

# Full wwPDB X-ray Structure Validation Report (i)

#### May 26, 2020 – 02:51 pm BST

PDB ID	:	4PW2
Title	:	Crystal structure of D-glucuronyl C5 epimerase
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Deposited on		
Resolution	:	1.90  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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

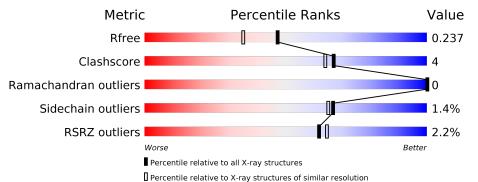
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December $25$ th $2019$ )
$\operatorname{Refmac}$	:	5.8.0158
CCP4	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.90 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	6207 (1.90-1.90)
Clashscore	141614	6847(1.90-1.90)
Ramachandran outliers	138981	6760(1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082(1.90-1.90)

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 <=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		
-			2%		
	A	585	80%	7% •	13%



# 2 Entry composition (i)

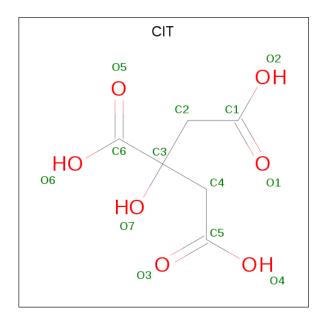
There are 3 unique types of molecules in this entry. The entry contains 4783 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 D-glucuronyl C5 epimerase B.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	510	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0
	11	010	4086	2611	699	761	15	0	0	0

• Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula:  $C_6H_8O_7$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	А	1	Total ( 13 (	CO 57	0	0

• Molecule 3 is water.

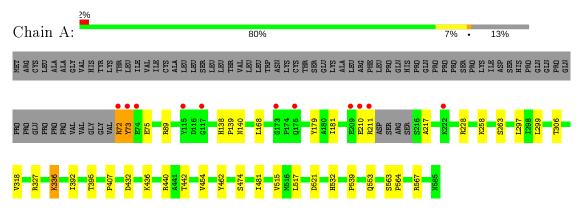
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	684	Total O 684 684	0	0



# 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: D-glucuronyl C5 epimerase B





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	66.38Å 66.38Å 337.57Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	47.38 - 1.90	Depositor
Resolution (A)	47.33 - 1.90	EDS
% Data completeness	99.9 (47.38-1.90)	Depositor
(in resolution range)	99.9(47.33-1.90)	EDS
R <sub>merge</sub>	0.10	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.65 (at 1.90 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
D D.	0.210 , $0.244$	Depositor
$R, R_{free}$	0.206 , $0.237$	DCC
$R_{free}$ test set	3094 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.9	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , $48.5$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.45, \langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4783	wwPDB-VP
Average B, all atoms $(Å^2)$	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



 $<sup>^1 {\</sup>rm Intensities}$  estimated from amplitudes.

# 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: CIT

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).

Mal	Chain	Bond	lengths	Bond angles		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.37	0/4190	0.56	0/5679	

There are no bond length outliers.

There are no bond angle outliers.

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	А	4086	0	4017	31	0
2	А	13	0	5	1	0
3	А	684	0	0	8	0
All	All	4783	0	4022	32	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 4.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1 Atom-2		$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	$egin{array}{clash} { m overlap} \ ({ m \AA}) \end{array}$
1:A:210:GLU:OE1	1:A:211:ARG:HG2	1.42	1.19

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Atoma 1	Atom 0	Interatomic	Clash	
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)	
1:A:210:GLU:OE1	1:A:211:ARG:CG	2.25	0.85	
1:A:72:ARG:N	1:A:72:ARG:HD3	1.96	0.81	
1:A:228:ARG:NH2	3:A:1052:HOH:O	2.34	0.59	
1:A:217:ALA:HB1	3:A:1379:HOH:O	2.05	0.56	
1:A:395:THR:HG22	1:A:407:PRO:HD3	1.87	0.56	
1:A:258:LYS:HE3	3:A:993:HOH:O	2.06	0.56	
1:A:327:ARG:HD3	3:A:1362:HOH:O	2.05	0.56	
1:A:481:ILE:HG21	1:A:553:GLN:HB3	1.90	0.54	
1:A:73:TYR:CD1	1:A:73:TYR:C	2.84	0.51	
1:A:436:LYS:O	1:A:440:ARG:HG3	2.12	0.49	
1:A:168:LEU:HD22	1:A:297:LEU:HD21	1.97	0.47	
1:A:75:GLU:HG2	3:A:1221:HOH:O	2.15	0.46	
1:A:138:HIS:ND1	1:A:140:ASN:OD1	2.39	0.46	
1:A:336:LYS:HB2	1:A:336:LYS:HE2	1.47	0.45	
1:A:210:GLU:HA	1:A:211:ARG:HA	1.58	0.44	
1:A:564:PRO:HA	1:A:567:ARG:HE	1.82	0.44	
2:A:601:CIT:O7	2:A:601:CIT:O1	2.36	0.43	
1:A:474:SER:HA	3:A:1290:HOH:O	2.18	0.43	
1:A:263:SER:HA	1:A:318:VAL:O	2.18	0.43	
1:A:462:TYR:CZ	1:A:515:VAL:HG11	2.54	0.43	
1:A:179:TYR:CE2	1:A:181:ILE:HB	2.55	0.42	
1:A:563:SER:HA	1:A:564:PRO:HD3	1.96	0.41	
1:A:432:ASP:HB3	1:A:436:LYS:NZ	2.35	0.41	
1:A:179:TYR:HE1	1:A:392:ILE:HG12	1.84	0.41	
1:A:72:ARG:N	1:A:72:ARG:CD	2.70	0.41	
1:A:138:HIS:HA	1:A:139:PRO:HD3	1.96	0.41	
1:A:228:ARG:NH2	3:A:1191:HOH:O	2.50	0.41	
1:A:299:LEU:HB2	1:A:306:THR:HB	2.02	0.41	
1:A:521:ASP:HB3	3:A:1171:HOH:O	2.21	0.40	
1:A:73:TYR:CD1	1:A:89:ARG:HD2	2.56	0.40	
1:A:532:HIS:HB3	1:A:539:PRO:HA	2.02	0.40	

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There are no symmetry-related clashes.

### 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

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	А	506/585~(86%)	493~(97%)	13 (3%)	0	100 100	

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

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.

$\mathbf{M}$	ol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1		А	439/507~(87%)	433~(99%)	6 (1%)	67 65	

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	72	ARG
1	А	73	TYR
1	А	336	LYS
1	А	442	THR
1	А	454	VAL
1	А	517	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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)

1 ligand is 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	Tuno	Chain	Res	Link	Bond lengths			Bond angles		
		Type				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
	2	CIT	А	601	-	3,12,12	1.35	1 (33%)	$3,\!17,\!17$	1.55	1 (33%)

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	CIT	А	601	-	-	1/6/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	601	CIT	C2-C3	-2.03	1.52	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	601	CIT	C3-C2-C1	-2.02	111.75	114.98

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	601	CIT	C1-C2-C3-C4



There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	CIT	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 (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,  $95^{th}$  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 $>2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	$\mathbf{Q}{<}0.9$
1	А	510/585~(87%)	0.10	11 (2%) 62 64	22, 31, 52, 103	0

All (11) RSRZ outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	А	72	ARG	6.8
1	А	210	GLU	4.6
1	А	211	ARG	3.4
1	А	173	GLY	2.9
1	А	74	GLU	2.7
1	А	222	LYS	2.4
1	А	73	TYR	2.4
1	А	209	GLU	2.3
1	А	115	TYR	2.2
1	А	117	GLY	2.2
1	А	175	GLN	2.2

## 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	$Q{<}0.9$
2	CIT	А	601	13/13	0.84	0.20	$52,\!56,\!59,\!59$	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

