



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 01:00 am BST

PDB ID : 4ZA6  
Title : Structure of the R. erythropolis transcriptional repressor QsdR from TetR family  
Authors : El Sahili, A.; Morera, S.  
Deposited on : 2015-04-13  
Resolution : 1.97 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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

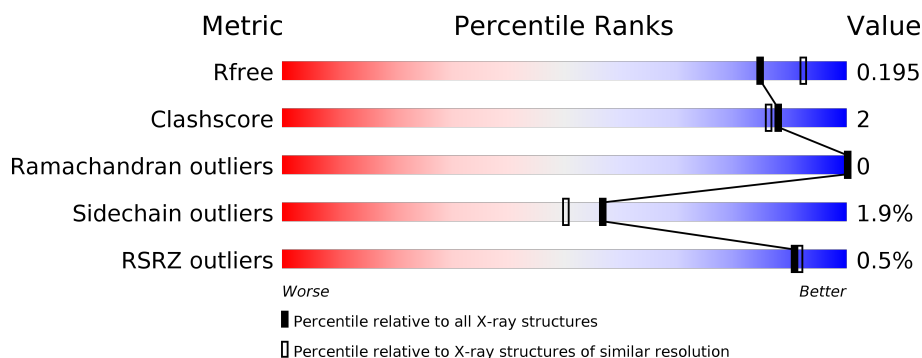
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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))
$R_{free}$	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 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	192	 92% 5% ••
1	B	192	 91% 7% •

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MPD	A	204	-	-	-	X
2	MPD	B	203	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3277 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 TetR family transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1451	909	257	277	8			
1	B	188	Total	C	N	O	S	0	0	0
			1451	909	257	277	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	HIS	-	expression tag	UNP A0A0C2W9F0
A	188	HIS	-	expression tag	UNP A0A0C2W9F0
A	189	HIS	-	expression tag	UNP A0A0C2W9F0
A	190	HIS	-	expression tag	UNP A0A0C2W9F0
A	191	HIS	-	expression tag	UNP A0A0C2W9F0
A	192	HIS	-	expression tag	UNP A0A0C2W9F0
B	187	HIS	-	expression tag	UNP A0A0C2W9F0
B	188	HIS	-	expression tag	UNP A0A0C2W9F0
B	189	HIS	-	expression tag	UNP A0A0C2W9F0
B	190	HIS	-	expression tag	UNP A0A0C2W9F0
B	191	HIS	-	expression tag	UNP A0A0C2W9F0
B	192	HIS	-	expression tag	UNP A0A0C2W9F0

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	172	Total	O	0	0
			172	172		
5	B	145	Total	O	0	0
			145	145		

### 3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

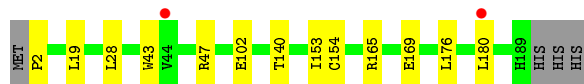
- Molecule 1: TetR family transcriptional regulator

Chain A:  92% 5% ..



- Molecule 1: TetR family transcriptional regulator

Chain B:  91% 7% .



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.63Å 91.63Å 145.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.81 – 1.97 45.81 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.81-1.97) 99.9 (45.81-1.97)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 1.97Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, $R_{free}$	0.206 , 0.228 0.171 , 0.195	Depositor DCC
$R_{free}$ test set	2108 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.0	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.269 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3277	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	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 52.46 % 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 4.8473e-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: CA, MPD, ACT

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	0.47	0/1470	0.60	0/1989
1	B	0.48	0/1470	0.61	0/1989
All	All	0.47	0/2940	0.61	0/3978

There are no bond length outliers.

There are no bond angle outliers.

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	1451	0	1490	7	0
1	B	1451	0	1490	5	0
2	A	32	0	56	0	0
2	B	16	0	28	0	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	172	0	0	1	0
5	B	145	0	0	0	0
All	All	3277	0	3070	12	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 2.

All (12) 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:153:ILE:HD13	1:B:176:LEU:HB3	1.74	0.68
1:A:73:GLN:O	1:A:76:GLU:HG2	1.98	0.62
1:A:153:ILE:HD13	1:A:180:LEU:HD13	1.89	0.54
1:B:165:ARG:HD3	1:B:169:GLU:OE1	2.09	0.52
1:A:76:GLU:HG3	5:A:376:HOH:O	2.09	0.51
1:A:165:ARG:HD2	1:A:169:GLU:OE1	2.11	0.50
1:A:153:ILE:HD12	1:A:176:LEU:HB3	1.95	0.48
1:B:153:ILE:HD12	1:B:154:CYS:SG	2.57	0.45
1:A:25:ASP:HB3	1:A:28:LEU:HB2	2.01	0.43
1:B:2:PRO:HB3	1:B:43:TRP:CD1	2.54	0.41
1:B:47:ARG:NH1	1:B:102:GLU:OE1	2.48	0.41
1:A:2:PRO:HB3	1:A:43:TRP:CD1	2.55	0.41

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	186/192 (97%)	186 (100%)	0	0	100	100
1	B	186/192 (97%)	186 (100%)	0	0	100	100
All	All	372/384 (97%)	372 (100%)	0	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	156/160 (98%)	154 (99%)	2 (1%)	69	64
1	B	156/160 (98%)	152 (97%)	4 (3%)	46	37
All	All	312/320 (98%)	306 (98%)	6 (2%)	57	50

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	180	LEU
1	B	19	LEU
1	B	28	LEU
1	B	140	THR
1	B	180	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	129	GLN
1	A	187	HIS
1	B	69	GLN
1	B	129	GLN
1	B	187	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 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	MPD	A	204	-	7,7,7	0.32	0	9,10,10	0.45	0
2	MPD	A	201	-	7,7,7	0.41	0	9,10,10	0.64	0
3	ACT	A	205	-	1,3,3	1.14	0	0,3,3	0.00	-
2	MPD	B	203	-	7,7,7	0.33	0	9,10,10	0.49	0
2	MPD	A	202	-	7,7,7	0.36	0	9,10,10	0.54	0
3	ACT	B	202	-	1,3,3	3.38	1 (100%)	0,3,3	0.00	-
2	MPD	B	201	-	7,7,7	0.34	0	9,10,10	0.83	0
2	MPD	A	203	-	7,7,7	0.28	0	9,10,10	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MPD	A	204	-	-	3/5/5/5	-
2	MPD	A	201	-	-	2/5/5/5	-
2	MPD	B	203	-	-	1/5/5/5	-
2	MPD	A	202	-	-	0/5/5/5	-
2	MPD	B	201	-	-	3/5/5/5	-
2	MPD	A	203	-	-	0/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	ACT	CH3-C	3.38	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	201	MPD	O2-C2-C3-C4
2	B	201	MPD	CM-C2-C3-C4
2	A	204	MPD	C2-C3-C4-C5
2	B	201	MPD	C1-C2-C3-C4
2	A	204	MPD	O2-C2-C3-C4
2	A	201	MPD	O2-C2-C3-C4
2	B	203	MPD	C2-C3-C4-C5
2	A	204	MPD	C2-C3-C4-O4
2	A	201	MPD	C2-C3-C4-O4

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	188/192 (97%)	0.07	0	100   100	26, 34, 55, 100	0
1	B	188/192 (97%)	0.08	2 (1%)	80   82	25, 36, 56, 100	0
All	All	376/384 (97%)	0.08	2 (0%)	91   91	25, 35, 56, 100	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	180	LEU	2.8
1	B	44	VAL	2.2

### 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(Å <sup>2</sup> )	Q<0.9
3	ACT	B	202	4/4	0.63	0.20	69,69,69,70	0
2	MPD	B	203	8/8	0.69	0.49	115,116,118,119	0
2	MPD	A	203	8/8	0.74	0.39	85,86,88,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MPD	A	202	8/8	0.78	0.16	86,87,89,90	0
2	MPD	B	201	8/8	0.79	0.21	40,42,43,48	0
2	MPD	A	204	8/8	0.79	0.87	80,82,84,84	0
4	CA	B	204	1/1	0.82	0.85	182,182,182,182	0
3	ACT	A	205	4/4	0.91	0.31	88,89,89,89	0
2	MPD	A	201	8/8	0.92	0.15	38,40,42,43	0
4	CA	A	206	1/1	0.99	0.05	46,46,46,46	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.