



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:50 am GMT

PDB ID : 3LUE
EMDB ID: : EMD-5170
Title : Model of alpha-actinin CH1 bound to F-actin
Authors : Galkin, V.E.; Orlova, A.; Salmazo, A.; Djinovic-Carugo, K.; Egelman, E.H.
Deposited on : 2010-02-17
Resolution : 15.00 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

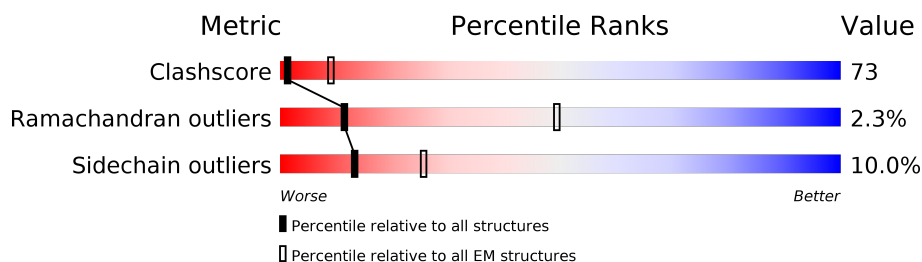
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 15.00 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.




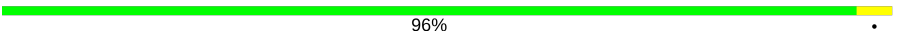

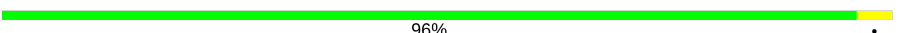

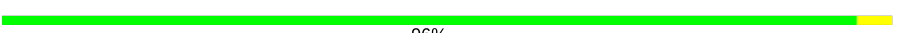


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

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	A	374	47% 39% 12% .
1	B	374	47% 40% 12% .
1	C	374	43% 41% 14% .
1	D	374	43% 41% 14% .
1	E	374	43% 41% 14% .
1	F	374	44% 41% 14% .
1	G	374	43% 41% 14% .
1	H	374	44% 41% 14% .
1	I	374	47% 40% 12% .

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Mol	Chain	Length	Quality of chain
1	J	374	 47% 40% 12%
2	K	109	 96%
2	L	109	 96%
2	M	109	 96%
2	N	109	 96%
2	O	109	 96%
2	P	109	 96%
2	Q	109	 96%
2	R	109	 96%
2	S	109	 96%
2	T	109	 96%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 37910 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 Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	B	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	C	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	D	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	E	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	F	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	G	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	H	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	I	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	J	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		

- Molecule 2 is a protein called Alpha-actinin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	M	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	L	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	O	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	N	109	Total	C	N	O	S	0	0
			874	561	157	151	5		

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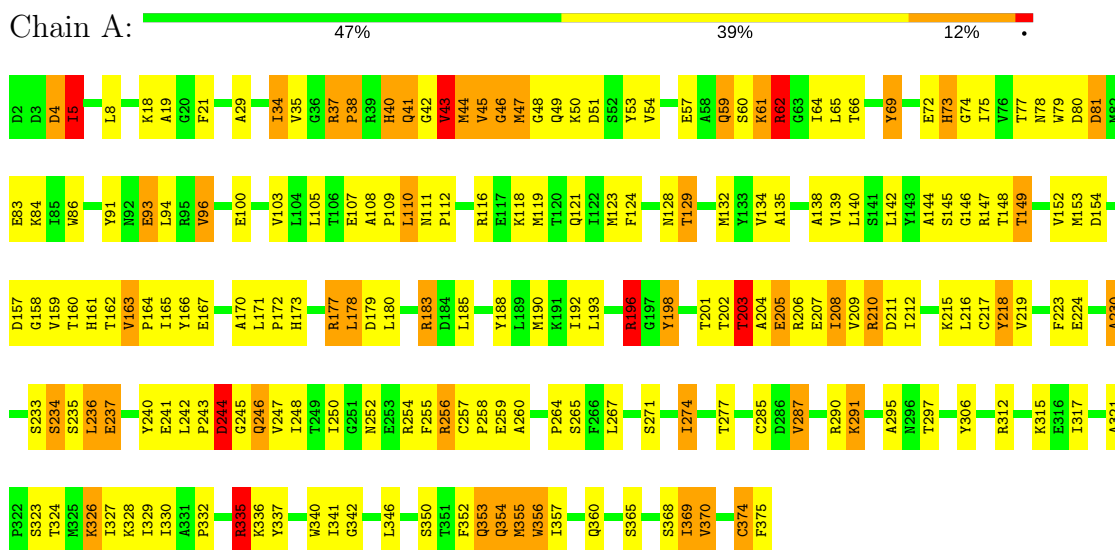
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Q	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	P	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	S	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	R	109	Total	C	N	O	S	0	0
			874	561	157	151	5		
2	T	109	Total	C	N	O	S	0	0
			874	561	157	151	5		

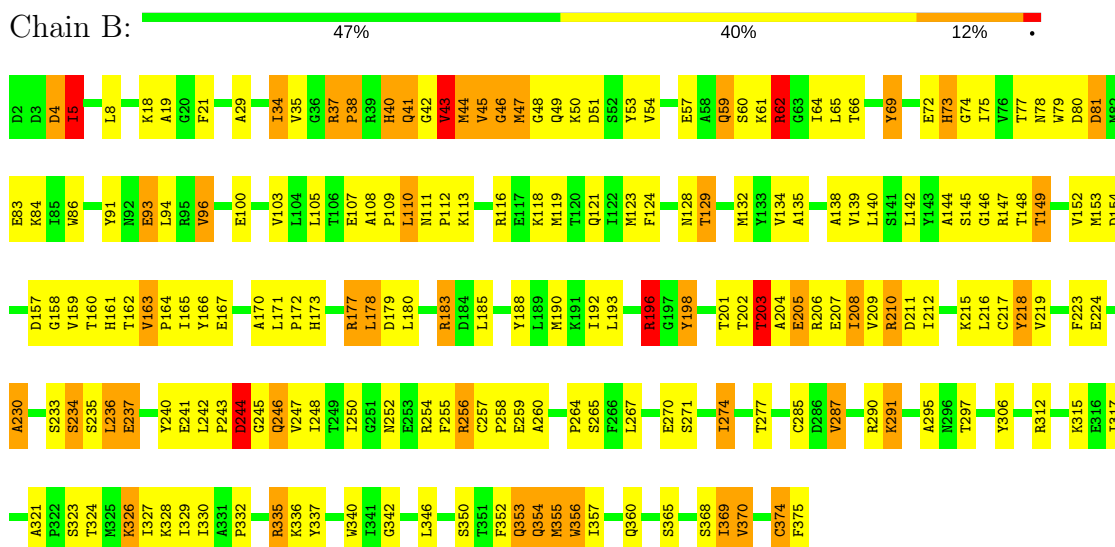
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Actin, cytoplasmic 1

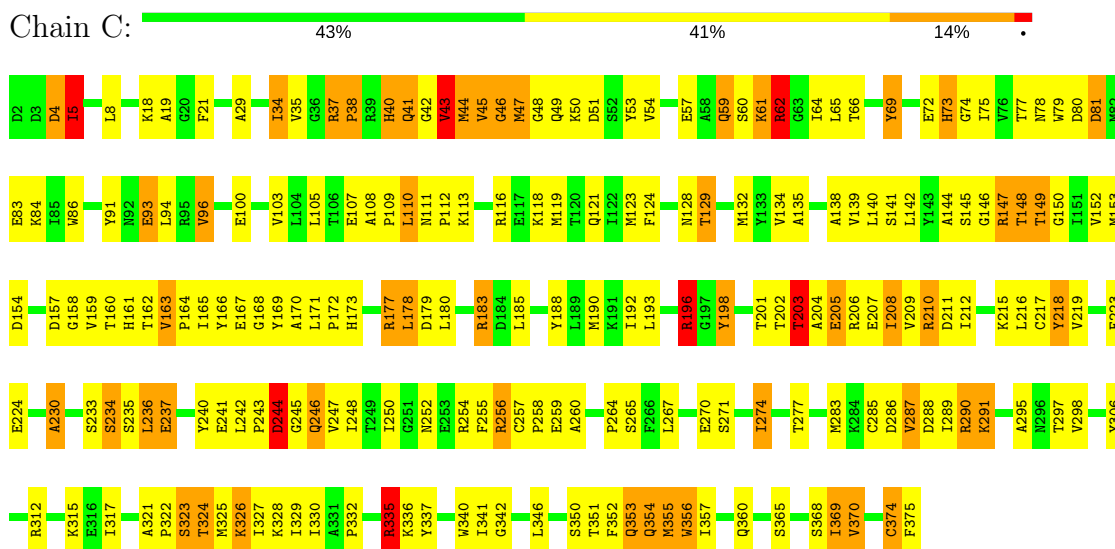


- Molecule 1: Actin, cytoplasmic 1



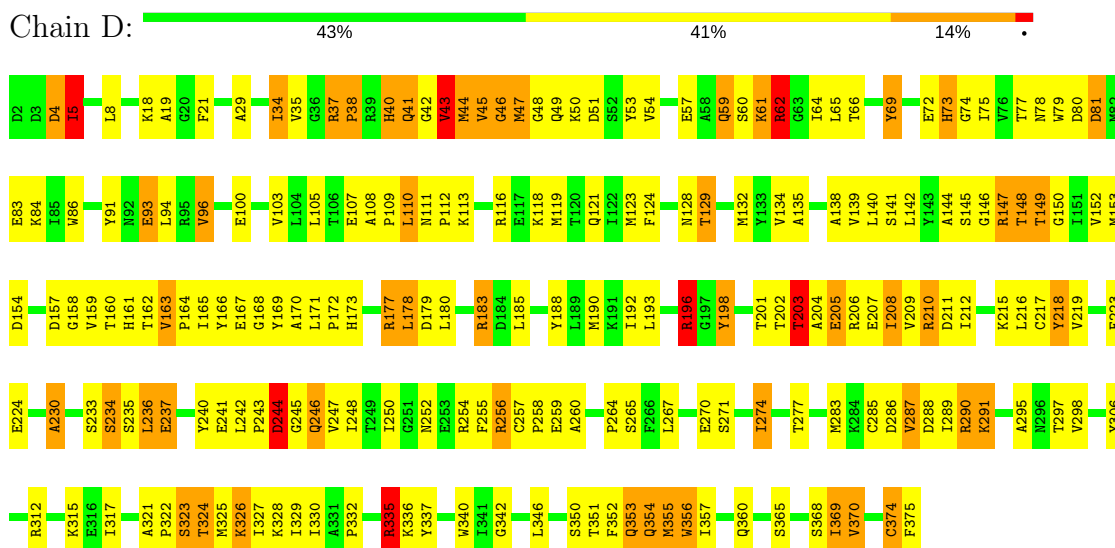
- Molecule 1: Actin, cytoplasmic 1

Chain C:



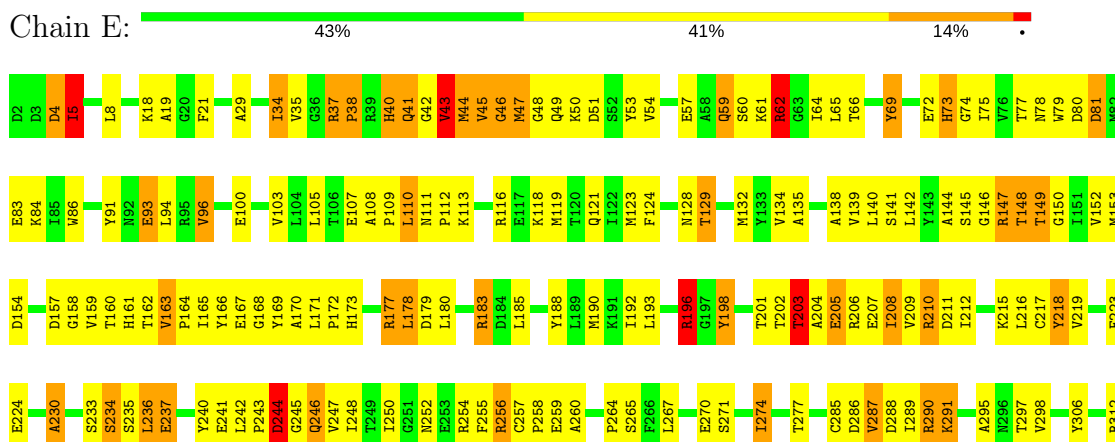
- Molecule 1: Actin, cytoplasmic 1

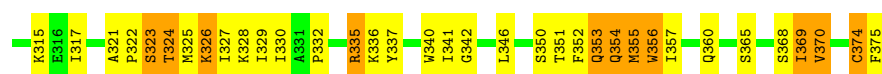
Chain D:



- Molecule 1: Actin, cytoplasmic 1

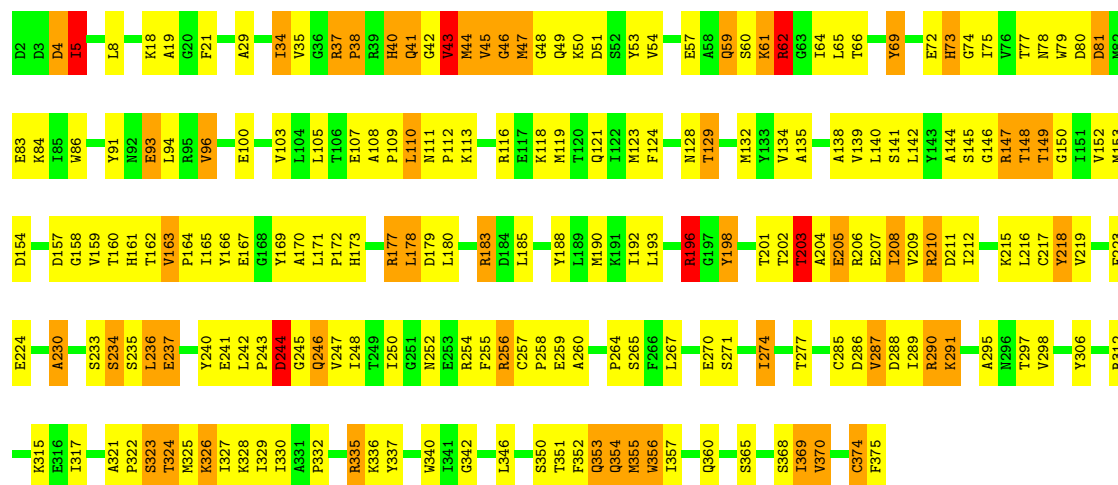
Chain E:





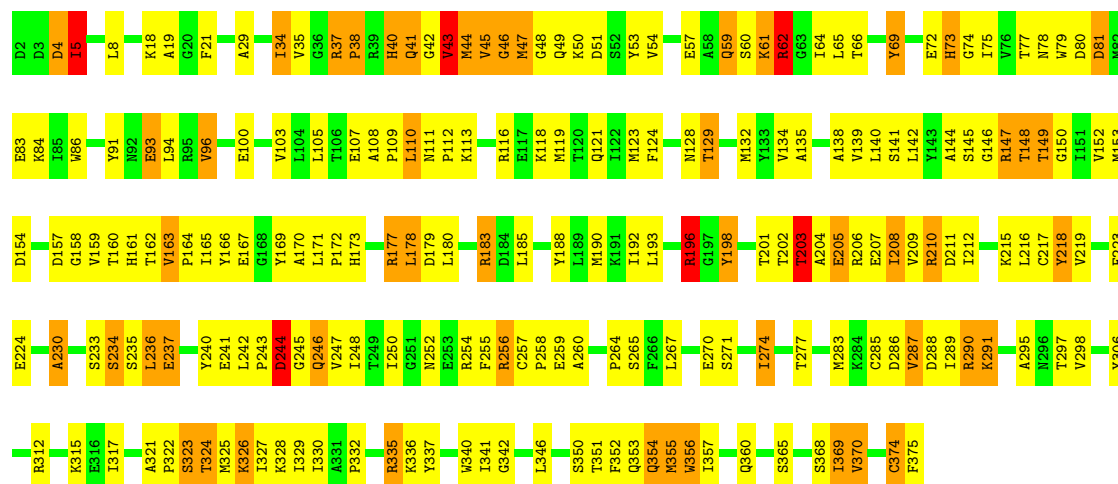
• Molecule 1: Actin, cytoplasmic 1

Chain F: 44% 41% 14%



• Molecule 1: Actin, cytoplasmic 1

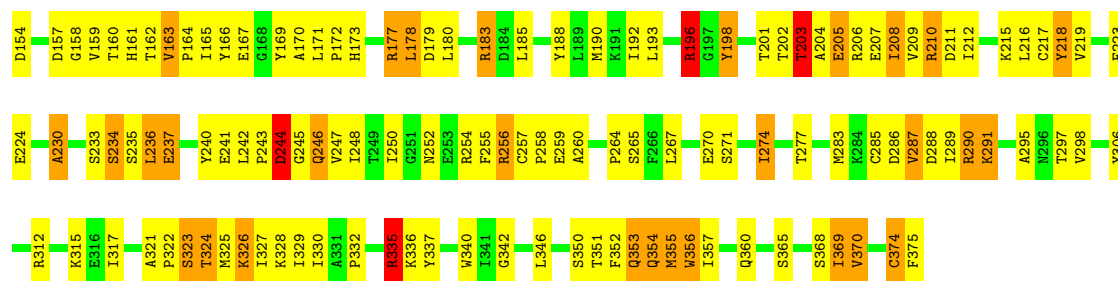
Chain G: 43% 41% 14%



• Molecule 1: Actin, cytoplasmic 1

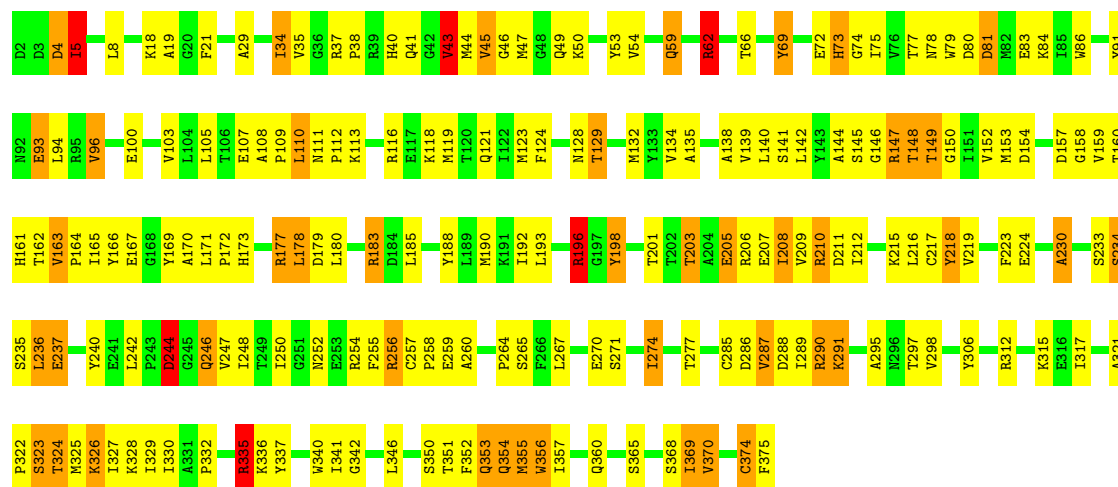
Chain H: 44% 41% 14%





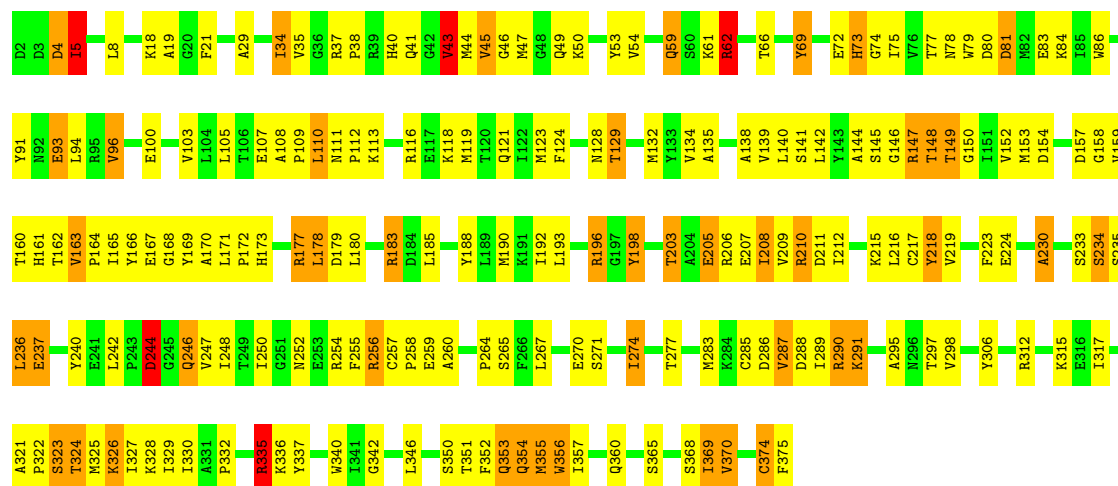
• Molecule 1: Actin, cytoplasmic 1

Chain I: 47% 40% 12%



• Molecule 1: Actin, cytoplasmic 1

Chain J: 47% 40% 12%



• Molecule 2: Alpha-actinin-3

Chain K: 96%



- Molecule 2: Alpha-actinin-3

Chain M:  96%



- Molecule 2: Alpha-actinin-3

Chain L:  96%



- Molecule 2: Alpha-actinin-3

Chain O:  96%



- Molecule 2: Alpha-actinin-3

Chain N:  96%



- Molecule 2: Alpha-actinin-3

Chain Q:  96%



- Molecule 2: Alpha-actinin-3

Chain P:  96%



- Molecule 2: Alpha-actinin-3

Chain S:  96%



- Molecule 2: Alpha-actinin-3

Chain R:  96% .



- Molecule 2: Alpha-actinin-3

Chain T:  96% .



4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of segments used	Not provided	Depositor
Resolution determination method	FSC at 0.5	Depositor
CTF correction method	Weiner filter	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	50000	Depositor
Image detector	Kodak SO163	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	A	1.01	0/2974	1.95	86/4016 (2.1%)
1	B	1.01	0/2974	1.95	85/4016 (2.1%)
1	C	1.01	0/2974	1.95	88/4016 (2.2%)
1	D	1.01	0/2974	1.95	89/4016 (2.2%)
1	E	1.01	0/2974	1.95	85/4016 (2.1%)
1	F	1.01	0/2974	1.95	86/4016 (2.1%)
1	G	1.01	0/2974	1.95	86/4016 (2.1%)
1	H	1.01	0/2974	1.95	87/4016 (2.2%)
1	I	1.01	0/2974	1.95	86/4016 (2.1%)
1	J	1.01	0/2974	1.95	88/4016 (2.2%)
2	K	0.37	0/888	0.56	0/1190
2	L	0.37	0/888	0.56	0/1190
2	M	0.37	0/888	0.56	0/1190
2	N	0.37	0/888	0.56	0/1190
2	O	0.37	0/888	0.56	0/1190
2	P	0.37	0/888	0.56	0/1190
2	Q	0.37	0/888	0.56	0/1190
2	R	0.37	0/888	0.56	0/1190
2	S	0.37	0/888	0.56	0/1190
2	T	0.37	0/888	0.56	0/1190
All	All	0.90	0/38620	1.73	866/52060 (1.7%)

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	A	1	1
1	B	1	1
1	C	1	1
1	D	1	1
1	E	1	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	1	1
1	G	1	1
1	H	1	1
1	I	1	1
1	J	1	1
All	All	10	10

There are no bond length outliers.

The worst 5 of 866 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	356	TRP	CD1-CG-CD2	13.48	117.09	106.30
1	G	356	TRP	CD1-CG-CD2	13.48	117.08	106.30
1	C	356	TRP	CD1-CG-CD2	13.46	117.07	106.30
1	H	356	TRP	CD1-CG-CD2	13.46	117.06	106.30
1	A	356	TRP	CD1-CG-CD2	13.45	117.06	106.30

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	73	HIS	CA
1	B	73	HIS	CA
1	C	73	HIS	CA
1	D	73	HIS	CA
1	E	73	HIS	CA

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	4	ASP	Mainchain
1	B	4	ASP	Mainchain
1	C	4	ASP	Mainchain
1	D	4	ASP	Mainchain
1	E	4	ASP	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	A	2917	0	2851	472	0
1	B	2917	0	2851	474	0
1	C	2917	0	2847	725	0
1	D	2917	0	2847	722	0
1	E	2917	0	2847	729	0
1	F	2917	0	2847	721	0
1	G	2917	0	2847	722	0
1	H	2917	0	2847	723	0
1	I	2917	0	2857	478	0
1	J	2917	0	2857	471	0
2	K	874	0	917	0	0
2	L	874	0	917	0	0
2	M	874	0	917	0	0
2	N	874	0	917	0	0
2	O	874	0	917	0	0
2	P	874	0	917	0	0
2	Q	874	0	917	0	0
2	R	874	0	917	0	0
2	S	874	0	917	0	0
2	T	874	0	917	0	0
All	All	37910	0	37668	4210	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 73.

The worst 5 of 4210 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)
1:H:142:LEU:HD13	1:H:152:VAL:CG2	1.18	1.62
1:A:69:TYR:CB	1:A:84:LYS:H	0.99	1.62
1:G:245:GLY:HA2	1:I:324:THR:CA	1.28	1.61
1:C:142:LEU:HD13	1:C:152:VAL:CG2	1.18	1.60
1:C:69:TYR:CB	1:C:84:LYS:H	0.99	1.60

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	A	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
1	B	361/374 (96%)	318 (88%)	33 (9%)	10 (3%)	6	39
1	C	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
1	D	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
1	E	361/374 (96%)	318 (88%)	33 (9%)	10 (3%)	6	39
1	F	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
1	G	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
1	H	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
1	I	361/374 (96%)	318 (88%)	33 (9%)	10 (3%)	6	39
1	J	361/374 (96%)	318 (88%)	32 (9%)	11 (3%)	5	37
2	K	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	L	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	M	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	N	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	O	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	P	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	Q	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	R	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	S	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
2	T	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
All	All	4680/4830 (97%)	4200 (90%)	373 (8%)	107 (2%)	11	43

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	VAL

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Mol	Chain	Res	Type
1	A	203	THR
1	A	233	SER
1	A	355	MET
1	B	43	VAL

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	A	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	B	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	C	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	D	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	E	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	F	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	G	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	H	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	I	317/317 (100%)	280 (88%)	37 (12%)	6	27
1	J	317/317 (100%)	280 (88%)	37 (12%)	6	27
2	K	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	L	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	M	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	N	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	O	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	P	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	Q	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	R	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	S	93/93 (100%)	89 (96%)	4 (4%)	33	64
2	T	93/93 (100%)	89 (96%)	4 (4%)	33	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	4100/4100 (100%)	3690 (90%)	410 (10%)	13	33

5 of 410 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	18	LYS
1	G	80	ASP
2	L	47	GLN
1	F	62	ARG
1	F	244	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	59	GLN
1	F	59	GLN
1	J	59	GLN
1	E	353	GLN
1	F	87	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.