



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:29 PM BST

PDB ID : 2W4A
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 Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

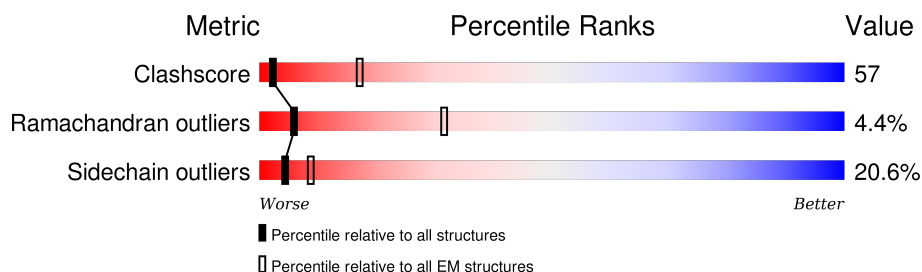
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 35.00 Å.

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







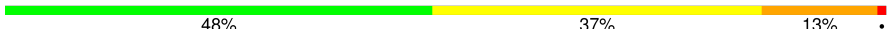
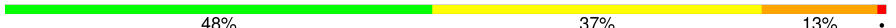
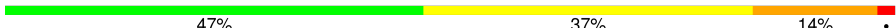









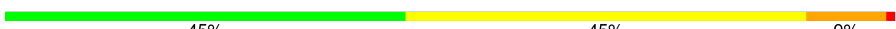








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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

Mol	Chain	Length	Quality of chain
1	1-B	150	49% 35% 13% .
1	10-B	150	49% 36% 13% .
1	11-B	150	48% 37% 13% .
1	12-B	150	50% 35% 13% .
1	13-B	150	48% 37% 13% .
1	14-B	150	49% 35% 14% .
1	15-B	150	49% 35% 14% .
1	16-B	150	49% 36% 13% .
1	17-B	150	47% 37% 13% .






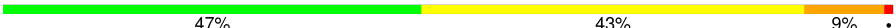




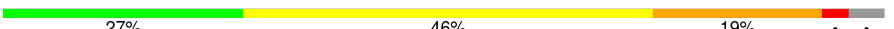
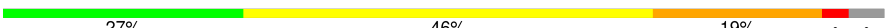
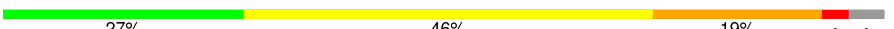
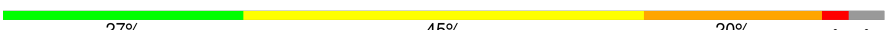
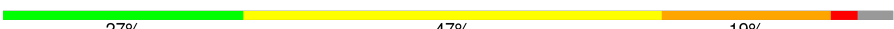
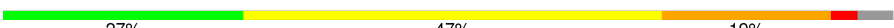
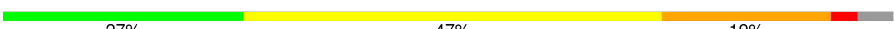
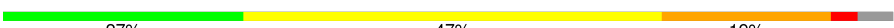
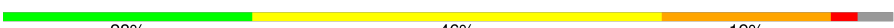
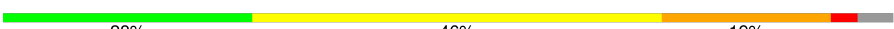
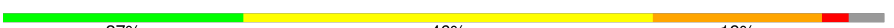
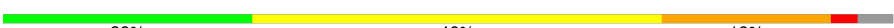
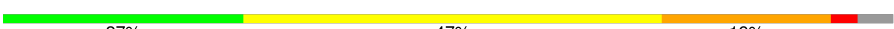


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Mol	Chain	Length	Quality of chain
1	18-B	150	 50% 35% 13% .
1	19-B	150	 49% 35% 14% .
1	2-B	150	 50% 35% 13% .
1	20-B	150	 49% 35% 13% .
1	21-B	150	 48% 37% 13% .
1	22-B	150	 48% 37% 13% .
1	3-B	150	 47% 37% 14% .
1	4-B	150	 49% 35% 13% .
1	5-B	150	 47% 37% 13% .
1	6-B	150	 49% 35% 14% .
1	7-B	150	 49% 35% 14% .
1	8-B	150	 50% 33% 15% .
1	9-B	150	 50% 35% 13% .
2	1-C	145	 52% 39% 8% .
2	10-C	145	 52% 39% 8% .
2	11-C	145	 52% 39% 8% .
2	12-C	145	 45% 45% 9% .
2	13-C	145	 52% 39% 8% .
2	14-C	145	 46% 44% 9% .
2	15-C	145	 52% 39% 8% .
2	16-C	145	 52% 38% 8% .
2	17-C	145	 52% 39% 8% .
2	18-C	145	 51% 40% 8% .
2	19-C	145	 49% 41% 9% .
2	2-C	145	 50% 41% 8% .

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Mol	Chain	Length	Quality of chain
2	20-C	145	 52% 39% 8% .
2	21-C	145	 49% 41% 8% .
2	22-C	145	 53% 38% 8% .
2	3-C	145	 52% 38% 9% .
2	4-C	145	 52% 39% 8% .
2	5-C	145	 47% 43% 9% .
2	6-C	145	 52% 39% 8% .
2	7-C	145	 52% 39% 8% .
2	8-C	145	 52% 38% 8% .
2	9-C	145	 52% 39% 8% .
3	1-M	840	 27% 46% 19% . .
3	10-M	840	 27% 46% 19% . .
3	11-M	840	 27% 46% 19% . .
3	12-M	840	 27% 45% 20% . .
3	13-M	840	 27% 47% 19% . .
3	14-M	840	 27% 47% 19% . .
3	15-M	840	 27% 47% 19% . .
3	16-M	840	 27% 47% 19% . .
3	17-M	840	 28% 46% 19% . .
3	18-M	840	 28% 46% 19% . .
3	19-M	840	 27% 46% 19% . .
3	2-M	840	 28% 46% 19% . .
3	20-M	840	 27% 47% 19% . .
3	21-M	840	 27% 46% 19% . .
3	22-M	840	 27% 46% 19% . .

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Mol	Chain	Length	Quality of chain
3	3-M	840	<div><div></div><div>28%</div><div>46%</div><div>19%</div><div></div><div></div></div>
3	4-M	840	<div><div></div><div>27%</div><div>47%</div><div>19%</div><div></div><div></div></div>
3	5-M	840	<div><div></div><div>27%</div><div>47%</div><div>19%</div><div></div><div></div></div>
3	6-M	840	<div><div></div><div>27%</div><div>47%</div><div>19%</div><div></div><div></div></div>
3	7-M	840	<div><div></div><div>28%</div><div>46%</div><div>18%</div><div></div><div></div></div>
3	8-M	840	<div><div></div><div>27%</div><div>46%</div><div>19%</div><div></div><div></div></div>
3	9-M	840	<div><div></div><div>28%</div><div>46%</div><div>19%</div><div></div><div></div></div>

2 Entry composition

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
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		
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
2	12-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	13-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	14-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
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		
2	21-C	145	Total	C	N	O	S	0	0
			1126	701	188	230	7		
2	22-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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		
3	21-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		
3	22-M	804	Total	C	N	O	S	0	0
			6455	4140	1089	1190	36		

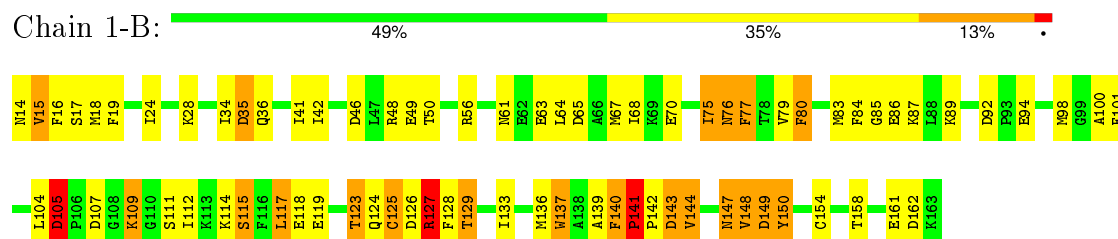
There is a discrepancy between the modelled and reference sequences:

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

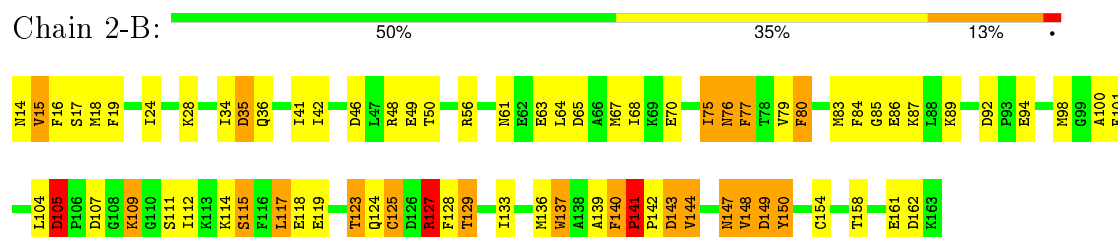
3 Residue-property plots

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

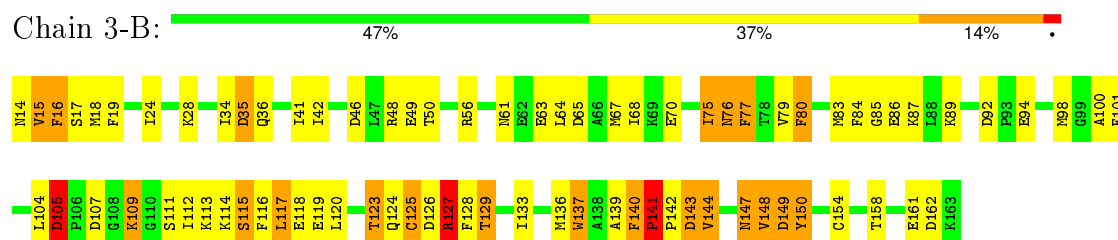
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



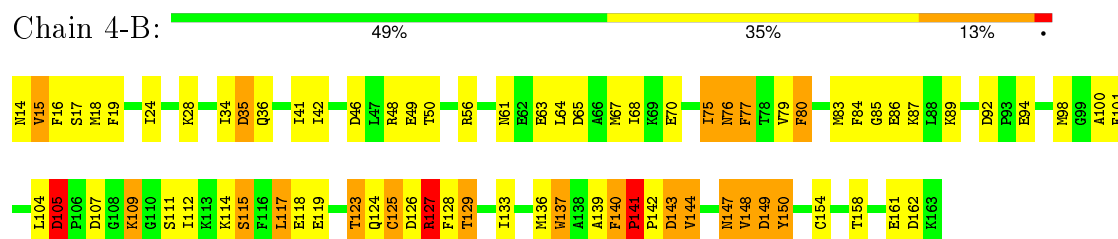
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



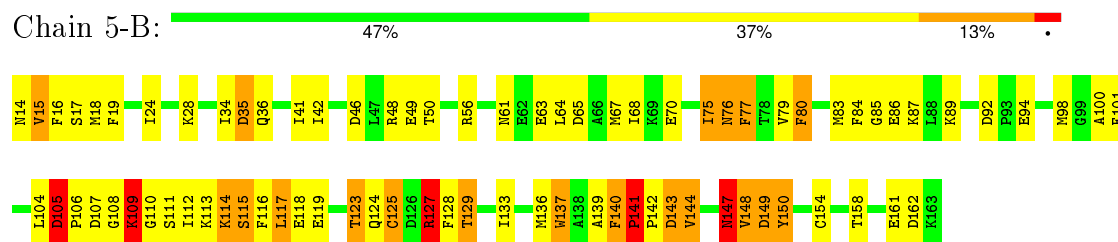
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



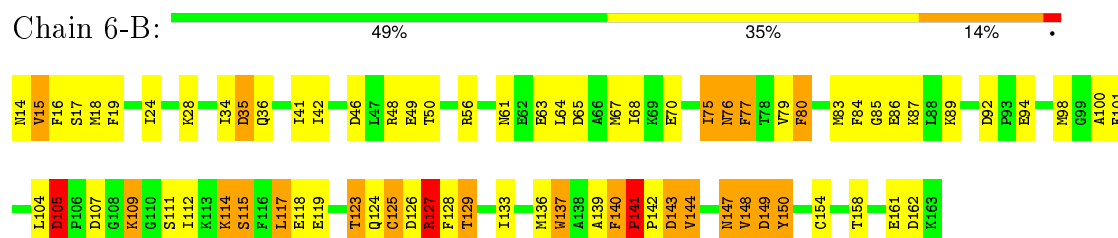
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



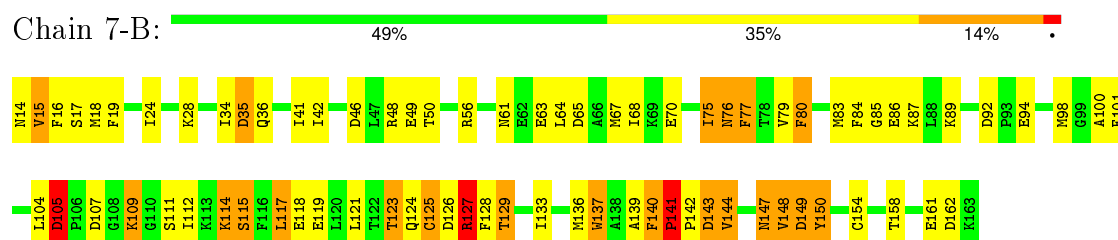
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



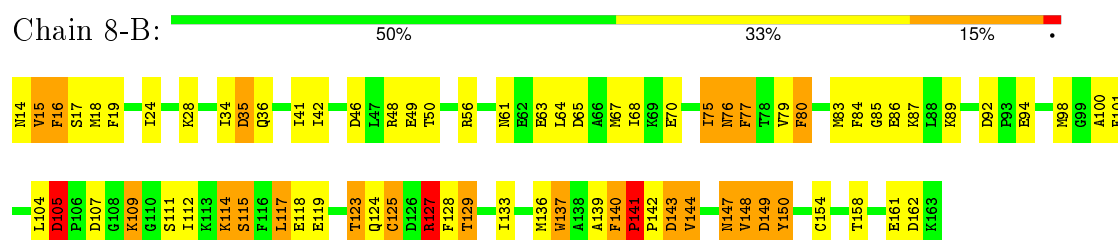
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



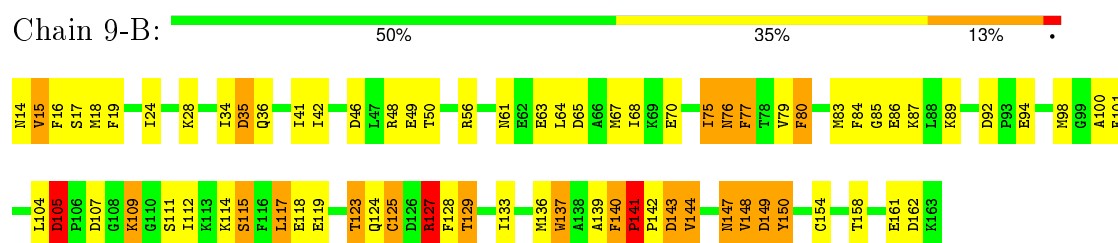
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



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

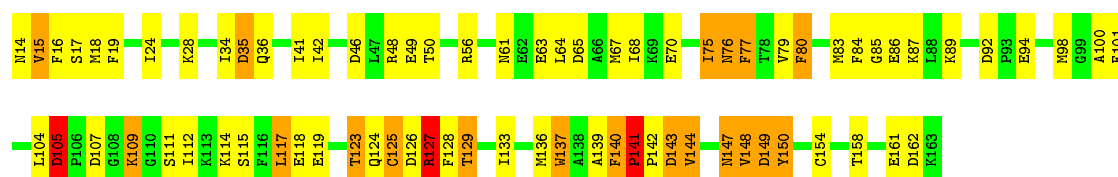


- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM



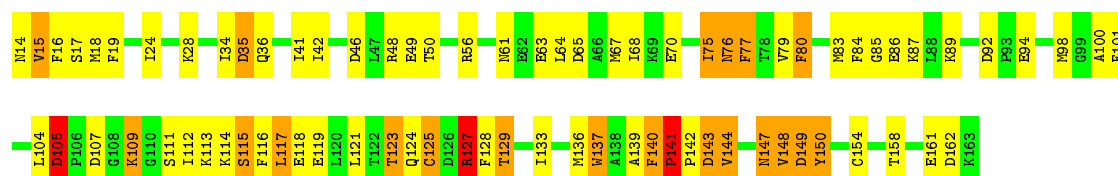
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM





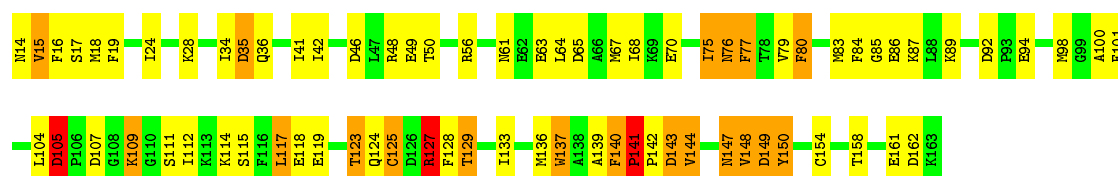
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 11-B: 48% 37% 13%



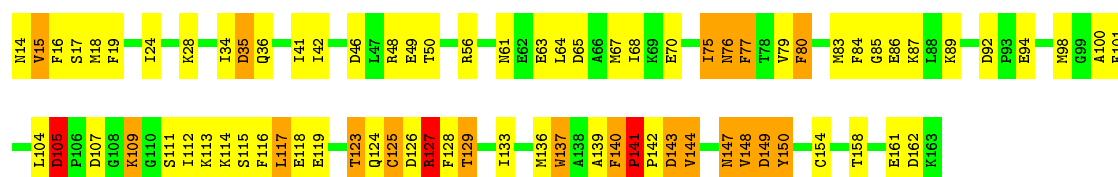
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 12-B: 50% 35% 13%



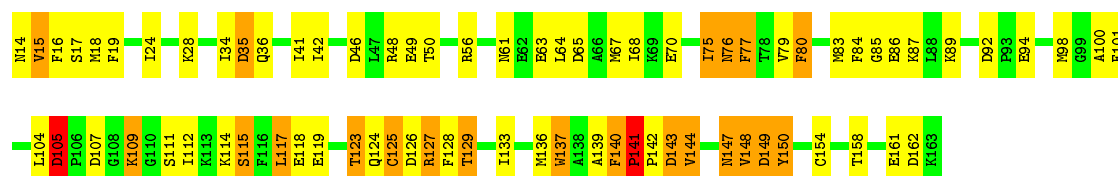
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 13-B: 48% 37% 13%



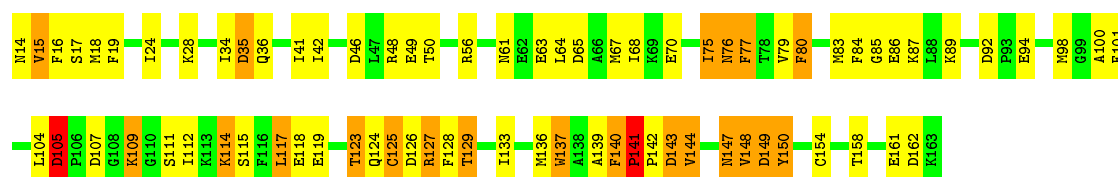
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 14-B: 49% 35% 14%



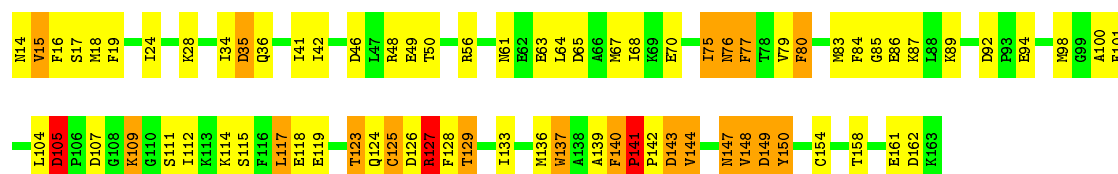
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 15-B: 49% 35% 14%



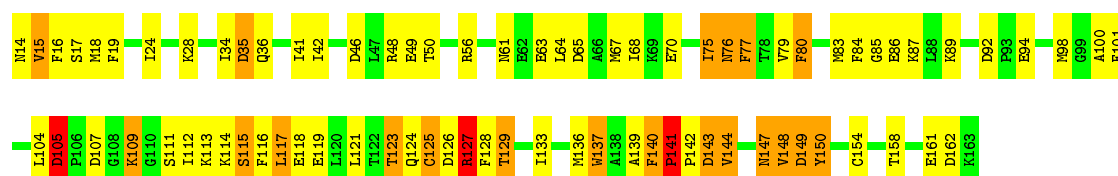
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 16-B: 49% 36% 13%



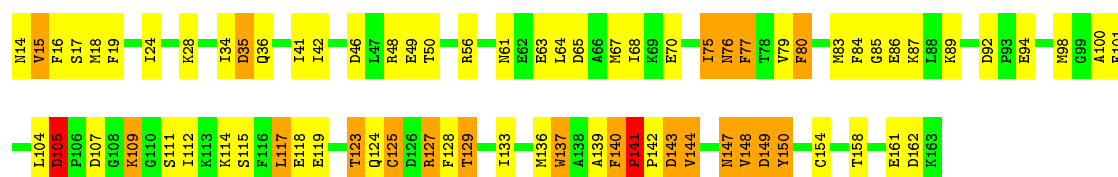
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 17-B: 47% 37% 13%



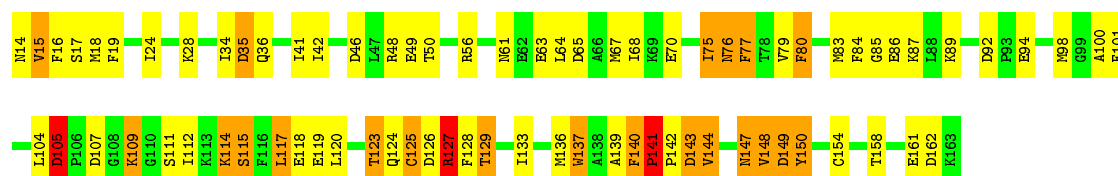
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 18-B: 50% 35% 13%



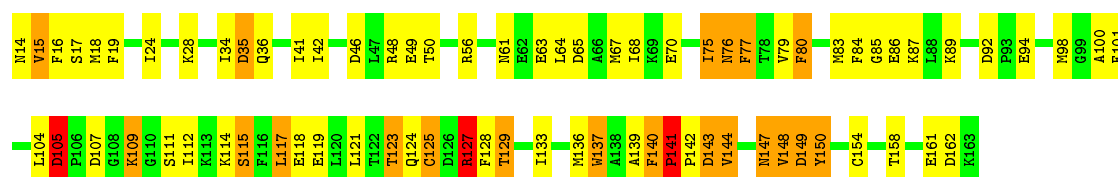
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 19-B: 49% 35% 14%



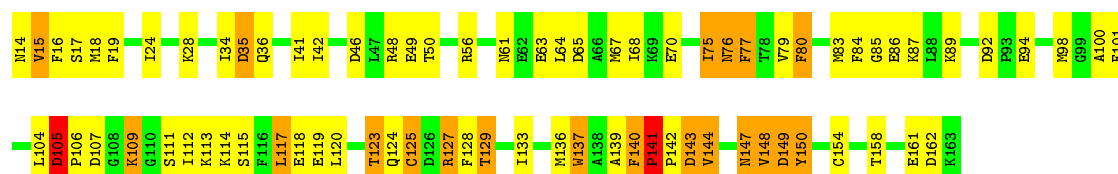
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 20-B: 49% 35% 13%



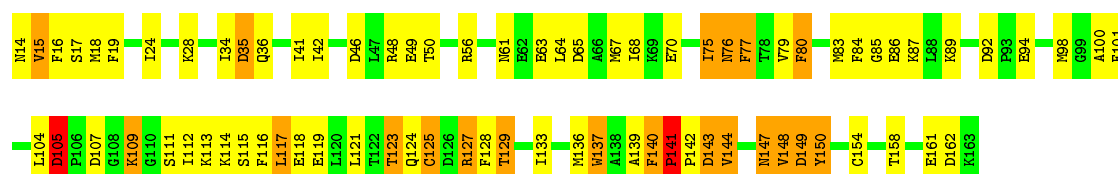
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 21-B: 48% 37% 13%



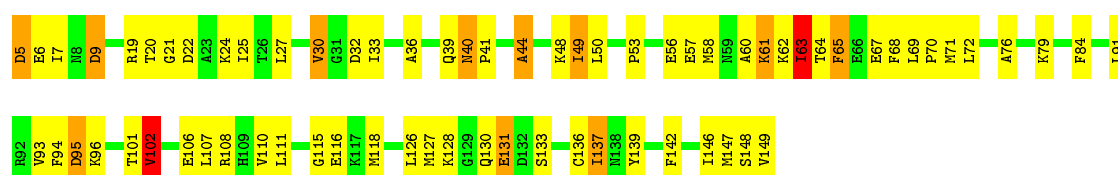
- Molecule 1: MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM

Chain 22-B: 48% 37% 13%



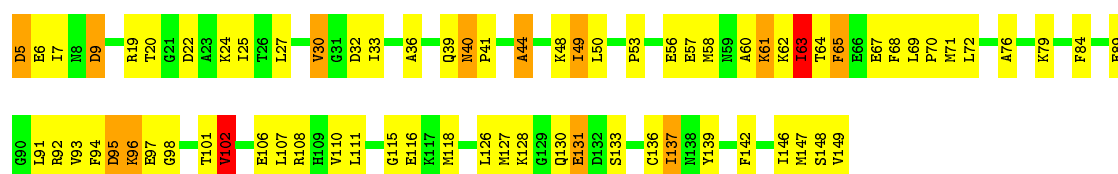
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 1-C: 52% 39% 8%



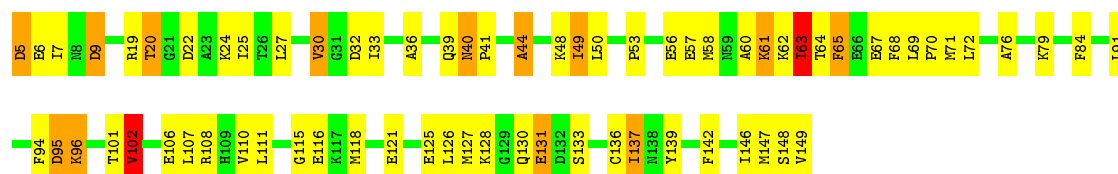
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 2-C: 50% 41% 8%

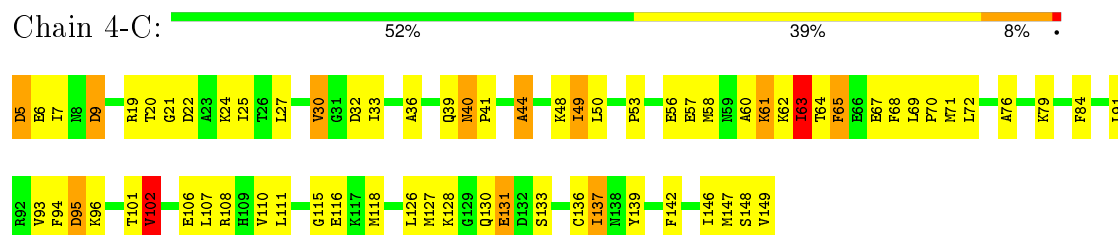


- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

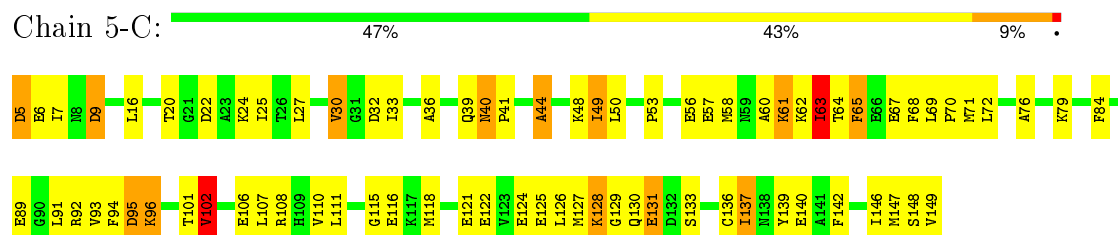
Chain 3-C: 52% 38% 9%



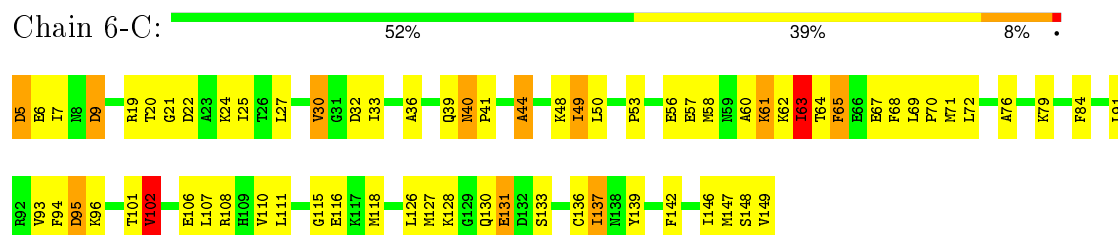
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



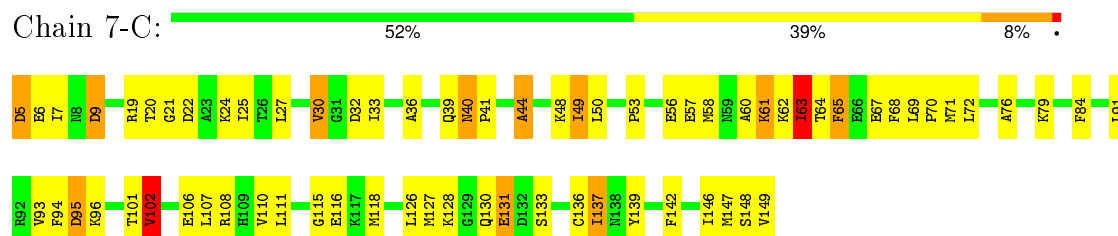
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



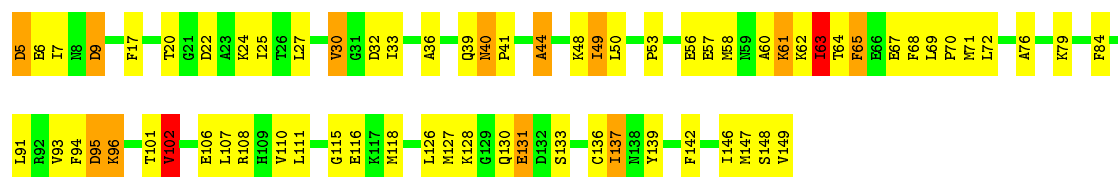
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



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

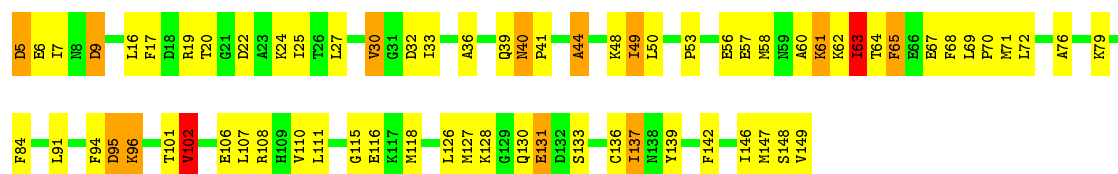


- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



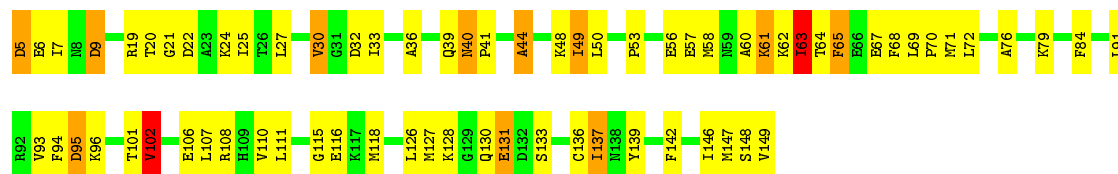
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 9-C: 52% 39% 8%



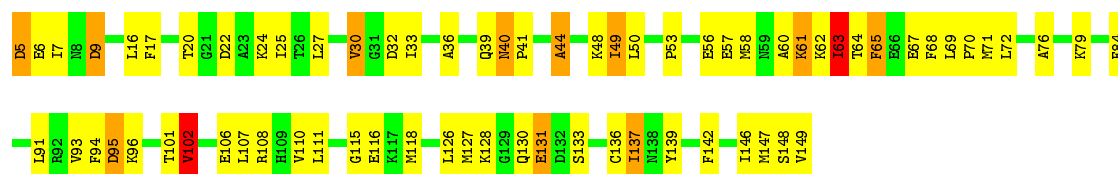
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 10-C: 52% 39% 8%



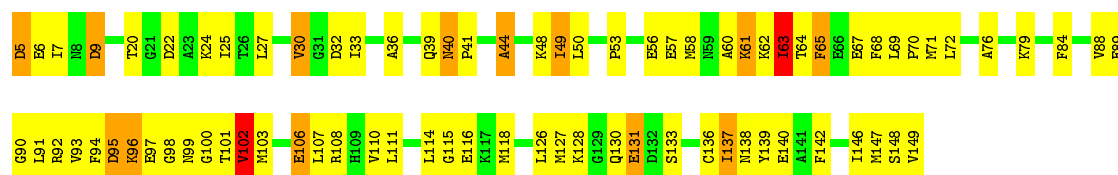
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 11-C: 52% 39% 8%



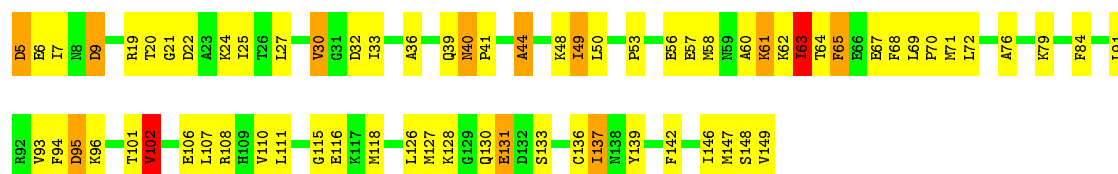
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 12-C: 45% 45% 9%

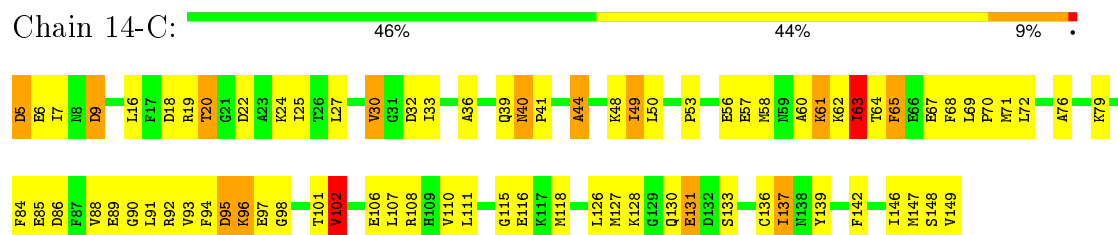


- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

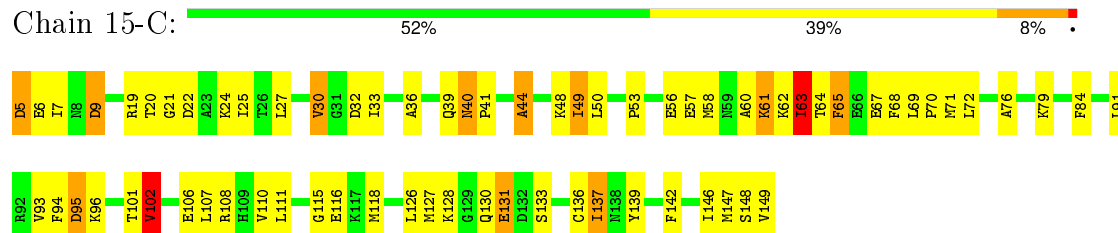
Chain 13-C: 52% 39% 8%



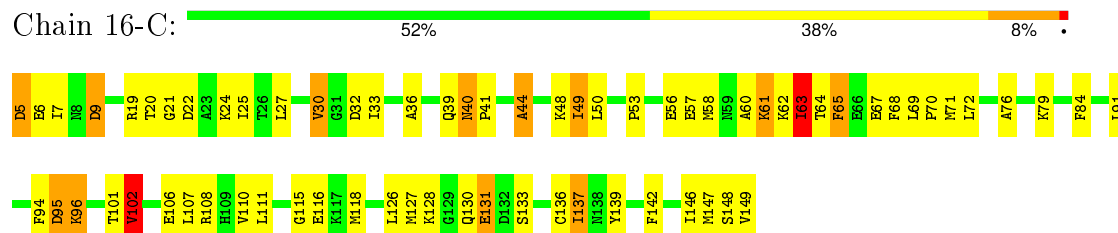
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



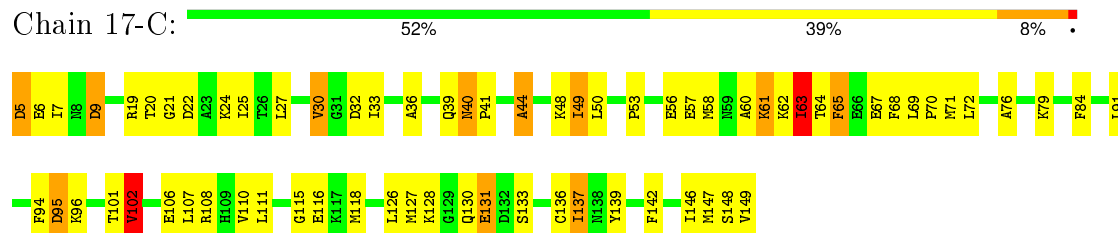
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



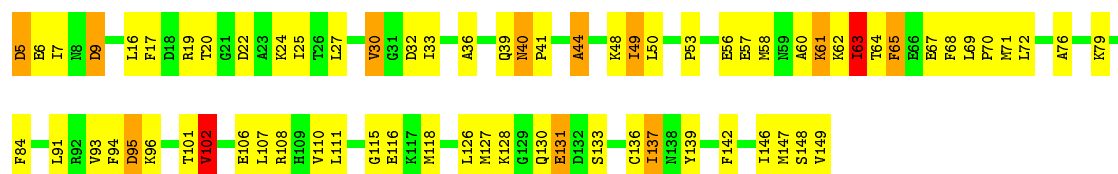
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



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

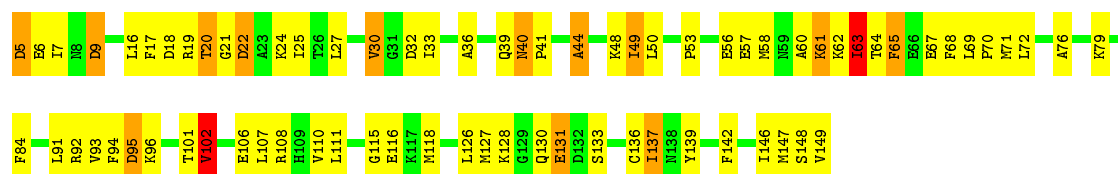


- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM



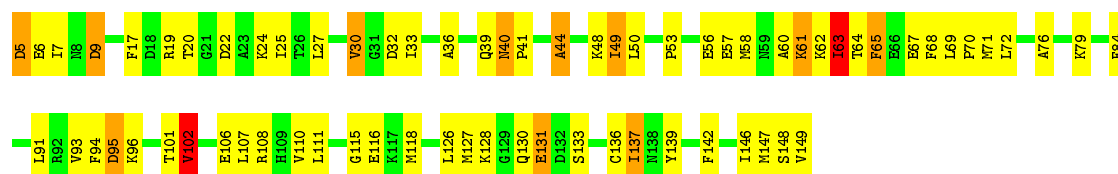
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 19-C: 49% 41% 9%



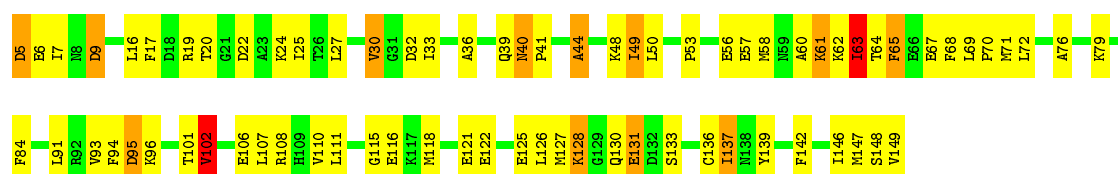
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 20-C: 52% 39% 8%



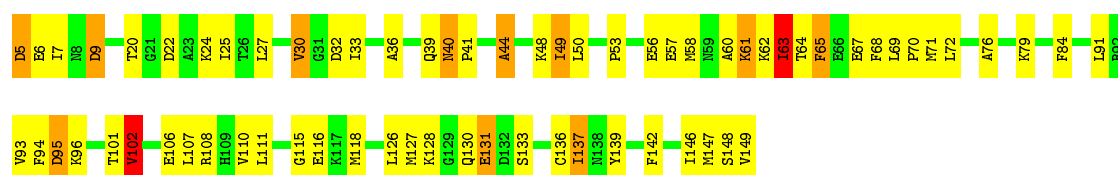
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 21-C: 49% 41% 8%



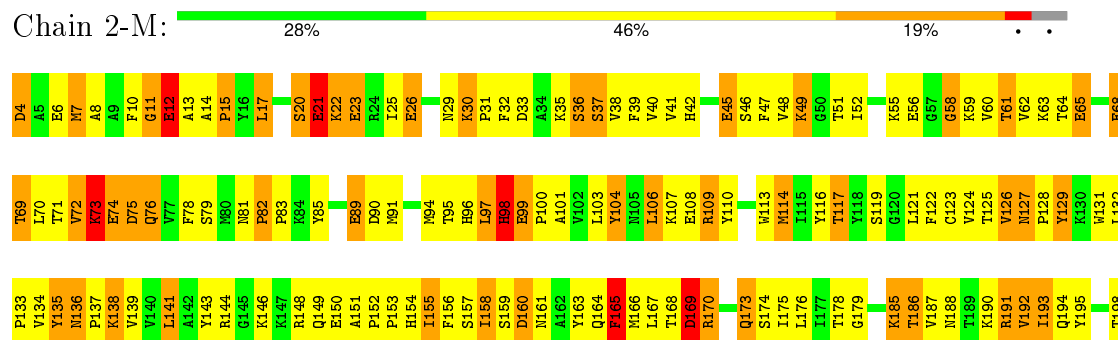
- Molecule 2: MYOSIN LIGHT CHAIN 3, SKELETAL MUSCLE ISOFORM

Chain 22-C: 53% 38% 8%

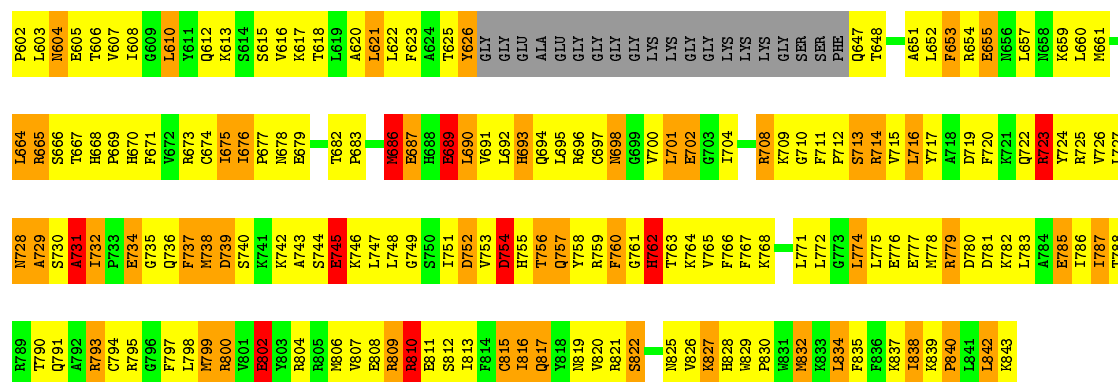


- Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 1-M: 27% 46% 19%

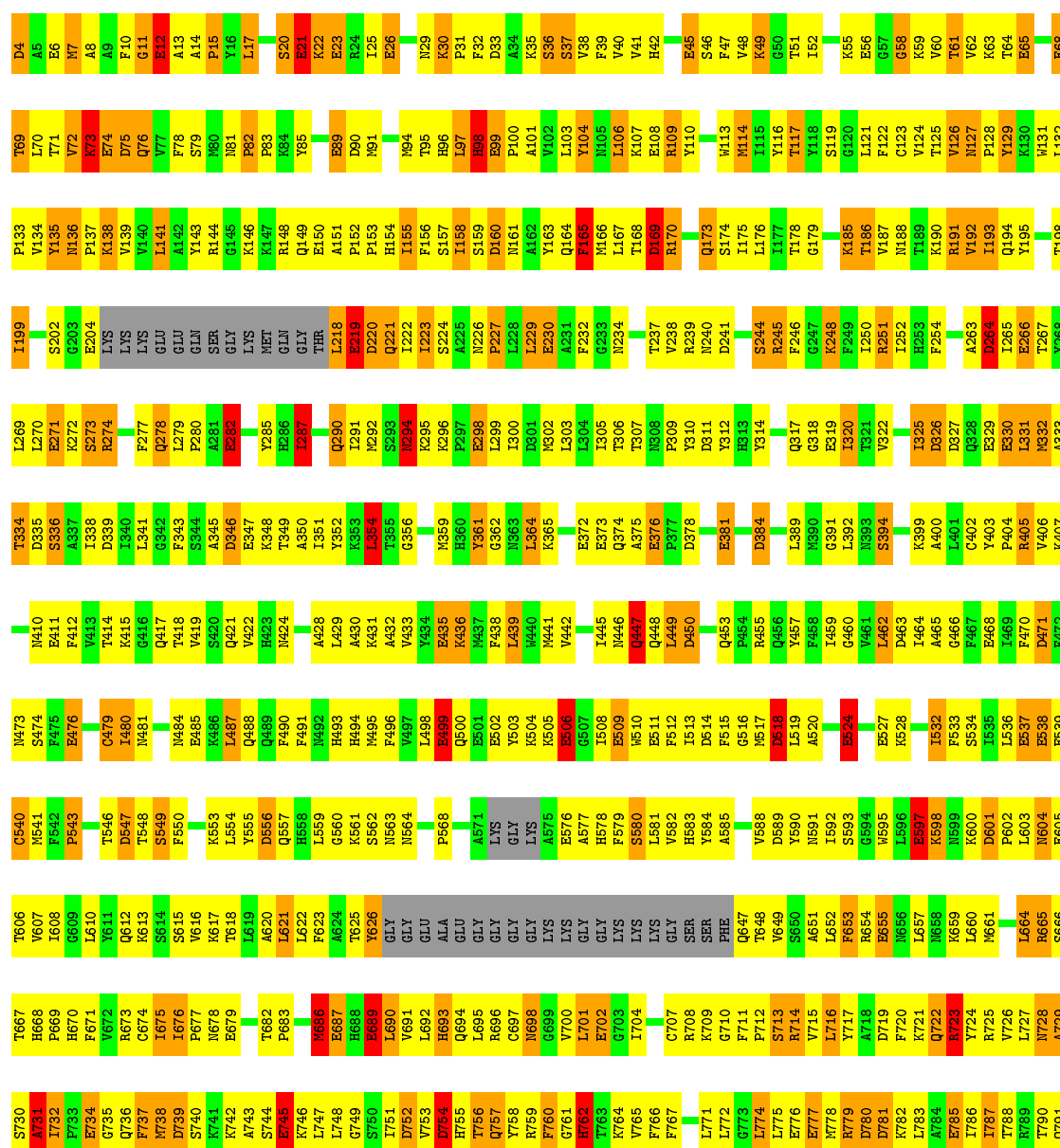


Chain 2-M:



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

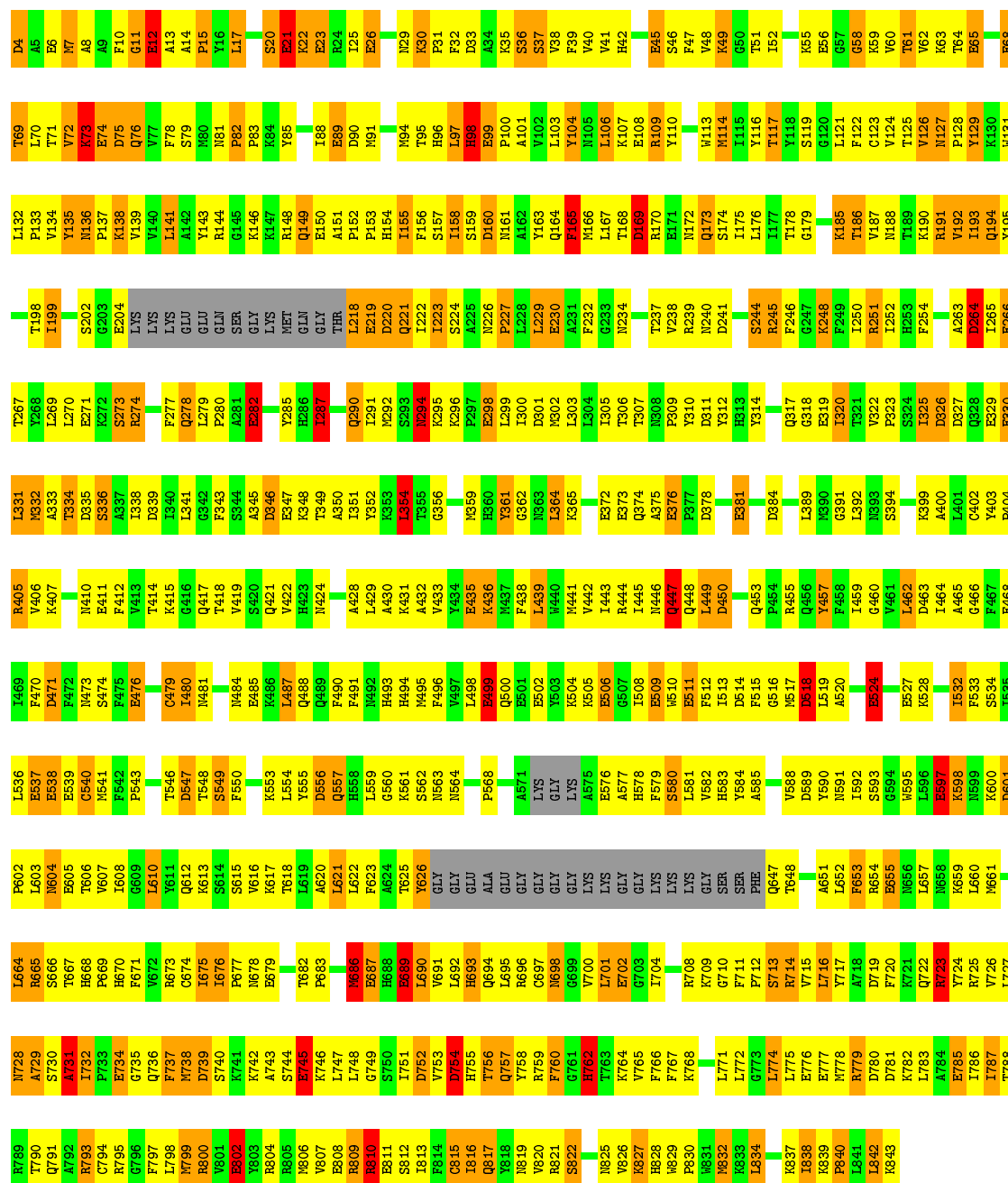
Chain 5-M: 27% 47% 19%





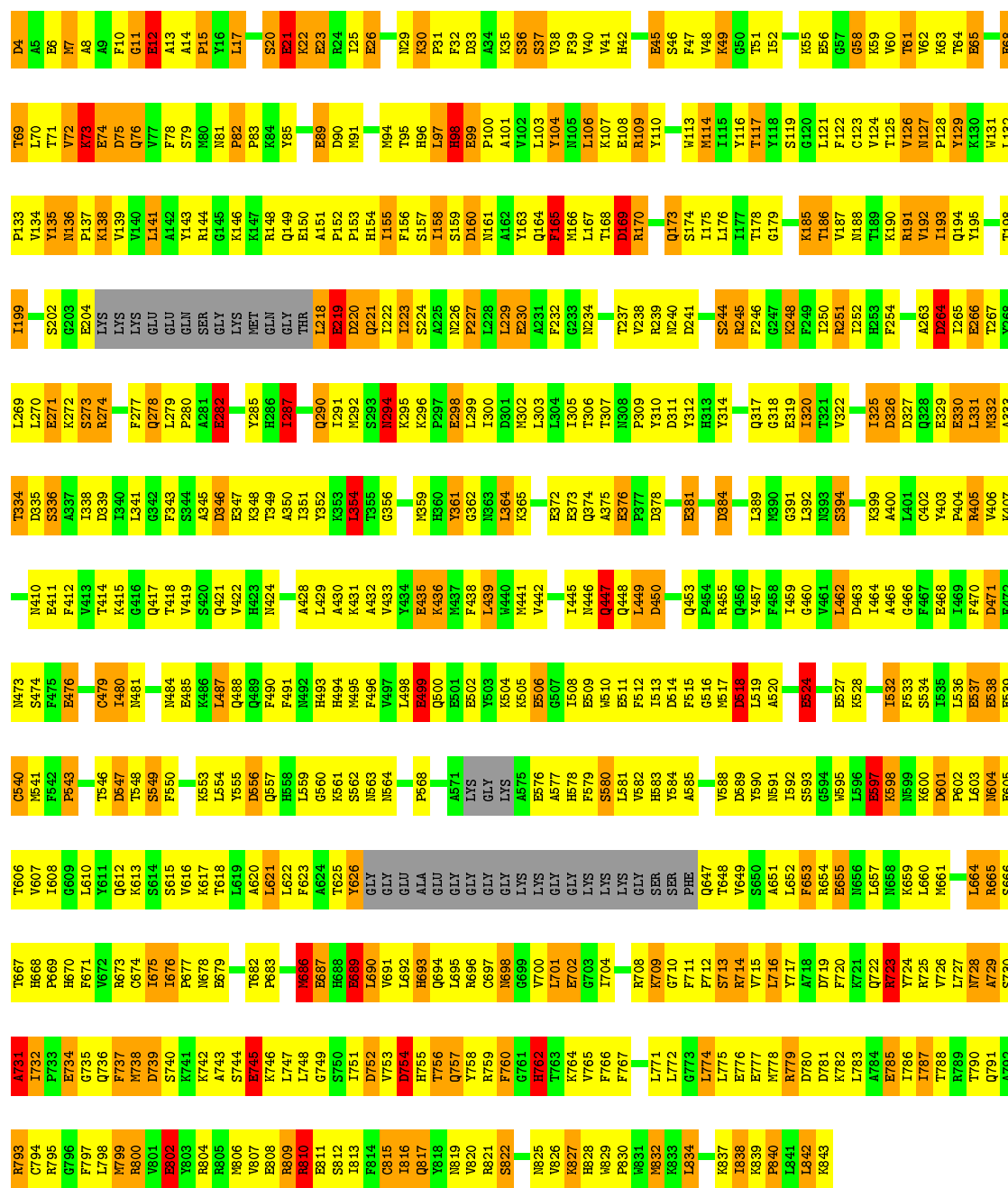
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 6-M: 27% 47% 19%



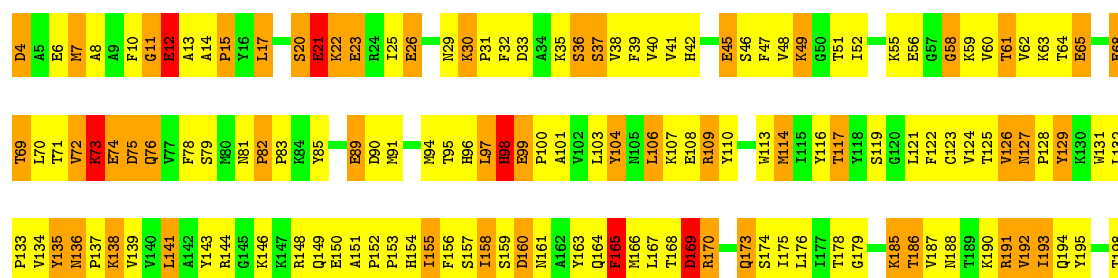
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

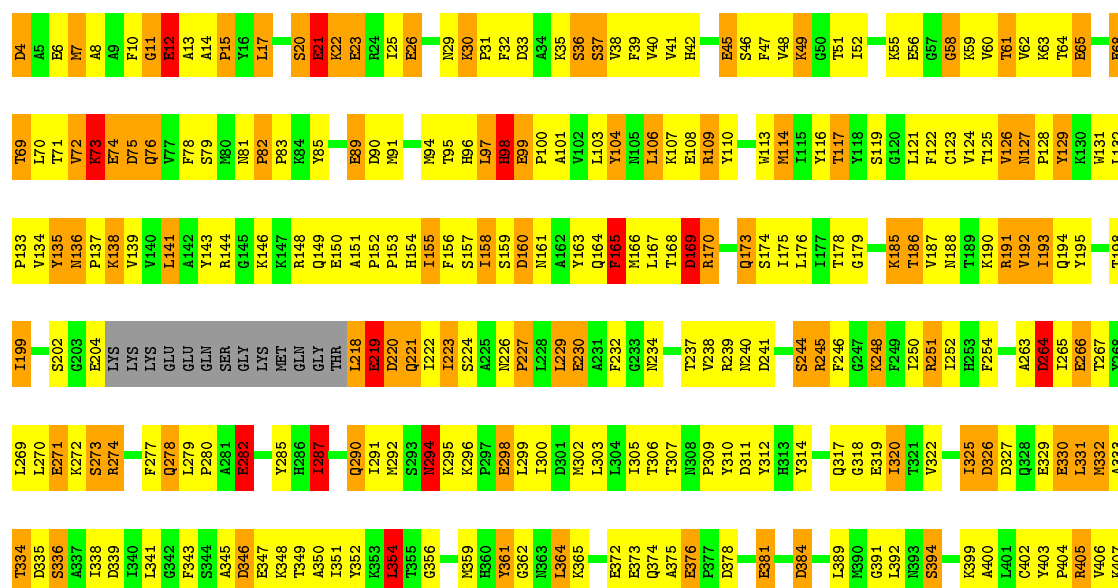
Chain 7-M: 28% 46% 18%



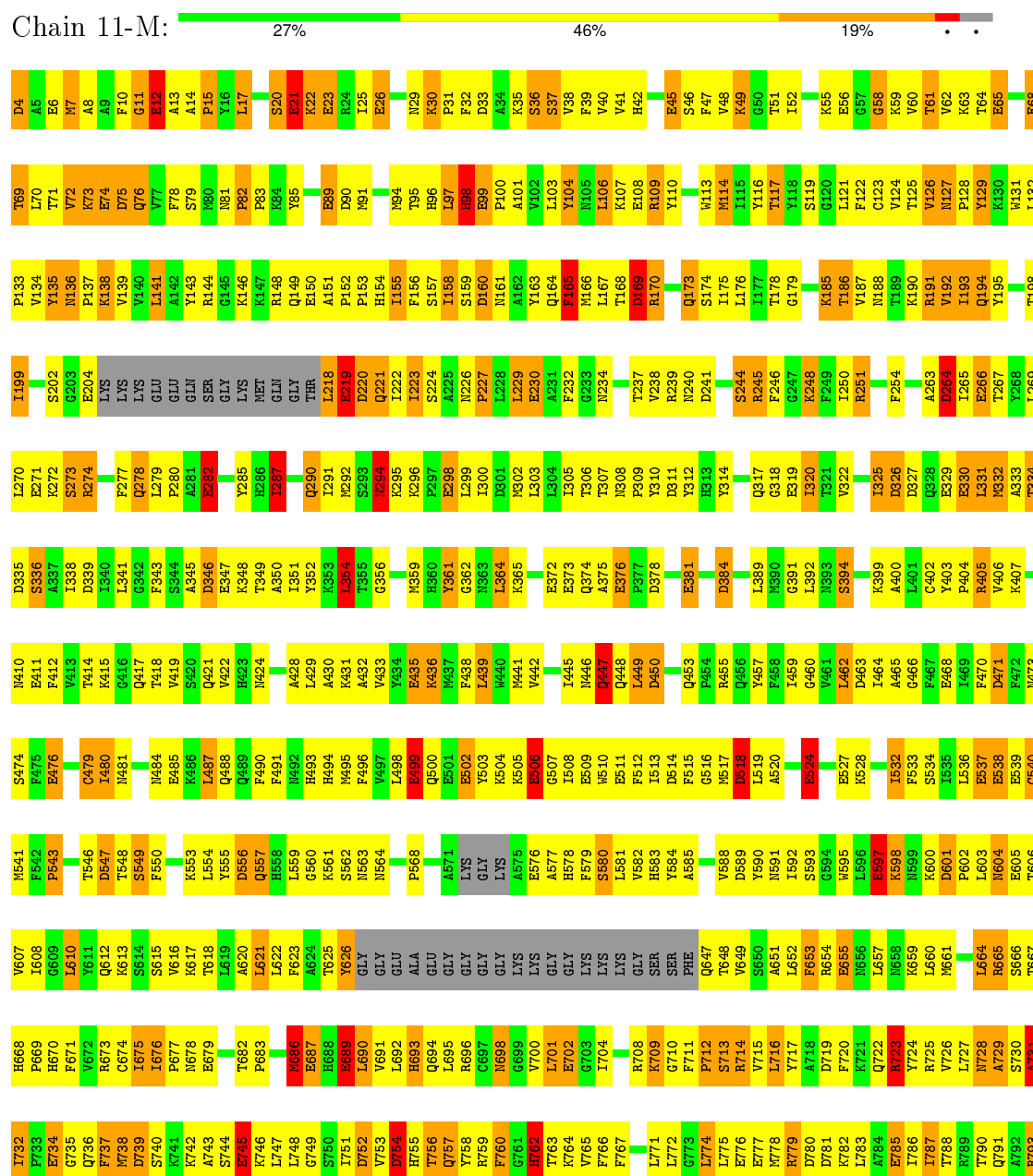
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 8-M: 27% 46% 19%





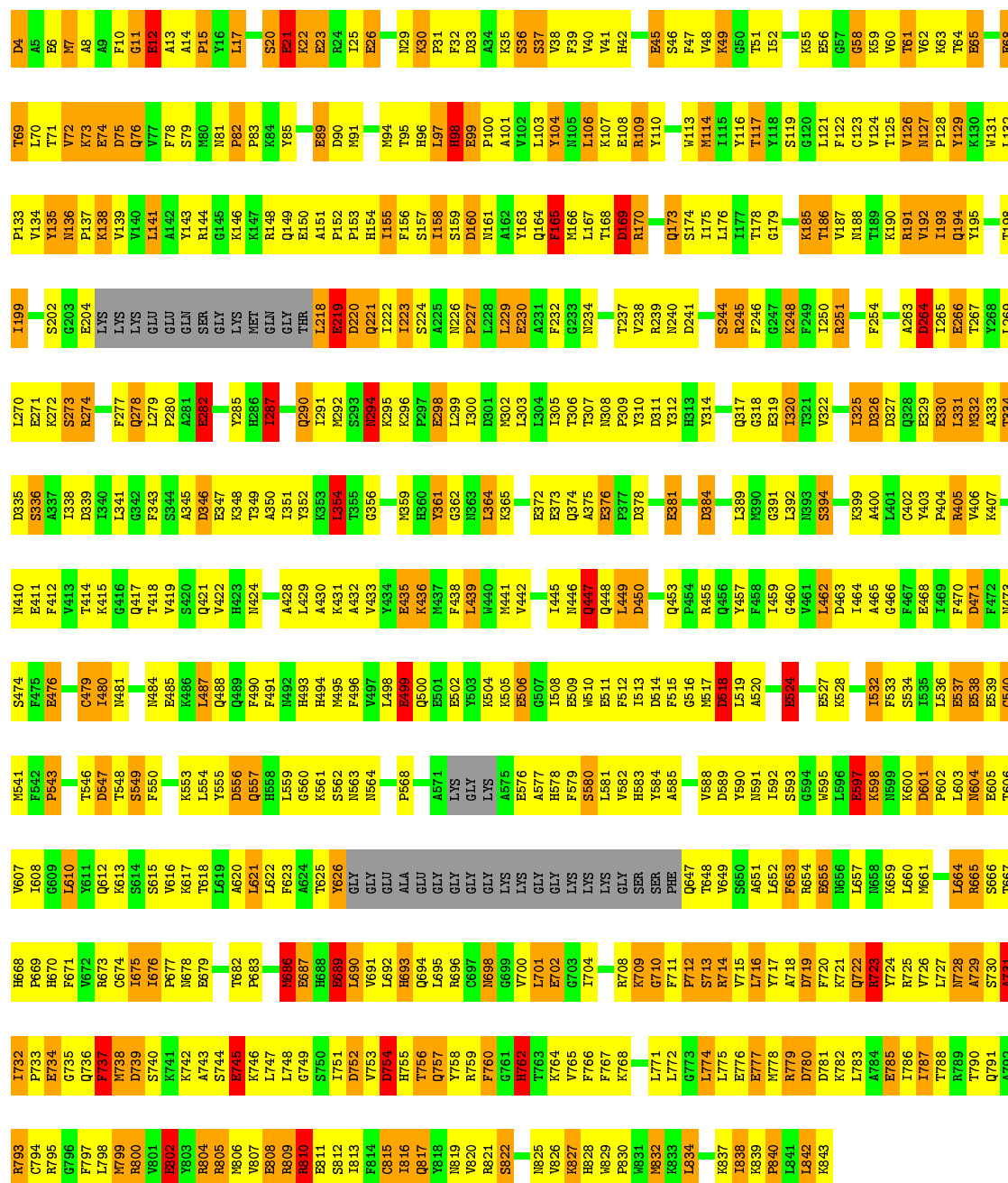
- Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT





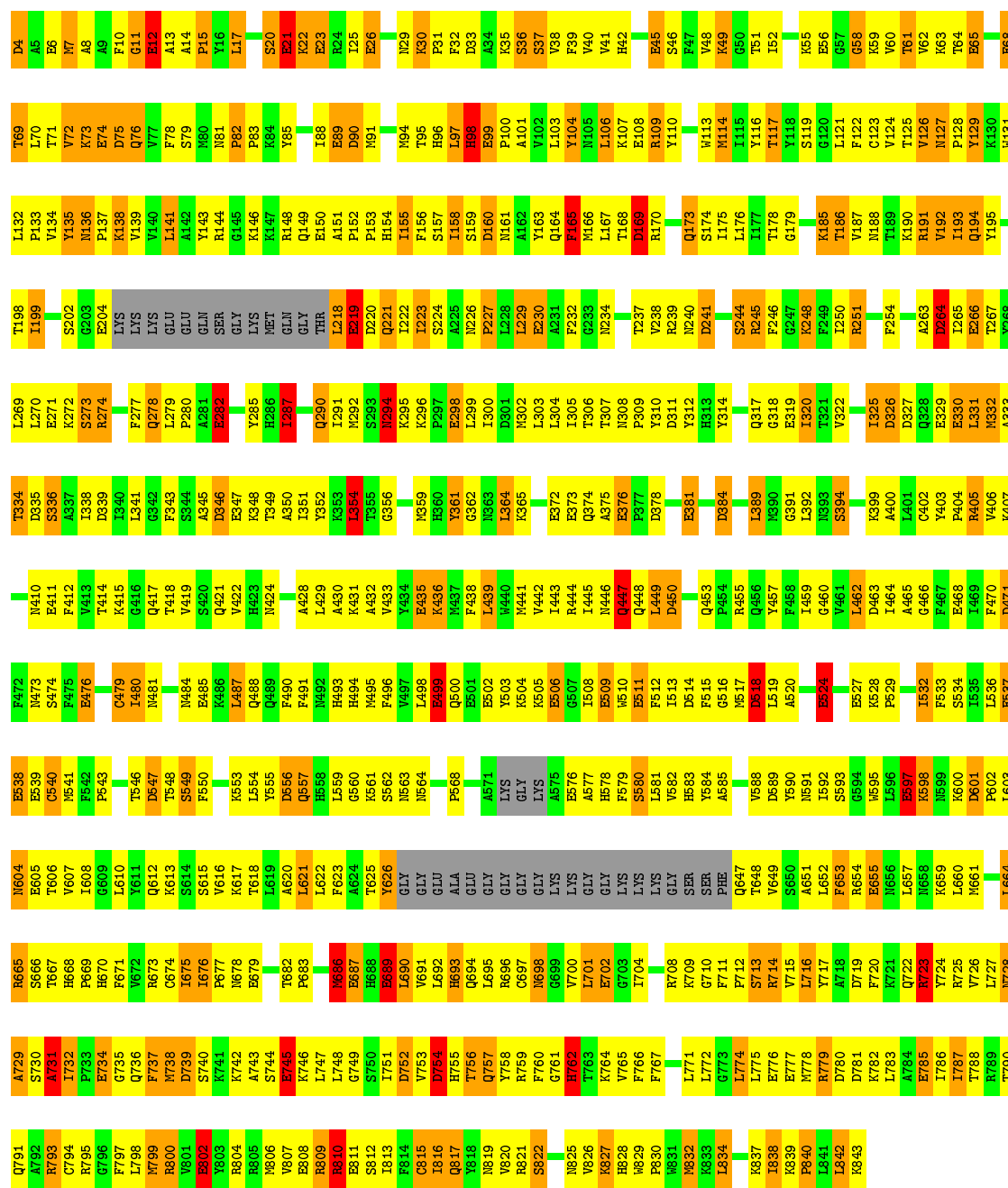
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 12-M: 27% 45% 20%

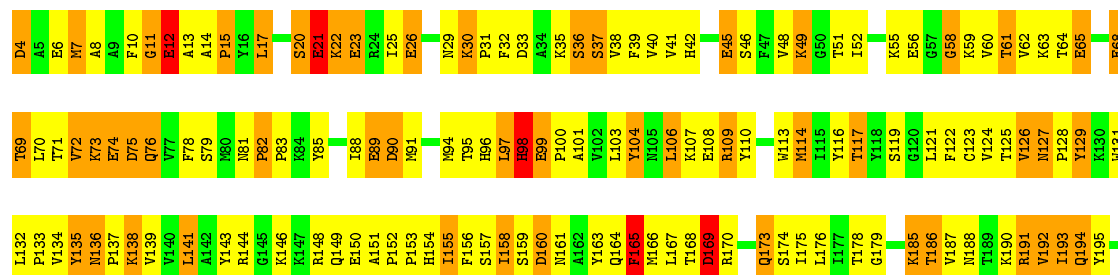


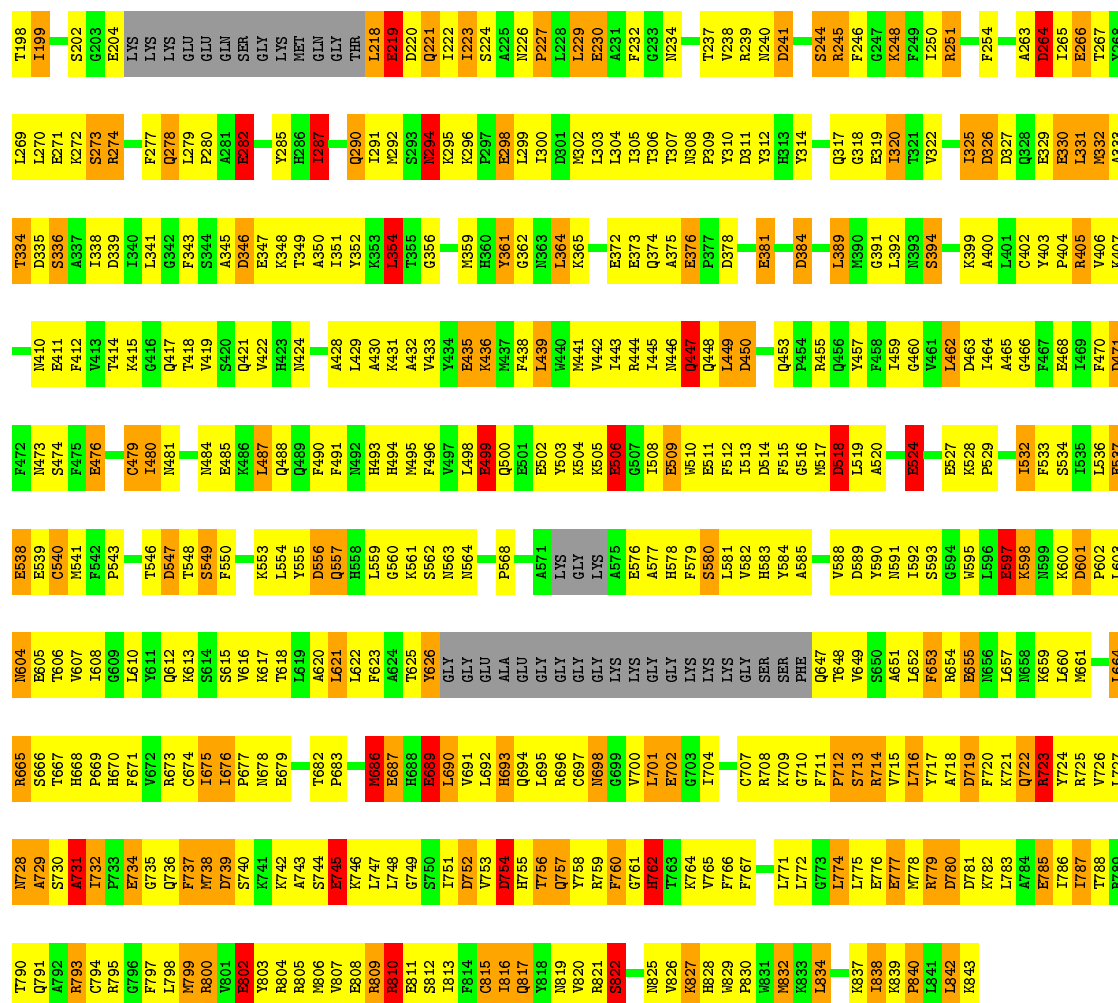
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 13-M: 27% 47% 19%



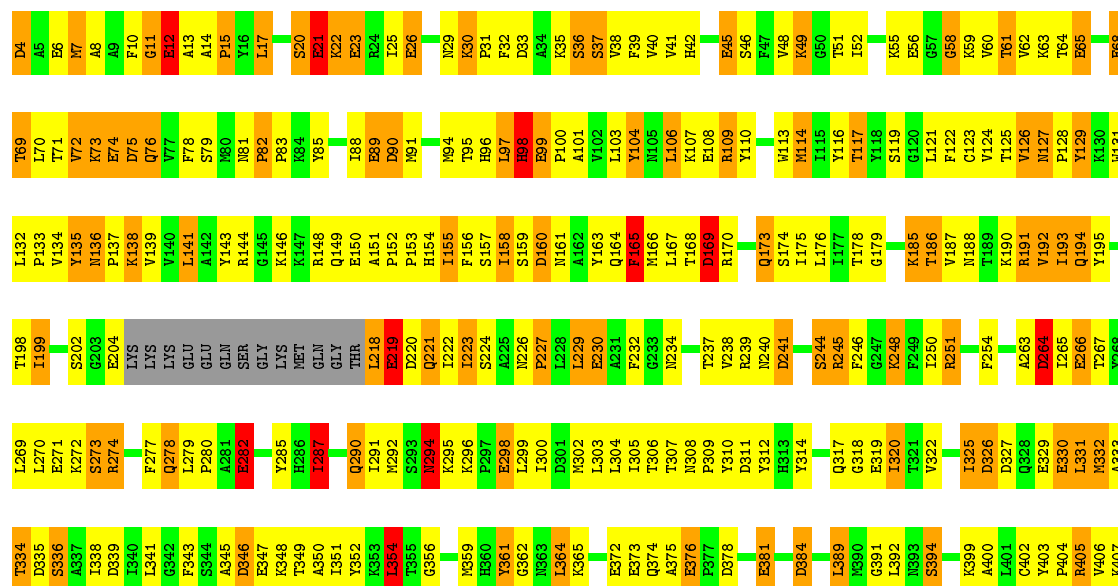
Chain 14-M: 27% 47% 19%

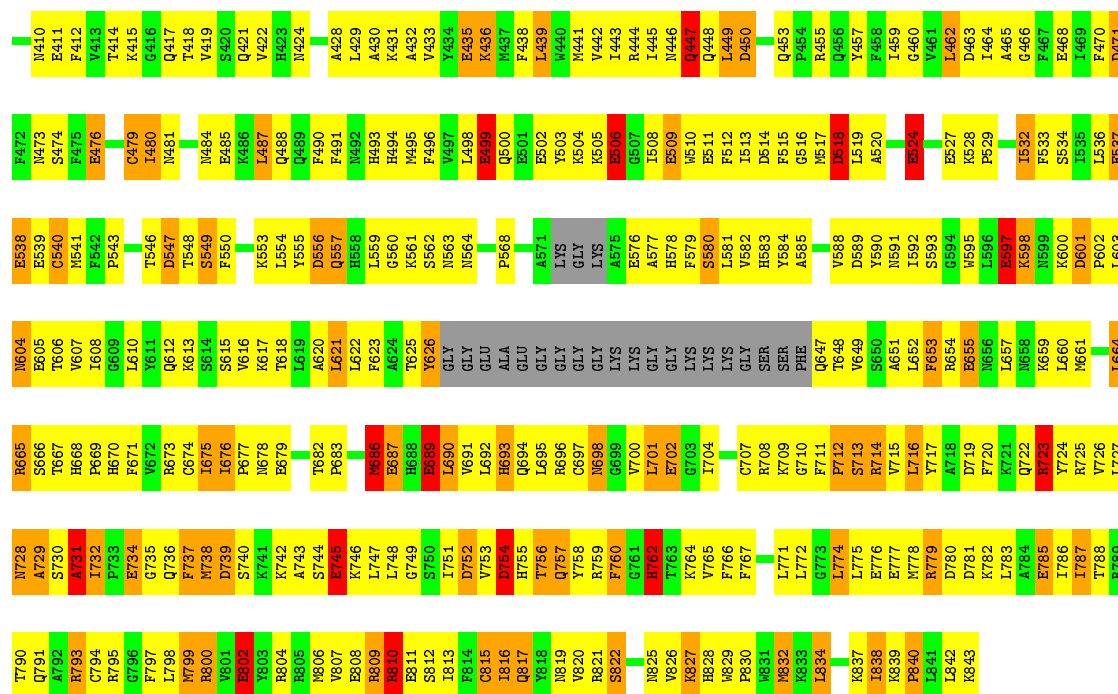




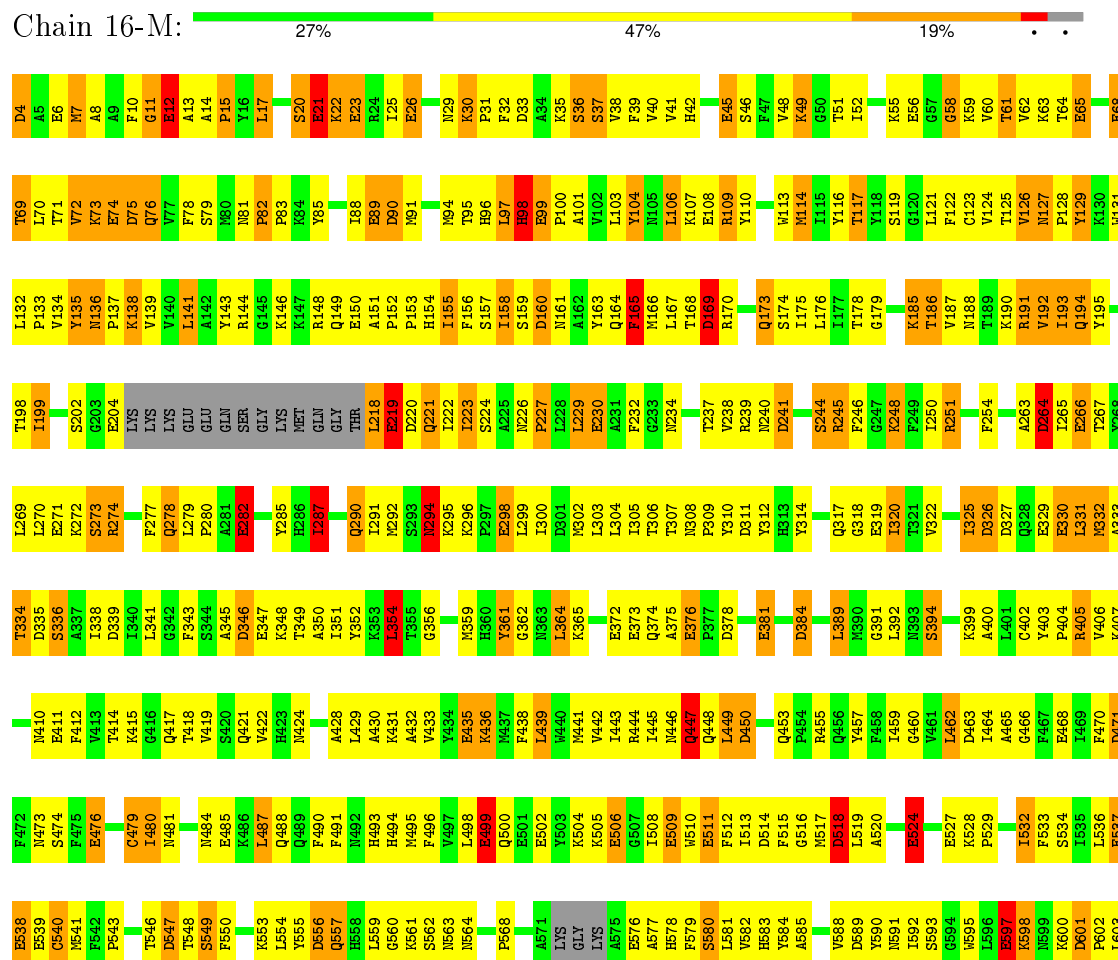
● Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

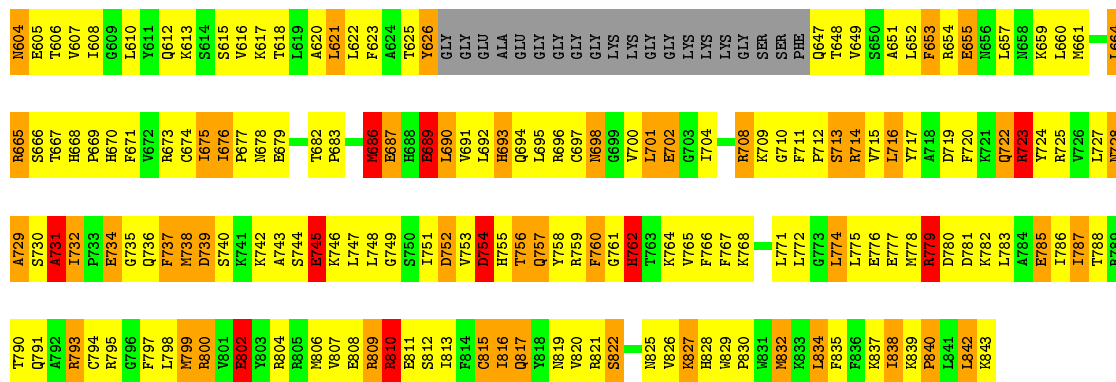
Chain 15-M: 27% 47% 19%





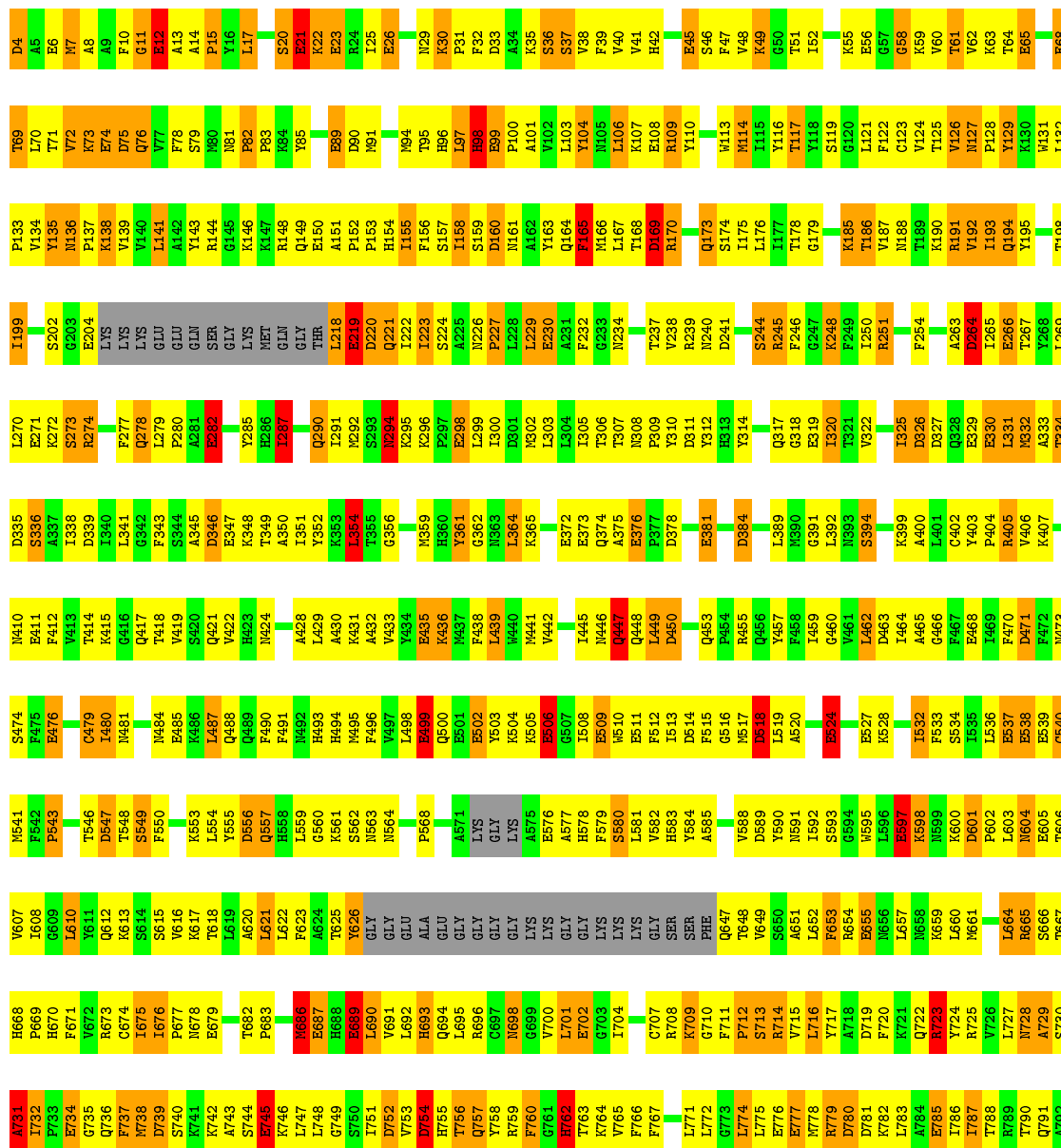
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT





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

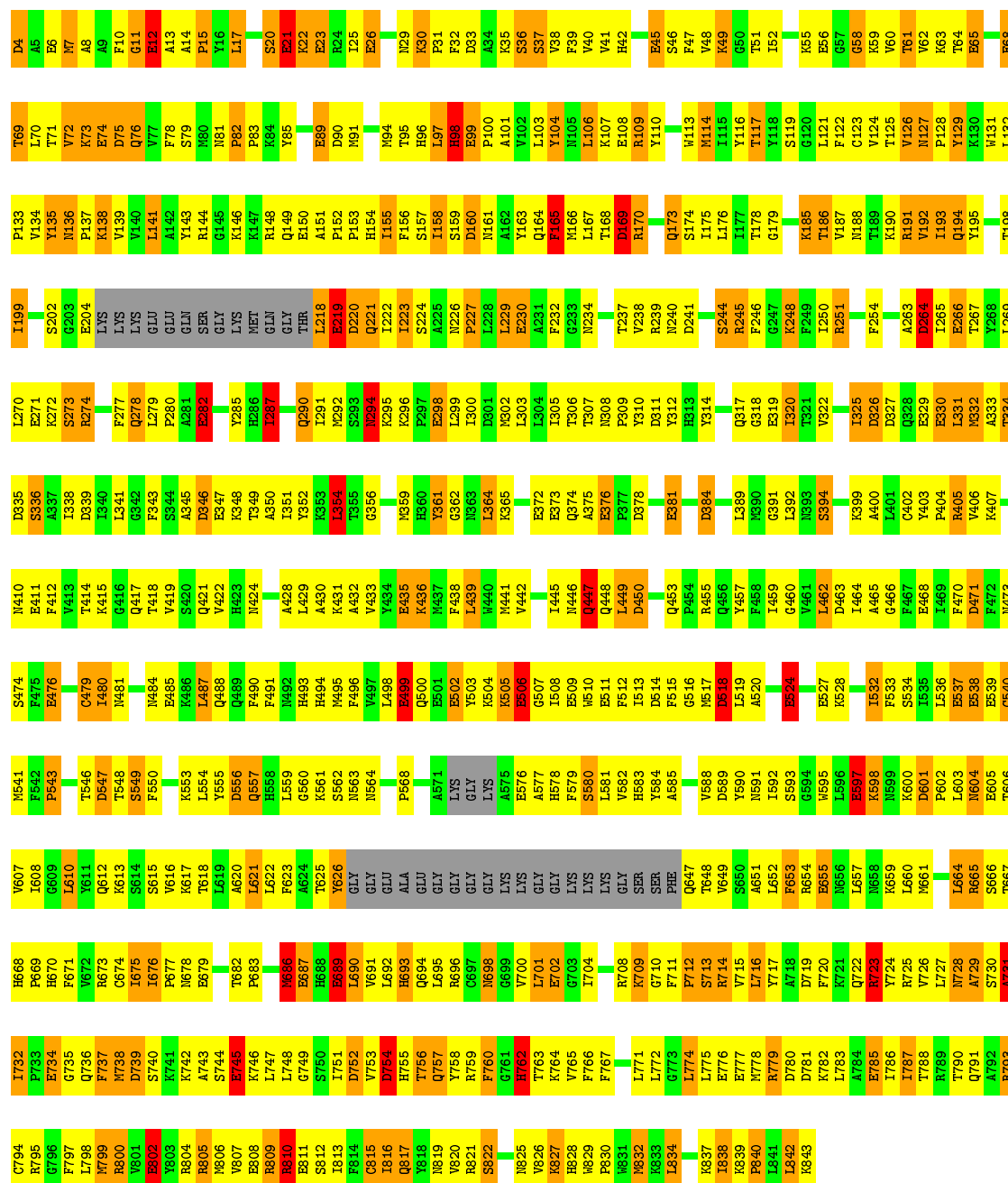
Chain 17-M: 28% 46% 19%





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

Chain 18-M: 28% 46% 19%



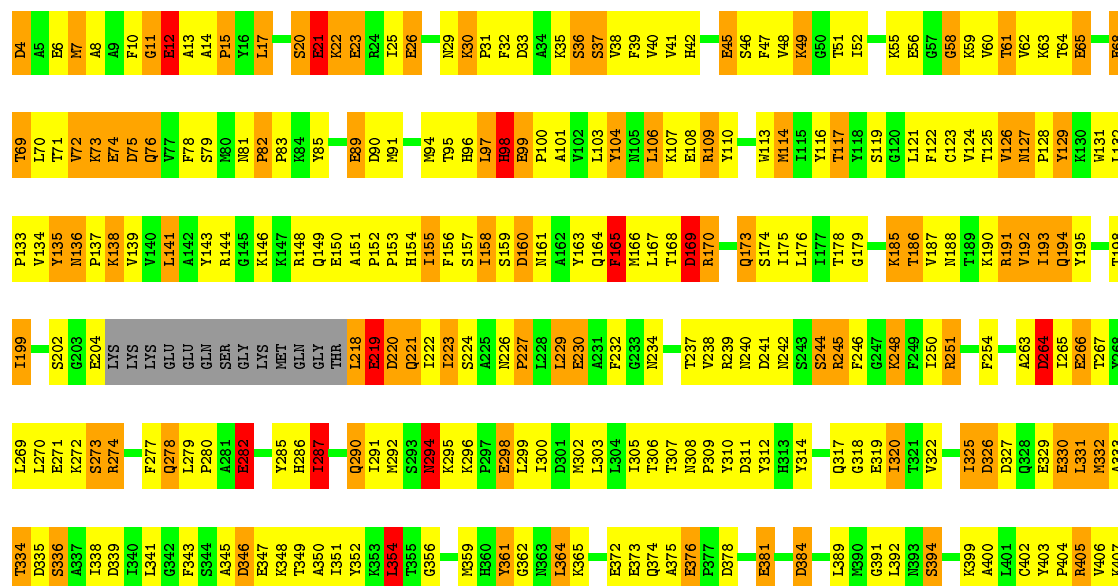
• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

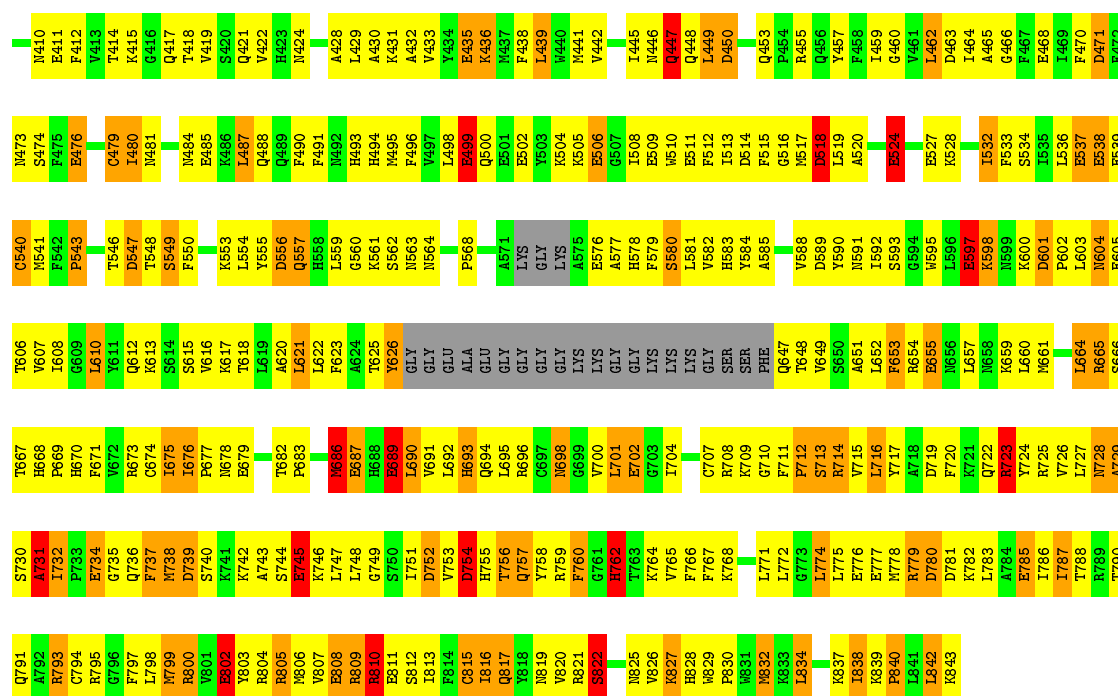
Chain 19-M: 27% 46% 19%



Frequency	Percentage
Daily	27%
Often	47%
Sometimes	19%
Never	5%

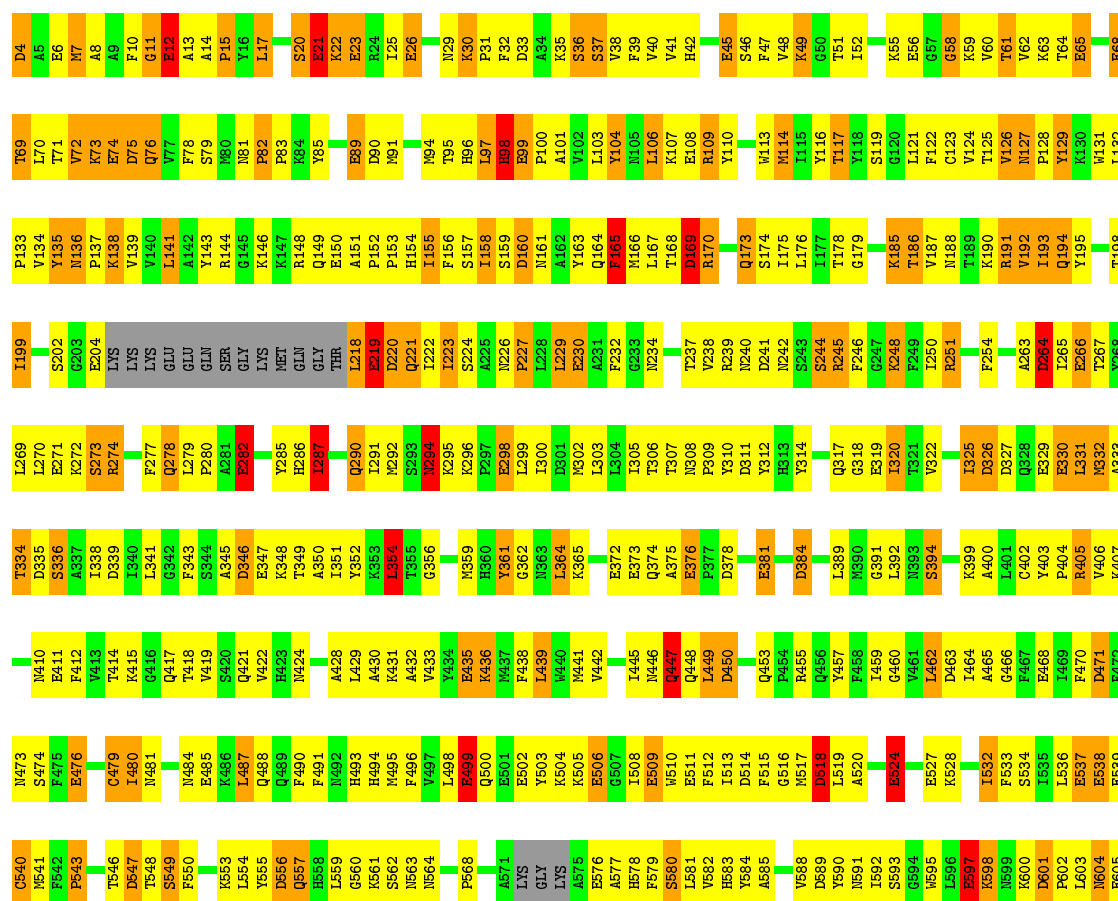






• Molecule 3: MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT

Chain 22-M:






4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	TIETZ TEM-CAM F224	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	1-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	10-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	11-B	0.69	0/1199	1.67	18/1617 (1.1%)
1	12-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	13-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	14-B	0.70	0/1199	1.67	17/1617 (1.1%)
1	15-B	0.70	0/1199	1.67	17/1617 (1.1%)
1	16-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	17-B	0.69	0/1199	1.67	18/1617 (1.1%)
1	18-B	0.70	0/1199	1.67	17/1617 (1.1%)
1	19-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	2-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	20-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	21-B	0.70	0/1199	1.67	17/1617 (1.1%)
1	22-B	0.70	0/1199	1.67	17/1617 (1.1%)
1	3-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	4-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	5-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	6-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	7-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	8-B	0.70	0/1199	1.67	18/1617 (1.1%)
1	9-B	0.70	0/1199	1.67	18/1617 (1.1%)
2	1-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	10-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	11-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	12-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	13-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	14-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	15-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	16-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	17-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	18-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	19-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	2-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
2	20-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	21-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	22-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	3-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	4-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	5-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	6-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
2	7-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	8-C	0.74	1/1140 (0.1%)	1.58	9/1530 (0.6%)
2	9-C	0.74	1/1140 (0.1%)	1.59	9/1530 (0.6%)
3	1-M	1.28	59/6593 (0.9%)	1.53	96/8881 (1.1%)
3	10-M	1.32	61/6594 (0.9%)	1.54	97/8884 (1.1%)
3	11-M	1.31	59/6593 (0.9%)	1.54	98/8881 (1.1%)
3	12-M	1.32	60/6593 (0.9%)	1.54	98/8881 (1.1%)
3	13-M	1.28	59/6593 (0.9%)	1.53	96/8881 (1.1%)
3	14-M	1.28	60/6592 (0.9%)	1.54	97/8878 (1.1%)
3	15-M	1.28	59/6593 (0.9%)	1.53	96/8881 (1.1%)
3	16-M	1.28	59/6593 (0.9%)	1.54	96/8881 (1.1%)
3	17-M	1.36	60/6594 (0.9%)	1.56	101/8884 (1.1%)
3	18-M	1.32	60/6594 (0.9%)	1.54	98/8884 (1.1%)
3	19-M	1.29	61/6593 (0.9%)	1.56	99/8881 (1.1%)
3	2-M	1.30	62/6593 (0.9%)	1.54	98/8881 (1.1%)
3	20-M	1.28	60/6593 (0.9%)	1.54	96/8881 (1.1%)
3	21-M	1.30	59/6593 (0.9%)	1.54	98/8881 (1.1%)
3	22-M	1.29	59/6593 (0.9%)	1.54	98/8881 (1.1%)
3	3-M	1.28	60/6593 (0.9%)	1.54	97/8881 (1.1%)
3	4-M	1.28	59/6593 (0.9%)	1.53	96/8881 (1.1%)
3	5-M	1.31	61/6592 (0.9%)	1.54	98/8878 (1.1%)
3	6-M	1.28	59/6593 (0.9%)	1.53	96/8881 (1.1%)
3	7-M	1.33	61/6594 (0.9%)	1.54	97/8884 (1.1%)
3	8-M	1.28	60/6592 (0.9%)	1.54	95/8878 (1.1%)
3	9-M	1.28	61/6593 (0.9%)	1.54	99/8881 (1.1%)
All	All	1.17	1340/196505 (0.7%)	1.56	2729/264619 (1.0%)

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	10-B	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
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	2-B	0	4
1	20-B	0	4
1	21-B	0	4
1	22-B	0	4
1	3-B	0	4
1	4-B	0	4
1	5-B	0	4
1	6-B	0	4
1	7-B	0	4
1	8-B	0	4
1	9-B	0	4
3	1-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	2-M	0	1
3	20-M	0	1
3	21-M	0	1
3	22-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

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

The worst 5 of 1340 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	17-M	709	LYS	C-N	36.40	1.98	1.33
3	7-M	709	LYS	C-N	30.92	1.88	1.33
3	10-M	709	LYS	C-N	27.52	1.82	1.33
3	18-M	709	LYS	C-N	26.92	1.81	1.33
3	12-M	709	LYS	C-N	26.38	1.80	1.33

The worst 5 of 2729 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8-M	731	ALA	O-C-N	-28.59	76.95	122.70
3	3-M	731	ALA	O-C-N	-28.59	76.97	122.70
3	9-M	731	ALA	O-C-N	-28.58	76.97	122.70
3	2-M	731	ALA	O-C-N	-28.57	76.98	122.70
3	5-M	731	ALA	O-C-N	-28.57	76.98	122.70

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	131	0
1	2-B	1177	0	1134	136	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3-B	1177	0	1132	176	0
1	4-B	1177	0	1134	133	0
1	5-B	1177	0	1132	251	0
1	6-B	1177	0	1134	135	0
1	7-B	1177	0	1134	139	0
1	8-B	1177	0	1134	134	0
1	9-B	1177	0	1134	136	0
1	10-B	1177	0	1134	133	0
1	11-B	1177	0	1134	134	0
1	12-B	1177	0	1134	127	0
1	13-B	1177	0	1134	132	0
1	14-B	1177	0	1134	161	0
1	15-B	1177	0	1134	134	0
1	16-B	1177	0	1134	136	0
1	17-B	1177	0	1134	137	0
1	18-B	1177	0	1134	134	0
1	19-B	1177	0	1131	185	0
1	20-B	1177	0	1134	146	0
1	21-B	1177	0	1131	193	0
1	22-B	1177	0	1134	131	0
2	1-C	1126	0	1084	88	0
2	2-C	1126	0	1084	210	0
2	3-C	1126	0	1082	134	0
2	4-C	1126	0	1084	87	0
2	5-C	1126	0	1077	211	0
2	6-C	1126	0	1084	88	0
2	7-C	1126	0	1084	89	0
2	8-C	1126	0	1084	94	0
2	9-C	1126	0	1084	89	0
2	10-C	1126	0	1084	89	0
2	11-C	1126	0	1084	91	0
2	12-C	1126	0	1072	320	0
2	13-C	1126	0	1084	85	0
2	14-C	1126	0	1079	205	0
2	15-C	1126	0	1084	89	0
2	16-C	1126	0	1084	91	0
2	17-C	1126	0	1084	85	0
2	18-C	1126	0	1084	90	0
2	19-C	1126	0	1079	166	0
2	20-C	1126	0	1084	102	0
2	21-C	1126	0	1082	153	0
2	22-C	1126	0	1084	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	1-M	6455	0	6382	873	0
3	2-M	6455	0	6379	961	0
3	3-M	6455	0	6378	852	0
3	4-M	6455	0	6382	830	0
3	5-M	6455	0	6375	957	0
3	6-M	6455	0	6376	824	0
3	7-M	6455	0	6383	836	0
3	8-M	6455	0	6382	914	0
3	9-M	6455	0	6383	832	0
3	10-M	6455	0	6379	863	0
3	11-M	6455	0	6379	890	0
3	12-M	6455	0	6370	1075	0
3	13-M	6455	0	6382	865	0
3	14-M	6455	0	6364	1004	0
3	15-M	6455	0	6379	843	0
3	16-M	6455	0	6378	862	0
3	17-M	6455	0	6380	850	0
3	18-M	6455	0	6381	854	0
3	19-M	6455	0	6378	887	0
3	20-M	6455	0	6381	842	0
3	21-M	6455	0	6380	842	0
3	22-M	6455	0	6382	835	0
All	All	192676	0	189086	21901	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 57.

The worst 5 of 21901 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	19
1	2-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	19
1	3-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	19
1	4-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	5-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	6-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	7-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	8-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	9-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	10-B	148/150 (99%)	120 (81%)	16 (11%)	12 (8%)	1	19
1	11-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	12-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	13-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	14-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	15-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	16-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	17-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	18-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	19-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	20-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	21-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
1	22-B	148/150 (99%)	119 (80%)	17 (12%)	12 (8%)	1	19
2	1-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	2-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	3-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	4-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	5-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	6-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	7-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	8-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	9-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	10-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	11-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	12-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	13-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	14-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	15-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	16-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	17-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	18-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	19-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	20-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	21-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
2	22-C	143/145 (99%)	111 (78%)	20 (14%)	12 (8%)	1	18
3	1-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	6	44
3	2-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	3-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	4-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	6	44
3	5-M	784/840 (93%)	647 (82%)	114 (14%)	23 (3%)	6	43
3	6-M	786/840 (94%)	649 (83%)	115 (15%)	22 (3%)	6	44
3	7-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	6	43
3	8-M	784/840 (93%)	646 (82%)	115 (15%)	23 (3%)	6	43
3	9-M	786/840 (94%)	648 (82%)	115 (15%)	23 (3%)	6	43
3	10-M	788/840 (94%)	651 (83%)	114 (14%)	23 (3%)	6	43
3	11-M	786/840 (94%)	648 (82%)	115 (15%)	23 (3%)	6	43
3	12-M	786/840 (94%)	647 (82%)	115 (15%)	24 (3%)	5	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	13-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	14-M	784/840 (93%)	646 (82%)	114 (14%)	24 (3%)	5	42
3	15-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	16-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	17-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	6	43
3	18-M	788/840 (94%)	650 (82%)	115 (15%)	23 (3%)	6	43
3	19-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	20-M	786/840 (94%)	649 (83%)	114 (14%)	23 (3%)	6	43
3	21-M	786/840 (94%)	647 (82%)	115 (15%)	24 (3%)	5	42
3	22-M	786/840 (94%)	648 (82%)	114 (14%)	24 (3%)	5	42
All	All	23696/24970 (95%)	19331 (82%)	3330 (14%)	1035 (4%)	6	33

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 ⓘ

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%)	11	42
1	2-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	3-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	4-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	5-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	6-B	128/130 (98%)	116 (91%)	12 (9%)	11	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	7-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	8-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	9-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	10-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	11-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	12-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	13-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	14-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	15-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	16-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	17-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	18-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	19-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	20-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	21-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
1	22-B	128/130 (98%)	116 (91%)	12 (9%)	11	42
2	1-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	2-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	3-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	4-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	5-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	6-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	7-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	8-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	9-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	10-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	11-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	12-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	13-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	14-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	15-C	120/122 (98%)	109 (91%)	11 (9%)	11	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	16-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	17-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	18-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	19-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	20-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	21-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
2	22-C	120/122 (98%)	109 (91%)	11 (9%)	11	43
3	1-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	2-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	3-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	4-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	5-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	6-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	7-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	8-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	9-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	10-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	11-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	12-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	13-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	14-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	15-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	16-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	17-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	18-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	19-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	20-M	693/724 (96%)	523 (76%)	170 (24%)	1	6
3	21-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
3	22-M	693/724 (96%)	522 (75%)	171 (25%)	1	6
All	All	20702/21472 (96%)	16443 (79%)	4259 (21%)	4	10

5 of 4259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	10-M	799	MET
3	13-M	159	SER
3	21-M	185	LYS
3	11-M	109	ARG
3	12-M	35	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 630 such sidechains are listed below:

Mol	Chain	Res	Type
2	11-C	40	ASN
3	13-M	317	GLN
3	21-M	188	ASN
3	11-M	290	GLN
3	12-M	188	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.