



# wwPDB X-ray Structure Validation Summary Report i

Sep 22, 2014 – 05:00 PM EDT

PDB ID : 4O8V  
Title : O-Acetyltransferase Domain of Pseudomonas putida AlgJ  
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Deposited on : 2013-12-30  
Resolution : 1.81 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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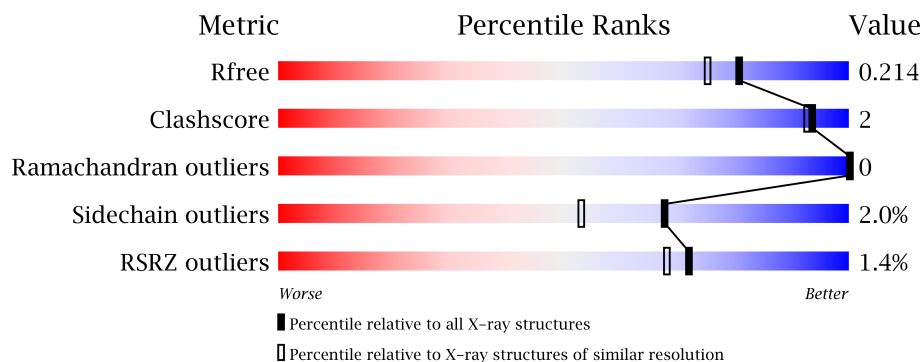
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.16 November 2013
Xtriage (Phenix)	:	dev-1439
EDS	:	stable23489
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)	:	stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 1.81 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	4101 (1.84-1.80)
Clashscore	79885	5140 (1.84-1.80)
Ramachandran outliers	78287	5077 (1.84-1.80)
Sidechain outliers	78261	5077 (1.84-1.80)
RSRZ outliers	66119	4103 (1.84-1.80)

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	308	
1	B	308	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4747 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 Alginate biosynthesis protein AlgJ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	Se	0	9	0
			2242	1419	399	418	6			
1	B	278	Total	C	N	O	Se	0	8	0
			2234	1413	399	416	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	GLY	-	EXPRESSION TAG	UNP Q88ND3
A	72	SER	-	EXPRESSION TAG	UNP Q88ND3
A	73	HIS	-	EXPRESSION TAG	UNP Q88ND3
A	74	MSE	-	EXPRESSION TAG	UNP Q88ND3
A	371	LEU	-	EXPRESSION TAG	UNP Q88ND3
A	372	GLU	-	EXPRESSION TAG	UNP Q88ND3
A	373	HIS	-	EXPRESSION TAG	UNP Q88ND3
A	374	HIS	-	EXPRESSION TAG	UNP Q88ND3
A	375	HIS	-	EXPRESSION TAG	UNP Q88ND3
A	376	HIS	-	EXPRESSION TAG	UNP Q88ND3
A	377	HIS	-	EXPRESSION TAG	UNP Q88ND3
A	378	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	71	GLY	-	EXPRESSION TAG	UNP Q88ND3
B	72	SER	-	EXPRESSION TAG	UNP Q88ND3
B	73	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	74	MSE	-	EXPRESSION TAG	UNP Q88ND3
B	371	LEU	-	EXPRESSION TAG	UNP Q88ND3
B	372	GLU	-	EXPRESSION TAG	UNP Q88ND3
B	373	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	374	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	375	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	376	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	377	HIS	-	EXPRESSION TAG	UNP Q88ND3
B	378	HIS	-	EXPRESSION TAG	UNP Q88ND3

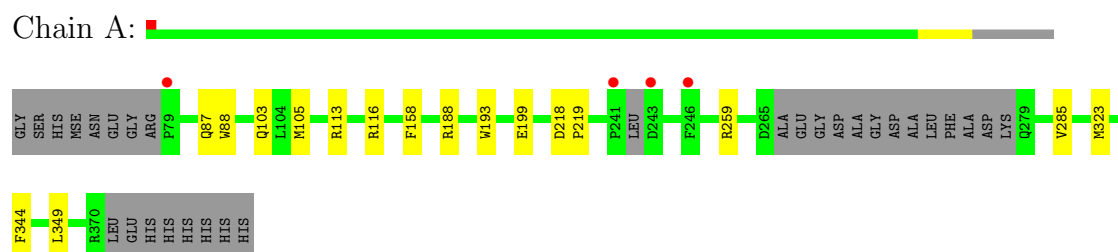
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	125	Total 125	O 125	0	0
2	B	146	Total 146	O 146	0	0

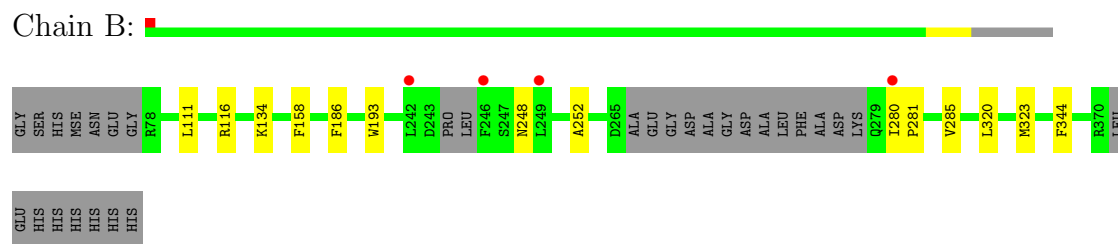
### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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: Alginate biosynthesis protein AlgJ



- Molecule 1: Alginate biosynthesis protein AlgJ



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	192.49Å 34.00Å 82.92Å 90.00° 91.93° 90.00°	Depositor
Resolution (Å)	48.10 – 1.81 48.10 – 1.81	Depositor EDS
% Data completeness (in resolution range)	95.5 (48.10-1.81) 95.1 (48.10-1.81)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.61 (at 1.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.176 , 0.215 0.175 , 0.214	Depositor DCC
$R_{free}$ test set	1959 reflections (4.17%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.3	Xtriage
Anisotropy	0.587	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 46.6	EDS
Estimated twinning fraction	0.015 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 47892 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4747	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.91% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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	0.43	0/2291	0.52	0/3109
1	B	0.46	0/2282	0.54	0/3097
All	All	0.45	0/4573	0.53	0/6206

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	2242	0	2159	10	0
1	B	2234	0	2144	7	0
2	A	125	0	0	2	0
2	B	146	0	0	0	0
All	All	4747	0	4303	14	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 2.

The worst 5 of 14 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:259[A]:ARG:NH2	2:A:513:HOH:O	2.26	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:199:GLU:OE2	1:A:259[A]:ARG:NH2	2.29	0.64
1:B:111:LEU:HD13	1:B:320:LEU:HD21	1.84	0.59
1:A:113:ARG:HD2	2:A:445:HOH:O	2.10	0.50
1:A:87[A]:GLN:HB2	1:B:252:ALA:HB2	1.97	0.46

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	281/308 (91%)	277 (99%)	4 (1%)	0	100	100
1	B	280/308 (91%)	275 (98%)	5 (2%)	0	100	100
All	All	561/616 (91%)	552 (98%)	9 (2%)	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	231/244 (95%)	226 (98%)	5 (2%)	64	48
1	B	228/244 (93%)	224 (98%)	4 (2%)	71	58
All	All	459/488 (94%)	450 (98%)	9 (2%)	68	53

5 of 9 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	344	PHE
1	B	344	PHE
1	B	158	PHE
1	A	158	PHE
1	B	116	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

There are no ligands in this entry.

## 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	278/308 (90%)	-0.23	4 (1%) 72 68	23, 34, 58, 83	0
1	B	278/308 (90%)	-0.22	4 (1%) 72 68	23, 33, 57, 100	0
All	All	556/616 (90%)	-0.22	8 (1%) 72 68	23, 34, 58, 100	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	246	PHE	2.8
1	A	79	PRO	2.8
1	A	246	PHE	2.7
1	B	242	LEU	2.5
1	A	243	ASP	2.4

### 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 ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.