



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 19, 2023 – 08:52 PM JST

PDB ID : 7BWG  
Title : A Glycoside Hydrolase Family 20 beta-N-Acetylglucosaminidase  
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Deposited on : 2020-04-14  
Resolution : 2.85 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.36  
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) : 2.36

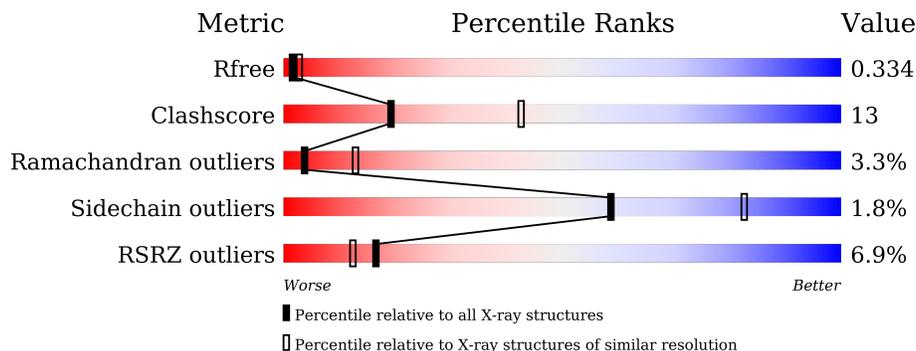
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 of 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	532	
1	B	532	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6618 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 Beta-N-acetylhexosaminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	485	3316	2113	565	631	7	0	0	0
1	B	473	3284	2103	558	616	7	0	0	0

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A1W6AQA7
A	2	GLU	-	expression tag	UNP A0A1W6AQA7
A	3	LEU	-	expression tag	UNP A0A1W6AQA7
A	4	ALA	-	expression tag	UNP A0A1W6AQA7
A	5	LEU	-	expression tag	UNP A0A1W6AQA7
A	521	LYS	-	expression tag	UNP A0A1W6AQA7
A	522	GLY	-	expression tag	UNP A0A1W6AQA7
A	523	GLN	-	expression tag	UNP A0A1W6AQA7
A	524	PHE	-	expression tag	UNP A0A1W6AQA7
A	525	LEU	-	expression tag	UNP A0A1W6AQA7
A	526	GLU	-	expression tag	UNP A0A1W6AQA7
A	527	HIS	-	expression tag	UNP A0A1W6AQA7
A	528	HIS	-	expression tag	UNP A0A1W6AQA7
A	529	HIS	-	expression tag	UNP A0A1W6AQA7
A	530	HIS	-	expression tag	UNP A0A1W6AQA7
A	531	HIS	-	expression tag	UNP A0A1W6AQA7
A	532	HIS	-	expression tag	UNP A0A1W6AQA7
B	1	MET	-	initiating methionine	UNP A0A1W6AQA7
B	2	GLU	-	expression tag	UNP A0A1W6AQA7
B	3	LEU	-	expression tag	UNP A0A1W6AQA7
B	4	ALA	-	expression tag	UNP A0A1W6AQA7
B	5	LEU	-	expression tag	UNP A0A1W6AQA7
B	521	LYS	-	expression tag	UNP A0A1W6AQA7
B	522	GLY	-	expression tag	UNP A0A1W6AQA7
B	523	GLN	-	expression tag	UNP A0A1W6AQA7

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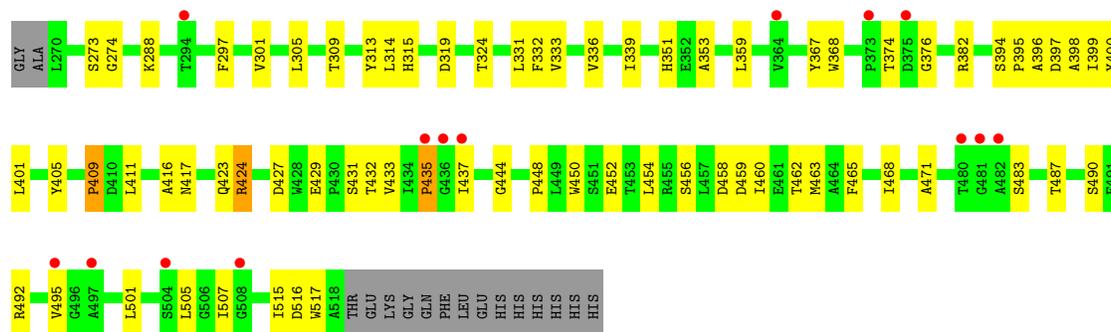
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Chain	Residue	Modelled	Actual	Comment	Reference
B	524	PHE	-	expression tag	UNP A0A1W6AQA7
B	525	LEU	-	expression tag	UNP A0A1W6AQA7
B	526	GLU	-	expression tag	UNP A0A1W6AQA7
B	527	HIS	-	expression tag	UNP A0A1W6AQA7
B	528	HIS	-	expression tag	UNP A0A1W6AQA7
B	529	HIS	-	expression tag	UNP A0A1W6AQA7
B	530	HIS	-	expression tag	UNP A0A1W6AQA7
B	531	HIS	-	expression tag	UNP A0A1W6AQA7
B	532	HIS	-	expression tag	UNP A0A1W6AQA7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	7	Total O 7 7	0	0
2	B	11	Total O 11 11	0	0





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.03Å 81.93Å 79.42Å 90.00° 94.08° 90.00°	Depositor
Resolution (Å)	57.61 – 2.85 57.61 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.6 (57.61-2.85) 99.7 (57.61-2.85)	Depositor EDS
$R_{merge}$	0.23	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.94 (at 2.86Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.292 , 0.335 0.292 , 0.334	Depositor DCC
$R_{free}$ test set	1190 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.0	Xtrriage
Anisotropy	0.839	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 42.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.000 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.81	EDS
Total number of atoms	6618	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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](#)

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	0.25	0/3400	0.45	0/4673
1	B	0.26	0/3372	0.45	0/4636
All	All	0.25	0/6772	0.45	0/9309

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	3
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	465	PHE	Peptide
1	B	235	MET	Peptide
1	B	257	ASP	Peptide
1	B	374	THR	Peptide

### 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	3316	0	2976	73	0
1	B	3284	0	2995	89	0
2	A	7	0	0	0	0
2	B	11	0	0	0	0
All	All	6618	0	5971	162	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 13.

The worst 5 of 162 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:78:LEU:HB3	1:A:108:LEU:HD21	1.73	0.69
1:B:147:ASP:HA	1:B:176:HIS:HB3	1.74	0.69
1:A:87:GLU:HG3	1:A:137:PRO:HG2	1.75	0.69
1:A:231:PRO:HG3	1:A:309:THR:HG21	1.72	0.69
1:B:454:LEU:HD23	1:B:460:ILE:HA	1.75	0.67

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	A	477/532 (90%)	426 (89%)	33 (7%)	18 (4%)	<b>3</b>   <b>10</b>
1	B	463/532 (87%)	420 (91%)	30 (6%)	13 (3%)	<b>5</b>   <b>16</b>
All	All	940/1064 (88%)	846 (90%)	63 (7%)	31 (3%)	<b>4</b>   <b>13</b>

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	260	ARG

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Mol	Chain	Res	Type
1	A	373	PRO
1	A	375	ASP
1	A	416	ALA
1	A	435	PRO

### 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	279/393 (71%)	274 (98%)	5 (2%)	59	82
1	B	286/393 (73%)	281 (98%)	5 (2%)	60	83
All	All	565/786 (72%)	555 (98%)	10 (2%)	59	82

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	411	LEU
1	B	424	ARG
1	B	516	ASP
1	A	257	ASP
1	A	411	LEU

Sometimes 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](#)

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, 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	485/532 (91%)	0.76	32 (6%) 18 14	15, 27, 43, 57	0
1	B	473/532 (88%)	0.73	34 (7%) 15 11	15, 26, 42, 62	0
All	All	958/1064 (90%)	0.75	66 (6%) 16 12	15, 27, 43, 62	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	508	GLY	4.2
1	B	98	VAL	4.0
1	A	32	ALA	3.8
1	A	235	MET	3.8
1	A	21	ALA	3.4

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.