Full wwPDB X-ray Structure Validation Report (i)

Dec 4, 2023 – 05:27 am GMT

PDB ID	:	2VN4
Title	:	Glycoside Hydrolase Family 15 Glucoamylase from Hypocrea jecorina
Authors	:	Bott, R.; Sandgren, M.; Hansson, H.
Deposited on	:	2008-01-30
Resolution	:	1.85 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 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
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
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 (i)

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

The reported resolution of this entry is 1.85 Å.

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

MolProbity failed to run properly; EDS was not executed - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5122 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.

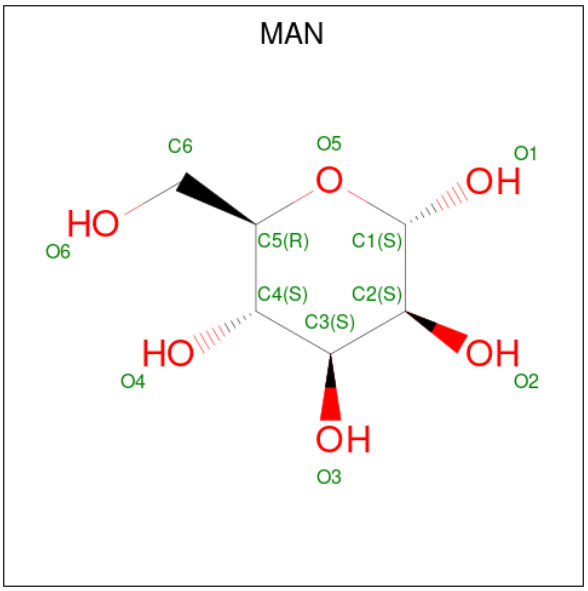
- Molecule 1 is a protein called GLUCOAMYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	599	4603	2910	763	919	11	0	21	0

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

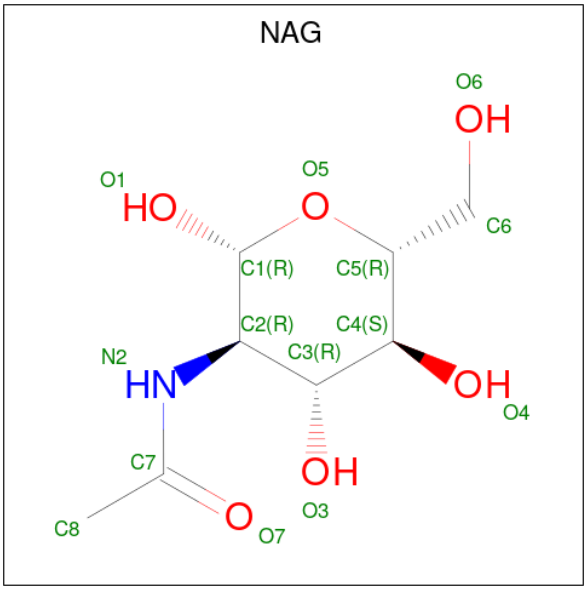
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0

- Molecule 3 is alpha-D-mannopyranose (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



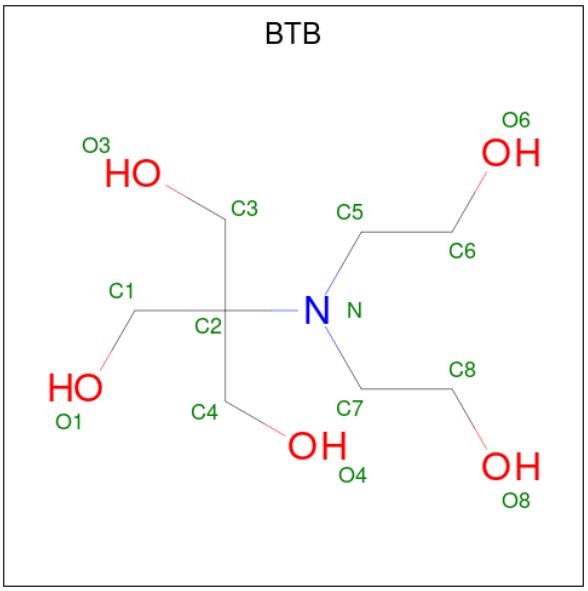
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0
			Total	C	O			
3	A	1	11	6	5		0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	14	8	1	5	0	0

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	14	8	1	5	0	0
			Total	C	N	O		
5	A	1	14	8	1	5	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	361	361	361	0	0

MolProbity failed to run properly; EDS was not executed - this section is therefore empty.

3 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	52.19Å 99.23Å 121.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.70 – 1.85	Depositor
% Data completeness (in resolution range)	98.1 (76.70-1.85)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.154 , 0.182	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5122	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

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)

2 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	B	1	2,1	14,14,15	0.52	0	17,19,21	1.10	2 (11%)
2	NAG	B	2	2	14,14,15	0.52	0	17,19,21	0.87	1 (5%)

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	NAG	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	NAG	O5-C1-C2	-2.78	106.91	111.29
2	B	1	NAG	C1-O5-C5	2.68	115.82	112.19
2	B	2	NAG	O5-C1-C2	-2.01	108.12	111.29

There are no chirality outliers.

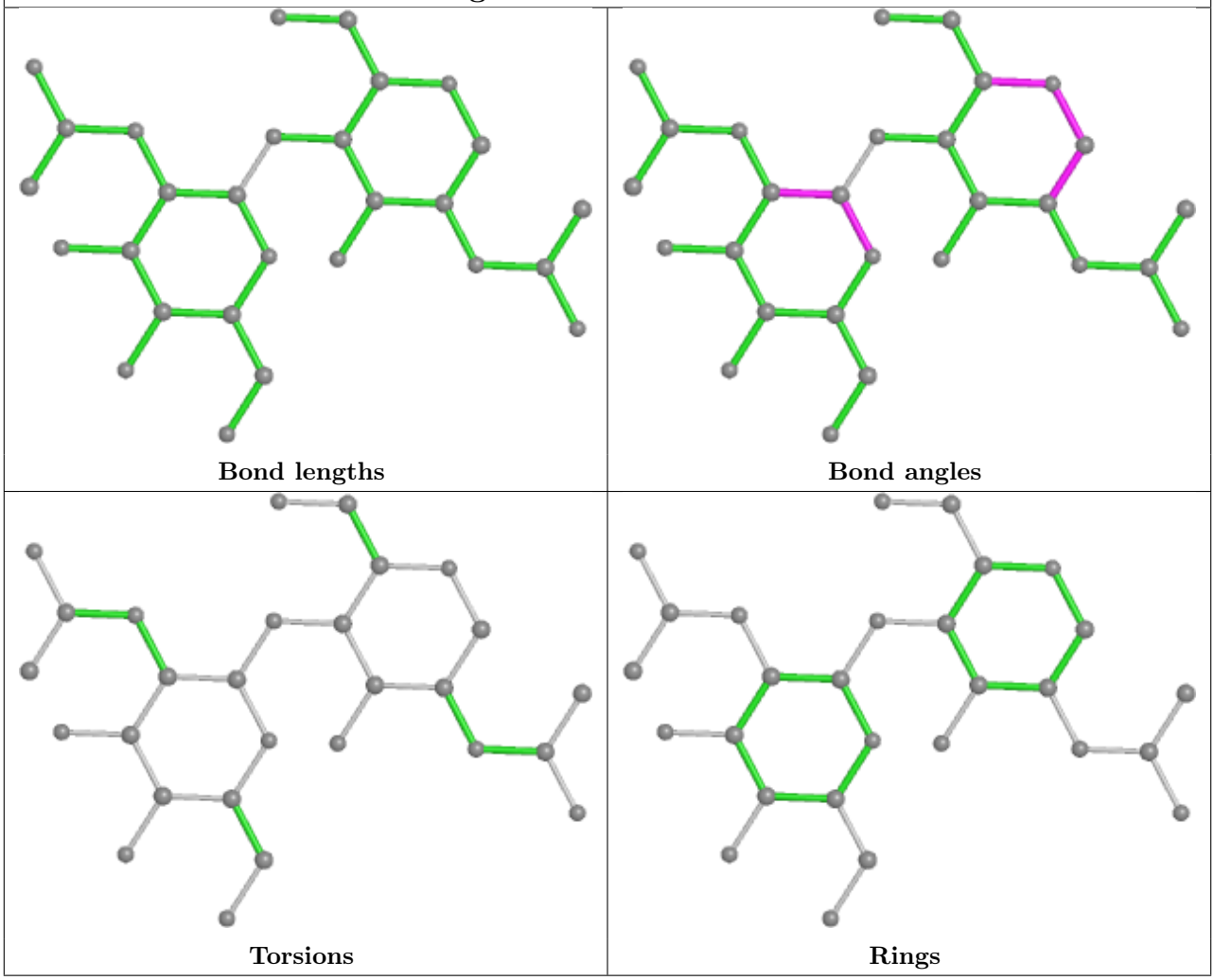
There are no torsion outliers.

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.

Oligosaccharide Chain B



4.6 Ligand geometry (i)

11 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	MAN	A	601	1	11,11,12	0.49	0	15,15,17	0.94	1 (6%)
3	MAN	A	605	1	11,11,12	0.54	0	15,15,17	0.88	1 (6%)
5	BTB	A	620	-	13,13,13	0.70	0	7,16,16	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	MAN	A	602	1	11,11,12	0.70	0	15,15,17	0.76	0
3	MAN	A	603	1	11,11,12	0.52	0	15,15,17	1.18	1 (6%)
4	NAG	A	613	1	14,14,15	0.53	0	17,19,21	1.02	1 (5%)
3	MAN	A	607	1	11,11,12	0.57	0	15,15,17	1.10	3 (20%)
3	MAN	A	609	1	11,11,12	0.61	0	15,15,17	1.02	1 (6%)
5	BTB	A	621	-	13,13,13	0.58	0	7,16,16	0.60	0
3	MAN	A	606	1	11,11,12	0.66	0	15,15,17	1.44	2 (13%)
3	MAN	A	608	1	11,11,12	0.51	0	15,15,17	1.00	1 (6%)

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	MAN	A	601	1	-	0/2/19/22	0/1/1/1
3	MAN	A	605	1	-	0/2/19/22	0/1/1/1
5	BTB	A	620	-	-	0/21/21/21	-
3	MAN	A	602	1	-	2/2/19/22	0/1/1/1
3	MAN	A	603	1	-	2/2/19/22	0/1/1/1
4	NAG	A	613	1	-	4/6/23/26	0/1/1/1
3	MAN	A	607	1	-	2/2/19/22	0/1/1/1
3	MAN	A	609	1	-	1/2/19/22	0/1/1/1
5	BTB	A	621	-	-	0/21/21/21	-
3	MAN	A	606	1	-	0/2/19/22	0/1/1/1
3	MAN	A	608	1	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	606	MAN	C1-O5-C5	3.99	117.60	112.19
3	A	603	MAN	C1-O5-C5	3.89	117.47	112.19
3	A	606	MAN	C1-C2-C3	2.97	113.31	109.67
3	A	607	MAN	O5-C5-C6	2.51	111.14	107.20
3	A	605	MAN	C1-O5-C5	2.41	115.46	112.19
3	A	609	MAN	C1-C2-C3	2.41	112.63	109.67
3	A	607	MAN	C1-O5-C5	2.39	115.43	112.19
3	A	608	MAN	O5-C5-C6	2.09	110.48	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	613	NAG	O5-C1-C2	-2.02	108.10	111.29
3	A	607	MAN	C1-C2-C3	2.02	112.15	109.67
3	A	601	MAN	O5-C1-C2	-2.00	107.68	110.77

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	603	MAN	O5-C5-C6-O6
3	A	608	MAN	O5-C5-C6-O6
3	A	602	MAN	C4-C5-C6-O6
4	A	613	NAG	C4-C5-C6-O6
3	A	607	MAN	O5-C5-C6-O6
3	A	603	MAN	C4-C5-C6-O6
3	A	602	MAN	O5-C5-C6-O6
4	A	613	NAG	O5-C5-C6-O6
4	A	613	NAG	C8-C7-N2-C2
3	A	608	MAN	C4-C5-C6-O6
3	A	607	MAN	C4-C5-C6-O6
4	A	613	NAG	O7-C7-N2-C2
3	A	609	MAN	C4-C5-C6-O6

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 was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

5.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

5.4 Ligands (i)

EDS was not executed - this section is therefore empty.

5.5 Other polymers (i)

EDS was not executed - this section is therefore empty.