



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 05:14 AM BST

PDB ID : 5FIB  
Title : Open form of murine Acid Sphingomyelinase  
Authors : Gorelik, A.; Illes, K.; Heinz, L.X.; Superti-Furga, G.; Nagar, B.  
Deposited on : 2015-12-22  
Resolution : 2.80 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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

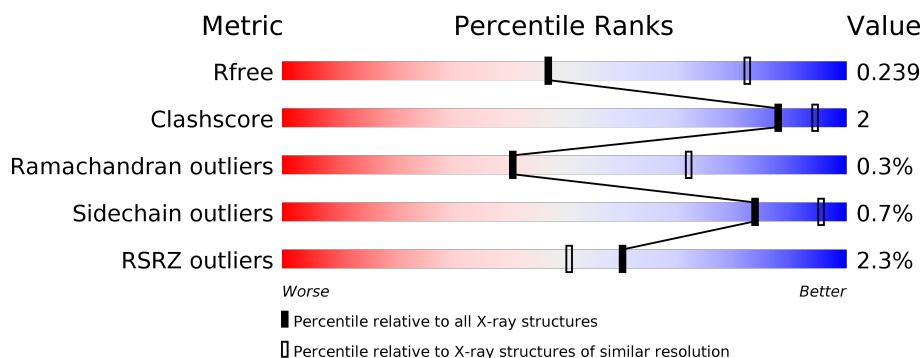
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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.





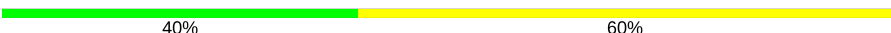

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 on 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	538	<div> <div>2%</div> <div>95%</div> <div>3%</div> </div>
1	B	538	<div> <div>2%</div> <div>94%</div> <div>5%</div> </div>
2	C	3	<div> <div>100%</div> </div>
2	D	3	<div> <div>33%</div> <div>67%</div> </div>
3	E	6	<div> <div>17%</div> <div>83%</div> </div>
3	H	6	<div> <div>17%</div> <div>67%</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
4	F	2	 50% 50%
5	G	4	 50% 50%
6	I	5	 40% 60%
7	J	5	 20% 80%

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
2	NAG	C	2	-	-	-	X
2	FUC	C	3	-	-	-	X
3	MAN	E	4	-	-	-	X
3	MAN	E	5	-	-	-	X
5	NAG	G	1	-	-	-	X
5	NAG	G	2	-	-	-	X
5	BMA	G	3	-	-	-	X
5	FUC	G	4	-	-	-	X
6	BMA	I	3	-	-	-	X
6	MAN	I	4	-	-	-	X
6	MAN	I	5	-	-	-	X
7	NAG	J	1	-	-	-	X
7	BMA	J	3	-	-	-	X
7	FUC	J	5	-	-	-	X
9	SO4	A	730	-	-	-	X
9	SO4	A	731	-	-	-	X
9	SO4	B	726	-	-	-	X

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 17590 atoms, of which 8565 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.

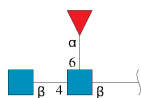
- Molecule 1 is a protein called SpHINGOMYELIN phosphodiesterase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	534	Total	C	H	N	O	S	0	0	0
			8303	2721	4073	735	751	23			
1	B	534	Total	C	H	N	O	S	0	1	0
			8326	2732	4082	737	752	23			

There are 20 discrepancies between the modelled and reference sequences:

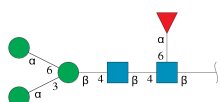
Chain	Residue	Modelled	Actual	Comment	Reference
A	74	ASP	-	expression tag	UNP Q04519
A	75	ARG	-	expression tag	UNP Q04519
A	76	HIS	-	expression tag	UNP Q04519
A	77	HIS	-	expression tag	UNP Q04519
A	78	HIS	-	expression tag	UNP Q04519
A	79	HIS	-	expression tag	UNP Q04519
A	80	HIS	-	expression tag	UNP Q04519
A	81	HIS	-	expression tag	UNP Q04519
A	82	LYS	-	expression tag	UNP Q04519
A	83	LEU	-	expression tag	UNP Q04519
B	74	ASP	-	expression tag	UNP Q04519
B	75	ARG	-	expression tag	UNP Q04519
B	76	HIS	-	expression tag	UNP Q04519
B	77	HIS	-	expression tag	UNP Q04519
B	78	HIS	-	expression tag	UNP Q04519
B	79	HIS	-	expression tag	UNP Q04519
B	80	HIS	-	expression tag	UNP Q04519
B	81	HIS	-	expression tag	UNP Q04519
B	82	LYS	-	expression tag	UNP Q04519
B	83	LEU	-	expression tag	UNP Q04519

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	3	Total	C	H	N	O	0	0	0
			75	22	37	2	14			
2	D	3	Total	C	H	N	O	0	0	0
			75	22	37	2	14			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



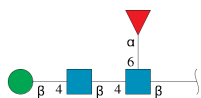
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	6	Total	C	H	N	O	0	0	0
			138	40	67	2	29			
3	H	6	Total	C	H	N	O	0	0	0
			138	40	67	2	29			

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



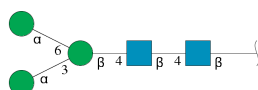
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



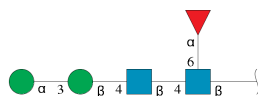
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	4	Total	C	H	N	O	0	0	0
			96	28	47	2	19			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	I	5	Total	C	H	N	O	0	0	0
			118	34	57	2	25			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.

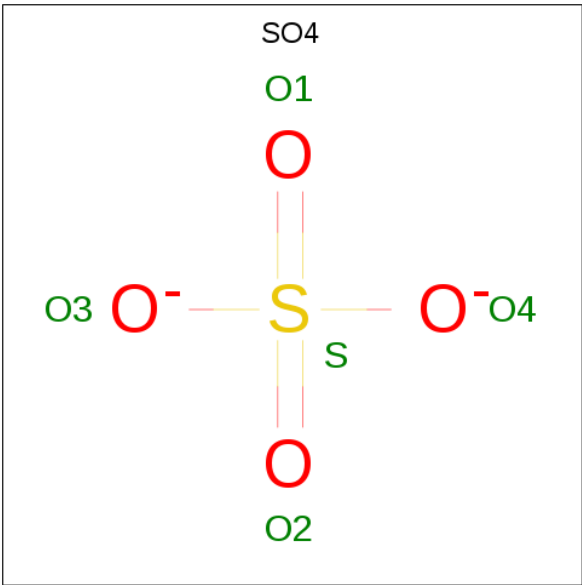


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	J	5	Total	C	H	N	O	0	0	0
			117	34	57	2	24			

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	3	Total	Zn	0	0
			3	3		
8	A	3	Total	Zn	0	0
			3	3		

- Molecule 9 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



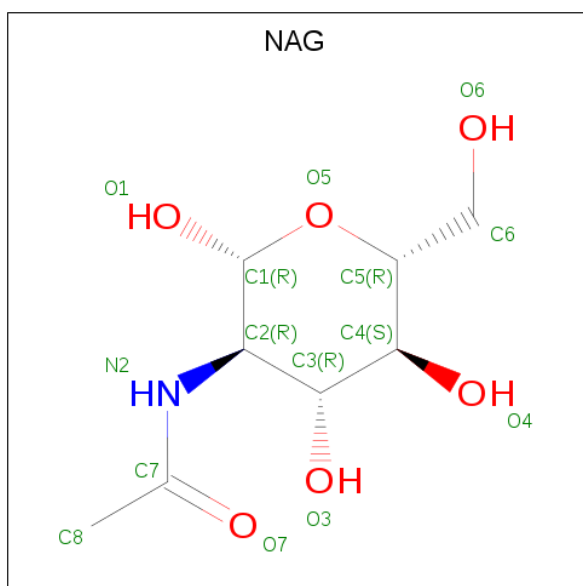
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	B	1	Total	O	S	0	0
			5	4	1		
9	B	1	Total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

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

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 11 is water.

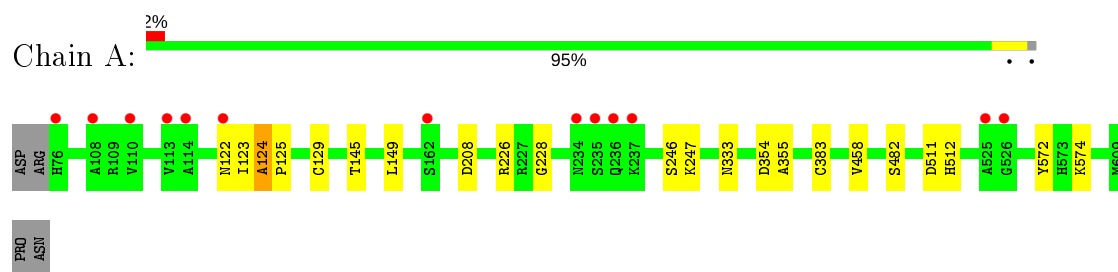
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	14	Total	O	0	0
			14	14		
11	B	16	Total	O	0	0
			16	16		



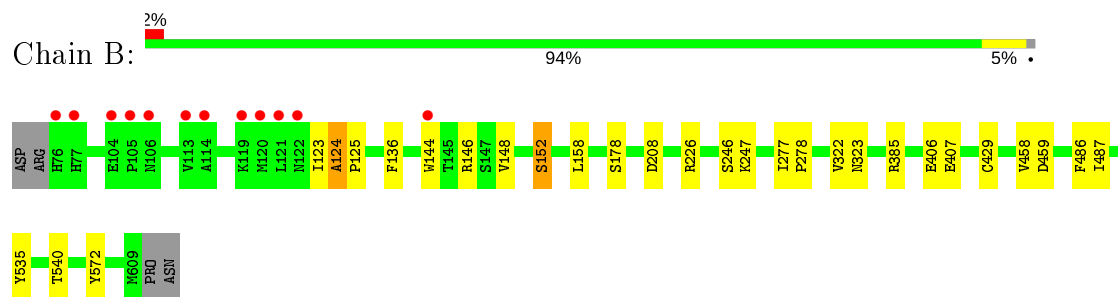
### 3 Residue-property plots

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.

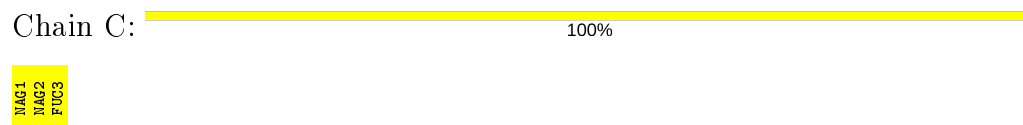
- Molecule 1: Sphingomyelin phosphodiesterase



- Molecule 1: Sphingomyelin phosphodiesterase



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  17% 83%



- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  17% 67% 17%



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

Chain F:  50% 50%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 50%



- Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  40% 60%



- Molecule 7: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  20% 80%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	181.17Å 181.17Å 109.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.70 – 2.80 45.70 – 2.50	Depositor EDS
% Data completeness (in resolution range)	73.2 (45.70-2.80) 65.4 (45.70-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, $R_{free}$	0.190 , 0.237 0.192 , 0.239	Depositor DCC
$R_{free}$ test set	2192 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.4	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 32.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	17590	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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: ZN, BMA, NAG, SO4, FUC, MAN

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	0.25	0/4379	0.42	0/5993
1	B	0.25	0/4395	0.42	0/6016
All	All	0.25	0/8774	0.42	0/12009

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	4230	4073	4072	13	1
1	B	4244	4082	4082	19	0
2	C	38	37	34	0	0
2	D	38	37	34	2	0
3	E	71	67	61	0	0
3	H	71	67	61	1	0
4	F	28	27	25	0	0
5	G	49	47	43	0	0
6	I	61	57	52	0	0
7	J	60	57	52	3	1
8	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	3	0	0	0	0
9	A	50	0	0	1	0
9	B	35	0	0	0	0
10	B	14	14	13	0	0
11	A	14	0	0	0	0
11	B	16	0	0	1	0
All	All	9025	8565	8529	35	1

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 35 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:SER:OG	7:J:4:MAN:O4	1.94	0.84
1:B:152:SER:HG	7:J:4:MAN:HO4	1.32	0.75
2:D:1:NAG:O5	2:D:3:FUC:O2	2.10	0.67
1:A:482:SER:O	1:A:574:LYS:NZ	2.28	0.66
1:B:124:ALA:HB1	1:B:125:PRO:CD	2.29	0.62

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ASN:O	7:J:5:FUC:O3[7_553]	2.07	0.13

## 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	532/538 (99%)	501 (94%)	29 (6%)	2 (0%)	34 66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	533/538 (99%)	502 (94%)	30 (6%)	1 (0%)	47 78
All	All	1065/1076 (99%)	1003 (94%)	59 (6%)	3 (0%)	41 72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	124	ALA
1	A	124	ALA
1	A	333	ASN

### 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	456/460 (99%)	454 (100%)	2 (0%)	91 97
1	B	457/460 (99%)	453 (99%)	4 (1%)	78 94
All	All	913/920 (99%)	907 (99%)	6 (1%)	84 95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	136	PHE
1	B	178	SER
1	B	146	ARG
1	A	383	CYS
1	B	152	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	HIS
1	A	334	GLN
1	B	290	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

34 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	NAG	C	1	1,2	14,14,15	0.47	0	17,19,21	1.01	1 (5%)
2	NAG	C	2	2	14,14,15	1.83	2 (14%)	17,19,21	1.10	2 (11%)
2	FUC	C	3	2	10,10,11	1.02	1 (10%)	14,14,16	1.13	1 (7%)
2	NAG	D	1	1,2	14,14,15	0.47	0	17,19,21	0.94	1 (5%)
2	NAG	D	2	2	14,14,15	0.65	0	17,19,21	0.92	1 (5%)
2	FUC	D	3	2	10,10,11	1.79	3 (30%)	14,14,16	1.59	3 (21%)
3	NAG	E	1	1,3	14,14,15	0.56	0	17,19,21	0.48	0
3	NAG	E	2	3	14,14,15	0.44	0	17,19,21	0.95	1 (5%)
3	BMA	E	3	3	11,11,12	1.16	0	15,15,17	1.49	3 (20%)
3	MAN	E	4	3	11,11,12	1.02	1 (9%)	15,15,17	1.26	3 (20%)
3	MAN	E	5	3	11,11,12	0.87	1 (9%)	15,15,17	1.17	2 (13%)
3	FUC	E	6	3	10,10,11	1.50	1 (10%)	14,14,16	2.19	4 (28%)
4	NAG	F	1	1,4	14,14,15	0.25	0	17,19,21	0.45	0
4	NAG	F	2	4	14,14,15	0.32	0	17,19,21	0.77	1 (5%)
5	NAG	G	1	1,5	14,14,15	0.39	0	17,19,21	0.51	0
5	NAG	G	2	5	14,14,15	0.26	0	17,19,21	0.46	0
5	BMA	G	3	5	11,11,12	0.61	0	15,15,17	0.95	1 (6%)
5	FUC	G	4	5	10,10,11	1.62	1 (10%)	14,14,16	2.30	4 (28%)
3	NAG	H	1	1,3	14,14,15	0.67	1 (7%)	17,19,21	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	H	2	3	14,14,15	0.23	0	17,19,21	0.49	0
3	BMA	H	3	3	11,11,12	0.67	0	15,15,17	1.24	1 (6%)
3	MAN	H	4	3	11,11,12	0.85	1 (9%)	15,15,17	1.70	4 (26%)
3	MAN	H	5	3	11,11,12	1.36	2 (18%)	15,15,17	1.93	4 (26%)
3	FUC	H	6	3	10,10,11	1.57	1 (10%)	14,14,16	2.18	4 (28%)
6	NAG	I	1	1,6	14,14,15	0.28	0	17,19,21	0.50	0
6	NAG	I	2	6	14,14,15	0.30	0	17,19,21	0.55	0
6	BMA	I	3	6	11,11,12	0.80	0	15,15,17	1.08	2 (13%)
6	MAN	I	4	6	11,11,12	0.87	1 (9%)	15,15,17	1.00	1 (6%)
6	MAN	I	5	6	11,11,12	0.74	0	15,15,17	1.10	2 (13%)
7	NAG	J	1	1,7	14,14,15	0.59	0	17,19,21	0.60	0
7	NAG	J	2	7	14,14,15	0.38	0	17,19,21	0.92	1 (5%)
7	BMA	J	3	7	11,11,12	1.00	0	15,15,17	1.42	3 (20%)
7	MAN	J	4	7	11,11,12	0.82	0	15,15,17	1.08	2 (13%)
7	FUC	J	5	7	10,10,11	1.73	3 (30%)	14,14,16	2.67	4 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	C	2	2	-	3/6/23/26	0/1/1/1
2	FUC	C	3	2	-	-	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	FUC	D	3	2	-	-	0/1/1/1
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	0/1/1/1
3	MAN	E	5	3	-	0/2/19/22	0/1/1/1
3	FUC	E	6	3	-	-	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
5	NAG	G	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	FUC	G	4	5	-	-	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
3	MAN	H	4	3	-	1/2/19/22	0/1/1/1
3	MAN	H	5	3	-	1/2/19/22	0/1/1/1
3	FUC	H	6	3	-	-	0/1/1/1
6	NAG	I	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	I	2	6	-	1/6/23/26	0/1/1/1
6	BMA	I	3	6	-	1/2/19/22	1/1/1/1
6	MAN	I	4	6	-	1/2/19/22	0/1/1/1
6	MAN	I	5	6	-	0/2/19/22	0/1/1/1
7	NAG	J	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	2/6/23/26	0/1/1/1
7	BMA	J	3	7	-	2/2/19/22	0/1/1/1
7	MAN	J	4	7	-	1/2/19/22	0/1/1/1
7	FUC	J	5	7	-	-	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	NAG	O5-C1	-4.97	1.35	1.43
5	G	4	FUC	C1-C2	4.41	1.62	1.52
3	H	6	FUC	C1-C2	4.38	1.62	1.52
3	E	6	FUC	C1-C2	4.18	1.61	1.52
2	D	3	FUC	C1-C2	4.10	1.61	1.52

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	5	FUC	C1-C2-C3	-6.84	101.26	109.67
5	G	4	FUC	C1-C2-C3	4.97	115.78	109.67
3	H	5	MAN	C1-C2-C3	4.96	115.76	109.67
7	J	5	FUC	O2-C2-C1	4.87	119.12	109.15
3	E	6	FUC	C1-C2-C3	4.81	115.57	109.67

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	2	NAG	O5-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6

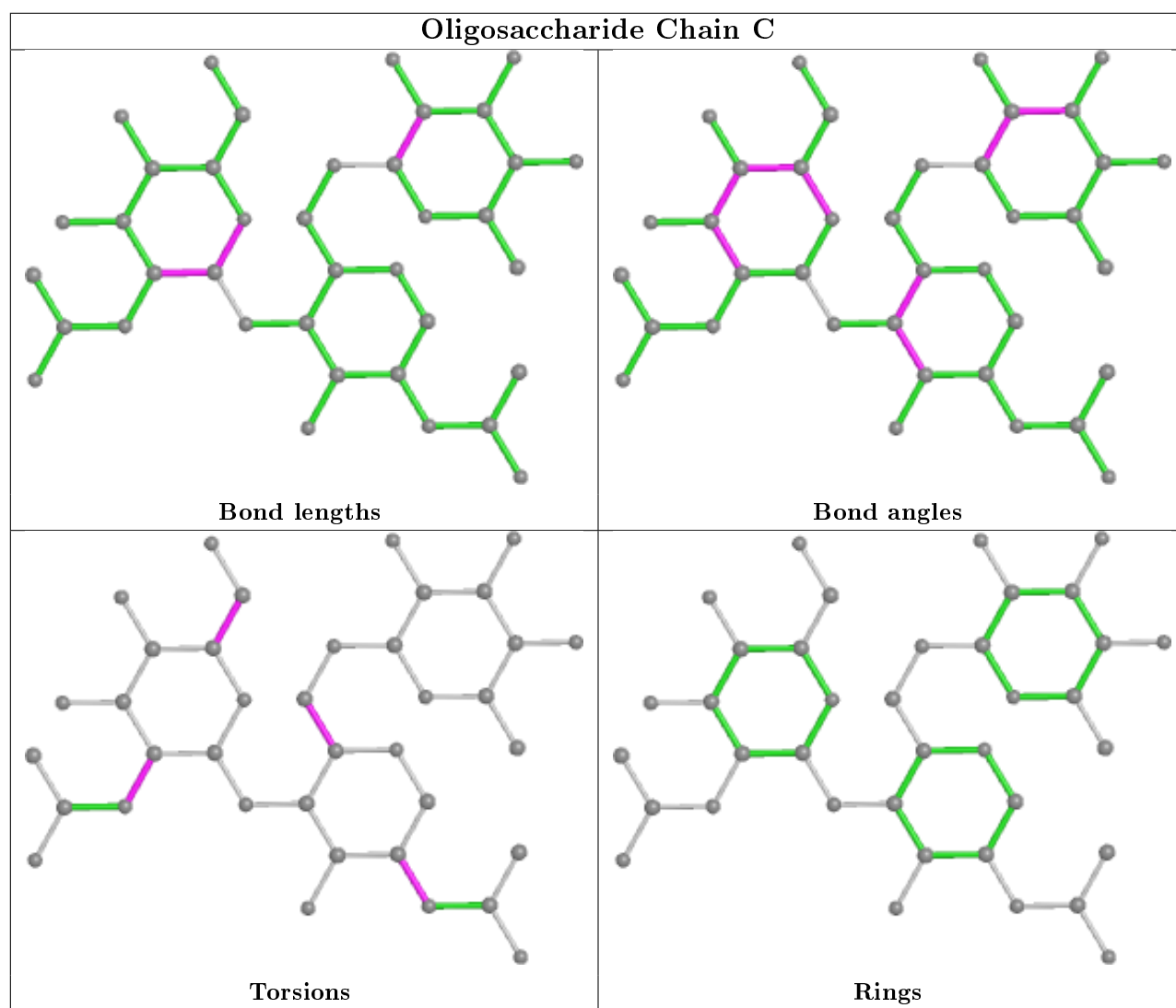
All (1) ring outliers are listed below:

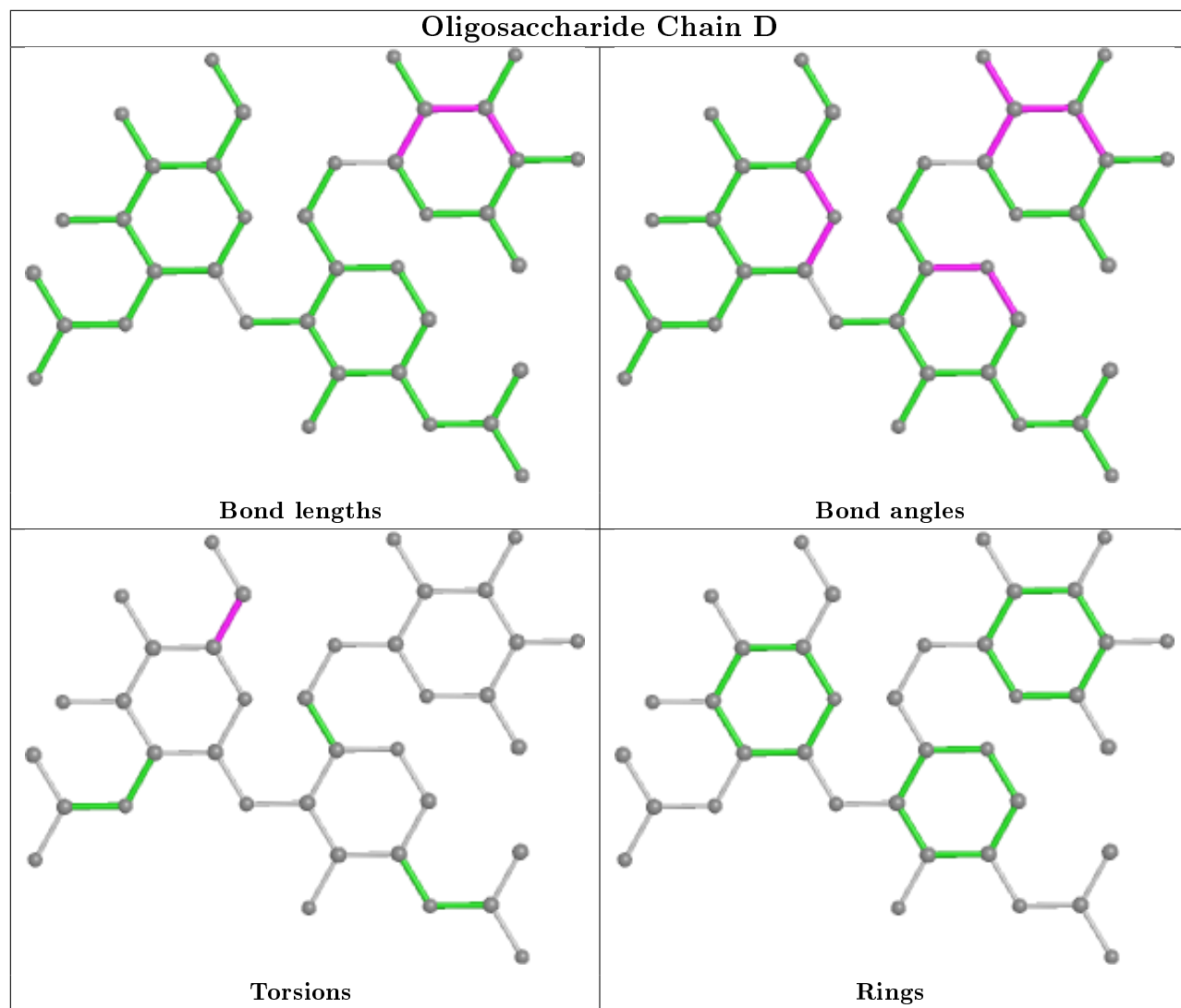
Mol	Chain	Res	Type	Atoms
6	I	3	BMA	C1-C2-C3-C4-C5-O5

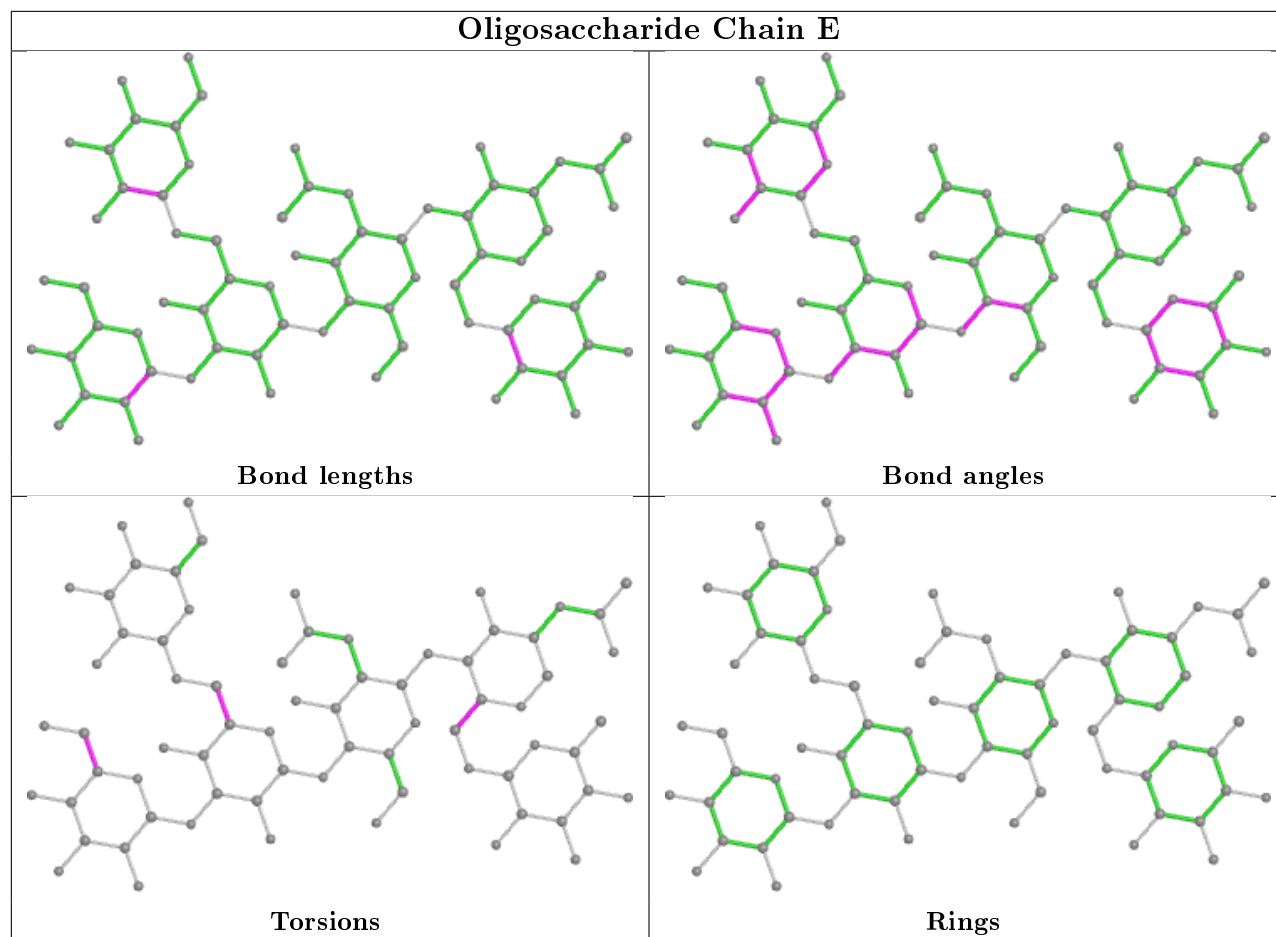
7 monomers are involved in 7 short contacts:

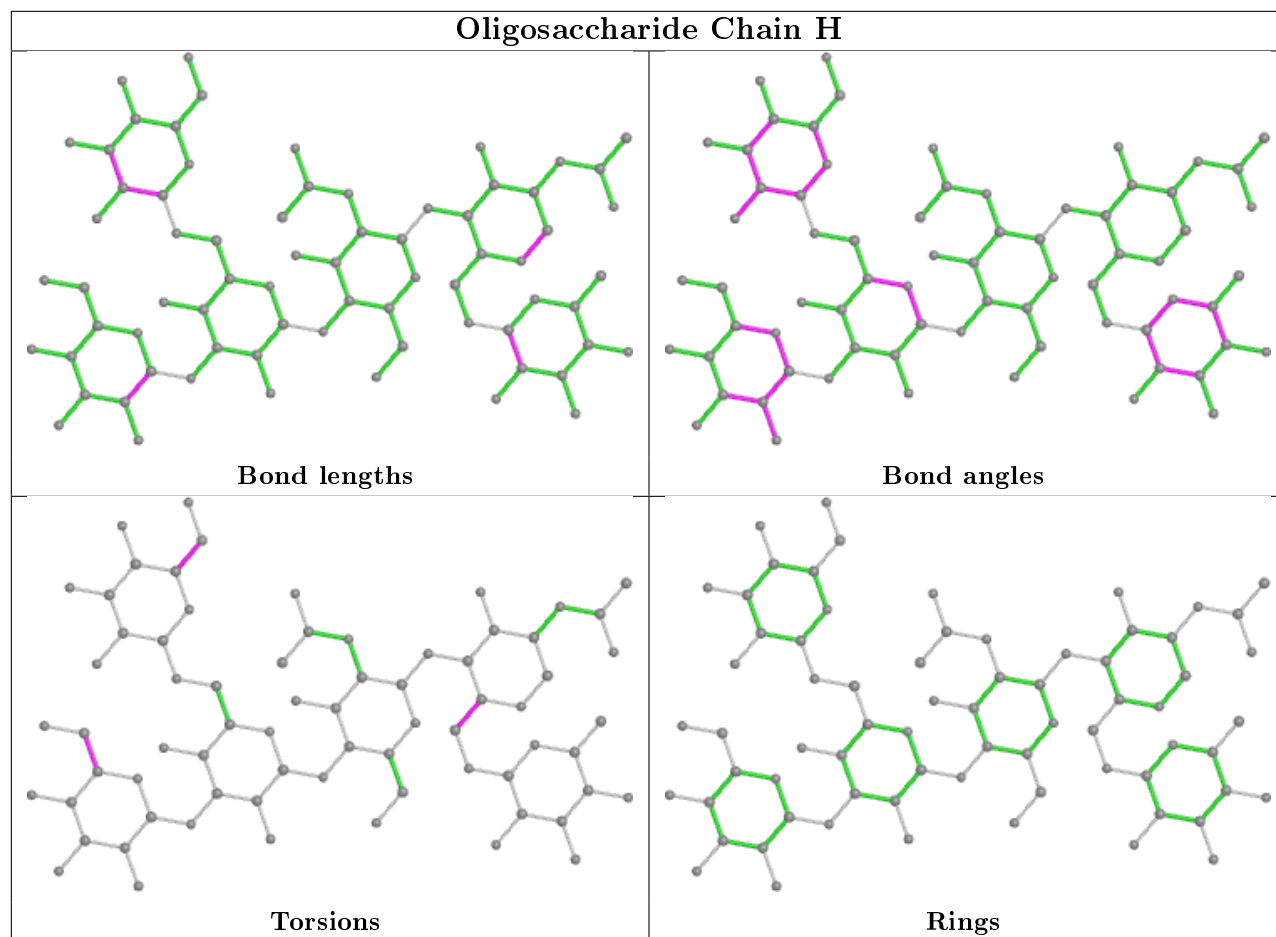
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	5	MAN	1	0
7	J	4	MAN	2	0
7	J	3	BMA	1	0
2	D	1	NAG	2	0
7	J	2	NAG	1	0
2	D	3	FUC	2	0
7	J	5	FUC	0	1

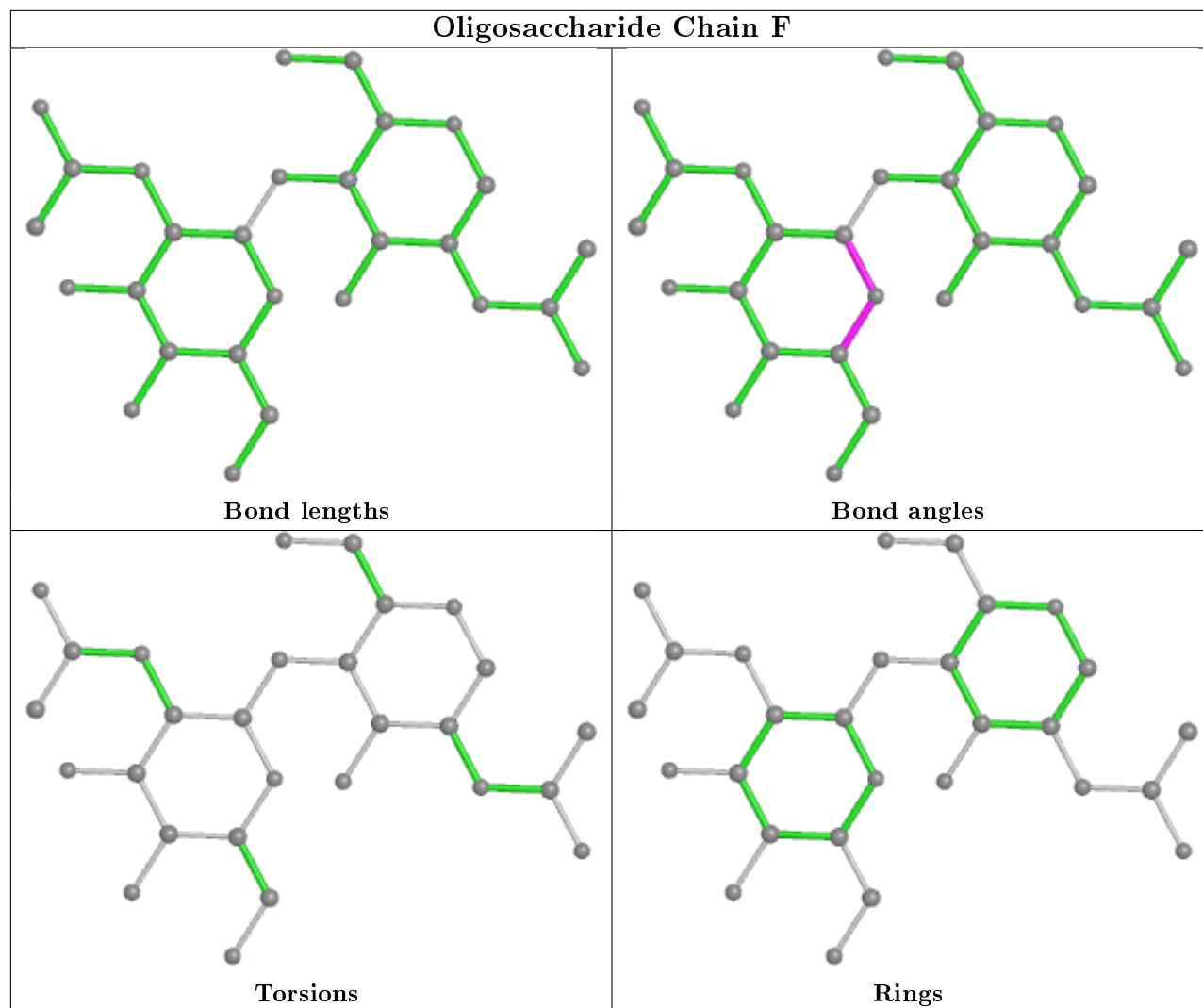
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

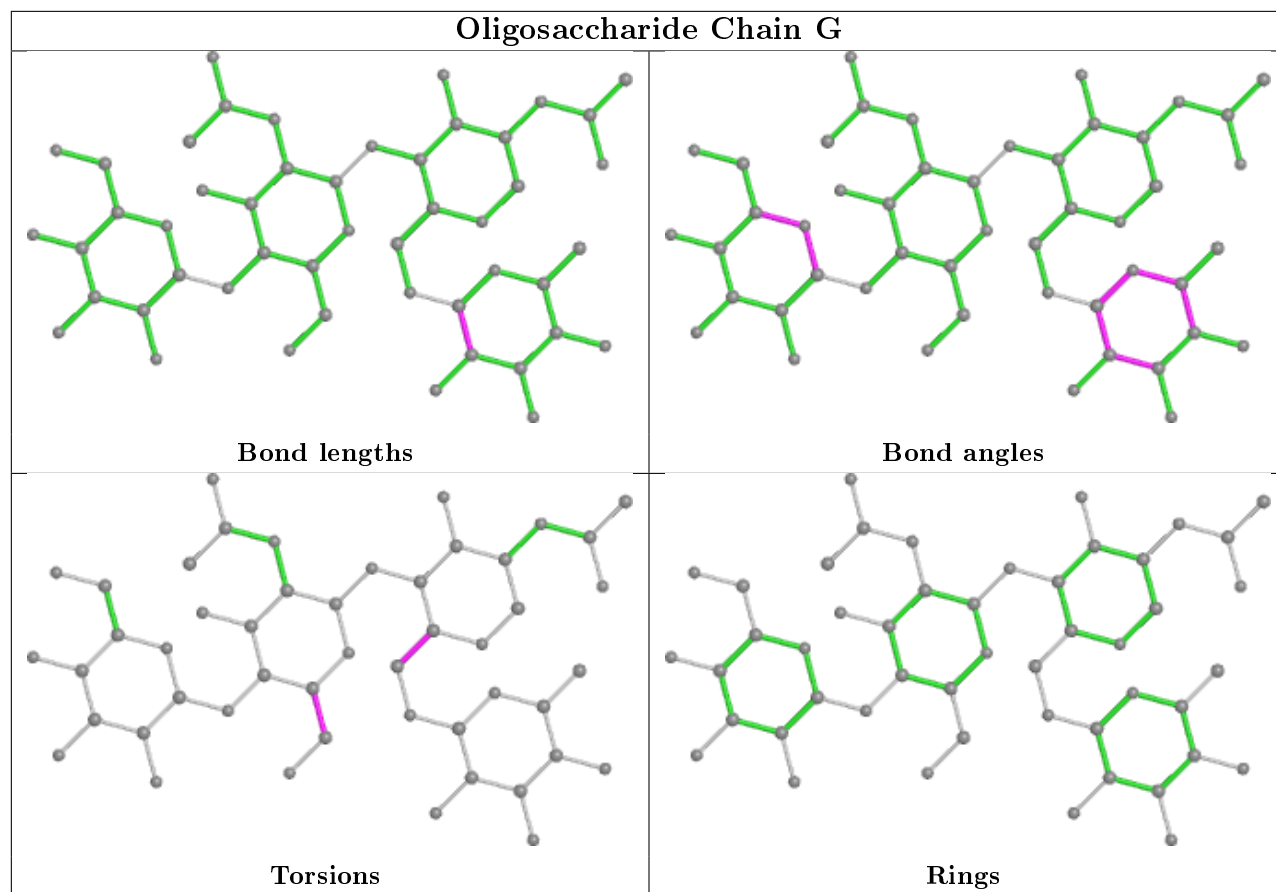




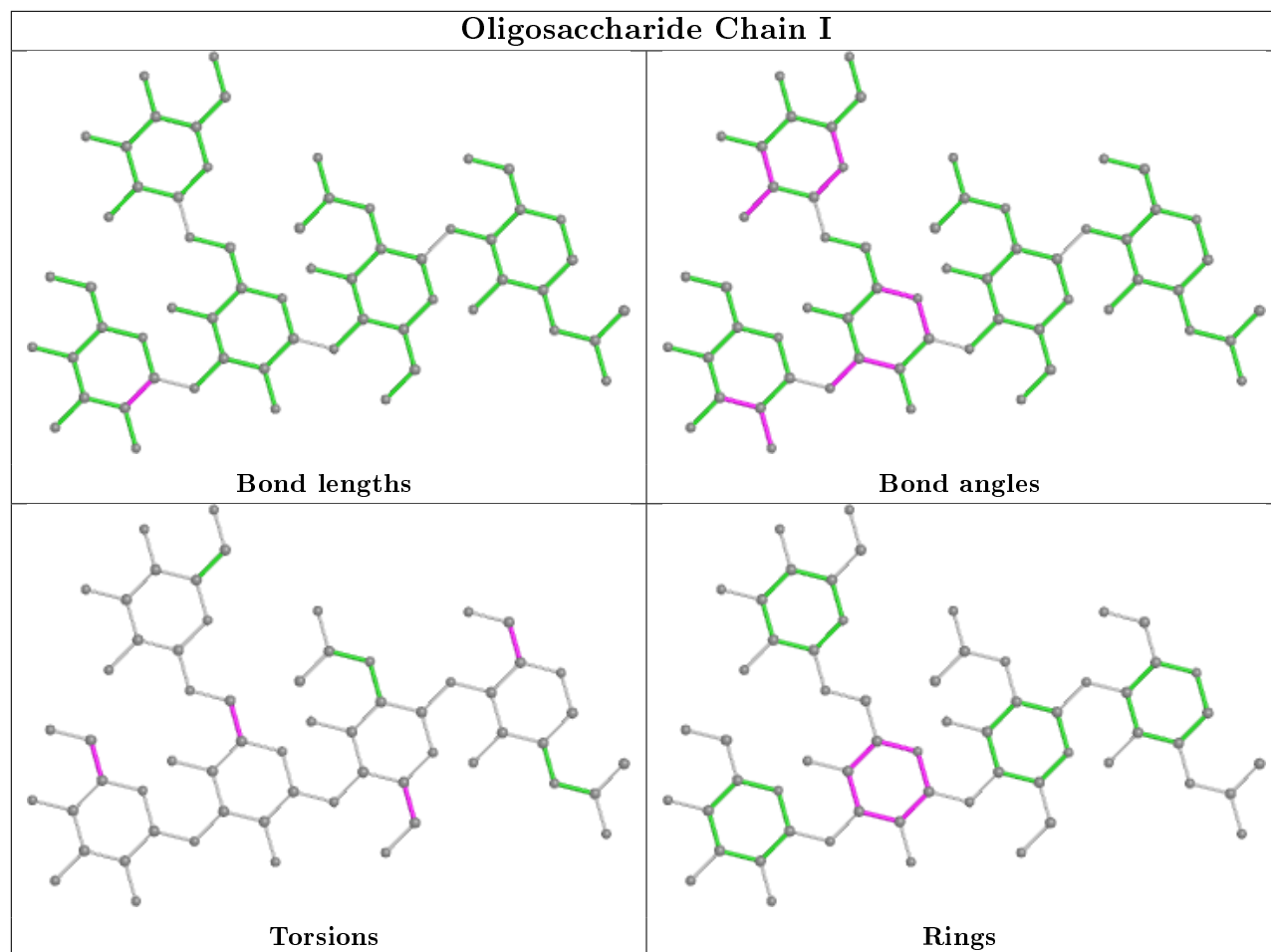


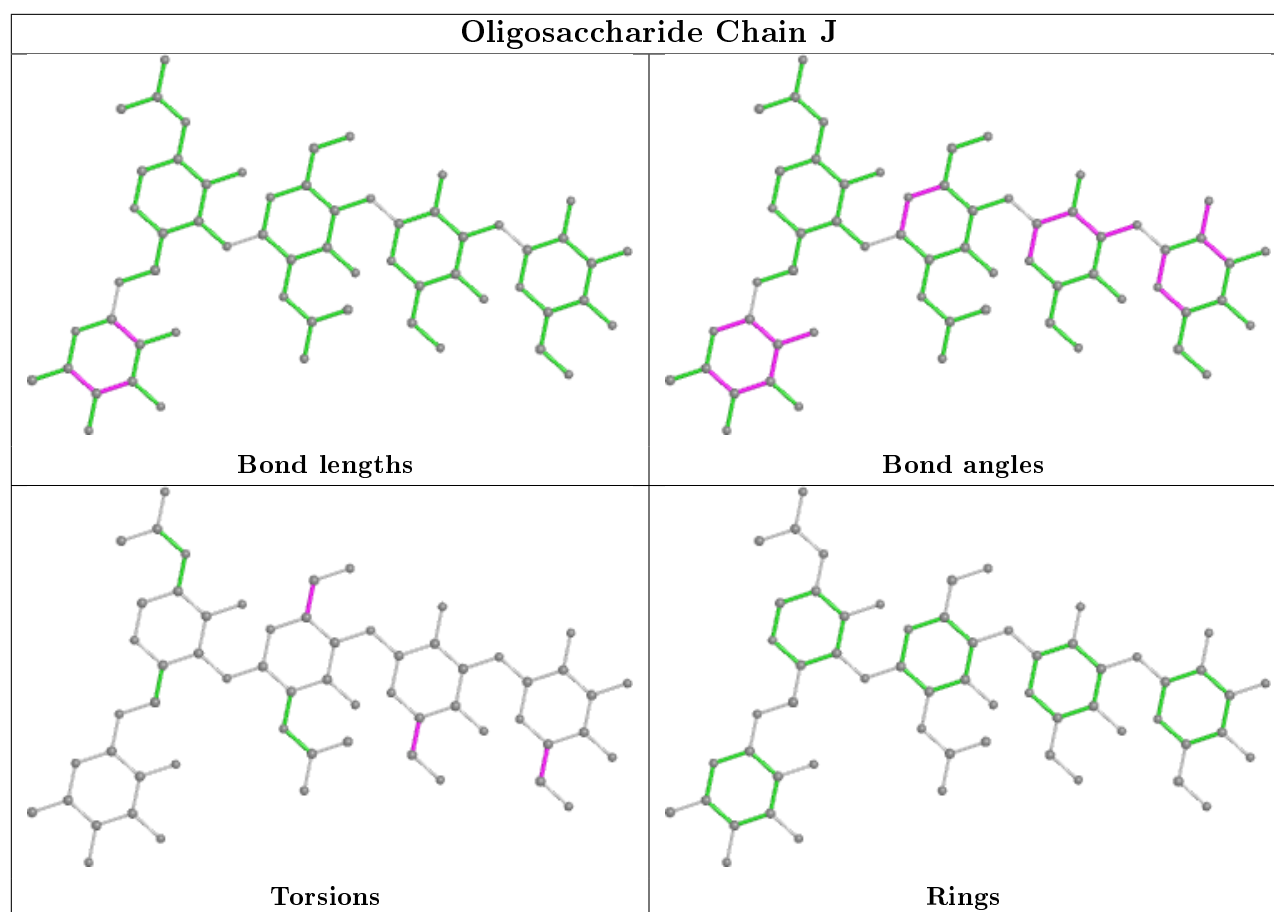












## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 6 are monoatomic - leaving 18 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	$\# Z  > 2$
9	SO4	B	722	-	4,4,4	0.13	0	6,6,6	0.05	0
9	SO4	A	722	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	B	726	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	A	731	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	B	727	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	B	723	-	4,4,4	0.14	0	6,6,6	0.05	0
10	NAG	B	704	1	14,14,15	0.20	0	17,19,21	0.46	0
9	SO4	A	725	-	4,4,4	0.14	0	6,6,6	0.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	SO4	B	725	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	A	724	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	B	724	-	4,4,4	0.14	0	6,6,6	0.04	0
9	SO4	A	728	-	4,4,4	0.14	0	6,6,6	0.04	0
9	SO4	A	729	-	4,4,4	0.14	0	6,6,6	0.06	0
9	SO4	A	723	-	4,4,4	0.14	0	6,6,6	0.06	0
9	SO4	B	721	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	A	730	-	4,4,4	0.14	0	6,6,6	0.04	0
9	SO4	A	727	-	4,4,4	0.14	0	6,6,6	0.05	0
9	SO4	A	726	-	4,4,4	0.14	0	6,6,6	0.05	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
10	NAG	B	704	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	729	SO4	1	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	534/538 (99%)	-0.21	13 (2%) 59 49	16, 38, 91, 130	0
1	B	534/538 (99%)	-0.43	12 (2%) 62 52	14, 32, 83, 120	0
All	All	1068/1076 (99%)	-0.32	25 (2%) 60 51	14, 35, 86, 130	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	235	SER	5.2
1	A	234	ASN	5.1
1	B	76	HIS	4.1
1	A	525	ALA	3.9
1	B	120	MET	3.9

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

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

### 6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	NAG	G	1	14/15	0.57	0.54	92,142,172,177	0
6	MAN	I	5	11/12	0.59	0.55	85,124,156,169	0
7	BMA	J	3	11/12	0.61	0.55	71,138,169,169	0
2	NAG	C	2	14/15	0.61	0.64	101,155,192,206	0

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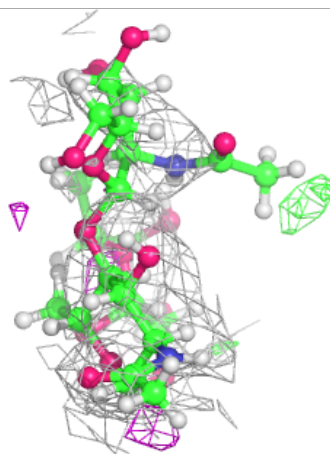
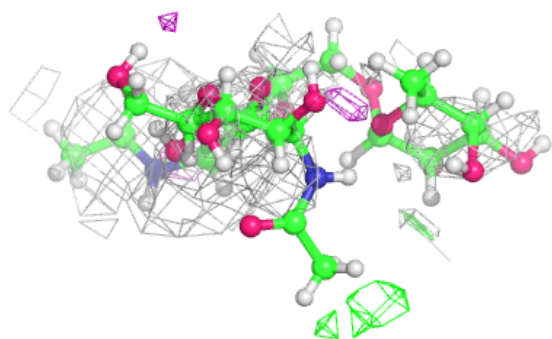
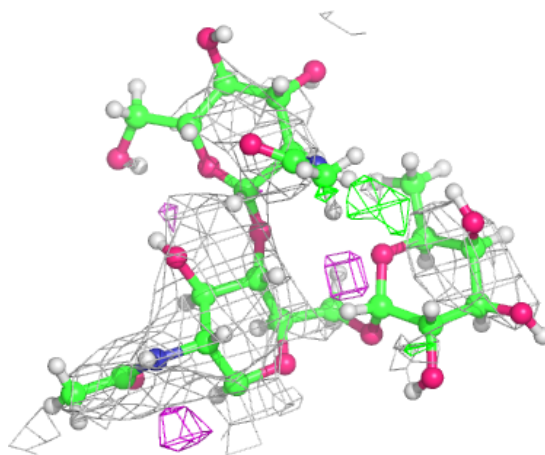
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	BMA	I	3	11/12	0.61	0.41	95,132,160,168	0
2	NAG	C	1	14/15	0.62	0.37	68,147,192,192	0
6	MAN	I	4	11/12	0.62	0.56	88,143,170,174	0
2	FUC	C	3	10/11	0.63	0.65	115,166,190,212	0
5	BMA	G	3	11/12	0.66	0.58	100,133,164,180	0
7	NAG	J	1	14/15	0.67	0.42	83,128,154,156	0
3	MAN	E	4	11/12	0.69	0.56	90,125,150,161	0
7	MAN	J	4	11/12	0.69	0.32	104,130,166,169	0
5	NAG	G	2	14/15	0.69	0.43	77,129,159,170	0
3	BMA	E	3	11/12	0.72	0.30	82,118,148,148	0
7	NAG	J	2	14/15	0.73	0.33	82,126,153,165	0
3	MAN	E	5	11/12	0.75	0.52	94,129,158,164	0
5	FUC	G	4	10/11	0.79	0.44	85,106,141,142	0
2	NAG	D	2	14/15	0.80	0.27	56,82,104,107	0
7	FUC	J	5	10/11	0.80	0.46	87,114,137,153	0
3	MAN	H	4	11/12	0.83	0.23	72,90,106,118	0
6	NAG	I	2	14/15	0.84	0.26	63,102,131,145	0
4	NAG	F	2	14/15	0.84	0.33	62,99,123,124	0
2	FUC	D	3	10/11	0.84	0.17	67,106,118,128	0
3	FUC	E	6	10/11	0.86	0.27	70,85,109,109	0
3	MAN	H	5	11/12	0.90	0.18	40,60,71,82	0
3	NAG	E	1	14/15	0.92	0.19	59,77,88,97	0
4	NAG	F	1	14/15	0.93	0.17	46,64,82,84	0
3	NAG	E	2	14/15	0.93	0.30	71,95,111,114	0
3	BMA	H	3	11/12	0.94	0.15	50,73,90,90	0
2	NAG	D	1	14/15	0.94	0.16	49,66,78,95	0
3	FUC	H	6	10/11	0.94	0.13	37,48,70,84	0
6	NAG	I	1	14/15	0.95	0.13	35,49,74,88	0
3	NAG	H	1	14/15	0.96	0.10	40,52,63,68	0
3	NAG	H	2	14/15	0.96	0.11	43,54,61,71	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.

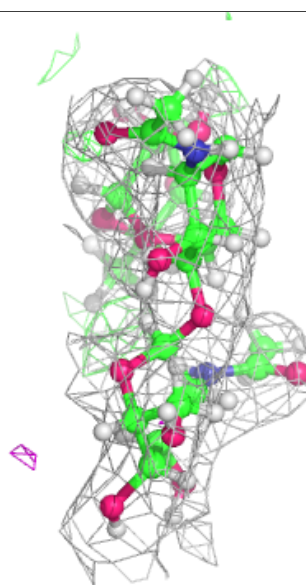
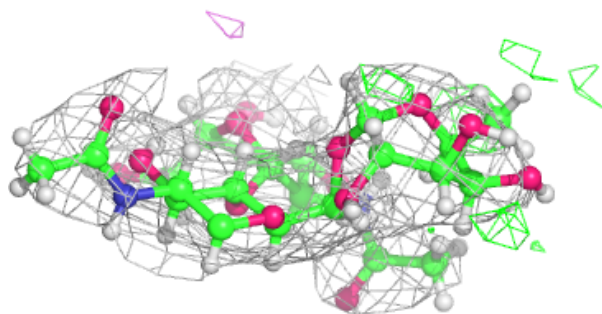
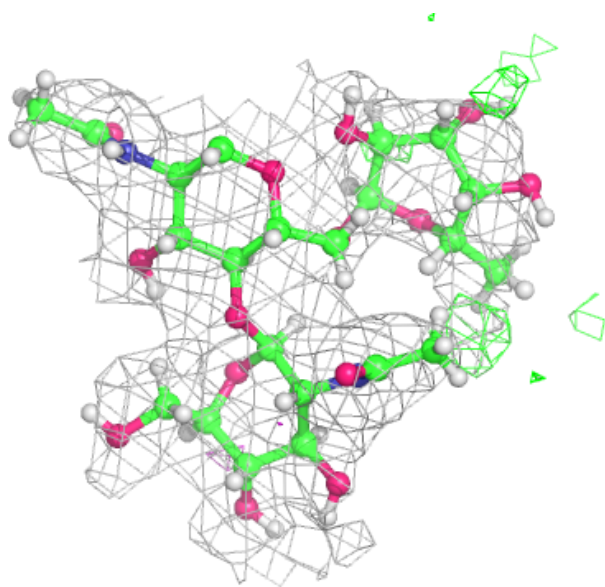
**Electron density around Chain C:**

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



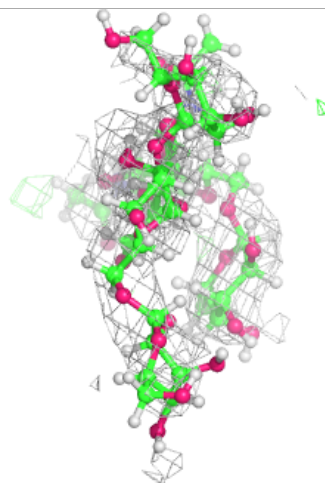
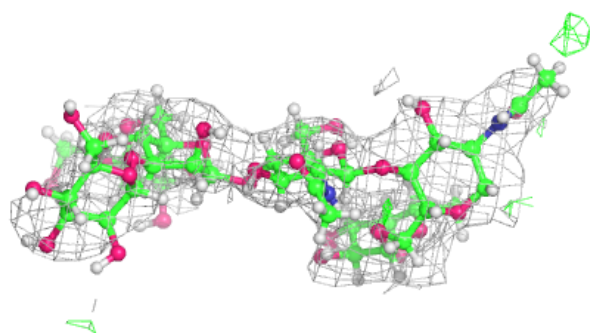
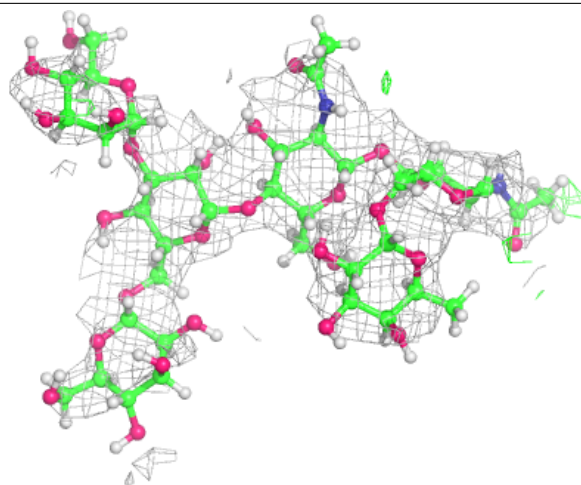
**Electron density around Chain D:**

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



**Electron density around Chain E:**

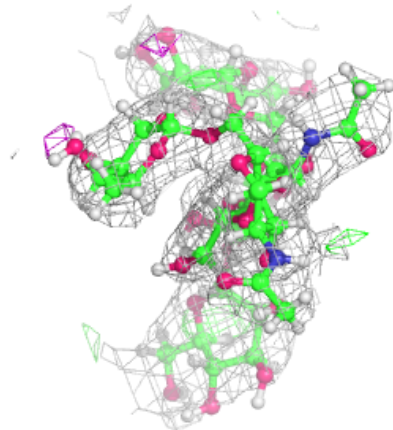
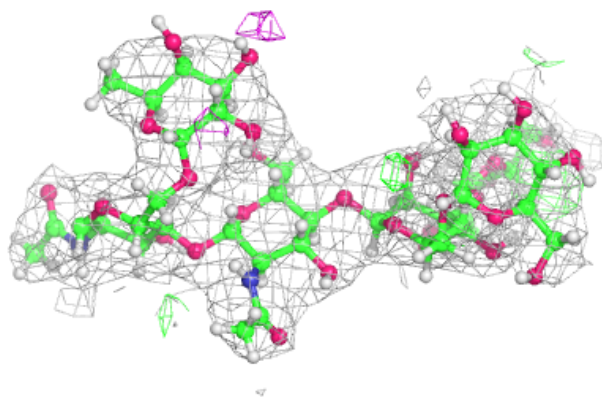
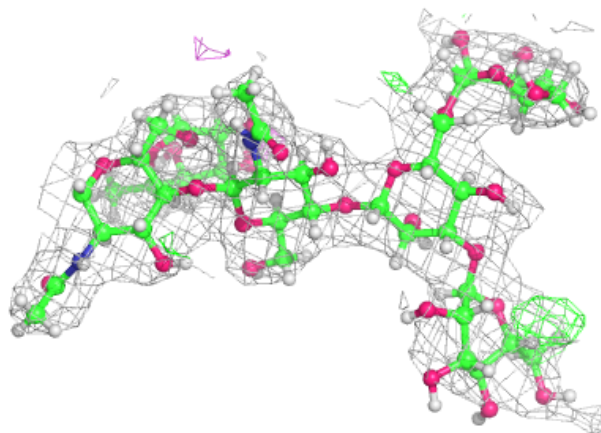
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





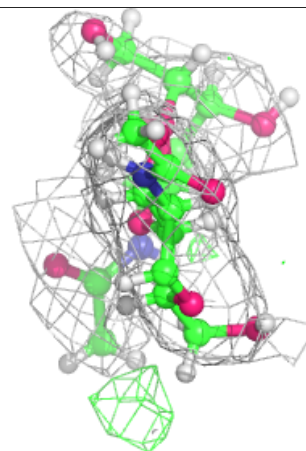
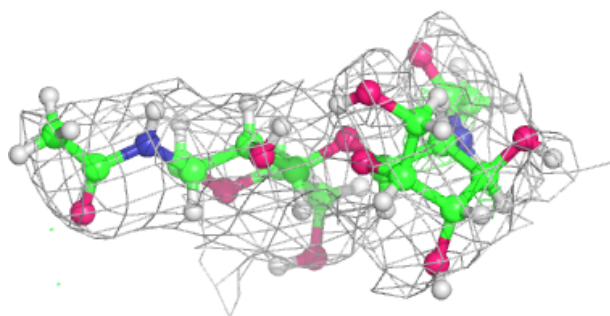
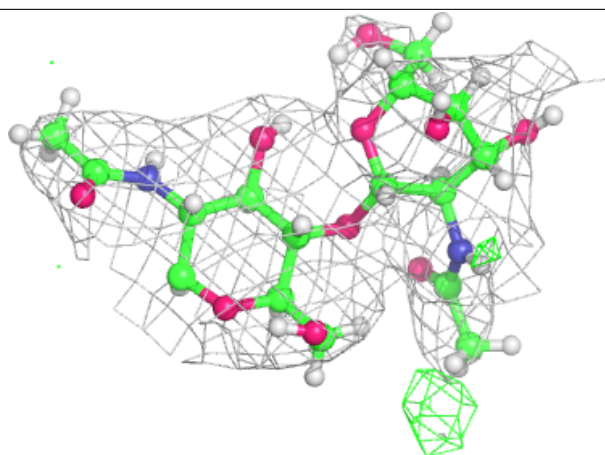
**Electron density around Chain H:**

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



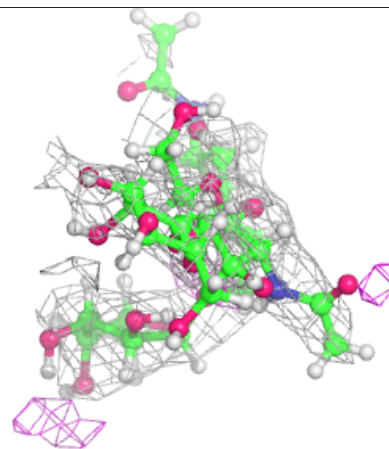
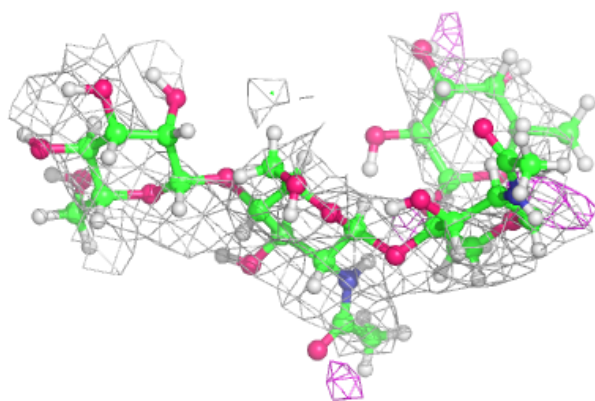
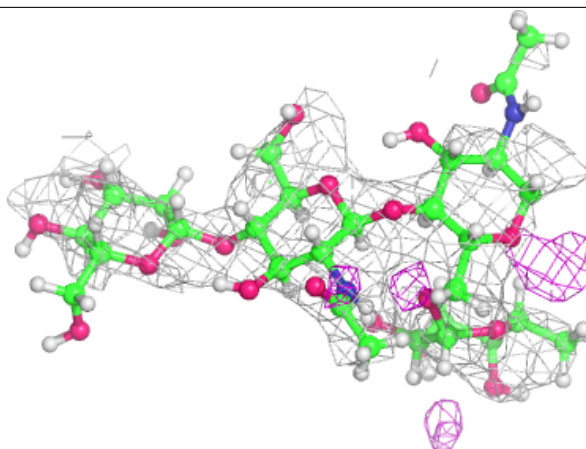
**Electron density around Chain F:**

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



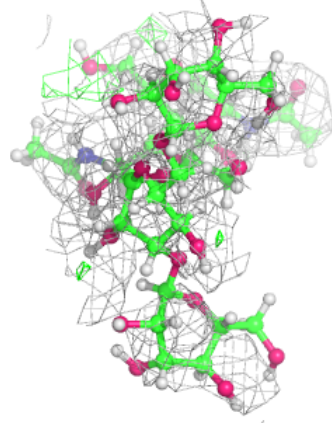
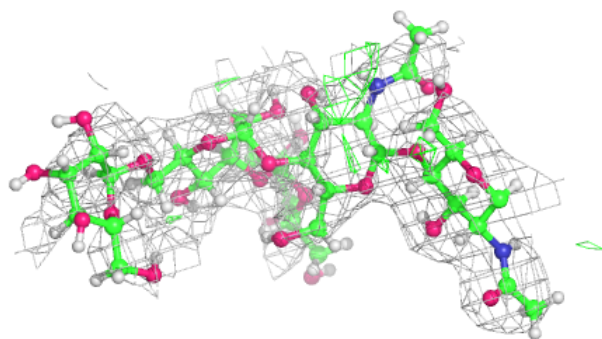
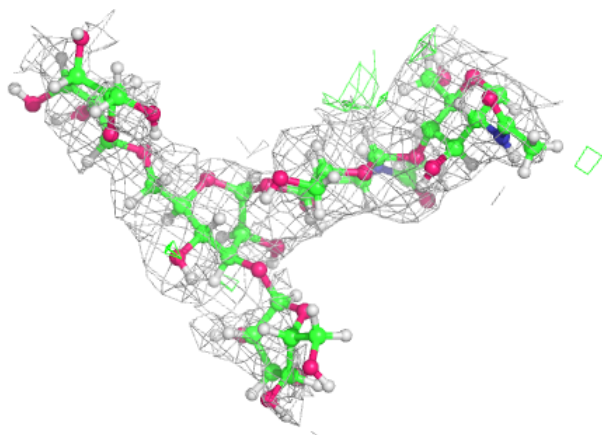
**Electron density around Chain G:**

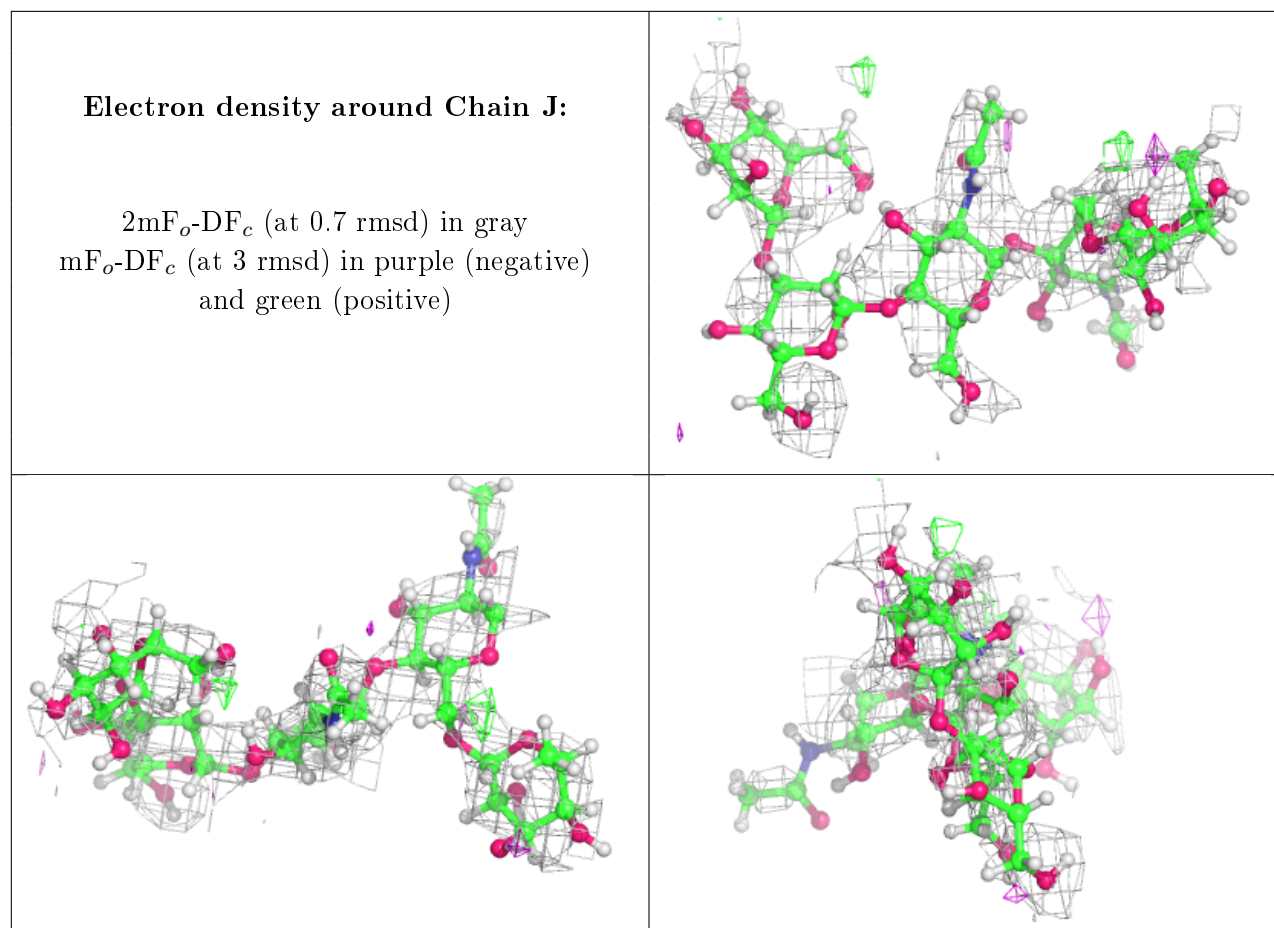
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain 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 ⓘ

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
9	SO4	A	731	5/5	0.59	0.54	94,108,128,155	0
9	SO4	A	730	5/5	0.72	0.61	73,77,116,138	0
10	NAG	B	704	14/15	0.78	0.39	67,103,130,135	0
9	SO4	A	728	5/5	0.78	0.25	94,96,106,133	0
9	SO4	B	726	5/5	0.78	0.66	79,85,104,136	0
9	SO4	B	724	5/5	0.81	0.37	72,81,82,122	0
9	SO4	A	727	5/5	0.83	0.56	122,122,134,147	0
9	SO4	A	729	5/5	0.84	0.36	77,83,116,117	0
9	SO4	B	727	5/5	0.85	0.35	78,99,140,145	0
9	SO4	A	724	5/5	0.89	0.22	60,61,104,125	0
9	SO4	B	721	5/5	0.90	0.19	55,61,78,85	0
9	SO4	B	725	5/5	0.90	0.33	73,80,100,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
9	SO4	B	723	5/5	0.92	0.26	73,77,85,112	0
9	SO4	B	722	5/5	0.92	0.42	63,69,102,118	0
9	SO4	A	726	5/5	0.93	0.27	52,78,95,110	0
9	SO4	A	722	5/5	0.94	0.19	56,67,82,84	0
9	SO4	A	725	5/5	0.94	0.30	77,78,91,105	0
9	SO4	A	723	5/5	0.94	0.14	34,44,66,73	0
8	ZN	A	703	1/1	0.96	0.08	47,47,47,47	0
8	ZN	A	702	1/1	0.98	0.16	30,30,30,30	0
8	ZN	B	702	1/1	0.98	0.19	31,31,31,31	0
8	ZN	A	701	1/1	0.99	0.15	29,29,29,29	0
8	ZN	B	703	1/1	0.99	0.04	54,54,54,54	0
8	ZN	B	701	1/1	0.99	0.15	24,24,24,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.