

Full wwPDB NMR Structure Validation Report (i)

Aug 6, 2020 – 08:47 AM BST

PDB ID : 1ZNT

Title : 18 NMR structures of AcAMP2-Like Peptide with non Natural Fluoroaromatic

Residue (AcAMP2F18Pff/Y20Pff) complex with N,N,N-triacetylchitotriose

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Deposited on : 2005-05-12

This is a Full wwPDB NMR 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

ShiftChecker : 2.13.1

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

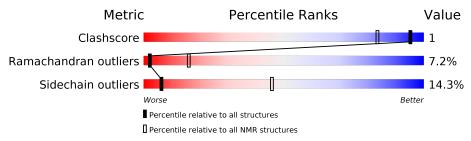
Validation Pipeline (wwPDB-VP) : 2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

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.



Metric	$egin{array}{c} ext{Whole archive} \ (\# ext{Entries}) \end{array}$	$ m NMR~archive \ (\#Entries)$
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length	Quality of chain					
1	A	31	65% 13% 23%					
2	В	3	100%					



2 Ensemble composition and analysis (i)

This entry contains 18 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: fewest violations.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues									
Well-defined core	Well-defined core Residue range (total) Backbone RMSD (Å) Medoid model								
1	A:3-A:17, A:19-A:19, A:21-	0.46	7						
	A:28 (24)								

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 1 single-model cluster was found.

Cluster number	Models
1	2, 3, 4, 7, 9, 10, 11, 12, 14, 15, 16, 17
2	1, 13, 18
3	5, 8
Single-model clusters	6



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 506 atoms, of which 245 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2.

Mol	Chain	Residues		${f Atoms}$					Trace	
1	Λ	2.1	Total	С	F	Н	N	О	S	1
1	A	91	422	130	2	204	43	36	7	1

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



Mol	Chain	Residues	Atoms					Trace
9	D	2	Total	С	Н	N	О	0
2	D	ა	84	24	41	3	16	U

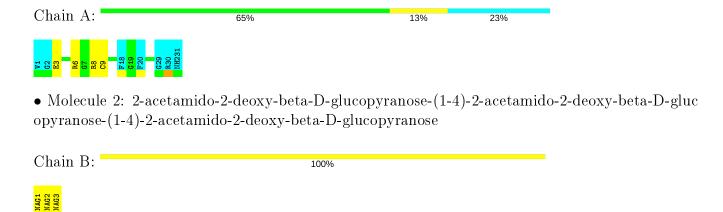


4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

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.

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





NAG1 NAG2 NAG3

4.2.2 Score per residue for model 2

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2

Chain A: 61% 10% • • 23%

• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

NAG1 NAG2 NAG3

4.2.3 Score per residue for model 3

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2

Chain A: 61% 13% • 23%

 $\bullet \ \, \text{Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2$

Chain B:

NAG1 NAG2 NAG3

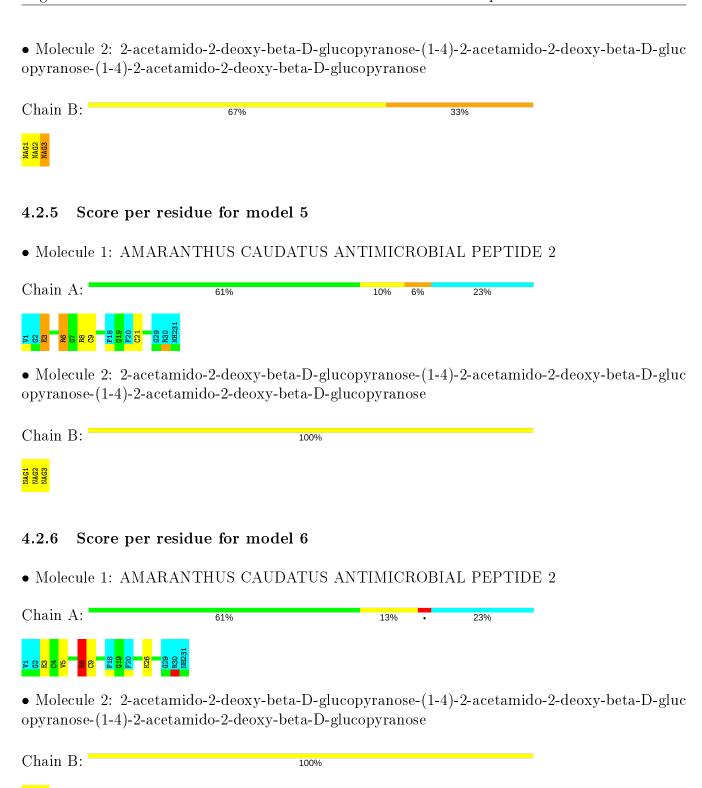
4.2.4 Score per residue for model 4

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2

Chain A: 58% 19% 23%



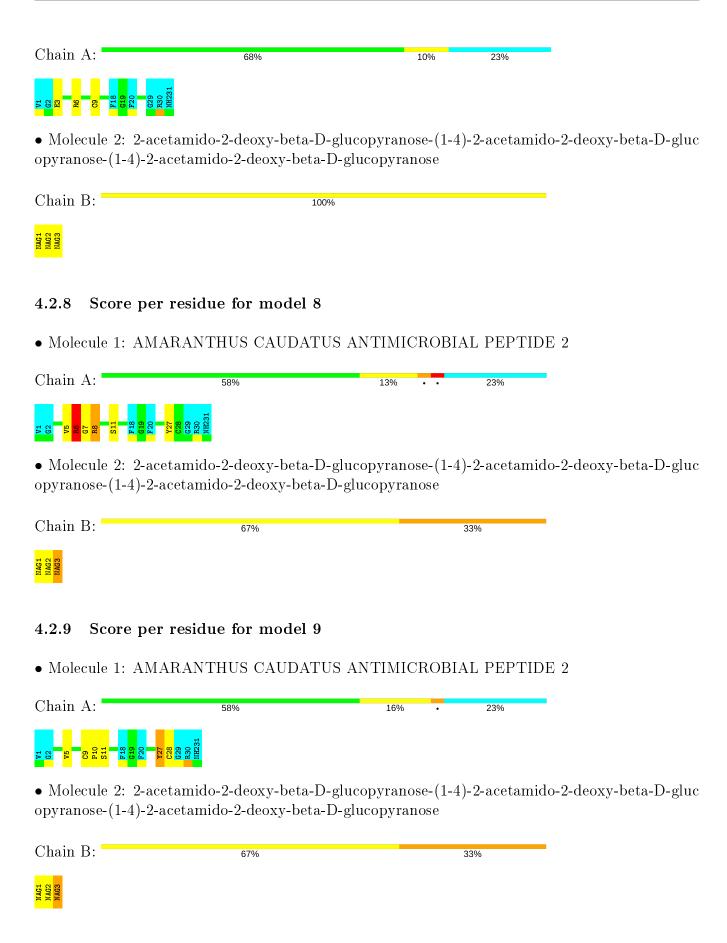




4.2.7 Score per residue for model 7 (medoid)

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2







4.2.10 Score per residue for model 10

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 100%

NAG1 NAG2 NAG3

4.2.11 Score per residue for model 11

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 100%

NAG1 NAG2 NAG3

4.2.12 Score per residue for model 12

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

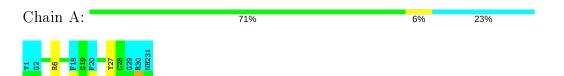
Chain B: 67% 33%





4.2.13 Score per residue for model 13

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 100%



4.2.14 Score per residue for model 14

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2

Chain A: 61% 10% 6% 23%

 $\bullet \ \, Molecule \ 2: \ 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \\$

Chain B:

NAG1 NAG2 NAG3

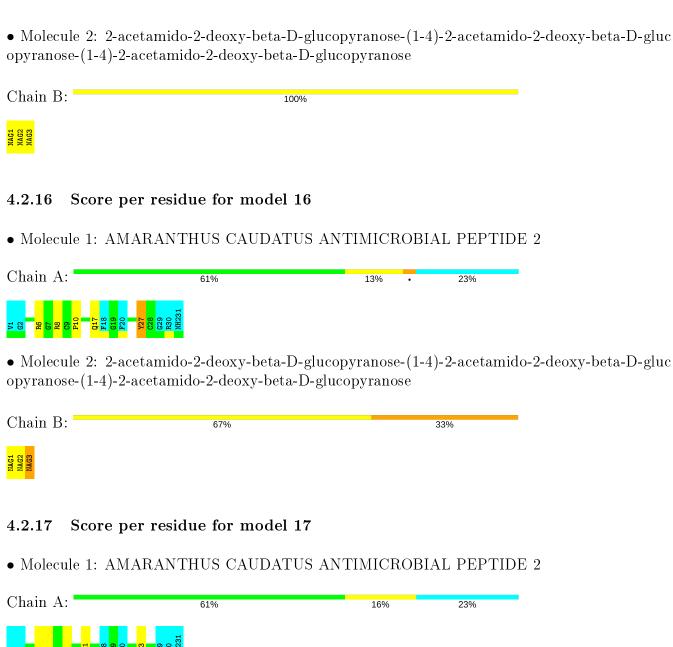
4.2.15 Score per residue for model 15

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2











• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-gluc opyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

4.2.18Score per residue for model 18

• Molecule 1: AMARANTHUS CAUDATUS ANTIMICROBIAL PEPTIDE 2



Chain A: 65% 13% 23%

 $\bullet \ \, \text{Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2$

Chain B:

NAG1 NAG2 NAG3



5 Refinement protocol and experimental data overview (i)



The models were refined using the following method: The structures are based on a total 314 cross peaks, 248 NOE-derived distance restraints, and finally 208 distance constraints and 18 come from cys-cys disulfide were used in the final round of calculation.

Of the 30 calculated structures, 18 were deposited, based on the following criterion: Fewest restraint violation, secondary lowest energy.

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

Software name	Classification	Version
DYANA	structure solution	1.5
Amber	refinement	5.0

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.



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: PFF, NAG, NH2

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 (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol Chain		E	ond lengths	Bond angles		
MIOI	Chain	RMSZ	#Z>5	RMSZ	#Z>5	
1	A	0.57 ± 0.01	$0\pm0/168~(~0.0\pm~0.0\%)$	1.13 ± 0.10	$1\pm1/219~(~0.4\pm~0.3\%)$	
All	All	0.57	0/3024 (0.0%)	1.13	16/3942 (0.4%)	

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	Planarity
1	A	0.0 ± 0.0	0.6 ± 0.6
All	All	0	10

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	$\begin{array}{c cccc} \textbf{Chain} & \textbf{Res} & \textbf{Type} & \textbf{Atoms} & \textbf{Z} & \textbf{Observed}(^o) \end{array}$		Type Atoms 7 Observed		$Observed(^o)$	$\mathrm{Ideal}(^{o})$	Mod	dels	
10101	Chain	nes	туре	Atoms	L	Observed(')	rved(°) Ideal(°)		Total
1	A	6	ARG	NE-CZ-NH1	10.42	125.51	120.30	8	4
1	A	8	ARG	NE-CZ-NH1	7.95	124.27	120.30	10	10
1	A	6	ARG	NE-CZ-NH2	5.52	123.06	120.30	4	2

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	6	ARG	Sidechain	4
1	A	27	TYR	Sidechain	3
1	A	8	ARG	Sidechain	3



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
1	A	167	156	156	0±1
2	В	43	41	39	0±1
All	All	3780	3546	3510	7

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 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	${f Models}$		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:27:TYR:CE1	2:B:3:NAG:H83	0.69	2.22	16	2	
1:A:27:TYR:CZ	2:B:3:NAG:H83	0.43	2.48	8	3	
1:A:27:TYR:CE2	2:B:3:NAG:H83	0.43	2.49	8	1	
1:A:17:GLN:CD	1:A:17:GLN:H	0.40	2.19	2	1	

6.3 Torsion angles (i)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	24/31 (77%)	19±2 (77±7%)	$4\pm 2 \ (16\pm 7\%)$	$2\pm1\ (7\pm5\%)$	2 16
All	All	432/558 (77%)	334 (77%)	67 (16%)	31 (7%)	2 16

All 9 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

\mathbf{Mol}	Chain	Res	Type	Models (Total)
1	A	11	SER	8
1	A	10	PRO	7
1	A	5	VAL	6

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Mol	Chain	Res	Type	Models (Total)
1	A	25	PRO	3
1	A	3	GLU	2
1	A	4	CYS	2
1	A	7	GLY	1
1	A	6	ARG	1
1	A	9	CYS	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	19/21 (90%)	16±1 (86±7%)	$3\pm1 \ (14\pm7\%)$	6	46	
All	All	342/378 (90%)	293 (86%)	49 (14%)	6	46	

All 9 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	9	CYS	13
1	A	6	ARG	12
1	A	8	ARG	7
1	A	3	GLU	5
1	A	23	LYS	3
1	A	26	LYS	3
1	A	28	CYS	2
1	A	17	GLN	2
1	A	21	CYS	2

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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.

Mal	Tuno	Chain	Dog	Tiple		Bond leng	${ m ths}$
WIOI	туре	Chain	nes	Link	Counts	RMSZ	#Z>2
1	PFF	A	20	1	11,12,13	1.14 ± 0.00	0±0 (0±0%)
1	PFF	A	18	1	11,12,13	1.16 ± 0.00	0±0 (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	Pog	Link		Bond ang	les
WIOI	туре	Chain	res	LIIIK	Counts	RMSZ	#Z>2
1	PFF	A	20	1	12,15,17	1.04 ± 0.00	0±0 (0±0%)
1	PFF	A	18	1	12,15,17	1.15 ± 0.00	0±0 (0±0%)

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	PFF	A	18	1	-	$0\pm0,5,6,8$	$0\pm0,1,1,1$
1	PFF	A	20	1	-	$0\pm0,5,6,8$	$0\pm0,1,1,1$

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.



6.5 Carbohydrates (i)

3 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.

Mal	Tuno	Chain	Pos	Link	Bond lengths			
WIOI	Type	Chain	res	LIIIK	Counts	RMSZ	#Z>2	
2	NAG	В	1	2	15,15,15	0.67 ± 0.00	0±0 (0±0%)	
2	NAG	В	2	2	14,14,15	0.72 ± 0.00	0±0 (0±0%)	
2	NAG	В	3	2	14,14,15	0.49 ± 0.00	0±0 (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	Tuno	Chain	Pos	Tiple	Bond angles			
WIOI	туре	Chain	res	LIIIK	Counts	RMSZ	#Z>2	
2	NAG	В	1	2	21,21,21	0.95 ± 0.00	0±0 (0±0%)	
2	NAG	В	2	2	17,19,21	1.66 ± 0.00	1±0 (5±0%)	
2	NAG	В	3	2	17,19,21	1.09 ± 0.00	0±0 (0±0%)	

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	В	1	2	-	$0\pm0,6,26,26$	$0\pm0,1,1,1$
2	NAG	В	2	2	-	$0\pm0,6,23,26$	$0\pm0,1,1,1$
2	NAG	В	3	2	=	$0\pm0,6,23,26$	$0\pm0,1,1,1$

There are no bond-length outliers.

All unique angle outliers are listed below.



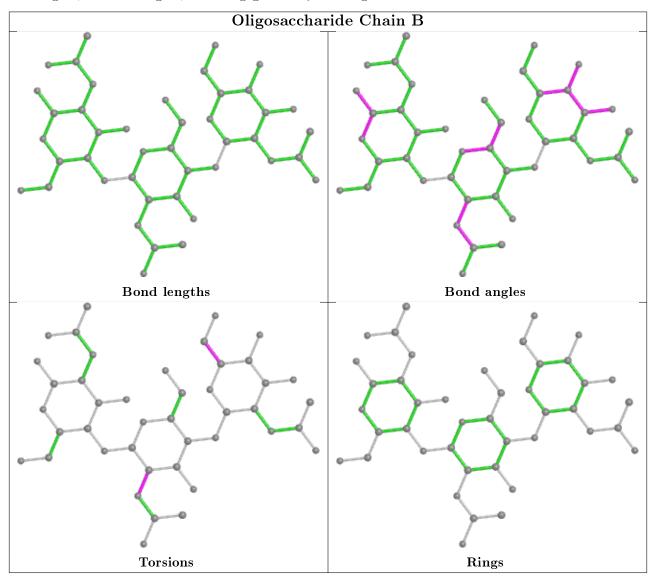
Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$	Models	
								Worst	Total
2	В	2	NAG	C2-N2-C7	5.23	130.35	122.90	1	18

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

