



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 19, 2017 – 08:21 PM EDT

PDB ID : 3NUZ
Title : Crystal structure of a putative acetyl xylan esterase (BF1801) from Bacteroides fragilis NCTC 9343 at 2.30 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : unknown
Resolution : 2.30 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

<http://wwpdb.org/validation/2016/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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

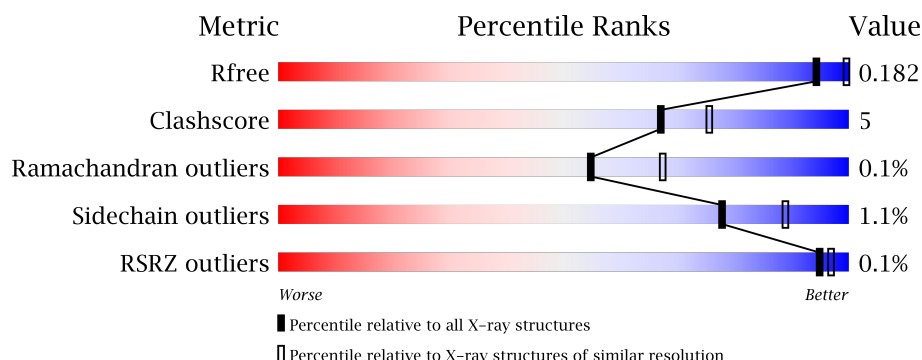
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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. 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	398	<div> <div>86%</div> <div>11%</div> <div>.</div> </div>
1	B	398	<div> <div>83%</div> <div>15%</div> <div>..</div> </div>
1	C	398	<div> <div>89%</div> <div>9%</div> <div>.</div> </div>
1	D	398	<div> <div>88%</div> <div>10%</div> <div>.</div> </div>
1	E	398	<div> <div>82%</div> <div>15%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	398	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: a green segment representing 86%, a yellow segment representing 11%, and a small grey segment at the end. A small black dot is located at the end of the grey segment.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19125 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 Putative acetyl xylan esterase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	Se	0	1	0
			3147	2027	540	566	4	10			
1	B	389	Total	C	N	O	S	Se	0	3	0
			3162	2038	542	568	4	10			
1	C	388	Total	C	N	O	S	Se	0	1	0
			3147	2028	541	564	4	10			
1	D	389	Total	C	N	O	S	Se	0	1	0
			3148	2029	539	566	4	10			
1	E	385	Total	C	N	O	S	Se	0	0	0
			3128	2017	536	561	4	10			
1	F	386	Total	C	N	O	S	Se	0	2	0
			3139	2026	535	564	4	10			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	EXPRESSION TAG	UNP Q5LEF1
B	0	GLY	-	EXPRESSION TAG	UNP Q5LEF1
C	0	GLY	-	EXPRESSION TAG	UNP Q5LEF1
D	0	GLY	-	EXPRESSION TAG	UNP Q5LEF1
E	0	GLY	-	EXPRESSION TAG	UNP Q5LEF1
F	0	GLY	-	EXPRESSION TAG	UNP Q5LEF1

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	61	Total	O	0	1
			62	62		
2	B	53	Total	O	0	0
			53	53		
2	C	55	Total	O	0	0
			55	55		

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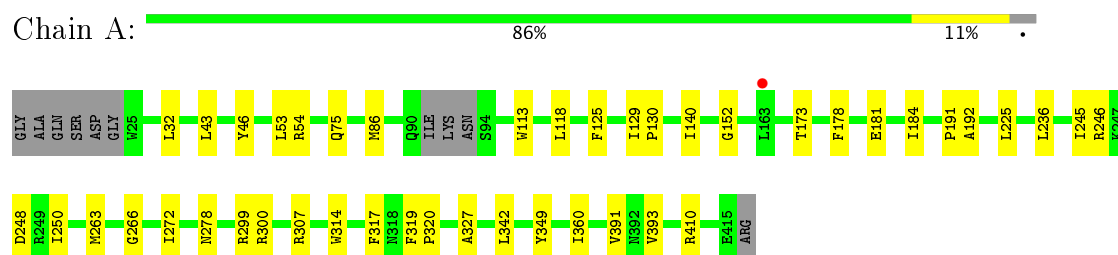
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	53	Total 53	O 53	0	0
2	E	21	Total 21	O 21	0	0
2	F	10	Total 10	O 10	0	0

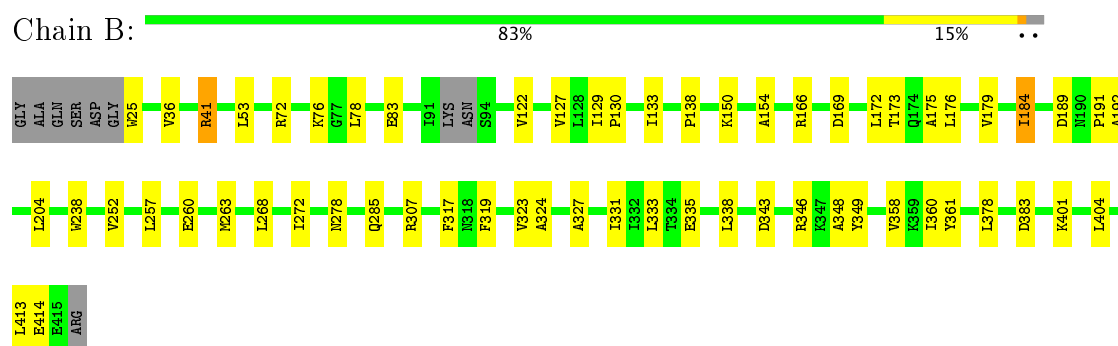
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

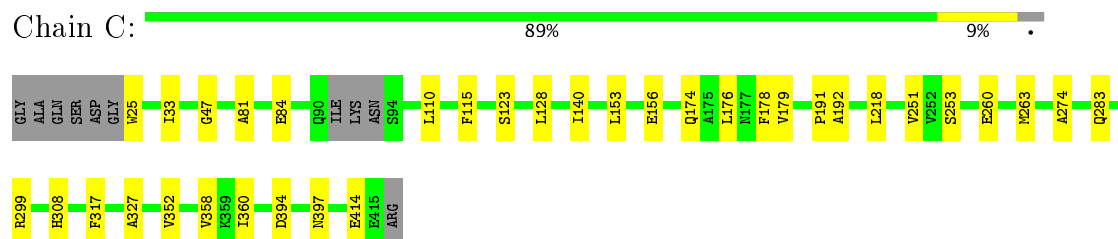
• Molecule 1: Putative acetyl xylan esterase



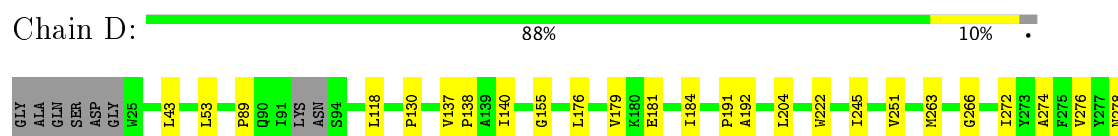
• Molecule 1: Putative acetyl xylan esterase



• Molecule 1: Putative acetyl xylan esterase

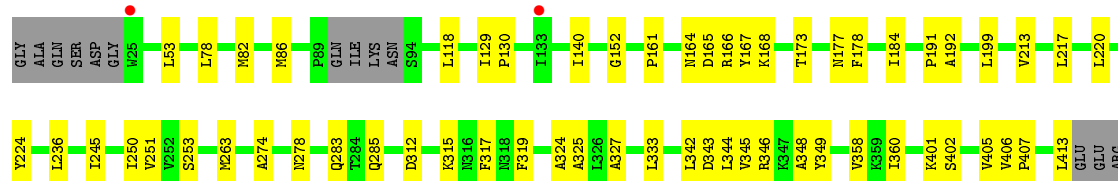
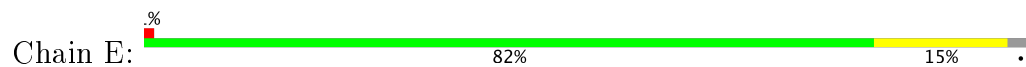


• Molecule 1: Putative acetyl xylan esterase

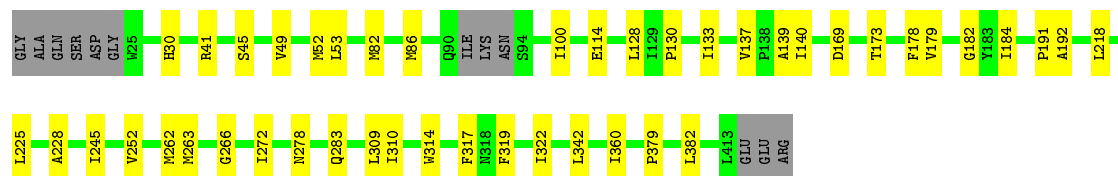
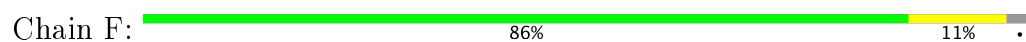




• Molecule 1: Putative acetyl xylan esterase



• Molecule 1: Putative acetyl xylan esterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	125.61Å 125.61Å 162.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.66 – 2.30 29.66 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.66-2.30) 99.3 (29.66-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.31Å)	Xtriage
Refinement program	PHENIX, REFMAC 5.5.0110	Depositor
R, R_{free}	0.152 , 0.182 0.154 , 0.182	Depositor DCC
R_{free} test set	6620 reflections (5.53%)	DCC
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.304 for -h,-k,l 0.460 for h,-h-k,-l 0.304 for -k,-h,-l	Xtriage
Reported twinning fraction	0.382 for H, K, L 0.136 for -H, H+K, -L 0.162 for -h,-k,l 0.320 for K, H, -L	Depositor
Outliers	0 of 126313 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19125	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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	0.44	0/3228	0.72	2/4364 (0.0%)
1	B	0.44	0/3249	0.71	2/4392 (0.0%)
1	C	0.45	0/3227	0.72	0/4360
1	D	0.44	0/3229	0.72	0/4366
1	E	0.45	0/3206	0.70	0/4332
1	F	0.43	0/3223	0.68	0/4357
All	All	0.44	0/19362	0.71	4/26171 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	54	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	B	72	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	307	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	B	41	ARG	NE-CZ-NH1	5.08	122.84	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 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	3147	0	3094	26	0
1	B	3162	0	3110	36	0
1	C	3147	0	3101	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3148	0	3091	22	0
1	E	3128	0	3093	43	0
1	F	3139	0	3096	33	0
2	A	62	0	0	0	0
2	B	53	0	0	0	0
2	C	55	0	0	0	0
2	D	53	0	0	2	0
2	E	21	0	0	0	0
2	F	10	0	0	0	0
All	All	19125	0	18585	170	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 5.

The worst 5 of 170 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:E:184:ILE:HD11	1:E:245:ILE:HG12	1.54	0.89
1:A:184:ILE:HD11	1:A:245:ILE:HG12	1.54	0.87
1:B:129:ILE:HA	1:B:184:ILE:HG22	1.66	0.77
1:F:263:MSE:HE1	1:F:319:PHE:CD1	2.21	0.75
1:F:263:MSE:HE1	1:F:319:PHE:CE1	2.25	0.71

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	385/398 (97%)	366 (95%)	19 (5%)	0	100	100
1	B	388/398 (98%)	373 (96%)	14 (4%)	1 (0%)	44	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	385/398 (97%)	370 (96%)	15 (4%)	0	100	100
1	D	386/398 (97%)	369 (96%)	16 (4%)	1 (0%)	44	55
1	E	381/398 (96%)	362 (95%)	19 (5%)	0	100	100
1	F	384/398 (96%)	367 (96%)	17 (4%)	0	100	100
All	All	2309/2388 (97%)	2207 (96%)	100 (4%)	2 (0%)	55	67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	414	GLU
1	D	414	GLU

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	338/340 (99%)	335 (99%)	3 (1%)	82	91
1	B	339/340 (100%)	334 (98%)	5 (2%)	70	83
1	C	338/340 (99%)	335 (99%)	3 (1%)	82	91
1	D	337/340 (99%)	333 (99%)	4 (1%)	75	87
1	E	338/340 (99%)	334 (99%)	4 (1%)	75	87
1	F	338/340 (99%)	335 (99%)	3 (1%)	82	91
All	All	2028/2040 (99%)	2006 (99%)	22 (1%)	78	89

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	283	GLN
1	D	222	TRP
1	F	283	GLN
1	C	317	PHE
1	D	43	LEU

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

Mol	Chain	Res	Type
1	A	207	ASN
1	E	55	ASN
1	E	164	ASN
1	E	177	ASN
1	F	392	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](#)

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, 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	378/398 (94%)	-0.48	1 (0%) 93 96	18, 31, 44, 51	0
1	B	379/398 (95%)	-0.47	0 100 100	19, 32, 44, 52	0
1	C	378/398 (94%)	-0.47	0 100 100	18, 31, 43, 51	0
1	D	379/398 (95%)	-0.41	0 100 100	18, 31, 43, 58	0
1	E	375/398 (94%)	-0.46	2 (0%) 90 93	28, 36, 46, 53	0
1	F	376/398 (94%)	-0.42	0 100 100	27, 37, 47, 56	0
All	All	2265/2388 (94%)	-0.45	3 (0%) 95 97	18, 34, 45, 58	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	133	ILE	2.1
1	A	163	LEU	2.1
1	E	25	TRP	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.