



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 03:01 AM UTC

PDB ID : 2W4U / pdb_00002w4u
EMDB ID : EMD-1584
Title : Isometrically contracting insect asynchronous flight muscle quick frozen after a length step
Authors : Wu, S.; Liu, J.; Reedy, M.C.; Tregear, R.T.; Winkler, H.; Franzini-Armstrong, C.; Sasaki, H.; Lucaveche, C.; Goldman, Y.E.; Reedy, M.K.; Taylor, K.A.
Deposited on : 2008-12-02
Resolution : 35.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

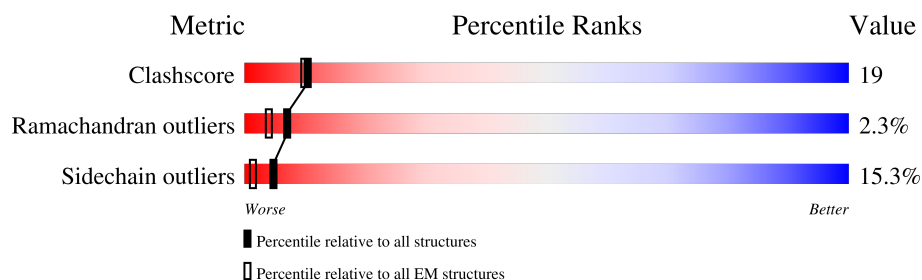
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 35.00 Å.

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



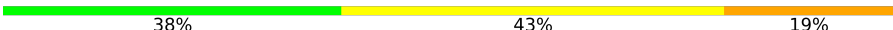
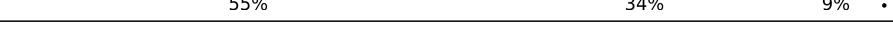
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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

Mol	Chain	Length	Quality of chain
1	0	159	43% 47% 8% .
1	3	159	44% 47% 8% .
1	6	159	42% 48% 8% .
1	9	159	43% 48% 8% .
2	1	90	51% 37% 12%
2	4	90	51% 36% 13%
2	7	90	51% 36% 13%
2	Y	90	51% 37% 12%
3	2	141	36% 44% 20%

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Mol	Chain	Length	Quality of chain
3	5	141	
3	8	141	
3	Z	141	
4	A	277	
4	B	277	
4	C	277	
4	T	277	
4	U	277	
4	V	277	
4	W	277	
4	X	277	
5	D	372	
5	E	372	
5	F	372	
5	G	372	
5	H	372	
5	I	372	
5	J	372	
5	K	372	
5	L	372	
5	M	372	
5	N	372	
5	O	372	
5	P	372	
5	Q	372	

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Mol	Chain	Length	Quality of chain
5	R	372	 55% 34% 10% •
5	S	372	 56% 33% 9% •

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 69221 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 TROPONIN C, SKELETAL MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	159	Total	C	N	O	S	0	0
			1252	770	199	272	11		
1	3	159	Total	C	N	O	S	0	0
			1252	770	199	272	11		
1	6	159	Total	C	N	O	S	0	0
			1252	770	199	272	11		
1	9	159	Total	C	N	O	S	0	0
			1252	770	199	272	11		

- Molecule 2 is a protein called TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	90	Total	C	N	O	0	0
			774	486	146	142		
2	4	90	Total	C	N	O	0	0
			774	486	146	142		
2	7	90	Total	C	N	O	0	0
			774	486	146	142		
2	Y	90	Total	C	N	O	0	0
			774	486	146	142		

- Molecule 3 is a protein called TROPONIN I, FAST SKELETAL MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	141	Total	C	N	O	S	0	0
			1140	709	214	212	5		
3	5	141	Total	C	N	O	S	0	0
			1140	709	214	212	5		
3	8	141	Total	C	N	O	S	0	0
			1140	709	214	212	5		
3	Z	141	Total	C	N	O	S	0	0
			1140	709	214	212	5		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	48	SER	CYS	conflict	UNP P68246
2	64	SER	CYS	conflict	UNP P68246
2	89	ILE	ASN	conflict	UNP P68246
5	48	SER	CYS	conflict	UNP P68246
5	64	SER	CYS	conflict	UNP P68246
5	89	ILE	ASN	conflict	UNP P68246
8	48	SER	CYS	conflict	UNP P68246
8	64	SER	CYS	conflict	UNP P68246
8	89	ILE	ASN	conflict	UNP P68246
Z	48	SER	CYS	conflict	UNP P68246
Z	64	SER	CYS	conflict	UNP P68246
Z	89	ILE	ASN	conflict	UNP P68246

- Molecule 4 is a protein called TROPOMYOSIN ALPHA-1 CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	260	Total	C	N	O	S	0	0
			2091	1278	353	456	4		
4	B	277	Total	C	N	O	S	0	0
			2230	1362	378	484	6		
4	C	39	Total	C	N	O	S	0	0
			316	198	48	69	1		
4	T	39	Total	C	N	O	S	0	0
			316	198	48	69	1		
4	U	277	Total	C	N	O	S	0	0
			2230	1362	378	484	6		
4	V	277	Total	C	N	O	S	0	0
			2230	1362	378	484	6		
4	W	39	Total	C	N	O	S	0	0
			316	198	48	69	1		
4	X	39	Total	C	N	O	S	0	0
			316	198	48	69	1		

- Molecule 5 is a protein called ACTIN, ALPHA SKELETAL MUSCLE.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	E	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	F	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	G	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		

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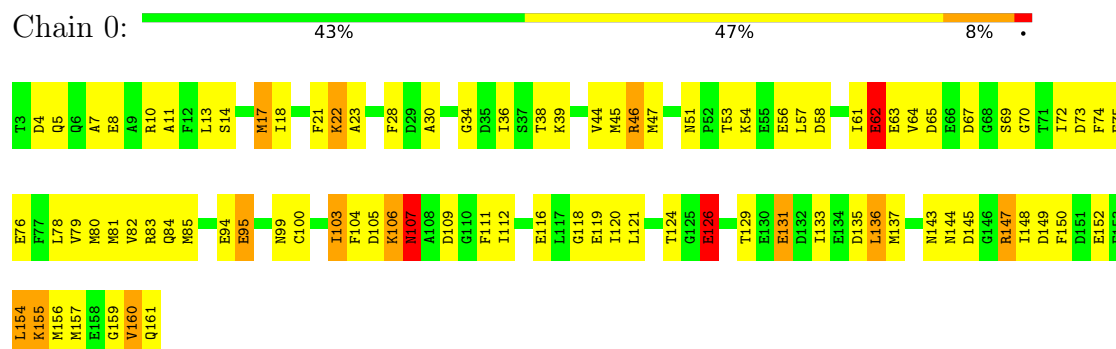
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Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	I	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	J	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	K	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	L	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	M	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	N	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	O	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	P	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	Q	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	R	372	Total 2907	C 1836	N 489	O 562	S 20	0	0
5	S	372	Total 2907	C 1836	N 489	O 562	S 20	0	0

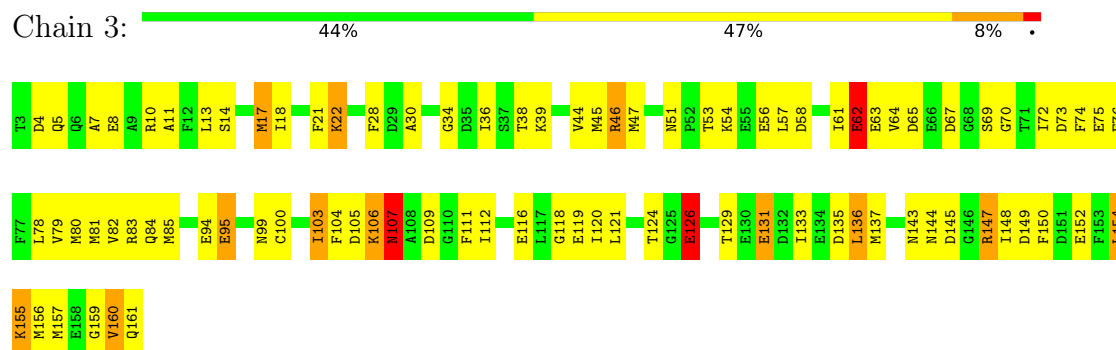
3 Residue-property plots

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.

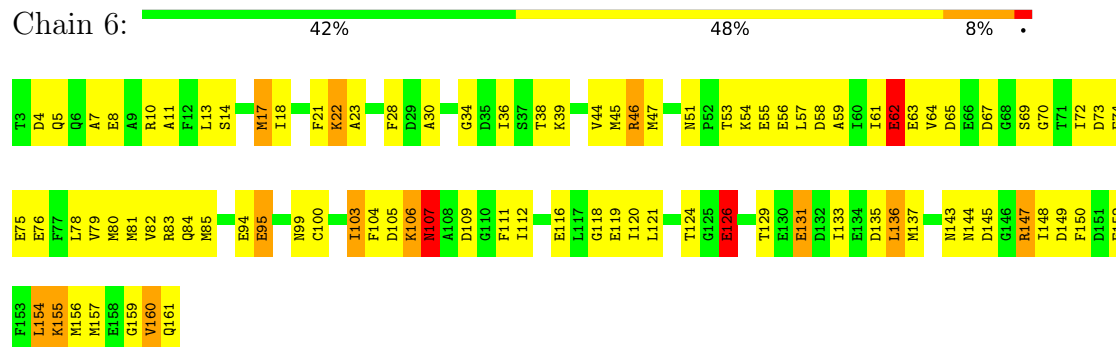
• Molecule 1: TROPONIN C, SKELETAL MUSCLE



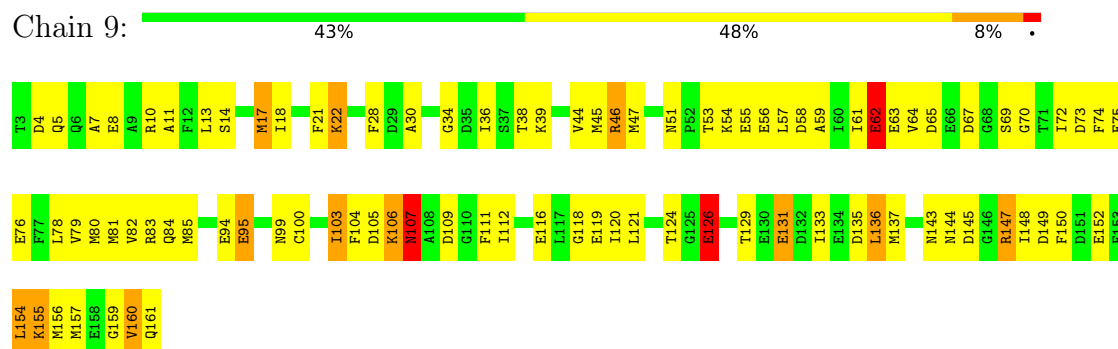
• Molecule 1: TROPONIN C, SKELETAL MUSCLE



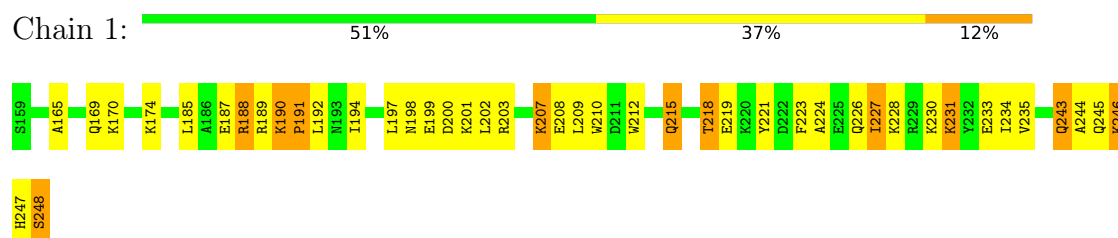
• Molecule 1: TROPONIN C, SKELETAL MUSCLE



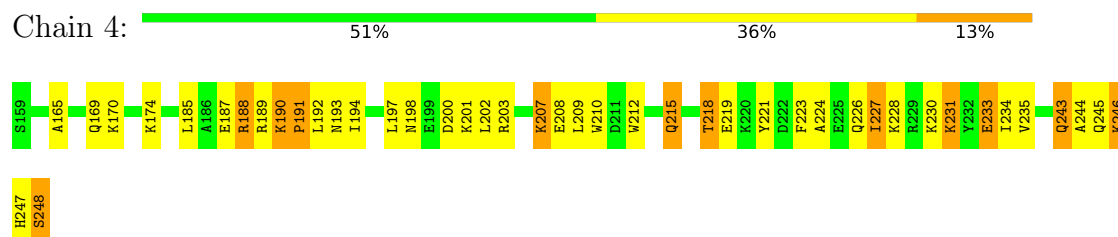
• Molecule 1: TROPONIN C, SKELETAL MUSCLE



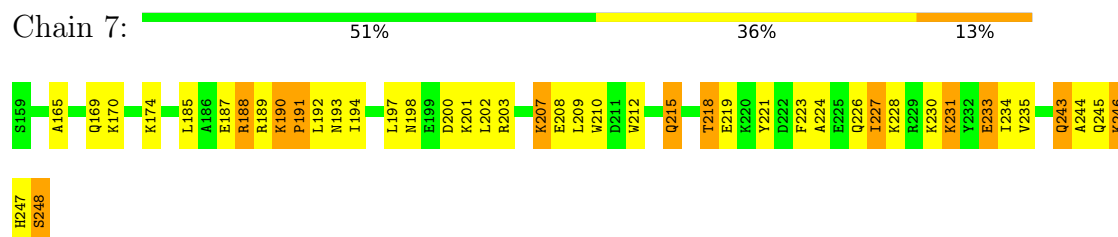
- Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS



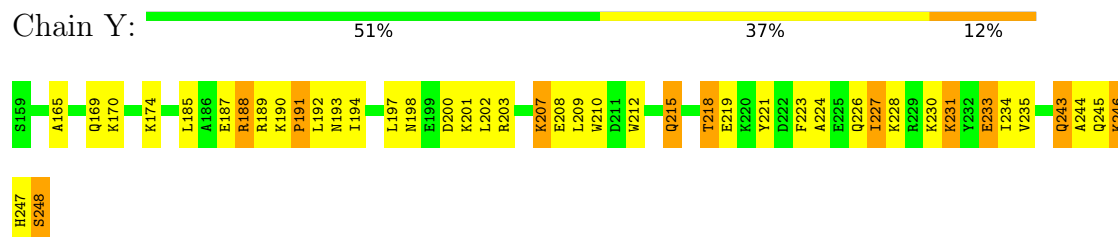
- Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS



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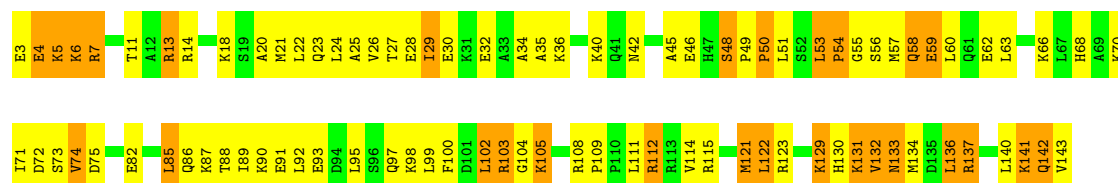


- Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS

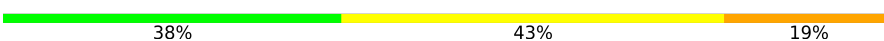


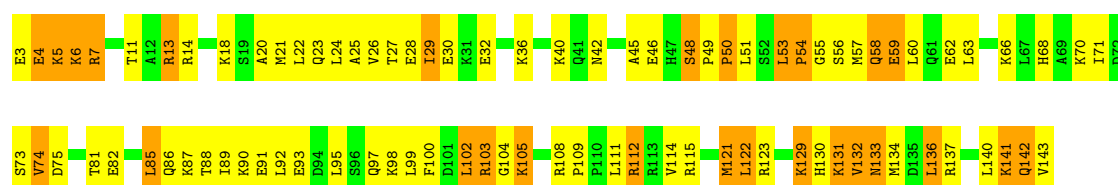
- Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE

Chain 2: 



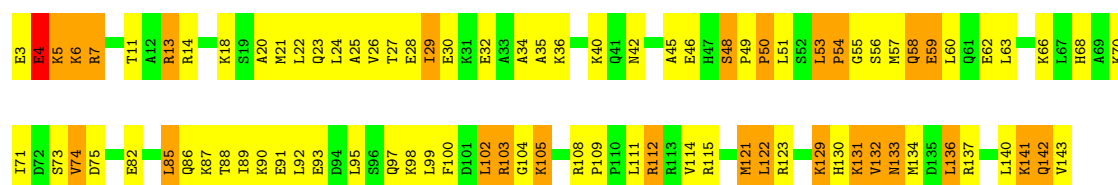
- Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE

Chain 5: 



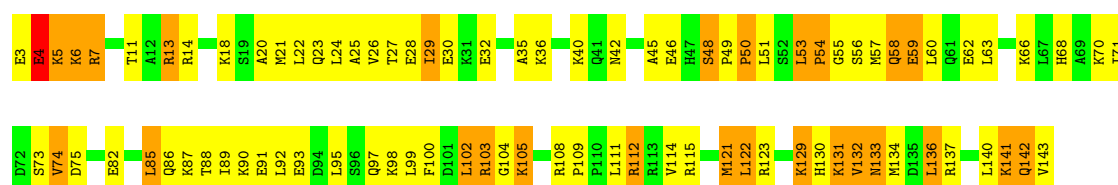
- Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE

Chain 8: 



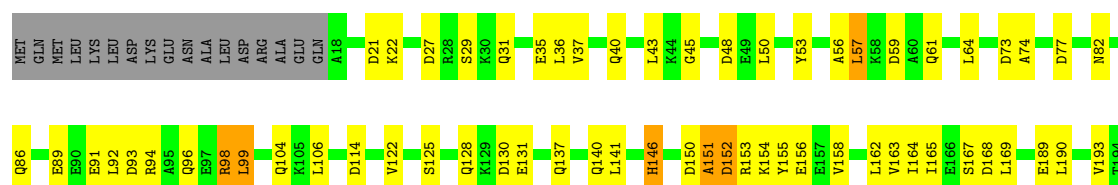
- Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE

Chain Z: 



- Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN

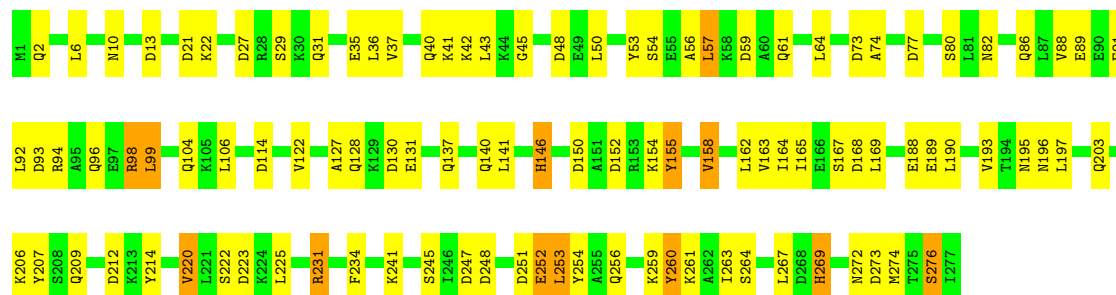
Chain A: 





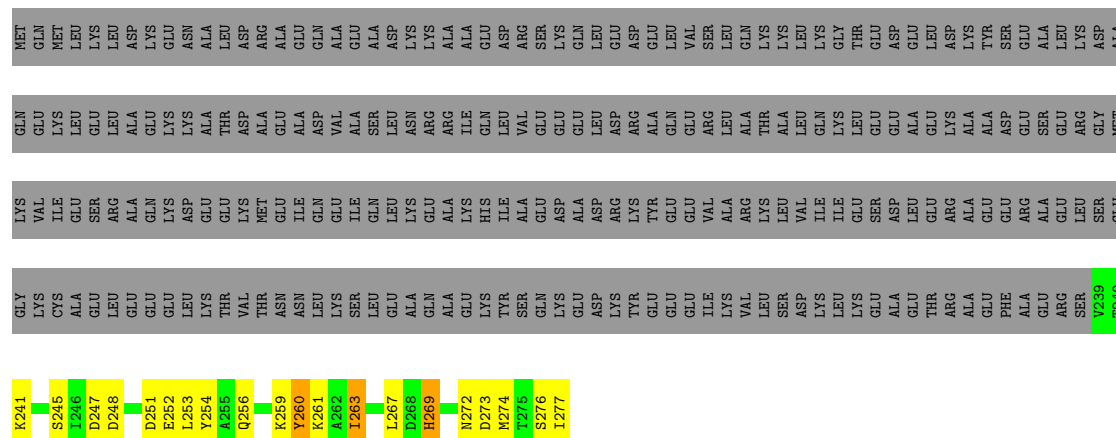
• Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN

Chain B: 62% 33% 5%



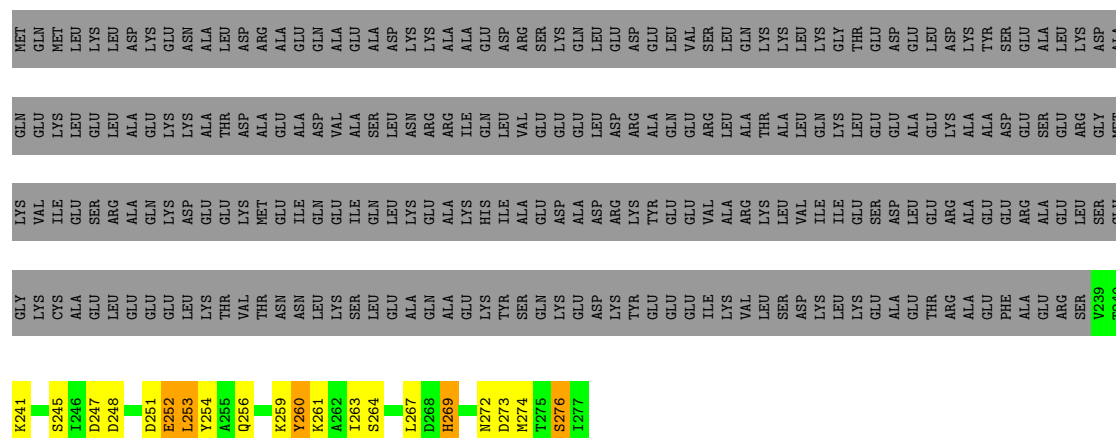
• Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN

Chain C: 7% 6% 86%

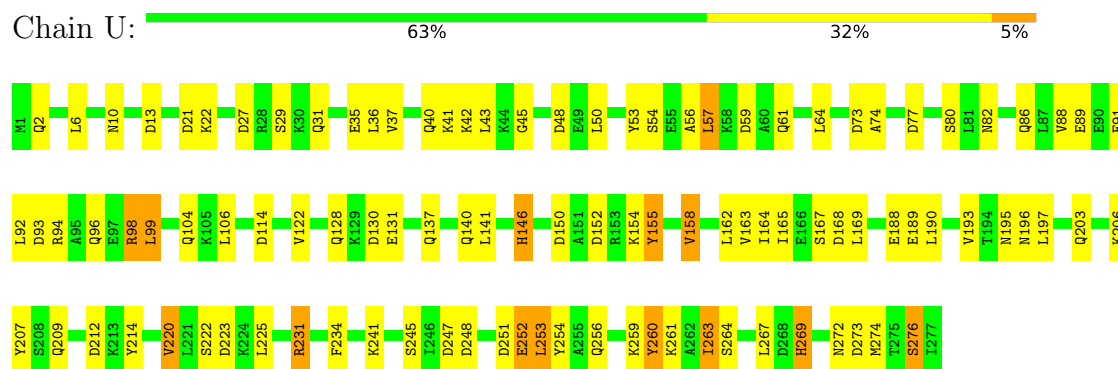


• Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN

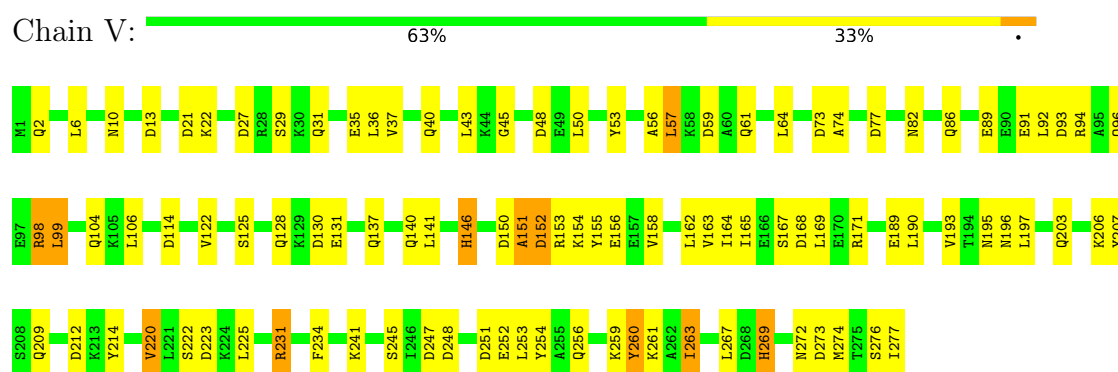
Chain T: 7% 5% 86%



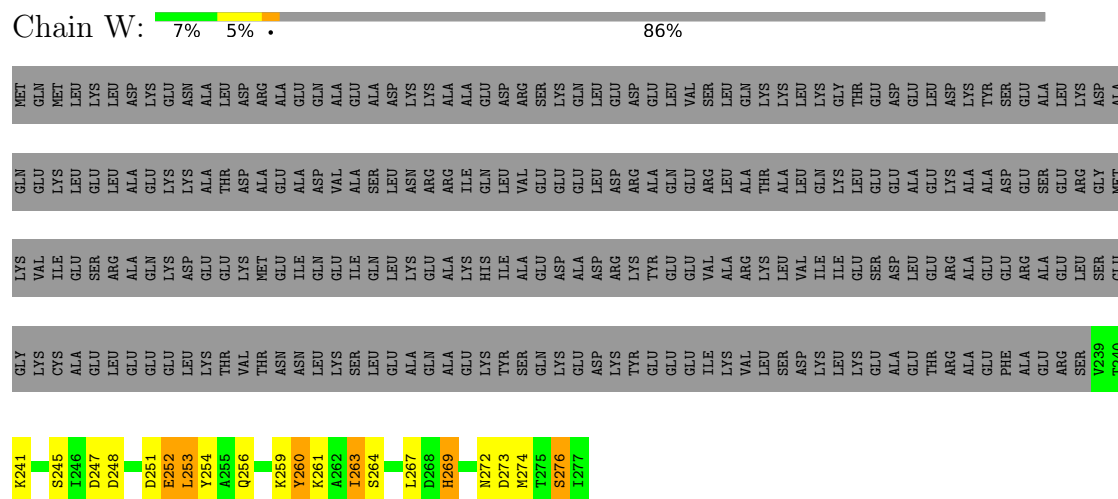
• Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN



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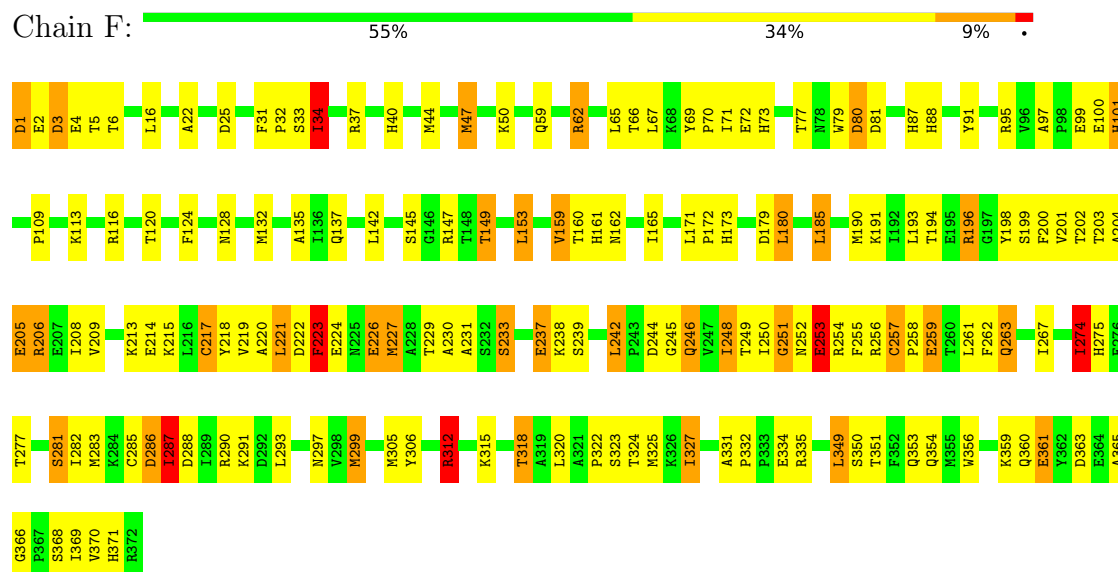
• Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN



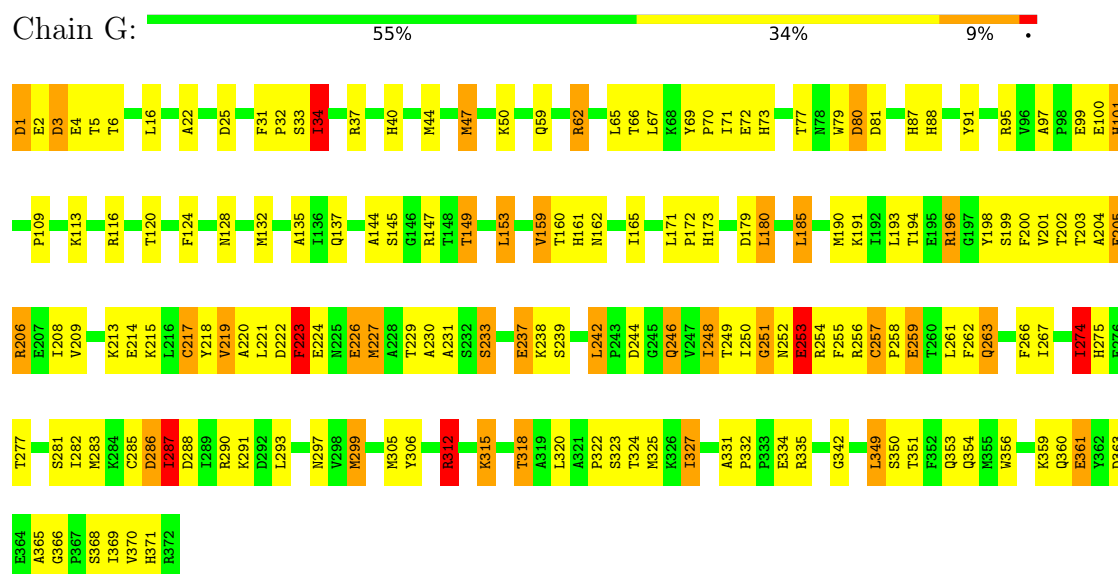
- Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

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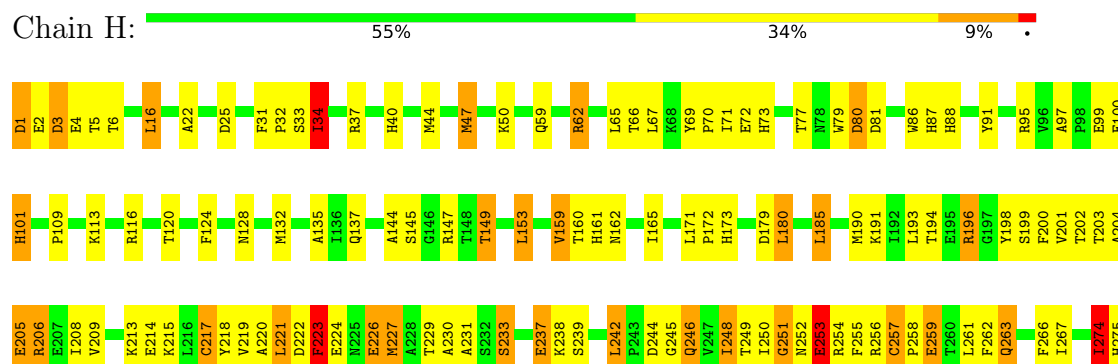
- Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

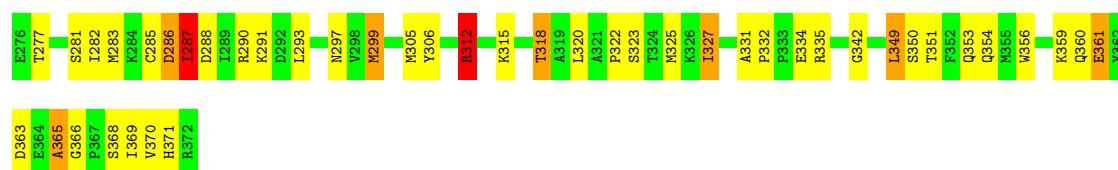


• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE



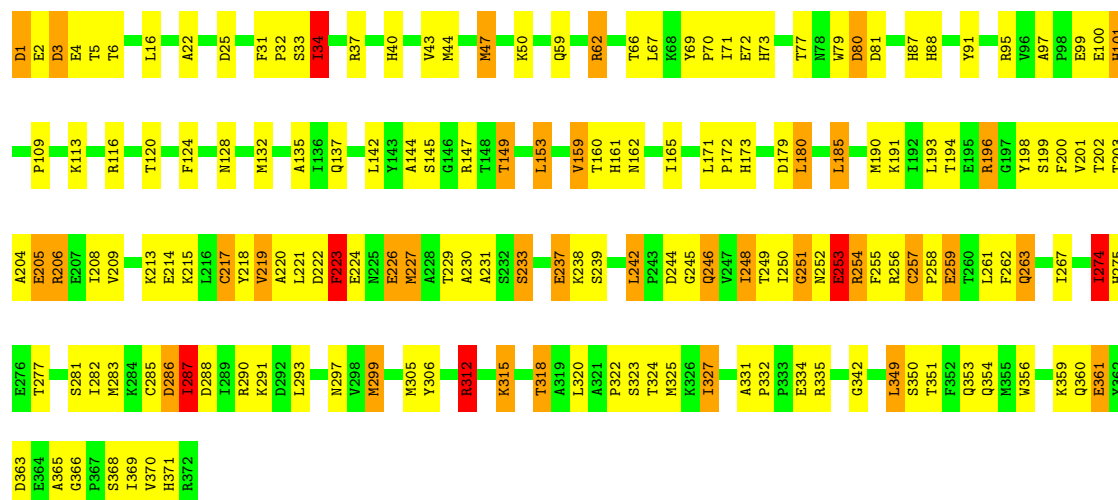
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE





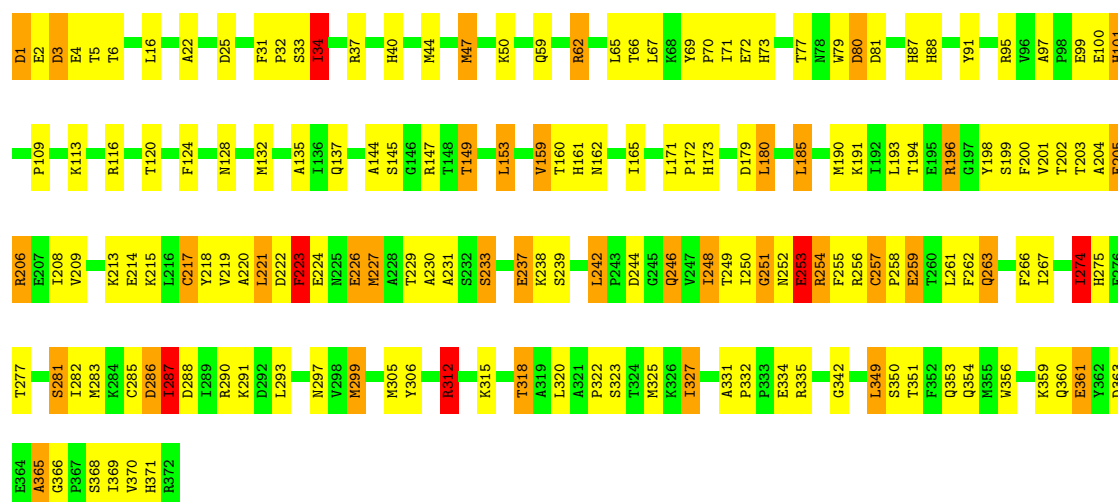
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

Chain I: 55% 34% 9%



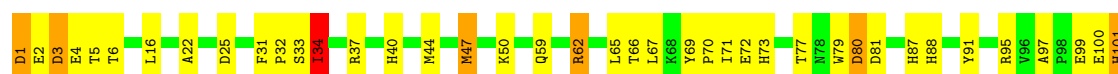
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

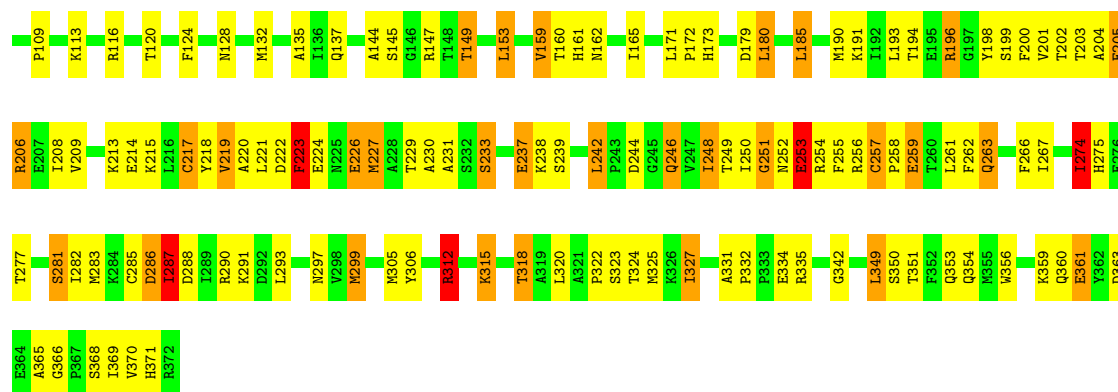
Chain J: 55% 34% 10%



• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

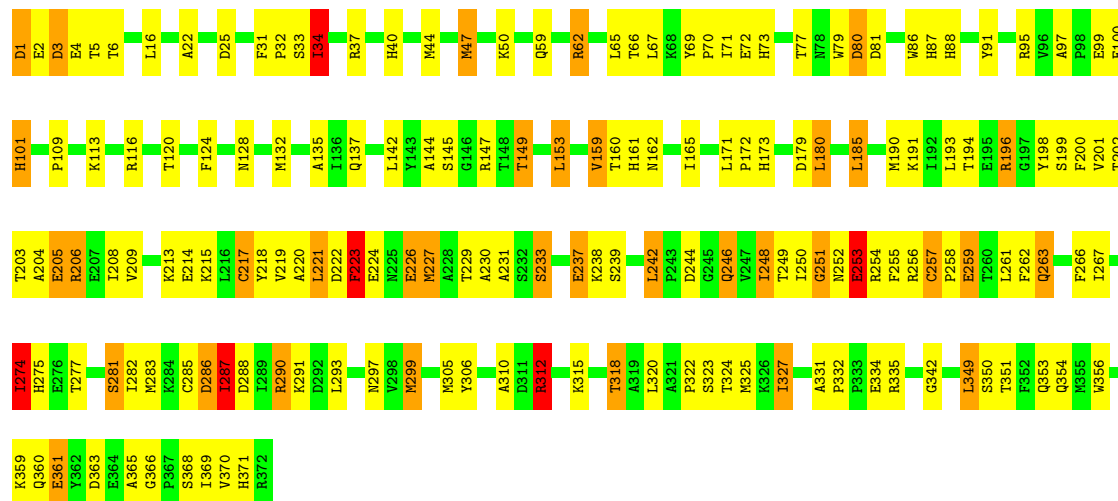
Chain K: 55% 34% 9%





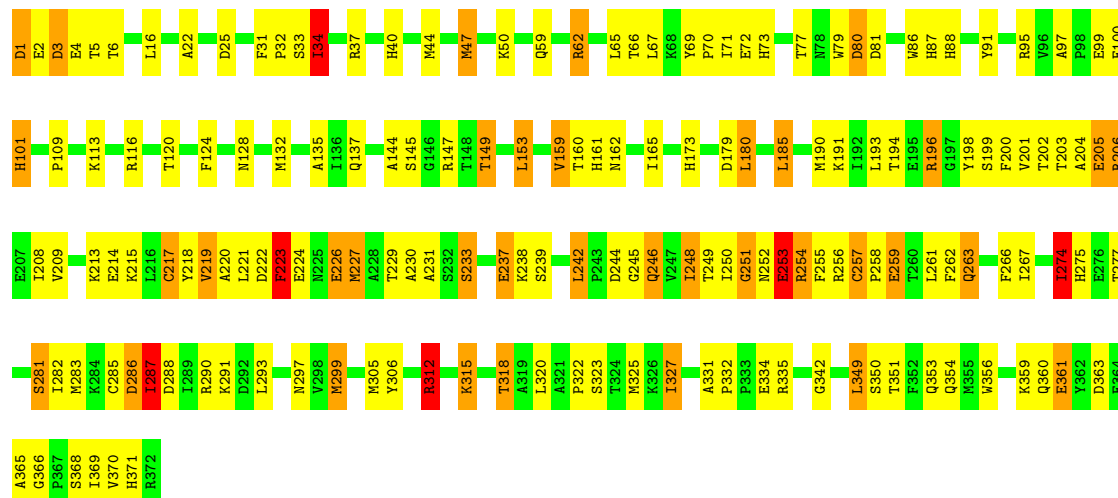
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

Chain L: 54% 35% 9% .

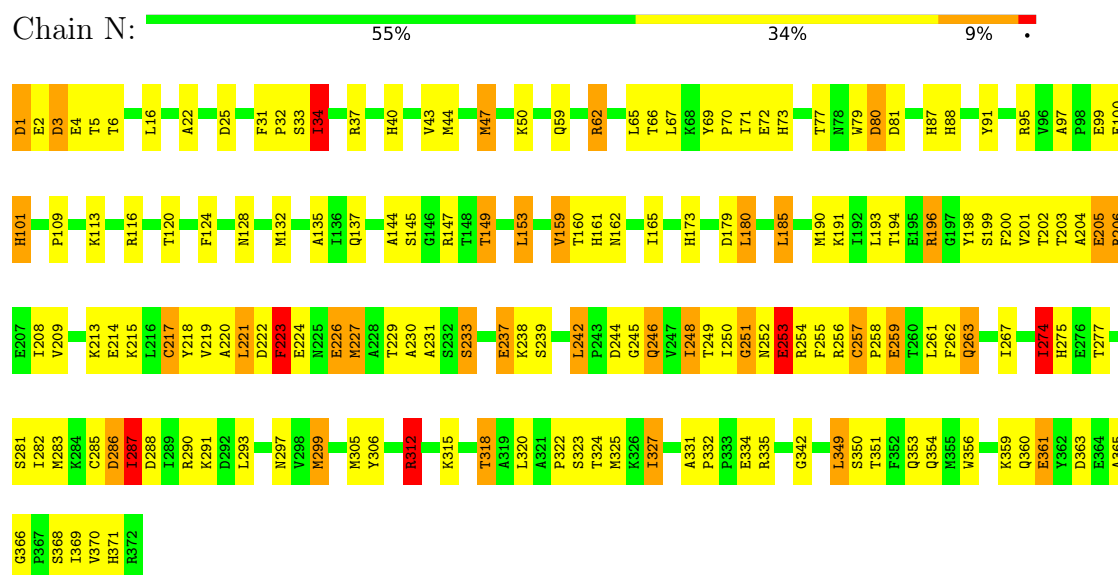


• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

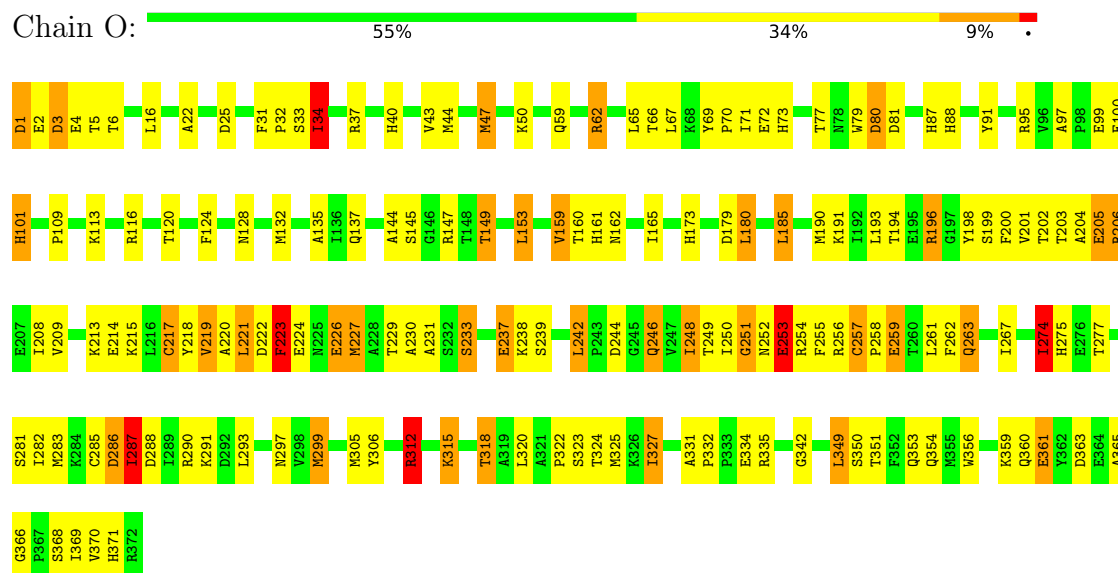
Chain M: 55% 34% 10% .



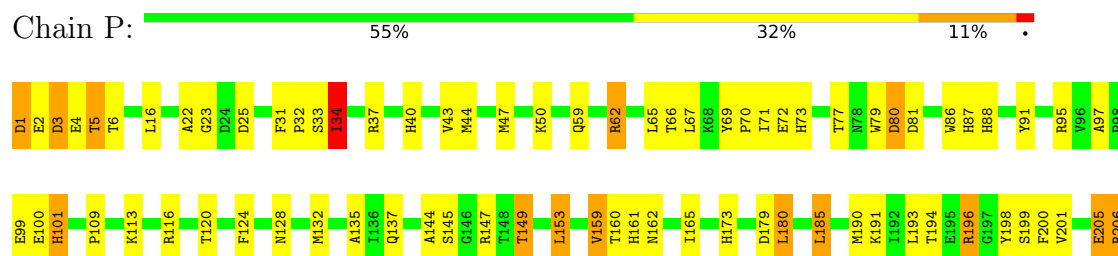
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

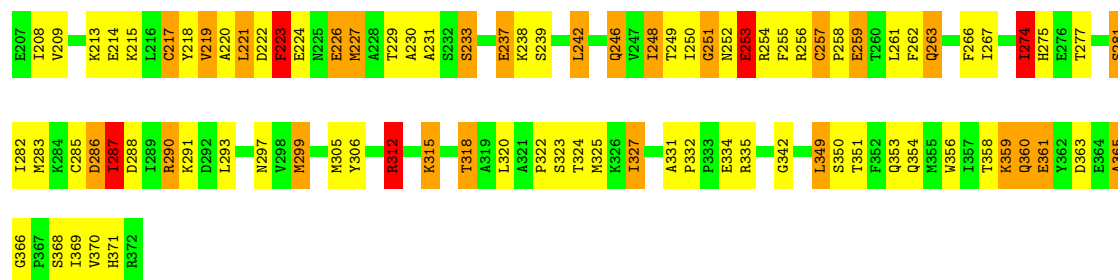


• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE



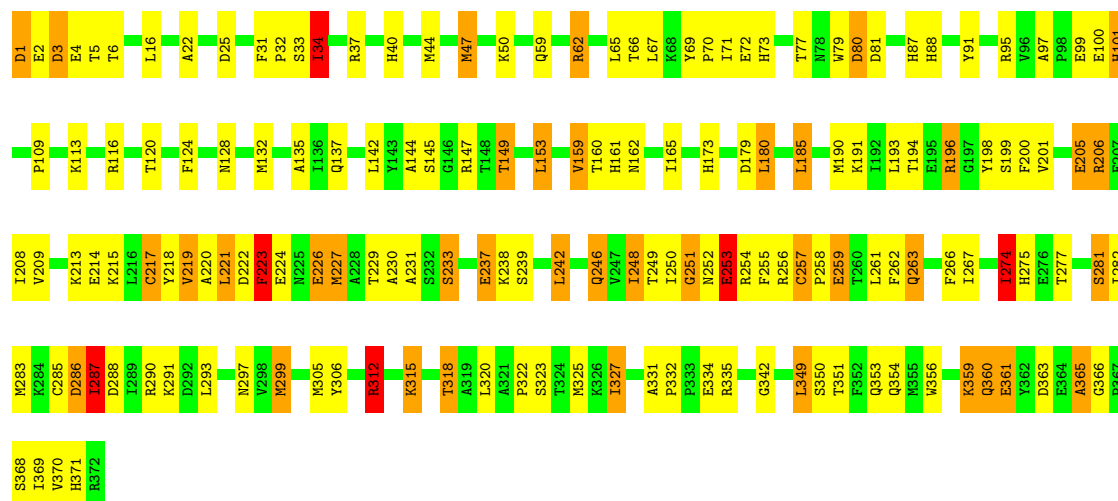
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE





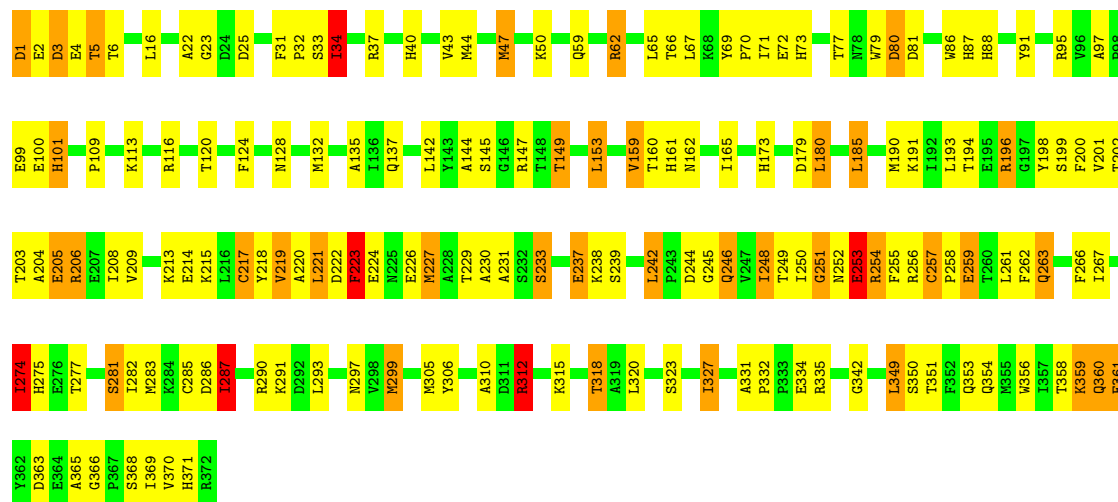
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

Chain Q: 56% 31% 10% .



• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

Chain R: 55% 34% 10% .



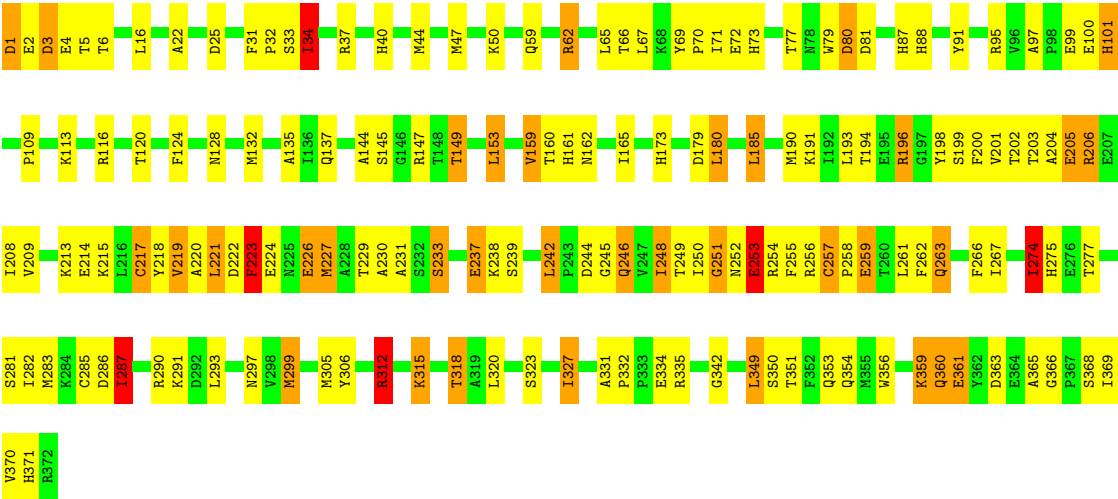
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

Chain S:

56%

33%

9%



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F224 (2k x 2k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.69	0/1264	0.96	2/1687 (0.1%)
1	3	0.69	0/1264	0.96	2/1687 (0.1%)
1	6	0.69	0/1264	0.96	2/1687 (0.1%)
1	9	0.69	0/1264	0.96	2/1687 (0.1%)
2	1	0.69	0/786	0.94	3/1046 (0.3%)
2	4	0.69	0/786	0.94	3/1046 (0.3%)
2	7	0.69	0/786	0.94	3/1046 (0.3%)
2	Y	0.69	0/786	0.94	3/1046 (0.3%)
3	2	0.70	1/1152 (0.1%)	1.13	7/1535 (0.5%)
3	5	0.70	1/1152 (0.1%)	1.13	7/1535 (0.5%)
3	8	0.70	1/1152 (0.1%)	1.13	7/1535 (0.5%)
3	Z	0.70	1/1152 (0.1%)	1.13	7/1535 (0.5%)
4	A	3.67	26/2099 (1.2%)	2.48	109/2799 (3.9%)
4	B	4.62	18/2238 (0.8%)	2.41	109/2983 (3.7%)
4	C	8.94	10/318 (3.1%)	2.86	23/425 (5.4%)
4	T	8.96	9/318 (2.8%)	2.85	23/425 (5.4%)
4	U	4.62	18/2238 (0.8%)	2.41	112/2983 (3.8%)
4	V	3.56	26/2238 (1.2%)	2.45	115/2983 (3.9%)
4	W	8.96	9/318 (2.8%)	2.84	24/425 (5.6%)
4	X	8.93	10/318 (3.1%)	2.86	23/425 (5.4%)
5	D	1.17	13/2969 (0.4%)	2.00	100/4023 (2.5%)
5	E	1.17	13/2969 (0.4%)	2.00	102/4023 (2.5%)
5	F	1.17	13/2969 (0.4%)	2.00	100/4023 (2.5%)
5	G	1.17	13/2969 (0.4%)	2.00	99/4023 (2.5%)
5	H	1.17	13/2969 (0.4%)	2.00	102/4023 (2.5%)
5	I	1.17	12/2969 (0.4%)	2.00	100/4023 (2.5%)
5	J	1.17	13/2969 (0.4%)	2.00	100/4023 (2.5%)
5	K	1.17	13/2969 (0.4%)	2.00	100/4023 (2.5%)
5	L	1.17	13/2969 (0.4%)	2.00	106/4023 (2.6%)
5	M	1.17	13/2969 (0.4%)	2.00	102/4023 (2.5%)
5	N	1.17	12/2969 (0.4%)	2.01	101/4023 (2.5%)
5	O	1.17	13/2969 (0.4%)	2.00	99/4023 (2.5%)
5	P	1.17	13/2969 (0.4%)	2.01	103/4023 (2.6%)
5	Q	1.17	13/2969 (0.4%)	2.01	102/4023 (2.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	R	1.17	13/2969 (0.4%)	2.00	104/4023 (2.6%)
5	S	1.17	13/2969 (0.4%)	2.00	100/4023 (2.5%)
All	All	2.15	336/70397 (0.5%)	1.95	2206/94888 (2.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	4
4	B	0	5
4	C	0	2
4	T	0	2
4	U	0	5
4	V	0	4
4	W	0	2
4	X	0	2
5	D	0	1
5	E	0	1
5	F	0	1
5	G	0	1
5	H	0	1
5	I	0	1
5	J	0	1
5	K	0	1
5	L	0	1
5	M	0	1
5	N	0	1
5	O	0	1
5	P	0	1
5	Q	0	1
5	R	0	1
5	S	0	1
All	All	0	42

The worst 5 of 336 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	T	260	TYR	CA-CB	155.18	3.97	1.53
4	W	260	TYR	CA-CB	155.10	3.97	1.53
4	B	260	TYR	CA-CB	155.08	3.97	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	U	260	TYR	CA-CB	155.07	3.97	1.53
4	C	260	TYR	CA-CB	154.66	3.96	1.53

The worst 5 of 2206 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	T	253	LEU	N-CA-C	25.38	138.55	111.14
4	B	253	LEU	N-CA-C	25.26	138.42	111.14
4	W	253	LEU	N-CA-C	24.73	138.49	111.03
4	U	253	LEU	N-CA-C	24.69	138.44	111.03
4	C	253	LEU	N-CA-C	24.36	137.52	110.97

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	231	ARG	Sidechain
4	A	260	TYR	Sidechain
4	A	261	LYS	Mainchain
4	A	98	ARG	Sidechain
4	B	98	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1252	0	1173	110	0
1	3	1252	0	1173	111	0
1	6	1252	0	1173	103	0
1	9	1252	0	1173	101	0
2	1	774	0	796	49	0
2	4	774	0	796	51	0
2	7	774	0	797	49	0
2	Y	774	0	791	48	0
3	2	1140	0	1201	109	0
3	5	1140	0	1201	109	0
3	8	1140	0	1201	108	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Z	1140	0	1201	103	0
4	A	2091	0	2082	0	0
4	B	2230	0	2227	0	0
4	C	316	0	314	0	0
4	T	316	0	312	0	0
4	U	2230	0	2227	0	0
4	V	2230	0	2227	0	0
4	W	316	0	307	0	0
4	X	316	0	314	0	0
5	D	2907	0	2862	110	0
5	E	2907	0	2862	114	0
5	F	2907	0	2864	107	0
5	G	2907	0	2864	112	0
5	H	2907	0	2864	106	0
5	I	2907	0	2864	113	0
5	J	2907	0	2864	107	0
5	K	2907	0	2864	109	0
5	L	2907	0	2864	108	0
5	M	2907	0	2864	110	0
5	N	2907	0	2864	107	0
5	O	2907	0	2864	109	0
5	P	2907	0	2860	124	0
5	Q	2907	0	2863	122	0
5	R	2907	0	2861	125	0
5	S	2907	0	2864	122	0
All	All	69221	0	68498	2220	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 19.

The worst 5 of 2220 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)
3:8:97:GLN:HE22	5:S:4:GLU:CG	1.19	1.53
3:5:97:GLN:HE22	5:Q:4:GLU:CG	1.19	1.51
1:3:62:GLU:CG	5:R:359:LYS:HD2	1.51	1.40
1:0:62:GLU:CG	5:P:360:GLN:HB2	1.52	1.39
1:3:62:GLU:CB	5:R:359:LYS:CD	1.76	1.39

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	0	157/159 (99%)	130 (83%)	20 (13%)	7 (4%)	2	17
1	3	157/159 (99%)	130 (83%)	20 (13%)	7 (4%)	2	17
1	6	157/159 (99%)	130 (83%)	20 (13%)	7 (4%)	2	17
1	9	157/159 (99%)	130 (83%)	20 (13%)	7 (4%)	2	17
2	1	88/90 (98%)	66 (75%)	18 (20%)	4 (4%)	2	17
2	4	88/90 (98%)	65 (74%)	19 (22%)	4 (4%)	2	17
2	7	88/90 (98%)	65 (74%)	19 (22%)	4 (4%)	2	17
2	Y	88/90 (98%)	66 (75%)	18 (20%)	4 (4%)	2	17
3	2	139/141 (99%)	107 (77%)	19 (14%)	13 (9%)	0	8
3	5	139/141 (99%)	108 (78%)	18 (13%)	13 (9%)	0	8
3	8	139/141 (99%)	108 (78%)	18 (13%)	13 (9%)	0	8
3	Z	139/141 (99%)	107 (77%)	19 (14%)	13 (9%)	0	8
4	A	258/277 (93%)	249 (96%)	7 (3%)	2 (1%)	16	54
4	B	275/277 (99%)	264 (96%)	11 (4%)	0	100	100
4	C	37/277 (13%)	34 (92%)	3 (8%)	0	100	100
4	T	37/277 (13%)	34 (92%)	3 (8%)	0	100	100
4	U	275/277 (99%)	264 (96%)	11 (4%)	0	100	100
4	V	275/277 (99%)	266 (97%)	7 (2%)	2 (1%)	18	56
4	W	37/277 (13%)	34 (92%)	3 (8%)	0	100	100
4	X	37/277 (13%)	34 (92%)	3 (8%)	0	100	100
5	D	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	E	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	F	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	G	370/372 (100%)	334 (90%)	30 (8%)	6 (2%)	7	38
5	H	370/372 (100%)	334 (90%)	30 (8%)	6 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	I	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	J	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	K	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	L	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	M	370/372 (100%)	334 (90%)	30 (8%)	6 (2%)	7	38
5	N	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	O	370/372 (100%)	333 (90%)	31 (8%)	6 (2%)	7	38
5	P	370/372 (100%)	334 (90%)	30 (8%)	6 (2%)	7	38
5	Q	370/372 (100%)	334 (90%)	30 (8%)	6 (2%)	7	38
5	R	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	S	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
All	All	8687/9728 (89%)	7744 (89%)	747 (9%)	196 (2%)	7	28

5 of 196 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	107	ASN
1	0	126	GLU
3	2	57	MET
3	2	142	GLN
1	3	107	ASN

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	0	134/134 (100%)	117 (87%)	17 (13%)	4	16
1	3	134/134 (100%)	117 (87%)	17 (13%)	4	16
1	6	134/134 (100%)	117 (87%)	17 (13%)	4	16
1	9	134/134 (100%)	117 (87%)	17 (13%)	4	16
2	1	82/82 (100%)	72 (88%)	10 (12%)	5	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	4	82/82 (100%)	72 (88%)	10 (12%)	5	17
2	7	82/82 (100%)	72 (88%)	10 (12%)	5	17
2	Y	82/82 (100%)	72 (88%)	10 (12%)	5	17
3	2	124/124 (100%)	108 (87%)	16 (13%)	4	15
3	5	124/124 (100%)	108 (87%)	16 (13%)	4	15
3	8	124/124 (100%)	108 (87%)	16 (13%)	4	15
3	Z	124/124 (100%)	108 (87%)	16 (13%)	4	15
4	A	224/239 (94%)	195 (87%)	29 (13%)	4	15
4	B	239/239 (100%)	203 (85%)	36 (15%)	3	12
4	C	36/239 (15%)	30 (83%)	6 (17%)	2	10
4	T	36/239 (15%)	27 (75%)	9 (25%)	0	4
4	U	239/239 (100%)	203 (85%)	36 (15%)	3	12
4	V	239/239 (100%)	210 (88%)	29 (12%)	5	17
4	W	36/239 (15%)	27 (75%)	9 (25%)	0	4
4	X	36/239 (15%)	30 (83%)	6 (17%)	2	10
5	D	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	E	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	F	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	G	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	H	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	I	315/315 (100%)	265 (84%)	50 (16%)	2	11
5	J	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	K	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	L	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	M	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	N	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	O	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	P	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	Q	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	R	315/315 (100%)	264 (84%)	51 (16%)	2	11
5	S	315/315 (100%)	264 (84%)	51 (16%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7485/8312 (90%)	6338 (85%)	1147 (15%)	5 12

5 of 1147 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	Q	353	GLN
3	Z	137	ARG
5	R	238	LYS
5	Q	351	THR
4	T	276	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 174 such sidechains are listed below:

Mol	Chain	Res	Type
5	M	252	ASN
5	Q	78	ASN
5	N	41	GLN
5	O	263	GLN
5	R	78	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

6 Map visualisation

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

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.