



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 04:41 AM UTC

PDB ID : 2W4V / pdb_00002w4v
EMDB ID : EMD-1584
Title : Isometrically contracting insect asynchronous flight muscle quick frozen after a quick release step
Authors : Wu, S.; Liu, J.; Reedy, M.C.; Tregear, R.T.; Winkler, H.; Franzini-Armstrong, C.; Sasaki, H.; Lucaveche, C.; Goldman, Y.E.; Reedy, M.K.; Taylor, K.A.
Deposited on : 2008-12-02
Resolution : 35.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

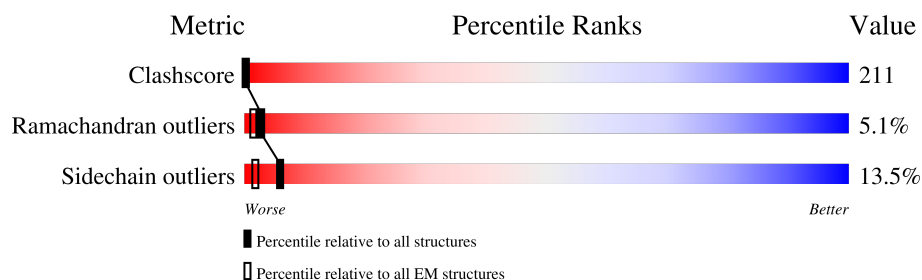
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 35.00 Å.

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



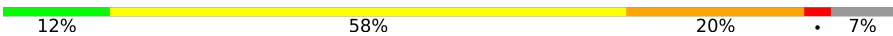
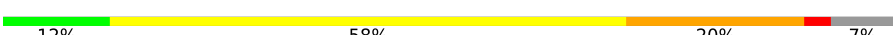
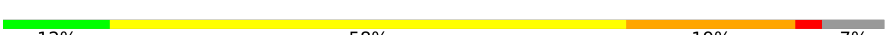
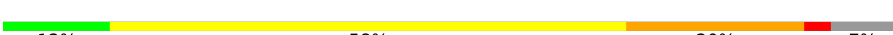
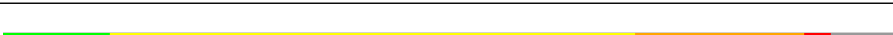
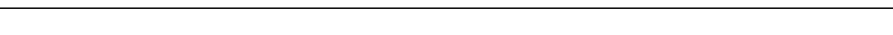
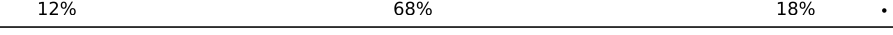
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1-C	831	12% 58% 20% • 7%
1	10-C	831	12% 59% 19% • 7%
1	11-C	831	12% 59% 19% • 7%
1	12-C	831	12% 59% 19% • 7%
1	13-C	831	12% 58% 20% • 7%
1	14-C	831	12% 58% 20% • 7%
1	15-C	831	12% 58% 20% • 7%
1	16-C	831	12% 59% 20% • 7%
1	17-C	831	12% 58% 20% • 7%

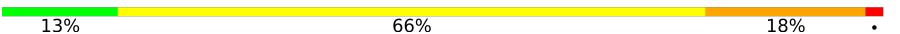
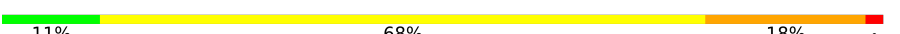
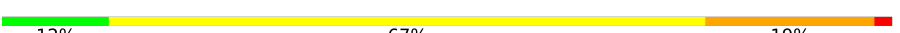
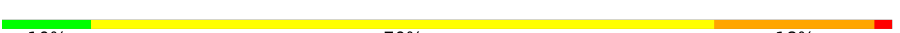
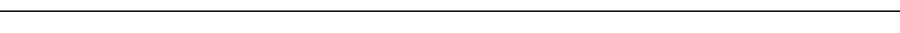
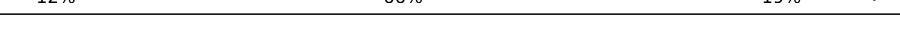
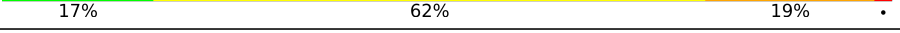
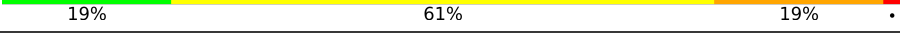
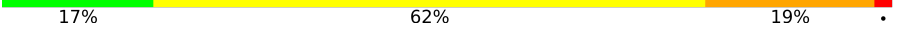
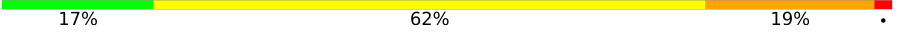
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	18-C	831	
1	19-C	831	
1	2-C	831	
1	20-C	831	
1	21-C	831	
1	22-C	831	
1	23-C	831	
1	24-C	831	
1	25-C	831	
1	26-C	831	
1	27-C	831	
1	3-C	831	
1	4-C	831	
1	5-C	831	
1	6-C	831	
1	7-C	831	
1	8-C	831	
1	9-C	831	
2	1-Y	136	
2	10-Y	136	
2	11-Y	136	
2	12-Y	136	
2	13-Y	136	
2	14-Y	136	
2	15-Y	136	

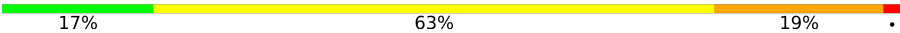
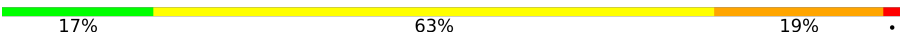
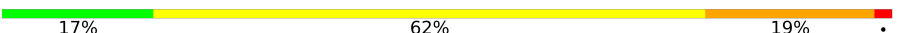
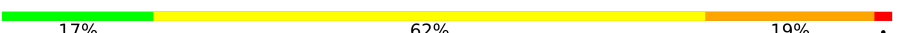
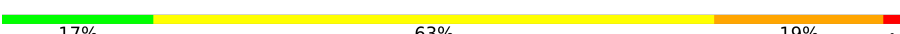
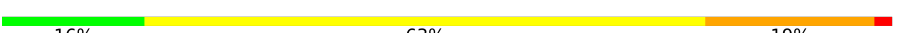
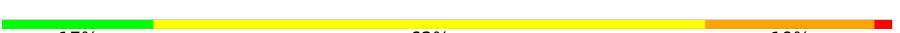
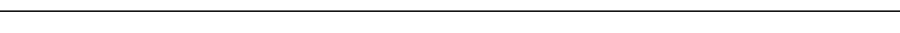
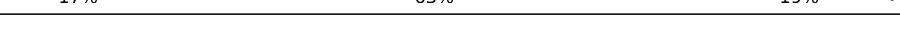
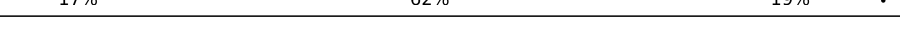
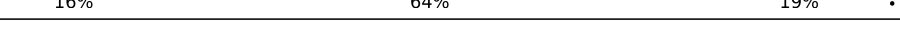
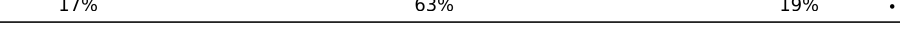
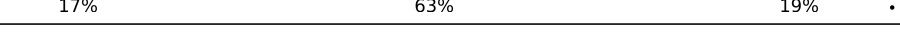
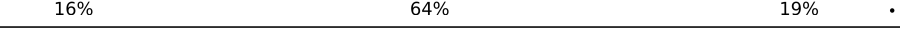
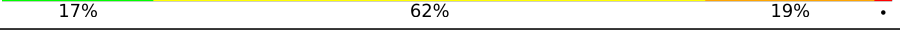
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	16-Y	136	 11% 68% 18% .
2	17-Y	136	 13% 66% 18% .
2	18-Y	136	 11% 68% 18% .
2	19-Y	136	 12% 67% 19% .
2	2-Y	136	 11% 68% 18% .
2	20-Y	136	 12% 67% 19% .
2	21-Y	136	 10% 70% 18% .
2	22-Y	136	 11% 68% 19% .
2	23-Y	136	 10% 69% 18% .
2	24-Y	136	 13% 66% 18% .
2	25-Y	136	 11% 68% 19% .
2	26-Y	136	 12% 67% 19% .
2	27-Y	136	 12% 66% 18% .
2	3-Y	136	 12% 67% 19% .
2	4-Y	136	 12% 66% 19% .
2	5-Y	136	 12% 66% 18% .
2	6-Y	136	 13% 65% 18% .
2	7-Y	136	 11% 68% 19% .
2	8-Y	136	 12% 68% 18% .
2	9-Y	136	 12% 67% 19% .
3	1-Z	151	 17% 62% 19% .
3	10-Z	151	 19% 61% 19% .
3	11-Z	151	 17% 62% 19% .
3	12-Z	151	 17% 62% 19% .
3	13-Z	151	 16% 64% 19% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	14-Z	151	 17% 63% 19% .
3	15-Z	151	 17% 63% 19% .
3	16-Z	151	 17% 62% 19% .
3	17-Z	151	 17% 62% 19% .
3	18-Z	151	 17% 63% 19% .
3	19-Z	151	 16% 63% 19% .
3	2-Z	151	 17% 62% 19% .
3	20-Z	151	 16% 64% 19% .
3	21-Z	151	 15% 65% 19% .
3	22-Z	151	 17% 63% 19% .
3	23-Z	151	 17% 63% 19% .
3	24-Z	151	 16% 63% 19% .
3	25-Z	151	 16% 64% 19% .
3	26-Z	151	 17% 63% 19% .
3	27-Z	151	 17% 63% 19% .
3	3-Z	151	 17% 62% 19% .
3	4-Z	151	 16% 64% 19% .
3	5-Z	151	 17% 63% 19% .
3	6-Z	151	 17% 63% 19% .
3	7-Z	151	 16% 64% 19% .
3	8-Z	151	 17% 62% 19% .
3	9-Z	151	 17% 63% 19% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 229527 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called MYOSIN HEAVY CHAIN, STRIATED MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	2-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	3-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	4-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	5-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	6-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	7-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	8-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	9-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	10-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	11-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	12-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	13-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	14-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	15-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	16-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		
1	17-C	772	Total	C	N	O	S	0	0
			6215	3957	1067	1155	36		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	18-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	19-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	20-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	21-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	22-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	23-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	24-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	25-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	26-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0
1	27-C	772	Total 6215	C 3957	N 1067	O 1155	S 36	0	0

- Molecule 2 is a protein called MYOSIN REGULATORY LIGHT CHAIN, STRIATED AD-
DUCTOR MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	2-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	3-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	4-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	5-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	6-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	7-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	8-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0
2	9-Y	136	Total 1088	C 687	N 173	O 219	S 9	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
2	10-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	11-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	12-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	13-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	14-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	15-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	16-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	17-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	18-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	19-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	20-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	21-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	22-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	23-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	24-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	25-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	26-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	27-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		

- Molecule 3 is a protein called MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	3-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	4-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	5-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	6-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	7-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	8-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	9-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	10-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	11-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	12-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	13-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	14-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	15-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	16-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	17-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	18-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	19-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	20-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	21-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	22-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		

Continued on next page...

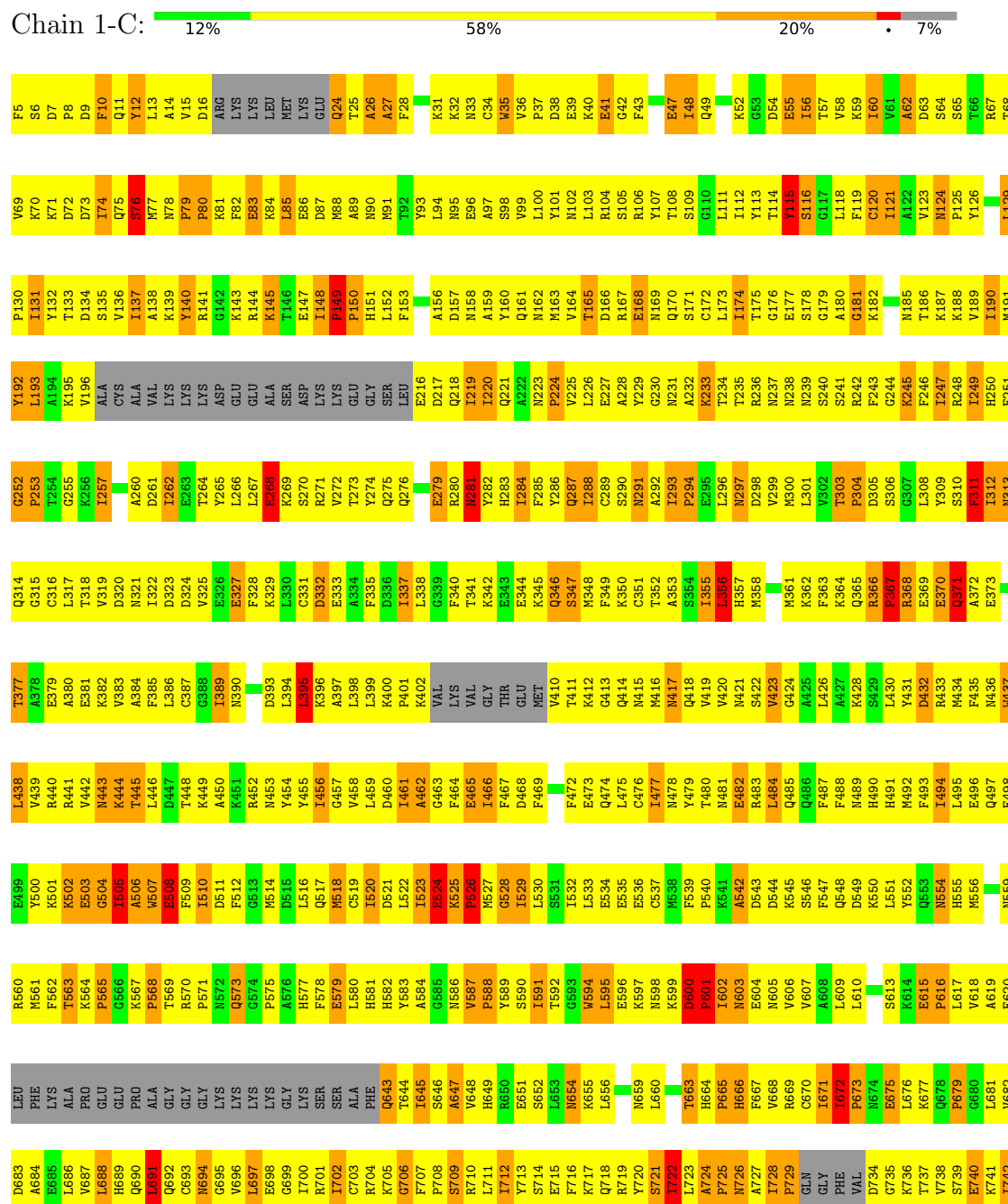
Continued from previous page...

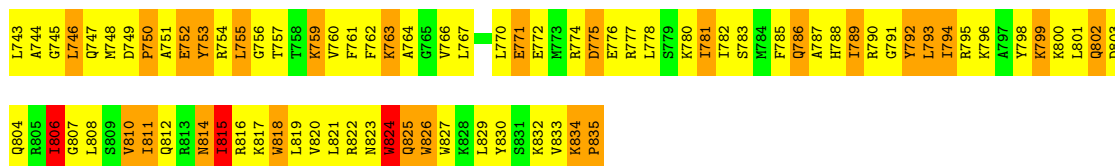
Mol	Chain	Residues	Atoms					AltConf	Trace
3	23-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	24-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	25-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	26-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	27-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

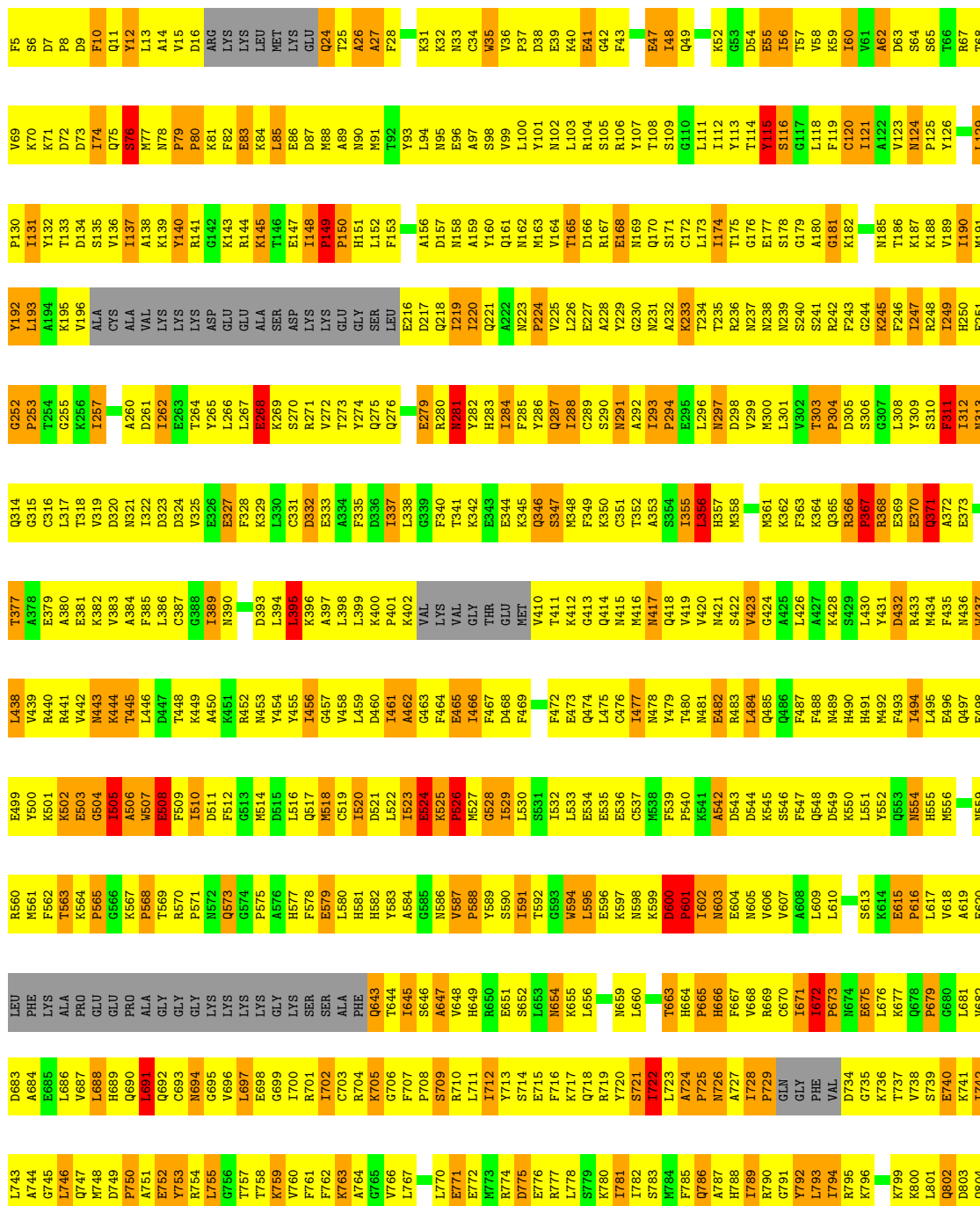
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

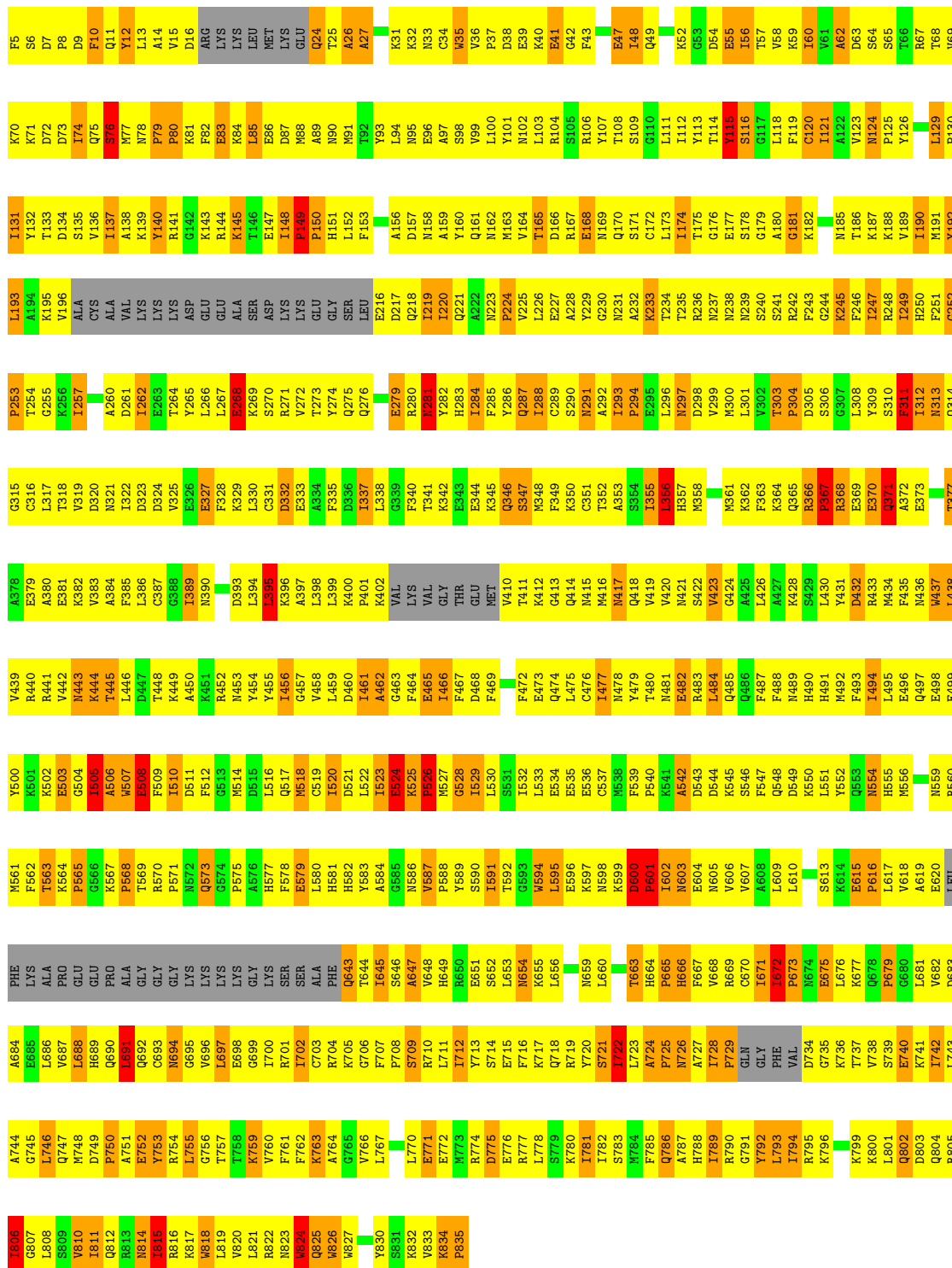




• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

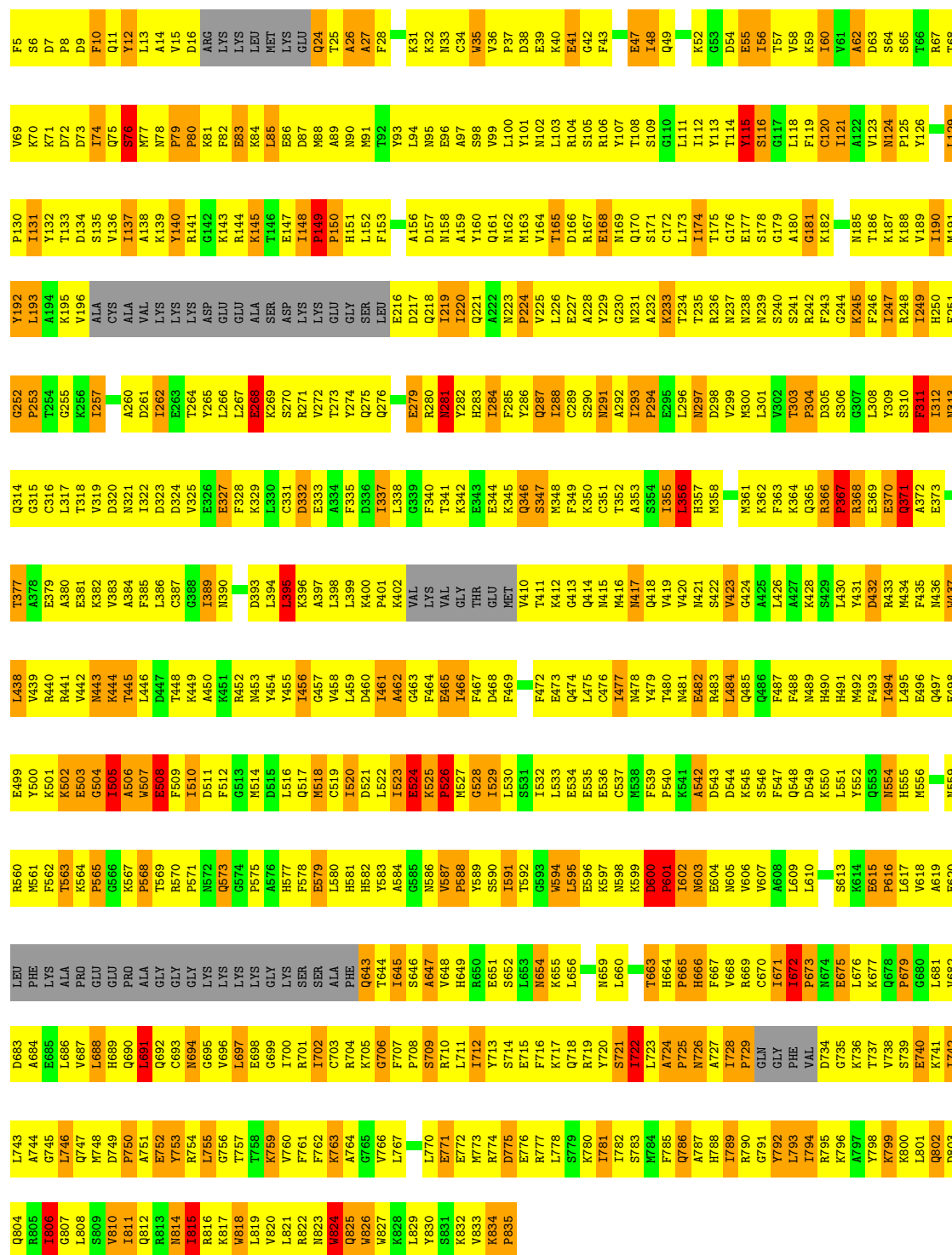
Chain 2-C: 12% 58% 20% 7%





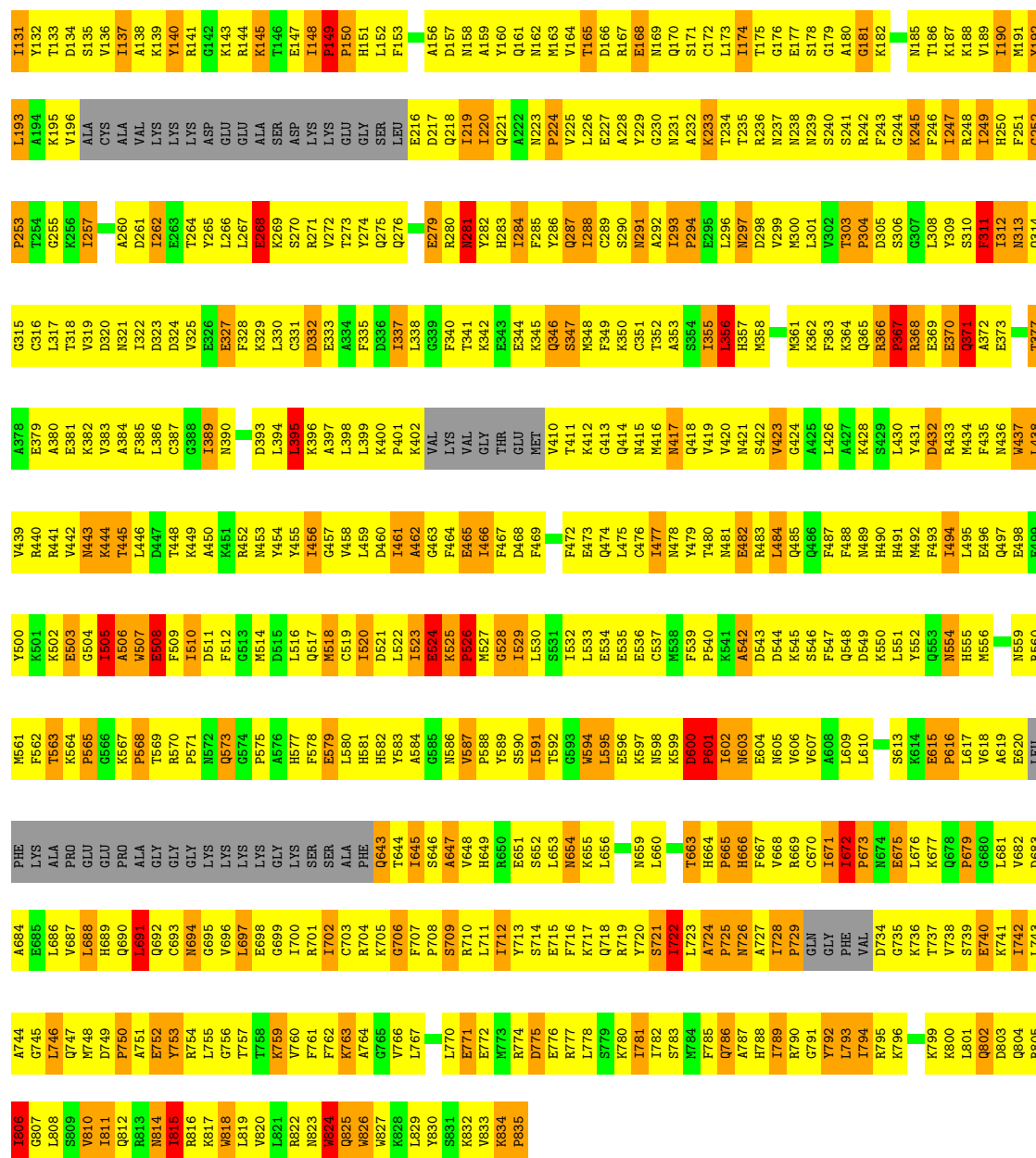
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 4-C: 12% 58% 20% 7%



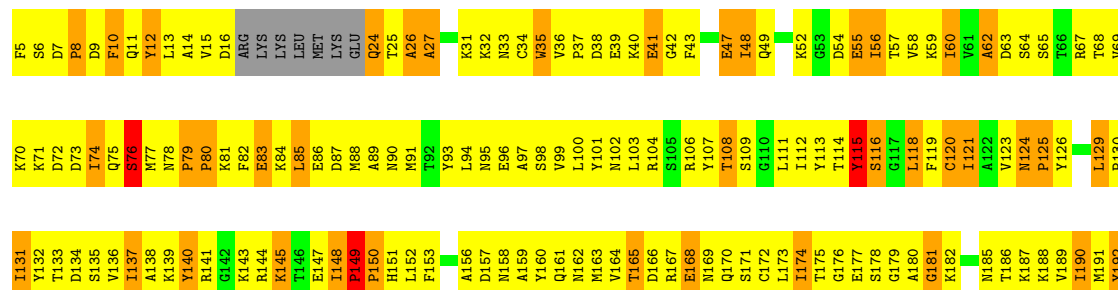
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 5-C: 12% 58% 19% 7%



● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 8-C: 12% 58% 20% 7%

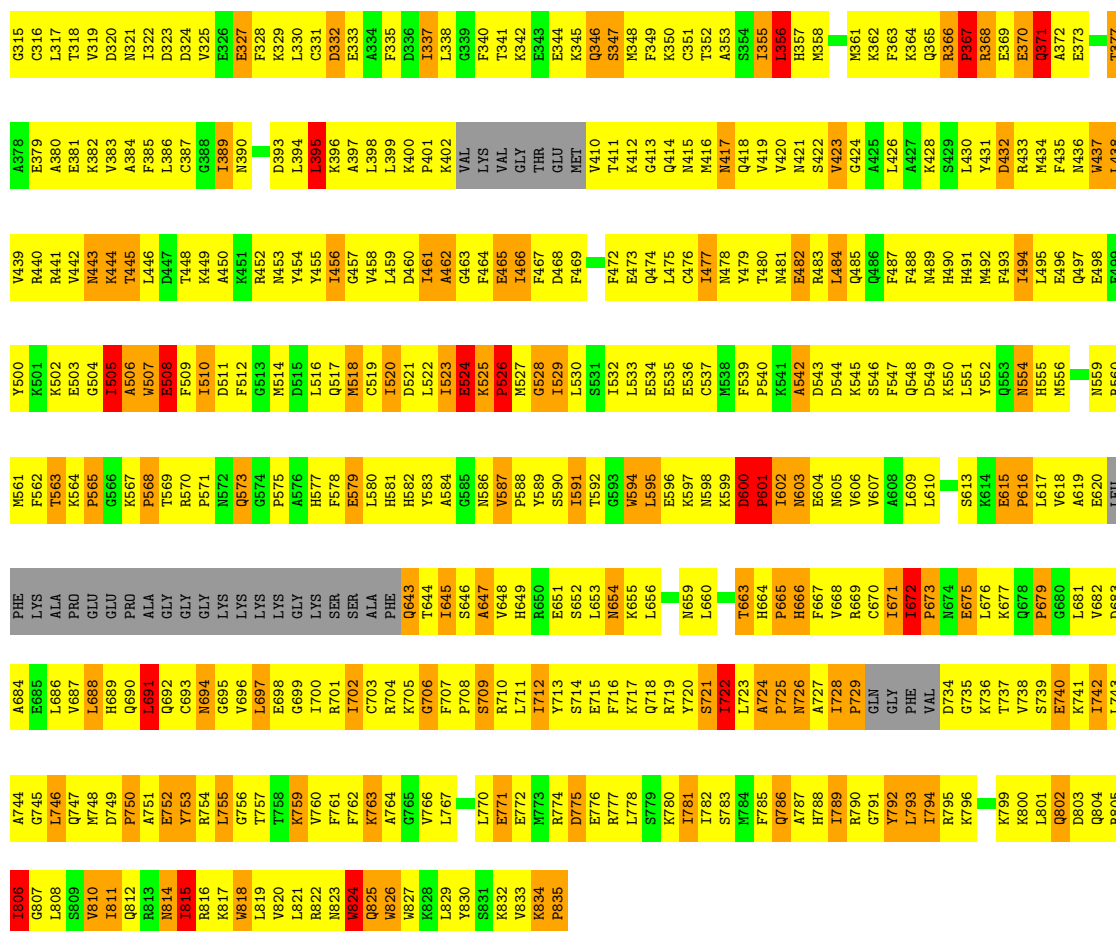


L193	A194	K196	V196	ALA	CYS	ALA	VAL	LYS	LYS	LYS	ASP	GLU	GLU	ALA	SER	ASP	LYS	LYS	GLY	SER	LEU	E216	D217	Q218	I219	I220	Q221	A222	N223	P224	V225	L226	E227	A228	Y229	G230	N231	A232	K233	T234	T235	R236	N237	N238	N239	S240	S241	R242	F243	G244	K245	F246	I247	R248	I249	H250	F251	G252																																																															
P253	T254	G255	K256	I257	A260	D261	L262	T263	T264	Y265	L266	L267	E268	K269	S270	R271	V272	T273	Y274	Q275	Q276	E279	R280	R281	H283	I284	F285	Y286	Q287	C289	K290	N291	A292	I293	P294	L296	N297	D298	V299	M300	L301	F302	T303	K364	Q365	R366	P367	S306	L308	Y309	E370	G371	A372	E373	N312	N313	Q314																																																																
G315	C316	L317	T318	V319	D320	N321	I322	D323	D324	V325	E326	E327	F328	K329	C331	D332	E333	A334	F335	D336	I337	L338	G339	F340	K342	E343	E344	K345	Q346	S347	M348	F349	K350	C351	T352	A353	S354	L355	L356	H357	M358	M361	K362	F363	K364	Q365	R366	P367	L430	Y431	D432	R433	L434	M435	F436	Q437	E438	E439																																																															
A378	E379	A380	E381	K382	V383	A384	F385	L386	C387	G388	I389	N390	R452	N453	L394	K395	L456	G457	L398	L399	K400	P401	K402	VAL	LYS	VAL	G465	F467	D468	F469	F472	E473	Q474	L475	N415	M416	M417	Q418	V419	V420	N421	E482	R483	L484	Q485	Q486	F487	F488	N489	H490	H491	M492	F493	L494	M495	H555	M556	N559	E560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	D600	F539	P601	T602	N603	E604	N605	V606	GLN	C670	L671	PHE	VAL	D734	G735	K736	T737	K800	L801	Q802	D803	T804	R805
V439	R440	R441	V442	N443	K444	T445	L446	D447	L448	K449	A450	K451	R452	N453	L454	Y455	L456	G457	L458	L459	D460	I461	A462	G463	F464	E465	L466	F467	D468	F469	F472	E473	Q474	L475	N415	M416	M417	Q418	V419	V420	N421	E482	R483	L484	Q485	Q486	F487	F488	N489	H490	H491	M492	F493	L494	M495	H555	M556	N559	E560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	D600	F539	P601	T602	N603	E604	N605	V606	GLN	C670	L671	PHE	VAL	D734	G735	K736	T737	K800	L801	Q802	D803	T804	R805
Y500	A501	K502	E503	L504	I505	A506	M507	F509	I510	D511	F512	G513	M514	D515	L516	Q517	M518	C519	I520	D521	L522	I523	E524	K525	P526	M527	G528	I529	L530	S531	I532	L533	E534	E535	E536	C537	P538	F539	P540	K541	A542	D543	D544	K545	S546	F547	L548	D549	K550	L551	Y552	Q553	M554	L555	M556	N559	E560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	D600	F539	P601	T602	N603	E604	N605	V606	GLN	C670	L671	PHE	VAL	D734	G735	K736	T737	K800	L801	Q802	D803	T804	R805		
M561	F562	K563	K564	P565	G566	K567	P568	T569	F570	P571	M572	Q573	G574	A575	L576	H577	F578	E579	L580	H581	H582	Y583	T584	E585	N586	V587	P588	Y589	S590	L591	T592	L593	M594	K595	L596	K597	N598	K599	D600	F601	T602	N603	E604	N605	V606	GLN	C670	L671	PHE	VAL	D734	G735	K736	T737	K800	L801	Q802	D803	T804	R805																																																													
PHE	LYS	ALA	PRO	GLU	GLU	PRO	ALA	GLY	GLY	GLY	LYS	LYS	LYS	GLY	LYS	LYS	SER	SER	ALA	PHE	Q643	T644	I645	S646	A647	V648	H649	R650	E651	S652	L653	M654	K655	L656	N659	L660	T663	H664	P665	H666	F667	V668	R669	GLN	C670	L671	PHE	VAL	D734	G735	K736	T737	K800	L801	Q802	D803	T804	R805																																																															
A684	E685	L686	V687	H688	L689	Q690	L691	E692	C693	N694	G695	V696	L697	E698	G699	T700	R701	I702	C703	R704	K705	Q643	T644	I645	S646	A647	V648	H649	R650	E651	S652	L653	M654	K655	L656	N659	L660	T663	H664	P665	H666	F667	V668	R669	GLN	C670	L671	PHE	VAL	D734	G735	K736	T737	K800	L801	Q802	D803	T804	R805																																																														
A744	G745	L746	Q747	M748	L749	P750	A751	E752	C753	R754	L755	G756	T757	E758	K759	V760	F761	F762	K763	A764	G765	V766	L767	L770	E771	M772	R773	R774	D775	E776	R777	L778	S779	K780	L781	L782	S783	F785	Q786	A787	H788	L789	R790	G791	Y792	L793	L794	R795	K796	K799	L800	L801	Q802	D803	T804	R805																																																																	
L806	G807	L808	S809	V810	I811	Q812	R813	R814	L815	R816	K817	K818	L819	W820	L821	R822	F823	R824	Q825	N826	K827	K828	L829	Y830	S831	R832	Y833	W834	V835	V836	P837	D838	E839	L840	E841	G842	F843	E847	I848	Q849	K853	E854	E855	I856	T857	V858	K859	L860	V861	A862	D863	S864	S865	L866	R867	L868	T869	L870	P871																																																														

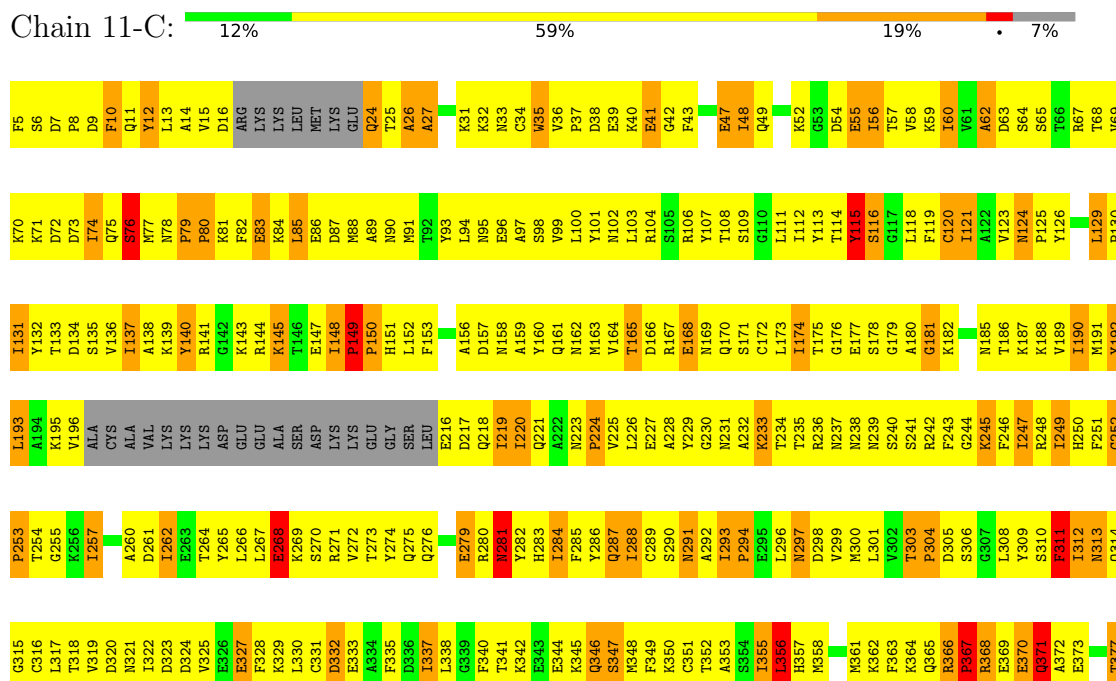
● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

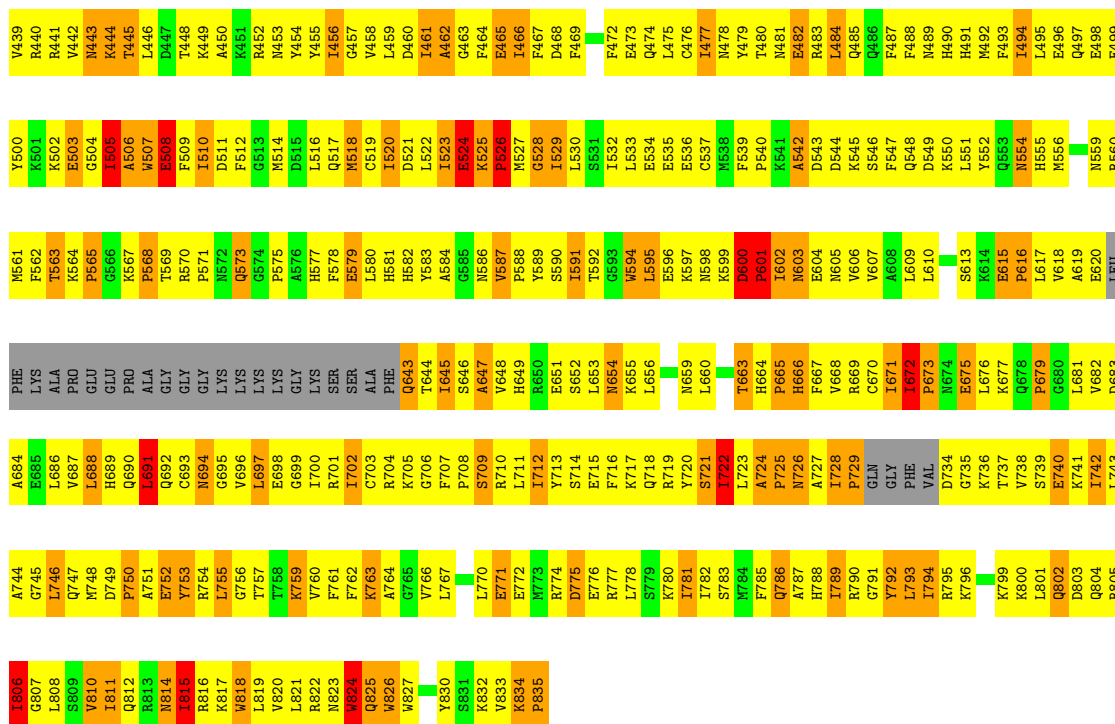
Chain 9-C: 12% 58% 20% 7%

F5	S6	D7	P8	D9	F10	Q11	Y12	L13	A14	V15	D16	A17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32	L33	L34	L35	L36	L37	L38	L39	L40	L41	L42	L43	L44	L45	L46	L47	L48	L49	L50	L51	L52	L53	L54	L55	L56	L57	L58	L59	L60	L61	L62	L63	L64	L65	L66	L67	L68	L69
K70	K71	D72	D73	I74	Q75	S76	M77	R78	P79	P80	K81	F82	E83	K84	L85	E86	D87	M88	A89	H90	L91	T92	Y93	L94	N95	E96	A97	S98	V99	L100	Y101	N102	L103	R104	S105	R106	Y107	T108	I109	G110	L111	I112	Y113	T114	E115	S116	G117	L118	F119	C120	V121	A122	V123	D124	S125	S126	P127	L128	M129	P130				
I131	Y132	T133	D134	S135	V136	I137	A138	L139	L140	R141	G142	K143	R144	K145	T146	E147	L148	P149	P150	H151	L152	F153	E156	D157	N158	I159	A160	Q161	N162	M163	V164	T165	D166	R167	E168	N169	Q170	S171	C172	L173	I174	T175	G176	E177	S178	G179	A180	G181	K182	N185	T186	K187	R188	P189	L190	M191	F192							
L193	A194	K196	V196	ALA	CYS	ALA	VAL	LYS	LYS	LYS	ASP	GLU	GLU	ALA	SER	ASP	LYS	LYS	GLY	SER	LEU	E216	D217	Q218	I219	I220	Q221	A222	N223	P224	V225	L226	E227	A228	Y229	G230	N231	A232	K233	T234	T235	R236	N237	N238	N239	S240	S241	R242	F243	G244	K245	F246	I247	R248	I249	H250	F251	G252						

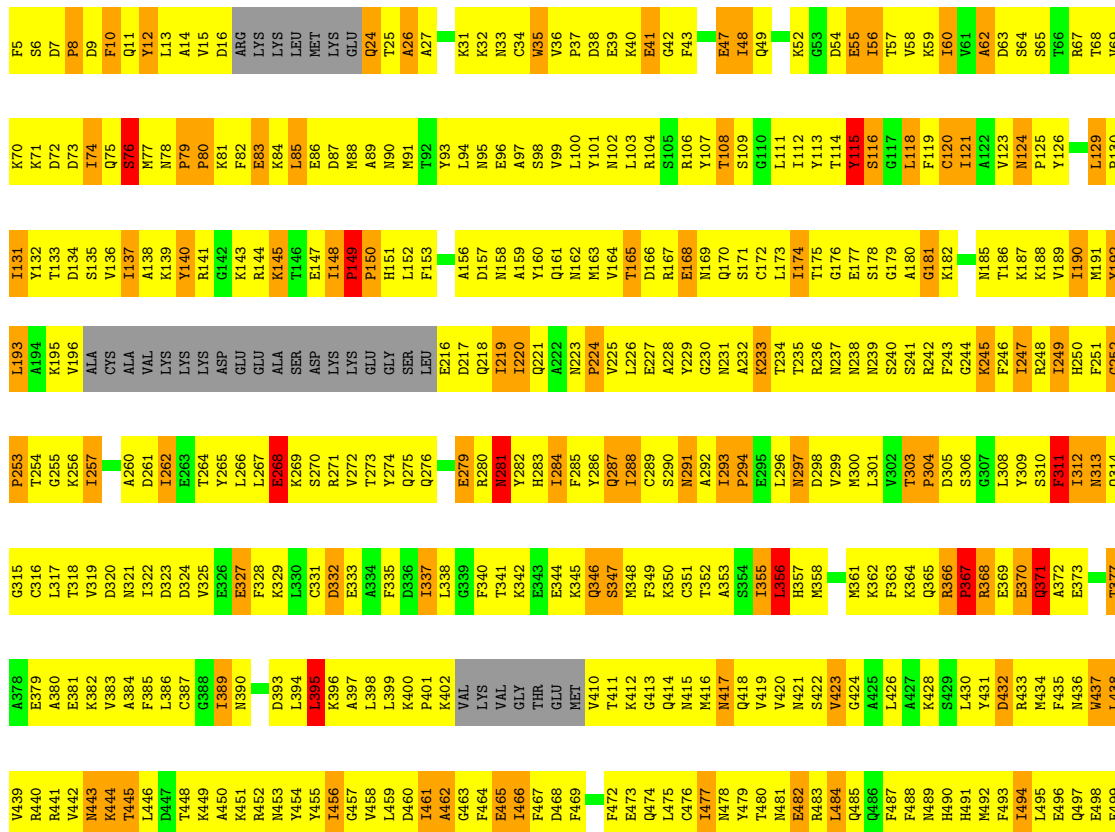
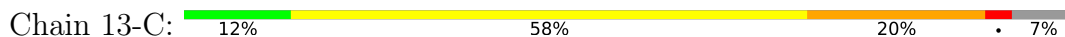


● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE





- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

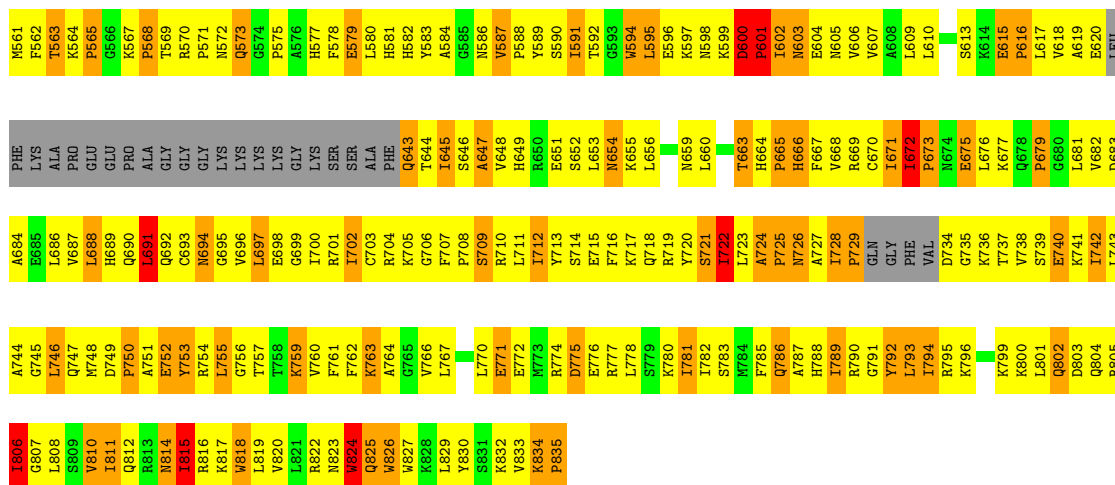


R805	R806	G807	L808	S809	V810	R811	Q812	R813	R814	R815	R816	R817	R818	R819	R820	R821	R822	R823	R824	R825	R826	R827	R828	R829	R830	S831	K832	K833	K834	P835																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
A744	G745	L746	Q747	M748	D749	P750	Q751	F752	Q753	F754	L755	F756	T757	T758	Q759	T760	F761	F762	K763	Q764	G765	F766	L767	G768	T769	T770	T771	T772	T773	T774	T775	T776	T777	L778	T779	T780	T781	T782	T783	T784	T785	T786	T787	T788	T789	T790	T791	T792	T793	T794	T795	T796	T797	T798	T799	K800	L801	Q802	D803	R804																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A684	E685	L686	V687	L688	H689	Q690	L691	Q692	G693	G694	G695	V696	L697	T698	G699	T700	R701	I702	C703	R704	K705	G706	F707	P708	T709	R710	L711	T712	T713	T714	T715	T716	T717	Q718	R719	T720	T721	T722	T723	T724	T725	T726	T727	T728	T729	G730	GLY	PHE	VAL	D734	G735	T736	T737	T738	T739	T740	T741	T742	T743	T744	T745	T746	T747	T748	T749	T750	T751	T752	T753	T754	T755	T756	T757	T758	T759	T760	T761	T762	T763	T764	T765	T766	T767	T768	T769	T770	T771	T772	T773	T774	T775	T776	T777	T778	T779	T780	T781	T782	T783	T784	T785	T786	T787	T788	T789	T790	T791	T792	T793	T794	T795	T796	T797	T798	T799	T800	T801	T802	T803	T804	T805	T806	T807	T808	T809	T810	T811	T812	T813	T814	T815	T816	T817	T818	T819	T820	T821	T822	T823	T824	T825	T826	T827	T828	T829	T830	T831	T832	T833	T834	T835	T836	T837	T838	T839	T840	T841	T842	T843	T844	T845	T846	T847	T848	T849	T850	T851	T852	T853	T854	T855	T856	T857	T858	T859	T860	T861	T862	T863	T864	T865	T866	T867	T868	T869	T870	T871	T872	T873	T874	T875	T876	T877	T878	T879	T880	T881	T882	T883	T884	T885	T886	T887	T888	T889	T890	T891	T892	T893	T894	T895	T896	T897	T898	T899	T900	T901	T902	T903	T904	T905	T906	T907	T908	T909	T910	T911	T912	T913	T914	T915	T916	T917	T918	T919	T920	T921	T922	T923	T924	T925	T926	T927	T928	T929	T930	T931	T932	T933	T934	T935	T936	T937	T938	T939	T940	T941	T942	T943	T944	T945	T946	T947	T948	T949	T950	T951	T952	T953	T954	T955	T956	T957	T958	T959	T960	T961	T962	T963	T964	T965	T966	T967	T968	T969	T970	T971	T972	T973	T974	T975	T976	T977	T978	T979	T980	T981	T982	T983	T984	T985	T986	T987	T988	T989	T990	T991	T992	T993	T994	T995	T996	T997	T998	T999	T1000	T1001	T1002	T1003	T1004	T1005	T1006	T1007	T1008	T1009	T1010	T1011	T1012	T1013	T1014	T1015	T1016	T1017	T1018	T1019	T1020	T1021	T1022	T1023	T1024	T1025	T1026	T1027	T1028	T1029	T1030	T1031	T1032	T1033	T1034	T1035	T1036	T1037	T1038	T1039	T1040	T1041	T1042	T1043	T1044	T1045	T1046	T1047	T1048	T1049	T1050	T1051	T1052	T1053	T1054	T1055	T1056	T1057	T1058	T1059	T1060	T1061	T1062	T1063	T1064	T1065	T1066	T1067	T1068	T1069	T1070	T1071	T1072	T1073	T1074	T1075	T1076	T1077	T1078	T1079	T1080	T1081	T1082	T1083	T1084	T1085	T1086	T1087	T1088	T1089	T1090	T1091	T1092	T1093	T1094	T1095	T1096	T1097	T1098	T1099	T1100	T1101	T1102	T1103	T1104	T1105	T1106	T1107	T1108	T1109	T1110	T1111	T1112	T1113	T1114	T1115	T1116	T1117	T1118	T1119	T1120	T1121	T1122	T1123	T1124	T1125	T1126	T1127	T1128	T1129	T1130	T1131	T1132	T1133	T1134	T1135	T1136	T1137	T1138	T1139	T1140	T1141	T1142	T1143	T1144	T1145	T1146	T1147	T1148	T1149	T1150	T1151	T1152	T1153	T1154	T1155	T1156	T1157	T1158	T1159	T1160	T1161	T1162	T1163	T1164	T1165	T1166	T1167	T1168	T1169	T1170	T1171	T1172	T1173	T1174	T1175	T1176	T1177	T1178	T1179	T1180	T1181	T1182	T1183	T1184	T1185	T1186	T1187	T1188	T1189	T1190	T1191	T1192	T1193	T1194	T1195	T1196	T1197	T1198	T1199	T1200	T1201	T1202	T1203	T1204	T1205	T1206	T1207	T1208	T1209	T1210	T1211	T1212	T1213	T1214	T1215	T1216	T1217	T1218	T1219	T1220	T1221	T1222	T1223	T1224	T1225	T1226	T1227	T1228	T1229	T1230	T1231	T1232	T1233	T1234	T1235	T1236	T1237	T1238	T1239	T1240	T1241	T1242	T1243	T1244	T1245	T1246	T1247	T1248	T1249	T1250	T1251	T1252	T1253	T1254	T1255	T1256	T1257	T1258	T1259	T1260	T1261	T1262	T1263	T1264	T1265	T1266	T1267	T1268	T1269	T1270	T1271	T1272	T1273	T1274	T1275	T1276	T1277	T1278	T1279	T1280	T1281	T1282	T1283	T1284	T1285	T1286	T1287	T1288	T1289	T1290	T1291	T1292	T1293	T1294	T1295	T1296	T1297	T1298	T1299	T1300	T1301	T1302	T1303	T1304	T1305	T1306	T1307	T1308	T1309	T1310	T1311	T1312	T1313	T1314	T1315	T1316	T1317	T1318	T1319	T1320	T1321	T1322	T1323	T1324	T1325	T1326	T1327	T1328	T1329	T1330	T1331	T1332	T1333	T1334	T1335	T1336	T1337	T1338	T1339	T1340	T1341	T1342	T1343	T1344	T1345	T1346	T1347	T1348	T1349	T1350	T1351	T1352	T1353	T1354	T1355	T1356	T1357	T1358	T1359	T1360	T1361	T1362	T1363	T1364	T1365	T1366	T1367	T1368	T1369	T1370	T1371	T1372	T1373	T1374	T1375	T1376	T1377	T1378	T1379	T1380	T1381	T1382	T1383	T1384	T1385	T1386	T1387	T1388	T1389	T1390	T1391	T1392	T1393	T1394	T1395	T1396	T1397	T1398	T1399	T1400	T1401	T1402	T1403	T1404	T1405	T1406	T1407	T1408	T1409	T1410	T1411	T1412	T1413	T1414	T1415	T1416	T1417	T1418	T1419	T1420	T1421	T1422	T1423	T1424	T1425	T1426	T1427	T1428	T1429	T1430	T1431	T1432	T1433	T1434	T1435	T1436	T1437	T1438	T1439	T1440	T1441	T1442	T1443	T1444	T1445	T1446	T1447	T1448	T1449	T1450	T1451	T1452	T1453	T1454	T1455	T1456	T1457	T1458	T1459	T1460	T1461	T1462	T1463	T1464	T1465	T1466	T1467	T1468	T1469	T1470	T1471	T1472	T1473	T1474	T1475	T1476	T1477	T1478	T1479	T1480	T1481	T1482	T1483	T1484	T1485	T1486	T1487	T1488	T1489	T1490	T1491	T1492	T1493	T1494	T1495	T1496	T1497	T1498	T1499	T1500	T1501	T1502	T1503	T1504	T1505	T1506	T1507	T1508	T1509	T1510	T1511	T1512	T1513	T1514	T1515	T1516	T1517	T1518	T1519	T1520	T1521	T1522	T1523	T1524	T1525	T1526	T1527	T1528	T1529	T1530	T1531	T1532	T1533	T1534	T1535	T1536	T1537	T1538	T1539	T1540	T1541	T1542	T1543	T1544	T1545	T1546	T1547	T1548	T1549	T1550	T1551	T1552	T1553	T1554	T1555	T1556	T1557	T1558	T1559	T1560	T1561	T1562	T1563	T1564	T1565	T1566	T1567	T1568	T1569	T1570	T1571	T1572	T1573	T1574	T1575	T1576	T1577	T1578	T1579	T1580	T1581	T1582	T1583	T1584	T1585	T1586	T1587	T1588	T1589	T1590	T1591	T1592	T1593	T1594	T1595	T1596	T1597	T1598	T1599	T1600	T1601	T1602	T1603	T1604	T1605	T1606	T1607	T1608	T1609	T1610	T1611	T1612	T1613	T1614	T1615	T1616	T1617	T1618	T1619	T1620	T1621	T1622	T1623	T1624	T1625	T1626	T1627	T1628	T1629	T1630	T1631	T1632	T1633	T1634	T1635	T1636	T1637	T1638	T1639	T1640	T1641	T1642	T1643	T1644	T1645	T1646	T1647	T1648	T1649	T1650	T1651	T1652	T1653	T1654	T1655	T1656	T1657	T1658	T1659	T1660	T1661	T1662	T1663	T1664	T1665	T1666	T1667	T1668	T1669	T1670	T1671	T1672	T1673	T1674	T1675	T1676	T1677	T1678	T1679	T1680	T1681	T1682	T1683	T1684	T1685	T1686	T1687	T1688	T1689	T1690	T1691	T1692	T1693	T1694	T1695	T1696	T1697	T1698	T1699	T1700	T1701	T1702	T1703	T1704	T1705	T1706	T1707	T1708	T1709	T1710	T1711	T1712	T1713	T1714	T1715	T1716	T1717	T1718	T1719	T1720	T1721	T1722	T1723	T1724	T1725	T1726	T1727	T1728	T1729	T1730	T1731	T1732	T1733	T1734	T1735	T1736	T1737	T1738	T1739	T1740	T1741	T1742	T1743	T1744	T1745	T1746	T1747	T1748	T1749	T1750	T1751	T1752	T1753	T1754	T1755	T1756	T1757	T1758	T1759	T1760	T1761	T1762	T1763	T1764	T1765	T1766	T1767	T1768	T1769	T1770	T1771	T1772	T1773	T1774	T1775	T1776	T1777	T1778	T1779	T1780	T1781	T1782	T1783	T1784	T1785	T1786	T1787	T1788	T1789	T1790	T1791	T1792	T1793	T1794	T1795	T1796	T1797	T1798	T1799	T1800	T1801	T1802	T1803	T1804	T1805	T1806	T1807	T1808	T1809	T1810	T1811	T1812	T1813	T1814	T1815	T1816	T1817	T1818	T1819	T1820	T1821	T1822	T1823	T1824	T1825	T1826	T1827	T1828	T1829	T1830	T1831	T1832	T1833	T1834	T1835	T1836	T1837	T1838	T1839	T1840	T1841	T1842	T1843	T1844	T1845	T1846	T1847	T1848	T1849	T1850	T1851	T1852	T1853	T1854	T1855	T1856	T1857	T1858	T1859	T1860	T1861	T1862	T1863	T1864	T1865	T1866	T1867	T1868	T1869	T1870	T1871	T1872	T1873	T1874	T1875	T1876	T1877	T1878	T1879	T1880	T1881	T1882	T1883	T1884	T1885	T1886	T1887	T1888	T1889	T1890	T1891	T1892	T1893	T1894	T1895	T1896	T1897	T1898	T1899	T1900	T1901	T1902	T1903	T1904	T1905	T1906	T1907	T1908	T1909	T1910	T1911	T1912	T1913	T1914	T1915	T1916	T1917	T1918	T1919	T1920	T1921	T1922	T1923	T1924	T1925	T1926	T1927	T1928	T1929	T1930	T1931	T1932	T1933	T1934	T1935	T1936	T1937	T1938	T1939	T1940	T1941	T1942	T1943	T1944	T1945	T1946	T1947	T1948	T1949	T1950	T1951	T1952	T1953	T1954	T1955	T1956	T1957	T1958	T1959	T1960	T1961	T1962	T1963	T1964	T1965	T1966	T1967	T1968	T1969	T1970	T1971	T1972	T1973	T1974	T1975	T1976	T1977	T1978	T1979	T1980	T1981	T1982	T1983	T1984	T1985	T1986	T1987	T1988	T1989	T1990	T1991	T1992	T1993	T1994	T1995	T1996	T1997	T1998	T1999	T2000	T2001	T2002	T2003	T2004	T2005	T2006	T2007	T2008	T2009	T2010	T20

• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

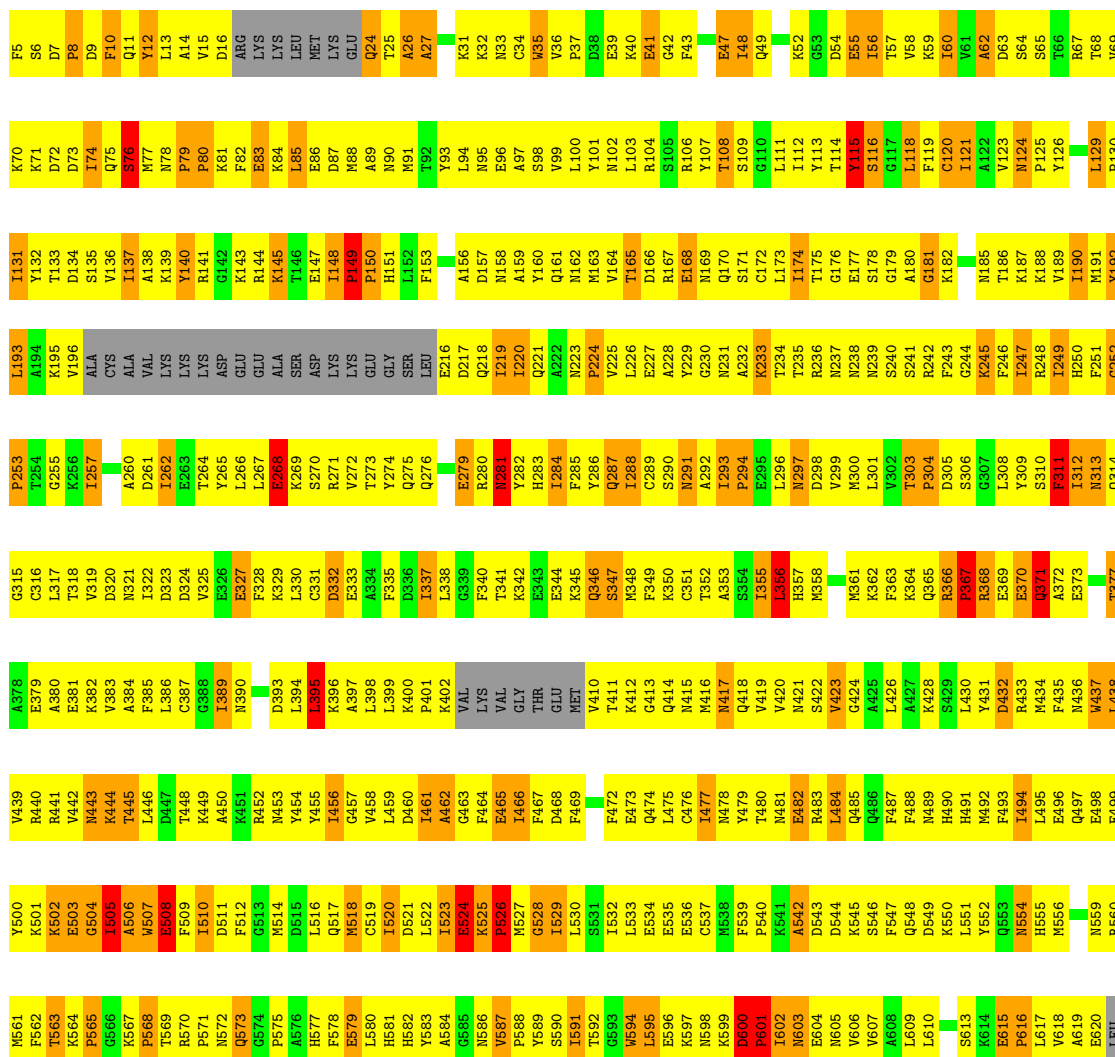
Chain 14-C: 12% 58% 20% 7%

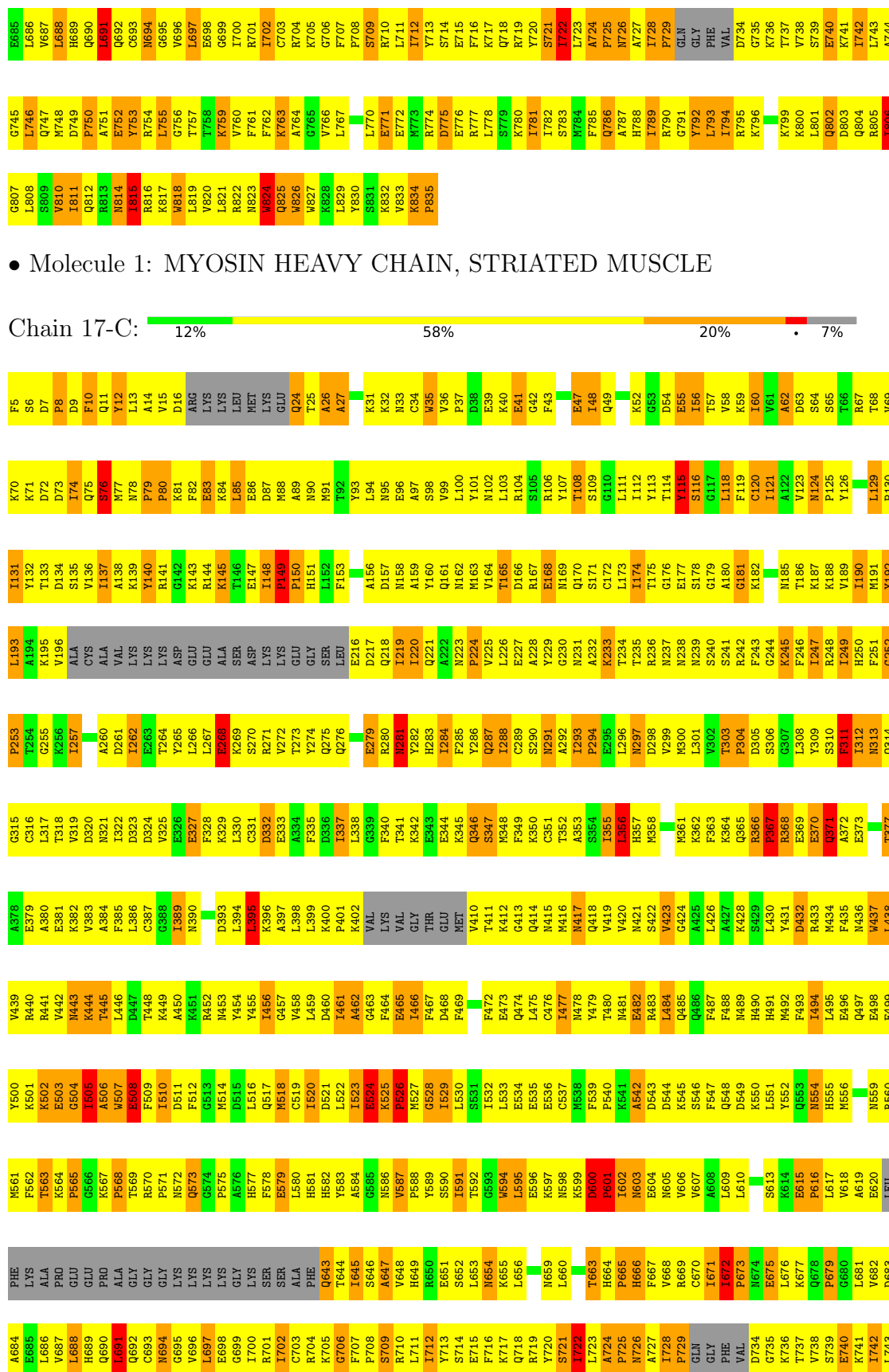
V439	Y500	K501	R440	K502	R441	K503	G504	K443	K444	A506	W507	E508	T447	F509	I510	K449	A510	A450	K389	N390		D393	L394	L395	K396	A397	L398	V458	I520	L459	D460	I461	A462	A463	A464	K525	P465	P526	M527	I466	F467	D468	P469		S531	F472	L532	L533	K473	L534	E534	K474	E535	L475	C476	E536	I477	M478	F539	P540	T480	K481	A542	R482	D543	D544	K485	K546	A486	F487	F488	N489	K550	L551	Y552	M492	F493	Q553	N554	L494	H555	M556	Q497	N559	L560																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
		E378	E379	A380	E381	K382	V383	A384	F385	L386	C387	G388	I389									D393	L394	L395	K396	A397	L398	V458	I520	L459	D460	I461	A462	A463	A464	K525	P465	P526	M527	I466	F467	D468	P469		S531	F472	L532	L533	K473	L534	E534	K474	E535	L475	C476	E536	I477	M478	F539	P540	T480	K481	A542	R482	D543	D544	K485	K546	A486	F487	F488	N489	K550	L551	Y552	M492	F493	Q553	N554	L494	H555	M556	Q497	N559	L560																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																

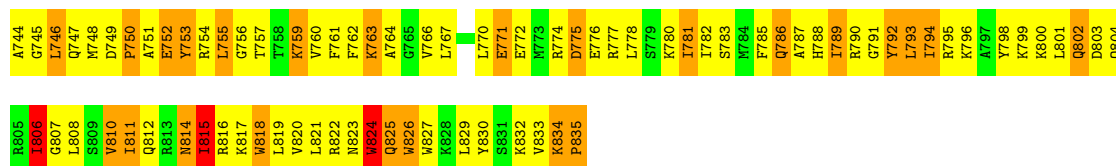


● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 15-C: 12% 58% 20% 7%

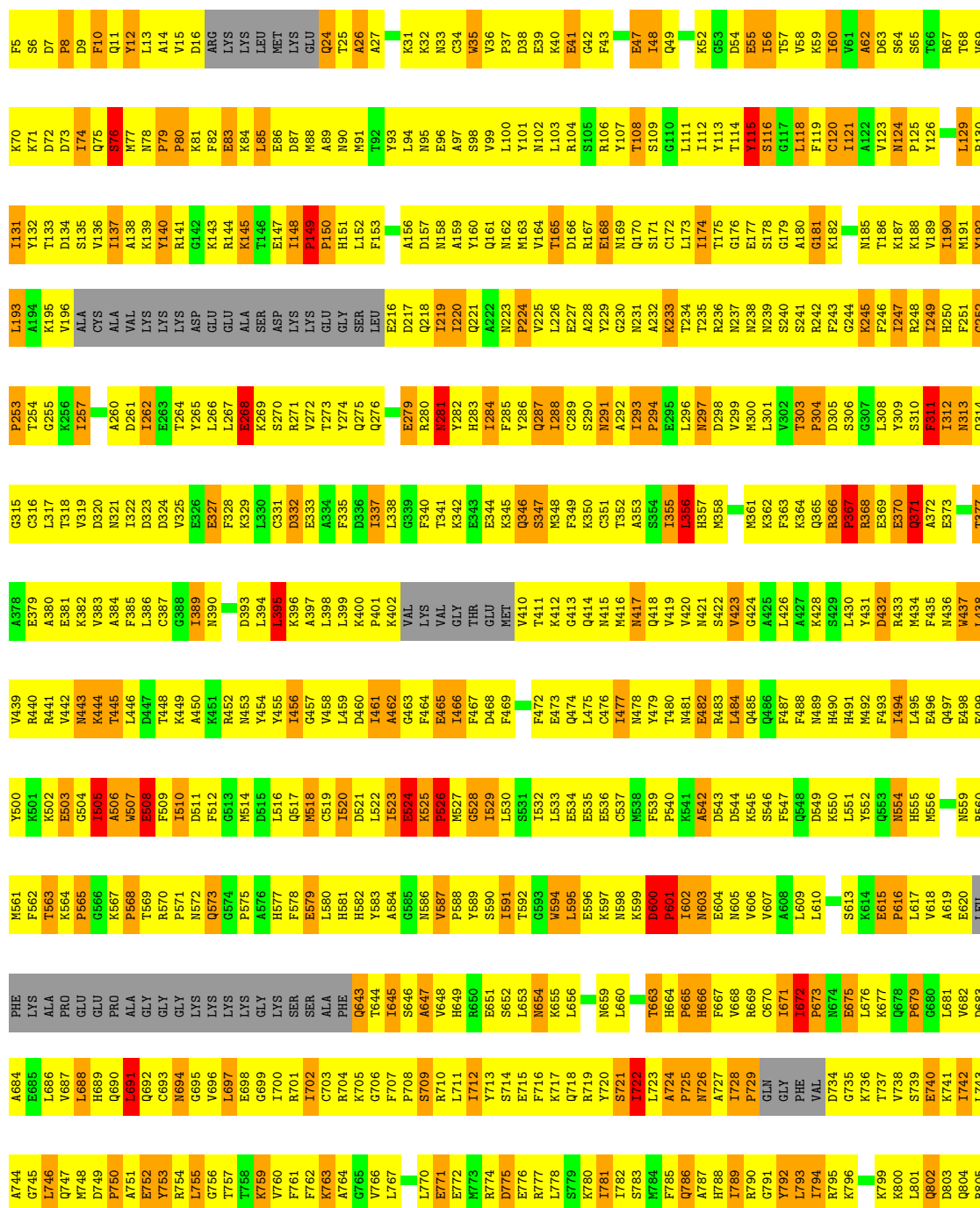






• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

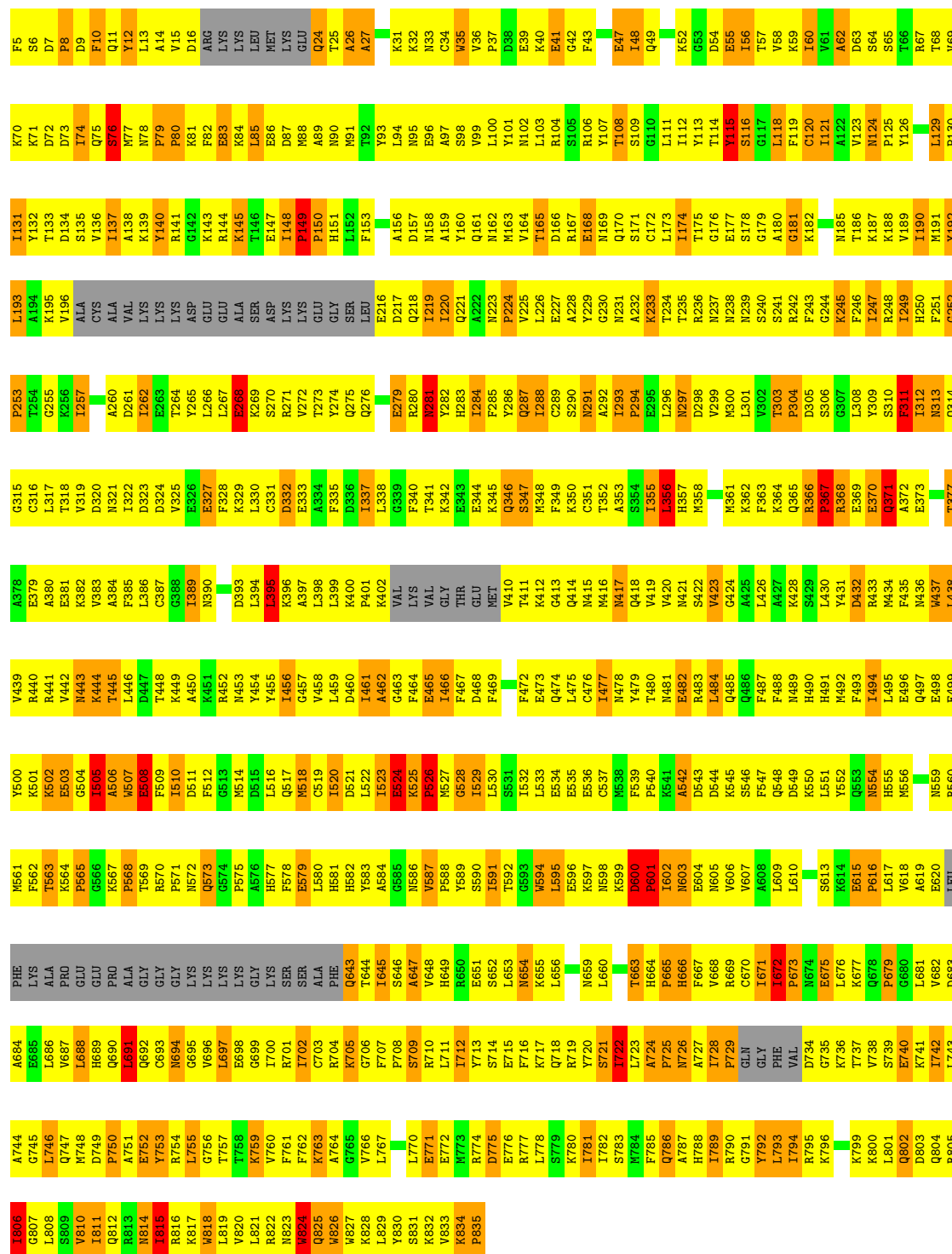
Chain 18-C: 12% 58% 20% 7%



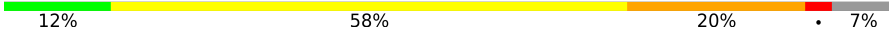


• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 19-C: 12% 58% 20% 7%



• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 20-C:  12% 58% 20% 7%

F5	S6	D7	P8	D9	F10	Q11	Y12	L13	P14	V15	D16	ARG	LYS	LYS	LEU	MET	LYS	GLU	Q24	T25	A26	A27	K31	K32	N33	C34	W35	V36	P37	D38	E39	K40	E41	G42	F43	E47	I48	Q49	K52	G53	D54	E55	I56	T57	V58	K59	I60	V61	A62	D63	S64	S65	T66	A67	T68	V69					
K70	K71	D72	D73	I74	Q75	S76	K77	M78	P79	P80	K81	F82	E83	K84	L85	E86	D87	M88	A89	N90	M91	L152	T92	Y93	L94	N95	E96	A97	S98	V99	L100	Y101	N102	L103	R104	S105	Y106	T107	T108	S109	G110	L111	I112	Y113	T114	Y115	S116	G117	L118	F119	C120	I121	A122	V123	N124	P125	V126	L129	T68	P130	
I131	Y132	D133	D134	V135	V136	I137	A138	L139	Y140	R141	L142	K143	R144	K145	T146	A147	I148	L149	P150	H151	L152	F153	E216	A156	D157	N158	A159	V160	Q161	N162	M163	V164	T165	D166	E227	A228	Y229	E168	N169	N231	A232	K233	T234	T235	R236	N237	N238	S240	S241	R242	F243	G244	N185	T245	I247	K187	P188	P189	I190	M191	Y192
L193	A194	K195	V196	ALA	CYS	ALA	VAL	LYS	LYS	LYS	ASP	GLU	GLU	ALA	SER	ASP	LYS	LYS	GLY	GLY	SER	LEU	D217	Q218	I219	L220	Q221	Q161	N223	P224	V225	L226	E227	A228	Y229	E229	G230	N231	A232	K233	T234	T235	R236	N237	N238	S240	S241	R242	F243	G244	N185	T245	I247	K187	P188	P189	I190	M191	Y192		
P253	T254	G255	K256	I257	K260	D261	T262	E263	T264	V265	L266	L267	E268	K269	S270	R271	V272	T273	Y274	Q275	Q276	E279	R280	N281	Y282	H283	L284	F285	T286	Q287	L288	C289	S290	N291	A292	L293	P294	E295	L296	D297	V298	N300	L301	V302	T303	P304	D305	S306	G307	L308	Y309	S310	P311	I312	F313	Q314					
G315	C316	L317	T318	V319	K320	N321	L322	D323	K324	V325	E326	F327	F328	K329	L330	C331	D332	E333	K334	F335	L337	K338	G339	F340	K341	K342	E343	E344	L345	Q346	S347	K348	F349	K350	C351	T352	A353	S354	L355	L356	H357	K358	K361	F362	K363	Q364	Q365	R366	P367	L368	Y369	A370	A371	A372	E373	T377					
A378	E379	A380	E381	K382	V383	A384	F385	L386	C387	G388	L389	N390	D393	L394	R395	L396	L397	L398	L399	K400	P401	K402	VAL	L410	T411	K412	Q413	Q414	Q415	N416	N417	Q418	V419	V420	N421	S422	V423	G424	L425	L426	A427	K428	S429	L430	Y431	D432	R433	L434	M435	F436	N437	L438									
V439	R440	R441	V442	N443	K444	T445	L446	D447	K448	K449	A450	V451	R452	M453	V454	L455	L456	G457	V458	D460	L461	A462	G463	F464	E465	L466	F467	E468	L469	F472	Q473	Q474	L475	C476	L477	M478	Y479	T480	N481	E482	R483	L484	Q485	F486	F487	M488	N489	H490	H491	Y492	M493	L494	L495	M496	Q497	E498	E499				
Y500	K501	K502	E503	G504	I505	A506	M507	E508	F509	L510	D511	F512	G513	M514	D515	L516	Q517	M518	C519	L520	D521	L522	E523	K524	E525	P526	G527	G528	L529	L530	S531	L532	L533	E534	E535	E536	E537	M538	F539	P540	K541	A542	N543	D544	K545	S546	F547	Q548	D549	K550	L551	Y552	Q553	N554	H555	M556	N559	R560			
M561	F562	T563	K564	P565	G566	K567	P568	R569	A570	P571	N572	G573	G574	P575	A576	H577	F578	E579	L580	H581	H582	Y583	A584	G585	N586	V587	P588	Y589	S590	L591	T592	G593	M594	L595	E596	K597	N598	K599	D600	R601	I602	N603	E604	N605	V606	V607	L608	L609	L610	S613	K614	E615	P616	L617	V618	A619	E620	LEU			
PHE	LYS	ALA	PRO	GLU	GLU	PRO	ALA	GLY	GLY	GLY	LYS	LYS	LYS	LYS	GLY	LYS	SER	SER	ALA	PHE	Q643	T644	I645	G646	A647	V648	H649	R650	G651	L652	L653	N654	K655	L656	N659	L660	T663	H664	P665	H666	F667	V668	R669	GLN	GLY	I671	I672	P673	M674	E675	L676	K677	V678	Q679	L680	G681	L682	L683			
A684	E685	L686	V687	L688	H689	Q690	L691	Q692	C693	N694	G695	V696	L697	E698	K699	I700	R701	I702	C703	R704	K705	G706	F707	P708	S709	L710	L711	L712	Y713	Y714	E715	F716	K717	Q718	R719	Y720	S721	T722	L723	A724	P725	P726	N727	I728	P729	GLN	GLY	PHE	VAL	D734	G735	K736	T737	V738	S739	L740	E741	Q742	L743		
A744	G745	L746	Q747	M748	D749	P750	A751	E752	Y753	R754	L755	G756	T757	F758	K759	V760	F761	F762	K763	A764	G765	V766	L767	L770	E771	E772	M773	R774	D775	E776	F777	L778	S779	K780	Y781	I782	S783	M784	F785	Q786	A787	H788	I789	G790	G791	Y792	L793	L794	R795	K796	K799	K800	L801	Q802	D803	Q804	R805				
L806	G807	L808	S809	V810	I811	Q812	R813	N814	R815	K816	K817	H818	L819	V820	L821	R822	N823	Q824	Q825	W826	K827	K828	L829	Y830	S831	K832	V833	K834	P835																																

• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

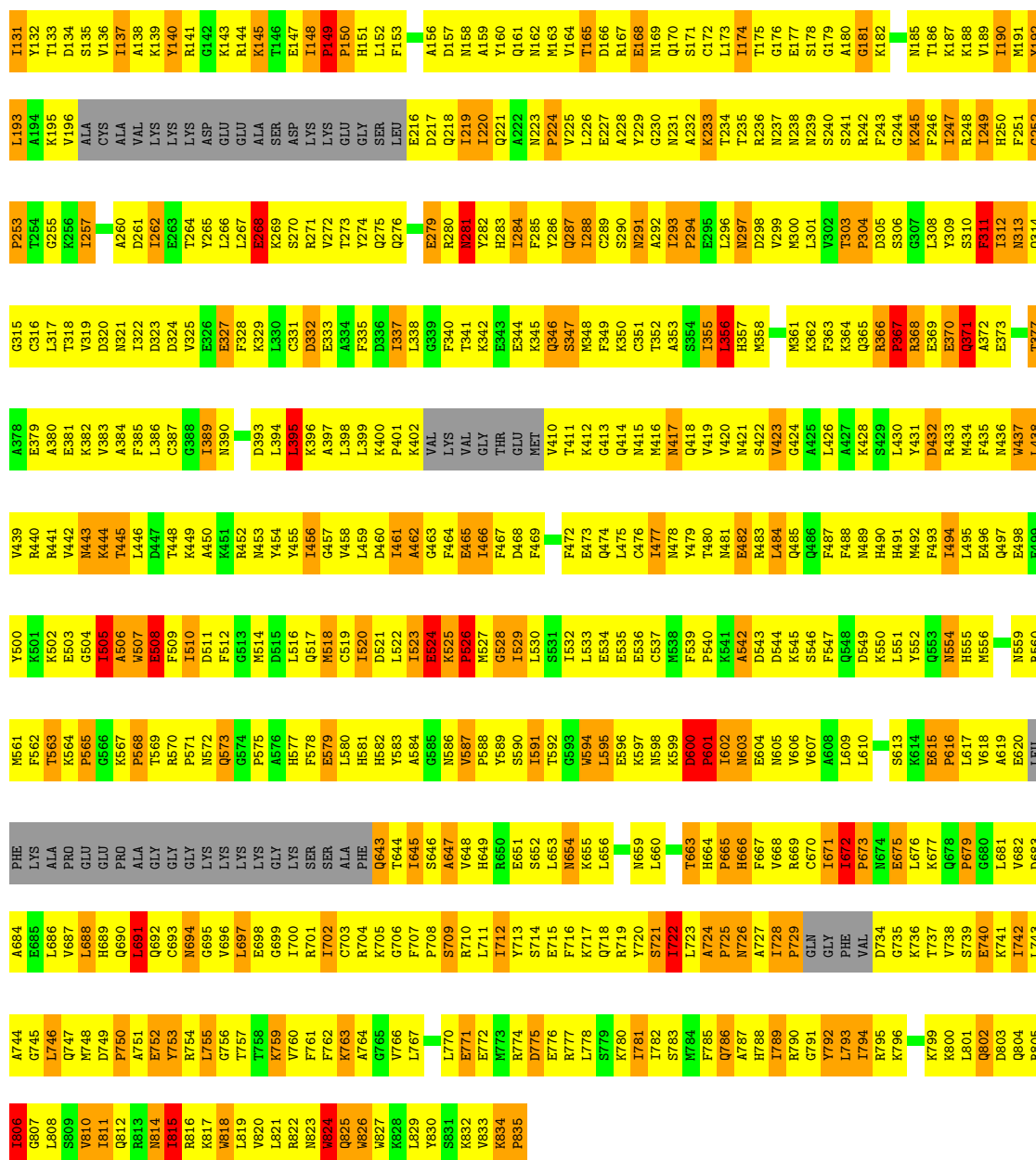
Chain 21-C:  11% 60% 20% 7%

K70	K71	D72	D73	I74	I75	S76	M77	M78	P79	P80	K81	F82	E83	K84	K85	E86	D87	M88	A89	N90	M91	T92	Y93	L94	N95	E96	A97	S98	V99	L100	Y101	N102	L103	R104	S105	R106	Y107	T108	S109	G110	L111	I112	Y113	T114	Y115	S116	G117	L118	F119	C120	I121	A122	T123	N124	P125	Y126	L129	M191	Y192								
I131	Y132	L133	D134	S135	V136	I137	ALA	I138	VAL	VAL	K139	K140	R141	K142	K143	E144	I145	P146	P147	H148	L149	F150	F151	F152	E216	D217	Q218	L219	I220	Q221	A222	N223	P224	V225	L226	E227	R167	E168	G230	N231	A232	K233	L234	L173	T235	R236	N237	N238	N239	S240	G179	A180	G181	F243	G244	K245	L308	I247	Y309	R248	S310	A372	E373	I312	H250	F251	Q314
P253	T254	G255	K256	I257	A260	D261	L262	E263	T264	Y265	L266	L267	E268	L269	S270	R271	Y272	T273	Y274	Q275	Q276	E279	R280	Y281	Y282	I283	H284	A285	Y286	Q287	L288	C289	S290	N291	A292	L293	P294	E295	L296	H357	D298	V299	M300	L301	V302	T303	K364	Q365	D305	P367	R368	L308	G307	Y309	R371	S310	A372	E373	I312	H250	F251	Q314					
G315	C316	L317	T318	V319	D320	N321	I322	D323	D324	V325	E326	E327	F328	K329	L330	C331	D332	E333	A334	F335	D336	I337	L338	G339	F340	T341	K342	E343	I284	K345	Q346	S347	M348	F349	Q413	K350	C351	T352	A353	E354	L356	H357	M358	M361	K362	F363	T303	Q365	D305	P367	R368	L308	G307	Y309	R371	S310	A372	E373	I312	H250	F251	Q314					
A378	E379	A380	E381	K382	V383	A384	F385	L386	C387	G388	I389	N390	D393	L394	Y455	K396	A397	L398	L399	K400	I401	A402	VAL	LYS	VAL	GLY	THR	GLU	GLU	MET	V410	T411	K412	Q413	Q414	N415	M416	M417	Q418	Q419	L355	V420	N421	S422	V423	G424	A425	L426	A427	K428	S429	L430	Y431	D432	R433	Y309	R371	S310	A372	E373	I312	H250	F251	Q314			
V439	R440	R441	V442	N443	K444	T445	L446	D447	T448	K449	A450	K451	R452	M453	Y454	Y455	A456	G457	V458	L459	D460	I461	A462	G463	F464	E465	L466	F467	D468	F469	F472	E473	Q474	L475	C476	I477	M478	Y479	T480	N481	E482	R483	S422	V423	G424	A425	L426	A427	K428	S429	L430	Y431	D432	R433	Y309	R371	S310	A372	E373	I312	H250	F251	Q314				
Y500	A501	E502	E503	E504	I505	A506	M507	E508	F509	I510	D511	F512	M513	M514	Y515	L516	M517	C519	I520	D521	L522	I523	E524	K525	P526	M527	G528	I529	L530	S531	I532	L533	E534	E535	E536	C537	M538	F539	P540	K541	A542	D543	D544	K545	S546	F547	F548	G549	K550	L551	Y552	Q553	N554	H555	M556	N559	R560										
M561	F562	T563	K564	P565	G566	K567	P568	T569	R570	P571	M572	Q573	S574	P575	A576	H577	F578	E579	L580	H581	H582	Y583	A584	E585	N586	P587	F588	Y589	E590	E591	T592	M593	W594	L595	E596	K597	N598	K599	D600	P601	T602	N603	E604	N605	V606	G607	L608	L609	L610	S613	K614	E615	P616	L617	V618	A619	E620	L621	D683								
PHE	LYS	ALA	PRO	GLU	GLU	PRO	ALA	GLY	GLY	GLY	LYS	LYS	LYS	LYS	GLY	LYS	LYS	LYS	ALA	PHE	Q643	T644	I645	S646	A647	V648	H649	R650	E651	S652	L653	N654	K655	L656	N659	L660	T663	H664	P665	H666	F667	V668	R669	C670	GLN	GLY	PHE	VAL	D734	G735	L676	T737	V738	W739	E740	K741	L742	L743									
A684	E685	L686	V687	L688	H689	Q690	L691	Q692	C693	N694	G695	V696	L697	E698	G699	I700	R701	I702	C703	R704	K705	G706	F707	P708	S709	L710	R711	I712	Y713	S714	E715	F716	Q717	K718	R719	Y720	S721	T722	L723	A724	P725	N726	A727	I728	P729	GLN	GLY	PHE	VAL	D734	G735	L676	T737	V738	W739	E740	K741	L742	L743								
A744	G745	L746	Q747	M748	D749	P750	A751	E752	V753	R754	L755	G756	T757	F758	K759	V760	F761	F762	K763	A764	G765	V766	L767	L770	E771	R772	M773	R774	D775	E776	R777	L778	S779	K780	L781	L782	S783	R784	Q785	Q786	A787	H788	L789	R790	G791	Y792	L793	L794	R795	K796	K799	L800	L801	Q802	D803	L804	R805										
L806	G807	S808	S809	V810	I811	Q812	R813	L814	R815	L816	K817	L818	L819	V820	L821	R822	N823	L824	Q825	W826	W827	K828	L829	Y830	S831	R832	C833	R834	P835	P836	P837	D838	N839	K840	E841	G842	F843	E847	I848	Q849	K852	G853	D854	E855	I856	T857	V858	K859	I860	V861	A862	D863	S864	S865	T866	R867	L868	R869									

• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

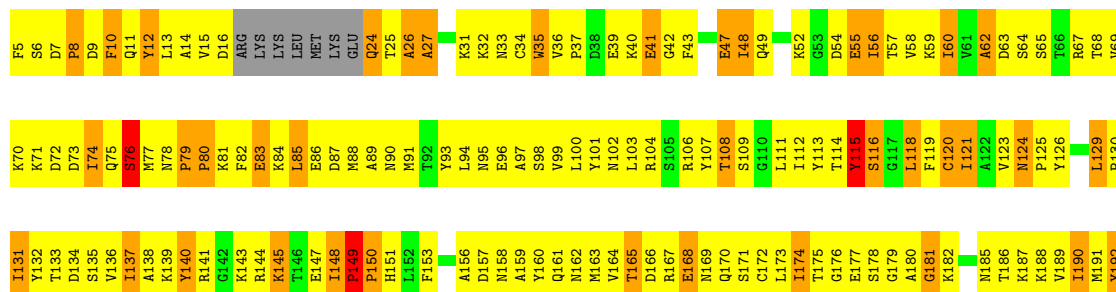
Chain 23-C: 12% 58% 19% 7%

F5	S6	D7	P8	D9	F10	Q11	Y12	L13	A14	V15	D16	A86	LYS	L85	L86	LEU	MET	LYS	GLY	Q24	T25	A26	A27	K31	K32	N33	C34	S35	W36	V37	D38	E39	N102	L103	R104	S105	R106	Y107	T108	I48	Q49	K52	G53	D54	E55	I56	T57	V58	K59	I80	V61	A62	D63	S64	S65	T66	R67	L88	P130
K70	K71	D72	D73	I74	I75	S76	M77	M78	P79	P80	K81	F82	E83	K84	K85	E86	D87	M88	A89	N90	M91	T92	Y93	L94	N95	E96	A97	S98	V99	L100	Y101	N102	L103	R104	S105	R106	Y107	T108	S109	G110	L111	I112	Y113	T114	Y115	S116	G117	L118	F119	C120	I121	A122	T123	N124	P125	Y126	L129	M191	Y192



● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 24-C: 12% 58% 20% 7%



R805	L743	D683	PHE	M661	Y500	V439	A378	G315	P253	L193
L744	L743	L743	L743	F562	K501	R440	E379	C316	P253	L193
G745	G745	E685	ALA	T563	K502	R441	A380	G316	K194	K194
L746	L746	L687	PRO	K564	G504	V442	E381	T318	G255	V196
Q747	Q747	V687	GLU	P565	G504	N443	K382	V319	K256	ALA
M748	M748	L688	GLU	G566	L505	K444	V383	D320	I257	CYS
D749	D749	H689	PRO	K567	A506	T445	A384	N321	A260	ALA
P750	P750	Q690	ALA	P568	H507	L446	F385	I322	D261	VAL
A751	A751	L691	GLY	T569	E508	D447	L386	D323	L262	LYS
E752	E752	Q692	GLY	R570	F509	T448	C387	D324	E263	LYS
Y753	Y753	C693	GLY	P571	I510	K449	V325	L326	T264	LYS
R754	R754	N694	LYS	N572	D511	A450	I389	E326	Y265	ASP
L755	L755	G695	LYS	Q573	F512	K451	N390	E327	L266	GLU
G756	G756	V696	LYS	G574	G513	R452	L453	F328	L267	GLU
L757	L757	L697	LYS	P575	M514	N453	D393	K329	E268	ALA
E758	E758	E698	GLY	A576	D615	L394	L394	L330	K269	SER
K759	K759	E699	LYS	H577	L516	Y455	L395	C331	S270	ASP
V760	V760	I700	SER	F578	Q517	L456	K396	D332	R271	LYS
F761	F761	R701	SER	E579	C519	G457	A397	E333	V272	LYS
L762	L762	I702	ALA	L580	M518	L458	L398	A334	T273	GLU
K763	K763	C703	PHE	H581	D520	L459	L399	F335	Y274	GLY
A764	A764	R704	Q643	H582	I521	D460	K400	D336	K275	SER
G765	G765	K705	T644	Y583	L522	I461	P401	I337	Q276	LEU
V766	V766	I645	I645	A584	I523	G462	K402	L338		
L767	L767	F707	S646	G585	E524	G463	VAL	G339	E279	E216
		P708	A647	N586	K525	F464	LYS	F340	R280	D217
L770	L770	S709	V648	V587	P526	E465	VAL	T341	N281	Q218
E771	E771	R710	H649	P588	M527	I466	L466	K342	Y282	I219
L772	L772	L711	R650	Y589	G528	F467	THR	F343	H283	L220
H773	H773	I712	E651	S590	I529	D468	GLU	E344	I284	Q221
R774	R774	Y713	S652	I591	L530	F469	MET	K345	T284	A222
D775	D775	S714	L653	T592	S531			Q346	Y286	N223
E776	E776	E715	M654	G593	I532	F472	T411	Q347	R287	P224
L777	L777	F716	K655	N594	L533	E473	K412	N348	I288	V225
L778	L778	K717	L656	L595	E534	Q474	G413	F349	C289	L226
S779	S779	Q718		E596	E535	L475	Q414	K350	S290	E227
K780	K780	R719	N659	K597	E536	C476	M415	C351	N291	A228
L781	L781	L660	L660	N598	C537	I477	M416	T352	A292	Y229
T782	T782	S721	Y661	K599	P538	N478	M417	A353	I293	G230
S783	S783	I722	T663	D600	F539	Y479	Q418	S354	P294	N231
H784	H784	L723	T663	P601	P540	T480	V419	I355	E295	A232
F785	F785	A724	H664	I602	K541	M481	V420	L358	F295	K233
Q786	Q786	P726	P665	N603	A542	E482	M421	H357	L296	T234
A787	A787	N725	H666	E604	D543	R483	S422	D298	N297	T235
H788	H788	A727	F667	N605	D544	L484	V423	V299	V299	R236
I789	I789	R728	V668	V606	K545	Q485	G424	M300	N237	N238
R790	R790	P729	R669	V607	S546	Q486	A425	L301	N239	N239
G791	G791	GLN	C670	A608	F547	F487	L426	K362	V302	S240
Y792	Y792	GLY	L609	L609	Q548	F488	A427	F363	S241	S240
L793	L793	PHE	L610	L610	D549	N489	K428	K364	T303	E241
I794	I794	VAL	P673		H490	H490	S429	Q365	R242	R242
R795	R795	D734	N674	S613	K550	H491	L430	R366	D305	F243
K796	K796	G735	E675	K614	Y552	M492	Y431	S306	G244	G244
		K736	L676	E815	Q553	F493	D432	G507	K245	K245
		T737	K677	P616	M554	I494	R433	E369	L308	F246
		V738	Q678	L617	H555	L495	M434	E370	Y309	I247
K799	K799	S739	P679	V618	M556	E496	F435	Q371	S310	R248
L800	L800	E740	G680	A619		Q497	N436	A372	F311	I249
Q802	Q802	K741		E620	N559	E498	W437	E373	I312	H250
D803	D803	L742	V682	L611	R560	E499	L439		P251	P251
E804	E804								C214	C252

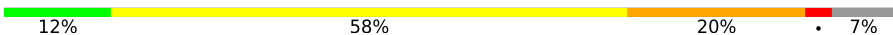
● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 25-C: 12% 58% 20% 7%

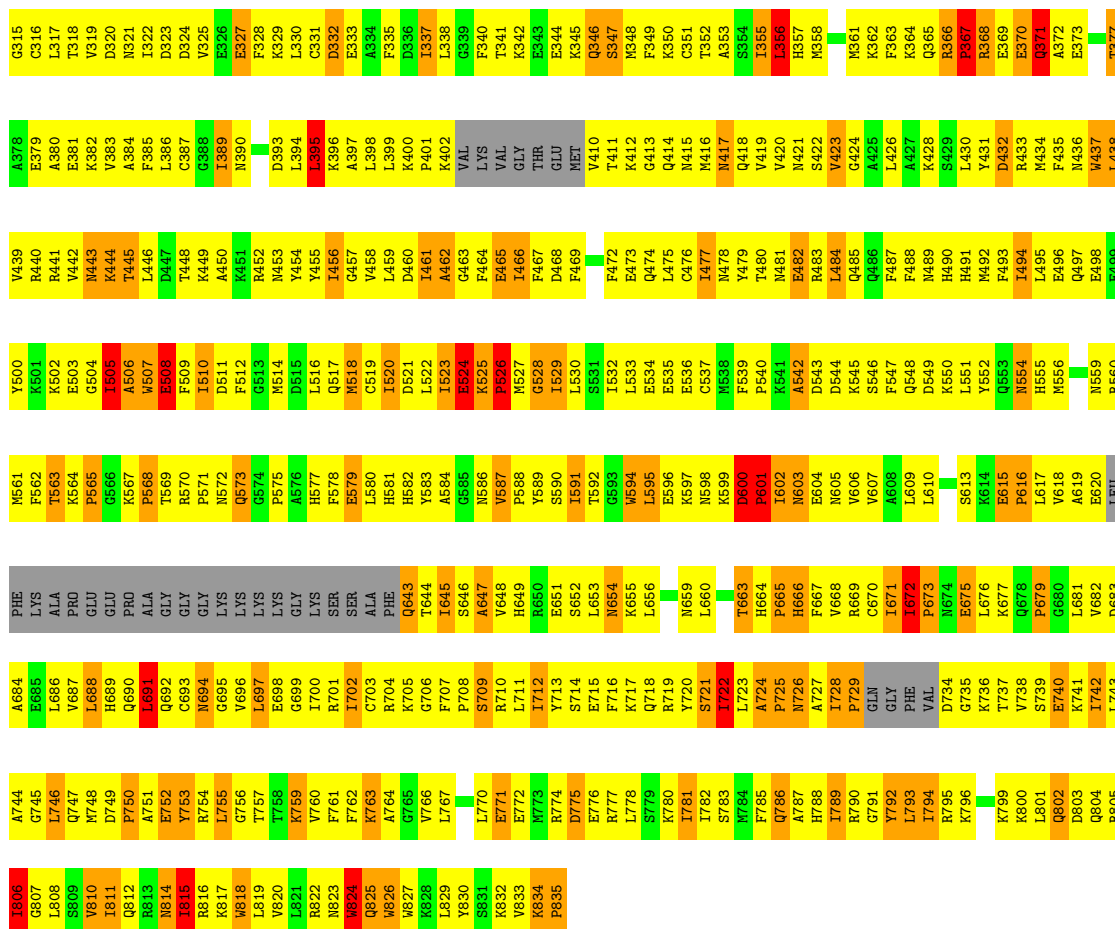
F5	S6	D7	P8	D9	F10	Q11	Y12	L13	A14	V15	D16	A17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32	L33	L34	L35	L36	L37	L38	L39	L40	L41	L42	L43	L44	L45	L46	L47	L48	L49	L50	L51	L52	L53	L54	L55	L56	L57	L58	L59	L60	L61	L62	L63	L64	L65	L66	L67	L68	L69
K70	K71	D72	D73	I74	Q75	S76	M77	K78	P79	P80	K81	F82	E83	K84	L85	E86	D87	M88	A89	H90	M91	T92	Y93	L94	N95	E96	A97	S98	V99	L100	L101	N102	L103	R104	S105	R106	Y107	T108	I109	G110	L111	I112	Y113	T114	E115	S116	G117	L118	F119	C120	V121	A122	D123	N124	S125	G126	R127	L128	P129	G130				
I131	Y132	T133	D134	S135	V136	I137	A138	L139	M140	R141	G142	K143	R144	E145	T146	E147	I148	P149	P150	H151	L152	F153	E154	D155	Q156	I157	A158	I159	V160	Q161	N162	M163	V164	T165	R166	E167	E168	M169	N170	K171	S172	L173	I174	T175	G176	E177	S178	G179	A180	R181	K182	L183	M185	T186	K187	K188	P189	H190	I191	Y192				
L193	A194	K195	V196	ALA	CYS	ALA	VAL	LYS	LYS	LYS	ASP	GLU	GLU	ALA	SER	ASP	LYS	LYS	GLY	SER	LEU	E216	D217	Q218	I219	I220	A221	Q222	Q223	N224	V225	L226	E227	A228	Y229	G230	N231	A232	K233	L234	T235	R236	N237	N238	S239	S240	S241	R242	F243	G244	K245	F246	I247	K248	P249	H250	F251	G252						

P253	A376	V439	Y500	M561	A694	A744	L306	F5	K70	T131	L193	P253
T254	E379	R440	A501	F562	E695	G745	G807	S6	K71	Y132	A194	T254
G255	A380	R441	K502	F563	L686	G746	G808	D7	D72	T133	K195	G255
K256	E381	R442	E503	K564	P687	Q747	S809	P8	D73	T134	V196	K256
I257	K382	V319	P665	G566	L688	M748	V810	D9	I74	S135	ALA	I257
A260	V383	K444	I505	K567	H689	P750	V811	F10	Q75	T137	ALA	A260
D261	N321	T445	A506	K568	Q690	A751	Q812	Q11	S76	M77	VAL	D261
I262	I322	L446	W507	P668	L691	E752	R813	Y12	M77	K139	LVS	I262
E263	D323	D324	F509	T569	Q692	G753	R814	A14	M78	P79	LVS	E263
T264	V325	K449	I510	A570	M694	R754	R816	V15	Y753	P80	LVS	T264
Y265	G388	T448	D511	P571	G695	R755	R817	D16	K81	K142	ASP	Y265
L266	I389	A450	D512	N572	V696	G756	W818	ARG	F82	G143	GLU	L266
L267	E327	K451	N390	Q573	L697	T757	L819	LVS	E83	R144	GLU	L267
E268	F328	R452	G513	G574	L698	T758	W820	LVS	E84	T145	ALA	E268
K269	K329	N453	M514	P575	E698	G759	L821	LVS	L85	T146	SER	K269
S270	L394	Y454	L516	A576	G699	W760	L822	LEU	K759	K147	ASP	S270
R271	G331	Y455	L517	H577	L700	V760	N823	MET	E86	I148	LVS	R271
V272	D332	Y456	L518	F578	R701	F761	N824	LVS	D87	P149	LVS	V272
T273	E333	G457	M518	E579	I702	F762	Q825	GLU	M88	P150	GLU	T273
Y274	A334	V458	C519	L580	C703	K763	Q826	Q24	A89	H151	GLY	Y274
Q275	F335	L459	D521	H581	R704	A764	W827	T25	N90	L152	SER	Q275
Q276	D336	D460	L522	Y583	T644	V766	R828	A26	M91	F153	LEU	Q276
Q277	I337	I461	L523	A584	F707	L767	Y830	A27	Y93	T92	LEU	Q277
Q278	L338	K462	I524	G585	P708	L768	S831	K31	L94	A156	D217	Q278
E279	G339	G463	E525	K586	S709	L770	S832	K32	N95	D157	Q218	E279
R280	F340	F464	K526	L586	S710	E771	R833	N33	E96	L158	I219	R280
K281	T341	E465	P526	P587	R710	E772	W834	N34	A97	A159	I220	K281
Y282	K342	I466	M527	P588	L711	E773	P835	W35	S98	Y160	Q221	Y282
H283	E343	F467	G528	Y589	T712	M773	R834	W36	V99	Q161	A222	H283
I284	G344	D468	I529	S590	Y713	R774	P835	P37	L100	N162	N223	I284
F285	K345	F469	L530	E591	S714	D775	L781	F43	P37	N163	P224	F285
Y286	Q346	Y410	S531	T592	S715	E776	T782	D38	E39	T165	Y225	Y286
Q287	S347	T411	I532	G593	F716	R777	L783	E39	N102	D166	E227	Q287
I288	M348	K412	L533	W594	K717	L778	W784	K40	L103	T167	L226	I288
C289	F349	Q413	E534	L595	Q718	S779	Q786	E41	R104	E167	A228	C289
S290	K350	L475	E535	E596	R719	K780	L787	G42	S105	R167	Y229	S290
N291	C351	K476	E536	K597	Y720	T781	T788	F43	R106	E168	Y230	N291
A292	T352	I477	C537	N598	S721	L782	W789	E47	Y107	N169	Q230	A292
I293	A353	M478	M538	K599	S722	S783	E784	I48	T108	Q170	N231	I293
P294	S354	Y479	F539	D600	L723	W784	Q785	I48	S109	S171	A232	P294
E295	I355	T480	P540	P601	A724	F785	Q786	Q49	G110	C172	K233	E295
L296	L356	N481	K541	I602	P725	P665	N726	K52	L111	L173	T234	L296
N297	H357	E482	A542	N603	N726	H666	A727	G53	I112	T174	T235	N297
D298	M358	R483	D543	E604	I728	V668	H788	D54	Y113	T175	R236	D298
V299	M361	L484	D544	N605	I728	V668	I789	E55	T114	G176	N237	V299
M300	K362	Q485	K545	V606	P729	R669	R790	I56	E55	E177	N238	M300
L301	F363	Q486	S546	V607	GLN	C670	G791	I56	S116	S178	N239	L301
V302	K364	F487	F547	A608	GLY	I671	Y792	T57	G117	G179	S240	V302
T303	K364	F488	G548	L609	PHE	I672	L793	V58	L118	A180	S241	T303
P304	Q365	N489	D549	L610	VAL	P673	I794	K59	F119	G181	R242	P304
D305	R366	H490	K550	L610	D734	R674	R795	I60	C120	K182	F243	D305
S306	P367	L430	L551	S613	G735	E675	K796	V61	T121	A122	G244	S306
G307	R368	Y431	Y552	K614	G736	E675	K799	A62	A122	N185	K245	G307
L308	E369	D432	F493	E615	T737	L676	K800	D63	V123	T186	F246	L308
Y309	A370	R433	F493	Q553	T737	K677	S64	S64	N124	K187	I247	Y309
S310	G371	I494	N554	P616	V738	Q678	L801	S65	P125	K188	R248	S310
F311	A372	L495	H555	L617	S739	Q679	Q802	T86	Y126	V189	I249	F311
I312	E373	E496	M556	V618	E740	G680	D803	R67	T260	L190	H250	I312
N313	W437	E498	N559	A619	K741	L681	Q804	T68	L129	M191	F251	N313
Q314	T377	E499	R560	LEU	L743	D683	R805	V69	P130	Y192	G252	Q314

● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

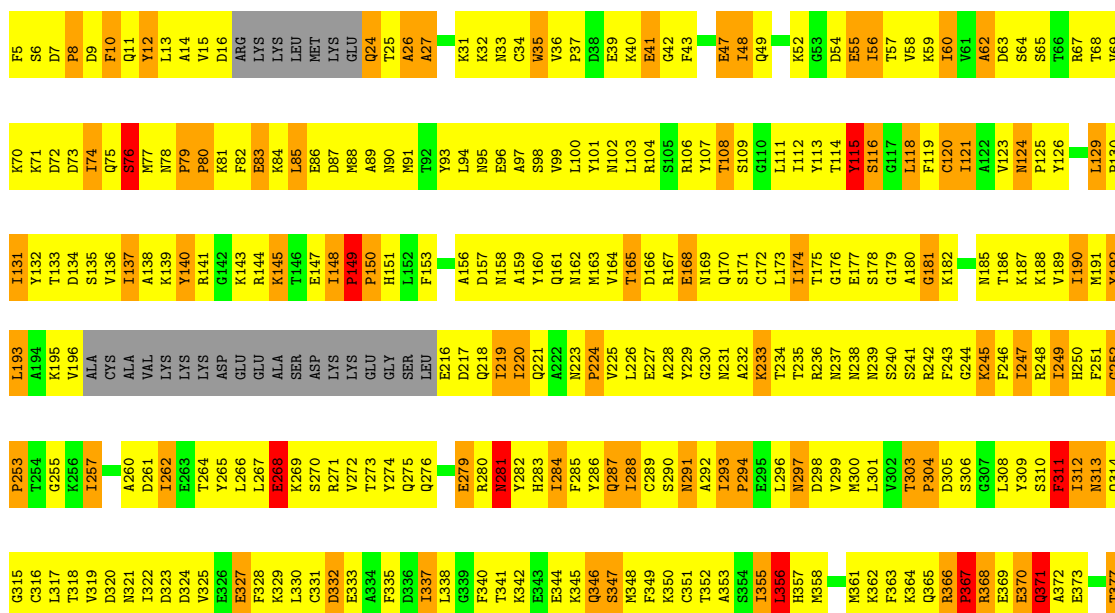
Chain 26-C:  12% 58% 20% 7%

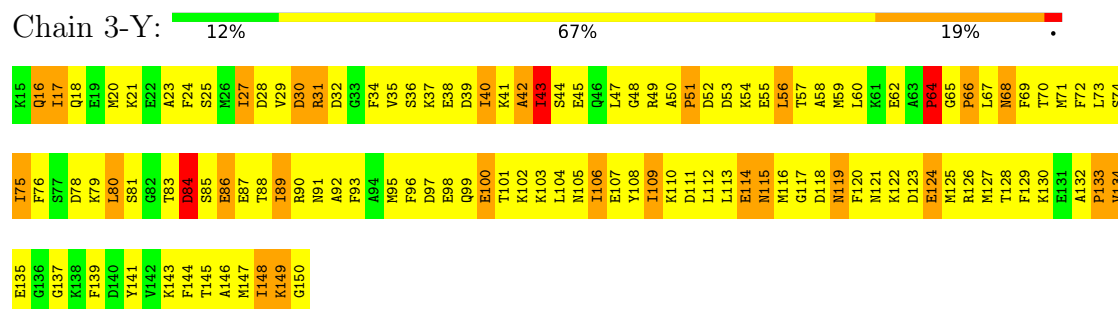
F5	K70	T131	L193	P253
S6	K71	Y132	A194	T254
D7	D72	T133	K195	G255
P8	D73	T134	V196	K256
D9	I74	S135	ALA	I257
F10	Q75	T137	ALA	A260
Q11	S76	M77	VAL	D261
Y12	M77	K139	LVS	I262
A14	P79	P80	LVS	E263
V15	K81	K142	ASP	T264
D16	F82	G143	GLU	Y265
ARG	E83	R144	GLU	L266
LVS	E84	T145	ALA	L267
LVS	L85	T146	ALA	E268
LEU	K759	K147	SER	K269
MET	E86	I148	ASP	S270
LVS	D87	P149	LVS	R271
GLU	M88	P150	LVS	V272
Q24	A89	H151	GLU	T273
T25	N90	L152	GLY	Y274
A26	M91	F153	SER	Q275
A27	Y93	T92	LEU	Q276
K31	L94	A156	D217	E279
K32	N95	D157	Q218	R280
N33	E96	L158	I219	K281
C34	A97	A159	I220	Y282
W35	S98	Y160	Q221	H283
V36	V99	Q161	A222	I284
P37	L100	N162	N223	F285
D38	P37	N163	P224	Y286
E39	N102	T165	Y225	Q287
K40	L103	D166	L226	I288
E41	R104	E167	E227	C289
G42	S105	R167	A228	S290
F43	R106	E168	Y229	N291
E47	Y107	N169	Q230	A292
I48	T108	Q170	N231	I293
Q49	S109	S171	A232	P294
K52	G110	C172	K233	E295
G53	L111	L173	T234	L296
D54	Y112	T174	T235	N297
E55	Y113	T175	R236	D298
I56	T114	G176	N237	V299
T57	E55	E177	N238	M300
V58	S116	S178	N239	L301
K59	G117	G179	S240	V302
I60	L118	A180	S241	T303
V61	F119	G181	R242	P304
A62	C120	K182	F243	D305
D63	T121	A122	G244	S306
S64	N185	N185	K245	G307
S64	V123	T186	F246	L308
S65	K800	K187	I247	Y309
S65	P125	K188	R248	S310
T86	Y126	V189	I249	F311
R67	T260	L190	H250	I312
T68	L129	M191	F251	N313
V69	P130	Y192	G252	Q314



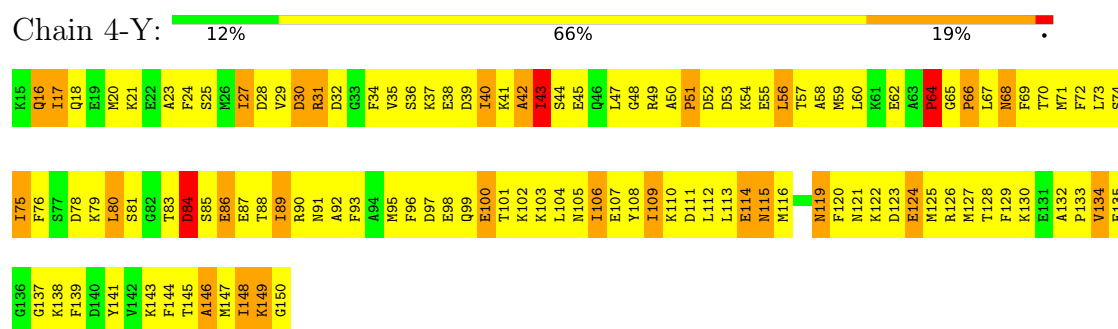
- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 27-C: 12% 58% 20% 7%

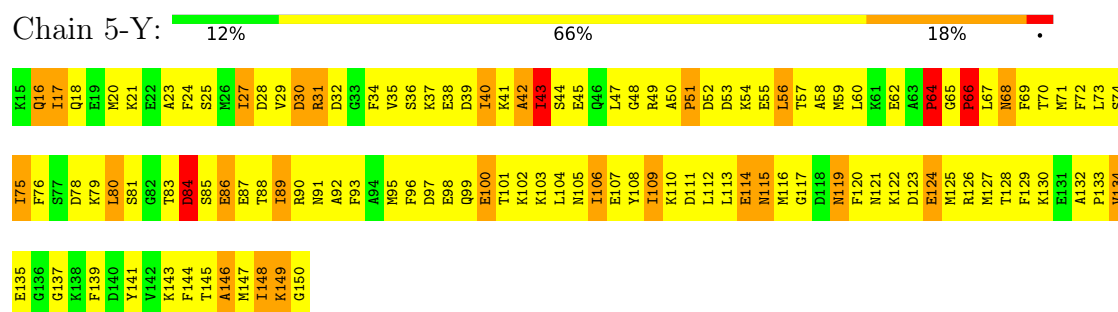




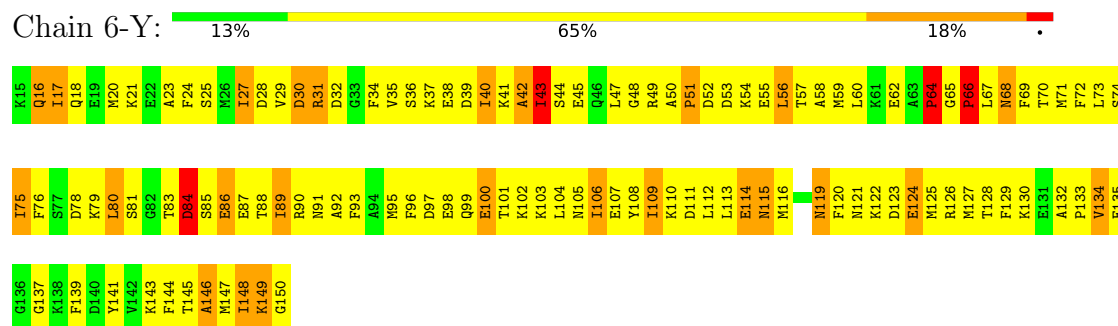
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

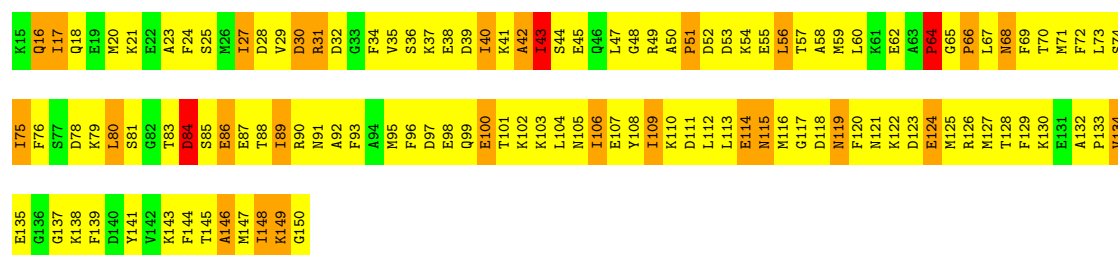


• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



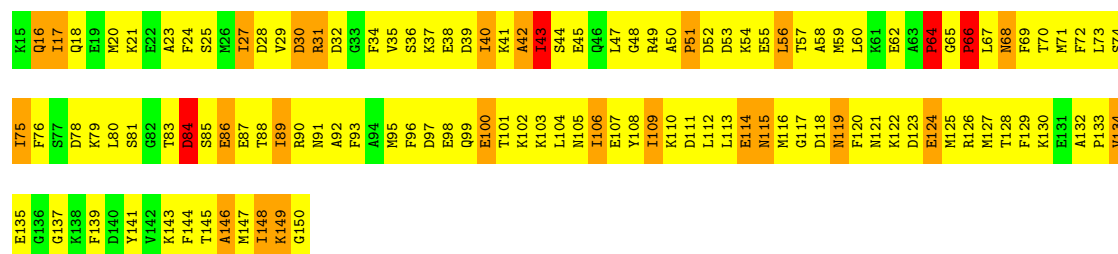
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE





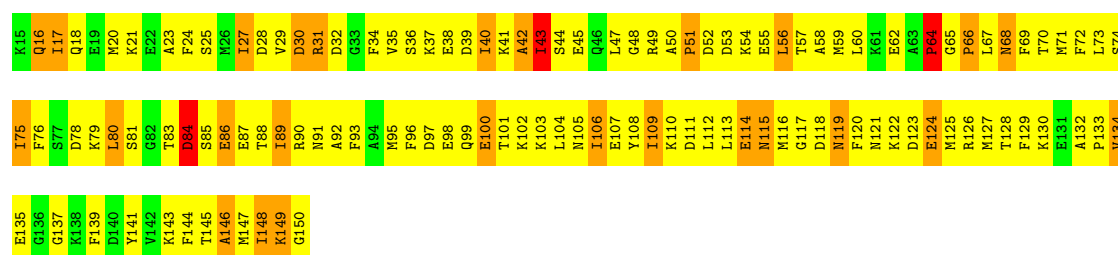
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 8-Y: 12% 68% 18% .



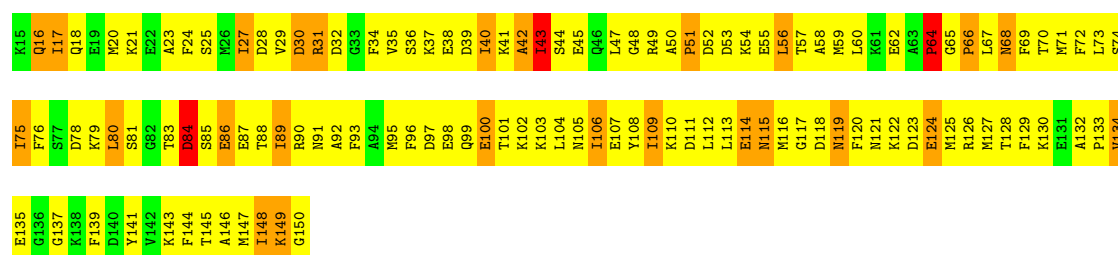
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 9-Y: 12% 67% 19% .



• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

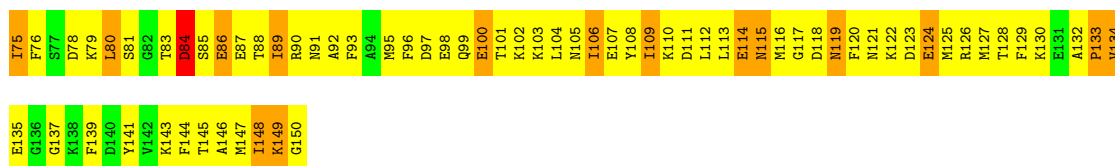
Chain 10-Y: 12% 68% 18% .



• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 11-Y: 12% 67% 19% .





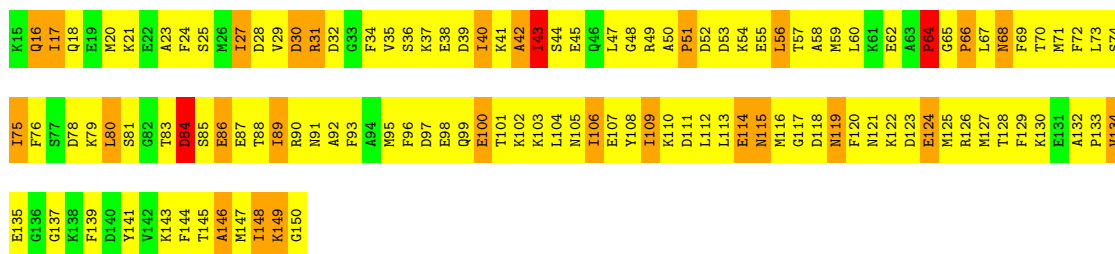
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 12-Y: 12% 67% 19%



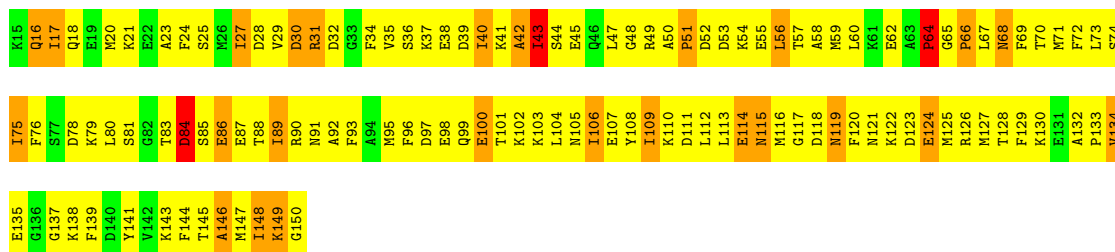
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 13-Y: 12% 67% 19%



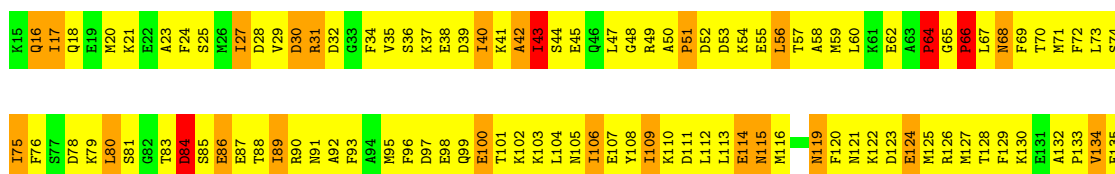
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 14-Y: 11% 68% 18%

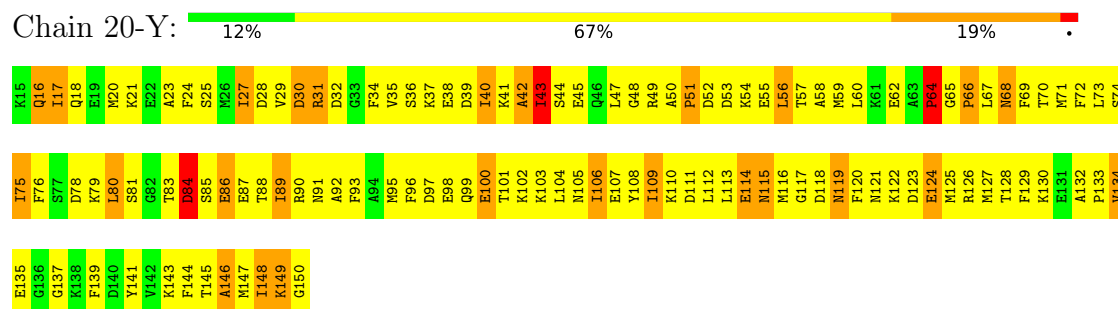


• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

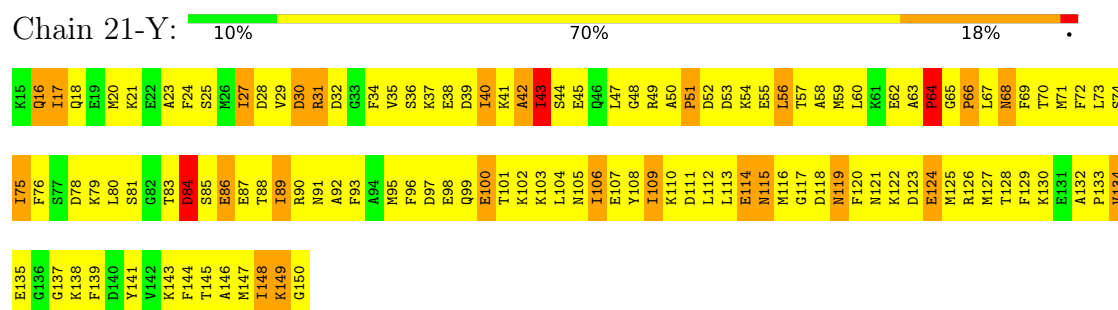
Chain 15-Y: 13% 65% 18%



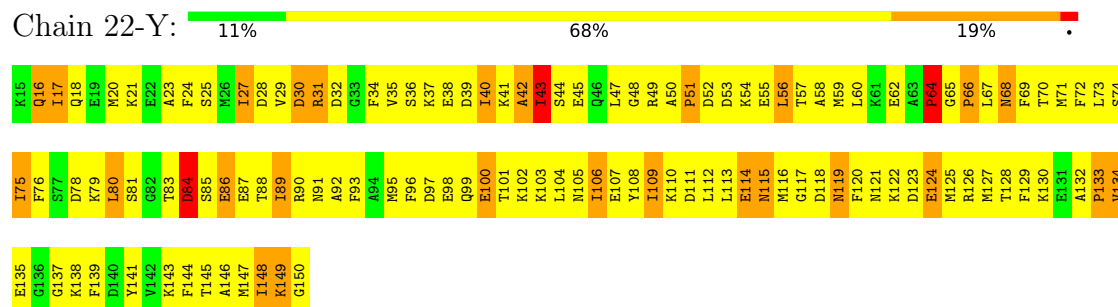
● Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



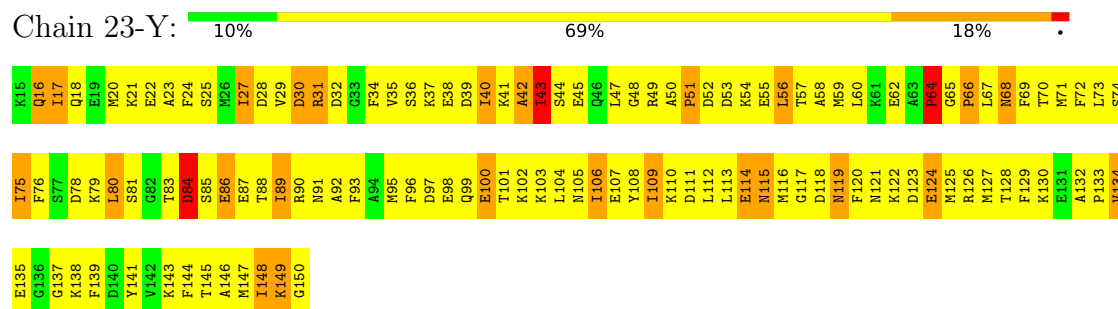
● Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



● Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

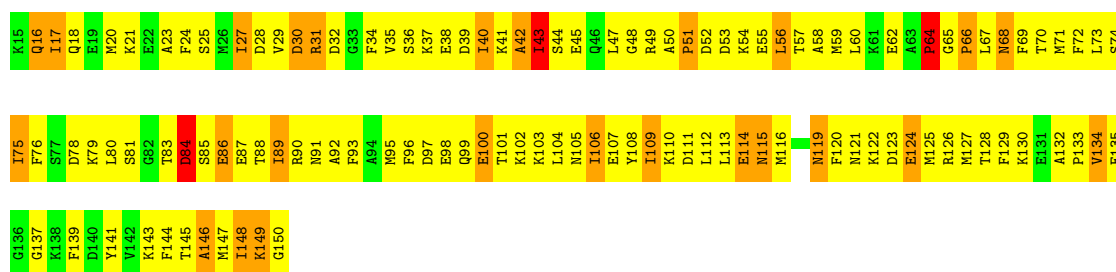


● Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

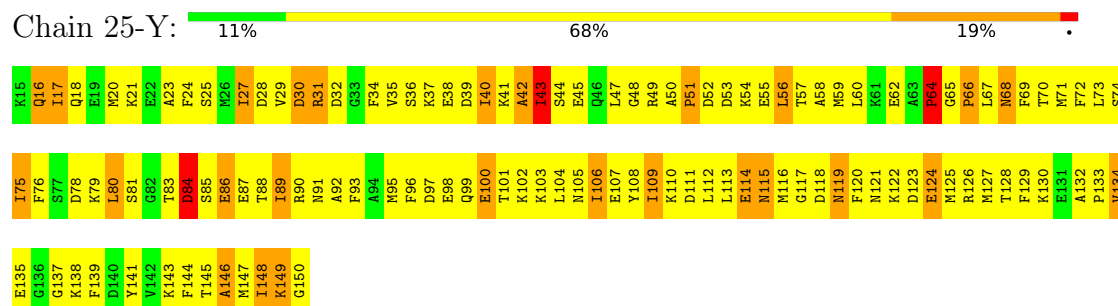


● Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

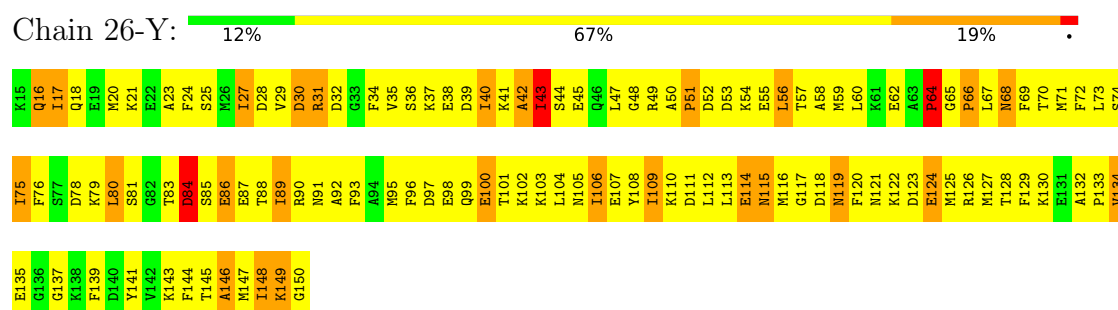




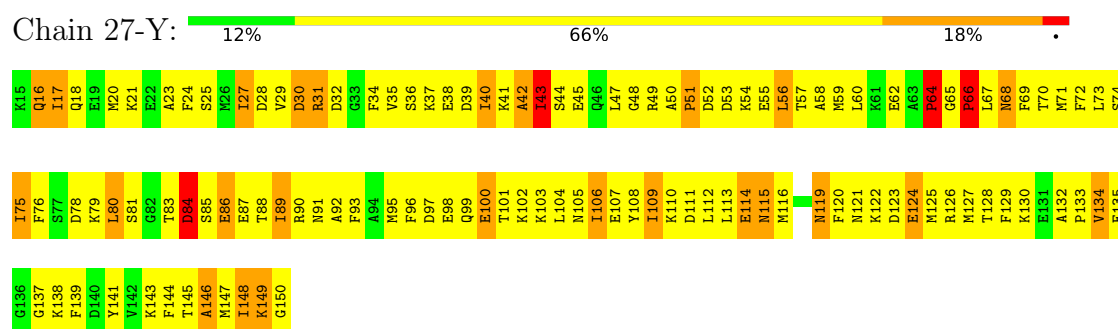
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



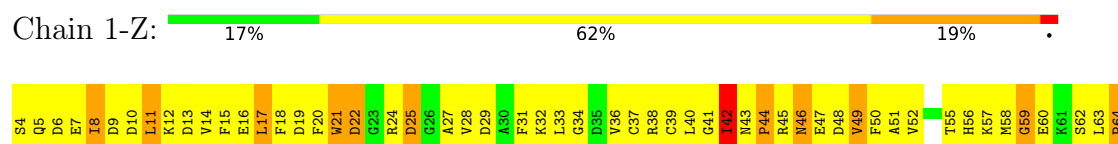
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

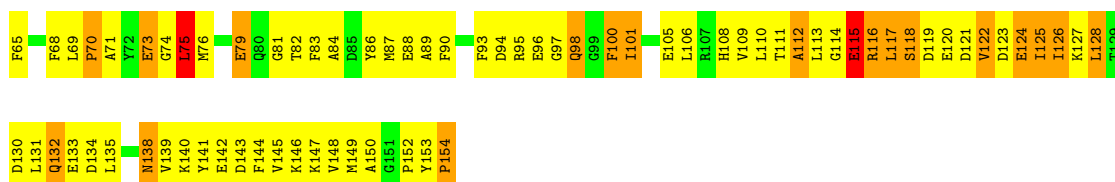


• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



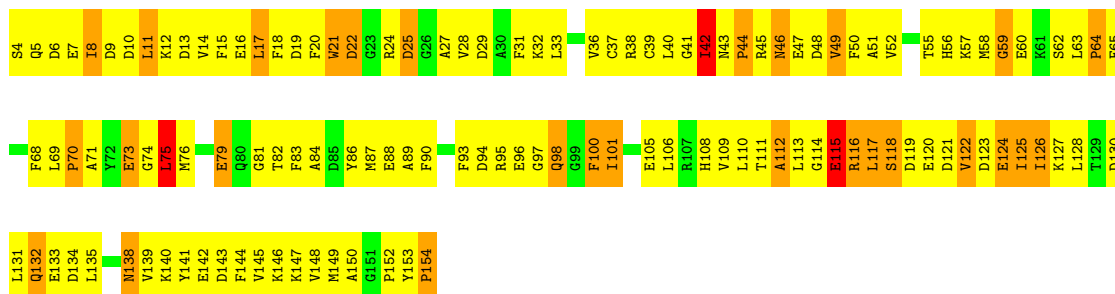
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE





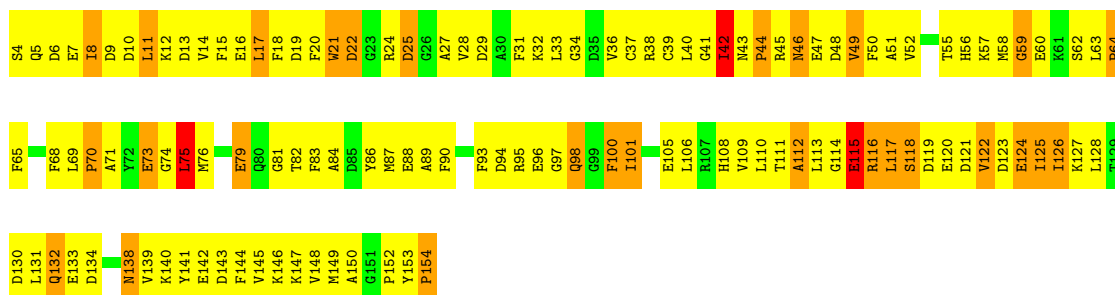
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 2-Z: 17% 62% 19%



- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 3-Z: 17% 62% 19%



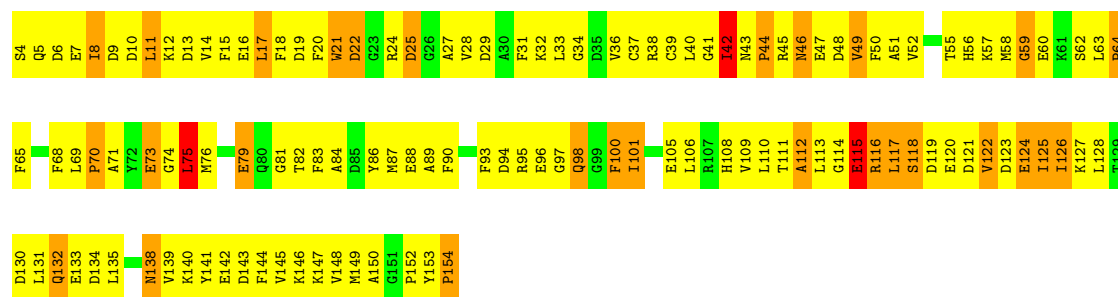
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 4-Z: 16% 64% 19%



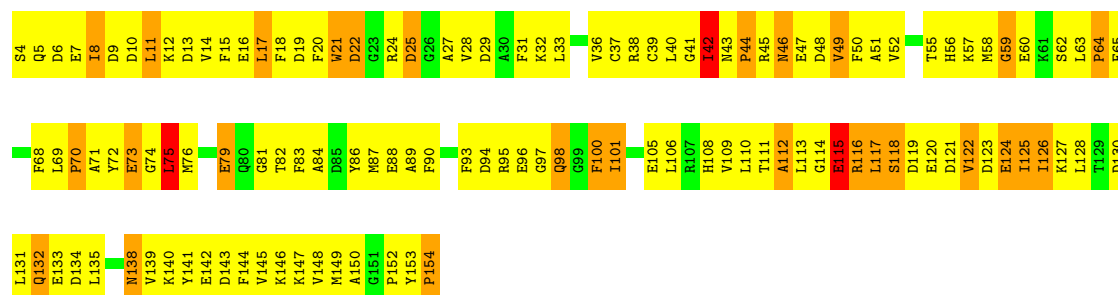
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 5-Z: 17% 63% 19%



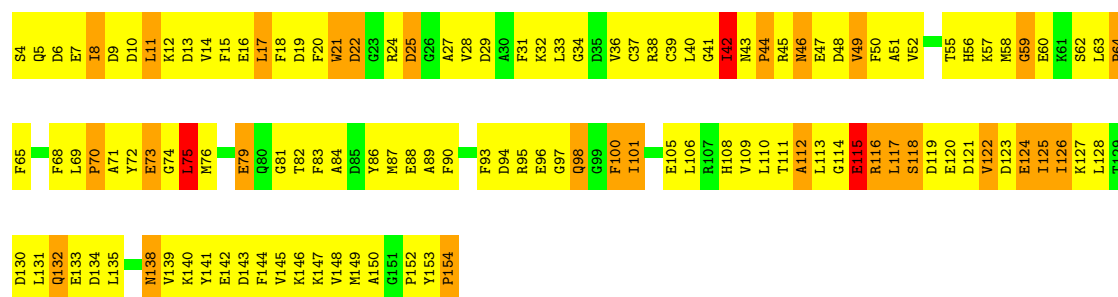
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 6-Z: 17% 63% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 7-Z: 16% 64% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

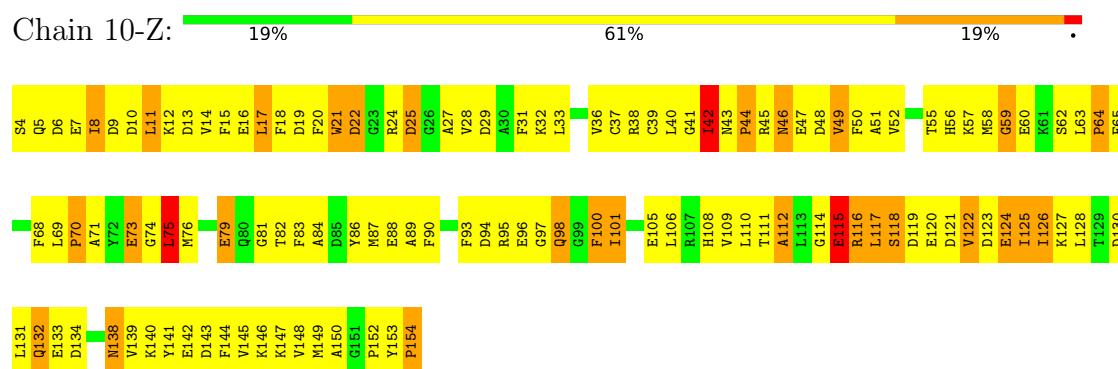
Chain 8-Z: 17% 62% 19%



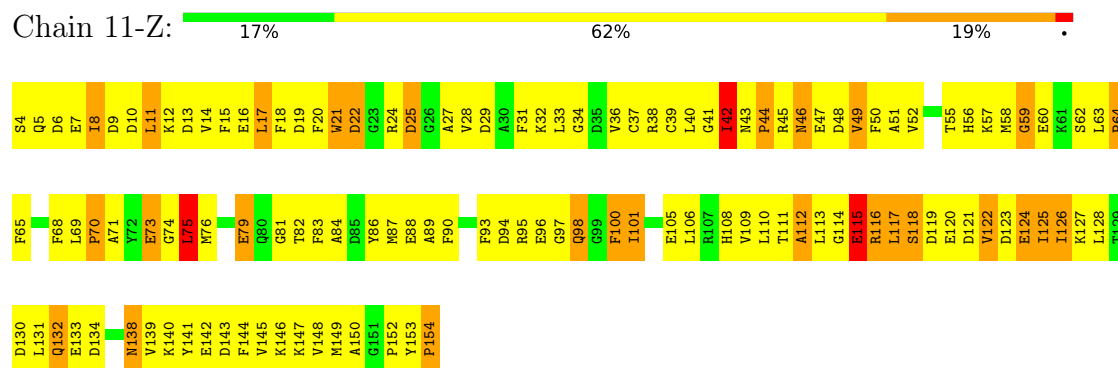
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



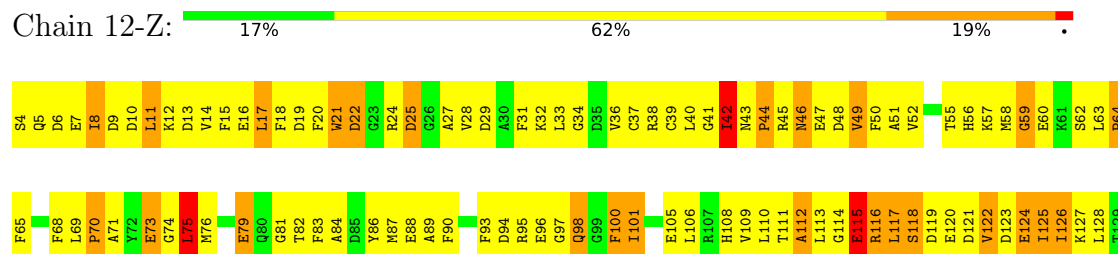
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

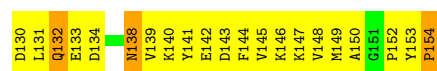


• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



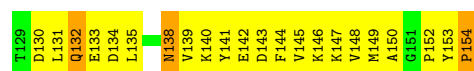
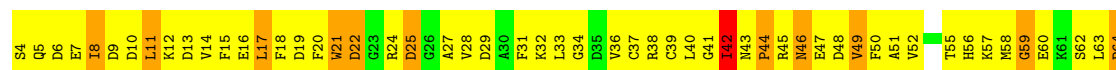
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE





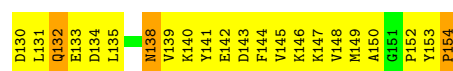
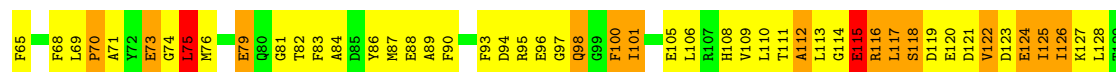
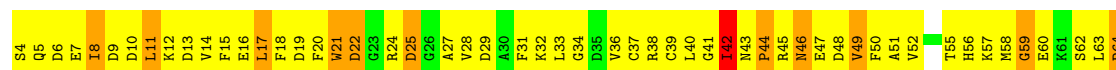
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 13-Z: 16% 64% 19%



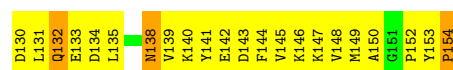
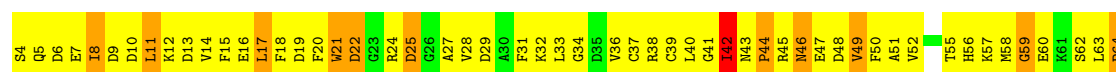
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 14-Z: 17% 63% 19%



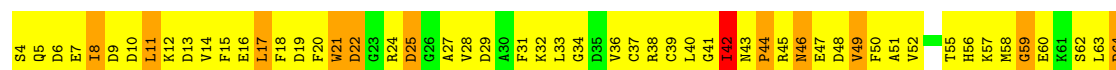
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

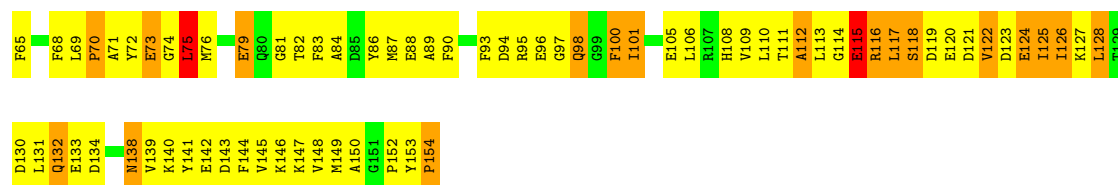
Chain 15-Z: 17% 63% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

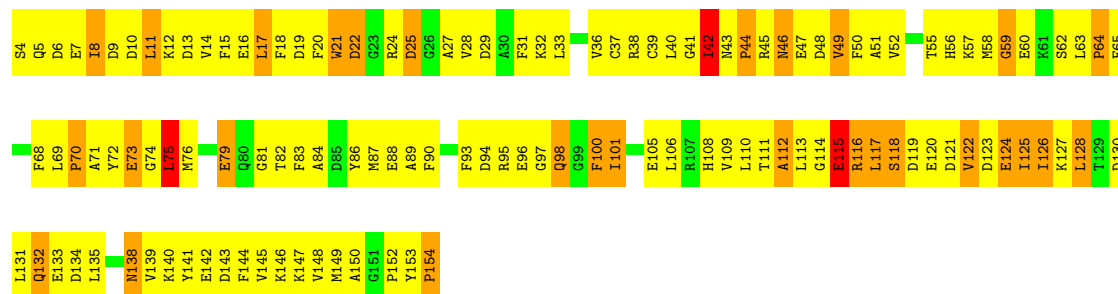
Chain 16-Z: 17% 62% 19%





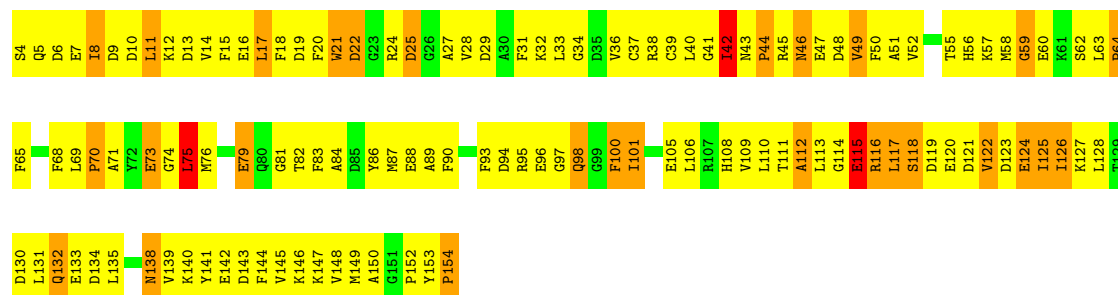
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 17-Z: 17% 62% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 18-Z: 17% 63% 19%



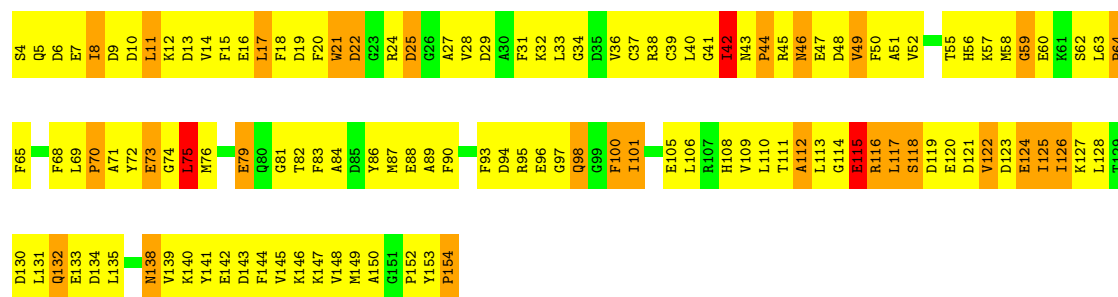
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 19-Z: 16% 63% 19%



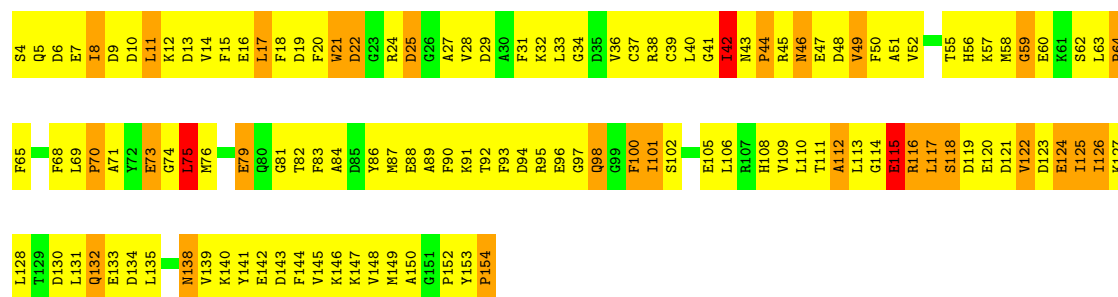
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 20-Z: 16% 64% 19%



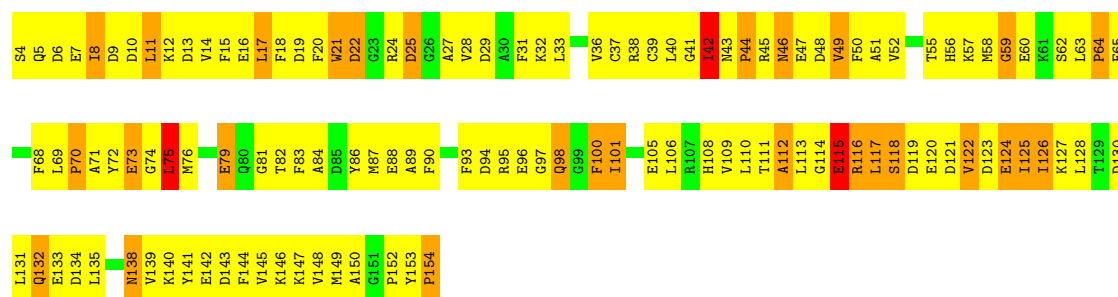
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 21-Z: 15% 65% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 22-Z: 17% 63% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 23-Z: 17% 63% 19%



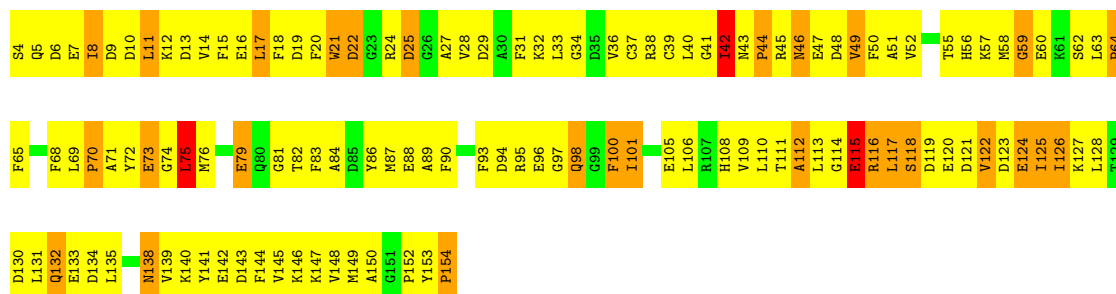
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 24-Z: 16% 63% 19%



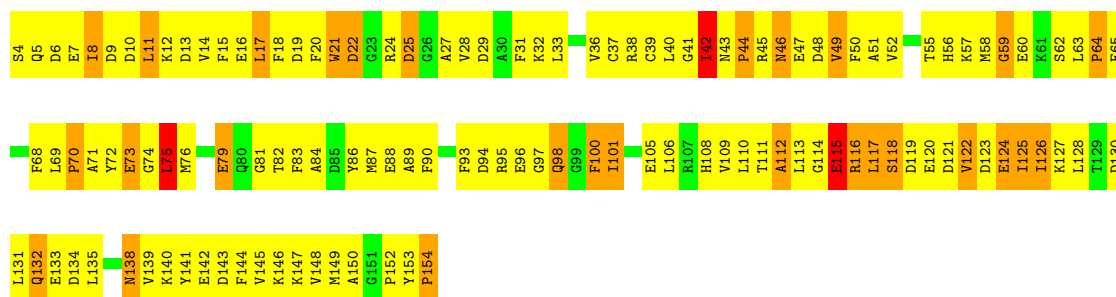
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 25-Z: 16% 64% 19%



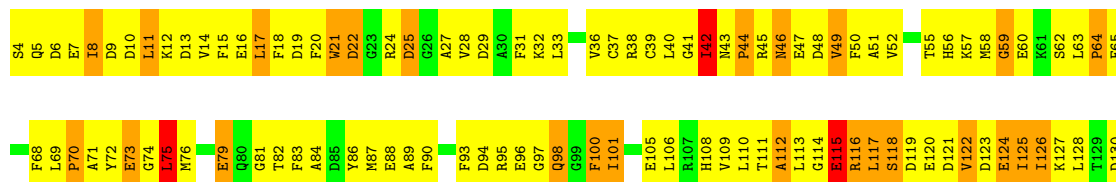
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 26-Z: 17% 63% 19%



• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 27-Z: 17% 63% 19%



L131	Q132		M138	V139
E133	D134		K140	Y141
L135			E142	D143
			F144	V145
			K146	K147
			V148	M149
			A150	G151
			P152	Y153
			P154	

4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F224 (2k x 2k)	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	1-C	2.06	86/6339 (1.4%)	2.10	94/8536 (1.1%)
1	2-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	3-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	4-C	2.06	86/6339 (1.4%)	2.10	94/8536 (1.1%)
1	5-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	6-C	2.06	86/6338 (1.4%)	2.10	94/8533 (1.1%)
1	7-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	8-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	9-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	10-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	11-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	12-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	13-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	14-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	15-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	16-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	17-C	2.06	86/6339 (1.4%)	2.10	94/8536 (1.1%)
1	18-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	19-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	20-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	21-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	22-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	23-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	24-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	25-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	26-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
1	27-C	2.06	86/6340 (1.4%)	2.10	94/8539 (1.1%)
2	1-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	2-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	3-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	4-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	5-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	6-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	7-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	8-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	9-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	10-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	11-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	12-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	13-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	14-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	15-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	16-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	17-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	18-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	19-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	20-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	21-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	22-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	23-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	24-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	25-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	26-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
2	27-Y	0.88	9/1104 (0.8%)	1.39	11/1472 (0.7%)
3	1-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	2-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	3-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	4-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	5-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	6-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	7-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	8-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	9-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	10-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	11-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	12-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	13-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	14-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	15-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	16-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	17-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	18-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	19-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	20-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	21-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	22-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	23-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	24-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	25-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	26-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
3	27-Z	0.76	8/1222 (0.7%)	1.35	11/1644 (0.7%)
All	All	1.81	2781/233977 (1.2%)	1.93	3132/314670 (1.0%)

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	1-C	0	4
1	2-C	0	6
1	3-C	0	4
1	4-C	0	4
1	5-C	0	4
1	6-C	0	4
1	7-C	0	4
1	8-C	0	5
1	9-C	0	4
1	10-C	0	4
1	11-C	0	4
1	12-C	0	4
1	13-C	0	5
1	14-C	0	4
1	15-C	0	6
1	16-C	0	4
1	17-C	0	4
1	18-C	0	4
1	19-C	0	6
1	20-C	0	4
1	21-C	0	4
1	22-C	0	4
1	23-C	0	4
1	24-C	0	7
1	25-C	0	4
1	26-C	0	4
1	27-C	0	6
2	1-Y	0	1
2	2-Y	0	1
2	3-Y	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
2	4-Y	0	1
2	5-Y	0	1
2	6-Y	0	1
2	7-Y	0	1
2	8-Y	0	1
2	9-Y	0	1
2	10-Y	0	1
2	11-Y	0	1
2	12-Y	0	1
2	13-Y	0	1
2	14-Y	0	1
2	15-Y	0	1
2	16-Y	0	1
2	17-Y	0	1
2	18-Y	0	1
2	19-Y	0	1
2	20-Y	0	1
2	21-Y	0	1
2	22-Y	0	1
2	23-Y	0	1
2	24-Y	0	1
2	25-Y	0	1
2	26-Y	0	1
2	27-Y	0	1
All	All	0	148

The worst 5 of 2781 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1-C	165	THR	C-N	98.05	2.70	1.33
1	2-C	165	THR	C-N	98.05	2.70	1.33
1	3-C	165	THR	C-N	98.05	2.70	1.33
1	4-C	165	THR	C-N	98.05	2.70	1.33
1	5-C	165	THR	C-N	98.05	2.70	1.33

The worst 5 of 3132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-C	165	THR	CA-C-N	-57.25	18.66	121.70
1	1-C	165	THR	C-N-CA	-57.25	18.66	121.70
1	2-C	165	THR	CA-C-N	-57.25	18.66	121.70
1	2-C	165	THR	C-N-CA	-57.25	18.66	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3-C	165	THR	CA-C-N	-57.25	18.66	121.70

There are no chirality outliers.

5 of 148 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-C	115	TYR	Mainchain
1	1-C	691	LEU	Mainchain
1	1-C	76	SER	Mainchain
1	1-C	824	TRP	Mainchain
2	1-Y	84	ASP	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-C	6215	0	6168	2860	0
1	2-C	6215	0	6174	2784	0
1	3-C	6215	0	6185	2643	0
1	4-C	6215	0	6176	2820	0
1	5-C	6215	0	6182	2654	0
1	6-C	6215	0	6180	2727	0
1	7-C	6215	0	6181	2665	0
1	8-C	6215	0	6179	2711	0
1	9-C	6215	0	6185	2665	0
1	10-C	6215	0	6183	2648	0
1	11-C	6215	0	6185	2643	0
1	12-C	6215	0	6185	2643	0
1	13-C	6215	0	6167	2881	0
1	14-C	6215	0	6185	2654	0
1	15-C	6215	0	6168	2851	0
1	16-C	6215	0	6185	2657	0
1	17-C	6215	0	6174	2887	0
1	18-C	6215	0	6185	2654	0
1	19-C	6215	0	6176	2737	0
1	20-C	6215	0	6184	2666	0
1	21-C	6215	0	6162	3008	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	22-C	6215	0	6183	2712	0
1	23-C	6215	0	6185	2653	0
1	24-C	6215	0	6168	2843	0
1	25-C	6215	0	6172	2768	0
1	26-C	6215	0	6185	2658	0
1	27-C	6215	0	6176	2791	0
2	1-Y	1088	0	1066	509	0
2	2-Y	1088	0	1066	480	0
2	3-Y	1088	0	1066	477	0
2	4-Y	1088	0	1066	504	0
2	5-Y	1088	0	1066	484	0
2	6-Y	1088	0	1066	482	0
2	7-Y	1088	0	1066	479	0
2	8-Y	1088	0	1066	474	0
2	9-Y	1088	0	1066	476	0
2	10-Y	1088	0	1066	485	0
2	11-Y	1088	0	1066	477	0
2	12-Y	1088	0	1066	477	0
2	13-Y	1088	0	1066	480	0
2	14-Y	1088	0	1066	480	0
2	15-Y	1088	0	1066	480	0
2	16-Y	1088	0	1066	482	0
2	17-Y	1088	0	1065	515	0
2	18-Y	1088	0	1066	480	0
2	19-Y	1088	0	1066	482	0
2	20-Y	1088	0	1066	483	0
2	21-Y	1088	0	1066	479	0
2	22-Y	1088	0	1066	480	0
2	23-Y	1088	0	1066	477	0
2	24-Y	1088	0	1066	474	0
2	25-Y	1088	0	1066	480	0
2	26-Y	1088	0	1066	482	0
2	27-Y	1088	0	1066	486	0
3	1-Z	1198	0	1119	514	0
3	2-Z	1198	0	1120	505	0
3	3-Z	1198	0	1120	504	0
3	4-Z	1198	0	1119	514	0
3	5-Z	1198	0	1120	507	0
3	6-Z	1198	0	1120	511	0
3	7-Z	1198	0	1120	510	0
3	8-Z	1198	0	1120	511	0
3	9-Z	1198	0	1120	504	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	10-Z	1198	0	1120	501	0
3	11-Z	1198	0	1120	504	0
3	12-Z	1198	0	1120	504	0
3	13-Z	1198	0	1120	552	0
3	14-Z	1198	0	1120	509	0
3	15-Z	1198	0	1120	510	0
3	16-Z	1198	0	1120	511	0
3	17-Z	1198	0	1118	545	0
3	18-Z	1198	0	1120	509	0
3	19-Z	1198	0	1120	508	0
3	20-Z	1198	0	1120	512	0
3	21-Z	1198	0	1118	630	0
3	22-Z	1198	0	1120	515	0
3	23-Z	1198	0	1120	512	0
3	24-Z	1198	0	1120	522	0
3	25-Z	1198	0	1118	535	0
3	26-Z	1198	0	1120	508	0
3	27-Z	1198	0	1120	507	0
All	All	229527	0	225831	96031	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 211.

The worst 5 of 96031 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:536:GLU:CB	1:C:547:PHE:HE1	1.04	1.67
1:C:536:GLU:CB	1:C:547:PHE:HE1	1.04	1.67
1:C:536:GLU:CB	1:C:547:PHE:HE1	1.04	1.67
1:C:536:GLU:CB	1:C:547:PHE:HE1	1.04	1.67
1:C:536:GLU:CB	1:C:547:PHE:HE1	1.04	1.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	1	15
1	2-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	3-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	1	16
1	4-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	1	15
1	5-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	1	15
1	6-C	754/831 (91%)	604 (80%)	112 (15%)	38 (5%)	1	16
1	7-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	1	15
1	8-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	9-C	758/831 (91%)	605 (80%)	115 (15%)	38 (5%)	1	16
1	10-C	758/831 (91%)	605 (80%)	114 (15%)	39 (5%)	1	15
1	11-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	1	16
1	12-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	1	16
1	13-C	758/831 (91%)	608 (80%)	112 (15%)	38 (5%)	1	16
1	14-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	15-C	758/831 (91%)	607 (80%)	112 (15%)	39 (5%)	1	15
1	16-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	17-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	1	15
1	18-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	19-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	20-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	1	15
1	21-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	22-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	1	16
1	23-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	1	16
1	24-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	1	15
1	25-C	758/831 (91%)	608 (80%)	112 (15%)	38 (5%)	1	16
1	26-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	1	16
1	27-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	1	16
2	1-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	2-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	3-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	4-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	5-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	6-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	7-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	8-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	9-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	10-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	11-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	12-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	13-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	14-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	15-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	16-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	17-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	18-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	19-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	20-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	21-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	22-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	23-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	24-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	25-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	26-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
2	27-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	2	17
3	1-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	12
3	2-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	3-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	4-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	5-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	6-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	7-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	8-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	12
3	9-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	10-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	11-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	12-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	13-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	14-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	15-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	16-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	12
3	17-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	12
3	18-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	19-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	12
3	20-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	21-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	22-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	23-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	24-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	12
3	25-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	26-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
3	27-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	1	13
All	All	28097/30186 (93%)	21738 (77%)	4913 (18%)	1446 (5%)	3	15

5 of 1446 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-C	27	ALA
1	1-C	366	ARG
1	1-C	368	ARG
1	1-C	371	GLN
1	1-C	542	ALA

5.3.2 Protein sidechains ⓘ

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	1-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	2-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	3-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	4-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	5-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	6-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	7-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	8-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	9-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	10-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	11-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	12-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	13-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	14-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	15-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	16-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	17-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	18-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	19-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	20-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	21-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	22-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	23-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	24-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	25-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	26-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
1	27-C	678/724 (94%)	579 (85%)	99 (15%)	3	13
2	1-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	2-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	4-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	5-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	6-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	7-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	8-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	9-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	10-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	11-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	12-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	13-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	14-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	15-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	16-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	17-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	18-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	19-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	20-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	21-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	22-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	23-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	24-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	25-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	26-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
2	27-Y	119/119 (100%)	106 (89%)	13 (11%)	6	21
3	1-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	2-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	3-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	4-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	5-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	6-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	7-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	8-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	9-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	10-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	11-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	12-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	13-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	14-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	15-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	16-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	17-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	18-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	19-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	20-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	21-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	22-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	23-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	24-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	25-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	26-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
3	27-Z	127/127 (100%)	114 (90%)	13 (10%)	7	23
All	All	24948/26190 (95%)	21573 (86%)	3375 (14%)	6	14

5 of 3375 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	15-Y	43	ILE
1	19-C	337	ILE
1	26-C	654	ASN
1	16-C	279	GLU
2	15-Y	27	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1290 such sidechains are listed below:

Mol	Chain	Res	Type
1	20-C	443	ASN
1	25-C	124	ASN
3	20-Z	138	ASN
1	20-C	436	ASN
2	22-Y	119	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	6-C	12
1	1-C	12
1	17-C	12
1	4-C	11
1	2-C	11
1	5-C	11
1	7-C	11
1	19-C	11

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
1	26-C	11
1	27-C	11
1	3-C	10
1	8-C	10
1	9-C	10
1	10-C	10
1	11-C	10
1	12-C	10
1	13-C	10
1	14-C	10
1	15-C	10
1	16-C	10
1	18-C	10
1	20-C	10
1	21-C	10
1	22-C	10
1	23-C	10
1	24-C	10
1	25-C	10

The worst 5 of 283 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
6	C	800:LYS	C	801:LEU	N	2.57
6	C	705:LYS	C	706:GLY	N	2.32
1	C	800:LYS	C	801:LEU	N	2.23
4	C	800:LYS	C	801:LEU	N	2.23
17	C	800:LYS	C	801:LEU	N	2.19

6 Tomogram visualisation

This section contains visualisations of the EMDB entry EMD-1584. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Mask visualisation

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

7 Tomogram analysis

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

7.1 Map-value distribution

This section was not generated.

8 Map-model fit

This section was not generated.