



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1R1U / pdb_00001r1u
Title : Crystal structure of the metal-sensing transcriptional repressor CzrA from *Staphylococcus aureus* in the apo-form
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Deposited on : 2003-09-25
Resolution : 2.00 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

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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

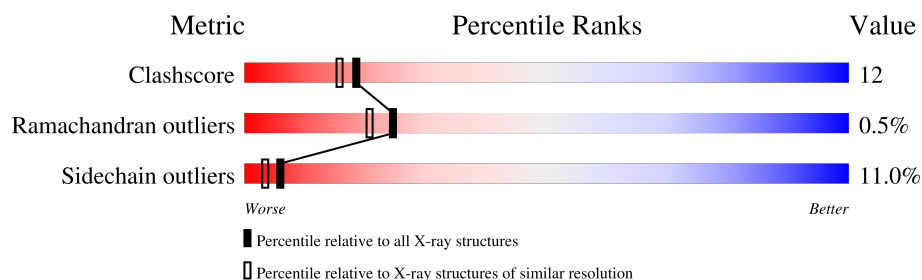
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	106	 66% 17% 5% • 11%
1	B	106	 67% 17% • 12%
1	C	106	 64% 20% 8% 8%
1	D	106	 63% 20% 7% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3214 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.

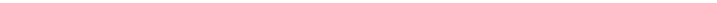
- Molecule 1 is a protein called repressor protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	94	Total	C	N	O	S	0	0	0
			746	466	140	137	3			
1	B	93	Total	C	N	O	S	0	0	0
			737	460	138	136	3			
1	C	98	Total	C	N	O	S	0	0	0
			778	485	144	146	3			
1	D	95	Total	C	N	O	S	0	0	0
			755	471	141	140	3			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	55	Total	O	0	0
			55	55		
2	B	56	Total	O	0	0
			56	56		
2	C	38	Total	O	0	0
			38	38		
2	D	49	Total	O	0	0
			49	49		

Note EDS was not executed.

- Chain A:  66% 17% 5% 11%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	50.11Å 50.11Å 153.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	18.90 – 2.00	Depositor
% Data completeness (in resolution range)	96.4 (18.90-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.202 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3214	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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	1.33	1/757 (0.1%)	1.20	4/1019 (0.4%)
1	B	1.33	4/748 (0.5%)	1.20	4/1008 (0.4%)
1	C	1.27	0/789	1.15	2/1062 (0.2%)
1	D	1.25	1/766 (0.1%)	1.20	3/1031 (0.3%)
All	All	1.30	6/3060 (0.2%)	1.19	13/4120 (0.3%)

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	C	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	78	MET	SD-CE	-6.04	1.64	1.79
1	B	85	ILE	C-O	-5.81	1.17	1.24
1	D	19	ILE	CA-CB	5.16	1.60	1.54
1	B	62	LEU	CA-C	5.14	1.59	1.52
1	B	30	ARG	CD-NE	-5.05	1.39	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	30	ARG	NE-CZ-NH2	-6.53	113.33	119.20
1	A	30	ARG	NE-CZ-NH2	-6.32	113.52	119.20
1	B	100	HIS	N-CA-C	6.20	120.25	110.58
1	B	77	SER	CA-CB-OG	5.79	122.67	111.10
1	C	51	LEU	N-CA-C	-5.75	100.41	109.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	7	GLU	Peptide

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	746	0	766	20	0
1	B	737	0	753	16	0
1	C	778	0	794	25	0
1	D	755	0	772	29	0
2	A	55	0	0	7	0
2	B	56	0	0	1	0
2	C	38	0	0	5	0
2	D	49	0	0	12	0
All	All	3214	0	3085	73	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 12.

The worst 5 of 73 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:D:16:VAL:HB	2:D:125:HOH:O	1.51	1.08
1:A:92:LYS:HG3	2:A:133:HOH:O	1.67	0.95
1:C:55:ASN:HD21	1:C:59:GLN:HE21	1.15	0.89
1:B:96:HIS:CE1	1:B:100:HIS:CD2	2.60	0.88
1:A:77:SER:HB3	2:A:125:HOH:O	1.76	0.83

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	92/106 (87%)	90 (98%)	1 (1%)	1 (1%)	11	7
1	B	91/106 (86%)	89 (98%)	2 (2%)	0	100	100
1	C	96/106 (91%)	88 (92%)	8 (8%)	0	100	100
1	D	93/106 (88%)	86 (92%)	6 (6%)	1 (1%)	11	7
All	All	372/424 (88%)	353 (95%)	17 (5%)	2 (0%)	24	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	PRO
1	D	76	GLN

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	85/96 (88%)	75 (88%)	10 (12%)	5	3
1	B	84/96 (88%)	79 (94%)	5 (6%)	17	14
1	C	89/96 (93%)	74 (83%)	15 (17%)	2	1
1	D	86/96 (90%)	78 (91%)	8 (9%)	8	5
All	All	344/384 (90%)	306 (89%)	38 (11%)	6	3

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	100	HIS
1	D	100	HIS
1	C	102	LYS
1	D	73	ARG
1	D	103	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	44	HIS
1	D	67	HIS
1	D	96	HIS
1	D	74	GLN
1	B	99	ASN

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.

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.