



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2017 – 04:24 pm GMT

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)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
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) : recalc29102

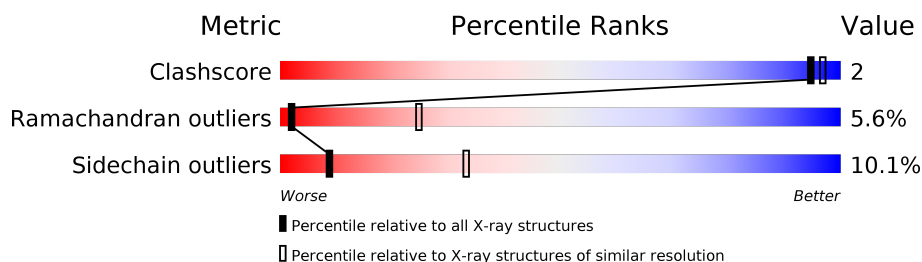
# 1 Overall quality at a glance

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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1037 (15.00-3.80)
Ramachandran outliers	110173	1004 (11.50-3.76)
Sidechain outliers	110143	1099 (11.50-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	863	 75% 20% . .
1	B	863	 73% 22% . .

## 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 ZeroOcc column contains the number of atoms modelled with zero occupancy, 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.

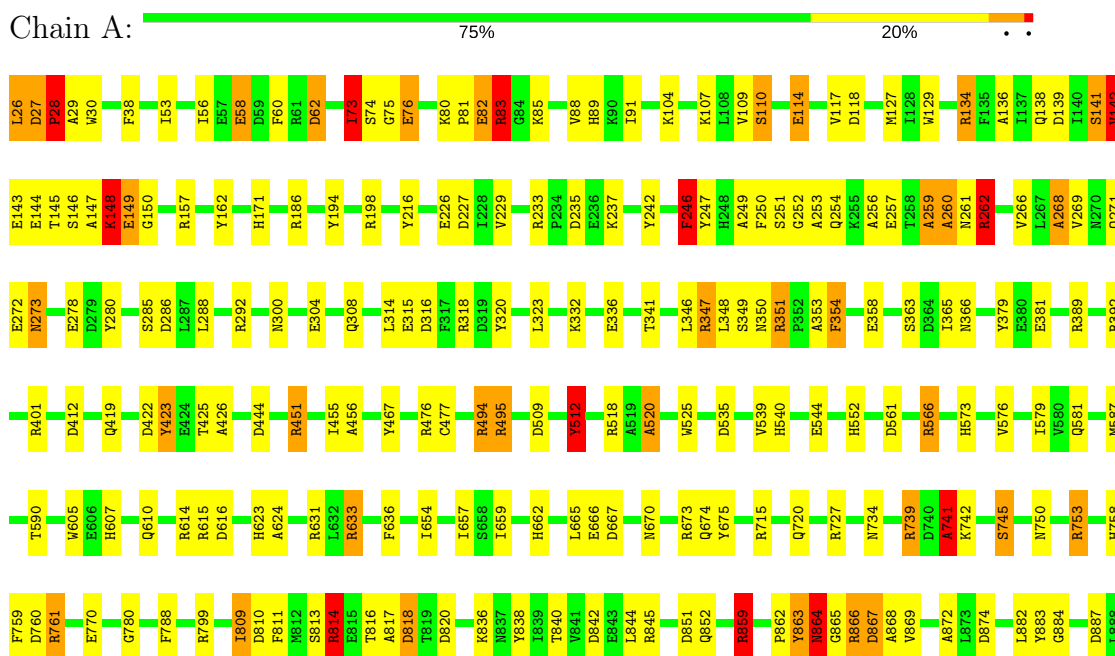
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	863	Total	C	N	O	S	0	0	0
			7007	4395	1236	1337	39			
1	B	863	Total	C	N	O	S	0	0	0
			7007	4395	1236	1337	39			

### 3 Residue-property plots

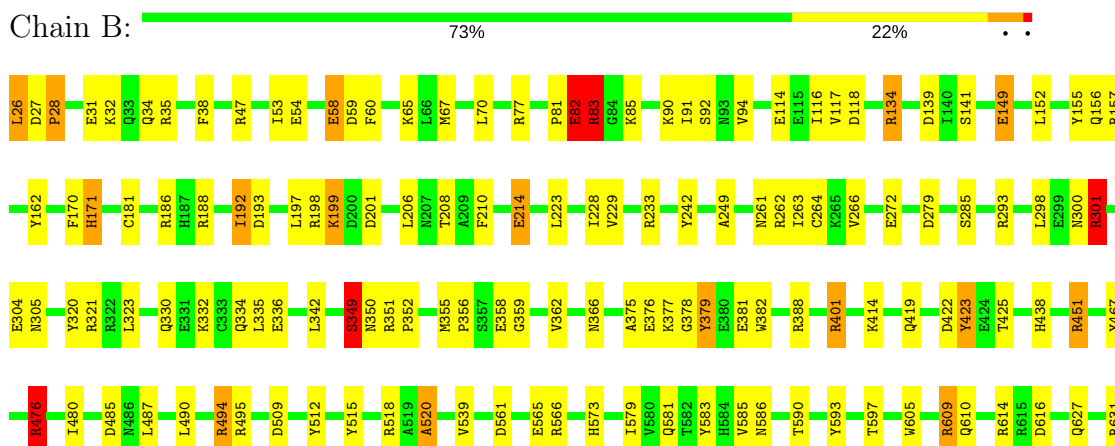
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

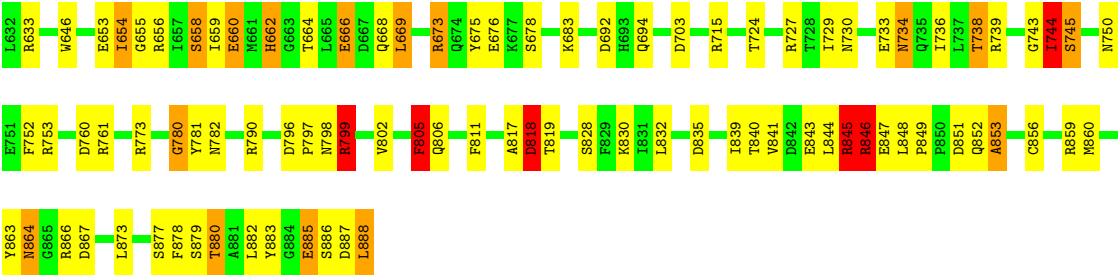
Note EDS was not executed.

#### • Molecule 1: actinin



#### • Molecule 1: actinin





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 1 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	263.10Å 203.70Å 100.00Å 90.00° 90.00° 107.10°	Depositor
Resolution (Å)	(Not available) – 20.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-20.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	unknown	Depositor
R, $R_{free}$	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14014	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

## 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 X-ray entries followed by that with respect to entries of similar resolution.

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%)	2	24
1	B	861/863 (100%)	698 (81%)	116 (14%)	47 (6%)	2	25
All	All	1722/1726 (100%)	1386 (80%)	239 (14%)	97 (6%)	2	25

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 X-ray entries followed by that with respect to entries of similar resolution.

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%)	10	36
1	B	750/750 (100%)	669 (89%)	81 (11%)	7	31
All	All	1500/1500 (100%)	1348 (90%)	152 (10%)	9	33

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

Mol	Chain	Res	Type
1	A	866	ARG

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Mol	Chain	Res	Type
1	B	199	LYS
1	B	845	ARG
1	A	882	LEU
1	B	70	LEU

Some 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	534	GLN
1	B	546	GLN
1	B	694	GLN
1	B	248	HIS
1	B	623	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.