

wwPDB X-ray Structure Validation Summary Report (i)

May 14, 2020 - 08:23 am BST

PDB ID	:	4BWT
Title	:	Three-dimensional structure of Paracoccus pantotrophus pseudoazurin at pH
		6.5
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Deposited on		
$\operatorname{Resolution}$:	1.76 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

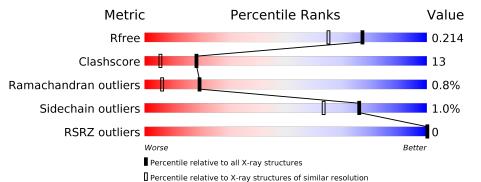
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\operatorname{CCP4}$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R _{free}	130704	$2340 \ (1.76-1.76)$
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437(1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 >=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 <=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	А	123	79%	19%	•
1	В	123	85%	12%	•



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2383 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.

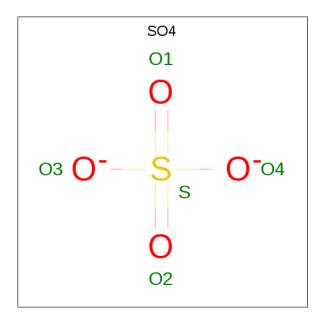
• Molecule 1 is a protein called PSEUDOAZURIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1 4	123	Total	С	Ν	Ο	S	0	6	0
	123	970	614	162	185	9	0	0	0	
1	р	123	Total	С	Ν	Ο	S	0	4	0
	I B	123	953	604	159	181	9	U		U

• Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Cu 1 1	0	0
2	А	1	Total Cu 1 1	0	0

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	239	Total O 239 239	0	0
4	В	199	Total O 199 199	0	0



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.

- Chain A:
 79%
 19%

 PRESSBERS
 PRESSBERS
- Molecule 1: PSEUDOAZURIN



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	107.28Å 57.87Å 67.10Å	Depositor
a, b, c, α , β , γ	90.00° 125.99° 90.00°	Depositor
Resolution (Å)	27.85 - 1.76	Depositor
Resolution (A)	27.85 - 1.76	EDS
% Data completeness	98.3 (27.85-1.76)	Depositor
(in resolution range)	98.4(27.85 - 1.76)	EDS
R _{merge}	0.06	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.41 (at 1.76 Å)	Xtriage
Refinement program	$\operatorname{REFMAC} 5.7.0032$	Depositor
R, R_{free}	0.166 , 0.206	Depositor
Π, Π_{free}	0.177 , 0.214	DCC
R_{free} test set	1653 reflections (5.08%)	wwPDB-VP
Wilson B-factor $(Å^2)$	11.9	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37 , 47.4	EDS
L-test for twinning ²	$< L >=0.46, < L^2>=0.29$	Xtriage
Estimated twinning fraction	0.073 for -h-2*l,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2383	wwPDB-VP
Average B, all atoms $(Å^2)$	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.81% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, $\rm CU$

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	Bo	nd lengths	Bond angles		
	Cham	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.08	3/1003~(0.3%)	1.13	5/1349~(0.4%)	
1	В	1.11	2/983~(0.2%)	1.11	5/1323~(0.4%)	
All	All	1.10	5/1986~(0.3%)	1.12	10/2672~(0.4%)	

All (5) bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms		Observed(Å)	Ideal(Å)
1	А	47	GLU	CD-OE1	7.08	1.33	1.25
1	А	4	GLU	CD-OE1	-6.59	1.18	1.25
1	В	114	ARG	CG-CD	-5.29	1.38	1.51
1	А	114	ARG	CG-CD	-5.10	1.39	1.51
1	В	4	GLU	CD-OE1	-5.03	1.20	1.25

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	86[A]	MET	CG-SD-CE	11.72	118.95	100.20
1	А	86[B]	MET	CG-SD-CE	11.72	118.95	100.20
1	В	24	ARG	NE-CZ-NH1	-8.50	116.05	120.30
1	В	112	ARG	NE-CZ-NH2	-8.09	116.25	120.30
1	В	112	ARG	NE-CZ-NH1	6.47	123.54	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	970	0	988	30	0
1	В	953	0	968	26	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	10	0	0	1	0
3	В	10	0	0	0	0
4	А	239	0	0	6	2
4	В	199	0	0	14	0
All	All	2383	0	1956	52	2

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.

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 13.

The worst 5 of 52 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:10:LYS:HB3	4:B:2026:HOH:O	1.33	1.28
1:A:16:MET:C	1:A:86[A]:MET:HE2	1.71	1.09
1:A:16:MET:HA	1:A:86[A]:MET:CE	1.91	1.01
1:A:17:VAL:N	1:A:86[A]:MET:HE2	1.81	0.96
1:B:103[A]:LYS:HE3	4:B:2177:HOH:O	1.69	0.92

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	Clash overlap (Å)
4:A:2177:HOH:O	4:A:2196:HOH:O[4_546]	1.53	0.67
4:A:2175:HOH:O	4:A:2196:HOH:O[4_546]	1.75	0.45

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percen	tiles
1	А	127/123~(103%)	121 (95%)	5~(4%)	1 (1%)	19	6
1	В	125/123~(102%)	120 (96%)	4 (3%)	1 (1%)	19	6
All	All	252/246~(102%)	241 (96%)	9 (4%)	2 (1%)	19	6

analysed, and the total number of residues.

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	В	39	SER	
1	А	39	SER	

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	Analysed Rotameric Outliers		Percentiles		
1	А	107/101~(106%)	105~(98%)	2(2%)	57 37		
1	В	104/101~(103%)	102~(98%)	2(2%)	57 37		
All	All	211/202~(104%)	207~(98%)	4 (2%)	76 37		

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	94[A]	ASP
1	А	94[B]	ASP
1	В	46[A]	LYS
1	В	46[B]	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type	
1	А	3	HIS	
1	А	6	HIS	
1	А	32	ASN	

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Mol	Chain	\mathbf{Res}	Type
1	В	3	HIS
1	В	32	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	Tune	Chain	Res	Link	Bond lengths			E	Bond ang	gles
	Type	Cham	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
3	SO4	В	1126	-	$4,\!4,\!4$	0.58	0	6,6,6	1.35	1(16%)
3	SO4	А	1125	-	4,4,4	0.59	0	$6,\!6,\!6$	0.60	0
3	SO4	А	1126	-	4,4,4	0.81	0	$6,\!6,\!6$	0.72	0
3	SO4	В	1125	-	4,4,4	0.63	0	6,6,6	0.88	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	1126	SO4	O4-S-O2	-2.51	96.22	109.31



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	1126	SO4	1	0

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^{th} 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 $>$	$\# RSRZ {>}2$		Z>2	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	А	123/123~(100%)	-0.05	0	100	100	5, 10, 21, 26	0
1	В	123/123~(100%)	-0.13	0	100	100	6, 10, 20, 24	0
All	All	246/246~(100%)	-0.09	0	100	100	5, 10, 21, 26	0

There are no RSRZ outliers to report.

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^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	SO4	А	1126	5/5	0.76	0.24	$35,\!45,\!52,\!57$	0
3	SO4	В	1125	5/5	0.84	0.25	$33,\!34,\!46,\!47$	0
3	SO4	А	1125	5/5	0.96	0.12	$33,\!34,\!35,\!41$	0
3	SO4	В	1126	5/5	0.96	0.16	$30,\!37,\!38,\!38$	0
2	CU	В	1124	1/1	1.00	0.02	9,9,9,9	0
2	CU	А	1124	1/1	1.00	0.02	8,8,8,8	0



6.5 Other polymers (i)

There are no such residues in this entry.

