



Full wwPDB EM Validation Report ⓘ

Aug 2, 2023 – 01:00 PM JST

PDB ID : 8J07
EMDB ID : EMD-35888
Title : 96nm repeat of human respiratory doublet microtubule and associated axonemal complexes
Authors : Gui, M.; Brown, A.
Deposited on : 2023-04-09
Resolution : 4.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev50
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

1 Overall quality at a glance

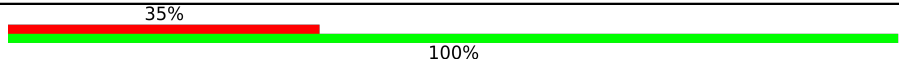
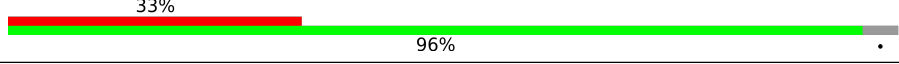


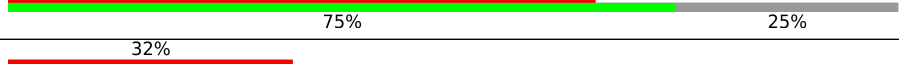

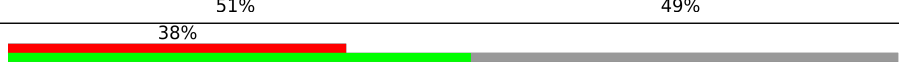
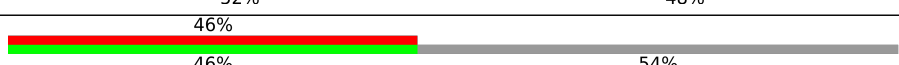



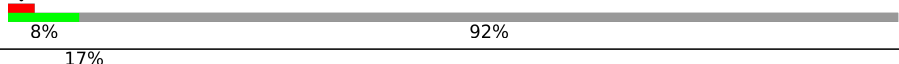





The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

There are no overall percentile quality scores available for this entry.

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

Mol	Chain	Length	Quality of chain
1	0	478	
1	4	478	
2	1	740	
3	10	449	
4	11	822	
5	12	269	
5	13	269	
5	14	269	
5	8	269	
6	1A	833	
6	1B	833	
6	1C	833	
7	1D	551	
7	1E	551	
7	1F	551	
7	1G	551	
7	1H	551	

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Mol	Chain	Length	Quality of chain
7	1I	551	24% 83% 17%
7	1J	551	17% 60% 40%
8	1L	620	98%
8	1M	620	98%
8	1N	620	98%
8	1O	620	98%
8	1P	620	98%
8	1Q	620	5% 98%
9	1R	514	5% 36% 64%
9	1S	514	12% 90% 10%
9	1T	514	64% 36%
10	1V	229	13% 64% 36%
10	1W	229	12% 64% 36%
11	1Y	194	8% 89% 10%
11	1Z	194	8% 89% 11%
12	2	484	39% 96%
13	2A	177	66% 34%
13	2B	177	66% 34%
13	2C	177	66% 34%
13	2D	177	66% 34%
13	2E	177	66% 34%
13	2F	177	66% 34%
13	2G	177	45% 55%
14	2I	101	5% 50% 50%
14	2J	101	50% 50%

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Mol	Chain	Length	Quality of chain
15	2L	301	14% 92% 8%
15	2M	301	9% 92% 8%
15	2N	301	12% 92% 8%
15	2O	301	9% 92% 8%
16	2Q	552	7% 52% 48%
16	2R	552	13% 92% 8%
16	2S	552	7% 48% 52%
17	2U	169	• 66% 34%
17	2V	169	5% 66% 34%
17	2W	169	• 66% 34%
17	2X	169	• 66% 34%
17	2Y	169	• 66% 34%
17	2Z	169	• 66% 34%
18	3	523	12% 99% •
19	3A	640	• 76% 24%
19	3B	640	• 76% 24%
19	3C	640	• 76% 24%
19	3D	640	• 76% 24%
19	3E	640	• 76% 24%
19	3F	640	5% 76% 24%
20	3G	749	10% 82% 18%
20	3H	749	11% 94% 6%
20	3I	749	11% 94% 6%
20	3J	749	8% 94% 6%
20	3K	749	9% 94% 6%

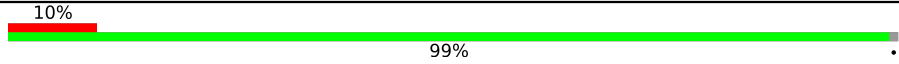
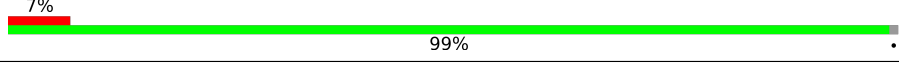
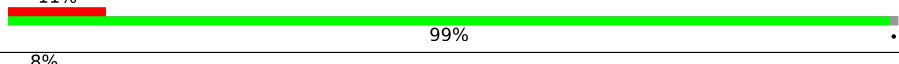
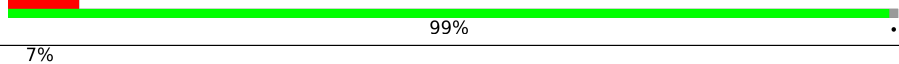

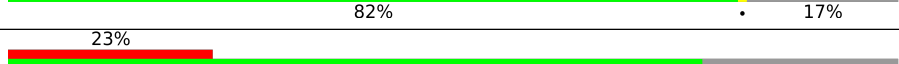
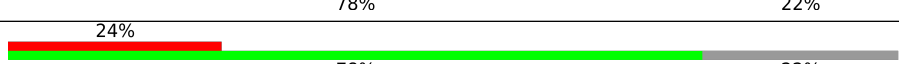
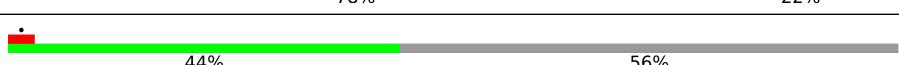


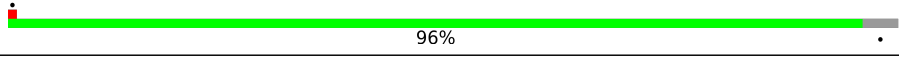


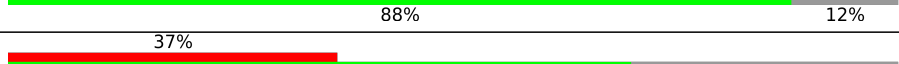

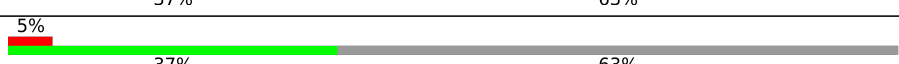
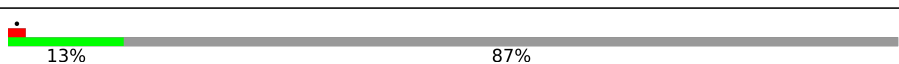








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Mol	Chain	Length	Quality of chain	
20	3L	749	23%	94% 6%
20	3M	749	11%	92% 8%
21	3O	256	11%	62% 38%
21	3P	256	13%	97% .
21	3Q	256	7%	98% .
21	3R	256	14%	98% .
21	3S	256	16%	97% .
21	3T	256	9%	98% .
21	3U	256	14%	98% .
22	3W	495	10%	79% 21%
22	3X	495	12%	97% .
22	3Y	495	5%	29% 71%
23	4A	275	.%	29% 71%
23	4B	275	46%	53% 47%
23	4C	275	17%	53% 47%
23	4D	275	39%	53% 47%
23	4E	275	11%	53% 47%
23	4F	275	50%	53% 47%
23	4G	275	13%	53% 47%
23	4H	275	46%	52% 47%
23	4I	275	13%	53% 47%
23	4J	275	28%	52% 47%
23	4K	275	24%	53% 47%
23	4L	275	52%	53% 47%
23	4M	275	19%	53% 47%

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Mol	Chain	Length	Quality of chain
24	4O	376	
24	4P	376	
24	4Q	376	
24	4R	376	
25	4S	136	
25	4T	136	
26	4U	121	
26	4V	121	
26	4W	121	
27	5	501	
28	5A	382	
28	5B	382	
28	5C	382	
29	5D	379	
29	5E	379	
29	5F	379	
30	5H	485	
30	5I	485	
30	5J	485	
31	5L	150	
31	5M	150	
32	5O	284	
32	5P	284	
32	5Q	284	
32	5R	284	

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Mol	Chain	Length	Quality of chain
32	5S	284	9% 80% 20%
32	5T	284	10% 79% 21%
32	5U	284	11% 80% 20%
32	5V	284	23% 77%
33	5X	147	86% 14%
33	5Y	147	5% 86% 14%
34	6A	222	14% 71% 29%
34	6C	222	35% 71% 28%
34	6E	222	17% 71% 29%
34	6G	222	37% 71% 29%
34	6I	222	40% 70% 29%
34	6K	222	48% 70% 29%
34	6L	222	14% 71% 29%
34	6N	222	33% 72% 28%
34	6O	222	17% 71% 29%
34	6Q	222	27% 71% 29%
34	6R	222	31% 71% 29%
34	6T	222	44% 71% 29%
34	6V	222	16% 71% 29%
35	7	874	35% 69% 31%
36	7A	201	17% 30% 70%
36	7B	201	33% 51% 49%
36	7C	201	42% 51% 49%
36	7D	201	13% 50% 50%
36	7E	201	30% 51% 49%

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Mol	Chain	Length	Quality of chain
36	7F	201	
36	7G	201	
37	7I	134	
37	7J	134	
38	8A	418	
38	8B	418	
38	8C	418	
38	8D	418	
38	8E	418	
38	8F	418	
38	8G	418	
38	8H	418	
39	8J	430	
39	8K	430	
39	8L	430	
39	8M	430	
39	8N	430	
39	8O	430	
39	8P	430	
39	8Q	430	
40	9	443	
41	A	309	
41	B	309	
41	C	309	
41	D	309	

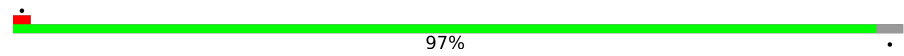
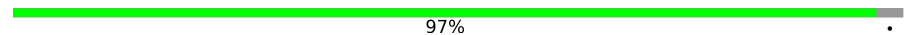
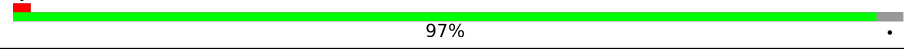
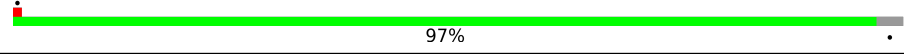
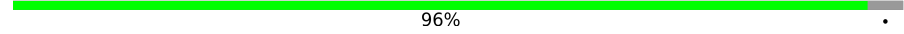
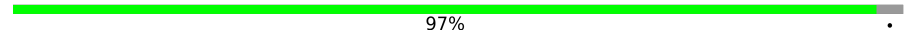
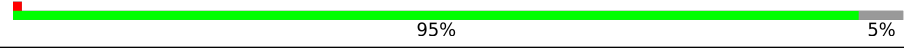
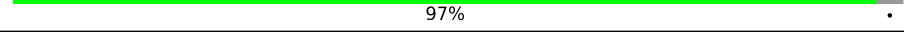
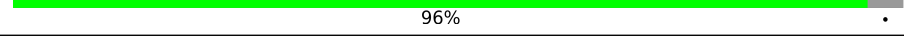
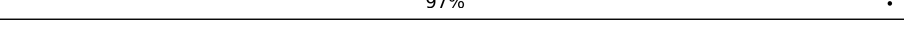
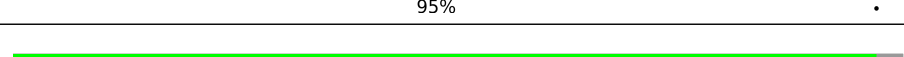
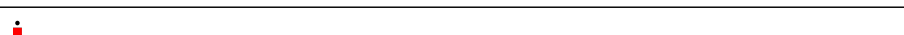
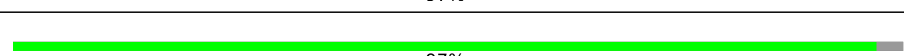

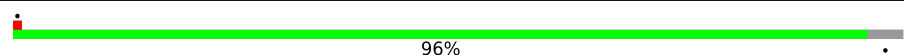
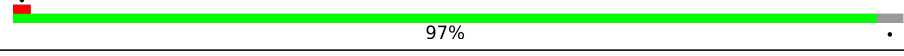
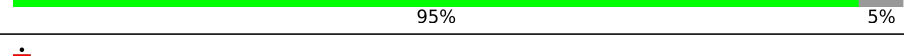
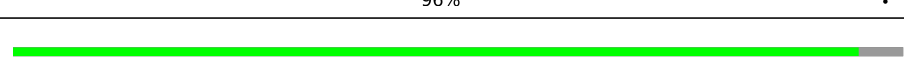
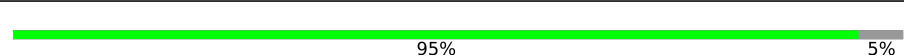
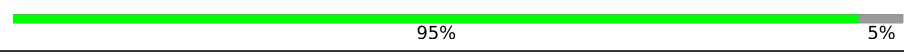
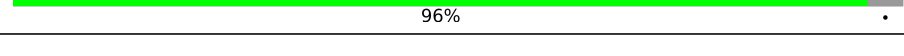
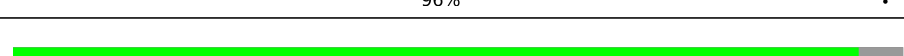



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Mol	Chain	Length	Quality of chain
41	a	309	
41	b	309	
41	c	309	
41	d	309	
42	AC	451	
42	AE	451	
42	AG	451	
42	AI	451	
42	AK	451	
42	AM	451	
42	AO	451	
42	AQ	451	
42	AS	451	
42	AU	451	
42	AW	451	
42	AY	451	
42	AZ	451	
42	BA	451	
42	BC	451	
42	BE	451	
42	BG	451	
42	BI	451	
42	BK	451	
42	BM	451	
42	BO	451	

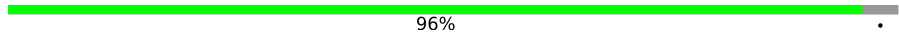
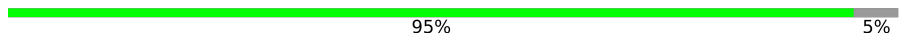
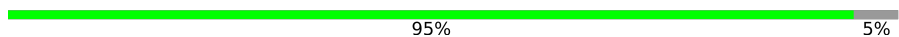
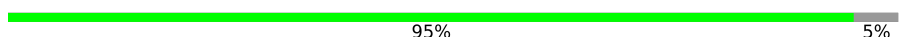
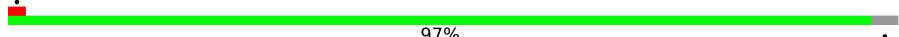
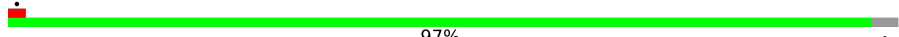




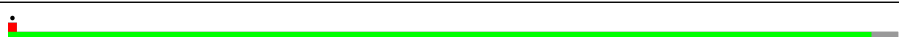


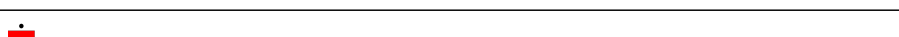
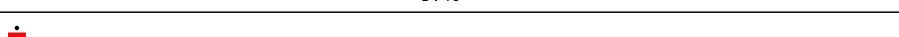
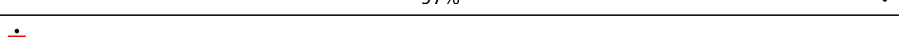
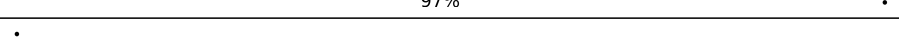
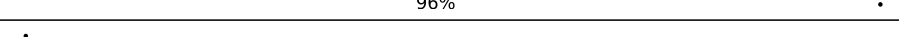
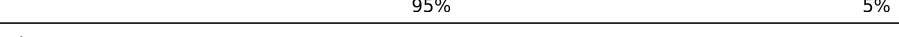
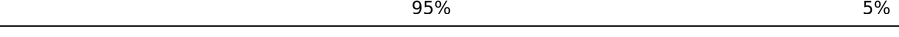
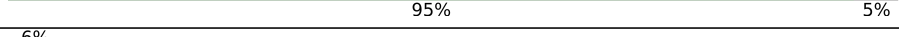
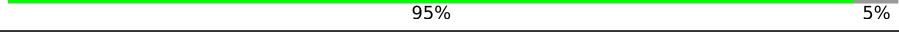
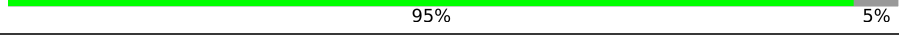
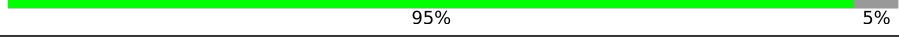
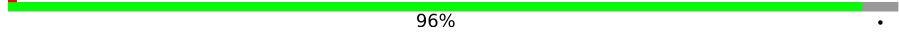
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Mol	Chain	Length	Quality of chain
42	BQ	451	 97%
42	BS	451	 97%
42	BU	451	 97%
42	BW	451	 97%
42	BY	451	 96%
42	CC	451	 97%
42	CE	451	 95% 5%
42	CG	451	 97%
42	CI	451	 96%
42	CK	451	 97%
42	CM	451	 95%
42	CO	451	 97%
42	CQ	451	 97%
42	CS	451	 97%
42	CU	451	 97%
42	CW	451	 96%
42	CY	451	 97%
42	DC	451	 95% 5%
42	DE	451	 96%
42	DG	451	 95% 5%
42	DI	451	 95% 5%
42	DK	451	 95% 5%
42	DM	451	 96%
42	DO	451	 96%
42	DQ	451	 95% 5%

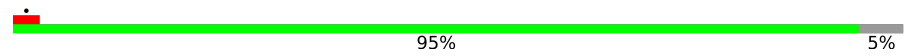
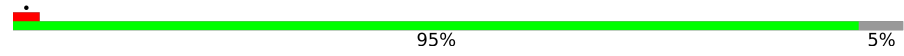
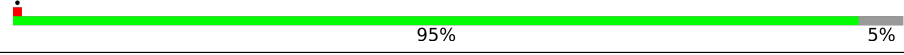
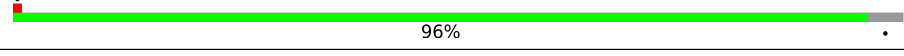
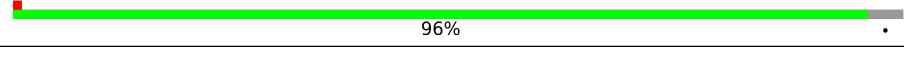
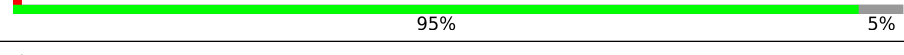
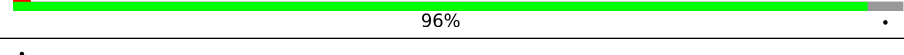
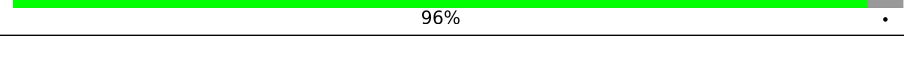
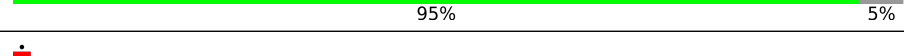
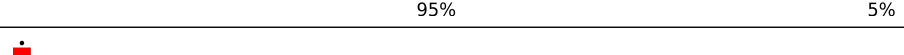
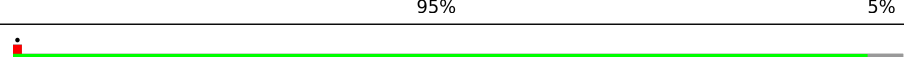
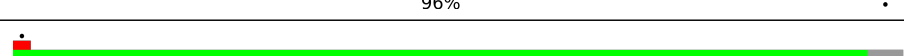
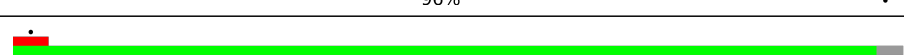
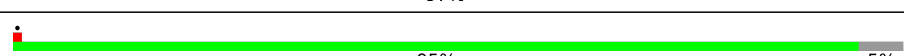
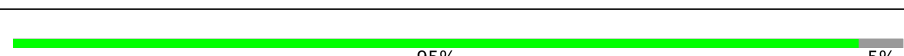
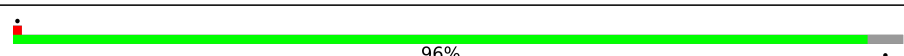
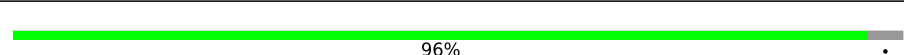
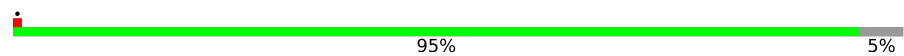
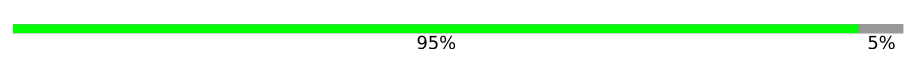
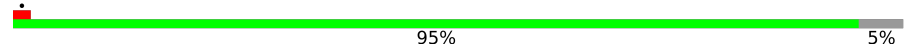
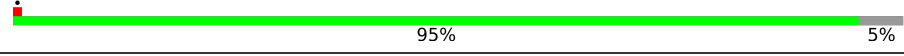
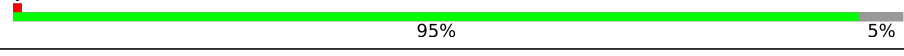
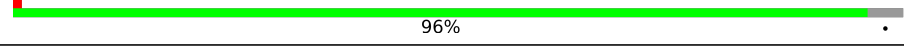
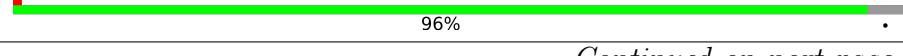

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Mol	Chain	Length	Quality of chain
42	DS	451	 96% .
42	DU	451	 95% 5% .
42	DW	451	 95% 5% .
42	DY	451	 95% 5% .
42	EC	451	 97% .
42	EE	451	 97% .
42	EG	451	 97% .
42	EI	451	 97% .
42	EK	451	 97% .
42	EM	451	 97% .
42	EO	451	 97% .
42	EQ	451	 97% .
42	ES	451	 97% .
42	EU	451	 97% .
42	EW	451	 97% .
42	EY	451	 97% .
42	FC	451	 96% .
42	FE	451	 95% 5% .
42	FG	451	 95% 5% .
42	FI	451	 95% 5% .
42	FK	451	 6% 95% 5% .
42	FM	451	 95% 5% .
42	FO	451	 95% 5% .
42	FQ	451	 96% .
42	FS	451	 96% .

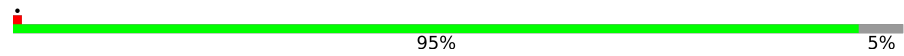
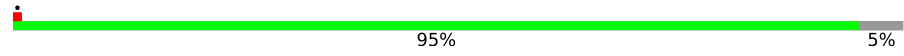
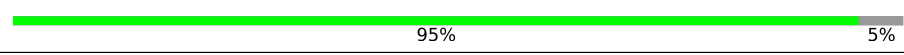
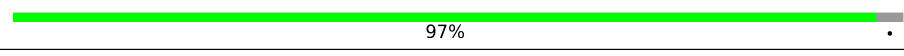
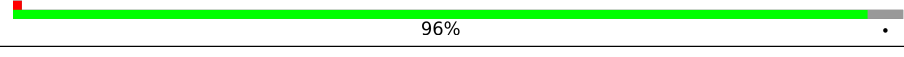
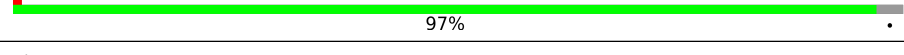
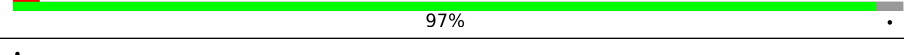
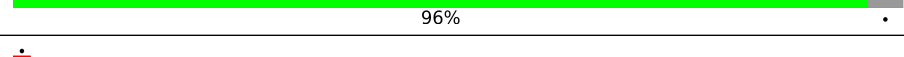
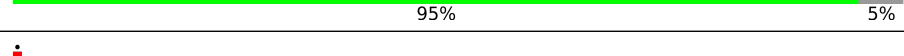
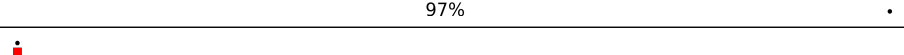
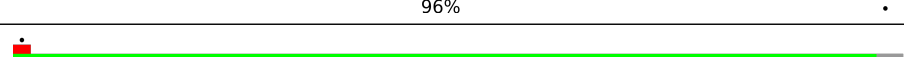
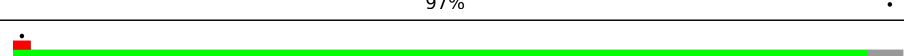
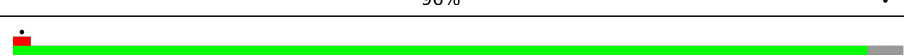
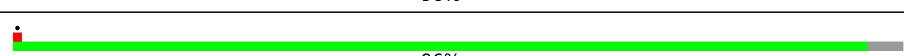
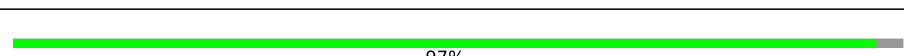
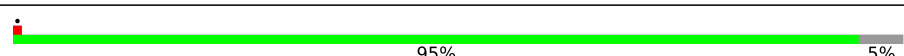
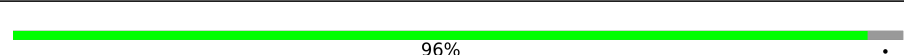
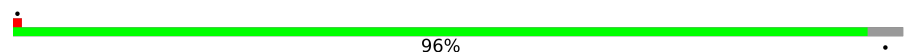
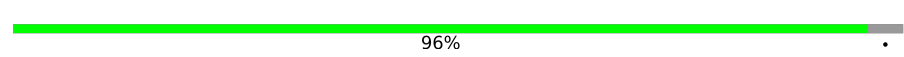
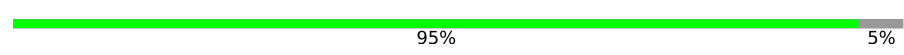
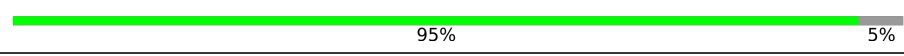
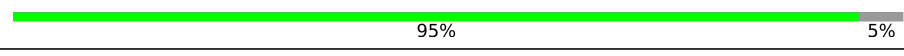
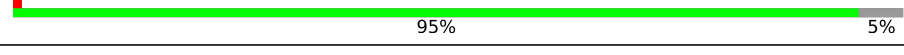
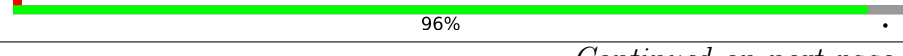

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Mol	Chain	Length	Quality of chain
42	FU	451	 95% 5%
42	FW	451	 95% 5%
42	FY	451	 95% 5%
42	GC	451	 96% .
42	GE	451	 96% .
42	GG	451	 95% 5%
42	GI	451	 96% .
42	GK	451	 96% .
42	GM	451	 95% 5%
42	GO	451	 95% 5%
42	GQ	451	 95% 5%
42	GS	451	 96% .
42	GU	451	 96% .
42	GW	451	 97% .
42	GY	451	 95% 5%
42	HA	451	 95% 5%
42	HC	451	 96% .
42	HE	451	 96% .
42	HG	451	 95% 5%
42	HI	451	 95% 5%
42	HK	451	 95% 5%
42	HM	451	 95% 5%
42	HO	451	 95% 5%
42	HQ	451	 96% .
42	HS	451	 96% .

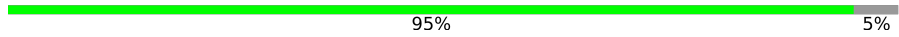
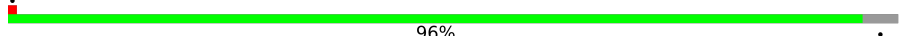
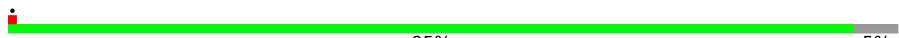
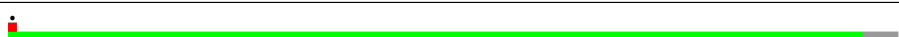
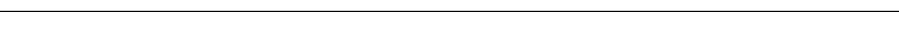
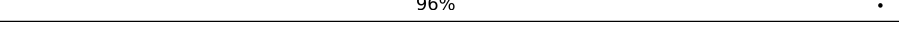
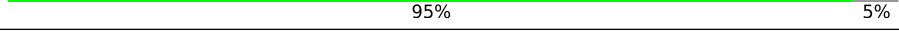
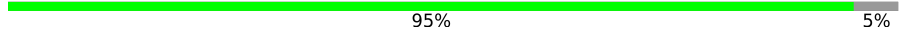
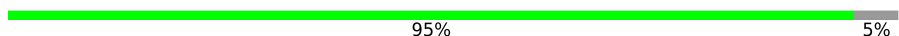
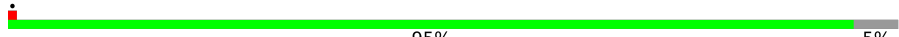

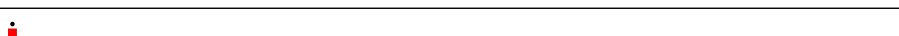
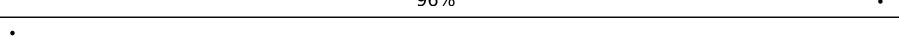
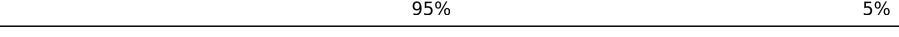
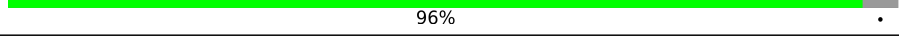
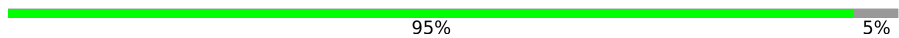
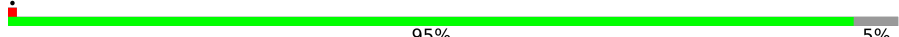


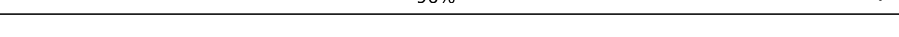
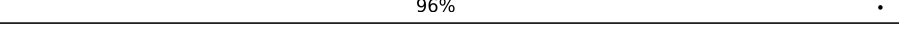
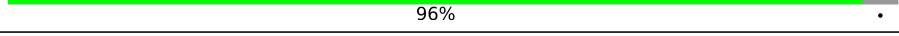
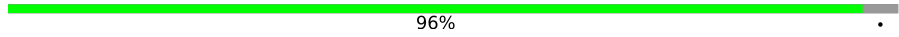
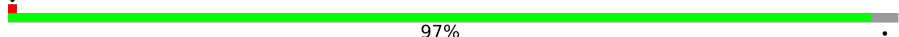

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Mol	Chain	Length	Quality of chain
42	HU	451	 95% 5%
42	HW	451	 95% 5%
42	HY	451	 95% 5%
42	IA	451	 97% .
42	IC	451	 96% .
42	IE	451	 97% .
42	IG	451	 97% .
42	II	451	 96% .
42	IK	451	 95% 5%
42	IM	451	 97% .
42	IO	451	 96% .
42	IQ	451	 97% .
42	IS	451	 96% .
42	IU	451	 96% .
42	IW	451	 96% .
42	IY	451	 97% .
42	JC	451	 95% 5%
42	JE	451	 96% .
42	JG	451	 96% .
42	JI	451	 96% .
42	JK	451	 95% 5%
42	JM	451	 95% 5%
42	JO	451	 95% 5%
42	JQ	451	 95% 5%
42	JS	451	 96% .

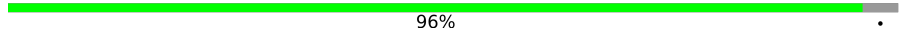
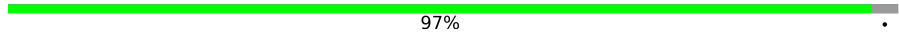
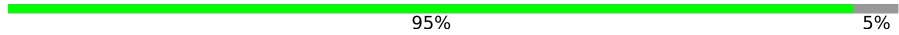
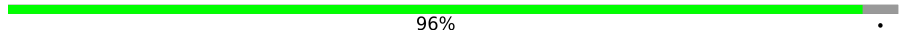
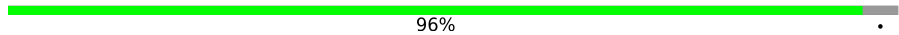
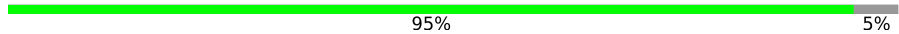
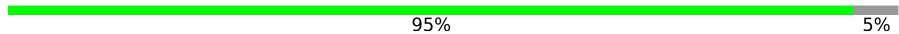
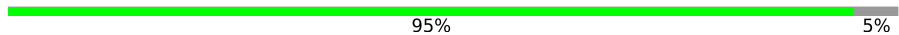
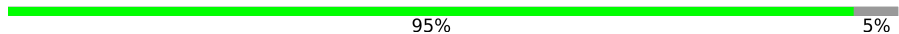
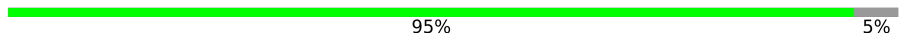
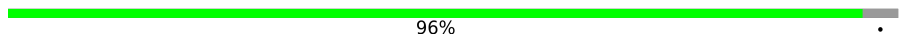
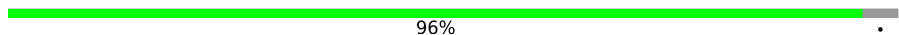
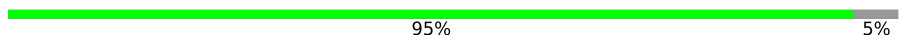
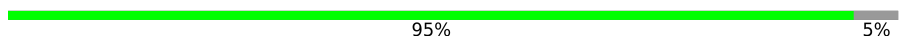
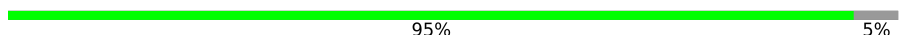
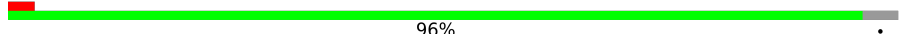
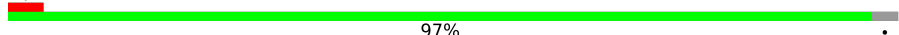
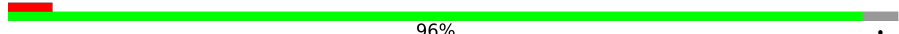
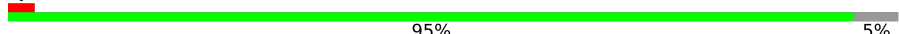
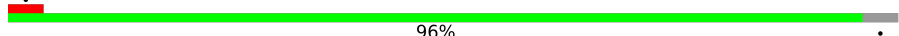
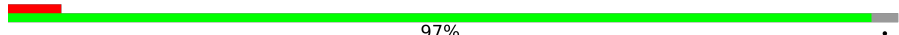
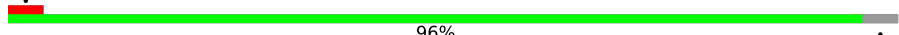
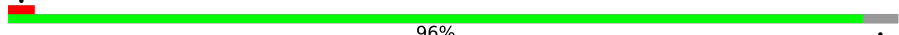
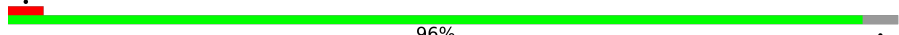
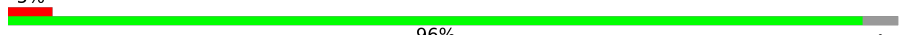
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Mol	Chain	Length	Quality of chain
42	JU	451	 95% 5%
42	JW	451	 96% .
42	JY	451	 95% 5%
42	KC	451	 96% .
42	KE	451	 96% .
42	KG	451	 95% 5%
42	KI	451	 95% 5%
42	KK	451	 95% 5%
42	KM	451	 95% 5%
42	KO	451	 95% 5%
42	KQ	451	 96% .
42	KS	451	 95% 5%
42	KU	451	 96% .
42	KW	451	 95% 5%
42	KY	451	 95% 5%
42	LC	451	 96% .
42	LE	451	 96% .
42	LG	451	 96% .
42	LI	451	 96% .
42	LK	451	 96% .
42	LM	451	 97% .
42	LO	451	 97% .
42	LQ	451	 97% .
42	LS	451	 97% .
42	LU	451	 96% .

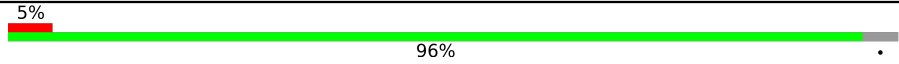
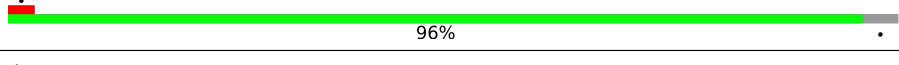
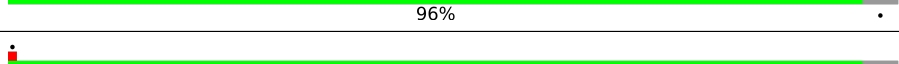
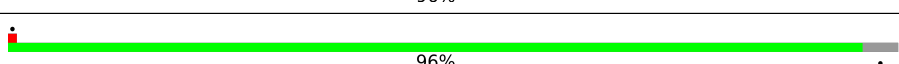
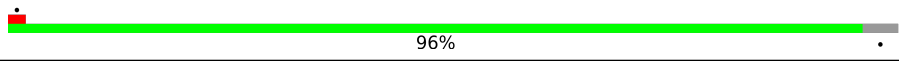
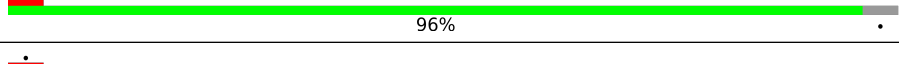
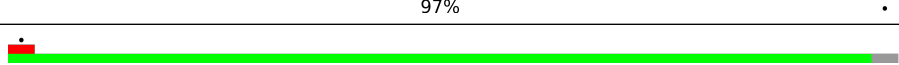
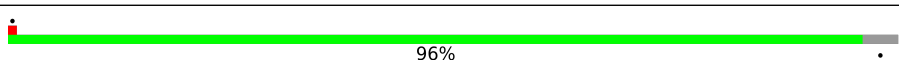
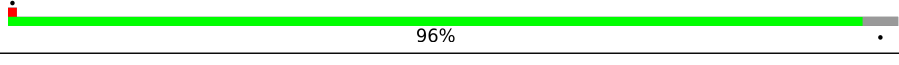
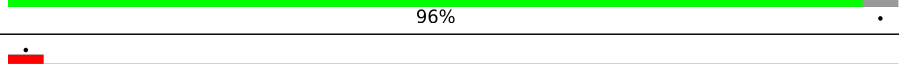
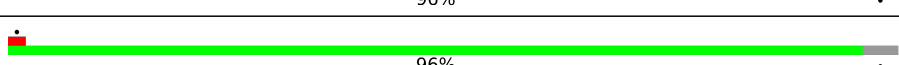
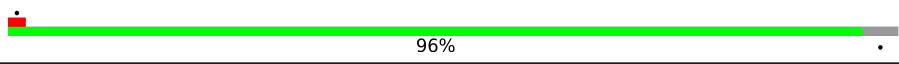
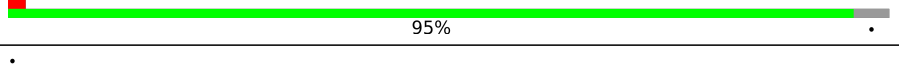
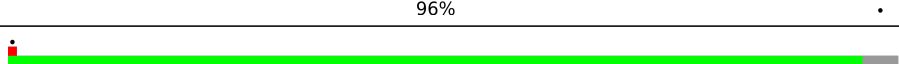
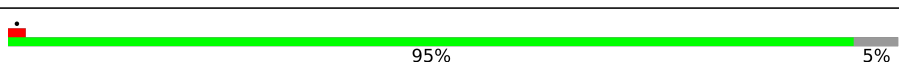
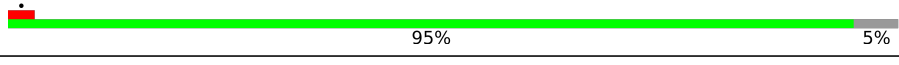
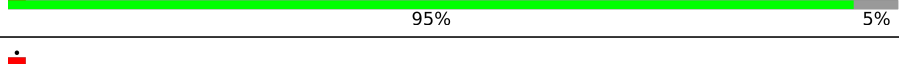
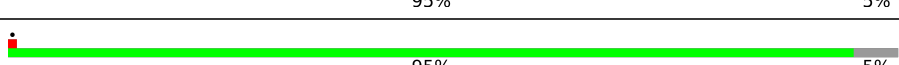
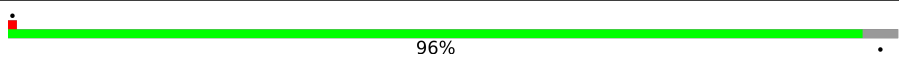
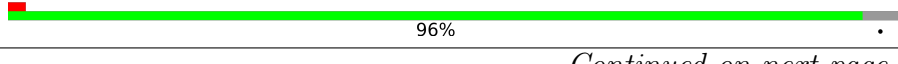



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Mol	Chain	Length	Quality of chain
42	LW	451	 96% .
42	LY	451	 97% .
42	MA	451	 95% 5% .
42	MC	451	 96% .
42	ME	451	 96% .
42	MG	451	 95% 5% .
42	MI	451	 95% 5% .
42	MK	451	 95% 5% .
42	MM	451	 95% 5% .
42	MO	451	 95% 5% .
42	MQ	451	 96% .
42	MS	451	 96% .
42	MU	451	 95% 5% .
42	MW	451	 95% 5% .
42	MY	451	 95% 5% .
42	NA	451	 96% .
42	NC	451	 97% .
42	NE	451	 5% 96% .
42	NG	451	 95% 5% .
42	NI	451	 96% .
42	NK	451	 6% 97% .
42	NM	451	 96% .
42	NO	451	 96% .
42	NQ	451	 96% .
42	NS	451	 5% 96% .

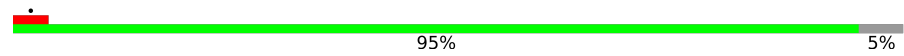
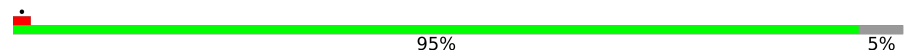
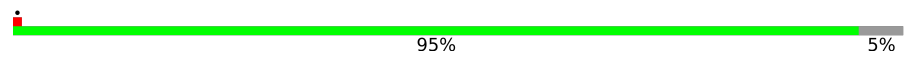
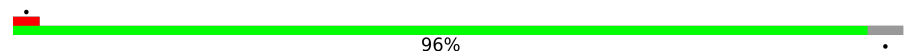
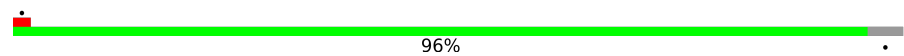
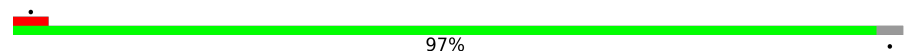
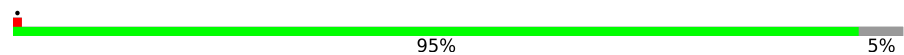
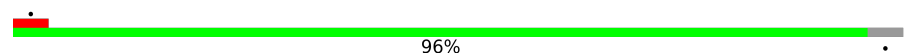
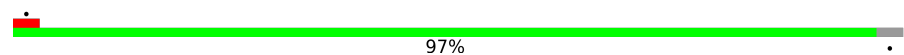
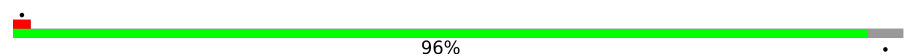
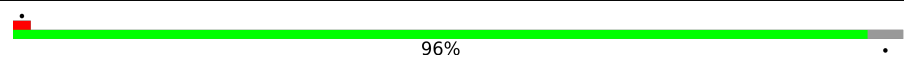
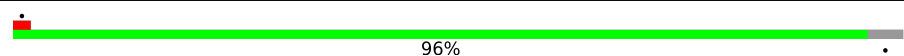
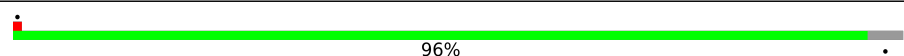
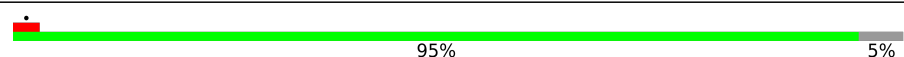
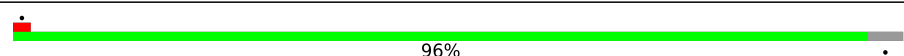
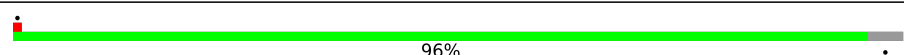
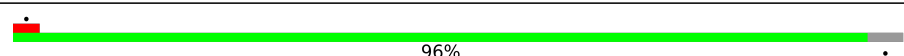
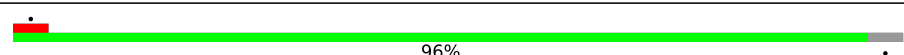
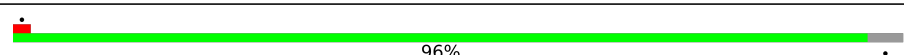
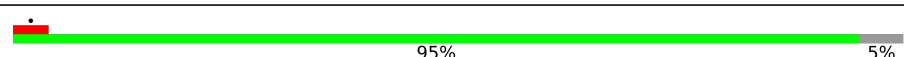
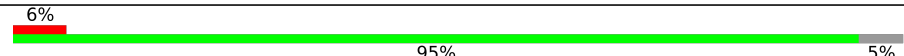
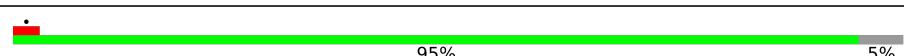
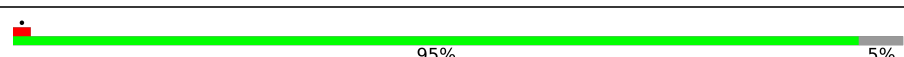
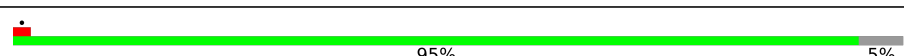
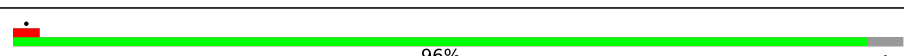
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Mol	Chain	Length	Quality of chain
42	NU	451	 5% 96%
42	NW	451	 5% 96%
42	OA	451	 5% 96%
42	OC	451	 5% 96%
42	OE	451	 5% 96%
42	OG	451	 5% 96%
42	OI	451	 5% 96%
42	OK	451	 5% 97%
42	OM	451	 5% 97%
42	OO	451	 5% 96%
42	OQ	451	 5% 96%
42	OS	451	 5% 96%
42	OU	451	 5% 96%
42	OW	451	 5% 96%
42	OY	451	 5% 96%
42	PA	451	 5% 95%
42	PC	451	 5% 96%
42	PE	451	 5% 96%
42	PG	451	 5% 95% 5%
42	PI	451	 5% 95% 5%
42	PK	451	 5% 95% 5%
42	PM	451	 5% 95% 5%
42	PO	451	 5% 95% 5%
42	PQ	451	5% 96%
42	PS	451	5% 96%

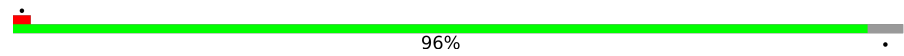
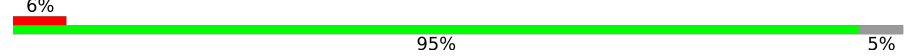
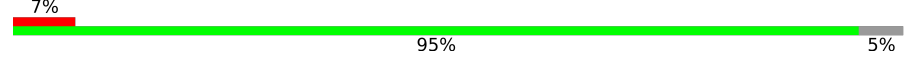
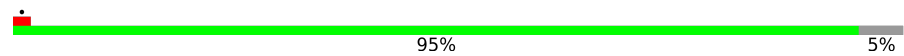
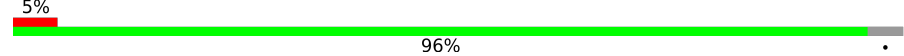
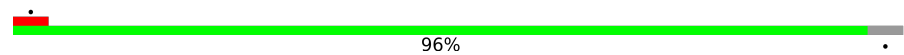
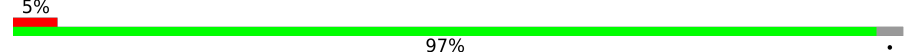
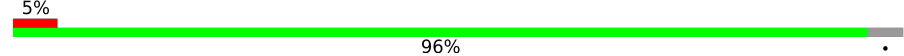
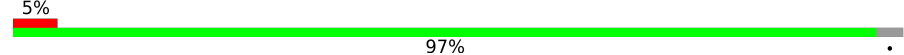
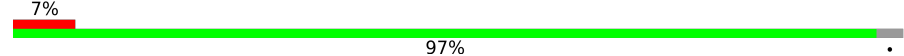
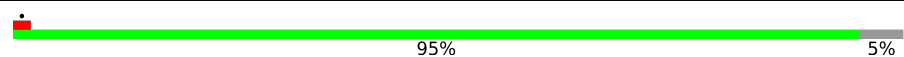
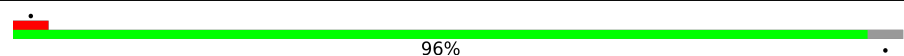
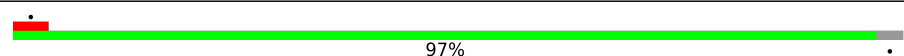
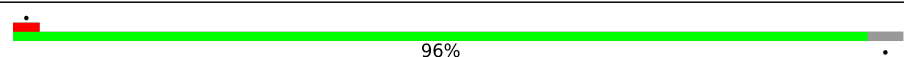
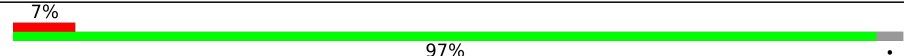
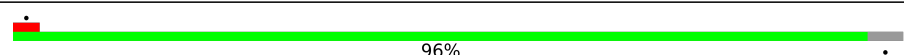
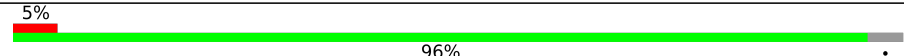
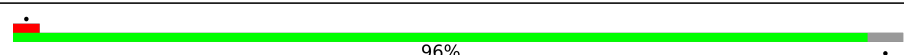
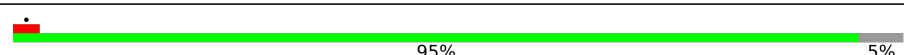
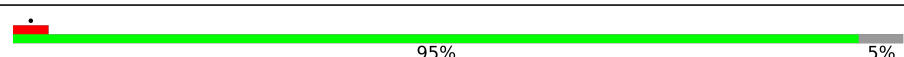
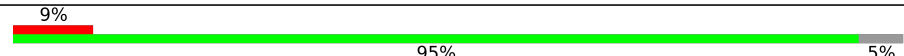
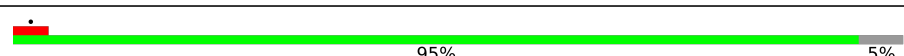
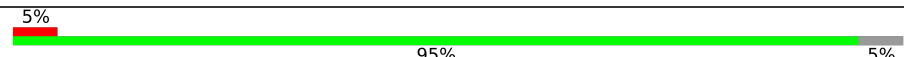
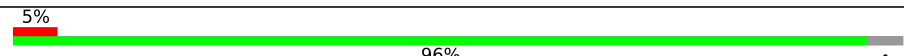
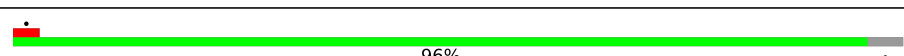
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Mol	Chain	Length	Quality of chain
42	PU	451	 95% 5%
42	PW	451	 95% 5%
42	PY	451	 95% 5%
42	QA	451	 96% .
42	QC	451	 96% .
42	QE	451	 97% .
42	QG	451	 95% 5%
42	QI	451	 96% .
42	QK	451	 97% .
42	QM	451	 96% .
42	QO	451	 96% .
42	QQ	451	 96% .
42	QS	451	 96% .
42	QU	451	 95% 5%
42	QW	451	 96% .
42	QY	451	 96% .
42	RA	451	 96% .
42	RC	451	 96% .
42	RE	451	 96% .
42	RG	451	 95% 5%
42	RI	451	 6% 95% 5%
42	RK	451	 95% 5%
42	RM	451	 95% 5%
42	RO	451	 95% 5%
42	RQ	451	 96% .

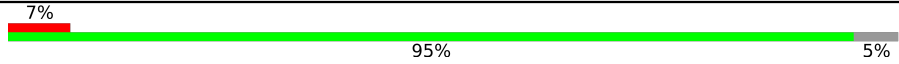
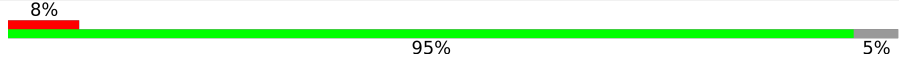
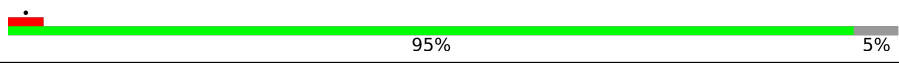
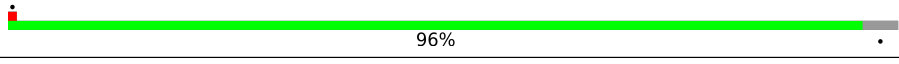
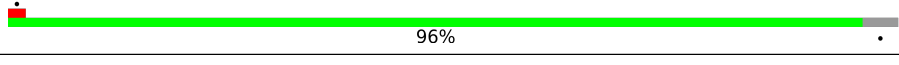
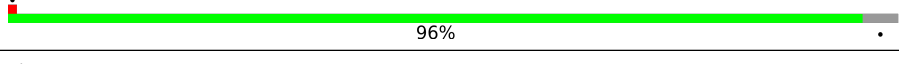
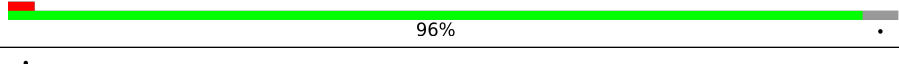
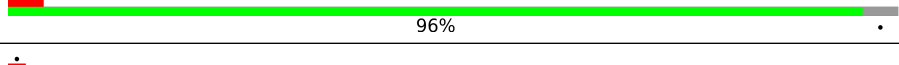
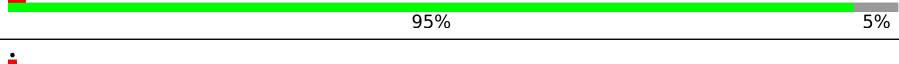
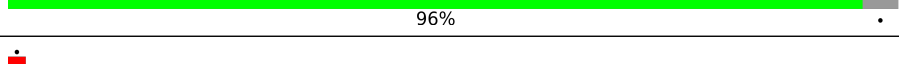
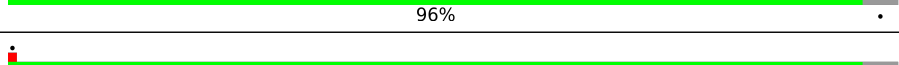
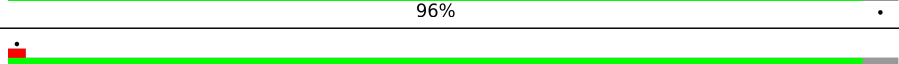
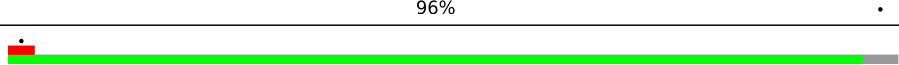
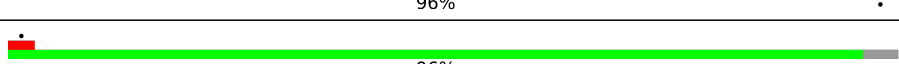
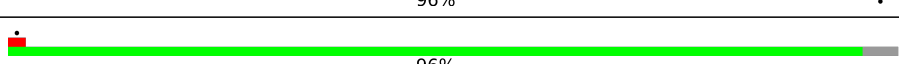
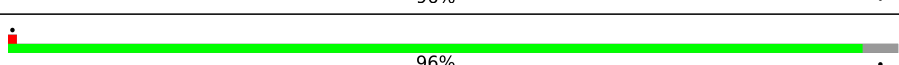
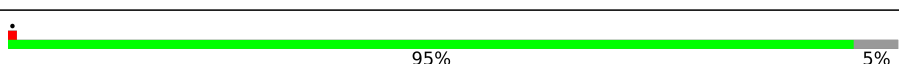
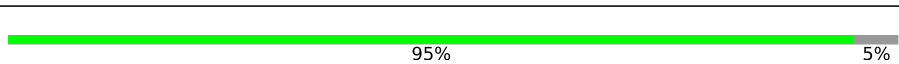
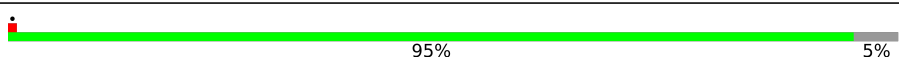
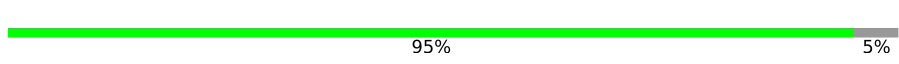
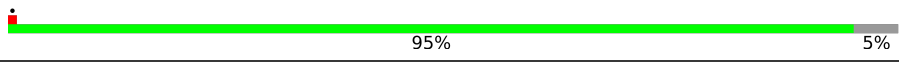
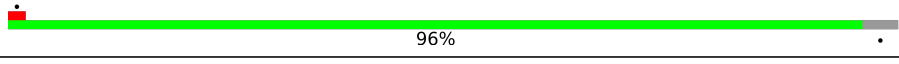
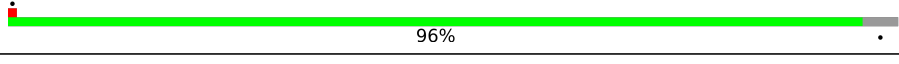
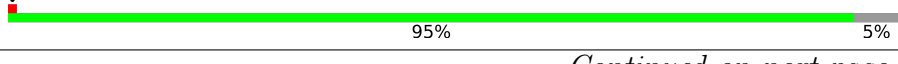

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Mol	Chain	Length	Quality of chain
42	RS	451	 96%
42	RU	451	 95%
42	RW	451	 95%
42	RY	451	 95%
42	SC	451	 96%
42	SE	451	 96%
42	SG	451	 97%
42	SI	451	 96%
42	SK	451	 97%
42	SM	451	 97%
42	SO	451	 95%
42	SQ	451	 96%
42	SS	451	 97%
42	SU	451	 96%
42	SW	451	 97%
42	SY	451	 96%
42	TC	451	 96%
42	TE	451	 96%
42	TG	451	 95%
42	TI	451	 95%
42	TK	451	 95%
42	TM	451	 95%
42	TO	451	 95%
42	TQ	451	 96%
42	TS	451	 96%

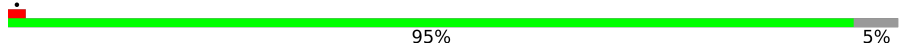
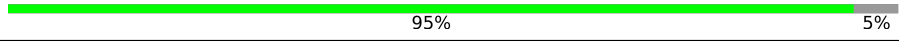
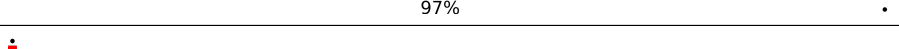
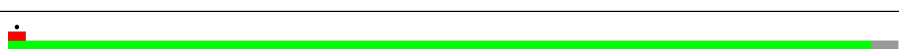

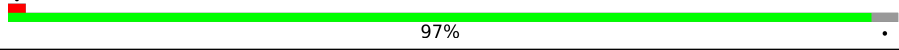
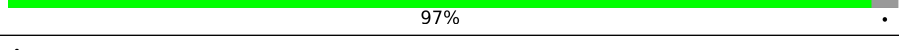
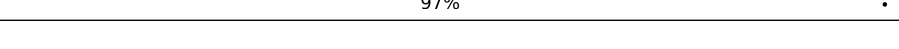
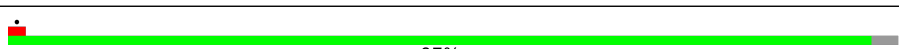
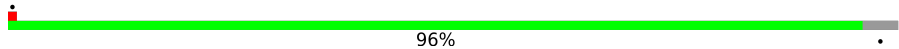
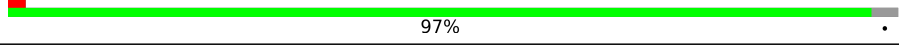
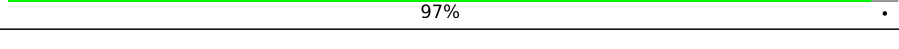
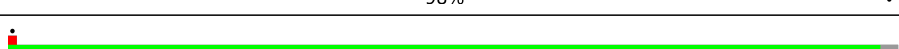
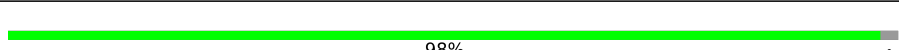
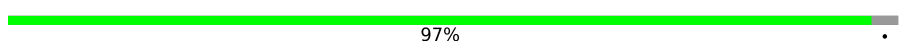
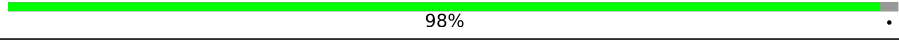
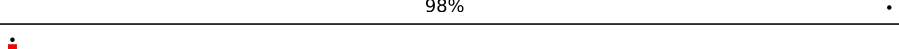

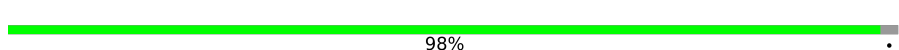
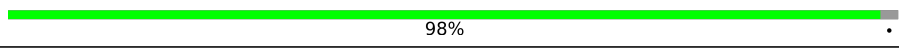
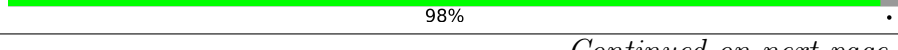



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Mol	Chain	Length	Quality of chain
42	TU	451	 7% 95% 5%
42	TW	451	 8% 95% 5%
42	TY	451	 95% 5%
42	UC	451	 96% .
42	UE	451	 96% .
42	UG	451	 96% .
42	UI	451	 96% .
42	UK	451	 96% .
42	UM	451	 95% 5%
42	UO	451	 96% .
42	UQ	451	 96% .
42	US	451	 96% .
42	UU	451	 96% .
42	UW	451	 96% .
42	UY	451	 96% .
42	VC	451	 96% .
42	VE	451	 96% .
42	VG	451	 95% 5%
42	VI	451	 95% 5%
42	VK	451	 95% 5%
42	VM	451	 95% 5%
42	VO	451	 95% 5%
42	VQ	451	 96% .
42	VS	451	 96% .
42	VU	451	 95% 5%

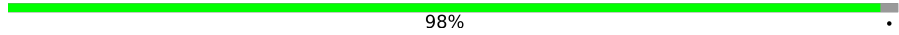
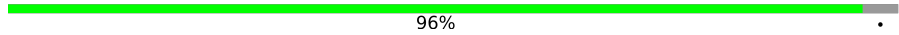
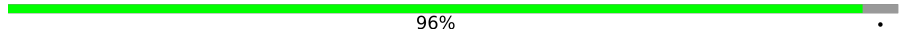
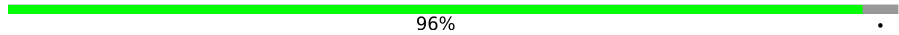
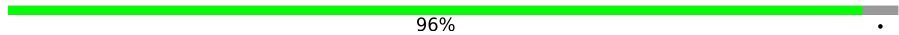
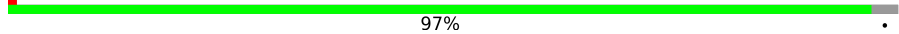
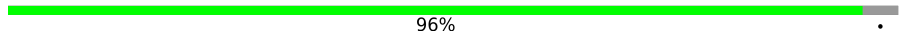
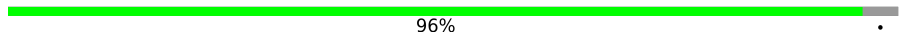
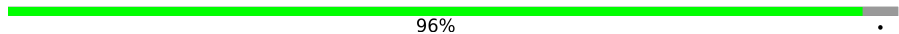
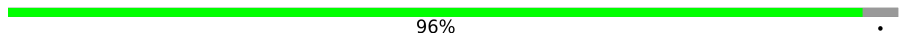
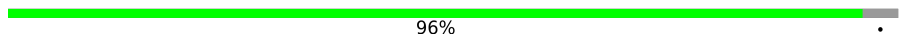
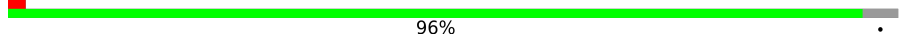
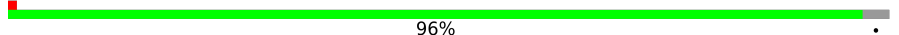
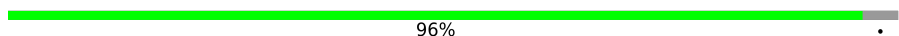
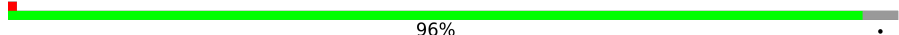
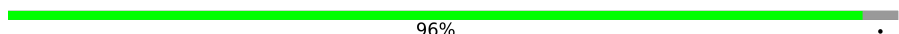
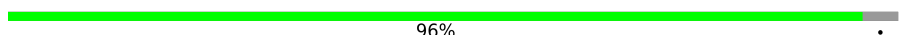
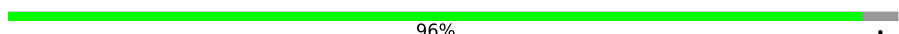
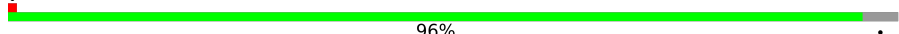
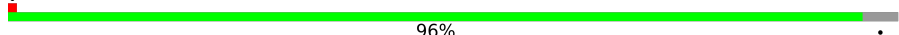
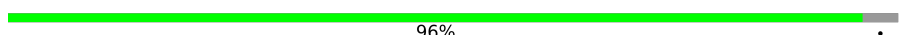
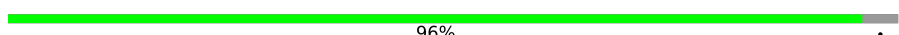
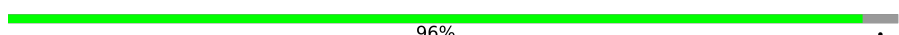
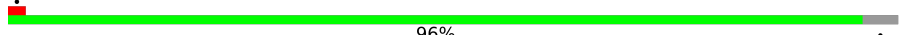
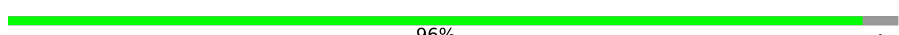
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Mol	Chain	Length	Quality of chain
42	VW	451	 95% 5%
42	VY	451	 95% 5%
42	WA	451	 97% .
42	WC	451	 96% .
42	WE	451	 97% .
42	WG	451	 96% .
42	WI	451	 97% .
42	WK	451	 97% .
42	WM	451	 97% .
42	WO	451	 96% .
42	WQ	451	 97% .
42	WS	451	 96% .
42	WU	451	 97% .
42	WW	451	 97% .
43	AB	445	 98% .
43	AD	445	 98% .
43	AF	445	 98% .
43	AH	445	 97% .
43	AJ	445	 98% .
43	AL	445	 98% .
43	AN	445	 98% .
43	AP	445	 98% .
43	AR	445	 98% .
43	AT	445	 98% .
43	AV	445	98% .

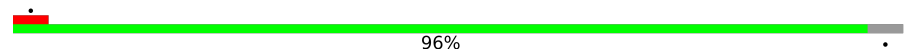
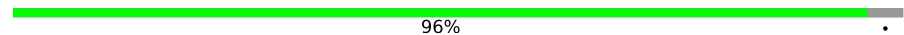
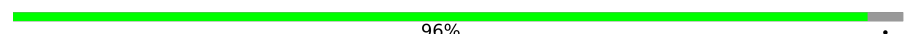
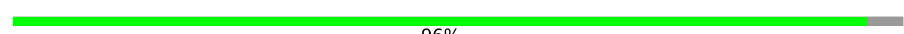


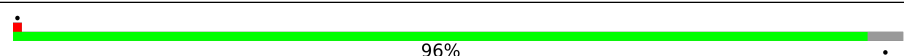
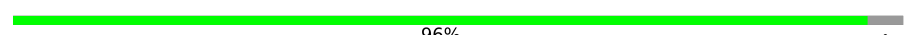
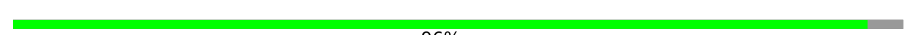


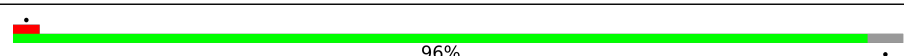
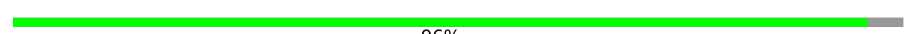

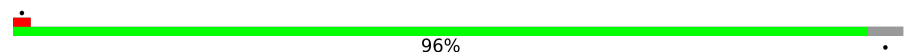
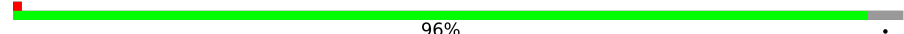
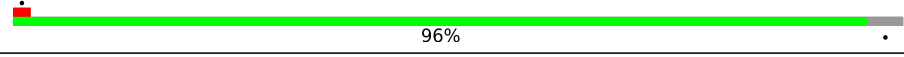
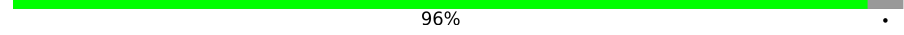
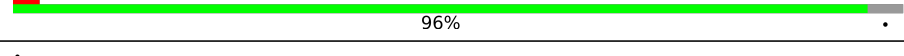
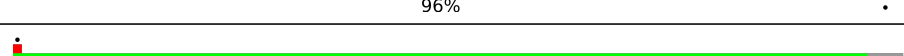
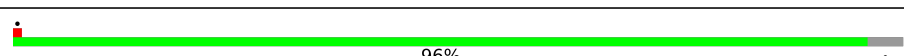
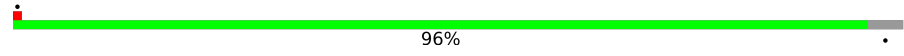
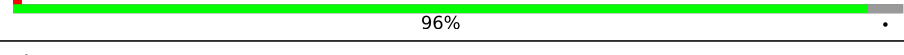
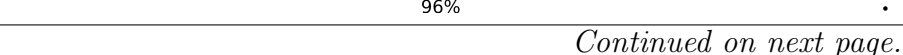

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Mol	Chain	Length	Quality of chain
43	AX	445	 98%
43	BB	445	 96%
43	BD	445	 96%
43	BF	445	 96%
43	BH	445	 96%
43	BJ	445	 97%
43	BL	445	 96%
43	BN	445	 96%
43	BP	445	 96%
43	BR	445	 96%
43	BT	445	 96%
43	BV	445	 96%
43	BX	445	 96%
43	CB	445	 96%
43	CD	445	 96%
43	CF	445	 96%
43	CH	445	 96%
43	CJ	445	 96%
43	CL	445	 96%
43	CN	445	 96%
43	CP	445	 96%
43	CR	445	 96%
43	CT	445	 96%
43	CV	445	 96%
43	CX	445	 96%

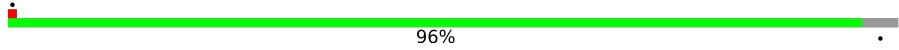
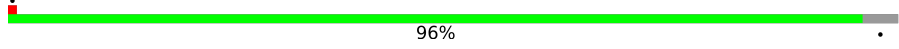
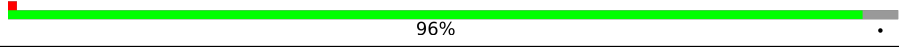
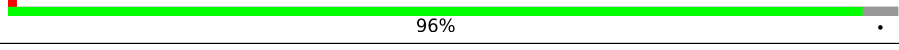
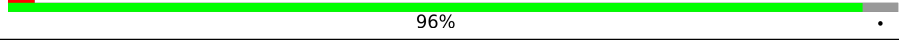
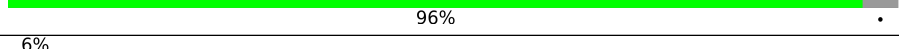
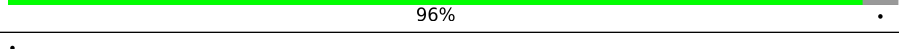
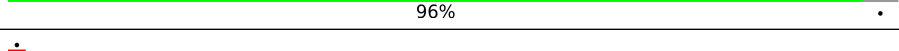
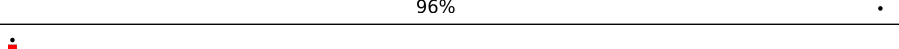
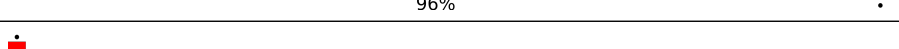
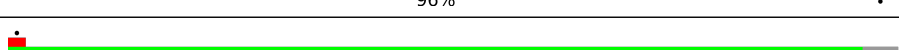
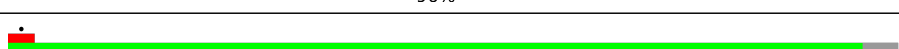
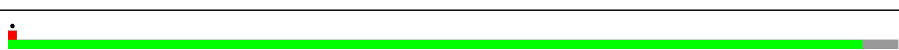
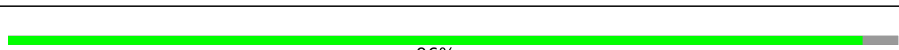
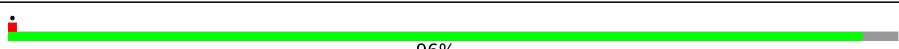
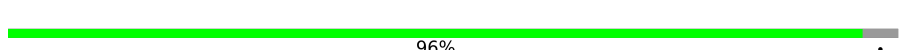
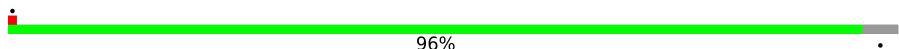
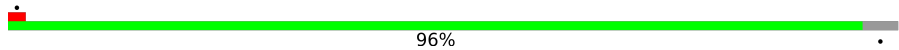
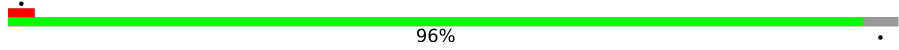
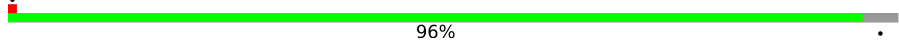
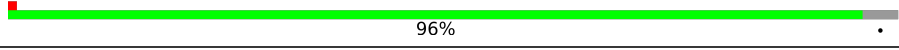
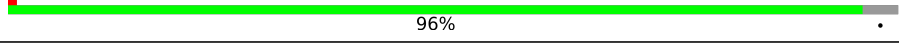
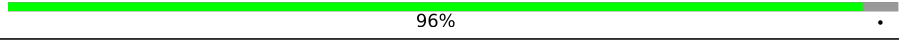
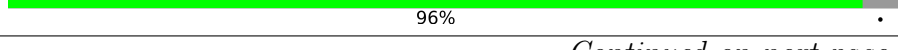

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Mol	Chain	Length	Quality of chain
43	CZ	445	 96%
43	DB	445	 96%
43	DD	445	 96%
43	DF	445	 96%
43	DH	445	 96%
43	DJ	445	 96%
43	DL	445	 96%
43	DN	445	 96%
43	DP	445	 96%
43	DR	445	 96%
43	DT	445	 96%
43	DV	445	 96%
43	DX	445	 96%
43	DZ	445	 96%
43	EB	445	 96%
43	ED	445	 96%
43	EF	445	 96%
43	EH	445	 96%
43	EJ	445	 96%
43	EL	445	 96%
43	EN	445	 96%
43	EP	445	 96%
43	ER	445	 96%
43	ET	445	 96%
43	EV	445	 96%

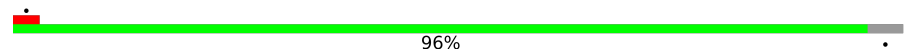
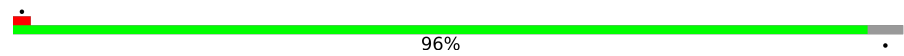
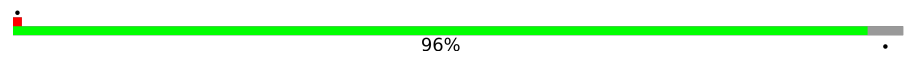
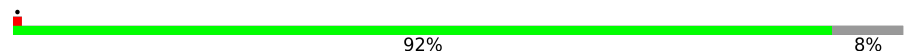
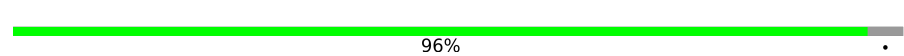
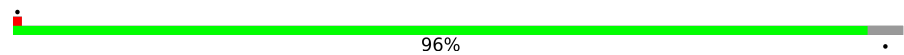
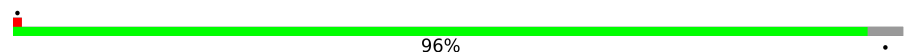
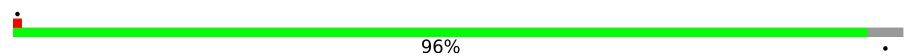
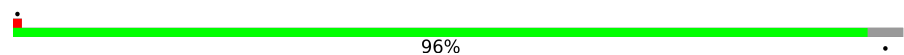
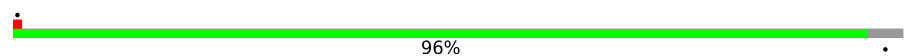
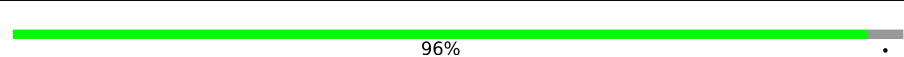
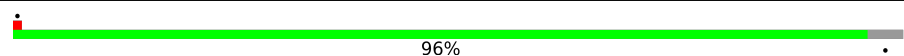
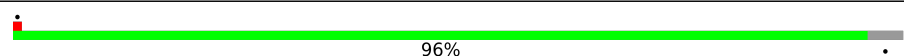
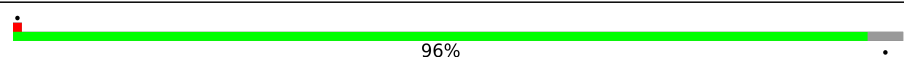
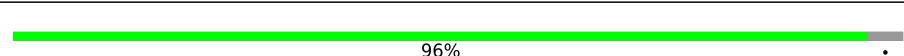
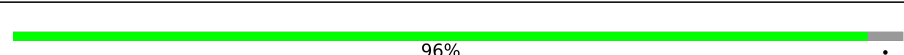
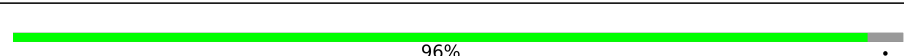
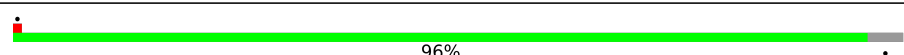
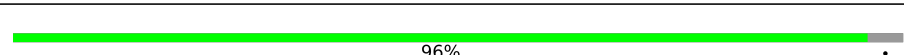
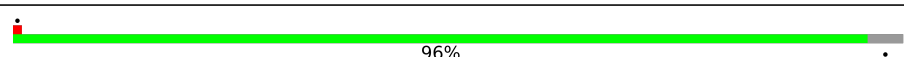
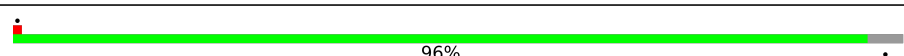
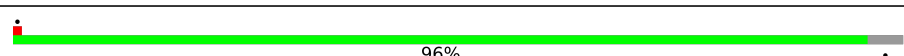
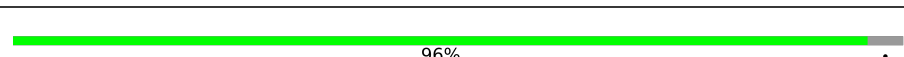
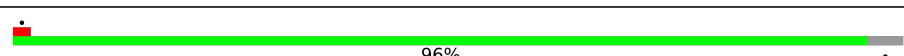
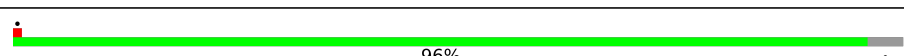
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Mol	Chain	Length	Quality of chain
43	EX	445	 96%
43	EZ	445	 96%
43	FB	445	 96%
43	FD	445	 96%
43	FF	445	 96%
43	FH	445	 96%
43	FJ	445	 96%
43	FL	445	 96%
43	FN	445	 96%
43	FP	445	 96%
43	FR	445	 96%
43	FT	445	 96%
43	FV	445	 96%
43	FX	445	 96%
43	FZ	445	 96%
43	GB	445	 96%
43	GD	445	 96%
43	GF	445	 96%
43	GH	445	 96%
43	GJ	445	 96%
43	GL	445	 96%
43	GN	445	 96%
43	GP	445	 96%
43	GR	445	 96%
43	GT	445	 96%

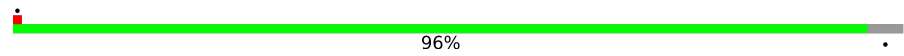
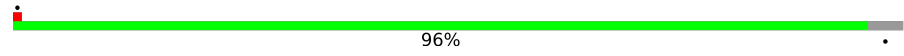
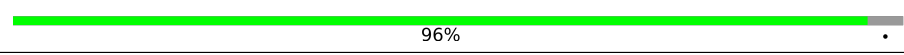
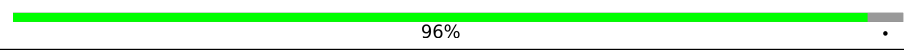
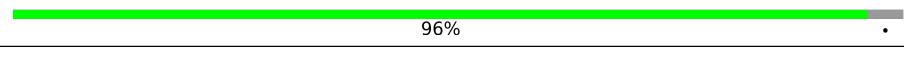
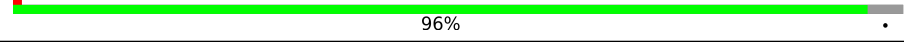
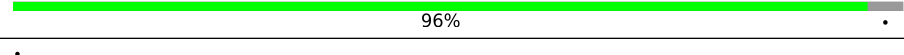
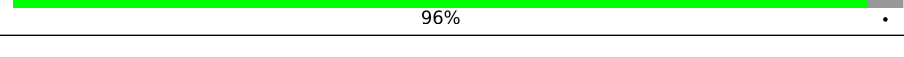
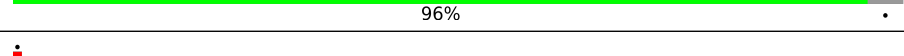
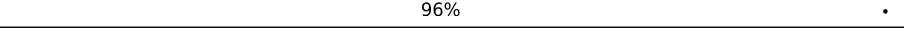
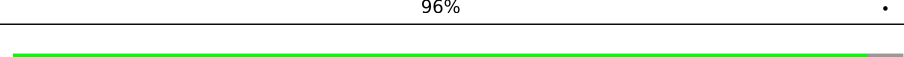
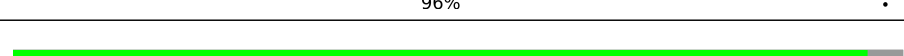
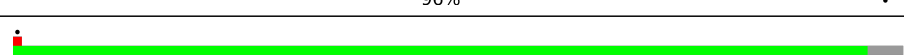
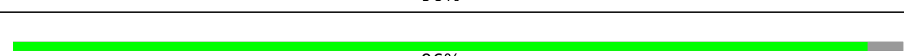
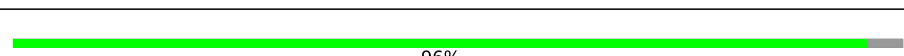
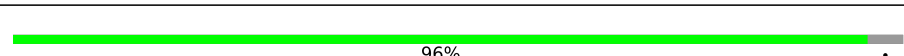
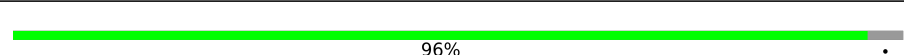
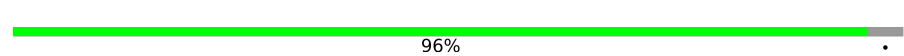
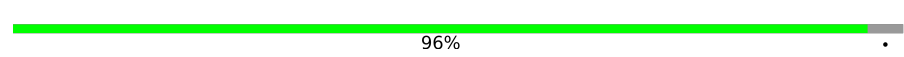
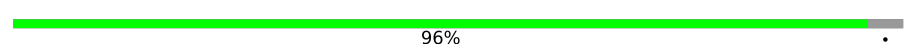
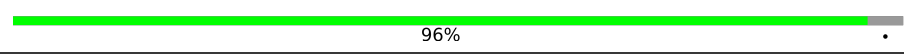
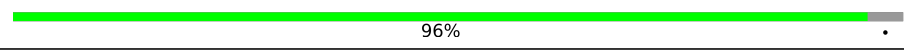
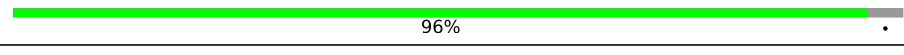
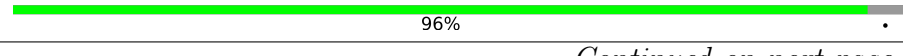

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Mol	Chain	Length	Quality of chain
43	GV	445	 96%
43	GX	445	 96%
43	GZ	445	 96%
43	HB	445	 92% 8%
43	HD	445	 96%
43	HF	445	 96%
43	HH	445	 96%
43	HJ	445	 96%
43	HL	445	 96%
43	HN	445	 96%
43	HP	445	 96%
43	HR	445	 96%
43	HT	445	 96%
43	HV	445	 96%
43	HX	445	 96%
43	HZ	445	 96%
43	IB	445	 96%
43	ID	445	 96%
43	IF	445	 96%
43	IH	445	 96%
43	IJ	445	 96%
43	IL	445	 96%
43	IN	445	 96%
43	IP	445	 96%
43	IR	445	 96%

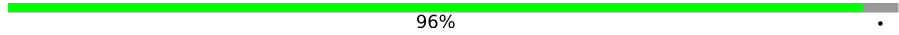
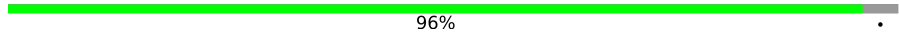
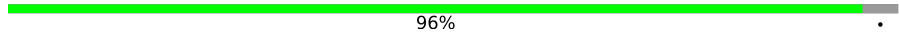
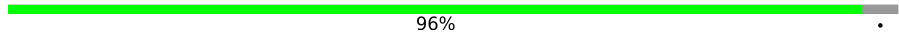
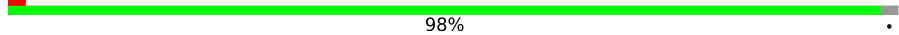
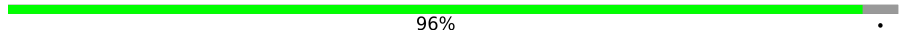
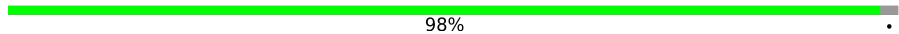
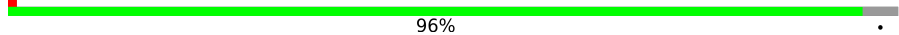
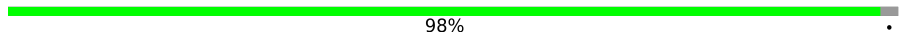
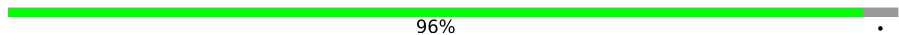
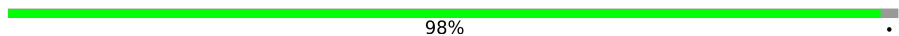
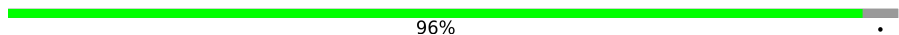
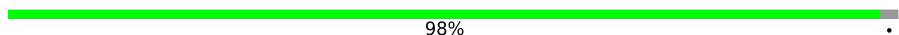
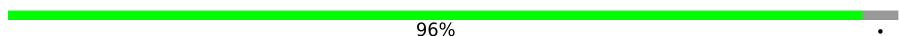
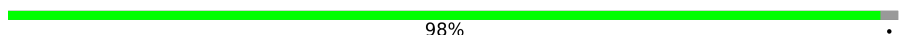
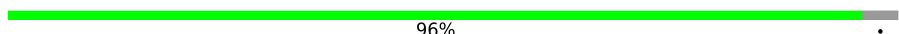
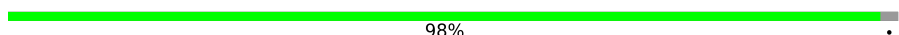
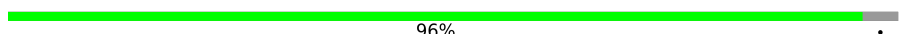
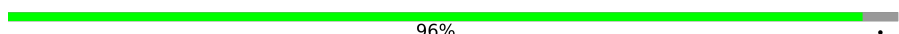
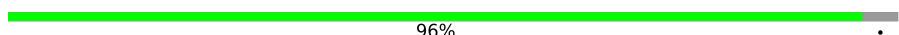
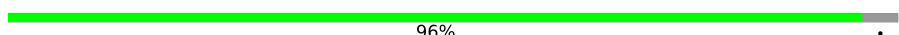
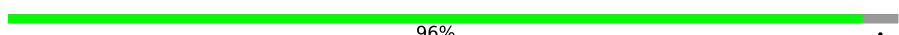
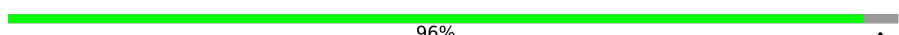
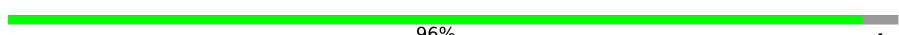
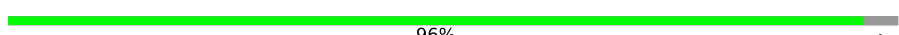
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Mol	Chain	Length	Quality of chain
43	IT	445	 96%
43	IV	445	 96%
43	IX	445	 96%
43	JB	445	 96%
43	JD	445	 96%
43	JF	445	 96%
43	JH	445	 96%
43	JJ	445	 96%
43	JL	445	 96%
43	JN	445	 96%
43	JP	445	 96%
43	JR	445	 96%
43	JT	445	 96%
43	JV	445	 96%
43	JX	445	 96%
43	JZ	445	 96%
43	KB	445	 96%
43	KD	445	 96%
43	KF	445	 96%
43	KH	445	 96%
43	KJ	445	 96%
43	KL	445	 96%
43	KN	445	 96%
43	KP	445	 96%
43	KR	445	 96%

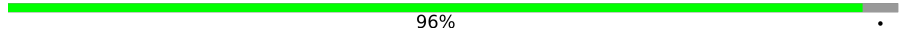
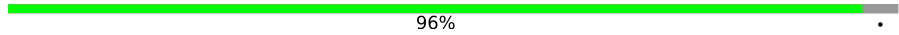
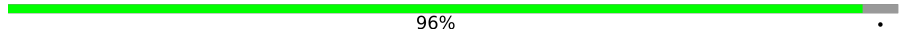
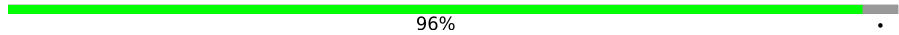
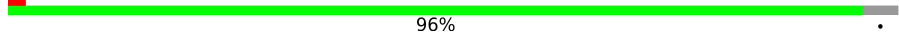
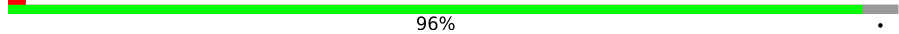
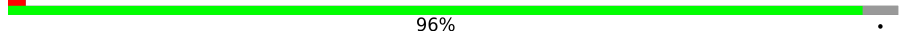
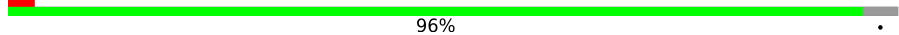
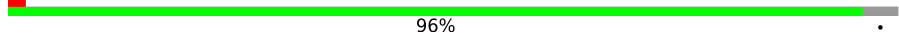
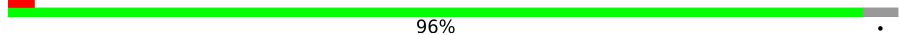
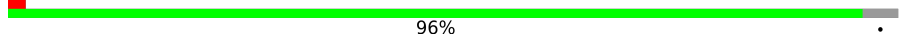
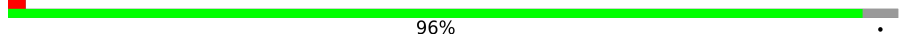
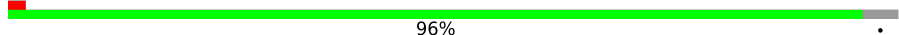
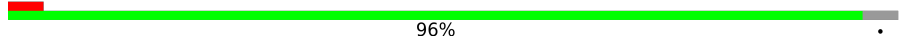
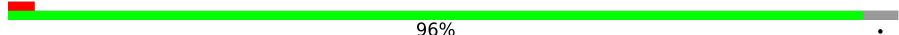
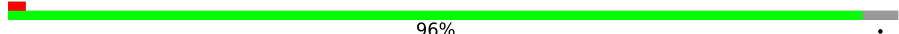
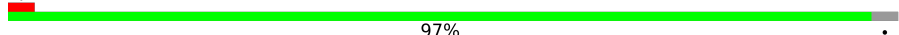
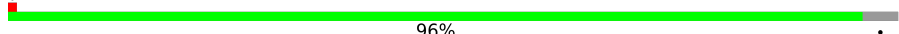
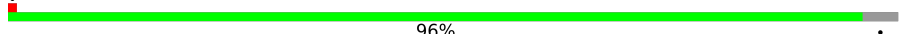
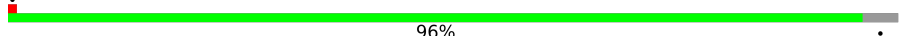
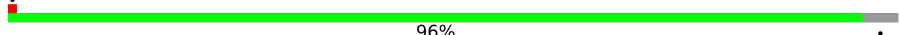
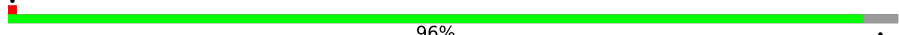
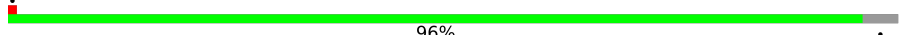
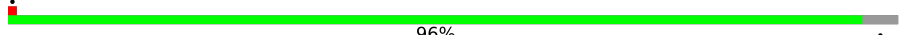
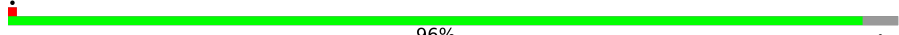
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Mol	Chain	Length	Quality of chain
43	KT	445	 96%
43	KV	445	 96%
43	KX	445	 96%
43	KZ	445	 96%
43	LB	445	 98%
43	LD	445	 96%
43	LF	445	 98%
43	LH	445	 96%
43	LJ	445	 98%
43	LL	445	 96%
43	LN	445	 98%
43	LP	445	 96%
43	LR	445	 98%
43	LT	445	 96%
43	LV	445	 98%
43	LX	445	 96%
43	LZ	445	 98%
43	MD	445	 96%
43	MF	445	 96%
43	MH	445	 96%
43	MJ	445	 96%
43	ML	445	 96%
43	MN	445	 96%
43	MP	445	 96%
43	MR	445	 96%

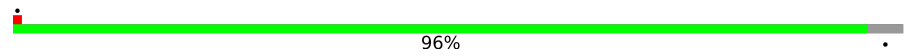
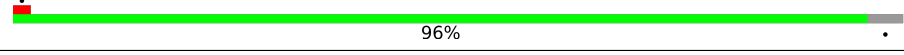
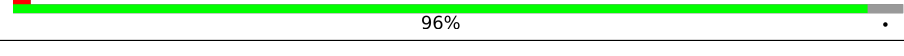
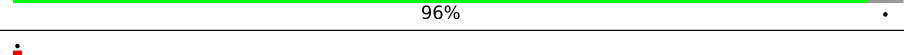
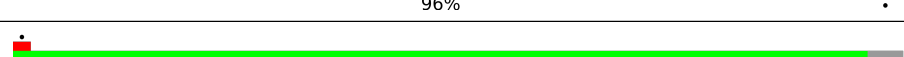
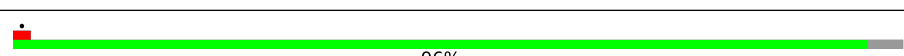

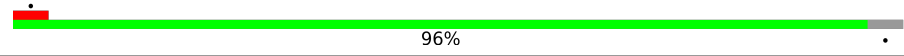
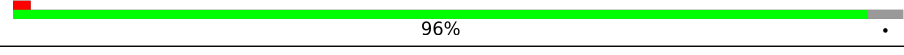
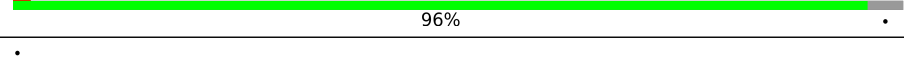
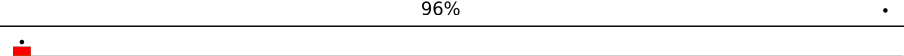
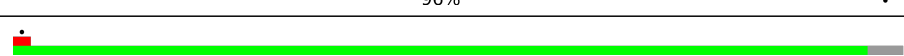
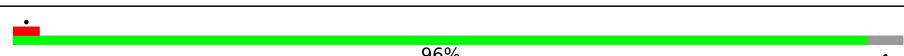
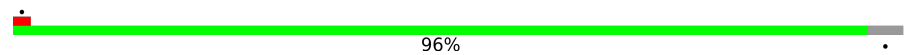
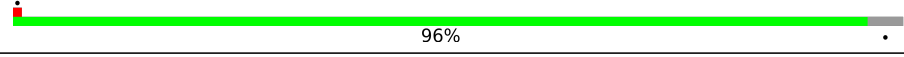
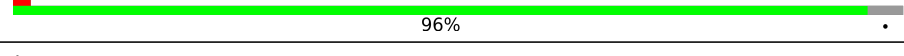
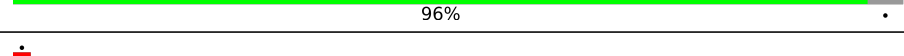
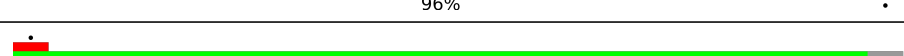
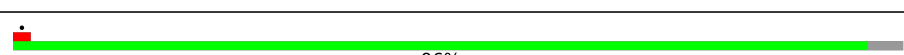
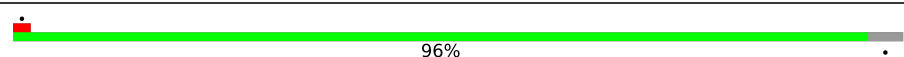
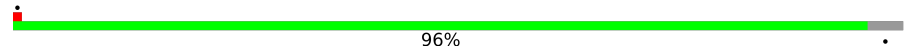
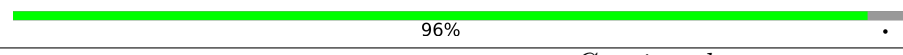



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Mol	Chain	Length	Quality of chain
43	MT	445	 96%
43	MV	445	 96%
43	MX	445	 96%
43	MZ	445	 96%
43	NB	445	 96%
43	ND	445	 96%
43	NF	445	 96%
43	NH	445	 96%
43	NJ	445	 96%
43	NL	445	 96%
43	NN	445	 96%
43	NP	445	 96%
43	NR	445	 96%
43	NT	445	 96%
43	NV	445	 96%
43	NX	445	 96%
43	NZ	445	 97%
43	OB	445	 96%
43	OD	445	 96%
43	OF	445	 96%
43	OH	445	 96%
43	OJ	445	 96%
43	OL	445	 96%
43	ON	445	 96%
43	OP	445	 96%

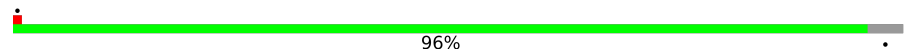
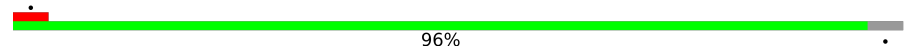
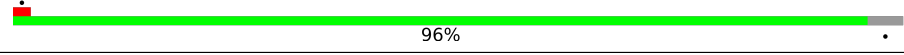
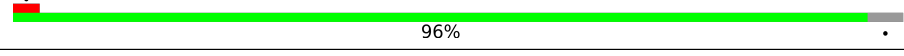
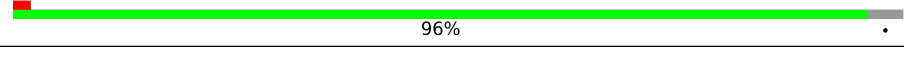
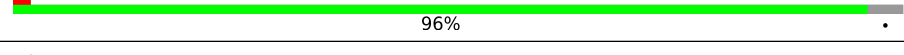
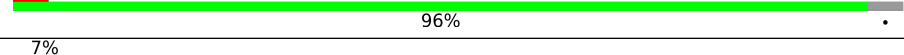
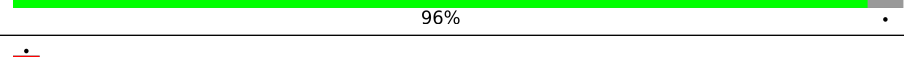
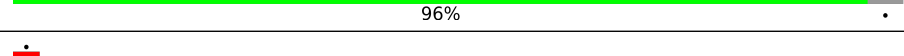
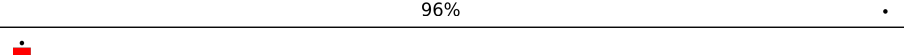
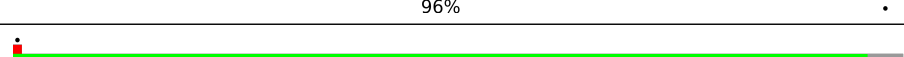
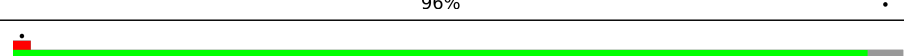
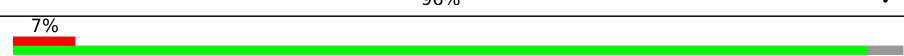
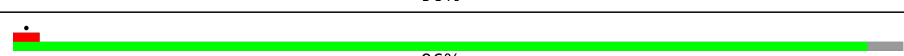
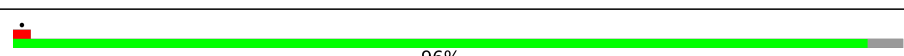
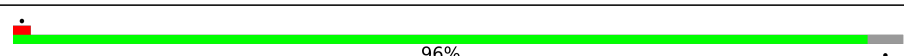
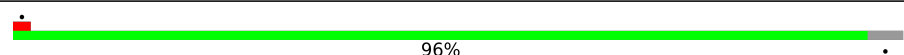
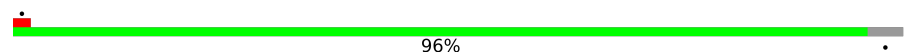
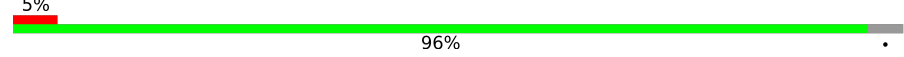
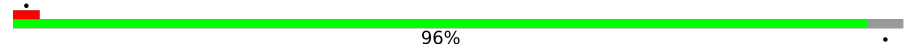
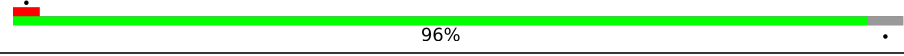
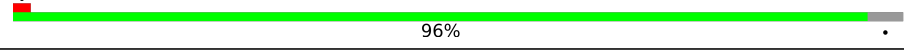
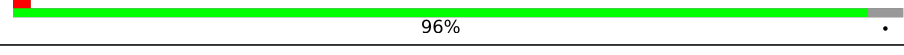
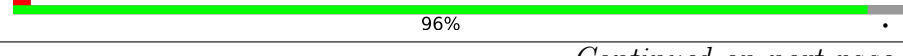

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Mol	Chain	Length	Quality of chain
43	OR	445	 96%
43	OT	445	 96%
43	OV	445	 96%
43	OX	445	 96%
43	PB	445	 96%
43	PD	445	 96%
43	PF	445	 96%
43	PH	445	 96%
43	PJ	445	 96%
43	PL	445	 96%
43	PN	445	 96%
43	PP	445	 96%
43	PR	445	 96%
43	PT	445	 96%
43	PV	445	 96%
43	PX	445	 96%
43	QB	445	 96%
43	QD	445	 96%
43	QF	445	 96%
43	QH	445	 96%
43	QJ	445	 96%
43	QL	445	 96%
43	QN	445	 96%
43	QP	445	 96%
43	QR	445	 96%

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Mol	Chain	Length	Quality of chain
43	QT	445	 96%
43	QV	445	 96%
43	QX	445	 96%
43	RB	445	 96%
43	RD	445	 96%
43	RF	445	 96%
43	RH	445	 96%
43	RJ	445	 96%
43	RL	445	 96%
43	RN	445	 96%
43	RP	445	 96%
43	RR	445	 96%
43	RT	445	 96%
43	RV	445	 96%
43	RX	445	 96%
43	SB	445	 96%
43	SD	445	 96%
43	SF	445	 96%
43	SH	445	 96%
43	SJ	445	 96%
43	SL	445	 96%
43	SN	445	 96%
43	SP	445	 96%
43	SR	445	 96%
43	ST	445	 96%

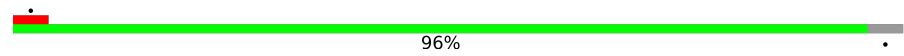
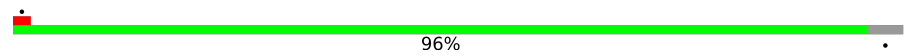
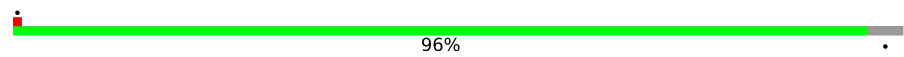
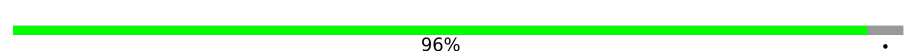
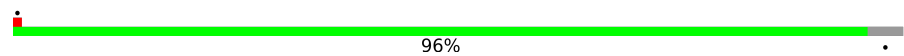
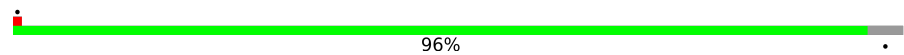
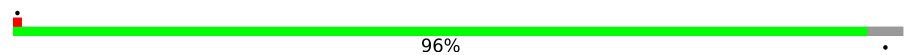
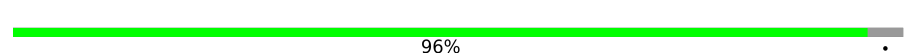
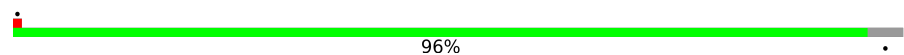
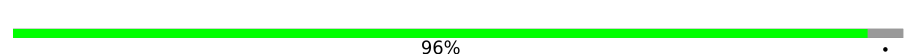
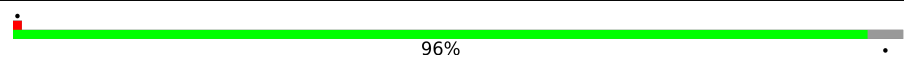
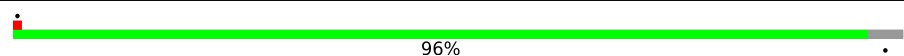
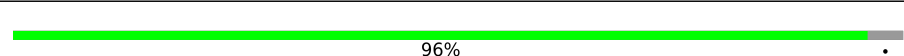
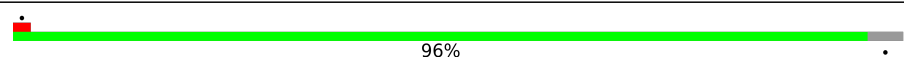
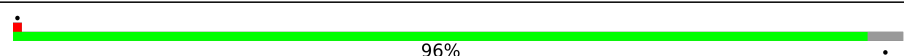
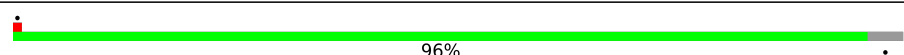
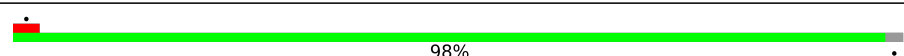
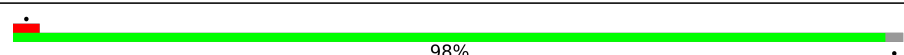
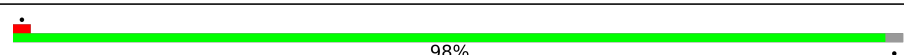
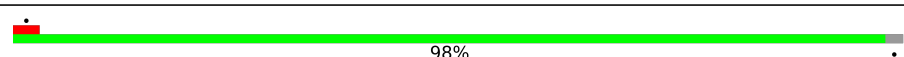
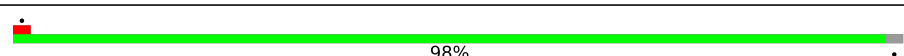
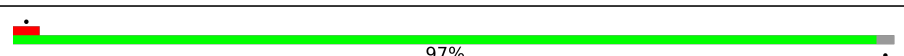
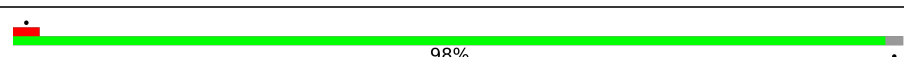
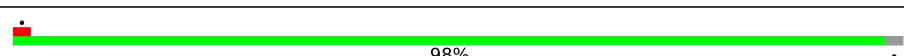
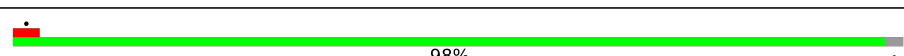
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Mol	Chain	Length	Quality of chain
43	SV	445	5% 96%
43	SX	445	96%
43	TB	445	96%
43	TD	445	96%
43	TF	445	96%
43	TH	445	96%
43	TJ	445	7% 96%
43	TL	445	7% 96%
43	TN	445	5% 96%
43	TP	445	96%
43	TR	445	96%
43	TT	445	96%
43	TV	445	7% 96%
43	TX	445	5% 96%
43	TZ	445	96%
43	UB	445	96%
43	UD	445	96%
43	UF	445	96%
43	UH	445	96%
43	UJ	445	96%
43	UL	445	96%
43	UN	445	96%
43	UP	445	96%
43	UR	445	96%
43	UT	445	96%

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Mol	Chain	Length	Quality of chain
43	UV	445	 96%
43	UX	445	 96%
43	UZ	445	 96%
43	VB	445	 96%
43	VD	445	 96%
43	VF	445	 96%
43	VH	445	 96%
43	VJ	445	 96%
43	VL	445	 96%
43	VN	445	 96%
43	VP	445	 96%
43	VR	445	 96%
43	VT	445	 96%
43	VV	445	 96%
43	VX	445	 96%
43	VZ	445	 96%
43	WB	445	 98%
43	WD	445	 98%
43	WF	445	 98%
43	WH	445	 98%
43	WJ	445	 98%
43	WL	445	 97%
43	WN	445	 98%
43	WP	445	 98%
43	WR	445	 98%

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Mol	Chain	Length	Quality of chain
43	WT	445	98%
43	WV	445	98%
43	WX	445	98%
44	E	560	13% 30% 70%
44	F	560	10% 39% 61%
44	e	560	13% 39% 61%
44	f	560	8% 38% 62%
45	G	716	9% 64% 36%
45	H	716	14% 65% 35%
45	I	716	9% 65% 35%
45	J	716	15% 66% 34%
45	g	716	32% 65% 35%
45	h	716	20% 66% 34%
45	i	716	17% 65% 35%
45	j	716	17% 66% 34%
46	K	151	13% 21% 79%
46	L	151	7% 23% 77%
46	k	151	21% 21% 79%
46	l	151	9% 25% 75%
47	M	276	15% 100%
47	N	276	32% 93% 7%
47	O	276	44% 100%
47	P	276	26% 95% 5%
47	m	276	29% 100%
47	n	276	49% 95% 5%

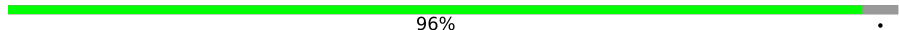
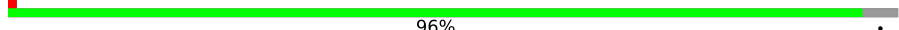
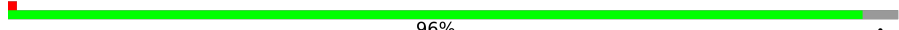
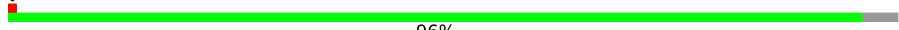
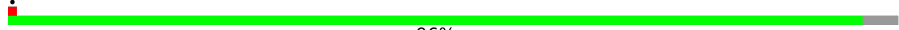





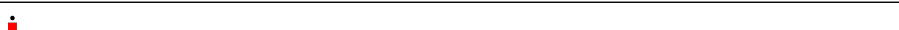

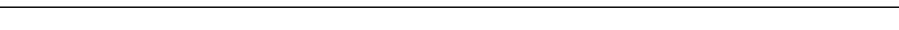
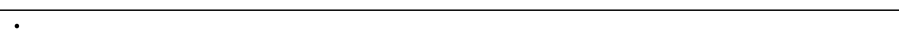





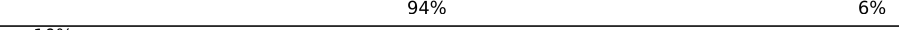
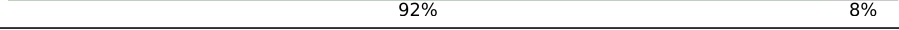
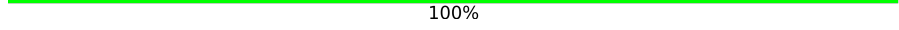
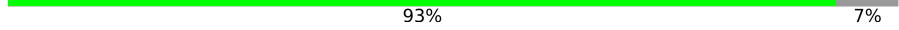
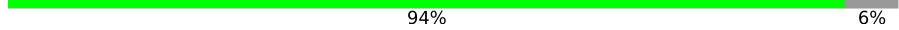
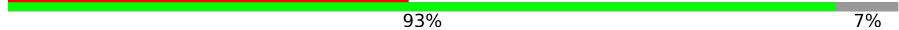
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Mol	Chain	Length	Quality of chain
47	o	276	28% 100%
47	p	276	21% 95% 5%
48	Q	230	25% 76% 24%
48	R	230	16% 84%
48	q	230	28% 90% 10%
48	r	230	18% 82%
49	S	311	31% 93% 7%
49	s	311	19% 93% 7%
50	T	348	15% 97% .
50	t	348	27% 93% 7%
51	U	316	27% 94% 6%
51	V	316	53% 94% 6%
51	u	316	37% 94% 6%
51	v	316	33% 94% 6%
52	W	149	51% 95% 5%
53	X	212	35% 91% 9%
53	Y	212	50% 91% 9%
53	x	212	18% 91% 9%
53	y	212	39% 91% 9%
54	XA	193	96% .
54	XB	193	96% .
54	XC	193	96% .
54	XD	193	96% .
54	XE	193	96% .
54	XF	193	96% .

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Mol	Chain	Length	Quality of chain
54	XG	193	 96%
54	XH	193	 96%
54	XI	193	 96%
54	XJ	193	 96%
54	XK	193	 96%
54	XL	193	 96%
54	XM	193	 96%
55	YB	257	 86% 14%
55	YC	257	 86% 14%
55	YD	257	 86% 14%
55	YF	257	 86% 14%
55	YG	257	 86% 14%
55	YH	257	 86% 14%
55	YI	257	 86% 14%
55	YJ	257	 86% 14%
55	YK	257	 86% 14%
55	YL	257	 86% 14%
55	YM	257	 86% 14%
56	Z	228	 26% 94% 6%
56	z	228	 10% 92% 8%
57	a0	72	 11% 100%
58	a1	89	 52% 93% 7%
58	a2	89	 49% 94% 6%
58	a3	89	 45% 93% 7%
58	a4	89	 40% 99%

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Mol	Chain	Length	Quality of chain
58	a5	89	8% 94% 6%
58	a6	89	6% 93% 7%
58	a7	89	24% 96% .
58	a8	89	19% 97% .
58	a9	89	47% 96% .
58	b0	89	35% 100%
58	b1	89	40% 94% ..
58	b2	89	85% 99% .
58	b3	89	52% 98% .
58	b4	89	40% 94% 6%
58	b5	89	47% 94% 6%
58	b6	89	40% 93% 7%
58	b7	89	31% 97% .
58	b8	89	42% 98% .
58	b9	89	37% 100%
58	c0	89	74% 96% .
58	l1	89	9% 100%
58	l2	89	. 100%
58	l3	89	. 100%
58	l4	89	. 100%
58	l5	89	100%
58	l6	89	. 100%
58	n1	89	31% 100%
58	n2	89	9% 100%
58	n3	89	17% 100%

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Mol	Chain	Length	Quality of chain
58	n4	89	8% 100%
58	n5	89	36% 100%
58	n6	89	9% 100%
58	p1	89	34% 100%
58	p2	89	12% 100%
58	p3	89	12% 100%
58	p4	89	9% 100%
58	p5	89	29% 100%
58	p6	89	11% 100%
58	r1	89	44% 100%
58	r2	89	17% 100%
58	r3	89	35% 100%
58	r4	89	9% 100%
58	r5	89	47% 100%
58	r6	89	19% 100%
59	c1	240	25% 95% 5%
60	c2	791	25% 80% 20%
61	c3	177	8% 25% 75%
61	c4	177	8% 31% 69%
61	c5	177	9% 34% 66%
61	c6	177	7% 34% 66%
62	d0	1237	45% 88% 12%
63	d1	767	20% 68% 32%
64	d2	1149	36% 79% 21%
65	d3	475	54% 88% 12%

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Mol	Chain	Length	Quality of chain
66	d4	365	53% 98%
67	d5	377	24% 100%
67	d6	377	17% 100%
67	d7	377	23% 98%
67	d8	377	66% 100%
67	d9	377	46% 97%
67	f1	377	28% 98%
68	e0	258	52% 81% 19%
68	e1	258	28% 77% 23%
68	e2	258	23% 81% 19%
68	e3	258	52% 77% 23%
68	e4	258	62% 78% 22%
68	e5	258	17% 77% 23%
68	e6	258	19% 77% 23%
68	e7	258	39% 77% 23%
68	e8	258	34% 81% 19%
68	e9	258	47% 77% 23%
69	f2	172	22% 85% 15%
70	g1	3960	49% 99%
71	g2	4024	10% 13% 87%
71	g4	4024	8% 11% 89%
72	g3	4116	6% 14% 86%
73	g5	4158	60% 96%
74	g6	4265	40% 98%
75	h1	941	41% 59%

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Mol	Chain	Length	Quality of chain
75	h2	941	
76	h3	1142	
76	h4	1142	
77	i1	555	
78	i2	377	
79	i3	233	
80	i4	1250	
80	i5	1250	
81	i6	1665	
81	i8	1665	
82	i7	1854	
82	i9	1854	
83	j1	872	
83	j2	872	
84	j3	308	
85	j4	611	
86	k1	891	
87	k2	848	
88	k3	716	
89	k4	96	
89	m4	96	
89	o4	96	
89	q4	96	
90	k5	96	
90	m5	96	

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Mol	Chain	Length	Quality of chain
90	o5	96	9% 100%
90	q5	96	18% 100%
91	k8	4589	29% 97%
92	k9	4427	58% 98%
93	l7	142	74% 26%
93	n7	142	56% 80% 20%
93	p7	142	54% 80% 20%
93	r7	142	61% 80% 20%
94	l8	113	90% 10%
94	n8	113	67% 91% 9%
94	p8	113	65% 91% 9%
94	r8	113	70% 80% 20%
95	m0	211	41% 100%
95	q0	211	42% 100%
95	s0	211	37% 100%
95	u0	211	40% 100%
96	m1	699	8% 75% 25%
96	o1	699	8% 75% 25%
96	q1	699	12% 75% 25%
96	s1	699	8% 59% 41%
97	m2	605	15% 87% 13%
97	o2	605	14% 87% 13%
97	q2	605	20% 87% 13%
97	s2	605	6% 66% 34%
98	m3	190	100% 100%

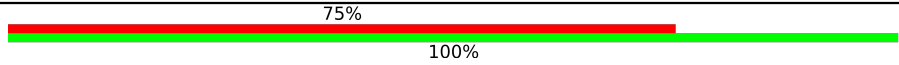
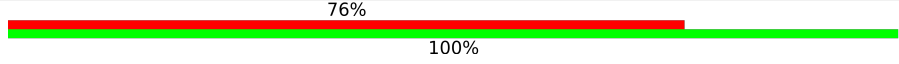



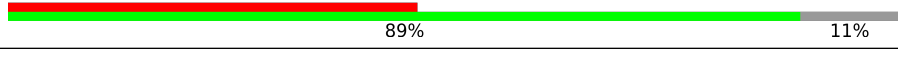
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Mol	Chain	Length	Quality of chain
98	o3	190	100% 100%
98	q3	190	100% 100%
99	m6	670	25% 52% 48%
99	o6	670	16% 28% 72%
99	q6	670	27% 52% 48%
99	s6	670	24% 52% 48%
99	u6	670	13% 32% 68%
100	m7	1044	21% 57% 43%
100	q7	1044	21% 57% 43%
100	s7	1044	19% 57% 43%
100	u7	1044	21% 57% 43%
101	m8	595	34% 70% 30%
101	o8	595	24% 40% 60%
101	q8	595	38% 70% 30%
101	s8	595	33% 70% 30%
101	u8	595	13% 39% 61%
102	m9	672	5% 30% 70%
102	q9	672	5% 30% 70%
102	s9	672	5% 30% 70%
102	u9	672	5% 30% 70%
103	n0	4624	51% 99%
103	p0	4624	51% 99%
103	r0	4624	55% 99%
103	t0	4624	18% 82%
104	n9	4486	75% 100%

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Mol	Chain	Length	Quality of chain
104	p9	4486	 <p>75% 100% 100%</p>
104	r9	4486	 <p>76% 100% 100%</p>
104	t9	4486	 <p>16% 84% 84%</p>
105	v1	330	 <p>40% 60% 60%</p>
105	v2	330	 <p>40% 60% 60%</p>
105	v3	330	 <p>40% 60% 60%</p>
106	w	464	 <p>46% 89% 11%</p>

2 Entry composition [i](#)

There are 109 unique types of molecules in this entry. The entry contains 3163608 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 Dynein regulatory complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	478	Total	C	N	O	S	0	0
			3952	2457	723	755	17		
1	4	459	Total	C	N	O	S	0	0
			3831	2381	702	731	17		

- Molecule 2 is a protein called Dynein regulatory complex protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	540	Total	C	N	O	S	0	0
			4537	2883	782	856	16		

- Molecule 3 is a protein called Dynein regulatory complex protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	10	346	Total	C	N	O	S	0	0
			2851	1772	519	546	14		

- Molecule 4 is a protein called Dynein regulatory complex protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	11	616	Total	C	N	O	S	0	0
			4998	3226	858	890	24		

- Molecule 5 is a protein called Dynein regulatory complex protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	12	118	Total	C	N	O	S	0	0
			961	610	161	186	4		
5	13	138	Total	C	N	O	S	0	0
			1128	717	190	216	5		
5	14	140	Total	C	N	O	S	0	0
			1143	725	195	218	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	8	124	1009	644	167	194	4	0	0

- Molecule 6 is a protein called EF-hand domain-containing family member B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	1A	523	4234	2686	744	789	15	0	0
6	1B	554	4483	2850	787	830	16	0	0
6	1C	90	729	477	129	121	2	0	0

- Molecule 7 is a protein called Cilia- and flagella-associated protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	1D	46	385	243	67	74	1	0	0
7	1E	382	3250	1975	624	632	19	0	0
7	1F	452	3849	2336	749	744	20	0	0
7	1G	121	1034	626	212	195	1	0	0
7	1H	176	1491	914	283	284	10	0	0
7	1I	456	3890	2362	756	751	21	0	0
7	1J	332	2861	1723	568	557	13	0	0

- Molecule 8 is a protein called Cilia- and flagella-associated protein 52.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	1L	610	4717	2978	827	882	30	0	0
8	1M	610	4717	2978	827	882	30	0	0
8	1N	610	4717	2978	827	882	30	0	0
8	1O	610	4717	2978	827	882	30	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	1P	610	Total	C	N	O	S	0	0
			4717	2978	827	882	30		
8	1Q	610	Total	C	N	O	S	0	0
			4717	2978	827	882	30		

- Molecule 9 is a protein called Cilia- and flagella-associated protein 53.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1R	186	Total	C	N	O	S	0	0
			1587	979	297	304	7		
9	1S	463	Total	C	N	O	S	0	0
			3926	2403	744	761	18		
9	1T	330	Total	C	N	O	S	0	0
			2794	1703	531	546	14		

- Molecule 10 is a protein called Cilia- and flagella-associated protein 95.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1V	146	Total	C	N	O	S	0	0
			1197	757	206	230	4		
10	1W	146	Total	C	N	O	S	0	0
			1197	757	206	230	4		

- Molecule 11 is a protein called Cilia- and flagella-associated protein 107.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	1Y	174	Total	C	N	O	S	0	0
			1470	945	263	259	3		
11	1Z	173	Total	C	N	O	S	0	0
			1463	940	262	258	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1Y	191	PHE	LEU	conflict	UNP Q8N1D5
1Z	191	PHE	LEU	conflict	UNP Q8N1D5

- Molecule 12 is a protein called Dynein regulatory complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	2	464	Total	C	N	O	S	0	0
			3869	2435	679	740	15		

- Molecule 13 is a protein called Protein Flattop.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2A	116	Total	C	N	O	S	0	0
			900	572	158	167	3		
13	2B	116	Total	C	N	O	S	0	0
			900	572	158	167	3		
13	2C	116	Total	C	N	O	S	0	0
			900	572	158	167	3		
13	2D	116	Total	C	N	O	S	0	0
			900	572	158	167	3		
13	2E	116	Total	C	N	O	S	0	0
			900	572	158	167	3		
13	2F	116	Total	C	N	O	S	0	0
			900	572	158	167	3		
13	2G	79	Total	C	N	O	S	0	0
			600	383	109	105	3		

- Molecule 14 is a protein called Cilia- and flagella-associated protein 141.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2I	50	Total	C	N	O	S	0	0
			423	269	75	76	3		
14	2J	50	Total	C	N	O	S	0	0
			423	269	75	76	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2L	277	Total	C	N	O	S	0	0
			2227	1403	397	415	12		
15	2M	277	Total	C	N	O	S	0	0
			2227	1403	397	415	12		
15	2N	277	Total	C	N	O	S	0	0
			2227	1403	397	415	12		
15	2O	277	Total	C	N	O	S	0	0
			2227	1403	397	415	12		

- Molecule 16 is a protein called Cilia- and flagella- associated protein 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2Q	289	Total	C	N	O	S	0	0
			2505	1552	480	463	10		
16	2R	506	Total	C	N	O	S	0	0
			4289	2667	796	810	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	2S	265	2205	1373	400	423	9	0	0

- Molecule 17 is a protein called Cilia- and flagella-associated protein 276.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	2U	112	906	568	166	171	1	0	0
17	2V	112	906	568	166	171	1	0	0
17	2W	112	906	568	166	171	1	0	0
17	2X	112	906	568	166	171	1	0	0
17	2Y	112	906	568	166	171	1	0	0
17	2Z	112	906	568	166	171	1	0	0

- Molecule 18 is a protein called Dynein regulatory complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	3	516	4225	2648	719	833	25	0	0

- Molecule 19 is a protein called EF-hand domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	3A	485	3992	2576	667	735	14	0	0
19	3B	485	3992	2576	667	735	14	0	0
19	3C	484	3984	2570	666	734	14	0	0
19	3D	485	3992	2576	667	735	14	0	0
19	3E	485	3992	2576	667	735	14	0	0
19	3F	484	3984	2570	666	734	14	0	0

- Molecule 20 is a protein called EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	3G	613	Total 5053	C 3263	N 841	O 925	S 24	0	0
20	3H	701	Total 5797	C 3742	N 964	O 1063	S 28	0	0
20	3I	702	Total 5808	C 3748	N 968	O 1064	S 28	0	0
20	3J	701	Total 5797	C 3742	N 964	O 1063	S 28	0	0
20	3K	701	Total 5797	C 3742	N 964	O 1063	S 28	0	0
20	3L	702	Total 5808	C 3748	N 968	O 1064	S 28	0	0
20	3M	687	Total 5692	C 3675	N 944	O 1045	S 28	0	0

- Molecule 21 is a protein called Enkurin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	3O	159	Total 1304	C 829	N 227	O 243	S 5	0	0
21	3P	248	Total 2010	C 1283	N 348	O 370	S 9	0	0
21	3Q	250	Total 2023	C 1290	N 350	O 373	S 10	0	0
21	3R	250	Total 2023	C 1290	N 350	O 373	S 10	0	0
21	3S	248	Total 2010	C 1283	N 348	O 370	S 9	0	0
21	3T	250	Total 2023	C 1290	N 350	O 373	S 10	0	0
21	3U	250	Total 2023	C 1290	N 350	O 373	S 10	0	0

- Molecule 22 is a protein called Meiosis-specific nuclear structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	3W	392	Total 3353	C 2065	N 611	O 656	S 21	0	0
22	3X	480	Total 4115	C 2547	N 753	O 793	S 22	0	0
22	3Y	143	Total 1225	C 770	N 223	O 227	S 5	0	0

- Molecule 23 is a protein called Protein FAM166B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	4A	80	Total	C	N	O	S	0	0
			619	405	108	103	3		
23	4B	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4C	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4D	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4E	146	Total	C	N	O	S	0	0
			1085	701	188	190	6		
23	4F	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4G	146	Total	C	N	O	S	0	0
			1085	701	188	190	6		
23	4H	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4I	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4J	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4K	146	Total	C	N	O	S	0	0
			1085	701	188	190	6		
23	4L	145	Total	C	N	O	S	0	0
			1080	698	187	189	6		
23	4M	146	Total	C	N	O	S	0	0
			1085	701	188	190	6		

- Molecule 24 is a protein called Nucleoside diphosphate kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	4O	371	Total	C	N	O	S	0	0
			2943	1873	506	543	21		
24	4P	371	Total	C	N	O	S	0	0
			2943	1873	506	543	21		
24	4Q	371	Total	C	N	O	S	0	0
			2943	1873	506	543	21		
24	4R	371	Total	C	N	O	S	0	0
			2943	1873	506	543	21		

- Molecule 25 is a protein called Piercer of microtubule wall 1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4S	113	Total	C	N	O	S	0	0
			905	566	165	169	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	4T	113	905	566	165	169	5	0	0

- Molecule 26 is a protein called Piercer of microtubule wall 2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	4U	94	750	478	127	139	6	0	0
26	4V	94	750	478	127	139	6	0	0
26	4W	53	411	267	64	74	6	0	0

- Molecule 27 is a protein called Dynein regulatory complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	5	303	2377	1498	427	442	10	0	0

- Molecule 28 is a protein called RIB43A-like with coiled-coils protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	5A	268	2218	1353	432	423	10	0	0
28	5B	368	3089	1886	608	584	11	0	0
28	5C	170	1423	871	278	271	3	0	0

- Molecule 29 is a protein called RIB43A-like with coiled-coils protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	5D	89	744	447	154	141	2	0	0
29	5E	335	2728	1650	530	533	15	0	0
29	5F	266	2158	1308	413	424	13	0	0

- Molecule 30 is a protein called Sperm-associated antigen 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5H	179	Total	C	N	O	S	0	0
			1459	919	260	271	9		
30	5I	179	Total	C	N	O	S	0	0
			1459	919	260	271	9		
30	5J	63	Total	C	N	O	S	0	0
			511	317	92	98	4		

- Molecule 31 is a protein called Uncharacterized protein CFAP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5L	89	Total	C	N	O	S	0	0
			763	481	135	143	4		
31	5M	89	Total	C	N	O	S	0	0
			763	481	135	143	4		

- Molecule 32 is a protein called Cilia- and flagella-associated protein 77.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5O	80	Total	C	N	O	S	0	0
			693	442	131	118	2		
32	5P	226	Total	C	N	O	S	0	0
			1849	1169	349	323	8		
32	5Q	224	Total	C	N	O	S	0	0
			1831	1158	345	320	8		
32	5R	226	Total	C	N	O	S	0	0
			1849	1169	349	323	8		
32	5S	226	Total	C	N	O	S	0	0
			1849	1169	349	323	8		
32	5T	224	Total	C	N	O	S	0	0
			1831	1158	345	320	8		
32	5U	226	Total	C	N	O	S	0	0
			1849	1169	349	323	8		
32	5V	66	Total	C	N	O	S	0	0
			522	330	95	94	3		

- Molecule 33 is a protein called Uncharacterized protein CFAP90.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	5X	127	Total	C	N	O	S	0	0
			1045	659	195	190	1		
33	5Y	127	Total	C	N	O	S	0	0
			1045	659	195	190	1		

- Molecule 34 is a protein called Sperm acrosome-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	6A	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6C	159	Total 1278	C 799	N 227	O 242	S 10	0	0
34	6E	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6G	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6I	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6K	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6L	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6N	159	Total 1278	C 799	N 227	O 242	S 10	0	0
34	6O	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6Q	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6R	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6T	157	Total 1263	C 788	N 225	O 240	S 10	0	0
34	6V	157	Total 1263	C 788	N 225	O 240	S 10	0	0

- Molecule 35 is a protein called Dynein regulatory complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	7	601	Total 4993	C 3174	N 854	O 931	S 34	0	0

- Molecule 36 is a protein called Protein FAM166C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	7A	60	Total 462	C 295	N 81	O 84	S 2	0	0
36	7B	102	Total 825	C 526	N 147	O 148	S 4	0	0
36	7C	102	Total 825	C 526	N 147	O 148	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
36	7D	101	Total	C	N	O	S	0	0
			818	521	146	147	4		
36	7E	102	Total	C	N	O	S	0	0
			825	526	147	148	4		
36	7F	102	Total	C	N	O	S	0	0
			825	526	147	148	4		
36	7G	101	Total	C	N	O	S	0	0
			818	521	146	147	4		

- Molecule 37 is a protein called Cilia- and flagella-associated protein 144.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	7I	111	Total	C	N	O	S	0	0
			945	594	179	170	2		
37	7J	111	Total	C	N	O	S	0	0
			945	594	179	170	2		

- Molecule 38 is a protein called Tektin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	8A	202	Total	C	N	O	S	0	0
			1615	1002	293	311	9		
38	8B	391	Total	C	N	O	S	0	0
			3185	1978	576	619	12		
38	8C	391	Total	C	N	O	S	0	0
			3185	1978	576	619	12		
38	8D	391	Total	C	N	O	S	0	0
			3185	1978	576	619	12		
38	8E	391	Total	C	N	O	S	0	0
			3185	1978	576	619	12		
38	8F	391	Total	C	N	O	S	0	0
			3185	1978	576	619	12		
38	8G	340	Total	C	N	O	S	0	0
			2770	1723	493	544	10		
38	8H	36	Total	C	N	O		0	0
			305	188	63	54			

- Molecule 39 is a protein called Tektin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	8J	58	Total	C	N	O	S	0	0
			498	300	100	97	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
39	8K	381	Total	C	N	O	S	0	0
			3088	1891	567	615	15		
39	8L	378	Total	C	N	O	S	0	0
			3063	1877	561	610	15		
39	8M	383	Total	C	N	O	S	0	0
			3109	1907	570	617	15		
39	8N	384	Total	C	N	O	S	0	0
			3117	1911	571	620	15		
39	8O	384	Total	C	N	O	S	0	0
			3117	1911	571	620	15		
39	8P	360	Total	C	N	O	S	0	0
			2916	1789	531	581	15		
39	8Q	23	Total	C	N	O	S	0	0
			192	117	38	36	1		

- Molecule 40 is a protein called Dynein regulatory complex protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	9	278	Total	C	N	O	S	0	0
			2336	1466	407	451	12		

- Molecule 41 is a protein called Radial spoke head 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	B	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	C	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	D	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	a	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	b	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	c	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		
41	d	210	Total	C	N	O	S	0	0
			1710	1066	308	334	2		

- Molecule 42 is a protein called Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AZ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AC	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AE	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AG	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AI	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AK	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AM	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AO	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AQ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AS	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AU	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AW	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	AY	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BA	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BC	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BE	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	BG	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BI	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	BK	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BM	433	Total 3387	C 2145	N 576	O 644	S 22	0	0
42	BO	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BQ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	BS	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BU	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BW	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	BY	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	CC	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CE	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	CG	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CI	431	Total 3377	C 2140	N 574	O 641	S 22	0	0
42	CK	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CM	431	Total 3377	C 2140	N 574	O 641	S 22	0	0
42	CO	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CQ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CS	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CU	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	CW	431	Total 3377	C 2140	N 574	O 641	S 22	0	0
42	CY	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	DC	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	DE	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	DG	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	DI	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	DK	430	Total 3371	C 2137	N 573	O 639	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	DM	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	DO	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	DQ	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	DS	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	DU	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	DW	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	DY	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	EC	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	EE	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	EG	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	EI	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	EK	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	EM	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	EO	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	EQ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	ES	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	EU	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	EW	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	EY	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	FC	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	FE	428	Total 3357	C 2130	N 571	O 634	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	FG	430	3371	2137	573	639	22	0	0
42	FI	430	3371	2137	573	639	22	0	0
42	FK	430	3371	2137	573	639	22	0	0
42	FM	430	3371	2137	573	639	22	0	0
42	FO	430	3371	2137	573	639	22	0	0
42	FQ	431	3379	2141	574	642	22	0	0
42	FS	431	3379	2141	574	642	22	0	0
42	FU	430	3371	2137	573	639	22	0	0
42	FW	430	3371	2137	573	639	22	0	0
42	FY	430	3371	2137	573	639	22	0	0
42	GC	431	3379	2141	574	642	22	0	0
42	GE	432	3385	2144	575	644	22	0	0
42	GG	430	3373	2138	573	640	22	0	0
42	GI	431	3379	2141	574	642	22	0	0
42	GK	433	3396	2151	577	646	22	0	0
42	GM	430	3373	2138	573	640	22	0	0
42	GO	430	3373	2138	573	640	22	0	0
42	GQ	430	3371	2137	573	639	22	0	0
42	GS	431	3379	2141	574	642	22	0	0
42	GU	432	3383	2143	575	643	22	0	0
42	GW	439	3429	2170	583	654	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	GY	428	Total	C	N	O	S	0	0
			3357	2130	571	634	22		
42	HA	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HC	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	HE	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	HG	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HI	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HK	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HM	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HO	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HQ	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	HS	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	HU	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HW	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	HY	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
42	IA	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
42	IC	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
42	IE	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
42	IG	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
42	II	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
42	IK	430	Total	C	N	O	S	0	0
			3373	2138	573	640	22		
42	IM	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	IO	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	IQ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	IS	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	IU	432	Total 3387	C 2145	N 575	O 645	S 22	0	0
42	IW	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	IY	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	JC	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	JE	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	JG	433	Total 3396	C 2151	N 577	O 646	S 22	0	0
42	JI	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	JK	429	Total 3365	C 2134	N 572	O 637	S 22	0	0
42	JM	429	Total 3365	C 2134	N 572	O 637	S 22	0	0
42	JO	430	Total 3373	C 2138	N 573	O 640	S 22	0	0
42	JQ	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	JS	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	JU	429	Total 3365	C 2134	N 572	O 637	S 22	0	0
42	JW	431	Total 3377	C 2140	N 574	O 641	S 22	0	0
42	JY	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KC	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	KE	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	KG	430	Total 3371	C 2137	N 573	O 639	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	KI	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KK	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KM	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KO	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KQ	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	KS	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KU	435	Total 3409	C 2160	N 579	O 648	S 22	0	0
42	KW	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	KY	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	LC	433	Total 3389	C 2146	N 576	O 645	S 22	0	0
42	LE	433	Total 3389	C 2146	N 576	O 645	S 22	0	0
42	LG	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	LI	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	LK	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	LM	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	LO	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	LQ	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	LS	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	LU	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	LW	434	Total 3397	C 2150	N 577	O 648	S 22	0	0
42	LY	439	Total 3429	C 2170	N 583	O 654	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	MA	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MC	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	ME	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	MG	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MI	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MK	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MM	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MO	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MQ	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	MS	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	MU	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MW	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	MY	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	NA	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	NC	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	NE	434	Total 3397	C 2150	N 577	O 648	S 22	0	0
42	NG	430	Total 3373	C 2138	N 573	O 640	S 22	0	0
42	NI	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	NK	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	NM	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	NO	432	Total 3387	C 2145	N 575	O 645	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	NQ	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
42	NS	435	Total	C	N	O	S	0	0
			3406	2156	579	649	22		
42	NU	433	Total	C	N	O	S	0	0
			3396	2151	577	646	22		
42	NW	433	Total	C	N	O	S	0	0
			3393	2148	576	647	22		
42	OA	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	OC	434	Total	C	N	O	S	0	0
			3402	2154	578	648	22		
42	OE	433	Total	C	N	O	S	0	0
			3393	2148	576	647	22		
42	OG	432	Total	C	N	O	S	0	0
			3383	2143	575	643	22		
42	OI	434	Total	C	N	O	S	0	0
			3402	2154	578	648	22		
42	OK	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
42	OM	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
42	OO	432	Total	C	N	O	S	0	0
			3387	2145	575	645	22		
42	OQ	433	Total	C	N	O	S	0	0
			3393	2148	576	647	22		
42	OS	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
42	OU	433	Total	C	N	O	S	0	0
			3396	2151	577	646	22		
42	OW	435	Total	C	N	O	S	0	0
			3406	2156	579	649	22		
42	OY	432	Total	C	N	O	S	0	0
			3387	2145	575	645	22		
42	PA	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	PC	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	PE	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
42	PG	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	PI	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	PK	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	PM	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	PO	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	PQ	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	PS	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	PU	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	PW	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	PY	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	QA	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	QC	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	QE	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	QG	430	Total 3373	C 2138	N 573	O 640	S 22	0	0
42	QI	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	QK	438	Total 3423	C 2167	N 582	O 652	S 22	0	0
42	QM	435	Total 3407	C 2157	N 579	O 649	S 22	0	0
42	QO	434	Total 3400	C 2153	N 578	O 647	S 22	0	0
42	QQ	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	QS	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	QU	429	Total 3365	C 2134	N 572	O 637	S 22	0	0
42	QW	431	Total 3379	C 2141	N 574	O 642	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	QY	432	3387	2145	575	645	22	0	0
42	RA	431	3379	2141	574	642	22	0	0
42	RC	431	3379	2141	574	642	22	0	0
42	RE	431	3379	2141	574	642	22	0	0
42	RG	430	3371	2137	573	639	22	0	0
42	RI	430	3371	2137	573	639	22	0	0
42	RK	430	3371	2137	573	639	22	0	0
42	RM	430	3371	2137	573	639	22	0	0
42	RO	430	3371	2137	573	639	22	0	0
42	RQ	431	3379	2141	574	642	22	0	0
42	RS	431	3379	2141	574	642	22	0	0
42	RU	430	3371	2137	573	639	22	0	0
42	RW	430	3371	2137	573	639	22	0	0
42	RY	430	3371	2137	573	639	22	0	0
42	SC	434	3402	2154	578	648	22	0	0
42	SE	432	3385	2144	575	644	22	0	0
42	SG	438	3423	2167	582	652	22	0	0
42	SI	434	3402	2154	578	648	22	0	0
42	SK	438	3423	2167	582	652	22	0	0
42	SM	438	3423	2167	582	652	22	0	0
42	SO	430	3373	2138	573	640	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	SQ	431	3379	2141	574	642	22	0	0
42	SS	439	3429	2170	583	654	22	0	0
42	SU	432	3387	2145	575	645	22	0	0
42	SW	439	3429	2170	583	654	22	0	0
42	SY	433	3391	2147	576	646	22	0	0
42	TC	431	3379	2141	574	642	22	0	0
42	TE	431	3379	2141	574	642	22	0	0
42	TG	430	3371	2137	573	639	22	0	0
42	TI	430	3371	2137	573	639	22	0	0
42	TK	430	3371	2137	573	639	22	0	0
42	TM	430	3371	2137	573	639	22	0	0
42	TO	430	3371	2137	573	639	22	0	0
42	TQ	431	3379	2141	574	642	22	0	0
42	TS	431	3379	2141	574	642	22	0	0
42	TU	430	3371	2137	573	639	22	0	0
42	TW	430	3371	2137	573	639	22	0	0
42	TY	430	3371	2137	573	639	22	0	0
42	UC	434	3397	2150	577	648	22	0	0
42	UE	431	3379	2141	574	642	22	0	0
42	UG	431	3377	2140	574	641	22	0	0
42	UI	431	3379	2141	574	642	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	UK	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	UM	430	Total 3373	C 2138	N 573	O 640	S 22	0	0
42	UO	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	UQ	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	US	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	UU	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	UW	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	UY	432	Total 3387	C 2145	N 575	O 645	S 22	0	0
42	VC	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	VE	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	VG	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VI	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VK	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VM	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VO	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VQ	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	VS	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	VU	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VW	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	VY	430	Total 3371	C 2137	N 573	O 639	S 22	0	0
42	WA	439	Total 3429	C 2170	N 583	O 654	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	WC	432	Total 3385	C 2144	N 575	O 644	S 22	0	0
42	WE	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	WG	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	WI	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	WK	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	WM	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	WO	431	Total 3379	C 2141	N 574	O 642	S 22	0	0
42	WQ	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	WS	432	Total 3383	C 2143	N 575	O 643	S 22	0	0
42	WU	439	Total 3429	C 2170	N 583	O 654	S 22	0	0
42	WW	439	Total 3429	C 2170	N 583	O 654	S 22	0	0

- Molecule 43 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	AB	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AD	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AF	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AH	433	Total 3400	C 2134	N 581	O 659	S 26	0	0
43	AJ	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AL	434	Total 3404	C 2136	N 582	O 660	S 26	0	0
43	AN	434	Total 3404	C 2136	N 582	O 660	S 26	0	0
43	AP	437	Total 3433	C 2155	N 585	O 667	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	AR	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AT	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AV	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	AX	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	BB	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	BD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	BF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	BH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	BJ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
43	BL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	BN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	BP	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	BR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	BT	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	BV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	BX	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
43	CB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	CD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	CF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	CH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	CJ	427	Total 3356	C 2109	N 575	O 646	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	CL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	CN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	CP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	CR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	CT	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	CV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	CX	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	CZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	DZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	EB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ED	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	EP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ER	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ET	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	EZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	FP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	FR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	FZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	GP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	GZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HB	411	Total 3214	C 2016	N 549	O 624	S 25	0	0
43	HD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	HH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	HP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	HZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ID	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	IP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	IV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	IX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	JP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	JZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	KB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	KD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	KF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	KH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	KJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	KL	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	KN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	KP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	KR	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	KT	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	KV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	KX	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	KZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	LB	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	LD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	LF	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	LH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	LJ	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	LL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	LN	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	LP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	LR	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	LT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	LV	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	LX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	LZ	436	Total 3424	C 2150	N 584	O 664	S 26	0	0
43	MD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	MH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ML	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	MP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	MZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	NB	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	ND	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NL	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NR	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	NV	428	Total 3361	C 2112	N 576	O 647	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	NX	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	NZ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
43	OB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	OD	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
43	OF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	OH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	OJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	OL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ON	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	OP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	OR	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	OT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	OV	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	OX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	PF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	PH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	PP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	PX	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	QB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	QP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	QX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	RJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	RP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	RX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	SP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	ST	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	SX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	TD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	TP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	TZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
43	UP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	UT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	UZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VH	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
43	VP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VR	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VT	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VV	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VX	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	VZ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
43	WB	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	WD	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	WF	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
43	WH	437	Total 3433	C 2155	N 585	O 667	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	WJ	434	Total	C	N	O	S	0	0
			3404	2136	582	660	26		
43	WL	434	Total	C	N	O	S	0	0
			3404	2136	582	660	26		
43	WN	437	Total	C	N	O	S	0	0
			3433	2155	585	667	26		
43	WP	437	Total	C	N	O	S	0	0
			3433	2155	585	667	26		
43	WR	437	Total	C	N	O	S	0	0
			3433	2155	585	667	26		
43	WT	437	Total	C	N	O	S	0	0
			3433	2155	585	667	26		
43	WV	437	Total	C	N	O	S	0	0
			3433	2155	585	667	26		
43	WX	437	Total	C	N	O	S	0	0
			3433	2155	585	667	26		

- Molecule 44 is a protein called Radial spoke head protein 3 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	E	169	Total	C	N	O	S	0	0
			1405	876	250	272	7		
44	F	217	Total	C	N	O	S	0	0
			1795	1125	311	350	9		
44	e	216	Total	C	N	O	S	0	0
			1783	1116	310	348	9		
44	f	213	Total	C	N	O	S	0	0
			1761	1104	304	344	9		

- Molecule 45 is a protein called Radial spoke head protein 4 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	G	460	Total	C	N	O	S	0	0
			3714	2353	600	753	8		
45	H	467	Total	C	N	O	S	0	0
			3767	2387	607	764	9		
45	I	464	Total	C	N	O	S	0	0
			3746	2374	604	760	8		
45	J	470	Total	C	N	O	S	0	0
			3788	2400	610	769	9		
45	g	466	Total	C	N	O	S	0	0
			3760	2382	606	763	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
45	h	470	Total	C	N	O	S	0	0
			3788	2400	610	769	9		
45	i	468	Total	C	N	O	S	0	0
			3772	2390	608	765	9		
45	j	470	Total	C	N	O	S	0	0
			3788	2400	610	769	9		

- Molecule 46 is a protein called Sperm surface protein Sp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	K	32	Total	C	N	O	0	0
			255	166	41	48		
46	L	35	Total	C	N	O	0	0
			277	178	45	54		
46	k	32	Total	C	N	O	0	0
			255	166	41	48		
46	l	38	Total	C	N	O	0	0
			306	195	52	59		

- Molecule 47 is a protein called Radial spoke head protein 9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	M	276	Total	C	N	O	S	0	0
			2205	1412	366	418	9		
47	N	257	Total	C	N	O	S	0	0
			2050	1314	343	384	9		
47	O	276	Total	C	N	O	S	0	0
			2205	1412	366	418	9		
47	P	262	Total	C	N	O	S	0	0
			2088	1339	348	392	9		
47	m	276	Total	C	N	O	S	0	0
			2205	1412	366	418	9		
47	n	262	Total	C	N	O	S	0	0
			2088	1339	348	392	9		
47	o	276	Total	C	N	O	S	0	0
			2205	1412	366	418	9		
47	p	262	Total	C	N	O	S	0	0
			2088	1339	348	392	9		

- Molecule 48 is a protein called Ropporin-1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Q	174	Total	C	N	O	S	0	0
			1392	896	240	246	10		
48	R	37	Total	C	N	O		0	0
			300	196	52	52			
48	q	206	Total	C	N	O	S	0	0
			1641	1053	279	298	11		
48	r	42	Total	C	N	O	S	0	0
			330	214	57	58	1		

- Molecule 49 is a protein called Probable inactive peptidyl-prolyl cis-trans isomerase-like 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	290	Total	C	N	O	S	0	0
			2336	1496	400	431	9		
49	s	290	Total	C	N	O	S	0	0
			2336	1496	400	431	9		

- Molecule 50 is a protein called Radial spoke head 14 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T	336	Total	C	N	O	S	0	0
			2612	1660	451	485	16		
50	t	325	Total	C	N	O	S	0	0
			2528	1608	437	467	16		

- Molecule 51 is a protein called DnaJ homolog subfamily B member 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	296	Total	C	N	O	S	0	0
			2397	1540	415	435	7		
51	V	297	Total	C	N	O	S	0	0
			2406	1545	417	437	7		
51	u	296	Total	C	N	O	S	0	0
			2397	1540	415	435	7		
51	v	297	Total	C	N	O	S	0	0
			2406	1545	417	437	7		

- Molecule 52 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	W	142	Total	C	N	O	S	0	0
			1121	687	180	245	9		

- Molecule 53 is a protein called Nucleoside diphosphate kinase homolog 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	X	192	Total	C	N	O	S	0	0
			1537	993	259	277	8		
53	Y	192	Total	C	N	O	S	0	0
			1537	993	259	277	8		
53	x	192	Total	C	N	O	S	0	0
			1537	993	259	277	8		
53	y	192	Total	C	N	O	S	0	0
			1537	993	259	277	8		

- Molecule 54 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	XA	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XB	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XC	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XD	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XE	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XF	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XG	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XH	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XI	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XJ	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XK	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XL	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
54	XM	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		

- Molecule 55 is a protein called Parkin coregulated gene protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	YB	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YC	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YD	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YF	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YG	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YH	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YI	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YJ	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YK	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YL	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		
55	YM	220	Total	C	N	O	S	0	0
			1771	1147	301	314	9		

- Molecule 56 is a protein called Cytochrome b5 domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Z	214	Total	C	N	O	S	0	0
			1784	1145	303	331	5		
56	z	209	Total	C	N	O	S	0	0
			1735	1111	297	322	5		

- Molecule 57 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	a0	72	Total	C	N	O	0	0
			360	216	72	72		

- Molecule 58 is a protein called DYNLL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	a1	83	Total	C	N	O	S	0	0
			680	438	112	126	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	a2	84	685	441	113	127	4	0	0
58	a3	83	684	442	113	125	4	0	0
58	a4	88	719	460	121	133	5	0	0
58	a5	84	690	445	114	127	4	0	0
58	a6	83	681	439	112	126	4	0	0
58	a7	85	694	447	115	128	4	0	0
58	a8	86	705	453	119	129	4	0	0
58	a9	85	694	447	115	128	4	0	0
58	b0	89	727	465	122	134	6	0	0
58	b1	85	694	447	115	128	4	0	0
58	b2	89	727	465	122	134	6	0	0
58	b3	87	717	460	120	131	6	0	0
58	b4	84	695	448	117	126	4	0	0
58	b5	84	695	448	117	126	4	0	0
58	b6	83	684	442	113	125	4	0	0
58	b7	86	705	453	119	129	4	0	0
58	b8	87	713	457	120	132	4	0	0
58	b9	89	727	465	122	134	6	0	0
58	c0	85	694	447	115	128	4	0	0
58	l1	89	727	465	122	134	6	0	0
58	l2	89	727	465	122	134	6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	l3	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	l4	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	l5	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	l6	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	n1	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	n2	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	n3	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	n4	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	n5	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	n6	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	p1	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	p2	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	p3	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	p4	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	p5	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	p6	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	r1	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	r2	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	r3	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	r4	89	Total	C	N	O	S	0	0
			727	465	122	134	6		
58	r5	89	Total	C	N	O	S	0	0
			727	465	122	134	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	r6	89	Total	C	N	O	S	0	0
			727	465	122	134	6		

- Molecule 59 is a protein called MORN repeat-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	c1	228	Total	C	N	O	S	0	0
			1858	1178	329	341	10		

- Molecule 60 is a protein called IQ and ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	c2	631	Total	C	N	O	S	0	0
			5234	3355	910	948	21		

- Molecule 61 is a protein called DPY30 domain-containing protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	c3	44	Total	C	N	O	S	0	0
			363	234	64	62	3		
61	c4	55	Total	C	N	O	S	0	0
			458	292	83	80	3		
61	c5	61	Total	C	N	O	S	0	0
			515	328	92	92	3		
61	c6	61	Total	C	N	O	S	0	0
			515	328	92	92	3		

- Molecule 62 is a protein called Cilia- and flagella-associated protein 61.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	d0	1092	Total	C	N	O	S	0	0
			8819	5669	1488	1608	54		

- Molecule 63 is a protein called Cilia- and flagella-associated protein 91.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	d1	523	Total	C	N	O	S	0	0
			4340	2753	774	794	19		

- Molecule 64 is a protein called Cilia- and flagella-associated protein 251.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	d2	907	7227	4652	1193	1342	40	0	0

- Molecule 65 is a protein called Tetratricopeptide repeat protein 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	d3	419	3431	2178	578	654	21	0	0

- Molecule 66 is a protein called Zinc finger MYND domain-containing protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	d4	358	2885	1846	485	537	17	0	0

- Molecule 67 is a protein called ACTA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	d5	377	2944	1859	495	567	23	0	0
67	d6	377	2944	1859	495	567	23	0	0
67	d7	370	2889	1829	488	551	21	0	0
67	d8	377	2944	1859	495	567	23	0	0
67	d9	367	2864	1813	485	546	20	0	0
67	f1	371	2895	1832	489	553	21	0	0

- Molecule 68 is a protein called Axonemal dynein light intermediate polypeptide 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	e0	209	1713	1060	312	333	8	0	0
68	e1	198	1635	1009	299	319	8	0	0
68	e2	209	1713	1060	312	333	8	0	0
68	e3	198	1635	1009	299	319	8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
68	e4	200	Total	C	N	O	S	0	0
			1645	1017	302	318	8		
68	e5	199	Total	C	N	O	S	0	0
			1639	1012	299	319	9		
68	e6	199	Total	C	N	O	S	0	0
			1639	1013	299	319	8		
68	e7	198	Total	C	N	O	S	0	0
			1635	1009	299	319	8		
68	e8	209	Total	C	N	O	S	0	0
			1713	1060	312	333	8		
68	e9	198	Total	C	N	O	S	0	0
			1635	1009	299	319	8		

- Molecule 69 is a protein called Centrin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	f2	147	Total	C	N	O	S	0	0
			1183	739	191	246	7		

- Molecule 70 is a protein called Dynein axonemal heavy chain 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	g1	3939	Total	C	N	O	S	0	0
			31794	20376	5309	5921	188		

- Molecule 71 is a protein called Dynein axonemal heavy chain 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	g2	507	Total	C	N	O	S	0	0
			4176	2676	697	775	28		
71	g4	437	Total	C	N	O	S	0	0
			3610	2320	604	664	22		

- Molecule 72 is a protein called Dynein axonemal heavy chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	g3	571	Total	C	N	O	S	0	0
			4660	2997	783	849	31		

- Molecule 73 is a protein called Dynein axonemal heavy chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	g5	3978	32054	20492	5401	5990	171	0	0

- Molecule 74 is a protein called Dynein axonemal heavy chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	g6	4174	33600	21465	5650	6286	199	0	0

- Molecule 75 is a protein called Coiled-coil domain-containing protein 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	h1	388	3183	1954	570	648	11	0	0
75	h2	475	3959	2468	689	784	18	0	0

- Molecule 76 is a protein called Coiled-coil domain-containing protein 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	h3	387	3152	1944	578	613	17	0	0
76	h4	480	3932	2425	732	757	18	0	0

- Molecule 77 is a protein called Coiled-coil domain-containing protein 96.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	i1	305	2509	1552	477	467	13	0	0

- Molecule 78 is a protein called Coiled-coil domain-containing protein 113.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	i2	364	2998	1866	548	570	14	0	0

- Molecule 79 is a protein called Cilia- and flagella-associated protein 299.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	i3	194	1592	1006	274	311	1	0	0

- Molecule 80 is a protein called Cilia- and flagella-associated protein 57.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	i4	1021	Total	C	N	O	S	0	0
			8344	5265	1440	1599	40		
80	i5	1049	Total	C	N	O	S	0	0
			8561	5402	1477	1641	41		

- Molecule 81 is a protein called Cilia- and flagella-associated protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	i6	165	Total	C	N	O	S	0	0
			1363	854	240	255	14		
81	i8	1379	Total	C	N	O	S	0	0
			11188	7146	1869	2111	62		

- Molecule 82 is a protein called Cilia- and flagella-associated protein 44.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	i7	160	Total	C	N	O	S	0	0
			1326	826	248	242	10		
82	i9	1338	Total	C	N	O	S	0	0
			10895	6968	1841	2028	58		

- Molecule 83 is a protein called Cilia- and flagella-associated protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
83	j1	458	Total	C	N	O	S	0	0
			3859	2403	710	734	12		
83	j2	471	Total	C	N	O	S	0	0
			3973	2477	732	752	12		

- Molecule 84 is a protein called Cilia- and flagella-associated protein 73.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	j3	254	Total	C	N	O	S	0	0
			2104	1304	412	383	5		

- Molecule 85 is a protein called Cilia- and flagella-associated protein 100.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	j4	244	Total	C	N	O	S	0	0
			2021	1266	342	404	9		

- Molecule 86 is a protein called Dynein axonemal intermediate chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
86	k1	590	4743	3035	781	897	30	0	0

- Molecule 87 is a protein called Dynein axonemal intermediate chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
87	k2	500	3991	2544	673	749	25	0	0

- Molecule 88 is a protein called Dynein axonemal intermediate chain 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
88	k3	497	4044	2608	666	751	19	0	0

- Molecule 89 is a protein called Dynein light chain roadblock-type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
89	k4	96	764	481	131	148	4	0	0
89	m4	96	764	481	131	148	4	0	0
89	o4	96	764	481	131	148	4	0	0
89	q4	96	764	481	131	148	4	0	0

- Molecule 90 is a protein called Dynein light chain roadblock-type 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
90	k5	96	758	476	134	143	5	0	0
90	m5	96	758	476	134	143	5	0	0
90	o5	96	758	476	134	143	5	0	0
90	q5	96	758	476	134	143	5	0	0

- Molecule 91 is a protein called Dynein axonemal heavy chain 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
91	k8	4443	36045	23070	6109	6666	200	0	0

- Molecule 92 is a protein called Dynein axonemal heavy chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
92	k9	4349	35139	22447	6004	6497	191	0	0

- Molecule 93 is a protein called Dynein light chain Tctex-type protein 2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
93	l7	105	854	545	141	159	9	0	0
93	n7	113	924	592	154	169	9	0	0
93	p7	113	924	592	154	169	9	0	0
93	r7	113	924	592	154	169	9	0	0

- Molecule 94 is a protein called Dynein light chain Tctex-type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
94	l8	102	785	497	130	152	6	0	0
94	n8	103	790	500	131	153	6	0	0
94	p8	103	790	500	131	153	6	0	0
94	r8	90	687	435	117	129	6	0	0

- Molecule 95 is a protein called Calaxin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
95	m0	211	1716	1091	284	326	15	0	0
95	q0	211	1716	1091	284	326	15	0	0
95	s0	211	1716	1091	284	326	15	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
95	u0	211	1716	1091	284	326	15	0	0

- Molecule 96 is a protein called Dynein axonemal intermediate chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
96	m1	527	4241	2704	729	788	20	0	0
96	o1	527	4241	2704	729	788	20	0	0
96	q1	527	4241	2704	729	788	20	0	0
96	s1	414	3320	2132	557	612	19	0	0

- Molecule 97 is a protein called Dynein axonemal intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
97	m2	529	4233	2669	723	812	29	0	0
97	o2	529	4233	2669	723	812	29	0	0
97	q2	529	4233	2669	723	812	29	0	0
97	s2	398	3161	2002	538	600	21	0	0

- Molecule 98 is a protein called Dynein axonemal light chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
98	m3	190	1509	960	254	287	8	0	0
98	o3	190	1509	960	254	287	8	0	0
98	q3	190	1509	960	254	287	8	0	0

- Molecule 99 is a protein called Outer dynein arm-docking complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
99	m6	349	2926	1816	554	547	9	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
99	o6	189	Total	C	N	O	S	0	0
			1567	986	278	297	6		
99	q6	349	Total	C	N	O	S	0	0
			2926	1816	554	547	9		
99	s6	349	Total	C	N	O	S	0	0
			2926	1816	554	547	9		
99	u6	212	Total	C	N	O	S	0	0
			1772	1085	352	330	5		

- Molecule 100 is a protein called Outer dynein arm-docking complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	m7	599	Total	C	N	O	S	0	0
			4591	2866	832	861	32		
100	q7	599	Total	C	N	O	S	0	0
			4591	2866	832	861	32		
100	s7	599	Total	C	N	O	S	0	0
			4591	2866	832	861	32		
100	u7	599	Total	C	N	O	S	0	0
			4591	2866	832	861	32		

- Molecule 101 is a protein called Outer dynein arm-docking complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	m8	419	Total	C	N	O	S	0	0
			3484	2160	657	655	12		
101	o8	239	Total	C	N	O	S	0	0
			1970	1214	370	378	8		
101	q8	419	Total	C	N	O	S	0	0
			3484	2160	657	655	12		
101	s8	419	Total	C	N	O	S	0	0
			3484	2160	657	655	12		
101	u8	231	Total	C	N	O	S	0	0
			1944	1210	370	359	5		

- Molecule 102 is a protein called Outer dynein arm-docking complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	m9	204	Total	C	N	O	S	0	0
			1656	1048	285	313	10		
102	q9	204	Total	C	N	O	S	0	0
			1656	1048	285	313	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
102	s9	204	Total	C	N	O	S	0	0
			1656	1048	285	313	10		
102	u9	204	Total	C	N	O	S	0	0
			1656	1048	285	313	10		

- Molecule 103 is a protein called Dynein axonemal heavy chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	n0	4575	Total	C	N	O	S	0	0
			36802	23465	6234	6895	208		
103	p0	4575	Total	C	N	O	S	0	0
			36802	23465	6234	6895	208		
103	r0	4575	Total	C	N	O	S	0	0
			36802	23465	6234	6895	208		
103	t0	836	Total	C	N	O	S	0	0
			6751	4318	1150	1251	32		

- Molecule 104 is a protein called Dynein axonemal heavy chain 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	n9	4486	Total	C	N	O	S	0	0
			36021	22986	6125	6720	190		
104	p9	4486	Total	C	N	O	S	0	0
			36021	22986	6125	6720	190		
104	r9	4486	Total	C	N	O	S	0	0
			36021	22986	6125	6720	190		
104	t9	718	Total	C	N	O	S	0	0
			5742	3642	1001	1072	27		

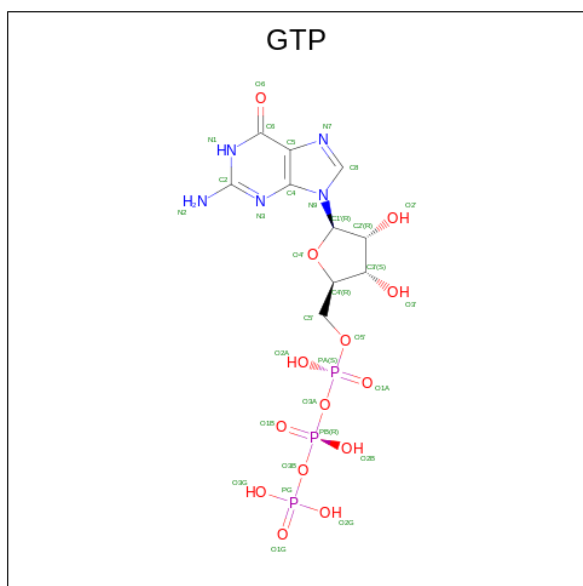
- Molecule 105 is a protein called Thioredoxin domain-containing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	v1	133	Total	C	N	O	S	0	0
			1043	664	173	200	6		
105	v2	133	Total	C	N	O	S	0	0
			1043	664	173	200	6		
105	v3	133	Total	C	N	O	S	0	0
			1043	664	173	200	6		

- Molecule 106 is a protein called Leucine-rich repeat-containing protein 34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
106	w	412	3229	2048	546	614	21	0	0

- Molecule 107 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	AZ	1	Total 32	C 10	N 5	O 14	P 3	0
107	AC	1	Total 32	C 10	N 5	O 14	P 3	0
107	AE	1	Total 32	C 10	N 5	O 14	P 3	0
107	AG	1	Total 32	C 10	N 5	O 14	P 3	0
107	AI	1	Total 32	C 10	N 5	O 14	P 3	0
107	AK	1	Total 32	C 10	N 5	O 14	P 3	0
107	AM	1	Total 32	C 10	N 5	O 14	P 3	0
107	AO	1	Total 32	C 10	N 5	O 14	P 3	0
107	AQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	AS	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	AU	1	Total 32	C 10	N 5	O 14	P 3	0
107	AW	1	Total 32	C 10	N 5	O 14	P 3	0
107	AY	1	Total 32	C 10	N 5	O 14	P 3	0
107	BA	1	Total 32	C 10	N 5	O 14	P 3	0
107	BC	1	Total 32	C 10	N 5	O 14	P 3	0
107	BE	1	Total 32	C 10	N 5	O 14	P 3	0
107	BG	1	Total 32	C 10	N 5	O 14	P 3	0
107	BI	1	Total 32	C 10	N 5	O 14	P 3	0
107	BK	1	Total 32	C 10	N 5	O 14	P 3	0
107	BM	1	Total 32	C 10	N 5	O 14	P 3	0
107	BO	1	Total 32	C 10	N 5	O 14	P 3	0
107	BQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	BS	1	Total 32	C 10	N 5	O 14	P 3	0
107	BU	1	Total 32	C 10	N 5	O 14	P 3	0
107	BW	1	Total 32	C 10	N 5	O 14	P 3	0
107	BY	1	Total 32	C 10	N 5	O 14	P 3	0
107	CC	1	Total 32	C 10	N 5	O 14	P 3	0
107	CE	1	Total 32	C 10	N 5	O 14	P 3	0
107	CG	1	Total 32	C 10	N 5	O 14	P 3	0
107	CI	1	Total 32	C 10	N 5	O 14	P 3	0
107	CK	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	CM	1	Total 32	C 10	N 5	O 14	P 3	0
107	CO	1	Total 32	C 10	N 5	O 14	P 3	0
107	CQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	CS	1	Total 32	C 10	N 5	O 14	P 3	0
107	CU	1	Total 32	C 10	N 5	O 14	P 3	0
107	CW	1	Total 32	C 10	N 5	O 14	P 3	0
107	CY	1	Total 32	C 10	N 5	O 14	P 3	0
107	DC	1	Total 32	C 10	N 5	O 14	P 3	0
107	DE	1	Total 32	C 10	N 5	O 14	P 3	0
107	DG	1	Total 32	C 10	N 5	O 14	P 3	0
107	DI	1	Total 32	C 10	N 5	O 14	P 3	0
107	DK	1	Total 32	C 10	N 5	O 14	P 3	0
107	DM	1	Total 32	C 10	N 5	O 14	P 3	0
107	DO	1	Total 32	C 10	N 5	O 14	P 3	0
107	DQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	DS	1	Total 32	C 10	N 5	O 14	P 3	0
107	DU	1	Total 32	C 10	N 5	O 14	P 3	0
107	DW	1	Total 32	C 10	N 5	O 14	P 3	0
107	DY	1	Total 32	C 10	N 5	O 14	P 3	0
107	EC	1	Total 32	C 10	N 5	O 14	P 3	0
107	EE	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	EG	1	Total 32	C 10	N 5	O 14	P 3	0
107	EI	1	Total 32	C 10	N 5	O 14	P 3	0
107	EK	1	Total 32	C 10	N 5	O 14	P 3	0
107	EM	1	Total 32	C 10	N 5	O 14	P 3	0
107	EO	1	Total 32	C 10	N 5	O 14	P 3	0
107	EQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	ES	1	Total 32	C 10	N 5	O 14	P 3	0
107	EU	1	Total 32	C 10	N 5	O 14	P 3	0
107	EW	1	Total 32	C 10	N 5	O 14	P 3	0
107	EY	1	Total 32	C 10	N 5	O 14	P 3	0
107	FC	1	Total 32	C 10	N 5	O 14	P 3	0
107	FE	1	Total 32	C 10	N 5	O 14	P 3	0
107	FG	1	Total 32	C 10	N 5	O 14	P 3	0
107	FI	1	Total 32	C 10	N 5	O 14	P 3	0
107	FK	1	Total 32	C 10	N 5	O 14	P 3	0
107	FM	1	Total 32	C 10	N 5	O 14	P 3	0
107	FN	1	Total 32	C 10	N 5	O 14	P 3	0
107	FQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	FS	1	Total 32	C 10	N 5	O 14	P 3	0
107	FU	1	Total 32	C 10	N 5	O 14	P 3	0
107	FW	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	FY	1	32	10	5	14	3	0
107	GC	1	32	10	5	14	3	0
107	GE	1	32	10	5	14	3	0
107	GG	1	32	10	5	14	3	0
107	GI	1	32	10	5	14	3	0
107	GK	1	32	10	5	14	3	0
107	GM	1	32	10	5	14	3	0
107	GO	1	32	10	5	14	3	0
107	GQ	1	32	10	5	14	3	0
107	GR	1	32	10	5	14	3	0
107	GU	1	32	10	5	14	3	0
107	GW	1	32	10	5	14	3	0
107	GX	1	32	10	5	14	3	0
107	HA	1	32	10	5	14	3	0
107	HC	1	32	10	5	14	3	0
107	HE	1	32	10	5	14	3	0
107	HF	1	32	10	5	14	3	0
107	HI	1	32	10	5	14	3	0
107	HK	1	32	10	5	14	3	0
107	HM	1	32	10	5	14	3	0
107	HN	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	HQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	HS	1	Total 32	C 10	N 5	O 14	P 3	0
107	HU	1	Total 32	C 10	N 5	O 14	P 3	0
107	HW	1	Total 32	C 10	N 5	O 14	P 3	0
107	HY	1	Total 32	C 10	N 5	O 14	P 3	0
107	IA	1	Total 32	C 10	N 5	O 14	P 3	0
107	IC	1	Total 32	C 10	N 5	O 14	P 3	0
107	ID	1	Total 32	C 10	N 5	O 14	P 3	0
107	IG	1	Total 32	C 10	N 5	O 14	P 3	0
107	II	1	Total 32	C 10	N 5	O 14	P 3	0
107	IK	1	Total 32	C 10	N 5	O 14	P 3	0
107	IM	1	Total 32	C 10	N 5	O 14	P 3	0
107	IO	1	Total 32	C 10	N 5	O 14	P 3	0
107	IQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	IS	1	Total 32	C 10	N 5	O 14	P 3	0
107	IU	1	Total 32	C 10	N 5	O 14	P 3	0
107	IW	1	Total 32	C 10	N 5	O 14	P 3	0
107	IY	1	Total 32	C 10	N 5	O 14	P 3	0
107	JC	1	Total 32	C 10	N 5	O 14	P 3	0
107	JD	1	Total 32	C 10	N 5	O 14	P 3	0
107	JG	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	JI	1	Total 32	C 10	N 5	O 14	P 3	0
107	JJ	1	Total 32	C 10	N 5	O 14	P 3	0
107	JM	1	Total 32	C 10	N 5	O 14	P 3	0
107	JO	1	Total 32	C 10	N 5	O 14	P 3	0
107	JQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	JR	1	Total 32	C 10	N 5	O 14	P 3	0
107	JU	1	Total 32	C 10	N 5	O 14	P 3	0
107	JW	1	Total 32	C 10	N 5	O 14	P 3	0
107	JY	1	Total 32	C 10	N 5	O 14	P 3	0
107	KC	1	Total 32	C 10	N 5	O 14	P 3	0
107	KE	1	Total 32	C 10	N 5	O 14	P 3	0
107	KF	1	Total 32	C 10	N 5	O 14	P 3	0
107	KI	1	Total 32	C 10	N 5	O 14	P 3	0
107	KK	1	Total 32	C 10	N 5	O 14	P 3	0
107	KM	1	Total 32	C 10	N 5	O 14	P 3	0
107	KN	1	Total 32	C 10	N 5	O 14	P 3	0
107	KQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	KS	1	Total 32	C 10	N 5	O 14	P 3	0
107	KU	1	Total 32	C 10	N 5	O 14	P 3	0
107	KW	1	Total 32	C 10	N 5	O 14	P 3	0
107	KY	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	LC	1	Total 32	C 10	N 5	O 14	P 3	0
107	LE	1	Total 32	C 10	N 5	O 14	P 3	0
107	LG	1	Total 32	C 10	N 5	O 14	P 3	0
107	LI	1	Total 32	C 10	N 5	O 14	P 3	0
107	LK	1	Total 32	C 10	N 5	O 14	P 3	0
107	LM	1	Total 32	C 10	N 5	O 14	P 3	0
107	LO	1	Total 32	C 10	N 5	O 14	P 3	0
107	LQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	LS	1	Total 32	C 10	N 5	O 14	P 3	0
107	LU	1	Total 32	C 10	N 5	O 14	P 3	0
107	LW	1	Total 32	C 10	N 5	O 14	P 3	0
107	LY	1	Total 32	C 10	N 5	O 14	P 3	0
107	MA	1	Total 32	C 10	N 5	O 14	P 3	0
107	MC	1	Total 32	C 10	N 5	O 14	P 3	0
107	ME	1	Total 32	C 10	N 5	O 14	P 3	0
107	MG	1	Total 32	C 10	N 5	O 14	P 3	0
107	MI	1	Total 32	C 10	N 5	O 14	P 3	0
107	MK	1	Total 32	C 10	N 5	O 14	P 3	0
107	MM	1	Total 32	C 10	N 5	O 14	P 3	0
107	MN	1	Total 32	C 10	N 5	O 14	P 3	0
107	MQ	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	MS	1	Total 32	C 10	N 5	O 14	P 3	0
107	MT	1	Total 32	C 10	N 5	O 14	P 3	0
107	MW	1	Total 32	C 10	N 5	O 14	P 3	0
107	MY	1	Total 32	C 10	N 5	O 14	P 3	0
107	NA	1	Total 32	C 10	N 5	O 14	P 3	0
107	NC	1	Total 32	C 10	N 5	O 14	P 3	0
107	ND	1	Total 32	C 10	N 5	O 14	P 3	0
107	NG	1	Total 32	C 10	N 5	O 14	P 3	0
107	NI	1	Total 32	C 10	N 5	O 14	P 3	0
107	NK	1	Total 32	C 10	N 5	O 14	P 3	0
107	NL	1	Total 32	C 10	N 5	O 14	P 3	0
107	NO	1	Total 32	C 10	N 5	O 14	P 3	0
107	NQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	NS	1	Total 32	C 10	N 5	O 14	P 3	0
107	NU	1	Total 32	C 10	N 5	O 14	P 3	0
107	NW	1	Total 32	C 10	N 5	O 14	P 3	0
107	OA	1	Total 32	C 10	N 5	O 14	P 3	0
107	OC	1	Total 32	C 10	N 5	O 14	P 3	0
107	OE	1	Total 32	C 10	N 5	O 14	P 3	0
107	OG	1	Total 32	C 10	N 5	O 14	P 3	0
107	OI	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	OK	1	Total 32	C 10	N 5	O 14	P 3	0
107	OM	1	Total 32	C 10	N 5	O 14	P 3	0
107	OO	1	Total 32	C 10	N 5	O 14	P 3	0
107	OQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	OS	1	Total 32	C 10	N 5	O 14	P 3	0
107	OU	1	Total 32	C 10	N 5	O 14	P 3	0
107	OW	1	Total 32	C 10	N 5	O 14	P 3	0
107	OY	1	Total 32	C 10	N 5	O 14	P 3	0
107	PA	1	Total 32	C 10	N 5	O 14	P 3	0
107	PC	1	Total 32	C 10	N 5	O 14	P 3	0
107	PE	1	Total 32	C 10	N 5	O 14	P 3	0
107	PG	1	Total 32	C 10	N 5	O 14	P 3	0
107	PI	1	Total 32	C 10	N 5	O 14	P 3	0
107	PK	1	Total 32	C 10	N 5	O 14	P 3	0
107	PM	1	Total 32	C 10	N 5	O 14	P 3	0
107	PN	1	Total 32	C 10	N 5	O 14	P 3	0
107	PQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	PS	1	Total 32	C 10	N 5	O 14	P 3	0
107	PT	1	Total 32	C 10	N 5	O 14	P 3	0
107	PW	1	Total 32	C 10	N 5	O 14	P 3	0
107	PY	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	QA	1	Total 32	C 10	N 5	O 14	P 3	0
107	QC	1	Total 32	C 10	N 5	O 14	P 3	0
107	QD	1	Total 32	C 10	N 5	O 14	P 3	0
107	QG	1	Total 32	C 10	N 5	O 14	P 3	0
107	QI	1	Total 32	C 10	N 5	O 14	P 3	0
107	QK	1	Total 32	C 10	N 5	O 14	P 3	0
107	QL	1	Total 32	C 10	N 5	O 14	P 3	0
107	QO	1	Total 32	C 10	N 5	O 14	P 3	0
107	QQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	QR	1	Total 32	C 10	N 5	O 14	P 3	0
107	QU	1	Total 32	C 10	N 5	O 14	P 3	0
107	QW	1	Total 32	C 10	N 5	O 14	P 3	0
107	QX	1	Total 32	C 10	N 5	O 14	P 3	0
107	RA	1	Total 32	C 10	N 5	O 14	P 3	0
107	RC	1	Total 32	C 10	N 5	O 14	P 3	0
107	RE	1	Total 32	C 10	N 5	O 14	P 3	0
107	RF	1	Total 32	C 10	N 5	O 14	P 3	0
107	RI	1	Total 32	C 10	N 5	O 14	P 3	0
107	RK	1	Total 32	C 10	N 5	O 14	P 3	0
107	RM	1	Total 32	C 10	N 5	O 14	P 3	0
107	RN	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	RQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	RS	1	Total 32	C 10	N 5	O 14	P 3	0
107	RT	1	Total 32	C 10	N 5	O 14	P 3	0
107	RW	1	Total 32	C 10	N 5	O 14	P 3	0
107	RY	1	Total 32	C 10	N 5	O 14	P 3	0
107	SC	1	Total 32	C 10	N 5	O 14	P 3	0
107	SE	1	Total 32	C 10	N 5	O 14	P 3	0
107	SG	1	Total 32	C 10	N 5	O 14	P 3	0
107	SI	1	Total 32	C 10	N 5	O 14	P 3	0
107	SK	1	Total 32	C 10	N 5	O 14	P 3	0
107	SL	1	Total 32	C 10	N 5	O 14	P 3	0
107	SO	1	Total 32	C 10	N 5	O 14	P 3	0
107	SQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	SR	1	Total 32	C 10	N 5	O 14	P 3	0
107	SU	1	Total 32	C 10	N 5	O 14	P 3	0
107	SW	1	Total 32	C 10	N 5	O 14	P 3	0
107	SX	1	Total 32	C 10	N 5	O 14	P 3	0
107	TB	1	Total 32	C 10	N 5	O 14	P 3	0
107	TE	1	Total 32	C 10	N 5	O 14	P 3	0
107	TG	1	Total 32	C 10	N 5	O 14	P 3	0
107	TI	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	TK	1	Total 32	C 10	N 5	O 14	P 3	0
107	TM	1	Total 32	C 10	N 5	O 14	P 3	0
107	TN	1	Total 32	C 10	N 5	O 14	P 3	0
107	TQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	TS	1	Total 32	C 10	N 5	O 14	P 3	0
107	TU	1	Total 32	C 10	N 5	O 14	P 3	0
107	TW	1	Total 32	C 10	N 5	O 14	P 3	0
107	TY	1	Total 32	C 10	N 5	O 14	P 3	0
107	UC	1	Total 32	C 10	N 5	O 14	P 3	0
107	UE	1	Total 32	C 10	N 5	O 14	P 3	0
107	UG	1	Total 32	C 10	N 5	O 14	P 3	0
107	UI	1	Total 32	C 10	N 5	O 14	P 3	0
107	UK	1	Total 32	C 10	N 5	O 14	P 3	0
107	UM	1	Total 32	C 10	N 5	O 14	P 3	0
107	UO	1	Total 32	C 10	N 5	O 14	P 3	0
107	UQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	US	1	Total 32	C 10	N 5	O 14	P 3	0
107	UU	1	Total 32	C 10	N 5	O 14	P 3	0
107	UW	1	Total 32	C 10	N 5	O 14	P 3	0
107	UY	1	Total 32	C 10	N 5	O 14	P 3	0
107	VC	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	VE	1	Total 32	C 10	N 5	O 14	P 3	0
107	VG	1	Total 32	C 10	N 5	O 14	P 3	0
107	VI	1	Total 32	C 10	N 5	O 14	P 3	0
107	VK	1	Total 32	C 10	N 5	O 14	P 3	0
107	VM	1	Total 32	C 10	N 5	O 14	P 3	0
107	VN	1	Total 32	C 10	N 5	O 14	P 3	0
107	VQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	VS	1	Total 32	C 10	N 5	O 14	P 3	0
107	VU	1	Total 32	C 10	N 5	O 14	P 3	0
107	VW	1	Total 32	C 10	N 5	O 14	P 3	0
107	VY	1	Total 32	C 10	N 5	O 14	P 3	0
107	WA	1	Total 32	C 10	N 5	O 14	P 3	0
107	WC	1	Total 32	C 10	N 5	O 14	P 3	0
107	WE	1	Total 32	C 10	N 5	O 14	P 3	0
107	WG	1	Total 32	C 10	N 5	O 14	P 3	0
107	WI	1	Total 32	C 10	N 5	O 14	P 3	0
107	WK	1	Total 32	C 10	N 5	O 14	P 3	0
107	WM	1	Total 32	C 10	N 5	O 14	P 3	0
107	WO	1	Total 32	C 10	N 5	O 14	P 3	0
107	WQ	1	Total 32	C 10	N 5	O 14	P 3	0
107	WS	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
107	WU	1	32	10	5	14	3	0
107	WW	1	32	10	5	14	3	0

- Molecule 108 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
108	AZ	1	Total	Mg	0
			1	1	
108	AC	1	Total	Mg	0
			1	1	
108	AE	1	Total	Mg	0
			1	1	
108	AG	1	Total	Mg	0
			1	1	
108	AI	1	Total	Mg	0
			1	1	
108	AK	1	Total	Mg	0
			1	1	
108	AM	1	Total	Mg	0
			1	1	
108	AO	1	Total	Mg	0
			1	1	
108	AQ	1	Total	Mg	0
			1	1	
108	AS	1	Total	Mg	0
			1	1	
108	AU	1	Total	Mg	0
			1	1	
108	AW	1	Total	Mg	0
			1	1	
108	AY	1	Total	Mg	0
			1	1	
108	BA	1	Total	Mg	0
			1	1	
108	BC	1	Total	Mg	0
			1	1	
108	BE	1	Total	Mg	0
			1	1	
108	BG	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	BI	1	1	1	0
108	BK	1	1	1	0
108	BM	1	1	1	0
108	BO	1	1	1	0
108	BP	1	1	1	0
108	BS	1	1	1	0
108	BU	1	1	1	0
108	BW	1	1	1	0
108	BY	1	1	1	0
108	CC	1	1	1	0
108	CE	1	1	1	0
108	CG	1	1	1	0
108	CI	1	1	1	0
108	CK	1	1	1	0
108	CM	1	1	1	0
108	CO	1	1	1	0
108	CQ	1	1	1	0
108	CS	1	1	1	0
108	CU	1	1	1	0
108	CW	1	1	1	0
108	CY	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	DC	1	1	1	0
108	DE	1	1	1	0
108	DG	1	1	1	0
108	DI	1	1	1	0
108	DK	1	1	1	0
108	DM	1	1	1	0
108	DO	1	1	1	0
108	DQ	1	1	1	0
108	DS	1	1	1	0
108	DU	1	1	1	0
108	DW	1	1	1	0
108	DY	1	1	1	0
108	EC	1	1	1	0
108	EE	1	1	1	0
108	EG	1	1	1	0
108	EI	1	1	1	0
108	EK	1	1	1	0
108	EM	1	1	1	0
108	EO	1	1	1	0
108	EQ	1	1	1	0
108	ES	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	EU	1	1	1	0
108	EW	1	1	1	0
108	EY	1	1	1	0
108	FB	1	1	1	0
108	FE	1	1	1	0
108	FG	1	1	1	0
108	FH	1	1	1	0
108	FK	1	1	1	0
108	FM	1	1	1	0
108	FO	1	1	1	0
108	FQ	1	1	1	0
108	FS	1	1	1	0
108	FU	1	1	1	0
108	FV	1	1	1	0
108	FY	1	1	1	0
108	GC	1	1	1	0
108	GE	1	1	1	0
108	GG	1	1	1	0
108	GI	1	1	1	0
108	GK	1	1	1	0
108	GM	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	GO	1	1	1	0
108	GQ	1	1	1	0
108	GS	1	1	1	0
108	GU	1	1	1	0
108	GW	1	1	1	0
108	GY	1	1	1	0
108	HA	1	1	1	0
108	HC	1	1	1	0
108	HE	1	1	1	0
108	HG	1	1	1	0
108	HH	1	1	1	0
108	HK	1	1	1	0
108	HM	1	1	1	0
108	HO	1	1	1	0
108	HQ	1	1	1	0
108	HS	1	1	1	0
108	HU	1	1	1	0
108	HV	1	1	1	0
108	HY	1	1	1	0
108	IA	1	1	1	0
108	IC	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	IE	1	1	1	0
108	IG	1	1	1	0
108	II	1	1	1	0
108	IK	1	1	1	0
108	IM	1	1	1	0
108	IO	1	1	1	0
108	IQ	1	1	1	0
108	IS	1	1	1	0
108	IU	1	1	1	0
108	IW	1	1	1	0
108	IY	1	1	1	0
108	JC	1	1	1	0
108	JE	1	1	1	0
108	JG	1	1	1	0
108	JI	1	1	1	0
108	JK	1	1	1	0
108	JM	1	1	1	0
108	JO	1	1	1	0
108	JQ	1	1	1	0
108	JS	1	1	1	0
108	JU	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	JW	1	1	1	0
108	JY	1	1	1	0
108	KC	1	1	1	0
108	KE	1	1	1	0
108	KG	1	1	1	0
108	KH	1	1	1	0
108	KK	1	1	1	0
108	KM	1	1	1	0
108	KO	1	1	1	0
108	KQ	1	1	1	0
108	KS	1	1	1	0
108	KU	1	1	1	0
108	KV	1	1	1	0
108	KY	1	1	1	0
108	LC	1	1	1	0
108	LE	1	1	1	0
108	LG	1	1	1	0
108	LI	1	1	1	0
108	LK	1	1	1	0
108	LM	1	1	1	0
108	LO	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	LQ	1	1	1	0
108	LS	1	1	1	0
108	LU	1	1	1	0
108	LW	1	1	1	0
108	LY	1	1	1	0
108	MA	1	1	1	0
108	MC	1	1	1	0
108	ME	1	1	1	0
108	MG	1	1	1	0
108	MH	1	1	1	0
108	MK	1	1	1	0
108	MM	1	1	1	0
108	MO	1	1	1	0
108	MQ	1	1	1	0
108	MS	1	1	1	0
108	MU	1	1	1	0
108	MV	1	1	1	0
108	MY	1	1	1	0
108	NA	1	1	1	0
108	NC	1	1	1	0
108	NE	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	NG	1	1	1	0
108	NI	1	1	1	0
108	NK	1	1	1	0
108	NM	1	1	1	0
108	NO	1	1	1	0
108	NQ	1	1	1	0
108	NS	1	1	1	0
108	NU	1	1	1	0
108	NW	1	1	1	0
108	OA	1	1	1	0
108	OC	1	1	1	0
108	OE	1	1	1	0
108	OG	1	1	1	0
108	OI	1	1	1	0
108	OK	1	1	1	0
108	OM	1	1	1	0
108	OO	1	1	1	0
108	OQ	1	1	1	0
108	OS	1	1	1	0
108	OU	1	1	1	0
108	OW	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	OY	1	1	1	0
108	PA	1	1	1	0
108	PC	1	1	1	0
108	PE	1	1	1	0
108	PG	1	1	1	0
108	PI	1	1	1	0
108	PK	1	1	1	0
108	PM	1	1	1	0
108	PO	1	1	1	0
108	PQ	1	1	1	0
108	PS	1	1	1	0
108	PU	1	1	1	0
108	PV	1	1	1	0
108	PY	1	1	1	0
108	QA	1	1	1	0
108	QC	1	1	1	0
108	QE	1	1	1	0
108	QG	1	1	1	0
108	QI	1	1	1	0
108	QK	1	1	1	0
108	QM	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	QO	1	1	1	0
108	QQ	1	1	1	0
108	QS	1	1	1	0
108	QU	1	1	1	0
108	QW	1	1	1	0
108	QY	1	1	1	0
108	RA	1	1	1	0
108	RC	1	1	1	0
108	RE	1	1	1	0
108	RG	1	1	1	0
108	RH	1	1	1	0
108	RK	1	1	1	0
108	RM	1	1	1	0
108	RO	1	1	1	0
108	RQ	1	1	1	0
108	RS	1	1	1	0
108	RT	1	1	1	0
108	RV	1	1	1	0
108	RY	1	1	1	0
108	SC	1	1	1	0
108	SE	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	SG	1	1	1	0
108	SI	1	1	1	0
108	SK	1	1	1	0
108	SM	1	1	1	0
108	SO	1	1	1	0
108	SQ	1	1	1	0
108	SS	1	1	1	0
108	SU	1	1	1	0
108	SW	1	1	1	0
108	SY	1	1	1	0
108	TB	1	1	1	0
108	TE	1	1	1	0
108	TG	1	1	1	0
108	TI	1	1	1	0
108	TK	1	1	1	0
108	TM	1	1	1	0
108	TO	1	1	1	0
108	TQ	1	1	1	0
108	TS	1	1	1	0
108	TU	1	1	1	0
108	TW	1	1	1	0

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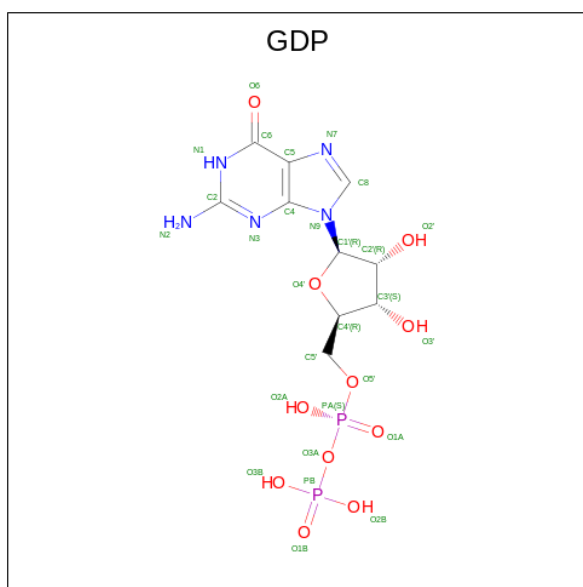
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
108	TY	1	1	1	0
108	UC	1	1	1	0
108	UE	1	1	1	0
108	UG	1	1	1	0
108	UI	1	1	1	0
108	UK	1	1	1	0
108	UM	1	1	1	0
108	UO	1	1	1	0
108	UQ	1	1	1	0
108	US	1	1	1	0
108	UU	1	1	1	0
108	UW	1	1	1	0
108	UY	1	1	1	0
108	VC	1	1	1	0
108	VE	1	1	1	0
108	VG	1	1	1	0
108	VH	1	1	1	0
108	VK	1	1	1	0
108	VM	1	1	1	0
108	VO	1	1	1	0
108	VQ	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
108	VS	1	Total 1	Mg 1	0
108	VU	1	Total 1	Mg 1	0
108	VV	1	Total 1	Mg 1	0
108	VY	1	Total 1	Mg 1	0
108	WA	1	Total 1	Mg 1	0
108	WC	1	Total 1	Mg 1	0
108	WE	1	Total 1	Mg 1	0
108	WG	1	Total 1	Mg 1	0
108	WI	1	Total 1	Mg 1	0
108	WK	1	Total 1	Mg 1	0
108	WM	1	Total 1	Mg 1	0
108	WO	1	Total 1	Mg 1	0
108	WQ	1	Total 1	Mg 1	0
108	WS	1	Total 1	Mg 1	0
108	WU	1	Total 1	Mg 1	0
108	WW	1	Total 1	Mg 1	0

- Molecule 109 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	AB	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AD	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AF	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AH	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AL	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AN	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AP	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AR	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AT	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AV	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	AX	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	BB	1	Total	C	N	O	P	0
			28	10	5	11	2	
109	BD	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	BF	1	Total 28	C 10	N 5	O 11	P 2	0
109	BH	1	Total 28	C 10	N 5	O 11	P 2	0
109	BJ	1	Total 28	C 10	N 5	O 11	P 2	0
109	BL	1	Total 28	C 10	N 5	O 11	P 2	0
109	BN	1	Total 28	C 10	N 5	O 11	P 2	0
109	BP	1	Total 28	C 10	N 5	O 11	P 2	0
109	BR	1	Total 28	C 10	N 5	O 11	P 2	0
109	BT	1	Total 28	C 10	N 5	O 11	P 2	0
109	BV	1	Total 28	C 10	N 5	O 11	P 2	0
109	BX	1	Total 28	C 10	N 5	O 11	P 2	0
109	CB	1	Total 28	C 10	N 5	O 11	P 2	0
109	CD	1	Total 28	C 10	N 5	O 11	P 2	0
109	CF	1	Total 28	C 10	N 5	O 11	P 2	0
109	CH	1	Total 28	C 10	N 5	O 11	P 2	0
109	CJ	1	Total 28	C 10	N 5	O 11	P 2	0
109	CL	1	Total 28	C 10	N 5	O 11	P 2	0
109	CN	1	Total 28	C 10	N 5	O 11	P 2	0
109	CP	1	Total 28	C 10	N 5	O 11	P 2	0
109	CR	1	Total 28	C 10	N 5	O 11	P 2	0
109	CT	1	Total 28	C 10	N 5	O 11	P 2	0
109	CV	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	CX	1	28	10	5	11	2	0
109	CZ	1	28	10	5	11	2	0
109	DB	1	28	10	5	11	2	0
109	DD	1	28	10	5	11	2	0
109	DF	1	28	10	5	11	2	0
109	DH	1	28	10	5	11	2	0
109	DJ	1	28	10	5	11	2	0
109	DL	1	28	10	5	11	2	0
109	DN	1	28	10	5	11	2	0
109	DP	1	28	10	5	11	2	0
109	DR	1	28	10	5	11	2	0
109	DT	1	28	10	5	11	2	0
109	DV	1	28	10	5	11	2	0
109	DX	1	28	10	5	11	2	0
109	DZ	1	28	10	5	11	2	0
109	EB	1	28	10	5	11	2	0
109	ED	1	28	10	5	11	2	0
109	EF	1	28	10	5	11	2	0
109	EH	1	28	10	5	11	2	0
109	EJ	1	28	10	5	11	2	0
109	EL	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	EN	1	Total 28	C 10	N 5	O 11	P 2	0
109	EP	1	Total 28	C 10	N 5	O 11	P 2	0
109	ER	1	Total 28	C 10	N 5	O 11	P 2	0
109	ET	1	Total 28	C 10	N 5	O 11	P 2	0
109	EV	1	Total 28	C 10	N 5	O 11	P 2	0
109	EX	1	Total 28	C 10	N 5	O 11	P 2	0
109	EZ	1	Total 28	C 10	N 5	O 11	P 2	0
109	FB	1	Total 28	C 10	N 5	O 11	P 2	0
109	FD	1	Total 28	C 10	N 5	O 11	P 2	0
109	FF	1	Total 28	C 10	N 5	O 11	P 2	0
109	FH	1	Total 28	C 10	N 5	O 11	P 2	0
109	FJ	1	Total 28	C 10	N 5	O 11	P 2	0
109	FL	1	Total 28	C 10	N 5	O 11	P 2	0
109	FN	1	Total 28	C 10	N 5	O 11	P 2	0
109	FP	1	Total 28	C 10	N 5	O 11	P 2	0
109	FR	1	Total 28	C 10	N 5	O 11	P 2	0
109	FT	1	Total 28	C 10	N 5	O 11	P 2	0
109	FV	1	Total 28	C 10	N 5	O 11	P 2	0
109	FX	1	Total 28	C 10	N 5	O 11	P 2	0
109	FZ	1	Total 28	C 10	N 5	O 11	P 2	0
109	GB	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	GD	1	28	10	5	11	2	0
109	GF	1	28	10	5	11	2	0
109	GH	1	28	10	5	11	2	0
109	GJ	1	28	10	5	11	2	0
109	GL	1	28	10	5	11	2	0
109	GN	1	28	10	5	11	2	0
109	GP	1	28	10	5	11	2	0
109	GR	1	28	10	5	11	2	0
109	GT	1	28	10	5	11	2	0
109	GV	1	28	10	5	11	2	0
109	GX	1	28	10	5	11	2	0
109	GZ	1	28	10	5	11	2	0
109	HB	1	28	10	5	11	2	0
109	HD	1	28	10	5	11	2	0
109	HF	1	28	10	5	11	2	0
109	HH	1	28	10	5	11	2	0
109	HJ	1	28	10	5	11	2	0
109	HL	1	28	10	5	11	2	0
109	HN	1	28	10	5	11	2	0
109	HP	1	28	10	5	11	2	0
109	HR	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	HT	1	28	10	5	11	2	0
109	HV	1	28	10	5	11	2	0
109	HX	1	28	10	5	11	2	0
109	HZ	1	28	10	5	11	2	0
109	IB	1	28	10	5	11	2	0
109	ID	1	28	10	5	11	2	0
109	IF	1	28	10	5	11	2	0
109	IH	1	28	10	5	11	2	0
109	IJ	1	28	10	5	11	2	0
109	IL	1	28	10	5	11	2	0
109	IN	1	28	10	5	11	2	0
109	IP	1	28	10	5	11	2	0
109	IR	1	28	10	5	11	2	0
109	IT	1	28	10	5	11	2	0
109	IV	1	28	10	5	11	2	0
109	IX	1	28	10	5	11	2	0
109	JB	1	28	10	5	11	2	0
109	JD	1	28	10	5	11	2	0
109	JF	1	28	10	5	11	2	0
109	JH	1	28	10	5	11	2	0
109	JJ	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	JL	1	28	10	5	11	2	0
109	JN	1	28	10	5	11	2	0
109	JP	1	28	10	5	11	2	0
109	JR	1	28	10	5	11	2	0
109	JT	1	28	10	5	11	2	0
109	JV	1	28	10	5	11	2	0
109	JX	1	28	10	5	11	2	0
109	JZ	1	28	10	5	11	2	0
109	KB	1	28	10	5	11	2	0
109	KD	1	28	10	5	11	2	0
109	KF	1	28	10	5	11	2	0
109	KH	1	28	10	5	11	2	0
109	KJ	1	28	10	5	11	2	0
109	KL	1	28	10	5	11	2	0
109	KN	1	28	10	5	11	2	0
109	KP	1	28	10	5	11	2	0
109	KR	1	28	10	5	11	2	0
109	KT	1	28	10	5	11	2	0
109	KV	1	28	10	5	11	2	0
109	KX	1	28	10	5	11	2	0
109	KZ	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	LB	1	28	10	5	11	2	0
109	LD	1	28	10	5	11	2	0
109	LF	1	28	10	5	11	2	0
109	LH	1	28	10	5	11	2	0
109	LJ	1	28	10	5	11	2	0
109	LL	1	28	10	5	11	2	0
109	LN	1	28	10	5	11	2	0
109	LP	1	28	10	5	11	2	0
109	LR	1	28	10	5	11	2	0
109	LT	1	28	10	5	11	2	0
109	LV	1	28	10	5	11	2	0
109	LX	1	28	10	5	11	2	0
109	LZ	1	28	10	5	11	2	0
109	MD	1	28	10	5	11	2	0
109	MF	1	28	10	5	11	2	0
109	MH	1	28	10	5	11	2	0
109	MJ	1	28	10	5	11	2	0
109	ML	1	28	10	5	11	2	0
109	MN	1	28	10	5	11	2	0
109	MP	1	28	10	5	11	2	0
109	MR	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	MT	1	28	10	5	11	2	0
109	MV	1	28	10	5	11	2	0
109	MX	1	28	10	5	11	2	0
109	MZ	1	28	10	5	11	2	0
109	NB	1	28	10	5	11	2	0
109	ND	1	28	10	5	11	2	0
109	NF	1	28	10	5	11	2	0
109	NH	1	28	10	5	11	2	0
109	NJ	1	28	10	5	11	2	0
109	NL	1	28	10	5	11	2	0
109	NN	1	28	10	5	11	2	0
109	NP	1	28	10	5	11	2	0
109	NR	1	28	10	5	11	2	0
109	NT	1	28	10	5	11	2	0
109	NV	1	28	10	5	11	2	0
109	NX	1	28	10	5	11	2	0
109	NZ	1	28	10	5	11	2	0
109	OB	1	28	10	5	11	2	0
109	OD	1	28	10	5	11	2	0
109	OF	1	28	10	5	11	2	0
109	OH	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	OJ	1	28	10	5	11	2	0
109	OL	1	28	10	5	11	2	0
109	ON	1	28	10	5	11	2	0
109	OP	1	28	10	5	11	2	0
109	OR	1	28	10	5	11	2	0
109	OT	1	28	10	5	11	2	0
109	OV	1	28	10	5	11	2	0
109	OX	1	28	10	5	11	2	0
109	PB	1	28	10	5	11	2	0
109	PD	1	28	10	5	11	2	0
109	PF	1	28	10	5	11	2	0
109	PH	1	28	10	5	11	2	0
109	PJ	1	28	10	5	11	2	0
109	PL	1	28	10	5	11	2	0
109	PN	1	28	10	5	11	2	0
109	PP	1	28	10	5	11	2	0
109	PR	1	28	10	5	11	2	0
109	PT	1	28	10	5	11	2	0
109	PV	1	28	10	5	11	2	0
109	PX	1	28	10	5	11	2	0
109	QB	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	QD	1	28	10	5	11	2	0
109	QF	1	28	10	5	11	2	0
109	QH	1	28	10	5	11	2	0
109	QJ	1	28	10	5	11	2	0
109	QL	1	28	10	5	11	2	0
109	QN	1	28	10	5	11	2	0
109	QP	1	28	10	5	11	2	0
109	QR	1	28	10	5	11	2	0
109	QT	1	28	10	5	11	2	0
109	QV	1	28	10	5	11	2	0
109	QX	1	28	10	5	11	2	0
109	RB	1	28	10	5	11	2	0
109	RD	1	28	10	5	11	2	0
109	RF	1	28	10	5	11	2	0
109	RH	1	28	10	5	11	2	0
109	RJ	1	28	10	5	11	2	0
109	RL	1	28	10	5	11	2	0
109	RN	1	28	10	5	11	2	0
109	RP	1	28	10	5	11	2	0
109	RR	1	28	10	5	11	2	0
109	RT	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	RV	1	28	10	5	11	2	0
109	RX	1	28	10	5	11	2	0
109	SB	1	28	10	5	11	2	0
109	SD	1	28	10	5	11	2	0
109	SF	1	28	10	5	11	2	0
109	SH	1	28	10	5	11	2	0
109	SJ	1	28	10	5	11	2	0
109	SL	1	28	10	5	11	2	0
109	SN	1	28	10	5	11	2	0
109	SP	1	28	10	5	11	2	0
109	SR	1	28	10	5	11	2	0
109	ST	1	28	10	5	11	2	0
109	SV	1	28	10	5	11	2	0
109	SX	1	28	10	5	11	2	0
109	TB	1	28	10	5	11	2	0
109	TD	1	28	10	5	11	2	0
109	TF	1	28	10	5	11	2	0
109	TH	1	28	10	5	11	2	0
109	TJ	1	28	10	5	11	2	0
109	TL	1	28	10	5	11	2	0
109	TN	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	TP	1	28	10	5	11	2	0
109	TR	1	28	10	5	11	2	0
109	TT	1	28	10	5	11	2	0
109	TV	1	28	10	5	11	2	0
109	TX	1	28	10	5	11	2	0
109	TZ	1	28	10	5	11	2	0
109	UB	1	28	10	5	11	2	0
109	UD	1	28	10	5	11	2	0
109	UF	1	28	10	5	11	2	0
109	UH	1	28	10	5	11	2	0
109	UJ	1	28	10	5	11	2	0
109	UL	1	28	10	5	11	2	0
109	UN	1	28	10	5	11	2	0
109	UP	1	28	10	5	11	2	0
109	UR	1	28	10	5	11	2	0
109	UT	1	28	10	5	11	2	0
109	UV	1	28	10	5	11	2	0
109	UX	1	28	10	5	11	2	0
109	UZ	1	28	10	5	11	2	0
109	VB	1	28	10	5	11	2	0
109	VD	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	VF	1	28	10	5	11	2	0
109	VH	1	28	10	5	11	2	0
109	VJ	1	28	10	5	11	2	0
109	VL	1	28	10	5	11	2	0
109	VN	1	28	10	5	11	2	0
109	VP	1	28	10	5	11	2	0
109	VR	1	28	10	5	11	2	0
109	VT	1	28	10	5	11	2	0
109	VV	1	28	10	5	11	2	0
109	VX	1	28	10	5	11	2	0
109	VZ	1	28	10	5	11	2	0
109	WB	1	28	10	5	11	2	0
109	WD	1	28	10	5	11	2	0
109	WF	1	28	10	5	11	2	0
109	WH	1	28	10	5	11	2	0
109	WJ	1	28	10	5	11	2	0
109	WL	1	28	10	5	11	2	0
109	WN	1	28	10	5	11	2	0
109	WP	1	28	10	5	11	2	0
109	WR	1	28	10	5	11	2	0
109	WT	1	28	10	5	11	2	0

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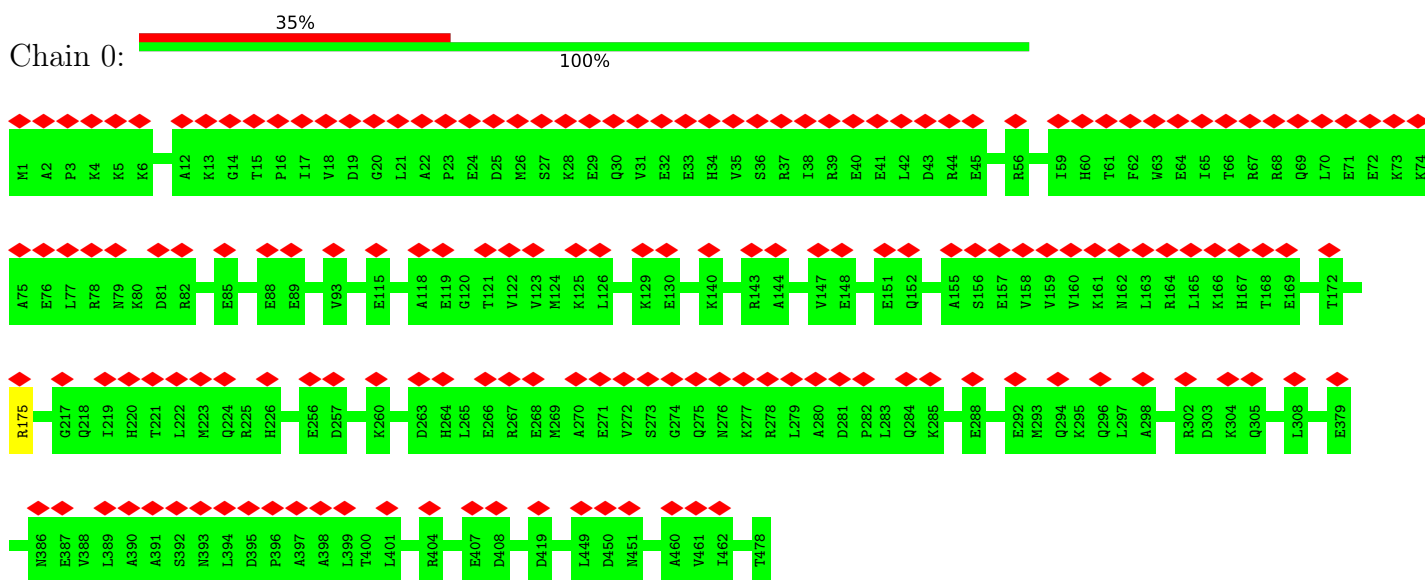
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
109	WV	1	28	10	5	11	2	0
109	WX	1	28	10	5	11	2	0

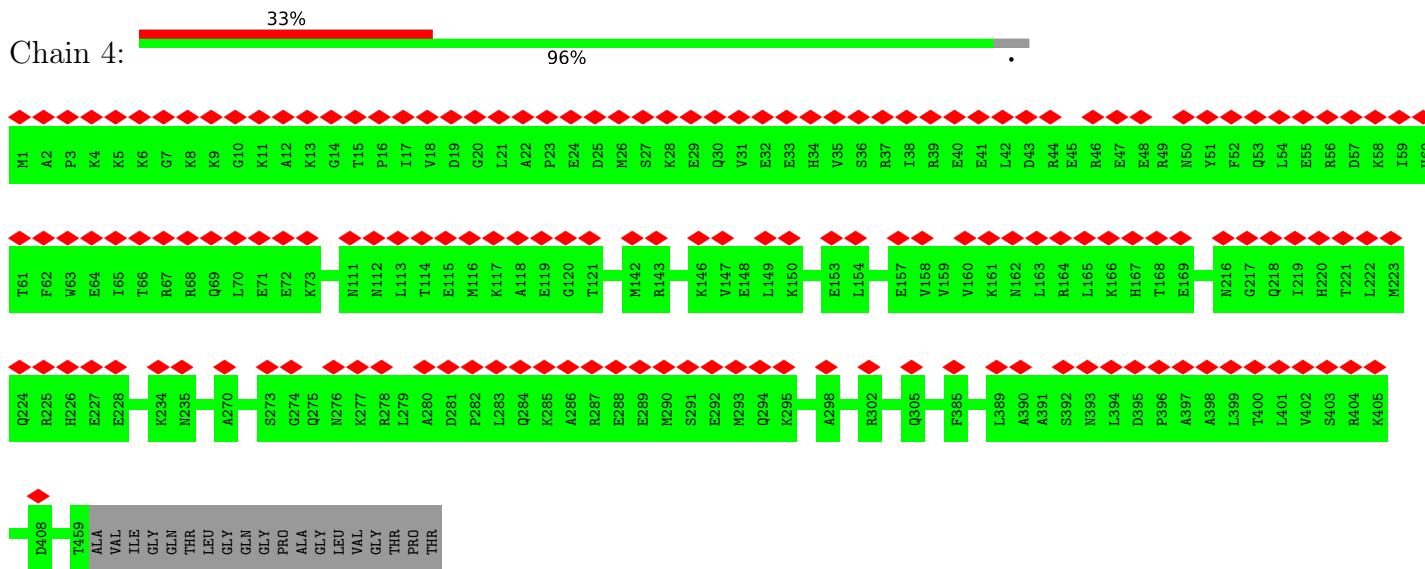
3 Residue-property plots [i](#)

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

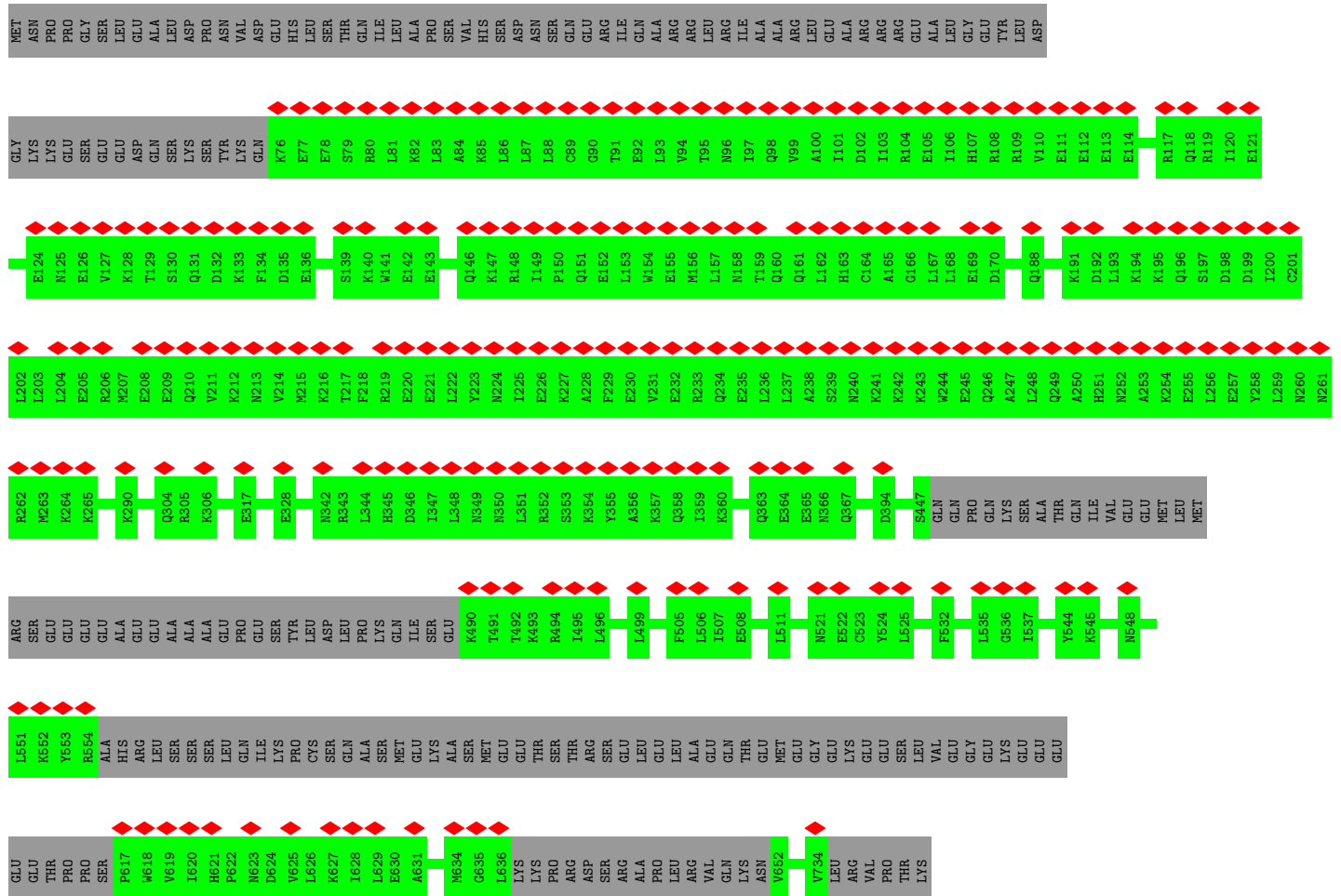
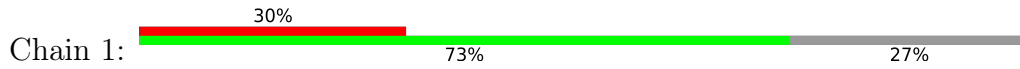
- Molecule 1: Dynein regulatory complex subunit 4



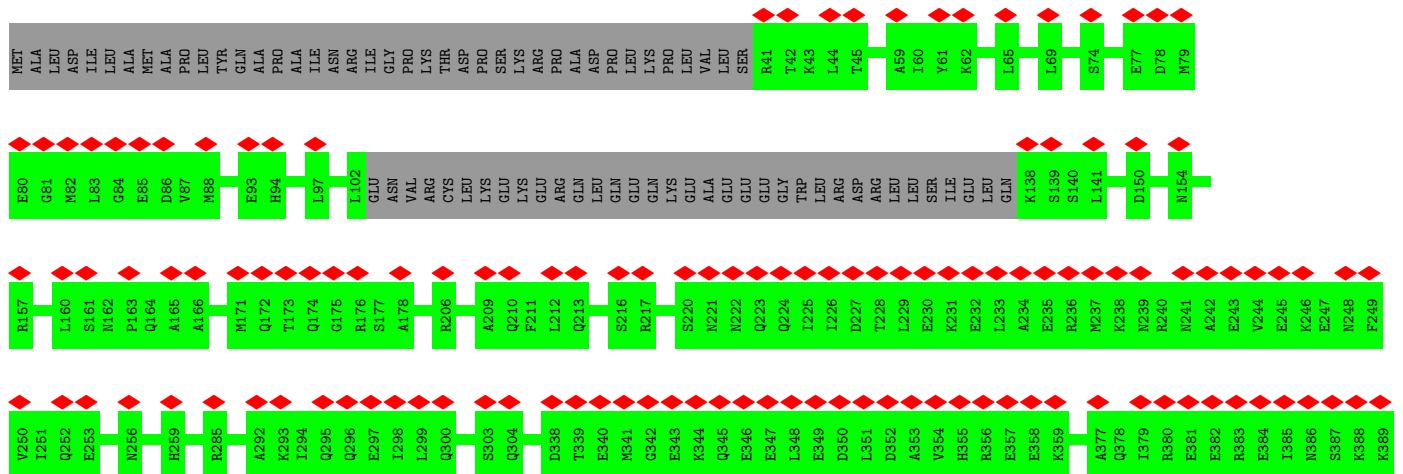
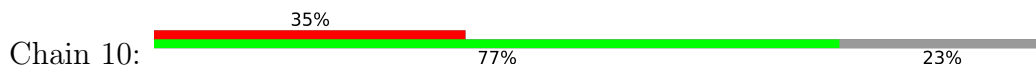
- Molecule 1: Dynein regulatory complex subunit 4



- Molecule 2: Dynein regulatory complex protein 1

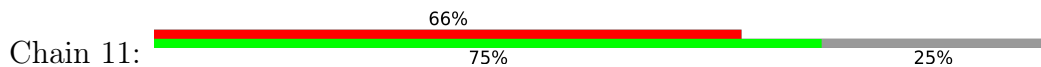


• Molecule 3: Dynein regulatory complex protein 10



R390	M391	E392	A393	E394	Q395	E396	M397	V398	R399	M400	V401	R402	A403	A404	T405	L406	I407	Q408	A409	L410	W411	K412	G413	Y414	L415	V416	R417	S418	L419	L420	R421	SER	LYS	LYS	LYS	ARG	GLY	LYS	LYS	ALA	ASP	LYS	GLU	LYS	LYS	GLN	LYS	LYS	LYS	LYS
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● Molecule 4: Dynein regulatory complex protein 11



M1	S2	N3	A4	Y5	M6	N7	K8	M9	W10	H11	Q12	T13	Q14	E15	A16	L17	G18	A19	L20	D22	K23	E24	P25	Q26	K27	M28	I29	E30	P31	Q32	R33	N34	Q35	V36	F37	I38	F39	Q40	T41	L42	A43	T44	F45	Y46	V47	K48	Y49	I52	N55	L56	E57	M58	V59	Y60	D61	O62
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F63	V64	H65	P66	Q67	K68	R69	I70	L71	I72	R73	K74	Q75	L76	W77	L84	E85	L86	K87	N88	E89	M90	V91	E92	L93	E94	L95	T96	E97	F98	H99	Y100	F101	D102	D103	V104	L105	Q106	D107	L108	K109	L110	A111	T112	Q113	Q114	L115	D116	I117	F118	I119	P120	K121	Y122	F123	L124	V125	E126	K127
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L128	E129	V130	I131	Q132	G133	R134	E135	K136	I137	L138	A139	Q140	I141	L142	A143	D144	G146	I147	D148	T149	S150	D151	M152	L153	Y154	P155	E156	K157	S158	I159	F160	D162	E163	I164	L165	K166	L167	I168	K169	I170	A171	E172	R173	A174	R175	Q176	I177	F178	L179	R180	A181	L182	F183	M184	K185	Q186	I187
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Y188	L189	Q190	E191	T253	R193	A194	K195	Q196	S197	K198	M199	L200	G201	K202	K203	V204	T205	D206	T207	W208	A209	A210	A211	L212	R213	I214	Q215	K216	V217	W218	R219	R220	F221	H222	Q223	R224	K225	E226	T227	E228	K229	L230	E233	E234	M235	I236	F237	L238	G239	M240	N241	P242	P243	P244	L245	F246	N247	E248
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V249	S250	A251	T252	I254	Q255	A256	E257	K258	D260	L261	R262	N264	E265	VAL	GLN	ILE	LYS	HIS	GLU	GLN	GLU	ASP	TYR	ASP	GLU	GLU	LEU	ASN	LEU	ASP	R219	R220	F221	H222	Q223	R224	K225	E226	T227	E228	K229	L230	E233	E234	M235	I236	F237	L238	G239	M240	N241	P242	P243	P244	L245	F246	N247	E248
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ARG	ASN	LEU	THR	GLY	THR	PHE	PRO	ASP	TYR	GLU	PRO	VAL	VAL	ILE	ILE	PHE	SER	ASP	LYS	THR	ILE	GLN	VAL	ILE	ASP	GLU	LEU	ASN	GLN	GLU	GLU	LYS	ASN	LYS	LYS	GLY	VAL	LYS	LYS	ILE	LYS	GLU	GLU	ASN	ALA	ALA	LYS	GLU	LYS	GLY	ASP	LYS
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GLN	LYS	GLY	THR	LYS	GLU	LYS	ASN	GLY	VAL	W384	K385	M386	S387	P388	S389	L390	F391	L392	F393	A394	M395	K396	E397	G398	C399	M400	A401	Y402	K403	E404	L405	W406	M407	K408	K409	D410	E411	S412	W413	M414	F415	S416	Q417	ASP	TYR	PRO	GLU	LEU	ILE	LYS	GLU	GLU	LYS
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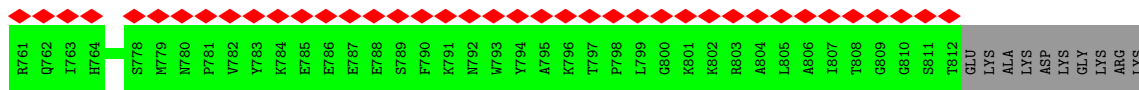
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LEU	THR	ALA	ASP	ARG	THR	ILE	E496	S497	L498	Y499	K500	E501	L502	V503	E504	E505	G506	L507	L508	I509	Q510	A511	L512	K513	V514	M515	L516	S517	D518	Y519	I520	E521	E522	Y523	S524	Y525	L526	G527	T528	T529	L530	R531	Q532	V533	S534	I535	E536	P537	M538	P539	Y551	P555	L556	G557	L558	A559	A560
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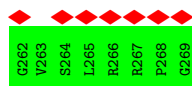
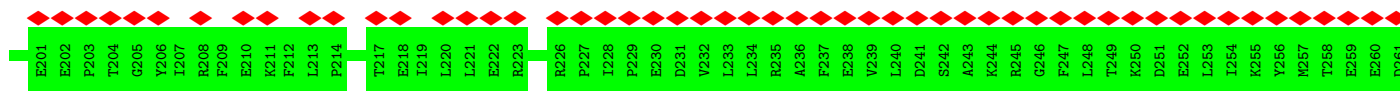
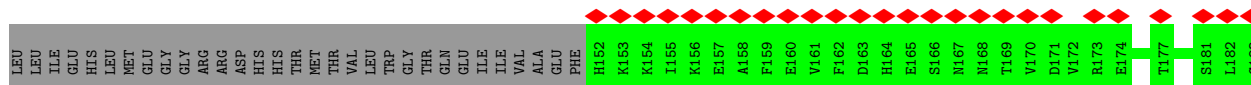
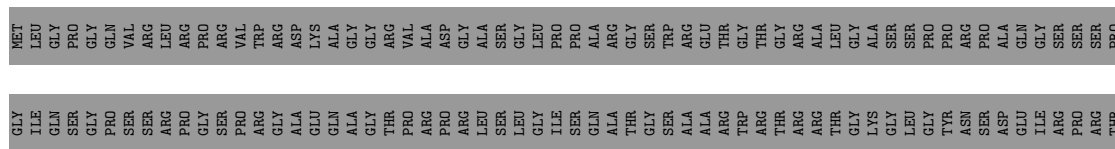
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V621	F622	K623	V624	A625	R626	Q627	L628	Q629	P630	S631	V632	M633	V634	I635	E636	D637	T638	E639	K640	T641	F642	Y643	K644	G645	K646	V647	M648	A649	E650	K651	M652	M653	E654	P655	K656	R657	L658	K659	K660	H661	L662	P663	Q664	I665	L666	K667	L668	L669	P671	D672	D673	R674	L675	L676	L677	V678	G679	T680
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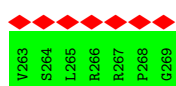
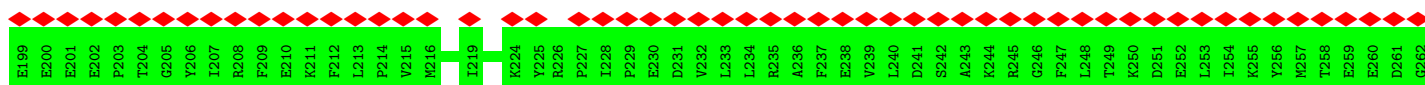
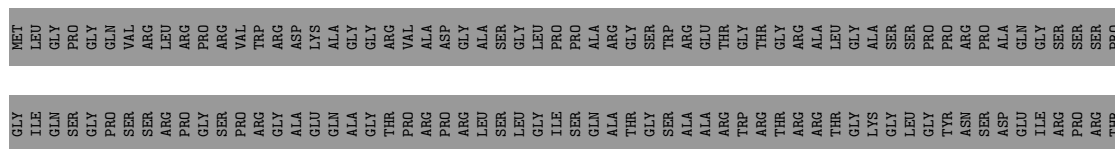
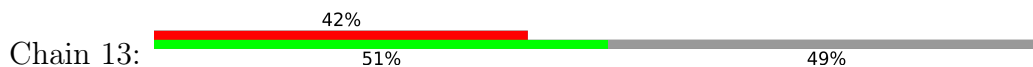
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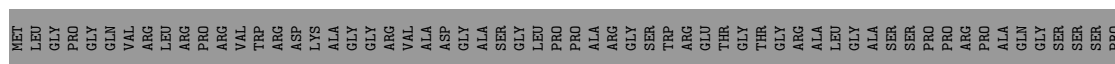
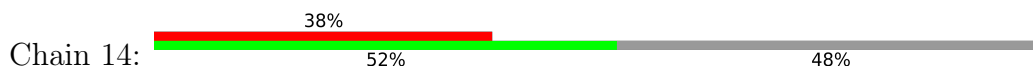
• Molecule 5: Dynein regulatory complex protein 8

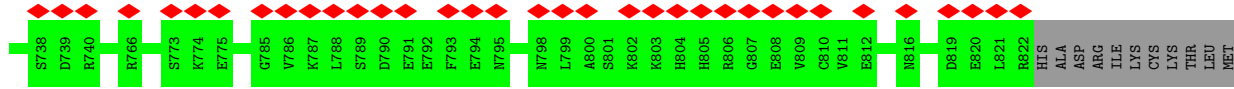


• Molecule 5: Dynein regulatory complex protein 8

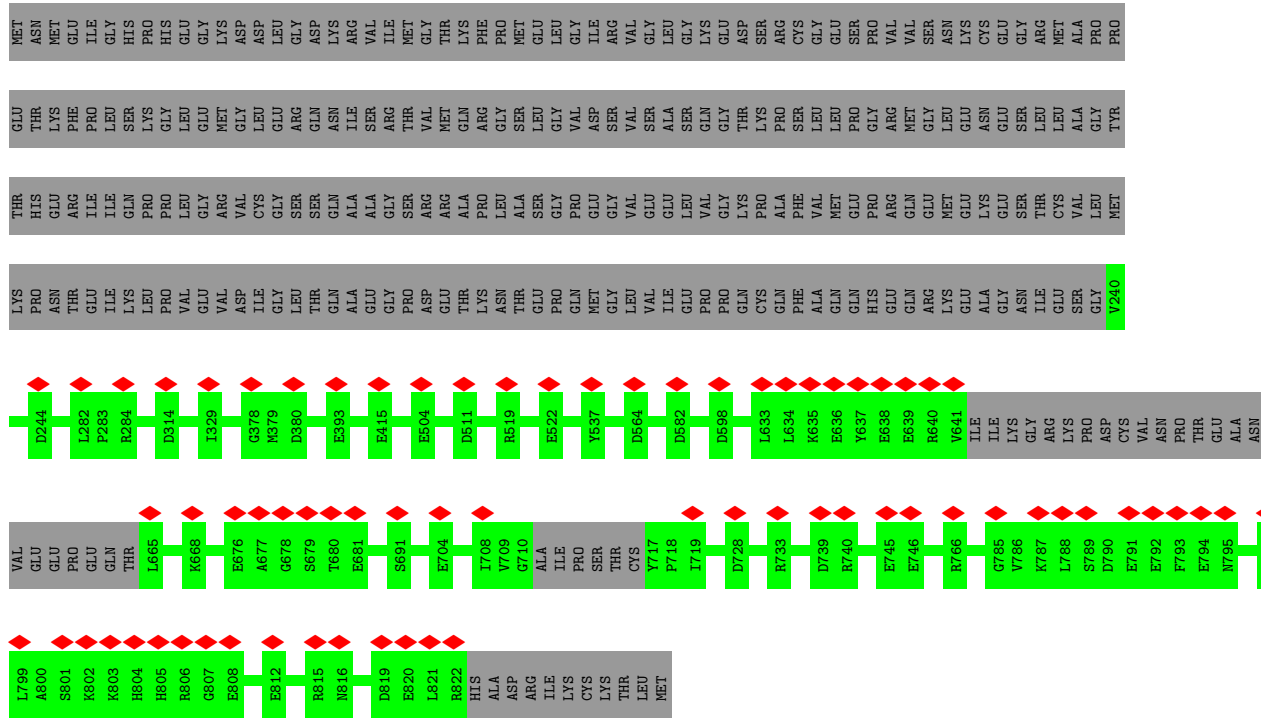


• Molecule 5: Dynein regulatory complex protein 8

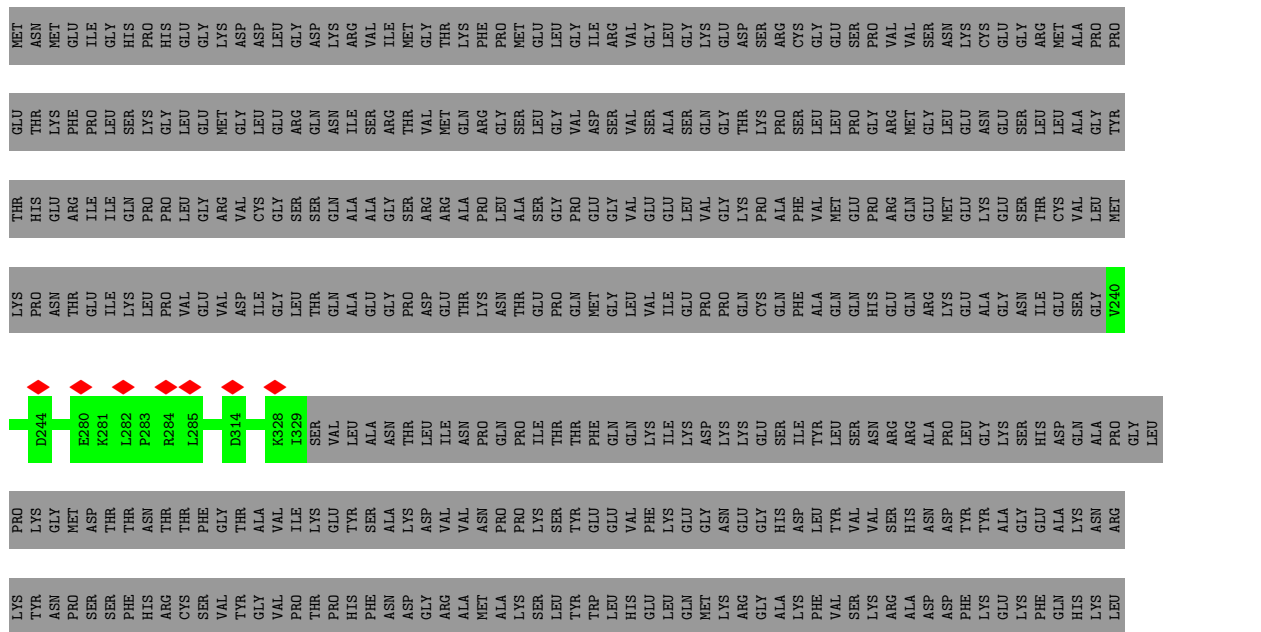


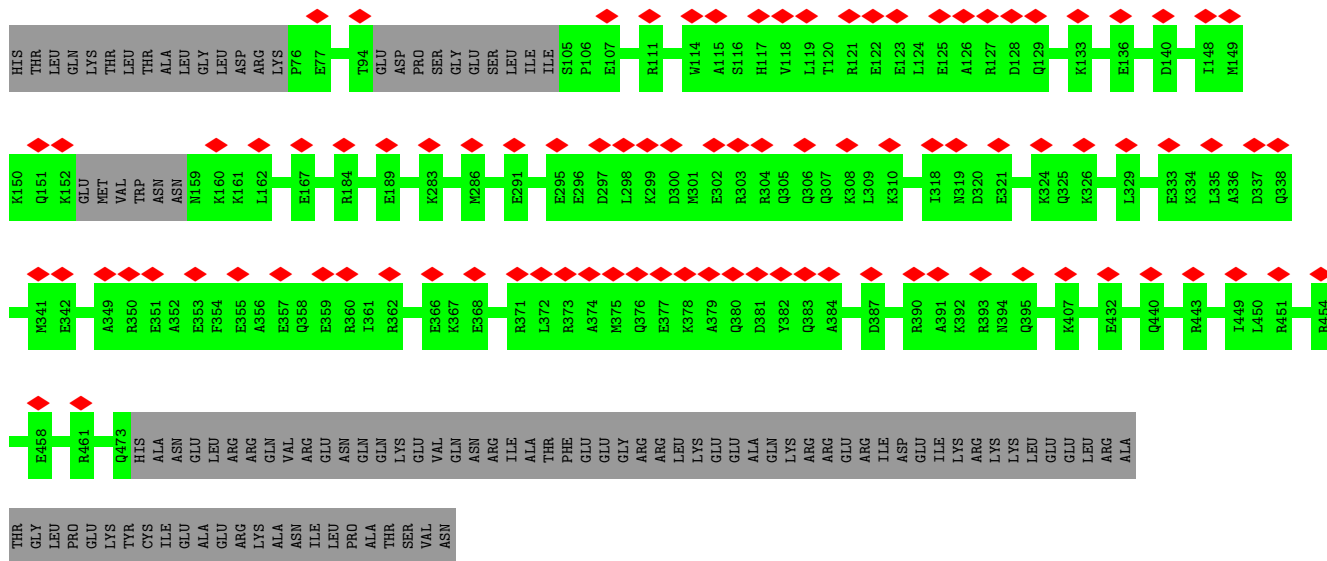


• Molecule 6: EF-hand domain-containing family member B

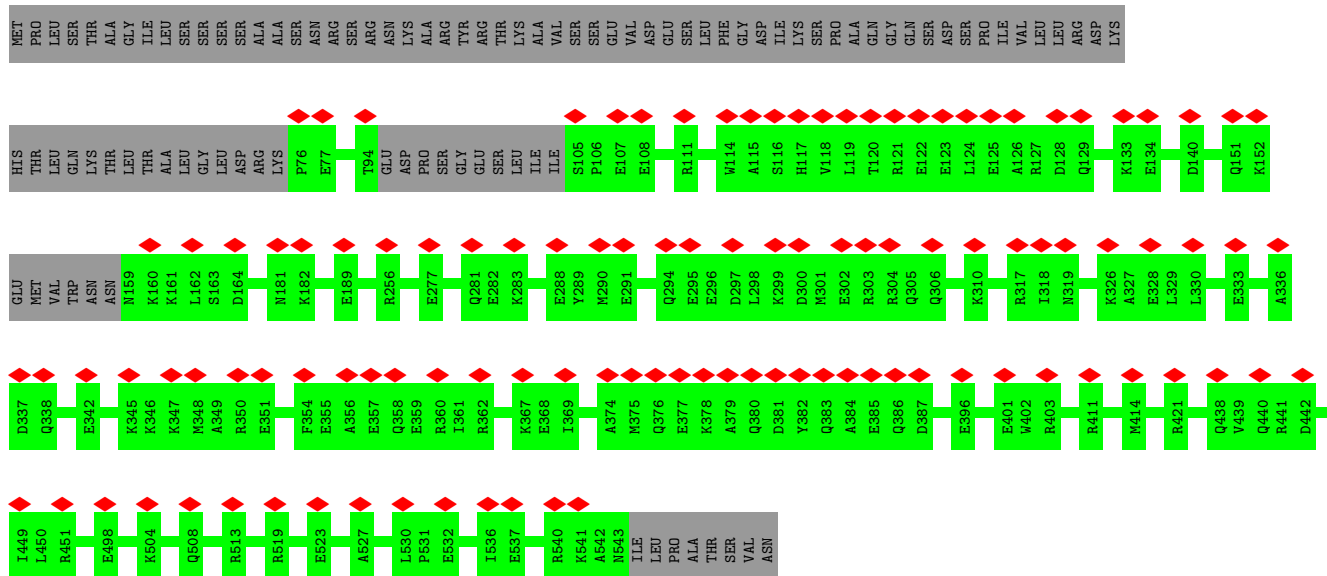
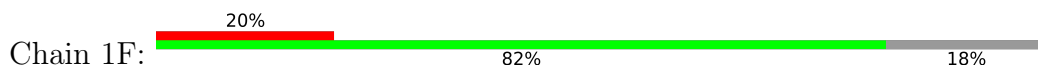


• Molecule 6: EF-hand domain-containing family member B

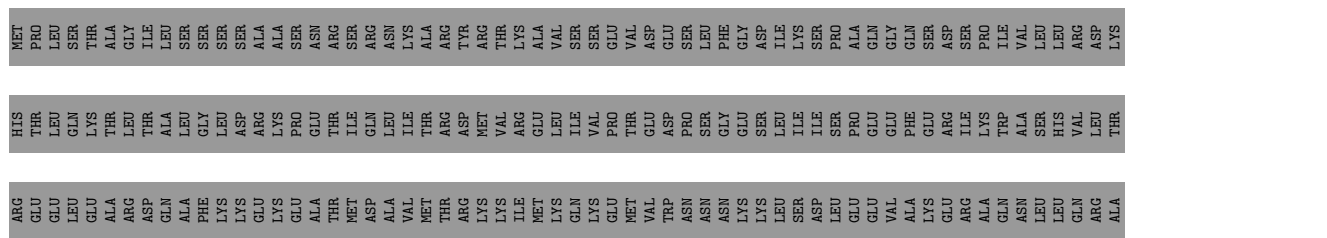


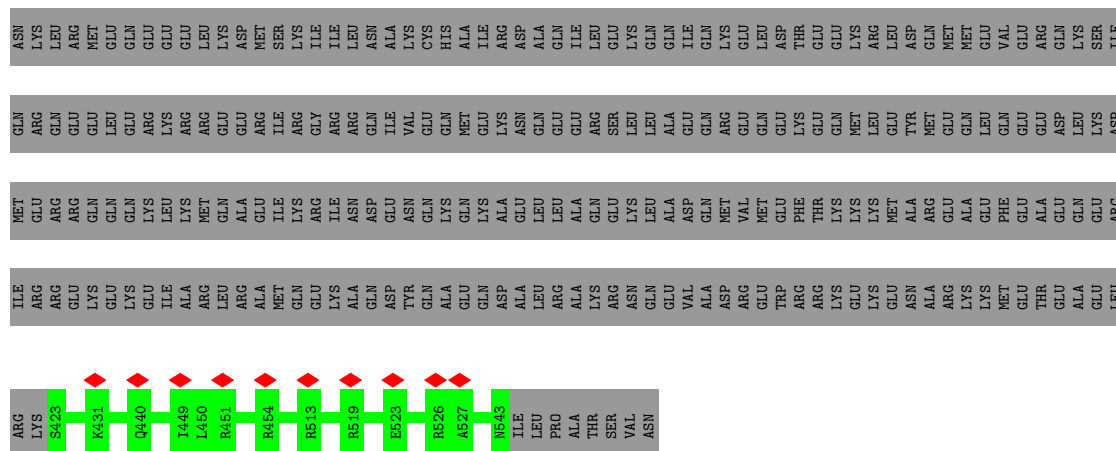


• Molecule 7: Cilia- and flagella-associated protein 45

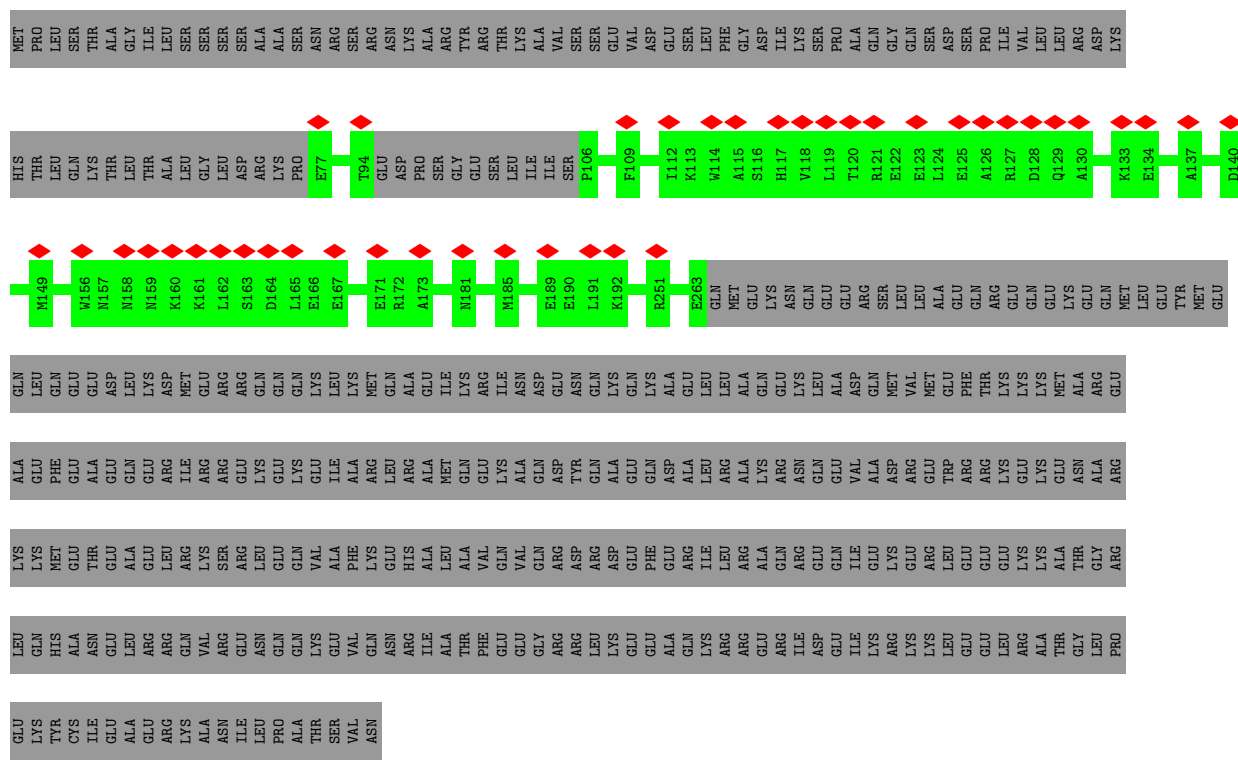


• Molecule 7: Cilia- and flagella-associated protein 45

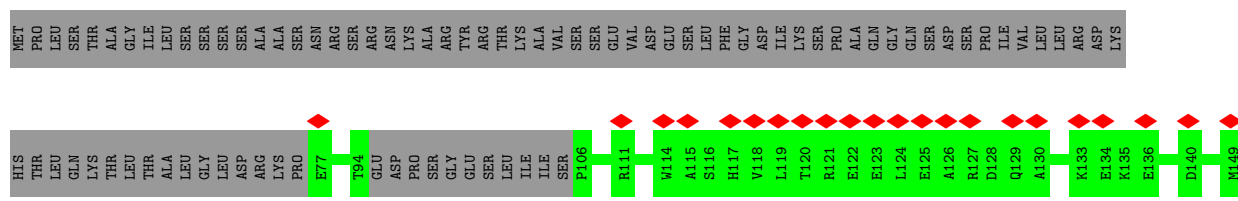
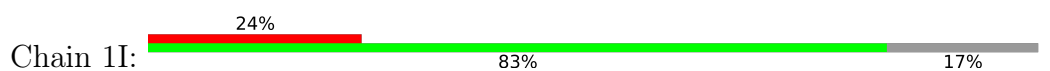


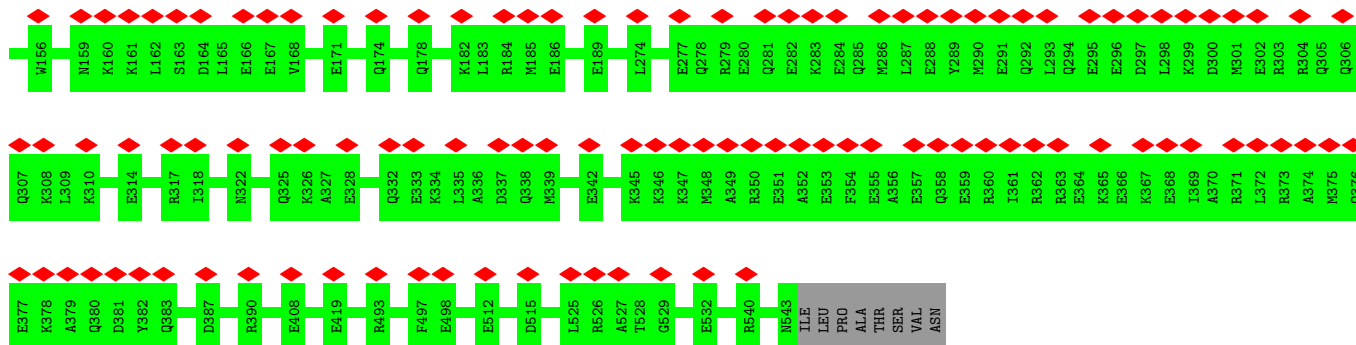


● Molecule 7: Cilia- and flagella-associated protein 45

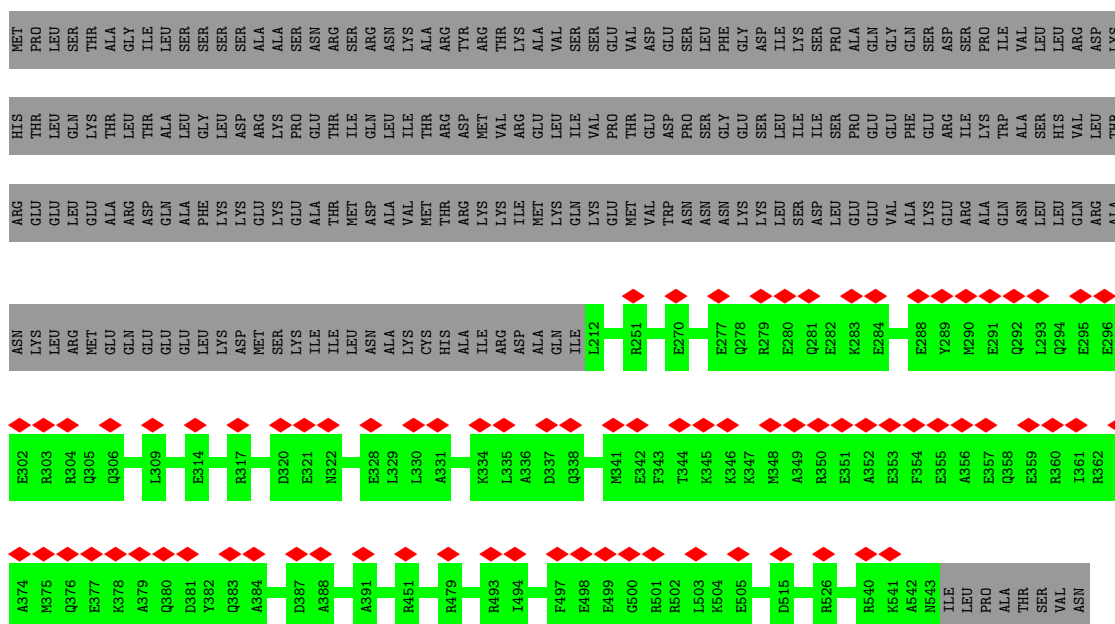


● Molecule 7: Cilia- and flagella-associated protein 45

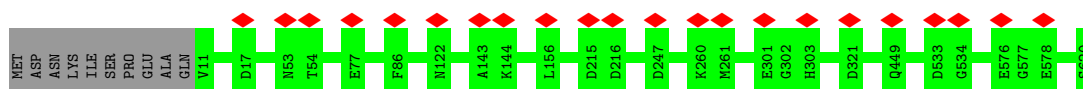




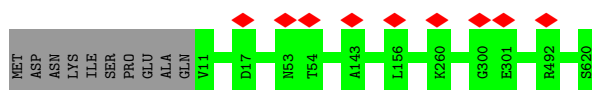
• Molecule 7: Cilia- and flagella-associated protein 45



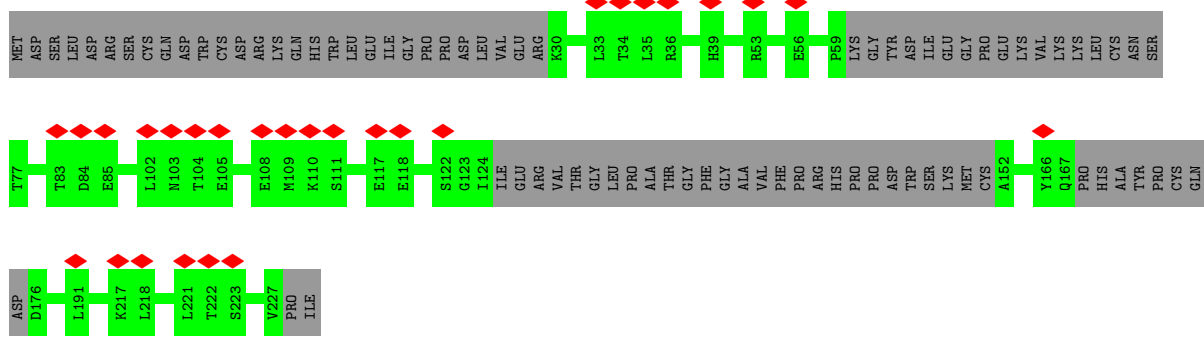
• Molecule 8: Cilia- and flagella-associated protein 52



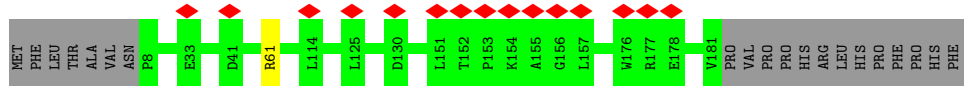
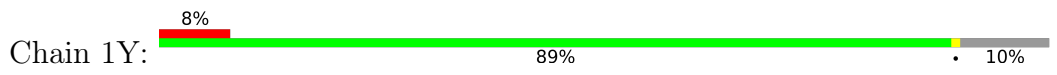
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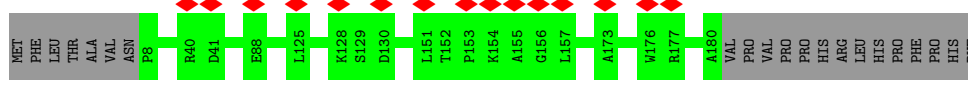
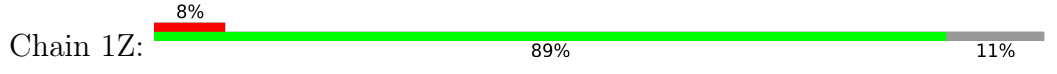
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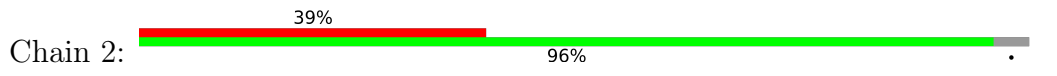
• Molecule 11: Cilia- and flagella-associated protein 107



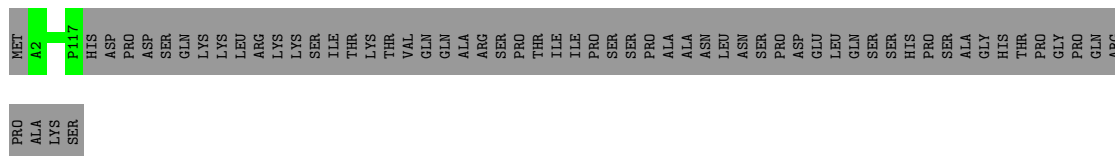
• Molecule 11: Cilia- and flagella-associated protein 107



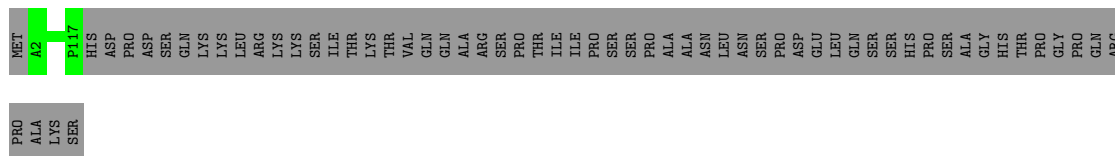
• Molecule 12: Dynein regulatory complex subunit 2



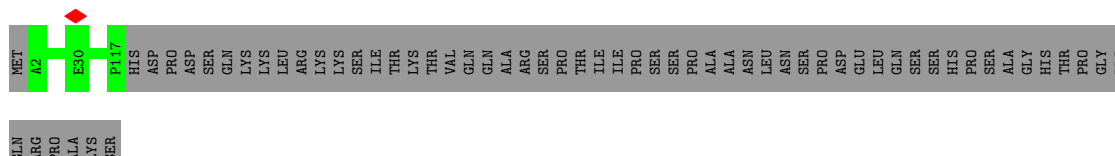
• Molecule 13: Protein Flattop



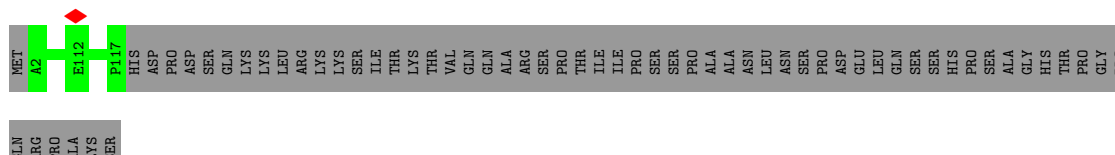
• Molecule 13: Protein Flattop



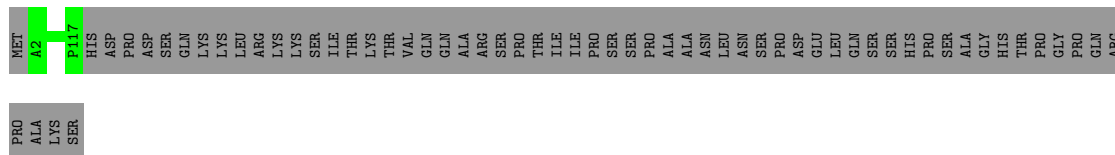
• Molecule 13: Protein Flattop



• Molecule 13: Protein Flattop



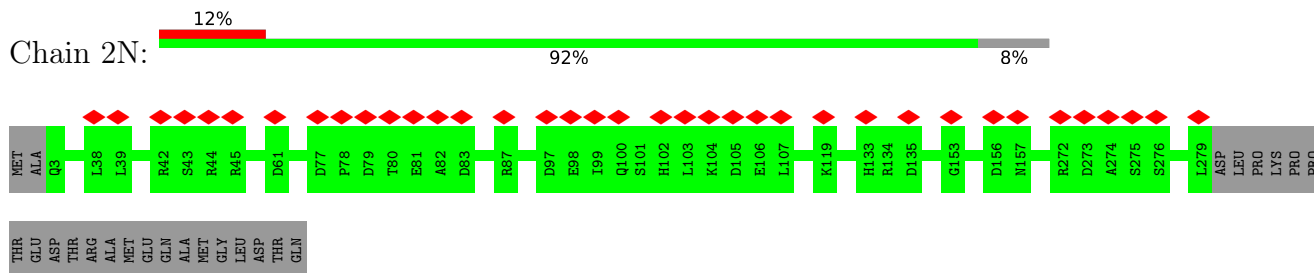
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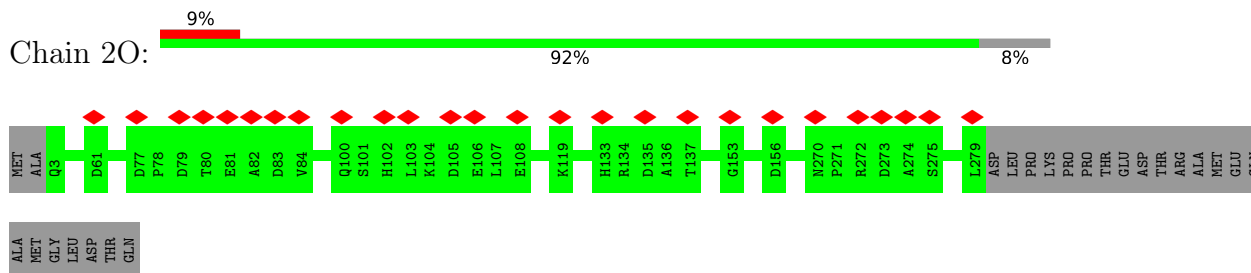
• Molecule 13: Protein Flattop



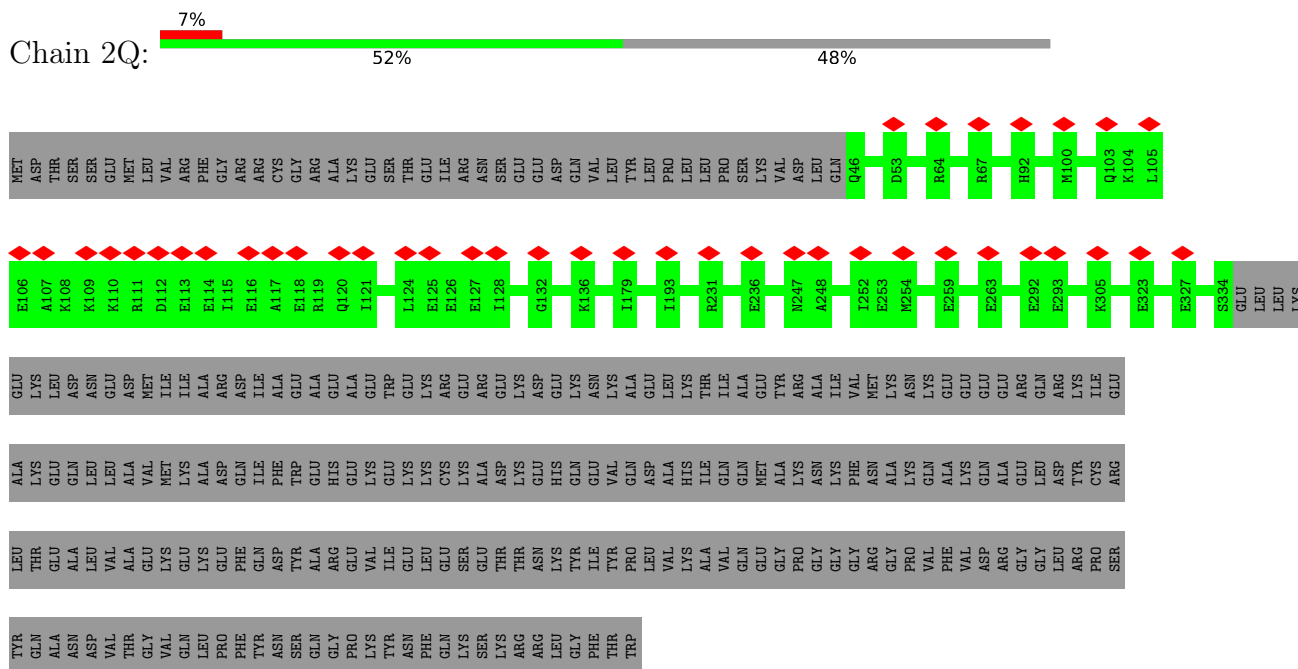
• Molecule 15: Cilia- and flagella-associated protein 161



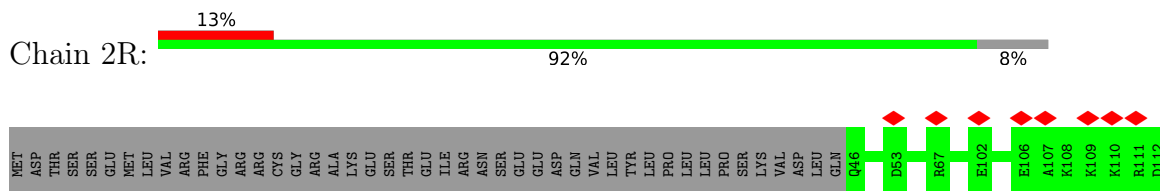
• Molecule 15: Cilia- and flagella-associated protein 161

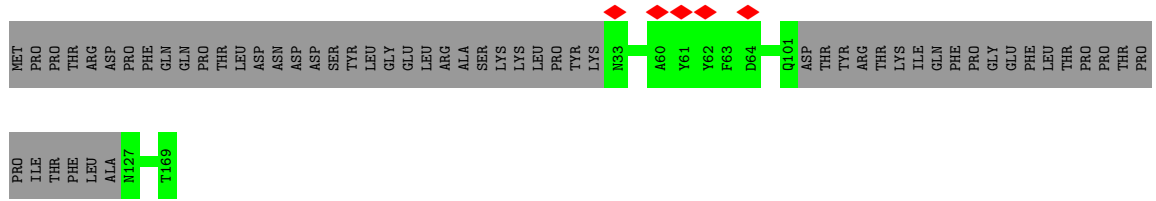


• Molecule 16: Cilia- and flagella-associated protein 210

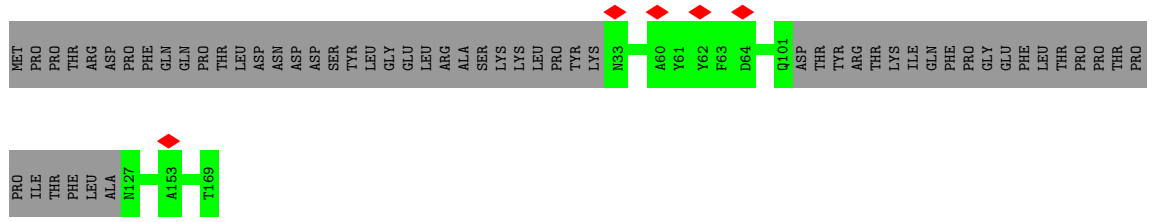


• Molecule 16: Cilia- and flagella-associated protein 210

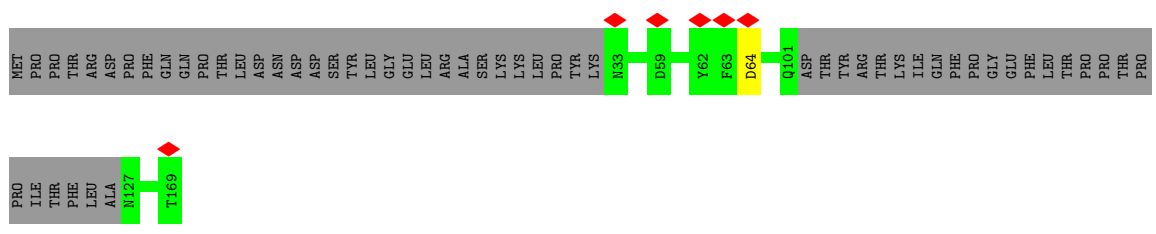




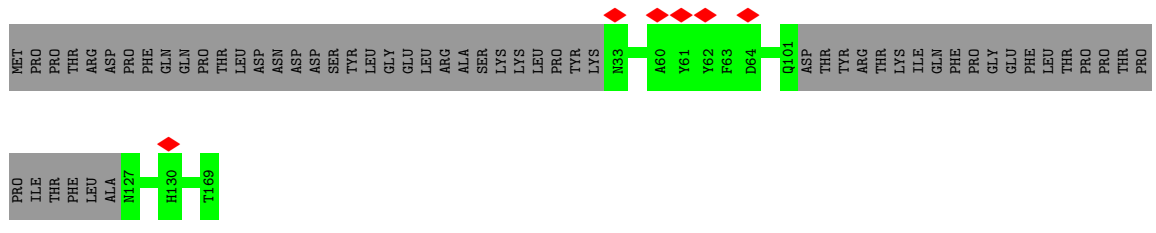
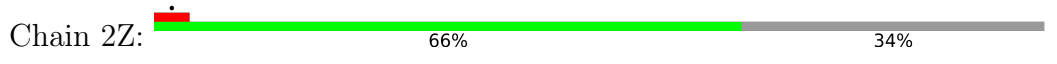
• Molecule 17: Cilia- and flagella-associated protein 276



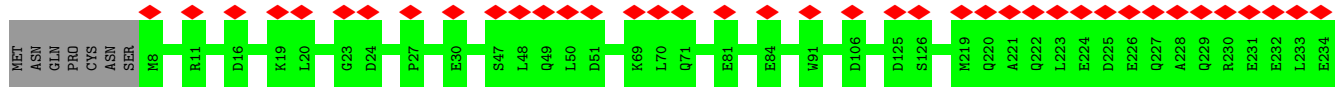
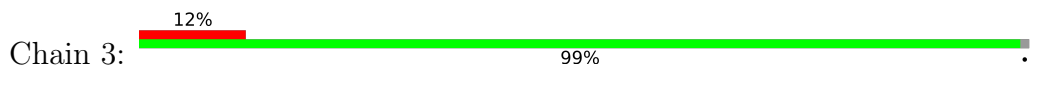
• Molecule 17: Cilia- and flagella-associated protein 276



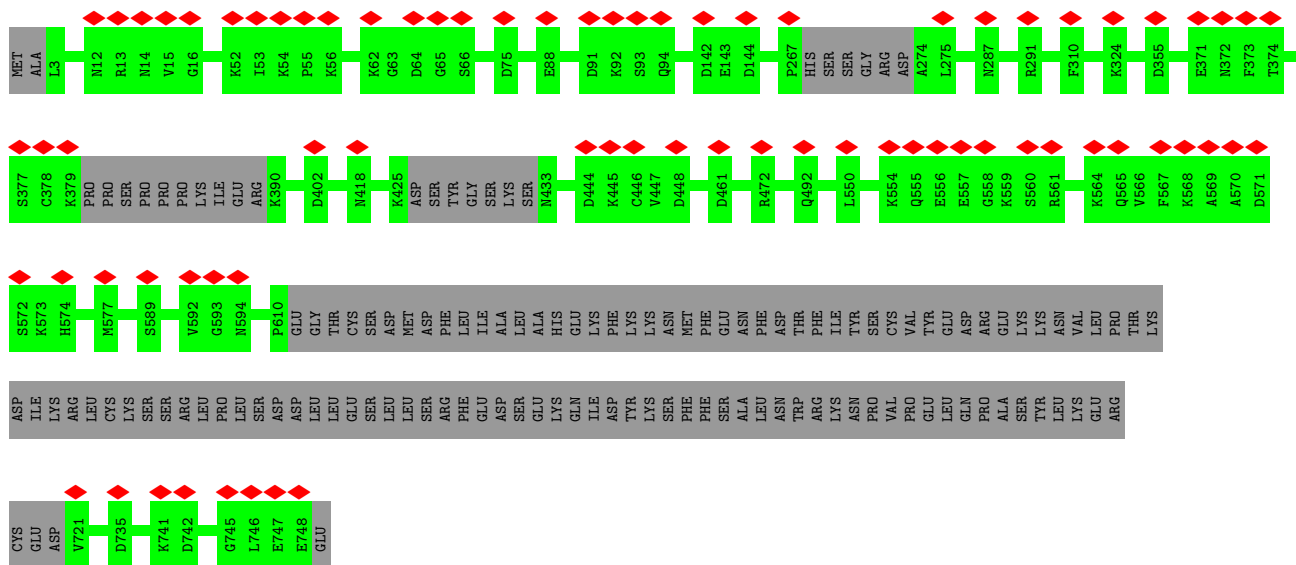
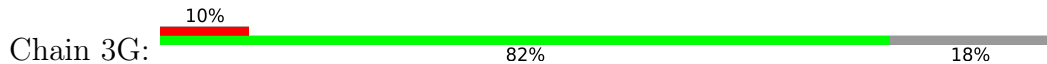
• Molecule 17: Cilia- and flagella-associated protein 276



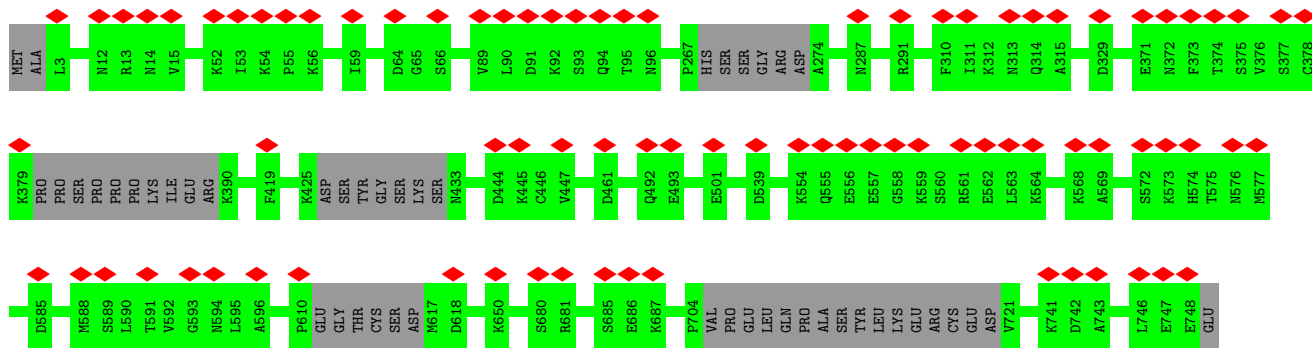
• Molecule 18: Dynein regulatory complex subunit 3



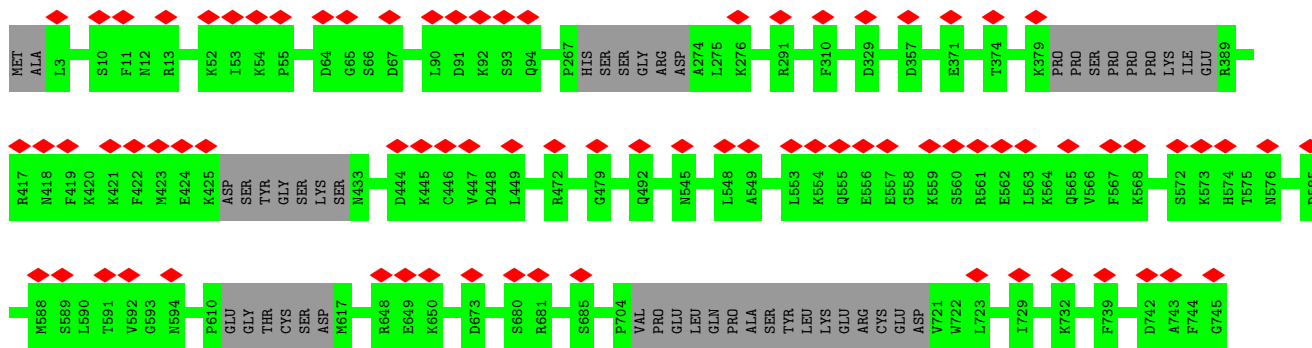
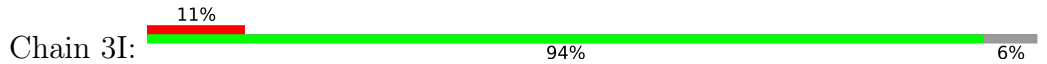
• Molecule 20: EF-hand domain-containing family member C2



• Molecule 20: EF-hand domain-containing family member C2

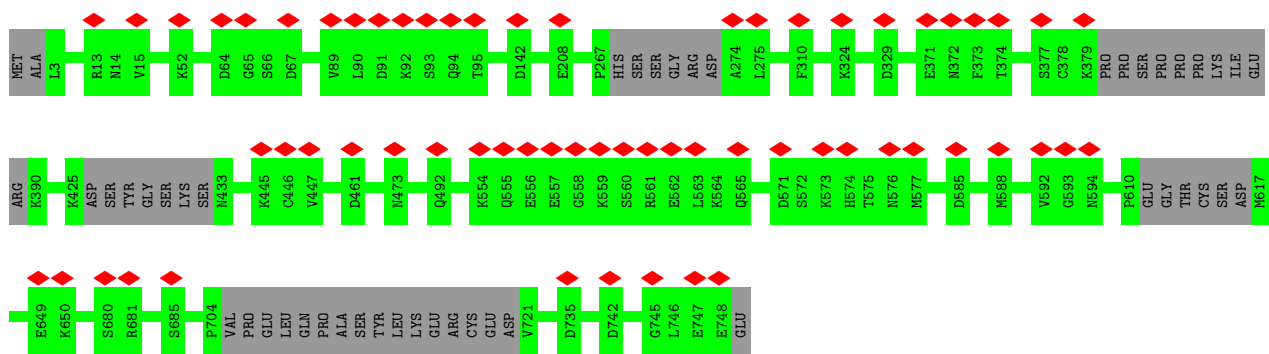


• Molecule 20: EF-hand domain-containing family member C2

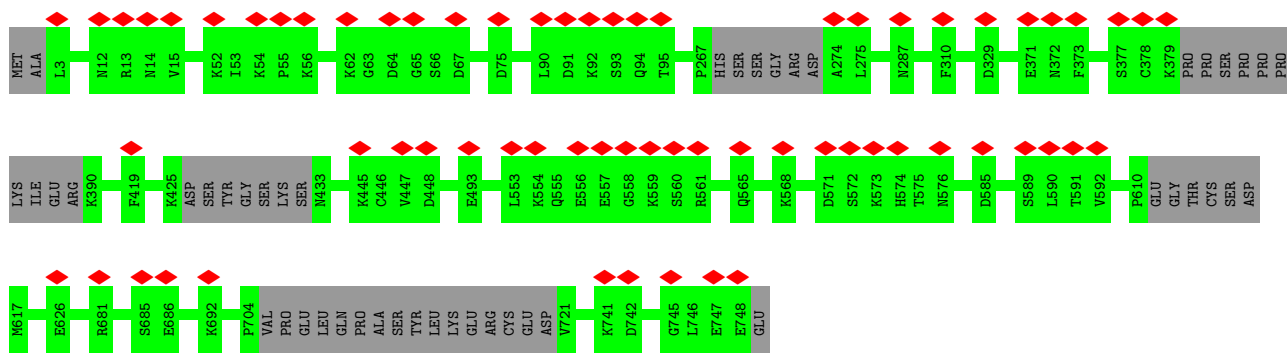




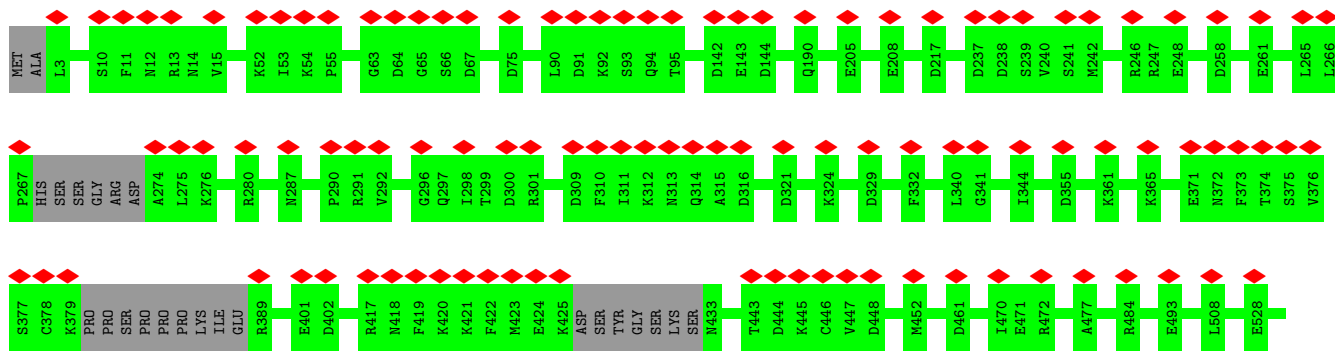
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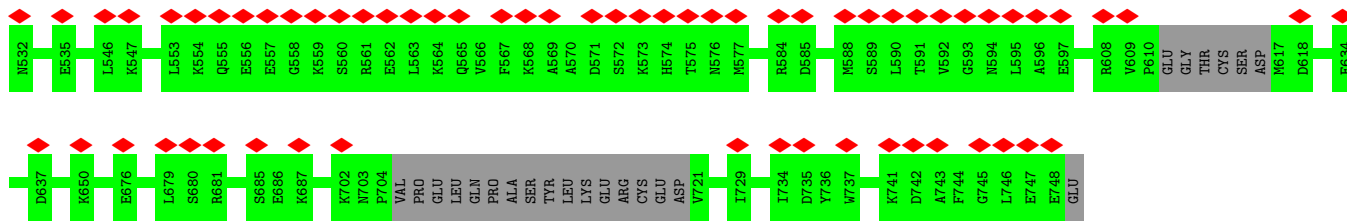


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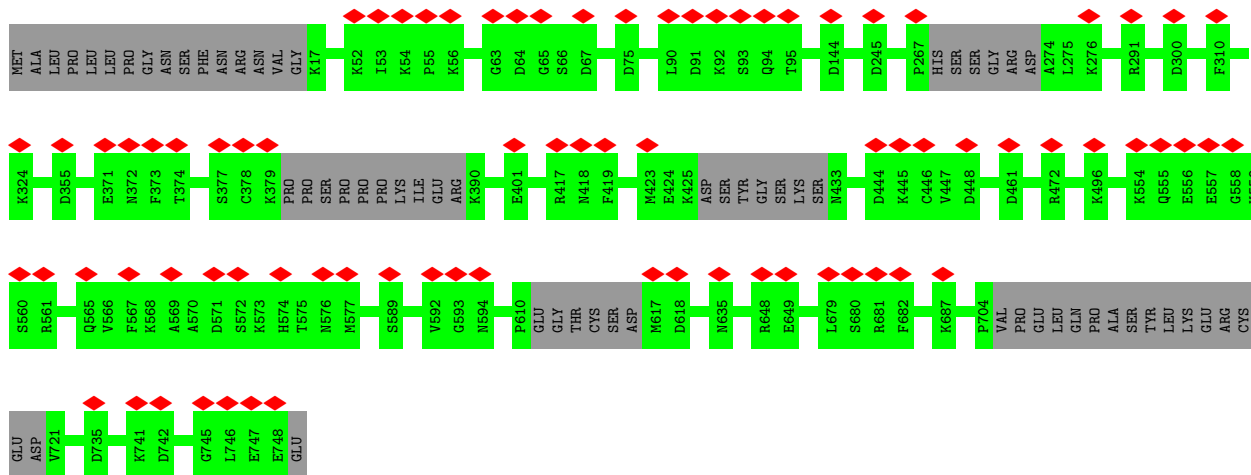
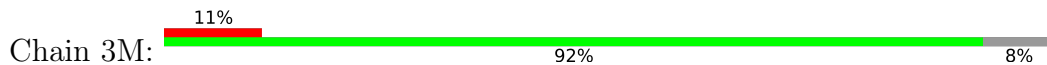


• Molecule 20: EF-hand domain-containing family member C2

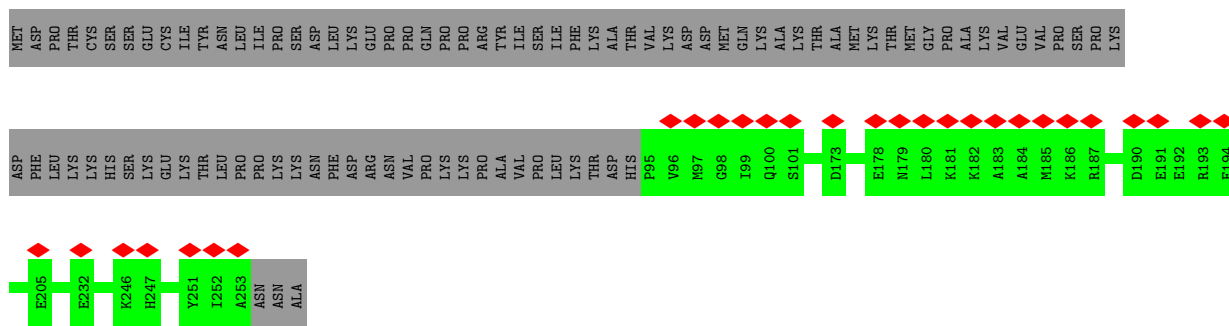




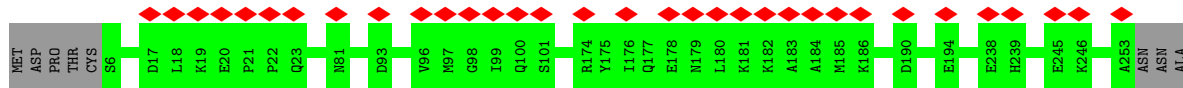
• Molecule 20: EF-hand domain-containing family member C2



• Molecule 21: Enkurin

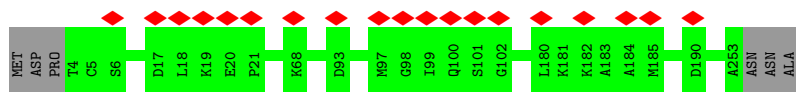


• Molecule 21: Enkurin

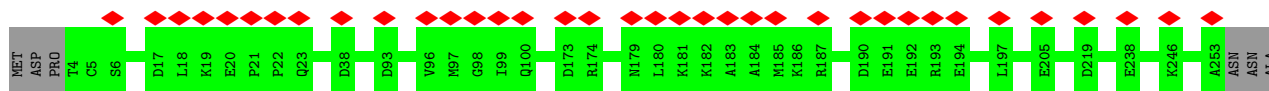


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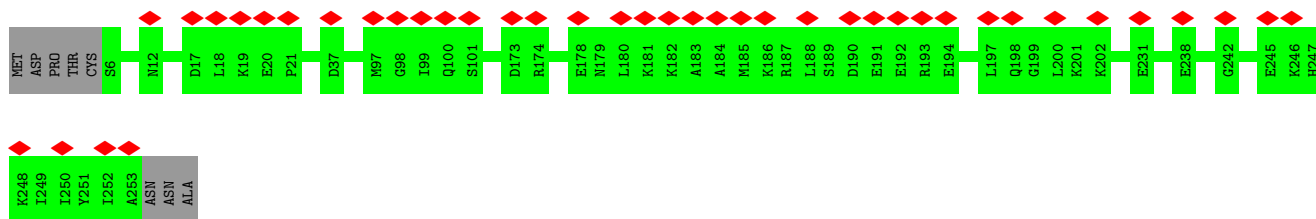




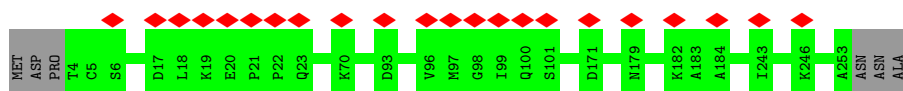
• Molecule 21: Enkurin



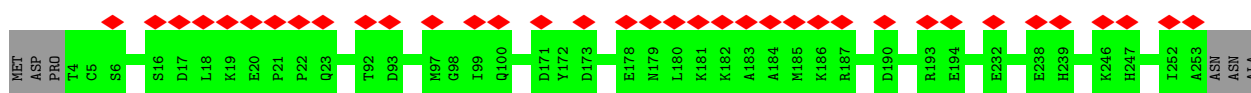
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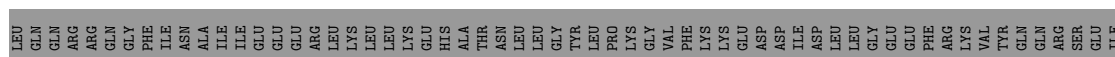
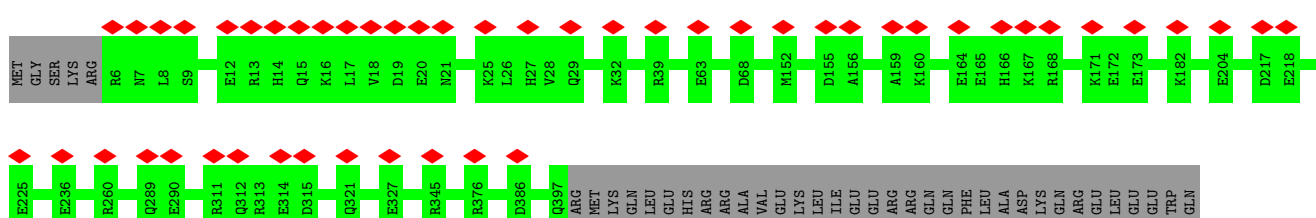
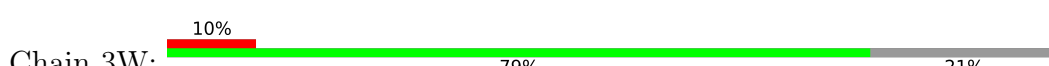
• Molecule 21: Enkurin



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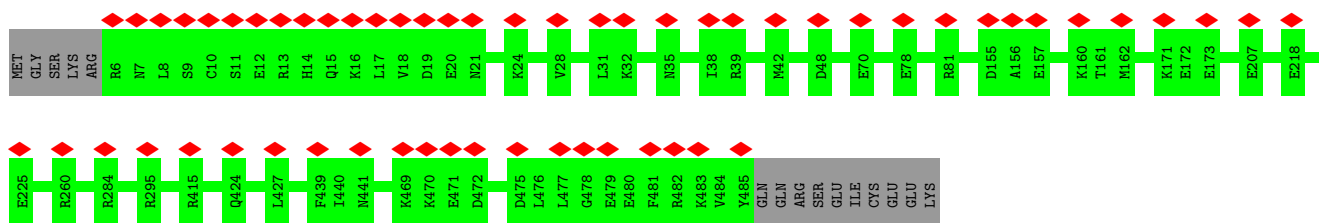


• Molecule 22: Meiosis-specific nuclear structural protein 1

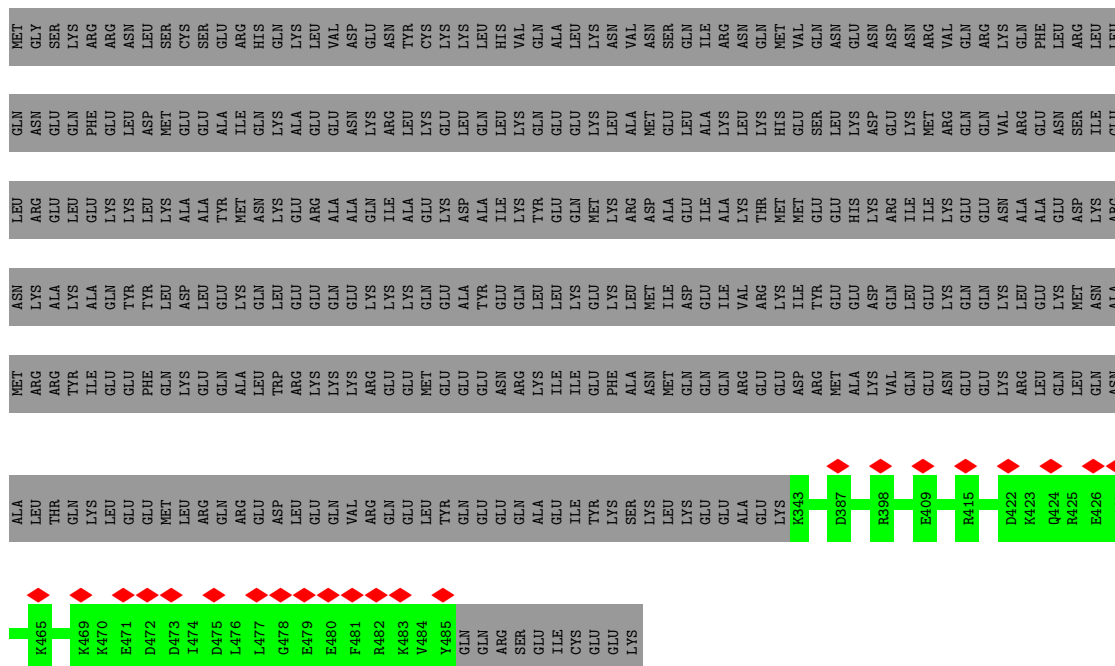


CYS
GLU
GLU
LYS

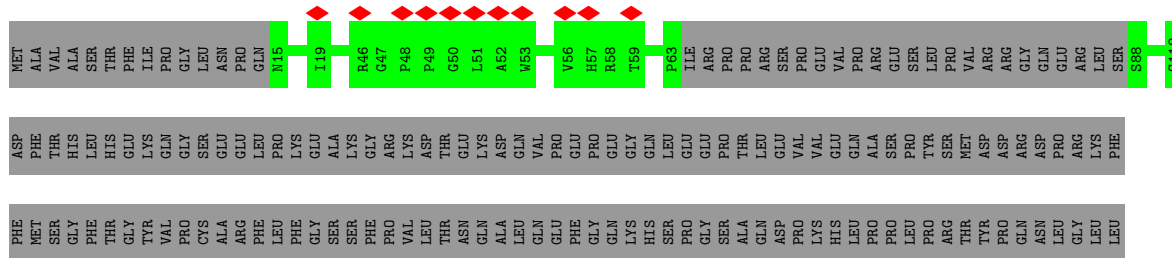
- Molecule 22: Meiosis-specific nuclear structural protein 1



- Molecule 22: Meiosis-specific nuclear structural protein 1



- Molecule 23: Protein FAM166B



PRO	ASN	TYR	GLY	GLY	VAL	PRO	GLY	TYR	LYS	PHE	PHE	GLY	HIS	THR	PHE	THR	GLY	HIS	LEU	THR	THR	PHE	GLN	LYS	LEU	LEU	ALA
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• Molecule 23: Protein FAM166B



MET	ALA	VAL	ALA	ALA	THR	SER	THR	PHE	ILE	PRO	GLY	LEU	LEU	ASN	PRO	GLN	N15	P16	H17	Y18	I19	P20	G21	Y22	T23	C26	P27	L28	L29	R30	F31	S32	V33	G34	Q35	T36	Y37	G38	Q39	L44	L45	R46	G47	P48	P49	G50	L51	A52	W53	P54	P55	V56	H57	R58	T59	L60	L61	P62	P63	ILE
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ARG	PRO	PRO	ARG	SER	PRO	GLU	VAL	PRO	PRO	ARG	GLY	LEU	LEU	PRO	VAL	S88	S89	M90	I91	P92	G93	Y94	T95	G96	F97	V98	P99	R100	A101	Q102	F103	I104	F105	A106	K107	N108	C109	S110	Q111	V112	W113	A114	E115	A116	L117	S118	ASP	PHE	THR	HIS	HIS	LEU	HIS
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GLU	LYS	GLN	TYR	SER	GLY	LEU	LEU	PRO	LYS	ALA	LYS	ARG	LYS	THR	GLY	LYS	ASP	GLN	VAL	PRO	PRO	GLU	PRO	THR	LEU	GLY	VAL	VAL	GLY	GLY	ALA	S166	P167	Y168	S169	M170	D171	D172	R173	D174	P175	R176	K177	F178	F179	M180	G182	F183	T184
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G185	Y186	V187	P188	C189	A190	R191	F192	L193	F194	G195	S196	S197	F198	P199	V200	L201	T202	N203	Q204	A205	L206	Q207	E208	F209	G210	Q211	LYS	HIS	SER	PRO	GLY	SER	GLY	ALA	GLN	ASP	PRO	LYS	HIS	LEU	LEU	THR	PRO	ASN	GLY	LEU	LEU	PRO	ASN	TYR	GLY	TYR
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VAL	PRO	GLY	TYR	LYS	PHE	GLN	PHE	G253	H254	T255	F256	G257	H258	L259	T260	H261	D262	A263	L264	G265	L266	F269	Q270	K271	GLN	LEU	LEU	ALA
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• Molecule 23: Protein FAM166B



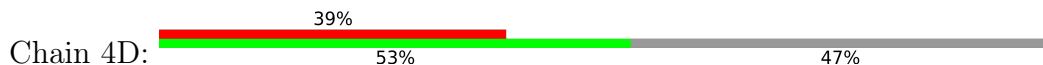
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S118	ASP	PHE	THR	HIS	HIS	GLY	GLN	GLY	PRO	LYS	GLU	LEU	LEU	LYS	ALA	ALA	L201	T202	N203	Q204	Q207	E208	F209	G210	Q211	LYS	HIS	SER	PRO	GLY	GLN	LEU	LEU	PRO	PRO	GLY	VAL	VAL	VAL	S166	P167	Y168	S169	M170	D171	D172	R173	D174	P175	R176
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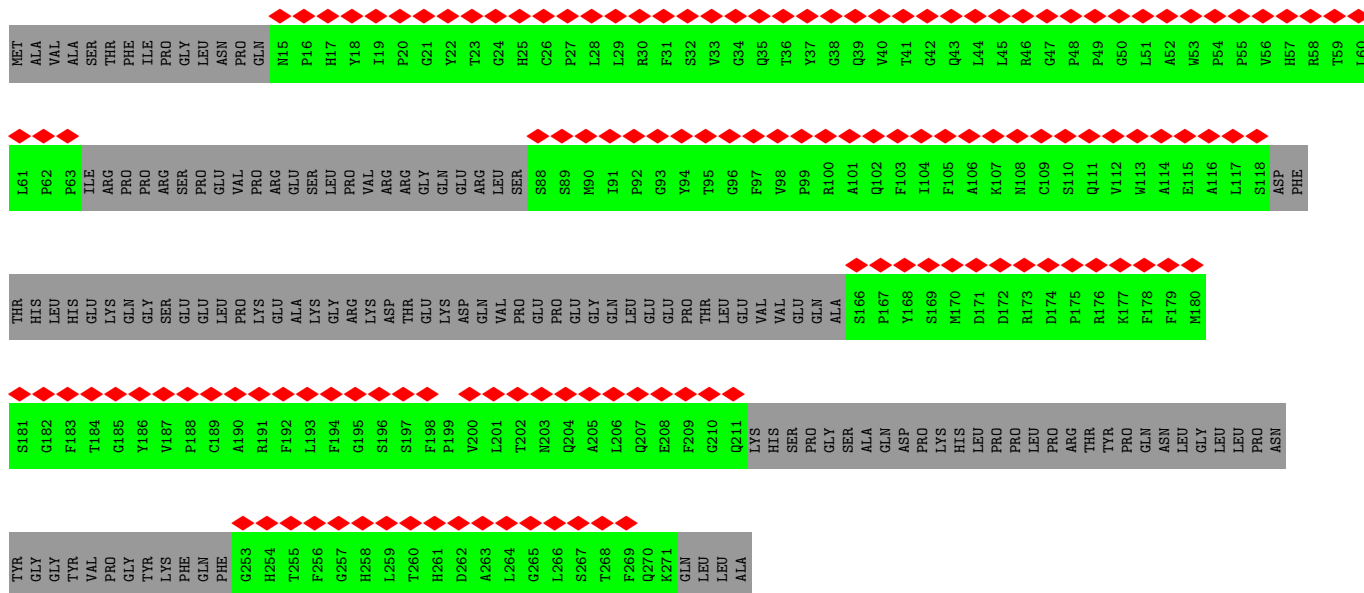
K177	F178	T184	C189	A190	R191	F198	L201	T202	N203	Q204	Q207	E208	F209	G210	Q211	LYS	HIS	SER	PRO	GLY	GLN	LEU	LEU	PRO	PRO	GLY	VAL	VAL	VAL	GLN	ASN	LEU	LEU	GLY	LEU	LEU	LEU	PRO	ASN	TYR	GLY	TYR	VAL	VAL	PRO	GLY	TYR	LYS	LYS	PHE
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GLN	PHE	G253	H254	T255	F256	G257	H258	L259	T260	H261	D262	A263	L264	G265	L266	F269	Q270	K271	GLN	LEU	LEU	ALA
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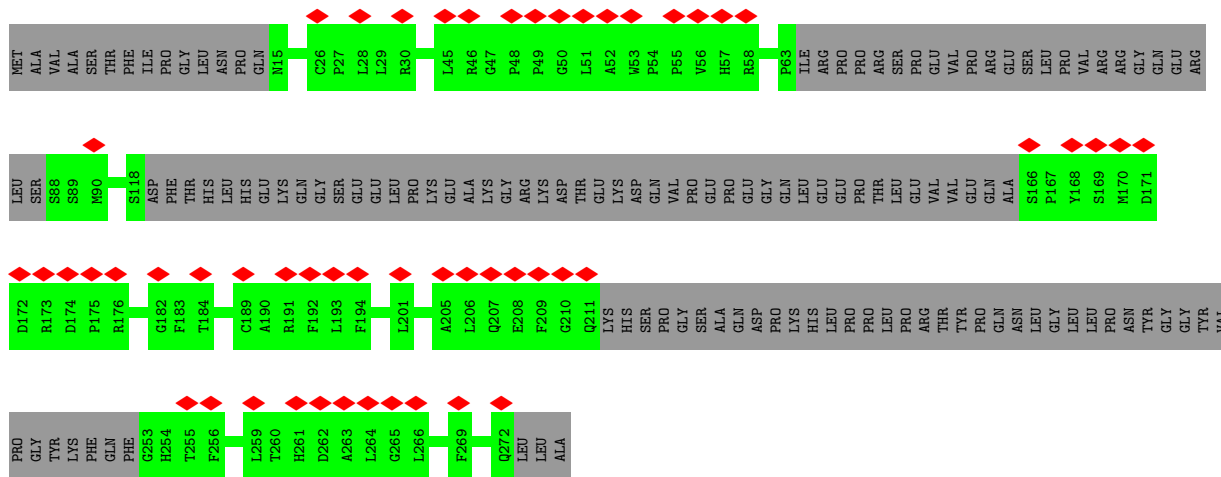
• Molecule 23: Protein FAM166B



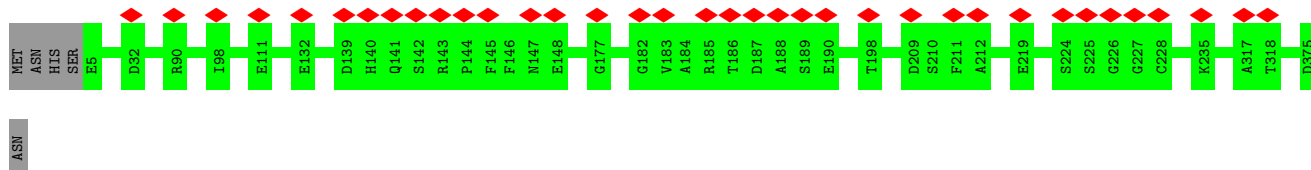
MET	ALA	VAL	VAL	SER	THR	PHE	ILE	PRO	GLY	LEU	LEU	ASN	PRO	GLN	N15	P16	H17	Y18	T23	C26	P27	L28	L29	R30	F31	Q35	G42	Q43	L44	L45	R46	G47	P48	P49	G50	L51	A52	W53	P54	P55	V56	H57	R58	T59	L60	P63	ILE	ARG	PRO	PRO	ARG	SER	PRO	GLU	VAL
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• Molecule 23: Protein FAM166B

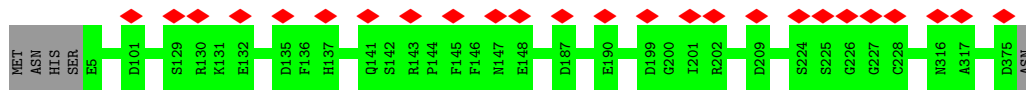


• Molecule 24: Nucleoside diphosphate kinase 7

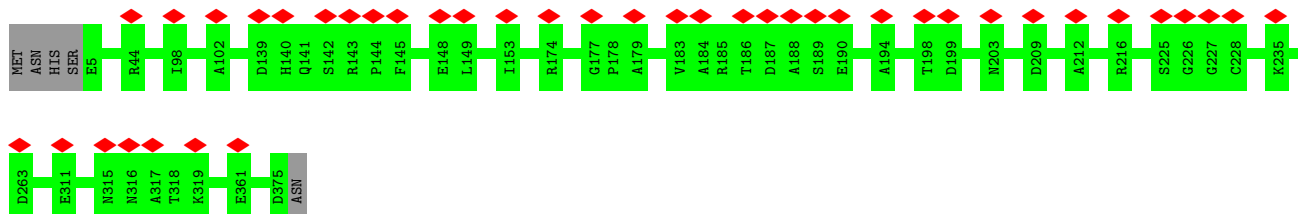


• Molecule 24: Nucleoside diphosphate kinase 7

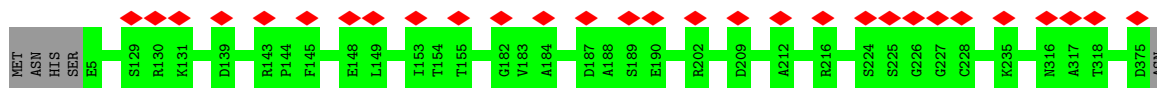




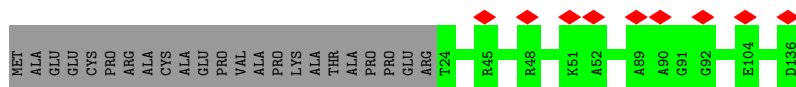
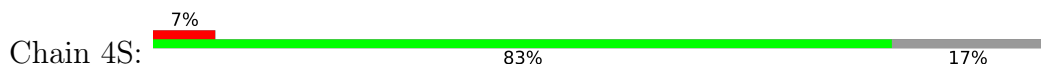
• Molecule 24: Nucleoside diphosphate kinase 7



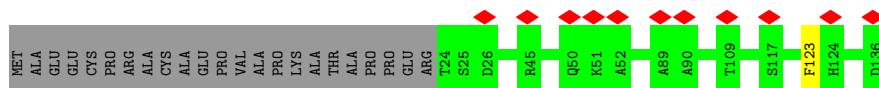
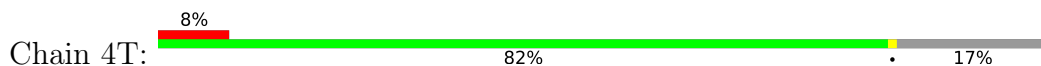
• Molecule 24: Nucleoside diphosphate kinase 7



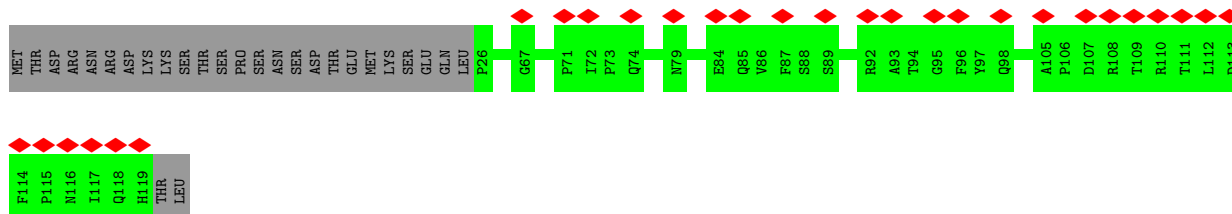
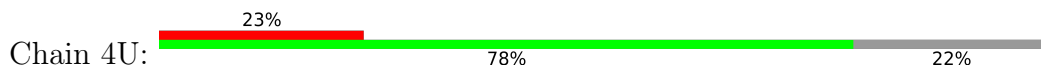
• Molecule 25: Piercer of microtubule wall 1 protein



• Molecule 25: Piercer of microtubule wall 1 protein

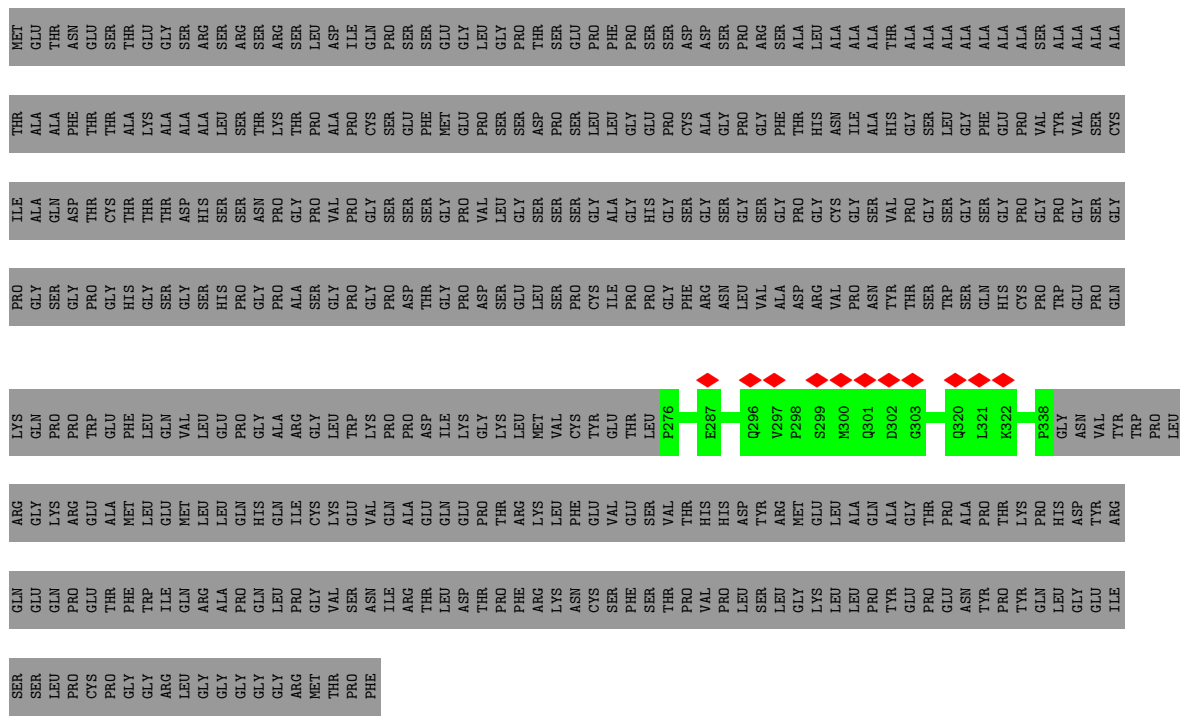


• Molecule 26: Piercer of microtubule wall 2 protein

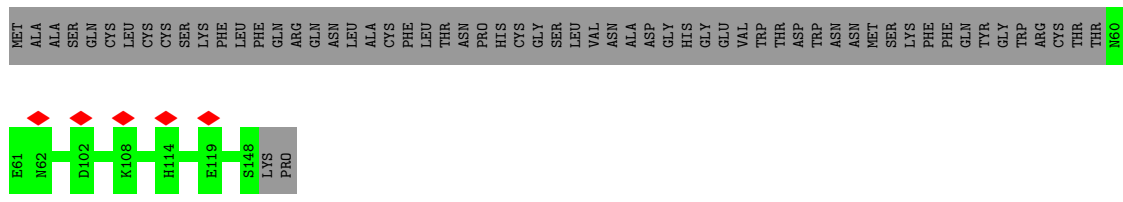


• Molecule 26: Piercer of microtubule wall 2 protein

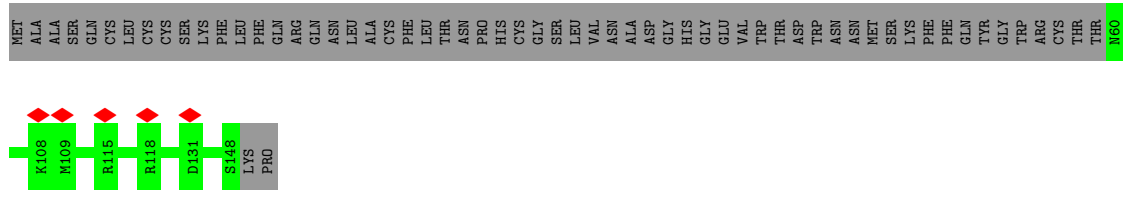




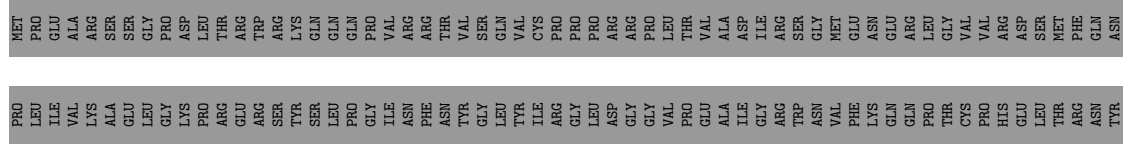
• Molecule 31: Uncharacterized protein CFAP68

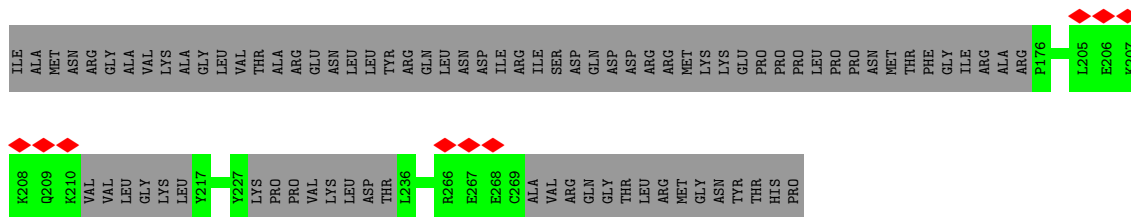


• Molecule 31: Uncharacterized protein CFAP68

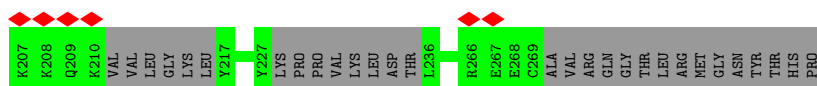
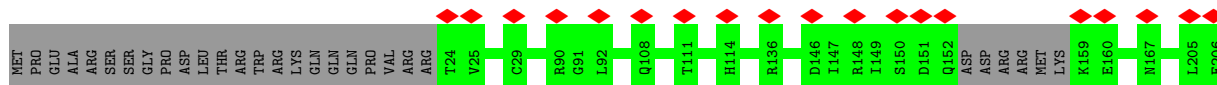
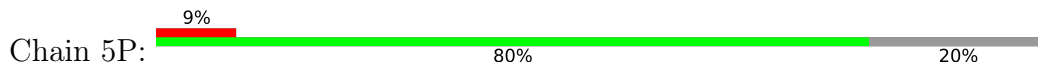


• Molecule 32: Cilia- and flagella-associated protein 77

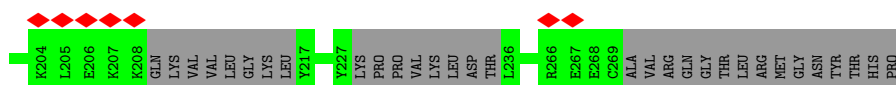
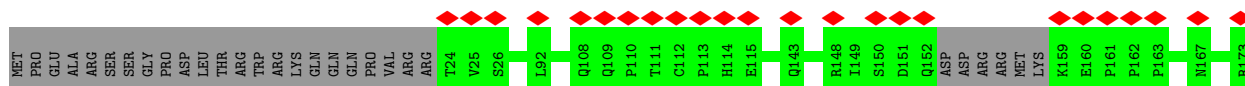
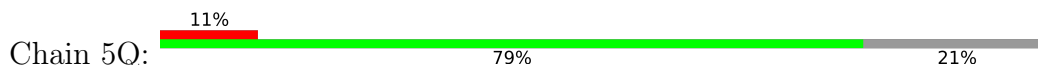




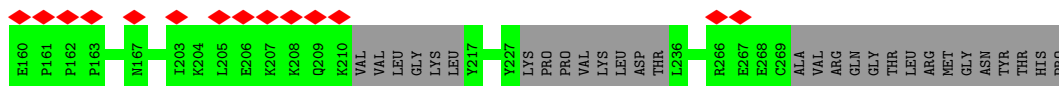
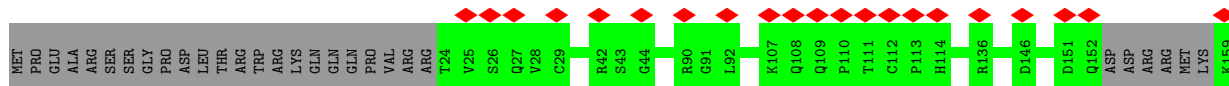
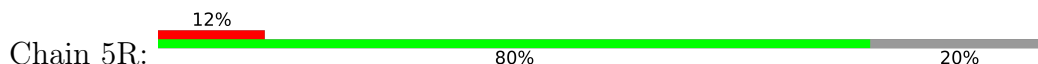
• Molecule 32: Cilia- and flagella-associated protein 77



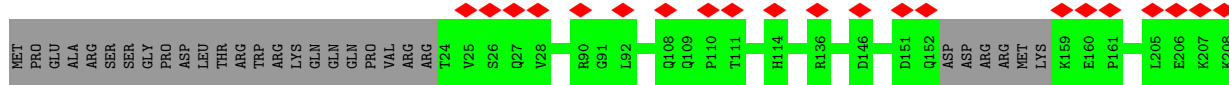
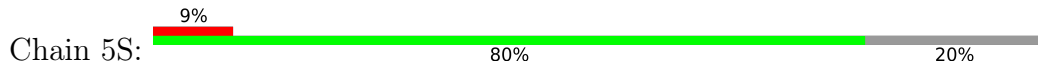
• Molecule 32: Cilia- and flagella-associated protein 77

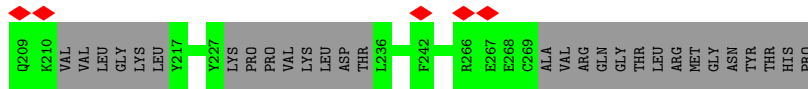


• Molecule 32: Cilia- and flagella-associated protein 77

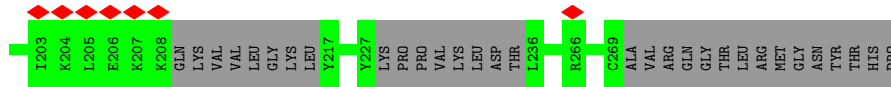
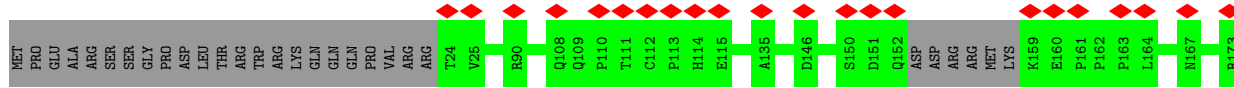
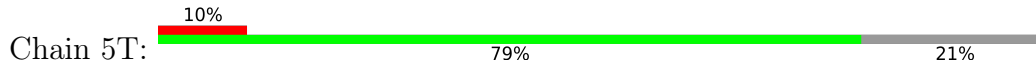


• Molecule 32: Cilia- and flagella-associated protein 77

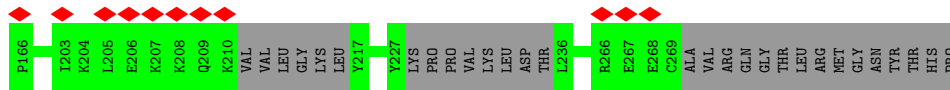
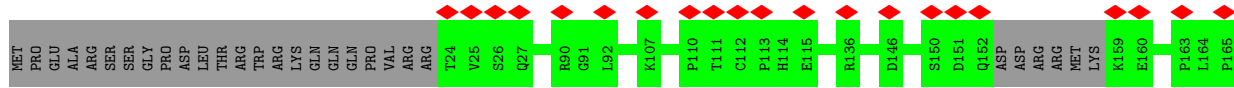
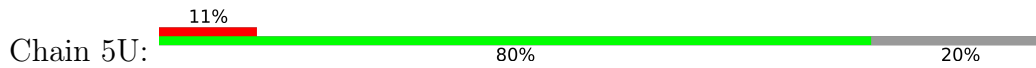




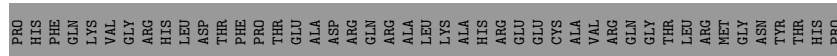
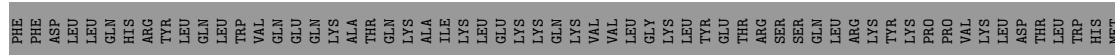
• Molecule 32: Cilia- and flagella-associated protein 77



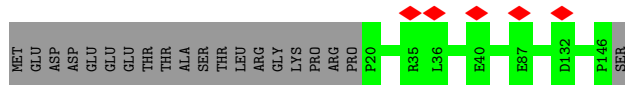
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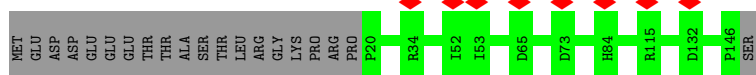
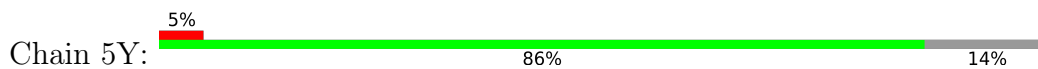
• Molecule 32: Cilia- and flagella-associated protein 77



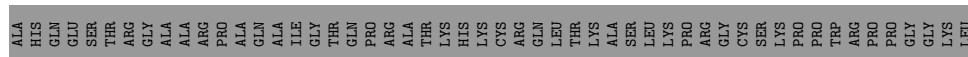
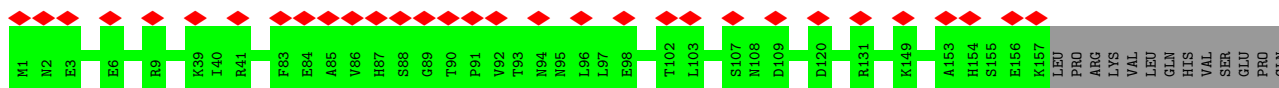
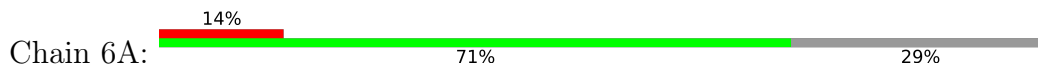
• Molecule 33: Uncharacterized protein CFAP90



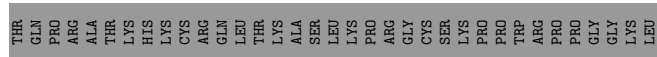
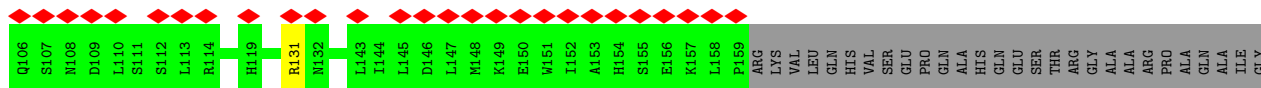
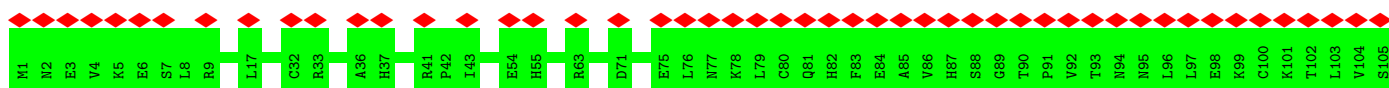
• Molecule 33: Uncharacterized protein CFAP90



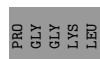
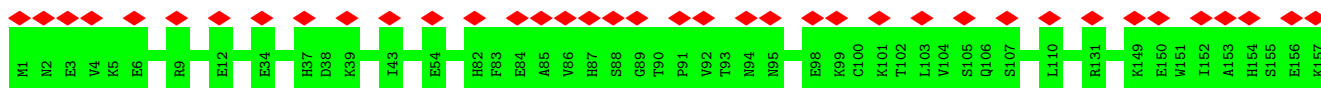
• Molecule 34: Sperm acrosome-associated protein 9



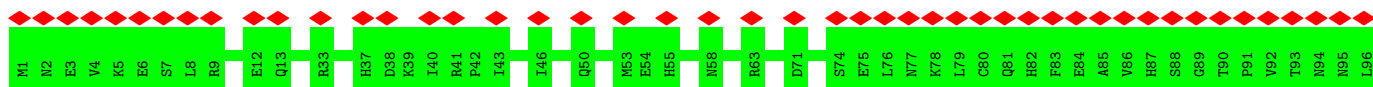
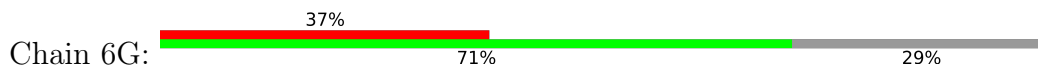
• Molecule 34: Sperm acrosome-associated protein 9

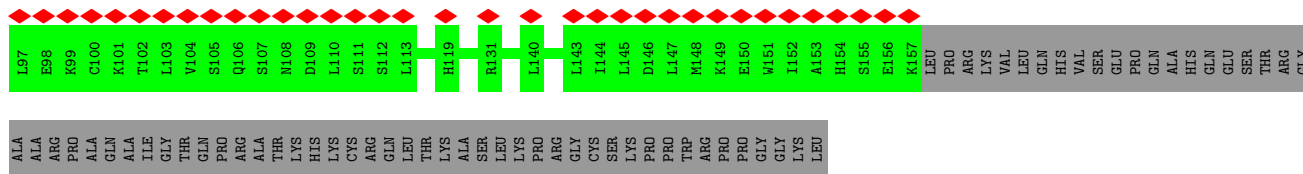


• Molecule 34: Sperm acrosome-associated protein 9

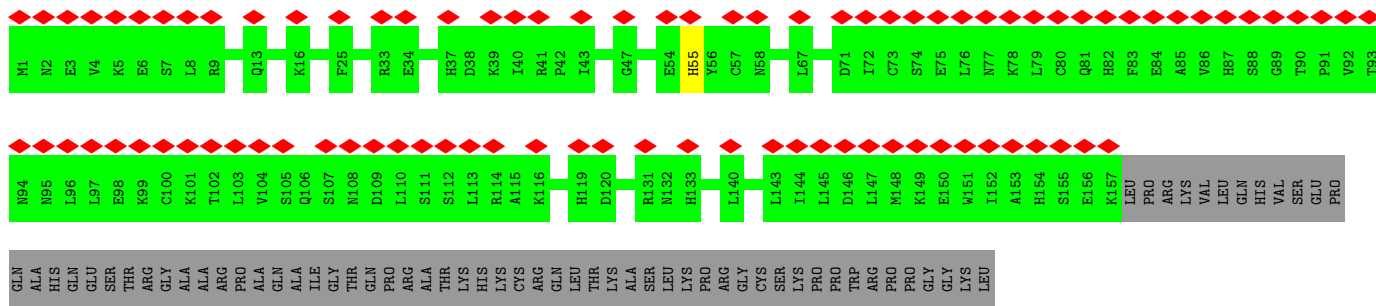
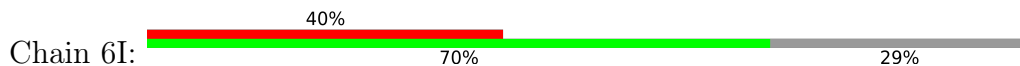


• Molecule 34: Sperm acrosome-associated protein 9

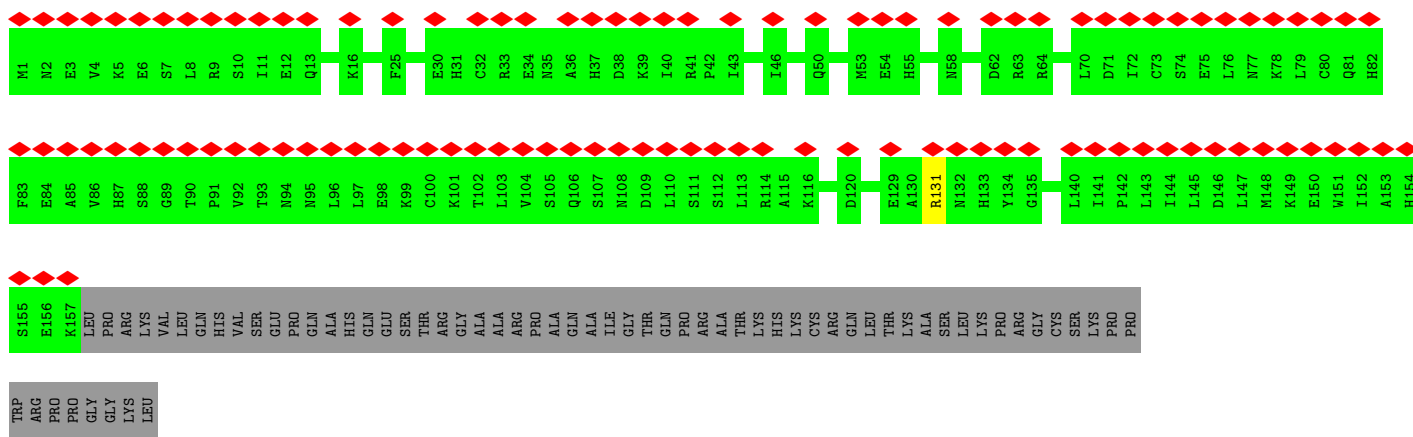
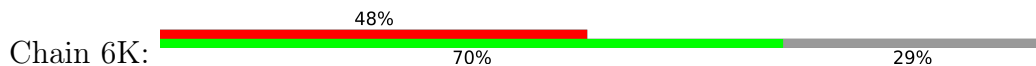




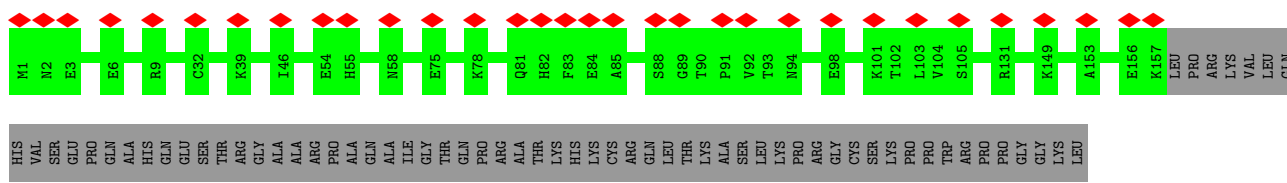
• Molecule 34: Sperm acrosome-associated protein 9



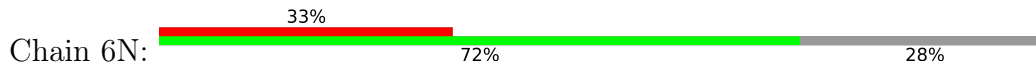
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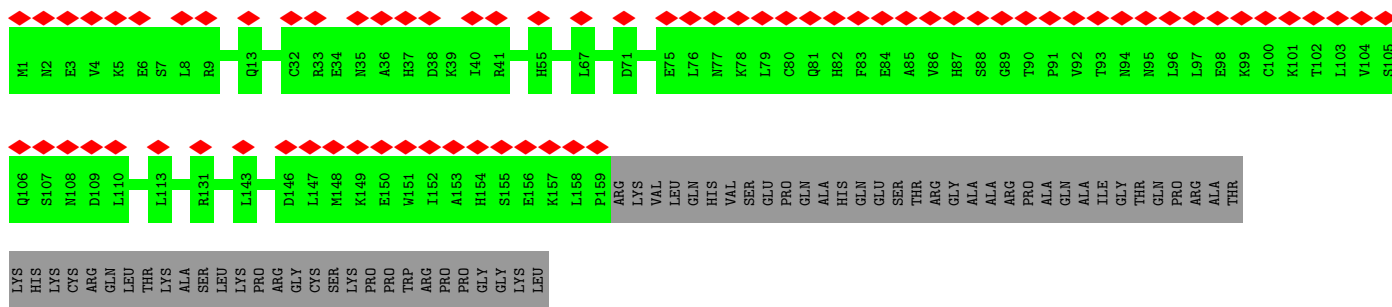


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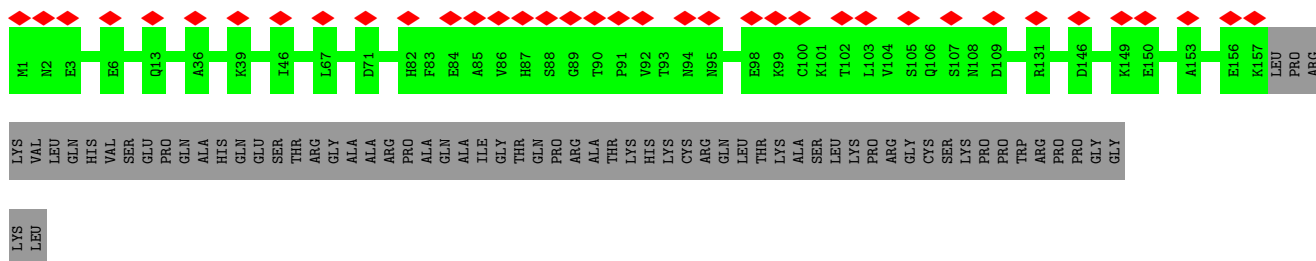


• Molecule 34: Sperm acrosome-associated protein 9

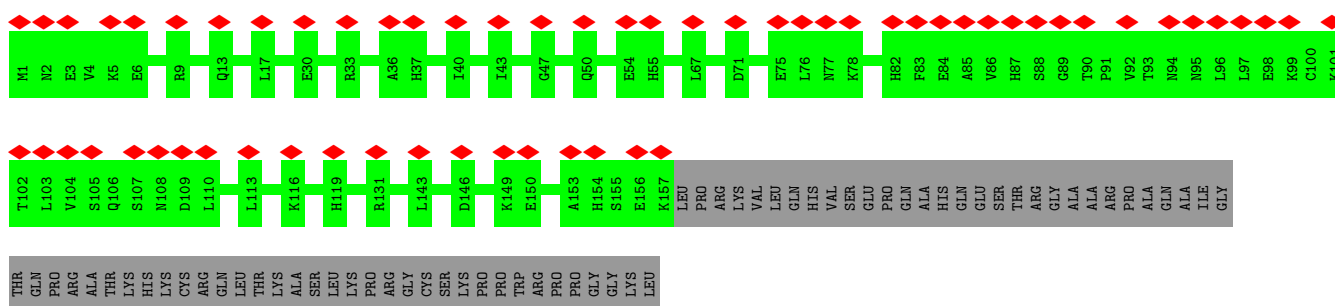
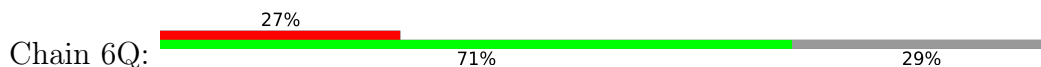




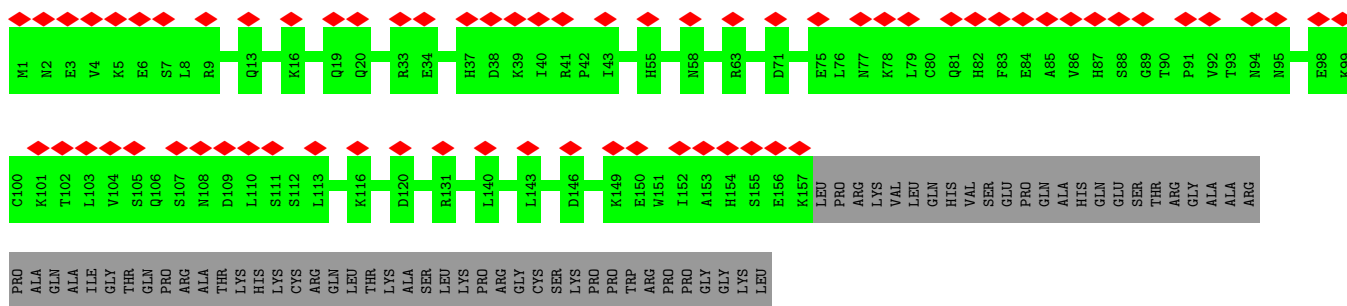
• Molecule 34: Sperm acrosome-associated protein 9



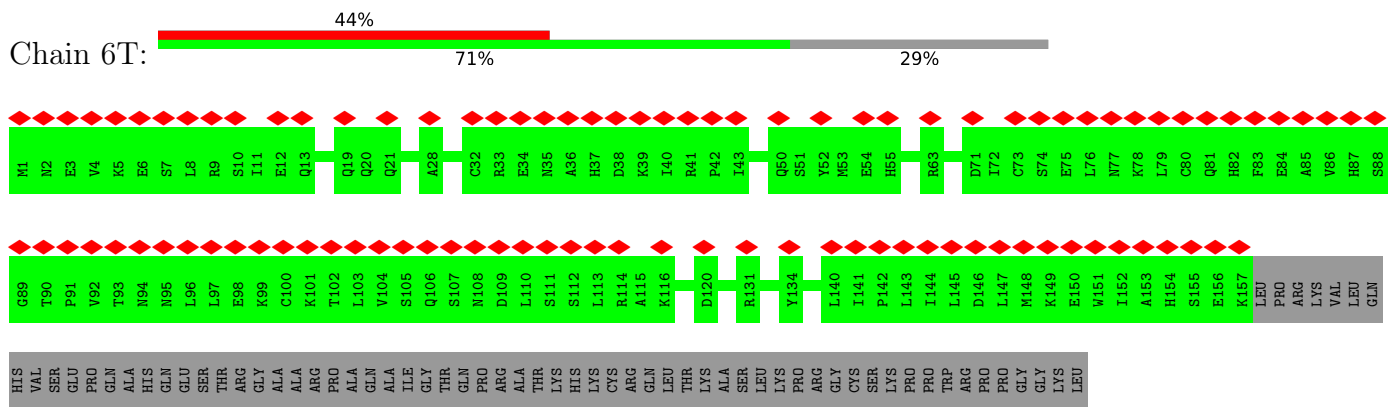
• Molecule 34: Sperm acrosome-associated protein 9



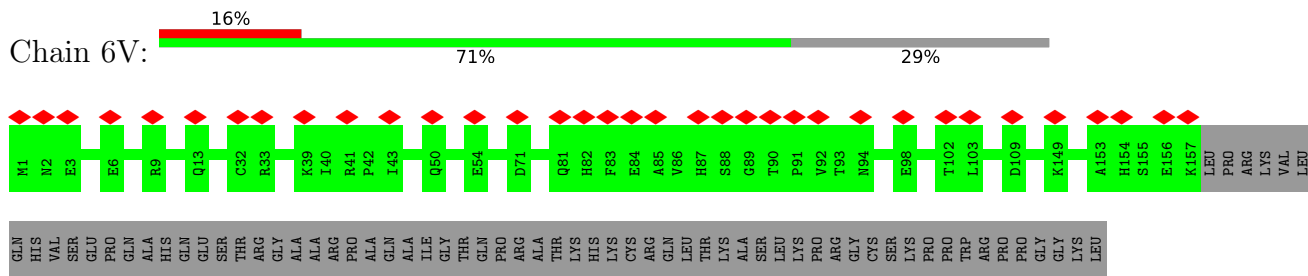
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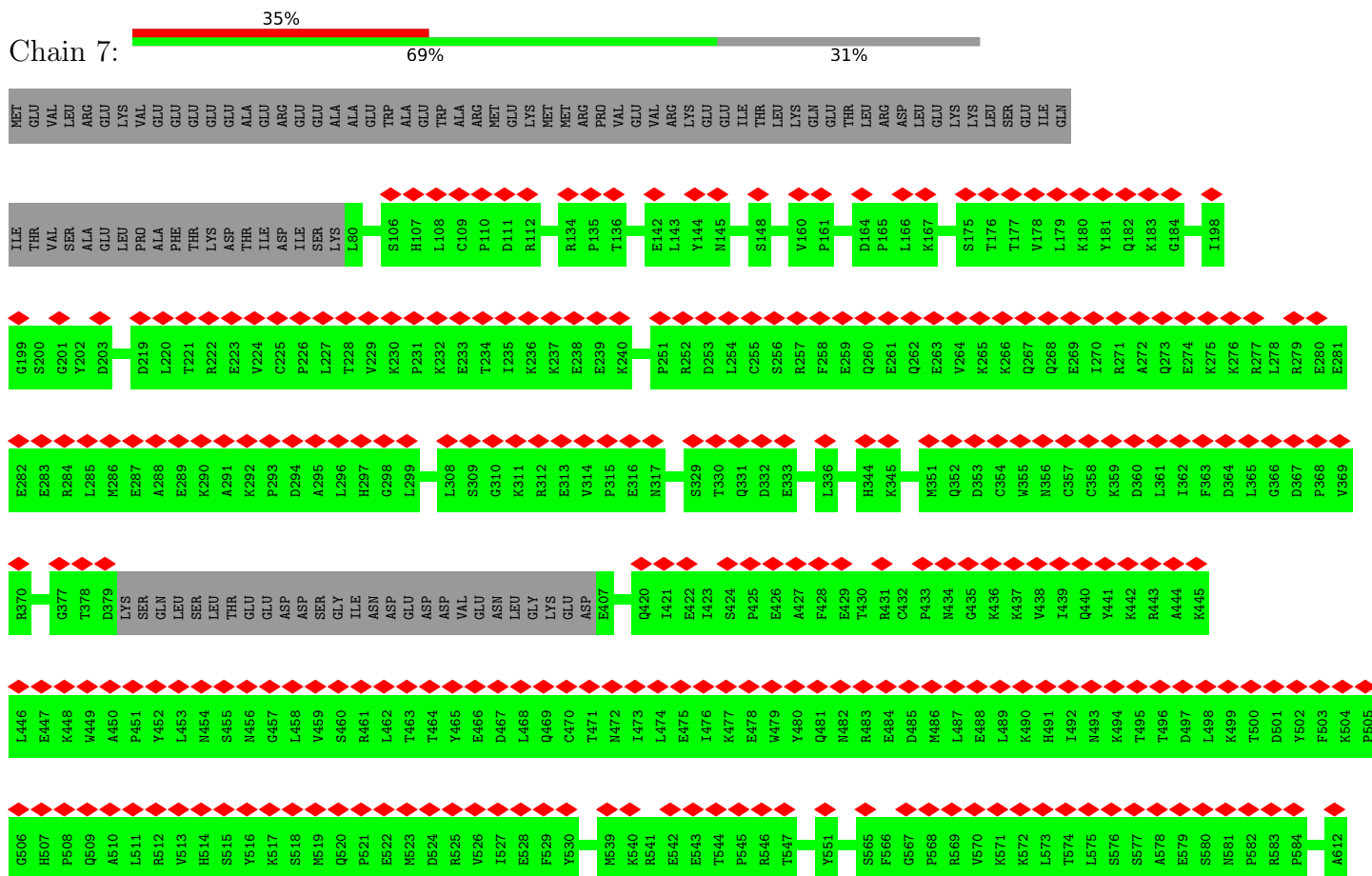
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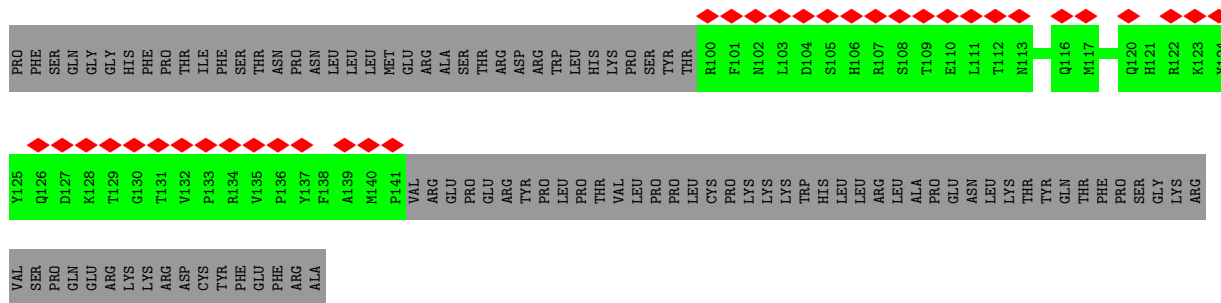


• Molecule 34: Sperm acrosome-associated protein 9

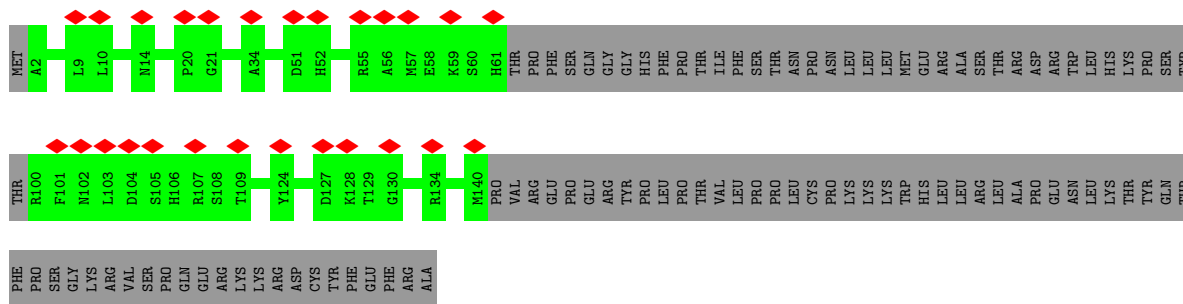


• Molecule 35: Dynein regulatory complex subunit 7

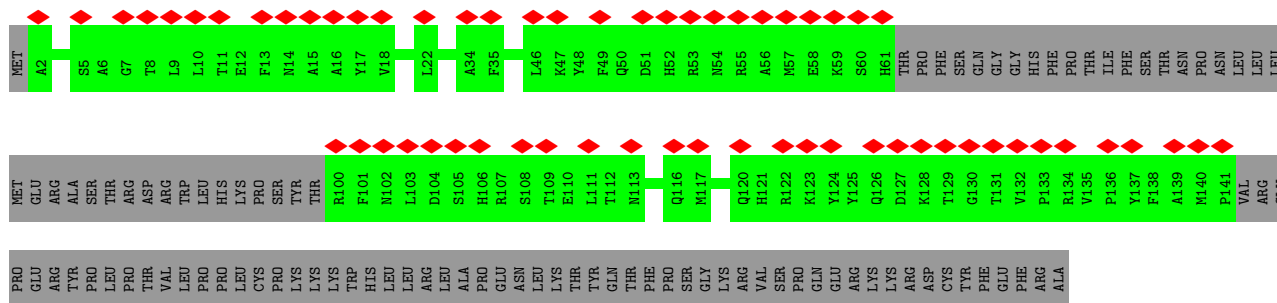




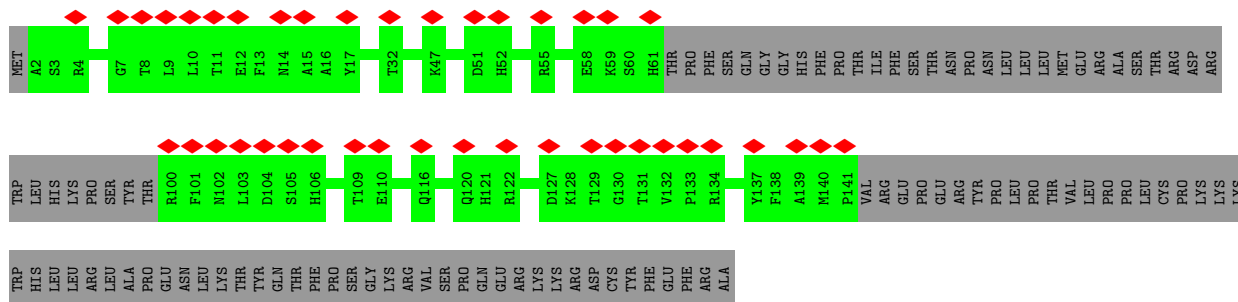
• Molecule 36: Protein FAM166C



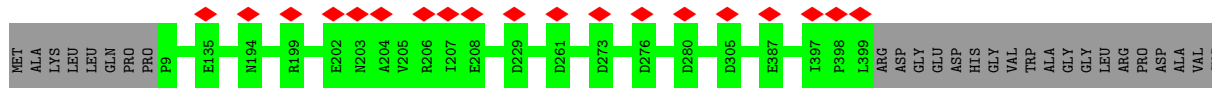
• Molecule 36: Protein FAM166C



• Molecule 36: Protein FAM166C



• Molecule 38: Tektin-1

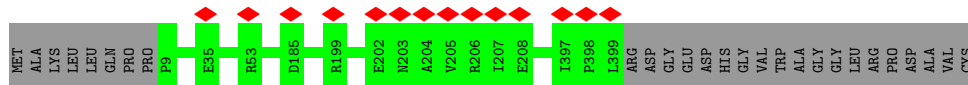


• Molecule 38: Tektin-1

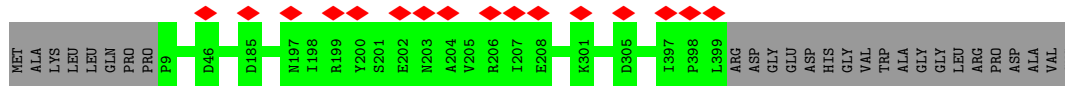


VAL
CYS

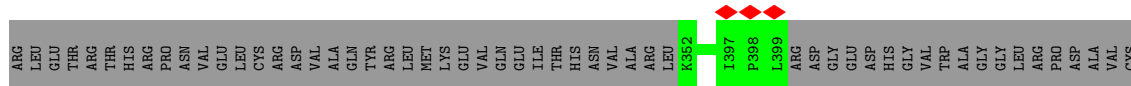
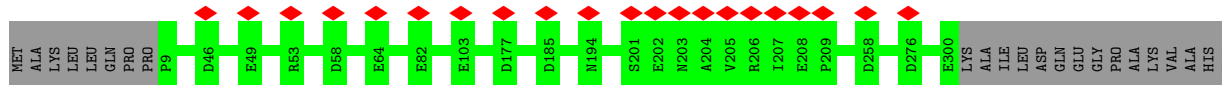
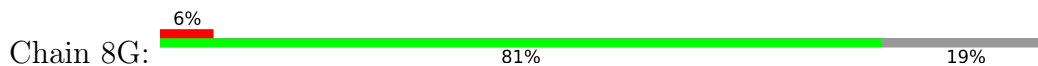
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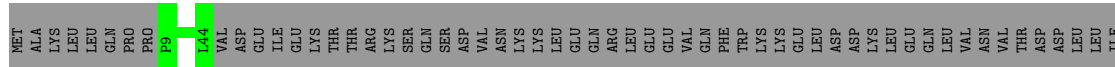
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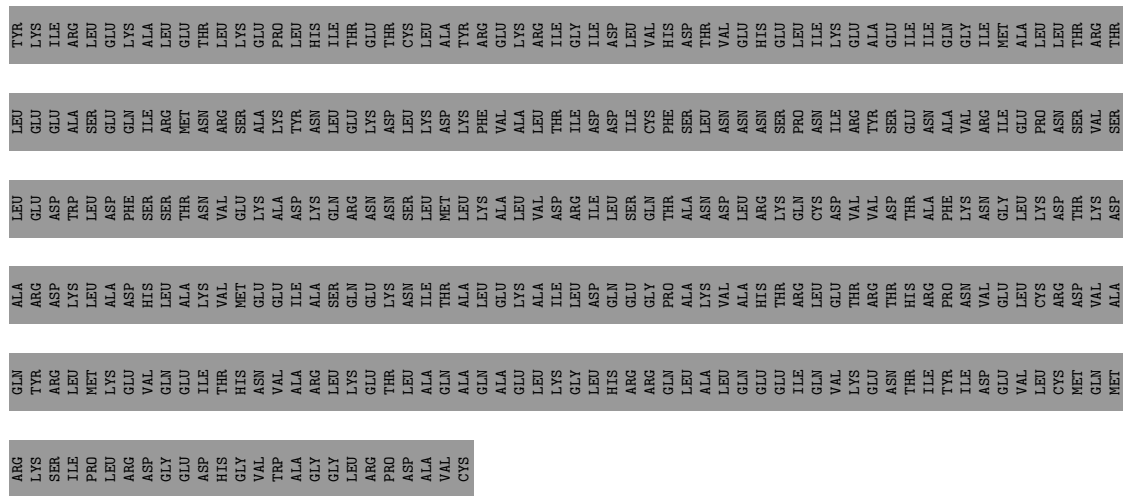


• Molecule 38: Tektin-1

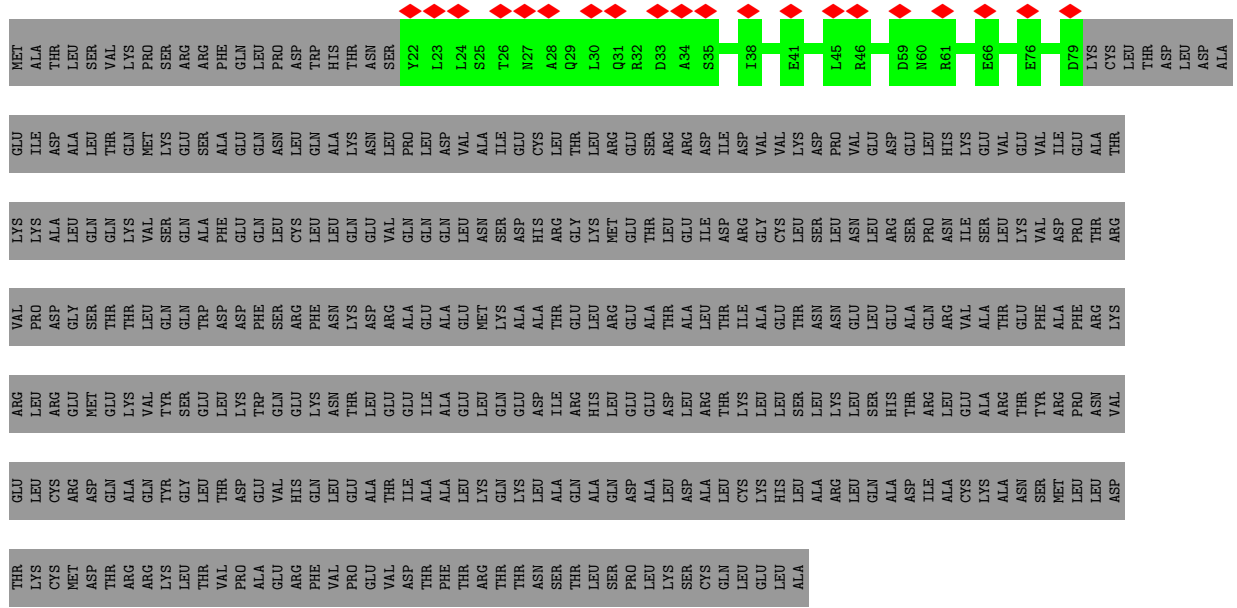


• Molecule 38: Tektin-1

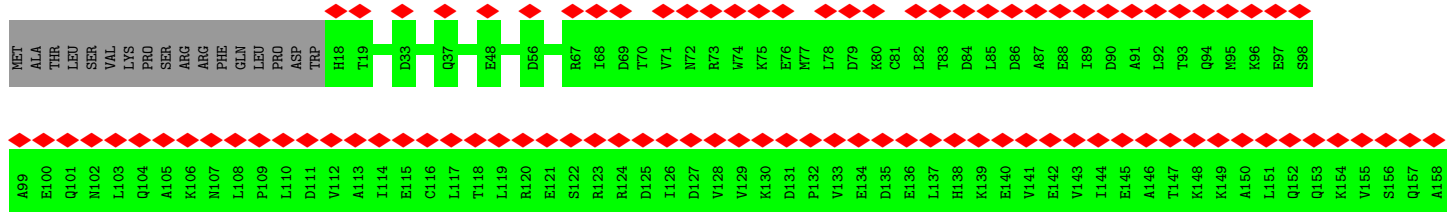
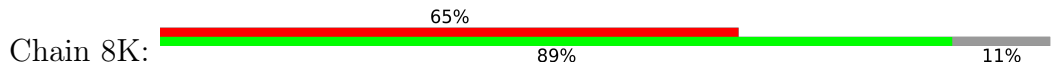


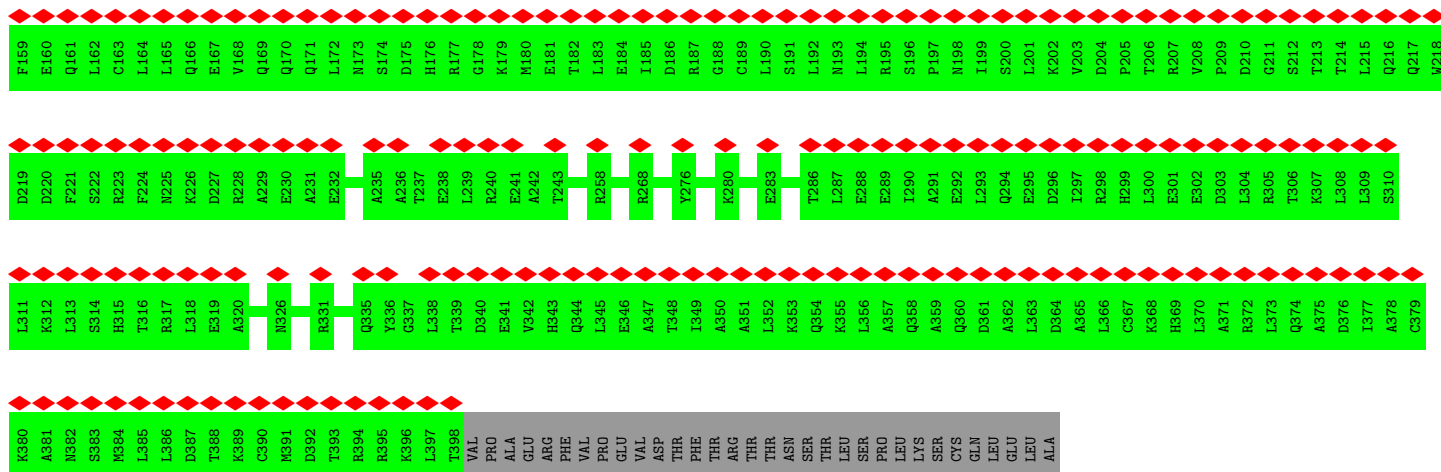


• Molecule 39: Tektin-2

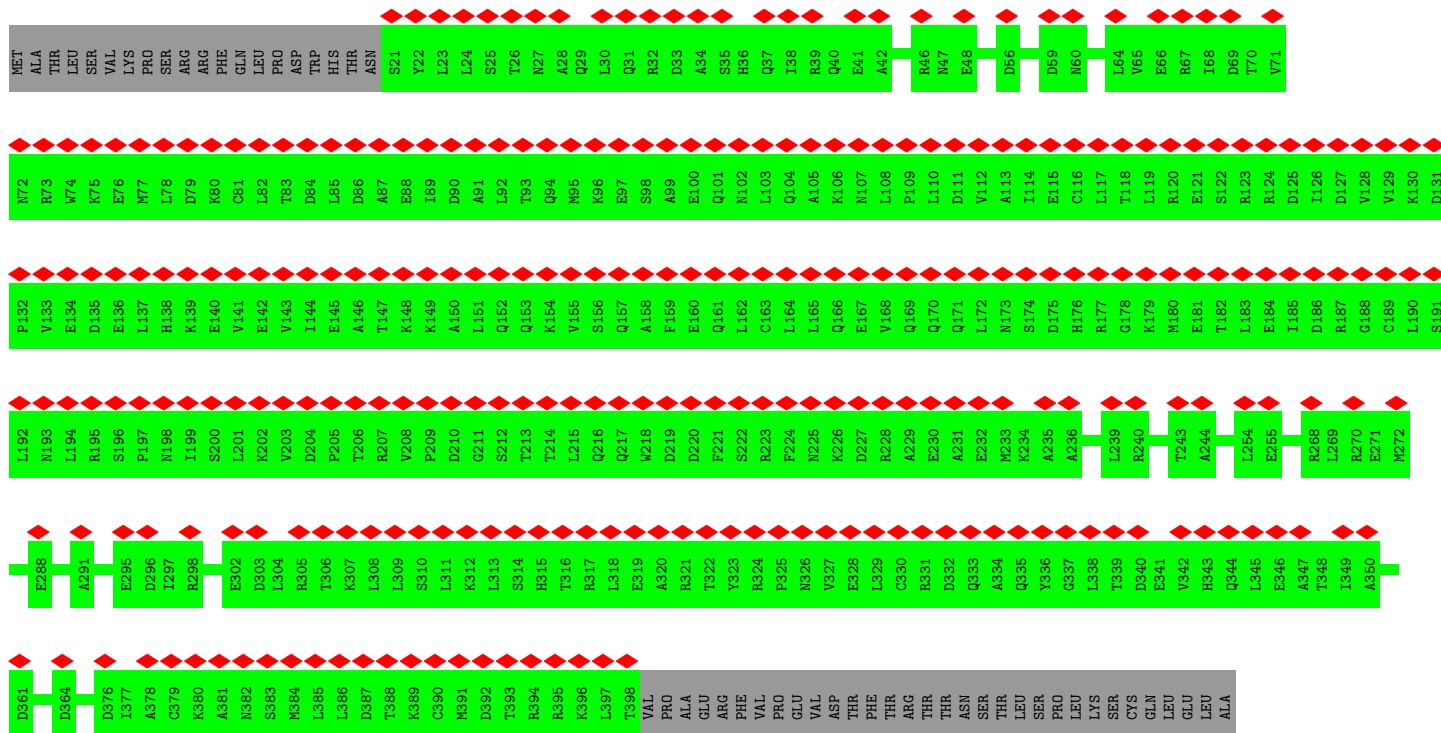
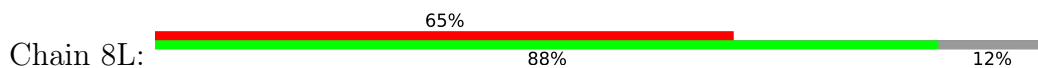


• Molecule 39: Tektin-2

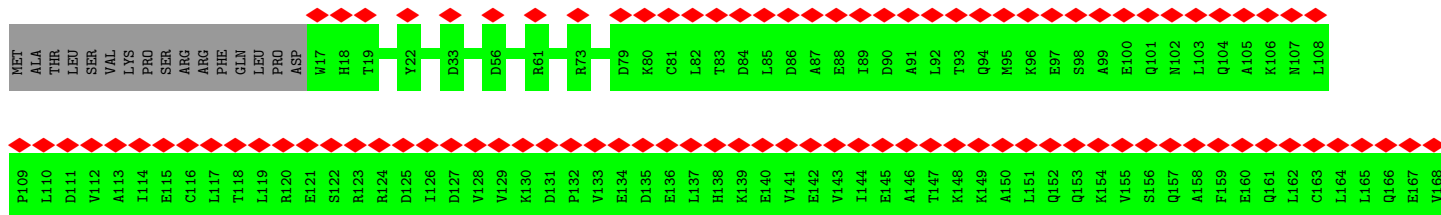
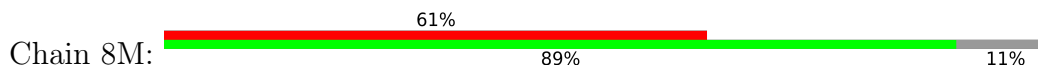


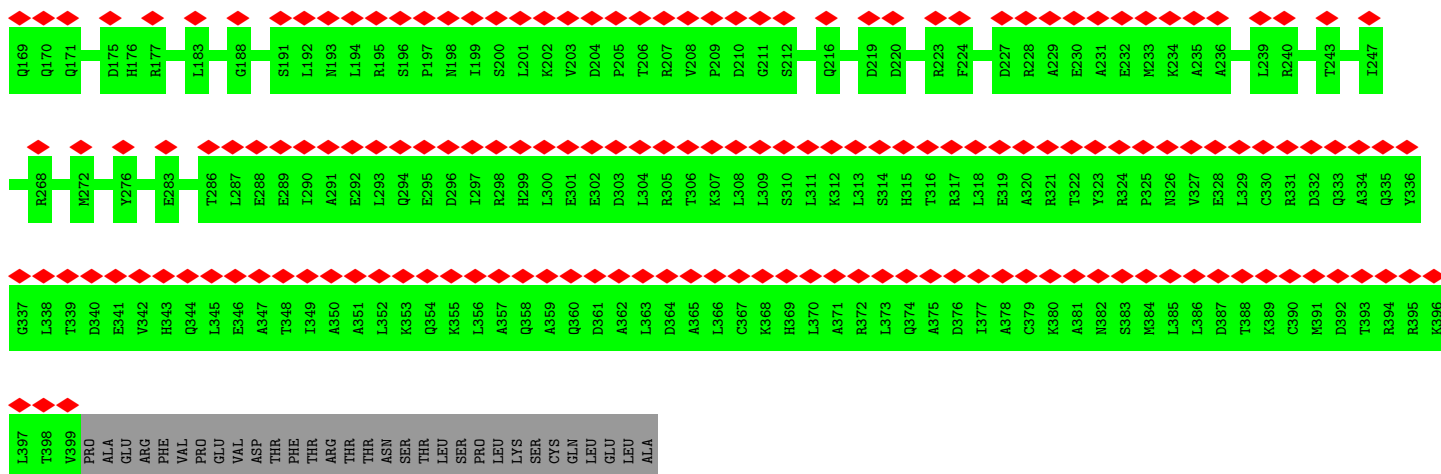


• Molecule 39: Tektin-2

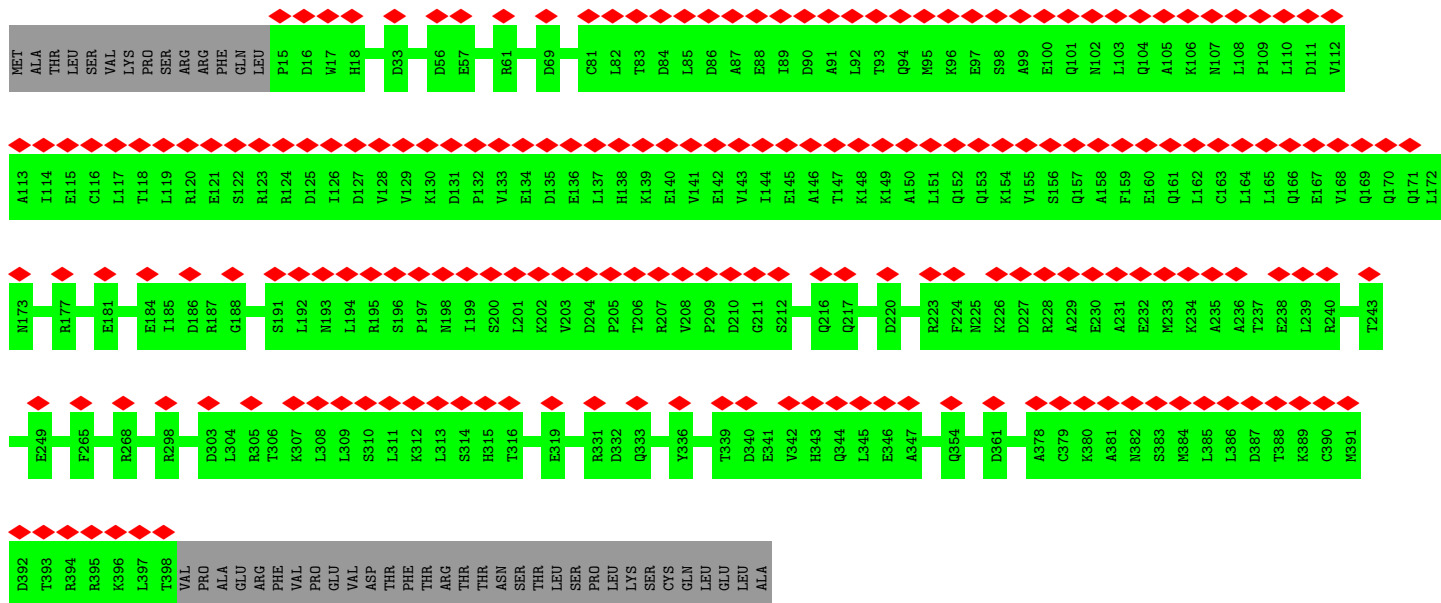
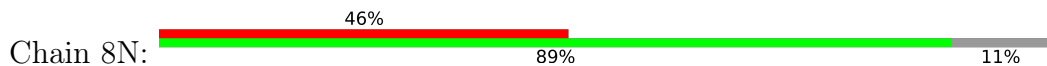


• Molecule 39: Tektin-2

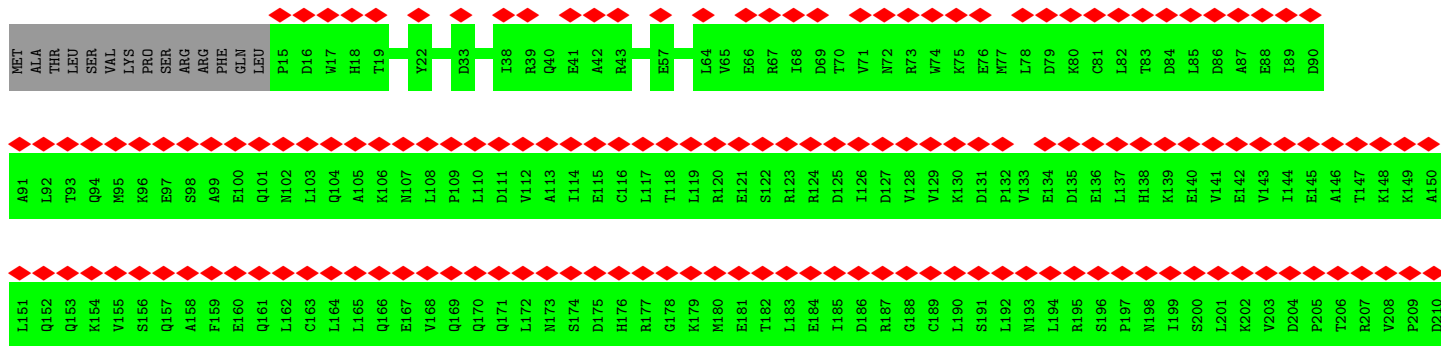
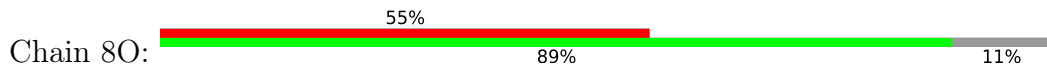


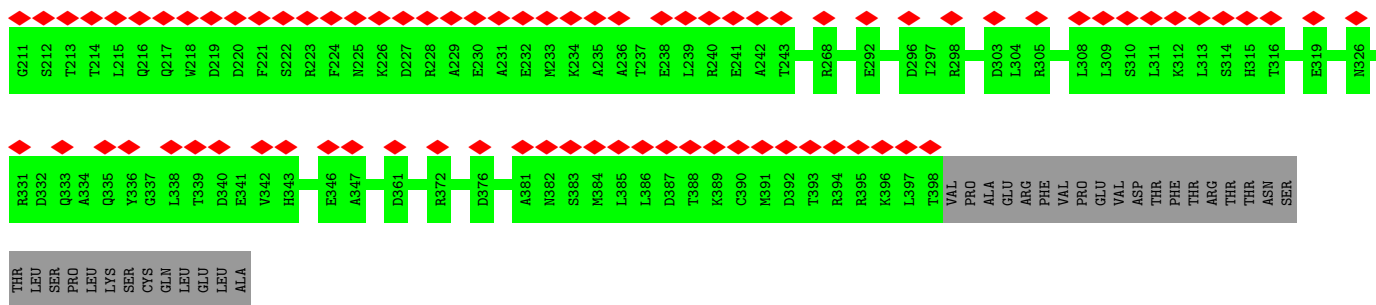


• Molecule 39: Tektin-2

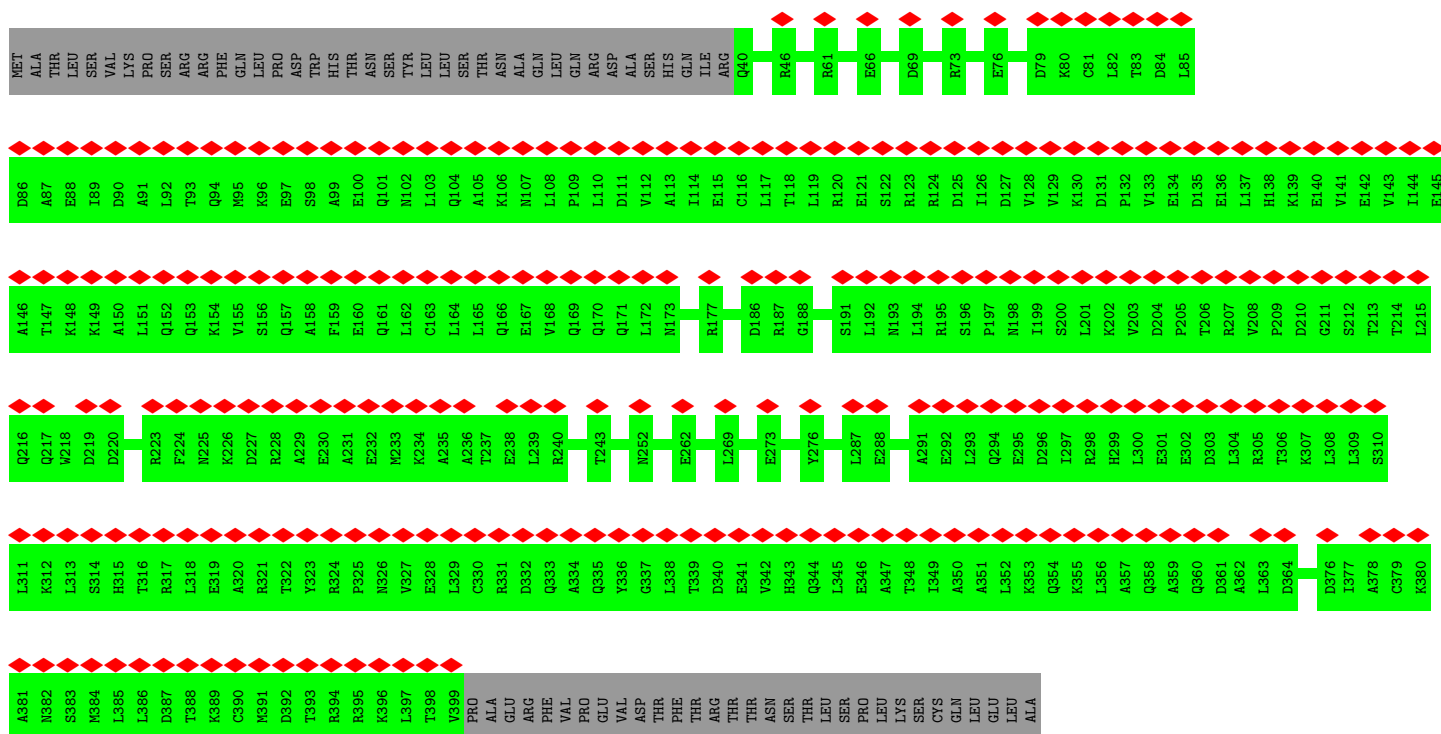
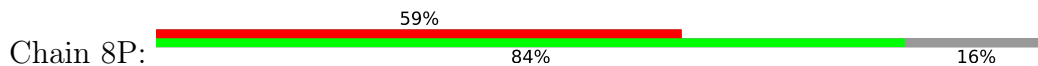


• Molecule 39: Tektin-2

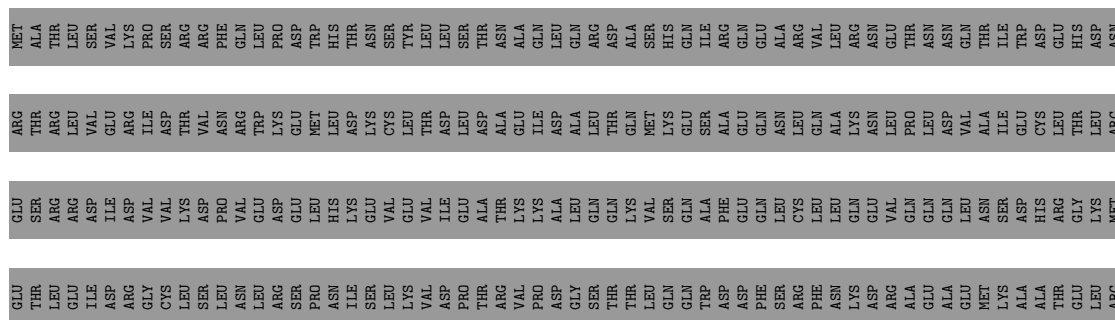


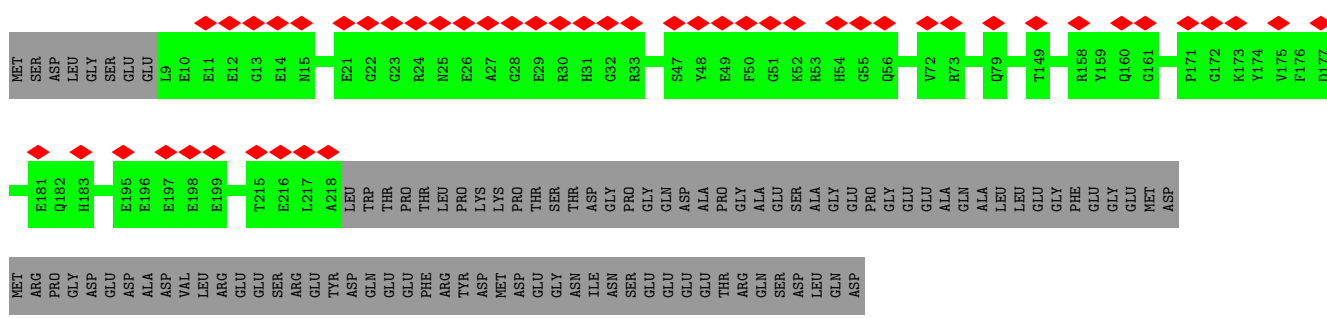


• Molecule 39: Tektin-2

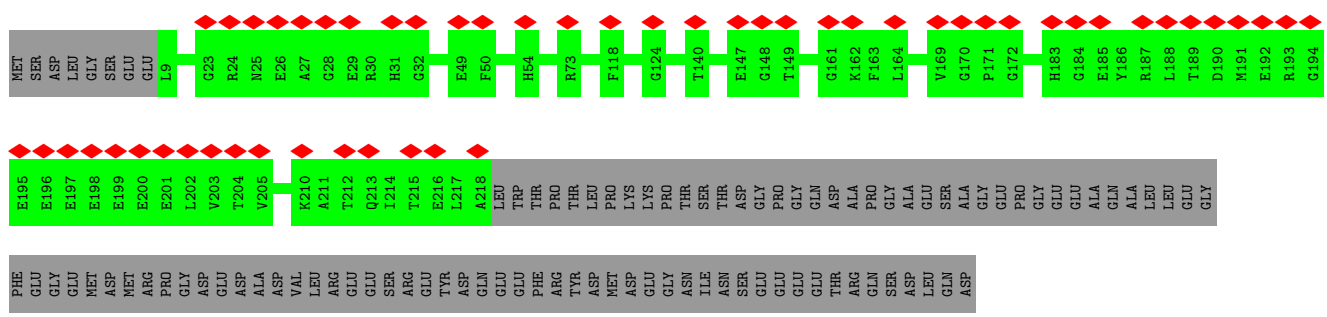


• Molecule 39: Tektin-2

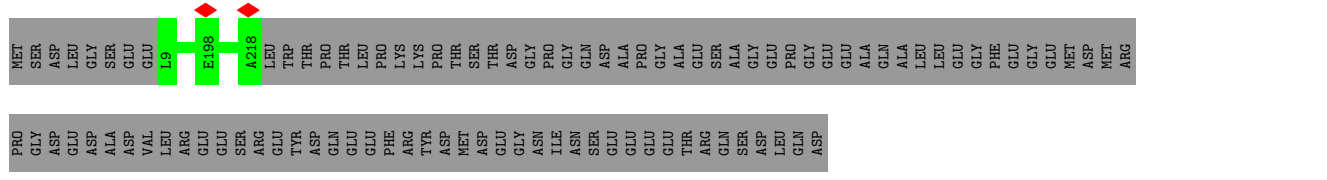




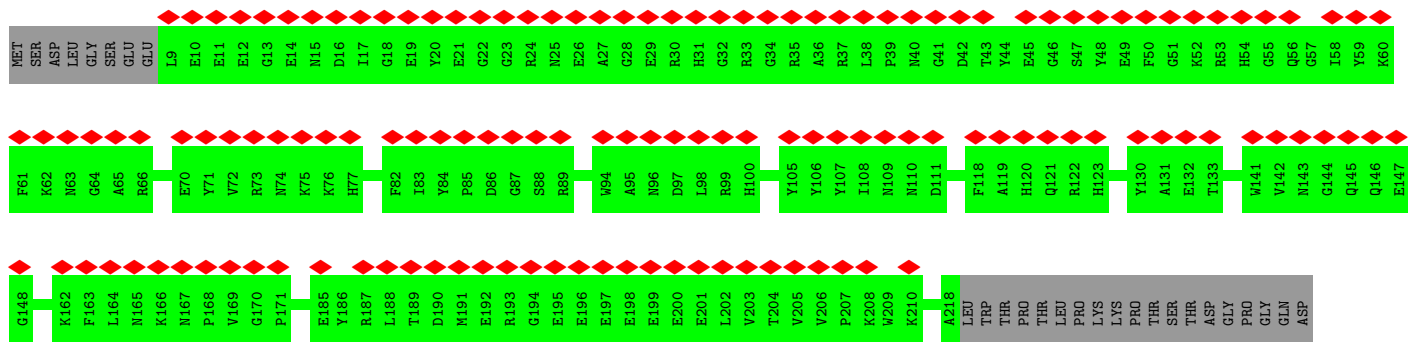
• Molecule 41: Radial spoke head 1 homolog



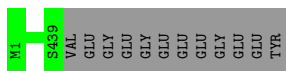
• Molecule 41: Radial spoke head 1 homolog



• Molecule 41: Radial spoke head 1 homolog

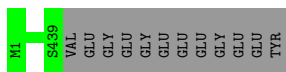


Chain AZ:  97%



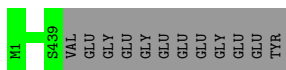
- Molecule 42: Tubulin alpha-1A chain

Chain AC:  97%



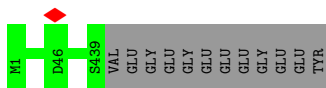
- Molecule 42: Tubulin alpha-1A chain

Chain AE:  97%



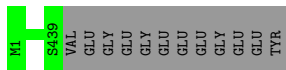
- Molecule 42: Tubulin alpha-1A chain

Chain AG:  97%



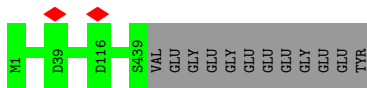
- Molecule 42: Tubulin alpha-1A chain

Chain AI:  97%



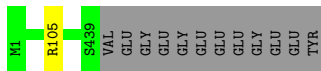
- Molecule 42: Tubulin alpha-1A chain

Chain AK:  97%



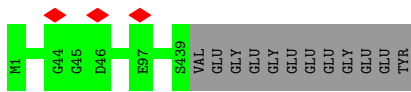
- Molecule 42: Tubulin alpha-1A chain

Chain AM:  97%



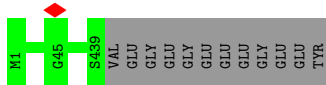
- Molecule 42: Tubulin alpha-1A chain

Chain AO:  97%



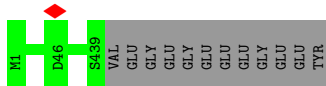
- Molecule 42: Tubulin alpha-1A chain

Chain AQ:  97%



- Molecule 42: Tubulin alpha-1A chain

Chain AS:  97%



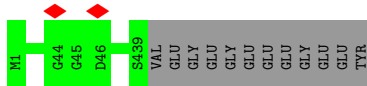
- Molecule 42: Tubulin alpha-1A chain

Chain AU:  97%



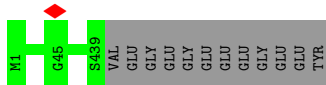
- Molecule 42: Tubulin alpha-1A chain

Chain AW:  97%



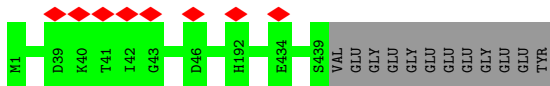
- Molecule 42: Tubulin alpha-1A chain

Chain AY:  97%

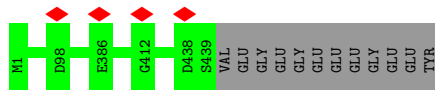


- Molecule 42: Tubulin alpha-1A chain

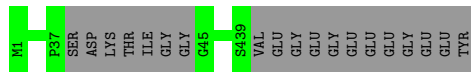
Chain BA:  97%



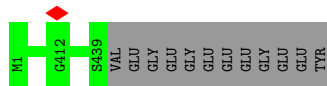
- Molecule 42: Tubulin alpha-1A chain



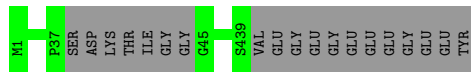
- Molecule 42: Tubulin alpha-1A chain



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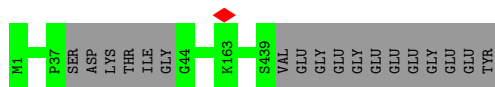
- Molecule 42: Tubulin alpha-1A chain



- Molecule 42: Tubulin alpha-1A chain

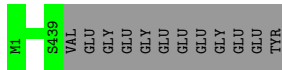


- Molecule 42: Tubulin alpha-1A chain



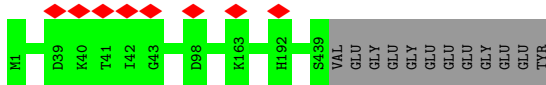
- Molecule 42: Tubulin alpha-1A chain





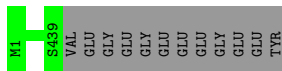
- Molecule 42: Tubulin alpha-1A chain

Chain BQ: 97%



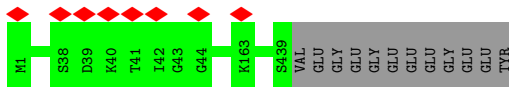
- Molecule 42: Tubulin alpha-1A chain

Chain BS: 97%



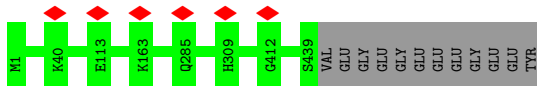
- Molecule 42: Tubulin alpha-1A chain

Chain BU: 97%



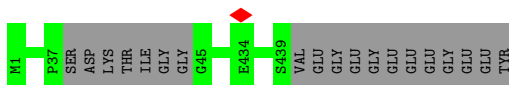
- Molecule 42: Tubulin alpha-1A chain

Chain BW: 97%



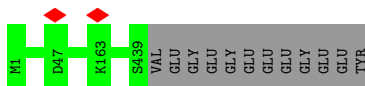
- Molecule 42: Tubulin alpha-1A chain

Chain BY: 96%



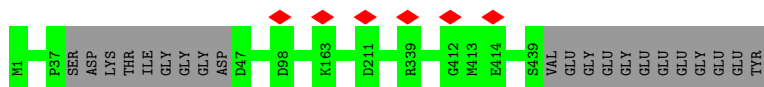
- Molecule 42: Tubulin alpha-1A chain

Chain CC: 97%



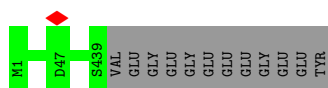
- Molecule 42: Tubulin alpha-1A chain

Chain CE:  95% 5%



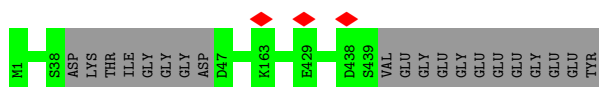
- Molecule 42: Tubulin alpha-1A chain

Chain CG:  97%



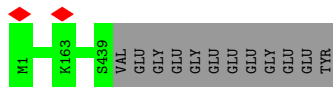
- Molecule 42: Tubulin alpha-1A chain

Chain CI:  96%



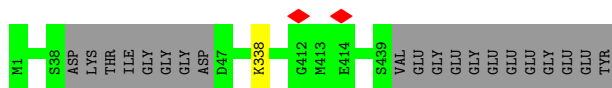
- Molecule 42: Tubulin alpha-1A chain

Chain CK:  97%



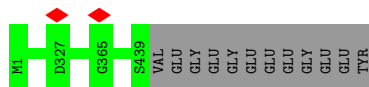
- Molecule 42: Tubulin alpha-1A chain

Chain CM:  95%



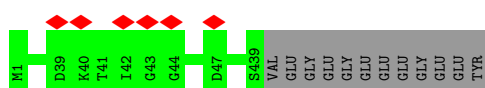
- Molecule 42: Tubulin alpha-1A chain

Chain CO:  97%

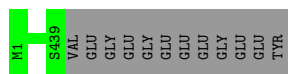


- Molecule 42: Tubulin alpha-1A chain

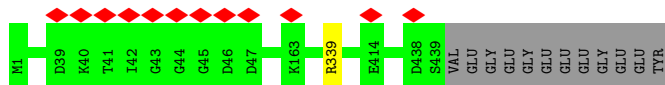
Chain CQ:  97%



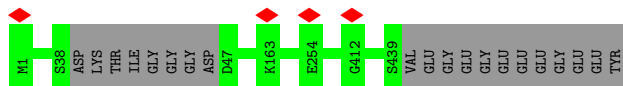
• Molecule 42: Tubulin alpha-1A chain



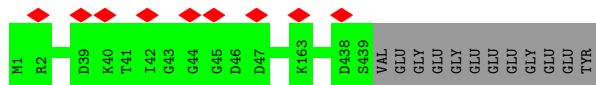
• Molecule 42: Tubulin alpha-1A chain



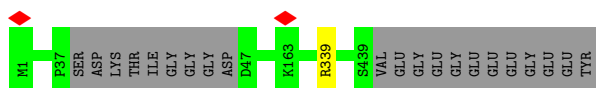
• Molecule 42: Tubulin alpha-1A chain



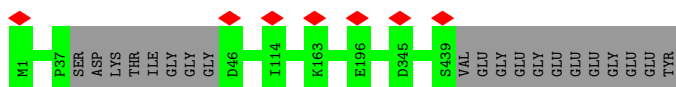
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

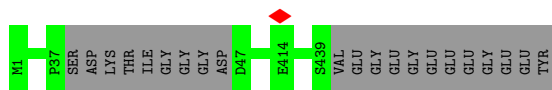


• Molecule 42: Tubulin alpha-1A chain



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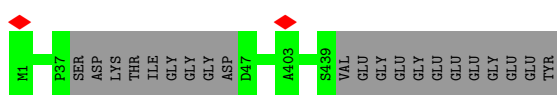




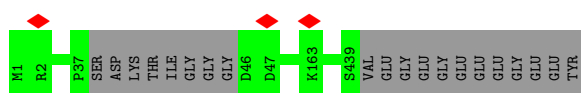
• Molecule 42: Tubulin alpha-1A chain



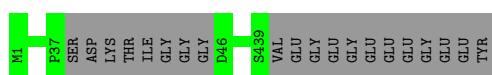
• Molecule 42: Tubulin alpha-1A chain



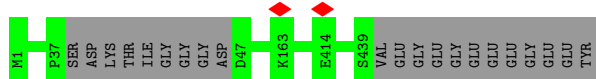
• Molecule 42: Tubulin alpha-1A chain



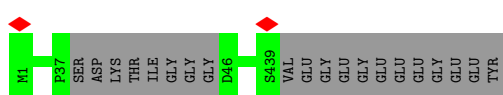
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

Chain DU:  95% 5%



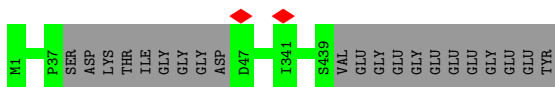
- Molecule 42: Tubulin alpha-1A chain

Chain DW:  95% 5%



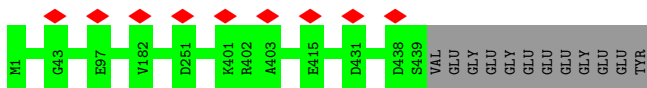
- Molecule 42: Tubulin alpha-1A chain

Chain DY:  95% 5%



- Molecule 42: Tubulin alpha-1A chain

Chain EC:  97% .



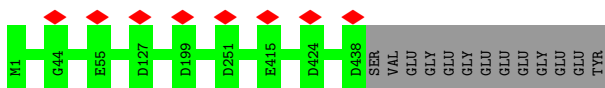
- Molecule 42: Tubulin alpha-1A chain

Chain EE:  97% .



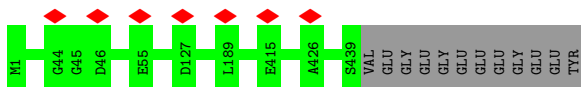
- Molecule 42: Tubulin alpha-1A chain

Chain EG:  97% .

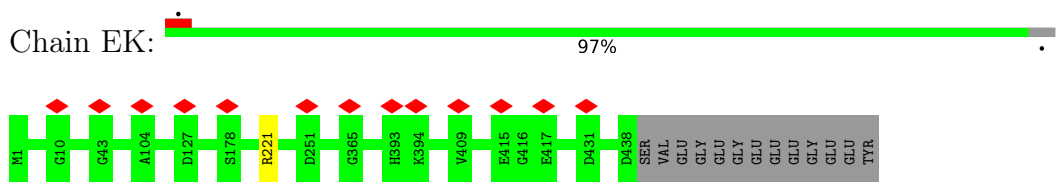


- Molecule 42: Tubulin alpha-1A chain

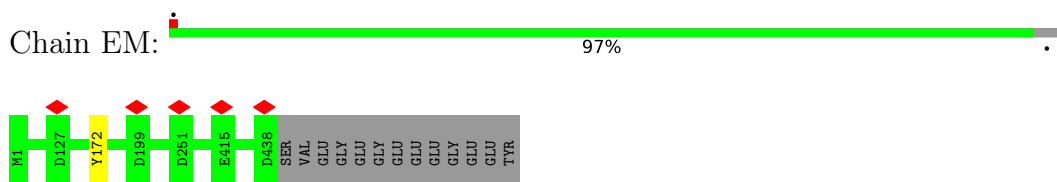
Chain EI:  97% .



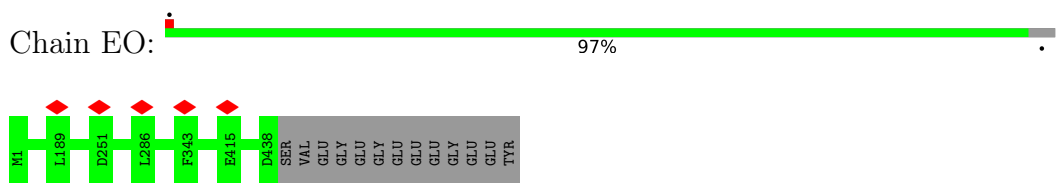
• Molecule 42: Tubulin alpha-1A chain



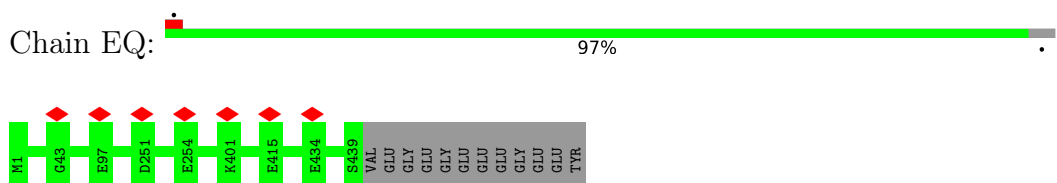
• Molecule 42: Tubulin alpha-1A chain



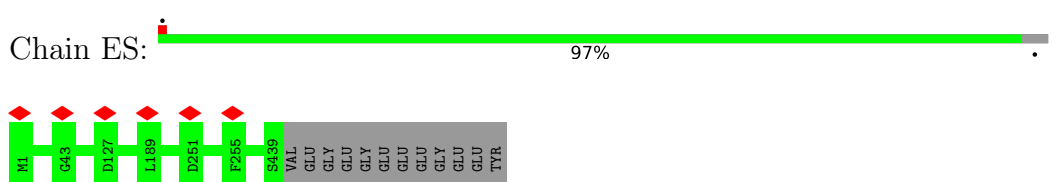
• Molecule 42: Tubulin alpha-1A chain



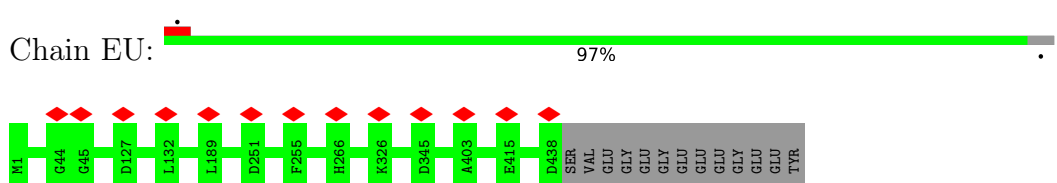
• Molecule 42: Tubulin alpha-1A chain



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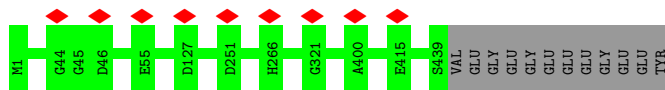


• Molecule 42: Tubulin alpha-1A chain

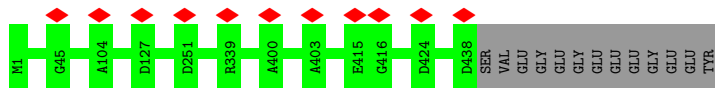


• Molecule 42: Tubulin alpha-1A chain

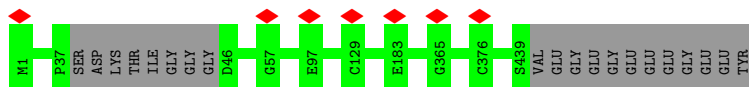




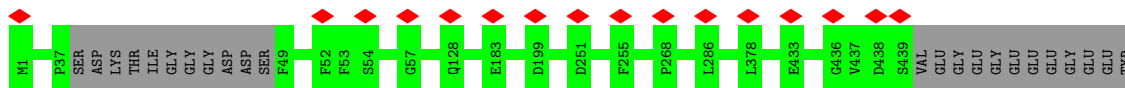
- Molecule 42: Tubulin alpha-1A chain



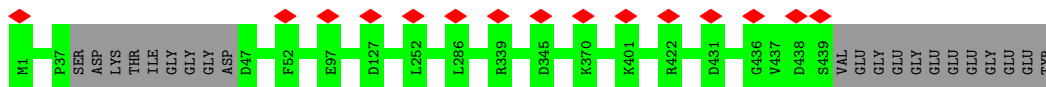
- Molecule 42: Tubulin alpha-1A chain



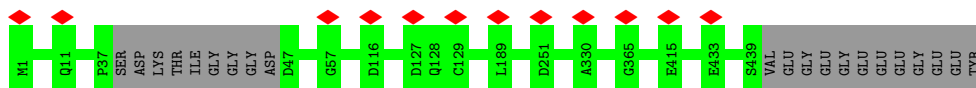
- Molecule 42: Tubulin alpha-1A chain



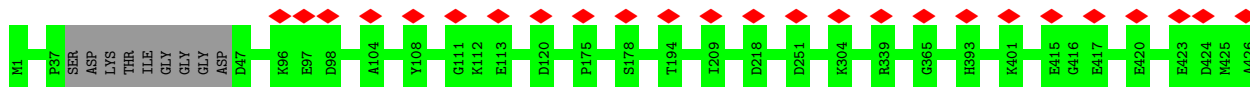
- Molecule 42: Tubulin alpha-1A chain

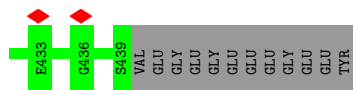


- Molecule 42: Tubulin alpha-1A chain



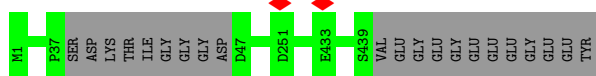
- Molecule 42: Tubulin alpha-1A chain





- Molecule 42: Tubulin alpha-1A chain

Chain FM: 95% 5%



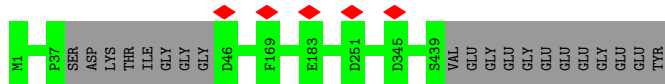
- Molecule 42: Tubulin alpha-1A chain

Chain FO: 95% 5%



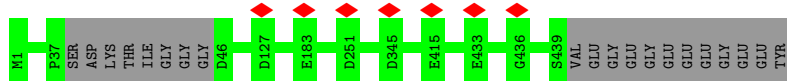
- Molecule 42: Tubulin alpha-1A chain

Chain FQ: 96% 5%



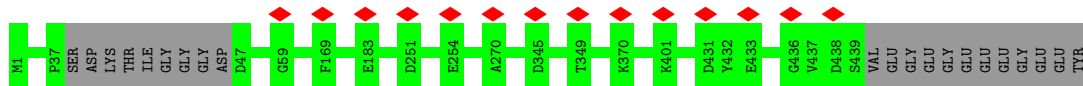
- Molecule 42: Tubulin alpha-1A chain

Chain FS: 96% 5%



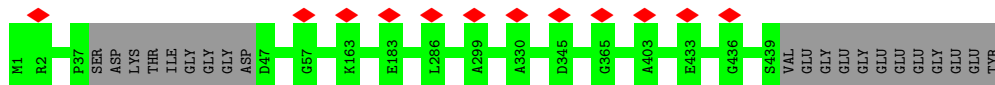
- Molecule 42: Tubulin alpha-1A chain

Chain FU: 95% 5%

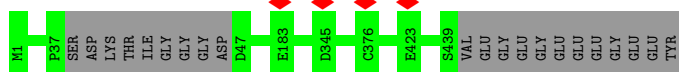


- Molecule 42: Tubulin alpha-1A chain

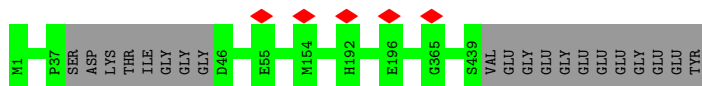
Chain FW: 95% 5%



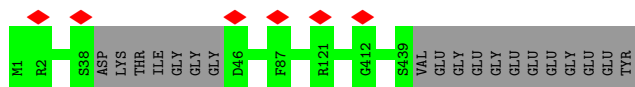
- Molecule 42: Tubulin alpha-1A chain



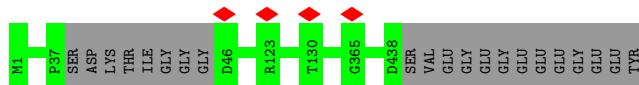
• Molecule 42: Tubulin alpha-1A chain



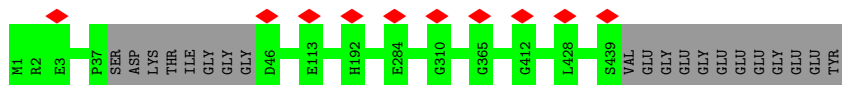
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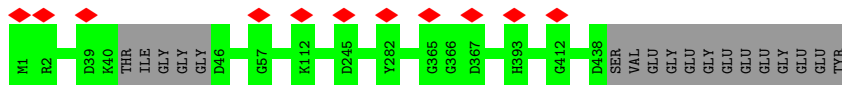
• Molecule 42: Tubulin alpha-1A chain



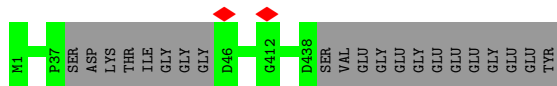
• Molecule 42: Tubulin alpha-1A chain



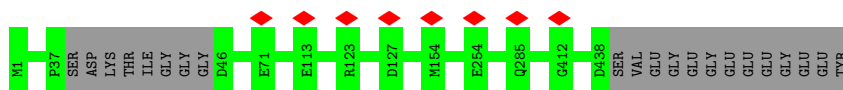
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain



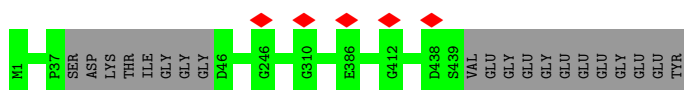
• Molecule 42: Tubulin alpha-1A chain



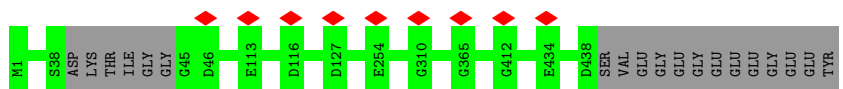
• Molecule 42: Tubulin alpha-1A chain



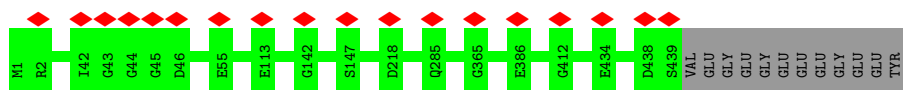
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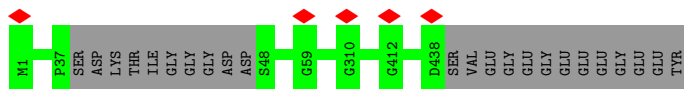
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

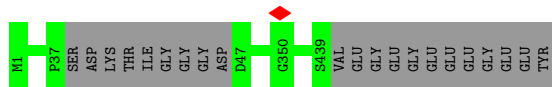


• Molecule 42: Tubulin alpha-1A chain

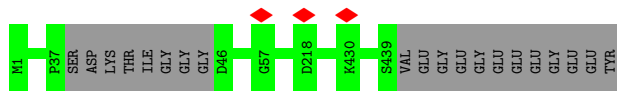


• Molecule 42: Tubulin alpha-1A chain

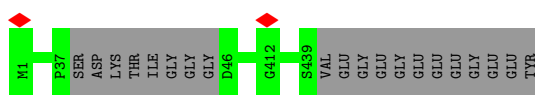




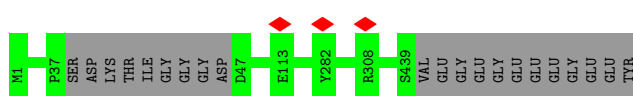
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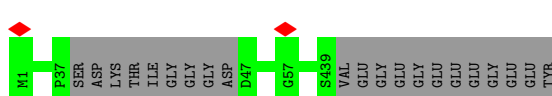
• Molecule 42: Tubulin alpha-1A chain



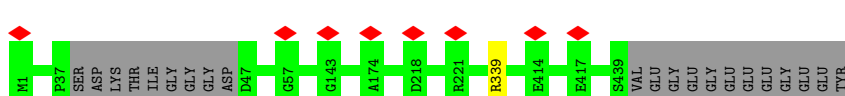
• Molecule 42: Tubulin alpha-1A chain



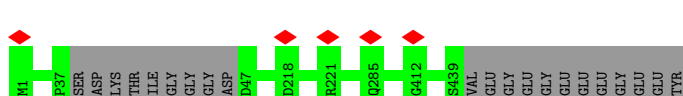
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

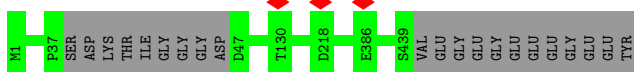


• Molecule 42: Tubulin alpha-1A chain



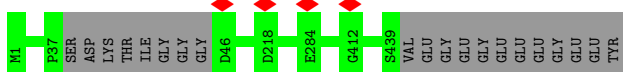
• Molecule 42: Tubulin alpha-1A chain

Chain HO:  95% 5%



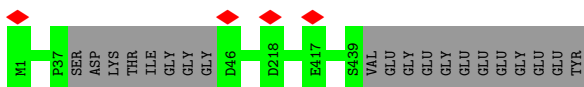
- Molecule 42: Tubulin alpha-1A chain

Chain HQ:  96% .



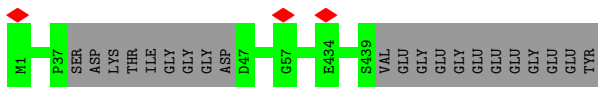
- Molecule 42: Tubulin alpha-1A chain

Chain HS:  96% .



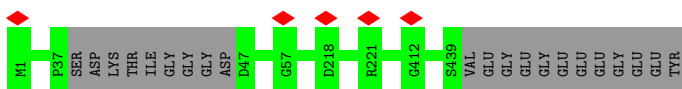
- Molecule 42: Tubulin alpha-1A chain

Chain HU:  95% 5%



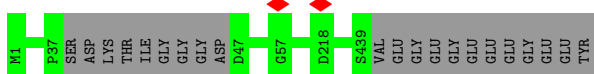
- Molecule 42: Tubulin alpha-1A chain

Chain HW:  95% 5%



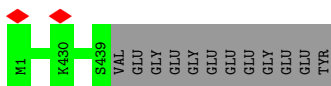
- Molecule 42: Tubulin alpha-1A chain

Chain HY:  95% 5%



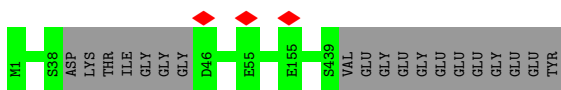
- Molecule 42: Tubulin alpha-1A chain

Chain IA:  97% .



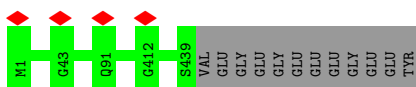
- Molecule 42: Tubulin alpha-1A chain

Chain IC:  96%



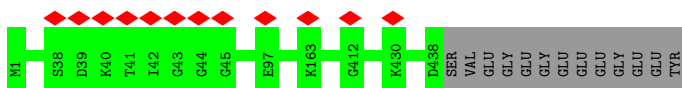
- Molecule 42: Tubulin alpha-1A chain

Chain IE:  97%



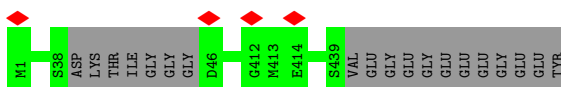
- Molecule 42: Tubulin alpha-1A chain

Chain IG:  97%



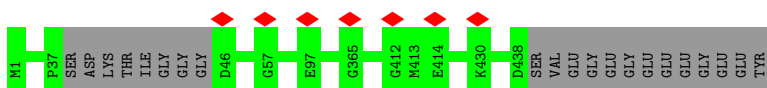
- Molecule 42: Tubulin alpha-1A chain

Chain II:  96%



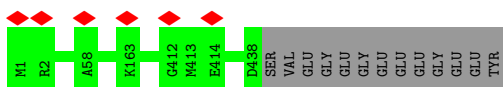
- Molecule 42: Tubulin alpha-1A chain

Chain IK:  95% 5%



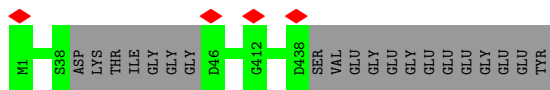
- Molecule 42: Tubulin alpha-1A chain

Chain IM:  97%

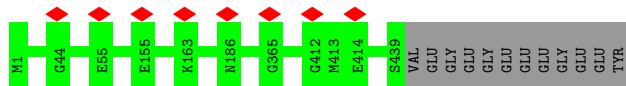


- Molecule 42: Tubulin alpha-1A chain

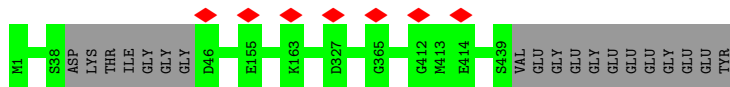
Chain IO:  96%



• Molecule 42: Tubulin alpha-1A chain



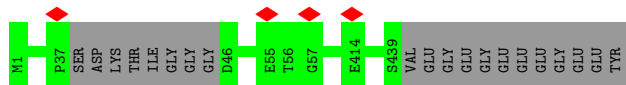
• Molecule 42: Tubulin alpha-1A chain



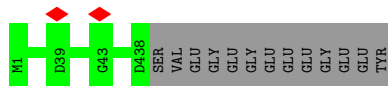
• Molecule 42: Tubulin alpha-1A chain



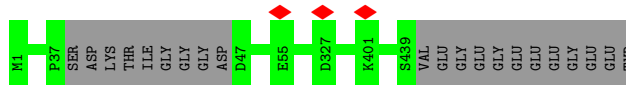
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

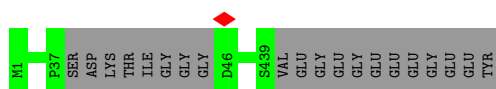


• Molecule 42: Tubulin alpha-1A chain



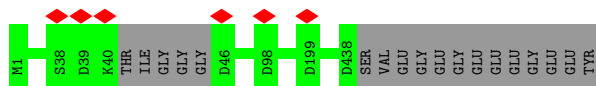
• Molecule 42: Tubulin alpha-1A chain

Chain JE:  96%



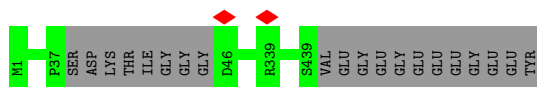
- Molecule 42: Tubulin alpha-1A chain

Chain JG:  96%



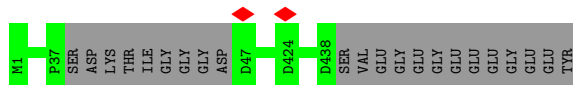
- Molecule 42: Tubulin alpha-1A chain

Chain JI:  96%



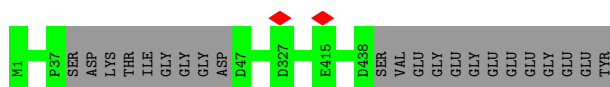
- Molecule 42: Tubulin alpha-1A chain

Chain JK:  95%



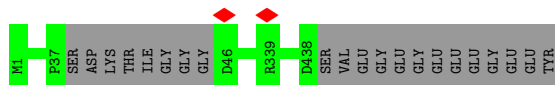
- Molecule 42: Tubulin alpha-1A chain

Chain JM:  95%



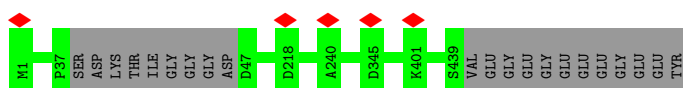
- Molecule 42: Tubulin alpha-1A chain

Chain JO:  95%



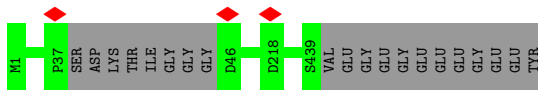
- Molecule 42: Tubulin alpha-1A chain

Chain JQ:  95%



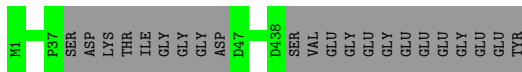
- Molecule 42: Tubulin alpha-1A chain

Chain JS:  96%



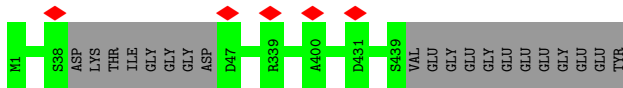
- Molecule 42: Tubulin alpha-1A chain

Chain JU:  95%



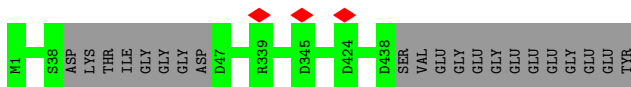
- Molecule 42: Tubulin alpha-1A chain

Chain JW:  96%



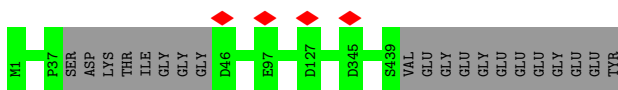
- Molecule 42: Tubulin alpha-1A chain

Chain JY:  95%



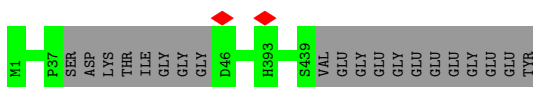
- Molecule 42: Tubulin alpha-1A chain

Chain KC:  96%



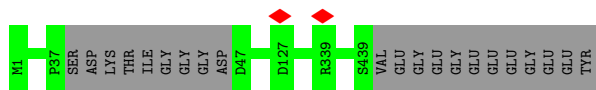
- Molecule 42: Tubulin alpha-1A chain

Chain KE:  96%



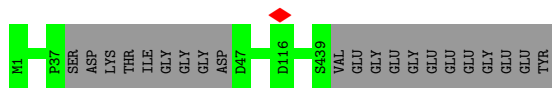
- Molecule 42: Tubulin alpha-1A chain

Chain KG:  95%



- Molecule 42: Tubulin alpha-1A chain

Chain KI: 95% 5%



- Molecule 42: Tubulin alpha-1A chain

Chain KK: 95% 5%



- Molecule 42: Tubulin alpha-1A chain

Chain KM: 95% 5%



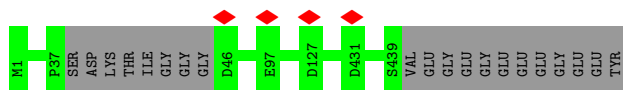
- Molecule 42: Tubulin alpha-1A chain

Chain KO: 95% 5%



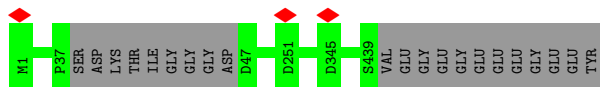
- Molecule 42: Tubulin alpha-1A chain

Chain KQ: 96% 5%

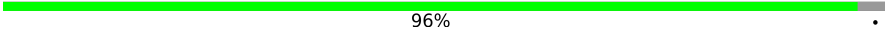


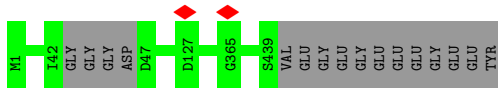
- Molecule 42: Tubulin alpha-1A chain

Chain KS: 95% 5%



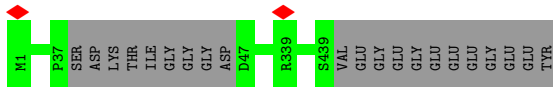
- Molecule 42: Tubulin alpha-1A chain

Chain KU:  96%



- Molecule 42: Tubulin alpha-1A chain

Chain KW:  95% 5%



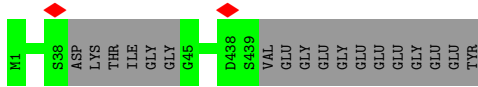
- Molecule 42: Tubulin alpha-1A chain

Chain KY:  95% 5%



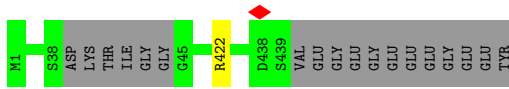
- Molecule 42: Tubulin alpha-1A chain

Chain LC:  96%



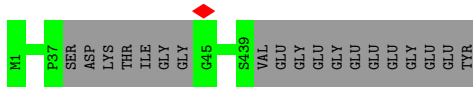
- Molecule 42: Tubulin alpha-1A chain

Chain LE:  96%



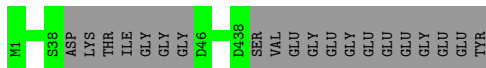
- Molecule 42: Tubulin alpha-1A chain

Chain LG:  96%



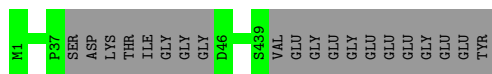
- Molecule 42: Tubulin alpha-1A chain

Chain LI:  96%



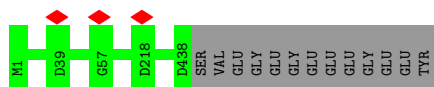
• Molecule 42: Tubulin alpha-1A chain

Chain LK:  96%



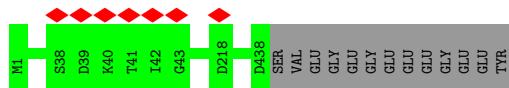
• Molecule 42: Tubulin alpha-1A chain

Chain LM:  97%



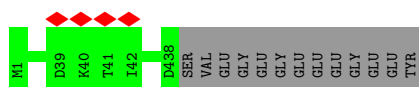
• Molecule 42: Tubulin alpha-1A chain

Chain LO:  97%



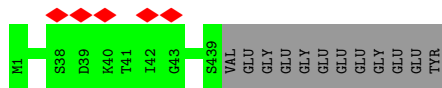
• Molecule 42: Tubulin alpha-1A chain

Chain LQ:  97%



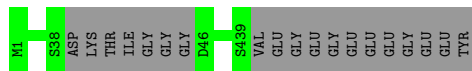
• Molecule 42: Tubulin alpha-1A chain

Chain LS:  97%



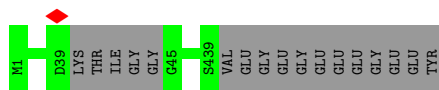
• Molecule 42: Tubulin alpha-1A chain

Chain LU:  96%

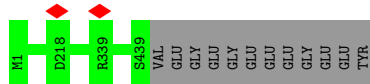


• Molecule 42: Tubulin alpha-1A chain

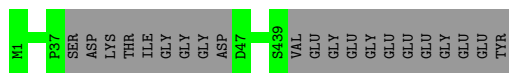
Chain LW:  96%



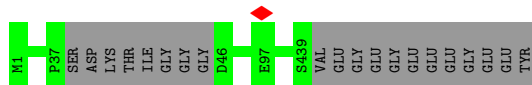
• Molecule 42: Tubulin alpha-1A chain



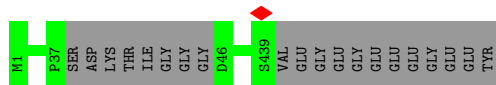
• Molecule 42: Tubulin alpha-1A chain



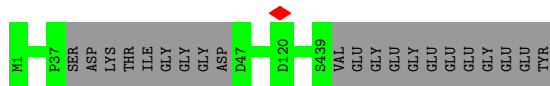
• Molecule 42: Tubulin alpha-1A chain



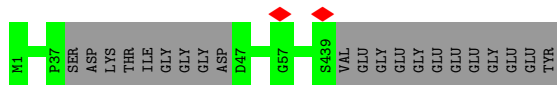
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

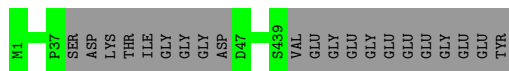


• Molecule 42: Tubulin alpha-1A chain



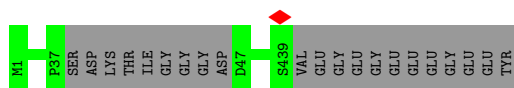
• Molecule 42: Tubulin alpha-1A chain

Chain MK:  95% 5%



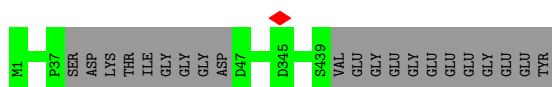
- Molecule 42: Tubulin alpha-1A chain

Chain MM:  95% 5%



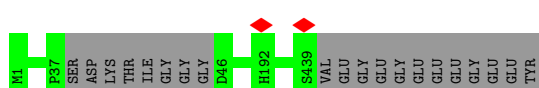
- Molecule 42: Tubulin alpha-1A chain

Chain MO:  95% 5%



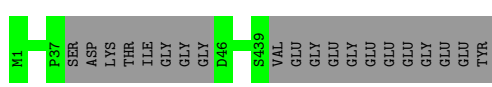
- Molecule 42: Tubulin alpha-1A chain

Chain MQ:  96% .



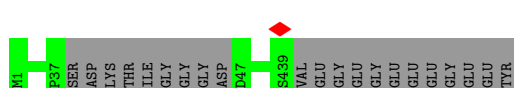
- Molecule 42: Tubulin alpha-1A chain

Chain MS:  96% .



- Molecule 42: Tubulin alpha-1A chain

Chain MU:  95% 5%



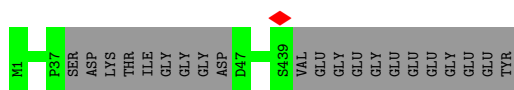
- Molecule 42: Tubulin alpha-1A chain

Chain MW:  95% 5%



• Molecule 42: Tubulin alpha-1A chain

Chain MY:  95% 5%



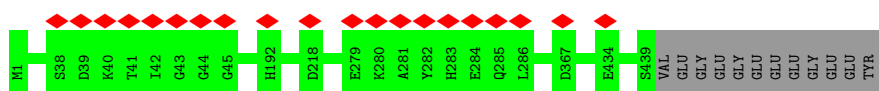
• Molecule 42: Tubulin alpha-1A chain

Chain NA:  96% 5%



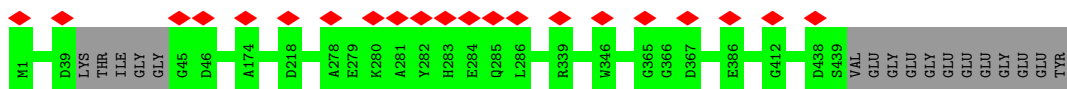
• Molecule 42: Tubulin alpha-1A chain

Chain NC:  97% 5%



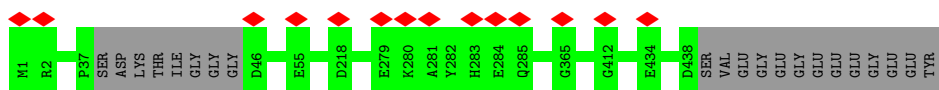
• Molecule 42: Tubulin alpha-1A chain

Chain NE:  5% 96% 5%



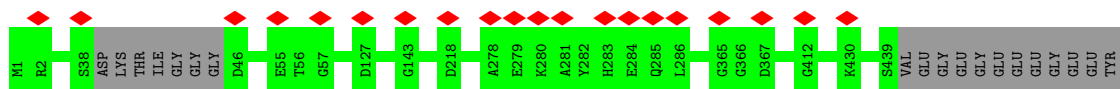
• Molecule 42: Tubulin alpha-1A chain

Chain NG:  5% 95% 5%



• Molecule 42: Tubulin alpha-1A chain

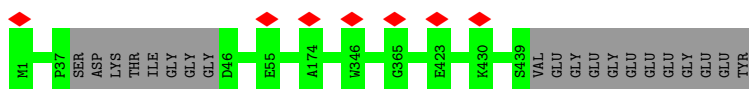
Chain NI:  5% 96% 5%



• Molecule 42: Tubulin alpha-1A chain

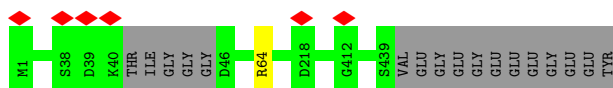
Chain NK:  6% 97% 5%

Chain OA:  96%



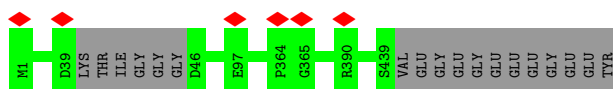
- Molecule 42: Tubulin alpha-1A chain

Chain OC:  96%



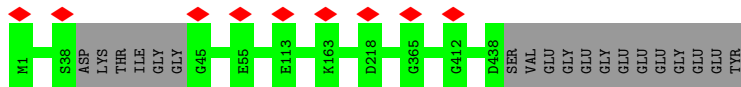
- Molecule 42: Tubulin alpha-1A chain

Chain OE:  96%



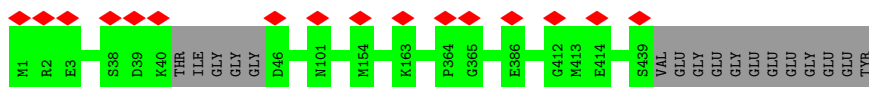
- Molecule 42: Tubulin alpha-1A chain

Chain OG:  96%



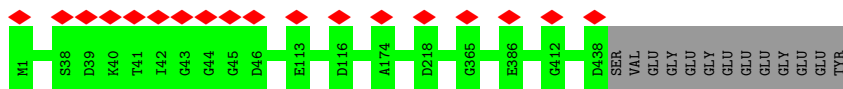
- Molecule 42: Tubulin alpha-1A chain

Chain OI:  96%



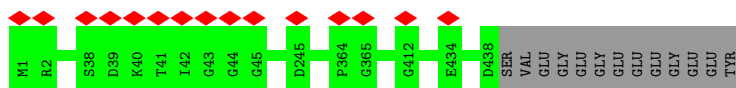
- Molecule 42: Tubulin alpha-1A chain

Chain OK:  97%

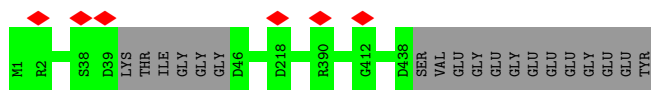


- Molecule 42: Tubulin alpha-1A chain

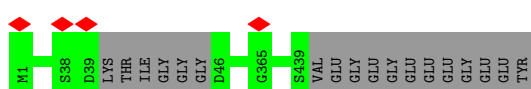
Chain OM:  97%



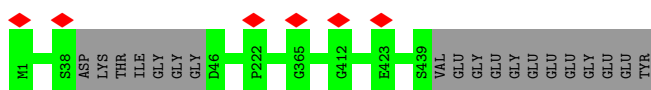
• Molecule 42: Tubulin alpha-1A chain



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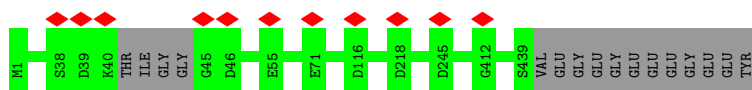
• Molecule 42: Tubulin alpha-1A chain



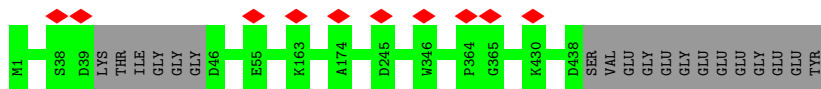
• Molecule 42: Tubulin alpha-1A chain



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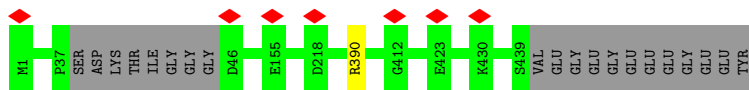


• Molecule 42: Tubulin alpha-1A chain

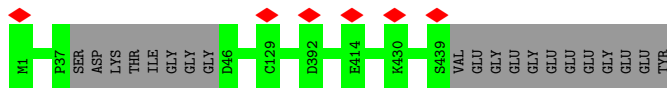


• Molecule 42: Tubulin alpha-1A chain

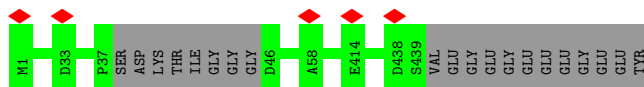




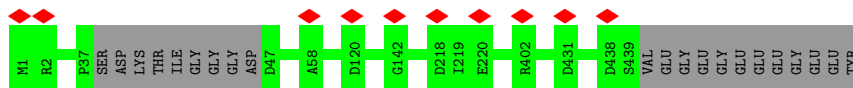
- Molecule 42: Tubulin alpha-1A chain



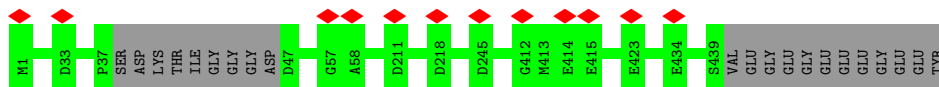
- Molecule 42: Tubulin alpha-1A chain



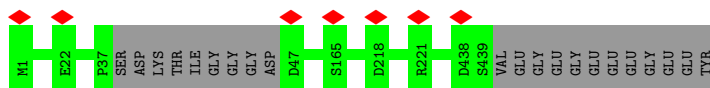
- Molecule 42: Tubulin alpha-1A chain



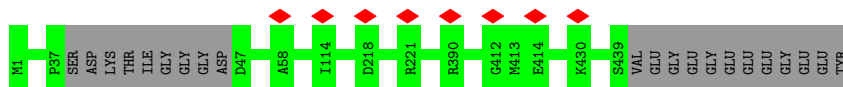
- Molecule 42: Tubulin alpha-1A chain



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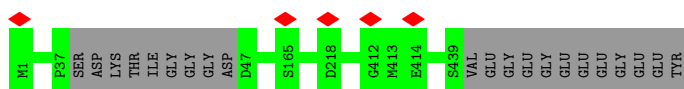


- Molecule 42: Tubulin alpha-1A chain



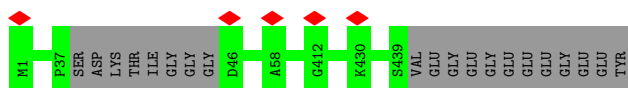
- Molecule 42: Tubulin alpha-1A chain

Chain PO:  95% 5%



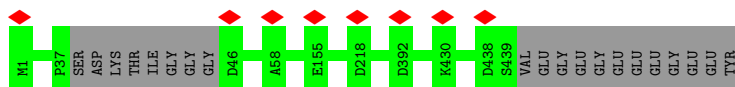
- Molecule 42: Tubulin alpha-1A chain

Chain PQ:  96% .



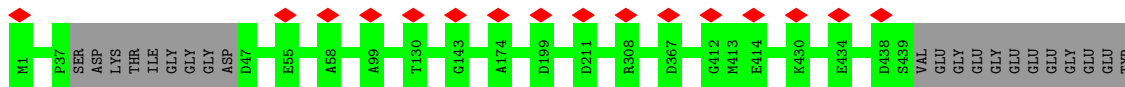
- Molecule 42: Tubulin alpha-1A chain

Chain PS:  96% .



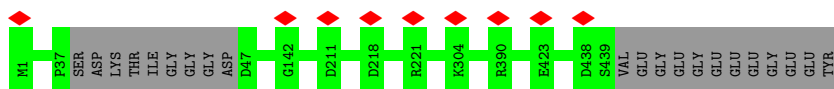
- Molecule 42: Tubulin alpha-1A chain

Chain PU:  95% 5%



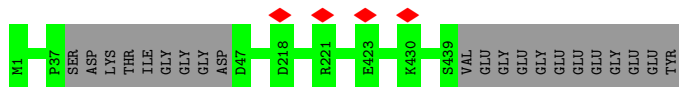
- Molecule 42: Tubulin alpha-1A chain

Chain PW:  95% 5%



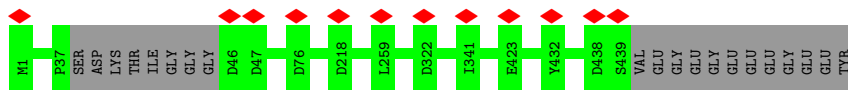
- Molecule 42: Tubulin alpha-1A chain

Chain PY:  95% 5%



- Molecule 42: Tubulin alpha-1A chain

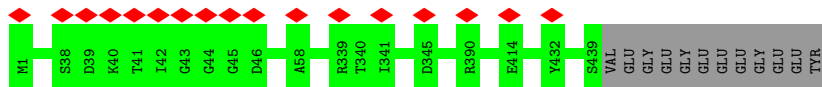
Chain QA:  96% .



• Molecule 42: Tubulin alpha-1A chain



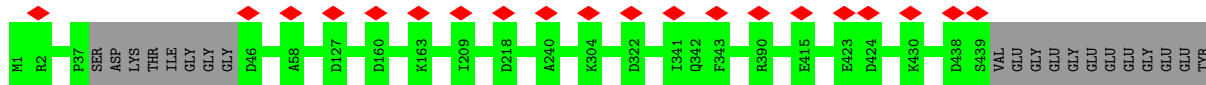
• Molecule 42: Tubulin alpha-1A chain



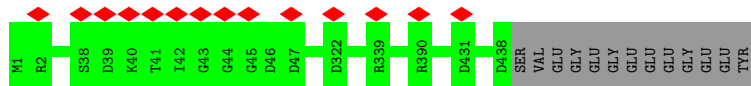
• Molecule 42: Tubulin alpha-1A chain



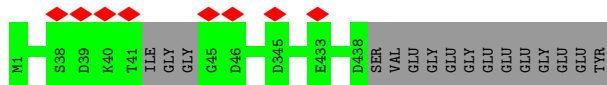
• Molecule 42: Tubulin alpha-1A chain



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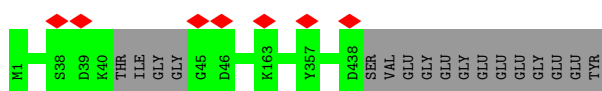


• Molecule 42: Tubulin alpha-1A chain



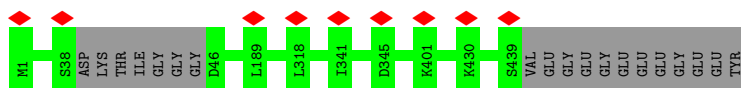
- Molecule 42: Tubulin alpha-1A chain

Chain QO:  96%



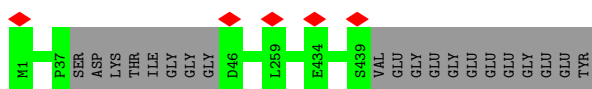
- Molecule 42: Tubulin alpha-1A chain

Chain QQ:  96%



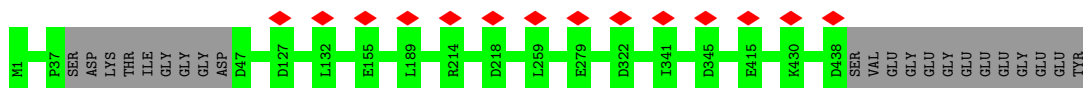
- Molecule 42: Tubulin alpha-1A chain

Chain QS:  96%



- Molecule 42: Tubulin alpha-1A chain

Chain QU:  95% 5%



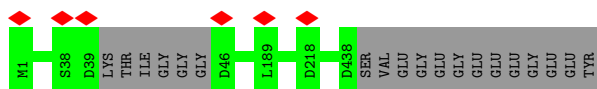
- Molecule 42: Tubulin alpha-1A chain

Chain QW:  96%



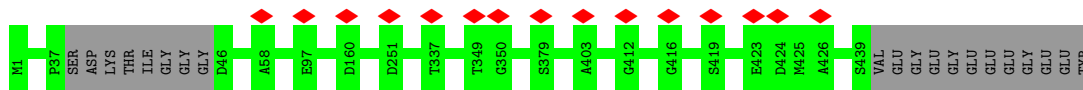
- Molecule 42: Tubulin alpha-1A chain

Chain QY:  96%

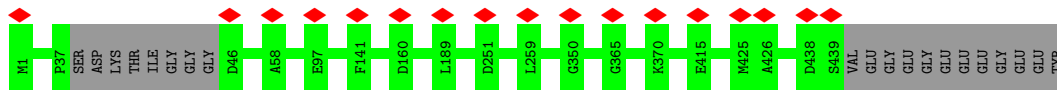


- Molecule 42: Tubulin alpha-1A chain

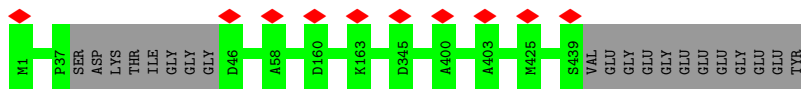
Chain RA:  96%



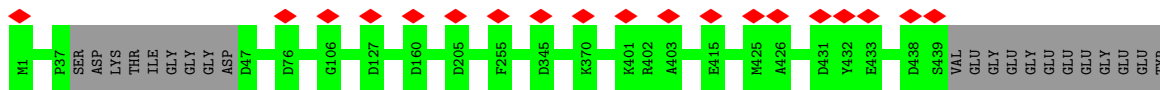
• Molecule 42: Tubulin alpha-1A chain



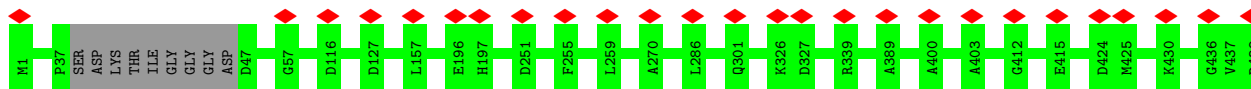
• Molecule 42: Tubulin alpha-1A chain



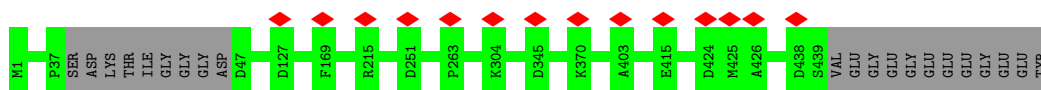
• Molecule 42: Tubulin alpha-1A chain



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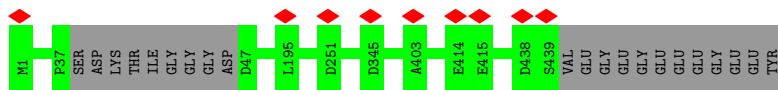


• Molecule 42: Tubulin alpha-1A chain

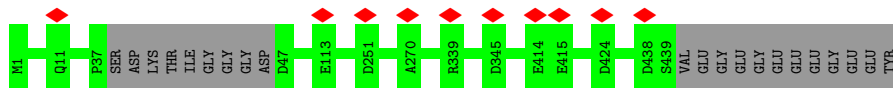


• Molecule 42: Tubulin alpha-1A chain

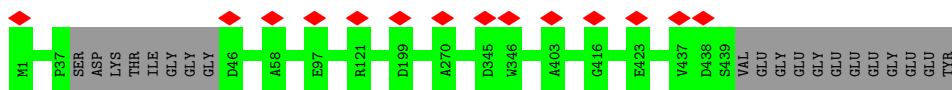




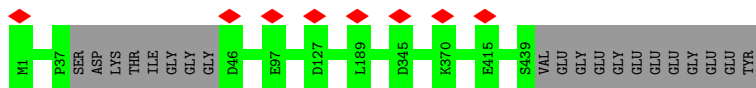
• Molecule 42: Tubulin alpha-1A chain



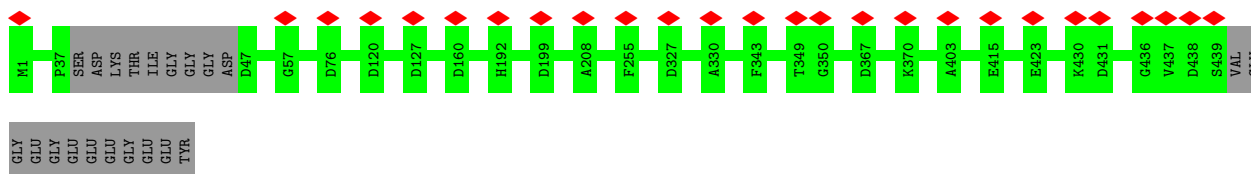
• Molecule 42: Tubulin alpha-1A chain



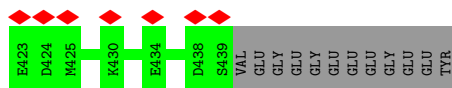
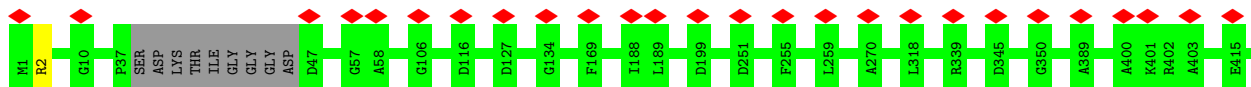
• Molecule 42: Tubulin alpha-1A chain



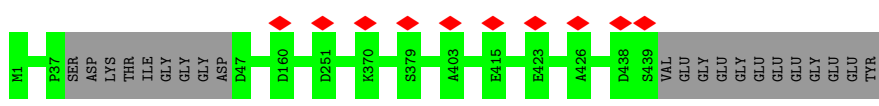
• Molecule 42: Tubulin alpha-1A chain



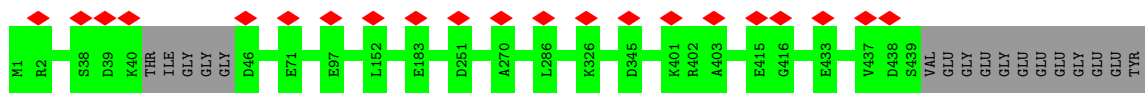
• Molecule 42: Tubulin alpha-1A chain



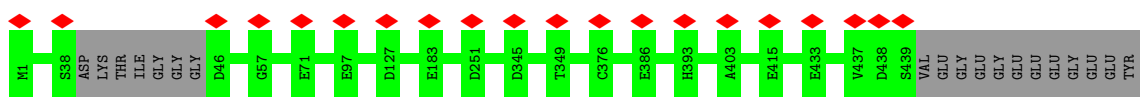
• Molecule 42: Tubulin alpha-1A chain



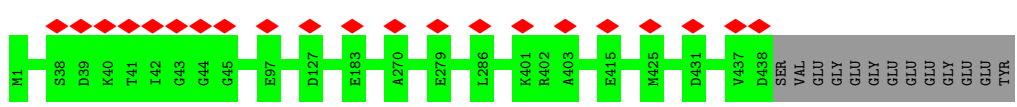
• Molecule 42: Tubulin alpha-1A chain



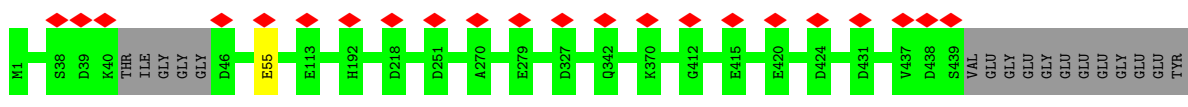
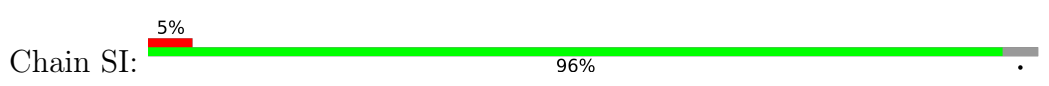
• Molecule 42: Tubulin alpha-1A chain



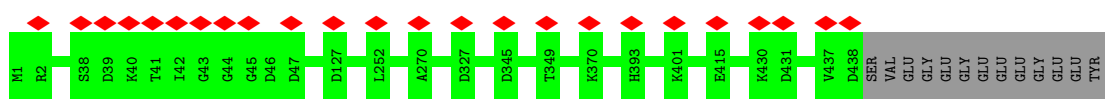
• Molecule 42: Tubulin alpha-1A chain



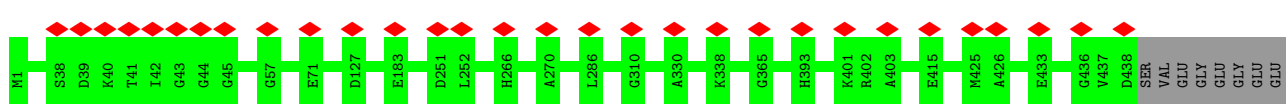
• Molecule 42: Tubulin alpha-1A chain



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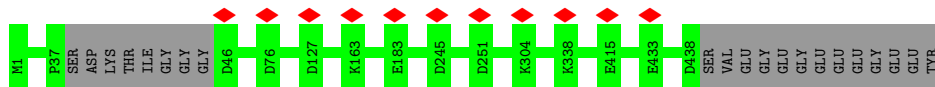


• Molecule 42: Tubulin alpha-1A chain

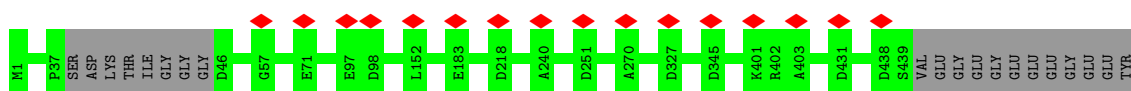


GLU
GLU
GLU
TYR

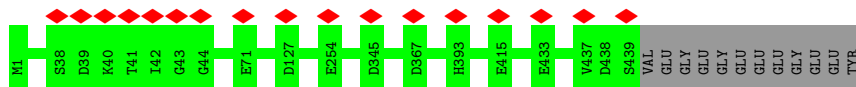
- Molecule 42: Tubulin alpha-1A chain



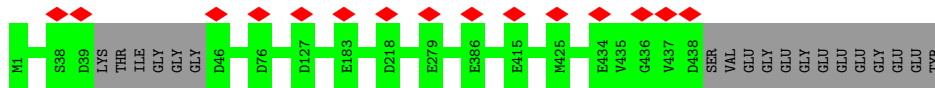
- Molecule 42: Tubulin alpha-1A chain



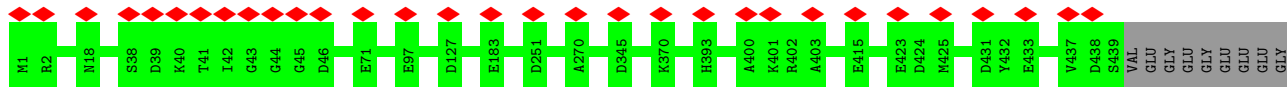
- Molecule 42: Tubulin alpha-1A chain



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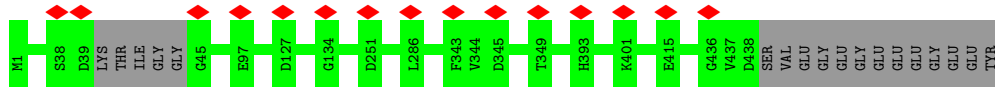


- Molecule 42: Tubulin alpha-1A chain

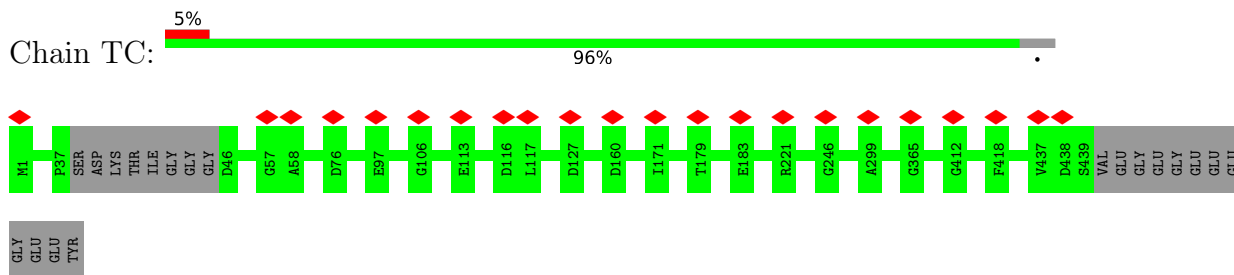


GLU
GLU
TYR

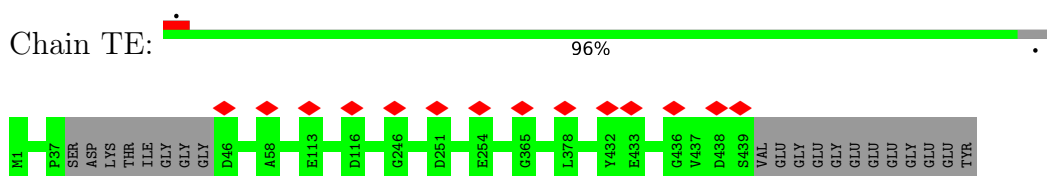
- Molecule 42: Tubulin alpha-1A chain



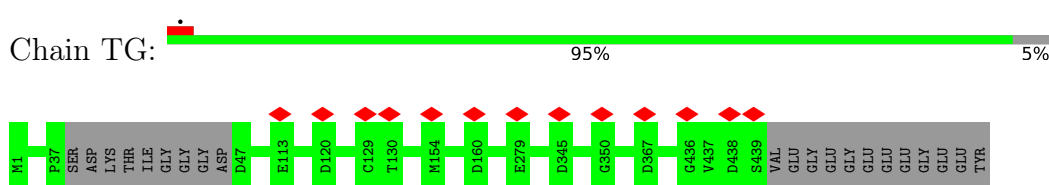
• Molecule 42: Tubulin alpha-1A chain



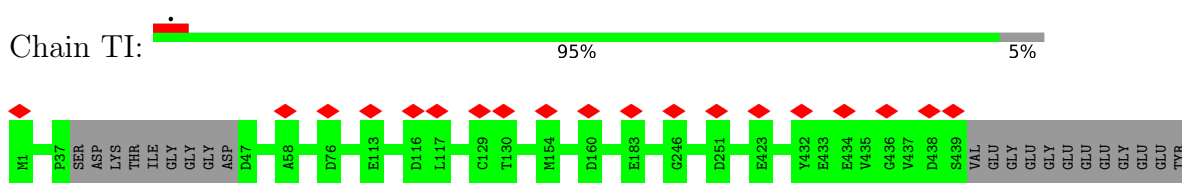
• Molecule 42: Tubulin alpha-1A chain



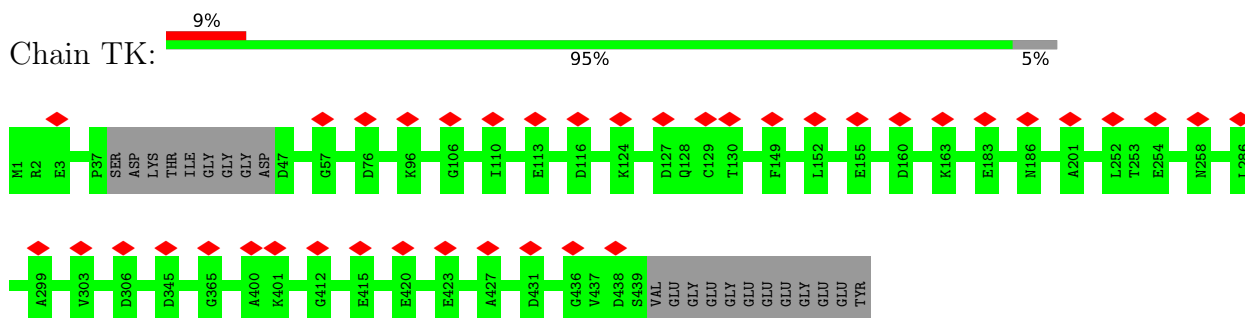
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

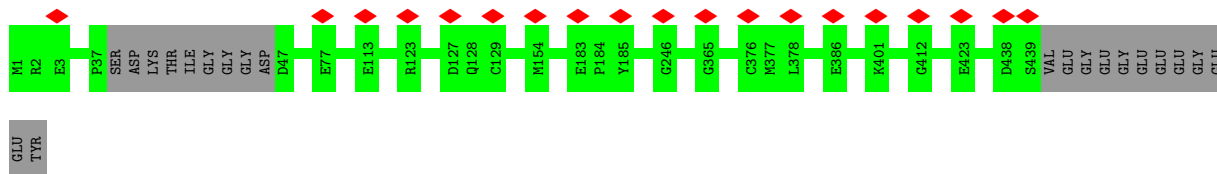


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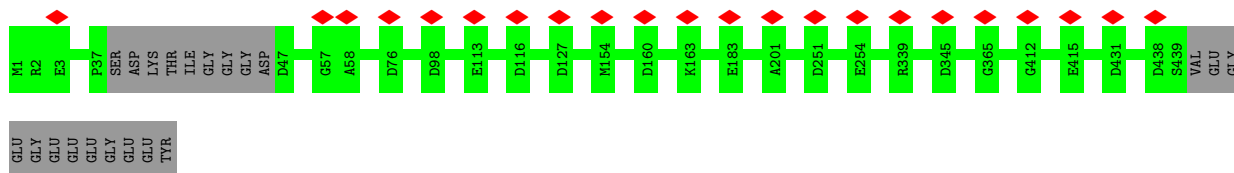


• Molecule 42: Tubulin alpha-1A chain

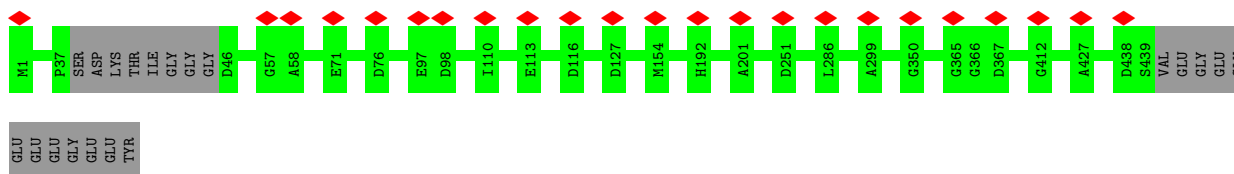




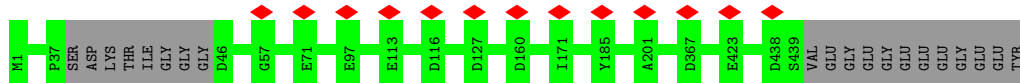
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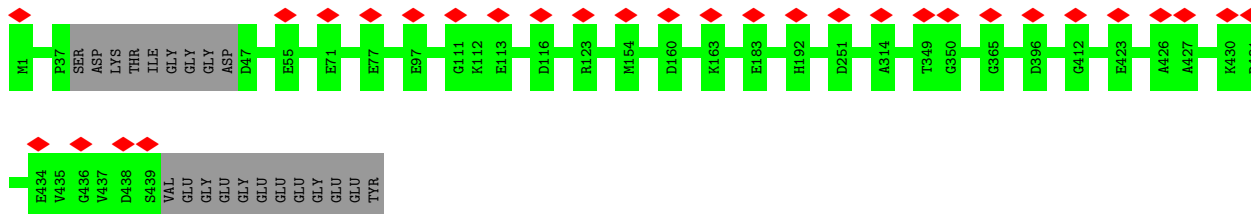
• Molecule 42: Tubulin alpha-1A chain



• Molecule 42: Tubulin alpha-1A chain

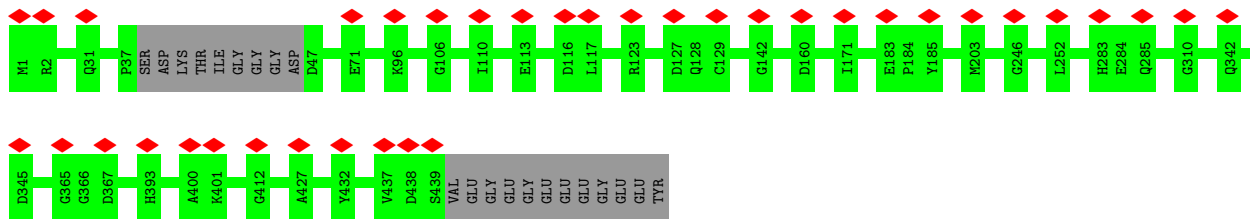


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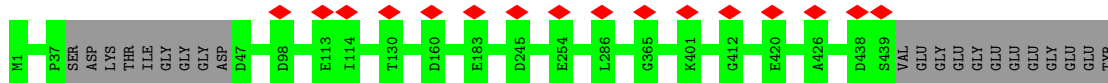


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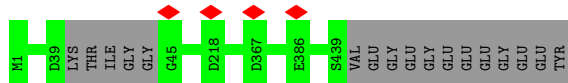




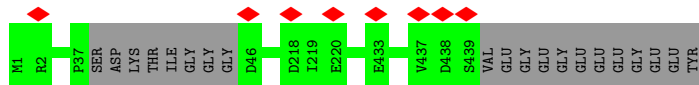
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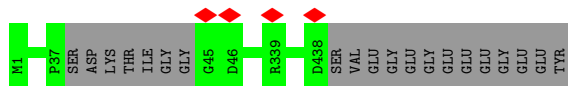
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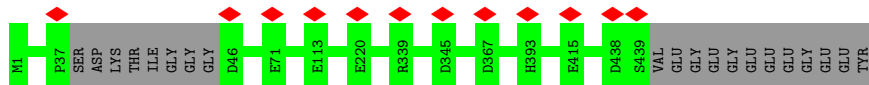
• Molecule 42: Tubulin alpha-1A chain



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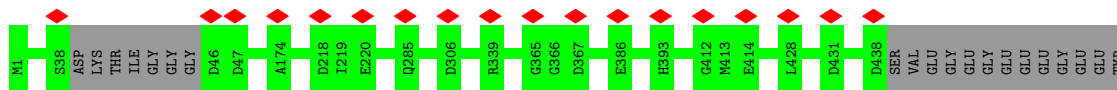


• Molecule 42: Tubulin alpha-1A chain

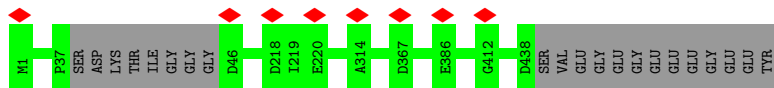


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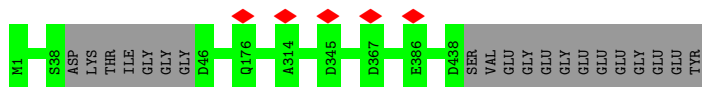




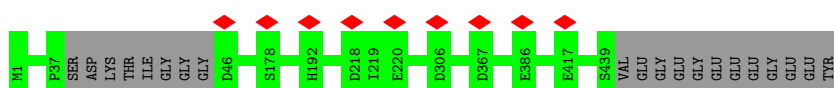
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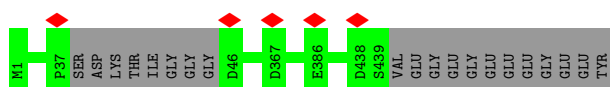
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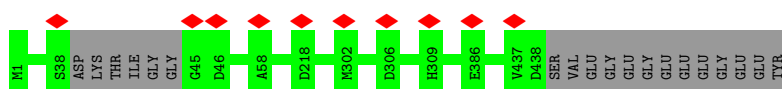
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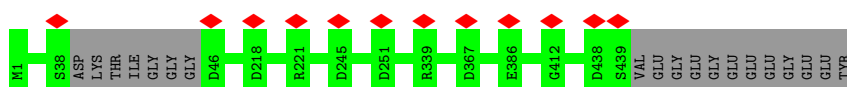
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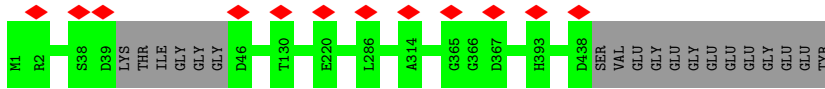
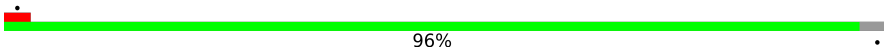


• Molecule 42: Tubulin alpha-1A chain



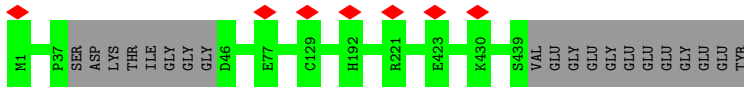
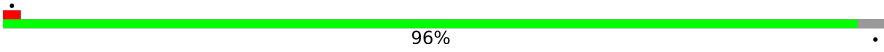
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Chain UY:



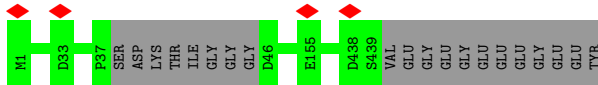
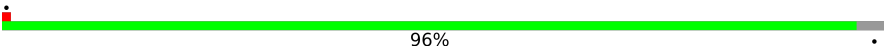
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Chain VC:



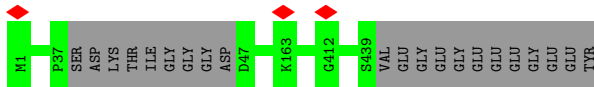
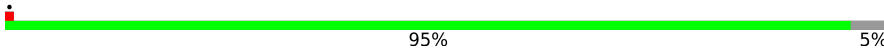
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Chain VE:



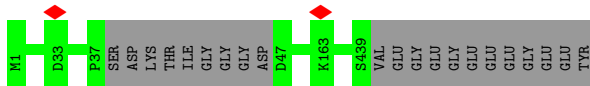
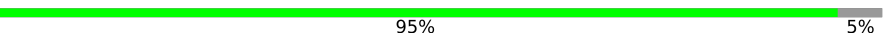
- Molecule 42: Tubulin alpha-1A chain

Chain VG:



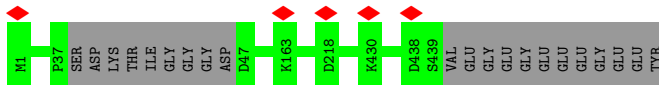
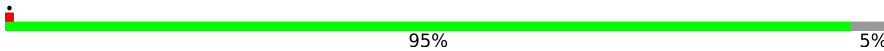
- Molecule 42: Tubulin alpha-1A chain

Chain VI:



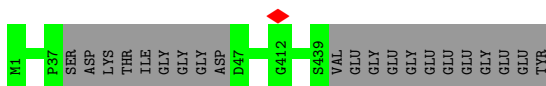
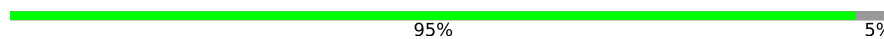
- Molecule 42: Tubulin alpha-1A chain

Chain VK:

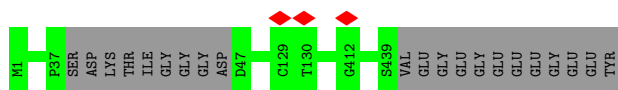


- Molecule 42: Tubulin alpha-1A chain

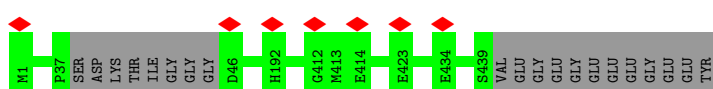
Chain VM:



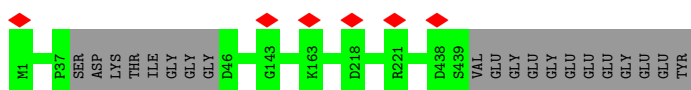
• Molecule 42: Tubulin alpha-1A chain



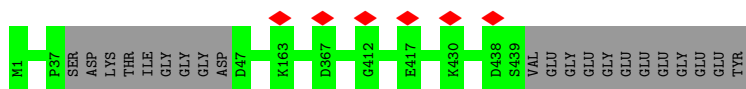
• Molecule 42: Tubulin alpha-1A chain



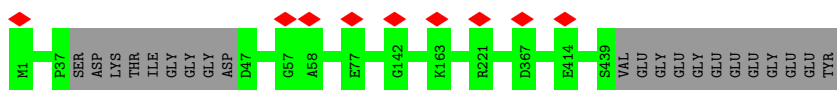
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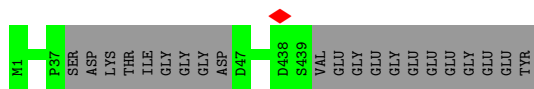
• Molecule 42: Tubulin alpha-1A chain



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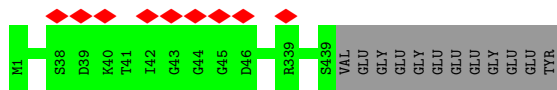


• Molecule 42: Tubulin alpha-1A chain



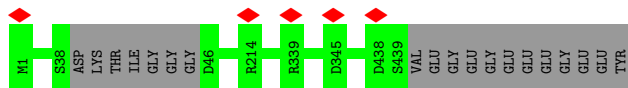
• Molecule 42: Tubulin alpha-1A chain





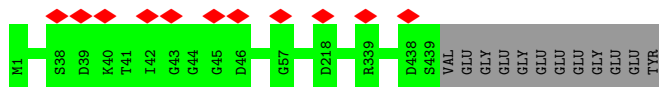
- Molecule 42: Tubulin alpha-1A chain

Chain WC: 96%



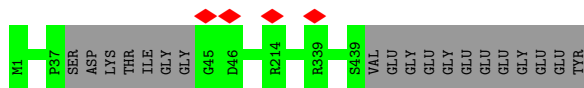
- Molecule 42: Tubulin alpha-1A chain

Chain WE: 97%



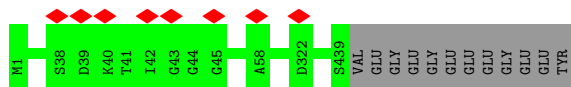
- Molecule 42: Tubulin alpha-1A chain

Chain WG: 96%



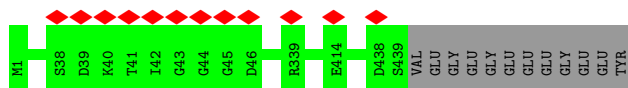
- Molecule 42: Tubulin alpha-1A chain

Chain WI: 97%



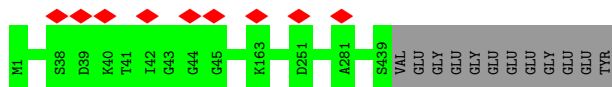
- Molecule 42: Tubulin alpha-1A chain

Chain WK: 97%



- Molecule 42: Tubulin alpha-1A chain

Chain WM: 97%



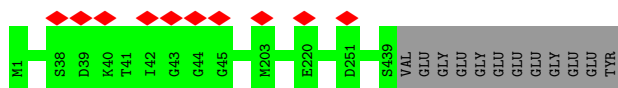
- Molecule 42: Tubulin alpha-1A chain

Chain WO:  96%



• Molecule 42: Tubulin alpha-1A chain

Chain WQ:  97%



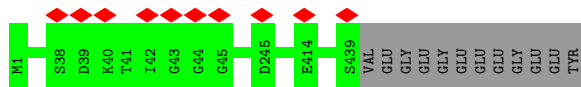
• Molecule 42: Tubulin alpha-1A chain

Chain WS:  96%



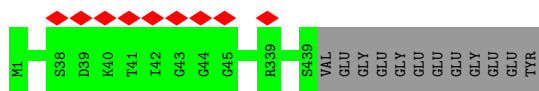
• Molecule 42: Tubulin alpha-1A chain

Chain WU:  97%



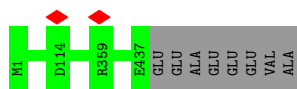
• Molecule 42: Tubulin alpha-1A chain

Chain WW:  97%



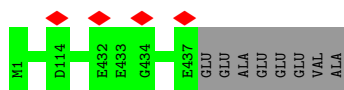
• Molecule 43: Tubulin beta-4B chain

Chain AB:  98%



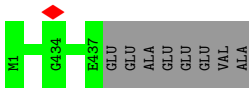
• Molecule 43: Tubulin beta-4B chain

Chain AD:  98%



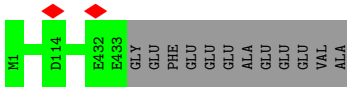
- Molecule 43: Tubulin beta-4B chain

Chain AF:  98%



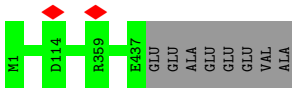
- Molecule 43: Tubulin beta-4B chain

Chain AH:  97%



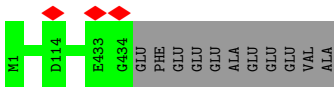
- Molecule 43: Tubulin beta-4B chain

Chain AJ:  98%



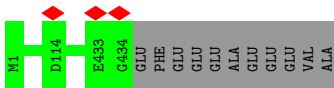
- Molecule 43: Tubulin beta-4B chain

Chain AL:  98%



- Molecule 43: Tubulin beta-4B chain

Chain AN:  98%



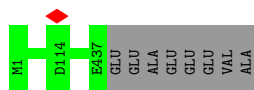
- Molecule 43: Tubulin beta-4B chain

Chain AP:  98%

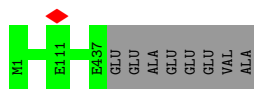


- Molecule 43: Tubulin beta-4B chain

Chain AR:  98%



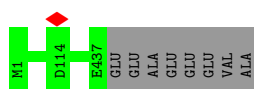
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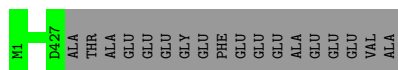
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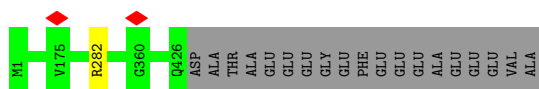
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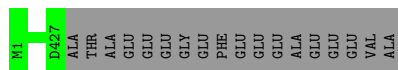
• Molecule 43: Tubulin beta-4B chain



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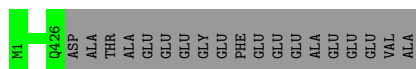


• Molecule 43: Tubulin beta-4B chain

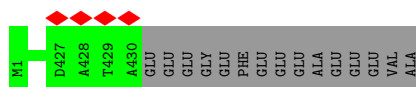


• Molecule 43: Tubulin beta-4B chain

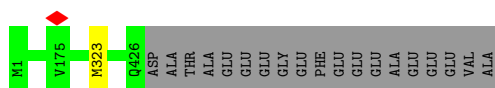




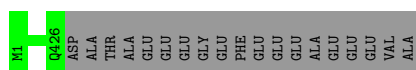
- Molecule 43: Tubulin beta-4B chain



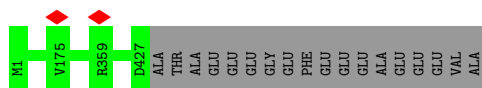
- Molecule 43: Tubulin beta-4B chain



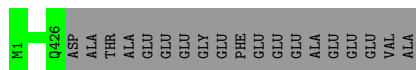
- Molecule 43: Tubulin beta-4B chain



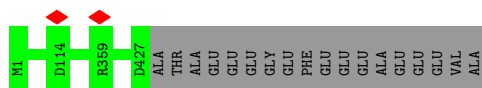
- Molecule 43: Tubulin beta-4B chain



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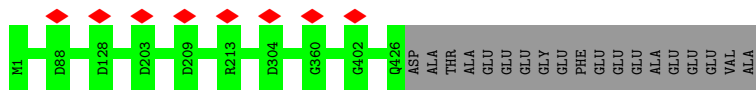


- Molecule 43: Tubulin beta-4B chain

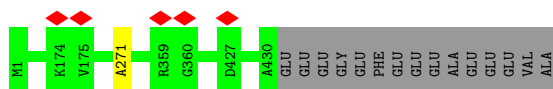


- Molecule 43: Tubulin beta-4B chain

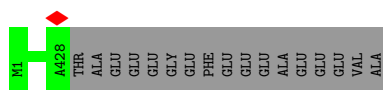




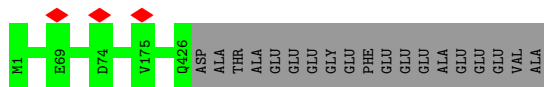
- Molecule 43: Tubulin beta-4B chain



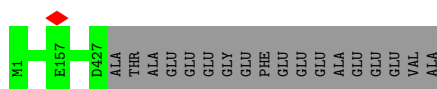
- Molecule 43: Tubulin beta-4B chain



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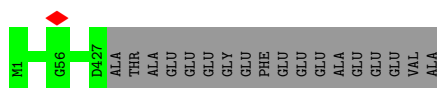
- Molecule 43: Tubulin beta-4B chain



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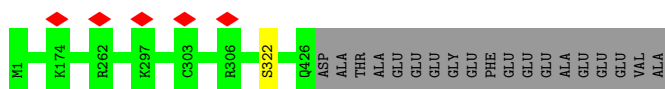


- Molecule 43: Tubulin beta-4B chain



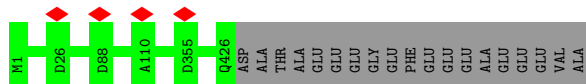
- Molecule 43: Tubulin beta-4B chain

Chain CL:  96%



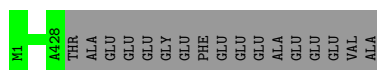
- Molecule 43: Tubulin beta-4B chain

Chain CN:  96%



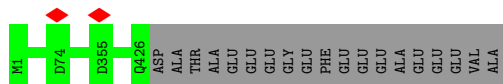
- Molecule 43: Tubulin beta-4B chain

Chain CP:  96%



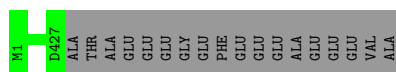
- Molecule 43: Tubulin beta-4B chain

Chain CR:  96%



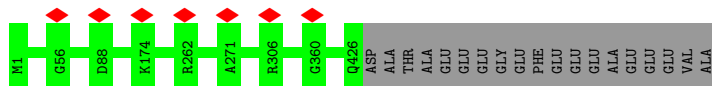
- Molecule 43: Tubulin beta-4B chain

Chain CT:  96%



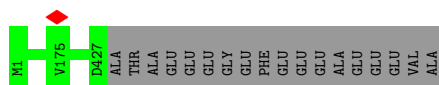
- Molecule 43: Tubulin beta-4B chain

Chain CV:  96%



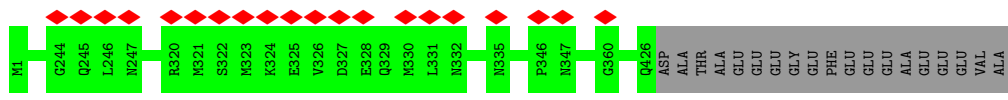
- Molecule 43: Tubulin beta-4B chain

Chain CX:  96%



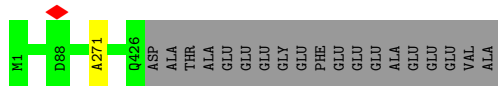
- Molecule 43: Tubulin beta-4B chain

Chain CZ:  96%



• Molecule 43: Tubulin beta-4B chain

Chain DB:  96%



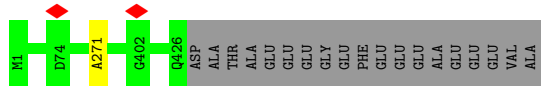
• Molecule 43: Tubulin beta-4B chain

Chain DD:  96%



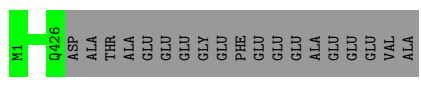
• Molecule 43: Tubulin beta-4B chain

Chain DF:  96%



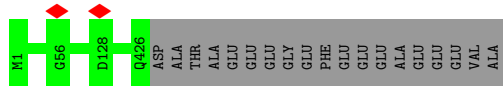
• Molecule 43: Tubulin beta-4B chain

Chain DH:  96%



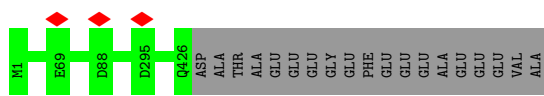
• Molecule 43: Tubulin beta-4B chain

Chain DJ:  96%



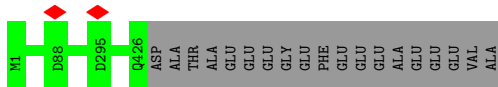
• Molecule 43: Tubulin beta-4B chain

Chain DL:  96%



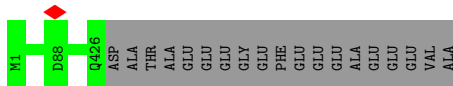
• Molecule 43: Tubulin beta-4B chain

Chain DN:  96%



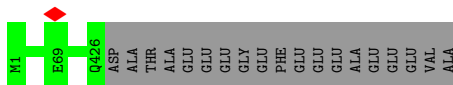
- Molecule 43: Tubulin beta-4B chain

Chain DP:  96%



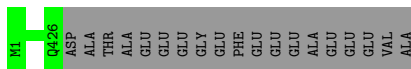
- Molecule 43: Tubulin beta-4B chain

Chain DR:  96%



- Molecule 43: Tubulin beta-4B chain

Chain DT:  96%



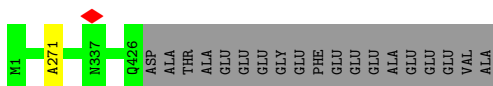
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Chain DV:  96%



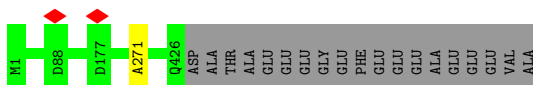
- Molecule 43: Tubulin beta-4B chain

Chain DX:  96%

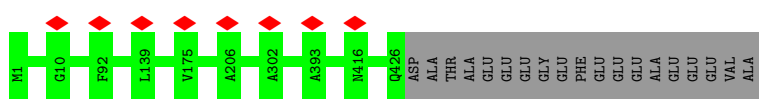


- Molecule 43: Tubulin beta-4B chain

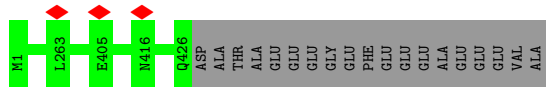
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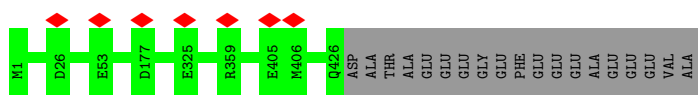
- Molecule 43: Tubulin beta-4B chain



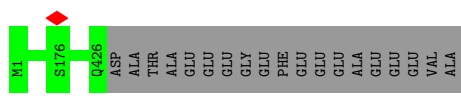
• Molecule 43: Tubulin beta-4B chain



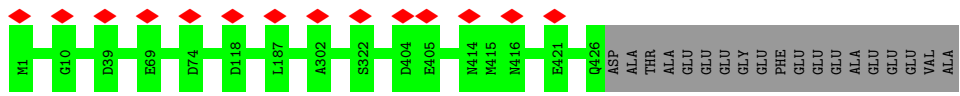
• Molecule 43: Tubulin beta-4B chain



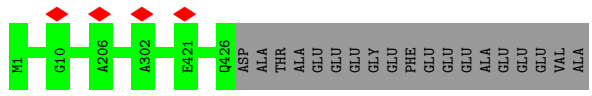
• Molecule 43: Tubulin beta-4B chain



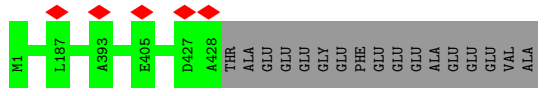
• Molecule 43: Tubulin beta-4B chain



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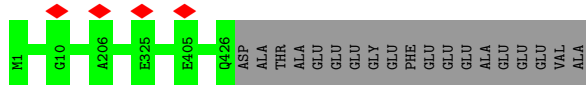
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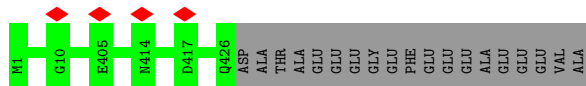
• Molecule 43: Tubulin beta-4B chain



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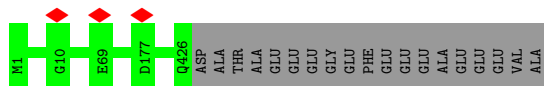
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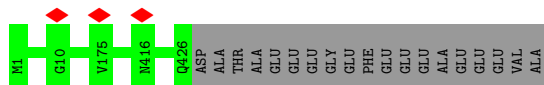
• Molecule 43: Tubulin beta-4B chain



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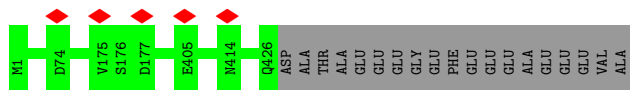


• Molecule 43: Tubulin beta-4B chain

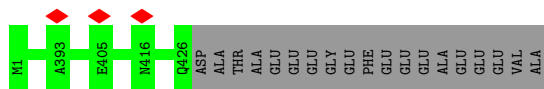


• Molecule 43: Tubulin beta-4B chain





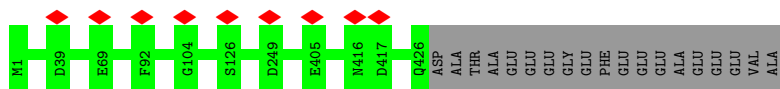
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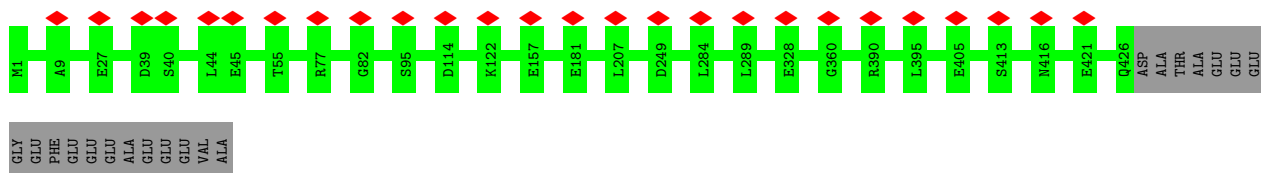
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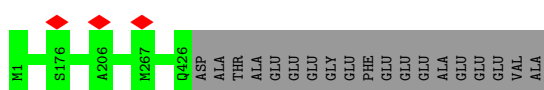
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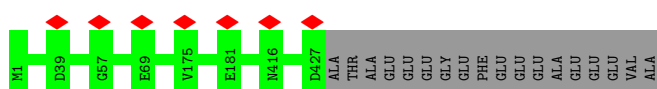
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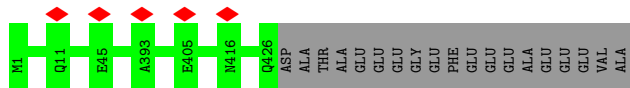
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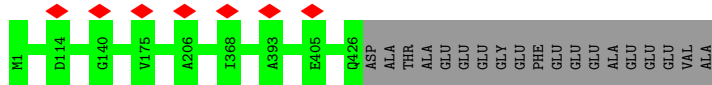
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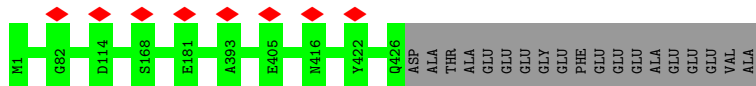
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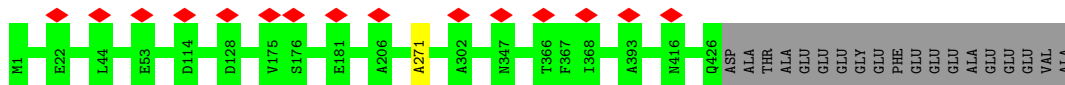
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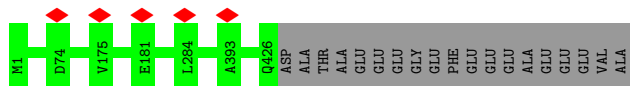
• Molecule 43: Tubulin beta-4B chain



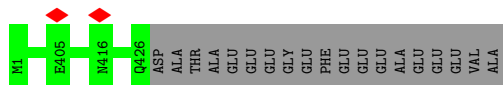
• Molecule 43: Tubulin beta-4B chain



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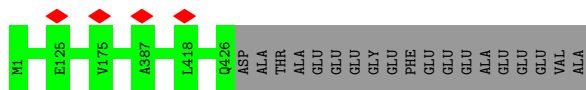


• Molecule 43: Tubulin beta-4B chain



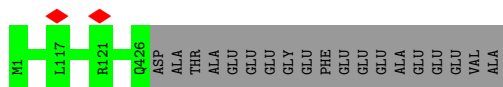
• Molecule 43: Tubulin beta-4B chain





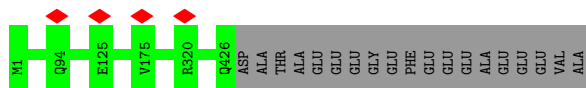
- Molecule 43: Tubulin beta-4B chain

Chain GD: 96%



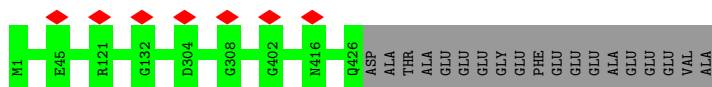
- Molecule 43: Tubulin beta-4B chain

Chain GF: 96%



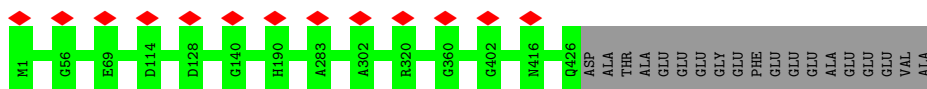
- Molecule 43: Tubulin beta-4B chain

Chain GH: 96%



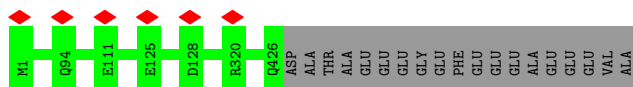
- Molecule 43: Tubulin beta-4B chain

Chain GJ: 96%



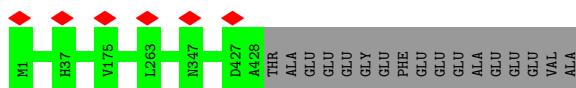
- Molecule 43: Tubulin beta-4B chain

Chain GL: 96%



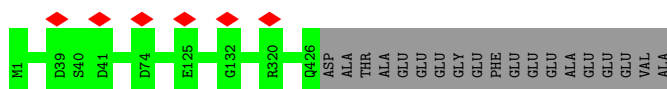
- Molecule 43: Tubulin beta-4B chain

Chain GN: 96%



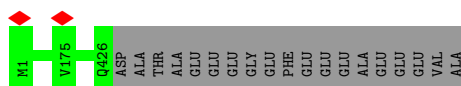
- Molecule 43: Tubulin beta-4B chain

Chain GP:  96%



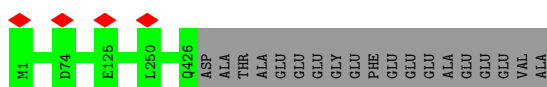
- Molecule 43: Tubulin beta-4B chain

Chain GR:  96%



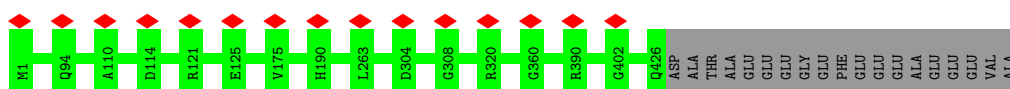
- Molecule 43: Tubulin beta-4B chain

Chain GT:  96%



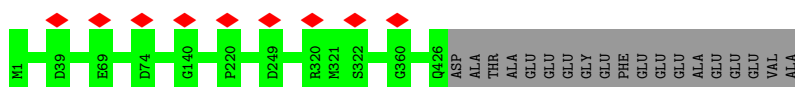
- Molecule 43: Tubulin beta-4B chain

Chain GV:  96%



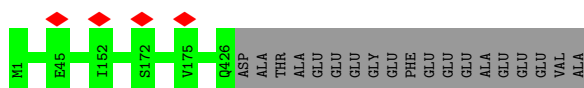
- Molecule 43: Tubulin beta-4B chain

Chain GX:  96%



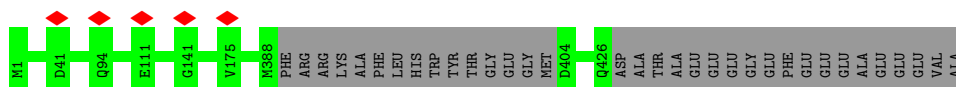
- Molecule 43: Tubulin beta-4B chain

Chain GZ:  96%



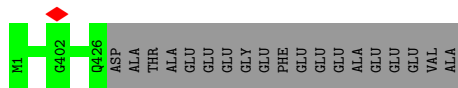
- Molecule 43: Tubulin beta-4B chain

Chain HB:  92% 8%



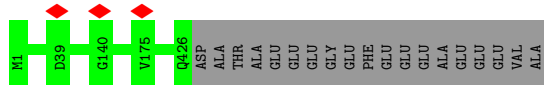
• Molecule 43: Tubulin beta-4B chain

Chain HD:  96%



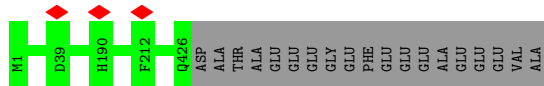
• Molecule 43: Tubulin beta-4B chain

Chain HF:  96%



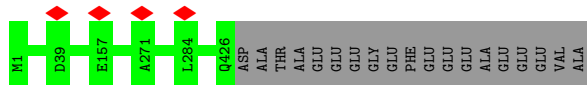
• Molecule 43: Tubulin beta-4B chain

Chain HH:  96%



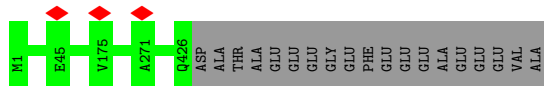
• Molecule 43: Tubulin beta-4B chain

Chain HJ:  96%



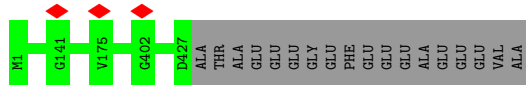
• Molecule 43: Tubulin beta-4B chain

Chain HL:  96%



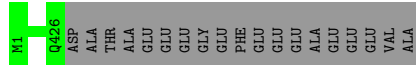
• Molecule 43: Tubulin beta-4B chain

Chain HN:  96%

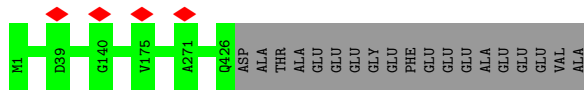


• Molecule 43: Tubulin beta-4B chain

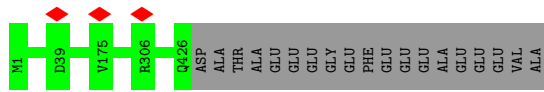
Chain HP:  96%



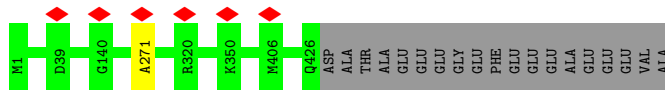
• Molecule 43: Tubulin beta-4B chain



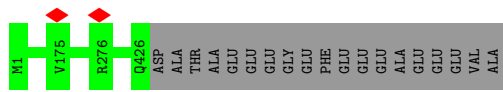
• Molecule 43: Tubulin beta-4B chain



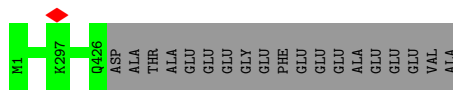
• Molecule 43: Tubulin beta-4B chain



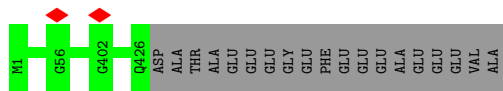
• Molecule 43: Tubulin beta-4B chain



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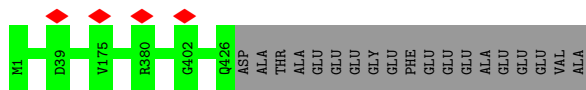


• Molecule 43: Tubulin beta-4B chain



• Molecule 43: Tubulin beta-4B chain





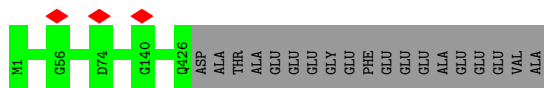
- Molecule 43: Tubulin beta-4B chain

Chain IF: 96%



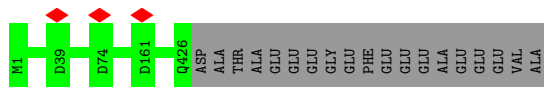
- Molecule 43: Tubulin beta-4B chain

Chain IH: 96%



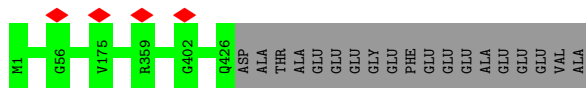
- Molecule 43: Tubulin beta-4B chain

Chain IJ: 96%



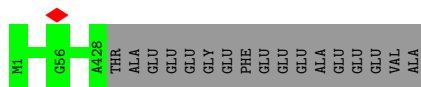
- Molecule 43: Tubulin beta-4B chain

Chain IL: 96%



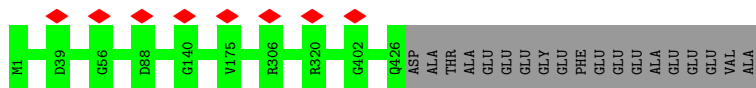
- Molecule 43: Tubulin beta-4B chain

Chain IN: 96%

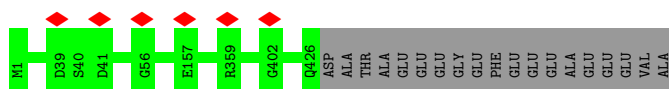


- Molecule 43: Tubulin beta-4B chain

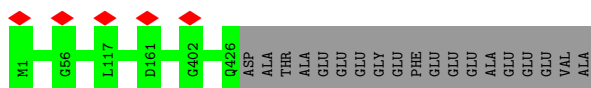
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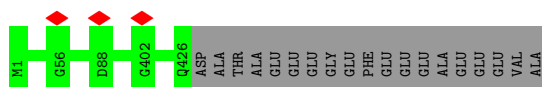
- Molecule 43: Tubulin beta-4B chain



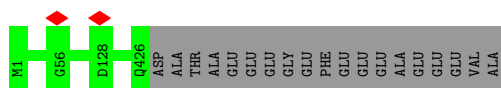
• Molecule 43: Tubulin beta-4B chain



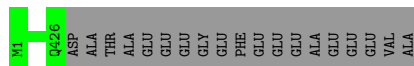
• Molecule 43: Tubulin beta-4B chain



• Molecule 43: Tubulin beta-4B chain



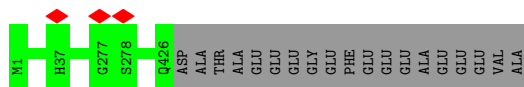
• Molecule 43: Tubulin beta-4B chain



• Molecule 43: Tubulin beta-4B chain

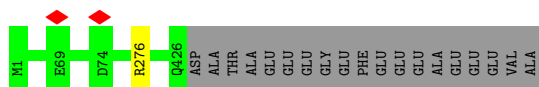


• Molecule 43: Tubulin beta-4B chain



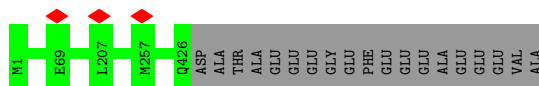
• Molecule 43: Tubulin beta-4B chain

Chain JH:  96%



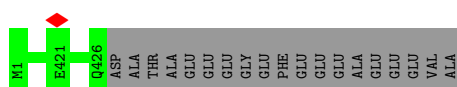
• Molecule 43: Tubulin beta-4B chain

Chain JJ:  96%



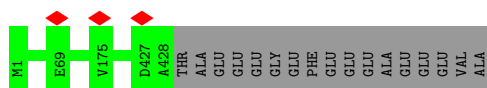
• Molecule 43: Tubulin beta-4B chain

Chain JL:  96%



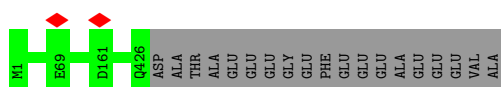
• Molecule 43: Tubulin beta-4B chain

Chain JN:  96%



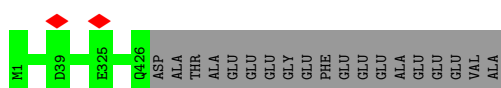
• Molecule 43: Tubulin beta-4B chain

Chain JP:  96%



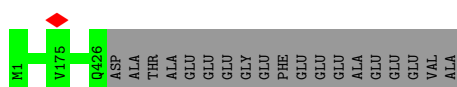
• Molecule 43: Tubulin beta-4B chain

Chain JR:  96%



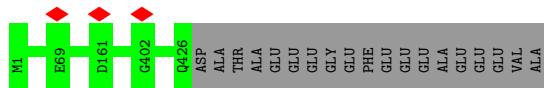
• Molecule 43: Tubulin beta-4B chain

Chain JT:  96%



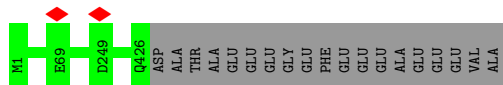
- Molecule 43: Tubulin beta-4B chain

Chain JV:  96%



- Molecule 43: Tubulin beta-4B chain

Chain JX:  96%



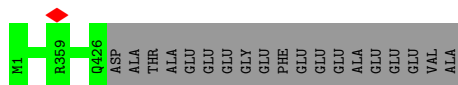
- Molecule 43: Tubulin beta-4B chain

Chain JZ:  96%



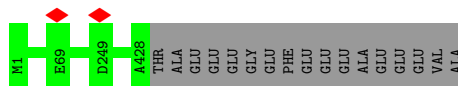
- Molecule 43: Tubulin beta-4B chain

Chain KB:  96%



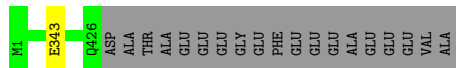
- Molecule 43: Tubulin beta-4B chain

Chain KD:  96%



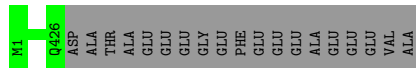
- Molecule 43: Tubulin beta-4B chain

Chain KF:  96%



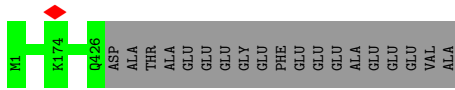
- Molecule 43: Tubulin beta-4B chain

Chain KH:  96%



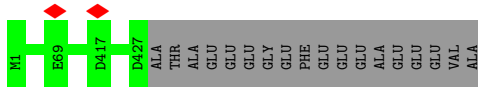
- Molecule 43: Tubulin beta-4B chain

Chain KJ:  96%



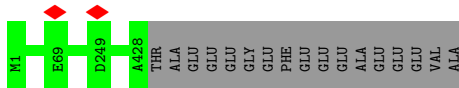
- Molecule 43: Tubulin beta-4B chain

Chain KL:  96%



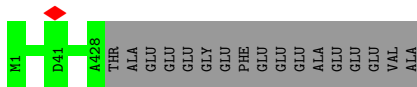
- Molecule 43: Tubulin beta-4B chain

Chain KN:  96%



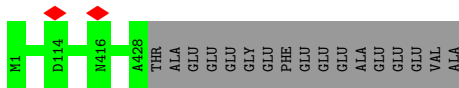
- Molecule 43: Tubulin beta-4B chain

Chain KP:  96%



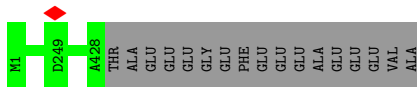
- Molecule 43: Tubulin beta-4B chain

Chain KR:  96%



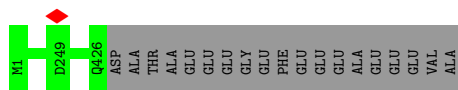
- Molecule 43: Tubulin beta-4B chain

Chain KT:  96%



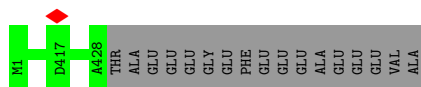
- Molecule 43: Tubulin beta-4B chain

Chain KV:  96%



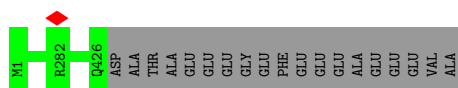
- Molecule 43: Tubulin beta-4B chain

Chain KX: 96%



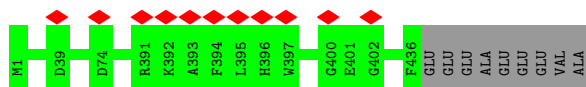
- Molecule 43: Tubulin beta-4B chain

Chain KZ: 96%



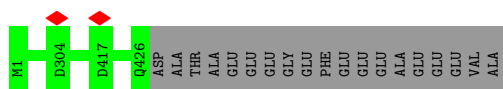
- Molecule 43: Tubulin beta-4B chain

Chain LB: 98%



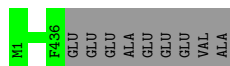
- Molecule 43: Tubulin beta-4B chain

Chain LD: 96%



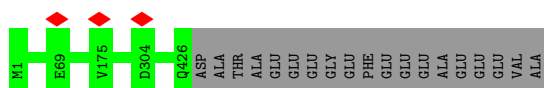
- Molecule 43: Tubulin beta-4B chain

Chain LF: 98%



- Molecule 43: Tubulin beta-4B chain

Chain LH: 96%



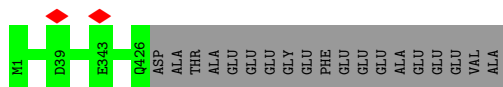
- Molecule 43: Tubulin beta-4B chain

Chain LJ: 98%



- Molecule 43: Tubulin beta-4B chain

Chain LL: 96%



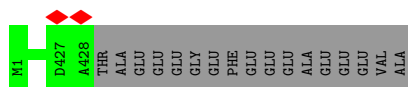
- Molecule 43: Tubulin beta-4B chain

Chain LN: 98%



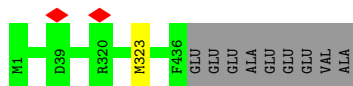
- Molecule 43: Tubulin beta-4B chain

Chain LP: 96%



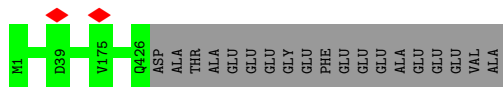
- Molecule 43: Tubulin beta-4B chain

Chain LR: 98%



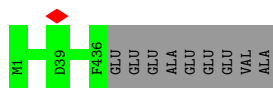
- Molecule 43: Tubulin beta-4B chain

Chain LT: 96%



- Molecule 43: Tubulin beta-4B chain

Chain LV: 98%



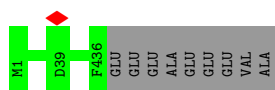
- Molecule 43: Tubulin beta-4B chain

Chain LX:  96%



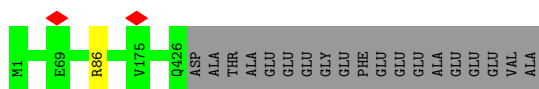
• Molecule 43: Tubulin beta-4B chain

Chain LZ:  98%



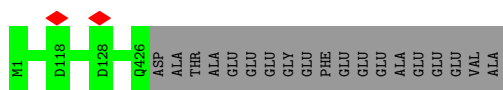
• Molecule 43: Tubulin beta-4B chain

Chain MD:  96%



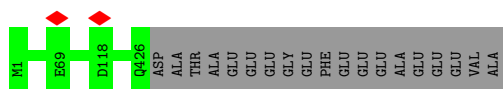
• Molecule 43: Tubulin beta-4B chain

Chain MF:  96%



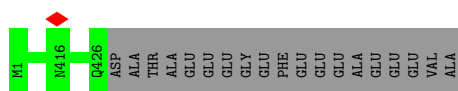
• Molecule 43: Tubulin beta-4B chain

Chain MH:  96%

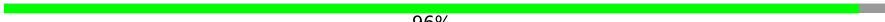


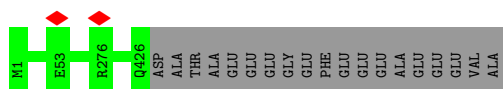
• Molecule 43: Tubulin beta-4B chain

Chain MJ:  96%



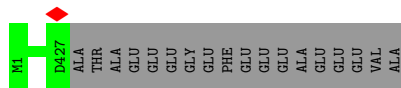
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Chain ML:  96%



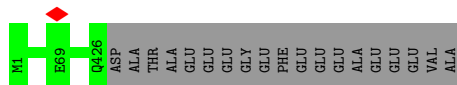
- Molecule 43: Tubulin beta-4B chain

Chain MN:  96%



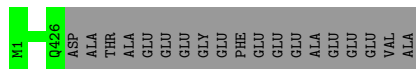
- Molecule 43: Tubulin beta-4B chain

Chain MP:  96%



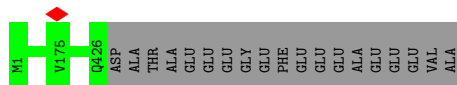
- Molecule 43: Tubulin beta-4B chain

Chain MR:  96%



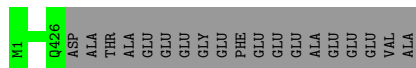
- Molecule 43: Tubulin beta-4B chain

Chain MT:  96%



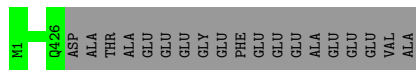
- Molecule 43: Tubulin beta-4B chain

Chain MV:  96%



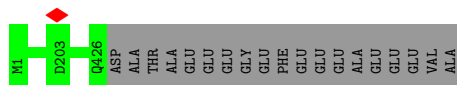
- Molecule 43: Tubulin beta-4B chain

Chain MX:  96%

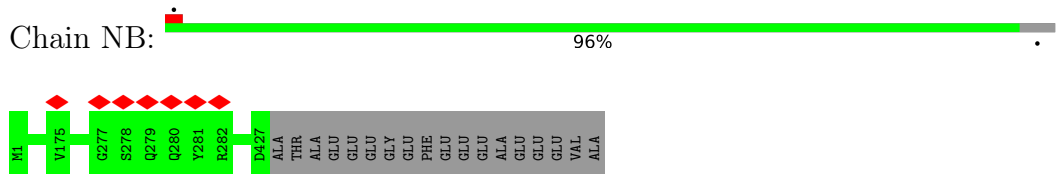


- Molecule 43: Tubulin beta-4B chain

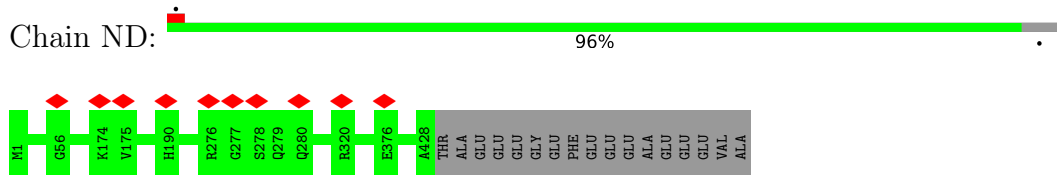
Chain MZ:  96%



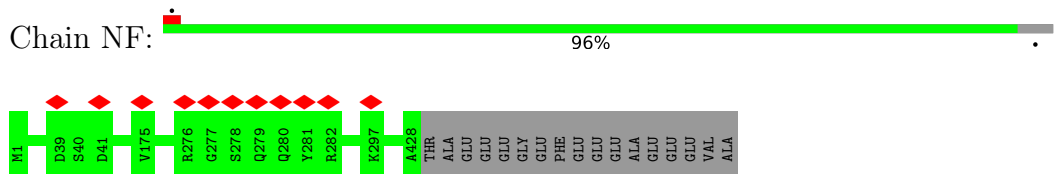
• Molecule 43: Tubulin beta-4B chain



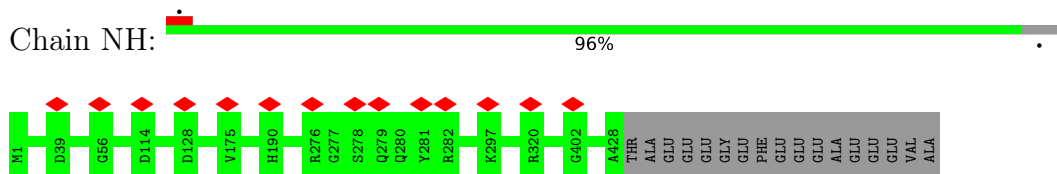
• Molecule 43: Tubulin beta-4B chain



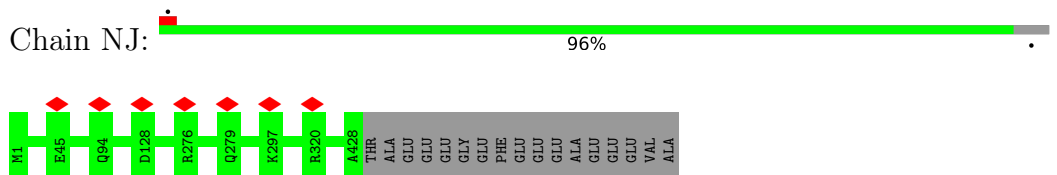
• Molecule 43: Tubulin beta-4B chain



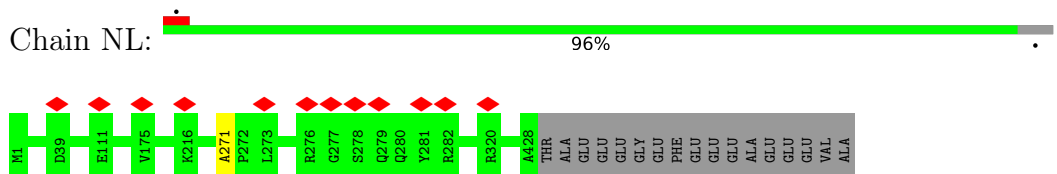
• Molecule 43: Tubulin beta-4B chain



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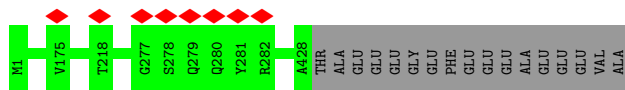


• Molecule 43: Tubulin beta-4B chain



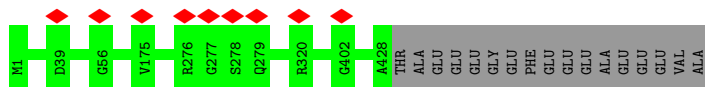
• Molecule 43: Tubulin beta-4B chain





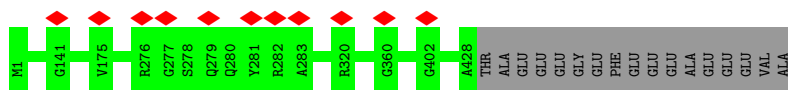
- Molecule 43: Tubulin beta-4B chain

Chain NP: 96%



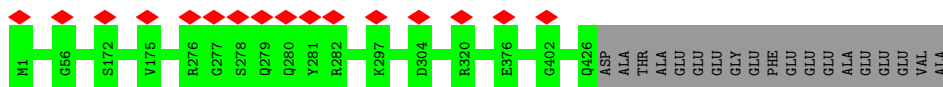
- Molecule 43: Tubulin beta-4B chain

Chain NR: 96%



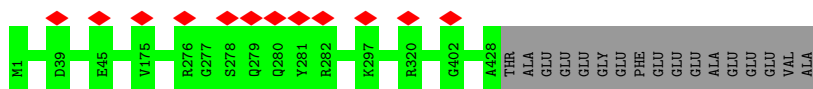
- Molecule 43: Tubulin beta-4B chain

Chain NT: 96%



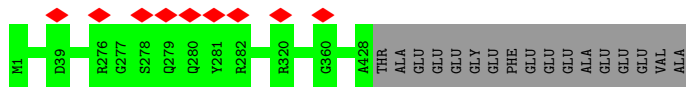
- Molecule 43: Tubulin beta-4B chain

Chain NV: 96%



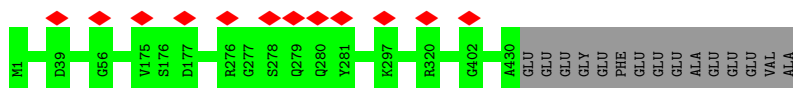
- Molecule 43: Tubulin beta-4B chain

Chain NX: 96%



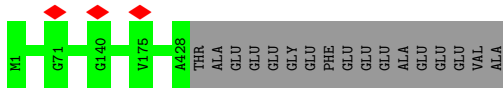
- Molecule 43: Tubulin beta-4B chain

Chain NZ: 97%



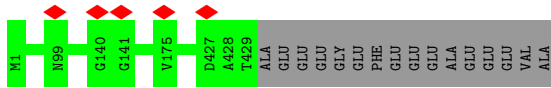
- Molecule 43: Tubulin beta-4B chain

Chain OB:  96%



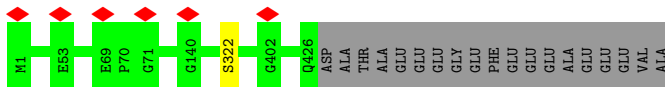
• Molecule 43: Tubulin beta-4B chain

Chain OD:  96%



• Molecule 43: Tubulin beta-4B chain

Chain OF:  96%



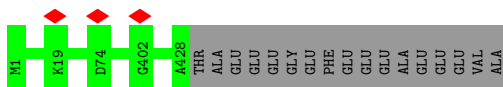
• Molecule 43: Tubulin beta-4B chain

Chain OH:  96%



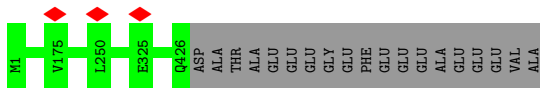
• Molecule 43: Tubulin beta-4B chain

Chain OJ:  96%



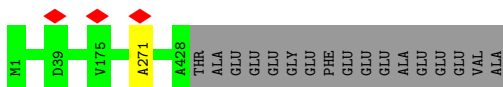
• Molecule 43: Tubulin beta-4B chain

Chain OL:  96%

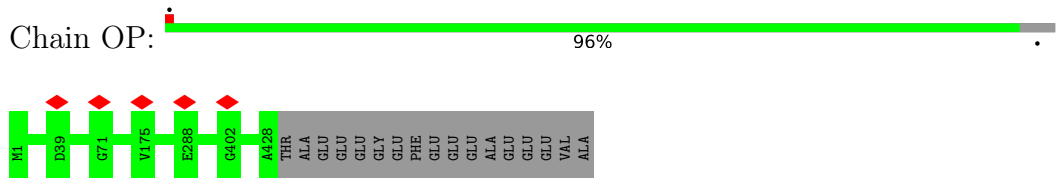


• Molecule 43: Tubulin beta-4B chain

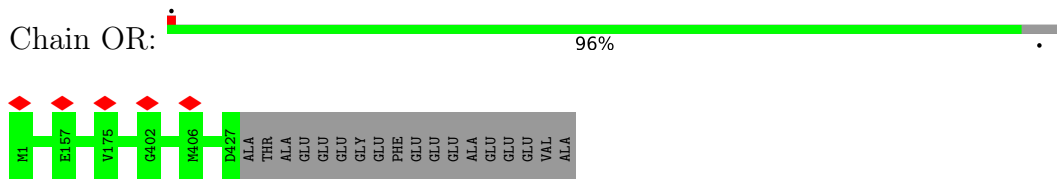
Chain ON:  96%



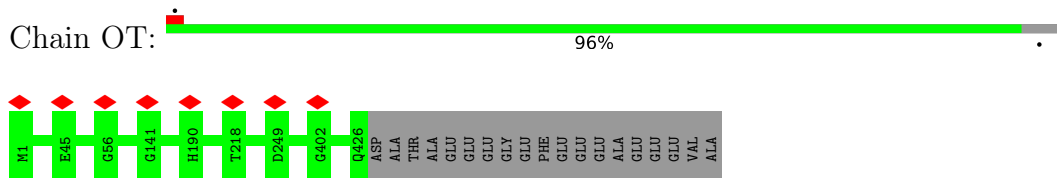
• Molecule 43: Tubulin beta-4B chain



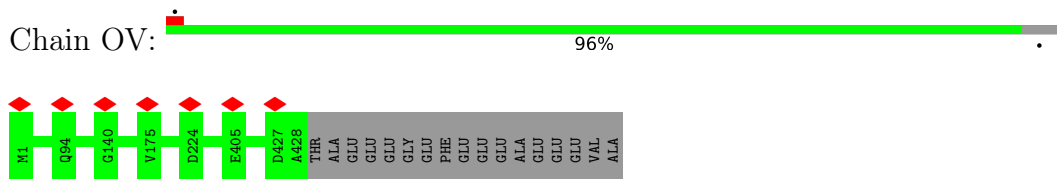
• Molecule 43: Tubulin beta-4B chain



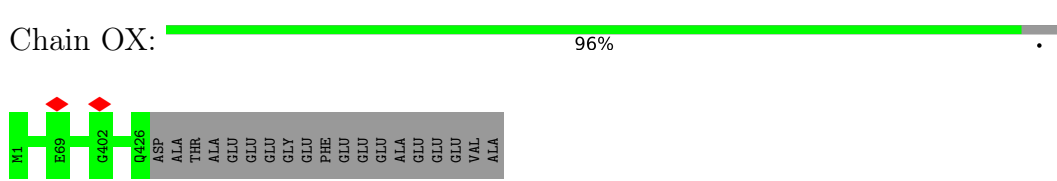
• Molecule 43: Tubulin beta-4B chain



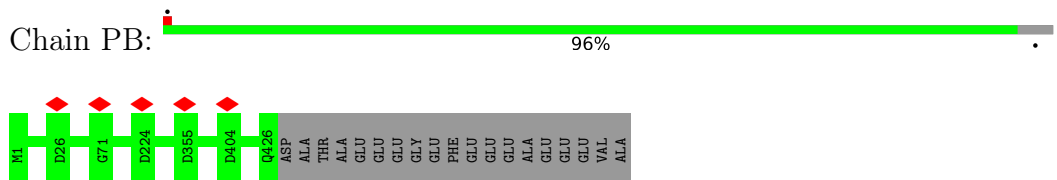
• Molecule 43: Tubulin beta-4B chain



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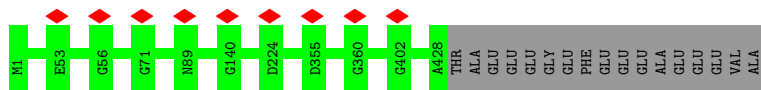


• Molecule 43: Tubulin beta-4B chain

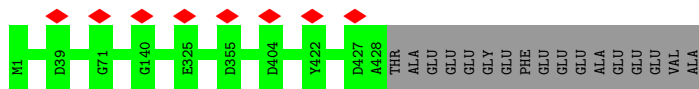


• Molecule 43: Tubulin beta-4B chain

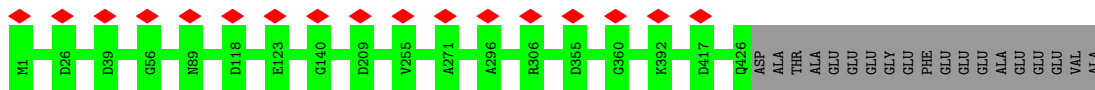




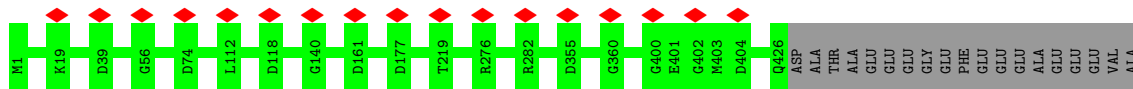
• Molecule 43: Tubulin beta-4B chain



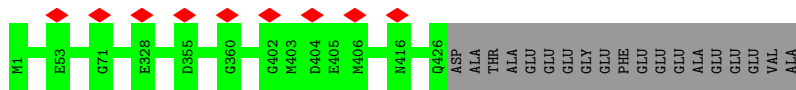
• Molecule 43: Tubulin beta-4B chain



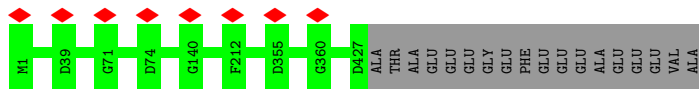
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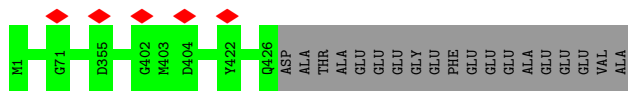
• Molecule 43: Tubulin beta-4B chain



• Molecule 43: Tubulin beta-4B chain

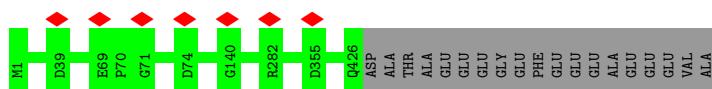


• Molecule 43: Tubulin beta-4B chain



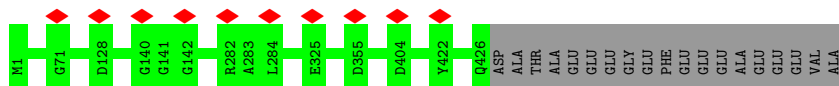
• Molecule 43: Tubulin beta-4B chain

Chain PR:  96%



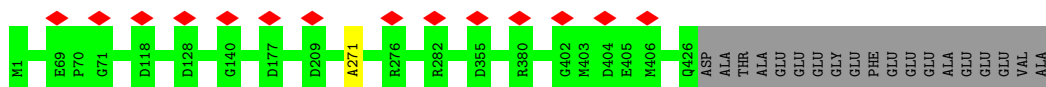
- Molecule 43: Tubulin beta-4B chain

Chain PT:  96%



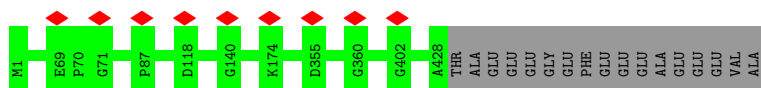
- Molecule 43: Tubulin beta-4B chain

Chain PV:  96%



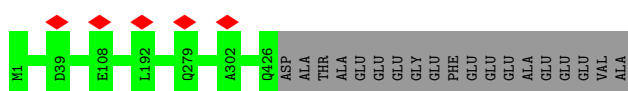
- Molecule 43: Tubulin beta-4B chain

Chain PX:  96%



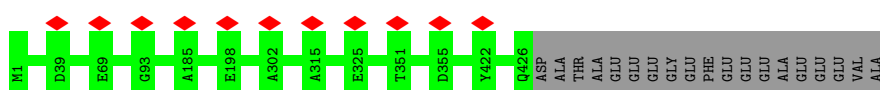
- Molecule 43: Tubulin beta-4B chain

Chain QB:  96%



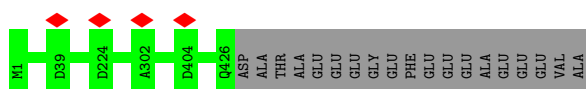
- Molecule 43: Tubulin beta-4B chain

Chain QD:  96%

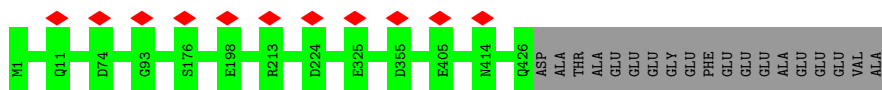


- Molecule 43: Tubulin beta-4B chain

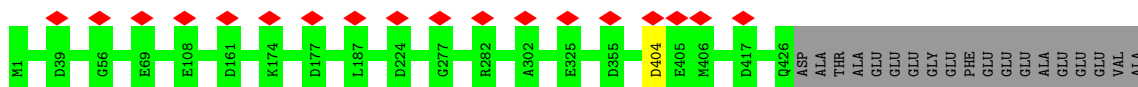
Chain QF:  96%



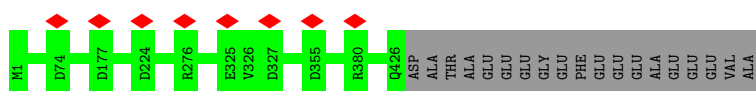
• Molecule 43: Tubulin beta-4B chain



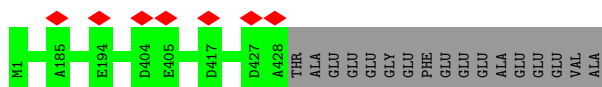
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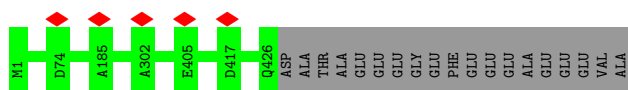
• Molecule 43: Tubulin beta-4B chain



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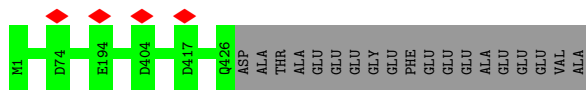


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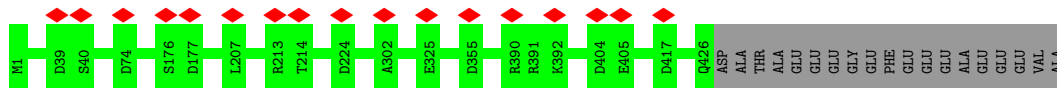
• Molecule 43: Tubulin beta-4B chain





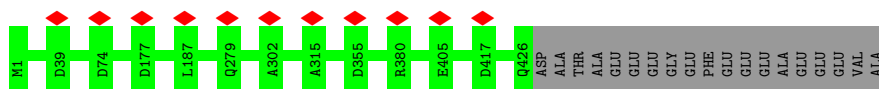
- Molecule 43: Tubulin beta-4B chain

Chain QV: 96%



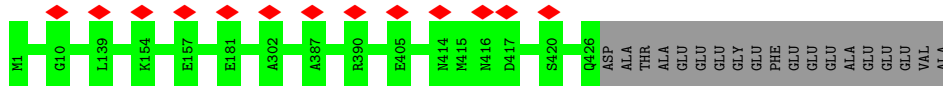
- Molecule 43: Tubulin beta-4B chain

Chain QX: 96%



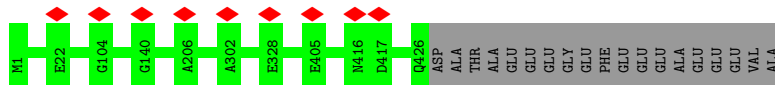
- Molecule 43: Tubulin beta-4B chain

Chain RB: 96%



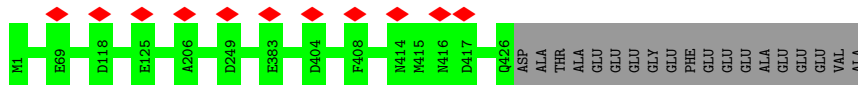
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Chain RD: 96%



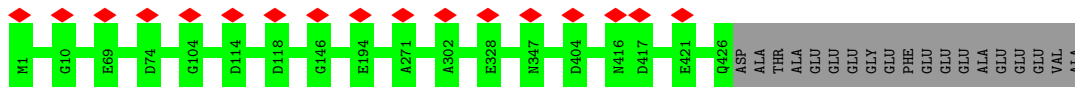
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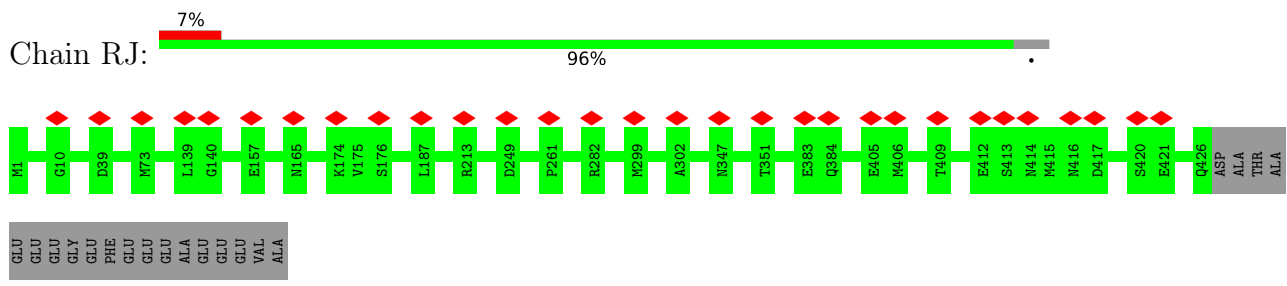


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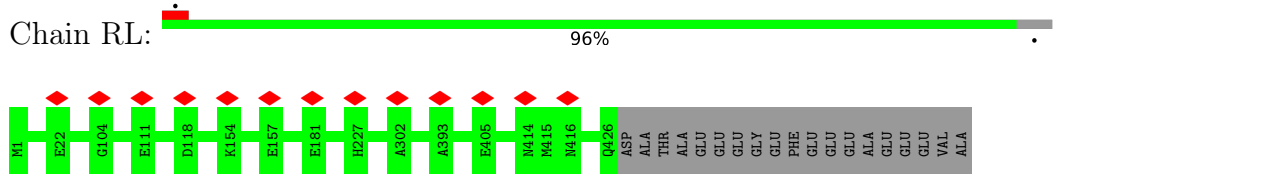
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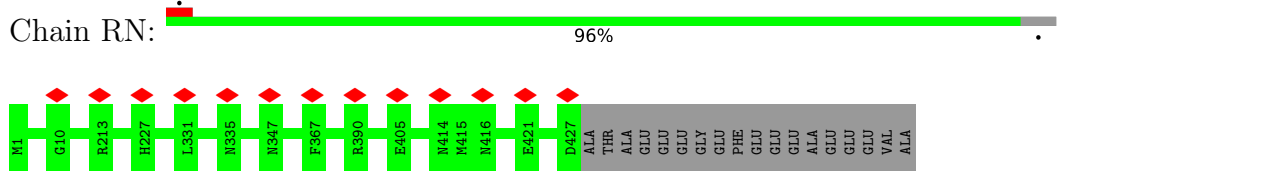
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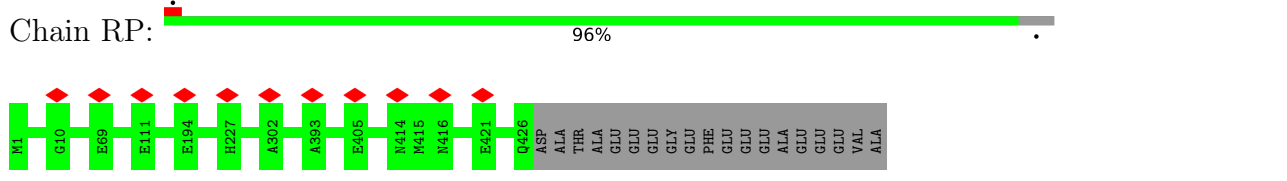
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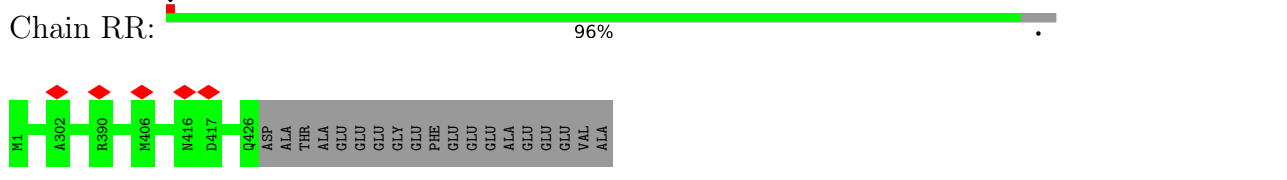
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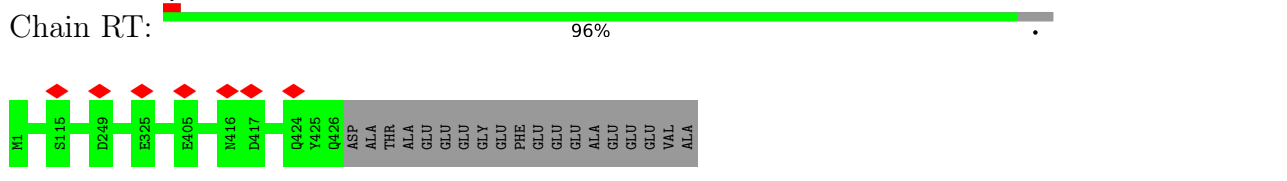
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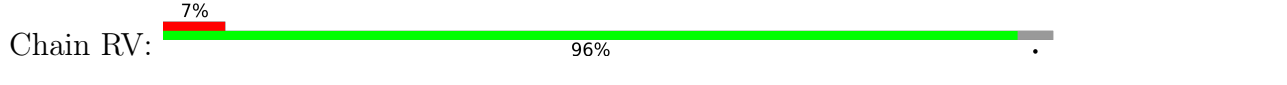
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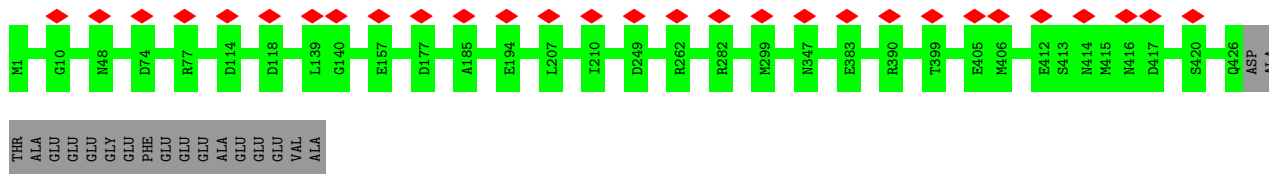


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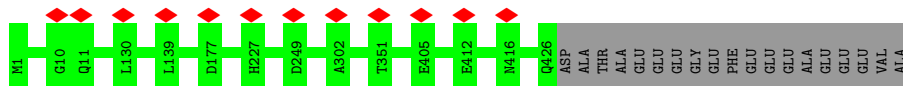


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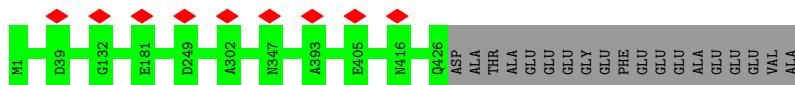




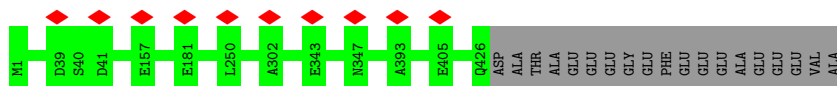
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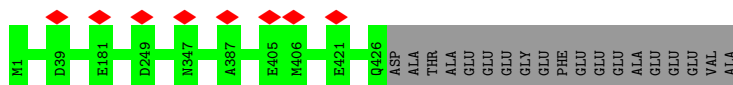
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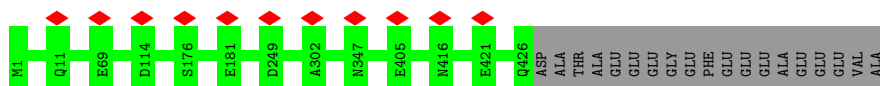
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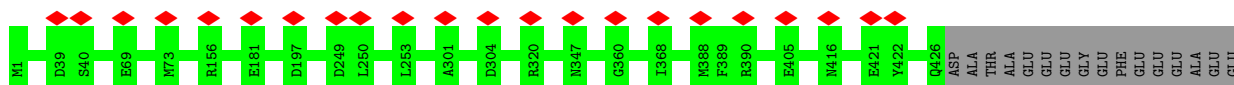
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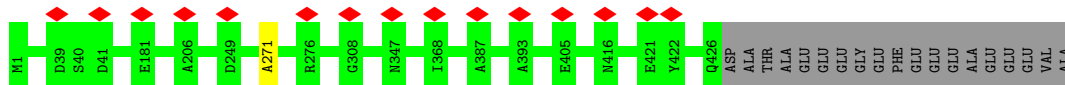


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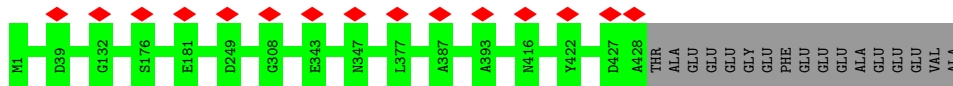


GLU
VAL
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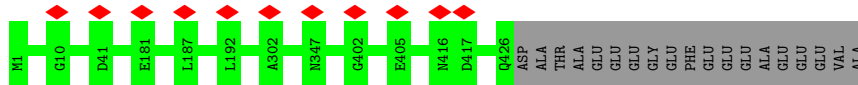
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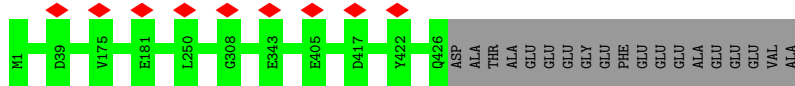
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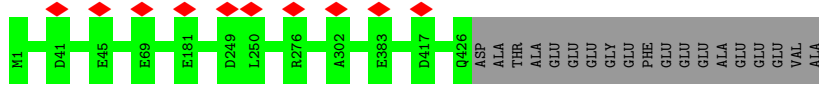
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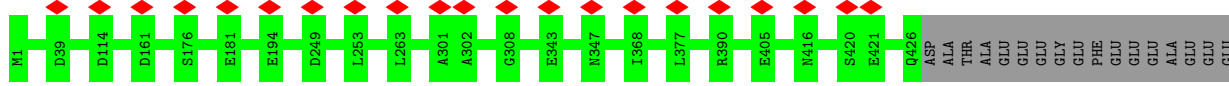
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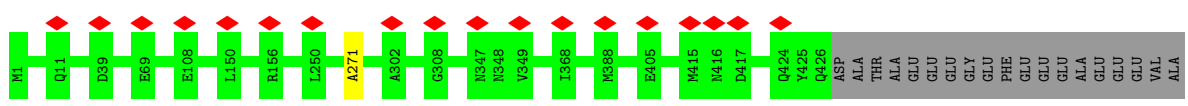


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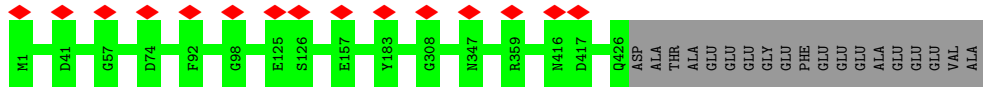


VAL
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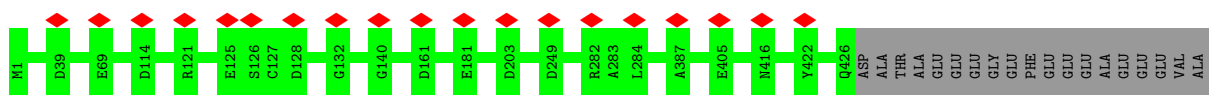
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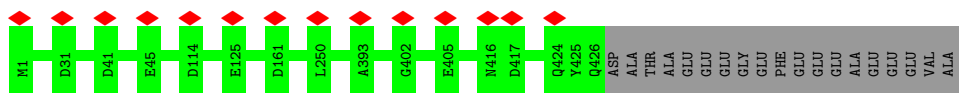
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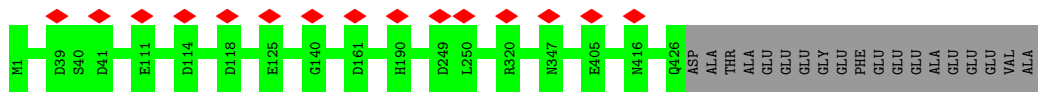
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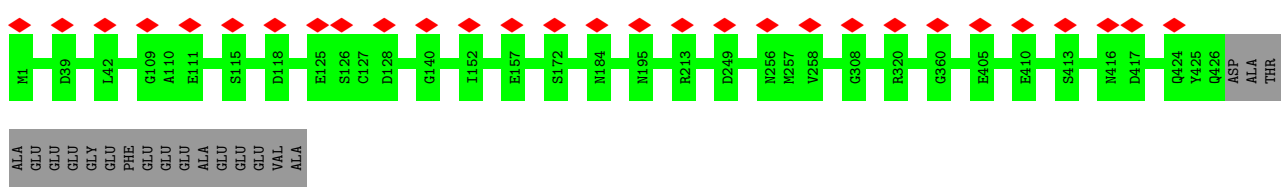
• Molecule 43: Tubulin beta-4B chain



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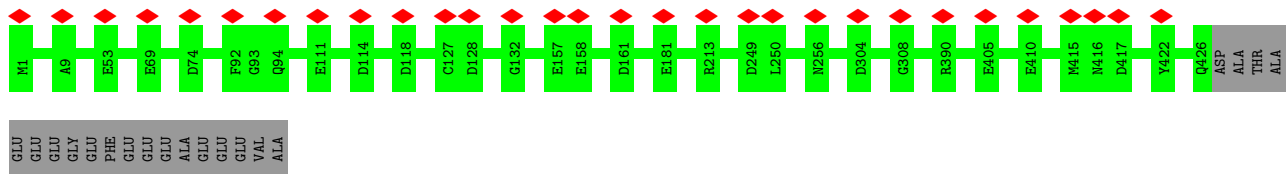


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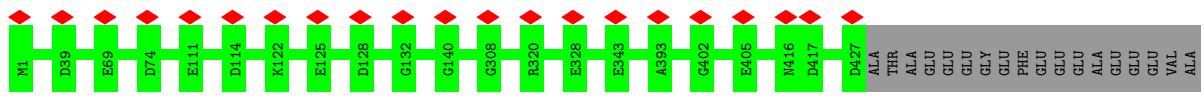


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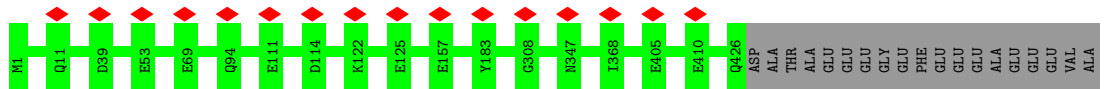




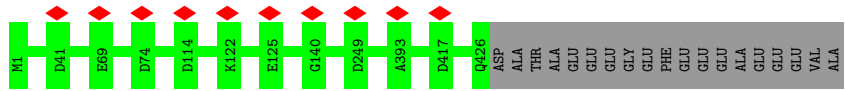
• Molecule 43: Tubulin beta-4B chain



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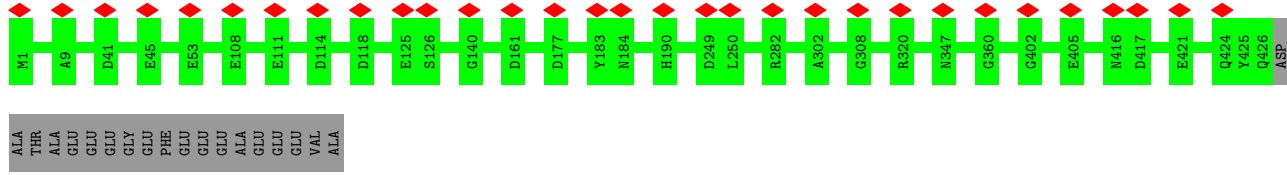
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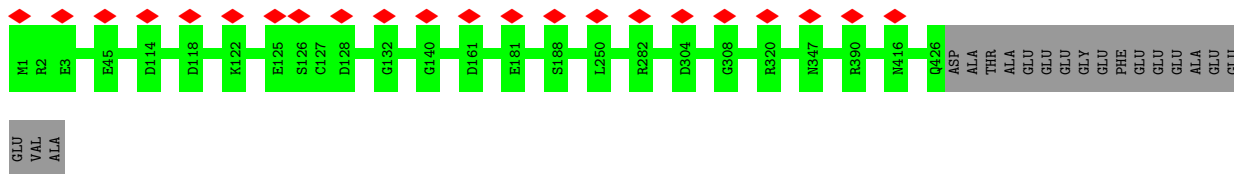


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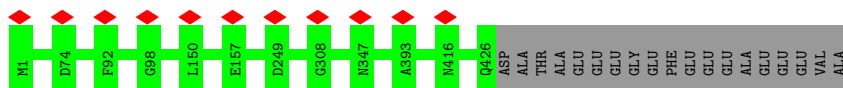


• Molecule 43: Tubulin beta-4B chain





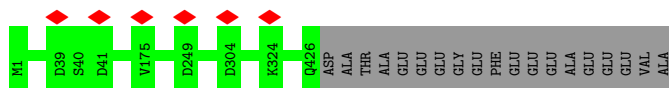
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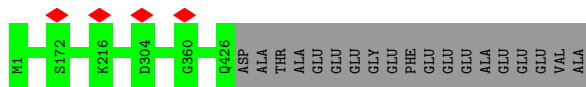
• Molecule 43: Tubulin beta-4B chain



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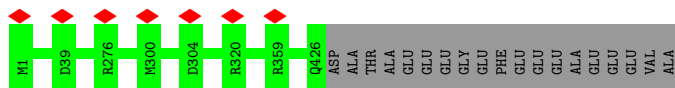
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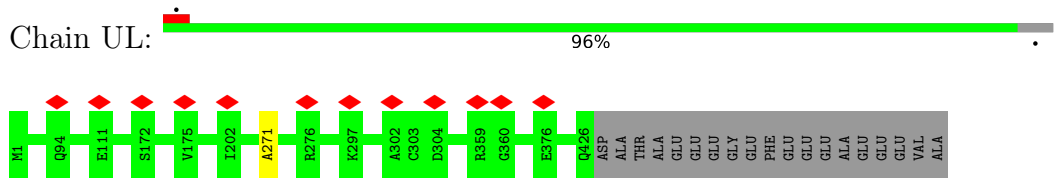
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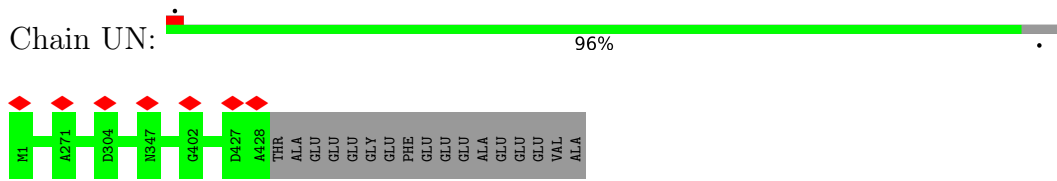
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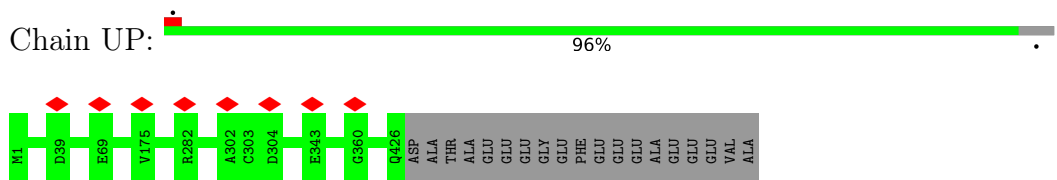
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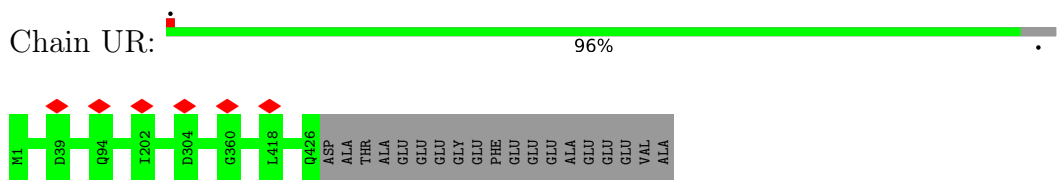
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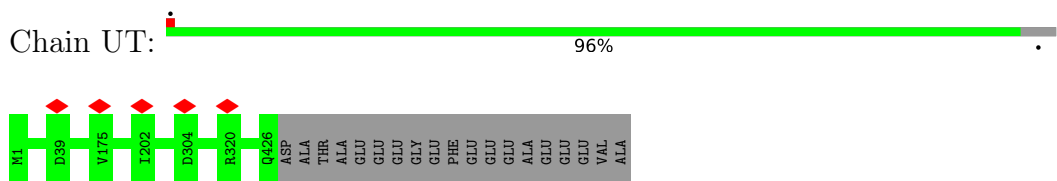
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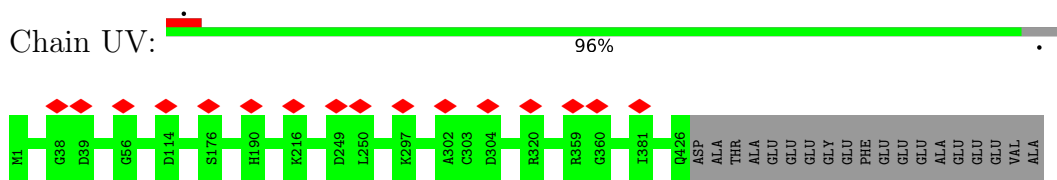
• Molecule 43: Tubulin beta-4B chain



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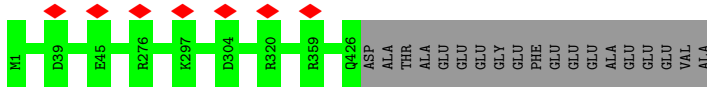


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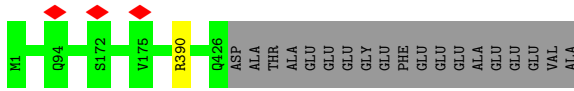


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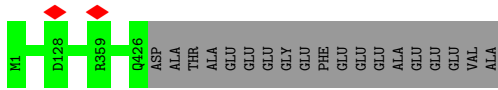




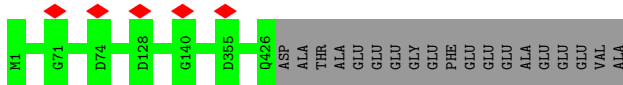
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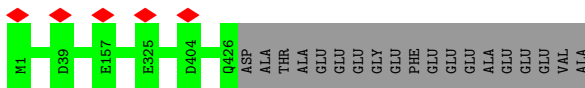
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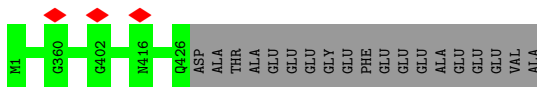
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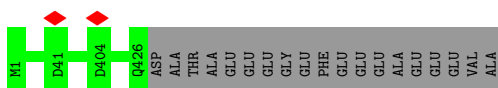
- Molecule 43: Tubulin beta-4B chain



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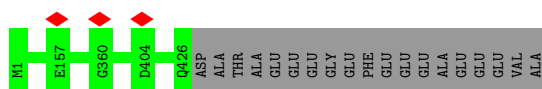


- Molecule 43: Tubulin beta-4B chain



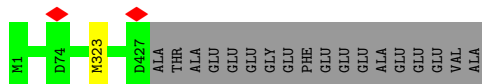
- Molecule 43: Tubulin beta-4B chain

Chain VL:  96%



• Molecule 43: Tubulin beta-4B chain

Chain VN:  96%



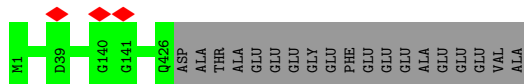
• Molecule 43: Tubulin beta-4B chain

Chain VP:  96%



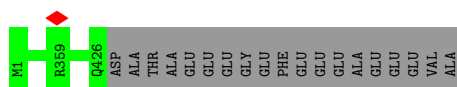
• Molecule 43: Tubulin beta-4B chain

Chain VR:  96%



• Molecule 43: Tubulin beta-4B chain

Chain VT:  96%



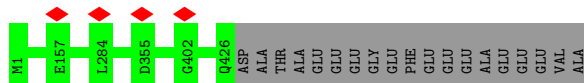
• Molecule 43: Tubulin beta-4B chain

Chain VV:  96%

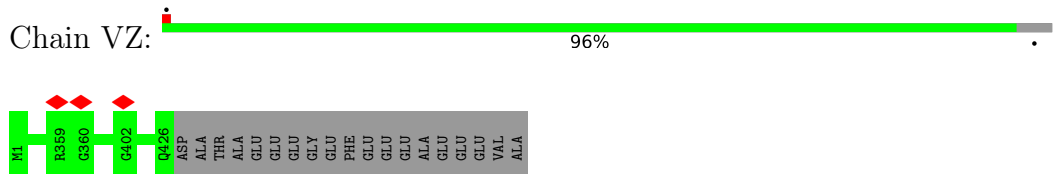


• Molecule 43: Tubulin beta-4B chain

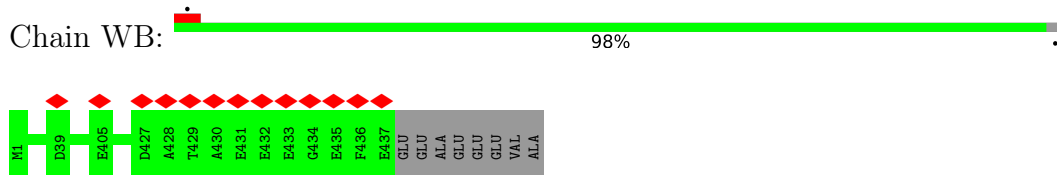
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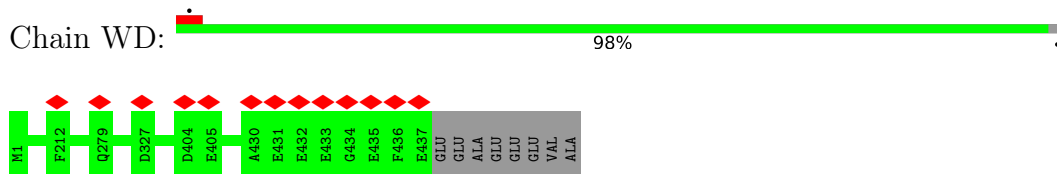
- Molecule 43: Tubulin beta-4B chain



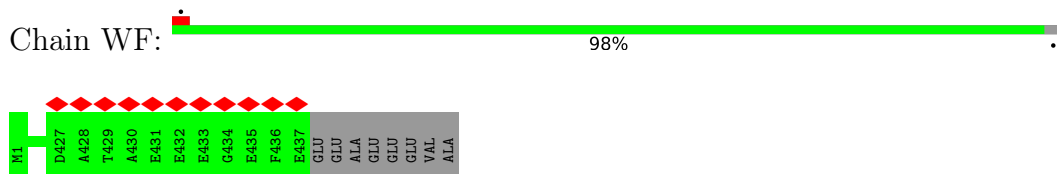
- Molecule 43: Tubulin beta-4B chain



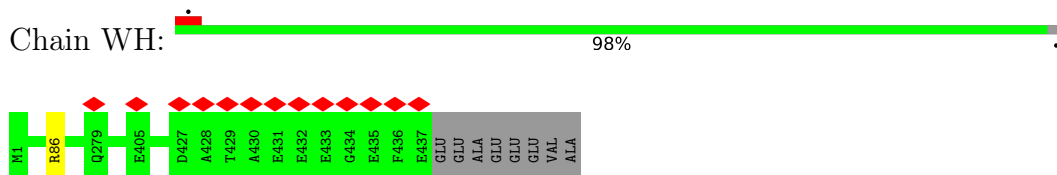
- Molecule 43: Tubulin beta-4B chain



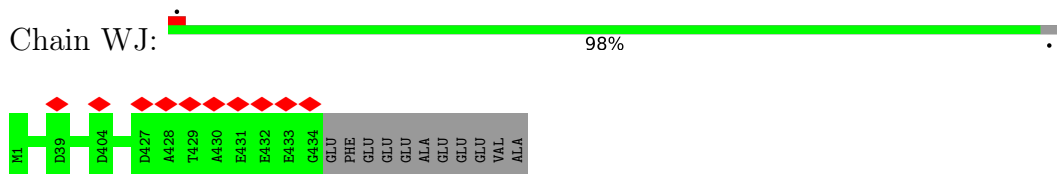
- Molecule 43: Tubulin beta-4B chain



- Molecule 43: Tubulin beta-4B chain

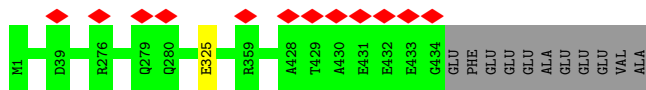


- Molecule 43: Tubulin beta-4B chain

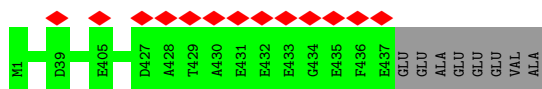


- Molecule 43: Tubulin beta-4B chain

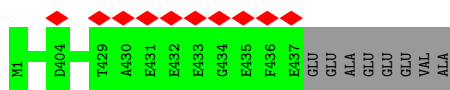




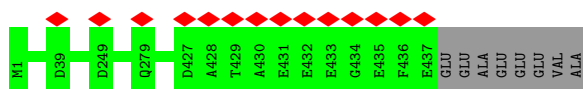
• Molecule 43: Tubulin beta-4B chain



• Molecule 43: Tubulin beta-4B chain



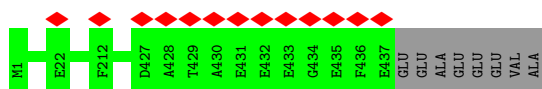
• Molecule 43: Tubulin beta-4B chain



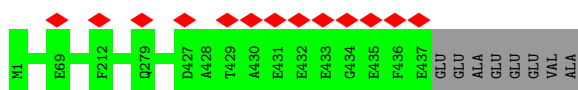
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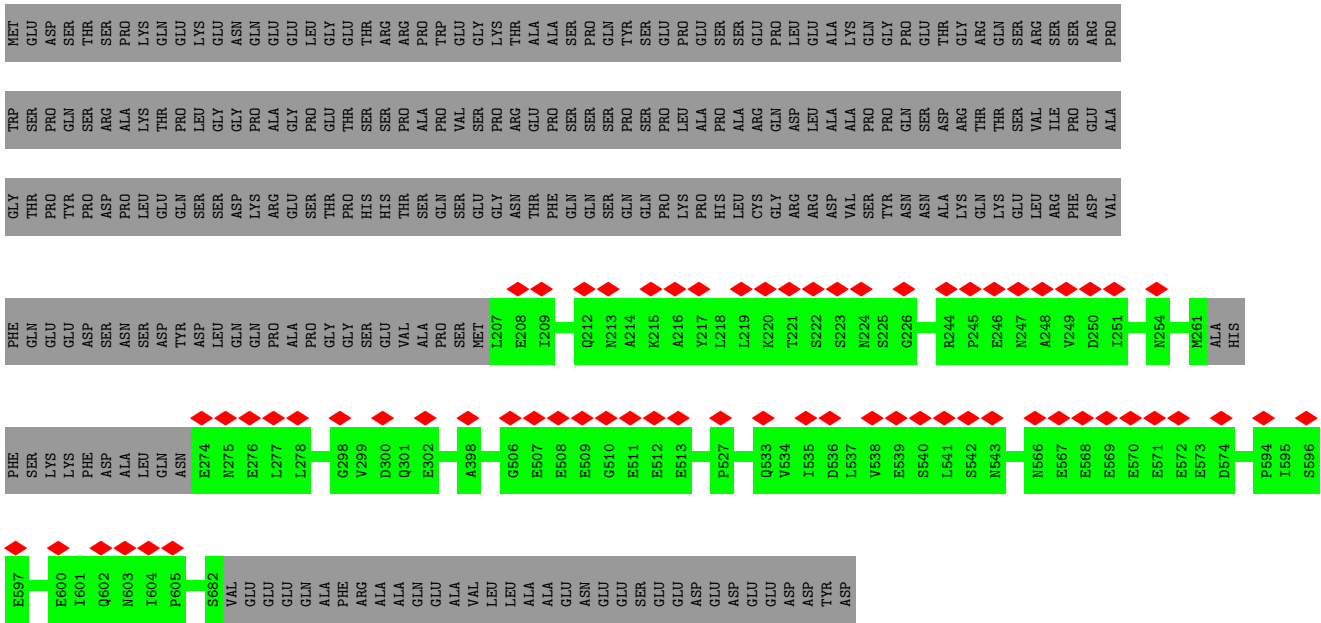
• Molecule 43: Tubulin beta-4B chain



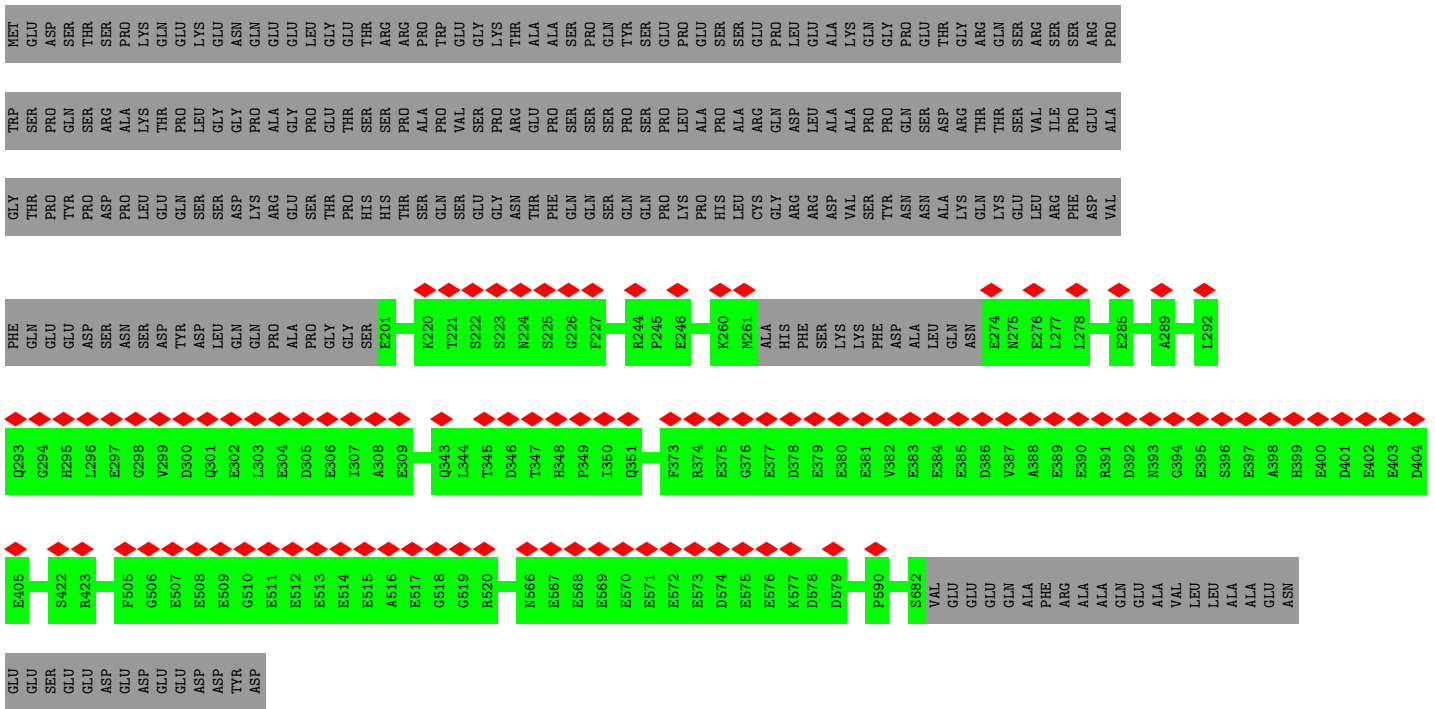
• Molecule 43: Tubulin beta-4B chain



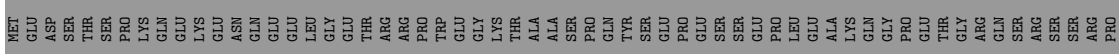
• Molecule 44: Radial spoke head protein 3 homolog



• Molecule 45: Radial spoke head protein 4 homolog A



• Molecule 45: Radial spoke head protein 4 homolog A



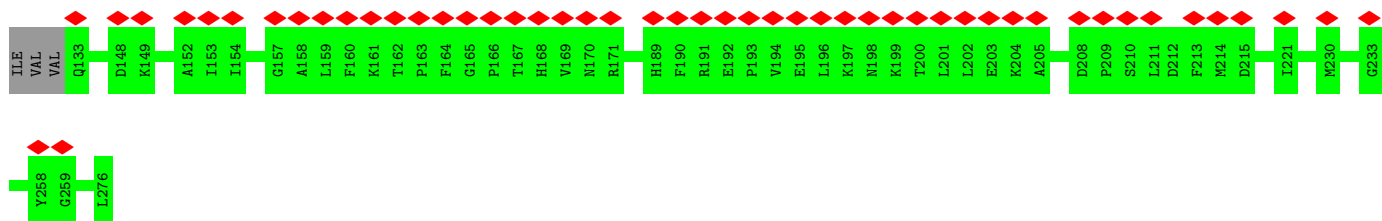
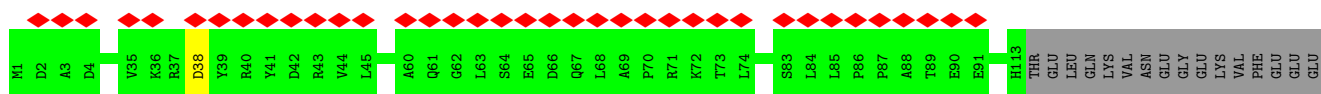
GLU LYS SER GLN ASP PRO GLU LYS GLN GLU GLU GLU GLN SER ILE LYS GLY LYS GLU GLU GLU THR SER VAL THR ILE LEU LEU ASP SER SER SER SER GLU GLU ASP LYS LYS LYS VAL THR ILE LEU LEU ASP SER SER SER SER GLU GLU VAL VAL ALA ALA VAL LYS ILE ILE GLN GLN ALA ALA PHE ARG ARG HIS ILE ILE ALA ARG ARG GLU GLU ALA ALA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

SER LEU GLN ASN GLU LYS GLU GLU ASN LYS

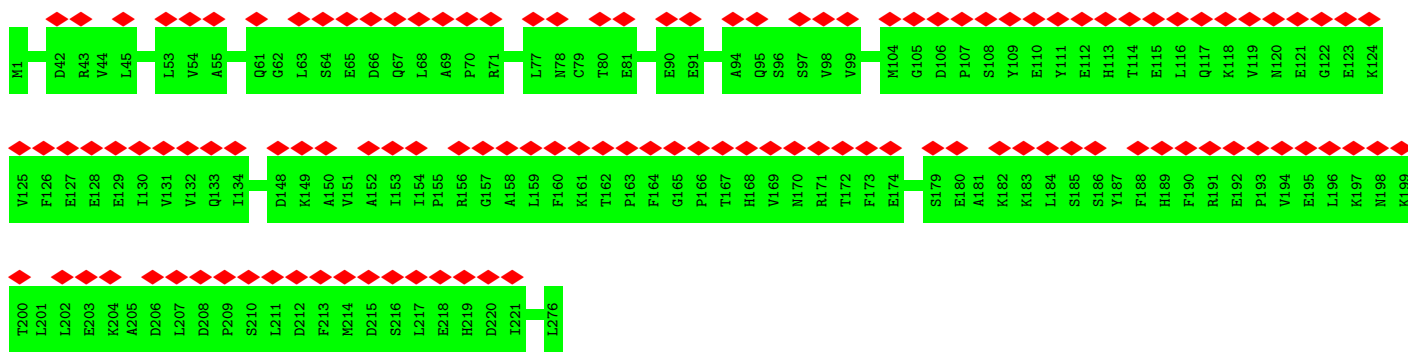
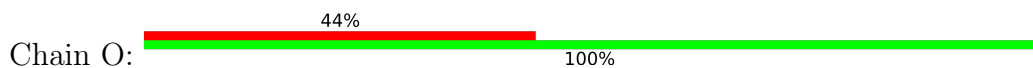
• Molecule 47: Radial spoke head protein 9 homolog



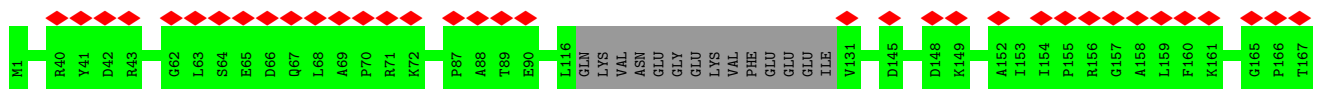
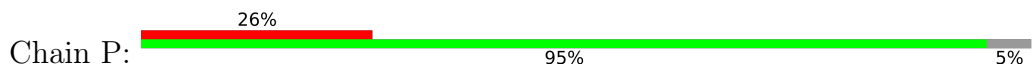
• Molecule 47: Radial spoke head protein 9 homolog

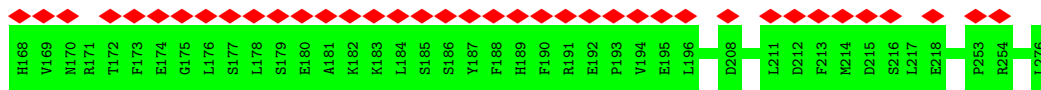


• Molecule 47: Radial spoke head protein 9 homolog

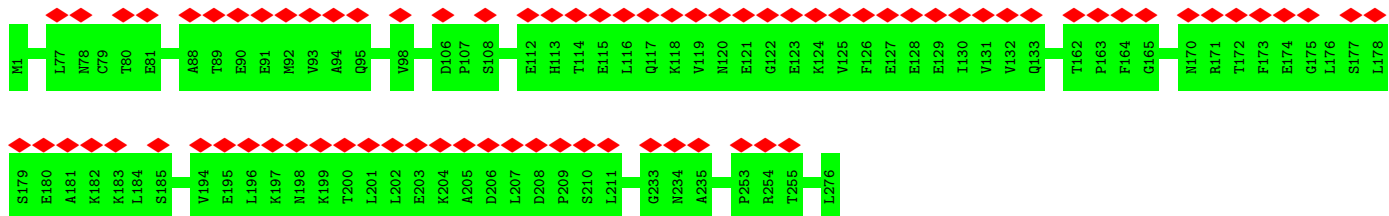


• Molecule 47: Radial spoke head protein 9 homolog

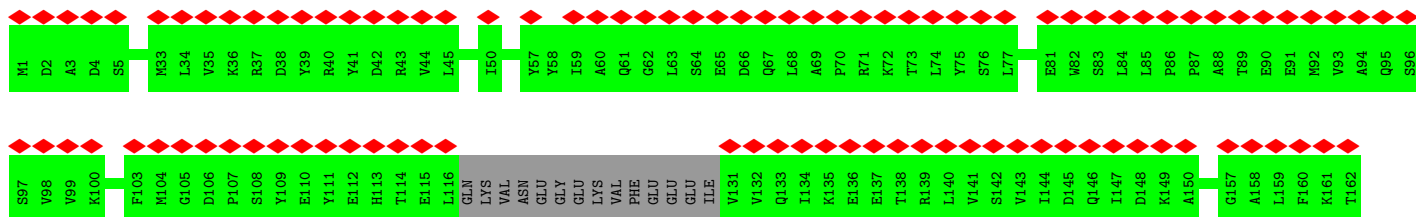
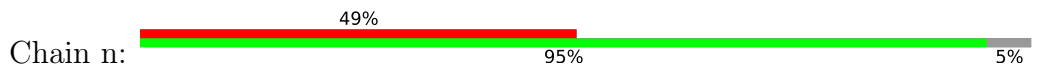




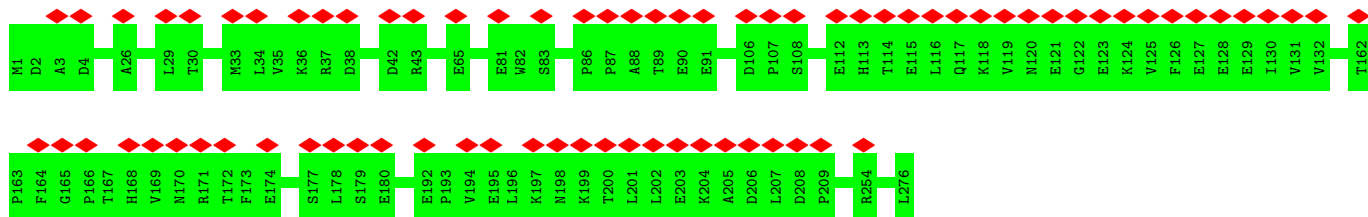
• Molecule 47: Radial spoke head protein 9 homolog



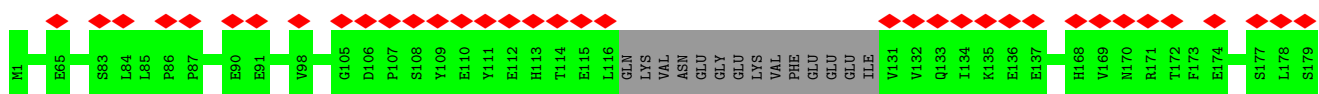
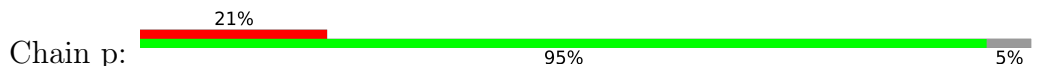
• Molecule 47: Radial spoke head protein 9 homolog

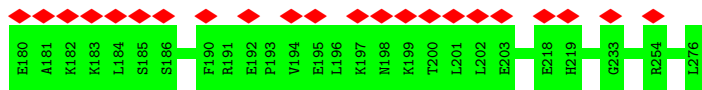


• Molecule 47: Radial spoke head protein 9 homolog

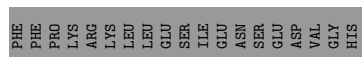
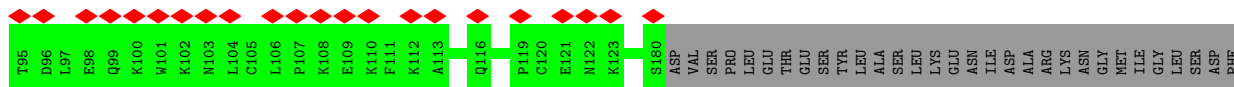
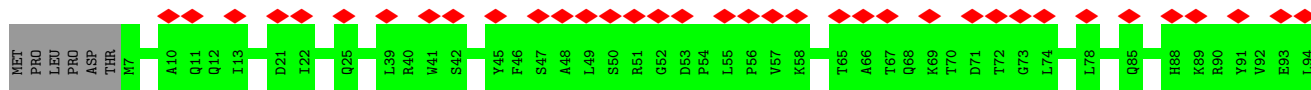
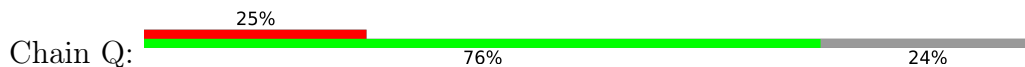


• Molecule 47: Radial spoke head protein 9 homolog

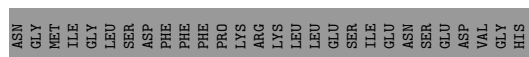
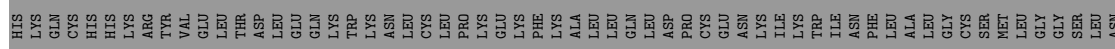
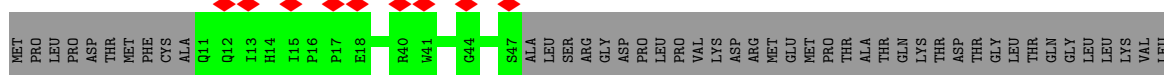




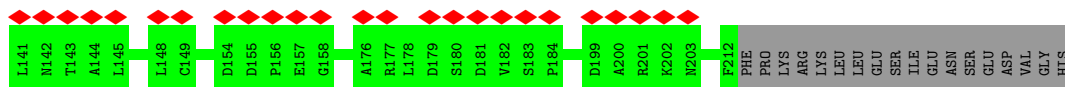
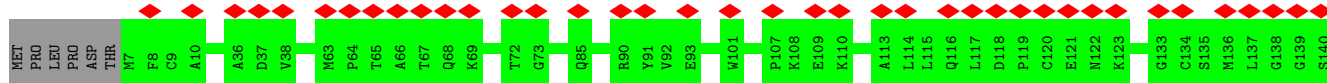
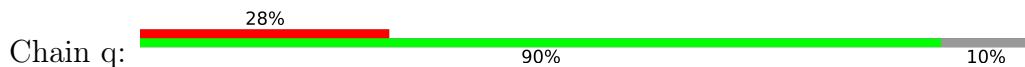
• Molecule 48: Roppurin-1-like protein



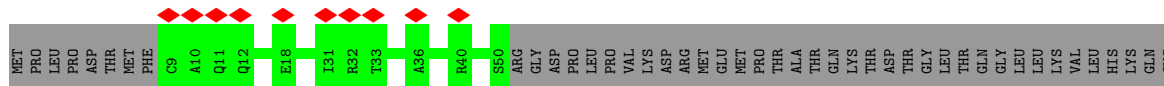
• Molecule 48: Roppurin-1-like protein

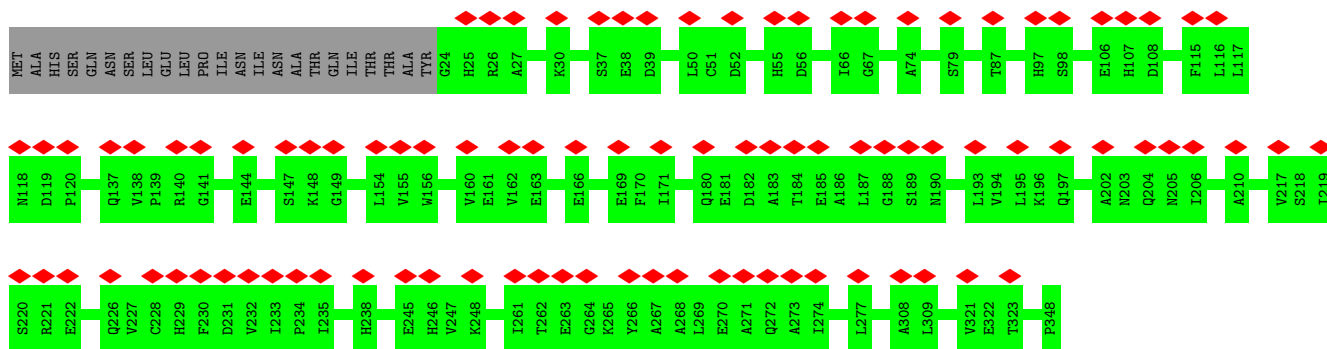


• Molecule 48: Roppurin-1-like protein

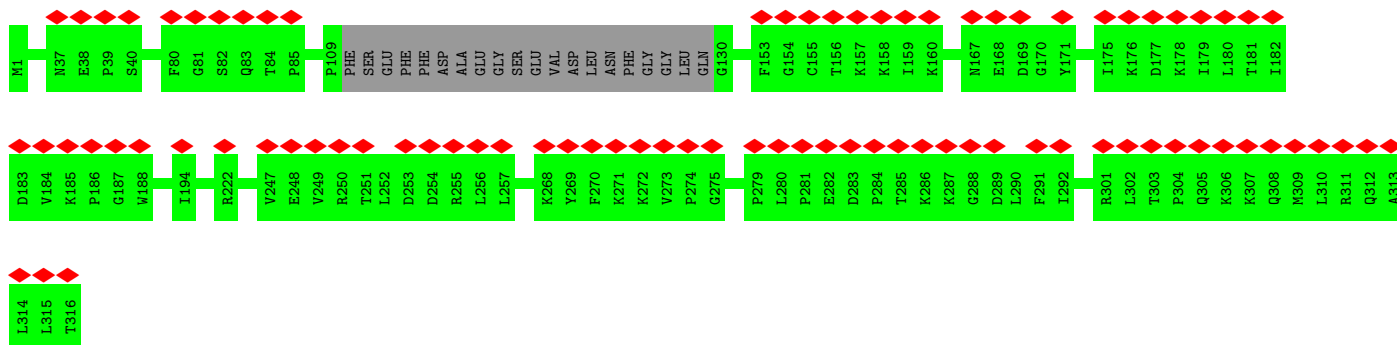


• Molecule 48: Roppurin-1-like protein

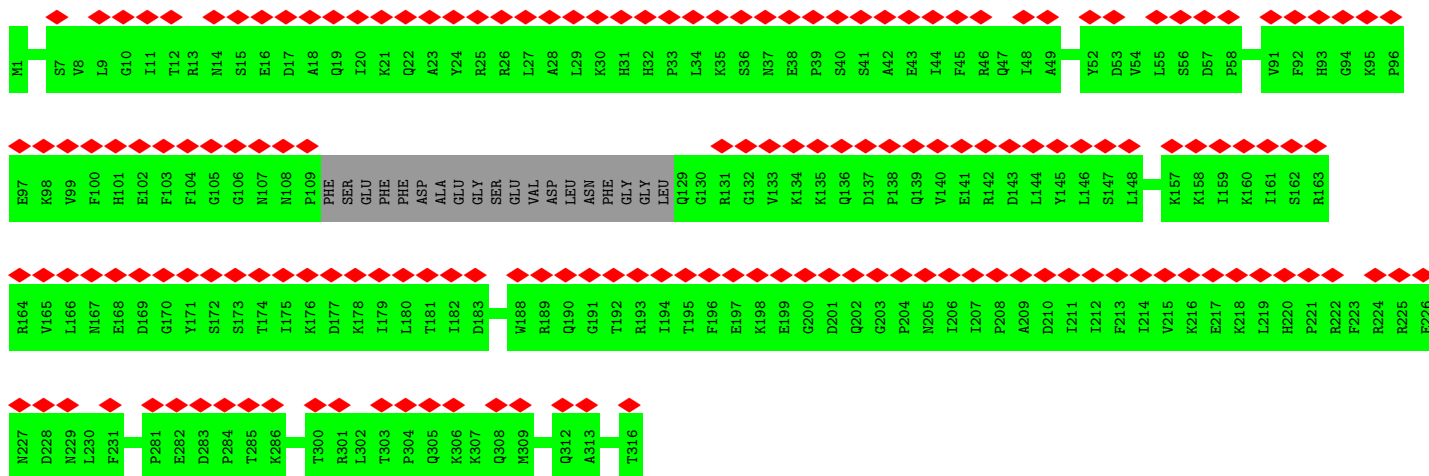




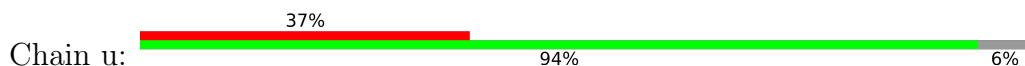
• Molecule 51: DnaJ homolog subfamily B member 13

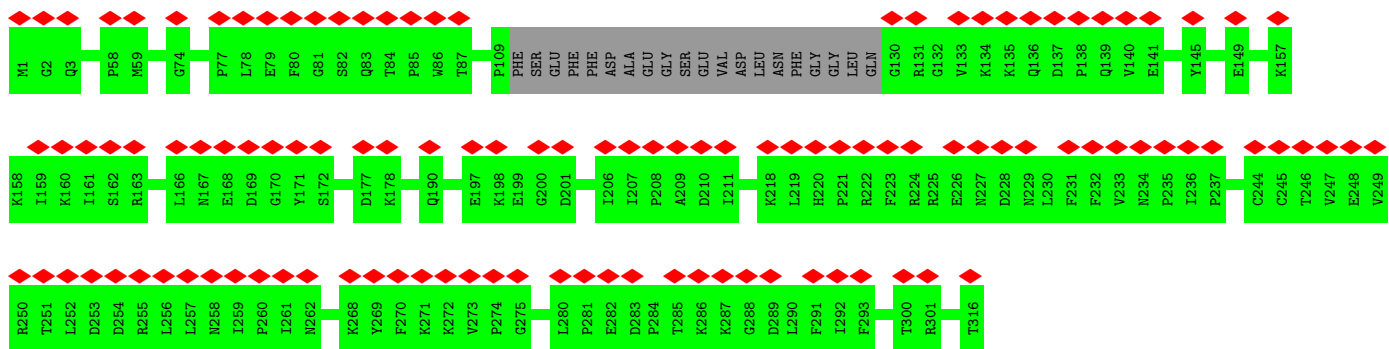


• Molecule 51: DnaJ homolog subfamily B member 13

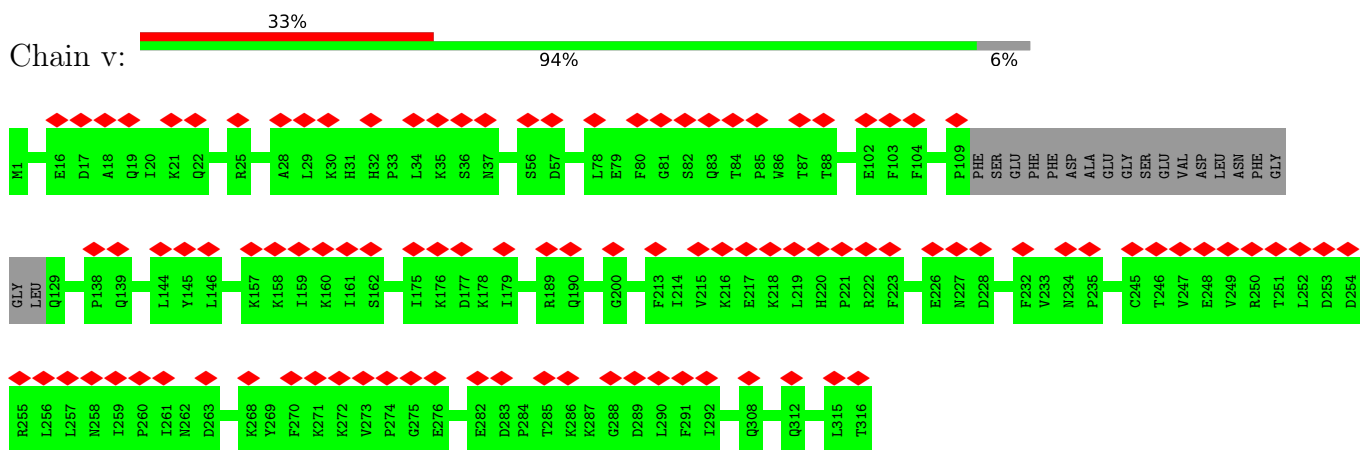


• Molecule 51: DnaJ homolog subfamily B member 13

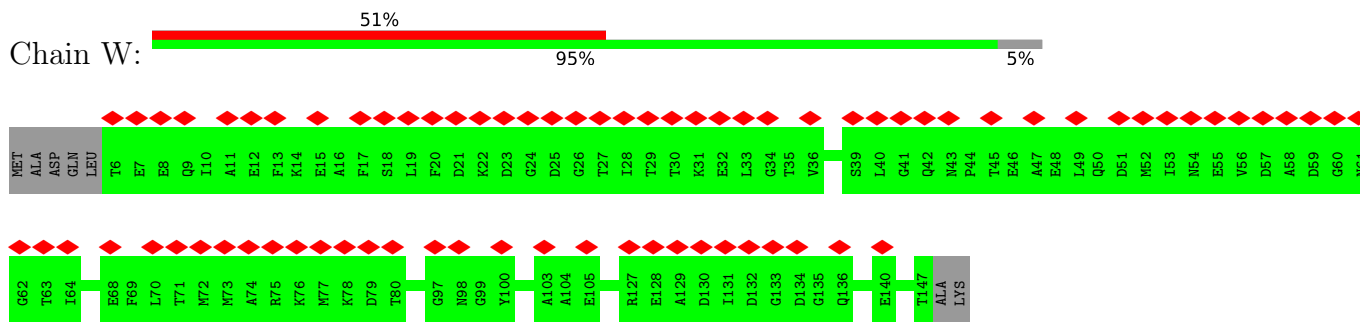




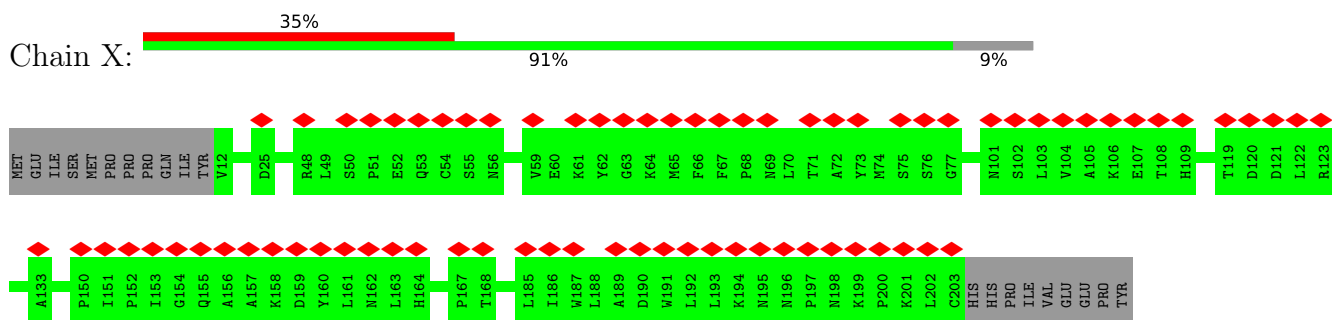
• Molecule 51: DnaJ homolog subfamily B member 13



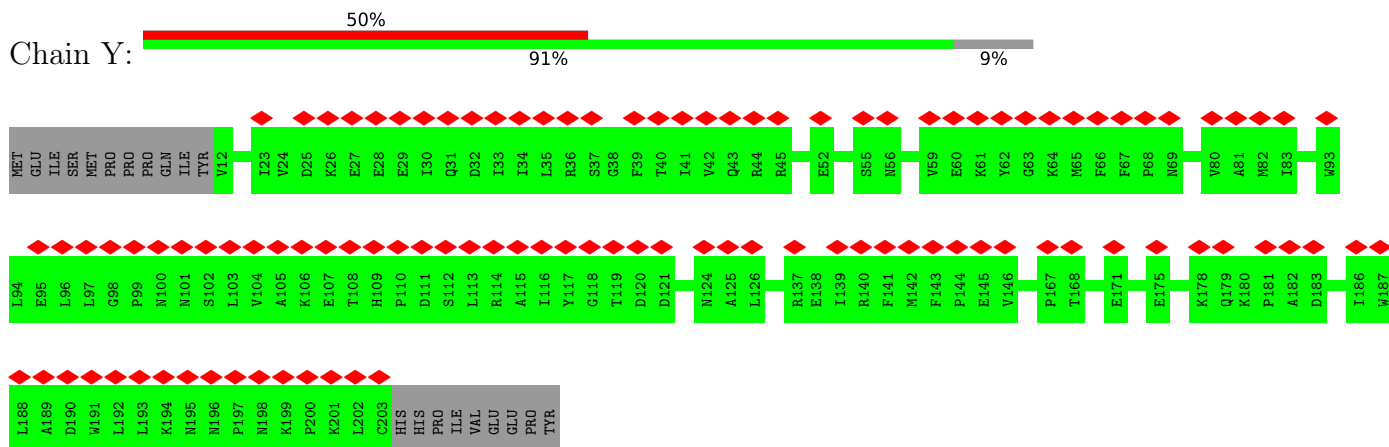
• Molecule 52: Calmodulin-1



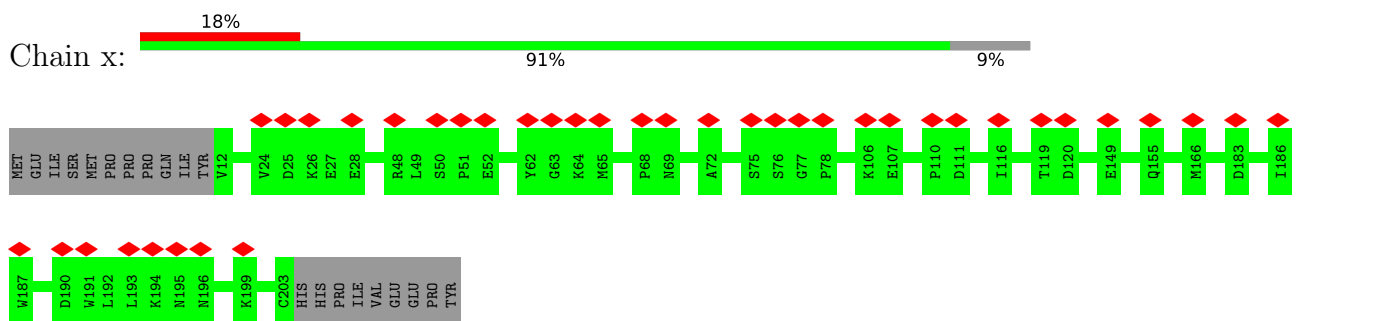
• Molecule 53: Nucleoside diphosphate kinase homolog 5



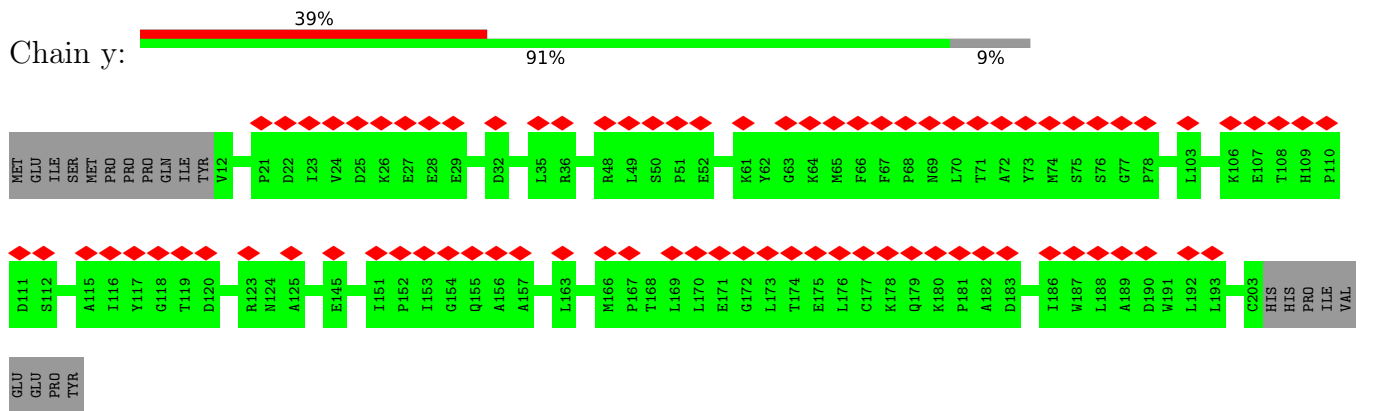
• Molecule 53: Nucleoside diphosphate kinase homolog 5



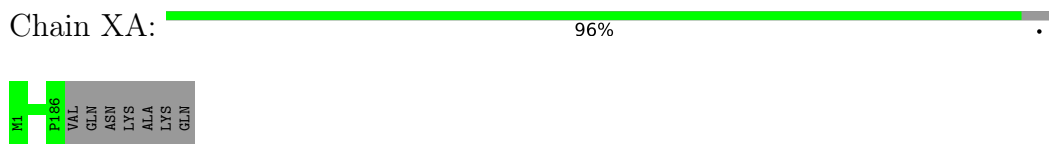
• Molecule 53: Nucleoside diphosphate kinase homolog 5



• Molecule 53: Nucleoside diphosphate kinase homolog 5

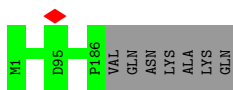


• Molecule 54: Cilia- and flagella-associated protein 20



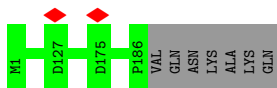
• Molecule 54: Cilia- and flagella-associated protein 20





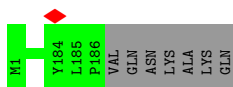
- Molecule 54: Cilia- and flagella-associated protein 20

Chain XC: 96%



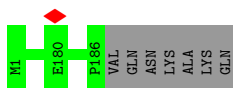
- Molecule 54: Cilia- and flagella-associated protein 20

Chain XD: 96%



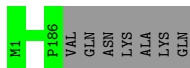
- Molecule 54: Cilia- and flagella-associated protein 20

Chain XE: 96%



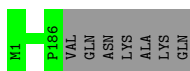
- Molecule 54: Cilia- and flagella-associated protein 20

Chain XF: 96%



- Molecule 54: Cilia- and flagella-associated protein 20

Chain XG: 96%



- Molecule 54: Cilia- and flagella-associated protein 20

Chain XH: 96%



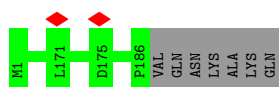
- Molecule 54: Cilia- and flagella-associated protein 20



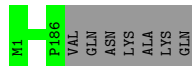
- Molecule 54: Cilia- and flagella-associated protein 20



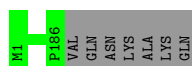
- Molecule 54: Cilia- and flagella-associated protein 20



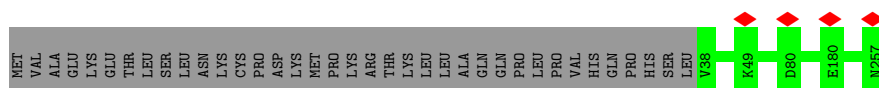
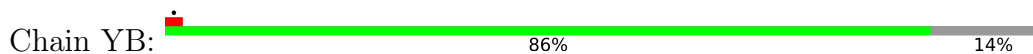
- Molecule 54: Cilia- and flagella-associated protein 20



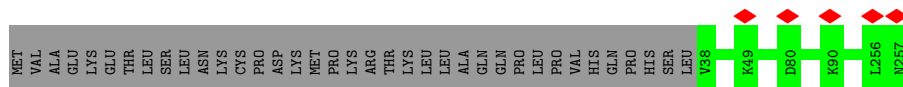
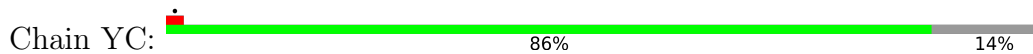
- Molecule 54: Cilia- and flagella-associated protein 20



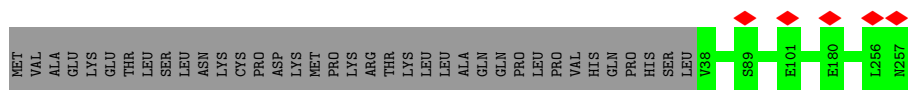
- Molecule 55: Parkin coregulated gene protein



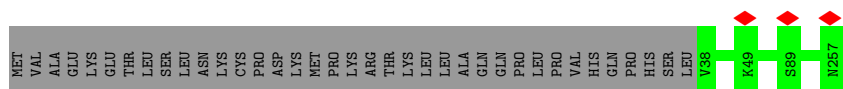
- Molecule 55: Parkin coregulated gene protein



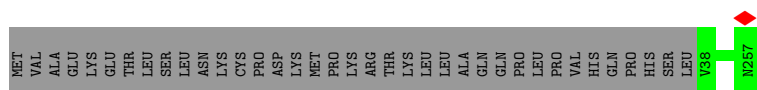
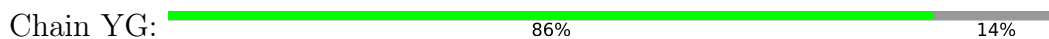
• Molecule 55: Parkin coregulated gene protein



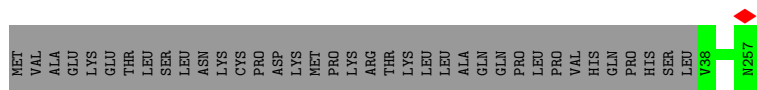
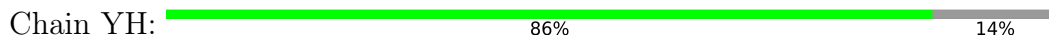
• Molecule 55: Parkin coregulated gene protein



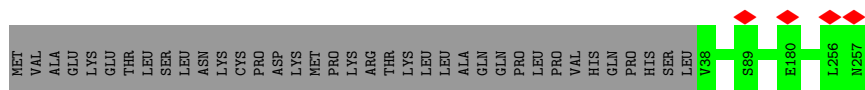
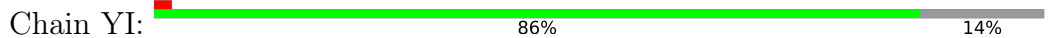
• Molecule 55: Parkin coregulated gene protein



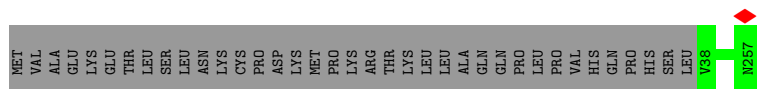
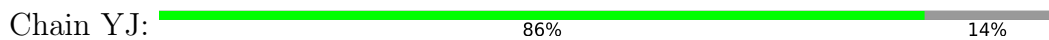
• Molecule 55: Parkin coregulated gene protein



• Molecule 55: Parkin coregulated gene protein

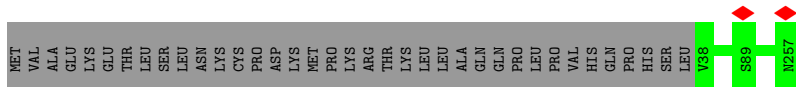


• Molecule 55: Parkin coregulated gene protein

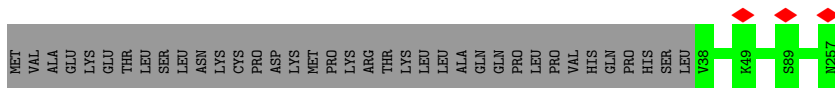
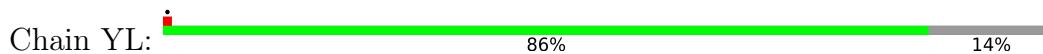


• Molecule 55: Parkin coregulated gene protein

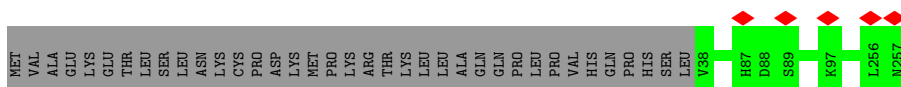




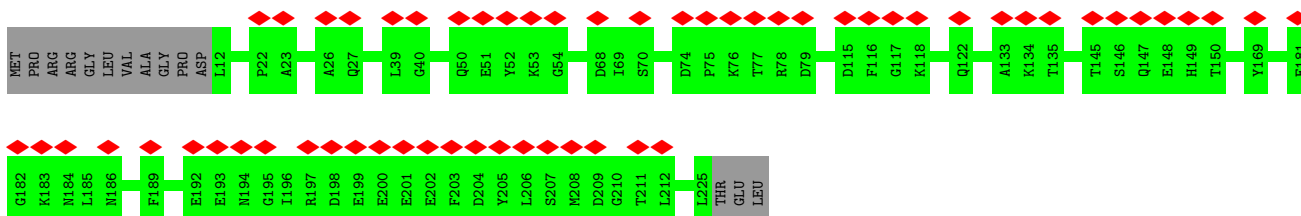
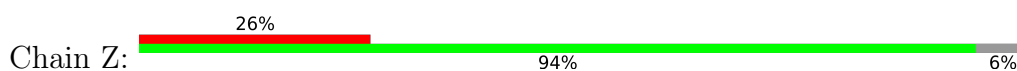
• Molecule 55: Parkin coregulated gene protein



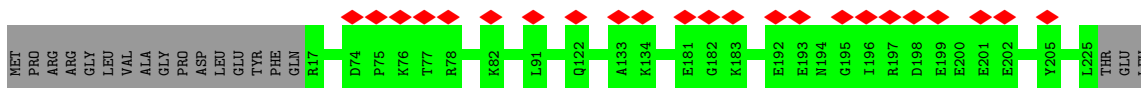
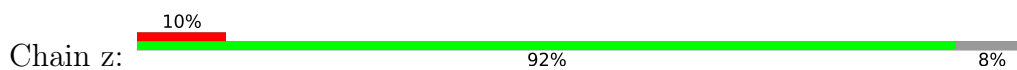
• Molecule 55: Parkin coregulated gene protein



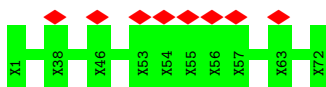
• Molecule 56: Cytochrome b5 domain-containing protein 1



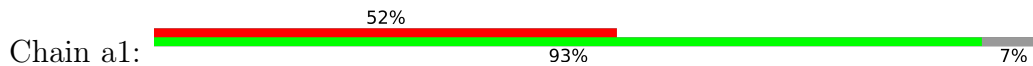
• Molecule 56: Cytochrome b5 domain-containing protein 1

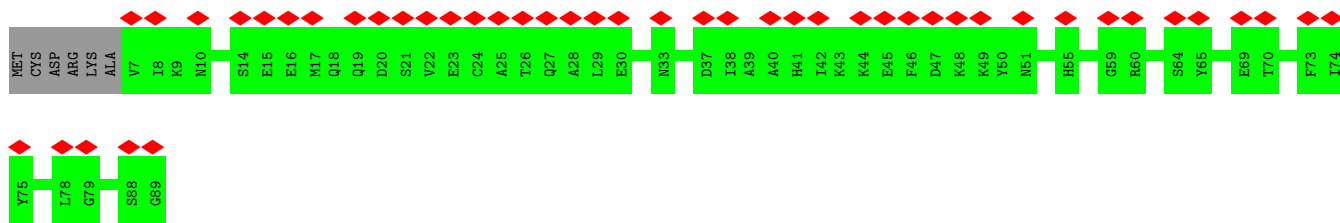


• Molecule 57: Unknown

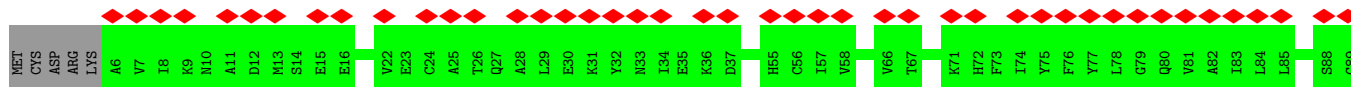
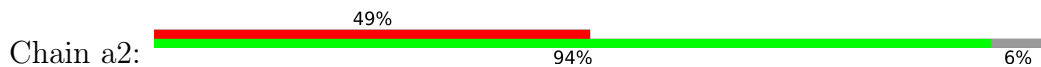


• Molecule 58: DYNLL1

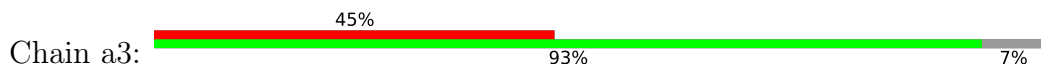




• Molecule 58: DYNLL1

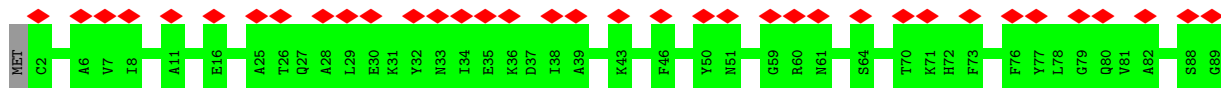
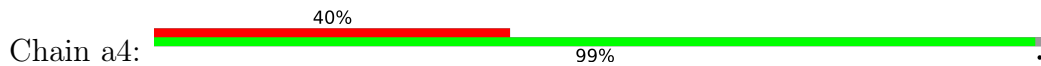


• Molecule 58: DYNLL1

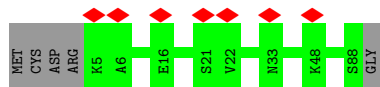


GLY

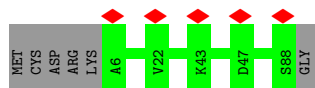
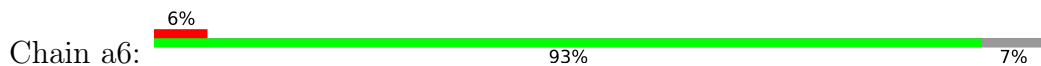
• Molecule 58: DYNLL1



• Molecule 58: DYNLL1

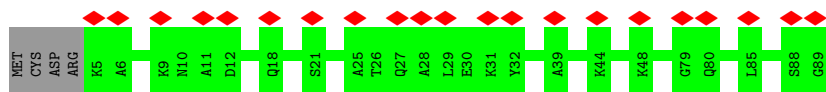


• Molecule 58: DYNLL1

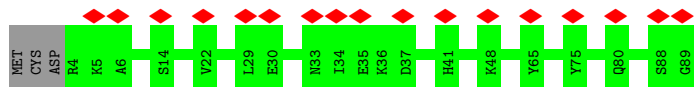


• Molecule 58: DYNLL1

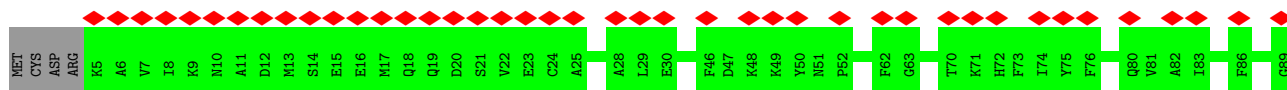




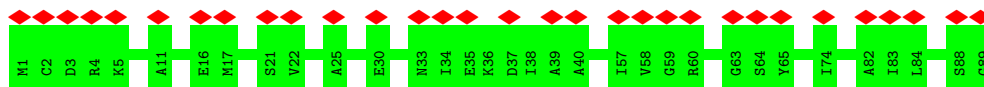
• Molecule 58: DYNLL1



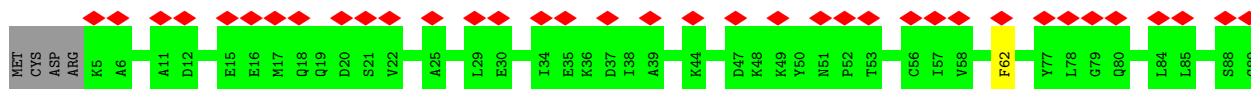
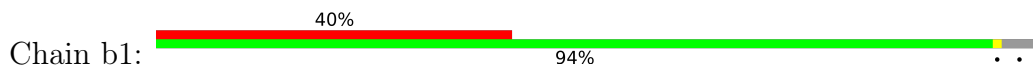
• Molecule 58: DYNLL1



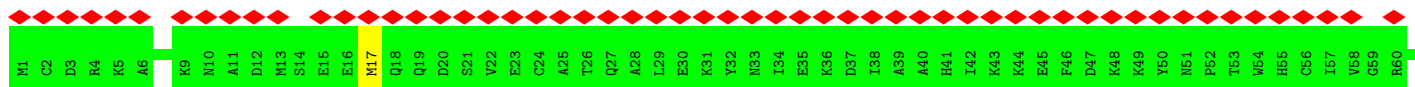
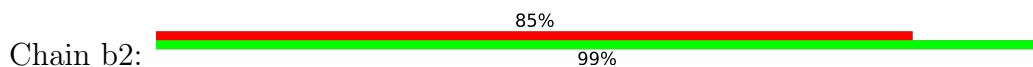
• Molecule 58: DYNLL1



• Molecule 58: DYNLL1

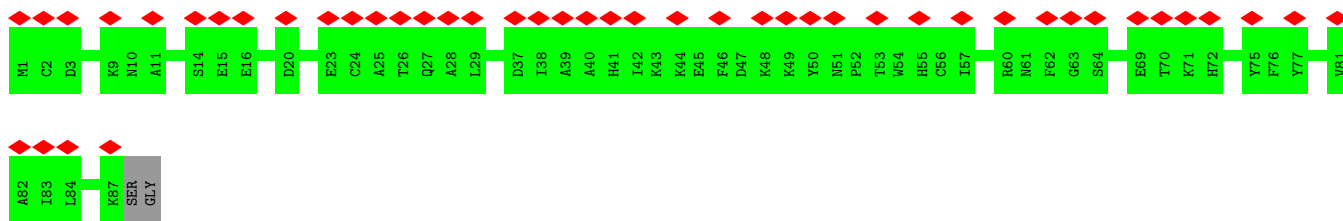


• Molecule 58: DYNLL1

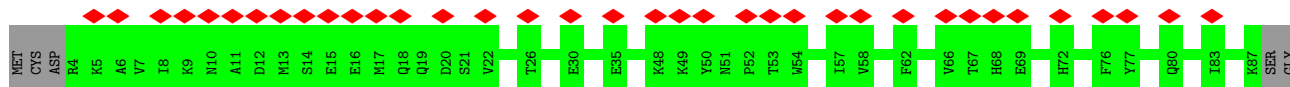
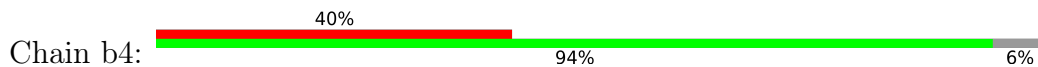


• Molecule 58: DYNLL1

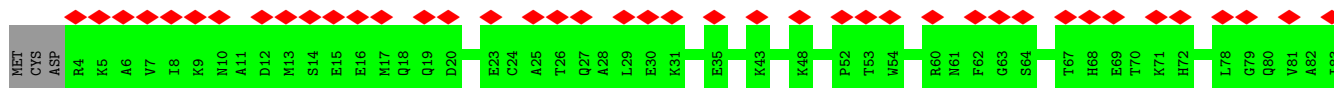




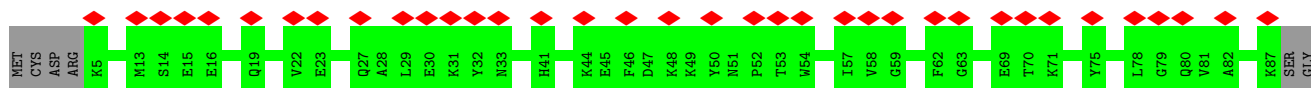
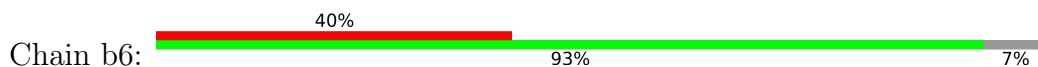
• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



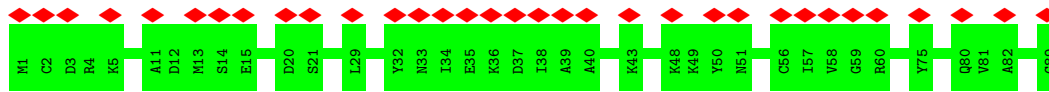
• Molecule 58: DYNLL1



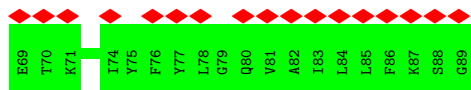
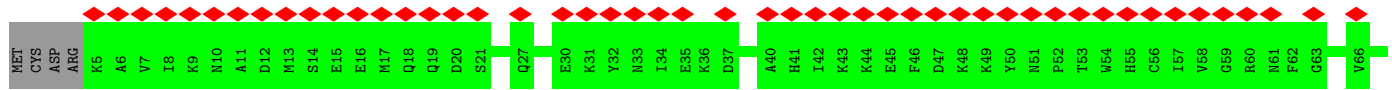
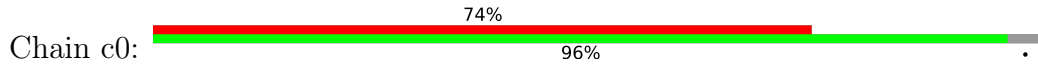
• Molecule 58: DYNLL1



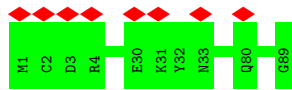
• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



• Molecule 58: DYNLL1



There are no outlier residues recorded for this chain.

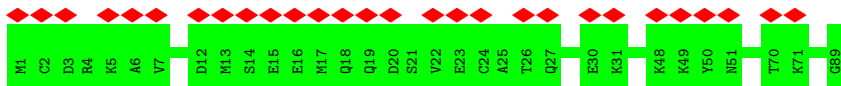
- Molecule 58: DYNLL1

Chain l6:  100%



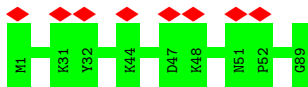
- Molecule 58: DYNLL1

Chain n1:  31% 100%



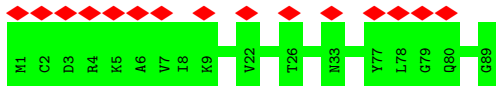
- Molecule 58: DYNLL1

Chain n2:  9% 100%



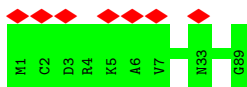
- Molecule 58: DYNLL1

Chain n3:  17% 100%



- Molecule 58: DYNLL1

Chain n4:  8% 100%



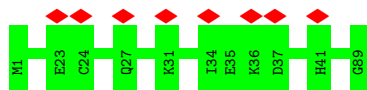
- Molecule 58: DYNLL1

Chain n5:  36% 100%

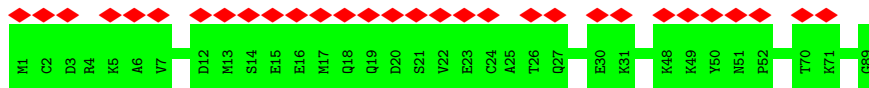


- Molecule 58: DYNLL1

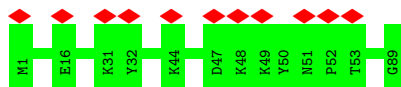
Chain n6:  9% 100%



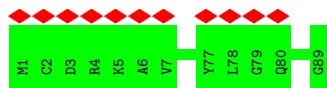
- Molecule 58: DYNLL1



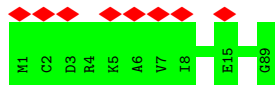
- Molecule 58: DYNLL1



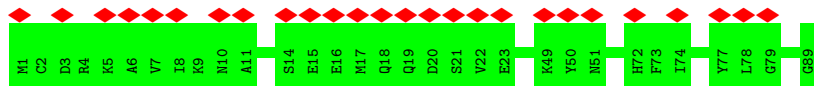
- Molecule 58: DYNLL1



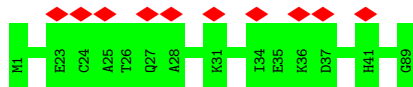
- Molecule 58: DYNLL1



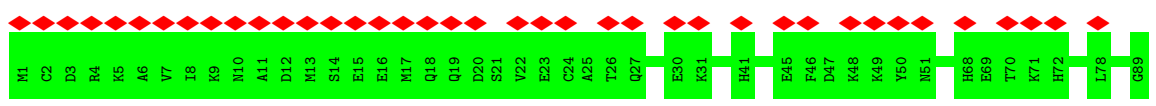
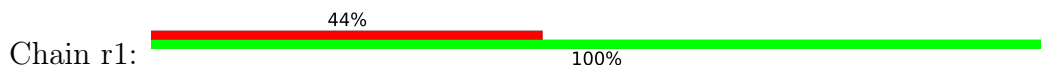
- Molecule 58: DYNLL1



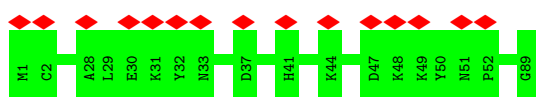
- Molecule 58: DYNLL1



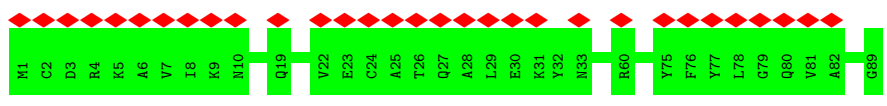
- Molecule 58: DYNLL1



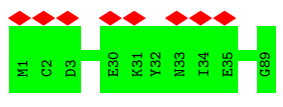
• Molecule 58: DYNLL1



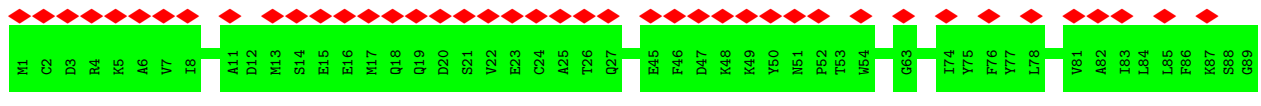
• Molecule 58: DYNLL1



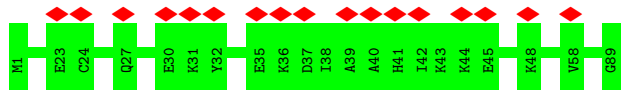
• Molecule 58: DYNLL1



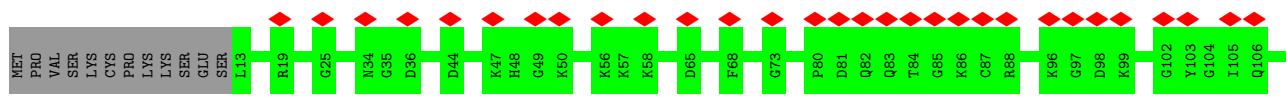
• Molecule 58: DYNLL1

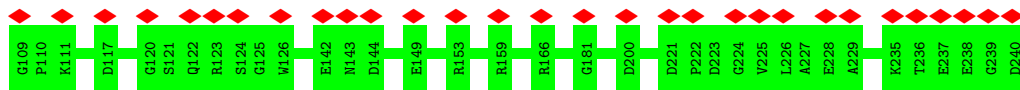


• Molecule 58: DYNLL1

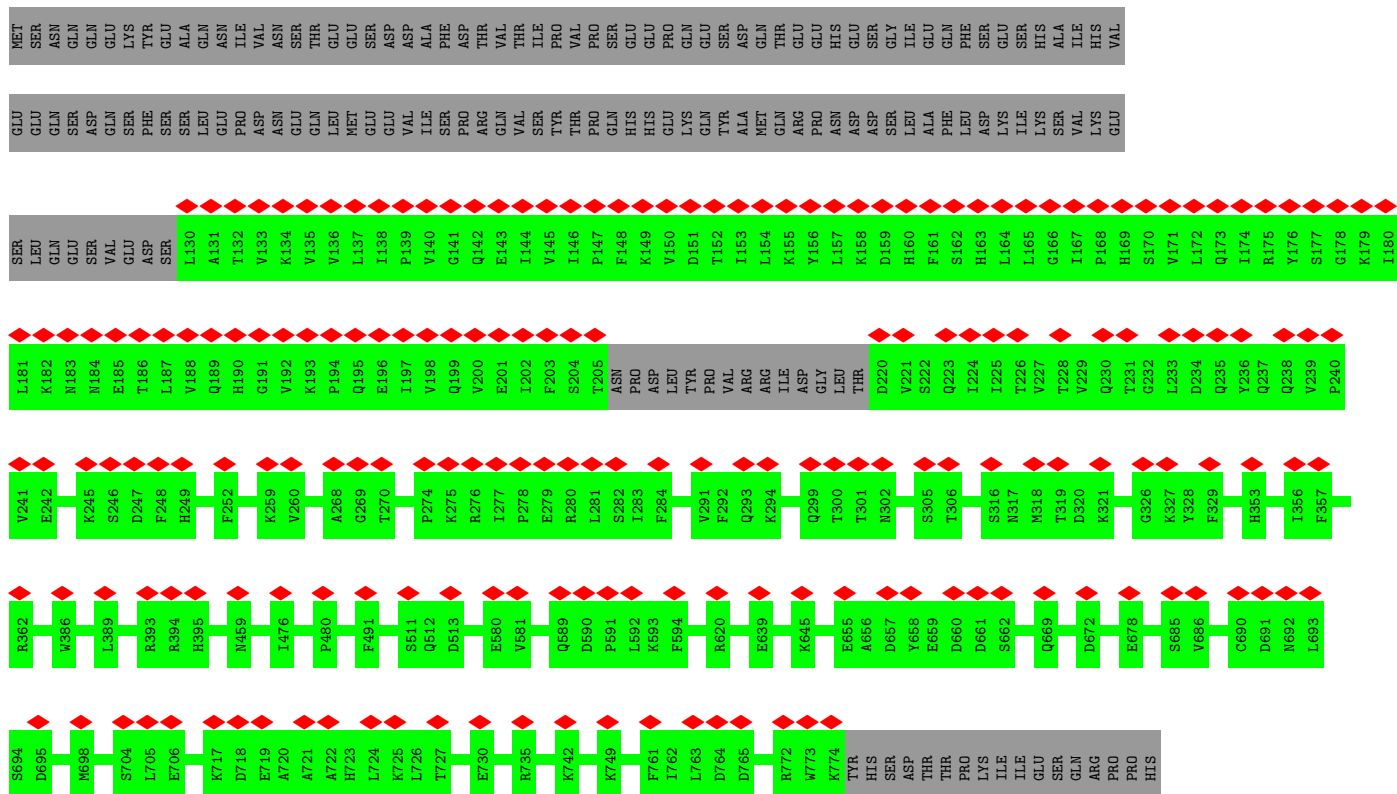
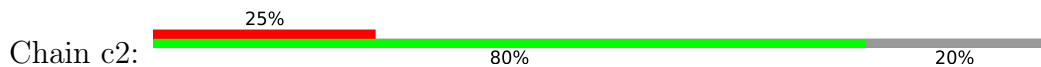


• Molecule 59: MORN repeat-containing protein 3

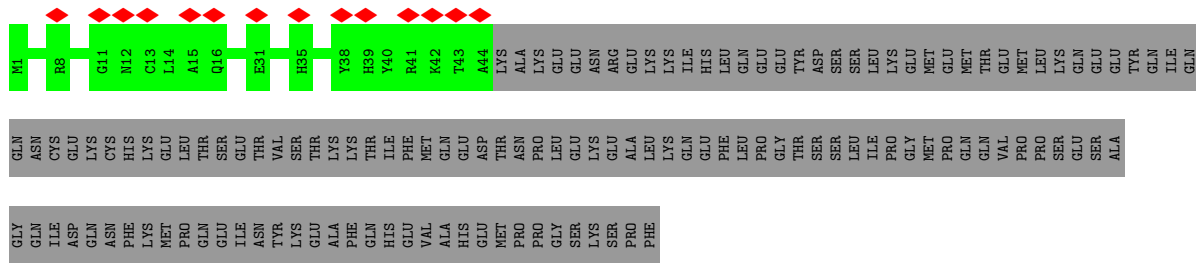




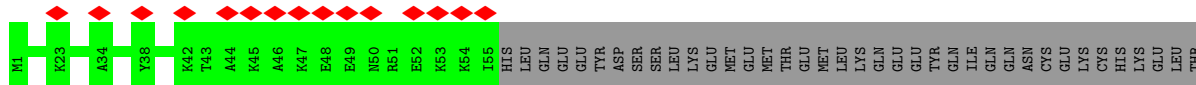
• Molecule 60: IQ and ubiquitin-like domain-containing protein

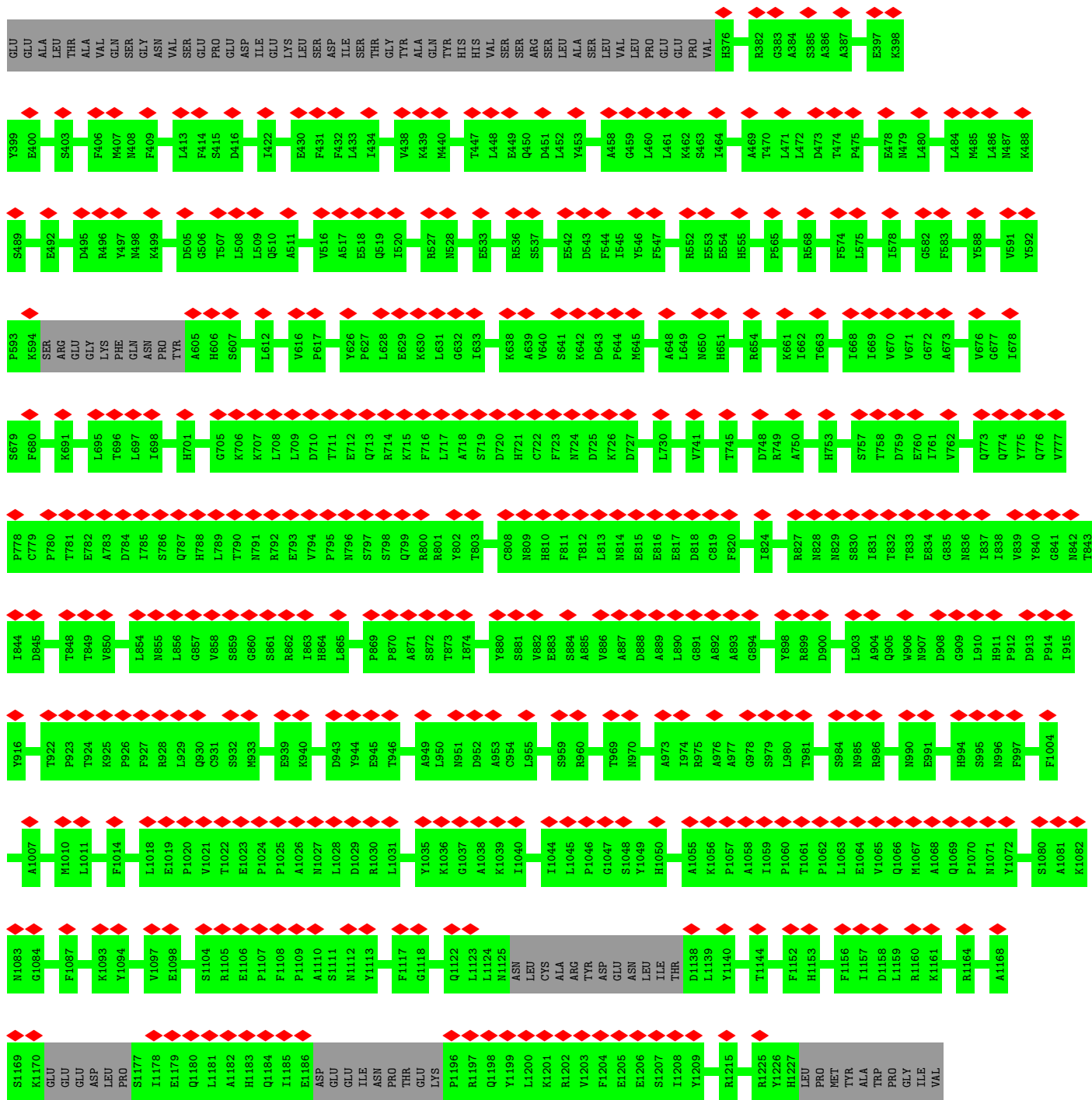


• Molecule 61: DPY30 domain-containing protein 2

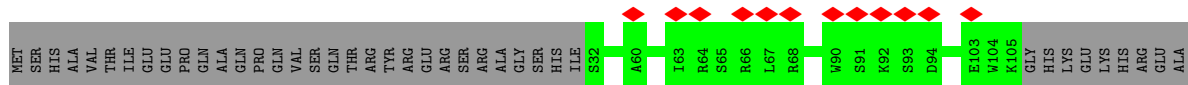


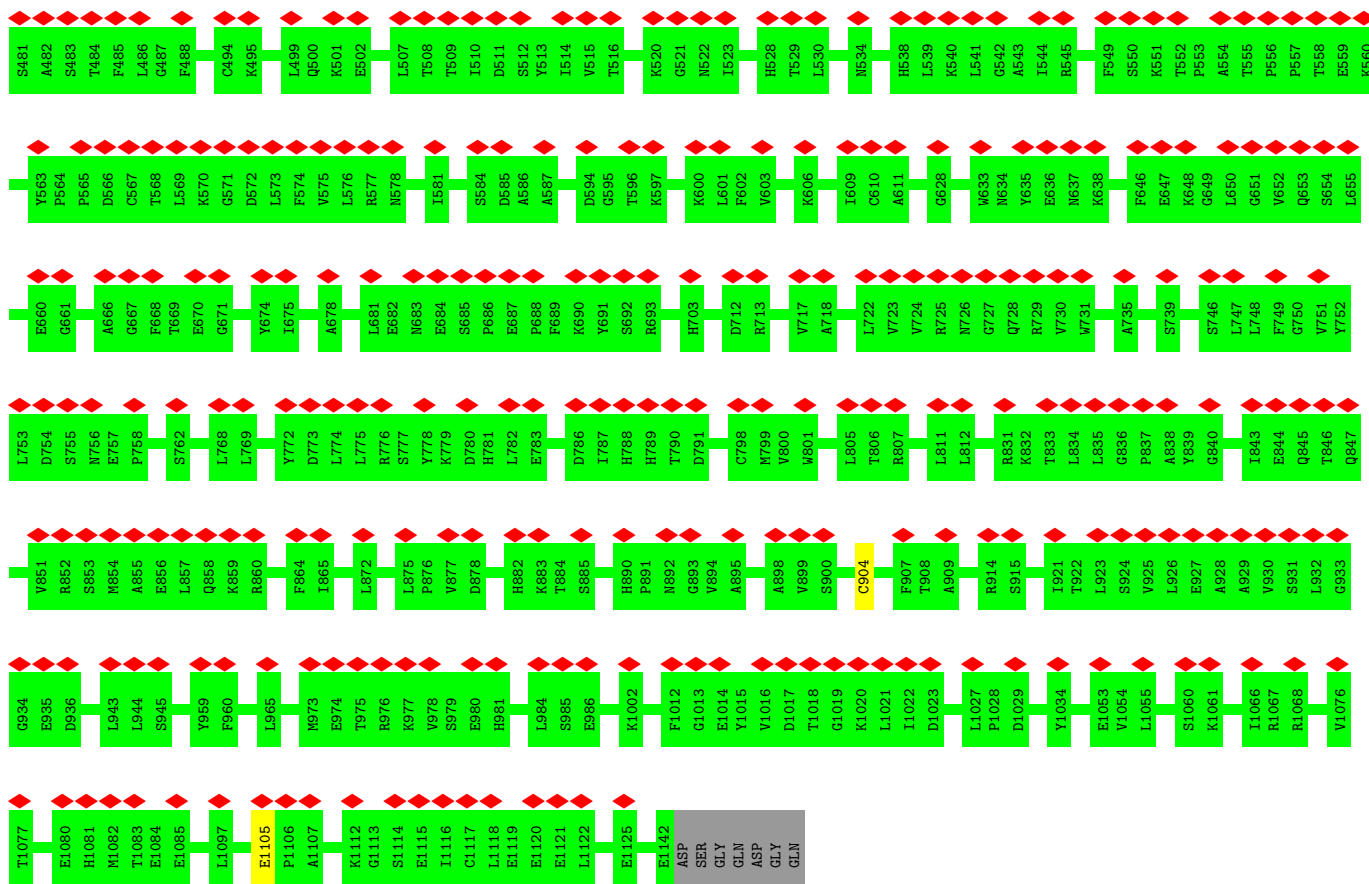
• Molecule 61: DPY30 domain-containing protein 2



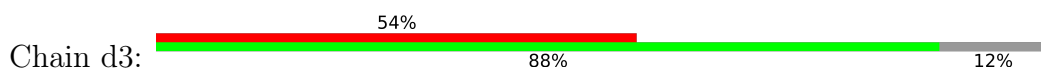


• Molecule 63: Cilia- and flagella-associated protein 91

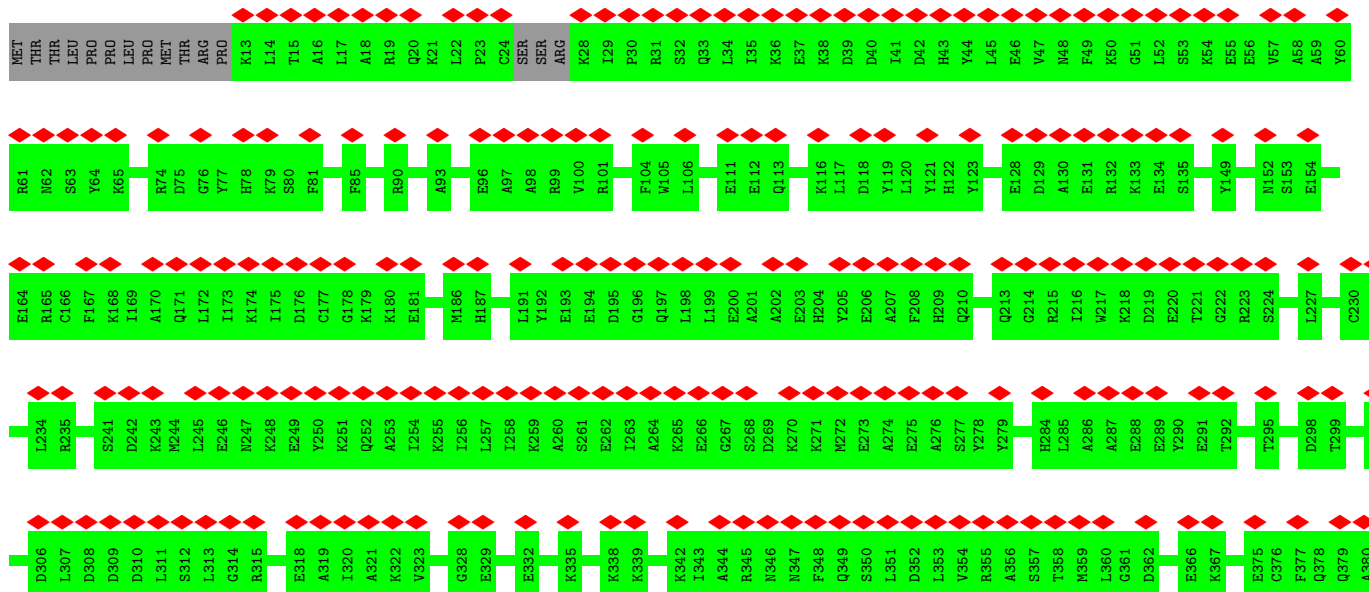


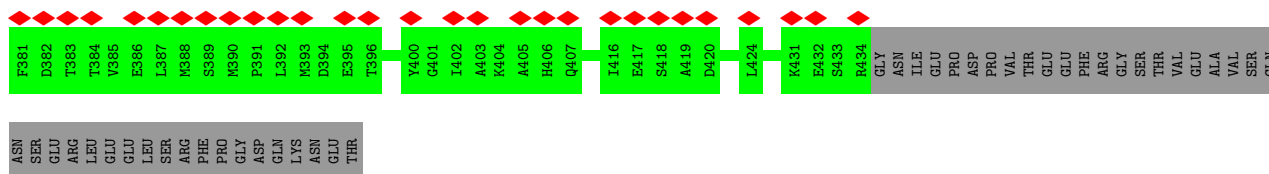


• Molecule 65: Tetratricopeptide repeat protein 29

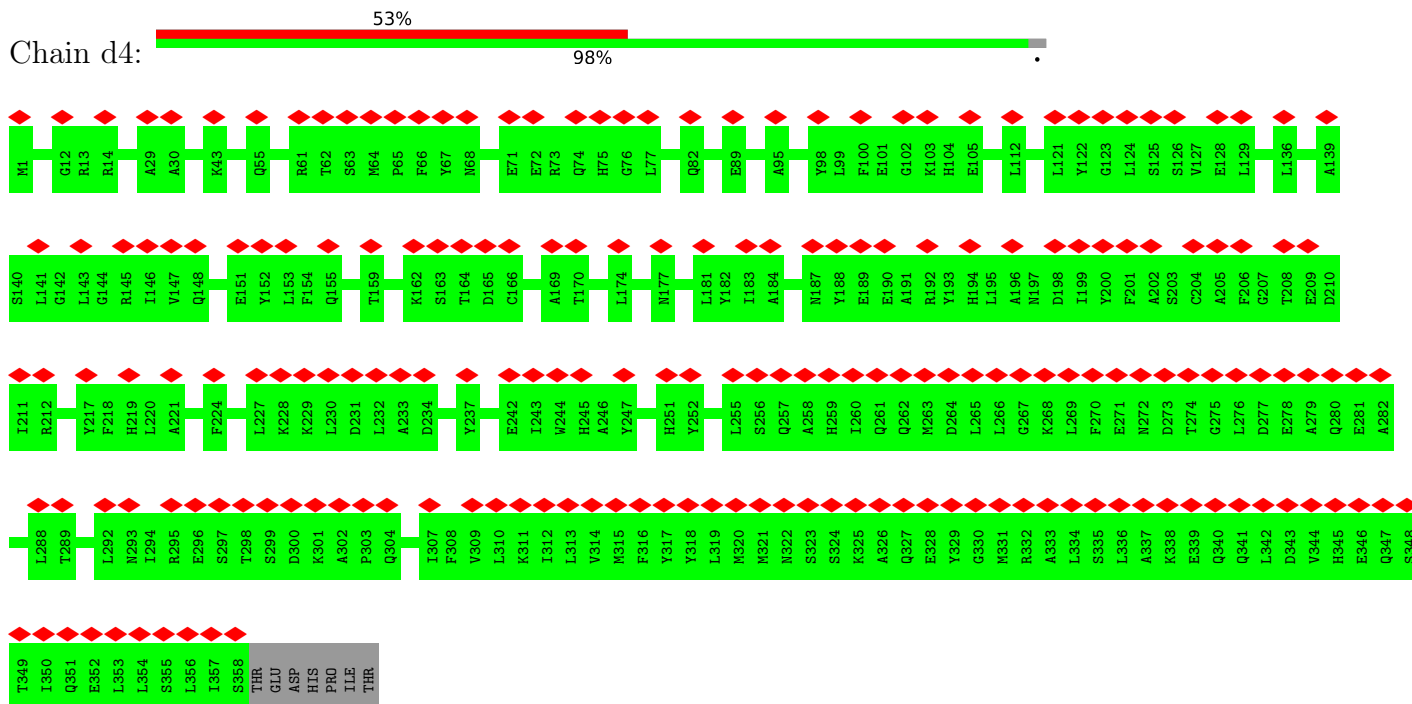


Chain d3:

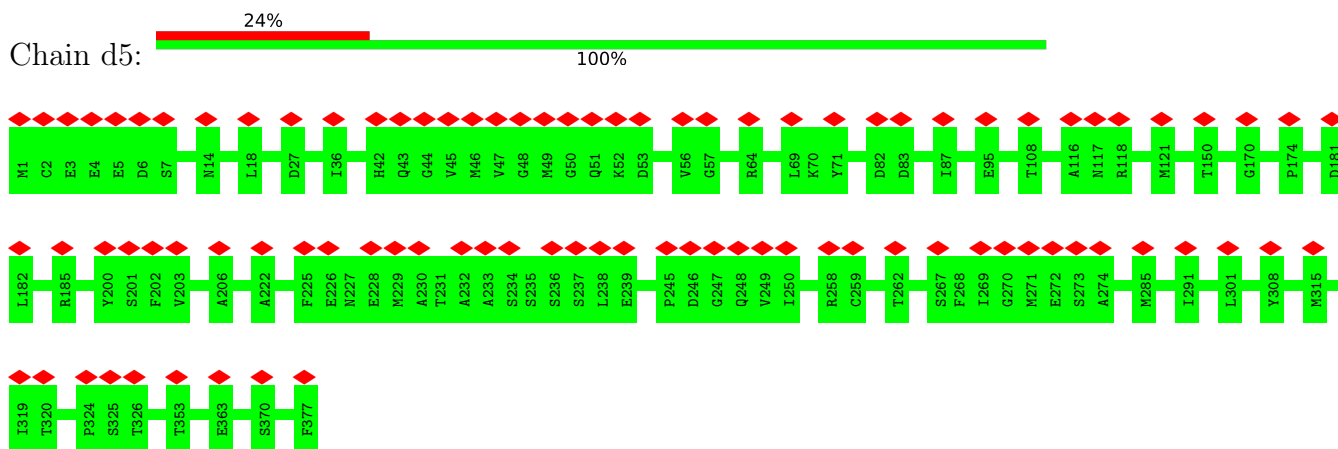




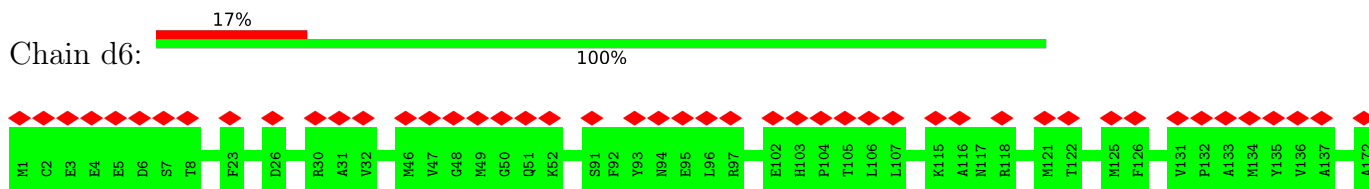
- Molecule 66: Zinc finger MYND domain-containing protein 12

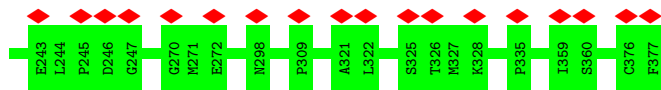


- Molecule 67: ACTA2

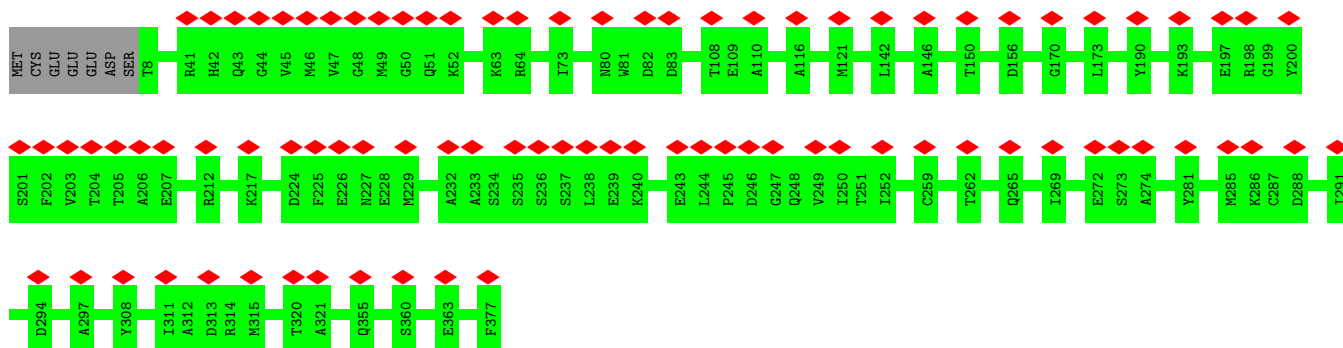


- Molecule 67: ACTA2

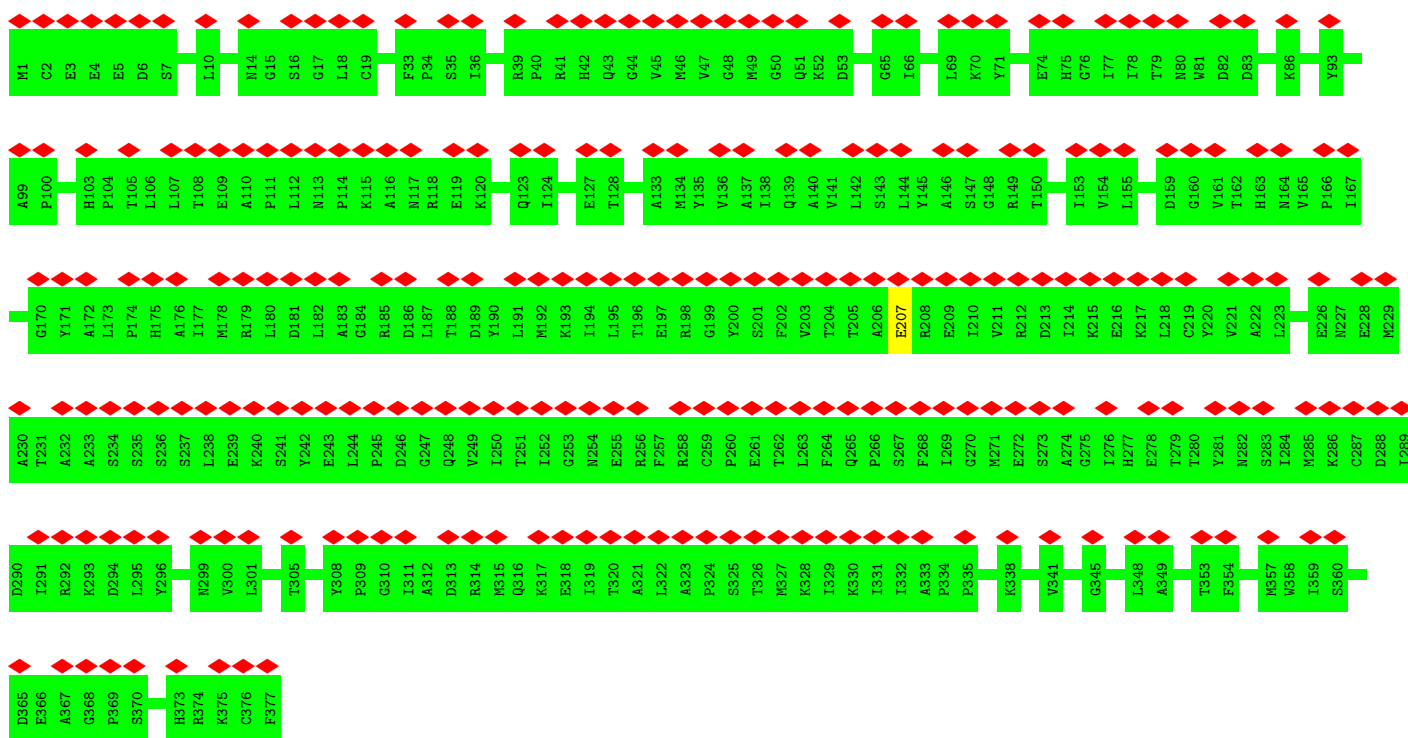




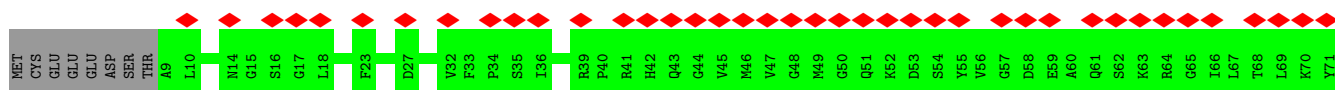
• Molecule 67: ACTA2

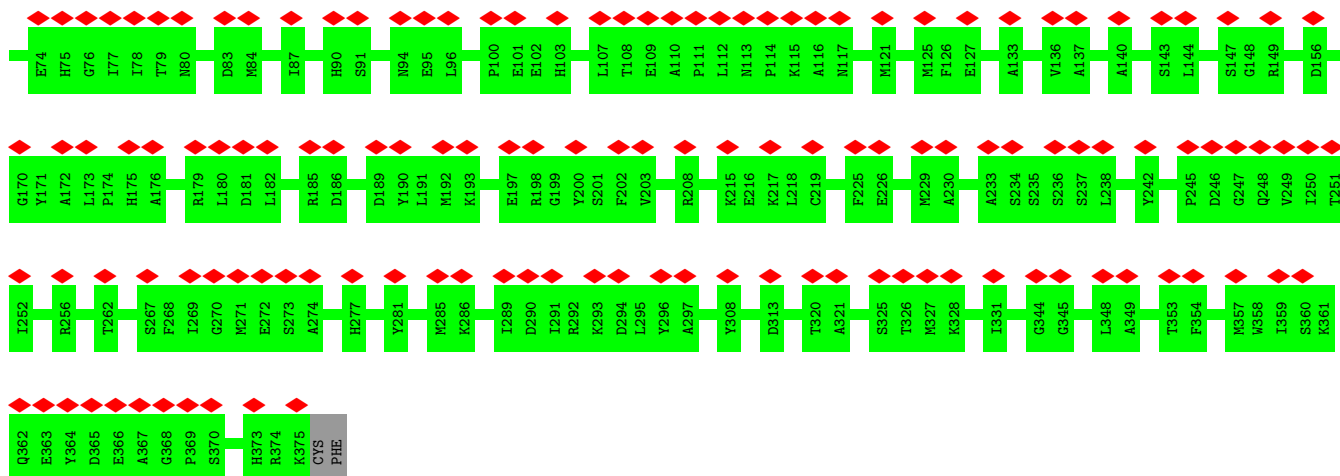


• Molecule 67: ACTA2

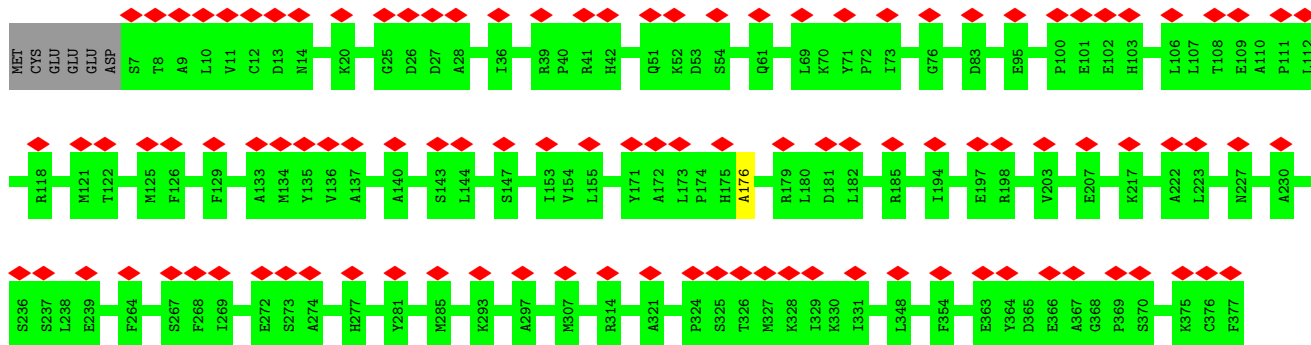


• Molecule 67: ACTA2

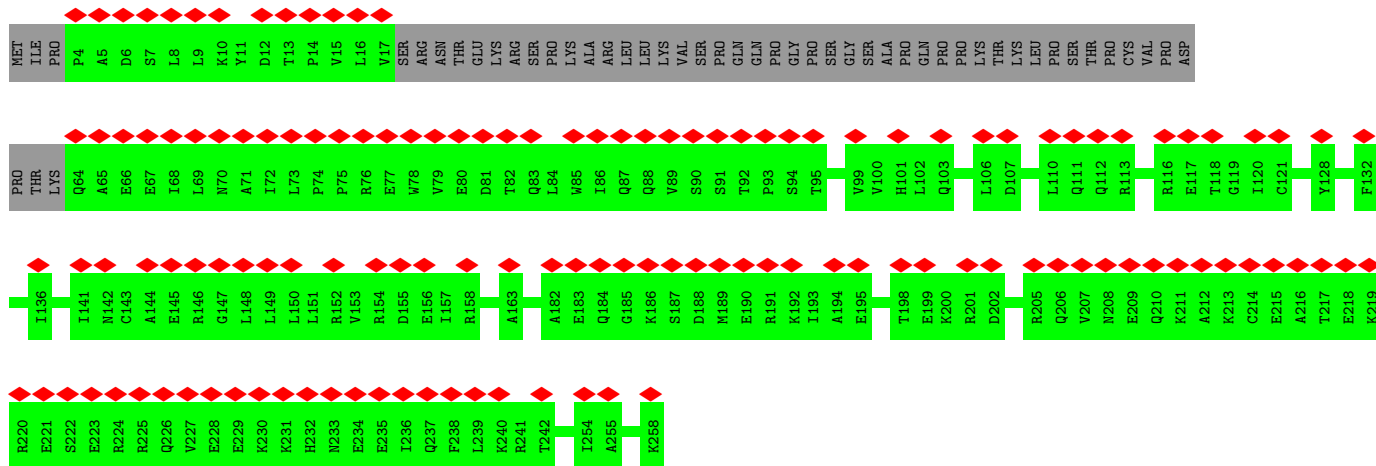
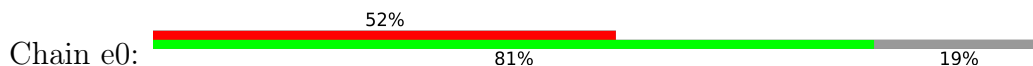




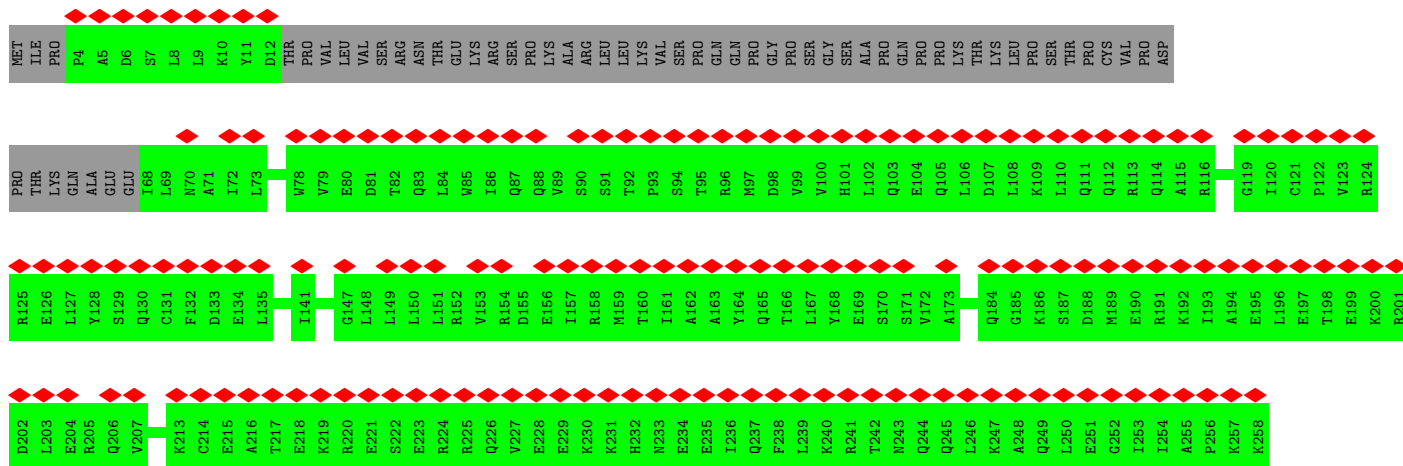
• Molecule 67: ACTA2



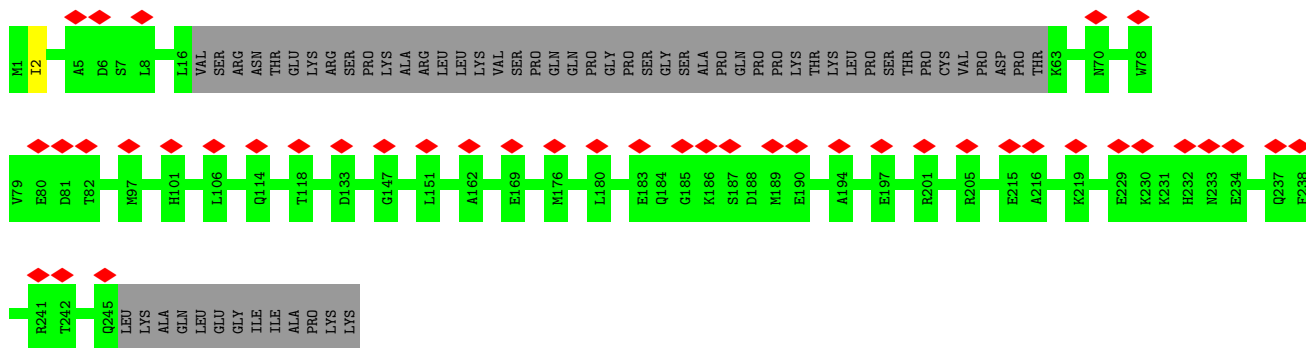
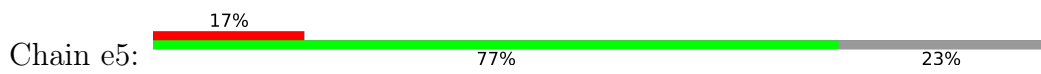
• Molecule 68: Axonemal dynein light intermediate polypeptide 1



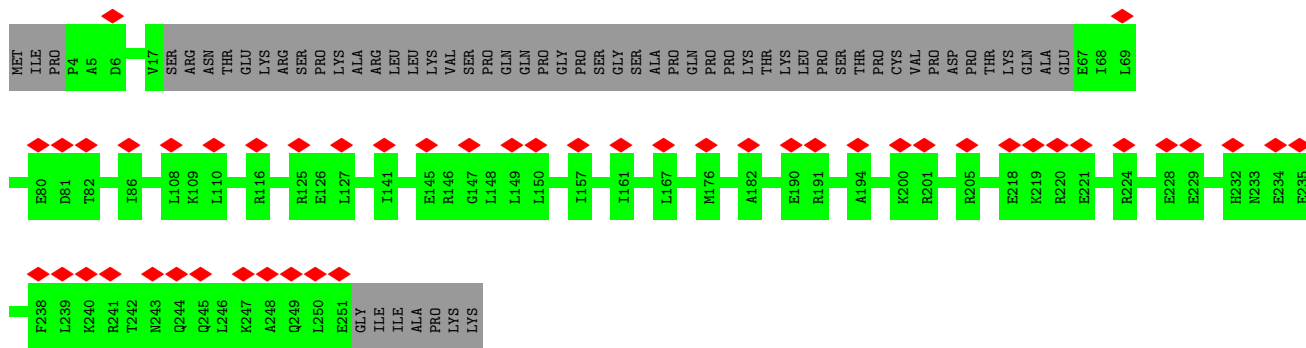
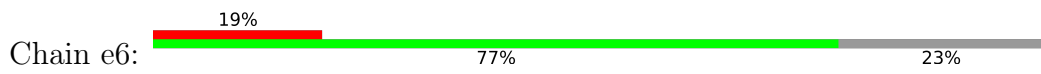
• Molecule 68: Axonemal dynein light intermediate polypeptide 1



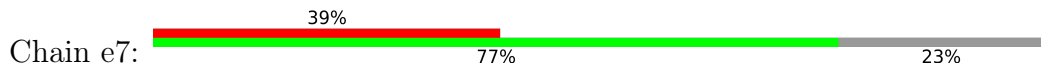
• Molecule 68: Axonemal dynein light intermediate polypeptide 1

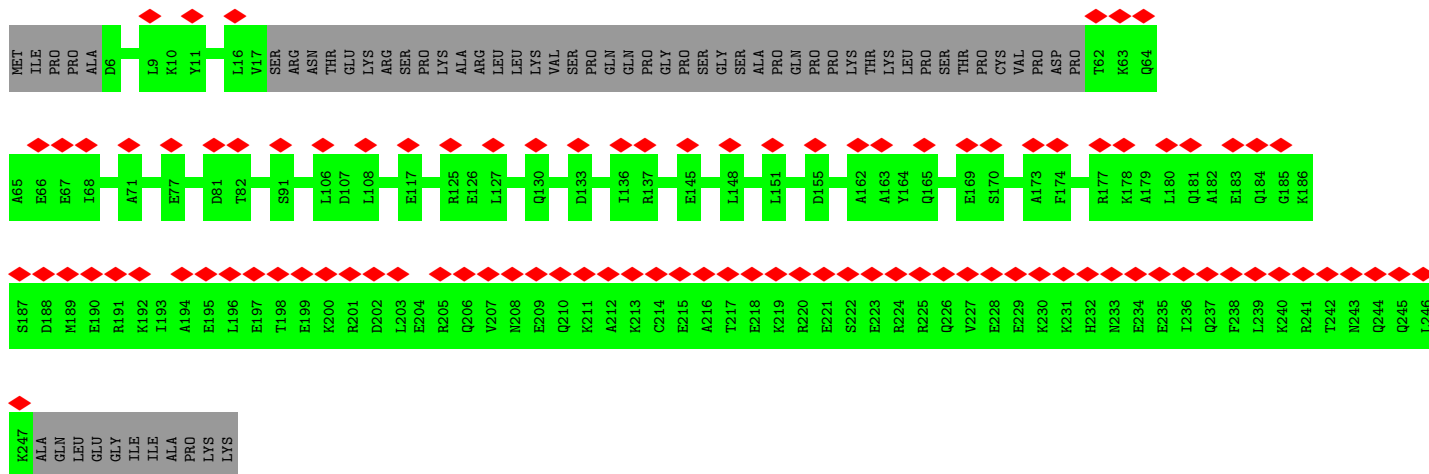


• Molecule 68: Axonemal dynein light intermediate polypeptide 1

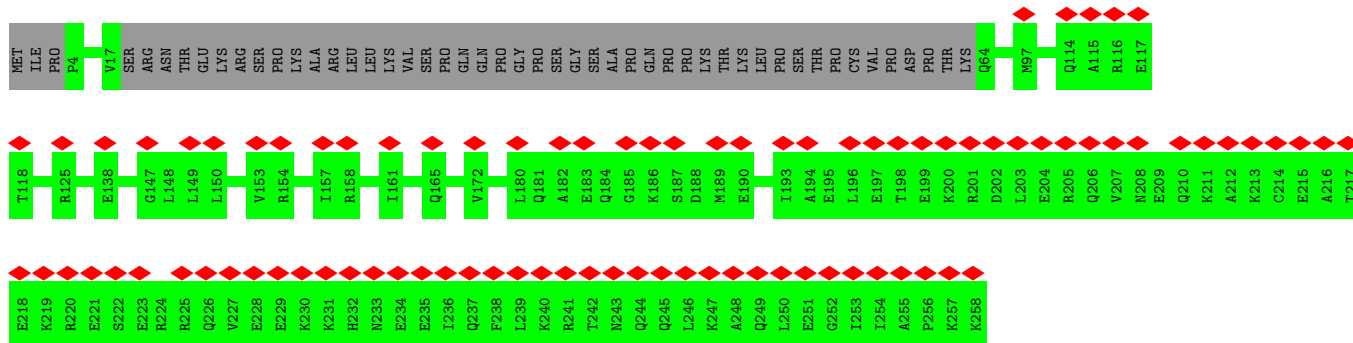
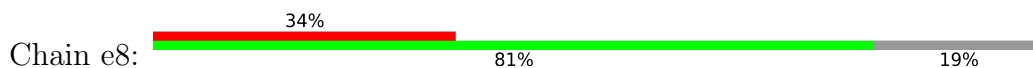


• Molecule 68: Axonemal dynein light intermediate polypeptide 1

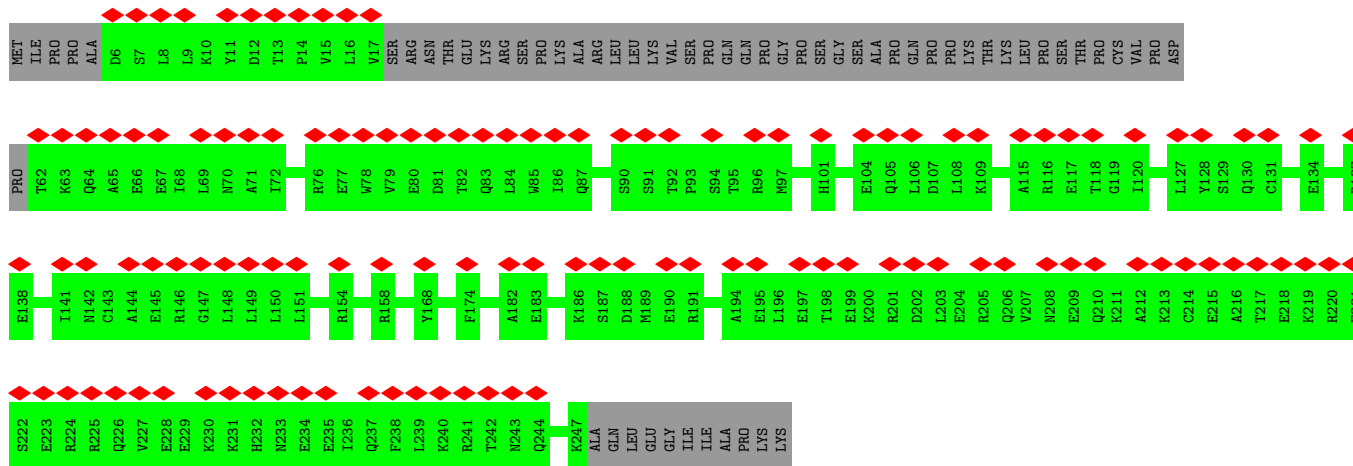
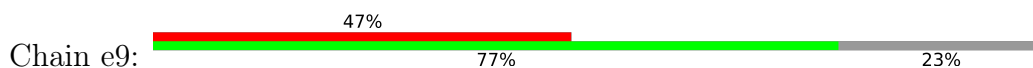




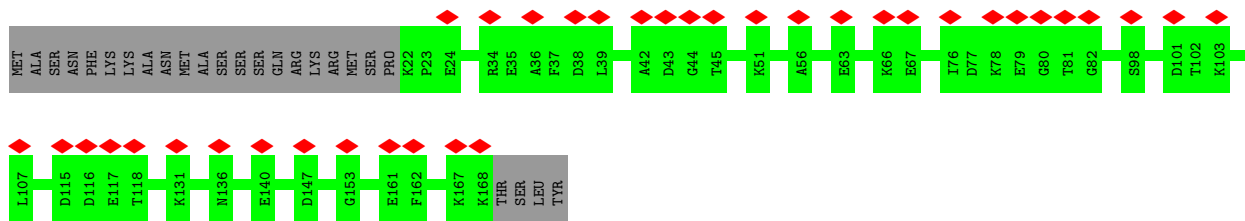
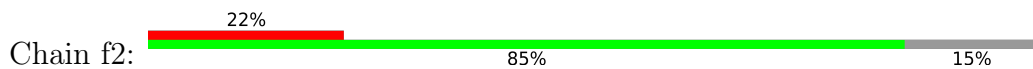
• Molecule 68: Axonemal dynein light intermediate polypeptide 1



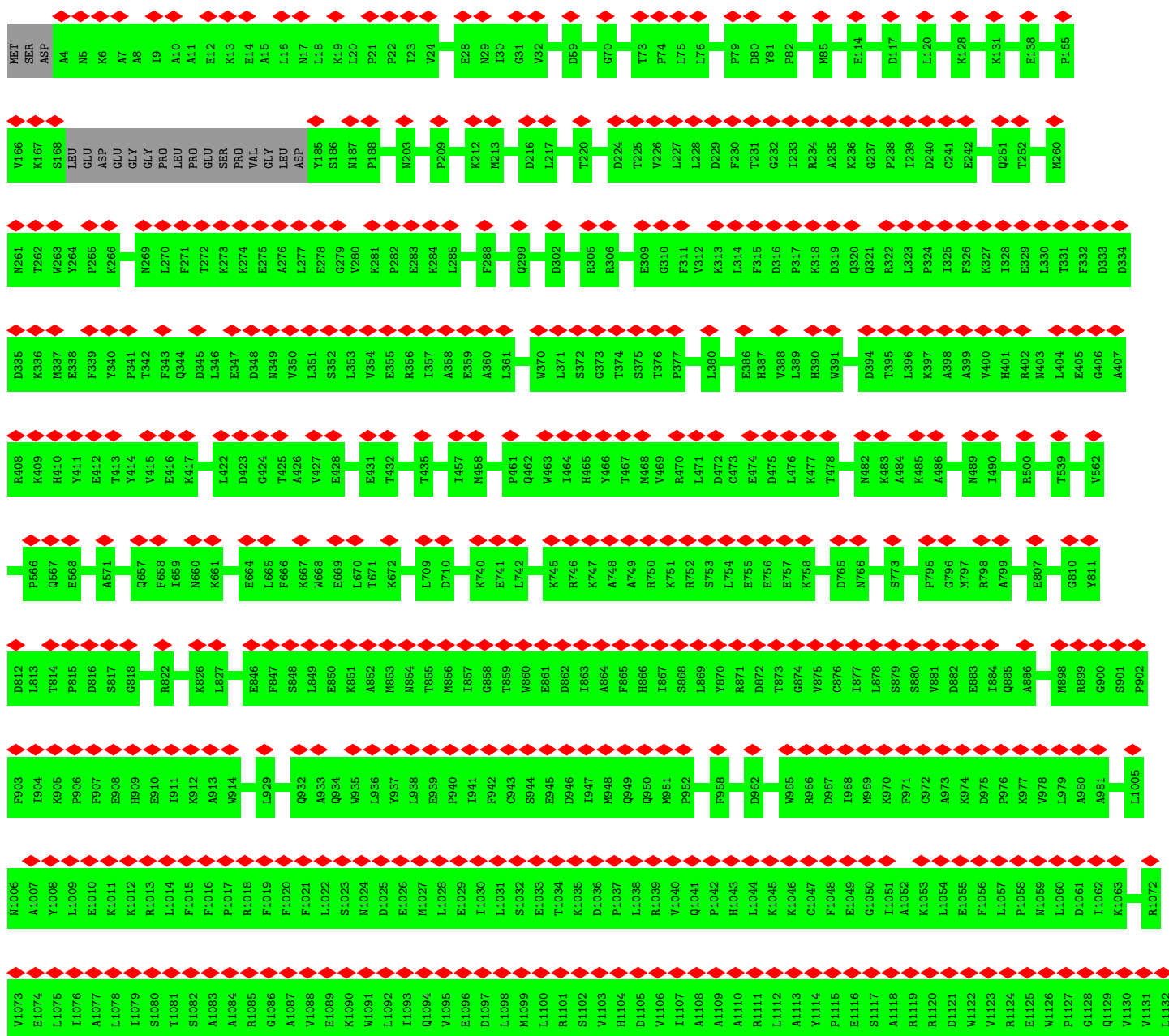
• Molecule 68: Axonemal dynein light intermediate polypeptide 1



• Molecule 69: Centrin-2

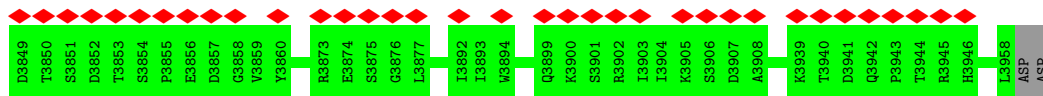


• Molecule 70: Dynein axonemal heavy chain 12

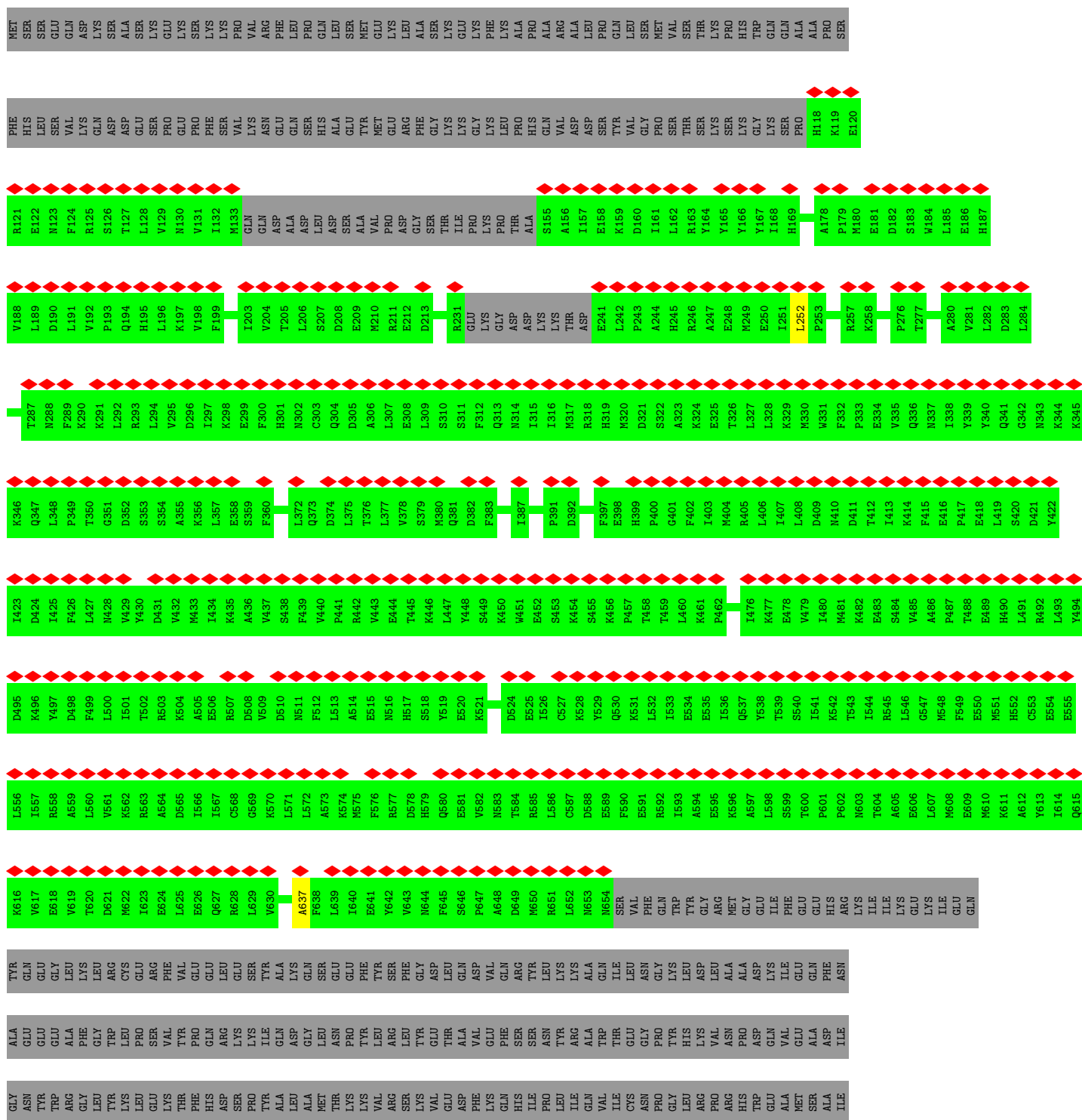


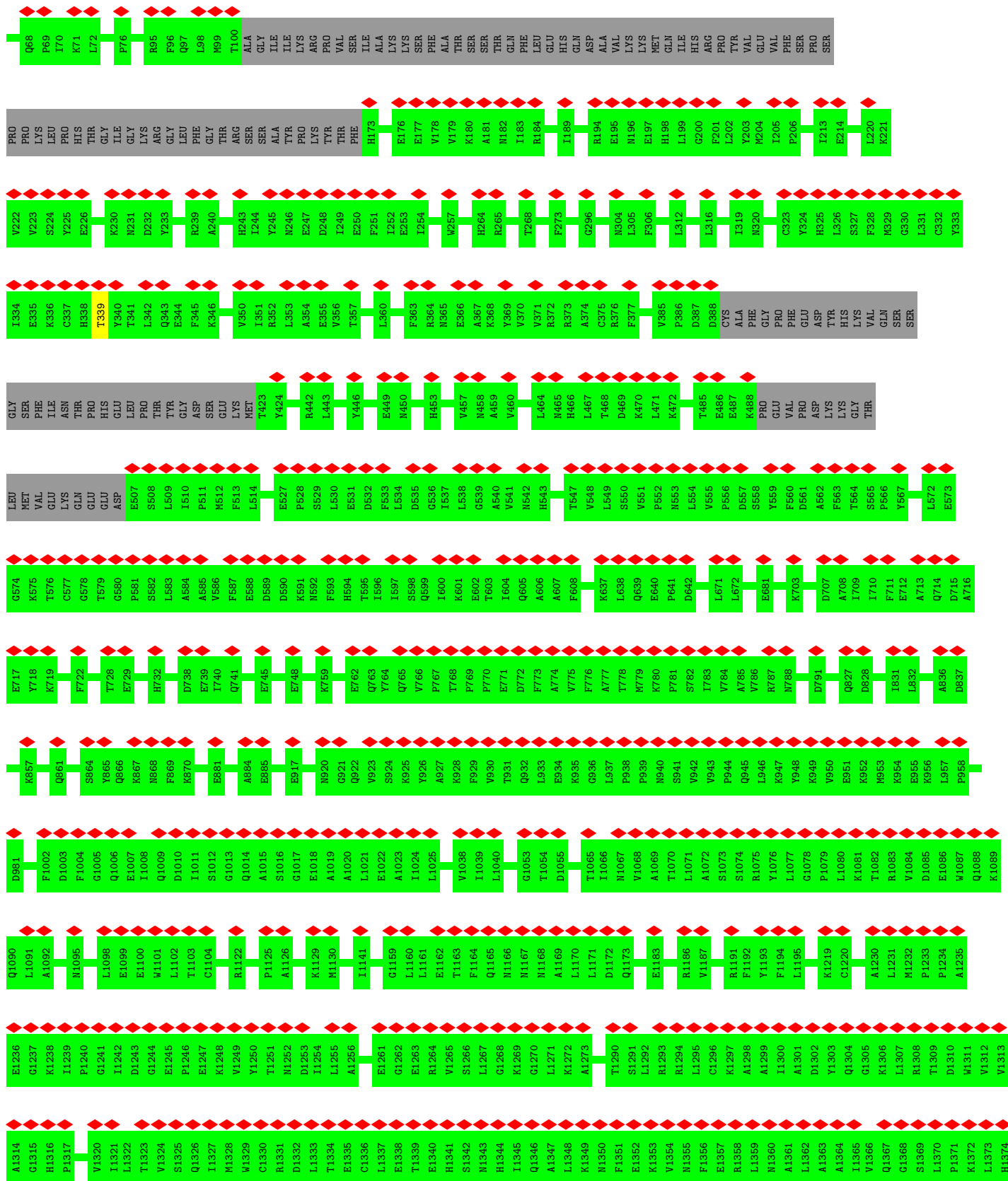
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● Molecule 71: Dynein axonemal heavy chain 7





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K3464	K3465	K3466	H3467	K3468	D3469	K3470	H3471	K3472	K3473	Q3474	E3475	K3477	A3478	A3479	H3480	Q3481	D3482	P3483	K3484	S3485	A3486	Q3487	L3488	S3489	S3490	F3491	H3492	K3493	L3494	I3495	L3496	I3497	K3498	C3499	C3500	K3501	E3502	E3503	K3504	V3505	V3506	F3507	A3508	L3509	T3510	D3511	F3512	V3513	I3514	E3515	N3516	L3517	D3518	K3519	Q3520	F3521	I3522	E3523	
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W1145	I4146	A4147	K4148	G4149	S4150	A4151	L4152	L4153	C4154	Q4155	L4156	SER	GLU																																														

• Molecule 74: Dynein axonemal heavy chain 1

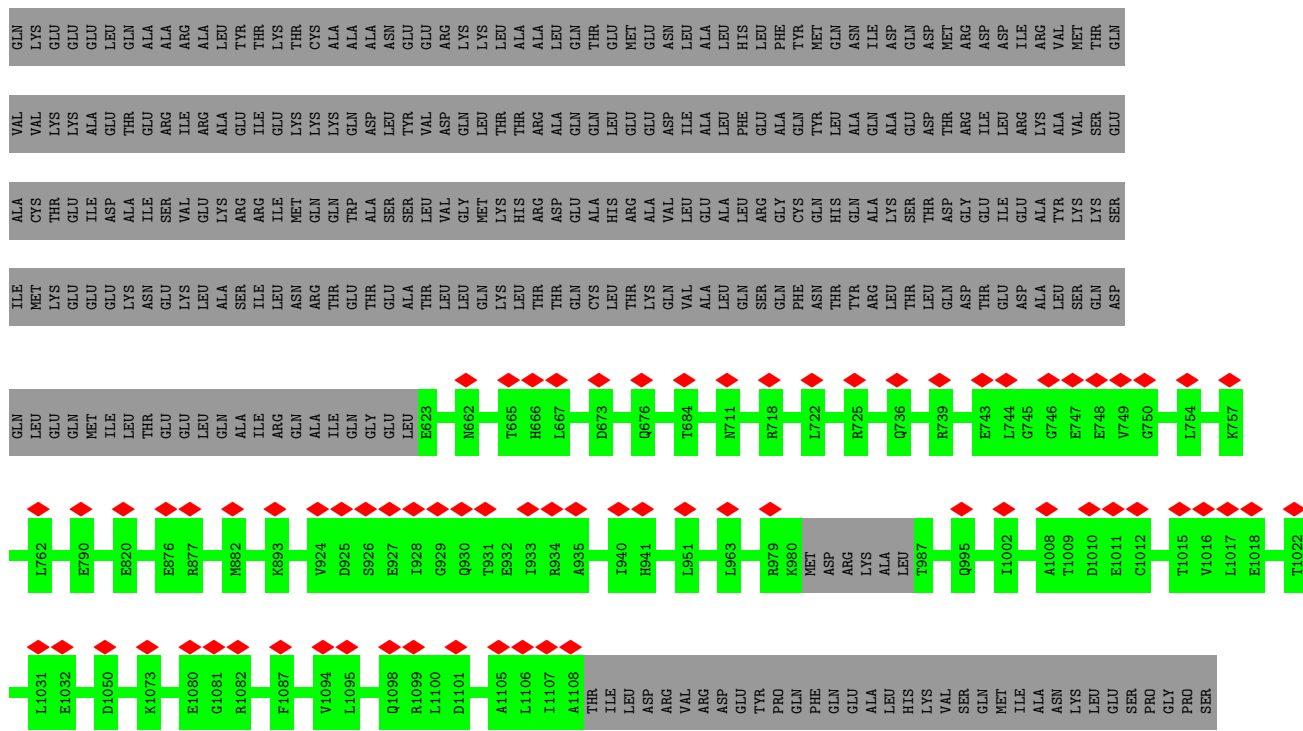


MET	GLU	GLN	PRO	PRO	ASN	PRO	LYS	GLY	TYR	THR	LEU	LEU	LEU	GLY	ARG	THR	PRO	GLN	GLY	PRO	PRO	GLU	CYS	SER	LEU	LEU	ALA	PRO	ALA	ALA	VAL	GLN	VAL	GLN	VAL	GLY	THR	HIS	ARG	GLY	LEU	GLU	GLU	TYR	ASN	PRO	PRO	GLY	LYS	ILE	LEU	PRO	GLY	SER	ASP	TYR	GLY	GLY	ASN	PRO	PRO	ALA	LEU	ASP	PRO	LYS	LEU	PRO
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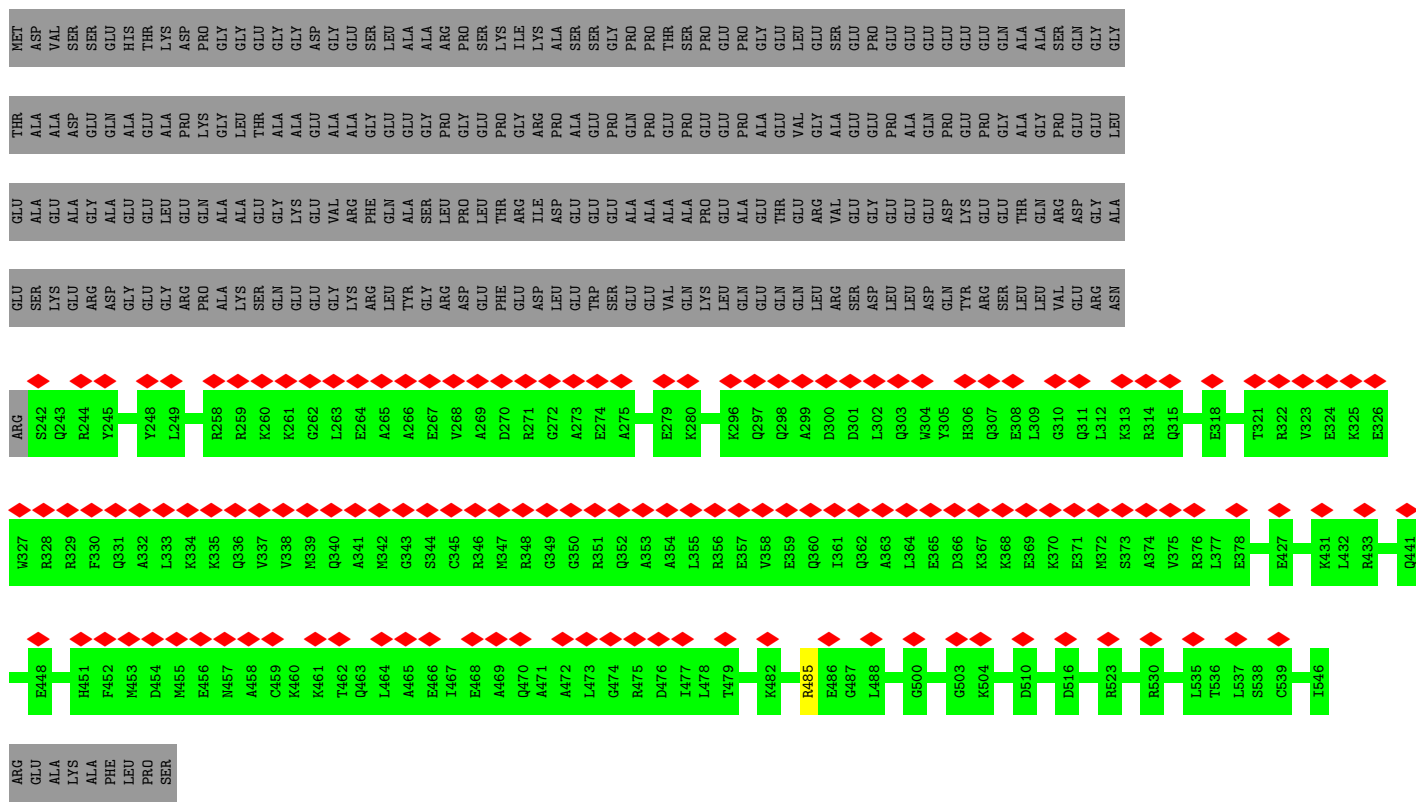
HIS	LEU	PRO	LEU	PRO	PRO	ALA	PRO	PRO	THR	THR	LEU	LEU	LEU	GLY	ASP	LEU	GLY	GLN	PRO	ARG	ARG	LYS	SER	PRO	PRO	LEU	LEU	THR	THR	THR	ASP	LYS	VAL	VAL	GLN	VAL	THR	L91	L92	K93	Q94	S99	G105	T106	L107	D108	Q109	C114	R118	L123	D128	L129	P134	R135	E143	I154	G155
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R159	L160	L161	A162	Q163	T164	D165	F166	Y171	E172	P173	F179	L182	L200	S201	L202	D203	I204	F209	S210	L213	D214	S215	N216	K217	L218	M219	P220	R221	H222	L223	Q226	H227	P228	Q229	T230	I231	E232	Q233	G234	H235	D236	P240	I241	L245	K246	D249	N250	E251	D252										
F253	D254	C255	R256	E260	N263	M264	G265	L266	E267	P268	G269	S270	L271	D272	R273	K274	G278	K279	A280	L281	T284	D285	L288	G289	D292	P293	K294	S295	Q296	K297	L298	K299	C303	E304	V307	L308	D309	Y310	D311	E312	E313	K314	K315	L316	Y317	H320	K321	T322	D323	E324									
K325	G326	L327	V328	R329	D330	E331	M332	G333	R334	P335	I336	L337	G340	V341	T342	T343	E344	G345	R346	P347	P348	L349	C352	Q353	Y354	K355	V356	P357	R358	I359	Q360	C364	A365	F371	R374	V375	V376	Q377	A380	D389	L381	N384	A387	Y391	N392	L393	Y394	M398	P399	S400									
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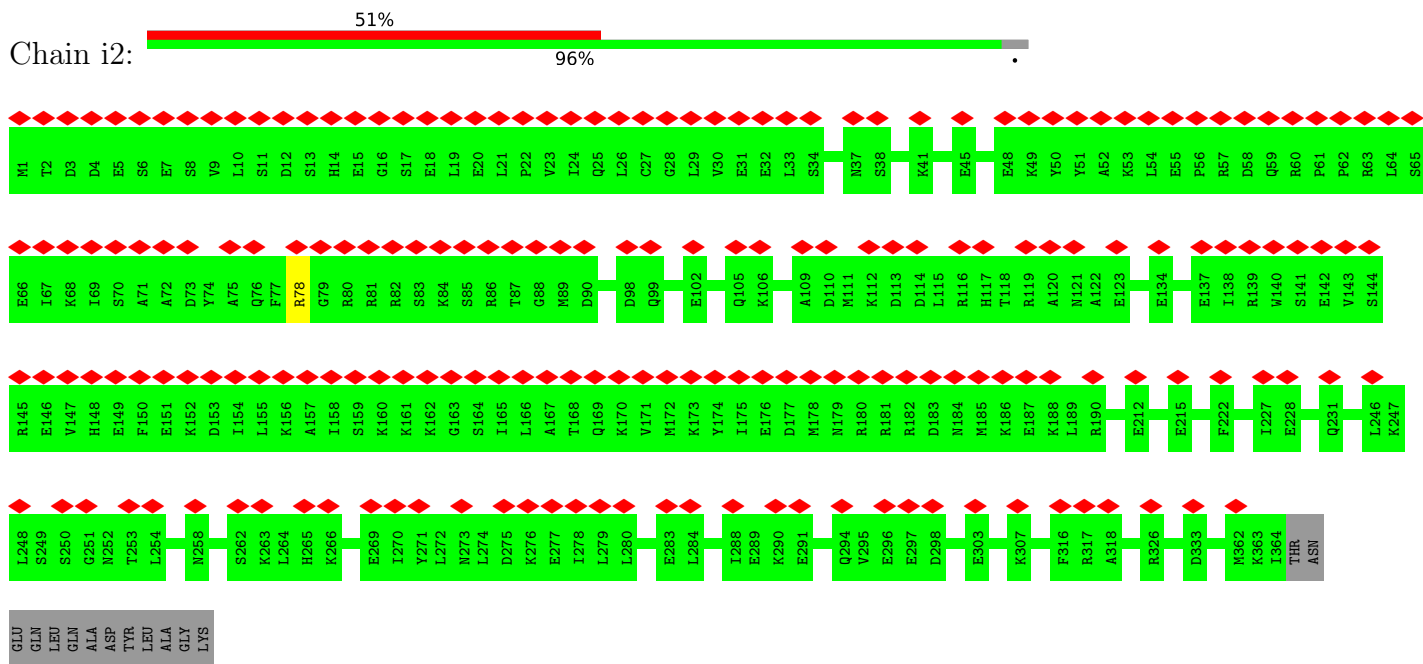
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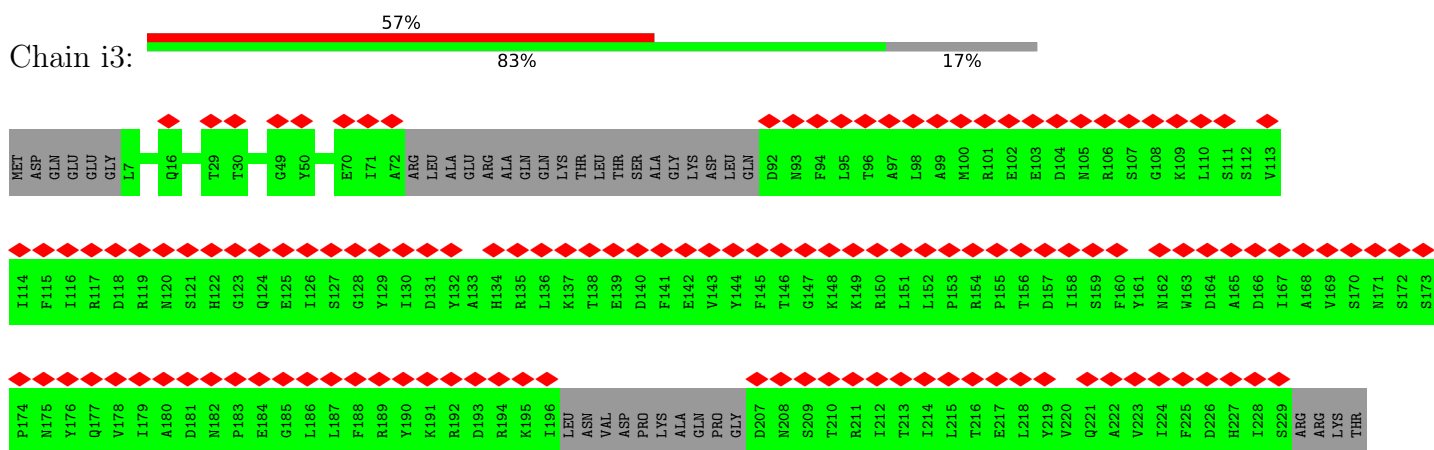
• Molecule 77: Coiled-coil domain-containing protein 96



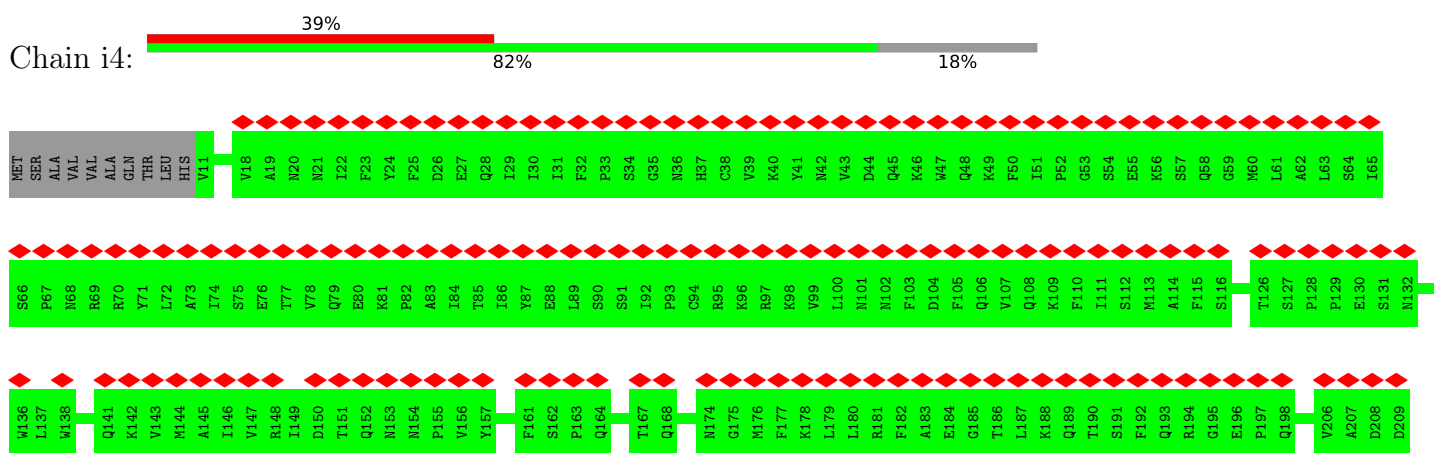
• Molecule 78: Coiled-coil domain-containing protein 113

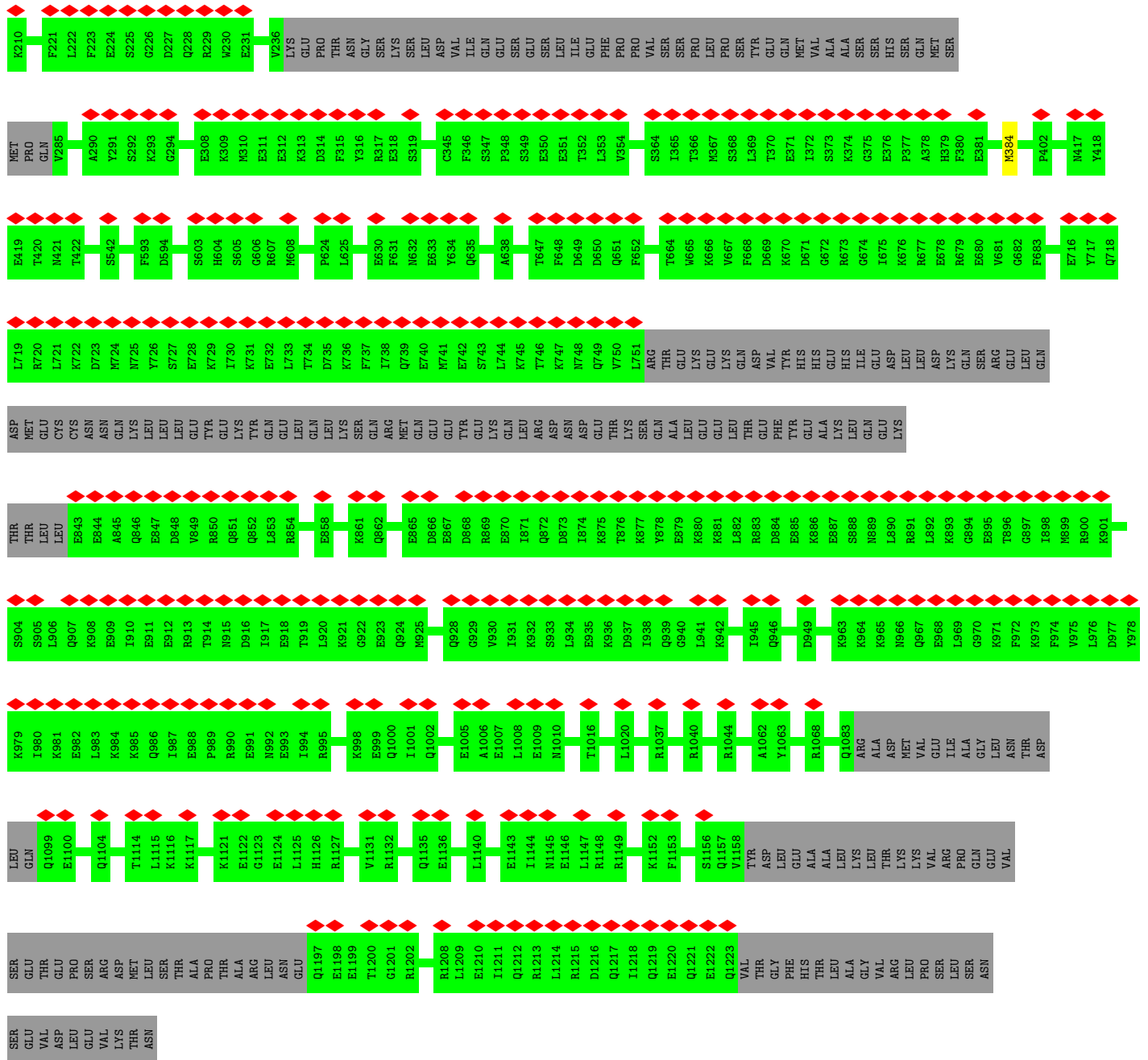


• Molecule 79: Cilia- and flagella-associated protein 299

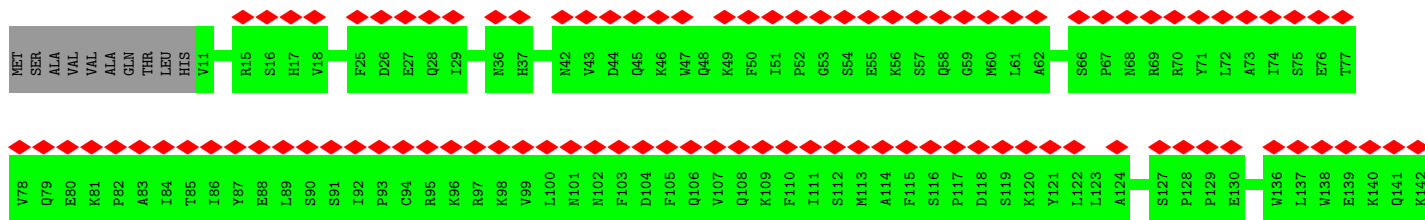
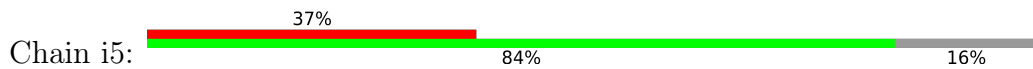


• Molecule 80: Cilia- and flagella-associated protein 57

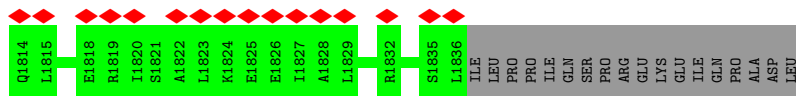




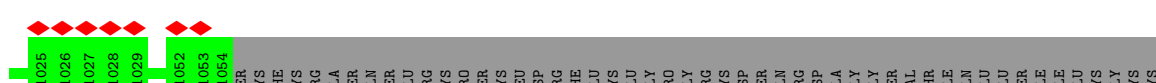
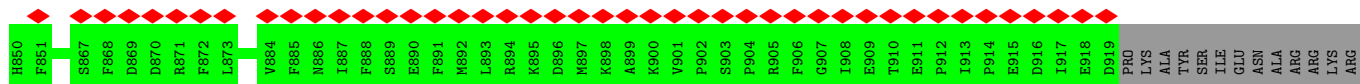
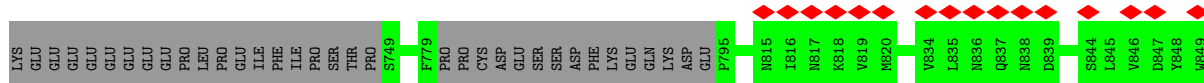
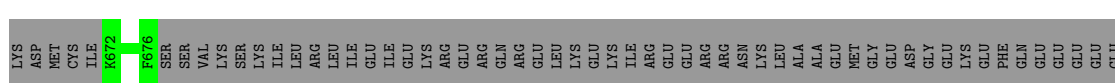
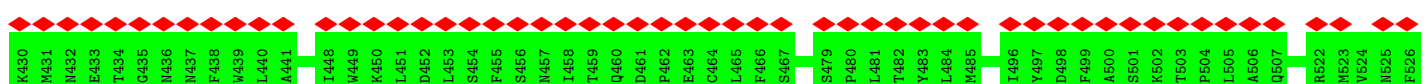
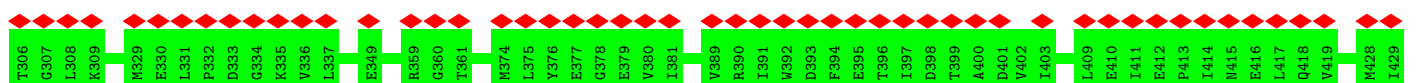
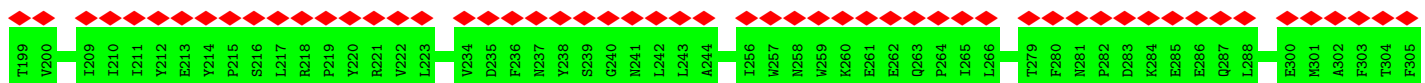
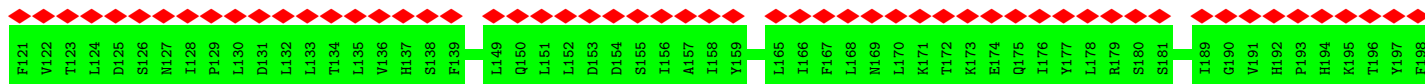
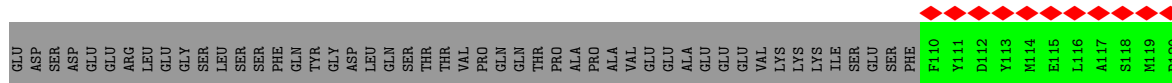
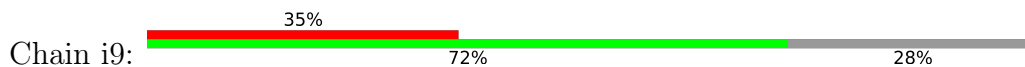
• Molecule 80: Cilia- and flagella-associated protein 57

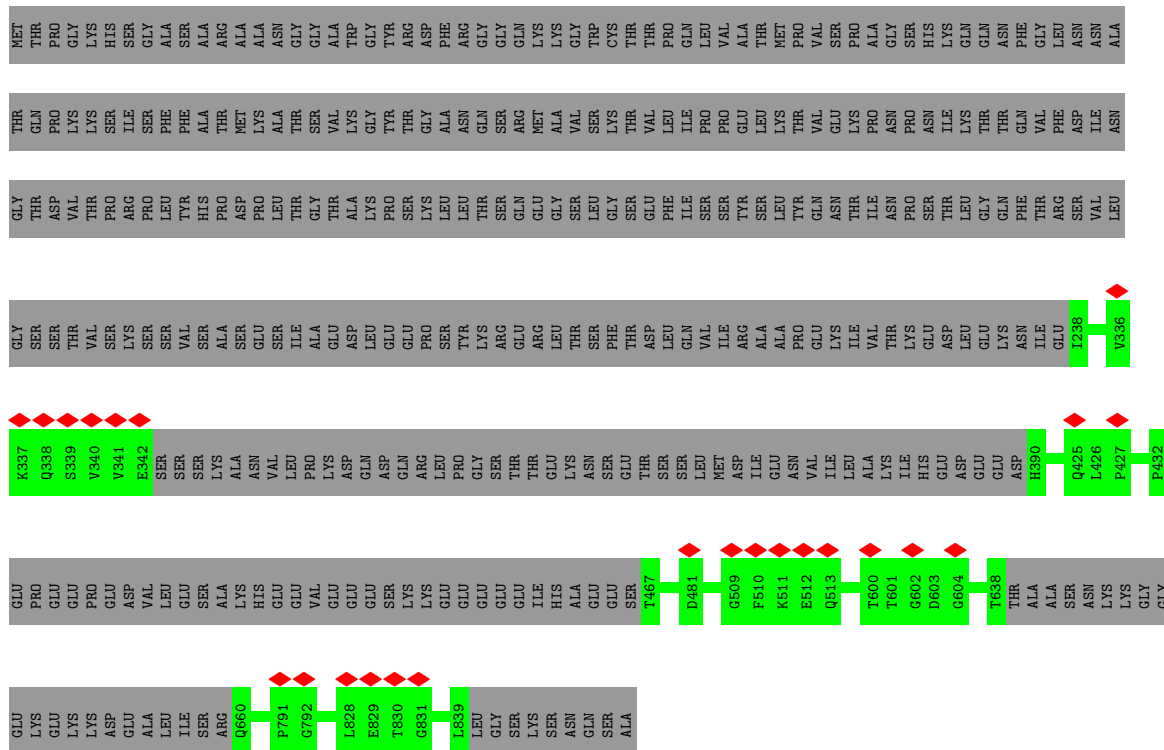






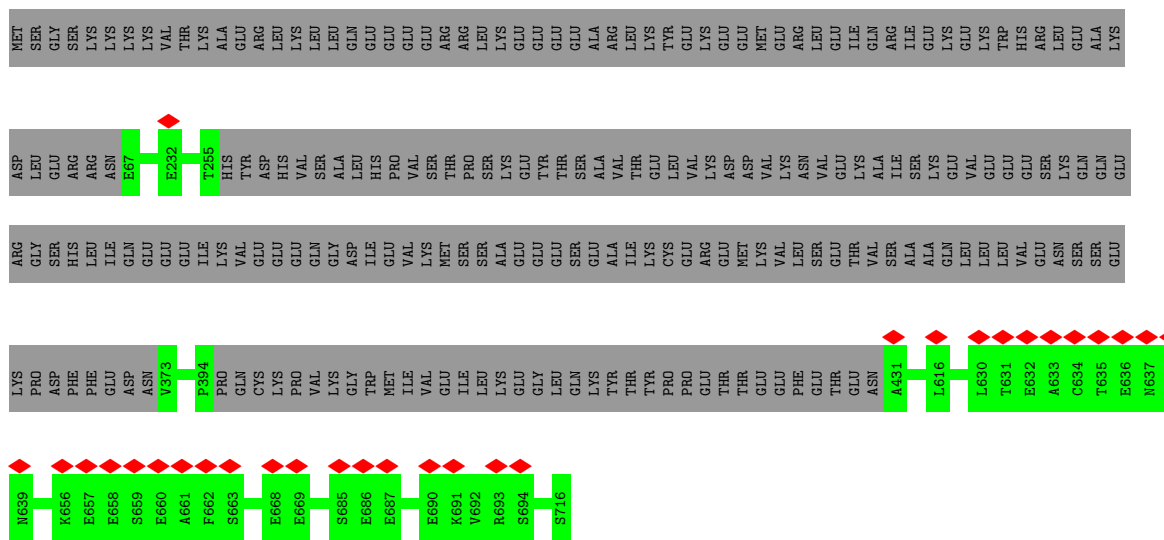
● Molecule 82: Cilia- and flagella-associated protein 44





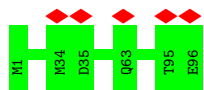
• Molecule 88: Dynein axonemal intermediate chain 7

Chain k3: 69% 31%



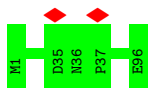
• Molecule 89: Dynein light chain roadblock-type 1

Chain k4: 100% 5%



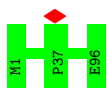
• Molecule 89: Dynein light chain roadblock-type 1

Chain m4:  100%



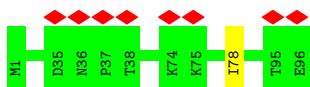
- Molecule 89: Dynein light chain roadblock-type 1

Chain o4:  100%



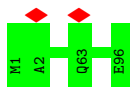
- Molecule 89: Dynein light chain roadblock-type 1

Chain q4:  8% 99%



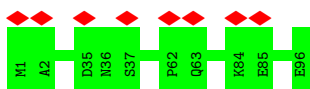
- Molecule 90: Dynein light chain roadblock-type 2

Chain k5:  100%



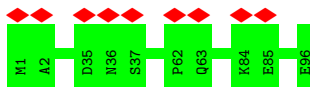
- Molecule 90: Dynein light chain roadblock-type 2

Chain m5:  8% 100%



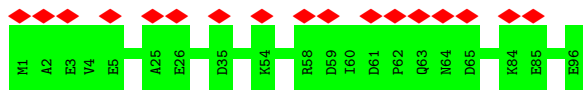
- Molecule 90: Dynein light chain roadblock-type 2

Chain o5:  9% 100%

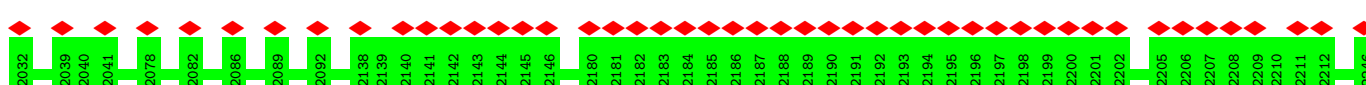
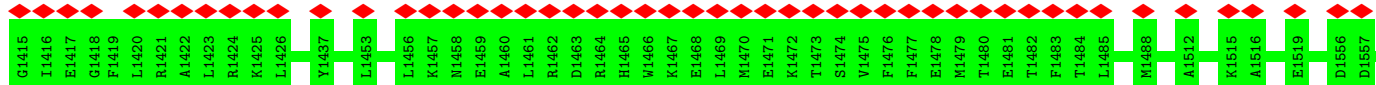
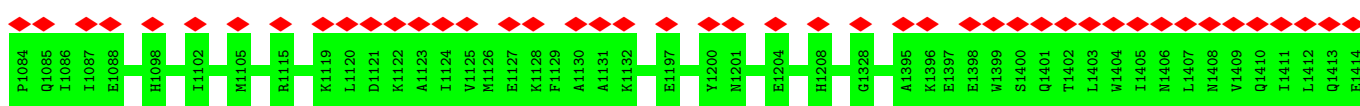
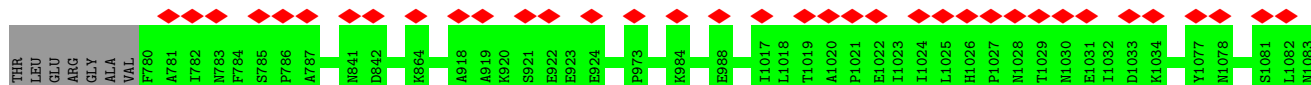
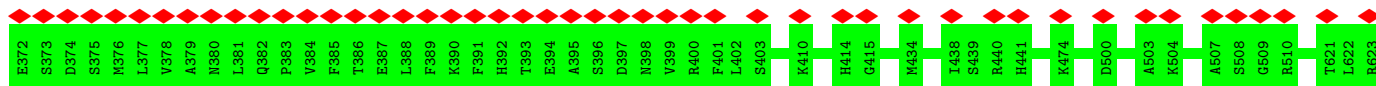
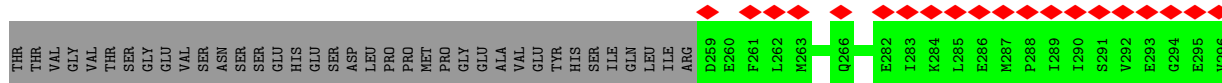
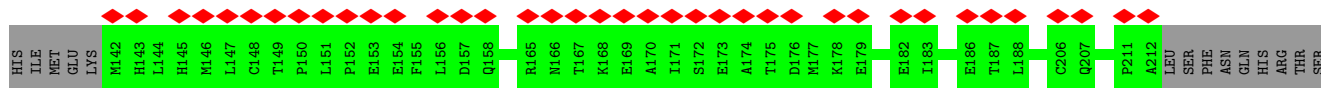
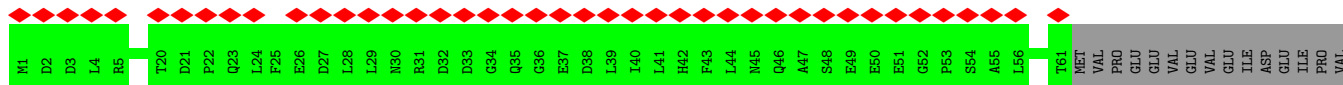


- Molecule 90: Dynein light chain roadblock-type 2

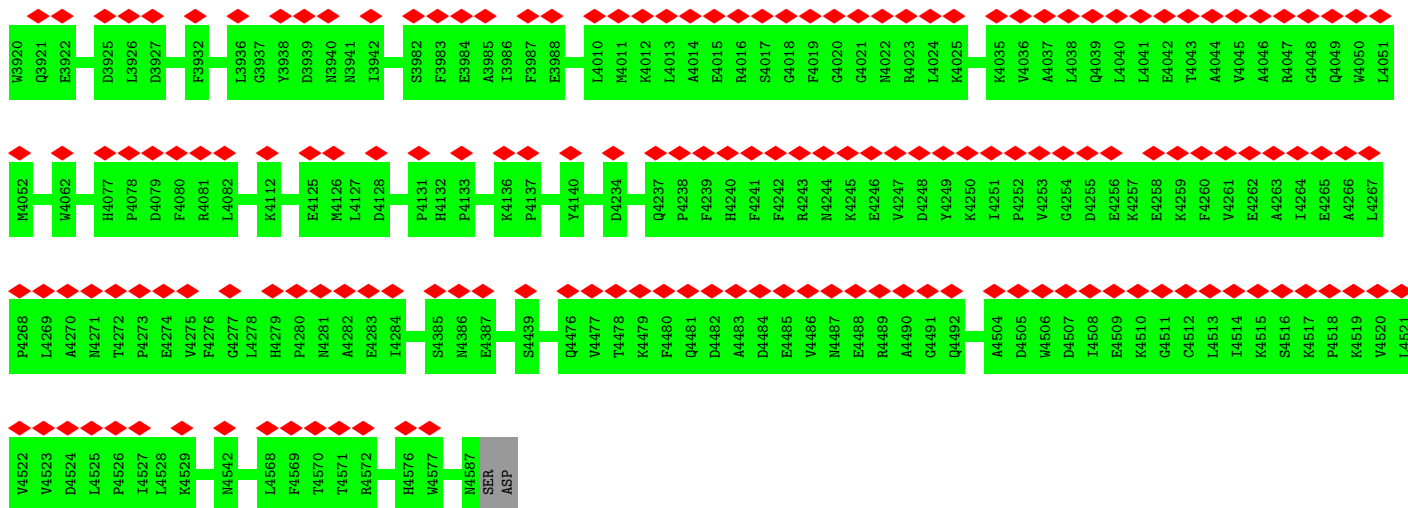
Chain q5:  18% 100%



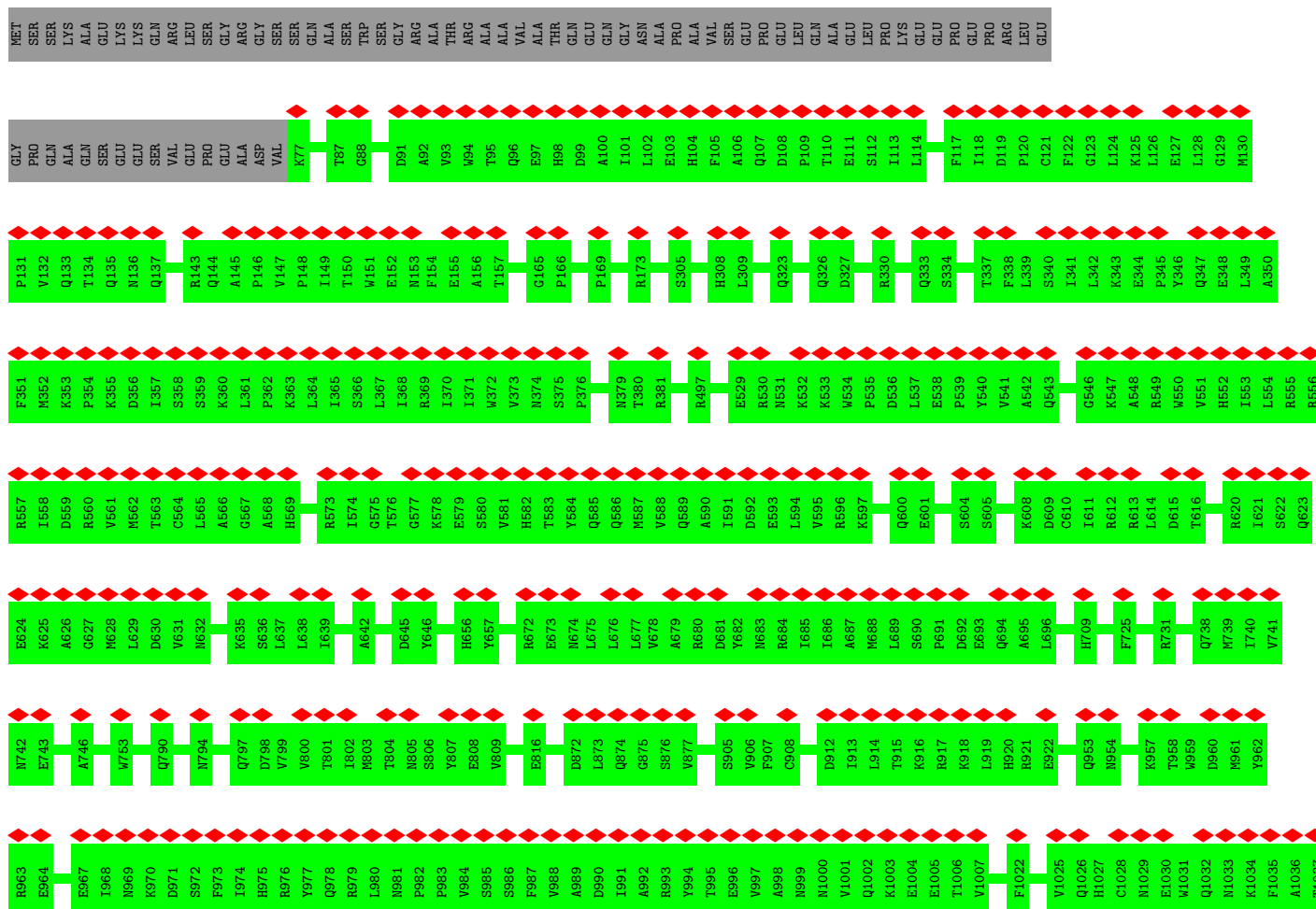
• Molecule 91: Dynein axonemal heavy chain 10



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V2383	N2384	Q2385	I2386	P2387	N2388	K2389	V2390	E2391	Q2392	Y2393	N2394	L2395	N2396	S2397	L2398	F2399	E2400	K2401	P2404	Y2405	E2447	G2448	E2449	L2450	E2451	D2452	L2453	D2454	E2496	G2497	V2498	A2500	N2501	E2504	I2535	H2536	A2537	P2538	E2539	K2564	S2591	E2592	E2593	T2594	N2595	E2616	A2617	E2620											
K2621	R2622	T2623	K2624	D2625	T2626	G2628	P2629	R2630	M2631	G2632	R2633	K2634	G2666	D2670	R2671	G2672	K2673	E2674	L2675	N2676	C2677	K2678	S2679	L2680	R2681	D2682	S2733	T2734	F2735	H2736	E2737	F2769	E2790	L2856	H2857	E2858	G2859	E2860	P2861	E2883	Y2884	N2885	E2886	S2887	M2888	S2939	L2946	L2947	S2948	R2949									
G2950	Y2951	S2952	E2953	N2954	S2955	F2956	R2957	E2958	D2959	L2960	K2961	S2962	L2965	K2966	L2967	G2968	L2969	E2970	L3003	L3004	F3005	S3006	E3007	E3008	E3009	K3010	E3011	S3012	L3013	L3014	S3015	Q3016	L3017	G3018	Q3019	E3020	A3021	L3022	K3023	Q3024	G3025	M3026	G3027	P3028	A3029	K3030	E3031	S3032	V3033	Q3035	Y3036	F3037	N3096						
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T3211	A3212	V3213	A3214	E3215	E3216	K3217	K3218	K3219	L3220	A3221	E3222	E3223	K3224	A3225	M3226	E3227	I3228	E3229	E3230	Q3231	N3232	K3233	V3234	I3235	K3236	M3237	E3238	K3239	A3240	E3241	A3242	E3243	T3244	T3245	L3246	A3247	E3248	V3249	M3250	P3251	L3252	L3253	E3254	A3255	K3256	K3257	L3258	E3259	L3260	Q3261	K3262	L3263	D3264	K3265	S3266	D3267	V3268	T3269	E3270
I3271	R3272	S3273	F3274	A3275	K3276	P3277	P3278	K3279	Q3280	V3281	Q3282	T3283	V3284	C3285	E3286	I3287	I3288	L3289	I3290	M3291	G3292	L3293	Y3294	K3295	E3296	L3297	N3298	W3299	K3300	T3301	A3302	K3303	G3304	V3305	M3306	S3307	F3308	P3309	N3310	F3311	L3312	R3313	P3314	L3315	M3316	E3317	I3318	F3319	D3320	R3321	S3322	L3323	T3324	Q3325	S3326	Q3327	V3328	K3329	N3330
I3331	K3332	G3333	L3334	L3335	K3336	T3337	L3338	N3339	T3340	T3342	E3343	E3344	M3345	E3346	A3347	V3348	S3349	K3350	A3351	G3352	L3353	G3354	M3355	L3356	K3357	F3358	V3359	E3360	A3361	V3362	M3363	G3364	Y3365	C3366	D3367	F3368	F3369	K3370	E3371	I3372	K3373	P3374	K3375	R3376	E3377	K3378	V3379	A3380	R3381	L3382	R3384	N3385	Q3386	Q3387	L3388	T3389	K3390		
R3391	E3392	L3393	E3394	R3395	I3396	Q3397	N3398	E3399	L3400	A3401	A3402	L3403	Q3404	K3405	E3406	L3407	E3408	T3409	L3410	G3411	A3412	K3413	Y3414	E3415	A3416	A3417	I3418	L3419	E3420	K3421	Q3422	K3423	L3424	Q3425	E3426	E3427	A3428	E3429	I3430	M3431	E3432	R3433	R3434	L3435	I3436	A3437	A3438	D3439	K3440	L3441	I3442	S3443	G3444	L3445	G3446	E3447	E3448	N3449	I3450
R3451	W3452	L3453	N3454	D3455	L3456	D3457	E3458	L3459	K3460	H3461	R3462	K3463	V3464	K3465	L3466	L3467	V3521	S3524	R3525	S3528	Q3529	R3566	T3667	V3668	T3669	L3670	E3673	K3677	V3680	L3681	V3682	A3683	Y3684	D3685	R3686	R3687	E3688	E3691	Q3692	R3693	E3694	H3695	L3696	Y3697	G3698	E3699	D3603	D3607	P3608	V3609	L3610	D3611	N3612	K3708					
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L3794	L3795	A3796	F3797	L3798	E3799	V3800	F3801	L3802	L3803	S3804	L3805	K3806	S3807	S3808	L3809	P3810	R3811	S3812	L3813	L3814	M3815	K3816	L3817	L3818	R3819	N3820	I3821	R3822	D3823	T3824	L3825	S3828	E3857	G3858	R3859	K3882	F3883	C3884	A3885	K3886	D3904	N3905	F3906	G3907	Q3908	D3911	D3912	V3913	E3914	N3915	N3916	Q3917	T3918	V3919					



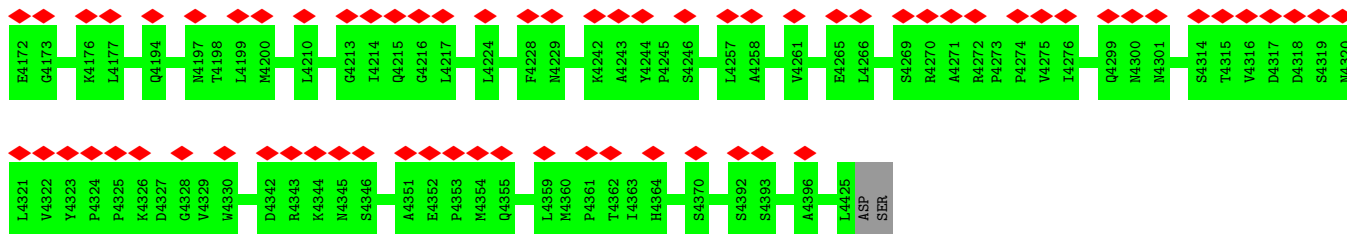
• Molecule 92: Dynein axonemal heavy chain 2



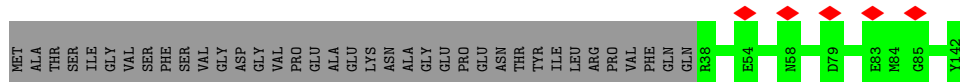
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E1106	V1107	P1108	V1109	D1110	D1111	S1112	V1113	L1114	E1115	M1116	L1117	D1118	S1119	L1120	N1121	E1122	E1123	V1124	V1125	V1126	F1127	Q1128	Q1129	T1130	L1131	L1132	D1133	S1134	K1135	Q1136	M1137	L1138	K1139	H1140	H1141	K1142	E1143	K1144	F1145	K1146	T1147	G1148	L1149	T1150	H1151	S1152	A1153	D1154	D1155	F1156	K1157	K1158	K1159	A1160	H1161	T1162	L1163	L1164	E1165	
D1166	F1167	E1168	F1169	K1170	G1171	H1172	L1173	T1174	S1175	M1176	V1177	G1178	Y1179	M1180	S1181	A1182	L1183	D1184	Q1185	I1186	T1187	Q1188	V1189	R1190	A1191	M1192	L1193	M1194	A1195	I1212	E1213	D1228	Q1231	Q1232	I1233	W1234	E1235	L1236	A1237	M1238	D1239	W1240	E1241	E1242	M1243	W1244	M1245	E1246	W1247	K1248	T1249	G1250	R1251	F1252	L1253	I1254				
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L1625	R1626	M1627	C1628	H1629	L1630	A1631	L1632	L1633	K1634	F1635	L1636	M1637	K1638	R1639	D1640	M1641	W1642	V1643	K1644	E1645	W1646	A1647	Q1648	G1649	V1650	V1651	I1652	T1653	A1654	S1655	S1688	I1689	L1690	M1691	K1692	Y1693	S1694	E1695	A1696	L1697	R1698	G1699	M1700	L1701	T1702	K1703	I1704	M1705	R1706	L1707	K1708	I1709	V1710	A1711	L1712	V1713	T1714	I1715		
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M1906	P1907	G1908	Y1909	A1910	G1911	R1912	V1929	V1930	P1931	D1932	S1933	T1934	L1935	I1936	A1937	E1938	I1939	L1940	F1942	G1943	E1944	G1945	F1946	G1947	N1948	C1949	K1950	V1956	Y1957	Y1960	S1961	R1969	Q1970	D1971	H1972	Y1973	D1974	F1975	F1976	L1977	R1978	A1979	L1980	T1981	S1982	L1983	L1984	R1985	Y1986	A1987	G1988	T1989	K1990	R1991						

R1992	L1993	Q1994	P1995	D1996	L1997	T1998	D1999	V2002	L2005	S2006	H2007	R2008	D2009	M2010	N2011	I2012	A2013	R2014	L2015	T2016	S2017	A2020	R2033	I2034	E2035	L2036	P2037	V2038	I2039	D2040	Y2041	G2042	R2043	E2044	R2045	E2046	T2047	V2048	E2049	Q2050	E2051	I2052	R2053	D2054	G2055	G2056	L2057	Q2058	S2059	T2060	F2061	F2062	T2063	L2064	T2065					
K2066	V2067	F2068	Q2069	L2070	Y2071	E2072	T2073	K2074	N2075	S2076	R2077	H2078	S2079	C2085	R2095	I2096	L2097	Q2098	A2099	S2100	L2101	S2102	S2103	L2104	C2105	R2106	A2107	G2108	D2109	P2110	N2111	F2112	N2113	I2114	V2115	R2116	E2117	E2133	Y2134	L2136	L2136	S2137	T2138	N2139	E2140	T2141	T2142	D2143	A2155	D2156	E2157	K2158	P2159	D2160	E2161					
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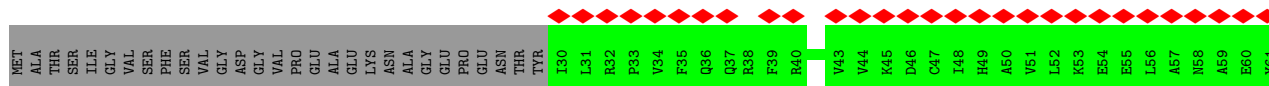
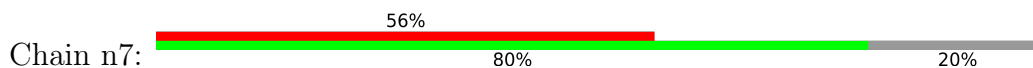
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G4090	G4090	E3884	P3819	P3758	F3618	L3617	R3557	F3481	N3334	V3212	M3272	V3212
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S4094	S4094	L3822	L3822	K3761	L3621	L3621	E3561	Y3484	W3337	P3215	K3275	P3215
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		T3810	T3810	T3810			R3608	R3608	V3385	E3263	E3263	E3263
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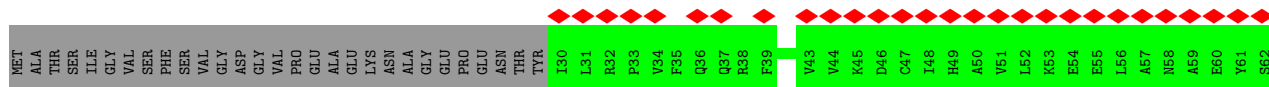
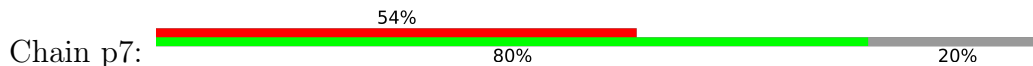
• Molecule 93: Dynein light chain Tctex-type protein 2B



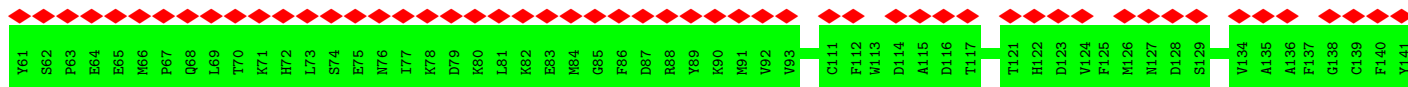
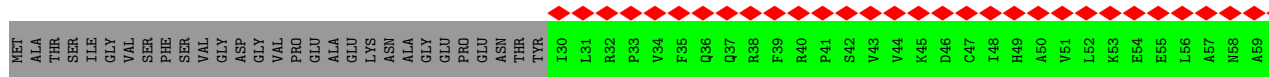
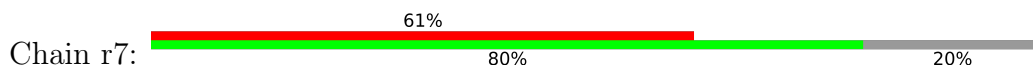
• Molecule 93: Dynein light chain Tctex-type protein 2B



• Molecule 93: Dynein light chain Tctex-type protein 2B

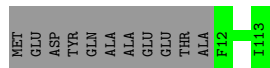
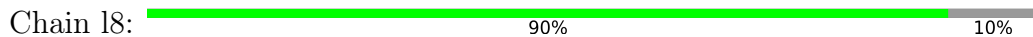


• Molecule 93: Dynein light chain Tctex-type protein 2B

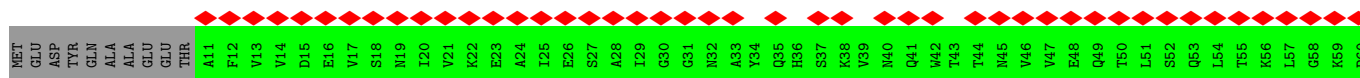
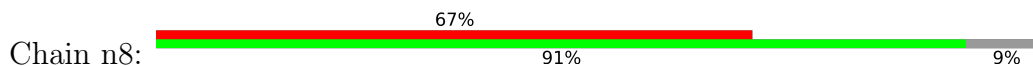


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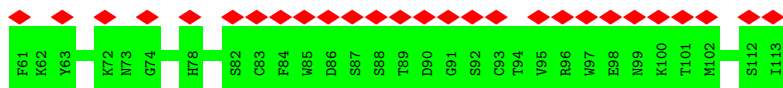
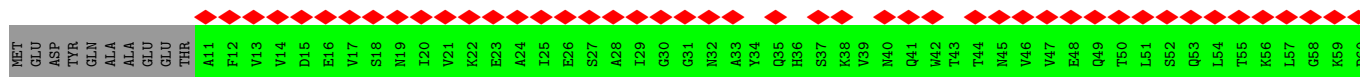
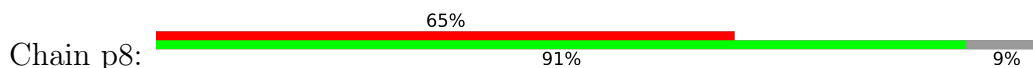
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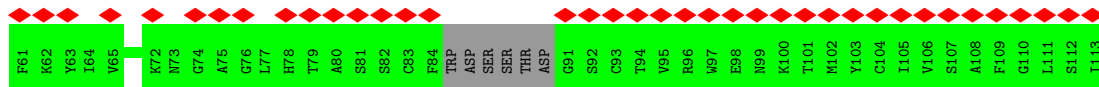
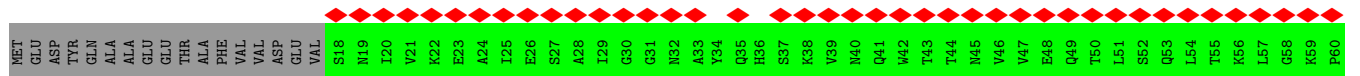
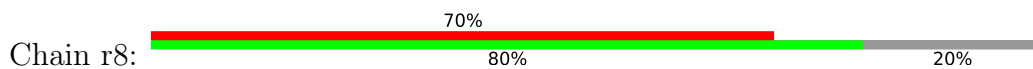
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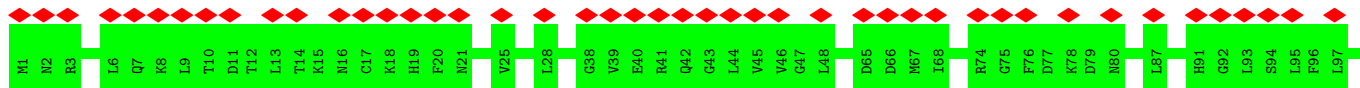
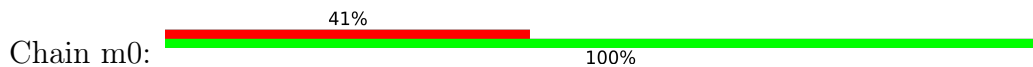
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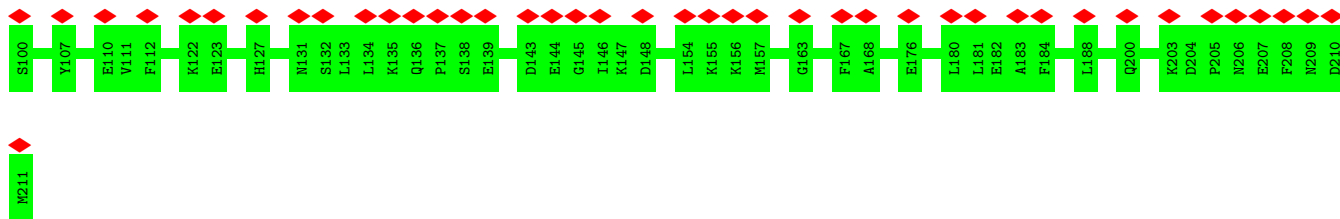


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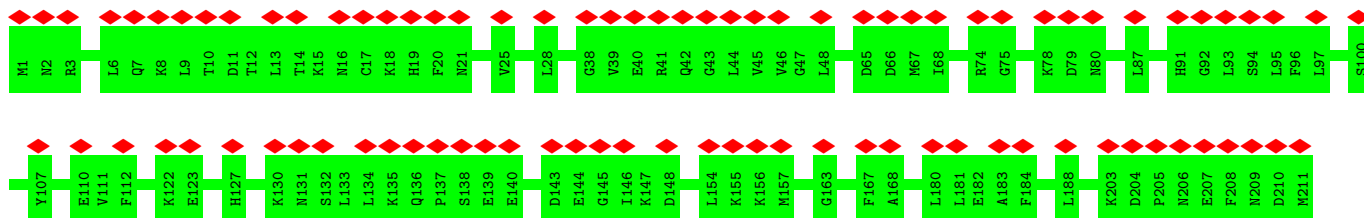
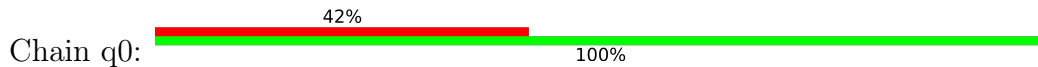


Molecule 95: Calaxin

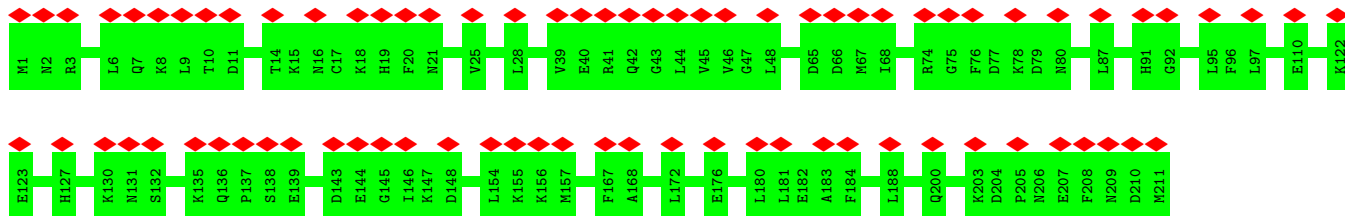




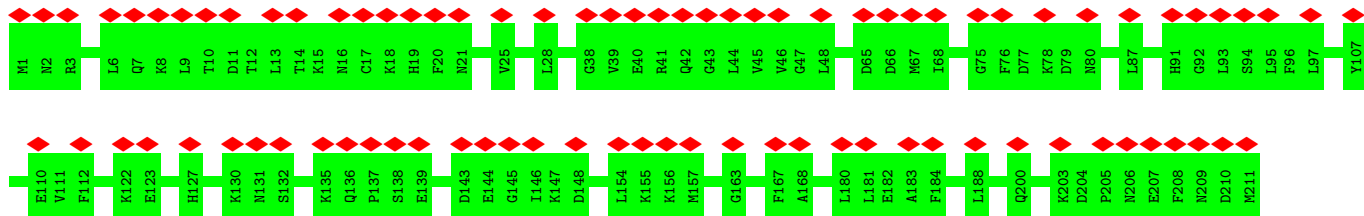
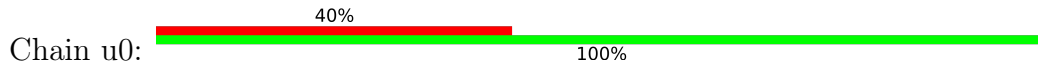
• Molecule 95: Calaxin



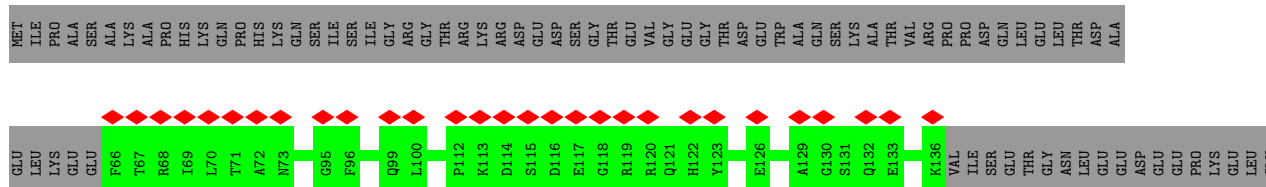
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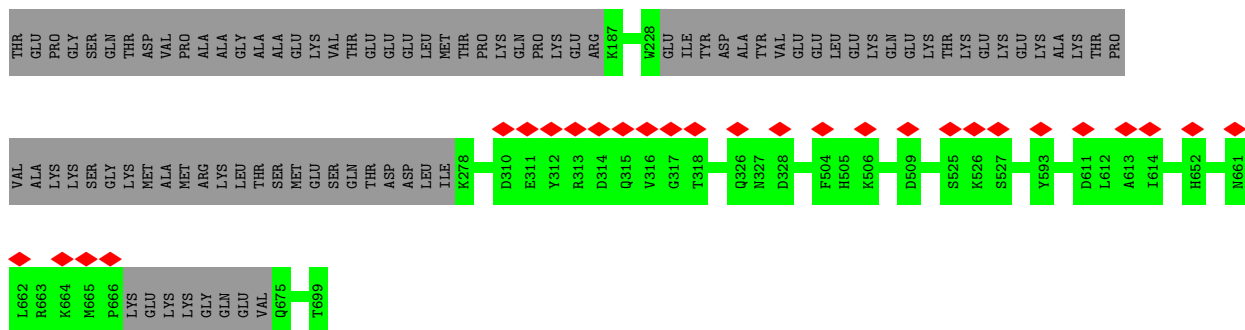


• Molecule 95: Calaxin

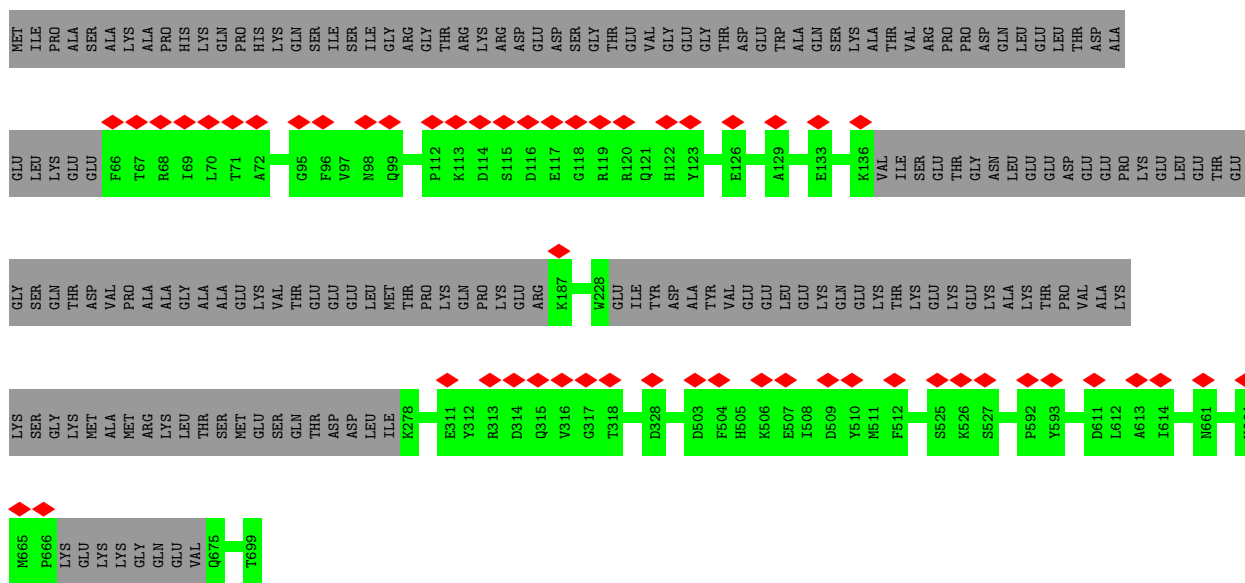
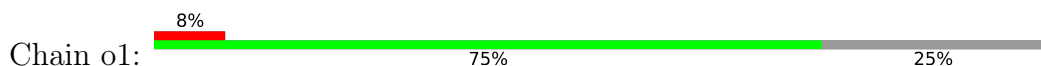


• Molecule 96: Dynein axonemal intermediate chain 1

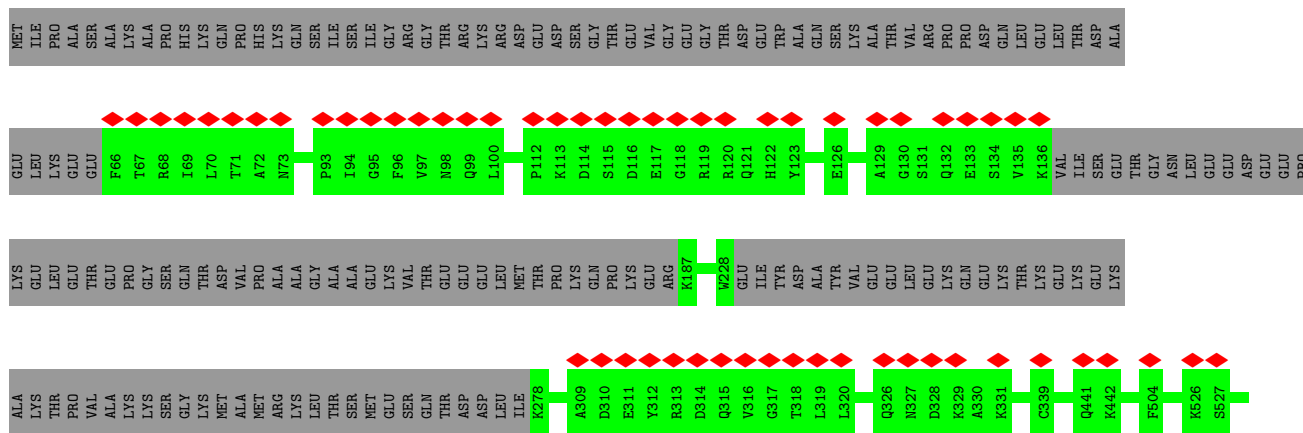
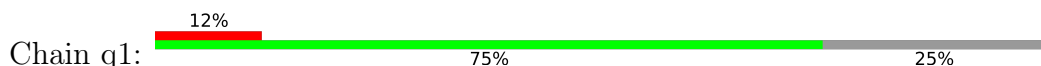


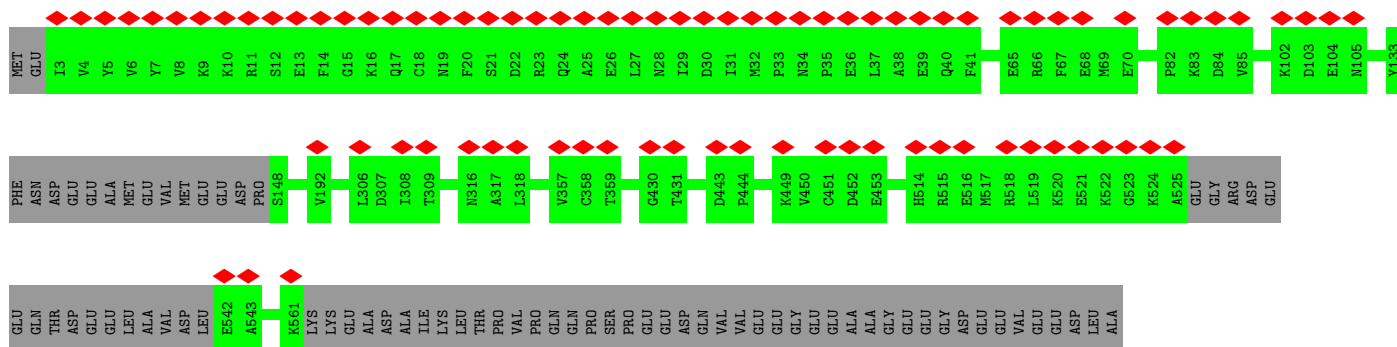


• Molecule 96: Dynein axonemal intermediate chain 1

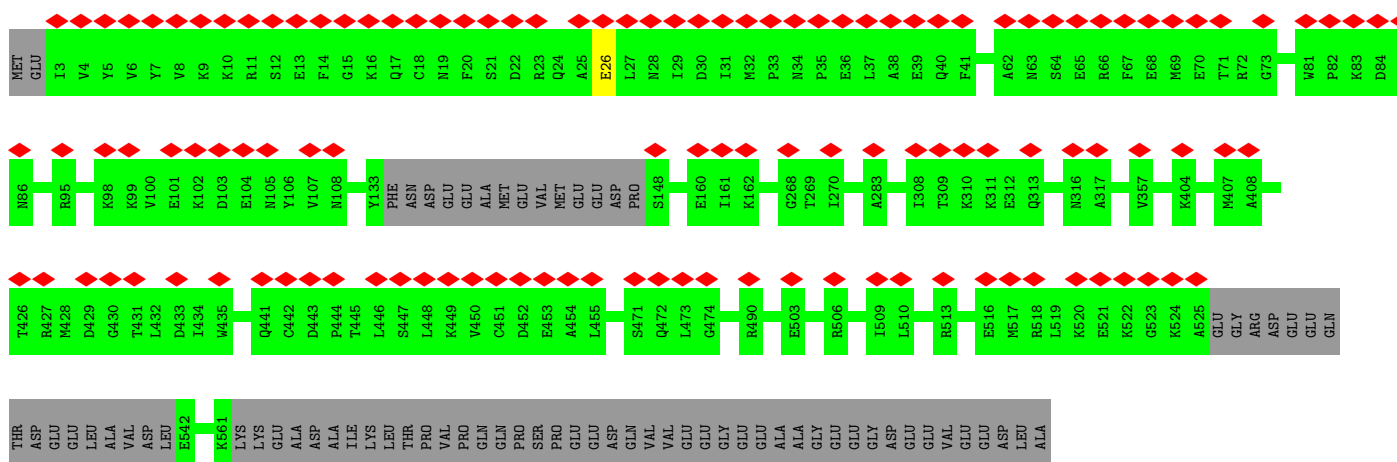
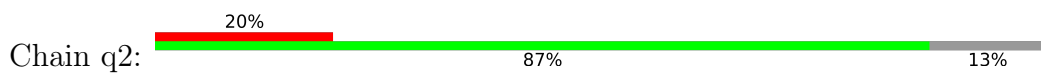


• Molecule 96: Dynein axonemal intermediate chain 1

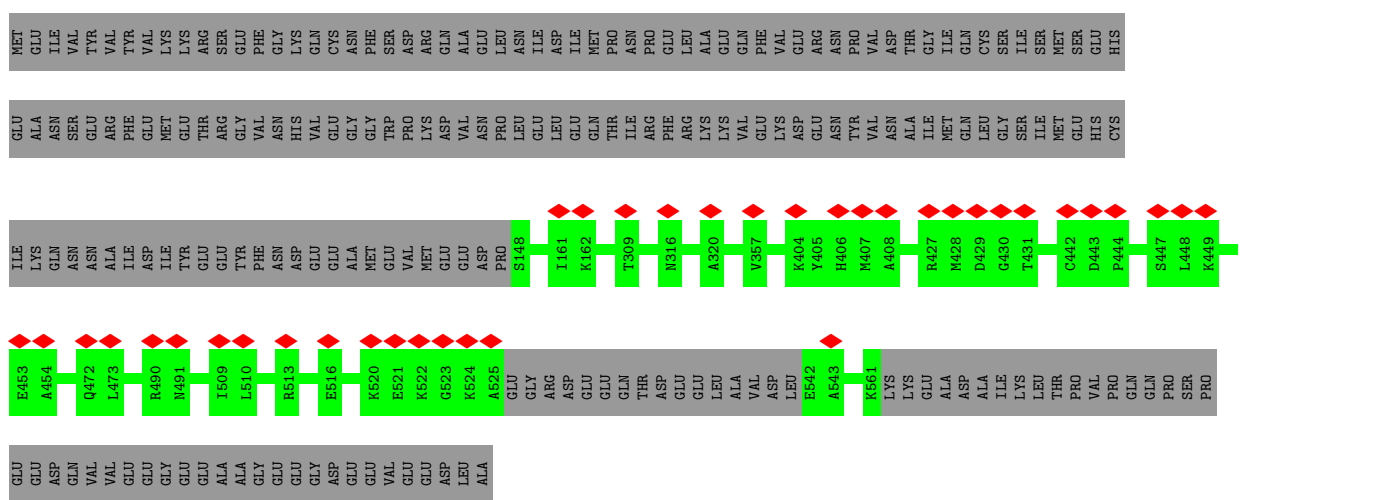




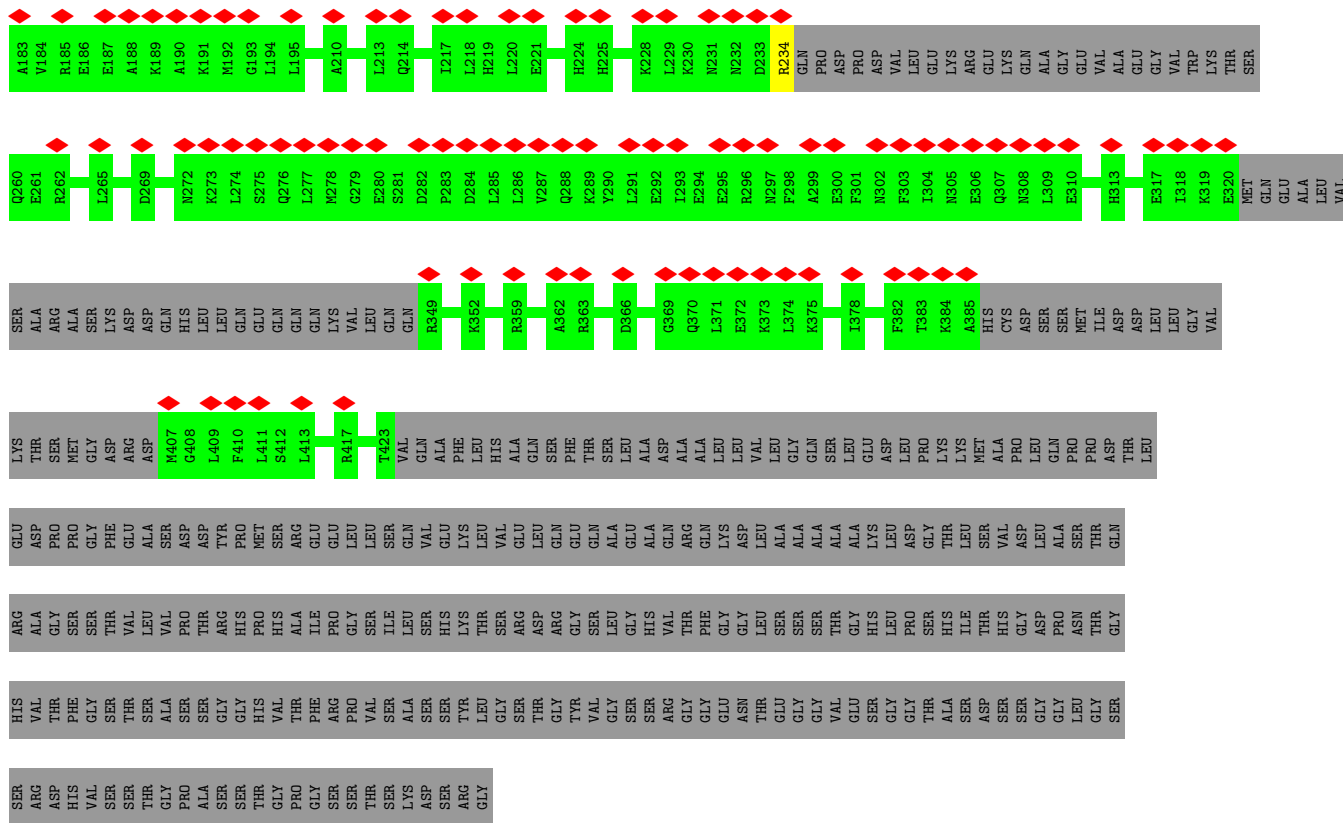
• Molecule 97: Dynein axonemal intermediate chain 2



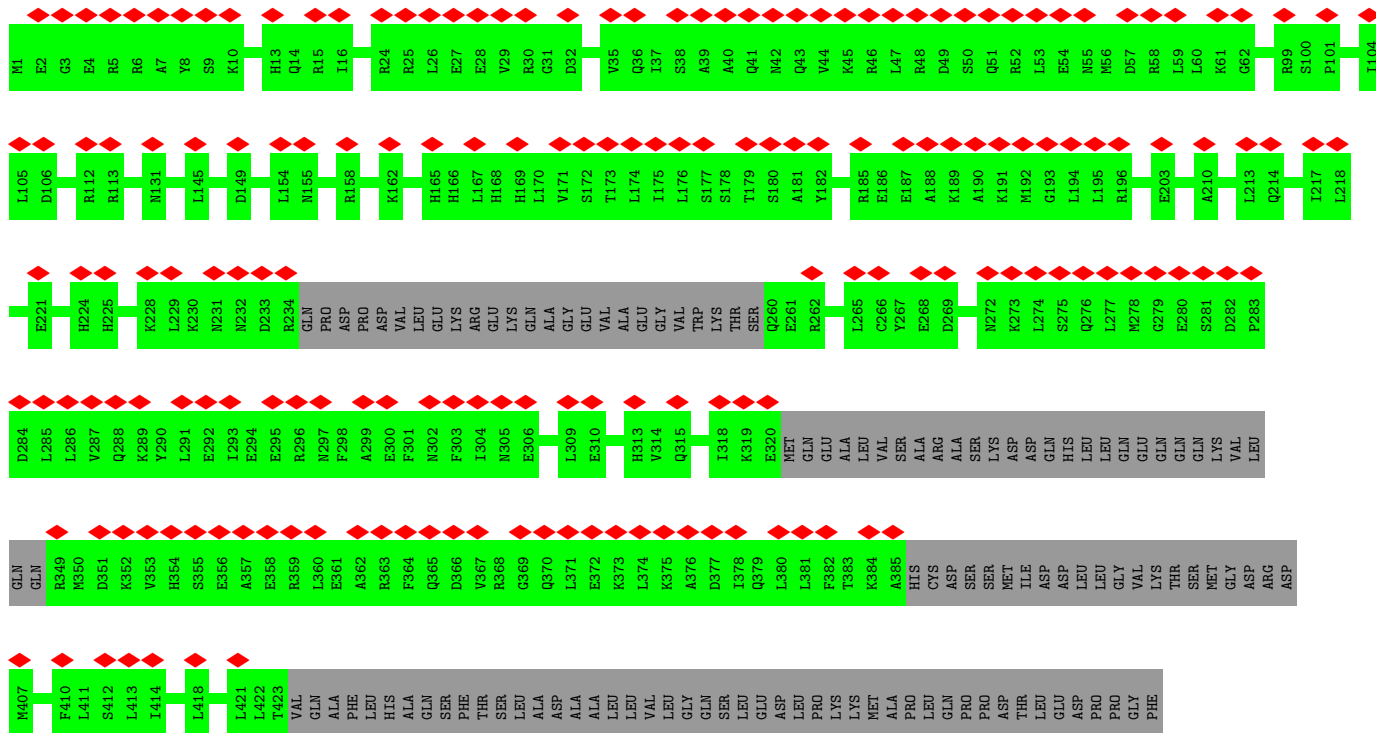
• Molecule 97: Dynein axonemal intermediate chain 2

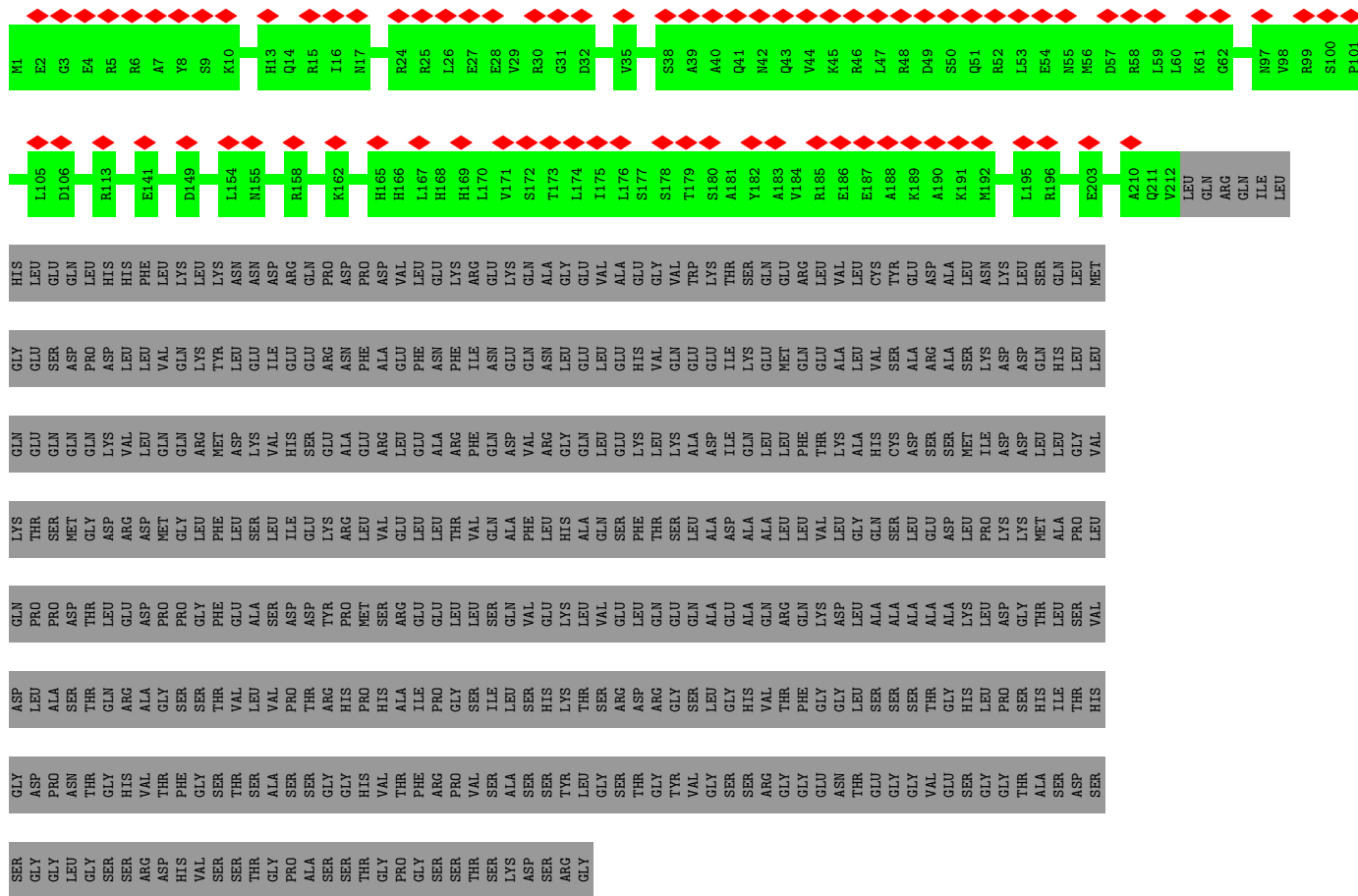


• Molecule 98: Dynein axonemal light chain 1

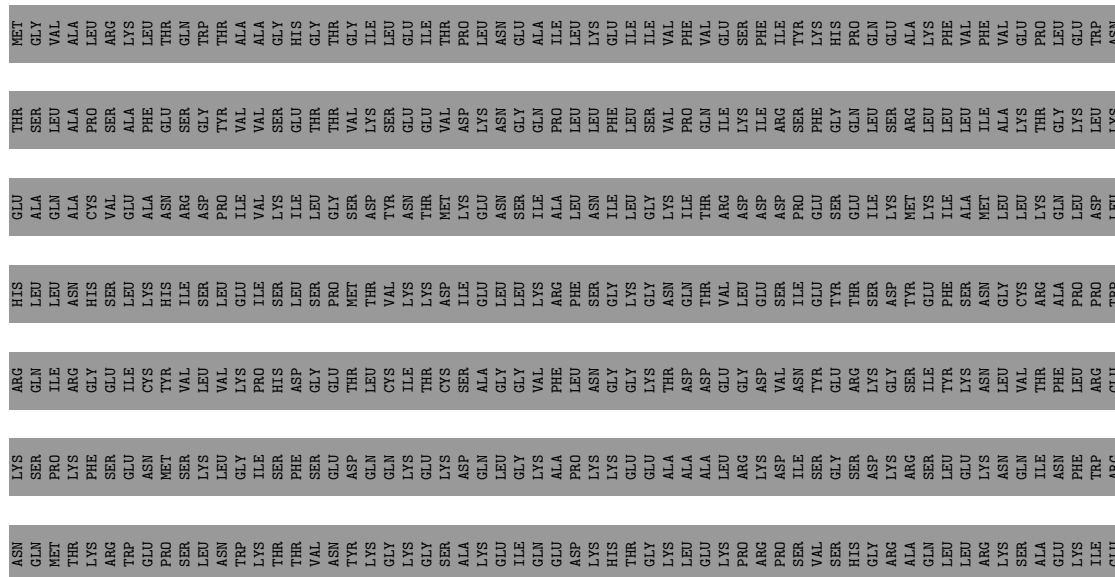


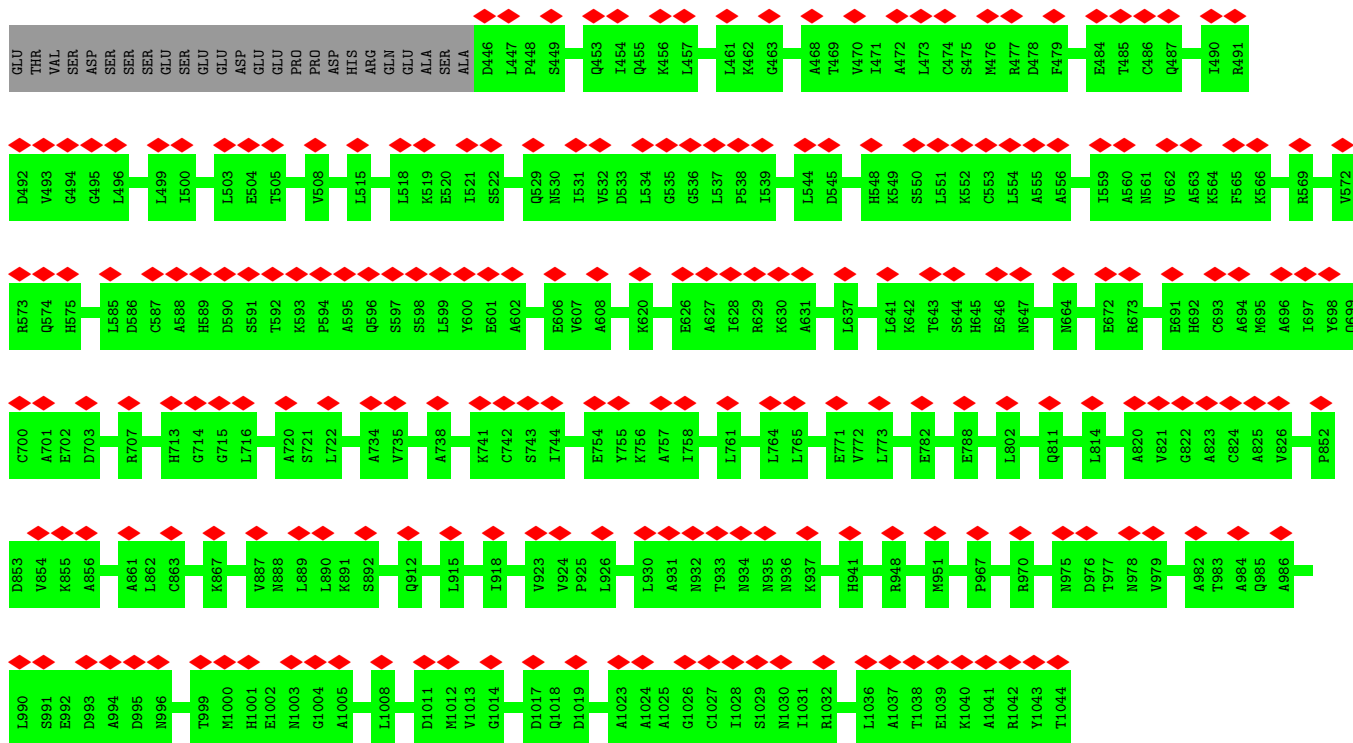
● Molecule 99: Outer dynein arm-docking complex subunit 1



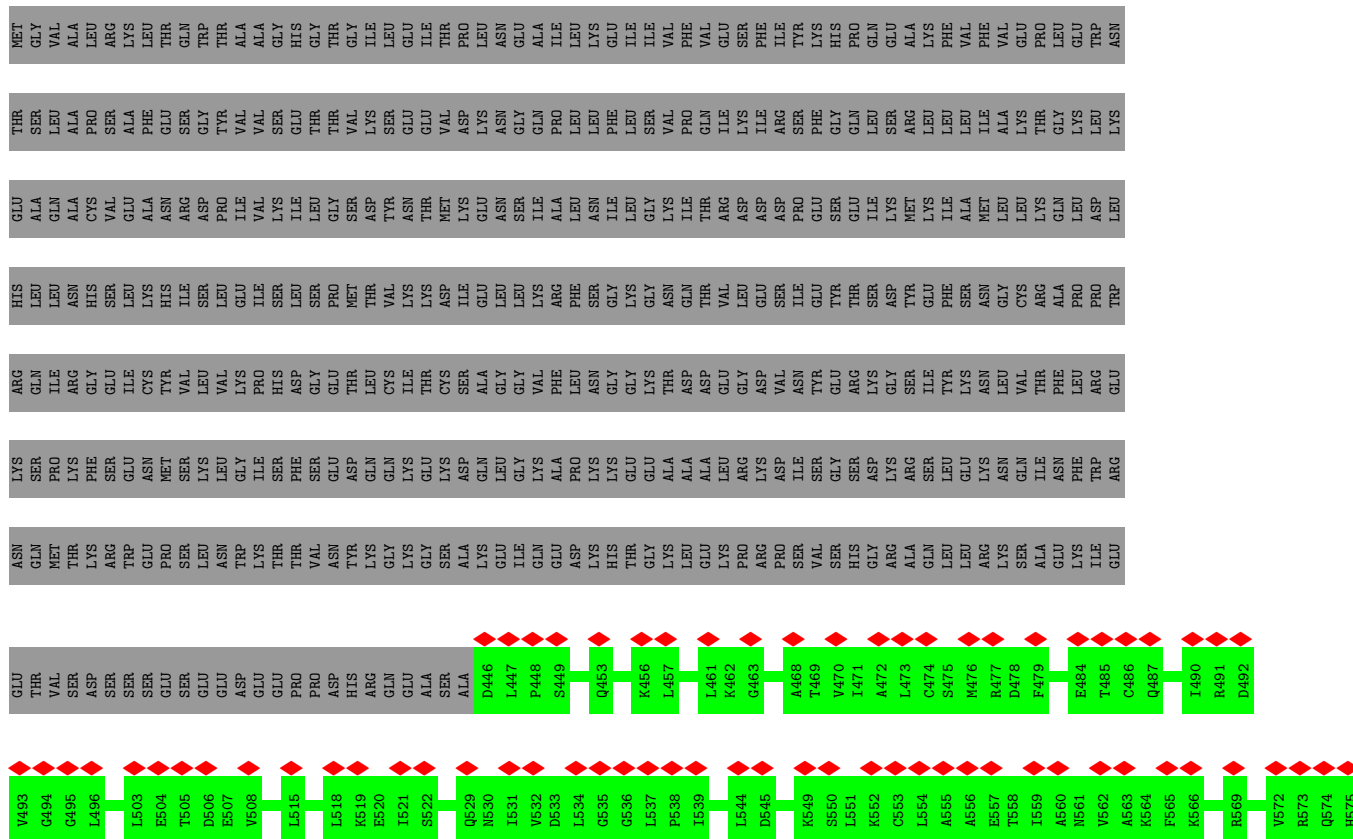


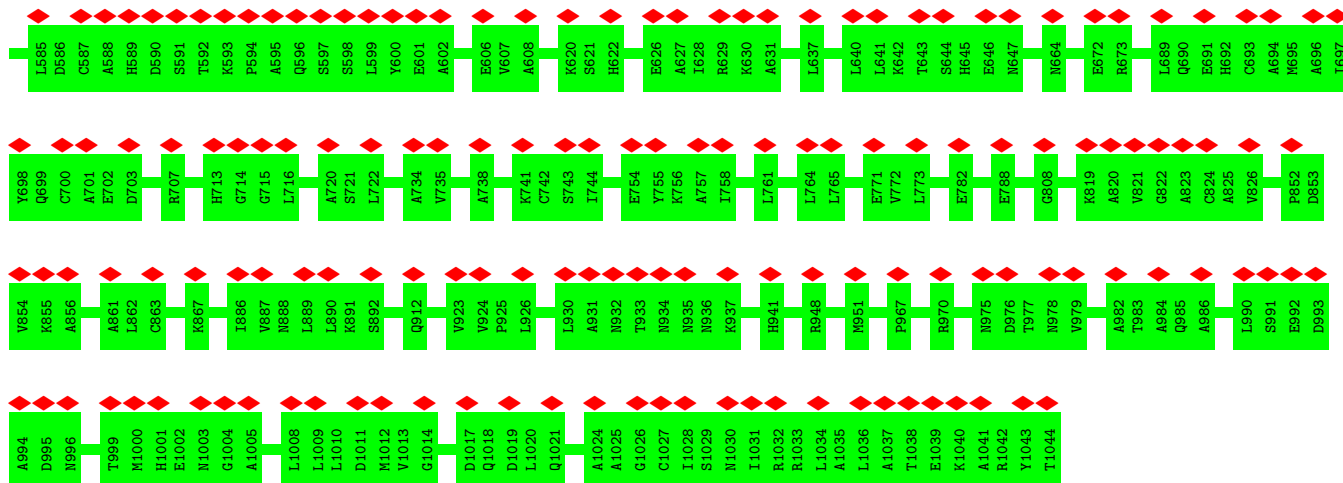
● Molecule 100: Outer dynein arm-docking complex subunit 2



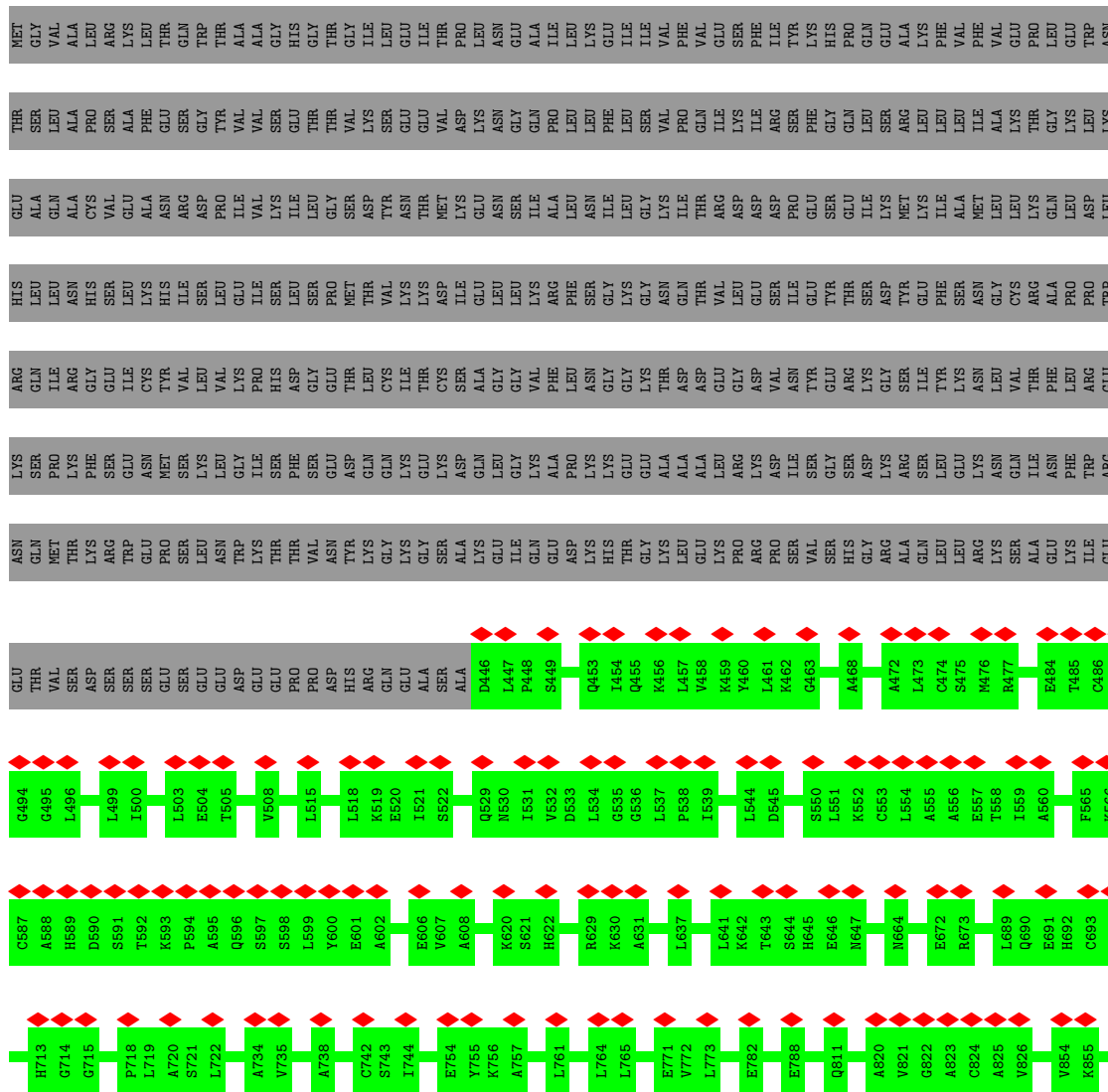


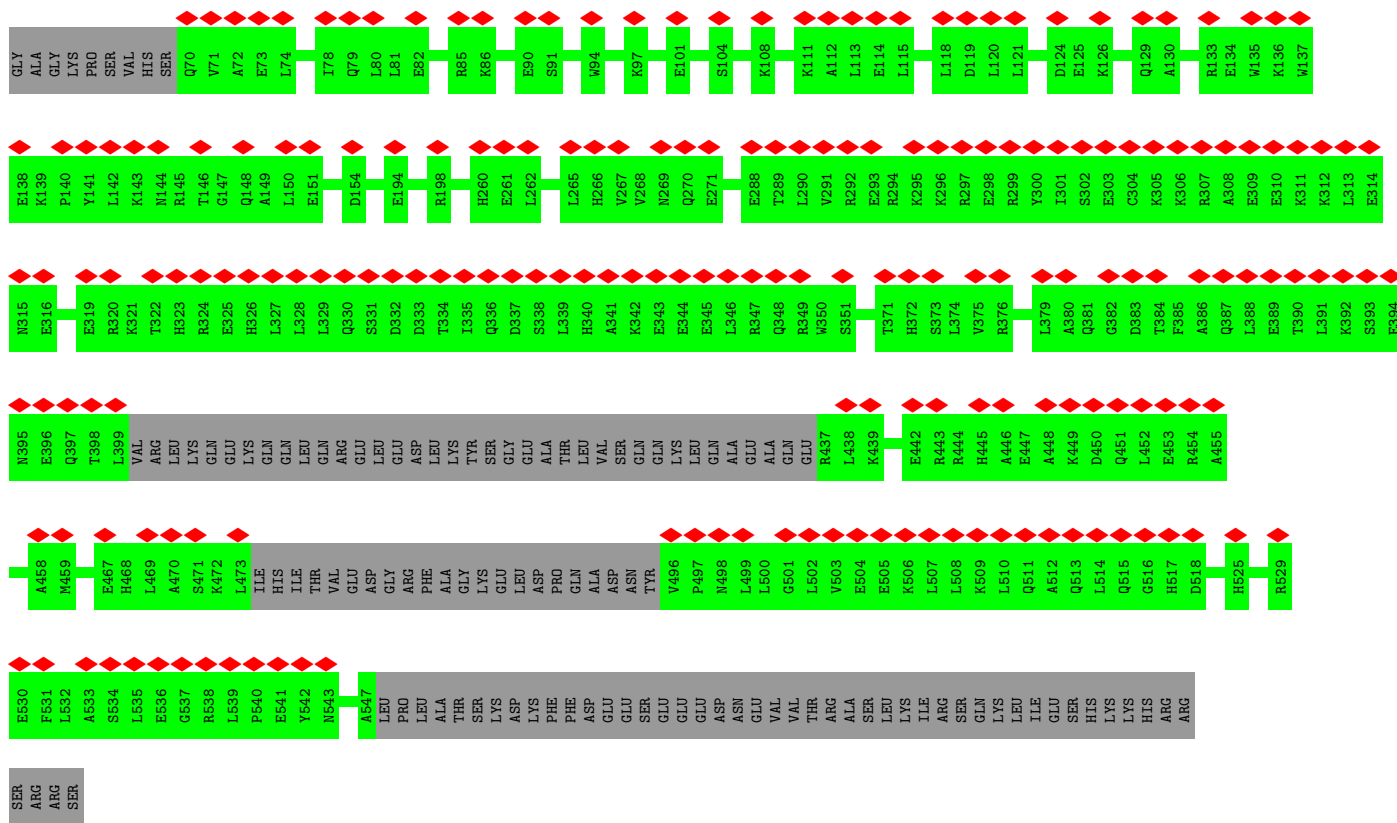
● Molecule 100: Outer dynein arm-docking complex subunit 2



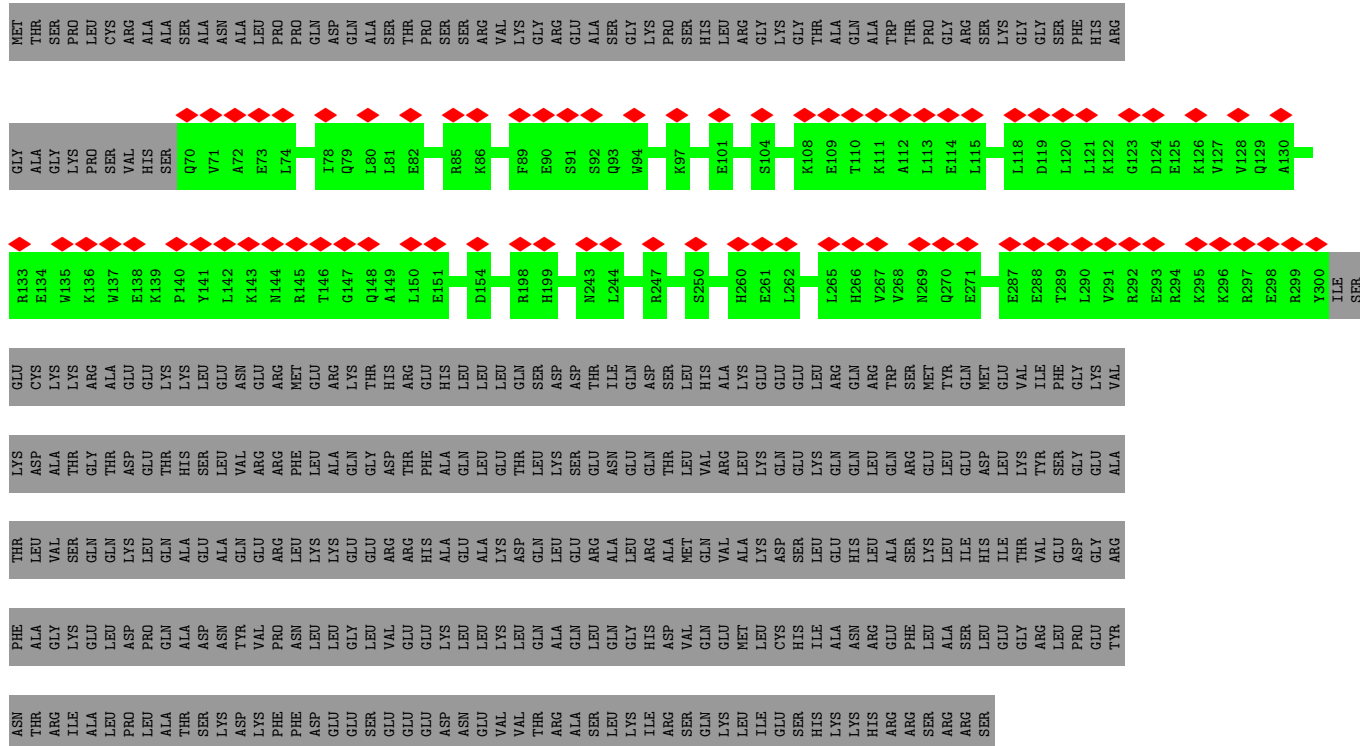


● Molecule 100: Outer dynein arm-docking complex subunit 2

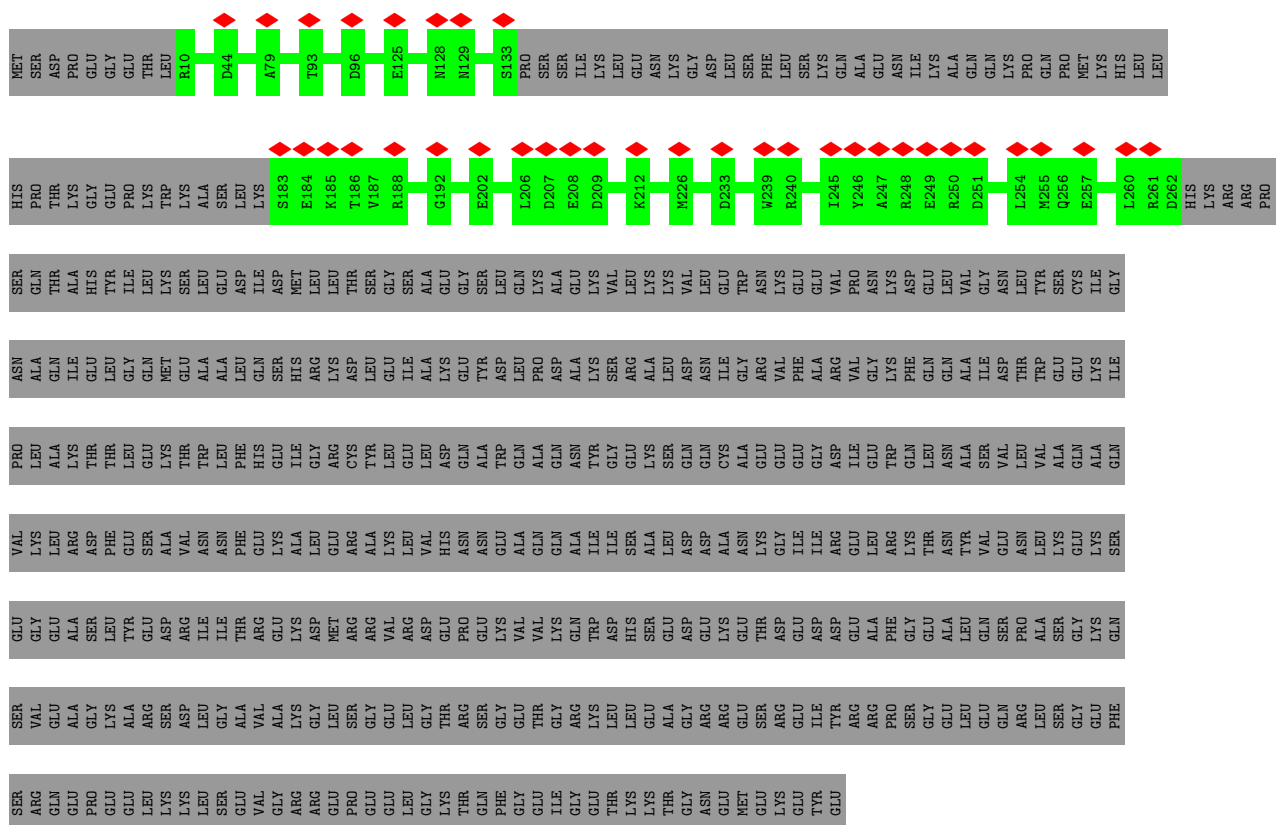




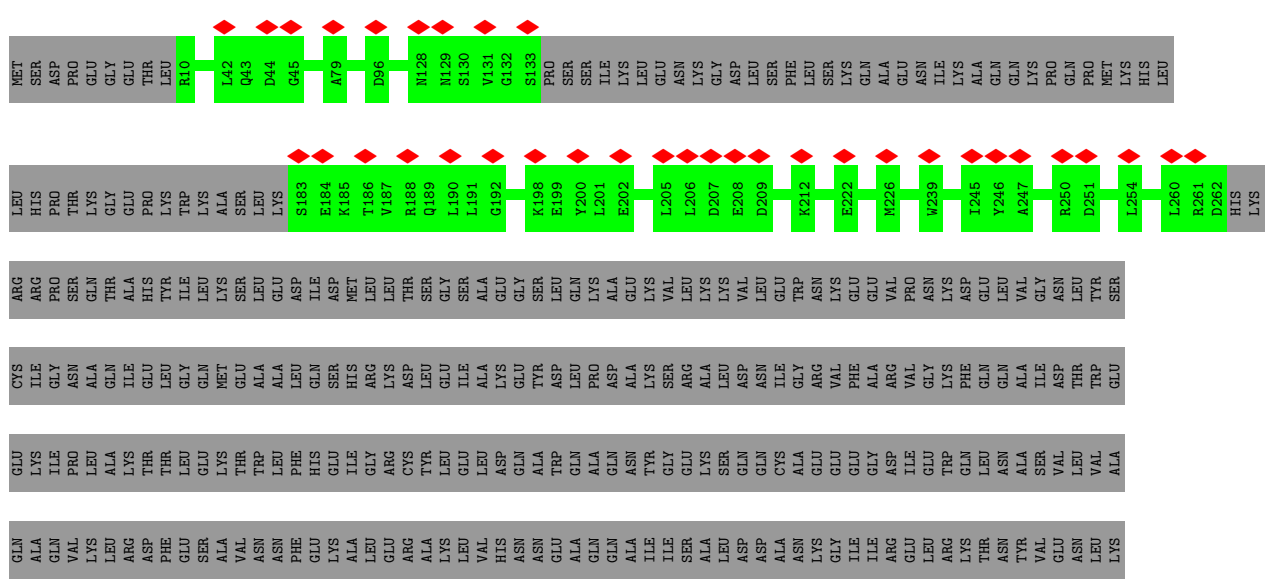
• Molecule 101: Outer dynein arm-docking complex subunit 3



● Molecule 102: Outer dynein arm-docking complex subunit 4



● Molecule 102: Outer dynein arm-docking complex subunit 4



F1639	V1640	G1641	G1642	D1643	I1644	A1645	K1646	Q1647	L1648	P1649	K1650	E1651	A1652	K1653	R1654	F1655	S1656	M1657	I1658	D1659	K1660	S1661	W1662	V1663	K1664	I1665	M1666	T1667	R1668	A1669	H1670	E1671	V1672	P1673	S1674	V1675	V1676	Q1677	C1678	C1679	V1680	G1681	D1682	E1683	T1684	L1685	G1686	Q1687	L1688	L1689	P1690	L1692	L1693	D1694	Q1695	L1696	E1697	I1698
C1699	Q1700	K1701	S1702	L1703	T1704	G1705	Y1706	L1707	E1708	K1709	K1710	V1720	S1721	D1722	P1723	A1724	L1725	L1726	E1727	I1728	L1729	G1730	Q1731	A1732	S1733	L1734	S1735	H1736	T1737	K1753	F1754	H1755	E1756	K1757	I1758	Y1759	D1760	R1761	E1774	L1775	D1776	K1777	P1778	V1779	M1780	A1781	E1782	G1783	Q1784	G1785	L1786	V1787	S1791	E1794				
E1795	S1798	S1799	L1800	H1801	L1802	V1803	I1804	R1805	Q1806	A1807	A1808	A1809	M1810	I1811	Q1812	E1813	T1814	G1815	F1816	Q1817	L1818	T1819	E1820	F1821	L1822	S1823	S1824	F1825	M1836	I1837	W1838	T1839	R1840	D1841	S1842	E1843	E1844	A1845	L1846	R1847	M1848	A1849	K1850	D1852	K1853	I1855	M1856	Q1857	K1858	L1859	M1860	Q1861	A1862	E1865				
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• Molecule 103: Dynein axonemal heavy chain 5

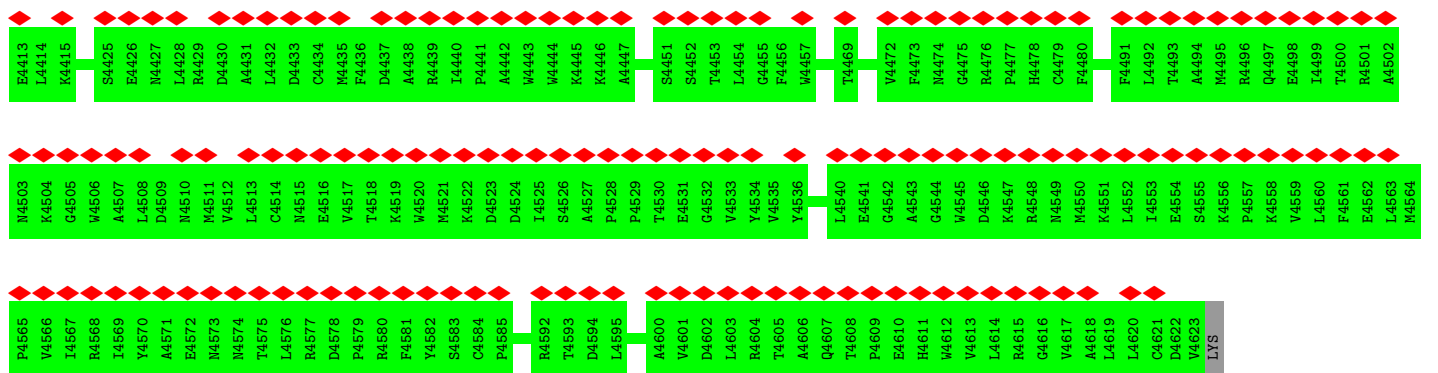


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A459	K460	Q461	R683	E687	A700	P701	T703	G704	E705	E846	E847	E852	E896	GLU	SER	LYS	ILE	SER	ASN	GLY	ASN	SER	VAL	ASN	TYR	LYS	ASN	GLU	V101	SER	SER	ALA	ALA	ARG	GLU	GLY	ASN	PHE	ASP	THR	LEU	LEU	THR	SER	SER	ILE	ASN	ALA	ARG	ALA	ALA	ALA						

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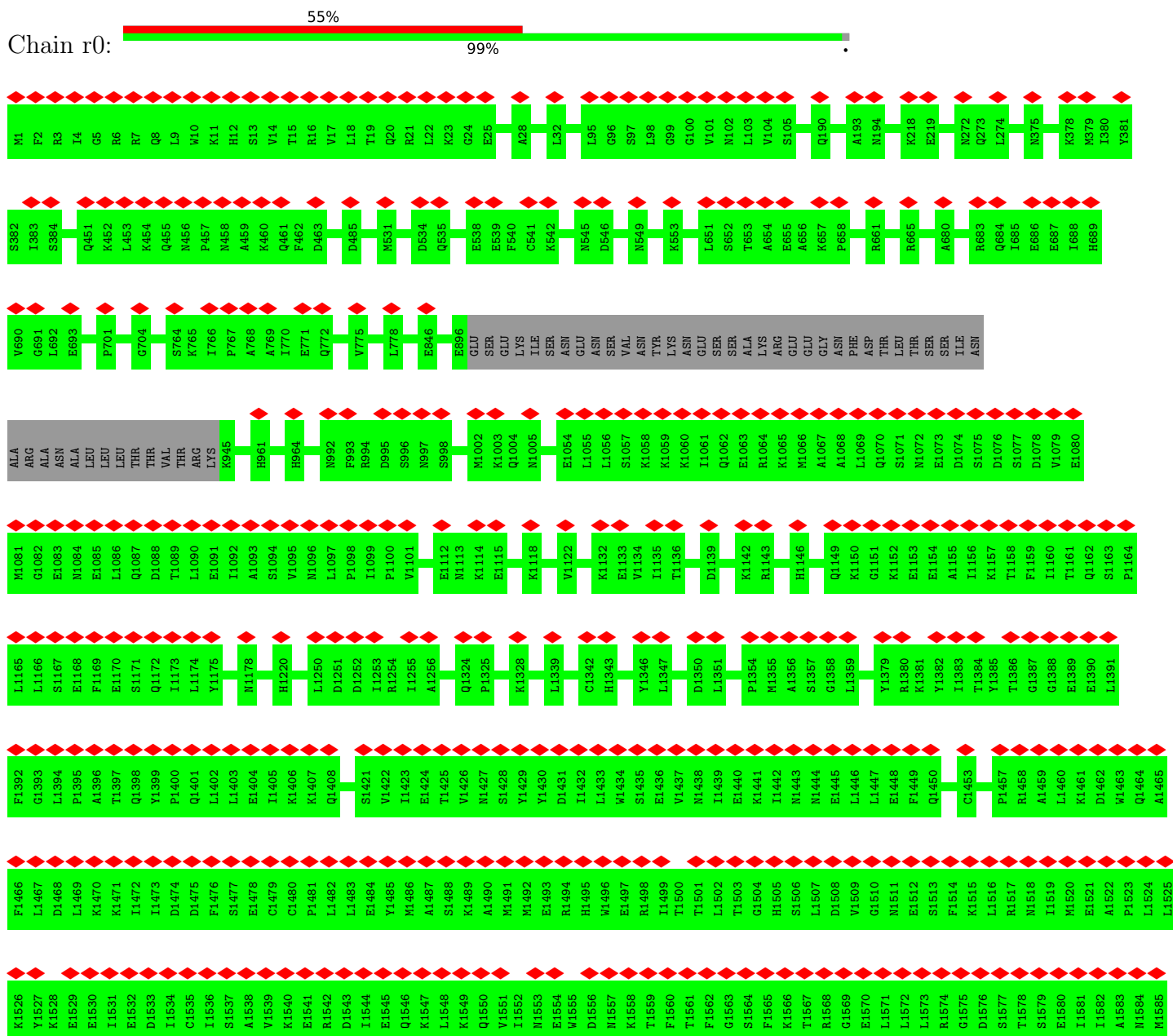
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N2728	C2729	T2730	L2731	R2732	S2733	C2750	T2751	Q2752	R2753	G2754	F2755	S2756	E2757	R2772	Q2775	N2776	T2777	K2778	L2779	K2780	N2781	L2782	P2783	L2784	P2785	V2791	S2809	E2810	W2811	L2812	K2813	E2814	A2846	S2849	L2850	V2851	E2852	E2853	E2854	F2855	G2856	E2857	E2858	K2859	K2860	L2861	L2862	V2863	D2864	C2865	L2866	L2867							
F2874	L2875	R2876	D2877	A2878	P2879	E2880	A2881	A2882	G2883	E2884	L2885	S2886	E2887	A2889	D2890	T2893	P2894	E2898	P2899	I2900	F2903	S2904	H2905	L2906	K2907	E2908	R2909	L2910	N2911	M2912	F2913	L2914	Q2915	Y2917	S2918	N2918	E2919	S2920	L2921	R2922	G2923	A2924	G2925	M2926	L2968	F2971	I2972	A2973	G2974	S2977									
T2981	L2982	T2983	R2984	S2985	Y2986	N2987	T2988	S2989	N2990	L2991	M2992	E2993	D2994	L2995	K2996	V2997	Y2999	R3000	T3001	Q3004	Q3005	K3019	D3020	E3021	S3022	F3023	L3024	E3025	Y3026	N3038	L3039	F3040	A3041	R3042	D3043	E3044	I3045	D3046	E3047	I3048	N3049	S3050	D3051	L3052	A3053	S3054	V3055	M3056	K3057	K3058	A2973	F3060	P3061	F3065					
T3066	N3067	E3068	N3069	L3070	H3071	D3072	Y3073	F3074	G3092	E3093	K3094	F3095	R3096	N3097	R3098	A3099	L3100	K3101	F3102	P3103	E3127	H3128	F3129	L3130	T3131	S3132	Y3133	D3134	I3135	D3136	C3137	S3138	L3139	E3140	I3141	K3142	K3143	G3190	E3191	K3192	H3193	V3194	E3195	V3196	L3197	T3198	L3199	A3200	N3201	K3202	R3203	K3263	D3264	F3265	G3206	L3207	E3208		
K3209	L3210	K3211	E3212	A3213	S3214	E3215	S3216	V3217	A3218	A3219	L3220	S3221	K3222	E3223	L3224	A3225	A3226	K3227	E3228	K3229	E3230	L3231	Q3232	V3233	A3234	N3235	D3236	K3237	A3238	D3239	K3240	V3241	L3242	K3243	E3244	V3245	T3246	M3247	K3248	A3249	Q3250	A3251	A3252	E3253	K3254	P3255	K3256	A3257	L3258	V3259	Q3260	K3261	V3262	K3263	D3264	A3265	L3266	Q3267	A3268
I3269	V3270	D3271	S3272	L3273	S3274	K3275	D3276	K3277	A3278	L3279	A3280	E3281	E3282	K3283	L3284	E3285	A3286	A3287	K3288	P3289	A3290	L3291	E3292	E3293	A3294	E3295	A3296	A3297	L3298	Q3299	T3300	I3301	P3302	P3303	S3304	D3305	L3306	A3307	T3308	V3309	R3310	T3311	L3312	G3313	R3314	P3315	P3316	H3317	L3318	I3319	M3320	R3321	L3322	M3323	D3324	C3325	R3326	L3327	L3328
L3329	F3330	Q3331	R3332	K3333	V3334	S3335	A3336	V3337	K3338	I3339	D3340	L3341	E3342	K3343	S3344	G3345	T3346	M3347	P3348	S3349	V3350	Q3351	E3352	S3353	L3354	K3355	L3356	M3357	T3358	A3359	G3360	N3361	F3362	L3363	Q3364	N3365	L3366	Q3367	Q3368	F3369	P3370	K3371	D3372	T3373	I3374	N3375	E3376	E3377	V3378	I3379	E3380	F3381	L3382	S3383	P3384	V3385	F3386	E3387	M3388
F3389	D3390	Y3391	N3392	L3393	E3394	T3395	A3396	K3397	R3398	V3399	C3400	G3401	N3402	V3403	A3404	G3405	C3407	S3408	N3409	T3410	K3411	A3412	R3413	A3414	S3415	F3416	F3417	S3418	I3419	N3420	K3421	E3422	V3423	L3424	F3425	L3426	K3427	A3428	N3429	L3430	V3431	V3432	Q3433	I3434	N3435	R3436	H3437	L3438	L3439	A3440	K3441	Q3442	D3443	L3444	Q3445	K3446	E3447	Q3448	

A3449	A3450	L3451	I3452	D3453	K3454	K3455	A3456	E3457	L3458	D3459	V3460	V3461	A3462	A3463	E3464	V3465	I3466	I3467	A3468	K3469	T3470	E3471	K3472	I3473	I3474	L3475	L3476	E3477	D3478	A3479	E3480	R3481	C3482	R3483	H3484	K3485	K3486	I3487	T3488	A3489	S3490	T3491	L3492	L3493	S3494	G3495	L3496	A3497	E3499	K3500	E3501	K3502	K3503	T3504	E3505	S3507	D3508											
E3509	F3510	A3511	A3512	Q3513	T3514	K3515	R3516	K3551	A3552	R3553	K3554	I3555	P3556	K3559	I3568	D3569	A3570	P3571	T3572	I3573	S3574	E3575	W3576	N3577	L3578	Q3579	I3604	D3605	I3606	K3607	T3608	K3611	I3612	K3615	N3616	K3617	E3618	S3619	R3620	N3621	E3622	L3623	Q3624	I3625	T3626	I3627	D3628	V3629	L3628	N3629	K3630	H3631	Y3632	F3633	R3634													
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L3699	P3699	N3700	P3701	A3702	V3703	T3717	G3729	R3730	S3731	V3731	I3732	L3733	T3734	E3735	K3736	Q3737	E3738	L3739	E3740	K3741	E3742	K3798	L3799	E3740	K3741	E3742	R3743	T3744	H3745	L3746	D3747	E3748	D3749	V3750	T3751	A3752	N3753	K3754	R3755	R3756	N3757	K3758	E3759	L3760	E3761	D3762	N3763	D3764	L3765	I3766	R3767	L3768	T3769	S3770	T3771	Q3772	G3773	S3774	L3775	V3776	E3777	D3778	E3779					
S3780	L3781	I3782	V3783	V3784	L3785	S3786	N3787	T3788	K3789	R3790	T3791	A3792	E3793	E3794	V3795	T3796	Q3797	K3798	L3799	E3800	K3801	S3802	A3803	E3804	T3805	E3806	V3807	I3808	I3809	N3810	S3811	A3812	R3813	E3814	E3815	V3816	R3817	P3818	V3819	D3852	L3853	S3854	L3855	A3856	K3857	S3858	V3859	K3860	S3861	P3862	I3863	T3864	S3865	T3866	K3867	L3868	S3869	L3869	I3870	L3871	S3872	L3873	S3874	L3875	V3876	E3877	N3878	L3879
I3871	K3885	G3886	L3887	V3888	E3889	E3890	K3891	K3892	F3893	D3904	R3907	N3908	R3909	V3910	K3911	H3912	E3913	E3914	F3915	T3916	L3917	L3918	L3919	K3920	G3921	G3922	A3923	S3924	L3925	D3926	L3927	K3928	A3929	C3930	K3931	K3932	K3933	P3934	S3935	K3936	W3937	T3938	L3939	D3940	I3941	T3942	W3943	L3944	N3945	V3946	E3947	L3948	S3949	K3950	K3951	L3952												
R3953	Q3954	F3955	S3956	D3957	V3958	L3959	D3960	Q3961	I3962	S3963	R3964	N3965	E3966	K3967	M3968	K3969	V3970	I3971	V3972	V3973	D3974	K3975	E3976	N3977	P3978	E3979	E3980	E3981	P3982	L3983	P3984	N3985	V3986	Y3987	D3988	K3989	S3990	L3991	D3992	C3993	P3994	R3995	R3996	L3997	L3998	L3999	I4000	R4001	K4002	W4003	C4004	P4005	D4006	L4007	T4008	I4009	A4010	Q4011	A4012									
R4013	K4014	Y4015	L4016	V4017	D4018	S4019	M4020	G4021	E4022	K4023	Y4024	A4025	E4026	G4027	V4028	L4029	L4030	D4031	L4032	E4033	K4034	T4035	W4036	E4037	E4038	S4039	D4040	P4041	R4042	T4043	P4044	L4045	L4046	C4047	L4048	L4049	S4050	M4051	G4052	S4053	D4054	P4055	T4056	D4057	S4058	L4059	L4060	A4061	L4062	G4063	K4064	R4065	L4066	K4067	L4068	E4069	T4070	R4071	Y4072									
V4073	S4074	M4075	Q4079	E4080	V4081	H4082	A4083	R4084	K4085	L4086	Q4088	Q4089	T4090	M4091	A4092	M4093	G4094	A4095	W4096	A4097	L4098	L4099	Q4100	M4101	A4102	H4103	D4107	F4108	M4109	L4110	E4111	L4112	M4113	D4114	I4115	I4116	I4117	E4118	T4119	E4120	L4121	V4122	H4123	D4124	A4125	F4126	R4127	L4128	W4129	M4130	T4131	T4132	E4133	K4136														
P4139	L4142	M4145	S4146	T4147	K4148	F4149	A4150	M4151	D4152	P4153	P4154	Q4155	G4156	R4158	A4159	G4160	L4161	K4162	R4163	T4164	Y4165	S4166	G4167	W4168	A4169	Q4170	D4171	L4172	L4173	L4174	V4175	S4176	F4177	G4178	S4179	Q4180	W4181	K4182	M4183	L4184	L4185	Y4186	A4187	V4188	L4189	F4190	L4191	H4192	S4193	T4194	V4195	Q4196	E4197	R4198	R4199	K4200												
F4201	G4202	A4203	L4204	G4205	W4206	M4207	L4208	P4209	Y4210	E4211	F4212	M4213	Q4214	A4215	D4216	F4217	N4218	A4219	T4220	W4221	L4228	D4229	D4230	M4231	D4232	V4233	K4234	K4235	G4236	V4237	S4238	W4239	Q4250	Y4251	G4252	G4253	R4254	V4255	L4256	D4257	D4258	Y4259	D4260	K4261	R4262	L4263	L4264	M4265	T4266	F4267	A4268	K4269	W4270	W4271	F4272	S4273	E4274											
M4275	M4276	F4277	G4278	P4279	D4280	F4281	S4282	F4283	Y4284	Q4285	G4286	M4287	N4288	I4289	P4290	K4291	C4292	S4293	T4294	V4295	D4296	M4297	Y4298	L4299	Q4300	Y4301	I4302	K4303	S4304	L4305	P4306	Y4307	A4308	D4309	S4310	P4311	E4312	V4313	F4314	G4315	L4316	H4317	P4318	M4319	A4320	D4321	I4322	T4323	Y4324	Q4325	S4326	K4327	L4328	A4329	K4330	D4331	W4332	L4333	D4334									
L4337	G4346	G4347	G4348	D4349	E4350	A4354	A4357	R4358	L4359	A4360	D4361	D4362	M4363	L4364	K4366	L4367	P4368	P4369	D4370	Y4371	V4372	P4373	Y4374	E4375	V4376	K4377	E4378	R4379	L4380	Q4381	K4382	M4383	G4384	P4385	F4386	Q4387	P4388	M4389	N4390	I4391	F4392	Q4401	R4402	V4403	L4404	S4405	L4406	V4407	R4408	S4409	T4410	L4411	T4412															



• Molecule 103: Dynein axonemal heavy chain 5

Chain r0:



E1586	D1587	S1588	L1589	M1590	L1591	L1592	G1593	S1594	L1595	L1596	S1597	M1598	R1599	Y1600	M1601	M1602	P1603	F1604	K1605	A1606	Q1607	I1608	V1612	L1615	S1616	M1617	S1618	T1619	D1620	I1621	I1622	E1623	S1624	M1625	M1626	I1627	V1628	Q1629	M1630	W1631	W1632	I1633	Y1634	L1635	L1636	L1637	V1638	F1639	V1640	G1641	G1642	D1643	I1644	A1645	K1646	Q1647	L1648																																																					
P1649	K1650	E1651	A1652	K1653	R1654	F1655	S1656	M1657	I1658	D1659	K1660	S1661	W1662	V1663	K1664	I1665	M1666	T1667	R1668	A1669	H1670	E1671	V1672	P1673	S1674	V1675	V1676	Q1677	C1678	C1679	V1680	G1681	D1682	E1683	T1684	L1685	M1686	I1687	L1688	L1689	P1690	H1691	W1692	L1693	D1694	Q1695	L1696	L1697	V1698	F1699	Q1700	K1701	S1702	L1703	T1704	G1705	Y1706	S1721																																																				
D1722	P1723	A1724	L1725	L1726	E1727	F1754	H1755	E1756	K1757	I1758	Y1759	D1760	E1774	L1775	D1776	K1777	V1779	M1780	S1798	S1799	L1800	H1801	L1802	V1803	I1804	R1805	Q1806	A1807	A1808	A1809	M1810	I1811	Q1812	E1813	T1814	G1815	F1816	Q1817	L1818	E1820	F1821	L1822	S1823	S1824	F1825	G1833	M1836	I1837	W1838	L1839	R1840	D1841	L1842	E1843	E1844	A1845	L1846	M1848	A1849	K1850	F1851	D1852	K1853	K1854	I1855	M1856	Q1857	K1858	T1859	M1860	Q1861	A1862	F1863	L1864	E1865	L1866	D1901	D1902	L1903	C1904	H1905	M1906	H1907	M1908	K1909	S1910	P1911	M1912	D1913	F1914	E2092	L2093	P2094	E2095	N2096	L2097	K2098	L2099	M2100	F2101	D2126	N2127	V2128	V2129	L2130	A2131	R2132	K2133	F2134	G1980
S1842	E1843	E1844	A1845	L1846	R1847	M1848	A1849	K1850	F1851	D1852	K1853	K1854	I1855	M1856	Q1857	K1858	T1859	M1860	Q1861	A1862	F1863	L1864	E1865	L1866	D1901	D1902	L1903	C1904	H1905	M1906	H1907	M1908	K1909	S1910	P1911	M1912	D1913	F1914	E2092	L2093	P2094	E2095	N2096	L2097	K2098	L2099	M2100	F2101	D2126	N2127	V2128	V2129	L2130	A2131	R2132	K2133	F2134	G1980																																																				
P1981	A1982	G1983	S2007	D2008	Q2009	G2014	L2015	G2016	R2017	I2018	F2019	E2033	F2034	N2035	R2036	I2037	L2042	S2043	V2044	A2045	A2046	Q2047	Q2048	I2049	S2050	M2083	P2085	G2086	Y2087	A2088	G2089	R2090	Q2091	E2092	L2093	P2094	E2095	N2096	L2097	K2098	L2099	M2100	F2101	D2126	N2127	V2128	V2129	L2130	A2131	R2132	K2133	F2134																																																										
F2135	T2136	L2137	Y2138	L2139	L2140	C2141	E2142	E2143	Q2144	L2145	S2146	K2147	Q2148	V2149	H2150	Y2151	T2176	E2177	S2178	T2179	L2180	V2181	R2182	R2183	V2184	L2185	R2186	D2187	N2188	L2189	L2190	S2191	L2192	L2193	L2194	D2195	E2196	D2197	E2198	F2199	L2200	F2201	L2202	S2203	L2204	I2205	E2206	D2207	F2209	P2210	N2211	L2212	L2213	L2214	D2215	K2216	A2217																																																					
G2218	Y2219	P2220	E2221	L2222	E2223	A2224	A2225	L2226	S2227	R2228	P2229	Q2229	V2230	E2231	E2232	A2233	G2234	L2235	I2236	N2237	H2238	P2239	P2240	W2241	K2242	K2244	V2245	I2246	L2248	F2249	R2253	G2257	M2258	M2259	T2260	L2261	D2262	P2263	S2264	G2265	G2266	G2267	K2268	T2269	T2270	C2271	I2272	H2273	T2274	L2275	M2276	L2277	L2278	L2279	T2280	D2281																																																						
C2282	G2283	K2284	P2285	H2286	R2287	E2288	M2289	R2290	M2291	N2292	P2293	K2294	A2295	L2296	T2297	A2298	P2299	Q2300	M2301	F2302	G2303	R2304	L2305	V2306	A2308	T2309	D2310	W2312	T2313	G2315	L2316	F2317	S2318	T2319	L2320	W2321	R2322	K2323	T2324	L2325	R2326	A2327	K2328	K2329	G2330	E2331	H2332	L2333	W2334	L2335	L2336	L2337	D2338	G2339	P2340	V2341																																																						
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E2410	G2411	F2412	L2413	K2414	K2415	R2416	S2417	P2418	Q2419	E2420	A2421	E2422	I2423	L2424	R2425	Q2426	L2427	Y2428	T2429	E2430	S2431	F2432	P2433	D2434	L2435	Y2436	R2437	F2438	C2439	I2440	Q2441	N2442	L2443	E2444	Y2445	K2446	M2447	E2448	V2449	L2450	E2451	A2452	F2453	V2454	I2455	T2456	Q2457	S2458	M2460	M2461	L2462	Q2463	G2464	L2465	I2466	L2468	K2469																																																					
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S3865	D3926	I3987	L4048	E4118	L4185	G4247	P4306	L4367	A4431	M4503	L4563	
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K3881	L3939	L3999	I4061	M4130	E4197	Y4259	M4319	R4379	G4455	M4515	T4576	
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Y3888	L3946	D4006	R4007	Q4137	L4204	F4267	K4327	Q4387	R4464	D4523	Y4582	
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D3904	I3962	K4023	L4087	K4162	V4221	F4281	F4341	L4405	C4479	G4537	Q4607	
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Q3906	R3964	A4025	Q4089	T4164	H4227	Q4285	D4343	L4407	W4481	E4541	P4609	
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V3910	W3969	I4029	A4092	V4168	H4230	I4289	D4349	T4410	F4486	M4545	V4613	
K3911	K3970	M4093	A4093	S4169	D4231	P4290	E4350	L4411	M4487	D4546	L4614	
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E3914	F3973	L4032	W4096	L4171	K4234	S4292	E4353	L4414	Q4489	G4549	A4618	
F3915	D3974	K4034	A4097	L4172	K4235	C4293	A4354	L4416	F4491	M4550	L4619	
	K3976	T4035	L4098	L4173		V4295	V4355	A4417		K4551		

● Molecule 103: Dynein axonemal heavy chain 5



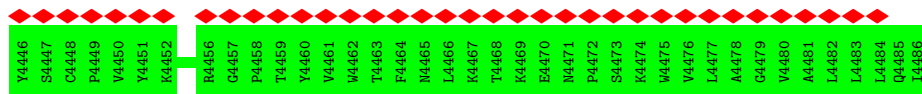
Table with 10 columns of amino acid residues and their corresponding three-letter codes. The residues are color-coded (green, red, grey) and some are marked with diamond symbols. The table lists residues from M1 to E219.

F1822	A1823	M1824	I1825	C1826	D1827	L1828	S1829	K1830	L1831	V1832	S1833	V1834	E1835	V1836	L1837	G1838	N1839	T1840	P1841	R1842	L1843	V1844	H1845	T1846	R1847	L1848	T1849	I1850	R1851	C1852	V1853	I1854	T1855	L1856	T1857	G1858	S1859	L1860	H1861	L1862	T1863	F1864	L1865	L1866	L1867	L1868	L1869	L1870	L1871	L1872	G1873	L1874	D1875	K1876	T1877	E1878	K1879	H1880	K1881		
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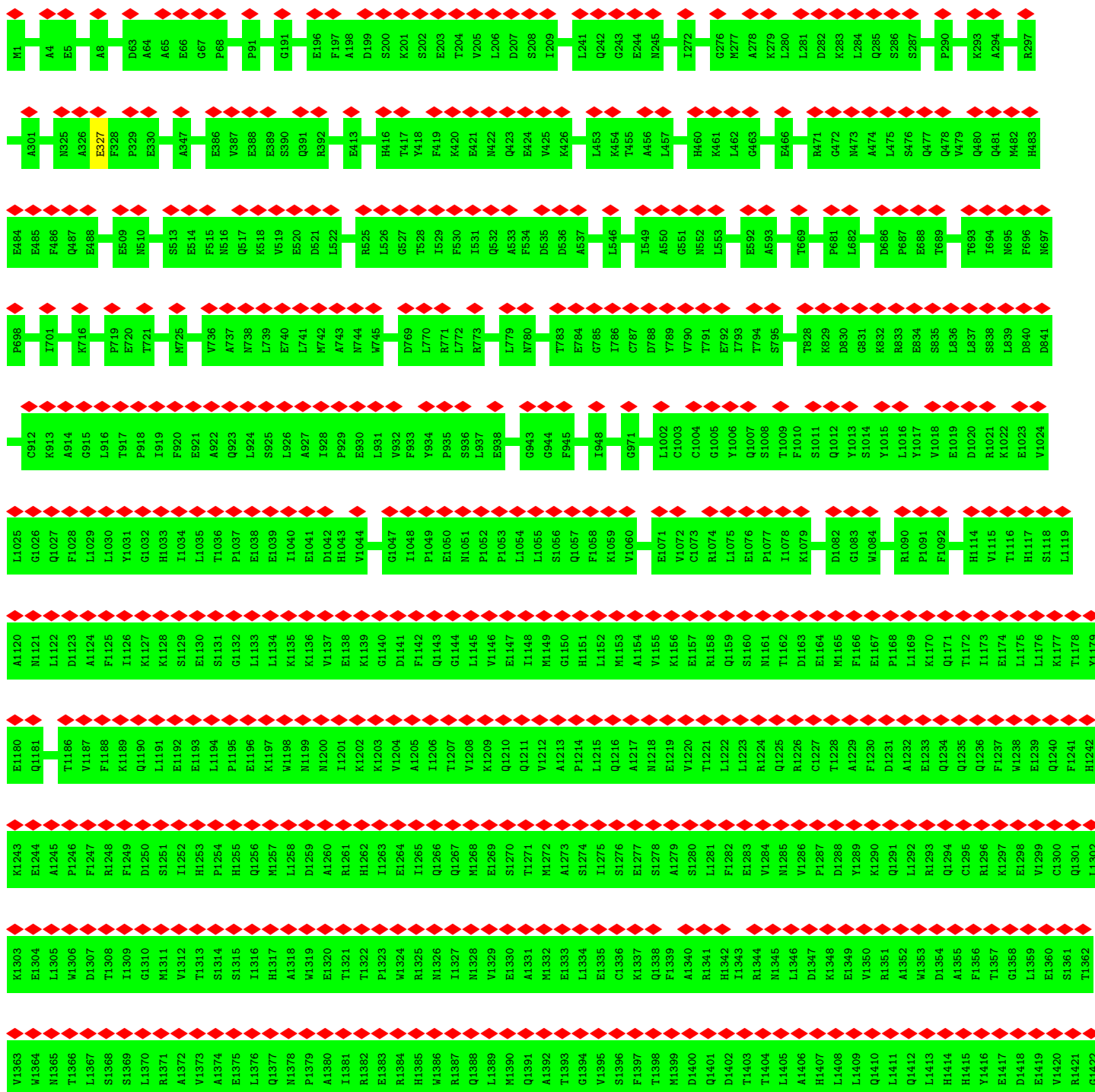
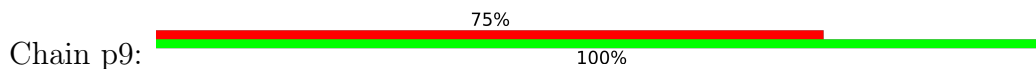
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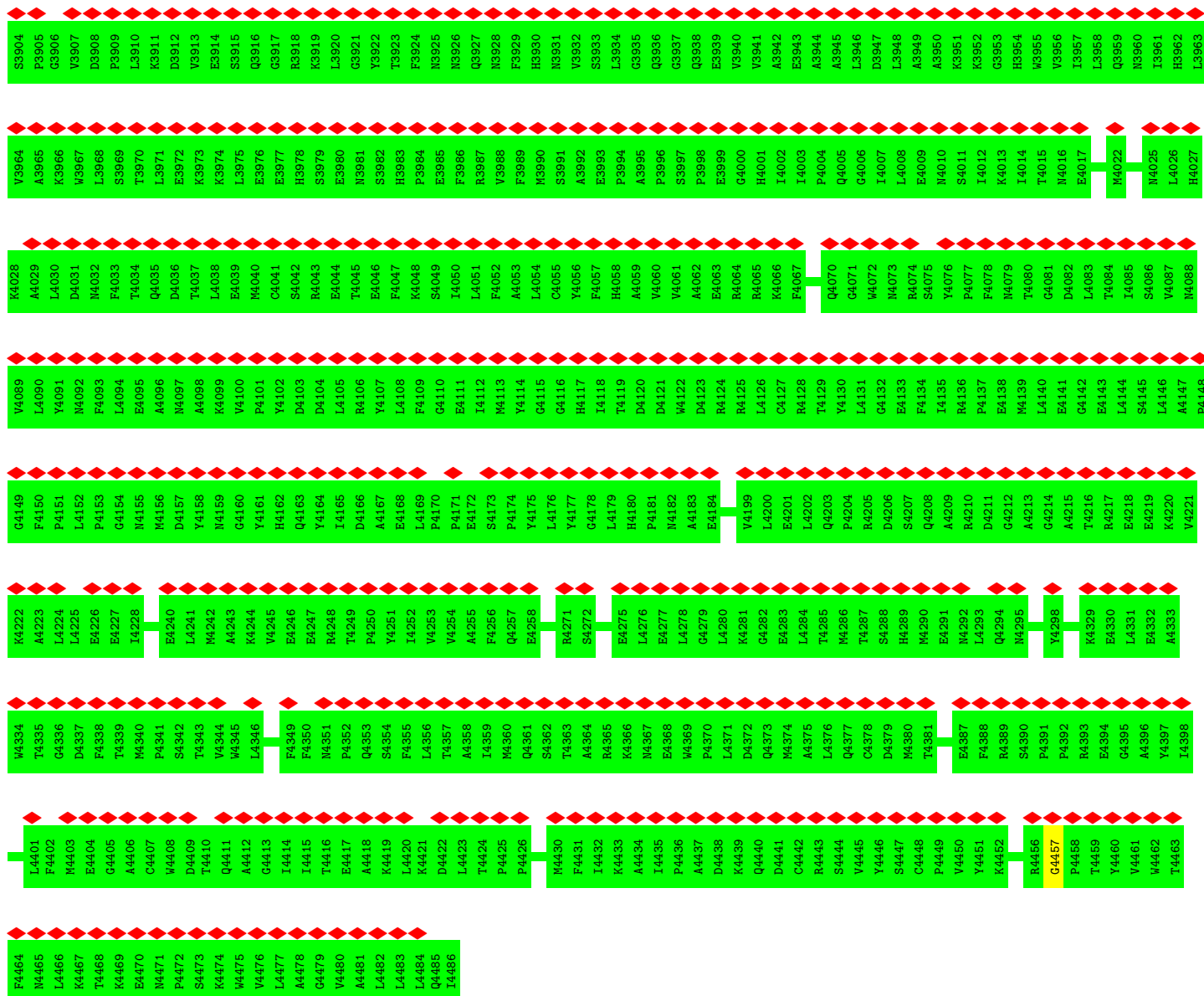
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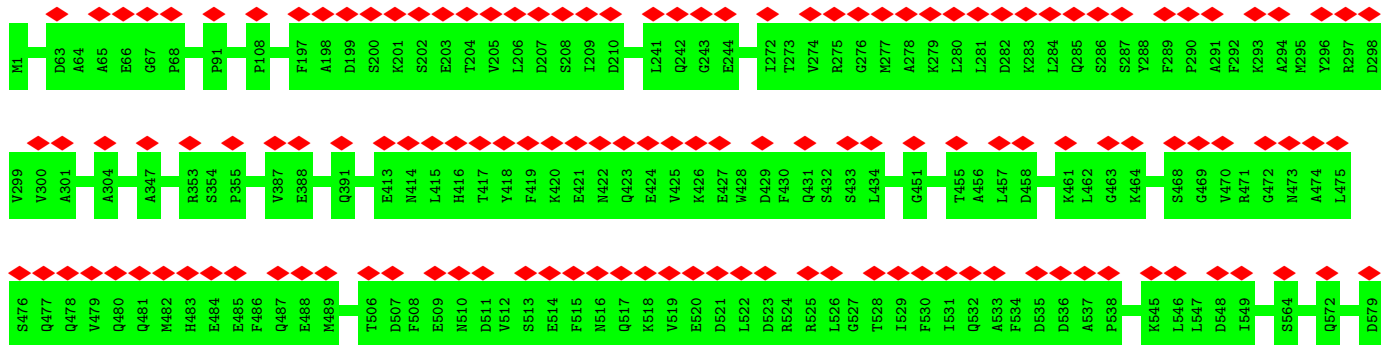
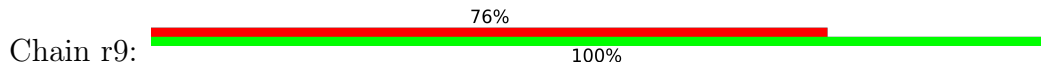
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V2147	M2087	Y2027	I1967	I1907	P1847	R1787	W1727	S1667	L1607	D1547	A1487	A1427
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G2154	I2094	L2034	M1973	A1913	Y1853	M1793	M1733	S1673	L1613	L1553	E1493	E1434
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V2160	A2100	Y2040	T1980	C1920	L1860	M1800	E1740	L1680	T1620	I1560	K1500	L1440
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	N2923	D2863	H2788	K2723	A2657	M2593	G2533	P2473	Q2414	Q2414	P2276	I2216
	E2924	L2864	N2789	D2724	F2658	N2594	P2534	V2474	G2415	G2415	A2277	T2217
	V2925	A2865	E2790	F2725	H2659	P2595	P2535	M2475	T2416	T2416	T2278	H2218
	K2926	S2866	H2659	D2726	Q2660	T2596	G2536	L2476	L2417	L2417	V2279	G2220
	S2927	L2867	K2661	L2727	K2661	A2597	N2537	V2477	F2418	F2418	S2280	D2221
	Q2928	T2793	L2662	F2728	G2598	G2598	K2538	G2478	D2419	D2419	R2281	K2222
	G2929	C2868	A2663	D2729	F2600	S2599	K2539	T2479	Y2420	Y2420	A2282	K2223
	R2929	L2869	A2663	K2730	L2540	F2600	L2540	A2480	Y2421	Y2421	G2283	W2224
	L2930	K2870	T2795	I2731	I2541	G2481	I2541	G2481	I2422	I2422	I2284	I2224
	V2931	A2871	T2665	Q2732	Y2542	T2602	Y2542	T2482	D2423	D2423	L2285	L2225
	D2932	G2872	F2666	T2733	F2543	N2603	F2543	G2483	P2424	P2424	Y2286	L2226
	N2933	V2873	L2667	Q2733	I2544	P2604	I2544	Q2484	E2425	E2425	Y2287	I2227
	R2934	K2874	P2668	E2734	D2545	R2605	D2545	S2485	T2426	T2426	N2288	G2228
	E2935	M2875	T2669	V2735	D2546	L2606	D2546	V2486	K2427	K2427	P2289	D2229
	N2936	L2876	G2670	L2736	Q2607	Q2607	M2547	L2487	R2428	R2428	A2290	I2230
	Q2937	E2801	K2671	K2737	R2608	R2608	N2548	V2488	F2429	F2429	D2291	D2231
	W2938	D2802	L2672	K2738	H2609	H2609	M2549	G2489	E2430	E2430	L2292	P2232
	V2939	A2803	F2673	T2739	F2610	F2610	P2550	A2490	A2431	A2431	G2293	K2233
	F2940	R2805	H2674	F2740	S2611	S2611	E2551	K2491	W2432	W2432	N2294	W2234
	F2941	H2806	Y2675	D2741	V2612	V2612	D2552	L2492	S2433	S2433	N2295	I2235
	I2942	L2813	L2676	D2742	F2613	F2613	D2553	A2493	K2434	K2434	P2296	E2236
	D2943	L2814	F2677	E2743	V2614	V2614	D2554	S2494	L2435	L2435	D2297	S2237
	R2944	D2884	M2678	I2744	L2615	L2615	Y2555	L2495	V2436	V2436	P2298	L2238
	I2945	A2885	S2616	D2745	S2616	S2616	G2556	D2496	P2437	P2437	S2299	N2239
	K2946	Q2886	R2680	P2746	R2680	R2680	T2557	D2497	Q2438	Q2438	S2300	T2240
	Q2947	V2887	D2681	V2747	F2681	F2681	V2558	E2498	F2439	F2439	W2301	W2241
	R2948	A2888	F2682	E2748	G2619	G2619	Q2559	A2499	E2440	E2440	I2302	H2242
	L2949	D2889	A2683	Q2749	A2620	A2620	P2560	Y2500	F2441	F2441	E2303	D2243
	K2950	E2890	M2684	T2750	D2621	D2621	H2561	L2501	D2442	D2442	K2304	D2244
	V2951	R2891	L2685	Q2751	A2622	A2622	T2562	V2502	P2443	P2443	R2305	H2245
	T2952	F2892	F2686	S2752	L2623	L2623	I2563	K2503	E2444	E2444	E2306	K2246
	L2953	G2893	Q2687	P2753	S2624	S2624	I2564	M2504	M2445	M2445	I2307	W2247
	K2954	V2894	Q2687	N2754	S2625	S2625	R2565	V2505	F2446	F2446	Q2308	L2248
	F2955	L2895	S2693	A2760	L2626	L2626	Q2566	P2506	L2447	L2447	T2309	T2249
	S2956	T2896	V2694	M2761	Y2627	Y2627	H2567	F2507	Q2448	Q2448	E2310	L2250
	V2957	G2897	E2695	G2762	S2628	S2628	L2568	N2508	A2449	A2449	R2311	A2251
	Q2958	D2898	C2696	I2763	I2629	I2629	D2569	Y2509	C2450	C2450	A2312	S2252
	G2959	L2899	V2697	G2764	L2630	L2630	Y2570	Y2510	L2451	L2451	N2313	H2253
	N2960	L2900	K2698	E2765	L2631	L2631	G2571	T2511	V2452	V2452	I2314	E2254
	K2961	A2901	T2700	Q2766	Q2633	Q2633	H2572	T2512	H2453	H2453	T2315	R2255
	L2962	S2902	T2701	K2767	H2634	H2634	Y2574	S2513	T2454	T2454	I2316	I2256
	R2963	G2903	D2702	D2702	N2639	N2639	D2575	A2514	E2455	E2455	L2317	F2257
	V2964	E2904	L2703	L2703	F2640	F2640	R2576	M2515	E2456	E2456	F2318	L2258
	R2965	I2905	L2704	L2704	P2641	P2641	S2577	Q2517	T2457	T2457	D2319	H2259
	S2966	D2906	R2705	R2705	A2642	A2642	K2578	L2518	I2458	I2458	K2320	T2261
	R2967	D2907	L2706	L2706								
	K2968	L2908										

R3767	E3808	S3702	E3642	L3582	N3512	E3451	G3391	K3331	A3151	A3091	S3031
E3768	E3809	L3703	N3643	E3583	L3513	N3452	F3392	L3332	K3152	A3092	N3032
V3769	E3810	K3704	L3644	D3584	E3514	A3453	F3393	K3333	K3153	A3093	E3033
N3770	E3811	A3705	E3645	Q3585	E3515	T3454	T3394	C3334	E3154	E3094	Q3034
V3771	E3812	F3706	L3646	L3586	S3516	K3455	K3395	Q3335	P3155	V3095	R3035
V3772	E3813	S3707	T3647	L3587	I3517	L3456	K3396	Q3336	A3156	E3096	R3036
E3773	E3814	I3708	K3648	A3588	D3518	I3457	Y3397	E3337	L3157	L3097	N3037
L3774	E3815	V3709	Q3649	A3589	P3519	N3458	R3398	A3338	T3158	K3098	Y3038
	E3816	F3710	T3650	A3590	V3520	C3459	F3399	E3339	F3279	Q3099	T3039
	E3817	Q3711	A3651	V3591	L3521	E3460	S3400	V3340	A3160	K3100	T3040
	E3818	K3712	A3652	G3522	G3522	R3461	L3401	T3341	Q3161	N3101	F3041
	E3819	A3713	E3653	P3523	P3523	W3462	L3402	A3342	A3162	E3102	K3042
	E3820	V3714	V3654	L3524	R3403	F3463	D3403	V3343	A3163	D3103	S3043
	E3821	E3715	E3655	R3404	R3405	L3464	R3405	T3344	L3164	A3104	F3044
	E3822	R3716	K3656	T3406	T3406	N3465	T3406	L3345	K3165	D3105	L3045
	E3823	A3717	K3657	W3407	W3407	V3466	W3406	S3346	T3166	E3046	E3046
	E3824	A3718	V3658	R3407	R3407	D3467	R3407	L3347	L3167	L3107	F3047
	E3825	F3719	Q3659	P3408	P3408	F3468	P3408	A3348	N3168	I3108	I3048
	E3826	D3720	E3660	Q3469	Q3469	Q3469	Y3409	N3349	K3169	Q3109	R3049
	E3827	E3721	A3661	L3470	L3470	L3470	R3410	R3350	T3170	V3110	L3050
	E3828	S3722	K3662	Q3471	Q3471	G3471	S3411	R3351	T3171	Q3111	Y3051
	E3829	L3723	S3663	G3472	G3472	G3472	Q3412	V3352	L3172	G3112	Q3052
	E3830	R3724	D3664	L3473	L3473	L3473	L3413	G3353	T3173	V3113	S3053
	E3831	E3725	E3665	K3474	K3474	K3474	K3414	G3354	E3174	A3114	L3054
	E3832	R3726	V3666	W3475	W3475	W3475	T3415	L3355	L3175	T3115	L3055
	E3833	V3727	K3667	L3476	L3476	L3476	R3416	A3356	K3176	R3116	H3056
	E3834	A3728	L3668	K3477	K3477	K3477	I3417	S3357	K3177	K3117	R3057
	E3835	N3729	N3669	M3478	M3478	M3478	P3418	E3358	F3178	V3118	H3058
	E3836	L3730	E3670	K3479	K3479	K3479	R3418	N3359	R3179	R3119	R3059
	E3837	I3731	G3671	Y3480	Y3480	Y3480	T3420	A3360	S3180	R3120	K3060
	E3838	D3732	R3672	E3481	E3481	E3481	P3421	R3361	P3181	E3121	E3061
	E3839	K3733	S3673	E3482	E3482	E3482	A3422	W3362	P3182	K3122	L3062
	E3840	R3734	K3674	D3483	D3483	D3483	L3423	A3363	L3183	A3123	K3063
	E3841	E3735	T3675	L3484	L3484	L3484	R3424	D3364	A3184	M3124	C3064
	E3842	F3736	R3676	R3485	R3485	R3485	P3425	A3365	V3185	A3125	K3065
	E3843	S3737	P3677	L3486	L3486	L3486	L3426	V3366	S3186	D3126	T3066
	E3844	V3738	A3678	T3487	T3487	T3487	R3427	Q3367	S3187	E3127	E3067
	E3845	Y3739	F3679	Q3488	Q3488	Q3488	M3428	K3368	V3188	A3128	R3068
	E3846	Q3740	A3680	L3489	L3489	L3489	L3429	F3369	S3189	E3129	L3069
	E3847	R3741	R3681	Q3490	Q3490	Q3490	M3430	K3370	A3190	Q3130	E3070
	E3848	T3742	E3682	Q3491	Q3491	Q3491	D3431	Q3371	A3191	K3131	N3071
	E3849	I3743	S3683	K3492	K3492	K3492	D3432	Q3372	V3192	V3132	G3072
	E3850	R3744	L3684	G3493	G3493	G3493	A3433	E3373	M3193	A3133	L3073
	E3851	K3745	L3685	Y3494	Y3494	Y3494	D3434	R3374	V3194	V3134	L3074
	E3852	F3746	S3686	L3495	L3495	L3495	W3435	T3375	L3195	I3135	K3075
	E3853	V3747	Y3687	Q3496	Q3496	Q3496	A3436	L3376	M3196	M3136	L3076
	E3854	L3748	L3688	I3497	I3497	I3497	A3437	C3377	A3197	L3137	H3077
	E3855	N3749	Q3689	L3498	L3498	L3498	W3438	Q3378	P3198	E3138	S3078
	E3856	A3750	A3690	E3499	E3499	E3499	Q3439	D3379	R3199	V3139	T3079
	E3857	Q3751	S3691	Q3500	Q3500	Q3500	R3440	L3380	G3200	K3140	S3080
	E3858	L3752	L3692	A3501	A3501	A3501	E3441	L3381	Q3201	Q3141	A3081
	E3859	T3753	S3693	L3502	L3502	L3502	G3442	L3382	V3202	K3142	Q3082
	E3860	R3754	K3694	E3503	E3503	E3503	L3443	T3383	P3203	Q3143	V3083
	E3861	V3755	L3695	A3504	A3504	A3504	P3444	T3384	K3144	K3144	D3084
	E3862	F3756	H3696	G3505	G3505	G3505	A3445	A3385	D3205	D3145	D3085
	E3863	I3757	V3697	V3576	V3576	V3576	R3446	F3386	C3146	C3146	L3086
	E3864	S3758	E3698	T3577	T3577	T3577	D3447	L3387	S3207	E3147	K3087
	E3865	K3759	L3699	L3578	L3578	L3578	M3448	T3388	W3208	E3148	A3088
	E3866	F3760	S3699	F3579	F3579	F3579	S3449	Y3389	K3209	D3149	K3089
	E3867	Q3761	H3699	G3581	G3581	G3581	V3450	L3390	A3210	L3150	L3090



● Molecule 104: Dynein axonemal heavy chain 9



A580	V581	R582	M583	I584	S586	Q587	A593	E637	S638	A639	E640	G641	K642	R643	Q646	K647	D650	T669	E672	K673	Y676	S679	Q680	P681	L682	L683	K684	R685	D686	P687	E688	T689	K690	E691	I692	T693	I694	M695	F696	N697	K716	H717	M718	F719	S728	Y732													
V736	A737	N738	L739	E740	L741	M742	A743	N744	M745	Y746	N747	K748	M750	K751	T752	L753	L754	E755	Q766	L770	E777	T778	L779	G785	I786	C787	D788	Y789	T791	E792	I793	T794	T828	K829	D830	G831	K832	R833	I694	E834	S835	L836	L837	S838	L839	D840	D841	D844	Y905	E908									
N909	T910	E911	C912	K913	A914	G915	L916	T917	P918	I919	F920	E921	L926	A927	I928	P929	E930	L931	T991	R996	Q997	R998	M999	M1000	G1001	L1002	C1003	C1004	G1005	Q1007	S1008	T1009	F1010	S1011	Q1012	Y1013	S1014	Y1015	L1016	Y1017	V1018	S835	L836	L837	S838	L839	D840	Q1027	F1028	L1029	L1030	Y1031	G1032	H1033					
I1034	L1035	T1036	D1037	E1038	E1039	D1046	I1048	P1049	N1051	P1052	P1053	L1054	L1055	T1056	Q1057	F1058	K1059	V1060	Q1061	D1063	S1064	Y1065	E1066	T1067	L1068	Y1069	E1070	E1071	V1072	C1073	I1074	L1075	E1076	I1077	I1078	K1079	V1080	F1081	D1082	G1083	W1084	M1085	K1086	I1087	D1088	I1089	R1090	P1091	K1093	L1096	K1108	Q1109							
H1110	L1111	V1112	D1113	H1114	V1115	T1116	H1117	S1118	L1119	A1120	M1121	L1122	D1123	A1124	F1125	I1126	K1127	Q1128	S1129	E1130	S1131	L1132	L1133	L1134	K1135	V1137	E1138	K1139	G1140	D1141	F1142	Q1143	L1144	L1145	V1146	E1147	I1148	M1149	G1150	H1151	L1152	M1153	A1154	V1155	E1157	R1158	Q1159	S1160	M1161	T1162	D1163	E1164	M1165	F1166	E1167	L1168	L1169		
K1170	Q1171	T1172	I1173	E1174	L1175	L1176	K1177	T1178	Y1179	E1180	Q1181	E1182	L1183	P1184	E1185	T1186	V1187	F1188	K1189	Q1190	L1191	E1192	E1193	L1194	P1195	M1198	M1199	L1200	I1201	K1202	L1203	V1204	A1205	L1206	T1207	V1208	K1209	Q1210	Q1211	L1212	A1213	P1214	L1215	Q1216	L1217	M1218	E1219	V1220	T1221	L1222	M1223	R1224	Q1225	R1226	C1227	T1228	A1229	F1230	
D1231	A1232	E1233	Q1234	Q1235	Q1236	F1237	W1238	E1239	Q1240	F1241	H1242	K1243	E1244	A1245	P1246	F1247	R1248	F1249	K1250	S1251	I1252	H1253	P1254	H1255	Q1256	M1257	L1258	D1259	A1260	R1261	H1262	I1263	E1264	L1265	Q1266	Q1267	M1268	E1269	S1270	T1271	M1272	A1273	S1274	L1275	S1276	E1277	S1278	A1279	I1280	L1281	F1282	E1283	V1284	N1285	V1286	P1287	D1288	Y1289	K1290
Q1291	L1292	R1293	Q1294	C1295	R1296	K1297	E1298	V1299	C1300	Q1301	L1302	K1303	E1304	L1305	W1306	D1307	T1308	I1309	G1310	M1311	V1312	T1313	S1314	S1315	I1316	H1317	A1318	W1319	E1320	T1321	T1322	P1323	V1324	R1325	M1326	I1327	N1328	V1329	E1330	A1331	M1332	E1333	L1334	E1335	C1336	K1337	Q1338	F1339	A1340	R1341	H1342	I1343	R1344	L1345	M1346	D1347	K1348	E1349	V1350
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L1411	Q1412	L1413	H1414	H1415	V1416	E1417	D1418	E1419	V1420	R1421	G1422	I1423	V1424	D1425	K1426	A1427	A1428	K1429	E1430	M1431	G1432	M1433	E1434	K1435	L1436	L1437	K1438	E1439	L1440	Q1441	T1442	V1443	W1444	A1445	G1446	M1447	E1448	F1449	Q1450	Y1451	P1453	H1454	P1455	L1456	T1457	N1458	V1459	P1460	L1461	L1462	C1463	S1464	D1465	E1466	D1467	L1468	I1469	E1470	
V1471	L1472	E1473	D1474	M1475	Q1476	V1477	Q1478	L1479	Q1480	M1481	L1482	V1483	M1484	S1485	K1486	Y1487	V1488	A1489	F1490	F1491	L1492	E1493	E1494	V1495	S1496	G1497	W1498	Q1499	K1500	K1501	L1502	S1503	T1504	V1505	D1506	A1507	V1508	I1509	S1510	I1511	W1512	F1513	E1514	V1515	L1516	R1517	T1518	V1519	Q1520	H1521	L1522	E1523	S1524	I1525	F1526	T1527	G1528	S1529	E1530
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A1591	E1592	V1593	L1594	D1595	T1596	K1597	R1598	L1599	A1600	F1601	P1602	F1603	F1604	Y1605	F1606	L1607	S1608	S1609	S1610	D1611	L1612	L1613	D1614	I1615	L1616	S1617	M1618	K1619	T1620	A1621	P1622	Q1623	Q1624	V1625	Q1626	R1627	H1628	L1629	S1630	K1631	L1632	F1633	D1634	M1635	M1636	A1637	K1638	M1639	R1640	F1641	Q1642	L1643	D1644	A1645	S1646	G1647	E1648	P1649	T1650

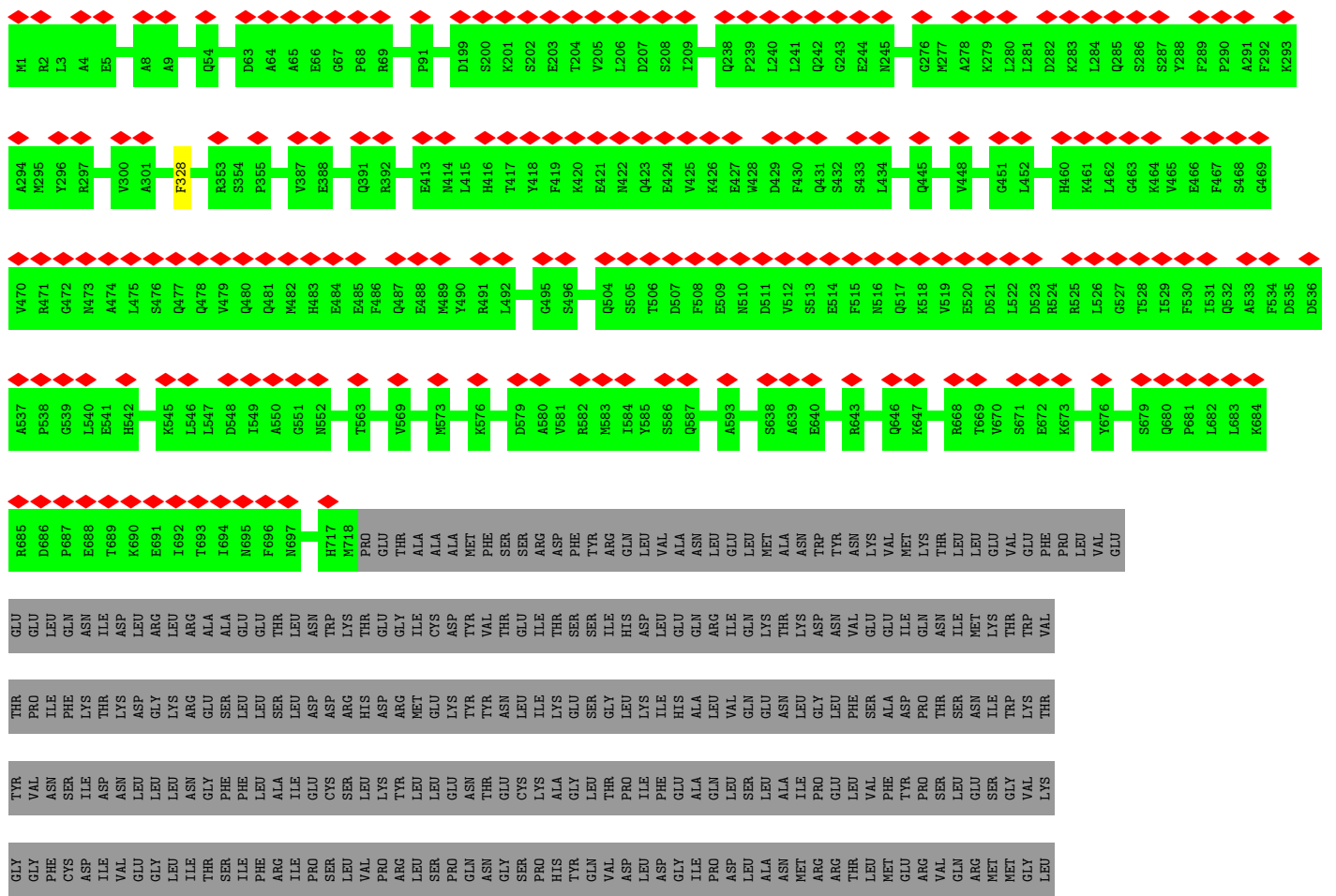
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A2378	A2312	S2252	G2192	L2132	R2072	G2012	W1952	Y1892	Y1832	D1772	F1712	T1652
I2379	M2313	M2253	I2193	K2133	S2073	F2013	F1953	V1893	S1833	R1773	D1713	S1653
W2380	L2314	E2254	I2194	V2134	L2074	I2014	S1954	F1894	Y1834	Q1774	H1714	L1654
L2315	T2315	R2255	M2195	Q2135	R2075	E2015	F1955	M1895	E1835	K1775	P1715	G1655
L2317	L2316	L2256	P2196	Q2136	D2076	A2016	L1956	C1896	Y1836	I1776	A1716	M1656
P2318	L2317	P2257	A2197	L2137	F2077	Q2017	G1957	S1897	L1837	M1777	Q1717	Y1657
D2319	P2318	L2258	T2198	E2138	M2078	S2018	E1958	E1898	G1838	T1778	V1718	S1658
M2385	D2319	M2259	E2199	E2139	I2079	L2019	E1959	Q1899	M1839	I1779	A1719	K1659
A2386	E2200	P2260	E2200	L2140	P2080	A2020	I1960	M1900	T1840	C1780	L1720	E1660
V2387	W2201	T2261	K2202	L2141	K2081	R2021	S1961	D1901	P1841	T1781	T1721	E1661
Q2388	K2203	M2262	I2082	A2142	I2082	K2022	L1962	Y1902	R1842	I1782	C1722	E1662
D2389	D2204	K2263	P2083	V2143	T2084	F2023	M1963	K1903	D1784	D1723	Q1723	Y1663
Q2390	G2204	L2264	T2084	R2144	T2084	I2024	P1964	S1904	V1844	W1784	Q1724	V1664
L2391	L2205	H2145	D2085	H2145	D2085	T2025	S1965	C1905	I1845	H1785	I1725	A1665
V2392	F2206	S2146	D2086	S2146	D2086	L2026	V1966	G1906	T1846	A1786	W1726	F1666
D2393	S2207	E2267	M2087	V2147	M2087	Y2027	G1967	N1907	P1847	W1727	W1727	S1667
Y2394	S2268	L2268	P2088	F2148	P2088	Q2028	I1968	I1908	L1848	D1788	T1728	E1668
R2395	I2209	S2269	I2089	V2149	I2089	L2029	F1969	Y1909	T1849	V1789	T1729	P1669
K2407	M2210	H2270	F2090	V2150	F2090	C2030	I1970	K1910	D1850	V1790	E1730	C1670
T2408	R2211	L2271	M2091	G2151	M2091	K2031	T1971	R1851	R1850	K1791	V1731	D1671
Q2414	L2213	E2272	G2092	G2152	G2092	L2033	M1973	L1912	C1852	K1792	G1732	C1672
G2415	A2214	A2274	L2094	A2153	L2093	L2033	M1973	A1913	Y1853	M1793	M1733	S1673
S2343	M2215	M2275	G2096	G2154	I2094	L2034	P1974	Q1914	I1854	I1794	A1734	G1674
M2344	A2216	P2276	D2096	G2155	G2096	S2036	G1975	G1916	T1855	A1795	F1735	Q1675
V2345	T2217	A2277	L2097	K2157	L2097	Q2037	A1977	A1917	L1856	Q1796	A1736	V1676
D2419	H2218	T2278	F2098	S2158	F2098	D2038	G1978	W1918	Q1858	V1798	L1738	E1677
Y2420	D2219	V2279	P2099	Q2159	P2099	H2039	R1979	W1919	S1859	V1799	E1739	I1678
T2421	G2220	S2280	A2100	V2160	A2100	Y2040	L1980	C1920	L1860	D1900	E1740	M1679
D2423	P2221	R2281	L2101	L2161	L2101	D2041	E1981	F1921	H1861	A1801	G1741	M1681
P2424	K2222	A2282	D2102	R2162	D2102	W2042	L1982	D1922	L1862	Q1802	Y1742	H1682
E2425	W2223	G2283	V2103	S2163	V2103	G2043	P1983	E1923	T1863	A1803	E1743	V1683
T2426	I2224	L2284	P2104	L2164	P2104	L2044	E1984	F1924	M1864	F1804	S1744	L1684
K2427	L2225	L2285	R2105	H2165	R2105	R2045	M1985	M1925	S1865	L1805	A1745	G1685
F2429	L2226	Y2286	R2106	K2166	R2106	A2046	L1986	R1926	G1866	W1806	M1746	H1686
E2430	D2227	L2287	K2107	T2167	K2107	O2047	L1987	I1927	A1867	L1807	K1747	M1687
P2431	G2228	M2288	D2108	Y2168	D2108	K2048	S1988	S1928	P1868	S1808	D1748	K1688
W2432	D2229	P2289	P2109	Q2169	P2109	S2049	L1989	V1929	A1869	Q1809	Y1749	A1689
S2433	I2230	A2290	M2110	I2170	M2110	V2050	F1990	E1930	G1870	L1810	K1750	T1690
K2434	D2231	D2291	F2111	M2171	F2111	L2051	R1991	V1931	P1871	R1811	K1751	V1691
L2435	M2233	L2292	E2112	K2172	E2112	V2052	C1993	S1933	G1873	H1812	K1752	R1692
V2436	W2234	W2294	A2113	R2173	A2113	V2053	C1993	S1933	G1873	R1813	Q1753	H1693
P2437	L2235	M2295	L2114	R2174	L2114	A2054	A1994	V1934	T1874	W1814	V1754	E1694
Q2438	E2236	W2296	V2115	G2055	G2055	G2055	M1995	V1935	G1875	D1815	A1755	M1695
F2439	S2237	P2297	R2116	V2175	R2116	S2056	V1996	A1936	K1876	D1816	Q1756	T1696
E2440	S2238	F2298	K2117	W2177	K2117	L2057	V1997	V1937	T1877	E1817	L1757	E1697
D2441	I2239	M2299	A2118	T2178	A2118	K2058	P1998	Q1938	E1878	V1818	K1758	G1698
F2443	M2239	S2299	I2119	D2179	I2119	R2059	D1999	V1939	T1879	R1819	T1759	P1699
E2444	T2240	T2240	V2120	L2180	V2120	G2060	F2000	K1940	T1880	H1820	L1760	T1700
P2445	V2241	W2301	D2121	M2181	D2121	D2061	E2001	S1941	K1881	C1821	I1761	A1701
E2446	M2242	L2302	L2122	K2183	L2122	P2062	L2002	I1942	D1882	F1822	T1762	Y1702
H2447	D2243	E2303	K2123	P2183	K2123	D2063	I2003	Q1943	L1883	A1823	M1763	E1703
Y2448	D2244	K2304	L2124	A2184	L2124	R2064	C2004	D1944	G1884	M1824	L1764	E1704
P2449	M2245	R2305	Q1215	V2185	Q1215	P2065	E2005	A1945	R1885	I1825	I1765	K1705
L2447	K2246	E2306	A2126	T2186	A2126	E2066	I2006	I1946	A1886	C1826	G1766	P1706
Q2448	V2247	L2307	E2127	D2187	E2127	D2067	M2007	R1947	L1887	D1827	Q1767	E1707
A2449	L2248	Q2308	D2128	M2188	D2128	Q2068	L2008	D1948	G1888	A1828	L1768	E1708
C2450	T2249	E2189	M2129	E2189	M2129	V2069	W2009	K1949	I1889	Q1829	S1769	Q1709
	L2250	L2190	F2130				A2010	K1950	L1890	F1830	K1770	W1710

F3203	K3144	V5083	N3023	L2962	S2902	S2842	G2762	K2698	L2631	G2571	T2511	L2451
K3204	K3145	D3084	Q3024	R2963	G2903	S2843	I2763	S2699	T2632	H2572	T2512	V2452
D3205	D3085	D3085	T3025	V2964	E2904	M2844	G2764	T2700	Q2633	W2573	S2513	H2453
R3206	C3146	L3086	S3026	R2965	I2905	D2845	E2765	W2701	H2634	Y2574	A2514	T2454
S3207	K3087	K3087	Q3027	R2966	P2906	V2846	F2770	D2702	M2639	R2576	M2515	S2455
K3208	A3088	A3088	S3028	S2967	D2907	F2847	V2771	L2703	F2640	K2577	L2516	E2456
K3209	K3089	K3089	Y3029	K2968	L2908	Q2848	W2772	L2704	P2641	S2578	A2518	T2457
A3210	L3090	L3090	L3030	F2969	Y2909	I2849	Q2773	R2705	A2642	K2578	V2519	I2458
K3211	A3091	A3091	S3031	P2970	S2910	T2850	W2774	L2706	S2643	L2579	A2644	R2459
K3212	A3092	A3092	N3032	A2971	D2911	L2851	E2775	Y2707	L2644	S2580	L2520	V2460
V3213	Q3093	Q3093	E3033	I2972	D2912	R2852	L2776	L2708	L2645	L2581	E2521	C2461
T3214	E3094	E3094	Q3034	V2973	E2913	K2853	L2777	S2711	Q2646	K2582	K2522	Y2462
R3215	V5095	V5095	R3035	M2974	E2914	G2854	L2778	M2712	S2647	E2583	P2523	F2463
A3216	E3096	E3096	Y3036	C2975	Y2915	T2855	Q2778	Y2715	I2648	L2584	L2524	M2464
R3217	L3097	L3097	Y3037	T2976	M2916	Q2856	Q2779	R2716	P2649	T2585	E2525	E2465
V3218	K3098	K3098	Y3038	A2977	I2917	I2857	L2780	D2717	P2650	N2586	K2526	R2466
K3219	Q3099	Q3099	T3039	I2978	I2918	Q2858	V2781	K2718	P2651	V2587	A2528	L2467
A3220	K3100	K3100	T3040	H2979	I2919	R2859	E2783	M2719	I2652	Q2588	A2529	M2468
F3221	Q3101	Q3101	P3041	W2980	M2920	K2861	A2784	V2720	D2653	V2590	R2530	R2470
L3222	E3102	E3102	K3042	F2981	V2921	M2862	L2785	V2721	L2654	S2591	N2531	Q2471
D3223	D3103	D3103	S3043	W2984	R2922	M2863	A2786	E2721	A2655	S2592	N2532	R2472
S3224	A3104	A3104	F3044	P2985	M2923	D2863	E2786	E2722	L2656	C2592	G2533	F2473
L3225	D3105	D3105	L3045	Q2986	E2924	L2864	N2787	K2723	L2657	M2593	P2534	P2474
L3226	K3106	K3106	E3046	Q2987	V2925	A2865	H2788	D2724	F2658	N2594	P2535	V2474
R3227	F3047	F3047	F3047	Q2988	K2926	I2867	I2789	F2725	H2659	T2595	G2536	M2475
N3228	I3048	I3048	I3048	A2988	S2927	L2867	E2790	L2726	Q2660	T2597	N2537	W2477
K3229	R3049	R3049	R3049	L2989	Q2928	C2868	V2791	L2727	K2661	G2598	K2538	G2478
K3230	L3050	L3050	L3050	E2990	G2929	L2869	N2792	F2728	I2662	S2599	K2539	T2479
E3231	Y3051	Y3051	Y3051	S2991	L2930	K2870	V2794	D2729	A2663	P2600	L2540	A2480
N3232	Q3052	Q3052	Q3052	V2992	M2931	A2871	M2796	K2730	T2664	T2601	I2541	G2481
I3233	S3053	S3053	S3053	S2993	D2932	G2872	D2796	I2731	T2665	L2602	Y2542	T2482
H3234	L3054	L3054	L3054	R2994	M2933	V2873	L2797	Q2732	F2666	N2603	F2543	G2483
E3235	L3055	L3055	L3055	R2995	R2934	K2874	L2799	T2733	L2667	P2604	I2544	G2484
N3236	H3056	H3056	H3056	F2996	E2935	N2875	L2799	E2734	P2668	R2605	D2545	S2485
S3237	R3057	R3057	R3057	L2997	M2936	L2876	F2800	L2736	T2669	L2606	D2546	V2486
L3238	H3058	H3058	H3058	Q2998	C2937	N2877	E2801	K2737	G2670	Q2607	M2547	L2487
K3239	R3059	R3059	R3059	M2999	W2938	T2878	D2802	L2738	K2672	R2608	N2548	V2488
A3240	K3060	K3060	K3060	T3000	Q2939	S2879	A2803	T2739	F2673	H2609	M2549	G2489
I3241	E3061	E3061	E3061	E3001	F2940	F2880	M2804	F2740	K2674	P2610	P2550	A2490
R3242	L3062	L3062	L3062	I3003	T2941	L2881	R2805	D2741	H2674	S2611	E2551	K2491
F3243	K3063	K3063	K3063	I3003	I2942	M2882	H2806	D2742	L2675	V2612	V2552	L2492
L3244	C3064	C3064	C3064	E3004	D2943	T2883	L2813	I2743	L2676	F2613	D2553	A2493
L3245	K3065	K3065	K3065	P3005	R2944	D2884	L2814	E2744	F2677	V2614	A2554	S2494
O3246	T3066	T3066	T3066	V3007	I2945	A2885	L2814	E2744	L2679	L2615	V2555	L2495
D3247	E3067	E3067	E3067	V3007	R2946	Q2886	F2817	D2745	L2679	S2616	G2556	D2496
R3248	R3068	R3068	R3068	K3008	R2947	V2887	R2818	P2746	R2680	L2617	V2557	P2497
E3249	L3069	L3069	L3069	Q3009	Q2948	A2888	R2819	V2747	D2681	F2618	T2557	P2497
F3250	E3070	E3070	E3070	S3010	L2949	D2889	G2819	E2748	F2682	P2619	V2558	E2498
N3251	N3071	N3071	N3071	I3011	K2950	R2890	N2820	Q2749	A2683	G2619	Q2559	A2499
V3252	G3072	G3072	G3072	S3012	M2951	S2891	L2822	T2750	N2684	A2620	V2560	Y2500
M3253	L3073	L3073	L3073	K3013	T2952	F2892	L2823	Q2751	L2685	D2621	H2561	L2501
F3254	L3074	L3074	L3074	F3014	L2953	L2893	L2823	S2752	F2686	A2622	T2562	V2502
L3255	K3075	K3075	K3075	M3015	C2954	V2894	V2824	P2753	L2687	S2624	I2563	K2503
M3256	L3076	L3076	L3076	A3016	G2955	L2895	G2825	N2754	L2755	S2625	I2564	M2504
A3257	H3077	H3077	H3077	F3017	S2956	L2896	V2826	Y2756	Q2687	L2627	R2565	V2505
R3258	S3078	S3078	S3078	H3018	P2957	N2897	G2827	A2760	V2689	T2627	Q2566	P2506
K3259	T3079	T3079	T3079	H3019	V2958	D2898	G2828	N2761	E2695	S2628	H2567	F2507
G3260	S3080	S3080	S3080	T3020	V2959	L2899	S2829	N2761	E2695	S2629	L2568	H2508
R3261	A3081	A3081	A3081	S3021	M2960	L2900	G2829	N2761	E2695	C2686	D2569	Y2509
A3262	Q3082	Q3082	Q3082	V3022	K2961	A2901						Y2510

F4077	E4009	A3949	A3887	A3756	D3691	S3631	T3571	E3503	L3443	T3383	R3323	A3263
F4078	M4010	A3950	T3888	Q3757	L3692	G3632	L3572	A3504	P3444	T3384	F3324	G3264
M4079	S4011	K3951	S3889	L3758	S3693	N3633	I3573	G3505	A3445	A3385	E3325	L3265
T4080	I4012	K3952	F3890	T3759	K3694	F3634	N3574	V3507	D3446	F3386	K3326	C3266
G4081	K4013	H3953	E3891	F3760	I3695	L3635	F3575	V3508	R3447	S3387	A3327	S3267
L4082	I4014	G3954	E3892	Q3761	H3696	L3636	T3576	L3509	M3448	S3388	T3328	M3268
T4083	T4015	M3955	S3893	I3762	P3697	E3637	V3577	I3510	S3449	F3389	A3329	V3269
T4084	M4016	V3956	G3894	L3763	M3698	T3638	T3578	E3511	V3450	L3390	D3330	I3270
M4025	M4025	I3957	P3895	L3764	Y3699	V3639	R3579	N3512	E3451	K3391	K3331	N3271
L4026	L4026	Q3959	A3896	M3765	Q3700	L3640	K3580	M3513	N3452	L3392	L3332	I3272
H4027	H4027	R3977	N3766	N3766	F3701	V3641	G3581	E3514	A3453	F3393	K3333	V3273
K4028	K4028	P3898	R3767	R3767	S3702	E3642	L3582	E3515	T3454	T3394	C3394	R3274
A4029	A4029	M3899	N3643	N3643	L3703	L3644	E3583	S3516	I3455	Q3395	Q3336	F3275
L4030	L4030	H3962	K3704	K3704	K3704	L3644	Q3584	I3517	L3456	K3396	Q3336	V3276
D4031	D4031	L3963	A3705	A3705	A3705	E3645	Q3585	D3518	I3457	R3398	E3337	E3277
M4032	M4032	F3901	F3706	F3706	F3706	I3646	L3586	P3519	N3458	K3399	A3338	V3278
F4033	F4033	I3902	S3707	S3707	S3707	T3647	L3587	V3520	C3459	Q3399	E3339	F3279
T4034	T4034	L3903	I3708	I3708	I3708	K3648	A3588	L3521	E3460	S3400	V3340	C3280
Q4035	Q4035	D3908	V3709	V3709	V3709	Q3649	A3589	L3521	R3461	L3401	T3341	D3281
A4036	A4036	P3909	F3710	F3710	F3710	T3650	N3590	G3522	N3462	L3402	A3342	V3282
T4037	T4037	L3910	Q3711	Q3711	Q3711	A3651	V3591	P3523	Q3463	D3403	V3343	E3283
L4038	L4038	K3911	K3712	K3712	K3712	A3652	S3592	L3524	L3464	R3404	T3344	R3284
E4039	E4039	K3912	A3713	A3713	A3713	E3653	K3593	L3525	M3465	T3405	I3345	K3285
M4040	M4040	D3912	V3714	V3714	V3714	V3654	E3594	G3526	V3466	W3406	S3346	K3286
C4041	C4041	E3819	E3715	E3715	E3715	E3655	K3595	V3529	D3467	R3407	L3347	Q3287
S4042	S4042	S3820	R3716	R3716	R3716	E3656	P3596	I3530	P3468	K3408	A3348	Q3288
R4043	R4043	A3821	A3717	A3717	A3717	K3656	D3597	K3537	Q3469	F3409	N3349	L3289
E4044	E4044	K3822	A3718	A3718	A3718	V3658	L3598	I3538	L3470	L3410	R3350	N3290
T4045	T4045	N3824	R3825	R3825	R3825	Q3659	E3599	F3535	Q3471	S3411	L3351	K3291
E4046	E4046	K3825	D3720	D3720	D3720	E3660	Q3600	I3536	G3472	Q3412	V3352	A3292
F4047	F4047	K3826	E3721	E3721	E3721	A3661	L3601	K3537	I3473	L3413	G3353	T3293
K4048	K4048	E3829	S3722	S3722	S3722	K3662	K3602	I3538	K3474	K3414	G3354	A3294
S4049	S4049	E3829	L3723	L3723	L3723	V3663	S3603	D3540	W3475	T3415	L3355	D3295
I4050	I4050	E3841	R3724	R3724	R3724	E3665	D3604	D3540	I3476	P3416	A3356	L3296
F4052	F4052	N3844	E3725	E3725	E3725	E3666	L3605	K3541	K3477	I3417	S3357	T3297
A4053	A4053	K3845	R3726	R3726	R3726	V3666	T3606	E3542	N3478	P3418	E3358	A3298
L4054	L4054	T3846	V3727	V3727	V3727	K3667	Q3607	C3543	K3479	F3419	N3359	A3299
C4055	C4055	K3846	N3729	N3729	N3729	N3669	Q3609	R3550	Y3480	T3420	V3360	Q3300
M4056	M4056	T3847	L3730	L3730	L3730	E3670	N3610	P3421	G3481	P3421	R3361	E3301
F4057	F4057	A3847	L3731	L3731	L3731	A3671	G3611	A3422	E3482	A3422	W3362	K3302
H4058	H4058	Q3849	D3732	D3732	D3732	E3672	F3612	L3484	D3483	L3423	A3363	L3303
A4059	A4059	F3859	K3733	K3733	K3733	E3673	K3613	H3554	R3485	D3424	A3364	A3304
V4060	V4060	E3872	I3734	I3734	I3734	H3674	L3614	T3555	V3486	L3426	A3365	A3305
W4061	W4061	K3873	T3735	T3735	T3735	V3675	T3615	K3556	T3487	K3427	Q3367	I3306
A4062	A4062	L3874	F3736	F3736	F3736	R3676	L3616	L3557	M3428	R3428	N3368	K3307
E4063	E4063	G3875	S3737	S3737	S3737	P3677	K3617	A3558	I3489	L3429	F3369	K3309
R4064	R4064	C3876	V3738	V3738	V3738	A3678	T3618	N3559	G3490	M3430	K3370	I3310
M4065	M4065	K3877	Q3740	Q3740	Q3740	E3680	L3619	H3561	Q3492	D3431	Q3371	A3311
K4066	K4066	Y3878	I3741	I3741	I3741	R3681	D3621	Y3562	K3492	A3433	E3373	H3312
Q4070	Q4070	T3742	T3742	T3742	T3742	A3682	S3622	Q3563	G3493	D3434	R3374	L3313
G4071	G4071	L3743	L3743	L3743	L3743	S3683	L3623	P3564	L3495	V3435	T3375	E3315
W4072	W4072	R3744	L3684	L3684	L3684	L3684	L3624	E3565	Q3496	A3436	L3376	N3316
M4073	M4073	G3745	L3685	L3685	L3685	S3625	S3625	L3566	I3497	A3437	C3377	L3317
R4074	R4074	L3746	Y3686	Y3686	Y3686	R3626	R3626	Q3567	T3498	W3438	G3378	A3318
S4075	S4075	F3747	F3687	F3687	F3687	F3687	L3627	A3568	E3499	Q3439	D3379	K3319
Y4076	Y4076	Y3754	S3628	S3628	S3628	L3688	S3628	Q3569	Q3500	N3440	I3380	F3321
R4136	R4136	L3755	M3689	M3689	M3689	N3690	A3630	A3570	L3502	G3442	L3382	A3322



● Molecule 104: Dynein axonemal heavy chain 9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90482	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	23.857	Depositor
Minimum map value	0.000	Depositor
Average map value	0.313	Depositor
Map value standard deviation	1.129	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	848.03, 885.02, 1093.26	wwPDB
Map dimensions	619, 646, 798	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	Depositor

5 Model quality i

5.1 Standard geometry i

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	1
11	1Y	0	2
17	2Y	0	1
23	4H	0	1
23	4J	0	1
25	4T	0	1
34	6C	0	1
34	6I	0	1
34	6K	0	1
42	AM	0	1
42	CM	0	1
42	CU	0	1
42	DC	0	1
42	EK	0	1
42	EM	0	1
42	GQ	0	1
42	HK	0	1
42	LE	0	1
42	OC	0	1
42	PA	0	1
42	RW	0	1
42	SI	0	1
43	BD	0	1
43	BL	0	1
43	BX	0	1
43	CL	0	1
43	DB	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	DF	0	1
43	DX	0	1
43	DZ	0	1
43	EV	0	1
43	FV	0	1
43	HV	0	1
43	JH	0	1
43	KF	0	1
43	LR	0	1
43	MD	0	1
43	NL	0	1
43	OF	0	1
43	ON	0	1
43	PV	0	1
43	QJ	0	1
43	SL	0	1
43	SX	0	1
43	UL	0	1
43	UZ	0	1
43	VN	0	1
43	WH	0	1
43	WL	0	1
45	j	0	1
47	N	0	1
58	b1	0	1
58	b2	0	1
64	d2	0	2
67	d8	0	1
67	f1	0	1
68	e5	0	1
70	g1	0	2
71	g2	0	2
73	g5	0	2
74	g6	0	5
75	h2	0	1
77	i1	0	1
78	i2	0	1
80	i4	0	1
82	i9	0	2
84	j3	0	2
89	q4	0	1
92	k9	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
97	q2	0	1
99	o6	0	1
101	m8	0	1
102	u9	0	1
103	n0	0	1
103	r0	0	3
104	n9	0	1
104	p9	0	2
104	r9	0	1
104	t9	0	1
All	All	0	94

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (94) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	175	ARG	Sidechain
11	1Y	61	ARG	Peptide,Sidechain
17	2Y	64	ASP	Peptide
23	4H	54	PRO	Peptide
23	4J	54	PRO	Peptide
25	4T	123	PHE	Peptide
34	6C	131	ARG	Sidechain
34	6I	55	HIS	Peptide
34	6K	131	ARG	Sidechain
42	AM	105	ARG	Sidechain
43	BD	282	ARG	Sidechain
43	BL	323	MET	Peptide
43	BX	271	ALA	Peptide
43	CL	322	SER	Peptide
42	CM	338	LYS	Peptide
42	CU	339	ARG	Sidechain
43	DB	271	ALA	Peptide
42	DC	339	ARG	Sidechain
43	DF	271	ALA	Peptide
43	DX	271	ALA	Peptide
43	DZ	271	ALA	Peptide
42	EK	221	ARG	Sidechain
42	EM	172	TYR	Peptide

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Mol	Chain	Res	Type	Group
43	EV	322	SER	Peptide
43	FV	271	ALA	Peptide
42	GQ	121	ARG	Sidechain
42	HK	339	ARG	Sidechain
43	HV	271	ALA	Peptide
43	JH	276	ARG	Sidechain
43	KF	343	GLU	Peptide
42	LE	422	ARG	Sidechain
43	LR	323	MET	Peptide
43	MD	86	ARG	Sidechain
47	N	38	ASP	Sidechain
43	NL	271	ALA	Peptide
42	OC	64	ARG	Sidechain
43	OF	322	SER	Peptide
43	ON	271	ALA	Peptide
42	PA	390	ARG	Sidechain
43	PV	271	ALA	Peptide
43	QJ	404	ASP	Peptide
42	RW	2	ARG	Sidechain
42	SI	55	GLU	Peptide
43	SL	271	ALA	Peptide
43	SX	271	ALA	Peptide
43	UL	271	ALA	Peptide
43	UZ	390	ARG	Peptide
43	VN	323	MET	Peptide
43	WH	86	ARG	Sidechain
43	WL	325	GLU	Peptide
58	b1	62	PHE	Peptide
58	b2	17	MET	Peptide
64	d2	1105	GLU	Peptide
64	d2	904	CYS	Peptide
67	d8	207	GLU	Peptide
68	e5	2	ILE	Peptide
67	f1	176	ALA	Peptide
70	g1	2202	MET	Peptide
70	g1	2436	SER	Peptide
71	g2	252	LEU	Peptide
71	g2	637	ALA	Peptide
73	g5	1445	LEU	Peptide
73	g5	339	THR	Peptide
74	g6	1089	GLU	Peptide
74	g6	1169	TRP	Peptide

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Mol	Chain	Res	Type	Group
74	g6	1702	ARG	Sidechain
74	g6	2027	PRO	Peptide
74	g6	893	GLN	Peptide
75	h2	811	ARG	Sidechain
77	i1	485	ARG	Sidechain
78	i2	78	ARG	Sidechain
80	i4	384	MET	Peptide
82	i9	1694	MET	Peptide
82	i9	1701	LEU	Peptide
45	j	260	LYS	Peptide
84	j3	141	GLU	Peptide
84	j3	268	GLN	Peptide
92	k9	2488	PRO	Peptide
92	k9	3757	TYR	Peptide
101	m8	207	ARG	Sidechain
103	n0	392	LYS	Peptide
104	n9	2507	PHE	Peptide
99	o6	234	ARG	Sidechain
104	p9	327	GLU	Peptide
104	p9	4457	GLY	Peptide
97	q2	26	GLU	Peptide
89	q4	78	ILE	Peptide
103	r0	2909	ARG	Sidechain
103	r0	3933	LYS	Peptide
103	r0	3953	ARG	Peptide
104	r9	995	ARG	Sidechain
104	t9	328	PHE	Peptide
102	u9	240	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 859 ligands modelled in this entry, 285 are monoatomic - leaving 574 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35888. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

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

6.2 Central slices [i](#)

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

6.3 Largest variance slices [i](#)

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

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

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](#)

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

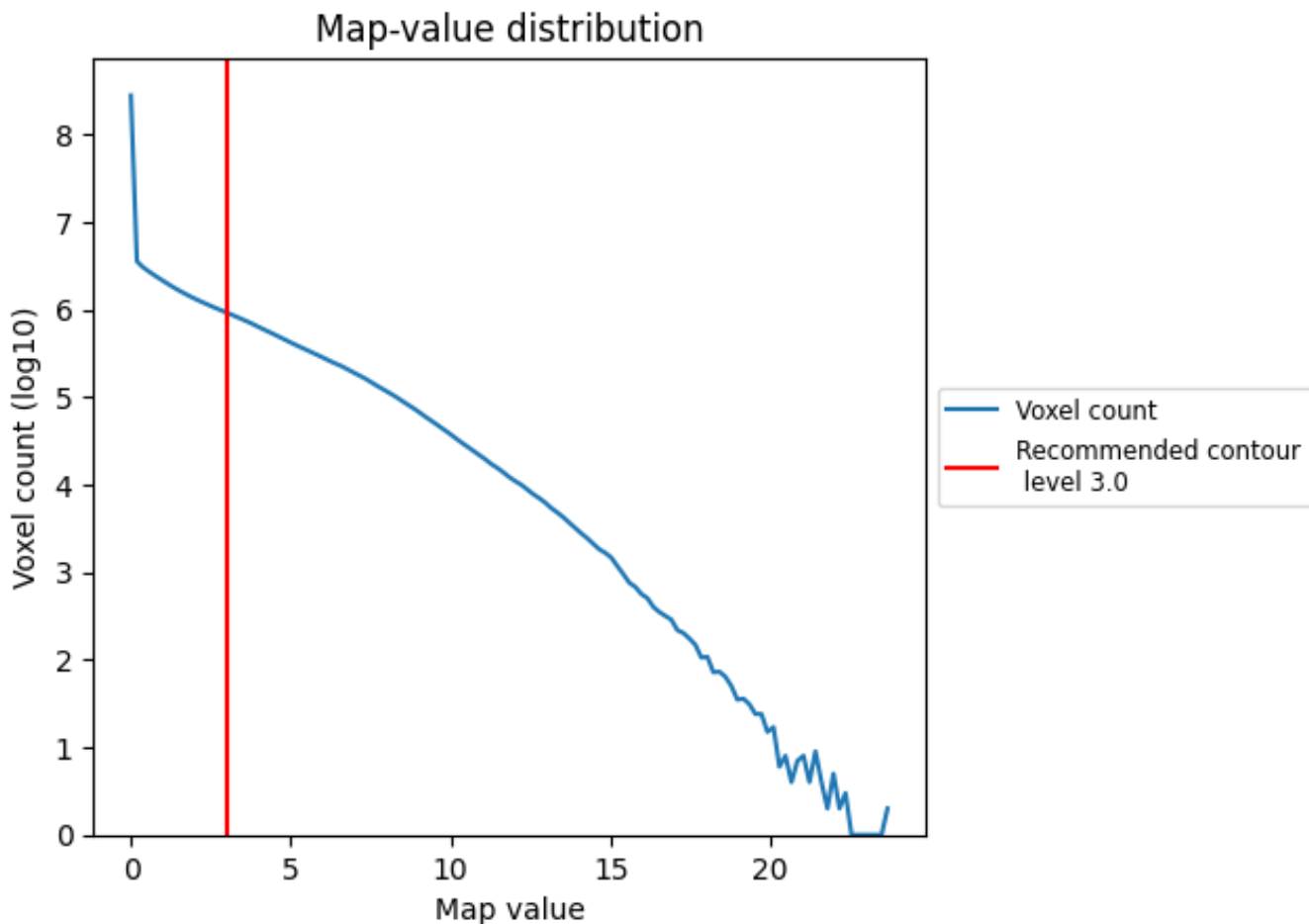
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

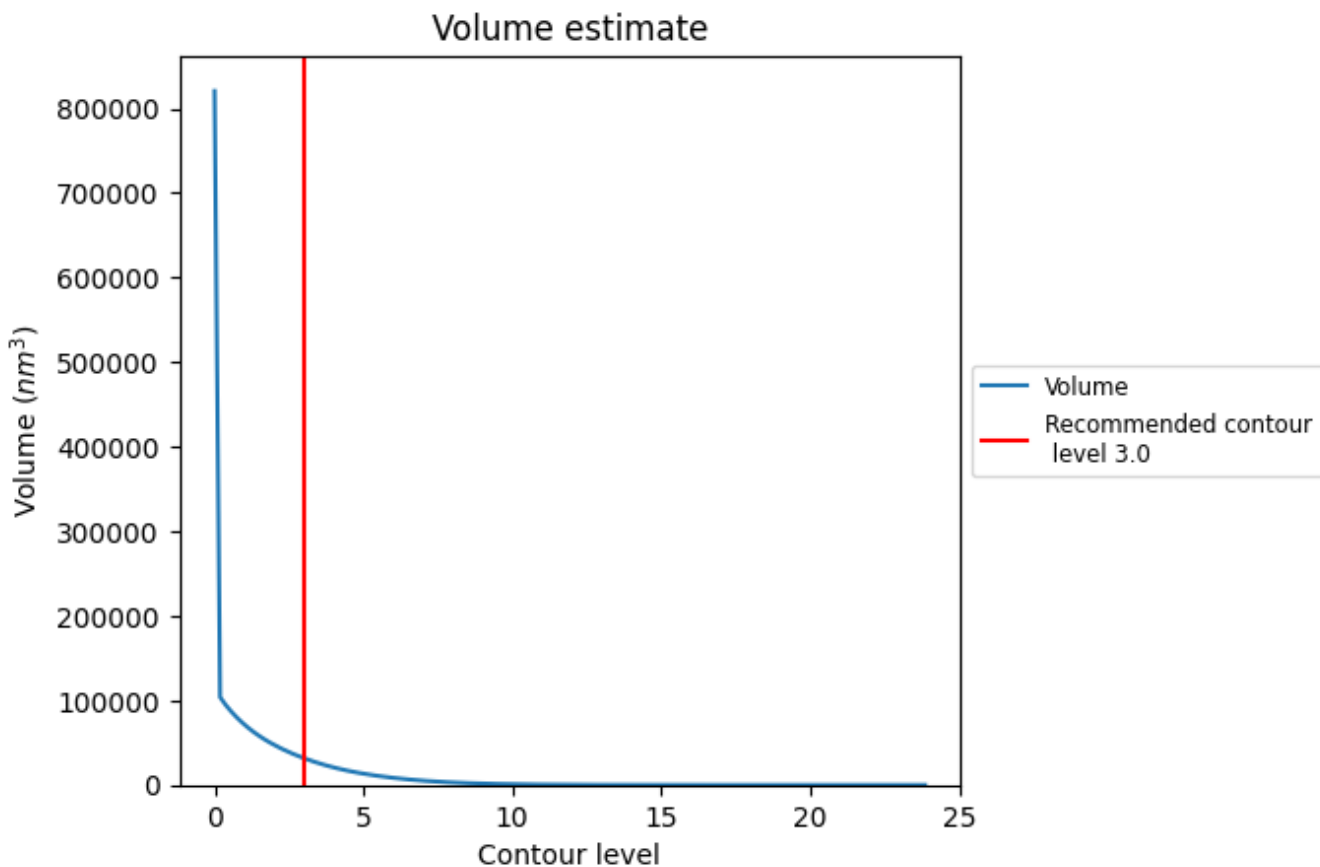
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 31677 nm^3 ; this corresponds to an approximate mass of 28615 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-35888 and PDB model 8J07. Per-residue inclusion information can be found in section 3 on page 141.

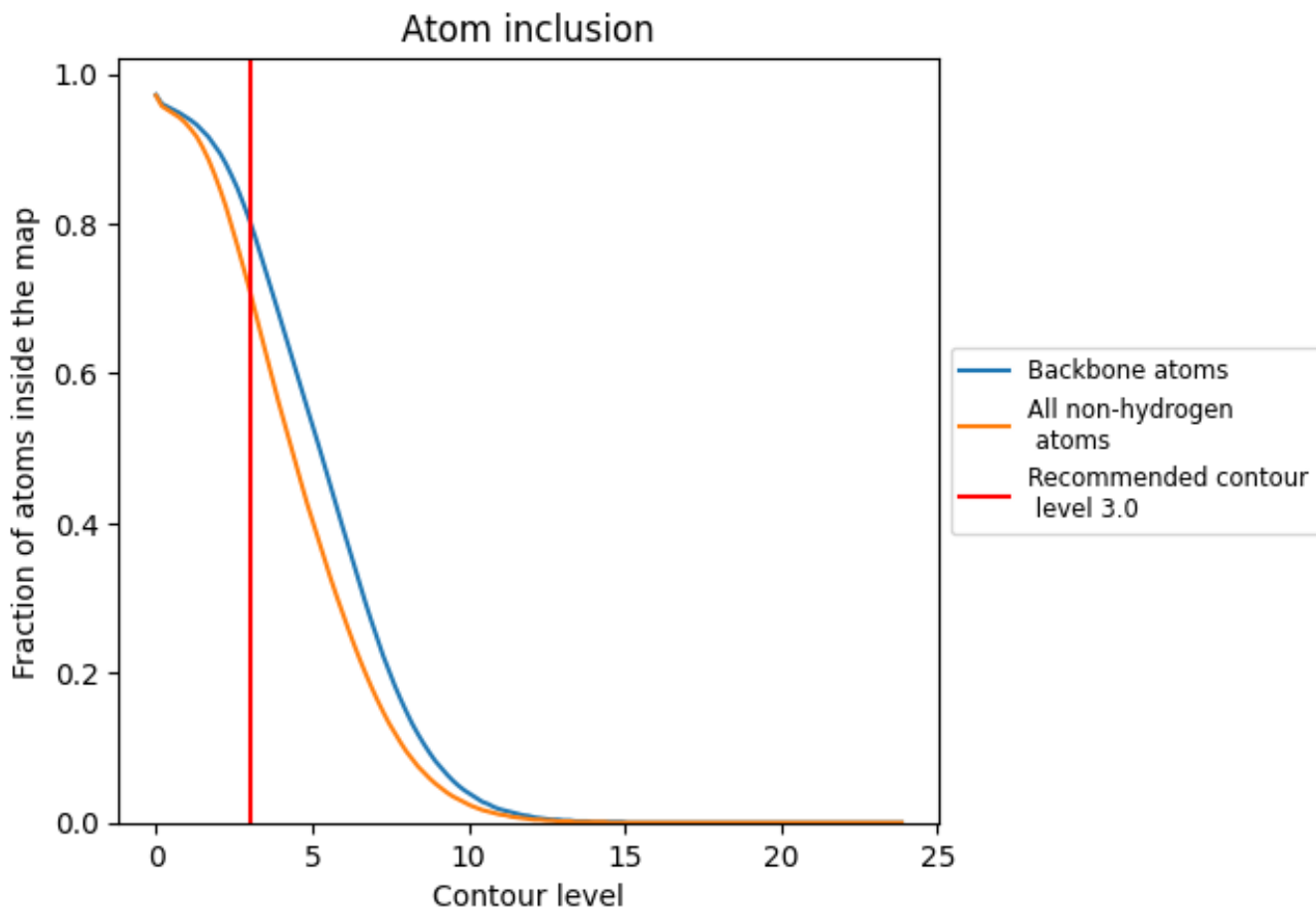
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

This section was not generated.

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 (3.0).

9.2 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.3 Map-model fit summary











































The table lists the average atom inclusion at the recommended contour level (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	0.7110
0	0.5630
1	0.4760
10	0.4370
11	0.1150
12	0.2450
13	0.1800
14	0.2660
1A	0.6540
1B	0.6620
1C	0.6960
1D	0.4570
1E	0.5410
1F	0.5470
1G	0.6150
1H	0.5700
1I	0.5260
1J	0.5440
1L	0.7500
1M	0.7650
1N	0.7420
1O	0.7440
1P	0.7620
1Q	0.7290
1R	0.6540
1S	0.6340
1T	0.6660
1V	0.6120
1W	0.6000
1Y	0.6950
1Z	0.7140
2	0.5030
2A	0.8260
2B	0.8360
2C	0.8330



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Chain	Atom inclusion
2D	 0.8450
2E	 0.8450
2F	 0.8390
2G	 0.8350
2I	 0.6710
2J	 0.6760
2L	 0.6680
2M	 0.7300
2N	 0.6780
2O	 0.7230
2Q	 0.6090
2R	 0.6020
2S	 0.6220
2U	 0.7460
2V	 0.7710
2W	 0.7610
2X	 0.7690
2Y	 0.7720
2Z	 0.7600
3	 0.8170
3A	 0.7950
3B	 0.8040
3C	 0.7580
3D	 0.7950
3E	 0.7740
3F	 0.7540
3G	 0.7120
3H	 0.7060
3I	 0.7060
3J	 0.7290
3K	 0.7340
3L	 0.5840
3M	 0.7090
3O	 0.6500
3P	 0.6620
3Q	 0.6930
3R	 0.6640
3S	 0.6610
3T	 0.7030
3U	 0.6520
3W	 0.6030
3X	 0.5930











































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Chain	Atom inclusion
3Y	0.5900
4	0.5530
4A	0.6430
4B	0.1460
4C	0.5460
4D	0.2550
4E	0.6330
4F	0.1130
4G	0.6020
4H	0.1740
4I	0.5900
4J	0.3880
4K	0.4360
4L	0.0520
4M	0.5090
4O	0.7180
4P	0.7110
4Q	0.7120
4R	0.6940
4S	0.7390
4T	0.7360
4U	0.5590
4V	0.5420
4W	0.7210
5	0.0510
5A	0.7510
5B	0.7580
5C	0.7660
5D	0.4100
5E	0.4320
5F	0.3880
5H	0.6490
5I	0.6630
5J	0.7020
5L	0.7250
5M	0.7290
5O	0.7170
5P	0.7090
5Q	0.6940
5R	0.6800
5S	0.7080
5T	0.6960











































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Chain	Atom inclusion
5U	 0.6880
5V	 0.7680
5X	 0.7180
5Y	 0.7000
6A	 0.5690
6C	 0.3700
6E	 0.5350
6G	 0.3420
6I	 0.3140
6K	 0.2640
6L	 0.5660
6N	 0.3700
6O	 0.5410
6Q	 0.4590
6R	 0.4220
6T	 0.2890
6V	 0.5660
7	 0.4620
7A	 0.3630
7B	 0.3190
7C	 0.2100
7D	 0.5340
7E	 0.3840
7F	 0.4580
7G	 0.3630
7I	 0.6780
7J	 0.6630
8	 0.0020
8A	 0.7190
8B	 0.6910
8C	 0.6750
8D	 0.6960
8E	 0.7110
8F	 0.7090
8G	 0.6920
8H	 0.7820
8J	 0.4840
8K	 0.1900
8L	 0.1990
8M	 0.2260
8N	 0.3440
8O	 0.2610

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Chain	Atom inclusion
8P	 0.2090
8Q	 0.4620
9	 0.5000
A	 0.7900
AB	 0.8810
AC	 0.8880
AD	 0.8780
AE	 0.8840
AF	 0.8950
AG	 0.9010
AH	 0.8730
AI	 0.8770
AJ	 0.8720
AK	 0.8760
AL	 0.8800
AM	 0.8900
AN	 0.8730
AO	 0.8920
AP	 0.8840
AQ	 0.9010
AR	 0.8860
AS	 0.8890
AT	 0.8890
AU	 0.8870
AV	 0.8730
AW	 0.8830
AX	 0.8820
AY	 0.8900
AZ	 0.9030
B	 0.7380
BA	 0.8610
BB	 0.8670
BC	 0.8590
BD	 0.8570
BE	 0.8500
BF	 0.8720
BG	 0.8750
BH	 0.8740
BI	 0.8660
BJ	 0.8500
BK	 0.8390
BL	 0.8410











































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Chain	Atom inclusion
BM	0.8610
BN	0.8580
BO	0.8570
BP	0.8650
BQ	0.8640
BR	0.8670
BS	0.8430
BT	0.8420
BU	0.8190
BV	0.7820
BW	0.8230
BX	0.8610
BY	0.8690
C	0.7310
CB	0.8710
CC	0.8660
CD	0.8620
CE	0.8120
CF	0.8420
CG	0.8590
CH	0.8580
CI	0.8530
CJ	0.8330
CK	0.8420
CL	0.8400
CM	0.8490
CN	0.8610
CO	0.8520
CP	0.8660
CQ	0.8640
CR	0.8800
CS	0.8710
CT	0.8560
CU	0.8180
CV	0.7680
CW	0.8500
CX	0.8490
CY	0.8550
CZ	0.8370
D	0.9810
DB	0.8580
DC	0.8520

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Chain	Atom inclusion
DD	 0.8680
DE	 0.8010
DF	 0.8460
DG	 0.8420
DH	 0.8730
DI	 0.8610
DJ	 0.8220
DK	 0.8370
DL	 0.8680
DM	 0.8470
DN	 0.8630
DO	 0.8480
DP	 0.8580
DQ	 0.8600
DR	 0.8930
DS	 0.8770
DT	 0.8790
DU	 0.8430
DV	 0.7870
DW	 0.8320
DX	 0.8590
DY	 0.8460
DZ	 0.8480
E	 0.5560
EB	 0.8170
EC	 0.8160
ED	 0.8470
EE	 0.7910
EF	 0.8090
EG	 0.8130
EH	 0.8340
EI	 0.8080
EJ	 0.7650
EK	 0.7790
EL	 0.8280
EM	 0.8190
EN	 0.8280
EO	 0.8230
EP	 0.8250
EQ	 0.8260
ER	 0.8440
ES	 0.8230

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Chain	Atom inclusion
ET	0.8350
EU	0.7890
EV	0.7690
EW	0.7800
EX	0.8190
EY	0.8100
EZ	0.8230
F	0.6970
FB	0.8150
FC	0.8260
FD	0.8400
FE	0.7940
FF	0.7610
FG	0.7820
FH	0.7860
FI	0.7820
FJ	0.7010
FK	0.7430
FL	0.8250
FM	0.8360
FN	0.8260
FO	0.8210
FP	0.8290
FQ	0.8440
FR	0.8340
FS	0.8300
FT	0.8100
FU	0.7820
FV	0.7420
FW	0.7860
FX	0.8160
FY	0.8260
FZ	0.8140
G	0.8630
GB	0.8100
GC	0.7990
GD	0.8280
GE	0.8020
GF	0.8330
GG	0.8210
GH	0.8040
GI	0.7910











































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Chain	Atom inclusion
GJ	0.7640
GK	0.7790
GL	0.8150
GM	0.8140
GN	0.8110
GO	0.7960
GP	0.8100
GQ	0.8290
GR	0.8190
GS	0.8180
GT	0.8090
GU	0.7930
GV	0.7500
GW	0.7680
GX	0.8060
GY	0.8070
GZ	0.8160
H	0.7680
HA	0.8310
HB	0.8230
HC	0.8320
HD	0.8560
HE	0.8510
HF	0.8360
HG	0.8270
HH	0.8260
HI	0.8310
HJ	0.7920
HK	0.8000
HL	0.8170
HM	0.8170
HN	0.8150
HO	0.8220
HP	0.8380
HQ	0.8400
HR	0.8300
HS	0.8290
HT	0.8250
HU	0.8070
HV	0.7900
HW	0.7950
HX	0.8170











































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Chain	Atom inclusion
HY	 0.8180
HZ	 0.8260
I	 0.8460
IA	 0.8320
IB	 0.8510
IC	 0.8520
ID	 0.8370
IE	 0.8280
IF	 0.8350
IG	 0.8100
IH	 0.7930
II	 0.8030
IJ	 0.8120
IK	 0.8200
IL	 0.8270
IM	 0.8240
IN	 0.8490
IO	 0.8430
IP	 0.8320
IQ	 0.8290
IR	 0.8240
IS	 0.8130
IT	 0.7990
IU	 0.8010
IV	 0.8140
IW	 0.8320
IX	 0.8330
IY	 0.8230
J	 0.7520
JB	 0.8300
JC	 0.8230
JD	 0.8440
JE	 0.8220
JF	 0.8200
JG	 0.8090
JH	 0.8200
JI	 0.8050
JJ	 0.8040
JK	 0.7980
JL	 0.8270
JM	 0.8190
JN	 0.8210











































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Chain	Atom inclusion
JO	 0.8270
JP	 0.8450
JQ	 0.8140
JR	 0.8240
JS	 0.8020
JT	 0.8190
JU	 0.8070
JV	 0.8210
JW	 0.8100
JX	 0.8220
JY	 0.8120
JZ	 0.8300
K	 0.3680
KB	 0.8580
KC	 0.8580
KD	 0.8720
KE	 0.8620
KF	 0.8620
KG	 0.8610
KH	 0.8720
KI	 0.8680
KJ	 0.8620
KK	 0.8580
KL	 0.8440
KM	 0.8430
KN	 0.8460
KO	 0.8560
KP	 0.8700
KQ	 0.8600
KR	 0.8550
KS	 0.8620
KT	 0.8450
KU	 0.8500
KV	 0.8450
KW	 0.8490
KX	 0.8380
KY	 0.8550
KZ	 0.8550
L	 0.6650
LB	 0.8310
LC	 0.8720
LD	 0.8610











































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Chain	Atom inclusion
LE	 0.8580
LF	 0.8570
LG	 0.8760
LH	 0.8640
LI	 0.8580
LJ	 0.8710
LK	 0.8830
LL	 0.8580
LM	 0.8450
LN	 0.8590
LO	 0.8620
LP	 0.8720
LQ	 0.8650
LR	 0.8680
LS	 0.8740
LT	 0.8610
LU	 0.8640
LV	 0.8640
LW	 0.8730
LX	 0.8550
LY	 0.8460
LZ	 0.8560
M	 0.8240
MA	 0.8770
MC	 0.8830
MD	 0.8700
ME	 0.8730
MF	 0.8660
MG	 0.8850
MH	 0.8750
MI	 0.8760
MJ	 0.8790
MK	 0.8940
ML	 0.8790
MM	 0.8700
MN	 0.8800
MO	 0.8860
MP	 0.8820
MQ	 0.8800
MR	 0.8840
MS	 0.8870
MT	 0.8810











































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Chain	Atom inclusion
MU	 0.8730
MV	 0.8910
MW	 0.8800
MX	 0.8760
MY	 0.8610
MZ	 0.8720
N	 0.6420
NA	 0.8000
NB	 0.8100
NC	 0.7980
ND	 0.8120
NE	 0.7940
NF	 0.8040
NG	 0.8000
NH	 0.7820
NI	 0.7770
NJ	 0.7850
NK	 0.7660
NL	 0.7960
NM	 0.7870
NN	 0.7990
NO	 0.7930
NP	 0.8010
NQ	 0.7900
NR	 0.7800
NS	 0.7640
NT	 0.7690
NU	 0.7680
NV	 0.7800
NW	 0.7850
NX	 0.8060
NZ	 0.7950
O	 0.5270
OA	 0.8130
OB	 0.8210
OC	 0.8210
OD	 0.8150
OE	 0.8150
OF	 0.8070
OG	 0.8010
OH	 0.7700
OI	 0.7540

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Chain	Atom inclusion
OJ	 0.7780
OK	 0.7760
OL	 0.8030
OM	 0.8060
ON	 0.8360
OO	 0.8330
OP	 0.8260
OQ	 0.8120
OR	 0.8150
OS	 0.7990
OT	 0.7780
OU	 0.7670
OV	 0.7730
OW	 0.7810
OX	 0.8140
OY	 0.8100
P	 0.6890
PA	 0.7870
PB	 0.8060
PC	 0.8150
PD	 0.8020
PE	 0.7950
PF	 0.7940
PG	 0.7690
PH	 0.7440
PI	 0.7220
PJ	 0.7400
PK	 0.7700
PL	 0.7850
PM	 0.7920
PN	 0.8080
PO	 0.8080
PP	 0.8010
PQ	 0.7990
PR	 0.8040
PS	 0.7940
PT	 0.7630
PU	 0.7270
PV	 0.7460
PW	 0.7640
PX	 0.7760
PY	 0.7890











































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Chain	Atom inclusion
Q	0.6250
QA	0.7740
QB	0.7950
QC	0.7930
QD	0.7900
QE	0.7670
QF	0.8010
QG	0.7900
QH	0.7560
QI	0.7080
QJ	0.7370
QK	0.7490
QL	0.7710
QM	0.7770
QN	0.7990
QO	0.7980
QP	0.7890
QQ	0.7900
QR	0.8180
QS	0.7940
QT	0.7740
QU	0.7220
QV	0.7300
QW	0.7490
QX	0.7770
QY	0.7730
R	0.6940
RA	0.7640
RB	0.7740
RC	0.7680
RD	0.7630
RE	0.7650
RF	0.7700
RG	0.7610
RH	0.7450
RI	0.7020
RJ	0.6980
RK	0.7340
RL	0.7540
RM	0.7650
RN	0.7770
RO	0.7710











































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Chain	Atom inclusion
RP	 0.7560
RQ	 0.7740
RR	 0.7940
RS	 0.7880
RT	 0.7640
RU	 0.7100
RV	 0.6970
RW	 0.7070
RX	 0.7540
RY	 0.7650
S	 0.6420
SB	 0.7640
SC	 0.7540
SD	 0.7670
SE	 0.7560
SF	 0.7720
SG	 0.7410
SH	 0.7470
SI	 0.7150
SJ	 0.6880
SK	 0.7060
SL	 0.7260
SM	 0.7290
SN	 0.7510
SO	 0.7610
SP	 0.7460
SQ	 0.7710
SR	 0.7920
SS	 0.7630
ST	 0.7740
SU	 0.7310
SV	 0.6940
SW	 0.7080
SX	 0.7370
SY	 0.7570
T	 0.7900
TB	 0.7750
TC	 0.7550
TD	 0.7640
TE	 0.7820
TF	 0.7830
TG	 0.7850











































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Chain	Atom inclusion
TH	 0.7630
TI	 0.7420
TJ	 0.6870
TK	 0.6830
TL	 0.7230
TM	 0.7540
TN	 0.7600
TO	 0.7440
TP	 0.7410
TQ	 0.7630
TR	 0.7890
TS	 0.7740
TT	 0.7480
TU	 0.7260
TV	 0.6920
TW	 0.7010
TX	 0.7280
TY	 0.7630
TZ	 0.7860
U	 0.6820
UB	 0.8180
UC	 0.8120
UD	 0.8080
UE	 0.8040
UF	 0.8050
UG	 0.7990
UH	 0.7970
UI	 0.7760
UJ	 0.7440
UK	 0.7400
UL	 0.7790
UM	 0.7950
UN	 0.8070
UO	 0.7900
UP	 0.7900
UQ	 0.7910
UR	 0.7990
US	 0.7860
UT	 0.7790
UU	 0.7600
UV	 0.7370
UW	 0.7630











































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Chain	Atom inclusion
UX	 0.7800
UY	 0.7930
UZ	 0.8230
V	 0.3930
VB	 0.8310
VC	 0.8180
VD	 0.8280
VE	 0.8350
VF	 0.8180
VG	 0.8260
VH	 0.8300
VI	 0.8140
VJ	 0.8140
VK	 0.8200
VL	 0.8330
VM	 0.8430
VN	 0.8350
VO	 0.8250
VP	 0.8320
VQ	 0.8320
VR	 0.8250
VS	 0.8170
VT	 0.8250
VU	 0.8170
VV	 0.8180
VW	 0.8170
VX	 0.8340
VY	 0.8420
VZ	 0.8400
W	 0.3910
WA	 0.8060
WB	 0.8150
WC	 0.8150
WD	 0.7960
WE	 0.8110
WF	 0.8150
WG	 0.8300
WH	 0.8020
WI	 0.8160
WJ	 0.8250
WK	 0.8200
WL	 0.8210











































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Chain	Atom inclusion
WM	 0.8090
WN	 0.8150
WO	 0.8250
WP	 0.8050
WQ	 0.8230
WR	 0.8120
WS	 0.8280
WT	 0.7930
WU	 0.8060
WV	 0.8070
WW	 0.8040
WX	 0.8020
X	 0.5930
XA	 0.8640
XB	 0.8590
XC	 0.8310
XD	 0.8770
XE	 0.8530
XF	 0.8650
XG	 0.8870
XH	 0.8670
XI	 0.8870
XJ	 0.8770
XK	 0.8730
XL	 0.8550
XM	 0.8570
Y	 0.4150
YB	 0.8320
YC	 0.7760
YD	 0.8410
YF	 0.8530
YG	 0.8710
YH	 0.8530
YI	 0.8030
YJ	 0.8700
YK	 0.8510
YL	 0.8360
YM	 0.7920
Z	 0.7030
a	 0.3170
a0	 0.7720
a1	 0.4200











































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Chain	Atom inclusion
a2	 0.4160
a3	 0.3730
a4	 0.4840
a5	 0.6920
a6	 0.7270
a7	 0.5510
a8	 0.5480
a9	 0.4120
b	 0.6280
b0	 0.4920
b1	 0.4490
b2	 0.1780
b3	 0.4360
b4	 0.4610
b5	 0.3970
b6	 0.4650
b7	 0.5420
b8	 0.4420
b9	 0.4910
c	 0.6510
c0	 0.1940
c1	 0.5640
c2	 0.5210
c3	 0.6730
c4	 0.6380
c5	 0.6750
c6	 0.7330
d	 0.7400
d0	 0.4040
d1	 0.5460
d2	 0.4240
d3	 0.3150
d4	 0.3550
d5	 0.5650
d6	 0.7660
d7	 0.5850
d8	 0.3070
d9	 0.4260
e	 0.5960
e0	 0.3040
e1	 0.4780
e2	 0.5610











































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Chain	Atom inclusion
e3	 0.3010
e4	 0.1870
e5	 0.5740
e6	 0.5580
e7	 0.3920
e8	 0.4510
e9	 0.3220
f	 0.7190
f1	 0.5200
f2	 0.5120
g	 0.4930
g1	 0.4800
g2	 0.1960
g3	 0.4200
g4	 0.1990
g5	 0.3490
g6	 0.5700
h	 0.6630
h1	 0.6860
h2	 0.6390
h3	 0.6900
h4	 0.6420
i	 0.7060
i1	 0.4590
i2	 0.3890
i3	 0.3190
i4	 0.4810
i5	 0.4930
i6	 0.2530
i7	 0.2490
i8	 0.7120
i9	 0.4860
j	 0.7220
j1	 0.2130
j2	 0.2310
j3	 0.5890
j4	 0.6530
k	 0.8000
k1	 0.8580
k2	 0.9370
k3	 0.9260
k4	 0.8910











































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Chain	Atom inclusion
k5	 0.9340
k8	 0.6790
k9	 0.3900
l	 0.5450
l1	 0.8910
l2	 0.9900
l3	 0.9830
l4	 0.9890
l5	 1.0000
l6	 0.9890
l7	 0.9250
l8	 0.9970
m	 0.6980
m0	 0.4830
m1	 0.8700
m2	 0.8090
m3	 0.0000
m4	 0.9670
m5	 0.8790
m6	 0.4270
m7	 0.5200
m8	 0.4300
m9	 0.6500
n	 0.4580
n0	 0.4650
n1	 0.6220
n2	 0.8590
n3	 0.8050
n4	 0.9080
n5	 0.6080
n6	 0.8880
n7	 0.2630
n8	 0.2440
n9	 0.2400
o	 0.6860
o1	 0.8670
o2	 0.8190
o3	 0.0000
o4	 0.9870
o5	 0.8950
o6	 0.3970
o8	 0.3500

















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Chain	Atom inclusion
p	 0.7240
p0	 0.4700
p1	 0.6500
p2	 0.8330
p3	 0.8690
p4	 0.8940
p5	 0.6580
p6	 0.8910
p7	 0.2810
p8	 0.2660
p9	 0.2420
q	 0.6310
q0	 0.4690
q1	 0.8220
q2	 0.7380
q3	 0.0000
q4	 0.8980
q5	 0.7790
q6	 0.4030
q7	 0.5160
q8	 0.3880
q9	 0.6510
r	 0.6510
r0	 0.4290
r1	 0.5120
r2	 0.8120
r3	 0.6530
r4	 0.8970
r5	 0.5090
r6	 0.7810
r7	 0.2170
r8	 0.1210
r9	 0.2280
s	 0.7530
s0	 0.5000
s1	 0.8420
s2	 0.8780
s6	 0.4440
s7	 0.5350
s8	 0.4370
s9	 0.6750
t	 0.6240

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Chain	Atom inclusion
t0	 0.8400
t9	 0.6980
u	 0.5650
u0	 0.4820
u6	 0.4800
u7	 0.5170
u8	 0.5120
u9	 0.6550
v	 0.6040
v1	 0.0000
v2	 0.0000
v3	 0.0000
w	 0.4010
x	 0.7410
y	 0.5520
z	 0.8360