



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 04:13 PM GMT

PDB ID : 2P4Z  
Title : A Ferredoxin-like Metallo-beta-lactamaseSuperfamily Protein from Thermoanaerobacter tengcongensis  
Authors : Liang, D.-C.; Gu, S.-Y.  
Deposited on : 2007-03-14  
Resolution : 2.10 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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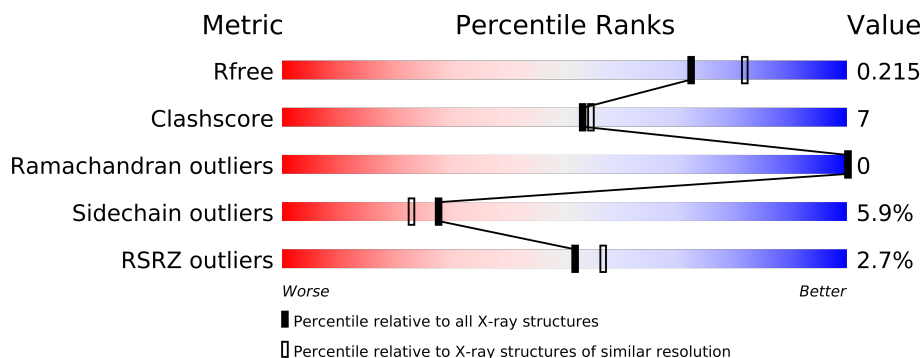
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.10 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))
$R_{free}$	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	284	
1	B	284	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	FE	A	1001	-	X
2	FE	A	1002	-	X
2	FE	B	1003	-	X
2	FE	B	1004	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4576 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Metal-dependent hydrolases of the beta-lactamase superfamily II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2182	1401	365	410	6			
1	B	276	Total	C	N	O	S	0	0	0
			2192	1407	368	411	6			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP Q8R8V2
A	2	ARG	-	EXPRESSION TAG	UNP Q8R8V2
A	3	GLY	-	EXPRESSION TAG	UNP Q8R8V2
A	4	SER	-	EXPRESSION TAG	UNP Q8R8V2
A	5	HIS	-	EXPRESSION TAG	UNP Q8R8V2
A	6	HIS	-	EXPRESSION TAG	UNP Q8R8V2
A	7	HIS	-	EXPRESSION TAG	UNP Q8R8V2
A	8	HIS	-	EXPRESSION TAG	UNP Q8R8V2
A	9	HIS	-	EXPRESSION TAG	UNP Q8R8V2
A	10	HIS	-	EXPRESSION TAG	UNP Q8R8V2
A	11	GLY	-	EXPRESSION TAG	UNP Q8R8V2
A	12	SER	-	EXPRESSION TAG	UNP Q8R8V2
A	13	VAL	-	EXPRESSION TAG	UNP Q8R8V2
B	1	MET	-	INITIATING METHIONINE	UNP Q8R8V2
B	2	ARG	-	EXPRESSION TAG	UNP Q8R8V2
B	3	GLY	-	EXPRESSION TAG	UNP Q8R8V2
B	4	SER	-	EXPRESSION TAG	UNP Q8R8V2
B	5	HIS	-	EXPRESSION TAG	UNP Q8R8V2
B	6	HIS	-	EXPRESSION TAG	UNP Q8R8V2
B	7	HIS	-	EXPRESSION TAG	UNP Q8R8V2
B	8	HIS	-	EXPRESSION TAG	UNP Q8R8V2
B	9	HIS	-	EXPRESSION TAG	UNP Q8R8V2
B	10	HIS	-	EXPRESSION TAG	UNP Q8R8V2
B	11	GLY	-	EXPRESSION TAG	UNP Q8R8V2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	12	SER	-	EXPRESSION TAG	UNP Q8R8V2
B	13	VAL	-	EXPRESSION TAG	UNP Q8R8V2

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Fe 2 2	0	0
2	A	2	Total Fe 2 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	98	Total O 98 98	0	0
3	B	100	Total O 100 100	0	0



## 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, $\alpha$ , $\beta$ , $\gamma$	77.20Å 138.31Å 52.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.10 14.88 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.2 (15.00-2.10) 96.2 (14.88-2.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.82 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.200 , 0.219 0.200 , 0.215	Depositor DCC
$R_{free}$ test set	1650 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.1	Xtriage
Anisotropy	0.846	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 34.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 32503 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4576	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.21 % 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 1.1827e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.53	0/2219	0.64	0/2980
1	B	0.51	0/2230	0.62	0/2995
All	All	0.52	0/4449	0.63	0/5975

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2182	0	2196	30	0
1	B	2192	0	2203	34	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	98	0	0	0	0
3	B	100	0	0	2	0
All	All	4576	0	4399	61	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 61 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:198:CYS:SG	1:A:227:HIS:HD2	1.88	0.96
1:A:156:TYR:H	1:A:205:ASN:HD21	1.13	0.96
1:B:21:ASN:HD21	1:B:32:HIS:HD2	1.13	0.96
1:B:156:TYR:H	1:B:205:ASN:HD21	1.14	0.89
1:A:100:HIS:HD2	1:A:102:GLU:H	1.26	0.84

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	273/284 (96%)	263 (96%)	10 (4%)	0	100	100
1	B	274/284 (96%)	264 (96%)	10 (4%)	0	100	100
All	All	547/568 (96%)	527 (96%)	20 (4%)	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	238/249 (96%)	222 (93%)	16 (7%)	23	18
1	B	239/249 (96%)	227 (95%)	12 (5%)	34	30
All	All	477/498 (96%)	449 (94%)	28 (6%)	28	23

5 of 28 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	252	LEU
1	A	283	VAL
1	B	235	LYS
1	A	269	LEU
1	A	276	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	227	HIS
1	B	16	GLN
1	B	132	ASN
1	A	193	ASN
1	A	205	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 4 ligands modelled in this entry, 4 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.

## 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

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	275/284 (96%)	0.02	7 (2%) 54 59	14, 24, 37, 53	0
1	B	276/284 (97%)	-0.04	5 (1%) 65 69	15, 24, 37, 51	0
All	All	551/568 (97%)	-0.01	12 (2%) 52 64	14, 24, 37, 53	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	112	LYS	5.5
1	B	9	HIS	4.7
1	B	112	LYS	4.7
1	A	111	ARG	4.2
1	A	113	GLY	3.8

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

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

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FE	A	1001	1/1	0.23	12.32	18,18,18,18	1
2	FE	B	1004	1/1	0.34	11.49	18,18,18,18	1
2	FE	A	1002	1/1	0.26	10.38	15,15,15,15	1
2	FE	B	1003	1/1	0.18	3.33	17,17,17,17	1

## 6.5 Other polymers ⓘ

There are no such residues in this entry.