



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 18, 2017 – 04:34 PM EST

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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

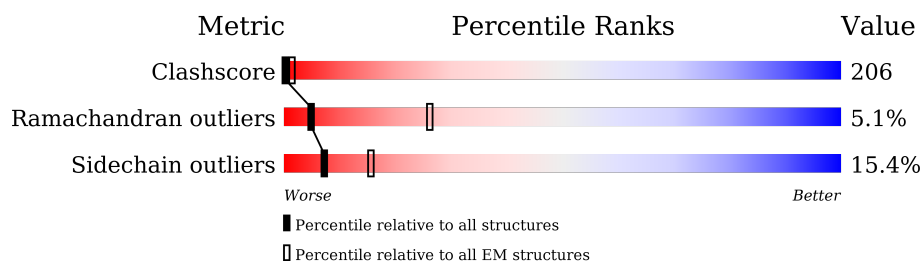
1 Overall quality at a glance

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.




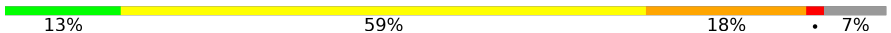
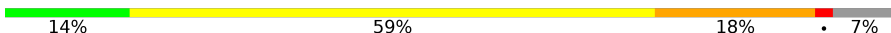


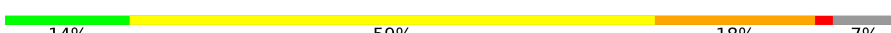
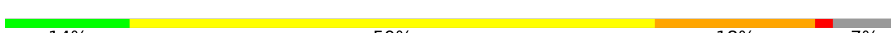




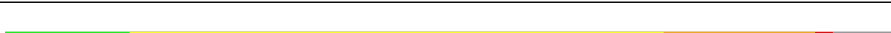







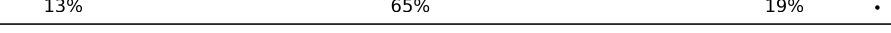
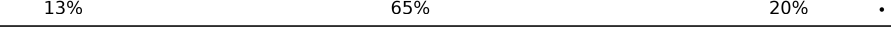


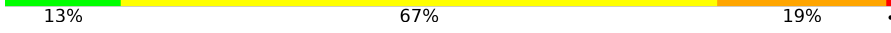
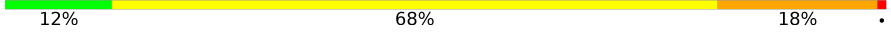
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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	<div> <div>13%</div> <div>59%</div> <div>18%</div> <div>• 7%</div> </div>
1	10-C	831	<div> <div>14%</div> <div>59%</div> <div>18%</div> <div>• 7%</div> </div>
1	11-C	831	<div> <div>14%</div> <div>60%</div> <div>17%</div> <div>• 7%</div> </div>
1	12-C	831	<div> <div>14%</div> <div>60%</div> <div>17%</div> <div>• 7%</div> </div>
1	13-C	831	<div> <div>13%</div> <div>60%</div> <div>18%</div> <div>• 7%</div> </div>
1	14-C	831	<div> <div>13%</div> <div>59%</div> <div>18%</div> <div>• 7%</div> </div>
1	15-C	831	<div> <div>13%</div> <div>59%</div> <div>18%</div> <div>• 7%</div> </div>
1	16-C	831	<div> <div>13%</div> <div>59%</div> <div>18%</div> <div>• 7%</div> </div>
1	17-C	831	<div> <div>13%</div> <div>59%</div> <div>18%</div> <div>• 7%</div> </div>


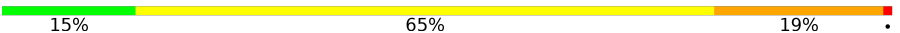
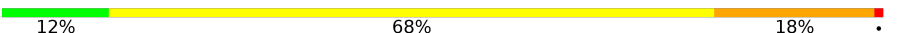
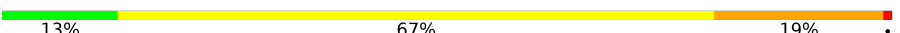

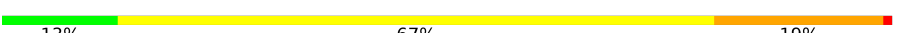
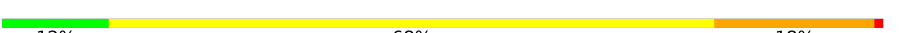




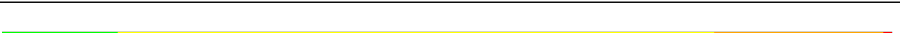





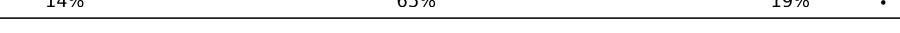


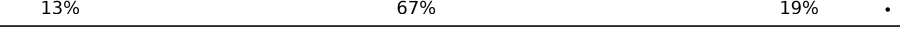
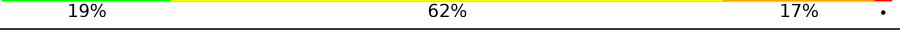
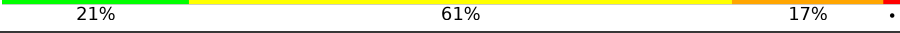
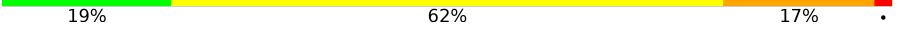
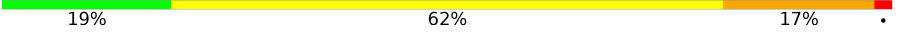
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Mol	Chain	Length	Quality of chain
1	18-C	831	
1	19-C	831	
1	2-C	831	
1	20-C	831	
1	21-C	831	
1	22-C	831	
1	23-C	831	
1	24-C	831	
1	25-C	831	
1	26-C	831	
1	27-C	831	
1	3-C	831	
1	4-C	831	
1	5-C	831	
1	6-C	831	
1	7-C	831	
1	8-C	831	
1	9-C	831	
2	1-Y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

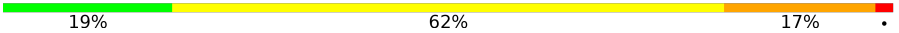
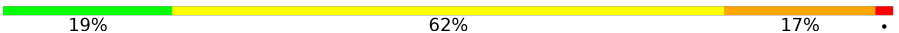
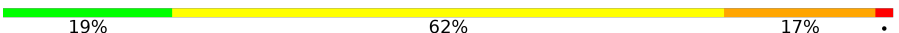
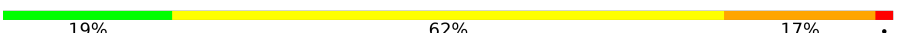
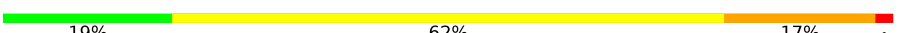
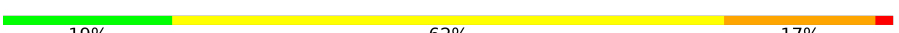
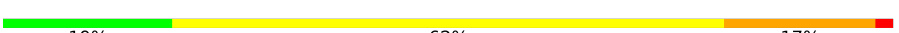




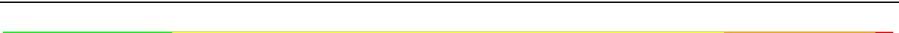



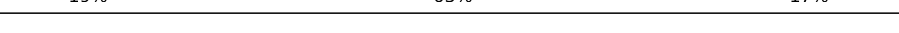
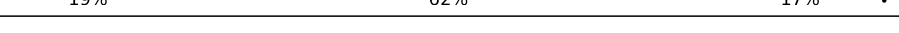
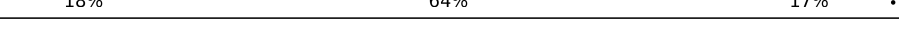
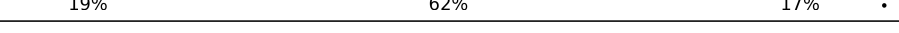
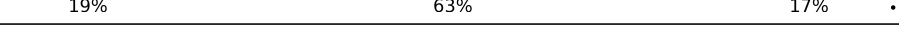
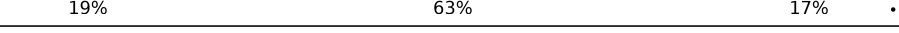
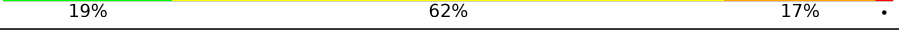
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Mol	Chain	Length	Quality of chain
2	16-Y	136	 12% 68% 18% .
2	17-Y	136	 15% 65% 19% .
2	18-Y	136	 12% 68% 18% .
2	19-Y	136	 13% 67% 19% .
2	2-Y	136	 12% 67% 20% .
2	20-Y	136	 13% 67% 19% .
2	21-Y	136	 12% 68% 18% .
2	22-Y	136	 13% 66% 20% .
2	23-Y	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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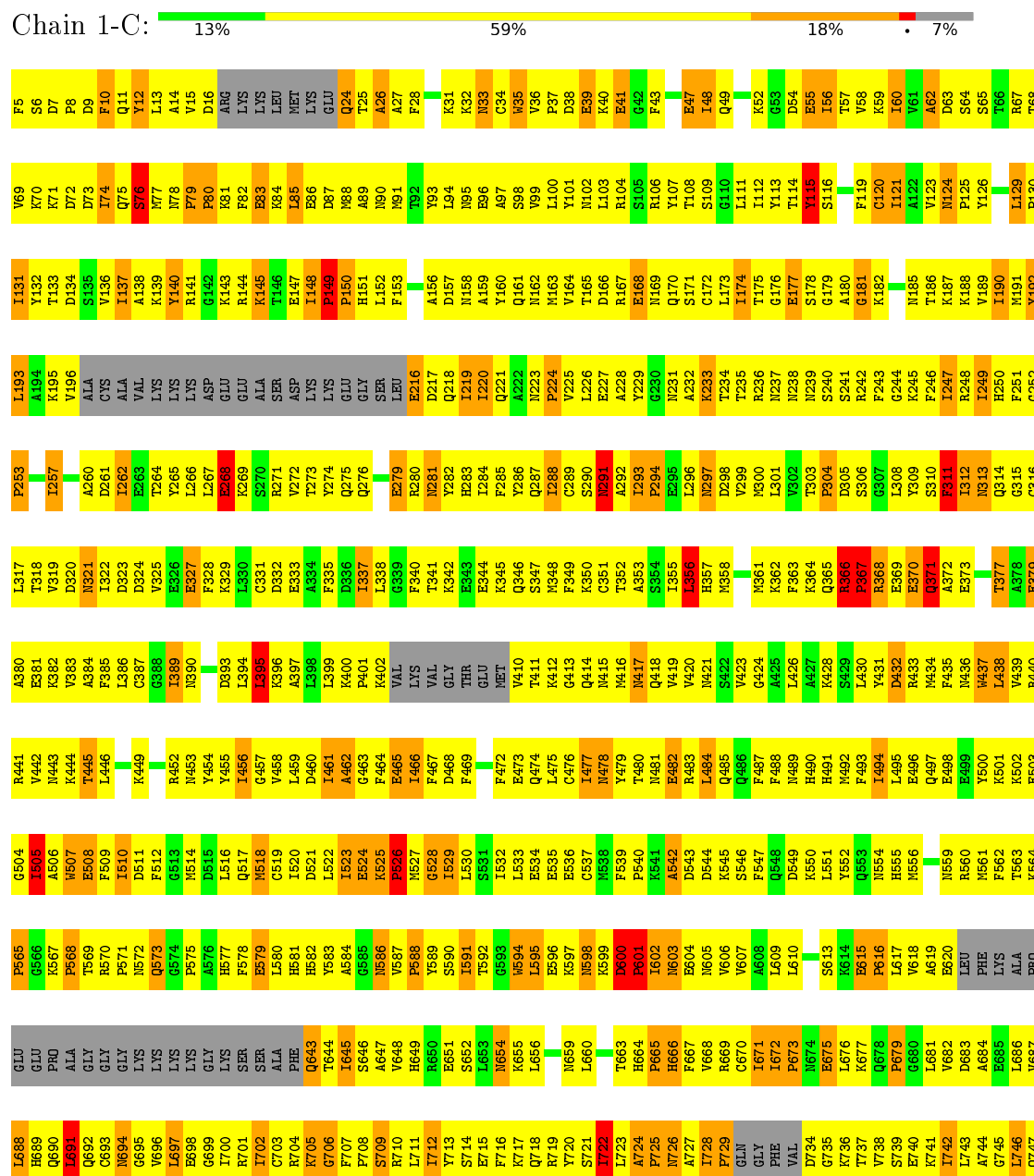
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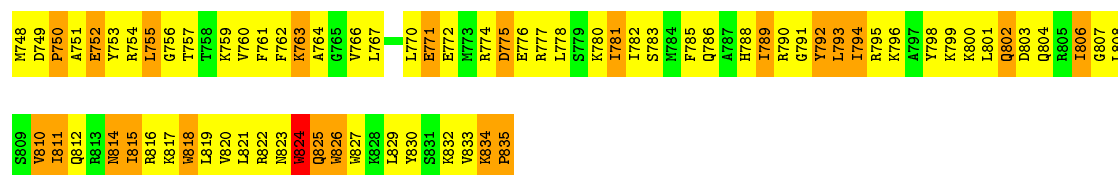
Mol	Chain	Residues	Atoms					AltConf	Trace
3	23-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	24-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	25-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	26-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		
3	27-Z	151	Total	C	N	O	S	0	0
			1198	757	190	244	7		

3 Residue-property plots

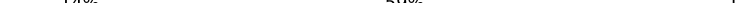
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric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

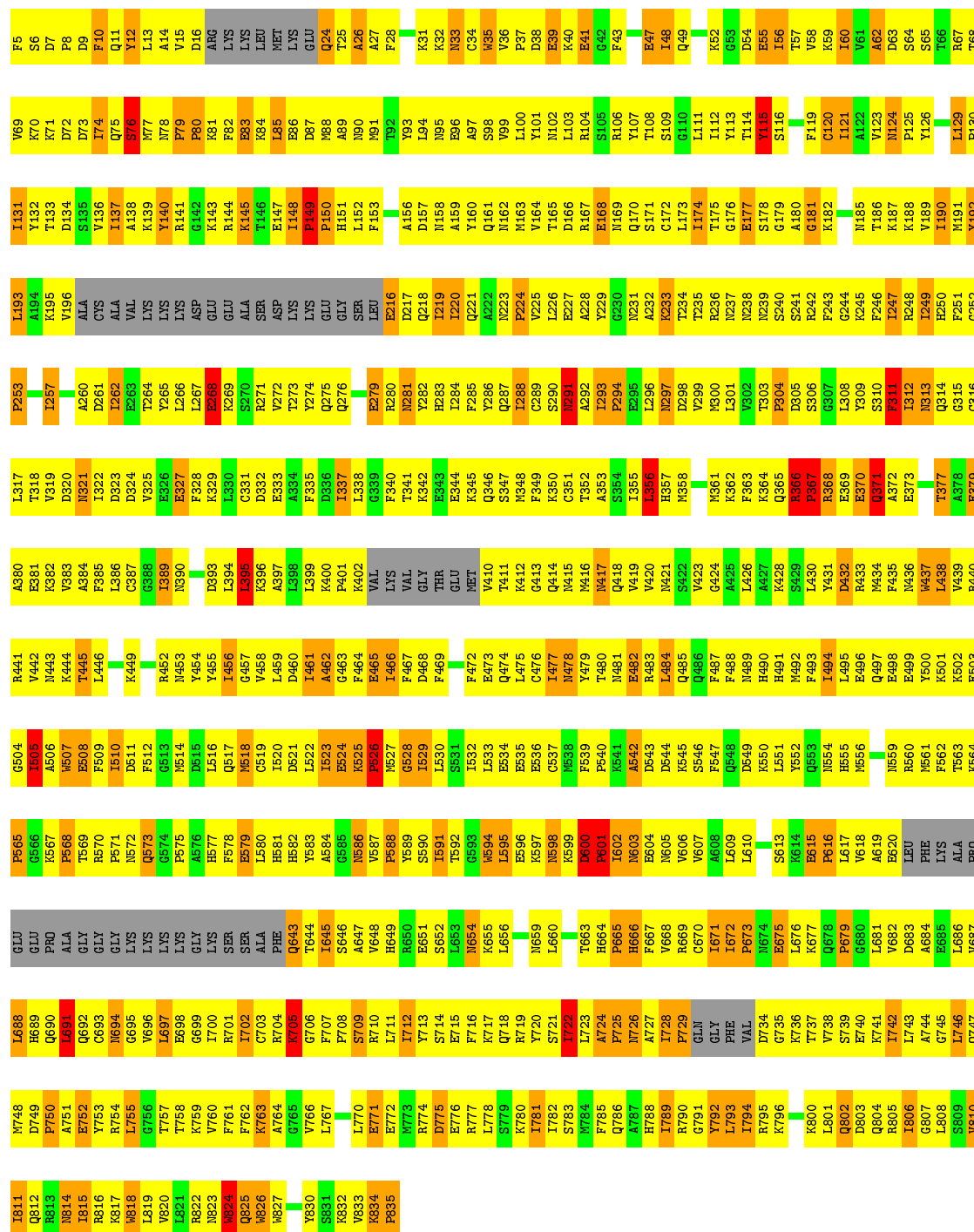
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE





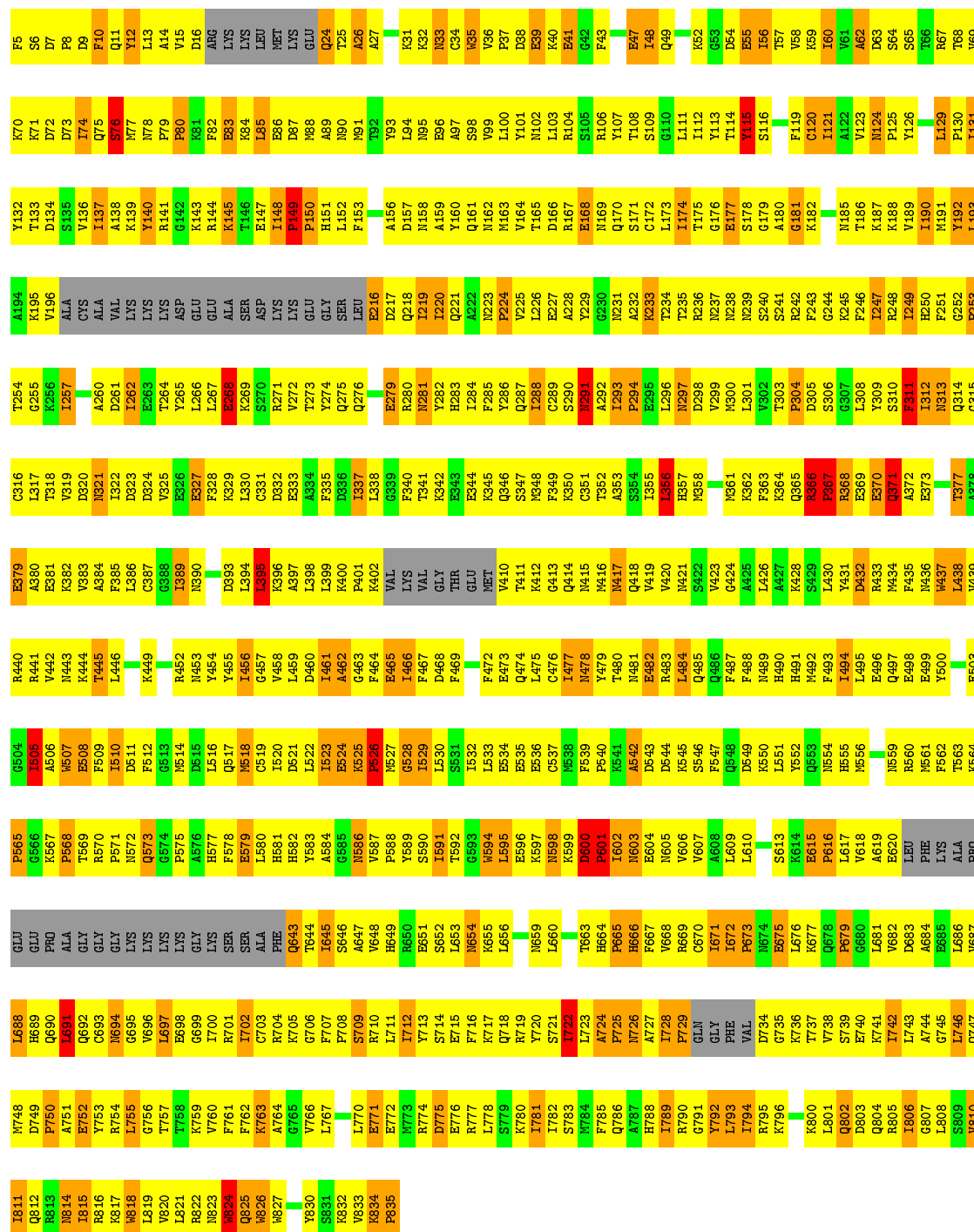
- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

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



• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 3-C: 14% 60% 17% 7%



• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 4-C: 13% 60% 18% 7%



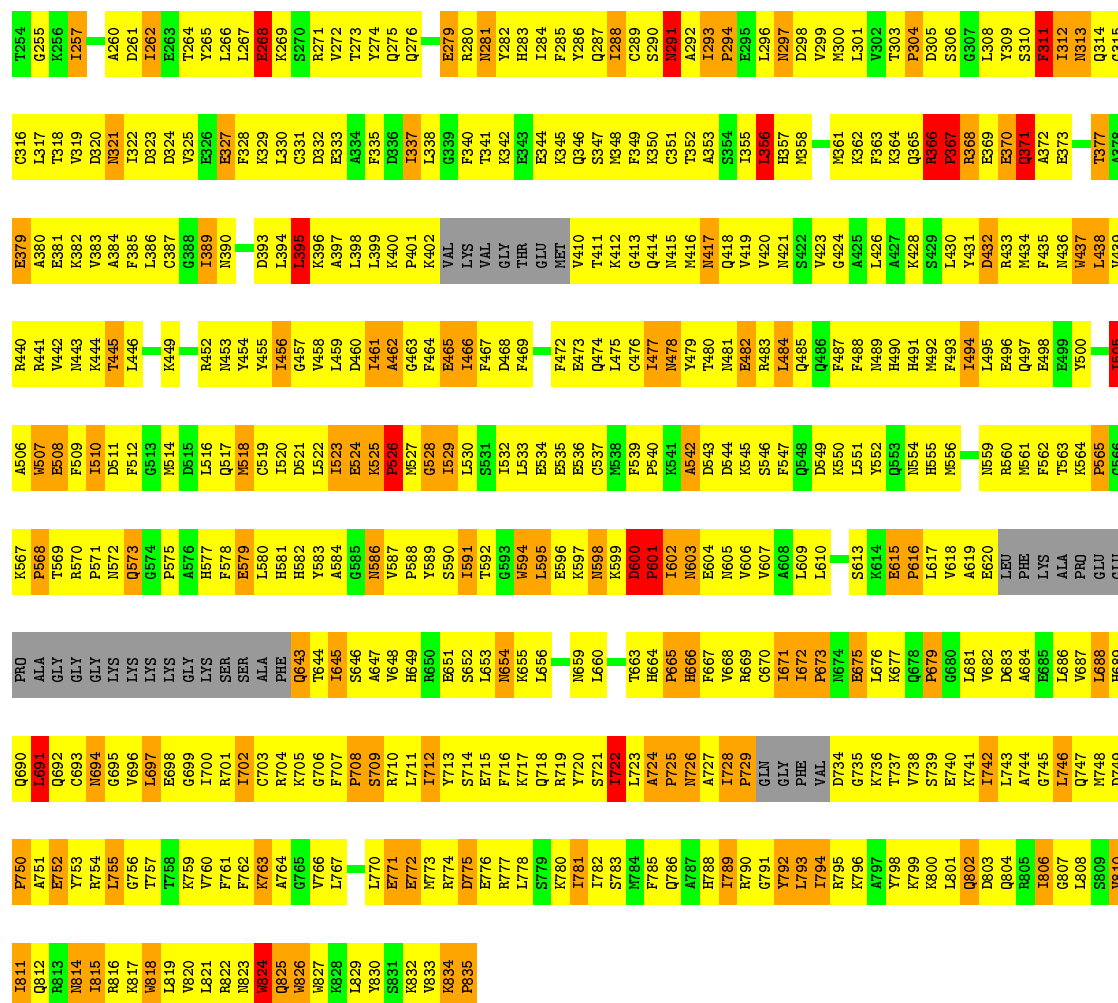
F5	S6	D7	P8	D9	F10	Q11	Y12	L13	A14	V15	D16	A18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32	L33	L34	L35	L36	L37	L38	L39	L40	L41	L42	L43	L44	L45	L46	L47	L48	L49	L50	L51	L52	L53	L54	L55	L56	L57	L58	L59	L60	L61	L62	L63	L64	L65	L66	L67	L68	L69	L70	L71	L72	L73	L74	L75	L76	L77	L78	L79	L80	L81	L82	L83	L84	L85	L86	L87	L88	L89	L90	L91	L92	L93	L94	L95	L96	L97	L98	L99	L100	L101	L102	L103	L104	L105	L106	L107	L108	L109	L110	L111	L112	L113	L114	L115	L116	L117	L118	L119	L120	L121	L122	L123	L124	L125	L126	L127	L128	L129	L130	L131	L132	L133	L134	L135	L136	L137	L138	L139	L140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	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
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Q812	P750	Q690	PR0	K567	A506	R440	E379	C316	T254	A194	Y132
R813	A751	L691	ALA	P568	E507	R441	A380	L317	G255	K195	T133
I814	E752	Q692	GLY	T569	B508	V442	E381	T318	K256	V196	D134
I815	Y753	C693	GLY	R570	F509	N443	K382	V319	I257	ALA	S135
R816	R754	M694	GLY	P571	F510	K444	V283	D320		CYS	I136
K817	L755	G695	LYS	N572	D511	T445	A384	R320		ALA	I137
H818	G756	V696	LYS	Q573	F512	L446		N321	A260	VAL	K138
L819	T757	L697	LYS	P574	G513		F385	I322	D261	LYS	K139
R820	T758	E698	LYS	P575	M514	K449	C387	D323	E263	LYS	L140
V821	K759	G699	GLY	A576	H515	R452	G388	V325	T264	LYS	R141
R822	V760	I700	LYS	H577	L516	R453	T389	G326	Y265	ASP	G142
N823	F761	R701	SER	F578	O517	N453	N390	E327	L266	GLU	K143
R824	F762	I702	SER	E579	M518	Y454		F328	L267	GLU	R144
K825	K763	G703	ALA	L580	C519	Y455	D393	K329	E268	ALA	K145
H826	A764	R704	PHE	H581	L520	I456	L394	L330	K269	SER	T146
R827	G765	K705	Q643	H582	D521	G457	L395	C331	S270	ASP	E147
K828	V766	G706	Q644	Y583	L522	V458	K396	D332	R271	LYS	I148
L829	L767	F707	T645	A584	L523	L459	A397	E333	V272	LYS	P149
Y830		F708	S646	G585	E524	D460	L398	A334	T273	GLU	P150
S831	L770	S709	A647	H586	K525	I461	L399	F335	Y274	GLY	H151
R832	E771	R710	V648	P587	P526	A462	K400	D336	Q275	LEU	F152
K833	E772	L711	H649	P588	N527	G463	P401	I337	Q276	SER	F153
K834	E773	I712	H650	Y589	G528	F464	K402	L338		E216	
P835	R774	Y713	E651	S590	L529	E465	VAL	G339	E279	D217	A156
	D775	S714	G652	I591	L530	I466	LYS	F340	R280	Q218	D157
	E776	F715	L653	T592	S531	F467	VAL	T341	M281	T219	N158
	R777	F716	H654	G593	L532	D468	GLY	K342	Y282	I220	A159
	L778	K717	K655	L594	L533	F469	THR	E343	H283	Q221	Y160
	S779	Q718	L656	L595	E534		GLU	E344	I284	A222	Q161
K780		R719		E596	E535		MET	K345	F285	N223	N162
I781	R782	Y720	M659	K597	E536	E473	V410	Q346	Y286	P224	M163
T783	L784	S721	L660	N598	C537	Q474	T411	S347	Q287	V225	V164
R784		L723	T663	K599	N538	L475	K412	N348	C289	L226	T165
F785	K786	L724	H664	D600	F539	C476	G413	F349	C289	E227	D166
R786		P725	P665	P601	P640	I477	G414	K350	S290	A228	R167
A787	R787	N726	H666	N602	E541	N478	N415	C351	R231	Y229	E168
H788		R727	H666	N603	A542	Y479	N416	T352	A292	G230	N169
L789	R789	A728	P667	E604	D543	Q474	N418	A353	N231	Q232	K170
P790	R790	I728	V668	N605	D544	N481	Q417	S354	P294	A232	S171
G791	R791	P729	H669	V606	K545	E482	V419	E295	K293	R233	G172
Y792		GLN	C670	V607	S546	R483	V420	L356	L296	T234	L173
L793	Y792	GLY	I671	A608	F547	L484	N421	K357	N297	T235	I174
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R796		G735	E675	S613	L551	F488	A425	N361	L301	N239	S178
		K736	L676	K614	L552	N489	L426	K362	V302	G240	G179
		T737	K677	E615	Q553	H490	A427	K363	T303	S241	A180
		V738	Q678	P616	N554	H491	K428	K364	D305	R242	G181
		E740	P679	L617	H555	M492	S429	R366	F243	G244	K182
		K741	G680	V618	M556	F493	L430	P367	S306	F243	
		L681	L681	A619		I494	D431	K368	G307	K245	N185
		I742	V682	E620	N559	L495	Y432	E369	L308	F246	T186
		L743	D683	LEU	R560	E496	R433	E370	Y309	D247	K187
		A744	A684	PHE	N561	Q497	F434	Q371	S310	R248	K187
		G745	E685	LYS	F562	E498	N435	F311	I249	K188	V189
		L746	L686	ALA	T563	E499	N436	E373	N312	H250	I190
		Q747	V687	PRO	K564	Y500	N437	E373	G131	F251	M191
		R748	L688	GLU	P565		L438	T377	Q314	G252	K192
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● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

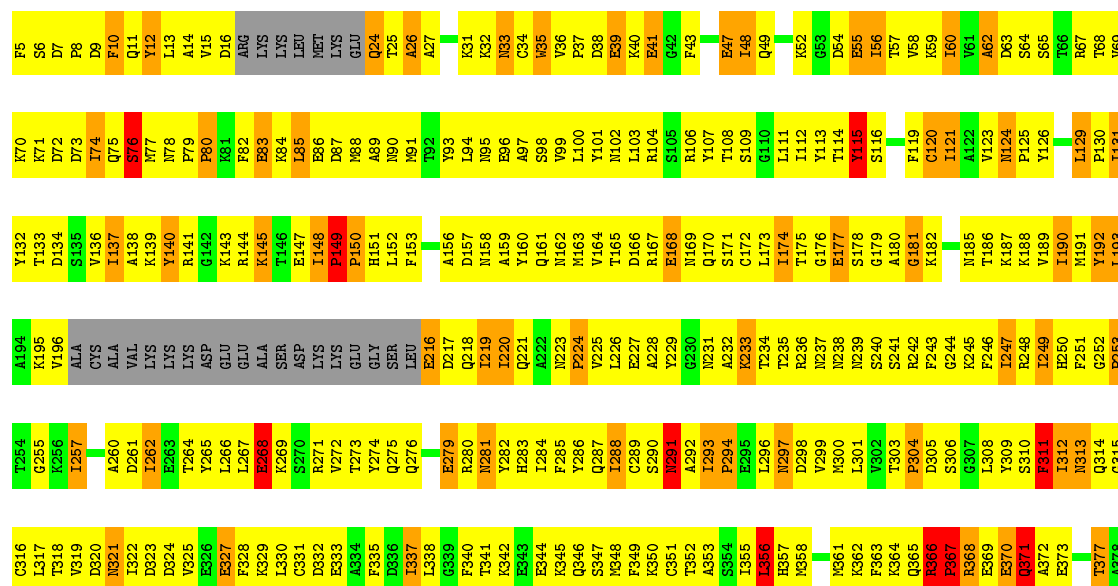
Chain 6-C: 13% 60% 18% 7%

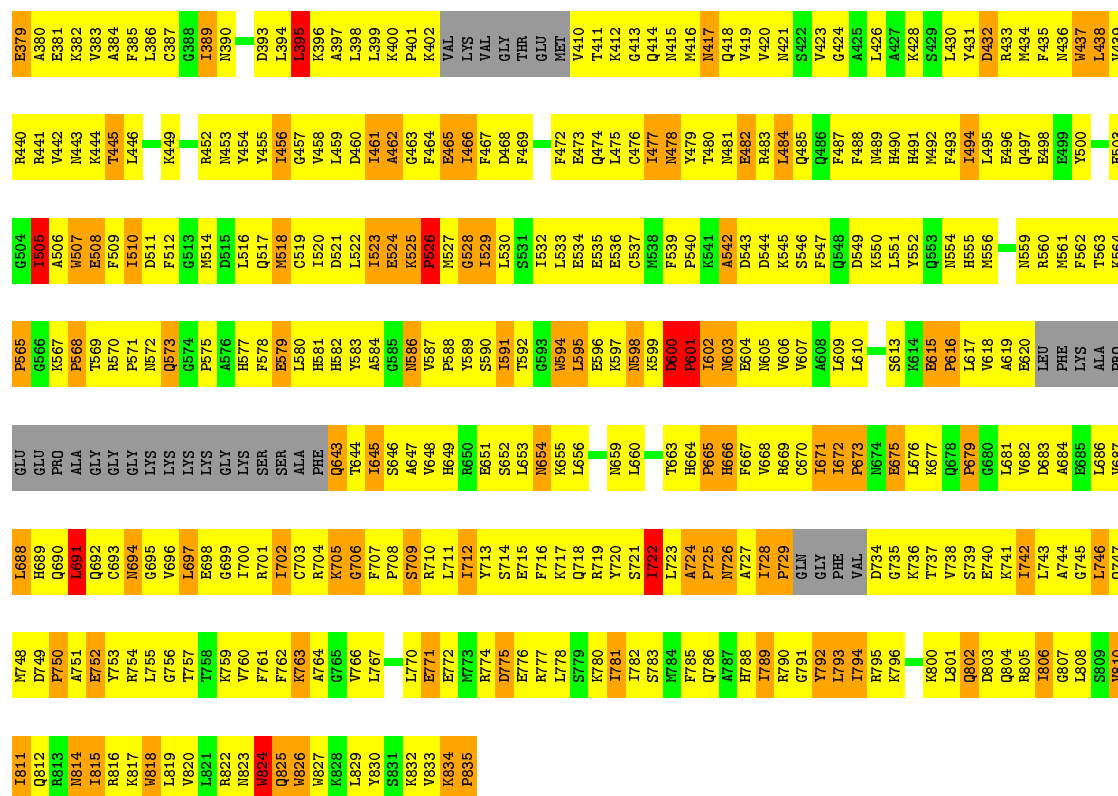
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	V196	T133	K71	S6
ALA	S135	D134	D72	D7
	CYS	I136	D73	P8
ALA	I137	S136	I74	D9
VAL	A138	S76	Q75	F10
LNS	K139	M77	S76	Q11
LNS	Y140	N78	M78	Y12
LNS	R141	P79	N79	L13
ASP	G142	P80	N80	A14
GLU	K143	K81	K81	V15
GLU	R144	F82	F82	D16
ALA	K145	E83	E83	A48
SER	T146	K84	K84	LVS
ASP	E147	L85	L85	LEU
LNS	I148	E86	E86	MET
LVS	P149	D87	D87	LVS
GLU	P150	N88	N88	GLU
GLU	H151	A89	A89	Q24
LNS	L152	N90	N90	T25
SER	F153	N91	N91	A26
E216	D217	T92	T92	A27
Q218	A156	Y93	Y93	K31
I219	D157	L94	L94	K32
I220	M158	N95	N95	N33
Q221	A159	E96	E96	C34
Q222	Y160	A97	A97	K35
Q223	Q161	S98	S98	V36
P224	N162	V99	V99	P37
V225	M163	L100	L100	D38
L226	V164	Y101	Y101	E39
E227	T165	N102	N102	K40
E228	D166	L103	L103	R41
E229	R167	R104	R104	G42
G230	E168	S105	S105	F43
N231	M169	R106	R106	E47
A232	Q170	Y107	Y107	I48
K233	S171	T108	T108	Q49
K234	C172	S109	S109	K52
T235	L173	G110	G110	G53
T236	I174	L111	L111	D54
R237	T175	I112	I112	E55
N238	G176	Y113	Y113	I56
N239	E177	T114	T114	T57
N239	S178	Y115	Y115	V58
S240	G179	S116	S116	K59
S241	A180	F119	F119	I60
R242	G181	C120	C120	V61
G243	K182	I121	I121	A62
G244	G244	A122	A122	D63
K245	N185	V123	V123	S64
F246	L186	M124	M124	S65
I247	K187	P125	P125	T66
R248	K188	Y126	Y126	R67
I249	V189	L129	L129	V69
E250	I190	P130	P130	
F251	M191	T131	T131	
G252	G192	L132	L132	



• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

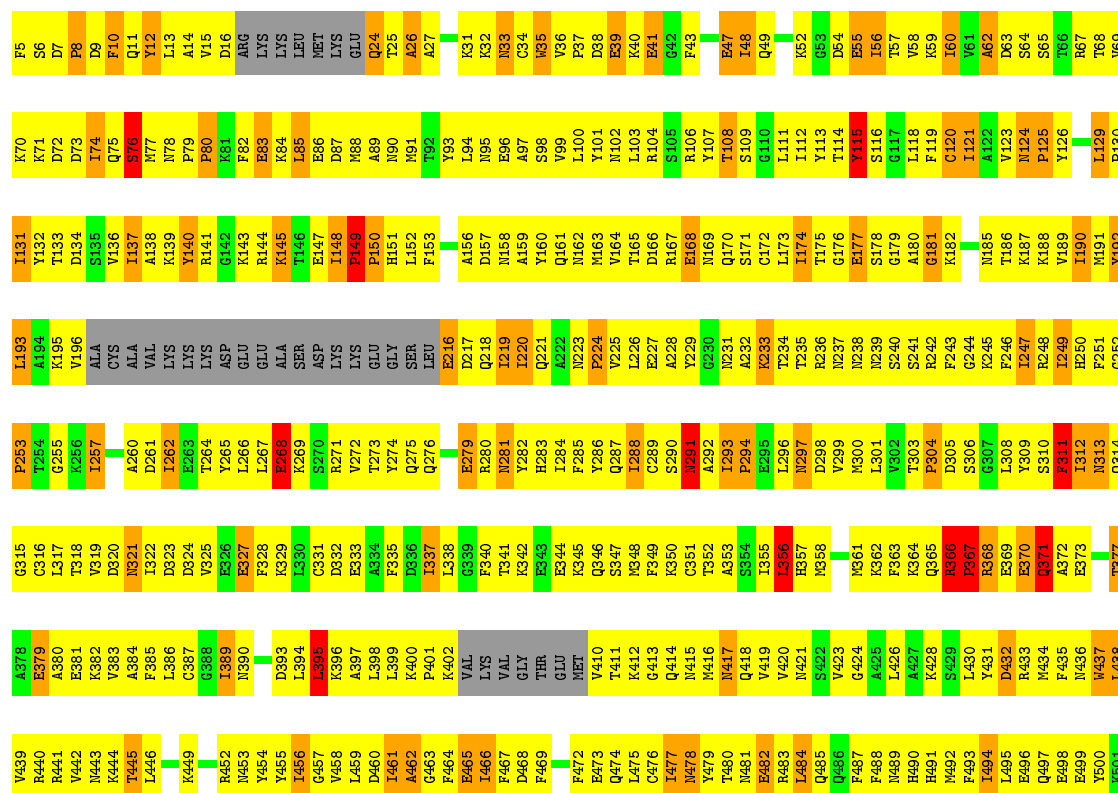
Chain 7-C: 14% 59% 18% 7%

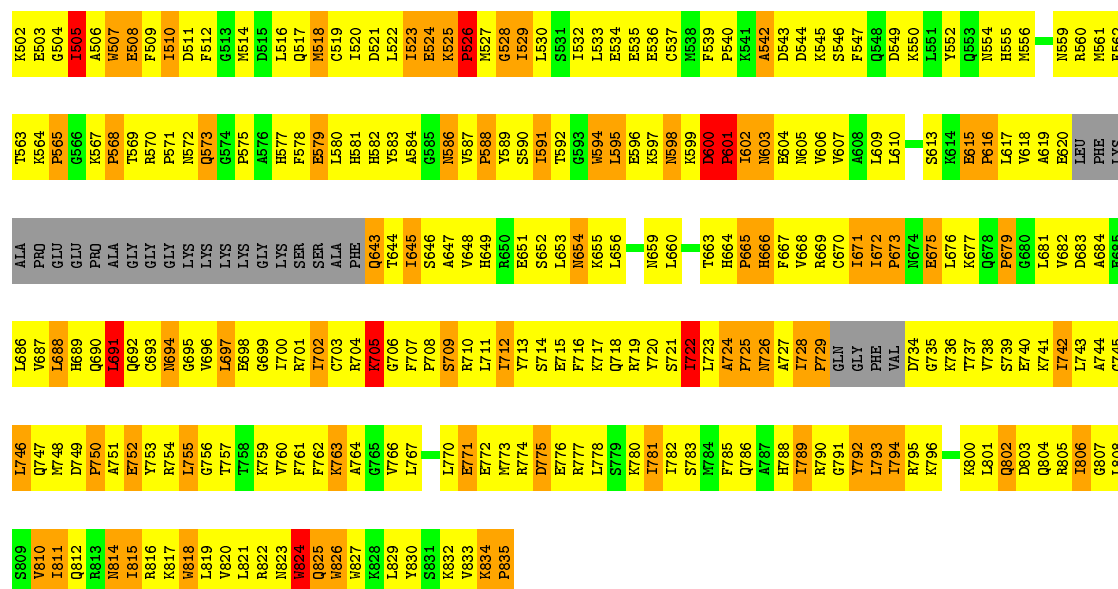




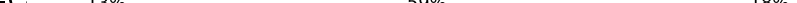
• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

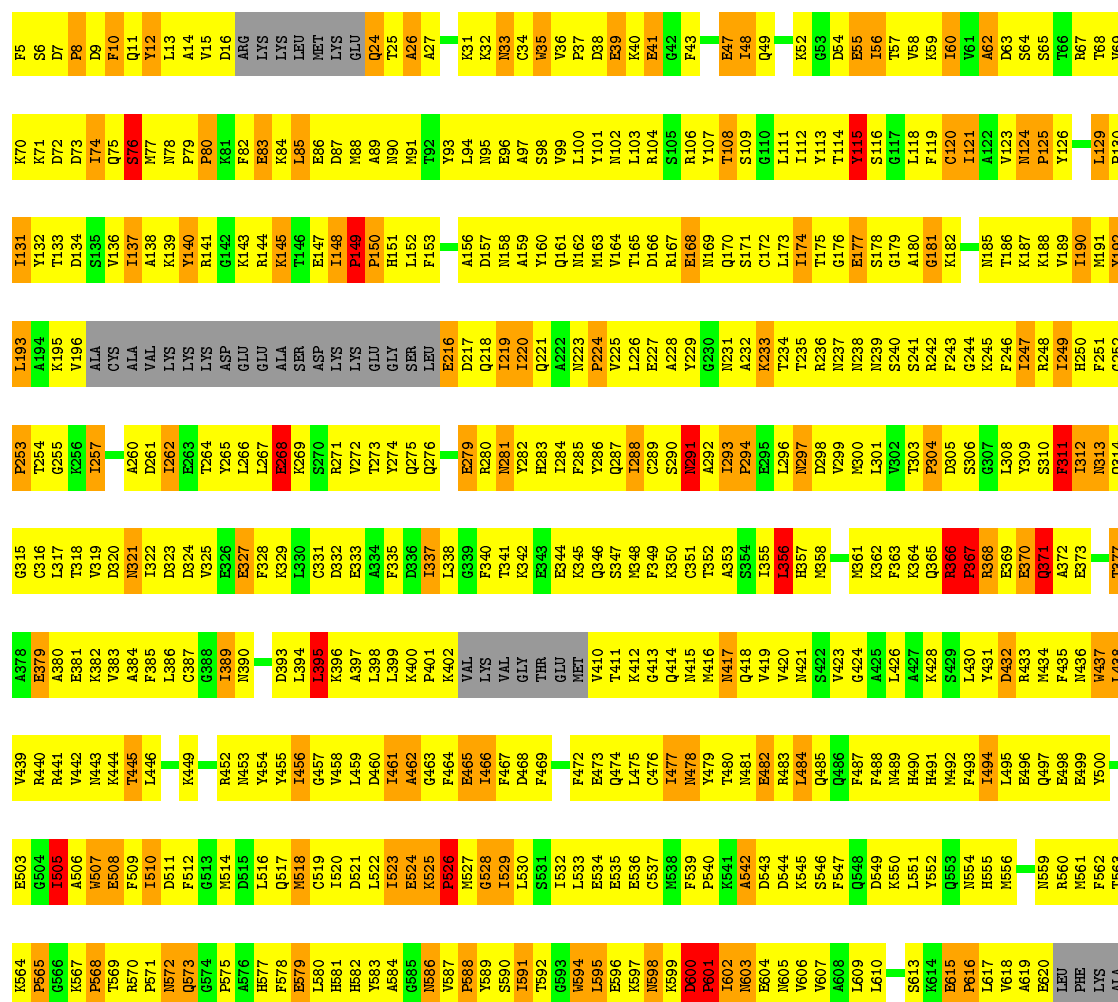
Chain 8-C: 13% 59% 18% 7%





- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 9-C:  13% 59% 18% 7%



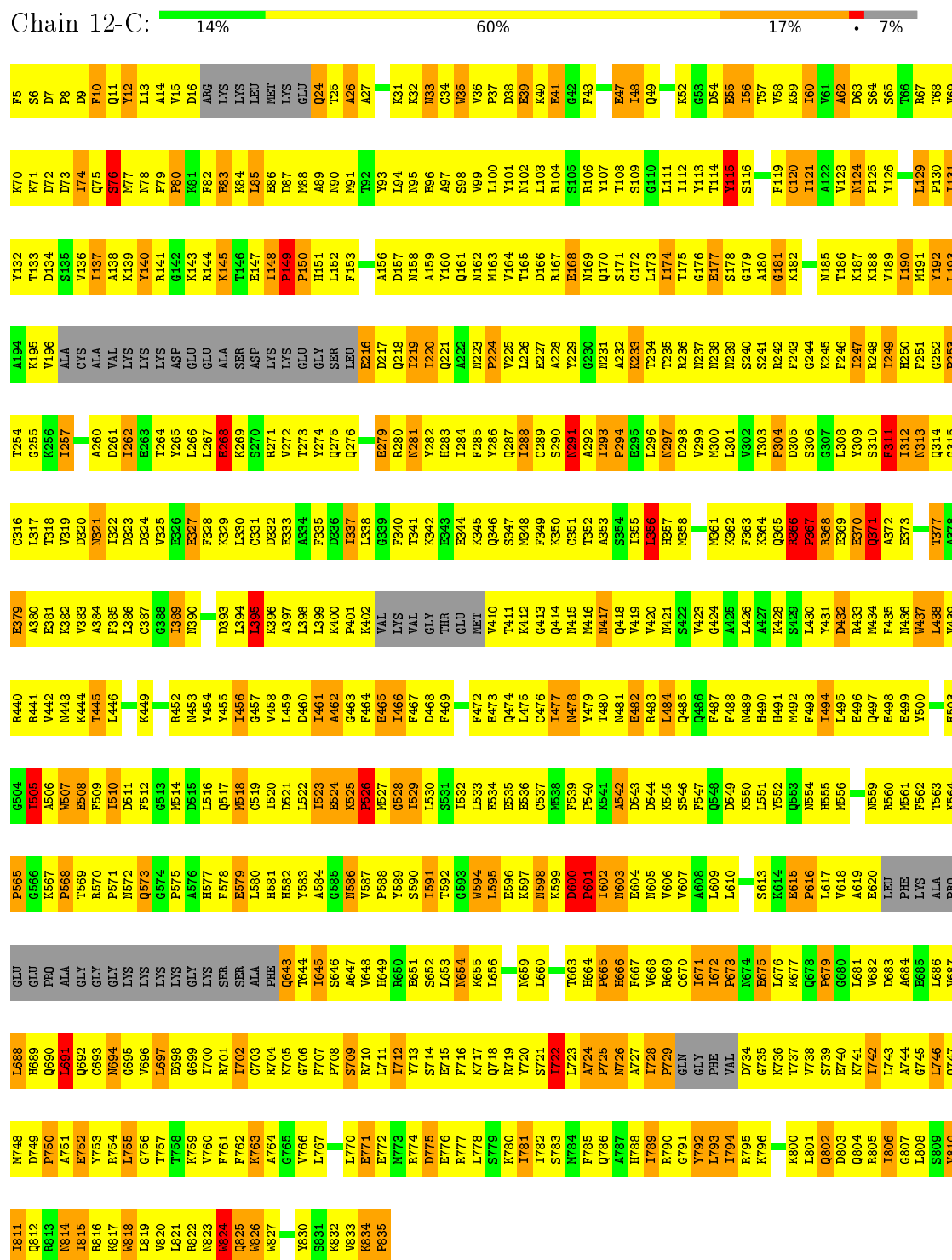
P750	P751	P752	P753	P754	P755	P756	P757	P758	P759	P760	P761	P762	P763	P764	P765	P766	P767	P768	P769	P770	P771	P772	P773	P774	P775	P776	P777	P778	P779	P780	P781	P782	P783	P784	P785	P786	P787	P788	P789	P790	P791	P792	P793	P794	P795	P796	P797	P798	P799	P800	P801	P802	P803	P804	P805	P806	P807	P808	P809	P810	P811	P812	P813	P814	P815	P816	P817	P818	P819	P820	P821	P822	P823	P824	P825	P826	P827	P828	P829	P830	P831	P832	P833	P834	P835
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• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

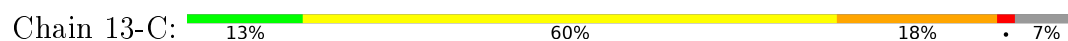
Chain 11-C: 14% 60% 17% 7%

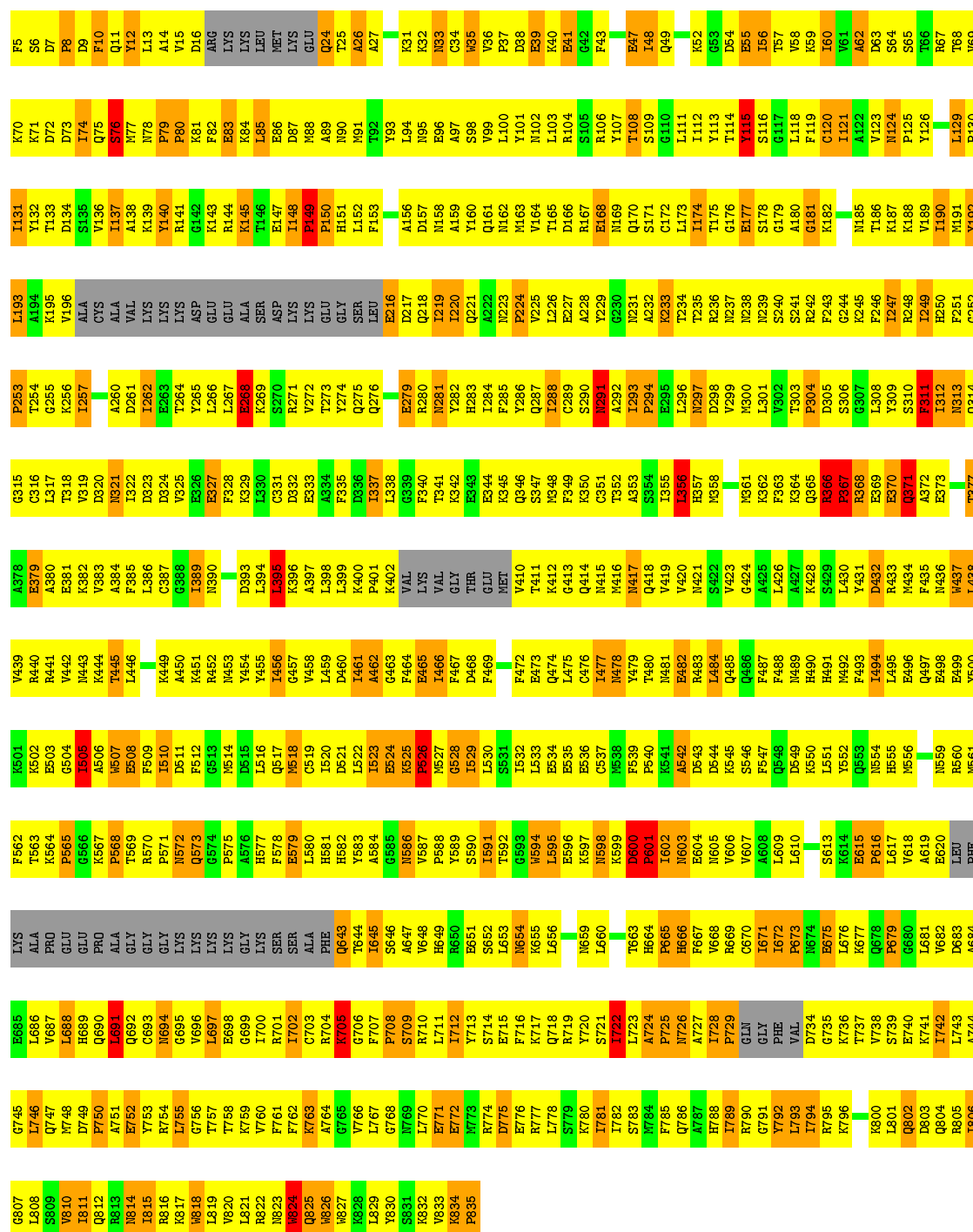
Y132	A194	T254	C316	E379	R440	G504	P565	GLU	I688	N748	I811	F5
K132	K195	G255	L317	A380	R441	A505	G566	GLU	H689	D749	Q812	S6
D134	V196	K256	T318	E381	V442	A506	K567	PRO	Q690	P750	R313	D7
S135	ALA	I257	V319	K382	K443	A507	P568	ALA	L691	A751	N814	P8
L136	CVS	L74	D320	K383	K444	A508	T569	GLY	Q692	P752	R815	D9
I137	ALA	L260	N321	A384	T445	A510	A570	GLY	Q693	P753	R816	F10
A138	VAL	D261	I322	F385	L446	L510	P571	GLY	H694	R754	K817	Q11
K139	LVS	L262	D323	L386	L512	D511	N572	LVS	G695	L755	N818	Y12
Y140	LVS	E263	D324	C387	L513	F512	Q573	LVS	G696	T756	L819	N78
R141	LVS	T264	G325	G388	G514	G513	G574	LVS	L697	T757	R820	P79
A142	ASP	Y265	A326	I389	R452	G515	P575	LVS	E698	T758	L821	P80
K143	GLU	L266	E327	N390	N453	P515	A576	GLY	G699	R759	R822	P81
R144	GLU	L267	F328	L392	N454	L516	H577	GLY	T700	V760	N823	A82
K145	ALA	E268	K329	L394	Y455	L517	F578	SER	R701	F761	Q824	LVS
T146	SER	K384	L330	L395	A456	N518	E579	SER	I702	F762	N826	LVS
E147	ASP	S270	C331	K396	G457	C519	L580	ALA	R704	K763	A764	L85
I148	LVS	R271	D332	K396	A458	T520	H581	PHE	T705	T764	R827	P86
P149	LVS	V272	E333	A397	L459	D521	H582	Q643	K706	T765	L828	MET
L150	GLY	T273	A334	L398	D460	L522	Y583	T644	F707	V766	K832	LVS
H151	GLU	Y274	D336	L399	A462	T523	A584	T645	T708	L767	R833	GLU
S152	SER	Q275	L336	K400	A463	E524	G585	A647	S709	L768	R834	Q24
N153	LEU	Q276	L337	P401	G463	K525	N586	G648	R710	E771	K834	T25
Y154	LEU	L216	L338	K402	F464	P526	V587	V648	L711	R772	R835	A26
A156	D217	E279	G339	VAL	E465	M527	P588	H649	I712	E773	P835	A27
D157	Q218	R280	F340	LVS	L466	G528	Y589	R650	T713	N774	R836	K31
N158	L219	N281	T341	VAL	F467	T529	S590	E651	S714	D775	R837	K32
A159	L220	Y282	K342	GLY	D468	L530	I591	S652	T715	E776	L778	N33
V160	Q221	H283	E343	GLU	F469	S531	T592	L653	E716	R777	L779	G34
Q161	Q222	L284	E344	THR	L470	L532	G593	N654	T717	L778	L780	H35
S162	N223	F285	K345	MET	F472	L533	M594	K655	K717	L778	L781	H36
L163	P224	Y286	Q346	V410	E473	E534	L595	L656	Q718	S780	L782	V36
V164	T225	Q287	S347	T411	Q474	E535	E596	L657	R719	K780	L783	V37
T165	L226	L288	K348	K412	L475	E536	K597	N659	T720	L781	L784	D38
D166	E227	K289	F349	G413	C476	C537	N598	L660	S721	L782	S783	E39
R167	A228	S290	K350	Q414	I477	N538	K599	L661	I722	L783	L785	K40
L168	Y229	E291	C351	N415	N478	P539	D600	T663	R723	K784	L786	G42
S169	G230	A292	T352	N416	Y479	P540	P601	H664	A724	F785	L787	G43
R106	N231	L293	A353	N417	T480	K541	I602	P665	T725	Q786	L788	E47
Y107	A232	P294	S354	Q418	N481	A542	N603	H666	N726	L788	L789	I48
T108	K233	E295	L355	V419	E482	D543	E504	F667	A727	L789	L790	Q49
S109	K234	L296	L356	V420	L483	D544	N605	V668	T728	L789	L791	L49
G110	T234	N297	K357	N421	L484	K545	V606	R669	P729	R790	L792	Q49
L111	T235	L297	N358	S422	Q485	S546	V607	C670	GLN	G791	L793	L11
L112	R236	D298	K361	V423	Q486	F547	A608	T671	PHE	Y792	L794	L12
Y113	N237	V299	K362	Q424	F488	Q548	D549	P672	VAL	L793	L795	L13
G114	M300	K301	K362	A425	K550	N550	K550	P673	D734	R795	L796	E55
E115	N238	L301	F363	L426	N489	L551	L551	L610	T735	R795	L796	E56
P116	S240	V302	K364	A427	H490	L552	S613	E675	G736	L796	L797	L56
A116	S241	T303	K365	K428	H491	L552	N614	T676	T737	R796	L798	L57
L180	R242	G481	K366	S429	M492	G553	E515	K677	T738	L801	L799	V58
N185	K245	F243	R367	L430	F493	N554	P616	Q678	S739	R802	L800	K59
V123	P246	S306	K368	Y431	I494	M555	L617	T680	E740	R803	L801	L60
L186	T247	K309	E369	D432	L495	M556	V618	G680	S740	R804	L802	V61
K187	T247	T247	E370	R433	E496	L559	A619	L681	K741	Q804	L803	A62
N124	K248	F310	E371	R434	Q497	N560	L619	T682	I742	R805	L804	D63
P125	S341	S311	Q371	F435	Q497	E560	L620	V683	L743	R806	L805	L64
L188	T249	F311	E372	N436	L497	N561	PHE	A684	A744	G807	L806	S64
S189	K250	I312	E373	N436	Y500	F562	LVS	E685	G745	L808	L807	S65
T66	N191	N313	E373	N437	Y500	T563	LVS	E686	L746	S809	L808	T66
L129	F251	K313	T377	L439	Y500	L564	ALA	L687	Q747	R810	L809	L67
L130	K252	Q314	A376	N439	E502	L564	ALA	L687	L747	L810	L810	L68
L131	K252	C315	L378	V430	E502	L564	ALA	L687	L747	L810	L810	L69

- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

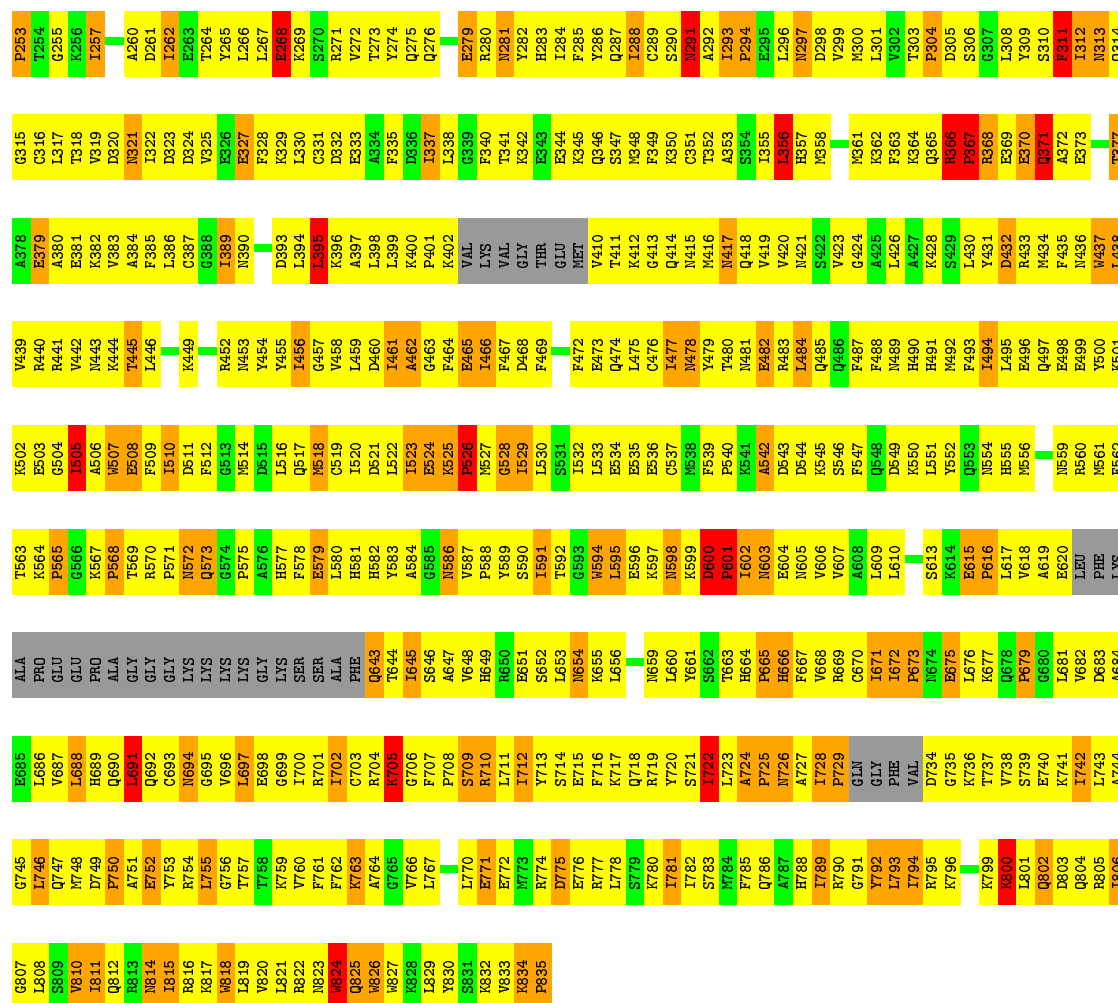


- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE



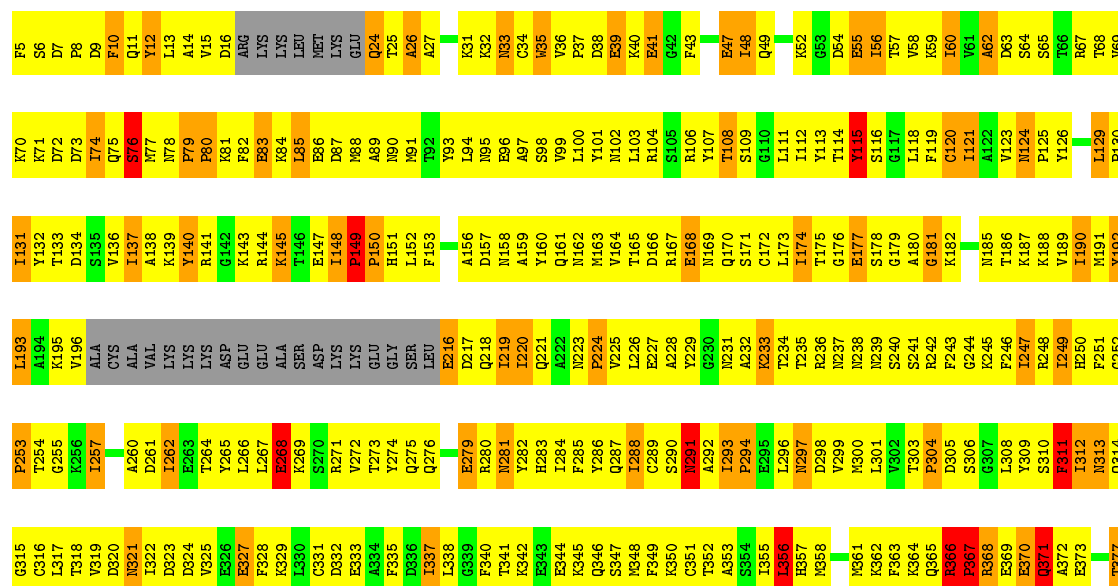


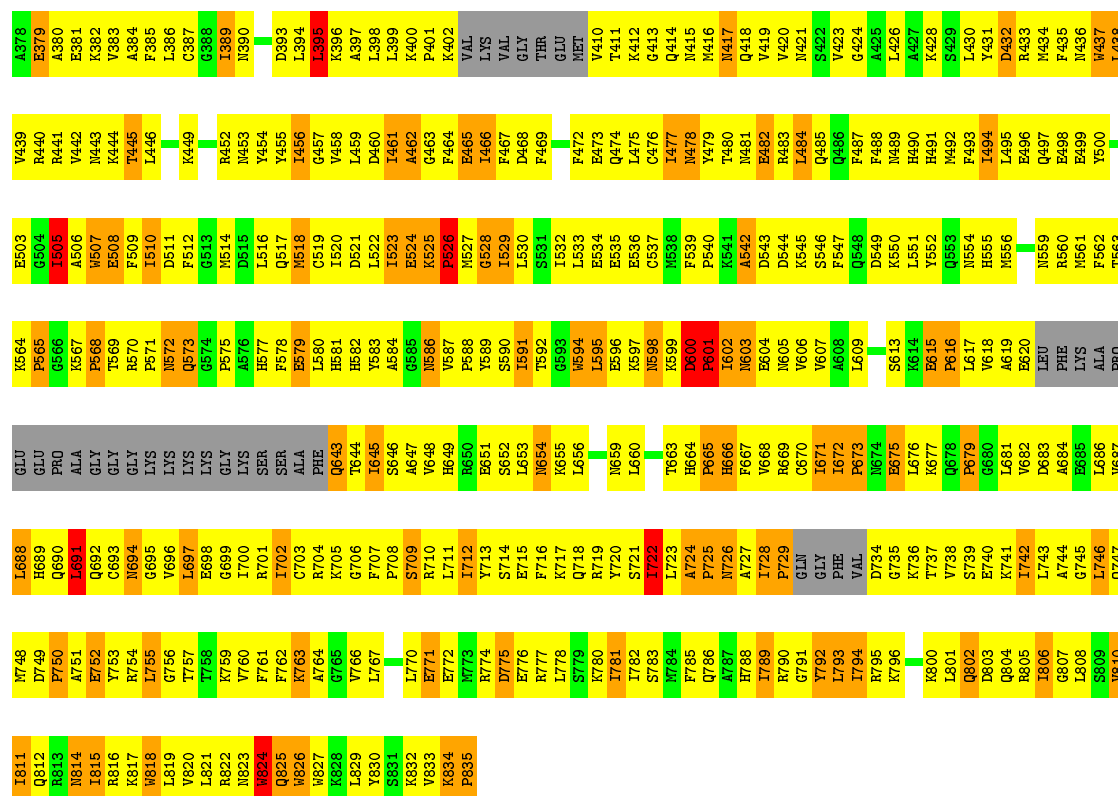
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● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

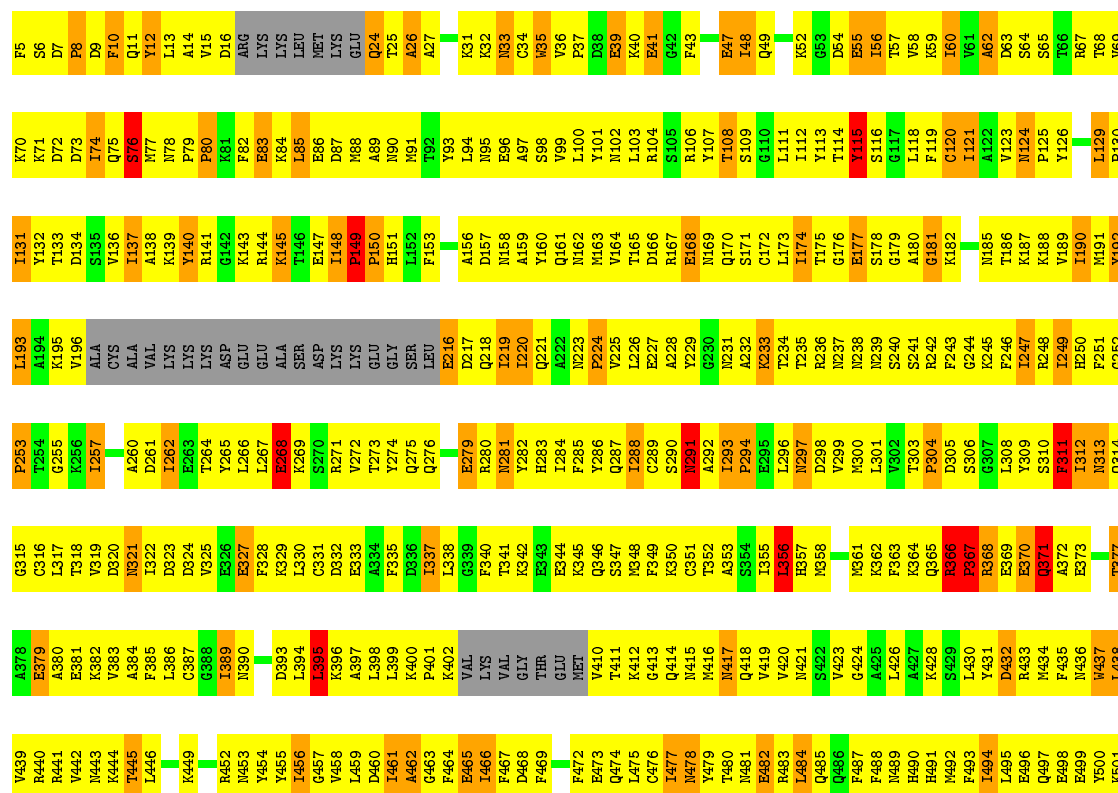
Chain 16-C: 13% 59% 18% 7%





● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

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

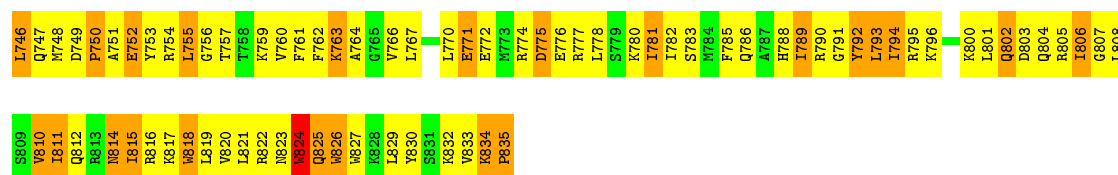


PRO	V687	Q747	V810	PRO	V687	Q747	V810
GLU	L688	M743	I811	GLU	L688	M743	I811
GLU	H889	D72	Q812	GLU	H889	D72	Q812
PRO	Q690	P750	Q813	PRO	Q690	P750	Q813
ALA	L691	D9	N814	ALA	L691	D9	N814
GLY	Q692	F10	I815	GLY	Q692	F10	I815
GLY	C693	Q11	I816	GLY	C693	Q11	I816
GLY	M694	Y12	K817	GLY	M694	Y12	K817
LYS	C695	L754	W818	LYS	C695	L754	W818
LYS	V696	G756	L319	LYS	V696	G756	L319
LYS	L697	T757	V820	LYS	L697	T757	V820
LYS	E698	T758	L321	LYS	E698	T758	L321
GLY	G699	K759	R822	GLY	G699	K759	R822
LYS	I700	V760	M823	LYS	I700	V760	M823
SER	R701	F761	W824	SER	R701	F761	W824
SER	I702	F762	Q825	SER	I702	F762	Q825
C703	R704	K763	W826	C703	R704	K763	W826
ALA	W704	LVS	W827	ALA	W704	LVS	W827
PHE	K705	G765	K828	PHE	K705	G765	K828
T644	G706	V766	Q24	T644	G706	V766	Q24
T645	F707	L767	L829	T645	F707	L767	L829
S646	P708	L767	S831	S646	P708	L767	S831
A647	S709	L770	L152	A647	S709	L770	L152
V648	R710	E771	N91	V648	R710	E771	N91
H649	L711	E772	F153	H649	L711	E772	F153
L650	I712	M773	L156	L650	I712	M773	L156
S652	Y713	R774	D157	S652	Y713	R774	D157
L653	S714	D775	N158	L653	S714	D775	N158
L654	E715	E776	A159	L654	E715	E776	A159
L655	F716	R777	Y160	L655	F716	R777	Y160
L656	K717	L778	Q161	L656	K717	L778	Q161
L659	Q718	S779	M162	L659	Q718	S779	M162
L660	R719	K780	M163	L660	R719	K780	M163
L663	Y720	I781	V164	L663	Y720	I781	V164
L664	S721	L782	D166	L664	S721	L782	D166
L665	T722	R783	R167	L665	T722	R783	R167
L666	L723	W784	E168	L666	L723	W784	E168
L667	A724	F785	M169	L667	A724	F785	M169
L668	P725	Q786	Q170	L668	P725	Q786	Q170
L669	M726	A787	S171	L669	M726	A787	S171
L670	A727	F788	C172	L670	A727	F788	C172
L671	I728	H789	L173	L671	I728	H789	L173
L672	P729	L790	L112	L672	P729	L790	L112
L673	GLN	Q791	T174	L673	GLN	Q791	T174
L674	GLY	Y792	G176	L674	GLY	Y792	G176
L675	PHE	L793	E177	L675	PHE	L793	E177
L676	VAL	I794	S116	L676	VAL	I794	S116
L677	D734	R795	G179	L677	D734	R795	G179
L678	T674	K796	L118	L678	T674	K796	L118
L679	G735	K800	A180	L679	G735	K800	A180
L680	K736	L801	G181	L680	K736	L801	G181
L681	T737	V738	K182	L681	T737	V738	K182
L682	V738	Q802	N185	L682	V738	Q802	N185
L683	S739	P679	A122	L683	S739	P679	A122
L684	E740	D63	L186	L684	E740	D63	L186
L685	K741	Q804	K187	L685	K741	Q804	K187
L686	I742	R805	L247	L686	I742	R805	L247
L687	L743	L806	R248	L687	L743	L806	R248
L688	A744	R607	L249	L688	A744	R607	L249
L689	G745	M91	H250	L689	G745	M91	H250
L690	L746	L808	F251	L690	L746	L808	F251
L691	L746	S809	G252	L691	L746	S809	G252

• Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

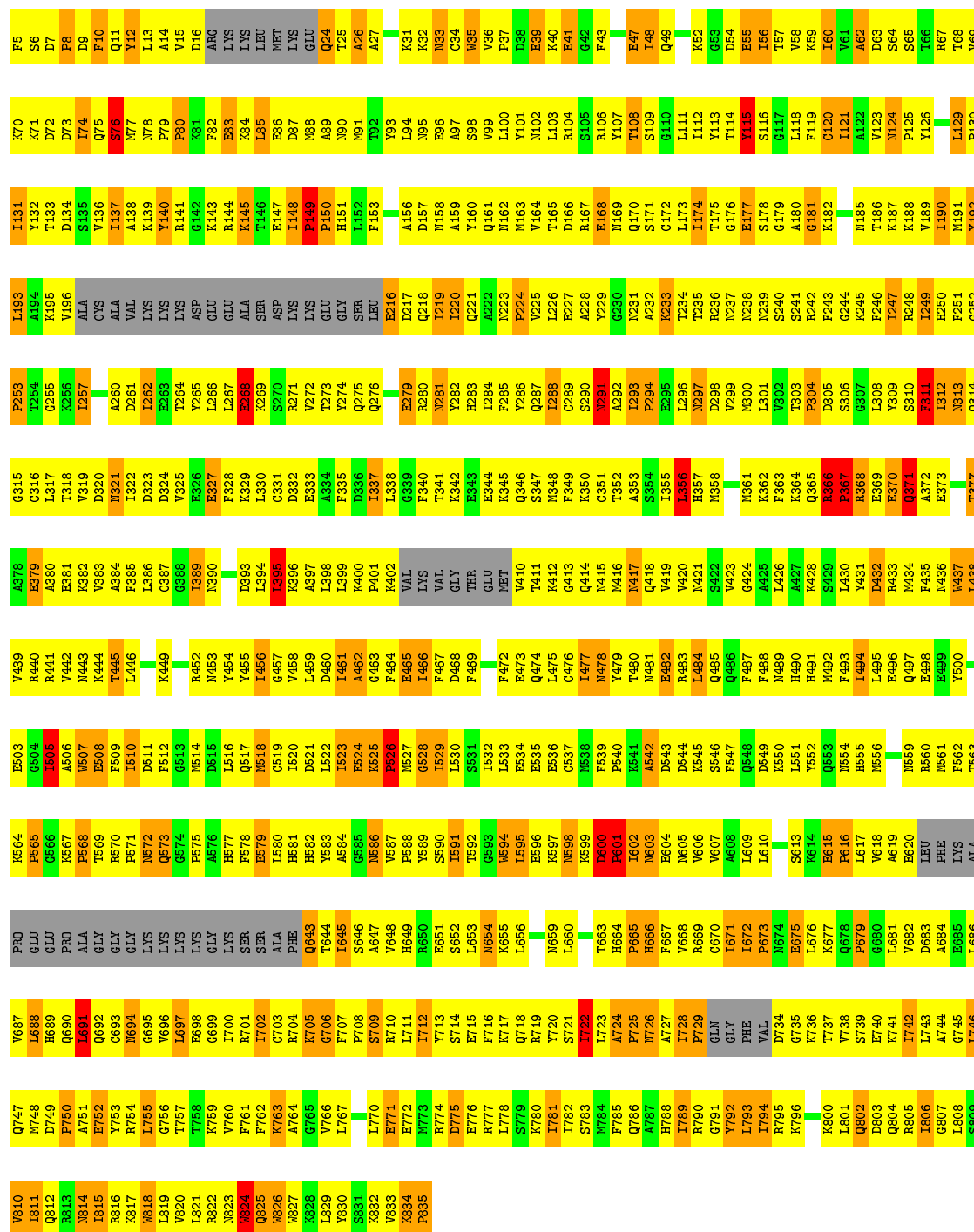
Chain 19-C: 13% 59% 18% 7%

F5	K70	I131	L193	P253	G315	A378	Y439	K502	T563	ALA	L686
S6	K71	Y132	A194	T254	C316	E379	R440	E503	K564	PRO	L687
D7	D72	T133	K195	G255	L317	A380	R441	E504	G565	GLU	L688
P8	D73	D134	Y196	K256	T318	E381	V442	G505	G566	GLU	H889
D9	I74	S135	ALA	I257	V319	K382	N443	A506	P567	PRO	Q690
F10	I75	V136	CVS	A280	D320	V383	K444	W507	P568	ALA	L691
Q11	S76	I137	ALA	D261	N321	A384	T445	W508	T569	GLY	Q692
Y12	R77	A138	VAL	I262	I322	P385	L446	F509	R570	GLY	C693
L13	M78	K139	LVS	E263	D323	L386	L447	D511	P571	GLY	M694
A14	P79	R140	LVS	E264	D324	C387	L448	D512	Q572	LVS	V696
V15	P80	R141	LVS	T265	V325	G388	L449	Q573	Q573	LVS	L697
LVS	K81	K142	ASP	Y266	E326	L389	R452	G513	G574	LVS	L698
GLY	R82	K143	GLU	L267	E327	N390	L453	M514	P575	LVS	E699
LVS	E83	R144	GLU	L268	F328	L391	Y454	B515	A576	GLY	G699
LVS	K84	K145	ALA	E269	K329	D393	Y455	L516	H577	LVS	I700
LVS	L85	T146	SER	K269	L330	L394	Y456	Q517	H578	SER	R701
MET	E86	L147	ASP	E270	C331	L395	G457	M518	E579	SER	I702
LVS	W87	I148	LVS	R271	D332	K396	V458	C519	H580	ALA	C703
GLU	N88	P149	LVS	V272	E333	A397	L459	I520	H581	PHE	R704
Q24	A89	F150	GLU	T273	A334	L398	D460	D521	H582	ALA	K705
T25	N90	H151	GLY	Y274	F335	L399	L461	L522	H583	T644	G706
A26	N91	L152	SER	Q275	D336	K400	G462	E524	G584	T645	F707
A27	T92	F153	LEU	Q276	I337	P401	G463	E525	G585	S646	F708
K31	Y93	L156	D216	E279	L338	K402	F464	K525	N586	A647	S709
K32	I94	D157	Q218	R280	G339	VAL	E465	E526	H587	V648	R710
N33	N95	N158	Q118	R281	F340	LVS	E466	M527	P588	H649	L711
C34	E96	A159	I219	Y282	T341	VAL	F467	G528	Y589	L650	I712
W35	A97	A159	L220	R283	K342	GLY	D468	I529	S590	E651	Y713
V36	N99	Q161	Q221	I284	E343	THR	F469	L530	I591	S652	S714
P37	V99	Q162	A222	L285	E344	GLU	L470	S531	T592	L653	E715
D38	Y101	M162	N223	Y286	K345	MET	F472	I532	G593	L654	F716
E39	N102	M163	P224	Q287	Q346	V410	E473	L533	M594	L655	K717
K40	L103	V164	V225	L288	K347	T411	Q474	E534	L595	L656	Q718
E41	R104	D166	L226	C289	K348	K412	L475	E535	E596	L659	R719
G42	R167	R167	A228	S290	Q413	K413	C476	E536	K597	L660	Y720
F43	S105	E168	Y229	K291	Q414	M415	I477	C537	N598	L663	S721
E47	Y107	M169	G230	A292	M416	M416	N478	M538	K599	T663	I722
L48	T108	Q170	N231	L293	M417	M417	Y479	F539	D600	L723	L723
Q49	S109	S171	A232	P294	Q418	Q418	T480	P540	P601	A724	A724
K52	G110	C172	K233	E295	V419	V419	E482	K541	L602	P725	P725
K53	L111	L173	T234	L296	V420	V420	R483	A542	N603	N726	N726
D54	Y113	T174	T235	D297	M421	M421	L484	D543	E604	A727	A727
E55	T114	G176	R236	D298	S422	S422	Q485	D544	N605	I728	I728
I56	L793	E177	N237	M300	V423	V423	Q486	K545	V606	P729	P729
T57	L795	S116	N238	L301	G424	G424	F487	S546	V607	GLN	GLN
V58	G117	A180	S240	F363	A425	A425	F488	Q548	A608	GLY	GLY
K59	F119	G181	R242	K364	A427	A427	M489	D549	L610	PHE	PHE
I60	G120	K182	F243	Q365	K428	K428	H490	L551	S613	VAL	VAL
V61	L121	N185	G244	R366	S429	S429	M492	L552	K614	D734	D734
A62	D63	A122	K245	P367	L430	L430	F493	Q553	E615	K736	K736
D63	D63	L186	F246	K368	Y431	Y431	I494	N554	P616	V738	V738
S64	S64	K187	K247	L308	D432	D432	L495	H555	P679	S739	S739
S65	S65	K188	R248	Y309	R433	R433	E496	M556	P679	E740	E740
T66	T66	L189	L249	F311	M434	M434	Q497	N559	L681	K741	K741
R67	R67	I190	H250	L312	F435	F435	E498	M560	V682	I742	I742
T68	T68	M91	F251	N313	M436	M436	E499	M561	D683	L743	L743
V69	P130	Y192	G252	Q314	L438	L438	Y500	M562	A684	A744	A744
							K501	F562	E685	G745	G745

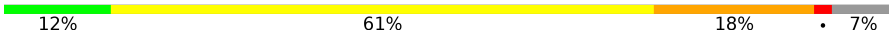
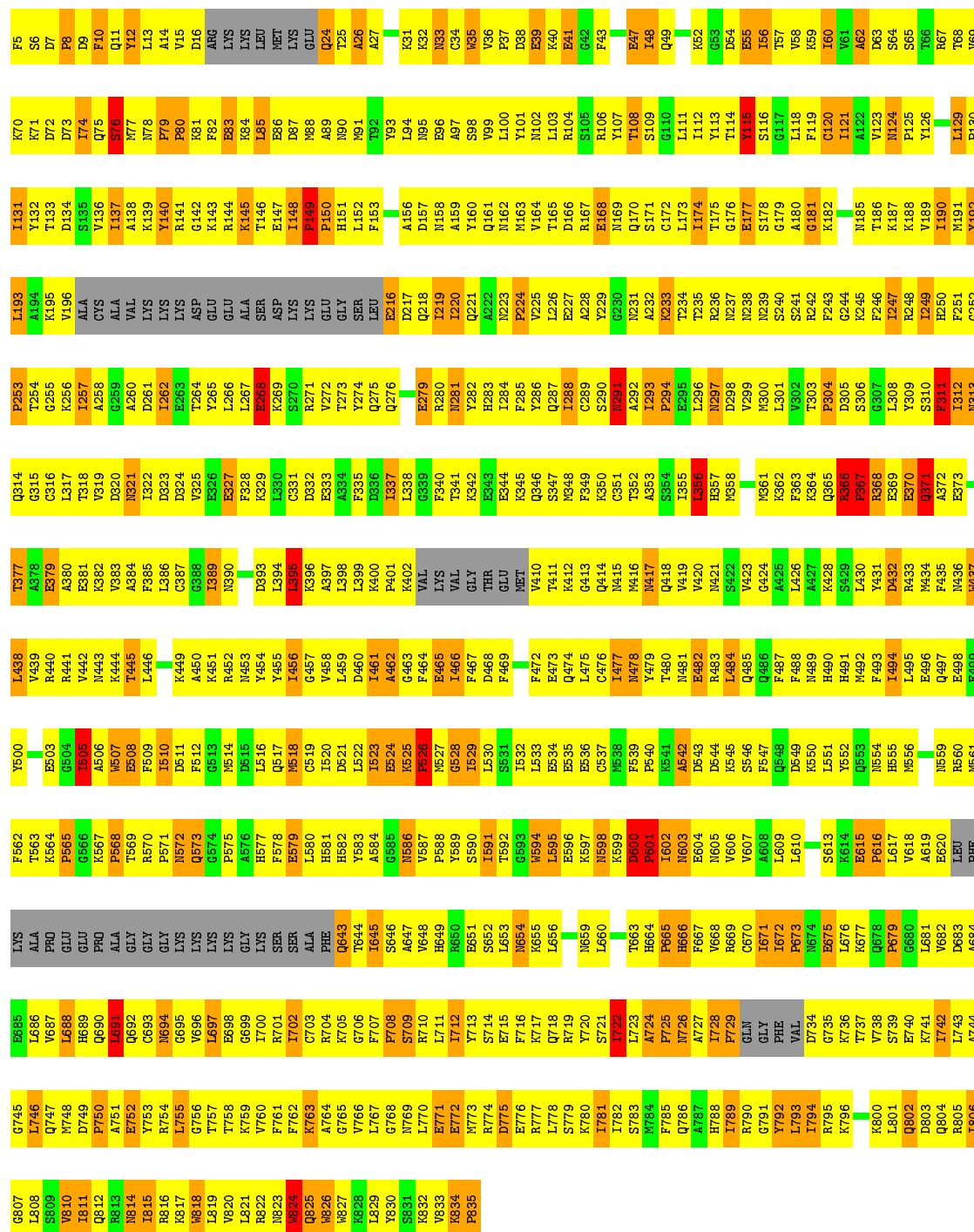


- Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

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



● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 21-C:  12% 61% 18% 7%

● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

Chain 22-C:  14% 59% 18% 7%

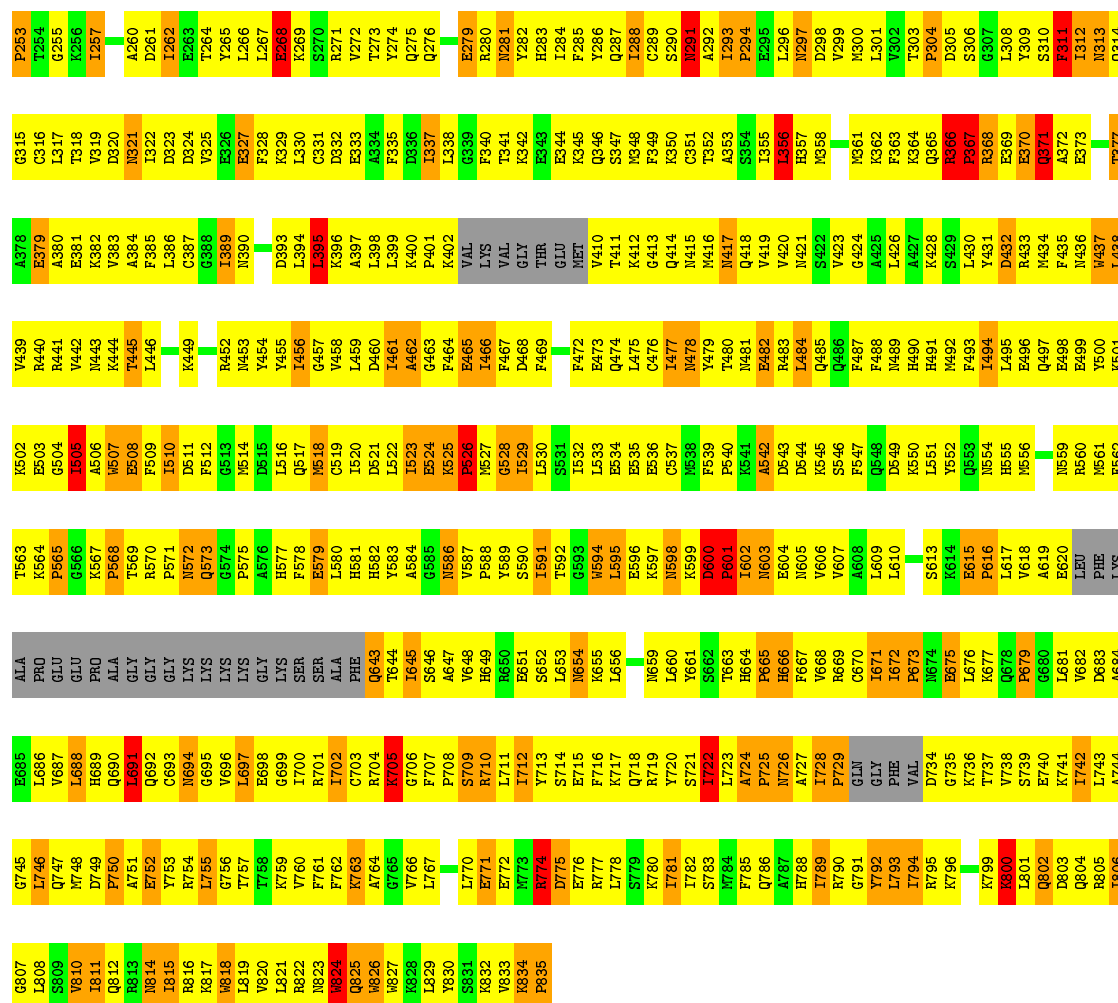
S809	L746	L686	ALA	T563	K502	V439	A378	G315	P253	L193	I131	K70	F5
V810	Q747	P687	PRO	K564	E503	R440	E379	C316	T254	A194	Y132	K71	S6
I811	M748	L688	GLU	P565	G504	R441	A380	L317	G255	K195	T133	D72	D7
Q812	D749	H689	GLU	G566	I505	V442	E381	T318	K256	V196	D134	D73	P8
K813	K750	P690	PRO	K567	A506	M443	K382	V219	I257	ALA	S135	I74	D9
N814	A751	L691	ALA	P568	M507	K444	V383	D320		CYS	V136	Q75	F10
L815	E752	Q692	GLY	T569	E508	T445	A384	N321	A260	VAL	I137	S76	Q11
R816	Y753	C693	GLY	R570	F509	L446	F385	I322	D261	ALA	A138	M77	Y12
K817	R754	H694	GLY	P571	I510	L449	L386	D324	L262	LYS	K139	N78	L13
L818	L755	G695	LYS	N572	D511	K449	C387	Q324	E263	LYS	Y140	P79	A14
L819	G756	V696	LYS	Q573	F512		G388	V325	T265	LYS	R141	P80	V15
R820	T757	L697	LYS	G574	G513	R452	I389	E326	Y264	ASP	G142	K81	D16
L821	V758	E698	LYS	P575	M514	M453	K390	E327	L266	GLU	K143	F82	ARG
R822	K759	G699	GLY	A576	L516	Y454	D393	F328	L267	GLU	R144	E83	LYS
N823	V760	I700	GLY	H577	D515	Y455	L394	K329	E268	ALA	K145	K84	LYS
K824	F761	R701	SER	F578	L517	L456	L394	L330	K269	SER	T146	L85	LEU
Q825	L762	I702	SER	E579	M518	G457	L395	C331	S270	ASP	E147	E86	MET
K826	K763	C703	ALA	L580	C519	V458	K396	D332	R271	LYS	I148	D87	LYS
N827	A764	R704	PHE	H581	I520	L459	A397	E333	V272	LYS	P149	M88	GLU
K828	G765	K705	Q643	H582	D521	D460	L398	A334	T273	GLU	P150	A89	Q24
L829	V766	G706	T644	L583	I522	L461	L399	F335	Y274	GLY	H151	N90	T25
V830	L767	F707	L645	A584	L523	A462	K400	D336	Q275	SER	L152	N91	A26
S831		P708	S646	G585	E524	G463	P401	I337	Q276	LEU	F153	T92	A27
K832	L770	S709	A647	N586	K525	F464	K402	L338		E216		Y93	
R833	E771	R710	V648	H587	P526	E465	VAL	G339	E279	D217	A156	L94	K31
K834	E772	L711	H649	P588	M527	L466	LYS	F340	R280	Q218	D157	N95	K32
P835	L773	I712	H650	L589	G528	F467	VAL	T341	N281	L219	N158	E96	N33
	R774	Y713	B651	S590	I529	D468	GLY	K342	T282	T220	A159	A97	G34
D775	L775	F714	S652	I591	L530	F469	THR	E343	H283	Q221	Y160	S98	K35
E776		E715	L653	T592	S531		GLU	E344	I284	K222	Q161	V99	V36
R777		K716	H654	G593	I532	F472	MET	K345	F285	N223	M162	L100	P37
L778		K717	L655	H594	L533	E473	V410	Q346	T286	P224	K163	Y101	D38
S779		Q718	L656	L595	E534	Q474	T411	S347	Q287	V225	T164	N102	E39
K780		R719		E596	E535	L475	K412	M348	L288	L226	T165	L103	K40
I781		Y720		K597	E536	C476	G413	F349	C289	E227	D166	R104	E41
L782		S721	L660	N598	C537	I477	Q414	K350	S290	A228	R167	S185	G42
S783		L722		K599	M538	M478	M415	C351	R291	Y229	E168	R106	F43
L784		R723	T663	P600	F539	K479	M416	T352	A292	G230	M169	Y107	
R785		A724	H664	L601	P540	T480	M417	A353	L293	K231	Q170	T108	E47
Q786		P725	P665	I602	K541	M481	Q418	S354	Q294	A232	S171	S109	I48
L787		N726	H666	N603	E542	E482	V419	L355	E295	K233	C172	G110	Q49
H788		A727	P667	E604	D543	R483	V420	L356	L296	T234	L173	L111	
I789		L728	V668	N605	D544	L484	M421	K357	N297	T235	I174	I112	K52
R790		P729	H669	V606	K545	Q485	S422	K358	D298	R236	T175	Y113	G53
G791		GLY	C670	V607	S546	Q486	V423	V299	V299	N237	G176	T114	D54
Y792		GLN	T671	A608	F547	F487	G424	K362	M300	N238	E177	Y115	E55
L793		PHE	L609	L610	O548	F488	A495	F363	L301	N239	S178	S116	I56
I794		VAL	P673		D549	M489	L426	K364	G302	S240	G179	G117	T57
R795		D734	H674	S613	D549	H490	A427	K364	T303	S241	A180	L118	V58
K796		G735	B675	K614	L551	H491	Q428	K366	P304	R242	F119	K359	
		K736	L676	L615	V552	M492	S429	K366	D305	F243	K182	C120	I60
		T737	K677	P616	O553	F493	L430	P367	S306	G244	I121	G120	
L800		V738	H678	L617	N554	L494	Y431	K368	G307	K245	N185	A122	A62
Q802		S739	P679	L618	H555	L495	D432	E369	L308	F246	T186	V123	D63
D803		E740	G680	V618	H556	E496	R433	E370	T309	I247	K187	N124	S64
Q804		K741	L681	A619	H599	Q497	F435	Q371	S310	R248	K188	P125	S65
R805		L742	V682	E620	N559	E498	F435	A372	F311	T249	L189	Y126	T66
L806		L743	D683	LEU	R560	E499	M436	E373	K132	K250	I190		R67
G807		A744	A684	PHE	M561	Y500	H437	A436	N131	T651	K191	L129	T68
L808		C745	H689	L581	P562	E504	L428	T377	Q344	C253	Y192	P130	V69

● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

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

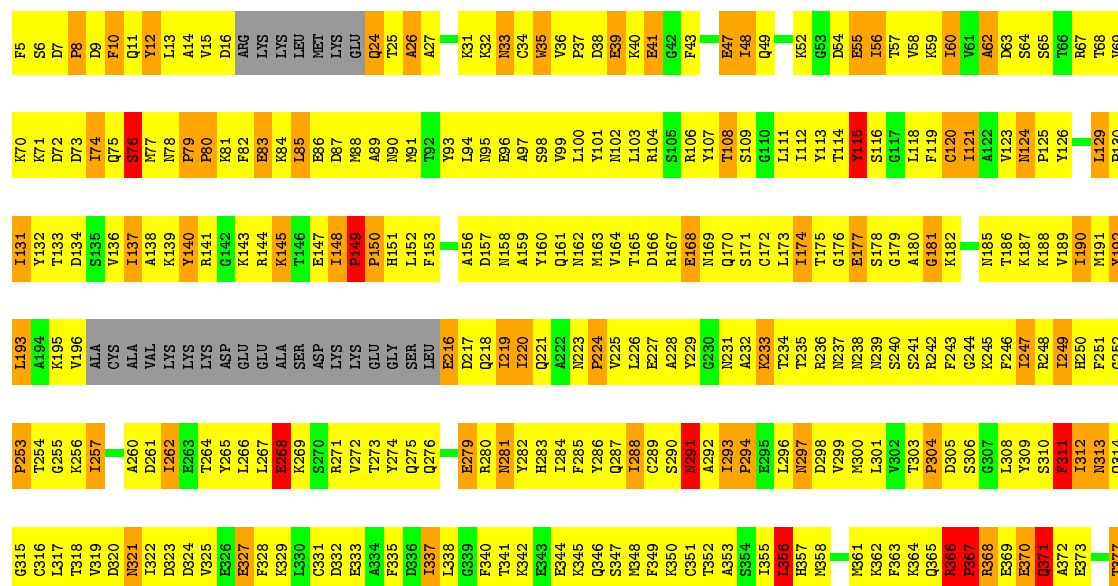
F5	S6	D7	P8	D9	F10	Q11	Y12	L13	A14	V15	D16	ARG	LYS	LYS	LEU	MET	LYS	GLU	Q24	T25	A26	A27	K31	K32	N33	C34	N35	V36	P37	D38	E39	K40	E41	S105	G42	F43	E47	T48	Q49	K52	G53	D54	E55	E56	T57	V58	K59	T60	V61	A62	D63	S64	S65	T66	R67	T68	P69			
K70	K71	D72	D73	I74	Q75	S76	M77	N78	P79	P80	K81	F82	E83	K84	L85	E86	D87	M88	A89	T90	M91	T92	Y93	L94	N95	E96	A97	S98	V99	L100	Y101	N102	L103	R104	S105	R106	Y107	T108	S109	G110	L111	I112	Y113	T114	E115	S116	G117	L118	V119	C120	I121	I122	A123	V124	P125	M126	Y127	L128	P129	V130

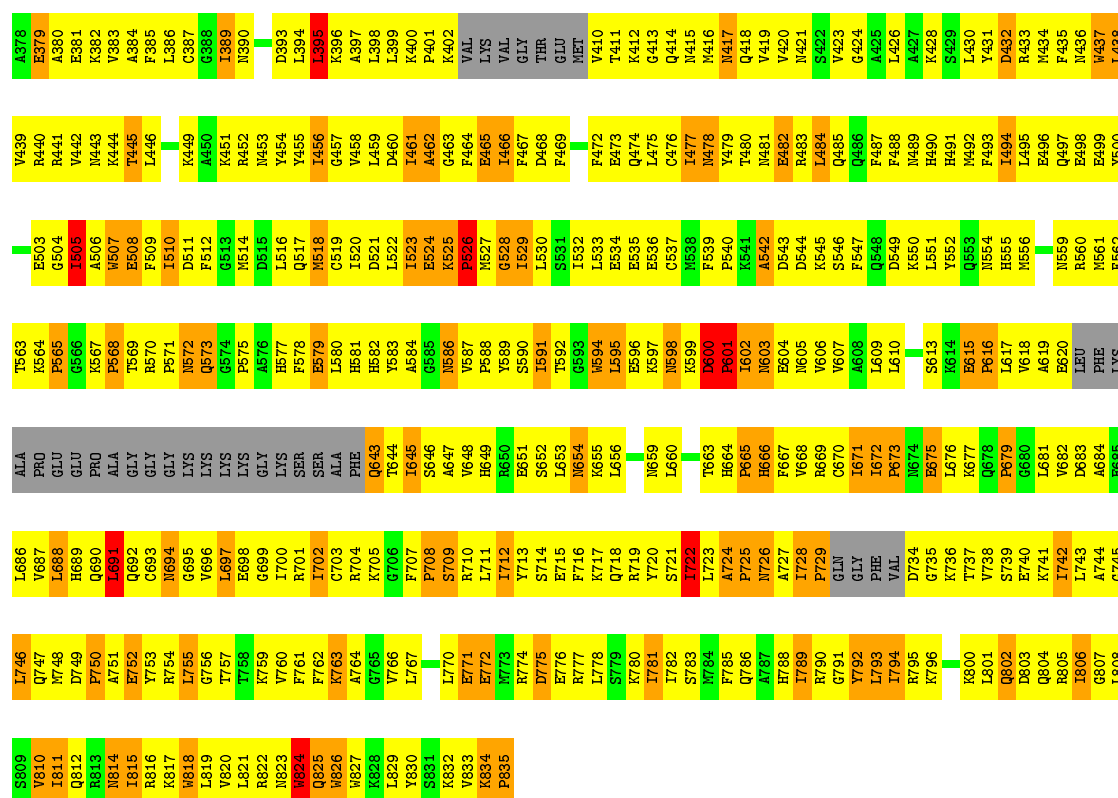
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● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

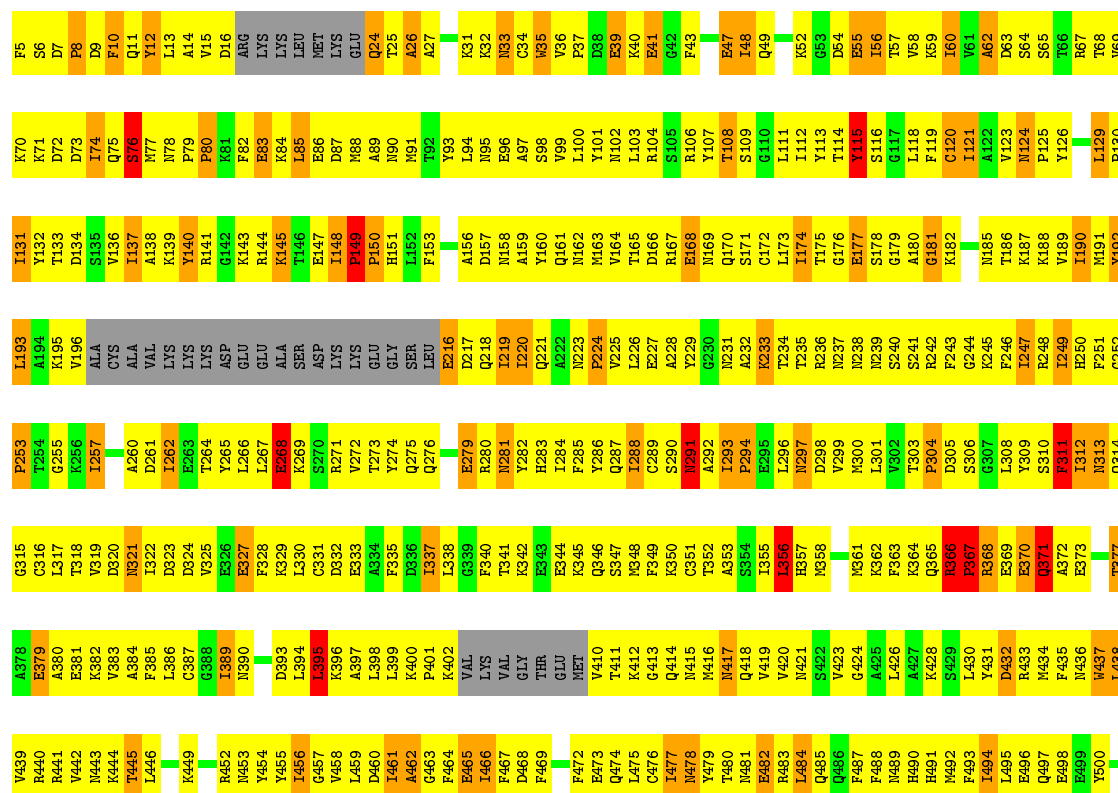
Chain 25-C: 13% 59% 18% 7%

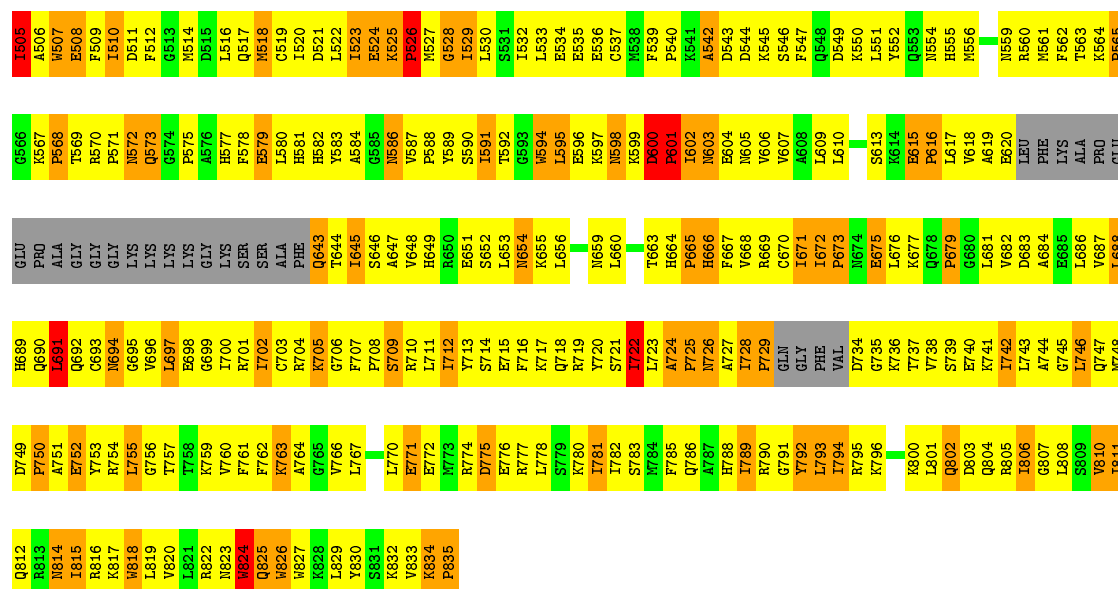




● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

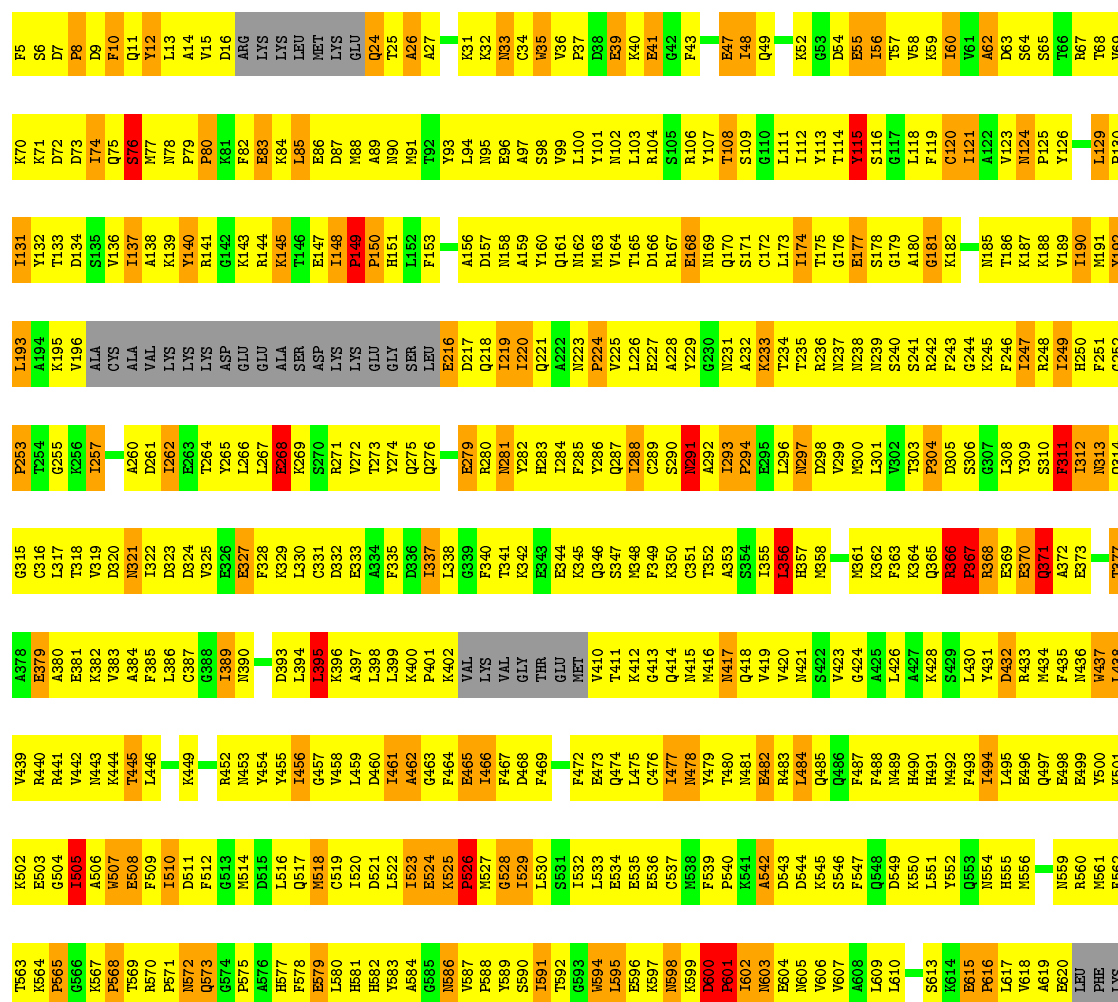
Chain 26-C: 14% 59% 18% 7%

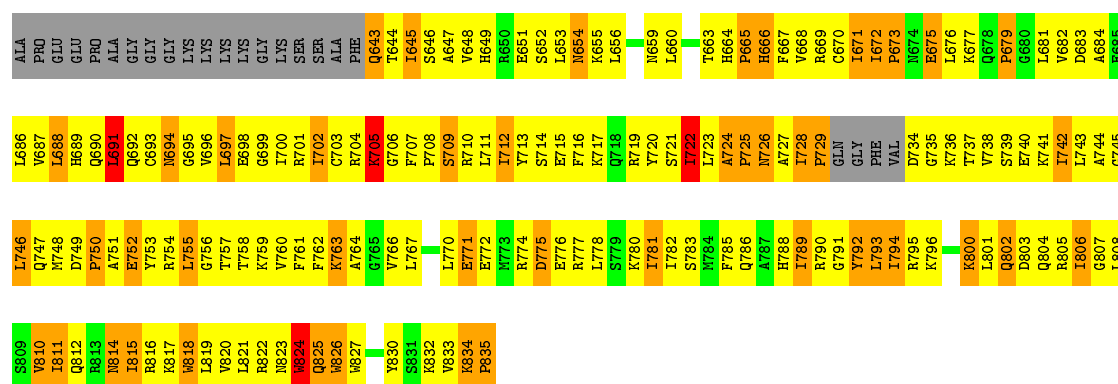




● Molecule 1: MYOSIN HEAVY CHAIN, STRIATED MUSCLE

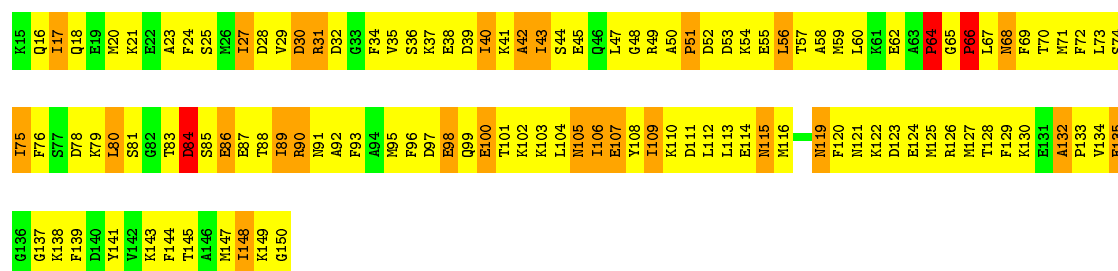
Chain 27-C: 13% 59% 18% 7%





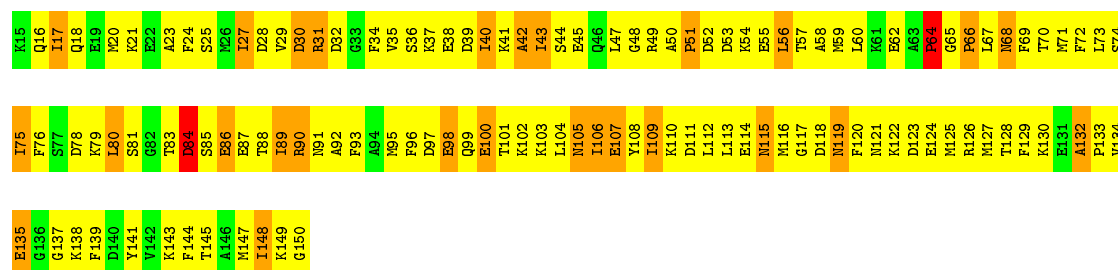
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 1-Y: 13% 65% 19%



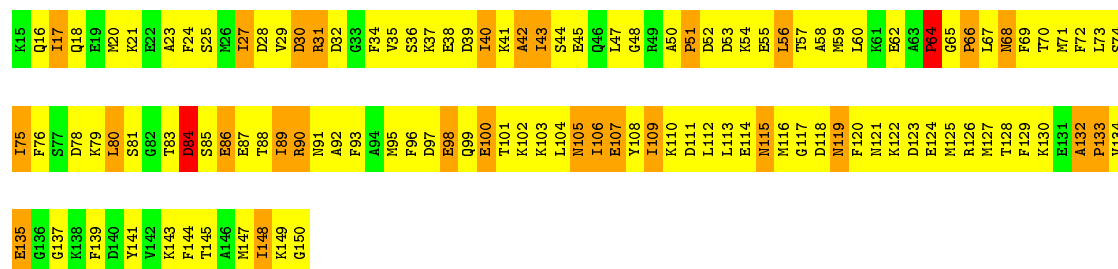
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 2-Y: 12% 67% 20%



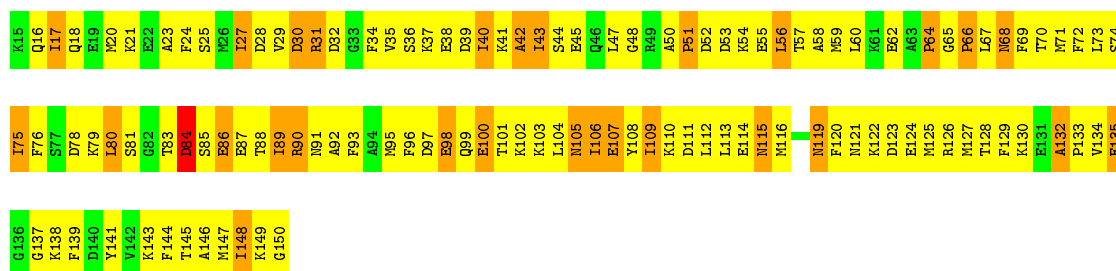
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 3-Y: 13% 65% 21%



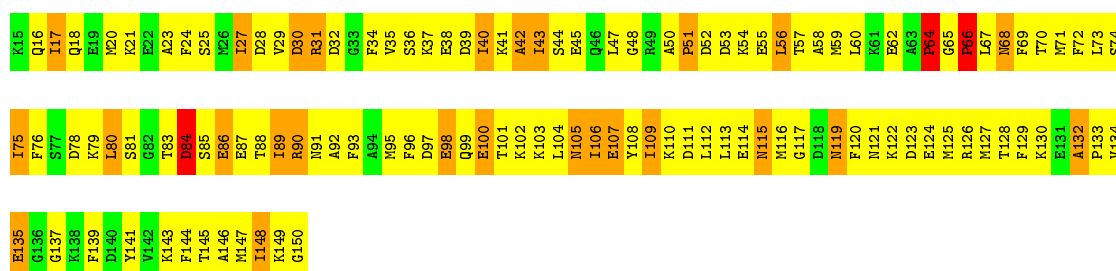
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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



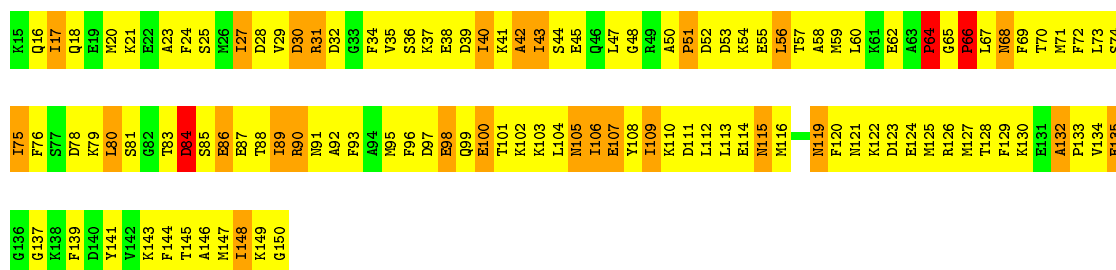
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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



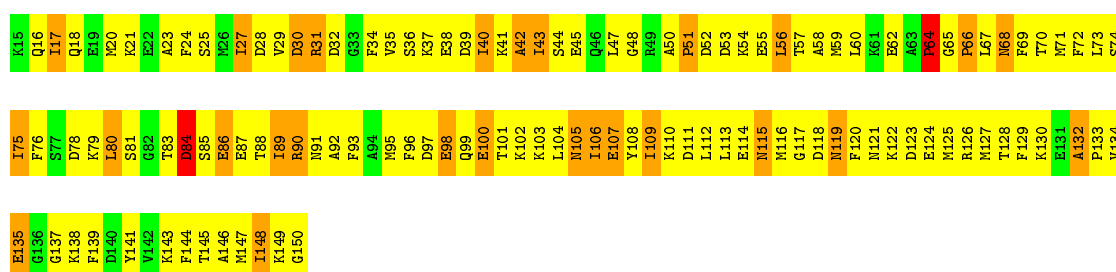
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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



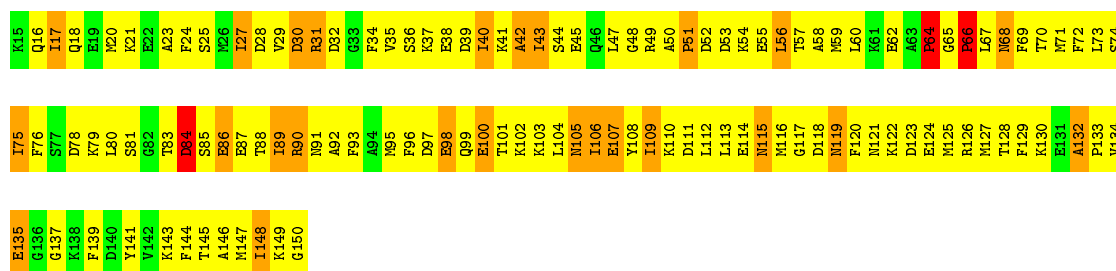
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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



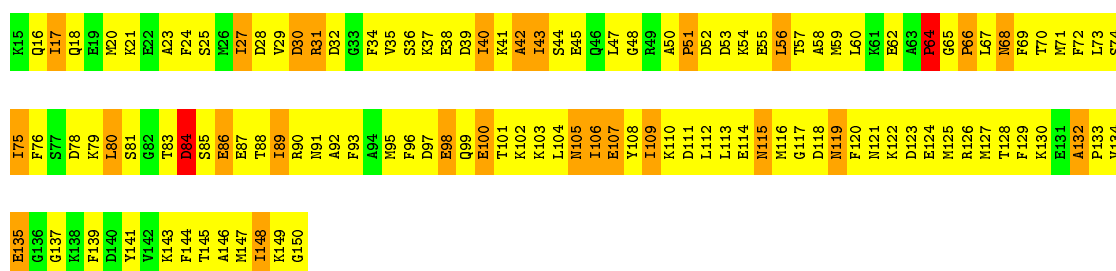
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 8-Y: 12% 68% 18%



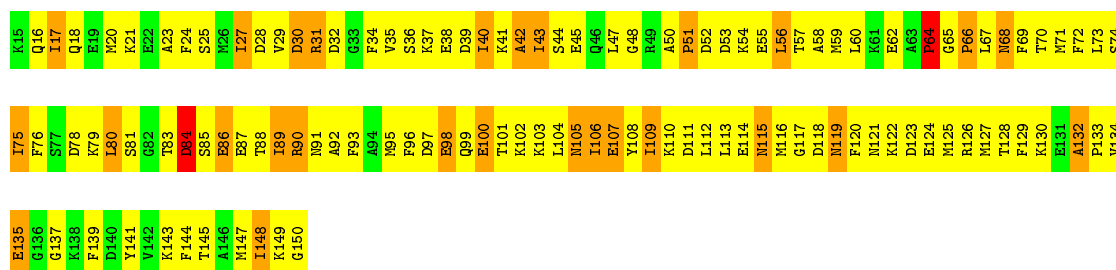
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 9-Y: 13% 67% 19%



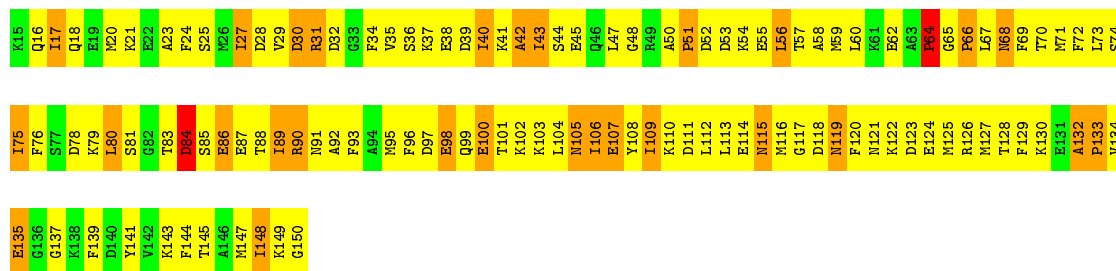
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 10-Y: 13% 65% 20%



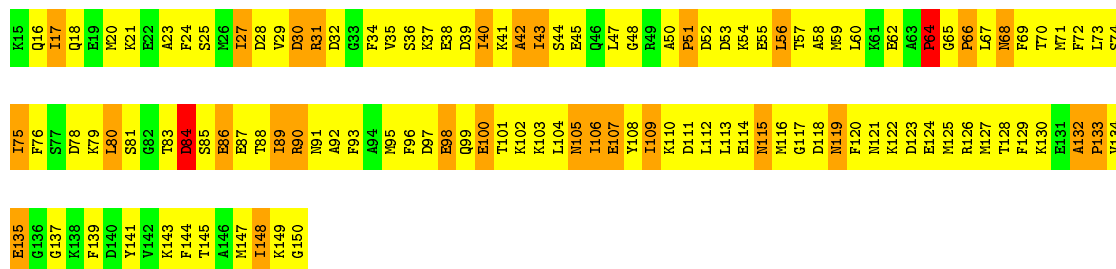
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 11-Y: 13% 65% 21%



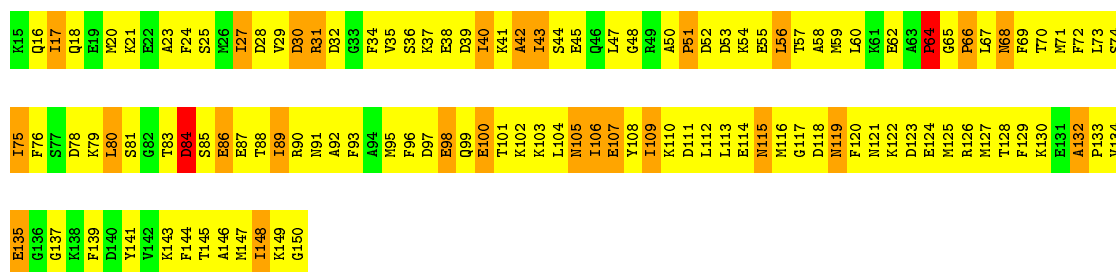
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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

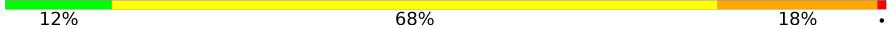


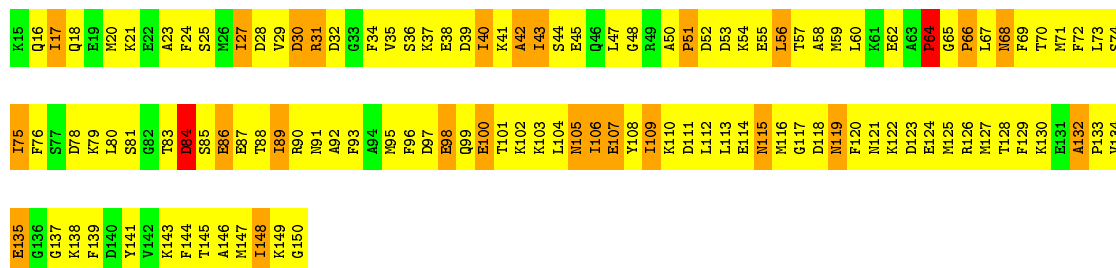
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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



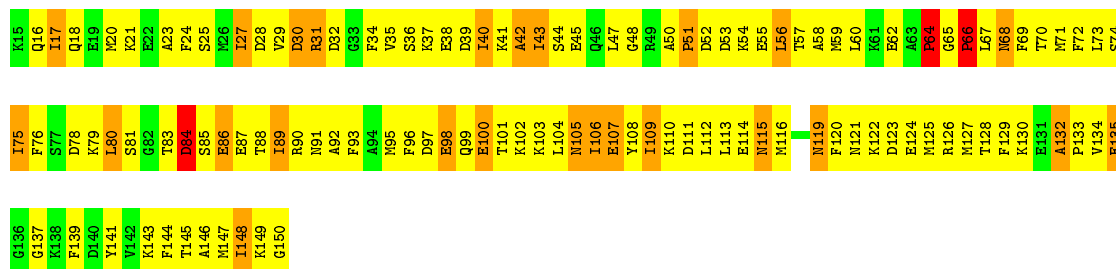
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

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

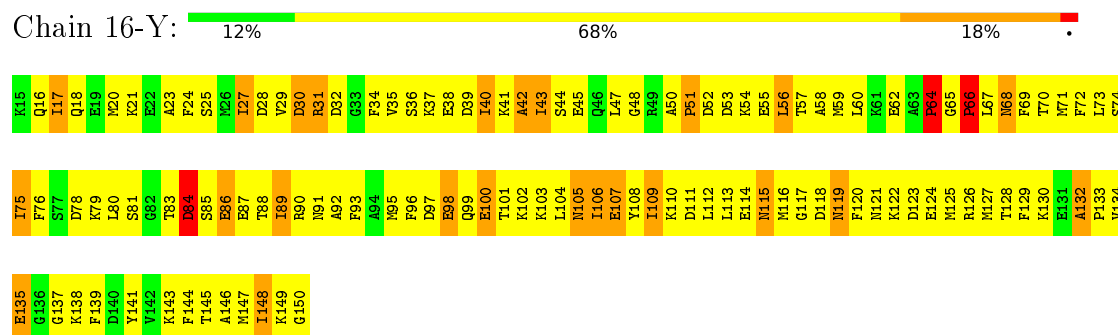


• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

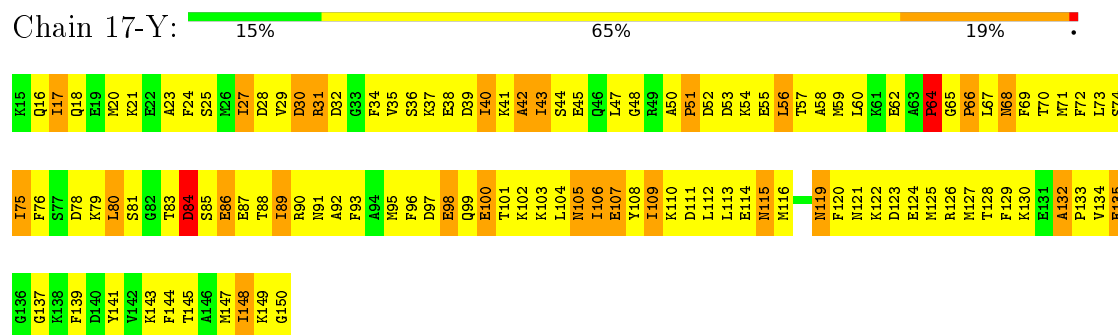
Chain 15-Y:  14% 65% 18% .



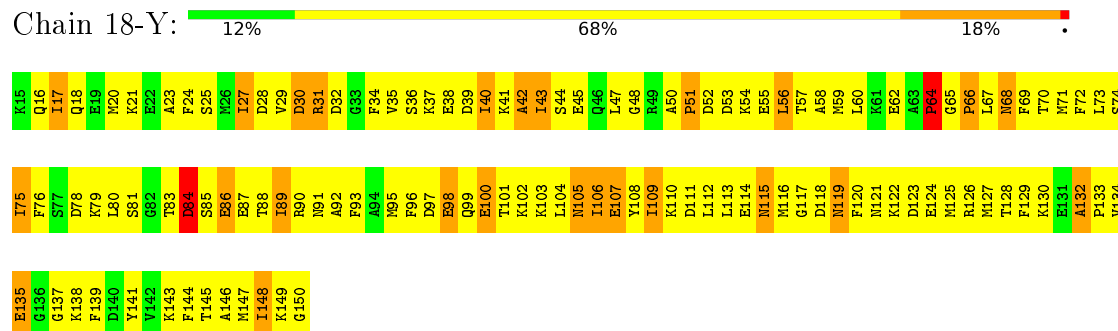
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



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



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

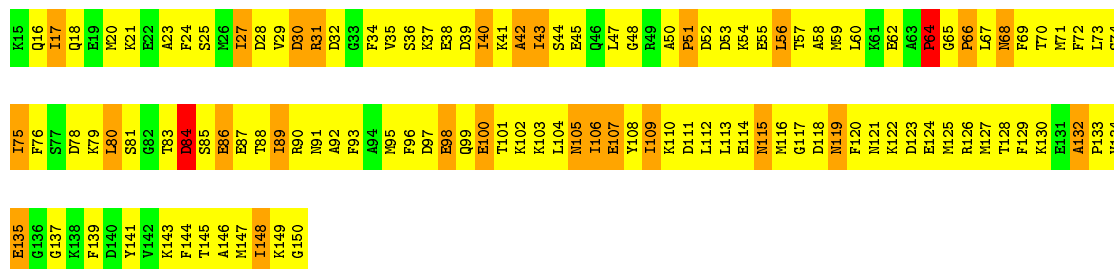


● Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



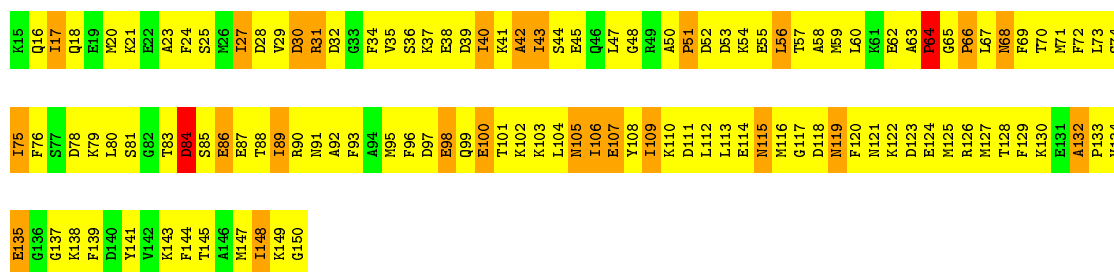
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 20-Y:  13% 67% 19%



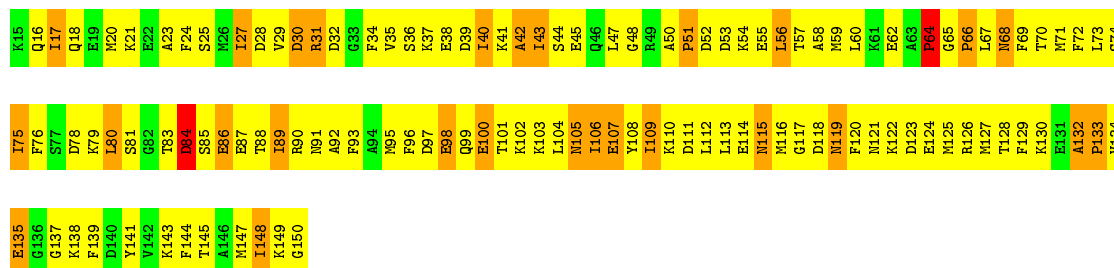
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 21-Y:  12% 68% 18%



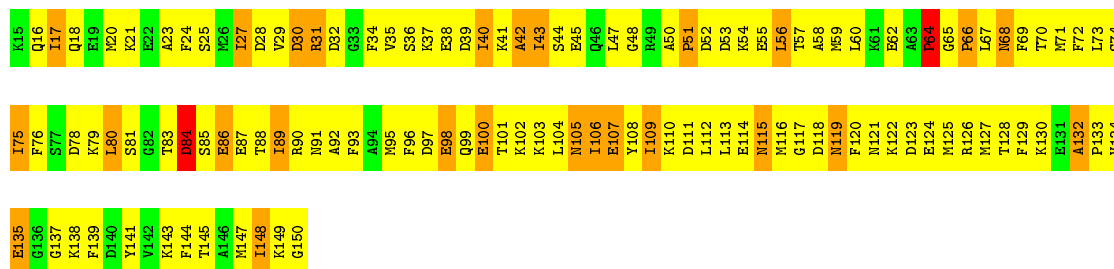
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

Chain 22-Y:  13% 66% 20%

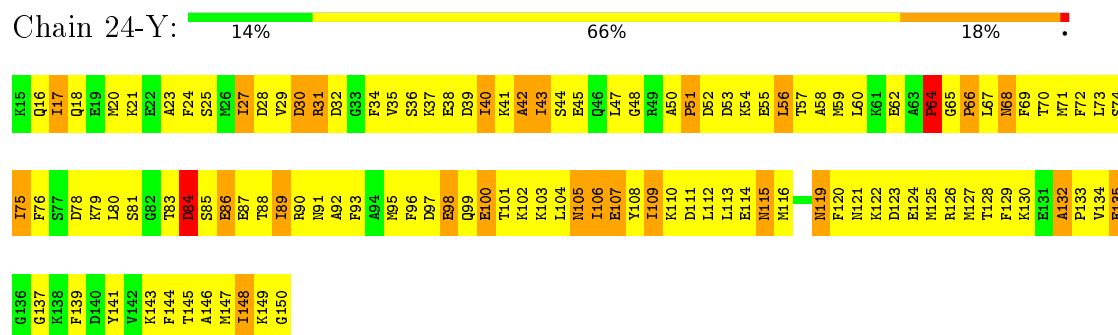


- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

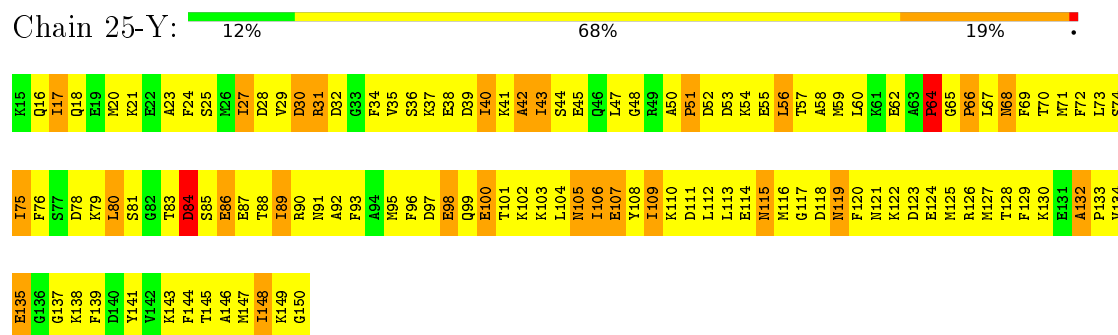
Chain 23-Y:  13% 67% 19%



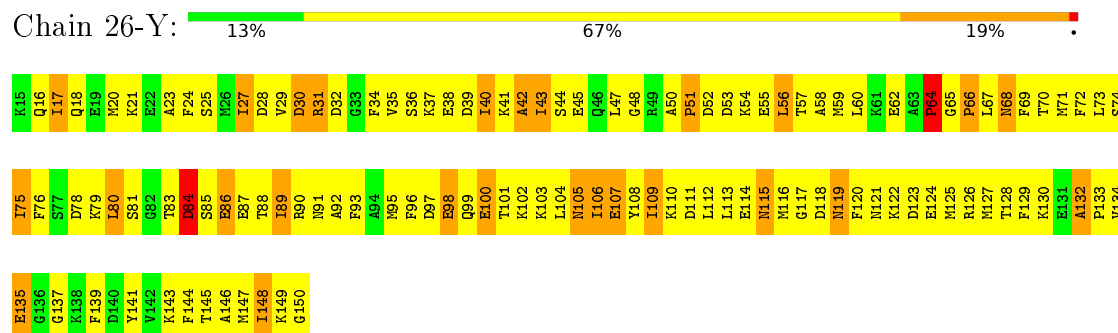
- Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



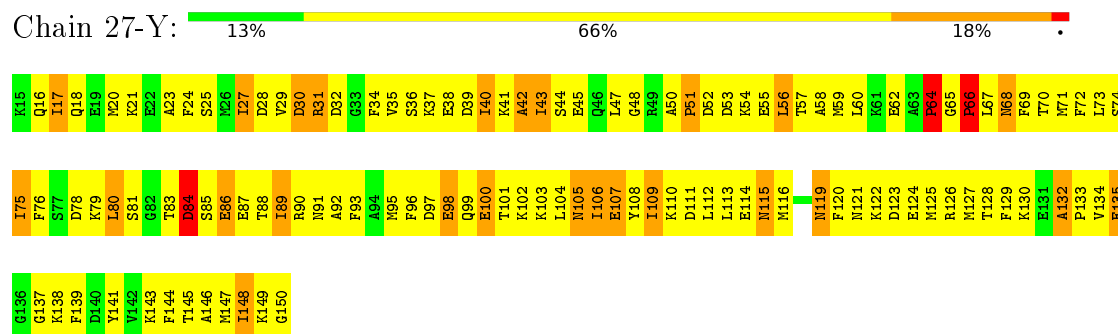
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



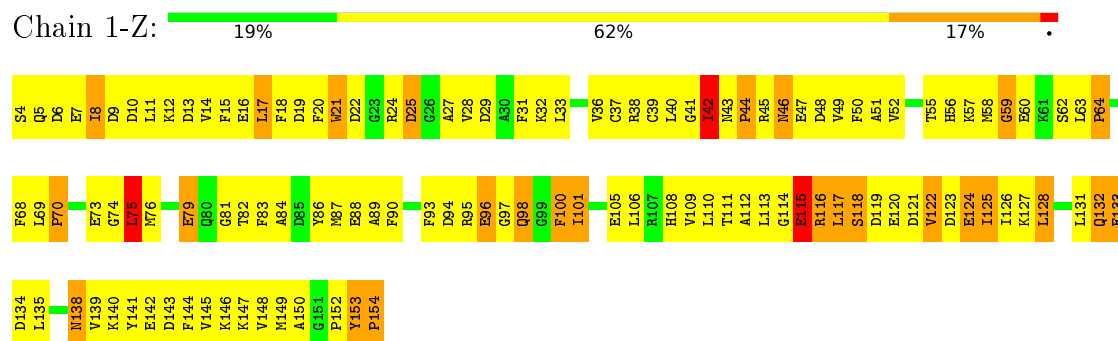
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



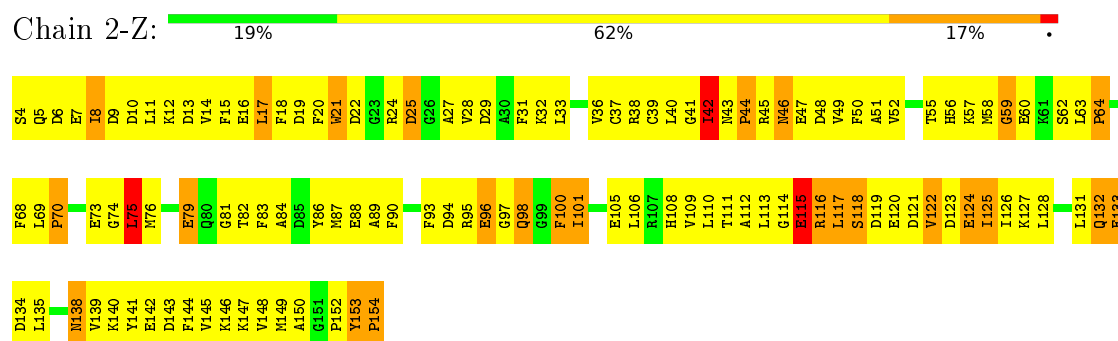
• Molecule 2: MYOSIN REGULATORY LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



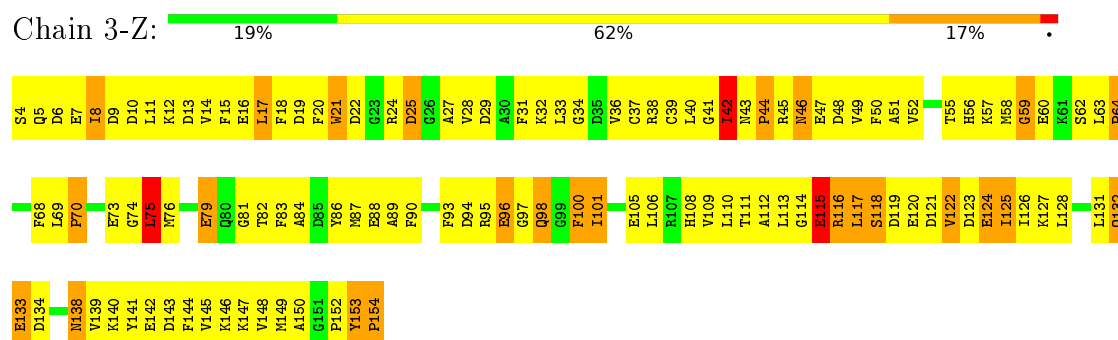
• Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



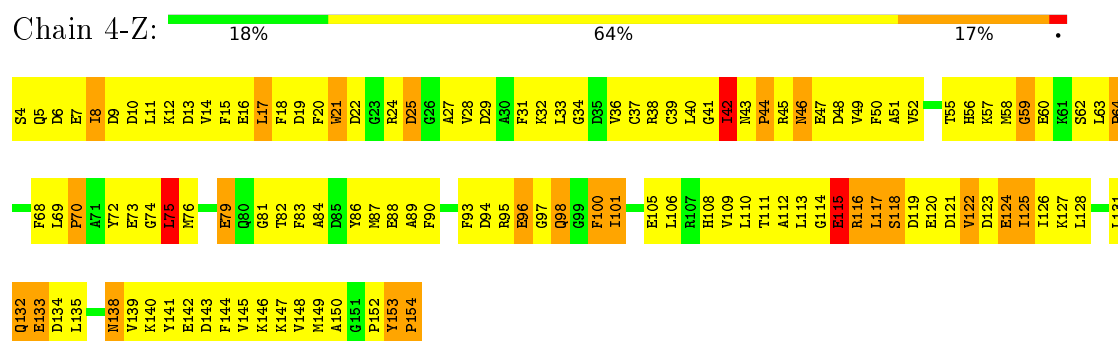
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



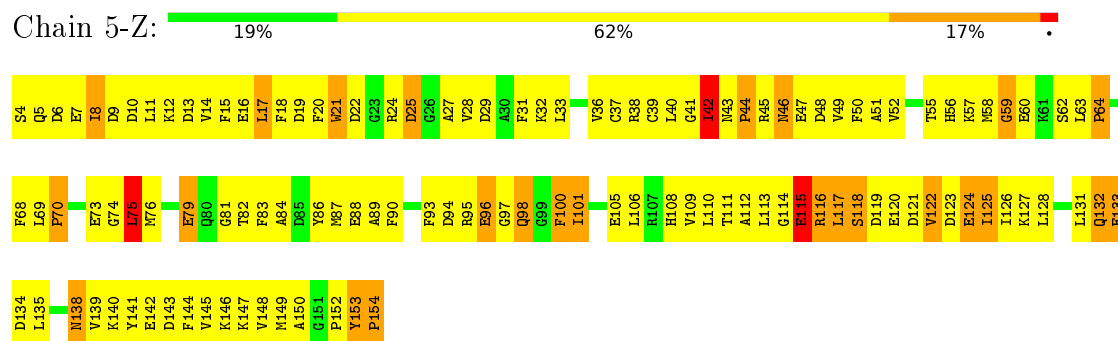
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



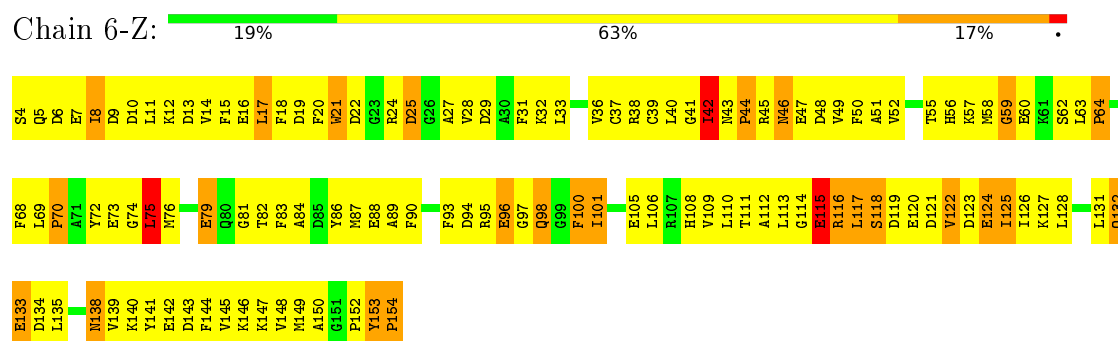
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



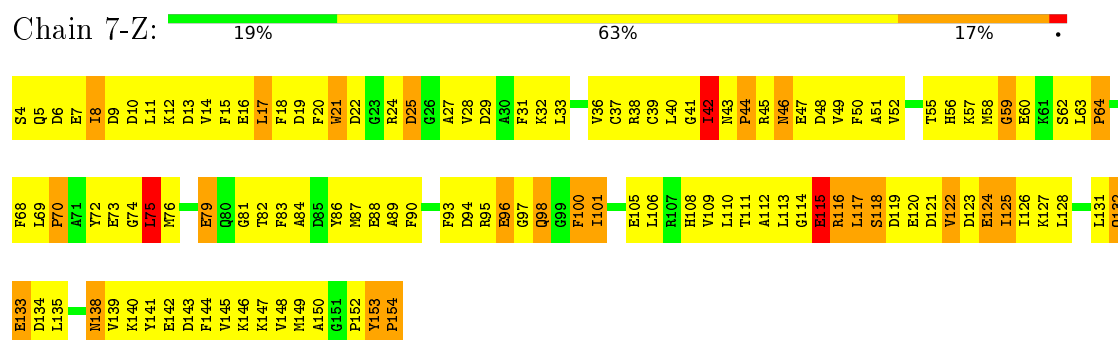
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



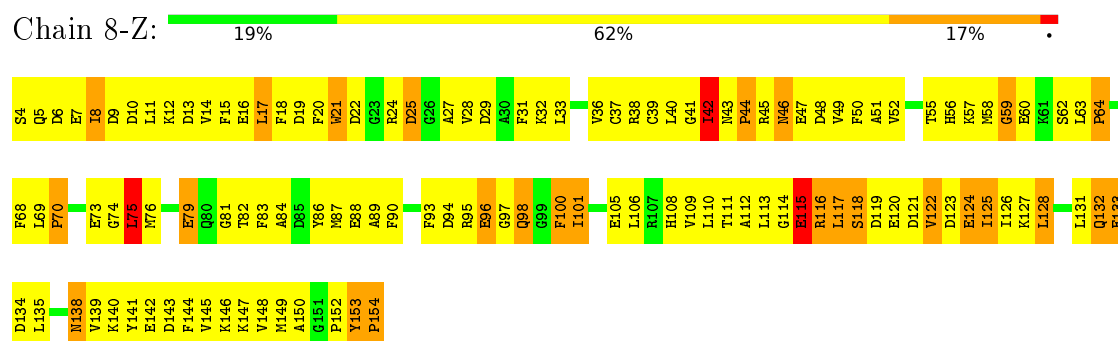
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



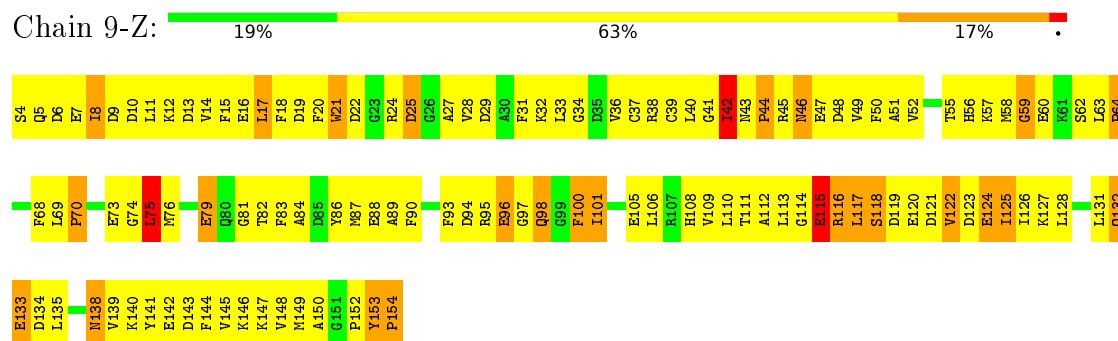
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



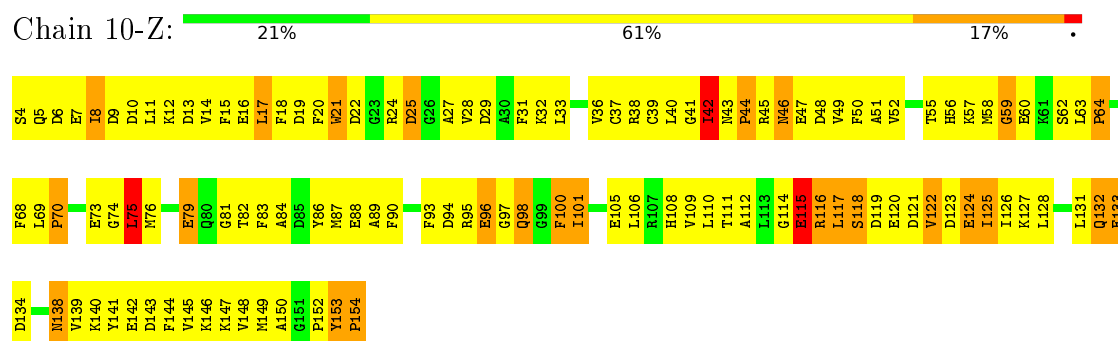
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



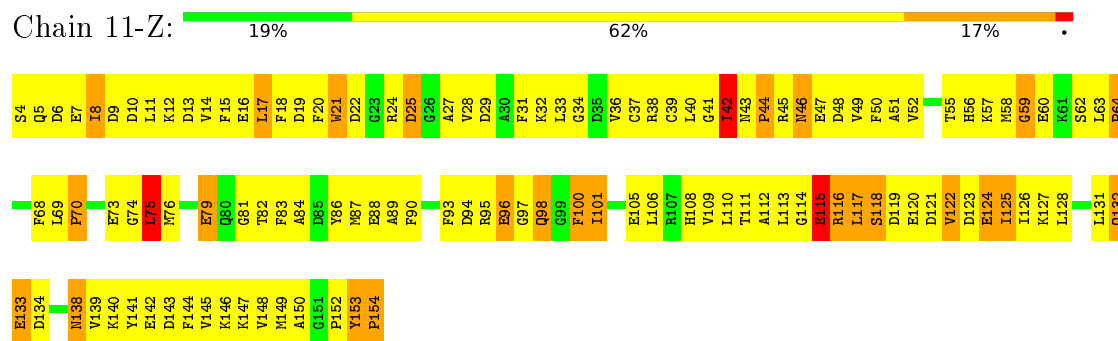
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



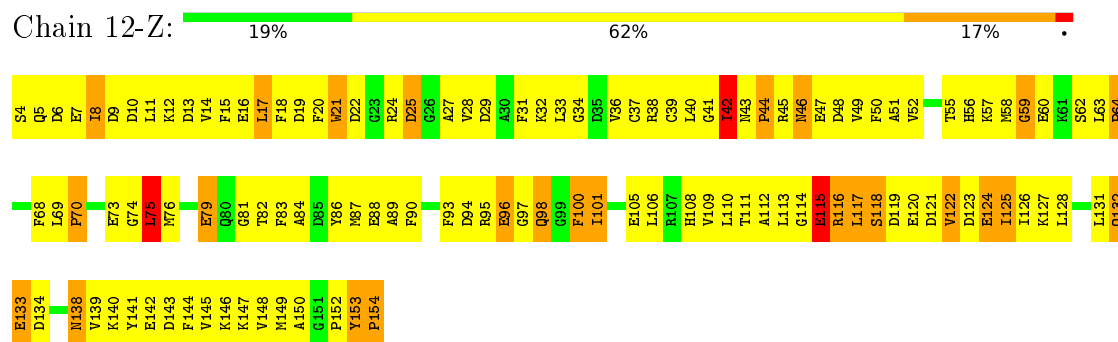
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



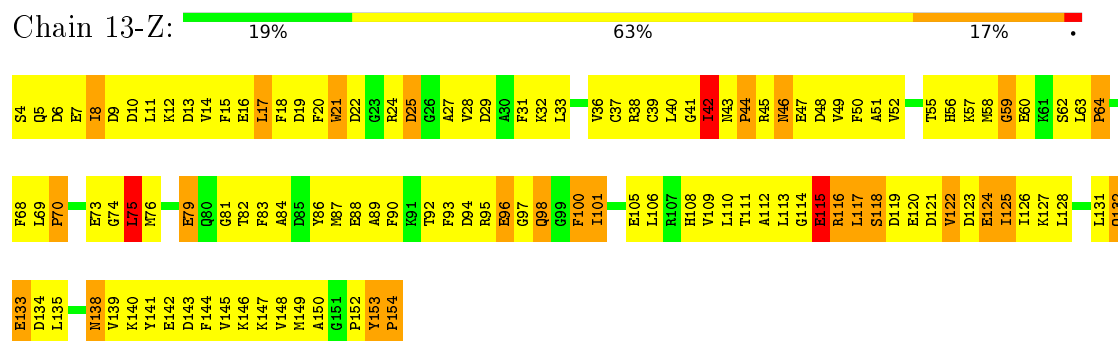
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



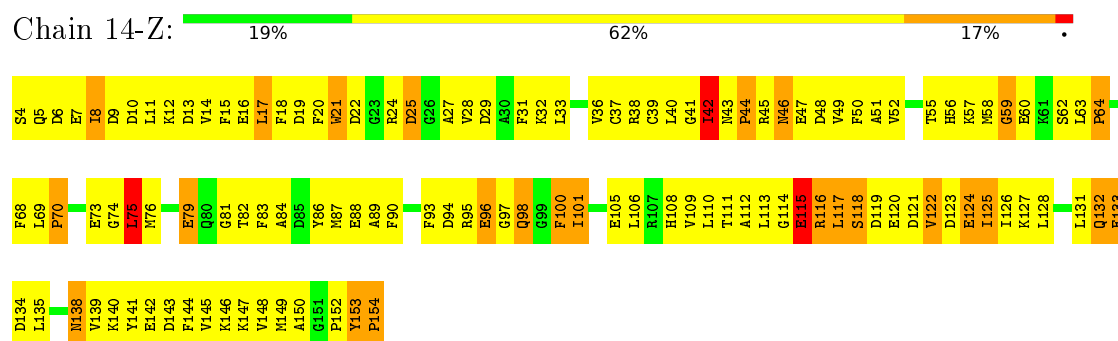
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



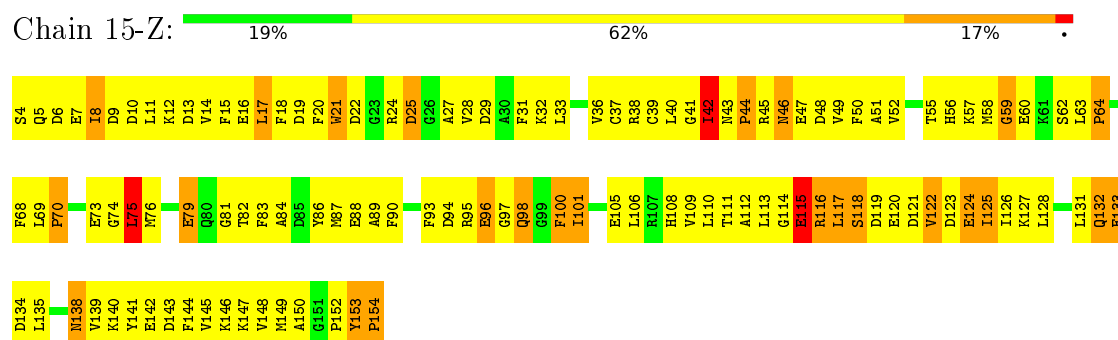
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



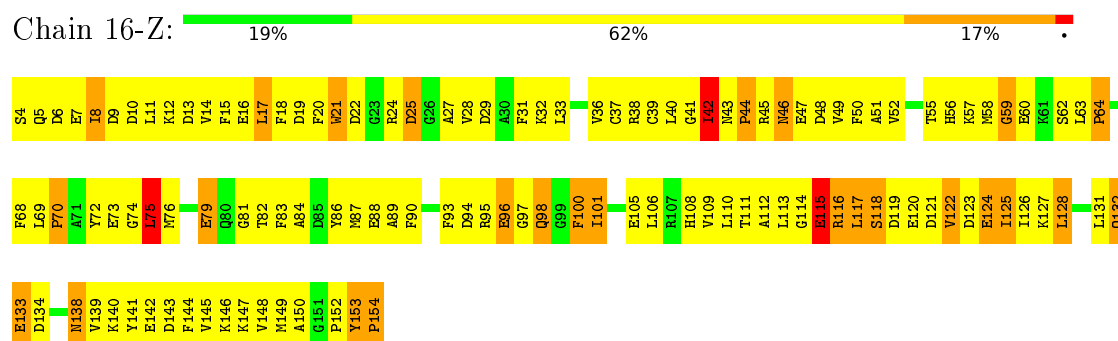
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



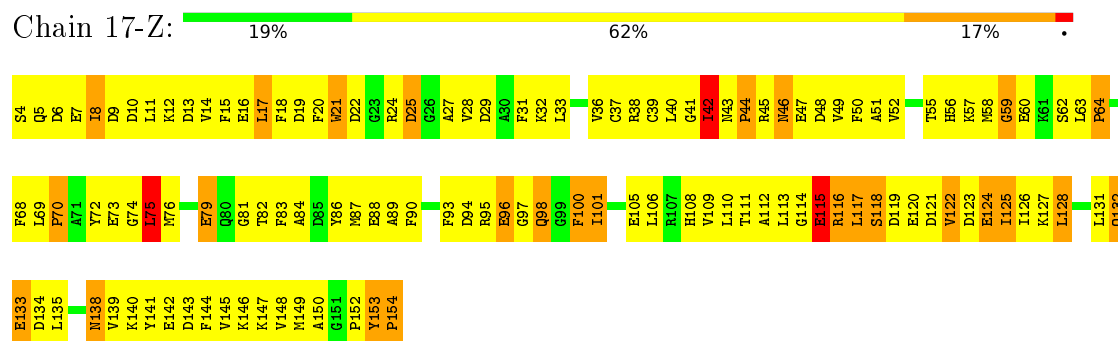
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

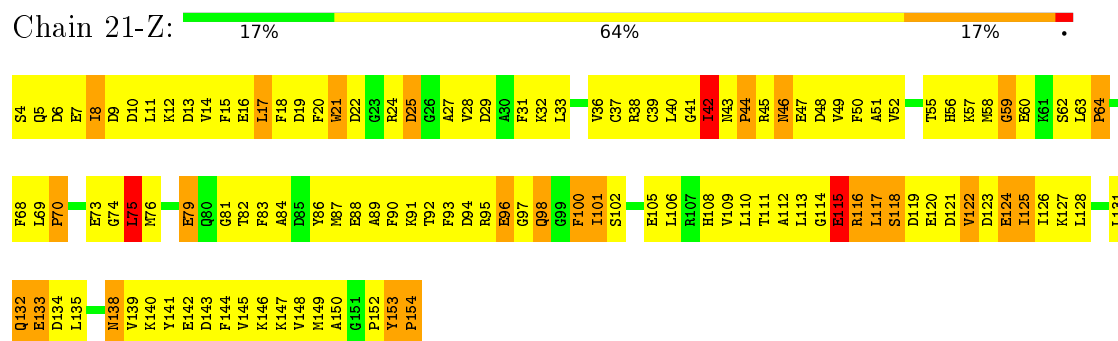


- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

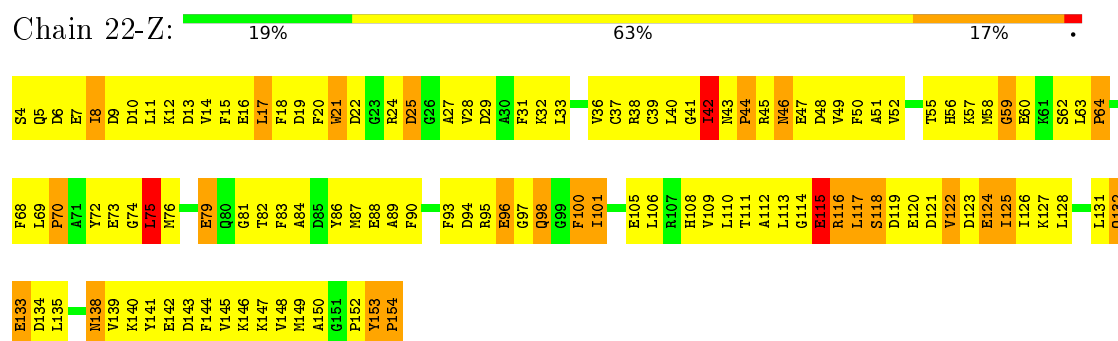


- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE

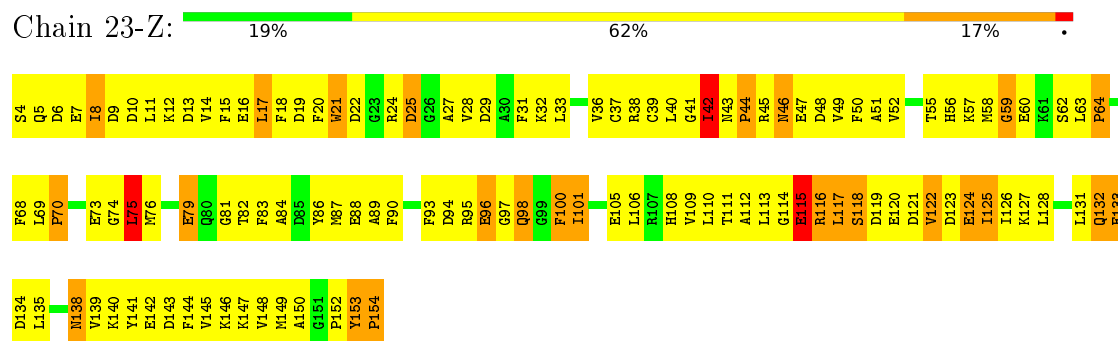




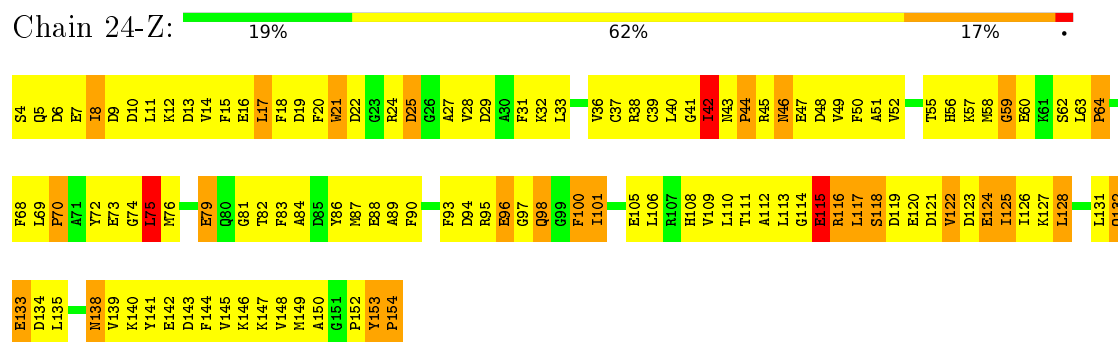
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



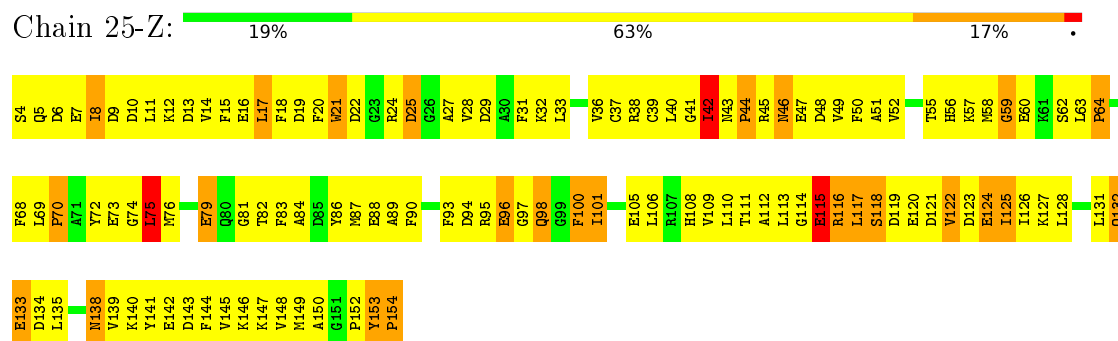
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



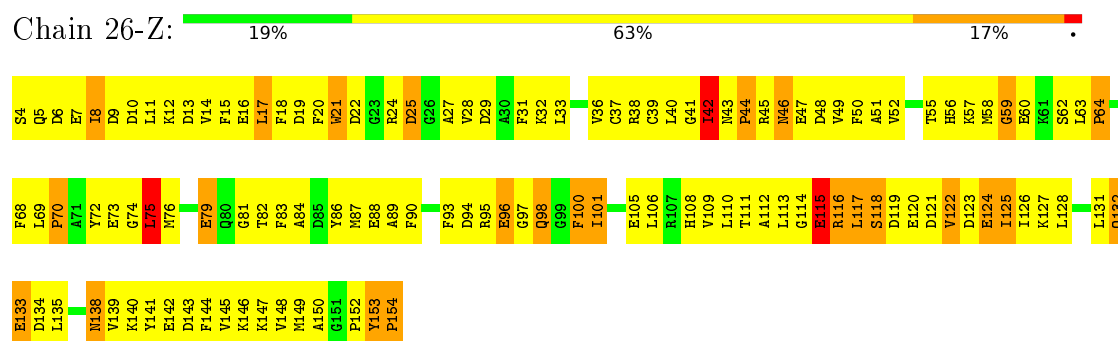
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



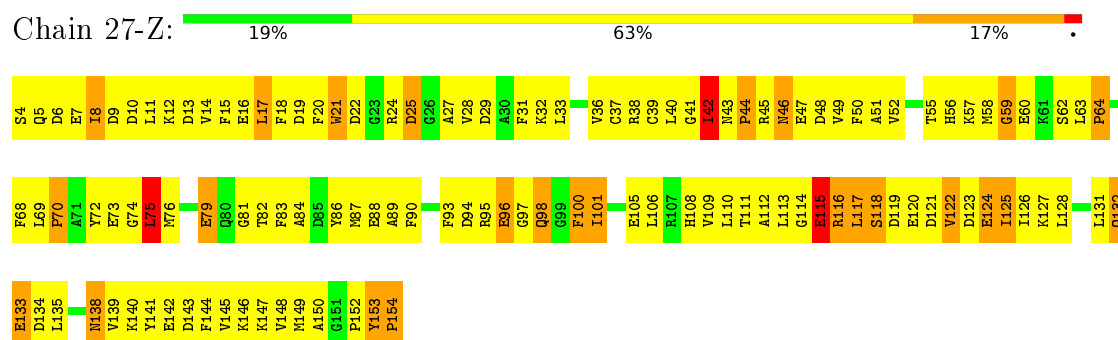
- Molecule 3: MYOSIN ESSENTIAL LIGHT CHAIN, STRIATED ADDUCTOR MUSCLE



- 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	30
1	2-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	3-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	3	31
1	4-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	2	30
1	5-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	30
1	6-C	754/831 (91%)	604 (80%)	112 (15%)	38 (5%)	3	31
1	7-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	30
1	8-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	9-C	758/831 (91%)	605 (80%)	115 (15%)	38 (5%)	3	31
1	10-C	758/831 (91%)	605 (80%)	114 (15%)	39 (5%)	2	30
1	11-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	3	31
1	12-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	3	31
1	13-C	758/831 (91%)	608 (80%)	112 (15%)	38 (5%)	3	31
1	14-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	15-C	758/831 (91%)	607 (80%)	112 (15%)	39 (5%)	2	30
1	16-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	17-C	756/831 (91%)	604 (80%)	113 (15%)	39 (5%)	2	30
1	18-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	19-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	20-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	30
1	21-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	22-C	758/831 (91%)	607 (80%)	113 (15%)	38 (5%)	3	31
1	23-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	3	31
1	24-C	758/831 (91%)	606 (80%)	113 (15%)	39 (5%)	2	30
1	25-C	758/831 (91%)	608 (80%)	112 (15%)	38 (5%)	3	31
1	26-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	3	31
1	27-C	758/831 (91%)	606 (80%)	114 (15%)	38 (5%)	3	31
2	1-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	33
2	2-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	33
2	3-Y	134/136 (98%)	95 (71%)	33 (25%)	6 (4%)	3	33

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	8-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	24
3	9-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	10-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	11-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	12-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	13-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	14-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	15-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	16-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	24
3	17-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	24
3	18-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	19-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	24
3	20-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	21-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	22-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	23-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	24-Z	149/151 (99%)	104 (70%)	35 (24%)	10 (7%)	1	24
3	25-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	26-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
3	27-Z	149/151 (99%)	104 (70%)	36 (24%)	9 (6%)	2	26
All	All	28097/30186 (93%)	21738 (77%)	4913 (18%)	1446 (5%)	5	30

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	4-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	5-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	6-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	7-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	8-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	9-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	10-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	11-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	12-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	13-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	14-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	15-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	16-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	17-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	18-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	19-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	20-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	21-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	22-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	23-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	24-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	25-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	26-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
2	27-Y	119/119 (100%)	100 (84%)	19 (16%)	3	21
3	1-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	2-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	3-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	4-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	5-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	6-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	7-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	8-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	9-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	10-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	11-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	12-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	13-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	14-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	15-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	16-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	17-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	18-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	19-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	20-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	21-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	22-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	23-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	24-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	25-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	26-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
3	27-Z	127/127 (100%)	111 (87%)	16 (13%)	5	29
All	All	24948/26190 (95%)	21114 (85%)	3834 (15%)	7	22

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