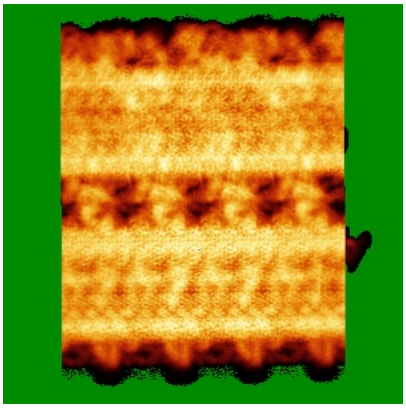
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



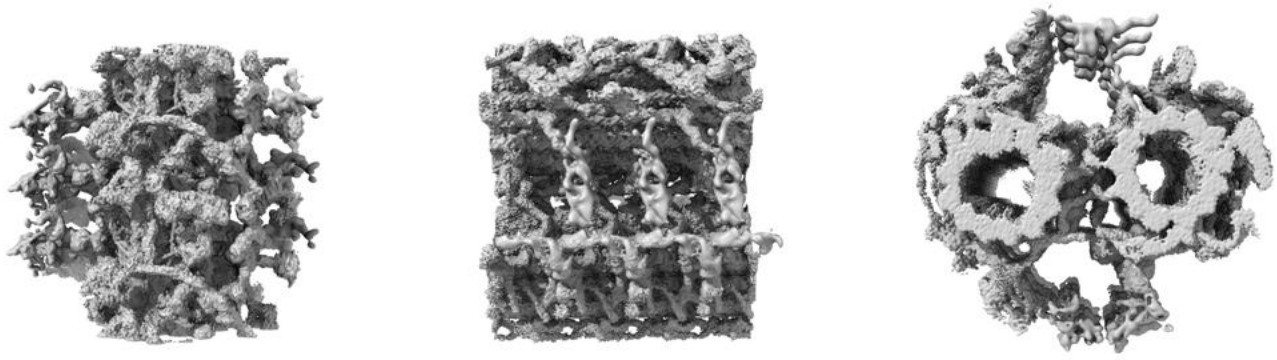
Y

Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

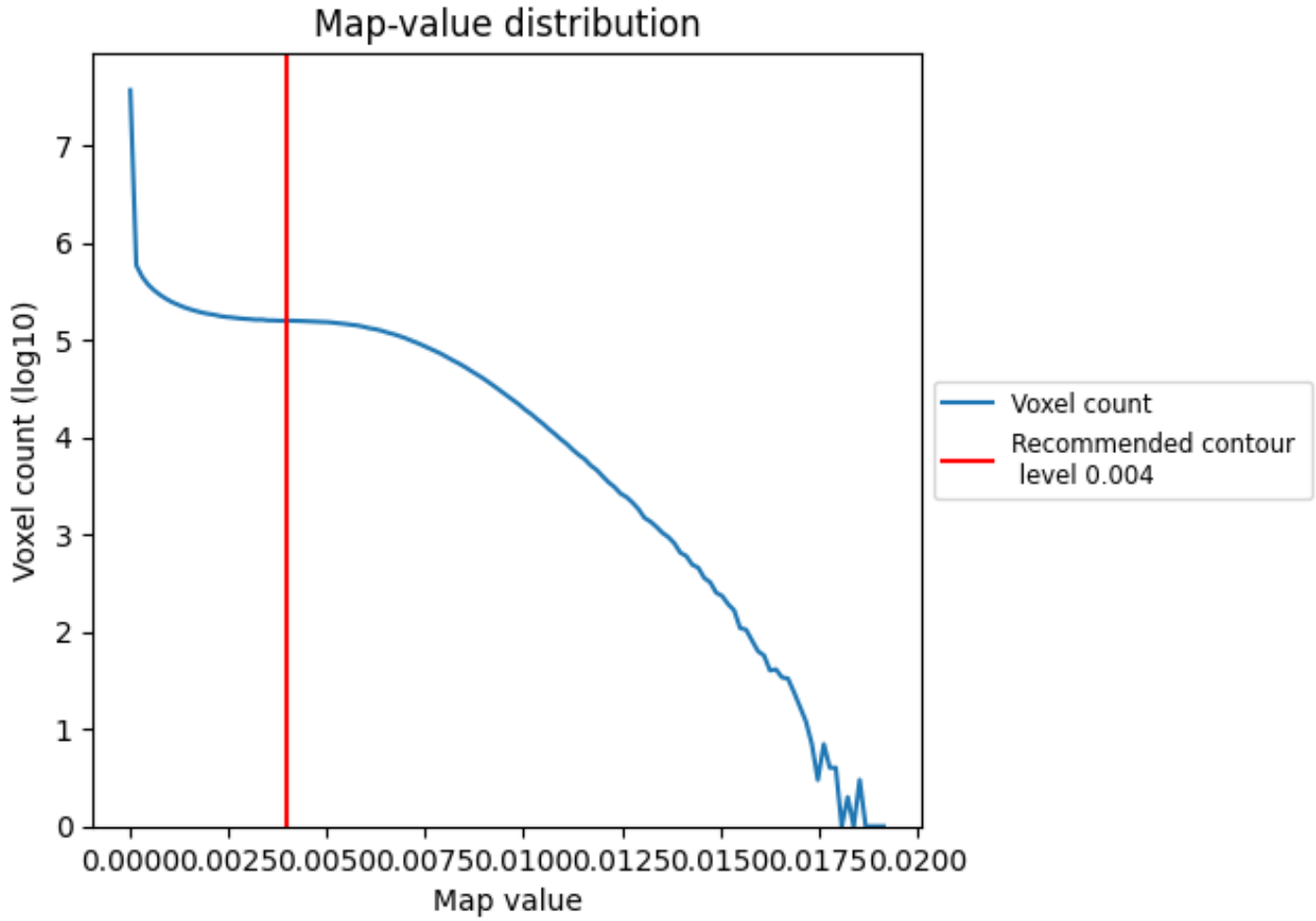
6.6 Mask visualisation (i)

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

7 Map analysis

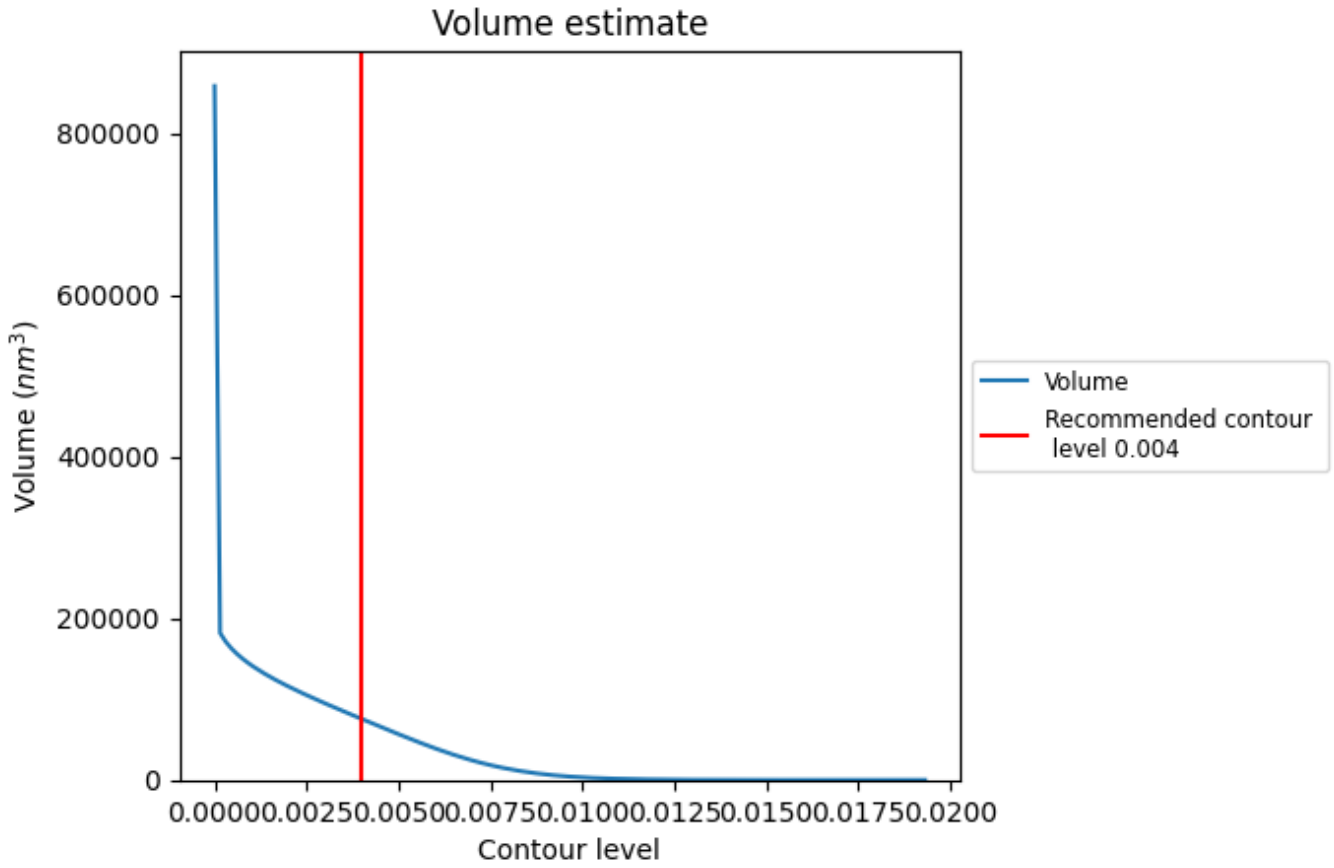
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

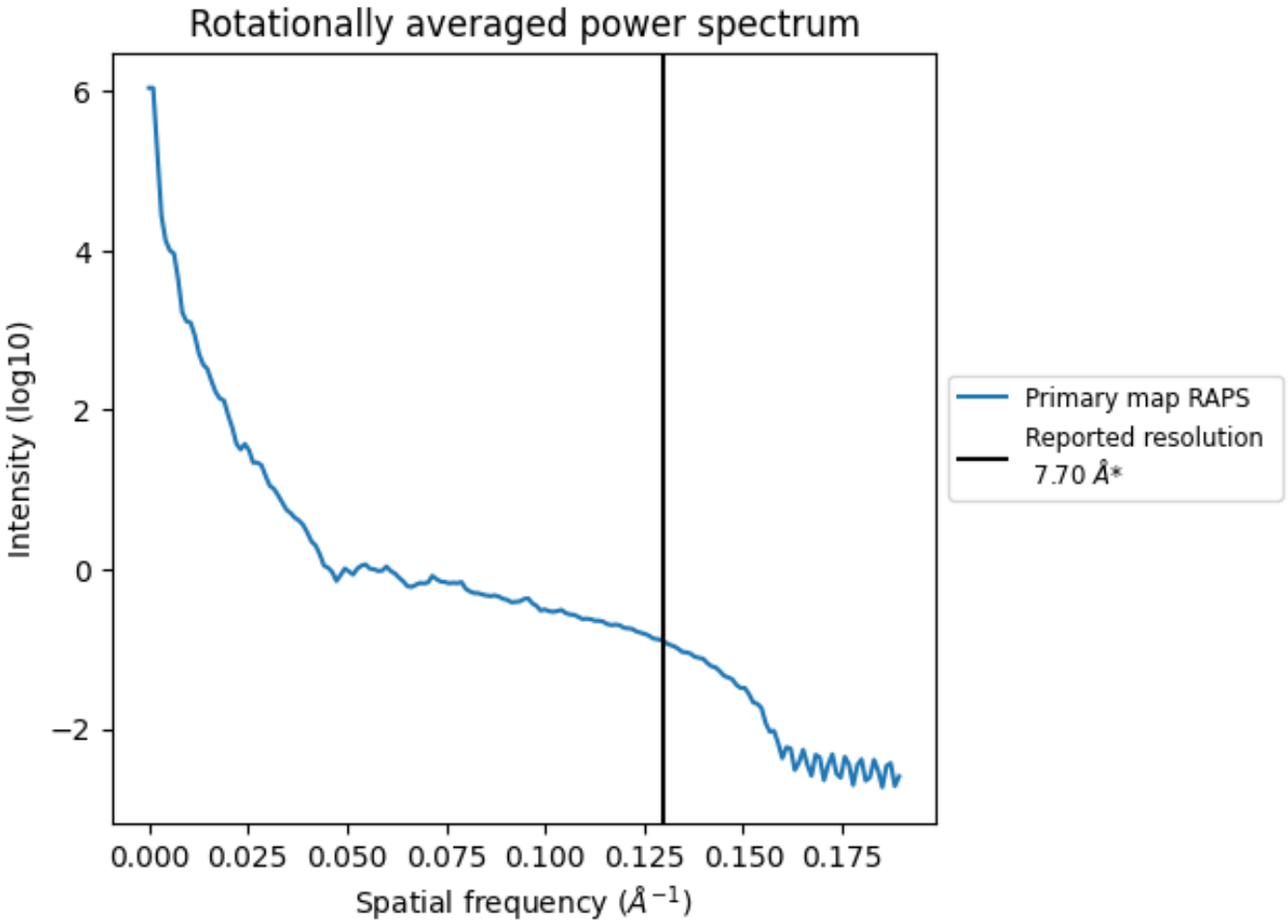
7.2 Volume estimate



The volume at the recommended contour level is 75468 nm^3; this corresponds to an approximate mass of 68172 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.130 Å^{-1}

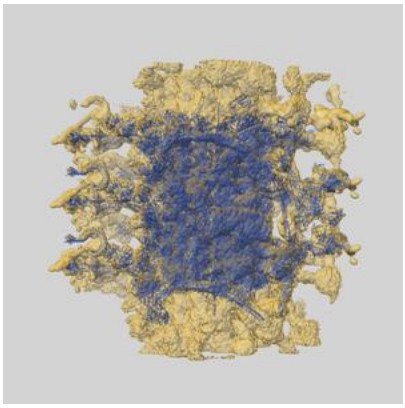
8 Fourier-Shell correlation

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

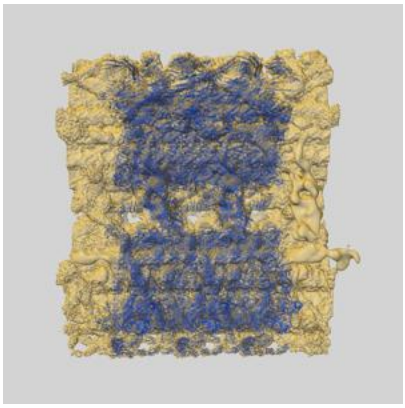
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-60633 and PDB model 9IJJ. Per-residue inclusion information can be found in section 3 on page 49.

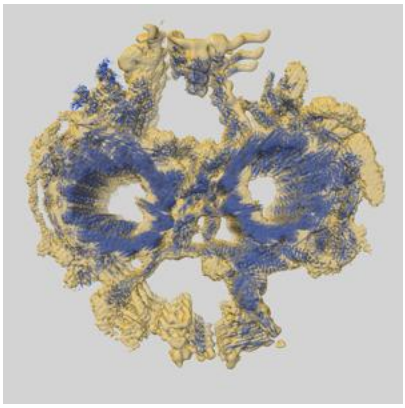
9.1 Map-model overlay



X



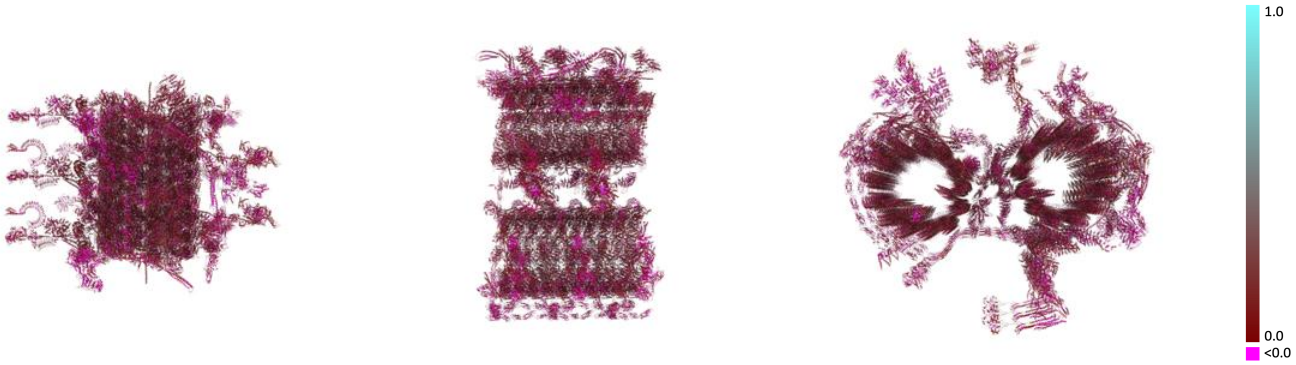
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

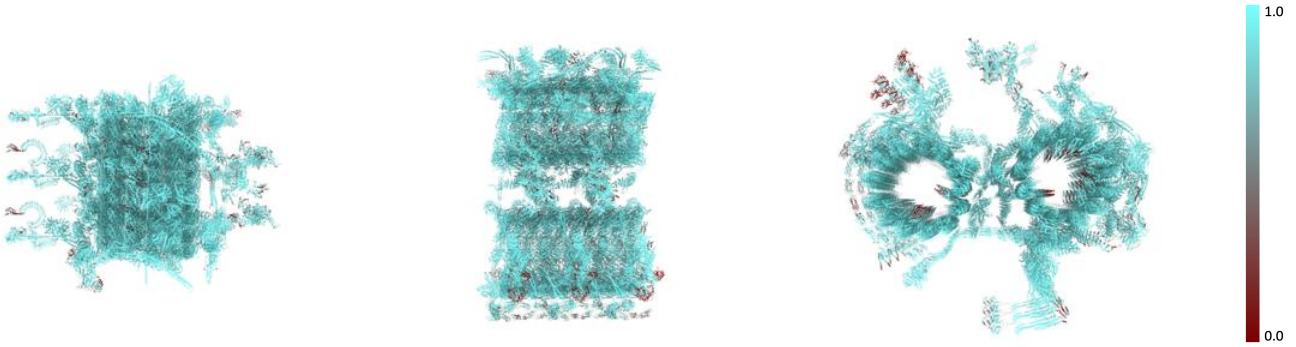
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

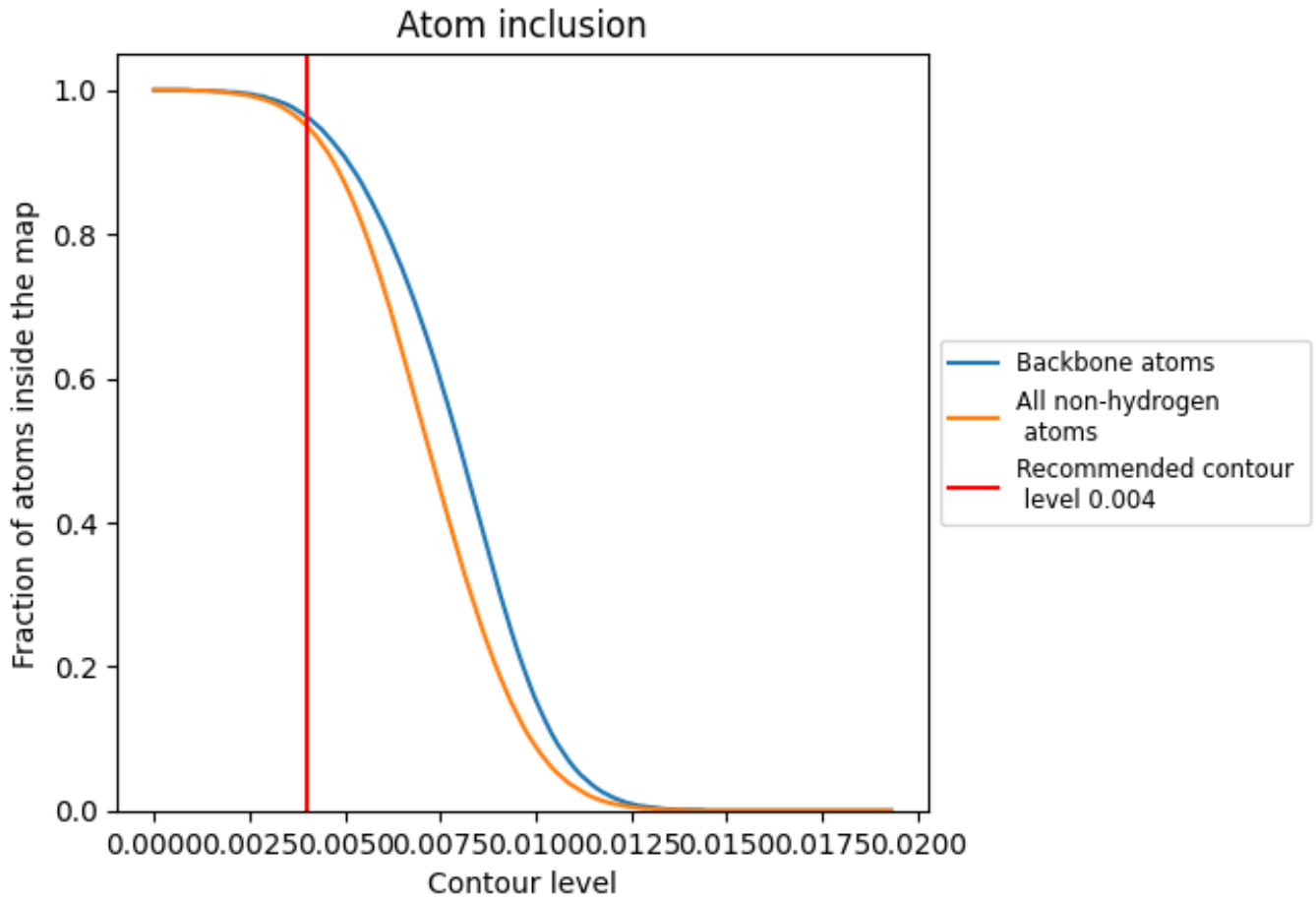
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.004).

9.4 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9500	0.1340
1A	0.9550	0.1500
1B	0.9760	0.1580
1C	0.9920	0.1500
1D	0.9920	0.1530
1E	0.9650	0.1590
1F	0.9640	0.1570
1G	0.9360	0.1480
1I	0.9590	0.1520
1J	0.9480	0.1600
1K	0.9770	0.1620
1L	0.9830	0.1600
1M	0.9830	0.1580
1N	0.9750	0.1650
1O	0.9470	0.1690
1P	0.5730	0.1480
1Q	0.4210	0.1080
1R	0.4910	0.1190
1S	0.8250	0.1470
1T	0.9110	0.1580
1U	0.8500	0.1610
1V	0.6580	0.1440
1W	0.8450	0.1610
1X	0.7380	0.1490
1Y	0.9060	0.1670
1Z	0.8680	0.1470
1a	0.9610	0.1630
1b	0.9760	0.1650
1c	0.9760	0.1620
1d	0.9480	0.1560
1e	0.5420	0.1190
1f	0.5040	0.1180
1g	0.4810	0.1120
1h	0.5250	0.1150
1i	0.5190	0.1240

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Chain	Atom inclusion	Q-score
1j	0.5300	0.1190
1k	0.3400	0.1020
2A	0.6320	0.1270
2B	0.7490	0.1440
2C	0.6230	0.1390
2D	0.3760	0.0320
2E	0.8300	0.1580
2F	0.7460	0.1450
2G	0.6570	0.1650
2H	0.7210	0.1390
2I	0.8290	0.1580
2J	0.8720	0.1630
2K	0.7680	0.1640
2L	0.6750	0.1540
2M	0.7750	0.1580
2N	0.8400	0.1650
2O	0.6560	0.1610
2P	0.6930	0.1440
2Q	0.8170	0.1540
2R	0.8700	0.1630
2S	0.7620	0.1610
2T	0.5990	0.1480
2U	0.7680	0.1470
2V	0.8440	0.1540
3A	0.9860	0.2010
3B	0.9040	0.1060
3C	0.8500	0.0920
3D	0.9420	0.1120
3E	0.6710	0.0860
3F	0.7990	0.0810
3G	0.7130	0.0770
3H	0.6730	0.0880
3I	0.7930	0.0810
3J	0.7260	0.0610
3K	0.8650	0.0550
3L	0.7160	0.0800
3M	0.8680	0.0530
3N	0.7230	0.0830
3O	0.9180	0.0670
3P	0.9260	0.0660
3Q	0.8030	0.0820
3R	0.7870	0.0850

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Chain	Atom inclusion	Q-score
3S	0.6220	0.0790
3T	0.9310	0.0180
3U	0.9700	0.0300
3V	0.7710	0.0350
3W	0.7990	0.0150
3X	0.7670	0.0300
3Y	0.7970	0.0140
3Z	0.9980	0.2310
3a	0.9960	0.2490
3b	1.0000	0.2740
3c	1.0000	0.2440
3d	1.0000	0.2160
3e	0.9960	0.2680
3f	1.0000	0.2940
3g	1.0000	0.2640
4A	0.9960	0.1520
4B	0.9940	0.1270
4C	0.9970	0.1500
4D	0.9990	0.1600
4E	0.9980	0.1270
4F	1.0000	0.1390
4G	0.8610	0.1080
4H	0.8800	0.0920
4I	0.8480	0.1000
4J	0.7180	0.1110
4K	0.6070	0.1060
4L	0.9240	0.1010
4M	0.9260	0.1140
4N	0.9160	0.0880
4O	1.0000	0.1300
4P	1.0000	0.1450
4Q	0.9950	0.0990
4R	0.9990	0.1420
4S	1.0000	0.1140
4T	1.0000	0.1380
4U	0.9990	0.1120
4V	0.9960	0.0940
4W	0.9970	0.0730
4X	0.8110	0.0950
4Y	0.8230	0.0940
4Z	1.0000	0.1290
4a	1.0000	0.1240

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Chain	Atom inclusion	Q-score
4b	1.0000	0.0870
4c	1.0000	0.0540
5A	1.0000	0.1840
5B	0.9940	0.0980
5C	0.8650	0.1190
A	0.8320	0.0410
A1	0.9880	0.1360
A2	0.9880	0.1210
A3	0.9940	0.1540
A4	0.9970	0.1430
AA	0.9830	0.1120
AB	0.9970	0.1390
AC	0.9420	0.0780
AD	0.9510	0.1090
AE	0.9780	0.1000
AF	0.9910	0.1240
AG	0.9010	0.1120
AH	0.9290	0.1210
AI	0.9630	0.1190
AJ	0.9300	0.1050
AK	0.9710	0.1170
AL	0.9670	0.1090
AM	0.9930	0.1150
AN	0.9460	0.1270
AO	0.9880	0.1290
AP	0.9170	0.0740
AQ	0.9840	0.1140
AR	0.9980	0.1440
AS	0.9870	0.0970
AT	0.9620	0.1260
AU	0.9870	0.1260
AV	0.9090	0.0710
AW	0.9740	0.0940
AX	0.8330	0.0850
AY	0.8340	0.0710
AZ	0.9850	0.1170
Ab	0.9940	0.1390
Ac	0.9920	0.1450
Ad	0.9990	0.1470
Ae	0.9960	0.1440
Af	0.9950	0.1450
Ag	0.9940	0.1440

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Chain	Atom inclusion	Q-score
Ah	0.9990	0.1560
Ai	0.9940	0.1420
Aj	0.9950	0.1430
Ak	0.9930	0.1400
An	0.9980	0.1580
Ao	0.9880	0.1560
Ap	0.9970	0.1610
Aq	0.9900	0.1580
Ar	0.9940	0.1690
As	0.9860	0.1570
At	0.9980	0.1630
Au	0.9920	0.1620
Av	0.9970	0.1670
Aw	0.9920	0.1560
B	0.8330	0.0390
Bb	0.9960	0.1460
Bc	0.9910	0.1370
Bd	0.9980	0.1430
Be	0.9900	0.1500
Bf	0.9930	0.1510
Bg	0.9890	0.1420
Bh	0.9960	0.1390
Bi	0.9890	0.1420
Bj	0.9920	0.1460
Bk	0.9910	0.1320
Bm	0.9890	0.1480
Bn	0.9910	0.1580
Bo	0.9860	0.1670
Bp	0.9960	0.1690
Bq	0.9810	0.1650
Br	0.9880	0.1640
Bs	0.9860	0.1690
Bt	0.9960	0.1600
Bu	0.9850	0.1580
Bv	0.9910	0.1530
C	0.8740	0.1000
Cb	0.9950	0.1450
Cc	0.9850	0.1460
Cd	0.9910	0.1440
Ce	0.9900	0.1400
Cf	0.9870	0.1470
Cg	0.9810	0.1370

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Chain	Atom inclusion	Q-score
Ch	0.9870	0.1430
Ci	0.9860	0.1470
Cj	0.9840	0.1460
Ck	0.9850	0.1370
Cm	0.9850	0.1490
Cn	0.9840	0.1660
Co	0.9770	0.1620
Cp	0.9860	0.1620
Cq	0.9770	0.1680
Cr	0.9780	0.1660
Cs	0.9760	0.1670
Ct	0.9870	0.1590
Cu	0.9800	0.1530
Cv	0.9890	0.1530
D	0.9740	0.1700
Db	0.9980	0.1280
Dc	0.9910	0.1370
Dd	0.9930	0.1500
De	0.9920	0.1290
Df	0.9920	0.1440
Dg	0.9850	0.1380
Dh	0.9890	0.1560
Di	0.9800	0.1450
Dj	0.9920	0.1390
Dk	0.9910	0.1430
Dm	0.9850	0.1550
Dn	0.9780	0.1600
Do	0.9780	0.1650
Dp	0.9810	0.1690
Dq	0.9670	0.1650
Dr	0.9700	0.1660
Ds	0.9730	0.1620
Dt	0.9840	0.1650
Du	0.9810	0.1590
Dv	0.9900	0.1560
E	0.8650	0.0670
Eb	0.9960	0.1360
Ec	0.9920	0.1450
Ed	0.9920	0.1420
Ee	0.9920	0.1310
Ef	0.9910	0.1470
Eg	0.9870	0.1370

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Chain	Atom inclusion	Q-score
Eh	0.9840	0.1490
Ei	0.9870	0.1370
Ej	0.9970	0.1400
Ek	0.9910	0.1410
Em	0.9810	0.1520
En	0.9850	0.1580
Eo	0.9840	0.1610
Ep	0.9880	0.1670
Eq	0.9740	0.1640
Er	0.9830	0.1660
Es	0.9840	0.1650
Et	0.9910	0.1610
Eu	0.9820	0.1560
Ev	0.9920	0.1500
F	0.8970	0.0860
Fa	0.9930	0.1330
Fb	0.9940	0.1380
Fc	0.9930	0.1470
Fd	0.9970	0.1460
Fe	0.9920	0.1370
Ff	0.9910	0.1510
Fg	0.9870	0.1410
Fh	0.9930	0.1470
Fi	0.9920	0.1450
Fj	0.9910	0.1440
Fn	0.9950	0.1520
Fo	0.9860	0.1620
Fp	0.9870	0.1590
Fq	0.9840	0.1500
Fr	0.9870	0.1630
Fs	0.9780	0.1640
Ft	0.9840	0.1590
Fu	0.9870	0.1560
Fv	0.9880	0.1590
Fw	0.9850	0.1540
G	0.9300	0.1060
Ga	0.9950	0.1300
Gb	0.9900	0.1390
Gc	0.9880	0.1440
Gd	0.9900	0.1520
Ge	0.9890	0.1400
Gf	0.9940	0.1470

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Chain	Atom inclusion	Q-score
Gg	0.9850	0.1400
Gh	0.9930	0.1480
Gi	0.9940	0.1390
Gj	0.9910	0.1350
Gn	0.9930	0.1500
Go	0.9870	0.1580
Gp	0.9870	0.1540
Gq	0.9840	0.1580
Gr	0.9860	0.1590
Gs	0.9840	0.1680
Gt	0.9860	0.1560
Gu	0.9860	0.1560
Gv	0.9900	0.1580
Gw	0.9880	0.1600
H	0.9860	0.1490
Ha	0.9880	0.1360
Hb	0.9910	0.1410
Hc	0.9810	0.1440
Hd	0.9790	0.1450
He	0.9870	0.1440
Hf	0.9920	0.1450
Hg	0.9810	0.1390
Hh	0.9880	0.1420
Hi	0.9890	0.1400
Hj	0.9950	0.1360
Hn	0.9910	0.1580
Ho	0.9810	0.1610
Hp	0.9840	0.1600
Hq	0.9870	0.1640
Hr	0.9870	0.1630
Hs	0.9790	0.1610
Ht	0.9810	0.1600
Hu	0.9880	0.1610
Hv	0.9910	0.1630
Hw	0.9880	0.1510
I	0.9880	0.1540
Ia	0.9910	0.1360
Ib	0.9860	0.1440
Ic	0.9840	0.1430
Id	0.9790	0.1380
Ie	0.9820	0.1440
If	0.9870	0.1460

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Chain	Atom inclusion	Q-score
Ig	0.9770	0.1440
Ih	0.9890	0.1440
Ii	0.9910	0.1410
Ij	0.9980	0.1440
In	0.9910	0.1570
Io	0.9810	0.1610
Ip	0.9900	0.1680
Iq	0.9850	0.1700
Ir	0.9870	0.1660
Is	0.9770	0.1650
It	0.9900	0.1670
Iu	0.9900	0.1650
Iv	0.9910	0.1640
Iw	0.9890	0.1540
J	0.9830	0.1740
Ja	0.9840	0.1420
Jb	0.9840	0.1400
Jc	0.9800	0.1460
Jd	0.9830	0.1540
Je	0.9700	0.1460
Jf	0.9720	0.1520
Jg	0.9720	0.1410
Jh	0.9760	0.1420
Ji	0.9830	0.1410
Jj	0.9890	0.1450
Jn	0.9950	0.1690
Jo	0.9780	0.1710
Jp	0.9900	0.1690
Jq	0.9810	0.1730
Jr	0.9880	0.1750
Js	0.9770	0.1780
Jt	0.9880	0.1640
Ju	0.9880	0.1710
Jv	0.9910	0.1690
Jw	0.9910	0.1670
K	0.9860	0.1710
Kb	0.9910	0.1500
Kc	0.9870	0.1390
Kd	0.9940	0.1500
Ke	0.9820	0.1440
Kf	0.9840	0.1530
Kg	0.9840	0.1450

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Chain	Atom inclusion	Q-score
Kh	0.9900	0.1550
Ki	0.9810	0.1460
Kj	0.9880	0.1520
Kk	0.9860	0.1370
Km	0.9920	0.1580
Kn	0.9950	0.1580
Ko	0.9840	0.1630
Kp	0.9890	0.1590
Kq	0.9830	0.1660
Kr	0.9930	0.1660
Ks	0.9840	0.1660
Kt	0.9900	0.1640
Ku	0.9880	0.1600
Kv	0.9960	0.1630
L	0.9940	0.1540
Lb	0.9920	0.1410
Lc	0.9900	0.1420
Ld	0.9980	0.1380
Le	0.9890	0.1500
Lf	0.9910	0.1490
Lg	0.9910	0.1430
Lh	0.9950	0.1500
Li	0.9900	0.1470
Lj	0.9920	0.1460
Lk	0.9930	0.1390
Lm	0.9880	0.1570
Ln	0.9960	0.1660
Lo	0.9870	0.1660
Lp	0.9850	0.1670
Lq	0.9810	0.1660
Lr	0.9930	0.1630
Ls	0.9880	0.1680
Lt	0.9880	0.1650
Lu	0.9860	0.1610
Lv	0.9980	0.1610
M	0.9930	0.1490
Mb	0.9980	0.1390
Mc	0.9910	0.1360
Md	0.9940	0.1480
Me	0.9910	0.1360
Mf	0.9970	0.1430
Mg	0.9900	0.1440

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Chain	Atom inclusion	Q-score
Mh	0.9930	0.1500
Mi	0.9910	0.1410
Mj	0.9970	0.1370
Mk	0.9930	0.1270
Mm	0.9900	0.1590
Mn	0.9940	0.1620
Mo	0.9880	0.1620
Mp	0.9960	0.1680
Mq	0.9860	0.1690
Mr	0.9950	0.1630
Ms	0.9880	0.1590
Mt	0.9960	0.1610
Mu	0.9900	0.1640
Mv	0.9970	0.1560
O	0.9540	0.0860
P	0.9410	0.0840
Q	0.9980	0.1270
R	0.9970	0.1260
S	0.9900	0.1340
T	0.9950	0.1280
U	0.9920	0.1320
V	0.9980	0.1180
W	0.9950	0.1590
X	0.9930	0.1690
Y	0.9950	0.1730
Z	0.9910	0.1780
a	0.9910	0.1680
b	0.9970	0.1550
c	0.9680	0.1370
d	0.9750	0.1450
e	0.9610	0.1480
f	0.9660	0.1300
g	0.9750	0.1500
h	0.9790	0.1150
i	0.9800	0.1070
j	0.9810	0.1100
k	0.6860	0.0590
l	0.7760	0.0530
m	0.6920	0.0520
n	0.7750	0.0590
o	0.6520	0.0560
p	0.7540	0.0580

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Chain	Atom inclusion	Q-score
q	0.9760	0.1600
r	0.9680	0.1490
s	0.9800	0.1440
t	0.9970	0.1390
u	0.9970	0.1430
v	0.9920	0.2060
w	0.9950	0.1940
x	0.8960	0.0520
y	0.8410	0.0670
z	0.8400	0.0670