



wwPDB EM Validation Summary Report ⓘ

Feb 20, 2025 – 07:47 AM EST

PDB ID : 1SJJ
Title : Cryo-EM Structure of Chicken Gizzard Smooth Muscle alpha-Actinin
Authors : Liu, J.; Taylor, D.W.; Taylor, K.A.
Deposited on : 2004-03-03
Resolution : 20.00 Å(reported)
Based on initial models : 1CFD, 1DXX, 1HCI

This is a wwPDB EM 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

<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:

MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

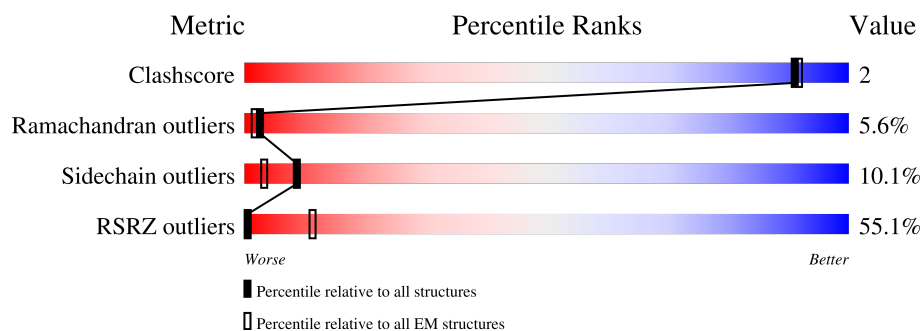
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 20.00 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RSRZ outliers	164674	54

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	A	863	<div> <div>56%</div> <div>75%</div> <div>20%</div> <div>• •</div> </div>
1	B	863	<div> <div>54%</div> <div>73%</div> <div>22%</div> <div>• •</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14014 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.

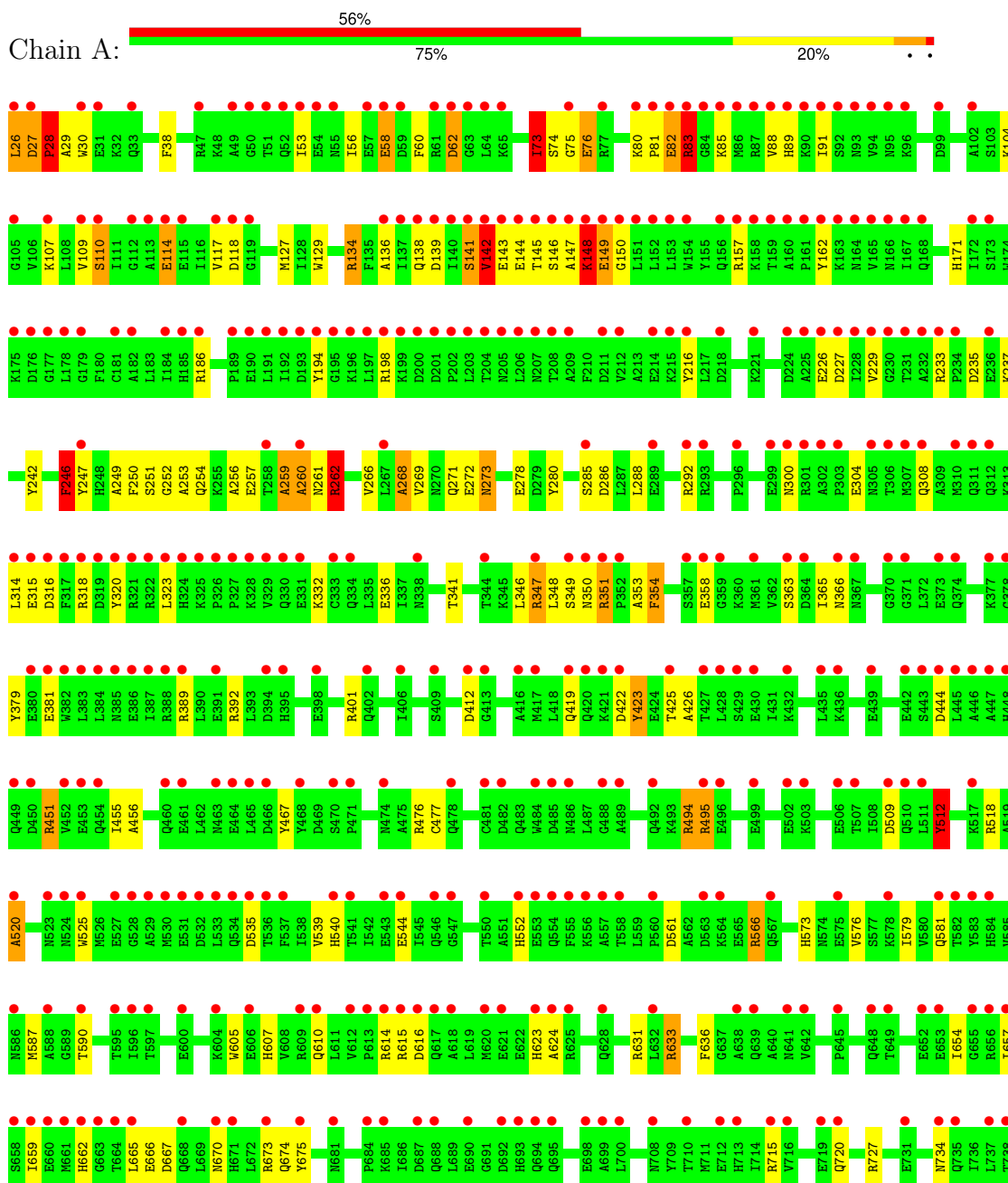
- Molecule 1 is a protein called actinin.

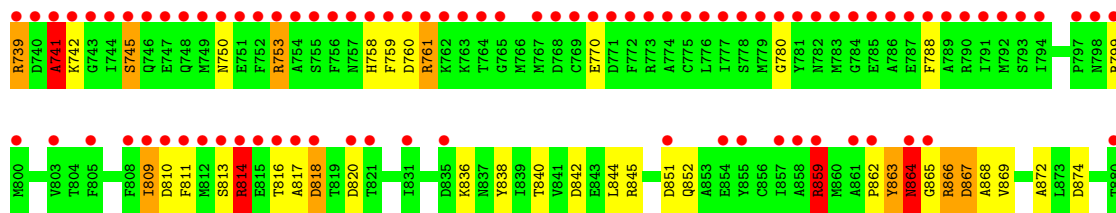
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	863	Total	C	N	O	S	0	0
			7007	4395	1236	1337	39		
1	B	863	Total	C	N	O	S	0	0
			7007	4395	1236	1337	39		

3 Residue-property plots

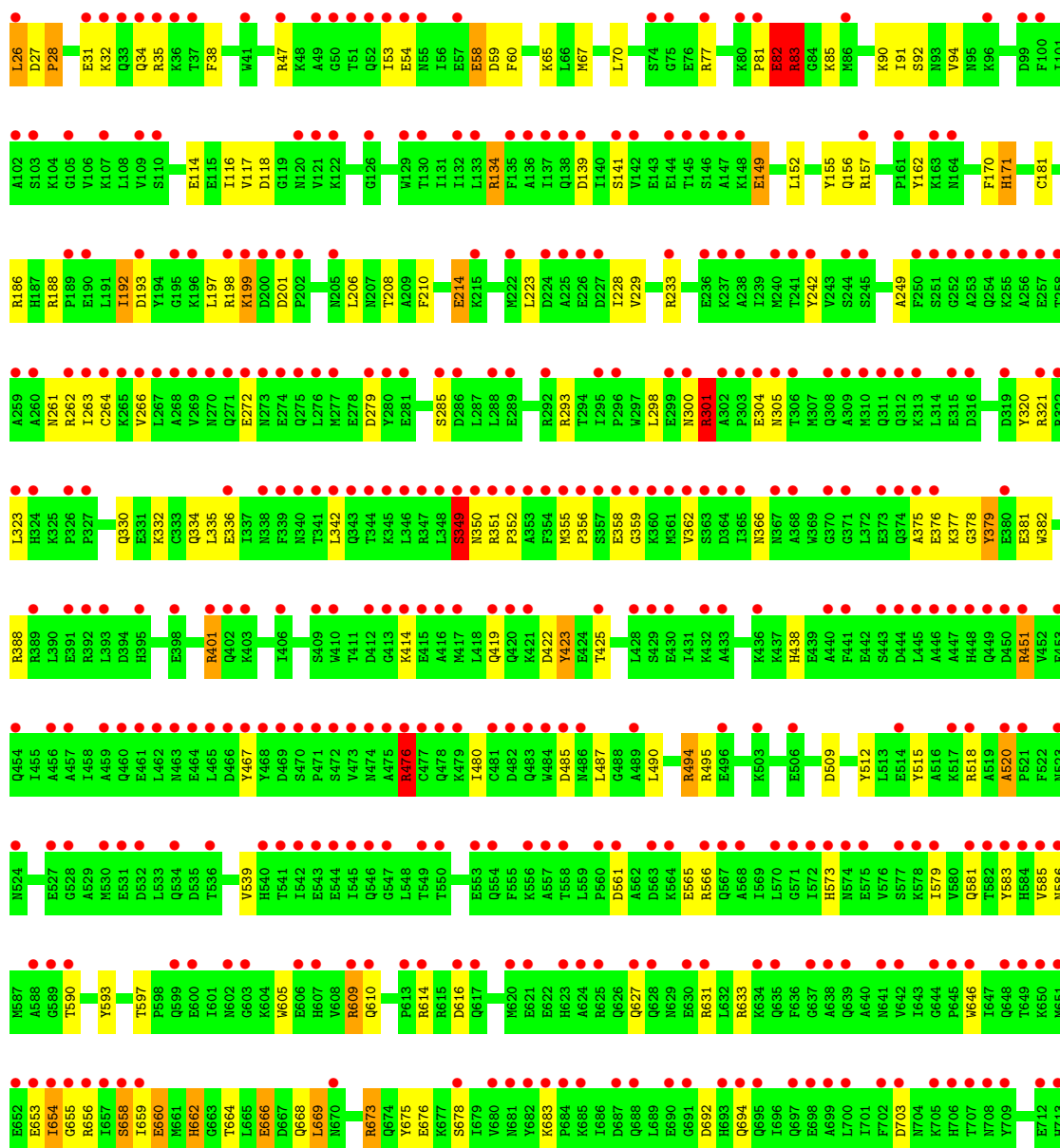
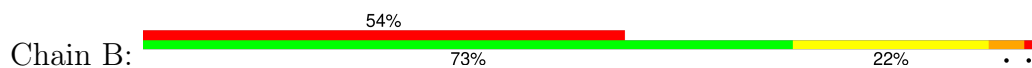
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

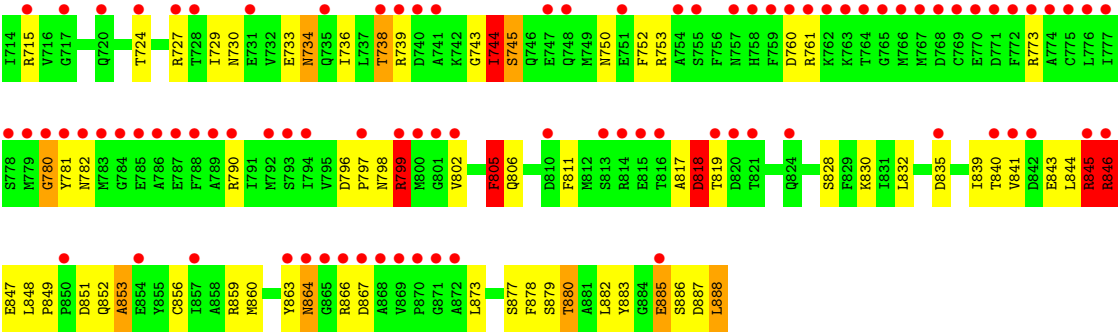
• Molecule 1: actinin





• Molecule 1: actinin





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 1 2	Depositor
Cell constants a, b, c, α , β , γ	263.10Å 203.70Å 100.00Å 90.00° 90.00° 107.10°	Depositor
Resolution (Å)	(Not available) – 20.00 200.00 – 14.81	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-20.00) 29.2 (200.00-14.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtrriage
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available) 0.385 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	(Not available)	Xtrriage
Anisotropy	(Not available)	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	3.94 , 999.0	EDS
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	14014	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	A	0.77	1/7139 (0.0%)	1.37	53/9633 (0.6%)
1	B	0.78	1/7139 (0.0%)	1.36	53/9633 (0.6%)
All	All	0.78	2/14278 (0.0%)	1.36	106/19266 (0.6%)

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	0	55
1	B	0	56
All	All	0	111

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	149	GLU	CD-OE2	10.05	1.36	1.25
1	A	149	GLU	CD-OE2	10.00	1.36	1.25

The worst 5 of 106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	149	GLU	CB-CA-C	-12.98	84.44	110.40
1	A	753	ARG	NE-CZ-NH1	10.24	125.42	120.30
1	B	566	ARG	NE-CZ-NH1	10.16	125.38	120.30
1	B	162	TYR	CB-CG-CD1	8.98	126.39	121.00
1	B	162	TYR	CB-CG-CD2	-8.68	115.79	121.00

There are no chirality outliers.

5 of 111 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	LEU	Peptide
1	A	27	ASP	Peptide
1	A	56	ILE	Peptide
1	A	58	GLU	Peptide
1	A	83	ARG	Sidechain

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	7007	0	6898	23	172
1	B	7007	0	6898	22	160
All	All	14014	0	13796	42	209

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 2.

The worst 5 of 42 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:A:149:GLU:HB2	1:A:150:GLY:CA	2.09	0.81
1:B:585:VAL:HG12	1:B:586:ASN:H	1.64	0.61
1:A:741:ALA:HB1	1:A:742:LYS:HA	1.83	0.60
1:A:149:GLU:HB2	1:A:150:GLY:HA3	1.88	0.56
1:A:852:GLN:NE2	1:B:149:GLU:OE2	2.32	0.55

The worst 5 of 209 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:864:ASN:CB	1:B:845:ARG:CZ[1_665]	0.31	1.89
1:A:836:LYS:CE	1:B:828:SER:CB[1_665]	0.32	1.88
1:A:89:HIS:CD2	1:A:813:SER:O[1_445]	0.48	1.72
1:B:81:PRO:CD	1:B:301:ARG:NH1[2_555]	0.68	1.52
1:B:81:PRO:CB	1:B:301:ARG:NH2[2_555]	0.68	1.52

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	A	861/863 (100%)	688 (80%)	123 (14%)	50 (6%)	1	14
1	B	861/863 (100%)	698 (81%)	116 (14%)	47 (6%)	1	15
All	All	1722/1726 (100%)	1386 (80%)	239 (14%)	97 (6%)	2	14

5 of 97 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	PRO
1	A	109	VAL
1	A	142	VAL
1	A	148	LYS
1	A	251	SER

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	A	750/750 (100%)	679 (90%)	71 (10%)	7	22
1	B	750/750 (100%)	669 (89%)	81 (11%)	5	19
All	All	1500/1500 (100%)	1348 (90%)	152 (10%)	9	20

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	590	THR

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Mol	Chain	Res	Type
1	B	864	ASN
1	B	627	GLN
1	B	750	ASN
1	B	885	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	573	HIS
1	B	623	HIS
1	B	852	GLN
1	B	694	GLN
1	B	156	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.