



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2024 – 01:02 AM EDT

PDB ID : 3GXT  
Title : Crystal structure of alpha-galactosidase A at pH 4.5 complexed with 1-deoxy galactonijirimycin  
Authors : Lieberman, R.L.  
Deposited on : 2009-04-02  
Resolution : 2.70 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  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

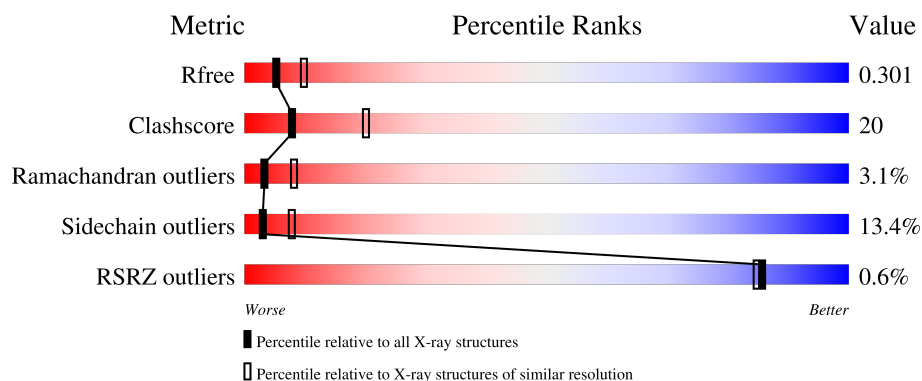
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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	398	<div> <div>55%</div> <div>35%</div> <div>7%</div> <div>..</div> </div>
1	B	398	<div> <div>58%</div> <div>33%</div> <div>6%</div> <div>..</div> </div>
2	C	2	<div> <div>100%</div> </div>
2	D	2	<div> <div>100%</div> </div>
2	F	2	<div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
3	E	2	 50% 50%
4	G	4	 100%
5	H	3	 33% 67%

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
3	MAN	E	2	X	-	-	-
4	NAG	G	1	X	-	-	-
4	MAN	G	3	X	-	-	-
5	MAN	H	3	X	-	-	-
6	SO4	A	2	-	-	X	-

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 6573 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 Alpha-galactosidase A.

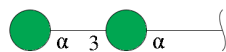
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3122	1988	534	574	26			
1	B	391	Total	C	N	O	S	0	0	0
			3131	1993	536	576	26			

- 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
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

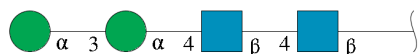
- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	E	2	Total	C	O	0	0	0
			22	12	10			

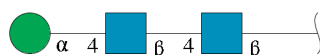
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose.

ose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



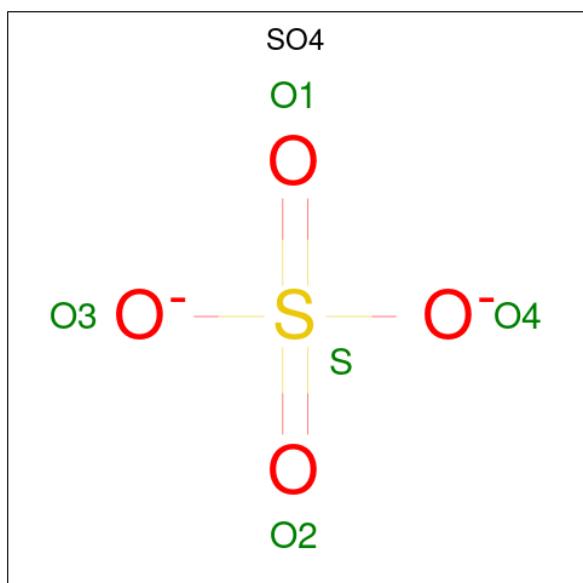
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



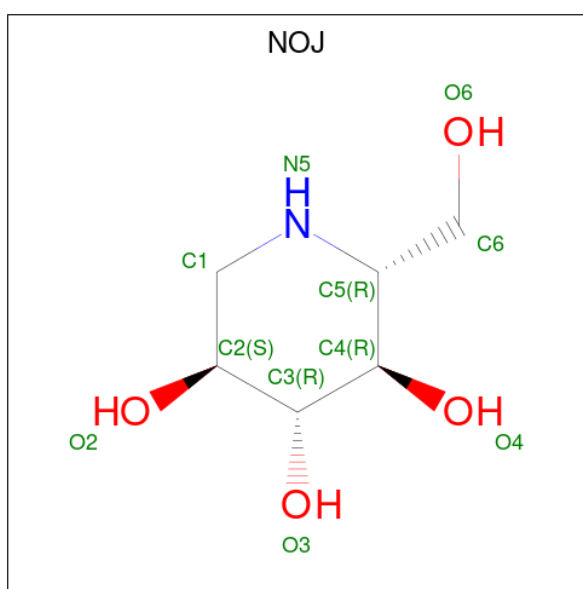
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is 1-DEOXYNOJIRIMYCIN (three-letter code: NOJ) (formula:  $C_6H_{13}NO_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			11	6	1	4		
7	B	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	36	Total	O	0	0
			36	36		
9	B	28	Total	O	0	0
			28	28		







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

Chain C: 100%



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

Chain D: 100%



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

Chain F: 50% 50%



- Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose

Chain E: 50% 50%



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

Chain G: 100%



- Molecule 5: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 33% 67%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.61Å 89.61Å 216.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.90 – 2.70 19.90 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.3 (19.90-2.70) 97.0 (19.90-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.03 (at 2.71Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.242 , 0.306 0.238 , 0.301	Depositor DCC
$R_{free}$ test set	1400 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.8	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 60.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6573	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, NOJ, MAN, SO4

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	0.84	2/3209 (0.1%)	0.91	5/4358 (0.1%)
1	B	0.79	0/3218	0.88	2/4370 (0.0%)
All	All	0.81	2/6427 (0.0%)	0.90	7/8728 (0.1%)

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	4
1	B	0	2
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	90	CYS	CB-SG	-5.34	1.73	1.81
1	A	229	PHE	CE1-CZ	5.13	1.47	1.37

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	332	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	392	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	A	286	LEU	CA-CB-CG	-5.30	103.11	115.30
1	A	220	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	B	388	LEU	CA-CB-CG	5.14	127.12	115.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	SER	Peptide
1	A	103	GLU	Peptide
1	A	104	GLY	Peptide
1	A	209	TRP	Peptide
1	B	102	SER	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	3122	0	2981	124	0
1	B	3131	0	2991	112	0
2	C	28	0	25	4	0
2	D	28	0	25	5	0
2	F	28	0	25	1	0
3	E	22	0	19	1	0
4	G	50	0	43	3	0
5	H	39	0	34	6	0
6	A	15	0	0	3	0
6	B	10	0	0	2	0
7	A	11	0	13	2	0
7	B	11	0	13	3	0
8	B	14	0	13	2	0
9	A	36	0	0	3	0
9	B	28	0	0	9	0
All	All	6573	0	6182	248	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 20.

The worst 5 of 248 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:103:GLU:HB3	1:A:104:GLY:HA3	1.15	1.15
1:A:332:ARG:HG3	1:A:332:ARG:HH11	1.08	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:ARG:HH11	1:B:332:ARG:HG3	1.28	0.95
1:A:363:ARG:HH11	1:A:363:ARG:HG2	1.34	0.93
1:A:103:GLU:HB3	1:A:104:GLY:CA	2.04	0.88

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	388/398 (98%)	332 (86%)	43 (11%)	13 (3%)	3	7
1	B	389/398 (98%)	333 (86%)	45 (12%)	11 (3%)	4	10
All	All	777/796 (98%)	665 (86%)	88 (11%)	24 (3%)	3	8

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	GLU
1	A	230	ALA
1	B	51	MET
1	B	359	ILE
1	B	420	THR

### 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	331/339 (98%)	289 (87%)	42 (13%)	3	9
1	B	332/339 (98%)	285 (86%)	47 (14%)	2	7
All	All	663/678 (98%)	574 (87%)	89 (13%)	3	8

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	175	ASP
1	B	326	LYS
1	B	235	SER
1	B	300	LEU
1	B	357	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	333	GLN
1	B	422	GLN
1	B	419	ASN
1	B	99	GLN
1	B	212	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

15 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	C	1	1,2	14,14,15	0.66	0	17,19,21	2.62	4 (23%)
2	NAG	C	2	2	14,14,15	0.58	0	17,19,21	2.10	4 (23%)
2	NAG	D	1	1,2	14,14,15	0.75	0	17,19,21	2.49	6 (35%)
2	NAG	D	2	2	14,14,15	0.98	0	17,19,21	2.50	3 (17%)
3	MAN	E	1	3	11,11,12	0.77	0	15,15,17	2.15	5 (33%)
3	MAN	E	2	3	11,11,12	0.93	1 (9%)	15,15,17	1.69	4 (26%)
2	NAG	F	1	1,2	14,14,15	0.83	0	17,19,21	1.61	4 (23%)
2	NAG	F	2	2	14,14,15	0.66	0	17,19,21	1.20	1 (5%)
4	NAG	G	1	1,4	14,14,15	0.67	0	17,19,21	1.85	3 (17%)
4	NAG	G	2	4	14,14,15	0.70	0	17,19,21	1.36	2 (11%)
4	MAN	G	3	4	11,11,12	0.77	0	15,15,17	1.57	3 (20%)
4	MAN	G	4	4	11,11,12	1.08	1 (9%)	15,15,17	2.02	5 (33%)
5	NAG	H	1	5	14,14,15	0.60	0	17,19,21	2.39	8 (47%)
5	NAG	H	2	5	14,14,15	0.73	0	17,19,21	1.73	4 (23%)
5	MAN	H	3	5	11,11,12	0.83	0	15,15,17	2.42	3 (20%)

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	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1
3	MAN	E	1	3	-	0/2/19/22	0/1/1/1
3	MAN	E	2	3	1/1/4/5	2/2/19/22	1/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
4	NAG	G	1	1,4	1/1/5/7	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	3/6/23/26	0/1/1/1
4	MAN	G	3	4	1/1/4/5	1/2/19/22	0/1/1/1
4	MAN	G	4	4	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	H	1	5	-	4/6/23/26	0/1/1/1
5	NAG	H	2	5	-	6/6/23/26	0/1/1/1
5	MAN	H	3	5	1/1/4/5	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	4	MAN	C2-C3	2.64	1.56	1.52
3	E	2	MAN	C2-C3	2.11	1.55	1.52

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C1-O5-C5	8.46	123.52	112.19
5	H	3	MAN	C1-O5-C5	7.73	122.55	112.19
2	D	1	NAG	C1-O5-C5	7.63	122.41	112.19
2	C	1	NAG	C1-O5-C5	6.62	121.05	112.19
5	H	1	NAG	C1-O5-C5	5.52	119.58	112.19

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	E	2	MAN	C1
4	G	1	NAG	C1
4	G	3	MAN	C1
5	H	3	MAN	C1

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	2	NAG	O7-C7-N2-C2
4	G	2	NAG	C8-C7-N2-C2
4	G	2	NAG	O7-C7-N2-C2
5	H	1	NAG	C8-C7-N2-C2
5	H	1	NAG	O7-C7-N2-C2

All (1) ring outliers are listed below:

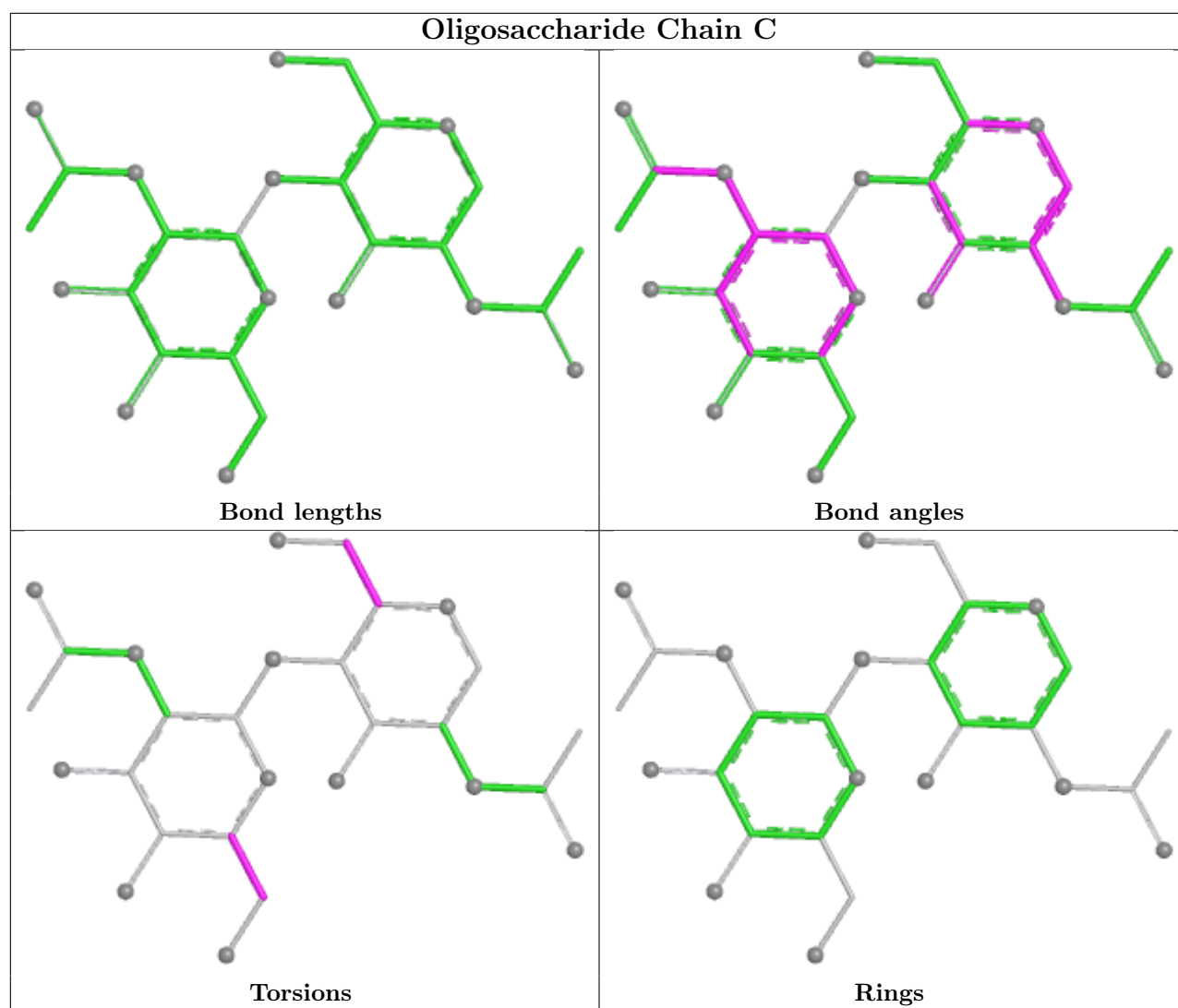
Mol	Chain	Res	Type	Atoms
3	E	2	MAN	C1-C2-C3-C4-C5-O5

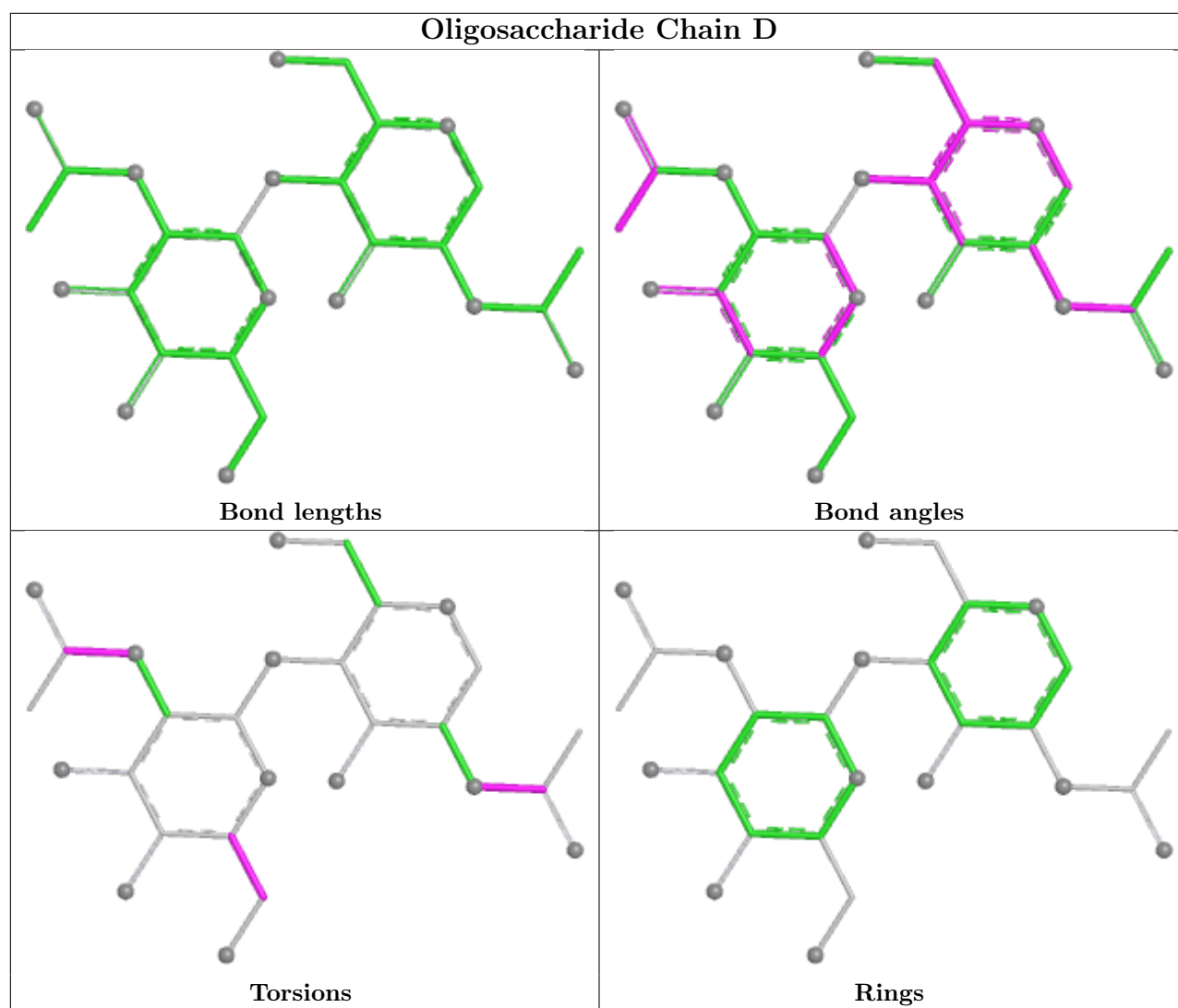


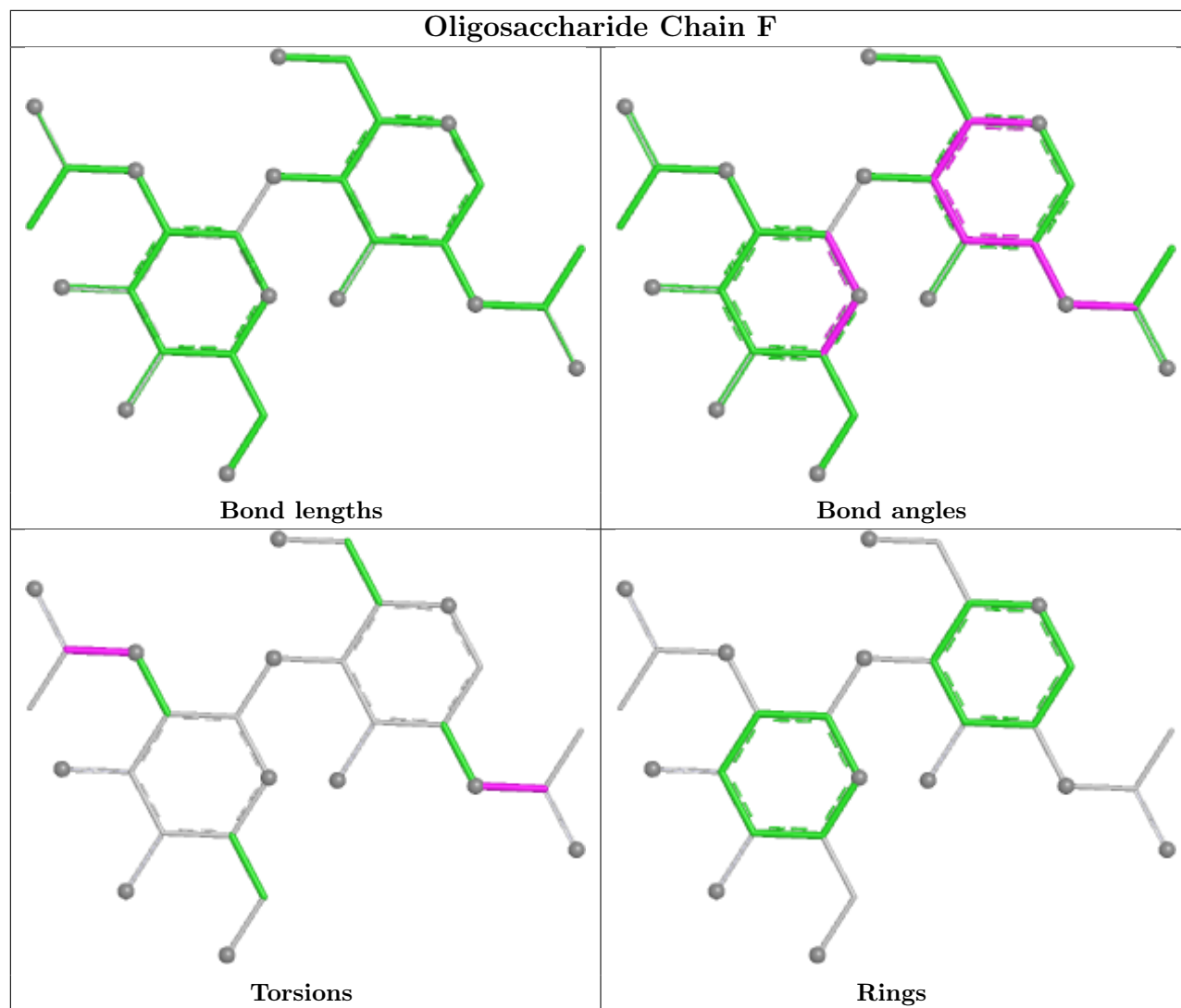
12 monomers are involved in 19 short contacts:

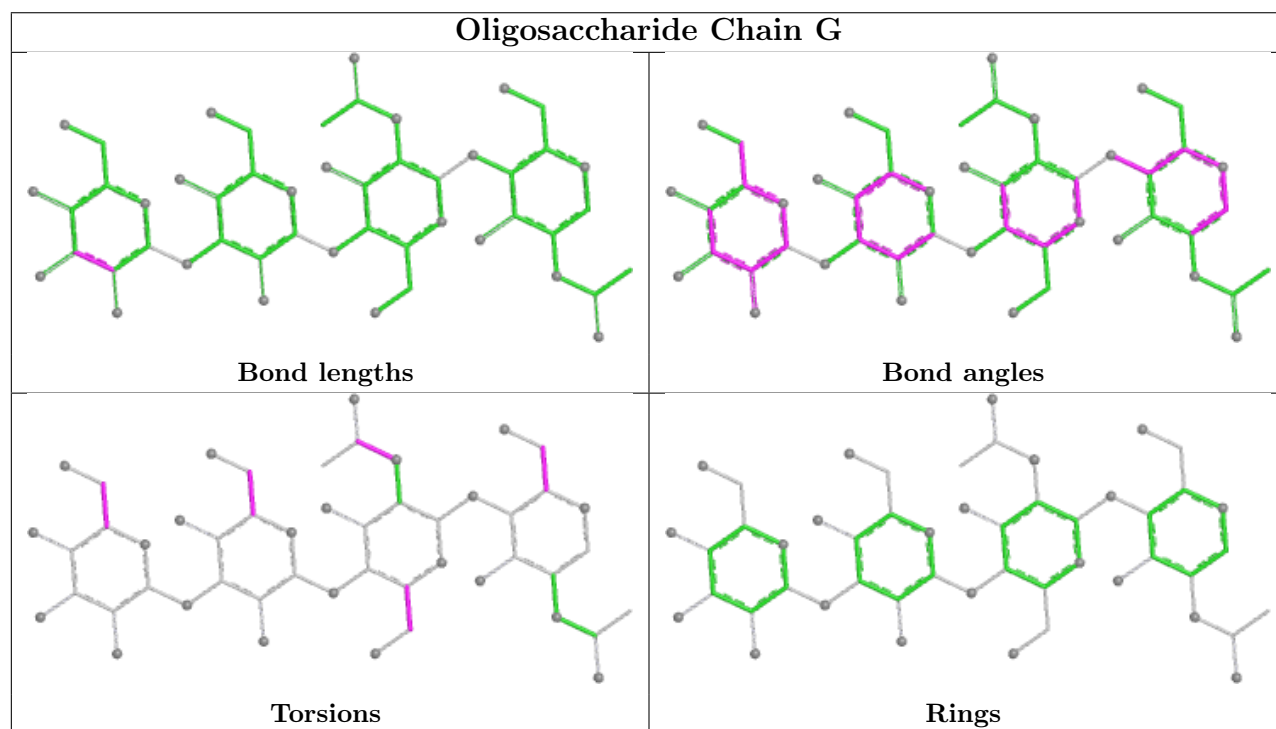
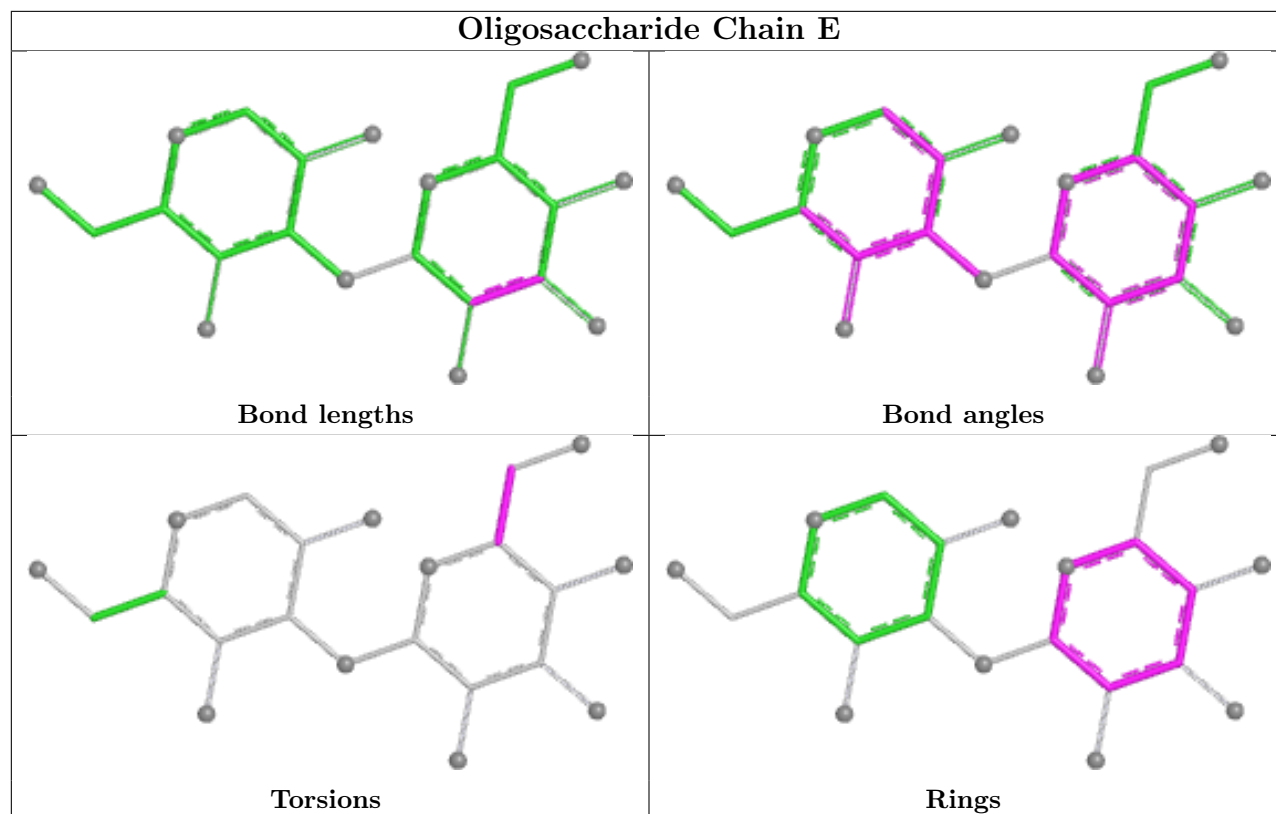
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
2	D	2	NAG	5	0
2	D	1	NAG	4	0
2	F	1	NAG	1	0
4	G	3	MAN	1	0
4	G	2	NAG	1	0
5	H	2	NAG	1	0
5	H	1	NAG	5	0
4	G	4	MAN	1	0
3	E	1	MAN	1	0
4	G	1	NAG	1	0
2	C	1	NAG	4	0

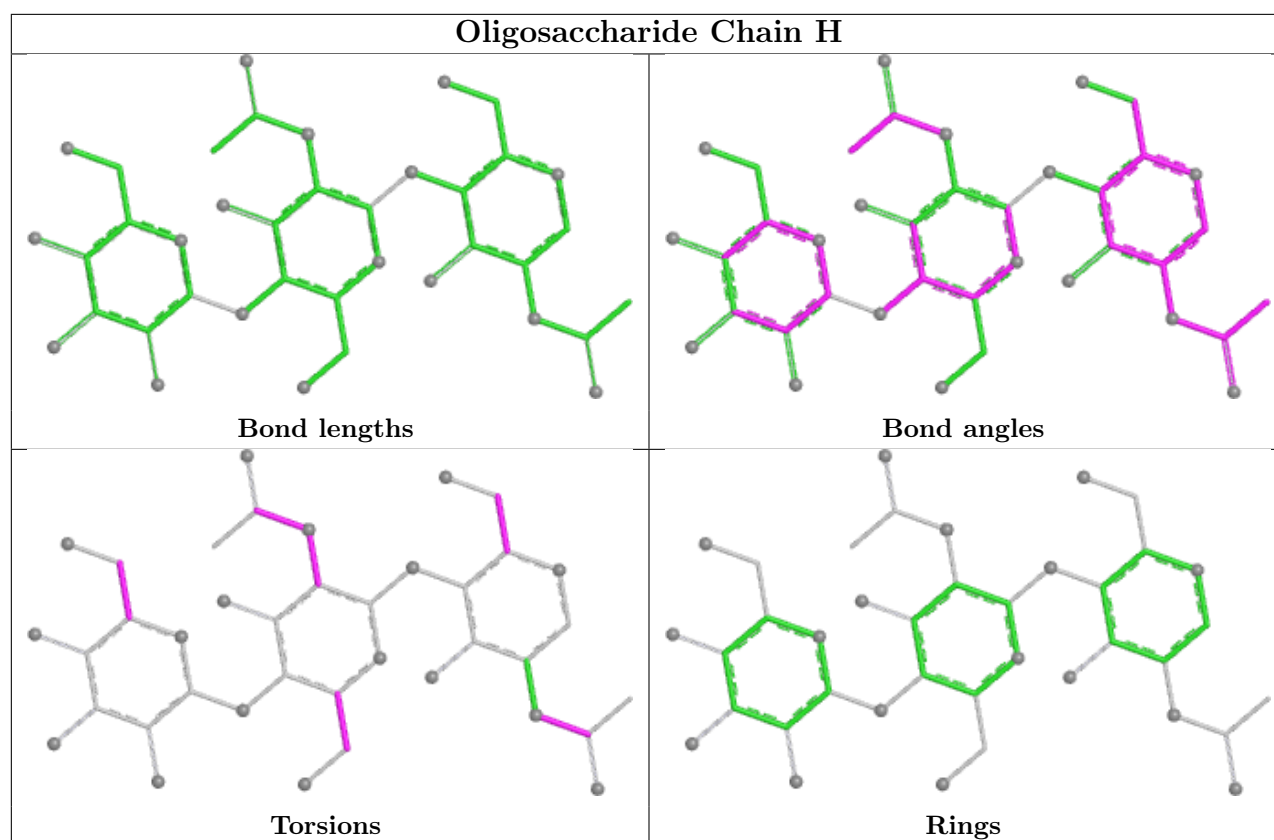
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











## 5.6 Ligand geometry [i](#)

8 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$
6	SO4	B	4	-	4,4,4	0.24	0	6,6,6	0.32	0
7	NOJ	B	1	-	11,11,11	1.76	1 (9%)	13,15,15	2.96	4 (30%)
6	SO4	A	5	-	4,4,4	0.48	0	6,6,6	0.19	0
6	SO4	B	3	-	4,4,4	0.23	0	6,6,6	0.36	0
8	NAG	B	639	-	14,14,15	0.70	0	17,19,21	2.39	7 (41%)
7	NOJ	A	430	-	11,11,11	1.00	1 (9%)	13,15,15	2.72	6 (46%)
6	SO4	A	1	-	4,4,4	0.47	0	6,6,6	1.29	0
6	SO4	A	2	-	4,4,4	0.35	0	6,6,6	0.59	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
7	NOJ	B	1	-	-	0/2/19/19	0/1/1/1
8	NAG	B	639	-	-	1/6/23/26	0/1/1/1
7	NOJ	A	430	-	-	0/2/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1	NOJ	C1-C2	4.75	1.56	1.52
7	A	430	NOJ	C1-C2	2.47	1.54	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	1	NOJ	C3-C4-C5	-8.94	97.92	111.02
7	A	430	NOJ	C2-C3-C4	-6.12	100.10	110.86
8	B	639	NAG	C1-O5-C5	5.52	119.59	112.19
7	A	430	NOJ	C3-C4-C5	-4.82	103.96	111.02
8	B	639	NAG	O5-C5-C4	3.54	119.44	110.83

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	639	NAG	C3-C2-N2-C7

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	4	SO4	1	0
7	B	1	NOJ	3	0
6	B	3	SO4	1	0
8	B	639	NAG	2	0
7	A	430	NOJ	2	0
6	A	1	SO4	1	0
6	A	2	SO4	2	0

## 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	390/398 (97%)	0.02	3 (0%) 82 82	54, 57, 59, 72	0
1	B	391/398 (98%)	0.16	2 (0%) 87 86	54, 57, 59, 71	0
All	All	781/796 (98%)	0.09	5 (0%) 85 85	54, 57, 59, 72	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	421	MET	2.6
1	B	211	PHE	2.3
1	B	359	ILE	2.2
1	A	102	SER	2.2
1	A	394	LEU	2.0

### 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

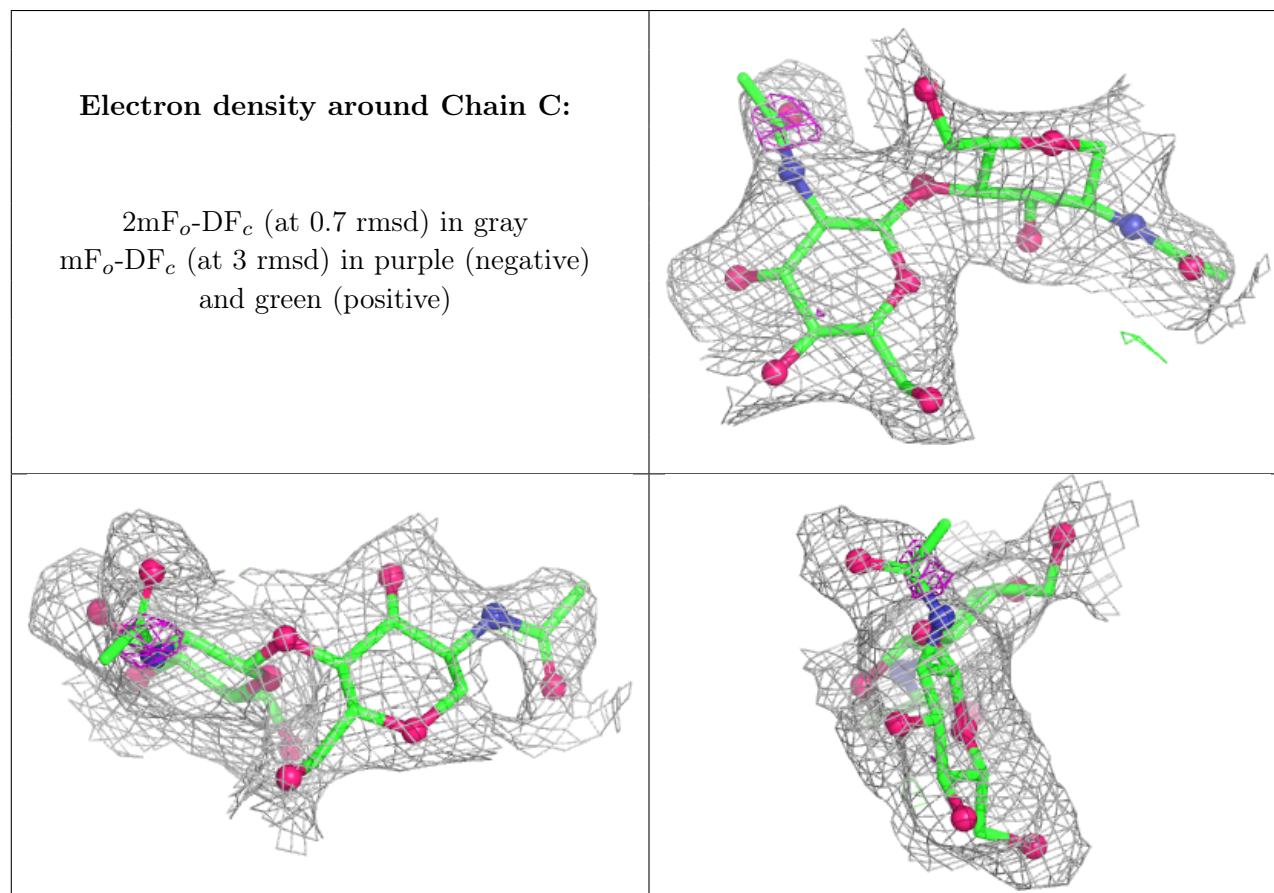
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	MAN	H	3	11/12	0.32	0.15	112,113,113,114	0
3	MAN	E	2	11/12	0.55	0.13	102,103,106,106	0
5	NAG	H	2	14/15	0.58	0.14	106,108,109,111	0
5	NAG	H	1	14/15	0.59	0.15	101,104,105,105	0

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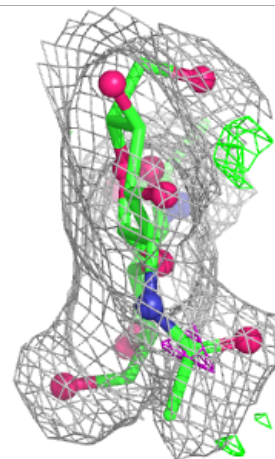
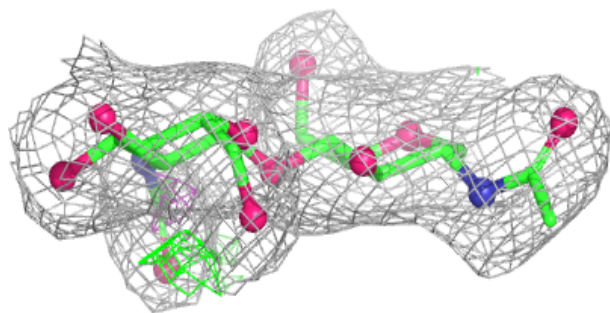
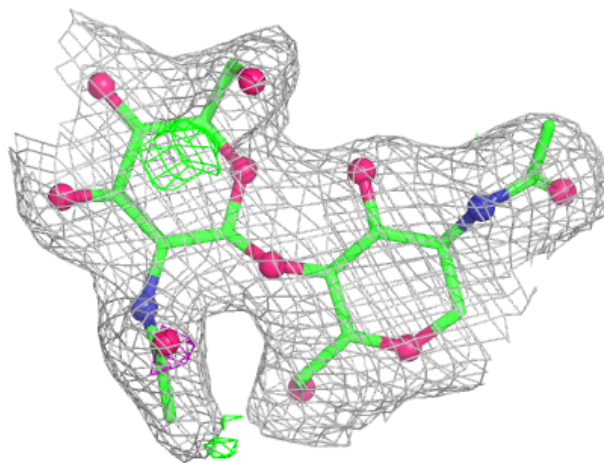
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	F	1	14/15	0.60	0.12	71,75,77,81	0
2	NAG	F	2	14/15	0.70	0.11	79,84,87,88	0
3	MAN	E	1	11/12	0.74	0.11	103,103,104,104	0
2	NAG	C	2	14/15	0.78	0.11	65,72,75,77	0
4	MAN	G	3	11/12	0.79	0.10	74,78,81,81	0
4	NAG	G	2	14/15	0.79	0.12	71,73,75,76	0
4	MAN	G	4	11/12	0.80	0.10	66,69,71,72	0
2	NAG	D	2	14/15	0.81	0.11	59,64,66,66	0
4	NAG	G	1	14/15	0.84	0.10	62,64,68,68	0
2	NAG	C	1	14/15	0.85	0.10	66,71,72,73	0
2	NAG	D	1	14/15	0.92	0.07	42,49,51,54	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



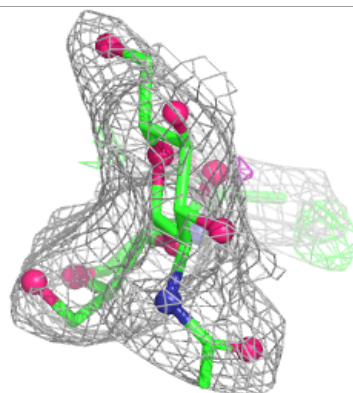
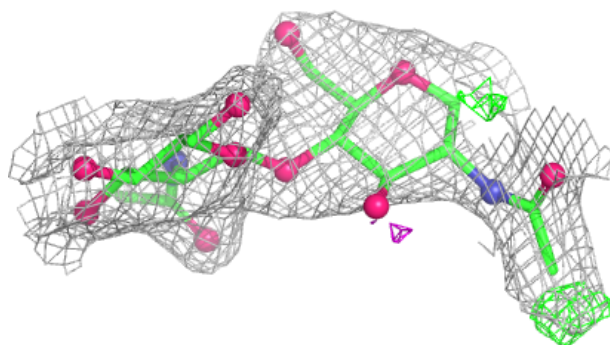
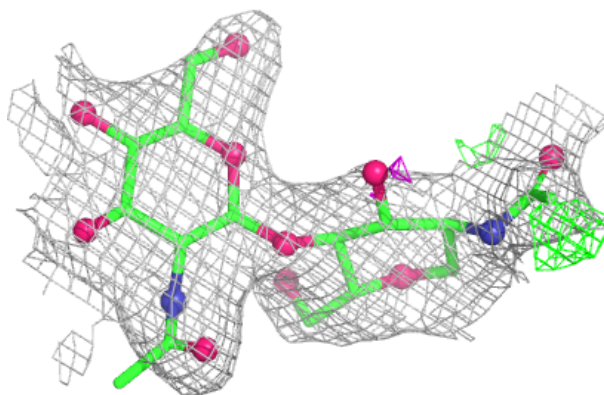
**Electron density around Chain D:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

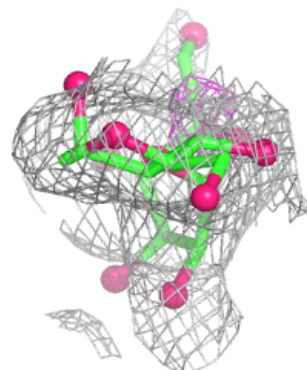
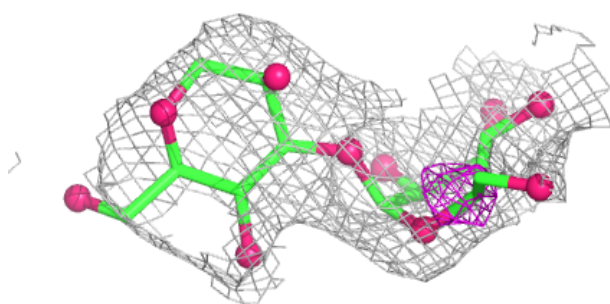
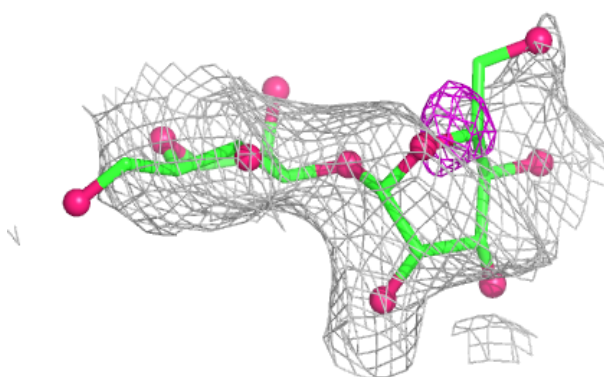


**Electron density around Chain F:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around Chain E:**

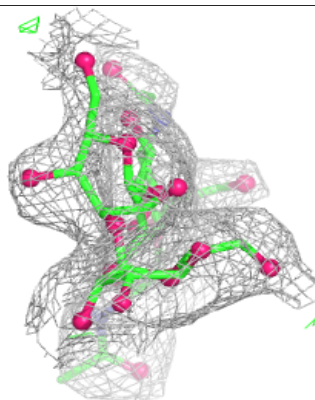
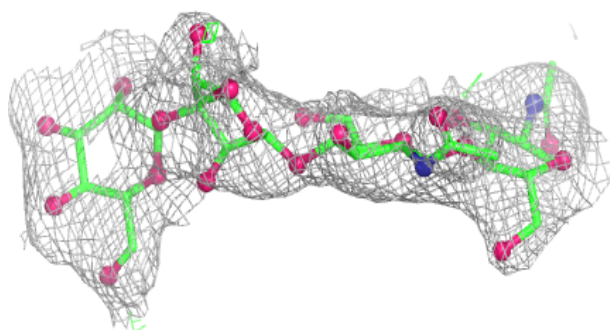
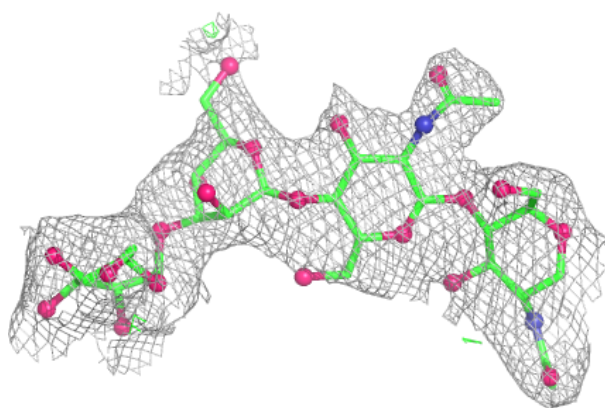
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



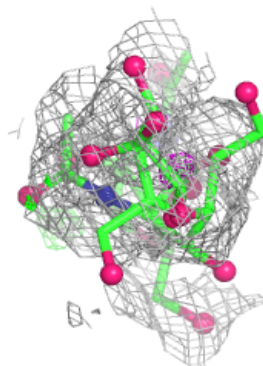
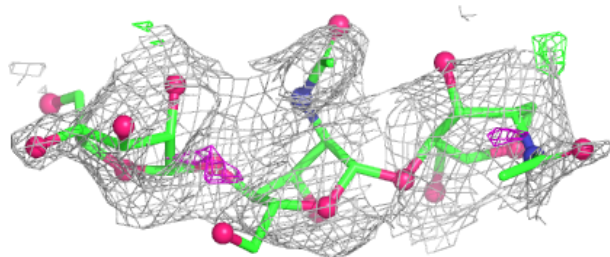
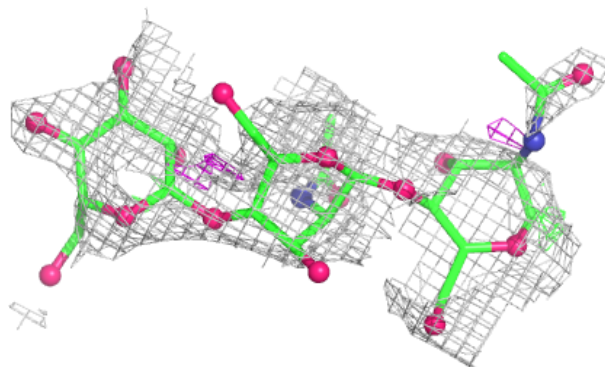


**Electron density around Chain G:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around Chain H:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	SO4	A	5	5/5	0.64	0.18	115,116,116,116	0
8	NAG	B	639	14/15	0.64	0.15	107,109,110,110	0
7	NOJ	B	1	11/11	0.87	0.15	46,52,56,56	0
6	SO4	B	4	5/5	0.88	0.14	81,82,83,83	0
6	SO4	A	2	5/5	0.90	0.13	68,68,70,70	0
6	SO4	B	3	5/5	0.91	0.13	85,85,86,87	0
6	SO4	A	1	5/5	0.91	0.14	58,58,59,60	0
7	NOJ	A	430	11/11	0.93	0.08	55,57,59,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.