



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 07:51 pm GMT

PDB ID : 2PS9  
Title : Structure and metal binding properties of ZnuA, a periplasmic zinc transporter from Escherichia coli  
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Deposited on : 2007-05-04  
Resolution : 2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

<https://www.wwpdb.org/validation/2017/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) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

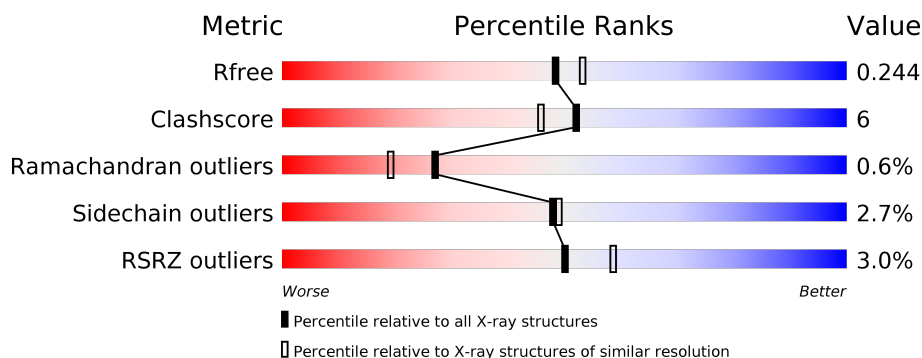
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
$R_{free}$	111664	1287 (2.16-2.16)
Clashscore	122126	1390 (2.16-2.16)
Ramachandran outliers	120053	1368 (2.16-2.16)
Sidechain outliers	120020	1367 (2.16-2.16)
RSRZ outliers	108989	1262 (2.16-2.16)

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.

Mol	Chain	Length	Quality of chain
1	A	284	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>7%</div> </div> </div>
1	B	284	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>13%</div> <div>7%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4365 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 High-affinity zinc uptake system protein znuA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	2	0
			2035	1302	345	380	8			
1	B	265	Total	C	N	O	S	0	0	0
			2037	1301	347	381	8			

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Co	0	0
			1	1		
2	A	1	Total	Co	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	168	Total	O	0	0
			168	168		
3	B	123	Total	O	0	0
			123	123		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.07Å 78.02Å 85.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 45.53 – 2.15	Depositor EDS
% Data completeness (in resolution range)	95.0 (50.00-2.15) 95.1 (45.53-2.15)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.25 (at 2.16Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.235 , 0.296 0.236 , 0.244	Depositor DCC
$R_{free}$ test set	1632 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.6	Xtrriage
Anisotropy	0.090	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 41.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4365	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.1572e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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

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	0.52	0/2083	0.64	1/2823 (0.0%)
1	B	0.47	0/2080	0.59	0/2820
All	All	0.50	0/4163	0.62	1/5643 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	ARG	NE-CZ-NH2	-5.85	117.37	120.30

There are no chirality outliers.

There are no planarity outliers.

### 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	2035	0	2061	24	0
1	B	2037	0	2050	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	168	0	0	5	0
3	B	123	0	0	1	0
All	All	4365	0	4111	49	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 6.

All (49) 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:B:255:ALA:HB2	1:B:264:VAL:HG21	1.48	0.94
1:B:119:HIS:CD2	1:B:224:HIS:HE1	1.94	0.85
1:A:116:LYS:HA	1:A:117:SER:HB2	1.57	0.85
1:B:42:ILE:HD11	1:B:155:ALA:HB1	1.69	0.73
1:A:116:LYS:HA	1:A:117:SER:CB	2.18	0.73
1:A:179:ASP:O	1:A:183:GLN:HG3	1.94	0.68
1:B:119:HIS:CD2	1:B:224:HIS:CE1	2.80	0.68
1:B:42:ILE:CD1	1:B:155:ALA:HB1	2.25	0.67
1:A:55:ASP:HB3	1:A:283:THR:HG23	1.79	0.64
1:B:147:SER:HB2	1:B:212:TYR:HB3	1.78	0.63
1:B:183:GLN:HE22	1:B:290:THR:HG22	1.63	0.62
1:A:159:HIS:HD2	3:A:484:HOH:O	1.82	0.61
1:A:147:SER:HB2	1:A:212:TYR:HB3	1.83	0.61
1:B:244:GLN:OE1	1:B:244:GLN:HA	2.01	0.60
1:A:152:ARG:HH22	1:A:188:GLU:CD	2.06	0.59
1:B:183:GLN:NE2	1:B:290:THR:HG22	2.19	0.58
1:A:34:PRO:HA	1:A:37:PHE:CD2	2.41	0.56
1:A:116:LYS:CA	1:A:117:SER:CB	2.85	0.53
1:A:152:ARG:NH2	1:A:188:GLU:OE2	2.40	0.53
1:B:42:ILE:HA	1:B:176:ASN:HB3	1.89	0.53
1:B:198:LEU:HA	1:B:201:LYS:HD2	1.92	0.52
1:A:52:LEU:HD11	1:A:72:LEU:HD11	1.92	0.52
1:B:207:HIS:HB3	1:B:256:GLU:OE2	2.10	0.51
1:A:224:HIS:CE1	3:A:506:HOH:O	2.63	0.51
1:A:152:ARG:HD3	1:A:181:GLU:OE1	2.11	0.51
1:A:159:HIS:CD2	3:A:484:HOH:O	2.61	0.51
1:B:34:PRO:HA	1:B:37:PHE:CD2	2.47	0.50
1:B:116:LYS:HD2	1:B:118:ILE:HD13	1.95	0.49
1:B:255:ALA:CB	1:B:264:VAL:HG21	2.32	0.49
1:A:285:ILE:HD13	1:A:295:PHE:HA	1.95	0.48
1:A:256:GLU:HG3	1:A:278:LEU:O	2.13	0.48
1:B:141:ASN:ND2	1:B:143:HIS:H	2.12	0.48
1:B:144:LEU:HB3	1:B:150:ILE:HG21	1.96	0.47
1:B:139:ASP:HB2	3:B:475:HOH:O	2.15	0.47
1:A:141:ASN:ND2	3:A:550:HOH:O	2.48	0.46
1:A:285:ILE:CD1	1:A:295:PHE:HA	2.46	0.46
1:B:52:LEU:HD11	1:B:72:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:PHE:HD2	1:A:255:ALA:HA	1.81	0.45
1:A:258[B]:GLN:HG2	3:A:530:HOH:O	2.18	0.44
1:B:205:VAL:O	1:B:224:HIS:HA	2.18	0.43
1:A:183:GLN:OE1	1:A:290:THR:HG22	2.17	0.43
1:A:89:MET:O	1:A:93:VAL:HB	2.18	0.43
1:A:207:HIS:HB3	1:A:256:GLU:OE2	2.19	0.42
1:B:152:ARG:HD3	1:B:181:GLU:OE1	2.19	0.42
1:B:234:GLY:O	1:B:238:LEU:HB2	2.19	0.42
1:A:32:LEU:HD22	1:A:53:LEU:HD22	2.01	0.41
1:B:195:LEU:HD13	1:B:219:LEU:HD11	2.01	0.41
1:B:27:ALA:N	1:B:47:THR:HG1	2.18	0.41
1:B:304:ALA:HB1	1:B:308:LYS:HE2	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	261/284 (92%)	254 (97%)	6 (2%)	1 (0%)	36	31
1	B	261/284 (92%)	252 (97%)	7 (3%)	2 (1%)	21	13
All	All	522/568 (92%)	506 (97%)	13 (2%)	3 (1%)	27	19

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	SER
1	B	117	SER
1	B	118	ILE



### 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	220/236 (93%)	214 (97%)	6 (3%)	48	49
1	B	219/236 (93%)	212 (97%)	7 (3%)	42	41
All	All	439/472 (93%)	426 (97%)	13 (3%)	48	43

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	LEU
1	A	73	GLN
1	A	226	THR
1	A	256	GLU
1	A	258[A]	GLN
1	A	258[B]	GLN
1	B	72	LEU
1	B	117	SER
1	B	119	HIS
1	B	141	ASN
1	B	164	GLU
1	B	227	VAL
1	B	253	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	106	GLN
1	A	159	HIS
1	A	193	ASN
1	A	228	ASN
1	B	73	GLN
1	B	90	GLN
1	B	106	GLN
1	B	119	HIS

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Mol	Chain	Res	Type
1	B	141	ASN
1	B	183	GLN
1	B	224	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 ⓘ

Of 2 ligands modelled in this entry, 2 are 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 ⓘ

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	263/284 (92%)	0.20	6 (2%) 60 68	20, 33, 51, 58	2 (0%)
1	B	265/284 (93%)	0.45	10 (3%) 40 48	25, 44, 61, 73	1 (0%)
All	All	528/568 (92%)	0.33	16 (3%) 50 58	20, 37, 57, 73	3 (0%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	120	GLY	11.3
1	B	117	SER	7.0
1	B	118	ILE	6.6
1	A	118	ILE	5.6
1	B	119	HIS	4.1
1	A	117	SER	3.5
1	A	309	GLY	2.7
1	B	240	GLU	2.6
1	A	230	GLU	2.5
1	B	230	GLU	2.4
1	A	245	LEU	2.3
1	B	226	THR	2.3
1	A	259	PHE	2.3
1	B	178	LYS	2.1
1	B	166	MET	2.0
1	B	264	VAL	2.0

### 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 carbohydrates 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, 95<sup>th</sup> 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	CO	B	401	1/1	0.99	0.12	36,36,36,36	0
2	CO	A	402	1/1	1.00	0.11	30,30,30,30	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.