



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 09:40 AM BST

PDB ID : 6YBR  
Title : RT structure of Glucose Isomerase obtained at 1.20 Å resolution from crystal grown in a Mylar microchip.  
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Deposited on : 2020-03-17  
Resolution : 1.20 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](mailto: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.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.13  
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) : 2.13

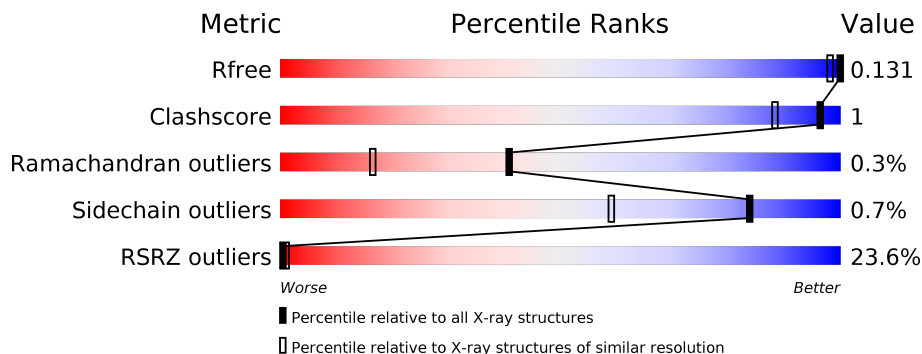
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.20 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	1223 (1.22-1.18)
Clashscore	141614	1286 (1.22-1.18)
Ramachandran outliers	138981	1240 (1.22-1.18)
Sidechain outliers	138945	1239 (1.22-1.18)
RSRZ outliers	127900	1200 (1.22-1.18)

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  $\geq 3$ , 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	388	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3703 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 Xylose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	385	3403	2126	621	646	10	0	46	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Na	0	0
			2	2		

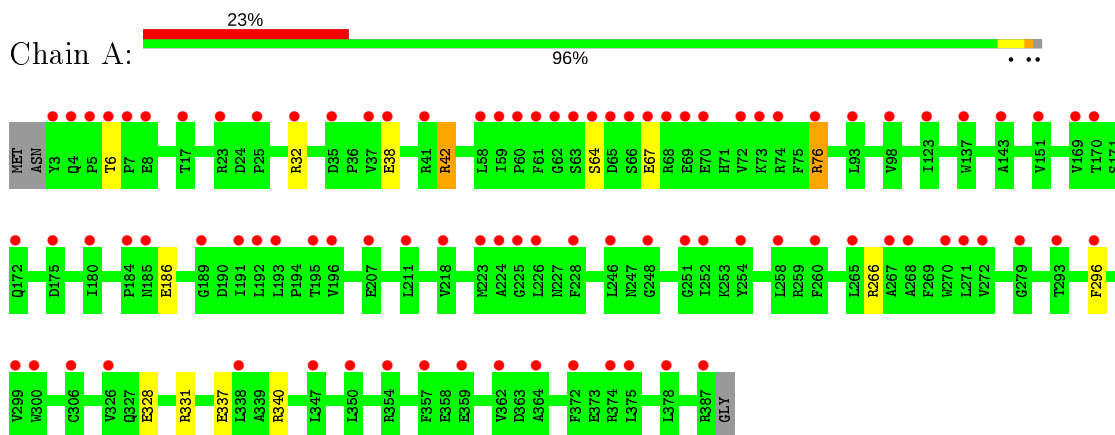
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	291	Total	O	0	5
			296	296		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Xylose isomerase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.99Å 99.38Å 103.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.99 – 1.20 46.99 – 1.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.99-1.20) 100.0 (46.99-1.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.56 (at 1.20Å)	Xtrriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.121 , 0.131 0.121 , 0.131	Depositor DCC
$R_{free}$ test set	7490 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.9	Xtrriage
Anisotropy	0.245	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.008 for -h,-l,-k	Xtrriage
$F_o, F_c$ correlation	0.99	EDS
Total number of atoms	3703	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: NA, MG

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	0.32	0/3507	0.63	2/4737 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	266	ARG	NE-CZ-NH1	-7.67	116.47	120.30
1	A	266	ARG	NE-CZ-NH2	6.01	123.30	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	3403	0	3264	7	0
2	A	2	0	0	0	0
3	A	2	0	0	0	0
4	A	296	0	0	2	2
All	All	3703	0	3264	7	2

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 (7) 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:38[B]:GLU:OE2	1:A:42[B]:ARG:NH1	2.17	0.77
1:A:328[B]:GLU:OE2	1:A:331[B]:ARG:NH2	2.33	0.56
1:A:6:THR:OG1	4:A:501:HOH:O	2.21	0.46
1:A:337:GLU:HG2	1:A:340[A]:ARG:NH2	2.31	0.45
1:A:64:SER:OG	1:A:67[B]:GLU:HG2	2.17	0.44
1:A:32[A]:ARG:HG2	1:A:296:PHE:HE2	1.85	0.42
1:A:76[B]:ARG:HD2	4:A:506:HOH:O	2.19	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:509:HOH:O	4:A:537:HOH:O[3_557]	2.10	0.10
4:A:525:HOH:O	4:A:724:HOH:O[4_557]	2.14	0.06

## 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	A	429/388 (111%)	415 (97%)	12 (3%)	2 (0%)	29 7

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186[A]	GLU
1	A	186[B]	GLU

### 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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	347/304 (114%)	343 (99%)	4 (1%)	71 37

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42[A]	ARG
1	A	42[B]	ARG
1	A	76[A]	ARG
1	A	76[B]	ARG

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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	385/388 (99%)	1.47	91 (23%) <b>0</b> <b>1</b>	12, 18, 35, 52	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	66[A]	SER	6.1
1	A	65[A]	ASP	5.0
1	A	62	GLY	4.2
1	A	252	ILE	4.2
1	A	61	PHE	4.0
1	A	357	PHE	4.0
1	A	70[A]	GLU	3.9
1	A	64	SER	3.8
1	A	23[A]	ARG	3.6
1	A	7	PRO	3.6
1	A	359	GLU	3.5
1	A	296	PHE	3.5
1	A	226	LEU	3.4
1	A	362[A]	VAL	3.4
1	A	4[A]	GLN	3.3
1	A	224	ALA	3.3
1	A	218	VAL	3.3
1	A	254	TYR	3.3
1	A	191	ILE	3.2
1	A	32[A]	ARG	3.2
1	A	354	ARG	3.2
1	A	69[A]	GLU	3.2
1	A	196[A]	VAL	3.2
1	A	387	ARG	3.1
1	A	258	LEU	3.0
1	A	74	ARG	3.0
1	A	68	ARG	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	3	TYR	2.8
1	A	170[A]	THR	2.8
1	A	211	LEU	2.8
1	A	67[A]	GLU	2.7
1	A	192	LEU	2.7
1	A	175[A]	ASP	2.7
1	A	279	GLY	2.6
1	A	41[A]	ARG	2.6
1	A	72	VAL	2.6
1	A	364	ALA	2.6
1	A	25[A]	PRO	2.5
1	A	123	ILE	2.5
1	A	223	MET	2.5
1	A	6	THR	2.4
1	A	38[A]	GLU	2.4
1	A	267	ALA	2.4
1	A	265	LEU	2.4
1	A	60	PRO	2.4
1	A	73[A]	LYS	2.4
1	A	207[A]	GLU	2.4
1	A	93	LEU	2.3
1	A	184	PRO	2.3
1	A	137	TRP	2.3
1	A	306	CYS	2.3
1	A	5	PRO	2.2
1	A	189	GLY	2.2
1	A	293	THR	2.2
1	A	268	ALA	2.2
1	A	195	THR	2.2
1	A	8[A]	GLU	2.2
1	A	228	PHE	2.2
1	A	260	PHE	2.2
1	A	374[A]	ARG	2.2
1	A	37	VAL	2.2
1	A	299	VAL	2.2
1	A	372	PHE	2.1
1	A	193	LEU	2.1
1	A	246	LEU	2.1
1	A	350	LEU	2.1
1	A	169[A]	VAL	2.1
1	A	326	VAL	2.1
1	A	270	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	300	TRP	2.1
1	A	172	GLN	2.1
1	A	271	LEU	2.1
1	A	35[A]	ASP	2.1
1	A	17	THR	2.1
1	A	59	ILE	2.1
1	A	76[A]	ARG	2.1
1	A	375	LEU	2.1
1	A	185	ASN	2.1
1	A	63	SER	2.1
1	A	180	ILE	2.1
1	A	248	GLY	2.0
1	A	347	LEU	2.0
1	A	98	VAL	2.0
1	A	151	VAL	2.0
1	A	225	GLY	2.0
1	A	251	GLY	2.0
1	A	272	VAL	2.0
1	A	143	ALA	2.0
1	A	58	LEU	2.0
1	A	338	LEU	2.0
1	A	378	LEU	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 monosaccharides 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	MG	A	402	1/1	0.97	0.42	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NA	A	403	1/1	0.99	0.09	28,28,28,28	0
3	NA	A	404	1/1	1.00	0.16	18,18,18,18	0
2	MG	A	401	1/1	1.00	0.35	8,8,8,8	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.