



wwPDB X-ray Structure Validation Summary Report

Nov 20, 2014 – 12:41 PM EST

PDB ID : 3WP3
Title : Xylanase 11C from Talaromyces cellulolyticus (formerly known as Acremonium cellulolyticus)
Authors : Ishikawa, K.; Inoue, H.; Kataoka, M.
Deposited on : 2014-01-09
Resolution : 1.98 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

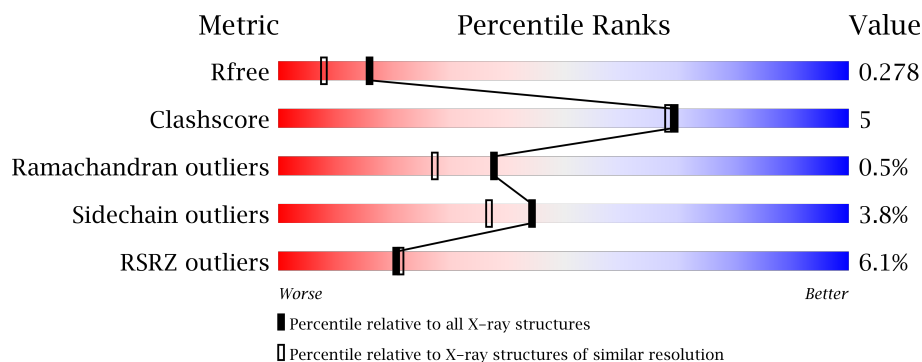
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable24195
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.1.3
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable24195

1 Overall quality at a glance

The reported resolution of this entry is 1.98 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	6577 (2.00-1.96)
Clashscore	79885	8091 (2.00-1.96)
Ramachandran outliers	78287	7989 (2.00-1.96)
Sidechain outliers	78261	7987 (2.00-1.96)
RSRZ outliers	66119	6578 (2.00-1.96)

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. 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	207	
1	B	207	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3167 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-xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1461	915	231	312	3			
1	B	190	Total	C	N	O	S	0	0	0
			1461	915	231	312	3			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	EXPRESSION TAG	UNP Q9HFH0
A	18	PHE	-	EXPRESSION TAG	UNP Q9HFH0
A	19	PRO	-	EXPRESSION TAG	UNP Q9HFH0
A	20	SER	-	EXPRESSION TAG	UNP Q9HFH0
A	21	GLY	-	EXPRESSION TAG	UNP Q9HFH0
A	22	LEU	-	EXPRESSION TAG	UNP Q9HFH0
A	23	THR	-	EXPRESSION TAG	UNP Q9HFH0
A	24	GLN	-	EXPRESSION TAG	UNP Q9HFH0
A	25	HIS	-	EXPRESSION TAG	UNP Q9HFH0
A	26	ALA	-	EXPRESSION TAG	UNP Q9HFH0
A	27	THR	-	EXPRESSION TAG	UNP Q9HFH0
A	75	ASN	ASP	ENGINEERED MUTATION	UNP Q9HFH0
A	101	THR	PRO	ENGINEERED MUTATION	UNP Q9HFH0
A	137	LEU	SER	ENGINEERED MUTATION	UNP Q9HFH0
A	157	ASP	ASN	ENGINEERED MUTATION	UNP Q9HFH0
B	17	MET	-	EXPRESSION TAG	UNP Q9HFH0
B	18	PHE	-	EXPRESSION TAG	UNP Q9HFH0
B	19	PRO	-	EXPRESSION TAG	UNP Q9HFH0
B	20	SER	-	EXPRESSION TAG	UNP Q9HFH0
B	21	GLY	-	EXPRESSION TAG	UNP Q9HFH0
B	22	LEU	-	EXPRESSION TAG	UNP Q9HFH0
B	23	THR	-	EXPRESSION TAG	UNP Q9HFH0
B	24	GLN	-	EXPRESSION TAG	UNP Q9HFH0
B	25	HIS	-	EXPRESSION TAG	UNP Q9HFH0
B	26	ALA	-	EXPRESSION TAG	UNP Q9HFH0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	27	THR	-	EXPRESSION TAG	UNP Q9HFH0
B	75	ASN	ASP	ENGINEERED MUTATION	UNP Q9HFH0
B	101	THR	PRO	ENGINEERED MUTATION	UNP Q9HFH0
B	137	LEU	SER	ENGINEERED MUTATION	UNP Q9HFH0
B	157	ASP	ASN	ENGINEERED MUTATION	UNP Q9HFH0

- Molecule 2 is water.

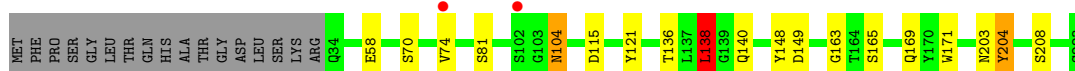
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	134	Total O 134 134	0	0
2	B	111	Total O 111 111	0	0

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.

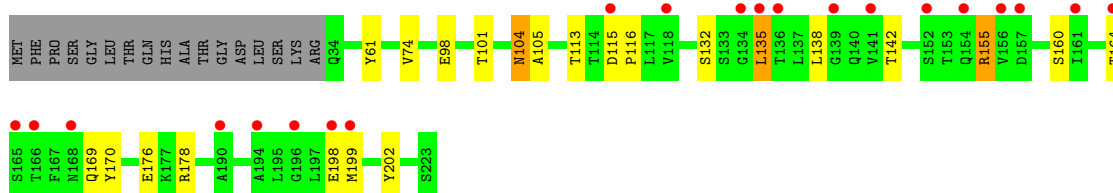
- Molecule 1: Endo-1,4-beta-xylanase

Chain A: 



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

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.51Å 60.11Å 106.98Å 90.00° 99.07° 90.00°	Depositor
Resolution (Å)	50.00 – 1.98 39.68 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-1.98) 99.7 (39.68-1.98)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.24 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.232 , 0.277 0.234 , 0.278	Depositor DCC
R_{free} test set	1773 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 40.3	EDS
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	3 of 35405 reflections (0.008%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3167	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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	1.20	3/1500 (0.2%)	1.00	1/2052 (0.0%)
1	B	1.07	4/1500 (0.3%)	0.92	1/2052 (0.0%)
All	All	1.14	7/3000 (0.2%)	0.96	2/4104 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	61	TYR	CD2-CE2	6.95	1.49	1.39
1	A	121	TYR	CD1-CE1	6.83	1.49	1.39
1	B	74	VAL	CB-CG1	5.98	1.65	1.52
1	A	204	TYR	CD1-CE1	5.35	1.47	1.39
1	B	98	GLU	CG-CD	5.16	1.59	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	LEU	CB-CG-CD1	7.14	123.14	111.00
1	B	178	ARG	NE-CZ-NH2	-6.45	117.08	120.30

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	1461	0	1320	12	0
1	B	1461	0	1320	14	0
2	A	134	0	0	4	0
2	B	111	0	0	1	0
All	All	3167	0	2640	26	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 5.

The worst 5 of 26 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:155:ARG:HH21	1:B:155:ARG:HG2	1.29	0.95
1:B:155:ARG:NH2	1:B:155:ARG:HG2	1.92	0.81
1:A:203:ASN:HD22	1:A:204:TYR:H	1.39	0.70
1:B:155:ARG:HH21	1:B:155:ARG:CG	2.06	0.64
1:B:113:THR:HG21	1:B:199:MET:CE	2.31	0.60

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	188/207 (91%)	181 (96%)	7 (4%)	0	100	100
1	B	188/207 (91%)	176 (94%)	10 (5%)	2 (1%)	21	10
All	All	376/414 (91%)	357 (95%)	17 (4%)	2 (0%)	38	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	135	LEU
1	B	164	THR

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	157/171 (92%)	151 (96%)	6 (4%)	44	37
1	B	157/171 (92%)	151 (96%)	6 (4%)	44	37
All	All	314/342 (92%)	302 (96%)	12 (4%)	44	37

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	SER
1	B	104	ASN
1	B	155	ARG
1	A	138	LEU
1	B	142	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	ASN
1	A	169	GLN
1	A	203	ASN
1	B	104	ASN

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, 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	190/207 (91%)	0.07	2 (1%) 77 80	10, 20, 37, 51	0
1	B	190/207 (91%)	0.58	21 (11%) 6 6	12, 26, 52, 60	0
All	All	380/414 (91%)	0.33	23 (6%) 21 21	10, 22, 49, 60	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	194	ALA	4.7
1	B	165	SER	4.5
1	B	136	THR	4.4
1	B	154	GLN	4.3
1	B	157	ASP	4.3

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.