



# wwPDB X-ray Structure Validation Summary Report

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PDB ID : 7DDY / pdb\_00007ddy  
Title : Crystal structure of an acetyl xylan esterase AlAXEase  
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Deposited on : 2020-10-30  
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

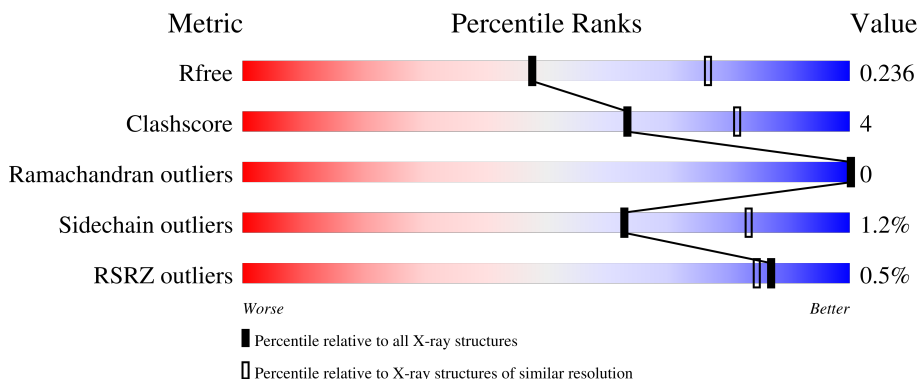
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 of 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	230	 79% 7% • 13%
1	B	230	 69% 18% 13%
1	C	230	 80% 6% • 13%
1	D	230	 80% 5% • 14%

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 6832 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 G-D-S-L family lipolytic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	D	198	Total 1574	C 992	N 274	O 302	S 6	0	0	0
1	A	199	Total 1581	C 997	N 275	O 303	S 6	0	0	0
1	B	200	Total 1590	C 1003	N 277	O 304	S 6	0	0	0
1	C	199	Total 1581	C 997	N 275	O 303	S 6	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	223	LEU	-	expression tag	UNP A0A2Z4G9P0
D	224	GLU	-	expression tag	UNP A0A2Z4G9P0
D	225	HIS	-	expression tag	UNP A0A2Z4G9P0
D	226	HIS	-	expression tag	UNP A0A2Z4G9P0
D	227	HIS	-	expression tag	UNP A0A2Z4G9P0
D	228	HIS	-	expression tag	UNP A0A2Z4G9P0
D	229	HIS	-	expression tag	UNP A0A2Z4G9P0
D	230	HIS	-	expression tag	UNP A0A2Z4G9P0
A	223	LEU	-	expression tag	UNP A0A2Z4G9P0
A	224	GLU	-	expression tag	UNP A0A2Z4G9P0
A	225	HIS	-	expression tag	UNP A0A2Z4G9P0
A	226	HIS	-	expression tag	UNP A0A2Z4G9P0
A	227	HIS	-	expression tag	UNP A0A2Z4G9P0
A	228	HIS	-	expression tag	UNP A0A2Z4G9P0
A	229	HIS	-	expression tag	UNP A0A2Z4G9P0
A	230	HIS	-	expression tag	UNP A0A2Z4G9P0
B	223	LEU	-	expression tag	UNP A0A2Z4G9P0
B	224	GLU	-	expression tag	UNP A0A2Z4G9P0
B	225	HIS	-	expression tag	UNP A0A2Z4G9P0
B	226	HIS	-	expression tag	UNP A0A2Z4G9P0
B	227	HIS	-	expression tag	UNP A0A2Z4G9P0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	228	HIS	-	expression tag	UNP A0A2Z4G9P0
B	229	HIS	-	expression tag	UNP A0A2Z4G9P0
B	230	HIS	-	expression tag	UNP A0A2Z4G9P0
C	223	LEU	-	expression tag	UNP A0A2Z4G9P0
C	224	GLU	-	expression tag	UNP A0A2Z4G9P0
C	225	HIS	-	expression tag	UNP A0A2Z4G9P0
C	226	HIS	-	expression tag	UNP A0A2Z4G9P0
C	227	HIS	-	expression tag	UNP A0A2Z4G9P0
C	228	HIS	-	expression tag	UNP A0A2Z4G9P0
C	229	HIS	-	expression tag	UNP A0A2Z4G9P0
C	230	HIS	-	expression tag	UNP A0A2Z4G9P0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	148	Total O 148 148	0	0
2	A	145	Total O 145 145	0	0
2	B	113	Total O 113 113	0	0
2	C	100	Total O 100 100	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.87Å 80.61Å 82.06Å 90.00° 103.13° 90.00°	Depositor
Resolution (Å)	49.33 – 2.50 49.33 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.1 (49.33-2.50) 98.1 (49.33-2.50)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.19 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, $R_{free}$	0.175 , 0.234 0.182 , 0.236	Depositor DCC
$R_{free}$ test set	1656 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtrriage
Anisotropy	0.769	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6832	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 [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	0.54	4/1607 (0.2%)	0.60	0/2167
1	B	0.73	6/1616 (0.4%)	0.66	2/2179 (0.1%)
1	C	0.53	2/1607 (0.1%)	0.56	0/2167
1	D	0.59	4/1599 (0.3%)	0.65	5/2156 (0.2%)
All	All	0.60	16/6429 (0.2%)	0.62	7/8669 (0.1%)

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	31	ASP	C-O	-10.98	1.12	1.23
1	B	31	ASP	C-O	-6.94	1.15	1.24
1	B	87	ASN	C-O	-6.68	1.20	1.23
1	A	117	LYS	C-O	-6.54	1.16	1.24
1	D	34	THR	C-O	-6.29	1.16	1.24

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	31	ASP	N-CA-C	11.09	127.08	109.79
1	B	56	MET	N-CA-C	-6.65	102.53	113.50
1	D	30	GLY	CA-C-N	5.55	131.02	121.86
1	D	30	GLY	C-N-CA	5.55	131.02	121.86
1	D	32	SER	N-CA-C	-5.29	106.09	112.54

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

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	1581	0	1570	7	0
1	B	1590	0	1582	24	0
1	C	1581	0	1570	12	0
1	D	1574	0	1562	7	0
2	A	145	0	0	0	0
2	B	113	0	0	1	0
2	C	100	0	0	1	0
2	D	148	0	0	1	0
All	All	6832	0	6284	50	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 4.

The worst 5 of 50 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:22:LYS:N	1:B:23:PRO:HD2	2.01	0.76
1:B:217:TRP:CE2	1:B:221:ILE:HD12	2.25	0.71
1:B:22:LYS:N	1:B:23:PRO:CD	2.53	0.71
1:C:52:LYS:HA	1:C:57:THR:HG22	1.73	0.70
1:B:22:LYS:O	1:B:22:LYS:HG2	1.91	0.70

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	197/230 (86%)	186 (94%)	11 (6%)	0	100	100
1	B	198/230 (86%)	185 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	197/230 (86%)	186 (94%)	11 (6%)	0	100	100
1	D	196/230 (85%)	183 (93%)	13 (7%)	0	100	100
All	All	788/920 (86%)	740 (94%)	48 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	Rotameric	Outliers	Percentiles	
1	A	172/202 (85%)	170 (99%)	2 (1%)	63	83
1	B	173/202 (86%)	169 (98%)	4 (2%)	44	72
1	C	172/202 (85%)	171 (99%)	1 (1%)	78	91
1	D	171/202 (85%)	170 (99%)	1 (1%)	78	91
All	All	688/808 (85%)	680 (99%)	8 (1%)	63	83

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	57	THR
1	B	86	LYS
1	B	53	THR
1	B	32	SER
1	B	59	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	147	HIS
1	B	151	GLN
1	D	187	ASN
1	A	120	GLN
1	A	169	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 oligosaccharides 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	199/230 (86%)	-0.45	0 <b>100</b>   <b>100</b>	17, 23, 38, 46	0
1	B	200/230 (86%)	-0.18	3 (1%) 72   68	18, 28, 47, 59	0
1	C	199/230 (86%)	-0.20	1 (0%) 87   85	20, 30, 49, 68	0
1	D	198/230 (86%)	-0.49	0 <b>100</b>   <b>100</b>	17, 23, 35, 45	0
All	All	796/920 (86%)	-0.33	4 (0%) 87   85	17, 26, 43, 68	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	55	GLY	3.0
1	B	57	THR	2.1
1	B	221	ILE	2.0
1	C	220	VAL	2.0

### 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 oligosaccharides 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.