



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 07:30 am BST

PDB ID : 4ZRX
Title : Crystal structure of a putative alpha-L-fucosidase (BACOVA_04357) from Bacteroides ovatus ATCC 8483 at 1.59 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2015-05-12
Resolution : 1.59 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

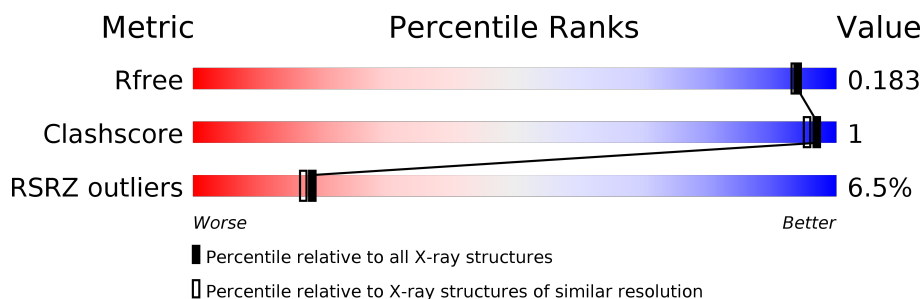
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

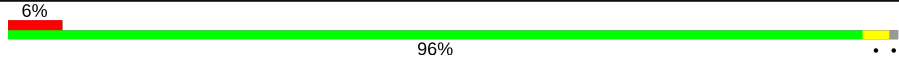
The reported resolution of this entry is 1.59 Å.

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}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 $\leq 5\%$. 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	586	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5399 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 F5/8 type C domain protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	581	4770	3051	811	889	4	15	0	18	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	LEADER SEQUENCE	UNP A7M2M0

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

Continued on next page...

Continued from previous page...

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

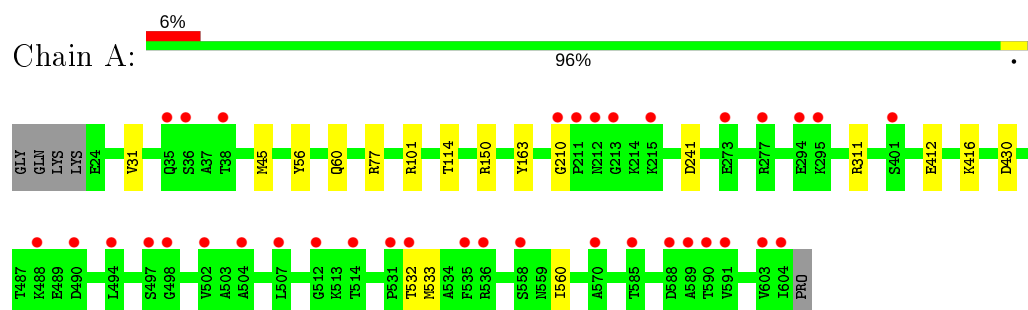
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	595	Total	O	0	8
			601	601		

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.

- Molecule 1: F5/8 type C domain protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.02Å 71.75Å 73.11Å 90.00° 106.98° 90.00°	Depositor
Resolution (Å)	28.60 – 1.59 28.60 – 1.59	Depositor EDS
% Data completeness (in resolution range)	97.7 (28.60-1.59) 97.7 (28.60-1.59)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.151 , 0.175 0.162 , 0.183	Depositor DCC
R_{free} test set	4082 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.639	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5399	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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: 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	0.90	1/4931 (0.0%)	0.90	10/6662 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	412	GLU	CB-CG	-5.22	1.42	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	ARG	NE-CZ-NH1	8.58	124.59	120.30
1	A	77	ARG	NE-CZ-NH2	-7.71	116.45	120.30
1	A	150	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	A	461	ARG	NE-CZ-NH1	6.90	123.75	120.30
1	A	461	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	A	101	ARG	NE-CZ-NH1	6.29	123.44	120.30
1	A	241	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	A	446	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	A	311	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	A	241	ASP	CB-CG-OD1	5.19	122.97	118.30

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 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	4770	0	4707	8	0
2	A	28	0	42	1	0
3	A	601	0	0	4	0
All	All	5399	0	4749	9	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 1.

All (9) 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:A:416:LYS:NZ	3:A:802:HOH:O	2.27	0.67
1:A:210:GLY:HA3	3:A:1316:HOH:O	2.03	0.58
1:A:532:THR:HG23	3:A:858:HOH:O	2.07	0.53
1:A:31:VAL:CG2	1:A:45:MSE:HE2	2.41	0.50
1:A:430[A]:ASP:OD1	3:A:801:HOH:O	2.20	0.49
1:A:114:THR:HA	1:A:163:TYR:HB3	1.95	0.47
2:A:705:EDO:H11	2:A:706:EDO:H22	1.97	0.46
1:A:56:TYR:O	1:A:60:GLN:HG2	2.18	0.43
1:A:533:MSE:HE2	1:A:560:ILE:HG12	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

7 ligands are modelled in this entry.

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	$\# Z > 2$
2	EDO	A	707	-	3,3,3	0.32	0	2,2,2	0.19	0
2	EDO	A	706	-	3,3,3	0.48	0	2,2,2	0.41	0
2	EDO	A	703	-	3,3,3	0.41	0	2,2,2	0.49	0
2	EDO	A	702	-	3,3,3	0.35	0	2,2,2	0.10	0
2	EDO	A	705	-	3,3,3	0.70	0	2,2,2	0.45	0
2	EDO	A	701	-	3,3,3	0.46	0	2,2,2	0.40	0
2	EDO	A	704	-	3,3,3	0.46	0	2,2,2	0.29	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
2	EDO	A	707	-	-	0/1/1/1	-
2	EDO	A	706	-	-	0/1/1/1	-
2	EDO	A	703	-	-	0/1/1/1	-
2	EDO	A	702	-	-	0/1/1/1	-
2	EDO	A	705	-	-	0/1/1/1	-
2	EDO	A	701	-	-	0/1/1/1	-
2	EDO	A	704	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	706	EDO	1	0
2	A	705	EDO	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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	568/586 (96%)	0.18	37 (6%) 18 17	13, 25, 47, 73	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	213	GLY	7.2
1	A	36	SER	5.7
1	A	211	PRO	5.5
1	A	558	SER	4.2
1	A	35	GLN	4.2
1	A	210	GLY	4.1
1	A	514	THR	4.0
1	A	494	LEU	3.9
1	A	604	ILE	3.8
1	A	590	THR	3.8
1	A	589	ALA	3.7
1	A	273[A]	GLU	3.3
1	A	502	VAL	3.2
1	A	488[A]	LYS	3.0
1	A	536	ARG	2.9
1	A	212	ASN	2.9
1	A	591	VAL	2.9
1	A	497	SER	2.8
1	A	215	LYS	2.8
1	A	603	VAL	2.8
1	A	504	ALA	2.8
1	A	295	LYS	2.8
1	A	588	ASP	2.7
1	A	486	THR	2.6
1	A	512	GLY	2.6
1	A	294	GLU	2.5
1	A	490	ASP	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	535	PHE	2.5
1	A	532	THR	2.3
1	A	498	GLY	2.3
1	A	531	PRO	2.2
1	A	38	THR	2.2
1	A	585	THR	2.2
1	A	507	LEU	2.1
1	A	277	ARG	2.1
1	A	570	ALA	2.1
1	A	401	SER	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 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, 95th 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	B-factors(Å ²)	Q<0.9
2	EDO	A	706	4/4	0.80	0.20	41,43,45,47	0
2	EDO	A	707	4/4	0.87	0.23	49,49,51,51	0
2	EDO	A	705	4/4	0.87	0.12	27,28,29,31	0
2	EDO	A	702	4/4	0.91	0.14	34,37,39,42	0
2	EDO	A	704	4/4	0.92	0.12	37,39,39,40	0
2	EDO	A	703	4/4	0.97	0.11	23,26,27,30	0
2	EDO	A	701	4/4	0.98	0.13	26,28,29,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.