



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 4, 2026 – 10:38 PM UTC

PDB ID : 9OZD / pdb\_00009ozd  
Title : Crystal structure of the polysaccharide lyase RbmB from *Vibrio cholerae* bound to *Vibrio* Polysaccharide  
Authors : Weerasekera, R.; Moreau, A.; Huang, X.; Potapova, A.; Schwechheimer, C.; Huynh, Y.; Cannizzo, O.; Gordon, R.; Hinbest, A.J.; Yang, Y.; Jiang, X.; Yan, J.; Yildiz, F.; Olson, R.  
Deposited on : 2025-06-05  
Resolution : 1.62 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)

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<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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

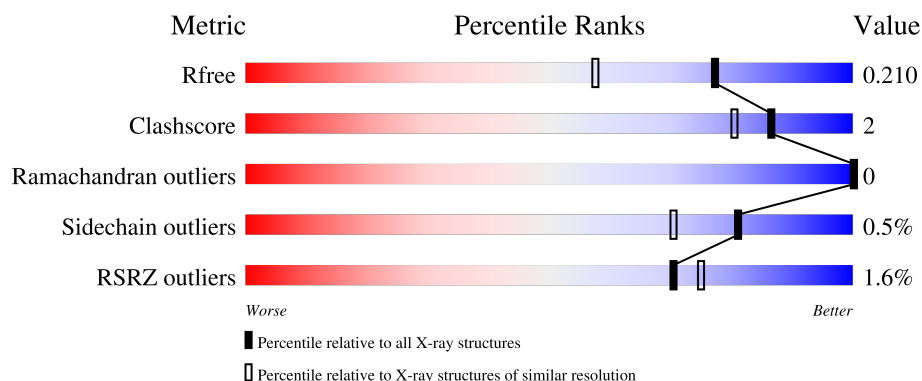
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.62 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.







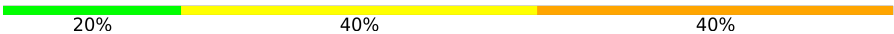
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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	380	<div> <div>92%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> </div>
1	B	380	<div> <div>91%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> </div>
1	C	380	<div> <div>92%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> </div>
1	D	380	<div> <div>91%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	E	4	 50% 25% 25%
2	F	4	 75% 25%
2	H	4	 25% 75%
2	J	4	 50% 50%
3	G	6	 17% 50% 33%
4	I	5	 20% 40% 40%

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 25213 atoms, of which 11656 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 Polysaccharide lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	366	Total	C	H	N	O	S	0	18	0
			5775	1849	2824	506	587	9			
1	B	368	Total	C	H	N	O	S	0	23	0
			5859	1874	2858	521	597	9			
1	C	367	Total	C	H	N	O	S	0	20	0
			5694	1824	2772	509	580	9			
1	D	366	Total	C	H	N	O	S	0	21	0
			5738	1844	2798	503	584	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	-	expression tag	UNP Q9KTH3
A	30	SER	-	expression tag	UNP Q9KTH3
A	31	THR	-	expression tag	UNP Q9KTH3
B	29	GLY	-	expression tag	UNP Q9KTH3
B	30	SER	-	expression tag	UNP Q9KTH3
B	31	THR	-	expression tag	UNP Q9KTH3
C	29	GLY	-	expression tag	UNP Q9KTH3
C	30	SER	-	expression tag	UNP Q9KTH3
C	31	THR	-	expression tag	UNP Q9KTH3
D	29	GLY	-	expression tag	UNP Q9KTH3
D	30	SER	-	expression tag	UNP Q9KTH3
D	31	THR	-	expression tag	UNP Q9KTH3

- Molecule 2 is an oligosaccharide called {[(2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	4	Total	C	H	N	O	0	0	0
			95	28	43	2	22			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	4	Total	C	H	N	O	0	0	0
			95	28	43	2	22			
2	H	4	Total	C	H	N	O	0	0	0
			95	28	43	2	22			
2	J	4	Total	C	H	N	O	0	0	0
			95	28	43	2	22			

- Molecule 3 is an oligosaccharide called {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose-(1-4)-{[(2R,3S,4R,5S,6R)-5-acetamido-3,4,6-trihydroxyoxane-2-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	6	Total	C	H	N	O	0	0	0
			148	44	66	4	34			

- Molecule 4 is an oligosaccharide called {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose-(1-4)-{[(2R,3S,4R,5S,6R)-5-acetamido-3,4,6-trihydroxyoxane-2-carbonyl]amino}acetic acid (non-preferred name).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	I	5	Total	C	H	N	O	0	0	0
			127	38	56	4	29			

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

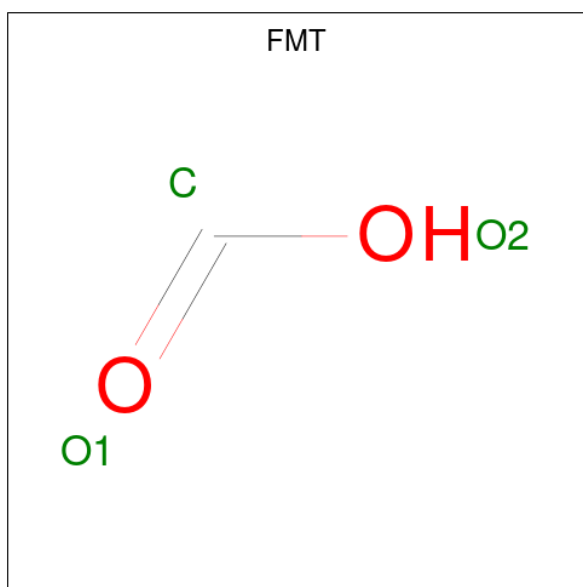
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		
5	B	1	Total	Na	0	0
			1	1		
5	C	1	Total	Na	0	0
			1	1		
5	D	1	Total	Na	0	0
			1	1		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	A	1	Total	C	H	O	0	0
			14	3	8	3		
6	B	1	Total	C	H	O	0	0
			14	3	8	3		
6	B	1	Total	C	H	O	0	0
			14	3	8	3		
6	B	1	Total	C	H	O	0	0
			14	3	8	3		
6	B	1	Total	C	H	O	0	0
			14	3	8	3		
6	C	1	Total	C	H	O	0	0
			14	3	8	3		
6	C	1	Total	C	H	O	0	0
			14	3	8	3		
6	D	1	Total	C	H	O	0	0
			14	3	8	3		
6	D	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 7 is FORMIC ACID (CCD ID: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			4	1	1	2		
7	A	1	Total	C	H	O	0	0
			4	1	1	2		
7	A	1	Total	C	H	O	0	0
			4	1	1	2		
7	B	1	Total	C	H	O	0	0
			4	1	1	2		
7	C	1	Total	C	H	O	0	0
			4	1	1	2		
7	D	1	Total	C	H	O	0	0
			4	1	1	2		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	370	Total	O	0	1
			370	370		
8	B	339	Total	O	0	2
			340	340		
8	C	255	Total	O	0	1
			256	256		
8	D	316	Total	O	0	0
			316	316		

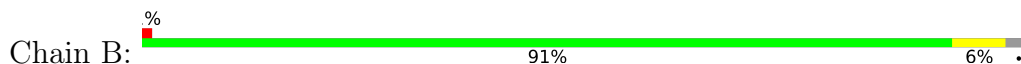
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

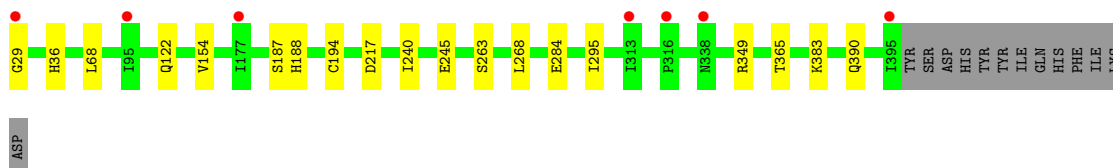
- Molecule 1: Polysaccharide lyase



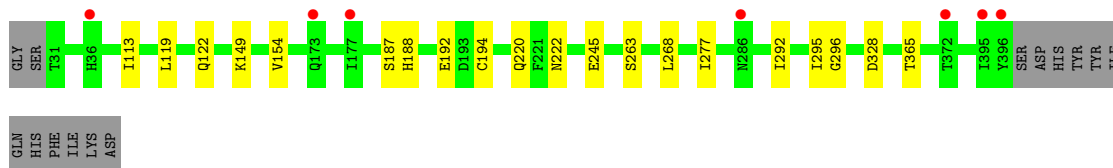
- Molecule 1: Polysaccharide lyase



- Molecule 1: Polysaccharide lyase



- Molecule 1: Polysaccharide lyase





- Molecule 2: {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose

Chain E: 



- Molecule 2: {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose

Chain F: 



- Molecule 2: {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose

Chain H: 

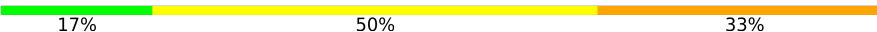


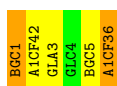
- Molecule 2: {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose

Chain J: 



- Molecule 3: {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-galactopyranose-(1-4)-{[(2R,3S,4R,5S,6R)-5-acetamido-3,4,6-trihydroxyoxane-2-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose

Chain G: 



- Molecule 4: {[ (2R,3S,4S)-3-acetamido-2,4-dihydroxy-3,4-dihydro-2H-pyran-6-carbonyl]amino}acetic acid (non-preferred name)-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-al

pha-D-galactopyranose-(1-4)-{[(2R,3S,4R,5S,6R)-5-acetamido-3,4,6-trihydroxyoxane-2-carbonyl]amino}acetic acid (non-preferred name)

Chain I: 20% 40% 40%

A1CF41  
GLA2  
GLC3  
BGC4  
A1CF35

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	123.56Å 52.56Å 133.23Å 90.00° 111.22° 90.00°	Depositor
Resolution (Å)	33.42 – 1.62 33.42 – 1.62	Depositor EDS
% Data completeness (in resolution range)	64.4 (33.42-1.62) 64.6 (33.42-1.62)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.25 (at 1.62Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.168 , 0.209 0.169 , 0.210	Depositor DCC
$R_{free}$ test set	6570 reflections (3.22%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.5	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 53.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	25213	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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: A1CF4, A1CF3, NA, GLA, GLC, BGC, GOL, FMT

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	0.15	0/3042	0.42	0/4127
1	B	0.14	0/3099	0.39	0/4201
1	C	0.12	0/3016	0.38	0/4090
1	D	0.14	0/3054	0.40	0/4143
All	All	0.14	0/12211	0.39	0/16561

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	2951	2824	2848	12	0
1	B	3001	2858	2874	12	0
1	C	2922	2772	2797	11	0
1	D	2940	2798	2841	11	0
2	E	52	43	29	1	0
2	F	52	43	29	2	0
2	H	52	43	29	0	0
2	J	52	43	29	0	0
3	G	82	66	38	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	71	56	27	6	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	30	40	40	0	0
6	B	24	32	32	0	0
6	C	12	16	16	0	0
6	D	12	16	16	0	0
7	A	9	3	3	0	0
7	B	3	1	1	0	0
7	C	3	1	1	0	0
7	D	3	1	1	0	0
8	A	370	0	0	0	0
8	B	340	0	0	0	0
8	C	256	0	0	3	0
8	D	316	0	0	2	0
All	All	13557	11656	11651	51	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 2.

The worst 5 of 51 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)
8:C:775[B]:HOH:O	4:I:2:GLA:O6	2.05	0.73
3:G:1:BGC:O6	4:I:1:A1CF4:O1	2.20	0.58
3:G:1:BGC:H6	4:I:1:A1CF4:C1	2.19	0.55
1:A:245:GLU:HA	1:A:268:LEU:O	2.09	0.53
1:C:263:SER:HA	1:C:295:ILE:O	2.09	0.53

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	382/380 (100%)	364 (95%)	18 (5%)	0	100	100
1	B	389/380 (102%)	373 (96%)	16 (4%)	0	100	100
1	C	385/380 (101%)	369 (96%)	16 (4%)	0	100	100
1	D	385/380 (101%)	367 (95%)	18 (5%)	0	100	100
All	All	1541/1520 (101%)	1473 (96%)	68 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	330/333 (99%)	328 (99%)	2 (1%)	78	66
1	B	333/333 (100%)	329 (99%)	4 (1%)	63	43
1	C	320/333 (96%)	317 (99%)	3 (1%)	70	54
1	D	328/333 (98%)	326 (99%)	2 (1%)	78	66
All	All	1311/1332 (98%)	1300 (99%)	11 (1%)	81	59

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	194[B]	CYS
1	C	383	LYS
1	D	194[B]	CYS
1	D	194[A]	CYS
1	B	194[A]	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	309	GLN
1	C	117	GLN
1	B	353	GLN
1	C	303	GLN
1	A	317	ASN

### 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 ⓘ

27 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	GLA	E	1	2	12,12,12	0.62	0	17,17,17	1.08	0
2	GLC	E	2	2	11,11,12	0.70	0	15,15,17	0.59	0
2	BGC	E	3	2	11,11,12	1.31	0	15,15,17	1.24	1 (6%)
2	A1CF3	E	4	2	18,18,19	2.38	6 (33%)	19,24,26	2.50	8 (42%)
2	GLA	F	1	2	12,12,12	0.61	0	17,17,17	0.96	1 (5%)
2	GLC	F	2	2	11,11,12	0.66	0	15,15,17	0.62	0
2	BGC	F	3	2	11,11,12	1.24	0	15,15,17	1.16	1 (6%)
2	A1CF3	F	4	2	18,18,19	2.35	6 (33%)	19,24,26	2.57	8 (42%)
3	BGC	G	1	3	12,12,12	1.17	0	17,17,17	1.33	3 (17%)
3	A1CF4	G	2	3	19,19,20	1.72	4 (21%)	22,26,28	1.07	1 (4%)
3	GLA	G	3	3	11,11,12	0.88	1 (9%)	15,15,17	1.21	1 (6%)
3	GLC	G	4	3	11,11,12	0.66	0	15,15,17	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	BGC	G	5	3	11,11,12	1.42	2 (18%)	15,15,17	1.29	2 (13%)
3	A1CF3	G	6	3	18,18,19	2.50	8 (44%)	19,24,26	2.73	10 (52%)
2	GLA	H	1	2	12,12,12	0.59	0	17,17,17	0.97	1 (5%)
2	GLC	H	2	2	11,11,12	0.69	0	15,15,17	0.62	0
2	BGC	H	3	2	11,11,12	1.27	0	15,15,17	1.13	1 (6%)
2	A1CF3	H	4	2	18,18,19	2.47	6 (33%)	19,24,26	2.48	8 (42%)
4	A1CF4	I	1	4	20,20,20	1.49	2 (10%)	28,28,28	1.48	4 (14%)
4	GLA	I	2	4	11,11,12	0.85	1 (9%)	15,15,17	1.17	2 (13%)
4	GLC	I	3	4	11,11,12	0.68	0	15,15,17	0.59	0
4	BGC	I	4	4	11,11,12	1.43	1 (9%)	15,15,17	1.27	3 (20%)
4	A1CF3	I	5	4	18,18,19	2.65	9 (50%)	19,24,26	2.82	9 (47%)
2	GLA	J	1	2	12,12,12	0.61	0	17,17,17	0.93	0
2	GLC	J	2	2	11,11,12	0.66	0	15,15,17	0.56	0
2	BGC	J	3	2	11,11,12	1.30	1 (9%)	15,15,17	1.17	1 (6%)
2	A1CF3	J	4	2	18,18,19	2.80	6 (33%)	19,24,26	2.84	9 (47%)

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	GLA	E	1	2	-	0/2/22/22	0/1/1/1
2	GLC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	3	2	-	0/2/19/22	0/1/1/1
2	A1CF3	E	4	2	-	0/13/26/29	0/1/1/1
2	GLA	F	1	2	-	0/2/22/22	0/1/1/1
2	GLC	F	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	3	2	-	0/2/19/22	0/1/1/1
2	A1CF3	F	4	2	-	0/13/26/29	0/1/1/1
3	BGC	G	1	3	-	2/2/22/22	0/1/1/1
3	A1CF4	G	2	3	-	1/13/30/33	0/1/1/1
3	GLA	G	3	3	-	0/2/19/22	0/1/1/1
3	GLC	G	4	3	-	0/2/19/22	0/1/1/1
3	BGC	G	5	3	-	0/2/19/22	0/1/1/1
3	A1CF3	G	6	3	-	0/13/26/29	0/1/1/1
2	GLA	H	1	2	-	0/2/22/22	0/1/1/1
2	GLC	H	2	2	-	0/2/19/22	0/1/1/1
2	BGC	H	3	2	-	0/2/19/22	0/1/1/1
2	A1CF3	H	4	2	-	0/13/26/29	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1CF4	I	1	4	-	2/13/33/33	0/1/1/1
4	GLA	I	2	4	-	0/2/19/22	0/1/1/1
4	GLC	I	3	4	-	0/2/19/22	0/1/1/1
4	BGC	I	4	4	-	2/2/19/22	0/1/1/1
4	A1CF3	I	5	4	-	3/13/26/29	0/1/1/1
2	GLA	J	1	2	-	0/2/22/22	0/1/1/1
2	GLC	J	2	2	-	0/2/19/22	0/1/1/1
2	BGC	J	3	2	-	0/2/19/22	0/1/1/1
2	A1CF3	J	4	2	-	0/13/26/29	0/1/1/1

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	5	A1CF3	C5-C6	5.97	1.59	1.47
2	J	4	A1CF3	C5-C6	5.92	1.59	1.47
2	H	4	A1CF3	C3-C2	5.63	1.59	1.53
2	J	4	A1CF3	C3-C2	5.53	1.59	1.53
3	G	6	A1CF3	C5-C6	5.44	1.58	1.47

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	5	A1CF3	O5-C5-C4	-6.86	118.64	124.94
3	G	6	A1CF3	O5-C5-C4	-6.24	119.21	124.94
4	I	5	A1CF3	C8-C7-N2	5.64	125.48	116.12
2	H	4	A1CF3	C8-C7-N2	5.57	125.35	116.12
3	G	6	A1CF3	C8-C7-N2	5.48	125.21	116.12

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

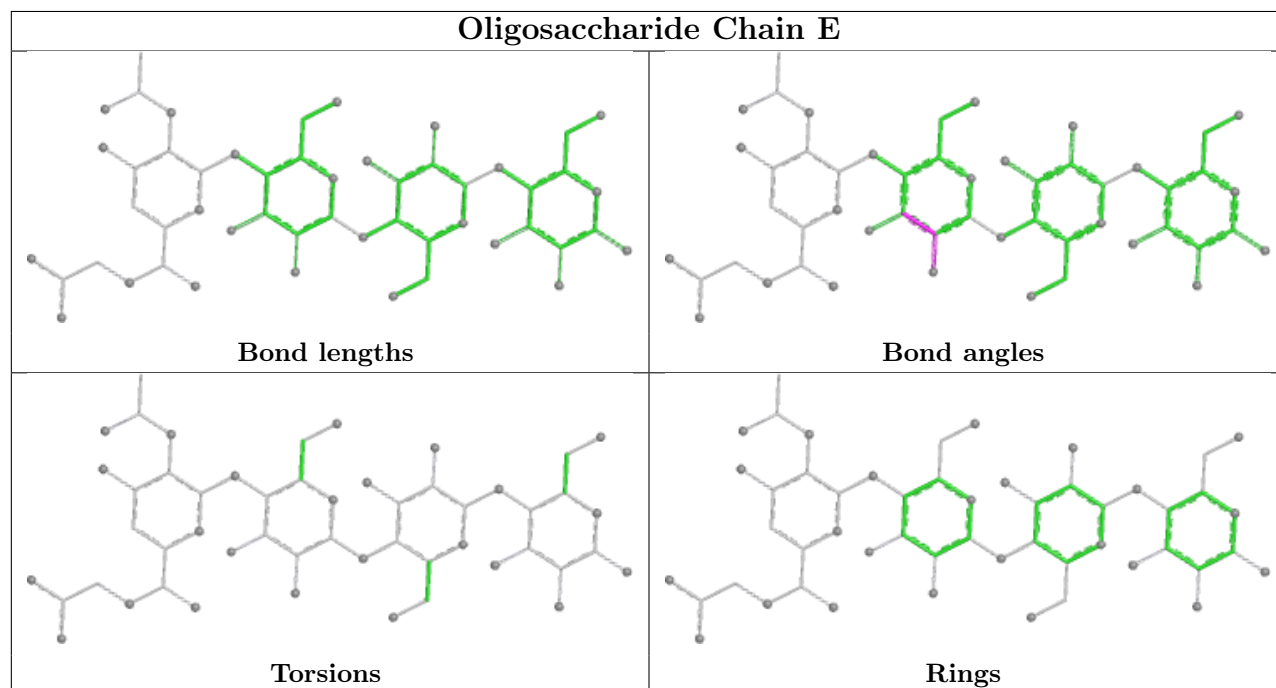
Mol	Chain	Res	Type	Atoms
4	I	4	BGC	O5-C5-C6-O6
3	G	1	BGC	O5-C5-C6-O6
4	I	4	BGC	C4-C5-C6-O6
3	G	1	BGC	C4-C5-C6-O6
4	I	1	A1CF4	O10A-C10-C9-N6

There are no ring outliers.

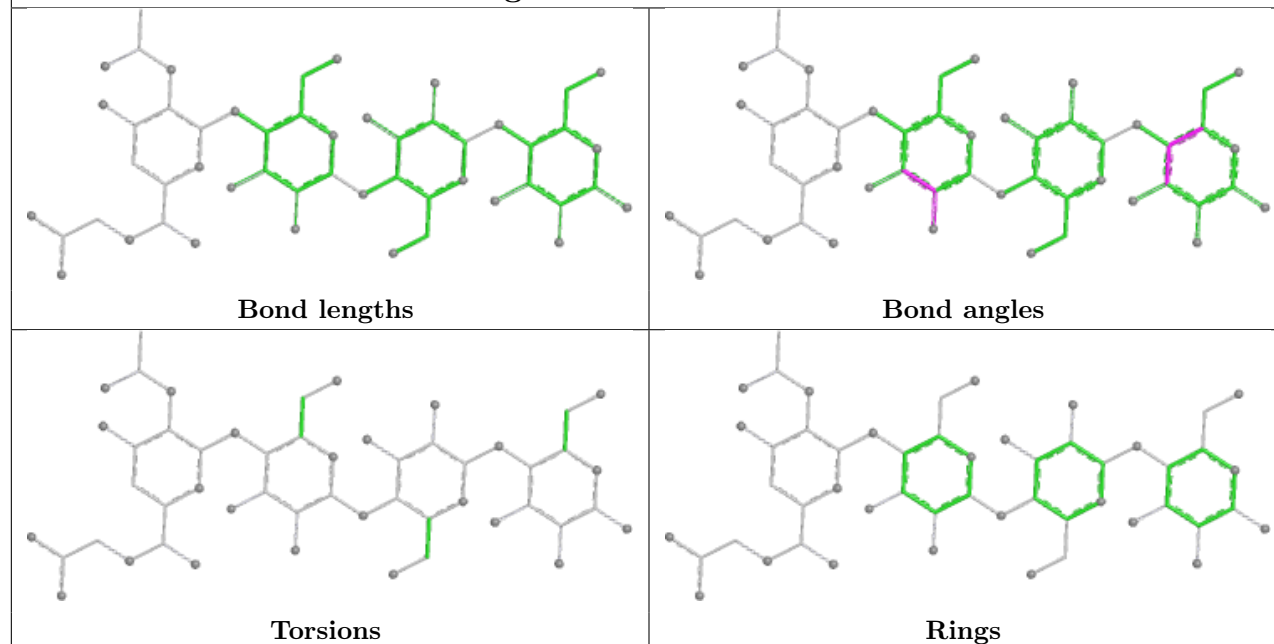
7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	1	BGC	3	0
2	E	4	A1CF3	1	0
4	I	2	GLA	2	0
3	G	6	A1CF3	1	0
2	F	1	GLA	1	0
2	F	2	GLC	1	0
4	I	1	A1CF4	4	0

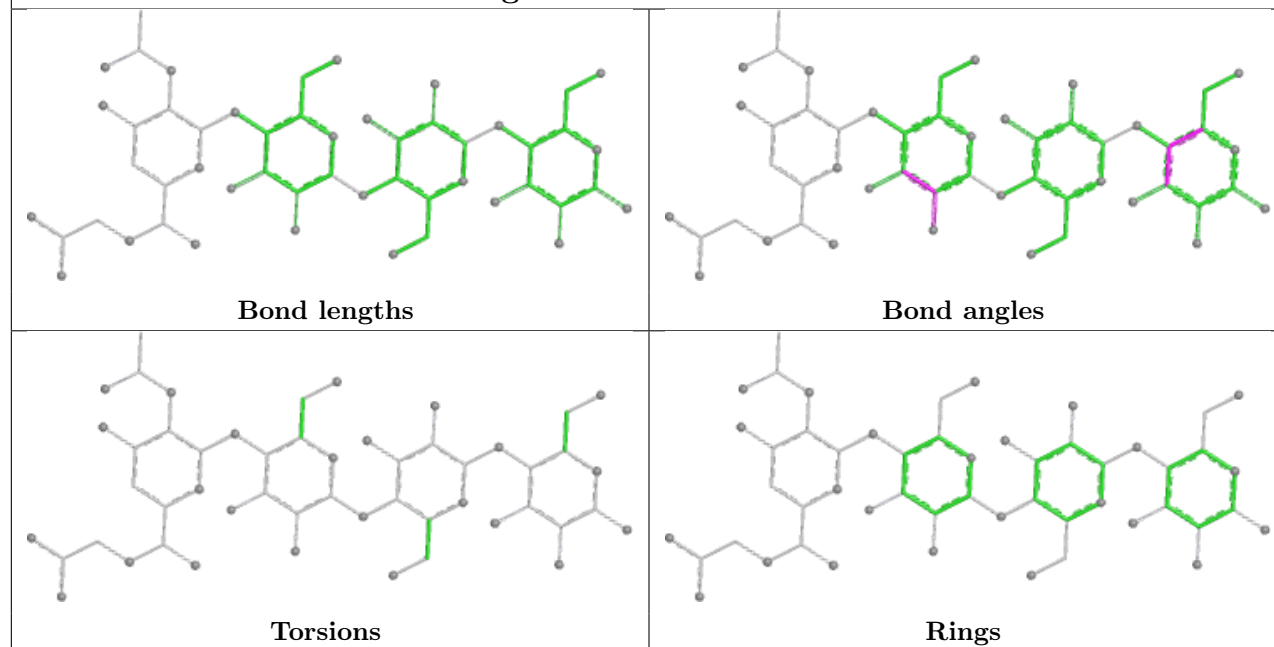
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



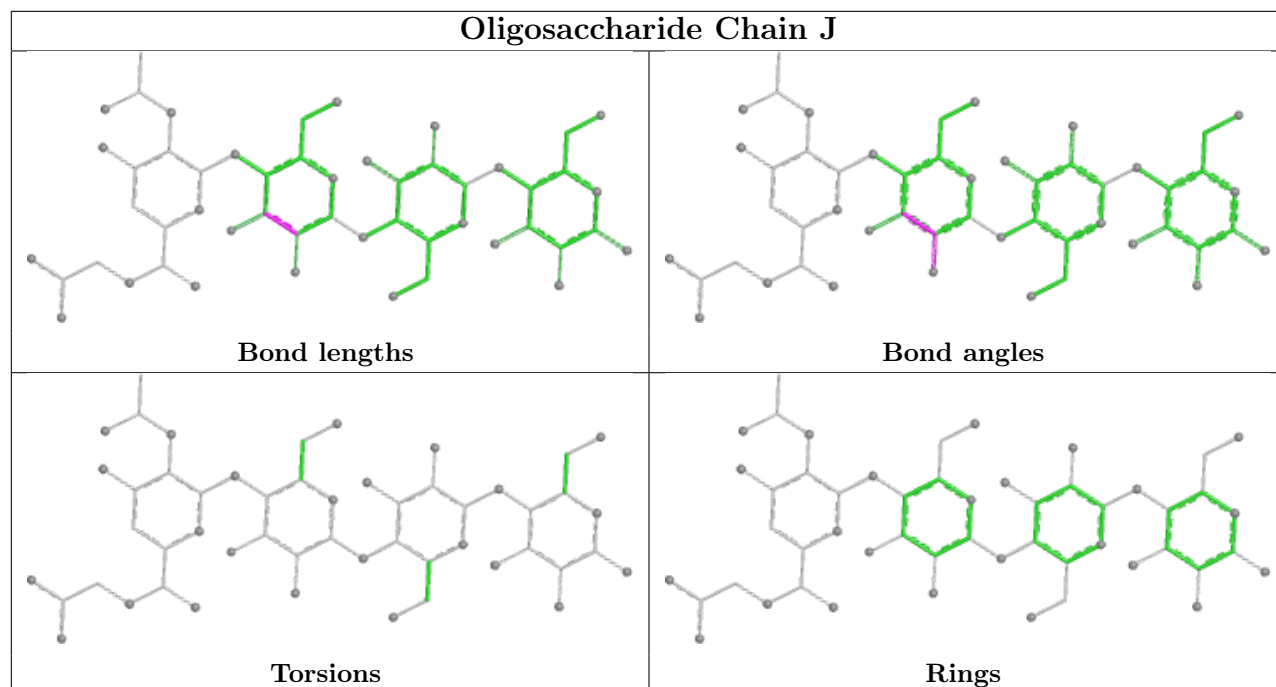
## Oligosaccharide Chain F



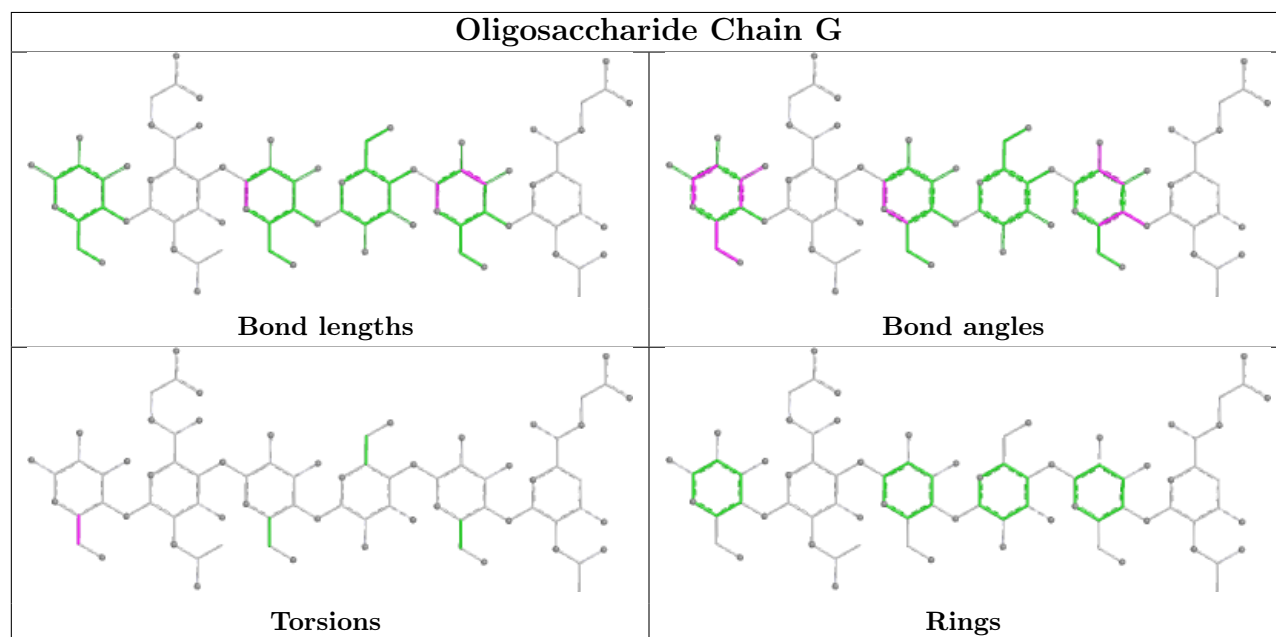
## Oligosaccharide Chain H

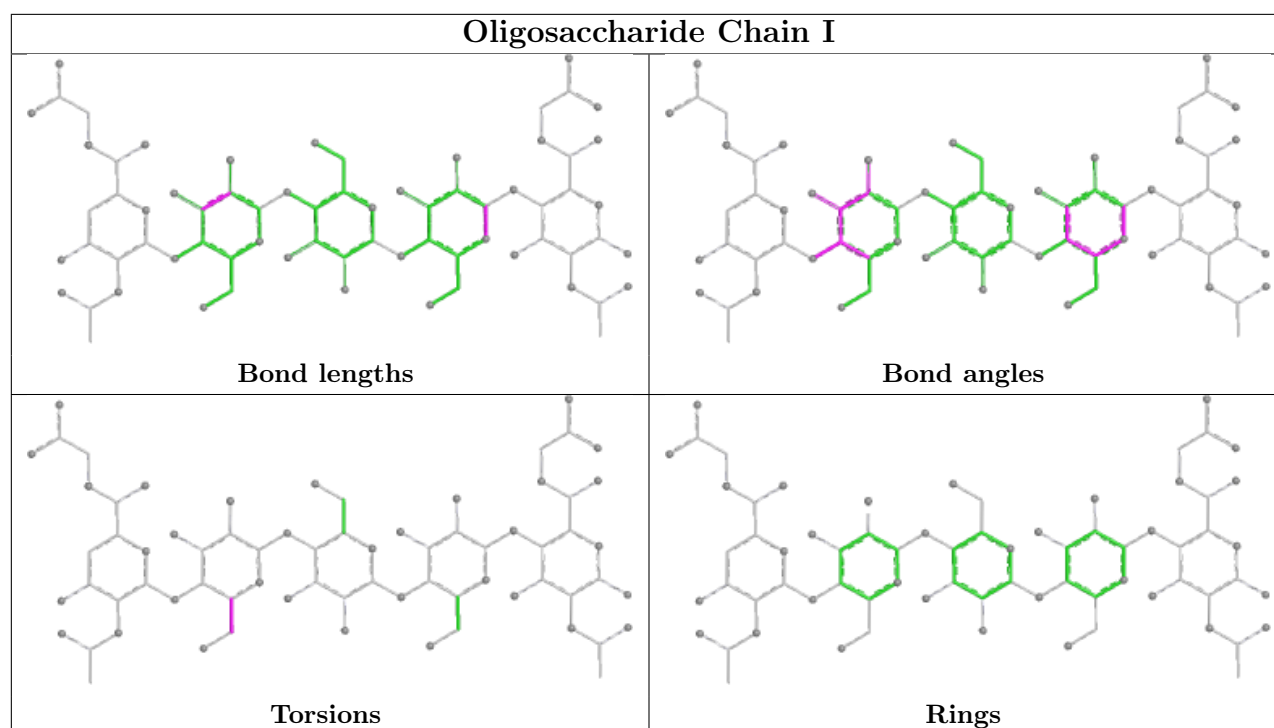


## Oligosaccharide Chain J



## Oligosaccharide Chain G





## 5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 4 are monoatomic - leaving 19 for Mogul analysis.

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	$\# Z  > 2$
7	FMT	A	507	-	2,2,2	0.64	0	1,1,1	0.62	0
7	FMT	D	504	-	2,2,2	0.64	0	1,1,1	0.61	0
6	GOL	D	502	-	5,5,5	0.35	0	5,5,5	0.34	0
7	FMT	A	508	-	2,2,2	0.64	0	1,1,1	0.62	0
6	GOL	A	505	-	5,5,5	0.38	0	5,5,5	0.59	0
7	FMT	C	504	-	2,2,2	0.64	0	1,1,1	0.63	0
6	GOL	A	502	-	5,5,5	0.34	0	5,5,5	0.48	0
6	GOL	B	502	-	5,5,5	0.36	0	5,5,5	0.48	0
7	FMT	B	506	-	2,2,2	0.64	0	1,1,1	0.61	0
6	GOL	B	503	-	5,5,5	0.35	0	5,5,5	0.56	0
6	GOL	A	506	-	5,5,5	0.34	0	5,5,5	0.37	0
6	GOL	C	503	-	5,5,5	0.35	0	5,5,5	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	GOL	B	504	-	5,5,5	0.35	0	5,5,5	0.45	0
6	GOL	A	503	-	5,5,5	0.38	0	5,5,5	0.42	0
6	GOL	D	503	-	5,5,5	0.34	0	5,5,5	0.45	0
6	GOL	C	502	-	5,5,5	0.33	0	5,5,5	0.38	0
6	GOL	A	504	-	5,5,5	0.29	0	5,5,5	0.39	0
7	FMT	A	509	-	2,2,2	0.65	0	1,1,1	0.60	0
6	GOL	B	505	-	5,5,5	0.31	0	5,5,5	0.52	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
6	GOL	A	503	-	-	4/4/4/4	-
6	GOL	D	503	-	-	0/4/4/4	-
6	GOL	D	502	-	-	3/4/4/4	-
6	GOL	A	505	-	-	2/4/4/4	-
6	GOL	B	505	-	-	0/4/4/4	-
6	GOL	C	502	-	-	4/4/4/4	-
6	GOL	A	504	-	-	2/4/4/4	-
6	GOL	C	503	-	-	1/4/4/4	-
6	GOL	B	503	-	-	0/4/4/4	-
6	GOL	A	502	-	-	0/4/4/4	-
6	GOL	A	506	-	-	3/4/4/4	-
6	GOL	B	502	-	-	0/4/4/4	-
6	GOL	B	504	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	504	GOL	O1-C1-C2-C3
6	B	504	GOL	O1-C1-C2-C3
6	A	504	GOL	O1-C1-C2-O2
6	D	502	GOL	O1-C1-C2-O2
6	A	503	GOL	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	366/380 (96%)	-0.51	4 (1%) 78 82	6, 17, 34, 48	18 (4%)
1	B	368/380 (96%)	-0.36	5 (1%) 73 78	7, 18, 39, 84	23 (6%)
1	C	367/380 (96%)	-0.10	7 (1%) 66 71	9, 23, 46, 79	20 (5%)
1	D	366/380 (96%)	-0.32	7 (1%) 66 71	9, 21, 39, 61	21 (5%)
All	All	1467/1520 (96%)	-0.32	23 (1%) 70 75	6, 20, 40, 84	82 (5%)

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	286	ASN	5.3
1	B	339	GLU	4.7
1	A	286	ASN	4.3
1	D	177	ILE	4.2
1	C	338	ASN	3.7

### 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
3	BGC	G	1	12/12	0.56	0.24	49,53,63,69	23
2	A1CF3	J	4	18/19	0.74	0.19	32,64,88,88	0

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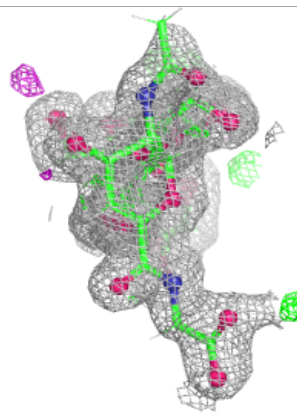
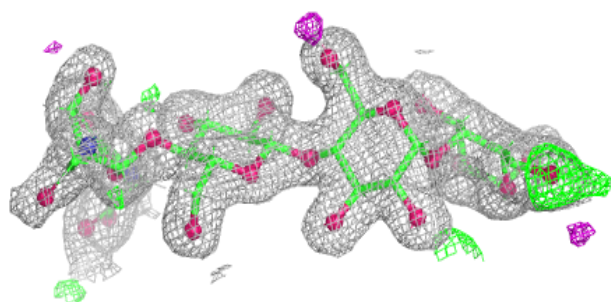
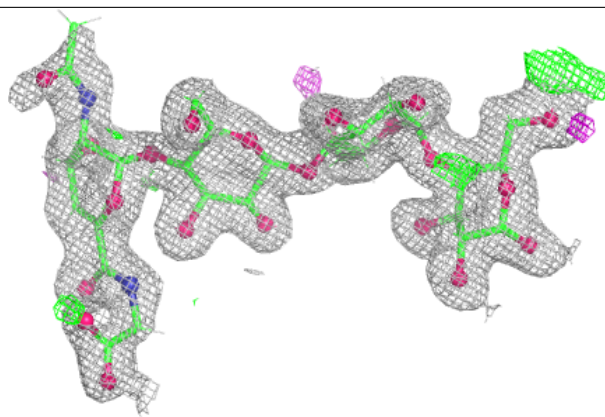
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GLA	I	2	11/12	0.77	0.16	24,42,49,55	21
4	A1CF4	I	1	20/20	0.83	0.15	21,43,56,66	34
4	BGC	I	4	11/12	0.84	0.14	27,41,50,59	21
3	BGC	G	5	11/12	0.87	0.14	22,37,52,55	21
4	GLC	I	3	11/12	0.88	0.11	21,28,34,41	21
3	A1CF4	G	2	19/20	0.88	0.14	19,38,46,50	32
3	A1CF3	G	6	18/19	0.89	0.15	16,37,53,68	30
4	A1CF3	I	5	18/19	0.89	0.16	21,30,62,62	30
3	GLA	G	3	11/12	0.90	0.10	20,33,45,47	21
3	GLC	G	4	11/12	0.91	0.11	17,30,36,37	21
2	A1CF3	E	4	18/19	0.93	0.10	15,26,49,49	30
2	GLA	H	1	12/12	0.93	0.09	16,27,39,49	0
2	BGC	J	3	11/12	0.93	0.09	18,30,44,48	0
2	GLA	F	1	12/12	0.94	0.07	14,19,31,59	23
2	A1CF3	H	4	18/19	0.94	0.09	16,28,43,43	0
2	GLC	J	2	11/12	0.94	0.07	17,23,32,38	0
2	A1CF3	F	4	18/19	0.94	0.08	14,25,34,38	30
2	BGC	H	3	11/12	0.95	0.06	18,22,26,29	0
2	GLC	E	2	11/12	0.95	0.06	11,15,24,29	21
2	GLA	J	1	12/12	0.96	0.06	17,21,35,38	0
2	GLC	F	2	11/12	0.96	0.06	14,21,27,29	21
2	GLC	H	2	11/12	0.96	0.06	16,25,30,36	0
2	BGC	F	3	11/12	0.96	0.06	13,18,24,26	21
2	BGC	E	3	11/12	0.96	0.06	11,18,23,26	21
2	GLA	E	1	12/12	0.97	0.04	12,17,21,22	23

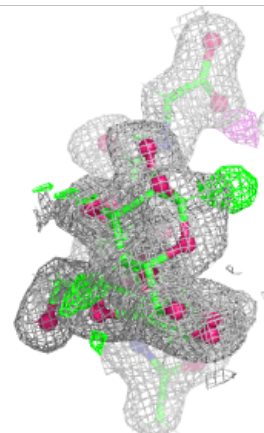
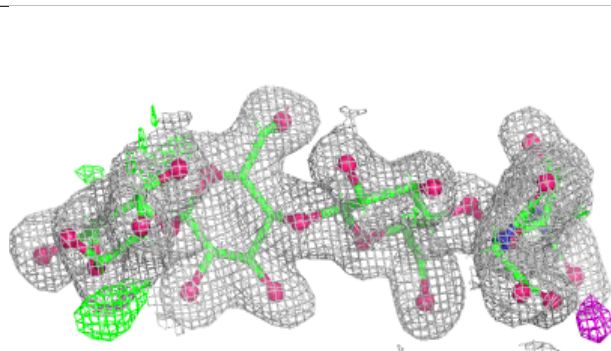
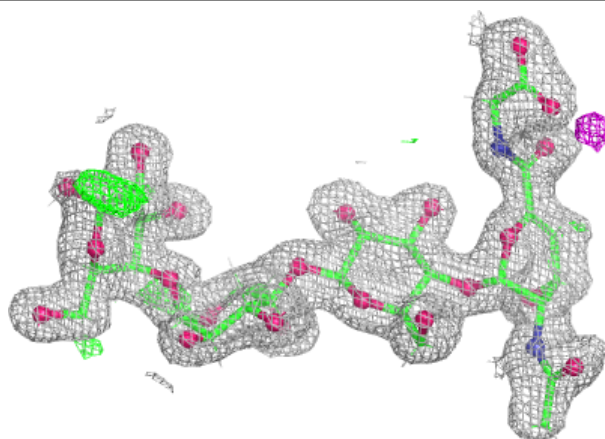
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain E:**

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

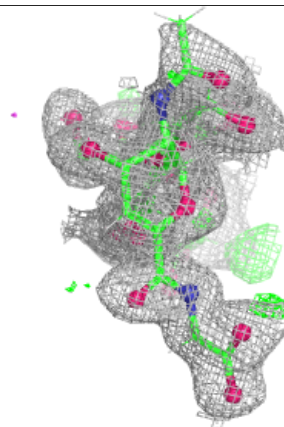
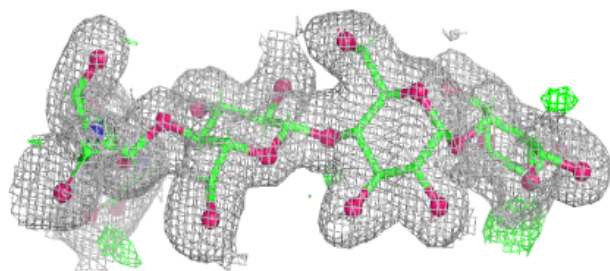
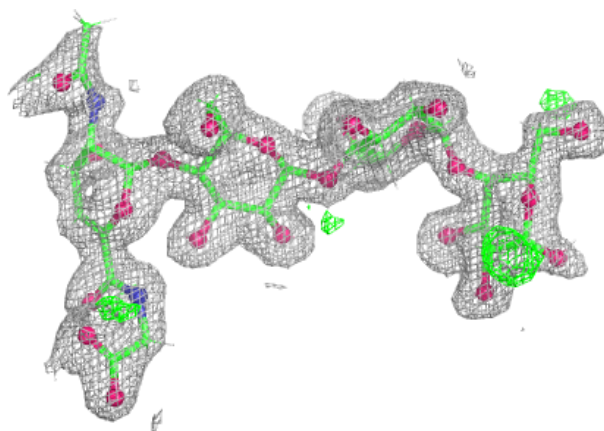
**Electron density around Chain F:**

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



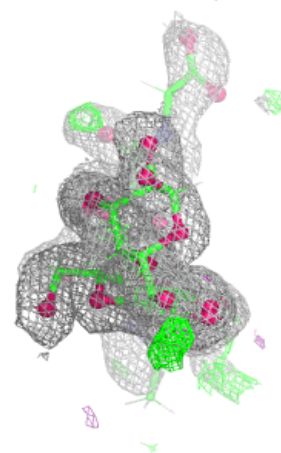
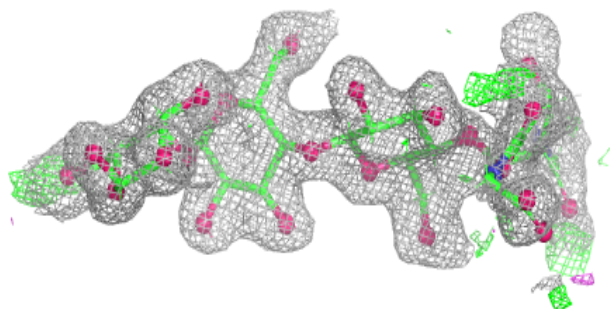
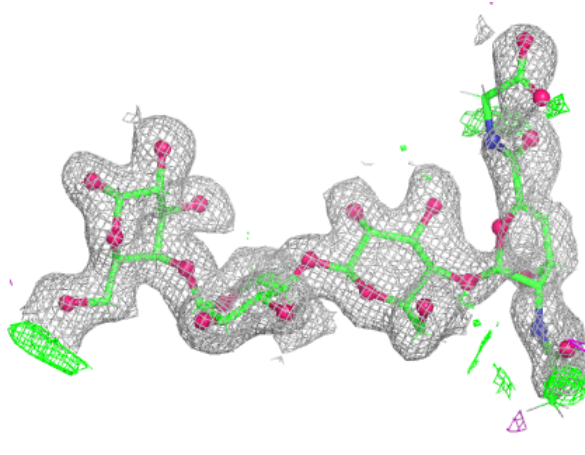
**Electron density around Chain H:**

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



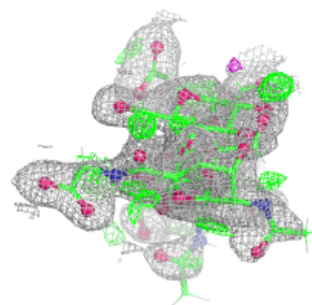
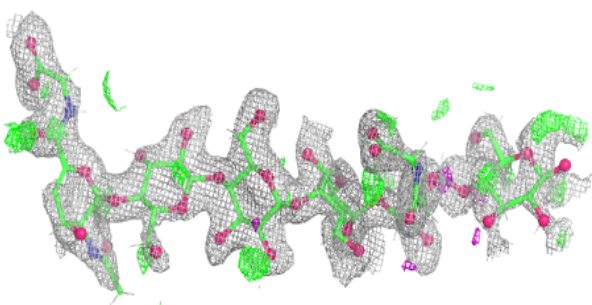
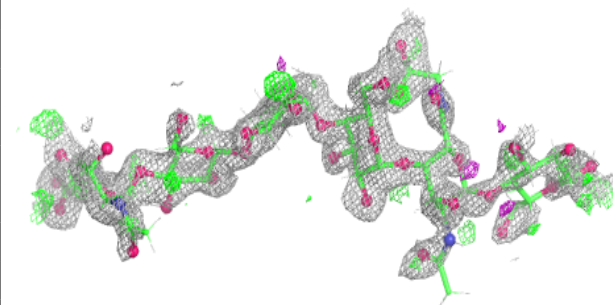
**Electron density around Chain J:**

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

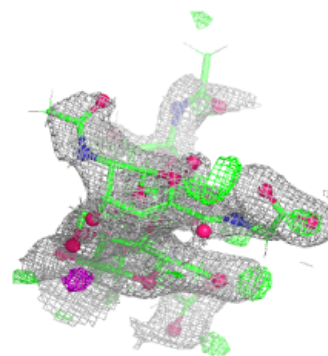
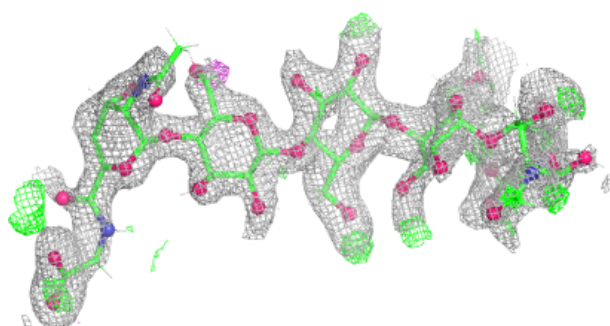
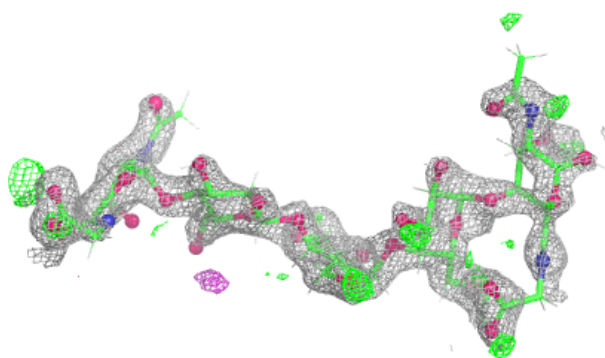


**Electron density around Chain G:**

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

**Electron density around Chain I:**

$2mF_o-DF_c$  (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
5	NA	B	501	1/1	0.71	0.19	13,13,13,13	1
6	GOL	A	506	6/6	0.75	0.15	25,43,53,60	6
6	GOL	A	505	6/6	0.78	0.18	29,37,47,56	6
6	GOL	C	503	6/6	0.78	0.16	32,45,53,59	4
6	GOL	B	505	6/6	0.85	0.11	12,33,39,47	6
6	GOL	B	503	6/6	0.85	0.14	26,42,54,65	4
6	GOL	A	504	6/6	0.86	0.10	16,29,39,41	3
6	GOL	A	502	6/6	0.88	0.13	18,35,42,45	3
6	GOL	B	504	6/6	0.88	0.13	27,36,47,54	5
5	NA	C	501	1/1	0.89	0.08	14,14,14,14	1
6	GOL	D	503	6/6	0.89	0.11	17,38,45,54	5
7	FMT	A	509	3/3	0.91	0.10	23,27,35,36	1
6	GOL	C	502	6/6	0.92	0.09	21,36,44,44	5
6	GOL	A	503	6/6	0.92	0.09	13,25,33,40	5
7	FMT	C	504	3/3	0.92	0.10	26,34,35,43	2
6	GOL	B	502	6/6	0.93	0.10	16,32,44,53	6
6	GOL	D	502	6/6	0.94	0.09	17,25,36,36	4
7	FMT	D	504	3/3	0.94	0.10	22,24,35,42	3
7	FMT	A	508	3/3	0.95	0.08	28,34,35,41	3
7	FMT	B	506	3/3	0.96	0.09	19,25,26,31	3
7	FMT	A	507	3/3	0.98	0.04	19,21,24,30	3
5	NA	A	501	1/1	0.98	0.05	14,14,14,14	1
5	NA	D	501	1/1	0.99	0.04	15,15,15,15	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.