



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 02:43 AM UTC

PDB ID : 2W4G / pdb_00002w4g
EMDB ID : EMD-1584
Title : ISOMETRICALLY CONTRACTING INSECT ASYNCHRONOUS FLIGHT
MUSCLE QUICK FROZEN AFTER A QUICK STRETCH 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

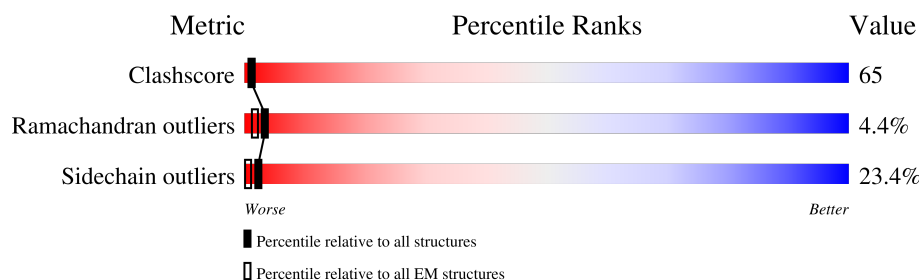
1 Overall quality at a glance

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.



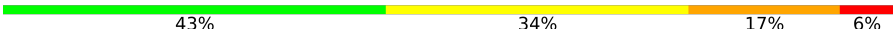
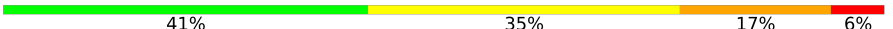
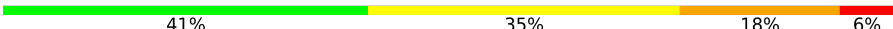
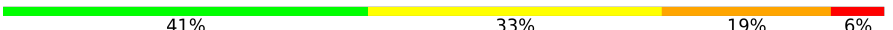
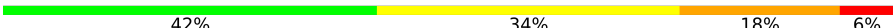
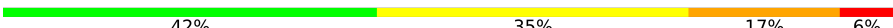
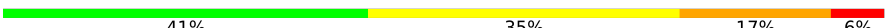
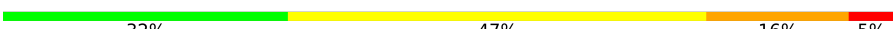
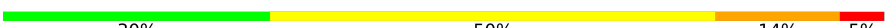
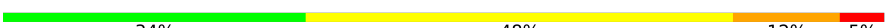
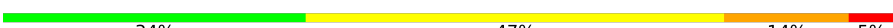
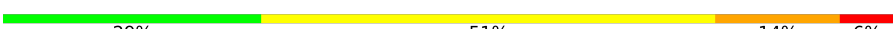
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	42% 35% 17% 6%
1	10-B	150	42% 33% 19% 6%
1	11-B	150	41% 35% 18% 6%
1	12-B	150	41% 35% 18% 6%
1	13-B	150	41% 35% 18% 6%
1	14-B	150	41% 35% 17% 6%
1	15-B	150	42% 35% 17% 6%
1	16-B	150	42% 35% 17% 6%
1	17-B	150	43% 34% 17% 6%

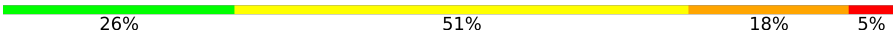
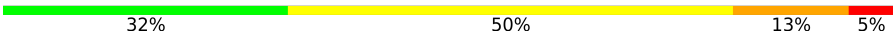
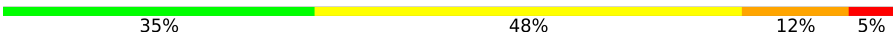
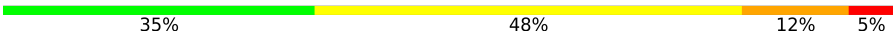
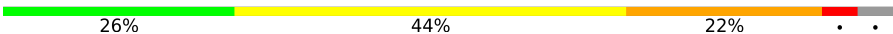
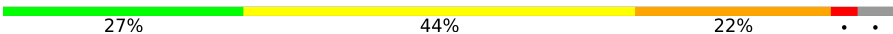
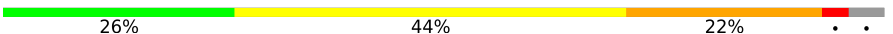
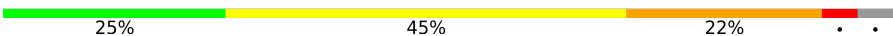
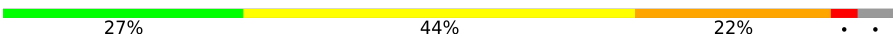
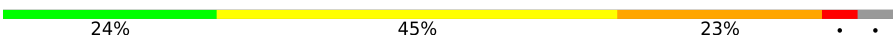
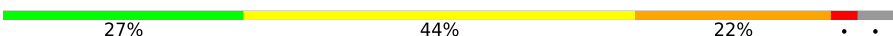
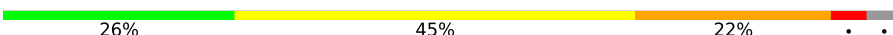
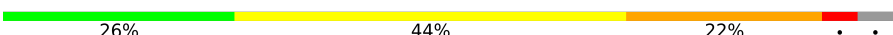
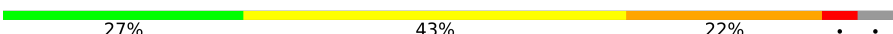
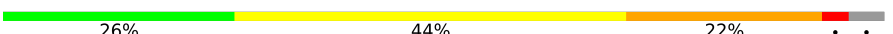
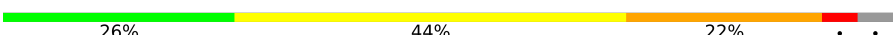
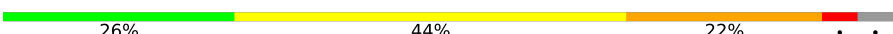
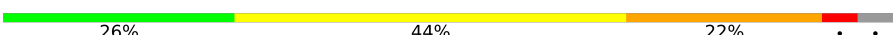
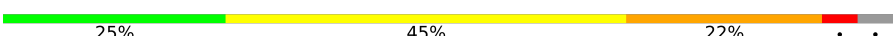
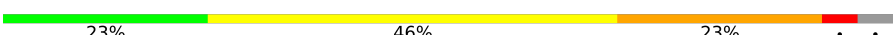
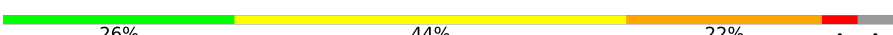
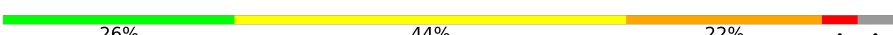
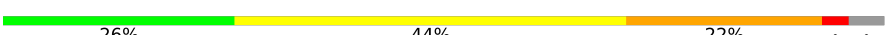
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Mol	Chain	Length	Quality of chain
1	18-B	150	
1	19-B	150	
1	2-B	150	
1	20-B	150	
1	3-B	150	
1	4-B	150	
1	5-B	150	
1	6-B	150	
1	7-B	150	
1	8-B	150	
1	9-B	150	
2	1-C	145	
2	10-C	145	
2	11-C	145	
2	12-C	145	
2	13-C	145	
2	14-C	145	
2	15-C	145	
2	16-C	145	
2	17-C	145	
2	18-C	145	
2	19-C	145	
2	2-C	145	
2	20-C	145	
2	3-C	145	

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Mol	Chain	Length	Quality of chain
2	4-C	145	
2	5-C	145	
2	6-C	145	
2	7-C	145	
2	8-C	145	
2	9-C	145	
3	1-M	840	
3	10-M	840	
3	11-M	840	
3	12-M	840	
3	13-M	840	
3	14-M	840	
3	15-M	840	
3	16-M	840	
3	17-M	840	
3	18-M	840	
3	19-M	840	
3	2-M	840	
3	20-M	840	
3	3-M	840	
3	4-M	840	
3	5-M	840	
3	6-M	840	
3	7-M	840	
3	8-M	840	

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Mol	Chain	Length	Quality of chain
3	9-M	840	26% 44% 22%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 175160 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		
1	15-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	16-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	17-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	18-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	19-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	20-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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	14-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	15-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	16-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	17-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	18-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	19-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	20-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		
3	6-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	7-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	8-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	9-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	10-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	11-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	12-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	13-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	14-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	15-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	16-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	17-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	18-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	19-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	20-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		

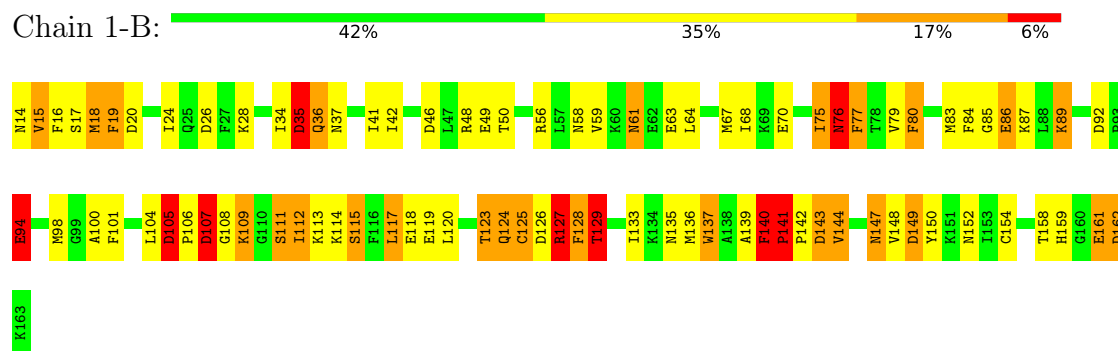
There is a discrepancy between the modelled and reference sequences:

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

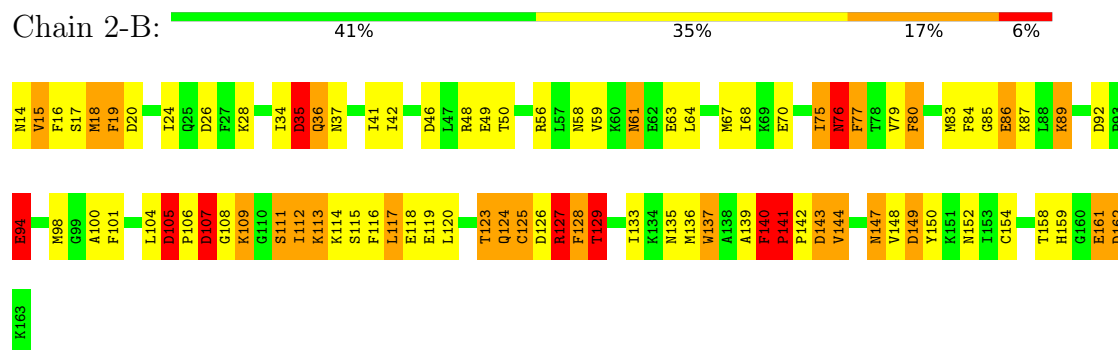
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

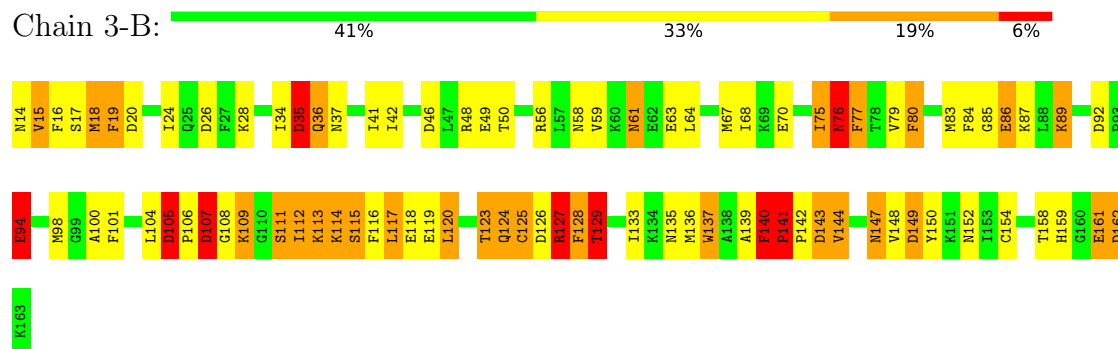
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



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

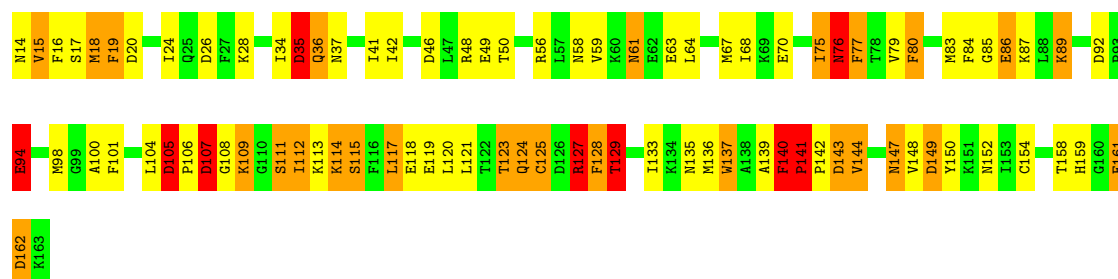


- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



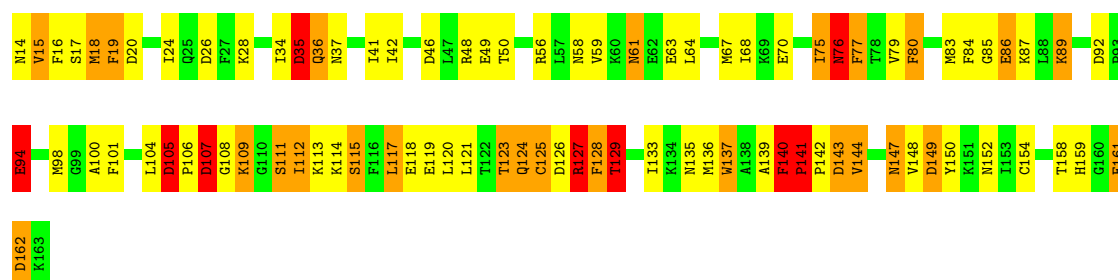
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 4-B: 



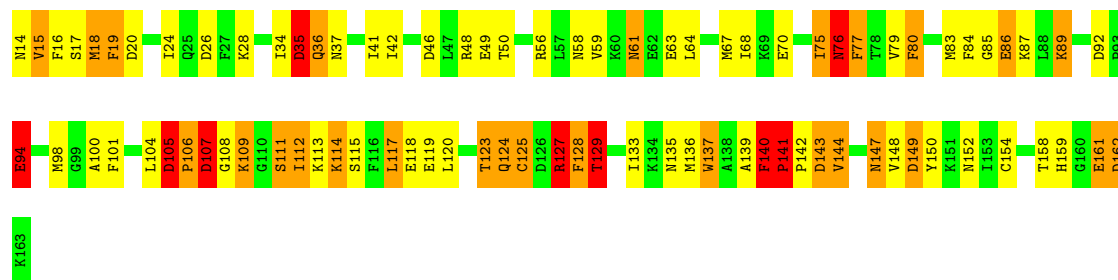
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 5-B: 

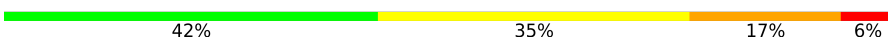


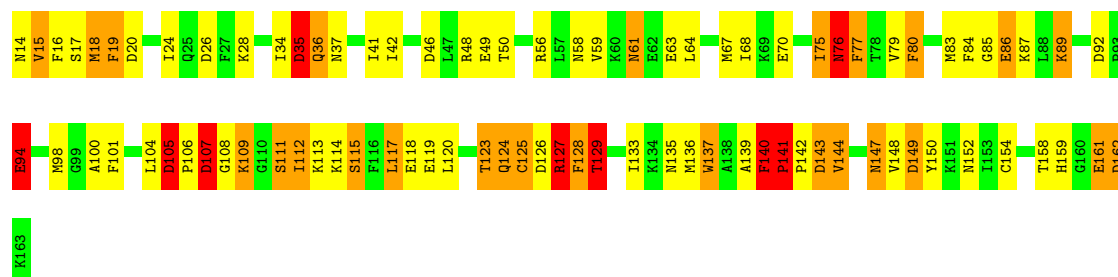
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 6-B: 

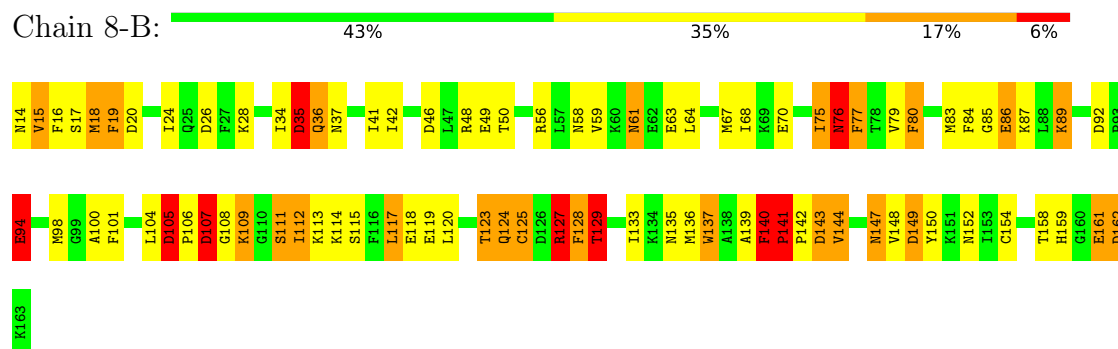


- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

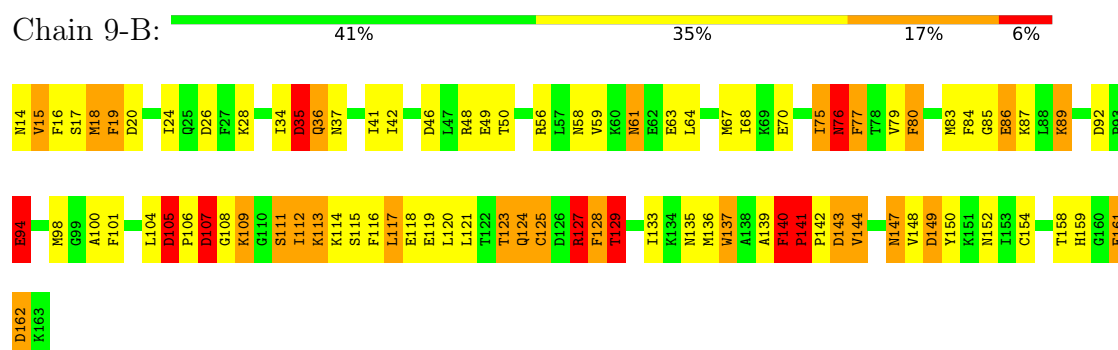
Chain 7-B: 



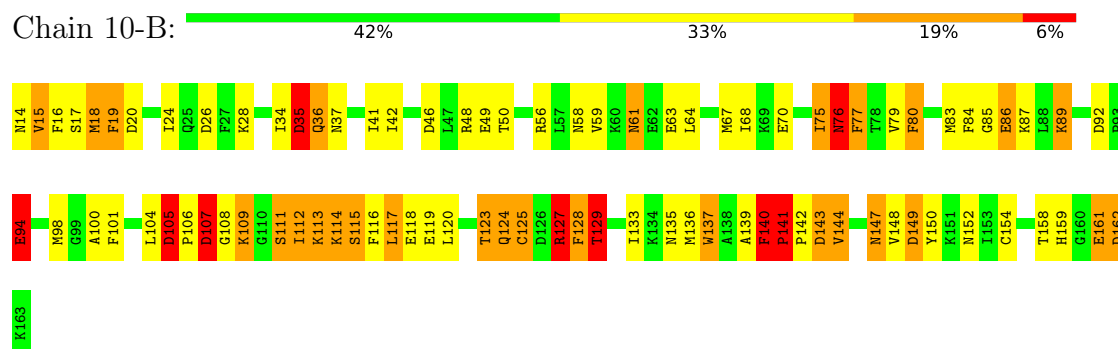
• Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



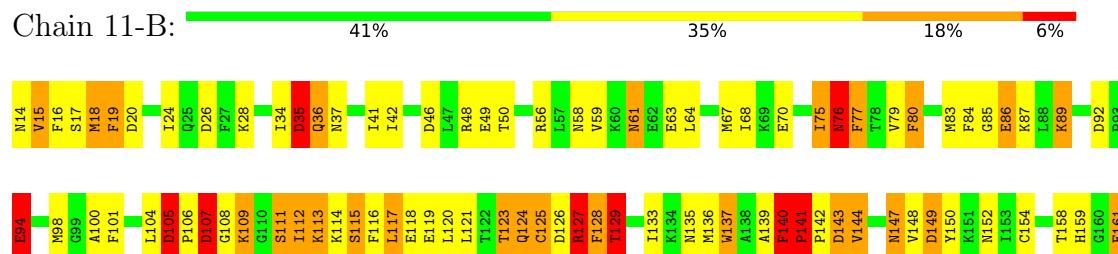
• Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



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



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



D162
K163

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

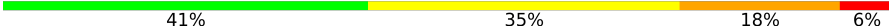
Chain 12-B:  41% 35% 18% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 Q36 N37 I41 L42 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 D92 P93

E94 M98 G99 A100 F101 L104 D105 P106 D107 G108 K109 G110 S111 I112 D113 K114 N115 F116 L117 E118 E119 L120 T123 Q124 C125 D126 R127 F128 T129 I133 K134 E135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 K151 N152 C154 T158 H159 G160 D162

K163

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

Chain 13-B:  41% 35% 18% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 Q36 N37 I41 L42 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 D92 P93

E94 M98 G99 A100 F101 L104 D105 P106 D107 G108 K109 G110 S111 I112 D113 K114 N115 F116 L117 E118 E119 L120 T123 Q124 C125 D126 R127 F128 T129 I133 K134 E135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 K151 N152 C154 T158 H159 G160 D162

K163

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

Chain 14-B:  41% 35% 17% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 Q36 N37 I41 L42 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 D92 P93

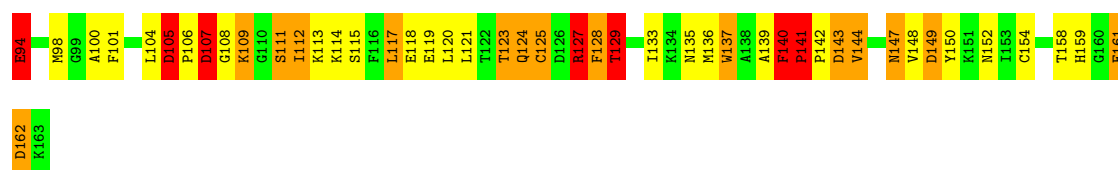
E94 M98 G99 A100 F101 L104 D105 P106 D107 G108 K109 G110 S111 I112 D113 K114 N115 F116 L117 E118 E119 L120 L121 T122 Q124 C125 D126 R127 F128 T129 I133 K134 E135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 K151 N152 C154 T158 H159 G160 E161

D162
K163

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

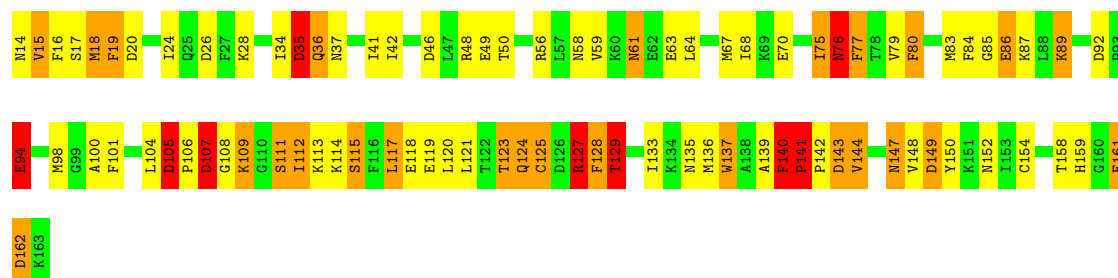
Chain 15-B:  42% 35% 17% 6%

N14 V15 F16 S17 M18 F19 D20 T24 Q25 D26 F27 K28 T34 D35 Q36 N37 I41 L42 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 D92 P93



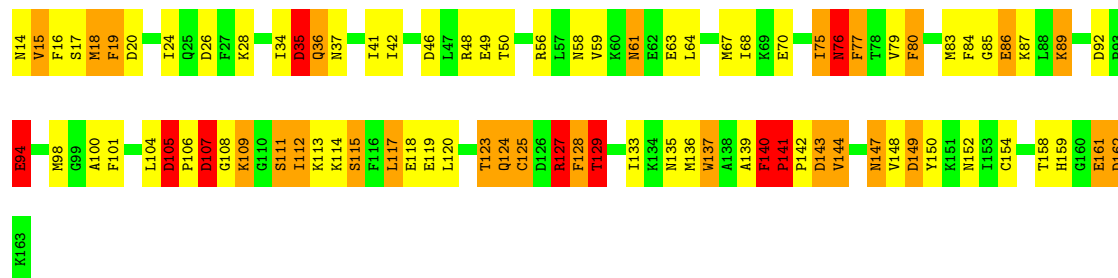
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 16-B: 42% 35% 17% 6%



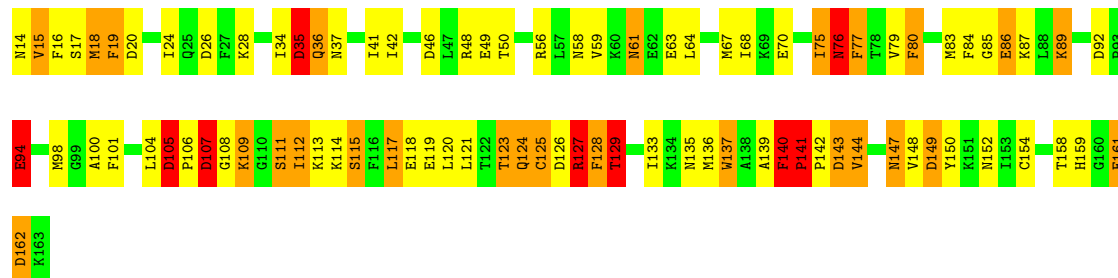
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 17-B: 43% 34% 17% 6%



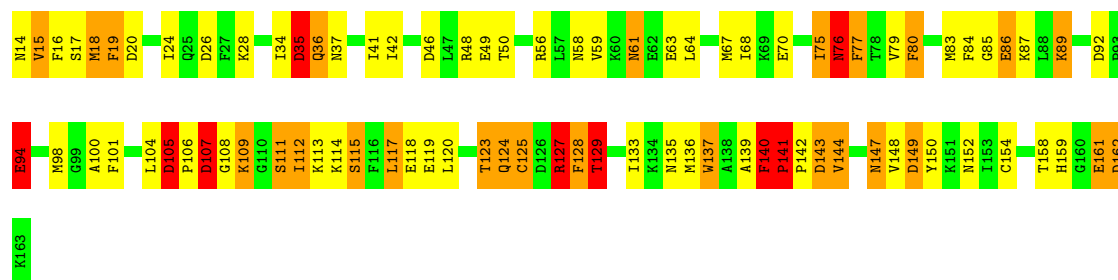
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 18-B: 41% 35% 17% 6%



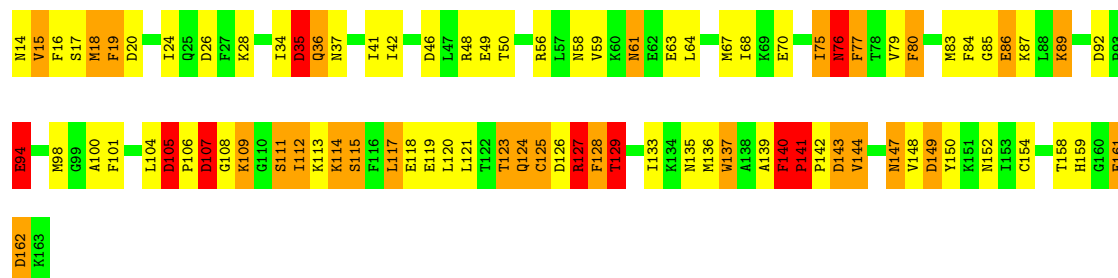
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 19-B: 43% 34% 17% 6%



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

Chain 20-B: 41% 35% 18% 6%



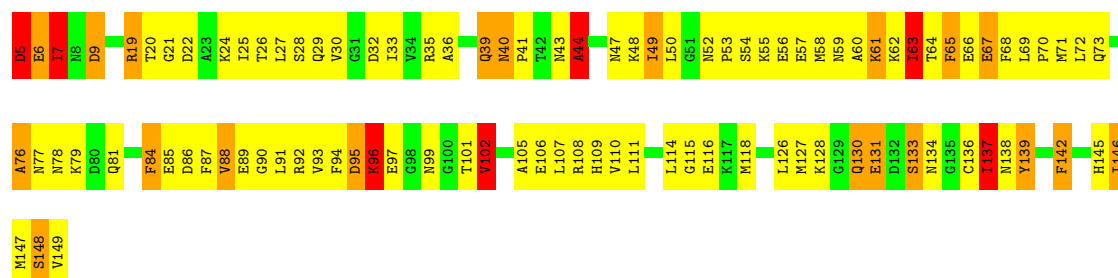
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 1-C: 29% 50% 17% 5%

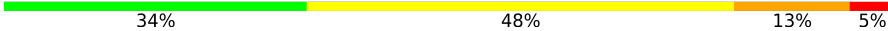


- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 2-C: 31% 50% 14% 5%



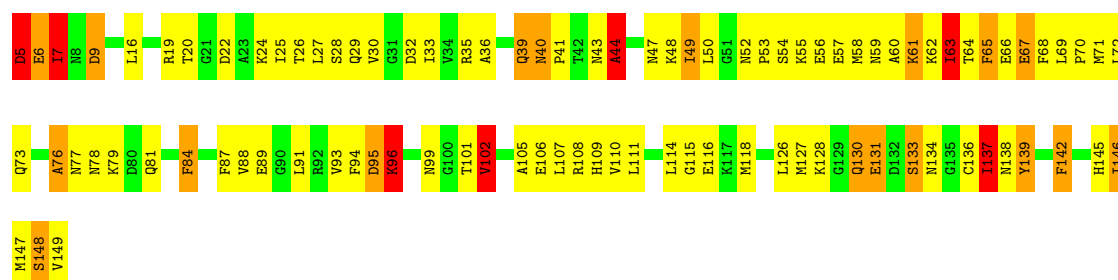
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 3-C: 

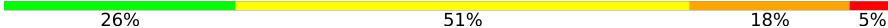


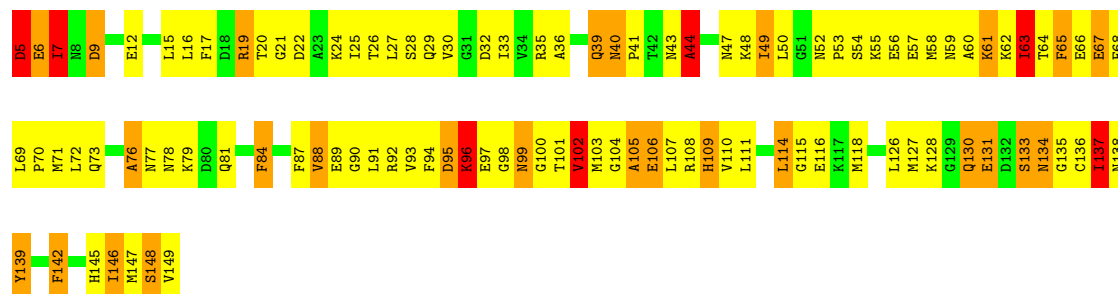
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 4-C: 



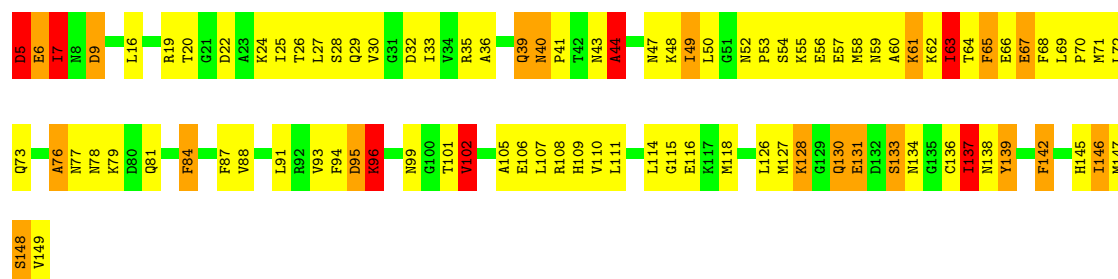
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 5-C: 

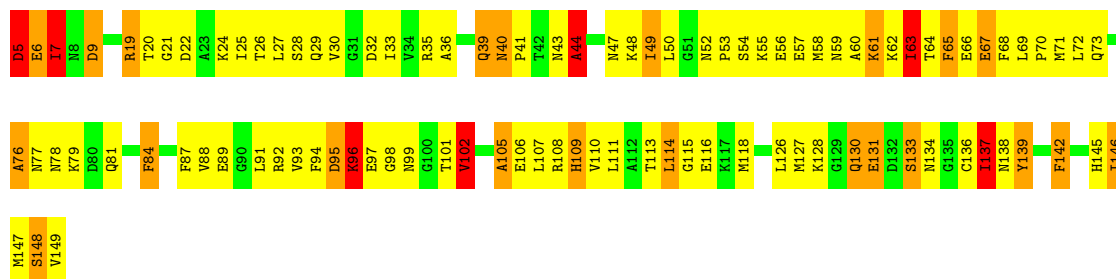


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 6-C: 

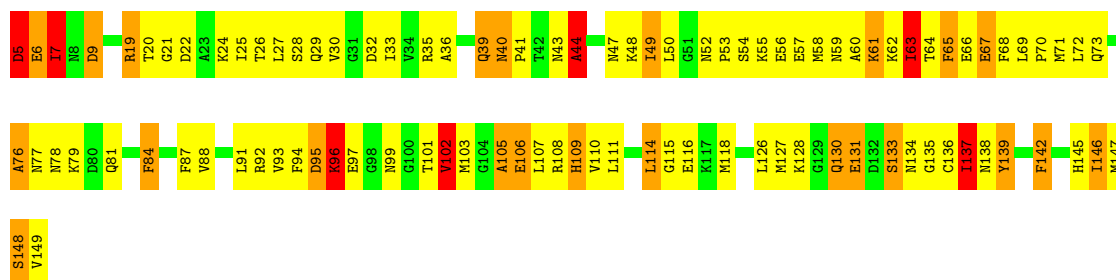


Chain 11-C: 32% 48% 15% 5%



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

Chain 12-C: 32% 47% 16% 5%



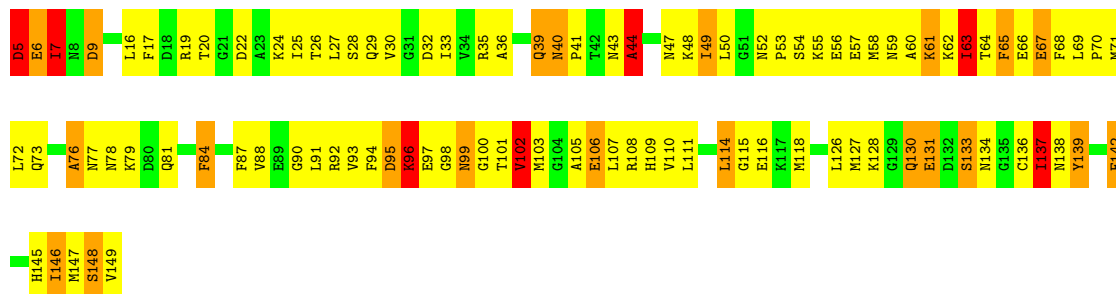
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 13-C: 29% 51% 14% 6%

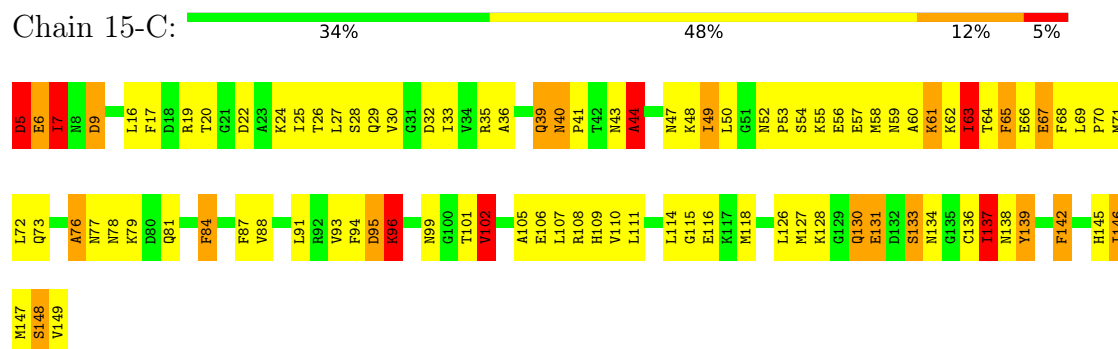


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

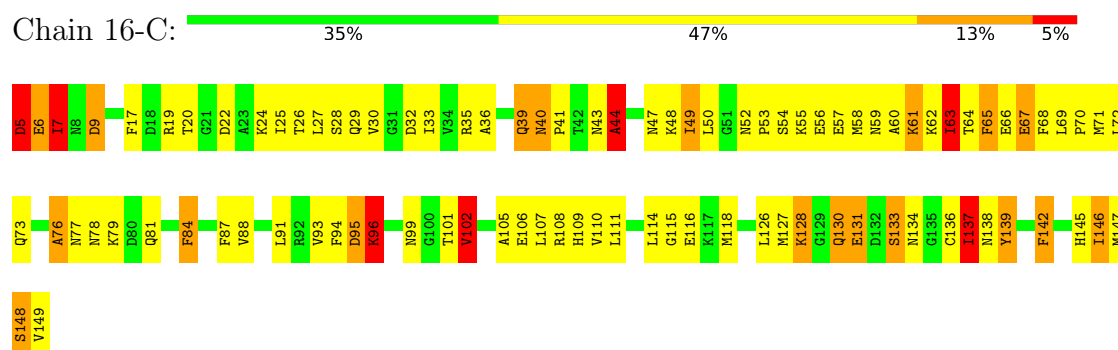
Chain 14-C: 30% 50% 14% 5%



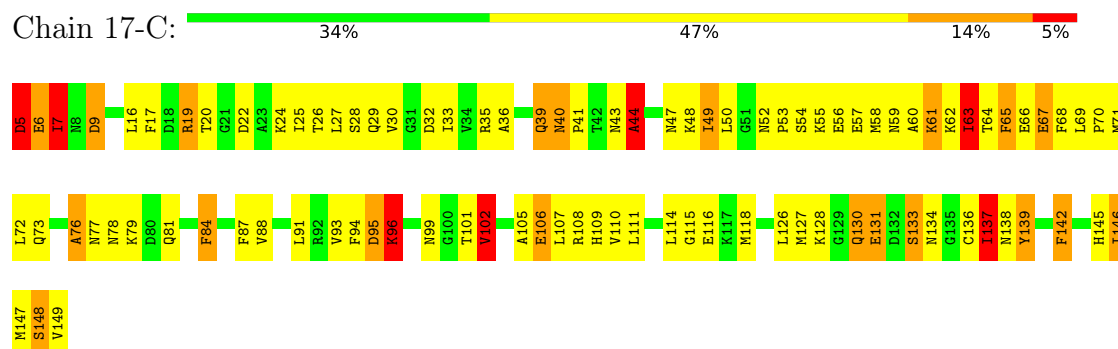
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



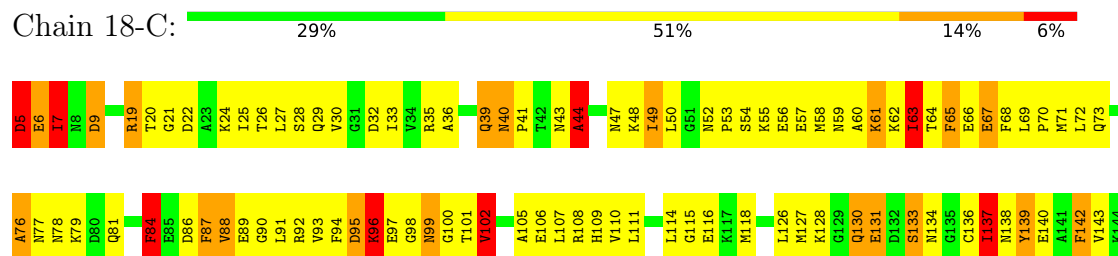
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



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



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



H145
I146
M147
S148
V149

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

Chain 19-C: 34% 48% 12% 5%

D5 E6 I7 N8 D9 R19 T20 G21 D22 A23 K24 I25 T26 L27 S28 Q29 V30 G31 D32 I33 V34 R35 A36 Q39 N40 P41 T42 N43 A44 N47 K48 L49 L50 G51 N52 P53 S54 K55 E56 E57 M58 N59 A60 K61 K62 K63 T64 T65 E66 E67 F68 L69 P70 M71 L72 Q73

A76 N77 K78 N79 D80 Q81 F84 F87 V88 E89 G90 L91 R92 V93 F94 D95 K96 E97 G98 N99 G100 T101 V102 A105 E106 L107 R108 H109 V110 L111 L114 G115 E116 K117 M118 L126 M127 K128 G129 Q130 E131 D132 N134 G135 C136 T137 N138 Y139 F142 H145 I146 M147 S148

V149

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

Chain 20-C: 33% 48% 14% 5%

D5 E6 I7 N8 D9 R19 T20 G21 D22 A23 K24 I25 T26 L27 S28 Q29 V30 G31 D32 I33 V34 R35 A36 Q39 N40 P41 T42 N43 A44 N47 K48 L49 L50 G51 N52 P53 S54 K55 E56 E57 M58 N59 A60 K61 K62 K63 T64 T65 E66 E67 F68 L69 P70 M71 L72 Q73

A76 N77 K78 N79 D80 Q81 F84 F87 V88 E89 G90 L91 R92 V93 F94 D95 K96 E97 G98 N99 G100 T101 V102 A105 E106 L114 G115 E116 K117 M118 L126 M127 K128 G129 Q130 E131 D132 N134 G135 C136 T137 N138 Y139 F142 H145 M147

S148
V149

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

Chain 1-M: 26% 44% 22%

D4 M7 A8 A9 F10 G11 E12 A13 A14 P15 Y16 L17 S20 E21 K22 E23 E24 I25 E26 N29 K30 P31 F32 K35 S36 A37 V38 F39 V40 V41 H42 E45 S46 F47 V48 K49 G50 T51 I52 K55 E56 G57 G58 K59 V60 T61 V62 K63 T64 E65 E68 T69 L70

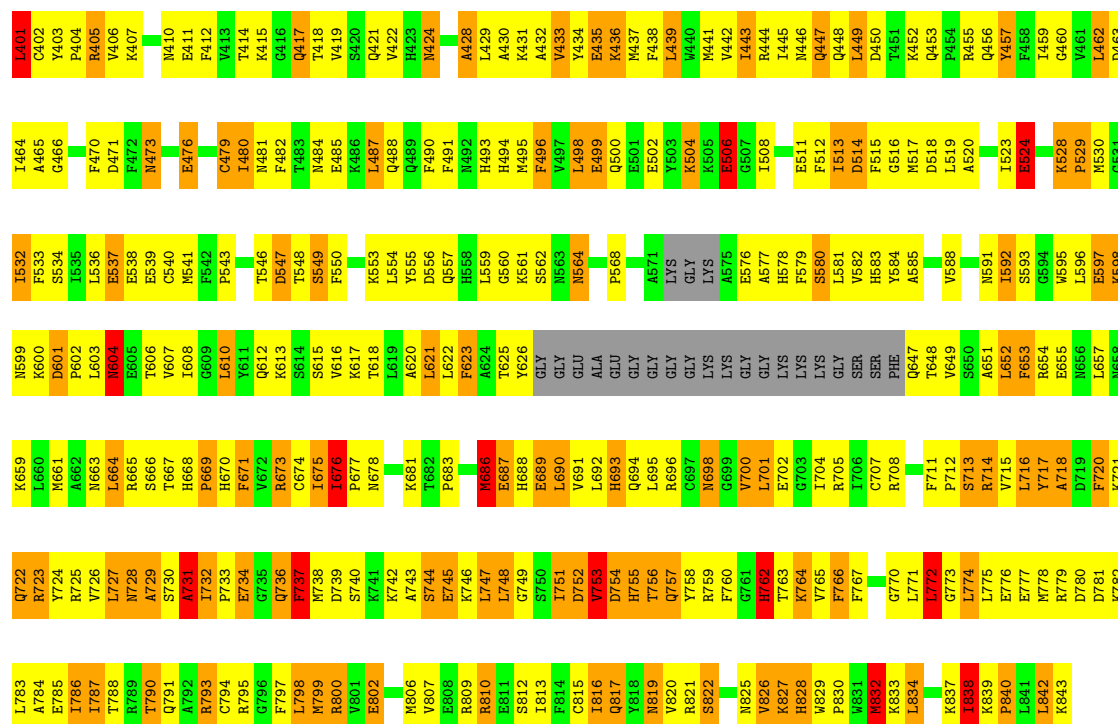
T71 V72 K73 E74 D75 A76 F77 F78 S79 M80 N81 M82 P83 K84 K85 F88 E89 D90 M91 M94 T95 H96 L97 H98 E99 P100 S101 A102 V103 E104 M105 L106 K107 T108 E109 Y110 A111 A112 M113 M114 I115 T116 T117 Y118 Y119 G120 L121 F122 C123 V124 V125 K126 T127 P128 Y129 L130 W131 L132

P133 V134 Y135 N136 P137 K138 V139 V140 L141 Y142 Y143 R144 K145 K146 Q149 E150 A151 P152 P153 H154 T155 F156 S157 T158 S159 D160 M161 A162 Y163 N164 F165 M166 L167 T168 D169 R170 E171 M172 Q173 S174 T175 L176 T177 T178 E179 E180 K185 T186 V187 M188 T189 K190 R191 V192 I193 Q194 Y195 F196

A197 T198 I199 A200 S201 G202 E203 L204 LYS LYS LYS GLU GLU GLN SER GLY MET LYS GLN THR L218 E219 F220 D221 I222 T223 S224 A225 N226 P227 L228 T229 E230 A231 N232 F232 G233 N234 A235 T236 T237 V238 R239 N240 S244 R245 F246 K248 F249 T250 R251 L252 L253 F254 T257 A263

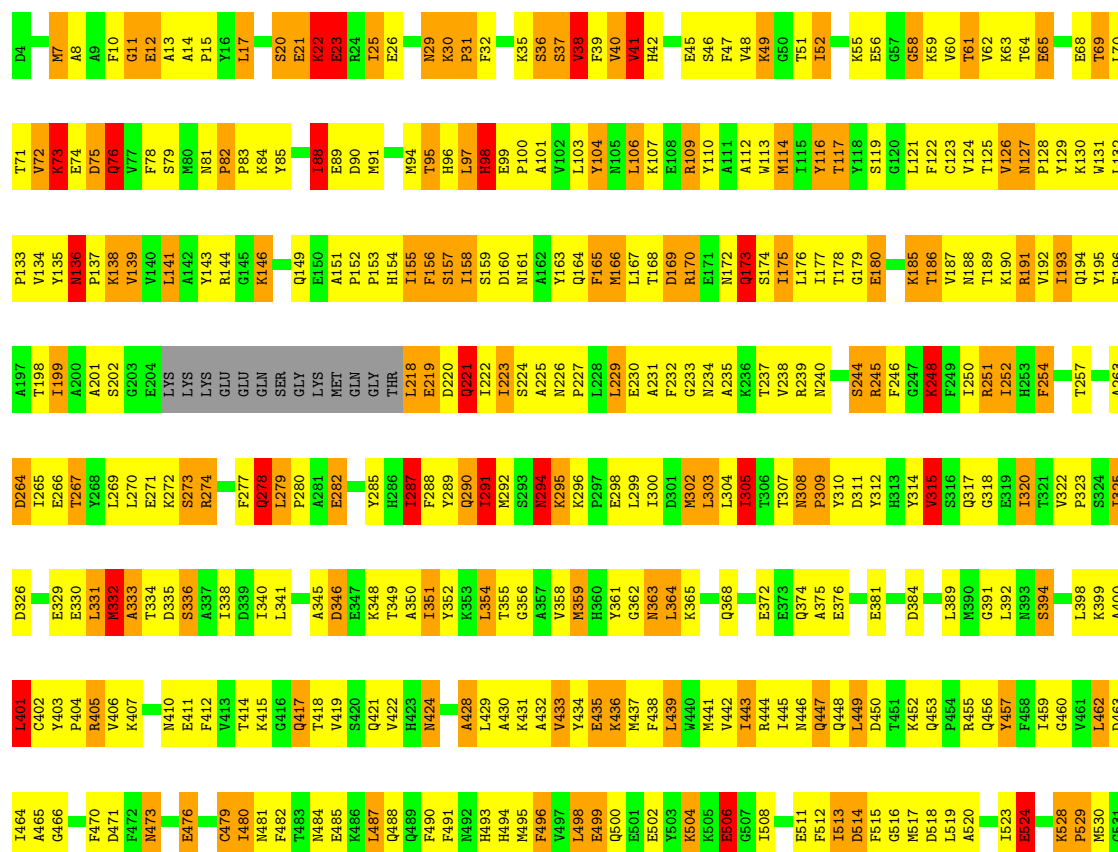
D264 I265 E266 T267 L268 L269 L270 E271 E272 D273 S274 F277 Q278 L279 P280 A281 E282 Y285 H286 T287 F288 Y289 Q290 T291 T292 S293 A294 K295 V296 M297 E298 E299 L299 T300 N301 L302 N303 L304 Q305 E306 T307 N308 A309 Y310 D311 Y312 H313 Y314 V315 S316 Q317 G318 L319 L320 N321 V322 P323 K324 I325

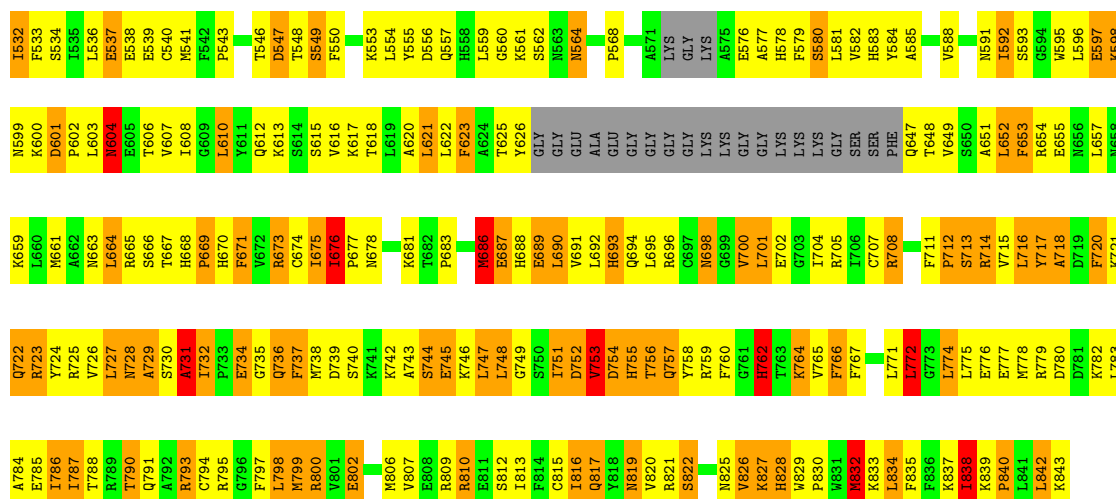
D326 E329 E330 L331 K332 A333 T334 D335 A337 I338 D339 L340 L341 A345 D346 E347 K348 A350 I351 Y352 K353 L354 T355 G356 A357 V358 K359 H360 E361 G362 N363 L364 K365 Q366 E372 E373 Q374 A375 E376 E381 D384 L389 R390 G391 L392 N393 S394 L398 K399 A400



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

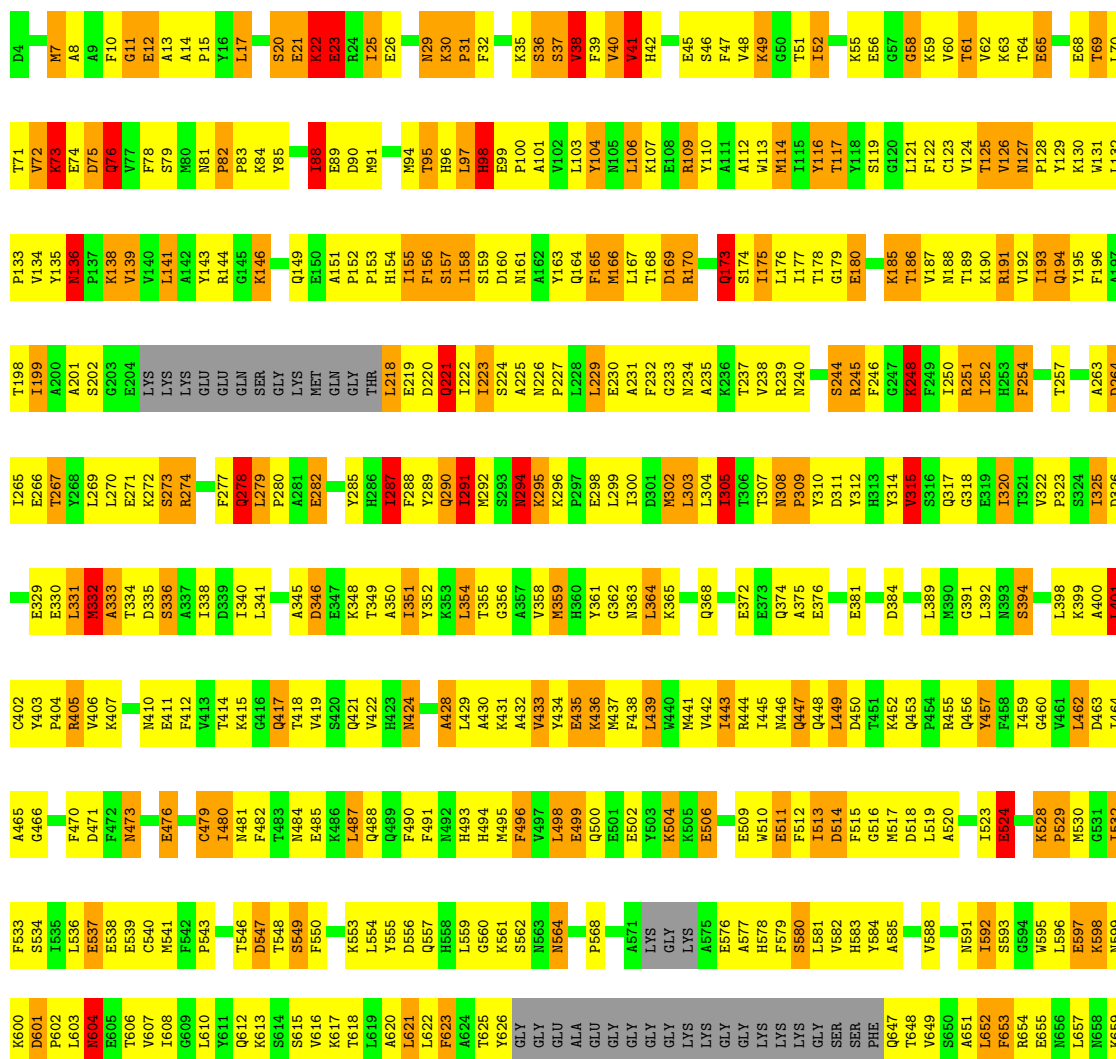
Chain 2-M: 26% 44% 22%





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

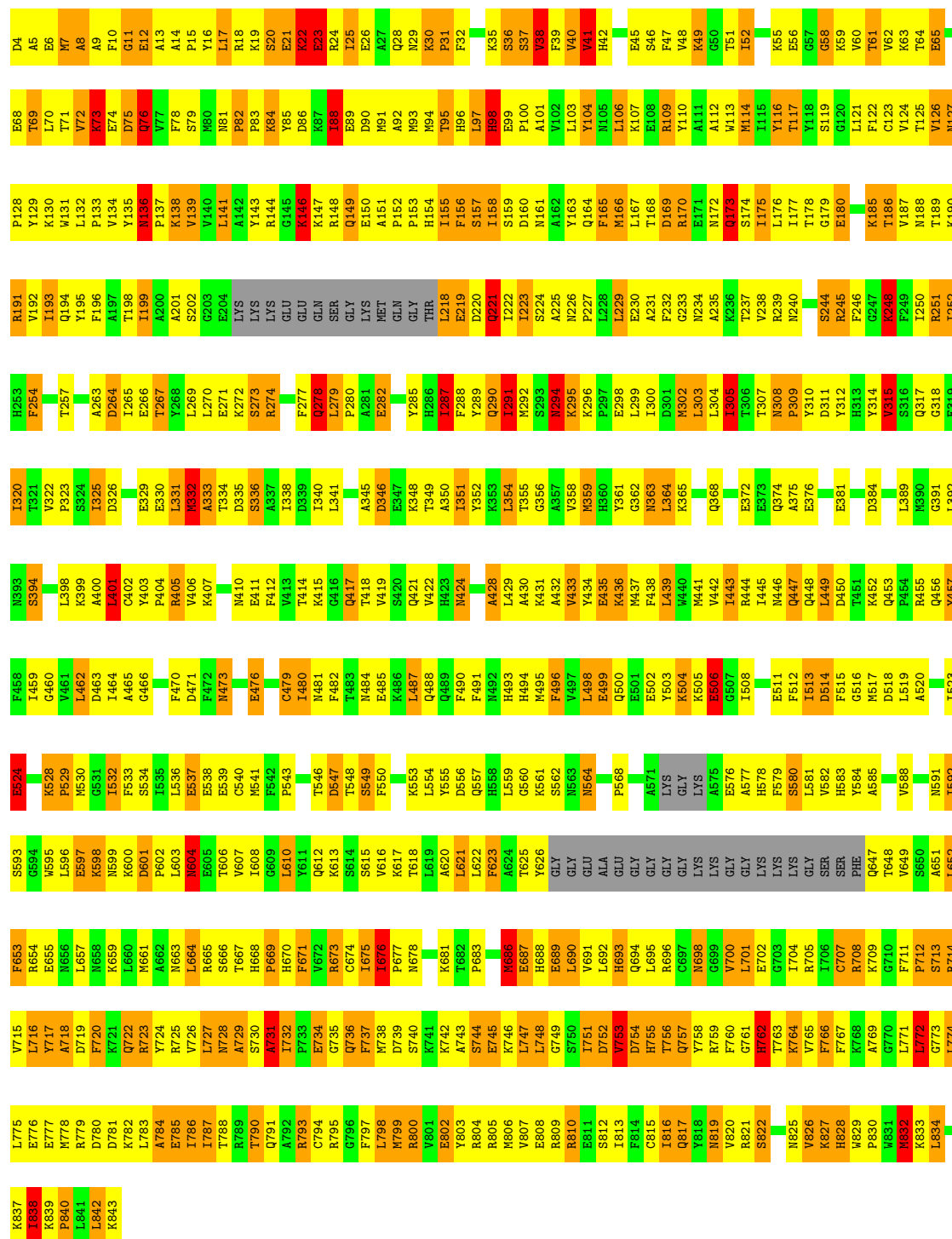
Chain 3-M: 26% 44% 22%





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

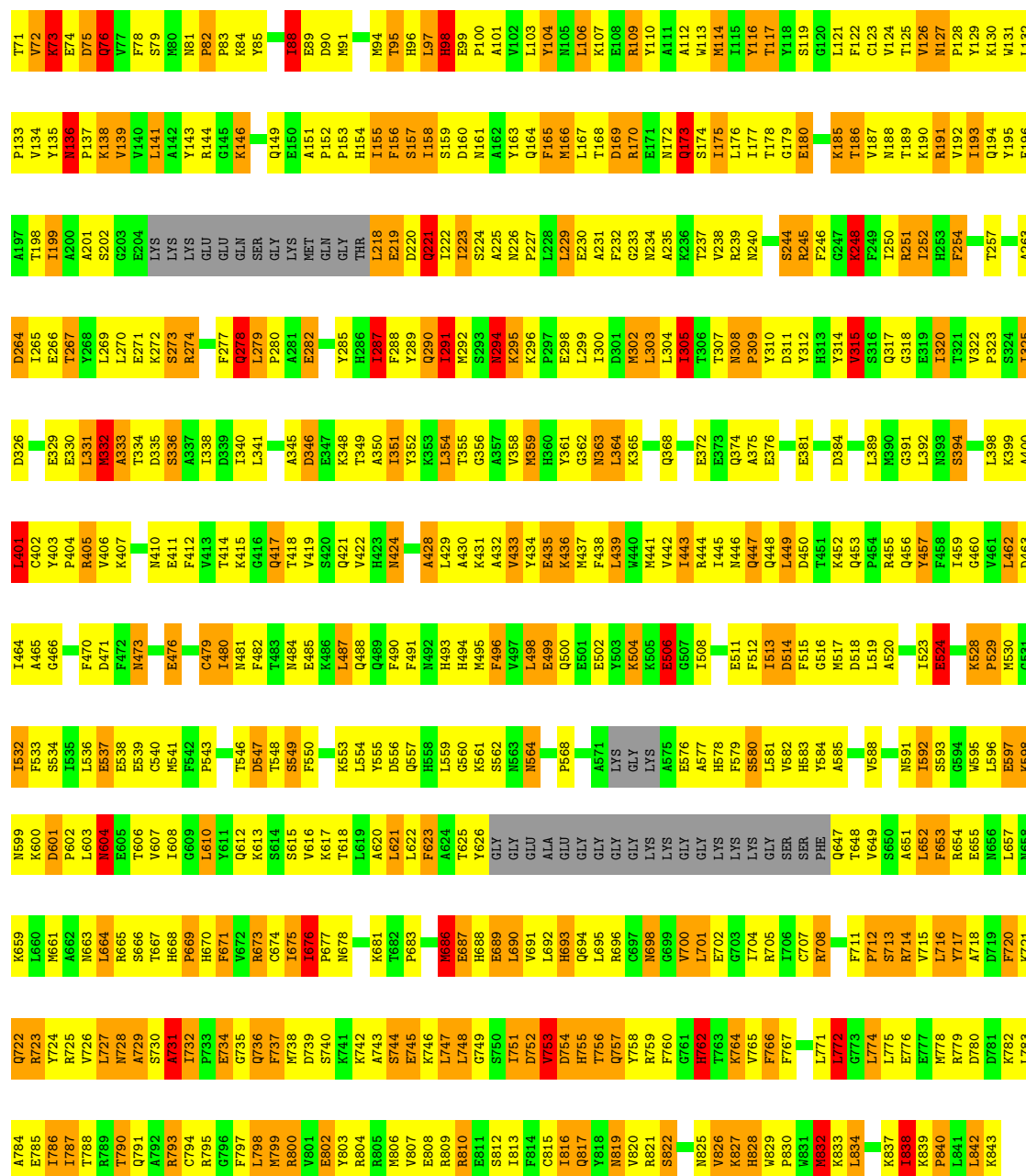
Chain 5-M: 23% 46% 23%



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

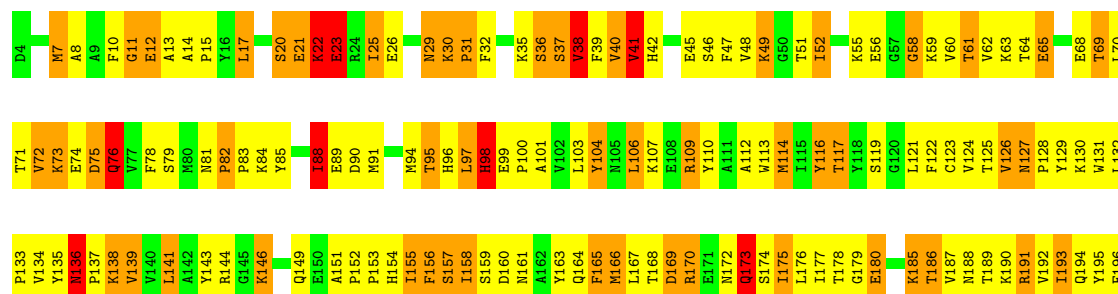
W782	W783	W784	W785	W786	W787	W788	W789	W790	W791	W792	W793	W794	W795	W796	W797	W798	W799	W800	W801	W802	W803	W804	W805	W806	W807	W808	W809	W810	W811	W812	W813	W814	W815	W816	W817	W818	W819	W820	W821	W822	W823	W824	W825	W826	W827	W828	W829	W830	W831	W832	W833	W834	W835	W836	W837	W838	W839	W840	W841	W842	W843	W844	W845	W846	W847	W848	W849	W850	W851	W852	W853	W854	W855	W856	W857	W858	W859	W860	W861	W862	W863	W864	W865	W866	W867	W868	W869	W870	W871	W872	W873	W874	W875	W876	W877	W878	W879	W880	W881	W882	W883	W884	W885	W886	W887	W888	W889	W890	W891	W892	W893	W894	W895	W896	W897	W898	W899	W900	W901	W902	W903	W904	W905	W906	W907	W908	W909	W910	W911	W912	W913	W914	W915	W916	W917	W918	W919	W920	W921	W922	W923	W924	W925	W926	W927	W928	W929	W930	W931	W932	W933	W934	W935	W936	W937	W938	W939	W940	W941	W942	W943	W944	W945	W946	W947	W948	W949	W950	W951	W952	W953	W954	W955	W956	W957	W958	W959	W960	W961	W962	W963	W964	W965	W966	W967	W968	W969	W970	W971	W972	W973	W974	W975	W976	W977	W978	W979	W980	W981	W982	W983	W984	W985	W986	W987	W988	W989	W990	W991	W992	W993	W994	W995	W996	W997	W998	W999	W1000	W1001	W1002	W1003	W1004	W1005	W1006	W1007	W1008	W1009	W1010	W1011	W1012	W1013	W1014	W1015	W1016	W1017	W1018	W1019	W1020	W1021	W1022	W1023	W1024	W1025	W1026	W1027	W1028	W1029	W1030	W1031	W1032	W1033	W1034	W1035	W1036	W1037	W1038	W1039	W1040	W1041	W1042	W1043	W1044	W1045	W1046	W1047	W1048	W1049	W1050	W1051	W1052	W1053	W1054	W1055	W1056	W1057	W1058	W1059	W1060	W1061	W1062	W1063	W1064	W1065	W1066	W1067	W1068	W1069	W1070	W1071	W1072	W1073	W1074	W1075	W1076	W1077	W1078	W1079	W1080	W1081	W1082	W1083	W1084	W1085	W1086	W1087	W1088	W1089</
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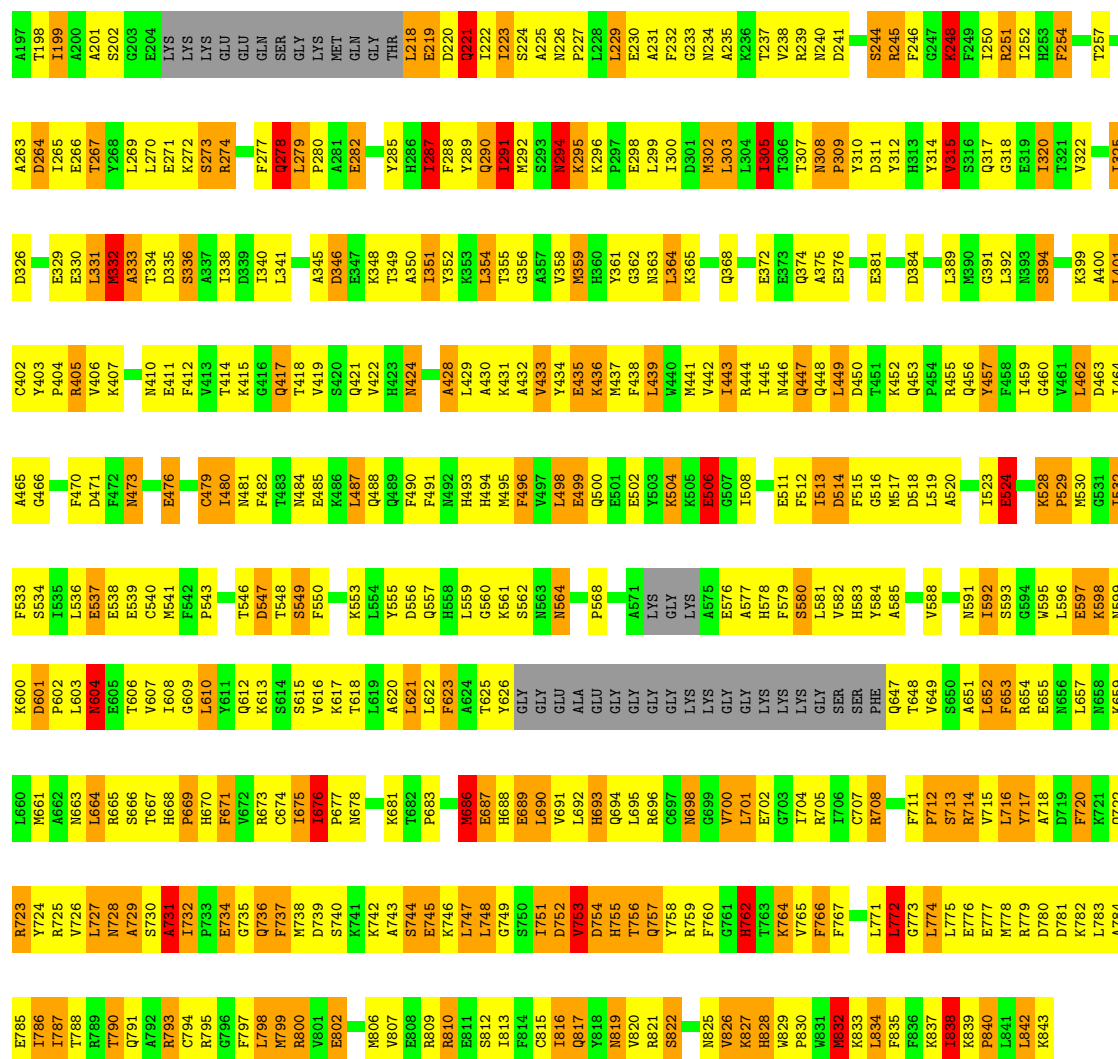
D4		M7		A8	A9	F10	G11	E12	A13	A14	P15	Y16	L17		S20	E21	K22	E23	E24	I25	E26			N29	K30	P31	F32		K35	S36	S37	V38	F39	V40	V41	H42			E45	S46	F47	V48	K49	G50	L51	I52		K55	E56	G57	G58	K59	V60	T61	V62	K63	T64	E65			E68	T69	I70
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● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

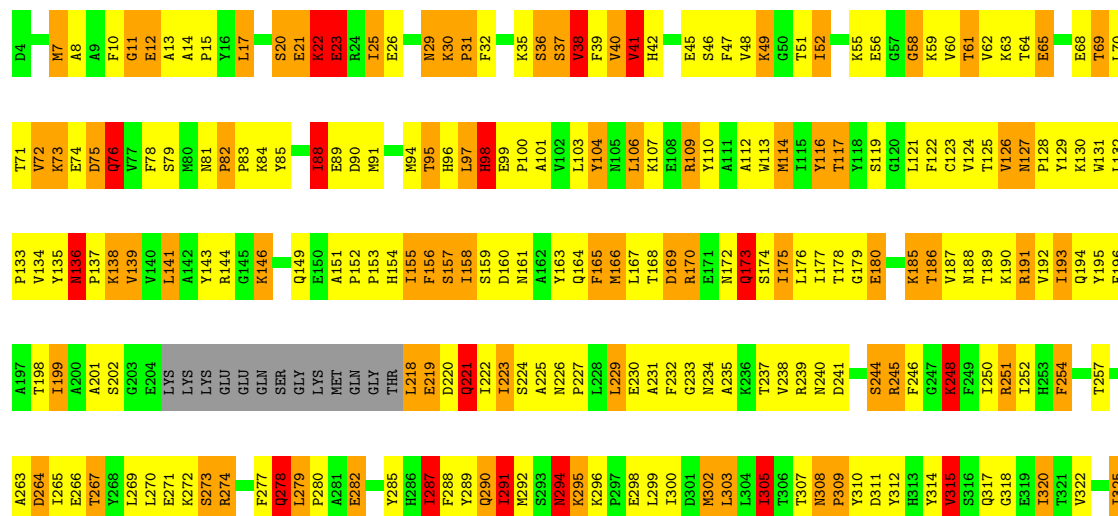
Chain 8-M: 26% 44% 22%

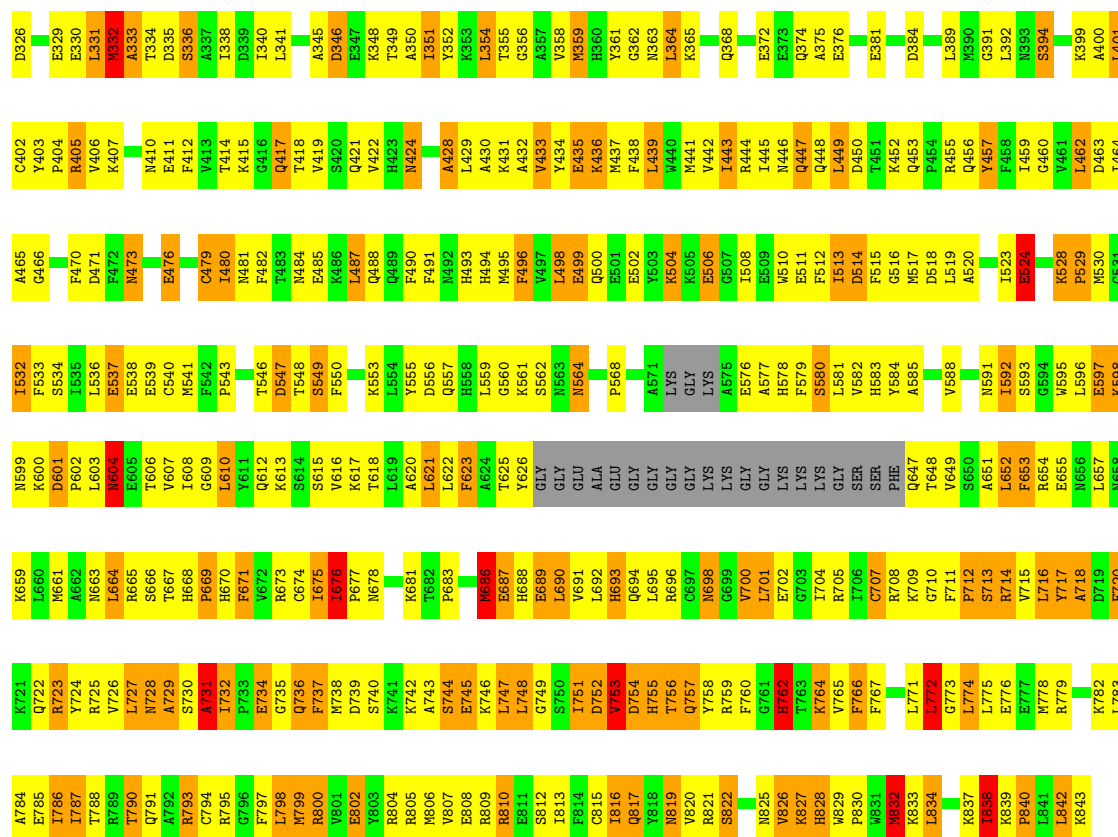




● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

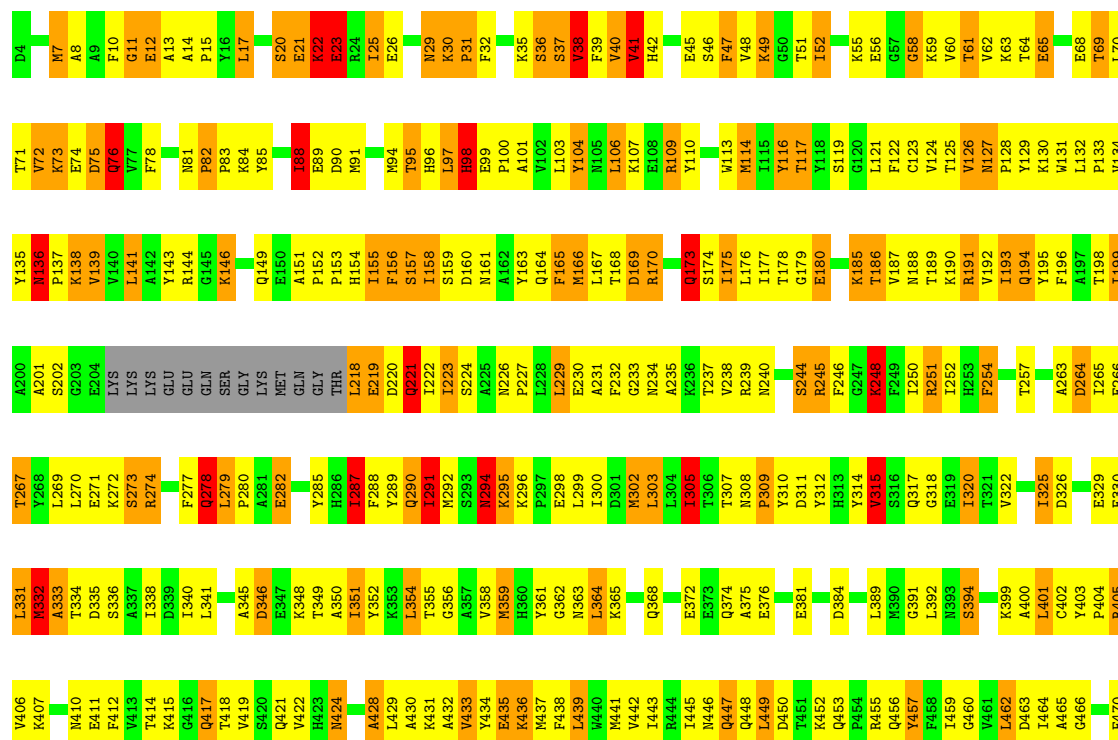
Chain 9-M: 26% 44% 22%

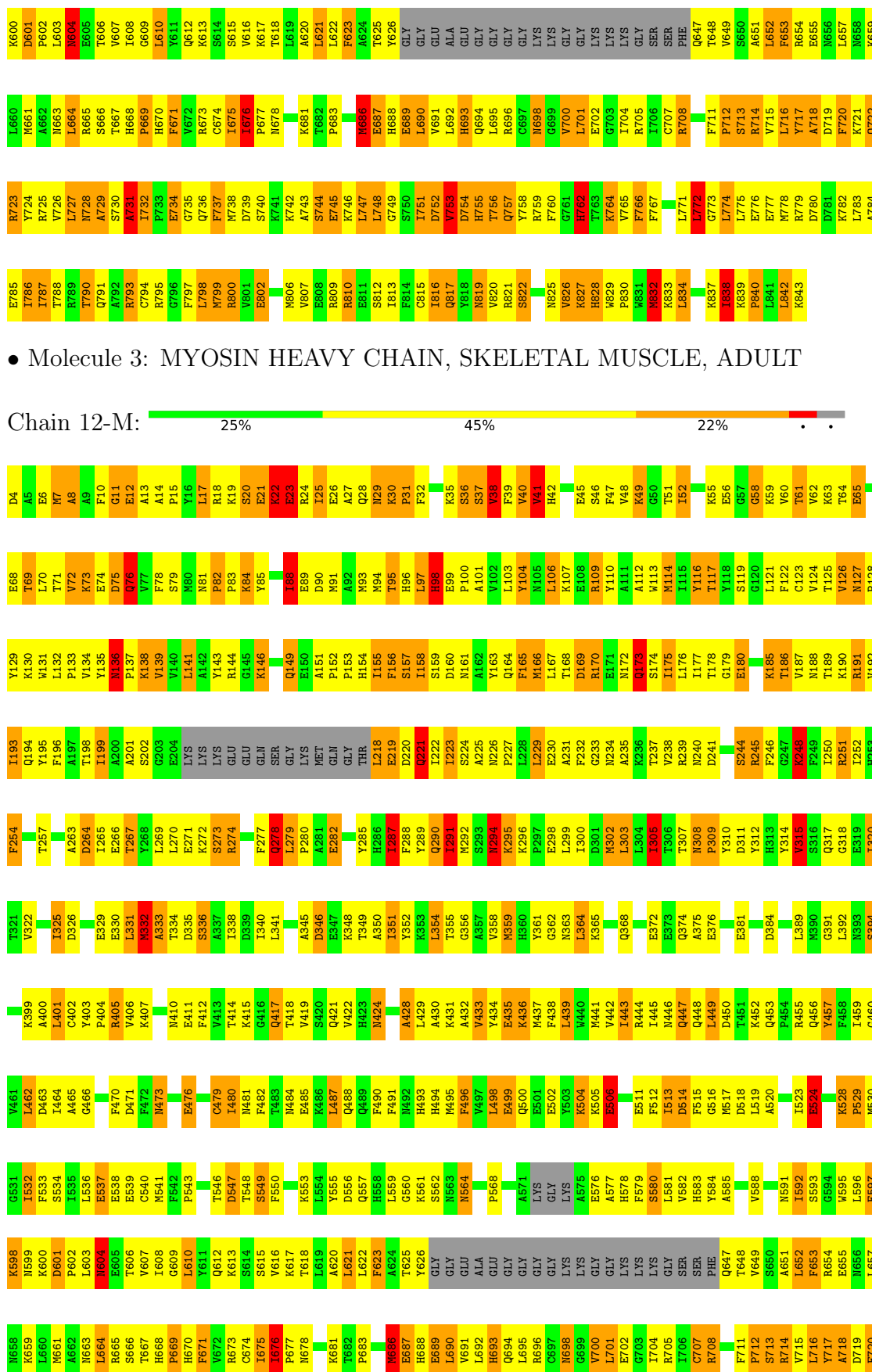


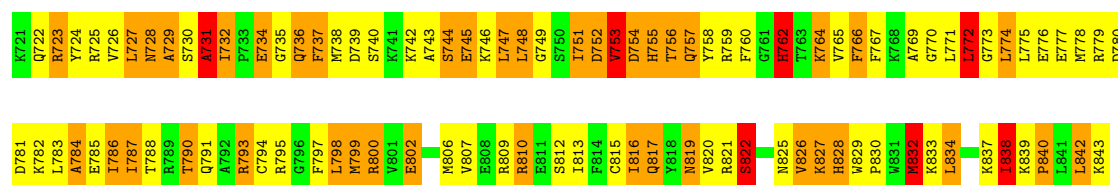


• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 10-M: 27% 44% 22%

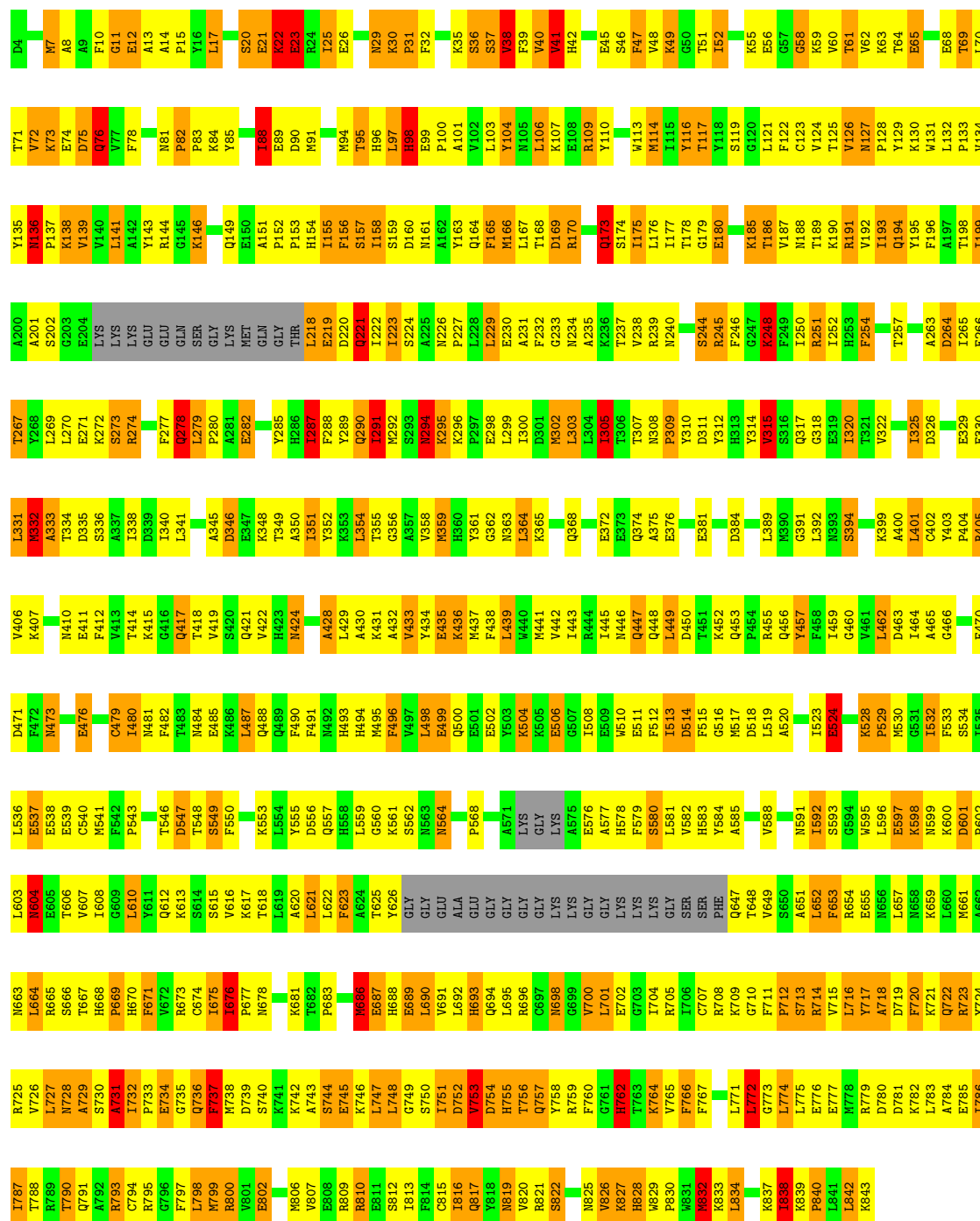






• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

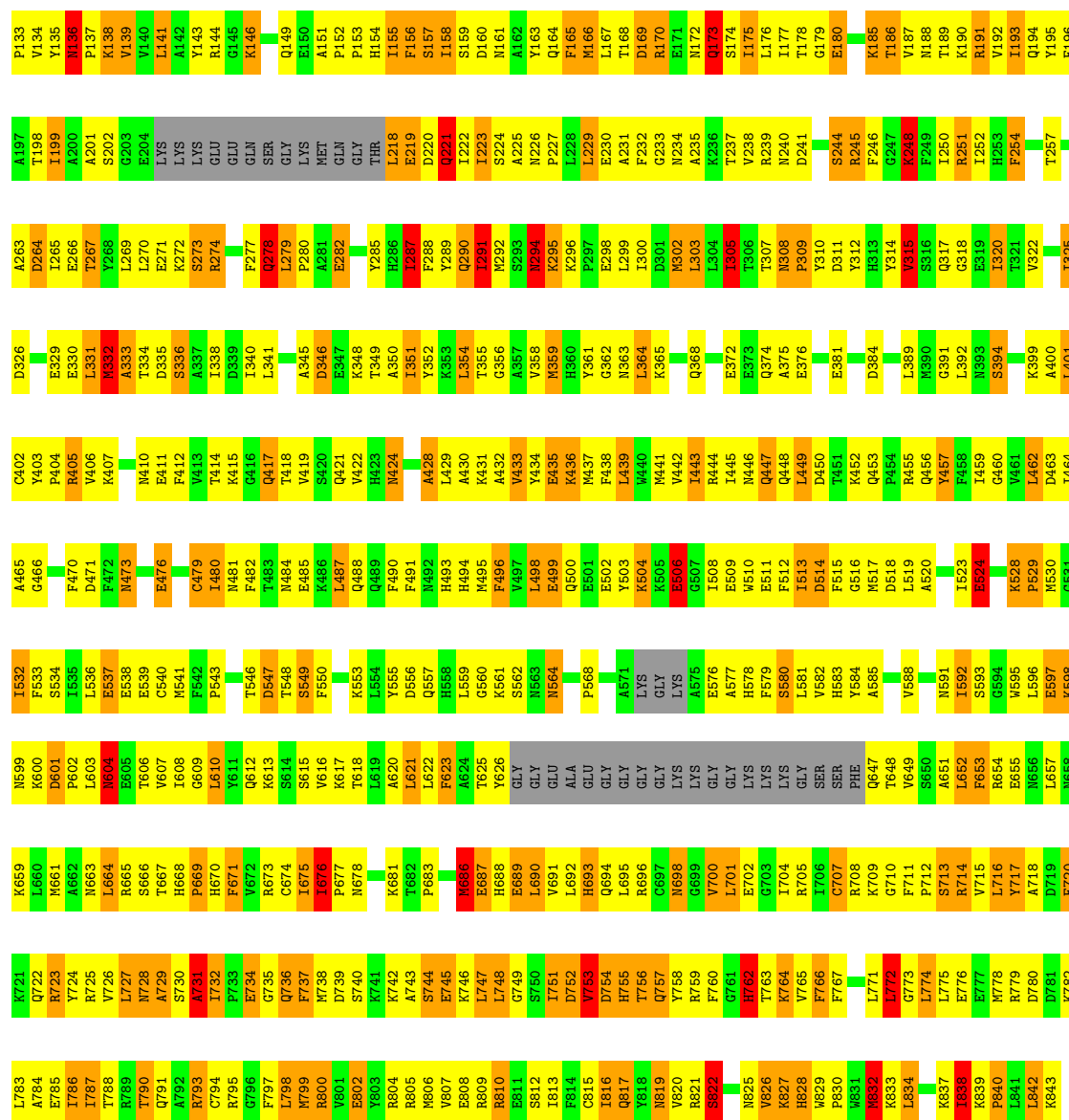
Chain 13-M: 27% 44% 22%



Chain 14-M: 24% 45% 23% . .

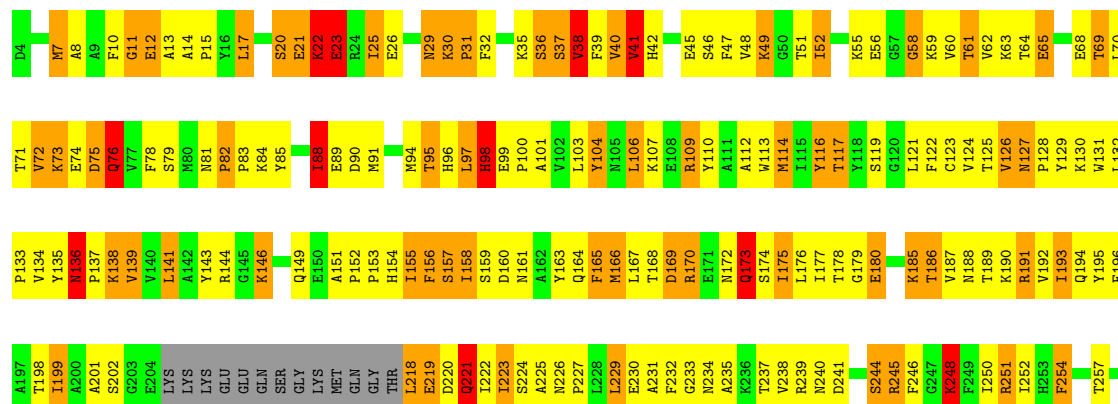


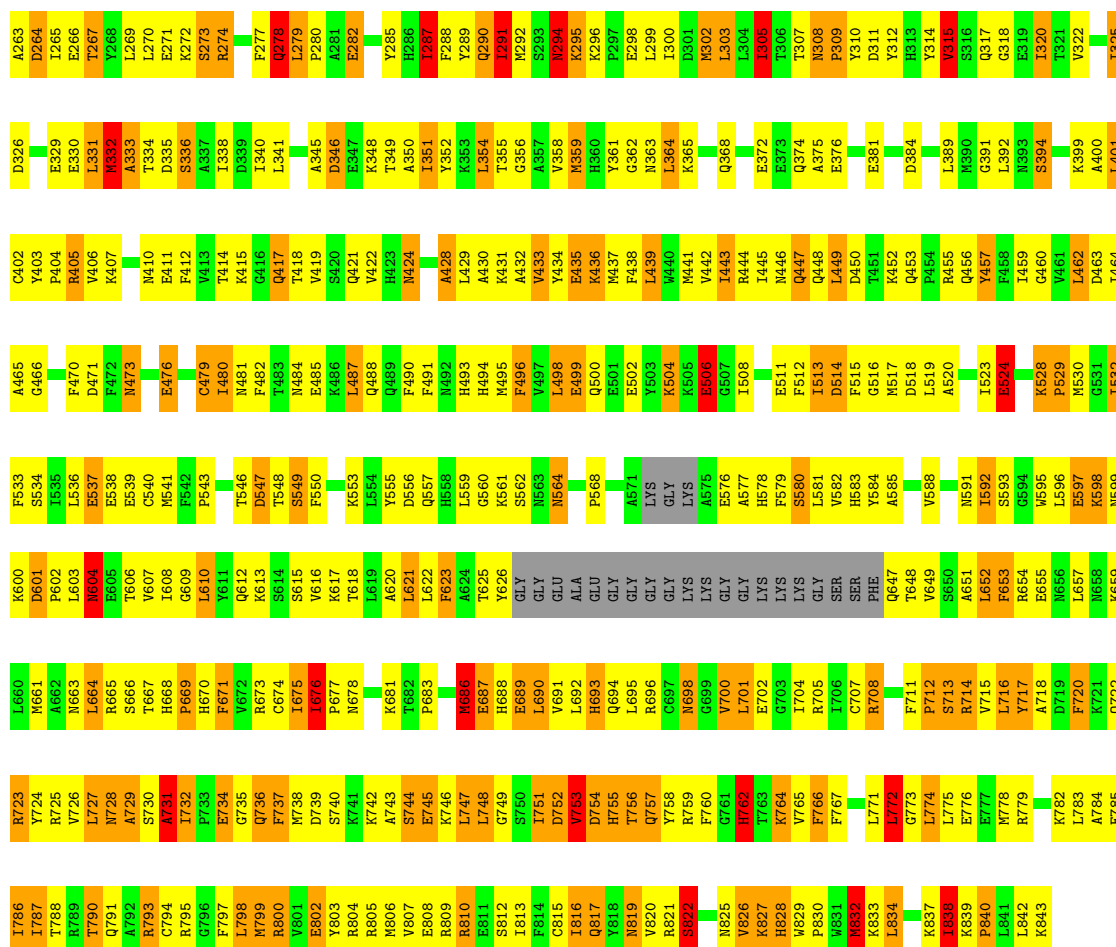
[illegible]



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

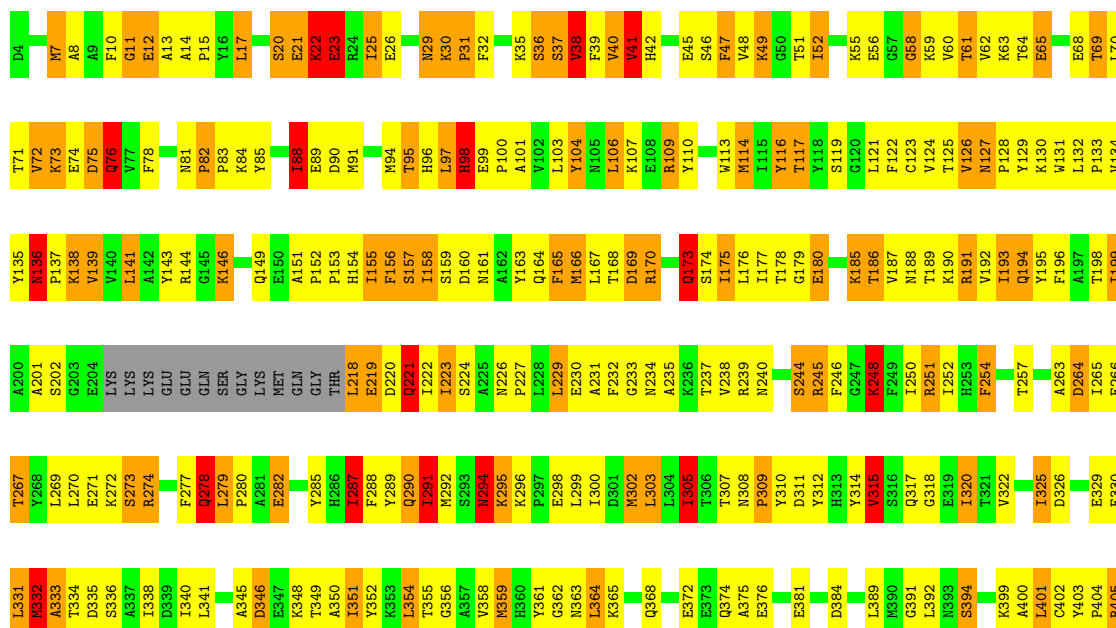
Chain 17-M: 26% 44% 22%

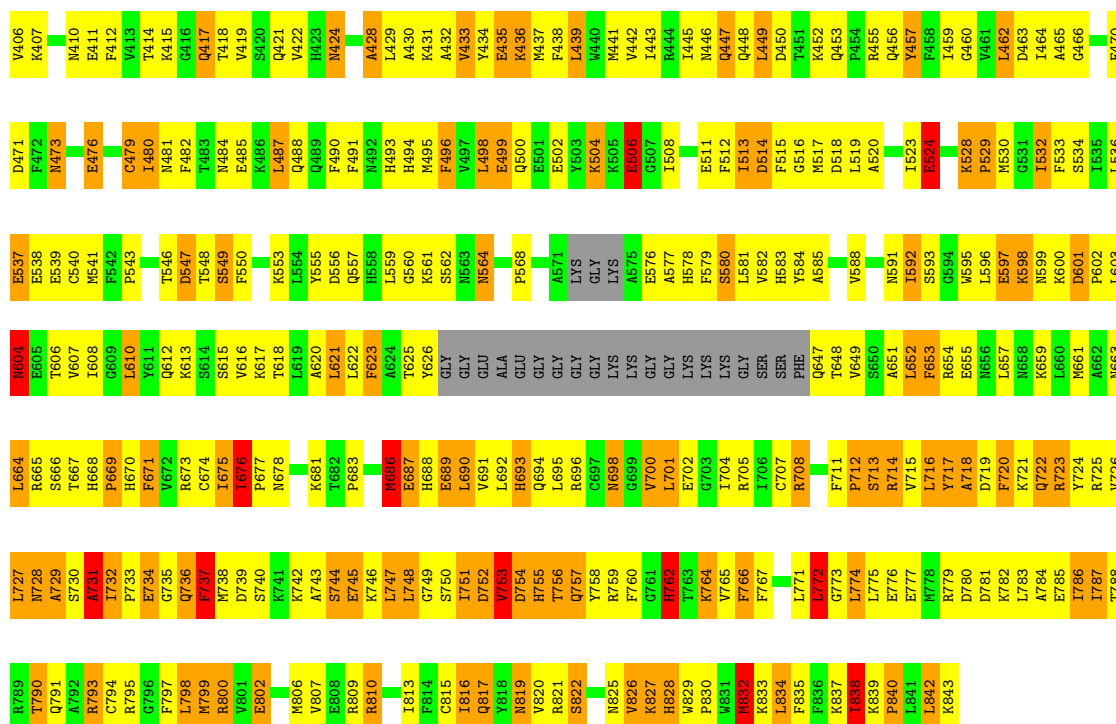




• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

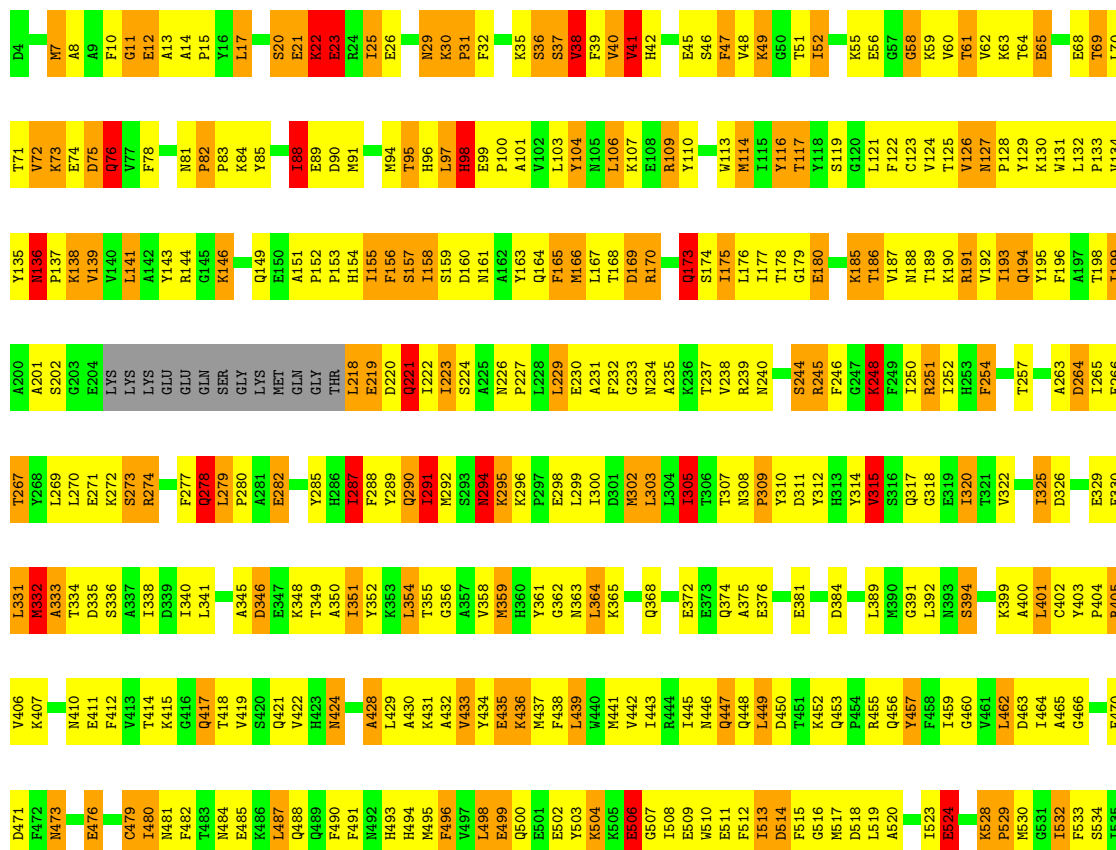
Chain 18-M: 27% 43% 22% • •





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

Chain 19-M: 26% 44% 22%



L660	M661	A662	N663	L664	R665	S666	T667	H668	P669	H670	F671	V672	R673	C674	I675	I676	P677	N678	K681	T682	P683	K686	E687	H688	E689	L690	V691	L692	H693	Q694	L695	R696	G697	N698	G699	V700	L701	E702	G703	I704	R705	I706	C707	R708	F711	P712	S713	R714	V715	L716	R717	A718	D719	F720	K721	Q722		
R723	Y724	R725	V726	L727	N728	A729	S730	A731	P732	P733	E734	G735	Q736	F737	M738	D739	S740	K741	K742	A743	S744	E745	K746	L747	L748	G749	S750	I751	D752	V753	D754	H755	I756	Q757	Y758	R759	F760	G761	R762	I763	K764	V765	F766	F767	L771	L772	G773	L774	L775	E776	E777	M778	R779	D780	D781	K782	L783	A784
E785	I786	I787	T788	R789	T790	Q791	A792	R793	C794	R795	G796	F797	L798	M799	R800	V801	E802	M806	V807	E808	R809	R810	E811	S812	I813	F814	C815	I816	Q817	Y818	M819	V820	R821	S822	N825	V826	K827	H828	W829	P830	W831	R832	K833	L834	F835	F836	K837	I838	K839	P840	L841	L842	K843					

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	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F224 (2k x 2k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	2-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	3-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	4-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	5-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	6-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	7-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	8-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	9-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	10-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	11-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	12-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	13-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	14-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	15-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	16-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	17-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	18-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	19-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
1	20-B	0.80	1/1199 (0.1%)	2.27	55/1617 (3.4%)
2	1-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	2-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	3-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	4-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	5-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	6-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	7-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	8-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	9-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	10-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	11-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	12-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	13-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	14-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	15-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	16-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	17-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	18-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	19-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	20-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
3	1-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	2-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	3-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	4-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	5-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	6-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	7-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	8-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	9-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	10-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	11-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	12-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	13-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	14-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	15-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	16-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	17-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
3	18-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	19-M	2.02	26/6593 (0.4%)	2.31	152/8881 (1.7%)
3	20-M	2.02	26/6594 (0.4%)	2.31	152/8884 (1.7%)
All	All	1.78	600/178649 (0.3%)	2.28	5360/240587 (2.2%)

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
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
1	15-B	0	4
1	16-B	0	4
1	17-B	0	4
1	18-B	0	4
1	19-B	0	4
1	20-B	0	4
3	1-M	0	1
3	2-M	0	1
3	3-M	0	4
3	4-M	0	1
3	5-M	0	4
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
3	13-M	0	1
3	14-M	0	3
3	15-M	0	1
3	16-M	0	1
3	17-M	0	1
3	18-M	0	1
3	19-M	0	1
3	20-M	0	1
All	All	0	108

The worst 5 of 600 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-M	31	PRO	C-N	68.84	2.29	1.33
3	2-M	31	PRO	C-N	68.84	2.29	1.33
3	3-M	31	PRO	C-N	68.84	2.29	1.33
3	4-M	31	PRO	C-N	68.84	2.29	1.33
3	5-M	31	PRO	C-N	68.84	2.29	1.33

The worst 5 of 5360 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-M	29	ASN	O-C-N	-47.04	47.74	123.00
3	2-M	29	ASN	O-C-N	-47.04	47.74	123.00
3	3-M	29	ASN	O-C-N	-47.04	47.74	123.00
3	4-M	29	ASN	O-C-N	-47.04	47.74	123.00
3	5-M	29	ASN	O-C-N	-47.04	47.74	123.00

There are no chirality outliers.

5 of 108 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 [i](#)

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	143	0
1	2-B	1177	0	1134	139	0
1	3-B	1177	0	1133	158	0
1	4-B	1177	0	1134	136	0
1	5-B	1177	0	1134	163	0
1	6-B	1177	0	1134	144	0
1	7-B	1177	0	1134	165	0
1	8-B	1177	0	1132	129	0
1	9-B	1177	0	1134	136	0
1	10-B	1177	0	1134	136	0
1	11-B	1177	0	1134	142	0
1	12-B	1177	0	1134	139	0
1	13-B	1177	0	1134	140	0
1	14-B	1177	0	1134	136	0
1	15-B	1177	0	1134	134	0
1	16-B	1177	0	1134	137	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	17-B	1177	0	1134	132	0
1	18-B	1177	0	1134	140	0
1	19-B	1177	0	1134	134	0
1	20-B	1177	0	1134	140	0
2	1-C	1126	0	1068	411	0
2	2-C	1126	0	1078	254	0
2	3-C	1126	0	1084	133	0
2	4-C	1126	0	1083	143	0
2	5-C	1126	0	1078	431	0
2	6-C	1126	0	1084	95	0
2	7-C	1126	0	1083	193	0
2	8-C	1126	0	1081	124	0
2	9-C	1126	0	1084	89	0
2	10-C	1126	0	1084	90	0
2	11-C	1126	0	1080	217	0
2	12-C	1126	0	1079	205	0
2	13-C	1126	0	1070	245	0
2	14-C	1126	0	1077	284	0
2	15-C	1126	0	1084	90	0
2	16-C	1126	0	1084	86	0
2	17-C	1126	0	1084	102	0
2	18-C	1126	0	1070	244	0
2	19-C	1126	0	1079	114	0
2	20-C	1126	0	1084	206	0
3	1-M	6455	0	6360	1258	0
3	2-M	6455	0	6376	1043	0
3	3-M	6455	0	6376	896	0
3	4-M	6455	0	6380	943	0
3	5-M	6455	0	6346	1513	0
3	6-M	6455	0	6381	895	0
3	7-M	6455	0	6376	961	0
3	8-M	6455	0	6382	874	0
3	9-M	6455	0	6382	877	0
3	10-M	6455	0	6381	875	0
3	11-M	6455	0	6376	964	0
3	12-M	6455	0	6363	1174	0
3	13-M	6455	0	6368	1076	0
3	14-M	6455	0	6345	1385	0
3	15-M	6455	0	6382	881	0
3	16-M	6455	0	6380	894	0
3	17-M	6455	0	6384	857	0
3	18-M	6455	0	6369	1047	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	19-M	6455	0	6377	926	0
3	20-M	6455	0	6381	975	0
All	All	175160	0	171740	22414	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 65.

The worst 5 of 22414 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)
2:C:139:TYR:CE2	3:M:725:ARG:HG3	1.24	1.71
3:M:508:ILE:HD13	3:M:766:PHE:CE2	1.26	1.70
2:C:93:VAL:CG1	3:M:724:TYR:CD1	1.76	1.65
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%)	120 (81%)	16 (11%)	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%)	120 (81%)	16 (11%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	9-B	148/150 (99%)	119 (80%)	17 (12%)	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
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
1	15-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	16-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	17-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	9
1	18-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	19-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	20-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%)	110 (77%)	21 (15%)	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
2	15-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	16-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	17-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	18-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	19-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	20-C	143/145 (99%)	110 (77%)	21 (15%)	12 (8%)	0	9
3	1-M	786/840 (94%)	649 (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%)	648 (82%)	116 (15%)	22 (3%)	4	24
3	4-M	788/840 (94%)	651 (83%)	114 (14%)	23 (3%)	3	23
3	5-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	6-M	786/840 (94%)	648 (82%)	114 (14%)	24 (3%)	3	22
3	7-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	8-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	9-M	786/840 (94%)	648 (82%)	115 (15%)	23 (3%)	3	23
3	10-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	11-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	12-M	788/840 (94%)	650 (82%)	114 (14%)	24 (3%)	3	23
3	13-M	786/840 (94%)	648 (82%)	116 (15%)	22 (3%)	4	24
3	14-M	788/840 (94%)	647 (82%)	116 (15%)	25 (3%)	3	21
3	15-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	16-M	786/840 (94%)	648 (82%)	114 (14%)	24 (3%)	3	22
3	17-M	788/840 (94%)	650 (82%)	114 (14%)	24 (3%)	3	23
3	18-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	19-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	20-M	788/840 (94%)	650 (82%)	114 (14%)	24 (3%)	3	23
All	All	21558/22700 (95%)	17584 (82%)	3032 (14%)	942 (4%)	3	17

5 of 942 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
1	15-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	16-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	17-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	18-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	19-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	20-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
2	6-C	120/122 (98%)	107 (89%)	13 (11%)	6	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
2	15-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	16-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	17-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	18-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	19-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	20-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
3	15-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	16-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	17-M	693/724 (96%)	498 (72%)	195 (28%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	18-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	19-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	20-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
All	All	18820/19520 (96%)	14420 (77%)	4400 (23%)	2	5

5 of 4400 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	17-M	708	ARG
3	18-M	175	ILE
3	17-M	702	GLU
3	19-M	754	ASP
2	8-C	28	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 645 such sidechains are listed below:

Mol	Chain	Res	Type
3	15-M	447	GLN
3	18-M	578	HIS
3	15-M	736	GLN
3	15-M	424	ASN
3	17-M	149	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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	19-M	9
3	3-M	8
3	4-M	8
3	6-M	8
3	7-M	8
3	9-M	8
3	10-M	8
3	13-M	8
3	14-M	8
3	15-M	8
3	16-M	8
3	1-M	7
3	2-M	7
3	5-M	7
3	8-M	7
3	11-M	7
3	12-M	7
3	18-M	7
3	20-M	7
3	17-M	6

The worst 5 of 151 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.