



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 01:16 AM GMT

PDB ID : 3QZ4  
Title : Crystal structure of an Endo-1,4-beta-xylanaseD (BT\_3675) from Bacteroides  
thetaiotaomicron VPI-5482 at 1.74 Å resolution  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2011-03-04  
Resolution : 1.74 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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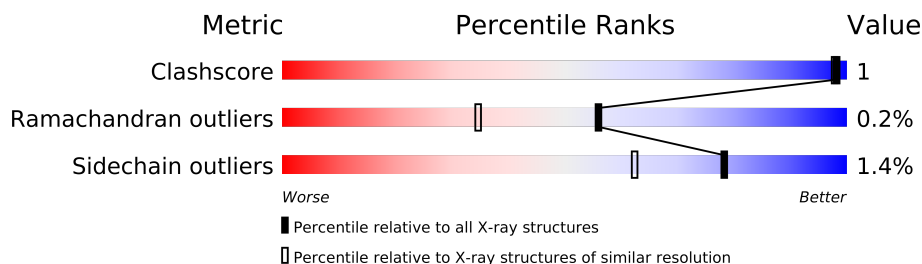
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	<b>FAILED</b>
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.74 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))
Clashscore	79885	1881 (1.76-1.72)
Ramachandran outliers	78287	1859 (1.76-1.72)
Sidechain outliers	78261	1859 (1.76-1.72)

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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	311	
1	B	311	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5633 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 Endo-1,4-beta-xylanaseD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	Se	0	4	0
			2430	1570	393	461	2	4			
1	B	306	Total	C	N	O	S	Se	0	2	0
			2440	1580	395	459	2	4			

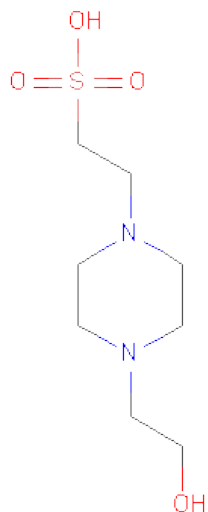
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	leader sequence	UNP Q8A1I6
B	0	GLY	-	leader sequence	UNP Q8A1I6

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	X	0	0
			2	2		
2	A	2	Total	X	0	0
			2	2		

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINEETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 8 4 4	0	1
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	272	Total O 280 280	0	8
5	B	396	Total O 409 409	0	13

### 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.

Note EDS failed to run properly.

- Molecule 1: Endo-1,4-beta-xylanaseD

Chain A: 



- Molecule 1: Endo-1,4-beta-xylanaseD

Chain B: 



## 4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.16Å 99.25Å 65.00Å 90.00° 97.92° 90.00°	Depositor
Resolution (Å)	29.86 – 1.74	Depositor
% Data completeness (in resolution range)	(Not available) (29.86-1.74)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.87 (at 1.74Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, $R_{free}$	0.159 , 0.202	Depositor
Wilson B-factor (Å <sup>2</sup> )	22.2	Xtriage
Anisotropy	0.581	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 65808 reflections (0.005%)	Xtriage
Total number of atoms	5633	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage'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.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UNX, EPE, EDO

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	0.49	1/2513 (0.0%)	0.64	0/3428
1	B	0.54	0/2522	0.63	0/3433
All	All	0.52	1/5035 (0.0%)	0.64	0/6861

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184	MSE	SE-CE	-5.42	1.63	1.95

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	2430	0	0	2	0
1	B	2440	0	0	1	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	15	0	17	0	0
3	B	15	0	17	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	16	0	24	0	0
4	B	24	0	36	1	0
5	A	280	0	0	1	0
5	B	409	0	0	0	0
All	All	5633	0	94	3	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 1.

All (3) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:175:SER:N	4:B:342:EDO:HO2	2.07	0.53
1:A:160:GLN:NE2	5:A:574:HOH:O	2.49	0.46
1:A:161:GLN:NE2	1:A:183:TYR:OH	2.52	0.42

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	308/311 (99%)	295 (96%)	13 (4%)	0	100	100
1	B	306/311 (98%)	293 (96%)	12 (4%)	1 (0%)	50	28
All	All	614/622 (99%)	588 (96%)	25 (4%)	1 (0%)	56	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	55	PRO

### 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	256/262 (98%)	249 (97%)	7 (3%)	57	30
1	B	259/262 (99%)	257 (99%)	2 (1%)	89	80
All	All	515/524 (98%)	506 (98%)	9 (2%)	78	53

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

Mol	Chain	Res	Type
1	A	252	SER
1	B	252	SER
1	A	304[B]	ASN
1	A	83[B]	THR
1	A	304[A]	ASN

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 ⓘ

Of 16 ligands modelled in this entry, 4 are unknown - leaving 12 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
3	EPE	A	338	-	15,15,15	1.02	1 (6%)	20,20,20	1.50	3 (15%)
4	EDO	A	339	-	3,3,3	0.49	0	2,2,2	0.58	0
4	EDO	A	340	-	3,3,3	0.52	0	2,2,2	0.39	0
4	EDO	A	344	-	3,3,3	0.50	0	2,2,2	0.39	0
4	EDO	A	345	-	3,3,3	0.56	0	2,2,2	0.32	0
3	EPE	B	337	-	15,15,15	0.86	1 (6%)	20,20,20	1.41	3 (15%)
4	EDO	B	340	-	3,3,3	0.57	0	2,2,2	0.06	0
4	EDO	B	341	-	3,3,3	0.57	0	2,2,2	0.33	0
4	EDO	B	342	-	3,3,3	0.61	0	2,2,2	0.10	0
4	EDO	B	343[A]	-	3,3,3	0.54	0	2,2,2	0.34	0
4	EDO	B	343[B]	-	3,3,3	0.54	0	2,2,2	0.38	0
4	EDO	B	346	-	3,3,3	0.57	0	2,2,2	0.72	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
3	EPE	A	338	-	-	0/9/19/19	0/1/1/1
4	EDO	A	339	-	-	0/1/1/1	0/0/0/0
4	EDO	A	340	-	-	0/1/1/1	0/0/0/0
4	EDO	A	344	-	-	0/1/1/1	0/0/0/0
4	EDO	A	345	-	-	0/1/1/1	0/0/0/0
3	EPE	B	337	-	-	0/9/19/19	0/1/1/1
4	EDO	B	340	-	-	0/1/1/1	0/0/0/0
4	EDO	B	341	-	-	0/1/1/1	0/0/0/0
4	EDO	B	342	-	-	0/1/1/1	0/0/0/0
4	EDO	B	343[A]	-	-	0/1/1/1	0/0/0/0
4	EDO	B	343[B]	-	-	0/1/1/1	0/0/0/0
4	EDO	B	346	-	-	0/1/1/1	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	338	EPE	C10-S	3.13	1.82	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	337	EPE	C10-S	2.60	1.81	1.77

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	337	EPE	O1S-S-C10	-4.04	103.34	106.81
3	A	338	EPE	O2S-S-C10	3.76	110.03	106.81
3	A	338	EPE	O1S-S-C10	3.18	109.53	106.81
3	B	337	EPE	C7-N4-C3	2.82	118.61	111.32
3	A	338	EPE	C7-N4-C5	2.58	117.98	111.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.