



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:53 PM UTC

PDB ID : 2W49 / pdb_00002w49
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

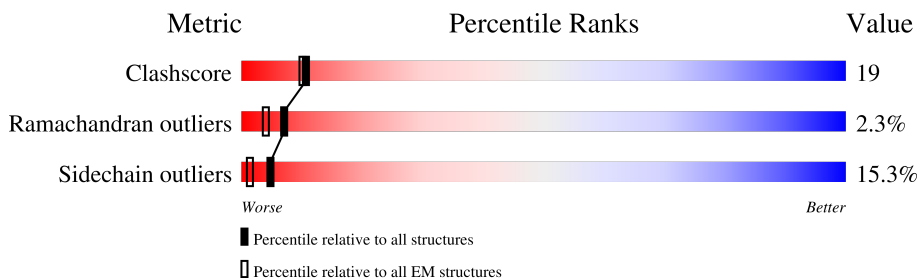
1 Overall quality at a glance i

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	0	159	43% 48% 8% .
1	3	159	42% 48% 8% .
1	6	159	43% 47% 8% .
1	9	159	42% 49% 8% .
2	1	90	50% 37% 13%
2	4	90	52% 34% 13%
2	7	90	51% 37% 12%
2	Y	90	52% 37% 11%
3	2	141	37% 43% 20% .



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Mol	Chain	Length	Quality of chain
3	5	141	36% 44% 20%
3	8	141	35% 46% 18% .
3	Z	141	37% 43% 19% .
4	A	277	64% 32% .
4	B	277	62% 33% 5%
4	C	277	7% 6% . 86%
4	T	277	7% 5% . 86%
4	U	277	63% 32% 5%
4	V	277	63% 32% .
4	W	277	7% 5% . 86%
4	X	277	7% 6% . 86%
5	D	372	55% 34% 9% .
5	E	372	55% 34% 10% .
5	F	372	55% 34% 9% .
5	G	372	55% 34% 9% .
5	H	372	55% 33% 10% .
5	I	372	56% 33% 10% .
5	J	372	55% 34% 9% .
5	K	372	55% 33% 10% .
5	L	372	55% 34% 10% .
5	M	372	55% 33% 10% .
5	N	372	55% 34% 9% .
5	O	372	55% 35% 9% .
5	P	372	55% 33% 10% .
5	Q	372	56% 33% 10% .

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

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 69376 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
			Total	C	N	O	S		
1	0	159	Total 1252	C 770	N 199	O 272	S 11	0	0
1	3	159	Total 1252	C 770	N 199	O 272	S 11	0	0
1	6	159	Total 1252	C 770	N 199	O 272	S 11	0	0
1	9	159	Total 1252	C 770	N 199	O 272	S 11	0	0

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

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

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

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

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	277	Total	C	N	O	S	0	0
			2230	1362	378	484	6		
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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Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	I	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	J	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	K	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	L	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	M	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	N	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	O	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	P	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	Q	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	R	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		
5	S	372	Total	C	N	O	S	0	0
			2907	1836	489	562	20		

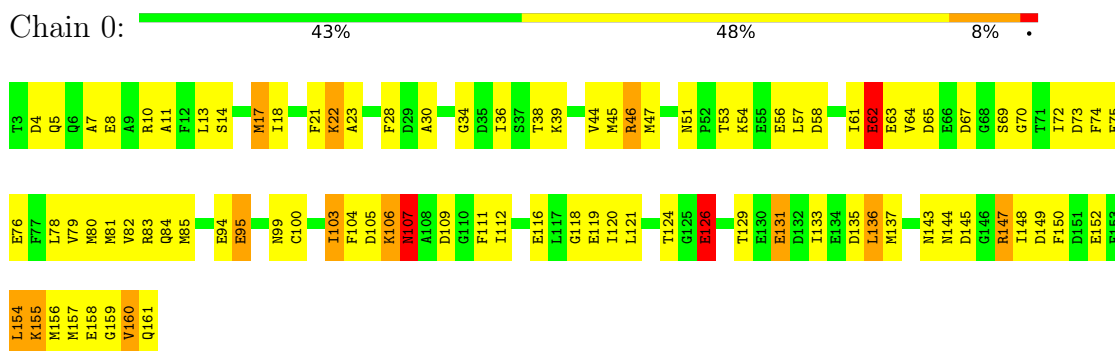
- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
6	0	4	Total	Ca	0
			4	4	
6	3	4	Total	Ca	0
			4	4	
6	6	4	Total	Ca	0
			4	4	
6	9	4	Total	Ca	0
			4	4	

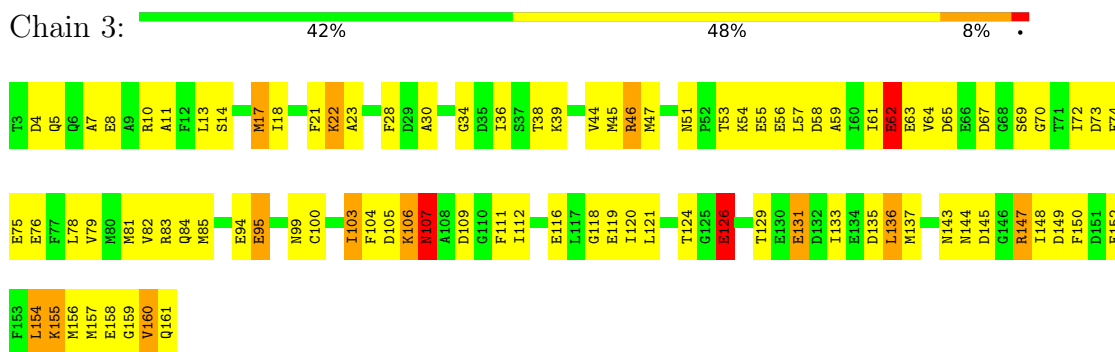
3 Residue-property plots

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.

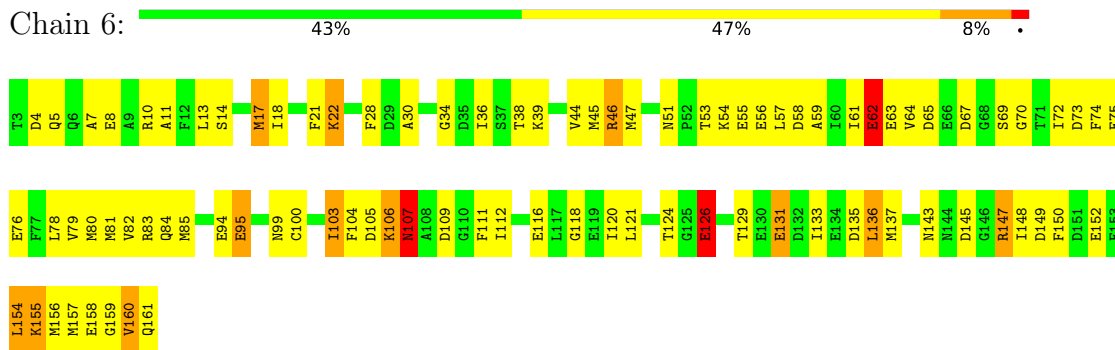
- Molecule 1: TROPONIN C, SKELETAL MUSCLE



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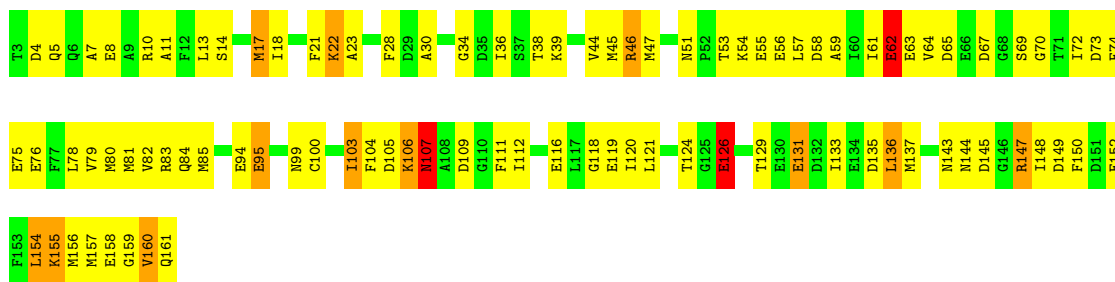


- Molecule 1: TROPONIN C, SKELETAL MUSCLE



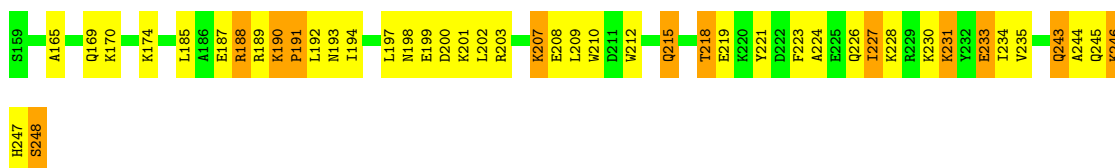
- Molecule 1: TROPONIN C, SKELETAL MUSCLE

Chain 9: 



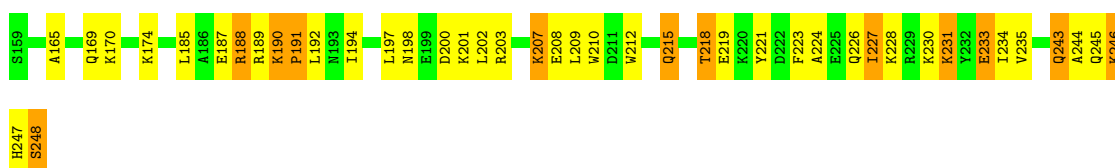
• Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS

Chain 1: 



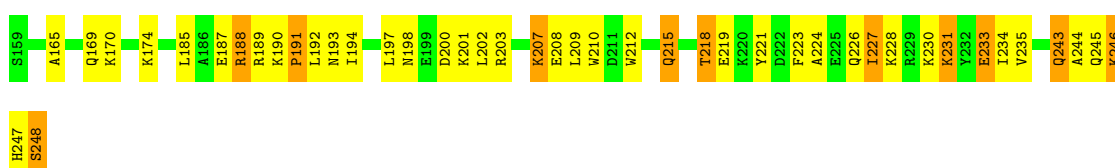
• Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS

Chain 4: 



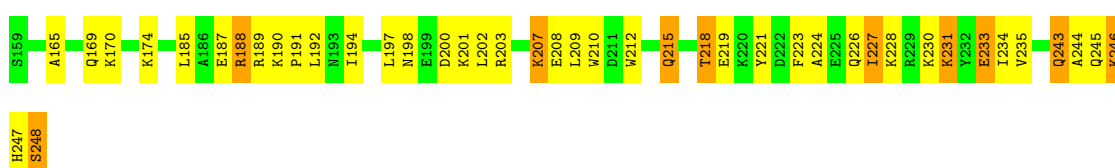
• Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS

Chain 7: 

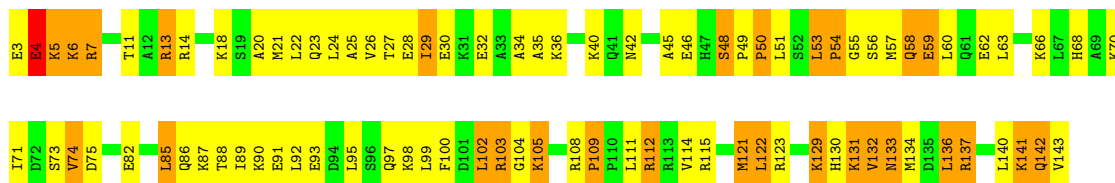
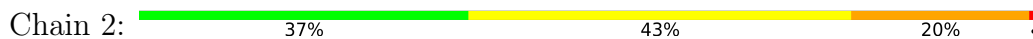


• Molecule 2: TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS

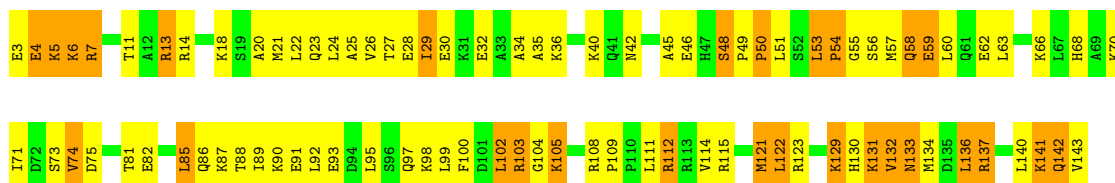
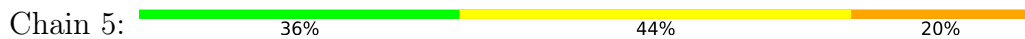
Chain Y: 



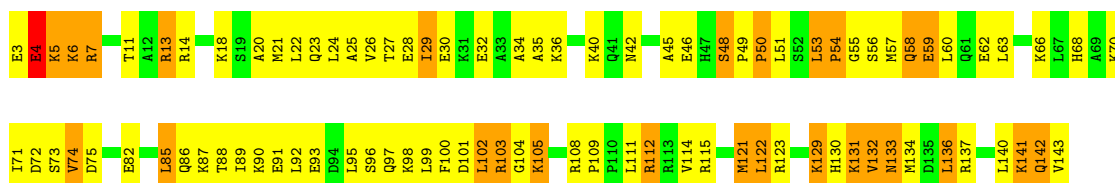
• Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE



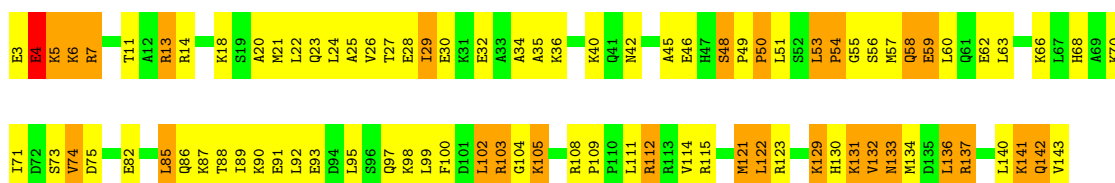
• Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE



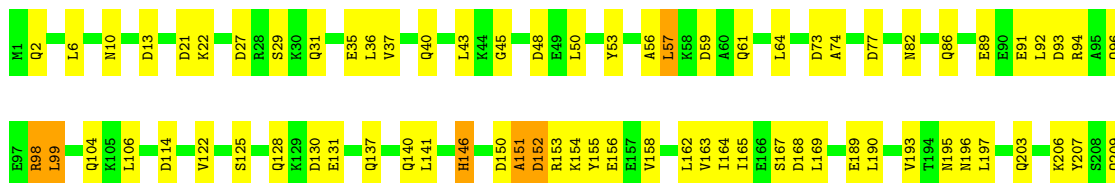
• Molecule 3: TROPONIN I, FAST SKELETAL MUSCLE



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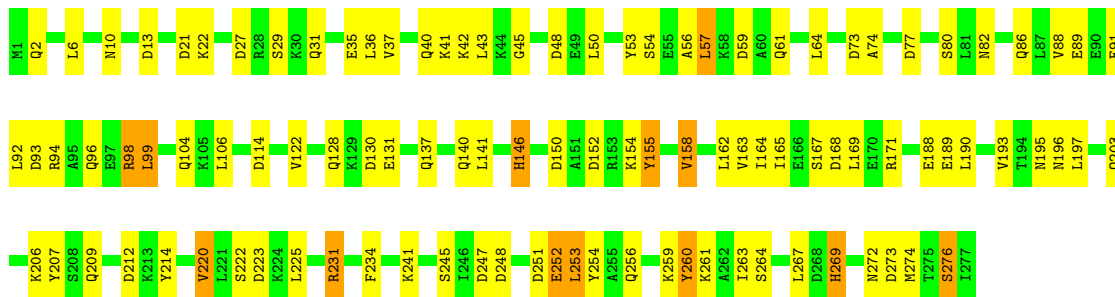


• Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN

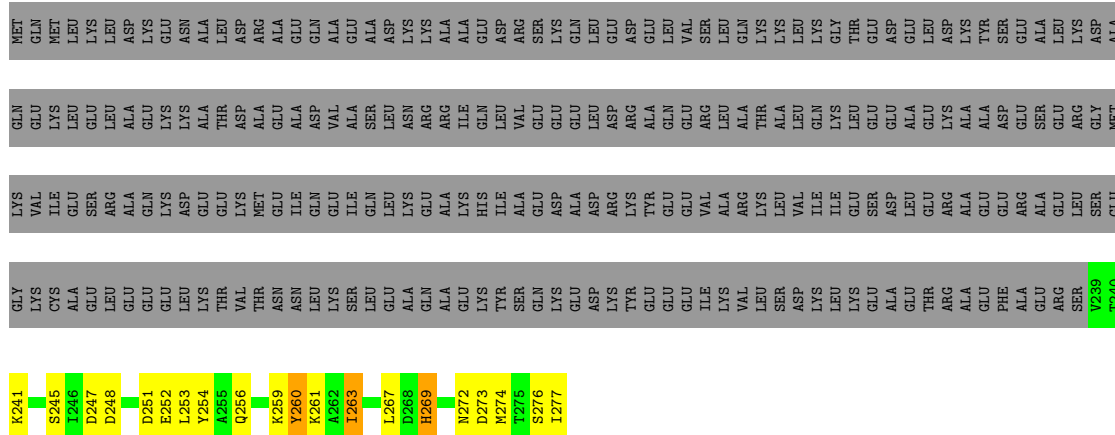




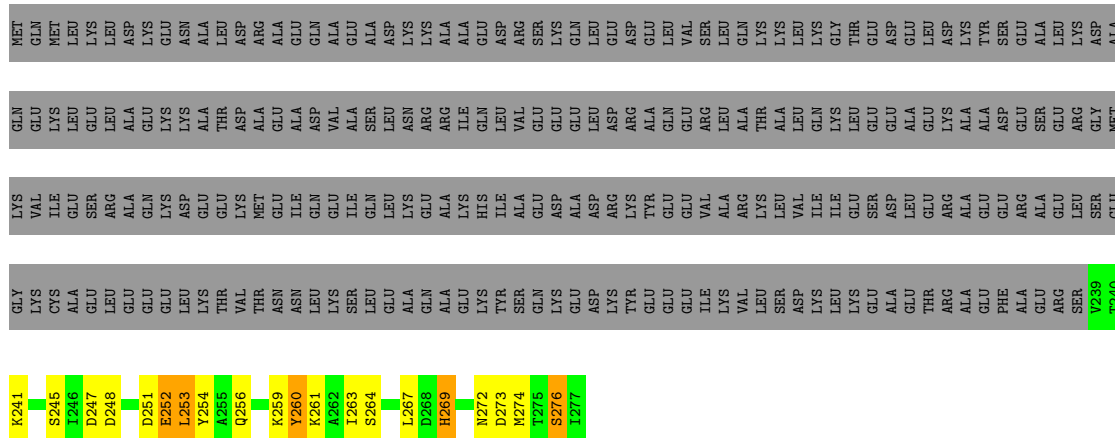
● Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN



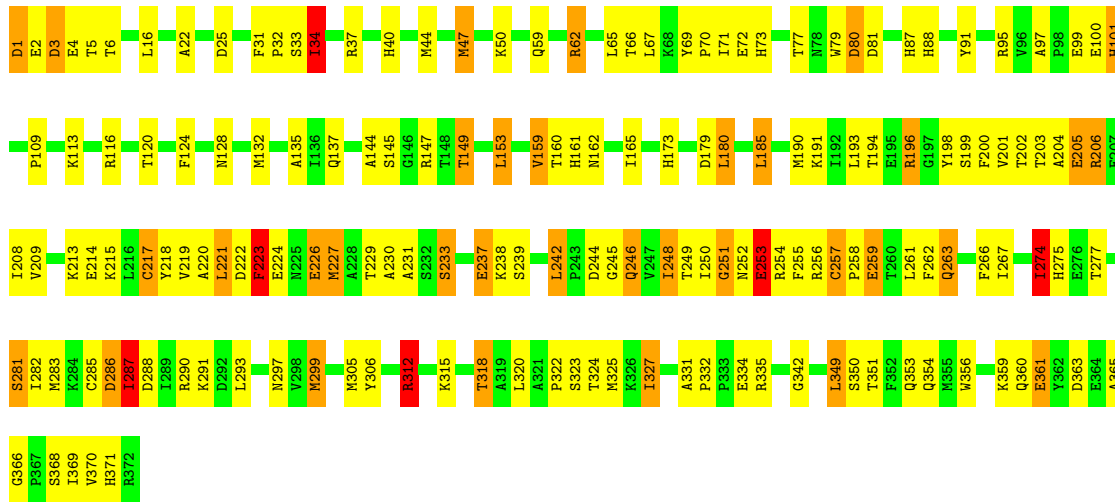
● Molecule 4: TROPOMYOSIN ALPHA-1 CHAIN



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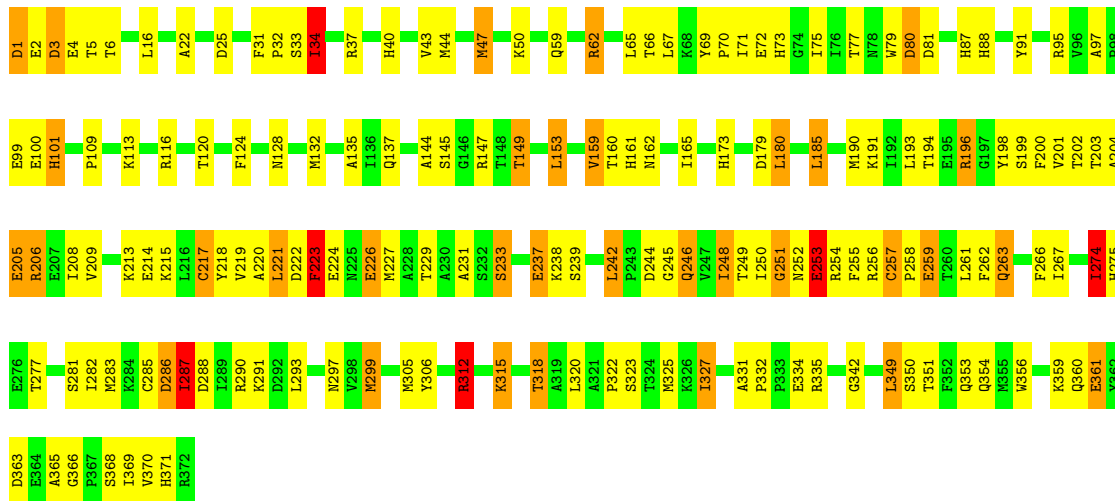


Chain F:  55% 34% 9%



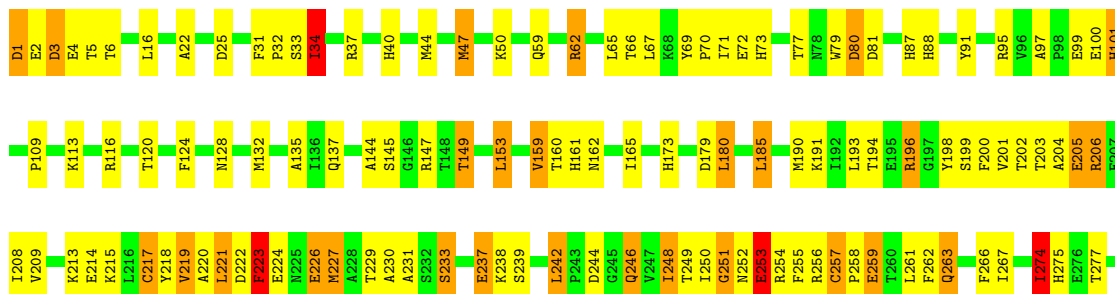
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

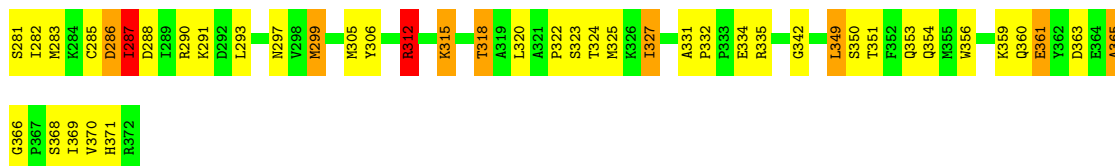
Chain G:  55% 34% 9%



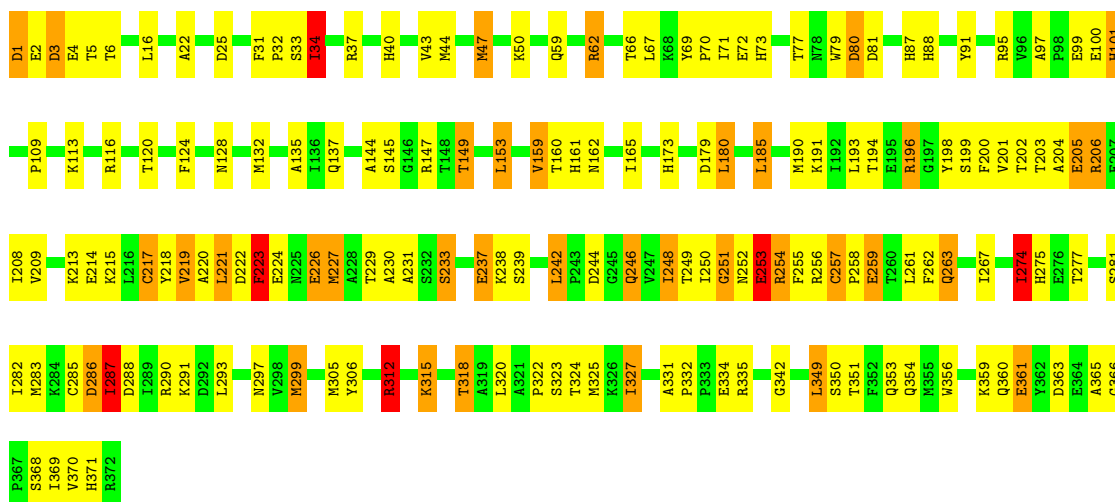
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

Chain H:  55% 33% 10%

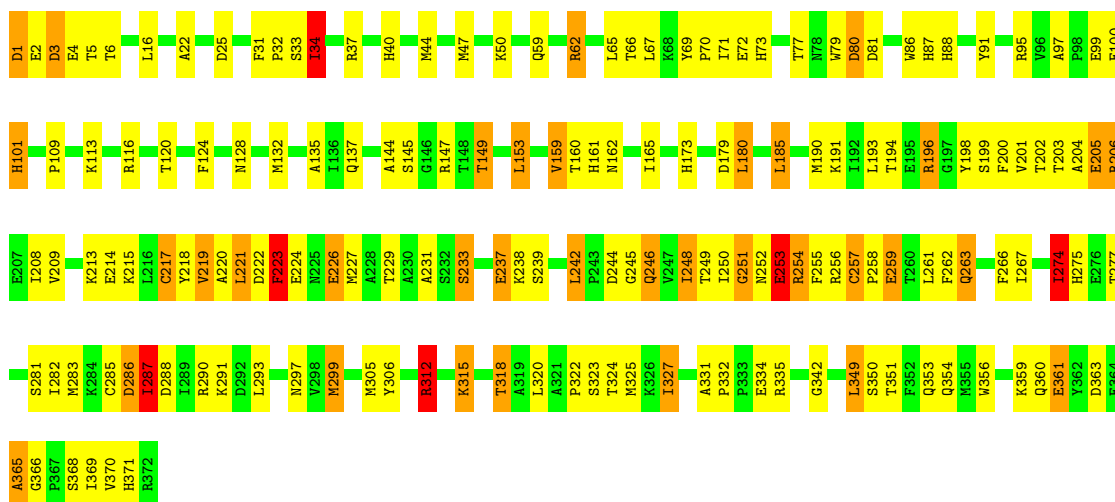




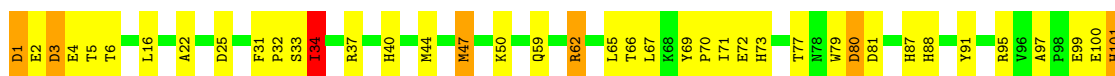
• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

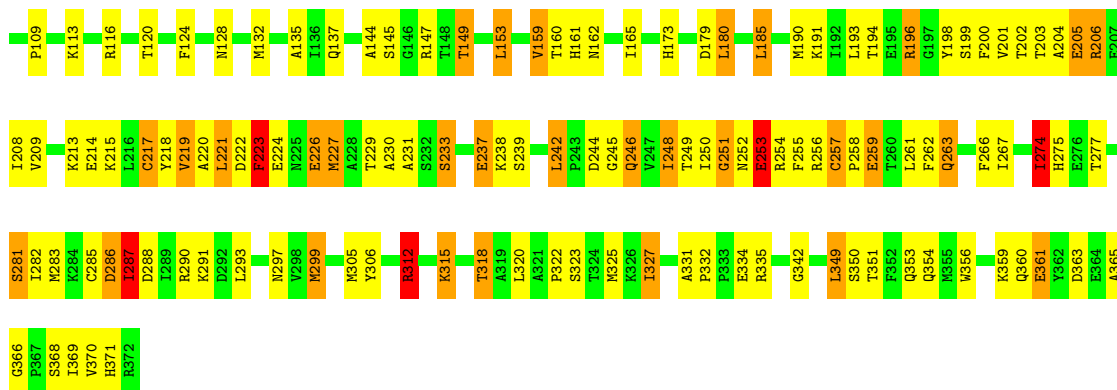


• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

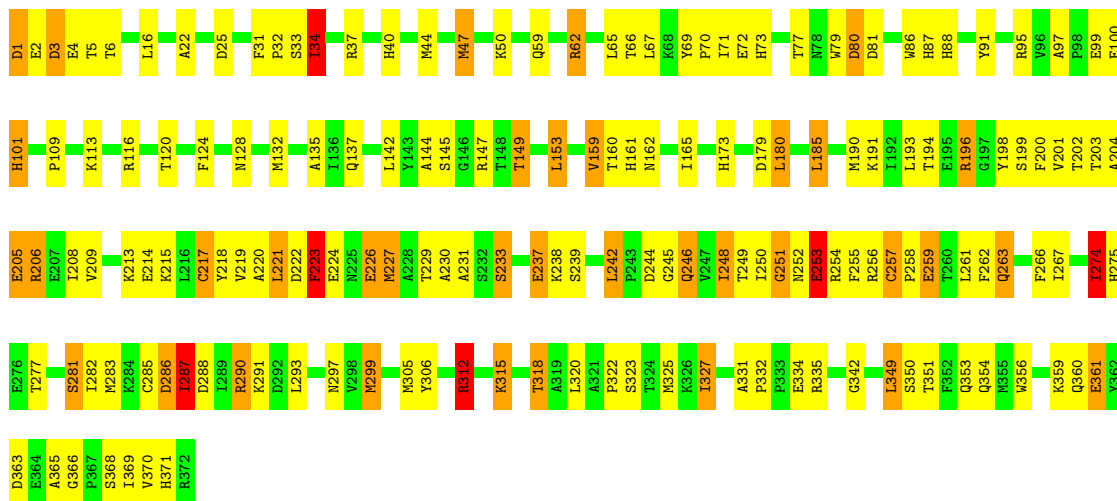


• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE

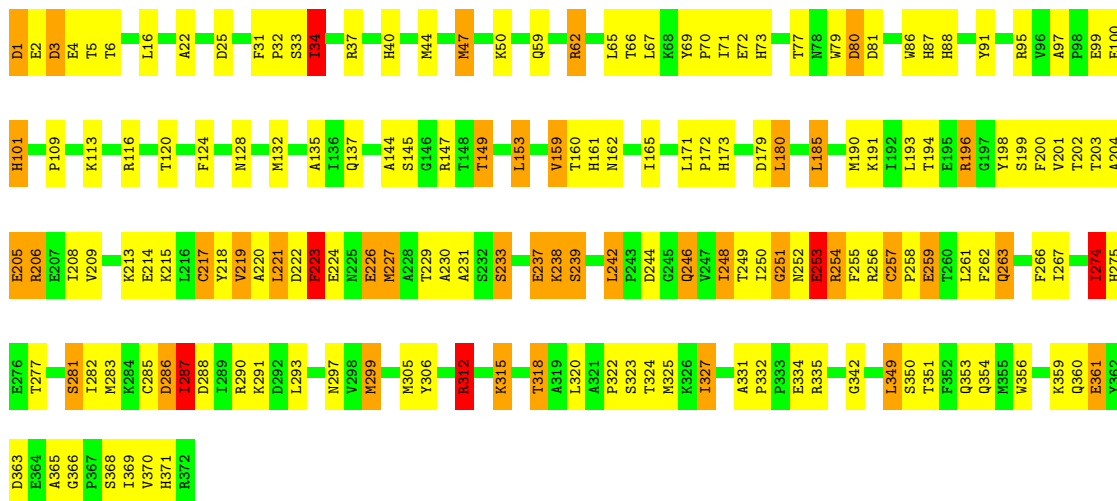




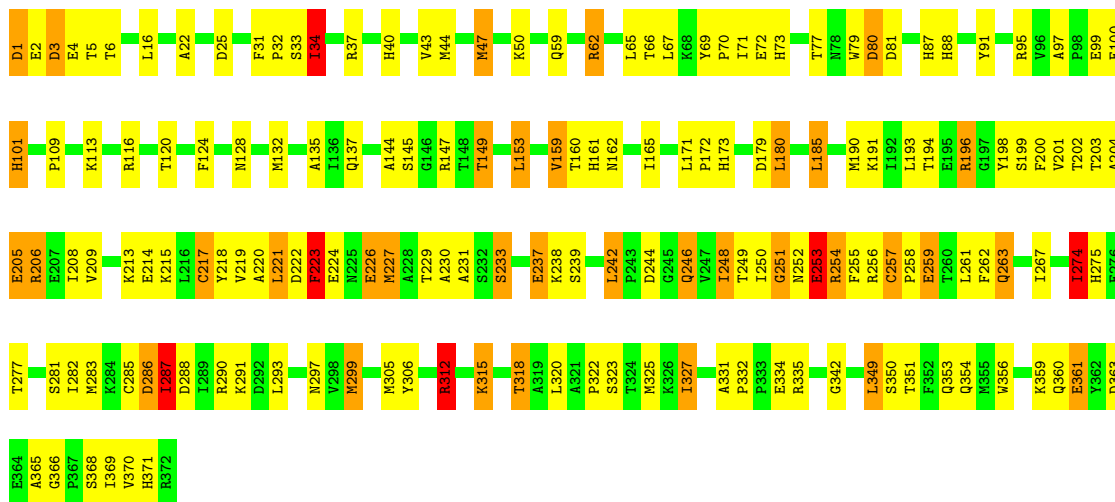
● Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE



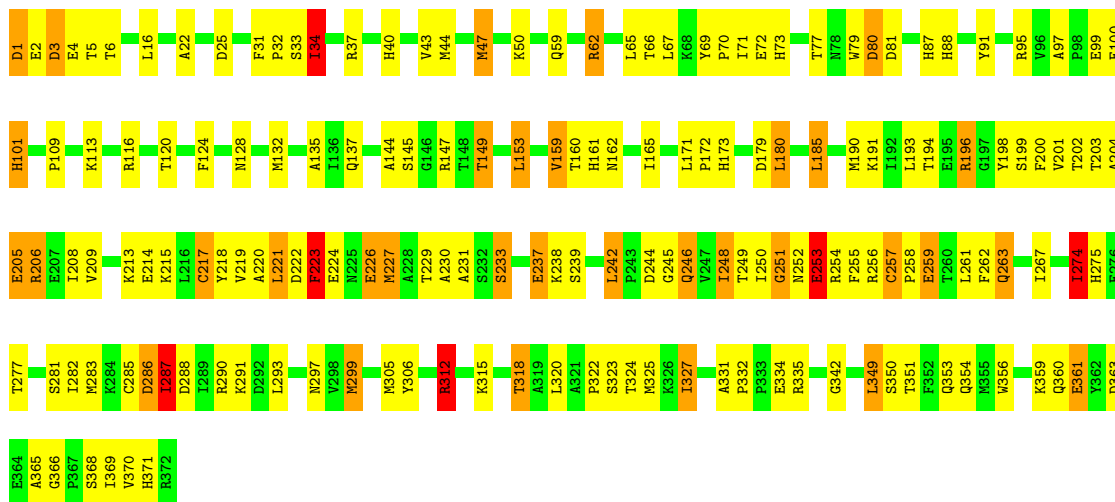
● Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE



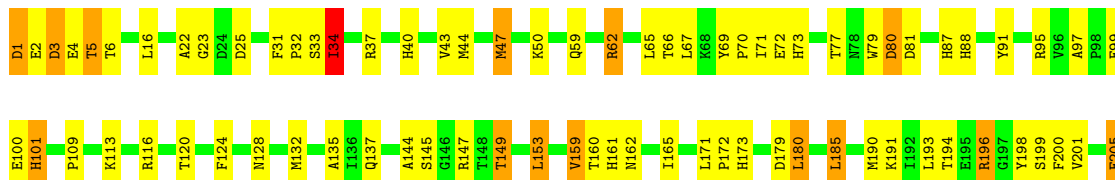
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• Molecule 5: ACTIN, ALPHA SKELETAL MUSCLE



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

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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%)	1.14	8/1535 (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	3.56	26/2238 (1.2%)	2.45	114/2983 (3.8%)
4	B	4.62	18/2238 (0.8%)	2.41	110/2983 (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	19/2238 (0.8%)	2.41	111/2983 (3.7%)
4	V	3.56	26/2238 (1.2%)	2.45	116/2983 (3.9%)
4	W	8.96	9/318 (2.8%)	2.84	24/425 (5.6%)
4	X	8.94	10/318 (3.1%)	2.86	23/425 (5.4%)
5	D	1.17	13/2969 (0.4%)	2.00	101/4023 (2.5%)
5	E	1.17	12/2969 (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	100/4023 (2.5%)
5	H	1.17	13/2969 (0.4%)	2.00	100/4023 (2.5%)
5	I	1.17	13/2969 (0.4%)	2.00	98/4023 (2.4%)
5	J	1.17	13/2969 (0.4%)	2.00	99/4023 (2.5%)
5	K	1.17	13/2969 (0.4%)	2.00	99/4023 (2.5%)
5	L	1.17	13/2969 (0.4%)	2.00	105/4023 (2.6%)
5	M	1.17	13/2969 (0.4%)	2.00	102/4023 (2.5%)
5	N	1.17	12/2969 (0.4%)	2.00	100/4023 (2.5%)
5	O	1.17	13/2969 (0.4%)	2.00	98/4023 (2.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	P	1.17	13/2969 (0.4%)	2.00	101/4023 (2.5%)
5	Q	1.17	13/2969 (0.4%)	2.01	101/4023 (2.5%)
5	R	1.17	13/2969 (0.4%)	2.01	101/4023 (2.5%)
5	S	1.17	13/2969 (0.4%)	2.00	101/4023 (2.5%)
All	All	2.15	337/70536 (0.5%)	1.95	2201/95072 (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 337 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	T	260	TYR	CA-CB	155.12	3.97	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	U	260	TYR	CA-CB	155.10	3.97	1.53
4	B	260	TYR	CA-CB	155.08	3.97	1.53
4	W	260	TYR	CA-CB	155.06	3.97	1.53
4	C	260	TYR	CA-CB	154.67	3.96	1.53

The worst 5 of 2201 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	T	253	LEU	N-CA-C	25.35	138.51	111.14
4	B	253	LEU	N-CA-C	25.31	138.47	111.14
4	W	253	LEU	N-CA-C	24.73	138.48	111.03
4	U	253	LEU	N-CA-C	24.70	138.45	111.03
4	V	253	LEU	N-CA-C	24.33	137.49	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	1172	112	0
1	3	1252	0	1172	90	0
1	6	1252	0	1172	103	0
1	9	1252	0	1172	88	0
2	1	774	0	797	49	0
2	4	774	0	796	50	0
2	7	774	0	797	50	0
2	Y	774	0	791	49	0
3	2	1140	0	1201	122	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	5	1140	0	1201	111	0
3	8	1140	0	1199	105	0
3	Z	1140	0	1201	104	0
4	A	2230	0	2227	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	108	0
5	E	2907	0	2862	109	0
5	F	2907	0	2864	109	0
5	G	2907	0	2864	106	0
5	H	2907	0	2864	110	0
5	I	2907	0	2864	108	0
5	J	2907	0	2864	108	0
5	K	2907	0	2864	108	0
5	L	2907	0	2864	102	0
5	M	2907	0	2864	111	0
5	N	2907	0	2864	111	0
5	O	2907	0	2864	111	0
5	P	2907	0	2860	125	0
5	Q	2907	0	2863	124	0
5	R	2907	0	2863	122	0
5	S	2907	0	2862	99	0
6	0	4	0	0	0	0
6	3	4	0	0	0	0
6	6	4	0	0	0	0
6	9	4	0	0	0	0
All	All	69376	0	68638	2199	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 2199 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)
3:2:100:PHE:CG	5:R:5:THR:HG22	1.40	1.54
3:5:97:GLN:HE22	5:Q:4:GLU:CG	1.19	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:62:GLU:CG	5:P:360:GLN:HB2	1.52	1.40
1:0:62:GLU:CG	5:P:359:LYS:HD2	1.52	1.38
3:5:97:GLN:NE2	5:Q:4:GLU:CG	1.85	1.37

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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%)	66 (75%)	18 (20%)	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%)	108 (78%)	18 (13%)	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	275/277 (99%)	266 (97%)	7 (2%)	2 (1%)	18	56
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	334 (90%)	30 (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
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%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	N	370/372 (100%)	335 (90%)	29 (8%)	6 (2%)	7	38
5	O	370/372 (100%)	334 (90%)	30 (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	8704/9728 (90%)	7764 (89%)	744 (8%)	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 [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	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
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	239/239 (100%)	210 (88%)	29 (12%)	5	17
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
All	All	7500/8312 (90%)	6353 (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 167 such sidechains are listed below:

Mol	Chain	Res	Type
5	N	40	HIS
5	R	78	ASN
5	N	263	GLN
5	P	137	GLN
5	S	78	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 16 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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-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.