

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2BVK
Title	:	Hyaluronan: the local solution conformation determined by NMR and com-
		puter modelling is close to a contracted left-handed four-fold helix
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Deposited on	:	2005-06-30

This is a wwPDB NMR Structure Validation Summary 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/NMRValidationReportHelp 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 (1)) were used in the production of this report:

MolProbity		
Mogul	:	1.8.4, CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

Clashscore

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: SOLUTION NMR, THEORETICAL MODEL

The overall completeness of chemical shifts assignment was not calculated.

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.

Metri	2	Percentile	Percentile Ranks				
Clashscore				0			
	Worse			Better			
	Percentile relative to all str	ructures					
	Percentile relative to all NI	MR structures					
Mada	Whole a	rchive	NMR archive				
Metri	c (#Entr	ries)	(# Entries)				

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The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

12864

Mol	Chain	Length	Quality of chain
1	Р	8	100%



2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 169 atoms, of which 64 are hydrogens and 0 are deuteriums.

• Molecule 1 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-bet a-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-gl ucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-glucopy ranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-glucopyranur onic acid.

																	((
β4	\bigtriangledown	β	3	β	4 🗸	β	3	β	4	\bigvee	β	3	β	4	\searrow	β)

Mol	Chain	Residues		Atoms					
1	D	0	Total	С	Η	Ν	0	0	
	I P	8	169	56	64	4	45	0	



4 Residue-property plots (i)

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

 $\label{eq:constraint} \bullet \mbox{Molecule 1: } 2\mbox{-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranuronic aci$

Chain P:

100%

BDP1 NAG2 BDP3 NAG4 BDP5 BDP5 NAG6 BDP7 NAG8



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *MOLECULAR DYNAMICS CONFIRMED* BY BA CALCULATION OF EXPERIMENTAL NMR PA.

Of the 250000 calculated structures, 1 were deposited, based on the following criterion: AVER-AGE CONFORMATION FROM A 50 NAN MOLECULAR DYNAMICS TRAJECTORY THAT EXPLICIT SOLVENT WATER AND CHARGE SODIUM IONS. THE 1-3 AND 1-4 LINKA FIXED AT (50.78, 9.78) AND (47.98, RESPECTIVELY USING THE H1-C1-OX-HX NOMEN-CLATURE.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CHARMM	refinement	
CHARMM	structure solution	

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BDP

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
All	All	105	64	75	-

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is -.

There are no clashes.

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

There are no protein molecules in this entry.

6.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

6.3.3 RNA (i)

There are no RNA molecules in this entry.



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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates (i)

8 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Tuno	vpe Chain Res Link			Bo	nd lengt	ths
MOI	Type	Ullalli	nes		Counts	RMSZ	#Z>2
1	BDP	Р	1	1	13,13,13	0.76	1 (7%)
1	NAG	Р	2	1	14,14,15	0.73	0 (0%)
1	BDP	Р	3	1	12,12,13	0.82	1 (8%)
1	NAG	Р	4	1	14,14,15	0.73	0 (0%)
1	BDP	Р	5	1	12,12,13	0.83	1 (8%)
1	NAG	Р	6	1	14,14,15	0.59	0 (0%)
1	BDP	Р	7	1	12,12,13	0.83	1 (8%)
1	NAG	Р	8	1	14,14,15	0.49	0 (0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res Link		B	ond ang	les
	туре	Unam	nes	LIIIK	Counts	RMSZ	#Z>2
1	BDP	Р	1	1	$18,\!19,\!19$	0.74	0 (0%)
1	NAG	Р	2	1	$17,\!19,\!21$	1.03	2 (11%)
1	BDP	Р	3	1	$14,\!17,\!19$	0.74	0 (0%)
1	NAG	Р	4	1	17,19,21	1.02	2 (11%)
1	BDP	Р	5	1	$14,\!17,\!19$	0.73	0 (0%)
1	NAG	Р	6	1	$17,\!19,\!21$	1.01	2 (11%)
1	BDP	Р	7	1	$14,\!17,\!19$	0.73	0 (0%)



Mol	Turne	Chain	Res	Link	Bond angles				
	туре				Counts	RMSZ	#Z>2		
1	NAG	Р	8	1	17,19,21	1.01	2 (11%)		

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	BDP	Р	1	1	-	$0,\!4,\!24,\!24$	0,1,1,1
1	NAG	Р	2	1	-	0,6,23,26	0,1,1,1
1	BDP	Р	3	1	-	0,4,21,24	0,1,1,1
1	NAG	Р	4	1	-	$0,\!6,\!23,\!26$	0,1,1,1
1	BDP	Р	5	1	-	0,4,21,24	0,1,1,1
1	NAG	Р	6	1	-	$0,\!6,\!23,\!26$	0,1,1,1
1	BDP	Р	7	1	-	0,4,21,24	0,1,1,1
1	NAG	Р	8	1	_	$0,\!6,\!23,\!26$	0,1,1,1

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	Р	7	BDP	O6B-C6	2.11	1.23	1.30
1	Р	5	BDP	O6B-C6	2.10	1.23	1.30
1	Р	1	BDP	O6B-C6	2.10	1.23	1.30
1	Р	3	BDP	O6B-C6	2.10	1.23	1.30

5 of 8 angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	Р	8	NAG	C8-C7-N2	2.10	112.54	116.10
1	Р	4	NAG	O7-C7-N2	2.10	125.81	121.95
1	Р	4	NAG	C8-C7-N2	2.10	112.55	116.10
1	Р	2	NAG	O7-C7-N2	2.08	125.78	121.95
1	Р	8	NAG	O7-C7-N2	2.08	125.78	121.95

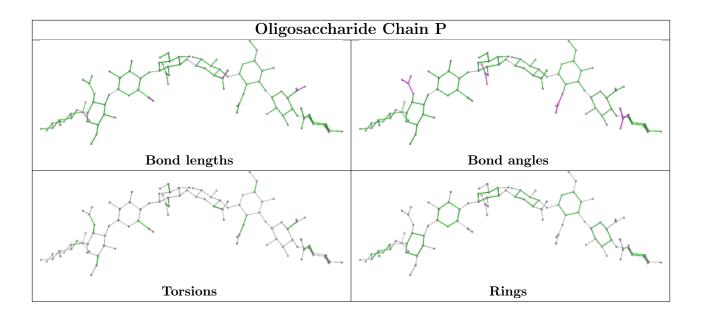
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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





6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



7 Chemical shift validation (i)

No chemical shift data were provided

