



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:39 PM UTC

PDB ID : 2VXJ / pdb\_00002vxj  
Title : CRYSTAL STRUCTURE OF PA-IL LECTIN COMPLEXED WITH AGAL13BGAL14GLC AT 1.9 Å RESOLUTION  
Authors : Blanchard, B.; Nurisso, A.; Hollville, E.; Tetaud, C.; Wiels, J.; Pokorna, M.; Wimmerova, M.; Varrot, A.; Imberty, A.  
Deposited on : 2008-07-04  
Resolution : 1.90 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 : 4-5-2 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

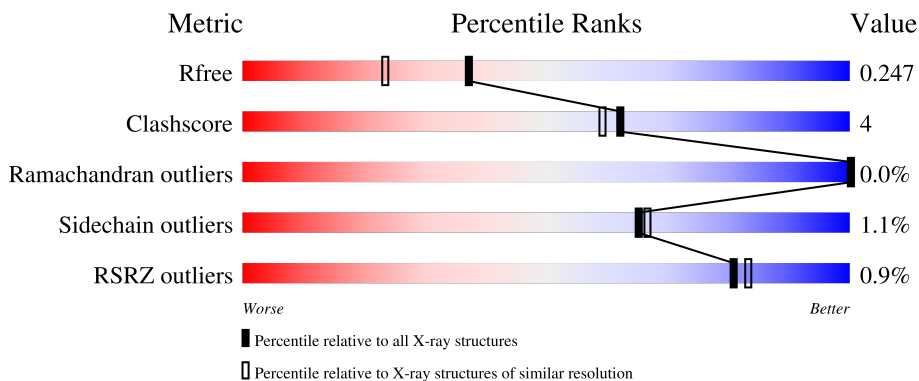
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	121	 2% 94% 6%
1	B	121	 87% 11%
1	C	121	 2% 90% 7%
1	D	121	 2% 91% 8%
1	E	121	 2% 91% 8%


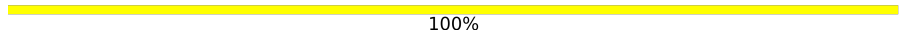
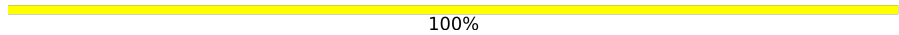
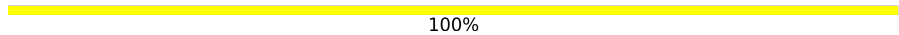
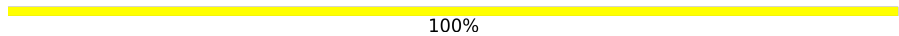
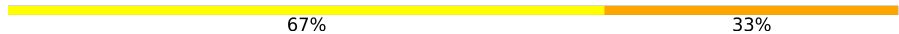
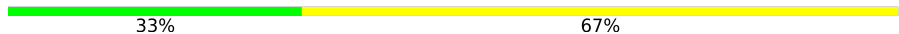
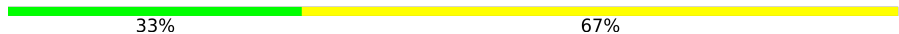
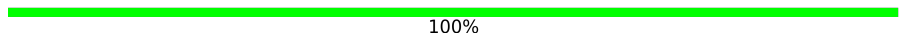
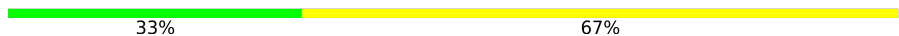
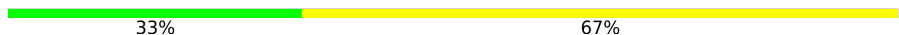
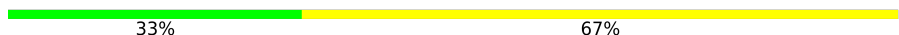
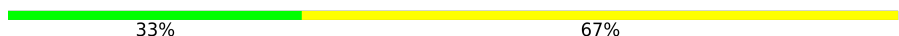



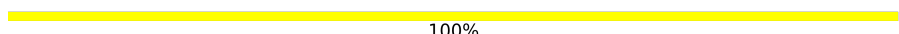
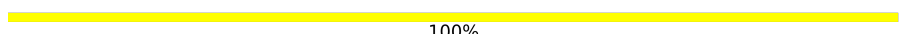
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Mol	Chain	Length	Quality of chain
1	F	121	89% 11%
1	G	121	3% 85% 14%
1	H	121	90% 10%
1	I	121	93% 6%
1	J	121	2% 87% 12%
1	K	121	91% 9%
1	L	121	89% 10%
1	M	121	2% 93% 7%
1	N	121	93% 6%
1	O	121	93% 7%
1	P	121	2% 90% 10%
1	Q	121	90% 9%
1	R	121	93% 6%
1	S	121	93% 7%
1	T	121	92% 8%
1	U	121	89% 11%
1	V	121	88% 12%
1	W	121	88% 12%
1	X	121	91% 9%
2	Y	3	33% 67%
2	Z	3	67% 33%
2	b	3	33% 67%
2	d	3	100%
2	e	3	100%
2	f	3	33% 67%

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Mol	Chain	Length	Quality of chain
2	g	3	 33% 67%
2	h	3	 100%
2	i	3	 100%
2	j	3	 100%
2	k	3	 100%
2	m	3	 67% 33%
2	n	3	 33% 67%
2	o	3	 33% 67%
2	p	3	 100%
2	q	3	 33% 67%
2	r	3	 33% 67%
2	s	3	 33% 67%
2	t	3	 33% 67%
2	u	3	 33% 67%
2	v	3	 33% 67%
3	a	3	 33% 67%
3	c	3	 100%
4	l	2	 100%

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
6	EDO	G	205	-	-	X	-
6	EDO	I	205	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 25600 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 PA-I GALACTOPHILIC LECTIN.

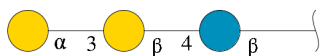
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	121	Total 901	C 567	N 156	O 175	S 3	0	0	0
1	B	118	Total 886	C 558	N 152	O 173	S 3	0	1	0
1	C	119	Total 886	C 558	N 153	O 172	S 3	0	0	0
1	D	120	Total 899	C 567	N 155	O 174	S 3	0	1	0
1	E	121	Total 907	C 572	N 157	O 175	S 3	0	1	0
1	F	121	Total 901	C 567	N 156	O 175	S 3	0	0	0
1	G	121	Total 897	C 564	N 155	O 175	S 3	0	0	0
1	H	121	Total 914	C 575	N 159	O 177	S 3	0	2	0
1	I	121	Total 901	C 567	N 156	O 175	S 3	0	0	0
1	J	120	Total 894	C 562	N 155	O 174	S 3	0	0	0
1	K	121	Total 901	C 567	N 156	O 175	S 3	0	0	0
1	L	121	Total 908	C 571	N 159	O 175	S 3	0	1	0
1	M	121	Total 906	C 570	N 157	O 176	S 3	0	1	0
1	N	120	Total 893	C 563	N 154	O 173	S 3	0	0	0
1	O	121	Total 907	C 571	N 156	O 177	S 3	0	1	0
1	P	121	Total 901	C 567	N 156	O 175	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	121	Total	C	N	O	S	0	1	0
			907	571	157	176	3			
1	R	121	Total	C	N	O	S	0	0	0
			901	567	156	175	3			
1	S	121	Total	C	N	O	S	0	0	0
			901	567	156	175	3			
1	T	121	Total	C	N	O	S	0	2	0
			910	573	156	178	3			
1	U	121	Total	C	N	O	S	0	1	0
			904	569	156	176	3			
1	V	121	Total	C	N	O	S	0	0	0
			901	567	156	175	3			
1	W	121	Total	C	N	O	S	0	0	0
			901	567	156	175	3			
1	X	121	Total	C	N	O	S	0	1	0
			907	571	156	177	3			

- Molecule 2 is an oligosaccharide called alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.



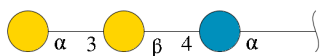
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	Y	3	Total	C	O	0	0	0
			34	18	16			
2	Z	3	Total	C	O	0	0	0
			34	18	16			
2	b	3	Total	C	O	0	0	0
			34	18	16			
2	d	3	Total	C	O	0	0	0
			34	18	16			
2	e	3	Total	C	O	0	0	0
			34	18	16			
2	f	3	Total	C	O	0	0	0
			34	18	16			
2	g	3	Total	C	O	0	0	0
			34	18	16			
2	h	3	Total	C	O	0	0	0
			34	18	16			
2	i	3	Total	C	O	0	0	0
			34	18	16			

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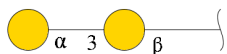
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	j	3	Total	C	O	0	0	0
			34	18	16			
2	k	3	Total	C	O	0	0	0
			34	18	16			
2	m	3	Total	C	O	0	0	0
			34	18	16			
2	n	3	Total	C	O	0	0	0
			34	18	16			
2	o	3	Total	C	O	0	0	0
			34	18	16			
2	p	3	Total	C	O	0	0	0
			34	18	16			
2	q	3	Total	C	O	0	0	0
			34	18	16			
2	r	3	Total	C	O	0	0	0
			34	18	16			
2	s	3	Total	C	O	0	0	0
			34	18	16			
2	t	3	Total	C	O	0	0	0
			34	18	16			
2	u	3	Total	C	O	0	0	0
			34	18	16			
2	v	3	Total	C	O	0	0	0
			34	18	16			

- Molecule 3 is an oligosaccharide called alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	a	3	Total	C	O	0	0	0
			34	18	16			
3	c	3	Total	C	O	0	0	0
			34	18	16			

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	1	2	Total	C	O	0	0	0
			22	12	10			

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

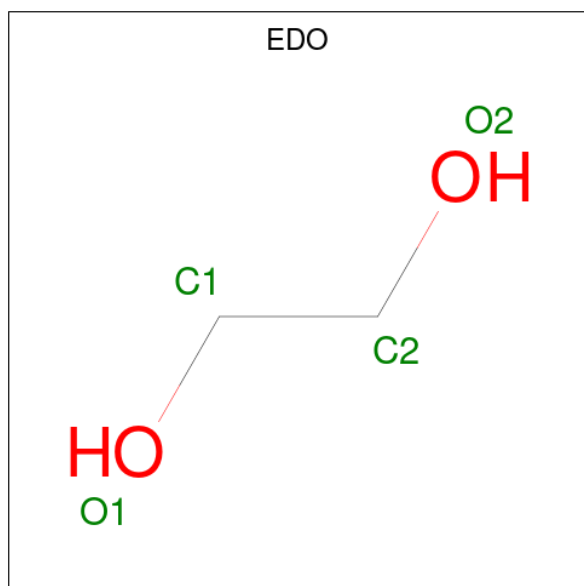
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	B	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		
5	D	1	Total	Ca	0	0
			1	1		
5	E	1	Total	Ca	0	0
			1	1		
5	F	1	Total	Ca	0	0
			1	1		
5	G	1	Total	Ca	0	0
			1	1		
5	H	1	Total	Ca	0	0
			1	1		
5	I	1	Total	Ca	0	0
			1	1		
5	J	1	Total	Ca	0	0
			1	1		
5	K	1	Total	Ca	0	0
			1	1		
5	L	1	Total	Ca	0	0
			1	1		
5	M	1	Total	Ca	0	0
			1	1		
5	N	1	Total	Ca	0	0
			1	1		
5	O	1	Total	Ca	0	0
			1	1		
5	P	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Q	1	Total Ca 1 1	0	0
5	R	1	Total Ca 1 1	0	0
5	S	1	Total Ca 1 1	0	0
5	T	1	Total Ca 1 1	0	0
5	U	1	Total Ca 1 1	0	0
5	V	1	Total Ca 1 1	0	0
5	W	1	Total Ca 1 1	0	0
5	X	1	Total Ca 1 1	0	0

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



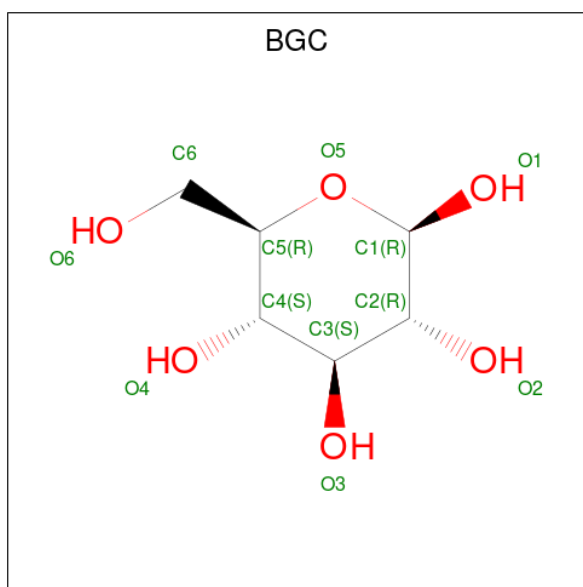
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	E	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	G	1	Total	C	O	0	0
			4	2	2		
6	H	1	Total	C	O	0	0
			4	2	2		
6	I	1	Total	C	O	0	0
			4	2	2		
6	I	1	Total	C	O	0	0
			4	2	2		
6	L	1	Total	C	O	0	0
			4	2	2		
6	M	1	Total	C	O	0	0
			4	2	2		
6	M	1	Total	C	O	0	0
			4	2	2		
6	N	1	Total	C	O	0	0
			4	2	2		
6	O	1	Total	C	O	0	0
			4	2	2		
6	Q	1	Total	C	O	0	0
			4	2	2		
6	Q	1	Total	C	O	0	0
			4	2	2		
6	S	1	Total	C	O	0	0
			4	2	2		
6	U	1	Total	C	O	0	0
			4	2	2		
6	V	1	Total	C	O	0	0
			4	2	2		
6	W	1	Total	C	O	0	0
			4	2	2		
6	W	1	Total	C	O	0	0
			4	2	2		
6	X	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is beta-D-glucopyranose (CCD ID: BGC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	N	1	Total	C O	0	0
			12	6 6		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	141	Total	O	0	0
			141	141		
8	B	122	Total	O	0	0
			122	122		
8	C	115	Total	O	0	0
			115	115		
8	D	124	Total	O	0	0
			124	124		
8	E	130	Total	O	0	0
			130	130		
8	F	113	Total	O	0	0
			113	113		
8	G	125	Total	O	0	0
			125	125		
8	H	135	Total	O	0	0
			135	135		
8	I	140	Total	O	0	0
			140	140		
8	J	123	Total	O	0	0
			123	123		
8	K	137	Total	O	0	0
			137	137		

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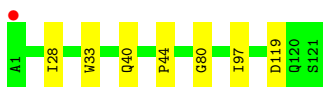
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
8	L	133	Total 133	O 133	0	0
8	M	124	Total 124	O 124	0	0
8	N	119	Total 119	O 119	0	0
8	O	107	Total 107	O 107	0	0
8	P	120	Total 120	O 120	0	0
8	Q	137	Total 137	O 137	0	0
8	R	125	Total 125	O 125	0	0
8	S	130	Total 130	O 130	0	0
8	T	134	Total 134	O 134	0	0
8	U	138	Total 138	O 138	0	0
8	V	122	Total 122	O 122	0	0
8	W	123	Total 123	O 123	0	0
8	X	129	Total 129	O 129	0	0

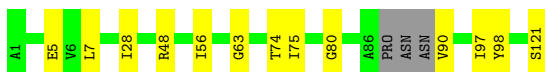
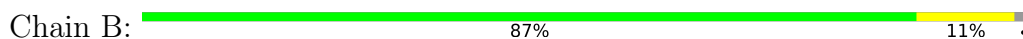
### 3 Residue-property plots [i](#)

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.

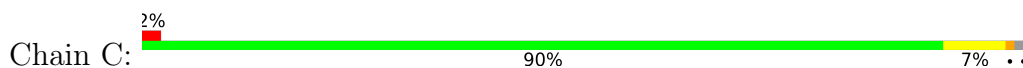
- Molecule 1: PA-I GALACTOPHILIC LECTIN



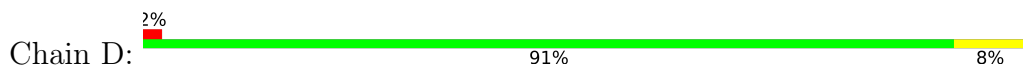
- Molecule 1: PA-I GALACTOPHILIC LECTIN



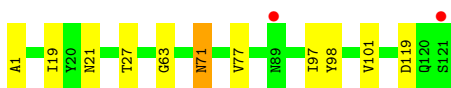
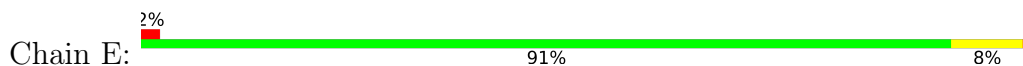
- Molecule 1: PA-I GALACTOPHILIC LECTIN




- Molecule 1: PA-I GALACTOPHILIC LECTIN

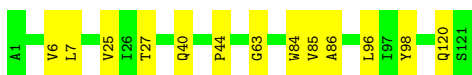


- Molecule 1: PA-I GALACTOPHILIC LECTIN




- Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain F:  89% 11%




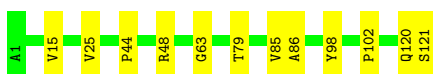
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain G:  3% 85% 14%




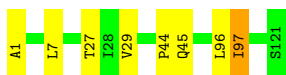
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain H:  90% 10%




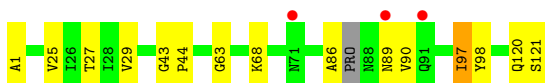
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain I:  93% 6%



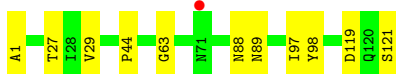
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain J:  2% 87% 12%




● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain K:  91% 9%



● Molecule 1: PA-I GALACTOPHILIC LECTIN

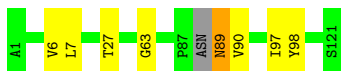
Chain L:  89% 10%



● Molecule 1: PA-I GALACTOPHILIC LECTIN



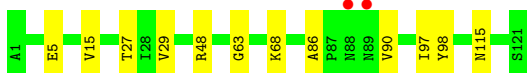
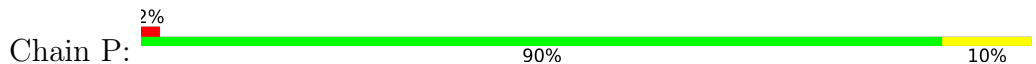
● Molecule 1: PA-I GALACTOPHILIC LECTIN



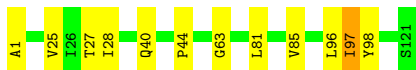
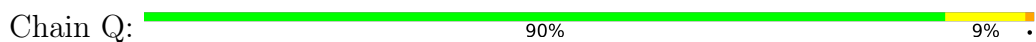
● Molecule 1: PA-I GALACTOPHILIC LECTIN



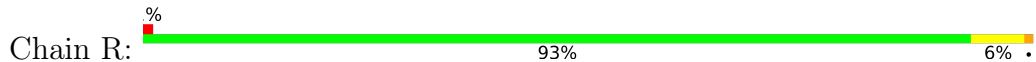
● Molecule 1: PA-I GALACTOPHILIC LECTIN



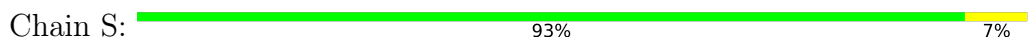
● Molecule 1: PA-I GALACTOPHILIC LECTIN



● Molecule 1: PA-I GALACTOPHILIC LECTIN



● Molecule 1: PA-I GALACTOPHILIC LECTIN




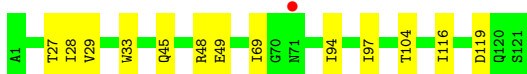
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain T:  92% 8%




● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain U:  89% 11%

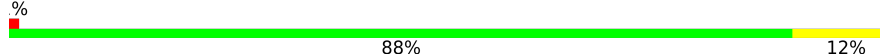


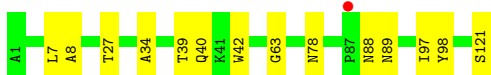
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain V:  88% 12%

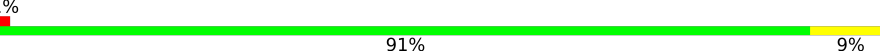


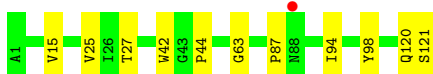
● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain W:  88% 12%

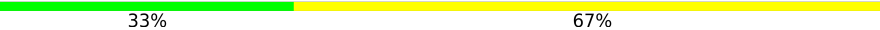


● Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain X:  91% 9%

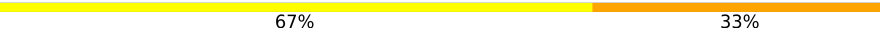


● Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain Y:  33% 67%



● Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain Z:  67% 33%

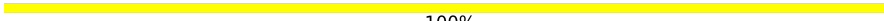


- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain b:  33% 67%

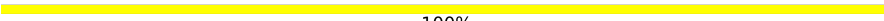
BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain d:  100%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain e:  100%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain f:  33% 67%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain g:  33% 67%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain h:  100%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain i:  100%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain j:  100%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain k:  100%


BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain m:  67% 33%


BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain n:  33% 67%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain o:  33% 67%

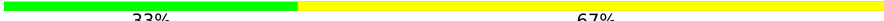
BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain p:  100%


BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain q:  33% 67%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain r:  33% 67%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain s:  33% 67%


BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain t:  33% 67%

BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain u:  33% 67%

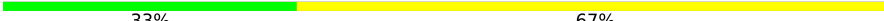
BGC1  
GAL2  
GLA3

- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain v:  33% 67%


BGC1  
GAL2  
GLA3

- Molecule 3: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain a:  33% 67%

GLC1  
GAL2  
GLA3

- Molecule 3: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain c:  100%

GIC1  
GAL2  
GLA3

- Molecule 4: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose

Chain l:  100%

GAL1  
GLA2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.18Å 86.52Å 119.08Å 93.93° 98.16° 90.08°	Depositor
Resolution (Å)	55.00 – 1.90 55.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.9 (55.00-1.90) 86.7 (55.00-1.90)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 1.90Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.185 , 0.245 0.190 , 0.247	Depositor DCC
$R_{free}$ test set	10734 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	11.4	Xtrriage
Anisotropy	0.966	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 45.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	25600	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8448e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: CA, GAL, GLA, BGC, EDO, GLC

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	0.98	0/924	0.89	0/1262
1	B	0.97	1/907 (0.1%)	0.88	0/1236
1	C	0.94	0/907	0.90	0/1236
1	D	0.92	0/924	0.87	0/1260
1	E	1.00	1/933 (0.1%)	0.96	5/1273 (0.4%)
1	F	0.97	0/924	0.91	0/1262
1	G	1.04	1/920 (0.1%)	0.87	0/1258
1	H	0.96	0/943	0.89	2/1287 (0.2%)
1	I	1.03	0/924	0.87	0/1262
1	J	0.94	0/915	0.90	0/1247
1	K	0.96	0/924	0.90	0/1262
1	L	0.99	0/935	0.87	0/1276
1	M	0.94	0/932	0.89	0/1273
1	N	0.99	1/915 (0.1%)	0.90	0/1248
1	O	1.01	0/933	0.87	0/1274
1	P	0.92	0/924	0.90	0/1262
1	Q	0.96	0/933	0.90	0/1274
1	R	0.97	0/924	0.93	0/1262
1	S	0.94	0/924	0.89	0/1262
1	T	1.00	0/939	0.92	0/1282
1	U	0.93	0/930	0.92	0/1270
1	V	1.00	0/924	0.88	0/1262
1	W	1.01	1/924 (0.1%)	0.90	0/1262
1	X	0.99	1/933 (0.1%)	0.89	0/1274
All	All	0.97	6/22215 (0.0%)	0.90	7/30326 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	6	VAL	CA-CB	5.84	1.61	1.53
1	B	75	ILE	CA-C	5.71	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	94	ILE	CA-CB	5.63	1.60	1.54
1	E	19	ILE	CA-CB	5.62	1.60	1.53
1	G	75	ILE	CA-CB	5.62	1.58	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	101	VAL	CA-C-N	-6.03	113.32	119.83
1	E	101	VAL	C-N-CA	-6.03	113.32	119.83
1	E	77	VAL	N-CA-C	-5.69	107.29	111.90
1	H	86	ALA	CA-C-N	-5.48	114.61	120.03
1	H	86	ALA	C-N-CA	-5.48	114.61	120.03

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	901	0	861	6	0
1	B	886	0	844	7	0
1	C	886	0	847	9	0
1	D	899	0	862	10	0
1	E	907	0	874	5	0
1	F	901	0	861	8	0
1	G	897	0	850	15	0
1	H	914	0	878	11	0
1	I	901	0	861	8	0
1	J	894	0	853	12	0
1	K	901	0	861	9	0
1	L	908	0	870	10	0
1	M	906	0	867	9	0
1	N	893	0	854	4	0
1	O	907	0	867	8	0
1	P	901	0	861	12	0
1	Q	907	0	869	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	901	0	861	6	0
1	S	901	0	861	8	0
1	T	910	0	872	7	0
1	U	904	0	866	11	0
1	V	901	0	861	12	0
1	W	901	0	861	11	0
1	X	907	0	867	8	0
2	Y	34	0	28	0	0
2	Z	34	0	28	1	0
2	b	34	0	28	0	0
2	d	34	0	28	0	0
2	e	34	0	28	0	0
2	f	34	0	28	0	0
2	g	34	0	28	0	0
2	h	34	0	28	0	0
2	i	34	0	28	0	0
2	j	34	0	28	0	0
2	k	34	0	28	0	0
2	m	34	0	28	3	0
2	n	34	0	28	0	0
2	o	34	0	29	0	0
2	p	34	0	28	0	0
2	q	34	0	28	0	0
2	r	34	0	28	0	0
2	s	34	0	28	0	0
2	t	34	0	28	0	0
2	u	34	0	28	0	0
2	v	34	0	28	0	0
3	a	34	0	28	0	0
3	c	34	0	28	0	0
4	l	22	0	17	0	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
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	1	0	0	0	0
5	M	1	0	0	0	0
5	N	1	0	0	0	0
5	O	1	0	0	0	0
5	P	1	0	0	0	0
5	Q	1	0	0	0	0
5	R	1	0	0	0	0
5	S	1	0	0	0	0
5	T	1	0	0	0	0
5	U	1	0	0	0	0
5	V	1	0	0	0	0
5	W	1	0	0	0	0
5	X	1	0	0	0	0
6	A	4	0	6	1	0
6	D	4	0	6	1	0
6	E	4	0	6	1	0
6	G	4	0	6	7	0
6	H	4	0	6	1	0
6	I	8	0	11	6	0
6	L	4	0	6	1	0
6	M	8	0	12	2	0
6	N	4	0	6	0	0
6	O	4	0	6	1	0
6	Q	8	0	12	1	0
6	S	4	0	6	1	0
6	U	4	0	6	1	0
6	V	4	0	6	2	0
6	W	8	0	12	1	0
6	X	4	0	6	2	0
7	N	12	0	11	0	0
8	A	141	0	0	3	0
8	B	122	0	0	1	0
8	C	115	0	0	0	0
8	D	124	0	0	4	0
8	E	130	0	0	1	0
8	F	113	0	0	0	0
8	G	125	0	0	2	0
8	H	135	0	0	2	0
8	I	140	0	0	0	0
8	J	123	0	0	1	0
8	K	137	0	0	2	0
8	L	133	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	M	124	0	0	3	0
8	N	119	0	0	0	0
8	O	107	0	0	2	0
8	P	120	0	0	5	0
8	Q	137	0	0	1	0
8	R	125	0	0	0	0
8	S	130	0	0	2	0
8	T	134	0	0	1	0
8	U	138	0	0	2	0
8	V	122	0	0	1	0
8	W	123	0	0	4	0
8	X	129	0	0	2	0
All	All	25600	0	21481	179	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 4.

The worst 5 of 179 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)
6:G:205:EDO:H22	1:H:44:PRO:HD2	1.45	0.98
8:O:320:HOH:O	2:m:2:GAL:H4	1.78	0.82
1:W:88:ASN:HB2	8:W:304:HOH:O	1.83	0.78
1:L:5:GLU:HG3	8:L:403:HOH:O	1.83	0.78
1:G:53:GLN:HG2	1:G:101:VAL:HG21	1.67	0.77

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	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
1	B	115/121 (95%)	112 (97%)	3 (3%)	0	100	100
1	C	115/121 (95%)	111 (96%)	4 (4%)	0	100	100
1	D	117/121 (97%)	114 (97%)	3 (3%)	0	100	100
1	E	120/121 (99%)	115 (96%)	5 (4%)	0	100	100
1	F	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
1	G	119/121 (98%)	114 (96%)	4 (3%)	1 (1%)	16	8
1	H	121/121 (100%)	118 (98%)	3 (2%)	0	100	100
1	I	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
1	J	116/121 (96%)	112 (97%)	4 (3%)	0	100	100
1	K	119/121 (98%)	117 (98%)	2 (2%)	0	100	100
1	L	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	M	120/121 (99%)	115 (96%)	5 (4%)	0	100	100
1	N	116/121 (96%)	113 (97%)	3 (3%)	0	100	100
1	O	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	P	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
1	Q	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	R	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
1	S	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
1	T	121/121 (100%)	118 (98%)	3 (2%)	0	100	100
1	U	120/121 (99%)	118 (98%)	2 (2%)	0	100	100
1	V	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
1	W	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
1	X	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
All	All	2851/2904 (98%)	2761 (97%)	89 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	54	GLY

### 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	94/94 (100%)	93 (99%)	1 (1%)	65	67
1	B	92/94 (98%)	90 (98%)	2 (2%)	45	42
1	C	92/94 (98%)	91 (99%)	1 (1%)	65	67
1	D	94/94 (100%)	94 (100%)	0	100	100
1	E	95/94 (101%)	93 (98%)	2 (2%)	47	44
1	F	94/94 (100%)	93 (99%)	1 (1%)	65	67
1	G	93/94 (99%)	90 (97%)	3 (3%)	34	27
1	H	96/94 (102%)	96 (100%)	0	100	100
1	I	94/94 (100%)	93 (99%)	1 (1%)	65	67
1	J	93/94 (99%)	92 (99%)	1 (1%)	65	67
1	K	94/94 (100%)	93 (99%)	1 (1%)	65	67
1	L	95/94 (101%)	92 (97%)	3 (3%)	34	27
1	M	95/94 (101%)	95 (100%)	0	100	100
1	N	93/94 (99%)	89 (96%)	4 (4%)	26	18
1	O	95/94 (101%)	95 (100%)	0	100	100
1	P	94/94 (100%)	94 (100%)	0	100	100
1	Q	95/94 (101%)	94 (99%)	1 (1%)	65	67
1	R	94/94 (100%)	93 (99%)	1 (1%)	65	67
1	S	94/94 (100%)	94 (100%)	0	100	100
1	T	96/94 (102%)	96 (100%)	0	100	100
1	U	95/94 (101%)	94 (99%)	1 (1%)	65	67
1	V	94/94 (100%)	94 (100%)	0	100	100
1	W	94/94 (100%)	92 (98%)	2 (2%)	47	44
1	X	95/94 (101%)	95 (100%)	0	100	100
All	All	2260/2256 (100%)	2235 (99%)	25 (1%)	65	67

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	48[B]	ARG
1	N	89	ASN
1	W	97	ILE
1	N	7	LEU
1	N	90	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	89	ASN
1	U	88	ASN
1	L	115	ASN
1	P	115	ASN
1	V	10	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

71 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	BGC	Y	1	2	12,12,12	0.89	0	17,17,17	0.83	0
2	GAL	Y	2	2	11,11,12	0.89	1 (9%)	15,15,17	1.14	2 (13%)
2	GLA	Y	3	5,2	11,11,12	0.91	0	15,15,17	1.23	1 (6%)
2	BGC	Z	1	2	12,12,12	0.46	0	17,17,17	1.13	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GAL	Z	2	2	11,11,12	1.01	1 (9%)	15,15,17	0.79	0
2	GLA	Z	3	5,2	11,11,12	0.84	0	15,15,17	1.20	1 (6%)
3	GLC	a	1	3	12,12,12	0.51	0	17,17,17	0.92	0
3	GAL	a	2	3	11,11,12	0.80	0	15,15,17	1.59	5 (33%)
3	GLA	a	3	5,3	11,11,12	0.54	0	15,15,17	1.30	2 (13%)
2	BGC	b	1	2	12,12,12	0.48	0	17,17,17	1.06	1 (5%)
2	GAL	b	2	2	11,11,12	0.77	0	15,15,17	1.03	0
2	GLA	b	3	5,2	11,11,12	0.59	0	15,15,17	1.02	1 (6%)
3	GLC	c	1	3	12,12,12	0.58	0	17,17,17	2.01	5 (29%)
3	GAL	c	2	3	11,11,12	0.88	0	15,15,17	1.11	1 (6%)
3	GLA	c	3	5,3	11,11,12	0.75	0	15,15,17	1.32	3 (20%)
2	BGC	d	1	2	12,12,12	0.58	0	17,17,17	0.83	1 (5%)
2	GAL	d	2	2	11,11,12	1.00	1 (9%)	15,15,17	0.95	0
2	GLA	d	3	5,2	11,11,12	0.71	0	15,15,17	1.30	1 (6%)
2	BGC	e	1	2	12,12,12	0.68	0	17,17,17	1.20	1 (5%)
2	GAL	e	2	2	11,11,12	0.75	0	15,15,17	0.96	1 (6%)
2	GLA	e	3	5,2	11,11,12	1.24	2 (18%)	15,15,17	1.96	3 (20%)
2	BGC	f	1	2	12,12,12	0.43	0	17,17,17	1.34	2 (11%)
2	GAL	f	2	2	11,11,12	0.65	0	15,15,17	0.87	0
2	GLA	f	3	5,2	11,11,12	0.54	0	15,15,17	1.29	2 (13%)
2	BGC	g	1	2	12,12,12	0.69	0	17,17,17	0.89	0
2	GAL	g	2	2	11,11,12	0.67	0	15,15,17	1.24	3 (20%)
2	GLA	g	3	5,2	11,11,12	0.85	0	15,15,17	1.56	3 (20%)
2	BGC	h	1	2	12,12,12	0.59	0	17,17,17	1.19	1 (5%)
2	GAL	h	2	2	11,11,12	0.98	1 (9%)	15,15,17	0.93	1 (6%)
2	GLA	h	3	5,2	11,11,12	0.57	0	15,15,17	1.20	1 (6%)
2	BGC	i	1	2	12,12,12	0.69	0	17,17,17	1.24	2 (11%)
2	GAL	i	2	2	11,11,12	0.56	0	15,15,17	1.12	1 (6%)
2	GLA	i	3	5,2	11,11,12	0.54	0	15,15,17	1.42	4 (26%)
2	BGC	j	1	2	12,12,12	0.58	0	17,17,17	1.50	3 (17%)
2	GAL	j	2	2	11,11,12	1.01	1 (9%)	15,15,17	1.07	0
2	GLA	j	3	5,2	11,11,12	0.42	0	15,15,17	1.26	2 (13%)
2	BGC	k	1	2	12,12,12	0.59	0	17,17,17	1.47	3 (17%)
2	GAL	k	2	2	11,11,12	1.22	1 (9%)	15,15,17	0.95	1 (6%)
2	GLA	k	3	5,2	11,11,12	0.79	0	15,15,17	1.18	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GAL	l	1	4	11,11,12	0.71	0	15,15,17	1.52	2 (13%)
4	GLA	l	2	4,5	11,11,12	0.59	0	15,15,17	1.53	4 (26%)
2	BGC	m	1	2	12,12,12	0.56	0	17,17,17	1.06	2 (11%)
2	GAL	m	2	2	11,11,12	0.80	0	15,15,17	0.88	0
2	GLA	m	3	5,2	11,11,12	0.87	0	15,15,17	1.16	1 (6%)
2	BGC	n	1	2	12,12,12	0.57	0	17,17,17	0.97	1 (5%)
2	GAL	n	2	2	11,11,12	0.68	0	15,15,17	0.69	0
2	GLA	n	3	5,2	11,11,12	0.53	0	15,15,17	1.18	1 (6%)
2	BGC	o	1	2	12,12,12	0.58	0	17,17,17	0.95	0
2	GAL	o	2	2	11,11,12	0.82	0	15,15,17	0.99	1 (6%)
2	GLA	o	3	5,2	11,11,12	0.77	0	15,15,17	1.69	5 (33%)
2	BGC	p	1	2	12,12,12	0.53	0	17,17,17	1.09	0
2	GAL	p	2	2	11,11,12	0.88	0	15,15,17	0.77	0
2	GLA	p	3	5,2	11,11,12	0.59	0	15,15,17	0.80	0
2	BGC	q	1	2	12,12,12	0.57	0	17,17,17	1.62	3 (17%)
2	GAL	q	2	2	11,11,12	0.69	0	15,15,17	0.74	0
2	GLA	q	3	5,2	11,11,12	0.56	0	15,15,17	1.65	2 (13%)
2	BGC	r	1	2	12,12,12	0.63	0	17,17,17	1.25	1 (5%)
2	GAL	r	2	2	11,11,12	0.60	0	15,15,17	1.07	0
2	GLA	r	3	5,2	11,11,12	0.43	0	15,15,17	1.41	3 (20%)
2	BGC	s	1	2	12,12,12	0.59	0	17,17,17	2.31	6 (35%)
2	GAL	s	2	2	11,11,12	0.58	0	15,15,17	0.96	0
2	GLA	s	3	5,2	11,11,12	0.62	0	15,15,17	1.35	1 (6%)
2	BGC	t	1	2	12,12,12	0.68	0	17,17,17	0.94	0
2	GAL	t	2	2	11,11,12	0.89	1 (9%)	15,15,17	1.07	1 (6%)
2	GLA	t	3	5,2	11,11,12	0.65	0	15,15,17	1.21	1 (6%)
2	BGC	u	1	2	12,12,12	0.55	0	17,17,17	1.21	2 (11%)
2	GAL	u	2	2	11,11,12	0.59	0	15,15,17	0.90	0
2	GLA	u	3	5,2	11,11,12	0.56	0	15,15,17	1.33	4 (26%)
2	BGC	v	1	2	12,12,12	0.65	0	17,17,17	0.94	0
2	GAL	v	2	2	11,11,12	0.90	1 (9%)	15,15,17	0.74	0
2	GLA	v	3	5,2	11,11,12	0.74	0	15,15,17	1.31	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	Y	1	2	-	0/2/22/22	0/1/1/1
2	GAL	Y	2	2	-	2/2/19/22	0/1/1/1
2	GLA	Y	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	Z	1	2	-	2/2/22/22	0/1/1/1
2	GAL	Z	2	2	-	0/2/19/22	0/1/1/1
2	GLA	Z	3	5,2	-	0/2/19/22	0/1/1/1
3	GLC	a	1	3	-	0/2/22/22	0/1/1/1
3	GAL	a	2	3	-	2/2/19/22	0/1/1/1
3	GLA	a	3	5,3	-	0/2/19/22	0/1/1/1
2	BGC	b	1	2	-	2/2/22/22	0/1/1/1
2	GAL	b	2	2	-	1/2/19/22	0/1/1/1
2	GLA	b	3	5,2	-	1/2/19/22	0/1/1/1
3	GLC	c	1	3	-	2/2/22/22	0/1/1/1
3	GAL	c	2	3	-	0/2/19/22	0/1/1/1
3	GLA	c	3	5,3	-	0/2/19/22	0/1/1/1
2	BGC	d	1	2	-	0/2/22/22	0/1/1/1
2	GAL	d	2	2	-	0/2/19/22	0/1/1/1
2	GLA	d	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	e	1	2	-	0/2/22/22	0/1/1/1
2	GAL	e	2	2	-	1/2/19/22	0/1/1/1
2	GLA	e	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	f	1	2	-	0/2/22/22	0/1/1/1
2	GAL	f	2	2	-	2/2/19/22	0/1/1/1
2	GLA	f	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	g	1	2	-	0/2/22/22	0/1/1/1
2	GAL	g	2	2	-	0/2/19/22	0/1/1/1
2	GLA	g	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	h	1	2	-	0/2/22/22	0/1/1/1
2	GAL	h	2	2	-	0/2/19/22	0/1/1/1
2	GLA	h	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	i	1	2	-	0/2/22/22	0/1/1/1
2	GAL	i	2	2	-	2/2/19/22	0/1/1/1
2	GLA	i	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	j	1	2	-	0/2/22/22	0/1/1/1
2	GAL	j	2	2	-	1/2/19/22	0/1/1/1
2	GLA	j	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	k	1	2	-	0/2/22/22	0/1/1/1
2	GAL	k	2	2	-	2/2/19/22	0/1/1/1
2	GLA	k	3	5,2	-	0/2/19/22	0/1/1/1
4	GAL	l	1	4	-	2/2/19/22	0/1/1/1
4	GLA	l	2	4,5	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	m	1	2	-	2/2/22/22	0/1/1/1
2	GAL	m	2	2	-	0/2/19/22	0/1/1/1
2	GLA	m	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	n	1	2	-	0/2/22/22	0/1/1/1
2	GAL	n	2	2	-	0/2/19/22	0/1/1/1
2	GLA	n	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	o	1	2	-	0/2/22/22	0/1/1/1
2	GAL	o	2	2	-	0/2/19/22	0/1/1/1
2	GLA	o	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	p	1	2	-	0/2/22/22	0/1/1/1
2	GAL	p	2	2	-	1/2/19/22	0/1/1/1
2	GLA	p	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	q	1	2	-	1/2/22/22	0/1/1/1
2	GAL	q	2	2	-	0/2/19/22	0/1/1/1
2	GLA	q	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	r	1	2	-	2/2/22/22	0/1/1/1
2	GAL	r	2	2	-	2/2/19/22	0/1/1/1
2	GLA	r	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	s	1	2	-	2/2/22/22	0/1/1/1
2	GAL	s	2	2	-	1/2/19/22	0/1/1/1
2	GLA	s	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	t	1	2	-	2/2/22/22	0/1/1/1
2	GAL	t	2	2	-	1/2/19/22	0/1/1/1
2	GLA	t	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	u	1	2	-	0/2/22/22	0/1/1/1
2	GAL	u	2	2	-	0/2/19/22	0/1/1/1
2	GLA	u	3	5,2	-	0/2/19/22	0/1/1/1
2	BGC	v	1	2	-	1/2/22/22	0/1/1/1
2	GAL	v	2	2	-	0/2/19/22	0/1/1/1
2	GLA	v	3	5,2	-	0/2/19/22	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	k	2	GAL	O5-C1	-3.18	1.38	1.43
2	e	3	GLA	O4-C4	3.17	1.50	1.43
2	h	2	GAL	O5-C1	-2.46	1.39	1.43
2	j	2	GAL	O5-C1	-2.42	1.39	1.43
2	Z	2	GAL	O5-C1	-2.41	1.39	1.43

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	s	1	BGC	C1-O5-C5	5.21	123.73	113.65
2	e	3	GLA	O4-C4-C5	5.18	122.08	109.32
2	s	1	BGC	O5-C1-C2	4.24	117.76	110.30
2	q	3	GLA	O4-C4-C5	4.00	119.18	109.32
2	s	1	BGC	O5-C5-C4	3.91	116.74	109.70

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

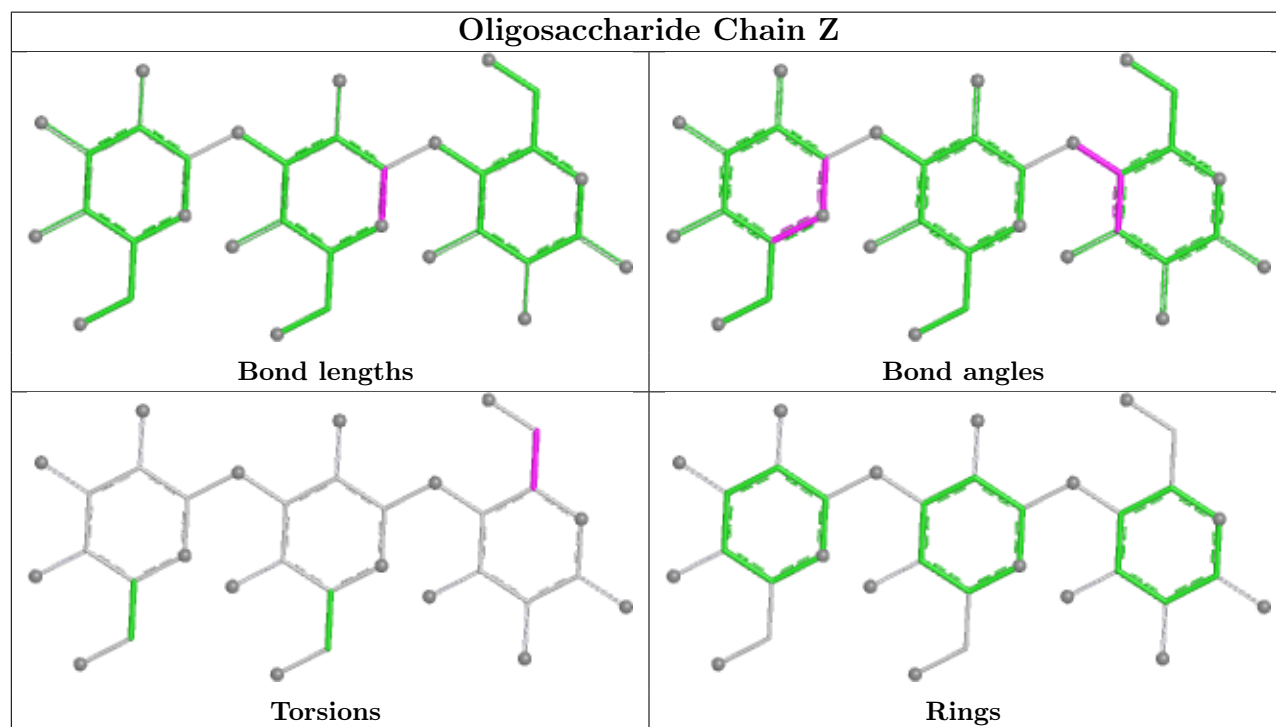
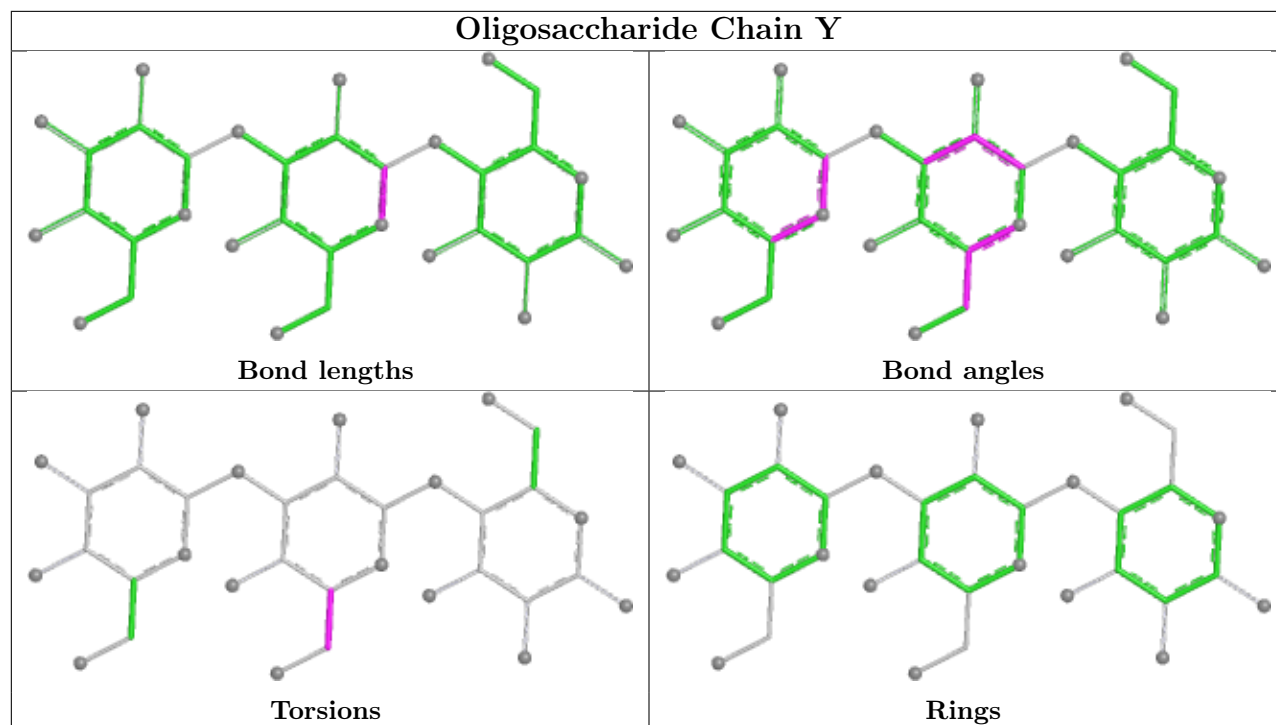
Mol	Chain	Res	Type	Atoms
4	l	1	GAL	C4-C5-C6-O6
2	s	1	BGC	O5-C5-C6-O6
2	i	2	GAL	O5-C5-C6-O6
2	s	1	BGC	C4-C5-C6-O6
4	l	1	GAL	O5-C5-C6-O6

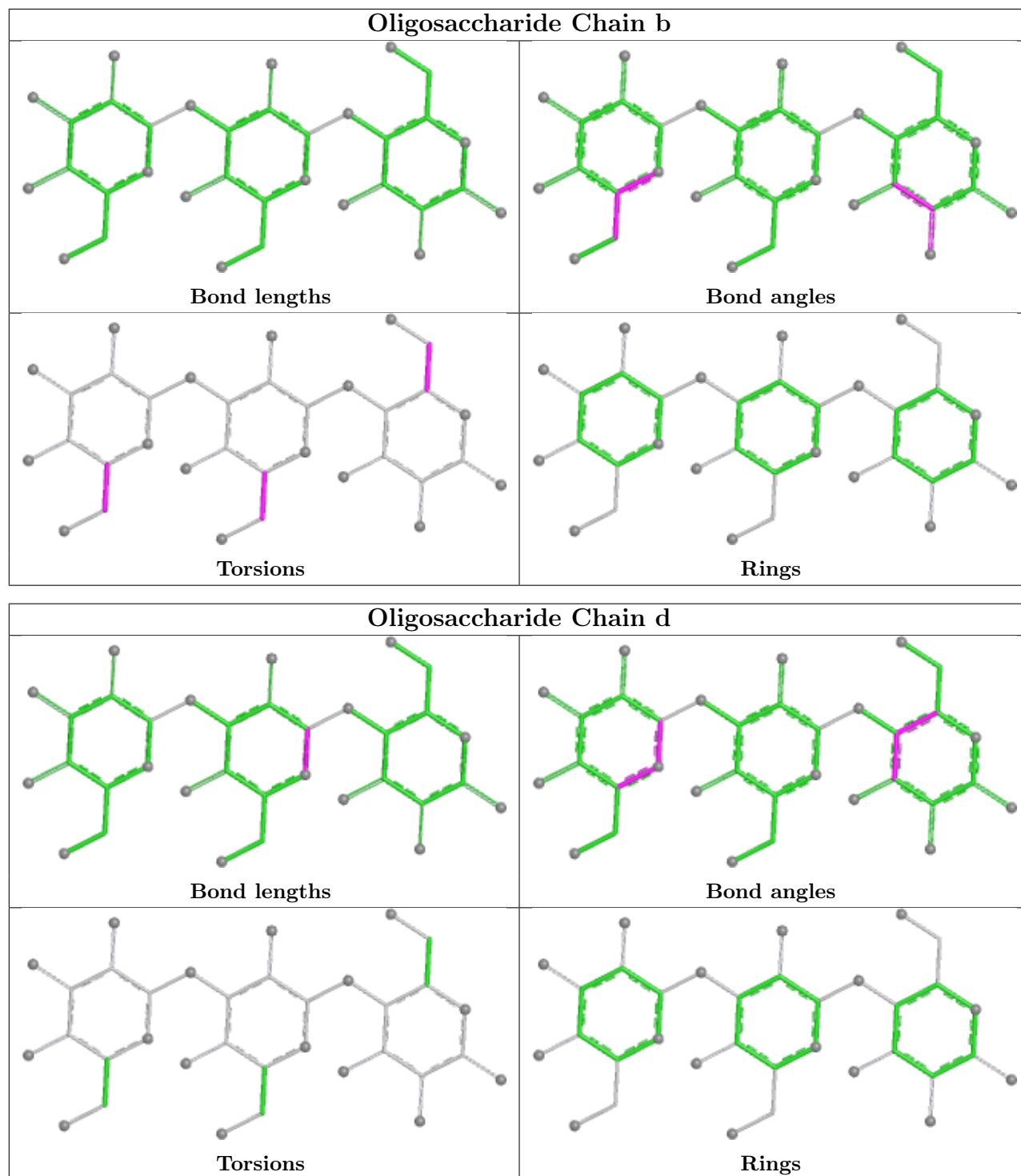
There are no ring outliers.

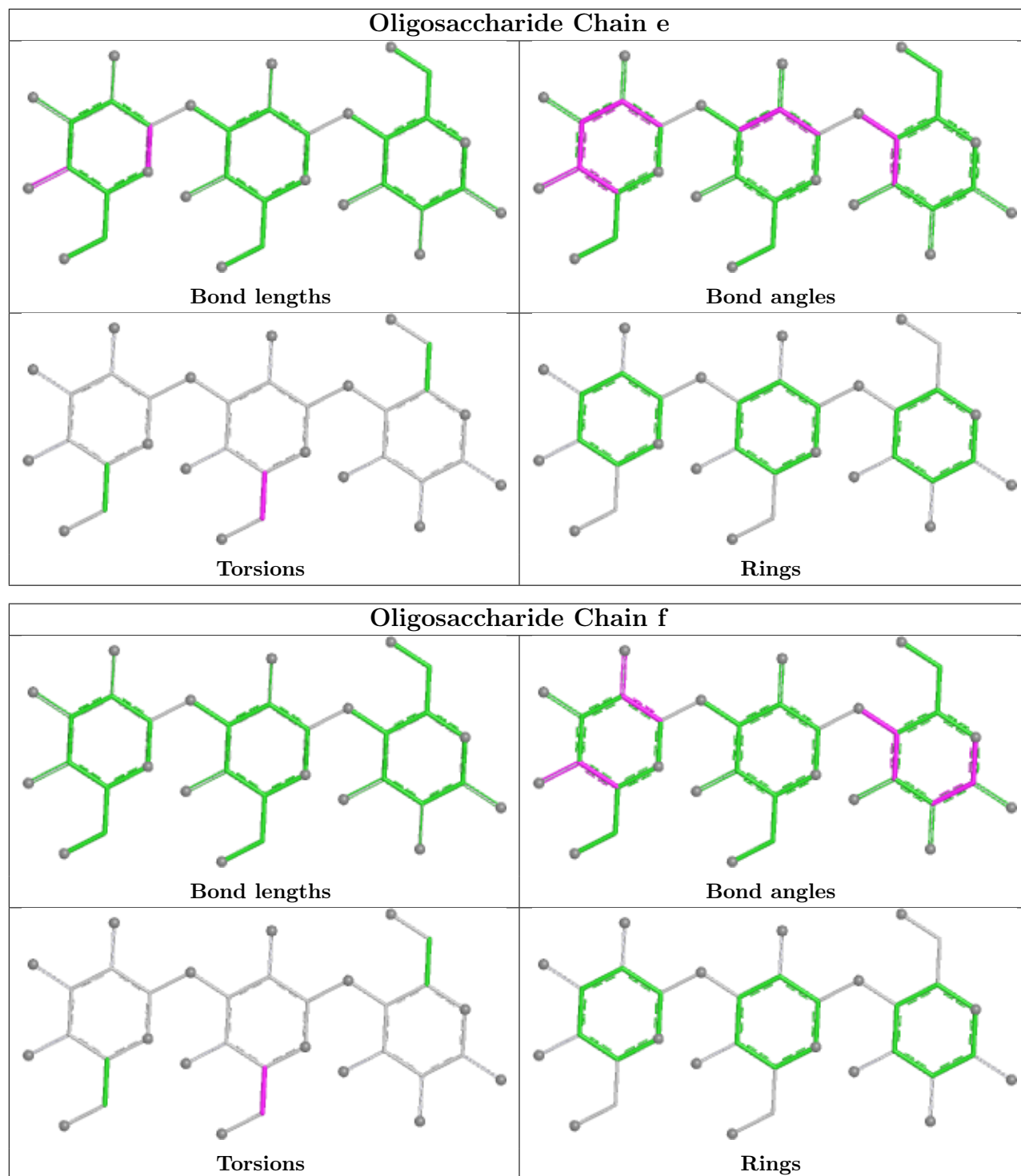
3 monomers are involved in 4 short contacts:

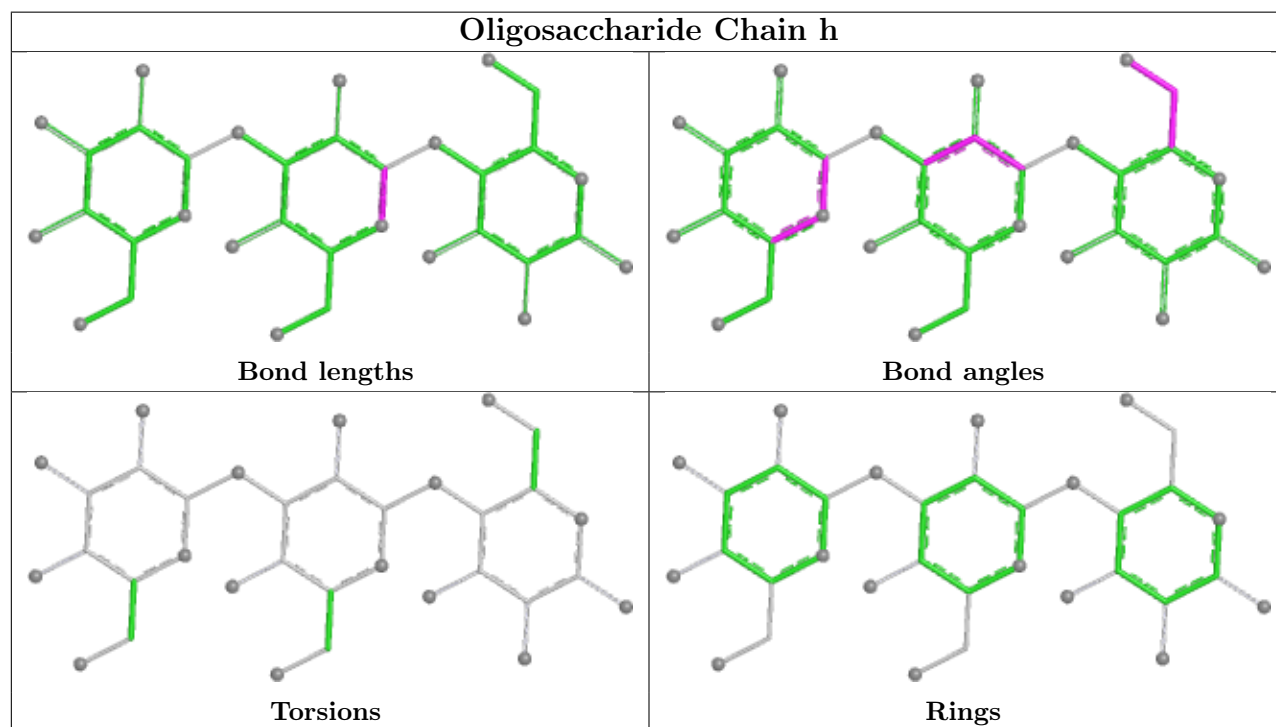
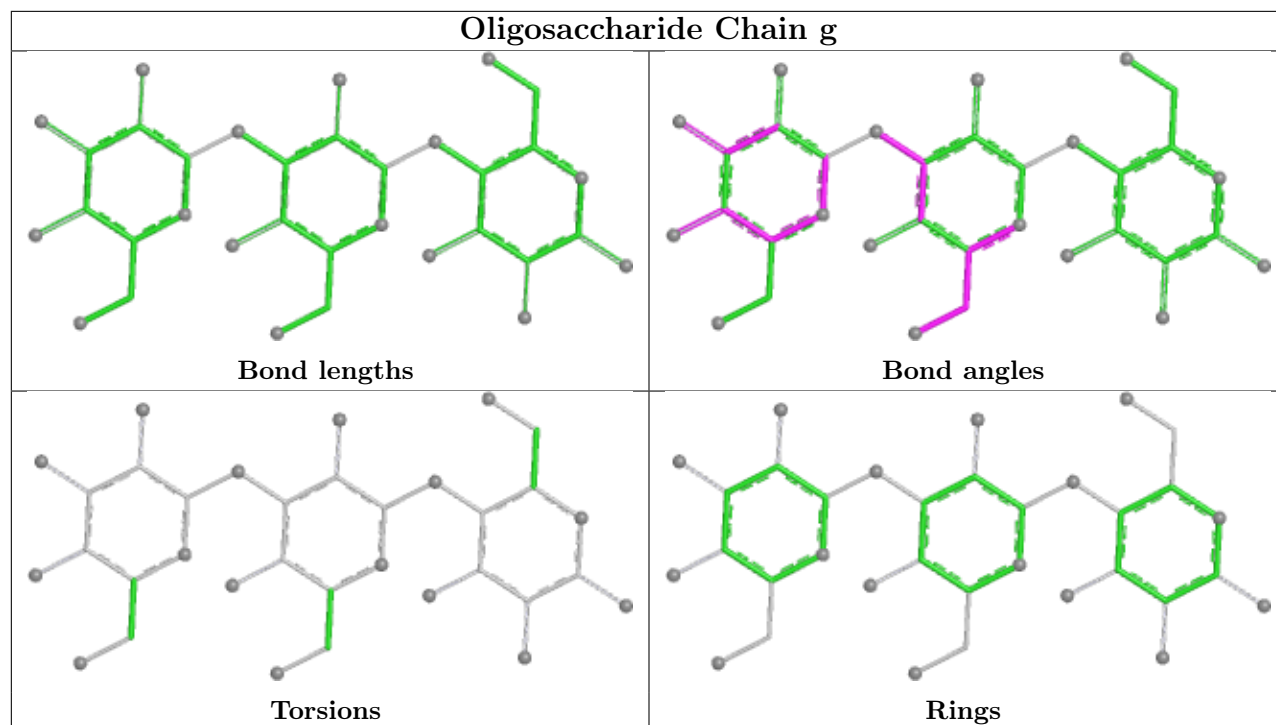
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Z	1	BGC	1	0
2	m	2	GAL	2	0
2	m	3	GLA	1	0

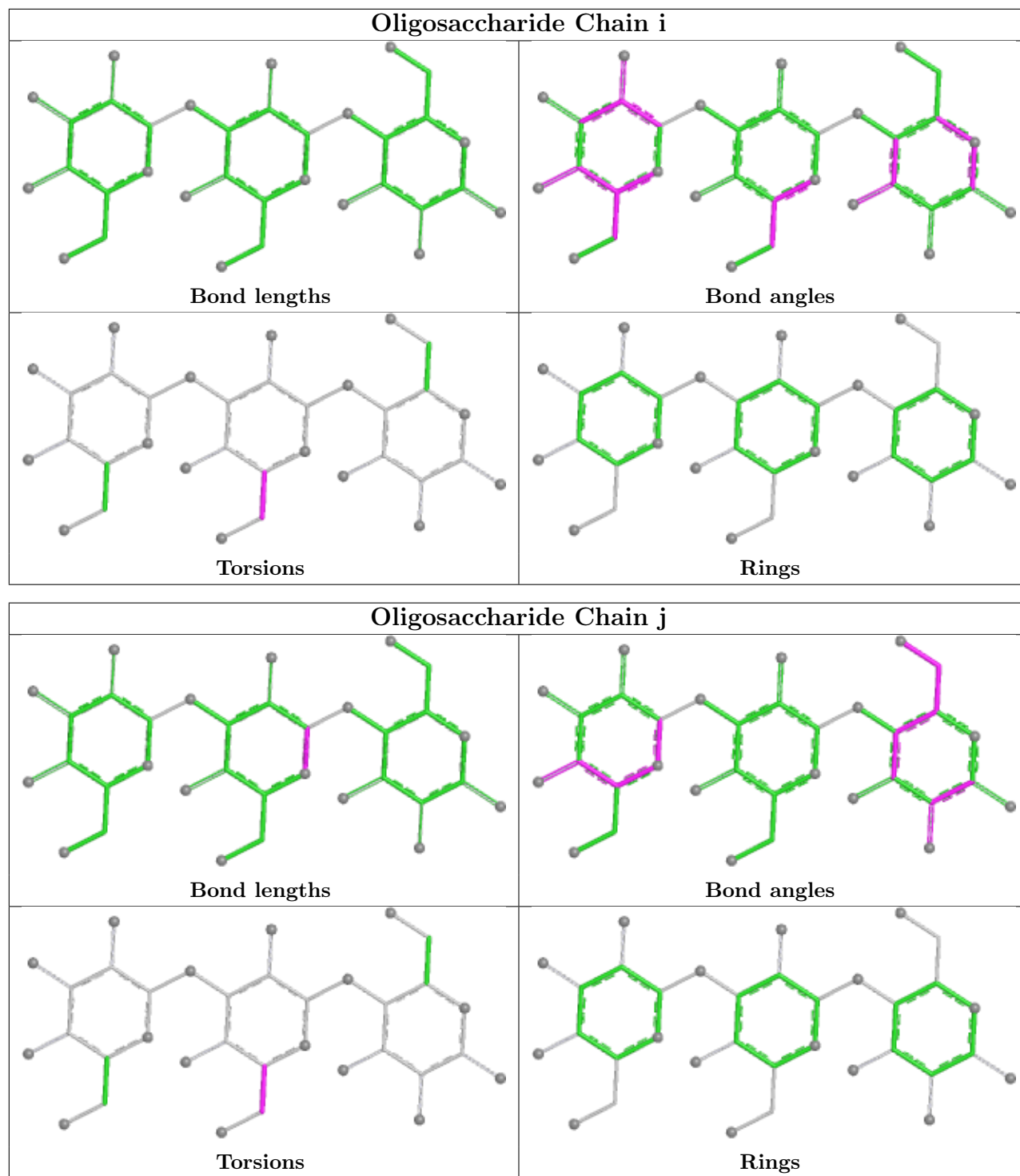
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

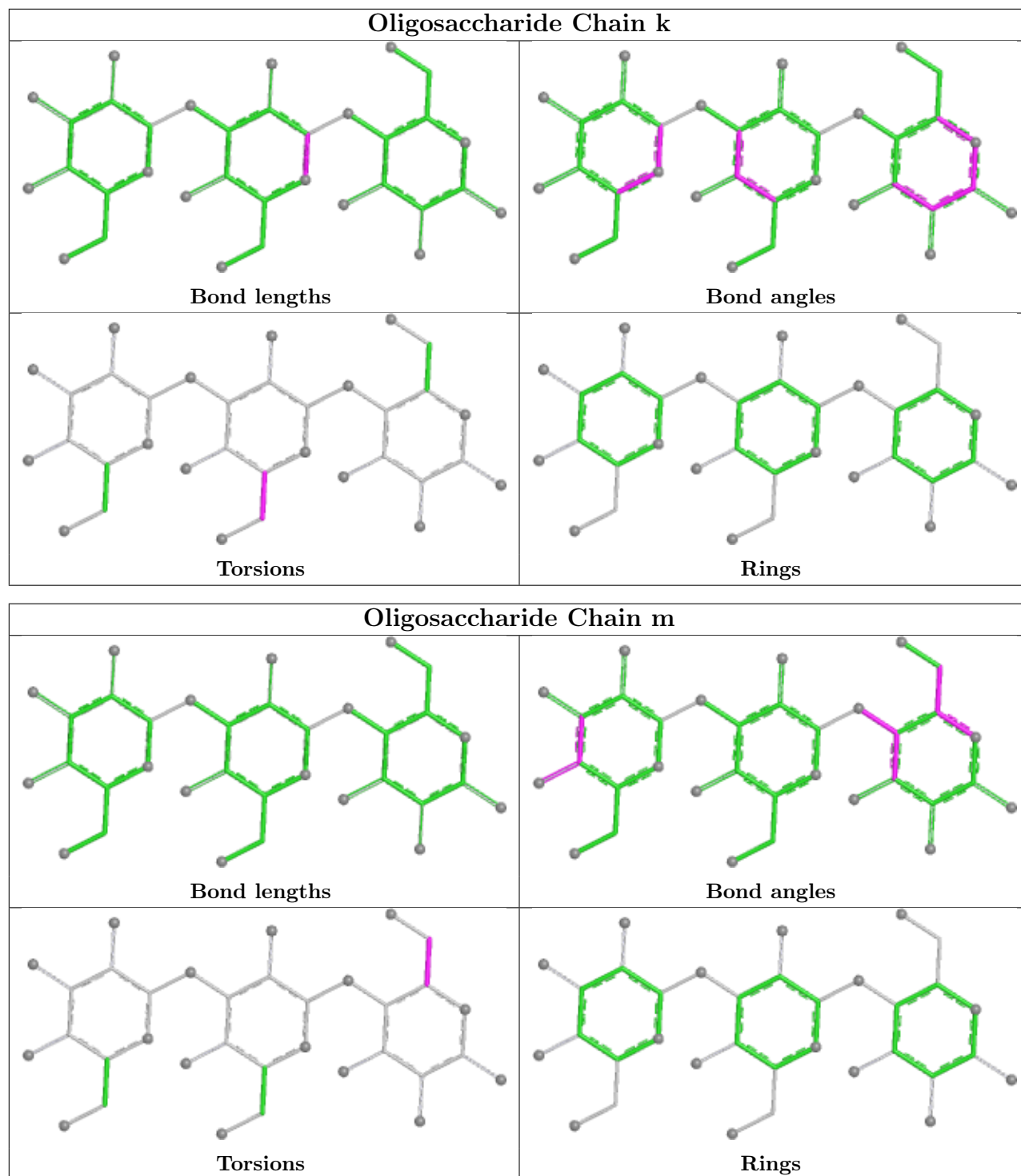


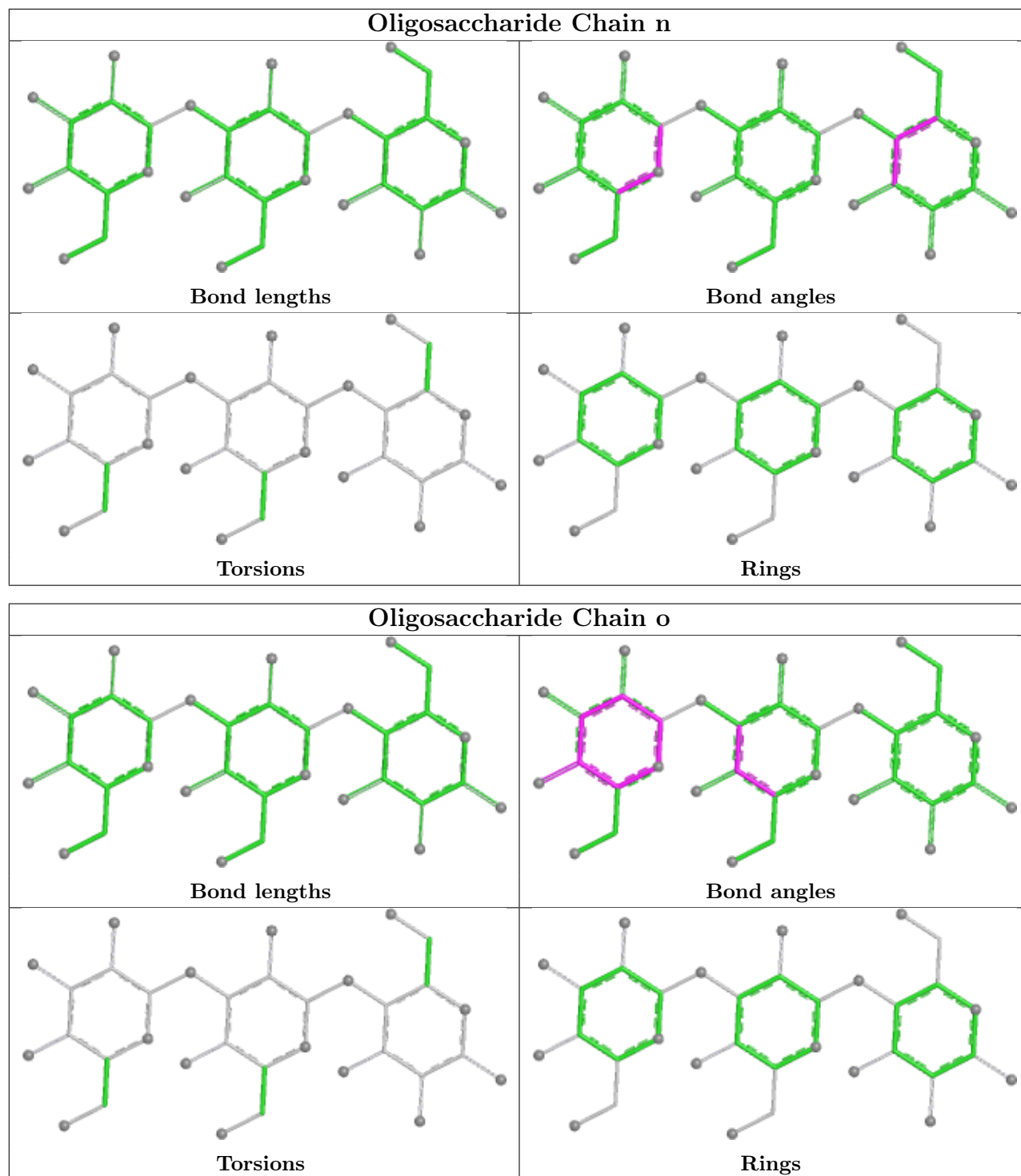


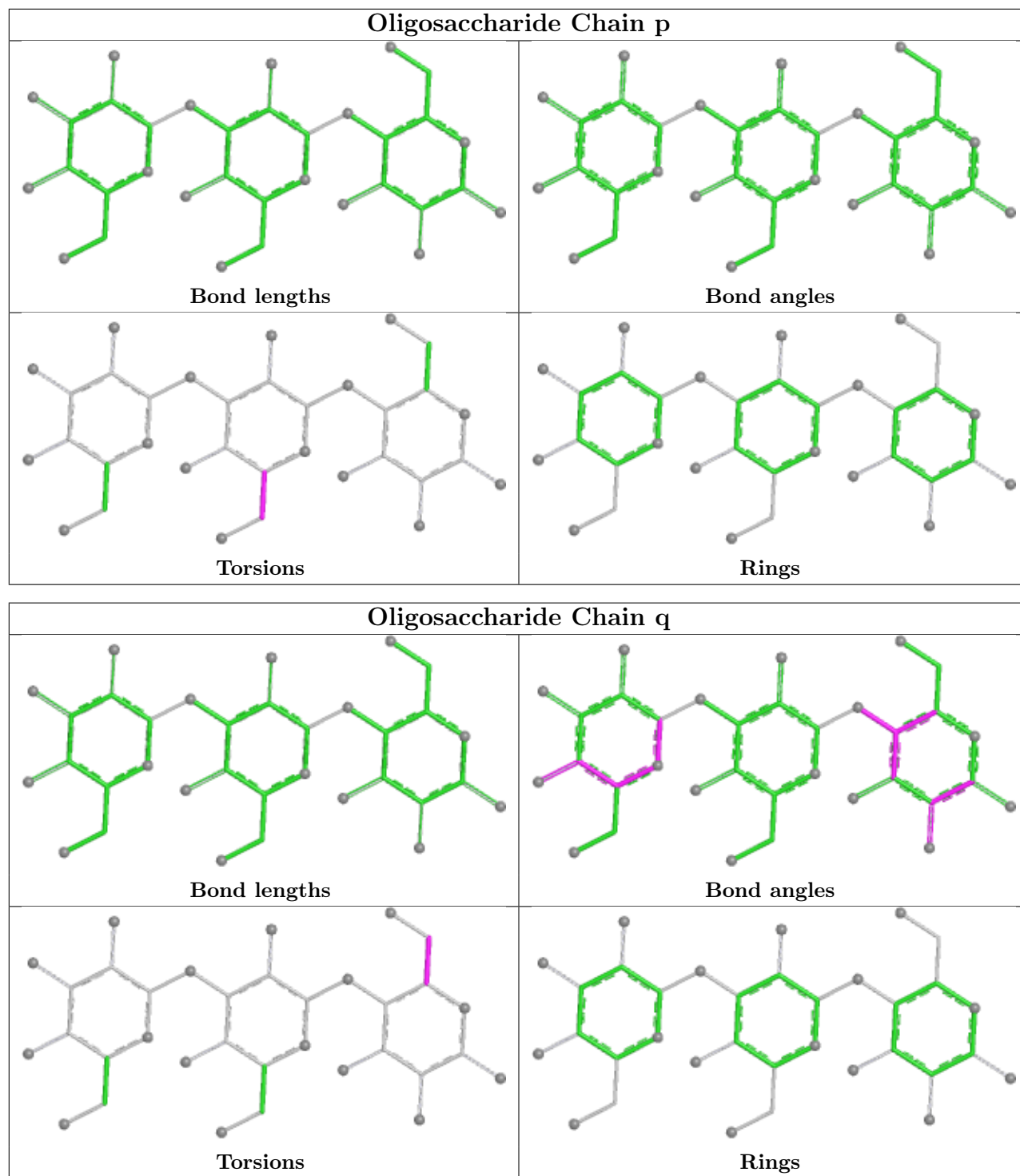


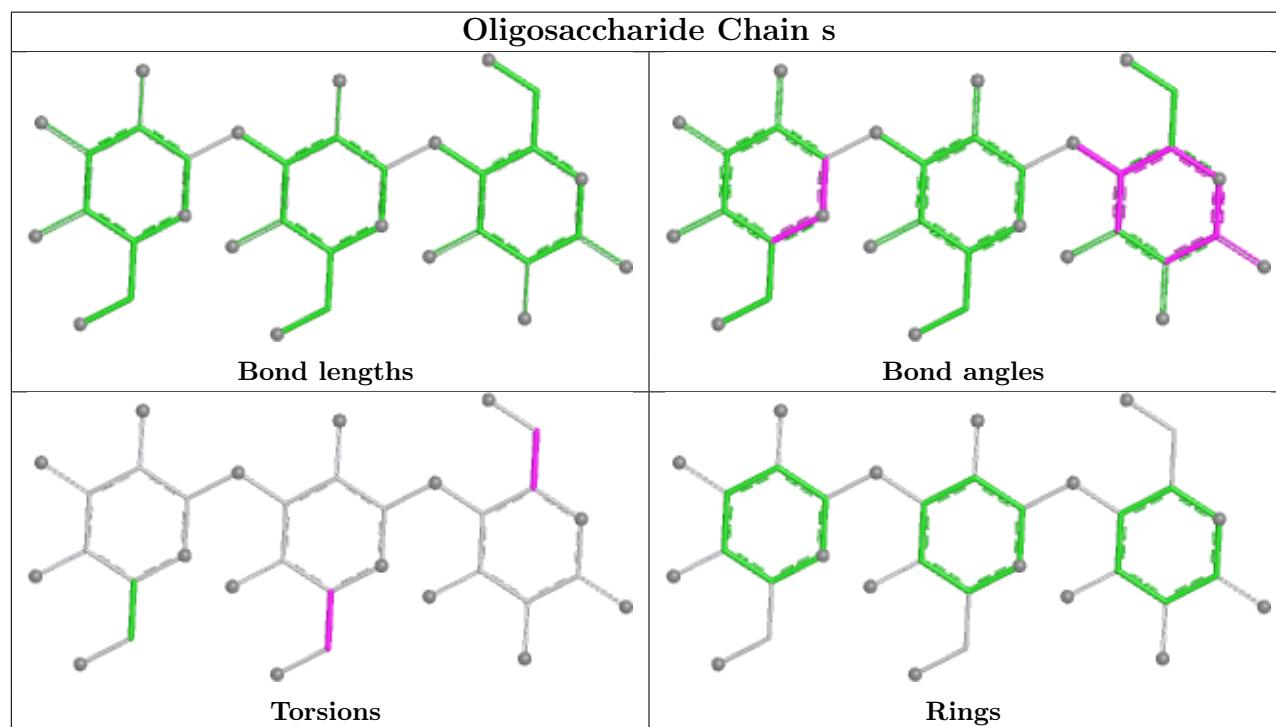
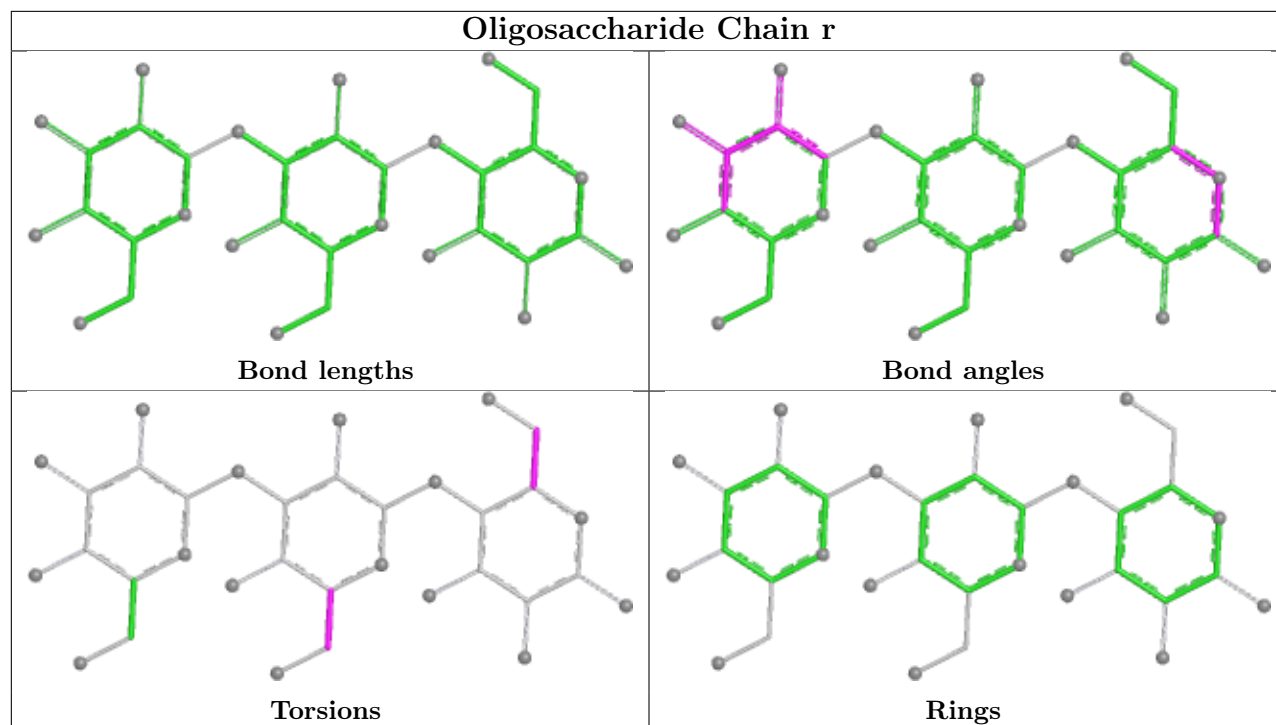


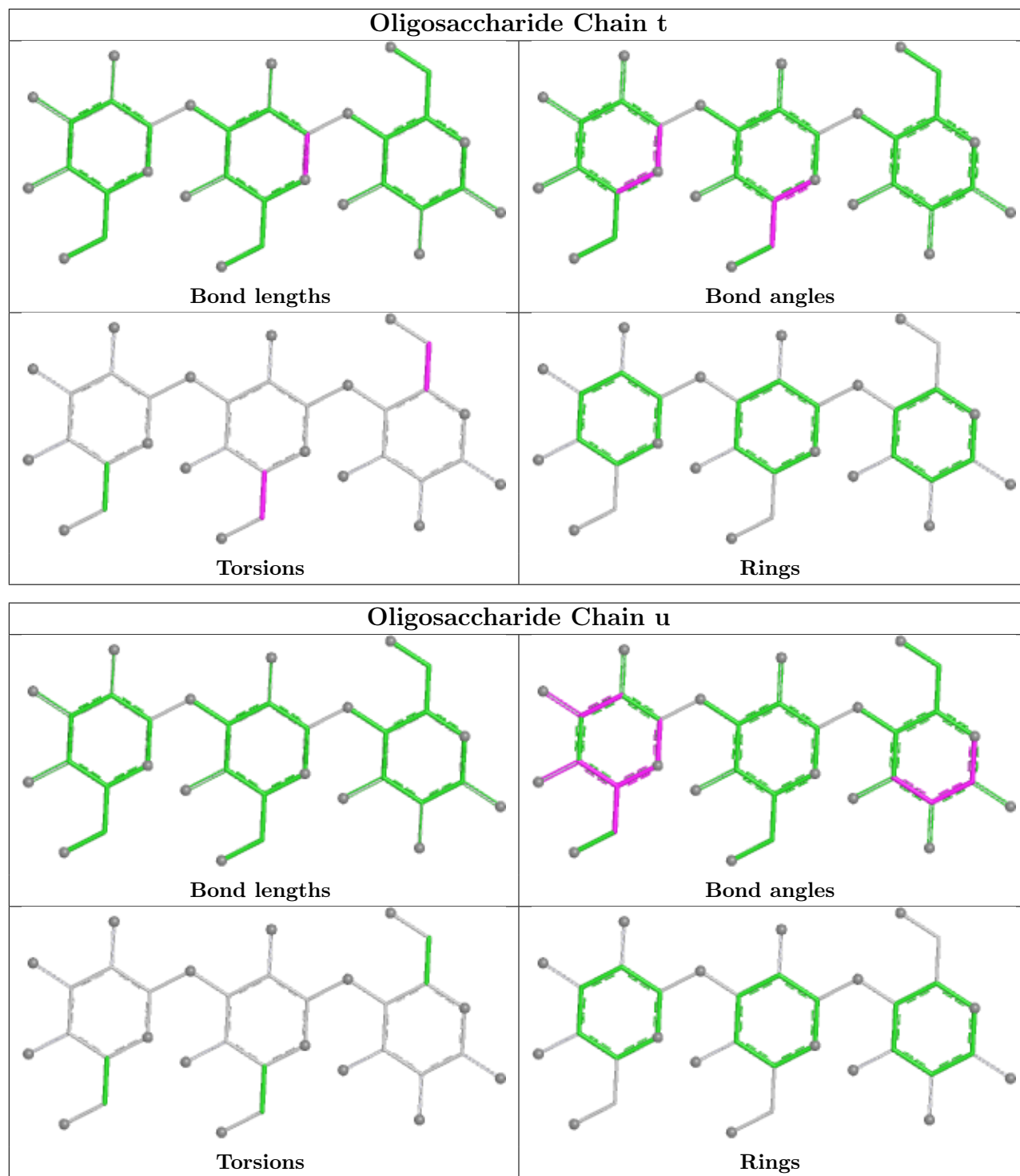


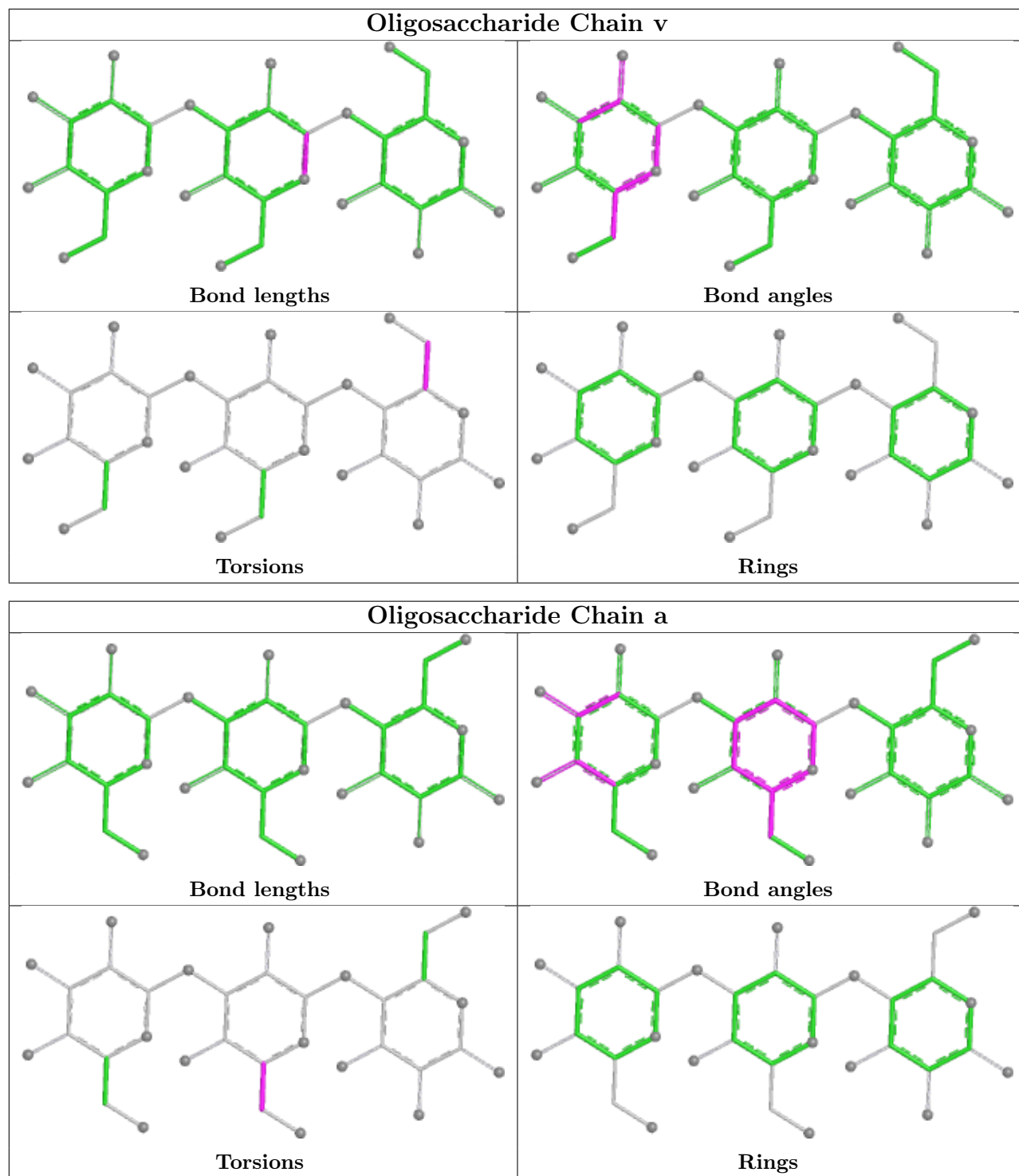


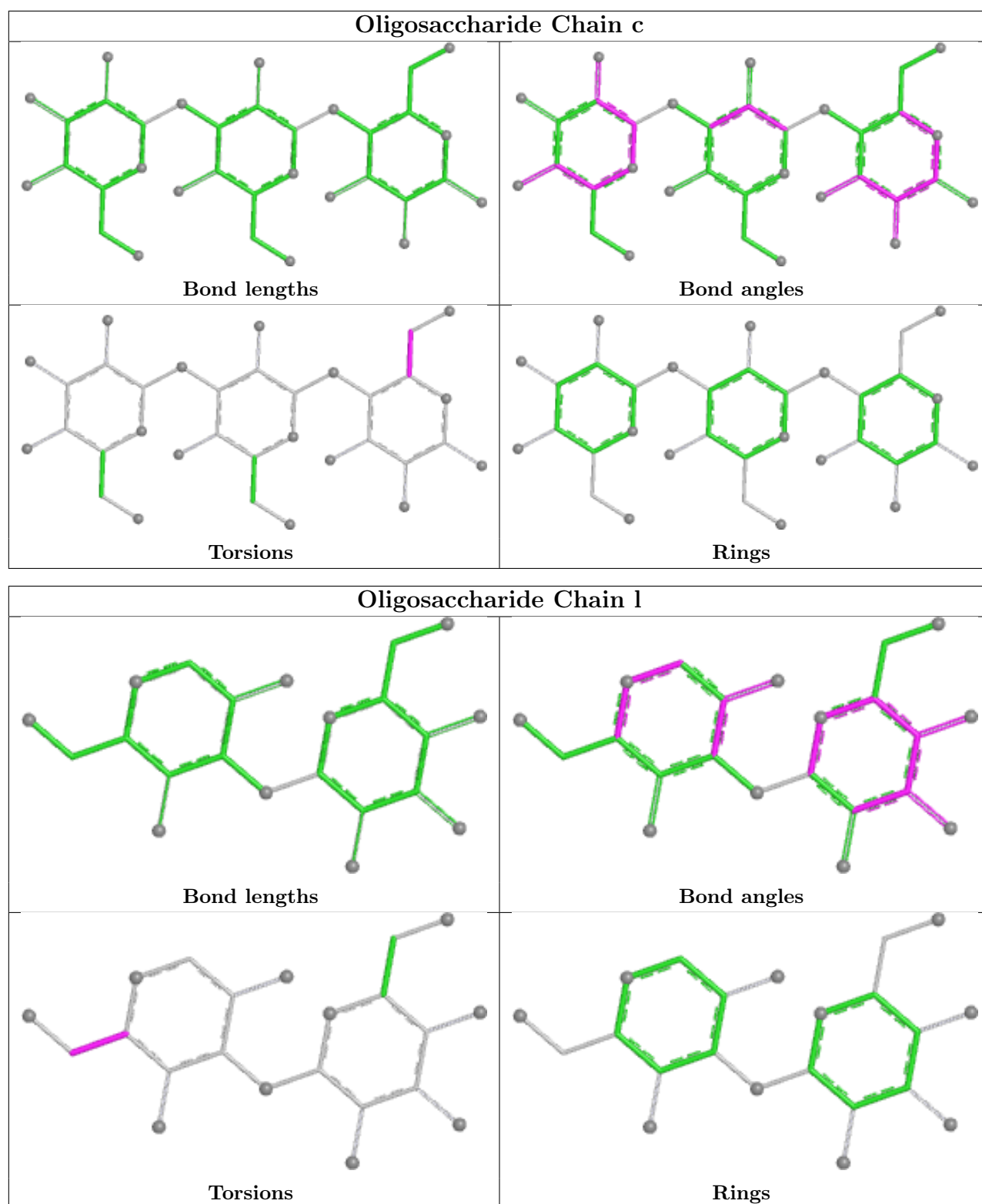












## 5.6 Ligand geometry [i](#)

Of 45 ligands modelled in this entry, 24 are monoatomic - leaving 21 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
6	EDO	N	205	-	3,3,3	0.51	0	2,2,2	0.40	0
6	EDO	A	205	-	3,3,3	0.36	0	2,2,2	0.32	0
6	EDO	X	205	-	3,3,3	0.42	0	2,2,2	0.69	0
6	EDO	W	205	-	3,3,3	0.33	0	2,2,2	0.33	0
6	EDO	Q	205	-	3,3,3	0.58	0	2,2,2	0.32	0
6	EDO	E	205	-	3,3,3	0.26	0	2,2,2	0.24	0
6	EDO	U	205	-	3,3,3	0.17	0	2,2,2	0.24	0
6	EDO	H	205	-	3,3,3	0.51	0	2,2,2	0.21	0
6	EDO	S	205	-	3,3,3	0.19	0	2,2,2	0.49	0
6	EDO	O	205	-	3,3,3	0.44	0	2,2,2	0.40	0
6	EDO	G	205	-	3,3,3	0.22	0	2,2,2	0.34	0
7	BGC	N	204	-	12,12,12	0.59	0	17,17,17	1.31	2 (11%)
6	EDO	L	205	-	3,3,3	0.27	0	2,2,2	0.05	0
6	EDO	Q	206	-	3,3,3	0.42	0	2,2,2	0.43	0
6	EDO	V	205	-	3,3,3	0.37	0	2,2,2	0.51	0
6	EDO	W	206	-	3,3,3	0.52	0	2,2,2	0.21	0
6	EDO	I	206	-	3,3,3	0.58	0	2,2,2	0.38	0
6	EDO	I	205	-	3,3,3	0.71	0	2,2,2	0.88	0
6	EDO	D	205	-	3,3,3	0.11	0	2,2,2	0.28	0
6	EDO	M	205	-	3,3,3	0.16	0	2,2,2	0.66	0
6	EDO	M	206	-	3,3,3	0.39	0	2,2,2	0.92	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	EDO	N	205	-	-	0/1/1/1	-
6	EDO	A	205	-	-	1/1/1/1	-
6	EDO	X	205	-	-	1/1/1/1	-
6	EDO	W	205	-	-	1/1/1/1	-
6	EDO	Q	205	-	-	1/1/1/1	-
6	EDO	E	205	-	-	1/1/1/1	-
6	EDO	U	205	-	-	1/1/1/1	-
6	EDO	H	205	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	S	205	-	-	1/1/1/1	-
6	EDO	O	205	-	-	1/1/1/1	-
6	EDO	G	205	-	-	0/1/1/1	-
7	BGC	N	204	-	-	0/2/22/22	0/1/1/1
6	EDO	L	205	-	-	1/1/1/1	-
6	EDO	Q	206	-	-	0/1/1/1	-
6	EDO	V	205	-	-	1/1/1/1	-
6	EDO	W	206	-	-	1/1/1/1	-
6	EDO	I	206	-	-	0/1/1/1	-
6	EDO	I	205	-	-	0/1/1/1	-
6	EDO	D	205	-	-	1/1/1/1	-
6	EDO	M	205	-	-	1/1/1/1	-
6	EDO	M	206	-	-	1/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	N	204	BGC	O4-C4-C3	-2.82	103.72	110.38
7	N	204	BGC	C3-C4-C5	2.15	114.13	110.23

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	205	EDO	O1-C1-C2-O2
6	U	205	EDO	O1-C1-C2-O2
6	H	205	EDO	O1-C1-C2-O2
6	V	205	EDO	O1-C1-C2-O2
6	W	205	EDO	O1-C1-C2-O2

There are no ring outliers.

16 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	205	EDO	1	0
6	X	205	EDO	2	0
6	W	205	EDO	1	0
6	Q	205	EDO	1	0
6	E	205	EDO	1	0
6	U	205	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	205	EDO	1	0
6	S	205	EDO	1	0
6	O	205	EDO	1	0
6	G	205	EDO	7	0
6	L	205	EDO	1	0
6	V	205	EDO	2	0
6	I	206	EDO	1	0
6	I	205	EDO	5	0
6	D	205	EDO	1	0
6	M	206	EDO	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	121/121 (100%)	-0.23	1 (0%) 82 85	7, 11, 19, 25	0
1	B	118/121 (97%)	-0.28	0 100 100	7, 11, 18, 21	1 (0%)
1	C	119/121 (98%)	0.12	2 (1%) 69 72	9, 14, 23, 25	2 (1%)
1	D	120/121 (99%)	-0.13	3 (2%) 58 62	8, 12, 20, 27	1 (0%)
1	E	121/121 (100%)	-0.04	2 (1%) 69 72	8, 13, 21, 30	1 (0%)
1	F	121/121 (100%)	-0.23	0 100 100	7, 12, 18, 29	0
1	G	121/121 (100%)	0.29	4 (3%) 49 52	7, 14, 24, 27	0
1	H	121/121 (100%)	-0.36	0 100 100	5, 10, 17, 24	2 (1%)
1	I	121/121 (100%)	-0.27	0 100 100	6, 10, 18, 23	0
1	J	120/121 (99%)	-0.29	3 (2%) 58 62	6, 10, 17, 24	1 (0%)
1	K	121/121 (100%)	-0.27	1 (0%) 82 85	7, 11, 17, 23	1 (0%)
1	L	121/121 (100%)	-0.23	0 100 100	7, 11, 18, 21	1 (0%)
1	M	121/121 (100%)	-0.01	2 (1%) 69 72	8, 13, 20, 29	1 (0%)
1	N	120/121 (99%)	-0.19	0 100 100	7, 12, 19, 24	0
1	O	121/121 (100%)	0.18	1 (0%) 82 85	7, 14, 22, 26	1 (0%)
1	P	121/121 (100%)	-0.29	2 (1%) 69 72	6, 10, 18, 24	0
1	Q	121/121 (100%)	-0.29	0 100 100	6, 11, 17, 27	1 (0%)
1	R	121/121 (100%)	-0.12	1 (0%) 82 85	1, 11, 18, 19	1 (0%)
1	S	121/121 (100%)	-0.26	0 100 100	6, 11, 18, 26	0
1	T	121/121 (100%)	-0.30	0 100 100	7, 11, 19, 23	2 (1%)
1	U	121/121 (100%)	-0.23	1 (0%) 82 85	7, 11, 18, 27	2 (1%)
1	V	121/121 (100%)	-0.31	1 (0%) 82 85	6, 11, 18, 24	0
1	W	121/121 (100%)	-0.00	1 (0%) 82 85	8, 14, 23, 33	0
1	X	121/121 (100%)	-0.20	1 (0%) 82 85	8, 12, 18, 22	2 (1%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
All	All	2896/2904 (99%)	-0.16	26 (0%) 81 83	1, 12, 20, 33	20 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	89	ASN	20.4
1	X	88	ASN	6.1
1	K	71	ASN	4.1
1	C	89	ASN	3.8
1	C	71	ASN	3.3

## 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
2	BGC	Z	1	12/12	0.81	0.13	24,31,34,34	0
2	BGC	Y	1	12/12	0.90	0.10	11,19,23,28	0
2	GAL	Z	2	11/12	0.93	0.09	21,24,29,30	0
2	GAL	Y	2	11/12	0.94	0.07	10,14,23,28	0
2	GLA	Z	3	11/12	0.94	0.08	16,18,19,20	0
2	GLA	Y	3	11/12	0.97	0.05	7,9,11,13	0
2	BGC	b	1	12/12	-	-	19,25,28,32	0
2	GAL	b	2	11/12	-	-	19,23,26,28	0
2	GLA	b	3	11/12	-	-	13,15,18,18	0
2	BGC	d	1	12/12	-	-	26,31,34,36	0
2	GAL	d	2	11/12	-	-	19,22,26,28	0
2	GLA	d	3	11/12	-	-	11,15,18,19	0
2	BGC	e	1	12/12	-	-	22,25,29,30	0
2	GAL	e	2	11/12	-	-	19,24,27,30	0
2	GLA	e	3	11/12	-	-	6,14,18,18	0
2	BGC	f	1	12/12	-	-	20,25,31,32	0
2	GAL	f	2	11/12	-	-	17,19,26,26	0

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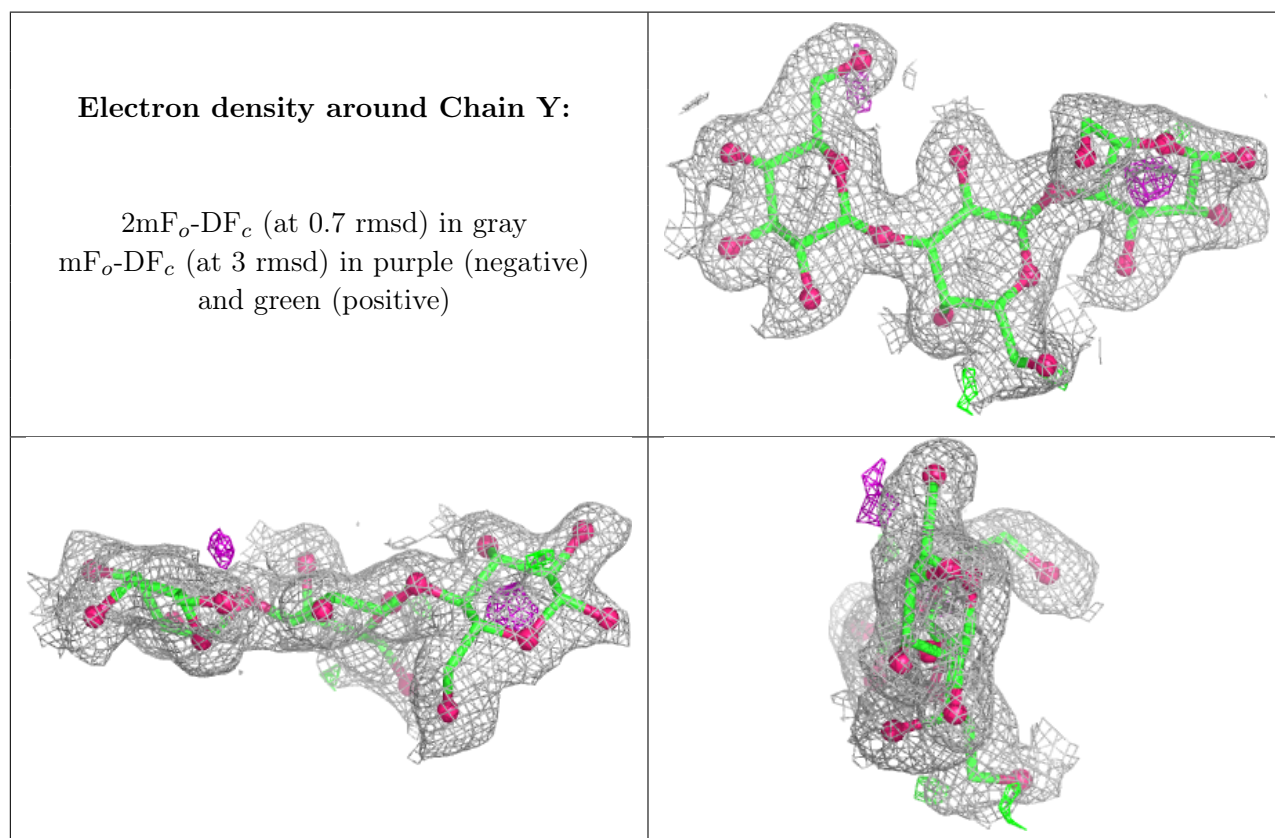
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLA	f	3	11/12	-	-	10,14,15,16	0
2	BGC	g	1	12/12	-	-	15,22,28,31	0
2	GAL	g	2	11/12	-	-	15,17,20,23	0
2	GLA	g	3	11/12	-	-	9,11,12,14	0
2	BGC	h	1	12/12	-	-	23,30,35,38	0
2	GAL	h	2	11/12	-	-	15,22,26,28	0
2	GLA	h	3	11/12	-	-	10,12,14,14	0
2	BGC	i	1	12/12	-	-	21,26,29,31	0
2	GAL	i	2	11/12	-	-	16,20,22,23	0
2	GLA	i	3	11/12	-	-	12,14,16,17	0
2	BGC	j	1	12/12	-	-	30,35,39,41	0
2	GAL	j	2	11/12	-	-	19,25,30,32	0
2	GLA	j	3	11/12	-	-	11,15,19,19	0
2	BGC	k	1	12/12	-	-	16,21,28,33	0
2	GAL	k	2	11/12	-	-	11,14,18,21	0
2	GLA	k	3	11/12	-	-	11,14,16,17	0
2	BGC	m	1	12/12	-	-	25,30,36,37	0
2	GAL	m	2	11/12	-	-	25,27,28,28	0
2	GLA	m	3	11/12	-	-	18,22,24,25	0
2	BGC	n	1	12/12	-	-	23,30,32,33	0
2	GAL	n	2	11/12	-	-	15,20,25,26	0
2	GLA	n	3	11/12	-	-	9,12,14,15	0
2	BGC	o	1	12/12	-	-	15,22,27,29	0
2	GAL	o	2	11/12	-	-	13,16,20,22	0
2	GLA	o	3	11/12	-	-	7,11,13,13	0
2	BGC	p	1	12/12	-	-	23,30,34,37	0
2	GAL	p	2	11/12	-	-	17,20,27,29	0
2	GLA	p	3	11/12	-	-	15,17,18,19	0
2	BGC	q	1	12/12	-	-	25,30,36,37	0
2	GAL	q	2	11/12	-	-	14,17,20,21	0
2	GLA	q	3	11/12	-	-	12,17,18,20	0
2	BGC	r	1	12/12	-	-	28,35,40,40	0
2	GAL	r	2	11/12	-	-	22,24,31,34	0
2	GLA	r	3	11/12	-	-	12,15,18,19	0
2	BGC	s	1	12/12	-	-	17,24,31,32	0
2	GAL	s	2	11/12	-	-	14,16,22,22	0
2	GLA	s	3	11/12	-	-	9,11,12,14	0
2	BGC	t	1	12/12	-	-	26,35,38,38	0
2	GAL	t	2	11/12	-	-	18,23,26,28	0
2	GLA	t	3	11/12	-	-	13,16,17,18	0
2	BGC	u	1	12/12	-	-	21,25,31,34	0
2	GAL	u	2	11/12	-	-	21,22,25,27	0

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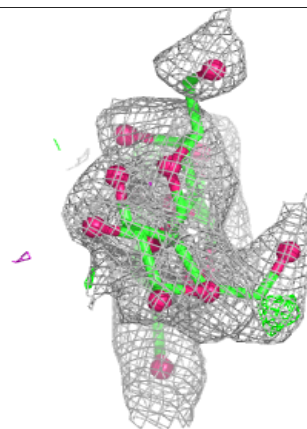
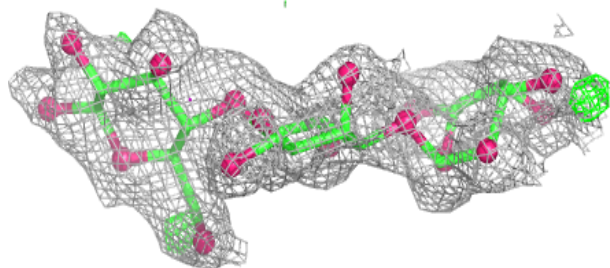
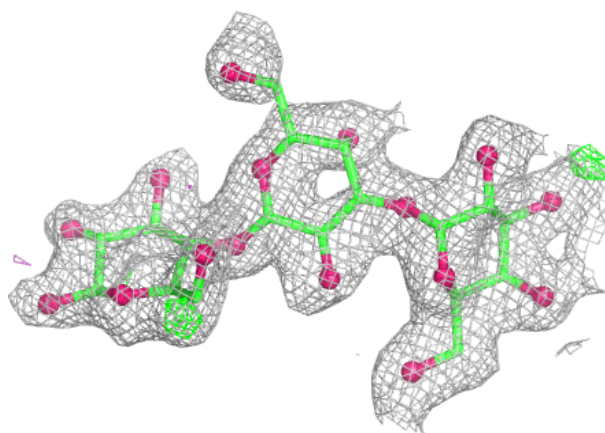
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLA	u	3	11/12	-	-	15,16,18,18	0
2	BGC	v	1	12/12	-	-	26,34,37,39	0
2	GAL	v	2	11/12	-	-	18,21,27,32	0
2	GLA	v	3	11/12	-	-	11,13,15,15	0
3	GLC	a	1	12/12	-	-	24,29,36,37	0
3	GAL	a	2	11/12	-	-	19,24,33,37	0
3	GLA	a	3	11/12	-	-	17,18,20,22	0
3	GLC	c	1	12/12	-	-	14,23,26,27	0
3	GAL	c	2	11/12	-	-	15,16,21,23	0
3	GLA	c	3	11/12	-	-	12,14,16,19	0
4	GAL	l	1	11/12	-	-	21,23,29,29	0
4	GLA	l	2	11/12	-	-	14,16,19,19	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.



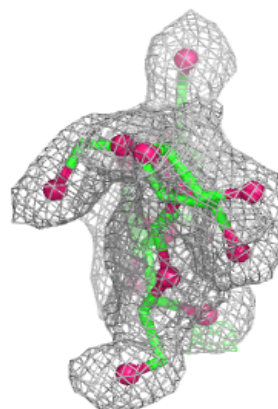
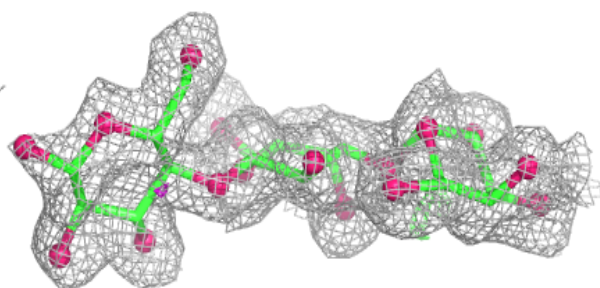
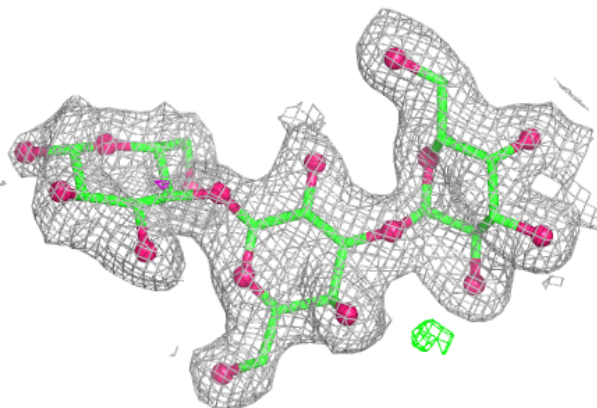
**Electron density around Chain Z:**

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

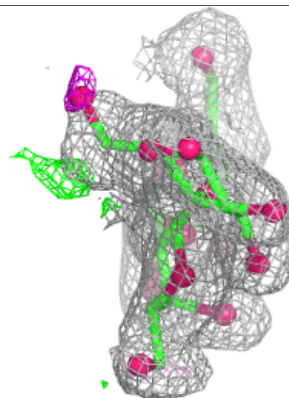
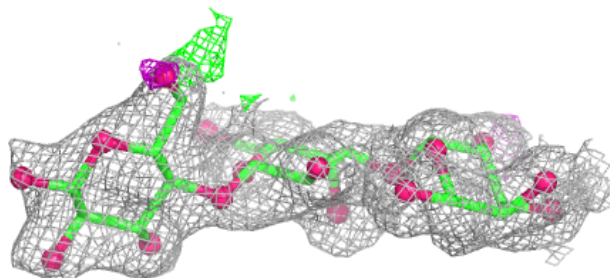
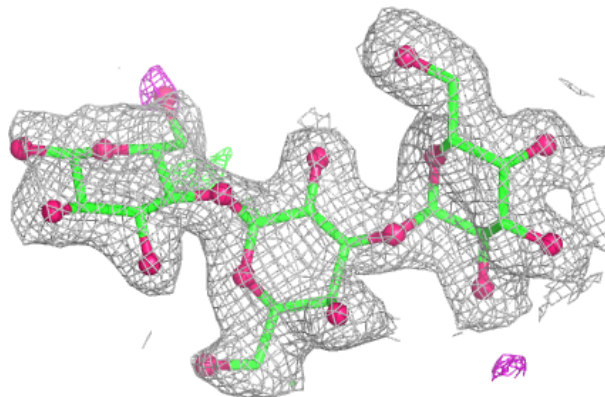


**Electron density around Chain b:**

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

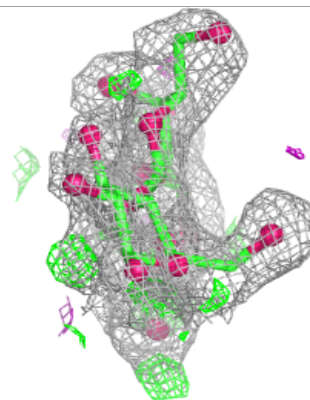
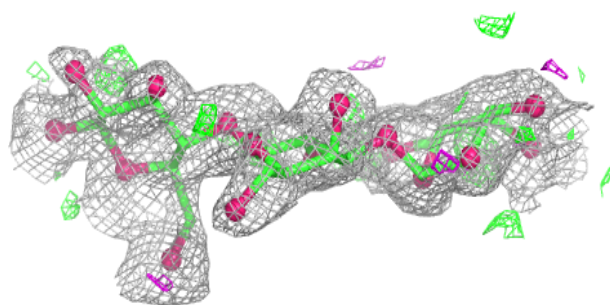
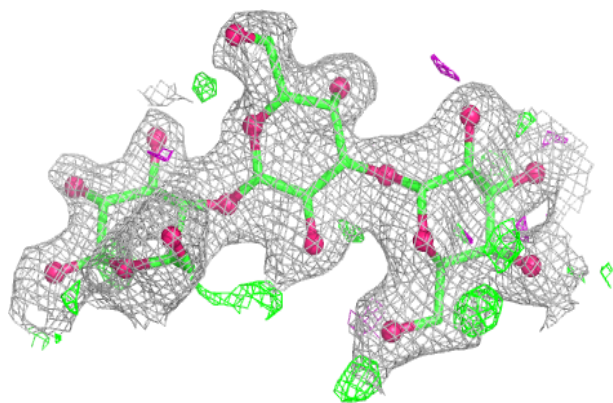
**Electron density around Chain d:**

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

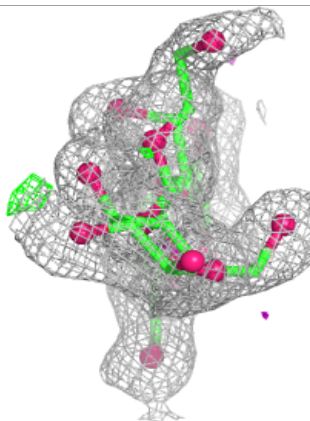
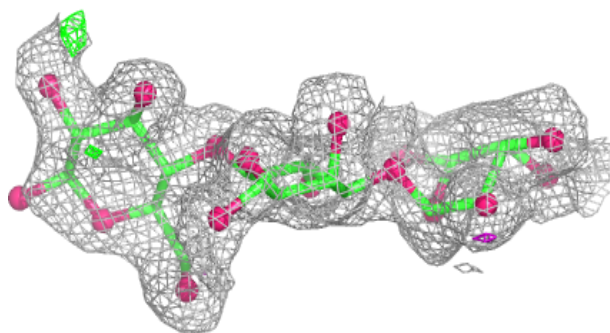
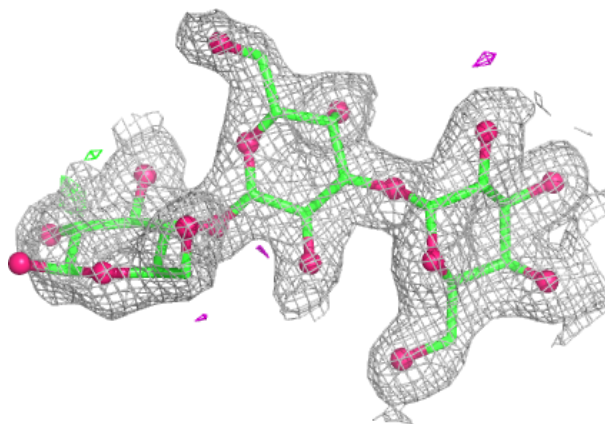


**Electron density around Chain e:**

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

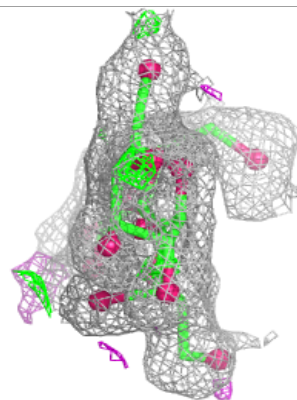
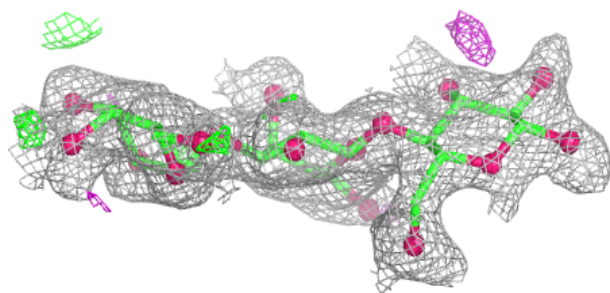
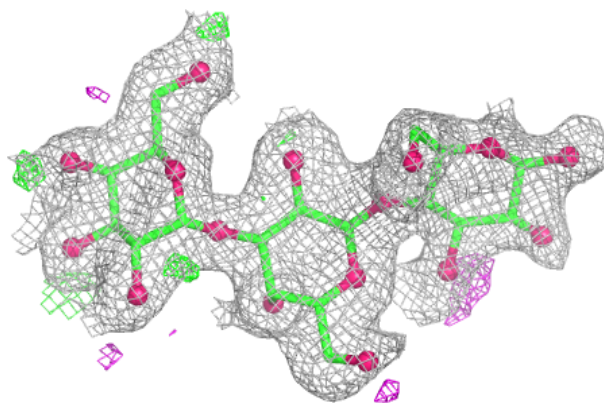
**Electron density around Chain f:**

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

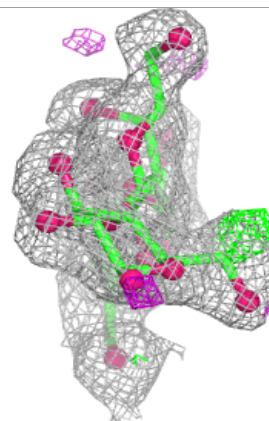
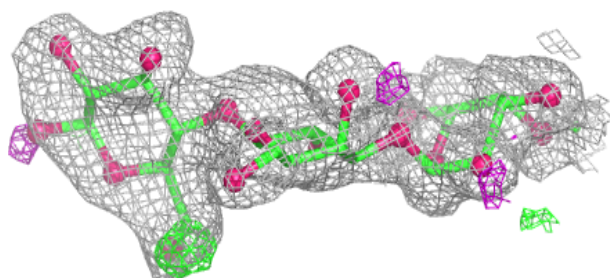
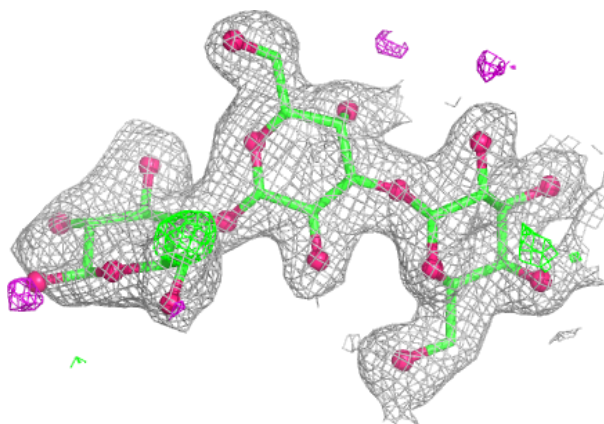


**Electron density around Chain g:**

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

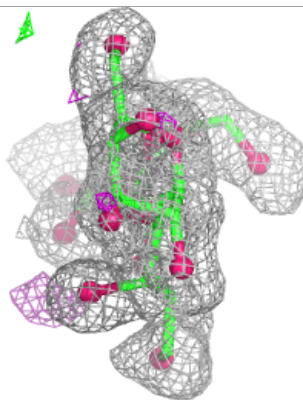
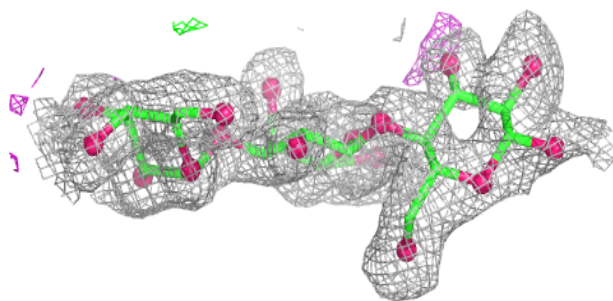
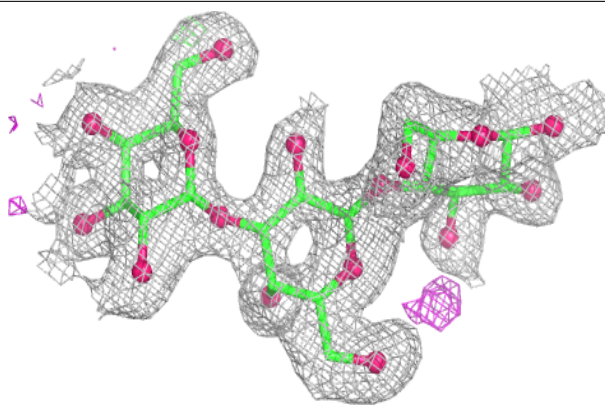
**Electron density around Chain h:**

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

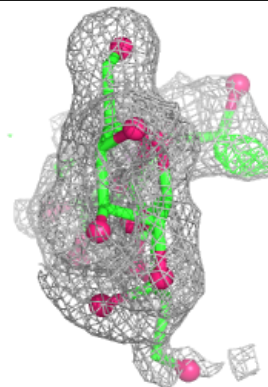
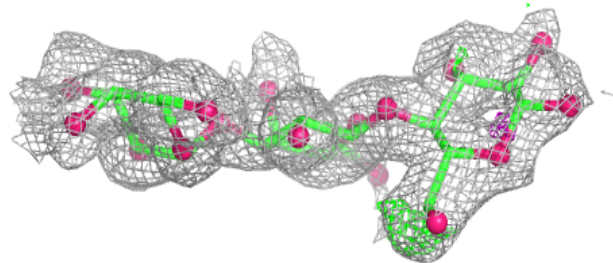
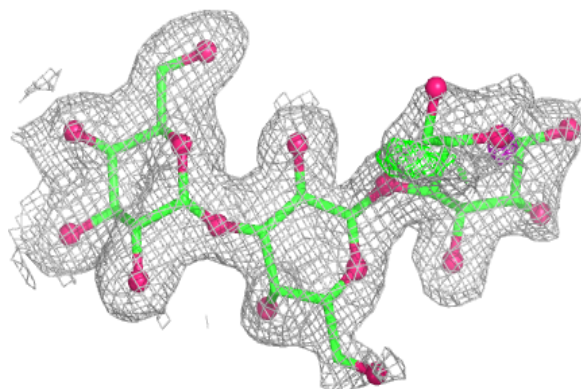


**Electron density around Chain i:**

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

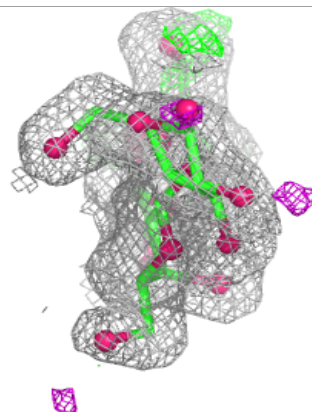
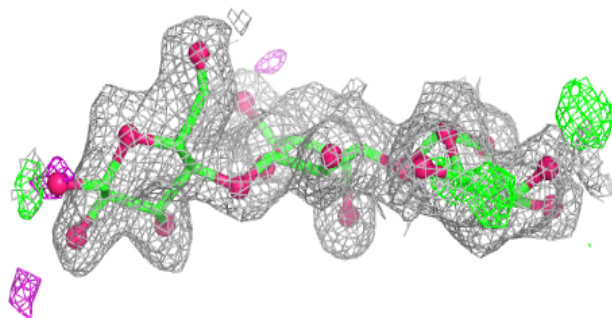
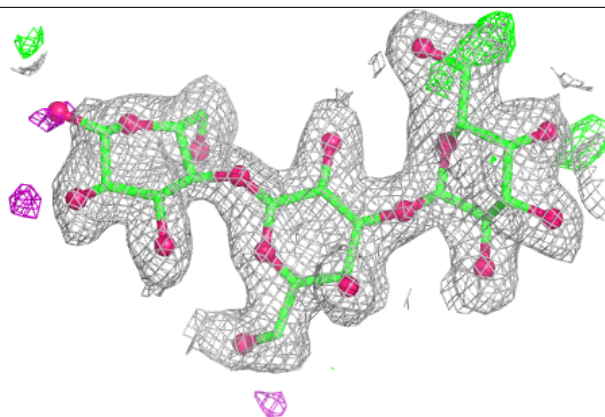
**Electron density around Chain j:**

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

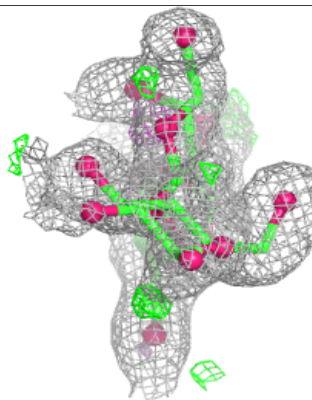
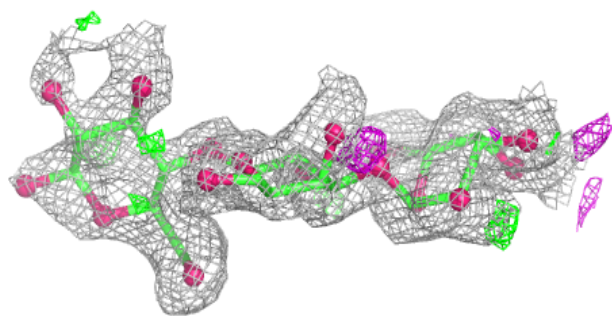
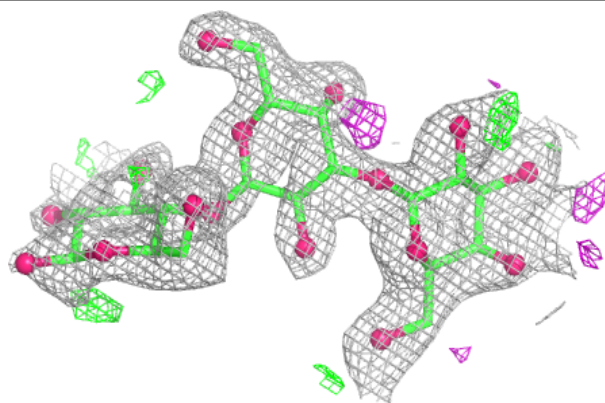


**Electron density around Chain k:**

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

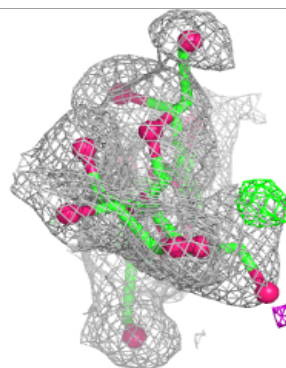
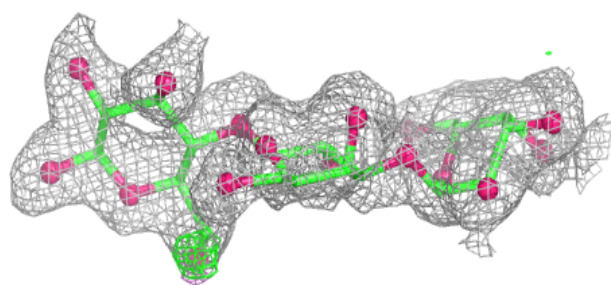
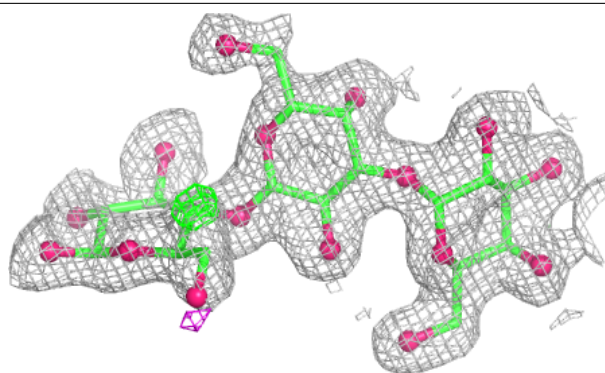
**Electron density around Chain m:**

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

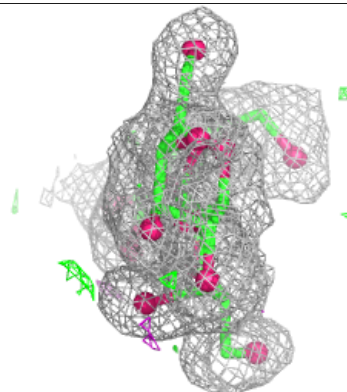
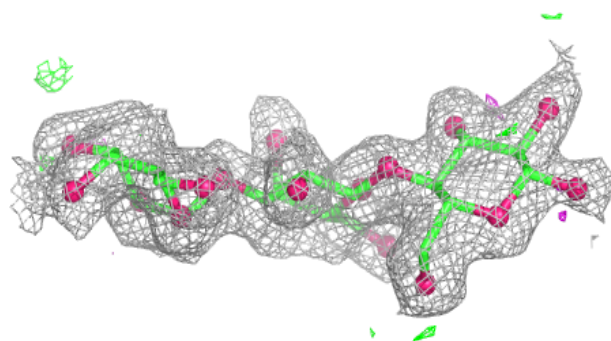
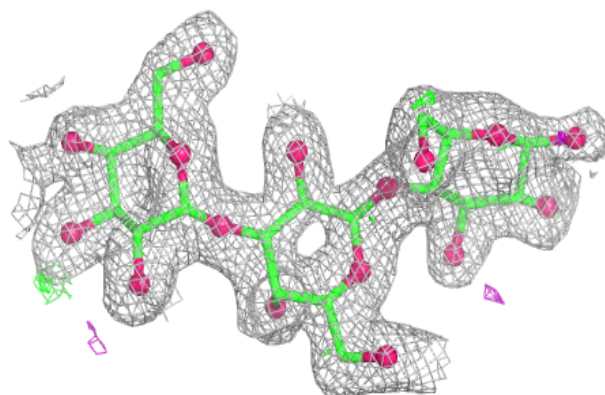


**Electron density around Chain n:**

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

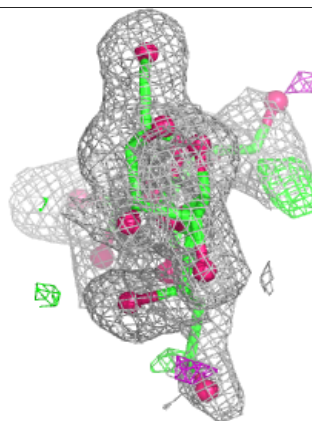
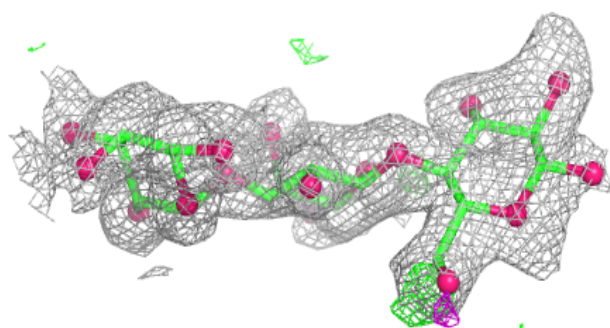
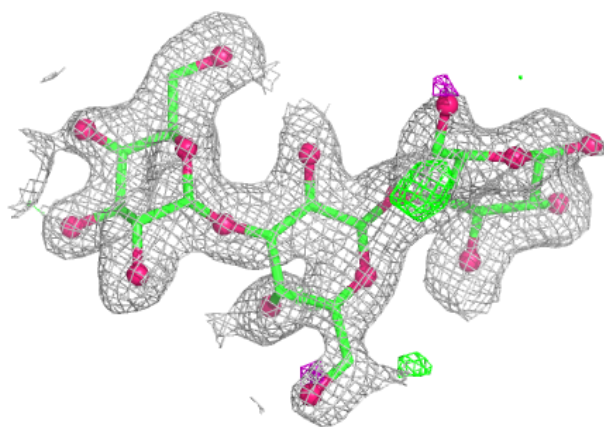
**Electron density around Chain o:**

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

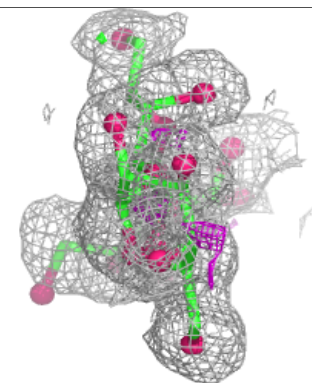
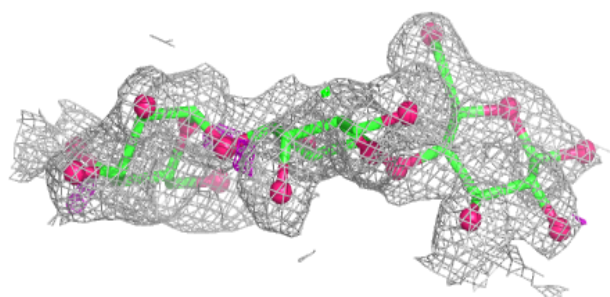
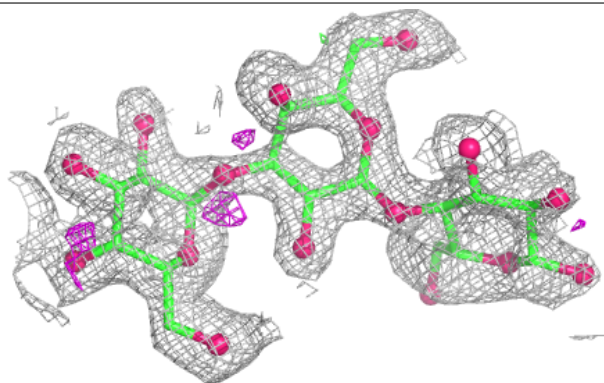


**Electron density around Chain p:**

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

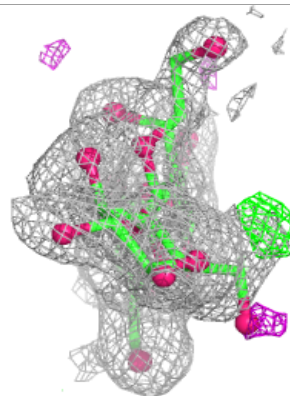
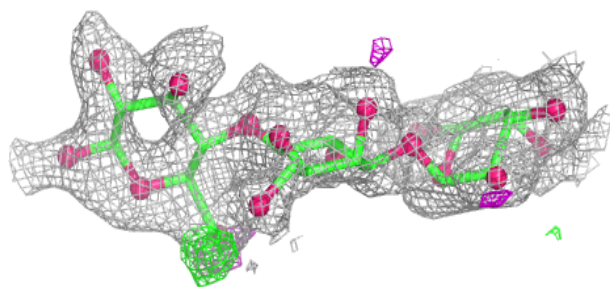
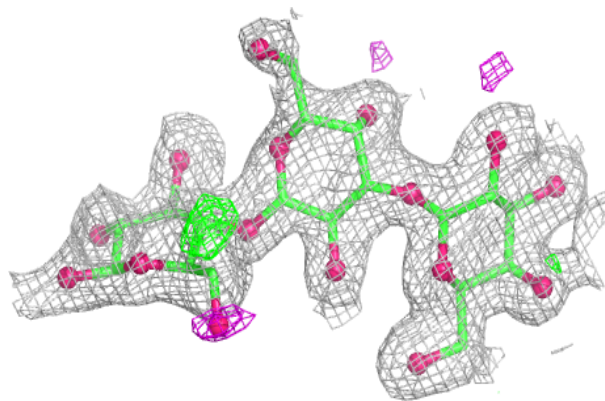
**Electron density around Chain q:**

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

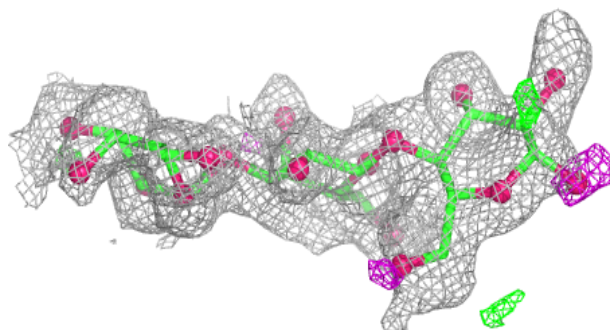
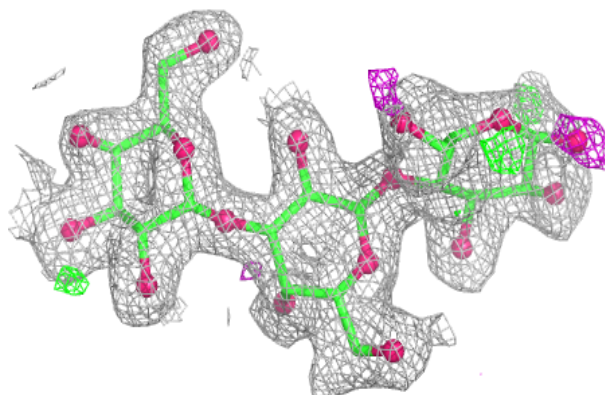


**Electron density around Chain r:**

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

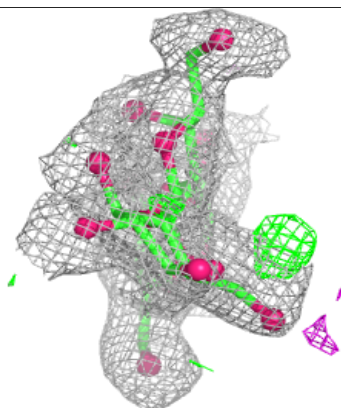
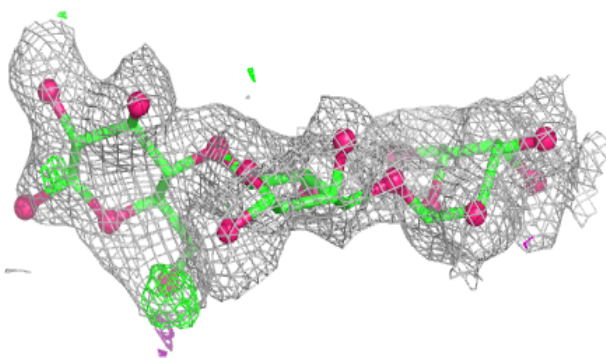
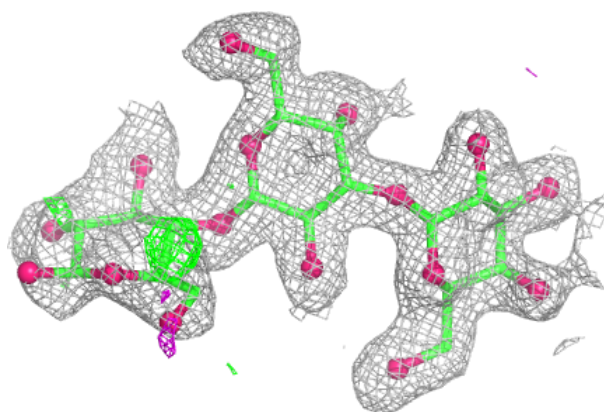
**Electron density around Chain s:**

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

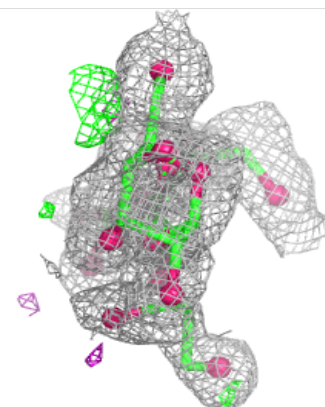
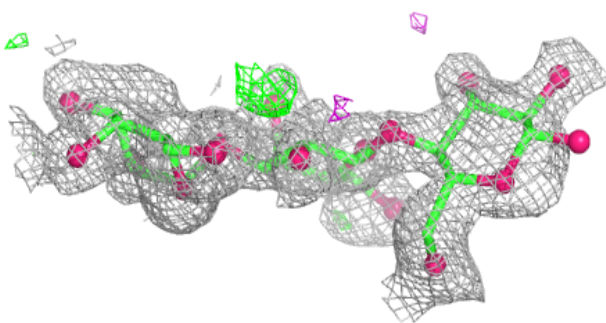
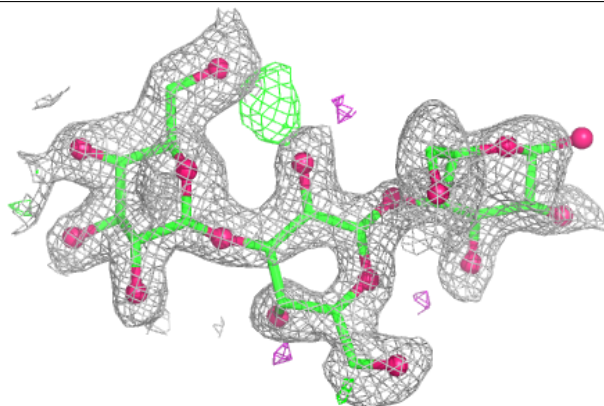


**Electron density around Chain t:**

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

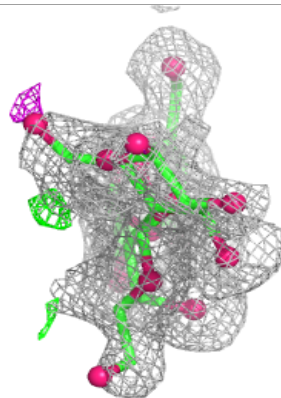
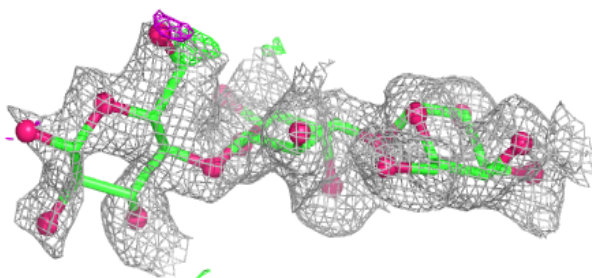
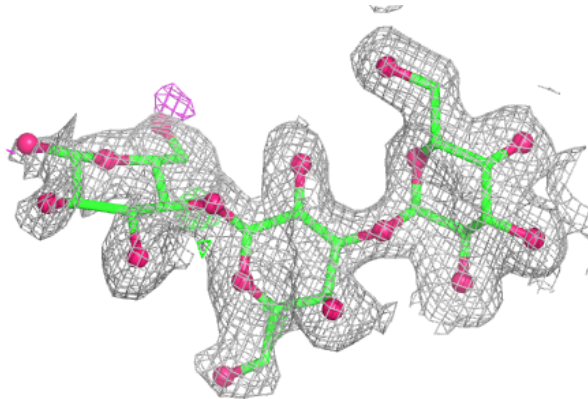
**Electron density around Chain u:**

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

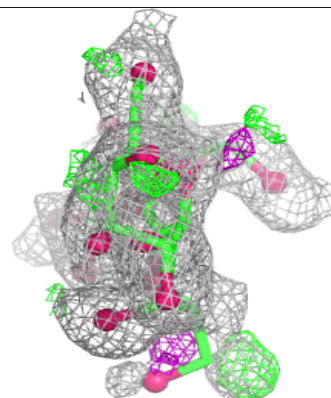
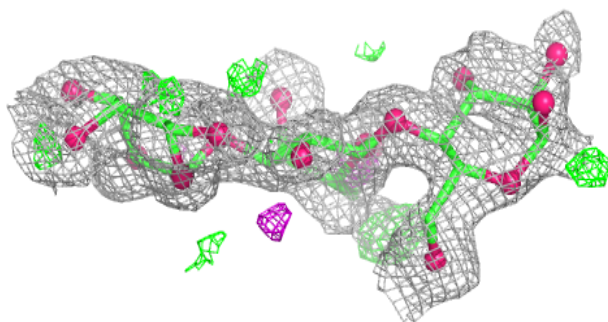
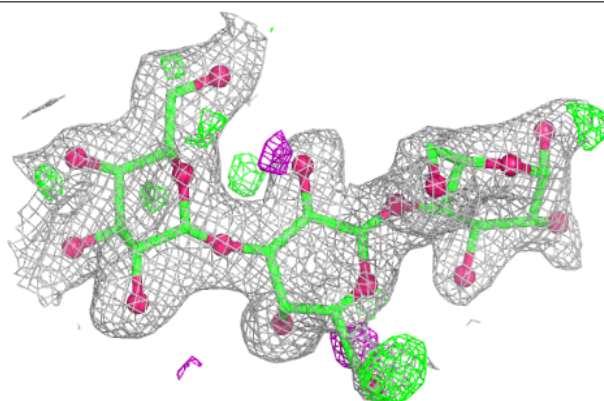


**Electron density around Chain v:**

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

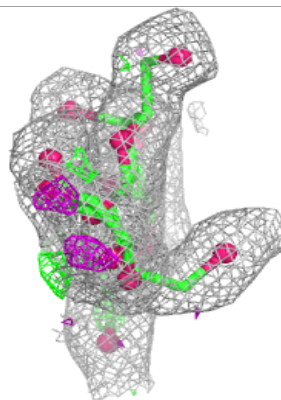
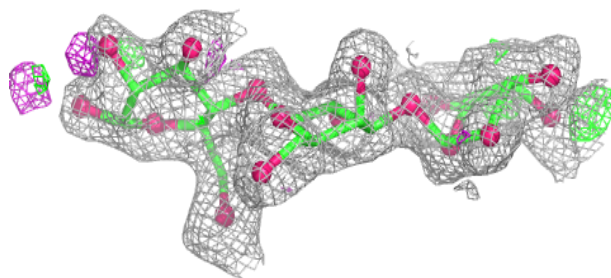
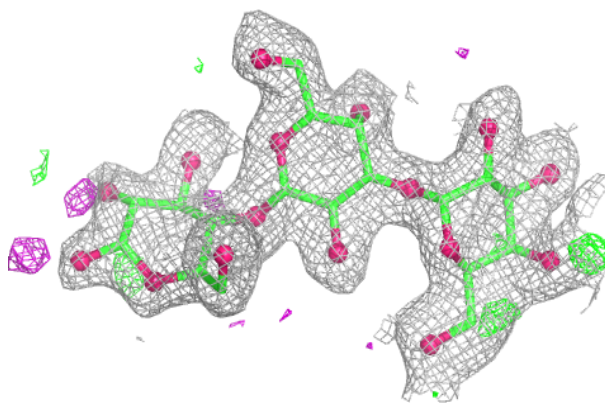
**Electron density around Chain a:**

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

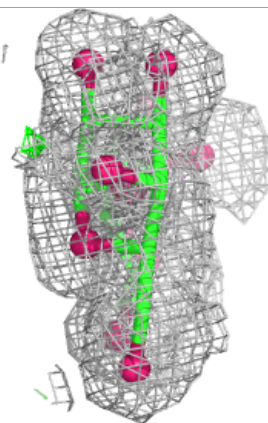
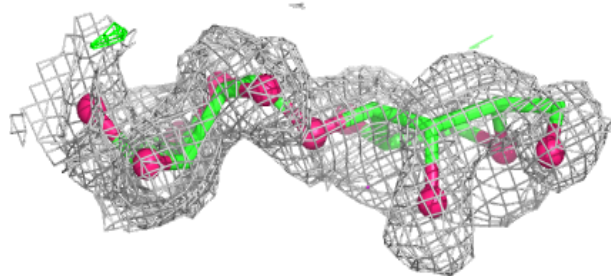
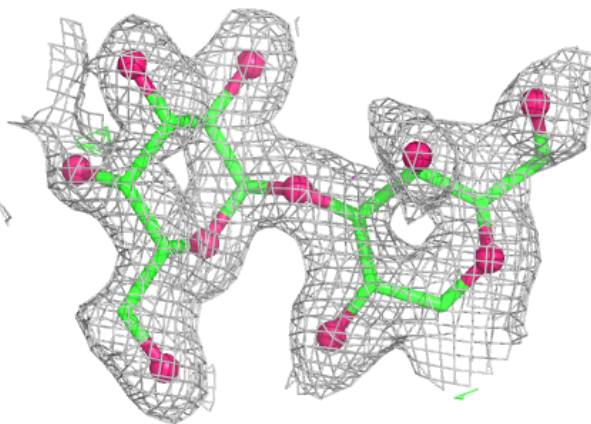


**Electron density around Chain c:**

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

**Electron density around Chain l:**

$2mF_o-DF_c$  (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
7	BGC	N	204	12/12	0.73	0.15	30,35,39,41	0
6	EDO	E	205	4/4	0.86	0.12	9,11,16,16	0
6	EDO	X	205	4/4	0.87	0.14	16,16,17,19	0
6	EDO	G	205	4/4	0.90	0.10	8,13,14,17	0
6	EDO	M	205	4/4	0.91	0.10	9,10,14,16	0
6	EDO	S	205	4/4	0.91	0.09	7,8,12,15	0
6	EDO	O	205	4/4	0.92	0.09	12,13,16,17	0
6	EDO	A	205	4/4	0.92	0.08	11,13,15,19	0
6	EDO	L	205	4/4	0.92	0.08	17,17,18,21	0
5	CA	O	201	1/1	0.92	0.08	19,19,19,19	0
6	EDO	W	205	4/4	0.93	0.08	12,13,14,15	0
6	EDO	U	205	4/4	0.94	0.08	11,12,12,18	0
6	EDO	V	205	4/4	0.94	0.11	16,17,17,18	0
6	EDO	D	205	4/4	0.94	0.08	13,14,17,20	0
6	EDO	W	206	4/4	0.94	0.08	20,23,24,26	0
6	EDO	Q	206	4/4	0.94	0.10	16,16,16,17	0
6	EDO	M	206	4/4	0.94	0.10	14,15,17,19	0
6	EDO	I	205	4/4	0.95	0.08	12,13,14,15	0
6	EDO	H	205	4/4	0.95	0.09	15,21,22,22	0
6	EDO	N	205	4/4	0.95	0.08	17,18,18,19	0
5	CA	C	200	1/1	0.96	0.04	16,16,16,16	0
6	EDO	Q	205	4/4	0.96	0.08	10,11,13,15	0
5	CA	G	201	1/1	0.97	0.04	16,16,16,16	0
5	CA	E	201	1/1	0.97	0.03	12,12,12,12	0
6	EDO	I	206	4/4	0.98	0.06	10,11,13,13	0
5	CA	N	201	1/1	0.98	0.03	15,15,15,15	0
5	CA	M	201	1/1	0.98	0.03	11,11,11,11	0
5	CA	P	200	1/1	0.99	0.02	10,10,10,10	0
5	CA	Q	201	1/1	0.99	0.03	10,10,10,10	0
5	CA	R	200	1/1	0.99	0.03	13,13,13,13	0
5	CA	S	201	1/1	0.99	0.03	11,11,11,11	0
5	CA	U	201	1/1	0.99	0.02	14,14,14,14	0
5	CA	W	201	1/1	0.99	0.04	14,14,14,14	0
5	CA	X	201	1/1	0.99	0.01	12,12,12,12	0
5	CA	I	201	1/1	0.99	0.02	10,10,10,10	0
5	CA	J	200	1/1	0.99	0.02	11,11,11,11	0
5	CA	K	200	1/1	0.99	0.04	12,12,12,12	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	CA	L	201	1/1	0.99	0.03	14,14,14,14	0
5	CA	B	200	1/1	0.99	0.02	13,13,13,13	0
5	CA	F	200	1/1	0.99	0.03	10,10,10,10	0
5	CA	A	201	1/1	0.99	0.02	10,10,10,10	0
5	CA	V	201	1/1	1.00	0.02	12,12,12,12	0
5	CA	D	201	1/1	1.00	0.02	13,13,13,13	0
5	CA	T	200	1/1	1.00	0.03	14,14,14,14	0
5	CA	H	201	1/1	1.00	0.01	8,8,8,8	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.