



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:56 PM UTC

PDB ID : 6I01 / pdb_00006i01
Title : Structure of human D-glucuronyl C5 epimerase in complex with substrate
Authors : Debarnot, C.; Monneau, Y.R.; Roig-Zamboni, V.; Le Narvor, C.; Goulet, A.;
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Deposited on : 2018-10-24
Resolution : 2.10 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

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>.

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

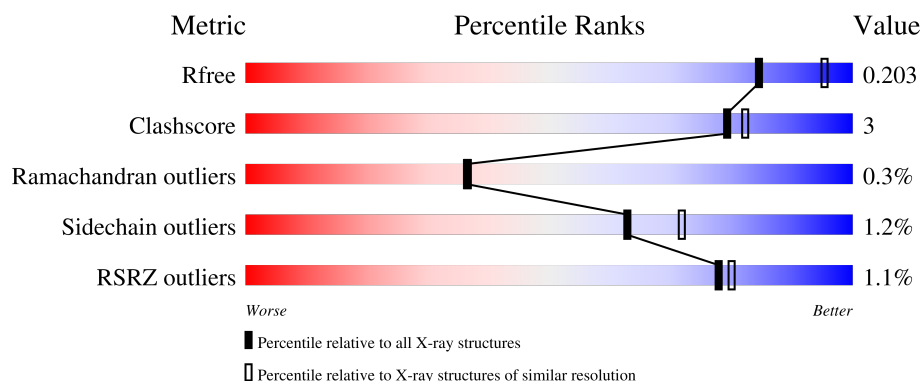
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



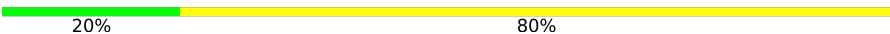
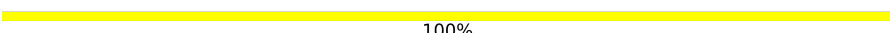
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 ≥ 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	527	% 90% 7% ••
1	B	527	2% 92% 6% •
2	C	7	14% 57% 29%
2	F	7	43% 57%
3	D	6	50% 50%

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Mol	Chain	Length	Quality of chain
4	E	5	 20% 80%
4	H	5	 20% 80%
5	G	5	 40% 40% 20%
6	I	2	 100%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 9546 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 D-glucuronyl C5-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	512	Total	C	N	O	S	0	12	0
			4192	2708	704	765	15			
1	B	516	Total	C	N	O	S	0	9	0
			4209	2717	703	773	16			

There are 16 discrepancies between the modelled and reference sequences:

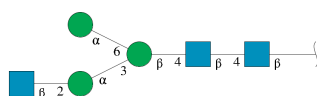
Chain	Residue	Modelled	Actual	Comment	Reference
A	91	ASP	-	expression tag	UNP O94923
A	92	TYR	-	expression tag	UNP O94923
A	93	LYS	-	expression tag	UNP O94923
A	94	ASP	-	expression tag	UNP O94923
A	95	ASP	-	expression tag	UNP O94923
A	96	ASP	-	expression tag	UNP O94923
A	97	ASP	-	expression tag	UNP O94923
A	578	PHE	TYR	engineered mutation	UNP O94923
B	91	ASP	-	expression tag	UNP O94923
B	92	TYR	-	expression tag	UNP O94923
B	93	LYS	-	expression tag	UNP O94923
B	94	ASP	-	expression tag	UNP O94923
B	95	ASP	-	expression tag	UNP O94923
B	96	ASP	-	expression tag	UNP O94923
B	97	ASP	-	expression tag	UNP O94923
B	578	PHE	TYR	engineered mutation	UNP O94923

- Molecule 2 is an oligosaccharide called beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid.



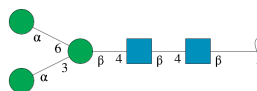
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	S	0	0	0
			94	42	3	46	3			
2	F	7	Total	C	N	O	S	0	0	0
			94	42	3	46	3			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-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
3	D	6	Total	C	N	O	0	0	0
			75	42	3	30			

- Molecule 4 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
4	E	5	Total	C	N	O	0	0	0
			61	34	2	25			
4	H	5	Total	C	N	O	0	0	0
			61	34	2	25			

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



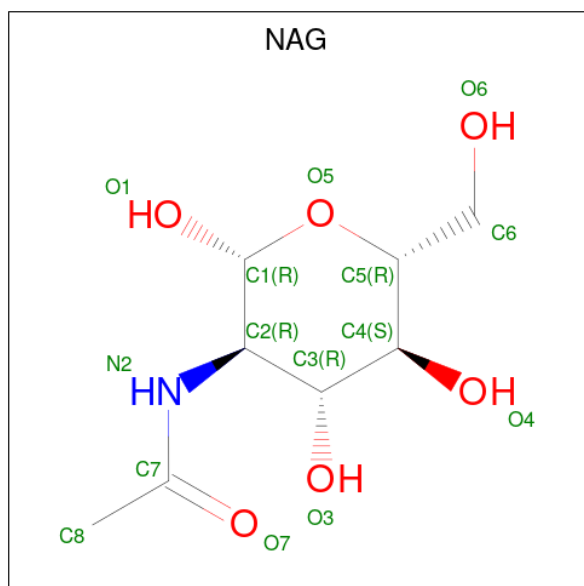
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	5	Total	C	N	O	0	0	0
			64	36	3	25			

- Molecule 6 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
6	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



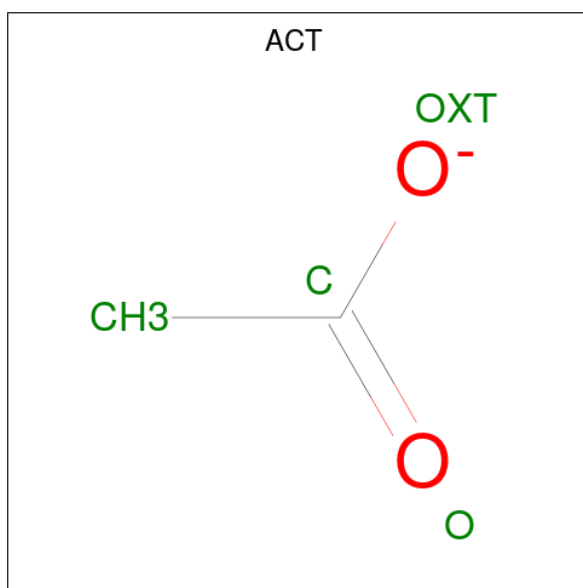
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 9 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	Ca	0	0
			1	1		
10	B	1	Total	Ca	0	0
			1	1		

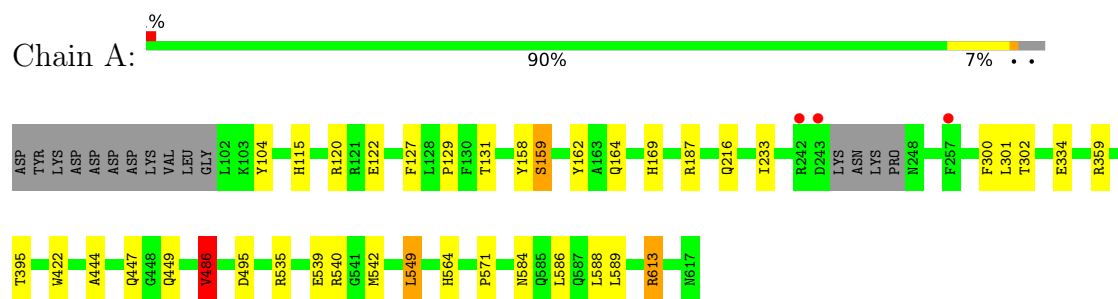
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	298	Total	O	0	0
			298	298		
11	B	266	Total	O	0	0
			266	266		

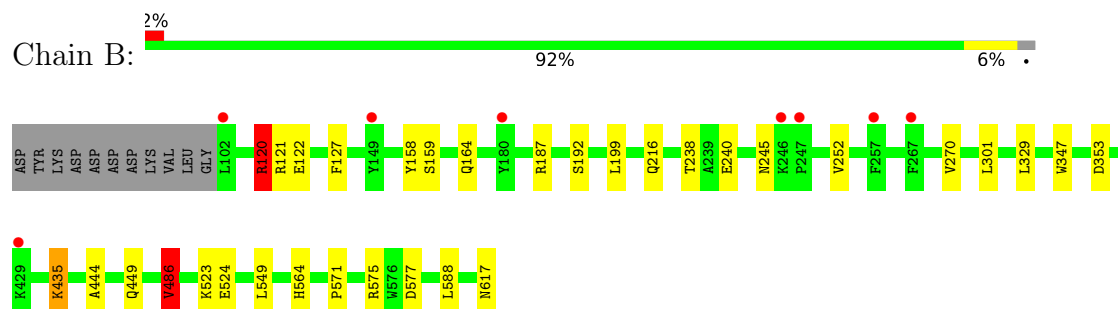
3 Residue-property plots [i](#)

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.

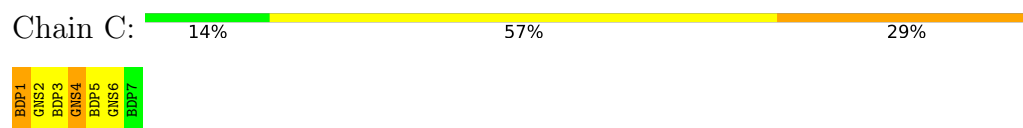
- Molecule 1: D-glucuronyl C5-epimerase



- Molecule 1: D-glucuronyl C5-epimerase



- Molecule 2: beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid



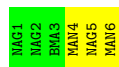
- Molecule 2: beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid-(1-4)-2-deoxy-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranuronic acid





- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-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 D: 50% 50%



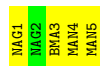
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 20% 80%



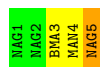
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 20% 80%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-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 G: 40% 40% 20%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	99.67Å 99.67Å 258.82Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.32 – 2.10 40.32 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.32-2.10) 99.9 (40.32-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.162 , 0.195 0.171 , 0.203	Depositor DCC
R_{free} test set	4259 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.059 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9546	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BDP, NAG, BMA, ACT, GNS, MAN, CA, GOL

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	0.69	0/4340	0.85	2/5872 (0.0%)
1	B	0.68	0/4345	0.85	2/5879 (0.0%)
All	All	0.68	0/8685	0.85	4/11751 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	2
All	All	0	6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	486	VAL	CB-CA-C	5.64	116.28	110.70
1	B	486	VAL	N-CA-CB	-5.59	104.11	112.67
1	B	486	VAL	CB-CA-C	5.44	116.09	110.70
1	A	486	VAL	N-CA-CB	-5.32	104.54	112.67

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	359[A]	ARG	Sidechain
1	A	359[B]	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	613[A]	ARG	Sidechain
1	A	613[B]	ARG	Sidechain
1	B	120	ARG	Sidechain

5.2 Too-close contacts

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	4192	0	4153	29	0
1	B	4209	0	4160	22	0
2	C	94	0	48	2	0
2	F	94	0	48	0	0
3	D	75	0	64	0	0
4	E	61	0	52	0	0
4	H	61	0	52	0	0
5	G	64	0	55	1	0
6	I	28	0	25	0	0
7	A	14	0	13	0	0
8	A	42	0	56	2	0
8	B	42	0	56	1	0
9	A	4	0	3	0	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
11	A	298	0	0	3	0
11	B	266	0	0	2	0
All	All	9546	0	8785	48	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 3.

The worst 5 of 48 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:ASP:OD2	1:A:540[B]:ARG:NH1	2.24	0.70
1:A:158:TYR:O	1:A:159:SER:CB	2.38	0.69
1:B:158:TYR:O	1:B:159:SER:CB	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:SER:HB2	1:B:199[B]:LEU:HD11	1.77	0.65
1:A:542:MET:HE1	1:A:589:LEU:HD22	1.79	0.65

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	520/527 (99%)	498 (96%)	20 (4%)	2 (0%)	30	28
1	B	523/527 (99%)	502 (96%)	20 (4%)	1 (0%)	43	44
All	All	1043/1054 (99%)	1000 (96%)	40 (4%)	3 (0%)	36	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	245	ASN
1	A	334	GLU
1	A	159	SER

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	455/459 (99%)	450 (99%)	5 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	456/459 (99%)	449 (98%)	7 (2%)	57	65
All	All	911/918 (99%)	899 (99%)	12 (1%)	63	69

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	240	GLU
1	B	301	LEU
1	B	549	LEU
1	B	435	LYS
1	A	486	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	202	GLN
1	B	468	ASN
1	B	587	GLN
1	B	510	ASN
1	A	447	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 ⓘ

37 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	BDP	C	1	2	13,13,13	0.88	0	18,19,19	1.21	2 (11%)
2	GNS	C	2	2	15,15,16	1.53	4 (26%)	17,22,24	1.50	3 (17%)
2	BDP	C	3	2	12,12,13	0.91	0	14,17,19	1.31	3 (21%)
2	GNS	C	4	2	15,15,16	4.74	2 (13%)	17,22,24	1.32	1 (5%)
2	BDP	C	5	2	12,12,13	0.71	0	14,17,19	1.36	2 (14%)
2	GNS	C	6	2	15,15,16	5.07	2 (13%)	17,22,24	1.77	2 (11%)
2	BDP	C	7	2	12,12,13	0.70	0	14,17,19	0.73	0
3	NAG	D	1	1,3	14,14,15	0.39	0	17,19,21	0.68	0
3	NAG	D	2	3	14,14,15	0.49	0	17,19,21	0.84	0
3	BMA	D	3	3	11,11,12	0.53	0	15,15,17	0.66	0
3	MAN	D	4	3	11,11,12	0.74	0	15,15,17	1.08	1 (6%)
3	NAG	D	5	3	14,14,15	0.38	0	17,19,21	1.23	2 (11%)
3	MAN	D	6	3	11,11,12	0.45	0	15,15,17	1.20	2 (13%)
4	NAG	E	1	1,4	14,14,15	0.25	0	17,19,21	1.12	1 (5%)
4	NAG	E	2	4	14,14,15	0.24	0	17,19,21	0.81	0
4	BMA	E	3	4	11,11,12	0.42	0	15,15,17	1.13	1 (6%)
4	MAN	E	4	4	11,11,12	0.30	0	15,15,17	1.15	1 (6%)
4	MAN	E	5	4	11,11,12	0.47	0	15,15,17	2.18	3 (20%)
2	BDP	F	1	2	13,13,13	0.81	0	18,19,19	1.18	1 (5%)
2	GNS	F	2	2	15,15,16	5.11	2 (13%)	17,22,24	1.56	2 (11%)
2	BDP	F	3	2	12,12,13	0.90	0	14,17,19	0.99	0
2	GNS	F	4	2	15,15,16	5.23	1 (6%)	17,22,24	1.44	2 (11%)
2	BDP	F	5	2	12,12,13	0.72	0	14,17,19	0.96	0
2	GNS	F	6	2	15,15,16	5.06	1 (6%)	17,22,24	1.44	1 (5%)
2	BDP	F	7	2	12,12,13	0.71	0	14,17,19	0.76	0
5	NAG	G	1	1,5	14,14,15	0.33	0	17,19,21	0.69	0
5	NAG	G	2	5	14,14,15	0.32	0	17,19,21	0.95	0
5	BMA	G	3	5	11,11,12	0.34	0	15,15,17	1.03	1 (6%)
5	MAN	G	4	5	11,11,12	0.47	0	15,15,17	1.57	1 (6%)
5	NAG	G	5	5	14,14,15	0.58	0	17,19,21	1.78	3 (17%)
4	NAG	H	1	1,4	14,14,15	0.32	0	17,19,21	1.26	1 (5%)
4	NAG	H	2	4	14,14,15	0.31	0	17,19,21	0.74	0
4	BMA	H	3	4	11,11,12	0.42	0	15,15,17	1.09	2 (13%)
4	MAN	H	4	4	11,11,12	0.27	0	15,15,17	1.10	2 (13%)
4	MAN	H	5	4	11,11,12	0.30	0	15,15,17	0.74	1 (6%)
6	NAG	I	1	1,6	14,14,15	0.33	0	17,19,21	0.75	1 (5%)
6	NAG	I	2	6	14,14,15	0.35	0	17,19,21	0.83	1 (5%)

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	BDP	C	1	2	-	0/4/24/24	0/1/1/1
2	GNS	C	2	2	-	2/7/24/27	0/1/1/1
2	BDP	C	3	2	-	0/4/21/24	0/1/1/1
2	GNS	C	4	2	-	3/7/24/27	0/1/1/1
2	BDP	C	5	2	-	0/4/21/24	0/1/1/1
2	GNS	C	6	2	-	3/7/24/27	0/1/1/1
2	BDP	C	7	2	-	0/4/21/24	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1
3	NAG	D	5	3	-	2/6/23/26	0/1/1/1
3	MAN	D	6	3	-	0/2/19/22	0/1/1/1
4	NAG	E	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	BMA	E	3	4	-	2/2/19/22	0/1/1/1
4	MAN	E	4	4	-	0/2/19/22	0/1/1/1
4	MAN	E	5	4	-	0/2/19/22	0/1/1/1
2	BDP	F	1	2	-	0/4/24/24	0/1/1/1
2	GNS	F	2	2	-	3/7/24/27	0/1/1/1
2	BDP	F	3	2	-	2/4/21/24	0/1/1/1
2	GNS	F	4	2	-	3/7/24/27	0/1/1/1
2	BDP	F	5	2	-	0/4/21/24	0/1/1/1
2	GNS	F	6	2	-	1/7/24/27	0/1/1/1
2	BDP	F	7	2	-	0/4/21/24	0/1/1/1
5	NAG	G	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	BMA	G	3	5	-	2/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
5	NAG	G	5	5	-	1/6/23/26	0/1/1/1
4	NAG	H	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	MAN	H	4	4	-	1/2/19/22	0/1/1/1
4	MAN	H	5	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	I	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	2/6/23/26	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	4	GNS	O3S-S1	19.99	1.64	1.42
2	F	2	GNS	O3S-S1	19.46	1.64	1.42
2	F	6	GNS	O2S-S1	19.43	1.64	1.42
2	C	6	GNS	O3S-S1	19.43	1.64	1.42
2	C	4	GNS	O2S-S1	18.04	1.62	1.42

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	5	MAN	C1-O5-C5	7.35	122.03	112.19
5	G	5	NAG	C1-O5-C5	6.27	120.58	112.19
5	G	4	MAN	C1-O5-C5	5.32	119.31	112.19
2	F	2	GNS	O2S-S1-O3S	-5.21	108.77	120.36
2	F	6	GNS	O2S-S1-O3S	-5.04	109.15	120.36

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

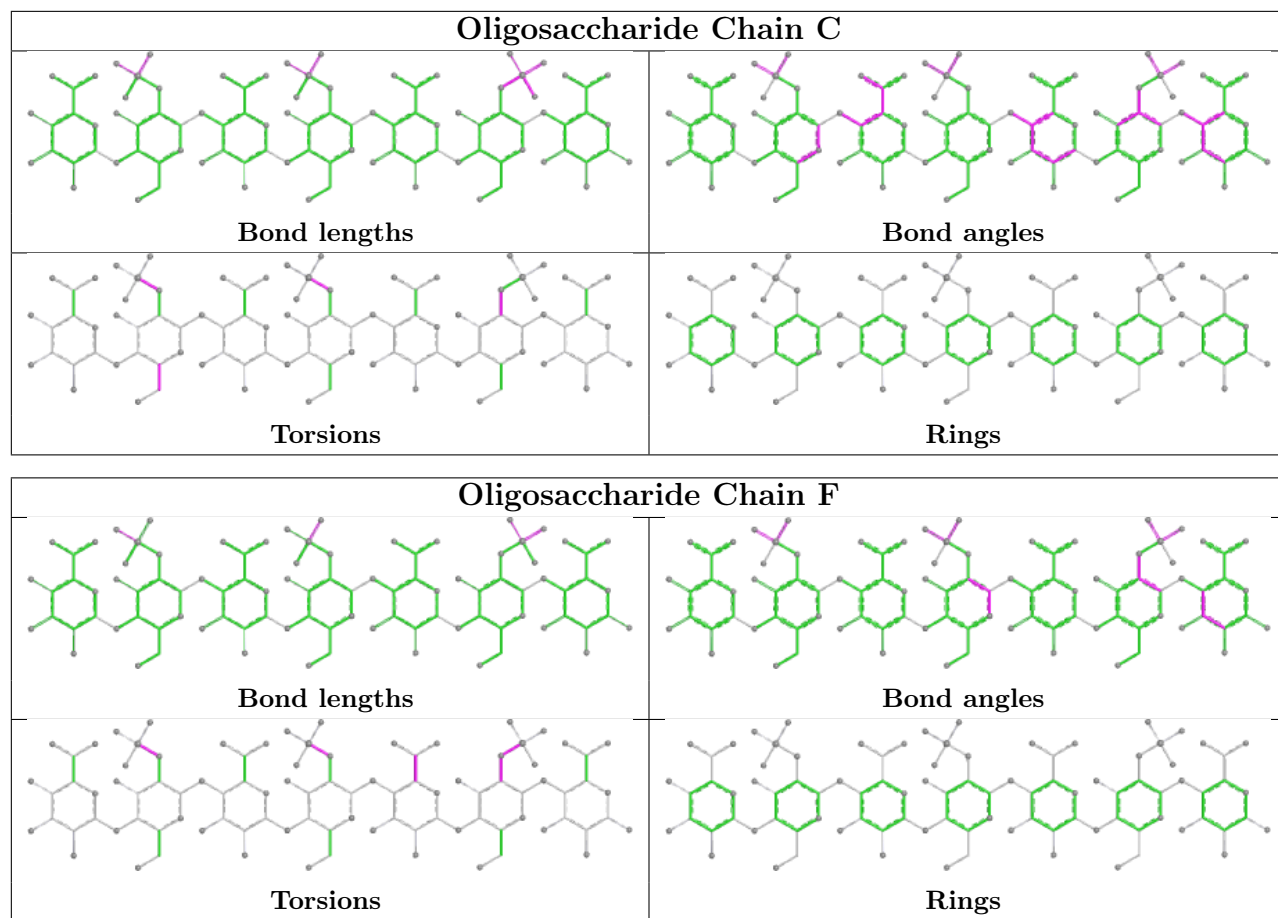
Mol	Chain	Res	Type	Atoms
2	C	4	GNS	C2-N2-S1-O1S
2	C	4	GNS	C2-N2-S1-O2S
2	F	4	GNS	C2-N2-S1-O1S
2	F	4	GNS	C2-N2-S1-O2S
2	F	4	GNS	C2-N2-S1-O3S

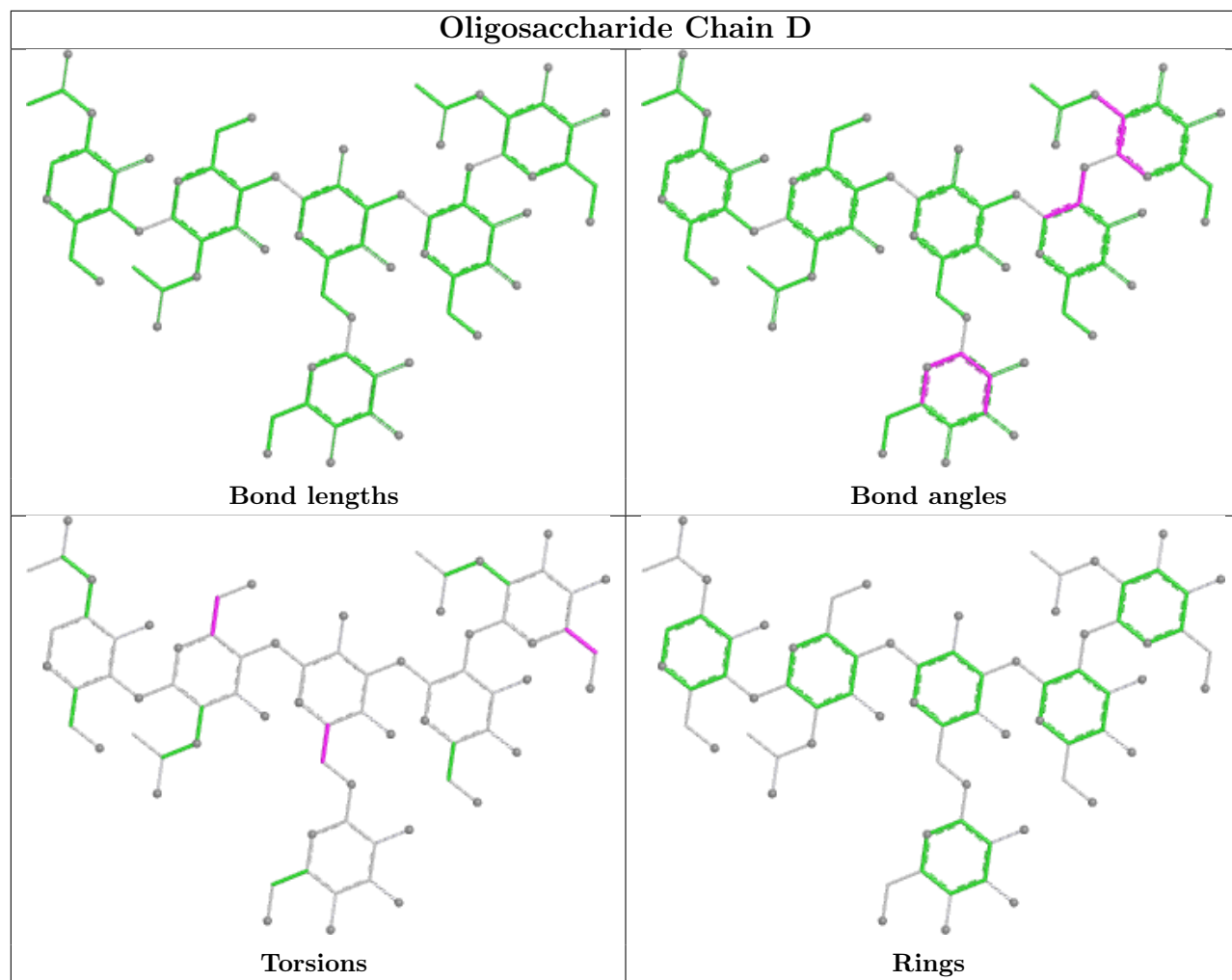
There are no ring outliers.

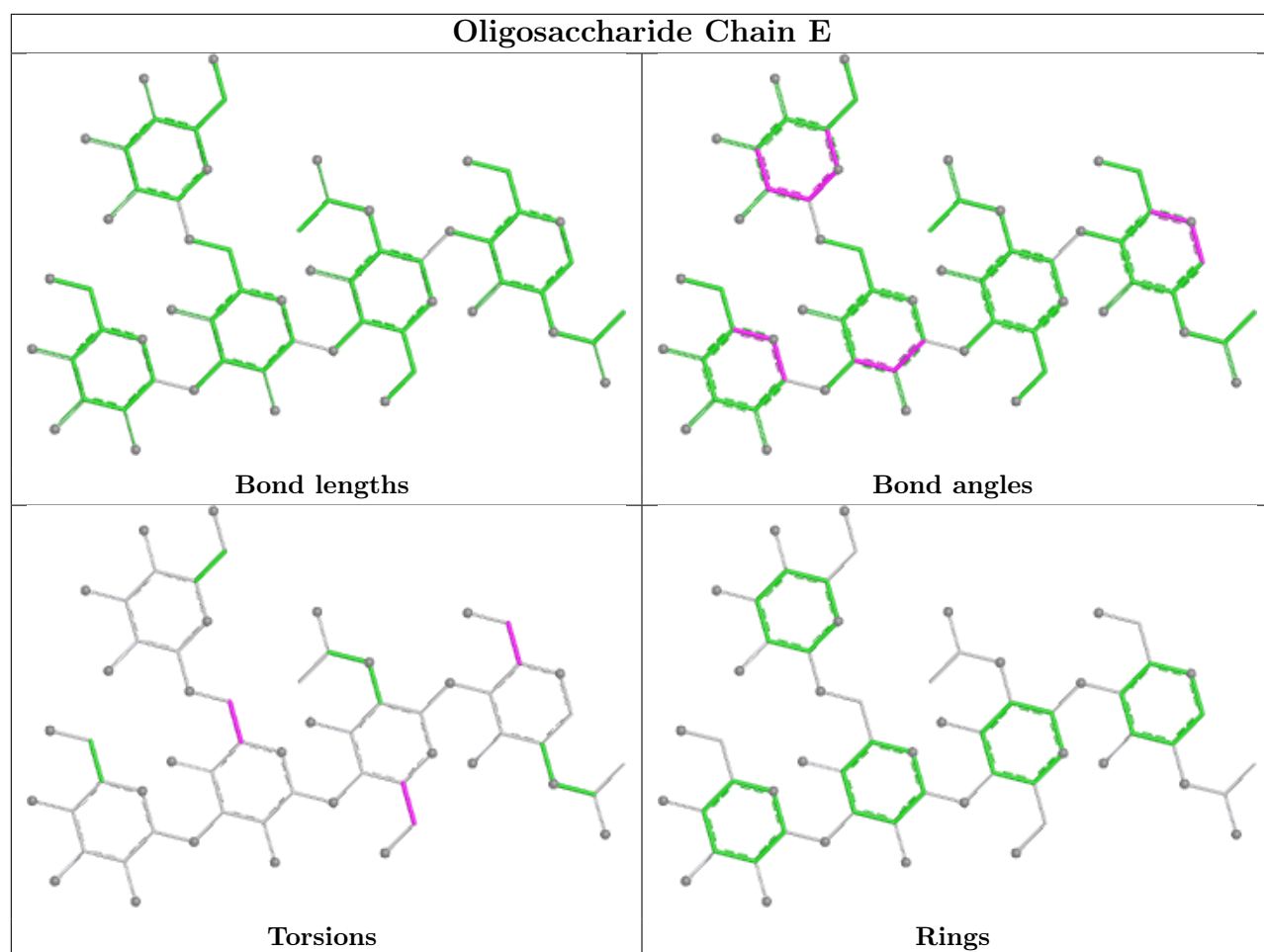
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	BDP	1	0
5	G	5	NAG	1	0
2	C	4	GNS	1	0

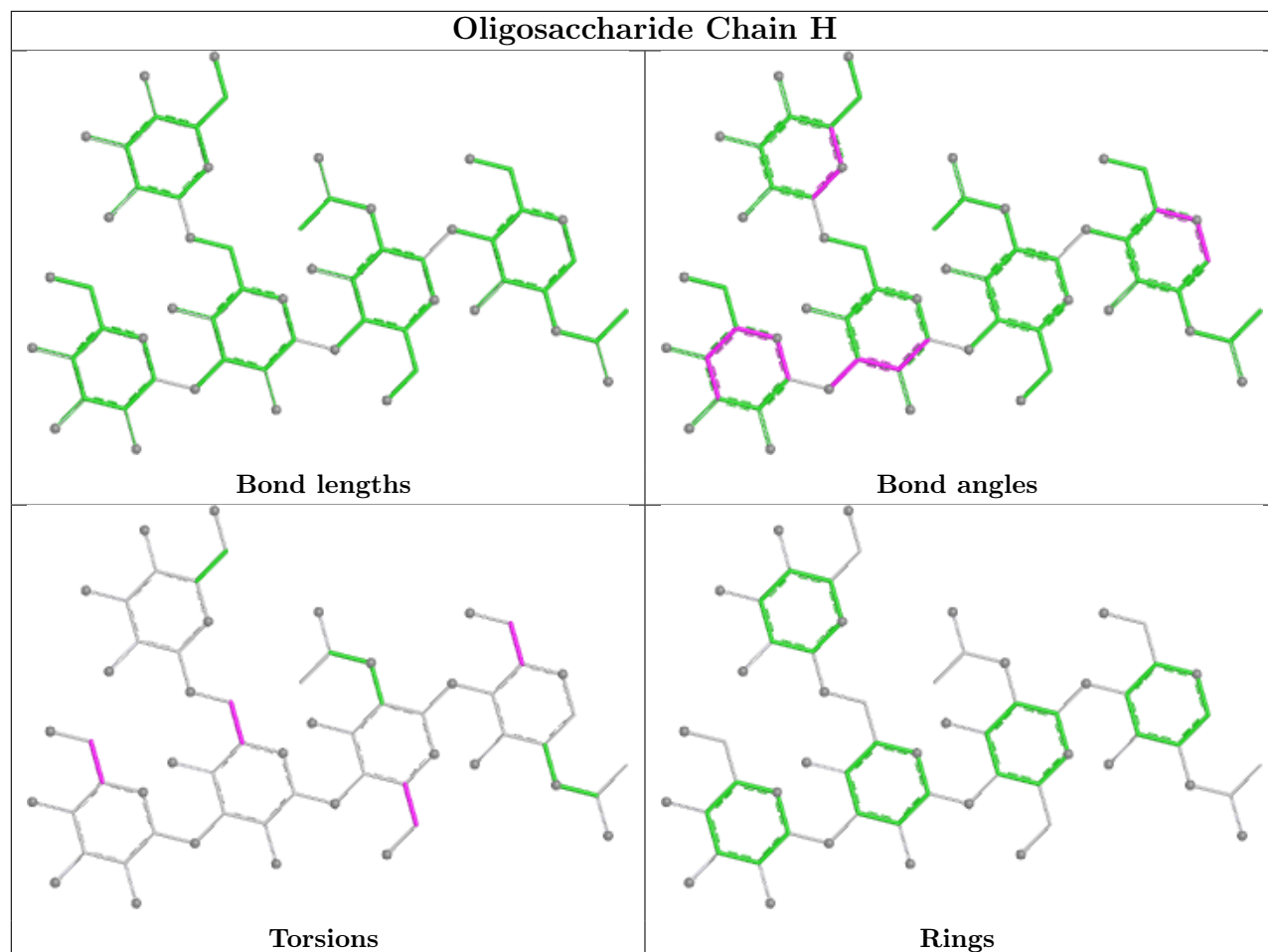
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



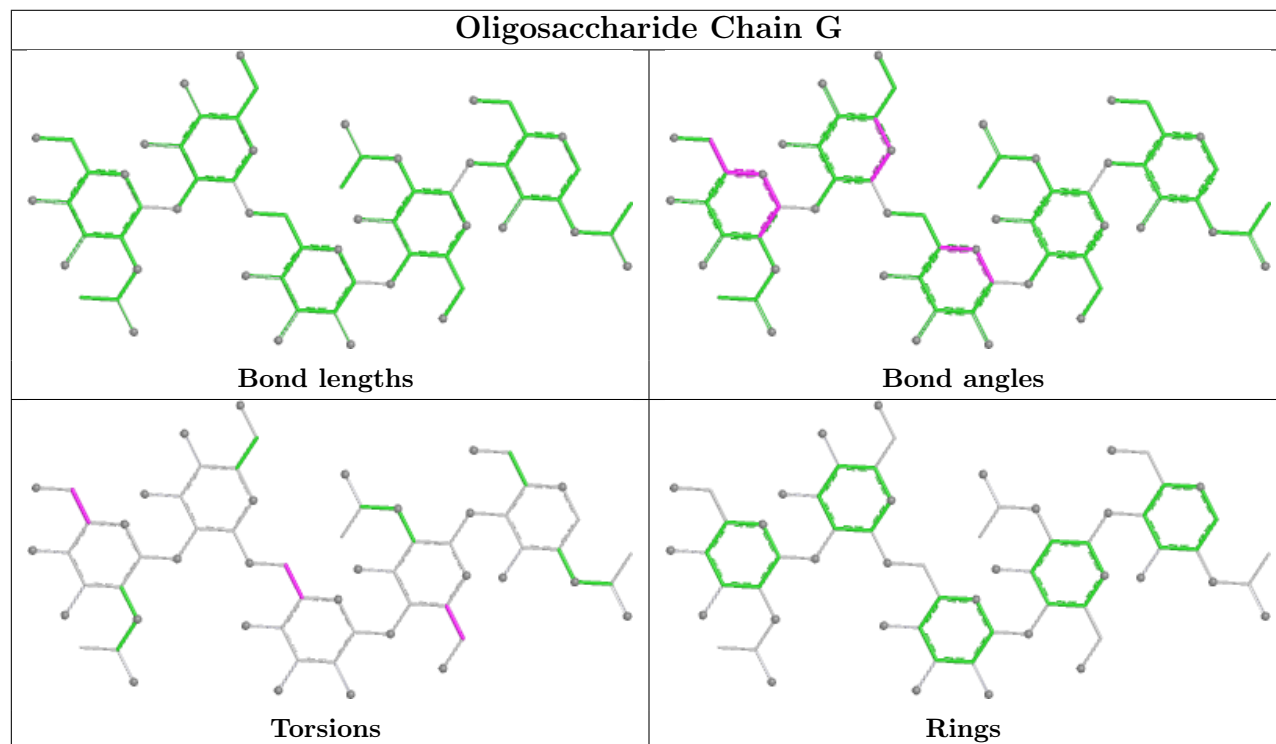


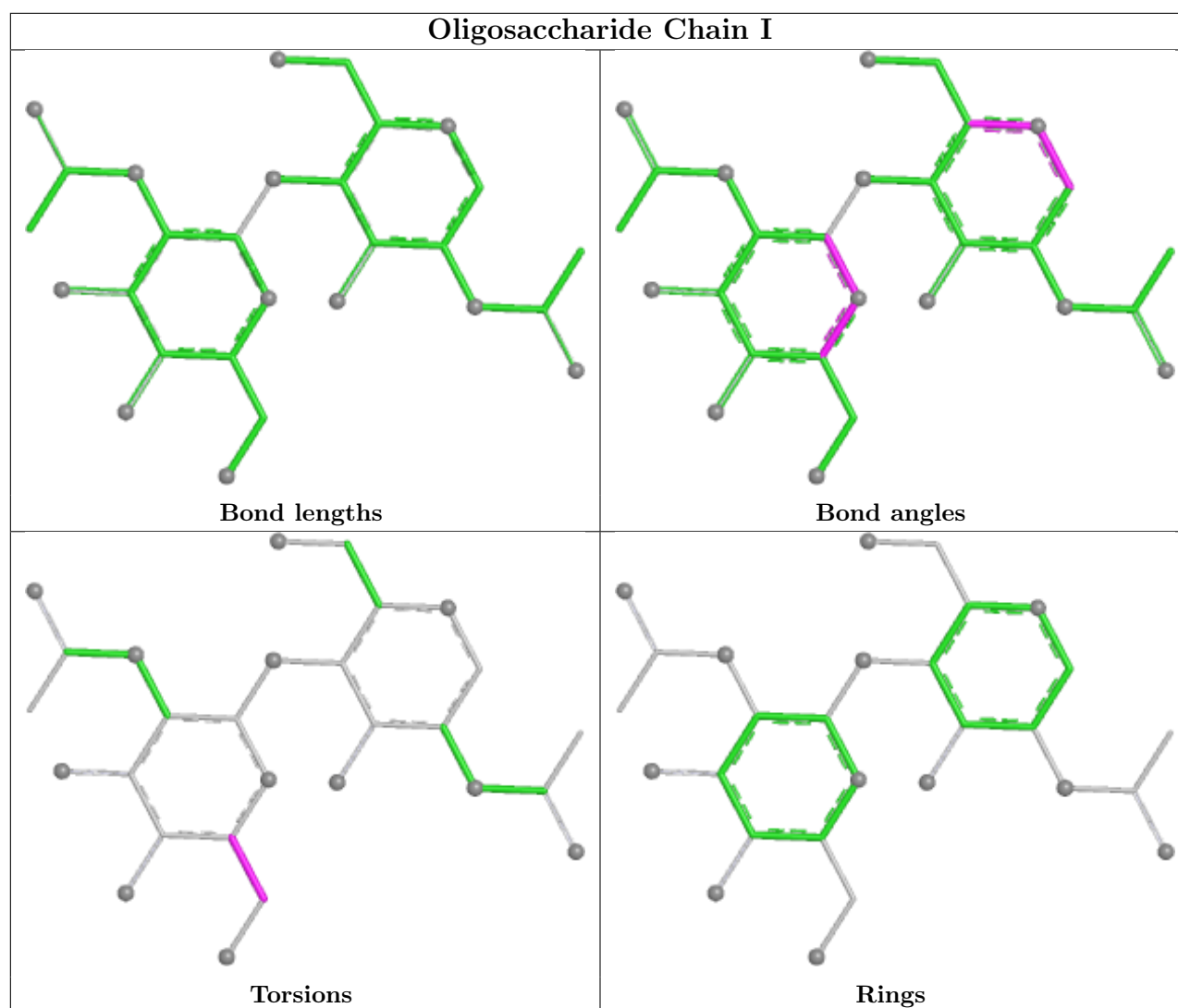


Oligosaccharide Chain H



Oligosaccharide Chain G





5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 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	$\# Z > 2$
8	GOL	B	726	-	5,5,5	0.11	0	5,5,5	0.57	0
8	GOL	B	720	-	5,5,5	0.52	0	5,5,5	1.16	0
8	GOL	A	721	-	5,5,5	0.26	0	5,5,5	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GOL	A	723	-	5,5,5	0.47	0	5,5,5	0.32	0
8	GOL	A	720	-	5,5,5	0.68	0	5,5,5	0.43	0
7	NAG	A	719	1	14,14,15	0.32	0	17,19,21	1.26	2 (11%)
8	GOL	B	722	-	5,5,5	0.55	0	5,5,5	0.74	0
8	GOL	B	725	-	5,5,5	0.49	0	5,5,5	0.33	0
8	GOL	A	724	-	5,5,5	0.43	0	5,5,5	0.12	0
8	GOL	B	721	-	5,5,5	0.14	0	5,5,5	0.93	0
8	GOL	B	723	-	5,5,5	0.44	0	5,5,5	0.42	0
8	GOL	A	726	-	5,5,5	0.24	0	5,5,5	0.20	0
8	GOL	A	722	-	5,5,5	0.41	0	5,5,5	0.45	0
8	GOL	B	724	-	5,5,5	0.43	0	5,5,5	0.29	0
8	GOL	A	725	-	5,5,5	0.43	0	5,5,5	0.48	0
9	ACT	A	727	-	3,3,3	0.81	0	3,3,3	0.77	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
8	GOL	B	726	-	-	3/4/4/4	-
8	GOL	B	720	-	-	0/4/4/4	-
8	GOL	A	721	-	-	4/4/4/4	-
8	GOL	A	723	-	-	0/4/4/4	-
8	GOL	A	720	-	-	4/4/4/4	-
7	NAG	A	719	1	-	1/6/23/26	0/1/1/1
8	GOL	B	722	-	-	1/4/4/4	-
8	GOL	B	725	-	-	4/4/4/4	-
8	GOL	A	724	-	-	2/4/4/4	-
8	GOL	B	721	-	-	0/4/4/4	-
8	GOL	B	723	-	-	0/4/4/4	-
8	GOL	A	726	-	-	0/4/4/4	-
8	GOL	A	722	-	-	2/4/4/4	-
8	GOL	B	724	-	-	4/4/4/4	-
8	GOL	A	725	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	719	NAG	O5-C1-C2	-2.44	107.51	111.29
7	A	719	NAG	C1-O5-C5	2.30	115.27	112.19

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	720	GOL	O1-C1-C2-O2
8	A	720	GOL	O1-C1-C2-C3
8	A	720	GOL	C1-C2-C3-O3
8	A	724	GOL	C1-C2-C3-O3
8	A	724	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	722	GOL	1	0
8	A	725	GOL	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, 95th 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 ²)	Q<0.9
1	A	512/527 (97%)	-0.24	3 (0%) 85 87	22, 42, 73, 109	12 (2%)
1	B	516/527 (97%)	-0.09	8 (1%) 70 73	24, 45, 89, 145	9 (1%)
All	All	1028/1054 (97%)	-0.17	11 (1%) 78 80	22, 43, 83, 145	21 (2%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	ASP	5.1
1	B	247	PRO	4.9
1	B	246	LYS	3.8
1	B	102	LEU	3.4
1	B	257	PHE	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, 95th 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 ²)	Q<0.9
4	MAN	E	5	11/12	0.39	0.12	117,119,121,123	0
4	MAN	H	5	11/12	0.44	0.12	120,129,131,131	0
4	MAN	H	4	11/12	0.45	0.11	115,123,127,127	0
6	NAG	I	2	14/15	0.45	0.15	109,112,116,116	0
4	MAN	E	4	11/12	0.47	0.12	109,114,117,119	0

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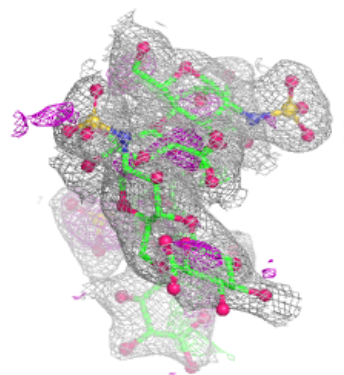
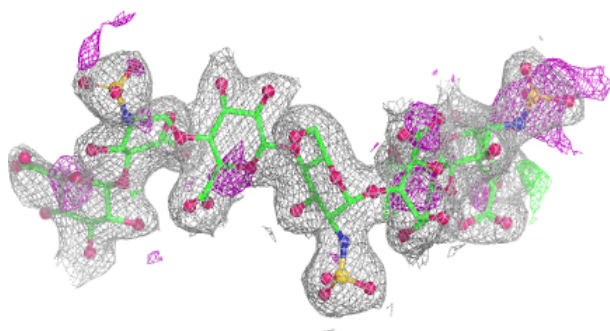
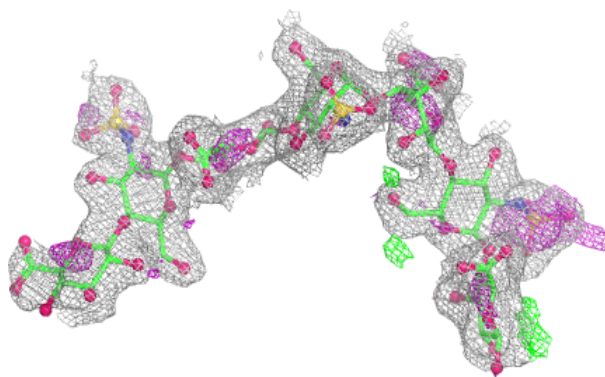
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	BMA	G	3	11/12	0.54	0.12	99,103,107,109	0
2	BDP	F	7	12/13	0.58	0.12	106,113,116,117	0
3	NAG	D	5	14/15	0.60	0.15	106,114,120,124	0
3	MAN	D	6	11/12	0.60	0.13	110,115,117,122	0
2	BDP	F	1	13/13	0.61	0.13	74,86,95,96	0
5	NAG	G	5	14/15	0.63	0.15	104,109,112,116	0
4	BMA	E	3	11/12	0.66	0.12	99,106,111,112	0
3	BMA	D	3	11/12	0.71	0.12	80,89,99,109	0
2	BDP	C	7	12/13	0.72	0.10	78,92,98,99	0
4	BMA	H	3	11/12	0.73	0.11	112,119,123,128	0
2	GNS	F	6	15/16	0.79	0.12	87,95,98,106	0
5	NAG	G	2	14/15	0.80	0.12	69,73,82,91	0
2	BDP	C	1	13/13	0.82	0.10	55,64,73,78	0
2	BDP	F	5	12/13	0.84	0.10	66,72,74,83	0
3	NAG	D	2	14/15	0.86	0.11	59,66,74,79	0
6	NAG	I	1	14/15	0.86	0.09	73,84,90,101	0
2	BDP	F	3	12/13	0.86	0.13	57,65,71,71	0
4	NAG	E	2	14/15	0.87	0.11	68,73,81,91	0
2	GNS	C	6	15/16	0.89	0.09	68,73,84,85	0
2	GNS	F	2	15/16	0.89	0.12	59,73,80,81	0
4	NAG	H	2	14/15	0.91	0.09	76,82,90,100	0
2	BDP	C	3	12/13	0.92	0.10	46,50,51,53	0
4	NAG	H	1	14/15	0.92	0.10	58,65,70,72	0
5	MAN	G	4	11/12	0.92	0.10	84,89,97,102	0
4	NAG	E	1	14/15	0.93	0.10	47,52,63,64	0
3	MAN	D	4	11/12	0.93	0.10	72,76,83,92	0
2	GNS	F	4	15/16	0.94	0.10	51,60,62,65	0
5	NAG	G	1	14/15	0.94	0.07	42,50,57,64	0
2	BDP	C	5	12/13	0.94	0.07	47,49,53,60	0
2	GNS	C	2	15/16	0.94	0.09	47,52,54,55	0
3	NAG	D	1	14/15	0.95	0.07	38,44,50,55	0
2	GNS	C	4	15/16	0.97	0.07	39,42,46,47	0

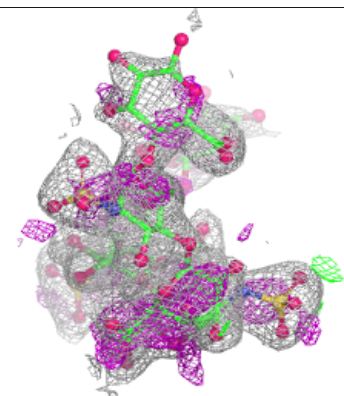
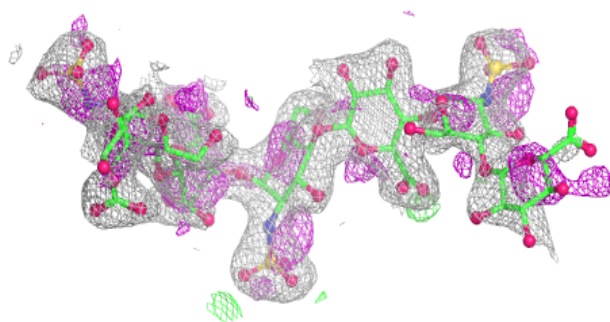
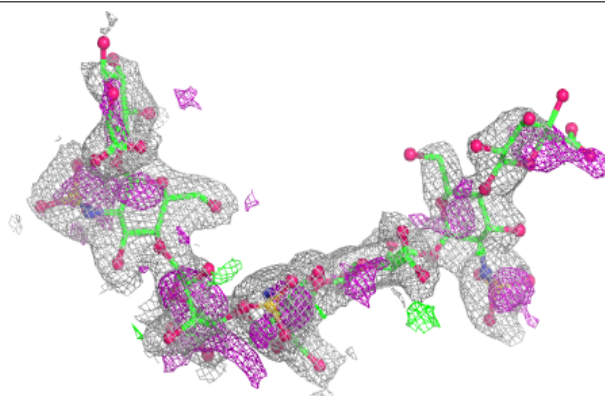
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

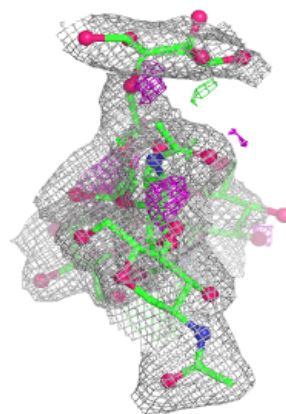
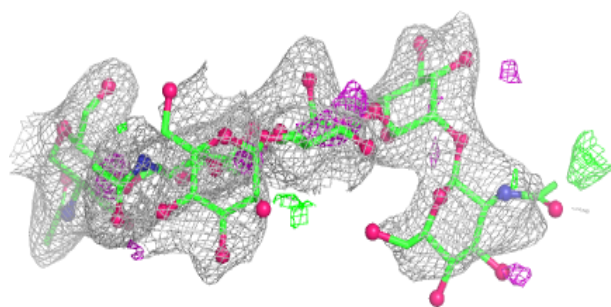
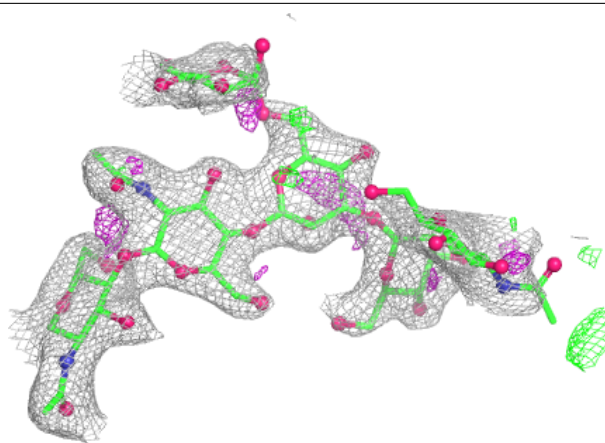
**Electron density around Chain F:**

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



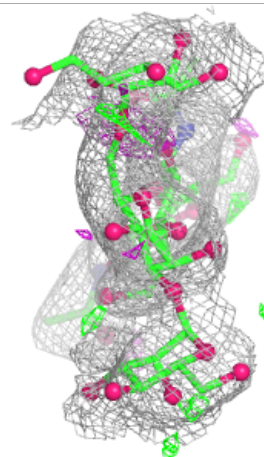
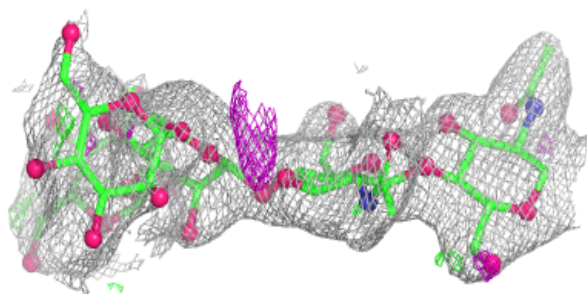
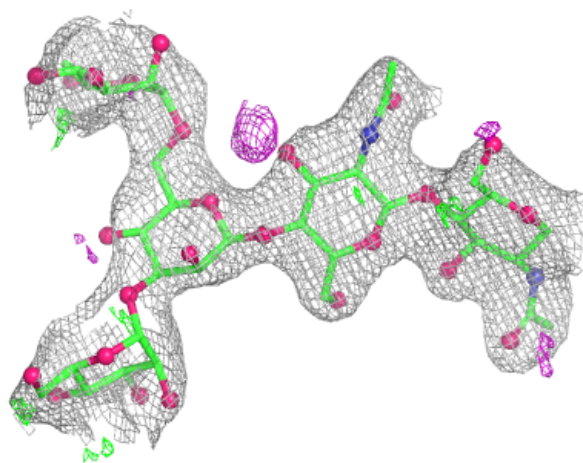
Electron density around Chain D:

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



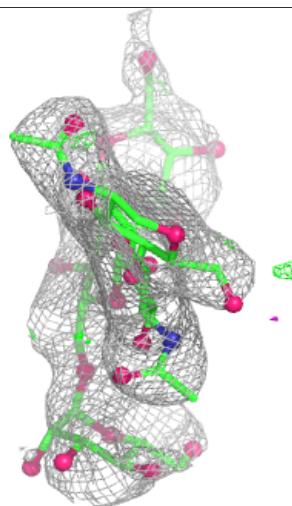
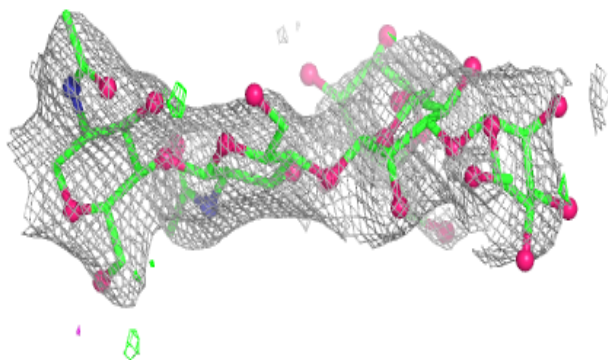
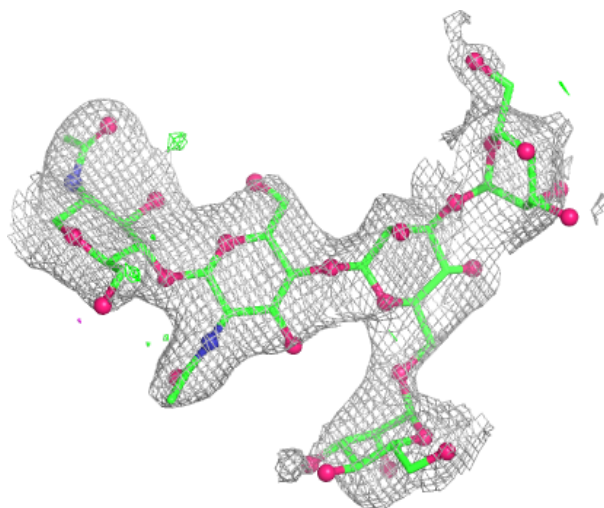
Electron density around Chain E:

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



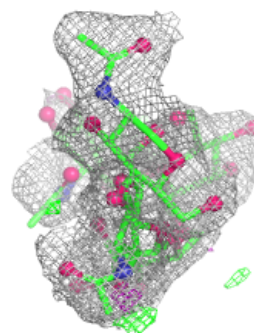
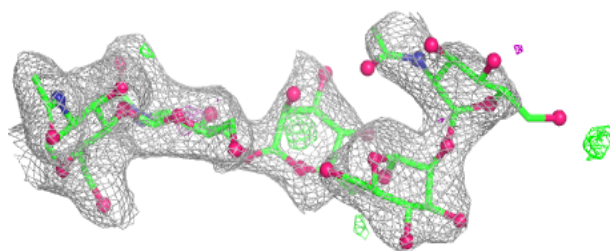
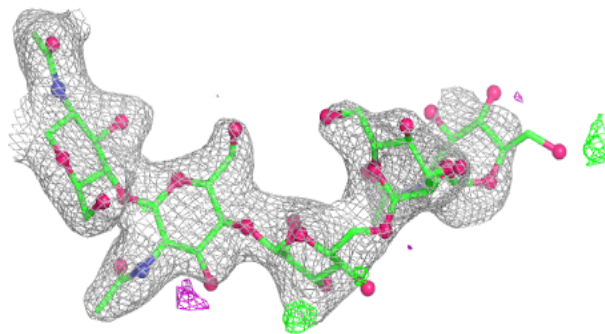
Electron density around Chain H:

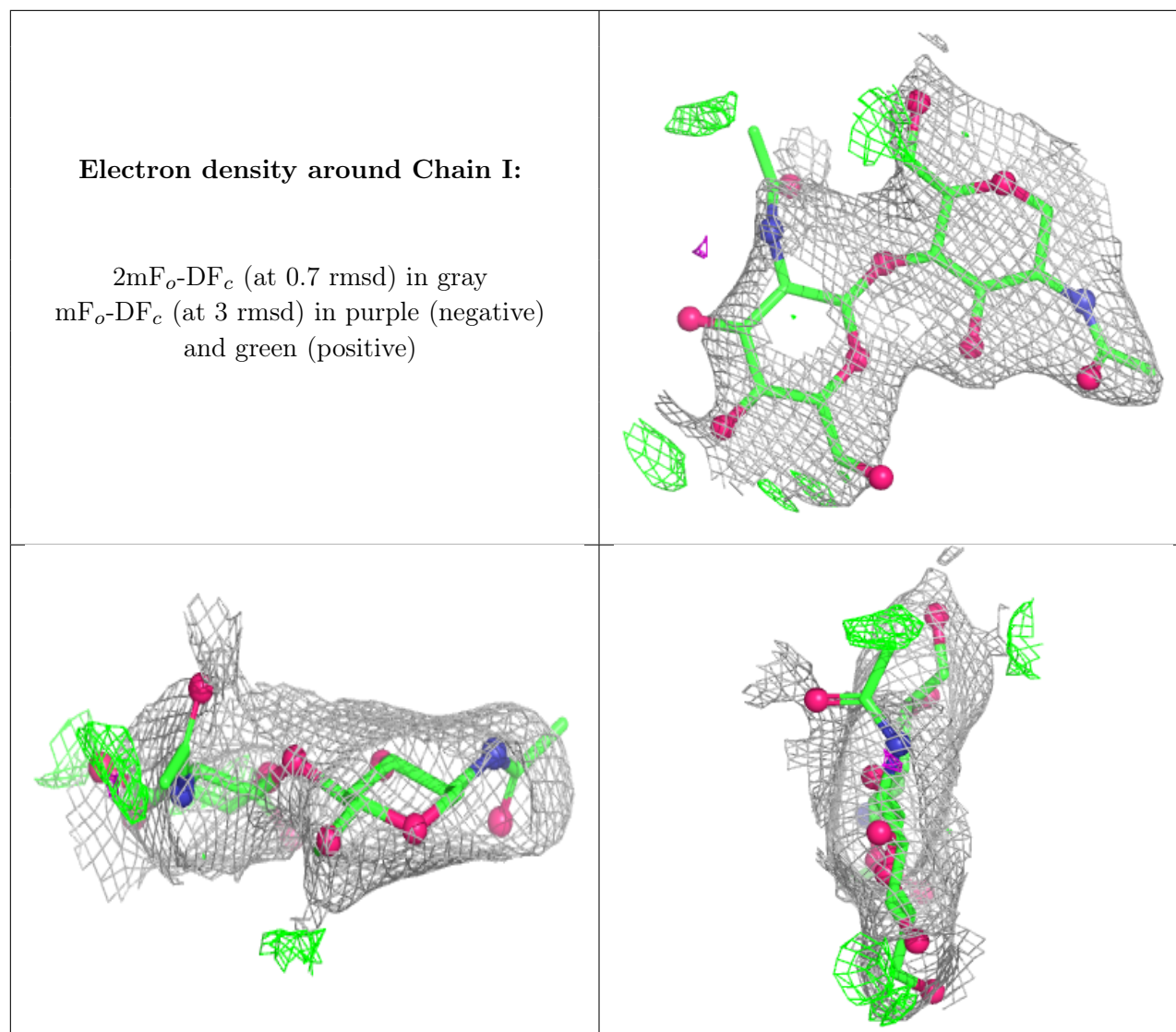
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

$2mF_o-DF_c$ (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, 95th 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 ²)	Q<0.9
7	NAG	A	719	14/15	0.66	0.12	85,93,101,104	0
9	ACT	A	727	4/4	0.75	0.21	62,64,67,69	0
8	GOL	B	726	6/6	0.77	0.22	73,74,79,83	0
8	GOL	B	722	6/6	0.79	0.21	61,64,66,67	0
8	GOL	B	724	6/6	0.79	0.17	63,68,73,73	0
8	GOL	B	725	6/6	0.83	0.17	67,74,76,78	0
8	GOL	A	723	6/6	0.84	0.13	52,63,67,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	GOL	B	720	6/6	0.85	0.16	41,52,58,65	0
8	GOL	A	725	6/6	0.85	0.17	46,52,60,69	0
8	GOL	B	721	6/6	0.86	0.15	51,57,60,65	0
8	GOL	A	726	6/6	0.87	0.14	71,79,82,83	0
8	GOL	A	724	6/6	0.89	0.13	73,77,78,79	0
8	GOL	A	720	6/6	0.90	0.13	39,47,56,62	0
8	GOL	A	721	6/6	0.94	0.11	48,53,59,70	0
8	GOL	A	722	6/6	0.95	0.10	44,49,54,55	0
8	GOL	B	723	6/6	0.95	0.08	51,53,54,55	0
10	CA	B	727	1/1	0.98	0.04	71,71,71,71	0
10	CA	A	728	1/1	0.99	0.04	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.