



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Apr 12, 2017 – 09:09 PM EDT

PDB ID : 2W4V
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/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029077

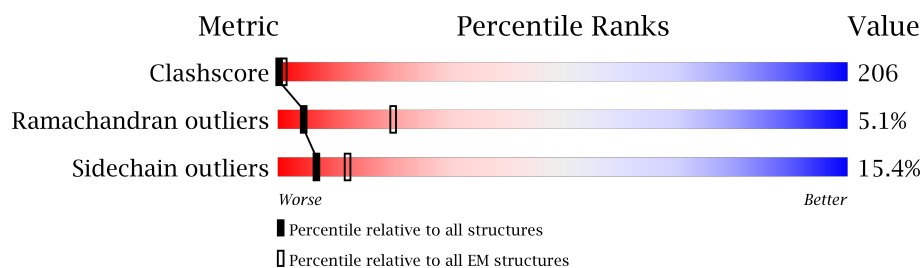
1 Overall quality at a glance

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.




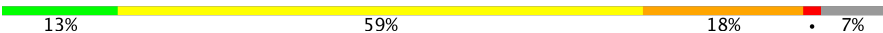
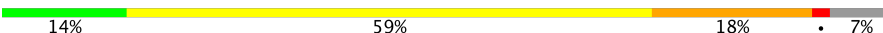


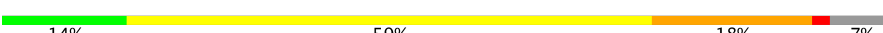
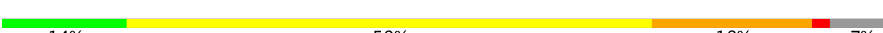




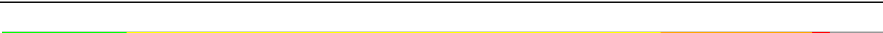






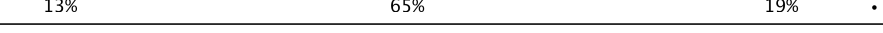



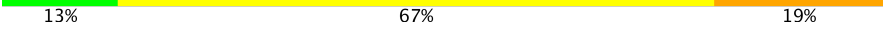
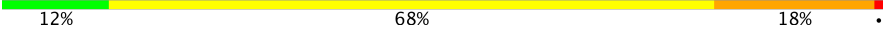
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	13% 59% 18% • 7%
1	10-C	831	14% 59% 18% • 7%
1	11-C	831	14% 60% 17% • 7%
1	12-C	831	14% 60% 17% • 7%
1	13-C	831	13% 60% 18% • 7%
1	14-C	831	13% 59% 18% • 7%
1	15-C	831	13% 59% 18% • 7%
1	16-C	831	13% 59% 18% • 7%
1	17-C	831	13% 59% 18% • 7%


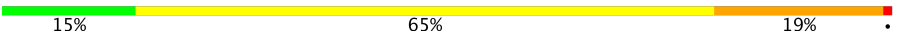
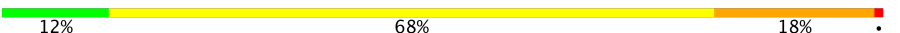


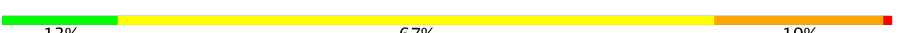
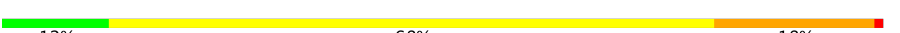




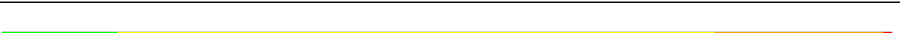





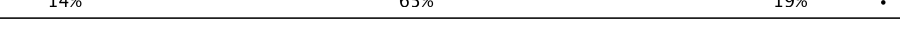


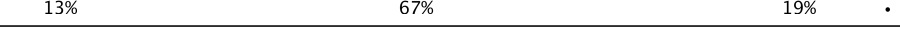
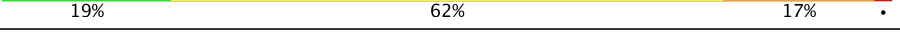
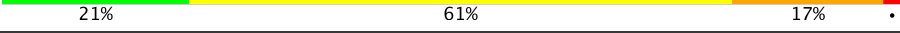
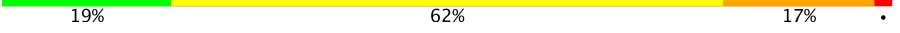
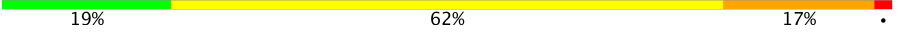
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Mol	Chain	Length	Quality of chain
1	18-C	831	
1	19-C	831	
1	2-C	831	
1	20-C	831	
1	21-C	831	
1	22-C	831	
1	23-C	831	
1	24-C	831	
1	25-C	831	
1	26-C	831	
1	27-C	831	
1	3-C	831	
1	4-C	831	
1	5-C	831	
1	6-C	831	
1	7-C	831	
1	8-C	831	
1	9-C	831	
2	1-Y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

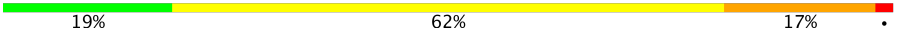
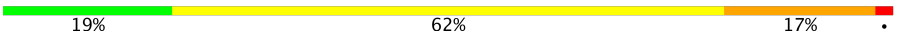
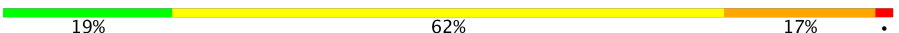
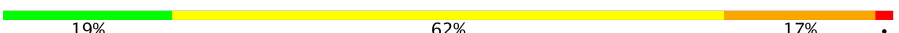
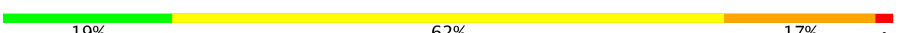
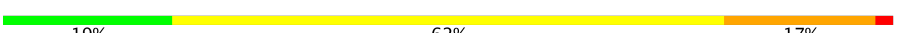
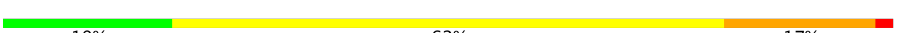




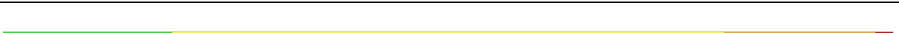



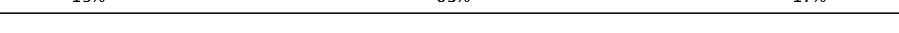
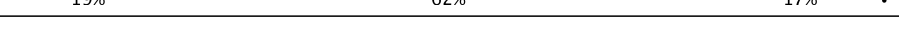
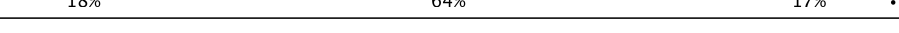
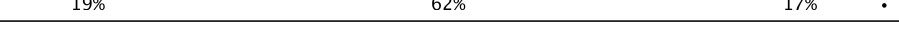
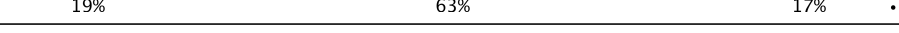
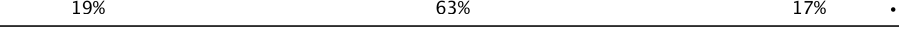
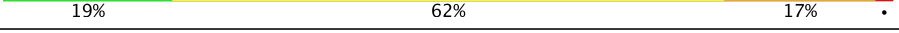
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Mol	Chain	Length	Quality of chain
2	16-Y	136	 12%68%18%.
2	17-Y	136	 15%65%19%.
2	18-Y	136	 12%68%18%.
2	19-Y	136	 13%67%19%.
2	2-Y	136	 12%67%20%.
2	20-Y	136	 13%67%19%.
2	21-Y	136	 12%68%18%.
2	22-Y	136	 13%66%20%.
2	23-Y	136	 13%67%19%.
2	24-Y	136	 14%66%18%.
2	25-Y	136	 12%68%19%.
2	26-Y	136	 13%67%19%.
2	27-Y	136	 13%66%18%.
2	3-Y	136	 13%65%21%.
2	4-Y	136	 13%65%21%.
2	5-Y	136	 13%65%19%.
2	6-Y	136	 14%65%19%.
2	7-Y	136	 12%67%20%.
2	8-Y	136	 12%68%18%.
2	9-Y	136	 13%67%19%.
3	1-Z	151	 19%62%17%.
3	10-Z	151	 21%61%17%.
3	11-Z	151	 19%62%17%.
3	12-Z	151	 19%62%17%.
3	13-Z	151	 19%63%17%.

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

2 Entry composition

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		

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

- 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	C	N	O	S	0	0
			1088	687	173	219	9		
2	2-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	3-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	4-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	5-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	6-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	7-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	8-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		
2	9-Y	136	Total	C	N	O	S	0	0
			1088	687	173	219	9		

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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		

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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		

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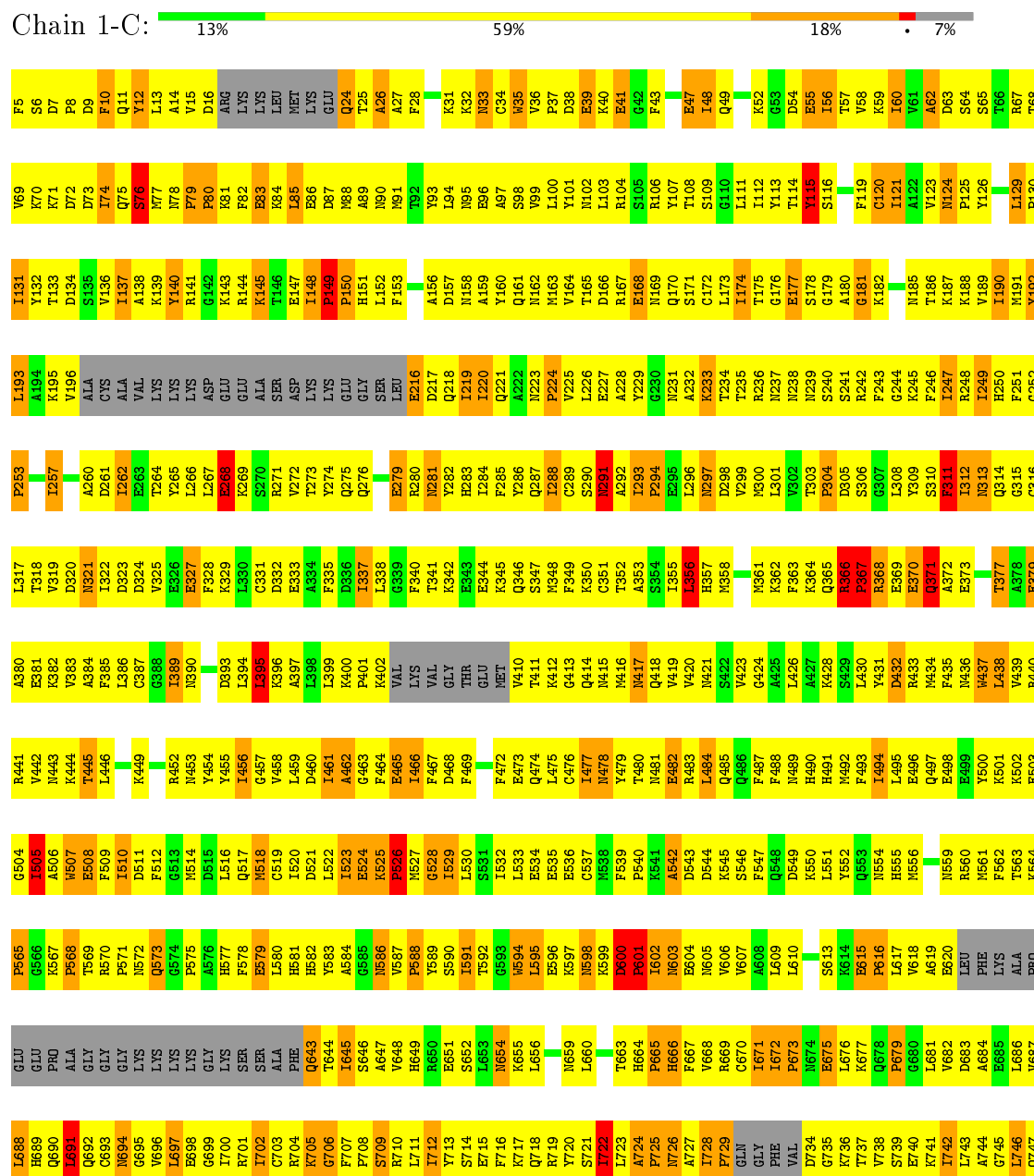
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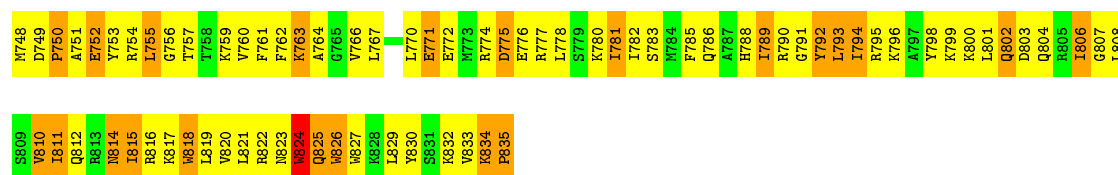
Mol	Chain	Residues	Atoms					AltConf	Trace
3	23-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	24-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	25-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	26-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	27-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244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

3 Residue-property plots

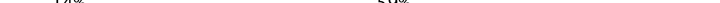
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according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

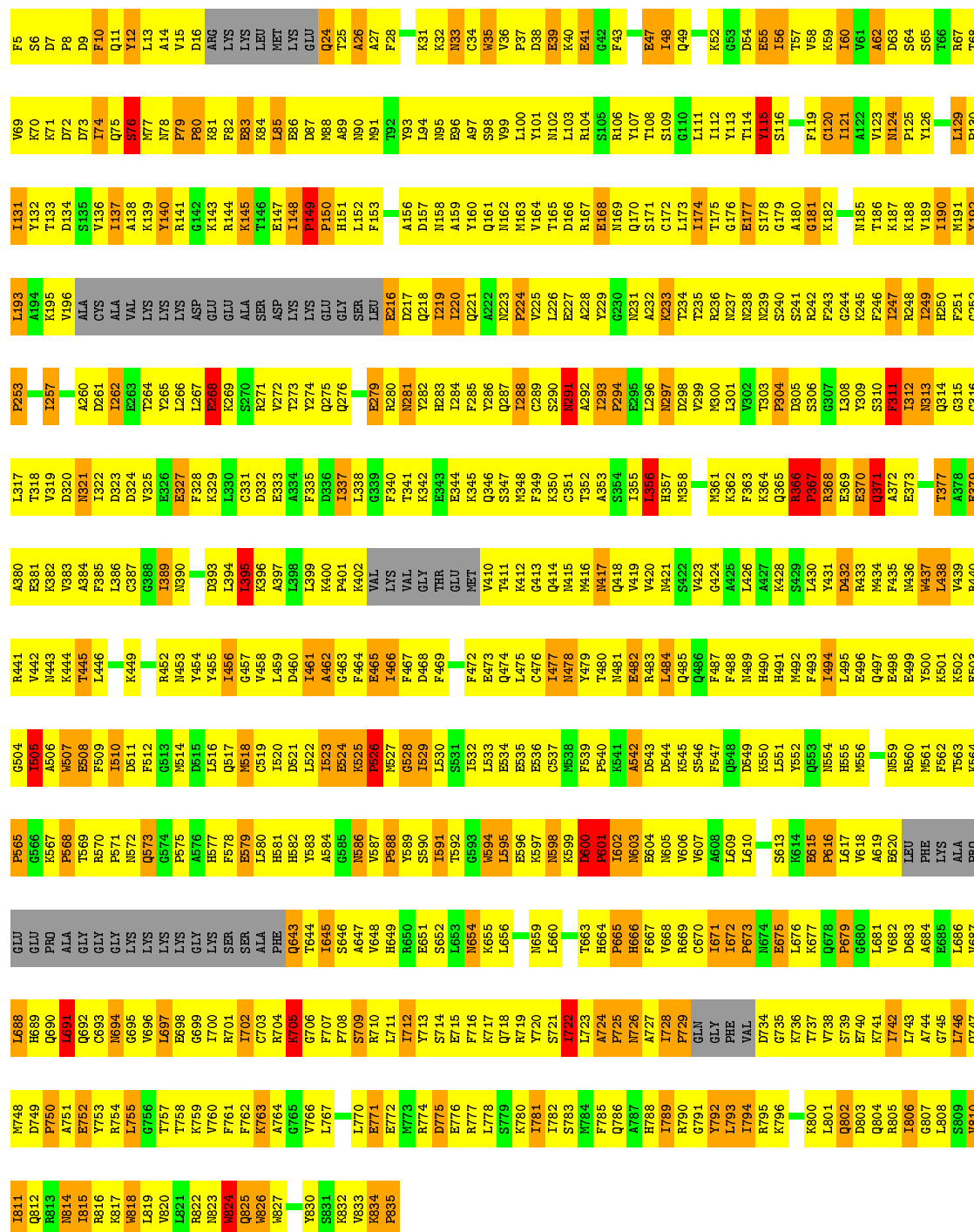
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE






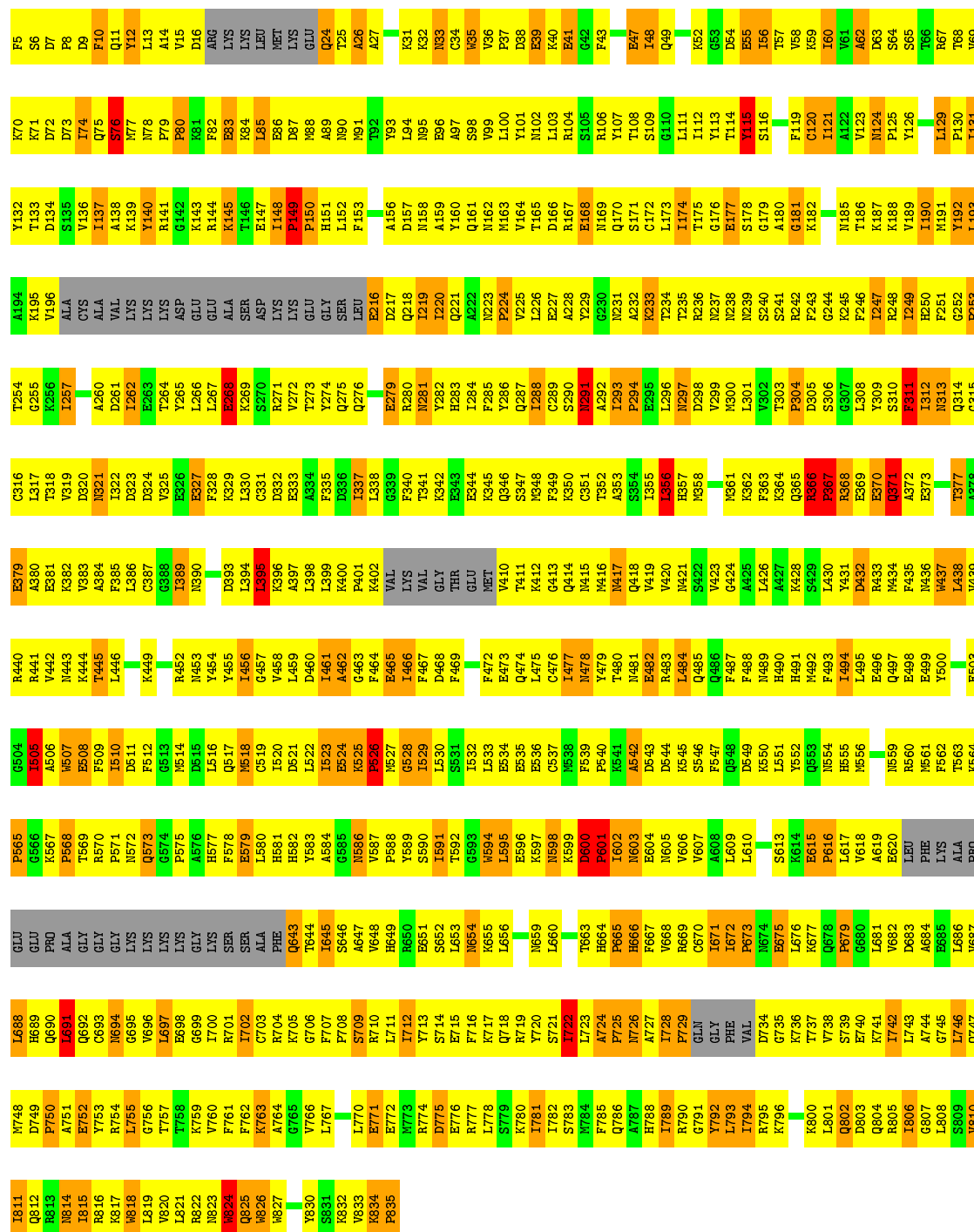
- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 2-C:  14% 59% 18% 7%




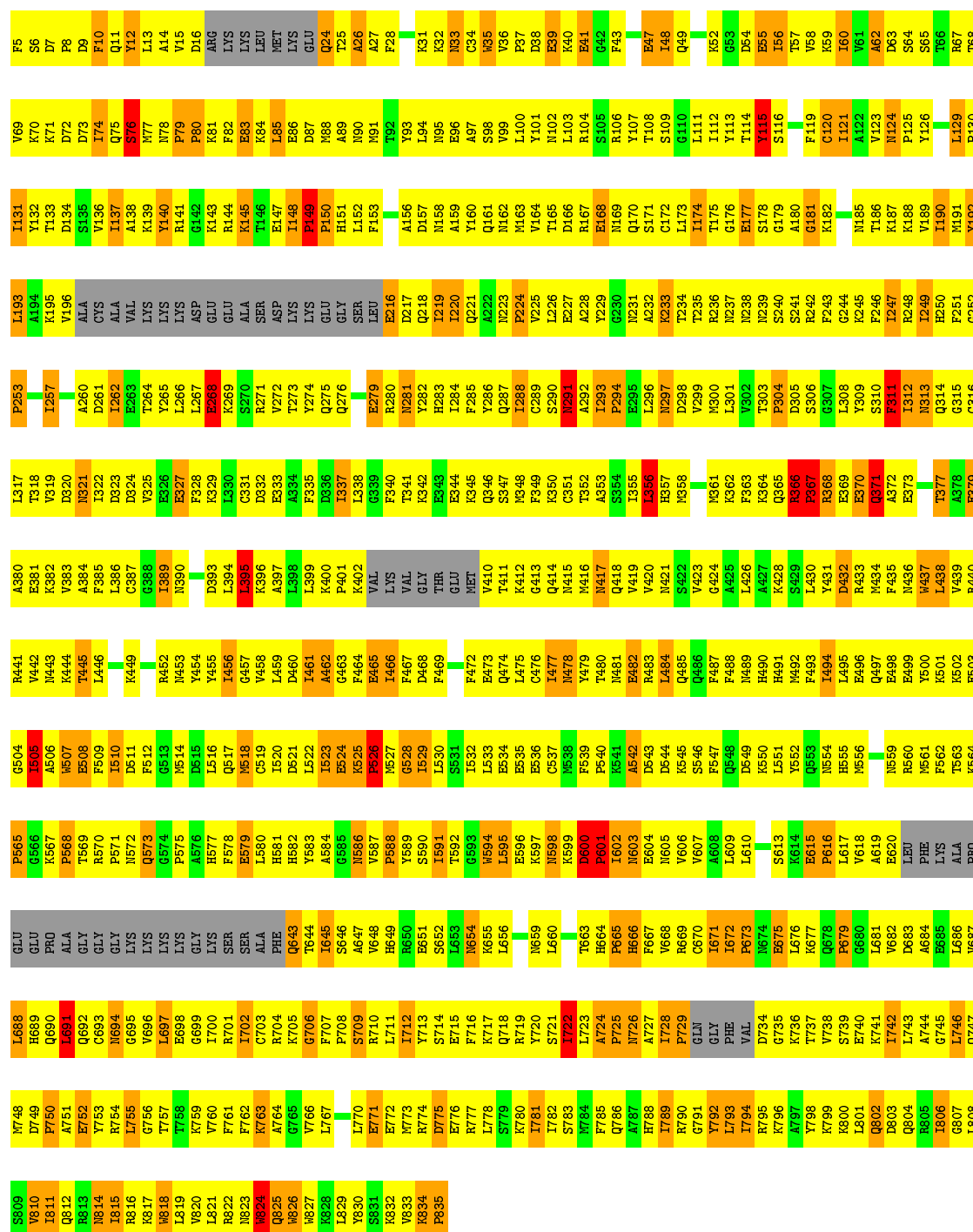
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 3-C: 

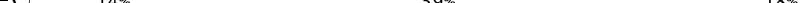


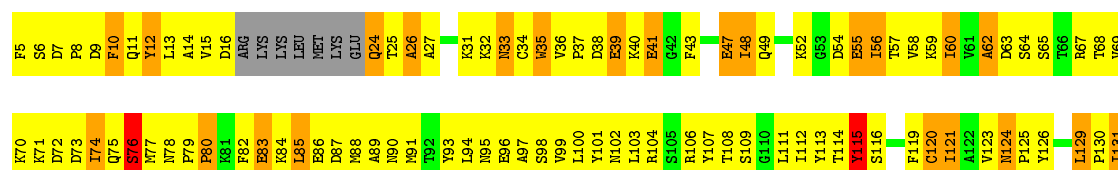
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 4-C: 

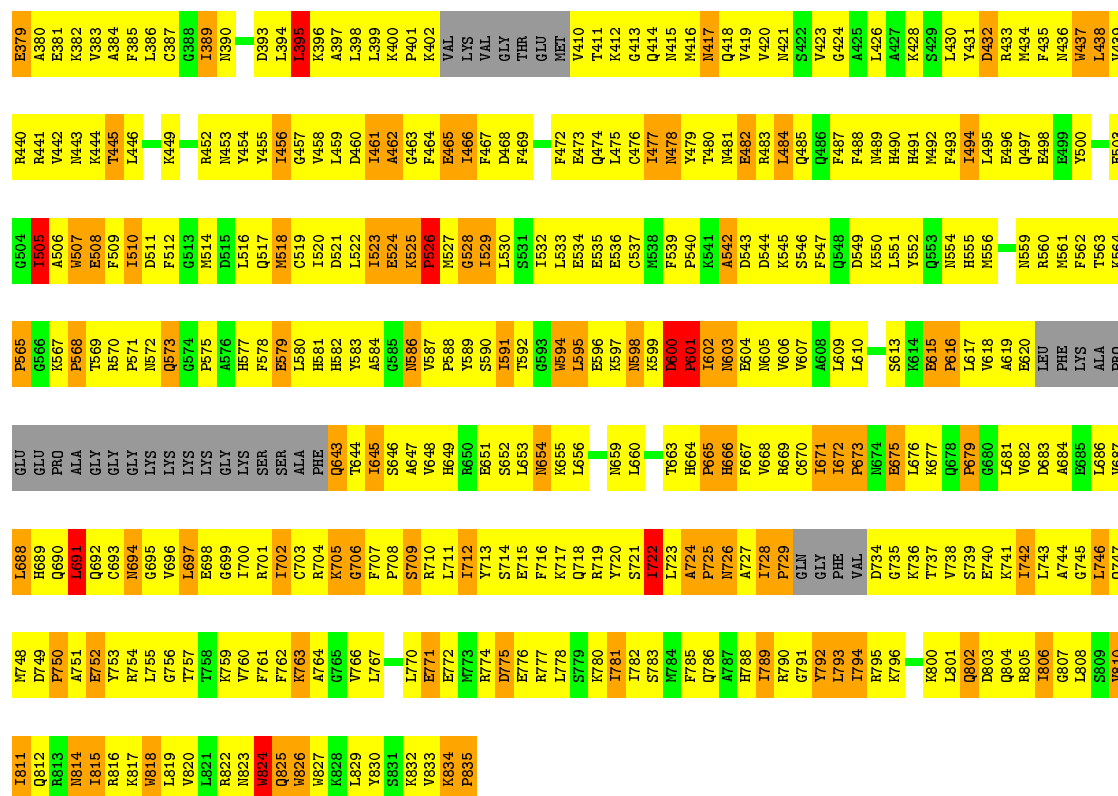


- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 5-C:  14% 59% 18% 7%

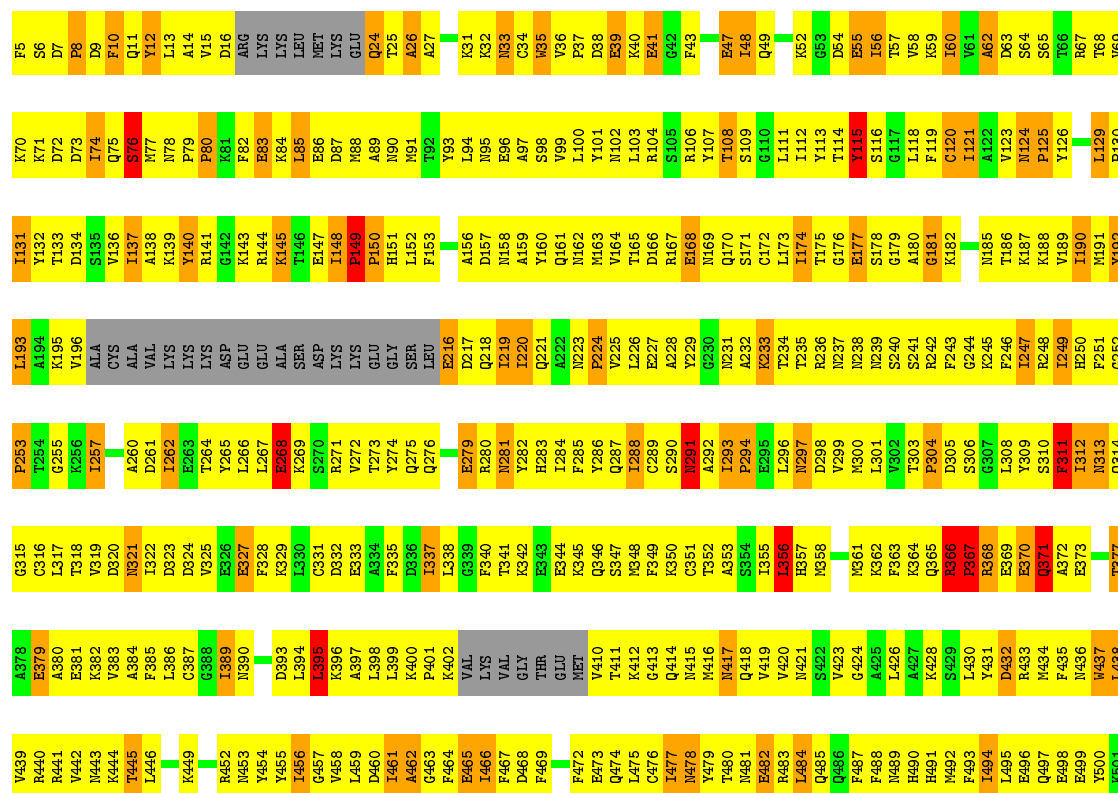


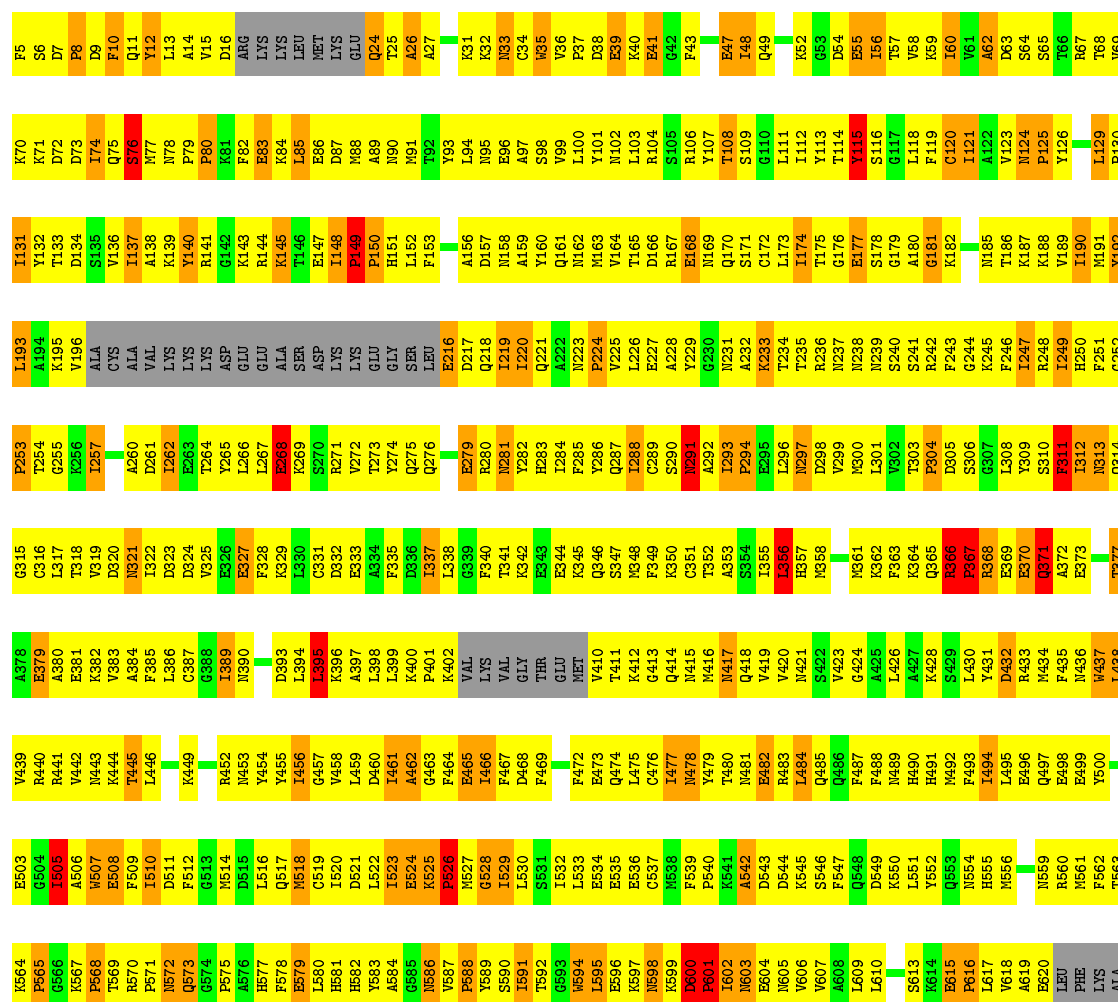
Y132	T133	D134	S135	I136	A137	A138	K139	Y140	G141	G142	K143	R144	K145	T146	E147	I148	P149	P150	H151	L152	F153	A156	D157	N158	A159	Y160	Q161	N162	M163	V164	T165	R166	R167	E168	N169	Q170	S171	G172	L173	T174	T175	G176	E177	S178	G179	A180	G181	K182	N185	T186	K187	K188	V189	I190	M191	G192	G252	P253																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
A194	K195	V196	ALA	CYS	ALA	VAL	LYS	LYS	ASP	GLU	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	R233	T234	T235	R236	N237	N238	N239	S240	S241	R242	F243	G244	K245	F246	I247	K187	K188	V189	I190	M191	G192	G252	P253																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
T254	G255	K256	T257	A260	D261	L262	E263	T264	Y265	L266	L267	E268	K269	C316	L317	T318	V319	D320	N321	I322	D323	D324	E325	E326	E327	F328	K329	L330	C331	R332	E333	V334	T335	T336	T337	T338	T339	T340	T341	T342	T343	T344	T345	T346	T347	T348	T349	T350	T351	T352	T353	T354	T355	T356	T357	T358	T359	T360	T361	T362	T363	T364	T365	T366	T367	T368	T369	T370	T371	T372	T373	T374	T375	T376	T377	T378	T379	T380	T381	T382	T383	T384	T385	T386	T387	T388	T389	T390	T391	T392	T393	T394	T395	T396	T397	T398	T399	T400	T401	T402	T403	T404	T405	T406	T407	T408	T409	T410	T411	T412	T413	T414	T415	T416	T417	T418	T419	T420	T421	T422	T423	T424	T425	T426	T427	T428	T429	T430	T431	T432	T433	T434	T435	T436	T437	T438	T439	T440	T441	T442	T443	T444	T445	T446	T447	T448	T449	T450	T451	T452	T453	T454	T455	T456	T457	T458	T459	T460	T461	T462	T463	T464	T465	T466	T467	T468	T469	T470	T471	T472	T473	T474	T475	T476	T477	T478	T479	T480	T481	T482	T483	T484	T485	T486	T487	T488	T489	T490	T491	T492	T493	T494	T495	T496	T497	T498	T499	T500	T501	T502	T503	T504	T505	T506	T507	T508	T509	T510	T511	T512	T513	T514	T515	T516	T517	T518	T519	T520	T521	T522	T523	T524	T525	T526	T527	T528	T529	T530	T531	T532	T533	T534	T535	T536	T537	T538	T539	T540	T541	T542	T543	T544	T545	T546	T547	T548	T549	T550	T551	T552	T553	T554	T555	T556	T557	T558	T559	T560	T561	T562	T563	T564	T565	T566	T567	T568	T569	T570	T571	T572	T573	T574	T575	T576	T577	T578	T579	T580	T581	T582	T583	T584	T585	T586	T587	T588	T589	T590	T591	T592	T593	T594	T595	T596	T597	T598	T599	T600	T601	T602	T603	T604	T605	T606	T607	T608	T609	T610	T611	T612	T613	T614	T615	T616	T617	T618	T619	T620	T621	T622	T623	T624	T625	T626	T627	T628	T629	T630	T631	T632	T633	T634	T635	T636	T637	T638	T639	T640	T641	T642	T643	T644	T645	T646	T647	T648	T649	T650	T651	T652	T653	T654	T655	T656	T657	T658	T659	T660	T661	T662	T663	T664	T665	T666	T667	T668	T669	T670	T671	T672	T673	T674	T675	T676	T677	T678	T679	T680	T681	T682	T683	T684	T685	T686	T687	T688	T689	T690	T691	T692	T693	T694	T695	T696	T697	T698	T699	T700	T701	T702	T703	T704	T705	T706	T707	T708	T709	T710	T711	T712	T713	T714	T715	T716	T717	T718	T719	T720	T721	T722	T723	T724	T725	T726	T727	T728	T729	T730	T731	T732	T733	T734	T735	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	T125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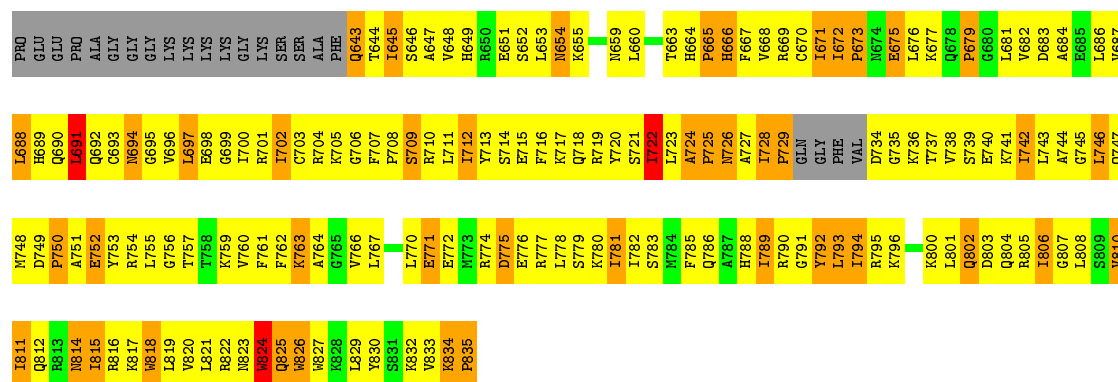


● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 8-C: 13% 59% 18% 7%

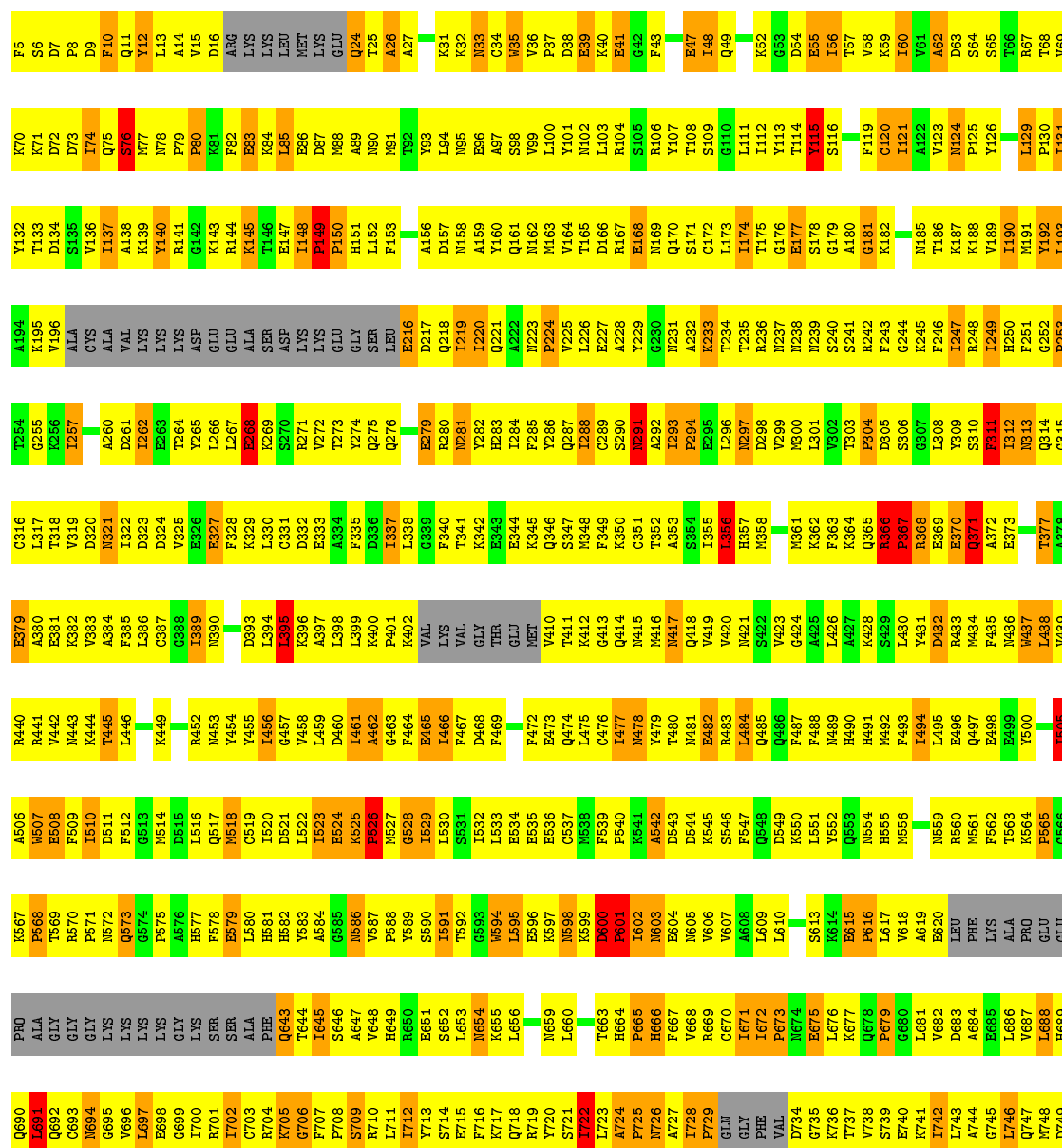


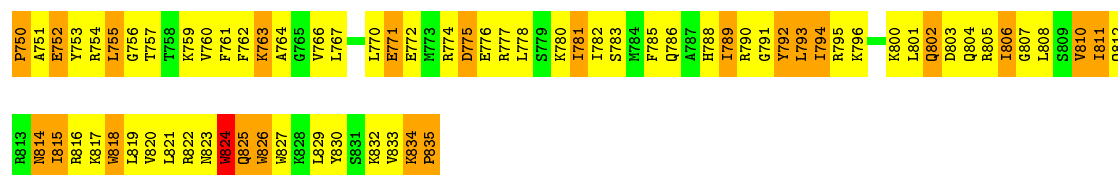




- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

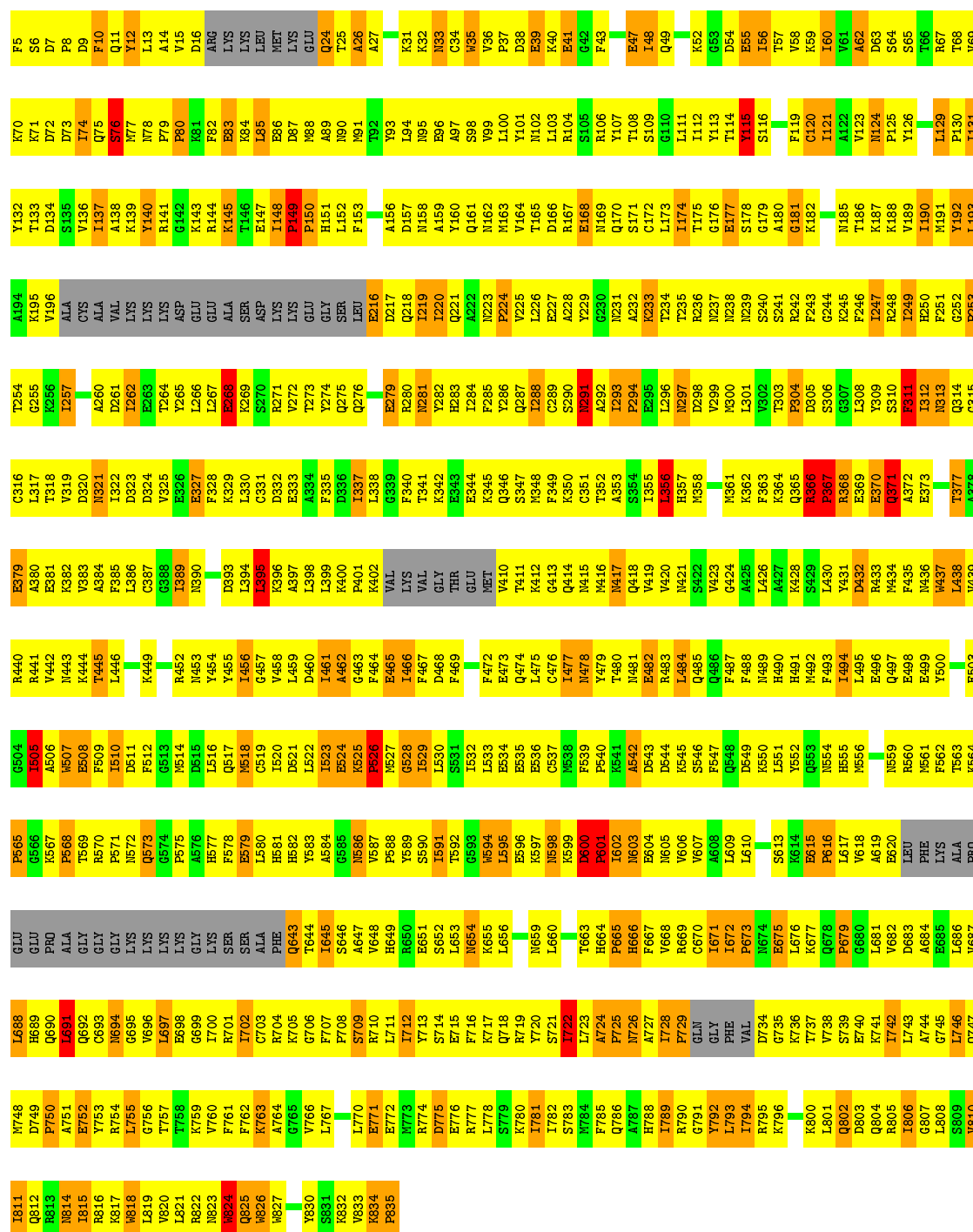
Chain 10-C:  14% 59% 18% 7%



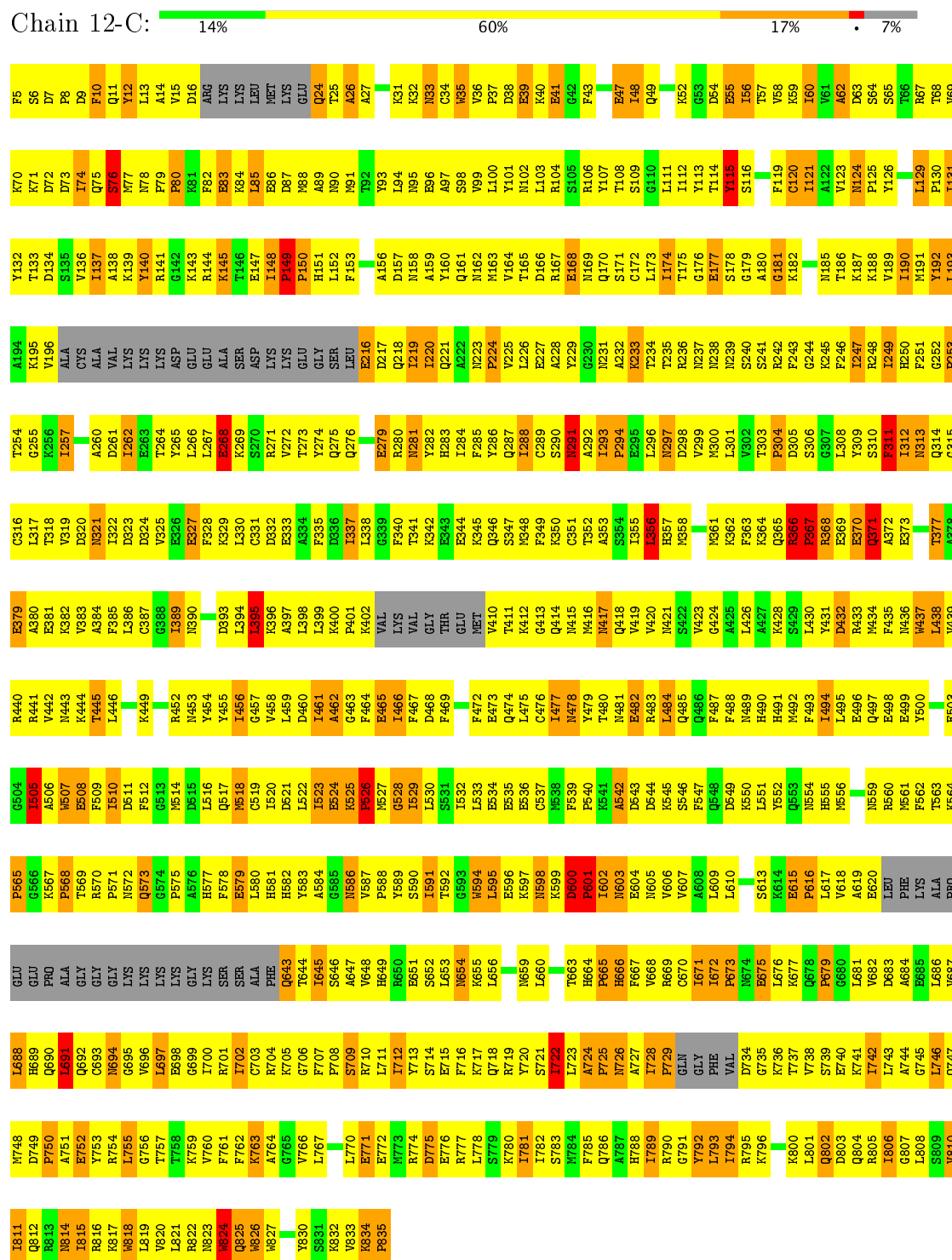


• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 11-C: 14% 60% 17% 7%

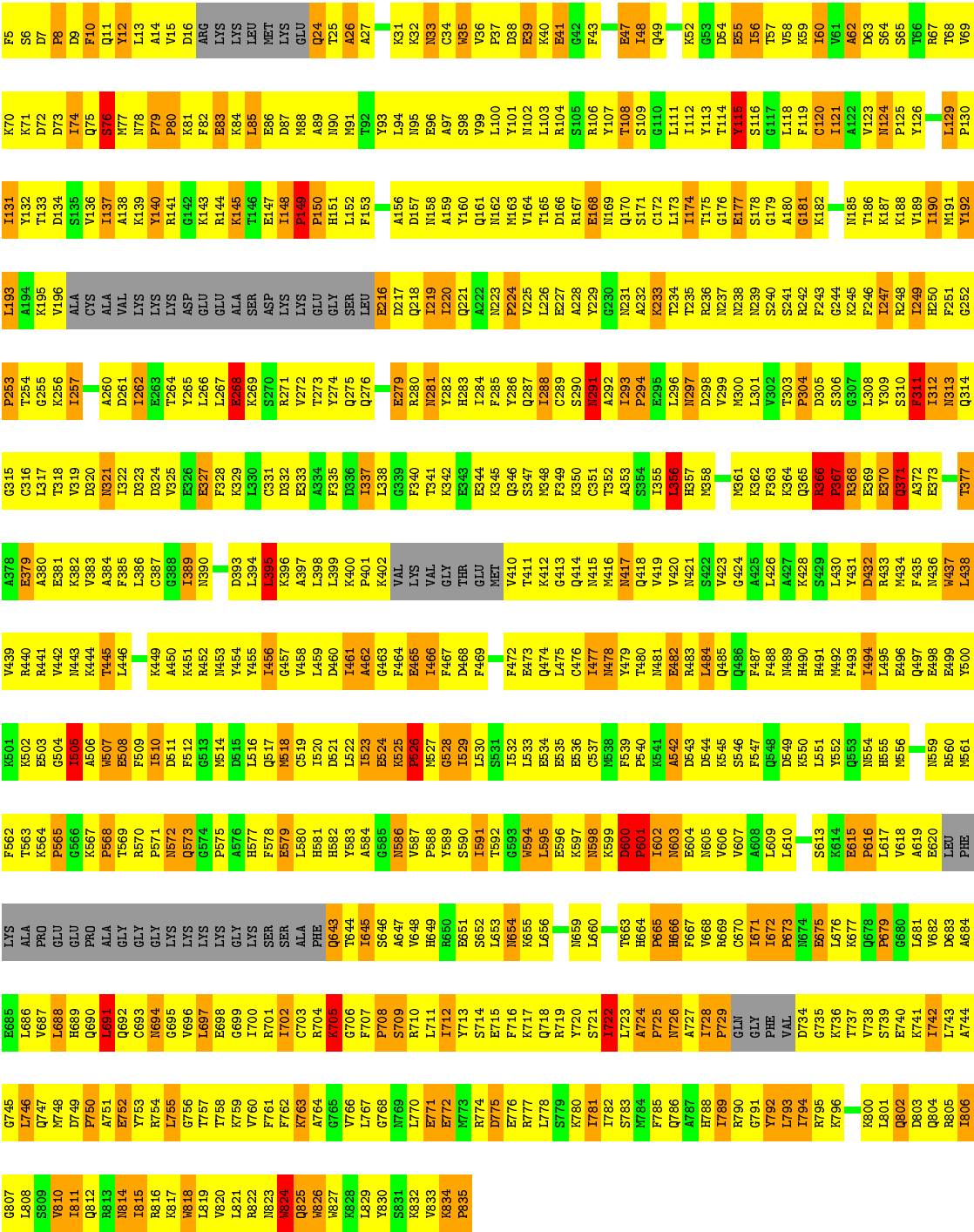


● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE



● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE



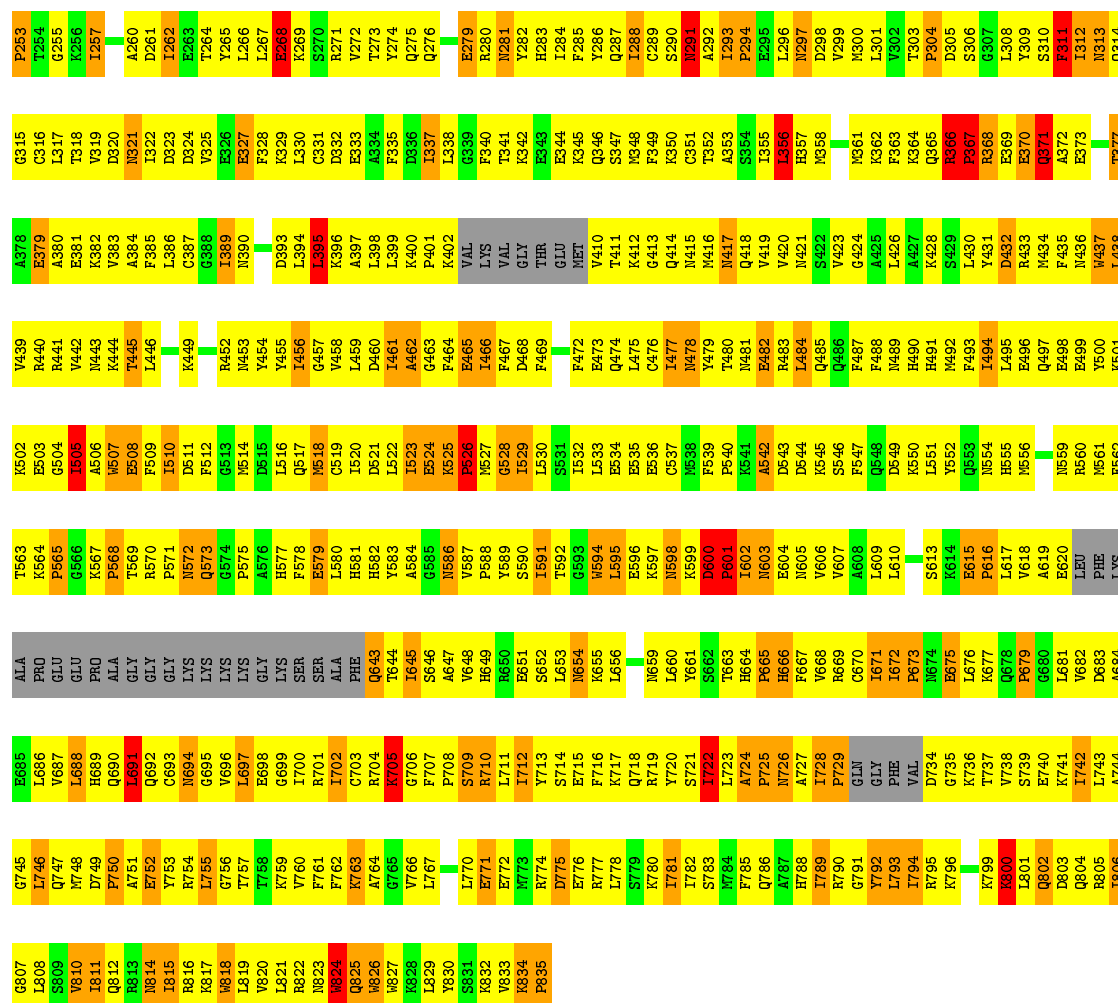


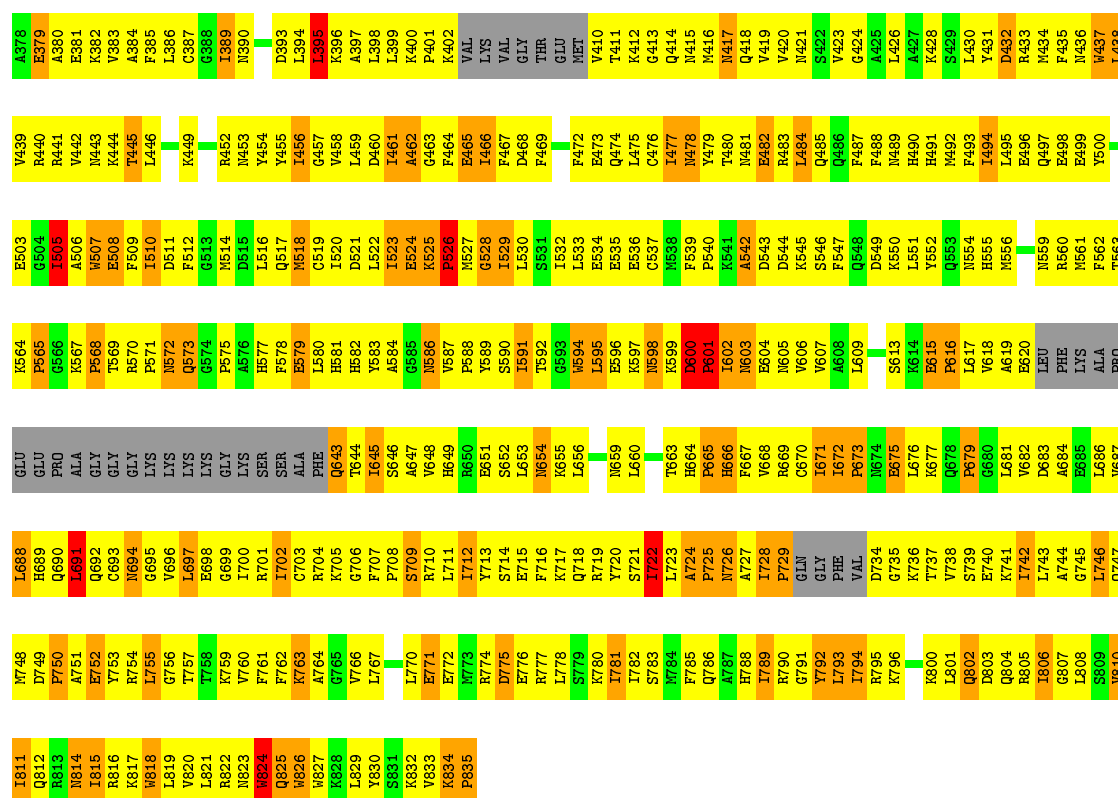
● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 14-C: 13% 59% 18% 7%



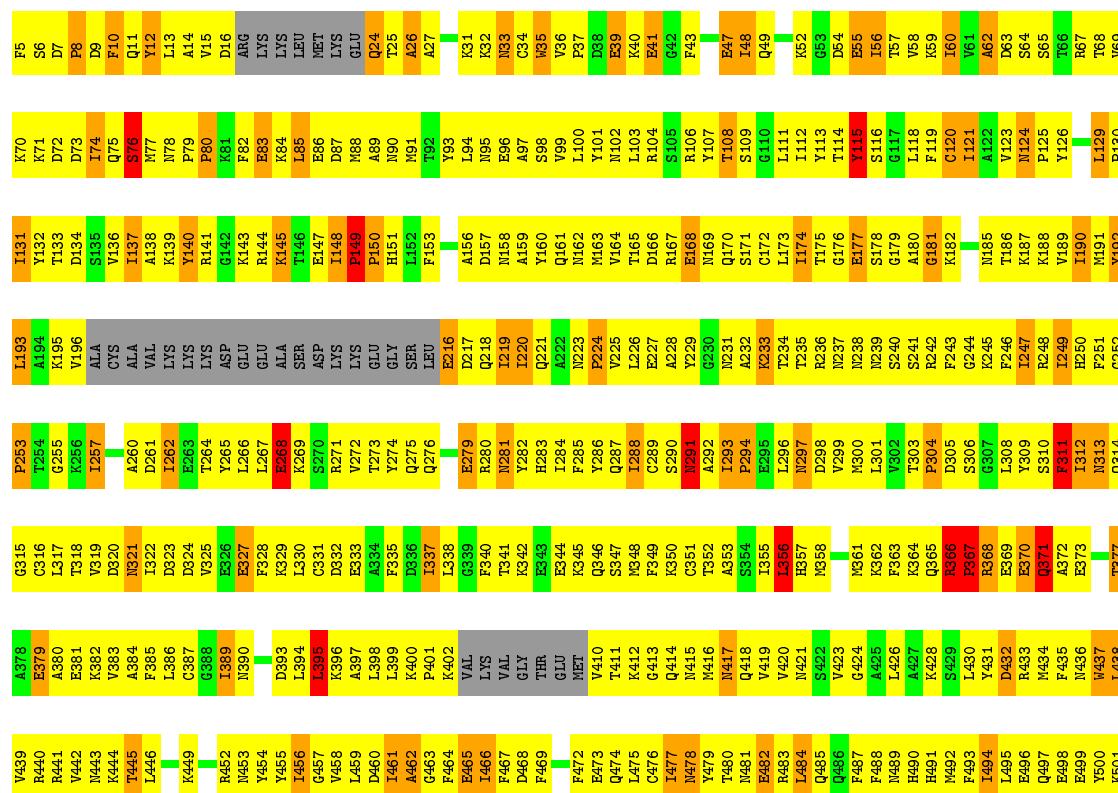
L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	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	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L1046	L1047	L1048	L1049	L1050	L1051	L1052	L1053	L1054	L1055	L1056	L1057	L1058	L1059	L1060	L1061	L1062	L1063	L1064	L1065	L1066	L1067	L1068	L1069	L1070	L1071	L1072	L1073	L1074	L1075	L1076	L1077	L1078	L1079	L1080	L1081	L1082	L1083	L1084	L1085	L1086	L1087	L1088	L1089	L1090	L1091	L1092	L1093	L1094	L1095	L1096	L1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157	L1158	L1159	L1160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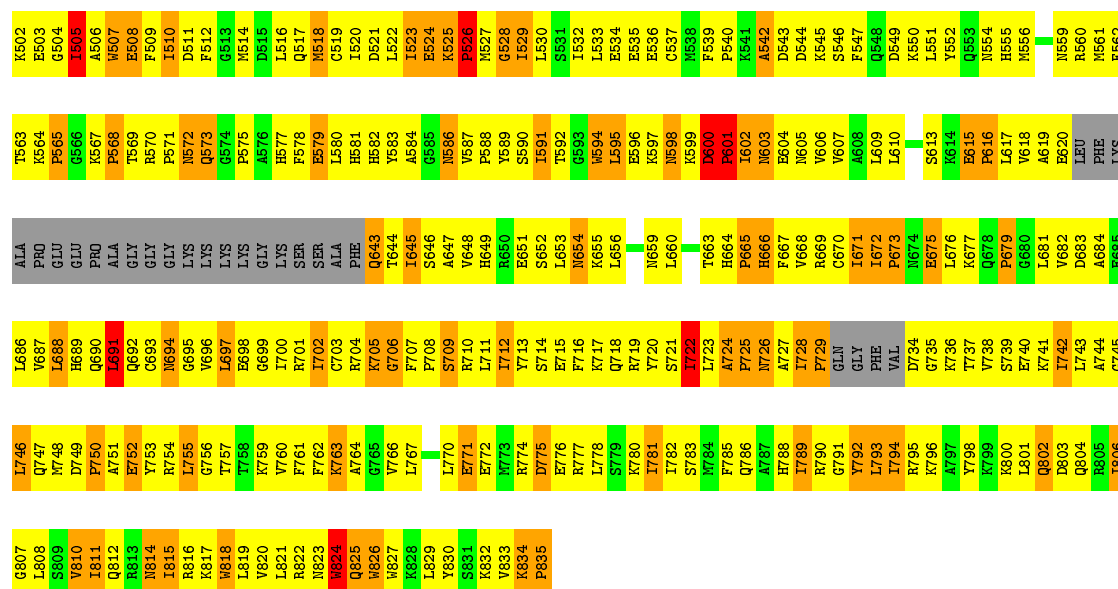




● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

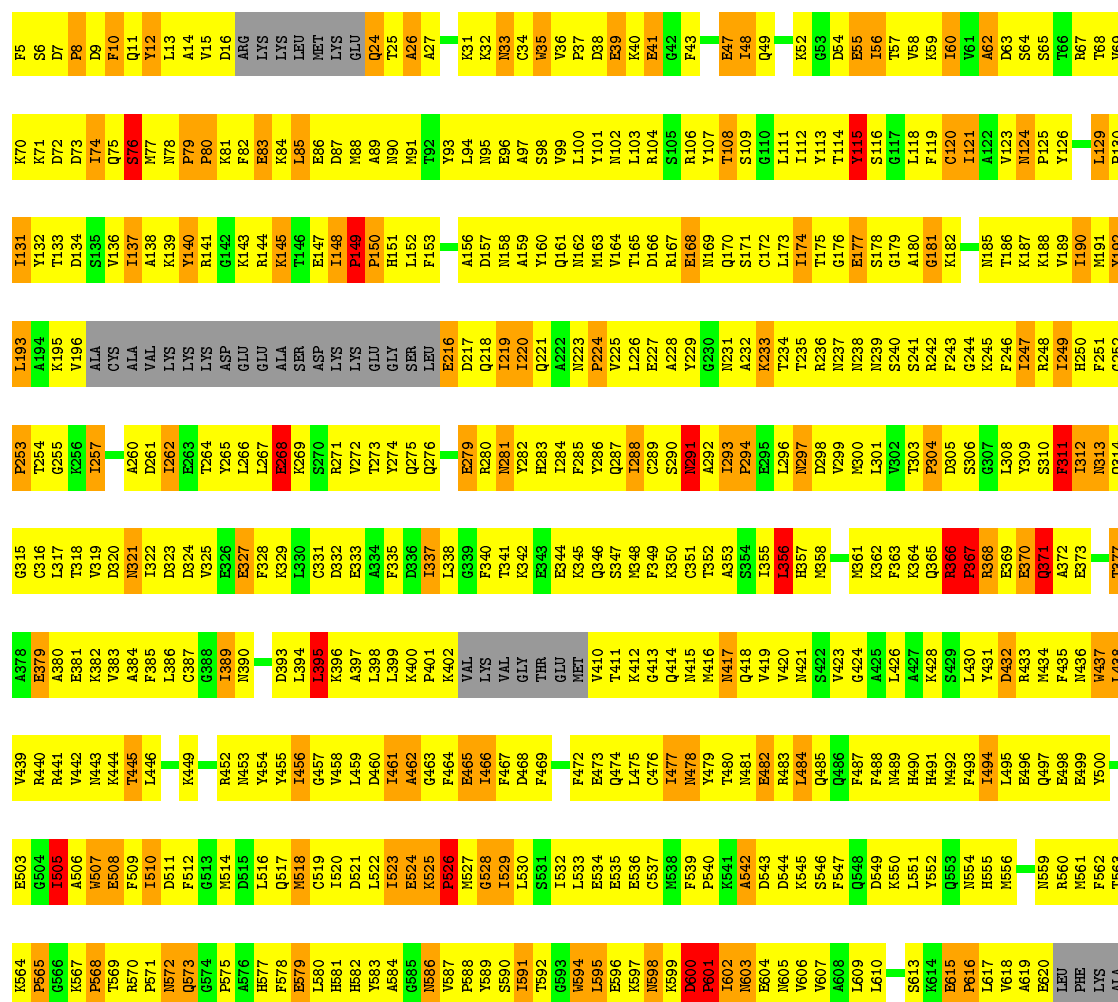
Chain 17-C: 13% 59% 18% 7%

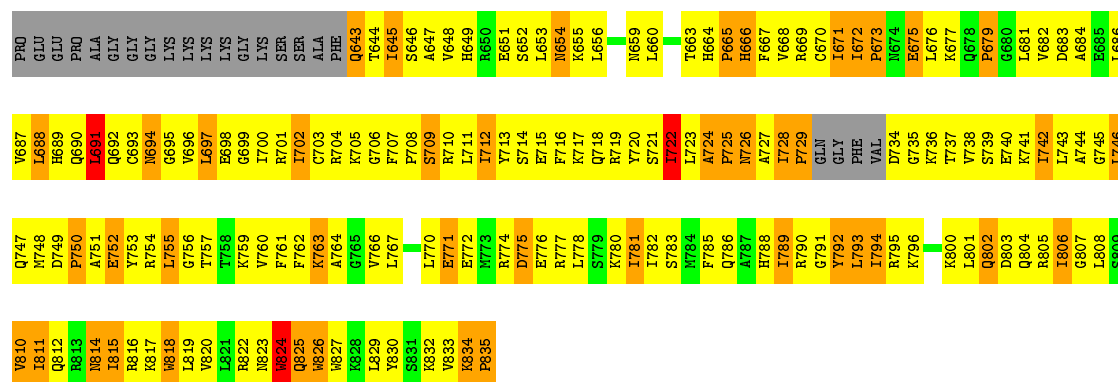




Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

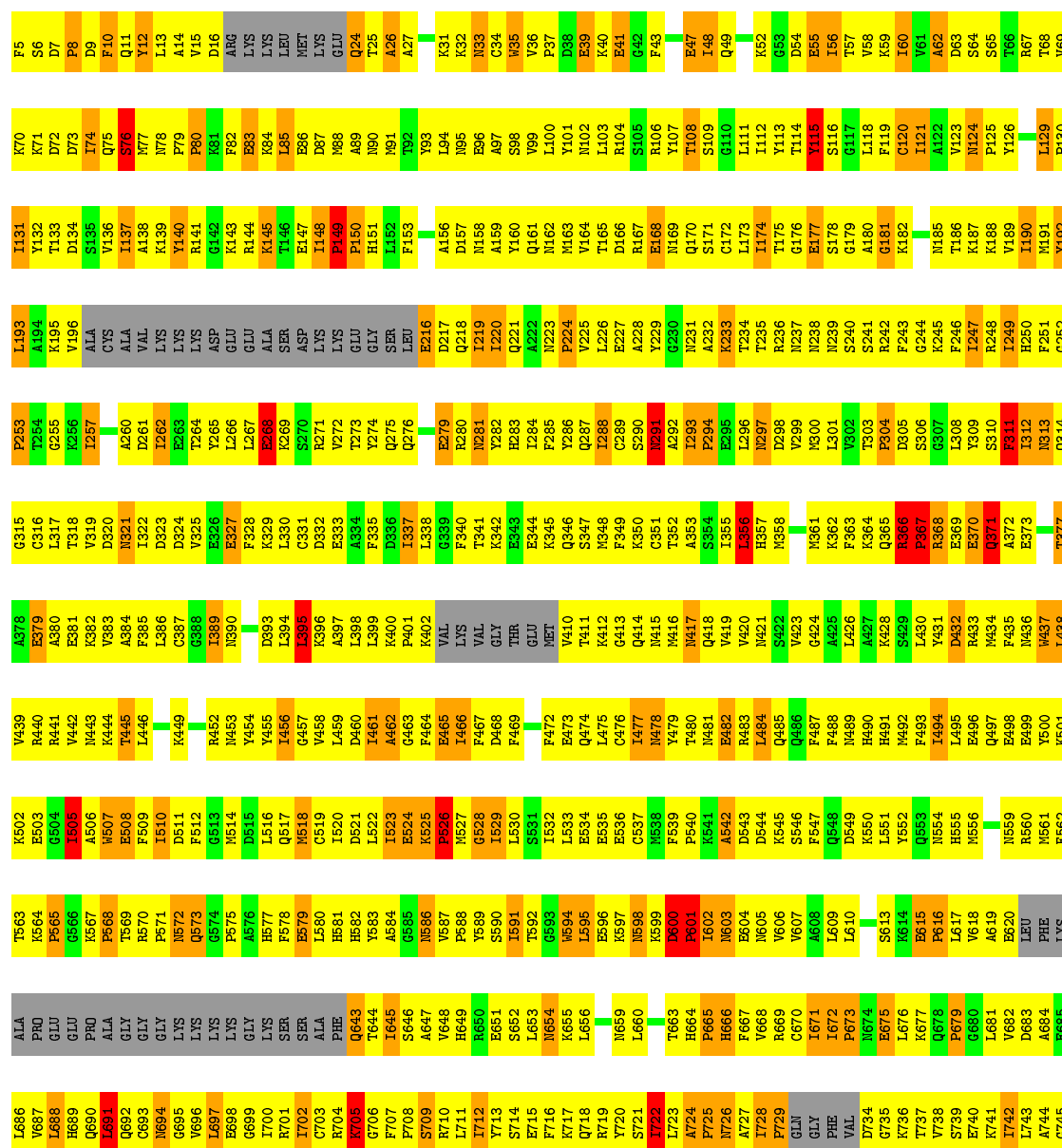
Chain 18-C:

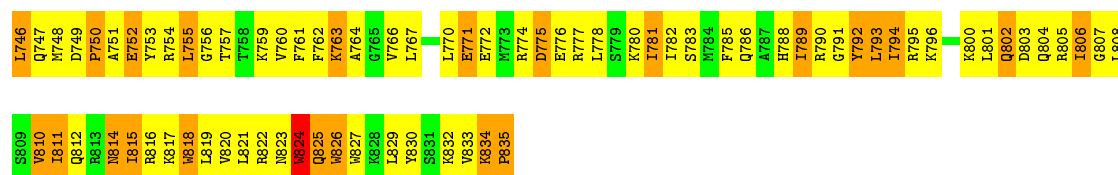




• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

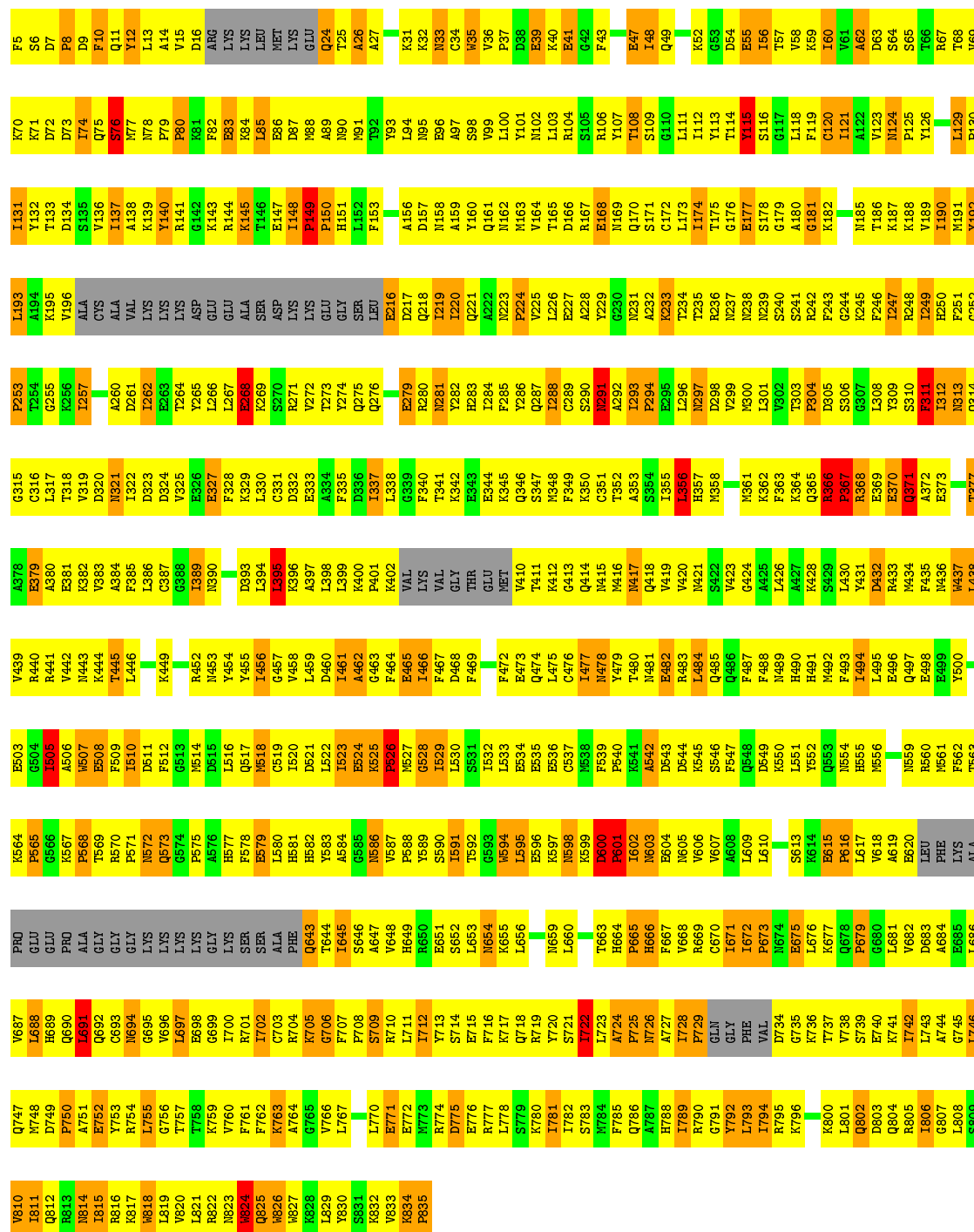
Chain 19-C: 13% 59% 18% 7%



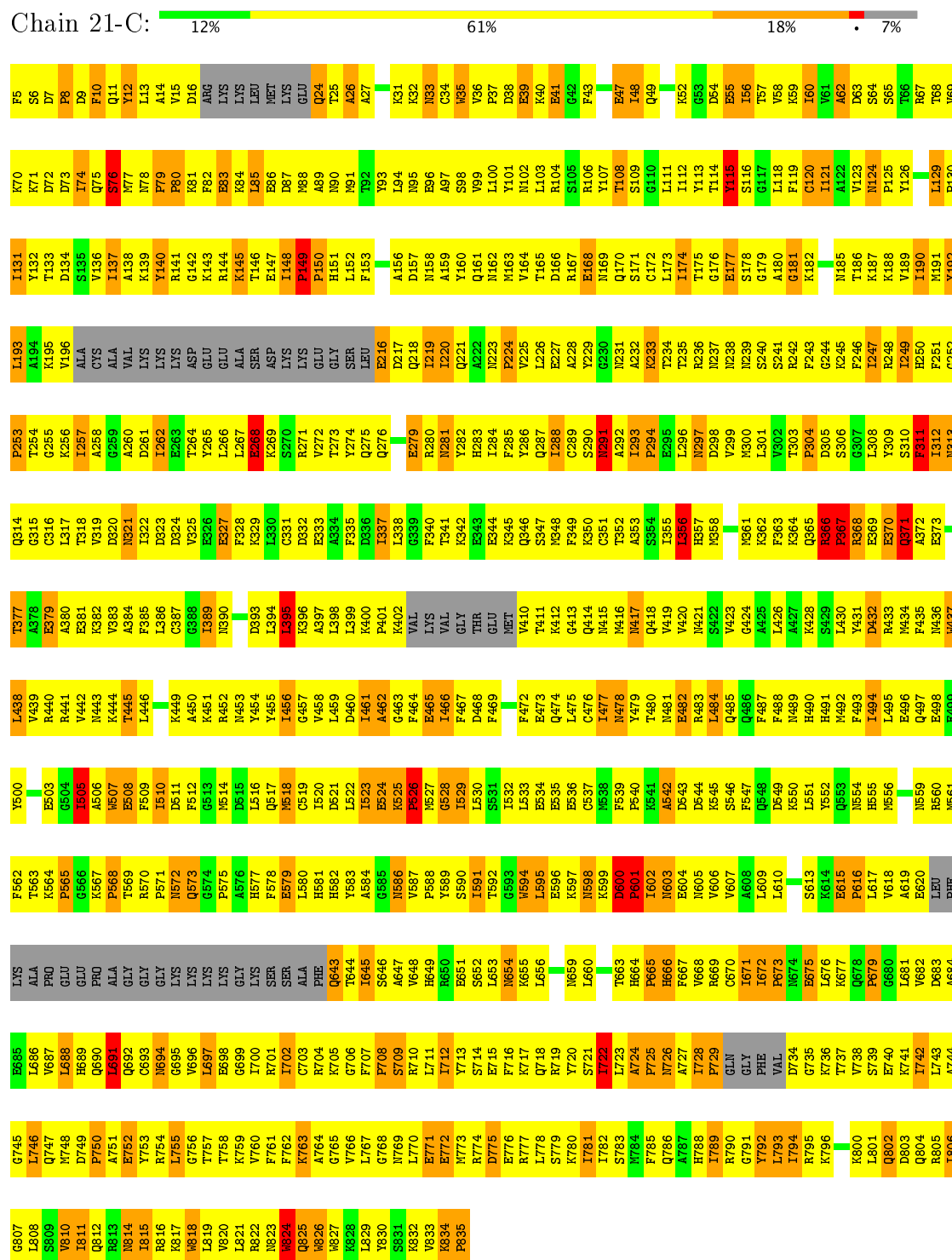


• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 20-C: 14% 59% 18% 7%

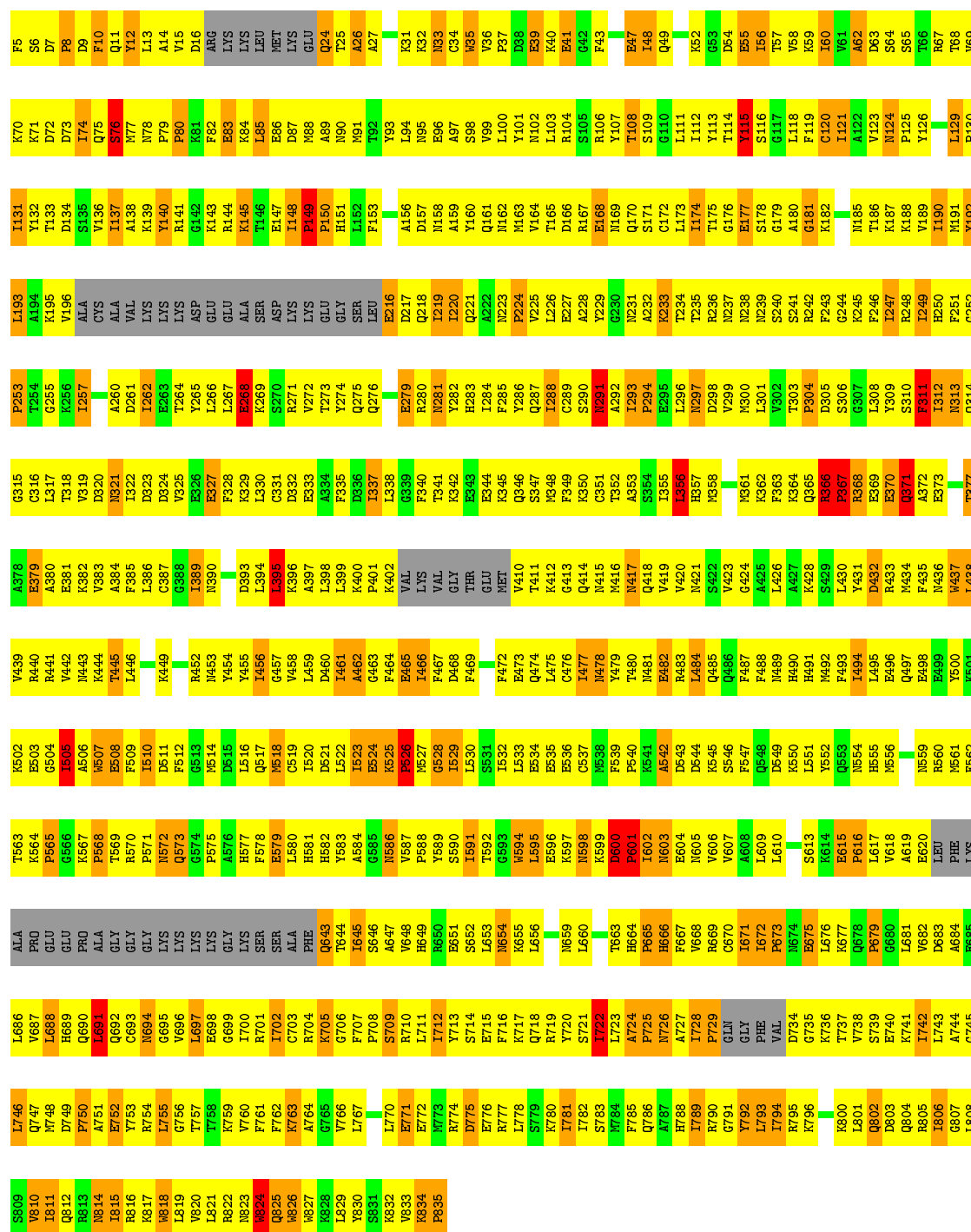


● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

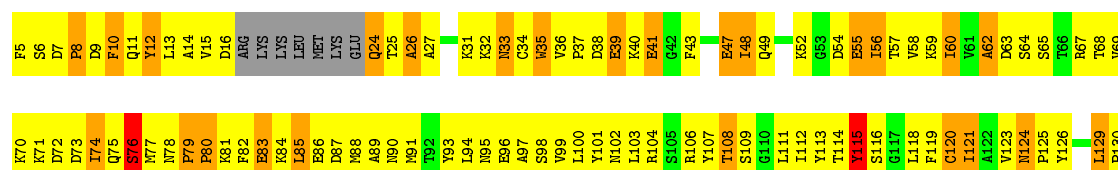


● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

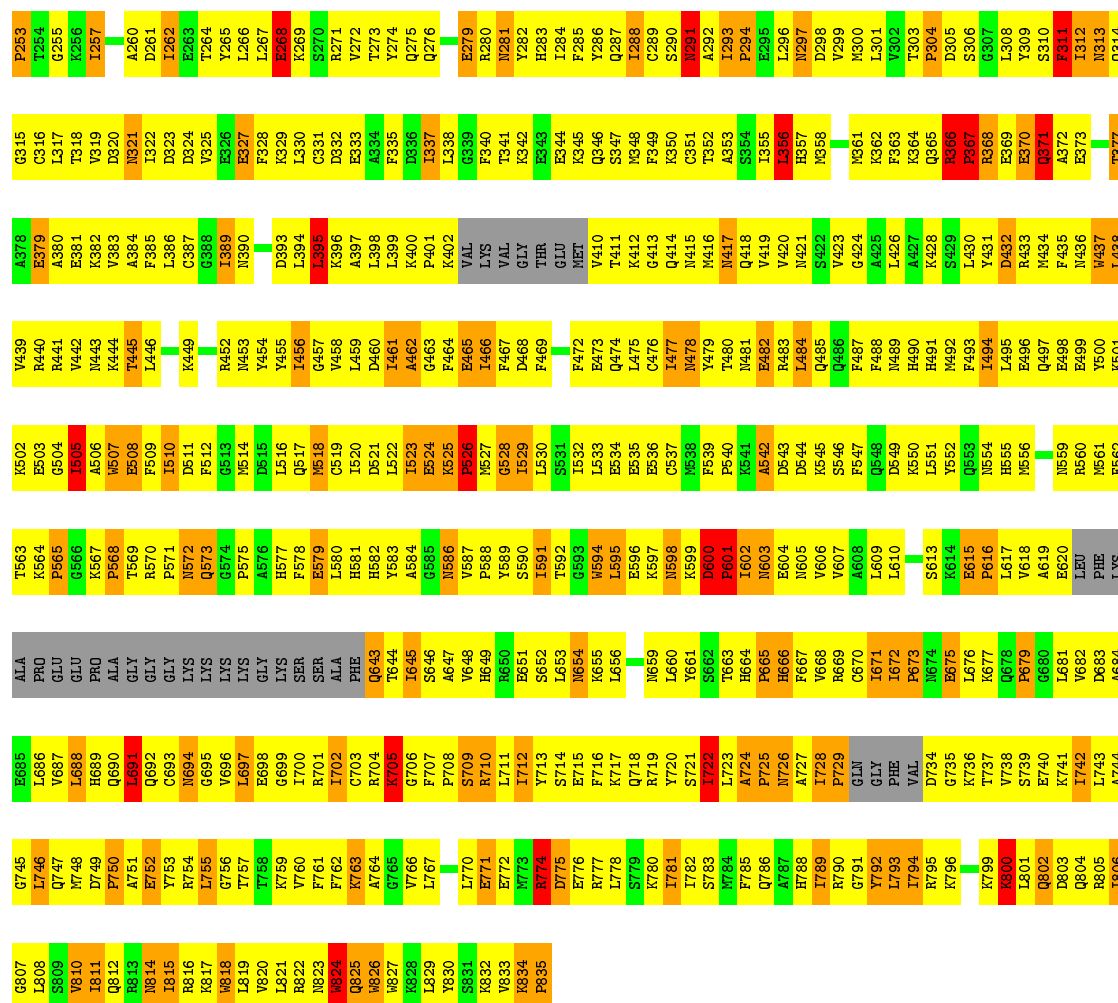




Chain 23-C:  14% 59% 18% 7%

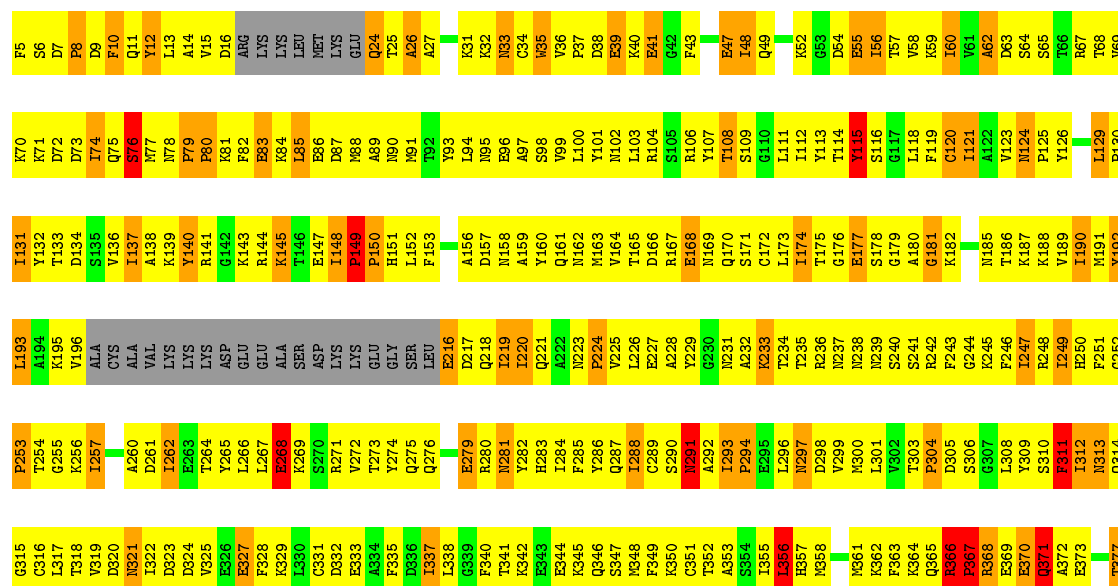


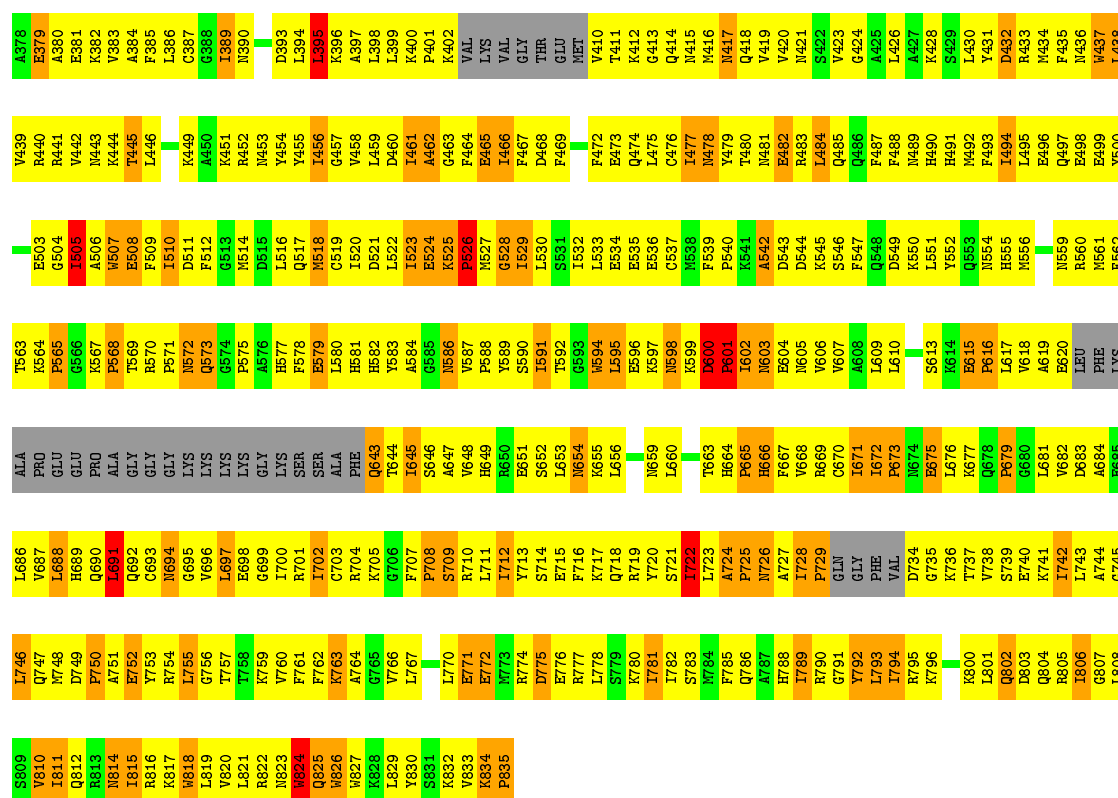
L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	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	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L1046	L1047	L1048	L1049	L1050	L1051	L1052	L1053	L1054	L1055	L1056	L1057	L1058	L1059	L1060	L1061	L1062	L1063	L1064	L1065	L1066	L1067	L1068	L1069	L1070	L1071	L1072	L1073	L1074	L1075	L1076	L1077	L1078	L1079	L1080	L1081	L1082	L1083	L1084	L1085	L1086	L1087	L1088	L1089	L1090	L1091	L1092	L1093	L1094	L1095	L1096	L1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157	L1158	L1159	L1160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• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

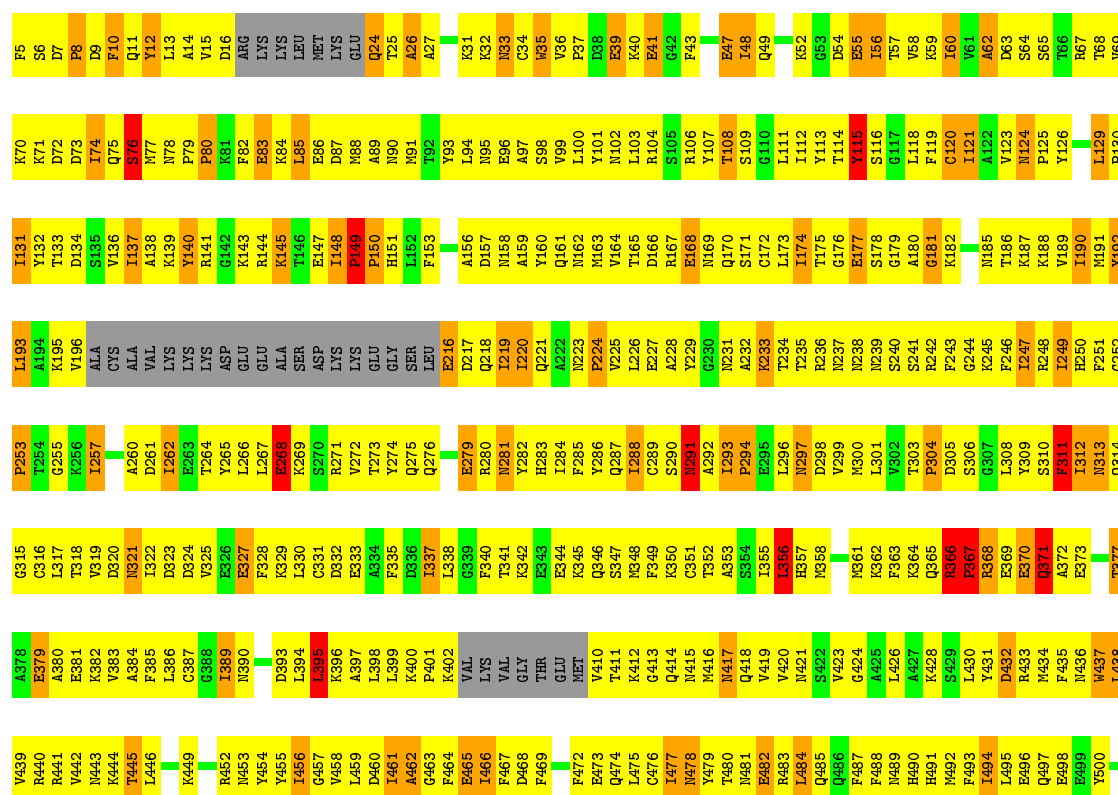
Chain 25-C: 13% 59% 18% 7%

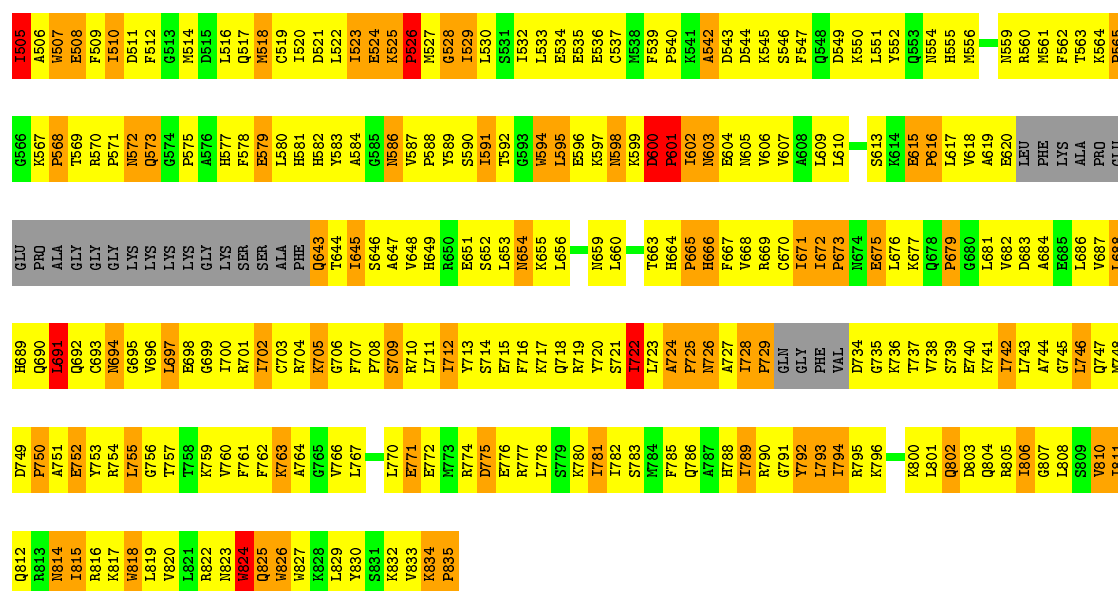




● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

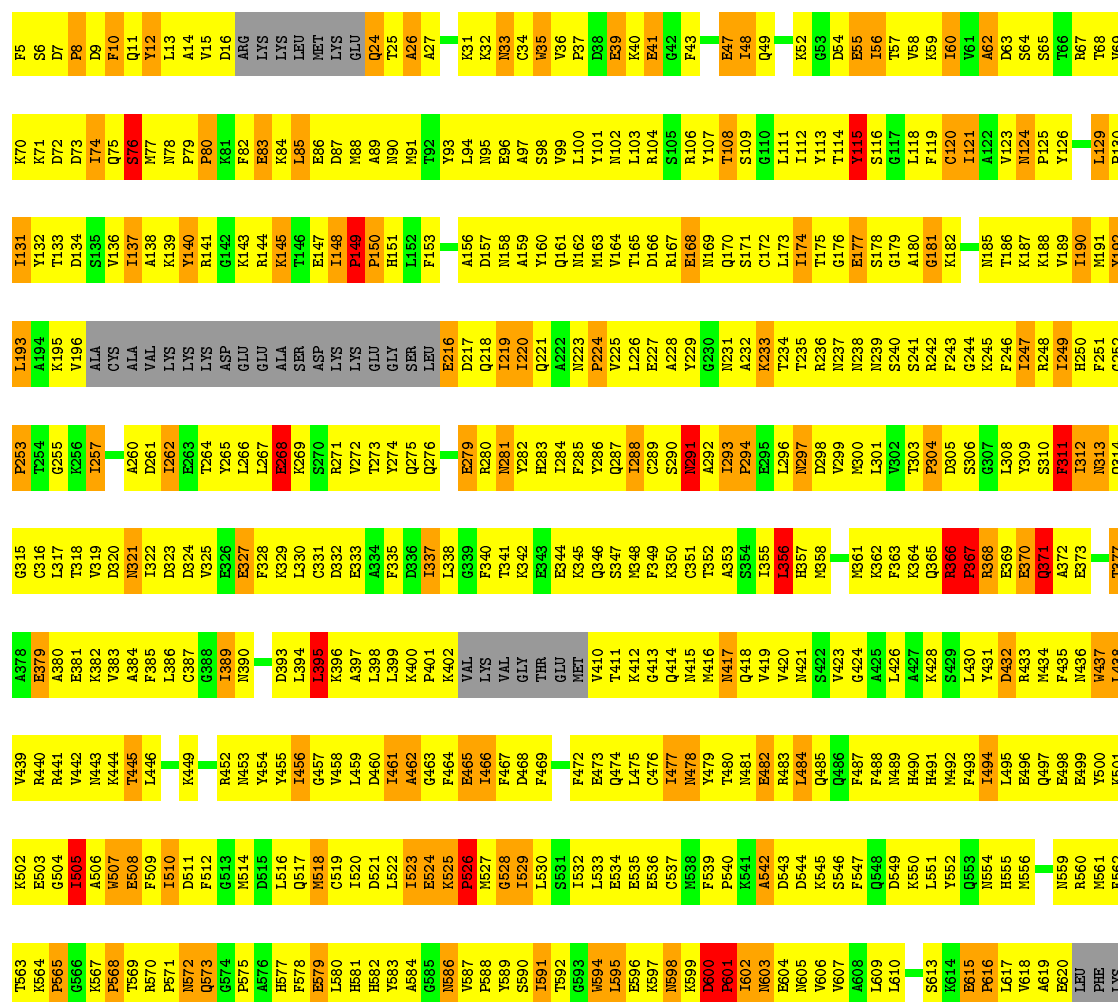
Chain 26-C: 14% 59% 18% 7%

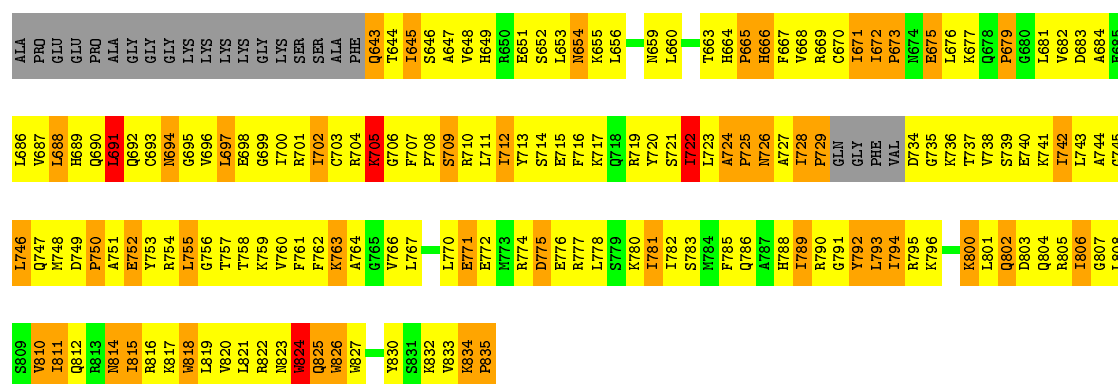




Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

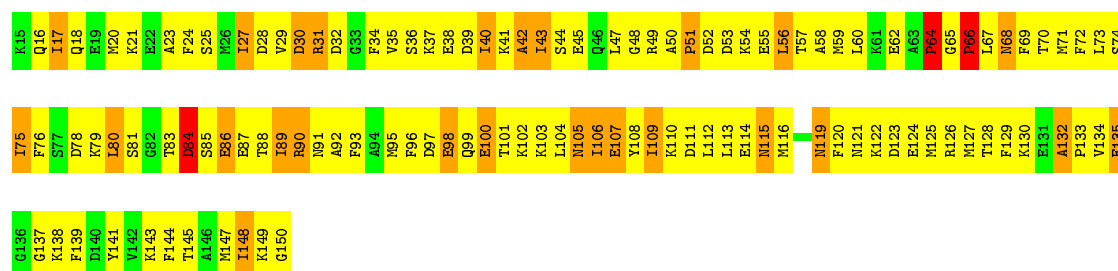
Chain 27-C: 13% 59% 18% 7%





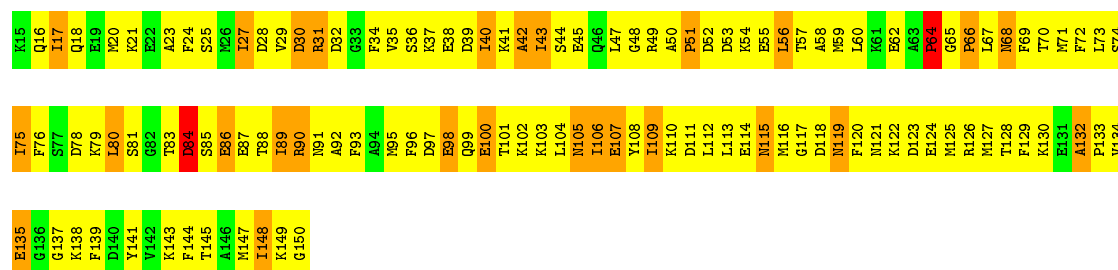
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 1-Y: 13% 65% 19%



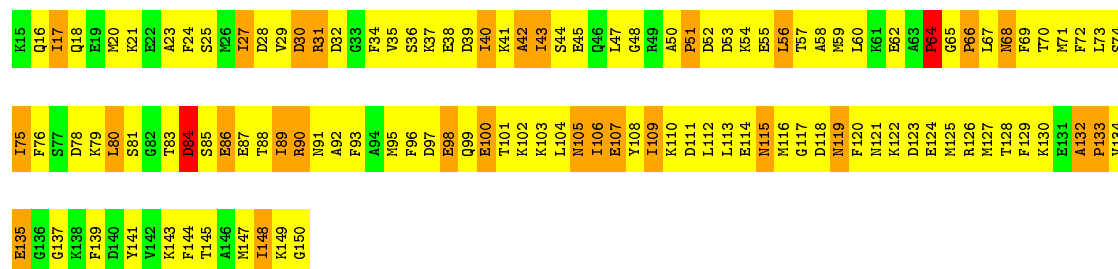
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 2-Y: 12% 67% 20%



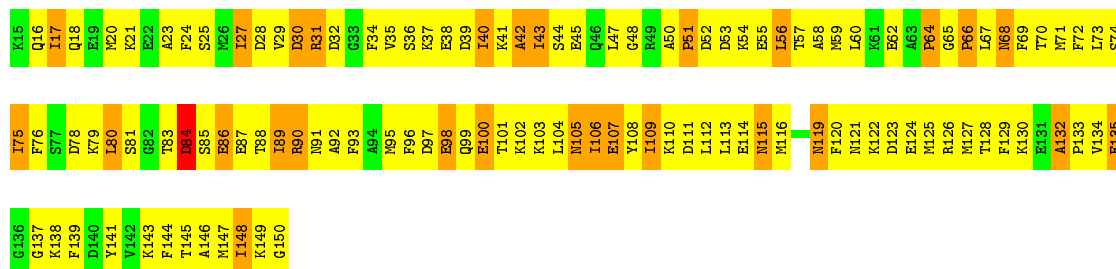
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 3-Y: 13% 65% 21%



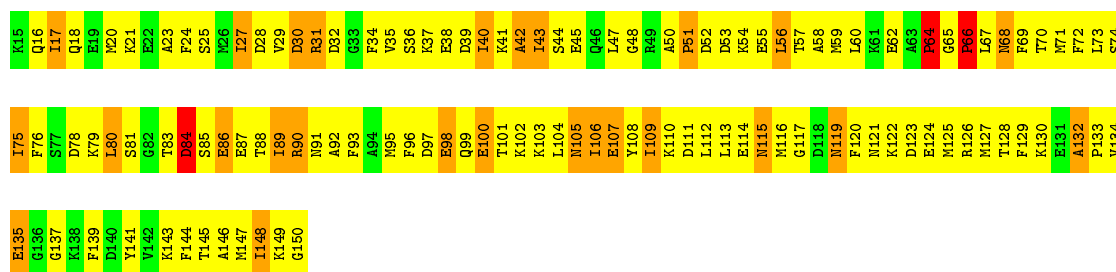
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 4-Y: 13% 65% 21% .



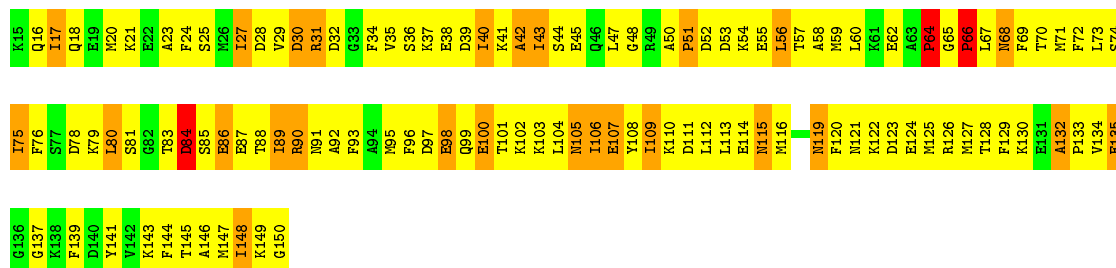
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 5-Y: 13% 65% 19% .



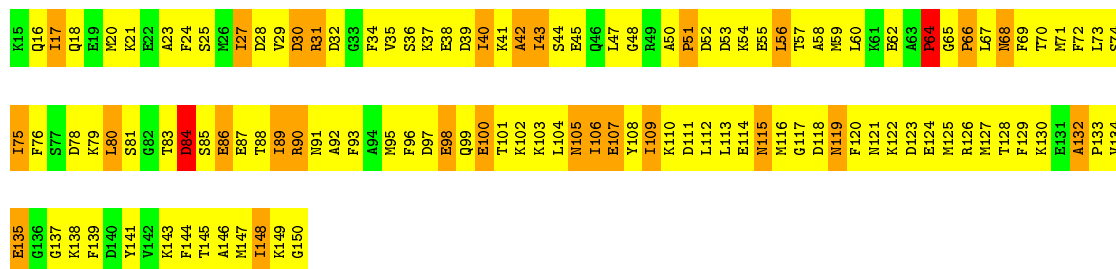
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 6-Y: 14% 65% 19% .



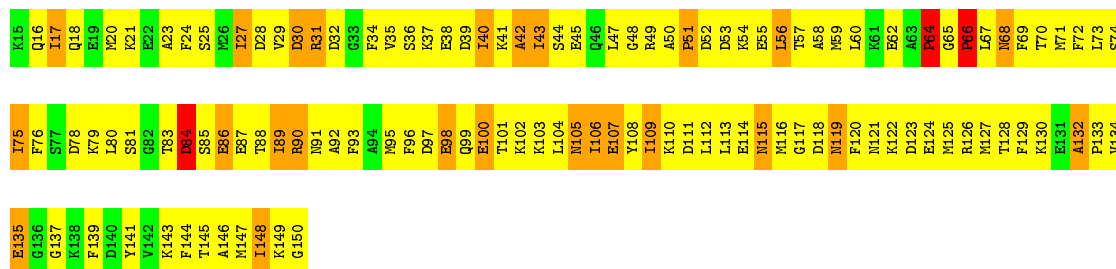
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 7-Y: 12% 67% 20% .



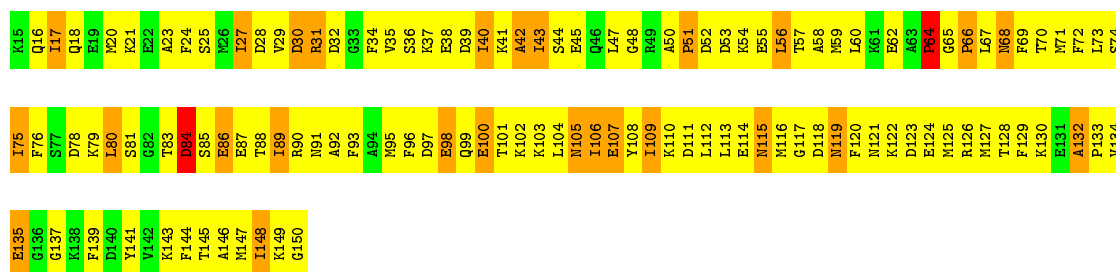
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 8-Y: 12% 68% 18%



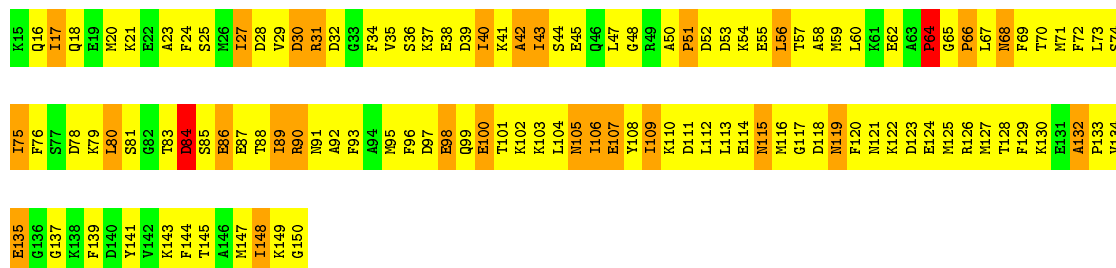
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 9-Y: 13% 67% 19%



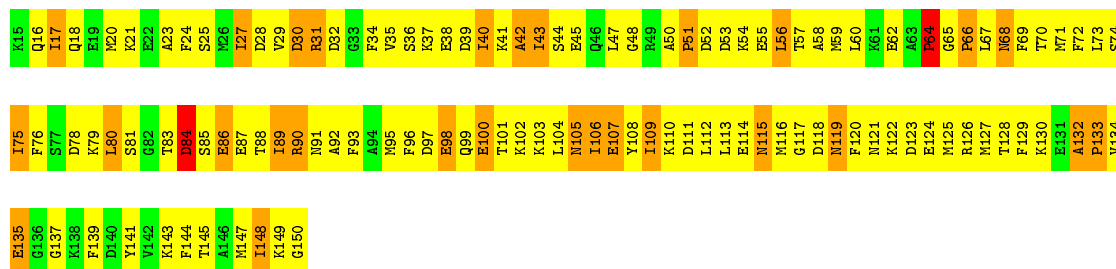
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 10-Y: 13% 65% 20%



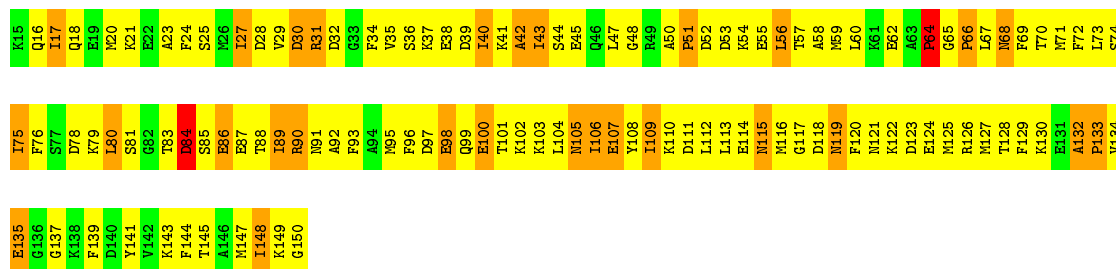
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 11-Y: 13% 65% 21%



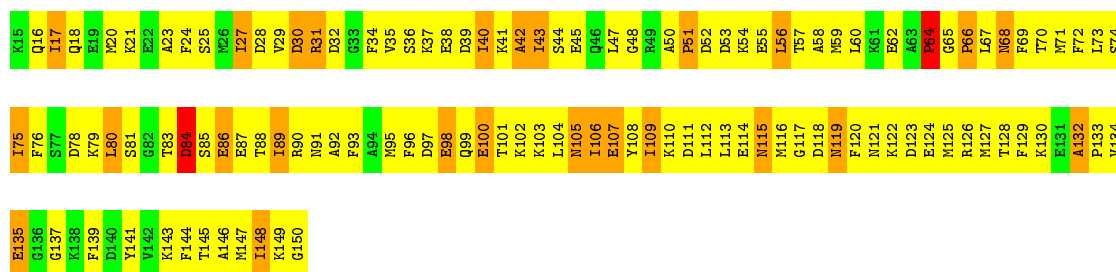
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 12-Y:  13% 65% 21% .




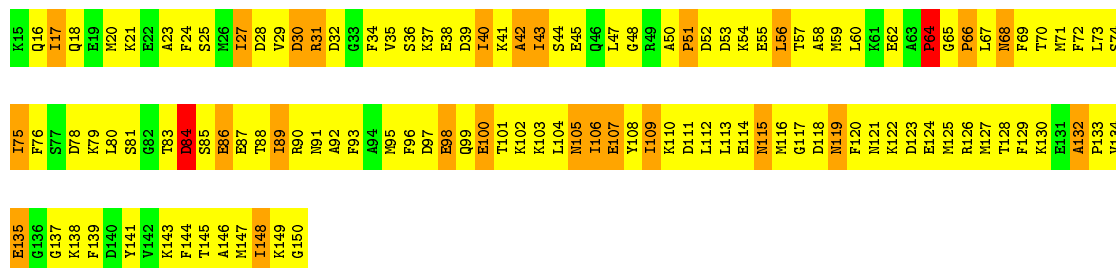
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 13-Y:  13% 67% 19% .



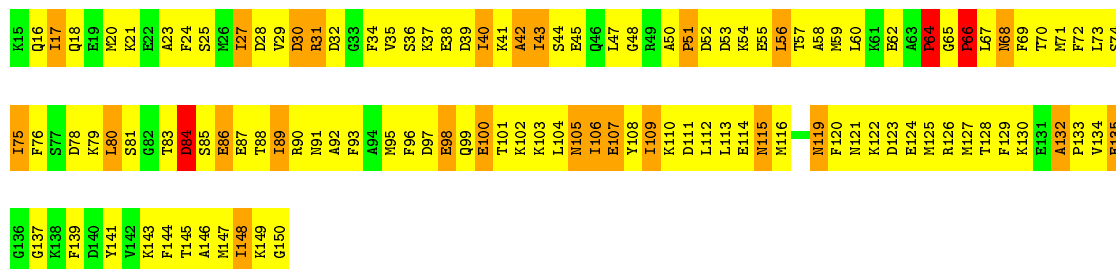
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 14-Y:  12% 68% 18% .



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

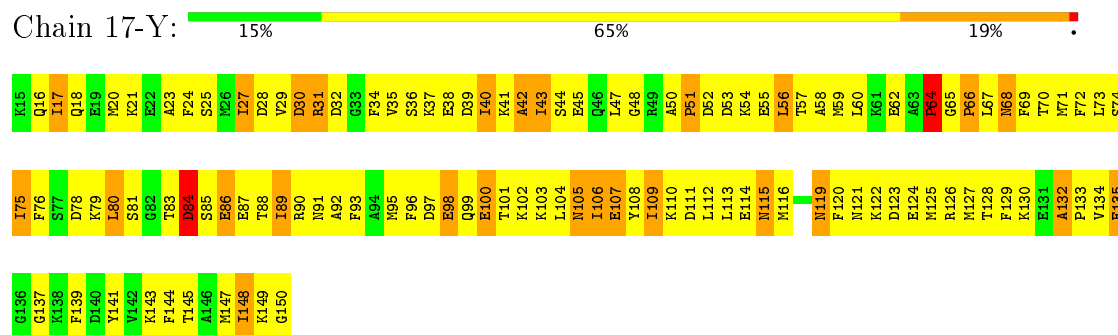
Chain 15-Y:  14% 65% 18% .



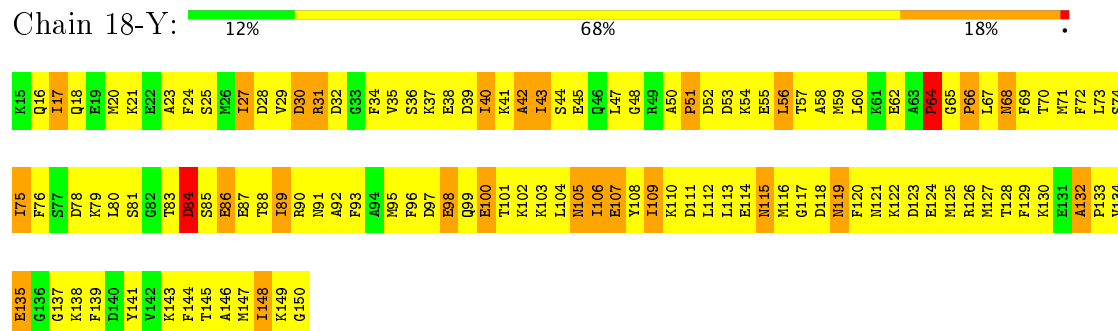
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



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



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

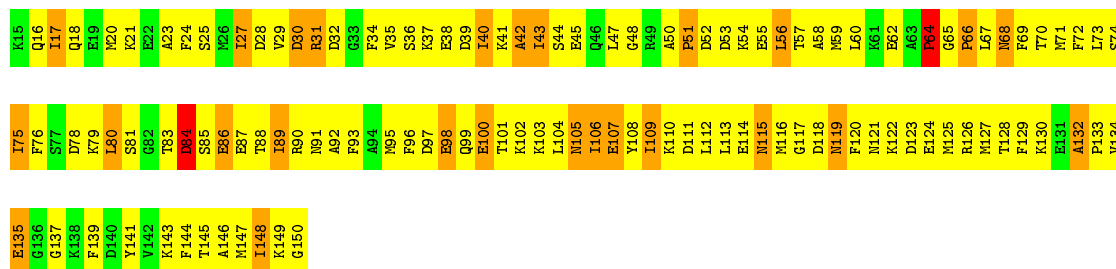


- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



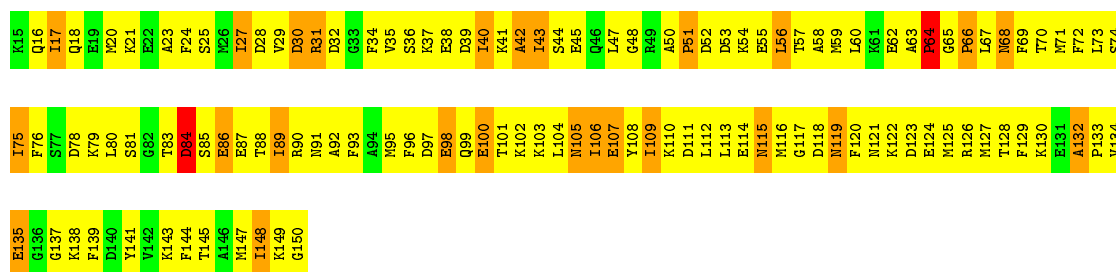
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 20-Y:  13% 67% 19%



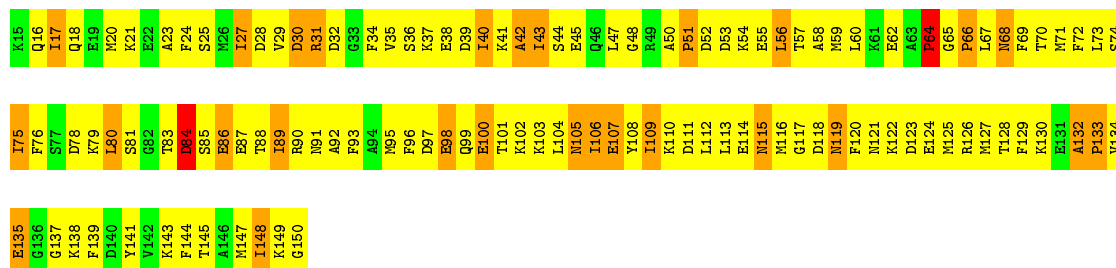
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 21-Y:  12% 68% 18%



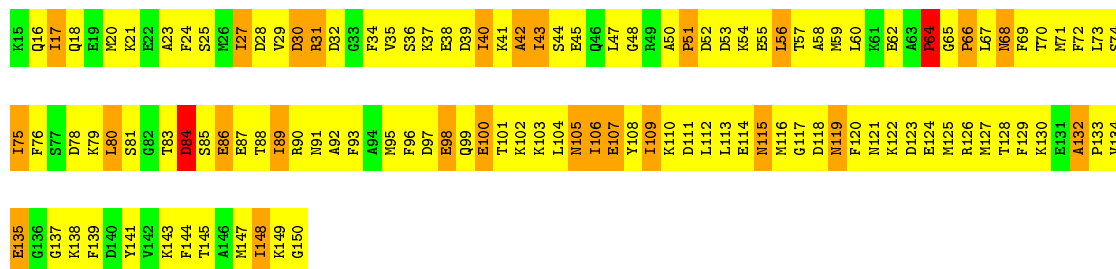
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 22-Y:  13% 66% 20%



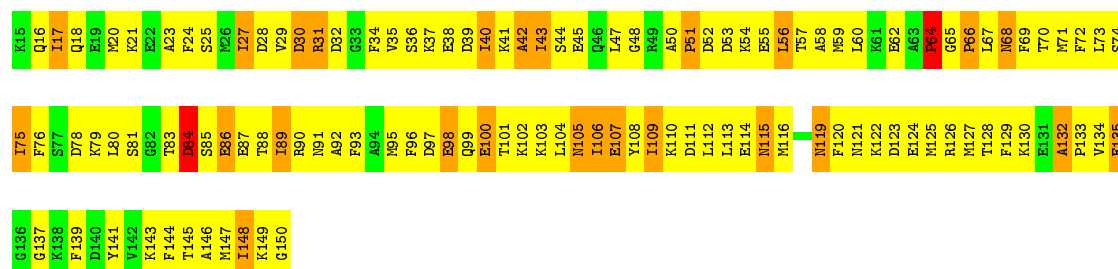
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 23-Y:  13% 67% 19%



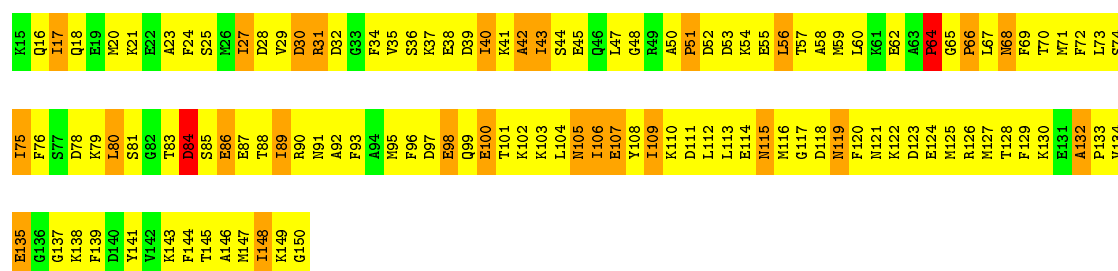
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 24-Y:  14% 66% 18%



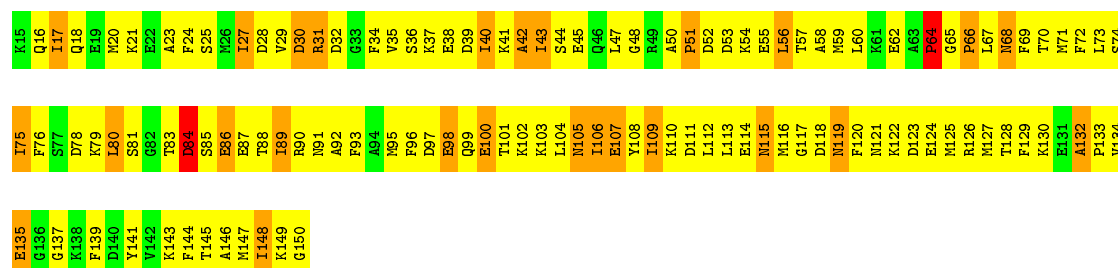
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 25-Y: 12% 68% 19%



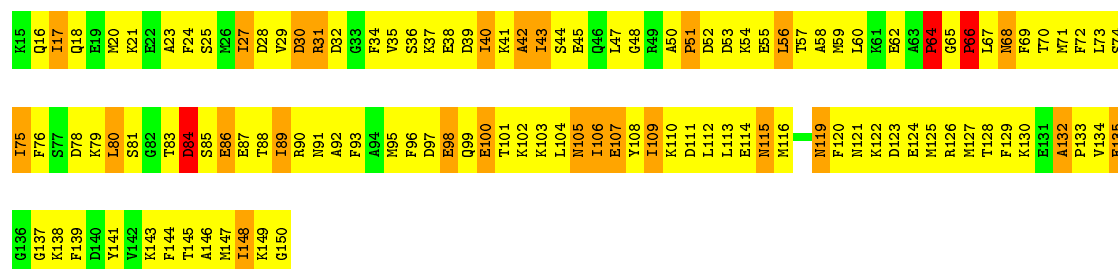
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 26-Y: 13% 67% 19%

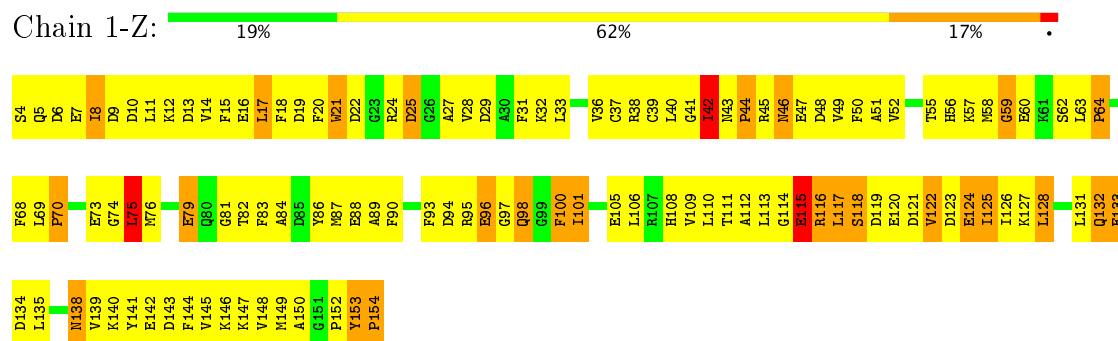


- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

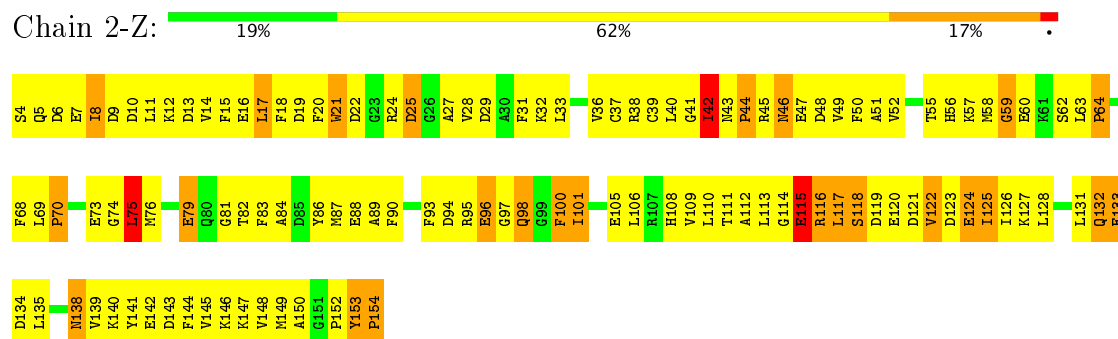
Chain 27-Y:  13% 66% 18% .



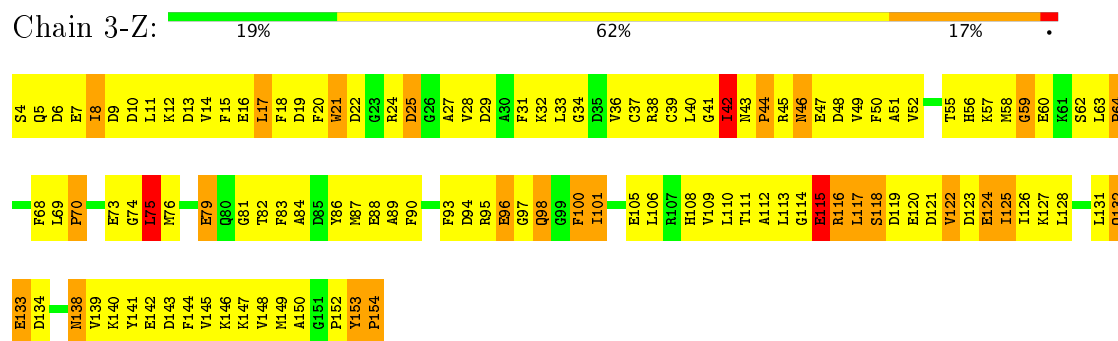
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



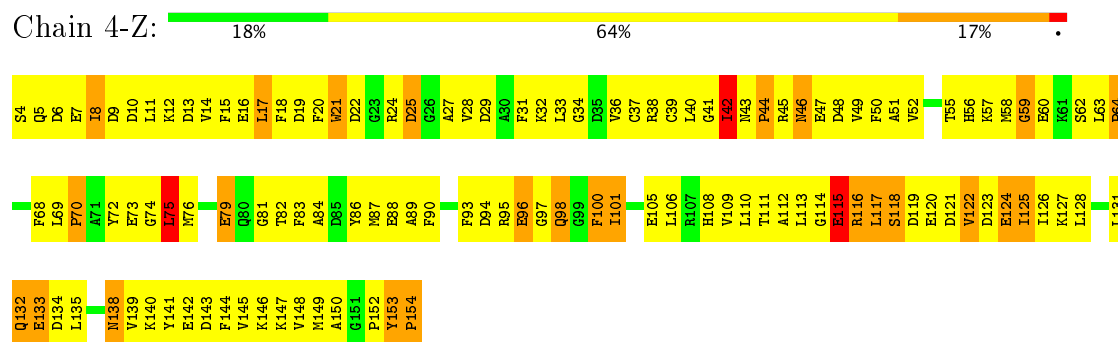
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



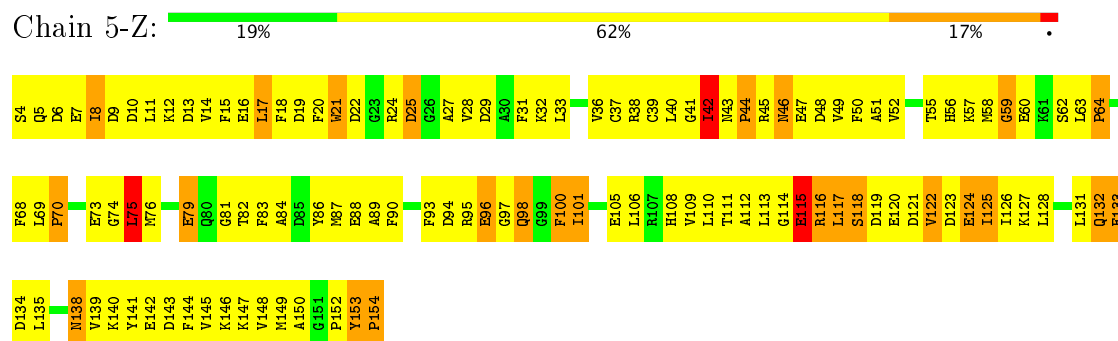
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



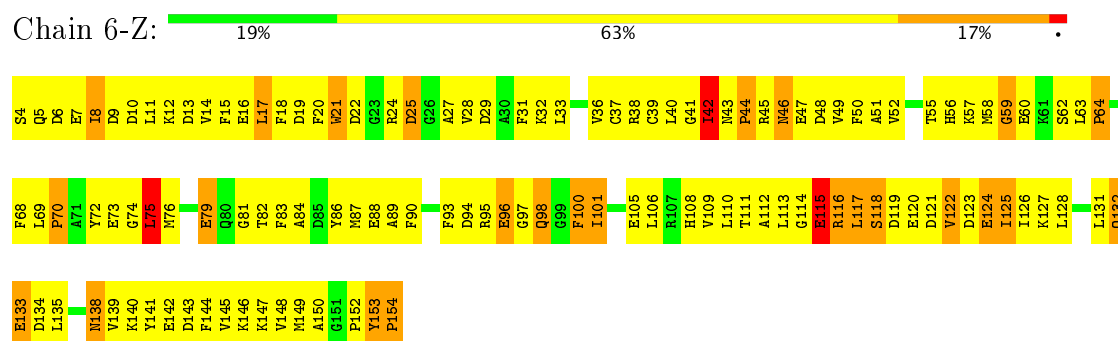
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



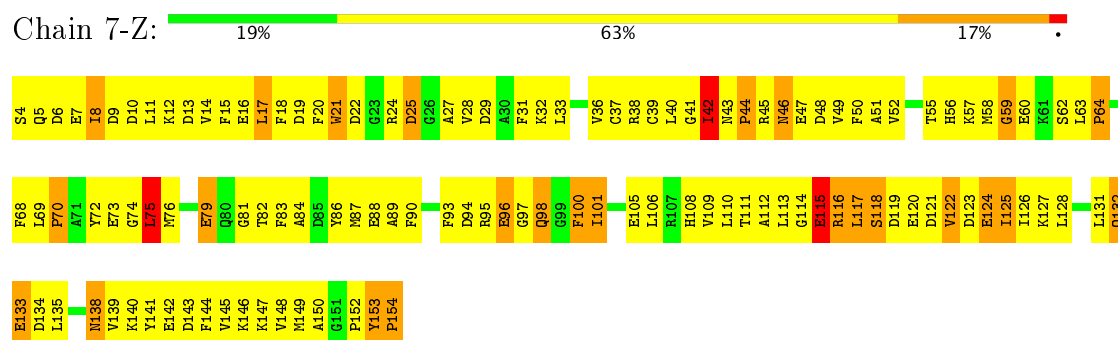
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



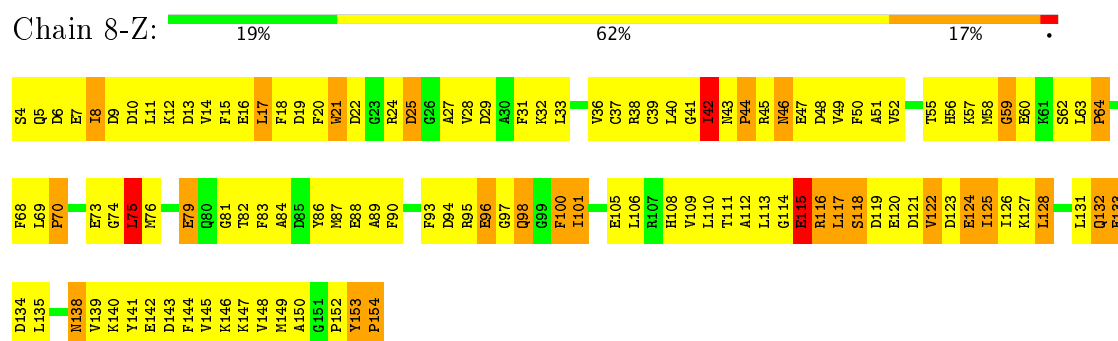
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



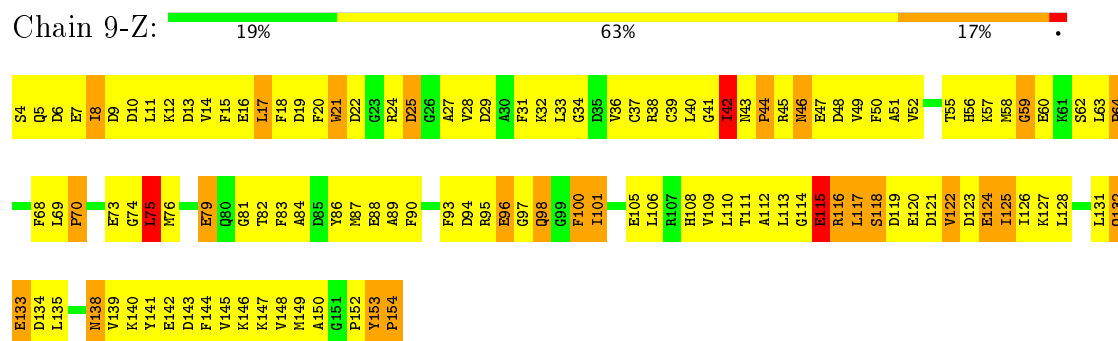
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



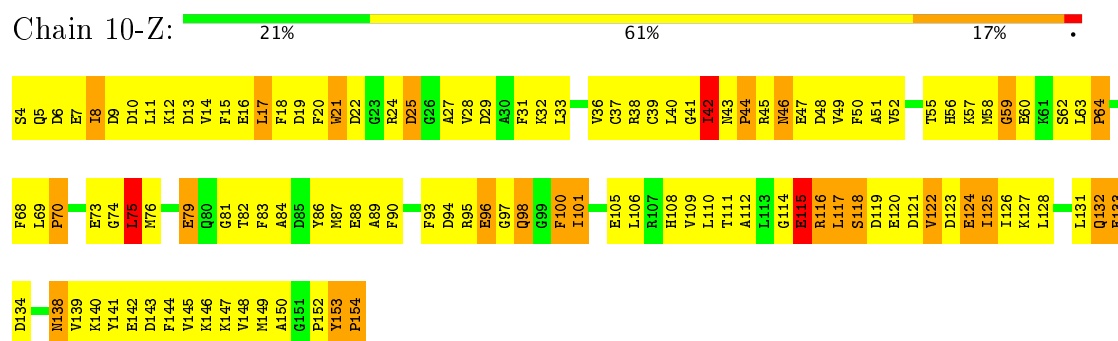
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



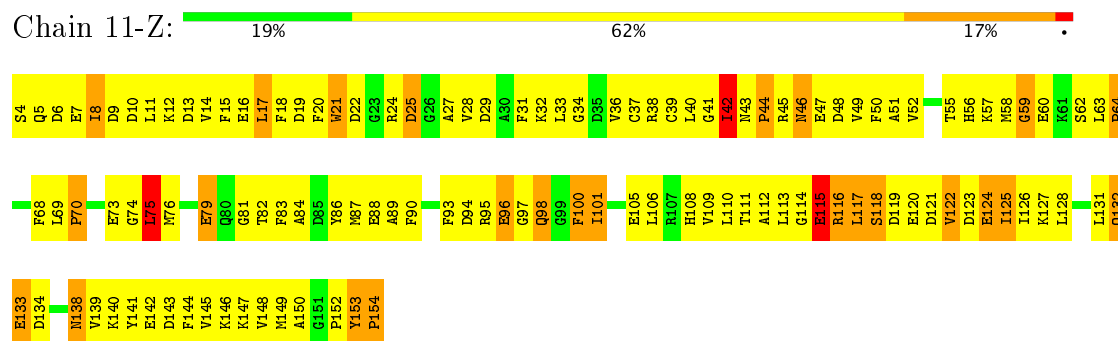
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



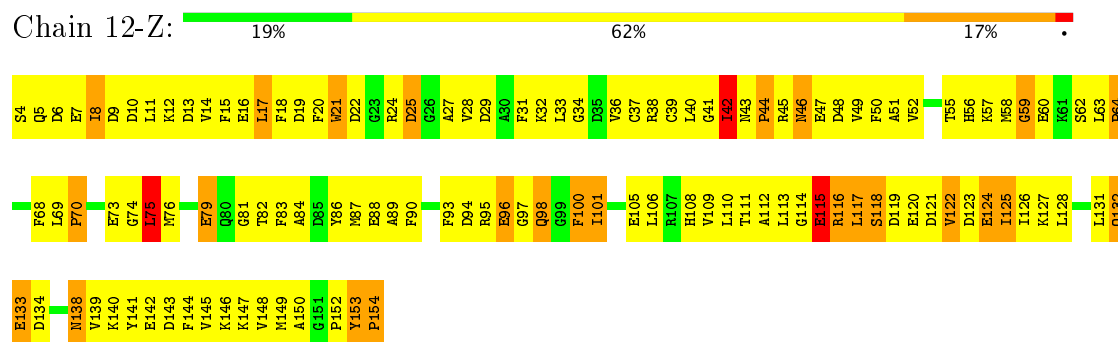
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



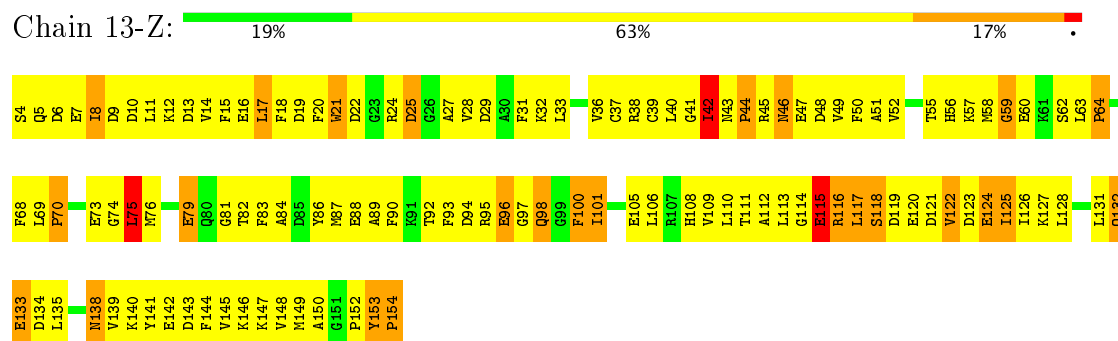
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



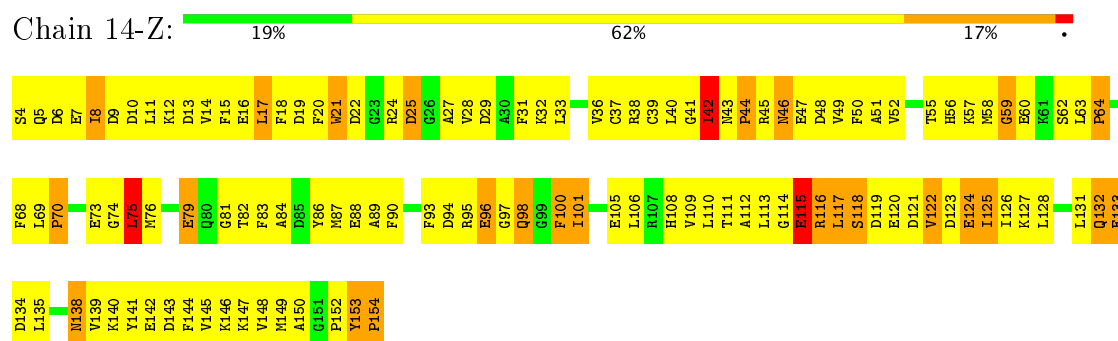
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



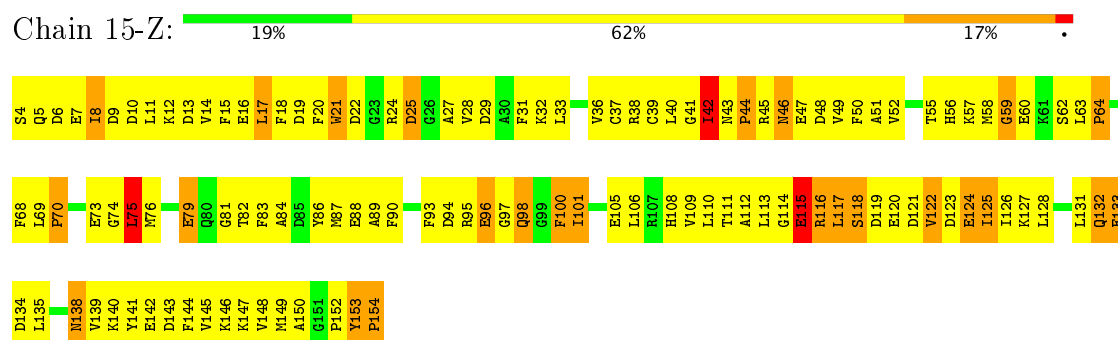
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



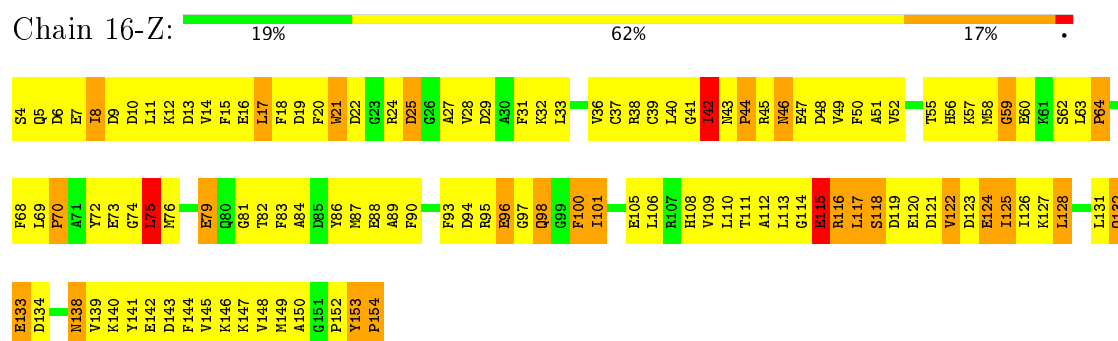
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



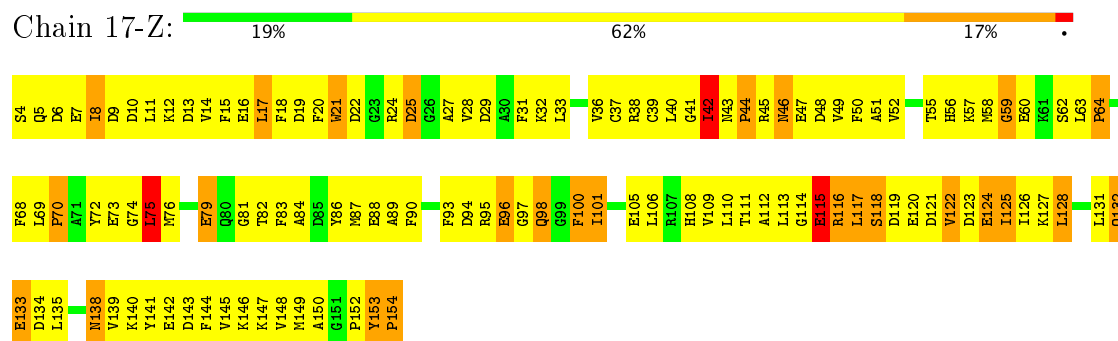
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

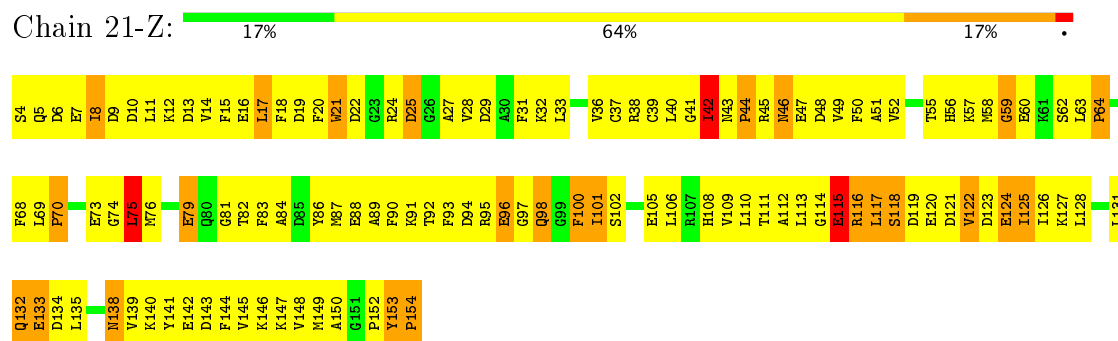


- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

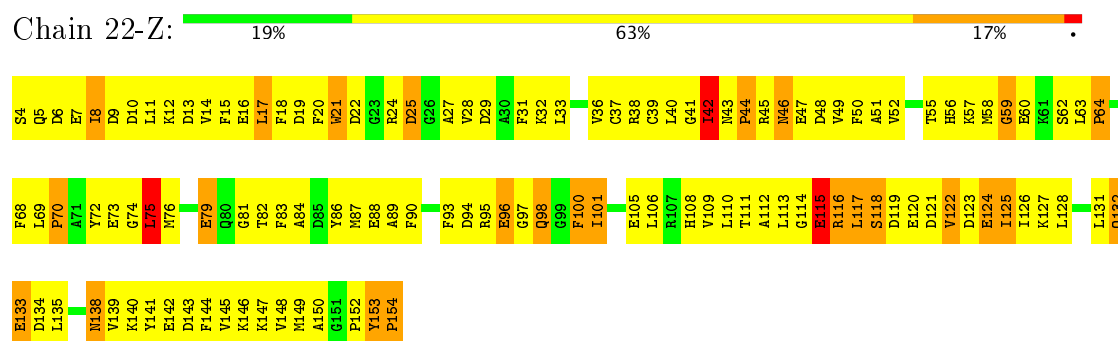


- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

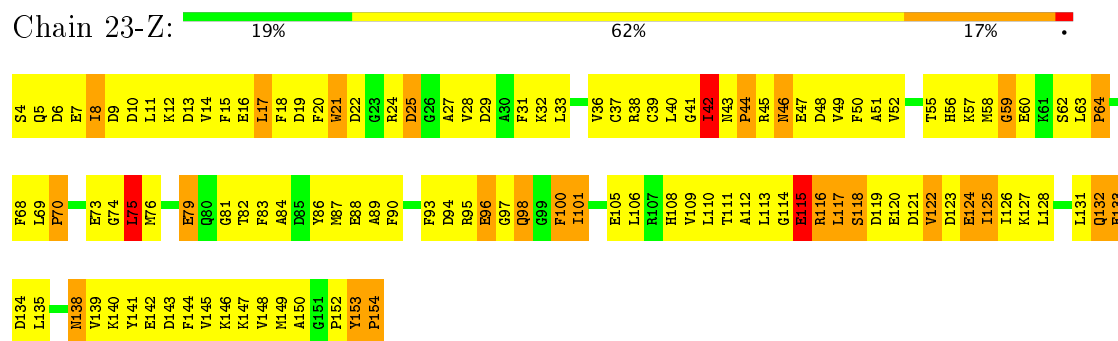




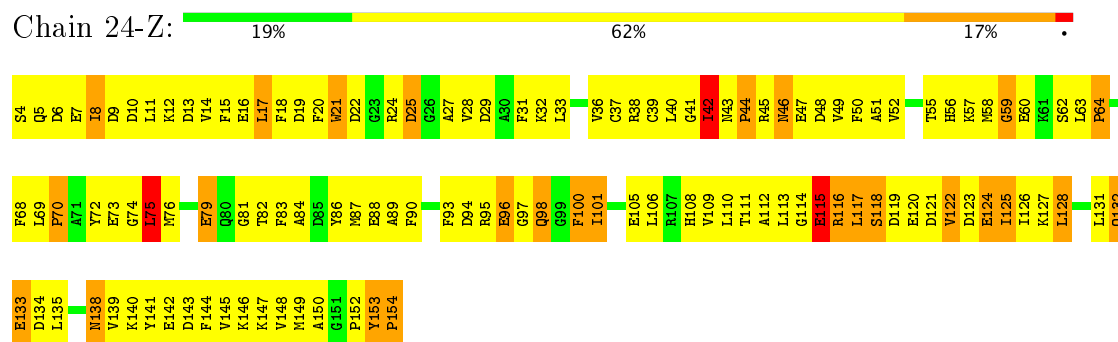
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



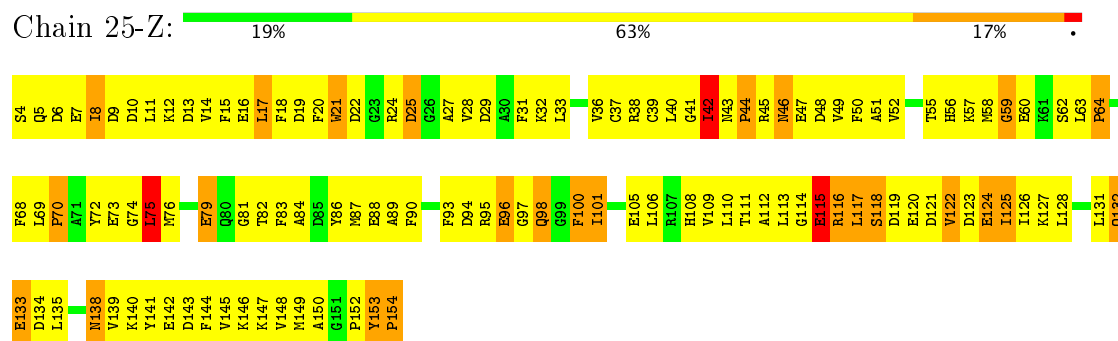
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



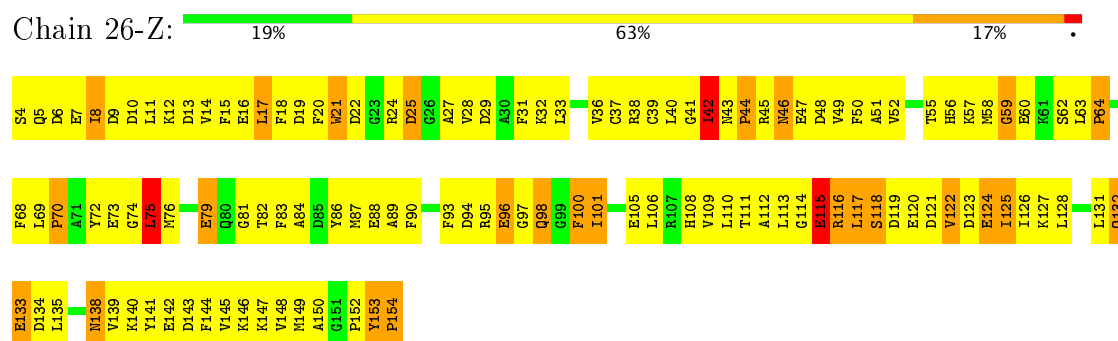
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



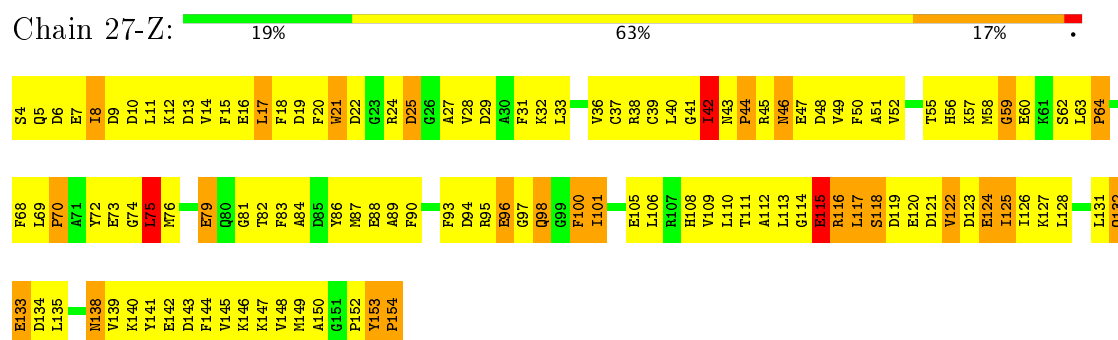
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



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



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



4 Experimental information

Property	Value	Source
Reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of tilted images used	Not provided	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	TIETZ TEM-CAM F224	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 > 2$	RMSZ	# $ Z > 2$
1	1-C	1.15	82/6339 (1.3%)	1.30	31/8536 (0.4%)
1	10-C	1.14	82/6340 (1.3%)	1.29	29/8539 (0.3%)
1	11-C	1.14	81/6340 (1.3%)	1.29	29/8539 (0.3%)
1	12-C	1.14	81/6340 (1.3%)	1.29	29/8539 (0.3%)
1	13-C	1.14	82/6340 (1.3%)	1.29	30/8539 (0.4%)
1	14-C	1.14	81/6340 (1.3%)	1.29	30/8539 (0.4%)
1	15-C	1.15	82/6340 (1.3%)	1.34	33/8539 (0.4%)
1	16-C	1.14	81/6340 (1.3%)	1.29	29/8539 (0.3%)
1	17-C	1.15	82/6339 (1.3%)	1.30	33/8536 (0.4%)
1	18-C	1.14	81/6340 (1.3%)	1.29	30/8539 (0.4%)
1	19-C	1.15	82/6340 (1.3%)	1.30	33/8539 (0.4%)
1	2-C	1.15	82/6340 (1.3%)	1.31	31/8539 (0.4%)
1	20-C	1.14	82/6340 (1.3%)	1.29	30/8539 (0.4%)
1	21-C	1.14	81/6340 (1.3%)	1.29	29/8539 (0.3%)
1	22-C	1.14	82/6340 (1.3%)	1.29	30/8539 (0.4%)
1	23-C	1.14	82/6340 (1.3%)	1.29	30/8539 (0.4%)
1	24-C	1.15	82/6340 (1.3%)	1.34	35/8539 (0.4%)
1	25-C	1.14	81/6340 (1.3%)	1.29	30/8539 (0.4%)
1	26-C	1.16	82/6340 (1.3%)	1.29	31/8539 (0.4%)
1	27-C	1.16	83/6340 (1.3%)	1.30	32/8539 (0.4%)
1	3-C	1.14	81/6340 (1.3%)	1.29	29/8539 (0.3%)
1	4-C	1.14	81/6339 (1.3%)	1.29	27/8536 (0.3%)
1	5-C	1.16	83/6340 (1.3%)	1.29	30/8539 (0.4%)
1	6-C	1.14	81/6338 (1.3%)	1.29	27/8533 (0.3%)
1	7-C	1.14	82/6340 (1.3%)	1.29	29/8539 (0.3%)
1	8-C	1.14	81/6340 (1.3%)	1.29	28/8539 (0.3%)
1	9-C	1.14	80/6340 (1.3%)	1.29	28/8539 (0.3%)
2	1-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	10-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	11-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	12-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	13-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
2	14-Y	0.80	9/1104 (0.8%)	1.06	1/1472 (0.1%)
2	15-Y	0.80	9/1104 (0.8%)	1.05	1/1472 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
2	16-Y	0.80	9/1104 (0.8%)	1.05	1/1472 (0.1%)
2	17-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
2	18-Y	0.80	9/1104 (0.8%)	1.06	1/1472 (0.1%)
2	19-Y	0.80	9/1104 (0.8%)	1.05	1/1472 (0.1%)
2	2-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	20-Y	0.80	9/1104 (0.8%)	1.05	1/1472 (0.1%)
2	21-Y	0.80	9/1104 (0.8%)	1.06	1/1472 (0.1%)
2	22-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
2	23-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
2	24-Y	0.80	8/1104 (0.7%)	1.05	1/1472 (0.1%)
2	25-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
2	26-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
2	27-Y	0.80	9/1104 (0.8%)	1.05	1/1472 (0.1%)
2	3-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	4-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	5-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	6-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	7-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	8-Y	0.80	9/1104 (0.8%)	1.06	2/1472 (0.1%)
2	9-Y	0.80	8/1104 (0.7%)	1.06	1/1472 (0.1%)
3	1-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	10-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	11-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	12-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	13-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	14-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	15-Z	0.82	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	16-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	17-Z	0.82	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	18-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	19-Z	0.82	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	2-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	20-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	21-Z	0.81	11/1222 (0.9%)	1.09	1/1644 (0.1%)
3	22-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	23-Z	0.81	11/1222 (0.9%)	1.09	1/1644 (0.1%)
3	24-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	25-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	26-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	27-Z	0.82	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	3-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	4-Z	0.82	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	5-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
3	6-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	7-Z	0.81	11/1222 (0.9%)	1.09	2/1644 (0.1%)
3	8-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
3	9-Z	0.81	10/1222 (0.8%)	1.09	2/1644 (0.1%)
All	All	1.06	2725/233977 (1.2%)	1.24	902/314670 (0.3%)

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	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	2-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
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
2	1-Y	0	1
2	10-Y	0	1
2	11-Y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
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	2-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
2	3-Y	0	1
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
All	All	0	148

The worst 5 of 2725 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	16-C	462	ALA	C-N	33.23	1.92	1.33
1	15-C	462	ALA	C-N	33.21	1.92	1.33
1	17-C	462	ALA	C-N	33.21	1.92	1.33
1	19-C	462	ALA	C-N	33.21	1.92	1.33
1	20-C	462	ALA	C-N	33.21	1.92	1.33

The worst 5 of 902 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	15-C	705	LYS	O-C-N	-27.34	76.73	123.20
1	24-C	705	LYS	O-C-N	-27.34	76.73	123.20
1	23-C	709	SER	O-C-N	27.20	166.23	122.70
1	14-C	709	SER	O-C-N	27.19	166.20	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	18-C	709	SER	O-C-N	27.19	166.20	122.70

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	2801	0
1	2-C	6215	0	6174	2730	0
1	3-C	6215	0	6185	2593	0
1	4-C	6215	0	6176	2764	0
1	5-C	6215	0	6182	2606	0
1	6-C	6215	0	6180	2671	0
1	7-C	6215	0	6181	2610	0
1	8-C	6215	0	6179	2653	0
1	9-C	6215	0	6185	2597	0
1	10-C	6215	0	6183	2596	0
1	11-C	6215	0	6185	2593	0
1	12-C	6215	0	6185	2593	0
1	13-C	6215	0	6167	2821	0
1	14-C	6215	0	6185	2599	0
1	15-C	6215	0	6168	2778	0
1	16-C	6215	0	6185	2591	0
1	17-C	6215	0	6173	2811	0
1	18-C	6215	0	6185	2599	0
1	19-C	6215	0	6176	2664	0
1	20-C	6215	0	6184	2596	0
1	21-C	6215	0	6162	2939	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	22-C	6215	0	6182	2642	0
1	23-C	6215	0	6185	2594	0
1	24-C	6215	0	6168	2770	0
1	25-C	6215	0	6172	2712	0
1	26-C	6215	0	6185	2588	0
1	27-C	6215	0	6176	2716	0
2	1-Y	1088	0	1066	501	0
2	2-Y	1088	0	1066	474	0
2	3-Y	1088	0	1066	471	0
2	4-Y	1088	0	1066	497	0
2	5-Y	1088	0	1066	476	0
2	6-Y	1088	0	1066	475	0
2	7-Y	1088	0	1066	472	0
2	8-Y	1088	0	1066	471	0
2	9-Y	1088	0	1066	467	0
2	10-Y	1088	0	1066	474	0
2	11-Y	1088	0	1066	471	0
2	12-Y	1088	0	1066	471	0
2	13-Y	1088	0	1066	472	0
2	14-Y	1088	0	1066	474	0
2	15-Y	1088	0	1066	470	0
2	16-Y	1088	0	1066	475	0
2	17-Y	1088	0	1065	503	0
2	18-Y	1088	0	1066	474	0
2	19-Y	1088	0	1066	474	0
2	20-Y	1088	0	1066	475	0
2	21-Y	1088	0	1066	467	0
2	22-Y	1088	0	1066	475	0
2	23-Y	1088	0	1066	472	0
2	24-Y	1088	0	1066	465	0
2	25-Y	1088	0	1066	468	0
2	26-Y	1088	0	1066	471	0
2	27-Y	1088	0	1066	475	0
3	1-Z	1198	0	1119	509	0
3	2-Z	1198	0	1120	499	0
3	3-Z	1198	0	1120	496	0
3	4-Z	1198	0	1119	508	0
3	5-Z	1198	0	1120	498	0
3	6-Z	1198	0	1120	505	0
3	7-Z	1198	0	1120	505	0
3	8-Z	1198	0	1120	500	0
3	9-Z	1198	0	1120	498	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	10-Z	1198	0	1120	497	0
3	11-Z	1198	0	1120	496	0
3	12-Z	1198	0	1120	496	0
3	13-Z	1198	0	1120	541	0
3	14-Z	1198	0	1120	502	0
3	15-Z	1198	0	1120	507	0
3	16-Z	1198	0	1120	504	0
3	17-Z	1198	0	1118	538	0
3	18-Z	1198	0	1120	502	0
3	19-Z	1198	0	1120	501	0
3	20-Z	1198	0	1120	505	0
3	21-Z	1198	0	1118	619	0
3	22-Z	1198	0	1120	507	0
3	23-Z	1198	0	1120	506	0
3	24-Z	1198	0	1120	512	0
3	25-Z	1198	0	1118	526	0
3	26-Z	1198	0	1120	504	0
3	27-Z	1198	0	1120	501	0
All	All	229527	0	225829	94003	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 206.

The worst 5 of 94003 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%)	2	26
1	2-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	3-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	2	27
1	4-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	2	26
1	5-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	26
1	6-C	754/831 (91%)	604 (80%)	112 (15%)	38 (5%)	2	27
1	7-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	26
1	8-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	9-C	758/831 (91%)	605 (80%)	115 (15%)	38 (5%)	2	27
1	10-C	758/831 (91%)	605 (80%)	114 (15%)	39 (5%)	2	26
1	11-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	2	27
1	12-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	2	27
1	13-C	758/831 (91%)	608 (80%)	112 (15%)	38 (5%)	2	27
1	14-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	15-C	758/831 (91%)	607 (80%)	112 (15%)	39 (5%)	2	26
1	16-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	17-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	2	26
1	18-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	19-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	20-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	26
1	21-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	22-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	2	27
1	23-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	2	27
1	24-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	26
1	25-C	758/831 (91%)	608 (80%)	112 (15%)	38 (5%)	2	27
1	26-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	2	27
1	27-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	2	27
2	1-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	2-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	3-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	4-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	5-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	6-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	7-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	8-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	9-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	10-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	11-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	12-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	13-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	14-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	15-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	16-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	17-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	18-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	19-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	20-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	21-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	22-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	23-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	24-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	25-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	26-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
2	27-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	29
3	1-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	21
3	2-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	3-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	4-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	5-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	6-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	7-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	8-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	21
3	9-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	10-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	11-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	12-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	13-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	14-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	15-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	16-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	21
3	17-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	21
3	18-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	19-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	21
3	20-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	21-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	22-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	23-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	24-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	21
3	25-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	26-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
3	27-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	23
All	All	28097/30186 (93%)	21738 (77%)	4913 (18%)	1446 (5%)	4	26

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%)	571 (84%)	107 (16%)	3	18
1	2-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	3-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	4-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	5-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	6-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	7-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	8-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	9-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	10-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	11-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	12-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	13-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	14-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	15-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	16-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	17-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	18-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	19-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	20-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	21-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	22-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	23-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	24-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	25-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	26-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
1	27-C	678/724 (94%)	571 (84%)	107 (16%)	3	18
2	1-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	2-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	4-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	5-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	6-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	7-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	8-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	9-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	10-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	11-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	12-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	13-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	14-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	15-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	16-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	17-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	18-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	19-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	20-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	21-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	22-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	23-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	24-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	25-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	26-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
2	27-Y	119/119 (100%)	100 (84%)	19 (16%)	3	18
3	1-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	2-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	3-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	4-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	5-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	6-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	7-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	8-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	9-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	10-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	11-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	12-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	13-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	14-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	15-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	16-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	17-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	18-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	19-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	20-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	21-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	22-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	23-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	24-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	25-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	26-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
3	27-Z	127/127 (100%)	111 (87%)	16 (13%)	5	26
All	All	24948/26190 (95%)	21114 (85%)	3834 (15%)	7	19

5 of 3834 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	13-C	220	ILE
1	16-C	124	ASN
3	25-Z	115	GLU
1	13-C	645	ILE
1	14-C	793	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1296 such sidechains are listed below:

Mol	Chain	Res	Type
1	13-C	237	ASN
1	16-C	95	ASN
3	25-Z	108	HIS
1	13-C	555	HIS
1	14-C	689	HIS

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 carbohydrates 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	17-C	12
1	1-C	12
1	7-C	11
1	26-C	11
1	27-C	11
1	2-C	11
1	5-C	11

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Mol	Chain	Number of breaks
1	19-C	11
1	4-C	11
1	25-C	10
1	18-C	10
1	14-C	10
1	11-C	10
1	3-C	10
1	9-C	10
1	20-C	10
1	16-C	10
1	10-C	10
1	13-C	10
1	8-C	10
1	21-C	10
1	24-C	10
1	12-C	10
1	22-C	10
1	15-C	10
1	23-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