



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:34 AM GMT

PDB ID : 2HR3  
Title : Crystal structure of putative transcriptional regulator protein from *Pseudomonas aeruginosa* PA01 at 2.4 Å resolution  
Authors : Kirillova, O.; Chruszcz, M.; Evdokimova, E.; Kudritska, M.; Cymborowski, M.; Savchenko, A.; Edwards, A.; Joachimiak, A.; Minor, W.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2006-07-19  
Resolution : 2.40 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

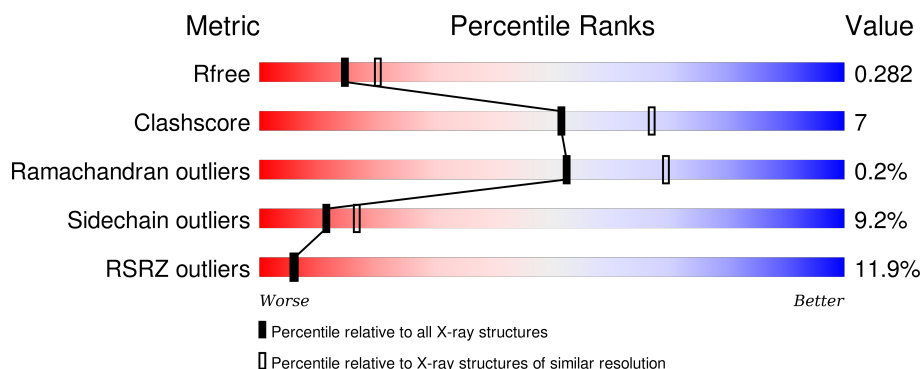
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	147	<div> <div>10%</div> <div>76%</div> <div>18%</div> <div>• 5%</div> </div>
1	B	147	<div> <div>12%</div> <div>72%</div> <div>18%</div> <div>•• 8%</div> </div>
1	C	147	<div> <div>13%</div> <div>69%</div> <div>23%</div> <div>• 6%</div> </div>
1	D	147	<div> <div>9%</div> <div>74%</div> <div>19%</div> <div>• 5%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4150 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 Probable transcriptional regulator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	139	Total	C	N	O	S	Se	0	0	0
			1032	637	196	196	1	2			
1	B	135	Total	C	N	O	S	Se	0	1	0
			1001	620	195	183	1	2			
1	C	138	Total	C	N	O	S	Se	0	0	0
			1012	625	198	186	1	2			
1	D	140	Total	C	N	O	S	Se	0	0	0
			1047	645	204	195	1	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
A	62	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
A	119	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
B	62	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
B	119	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
C	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
C	62	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
C	119	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
D	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
D	62	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1
D	119	MSE	MET	MODIFIED RESIDUE	UNP Q9HZE1

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	13	Total	O	0	0
			13	13		
2	B	16	Total	O	0	0
			16	16		

*Continued on next page...*

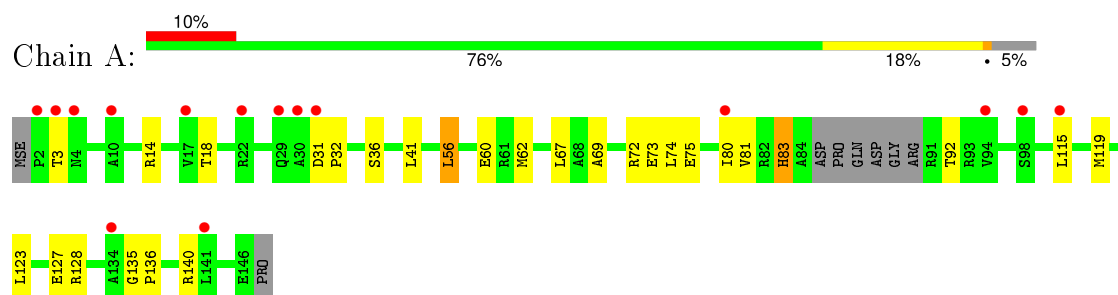
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	19	Total	O	0	0
			19	19		
2	D	10	Total	O	0	0
			10	10		

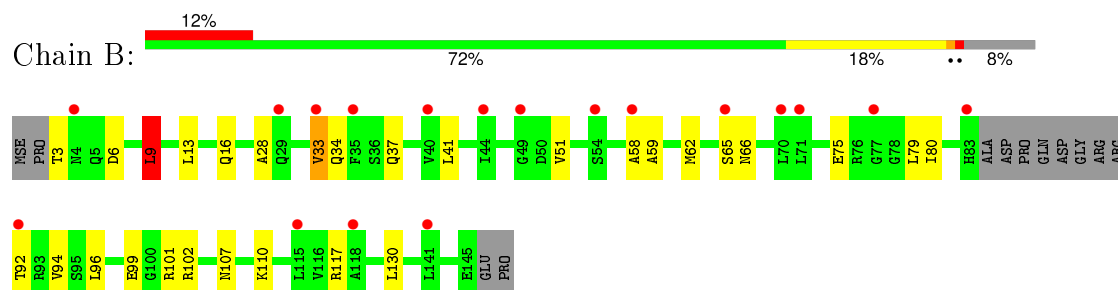
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

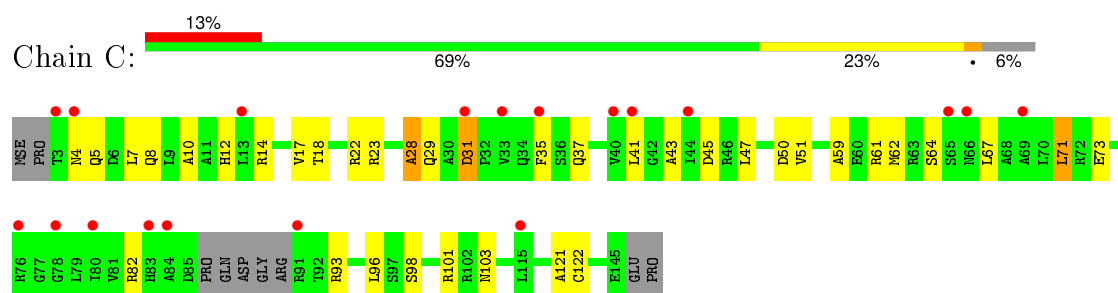
#### • Molecule 1: Probable transcriptional regulator



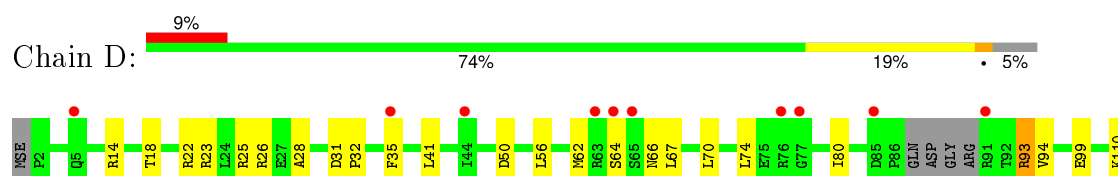
#### • Molecule 1: Probable transcriptional regulator



#### • Molecule 1: Probable transcriptional regulator



#### • Molecule 1: Probable transcriptional regulator





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.25Å 72.28Å 70.04Å 90.00° 101.43° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 19.70 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-2.40) 99.6 (19.70-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.04 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.208 , 0.280 0.211 , 0.282	Depositor DCC
$R_{free}$ test set	1179 reflections (5.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	55.0	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 71.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 22942 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4150	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	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 24.70 % 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 3.6459e-03. 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	1.05	1/1040 (0.1%)	1.07	2/1403 (0.1%)
1	B	0.98	0/1010	0.98	2/1362 (0.1%)
1	C	0.91	2/1019 (0.2%)	0.96	3/1376 (0.2%)
1	D	0.98	0/1056	0.94	1/1425 (0.1%)
All	All	0.98	3/4125 (0.1%)	0.99	8/5566 (0.1%)

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	A	0	1
1	C	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	122	CYS	CB-SG	-6.86	1.70	1.82
1	A	75	GLU	CG-CD	5.79	1.60	1.51
1	C	43	ALA	CA-CB	5.49	1.64	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128	ARG	NE-CZ-NH2	-9.88	115.36	120.30
1	A	128	ARG	NE-CZ-NH1	8.18	124.39	120.30
1	C	22	ARG	NE-CZ-NH2	-6.91	116.85	120.30
1	C	23	ARG	NE-CZ-NH2	-6.21	117.20	120.30
1	D	23	ARG	NE-CZ-NH2	-5.89	117.36	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	HIS	Peptide
1	C	28	ALA	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	1032	0	1012	14	0
1	B	1001	0	1003	16	0
1	C	1012	0	995	16	0
1	D	1047	0	1043	18	0
2	A	13	0	0	0	0
2	B	16	0	0	0	0
2	C	19	0	0	0	0
2	D	10	0	0	0	0
All	All	4150	0	4053	55	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 7.

The worst 5 of 55 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:96:LEU:HD12	1:B:101[B]:ARG:HH11	1.46	0.81
1:A:119:MSE:HE1	1:B:9:LEU:HD13	1.75	0.68
1:A:119:MSE:CE	1:B:9:LEU:HD13	2.27	0.65
1:B:33:VAL:O	1:B:37:GLN:HG3	1.98	0.63
1:B:99:GLU:HG3	1:B:102:ARG:NH1	2.13	0.62

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	135/147 (92%)	129 (96%)	6 (4%)	0	100	100
1	B	132/147 (90%)	122 (92%)	10 (8%)	0	100	100
1	C	134/147 (91%)	129 (96%)	4 (3%)	1 (1%)	26	38
1	D	136/147 (92%)	130 (96%)	6 (4%)	0	100	100
All	All	537/588 (91%)	510 (95%)	26 (5%)	1 (0%)	52	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	64	SER

### 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	99/116 (85%)	92 (93%)	7 (7%)	18	28
1	B	96/116 (83%)	87 (91%)	9 (9%)	11	16
1	C	95/116 (82%)	85 (90%)	10 (10%)	8	12
1	D	103/116 (89%)	93 (90%)	10 (10%)	10	15
All	All	393/464 (85%)	357 (91%)	36 (9%)	11	16

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	7	LEU
1	C	45	ASP
1	D	116	VAL
1	C	31	ASP
1	C	62	MSE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	C	12	HIS
1	C	143	GLN

### 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 carbohydrates 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](#)

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	137/147 (93%)	0.69	15 (10%) 7 7	45, 60, 73, 80	0
1	B	133/147 (90%)	0.91	18 (13%) 4 4	38, 60, 79, 88	0
1	C	136/147 (92%)	0.87	19 (13%) 4 4	48, 64, 84, 87	0
1	D	138/147 (93%)	0.71	13 (9%) 11 10	51, 63, 85, 88	0
All	All	544/588 (92%)	0.79	65 (11%) 6 6	38, 62, 82, 88	0

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	92	THR	6.6
1	C	65	SER	5.8
1	D	115	LEU	5.0
1	A	98	SER	4.9
1	C	4	ASN	4.9

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.