



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:23 AM UTC

PDB ID : 7SHJ / pdb_00007shj
Title : Crystal structure of Acinetobacter baumannii ZnuA in the metal-free state
Authors : Luo, Z.; McDevitt, C.A.; Kobe, B.
Deposited on : 2021-10-09
Resolution : 2.13 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 ⓘ 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

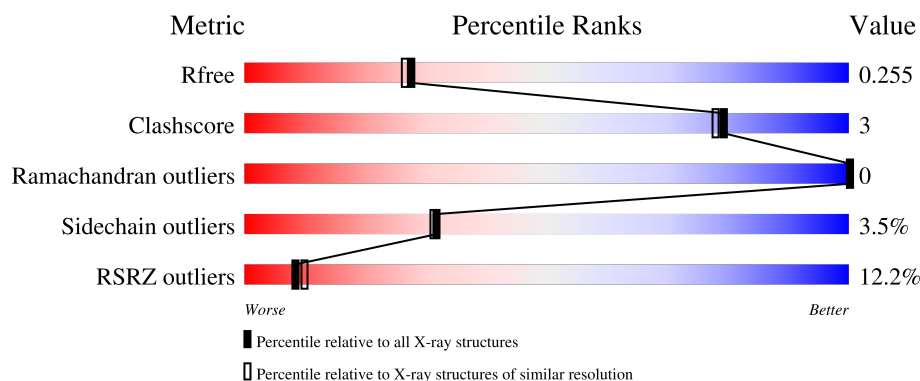
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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))
R_{free}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	286	10% 69% 14% • 16%
1	B	286	10% 71% 11% • 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7710 atoms, of which 3761 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 Zinc ABC transporter solute-binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	240	Total	C	H	N	O	S	0	0	0
			3780	1205	1889	333	348	5			
1	B	236	Total	C	H	N	O	S	0	0	0
			3738	1190	1872	327	344	5			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	initiating methionine	UNP A0A6B2IEQ3
A	268	ALA	-	expression tag	UNP A0A6B2IEQ3
A	269	SER	-	expression tag	UNP A0A6B2IEQ3
A	270	LEU	-	expression tag	UNP A0A6B2IEQ3
A	271	GLU	-	expression tag	UNP A0A6B2IEQ3
A	272	VAL	-	expression tag	UNP A0A6B2IEQ3
A	273	LEU	-	expression tag	UNP A0A6B2IEQ3
A	274	PHE	-	expression tag	UNP A0A6B2IEQ3
A	275	GLN	-	expression tag	UNP A0A6B2IEQ3
A	276	GLY	-	expression tag	UNP A0A6B2IEQ3
A	277	PRO	-	expression tag	UNP A0A6B2IEQ3
A	278	GLY	-	expression tag	UNP A0A6B2IEQ3
A	279	SER	-	expression tag	UNP A0A6B2IEQ3
A	280	ALA	-	expression tag	UNP A0A6B2IEQ3
A	281	HIS	-	expression tag	UNP A0A6B2IEQ3
A	282	HIS	-	expression tag	UNP A0A6B2IEQ3
A	283	HIS	-	expression tag	UNP A0A6B2IEQ3
A	284	HIS	-	expression tag	UNP A0A6B2IEQ3
A	285	HIS	-	expression tag	UNP A0A6B2IEQ3
A	286	HIS	-	expression tag	UNP A0A6B2IEQ3
A	287	HIS	-	expression tag	UNP A0A6B2IEQ3
A	288	HIS	-	expression tag	UNP A0A6B2IEQ3
A	289	HIS	-	expression tag	UNP A0A6B2IEQ3
A	290	HIS	-	expression tag	UNP A0A6B2IEQ3
A	291	HIS	-	expression tag	UNP A0A6B2IEQ3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	292	HIS	-	expression tag	UNP A0A6B2IEQ3
B	7	MET	-	initiating methionine	UNP A0A6B2IEQ3
B	268	ALA	-	expression tag	UNP A0A6B2IEQ3
B	269	SER	-	expression tag	UNP A0A6B2IEQ3
B	270	LEU	-	expression tag	UNP A0A6B2IEQ3
B	271	GLU	-	expression tag	UNP A0A6B2IEQ3
B	272	VAL	-	expression tag	UNP A0A6B2IEQ3
B	273	LEU	-	expression tag	UNP A0A6B2IEQ3
B	274	PHE	-	expression tag	UNP A0A6B2IEQ3
B	275	GLN	-	expression tag	UNP A0A6B2IEQ3
B	276	GLY	-	expression tag	UNP A0A6B2IEQ3
B	277	PRO	-	expression tag	UNP A0A6B2IEQ3
B	278	GLY	-	expression tag	UNP A0A6B2IEQ3
B	279	SER	-	expression tag	UNP A0A6B2IEQ3
B	280	ALA	-	expression tag	UNP A0A6B2IEQ3
B	281	HIS	-	expression tag	UNP A0A6B2IEQ3
B	282	HIS	-	expression tag	UNP A0A6B2IEQ3
B	283	HIS	-	expression tag	UNP A0A6B2IEQ3
B	284	HIS	-	expression tag	UNP A0A6B2IEQ3
B	285	HIS	-	expression tag	UNP A0A6B2IEQ3
B	286	HIS	-	expression tag	UNP A0A6B2IEQ3
B	287	HIS	-	expression tag	UNP A0A6B2IEQ3
B	288	HIS	-	expression tag	UNP A0A6B2IEQ3
B	289	HIS	-	expression tag	UNP A0A6B2IEQ3
B	290	HIS	-	expression tag	UNP A0A6B2IEQ3
B	291	HIS	-	expression tag	UNP A0A6B2IEQ3
B	292	HIS	-	expression tag	UNP A0A6B2IEQ3

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	110	Total O 110 110	0	0
3	B	81	Total O 81 81	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.52Å 45.61Å 97.66Å 90.00° 97.07° 90.00°	Depositor
Resolution (Å)	45.55 – 2.13 45.55 – 2.13	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.55-2.13) 99.6 (45.55-2.13)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.230 , 0.253 0.232 , 0.255	Depositor DCC
R_{free} test set	1403 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	34.3	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7710	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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

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	1.19	17/1932 (0.9%)	1.43	11/2624 (0.4%)
1	B	0.94	10/1904 (0.5%)	1.14	5/2583 (0.2%)
All	All	1.07	27/3836 (0.7%)	1.29	16/5207 (0.3%)

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	62	LEU	C-O	-8.53	1.13	1.24
1	B	256	ILE	C-O	-8.01	1.15	1.24
1	B	32	GLN	C-O	-8.01	1.15	1.24
1	B	71	ASN	C-O	-7.55	1.15	1.24
1	A	61	TRP	C-O	-7.47	1.14	1.23

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61	TRP	CA-C-O	-7.47	112.96	121.40
1	A	61	TRP	CA-C-O	-6.75	113.78	121.40
1	A	49	HIS	N-CA-C	-6.50	104.20	111.28
1	B	256	ILE	CA-C-O	-6.22	114.14	121.05
1	A	216	LEU	CA-C-O	-5.97	114.17	120.80

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	1891	1889	1892	10	0
1	B	1866	1872	1871	11	0
2	A	1	0	0	0	0
3	A	110	0	0	1	0
3	B	81	0	0	2	0
All	All	3949	3761	3763	20	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 3.

The worst 5 of 20 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:69:PRO:O	3:A:401:HOH:O	1.99	0.81
1:B:159:SER:O	3:B:301:HOH:O	2.07	0.71
1:B:53:ILE:HD13	1:B:74:LEU:HD21	1.78	0.64
1:A:35:LEU:HD11	1:A:70:LEU:HD11	1.88	0.55
1:A:91:ILE:HG23	1:A:106:VAL:HG13	1.89	0.54

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	232/286 (81%)	229 (99%)	3 (1%)	0	100	100
1	B	226/286 (79%)	220 (97%)	6 (3%)	0	100	100
All	All	458/572 (80%)	449 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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 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	202/241 (84%)	194 (96%)	8 (4%)	28	25
1	B	199/241 (83%)	193 (97%)	6 (3%)	36	37
All	All	401/482 (83%)	387 (96%)	14 (4%)	32	31

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	256	ILE
1	B	30	GLU
1	B	226	TYR
1	B	138	LYS
1	B	210	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	ASN
1	B	32	GLN
1	B	135	ASN
1	B	49	HIS
1	A	212	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	240/286 (83%)	0.67	29 (12%) 8 10	22, 36, 85, 129	0
1	B	236/286 (82%)	0.83	29 (12%) 8 10	27, 48, 94, 117	0
All	All	476/572 (83%)	0.74	58 (12%) 8 10	22, 42, 90, 129	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	35	LEU	4.9
1	B	73	LEU	4.3
1	A	73	LEU	4.3
1	B	219	SER	4.2
1	B	226	TYR	4.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NA	A	301	1/1	0.96	0.09	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.