wwPDB EM Validation Summary Report

Nov 25, 2023 – 10:55 PM EST

PDB ID	:	8G4L
EMDB ID	:	EMD-29722
Title	:	Cryo-EM structure of the human cardiac myosin filament
Authors	:	Dutta, D.; Nguyen, V.; Padron, R.; Craig, R.
Deposited on	:	2023-02-10
Resolution	:	6.40 Å(reported)
Based on initial models	:	., 2FXO, 5N69

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

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

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

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

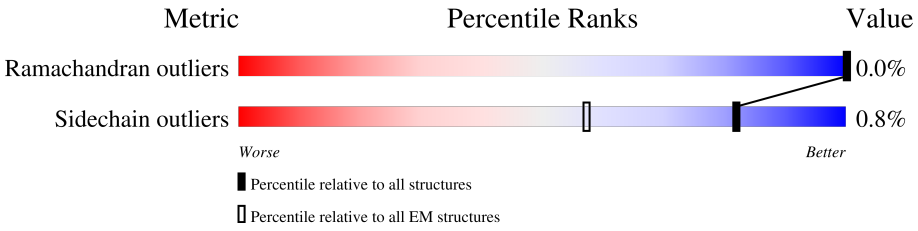
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 6.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	A	1935	41% 58% 41%
1	AA	1935	36% 58% 41%
1	AB	1935	44% 58% 41%
1	AG	1935	18% 82%
1	AH	1935	18% 82%
1	AI	1935	18% 82%
1	AJ	1935	18% 82%
1	AK	1935	18% 82%
1	AL	1935	18% 82%

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Mol	Chain	Length	Quality of chain
1	AM	1935	7% 19% 81%
1	AN	1935	7% 18% 81%
1	AO	1935	18% 81%
1	AP	1935	18% 81%
1	AQ	1935	18% 82%
1	AR	1935	18% 82%
1	AS	1935	6% 19% 81%
1	AT	1935	5% 18% 81%
1	AU	1935	17% 83%
1	AV	1935	17% 83%
1	AW	1935	12% 88%
1	AX	1935	12% 88%
1	AY	1935	6% 51% 48%
1	AZ	1935	51% 48%
1	B	1935	42% 58% 41%
1	BA	1935	43% 58% 41%
1	BB	1935	40% 58% 41%
1	BG	1935	18% 82%
1	BH	1935	18% 82%
1	BI	1935	18% 82%
1	BJ	1935	18% 82%
1	BK	1935	18% 82%
1	BL	1935	18% 82%
1	BM	1935	5% 19% 81%
1	BN	1935	5% 18% 81%

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Mol	Chain	Length	Quality of chain
1	BO	1935	18% 81%
1	BP	1935	18% 81%
1	BQ	1935	18% 82%
1	BR	1935	18% 82%
1	BS	1935	5% 19% 81%
1	BT	1935	18% 81%
1	BU	1935	17% 83%
1	BV	1935	17% 83%
1	BW	1935	11% 88%
1	BX	1935	12% 88%
1	BY	1935	7% 52% 48%
1	BZ	1935	51% 48%
1	G	1935	18% 82%
1	H	1935	18% 82%
1	I	1935	18% 82%
1	J	1935	18% 82%
1	K	1935	18% 82%
1	L	1935	18% 82%
1	M	1935	6% 19% 81%
1	N	1935	7% 18% 81%
1	O	1935	18% 81%
1	P	1935	18% 81%
1	Q	1935	18% 82%
1	R	1935	18% 82%
1	S	1935	7% 19% 81%

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Mol	Chain	Length	Quality of chain
1	T	1935	5% 18% 81%
1	U	1935	17% 83%
1	V	1935	17% 83%
1	W	1935	11% 88%
1	X	1935	12% 88%
1	Y	1935	6% 52% 48%
1	Z	1935	51% 48%
1	ae	1935	8% 47% 53%
1	af	1935	6% 47% 53%
1	ak	1935	7% 93%
1	al	1935	7% 93%
1	be	1935	10% 47% 53%
1	bf	1935	47% 53%
1	bk	1935	7% 93%
1	bl	1935	7% 93%
1	e	1935	9% 47% 53%
1	f	1935	47% 53%
1	k	1935	7% 93%
1	l	1935	7% 93%
2	AE	195	70% 82% 17%
2	AF	195	78% 82% 17%
2	BE	195	79% 82% 17%
2	BF	195	73% 82% 17%
2	E	195	77% 82% 17%
2	F	195	76% 82% 17%

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Mol	Chain	Length	Quality of chain
2	a	195	21% 82% 17%
2	aa	195	22% 82% 17%
2	ab	195	9% 82% 17%
2	ag	195	39% 82% 17%
2	ah	195	5% 82% 17%
2	b	195	9% 82% 17%
2	ba	195	22% 82% 17%
2	bb	195	8% 82% 17%
2	bg	195	26% 82% 17%
2	bh	195	82% 17%
2	g	195	31% 82% 17%
2	h	195	82% 17%
3	ac	166	15% 92% 8%
3	ad	166	13% 100%
3	ai	166	30% 92% 8%
3	aj	166	30% 99%
3	aq	166	90% 100%
3	ar	166	95% 100%
3	bc	166	19% 92% 8%
3	bd	166	16% 100%
3	bi	166	22% 92% 8%
3	bj	166	23% 99%
3	bq	166	89% 100%
3	br	166	88% 100%
3	c	166	19% 92% 8%

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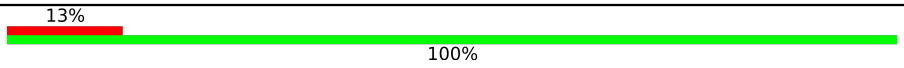
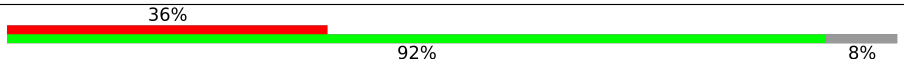
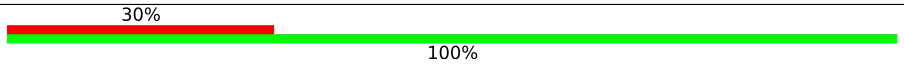
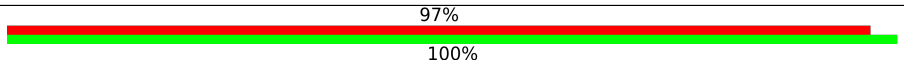
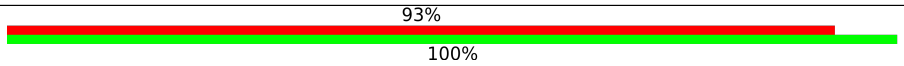
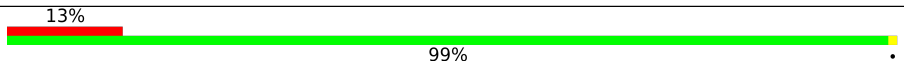
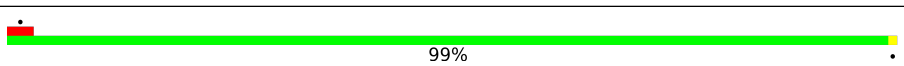
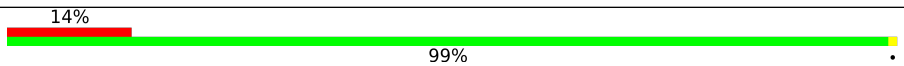
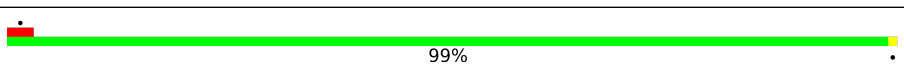
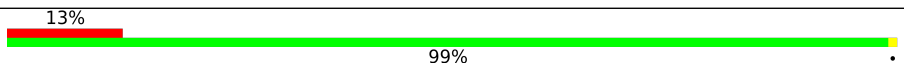
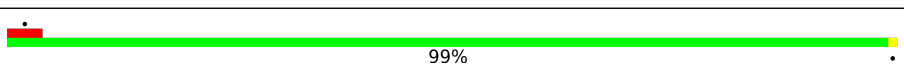
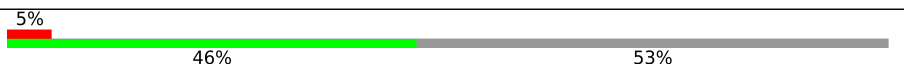
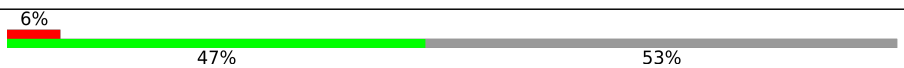
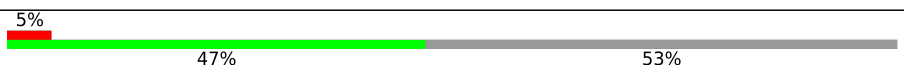
Mol	Chain	Length	Quality of chain
3	d	166	
3	i	166	
3	j	166	
3	q	166	
3	r	166	
4	am	1084	
4	an	1084	
4	bm	1084	
4	bn	1084	
4	m	1084	
4	n	1084	
5	ao	1274	
5	bo	1274	
5	o	1274	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 828952 atoms, of which 415168 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 Myosin-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	BB	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	BA	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	BG	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	BH	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	BI	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	BJ	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	BK	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	BL	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	BM	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	BN	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	BO	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	BP	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	BQ	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	BR	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	BS	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	BT	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	BU	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	BV	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		
1	BW	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	BX	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	BY	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	BZ	1005	Total	C	H	N	O	S	0	0
			16317	5163	8185	1391	1535	43		
1	be	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	bf	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	bk	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	bl	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	AA	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	AB	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	AG	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	AH	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	AI	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	AJ	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	AK	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	AL	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	AM	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	AN	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	AO	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	AP	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	AQ	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	AR	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	AS	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	AT	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	AU	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		
1	AV	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		
1	AW	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	AX	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	AY	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	AZ	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	ae	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	af	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	ak	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	al	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	A	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	B	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	G	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	H	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	I	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	J	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	K	350	Total	C	H	N	O	S	0	0
			5682	1723	2842	521	587	9		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	L	350	Total	C	H	N	O	S	0	0
			5682	1723	2842	521	587	9		
1	M	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	N	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	O	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	P	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	Q	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	R	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	S	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	T	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	U	325	Total	C	H	N	O	S	0	0
			5316	1592	2681	493	540	10		
1	V	325	Total	C	H	N	O	S	0	0
			5316	1592	2681	493	540	10		
1	W	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	X	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	Y	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	Z	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	e	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	f	908	Total	C	H	N	O	S	0	0
			14752	4688	7391	1261	1370	42		
1	k	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	l	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		

- Molecule 2 is a protein called Myosin light chain 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	BE	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	BF	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ba	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	bb	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	bg	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	bh	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	AE	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	AF	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	aa	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ab	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ag	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ah	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	E	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	F	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	a	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	b	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	g	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	h	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		

- Molecule 3 is a protein called Myosin regulatory light chain 2, ventricular/cardiac muscle isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	bc	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
3	bd	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	bi	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	bj	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	bq	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	br	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	ac	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	ad	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	ai	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	aj	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	aq	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	ar	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	c	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	d	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	i	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	j	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	q	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	r	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		

- Molecule 4 is a protein called Titin.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	bm	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	bn	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		

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Mol	Chain	Residues	Atoms						AltConf	Trace
4	am	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	an	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	m	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	n	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		

- Molecule 5 is a protein called Myosin-binding protein C, cardiac-type.

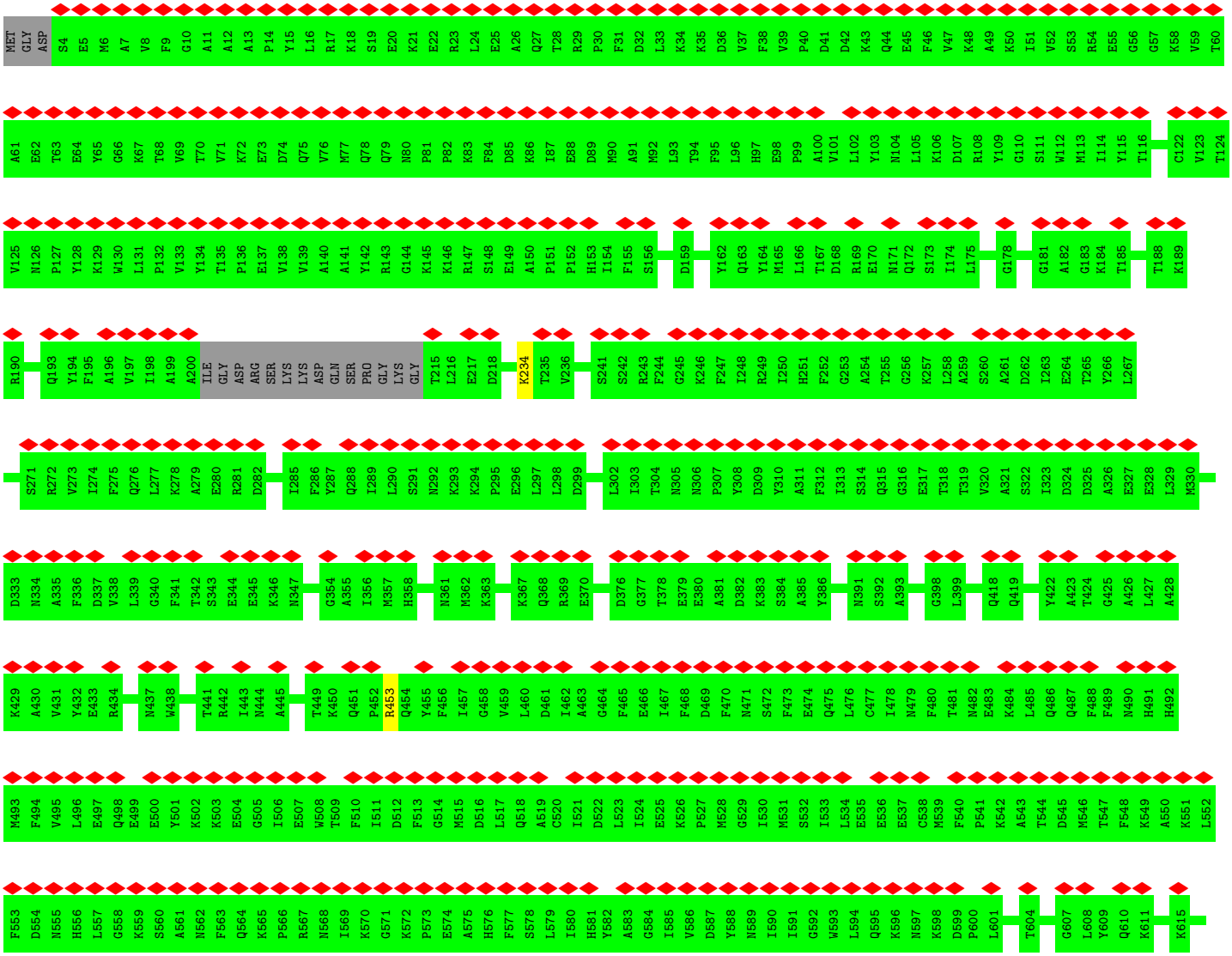
Mol	Chain	Residues	Atoms						AltConf	Trace
5	bo	598	Total	C	H	N	O	S	0	0
			9440	2992	4728	825	873	22		
5	ao	598	Total	C	H	N	O	S	0	0
			9440	2992	4728	825	873	22		
5	o	598	Total	C	H	N	O	S	0	0
			9440	2992	4728	825	873	22		

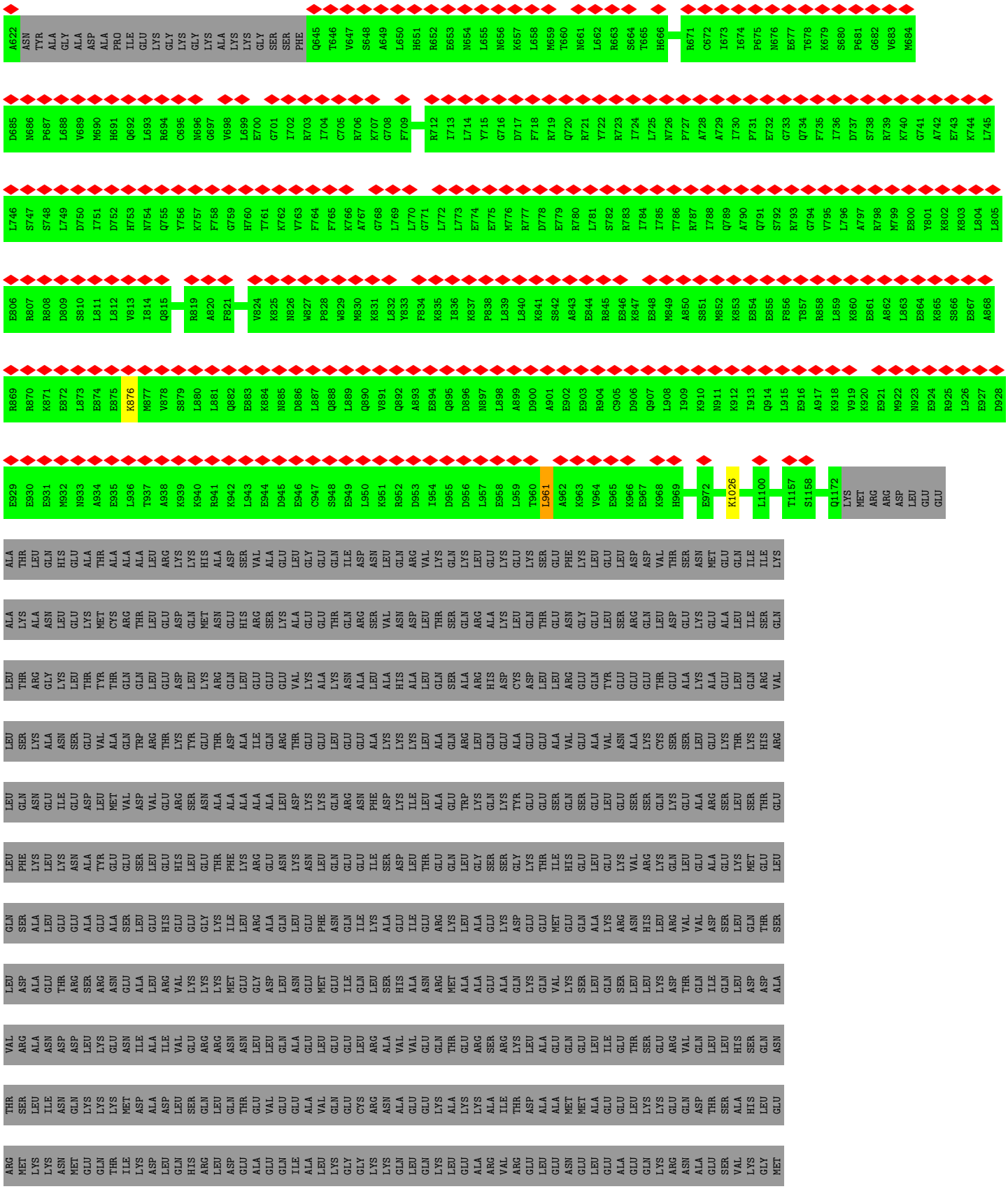
3 Residue-property plots (i)

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: Myosin-7

Chain BB:

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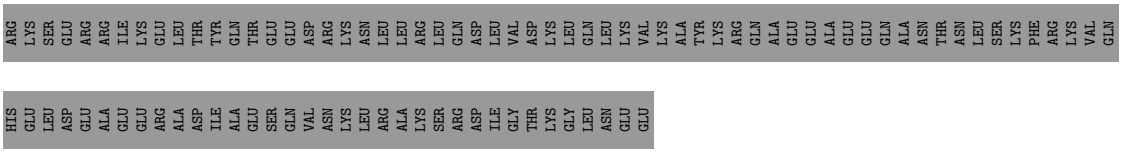
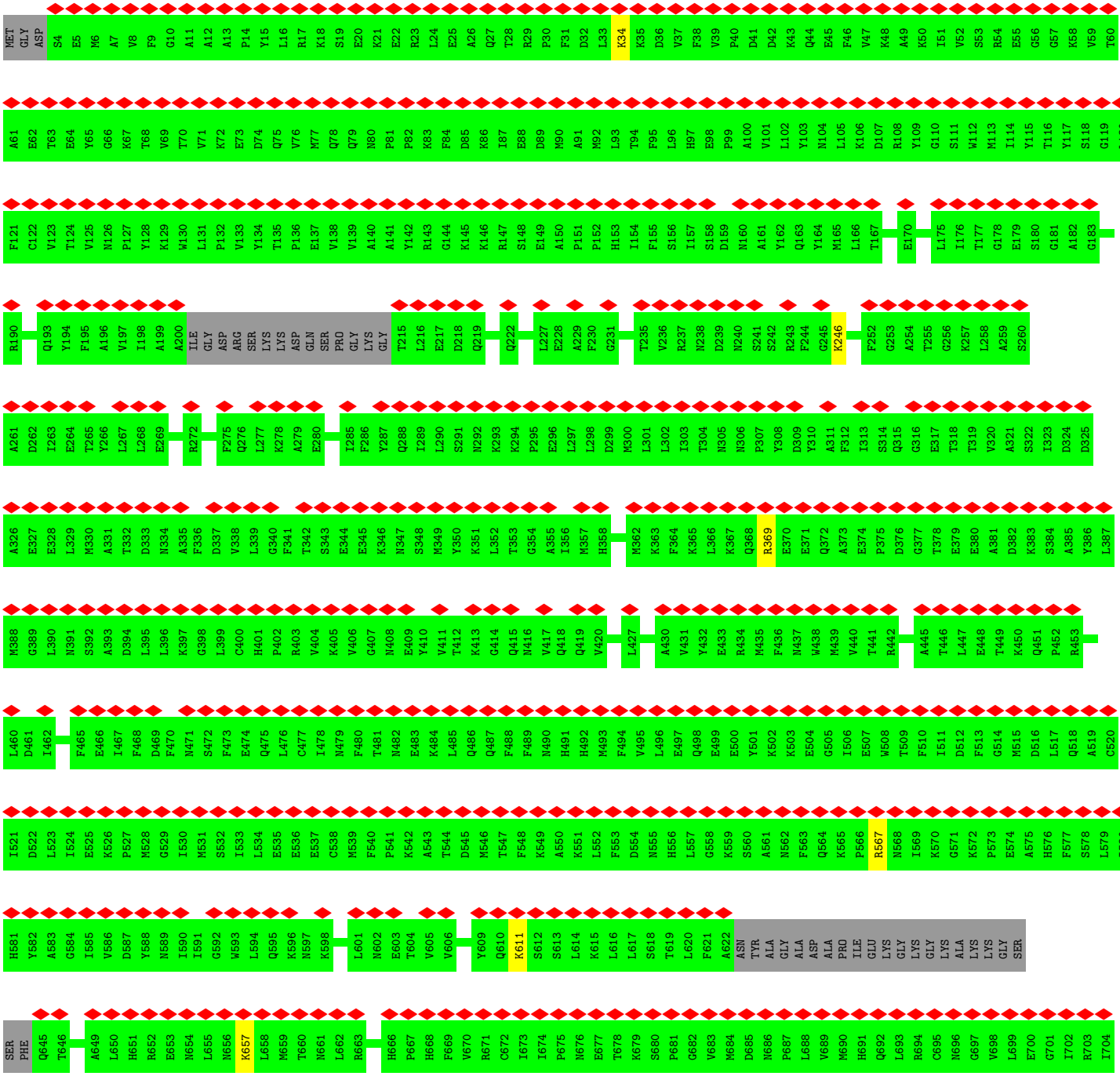
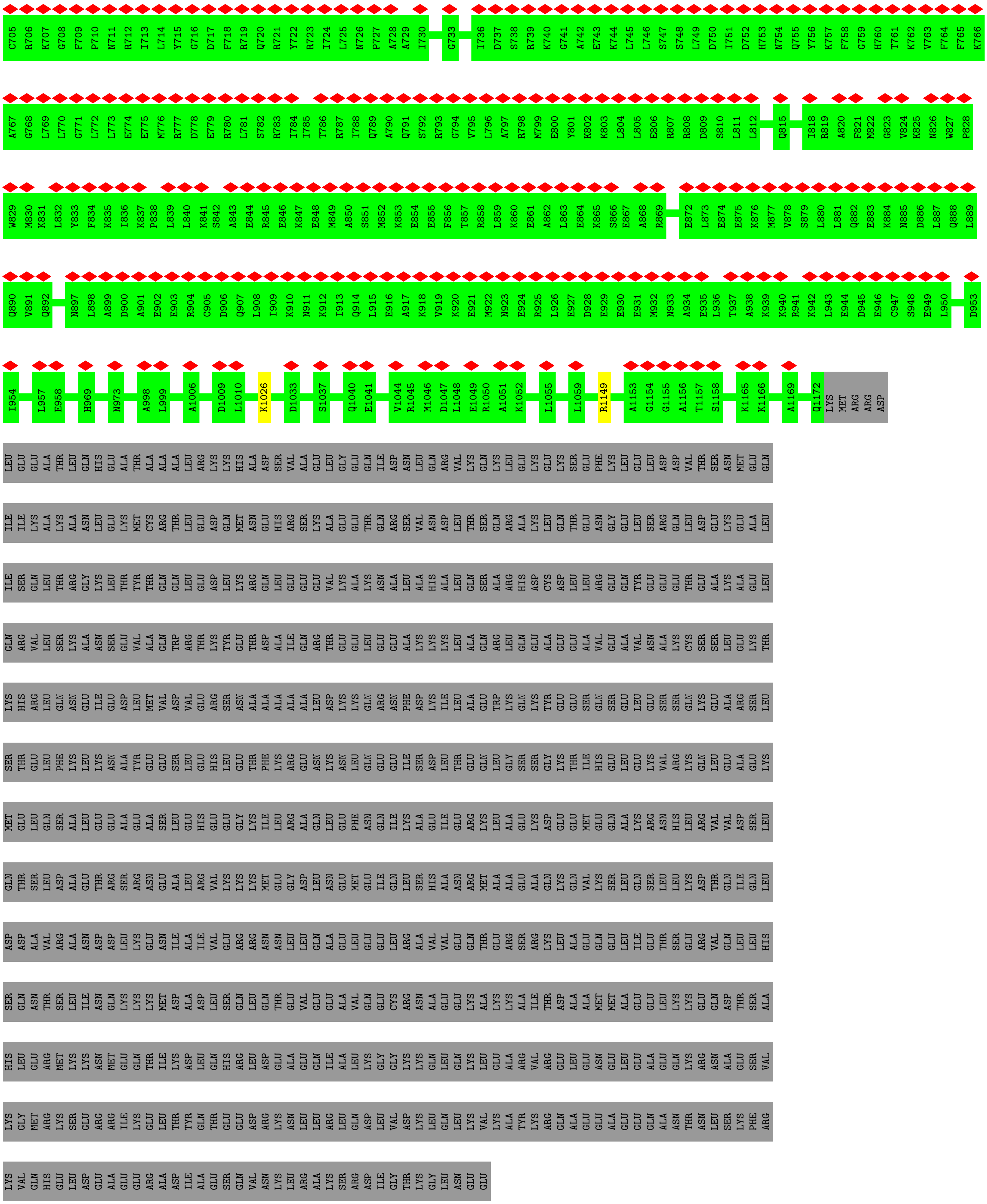
Q645 T646 V647 S648 A649 L650 H651 R652 E653 N654 L655 N656 K657 L658 M659 T660 N661 L662 R663 S664 T665 H666
R671 C672 I673 I674 P675 N676 E677 T678 K679 S680 P681 G682 V683 M684
D685 N686 P687 L688 V689 M690 H691 Q692 L693 R694 C695 N696 G697 V698 L699 E700 G701 T702 R703 I704 C705 R706 K707 G708 F709
R712 I713 L714 Y715 G716 D717 F718 R719 Q720 R721 Y722 R723 I724 L725 N726 P727 A728 A729 I730 P731 E732 G733 Q734 F735 I736 D737 S738 R739 K740 G741 A742 E743 K744 L745
L746 S747 S748 L749 D750 I751 D752 H753 N754 Q755 Y756 K757 F758 G759 H760 T761 K762 V763 F764 F765 K766 A767 G768 L769 L770 G771 L772 L773 E774 E775 M776 R777 D778 E779 R780 L781 S782 R783 I784 I785 T786 R787 I788 Q789 A790 Q791 S792 R793 G794 V795 L796 A797 R798 M799 E800 Y801 K802 K803 L804 L805
E806 R807 R808 D809 S810 L811 L812 V813 I814 Q815
R819 A820 F821
V824 K825 N826 W827 P828 W829 M830 K831 L832 Y833 F834 K835 I836 K837 P838 L839 L840 K841 S842 A843 E844 R845 E846 K847 E848 M849 A850 S851 M852 K853 E854 E855 F856 T857 R858 L859 K860 E861 A862 L863 E864 K865 S866 E867 A868
R869 R870 K871 E872 L873 E874 E875
K876
M877 V878 S879 L880 L881 Q882 E883 K884 N885 D886 L887 Q888 L889 Q890 V891 Q892 A893 E894 Q895 D896 N897 L898 A899 D900 A901 E902 E903 R904 C905 D906 Q907 L908 I909 K910 N911 K912 I913 Q914 L915 E916 A917 K918 V919 K920 E921 M922 N923 E924 R925 L926 E927 D928
E929 E930 E931 M932 N933 A934 E935 L936 T937 A938 K939 K940 R941 K942 L943 E944 D945 E946 C947 S948 E949 L950 K951 R952 D953 I954 D955 D956 L957 E958 L959 T960
L961
A962 K963 V964 E965 K966 E967 K968 H969
E972
K1026
L1100
T1157 S1158
Q1172
LYS MET ARG ARG ASP LEU GLU GLU
ALA THR LEU GLN HIS GLU ALA THR ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU GLU GLU ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS
ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN
LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU ARG GLU GLN LEU GLU GLU THR GLN ARG VAL
LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LYS LEU ALA GLN ARG LEU GLN GLU ALA GLU GLU ALA VAL GLU ALA VAL ASN ALA LYS CYS SER SER LEU GLU LYS THR LYS HIS ARG
LEU GLN ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG SER ASN ALA ALA ALA ALA ALA LEU ASP LYS LYS GLU ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU
LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER THR PHE LYS ARG GLU ASN LYS ASN LEU GLN GLU GLU ILE SER ASP LEU THR GLU GLN LEU GLY SER SER SER GLY LYS THR ILE HIS GLU LEU GLU GLU LYS VAL ARG LYS GLN LEU GLU LEU ALA GLU LYS MET GLU GLU
GLN SER ALA LEU GLU GLU ALA SER LEU GLU HIS GLU LEU GLU GLY LYS ILE LEU ARG ALA GLN LEU GLU PHE ASN GLN ILE ILE LYS ALA GLU ILE LEU ARG GLU ILE GLU ARG LYS LEU ALA GLU LYS ASP GLU GLU MET GLU GLN ALA LYS ARG ASN HIS LEU ARG VAL VAL ASP SER LEU GLN THR SER
LEU ASP ALA GLU THR ARG SER ARG ASN GLU ALA LEU ARG VAL LYS LYS MET GLU GLY ASP LEU ASN GLU MET GLU ILE GLN LEU SER HIS ALA ASN ARG MET ALA ALA GLU ALA GLN LYS GLN VAL LYS SER LEU GLN SER LEU LEU LYS ASP THR GLN ILE GLN LEU ASP ALA
VAL ARG ALA ASN ASP ASP LEU LYS GLU ASN ILE ALA VAL VAL GLU GLN THR GLU ARG SER ARG LYS LEU ALA GLU GLN GLU LEU ILE GLU THR SER GLU ARG VAL GLN LEU LEU HIS SER GLN ASN
THR SER LEU ILE ASN GLN LYS LYS LYS MET ASP ALA ASP LEU SER GLN LEU CLN THR GLU VAL GLU GLU ALA VAL GLN GLU CYS ARG ASN ALA GLU GLN GLU LYS ALA LYS LYS ALA ILE THR ASP ALA ALA MET MET ALA GLU GLU GLU LEU LYS LYS GLU GLN LYS LEU GLU
ARG MET LYS LYS ASN MET GLU GLN LYS LYS LYS GLN LEU GLN LEU LYS LEU GLU GLU ALA ARG VAL ARG GLU LEU GLU ASN GLU LEU GLU GLU ALA GLU GLN LYS ARG ASN ALA GLU SER VAL LYS GLY MET



• Molecule 1: Myosin-7

Chain BA:

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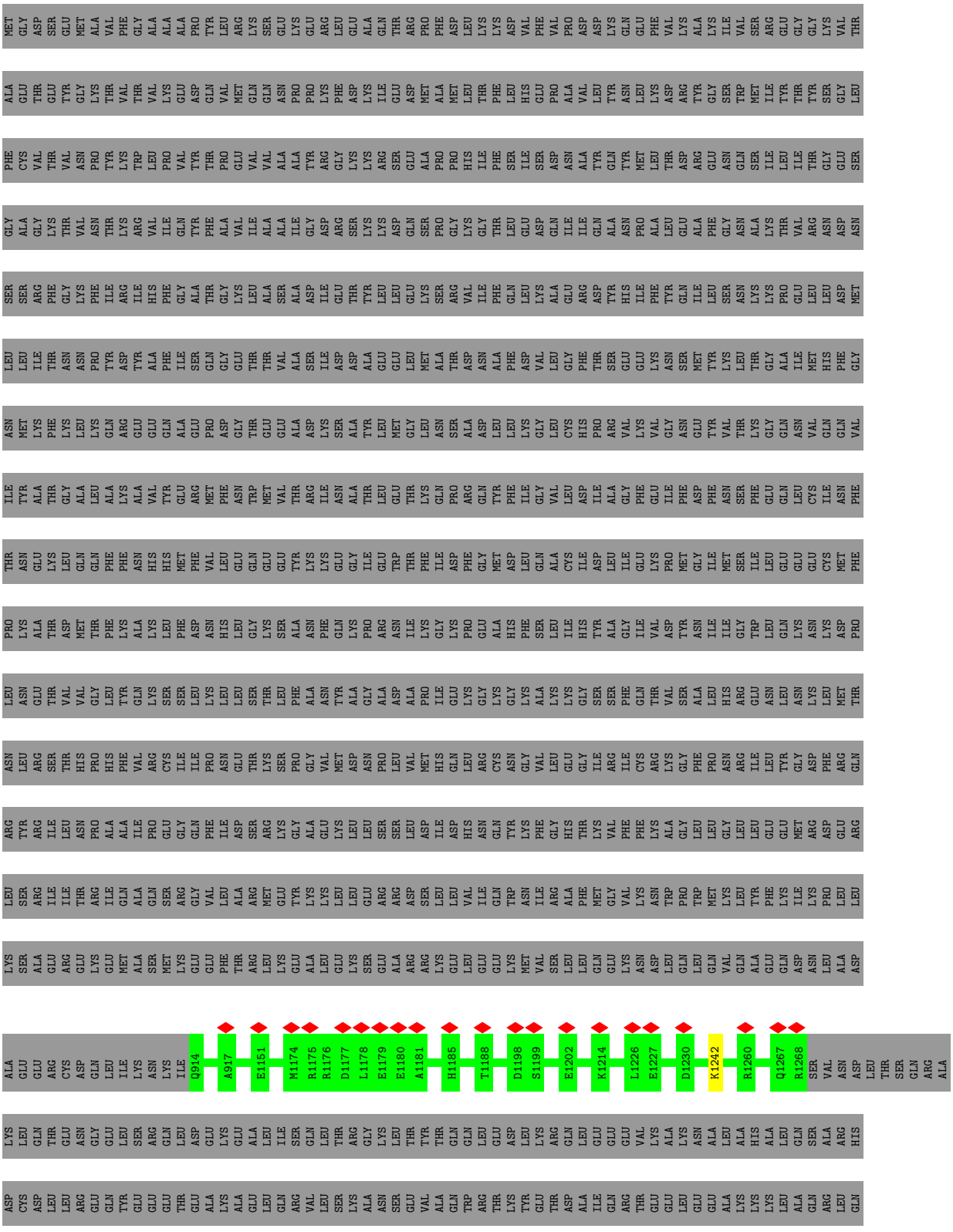
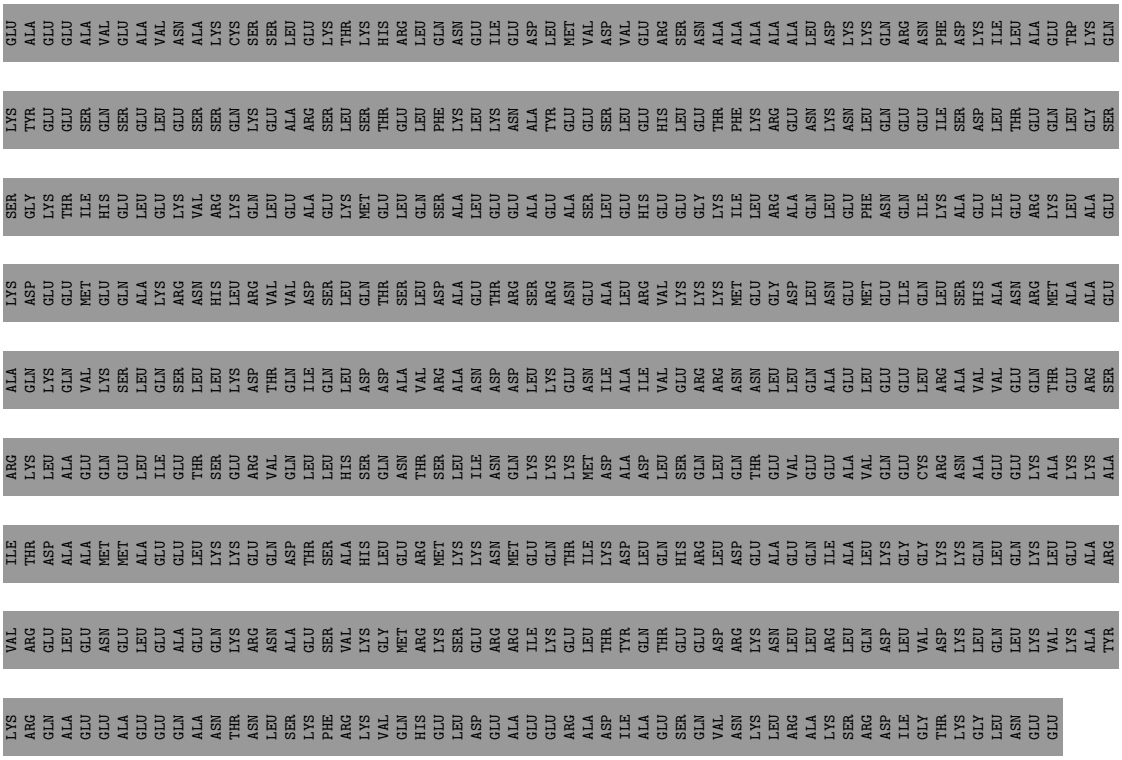
A767 G768 L769 L770 G771 L772 L773 E774 E775 M776 R777 D778 E779 R780 L781 S782 R783 I784 I785 T786 R787 I788 Q789 A790 Q791 S792 R793 G794 V795 L796 A797 R798 M799 E800 Y801 K802 K803 L804 L805 E806 R807 R808 D809 S810 L811 L812 Q815 I818 R819 A820 F821 M822 G823 V824 K825 N826 W827 P828
W829 M830 K831 L832 Y833 F834 K835 I836 K837 P838 L839 L840 K841 S842 A843 E844 R845 E846 K847 E848 M849 A850 S851 M852 K853 E854 E855 F856 T857 R858 L859 K860 E861 A862 L863 E864 K865 S866 E867 A868 R869 E872 L873 E874 E875 K876 M877 V878 S879 L880 L881 Q882 E883 K884 N885 D886 L887 Q888 L889
Q890 V891 Q892 N897 L898 A899 D900 A901 E902 E903 R904 C905 D906 Q907 L908 I909 K910 N911 K912 I913 Q914 L915 E916 A917 K918 V919 K920 E921 M922 N923 E924 R925 L926 E927 D928 E929 E930 E931 M932 N933 A934 E935 L936 T937 A938 K939 K940 R941 K942 L943 E944 D945 E946 C947 S948 E949 L950 D953
I954 L957 E958 H969 N973 A998 L999 A1006 D1009 L1010 K1026 D1033 S1037 Q1040 E1041 V1044 R1045 M1046 D1047 L1048 E1049 R1050 A1051 K1052 L1055 L1059 R1149 A1153 G1154 G1155 A1156 T1157 S1158 K1165 K1166 A1169 Q1172 LYS MET ARG ARG ASP
LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU GLU LEU ASP ASP VAL THR SER ASN MET GLU GLN
ILE ILE LYS ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU
ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU ARG GLU GLN TYR GLU GLU GLU THR GLU ALA LYS ALA GLU LEU
GLN ARG VAL LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LYS LEU ALA GLN ARG LEU GLN GLU ALA GLU GLU ALA VAL GLU ALA VAL ASN ALA LYS CYS SER SER LEU GLU LYS THR
LYS HIS ARG LEU GLN ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG SER ASN ALA ALA ALA ALA ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU
SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG GLU ASN LYS ASN LEU GLN GLU GLU ILE SER ASP LEU THR GLU GLN LEU GLY SER SER GLY LYS THR ILE HIS GLU LEU GLU LYS VAL ARG LYS GLN LEU GLU ALA GLU LYS
MET GLU LEU GLN SER ALA LEU GLU GLU ALA GLU ALA SER LEU GLU HIS GLU GLU GLY LYS ILE LEU ARG ALA GLN LEU GLU PHE ASN GLN ILE LYS ALA GLU ILE GLU ARG LYS LEU ALA GLU LYS ASP GLU GLU MET GLU GLN ALA LYS ARG ASN HIS LEU ARG VAL VAL ASP SER LEU
GLN THR SER LEU ASP ALA GLU THR ARG SER ARG ASN GLU ALA LEU ARG VAL LYS LYS MET GLU GLY ASP LEU ASN GLU MET GLU ILE GLN LEU SER HIS ALA ASN ARG MET ALA ALA GLU ALA GLN LYS GLN VAL LYS SER LEU GLN SER LEU LEU LYS ASP THR GLN ILE GLN LEU
ASP ASP ALA VAL ARG ALA ASN ASP ASP LEU LYS GLU ASN ILE ALA ILE VAL GLU ARG ARG ASN ASN LEU LEU GLN ALA GLU LEU GLU GLU LEU ARG ALA VAL VAL GLU GLN THR GLU ARG SER ARG LYS LEU ALA GLU GLN GLU LEU ILE GLU THR SER GLU ARG VAL GLN LEU LEU HIS
SER GLN ASN THR SER LEU ILE ASN GLN LYS LYS LYS MET ASP ALA ASP LEU SER GLN LEU GLN THR GLU VAL GLU GLU ALA VAL GLN GLU CYS ARG ASN ALA GLU GLU LYS ALA LYS LYS ALA ILE THR ASP ALA ALA MET MET ALA GLU GLU LEU LYS LYS GLU GLN ASP THR SER ALA
HIS LEU GLU ARG MET LYS LYS ASN MET GLU GLN THR ILE LYS ASP LEU GLN HIS ARG LEU ASP GLU ALA GLU GLN ILE ALA LEU LYS GLY GLY LYS LYS GLN LEU GLN LYS LEU GLU ALA ARG VAL ARG GLU LEU GLU ASN GLU LEU GLU ALA GLU GLN LYS ARG ASN ALA GLU SER VAL
LYS GLY MET ARG LYS SER GLU ARG ARG ILE LYS GLU LEU THR TYR GLN THR GLU GLU ASP ARG LYS ASN LEU LEU ARG LEU GLN ASP LEU VAL ASP LYS LEU GLN LEU LYS VAL LYS ALA TYR LYS ARG GLN ALA GLU GLU ALA GLU GLU GLN ALA ASN THR ASN LEU SER LYS PHE ARG
LYS VAL GLN HIS GLU LEU ASP GLU ALA GLU GLU ARG ALA ASP ILE ALA GLU SER GLN VAL ASN LYS LEU ARG ALA LYS SER ARG ASP ILE GLY THR LYS GLY LEU ASN GLU GLU

• Molecule 1: Myosin-7

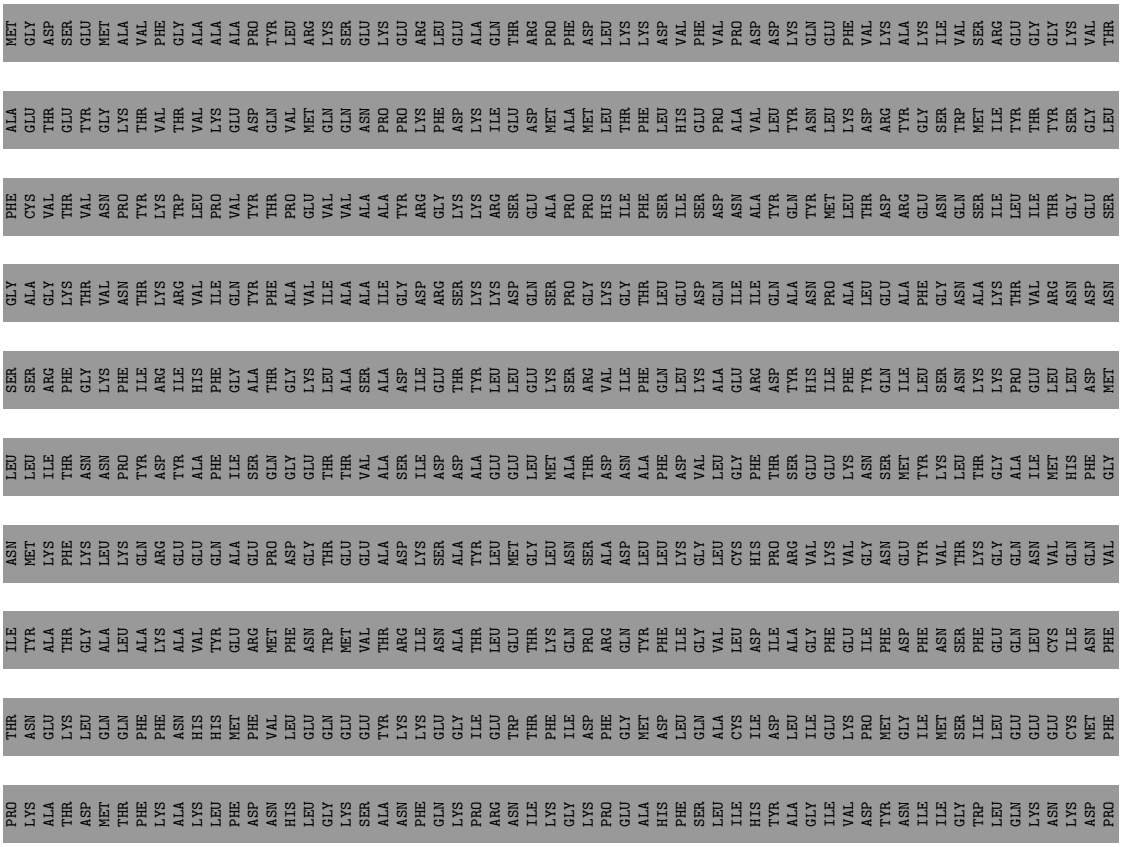
Chain BG:

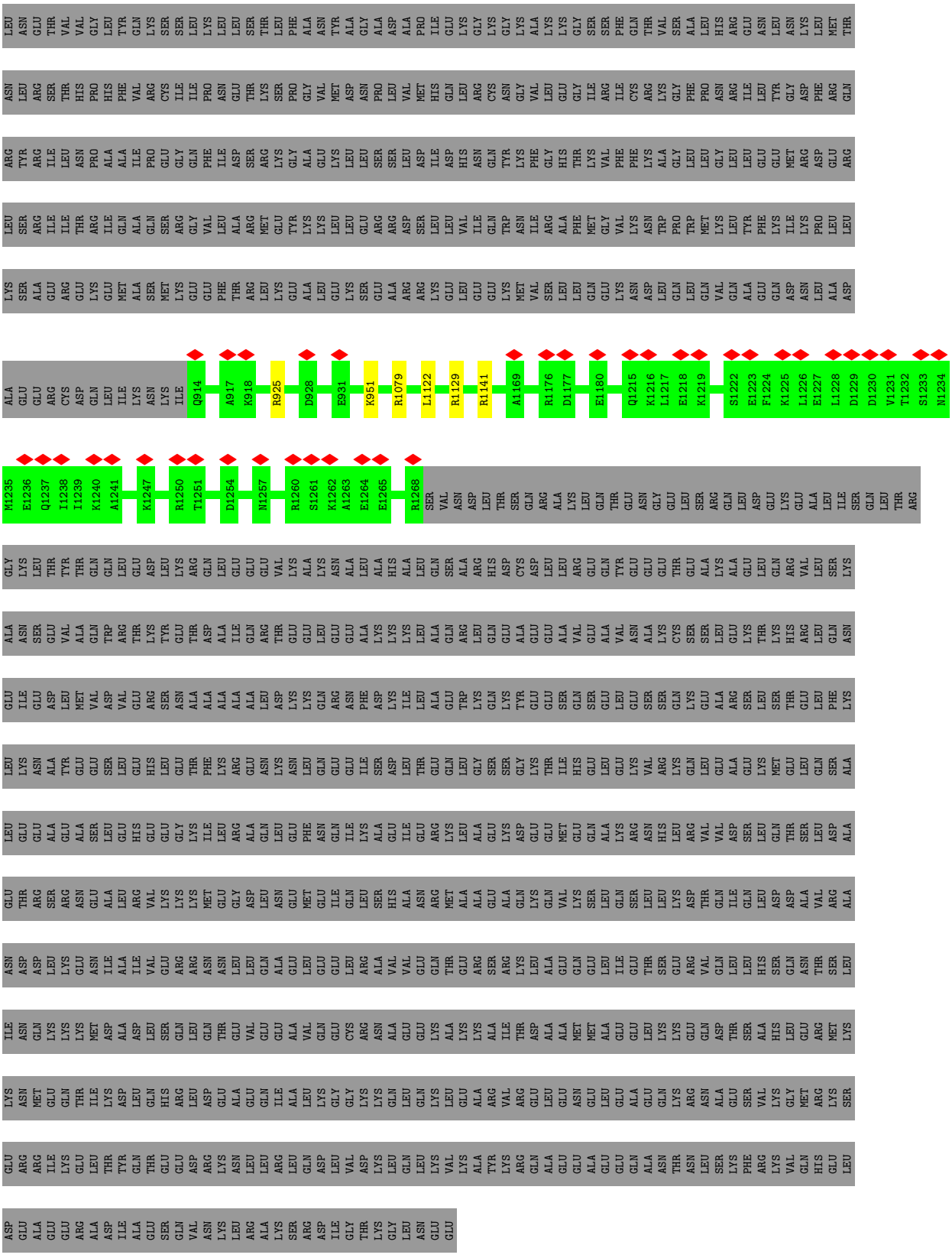




• Molecule 1: Myosin-7

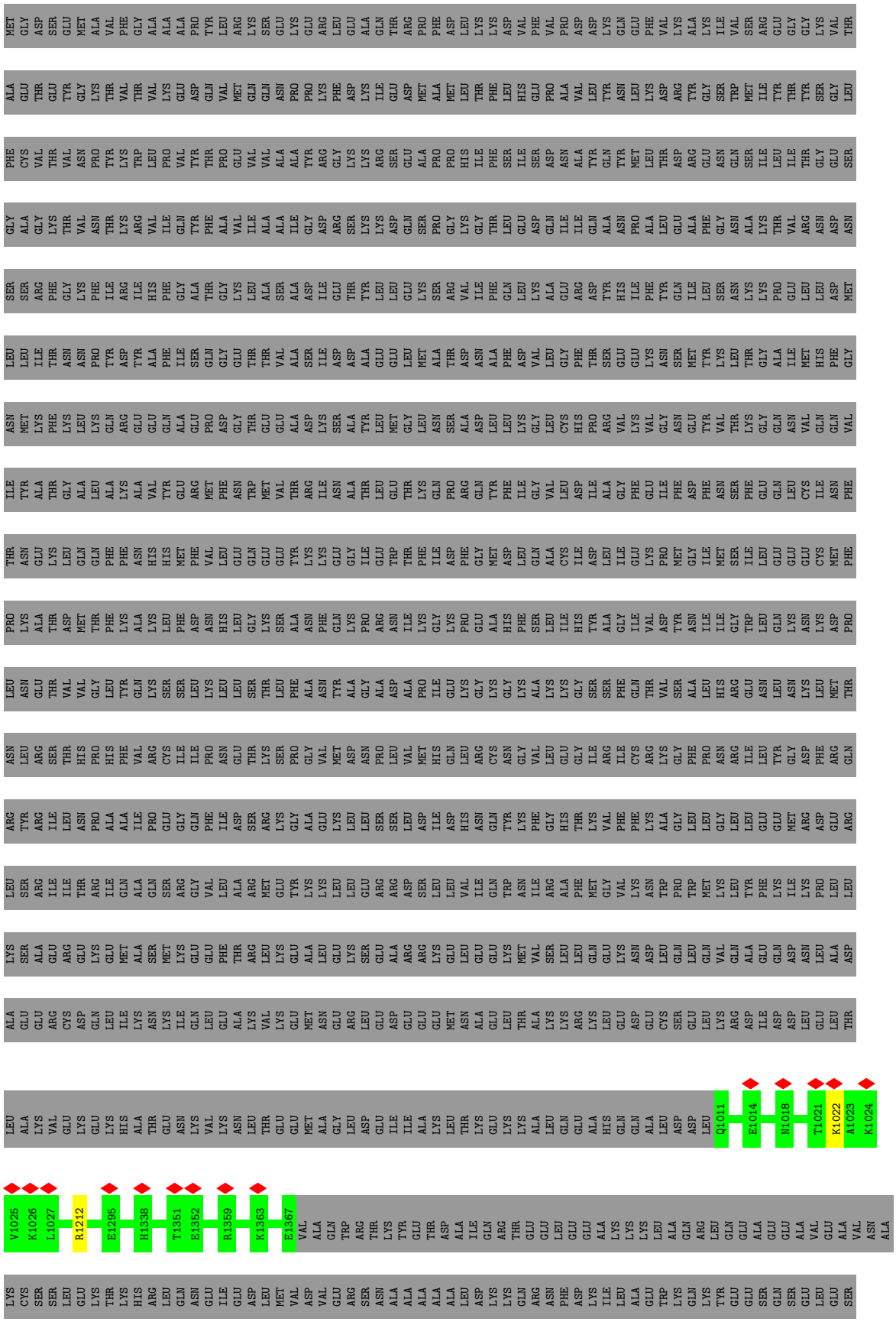
Chain BH:





• Molecule 1: Myosin-7

Chain BI: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E1014
N1018
T1021
K1022
A1023
K1024
V1025
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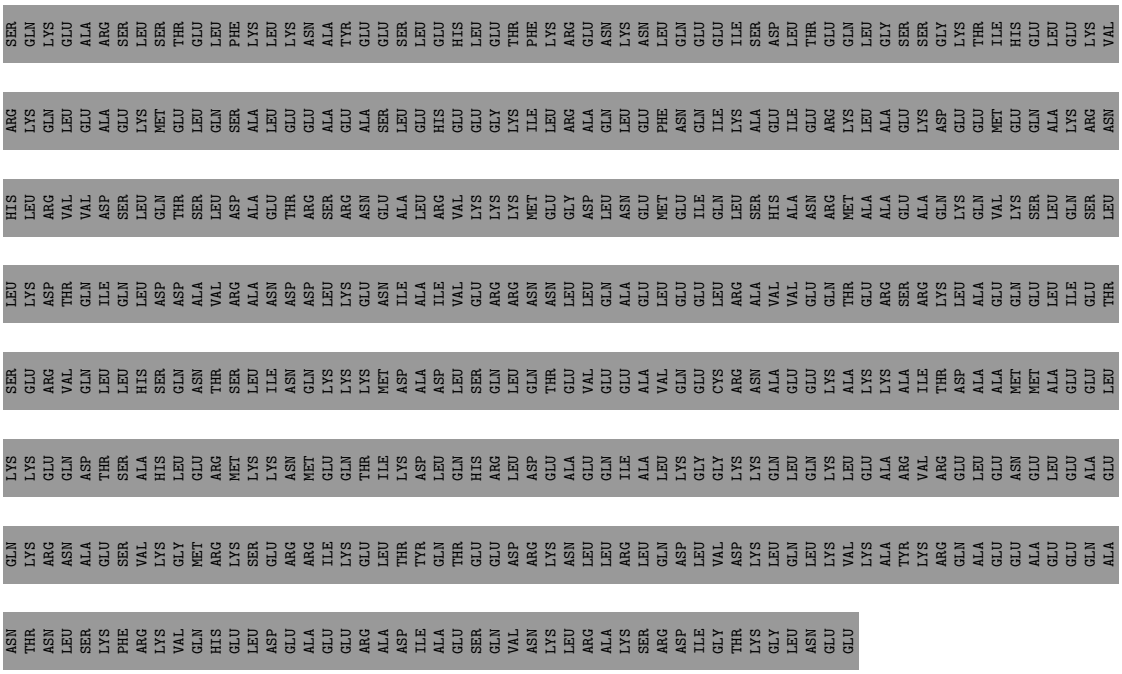
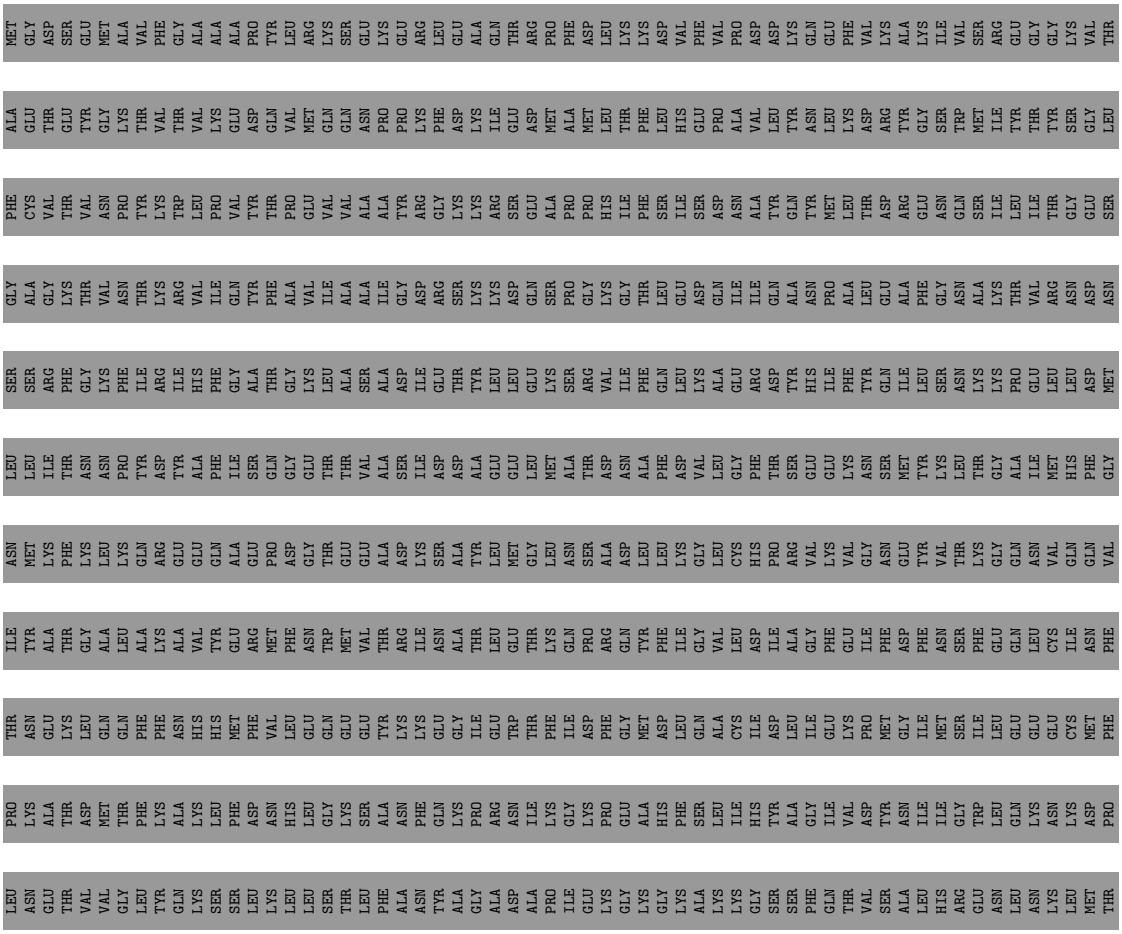
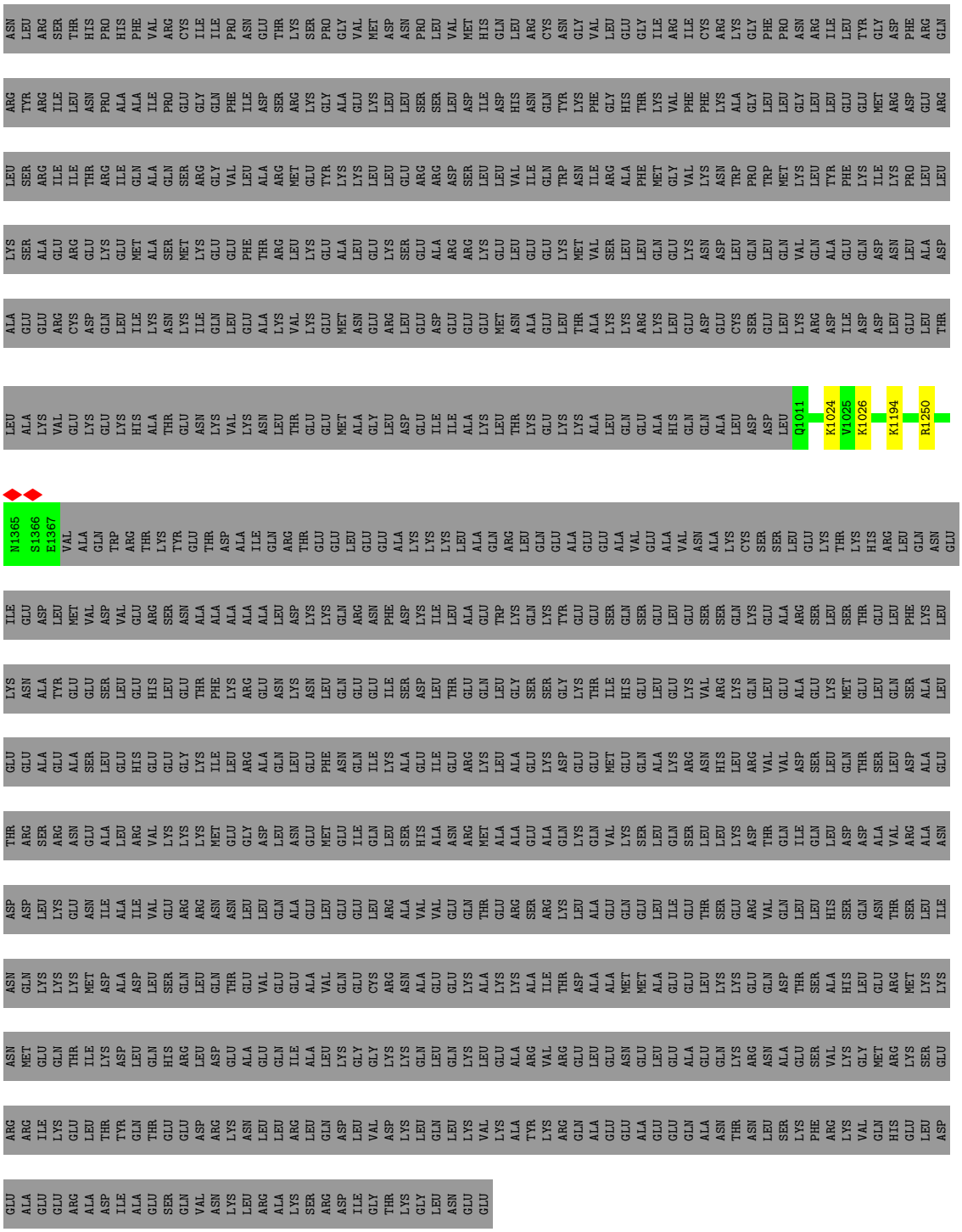
K1363
E1367



• Molecule 1: Myosin-7

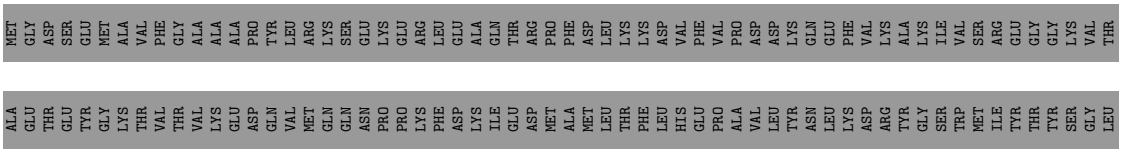
Chain BJ: 18% 82%

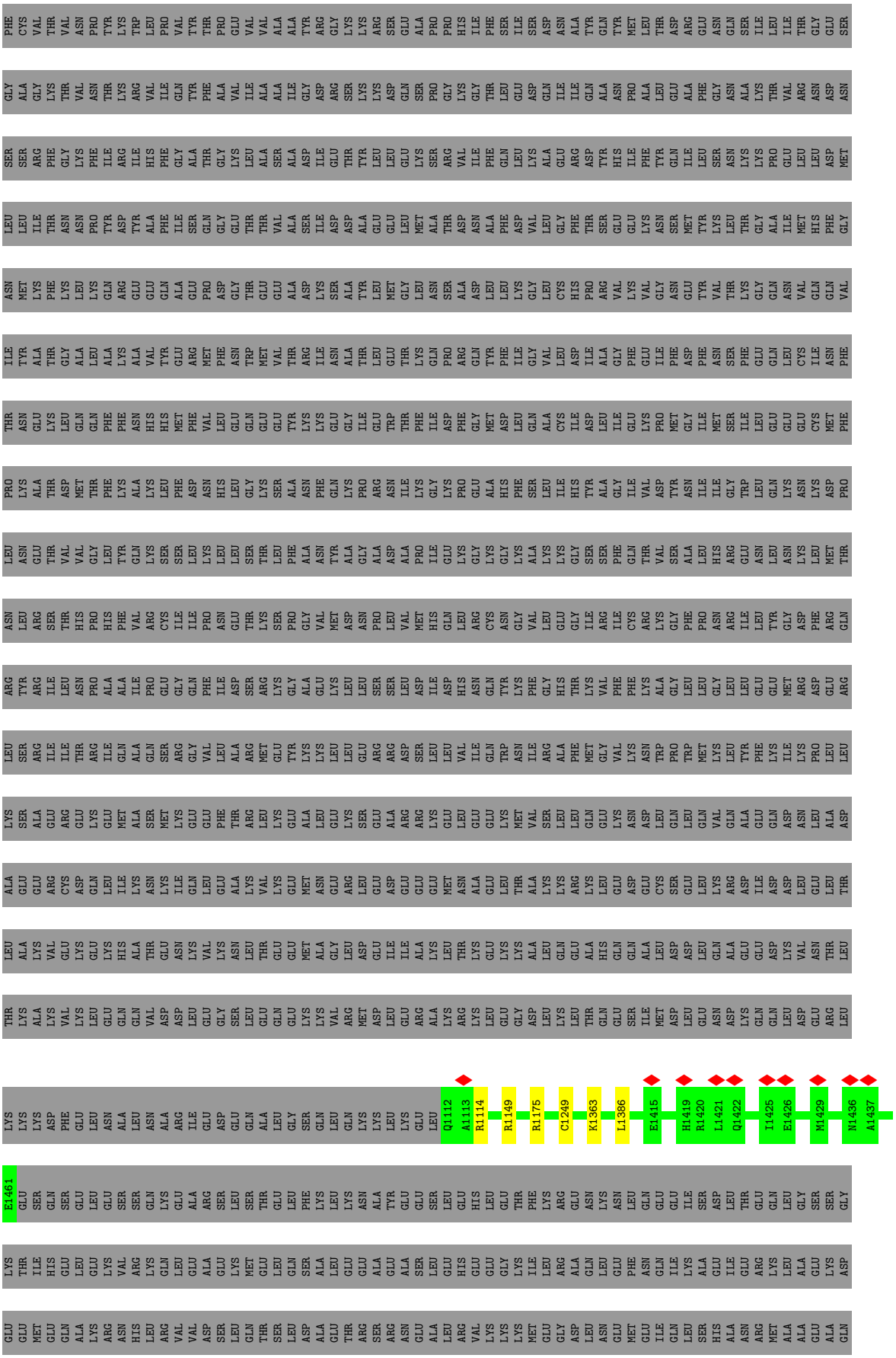




• Molecule 1: Myosin-7

Chain BK:

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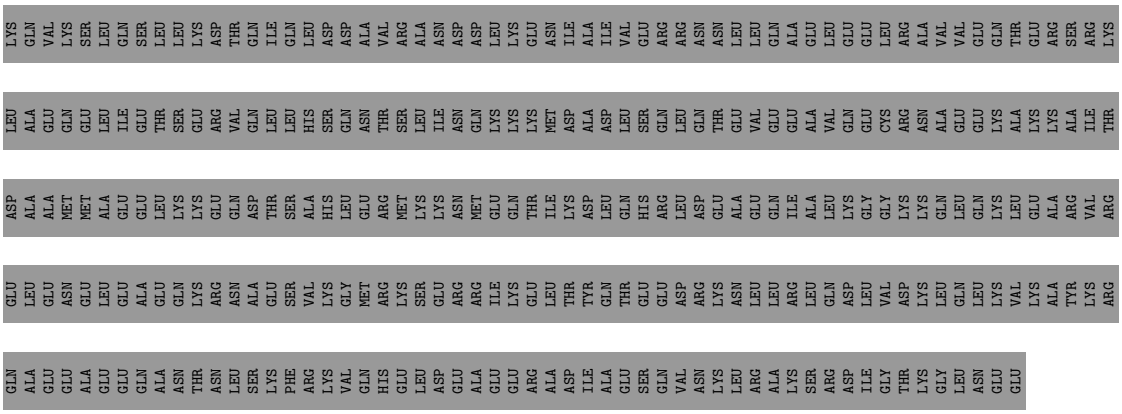
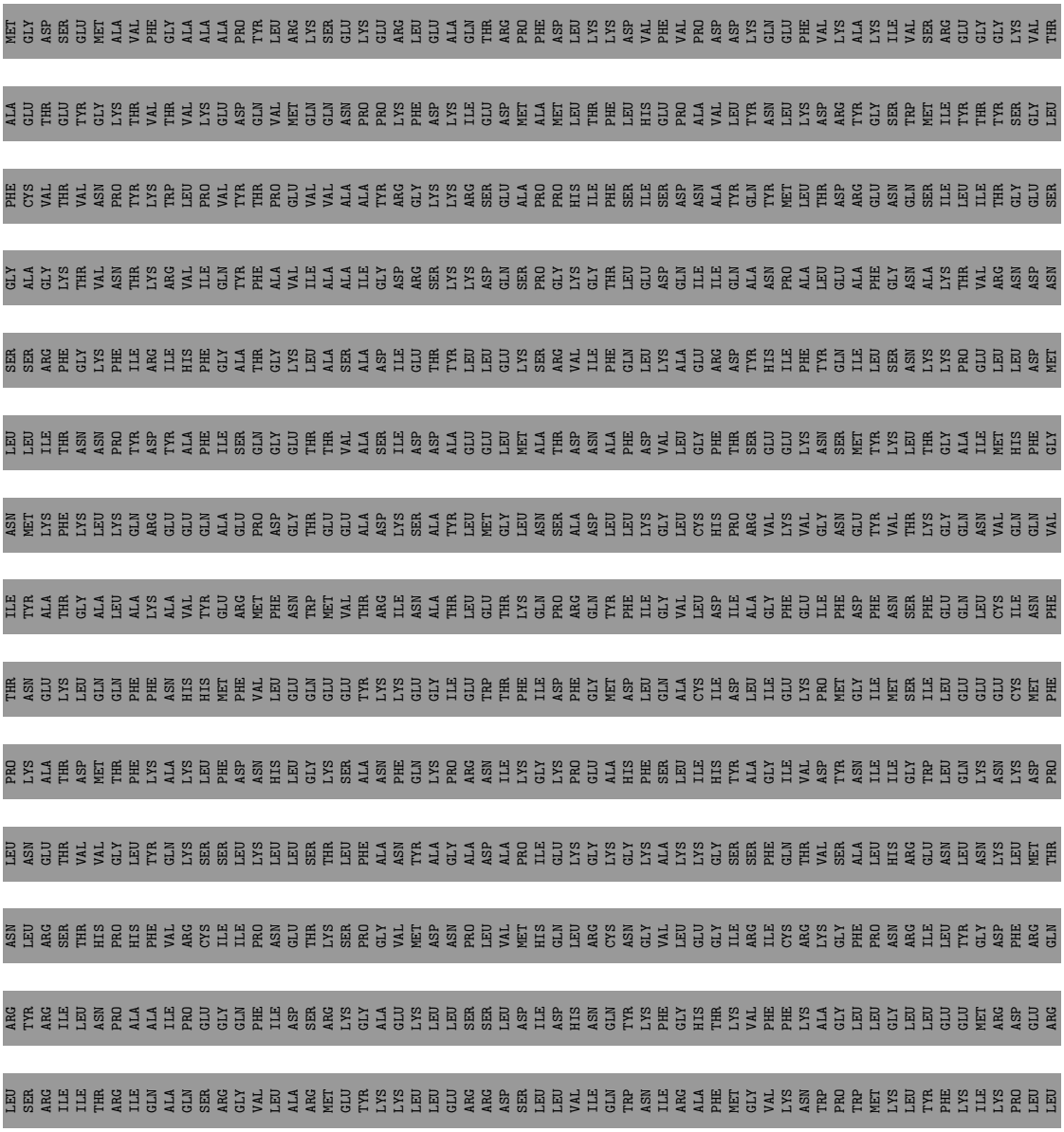
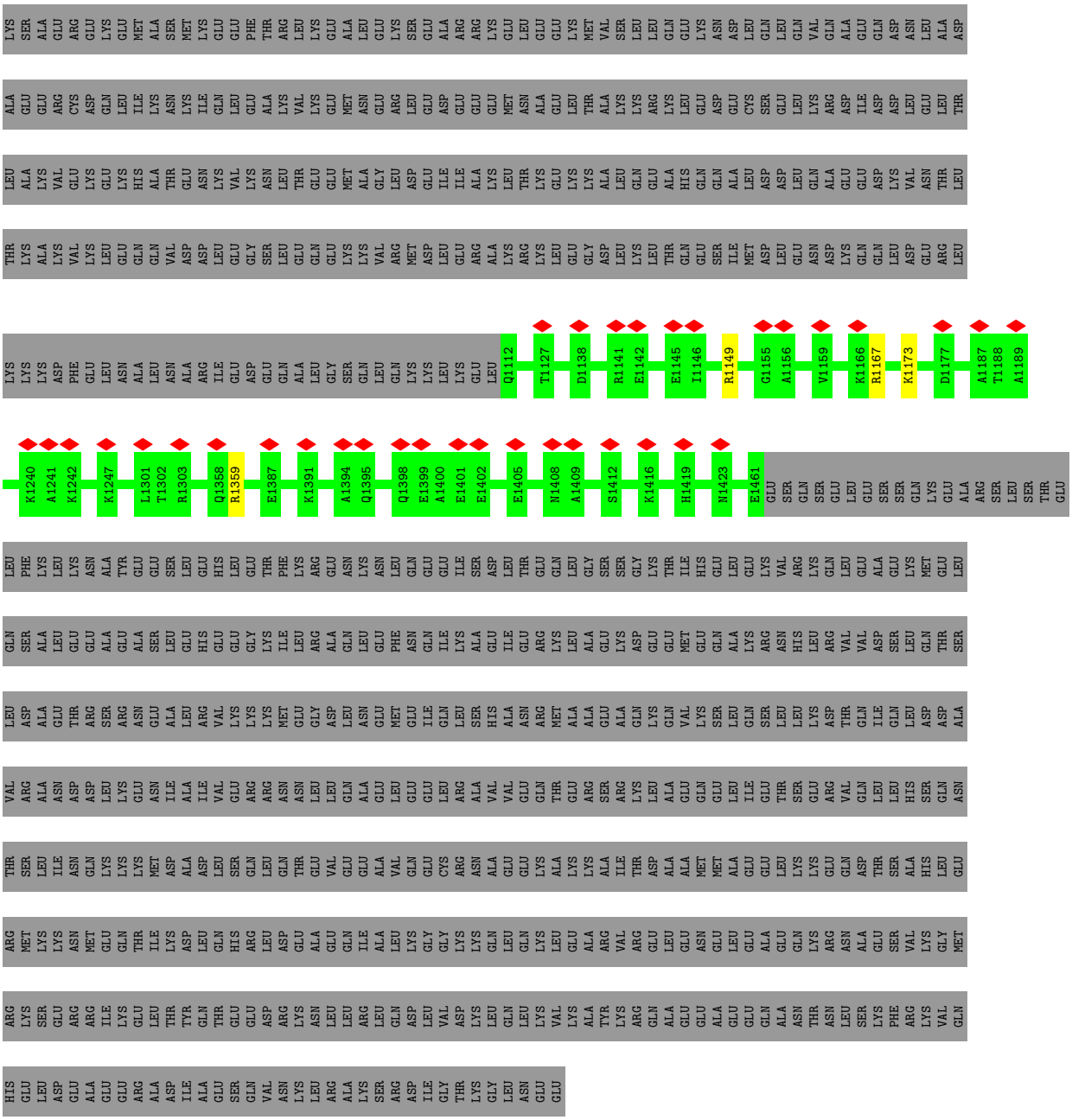


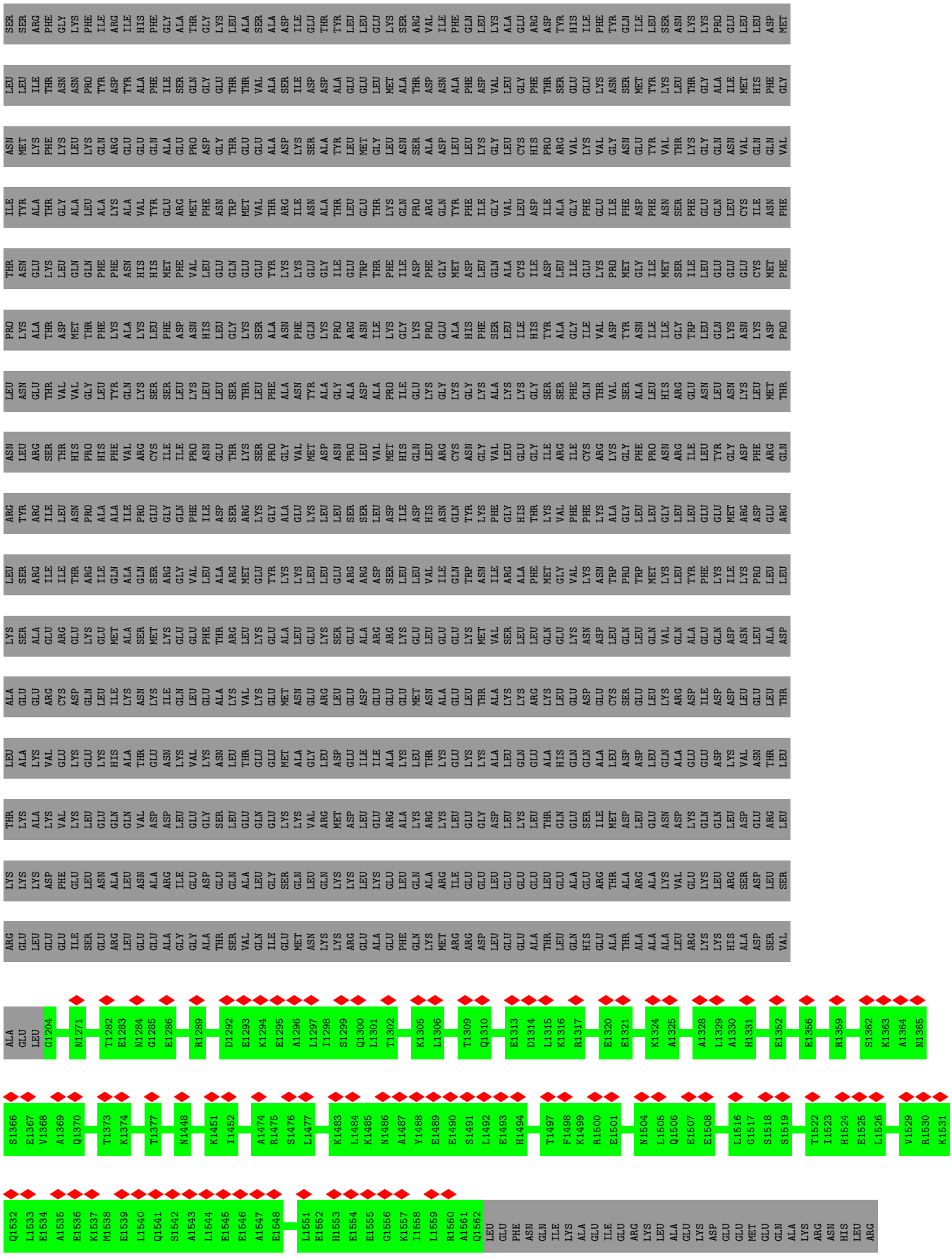
• Molecule 1: Myosin-7

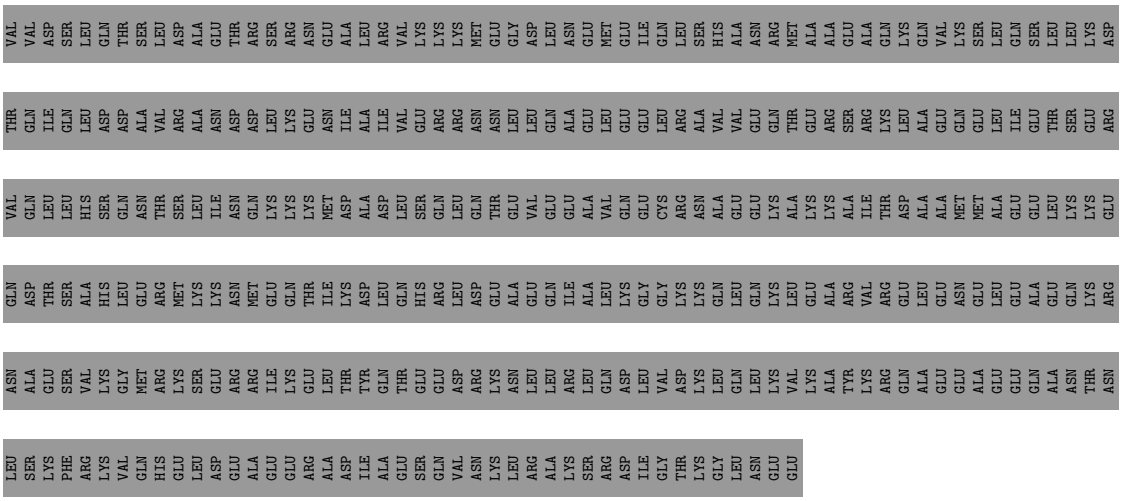
Chain BL:



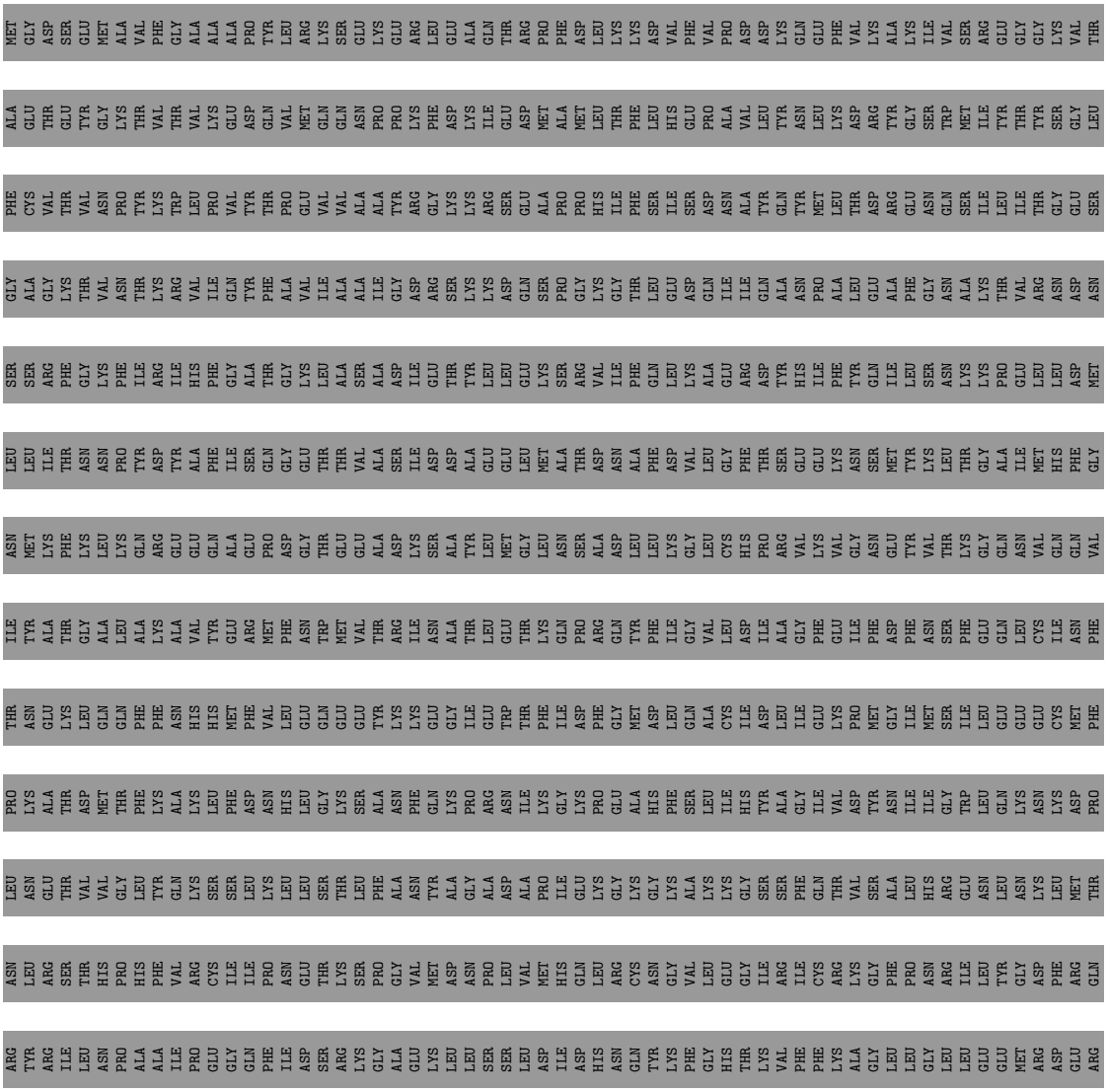


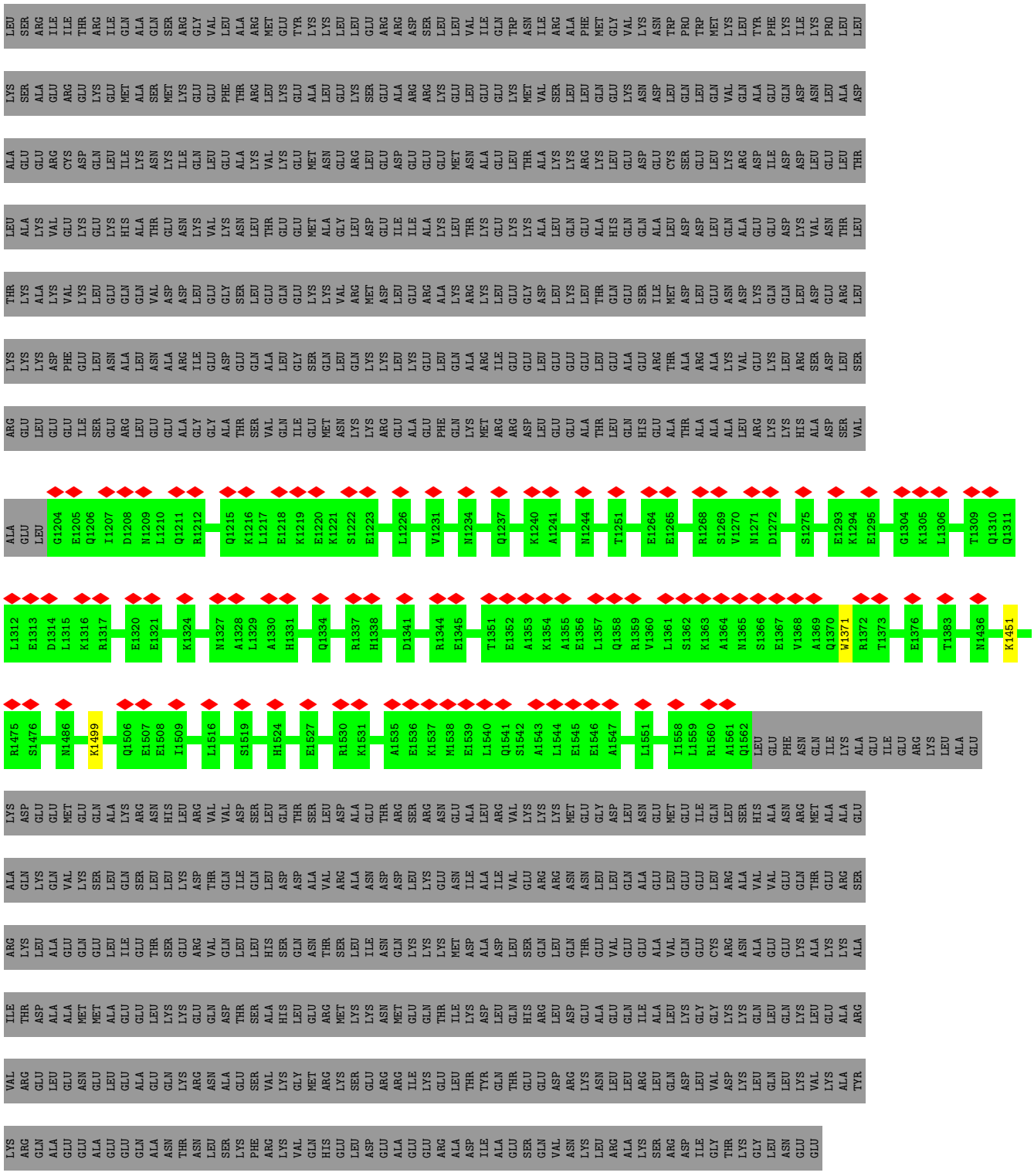
- Molecule 1: Myosin-7





• Molecule 1: Myosin-7





• Molecule 1: Myosin-7

Chain BO:

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

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

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

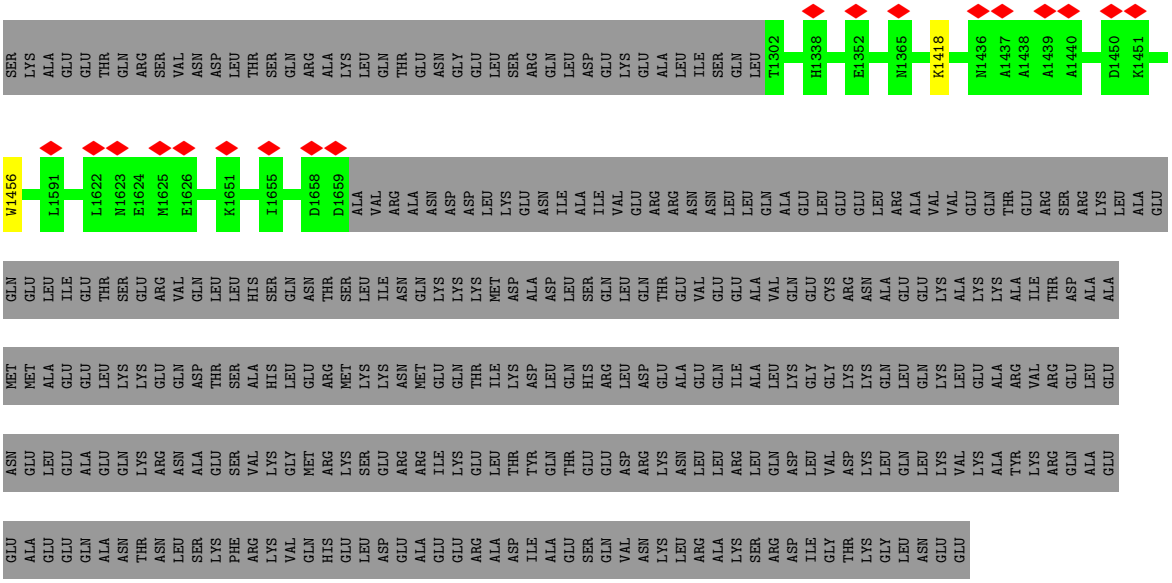
LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

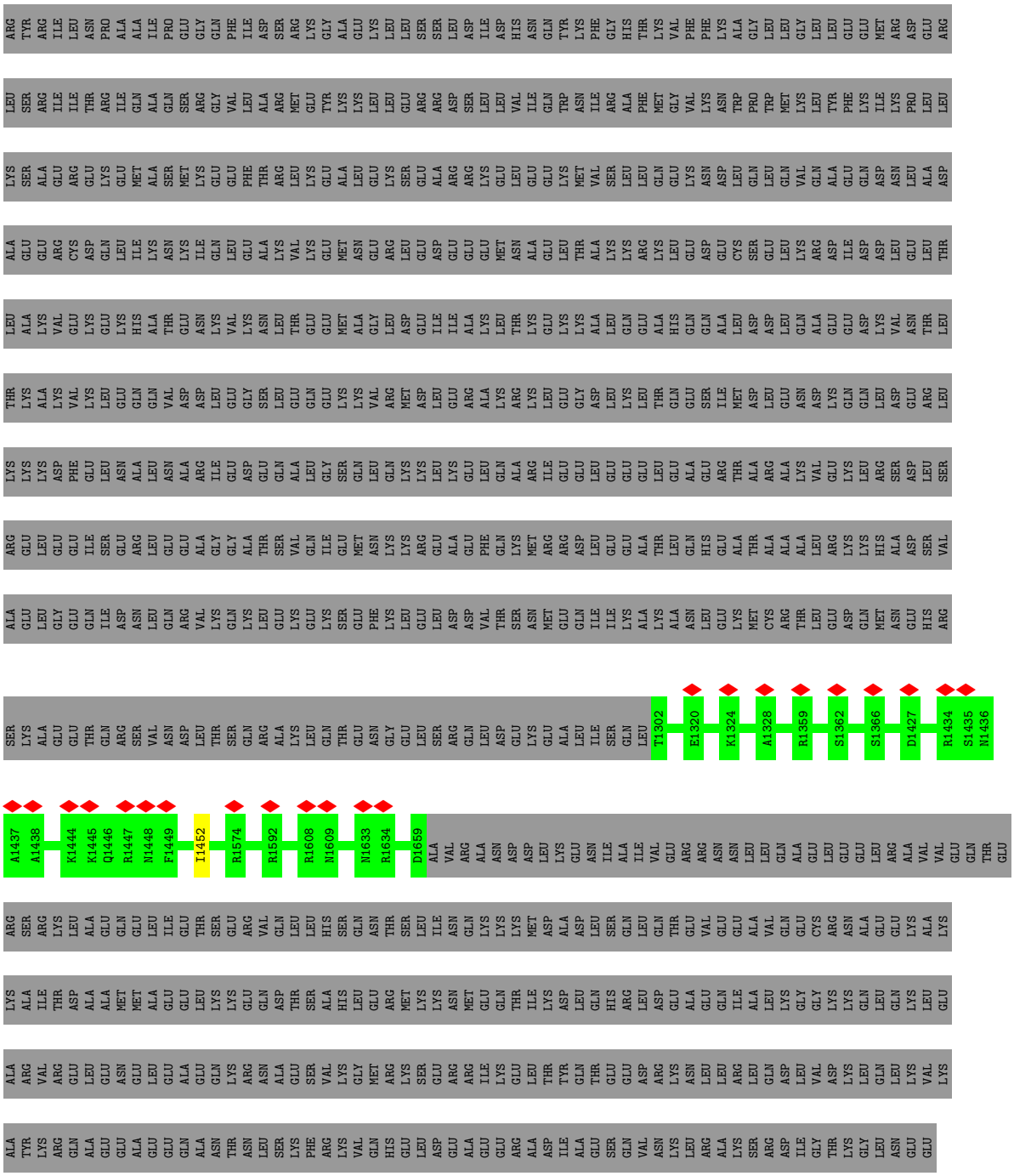
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

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

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

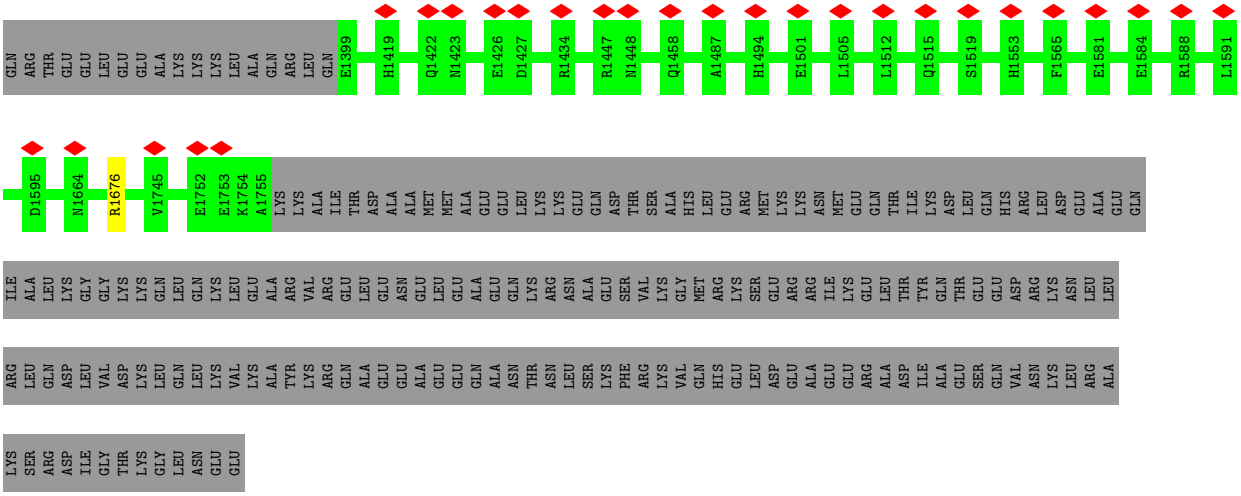


• Molecule 1: Myosin-7



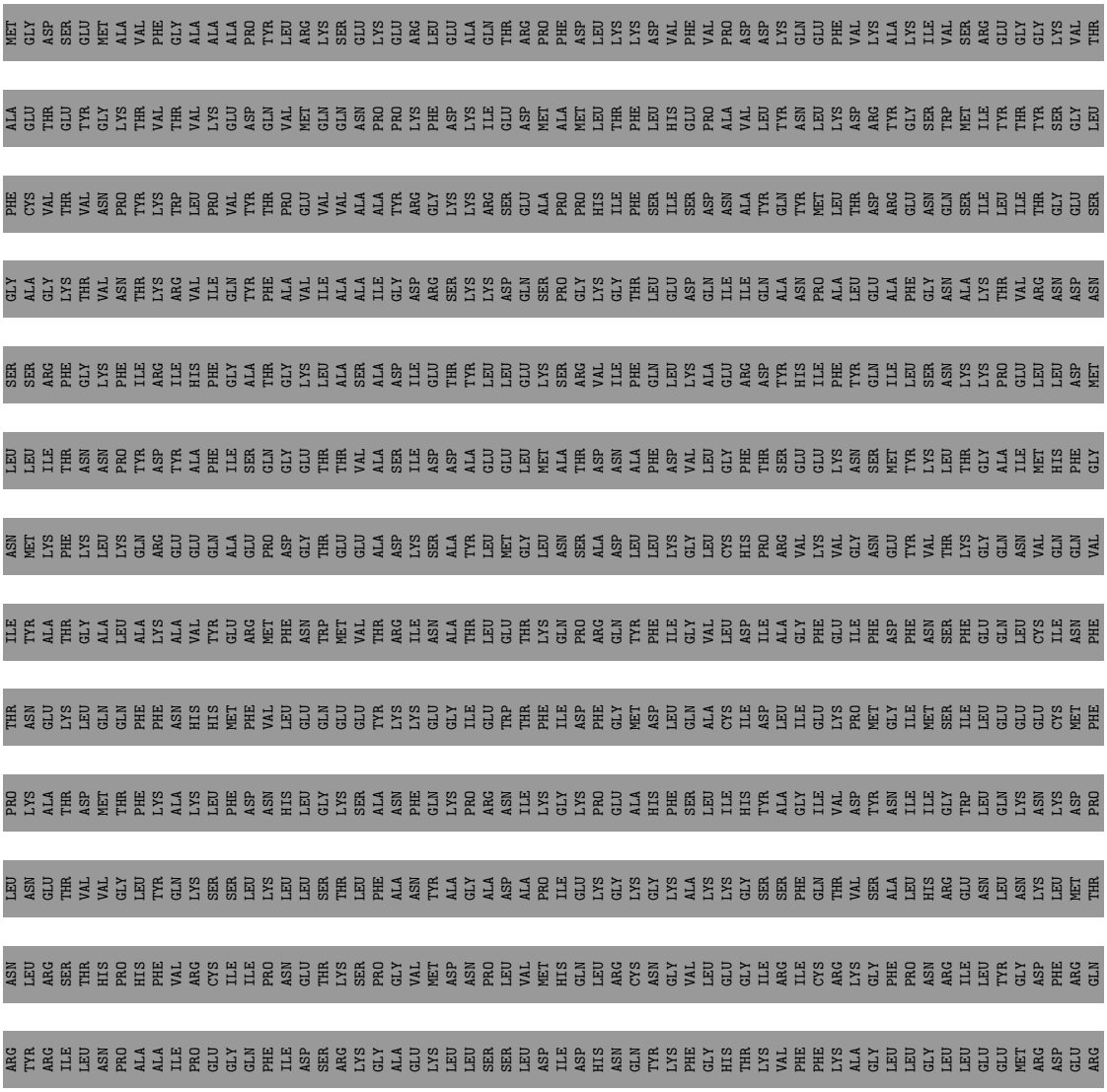
• Molecule 1: Myosin-7

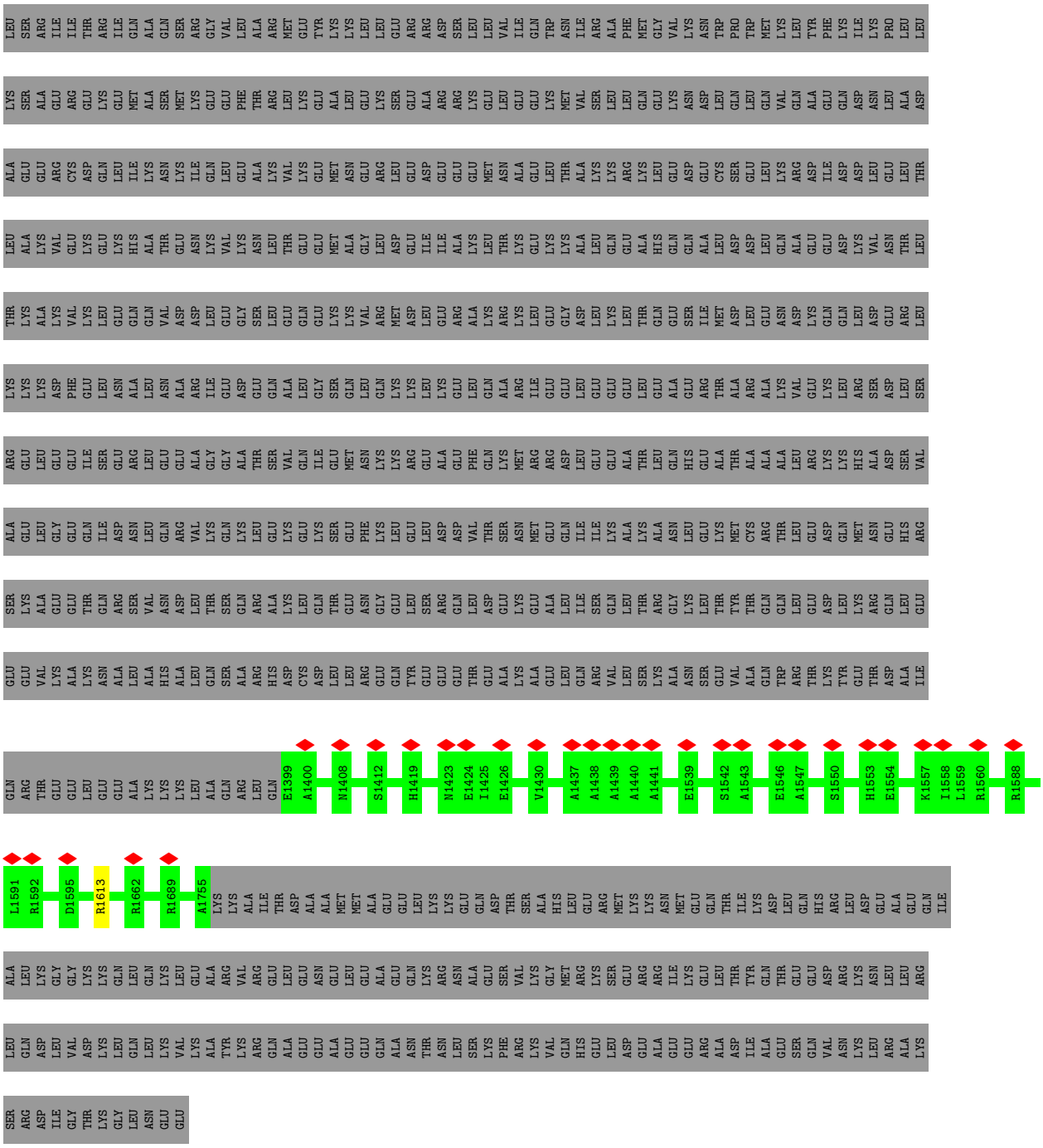
Chain BQ:



• Molecule 1: Myosin-7

Chain BR:





• Molecule 1: Myosin-7

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

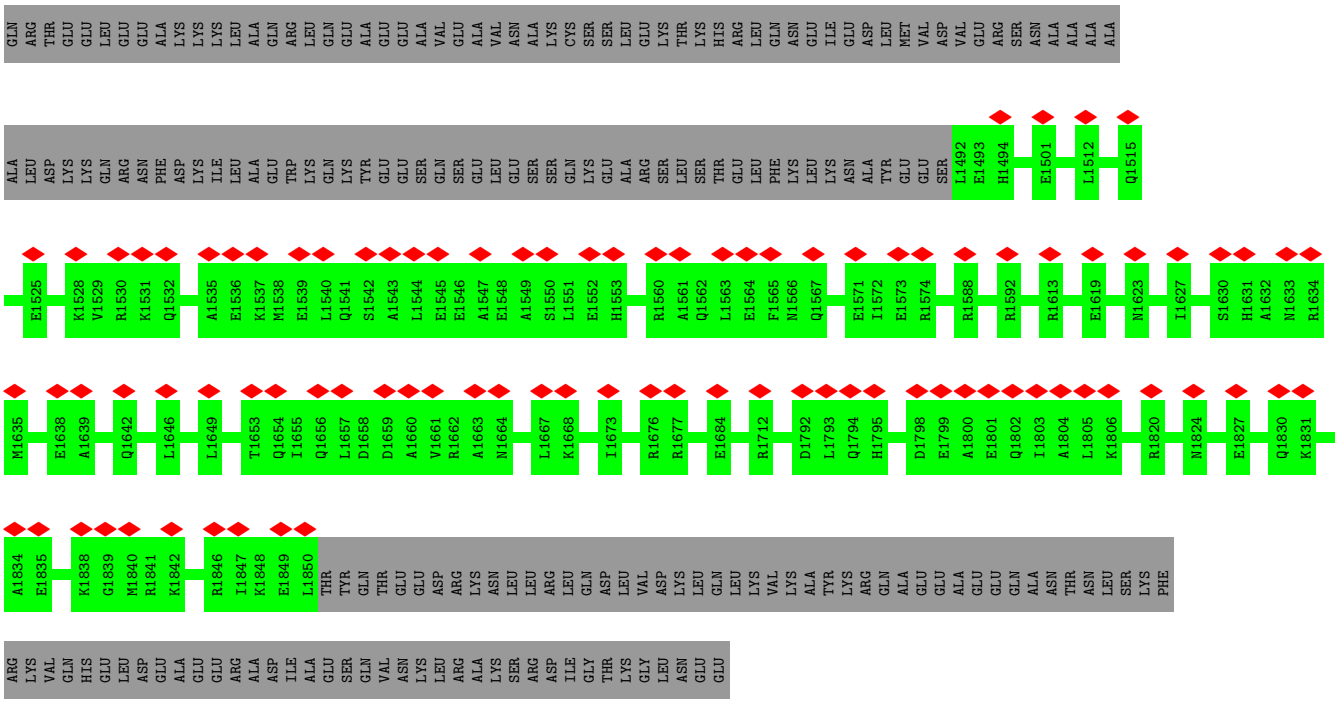
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

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

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

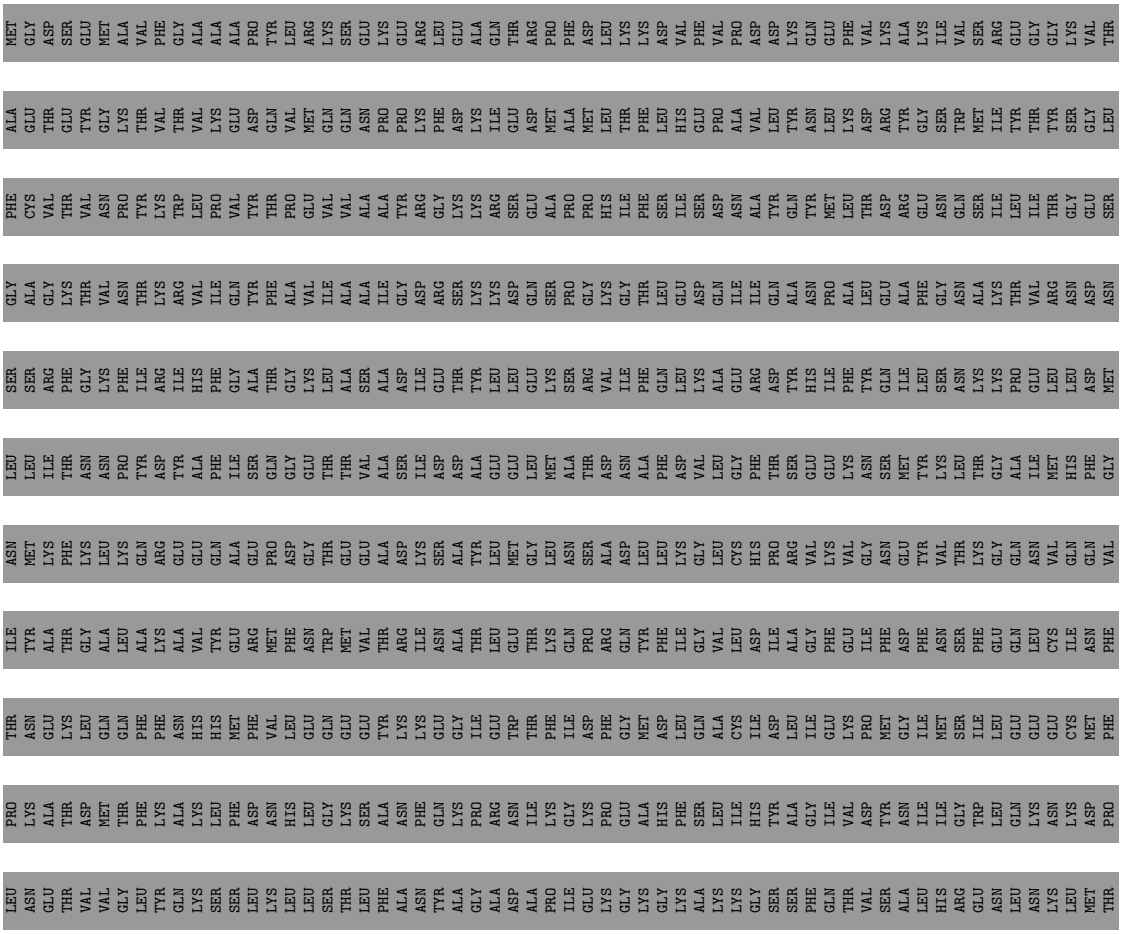
SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU

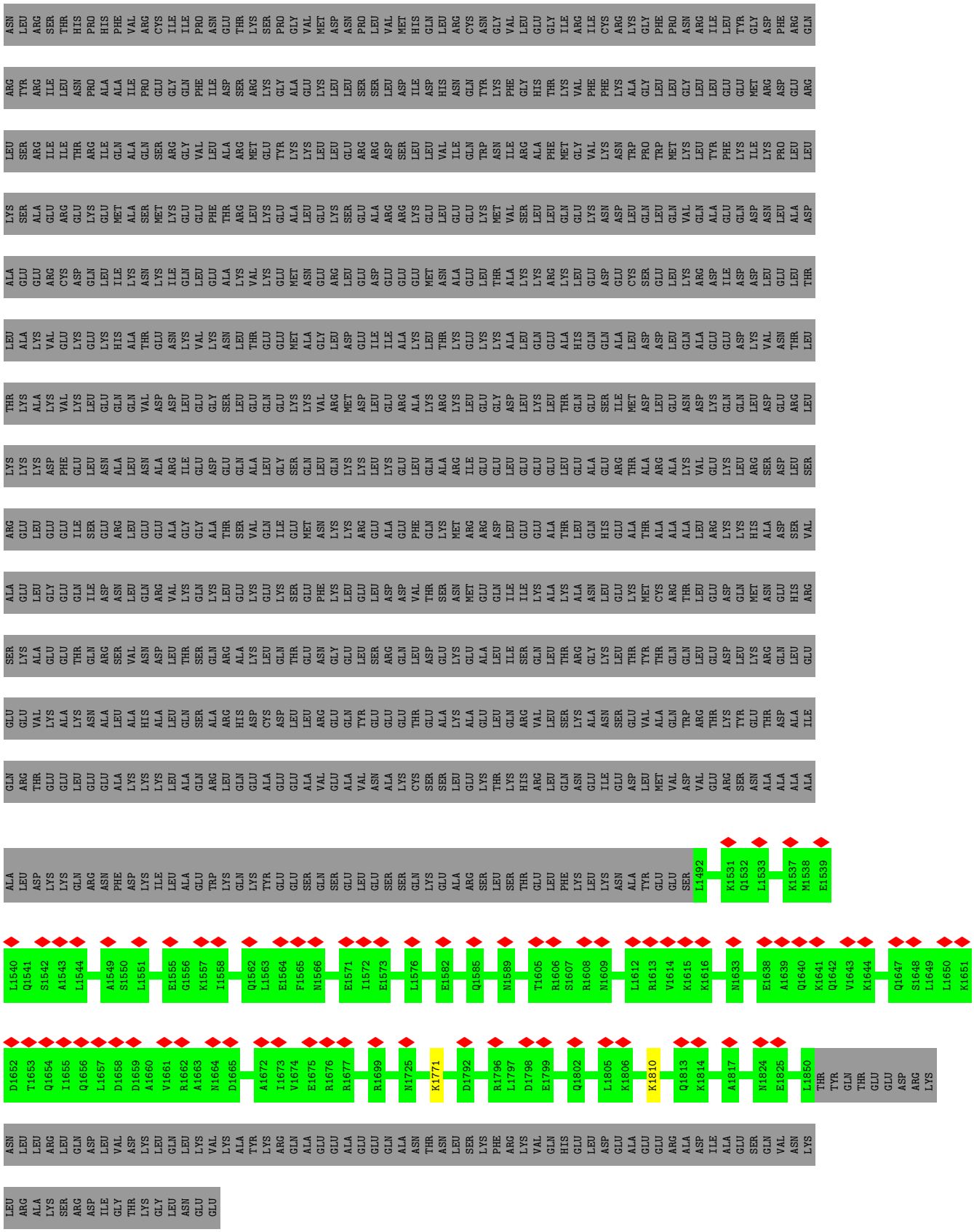
GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU ARG GLU GLN TYR GLU GLU GLU THR GLU ALA LYS ALA GLU LEU GLN ARG VAL LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE



- Molecule 1: Myosin-7

Chain BT:





• Molecule 1: Myosin-7

Chain BU:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

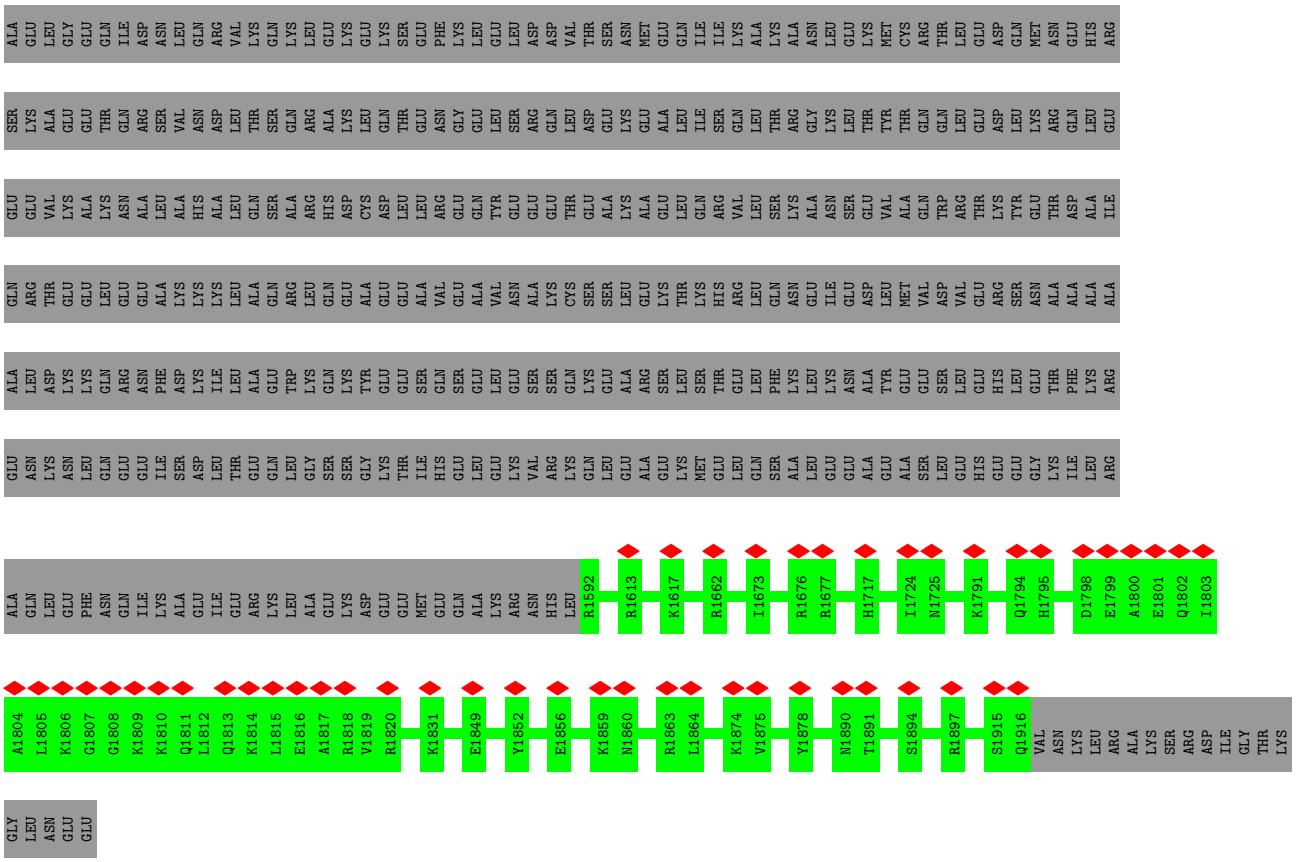
ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

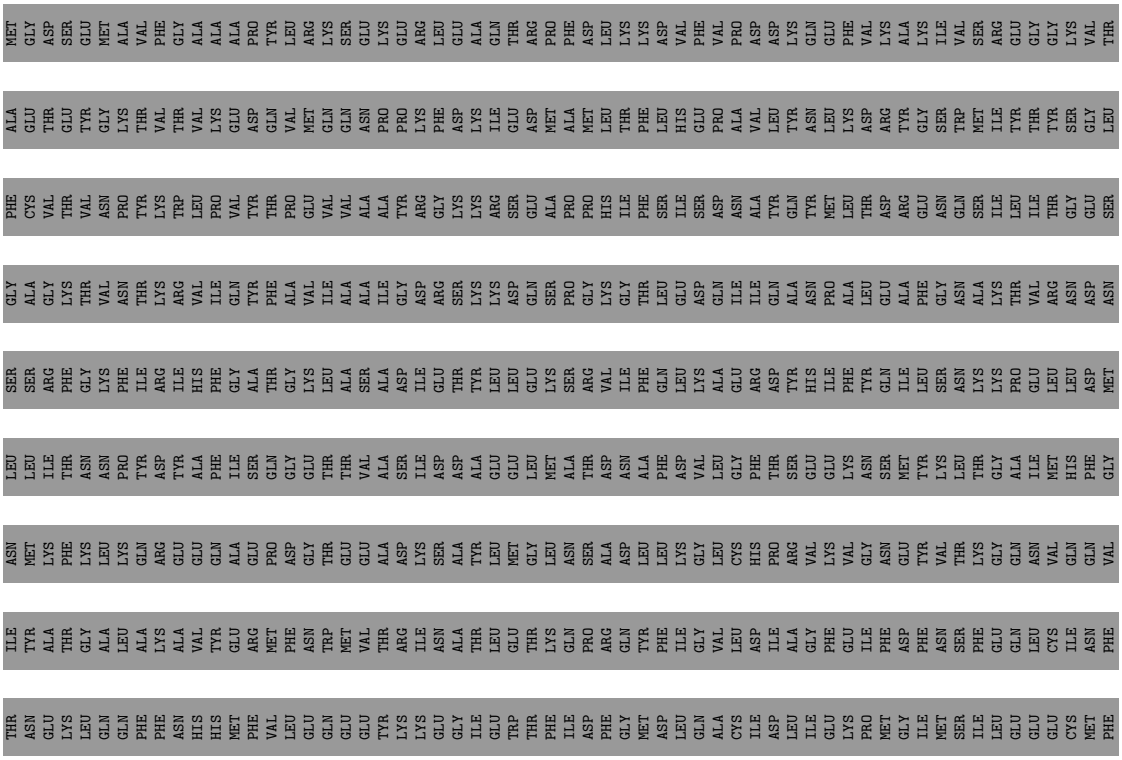
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

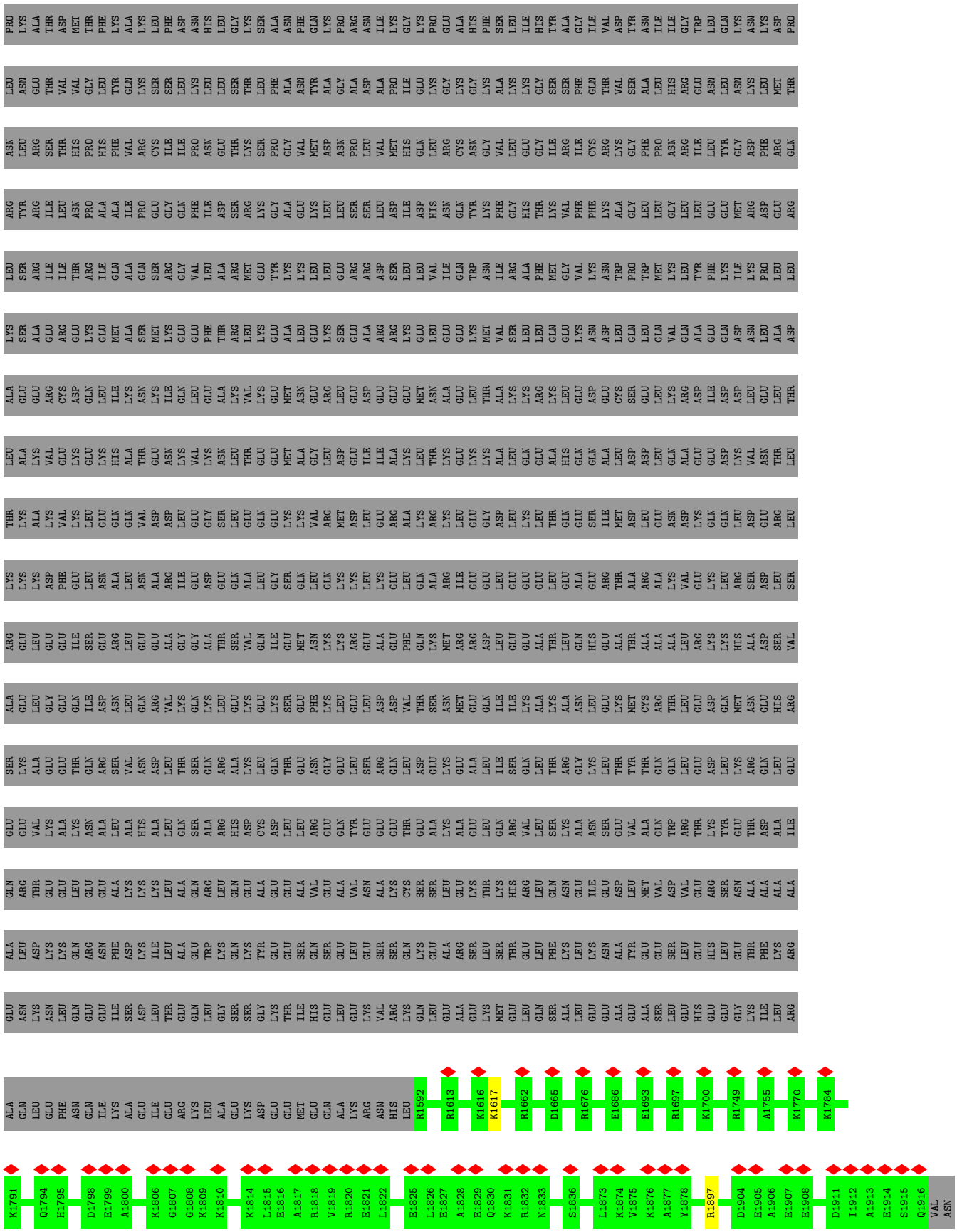
ARG GLU LEU GLU GLU ILE SER GLU ARG LEU GLU GLU ALA GLY GLY ALA THR SER VAL GLN ILE GLU MET ASN LYS LYS ARG GLU ALA GLU PHE GLN LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL



- Molecule 1: Myosin-7

Chain BV:

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K1770
K1784
K1791
Q1794
H1795
D1798
E1799
A1800
K1806
G1807
G1808
K1809
K1810
K1814
L1815
E1816
A1817
R1818
V1819
R1820
E1821
L1822
E1825
L1826
E1827
A1828
E1829
Q1830
K1831
R1832
N1833
S1836
L1873
K1874
V1875
K1876
A1877
Y1878
R1897
D1904
E1905
A1906
E1907
E1908
D1911
I1912
A1913
E1914
S1915
Q1916
VAL
ASN

LYS LEU ARG ALA LYS SER ARG ASP ILE GLY THR LYS GLY LEU ASN GLU GLU

• Molecule 1: Myosin-7

Chain BW:

11% 88%

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

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

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

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

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

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

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

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

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

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

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

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

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

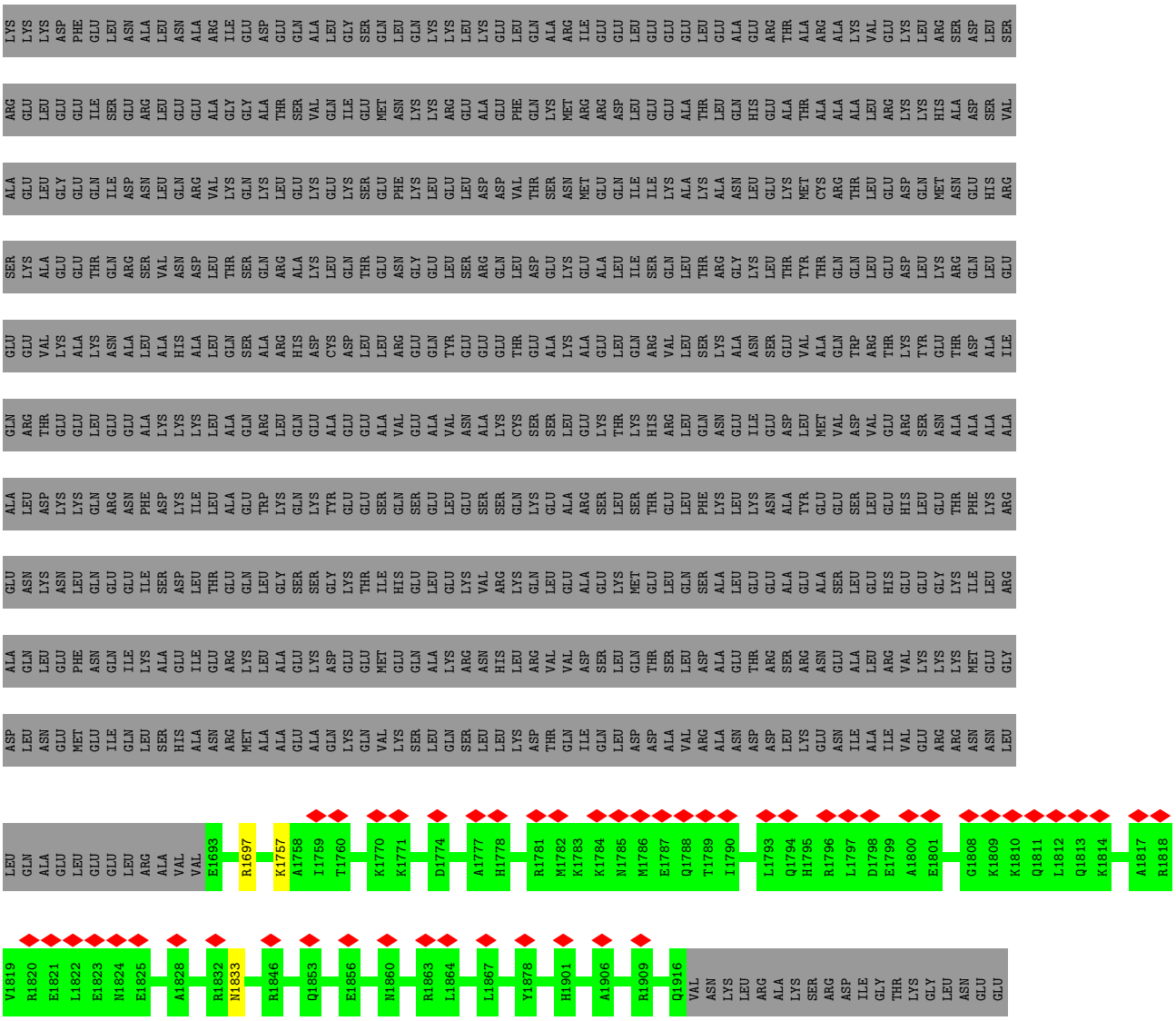
LEU SER ARG ILE ILE THR ARG ILE GLN ALA GLN SER ARG GLY VAL LEU ALA ARG MET GLU TYR LYS LYS LEU LEU GLU ARG ARG ASP SER LEU LEU VAL ILE GLN TRP ASN ILE ARG ALA PHE MET GLY VAL LYS ASN TRP PRO TRP MET LYS LEU TYR PHE LYS ILE LYS PRO LEU LEU

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

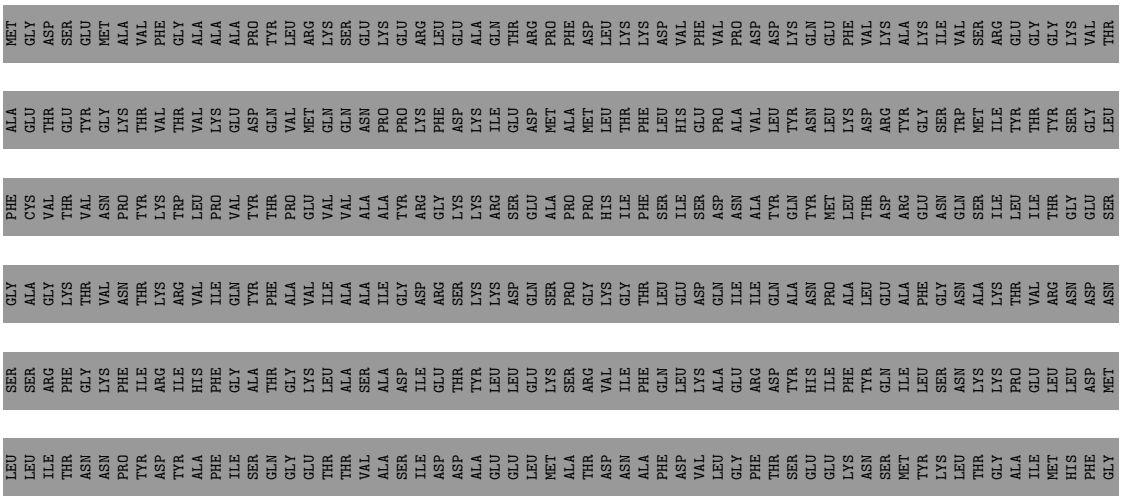
LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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



• Molecule 1: Myosin-7

Chain BX:



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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

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

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

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

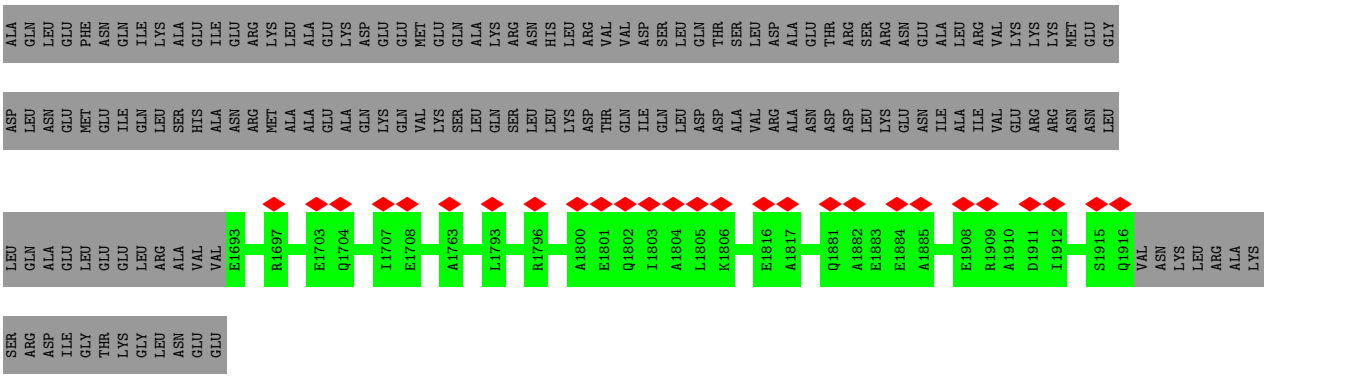
SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU

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

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

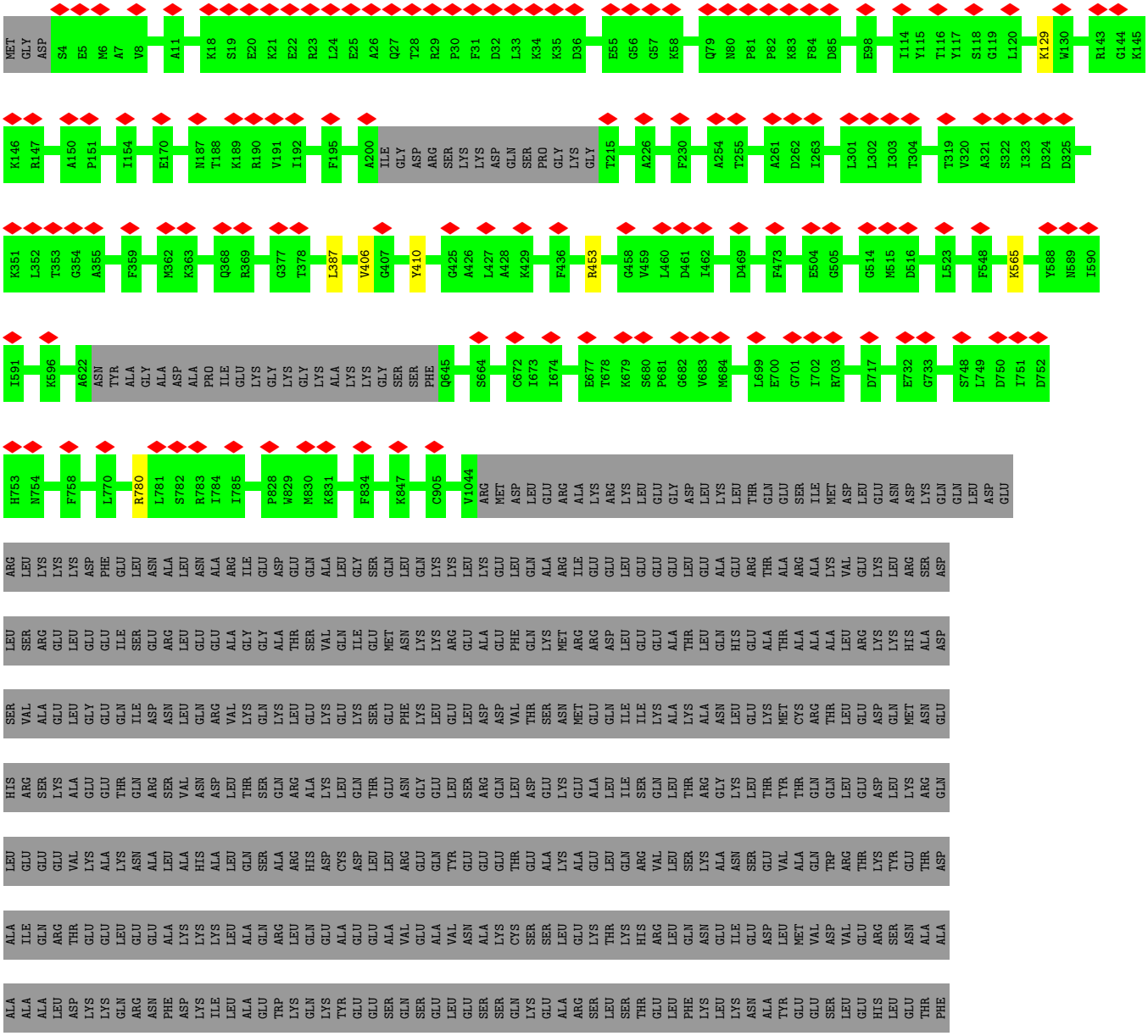
ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG

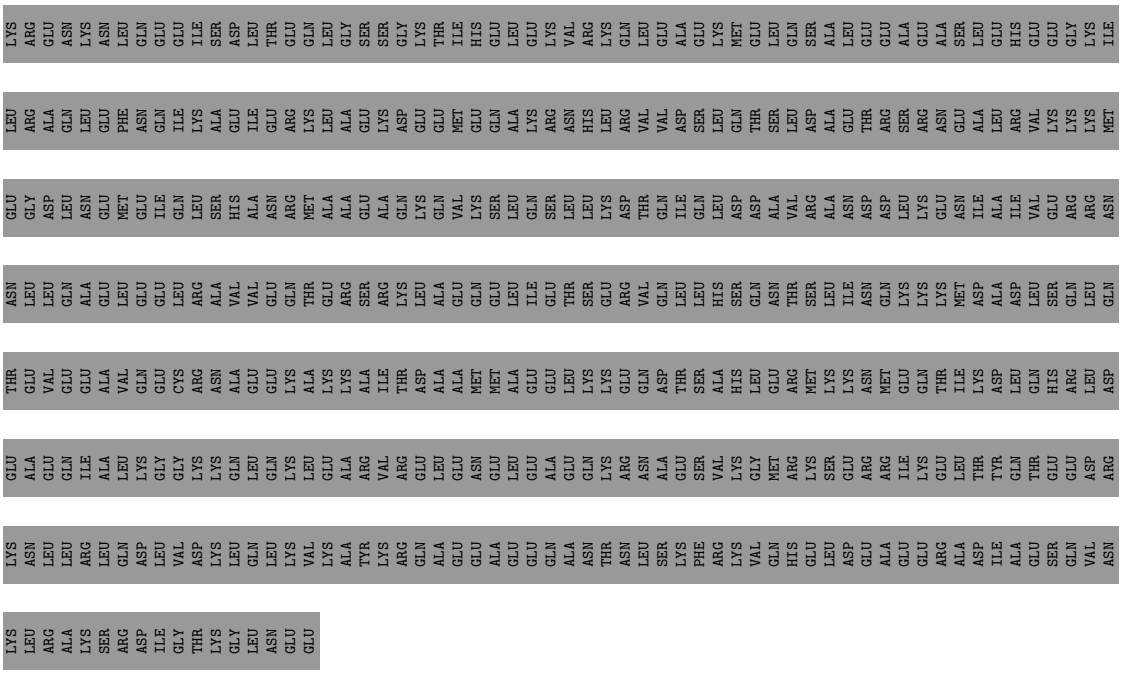
GLU ASN LYS ASN LEU GLN GLU GLU ILE SER ASP LEU THR GLU GLN LEU GLY SER SER GLY LYS THR ILE HIS GLU LEU GLU LYS VAL ARG LYS GLN LEU GLU ALA GLU LYS MET GLU LEU GLN SER ALA LEU GLU GLU ALA GLU ALA SER LEU GLU HIS GLU GLU GLY LYS ILE LEU ARG



• Molecule 1: Myosin-7

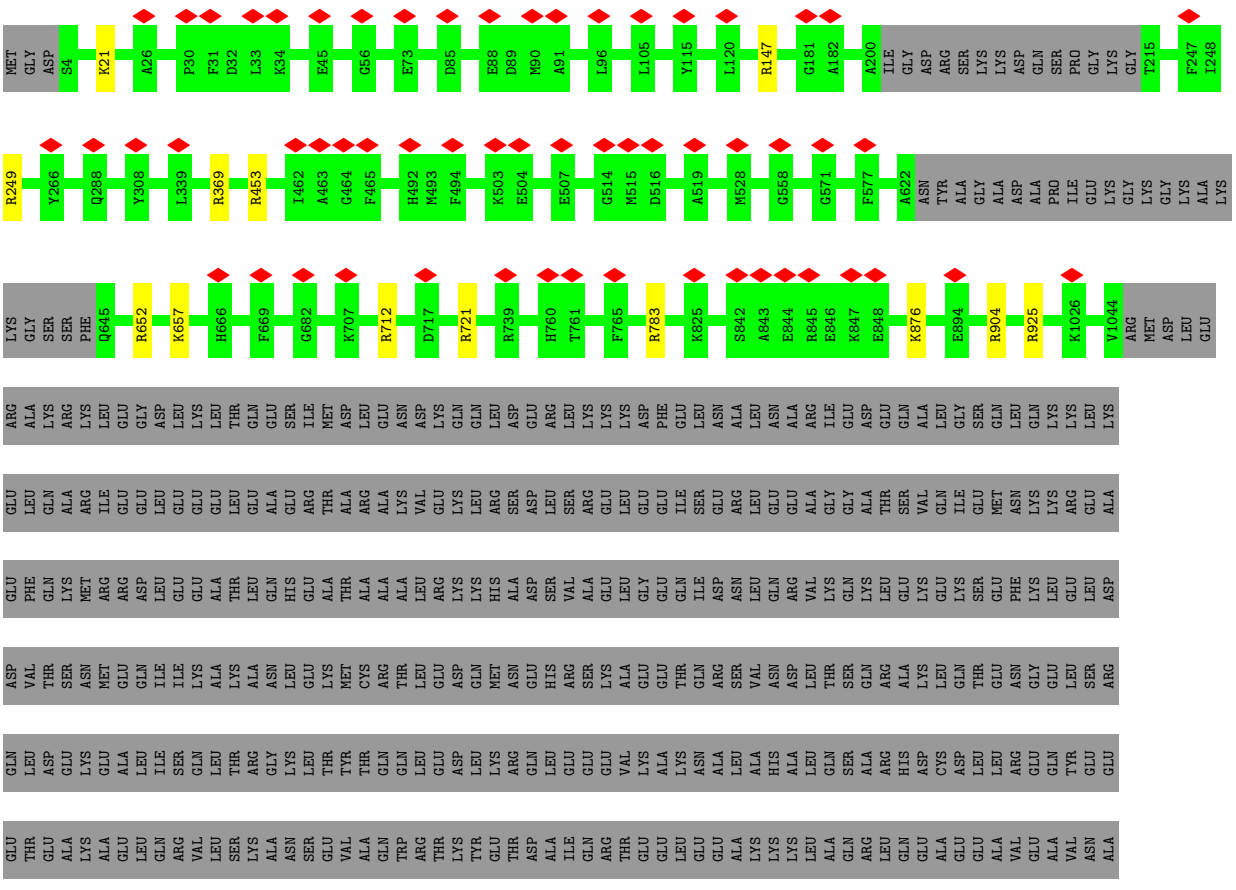
Chain BY:

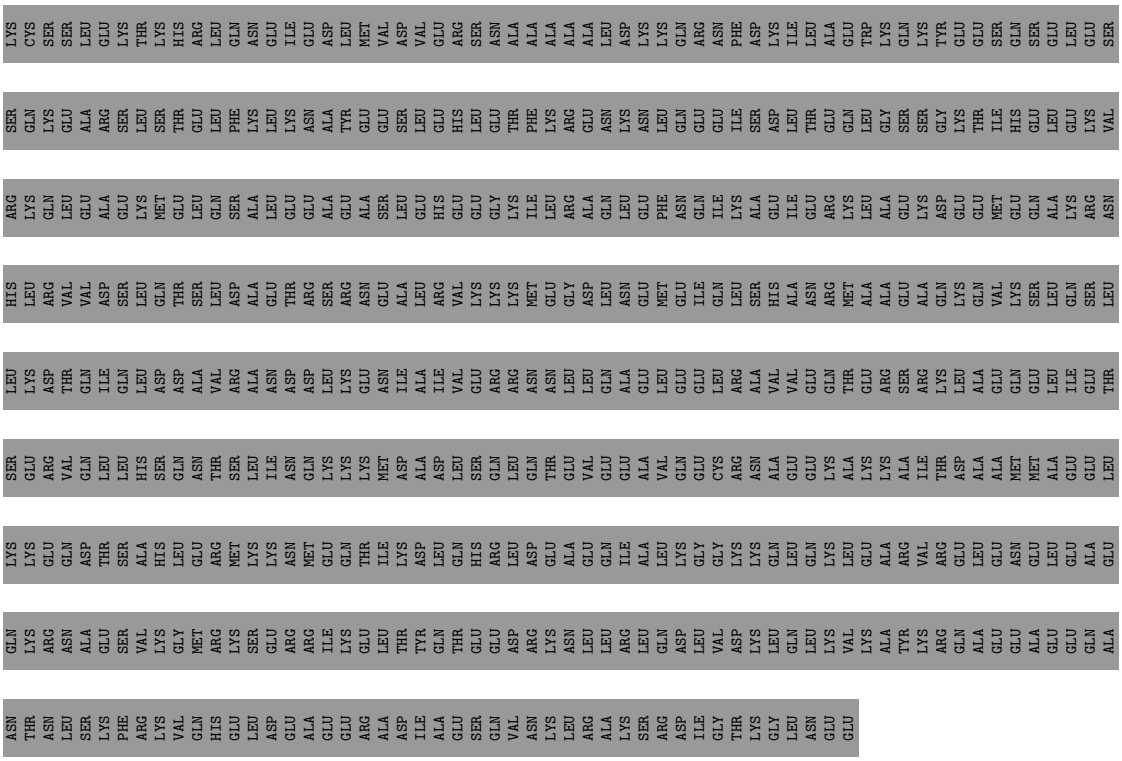




• Molecule 1: Myosin-7

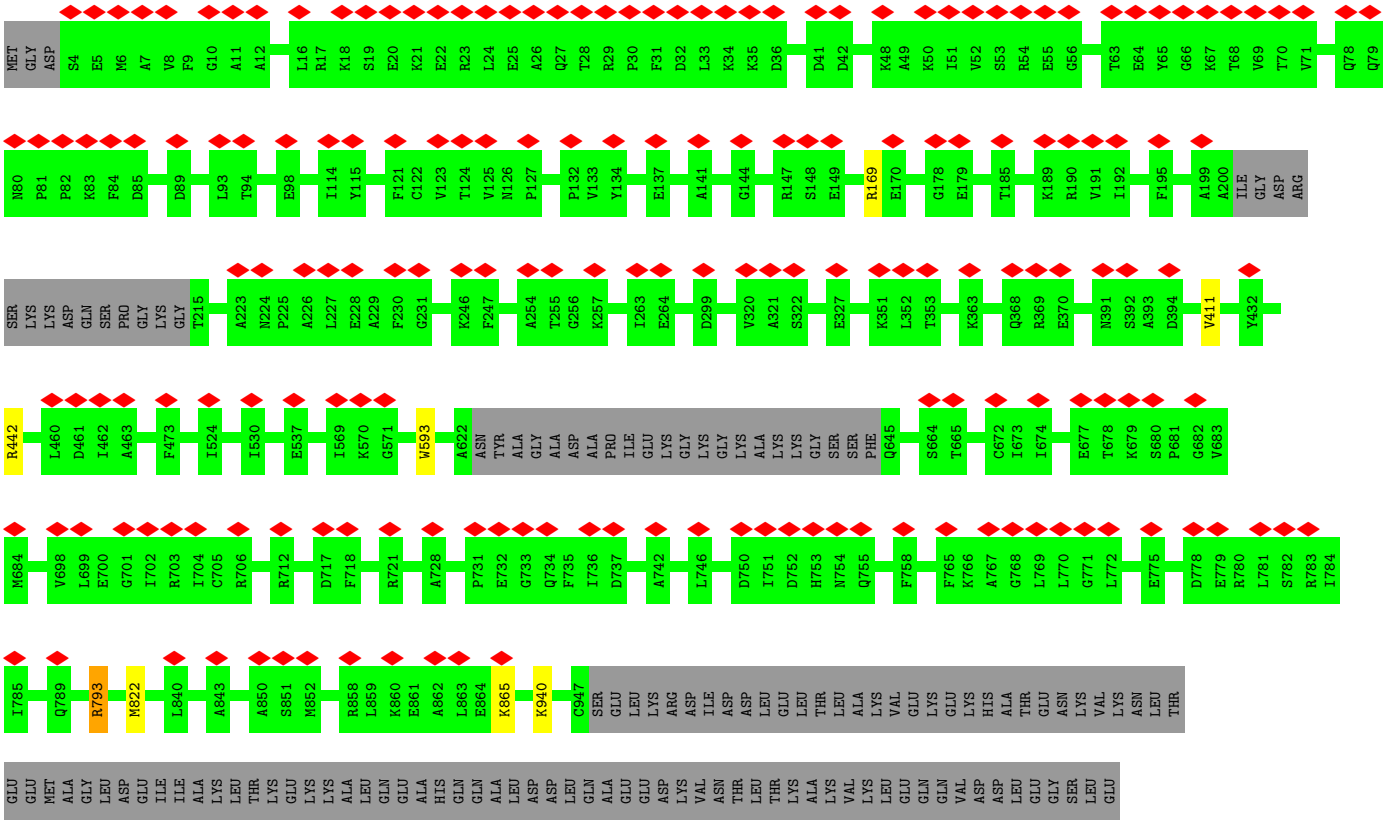
Chain BZ:

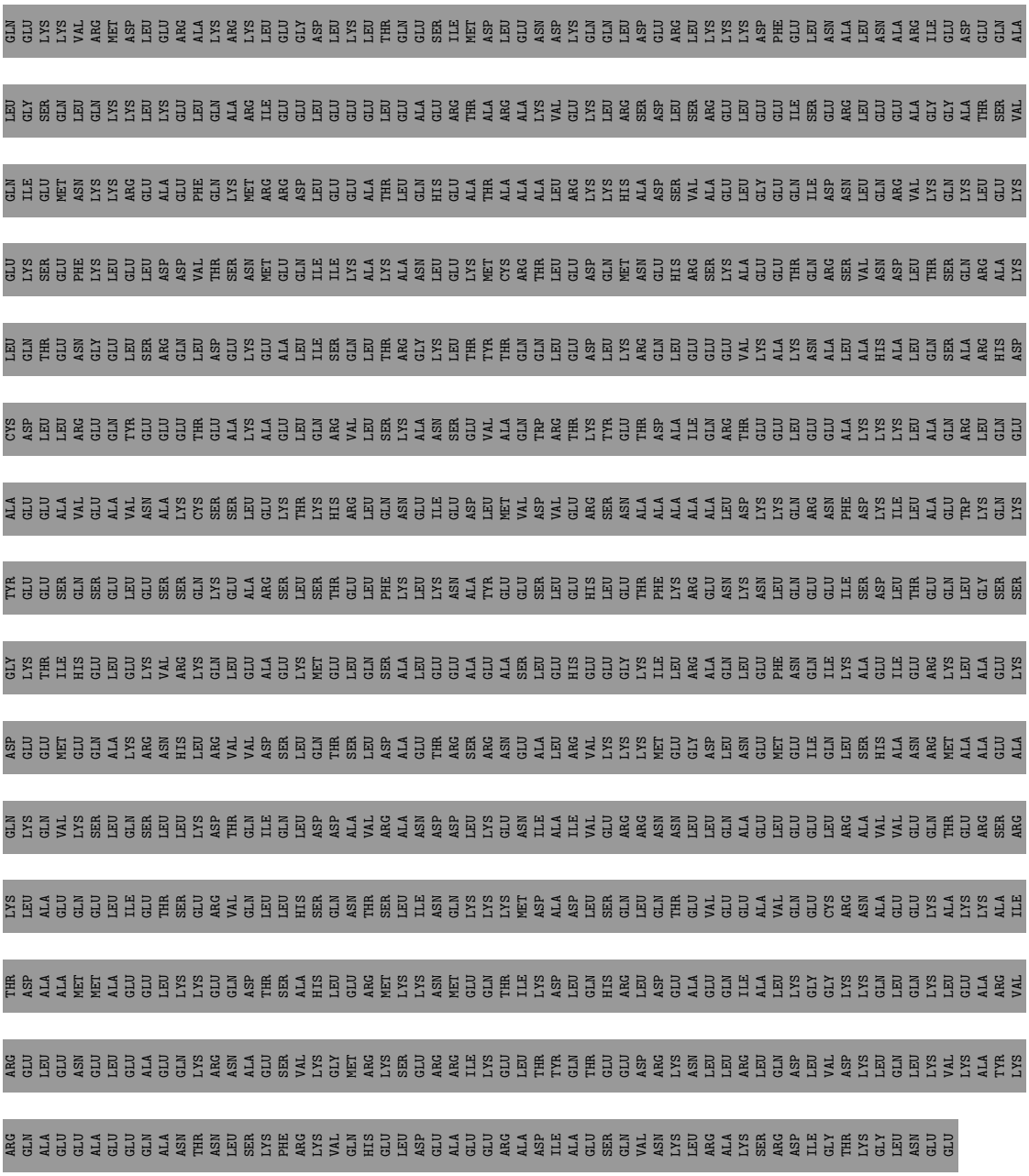




• Molecule 1: Myosin-7

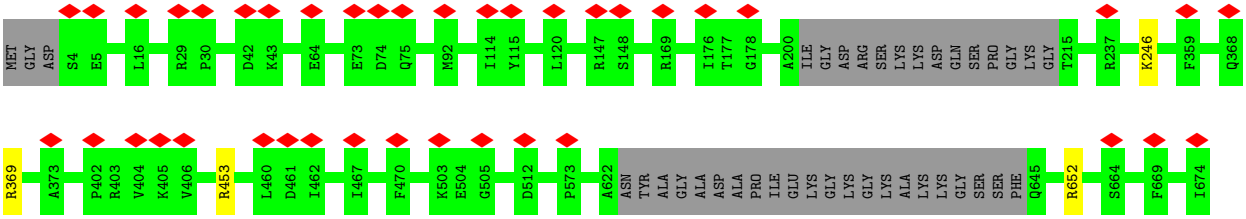
Chain be:

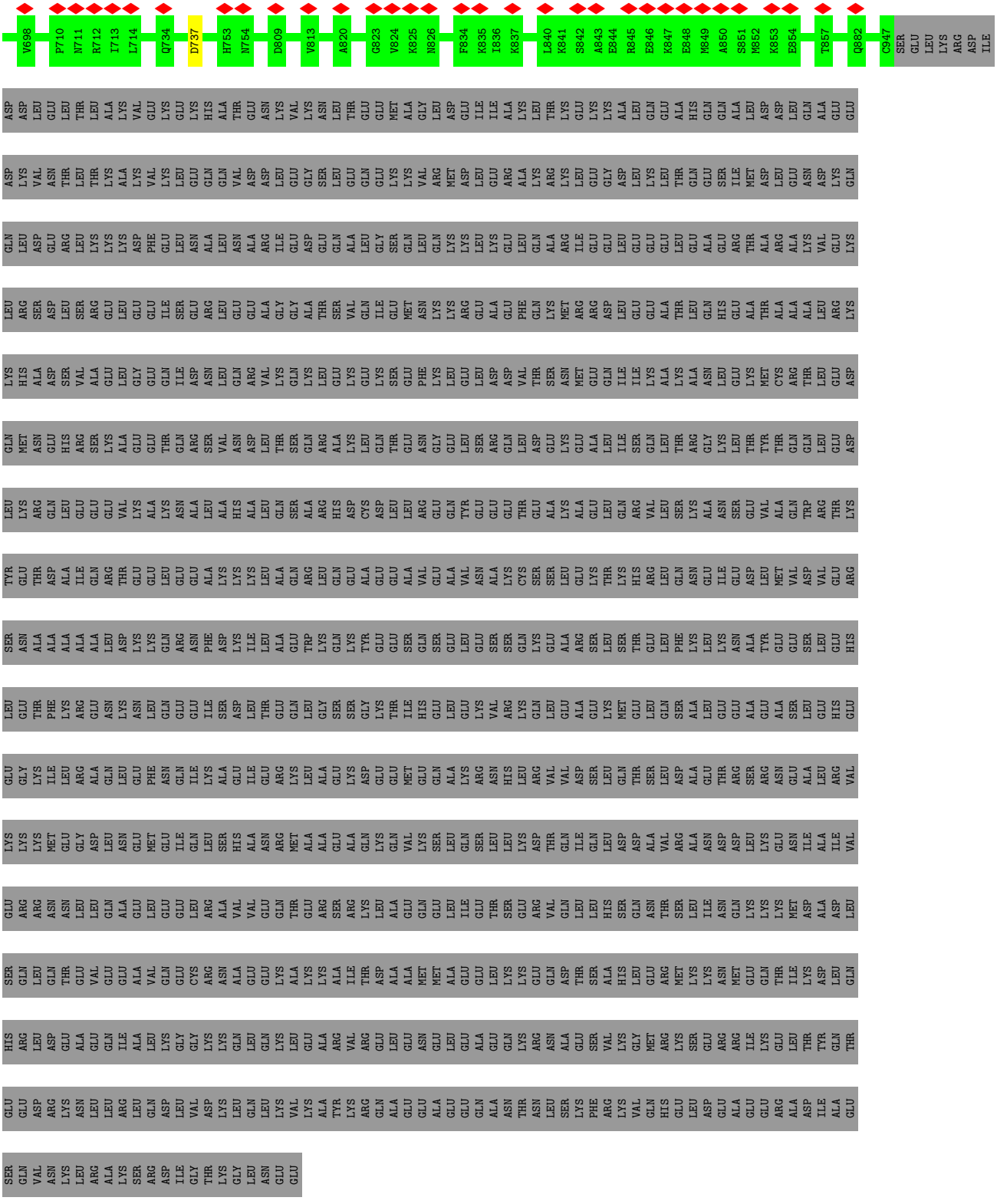




- Molecule 1: Myosin-7

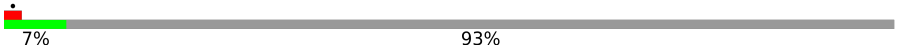
Chain bf:

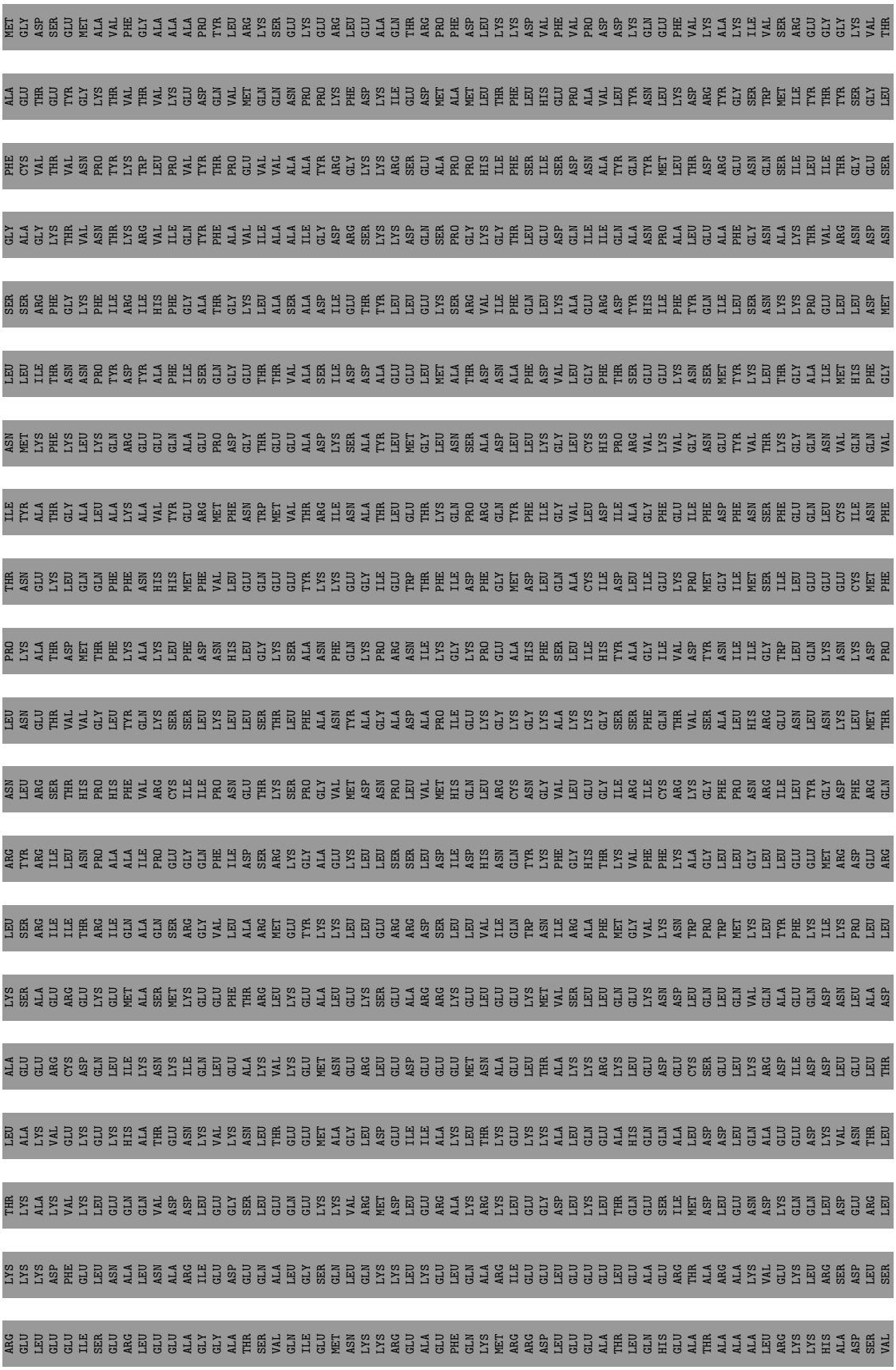


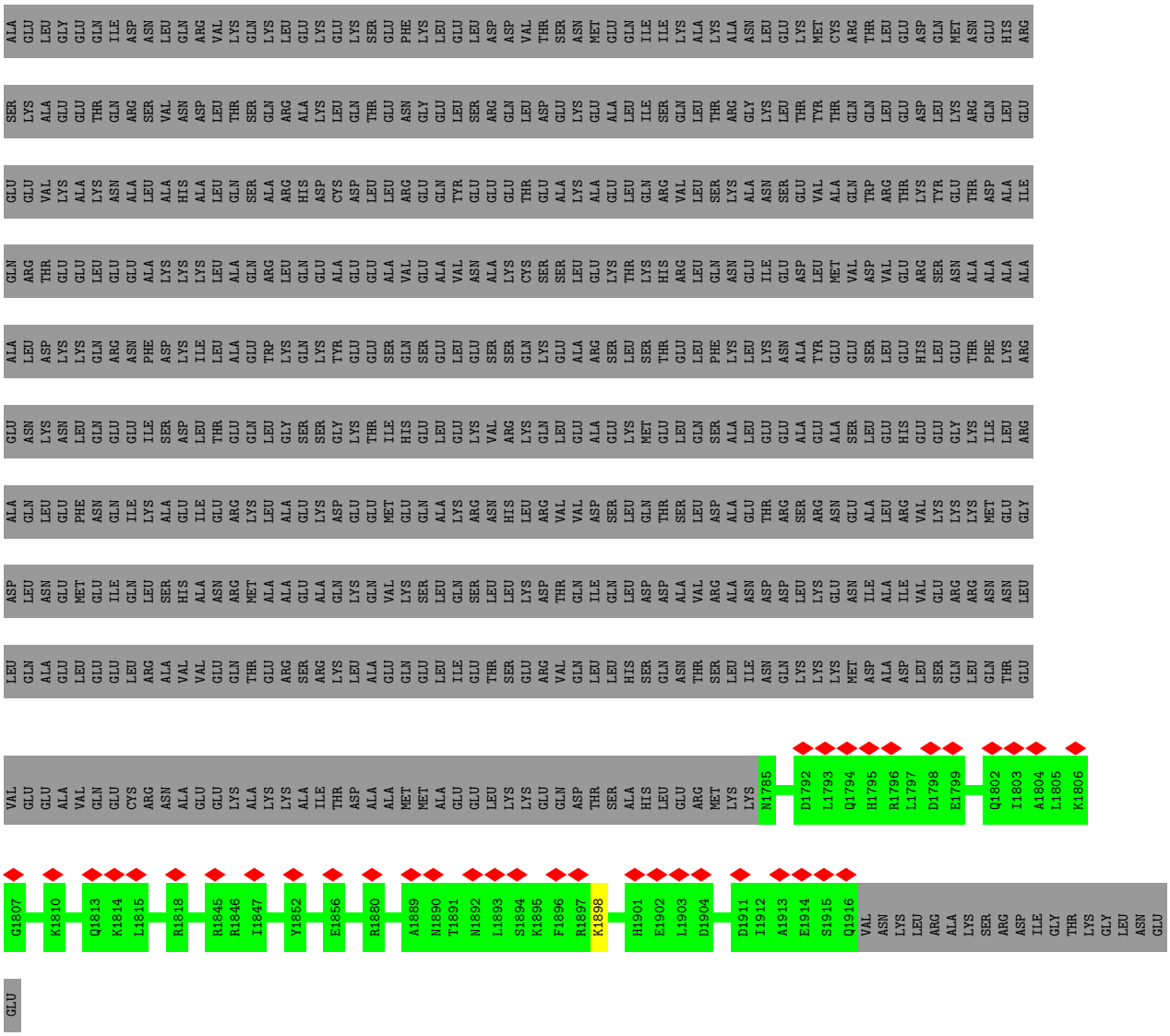


• Molecule 1: Myosin-7

Chain bk:

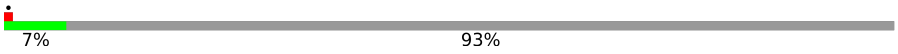


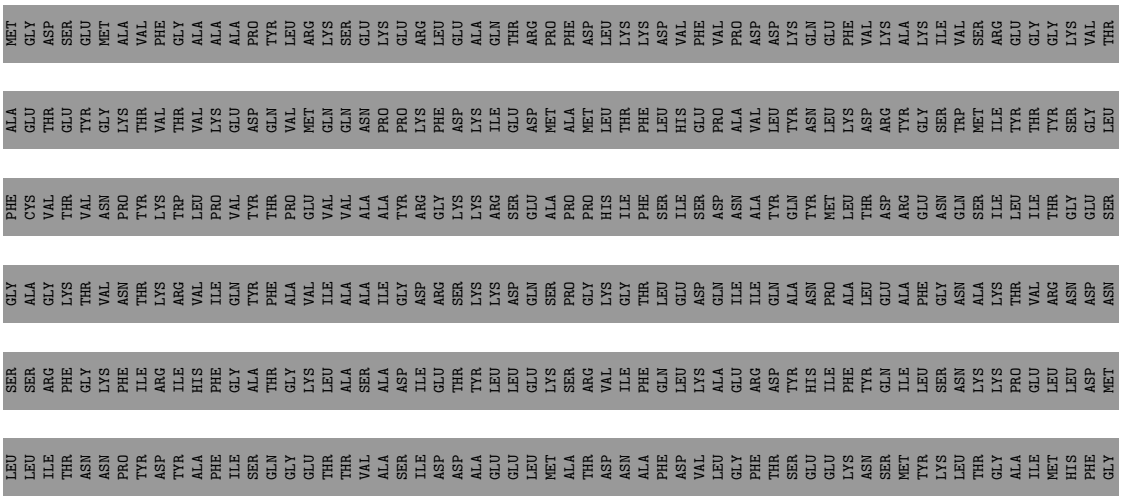


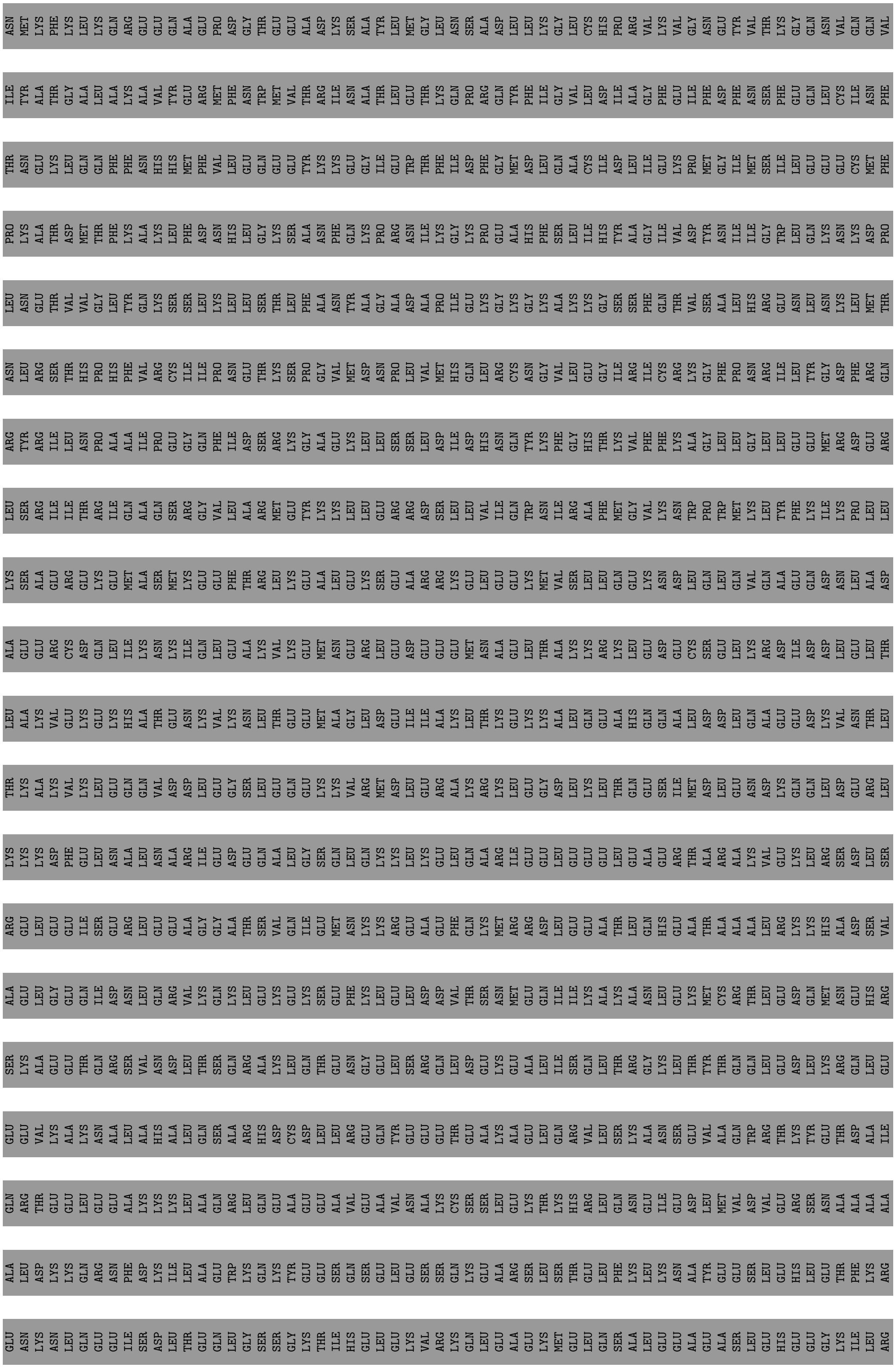


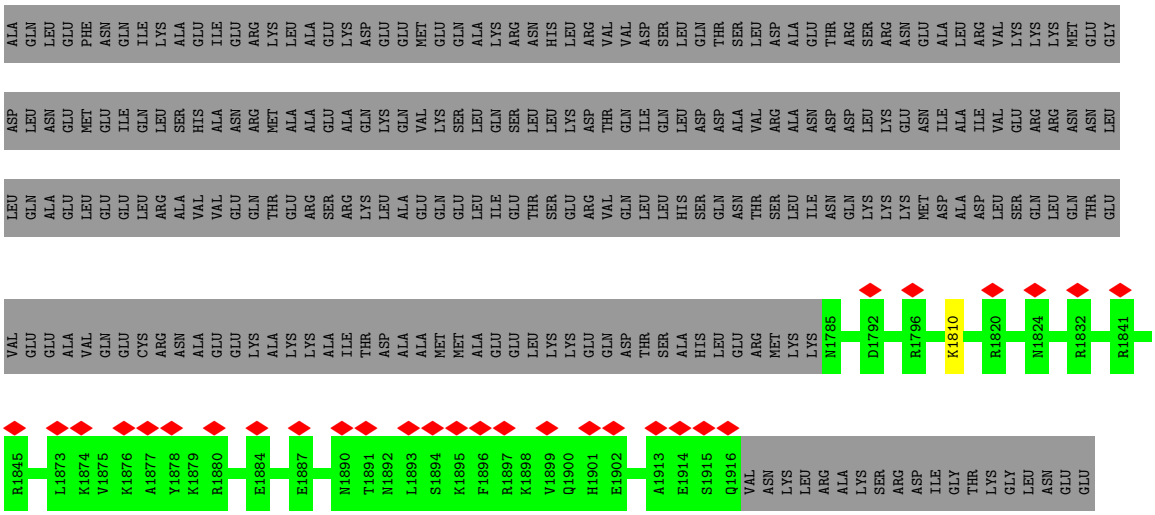
• Molecule 1: Myosin-7

Chain bl:



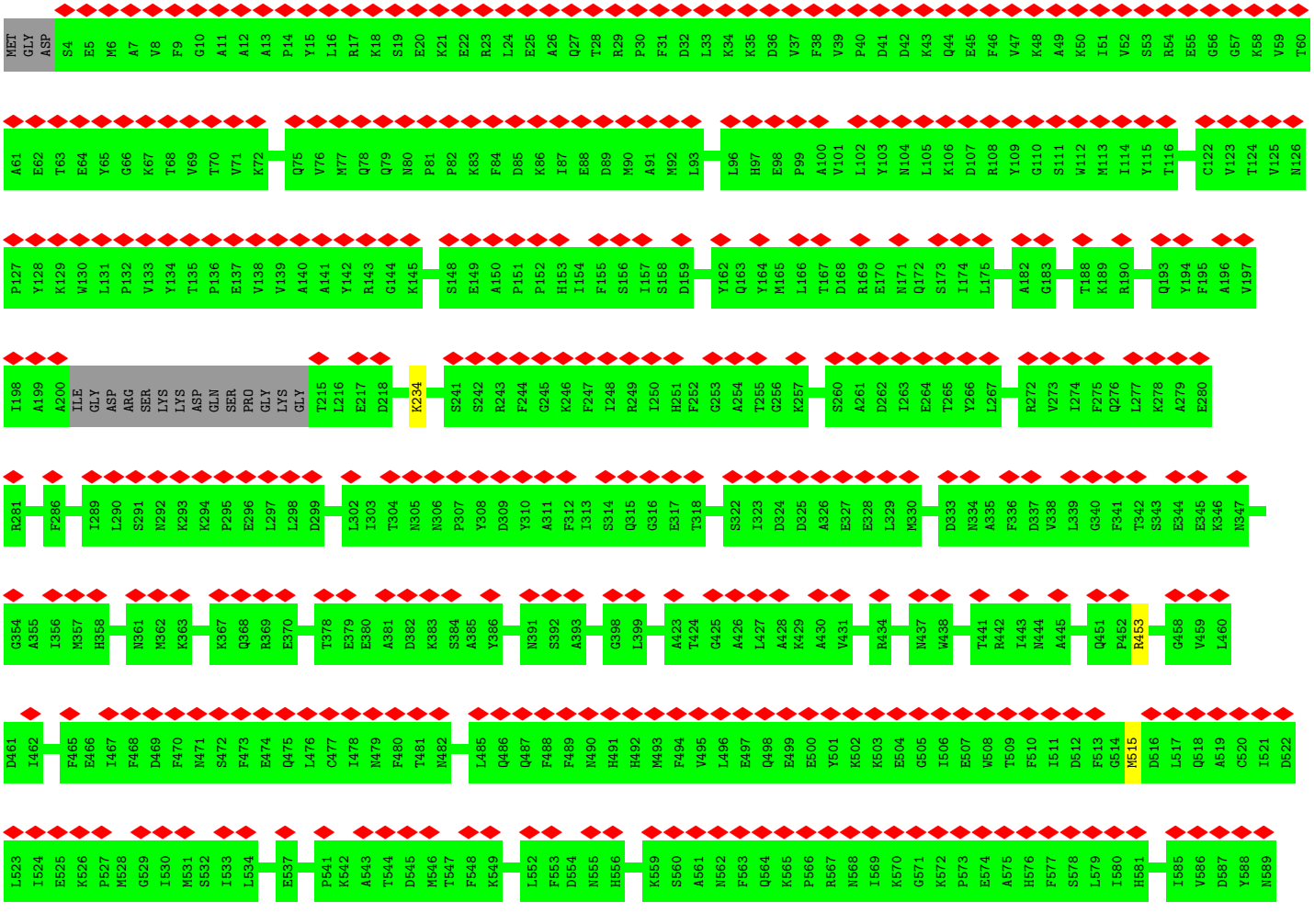


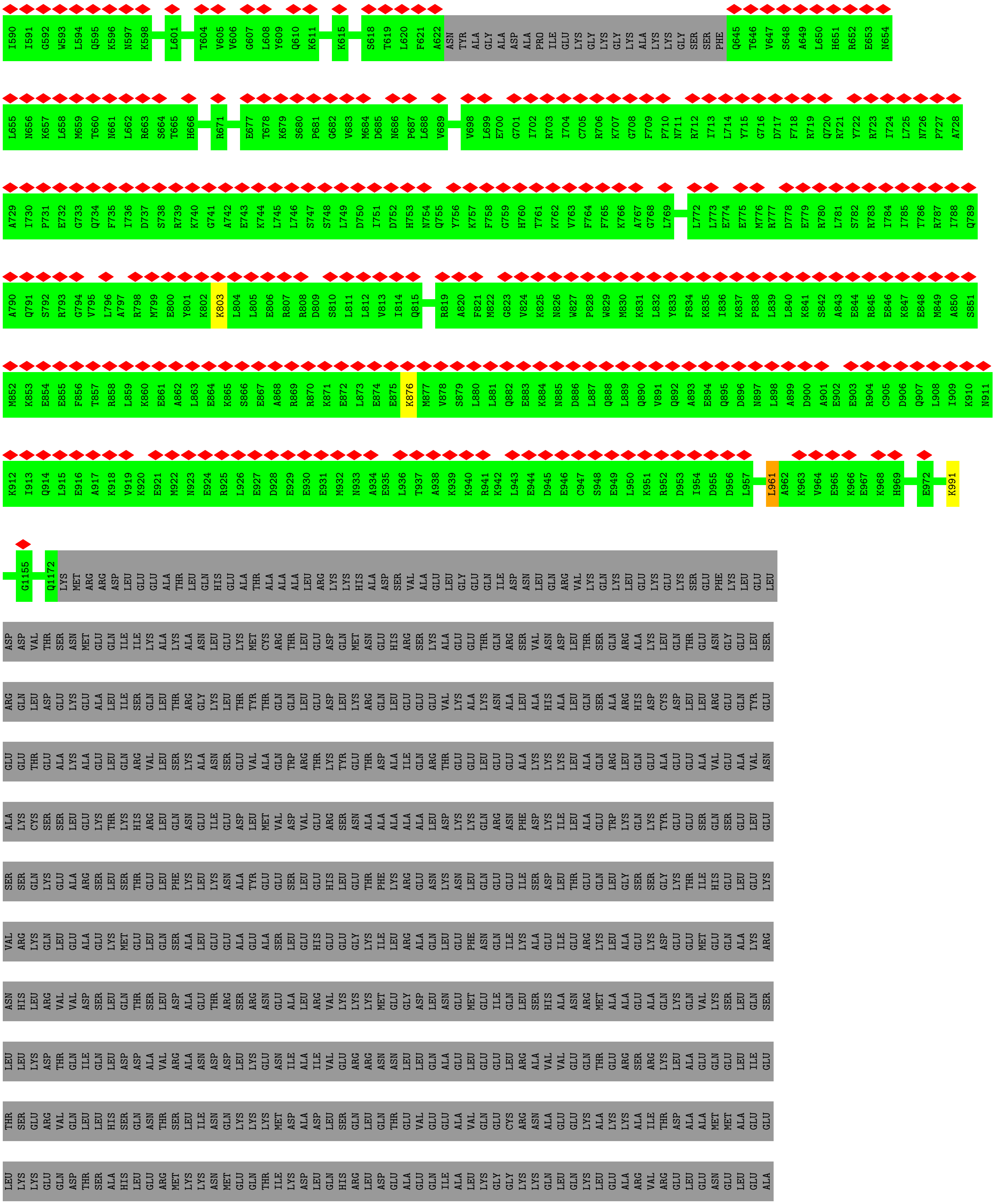

ASN MET LYS PHE LYS LEU LYS GLN ARG GLU GLU GLN ALA GLU PRO ASP GLY THR GLU GLU ALA ASP LYS SER ALA TYR LEU MET GLY LEU ASN SER ALA ASP LEU LEU LYS GLY LEU CYS HIS PRO ARG VAL LYS VAL GLY ASN GLU TYR VAL THR LYS GLY GLN ASN VAL GLN GLN VAL
ILE TYR ALA THR GLY ALA LEU ALA LYS ALA VAL TYR GLU ARG MET PHE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

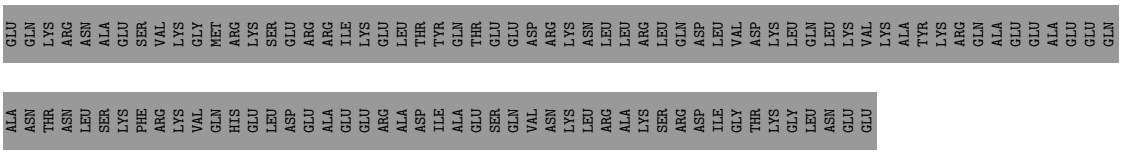


• Molecule 1: Myosin-7

Chain AA:

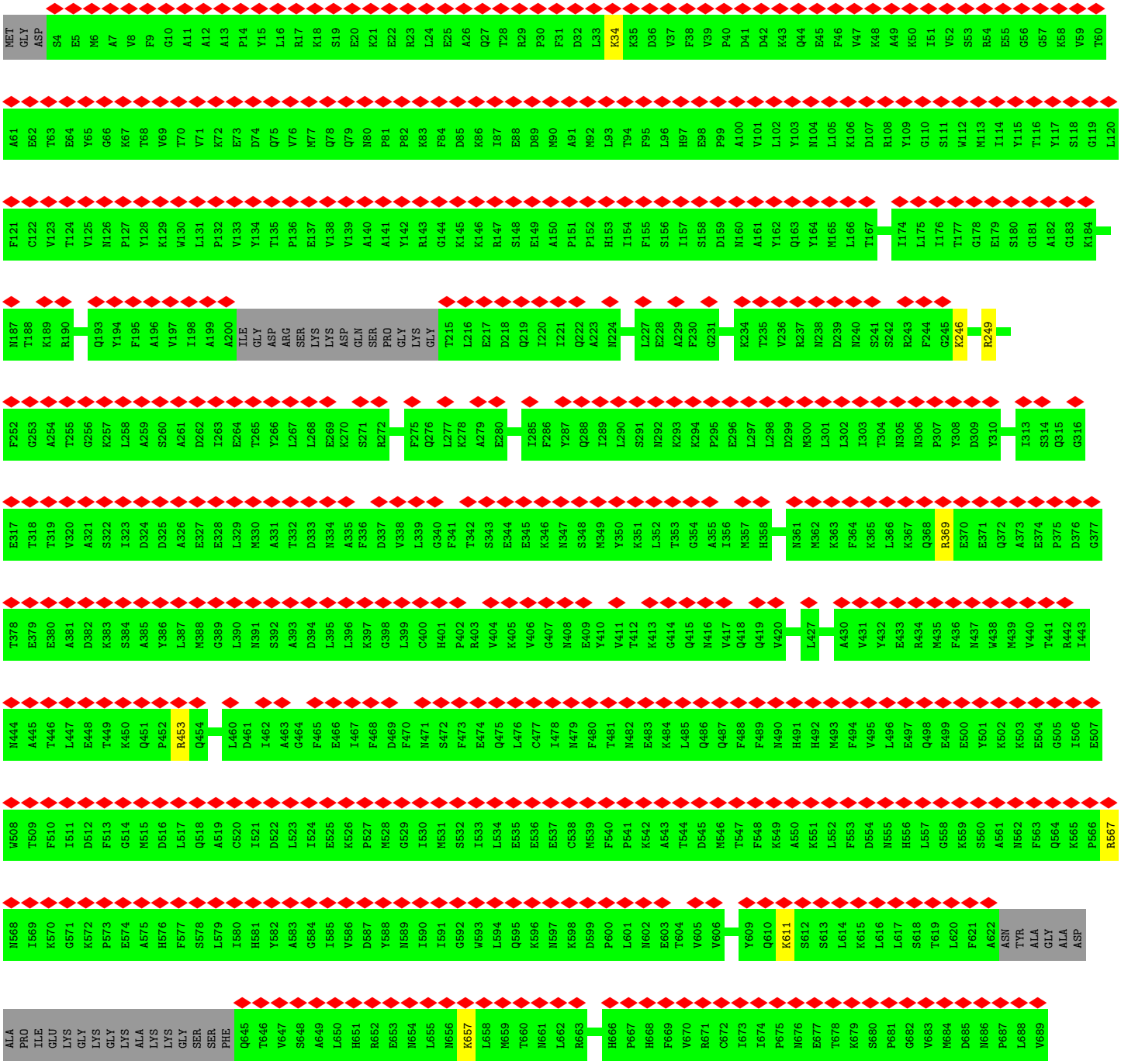


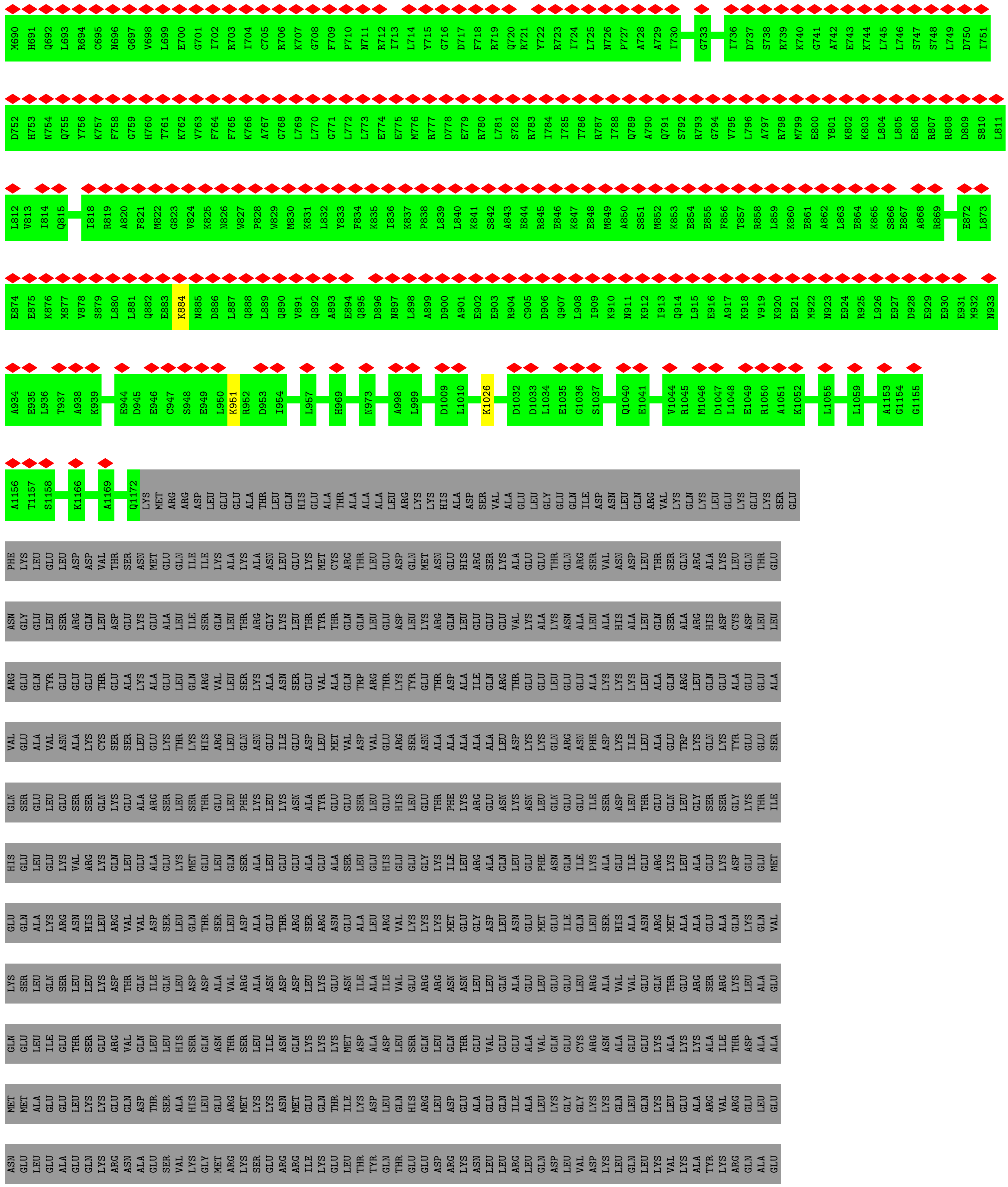

I590 I591 G592 W593 L594 Q595 K596 N597 K598 L601 T604 V605 V606 G607 L608 Y609 Q610 K611 K615 S618 T619 L620 F621 A622 ASN TYR ALA GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS GLY LYS ALA LYS LYS GLY SER SER PHE Q645 T646 V647 S648 A649 L650 H651 R652 E653 N654
L655 N656 K657 L658 M659 T660 N661 L662 R663 S664 T665 H666 R671 E677 T678 K679 S680 P681 G682 V683 M684 D685 N686 P687 L688 V689 V698 L699 E700 G701 I702 R703 I704 C705 R706 K707 G708 F709 P710 N711 R712 I713 L714 Y715 G716 D717 F718 R719 Q720 R721 Y722 R723 I724 L725 N726 P727 A728
A729 I730 P731 E732 G733 Q734 F735 I736 D737 S738 R739 K740 G741 A742 E743 K744 L745 L746 S747 S748 L749 D750 I751 D752 H753 N754 Q755 Y756 K757 F758 G759 H760 T761 K762 V763 F764 F765 K766 A767 G768 L769 L772 L773 E774 E775 M776 R777 D778 E779 R780 L781 S782 R783 I784 I785 T786 R787 I788 Q789
A790 Q791 S792 R793 G794 V795 L796 A797 R798 M799 E800 Y801 K802 K803 L804 L805 E806 R807 R808 D809 S810 L811 L812 V813 I814 Q815 R819 A820 F821 M822 G823 V824 K825 N826 W827 P828 W829 M830 K831 L832 Y833 F834 K835 I836 K837 P838 L839 L840 K841 S842 A843 E844 R845 E846 K847 E848 M849 A850 S851
M852 K853 E854 E855 F856 T857 R858 L859 K860 E861 A862 L863 E864 K865 S866 E867 A868 R869 R870 K871 E872 L873 E874 E875 K876 M877 V878 S879 L880 L881 Q882 E883 K884 N885 D886 L887 Q888 L889 Q890 V891 Q892 A893 E894 Q895 D896 N897 L898 A899 D900 A901 E902 E903 R904 C905 D906 Q907 L908 I909 K910 N911
K912 I913 Q914 L915 E916 A917 K918 V919 K920 E921 M922 N923 E924 R925 L926 E927 D928 E929 E930 E931 M932 N933 A934 E935 L936 T937 A938 K939 K940 R941 K942 L943 E944 D945 E946 C947 S948 E949 L950 K951 R952 D953 I954 D955 D956 L957 L961 A962 K963 V964 E965 K966 E967 K968 H969 E972 K991
G1155 Q1172 LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU LEU
ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER
ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU ARG GLU GLN TYR GLU
GLU GLU THR GLU ALA LYS ALA GLU LEU GLN ARG VAL LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LYS LEU ALA GLN ARG LEU GLN GLU ALA GLU GLU ALA VAL GLU ALA VAL ASN
ALA LYS CYS SER SER LEU GLU LYS THR LYS HIS ARG LEU GLN ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG SER ASN ALA ALA ALA ALA ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU
SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG GLU ASN LYS ASN LEU GLN GLU GLU ILE SER ASP LEU THR GLU GLN LEU GLY SER SER GLY LYS THR ILE HIS GLU LEU GLU LYS
VAL ARG LYS GLN LEU GLU ALA GLU LYS MET GLU LEU GLN SER ALA LEU GLU GLU ALA GLU ALA SER LEU GLU HIS GLU GLY LYS ILE LEU ARG ALA GLN LEU GLU PHE ASN GLN ILE LYS ALA GLU ILE GLU ARG LYS LEU ALA GLU LYS ASP GLU GLU MET GLU GLN ALA LYS ARG
ASN HIS LEU ARG VAL VAL ASP SER LEU GLN THR SER LEU ASP ALA GLU THR ARG SER ARG ASN GLU ALA LEU ARG VAL LYS LYS LYS MET GLU GLY ASP LEU ASN GLU MET GLU ILE GLN LEU SER HIS ALA ASN ARG MET ALA ALA GLU ALA GLN LYS GLN VAL LYS SER LEU GLN SER
LEU LEU LYS ASP THR GLN ILE GLN LEU ASP ASP ALA VAL ARG ALA ASN ASP ASP LEU LYS GLU ASN ILE ALA ILE VAL GLU ARG ARG ASN ASN LEU LEU GLN ALA GLU LEU GLU GLU LEU ARG ALA VAL VAL GLU GLN THR GLU ARG SER ARG LYS LEU ALA GLU GLN GLU LEU ILE GLU
THR SER GLU ARG VAL GLN LEU LEU HIS SER GLN ASN THR SER LEU ILE ASN GLN LYS LYS LYS MET ASP ALA ASP LEU SER GLN LEU GLN THR GLU VAL GLU GLU ALA VAL GLN GLU CYS ARG ASN ALA GLU GLU LYS ALA LYS LYS ALA ILE THR ASP ALA ALA MET MET ALA GLU GLU
LEU LYS LYS GLU GLN ASP THR SER ALA HIS LEU GLU ARG MET LYS LYS ASN MET GLU GLN THR ILE LYS ASP LEU GLN HIS ARG LEU ASP GLU ALA GLU GLN ILE ALA LEU LYS GLY GLY LYS LYS GLN LEU GLN LYS LEU GLU ALA ARG VAL ARG GLU LEU GLU ASN GLU LEU GLU ALA



• Molecule 1: Myosin-7

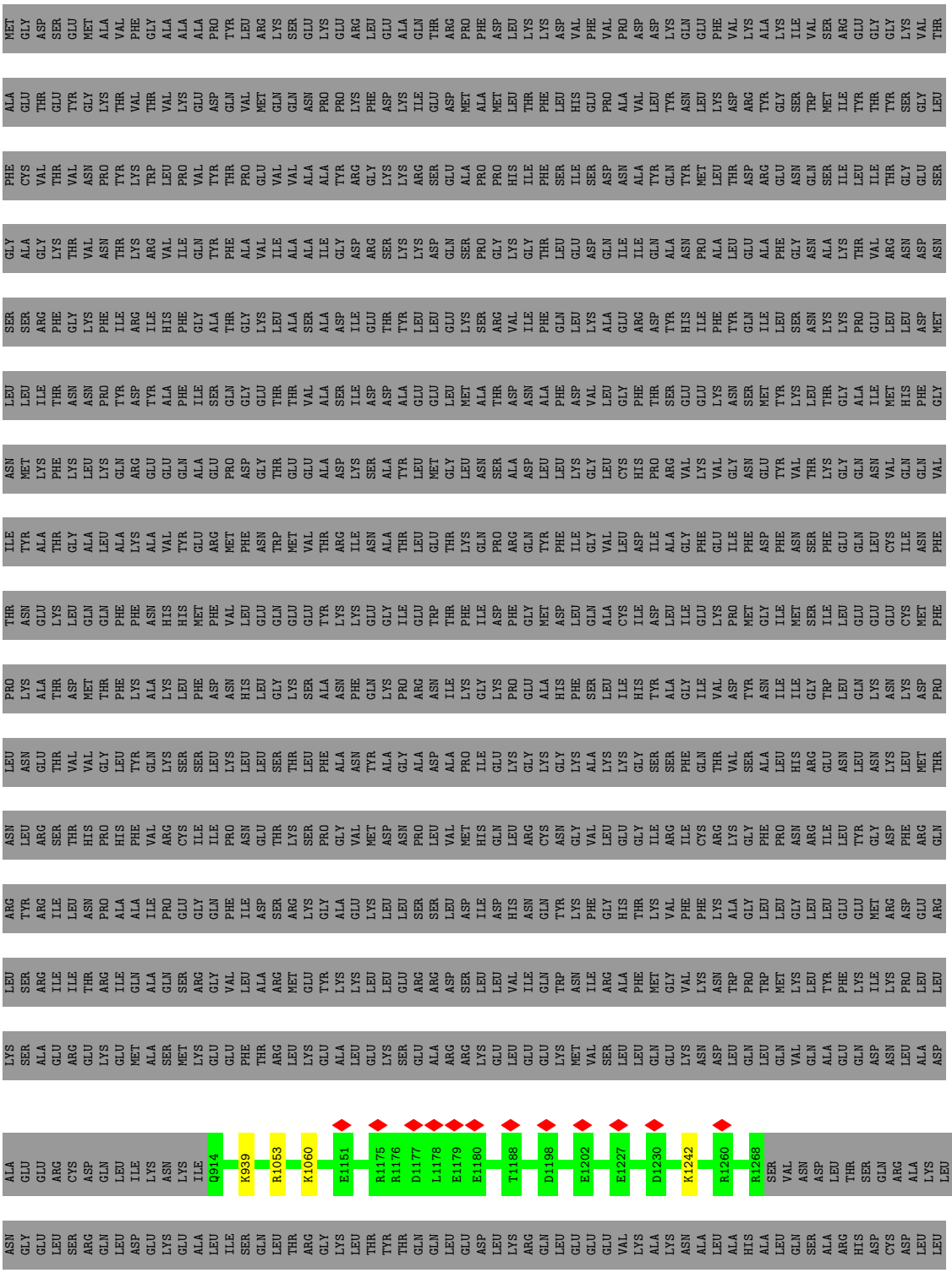
Chain AB:

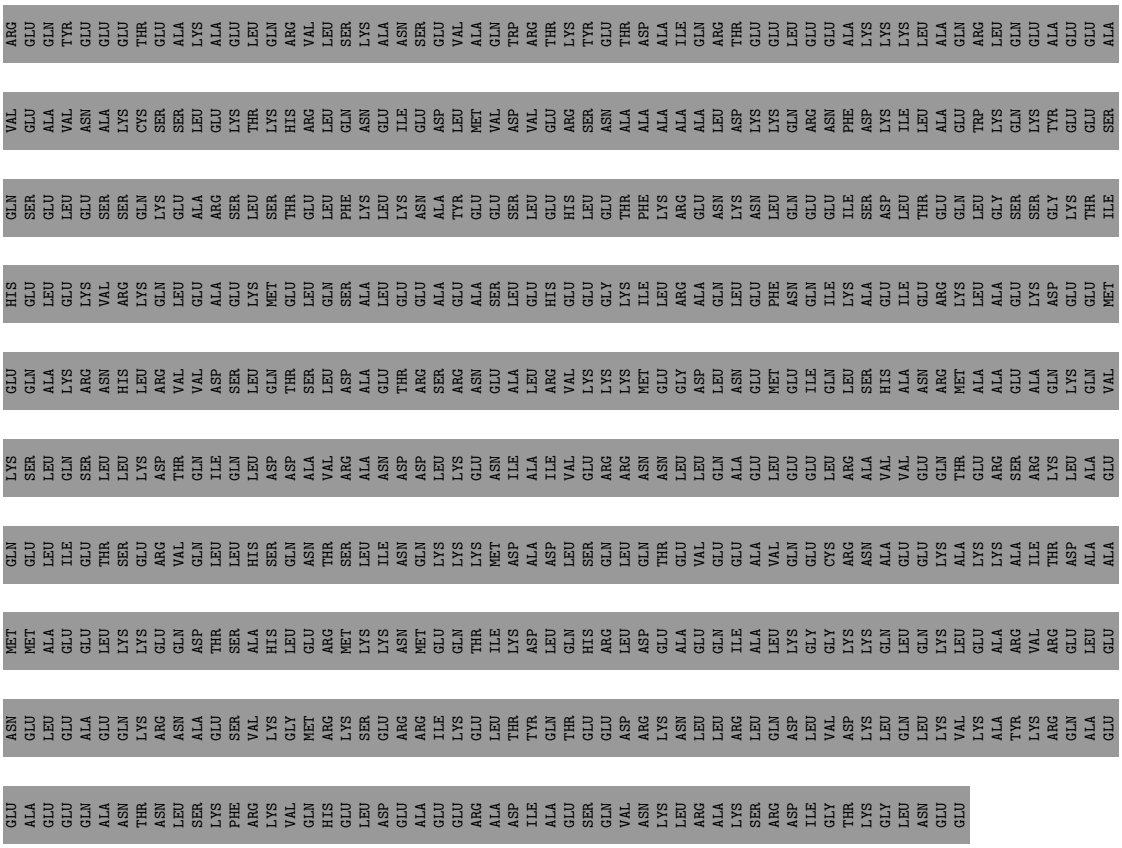



M690 H691 Q692 L693 R694 C695 N696 G697 V698 L699 E700 G701 I702 R703 I704 C705 R706 K707 G708 F709 P710 N711 R712 I713 L714 Y715 G716 D717 F718 R719 Q720 R721 Y722 R723 I724 L725 N726 P727 A728 A729 I730 G733 I736 D737 S738 R739 K740 G741 A742 E743 K744 L745 L746 S747 S748 L749 D750 I751
D752 H753 N754 Q755 Y756 K757 F758 G759 H760 T761 K762 V763 F764 F765 K766 A767 G768 L769 L770 G771 L772 L773 E774 E775 M776 R777 D778 E779 R780 L781 S782 R783 I784 I785 T786 R787 I788 Q789 A790 Q791 S792 R793 G794 V795 L796 A797 R798 M799 E800 Y801 K802 K803 L804 L805 E806 R807 R808 D809 S810 L811
L812 V813 I814 Q815 I818 R819 A820 F821 M822 G823 V824 K825 N826 W827 P828 W829 M830 K831 L832 Y833 F834 K835 I836 K837 P838 L839 L840 K841 S842 A843 E844 R845 E846 K847 E848 M849 A850 S851 M852 K853 E854 E855 F856 T857 R858 L859 K860 E861 A862 L863 E864 K865 S866 E867 A868 R869 E872 L873
E874 E875 K876 M877 V878 S879 L880 L881 Q882 E883 K884 N885 D886 L887 Q888 L889 Q890 V891 Q892 A893 E894 Q895 D896 N897 L898 A899 D900 A901 E902 E903 R904 C905 D906 Q907 L908 I909 K910 N911 K912 I913 Q914 L915 E916 A917 K918 V919 K920 E921 M922 N923 E924 R925 L926 E927 D928 E929 E930 E931 M932 N933
A934 E935 L936 T937 A938 K939 E944 D945 E946 C947 S948 E949 L950 K951 R952 D953 I954 L957 H969 N973 A998 L999 D1009 L1010 K1026 D1032 D1033 L1034 E1035 G1036 S1037 Q1040 E1041 V1044 R1045 M1046 D1047 L1048 E1049 R1050 A1051 K1052 L1055 L1059 A1153 G1154 G1155
A1156 T1157 S1158 K1166 A1169 Q1172 LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU
PHE LYS LEU GLU LEU ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU
ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU
ARG GLU GLN TYR GLU GLU GLU THR GLU ALA LYS ALA GLU LEU GLN ARG VAL LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LEU ALA GLN ARG LEU GLN GLU ALA GLU GLU ALA
VAL GLU ALA VAL ASN ALA LYS CYS SER SER LEU GLU LYS THR LYS HIS ARG LEU GLN ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG SER ASN ALA ALA ALA ALA ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER
GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG GLU ASN LYS ASN LEU GLN GLU GLU ILE SER ASP LEU THR GLU GLN LEU GLY SER SER GLY LYS THR ILE
HIS GLU LEU GLU LYS VAL ARG LYS GLN LEU GLU ALA GLU LYS MET GLU LEU GLN SER ALA LEU GLU GLU ALA GLU ALA SER LEU GLU HIS GLU GLY LYS ILE LEU ARG ALA GLN LEU GLU PHE ASN GLN ILE LYS ALA GLU ILE GLU ARG LYS LEU ALA GLU LYS ASP GLU GLU MET
GLU GLN ALA LYS ARG ASN HIS LEU ARG VAL VAL ASP SER LEU GLN THR SER LEU ASP ALA GLU THR ARG SER ARG ASN GLU ALA LEU ARG VAL LYS LYS MET GLU GLY ASP LEU ASN GLU MET GLU ILE GLN LEU SER HIS ALA ASN ARG MET ALA ALA GLU ALA GLN LYS GLN VAL
LYS SER LEU GLN SER LEU LEU LYS ASP THR GLN ILE GLN LEU ASP ASP ALA VAL ARG ALA ASN ASP ASP LEU LYS GLU ASN ILE ALA ILE VAL GLU ARG ARG ASN ASN LEU LEU GLN ALA GLU LEU GLU GLU LEU ARG ALA VAL VAL GLU GLN THR GLU ARG SER ARG LYS LEU ALA GLU
GLN GLU LEU ILE GLU THR SER GLU ARG VAL GLN LEU LEU HIS SER GLN ASN THR SER LEU ILE ASN GLN LYS LYS LYS MET ASP ALA ASP LEU SER GLN LEU GLN THR GLU VAL GLU GLU ALA VAL GLN GLU CYS ARG ASN ALA GLU GLU LYS ALA LYS LYS ALA ILE THR ASP ALA ALA
MET MET ALA GLU GLU LEU LYS LYS GLU GLN ASP THR SER ALA HIS LEU GLU ARG MET LYS LYS ASN MET GLU GLN THR ILE LYS ASP LEU GLN HIS ARG LEU ASP GLU ALA GLU GLN ILE ALA LEU LYS GLY GLY LYS LYS GLN LEU GLN LYS LEU GLU ALA ARG VAL ARG GLU LEU GLU
ASN GLU LEU GLU ALA GLU GLN LYS ARG ASN ALA GLU SER VAL LYS GLY MET ARG LYS SER GLU ARG ARG ILE LYS GLU LEU THR TYR GLN THR GLU GLU ASP ARG LYS ASN LEU LEU ARG LEU GLN ASP LEU VAL ASP LYS LEU GLN LEU LYS VAL LYS ALA TYR LYS ARG GLN ALA GLU

• Molecule 1: Myosin-7

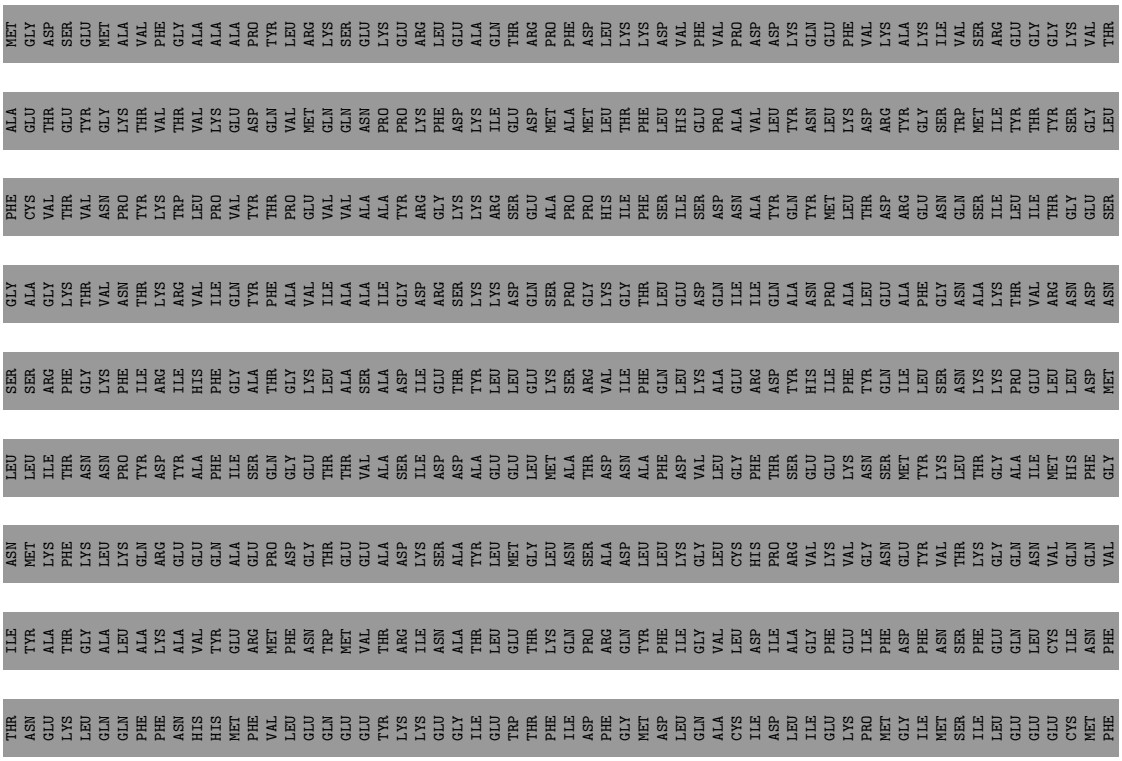
Chain AG:

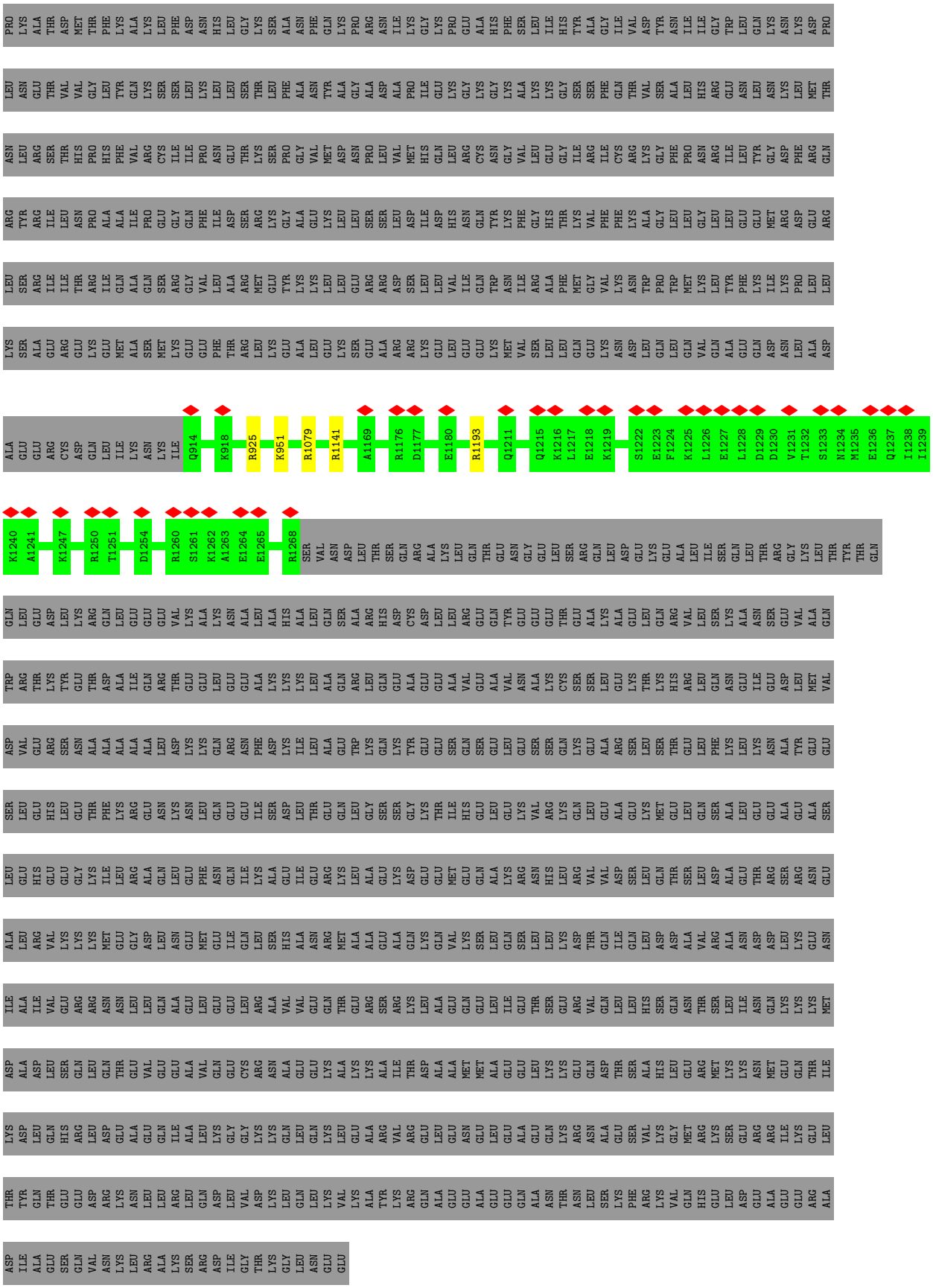




• Molecule 1: Myosin-7

Chain AH:

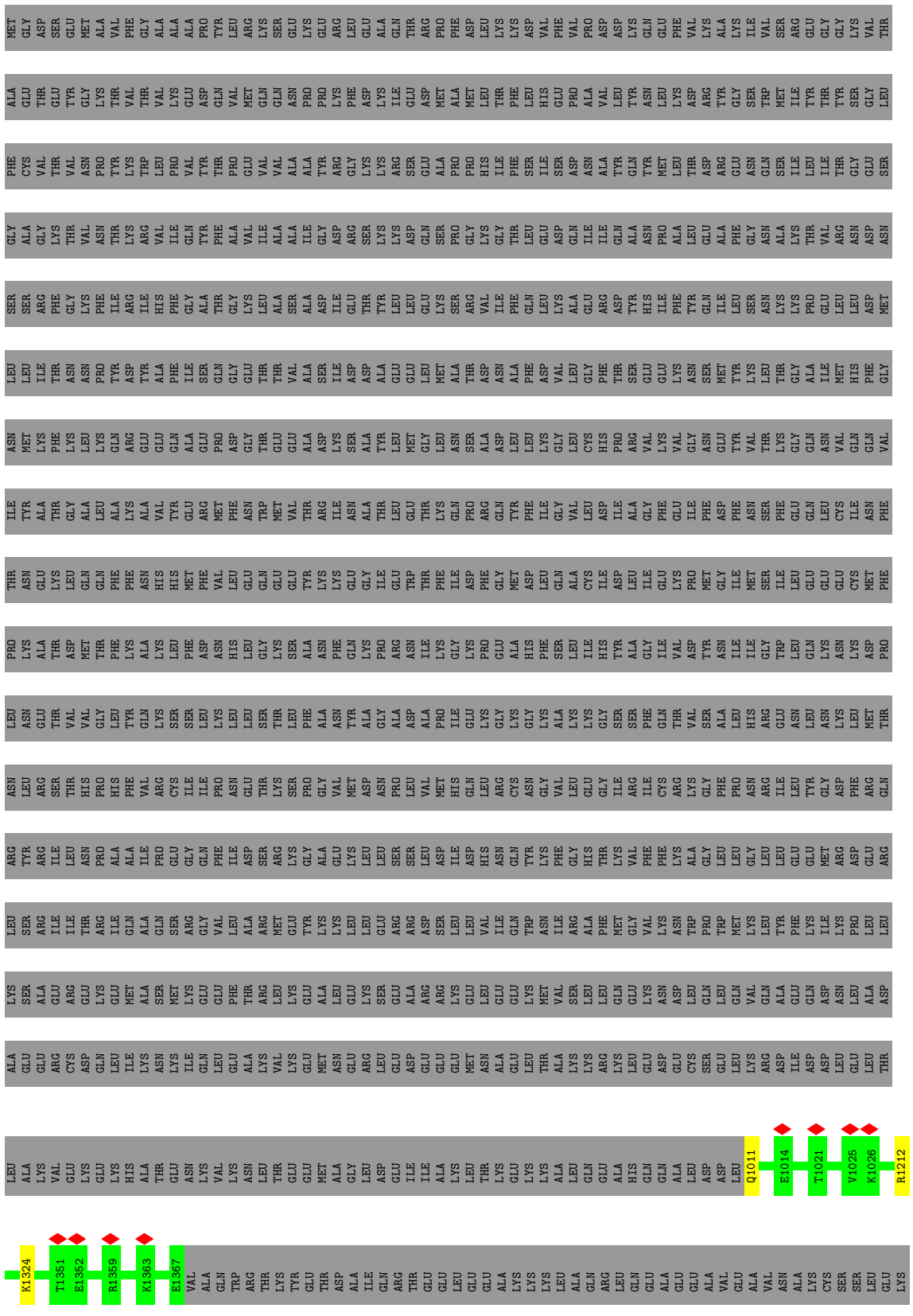




- Molecule 1: Myosin-7

Chain AI:


18%
82%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E1014
T1021
V1025
K1026
R1212
K1324
T1351
E1352
R1359
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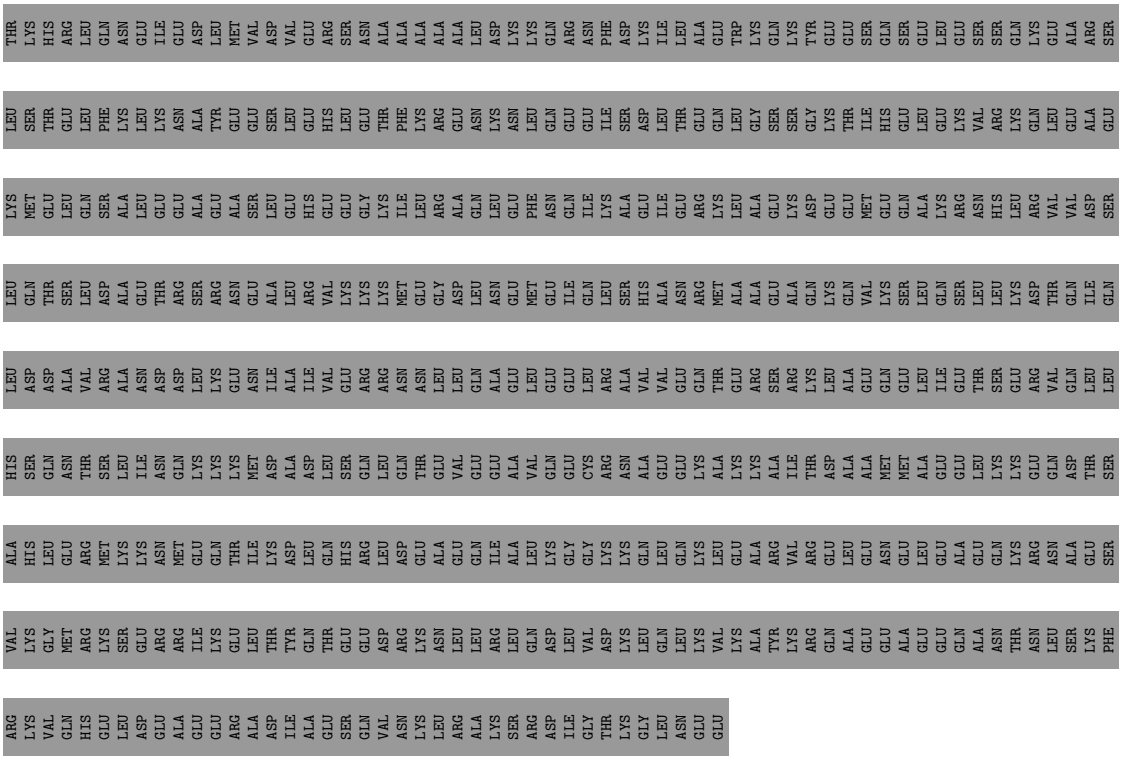
E1367



- Molecule 1: Myosin-7

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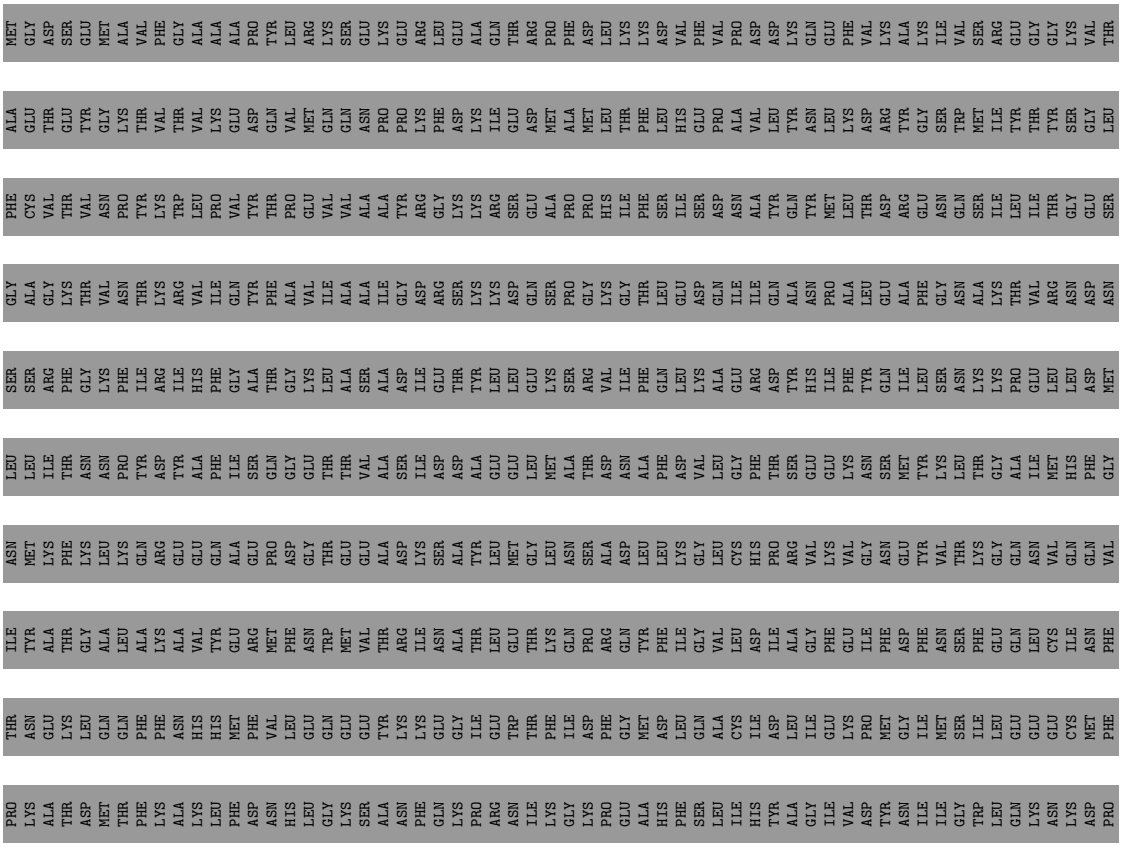

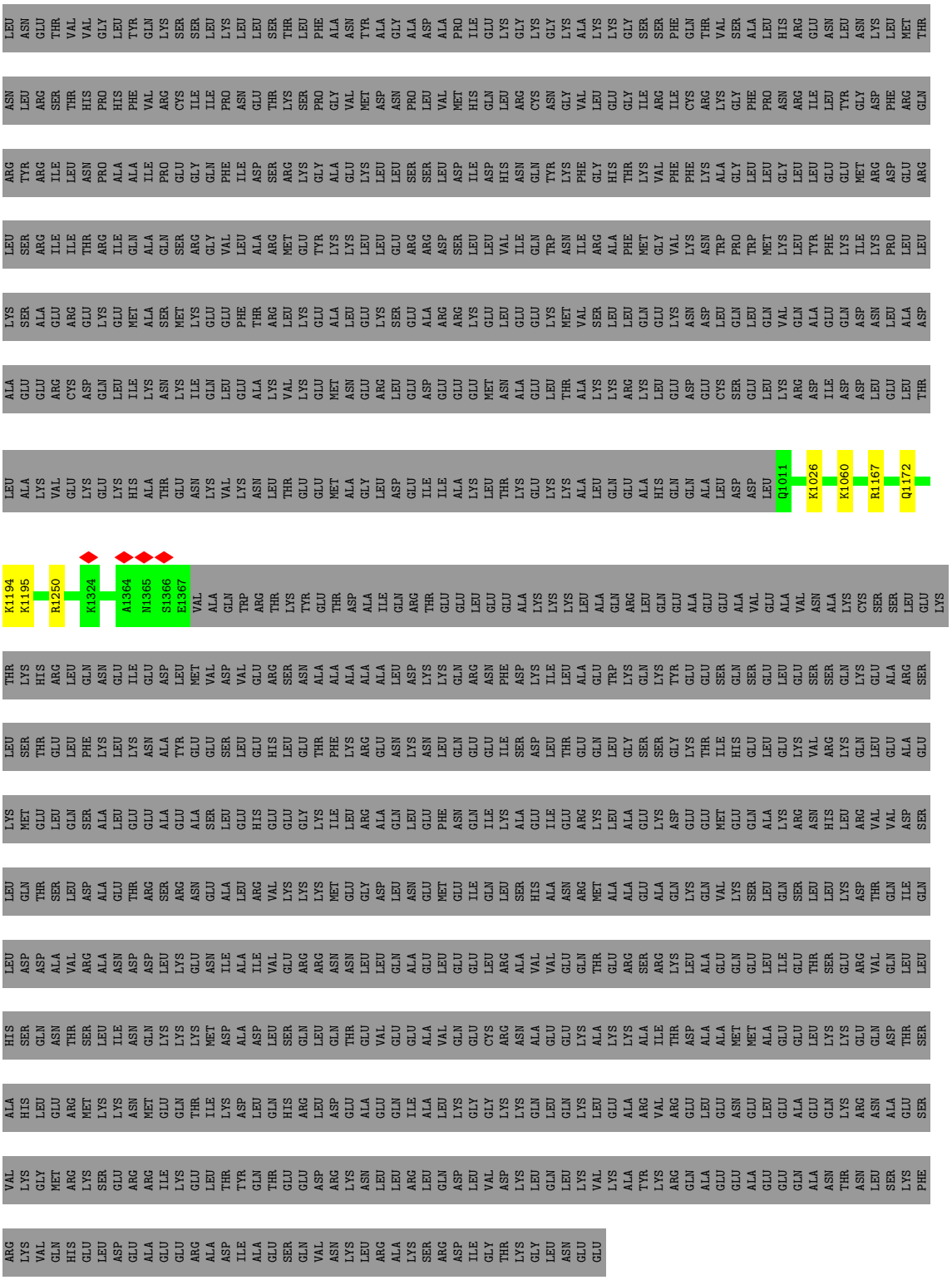

• Molecule 1: Myosin-7

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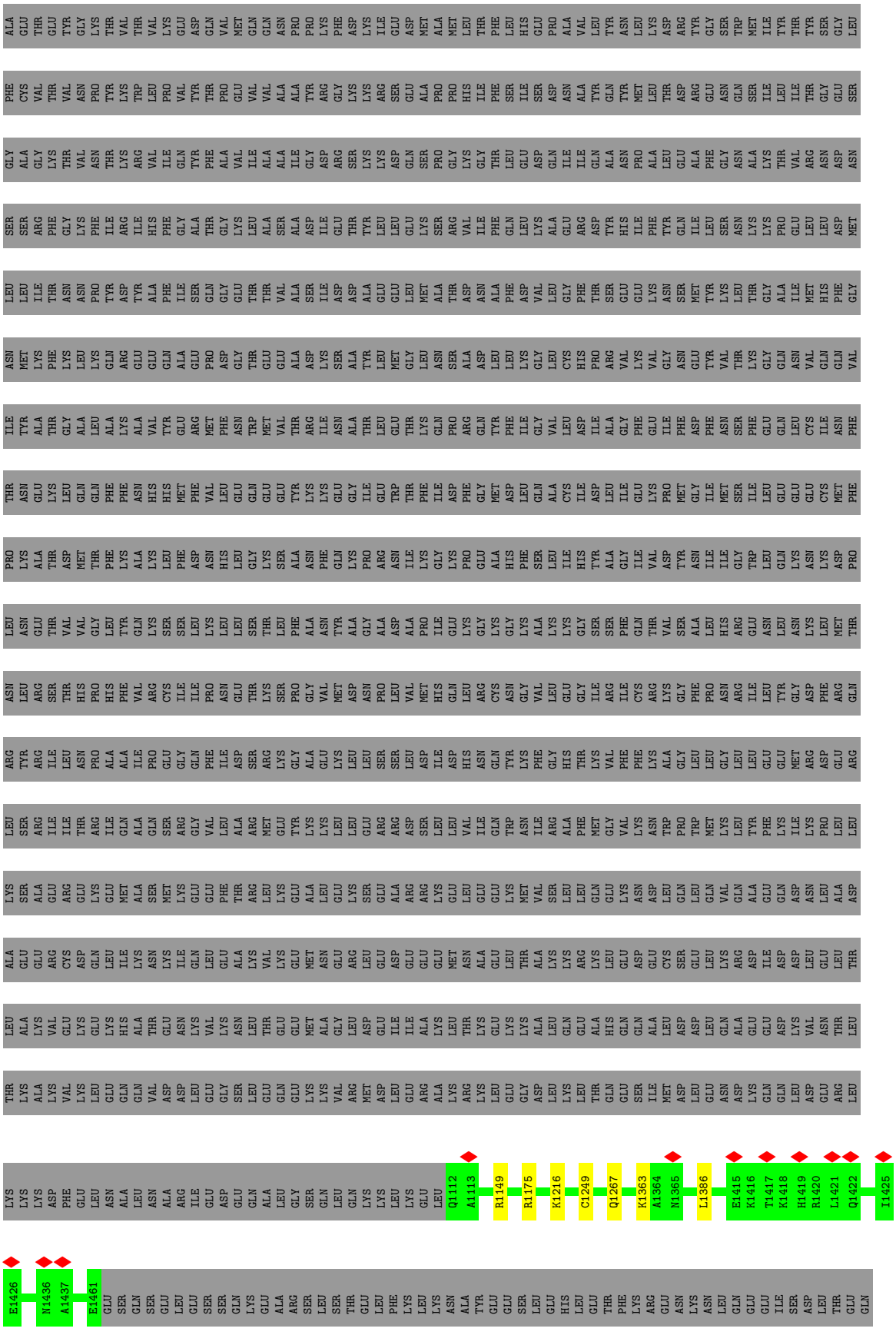
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C1249
Q1267
K1363
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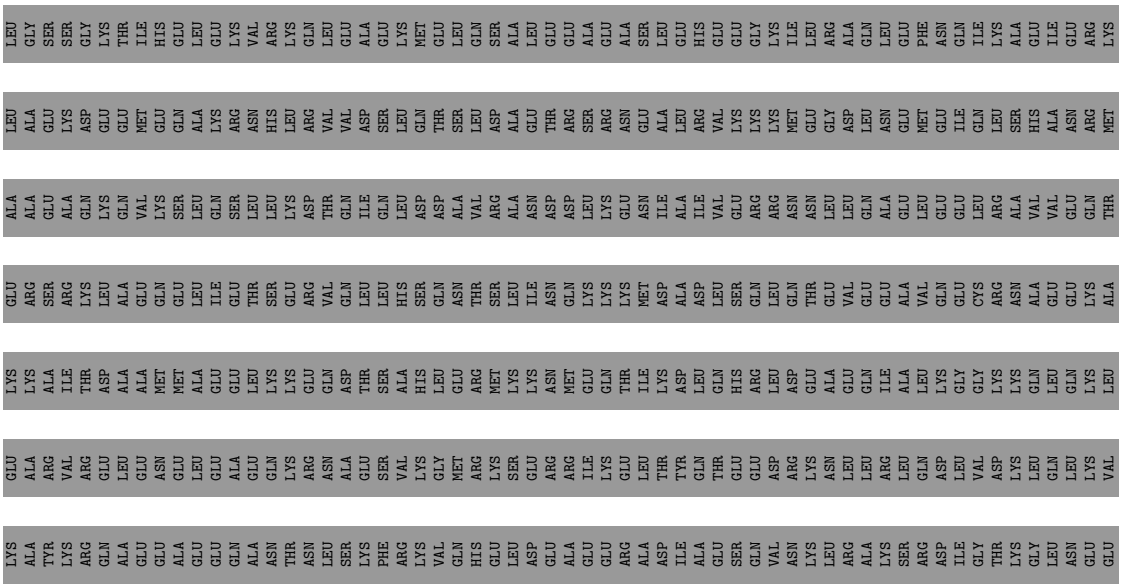
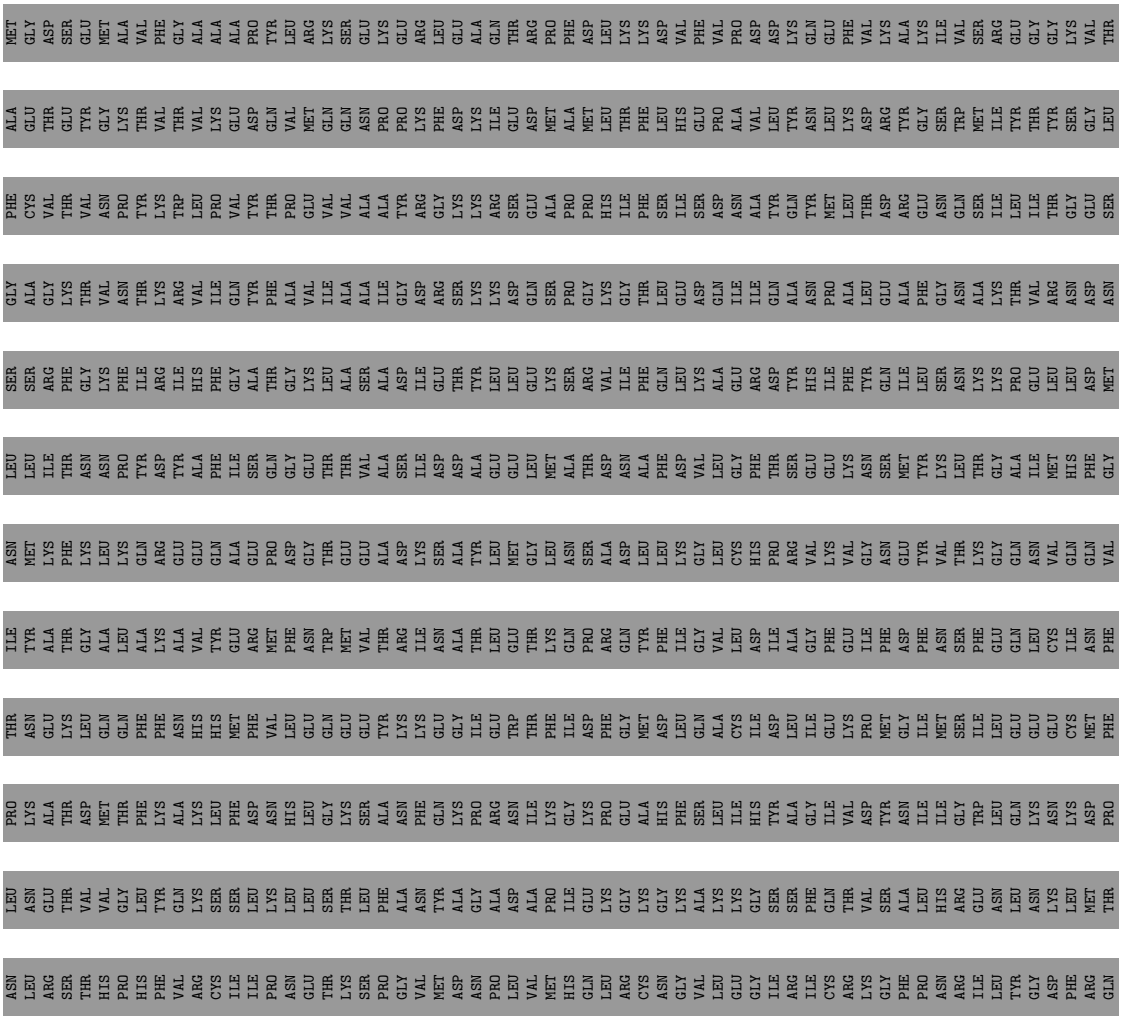
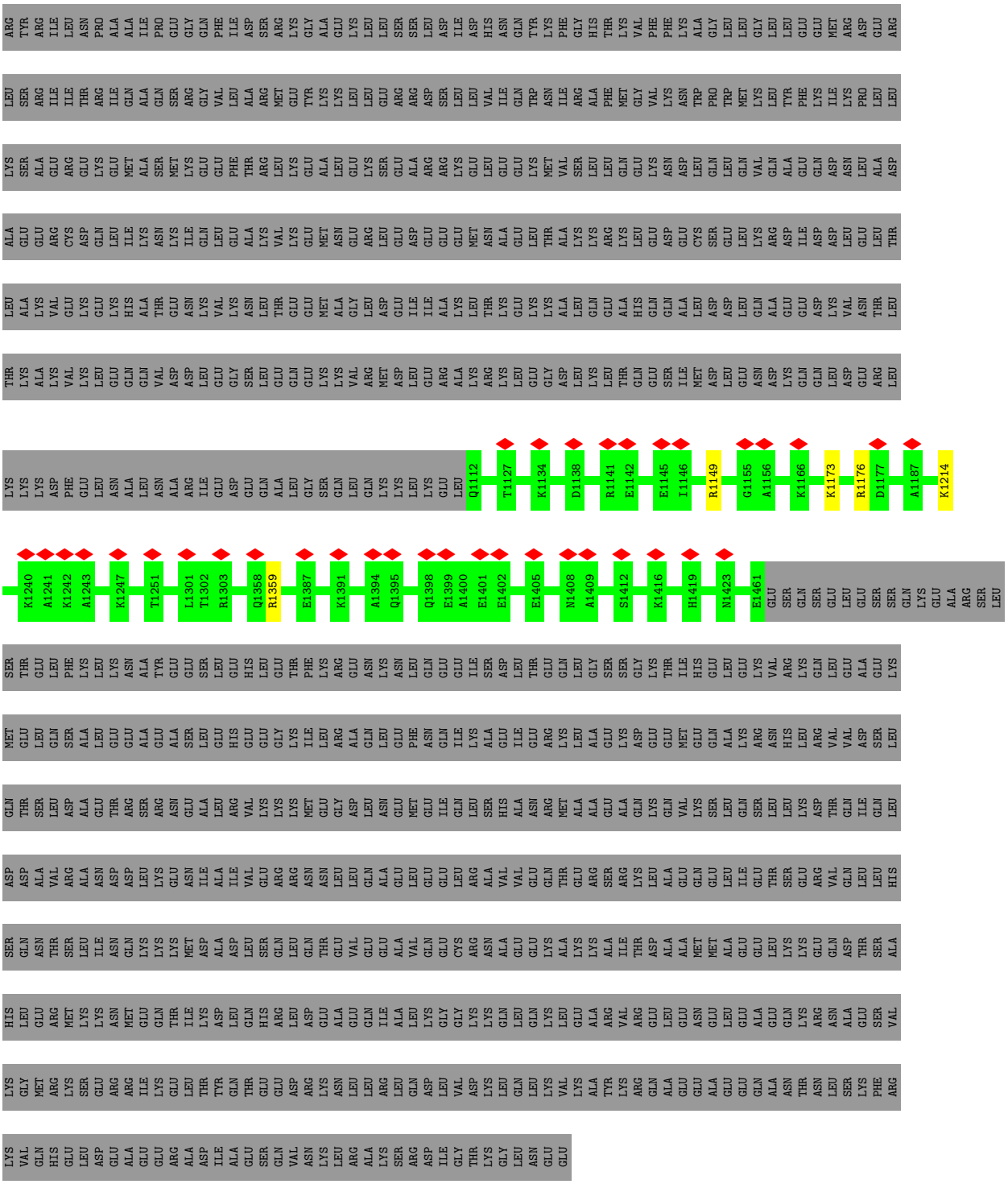


• Molecule 1: Myosin-7

Chain AL:





• Molecule 1: Myosin-7

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

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

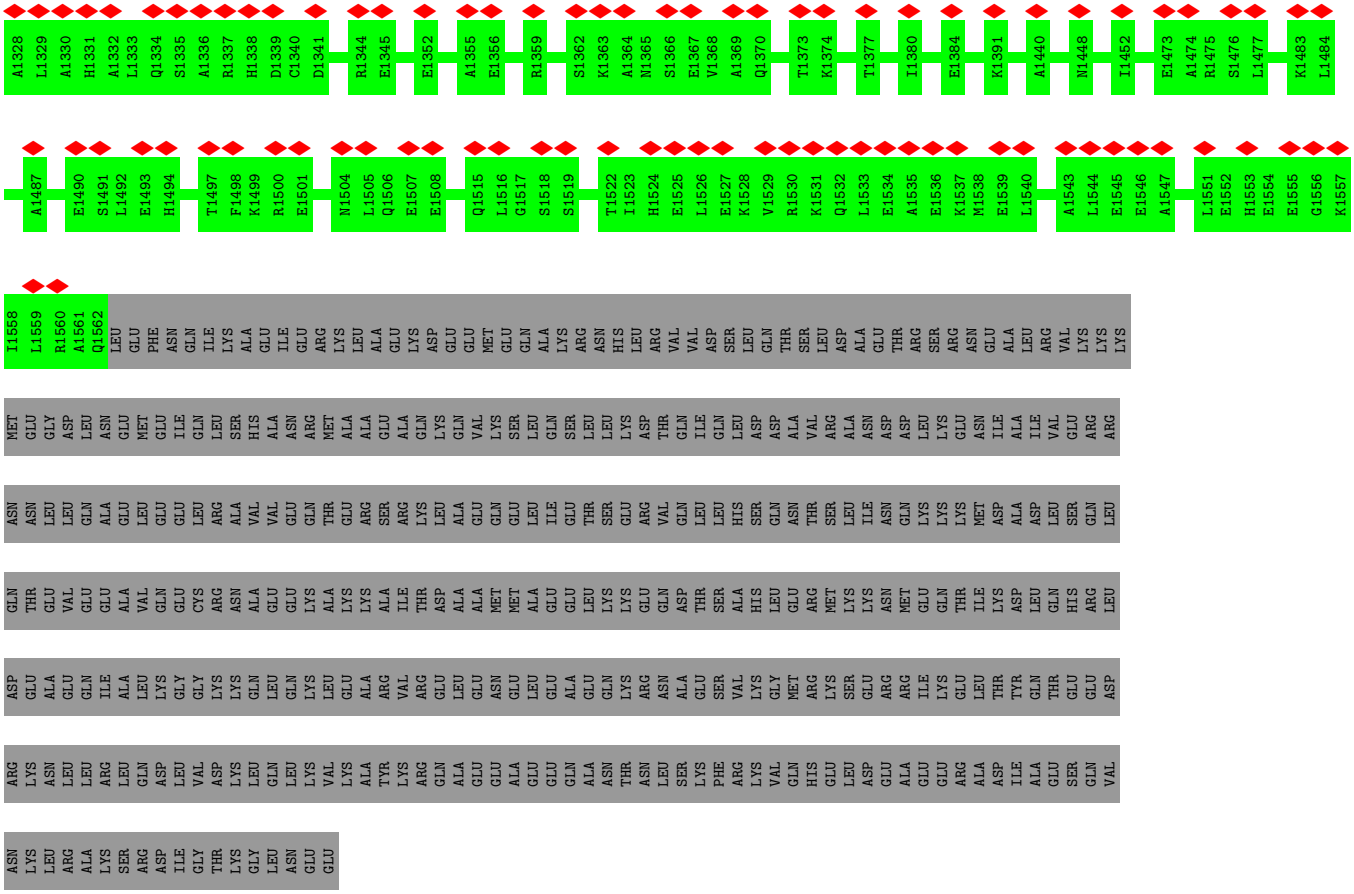
LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

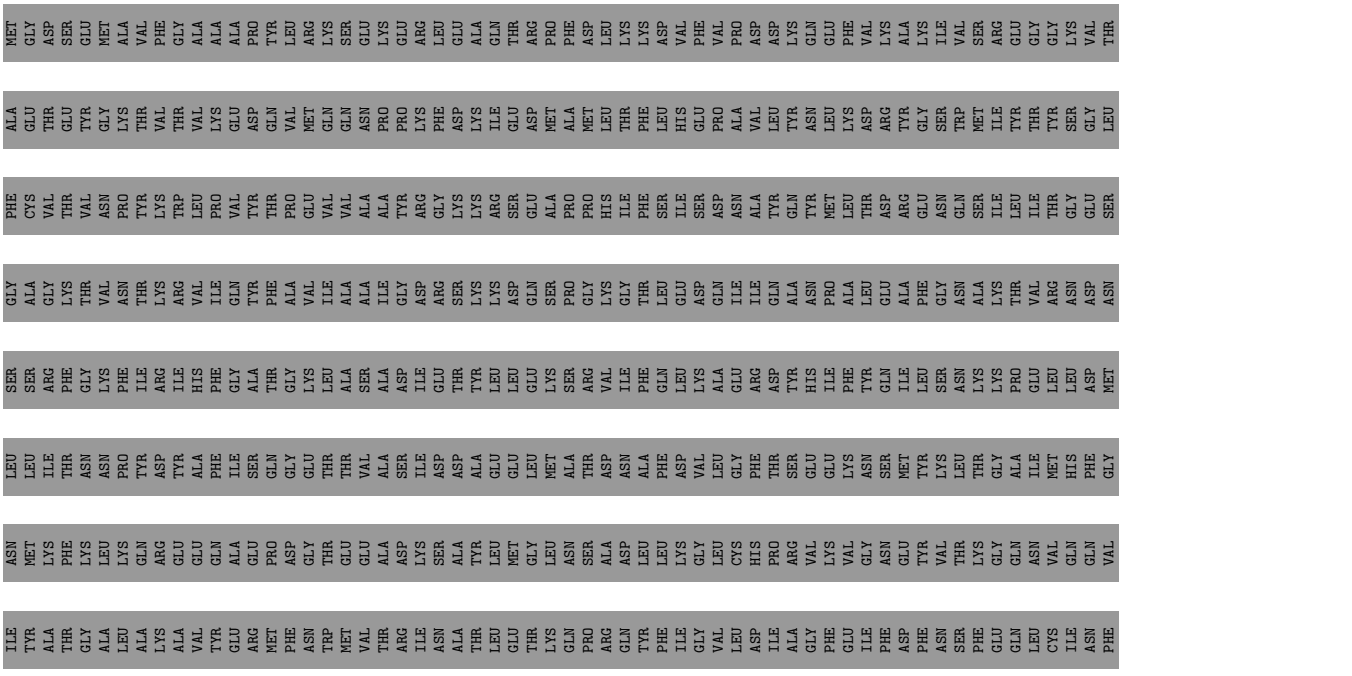
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

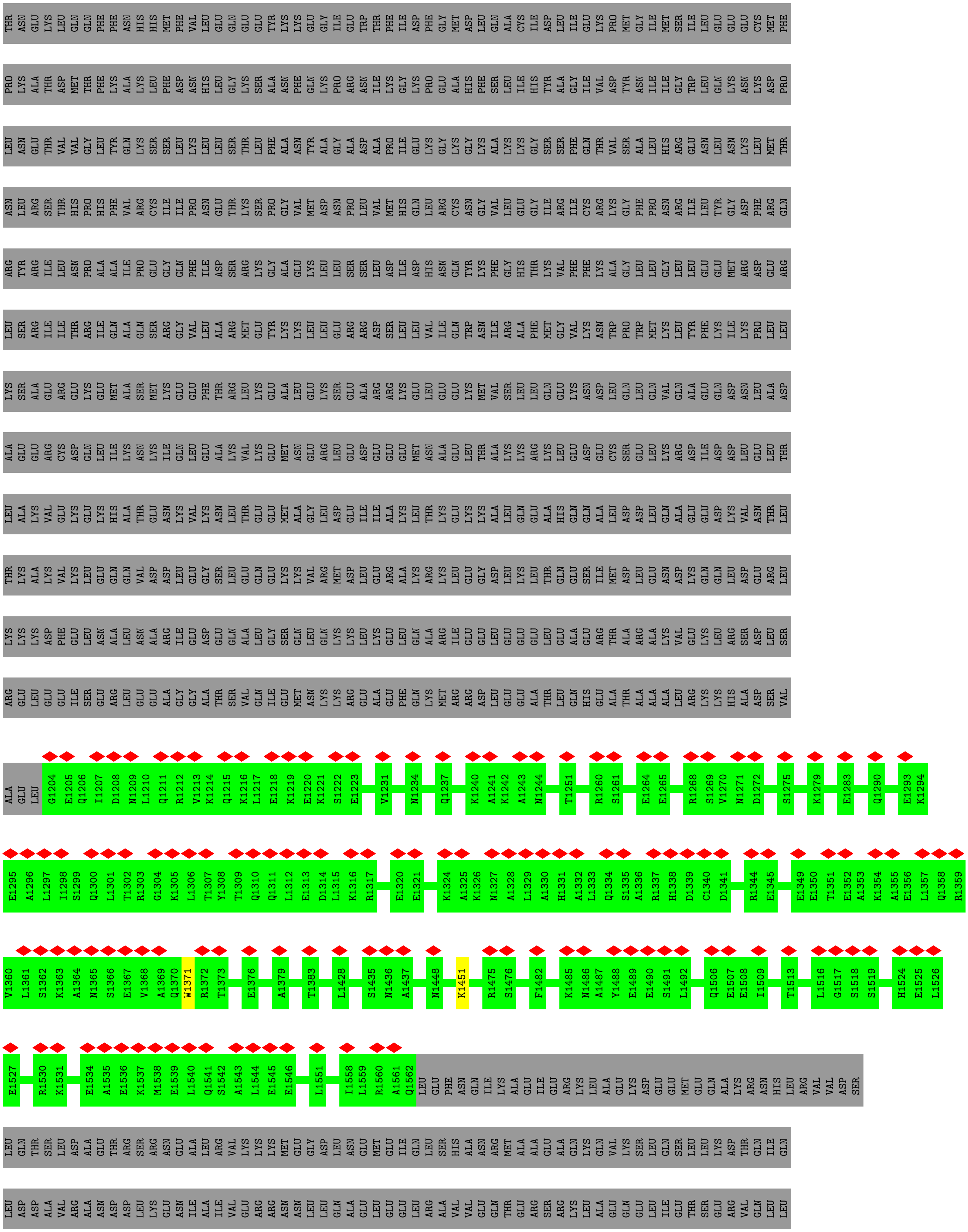
ARG GLU LEU GLU GLU ILE SER GLU ARG LEU GLU GLU ALA GLY GLY ALA THR SER VAL GLN ILE GLU MET ASN LYS LYS ARG GLU ALA GLU PHE GLN LYS MET ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL

ALA GLU LEU G1204 D1230 D1254 R1260 S1261 K1262 A1263 E1264 N1271 D1272 T1282 E1283 N1284 R1289 D1292 E1293 K1294 E1295 A1296 L1297 I1298 S1299 Q1300 L1301 T1302 R1303 G1304 K1305 L1306 T1307 Y1308 T1309 Q1310 Q1311 L1312 E1313 D1314 L1315 K1316 R1317 Q1318 L1319 E1320 E1321 E1322 V1323 K1324 A1325 K1326 N1327



- Molecule 1: Myosin-7

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PRO LYS ALA THR ASP MET THR PHE LYS ALA LYS LEU PHE ASP ASN HIS LEU GLY LYS SER ALA ASN PHE GLN LYS PRO ARG ASN ILE LYS GLY LYS PRO GLU ALA HIS PHE SER LEU ILE HIS TYR ALA GLY ILE VAL ASP TYR ASN ILE ILE GLY TRP LEU GLN LYS ASN LYS ASP PRO
LEU ASN GLU THR VAL VAL GLY LEU TYR GLN LYS SER SER LEU LYS LEU LEU SER THR LEU PHE ALA ASN TYR ALA GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS GLY LYS ALA LYS LYS GLY SER SER PHE GLN THR VAL SER ALA LEU HIS ARG GLU ASN LEU ASN LYS LEU MET THR
ASN LEU ARG SER THR HIS PRO HIS PHE VAL ARG CYS ILE ILE PRO ASN GLU THR LYS SER PRO GLY VAL MET ASP ASN PRO LEU VAL MET HIS GLN LEU ARG CYS ASN GLY VAL LEU GLU GLY ILE ARG ILE CYS ARG LYS GLY PHE PRO ASN ARG ILE LEU TYR GLY ASP PHE ARG GLN
ARG TYR ARG ILE LEU ASN PRO ALA ALA ILE PRO GLU GLY GLN PHE ILE ASP SER ARG LYS GLY ALA GLU LYS LEU LEU SER SER LEU ASP ILE ASP HIS ASN GLN TYR LYS PHE GLY HIS THR LYS VAL PHE PHE LYS ALA GLY LEU LEU GLY LEU LEU GLU GLU MET ARG ASP GLU ARG
LEU SER ARG ILE ILE THR ARG ILE GLN ALA GLN SER ARG GLY VAL LEU ALA ARG MET GLU TYR LYS LYS LEU LEU GLU ARG ARG ASP SER LEU LEU VAL ILE GLN TRP ASN ILE ARG ALA PHE MET GLY VAL LYS ASN TRP PRO TRP MET LYS LEU TYR PHE LYS ILE LYS PRO LEU LEU
LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP
ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR
LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU
THR LYS ALA LYS VAL LYS LEU GLU GLN GLN VAL ASP ASP LEU GLU GLY SER LEU GLU GLN GLU LYS LYS VAL ARG MET ASP LEU GLU ARG ALA LYS ARG LYS LEU GLU GLY ASP LEU LYS LEU THR GLN GLU SER ILE MET ASP LEU GLU ASN ASP LYS GLN GLN LEU ASP GLU ARG LEU
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER
ARG GLU LEU GLU GLU ILE SER GLU ARG LEU GLU GLU ALA GLY GLY ALA THR SER VAL GLN ILE GLU MET ASN LYS LYS ARG GLU ALA GLU PHE GLN LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL
ALA GLU LEU G1204 E1205 Q1206 I1207 D1208 N1209 L1210 Q1211 R1212 V1213 K1214 Q1215 K1216 L1217 E1218 K1219 E1220 K1221 S1222 E1223 V1231 N1234 Q1237 K1240 A1241 K1242 A1243 N1244 T1251 R1260 S1261 E1264 E1265 R1268 S1269 V1270 N1271 D1272 S1275 K1279 E1283 Q1290 E1293 K1294
E1295 A1296 L1297 I1298 S1299 Q1300 L1301 T1302 R1303 G1304 K1305 L1306 T1307 Y1308 T1309 Q1310 Q1311 L1312 E1313 D1314 L1315 K1316 R1317 E1320 E1321 K1324 A1325 K1326 N1327 A1328 L1329 A1330 H1331 A1332 L1333 Q1334 S1335 A1336 R1337 H1338 D1339 C1340 D1341 R1344 E1345 E1349 E1350 T1351 E1352 A1353 K1354 A1355 E1356 L1357 Q1358 R1359
V1360 L1361 S1362 K1363 A1364 N1365 S1366 E1367 V1368 A1369 Q1370 W1371 R1372 T1373 E1376 A1379 T1383 L1428 S1435 N1436 A1437 N1448 K1451 R1475 S1476 F1482 K1485 N1486 A1487 Y1488 E1489 E1490 S1491 L1492 Q1506 E1507 E1508 I1509 T1513 L1516 G1517 S1518 S1519 H1524 E1525 L1526
E1527 R1530 K1531 E1534 A1535 E1536 K1537 M1538 E1539 L1540 Q1541 S1542 A1543 L1544 E1545 E1546 L1551 I1558 L1559 R1560 A1561 Q1562 LEU GLU PHE ASN GLN ILE LYS ALA GLU ILE GLU ARG LYS LEU ALA GLU LYS ASP GLU GLU MET GLU GLN ALA LYS ARG ASN HIS LEU ARG VAL VAL ASP SER
LEU GLN THR SER LEU ASP ALA GLU THR ARG SER ARG ASN GLU ALA LEU ARG VAL LYS LYS MET GLU GLY ASP LEU ASN GLU MET GLU ILE GLN LEU SER HIS ALA ASN ARG MET ALA ALA GLU ALA GLN LYS GLN VAL LYS SER LEU GLN SER LEU LEU LYS ASP THR GLN ILE GLN
LEU ASP ASP ALA VAL ARG ALA ASN ASP ASP LEU LYS GLU ASN ILE ALA ILE VAL GLU ARG ARG ASN ASN LEU LEU GLN ALA GLU LEU GLU GLU LEU ARG ALA VAL VAL GLU GLN THR GLU ARG SER ARG LYS LEU ALA GLU GLN GLU LEU ILE GLU THR SER GLU ARG VAL GLN LEU LEU

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

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

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

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

- Molecule 1: Myosin-7

Chain AO:

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

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

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

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

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

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

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

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

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

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

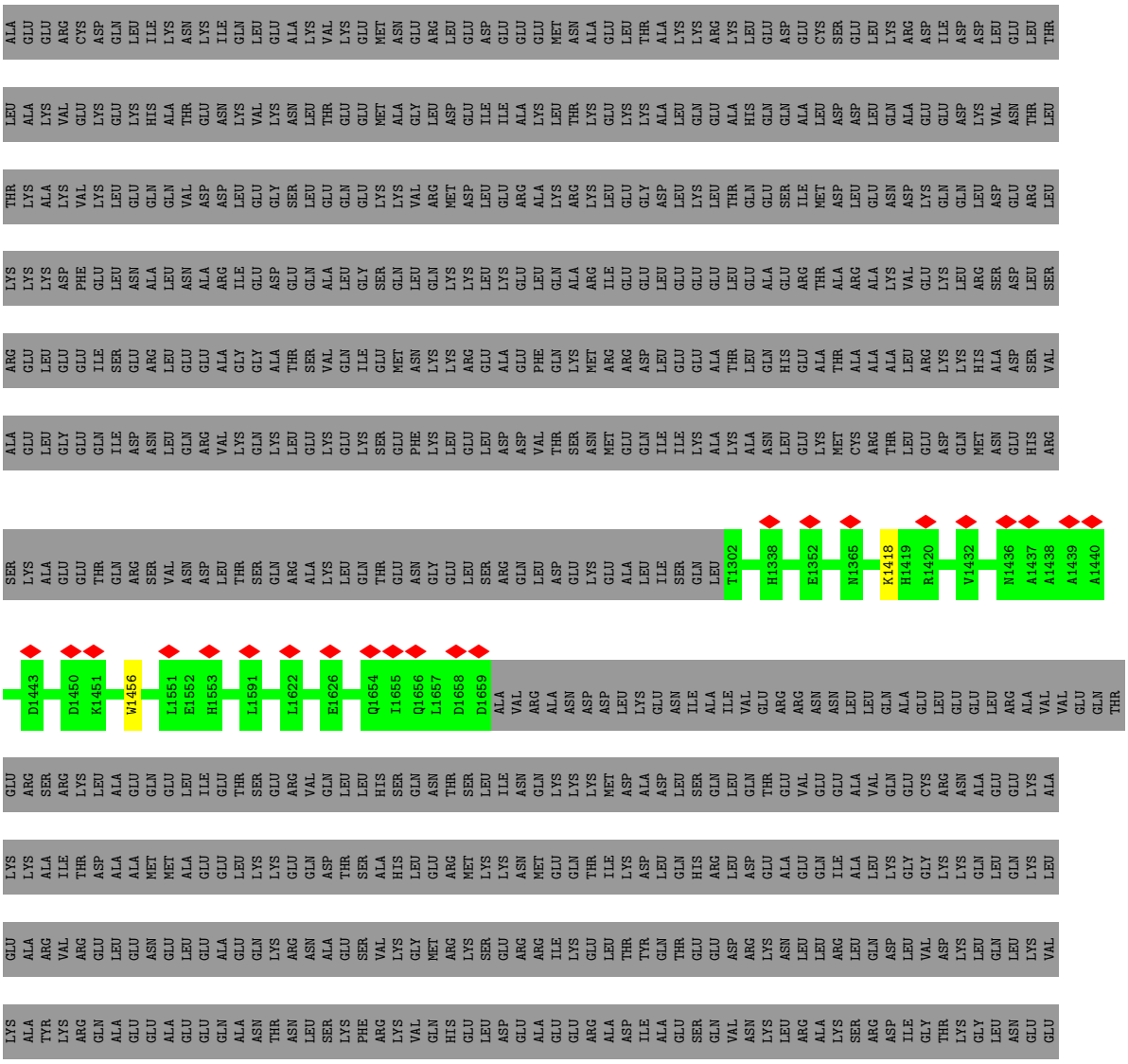
LEU ASN GLU THR VAL VAL GLY LEU TYR GLN LYS SER SER LEU LYS LEU LEU SER THR LEU PHE ALA ASN TYR ALA GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS GLY LYS ALA LYS LYS GLY SER SER PHE GLN THR VAL SER ALA LEU HIS ARG GLU ASN LEU ASN LYS LEU MET THR

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

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

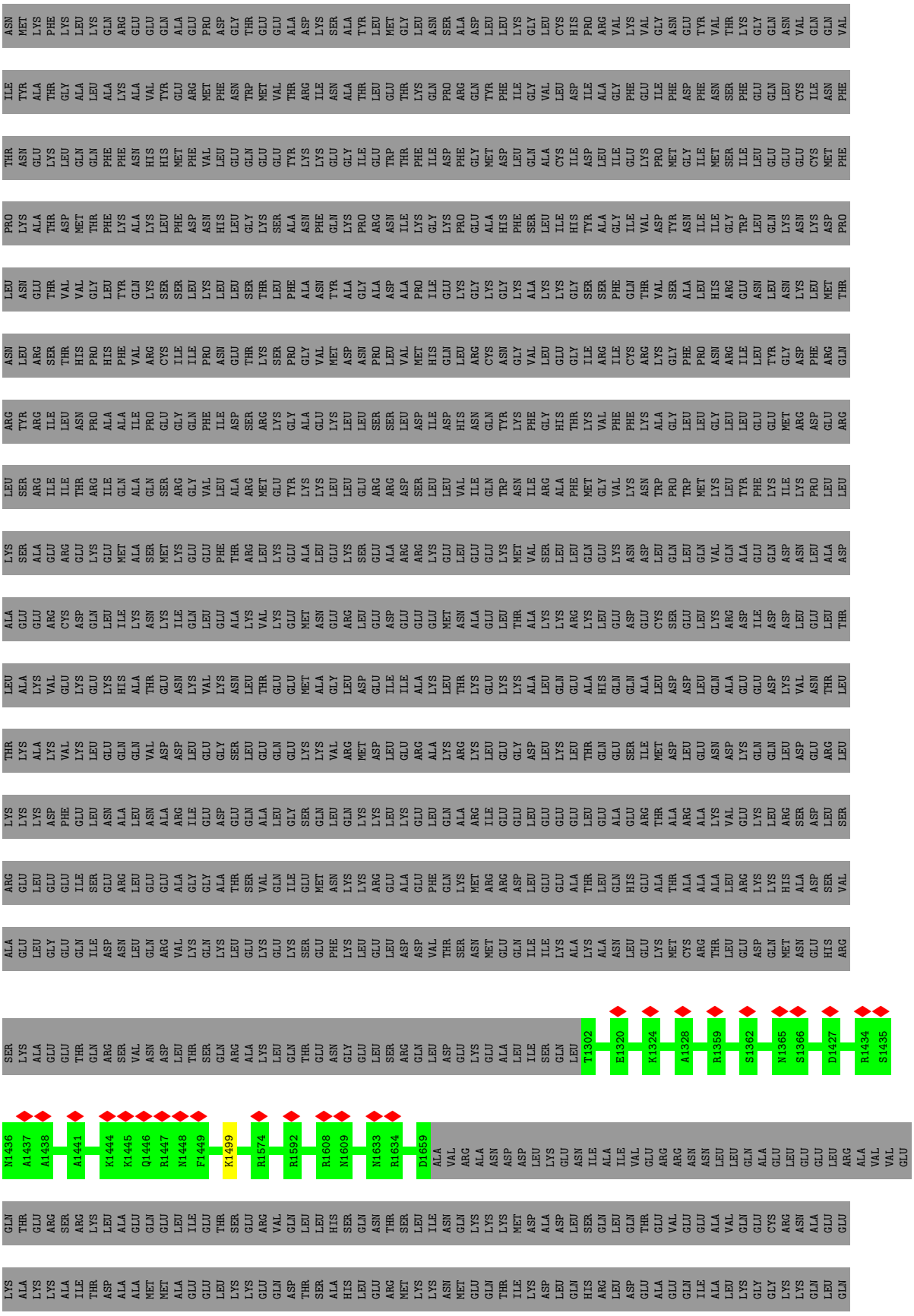
LEU SER ARG ILE ILE THR ARG ILE GLN ALA GLN SER ARG GLY VAL LEU ALA ARG MET GLU TYR LYS LYS LEU LEU GLU ARG ARG ASP SER LEU LEU VAL ILE GLN TRP ASN ILE ARG ALA PHE MET GLY VAL LYS ASN TRP PRO TRP MET LYS LEU TYR PHE LYS ILE LYS PRO LEU LEU

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP



• Molecule 1: Myosin-7

Chain AP: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Q1446
R1447
N1448
F1449
K1499
R1574
R1592
R1608
N1609
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R1634
D1659

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

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

GLU GLU

• Molecule 1: Myosin-7

Chain AQ: 18% 82%

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

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

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

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

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

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

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

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

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

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

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

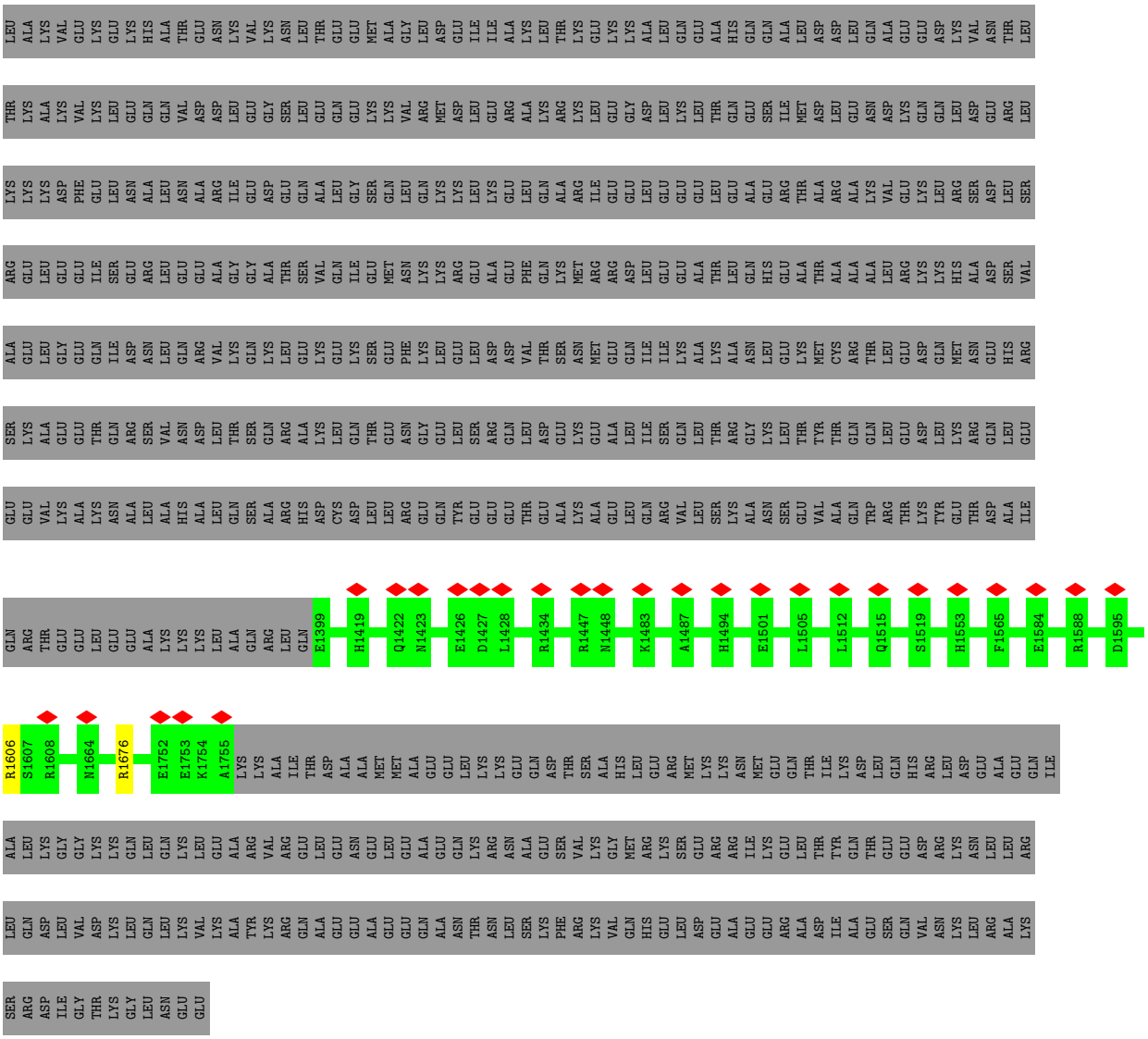
ASN LEU ARG SER THR HIS PHE VAL ARG CYS ILE ILE PRO ASN GLU THR LYS SER PRO GLY VAL MET ASP ASN PRO LEU VAL MET HIS GLN LEU ARG GLN GLU LYS ILE ARG ILE CYS ARG LYS GLY PHE PRO ASN ARG ILE GLU LEU LEU GLU GLU MET ARG ASP GLU ARG

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

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

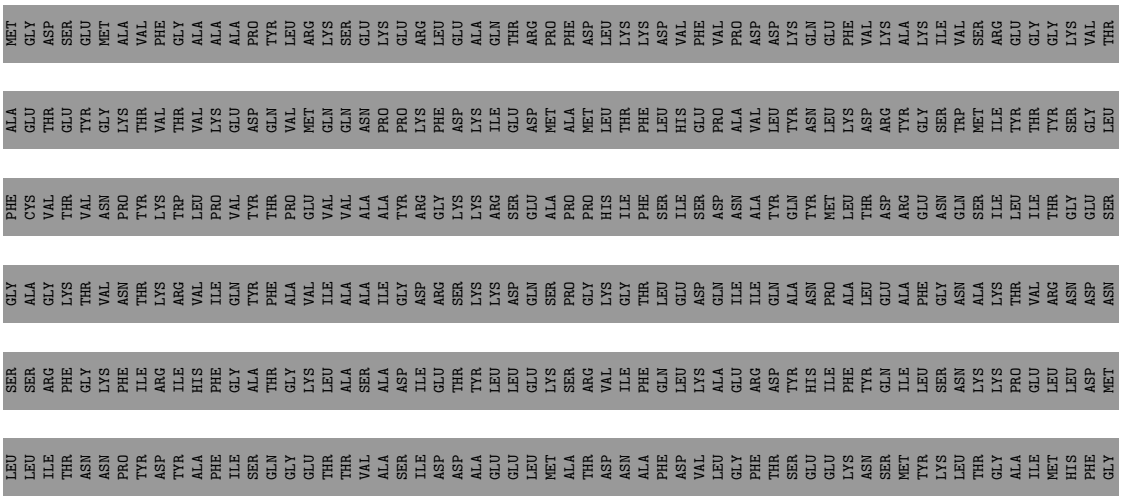
LYS SER ALA GLU ARG GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG ARG LYS GLU GLU LYS MET VAL SER LEU LEU GLN GLU GLN GLN ASP ASN ASP LEU ALA ASP

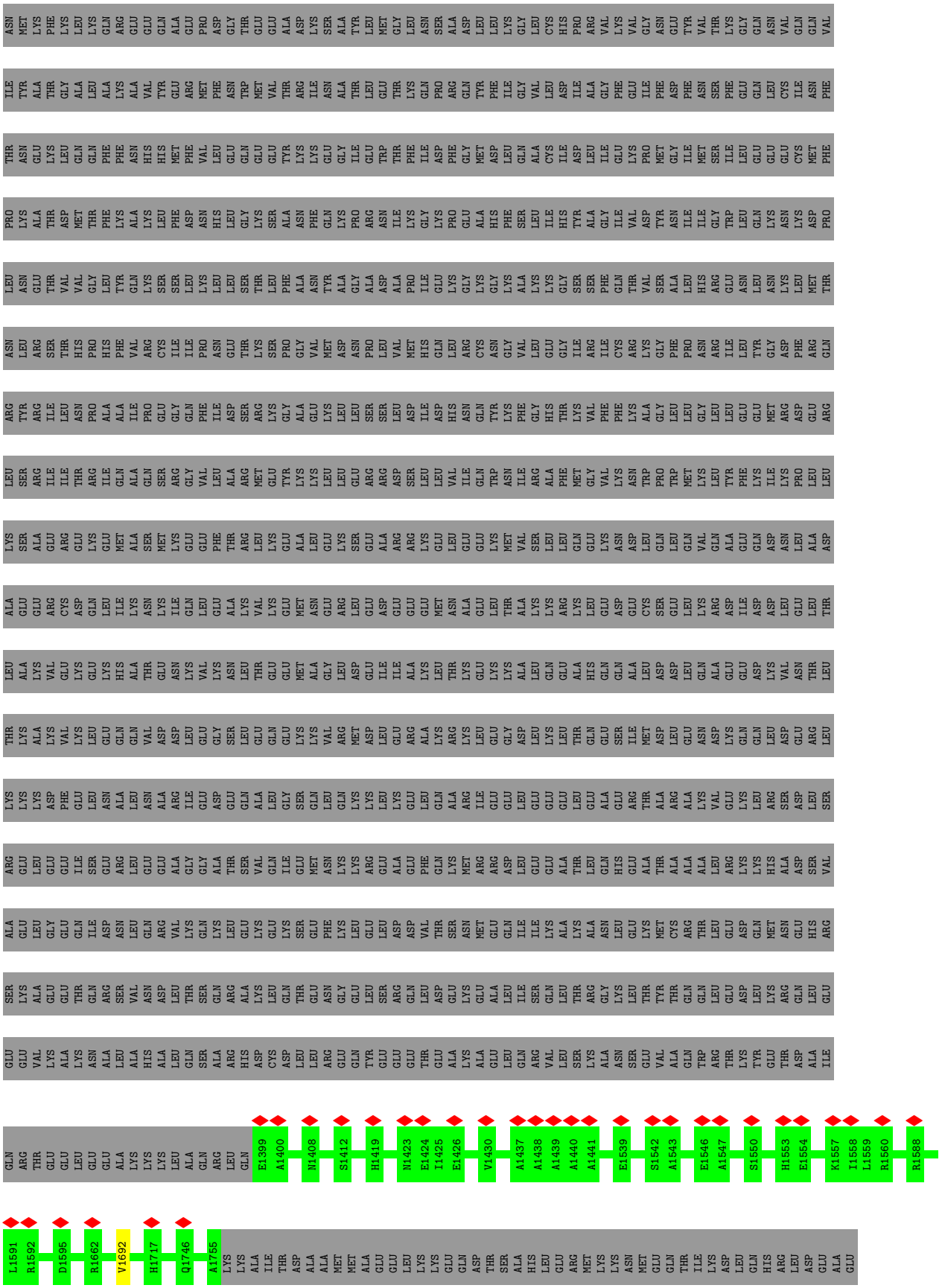
ALA GLU GLU LEU ILE LYS VAL LYS GLU MET ASN GLU ARG LEU GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU THR



• Molecule 1: Myosin-7

Chain AR:

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N1408
S1412
H1419
N1423
E1424
I1425
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V1430
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A1440
A1441
E1539
S1542
A1543
E1546
A1547
S1550
H1553
E1554
K1557
I1558
L1559
R1560
R1588
L1591
R1592
D1595
R1662
V1692
H1717
Q1746
A1755

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

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

ALA LYS SER ARG ASP ILE GLY THR LYS GLY LEU ASN GLU GLU

- Molecule 1: Myosin-7

Chain AS: 6% 19% 81%

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

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

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

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

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

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

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

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

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

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

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

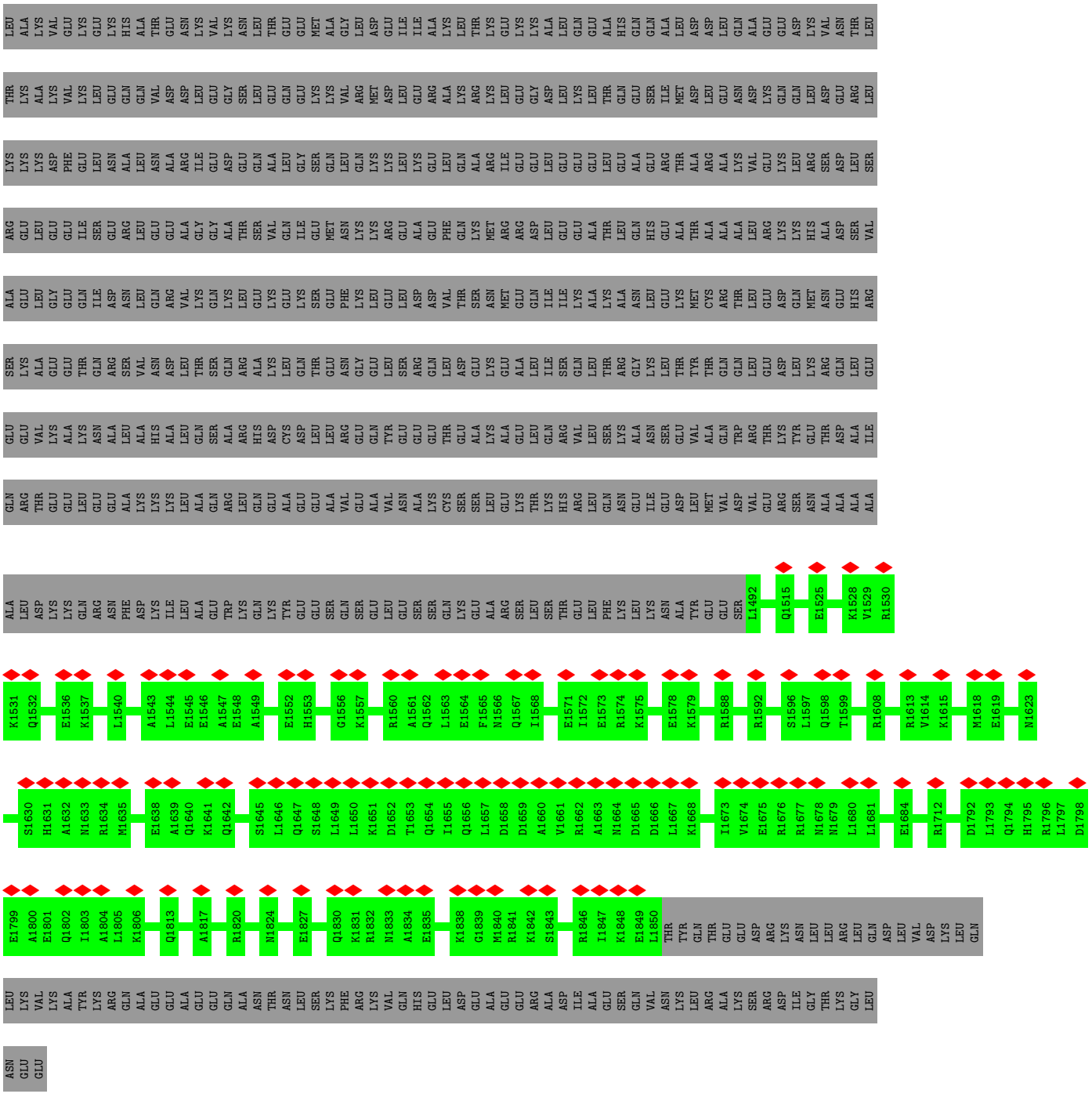
ASN LEU ARG SER THR HIS PRO HIS PHE VAL ARG CYS ILE ILE PRO ASN GLU THR LYS SER PRO GLY VAL MET ASP ASN PRO LEU VAL MET HIS GLN LEU ARG CYS ASN GLY VAL LEU GLU GLY ILE ARG ILE CYS ARG LYS GLY PHE PRO ASN ARG ILE LEU TYR GLY ASP PHE ARG GLN

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

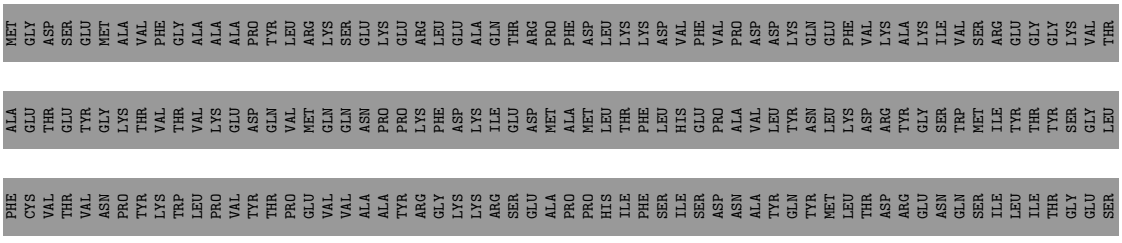
LEU SER ARG ILE ILE THR ARG ILE GLN ALA GLN SER ARG GLY VAL LEU ALA ARG MET GLU TYR LYS LYS LEU LEU GLU ARG ARG ASP SER LEU LEU VAL ILE GLN TRP ASN ILE ARG ALA PHE MET GLY VAL LYS ASN TRP PRO TRP MET LYS LEU TYR PHE LYS ILE LYS PRO LEU LEU

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR



• Molecule 1: Myosin-7



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

ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER L1492 K1503 K1528 K1531 Q1532 L1533

E1534 K1537 M1538 E1539 L1540 Q1541 S1542 A1543 L1544 L1551 K1557 I1558 Q1562 F1565 N1566 I1572 E1573 L1576 E1582 Q1585 N1589 T1605 R1606 S1607 R1608 N1609 L1612 R1613 V1614 K1615 K1616 Q1628 L1629 S1630 H1631 A1632 N1633 A1637 E1638 A1639 Q1640 K1641 Q1642 V1643 K1644 S1645

L1646 Q1647 S1648 L1649 L1650 K1651 D1652 T1653 Q1654 I1655 Q1656 L1657 D1658 D1659 A1660 V1661 R1662 A1663 N1664 D1665 K1668 A1672 I1673 V1674 E1675 R1676 R1677 K1728 K1771 D1792 L1793 R1796 L1797 D1798 E1799 Q1802 K1806 K1809 Q1813 K1814 A1817 N1824 E1825 M1840 R1841 K1842

R1845 R1846 I1847 K1848 E1849 L1850 THR TYR GLN THR GLU GLU ASP ARG LYS ASN LEU LEU ARG LEU GLN ASP LEU VAL ASP LYS LEU GLN LEU LYS VAL LYS ALA TYR LYS ARG GLN ALA GLU GLU ALA GLU GLU GLN ALA ASN THR ASN LEU SER LYS PHE ARG LYS VAL GLN HIS GLU LEU ASP

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

• Molecule 1: Myosin-7

Chain AU: 17% 83%

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

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

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

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

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

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

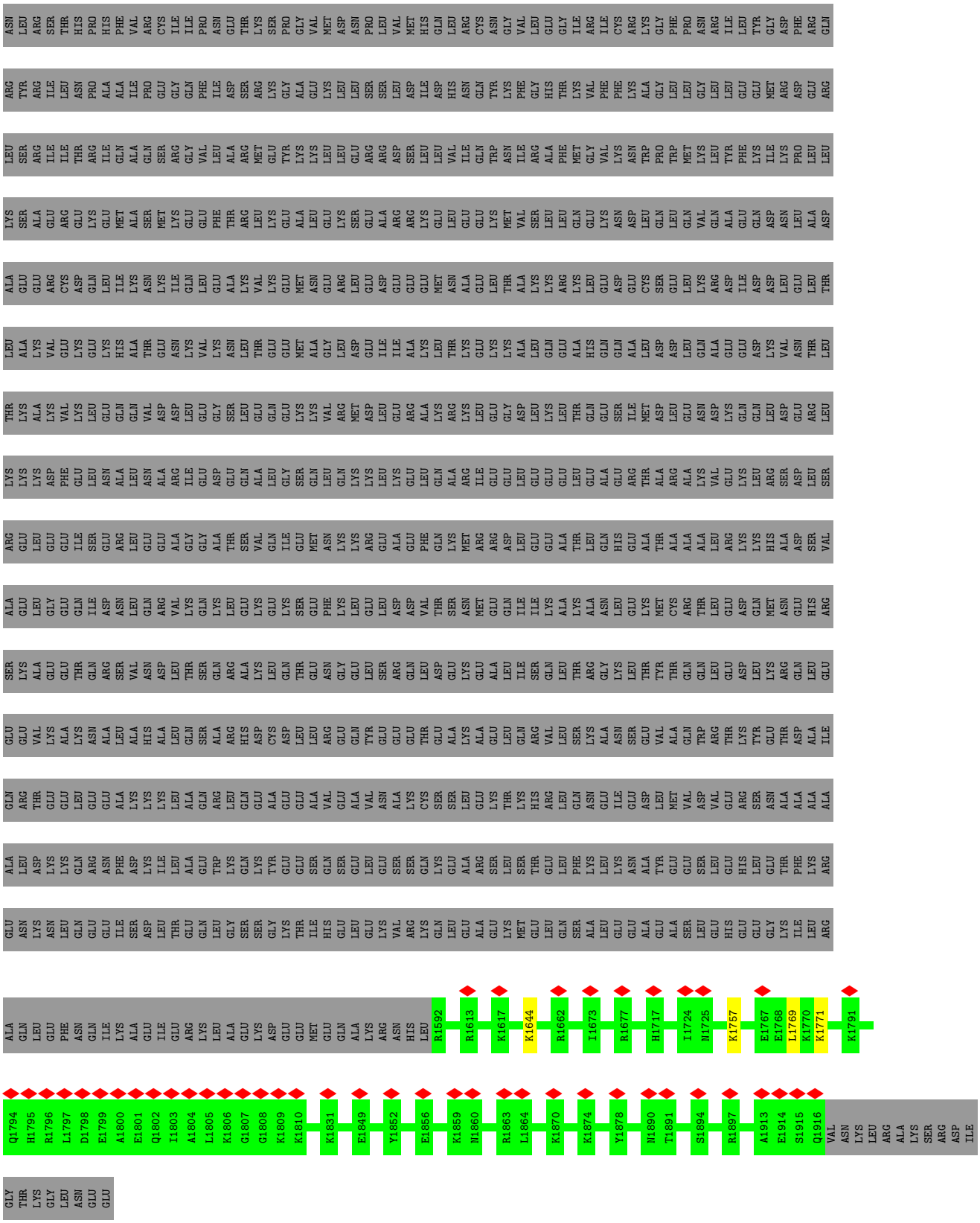
ASN MET LYS PHE LYS LEU LYS GLN ARG GLU GLU GLN ALA GLU PRO ASP GLY THR GLU GLU ALA ASP LYS SER ALA TYR LEU MET GLY LEU ASN SER ALA ASP LEU LEU LYS GLY LEU CYS HIS PRO ARG VAL LYS VAL GLY ASN GLU TYR VAL THR LYS GLY GLN ASN VAL GLN GLN VAL

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

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

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

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



• Molecule 1: Myosin-7

Chain AV:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

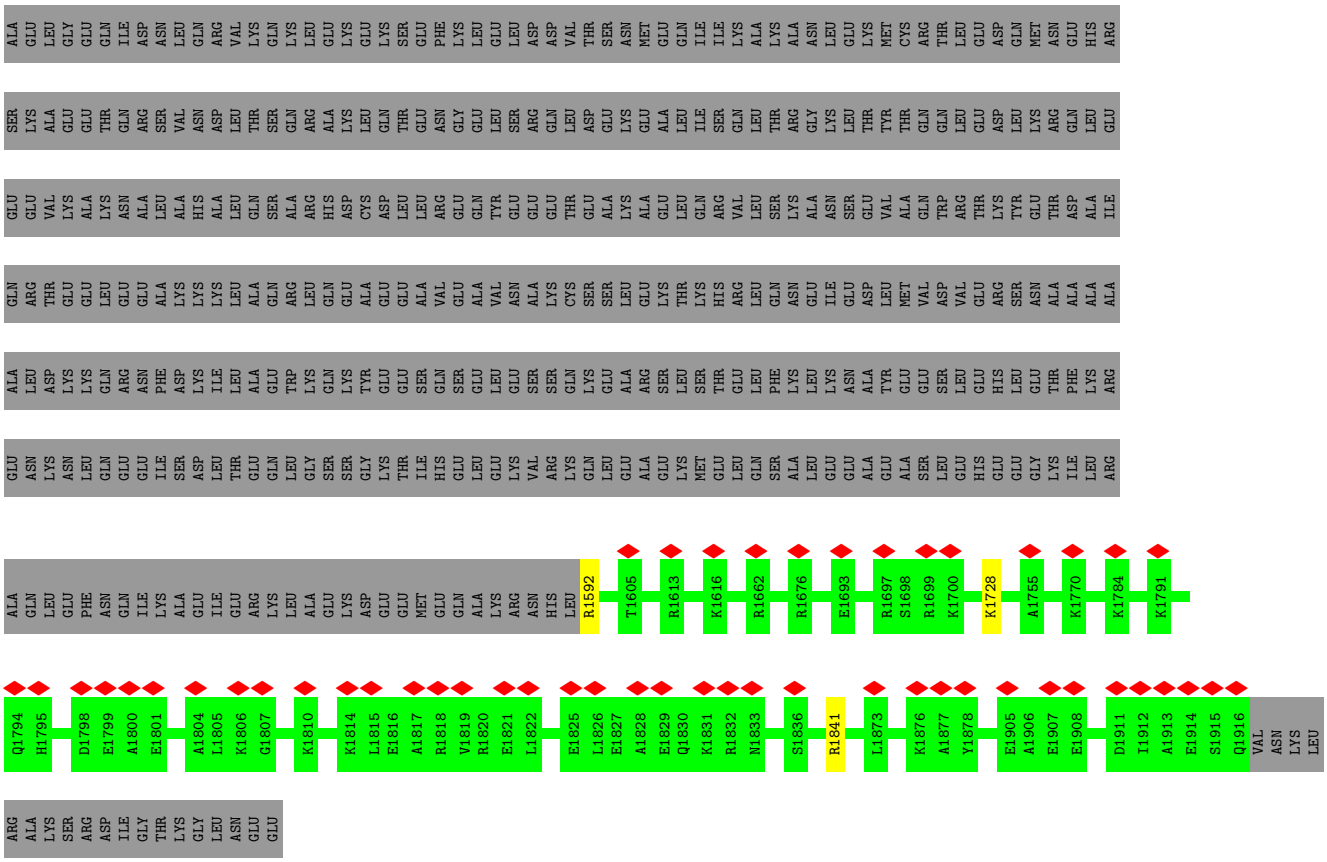
ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

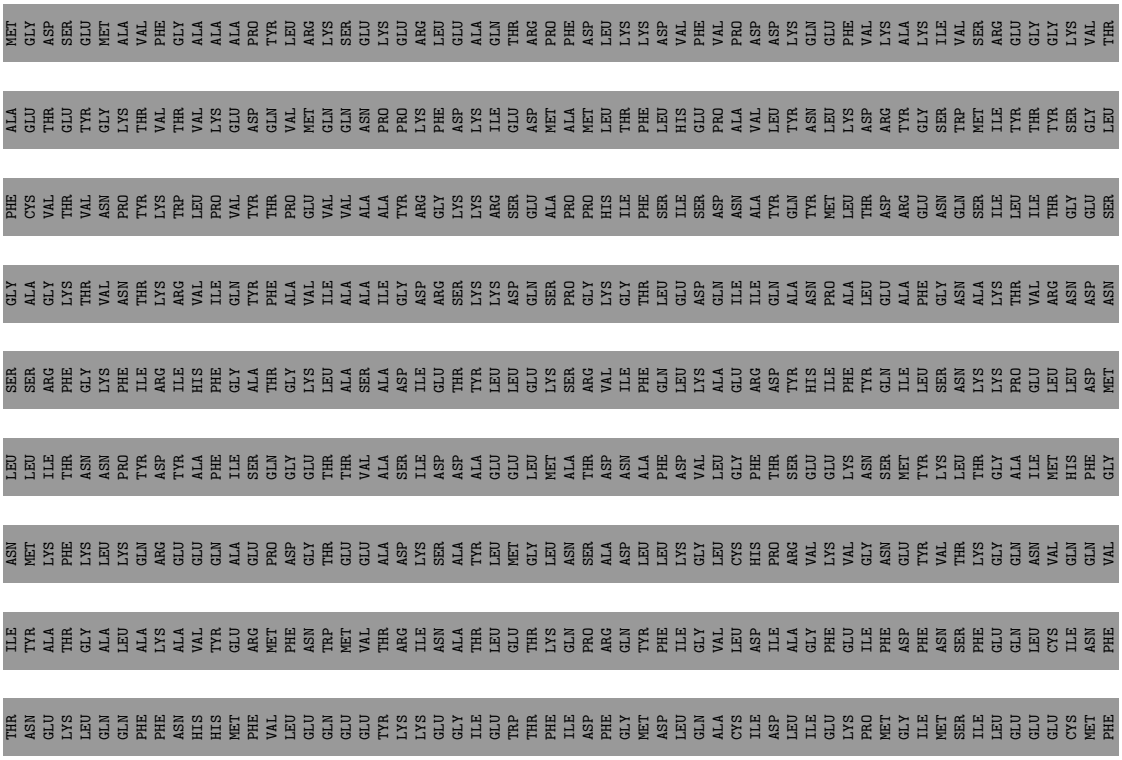
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

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



- Molecule 1: Myosin-7

Chain AW:



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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

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

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

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

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

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

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

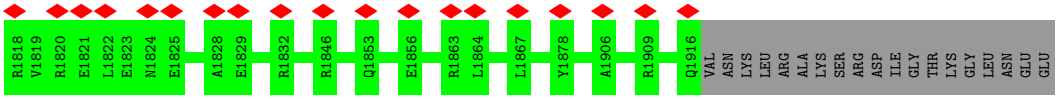
ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG

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

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

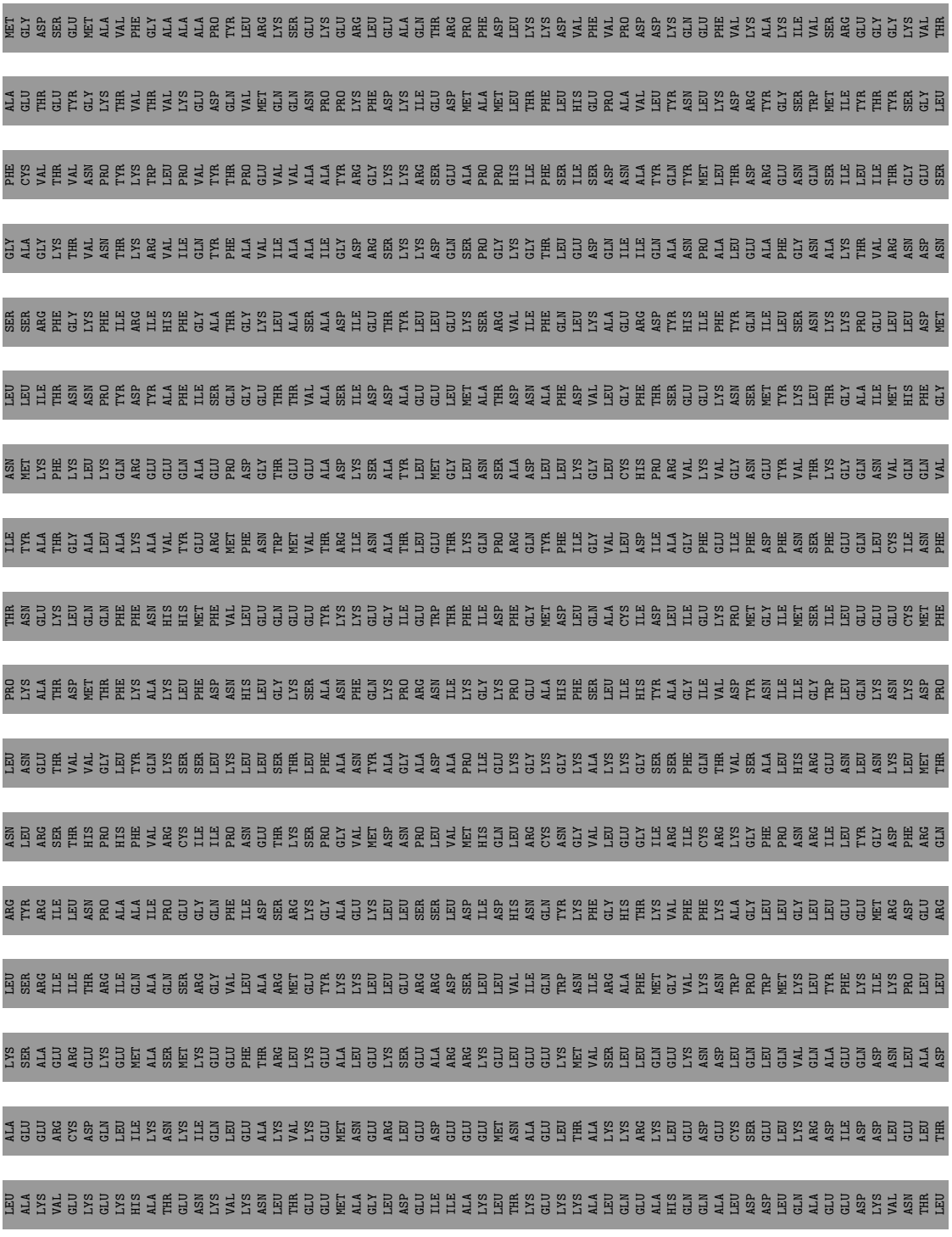
ASP LEU ASN GLU MET GLU ILE GLN LEU SER HIS ALA ASN ARG MET ALA ALA GLU ALA GLN LYS GLN VAL LYS SER LEU GLN SER LEU LEU LYS ASP THR GLN ILE GLN LEU ASP ASP ALA VAL ARG ALA ASN ASP ASP LEU LYS GLU ASN ILE ALA ILE VAL GLU ARG ARG ASN ASN LEU

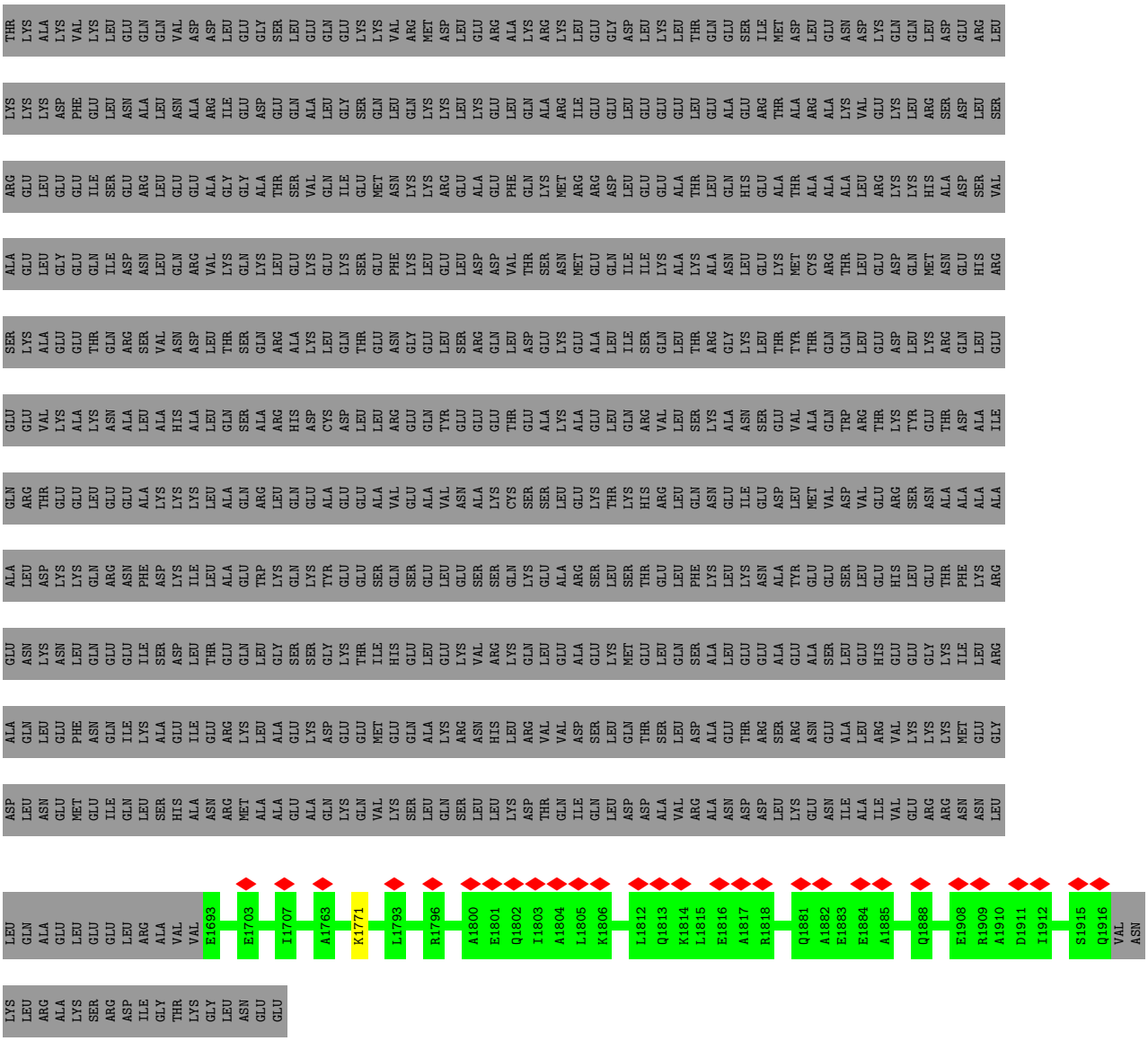
LEU GLN ALA GLU LEU GLU GLU LEU ARG ALA VAL VAL E1693 I1759 T1760 E1767 K1770 K1771 D1774 T1775 S1776 A1777 H1778 R1781 M1782 K1783 K1784 N1785 M1786 E1787 Q1788 T1789 I1790 K1791 D1792 L1793 Q1794 H1795 R1796 L1797 D1798 E1799 A1800 E1801 G1808 K1809 K1810 Q1811 L1812 Q1813 K1814 L1815 E1816 A1817



• Molecule 1: Myosin-7

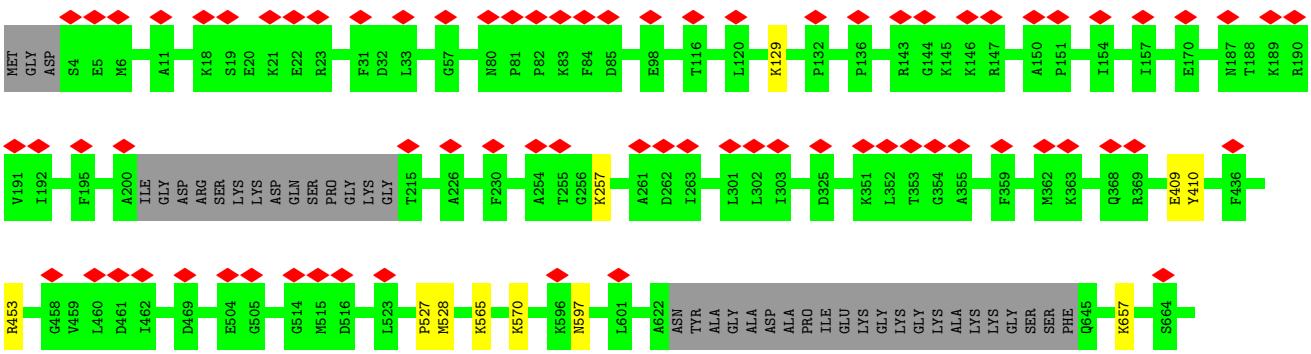
Chain AX:

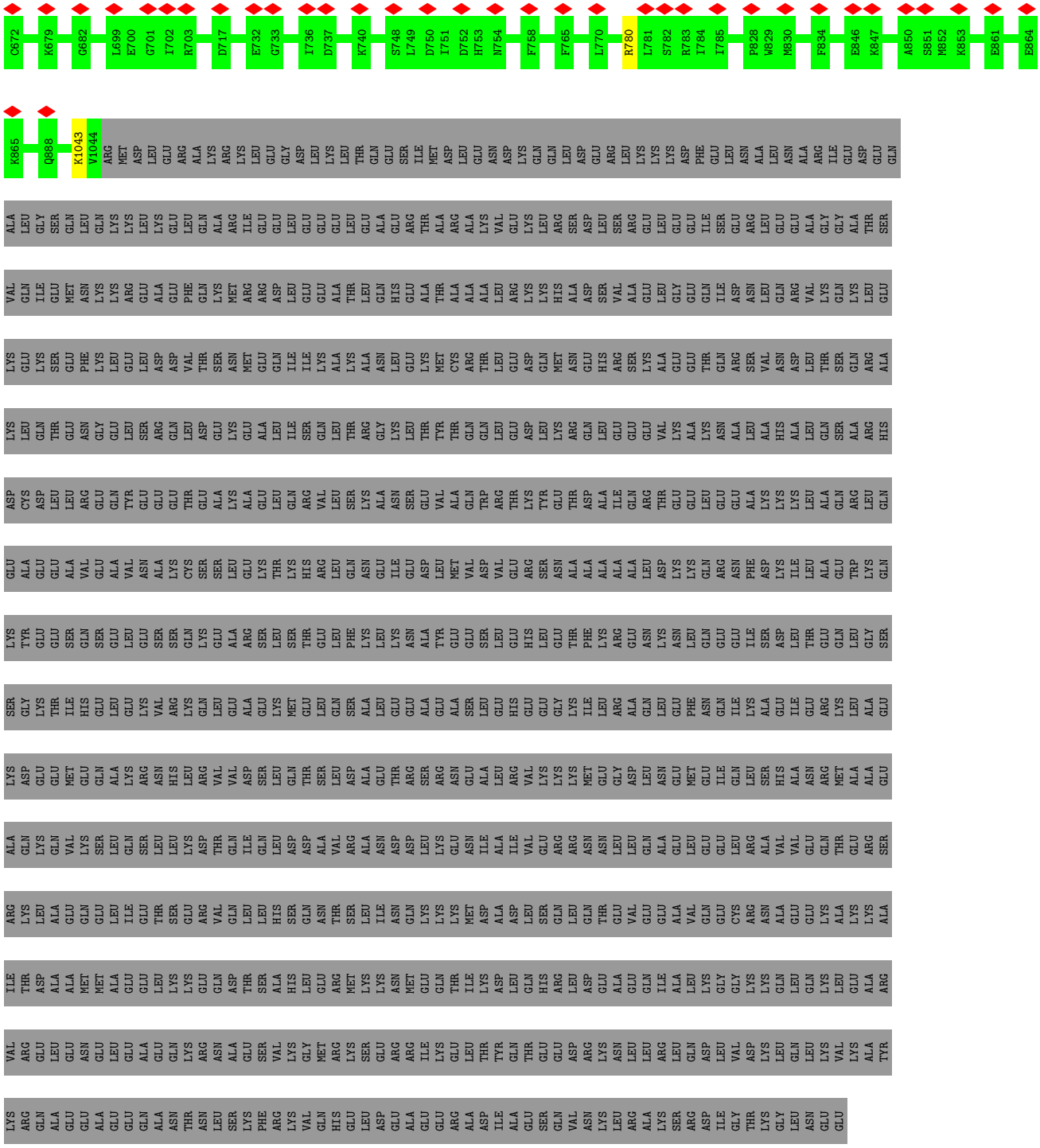




• Molecule 1: Myosin-7

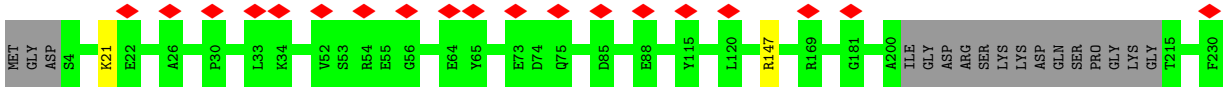
Chain AY:

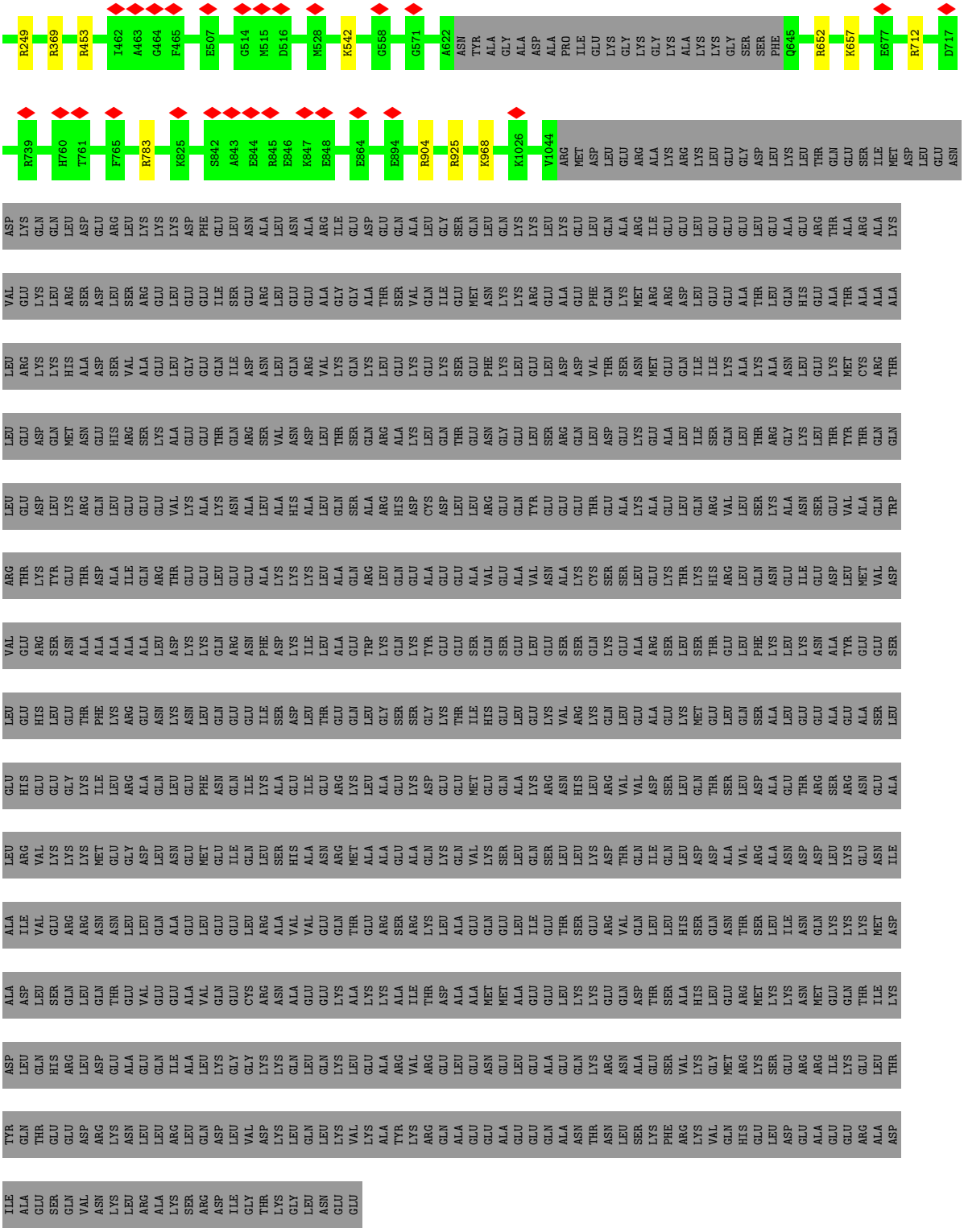




• Molecule 1: Myosin-7

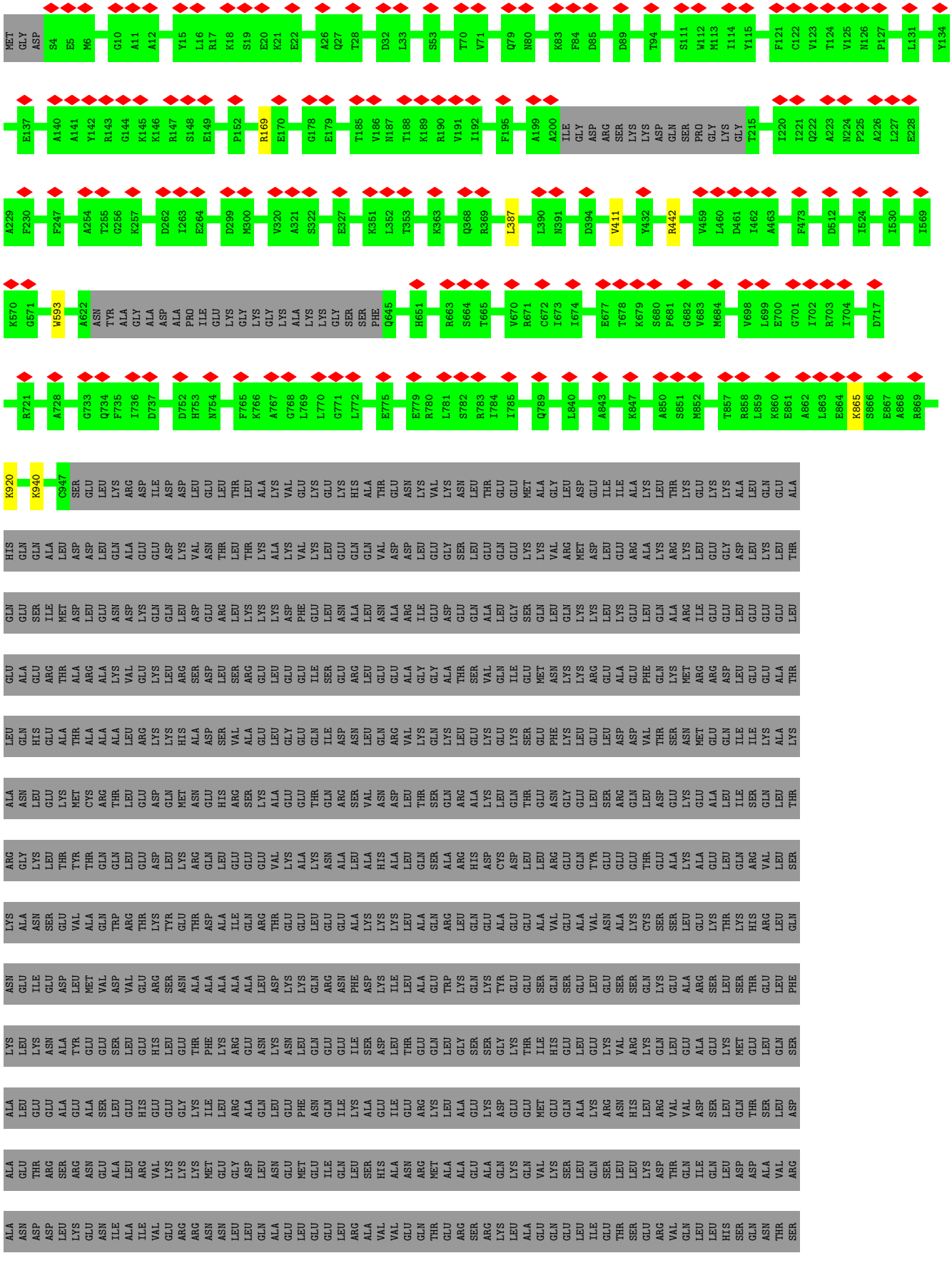
Chain AZ:

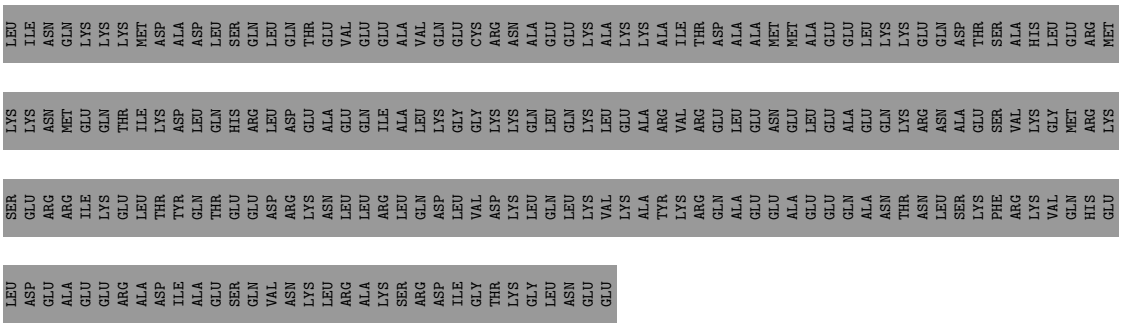




- Molecule 1: Myosin-7

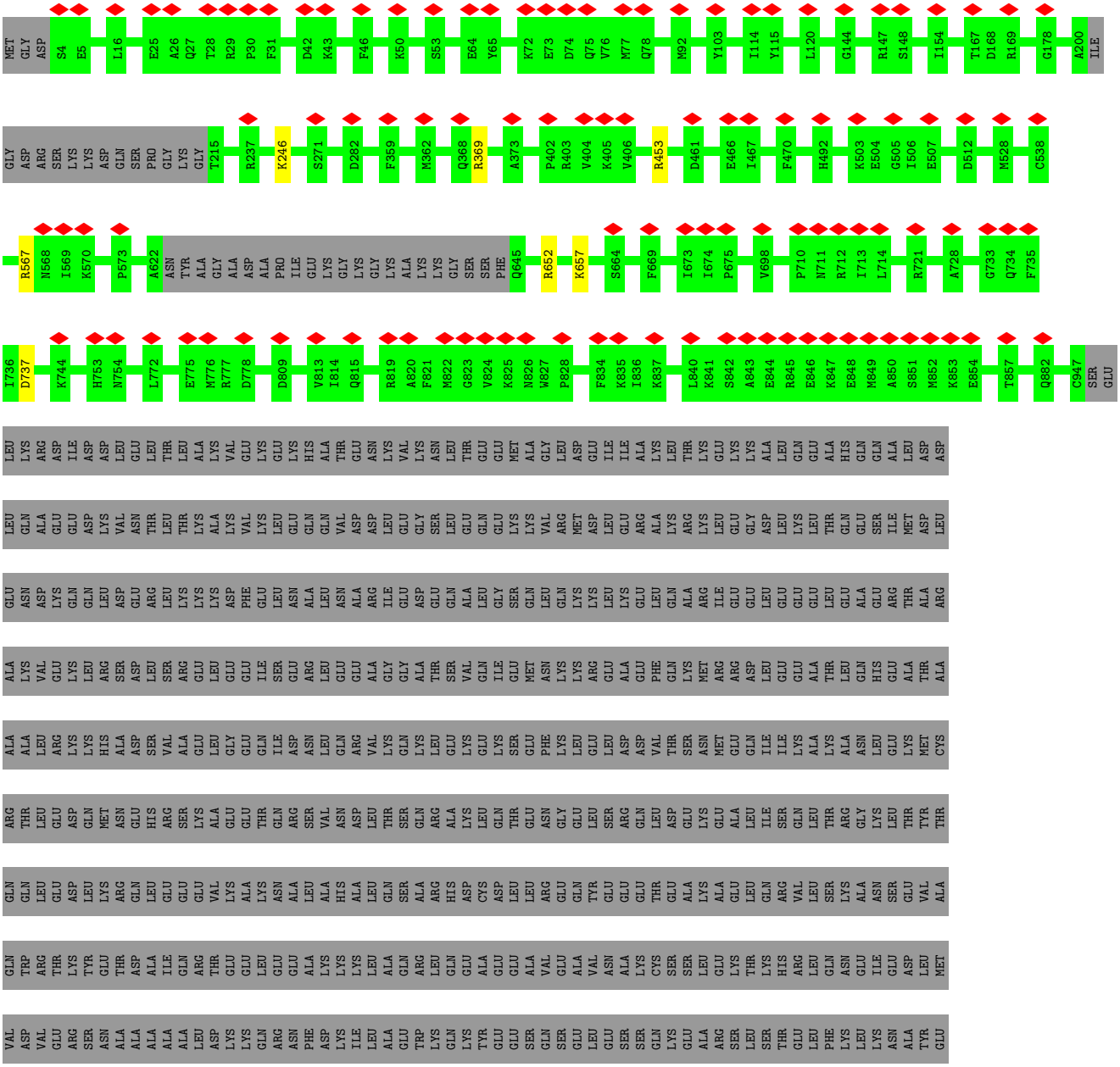
Chain ae:

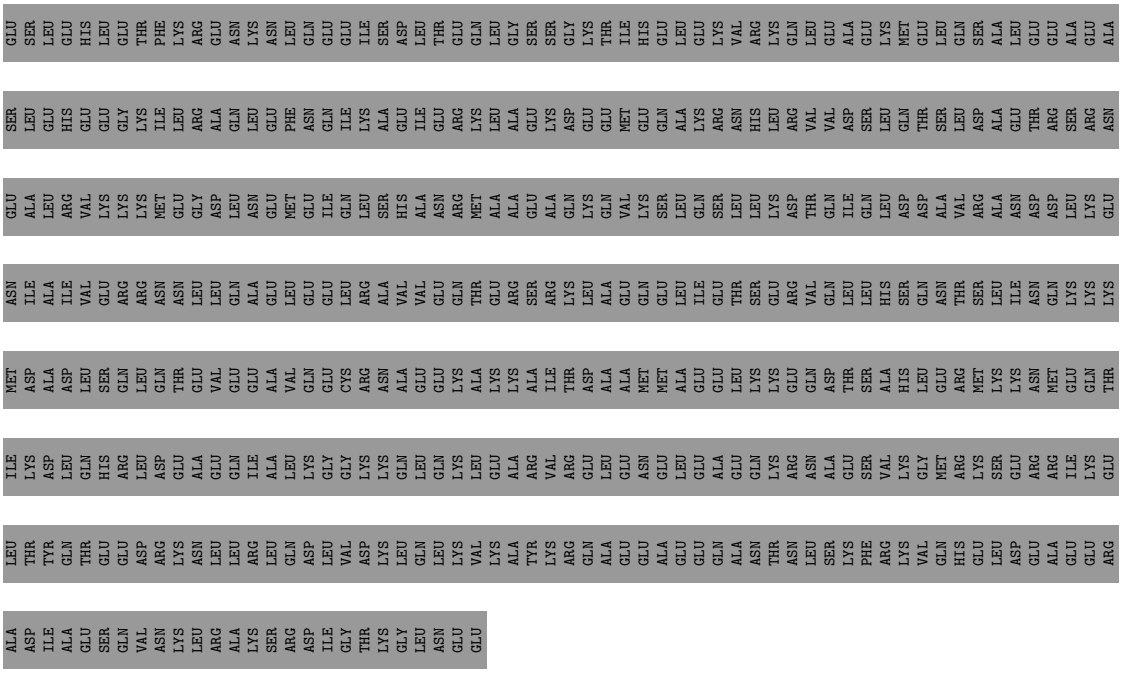

MET GLY ASP S4 E5 M6 G10 A11 A12 Y15 L16 R17 K18 S19 E20 K21 E22 A26 Q27 T28 D32 L33 S53 T70 V71 Q79 N80 K83 F84 D85 D89 T94 S111 W112 M113 I114 Y115 F121 C122 V123 T124 V125 N126 P127 L131 Y134
E137 A140 A141 Y142 R143 G144 K145 K146 R147 S148 E149 P152 R169 E170 G178 E179 T185 V186 N187 T188 K189 R190 V191 I192 F195 A199 A200 ILE GLY ASP ARG SER LYS LYS ASP GLN SER PRO GLY LYS GLY T215 I220 I221 Q222 A223 N224 P225 A226 L227 E228
A229 F230 F247 A254 T255 G256 K257 D262 I263 E264 D299 M300 V320 A321 S322 E327 K351 L352 T353 K363 Q368 R369 L387 L390 N391 D394 V411 Y432 R442 V459 L460 D461 I462 A463 F473 D512 I524 I530 I569
K570 G571 W593 A622 ASN TYR ALA GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS GLY LYS ALA LYS LYS GLY SER SER PHE Q645 H651 R663 S664 T665 V670 R671 C672 I673 I674 E677 T678 K679 S680 P681 G682 V683 M684 V698 L699 E700 G701 I702 R703 I704 D717
R721 A728 G733 Q734 F735 I736 D737 D752 H753 N754 F765 K766 A767 G768 L769 L770 G771 L772 E775 E779 R780 L781 S782 R783 I784 I785 Q789 L840 A843 K847 A850 S851 M852 T857 R858 L859 K860 E861 A862 L863 E864 K865 S866 E867 A868 R869
K920 K940 C947 SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA
HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU THR LYS ALA LYS VAL LYS LEU GLU VAL ASP ASP LEU LEU GLU GLY SER LEU GLU GLN GLU GLN GLU LYS LYS VAL ARG MET ASP LEU GLU GLU ARG ALA LYS ARG LYS LEU GLU GLU GLY ASP LEU LYS LEU THR
GLN GLU SER ILE MET ASP LEU GLU GLU ASN ASP LYS GLN GLN LEU ASP GLU ARG LEU LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU GLU ALA ARG ILE GLU GLU LEU GLU GLU LEU
GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER ARG GLU LEU GLU ILE SER GLU ARG LEU GLU GLU ALA GLY GLY ALA THR SER VAL GLN ILE GLU MET ASN LYS LYS ARG GLU ALA GLU PHE GLN LYS MET ARG ARG ASP LEU GLU LEU GLU ALA THR
LEU GLN HIS GLU ALA THR ALA ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL ALA GLU LEU GLY GLU GLN ILE ASP ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU MET PHE LYS LEU GLU ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA LYS
ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU GLU ASP GLN MET ASN GLU HIS ARG SER LYS ALA GLU GLU GLU THR GLN ARG GLU ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU GLY ASN GLY GLU GLU LEU SER ARG GLN LEU ASP GLU LYS GLU LEU ILE SER THR LEU
ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU GLU ASP LEU LYS ARG GLN LEU GLU GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU LEU ARG GLU GLN TYR GLU GLU GLU THR GLU ALA LYS ALA GLU LEU GLN ARG VAL LEU SER
LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ALA ILE GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LYS LEU ALA GLU GLN ARG LEU ALA GLU GLU ALA ALA VAL GLU ALA ALA VAL ASN ALA LYS CYS SER SER LEU GLU LYS THR LYS HIS ARG LEU GLN
ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG ASN PHE ASP LYS LYS ILE LEU ALA GLU TRP LYS GLN LYS GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE
LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG GLU ASN LYS ASN LEU GLN GLU GLU ILE SER ASP LEU THR GLU GLN LEU GLY SER SER GLY LYS THR ILE HIS GLU LEU GLU LEU GLU LYS VAL ARG LYS GLN LEU GLU ALA GLU LYS MET GLU LEU GLN SER
ALA LEU GLU GLU ALA SER LEU GLU HIS GLU GLY LYS ILE LEU ARG ALA GLN LEU GLU PHE ASN GLN ILE LYS ALA GLU ILE GLU GLU ARG LYS LEU ALA GLU LYS ASP GLU GLU MET GLU GLN ALA LYS ARG ASN HIS LEU ARG VAL VAL ASP SER LEU GLN THR SER LEU ASP
ALA GLU THR ARG SER ARG LYS ARG ASN GLU GLY ASP LEU ASN GLU MET GLU ILE GLN LEU GLU ARG MET ALA ALA GLU ALA GLN LYS LYS GLN VAL LYS SER LEU LEU GLN SER LEU LYS ASP THR GLN ILE LEU ASP ASP ALA VAL ARG
ALA ASN ASP LEU LYS GLU ASN ILE ALA VAL GLU LEU GLU ARG ALA VAL VAL GLU GLN THR GLU ARG SER ARG LYS LEU ALA GLU GLN GLU LEU ILE GLU THR SER GLU ARG VAL GLN LEU LEU LEU HIS SER GLN ASN ALA THR SER



• Molecule 1: Myosin-7

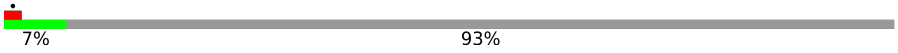
Chain af:

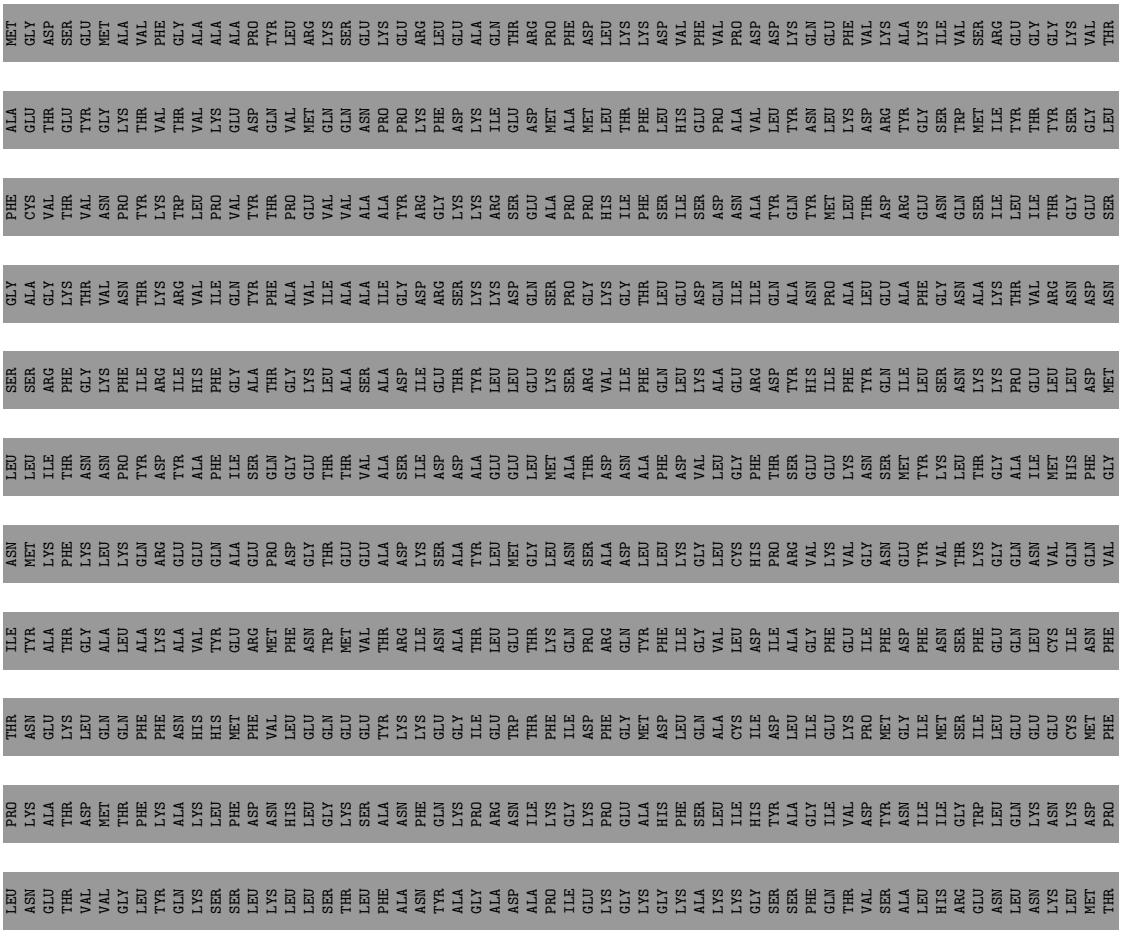


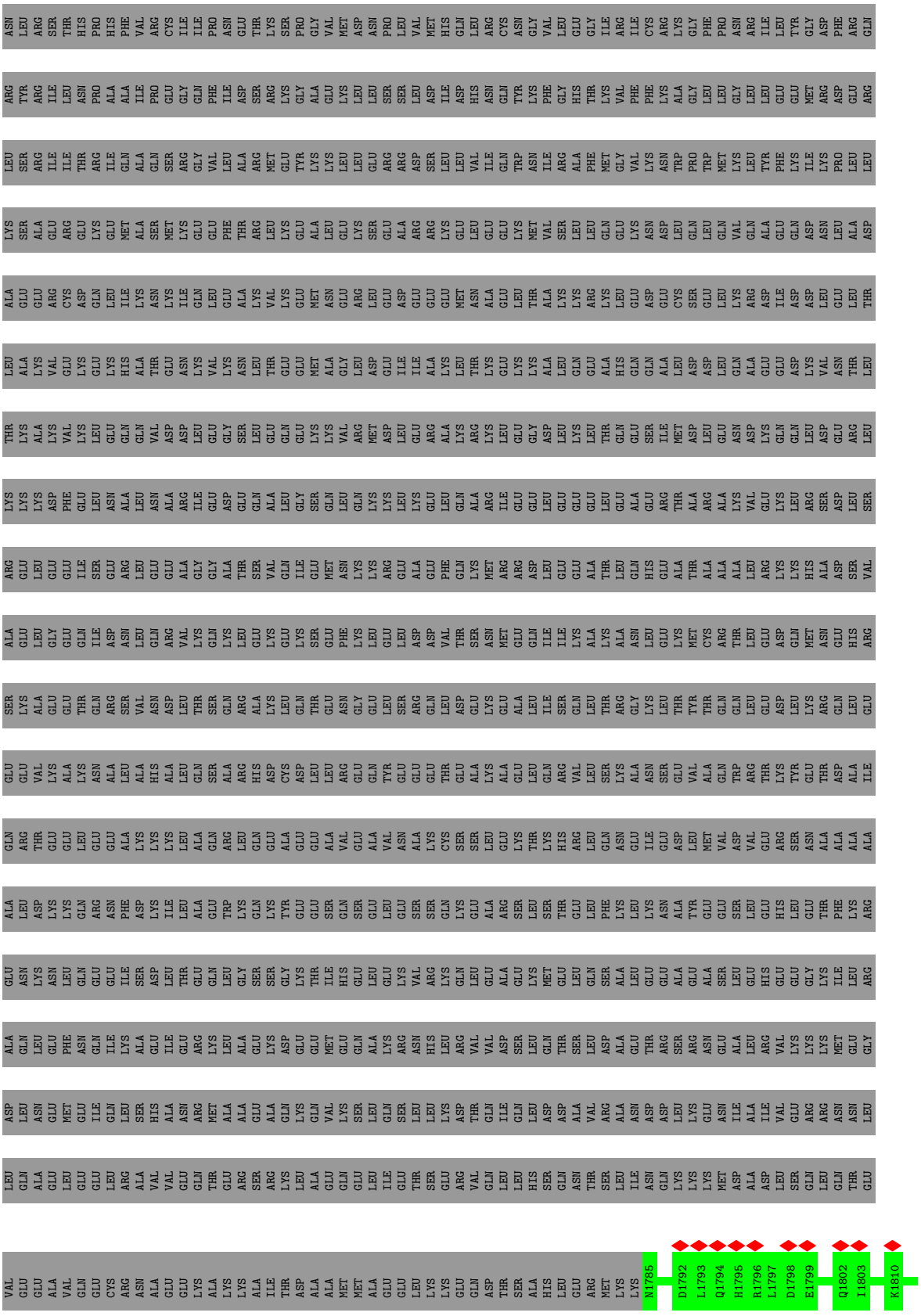


• Molecule 1: Myosin-7

Chain ak:



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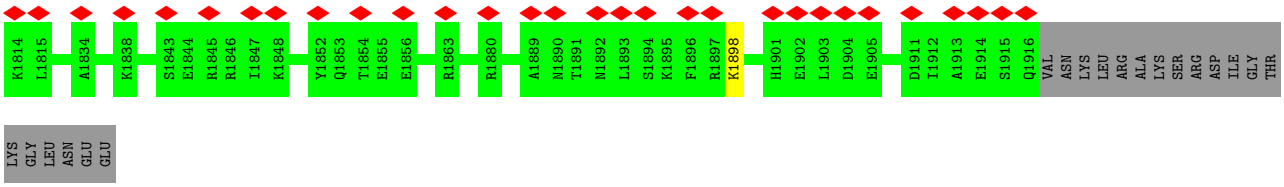
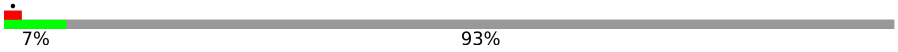
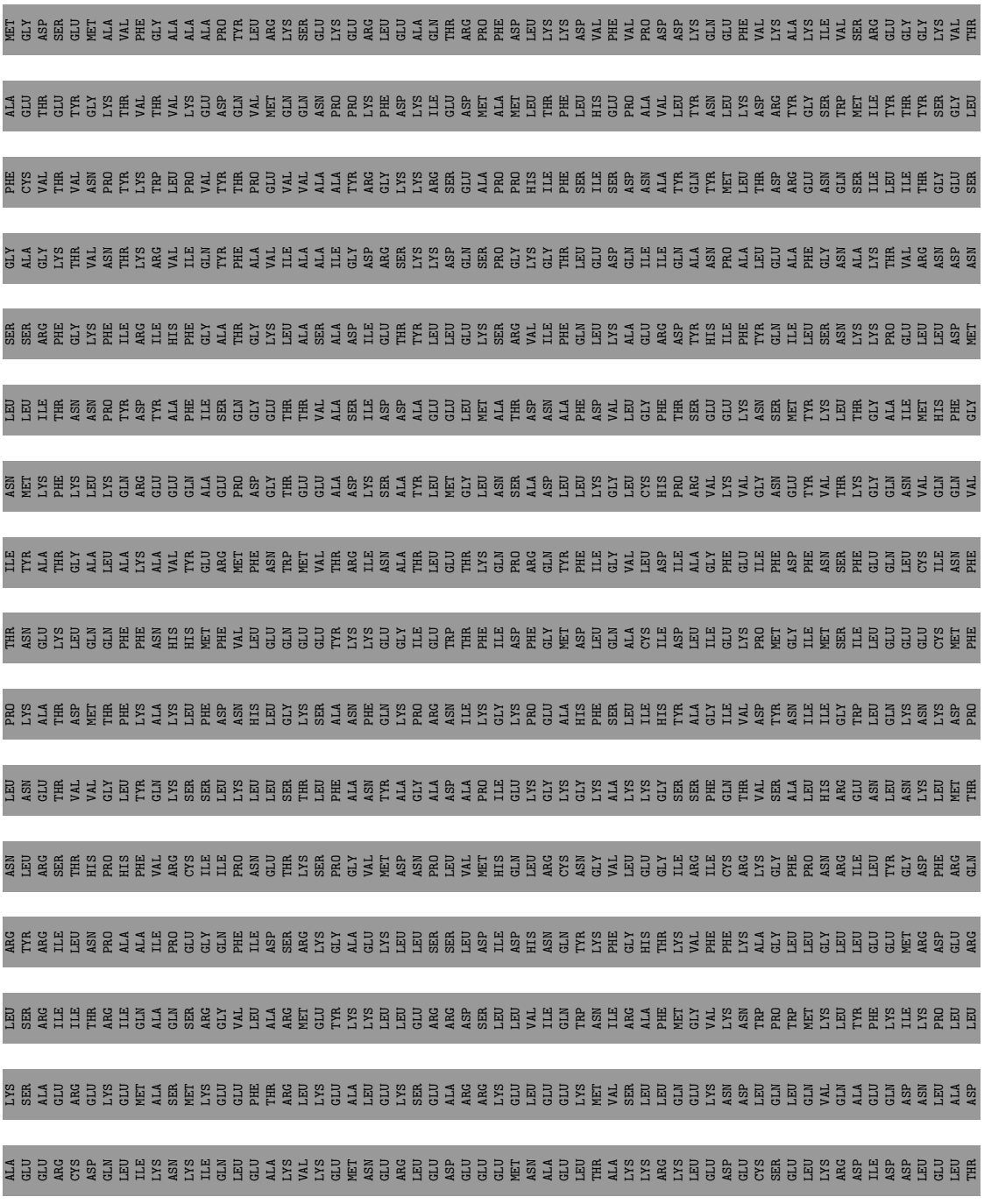
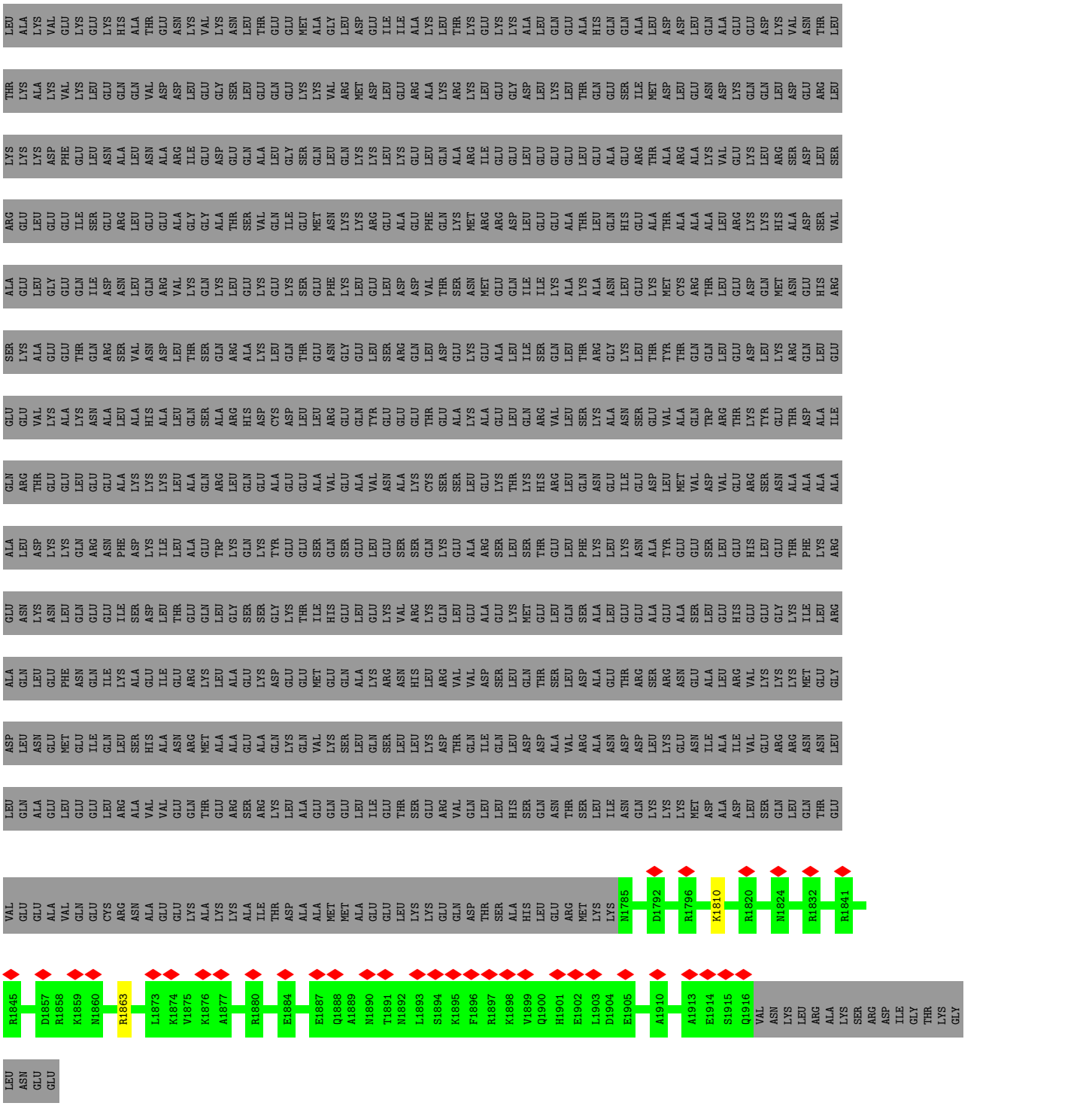


• Molecule 1: Myosin-7

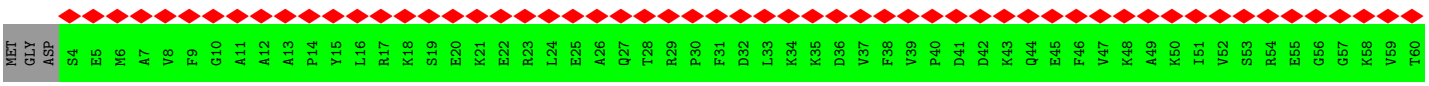
Chain a1:

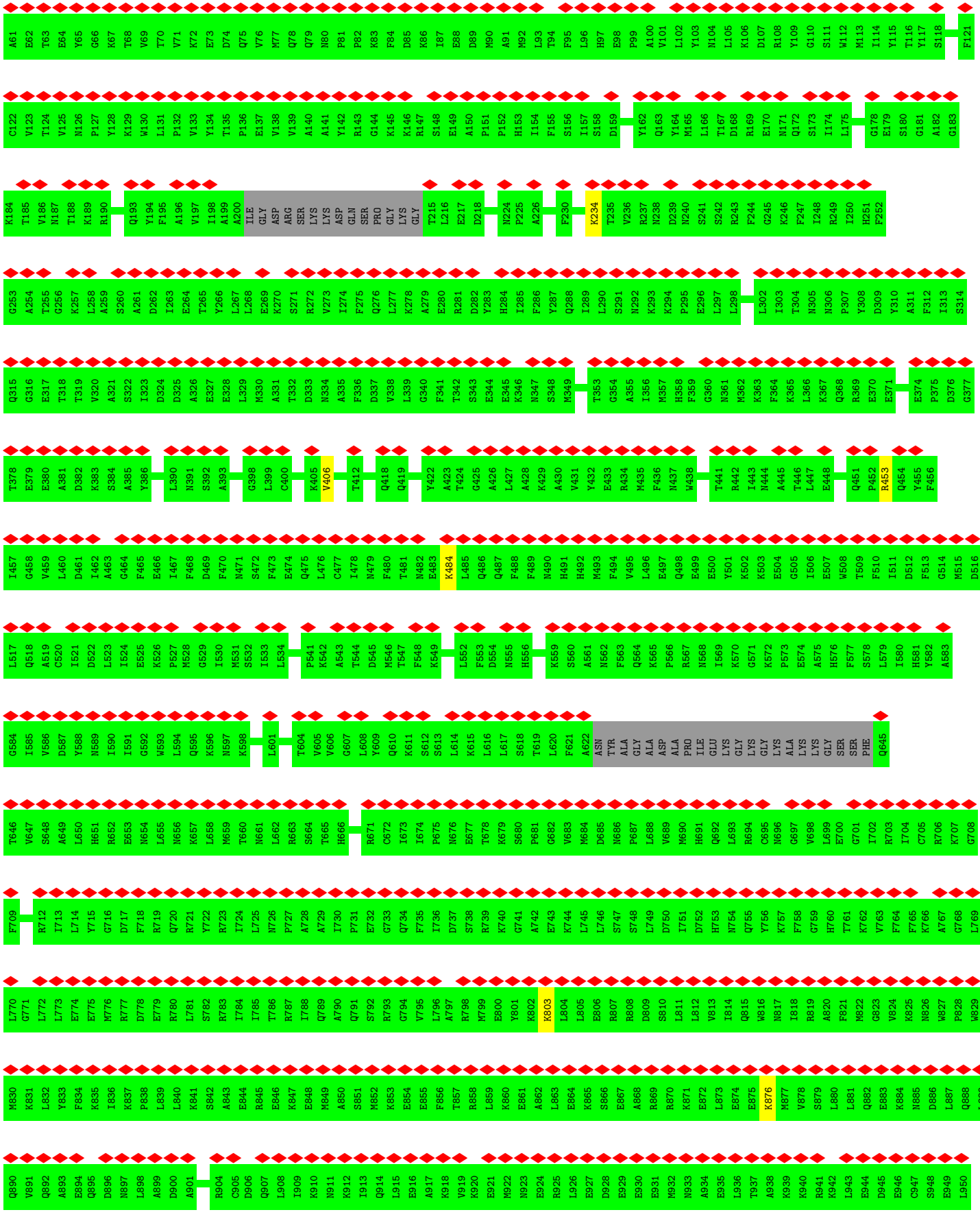






• Molecule 1: Myosin-7

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C122 V123 T124 V125 N126 P127 Y128 K129 W130 L131 P132 V133 Y134 T135 P136 E137 V138 V139 A140 A141 Y142 R143 G144 K145 K146 R147 S148 E149 A150 P151 P152 H153 I154 F155 S156 I157 S158 D159 Y162 Q163 Y164 M165 L166 T167 D168 R169 E170 N171 Q172 S173 I174 L175 G178 E179 S180 G181 A182 G183
K184 T185 V186 N187 T188 K189 R190 Q193 Y194 F195 A196 V197 I198 A199 A200 ILE GLY ASP ARG SER LYS LYS ASP GLN SER PRO GLY LYS GLY T215 L216 E217 D218 N224 P225 A226 F230 K234 T235 V236 R237 N238 D239 N240 S241 S242 R243 F244 G245 K246 F247 I248 R249 I250 H251 F252
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Q315 G316 E317 T318 T319 V320 A321 S322 I323 D324 D325 A326 E327 E328 L329 M330 A331 T332 D333 N334 A335 F336 D337 V338 L339 G340 F341 T342 S343 E344 E345 K346 N347 S348 M349 T353 G354 A355 I356 M357 H358 F359 G360 N361 M362 K363 F364 K365 L366 K367 Q368 R369 E370 E371 E374 P375 D376 G377
T378 E379 E380 A381 D382 K383 S384 A385 Y386 L390 N391 S392 A393 G398 L399 C400 K405 V406 T412 Q418 Q419 Y422 A423 T424 G425 A426 L427 A428 K429 A430 V431 Y432 E433 R434 M435 F436 N437 W438 T441 R442 T443 N444 A445 T446 L447 E448 Q451 P452 R453 Q454 Y455 F456
I457 G458 V459 L460 D461 I462 A463 G464 F465 E466 I467 F468 D469 F470 N471 S472 F473 E474 Q475 L476 C477 I478 N479 F480 T481 N482 E483 K484 L485 Q486 Q487 F488 F489 N490 H491 H492 M493 F494 V495 L496 E497 Q498 E499 E500 Y501 K502 K503 E504 G505 I506 E507 W508 T509 F510 I511 D512 F513 G514 M515 D516
L517 Q518 A519 C520 I521 D522 L523 I524 E525 K526 P527 M528 G529 I530 M531 S532 I533 L534 P541 K542 A543 T544 D545 M546 T547 F548 K549 L552 F553 D554 N555 H556 K559 S560 A561 N562 F563 Q564 K565 P566 R567 N568 I569 K570 G571 K572 P573 E574 A575 H576 F577 S578 L579 I580 H581 Y582 A583
G584 I585 V586 D587 Y588 N589 I590 I591 G592 W593 L594 Q595 K596 N597 K598 L601 T604 V605 V606 G607 L608 Y609 Q610 K611 S612 S613 L614 K615 L616 L617 S618 T619 L620 F621 A622 ASN TYR ALA GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS LYS GLY LYS ALA LYS LYS GLY SER SER PHE Q645
T646 V647 S648 A649 L650 H651 R652 E653 N654 L655 N656 K657 L658 M659 T660 N661 L662 R663 S664 T665 H666 R671 C672 I673 I674 P675 N676 E677 T678 K679 S680 P681 G682 V683 M684 D685 N686 P687 L688 V689 M690 H691 Q692 L693 R694 C695 N696 G697 V698 L699 E700 G701 I702 R703 I704 C705 R706 K707 G708
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L770 G771 L772 L773 E774 E775 M776 R777 D778 E779 R780 L781 S782 R783 I784 I785 T786 R787 I788 Q789 A790 Q791 S792 R793 G794 V795 L796 A797 R798 M799 E800 Y801 K802 K803 L804 L805 E806 R807 R808 D809 S810 L811 L812 V813 I814 Q815 W816 N817 I818 R819 A820 P821 M822 G823 V824 K825 N826 W827 P828 W829
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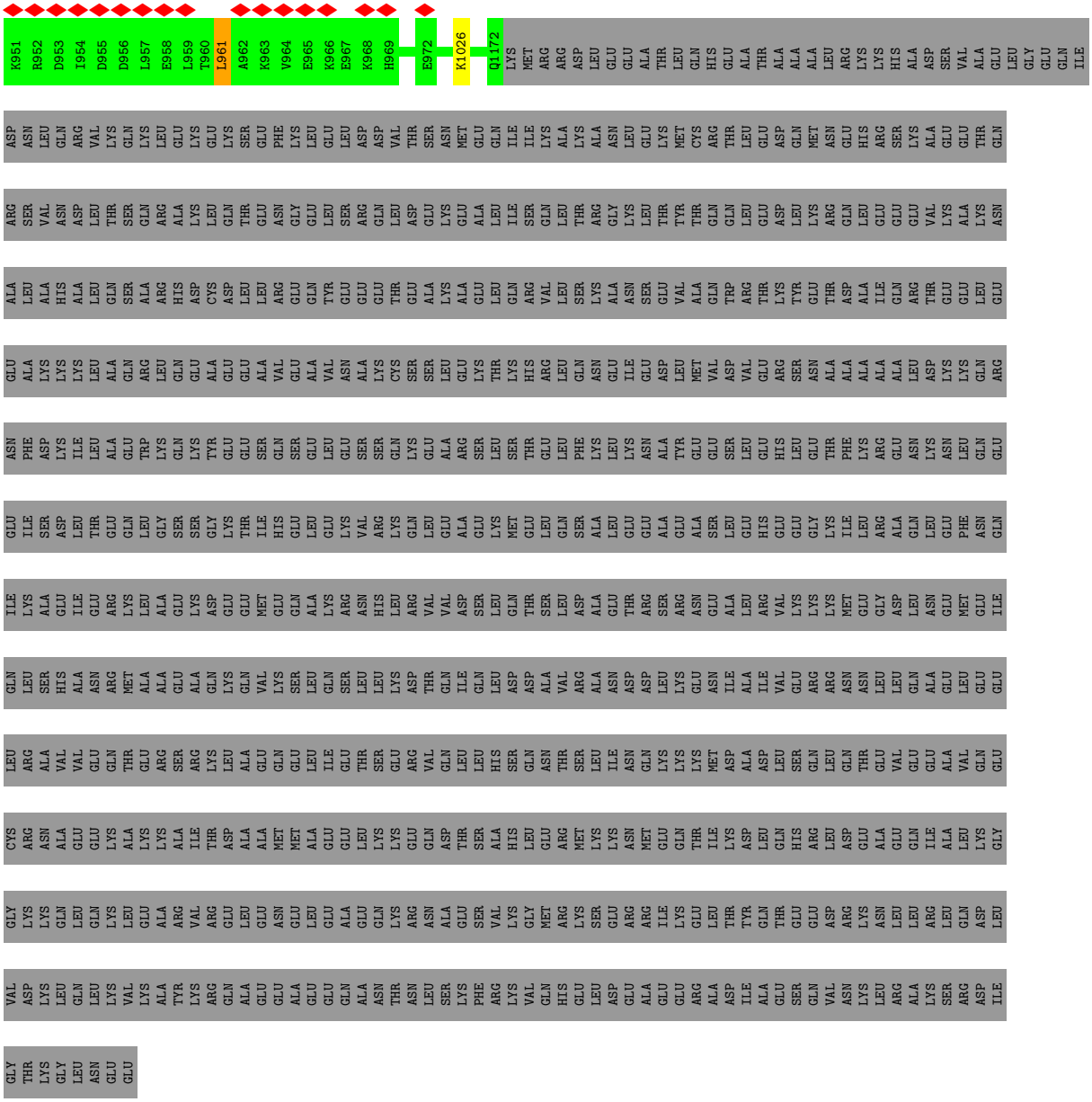
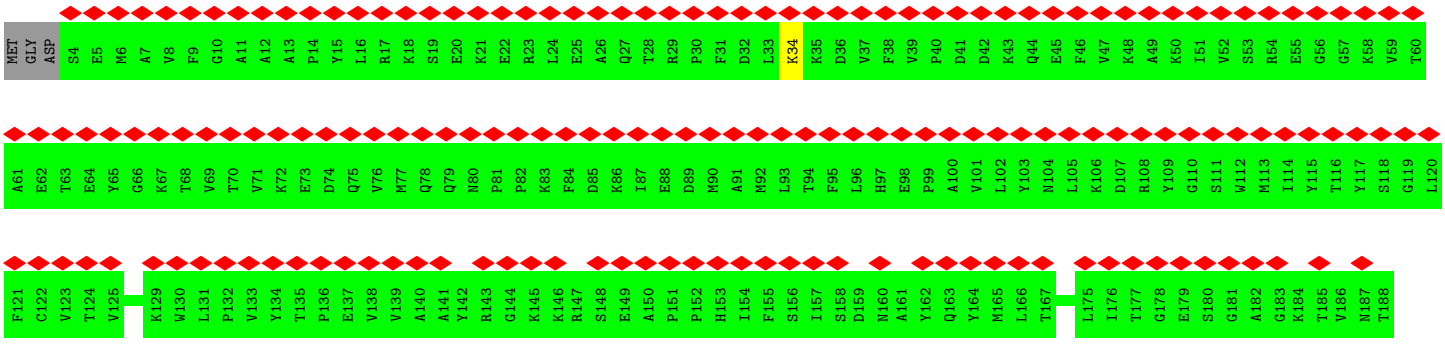
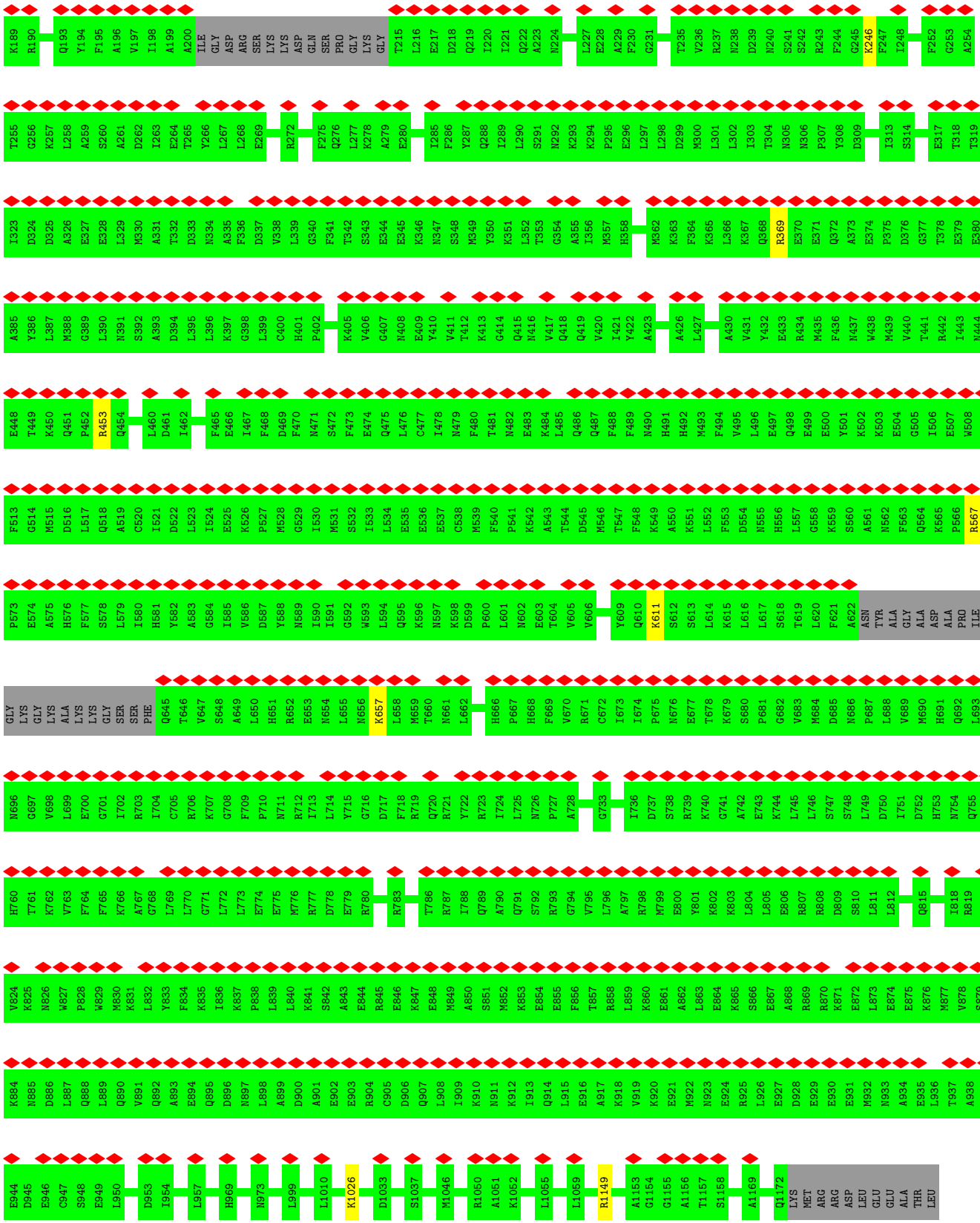


• Molecule 1: Myosin-7

Chain B:

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T255 G256 K257 L258 A259 S260 A261 D262 I263 E264 T265 Y266 L267 L268 E269 R272 F275 Q276 L277 K278 A279 E280 I285 F286 Y287 Q288 I289 L290 S291 N292 K293 K294 P295 E296 L297 L298 D299 M300 L301 L302 I303 T304 N305 N306 P307 Y308 D309 I313 S314 E317 T318 T319 V320 A321 S322
I323 D324 D325 A326 E327 E328 L329 M330 A331 T332 D333 N334 A335 F336 D337 V338 L339 G340 F341 T342 S343 E344 E345 K346 N347 S348 M349 Y350 K351 L352 T353 G354 A355 I356 M357 H358 M362 K363 F364 K365 L366 K367 Q368 R369 E370 E371 Q372 A373 E374 P375 D376 G377 T378 E379 E380 A381 D382 K383 S384
A385 Y386 L387 M388 G389 L390 N391 S392 A393 D394 L395 L396 K397 G398 L399 C400 H401 P402 K405 V406 G407 N408 E409 Y410 V411 T412 K413 G414 Q415 N416 V417 Q418 Q419 V420 I421 Y422 A423 A426 L427 A430 V431 Y432 E433 R434 M435 F436 N437 W438 M439 V440 T441 R442 I443 N444 A445 T446 L447
E448 T449 K450 Q451 P452 R453 Q454 L460 D461 I462 F465 E466 I467 F468 D469 F470 N471 S472 F473 E474 Q475 L476 C477 I478 N479 F480 T481 N482 E483 K484 L485 Q486 Q487 F488 F489 N490 H491 H492 M493 F494 V495 L496 E497 Q498 E499 E500 Y501 K502 K503 E504 G505 I506 E507 W508 T509 F510 I511 D512
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GLY LYS GLY LYS ALA LYS LYS GLY SER SER PHE Q645 T646 V647 S648 A649 L650 H651 R652 E653 N654 L655 M656 K657 L658 M659 T660 N661 L662 H666 P667 H668 F669 V670 R671 C672 I673 I674 P675 N676 E677 T678 K679 S680 P681 G682 V683 M684 D685 N686 P687 L688 V689 M690 H691 Q692 L693 R694 C695
N696 G697 V698 L699 E700 G701 I702 R703 I704 C705 R706 K707 G708 F709 P710 N711 R712 I713 L714 Y715 G716 D717 F718 R719 Q720 R721 Y722 R723 I724 L725 N726 P727 A728 G733 I736 D737 S738 R739 K740 G741 A742 E743 K744 L745 L746 S747 S748 L749 D750 I751 D752 H753 N754 Q755 Y756 K757 F758 G759
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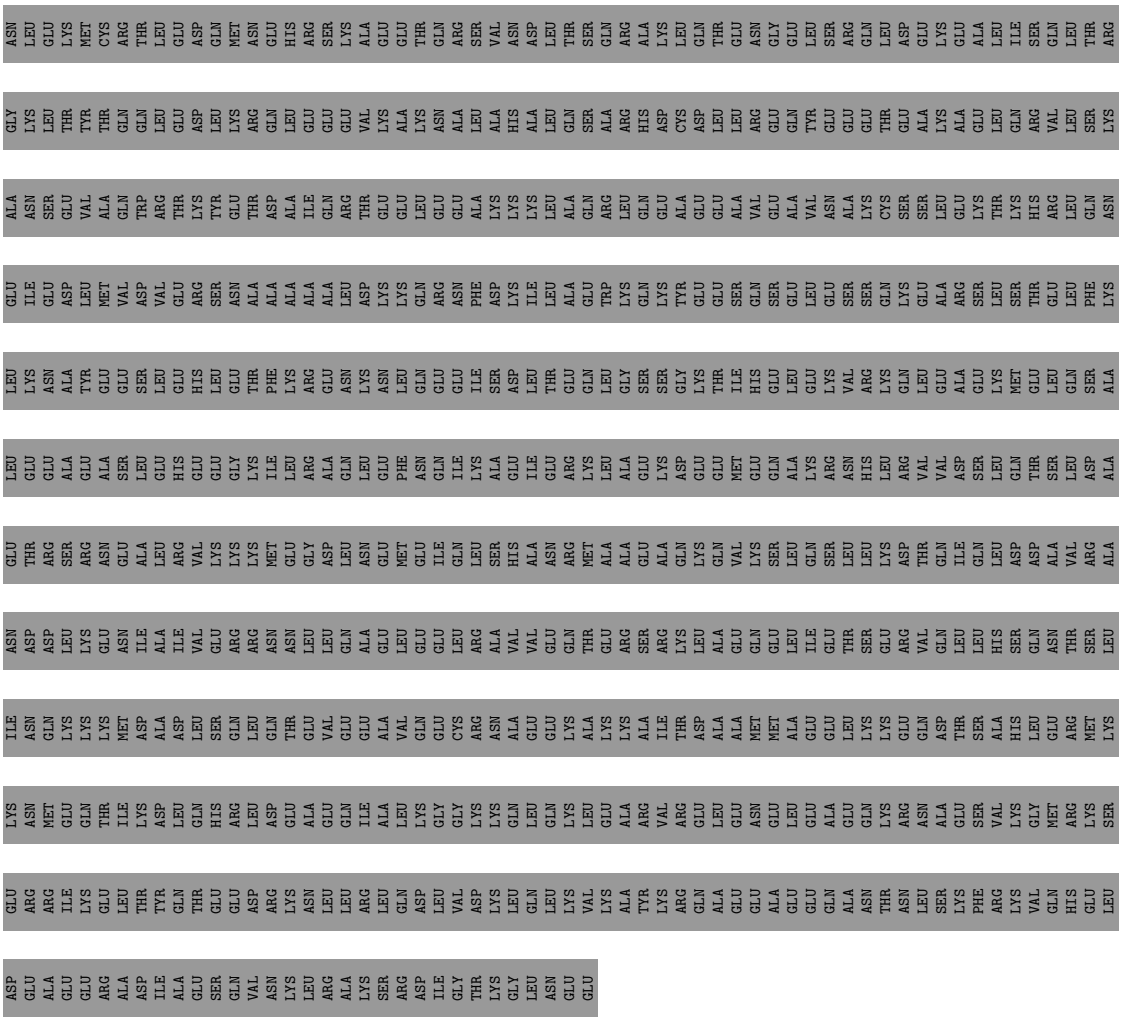
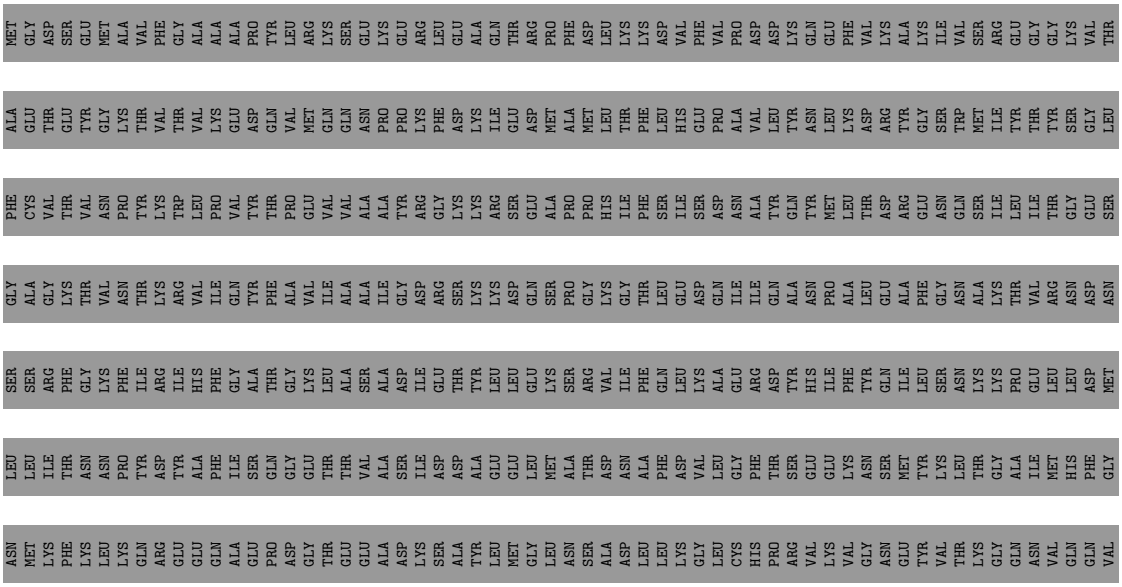
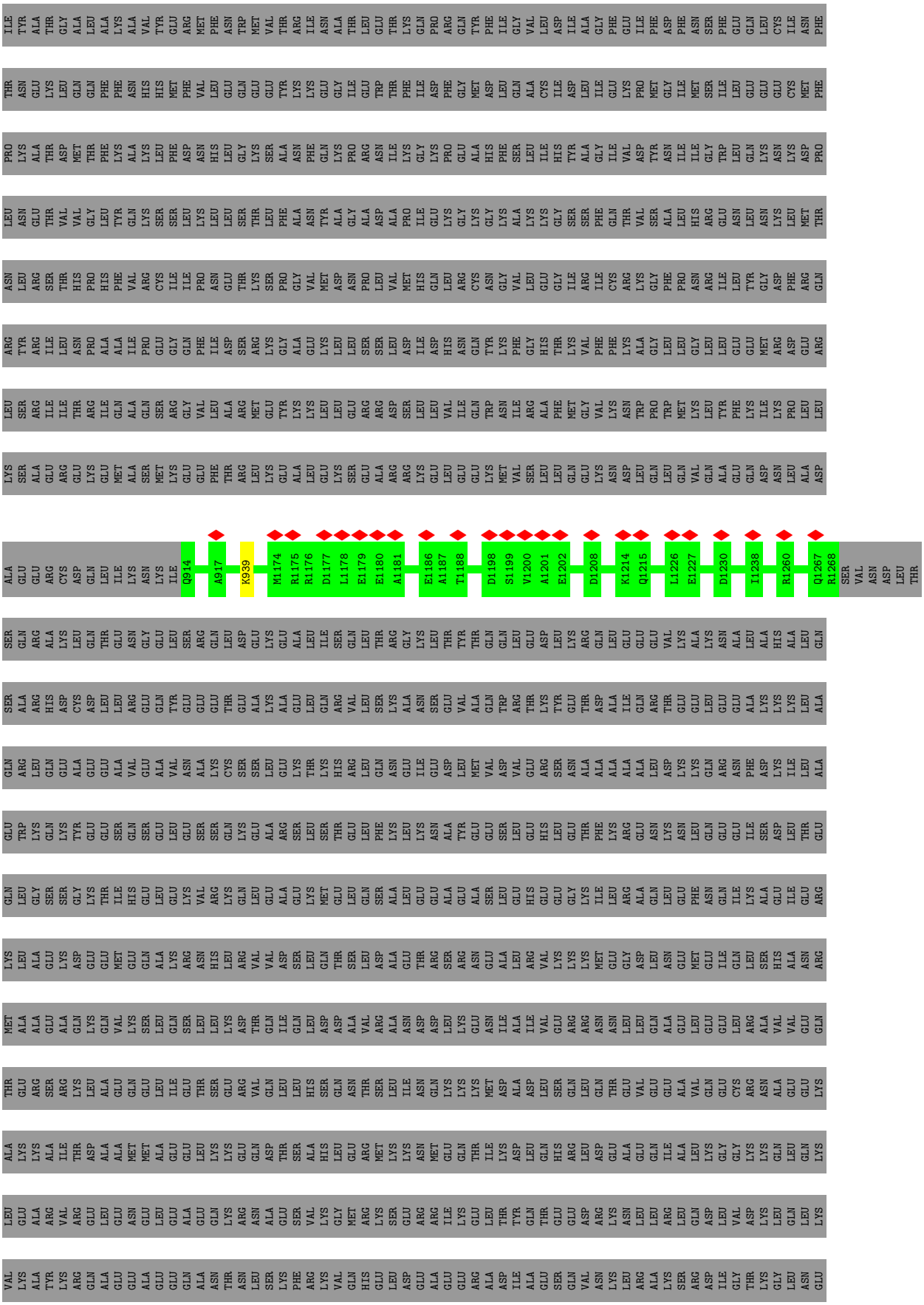
V824 K825 N826 W827 P828 W829 M830 K831 L832 Y833 F834 K835 I836 K837 P838 L839 L840 K841 S842 A843 E844 R845 E846 K847 E848 M849 A850 S851 M852 K853 E854 E855 F856 T857 R858 L859 K860 E861 A862 L863 E864 K865 S866 E867 A868 R869 R870 K871 E872 L873 E874 E875 K876 M877 V878 S879 L880 L881 Q882 E883
K884 N885 D886 L887 Q888 L889 Q890 V891 Q892 A893 E894 Q895 D896 N897 L898 A899 D900 A901 E902 E903 R904 C905 D906 Q907 L908 I909 K910 N911 K912 I913 Q914 L915 E916 A917 K918 V919 K920 E921 M922 N923 E924 R925 L926 E927 D928 E929 E930 E931 M932 N933 A934 E935 L936 T937 A938 K939 K940 R941 K942 L943
E944 D945 E946 C947 S948 E949 L950 D953 I954 L957 H969 N973 L999 L1010 K1026 D1033 S1037 M1046 R1050 A1051 K1052 L1055 L1059 R1149 A1153 G1154 G1155 A1156 T1157 S1158 A1169 Q1172 LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU
GLN GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU GLU LEU ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA ALA LYS ALA



• Molecule 1: Myosin-7

Chain G:

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S1199
V1200
A1201
E1202
D1208
K1214
Q1215
L1226
E1227
D1230
I1238
R1260
Q1267
R1268

GLU

- Molecule 1: Myosin-7

Chain H:

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

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

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

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

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

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

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

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

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

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

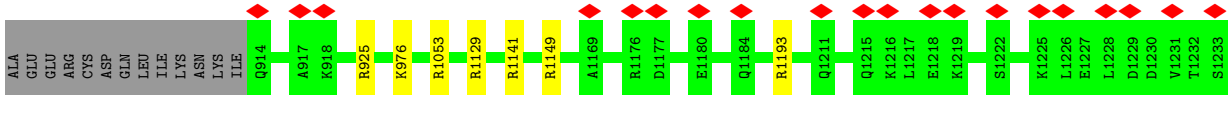
LEU ASN GLU THR VAL GLN LYS SER SER LEU LYS LEU LEU SER THR LEU PHE ALA ASN TYR ALA GLY GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS GLY LYS LYS GLY SER SER PHE GLN THR VAL SER ALA LEU LEU ASN ILE ILE GLY LEU ILE MET SER ILE LEU LEU GLU GLU GLU CYS MET THR

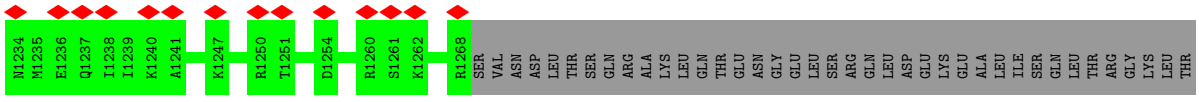
ASN LEU ARG SER THR HIS PRO HIS PHE VAL ARG CYS ILE ILE PRO ASN GLU THR LYS SER PRO GLY VAL LEU GLU VAL MET HIS GLN LEU ARG GLN CYS ASN GLY VAL LEU GLU GLY GLY ILE ARG ILE CYS ARG LYS GLY PHE PRO ASN ARG ILE LEU LEU ASN GLU GLY PHE GLN ASP ASN PRO ALA ASP ASP ARG ASP ASP LEU

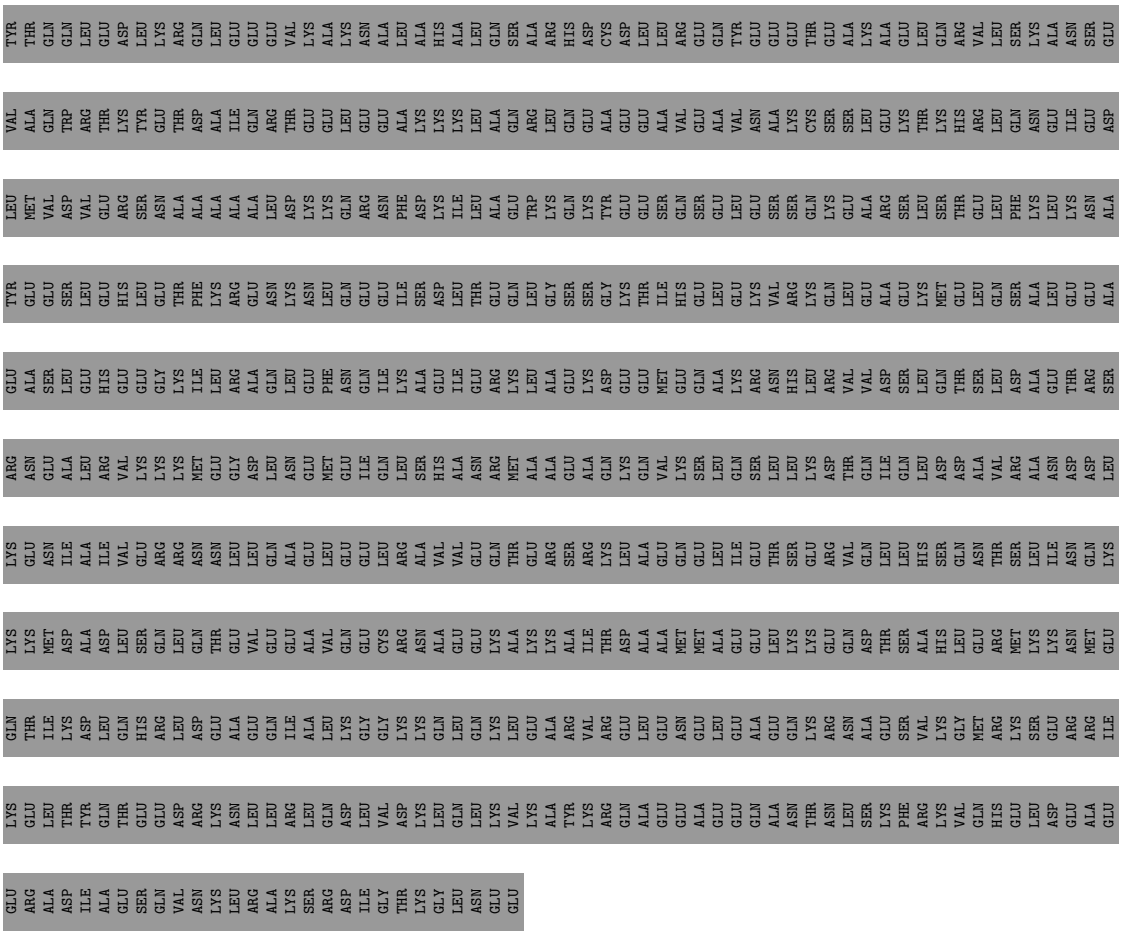
ARG TYR ARG ILE LEU ASN PRO ALA ILE PRO GLU GLY GLN PHE ILE ASP SER ARG LYS GLY PHE ALA GLU LYS LEU LEU SER ASP ILE GLU LEU ASP HIS ASN GLN TYR LYS PHE GLY HIS THR LYS VAL PHE PHE LYS ALA GLY LEU LEU LEU GLU GLU MET ARG ASP GLU ARG

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

LYS SER ALA GLU ARG LYS SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ARG ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS VAL ASN ASP LEU GLN LEU GLN VAL LYS ASP ASN LEU ASP

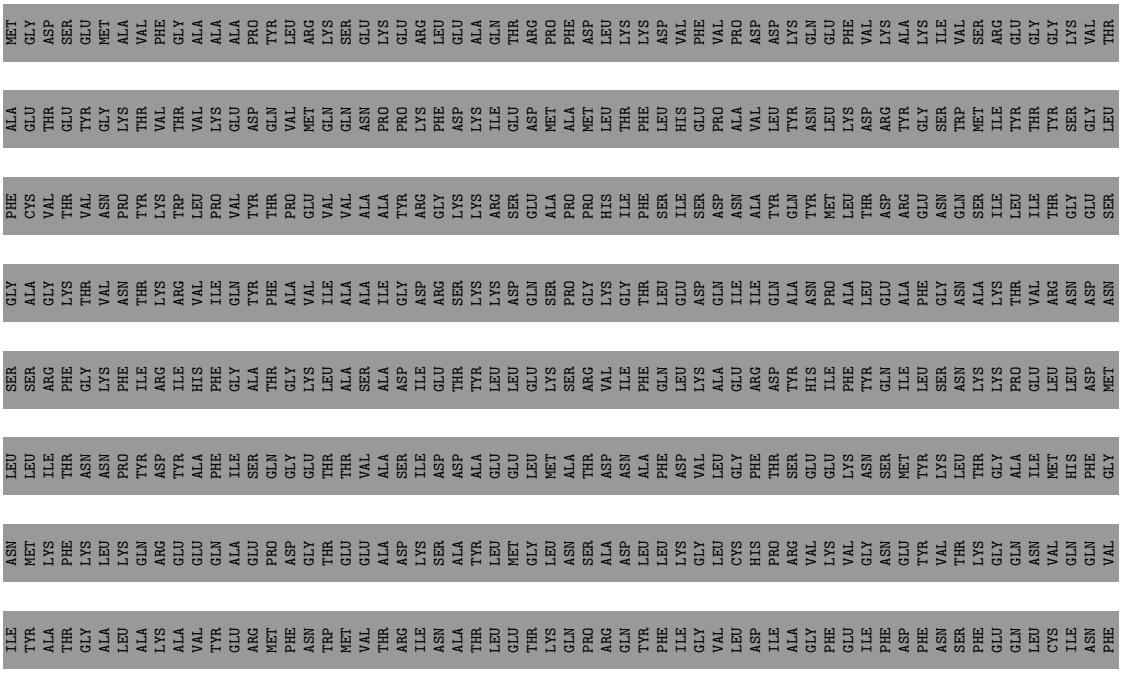


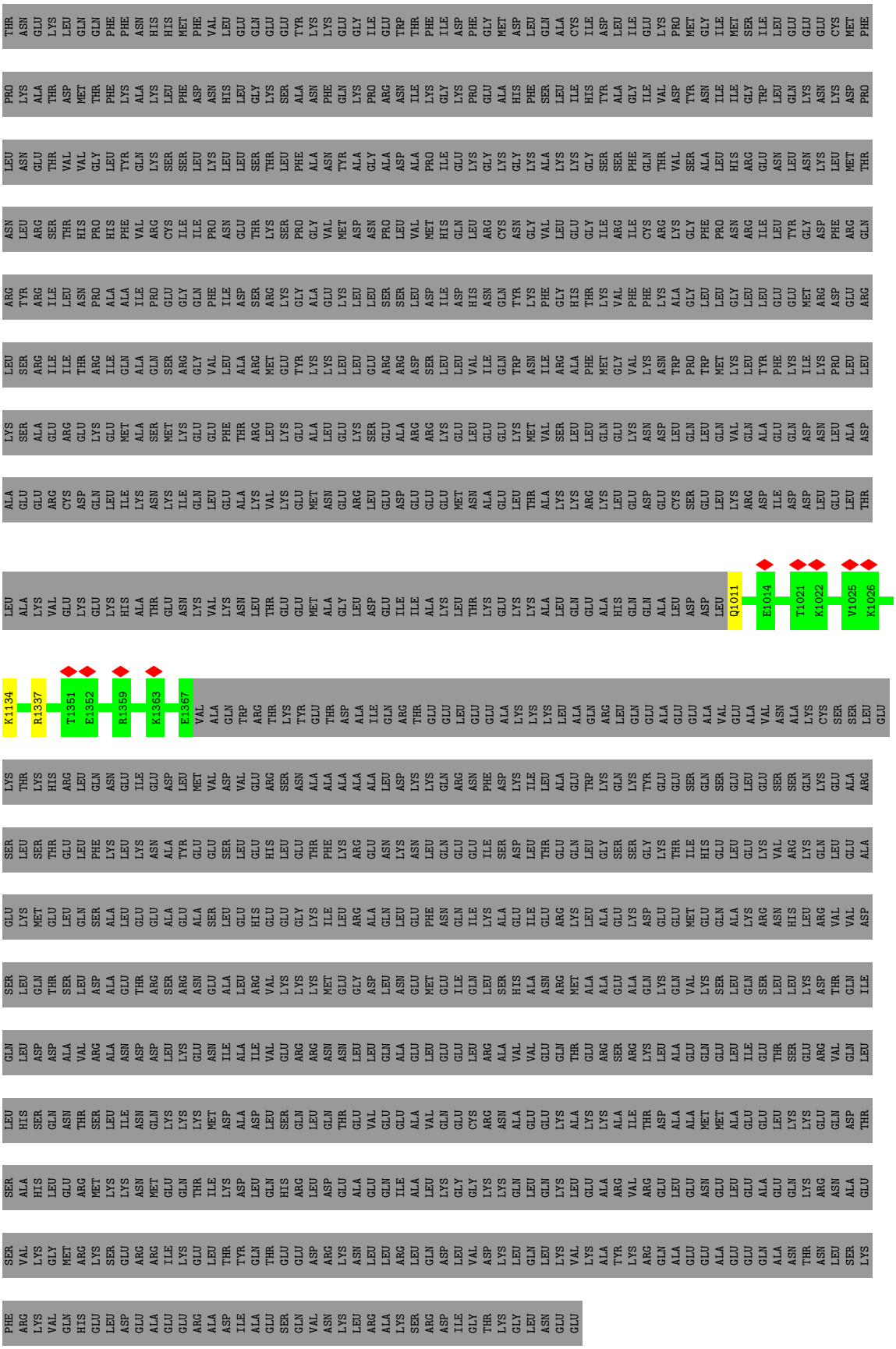




• Molecule 1: Myosin-7

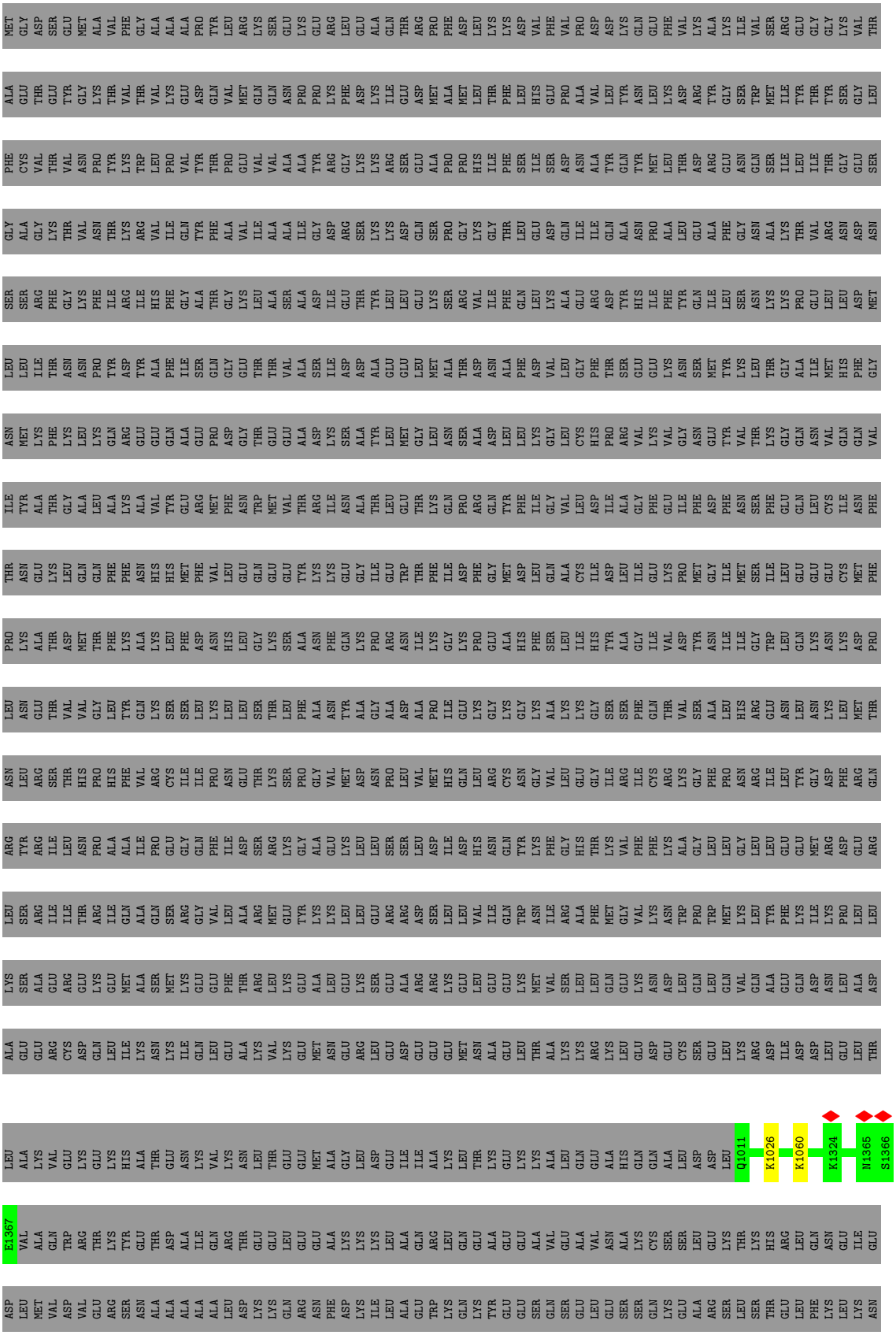
Chain I:

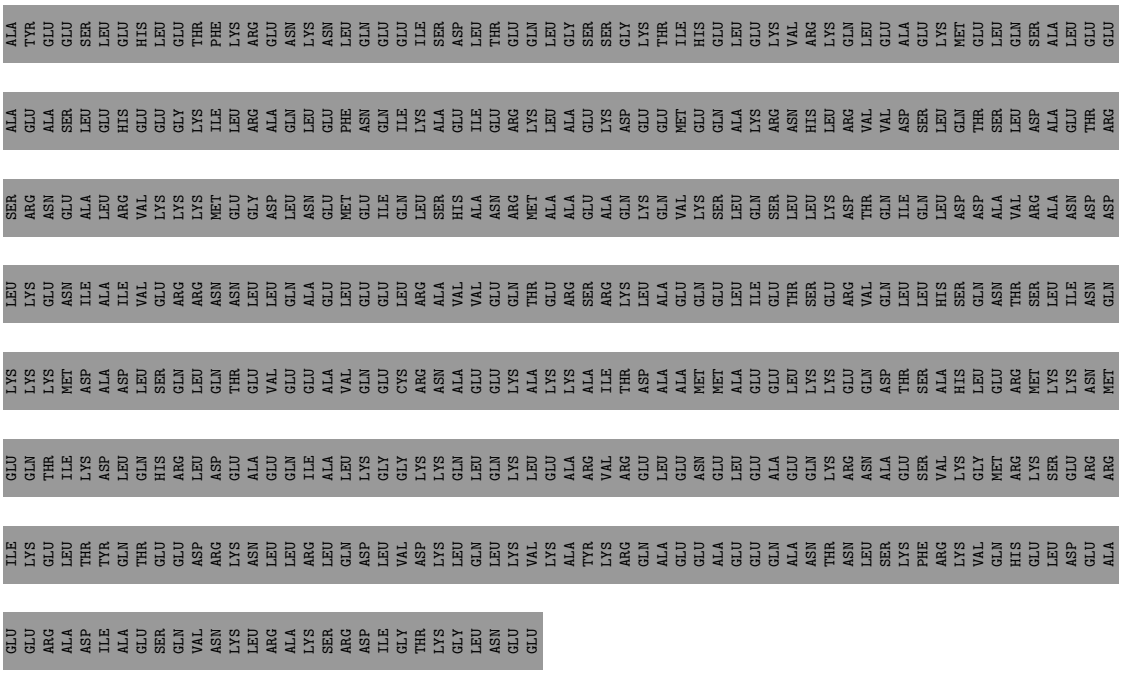




• Molecule 1: Myosin-7

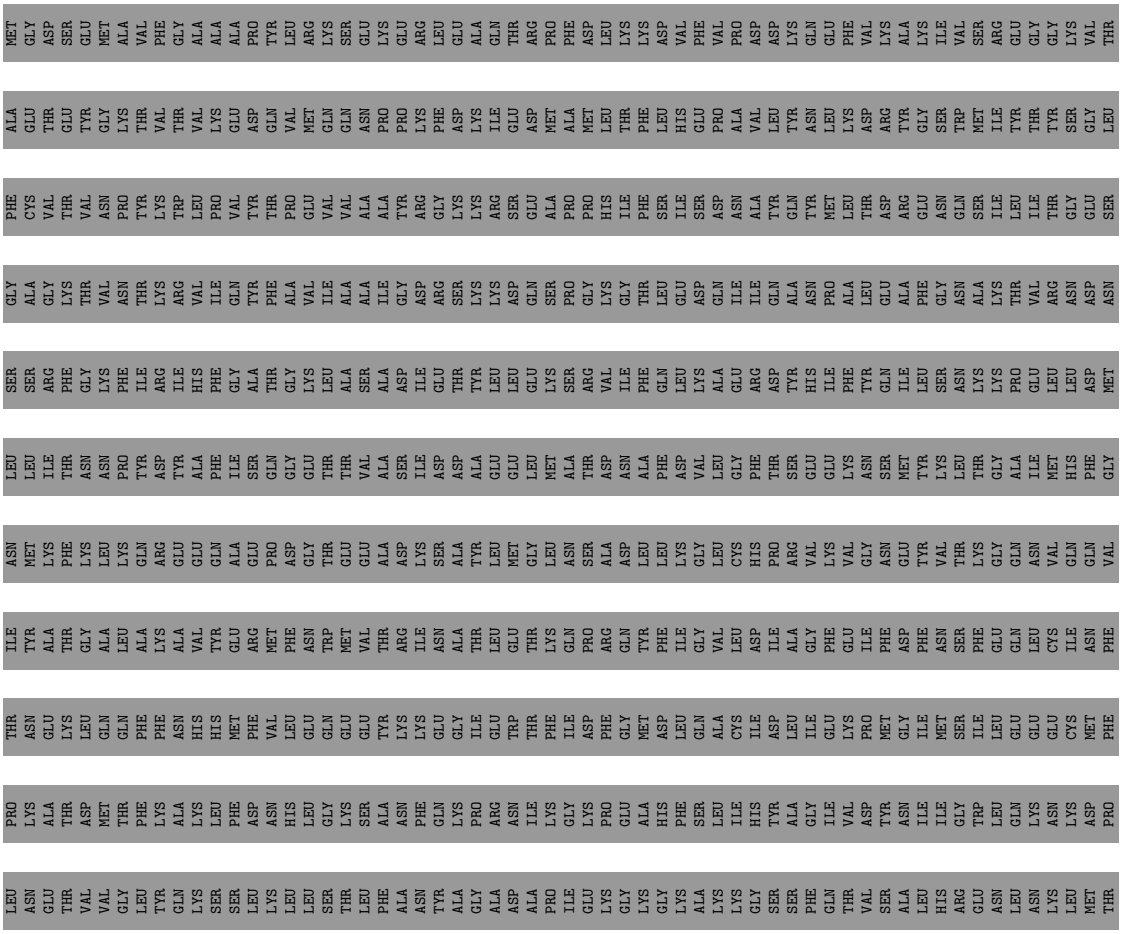
Chain J:

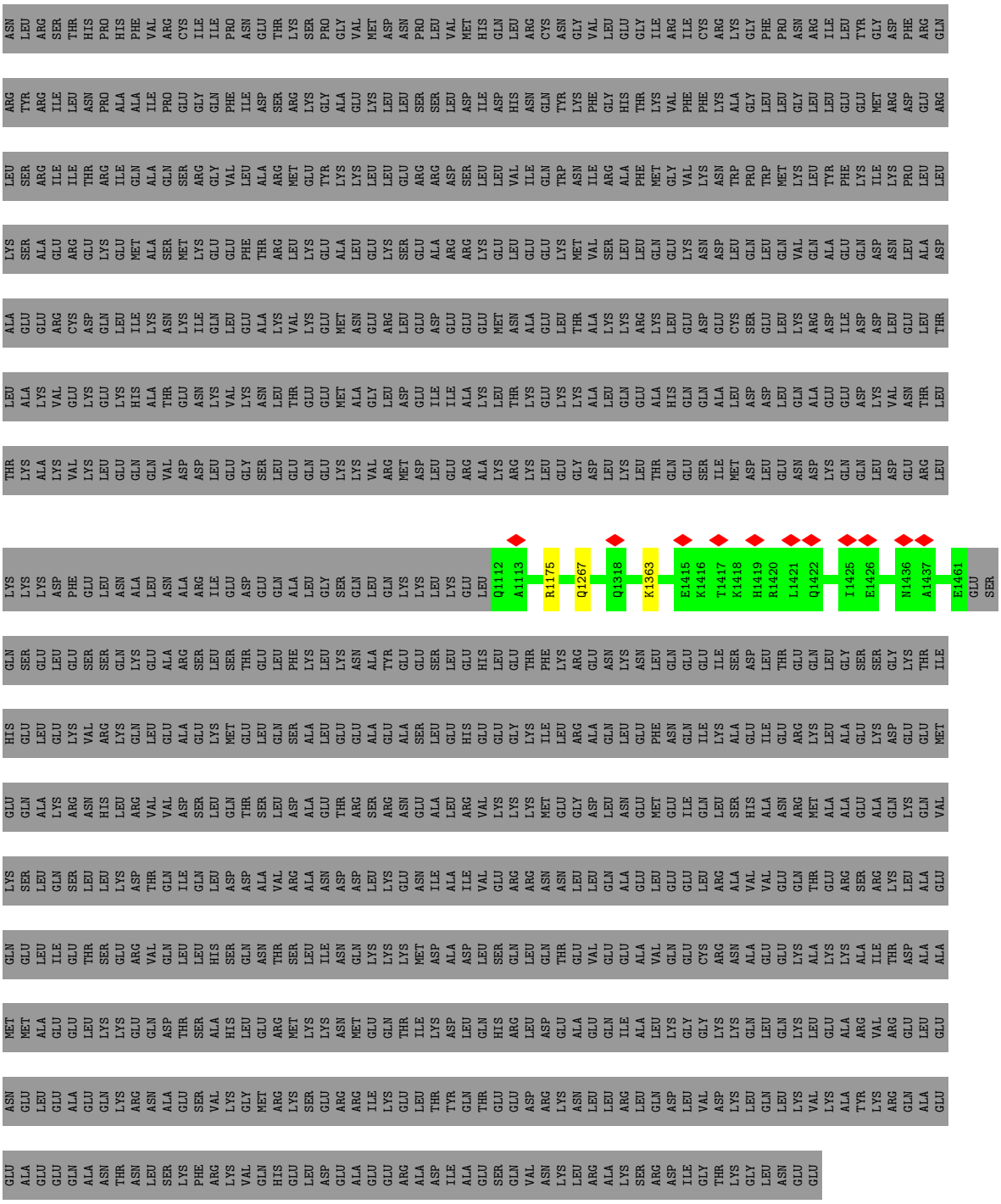




• Molecule 1: Myosin-7

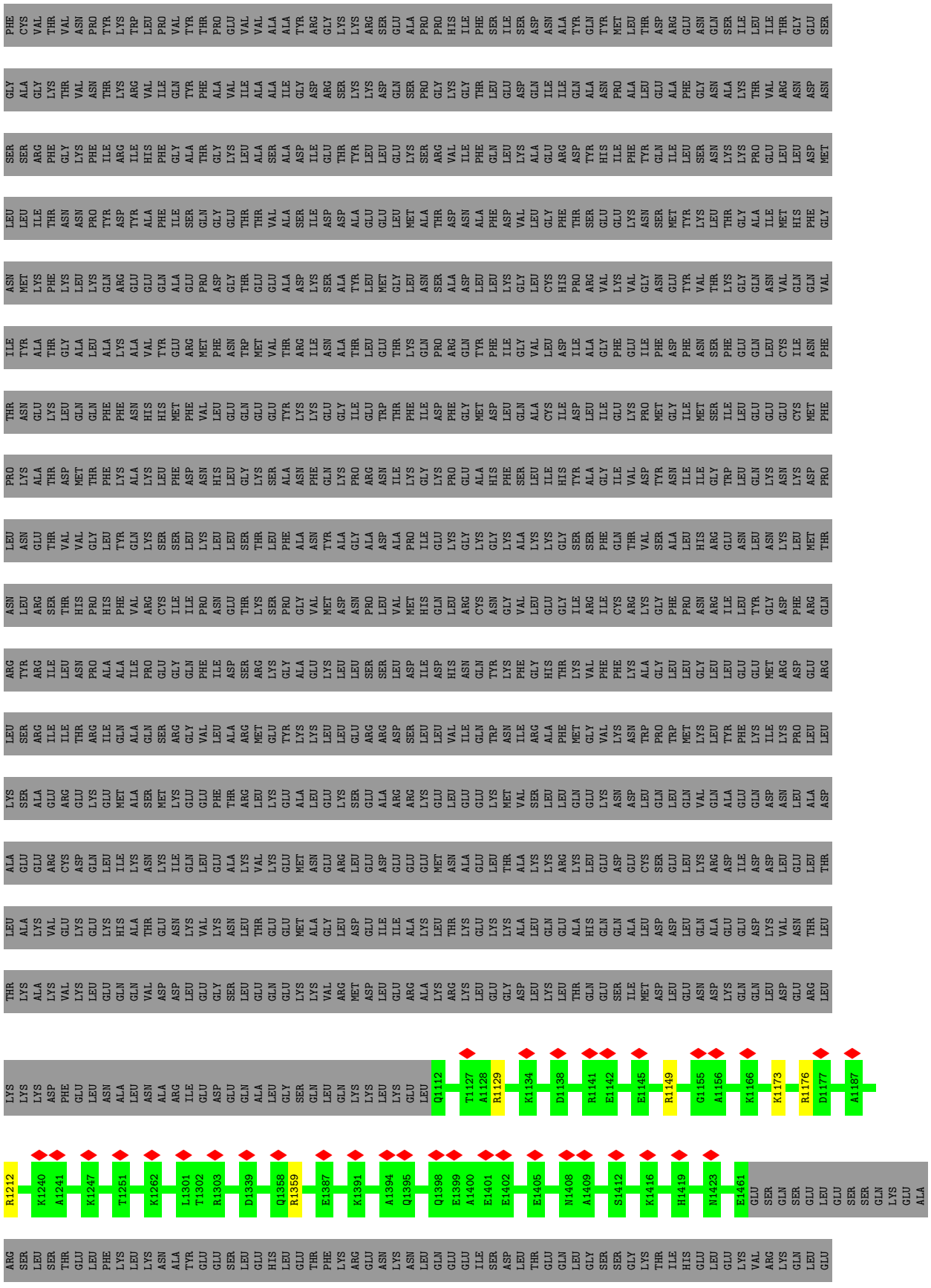
Chain K:





• Molecule 1: Myosin-7

Chain L: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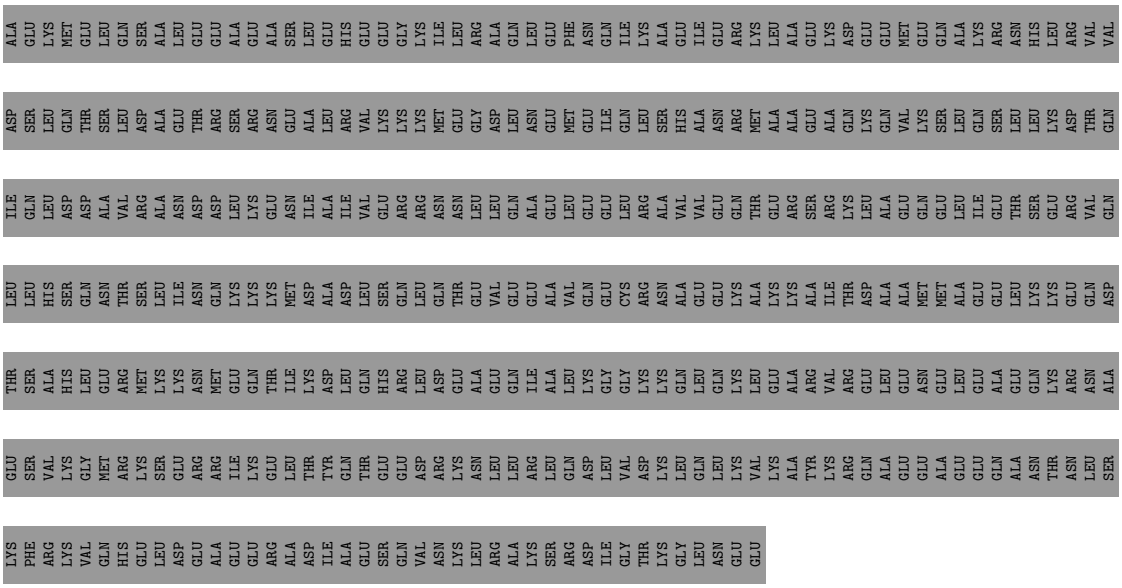
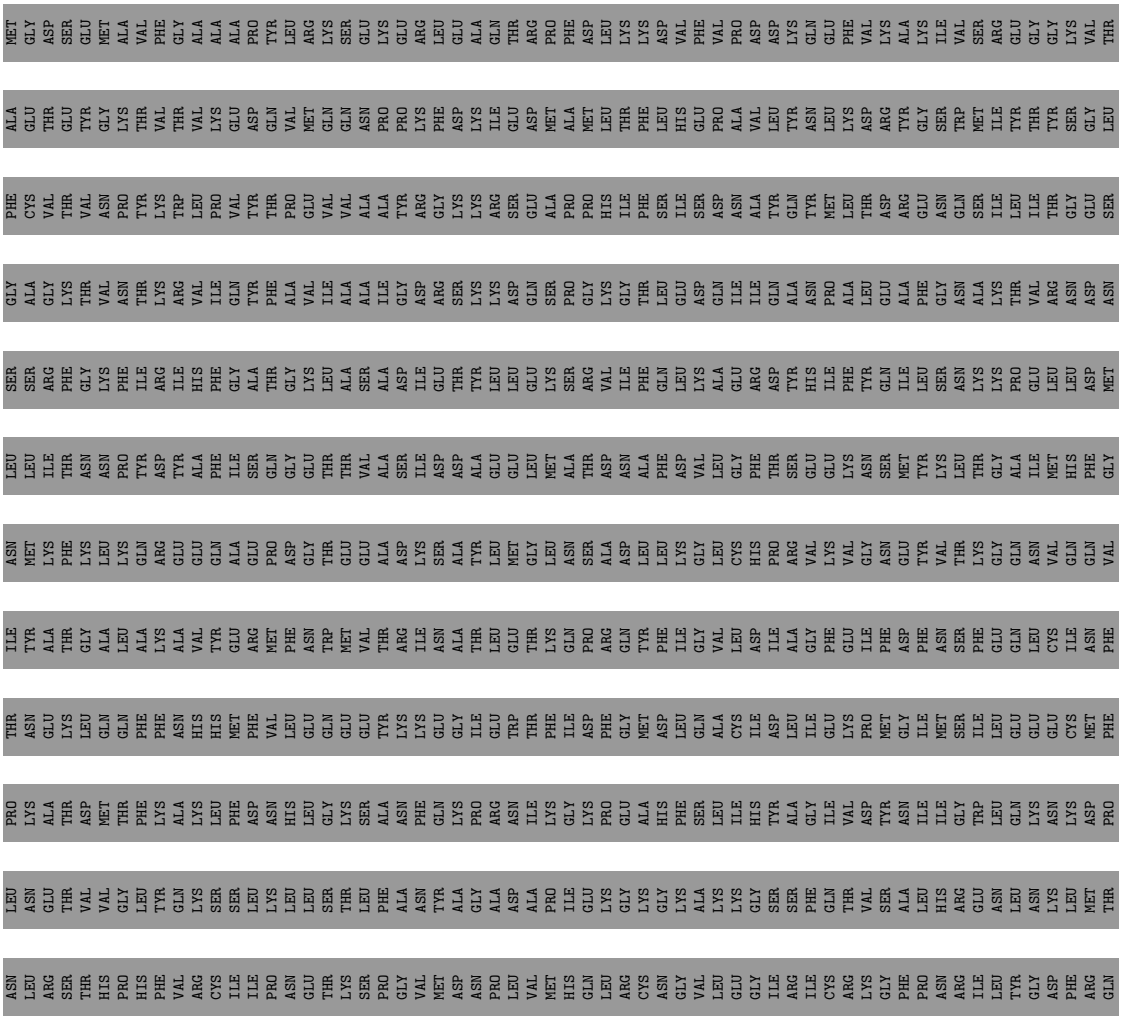
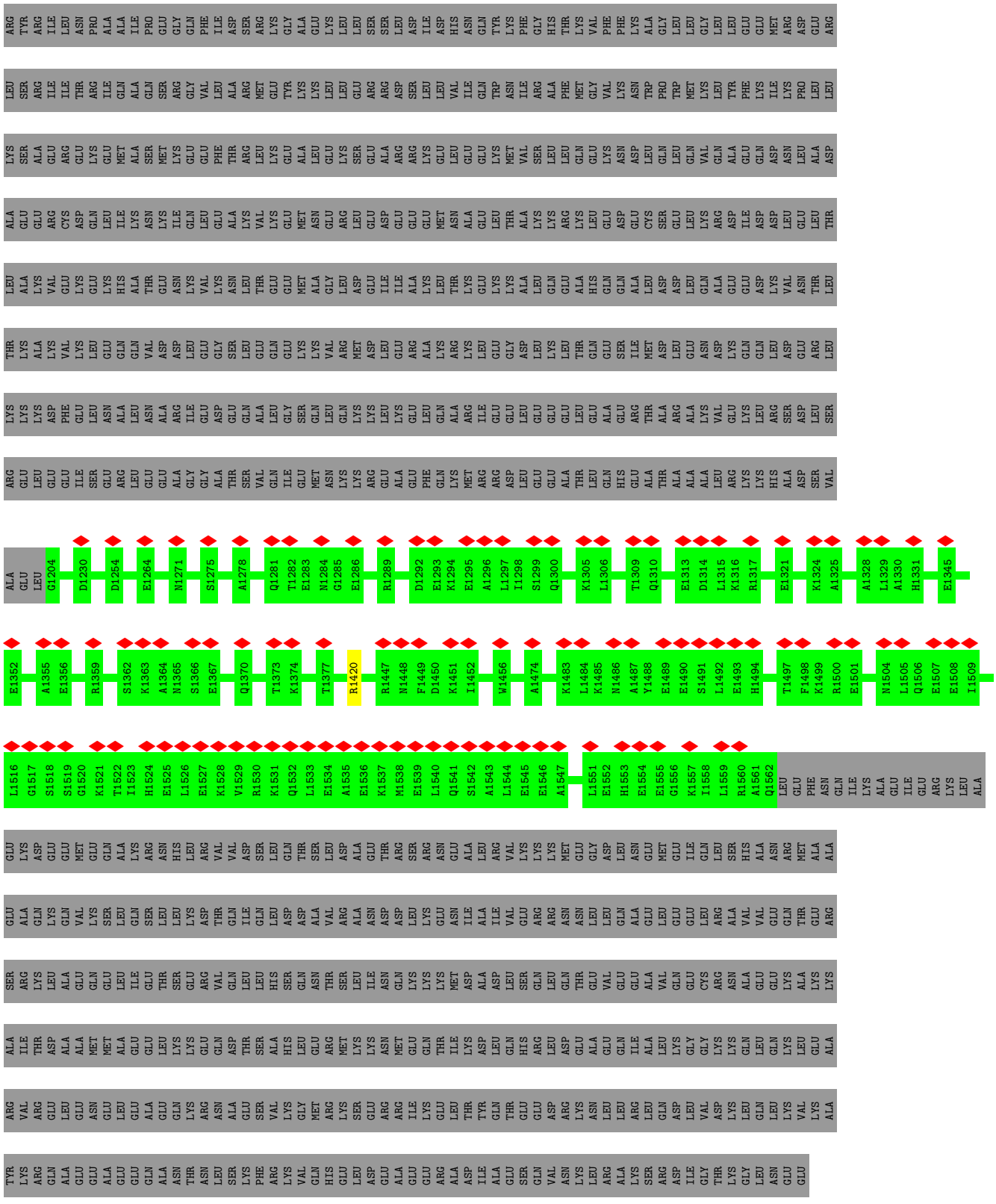


• Molecule 1: Myosin-7

Chain M:





• Molecule 1: Myosin-7

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

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

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

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

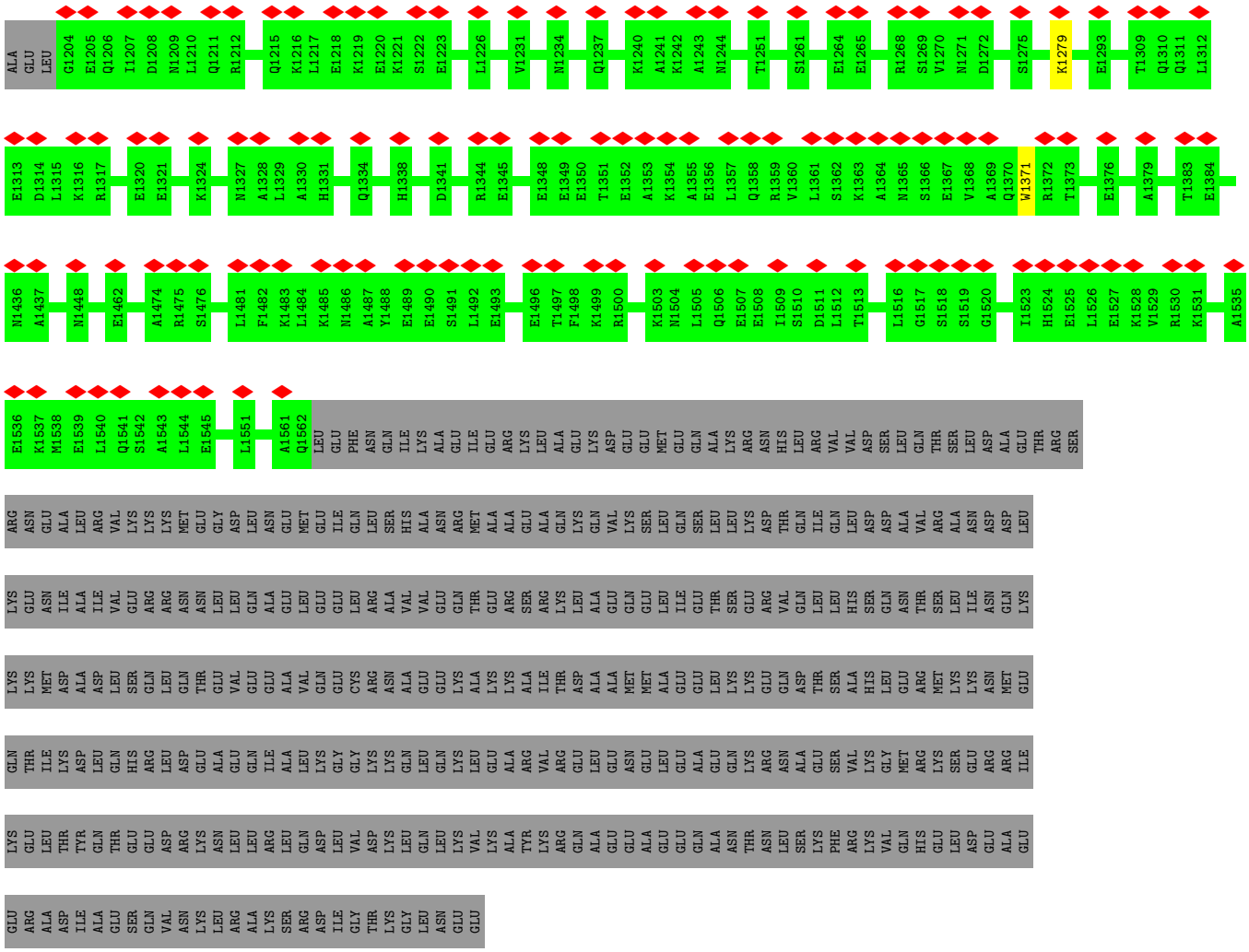
ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

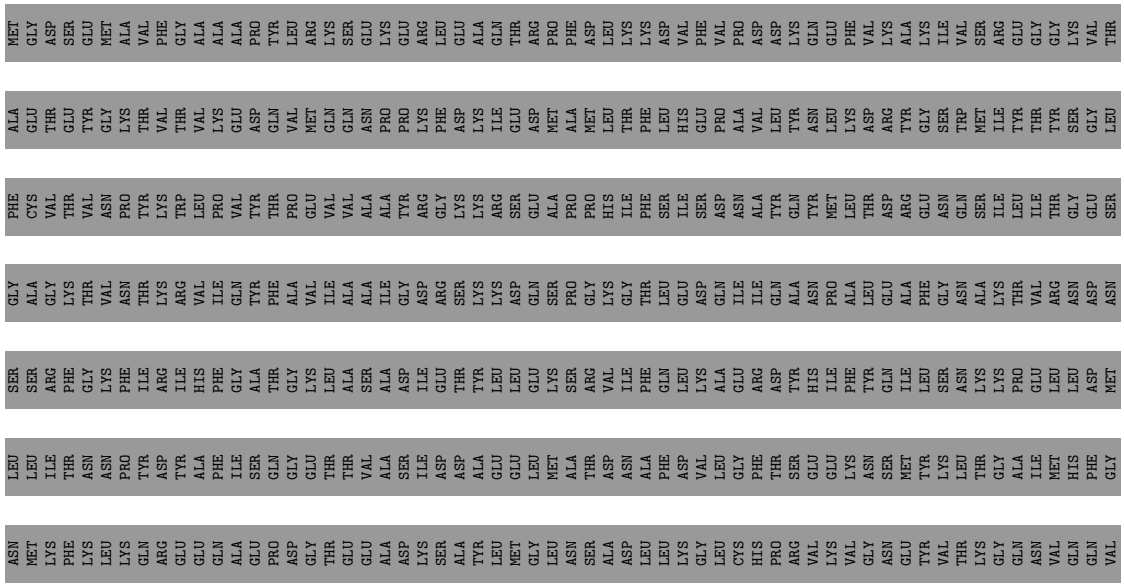
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

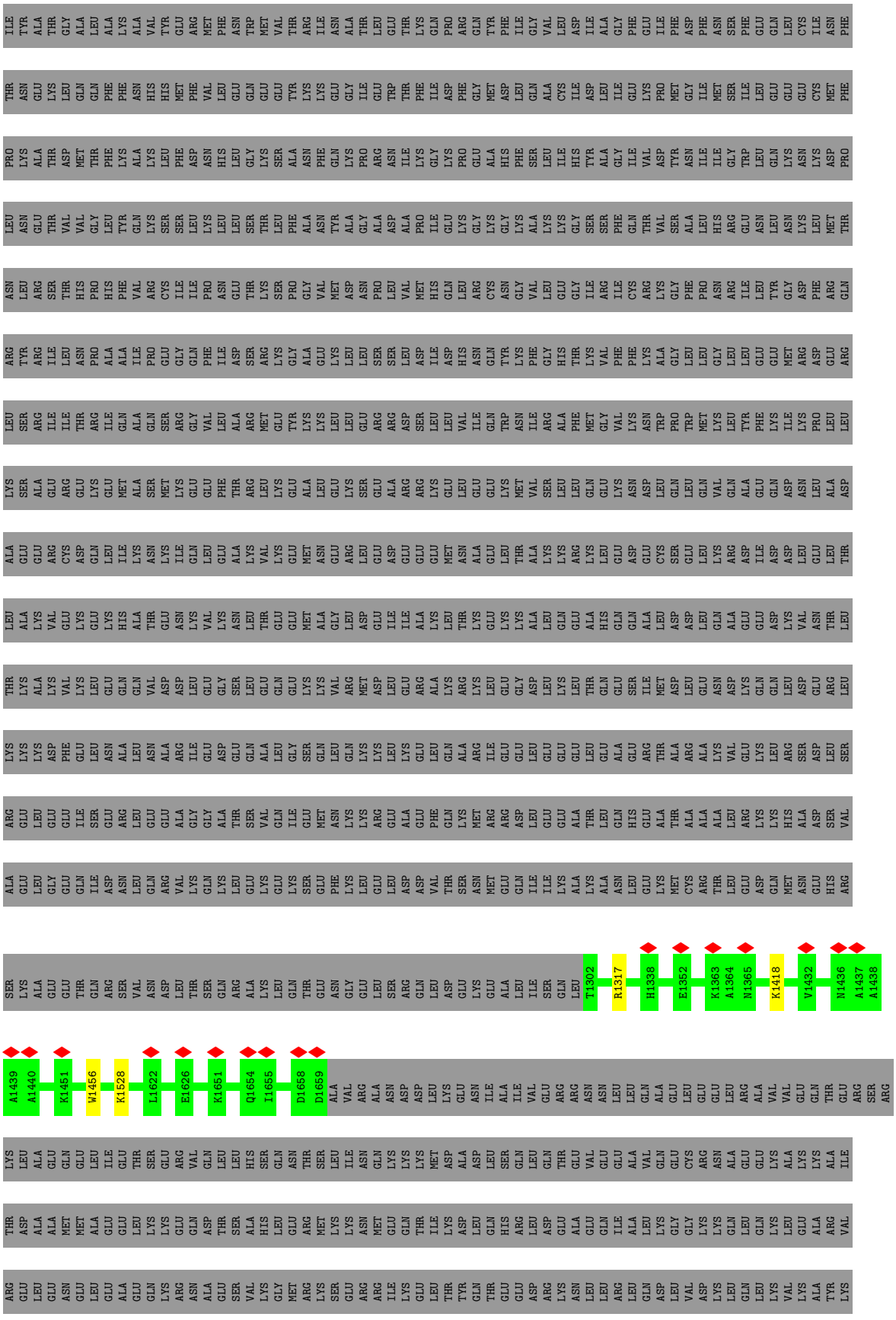
ARG GLU LEU GLU GLU ILE SER GLU ARG LEU GLU GLU ALA GLY GLY ALA THR SER VAL GLN ILE GLU MET ASN LYS LYS ARG GLU ALA GLU PHE GLN LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL



• Molecule 1: Myosin-7

Chain O:

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E1352
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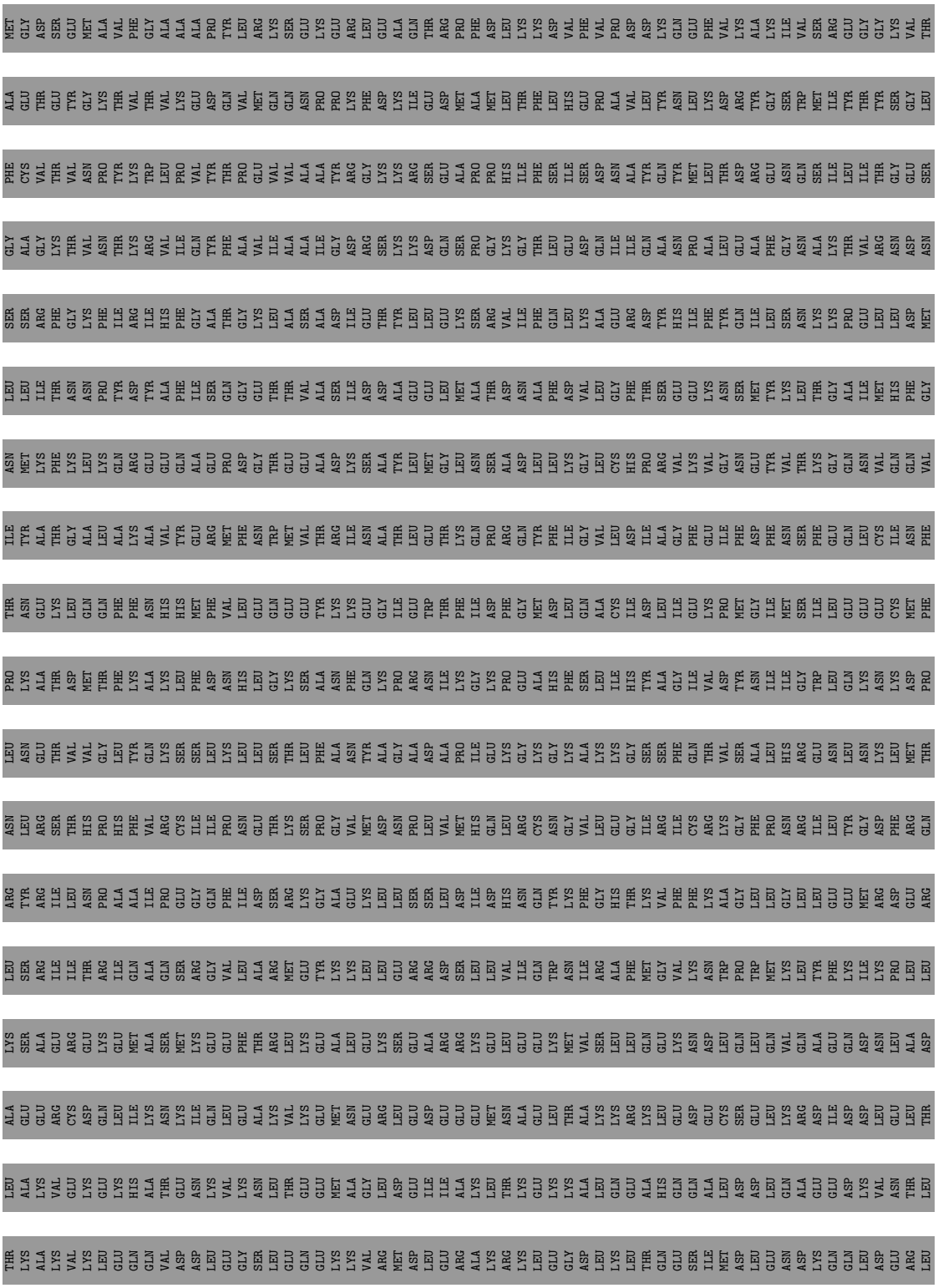
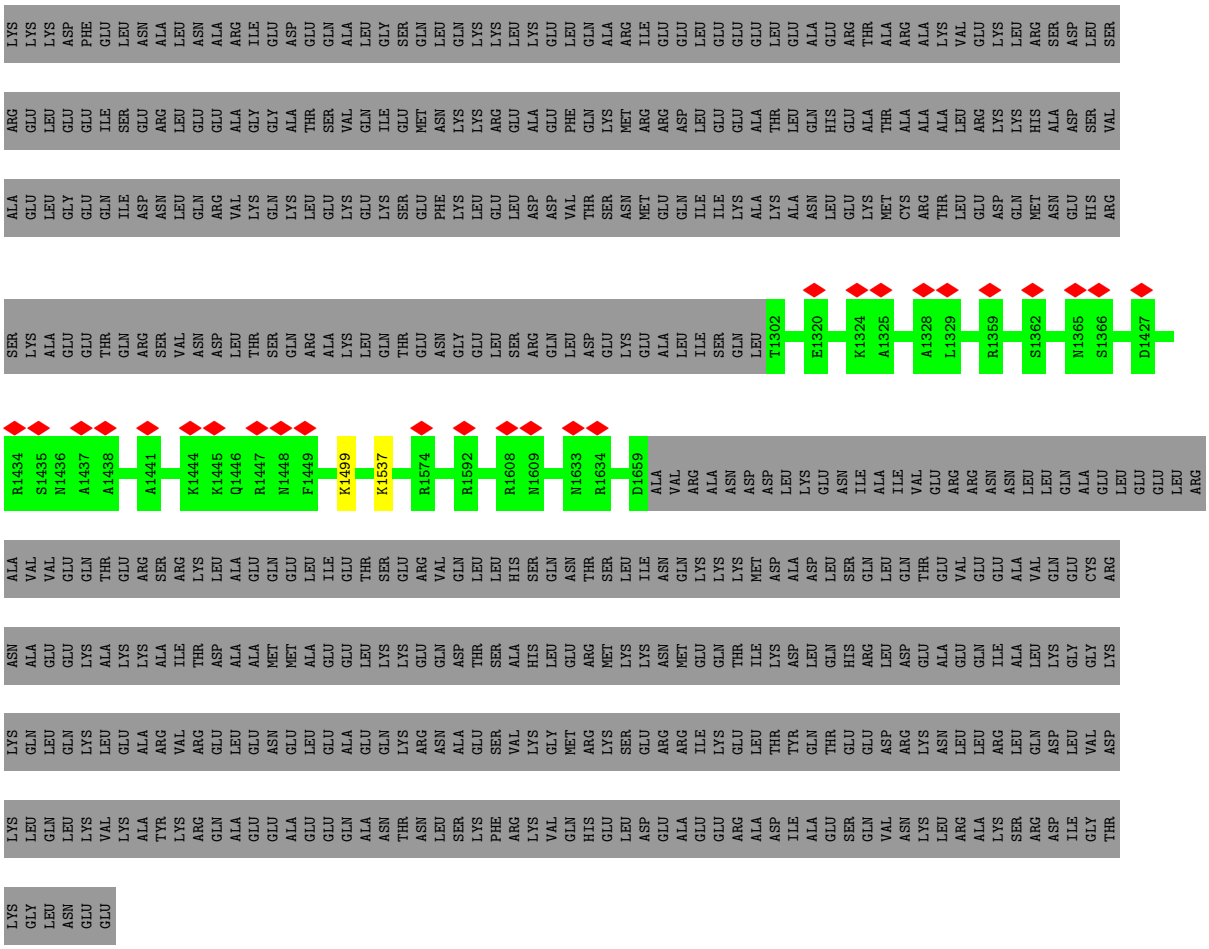
A1364
N1365
K1418
V1432
N1436
A1437
A1438
A1439
A1440
K1451
W1456
K1528
L1622
E1626
K1651
Q1654
I1655
D1658
D1659

- Molecule 1: Myosin-7

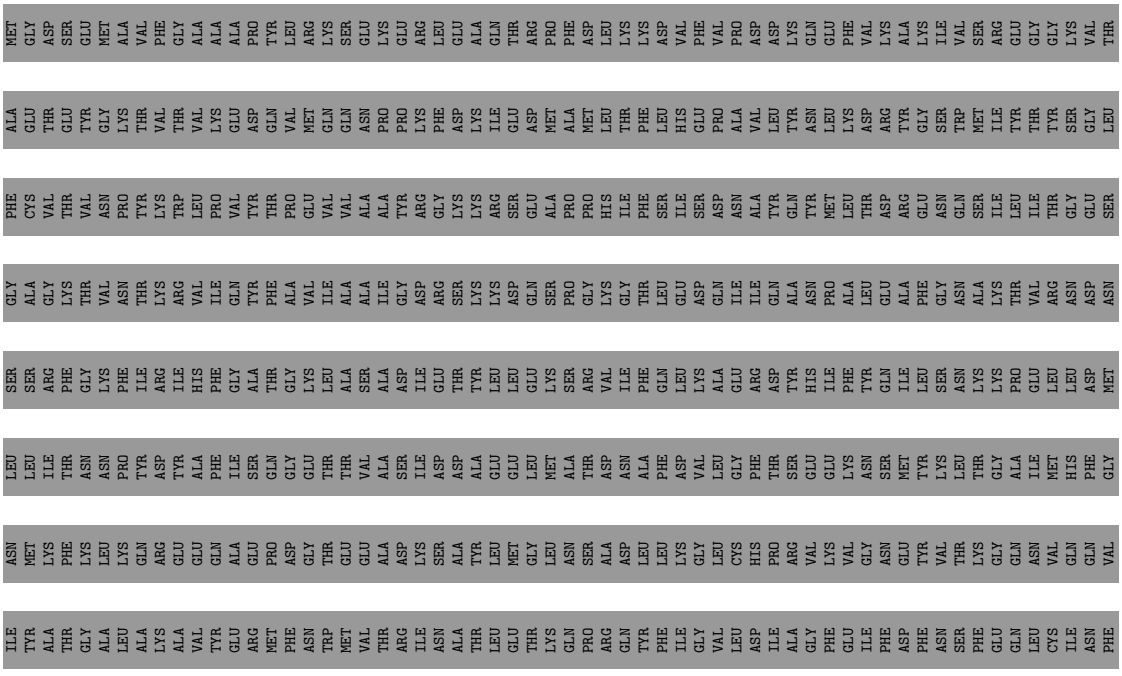
Chain P:

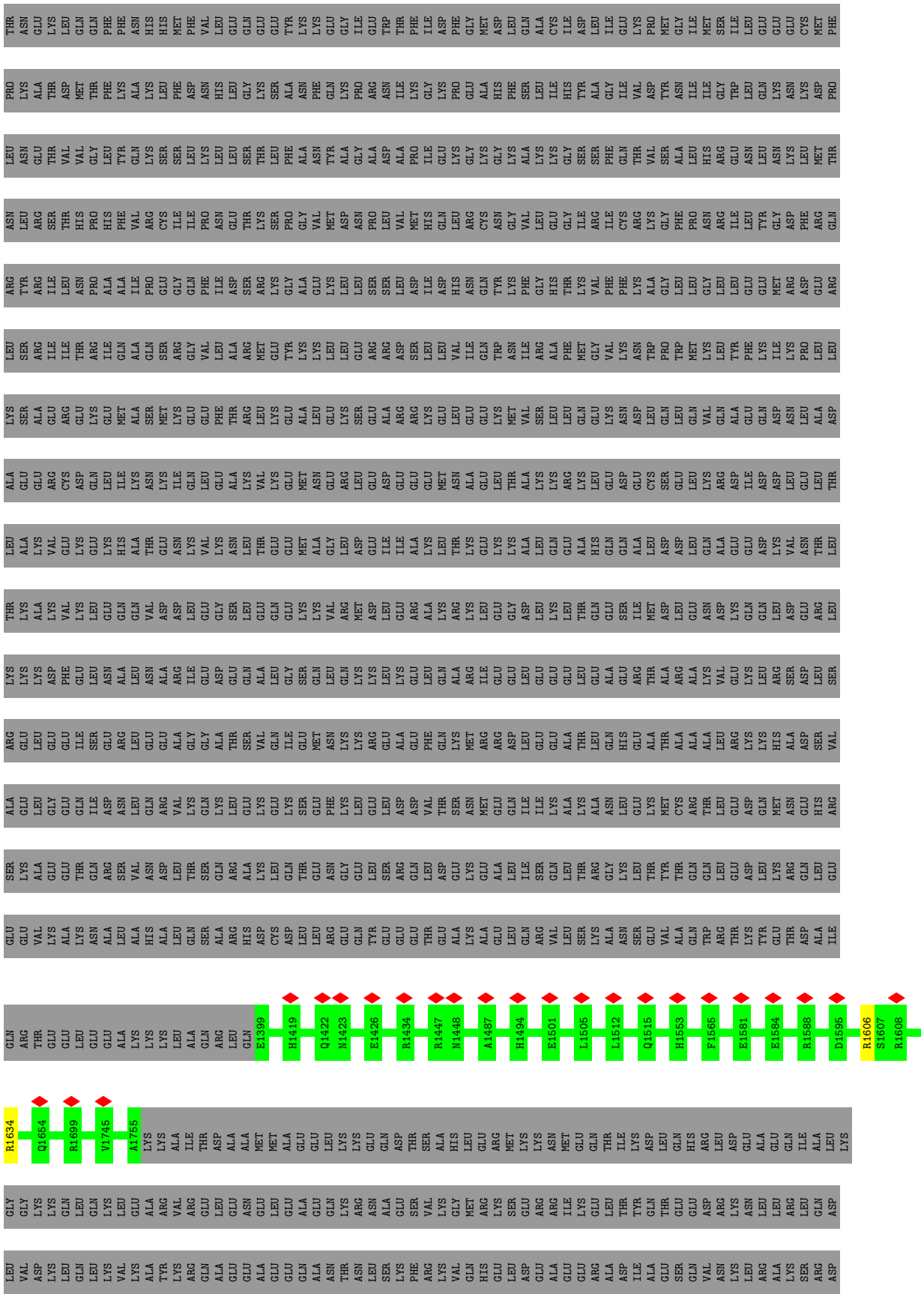




• Molecule 1: Myosin-7

Chain Q:

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Q1515
H1553
F1565
E1581
E1584
R1588
D1595
R1606
S1607
R1608
R1634
Q1654
R1699
V1745
A1755

ILE GLY THR LYS GLY LEU ASN GLU GLU

• Molecule 1: Myosin-7

Chain R:

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

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

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

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

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

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

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

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

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

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

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

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

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

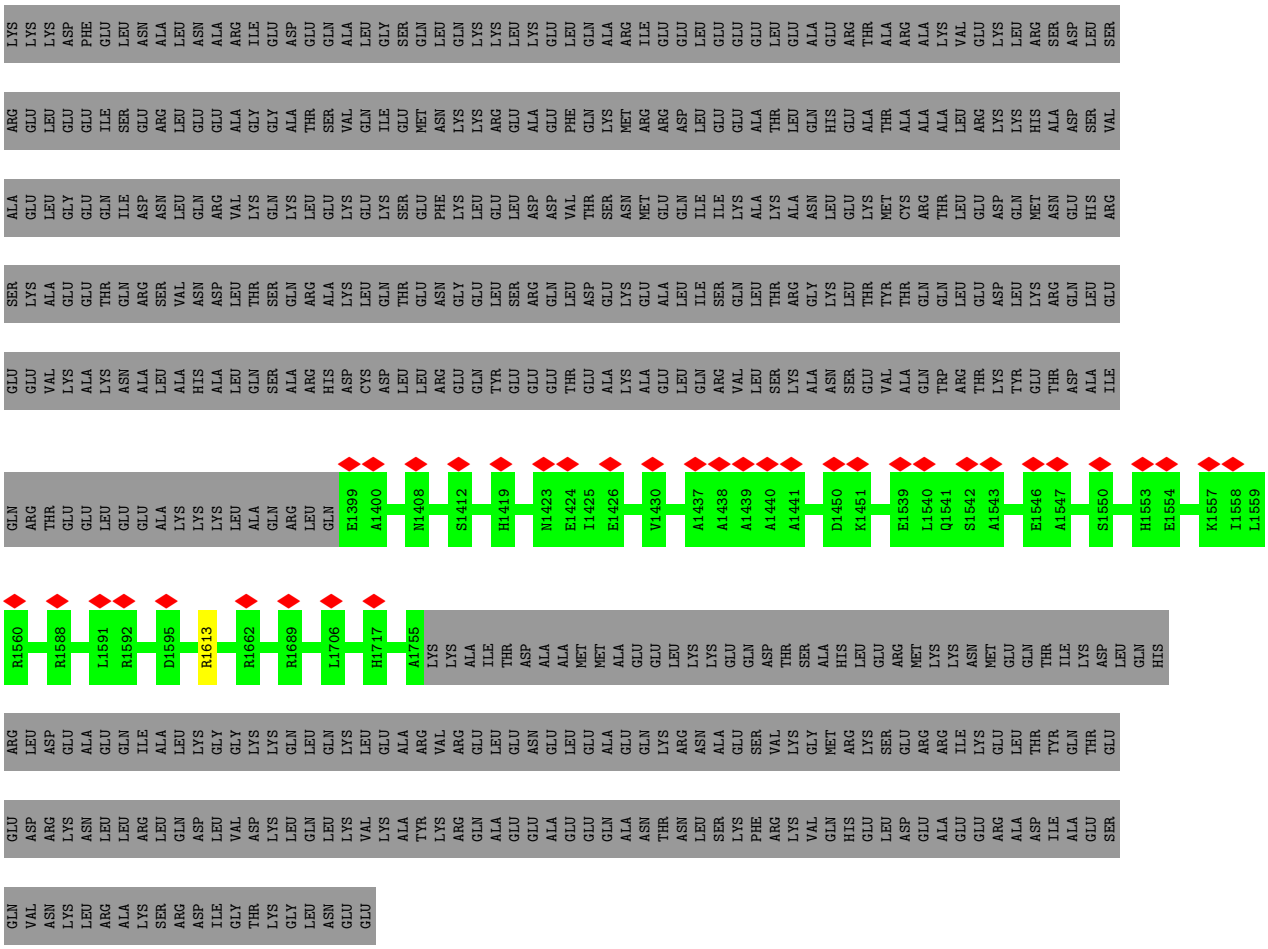
LEU SER ARG ILE ILE THR ARG ILE GLN ALA GLN SER ARG GLY VAL LEU ALA ARG MET GLU TYR LYS LYS LEU LEU GLU ARG ARG ASP SER LEU LEU VAL ILE GLN TRP ASN ILE ARG ALA PHE MET GLY VAL LYS ASN TRP PRO TRP MET LYS LEU TYR PHE LYS ILE LYS PRO LEU

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

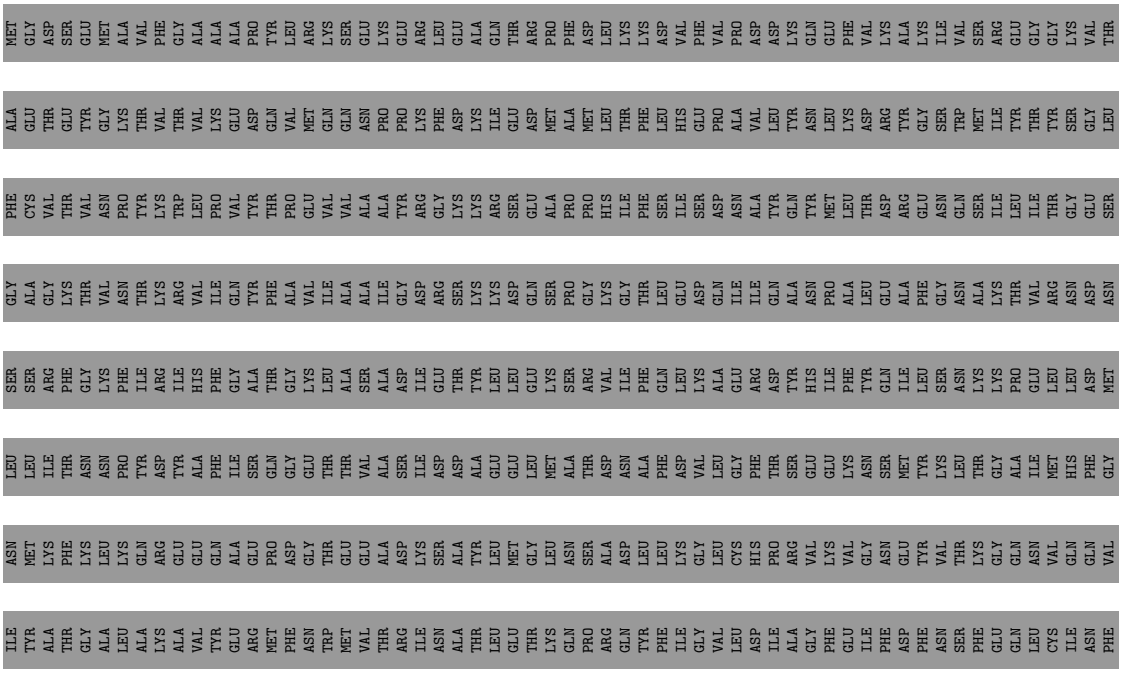
ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

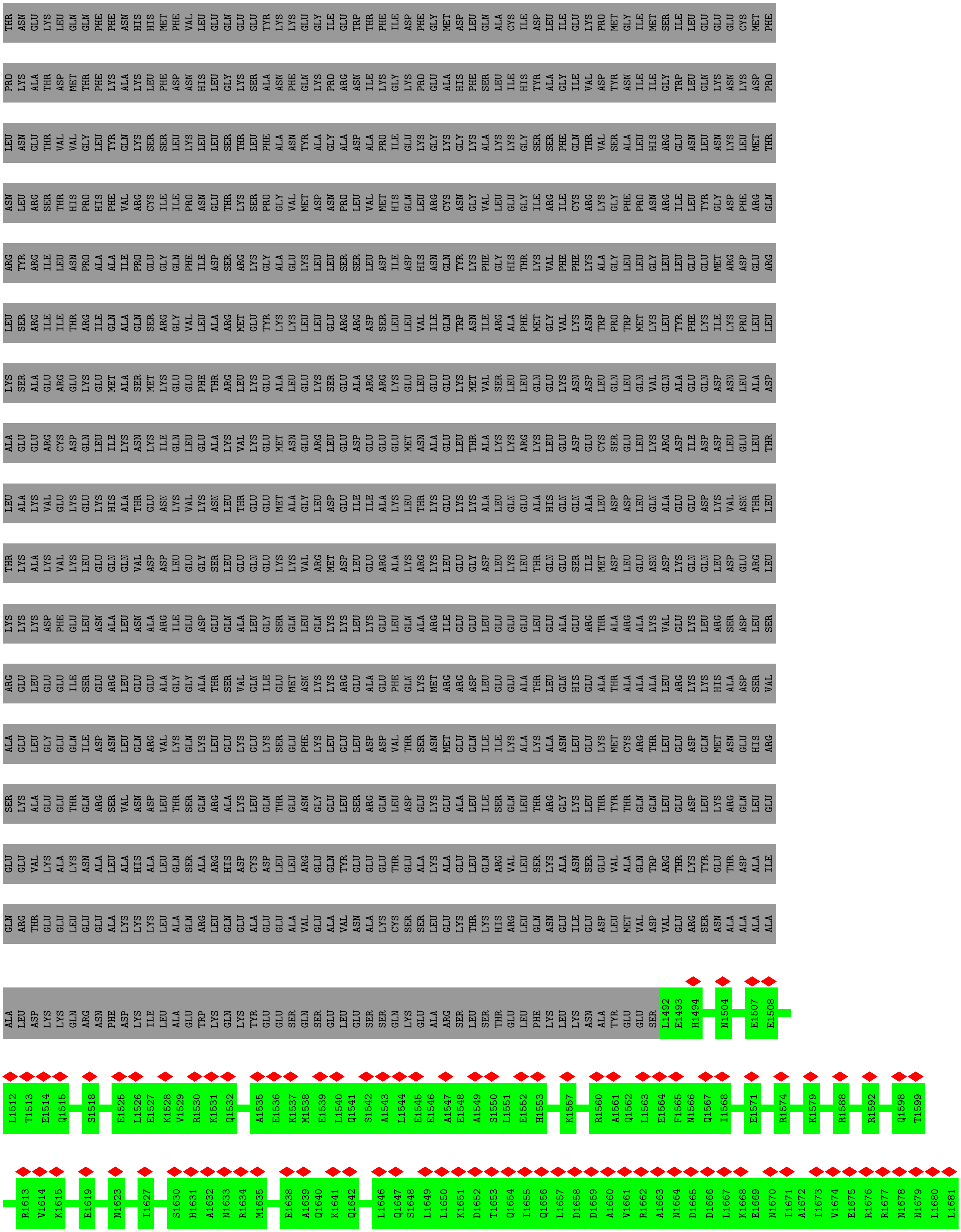
LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

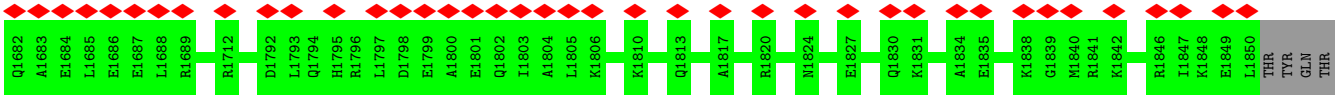
THR LYS ALA LYS VAL LYS LEU GLU GLN GLN VAL ASP ASP LEU GLU GLY SER LEU GLU GLN GLU LYS LYS VAL ARG MET ASP LEU GLU ARG ALA LYS ARG LYS LEU GLU GLY ASP LEU LYS LEU THR GLN GLU SER ILE MET ASP LEU GLU ASN ASP LYS GLN GLN LEU ASP GLU ARG LEU

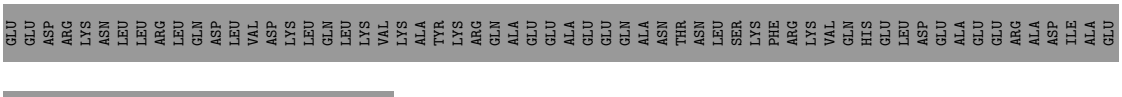


• Molecule 1: Myosin-7

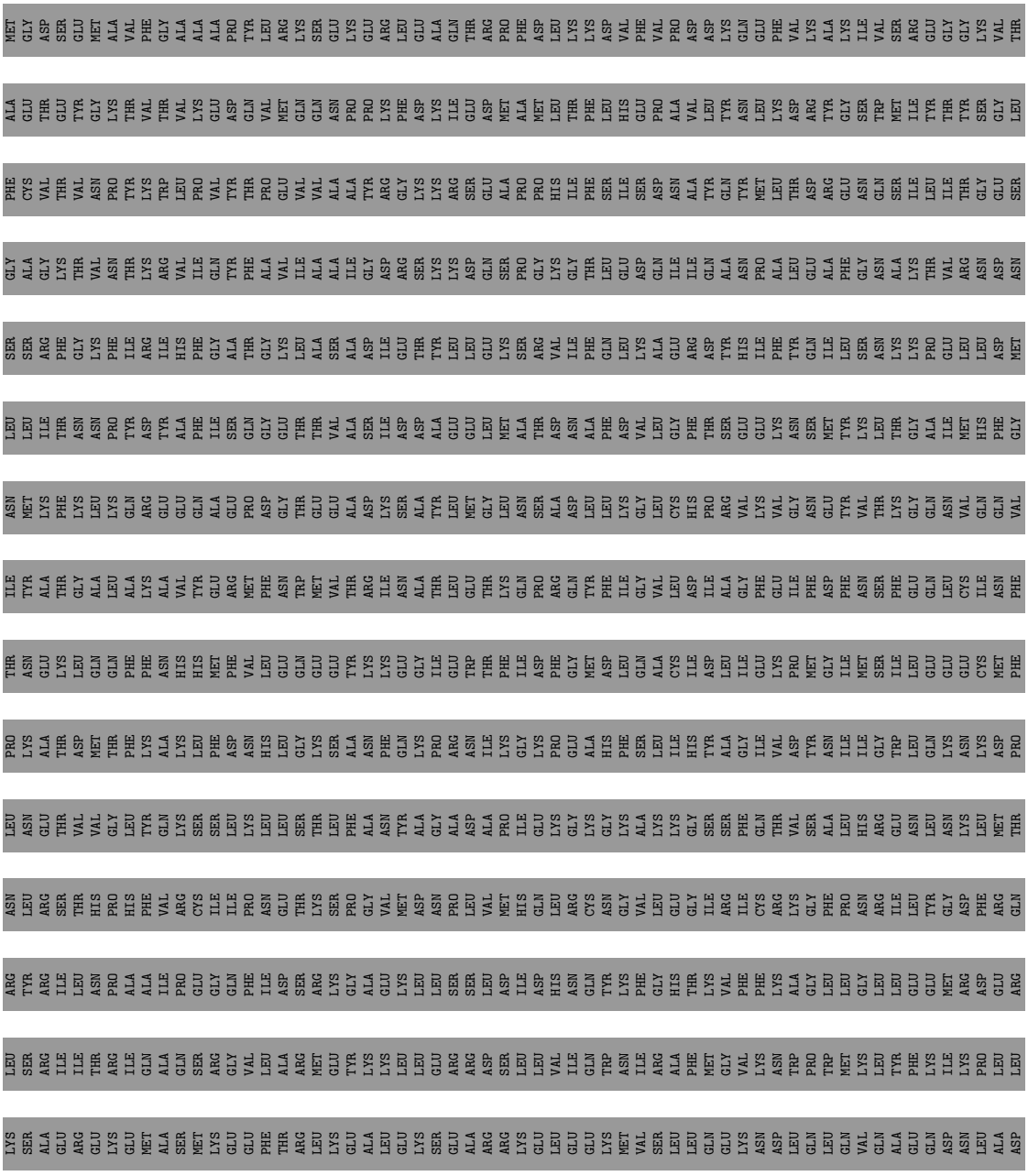


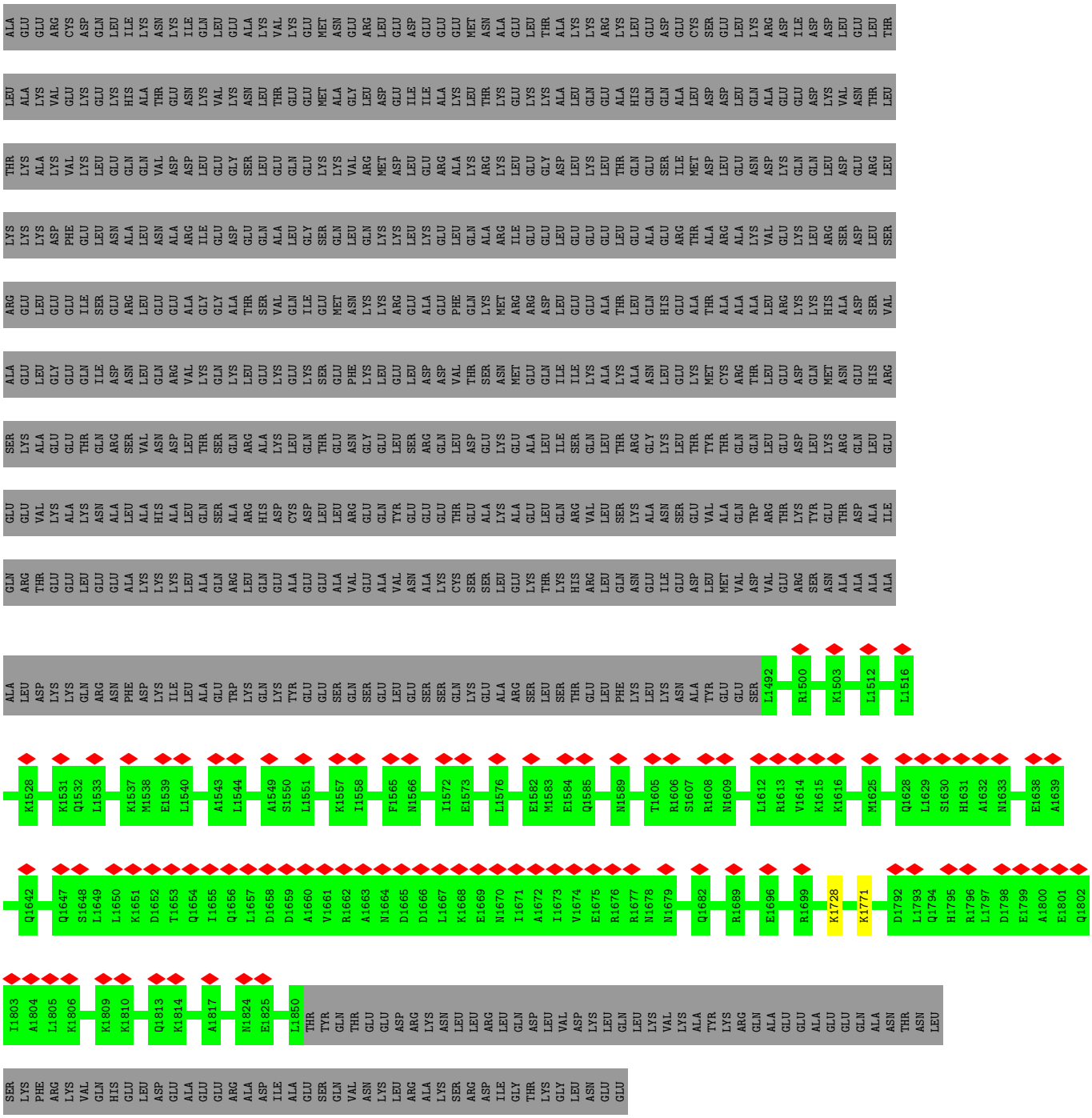

THR ASN GLU LYS LEU GLN GLN PHE PHE ASN HIS HIS MET PHE VAL LEU GLU GLN GLU GLU TYR LYS LYS GLU GLY ILE GLU TRP THR PHE ILE ASP PHE GLY MET ASP LEU GLN ALA CYS ILE ASP LEU ILE GLU LYS PRO MET GLY ILE MET SER ILE LEU GLU GLU GLU CYS MET PHE
PRO LYS ALA THR ASP MET THR PHE LYS ALA LYS LEU PHE ASP ASN HIS LEU GLY LYS SER ALA ASN PHE GLN LYS PRO ARG ASN ILE LYS GLY LYS PRO GLU ALA HIS PHE SER LEU ILE HIS TYR ALA GLY ILE VAL ASP TYR ASN ILE ILE GLY TRP LEU GLN LYS ASN LYS ASP PRO
LEU ASN GLU THR VAL VAL GLY LEU TYR GLN LYS SER SER LEU LYS LEU LEU SER THR LEU PHE ALA ASN TYR ALA GLY ALA ASP ALA PRO ILE GLU LYS GLY LYS GLY LYS ALA LYS LYS GLY SER SER PHE GLN THR VAL SER ALA LEU HIS ARG GLU ASN LEU ASN LYS LEU MET THR
ASN LEU ARG SER THR HIS PRO HIS PHE VAL ARG CYS ILE ILE PRO ASN GLU THR LYS SER PRO GLY VAL MET ASP ASN PRO LEU VAL MET HIS GLN LEU ARG CYS ASN GLY VAL LEU GLU GLY ILE ARG ILE CYS ARG LYS GLY PHE PRO ASN ARG ILE LEU TYR GLY ASP PHE ARG GLN
ARG TYR ARG ILE LEU ASN PRO ALA ALA ILE PRO GLU GLY GLN PHE ILE ASP SER ARG LYS GLY ALA GLU LYS LEU LEU SER SER LEU ASP ILE ASP HIS ASN GLN TYR LYS PHE GLY HIS THR LYS VAL PHE PHE LYS ALA GLY LEU LEU GLY LEU LEU GLU GLU MET ARG ASP GLU ARG
LEU SER ARG ILE ILE THR ARG ILE GLN ALA GLN SER ARG GLY VAL LEU ALA ARG MET GLU TYR LYS LYS LEU LEU GLU ARG ARG ASP SER LEU LEU VAL ILE GLN TRP ASN ILE ARG ALA PHE MET GLY VAL LYS ASN TRP PRO TRP MET LYS LEU TYR PHE LYS ILE LYS PRO LEU LEU
LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP
ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR
LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU
THR LYS ALA LYS VAL LYS LEU GLU GLN GLN VAL ASP ASP LEU GLU GLY SER LEU GLU GLN GLU LYS LYS VAL ARG MET ASP LEU GLU ARG ALA LYS ARG LYS LEU GLU GLY ASP LEU LYS LEU THR GLN GLU SER ILE MET ASP LEU GLU ASN ASP LYS GLN GLN LEU ASP GLU ARG LEU
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER
ARG GLU LEU GLU GLU ILE SER GLU ARG LEU GLU GLU ALA GLY GLY ALA THR SER VAL GLN ILE GLU MET ASN LYS LYS ARG GLU ALA GLU PHE GLN LYS MET ARG ARG ASP LEU GLU GLU ALA THR LEU GLN HIS GLU ALA THR ALA ALA ALA LEU ARG LYS LYS HIS ALA ASP SER VAL
ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU GLU LEU ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG
SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU
GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU ARG GLU GLN TYR GLU GLU GLU THR GLU ALA LYS ALA GLU LEU GLN ARG VAL LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE
GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LYS LEU ALA GLN ARG LEU GLN GLU ALA GLU GLU ALA VAL GLU ALA VAL ASN ALA LYS CYS SER SER LEU GLU LYS THR LYS HIS ARG LEU GLN ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG SER ASN ALA ALA ALA ALA
ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER L1492 E1493 H1494 N1504 E1507 E1508
L1512 T1513 E1514 Q1515 S1518 E1525 L1526 E1527 K1528 V1529 R1530 K1531 Q1532 A1535 E1536 K1537 M1538 E1539 L1540 Q1541 S1542 A1543 L1544 E1545 E1546 A1547 E1548 A1549 S1550 L1551 E1552 H1553 K1557 R1560 A1561 Q1562 L1563 E1564 F1565 N1566 Q1567 I1568 E1571 R1574 K1579 R1588 R1592 Q1598 T1599
R1613 V1614 K1615 E1619 N1623 I1627 S1630 H1631 A1632 N1633 R1634 M1635 E1638 A1639 Q1640 K1641 Q1642 L1646 Q1647 S1648 L1649 L1650 K1651 D1652 T1653 Q1654 I1655 Q1656 L1657 D1658 D1659 A1660 V1661 R1662 A1663 N1664 D1665 D1666 L1667 K1668 E1669 N1670 I1671 A1672 I1673 V1674 E1675 R1676 R1677 N1678 N1679 L1680 L1681





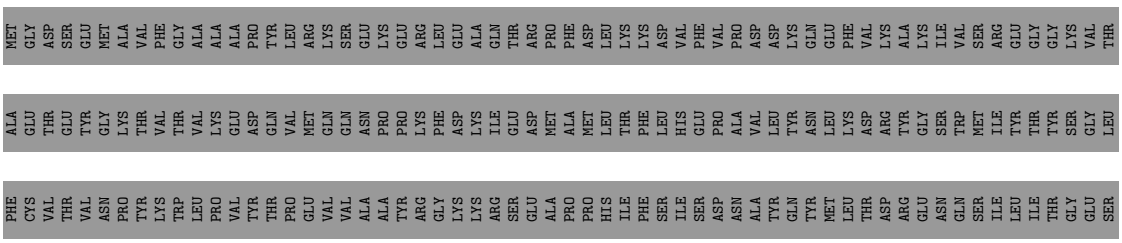
- Molecule 1: Myosin-7





• Molecule 1: Myosin-7

Chain U:



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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

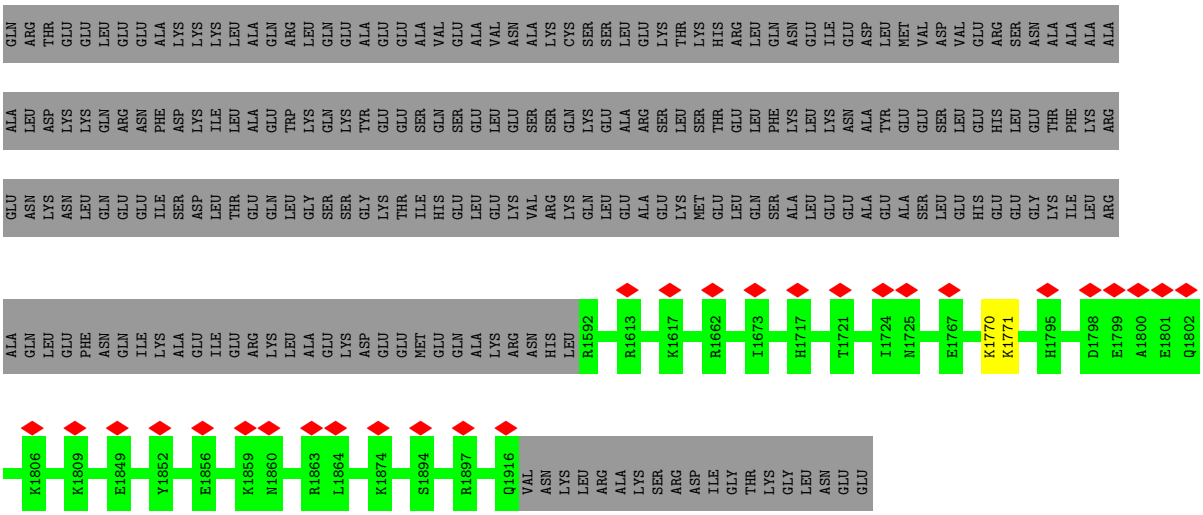
LYS LYS LYS ASP PHE GLU LEU ASN ALA LEU ASN ALA ARG ILE GLU ASP GLU GLN ALA LEU GLY SER GLN LEU GLN LYS LYS LEU LYS GLU LEU GLN ALA ARG ILE GLU GLU LEU GLU GLU GLU LEU GLU ALA GLU ARG THR ALA ARG ALA LYS VAL GLU LYS LEU ARG SER ASP LEU SER

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

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

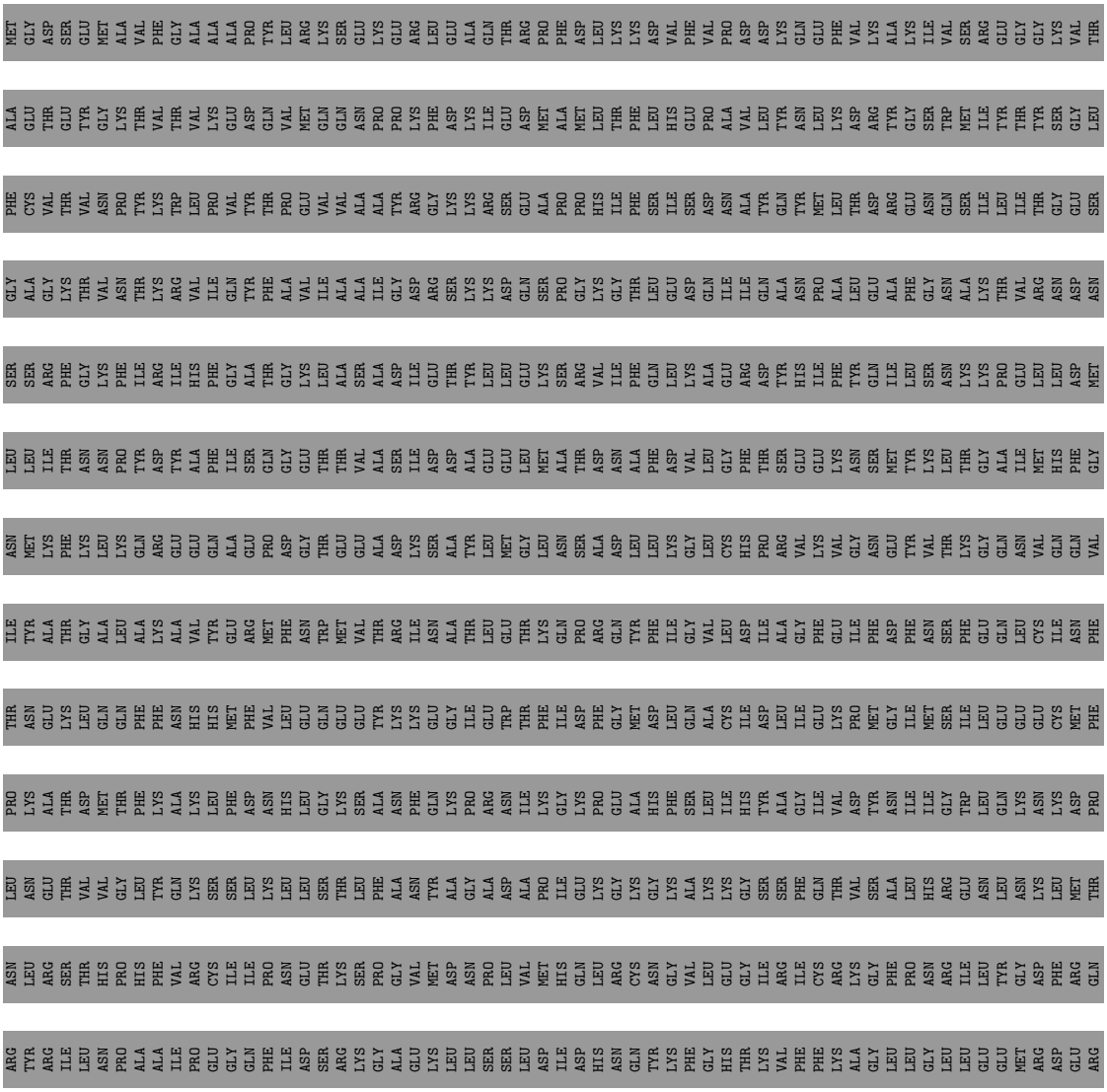
SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU

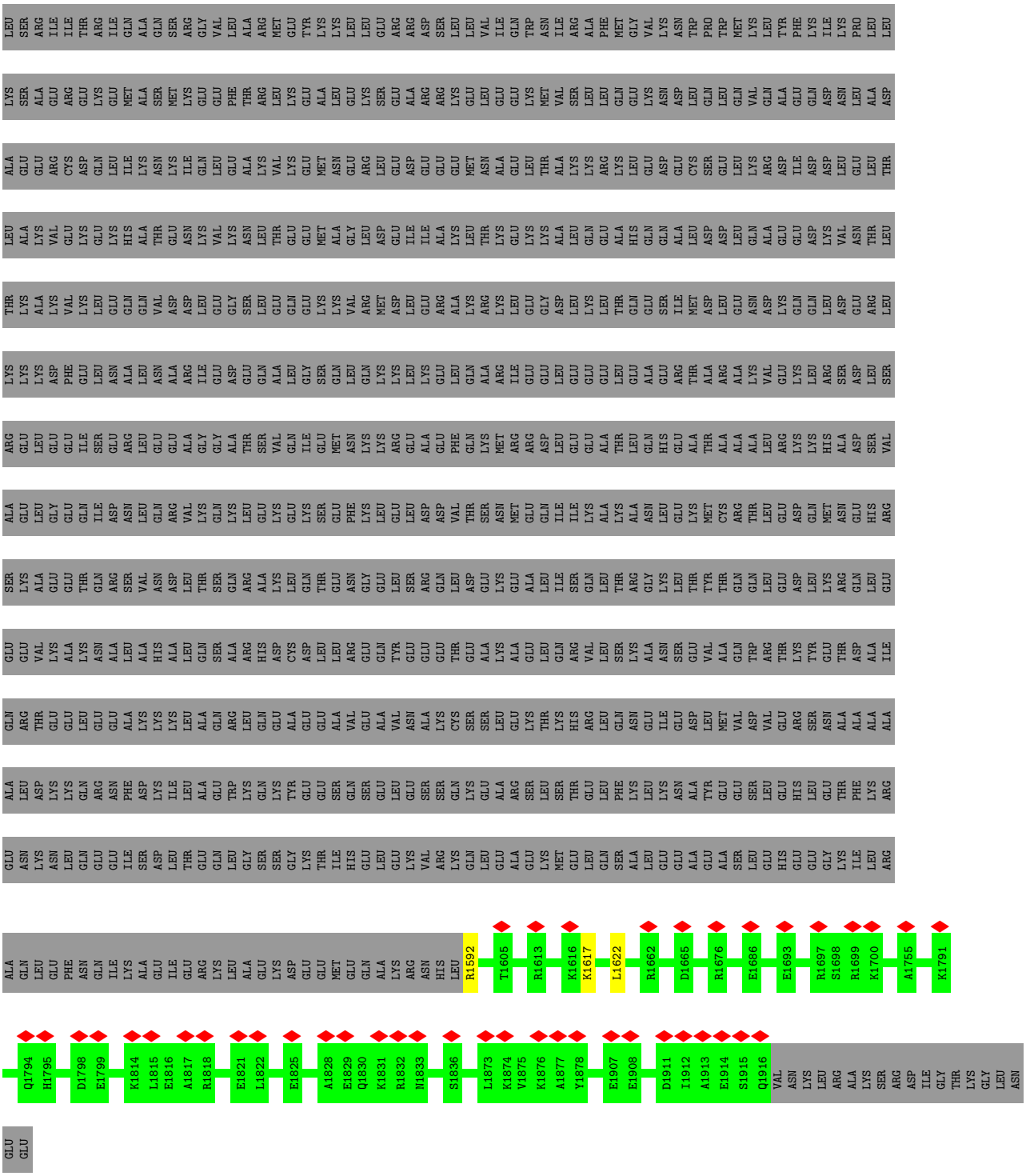
GLU GLU VAL LYS ALA LYS ASN ALA LEU ALA HIS ALA LEU GLN SER ALA ARG HIS ASP CYS ASP LEU LEU ARG GLU GLN TYR GLU GLU GLU THR GLU ALA LYS ALA GLU LEU GLN ARG VAL LEU SER LYS ALA ASN SER GLU VAL ALA GLN TRP ARG THR LYS TYR GLU THR ASP ALA ILE



• Molecule 1: Myosin-7

Chain V:





• Molecule 1: Myosin-7

Chain W:

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

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

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

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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

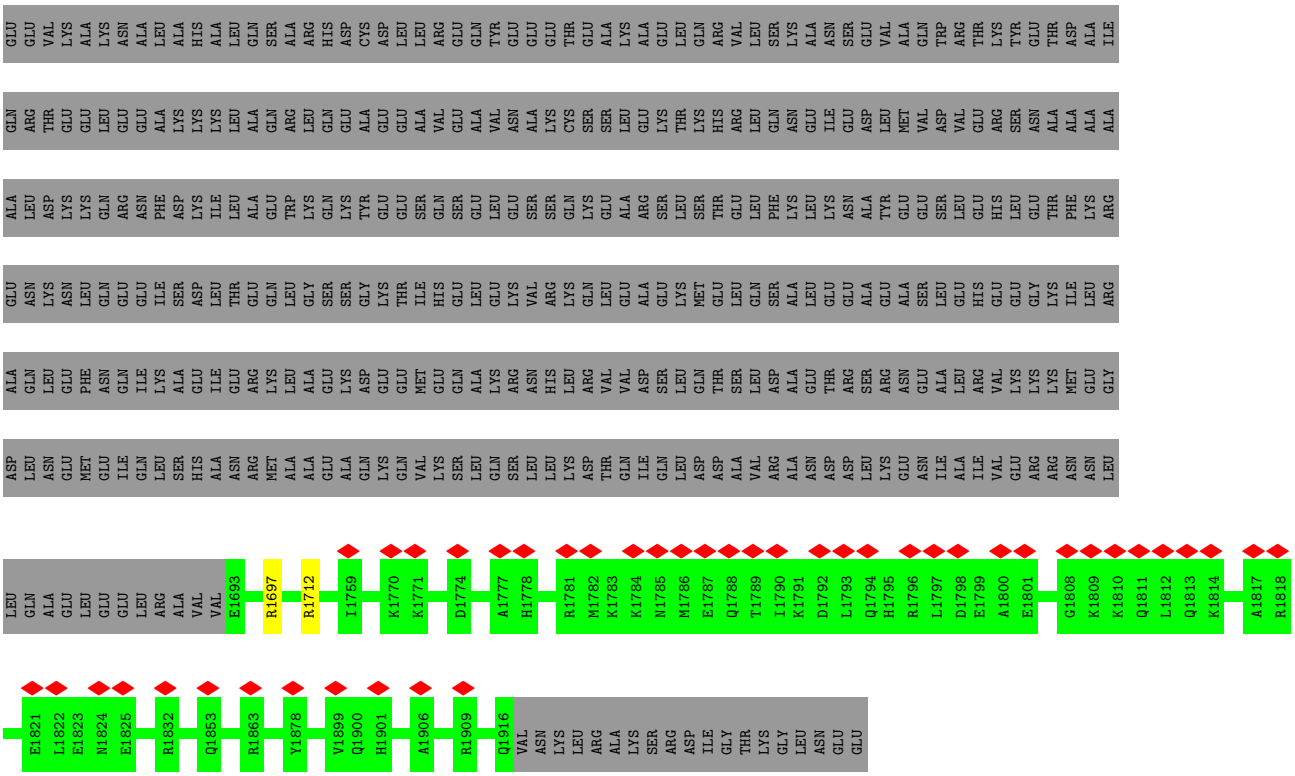
THR LYS ALA LYS VAL LYS LEU GLU GLN GLN VAL ASP ASP LEU GLU GLY SER LEU GLU GLN GLU LYS LYS VAL ARG MET ASP LEU GLU ARG ALA LYS ARG LYS LEU GLU GLY ASP LEU LYS LEU THR GLN GLU SER ILE MET ASP LEU GLU ASN ASP LYS GLN GLN LEU ASP GLU ARG LEU

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

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

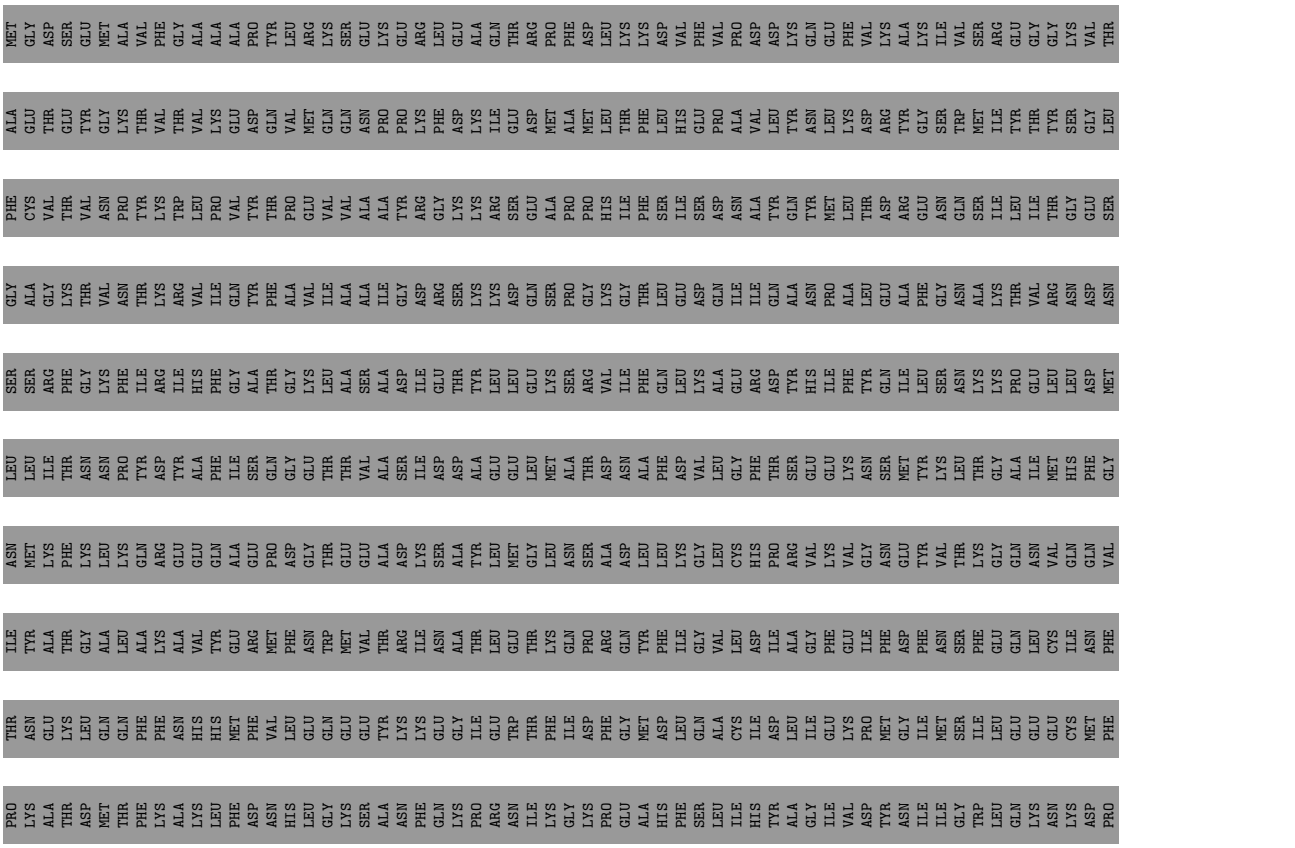
ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU GLU LEU ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG

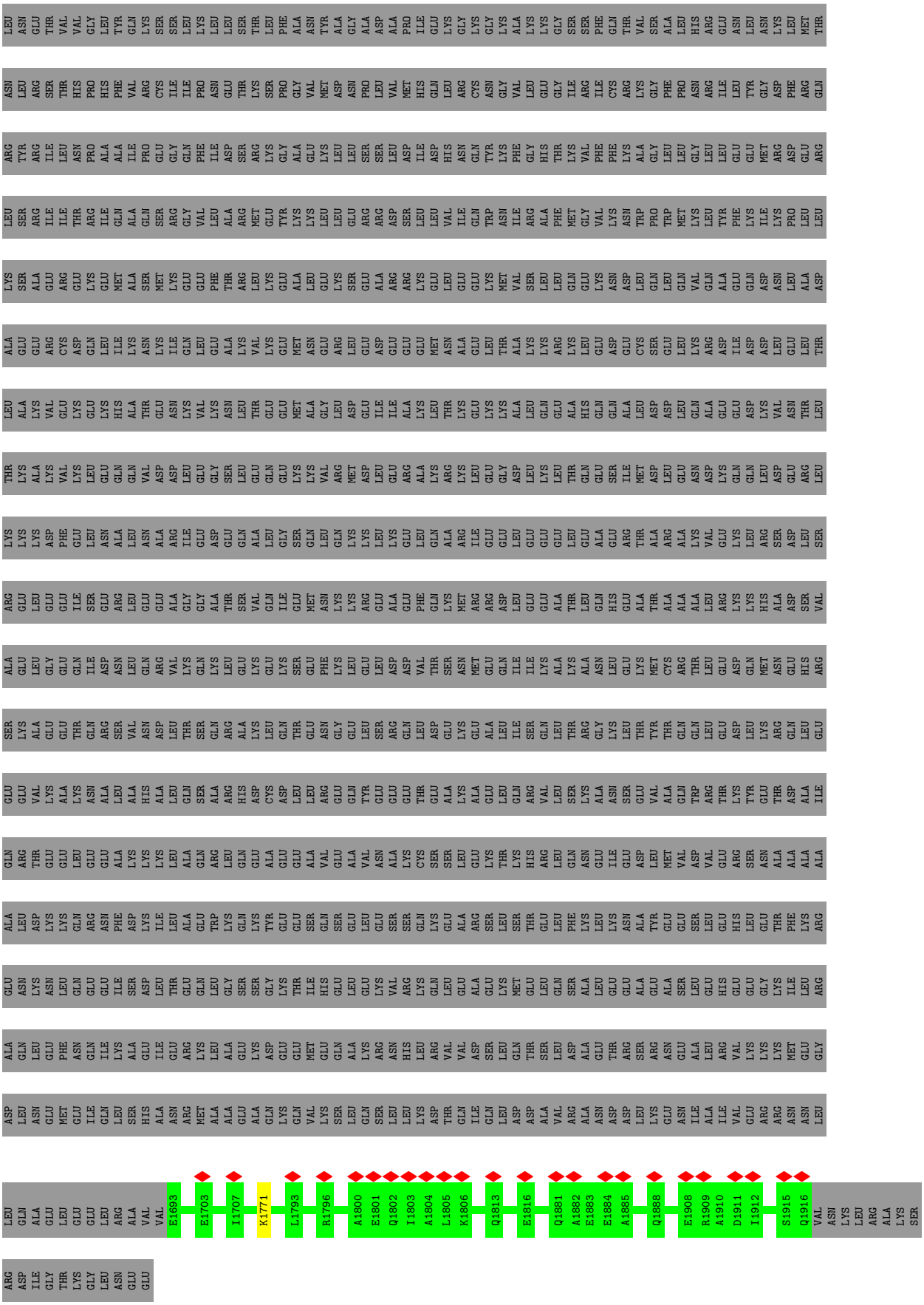
SER LYS ALA GLU GLU THR GLN ARG SER VAL ASN ASP LEU THR SER GLN ARG ALA LYS LEU GLN THR GLU ASN GLY GLU LEU SER ARG GLN LEU ASP GLU LYS GLU ALA LEU ILE SER GLN LEU THR ARG GLY LYS LEU THR TYR THR GLN GLN LEU GLU ASP LEU LYS ARG GLN LEU GLU



• Molecule 1: Myosin-7

Chain X:

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E1703
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K1771
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A1800
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Q1813
E1816
Q1881
A1882
E1883
E1884
A1885
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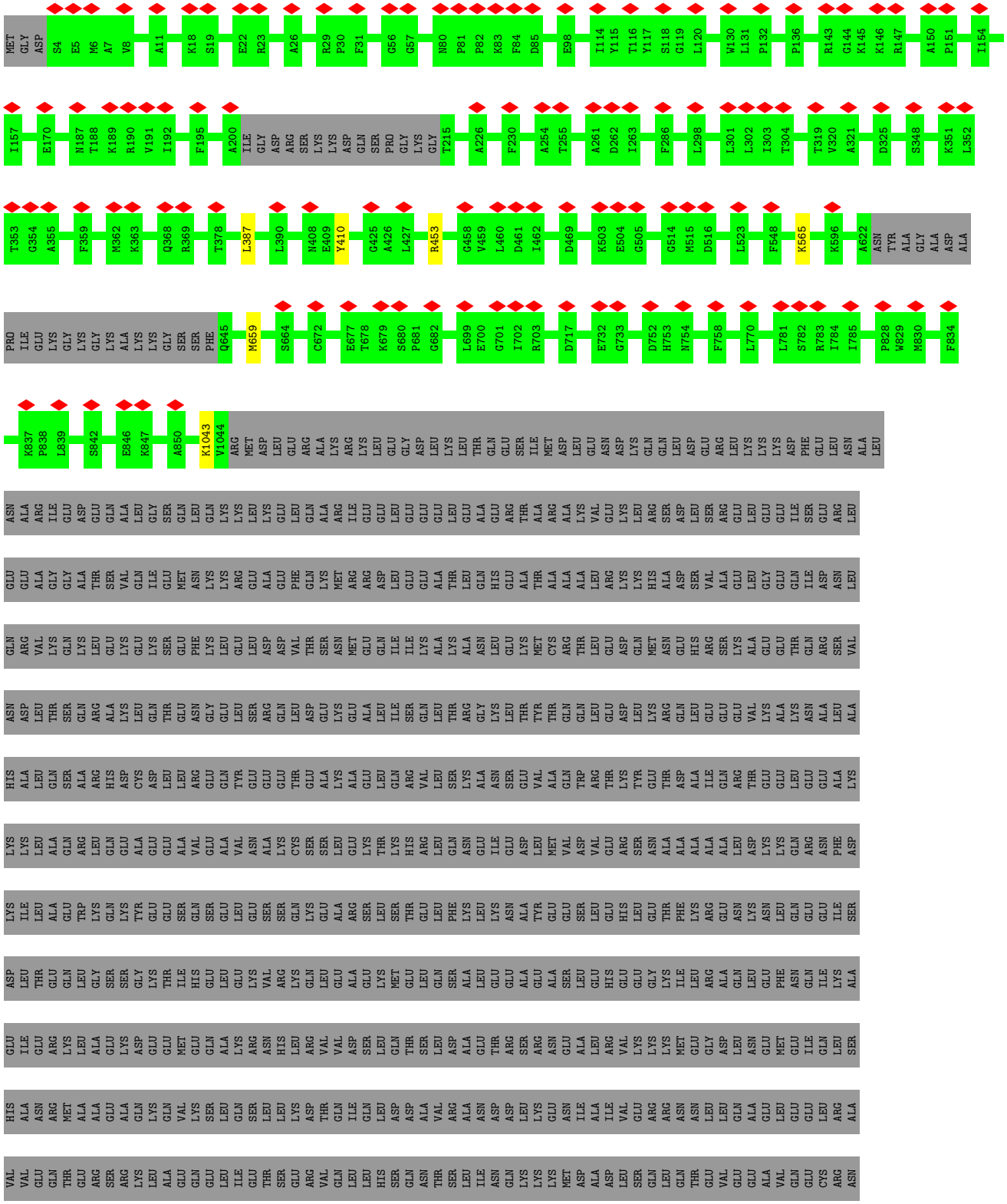
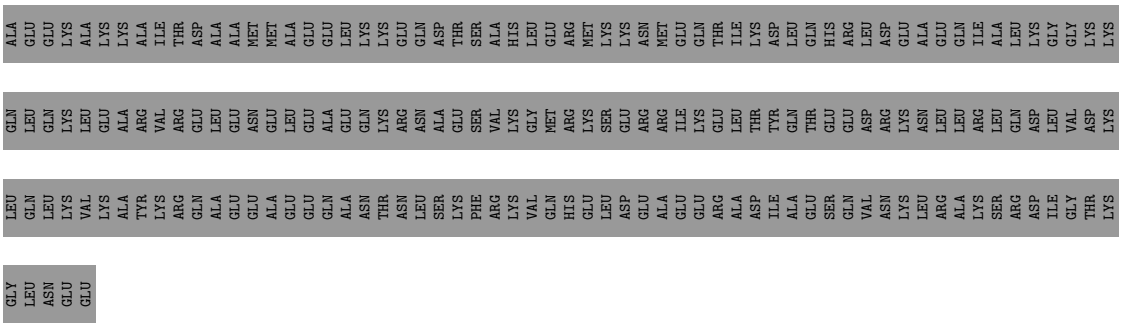
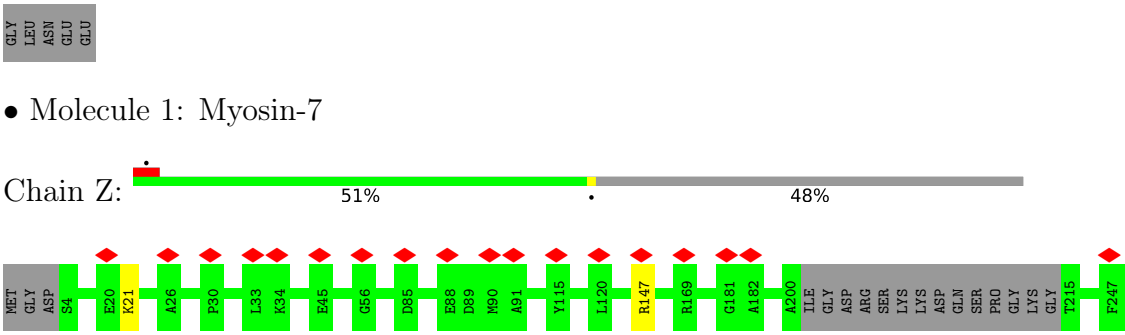
A1910
D1911
I1912
S1915
Q1916

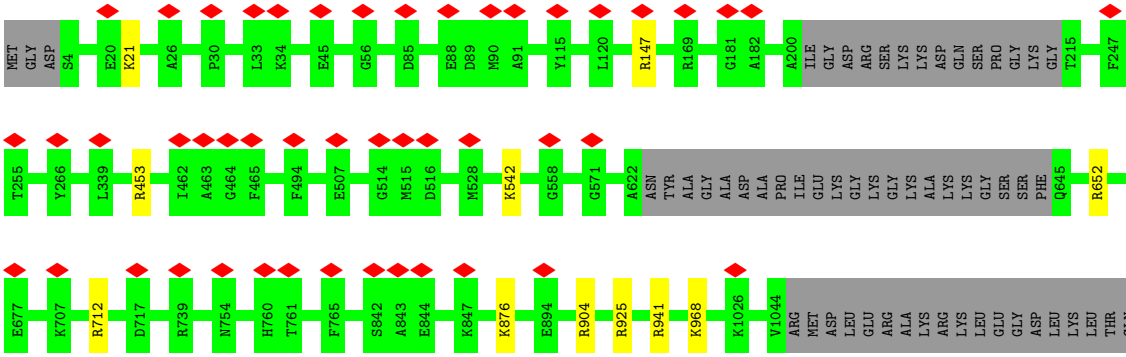
• Molecule 1: Myosin-7

Chain Y:



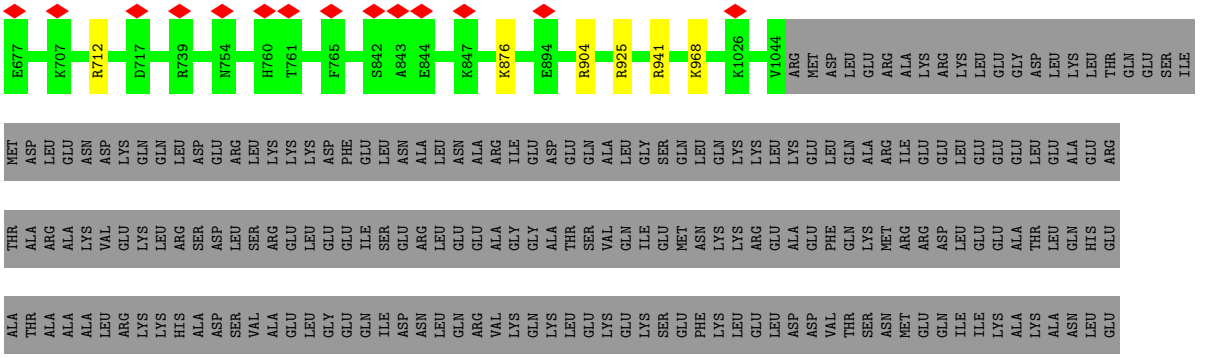


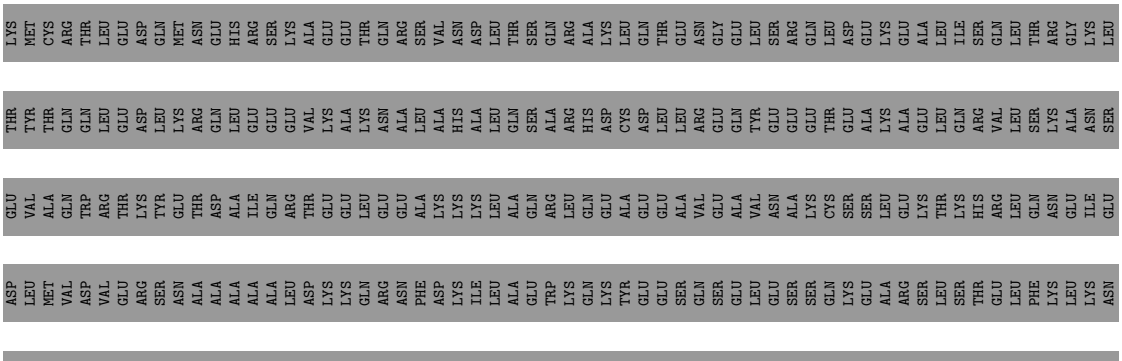


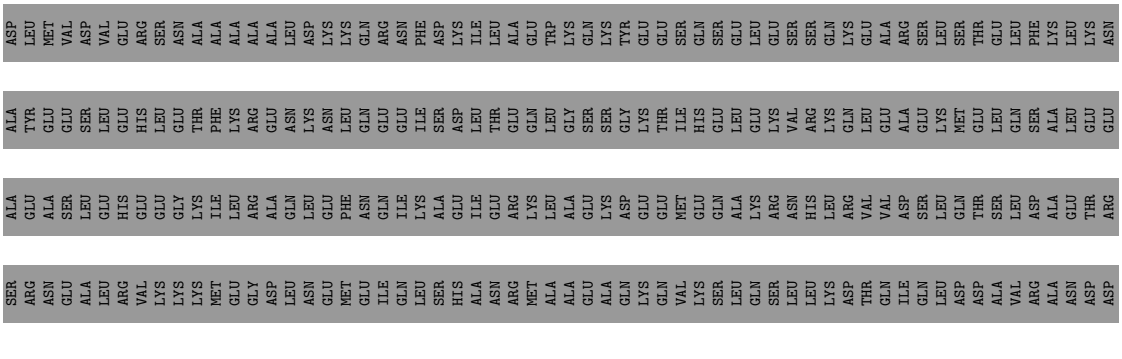


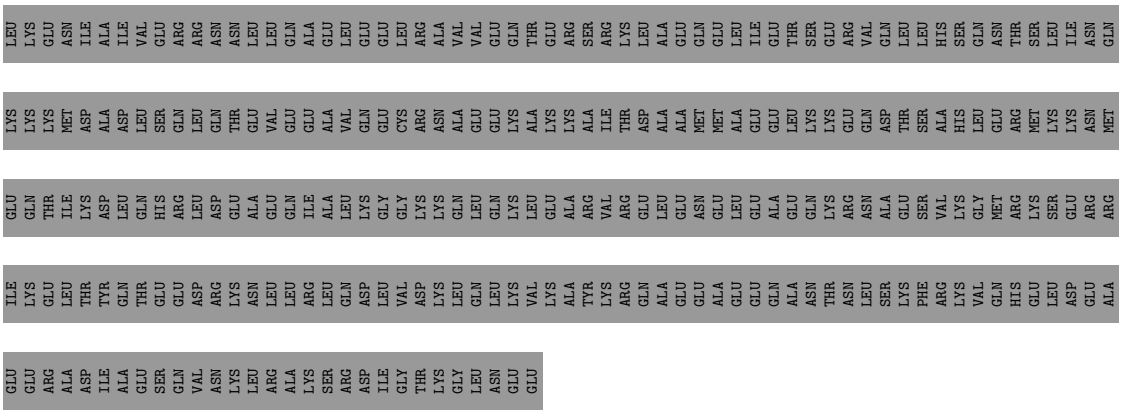
• Molecule 1: Myosin-7

Chain Z:



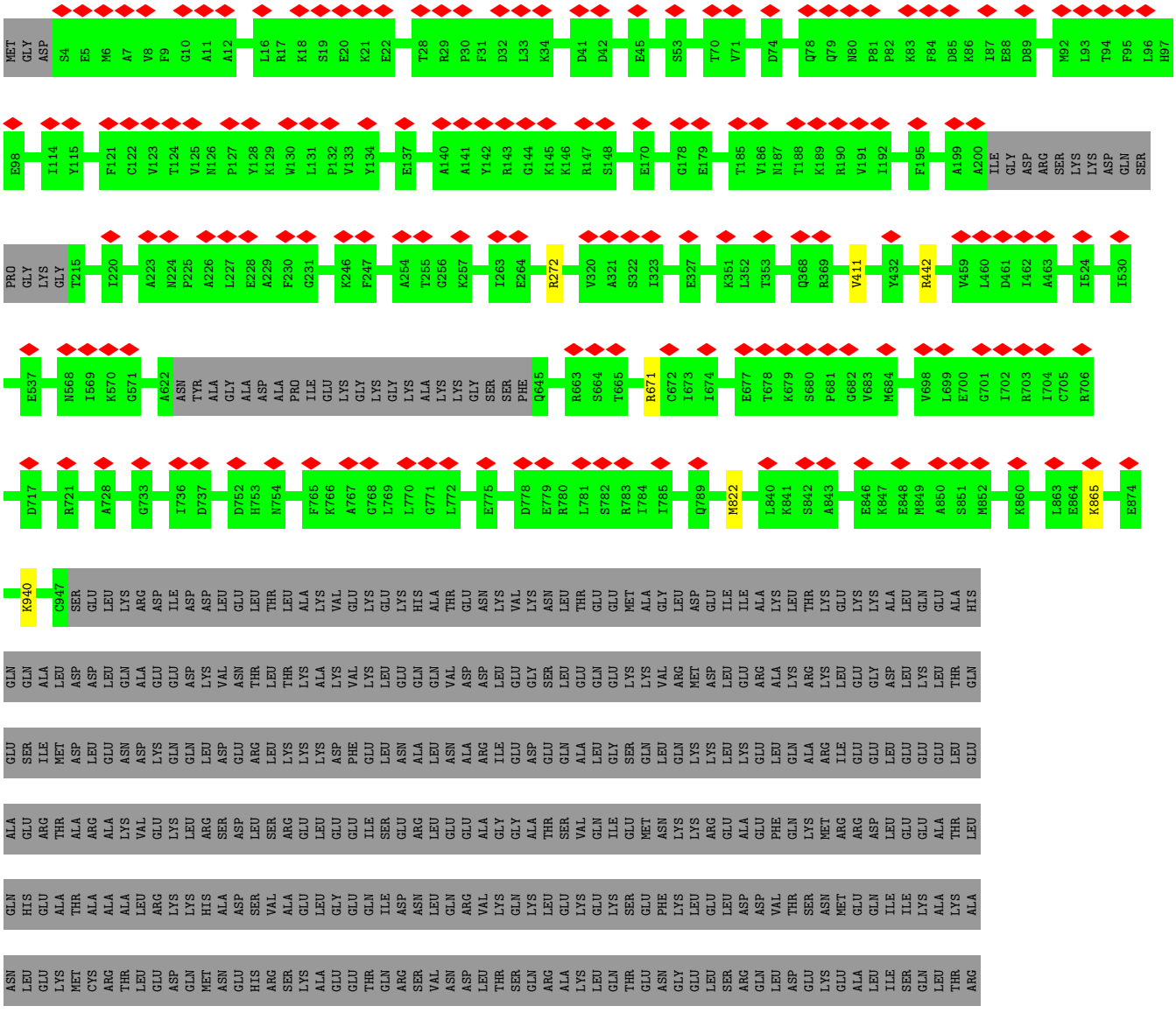


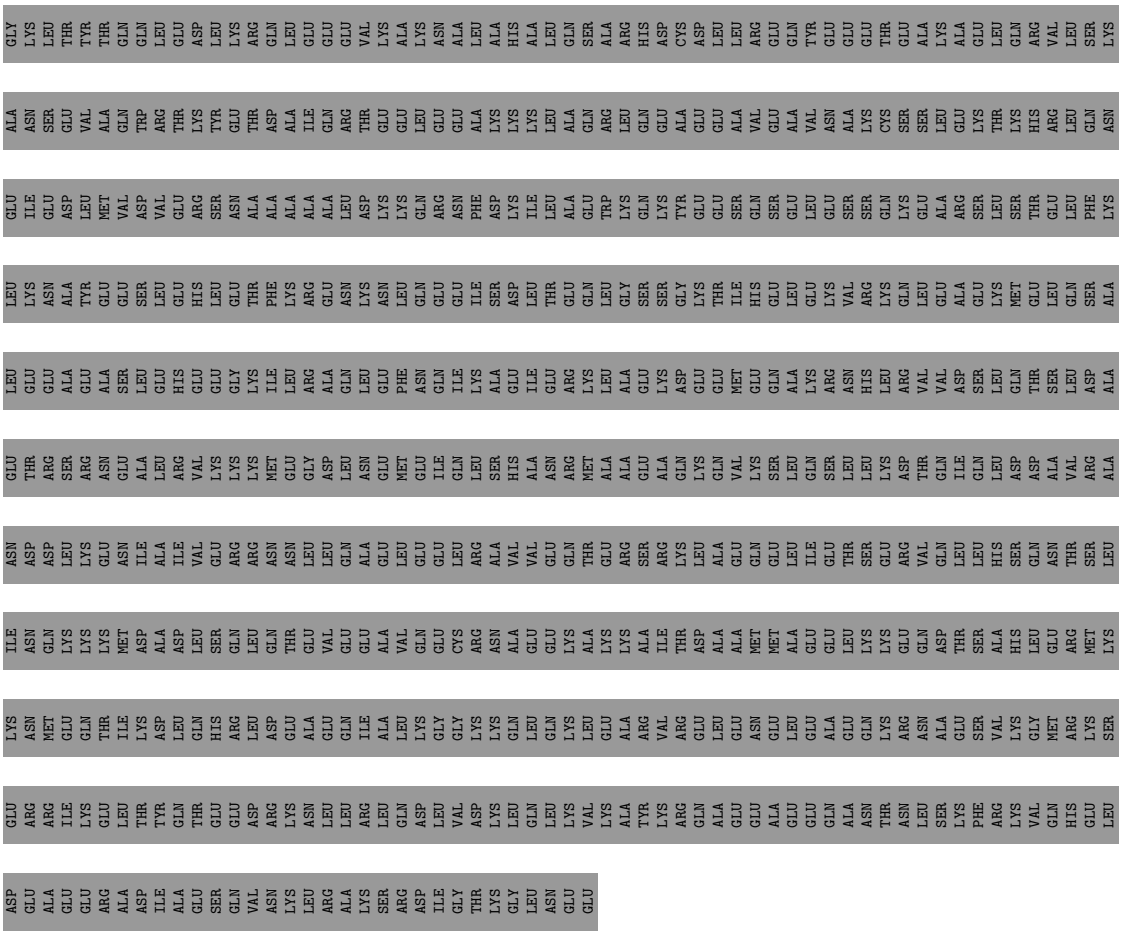




• Molecule 1: Myosin-7

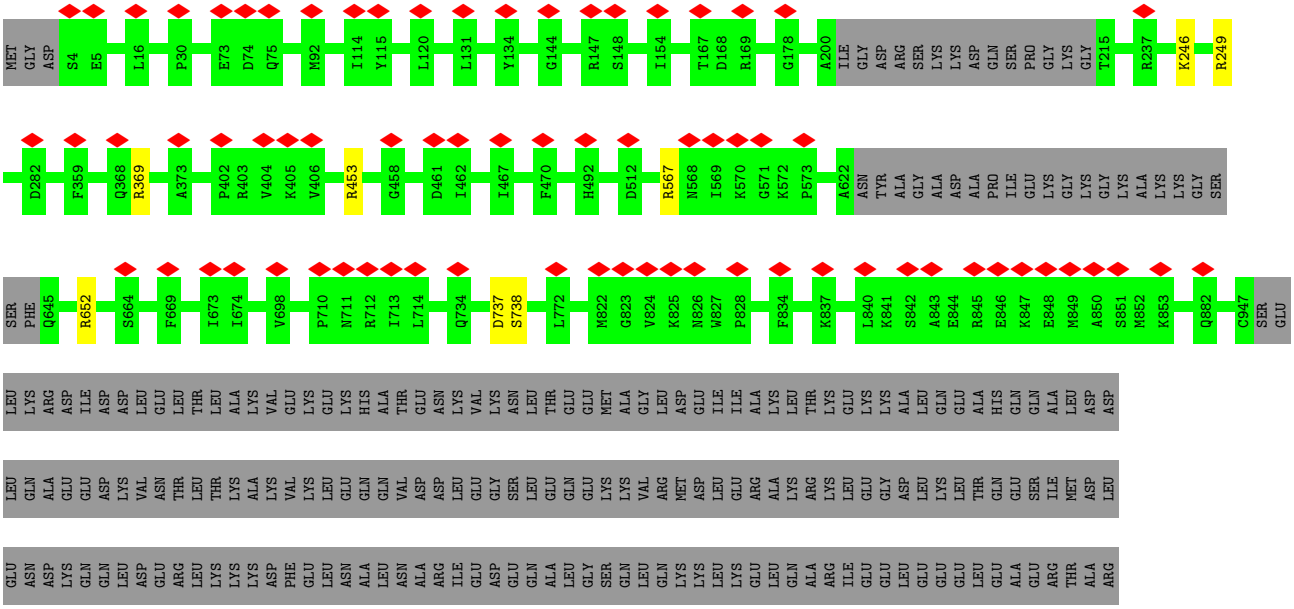
Chain e:

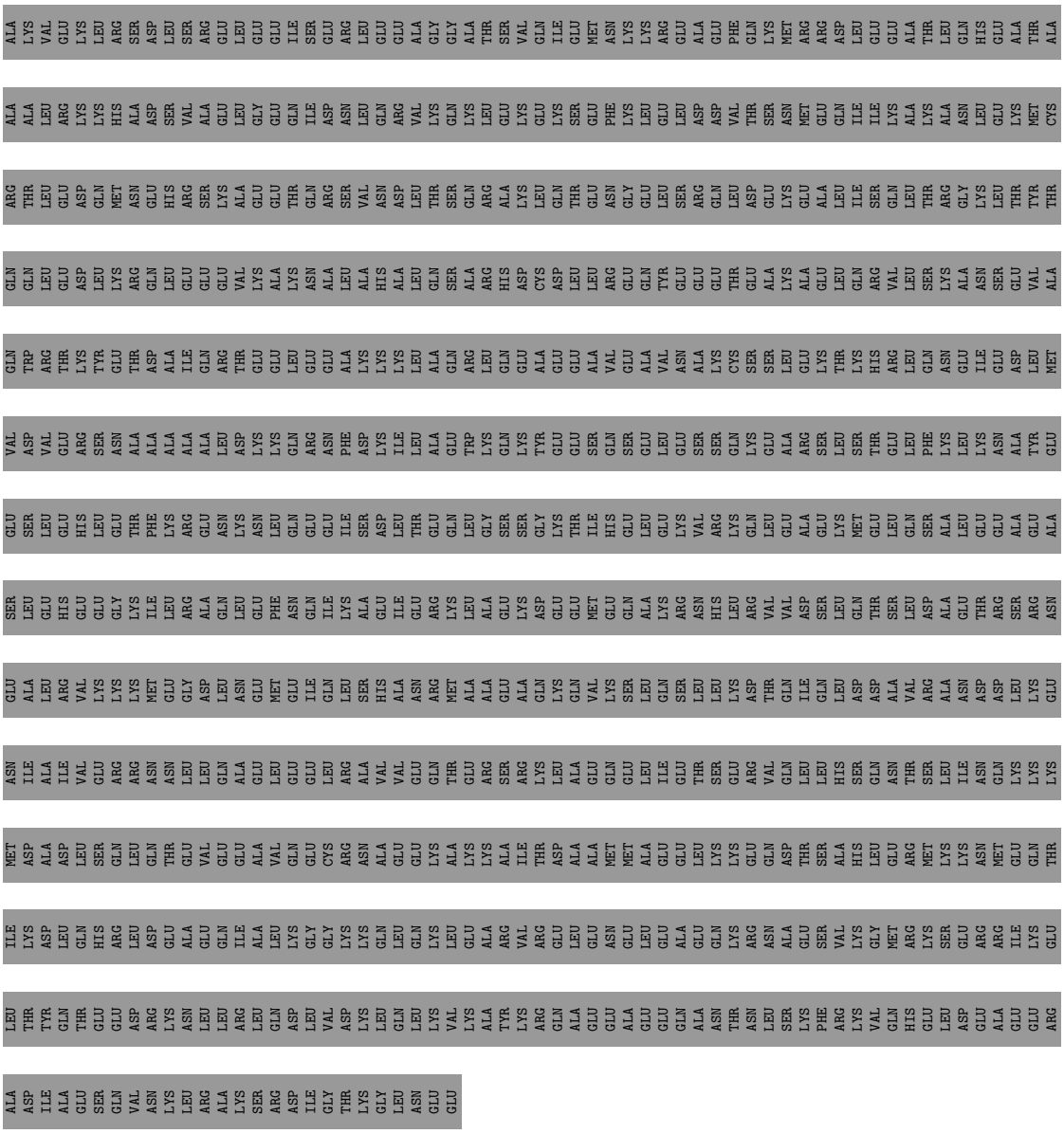




• Molecule 1: Myosin-7

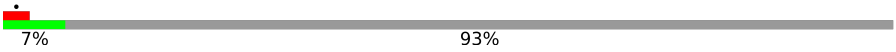
Chain f:

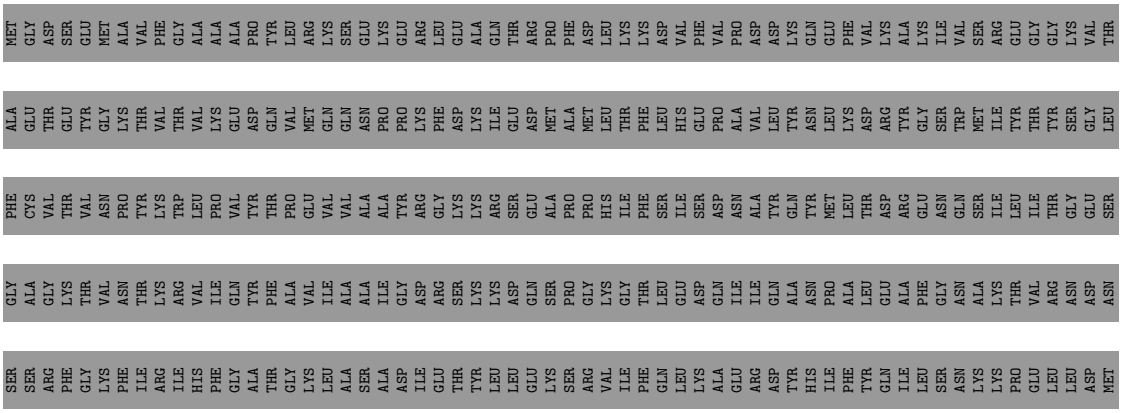




• Molecule 1: Myosin-7

Chain k:





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

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

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

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

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

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

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

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

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

LYS SER ALA GLU ARG GLU LYS GLU MET ALA SER MET LYS GLU GLU PHE THR ARG LEU LYS GLU ALA LEU GLU LYS SER GLU ALA ARG ARG LYS GLU LEU GLU GLU LYS MET VAL SER LEU LEU GLN GLU LYS ASN ASP LEU GLN LEU GLN VAL GLN ALA GLU GLN ASP ASN LEU ALA ASP

ALA GLU GLU ARG CYS ASP GLN LEU ILE LYS ASN LYS ILE GLN LEU GLU ALA LYS VAL LYS GLU MET ASN GLU ARG LEU GLU ASP GLU GLU GLU MET ASN ALA GLU LEU THR ALA LYS LYS ARG LYS LEU GLU ASP GLU CYS SER GLU LEU LYS ARG ASP ILE ASP ASP LEU GLU LEU THR

LEU ALA LYS VAL GLU LYS GLU LYS HIS ALA THR GLU ASN LYS VAL LYS ASN LEU THR GLU GLU MET ALA GLY LEU ASP GLU ILE ILE ALA LYS LEU THR LYS GLU LYS LYS ALA LEU GLN GLU ALA HIS GLN GLN ALA LEU ASP ASP LEU GLN ALA GLU GLU ASP LYS VAL ASN THR LEU

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

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

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

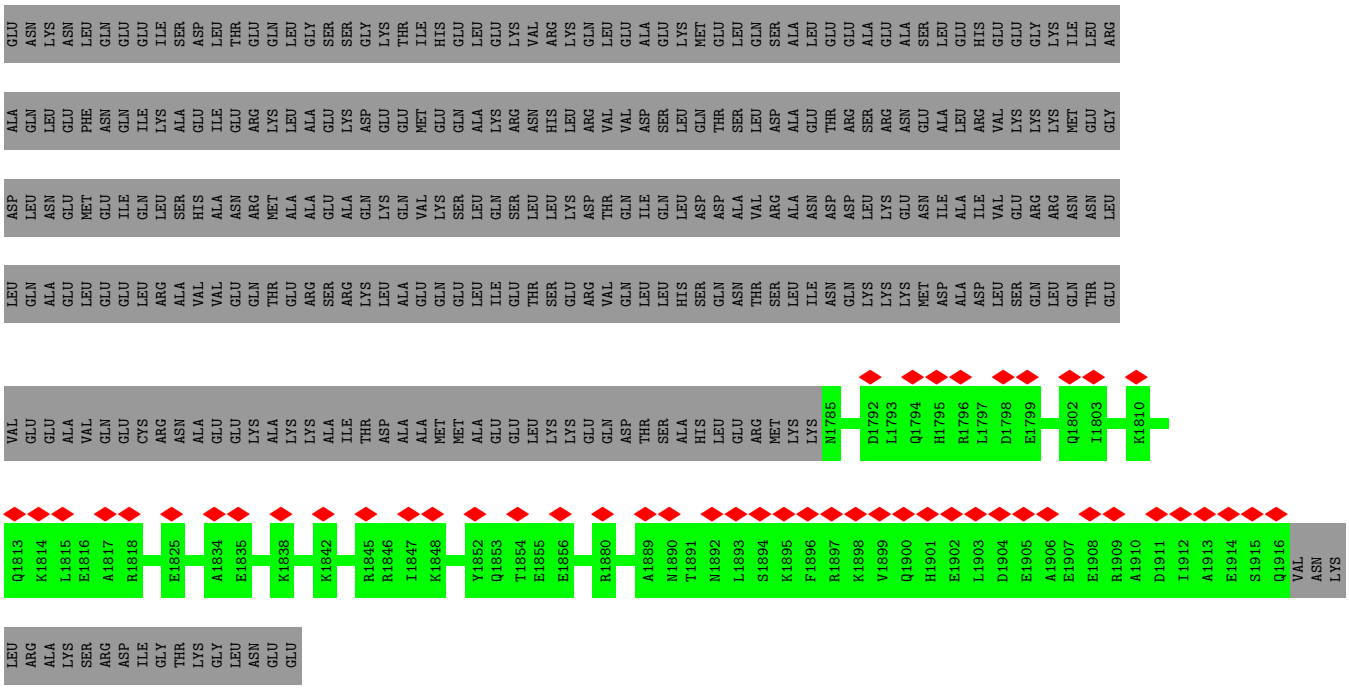
ALA GLU LEU GLY GLU GLN ILE ASP ASN LEU GLN ARG VAL LYS GLN LYS LEU GLU LYS GLU LYS SER GLU PHE LYS LEU GLU LEU ASP ASP VAL THR SER ASN MET GLU GLN ILE ILE LYS ALA LYS ALA ASN LEU GLU LYS MET CYS ARG THR LEU GLU ASP GLN MET ASN GLU HIS ARG

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

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

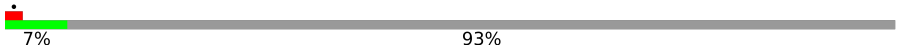
GLN ARG THR GLU GLU LEU GLU GLU ALA LYS LYS LEU ALA GLN ARG LEU GLN GLU ALA GLU GLU ALA VAL GLU ALA VAL ASN ALA LYS CYS SER SER LEU GLU LYS THR LYS HIS ARG LEU GLN ASN GLU ILE GLU ASP LEU MET VAL ASP VAL GLU ARG SER ASN ALA ALA ALA ALA

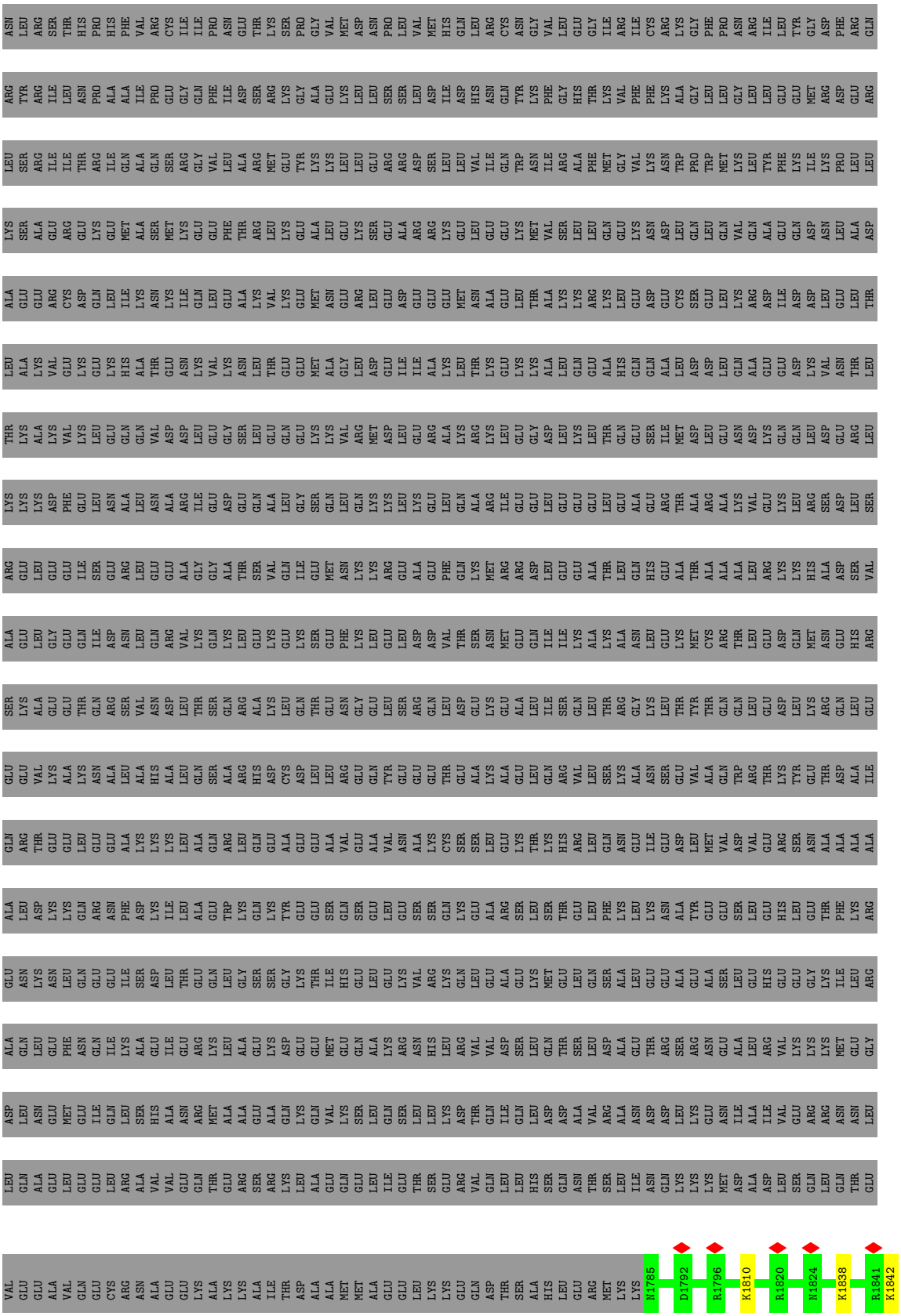
ALA LEU ASP LYS LYS GLN ARG ASN PHE ASP LYS ILE LEU ALA GLU TRP LYS GLN LYS TYR GLU GLU SER GLN SER GLU LEU GLU SER SER GLN LYS GLU ALA ARG SER LEU SER THR GLU LEU PHE LYS LEU LYS ASN ALA TYR GLU GLU SER LEU GLU HIS LEU GLU THR PHE LYS ARG



- Molecule 1: Myosin-7

Chain l:

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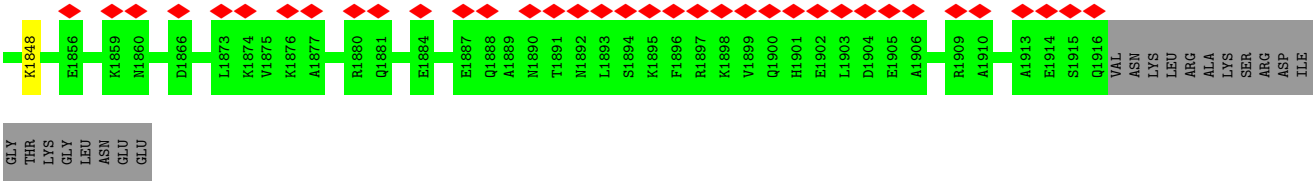
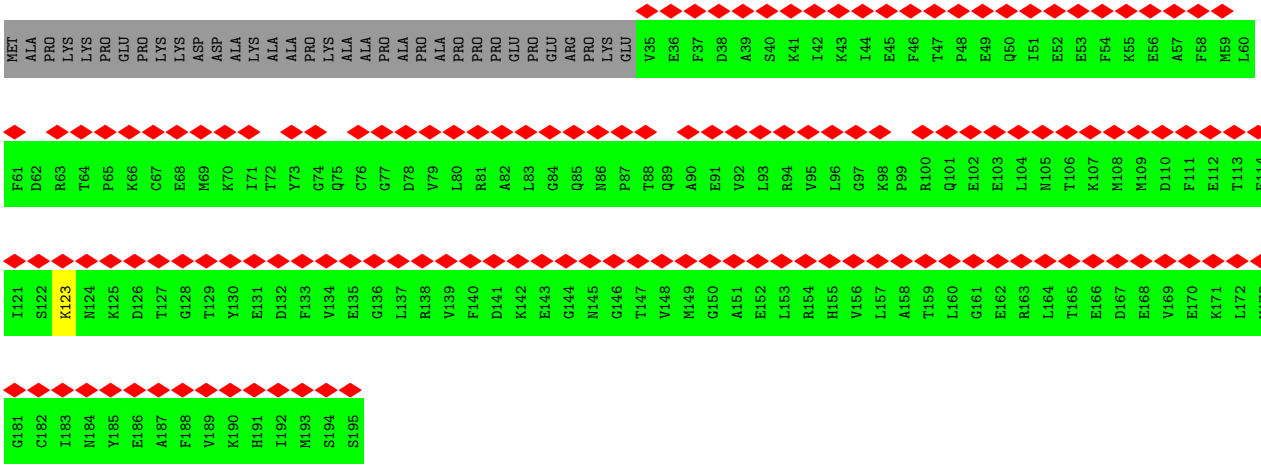
K1810
R1820
N1824
K1838
R1841
K1842



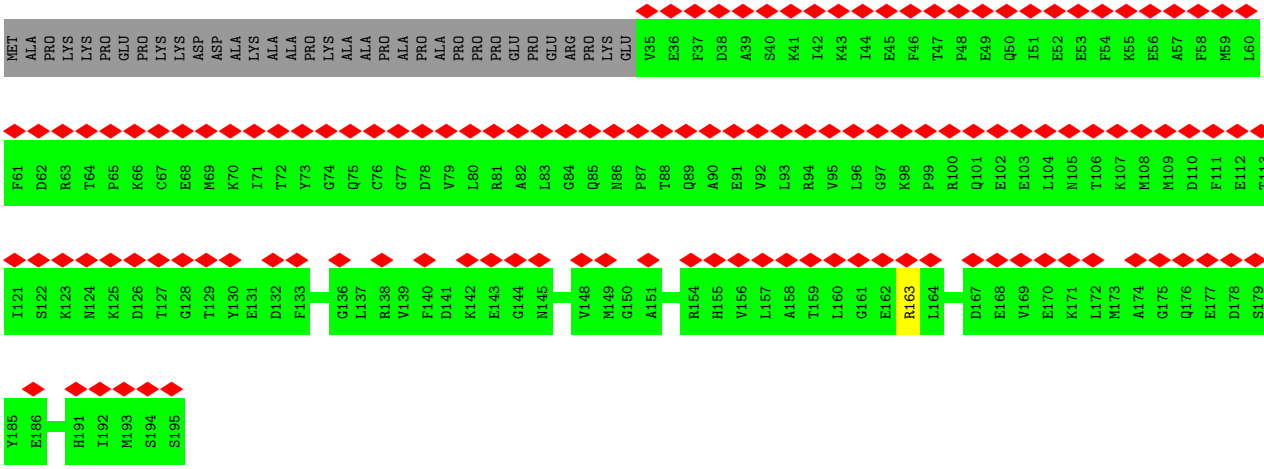
• Molecule 2: Myosin light chain 3

Chain BE:



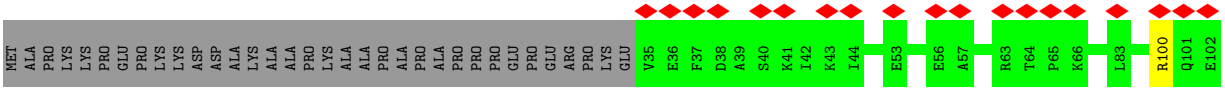
• Molecule 2: Myosin light chain 3

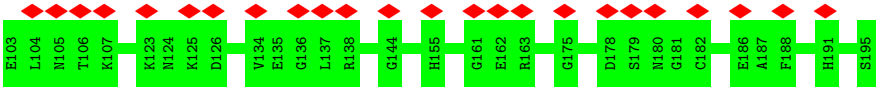
Chain BF:



• Molecule 2: Myosin light chain 3

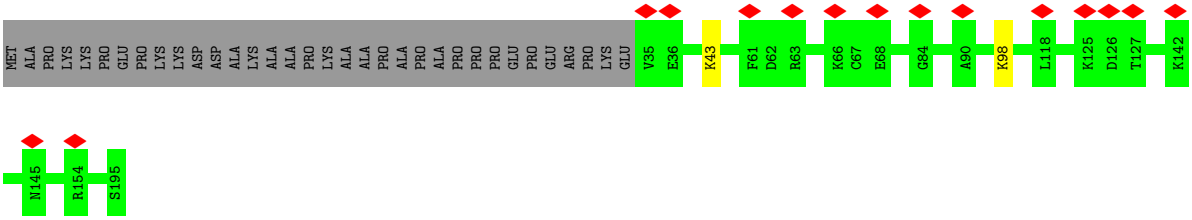
Chain ba:





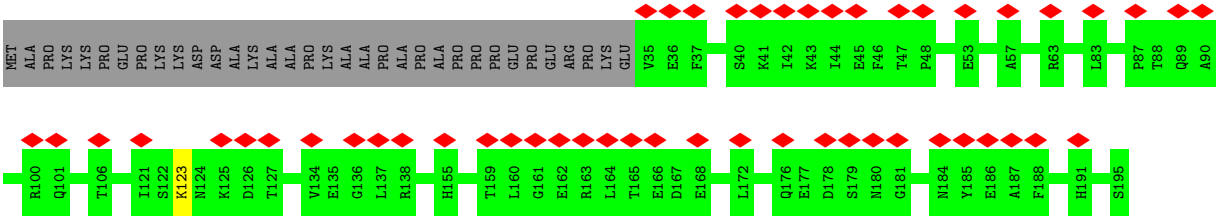
• Molecule 2: Myosin light chain 3

Chain bb:



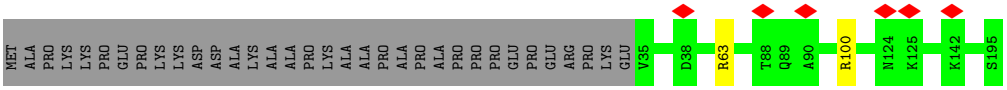
• Molecule 2: Myosin light chain 3

Chain bg:



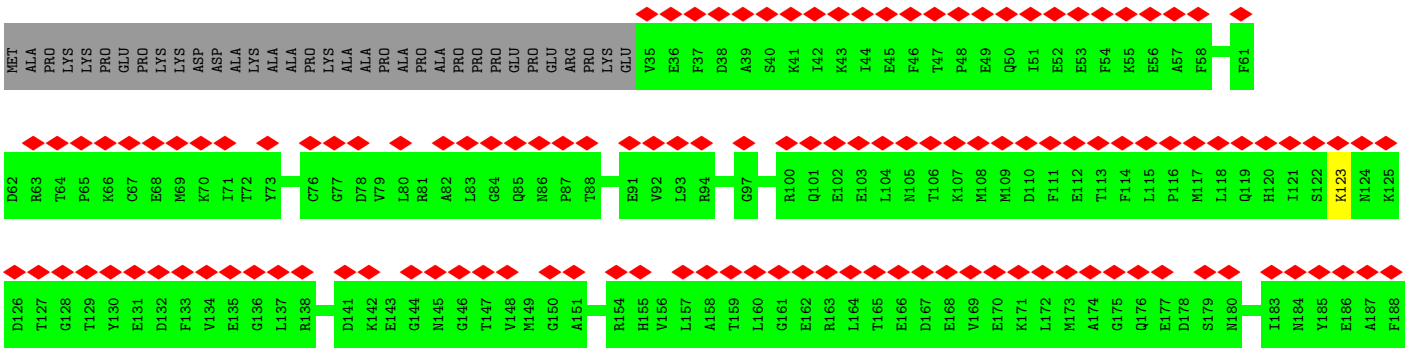
• Molecule 2: Myosin light chain 3

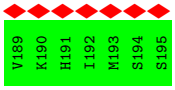
Chain bh:



• Molecule 2: Myosin light chain 3

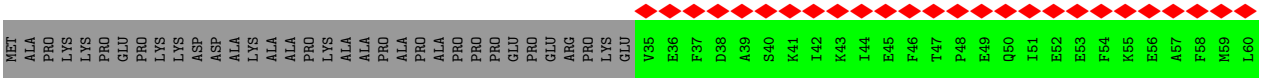
Chain AE:

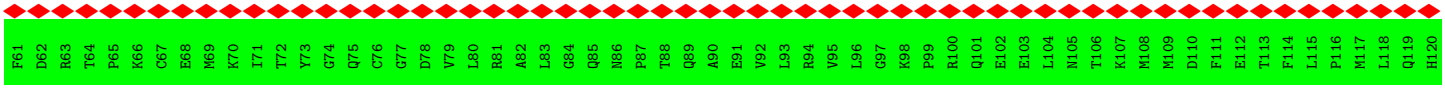


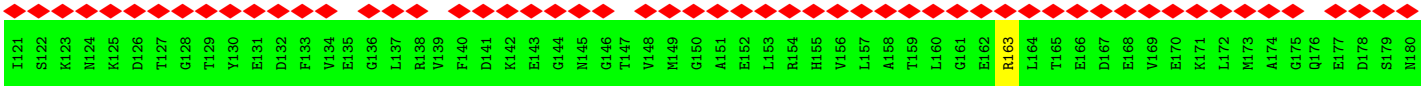


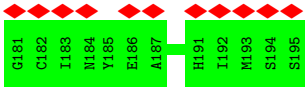
• Molecule 2: Myosin light chain 3

Chain AF:



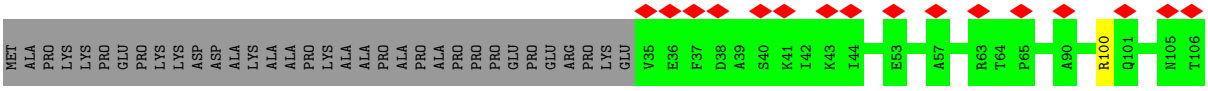


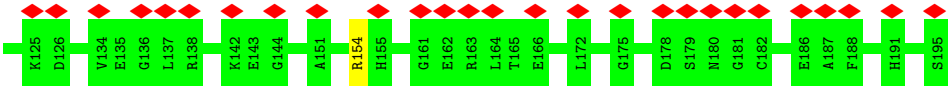




• Molecule 2: Myosin light chain 3

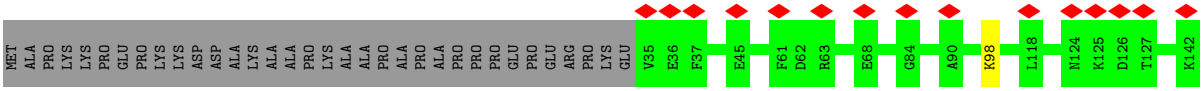
Chain aa:

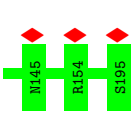




• Molecule 2: Myosin light chain 3

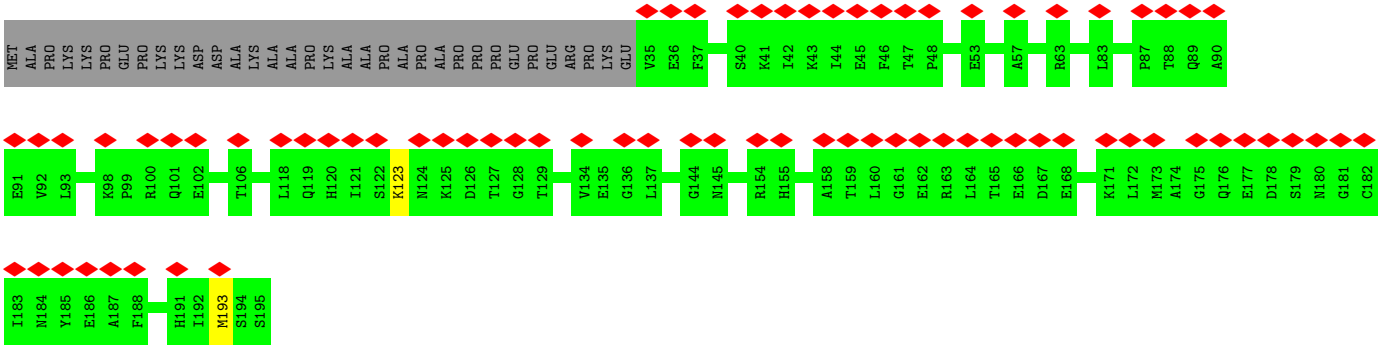
Chain ab:



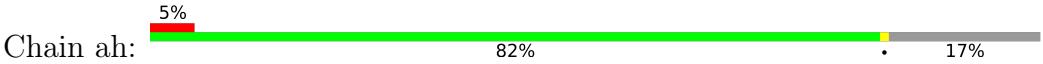


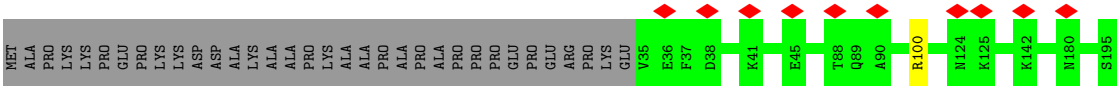
• Molecule 2: Myosin light chain 3

Chain ag:

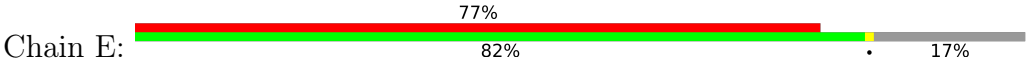


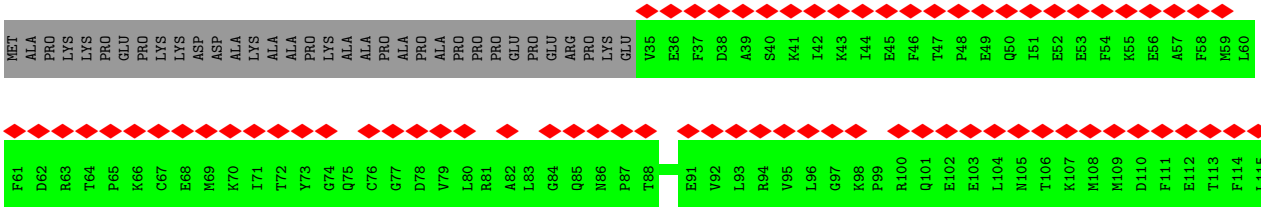
• Molecule 2: Myosin light chain 3



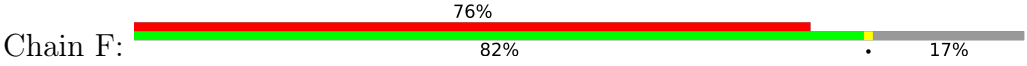


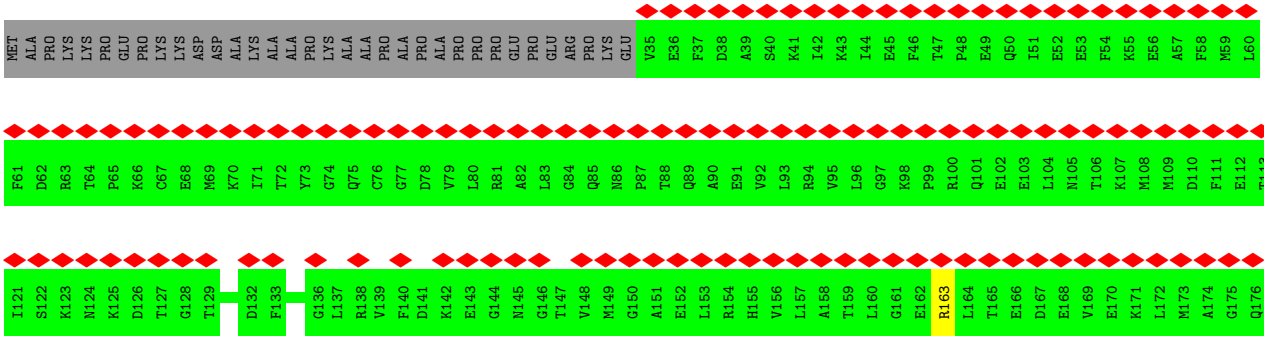
• Molecule 2: Myosin light chain 3

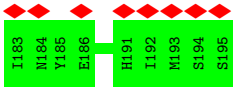




• Molecule 2: Myosin light chain 3

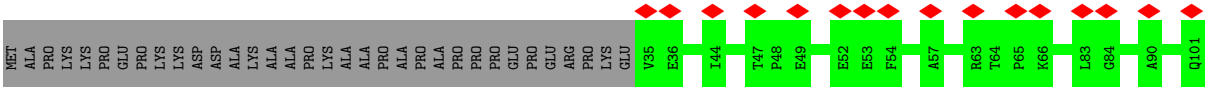


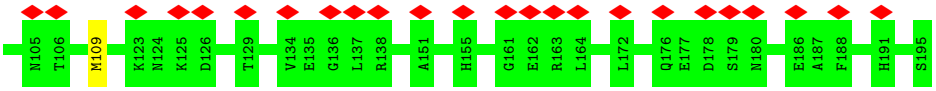




• Molecule 2: Myosin light chain 3

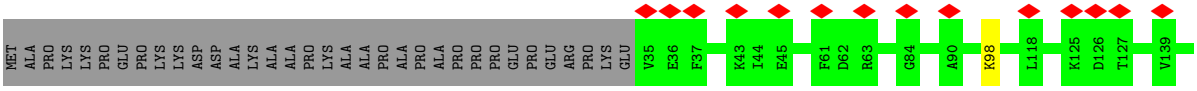
Chain a:

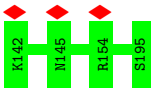




• Molecule 2: Myosin light chain 3

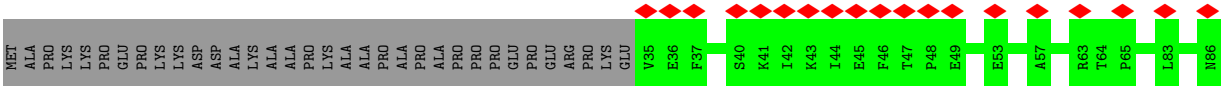
Chain b:

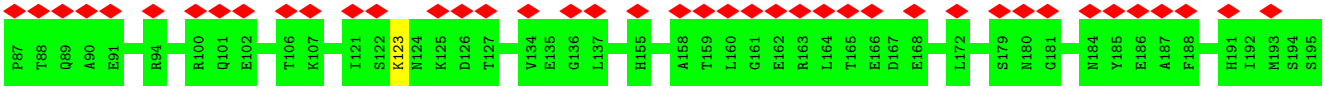




• Molecule 2: Myosin light chain 3

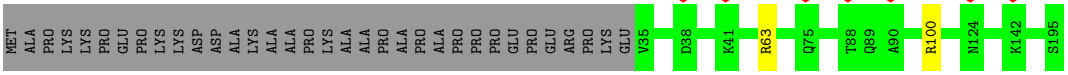
Chain g:





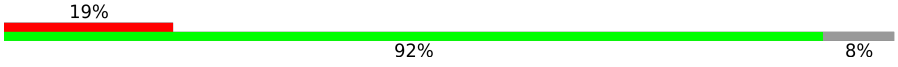
• Molecule 2: Myosin light chain 3

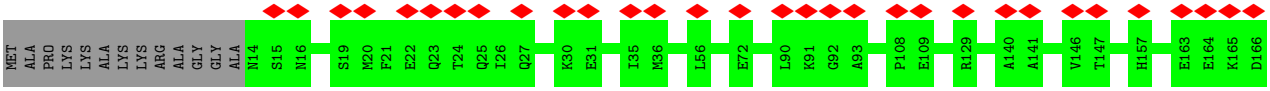
Chain h:



• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

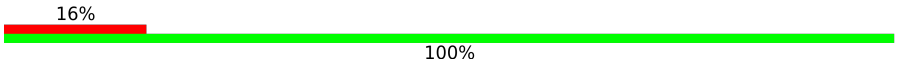
Chain bc:

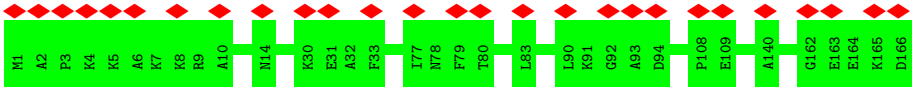




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

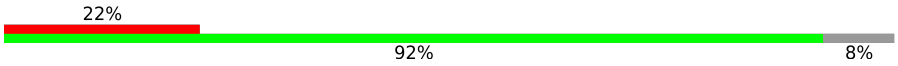
Chain bd:

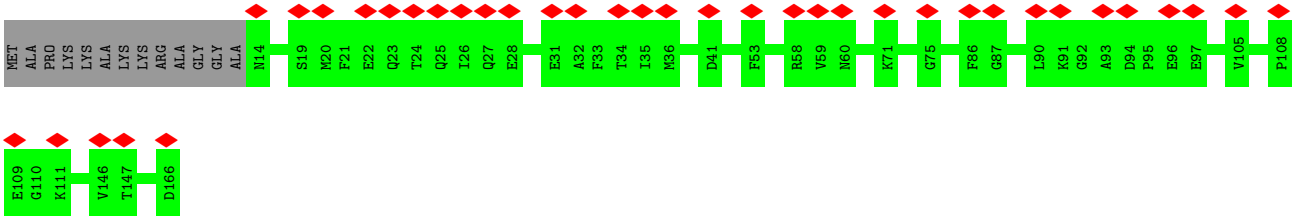




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

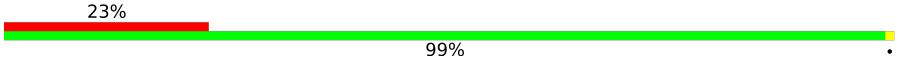
Chain bi:

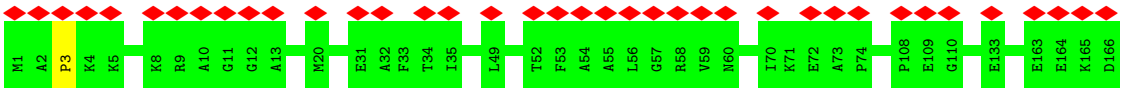




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

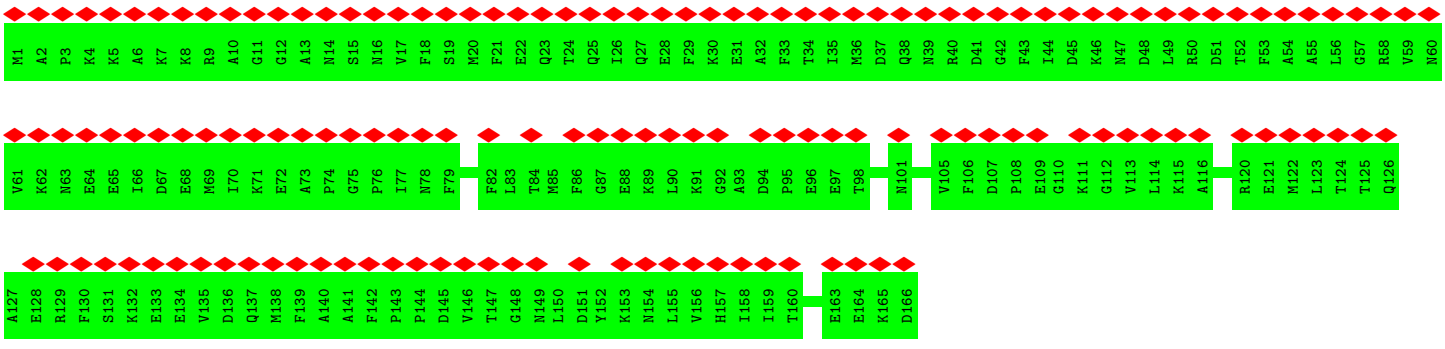
Chain bj:





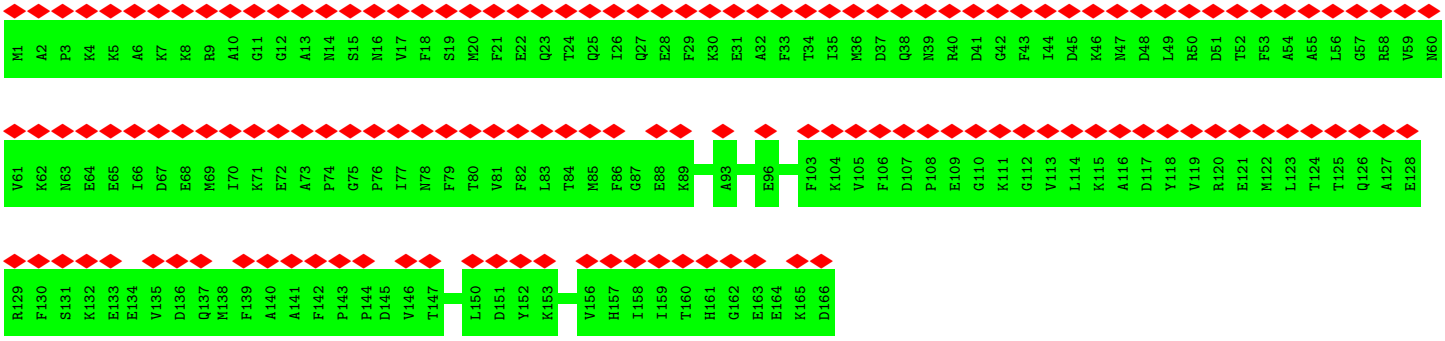
• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

Chain bq:

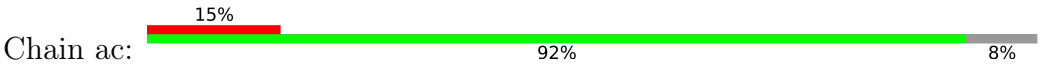


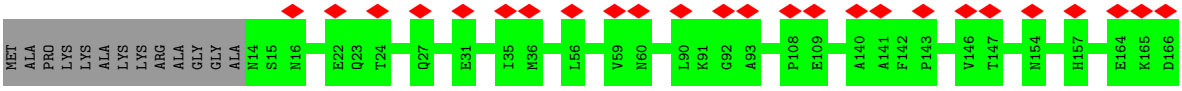
• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

Chain br:

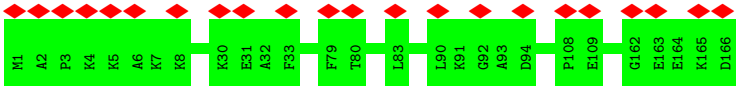


• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

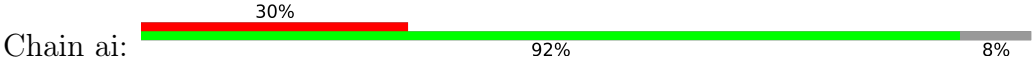


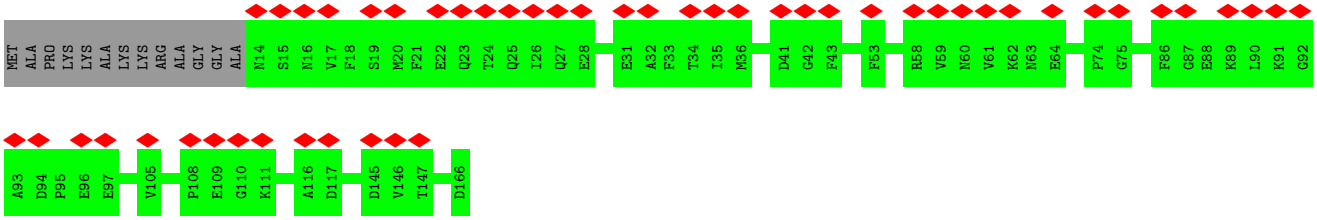


• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

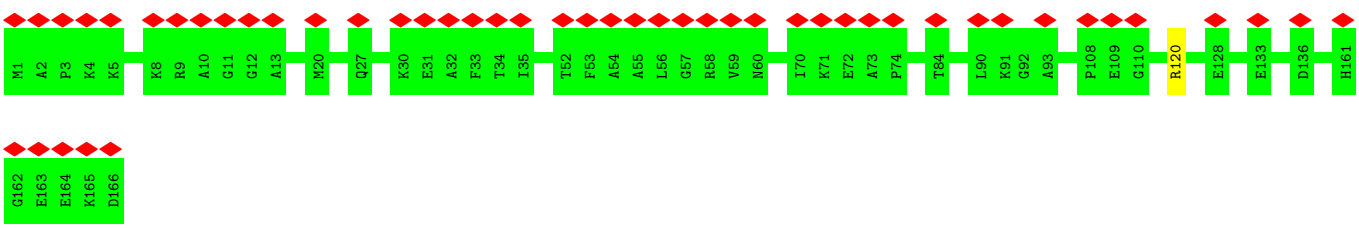


• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



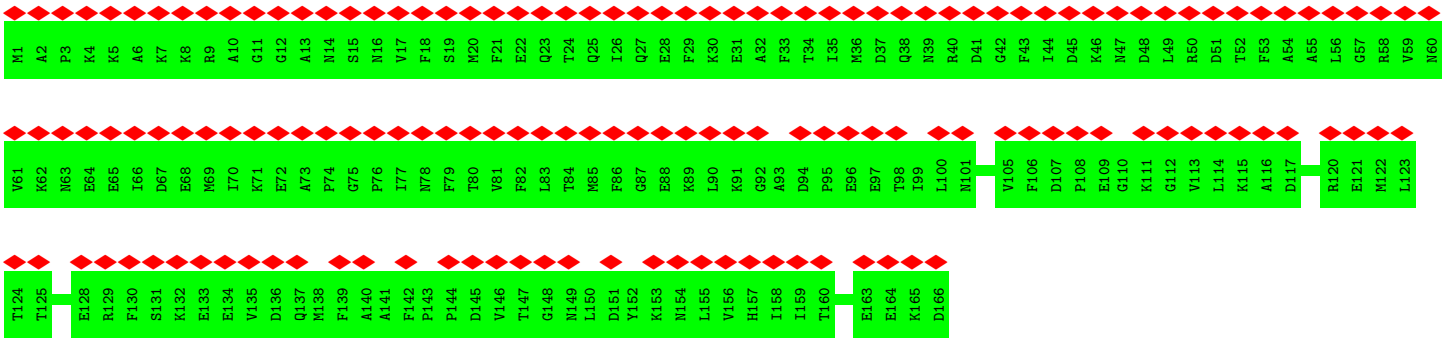


• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



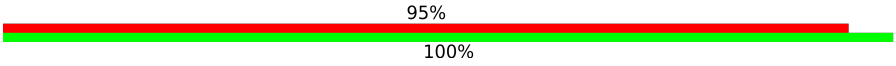
• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

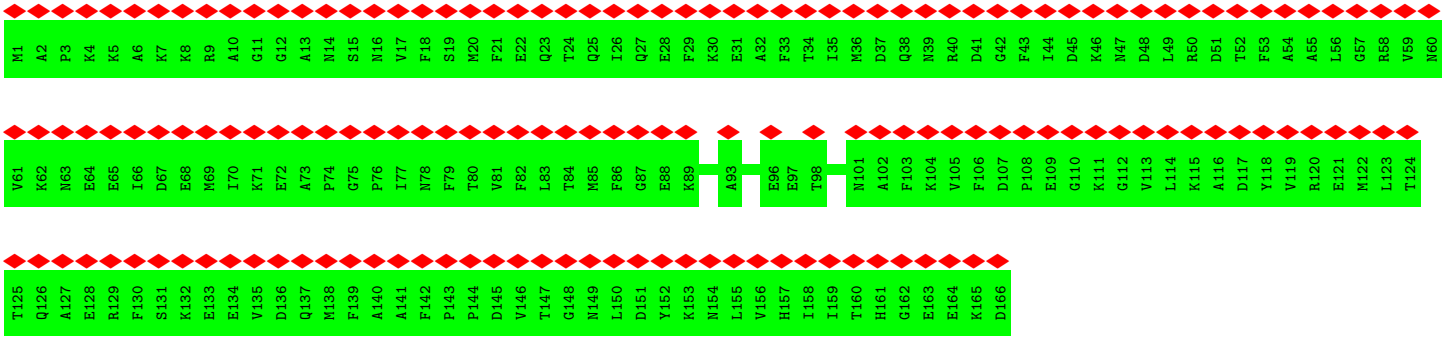
Chain aq:



• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

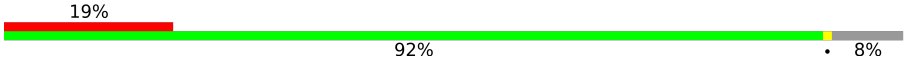
Chain ar:

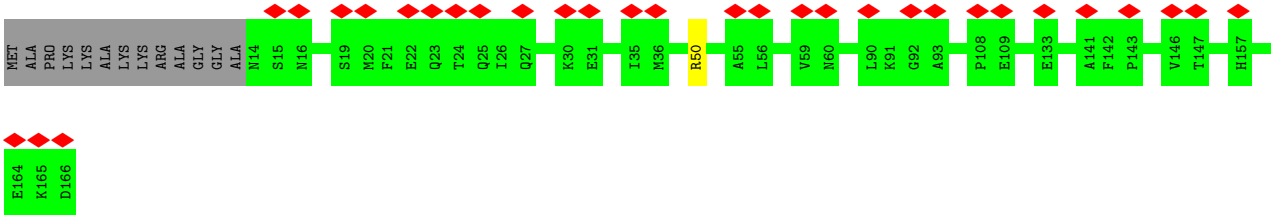




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

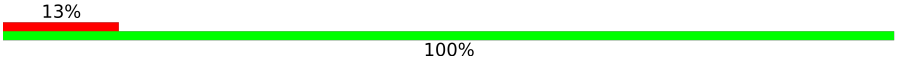
Chain c:

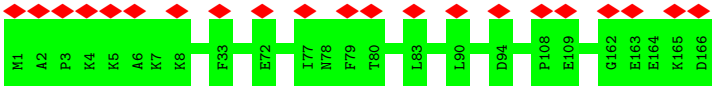




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

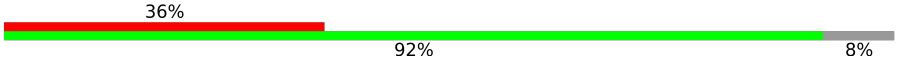
Chain d:

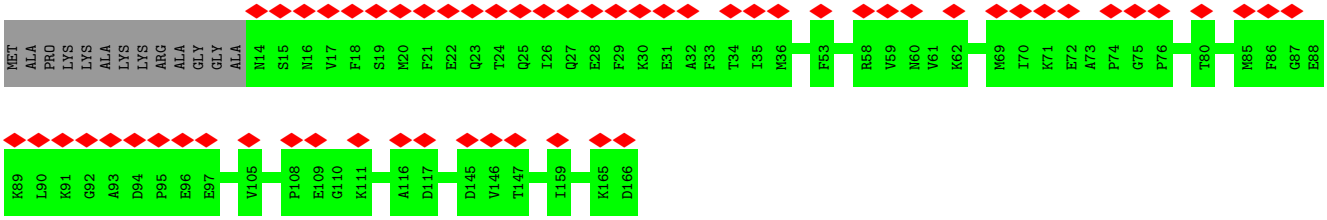




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

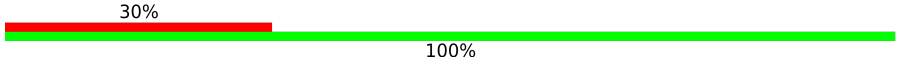
Chain i:

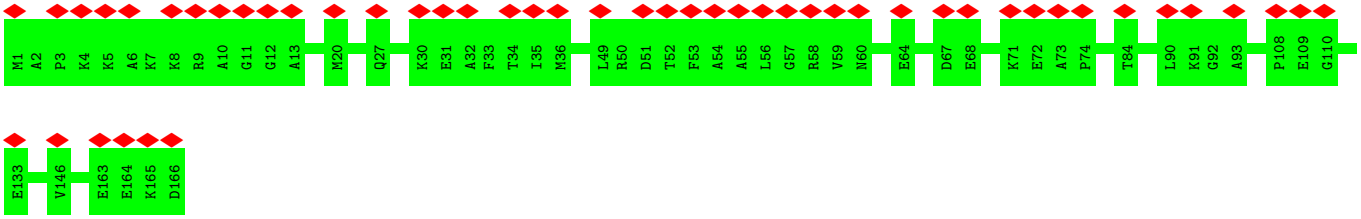




• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

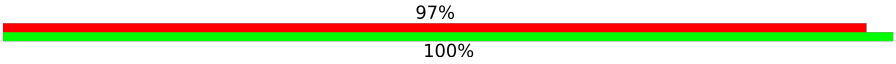
Chain j:





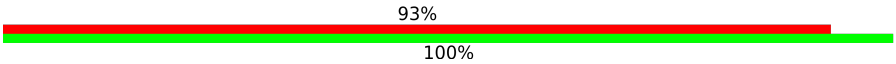
• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

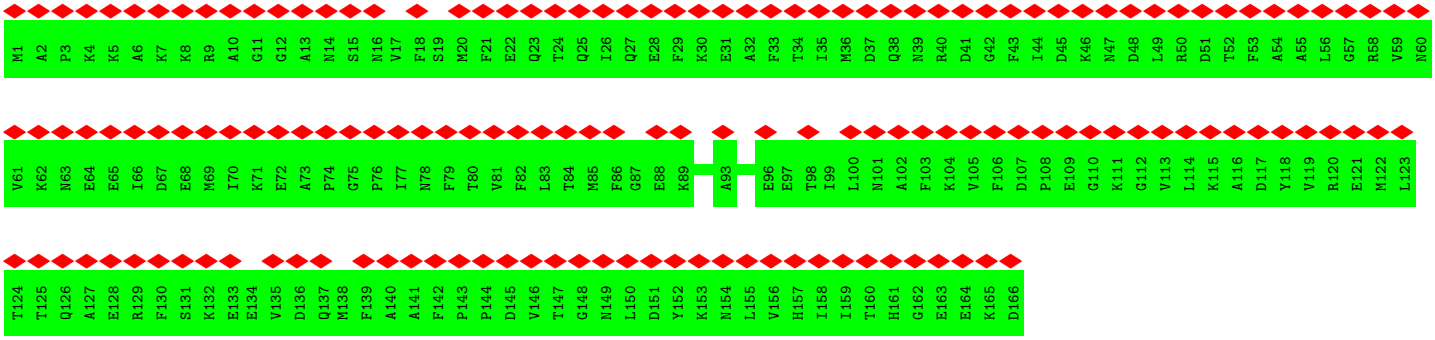
Chain q:



• Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform

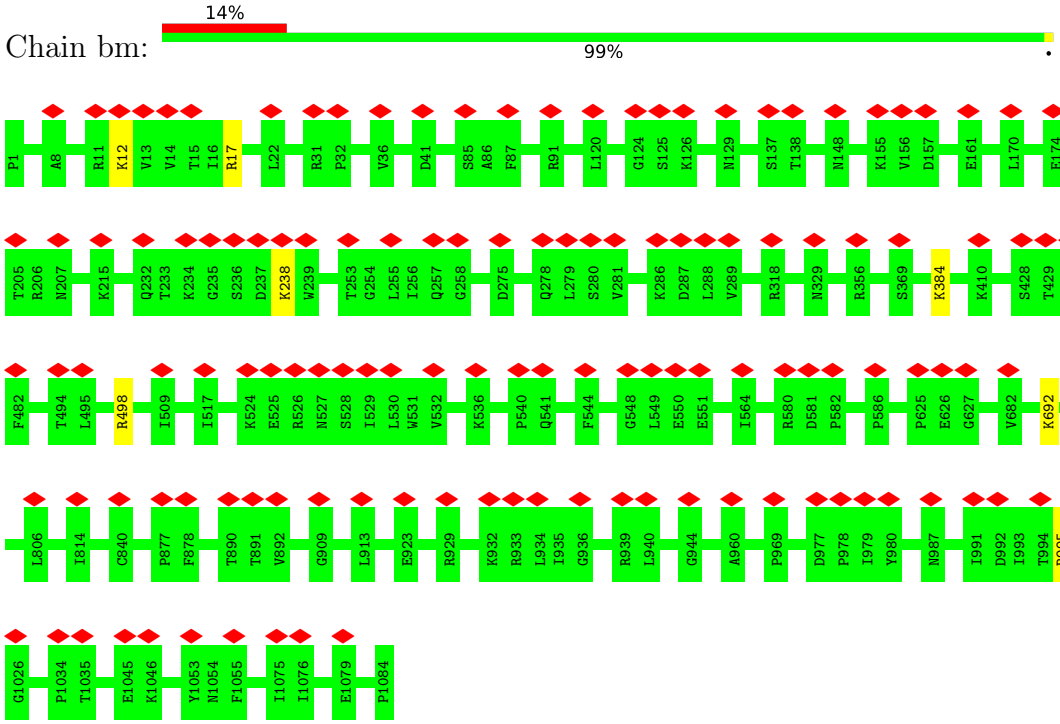
Chain r:





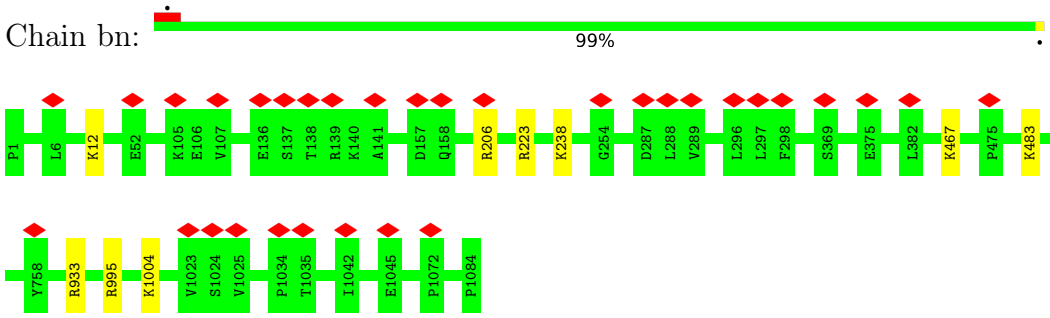
• Molecule 4: Titin

Chain bm:



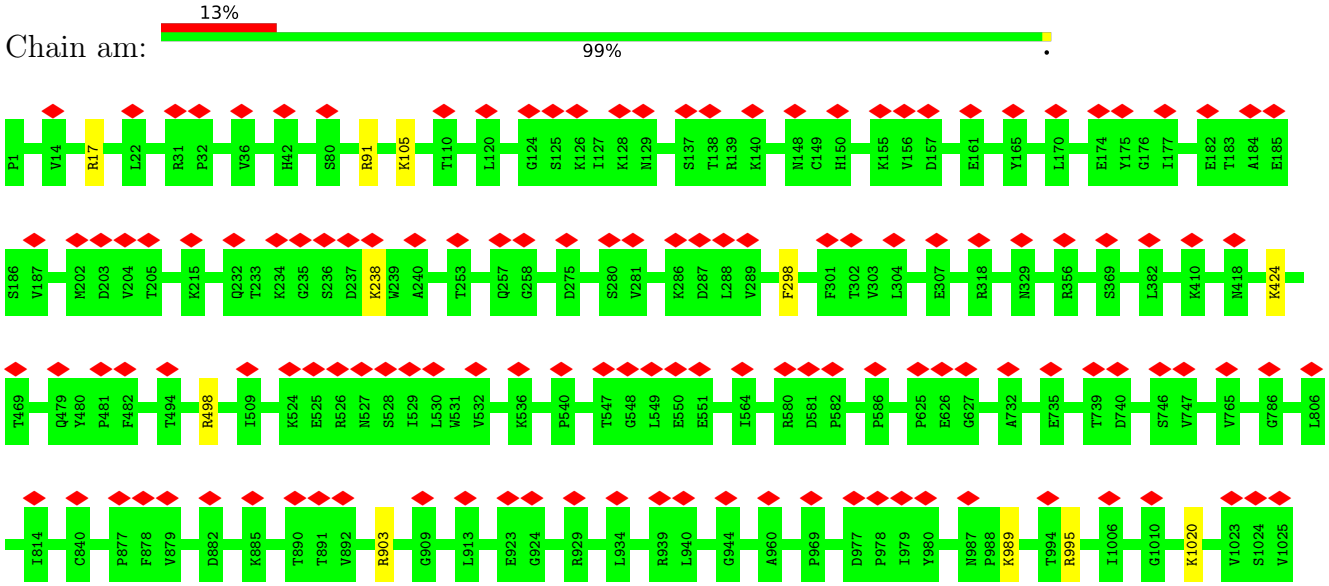
• Molecule 4: Titin

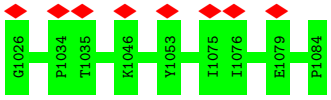
Chain bn:



• Molecule 4: Titin

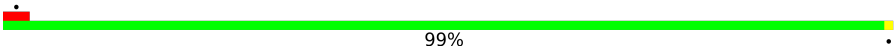
Chain am:

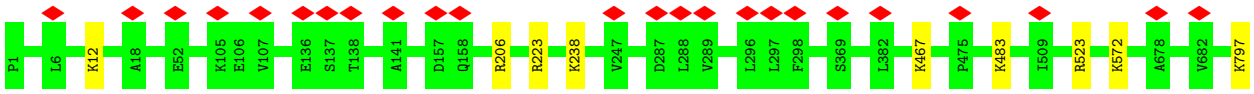


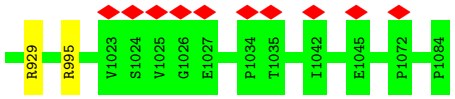


• Molecule 4: Titin

Chain an:

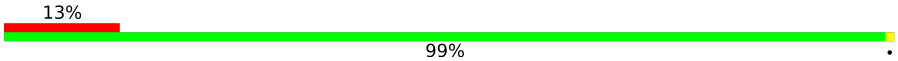


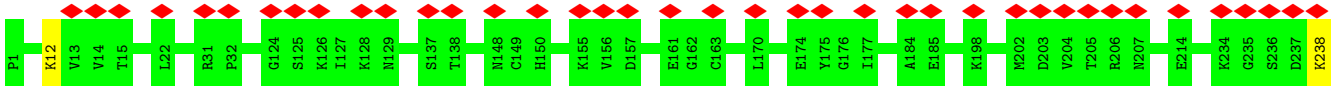


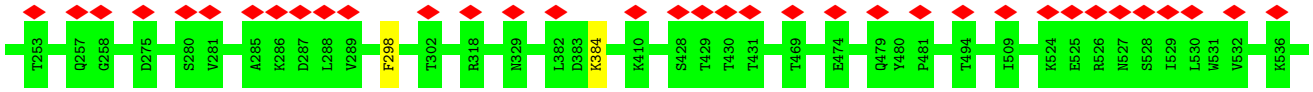


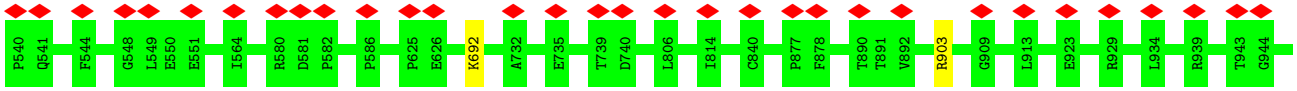
• Molecule 4: Titin

Chain m:



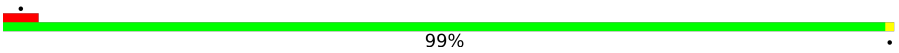


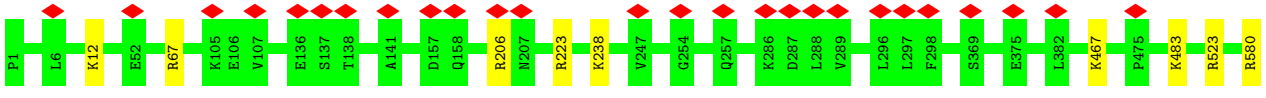


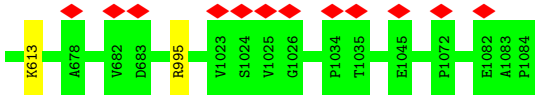


• Molecule 4: Titin

Chain n:

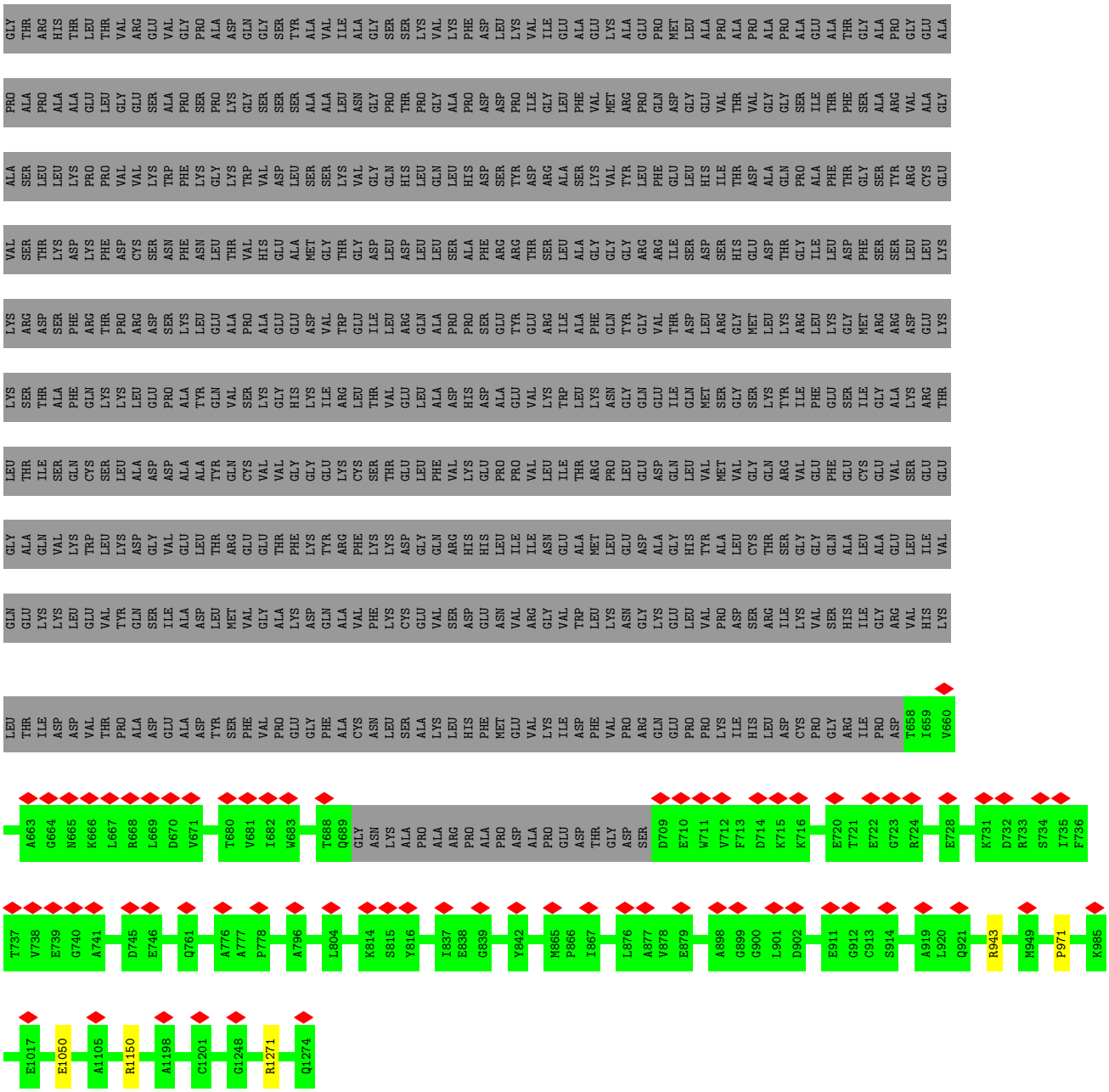






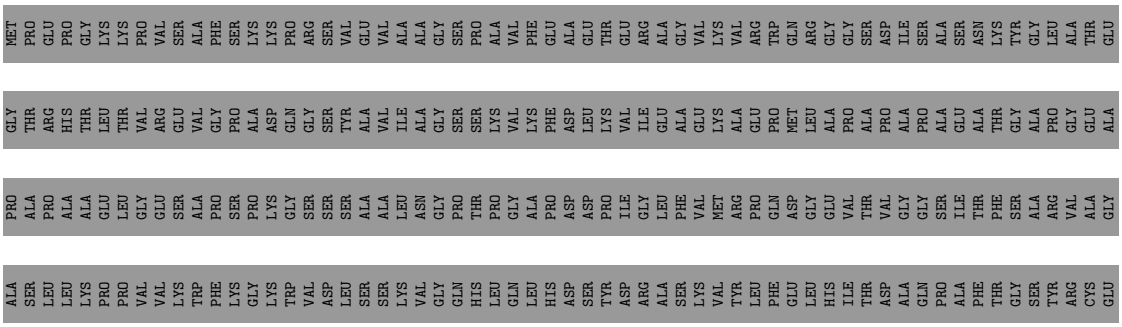
• Molecule 5: Myosin-binding protein C, cardiac-type

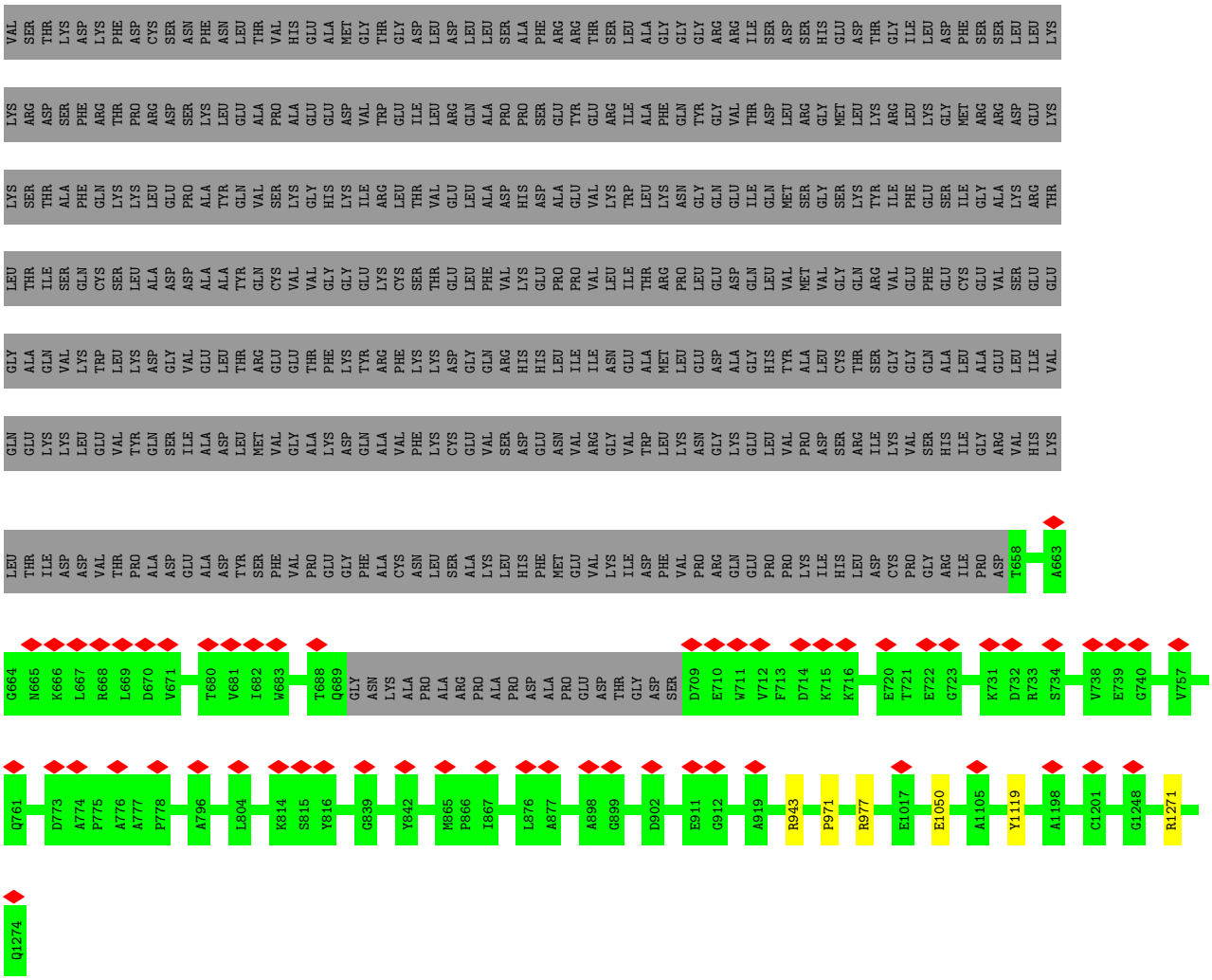
Chain bo:



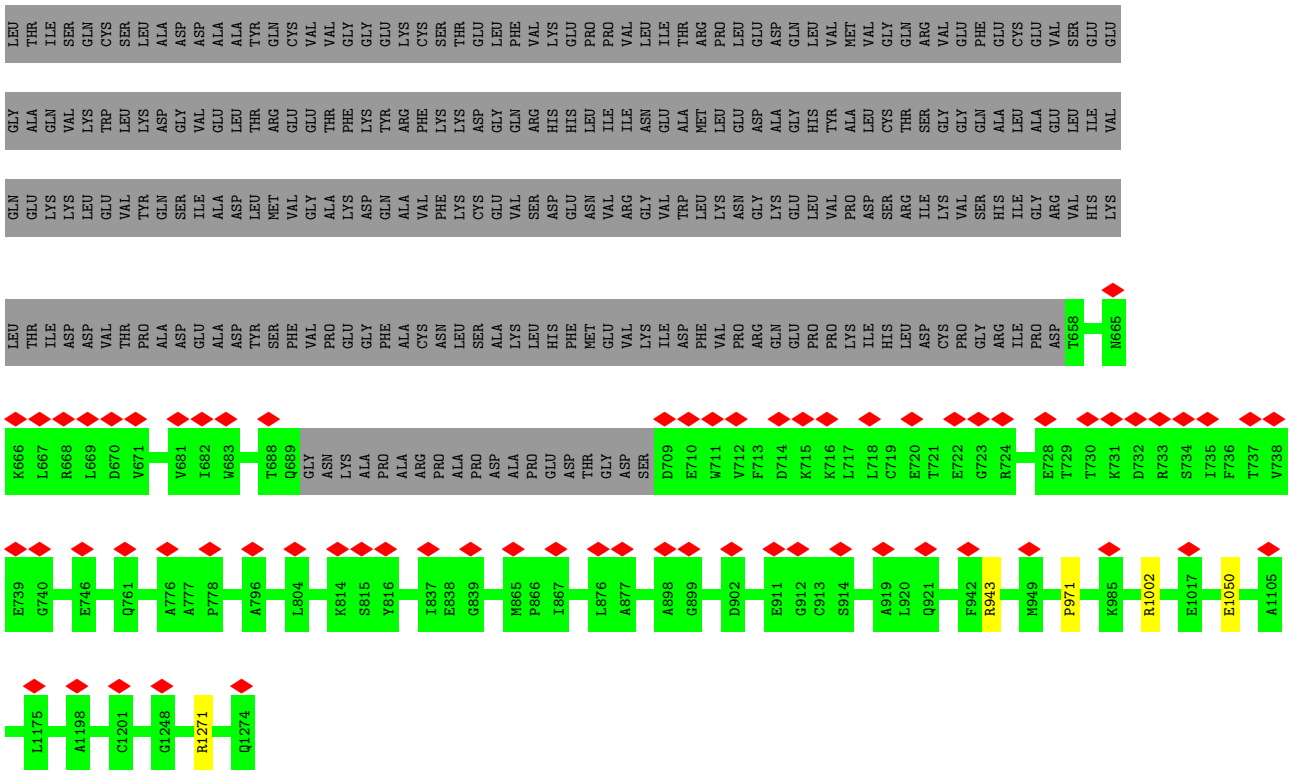
• Molecule 5: Myosin-binding protein C, cardiac-type

Chain ao:





• Molecule 5: Myosin-binding protein C, cardiac-type


LEU THR ILE SER GLN CYS SER LEU ALA ASP ASP ALA ALA TYR GLN CYS VAL VAL GLY GLY GLU LYS CYS SER THR GLU LEU PHE VAL LYS GLU PRO PRO VAL LEU ILE THR ARG PRO LEU GLU ASP GLN LEU VAL MET VAL GLY GLN ARG VAL GLU PHE GLU CYS GLU VAL SER GLU GLU
GLY ALA GLN VAL LYS TRP LEU LYS ASP GLY VAL GLU LEU THR ARG GLU GLU THR PHE LYS TYR ARG PHE LYS LYS ASP GLY GLN ARG HIS HIS LEU ILE ILE ASN GLU ALA MET LEU GLU ASP ALA GLY HIS TYR ALA LEU CYS THR SER GLY GLY GLN ALA LEU ALA GLU LEU ILE VAL
GLN GLU LYS LYS LEU GLU VAL TYR GLN SER ILE ALA ASP LEU MET VAL GLY ALA LYS ASP GLN ALA VAL PHE LYS CYS GLU VAL SER ASP GLU ASN VAL ARG GLY VAL TRP LEU LYS ASN GLY LYS GLU LEU VAL PRO ASP SER ARG ILE LYS VAL SER HIS ILE GLY ARG VAL HIS LYS
LEU THR ILE ASP ASP VAL THR PRO ALA ASP GLU ALA ASP TYR SER PHE VAL PRO GLU GLY PHE ALA CYS ASN LEU SER ALA LYS LEU HIS PHE MET GLU VAL LYS ILE ASP PHE VAL PRO ARG GLN GLU PRO PRO LYS ILE HIS LEU ASP CYS PRO GLY ARG ILE PRO ASP T658 M665
K666 L667 R668 L669 D670 V671 V681 I682 W683 T688 Q689 GLY ASN LYS ALA PRO ALA ARG PRO ALA PRO ASP ALA PRO GLU ASP THR GLY ASP SER D709 E710 W711 V712 F713 D714 K715 K716 L717 L718 C719 E720 T721 E722 G723 R724 E728 T729 T730 K731 D732 R733 S734 I735 F736 T737 V738
E739 G740 E746 Q761 A776 A777 P778 A796 L804 K814 S815 Y816 I837 E838 G839 M865 P866 I867 L876 A877 A898 G899 D902 E911 G912 C913 S914 A919 L920 Q921 F942 R943 M949 P971 K985 R1002 E1017 E1050 A1105
L1175 A1198 C1201 G1248 R1271 Q1274

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	102581	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	61	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.360	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	869.83997, 869.83997, 869.83997	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0873, 1.0873, 1.0873	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.26	0/9326	0.51	1/12520 (0.0%)
1	AA	0.27	0/9326	0.51	1/12520 (0.0%)
1	AB	0.26	0/9326	0.49	0/12520
1	AG	0.29	0/2888	0.53	0/3841
1	AH	0.32	0/2888	0.56	0/3841
1	AI	0.32	0/2903	0.57	0/3868
1	AJ	0.31	0/2903	0.56	0/3868
1	AK	0.31	0/2856	0.60	2/3815 (0.1%)
1	AL	1.16	2/2856 (0.1%)	0.57	2/3815 (0.1%)
1	AM	0.31	0/2936	0.53	0/3922
1	AN	0.35	1/2936 (0.0%)	0.52	0/3922
1	AO	0.38	1/2927 (0.0%)	0.58	0/3911
1	AP	0.33	0/2927	0.57	0/3911
1	AQ	0.31	0/2894	0.53	0/3869
1	AR	0.35	0/2894	0.57	0/3869
1	AS	0.32	0/2915	0.58	0/3883
1	AT	0.31	0/2915	0.54	0/3883
1	AU	0.31	0/2642	0.55	1/3524 (0.0%)
1	AV	0.29	0/2642	0.55	0/3524
1	AW	0.33	0/1838	0.57	0/2445
1	AX	0.31	0/1838	0.52	0/2445
1	AY	0.28	0/8275	0.53	1/11125 (0.0%)
1	AZ	0.30	0/8275	0.52	0/11125
1	B	0.26	0/9326	0.49	0/12520
1	BA	0.26	0/9326	0.48	0/12520
1	BB	0.26	0/9326	0.49	1/12520 (0.0%)
1	BG	0.28	0/2888	0.51	0/3841
1	BH	0.33	0/2888	0.57	1/3841 (0.0%)
1	BI	0.31	0/2903	0.59	0/3868
1	BJ	0.31	0/2903	0.55	0/3868
1	BK	0.32	0/2856	0.60	2/3815 (0.1%)
1	BL	0.32	0/2856	0.55	0/3815
1	BM	0.30	0/2936	0.51	0/3922
1	BN	0.35	1/2936 (0.0%)	0.52	0/3922

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	BO	0.41	1/2927 (0.0%)	0.59	0/3911
1	BP	0.33	0/2927	0.58	1/3911 (0.0%)
1	BQ	0.32	0/2894	0.53	0/3869
1	BR	0.34	0/2894	0.56	0/3869
1	BS	0.30	0/2915	0.56	0/3883
1	BT	0.31	0/2915	0.53	0/3883
1	BU	0.29	0/2642	0.52	0/3524
1	BV	0.31	0/2642	0.56	0/3524
1	BW	0.32	0/1838	0.56	0/2445
1	BX	0.31	0/1838	0.53	0/2445
1	BY	0.28	0/8275	0.52	2/11125 (0.0%)
1	BZ	0.28	0/8275	0.51	0/11125
1	G	0.28	0/2888	0.53	0/3841
1	H	0.31	0/2888	0.54	0/3841
1	I	0.32	0/2903	0.58	0/3868
1	J	0.32	0/2903	0.57	0/3868
1	K	0.32	0/2856	0.59	0/3815
1	L	1.16	2/2856 (0.1%)	0.56	2/3815 (0.1%)
1	M	0.30	0/2936	0.53	0/3922
1	N	0.36	1/2936 (0.0%)	0.51	0/3922
1	O	0.42	1/2927 (0.0%)	0.58	1/3911 (0.0%)
1	P	0.33	0/2927	0.56	0/3911
1	Q	0.31	0/2894	0.51	0/3869
1	R	0.35	0/2894	0.56	0/3869
1	S	0.30	0/2915	0.55	0/3883
1	T	0.30	0/2915	0.53	0/3883
1	U	0.30	0/2642	0.55	0/3524
1	V	0.29	0/2642	0.56	1/3524 (0.0%)
1	W	0.33	0/1838	0.57	0/2445
1	X	0.30	0/1838	0.54	0/2445
1	Y	0.28	0/8275	0.52	2/11125 (0.0%)
1	Z	0.28	0/8275	0.52	0/11125
1	ae	0.27	0/7502	0.51	1/10091 (0.0%)
1	af	0.27	0/7502	0.51	0/10091
1	ak	0.32	0/1098	0.55	0/1459
1	al	0.32	0/1098	0.52	0/1459
1	be	0.28	0/7502	0.53	1/10091 (0.0%)
1	bf	0.28	0/7502	0.52	0/10091
1	bk	0.33	0/1098	0.57	0/1459
1	bl	0.34	0/1098	0.58	0/1459
1	e	0.27	0/7502	0.52	1/10091 (0.0%)
1	f	0.29	0/7502	0.53	0/10091
1	k	0.33	0/1098	0.54	0/1459

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	l	0.36	0/1098	0.59	0/1459
2	AE	0.25	0/1304	0.49	0/1748
2	AF	0.25	0/1304	0.47	0/1748
2	BE	0.25	0/1304	0.48	0/1748
2	BF	0.25	0/1304	0.46	0/1748
2	E	0.25	0/1304	0.51	0/1748
2	F	0.25	0/1304	0.48	0/1748
2	a	0.27	0/1304	0.52	0/1748
2	aa	0.29	0/1304	0.53	0/1748
2	ab	0.30	0/1304	0.53	0/1748
2	ag	0.27	0/1304	0.50	0/1748
2	ah	0.28	0/1304	0.54	0/1748
2	b	0.30	0/1304	0.56	0/1748
2	ba	0.27	0/1304	0.52	0/1748
2	bb	0.32	0/1304	0.56	0/1748
2	bg	0.27	0/1304	0.48	0/1748
2	bh	0.29	0/1304	0.52	0/1748
2	g	0.29	0/1304	0.52	0/1748
2	h	0.28	0/1304	0.51	0/1748
3	ac	0.27	0/1254	0.48	0/1687
3	ad	0.29	0/1345	0.51	0/1805
3	ai	0.27	0/1254	0.50	0/1687
3	aj	0.28	0/1345	0.50	0/1805
3	aq	0.26	0/1345	0.46	0/1805
3	ar	0.26	0/1345	0.46	0/1805
3	bc	0.27	0/1254	0.50	0/1687
3	bd	0.28	0/1345	0.51	0/1805
3	bi	0.28	0/1254	0.49	0/1687
3	bj	0.28	0/1345	0.50	0/1805
3	bq	0.26	0/1345	0.47	0/1805
3	br	0.26	0/1345	0.46	0/1805
3	c	0.26	0/1254	0.47	0/1687
3	d	0.28	0/1345	0.52	0/1805
3	i	0.27	0/1254	0.48	0/1687
3	j	0.28	0/1345	0.52	0/1805
3	q	0.26	0/1345	0.47	0/1805
3	r	0.26	0/1345	0.46	0/1805
4	am	0.62	6/8610 (0.1%)	0.54	0/11717
4	an	0.30	0/8610	0.55	0/11717
4	bm	0.28	0/8610	0.54	0/11717
4	bn	0.30	0/8610	0.54	0/11717
4	m	0.62	6/8610 (0.1%)	0.54	0/11717
4	n	0.29	0/8610	0.55	0/11717

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	ao	0.29	0/4827	0.57	0/6572
5	bo	0.28	0/4827	0.56	0/6572
5	o	0.29	0/4827	0.56	0/6572
All	All	0.34	22/419277 (0.0%)	0.53	24/562902 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	AA	0	1
1	AY	0	3
1	BB	0	1
1	BY	0	2
1	O	0	1
1	Y	0	1
1	ae	0	1
1	be	0	2
1	e	0	1
2	aa	0	1
2	ag	0	1
4	n	0	1
5	ao	0	1
All	All	0	18

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AL	1176	ARG	CG-CD	59.47	3.00	1.51
1	L	1176	ARG	CG-CD	59.41	3.00	1.51
4	m	298	PHE	CE1-CZ	25.30	1.85	1.37
4	am	298	PHE	CE1-CZ	24.76	1.84	1.37
4	m	298	PHE	CD1-CE1	22.96	1.85	1.39

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	961	LEU	CA-CB-CG	12.33	143.66	115.30
1	BB	961	LEU	CA-CB-CG	12.27	143.52	115.30
1	AA	961	LEU	CA-CB-CG	11.82	142.49	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AK	1386	LEU	CA-CB-CG	8.05	133.81	115.30
1	AU	1769	LEU	CA-CB-CG	7.25	131.99	115.30

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BB	961	LEU	Peptide
1	BY	406	VAL	Peptide
1	BY	410	TYR	Peptide
1	be	593	TRP	Peptide
1	be	793	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)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1127/1935 (58%)	1073 (95%)	53 (5%)	1 (0%)	51	85
1	AA	1127/1935 (58%)	1065 (94%)	62 (6%)	0	100	100
1	AB	1127/1935 (58%)	1067 (95%)	60 (5%)	0	100	100
1	AG	353/1935 (18%)	351 (99%)	2 (1%)	0	100	100
1	AH	353/1935 (18%)	348 (99%)	5 (1%)	0	100	100
1	AI	355/1935 (18%)	351 (99%)	4 (1%)	0	100	100
1	AJ	355/1935 (18%)	348 (98%)	7 (2%)	0	100	100
1	AK	348/1935 (18%)	345 (99%)	3 (1%)	0	100	100
1	AL	348/1935 (18%)	339 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AM	357/1935 (18%)	350 (98%)	7 (2%)	0	100	100
1	AN	357/1935 (18%)	351 (98%)	6 (2%)	0	100	100
1	AO	356/1935 (18%)	349 (98%)	7 (2%)	0	100	100
1	AP	356/1935 (18%)	345 (97%)	11 (3%)	0	100	100
1	AQ	355/1935 (18%)	352 (99%)	3 (1%)	0	100	100
1	AR	355/1935 (18%)	343 (97%)	11 (3%)	1 (0%)	41	76
1	AS	357/1935 (18%)	347 (97%)	10 (3%)	0	100	100
1	AT	357/1935 (18%)	354 (99%)	3 (1%)	0	100	100
1	AU	323/1935 (17%)	317 (98%)	6 (2%)	0	100	100
1	AV	323/1935 (17%)	317 (98%)	6 (2%)	0	100	100
1	AW	222/1935 (12%)	216 (97%)	6 (3%)	0	100	100
1	AX	222/1935 (12%)	219 (99%)	3 (1%)	0	100	100
1	AY	999/1935 (52%)	925 (93%)	74 (7%)	0	100	100
1	AZ	999/1935 (52%)	920 (92%)	79 (8%)	0	100	100
1	B	1127/1935 (58%)	1059 (94%)	68 (6%)	0	100	100
1	BA	1127/1935 (58%)	1059 (94%)	68 (6%)	0	100	100
1	BB	1127/1935 (58%)	1067 (95%)	60 (5%)	0	100	100
1	BG	353/1935 (18%)	351 (99%)	2 (1%)	0	100	100
1	BH	353/1935 (18%)	350 (99%)	3 (1%)	0	100	100
1	BI	355/1935 (18%)	351 (99%)	4 (1%)	0	100	100
1	BJ	355/1935 (18%)	352 (99%)	3 (1%)	0	100	100
1	BK	348/1935 (18%)	346 (99%)	2 (1%)	0	100	100
1	BL	348/1935 (18%)	340 (98%)	8 (2%)	0	100	100
1	BM	357/1935 (18%)	353 (99%)	4 (1%)	0	100	100
1	BN	357/1935 (18%)	353 (99%)	4 (1%)	0	100	100
1	BO	356/1935 (18%)	346 (97%)	10 (3%)	0	100	100
1	BP	356/1935 (18%)	344 (97%)	12 (3%)	0	100	100
1	BQ	355/1935 (18%)	353 (99%)	2 (1%)	0	100	100
1	BR	355/1935 (18%)	345 (97%)	10 (3%)	0	100	100
1	BS	357/1935 (18%)	346 (97%)	11 (3%)	0	100	100
1	BT	357/1935 (18%)	351 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BU	323/1935 (17%)	321 (99%)	2 (1%)	0	100	100
1	BV	323/1935 (17%)	317 (98%)	6 (2%)	0	100	100
1	BW	222/1935 (12%)	218 (98%)	4 (2%)	0	100	100
1	BX	222/1935 (12%)	218 (98%)	4 (2%)	0	100	100
1	BY	999/1935 (52%)	920 (92%)	79 (8%)	0	100	100
1	BZ	999/1935 (52%)	912 (91%)	87 (9%)	0	100	100
1	G	353/1935 (18%)	352 (100%)	1 (0%)	0	100	100
1	H	353/1935 (18%)	349 (99%)	4 (1%)	0	100	100
1	I	355/1935 (18%)	350 (99%)	5 (1%)	0	100	100
1	J	355/1935 (18%)	350 (99%)	5 (1%)	0	100	100
1	K	348/1935 (18%)	345 (99%)	3 (1%)	0	100	100
1	L	348/1935 (18%)	341 (98%)	7 (2%)	0	100	100
1	M	357/1935 (18%)	352 (99%)	5 (1%)	0	100	100
1	N	357/1935 (18%)	352 (99%)	5 (1%)	0	100	100
1	O	356/1935 (18%)	349 (98%)	7 (2%)	0	100	100
1	P	356/1935 (18%)	350 (98%)	6 (2%)	0	100	100
1	Q	355/1935 (18%)	353 (99%)	2 (1%)	0	100	100
1	R	355/1935 (18%)	346 (98%)	9 (2%)	0	100	100
1	S	357/1935 (18%)	347 (97%)	10 (3%)	0	100	100
1	T	357/1935 (18%)	352 (99%)	5 (1%)	0	100	100
1	U	323/1935 (17%)	318 (98%)	5 (2%)	0	100	100
1	V	323/1935 (17%)	317 (98%)	6 (2%)	0	100	100
1	W	222/1935 (12%)	218 (98%)	4 (2%)	0	100	100
1	X	222/1935 (12%)	220 (99%)	2 (1%)	0	100	100
1	Y	999/1935 (52%)	930 (93%)	69 (7%)	0	100	100
1	Z	999/1935 (52%)	913 (91%)	86 (9%)	0	100	100
1	ae	902/1935 (47%)	826 (92%)	75 (8%)	1 (0%)	51	85
1	af	902/1935 (47%)	818 (91%)	83 (9%)	1 (0%)	51	85
1	ak	130/1935 (7%)	128 (98%)	2 (2%)	0	100	100
1	al	130/1935 (7%)	128 (98%)	2 (2%)	0	100	100
1	be	902/1935 (47%)	826 (92%)	75 (8%)	1 (0%)	51	85

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	bf	902/1935 (47%)	821 (91%)	80 (9%)	1 (0%)	51	85
1	bk	130/1935 (7%)	128 (98%)	2 (2%)	0	100	100
1	bl	130/1935 (7%)	129 (99%)	1 (1%)	0	100	100
1	e	902/1935 (47%)	826 (92%)	75 (8%)	1 (0%)	51	85
1	f	902/1935 (47%)	828 (92%)	72 (8%)	2 (0%)	47	81
1	k	130/1935 (7%)	127 (98%)	3 (2%)	0	100	100
1	l	130/1935 (7%)	128 (98%)	2 (2%)	0	100	100
2	AE	159/195 (82%)	146 (92%)	13 (8%)	0	100	100
2	AF	159/195 (82%)	151 (95%)	8 (5%)	0	100	100
2	BE	159/195 (82%)	150 (94%)	9 (6%)	0	100	100
2	BF	159/195 (82%)	150 (94%)	9 (6%)	0	100	100
2	E	159/195 (82%)	145 (91%)	14 (9%)	0	100	100
2	F	159/195 (82%)	151 (95%)	8 (5%)	0	100	100
2	a	159/195 (82%)	144 (91%)	15 (9%)	0	100	100
2	aa	159/195 (82%)	145 (91%)	14 (9%)	0	100	100
2	ab	159/195 (82%)	150 (94%)	9 (6%)	0	100	100
2	ag	159/195 (82%)	149 (94%)	10 (6%)	0	100	100
2	ah	159/195 (82%)	141 (89%)	18 (11%)	0	100	100
2	b	159/195 (82%)	148 (93%)	11 (7%)	0	100	100
2	ba	159/195 (82%)	145 (91%)	14 (9%)	0	100	100
2	bb	159/195 (82%)	147 (92%)	12 (8%)	0	100	100
2	bg	159/195 (82%)	144 (91%)	15 (9%)	0	100	100
2	bh	159/195 (82%)	145 (91%)	14 (9%)	0	100	100
2	g	159/195 (82%)	144 (91%)	15 (9%)	0	100	100
2	h	159/195 (82%)	145 (91%)	14 (9%)	0	100	100
3	ac	151/166 (91%)	137 (91%)	14 (9%)	0	100	100
3	ad	164/166 (99%)	147 (90%)	17 (10%)	0	100	100
3	ai	151/166 (91%)	140 (93%)	11 (7%)	0	100	100
3	aj	164/166 (99%)	147 (90%)	17 (10%)	0	100	100
3	aq	164/166 (99%)	159 (97%)	5 (3%)	0	100	100
3	ar	164/166 (99%)	151 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	bc	151/166 (91%)	141 (93%)	10 (7%)	0	100	100
3	bd	164/166 (99%)	146 (89%)	18 (11%)	0	100	100
3	bi	151/166 (91%)	138 (91%)	13 (9%)	0	100	100
3	bj	164/166 (99%)	147 (90%)	16 (10%)	1 (1%)	25	66
3	bq	164/166 (99%)	159 (97%)	5 (3%)	0	100	100
3	br	164/166 (99%)	152 (93%)	12 (7%)	0	100	100
3	c	151/166 (91%)	139 (92%)	12 (8%)	0	100	100
3	d	164/166 (99%)	148 (90%)	16 (10%)	0	100	100
3	i	151/166 (91%)	139 (92%)	12 (8%)	0	100	100
3	j	164/166 (99%)	143 (87%)	21 (13%)	0	100	100
3	q	164/166 (99%)	158 (96%)	6 (4%)	0	100	100
3	r	164/166 (99%)	151 (92%)	13 (8%)	0	100	100
4	am	1082/1084 (100%)	988 (91%)	94 (9%)	0	100	100
4	an	1082/1084 (100%)	972 (90%)	110 (10%)	0	100	100
4	bm	1082/1084 (100%)	984 (91%)	98 (9%)	0	100	100
4	bn	1082/1084 (100%)	982 (91%)	100 (9%)	0	100	100
4	m	1082/1084 (100%)	987 (91%)	95 (9%)	0	100	100
4	n	1082/1084 (100%)	987 (91%)	95 (9%)	0	100	100
5	ao	594/1274 (47%)	540 (91%)	52 (9%)	2 (0%)	41	76
5	bo	594/1274 (47%)	545 (92%)	47 (8%)	2 (0%)	41	76
5	o	594/1274 (47%)	546 (92%)	46 (8%)	2 (0%)	41	76
All	All	51114/167754 (30%)	48294 (94%)	2804 (6%)	16 (0%)	100	100

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	ae	411	VAL
1	bf	737	ASP
5	bo	1050	GLU
1	f	737	ASP
1	be	411	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	995/1695 (59%)	989 (99%)	6 (1%)	86	92
1	AA	995/1695 (59%)	989 (99%)	6 (1%)	86	92
1	AB	995/1695 (59%)	984 (99%)	11 (1%)	73	84
1	AG	315/1695 (19%)	311 (99%)	4 (1%)	69	82
1	AH	315/1695 (19%)	310 (98%)	5 (2%)	62	79
1	AI	316/1695 (19%)	313 (99%)	3 (1%)	78	87
1	AJ	316/1695 (19%)	309 (98%)	7 (2%)	52	71
1	AK	304/1695 (18%)	299 (98%)	5 (2%)	62	79
1	AL	304/1695 (18%)	300 (99%)	4 (1%)	69	82
1	AM	319/1695 (19%)	318 (100%)	1 (0%)	92	95
1	AN	319/1695 (19%)	318 (100%)	1 (0%)	92	95
1	AO	315/1695 (19%)	314 (100%)	1 (0%)	92	95
1	AP	315/1695 (19%)	314 (100%)	1 (0%)	92	95
1	AQ	317/1695 (19%)	315 (99%)	2 (1%)	86	92
1	AR	317/1695 (19%)	317 (100%)	0	100	100
1	AS	318/1695 (19%)	318 (100%)	0	100	100
1	AT	318/1695 (19%)	316 (99%)	2 (1%)	86	92
1	AU	288/1695 (17%)	285 (99%)	3 (1%)	76	86
1	AV	288/1695 (17%)	285 (99%)	3 (1%)	76	86
1	AW	199/1695 (12%)	199 (100%)	0	100	100
1	AX	199/1695 (12%)	198 (100%)	1 (0%)	88	93
1	AY	882/1695 (52%)	873 (99%)	9 (1%)	76	86
1	AZ	882/1695 (52%)	869 (98%)	13 (2%)	65	80
1	B	995/1695 (59%)	985 (99%)	10 (1%)	76	86
1	BA	995/1695 (59%)	987 (99%)	8 (1%)	81	89
1	BB	995/1695 (59%)	991 (100%)	4 (0%)	91	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	BG	315/1695 (19%)	314 (100%)	1 (0%)	92 95
1	BH	315/1695 (19%)	310 (98%)	5 (2%)	62 79
1	BI	316/1695 (19%)	314 (99%)	2 (1%)	86 92
1	BJ	316/1695 (19%)	312 (99%)	4 (1%)	69 82
1	BK	304/1695 (18%)	300 (99%)	4 (1%)	69 82
1	BL	304/1695 (18%)	300 (99%)	4 (1%)	69 82
1	BM	319/1695 (19%)	319 (100%)	0	100 100
1	BN	319/1695 (19%)	317 (99%)	2 (1%)	86 92
1	BO	315/1695 (19%)	314 (100%)	1 (0%)	92 95
1	BP	315/1695 (19%)	315 (100%)	0	100 100
1	BQ	317/1695 (19%)	316 (100%)	1 (0%)	92 95
1	BR	317/1695 (19%)	316 (100%)	1 (0%)	92 95
1	BS	318/1695 (19%)	318 (100%)	0	100 100
1	BT	318/1695 (19%)	316 (99%)	2 (1%)	86 92
1	BU	288/1695 (17%)	288 (100%)	0	100 100
1	BV	288/1695 (17%)	286 (99%)	2 (1%)	84 90
1	BW	199/1695 (12%)	196 (98%)	3 (2%)	65 80
1	BX	199/1695 (12%)	199 (100%)	0	100 100
1	BY	882/1695 (52%)	878 (100%)	4 (0%)	88 93
1	BZ	882/1695 (52%)	869 (98%)	13 (2%)	65 80
1	G	315/1695 (19%)	314 (100%)	1 (0%)	92 95
1	H	315/1695 (19%)	308 (98%)	7 (2%)	52 71
1	I	316/1695 (19%)	313 (99%)	3 (1%)	78 87
1	J	316/1695 (19%)	314 (99%)	2 (1%)	86 92
1	K	304/1695 (18%)	301 (99%)	3 (1%)	76 86
1	L	304/1695 (18%)	299 (98%)	5 (2%)	62 79
1	M	319/1695 (19%)	318 (100%)	1 (0%)	92 95
1	N	319/1695 (19%)	318 (100%)	1 (0%)	92 95
1	O	315/1695 (19%)	313 (99%)	2 (1%)	86 92
1	P	315/1695 (19%)	313 (99%)	2 (1%)	86 92
1	Q	317/1695 (19%)	315 (99%)	2 (1%)	86 92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	317/1695 (19%)	316 (100%)	1 (0%)	92	95
1	S	318/1695 (19%)	318 (100%)	0	100	100
1	T	318/1695 (19%)	316 (99%)	2 (1%)	86	92
1	U	288/1695 (17%)	286 (99%)	2 (1%)	84	90
1	V	288/1695 (17%)	286 (99%)	2 (1%)	84	90
1	W	199/1695 (12%)	197 (99%)	2 (1%)	76	86
1	X	199/1695 (12%)	198 (100%)	1 (0%)	88	93
1	Y	882/1695 (52%)	878 (100%)	4 (0%)	88	93
1	Z	882/1695 (52%)	869 (98%)	13 (2%)	65	80
1	ae	796/1695 (47%)	791 (99%)	5 (1%)	86	92
1	af	796/1695 (47%)	790 (99%)	6 (1%)	81	89
1	ak	117/1695 (7%)	116 (99%)	1 (1%)	78	87
1	al	117/1695 (7%)	115 (98%)	2 (2%)	60	78
1	be	796/1695 (47%)	791 (99%)	5 (1%)	86	92
1	bf	796/1695 (47%)	792 (100%)	4 (0%)	88	93
1	bk	117/1695 (7%)	116 (99%)	1 (1%)	78	87
1	bl	117/1695 (7%)	116 (99%)	1 (1%)	78	87
1	e	796/1695 (47%)	792 (100%)	4 (0%)	88	93
1	f	796/1695 (47%)	790 (99%)	6 (1%)	81	89
1	k	117/1695 (7%)	117 (100%)	0	100	100
1	l	117/1695 (7%)	113 (97%)	4 (3%)	37	60
2	AE	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	AF	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	BE	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	BF	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	E	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	F	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	a	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	aa	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	ab	141/167 (84%)	140 (99%)	1 (1%)	84	90
2	ag	141/167 (84%)	140 (99%)	1 (1%)	84	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	ah	141/167 (84%)	140 (99%)	1 (1%)	84 90
2	b	141/167 (84%)	140 (99%)	1 (1%)	84 90
2	ba	141/167 (84%)	140 (99%)	1 (1%)	84 90
2	bb	141/167 (84%)	139 (99%)	2 (1%)	67 80
2	bg	141/167 (84%)	140 (99%)	1 (1%)	84 90
2	bh	141/167 (84%)	139 (99%)	2 (1%)	67 80
2	g	141/167 (84%)	140 (99%)	1 (1%)	84 90
2	h	141/167 (84%)	139 (99%)	2 (1%)	67 80
3	ac	134/141 (95%)	134 (100%)	0	100 100
3	ad	141/141 (100%)	141 (100%)	0	100 100
3	ai	134/141 (95%)	134 (100%)	0	100 100
3	aj	141/141 (100%)	140 (99%)	1 (1%)	84 90
3	aq	141/141 (100%)	141 (100%)	0	100 100
3	ar	141/141 (100%)	141 (100%)	0	100 100
3	bc	134/141 (95%)	134 (100%)	0	100 100
3	bd	141/141 (100%)	141 (100%)	0	100 100
3	bi	134/141 (95%)	134 (100%)	0	100 100
3	bj	141/141 (100%)	141 (100%)	0	100 100
3	bq	141/141 (100%)	141 (100%)	0	100 100
3	br	141/141 (100%)	141 (100%)	0	100 100
3	c	134/141 (95%)	133 (99%)	1 (1%)	84 90
3	d	141/141 (100%)	141 (100%)	0	100 100
3	i	134/141 (95%)	134 (100%)	0	100 100
3	j	141/141 (100%)	141 (100%)	0	100 100
3	q	141/141 (100%)	141 (100%)	0	100 100
3	r	141/141 (100%)	141 (100%)	0	100 100
4	am	944/944 (100%)	934 (99%)	10 (1%)	73 84
4	an	944/944 (100%)	933 (99%)	11 (1%)	71 83
4	bm	944/944 (100%)	935 (99%)	9 (1%)	76 86
4	bn	944/944 (100%)	934 (99%)	10 (1%)	73 84
4	m	944/944 (100%)	937 (99%)	7 (1%)	84 90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	n	944/944 (100%)	934 (99%)	10 (1%)	73 84
5	ao	519/1076 (48%)	516 (99%)	3 (1%)	86 92
5	bo	519/1076 (48%)	516 (99%)	3 (1%)	86 92
5	o	519/1076 (48%)	516 (99%)	3 (1%)	86 92
All	All	45141/146646 (31%)	44798 (99%)	343 (1%)	82 89

5 of 343 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	484	LYS
1	Y	453	ARG
1	B	453	ARG
1	K	1175	ARG
1	Z	925	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 388 such sidechains are listed below:

Mol	Chain	Res	Type
1	AY	686	ASN
1	I	1185	HIS
1	AZ	1030	GLN
4	am	948	ASN
1	M	1471	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

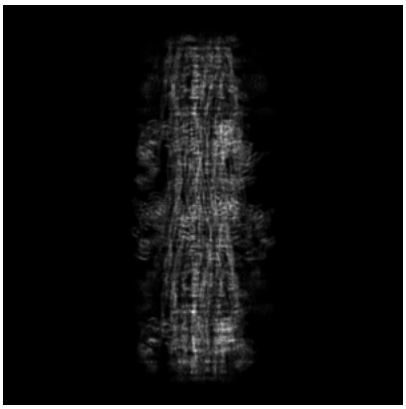
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-29722. These allow visual inspection of the internal detail of the map and identification of artifacts.

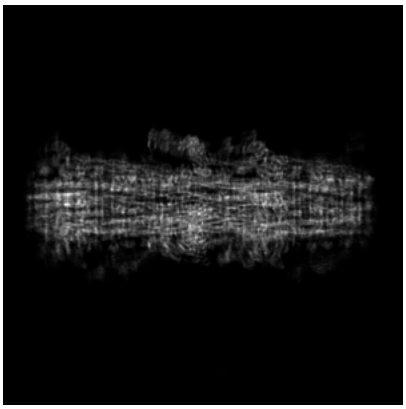
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

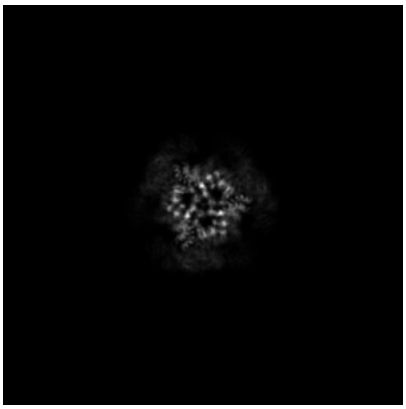
6.1.1 Primary map



X

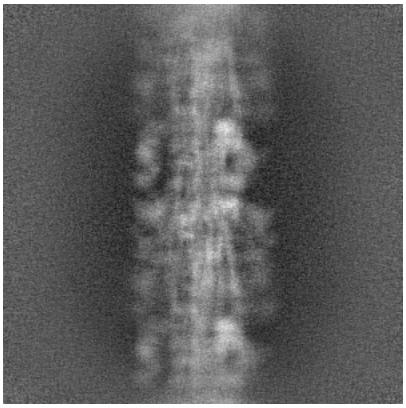


Y

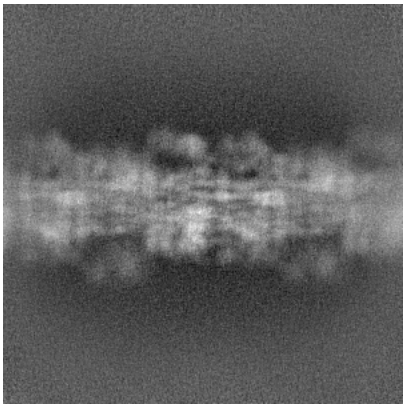


Z

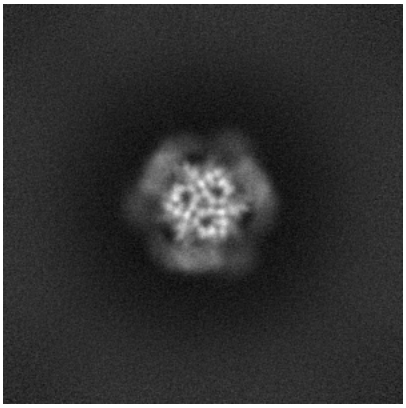
6.1.2 Raw map



X



Y

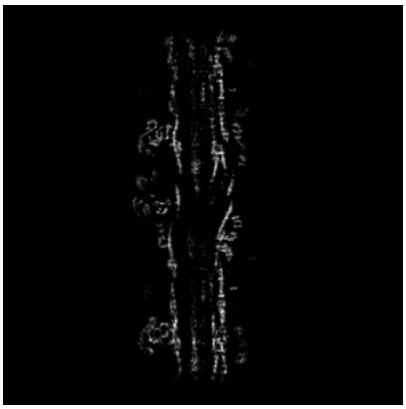


Z

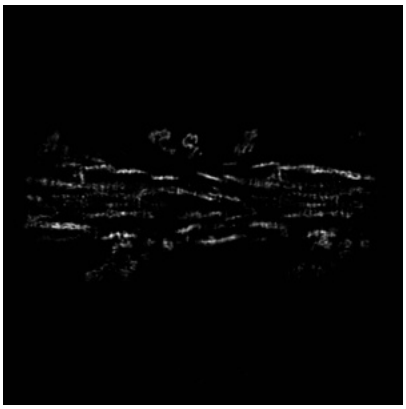
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



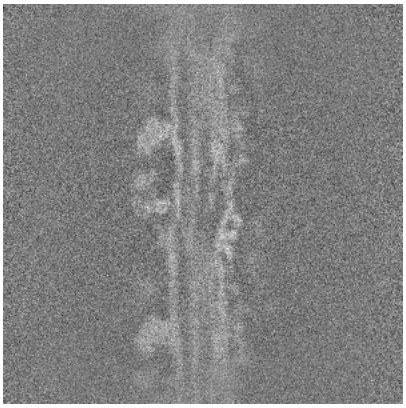
X Index: 400



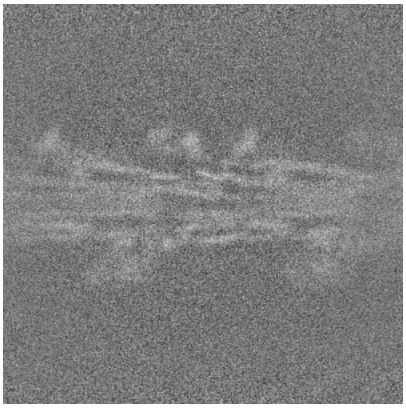
Y Index: 400

Z Index: 400

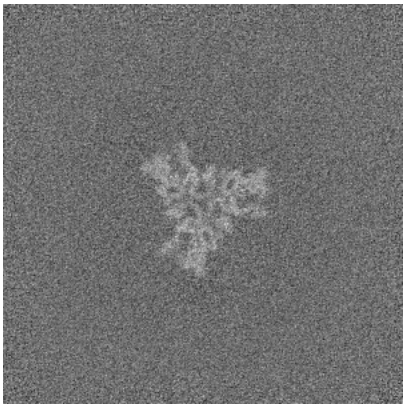
6.2.2 Raw map



X Index: 400



Y Index: 400



Z Index: 400

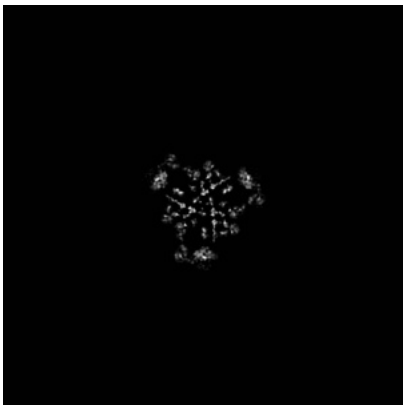
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

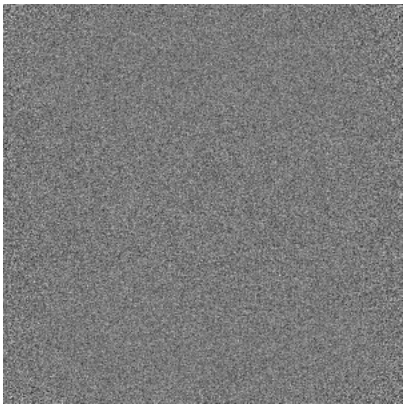
X Index: 368

Y Index: 381

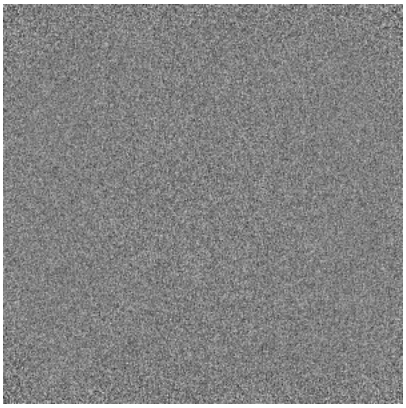


Z Index: 129

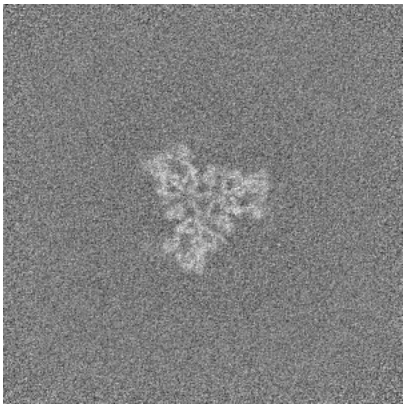
6.3.2 Raw map



X Index: 0



Y Index: 0

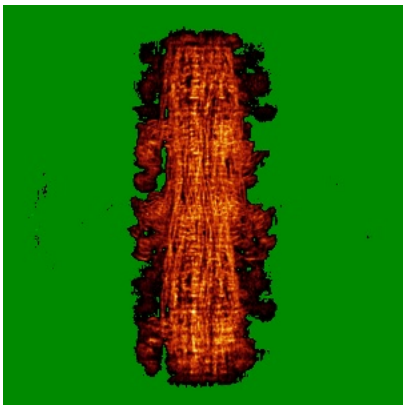


Z Index: 396

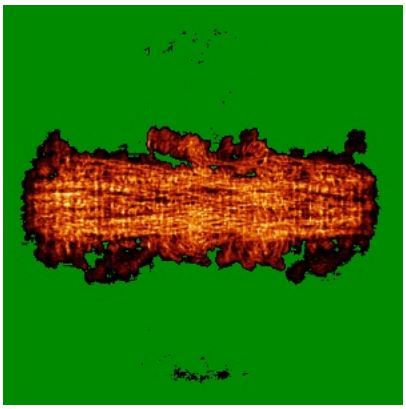
The images above show the largest variance slices of the map in three orthogonal directions.

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

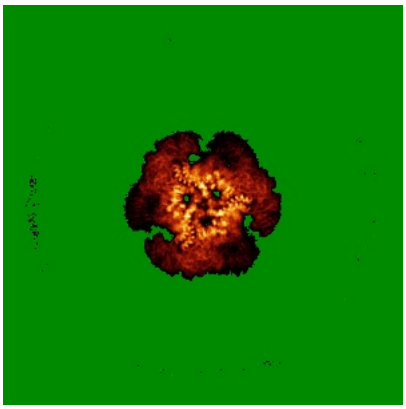
6.4.1 Primary map



X

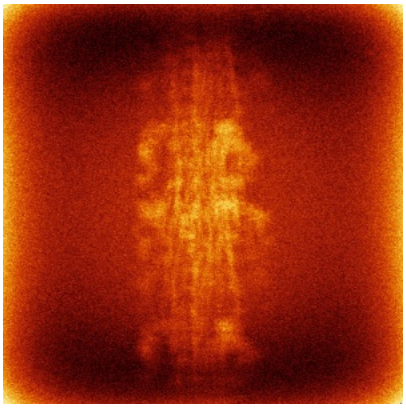


Y

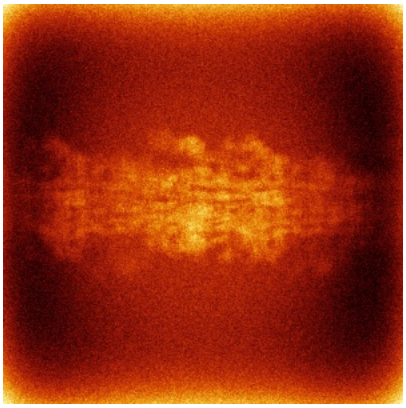


Z

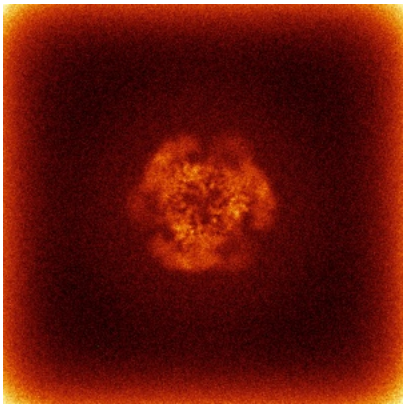
6.4.2 Raw map



X



Y

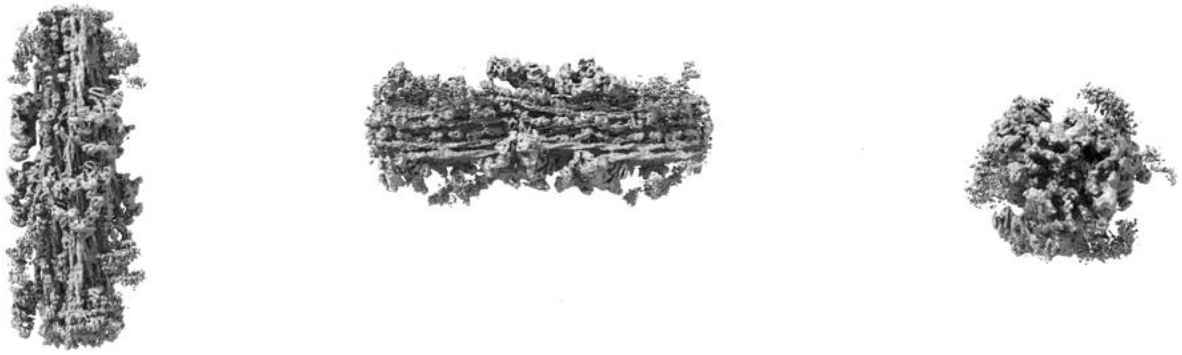


Z

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

6.5 Orthogonal surface views (i)

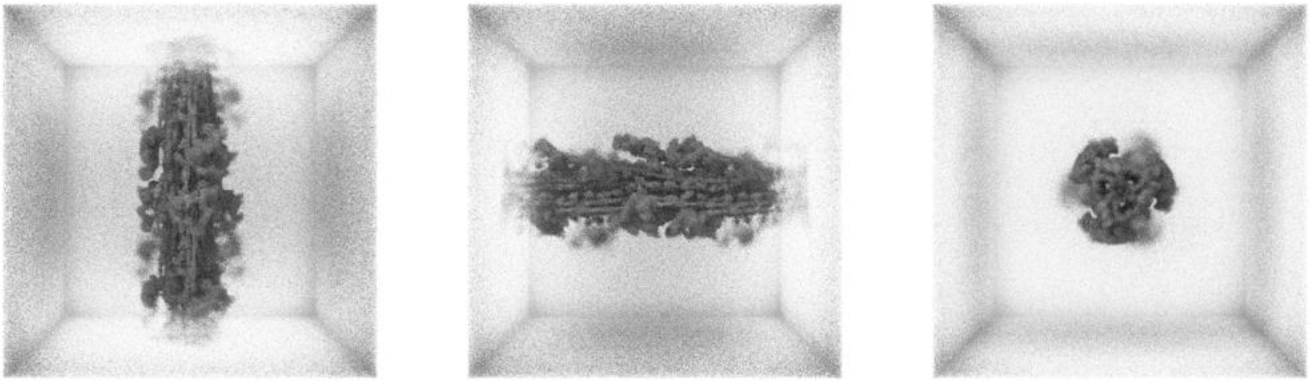
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

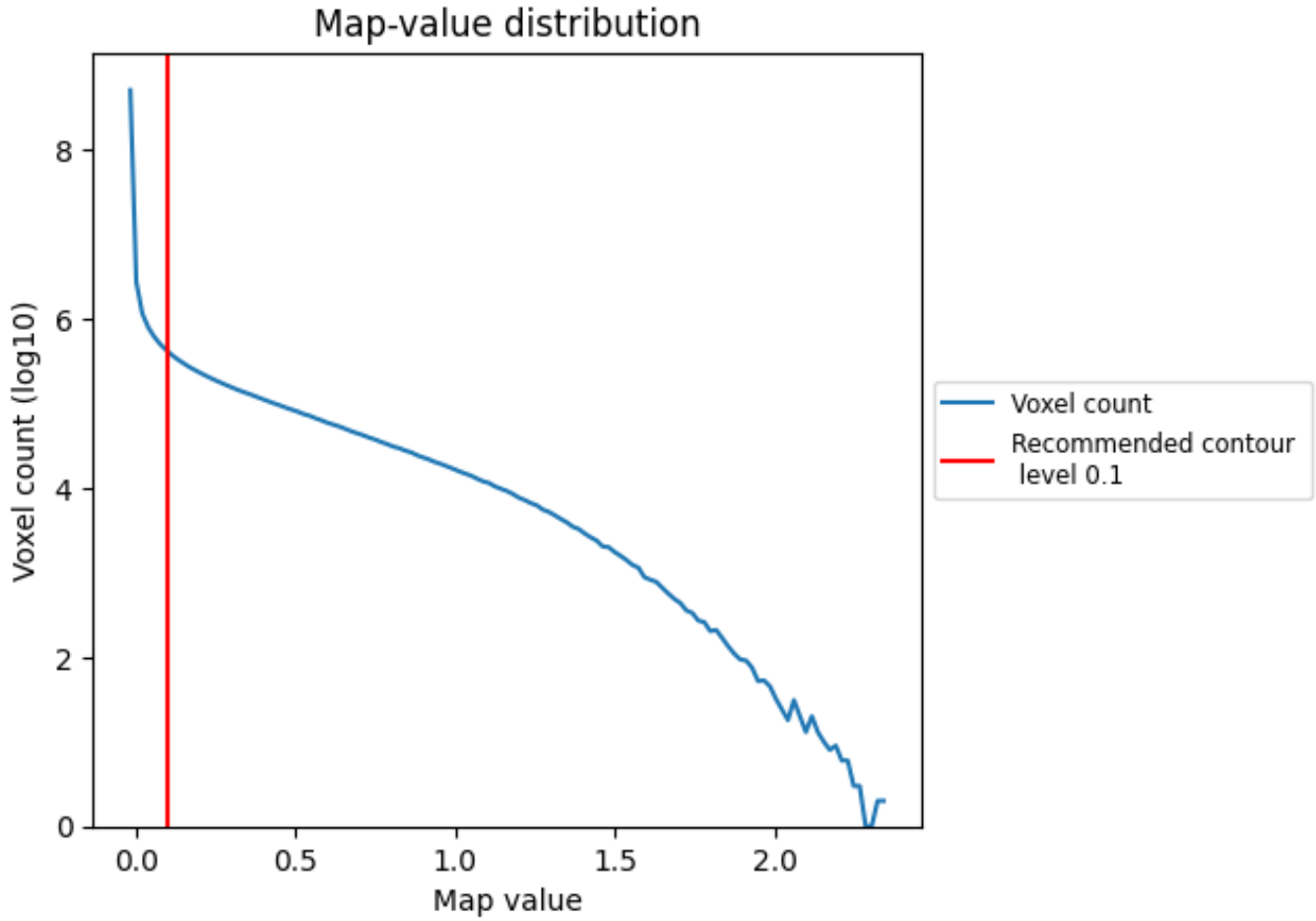
6.6 Mask visualisation (i)

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

7 Map analysis

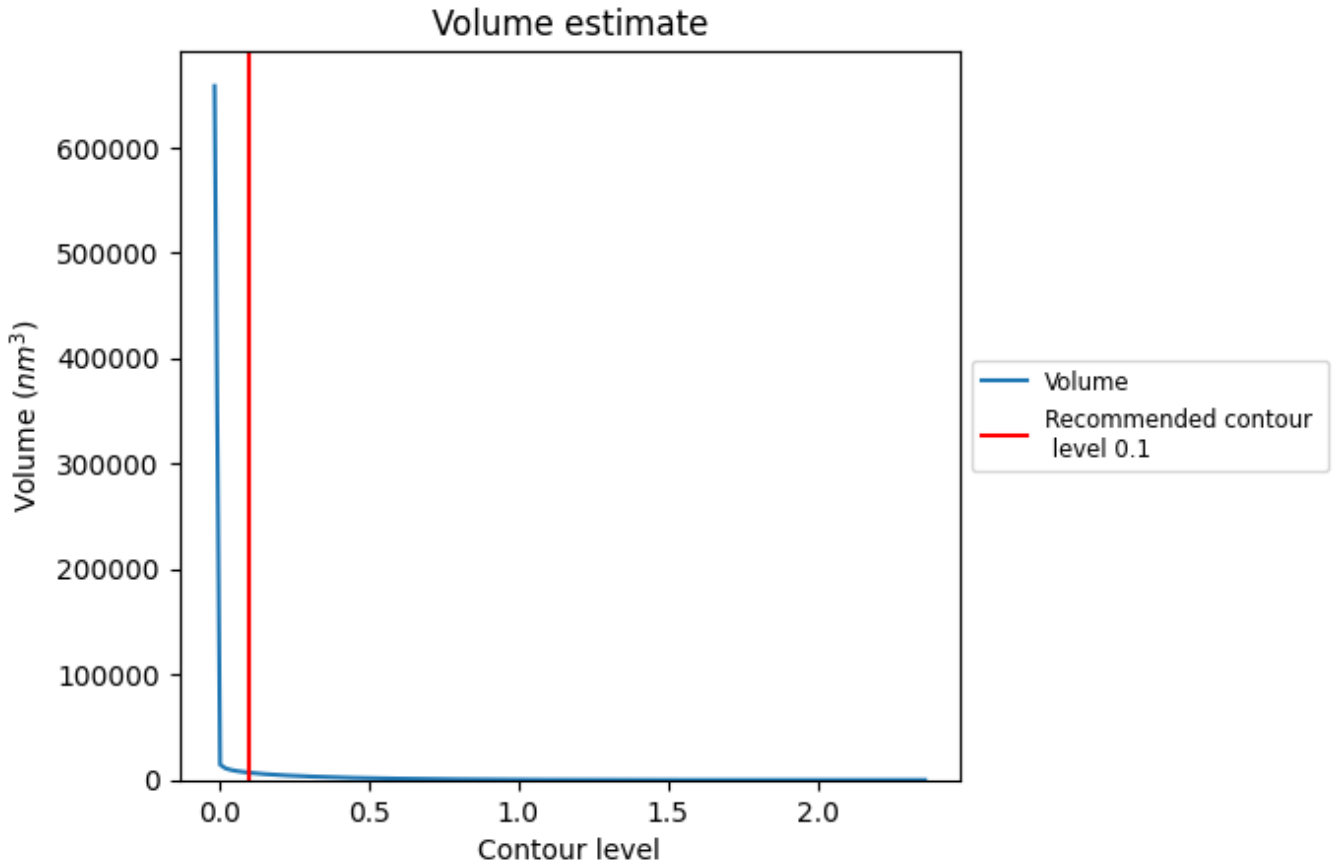
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

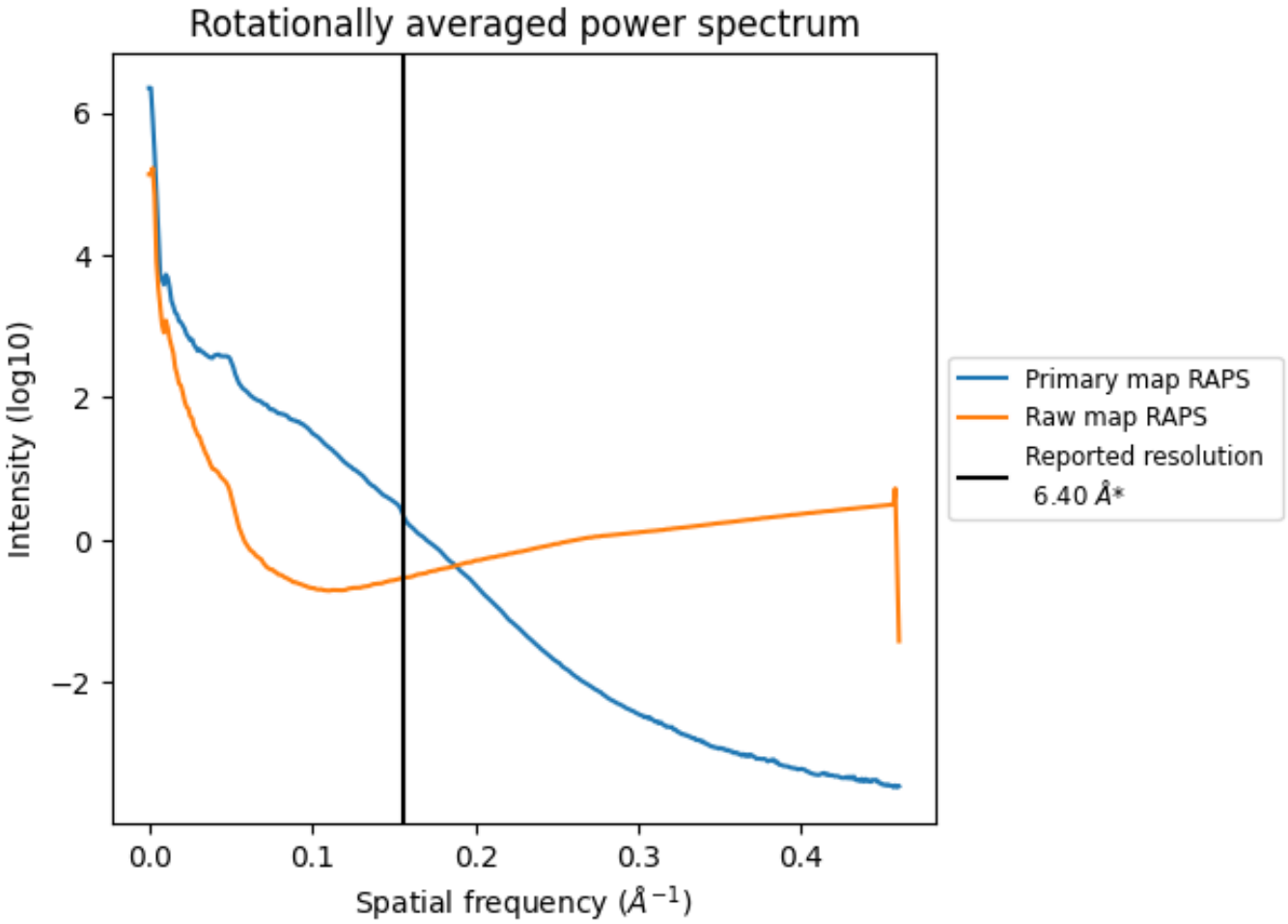
7.2 Volume estimate



The volume at the recommended contour level is 6910 nm^3; this corresponds to an approximate mass of 6242 kDa.

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

7.3 Rotationally averaged power spectrum (i)

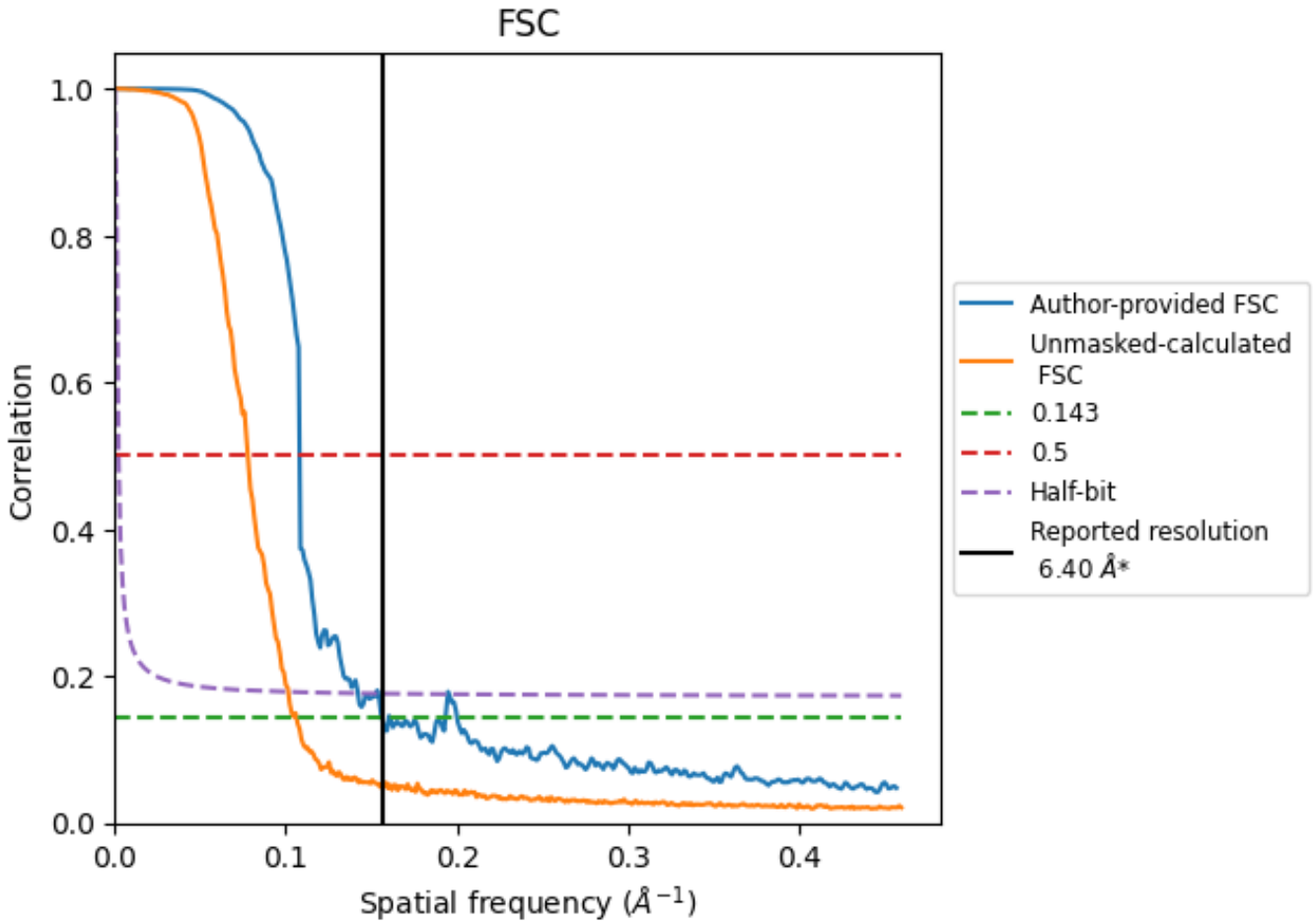


*Reported resolution corresponds to spatial frequency of 0.156 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.156 Å^{-1}

8.2 Resolution estimates (i)

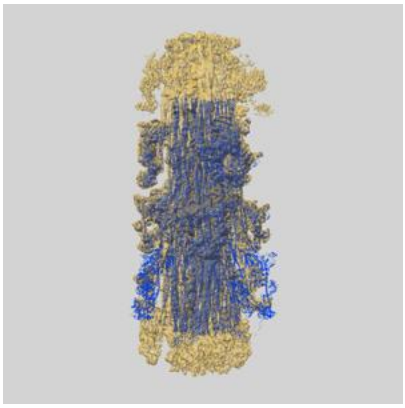
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.40	-	-
Author-provided FSC curve	6.41	9.25	7.03
Unmasked-calculated*	9.41	12.84	9.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.41 differs from the reported value 6.4 by more than 10 %

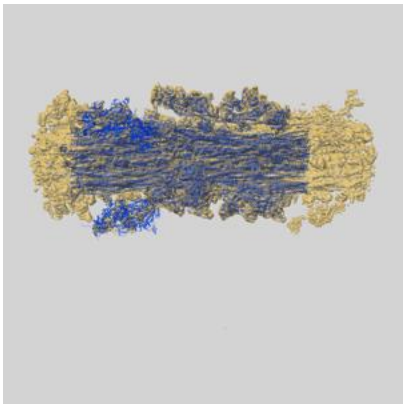
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-29722 and PDB model 8G4L. Per-residue inclusion information can be found in section 3 on page 15.

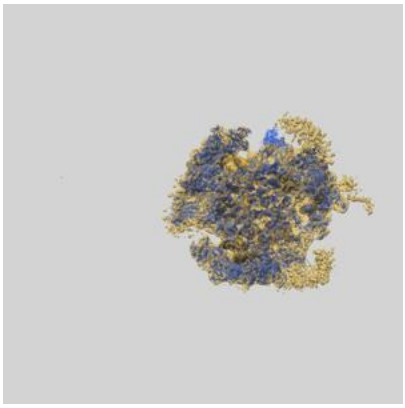
9.1 Map-model overlay



X



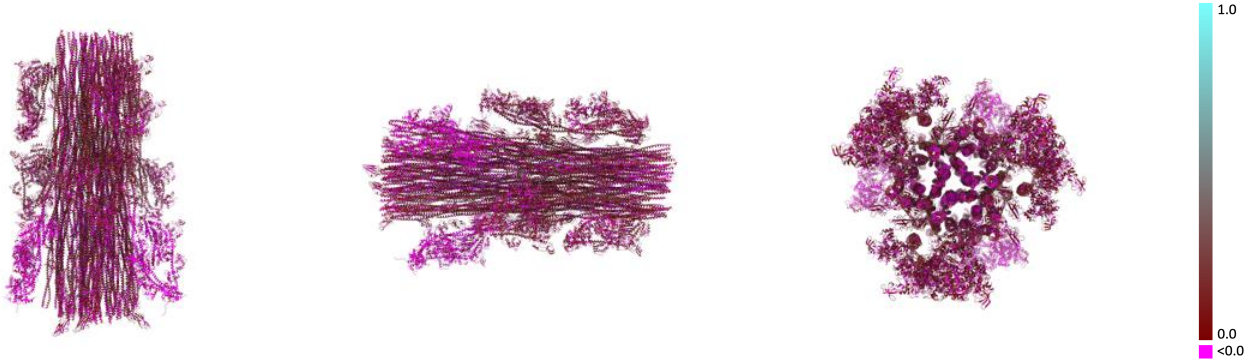
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

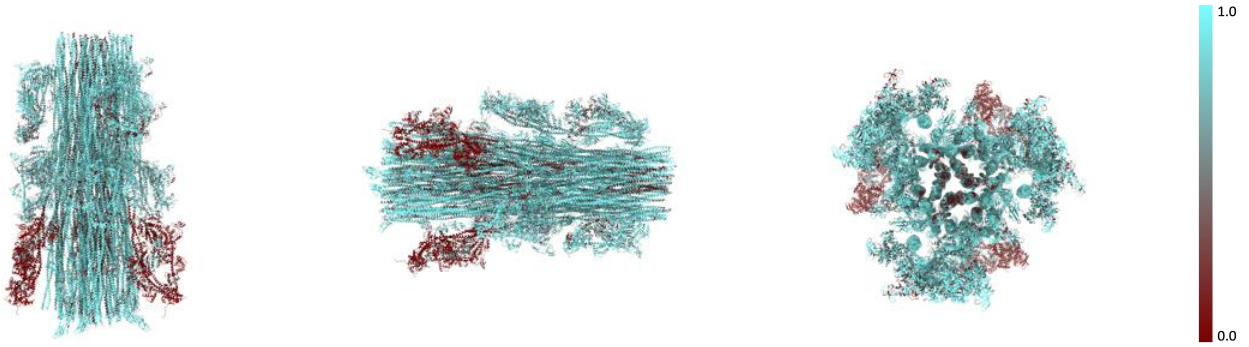
9.2 Q-score mapped to coordinate model



X Y Z

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

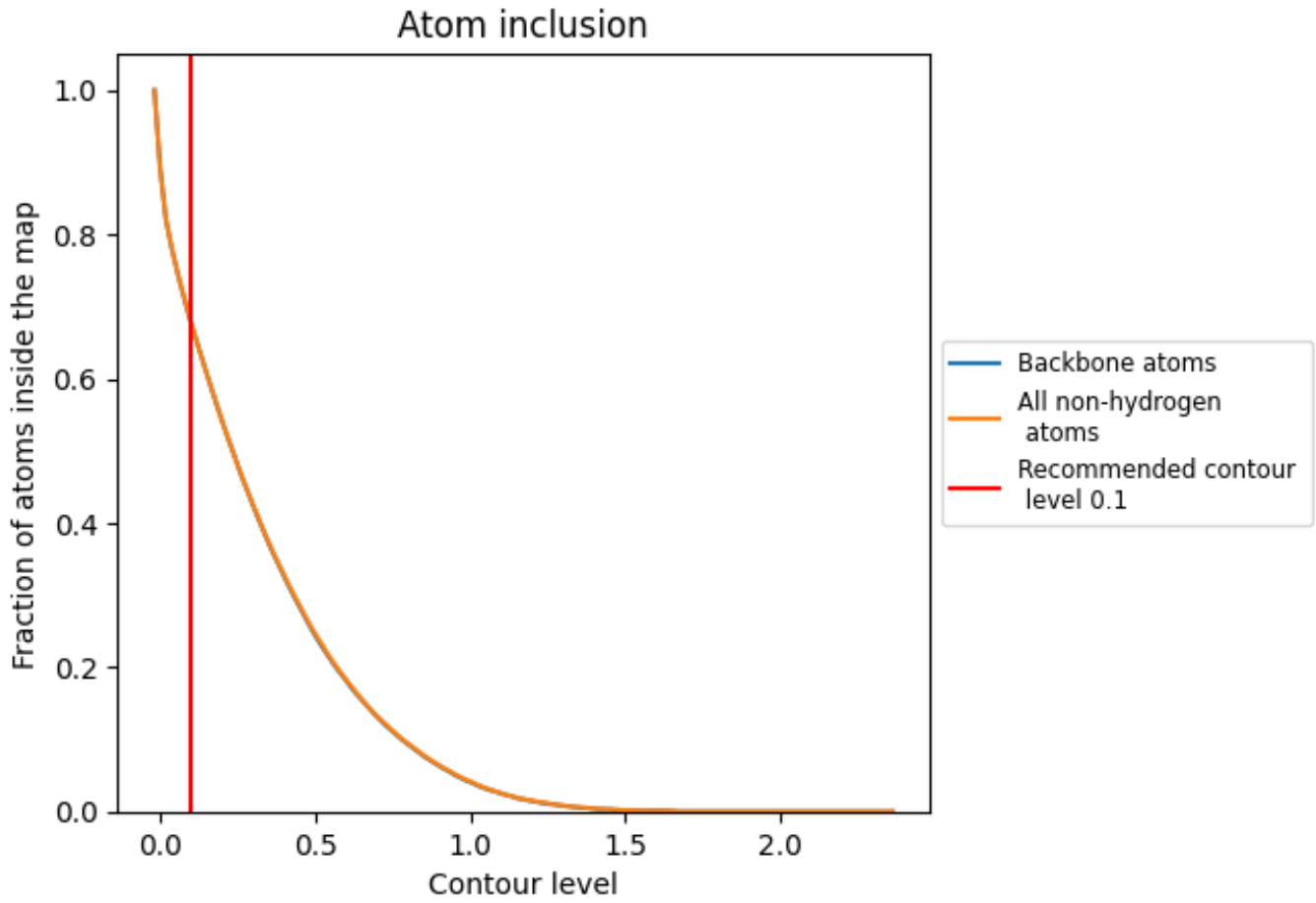
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6810	0.0790
A	0.2650	-0.0250
AA	0.3430	-0.0170
AB	0.2210	-0.0370
AE	0.1360	-0.0560
AF	0.0470	-0.0230
AG	0.8700	0.1190
AH	0.8280	0.1130
AI	0.9140	0.1360
AJ	0.9200	0.1450
AK	0.8660	0.1180
AL	0.8090	0.0960
AM	0.5970	0.0480
AN	0.5480	0.0270
AO	0.8540	0.1170
AP	0.8470	0.1070
AQ	0.8280	0.1020
AR	0.8060	0.1010
AS	0.6000	0.0520
AT	0.6740	0.0720
AU	0.7840	0.0970
AV	0.7500	0.0830
AW	0.6910	0.0580
AX	0.7710	0.0920
AY	0.7880	0.1070
AZ	0.7950	0.1310
B	0.2460	-0.0360
BA	0.2410	-0.0350
BB	0.2940	-0.0170
BE	0.0480	-0.0570
BF	0.1030	-0.0320
BG	0.8580	0.1180
BH	0.8210	0.1100
BI	0.9000	0.1350
BJ	0.9150	0.1440

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Chain	Atom inclusion	Q-score
BK	0.8730	0.1170
BL	0.8090	0.0940
BM	0.6520	0.0510
BN	0.6230	0.0340
BO	0.8630	0.1130
BP	0.8610	0.1140
BQ	0.8260	0.0970
BR	0.8100	0.1020
BS	0.6620	0.0540
BT	0.7050	0.0770
BU	0.7720	0.0900
BV	0.7530	0.0830
BW	0.6920	0.0600
BX	0.7870	0.0940
BY	0.7550	0.1010
BZ	0.7730	0.1250
E	0.0840	-0.0520
F	0.0780	-0.0230
G	0.8420	0.1140
H	0.8320	0.1150
I	0.9020	0.1370
J	0.9260	0.1440
K	0.8740	0.1230
L	0.8080	0.0920
M	0.6410	0.0510
N	0.5670	0.0180
O	0.8680	0.1230
P	0.8520	0.1060
Q	0.8310	0.1010
R	0.8030	0.0990
S	0.5610	0.0520
T	0.6430	0.0730
U	0.8290	0.1000
V	0.7780	0.0870
W	0.7190	0.0660
X	0.7940	0.0950
Y	0.7630	0.1030
Z	0.7840	0.1280
a	0.6540	0.0680
aa	0.6300	0.0580
ab	0.7810	0.1180
ac	0.7780	0.0770

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Chain	Atom inclusion	Q-score
ad	0.7960	0.1070
ae	0.7370	0.0900
af	0.7700	0.1050
ag	0.4740	0.0350
ah	0.8570	0.1060
ai	0.6190	0.0530
aj	0.6560	0.0620
ak	0.5980	0.0130
al	0.6600	0.0560
am	0.7840	0.1050
an	0.9080	0.1470
ao	0.8150	0.1500
aq	0.0860	-0.0700
ar	0.0370	-0.0590
b	0.7620	0.1120
ba	0.6380	0.0550
bb	0.8040	0.1230
bc	0.7290	0.0750
bd	0.7790	0.1030
be	0.7170	0.0870
bf	0.8090	0.1110
bg	0.6160	0.0500
bh	0.8780	0.1170
bi	0.7290	0.0460
bj	0.7150	0.0740
bk	0.6390	0.0250
bl	0.7100	0.0590
bm	0.7780	0.1020
bn	0.9050	0.1440
bo	0.7900	0.1420
bq	0.1160	-0.0660
br	0.1350	-0.0600
c	0.7080	0.0660
d	0.7870	0.1030
e	0.7280	0.0910
f	0.8130	0.1110
g	0.5370	0.0360
h	0.8800	0.1170
i	0.5490	0.0400
j	0.6630	0.0610
k	0.5490	0.0130
l	0.6400	0.0490

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Chain	Atom inclusion	Q-score
m	0.7930	0.1050
n	0.9000	0.1450
o	0.7960	0.1470
q	0.0340	-0.0740
r	0.0680	-0.0630