



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 05:23 AM BST

PDB ID : 1HYA  
Title : HYALURONIC ACID, STRUCTURE OF A FULLY EXTENDED 3-FOLD  
HELICAL SODIUM SALT AND COMPARISON WITH THE LESS EX-  
TENDED 4-FOLD HELICAL FORMS  
Authors : Arnott, S.  
Deposited on : 1977-11-20  
Resolution : 3.00 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.

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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  
Mogul : 1.8.5 (274361), 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) : 2.13.1

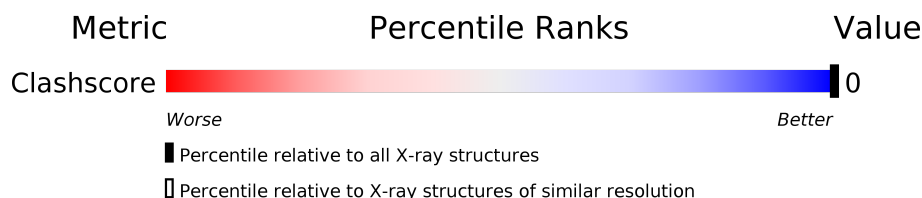
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
Clashscore	141614	2416 (3.00-3.00)

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  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	6	 50% 50%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	GCU	A	1	-	-	X	-
1	NAG	A	2	-	-	X	-
1	GCU	A	3	X	-	X	-
1	NAG	A	4	-	-	X	-
1	GCU	A	5	X	-	X	-
1	NAG	A	6	-	-	X	-
2	NA	A	771	-	-	X	-
2	NA	A	772	-	-	X	-
2	NA	A	773	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 141 atoms, of which 48 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 an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranuronic acid.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	6	Total	C	H	N	O	0	0	0
			126	42	48	3	33			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		

### 3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

- Molecule 1: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranuronic acid

Chain A: 

GCU1
MA62
GCU3
MA64
GCU5
MA66

## 4 Data and refinement statistics

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

Property	Value
Space group	P 32 2 1
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	11.70 Å 11.70 Å 28.50 Å 90.00° 90.00° 120.00°
Resolution (Å)	(Not available) – 3.00
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)
$R_{merge}$	(Not available)
$R_{sym}$	(Not available)
Refinement program	LINKED-ATOM LEAST-SQUARES MODEL-BUILDING PROCEDURE, L
R, $R_{free}$	(Not available) , (Not available)
Estimated twinning fraction	No twinning to report.
Total number of atoms	141
Average B, all atoms (Å <sup>2</sup> )	0.0

## 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, GCU, NAG

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	A	78	48	55	0	391
2	A	3	0	0	0	3
3	A	12	0	0	0	6
All	All	93	48	55	0	400

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 0.

There are no clashes within the asymmetric unit.

The worst 5 of 400 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)
1:A:4:NAG:O4	1:A:6:NAG:O4[2_654]	0.00	2.20
1:A:4:NAG:C2	1:A:6:NAG:C2[2_654]	0.00	2.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:NAG:O5	1:A:6:NAG:O5[2_654]	0.00	2.20
3:A:993:HOH:O	3:A:1001:HOH:O[3_664]	0.00	2.20
1:A:1:GCU:O6A	1:A:3:GCU:O6A[2_654]	0.00	2.20

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

### 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](#)

6 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	$\# Z  > 2$
1	GCU	A	1	1	9,12,13	0.22	0	12,17,19	0.47	0
1	NAG	A	2	1	14,14,15	0.49	0	17,19,21	0.92	1 (5%)
1	GCU	A	3	1	9,12,13	0.21	0	12,17,19	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	NAG	A	4	1	14,14,15	0.50	0	17,19,21	0.93	1 (5%)
1	GCU	A	5	1	9,12,13	0.21	0	12,17,19	0.47	0
1	NAG	A	6	1	14,14,15	0.50	0	17,19,21	0.93	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
1	GCU	A	1	1	-	0/0/21/24	0/1/1/1
1	NAG	A	2	1	-	0/6/23/26	0/1/1/1
1	GCU	A	3	1	1/1/6/6	0/0/21/24	0/1/1/1
1	NAG	A	4	1	-	0/6/23/26	0/1/1/1
1	GCU	A	5	1	1/1/6/6	0/0/21/24	0/1/1/1
1	NAG	A	6	1	-	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(°)	Ideal(°)
1	A	6	NAG	C2-N2-C7	-2.81	118.90	122.90
1	A	4	NAG	C2-N2-C7	-2.81	118.91	122.90
1	A	2	NAG	C2-N2-C7	-2.79	118.93	122.90

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	3	GCU	C1
1	A	5	GCU	C1

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 391 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	6	NAG	0	155
1	A	4	NAG	0	154
1	A	2	NAG	0	154
1	A	3	GCU	0	106

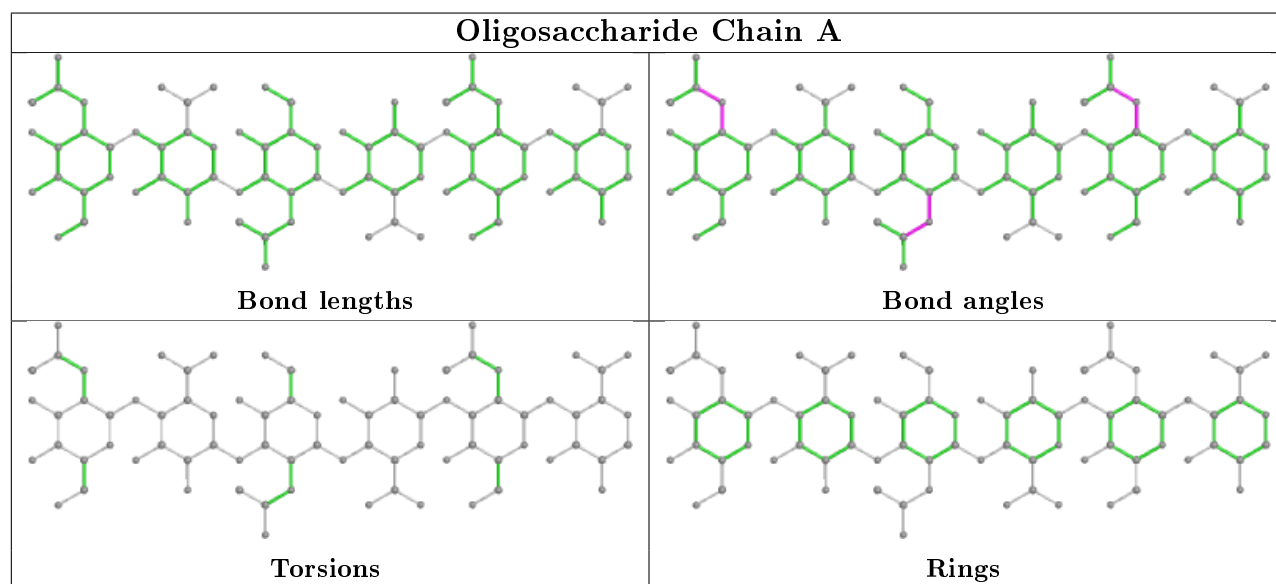
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	5	GCU	0	106
1	A	1	GCU	0	107

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 ⓘ

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.