



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:45 PM UTC

PDB ID : 2W4A / pdb_00002w4a
EMDB ID : EMD-1561
Title : ISOMETRICALLY CONTRACTING INSECT ASYNCHRONOUS FLIGHT MUSCLE
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 : 2008-11-24
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

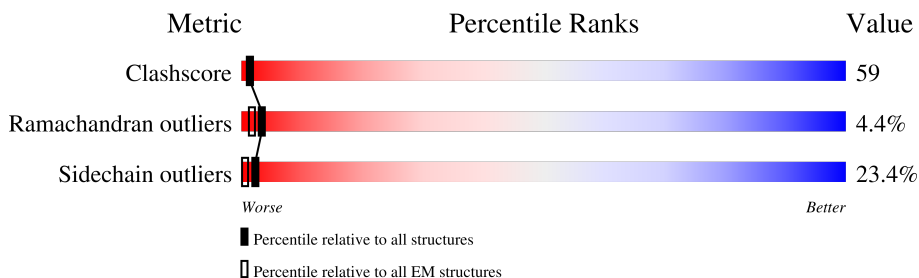
1 Overall quality at a glance i

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	42% 35% 17% 6%
1	13-B	150	41% 36% 17% 6%
1	14-B	150	41% 35% 17% 6%
1	15-B	150	41% 35% 17% 6%
1	16-B	150	41% 36% 17% 6%
1	17-B	150	40% 36% 18% 6%

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Mol	Chain	Length	Quality of chain			
1	18-B	150	42%	35%	17%	6%
1	19-B	150	41%	34%	19%	6%
1	2-B	150	42%	35%	17%	6%
1	20-B	150	41%	35%	17%	6%
1	21-B	150	42%	33%	19%	6%
1	22-B	150	41%	36%	17%	6%
1	3-B	150	41%	34%	19%	6%
1	4-B	150	41%	35%	17%	6%
1	5-B	150	41%	33%	19%	7%
1	6-B	150	41%	35%	18%	6%
1	7-B	150	41%	35%	18%	6%
1	8-B	150	42%	33%	19%	6%
1	9-B	150	42%	35%	17%	6%
2	1-C	145	35%	47%	13%	5%
2	10-C	145	35%	47%	13%	5%
2	11-C	145	34%	48%	12%	5%
2	12-C	145	30%	49%	16%	5%
2	13-C	145	35%	47%	13%	5%
2	14-C	145	30%	51%	14%	5%
2	15-C	145	35%	47%	13%	5%
2	16-C	145	36%	46%	13%	5%
2	17-C	145	36%	46%	13%	5%
2	18-C	145	34%	48%	13%	5%
2	19-C	145	32%	48%	14%	5%
2	2-C	145	33%	49%	13%	5%

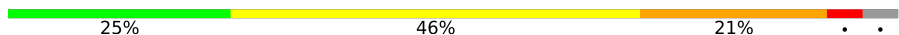
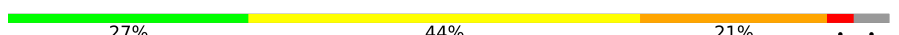
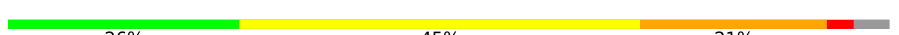
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Mol	Chain	Length	Quality of chain			
2	20-C	145	35%	47%	13%	5%
2	21-C	145	32%	49%	14%	5%
2	22-C	145	36%	47%	12%	5%
2	3-C	145	34%	47%	14%	5%
2	4-C	145	35%	47%	13%	5%
2	5-C	145	30%	52%	13%	5%
2	6-C	145	35%	47%	13%	5%
2	7-C	145	35%	47%	13%	5%
2	8-C	145	34%	48%	12%	5%
2	9-C	145	35%	47%	13%	5%
3	1-M	840	27%	44%	22%	• •
3	10-M	840	26%	45%	21%	• •
3	11-M	840	26%	45%	22%	• •
3	12-M	840	26%	45%	22%	• •
3	13-M	840	26%	45%	22%	• •
3	14-M	840	26%	45%	22%	• •
3	15-M	840	26%	44%	22%	• •
3	16-M	840	26%	44%	22%	• •
3	17-M	840	26%	44%	22%	• •
3	18-M	840	26%	45%	21%	• •
3	19-M	840	26%	44%	22%	• •
3	2-M	840	26%	44%	21%	• •
3	20-M	840	26%	44%	22%	• •
3	21-M	840	26%	45%	22%	• •
3	22-M	840	26%	45%	22%	• •

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Mol	Chain	Length	Quality of chain	
3	3-M	840		
3	4-M	840		
3	5-M	840		
3	6-M	840		
3	7-M	840		
3	8-M	840		
3	9-M	840		

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 192676 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
			Total	C	N	O	S		
1	1-B	150	1177	748	187	234	8	0	0
1	2-B	150	1177	748	187	234	8	0	0
1	3-B	150	1177	748	187	234	8	0	0
1	4-B	150	1177	748	187	234	8	0	0
1	5-B	150	1177	748	187	234	8	0	0
1	6-B	150	1177	748	187	234	8	0	0
1	7-B	150	1177	748	187	234	8	0	0
1	8-B	150	1177	748	187	234	8	0	0
1	9-B	150	1177	748	187	234	8	0	0
1	10-B	150	1177	748	187	234	8	0	0
1	11-B	150	1177	748	187	234	8	0	0
1	12-B	150	1177	748	187	234	8	0	0
1	13-B	150	1177	748	187	234	8	0	0
1	14-B	150	1177	748	187	234	8	0	0
1	15-B	150	1177	748	187	234	8	0	0
1	16-B	150	1177	748	187	234	8	0	0

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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		
1	21-B	150	Total	C	N	O	S	0	0
			1177	748	187	234	8		
1	22-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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	12-C	145	1126	701	188	230	7	0	0
2	13-C	145	1126	701	188	230	7	0	0
2	14-C	145	1126	701	188	230	7	0	0
2	15-C	145	1126	701	188	230	7	0	0
2	16-C	145	1126	701	188	230	7	0	0
2	17-C	145	1126	701	188	230	7	0	0
2	18-C	145	1126	701	188	230	7	0	0
2	19-C	145	1126	701	188	230	7	0	0
2	20-C	145	1126	701	188	230	7	0	0
2	21-C	145	1126	701	188	230	7	0	0
2	22-C	145	1126	701	188	230	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	1-M	804	6455	4140	1089	1190	36	0	0
3	2-M	804	6455	4140	1089	1190	36	0	0
3	3-M	804	6455	4140	1089	1190	36	0	0
3	4-M	804	6455	4140	1089	1190	36	0	0
3	5-M	804	6455	4140	1089	1190	36	0	0
3	6-M	804	6455	4140	1089	1190	36	0	0
3	7-M	804	6455	4140	1089	1190	36	0	0
3	8-M	804	6455	4140	1089	1190	36	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
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
3	15-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	16-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	17-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	18-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	19-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	20-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	21-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0
3	22-M	804	Total 6455	C 4140	N 1089	O 1190	S 36	0	0

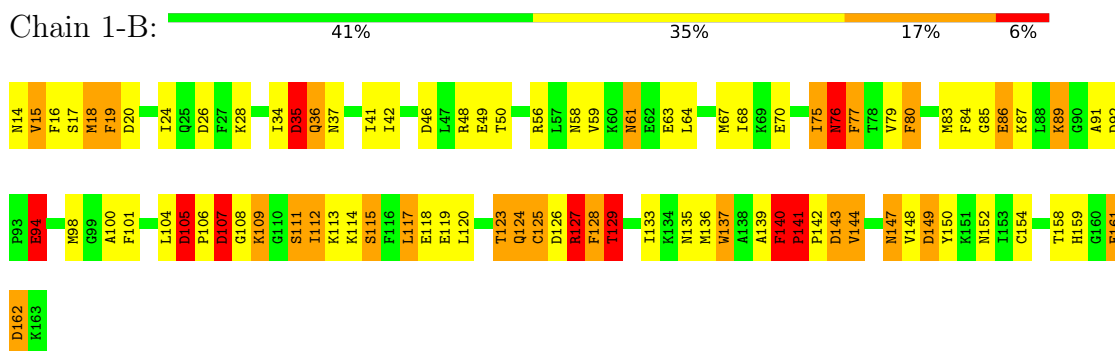
There is a discrepancy between the modelled and reference sequences:

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

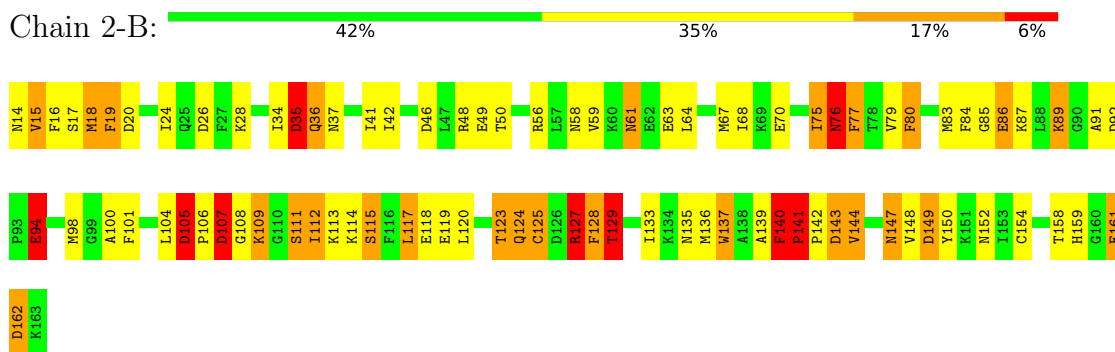
3 Residue-property plots

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.

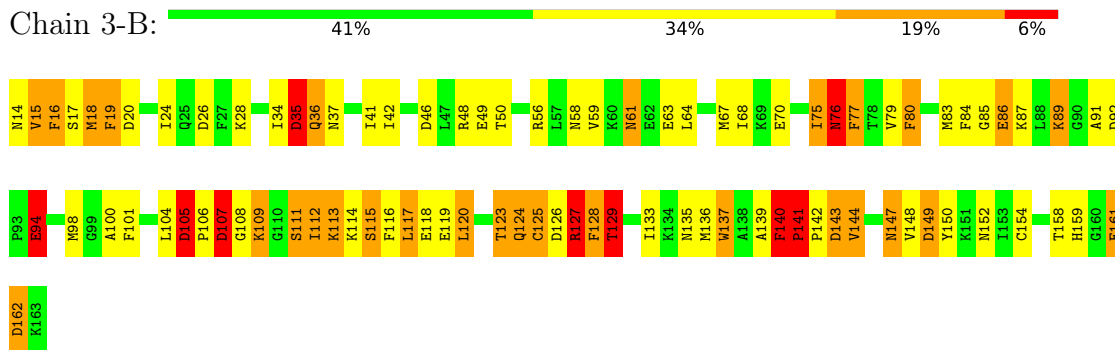
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



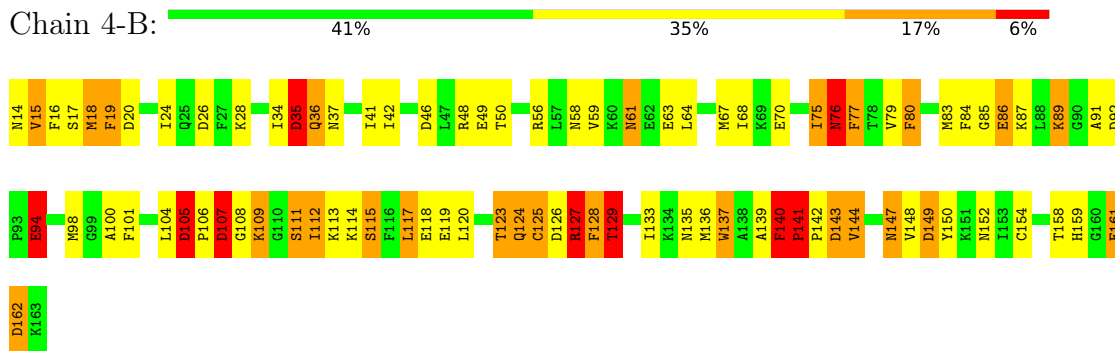
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



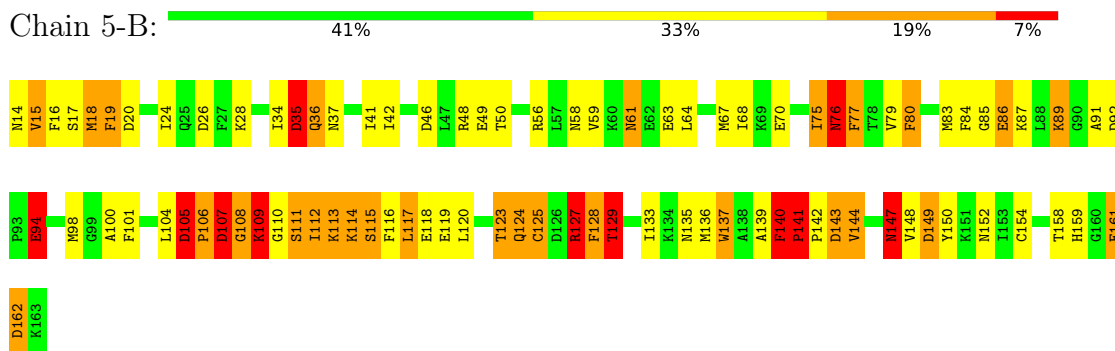
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



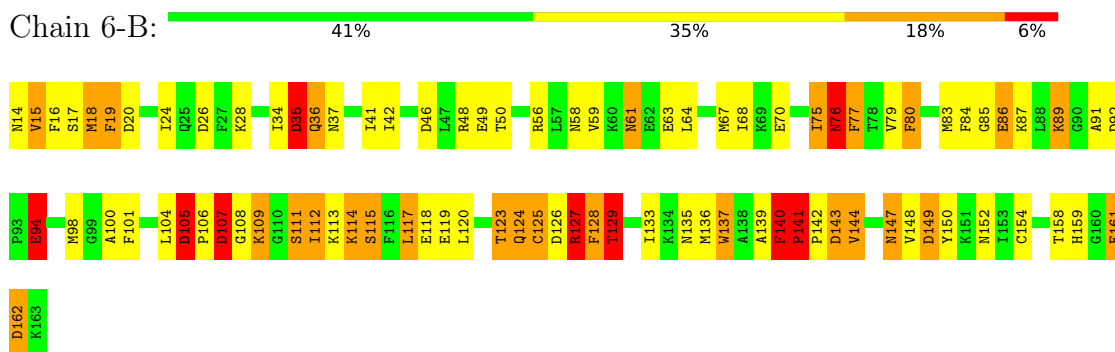
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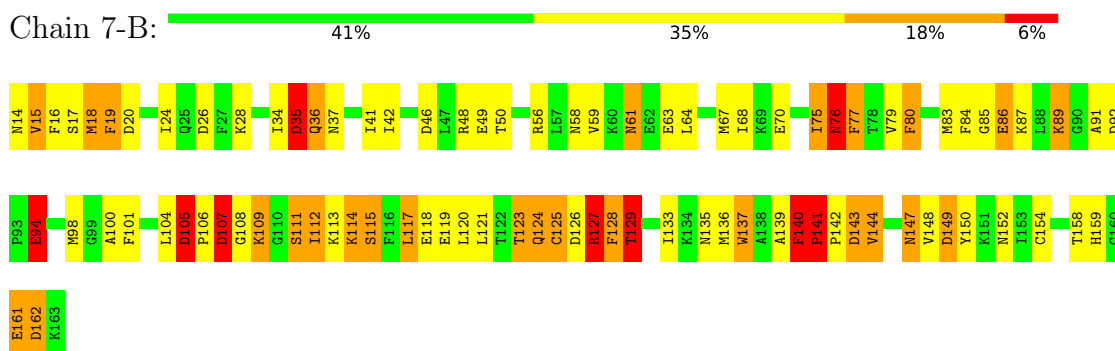
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



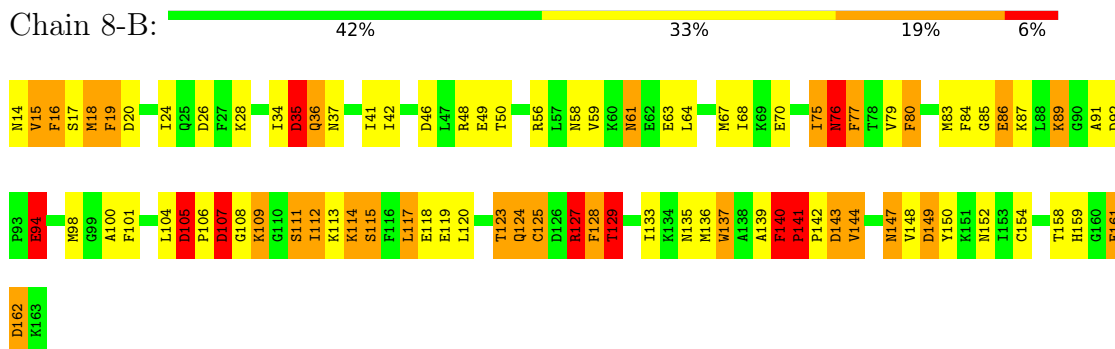
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



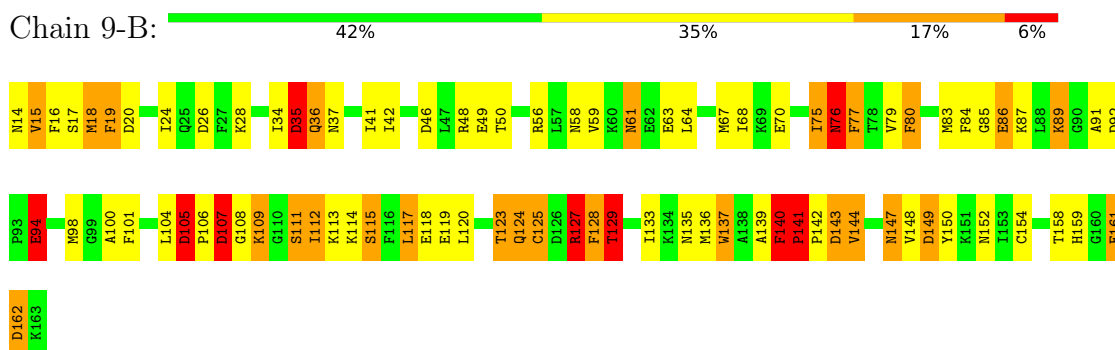
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



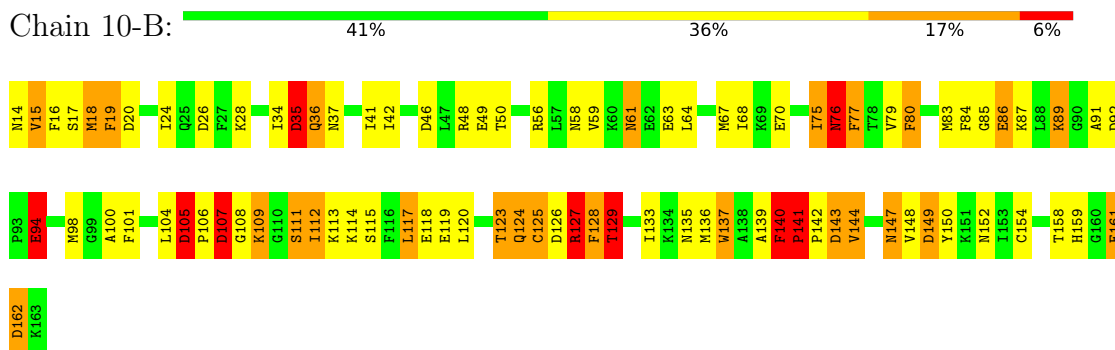
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



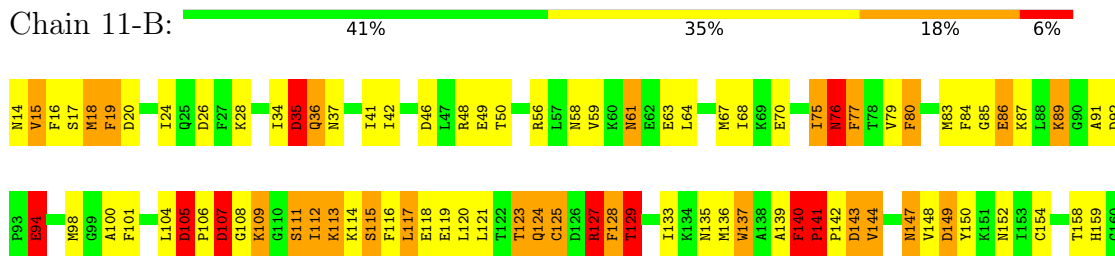
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



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



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



E161
D162
K163

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

Chain 12-B:  42% 35% 17% 6%

N14 V15 F16 S17 M18 F19 D20 I24 Q25 D26 F27 K28 I34 D35 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 G108 K109 G110 S111 D112 K113 K114 S115 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 K151 N152 I153 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 I24 Q25 D26 F27 K28 I34 D35 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 G108 K109 G110 S111 D112 K113 K114 S115 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 K151 N152 I153 C154 T158 H159 G160 E161

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 I24 Q25 D26 F27 K28 I34 D35 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

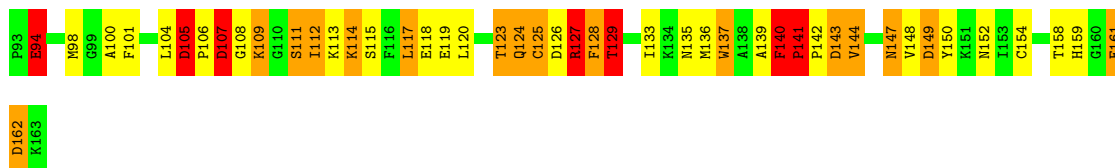
P93 E94 M98 G99 A100 F101 L104 D105 P106 D107 G108 K109 G110 S111 D112 K113 K114 S115 F116 L117 E118 E119 L120 T123 Q124 C125 D126 R127 F128 T129 I133 K134 N135 M136 W137 A138 A139 F140 P141 P142 D143 V144 N147 V148 D149 Y150 K151 N152 I153 C154 T158 H159 G160 E161

D162
K163

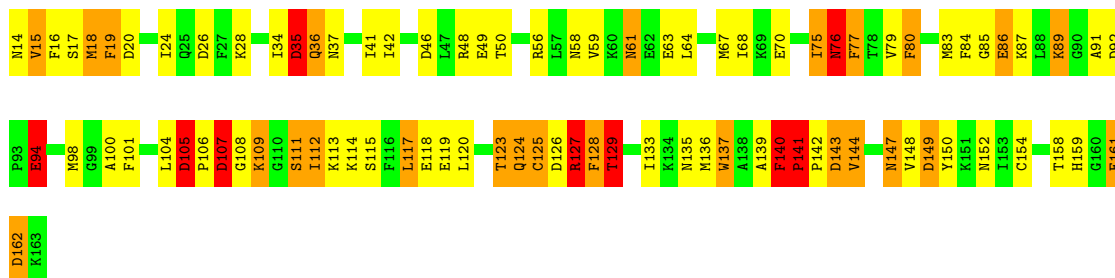
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 15-B:  41% 35% 17% 6%

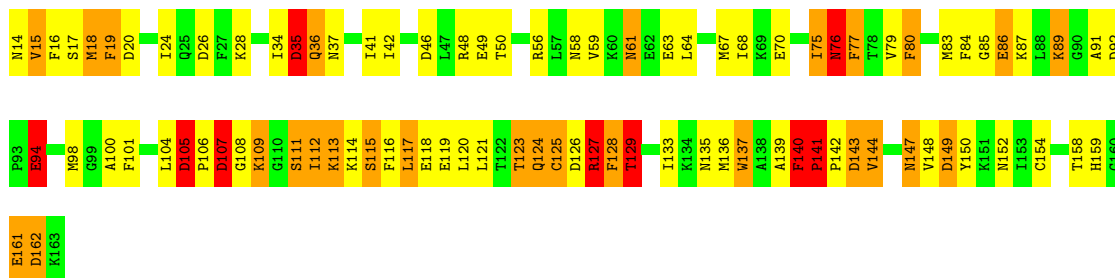
N14 V15 F16 S17 M18 F19 D20 I24 Q25 D26 F27 K28 I34 D35 Q36 N37 I41 I42 D46 L47 R48 E49 T50 R56 L57 N58 V59 R60 N61 E62 E63 L64 M67 I68 R69 E70 I75 R76 F77 T78 V79 F80 M83 F84 G85 E86 K87 L88 K89 G90 A91 D92



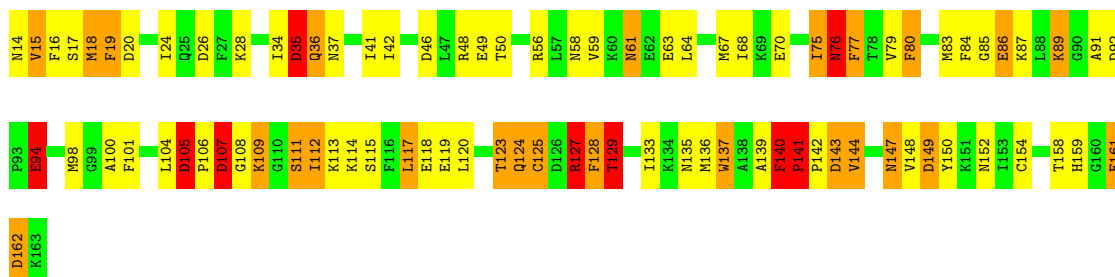
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



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

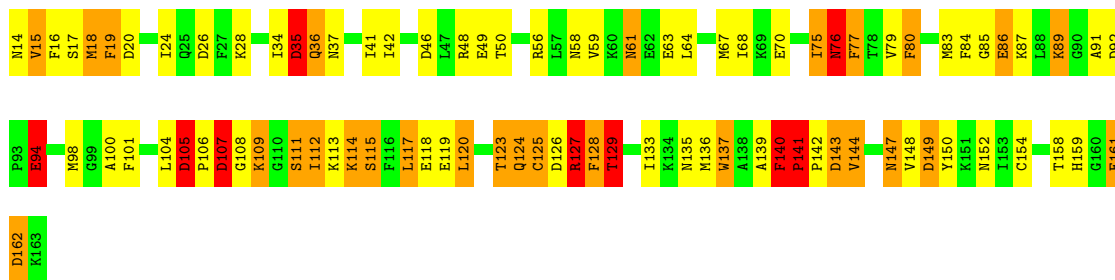


● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



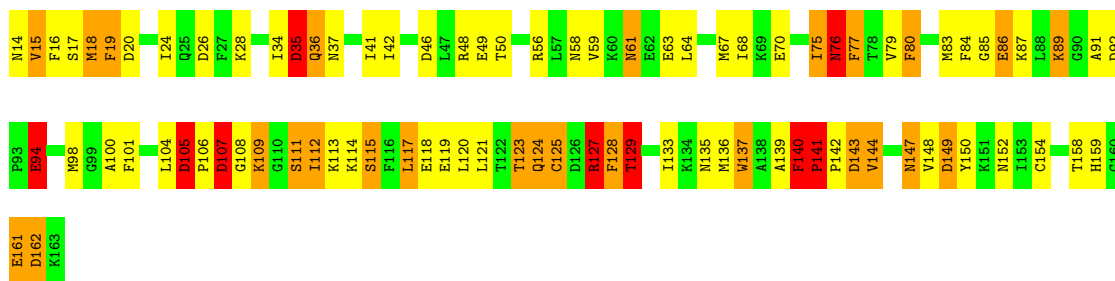
● Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM





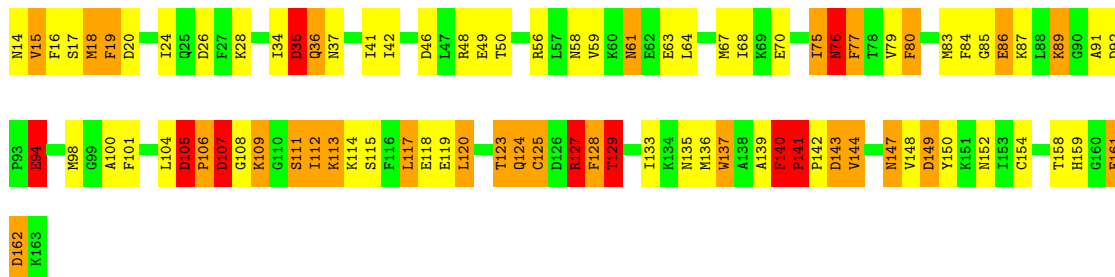
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 20-B: 41% 35% 17% 6%



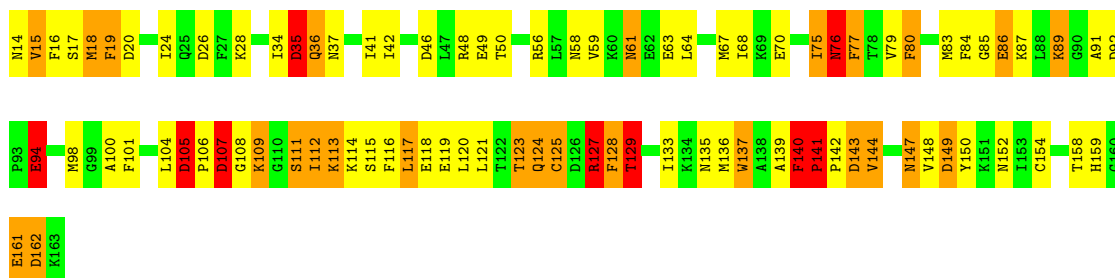
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 21-B: 42% 33% 19% 6%




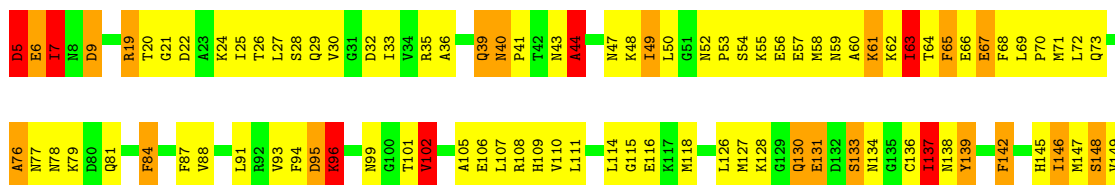
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 22-B: 41% 36% 17% 6%




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

Chain 1-C: 



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

Chain 2-C: 



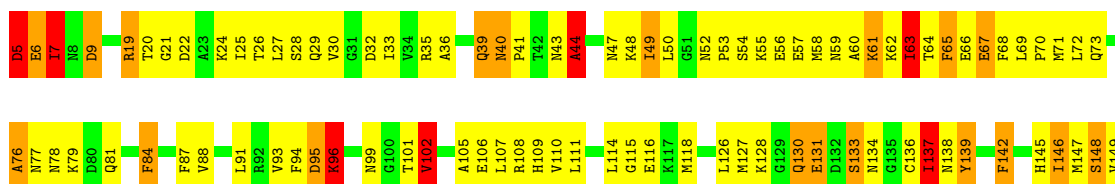
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 3-C: 

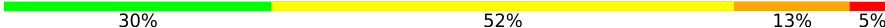


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 4-C: 

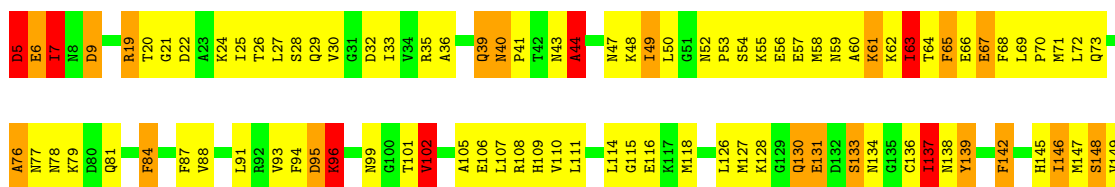


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

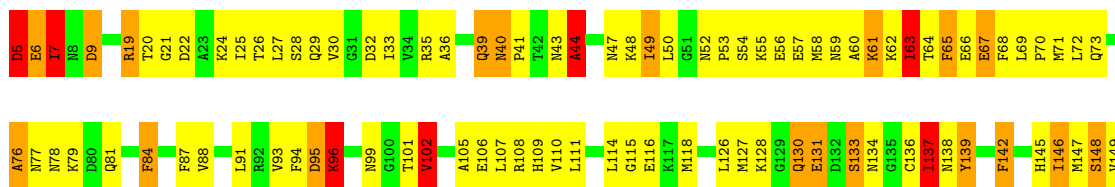
Chain 5-C: 



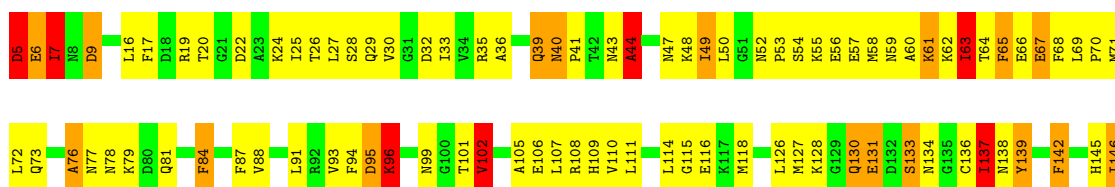
● Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



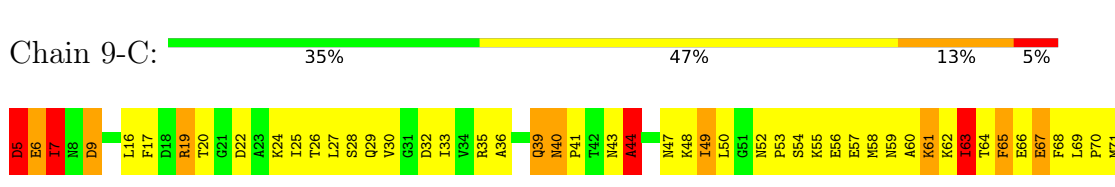
● Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

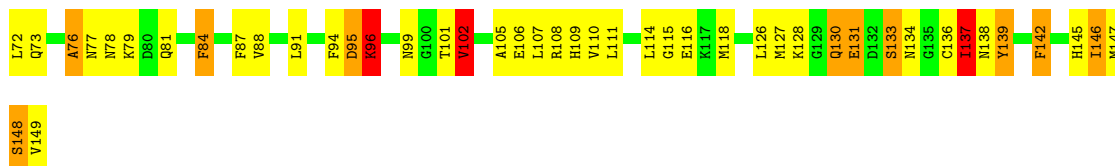


● Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

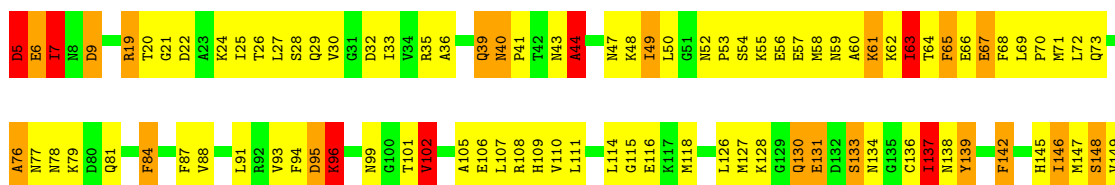


● Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

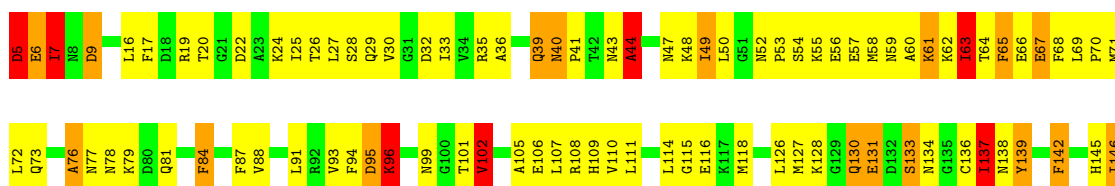




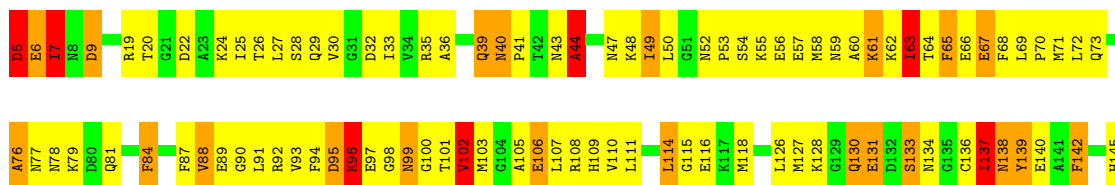
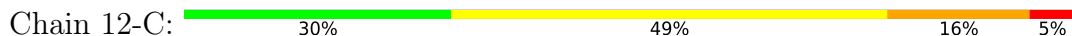
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



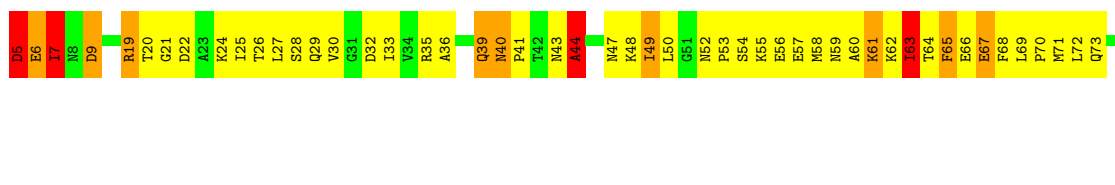
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

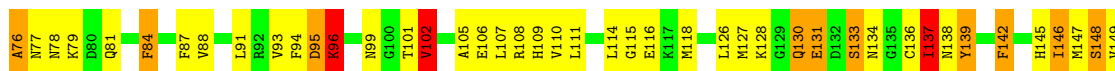


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

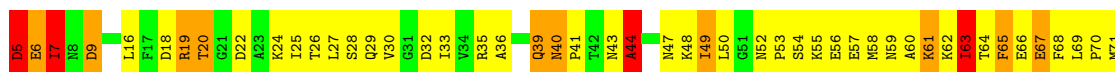


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

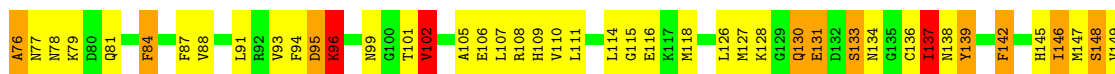
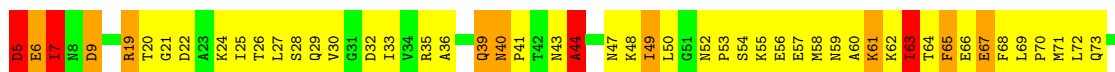
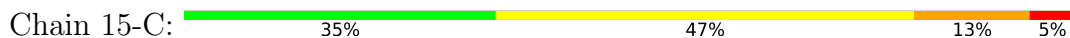




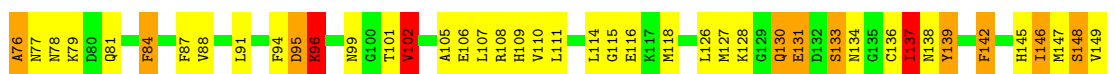
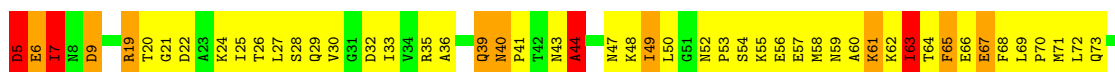
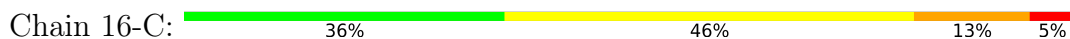
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



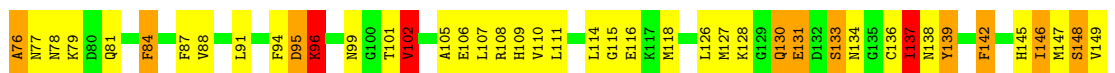
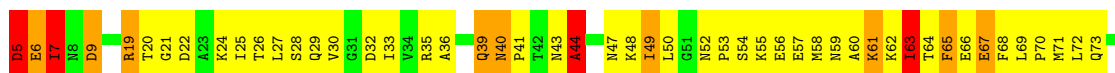
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



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



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

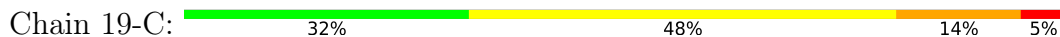


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

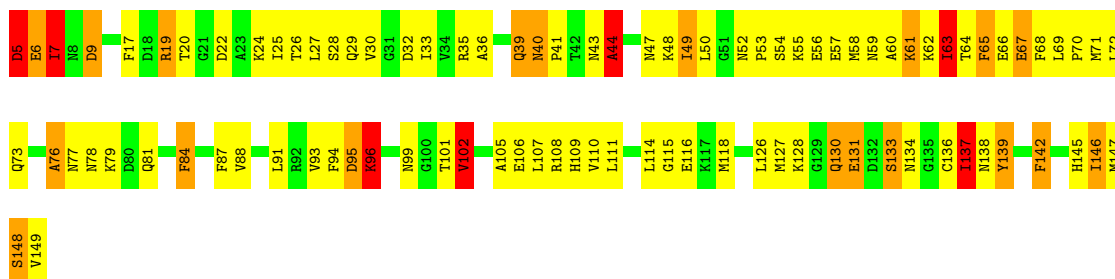




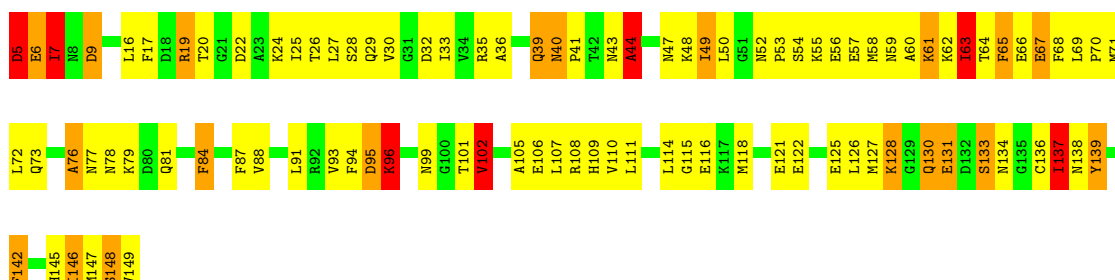
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



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

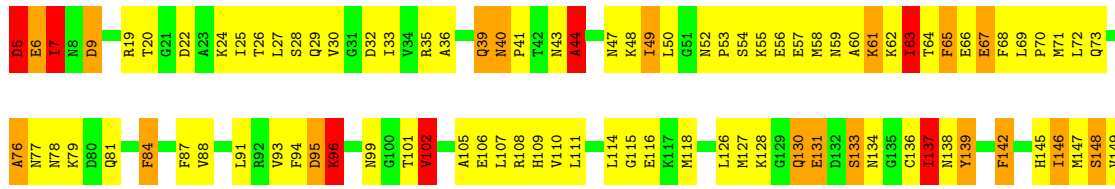


• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



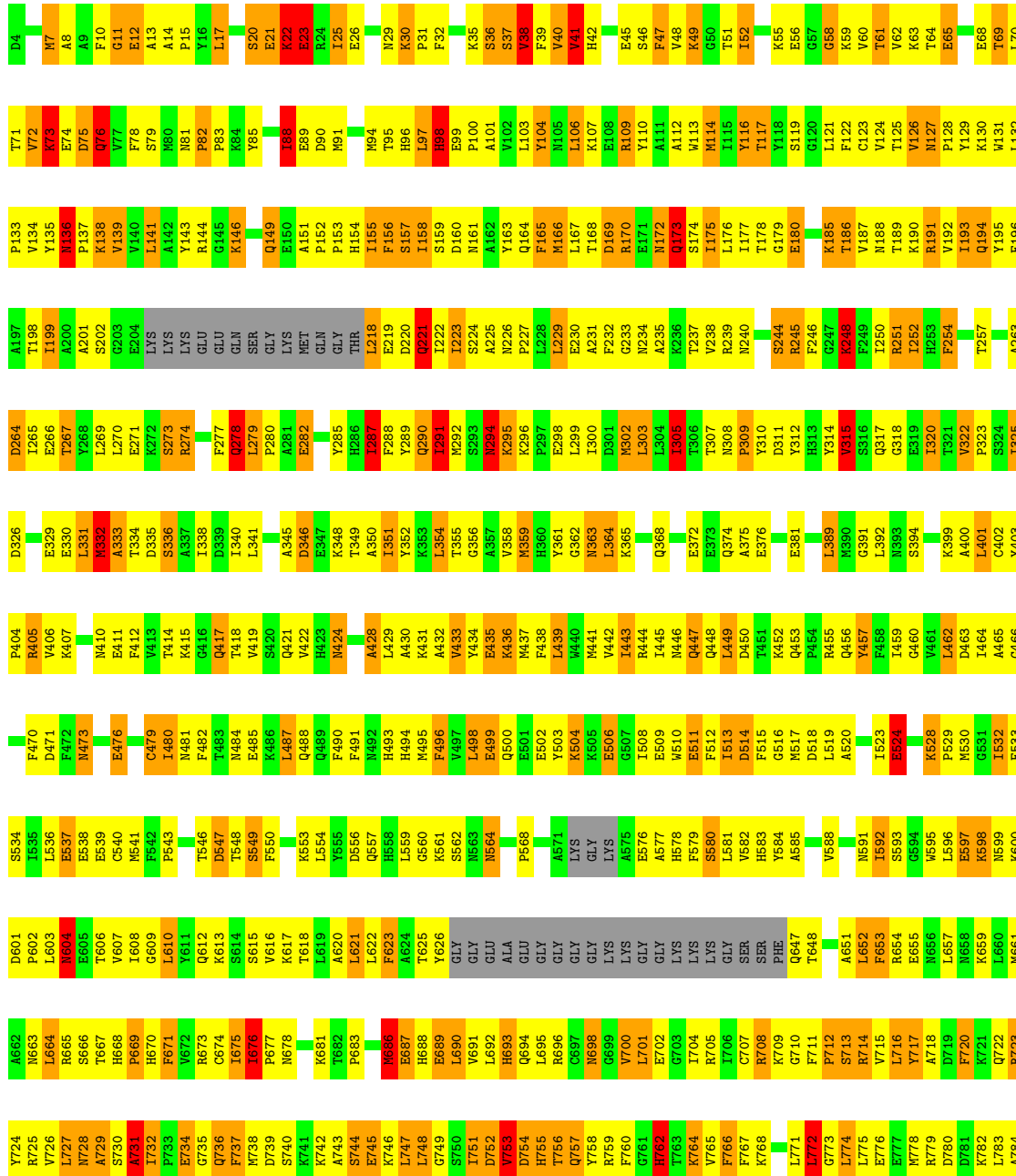
• Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

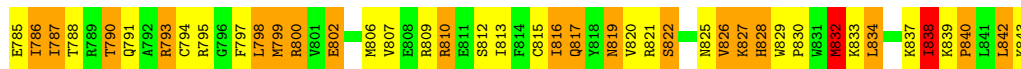
Chain 22-C: 36% 47% 12% 5%



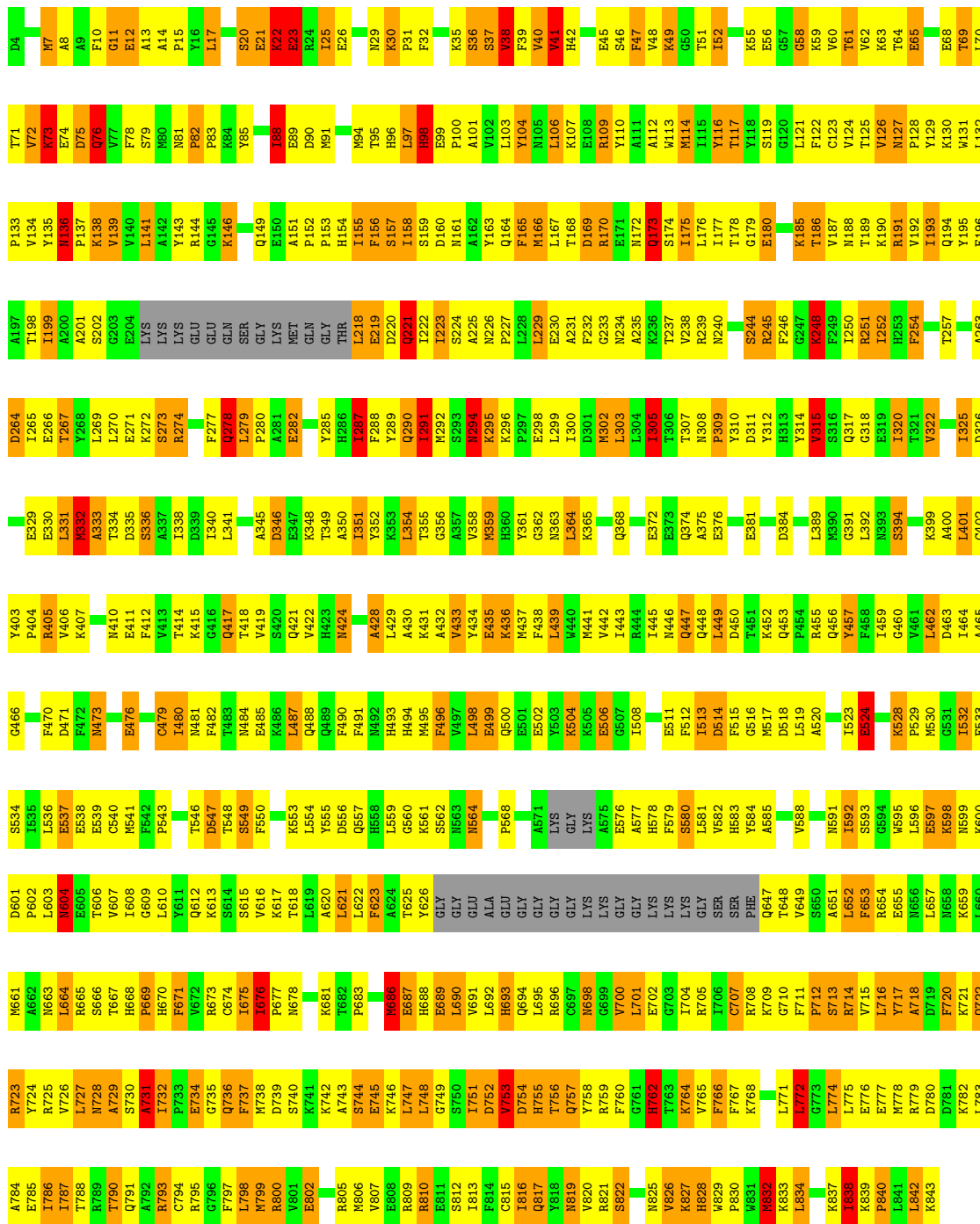
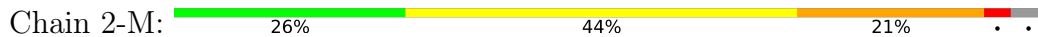
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 1-M: 27% 44% 22%



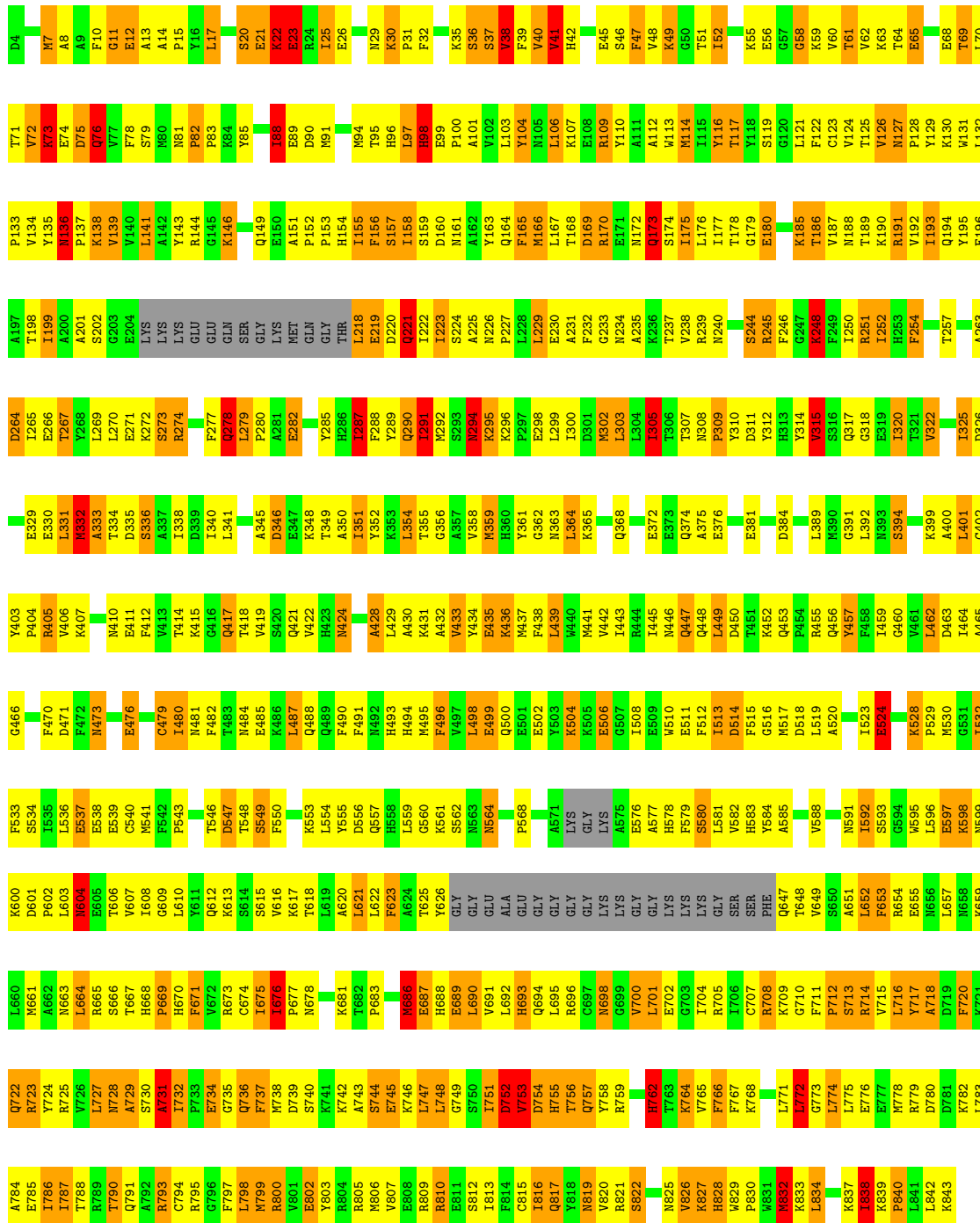


● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT



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

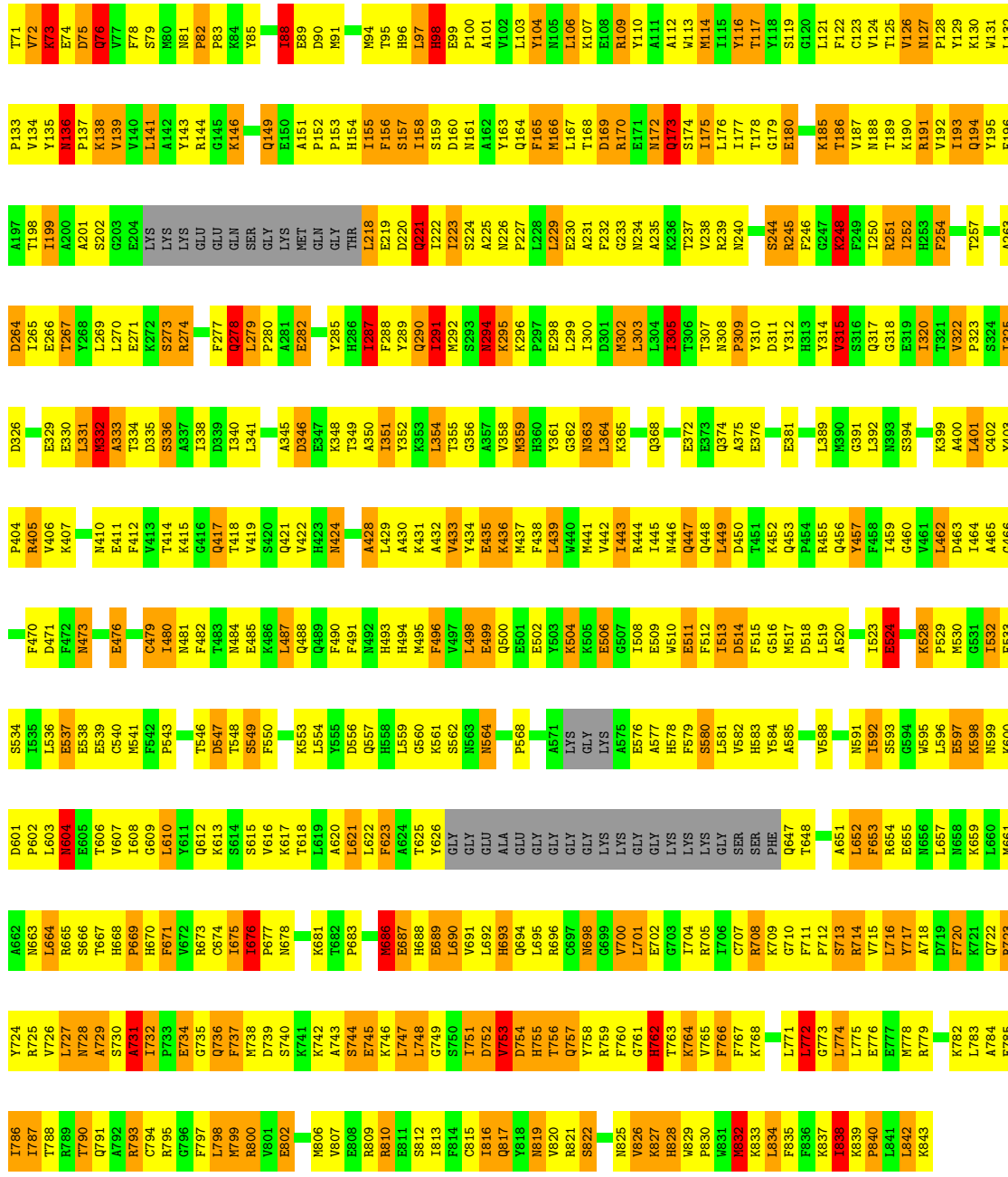
Chain 3-M: 27% 44% 21%



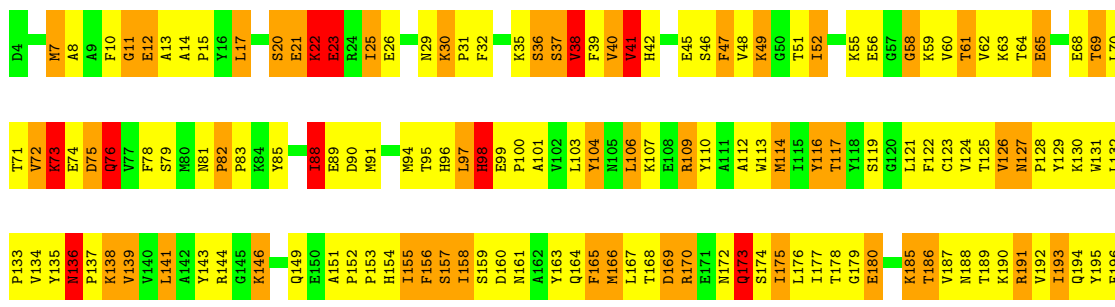
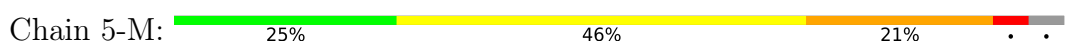
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

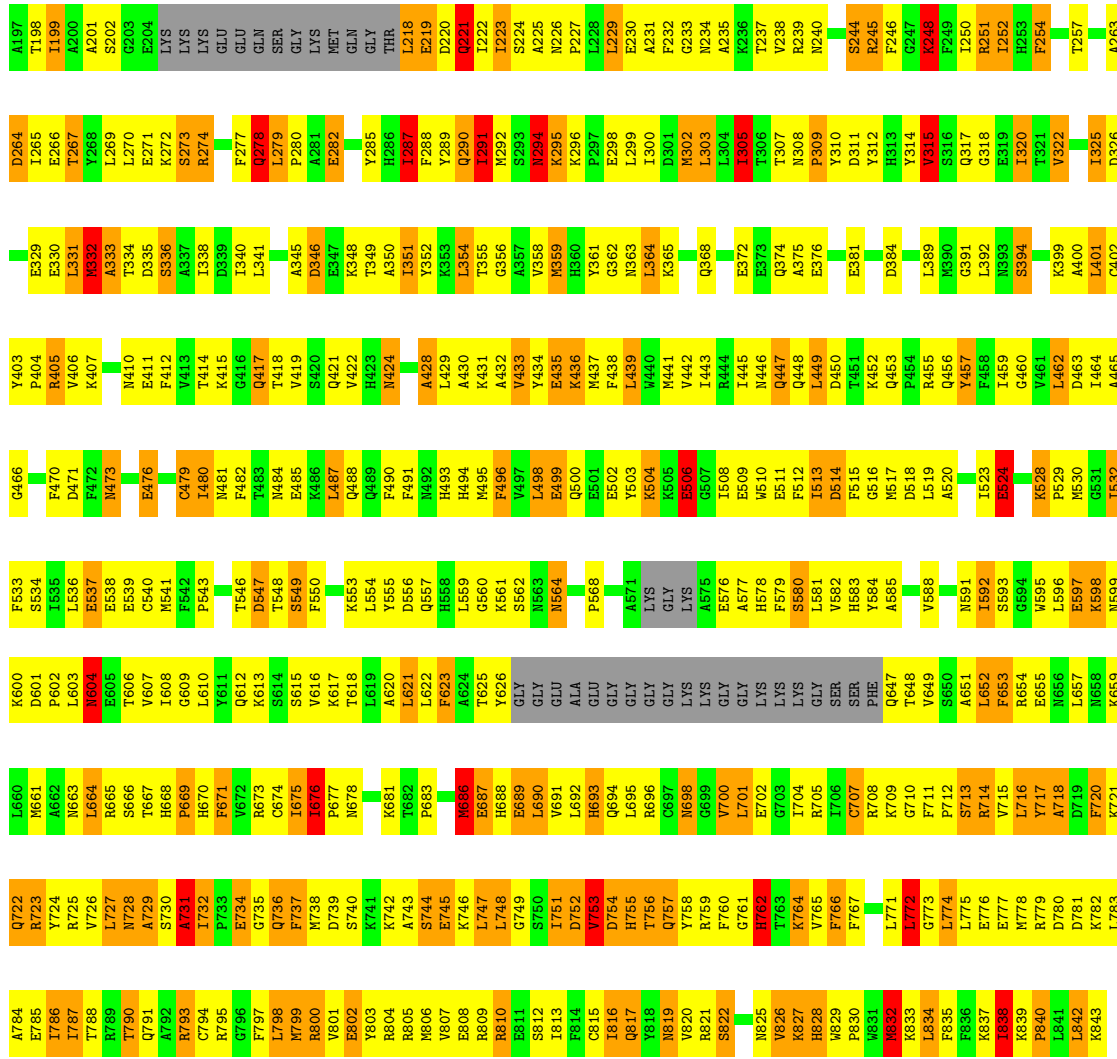
Chain 4-M: 26% 44% 22%



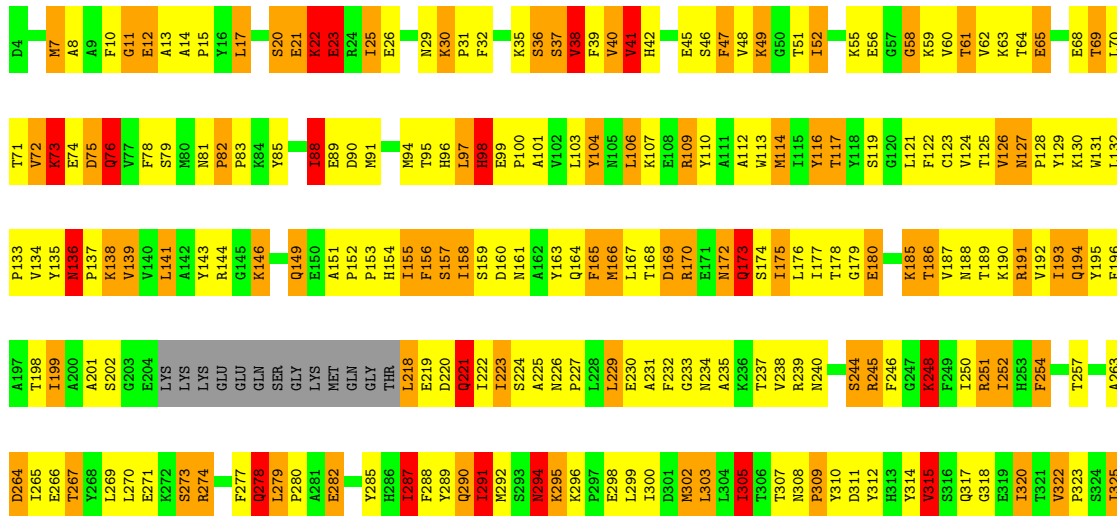
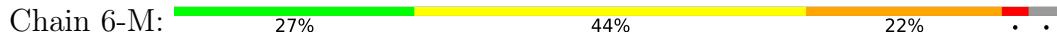


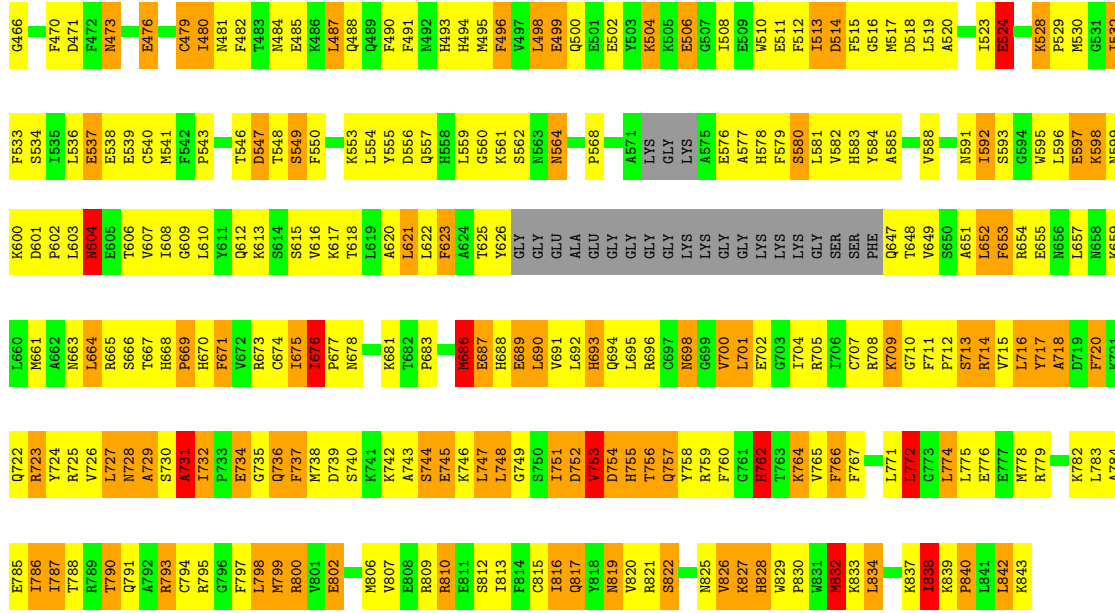
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT





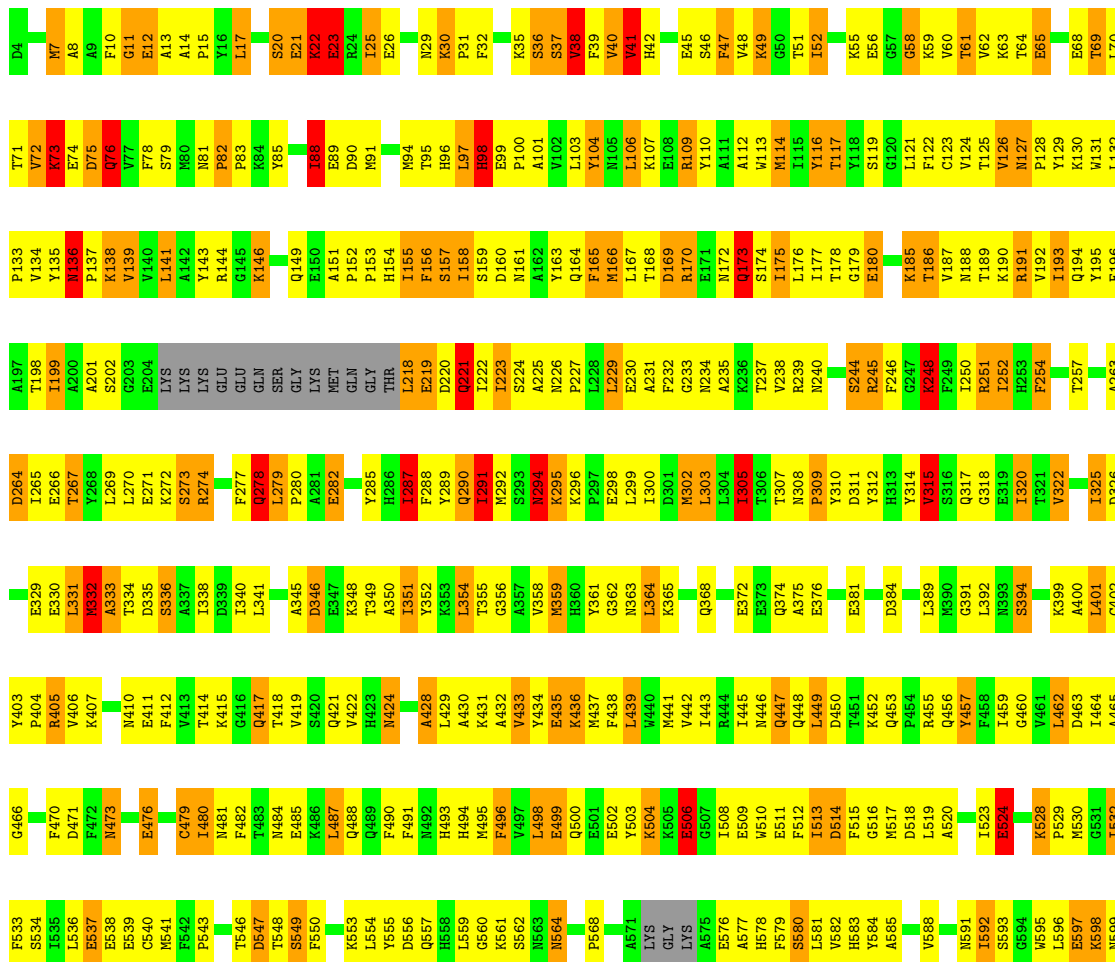
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT





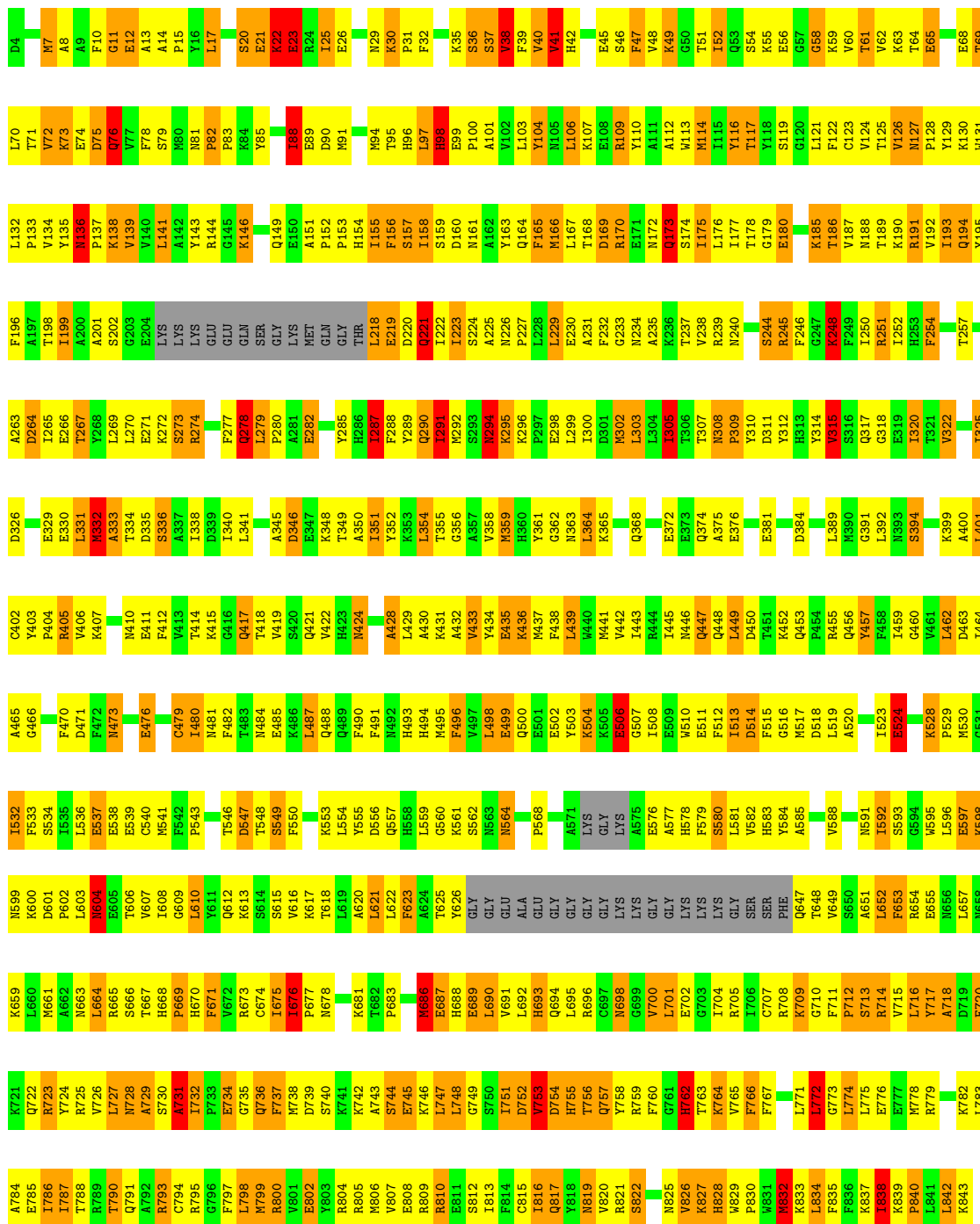
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 8-M: 26% 45% 21%



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

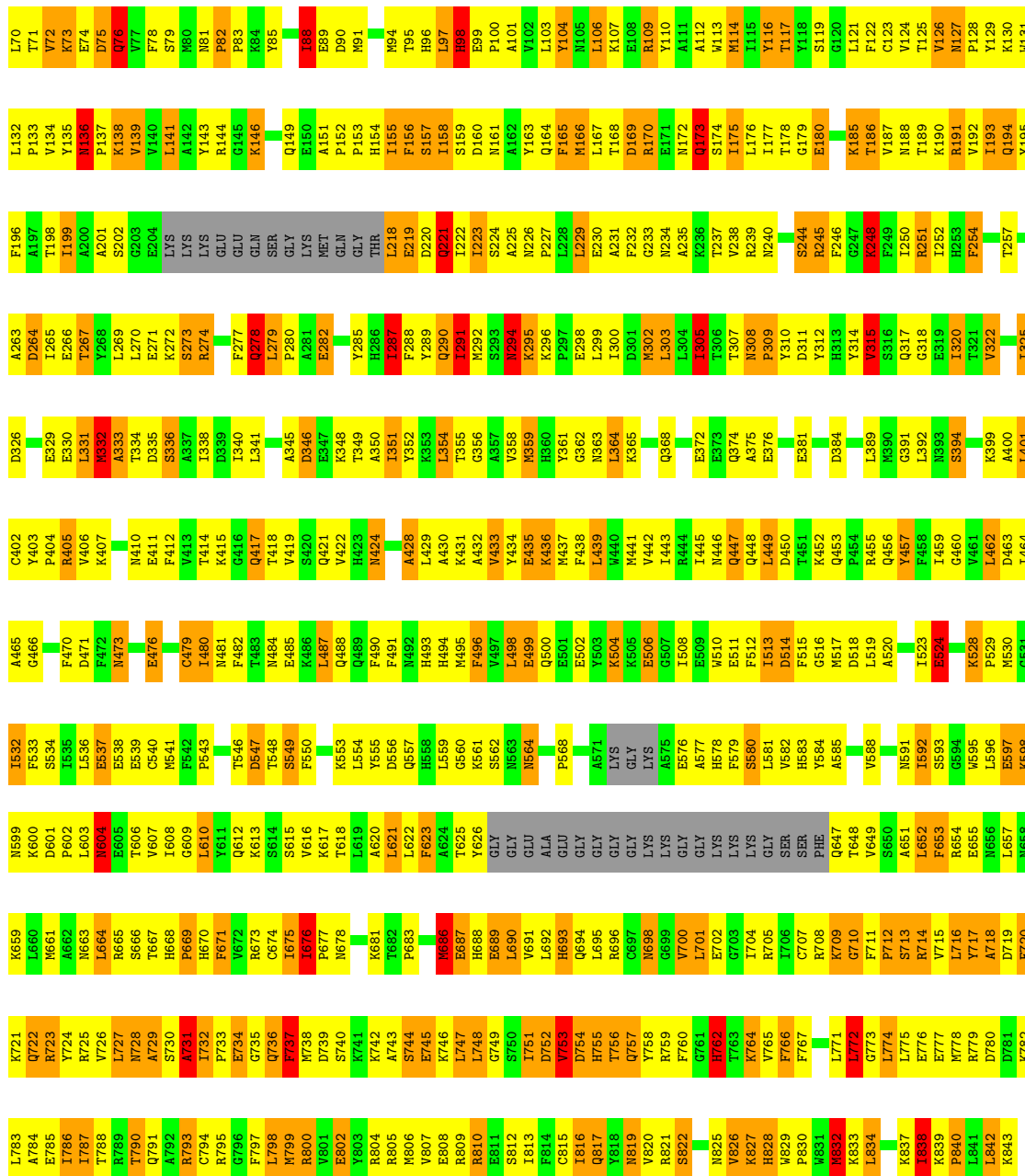
Chain 11-M: 26% 45% 22%



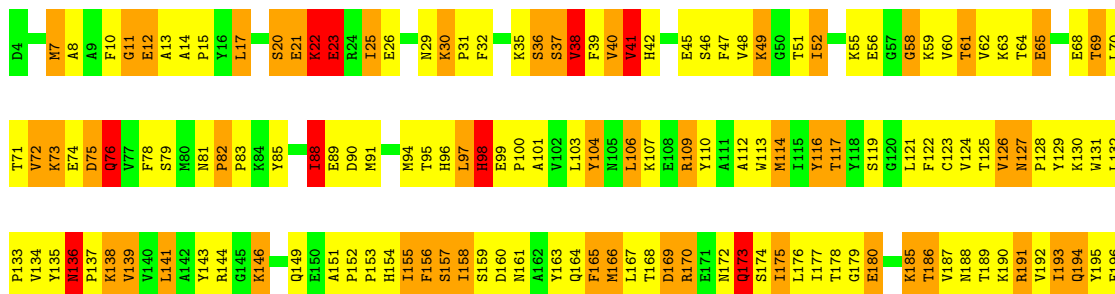
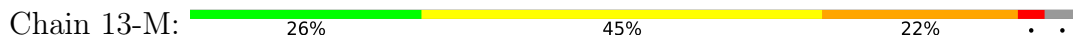
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

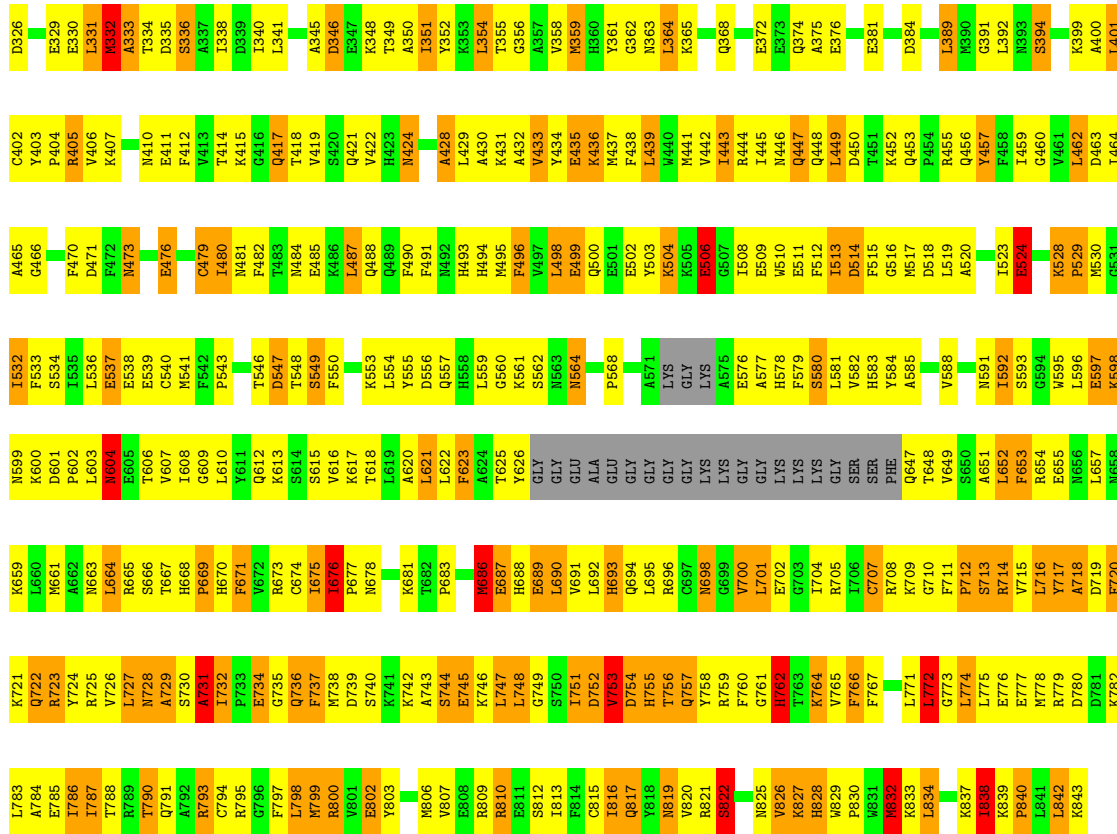
Chain 12-M: 26% 45% 22%



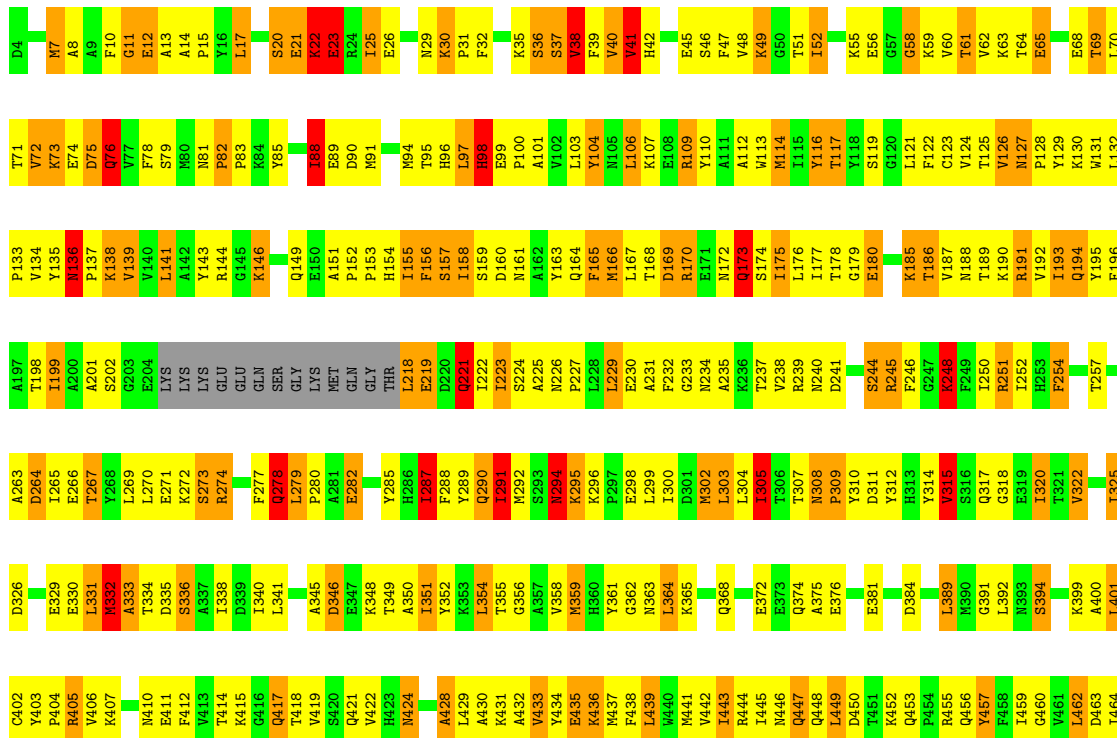
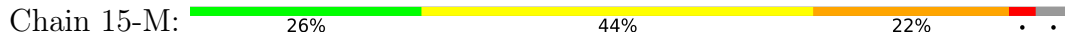


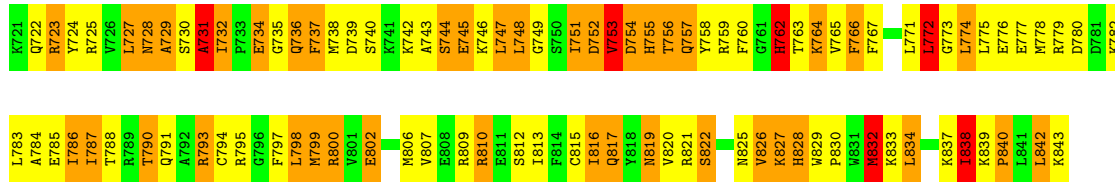
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT



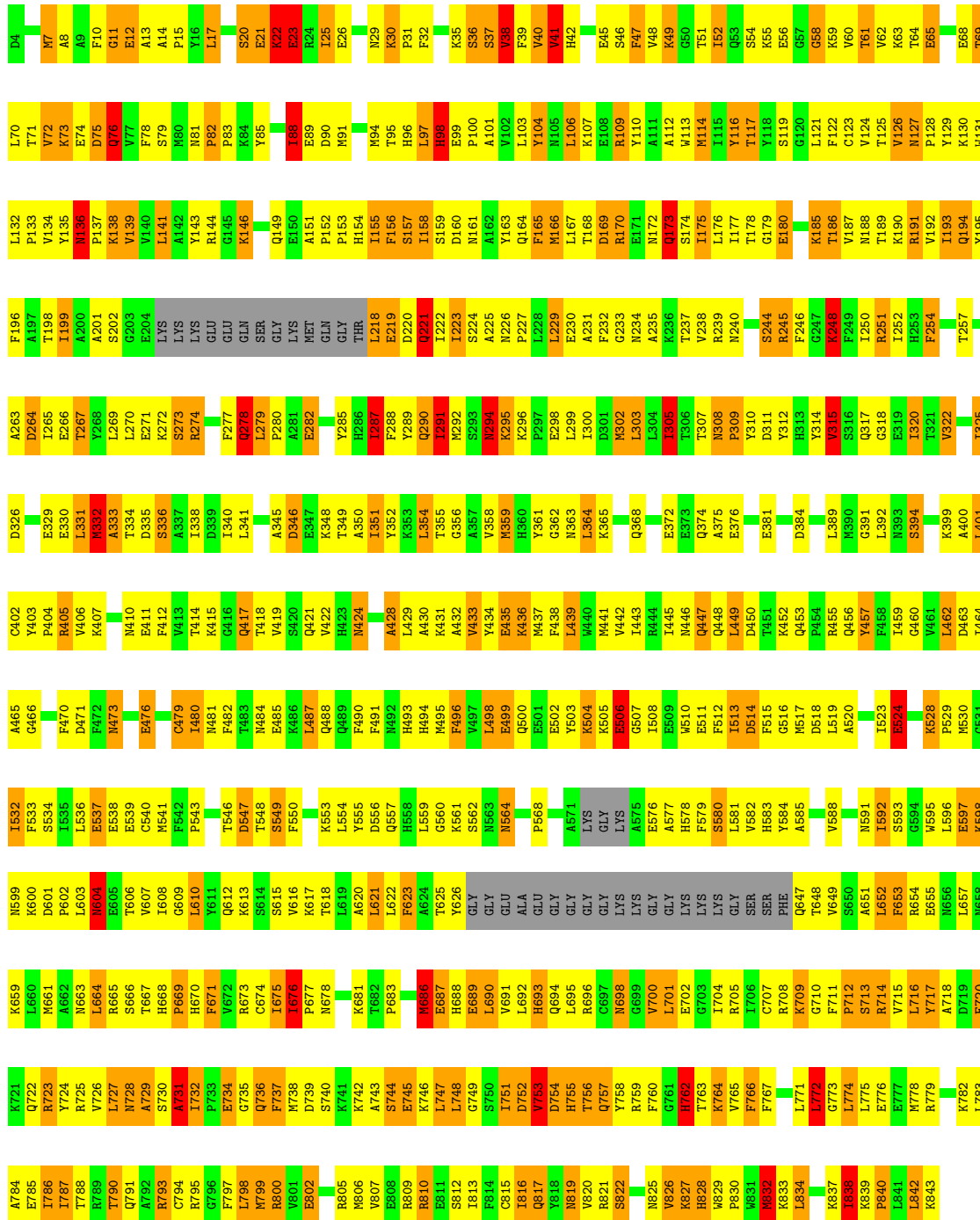
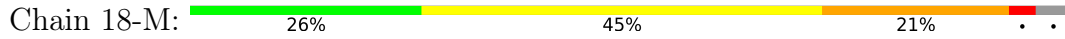


● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT



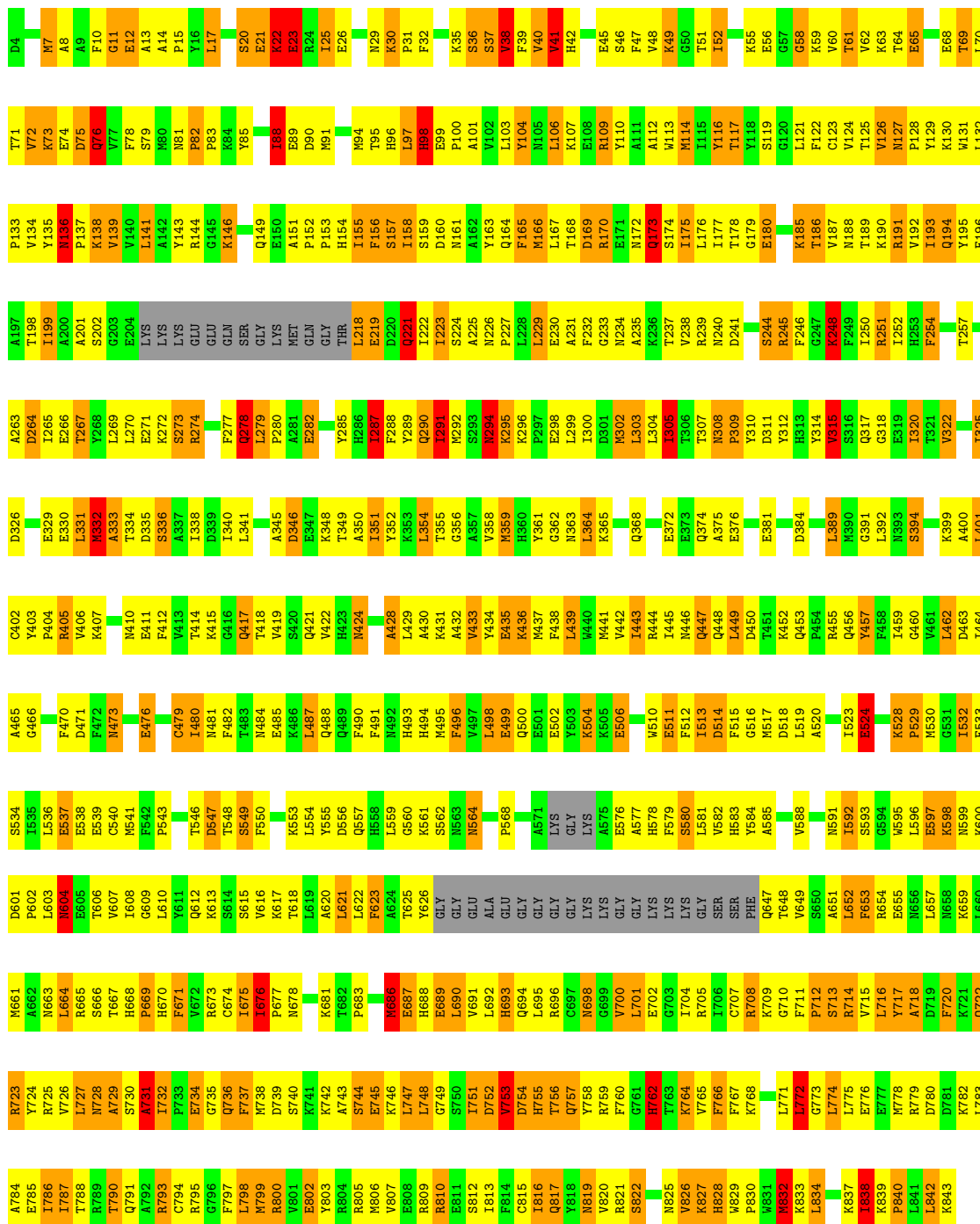


• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT



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

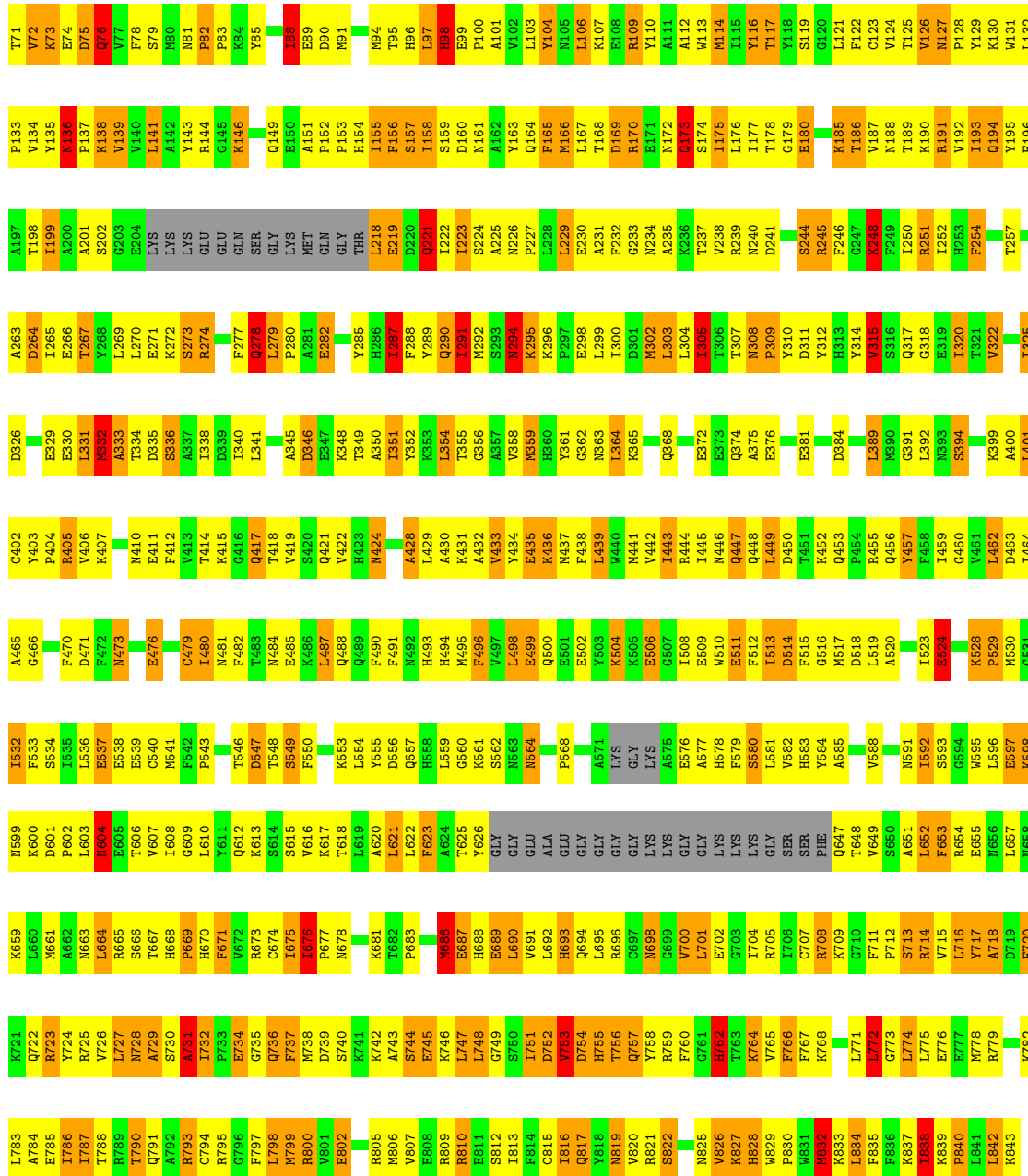
Chain 19-M: 26% 44% 22%



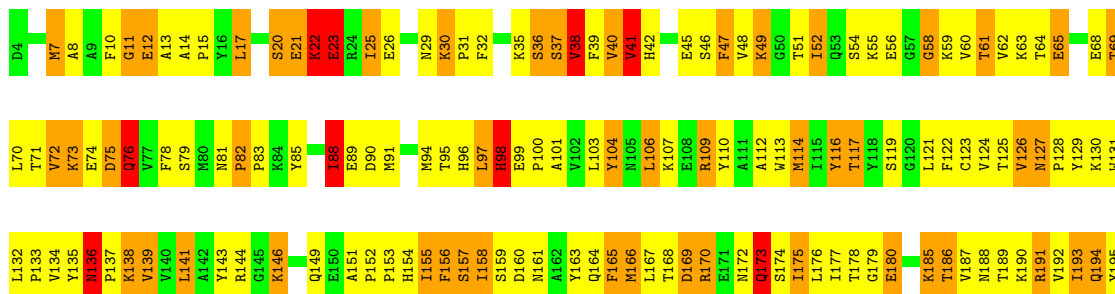
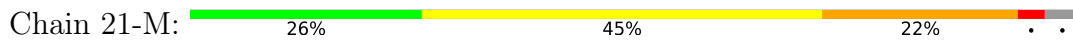
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 20-M: 26% 44% 22%





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



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 ($e^-/\text{Å}^2$)	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 i

5.1 Standard geometry i

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	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	2-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	3-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	4-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	5-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	6-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	7-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	8-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	9-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	10-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	11-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	12-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	13-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	14-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	15-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	16-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	17-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	18-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	19-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	20-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	21-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
1	22-B	0.79	1/1199 (0.1%)	2.27	58/1617 (3.6%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
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%)
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%)
2	21-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
2	22-C	0.83	3/1140 (0.3%)	2.15	61/1530 (4.0%)
3	1-M	1.63	22/6593 (0.3%)	1.87	139/8881 (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	22/6592 (0.3%)	1.87	139/8878 (1.6%)
3	6-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	7-M	1.66	23/6594 (0.3%)	1.88	141/8884 (1.6%)
3	8-M	1.63	22/6592 (0.3%)	1.87	139/8878 (1.6%)
3	9-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	10-M	1.66	23/6594 (0.3%)	1.88	141/8884 (1.6%)
3	11-M	1.66	23/6593 (0.3%)	1.88	141/8881 (1.6%)
3	12-M	1.66	23/6593 (0.3%)	1.88	141/8881 (1.6%)
3	13-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	14-M	1.63	22/6592 (0.3%)	1.87	139/8878 (1.6%)
3	15-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	16-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	17-M	1.66	23/6594 (0.3%)	1.88	141/8884 (1.6%)
3	18-M	1.66	23/6594 (0.3%)	1.88	141/8884 (1.6%)
3	19-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	20-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	21-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
3	22-M	1.63	22/6593 (0.3%)	1.87	139/8881 (1.6%)
All	All	1.47	578/196505 (0.3%)	1.97	5688/264619 (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

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Mol	Chain	#Chirality outliers	#Planarity outliers
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
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
1	21-B	0	4
1	22-B	0	4
3	1-M	0	1
3	2-M	0	1
3	3-M	0	2
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
3	13-M	0	1
3	14-M	0	1
3	15-M	0	1
3	16-M	0	2
3	17-M	0	1
3	18-M	0	1
3	19-M	0	3
3	20-M	0	1
3	21-M	0	1
3	22-M	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	114

The worst 5 of 578 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-M	731	ALA	C-N	51.68	1.91	1.33
3	2-M	731	ALA	C-N	51.68	1.91	1.33
3	3-M	731	ALA	C-N	51.68	1.91	1.33
3	4-M	731	ALA	C-N	51.68	1.91	1.33
3	5-M	731	ALA	C-N	51.68	1.91	1.33

The worst 5 of 5688 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-M	731	ALA	O-C-N	-34.24	77.05	122.59
3	2-M	731	ALA	O-C-N	-34.24	77.05	122.59
3	3-M	731	ALA	O-C-N	-34.24	77.05	122.59
3	4-M	731	ALA	O-C-N	-34.24	77.05	122.59
3	5-M	731	ALA	O-C-N	-34.24	77.05	122.59

There are no chirality outliers.

5 of 114 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	136	0
1	2-B	1177	0	1134	141	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3-B	1177	0	1132	180	0
1	4-B	1177	0	1134	138	0
1	5-B	1177	0	1132	256	0
1	6-B	1177	0	1134	140	0
1	7-B	1177	0	1134	144	0
1	8-B	1177	0	1134	137	0
1	9-B	1177	0	1134	139	0
1	10-B	1177	0	1134	138	0
1	11-B	1177	0	1134	137	0
1	12-B	1177	0	1134	132	0
1	13-B	1177	0	1134	136	0
1	14-B	1177	0	1134	162	0
1	15-B	1177	0	1134	139	0
1	16-B	1177	0	1134	140	0
1	17-B	1177	0	1134	143	0
1	18-B	1177	0	1134	137	0
1	19-B	1177	0	1131	191	0
1	20-B	1177	0	1134	149	0
1	21-B	1177	0	1131	197	0
1	22-B	1177	0	1134	134	0
2	1-C	1126	0	1084	89	0
2	2-C	1126	0	1084	212	0
2	3-C	1126	0	1082	137	0
2	4-C	1126	0	1084	89	0
2	5-C	1126	0	1077	213	0
2	6-C	1126	0	1084	90	0
2	7-C	1126	0	1084	90	0
2	8-C	1126	0	1084	96	0
2	9-C	1126	0	1084	87	0
2	10-C	1126	0	1084	90	0
2	11-C	1126	0	1084	90	0
2	12-C	1126	0	1072	323	0
2	13-C	1126	0	1084	87	0
2	14-C	1126	0	1080	207	0
2	15-C	1126	0	1084	90	0
2	16-C	1126	0	1084	92	0
2	17-C	1126	0	1084	85	0
2	18-C	1126	0	1084	91	0
2	19-C	1126	0	1079	167	0
2	20-C	1126	0	1084	102	0
2	21-C	1126	0	1082	154	0
2	22-C	1126	0	1084	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	1-M	6455	0	6382	908	0
3	2-M	6455	0	6379	991	0
3	3-M	6455	0	6378	879	0
3	4-M	6455	0	6382	862	0
3	5-M	6455	0	6375	979	0
3	6-M	6455	0	6376	853	0
3	7-M	6455	0	6383	861	0
3	8-M	6455	0	6382	942	0
3	9-M	6455	0	6383	853	0
3	10-M	6455	0	6379	887	0
3	11-M	6455	0	6379	915	0
3	12-M	6455	0	6372	1102	0
3	13-M	6455	0	6382	895	0
3	14-M	6455	0	6364	1034	0
3	15-M	6455	0	6379	869	0
3	16-M	6455	0	6378	887	0
3	17-M	6455	0	6380	876	0
3	18-M	6455	0	6381	876	0
3	19-M	6455	0	6378	914	0
3	20-M	6455	0	6381	869	0
3	21-M	6455	0	6380	867	0
3	22-M	6455	0	6382	860	0
All	All	192676	0	189089	22520	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 59.

The worst 5 of 22520 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:HZ3	3:M:766:PHE:CE2	1.08	1.71
3:M:508:ILE:HD13	3:M:766:PHE:CE2	1.23	1.66
3:M:510:TRP:CE3	3:M:766:PHE:CD2	1.74	1.65
3:M:510:TRP:CZ3	3:M:766:PHE:HB3	1.33	1.64
3:M:508:ILE:CD1	3:M:714:ARG:HD3	1.16	1.63

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	2-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	9
1	3-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	9
1	4-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	5-B	148/150 (99%)	119 (80%)	17 (12%)	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%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	10-B	148/150 (99%)	120 (81%)	16 (11%)	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%)	119 (80%)	17 (12%)	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
1	21-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	9
1	22-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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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
2	20-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	21-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
2	22-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	0	9
3	1-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	2-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	3-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	4-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	5-M	784/840 (93%)	647 (82%)	114 (14%)	23 (3%)	3	23
3	6-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	4	24
3	7-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	8-M	784/840 (93%)	646 (82%)	115 (15%)	23 (3%)	3	23
3	9-M	786/840 (94%)	648 (82%)	115 (15%)	23 (3%)	3	23
3	10-M	788/840 (94%)	651 (83%)	114 (14%)	23 (3%)	3	23
3	11-M	786/840 (94%)	648 (82%)	115 (15%)	23 (3%)	3	23
3	12-M	786/840 (94%)	647 (82%)	115 (15%)	24 (3%)	3	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	13-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	14-M	784/840 (93%)	646 (82%)	114 (14%)	24 (3%)	3	22
3	15-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	16-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	17-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	18-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	3	23
3	19-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	20-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	3	23
3	21-M	786/840 (94%)	647 (82%)	115 (15%)	24 (3%)	3	22
3	22-M	786/840 (94%)	648 (82%)	114 (14%)	24 (3%)	3	22
All	All	23696/24970 (95%)	19331 (82%)	3330 (14%)	1035 (4%)	3	17

5 of 1035 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 [i](#)

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
1	21-B	128/130 (98%)	116 (91%)	12 (9%)	8	26
1	22-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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
2	21-C	120/122 (98%)	107 (89%)	13 (11%)	6	21
2	22-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
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
3	21-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
3	22-M	693/724 (96%)	498 (72%)	195 (28%)	0	3
All	All	20702/21472 (96%)	15862 (77%)	4840 (23%)	2	5

5 of 4840 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	17-M	708	ARG
3	21-M	708	ARG
3	18-M	175	ILE
3	17-M	702	GLU
3	19-M	754	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 703 such sidechains are listed below:

Mol	Chain	Res	Type
3	15-M	481	ASN
1	19-B	36	GLN
1	16-B	23	GLN
3	15-M	453	GLN
3	17-M	360	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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	5-M	9
3	14-M	9
3	2-M	8
3	8-M	8
3	11-M	8
3	12-M	8
3	17-M	8
3	19-M	8
3	21-M	8
3	22-M	8
3	1-M	7
3	3-M	7
3	4-M	7
3	6-M	7
3	7-M	7
3	9-M	7
3	10-M	7
3	13-M	7
3	15-M	7
3	16-M	7
3	18-M	7
3	20-M	7

The worst 5 of 166 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-1561. 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.