

Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 – 11:46 PM EDT

PDB ID : 6OJK

Title : Structure of YePL2A K291W in Complex with Tetragalacturonic Acid

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2019-04-11 Deposited on

: 1.50 Å(reported) Resolution

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 (i) symbol.

> The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity **FAILED**

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13

EDS FAILED

20191225.v01 (using entries in the PDB archive December 25th 2019) Percentile statistics

Ideal geometry (proteins) Engh & Huber (2001) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) 2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4869 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 Periplasmic pectate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	542	Total 4290	C 2725	N 739	O 815	S 11	0	3	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A0T9S209
A	2	GLY	-	expression tag	UNP A0A0T9S209
A	3	SER	-	expression tag	UNP A0A0T9S209
A	4	SER	-	expression tag	UNP A0A0T9S209
A	5	HIS	-	expression tag	UNP A0A0T9S209
A	6	HIS	-	expression tag	UNP A0A0T9S209
A	7	HIS	-	expression tag	UNP A0A0T9S209
A	8	HIS	-	expression tag	UNP A0A0T9S209
A	9	HIS	-	expression tag	UNP A0A0T9S209
A	10	HIS	-	expression tag	UNP A0A0T9S209
A	11	SER	-	expression tag	UNP A0A0T9S209
A	12	SER	-	expression tag	UNP A0A0T9S209
A	13	GLY	-	expression tag	UNP A0A0T9S209
A	14	LEU	-	expression tag	UNP A0A0T9S209
A	15	VAL	-	expression tag	UNP A0A0T9S209
A	16	PRO	-	expression tag	UNP A0A0T9S209
A	17	ARG	-	expression tag	UNP A0A0T9S209
A	18	GLY	-	expression tag	UNP A0A0T9S209
A	19	SER	-	expression tag	UNP A0A0T9S209
A	20	HIS	-	expression tag	UNP A0A0T9S209
A	21	MET	-	expression tag	UNP A0A0T9S209
A	22	ALA	-	expression tag	UNP A0A0T9S209
A	23	SER	-	expression tag	UNP A0A0T9S209
A	291	TRP	LYS	engineered mutation	UNP A0A0T9S209

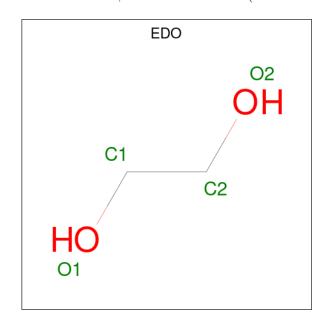
• Molecule 2 is an oligosaccharide called alpha-D-galactopyranuronic acid-(1-4)-alpha-D-galactopyranuronic acid-(1-4)-alpha-D-galactopyranuronic acid-(1-4)-alpha-D-galactopyranuroni



c acid.

I	Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace
	2	В	4	Total 49	C 24	O 25	0	0	0

 \bullet Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$



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

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	522	Total O 522 522	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	58.24Å 94.93Å 126.77Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.22 - 1.50	Depositor
% Data completeness	99.7 (46.22-1.50)	Depositor
(in resolution range)	, , ,	
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.35 (at 1.50Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.173 , 0.188	Depositor
Wilson B-factor (\mathring{A}^2)	16.9	Xtriage
Anisotropy	0.560	Xtriage
L-test for twinning ²	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4869	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

4 monosaccharides 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	Tuno	Chain	ain Res	s Link	Вс	ond leng	ths	Bond angles			
MIOI	Type	Chain			Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
2	ADA	В	1	2	13,13,13	0.99	0	18,19,19	0.82	0	
2	ADA	В	2	2	12,12,13	2.13	4 (33%)	14,17,19	1.60	2 (14%)	
2	ADA	В	3	2	12,12,13	0.67	0	14,17,19	0.94	0	
2	ADA	В	4	2	12,12,13	0.92	0	14,17,19	0.80	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	ADA	В	1	2	-	1/4/24/24	0/1/1/1
2	ADA	В	2	2	-	0/4/21/24	0/1/1/1
2	ADA	В	3	2	-	0/4/21/24	0/1/1/1
2	ADA	В	4	2	-	1/4/21/24	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
2	В	2	ADA	O4-C4	5.83	1.56	1.43
2	В	2	ADA	O5-C5	2.19	1.47	1.43
2	В	2	ADA	O5-C1	2.18	1.47	1.43
2	В	2	ADA	C2-C3	-2.11	1.49	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
2	В	2	ADA	C2-C3-C4	-3.39	105.02	110.89
2	В	2	ADA	O4-C4-C5	2.53	115.42	109.74

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	1	ADA	O5-C5-C6-O6B
2	В	4	ADA	O5-C5-C6-O6B

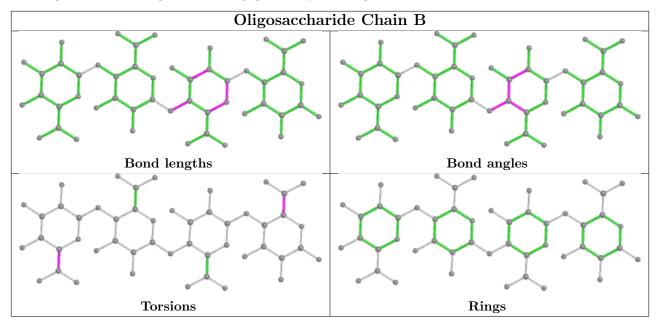
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,



bond angles, torsion angles, and ring geometry for oligosaccharide.



4.6 Ligand geometry (i)

2 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	Truss	Chain	Dag	Link	В	ond leng	gths	Bond angles		
MIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	EDO	A	1005	-	3,3,3	0.47	0	2,2,2	0.33	0
3	EDO	A	1006	-	3,3,3	0.40	0	2,2,2	0.55	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	EDO	A	1005	-	-	1/1/1/1	-
3	EDO	A	1006	_	-	0/1/1/1	-

There are no bond length outliers.



There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1005	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

