

wwPDB X-ray Structure Validation Summary Report (i)

Sep 18, 2021 – 08:03 AM BST

PDB ID : 7AW8

Title : Alpha-actinin in Rhodamnia argentea

Authors : Persson, K.; Backman, L.

Deposited on : 2020-11-06

Resolution : 1.50 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

A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

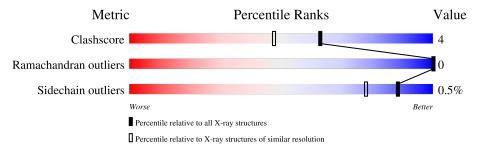
Validation Pipeline (wwPDB-VP) : 2.23.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.50 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)

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 of the lower 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	A	280	78%	7%	15%			

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

\mathbf{Mol}	Type	Chain	\mathbf{Res}	Chirality	Geometry	Clashes	Electron density
2	ACY	A	301	-	-	X	-
2	ACY	A	302	-	-	X	-



2 Entry composition (i)

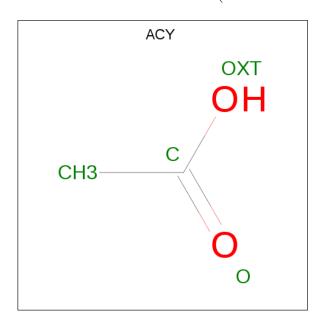
There are 4 unique types of molecules in this entry. The entry contains 4106 atoms, of which 1964 are hydrogens and 0 are deuteriums.

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 Alpha actinin, actin binding domain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	Δ	239	Total	С	Н	N	О	S	0	0	0
1	11	200	3899	1243	1948	339	360	9		U	

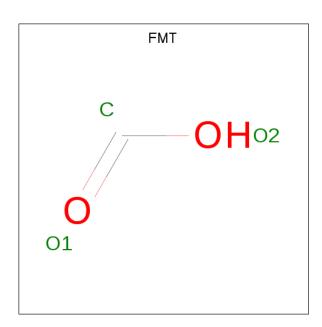
• Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 7		H 3		0	0
2	A	1	Total 7		H 3	O 2	0	0

• Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	Δ	1	Total C H O	0	0
	Λ	1	5 1 2 2	U	U
3	A	1	Total C H O	0	0
	3 A	1	5 1 2 2	U	
3	Δ	1	Total C H O	0	0
	5 A	1	5 1 2 2	U	
3	Δ	1	Total C H O	0	0
	11	1	5 1 2 2	0	U
3	Δ	1	Total C H O		
"	11	1	$\begin{bmatrix} 5 & 1 & 2 & 2 \end{bmatrix}$		

• Molecule 4 is water.

\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	$\mathbf{AltConf}$
4	A	168	Total O 168 168	0	0

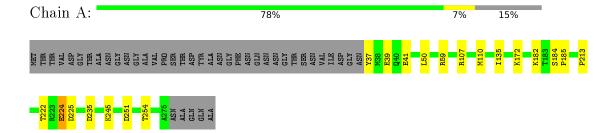


3 Residue-property plots (i)

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.

Note EDS was not executed.

• Molecule 1: Alpha actinin, actin binding domain





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 31 2 1	Depositor	
Cell constants	37.22Å 37.22Å 290.27Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	48.38 - 1.50	Depositor	
% Data completeness	99.9 (48.38-1.50)	Depositor	
(in resolution range)	33.3 (40.00 1.00)		
R_{merge}	0.10	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	PHENIX 1.17.1_3660	Depositor	
R, R_{free}	0.167 , 0.190	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	4106	wwPDB-VP	
Average B, all atoms (Å ²)	32.0	wwPDB-VP	



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: FMT, ACY

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	Boı	nd lengths	Bond angles		
MIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.67	3/1993~(0.2%)	0.73	4/2694 (0.1%)	

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
1	A	213	PRO	N-CA	10.74	1.65	1.47
1	A	224	GLU	CG-CD	-8.47	1.39	1.51
1	A	224	GLU	CD-OE2	-5.30	1.19	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^o)$
1	A	224	GLU	CG-CD-OE2	-7.44	103.41	118.30
1	A	224	GLU	CG-CD-OE1	6.82	131.94	118.30
1	A	107	ARG	CG-CD-NE	5.31	122.94	111.80
1	A	213	PRO	CA-N-CD	-5.12	104.33	111.50

There are no chirality outliers.

There are no planarity outliers.

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	A	1951	1948	1948	15	0

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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
2	A	8	6	6	6	0
3	A	15	10	5	0	0
4	A	168	0	0	7	0
All	All	2142	1964	1959	17	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 4.

The worst 5 of 17 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance } (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:222:THR:OG1	1:A:224:GLU:HG2	1.76	0.86
1:A:59:ARG:HH11	2:A:301:ACY:H1	1.51	0.74
1:A:110:MET:HE3	4:A:540:HOH:O	1.91	0.69
1:A:224:GLU:HG3	4:A:460:HOH:O	1.94	0.68
1:A:254:THR:OG1	2:A:302:ACY:H1	1.94	0.67

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 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	$237/280 \ (85\%)$	230 (97%)	7 (3%)	0	100	100	

There are no Ramachandran outliers to report.

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	212/242 (88%)	211 (100%)	1 (0%)	88 78		

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Mol Type Chain		n Dog	Dog	Dog	Dog	Dog	Dog	Dag	Peg	Dog	${ m Res}$	Dog	Dog	Link	В	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2												
3	FMT	A	303	-	0,2,2	0.00	-	0,1,1	0.00	-												
2	ACY	A	301	-	1,3,3	4.04	1 (100%)	0,3,3	0.00	-												



Mol	Type Chain Res		Link	Bond lengths			Bond angles			
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FMT	A	306	-	0,2,2	0.00	-	0,1,1	0.00	=
3	FMT	A	304	_	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	A	305	_	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	A	307	_	0,2,2	0.00	-	0,1,1	0.00	-
2	ACY	A	302	_	1,3,3	7.38	1 (100%)	0,3,3	0.00	_

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	A	302	ACY	СН3-С	7.38	1.58	1.48
2	A	301	ACY	СН3-С	4.04	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	ACY	2	0
2	A	302	ACY	4	0

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 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

