



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 01:38 AM UTC

PDB ID : 2W4H / pdb_00002w4h
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 : 2008-11-25
Resolution : 35.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

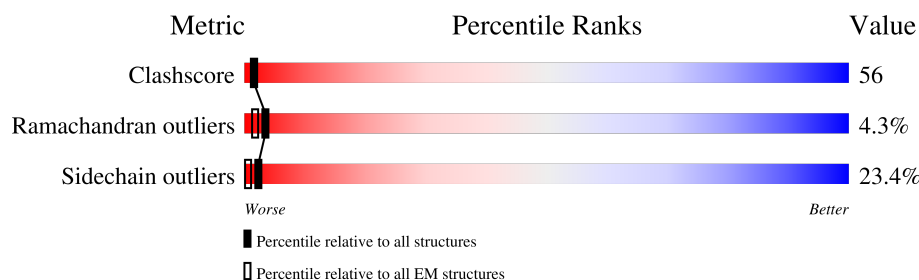
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 35.00 Å.

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



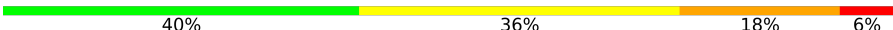
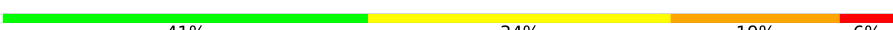
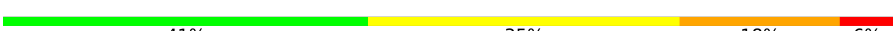
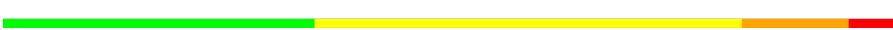
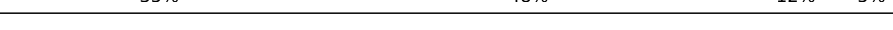
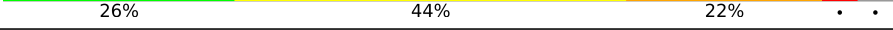
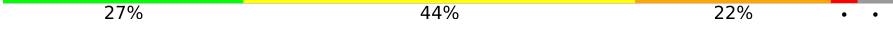
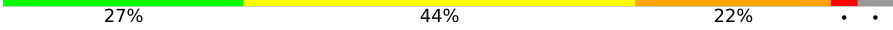
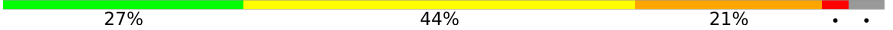
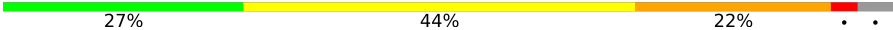
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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

Mol	Chain	Length	Quality of chain
1	1-B	150	41% 35% 17% 6%
1	10-B	150	41% 36% 17% 6%
1	11-B	150	41% 35% 18% 6%
1	12-B	150	41% 34% 19% 6%
1	13-B	150	41% 36% 17% 6%
1	14-B	150	41% 35% 18% 6%
1	2-B	150	41% 35% 18% 6%
1	3-B	150	41% 36% 17% 6%
1	4-B	150	41% 35% 17% 6%

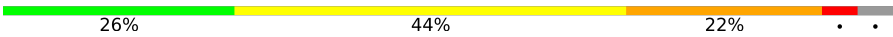
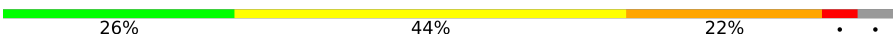
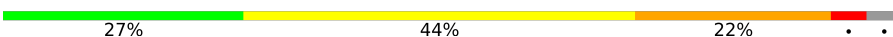
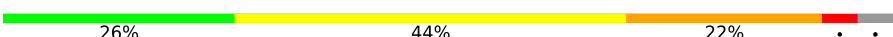
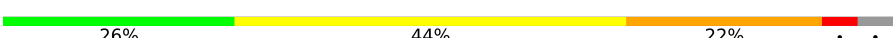
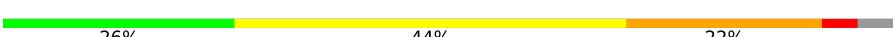
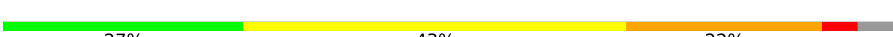
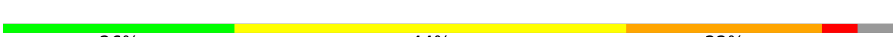
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Mol	Chain	Length	Quality of chain
1	5-B	150	 40%36%18%6%
1	6-B	150	 41%36%17%6%
1	7-B	150	 41%34%19%6%
1	8-B	150	 41%34%19%6%
1	9-B	150	 41%35%18%6%
2	1-C	145	 35%48%12%5%
2	10-C	145	 35%48%12%5%
2	11-C	145	 35%48%12%5%
2	12-C	145	 35%48%12%5%
2	13-C	145	 35%48%12%5%
2	14-C	145	 35%48%12%5%
2	2-C	145	 35%48%12%5%
2	3-C	145	 35%48%12%5%
2	4-C	145	 35%48%12%5%
2	5-C	145	 35%48%12%5%
2	6-C	145	 35%48%12%5%
2	7-C	145	 35%48%12%5%
2	8-C	145	 35%47%13%5%
2	9-C	145	 35%48%12%5%
3	1-M	840	 26%44%22%. .
3	10-M	840	 27%44%22%. .
3	11-M	840	 27%44%22%. .
3	12-M	840	 27%44%21%. .
3	13-M	840	 27%44%22%. .
3	14-M	840	 27%44%21%. .

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Mol	Chain	Length	Quality of chain
3	2-M	840	 26% 44% 22% . .
3	3-M	840	 26% 44% 22% . .
3	4-M	840	 27% 44% 22% . .
3	5-M	840	 26% 44% 22% . .
3	6-M	840	 26% 44% 22% . .
3	7-M	840	 26% 44% 22% . .
3	8-M	840	 27% 43% 22% . .
3	9-M	840	 26% 44% 22% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 122612 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 REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	2-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	3-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	4-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	5-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	6-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	7-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	8-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	9-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	10-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	11-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	12-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	13-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	14-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	26	ASP	GLU	conflict	UNP P02609

- Molecule 2 is a protein called MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	2-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	3-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	4-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	5-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	6-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	7-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	8-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	9-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	10-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	11-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	12-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	13-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	14-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		

- Molecule 3 is a protein called MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	2-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	3-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	4-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	5-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	6-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	7-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	8-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	9-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	10-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	11-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	12-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	13-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	14-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0

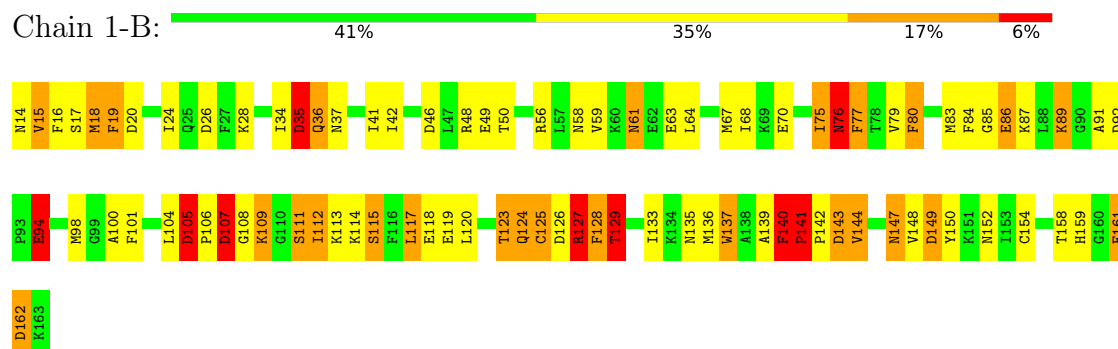
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	138	LYS	GLU	conflict	UNP P02609

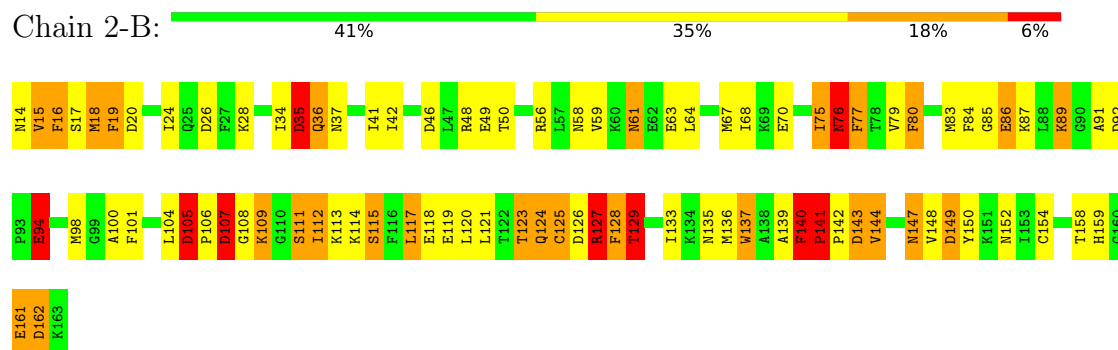
3 Residue-property plots [i](#)

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

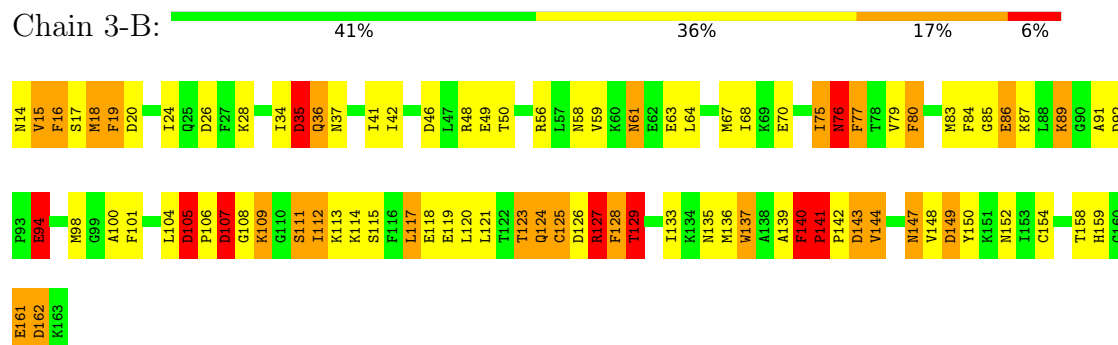
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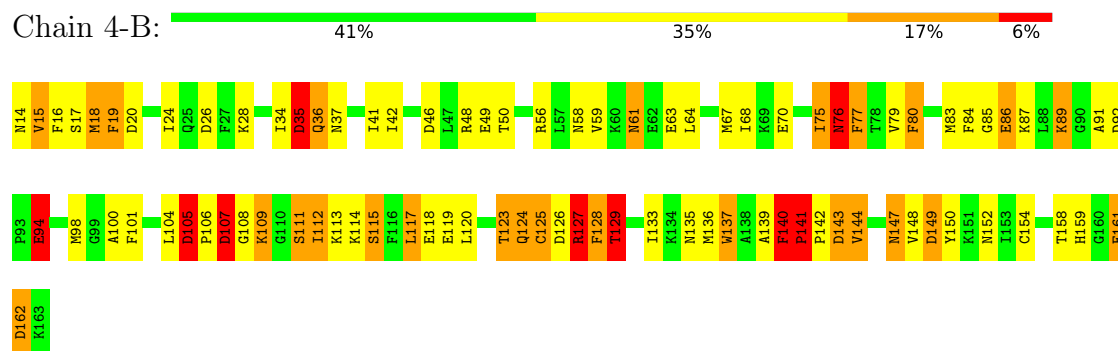
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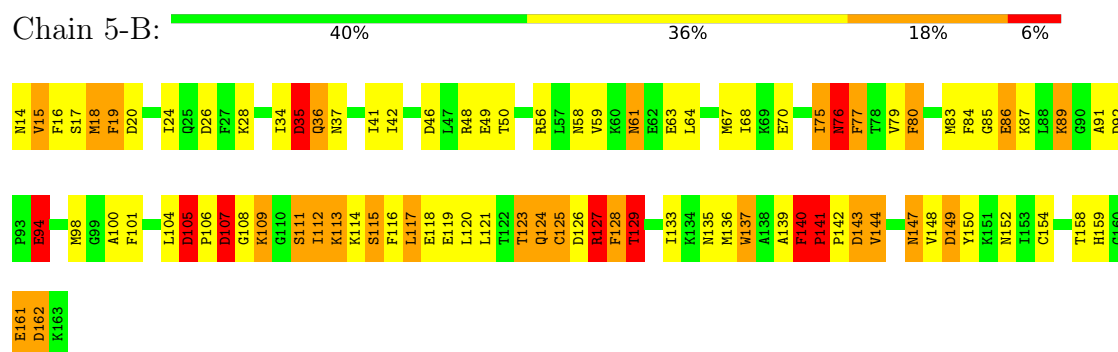
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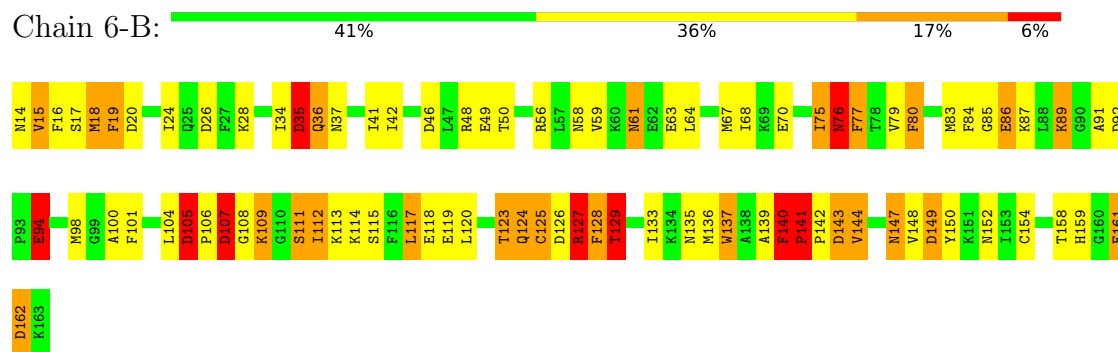
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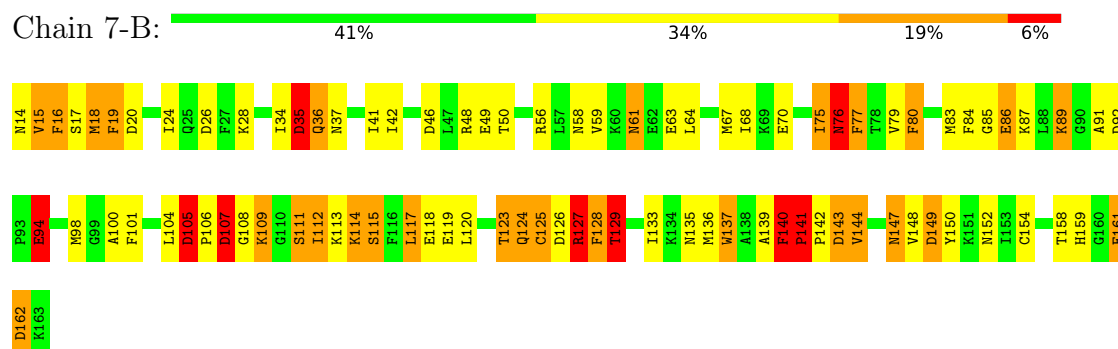
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



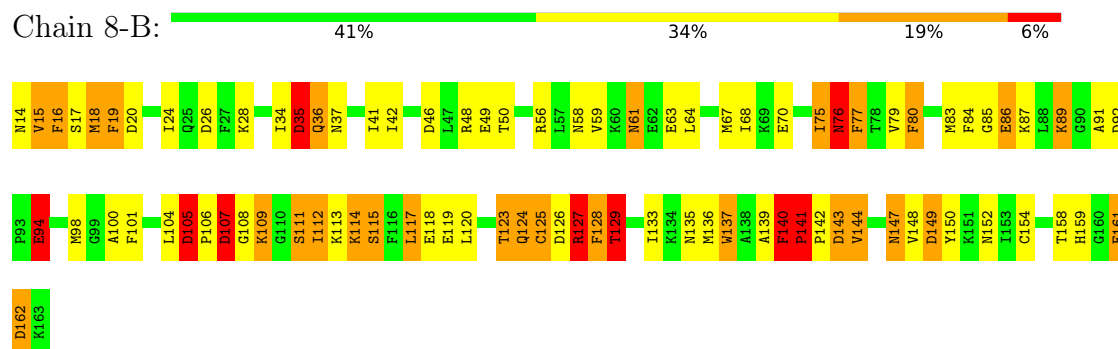
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



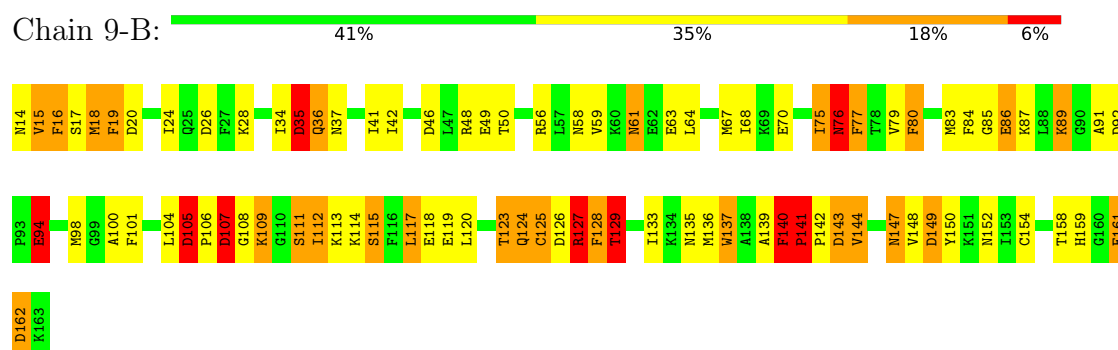
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



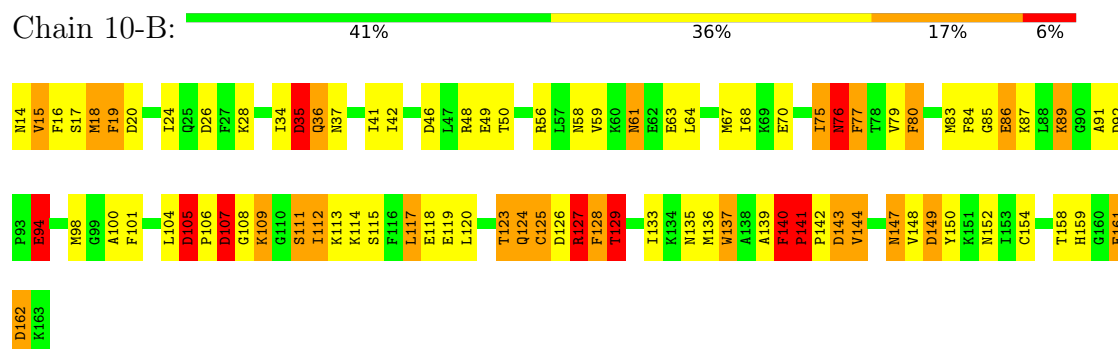
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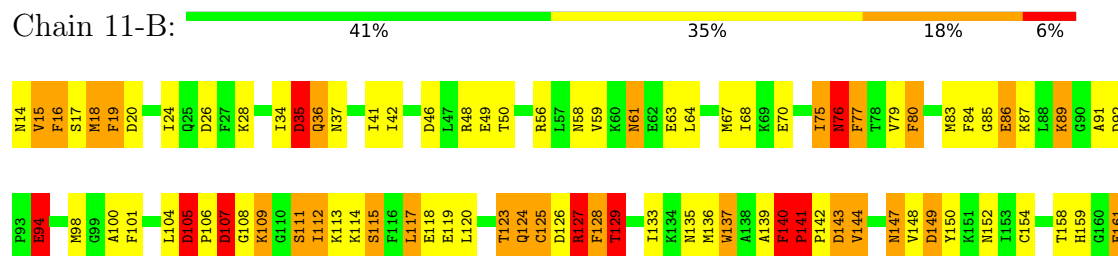
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



D162
K163

- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 12-B: 41% 34% 19% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 S11 D36 Q36 N37 I41 I42 D46 L47 R48 E49 T50 R56 L57 N58 V59 R60 N61 E62 E63 L64 M67 I68 R69 E70 I75 R76 F77 T78 V79 F80 M83 F84 G85 E86 K87 L88 K89 G90 A91 D92

P93 E94 M98 G99 A100 F101 L104 D105 P106 D107 F107 G108 K109 G110 S111 I112 K113 K114 K115 S116 F116 L117 E118 E119 L120 T123 Q124 C125 D126 R127 F128 T129 I133 K134 N135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 N152 N153 C154 T158 H159 G160 E161

D162
K163

- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 13-B: 41% 36% 17% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 S11 D36 Q36 N37 I41 I42 D46 L47 R48 E49 T50 R56 L57 N58 V59 R60 N61 E62 E63 L64 M67 I68 R69 E70 I75 R76 F77 T78 V79 F80 M83 F84 G85 E86 K87 L88 K89 G90 A91 D92

P93 E94 M98 G99 A100 F101 L104 D105 P106 D107 F107 G108 K109 G110 S111 I112 K113 K114 K115 S116 F116 L117 E118 E119 L120 T123 Q124 C125 D126 R127 F128 T129 I133 K134 N135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 N152 N153 C154 T158 H159 G160 E161

D162
K163

- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 14-B: 41% 35% 18% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 S11 D36 Q36 N37 I41 I42 D46 L47 R48 E49 T50 R56 L57 N58 V59 R60 N61 E62 E63 L64 M67 I68 R69 E70 I75 R76 F77 T78 V79 F80 M83 F84 G85 E86 K87 L88 K89 G90 A91 D92

P93 E94 M98 G99 A100 F101 L104 D105 P106 D107 F107 G108 K109 G110 S111 I112 K113 K114 K115 S116 F116 L117 E118 E119 L120 L121 T122 T123 Q124 C125 D126 R127 F128 T129 I133 K134 N135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 N152 N153 C154 T158 H159 G160

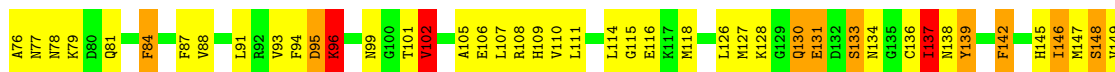
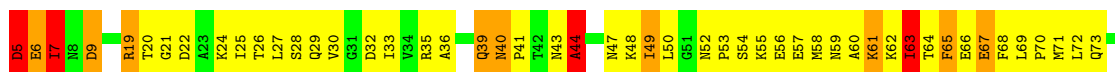
E161
D162
K163

- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

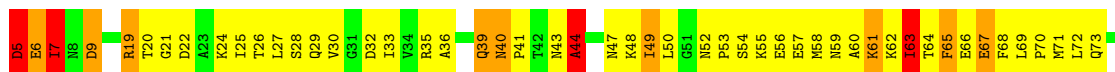
Chain 1-C: 35% 48% 12% 5%

D5 E6 I7 N8 D9 R19 T20 G21 D22 A23 K24 T25 T26 T27 S28 S29 Q29 V30 Q31 D32 I33 R35 V34 A36 Q39 N40 P41 T42 N43 N44 N47 K48 I49 L50 G51 N52 P53 S54 K55 E56 E57 M58 N59 A60 K61 K62 I63 T64 F65 E66 E67 F68 L69 P70 M71 L72 Q73

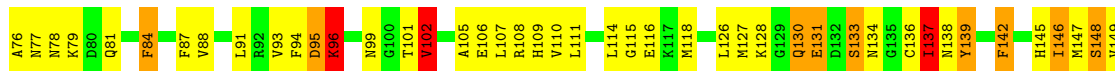
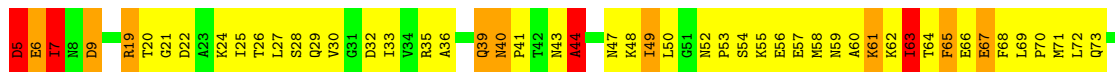
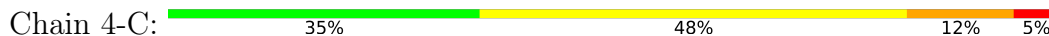
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



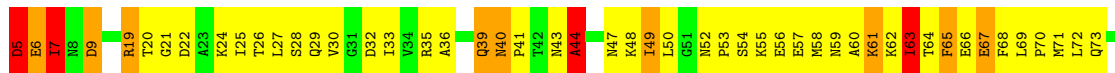
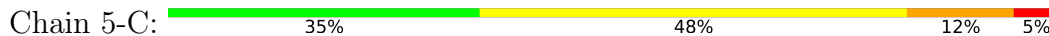
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



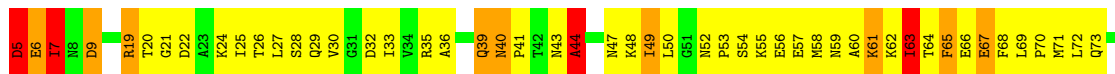
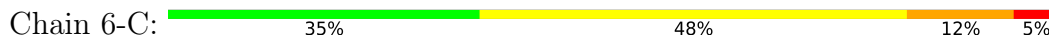
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

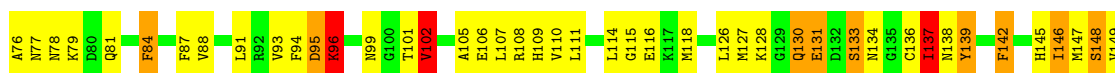


- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



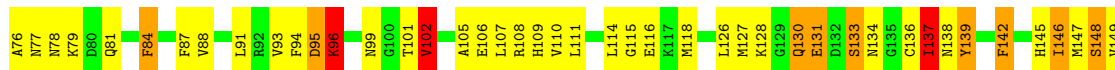
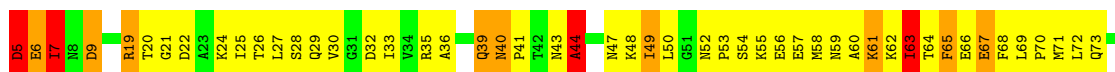
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM





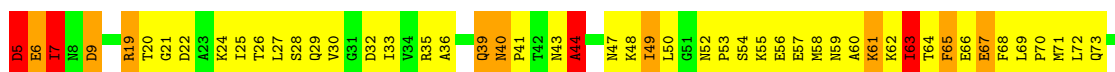
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 7-C: 35% 48% 12% 5%



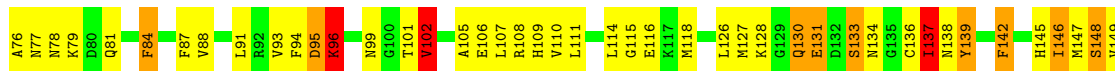
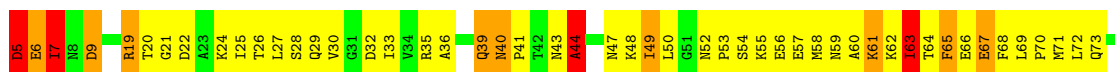
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 8-C: 35% 47% 13% 5%



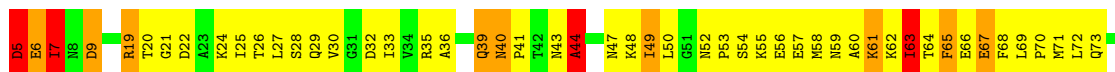
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 9-C: 35% 48% 12% 5%



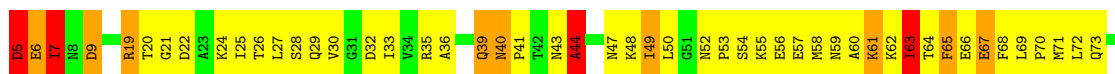
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

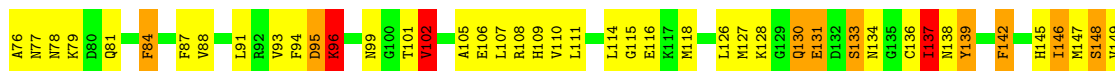
Chain 10-C: 35% 48% 12% 5%



• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

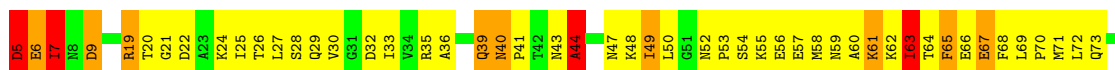
Chain 11-C: 35% 48% 12% 5%





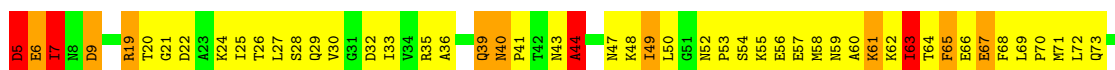
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 12-C: 35% 48% 12% 5%



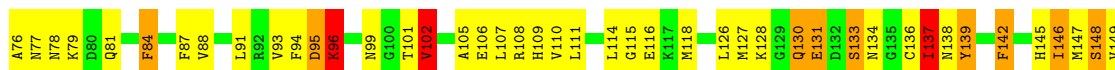
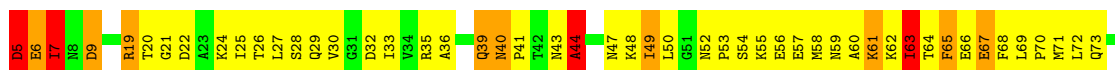
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 13-C: 35% 48% 12% 5%



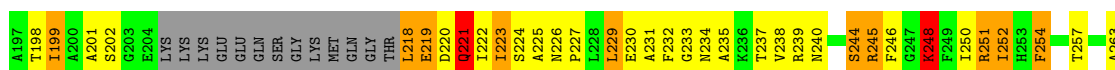
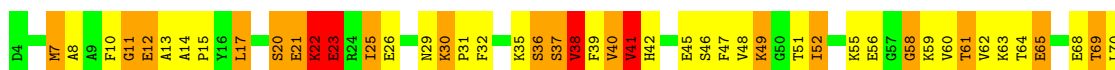
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

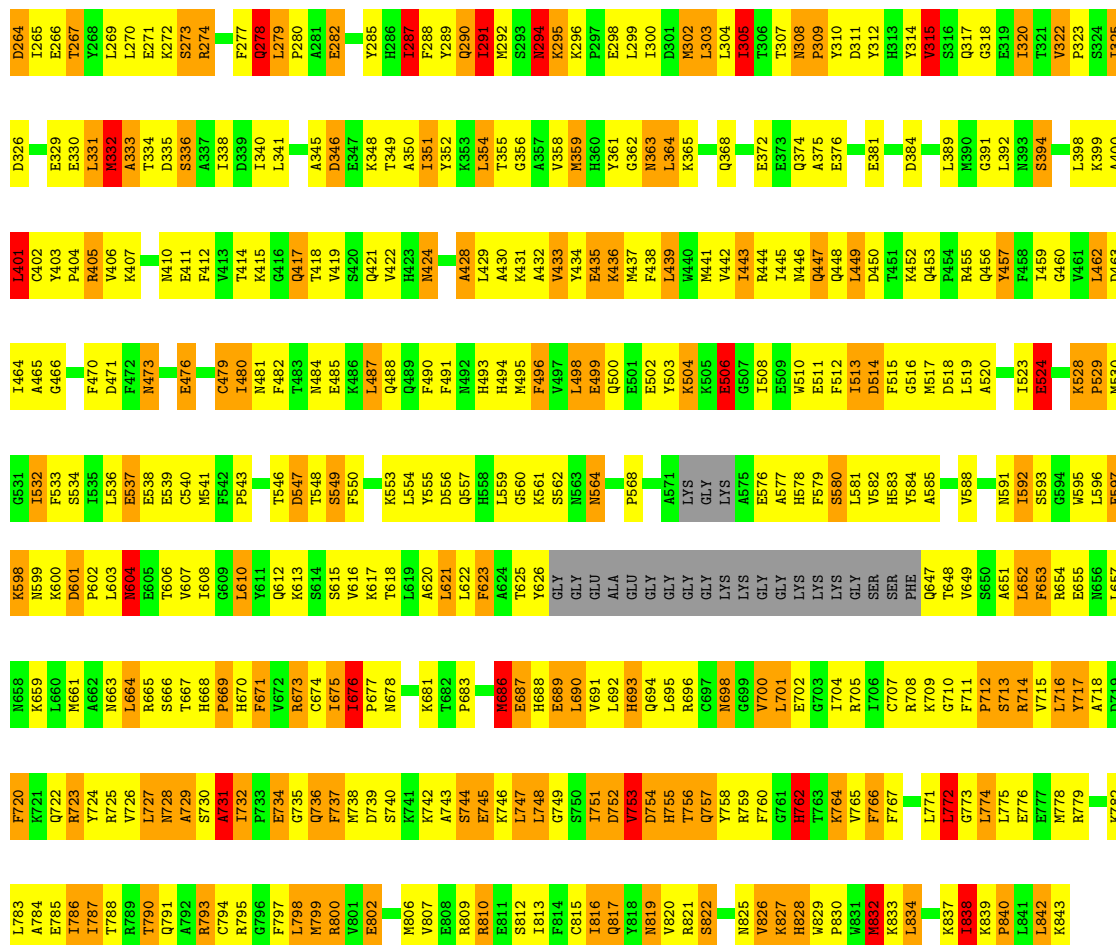
Chain 14-C: 35% 48% 12% 5%



• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

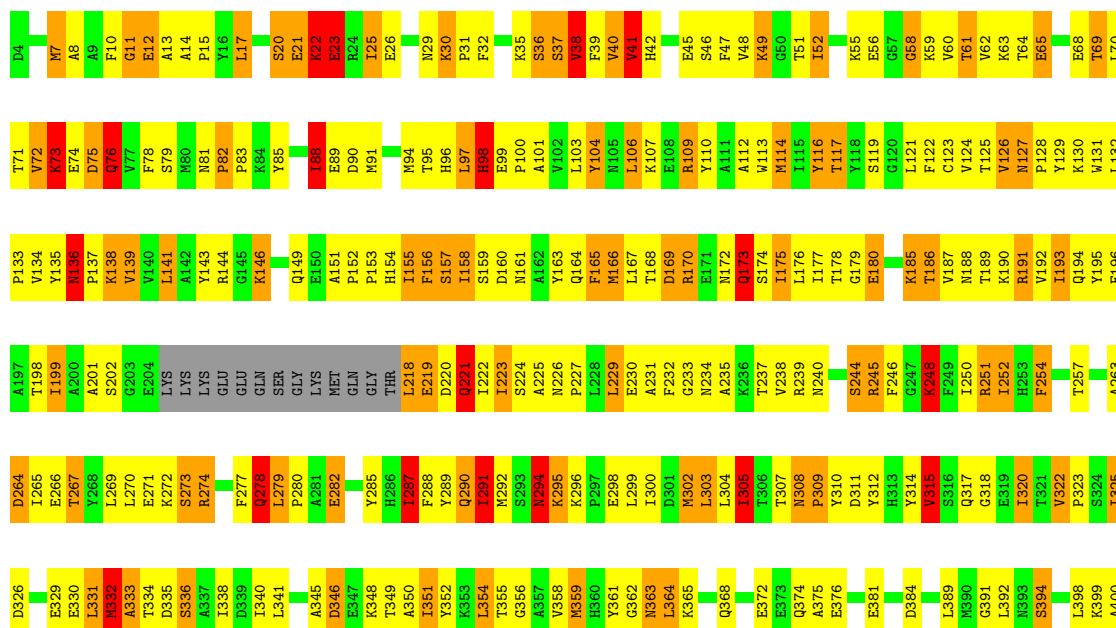
Chain 1-M: 26% 44% 22%





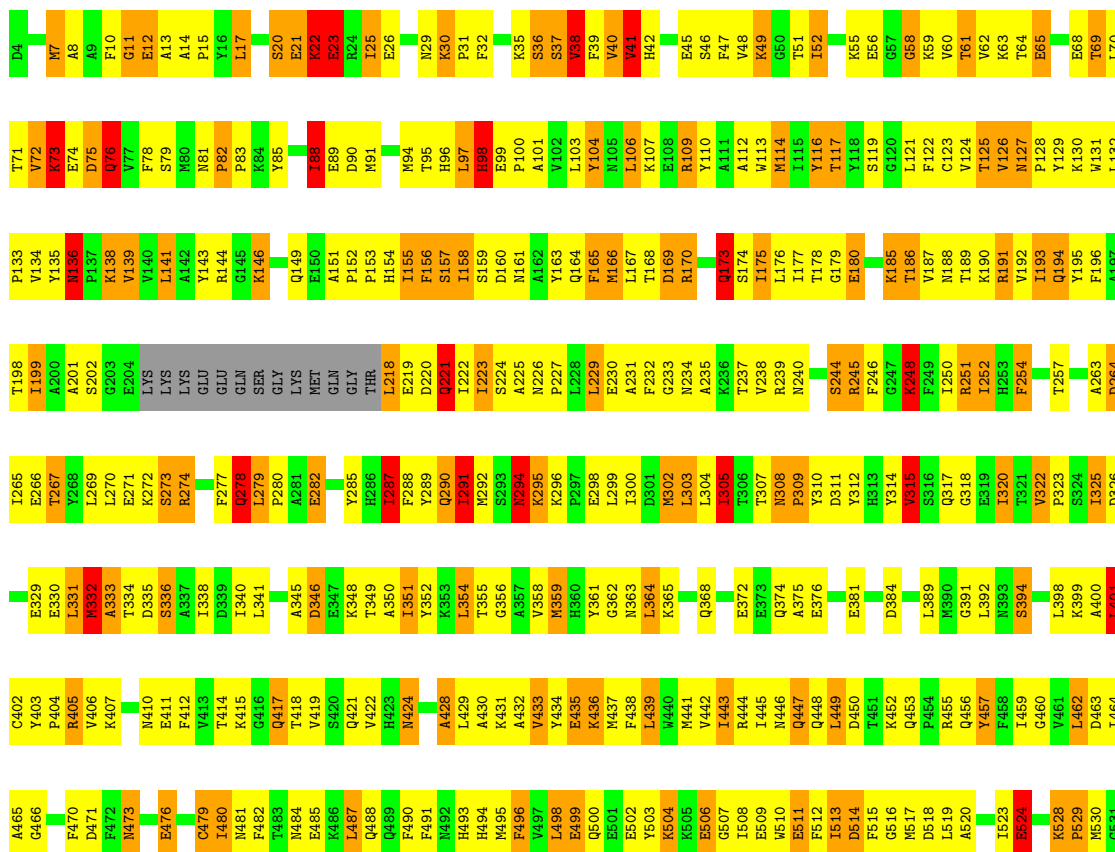
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 2-M: 26% 44% 22%

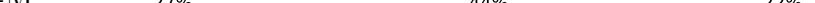


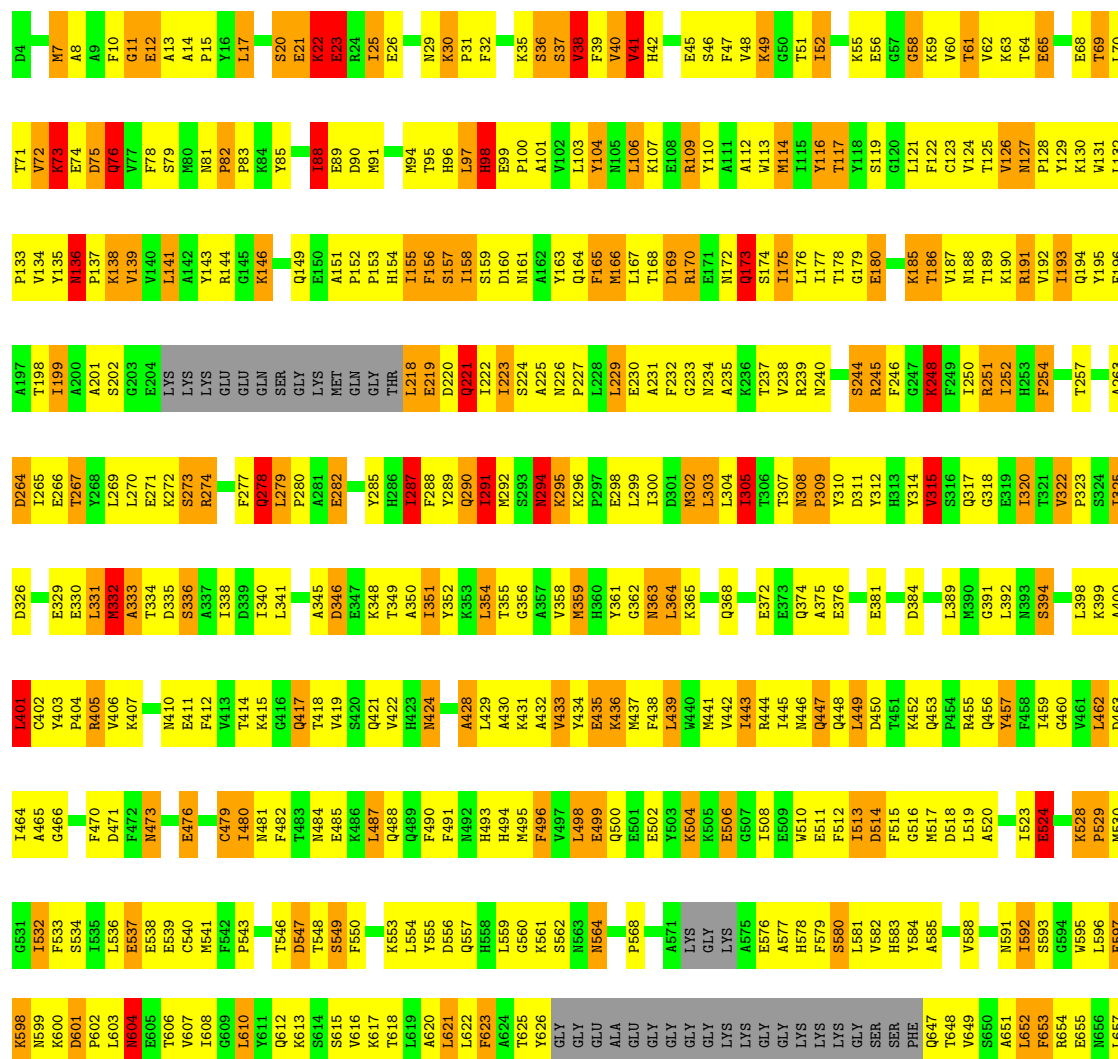


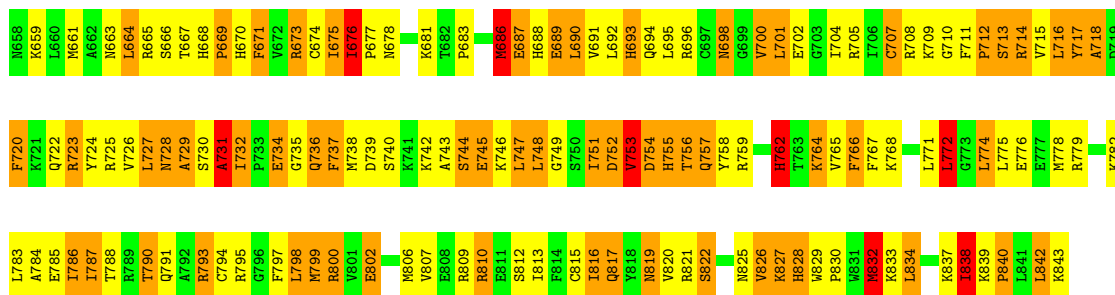
Chain 3-M: 26% 44% 22% . .



- Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

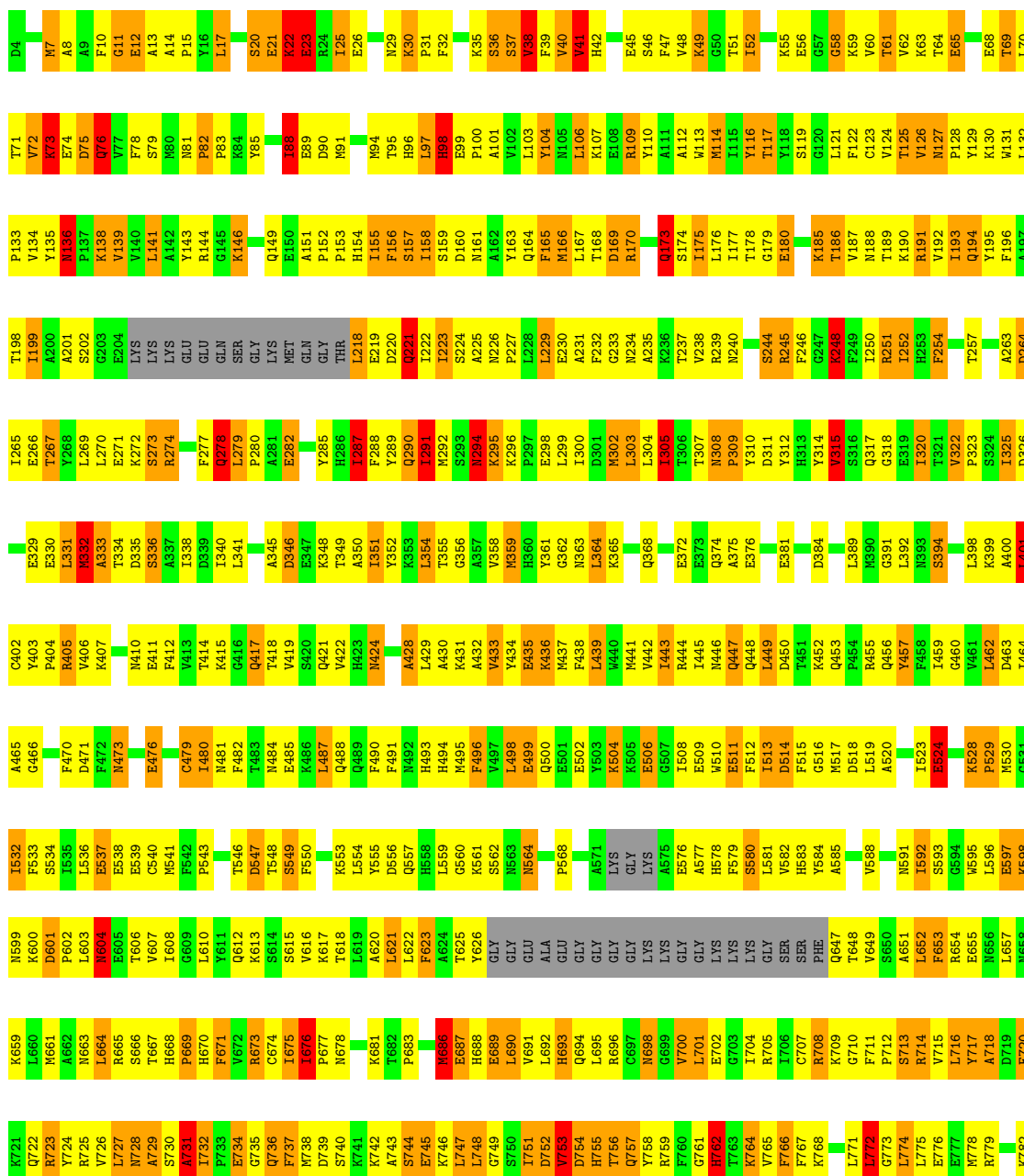
Chain 4-M:  27% 44% 22% . .





• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

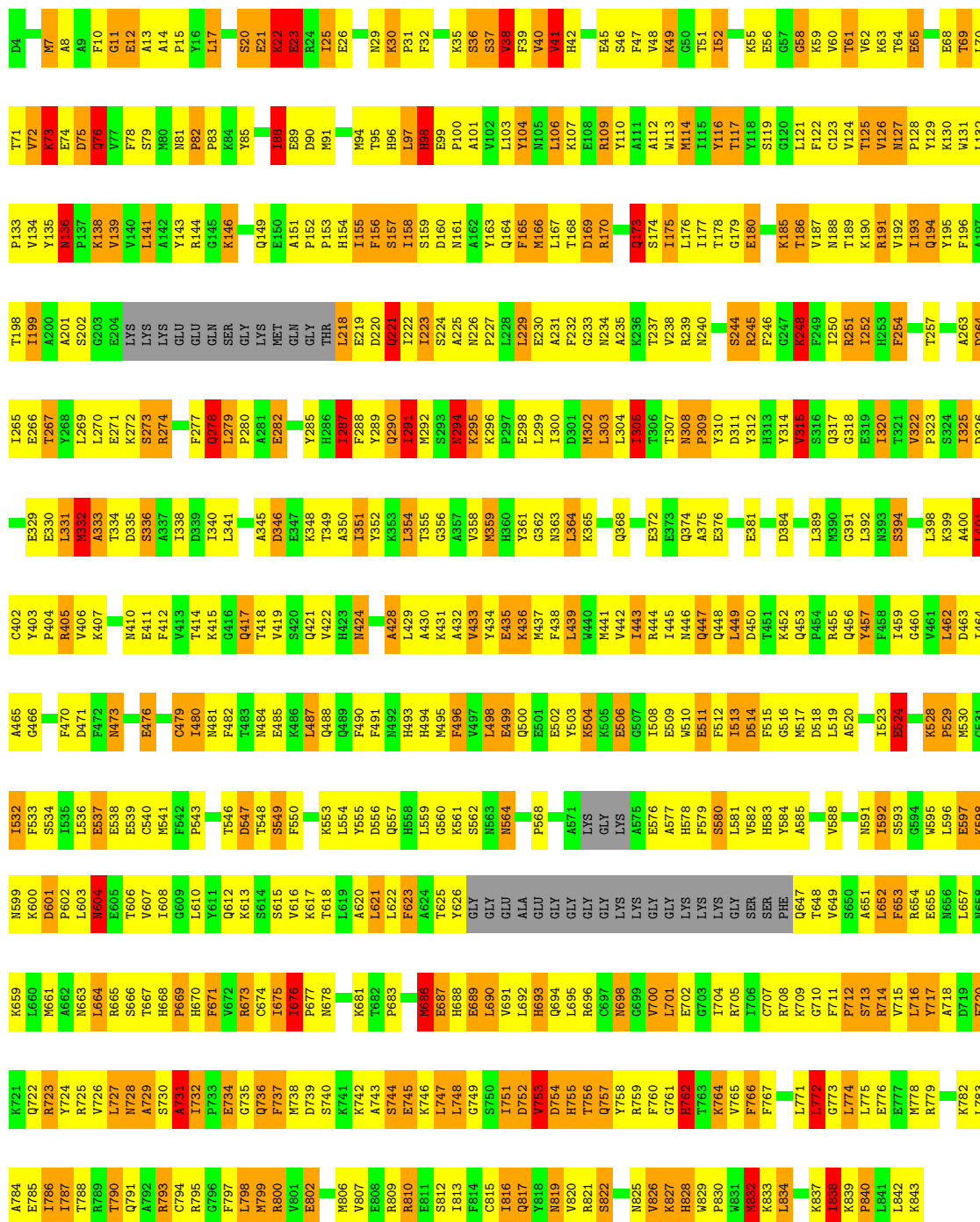
Chain 5-M: 26% 44% 22%





• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

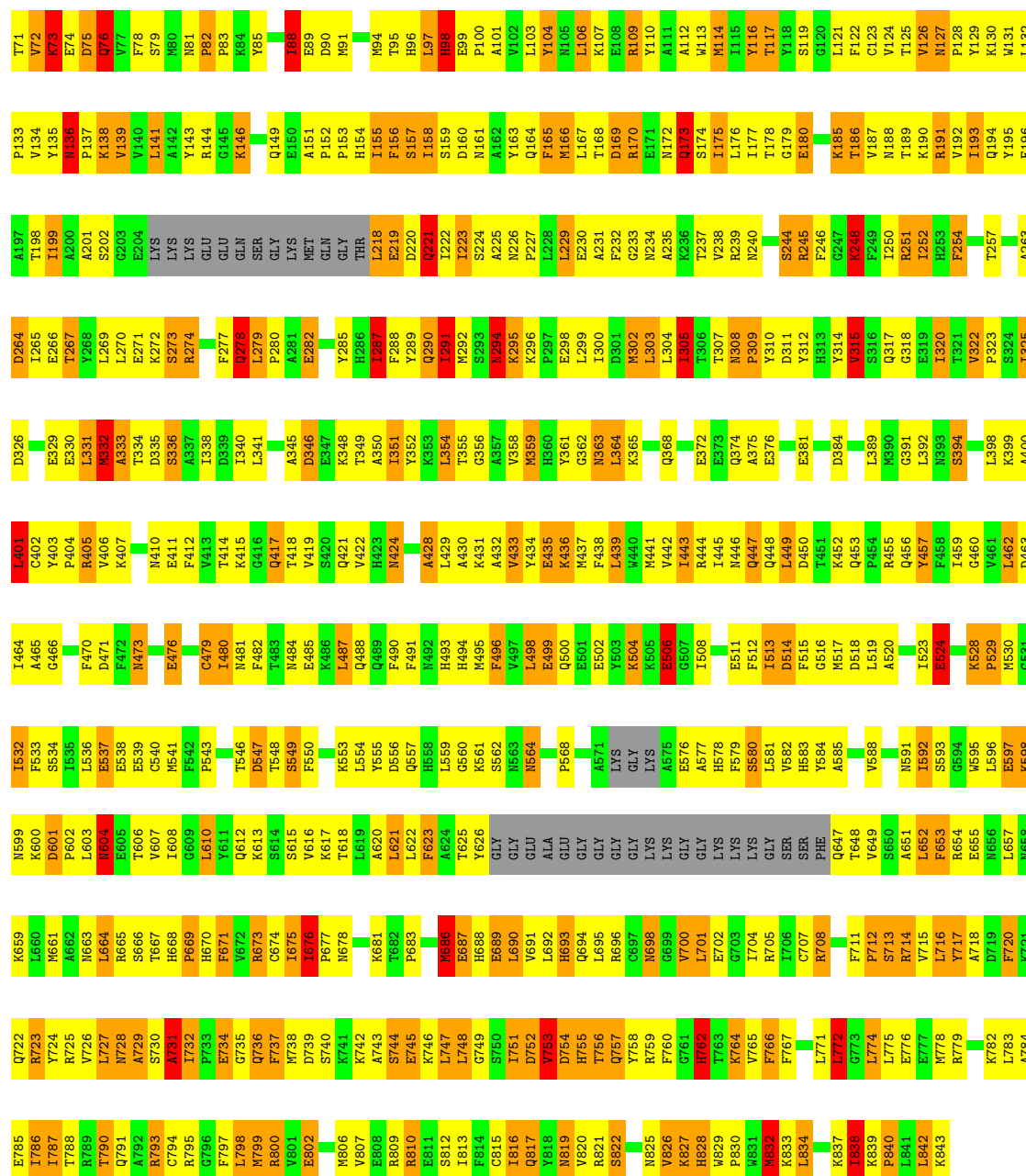
Chain 6-M: 26% 44% 22%



• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

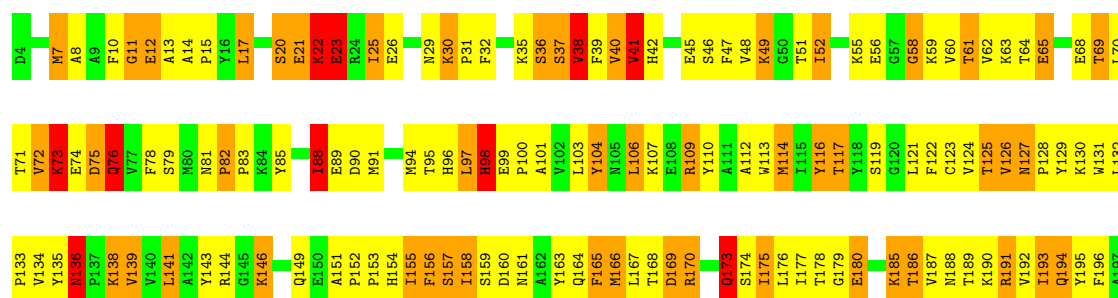
L783	F720	M658	K598	G531	T464	L401	D326	D264	A197	P133	T71	D4
L784	K721	K659	M599	L532	A465	C402	L265	L265	T198	V134	V72	M7
L785	K722	L680	K600	F533	C466	Y403	E329	E266	T199	Y135	K73	A8
L786	K723	M661	D601	S534	P404	P404	E330	T267	A200	N138	E74	A9
L787	K724	A682	P602	L535	F470	R405	L331	V268	A201	P137	D75	F10
L788	K725	M663	L603	L536	D471	V406	K332	L269	S202	K138	K76	G11
L789	V726	L684	M604	E537	F472	K407	A333	L270	G203	V139	V77	G11
L790	L727	L685	E605	E538	N473	N410	D335	L271	E204	V140	F78	E12
L791	M728	S666	E539	E539	K791	E411	D335	K272	LVS	L141	S79	A13
L792	A729	T667	V607	C540	E476	F412	K336	S273	LVS	A142	N80	A14
L793	S730	H668	L608	M541	F412	F412	A337	R274	LVS	Y143	P15	P15
L794	A731	H669	H609	F542	C479	V413	L338		GLU	Y143	P82	Y16
L795	L732	H670	L610	P543	L480	T414	D339	F277	GLU	G145	P83	L17
L796	F733	F671	Y611	T546	N481	K415	L340	K278	GLN	K146	K84	S20
L797	E734	F672	Q612	C416	F482	C416	L341	L279	SER		Y85	E21
L798	G735	K673	K613	D547	L483	Q417	A345	K281	GLY	F150	K88	K22
L799	Q736	C674	S614	T548	N484	T418	D346	E282	LVS	A151	E89	E23
L800	F737	L675	S615	S649	E485	V419	E347		GLY	P152	D90	R24
L801	M738	L676	V616	F550	K486	S420	K348	Y285	GLY	P153	N91	L25
L802	D739	F677	K617	L487	Q421	Q421	T349	H286	GLY	H154		E26
L803	M740	N678	T618	K563	Q488	V422	A350	L287	THR		N94	
L804	K741		L619	L554	Q489	H423	L351	L218	GLY	F155	N94	
L805	K742	K681	A620	Y555	F490	N424	F382	E219	LVS	F156	T95	N29
L806	A743	L682	L621	D556	F491		K353	F288	E219	S157	H96	K30
L807	S744	P683	L622	Q557	N492	A428	Q290	K289	D221	S158	L97	P31
L808	K745	F684	F623	H558	H493	L429	L354	T291	T222	S159	H98	F32
L809	E746	L685	K624	L559	H494	A430	T355	N292	L223	D160	E99	
L810	K746	M686	L625	C560	H494	A430	K356	S293	S224	N161	P100	K35
L811	L747	E687	T625	M561	N495	K431	A357	K294	A225	A162	A101	S36
L812	L748	H688	V626	K561	F496	A432	V358	K295	N226	Y163	S37	S36
L813	K749	E689	GLY	S562	N497	V433	K359	K296	P227	L103	V102	S37
L814	S750	L690	GLY	N563	L498	Y434	K360	K297	L228	F165	Y104	V38
L815	L751	F691	E499	M564	E499	E435	Y361	E298	L229	N105	F39	V40
L816	D752	L692	ALA	Q500	K436	K436	G362	L299	E230	L167	L106	V41
L817	K753	H693	GLU	P568	E501	N437	N363	L300	A231	T168	K107	H42
L818	D754	Q694	GLY		E502	F438	K364	K301	F232	D169	E108	
L819	M819	L695	GLY	A571	Y503	L439	K365	R302	G233	R170	R109	E45
L820	H755	L696	GLY	LVS	K504	Q440	L303	K301	N234	E171	Y110	S46
L821	T756	E697	GLY	LVS	M441	M441	L304	L304	A235	N172	A111	F47
L8												

D4	M7	A8	A9	F10	G11	E12	A13	A14	P15	Y16	L17	S20	E21	K22	E23	E24	L25	E26	N29	K30	P31	F32	K35	S36	S37	V38	F39	V40	V41	H42	E45	S46	F47	V48	K49	G50	T51	L52	K55	E56	G57	G58	K59	V60	T61	V62	K63	T64	E65	E68	T69	L70
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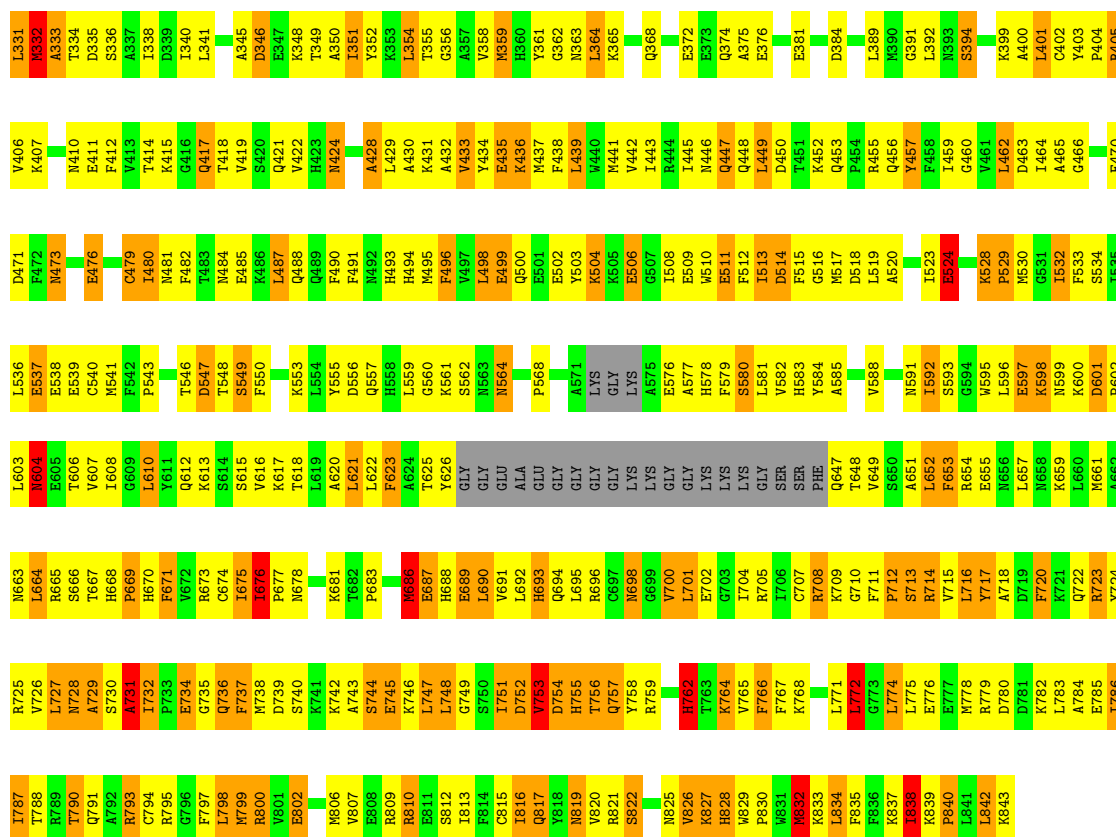
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 9-M: 26% 44% 22%



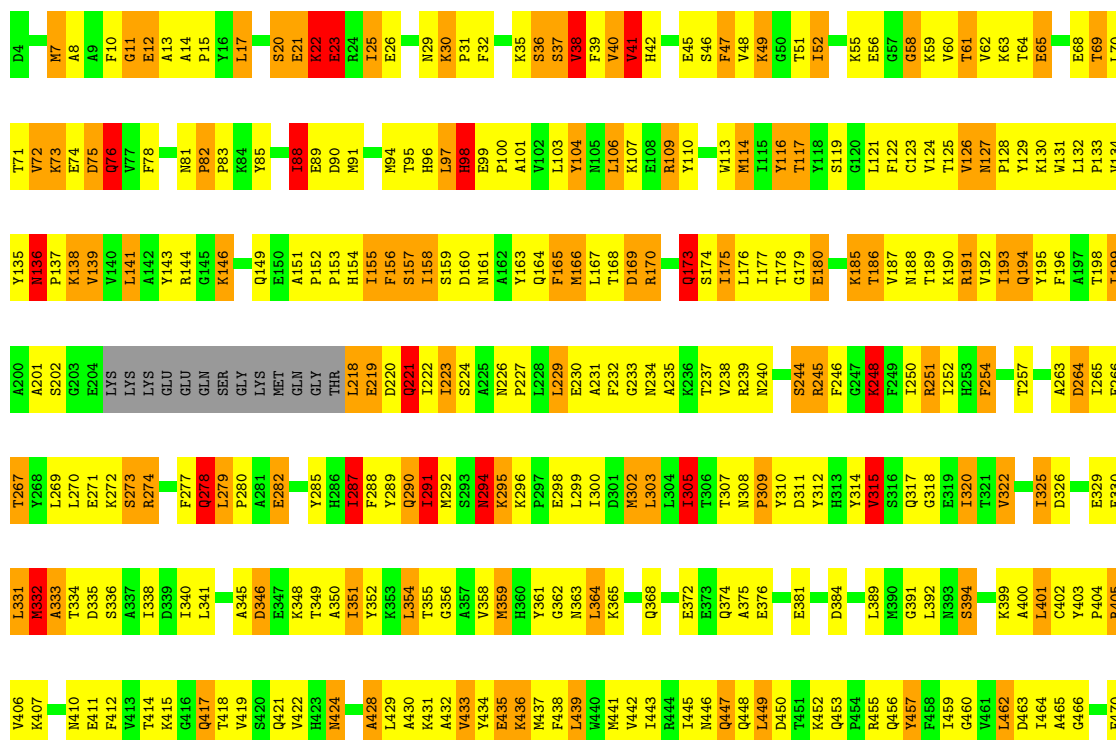


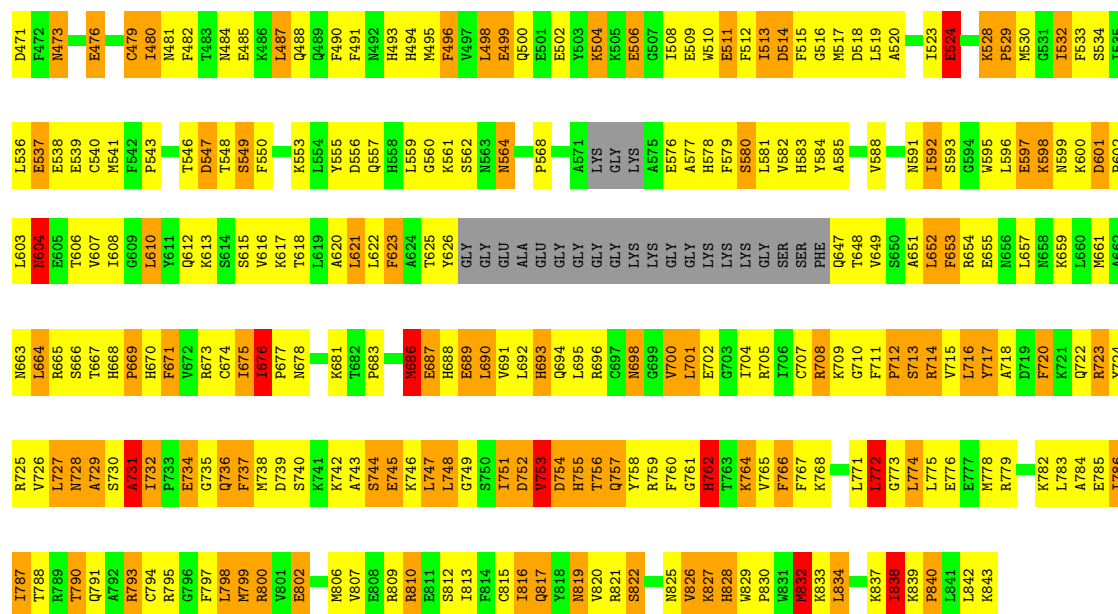
T267	A200	Y135	T71	D4
Y268	A201	M136	V72	M7
L269	S202	P137	K73	A8
L270	G203	K138	E74	A9
L271	E204	V139	D75	F10
K272	L1S	V140	Q76	G11
S273	L1S	L141	V77	E12
R274	L1S	A142	F78	A13
F277	GLU	Y143	N81	A14
Q278	GLU	R144	P82	P15
L279	GLN	G145	O83	Y16
L280	SER	K146	P83	L17
A281	GLY	Q149	K84	
L282	L1S	E150	Y85	S20
Y285	MET	M151	I88	E21
H286	GLN	A152	E89	K22
L287	THR	P153	D90	E23
F288	L218	H154	M91	R24
Y289	E219	I155	M94	I25
Q290	D220	F156	T95	N29
L291	Q221	S157	H96	K30
K292	L222	I158	L97	P31
S293	L223	S159	H98	F32
K294	E225	D160	E99	
K295	A226	A161	P100	K35
K296	P227	Y163	A101	S36
F297	L228	Q164	V102	S37
E298	L229	F165	L103	V38
L299	L299	M166	Y104	F39
I300	A231	P167	N105	V40
K302	F232	T168	L106	V41
M303	G233	D169	K107	H42
L304	K234	R170	E108	
L305	A235	Q173	R109	E45
T306	K236	S174	Y110	S46
T307	T306	I175	W113	F47
K308	T238	L176	M114	K48
P309	R239	I177	T115	K49
Y310	N240	T178	Y116	G50
D311	S244	G179	T117	S1
Y312	R245	E180	Y118	I52
Y314	G247		S119	
K315	F248	K185	G120	K55
S316	K248	T186	L121	E56
Q317	F249	V187	F122	G57
G318	L250	N188	C123	K59
E319	R251	T189	V124	V60
I320	L252	K190	T125	T61
T321	H253	R191	N126	V62
V322	F254	V192	M127	K63
		I193	P128	E65
I325	T257	Q194	Y129	
K326	A263	Y195	T130	E68
	D264	A197	L132	T69
E329	L265	T198	P133	L70
F329	T266	I199	V134	



• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

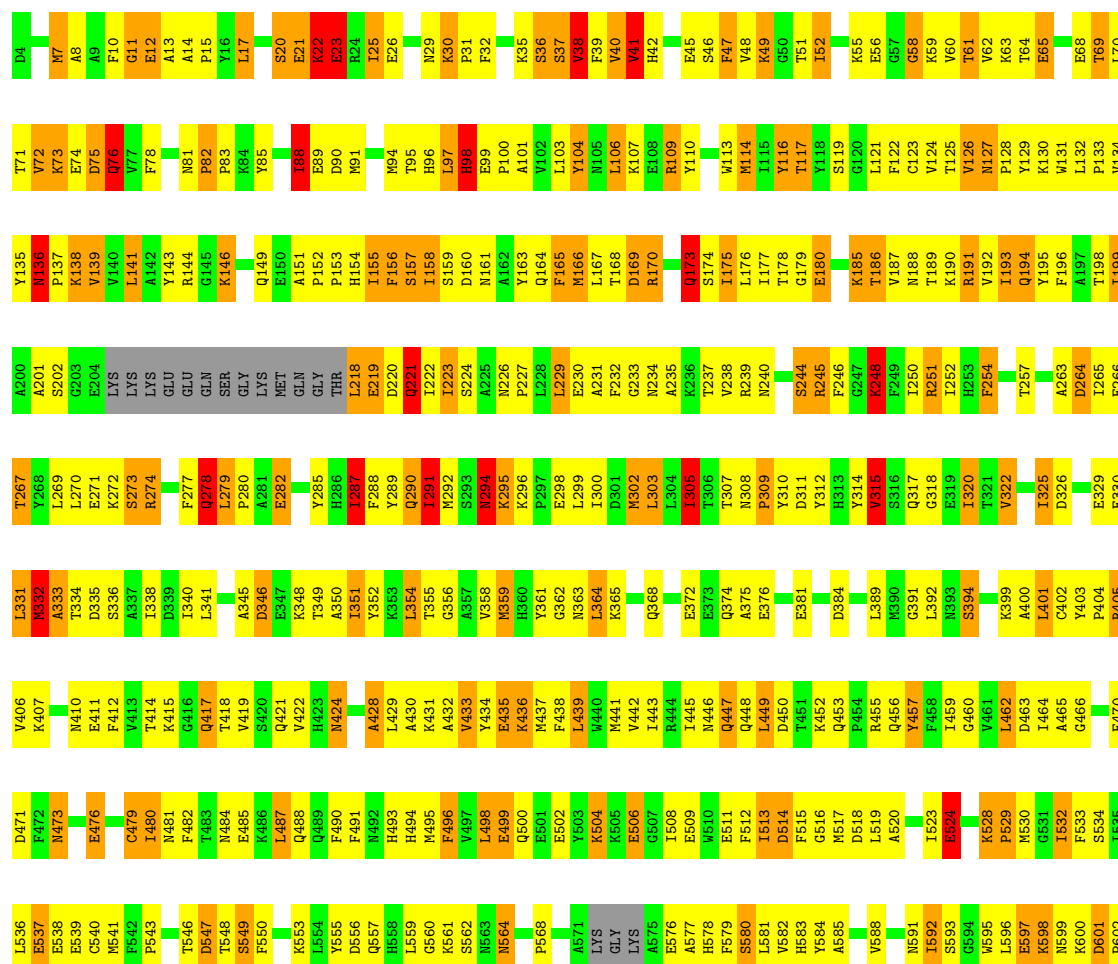
Chain 11-M: 27% 44% 22%

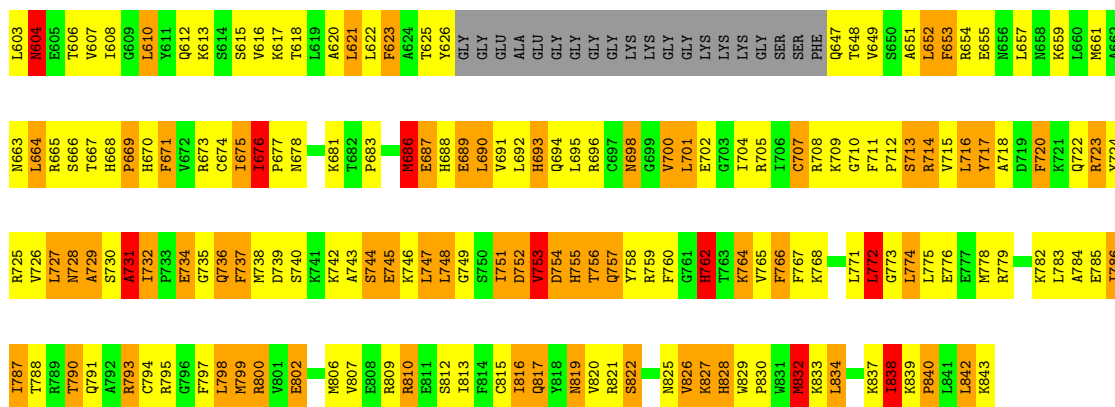




● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

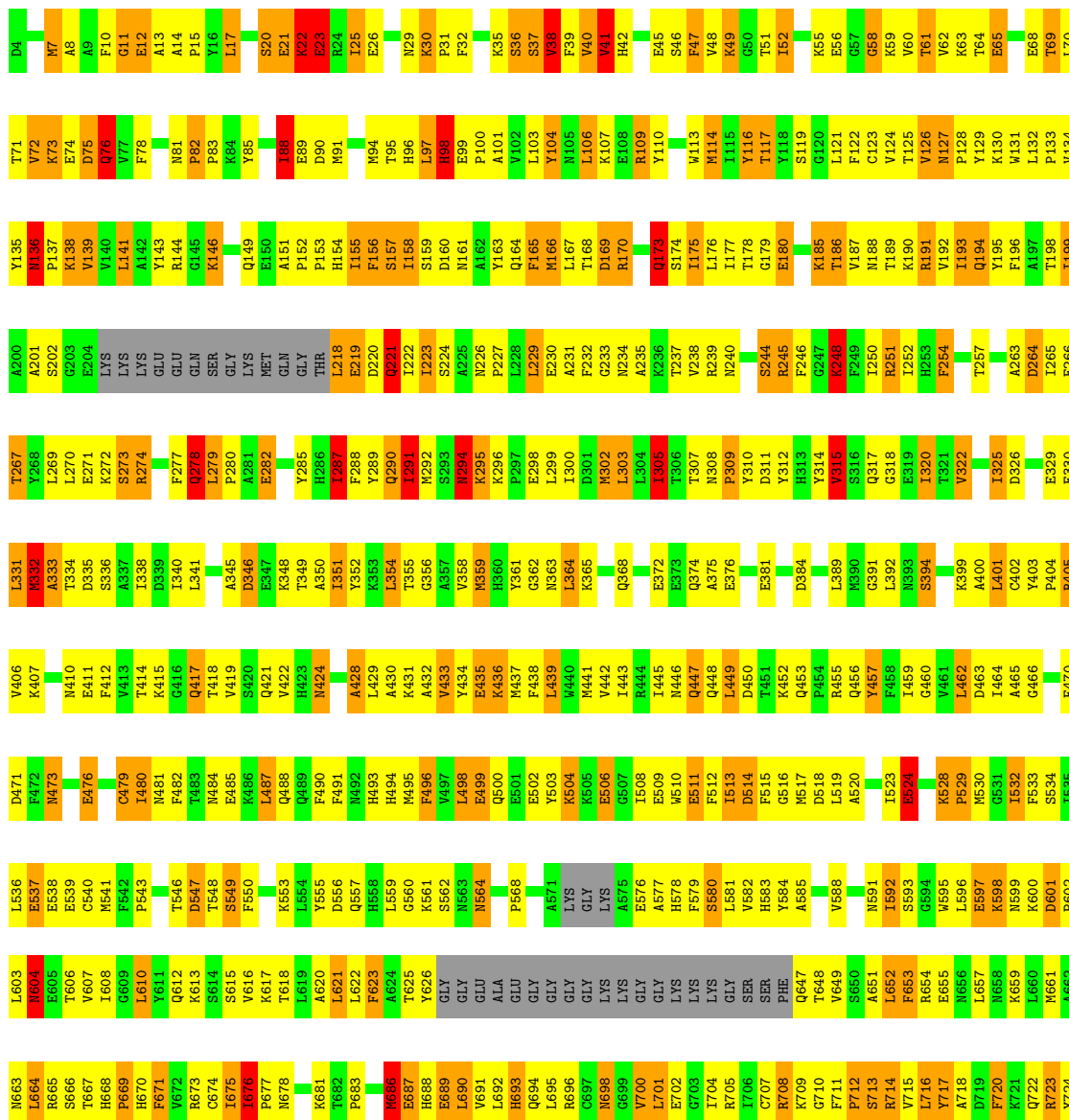
Chain 12-M: 27% 44% 21%

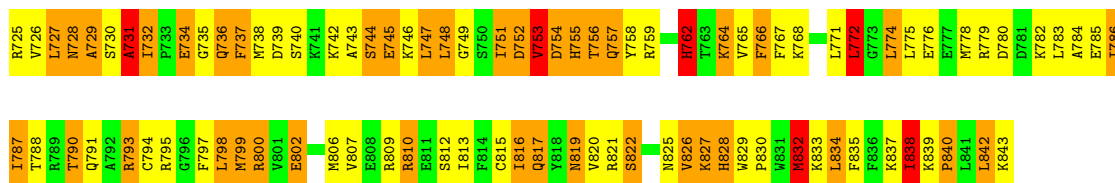




● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

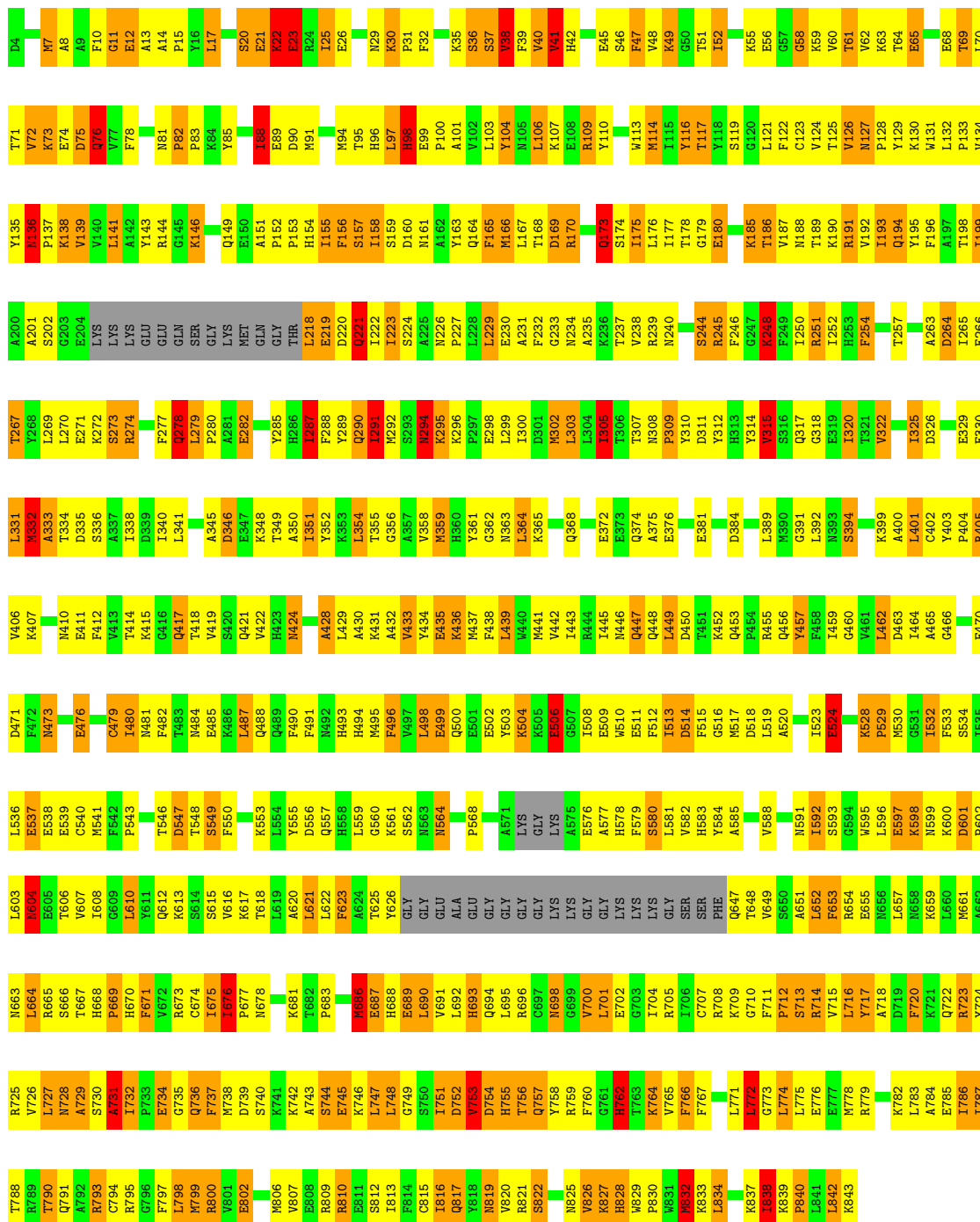
Chain 13-M: 27% 44% 22%





• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 14-M: 27% 44% 21%



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F224 (2k x 2k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	2-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	3-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	4-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	5-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	6-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	7-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	8-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	9-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	10-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	11-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	12-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	13-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
1	14-B	0.80	1/1199 (0.1%)	2.28	57/1617 (3.5%)
2	1-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	2-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	3-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	4-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	5-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	6-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	7-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	8-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	9-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	10-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	11-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	12-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	13-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
2	14-C	0.84	3/1140 (0.3%)	2.16	60/1530 (3.9%)
3	1-M	1.63	22/6594 (0.3%)	1.87	139/8884 (1.6%)
3	2-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	3-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	4-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	5-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	6-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	7-M	1.63	22/6594 (0.3%)	1.87	139/8884 (1.6%)
3	8-M	1.63	22/6594 (0.3%)	1.87	139/8884 (1.6%)
3	9-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	10-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	11-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	12-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	13-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	14-M	1.63	22/6594 (0.3%)	1.87	139/8884 (1.6%)
All	All	1.46	364/125052 (0.3%)	1.97	3584/168404 (2.1%)

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-B	0	4
1	2-B	0	4
1	3-B	0	4
1	4-B	0	4
1	5-B	0	4
1	6-B	0	4
1	7-B	0	4
1	8-B	0	4
1	9-B	0	4
1	10-B	0	4
1	11-B	0	4
1	12-B	0	4
1	13-B	0	4
1	14-B	0	4
3	1-M	0	1
3	2-M	0	1
3	3-M	0	1
3	4-M	0	1
3	5-M	0	1
3	6-M	0	1
3	7-M	0	1
3	8-M	0	1
3	9-M	0	1
3	10-M	0	1
3	11-M	0	1
3	12-M	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	13-M	0	1
3	14-M	0	1
All	All	0	70

The worst 5 of 364 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-M	731	ALA	C-N	51.63	1.91	1.33
3	2-M	731	ALA	C-N	51.63	1.91	1.33
3	3-M	731	ALA	C-N	51.63	1.91	1.33
3	4-M	731	ALA	C-N	51.63	1.91	1.33
3	5-M	731	ALA	C-N	51.63	1.91	1.33

The worst 5 of 3584 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-M	731	ALA	O-C-N	-34.23	77.07	122.59
3	2-M	731	ALA	O-C-N	-34.23	77.07	122.59
3	3-M	731	ALA	O-C-N	-34.23	77.07	122.59
3	4-M	731	ALA	O-C-N	-34.23	77.07	122.59
3	5-M	731	ALA	O-C-N	-34.23	77.07	122.59

There are no chirality outliers.

5 of 70 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-B	105	ASP	Peptide
1	1-B	127	ARG	Peptide
1	1-B	140	PHE	Peptide
1	1-B	141	PRO	Peptide
3	1-M	98	HIS	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-B	1177	0	1134	141	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2-B	1177	0	1134	138	0
1	3-B	1177	0	1134	138	0
1	4-B	1177	0	1134	138	0
1	5-B	1177	0	1134	140	0
1	6-B	1177	0	1134	137	0
1	7-B	1177	0	1134	145	0
1	8-B	1177	0	1134	144	0
1	9-B	1177	0	1134	141	0
1	10-B	1177	0	1134	137	0
1	11-B	1177	0	1134	139	0
1	12-B	1177	0	1134	141	0
1	13-B	1177	0	1134	137	0
1	14-B	1177	0	1134	138	0
2	1-C	1126	0	1084	90	0
2	2-C	1126	0	1084	91	0
2	3-C	1126	0	1084	88	0
2	4-C	1126	0	1084	89	0
2	5-C	1126	0	1084	90	0
2	6-C	1126	0	1084	87	0
2	7-C	1126	0	1084	91	0
2	8-C	1126	0	1084	91	0
2	9-C	1126	0	1084	89	0
2	10-C	1126	0	1084	91	0
2	11-C	1126	0	1084	91	0
2	12-C	1126	0	1084	91	0
2	13-C	1126	0	1084	91	0
2	14-C	1126	0	1084	90	0
3	1-M	6455	0	6383	880	0
3	2-M	6455	0	6377	862	0
3	3-M	6455	0	6379	897	0
3	4-M	6455	0	6383	854	0
3	5-M	6455	0	6383	909	0
3	6-M	6455	0	6382	912	0
3	7-M	6455	0	6383	873	0
3	8-M	6455	0	6384	839	0
3	9-M	6455	0	6382	882	0
3	10-M	6455	0	6383	850	0
3	11-M	6455	0	6381	851	0
3	12-M	6455	0	6381	834	0
3	13-M	6455	0	6383	850	0
3	14-M	6455	0	6383	856	0
All	All	122612	0	120399	13620	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 56.

The worst 5 of 13620 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)
3:M:510:TRP:CE3	3:M:766:PHE:HB3	1.18	1.70
3:M:510:TRP:CH2	3:M:711:PHE:CE2	1.76	1.68
3:M:510:TRP:CZ3	3:M:766:PHE:CB	1.79	1.64
3:M:540:CYS:CB	3:M:602:PRO:HG2	1.27	1.63
3:M:540:CYS:CB	3:M:602:PRO:HG2	1.27	1.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	2-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	3-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	4-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	5-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	9
1	6-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	7-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	8-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	9-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	9
1	10-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	11-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	12-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	13-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	14-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
2	1-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	2-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	3-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	4-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	5-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	6-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	7-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	8-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	9-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	10-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	11-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	12-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	13-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	14-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
3	1-M	788/840 (94%)	651 (83%)	114 (14%)	23 (3%)	3	23
3	2-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	3-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	4-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	5-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	6-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	7-M	788/840 (94%)	651 (83%)	113 (14%)	24 (3%)	3	23
3	8-M	788/840 (94%)	651 (83%)	114 (14%)	23 (3%)	3	23
3	9-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	10-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	11-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	12-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	13-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	14-M	788/840 (94%)	651 (83%)	115 (15%)	22 (3%)	4	24
All	All	15086/15890 (95%)	12316 (82%)	2120 (14%)	650 (4%)	3	17

5 of 650 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-B	76	ASN
1	1-B	109	LYS
1	1-B	115	SER
1	1-B	141	PRO
1	1-B	142	PRO

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-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	2-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	3-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	4-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	5-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	6-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	7-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	8-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	9-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	10-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	11-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	12-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	13-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	14-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
2	1-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	2-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	3-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	4-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	5-C	120/122 (98%)	107 (89%)	13 (11%)	6	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	6-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	7-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	8-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	9-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	10-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	11-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	12-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	13-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	14-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
3	1-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	2-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	3-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	4-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	5-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	6-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	7-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	8-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	9-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	10-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	11-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	12-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	13-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	14-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
All	All	13174/13664 (96%)	10094 (77%)	3080 (23%)	2	5

5 of 3080 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	9-M	245	ARG
3	11-M	245	ARG
3	9-M	513	ILE
3	9-M	229	LEU
3	10-M	290	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 468 such sidechains are listed below:

Mol	Chain	Res	Type
1	8-B	36	GLN
3	14-M	188	ASN
3	9-M	564	ASN
3	14-M	76	GLN
1	13-B	23	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	1-M	7
3	2-M	7
3	3-M	7
3	4-M	7
3	5-M	7

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Mol	Chain	Number of breaks
3	6-M	7
3	7-M	7
3	9-M	7
3	10-M	7
3	11-M	7
3	12-M	7
3	13-M	7
3	14-M	7
3	8-M	6

The worst 5 of 97 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	601:ASP	C	602:PRO	N	9.78
2	M	601:ASP	C	602:PRO	N	9.78
3	M	601:ASP	C	602:PRO	N	9.78
4	M	601:ASP	C	602:PRO	N	9.78
5	M	601:ASP	C	602:PRO	N	9.78

6 Map visualisation

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

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.