



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:10 PM UTC

PDB ID : 3UGH / pdb_00003ugh
Title : Crystal structure of a 6-SST/6-SFT from *Pachysandra terminalis* in complex with 6-kestose
Authors : Lammens, W.; Rabijns, A.; Van Laere, A.; Strelkov, S.V.; Van den Ende, W.
Deposited on : 2011-11-02
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

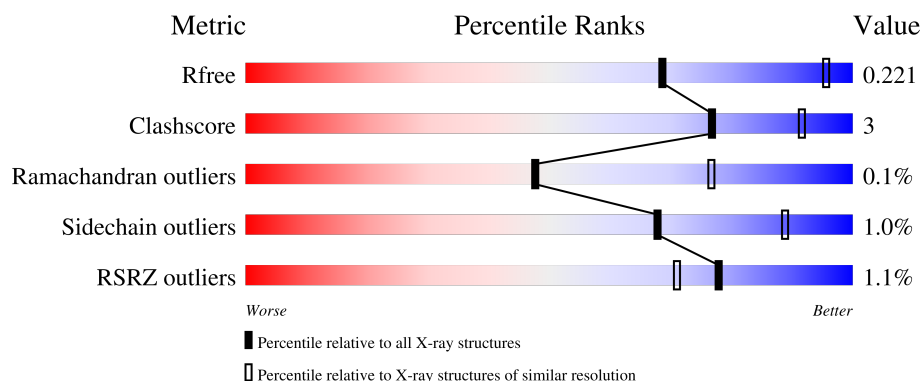
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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.



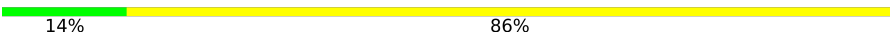
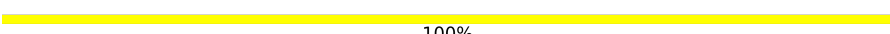
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 ≥ 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	546	% 87% 9% .
1	B	546	% 89% 7% .
2	C	3	67% 33%
2	G	3	67% 33%
3	D	3	33% 67%

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Mol	Chain	Length	Quality of chain
3	F	3	 67% 33%
4	E	7	 14% 86%
5	H	5	 40% 40% 20%
5	I	5	 20% 80%
6	J	3	 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
9	GOL	B	564	-	-	X	-

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 8752 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.

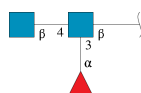
- Molecule 1 is a protein called Sucrose:(Sucrose/fructan) 6-fructosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			4164	2687	679	784	14			
1	B	524	Total	C	N	O	S	0	0	0
			4164	2687	679	784	14			

There are 4 discrepancies between the modelled and reference sequences:

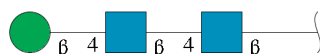
Chain	Residue	Modelled	Actual	Comment	Reference
A	133	VAL	ALA	SEE REMARK 999	UNP E3PQS3
A	361	GLY	ARG	SEE REMARK 999	UNP E3PQS3
B	133	VAL	ALA	SEE REMARK 999	UNP E3PQS3
B	361	GLY	ARG	SEE REMARK 999	UNP E3PQS3

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			38	22	2	14			
2	G	3	Total	C	N	O	0	0	0
			38	22	2	14			

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



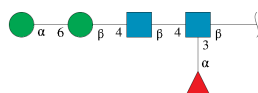
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	7	Total	C	N	O	0	0	0
			80	45	2	33			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	5	Total	C	N	O	0	0	0
			60	34	2	24			
5	I	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 6 is an oligosaccharide called beta-D-fructofuranose-(2-6)-beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



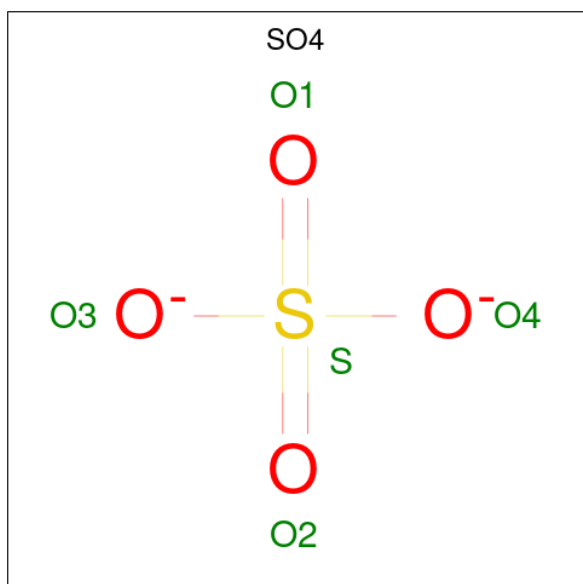
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
6	J	3	Total	C	O	0	0	0
			34	18	16			

- 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 SULFATE ION (CCD ID: SO4) (formula: O_4S).



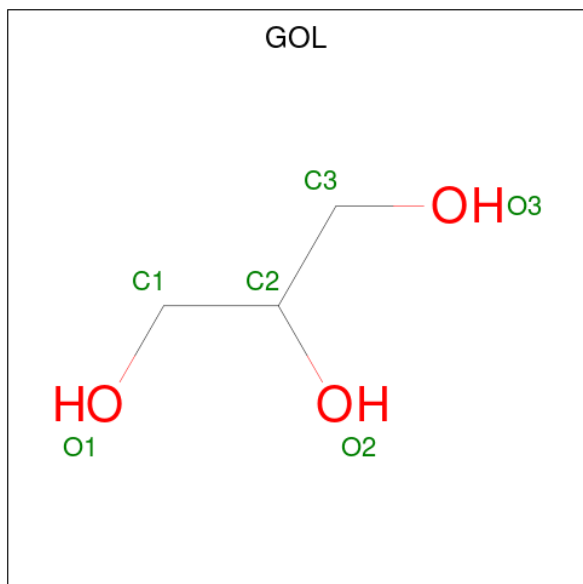
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 9 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).

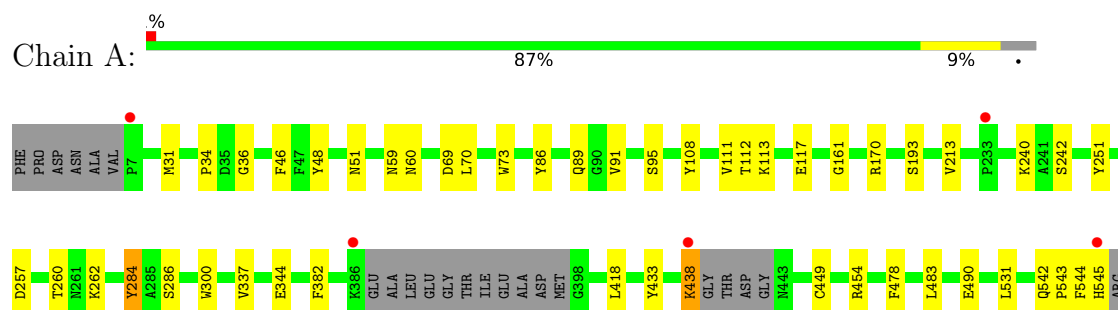


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			6	3	3		
9	B	1	Total	C	O	0	0
			6	3	3		

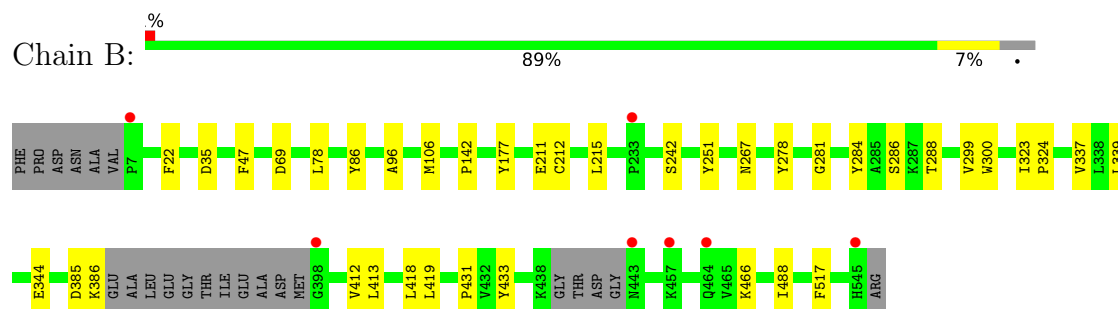
3 Residue-property plots

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.

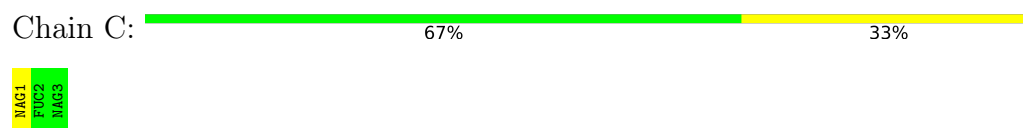
- Molecule 1: Sucrose:(Sucrose/fructan) 6-fructosyltransferase



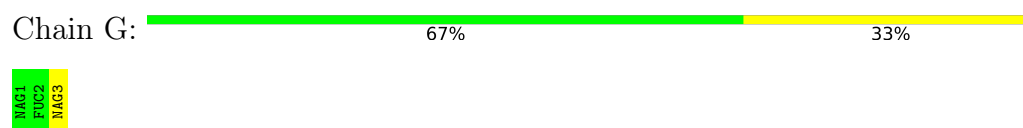
- Molecule 1: Sucrose:(Sucrose/fructan) 6-fructosyltransferase



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



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



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

Chain D:  33% 67%

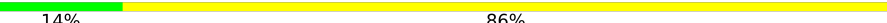
MAG1
MAG2
BMA3

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

Chain F:  67% 33%

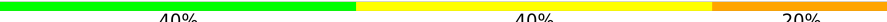
MAG1
MAG2
BMA3

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

Chain E:  14% 86%

MAG1
MAG2
BMA3
XYSA
MAN5
MAN6
FUC7

- Molecule 5: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  40% 40% 20%

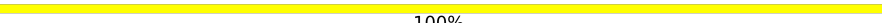
MAG1
MAG2
BMA3
MAN4
FUC5

- Molecule 5: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  20% 80%

MAG1
MAG2
BMA3
MAN4
FUC5

- Molecule 6: beta-D-fructofuranose-(2-6)-beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain J:  100%

GLC1
FRU2
FRU3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.29Å 123.89Å 146.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.71 – 2.90 29.71 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.71-2.90) 95.4 (29.71-2.90)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.197 , 0.240 (Not available) , 0.221	Depositor DCC
R_{free} test set	1836 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 16.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8752	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, GOL, FUC, MAN, FRU, SO4, GLC, NAG, XYS

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	0.45	0/4287	0.73	3/5841 (0.1%)
1	B	0.44	0/4287	0.73	4/5841 (0.1%)
All	All	0.45	0/8574	0.73	7/11682 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	ASN	N-CA-C	5.78	118.96	110.30
1	B	433	TYR	N-CA-C	5.71	117.86	109.24
1	B	267	ASN	CA-C-N	5.26	125.07	119.28
1	B	267	ASN	C-N-CA	5.26	125.07	119.28
1	B	488	ILE	N-CA-C	5.20	115.76	108.17
1	A	433	TYR	N-CA-C	5.20	116.97	109.07
1	A	284	TYR	N-CA-C	5.06	117.08	109.23

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	4164	0	4021	28	0
1	B	4164	0	4021	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	38	0	34	0	0
2	G	38	0	34	0	0
3	D	39	0	34	2	0
3	F	39	0	34	0	0
4	E	80	0	68	0	0
5	H	60	0	52	1	0
5	I	60	0	52	0	0
6	J	34	0	31	0	0
7	A	14	0	13	0	0
8	A	5	0	0	0	0
8	B	5	0	0	0	0
9	A	6	0	8	3	0
9	B	6	0	8	4	0
All	All	8752	0	8410	50	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.

All (50) 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:257:ASP:HB3	1:A:260:THR:HG22	1.58	0.85
1:A:454:ARG:HH12	3:D:1:NAG:H82	1.44	0.81
3:D:2:NAG:H4	3:D:3:BMA:O2	1.84	0.77
1:B:385:ASP:O	1:B:386:LYS:HB2	1.85	0.75
1:A:89:GLN:HG3	1:A:113:LYS:HA	1.74	0.69
1:A:257:ASP:HB3	1:A:260:THR:CG2	2.26	0.65
1:A:73:TRP:CD1	9:A:562:GOL:H32	2.32	0.64
1:B:323:ILE:HA	9:B:564:GOL:H32	1.82	0.60
1:B:323:ILE:HD13	9:B:564:GOL:H31	1.83	0.60
1:A:418:LEU:HD21	1:A:531:LEU:HD21	1.82	0.59
1:A:73:TRP:HD1	9:A:562:GOL:H32	1.69	0.57
1:A:89:GLN:CG	1:A:113:LYS:HA	2.35	0.57
1:B:22:PHE:O	9:B:564:GOL:H11	2.06	0.55
1:A:382:PHE:HB2	1:A:478:PHE:HB2	1.90	0.54
1:A:91:VAL:HG13	1:A:108:TYR:CD2	2.43	0.53
1:A:251:TYR:CZ	1:A:337:VAL:HG22	2.44	0.53
1:A:438:LYS:HD3	1:A:438:LYS:H	1.74	0.52
1:B:419:LEU:HB2	1:B:517:PHE:HB2	1.96	0.48
1:B:324:PRO:HD3	9:B:564:GOL:H32	1.97	0.47
1:B:86:TYR:HB2	1:B:142:PRO:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:MET:HG3	1:A:48:TYR:CD2	2.50	0.46
1:A:161:GLY:HA2	1:A:170:ARG:O	2.15	0.46
1:B:69:ASP:HB2	1:B:344:GLU:HG2	1.97	0.46
1:A:111:VAL:HG22	1:A:117:GLU:HG2	1.98	0.45
1:A:286:SER:HA	1:A:300:TRP:O	2.17	0.45
1:B:211:GLU:O	1:B:212:CYS:C	2.60	0.44
1:A:70:LEU:O	9:A:562:GOL:O2	2.36	0.44
1:A:483:LEU:HB2	1:A:490:GLU:HB2	2.00	0.43
1:B:251:TYR:CZ	1:B:337:VAL:HG22	2.53	0.43
1:A:69:ASP:HB2	1:A:344:GLU:HG2	2.01	0.43
1:A:34:PRO:HB3	1:A:46:PHE:HE2	1.83	0.42
1:A:51:ASN:CG	1:A:59:ASN:H	2.26	0.42
1:A:260:THR:HG23	1:A:262:LYS:H	1.84	0.42
1:A:542:GLN:HG2	1:A:543:PRO:HD2	2.00	0.42
1:B:418:LEU:O	1:B:431:PRO:HA	2.19	0.42
1:B:242:SER:HB3	1:B:284:TYR:CE1	2.55	0.42
1:B:86:TYR:CB	1:B:142:PRO:HG3	2.50	0.42
1:A:86:TYR:HA	1:A:112:THR:HG22	2.02	0.42
1:B:278:TYR:HB3	1:B:339:LEU:HD11	2.02	0.42
1:B:281:GLY:HA2	1:B:466:LYS:HD3	2.02	0.41
1:B:286:SER:HA	1:B:300:TRP:O	2.19	0.41
1:A:242:SER:HB3	1:A:284:TYR:CZ	2.55	0.41
1:A:544:PHE:O	1:A:545:HIS:C	2.64	0.41
1:B:35:ASP:O	1:B:47:PHE:HB2	2.21	0.41
1:B:96:ALA:HB2	1:B:106:MET:SD	2.61	0.41
1:B:412:VAL:HG12	1:B:413:LEU:HG	2.02	0.41
1:B:177:TYR:HB3	5:H:1:NAG:H82	2.02	0.41
1:B:288:THR:HG22	1:B:299:VAL:HB	2.02	0.40
1:A:257:ASP:CB	1:A:260:THR:HG22	2.38	0.40
1:A:213:VAL:HA	1:A:240:LYS:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	518/546 (95%)	488 (94%)	29 (6%)	1 (0%)	43	72
1	B	518/546 (95%)	490 (95%)	28 (5%)	0	100	100
All	All	1036/1092 (95%)	978 (94%)	57 (6%)	1 (0%)	48	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	GLY

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	376/463 (81%)	372 (99%)	4 (1%)	65	88
1	B	226/463 (49%)	224 (99%)	2 (1%)	70	90
All	All	602/926 (65%)	596 (99%)	6 (1%)	68	89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	SER
1	A	193	SER
1	A	438	LYS
1	A	449	CYS
1	B	78	LEU
1	B	215	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	267	ASN

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Mol	Chain	Res	Type
1	A	295	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 ⓘ

32 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	0.61	0	17,19,21	1.41	2 (11%)
2	FUC	C	2	2	10,10,11	0.46	0	14,14,16	0.51	0
2	NAG	C	3	2	14,14,15	0.53	0	17,19,21	0.83	0
3	NAG	D	1	3,1	14,14,15	0.52	0	17,19,21	1.08	0
3	NAG	D	2	3	14,14,15	0.61	0	17,19,21	1.14	1 (5%)
3	BMA	D	3	3	11,11,12	0.54	0	15,15,17	1.13	2 (13%)
4	NAG	E	1	4,1	14,14,15	0.46	0	17,19,21	1.20	3 (17%)
4	NAG	E	2	4	14,14,15	0.51	0	17,19,21	1.23	4 (23%)
4	BMA	E	3	4	11,11,12	0.64	0	15,15,17	0.80	1 (6%)
4	XYX	E	4	4	9,9,10	1.04	1 (11%)	10,12,14	1.44	1 (10%)
4	MAN	E	5	4	11,11,12	0.68	0	15,15,17	1.37	4 (26%)
4	MAN	E	6	4	11,11,12	0.65	0	15,15,17	0.97	1 (6%)
4	FUC	E	7	4	10,10,11	0.51	0	14,14,16	1.05	0
3	NAG	F	1	3,1	14,14,15	0.57	0	17,19,21	0.70	0
3	NAG	F	2	3	14,14,15	0.58	0	17,19,21	1.04	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BMA	F	3	3	11,11,12	0.45	0	15,15,17	0.77	0
2	NAG	G	1	1,2	14,14,15	0.53	0	17,19,21	0.99	0
2	FUC	G	2	2	10,10,11	0.54	0	14,14,16	0.73	0
2	NAG	G	3	2	14,14,15	0.50	0	17,19,21	1.00	1 (5%)
5	NAG	H	1	1,5	14,14,15	0.47	0	17,19,21	1.08	1 (5%)
5	NAG	H	2	5	14,14,15	0.60	0	17,19,21	0.98	1 (5%)
5	BMA	H	3	5	11,11,12	0.55	0	15,15,17	0.71	0
5	MAN	H	4	5	11,11,12	0.58	0	15,15,17	1.33	1 (6%)
5	FUC	H	5	5	10,10,11	0.48	0	14,14,16	0.68	0
5	NAG	I	1	1,5	14,14,15	0.48	0	17,19,21	1.35	3 (17%)
5	NAG	I	2	5	14,14,15	0.57	0	17,19,21	1.36	2 (11%)
5	BMA	I	3	5	11,11,12	0.68	0	15,15,17	1.20	2 (13%)
5	MAN	I	4	5	11,11,12	0.57	0	15,15,17	1.24	1 (6%)
5	FUC	I	5	5	10,10,11	0.52	0	14,14,16	0.78	0
6	GLC	J	1	6	11,11,12	0.63	0	15,15,17	1.70	2 (13%)
6	FRU	J	2	6	11,12,12	0.87	1 (9%)	10,18,18	0.83	0
6	FRU	J	3	6	11,11,12	0.35	0	15,15,18	1.08	1 (6%)

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	2/2/19/22	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	FUC	G	2	2	-	-	0/1/1/1
2	NAG	G	3	2	-	2/6/23/26	0/1/1/1
5	NAG	H	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	H	2	5	-	2/6/23/26	0/1/1/1
5	BMA	H	3	5	-	0/2/19/22	0/1/1/1
5	MAN	H	4	5	-	2/2/19/22	0/1/1/1
5	FUC	H	5	5	-	-	0/1/1/1
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1
5	BMA	I	3	5	-	1/2/19/22	0/1/1/1
5	MAN	I	4	5	-	2/2/19/22	0/1/1/1
5	FUC	I	5	5	-	-	0/1/1/1
6	GLC	J	1	6	-	2/2/19/22	0/1/1/1
6	FRU	J	2	6	-	0/5/24/24	0/1/1/1
6	FRU	J	3	6	-	4/4/20/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	2	FRU	O2-C2	2.72	1.45	1.40
4	E	4	XYS	O5-C1	-2.72	1.37	1.43

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	1	GLC	C1-C2-C3	5.16	117.15	109.64
5	H	4	MAN	C1-O5-C5	4.11	117.70	112.19
5	I	2	NAG	C4-C3-C2	4.04	116.94	111.02
4	E	4	XYS	C5-O5-C1	3.90	117.72	111.42
5	I	4	MAN	C1-O5-C5	3.67	117.10	112.19
5	I	1	NAG	C1-O5-C5	3.46	116.82	112.19
3	D	2	NAG	C4-C3-C2	3.34	115.92	111.02
2	C	1	NAG	C1-C2-N2	-3.28	105.26	110.43
4	E	5	MAN	C1-C2-C3	3.27	114.40	109.64
3	F	2	NAG	C4-C3-C2	2.99	115.40	111.02
5	I	1	NAG	O5-C1-C2	-2.93	106.76	111.29
4	E	1	NAG	C1-O5-C5	2.86	116.02	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	BMA	C1-O5-C5	2.73	115.85	112.19
5	I	3	BMA	O5-C5-C6	2.59	112.71	107.66
4	E	1	NAG	O5-C1-C2	-2.58	107.30	111.29
4	E	2	NAG	C8-C7-N2	2.56	120.37	116.12
2	G	3	NAG	C1-O5-C5	2.55	115.60	112.19
5	I	3	BMA	C1-C2-C3	2.50	113.28	109.64
2	C	1	NAG	C4-C3-C2	2.45	114.60	111.02
6	J	3	FRU	C1-C2-C3	-2.42	109.39	115.10
3	D	3	BMA	C1-C2-C3	2.40	113.13	109.64
6	J	1	GLC	C2-C3-C4	2.34	114.98	110.86
4	E	2	NAG	O7-C7-C8	-2.31	117.95	122.05
4	E	6	MAN	C1-C2-C3	2.31	113.00	109.64
5	I	2	NAG	O4-C4-C3	-2.25	105.06	110.38
4	E	5	MAN	C2-C3-C4	2.23	114.79	110.86
4	E	5	MAN	C3-C4-C5	2.21	114.25	110.23
4	E	3	BMA	C1-O5-C5	2.16	115.08	112.19
4	E	2	NAG	C2-N2-C7	2.15	125.79	122.90
4	E	2	NAG	C1-O5-C5	2.14	115.05	112.19
5	H	1	NAG	C1-O5-C5	2.13	115.05	112.19
5	I	1	NAG	C8-C7-N2	2.06	119.53	116.12
5	H	2	NAG	O5-C5-C6	2.03	111.61	107.66
4	E	1	NAG	C8-C7-N2	2.00	119.44	116.12
4	E	5	MAN	O5-C5-C6	2.00	111.56	107.66

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	5	MAN	O5-C5-C6-O6
6	J	1	GLC	O5-C5-C6-O6
4	E	6	MAN	O5-C5-C6-O6
4	E	5	MAN	C4-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
5	H	4	MAN	O5-C5-C6-O6
4	E	6	MAN	C4-C5-C6-O6
3	D	3	BMA	O5-C5-C6-O6
6	J	1	GLC	C4-C5-C6-O6
3	F	3	BMA	O5-C5-C6-O6
2	C	3	NAG	O5-C5-C6-O6
5	I	4	MAN	O5-C5-C6-O6
2	C	3	NAG	C4-C5-C6-O6
5	I	4	MAN	C4-C5-C6-O6

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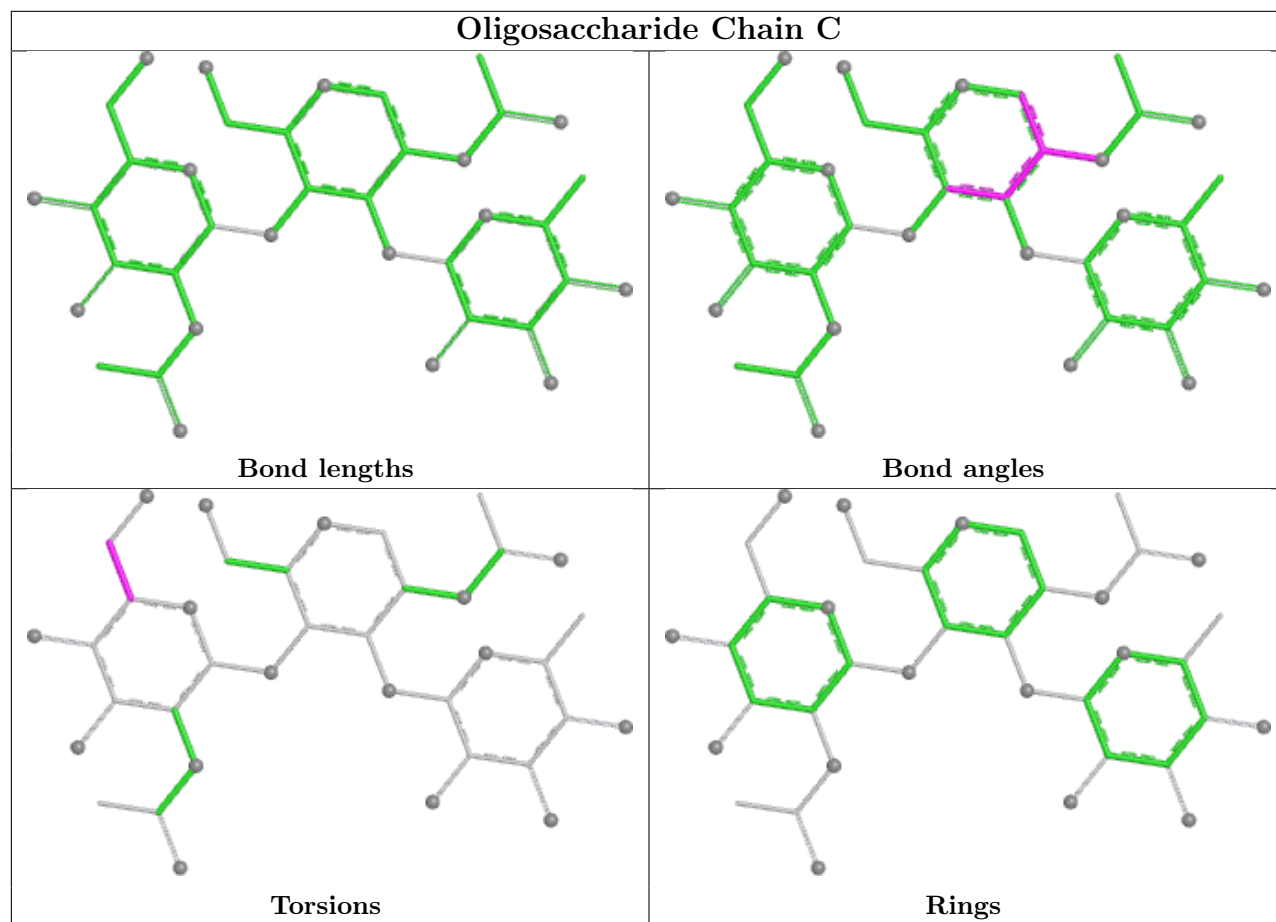
Mol	Chain	Res	Type	Atoms
6	J	3	FRU	O1-C1-C2-O5
3	F	3	BMA	C4-C5-C6-O6
3	D	1	NAG	C8-C7-N2-C2
3	D	1	NAG	O7-C7-N2-C2
4	E	1	NAG	C8-C7-N2-C2
4	E	1	NAG	O7-C7-N2-C2
4	E	2	NAG	C8-C7-N2-C2
4	E	2	NAG	O7-C7-N2-C2
5	I	1	NAG	C8-C7-N2-C2
5	I	1	NAG	O7-C7-N2-C2
5	H	4	MAN	C4-C5-C6-O6
6	J	3	FRU	O1-C1-C2-C3
5	I	2	NAG	C4-C5-C6-O6
5	I	2	NAG	O5-C5-C6-O6
2	G	3	NAG	C4-C5-C6-O6
2	G	3	NAG	O5-C5-C6-O6
5	I	3	BMA	O5-C5-C6-O6
5	H	2	NAG	C4-C5-C6-O6
6	J	3	FRU	O5-C5-C6-O6
5	H	2	NAG	O5-C5-C6-O6
6	J	3	FRU	C4-C5-C6-O6

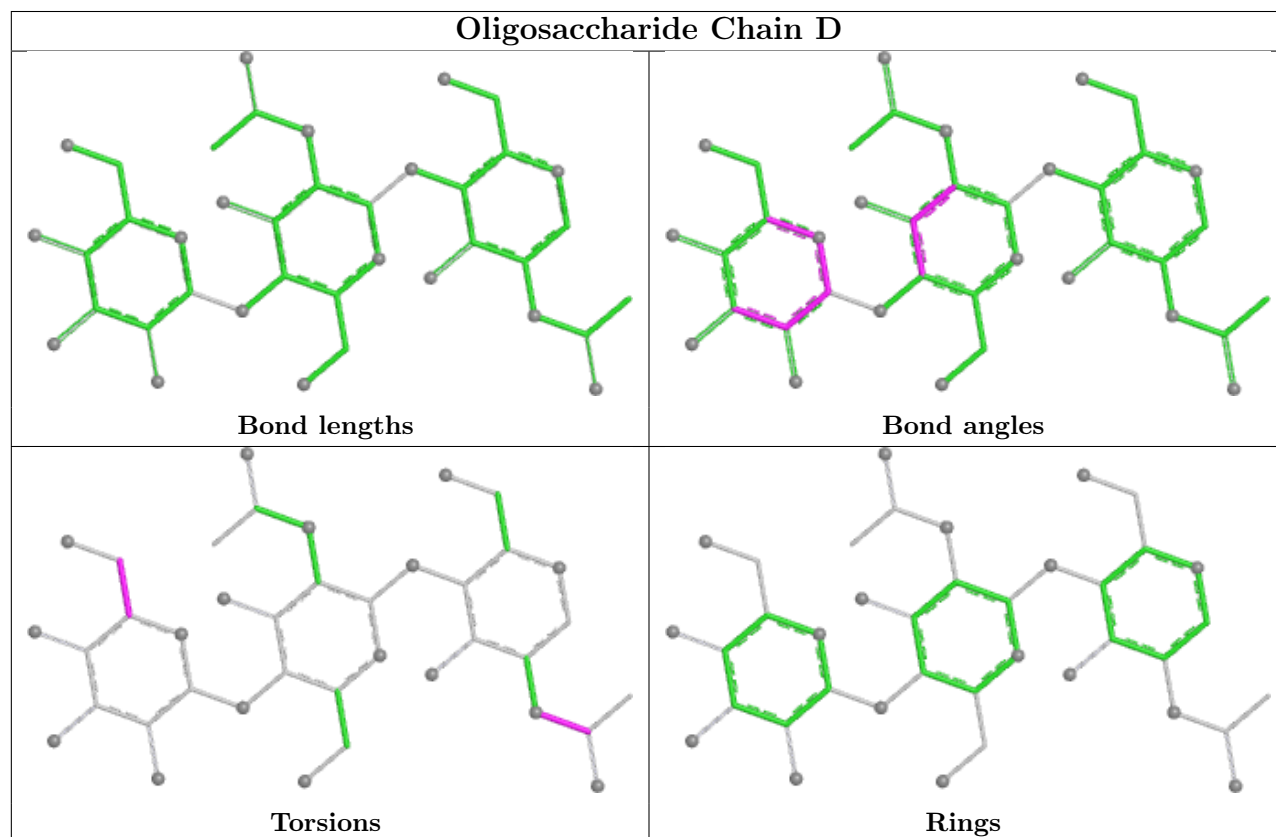
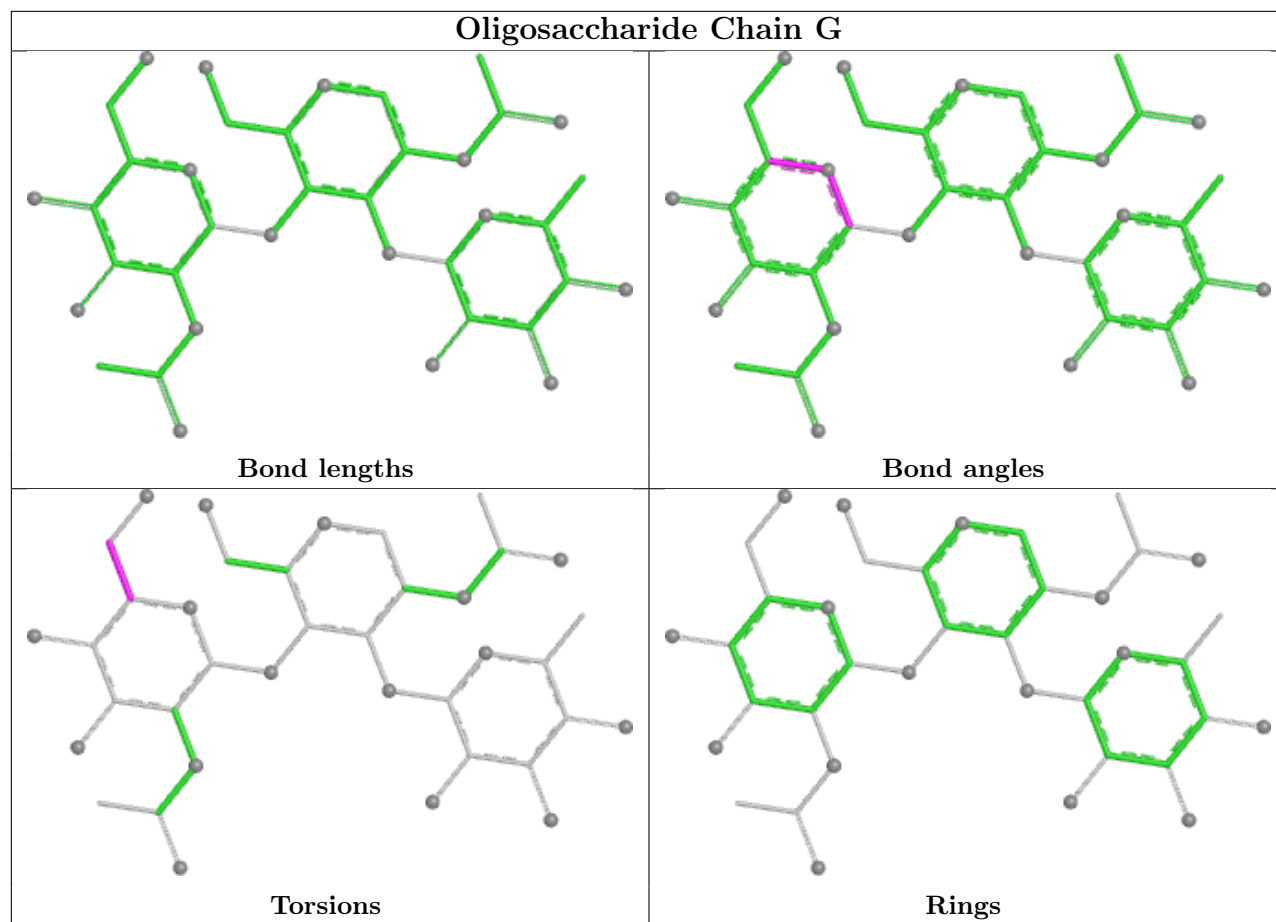
There are no ring outliers.

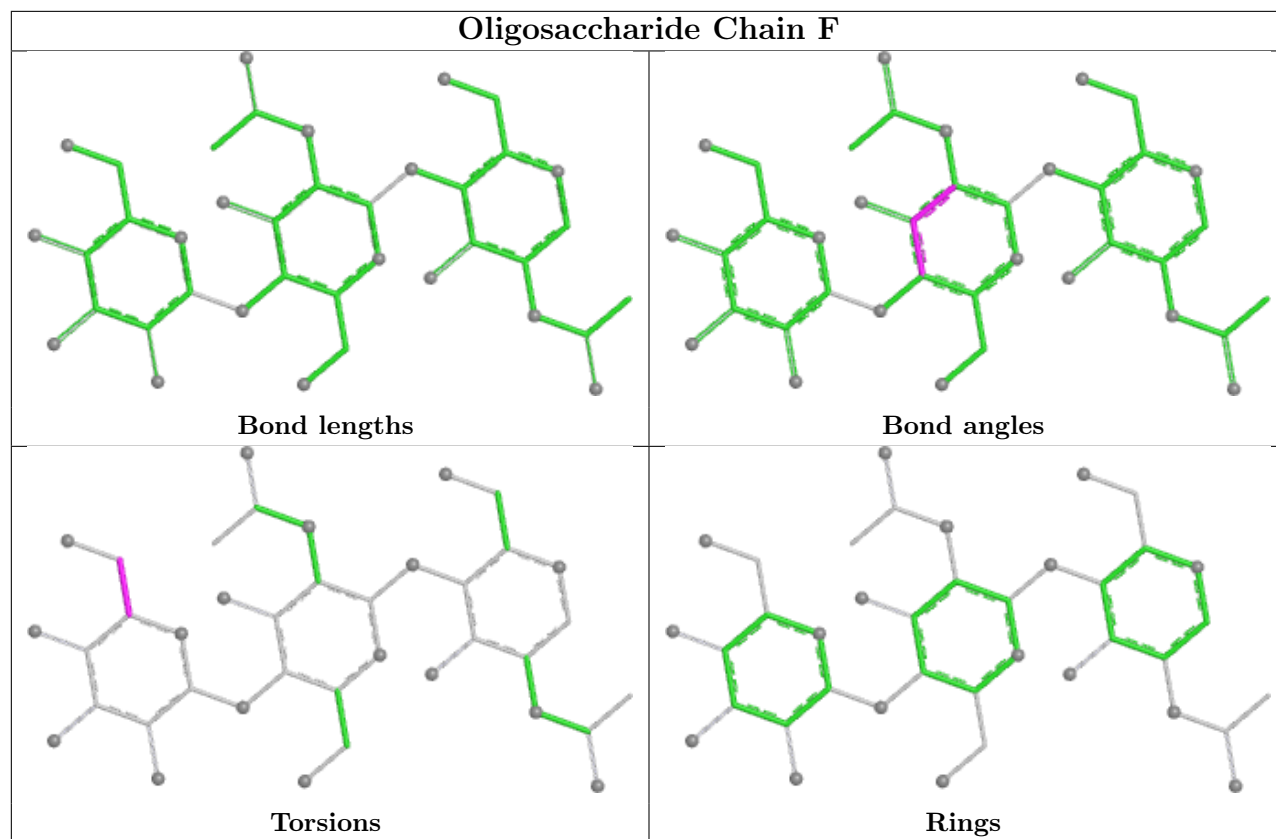
4 monomers are involved in 3 short contacts:

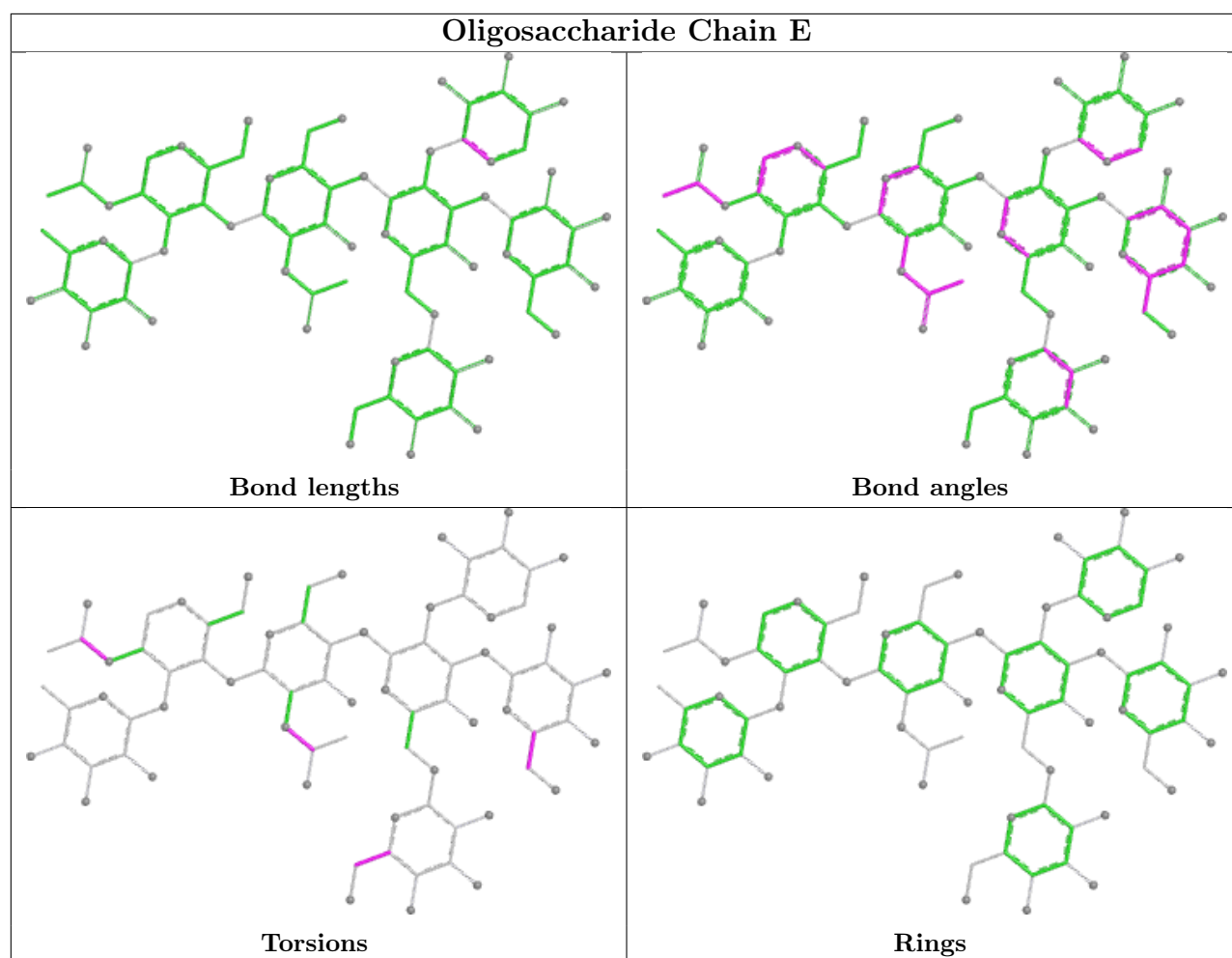
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1	NAG	1	0
3	D	2	NAG	1	0
5	H	1	NAG	1	0
3	D	3	BMA	1	0

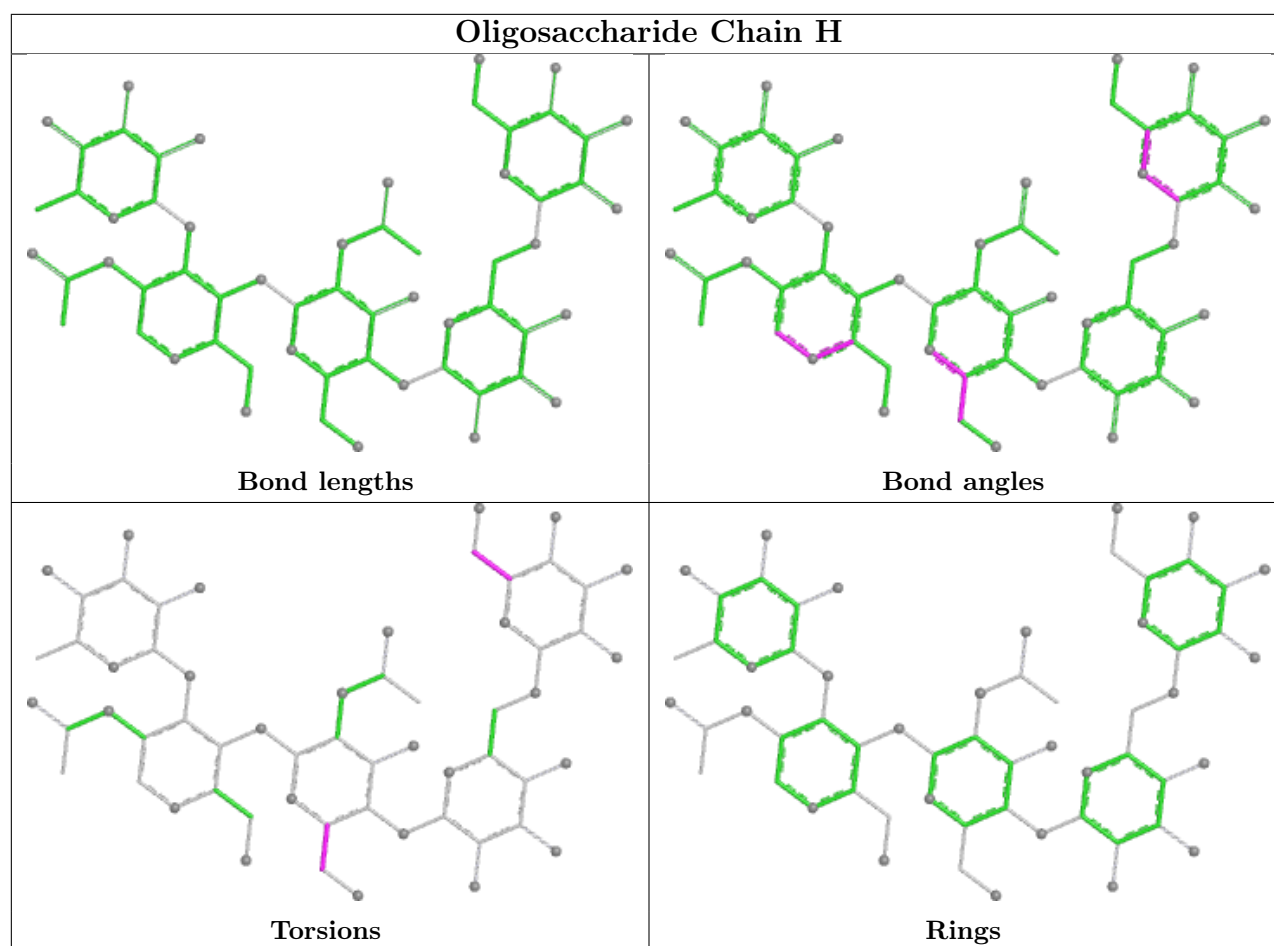
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

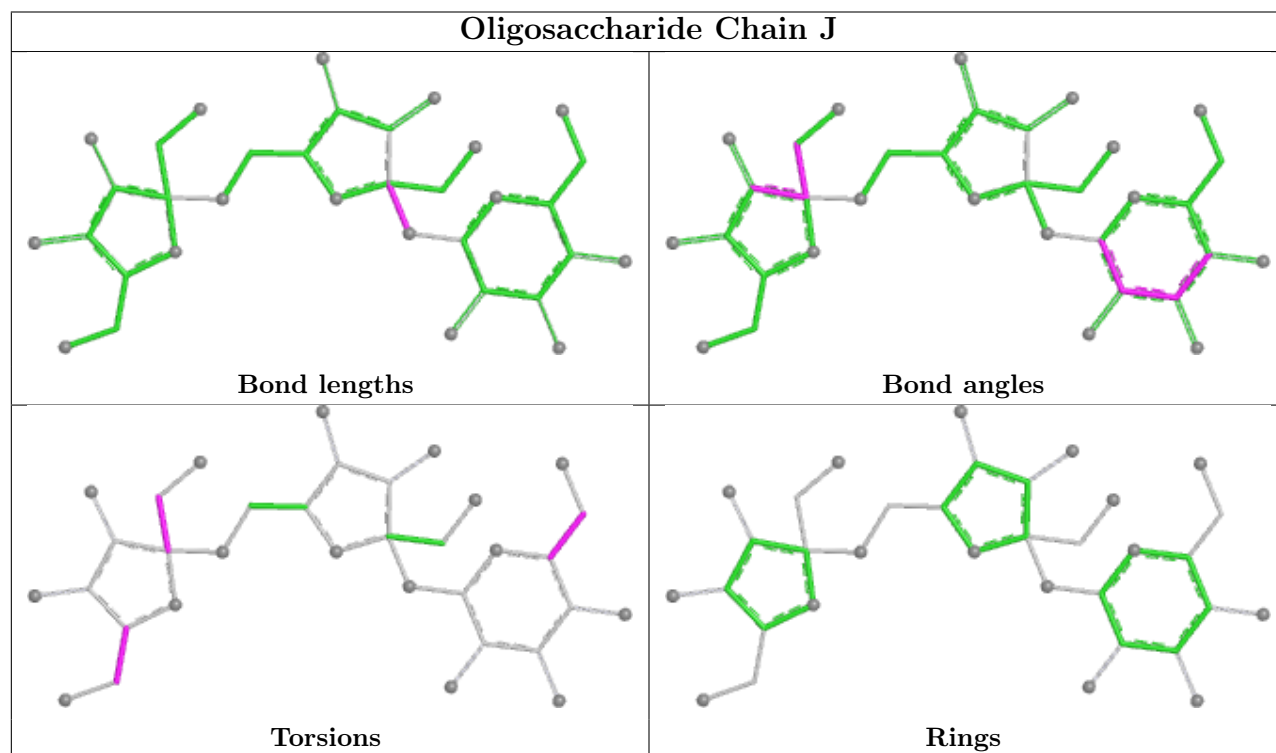
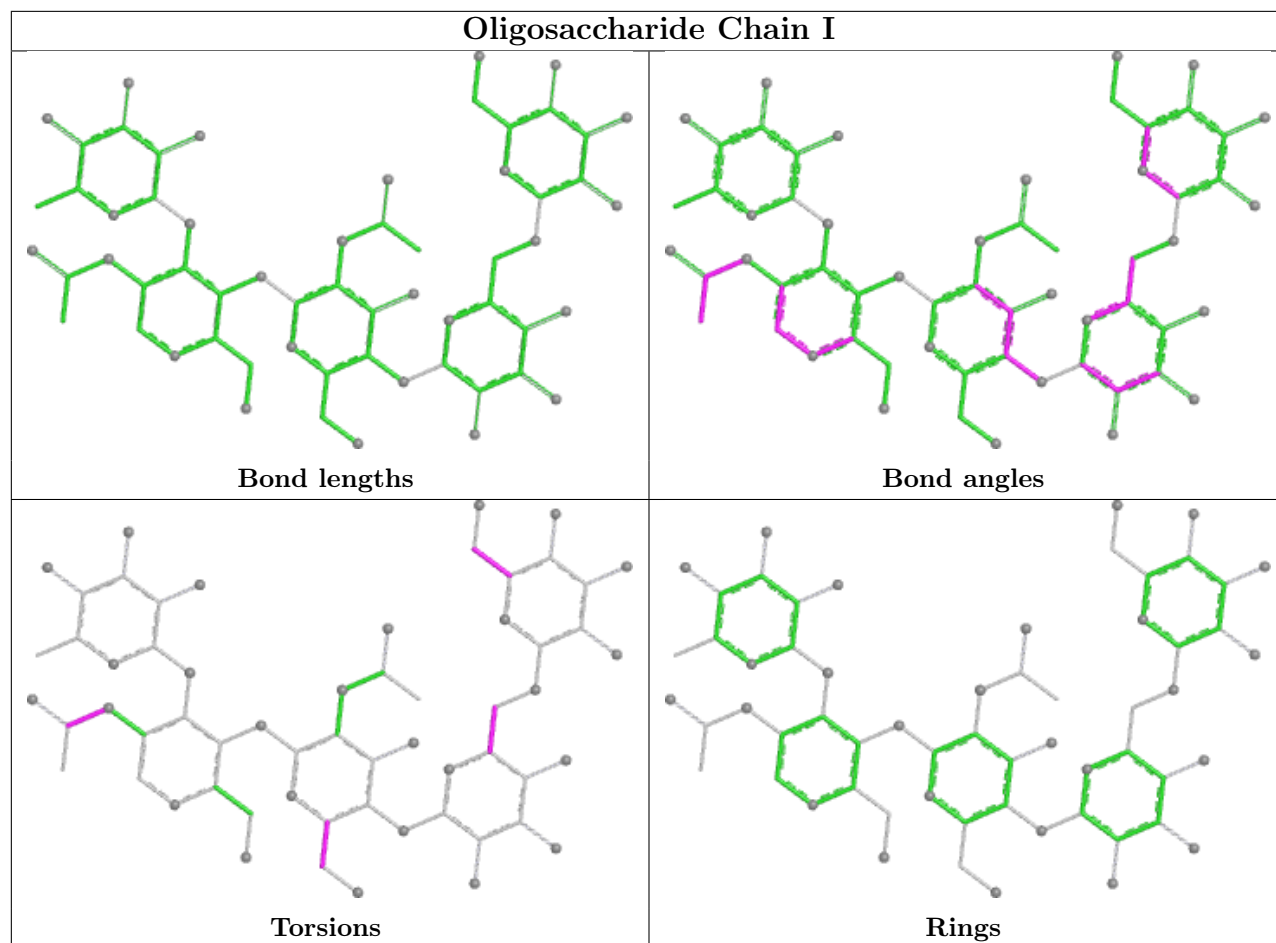












5.6 Ligand geometry

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
7	NAG	A	547	1	14,14,15	0.57	0	17,19,21	1.75	3 (17%)
9	GOL	A	562	-	5,5,5	0.42	0	5,5,5	0.29	0
8	SO4	B	563	-	4,4,4	0.25	0	6,6,6	0.09	0
8	SO4	A	561	-	4,4,4	0.25	0	6,6,6	0.12	0
9	GOL	B	564	-	5,5,5	0.43	0	5,5,5	0.24	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
9	GOL	B	564	-	-	4/4/4/4	-
7	NAG	A	547	1	-	4/6/23/26	0/1/1/1
9	GOL	A	562	-	-	2/4/4/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	547	NAG	C1-O5-C5	4.06	117.62	112.19
7	A	547	NAG	C4-C3-C2	-3.80	105.44	111.02
7	A	547	NAG	C3-C4-C5	-2.39	105.90	110.23

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	564	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
9	B	564	GOL	O1-C1-C2-C3
9	B	564	GOL	C1-C2-C3-O3
9	B	564	GOL	O2-C2-C3-O3
7	A	547	NAG	O5-C5-C6-O6
7	A	547	NAG	C4-C5-C6-O6
7	A	547	NAG	C8-C7-N2-C2
7	A	547	NAG	O7-C7-N2-C2
9	A	562	GOL	O1-C1-C2-O2
9	A	562	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	562	GOL	3	0
9	B	564	GOL	4	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	524/546 (95%)	-0.21	5 (0%) 79 73	8, 19, 29, 46	0
1	B	524/546 (95%)	-0.22	7 (1%) 75 67	7, 19, 31, 42	0
All	All	1048/1092 (95%)	-0.21	12 (1%) 78 71	7, 19, 30, 46	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	386	LYS	3.8
1	A	545	HIS	3.5
1	B	545	HIS	3.5
1	A	438	LYS	3.2
1	B	233	PRO	2.6
1	B	398	GLY	2.5
1	B	457	LYS	2.5
1	B	443	ASN	2.5
1	A	7	PRO	2.4
1	B	7	PRO	2.2
1	A	233	PRO	2.1
1	B	464	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

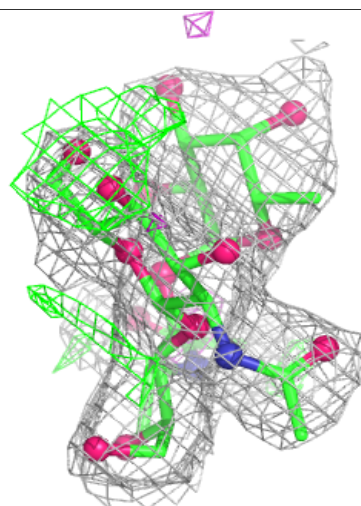
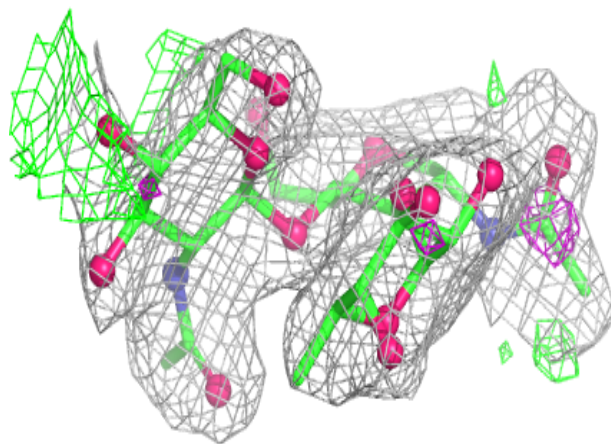
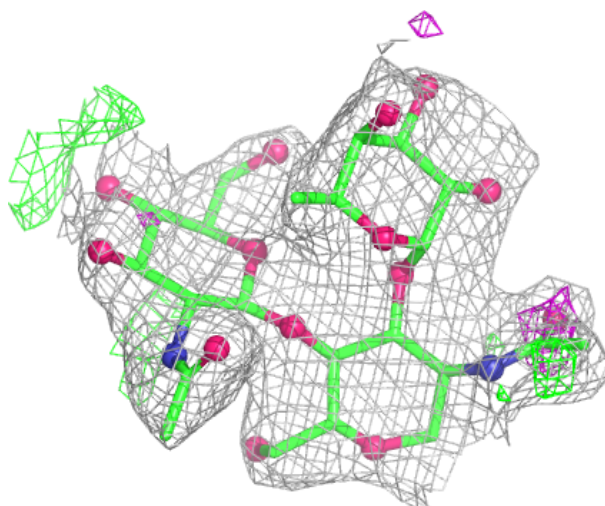
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MAN	E	6	11/12	0.58	0.21	67,67,68,68	0
4	XYS	E	4	9/10	0.59	0.22	65,65,66,66	0
4	MAN	E	5	11/12	0.63	0.21	61,62,62,63	0
3	BMA	F	3	11/12	0.66	0.18	48,50,51,51	0
5	BMA	I	3	11/12	0.67	0.19	60,61,64,66	0
6	GLC	J	1	11/12	0.68	0.23	66,67,69,70	0
5	MAN	I	4	11/12	0.69	0.19	67,67,68,68	0
5	MAN	H	4	11/12	0.70	0.18	56,57,57,57	0
2	NAG	G	3	14/15	0.76	0.18	46,49,50,50	0
6	FRU	J	2	12/12	0.76	0.17	61,65,67,67	0
5	BMA	H	3	11/12	0.79	0.12	45,47,51,54	0
2	NAG	C	3	14/15	0.82	0.15	34,38,40,41	0
2	NAG	C	1	14/15	0.83	0.14	27,31,33,34	0
3	BMA	D	3	11/12	0.84	0.12	29,30,30,30	0
5	FUC	I	5	10/11	0.85	0.14	45,45,45,45	0
6	FRU	J	3	11/12	0.86	0.17	57,59,60,60	0
4	NAG	E	2	14/15	0.87	0.14	48,49,52,56	0
5	NAG	I	2	14/15	0.87	0.14	51,53,55,58	0
2	FUC	C	2	10/11	0.88	0.13	33,33,34,34	0
4	NAG	E	1	14/15	0.88	0.12	34,38,40,44	0
2	FUC	G	2	10/11	0.88	0.14	39,40,41,41	0
4	BMA	E	3	11/12	0.88	0.11	60,62,64,66	0
5	NAG	I	1	14/15	0.89	0.11	37,41,44,47	0
3	NAG	D	2	14/15	0.89	0.11	23,26,27,29	0
4	FUC	E	7	10/11	0.90	0.13	41,42,42,43	0
3	NAG	D	1	14/15	0.91	0.10	19,20,21,23	0
5	NAG	H	1	14/15	0.91	0.10	24,28,29,32	0
2	NAG	G	1	14/15	0.92	0.10	29,33,37,42	0
5	NAG	H	2	14/15	0.92	0.11	31,36,39,43	0
3	NAG	F	2	14/15	0.92	0.09	37,40,42,45	0
5	FUC	H	5	10/11	0.93	0.10	28,28,28,29	0
3	NAG	F	1	14/15	0.95	0.10	23,27,28,33	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.

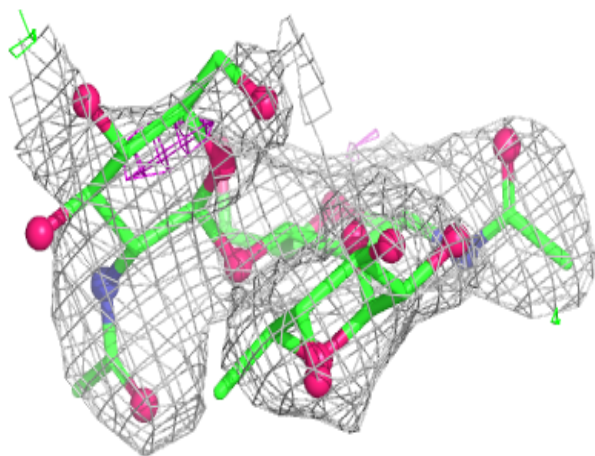
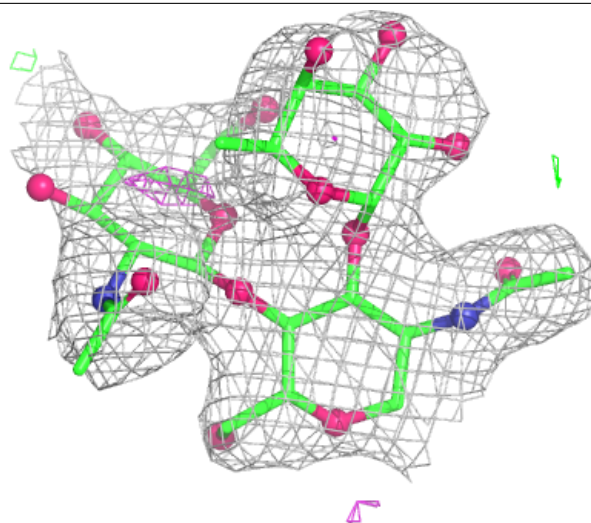
Electron density around Chain C:

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



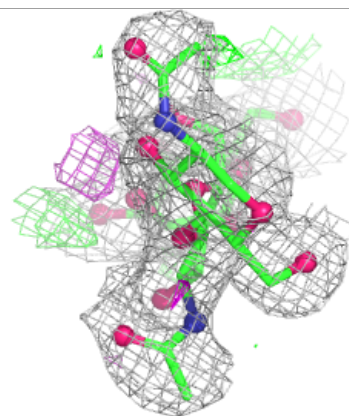
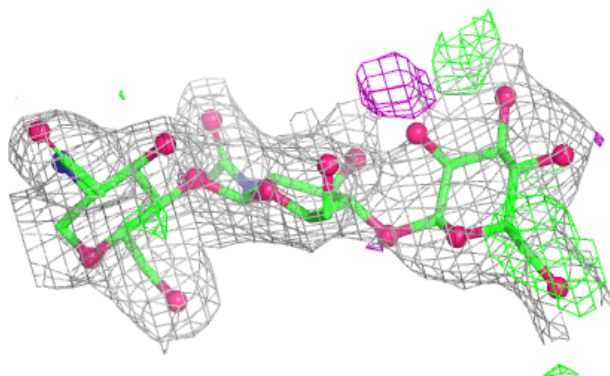
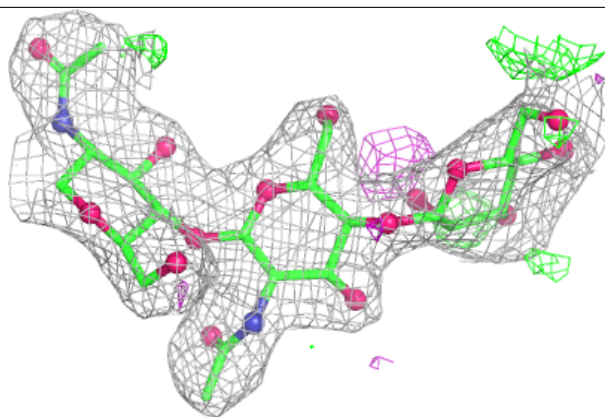
Electron density around Chain G:

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

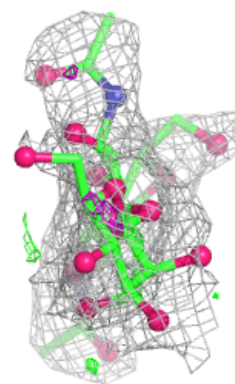
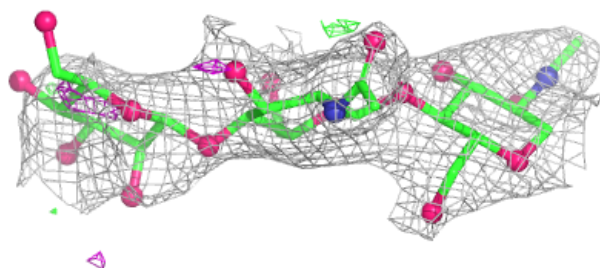
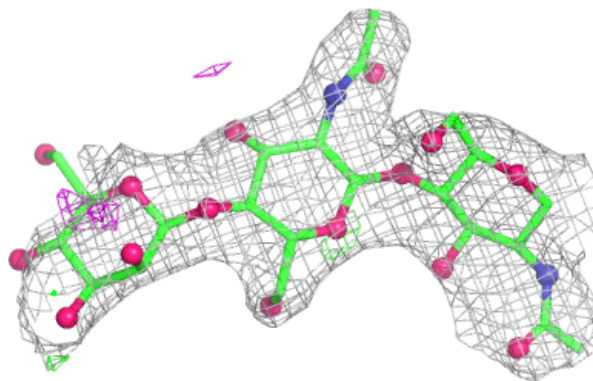


Electron density around Chain D:

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

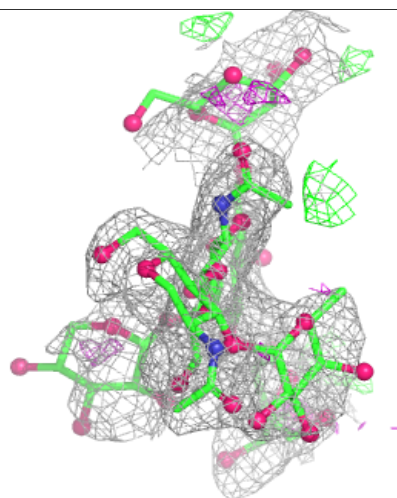
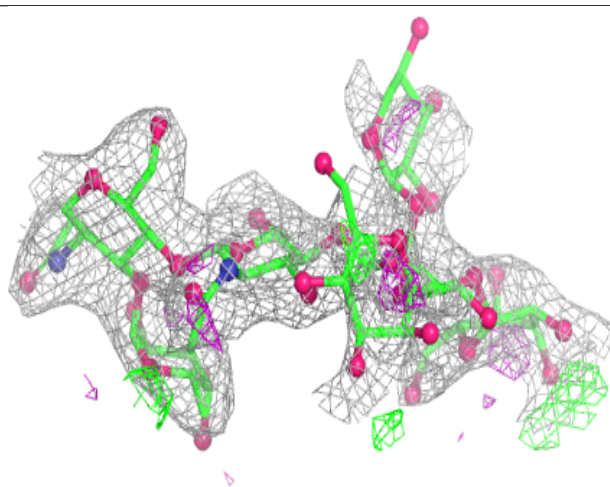
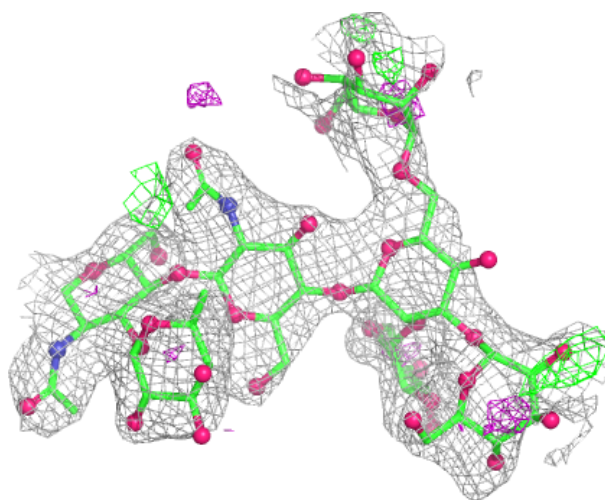
**Electron density around Chain F:**

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



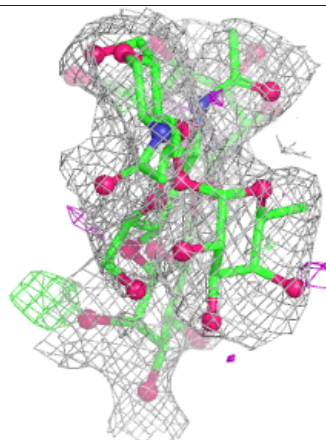
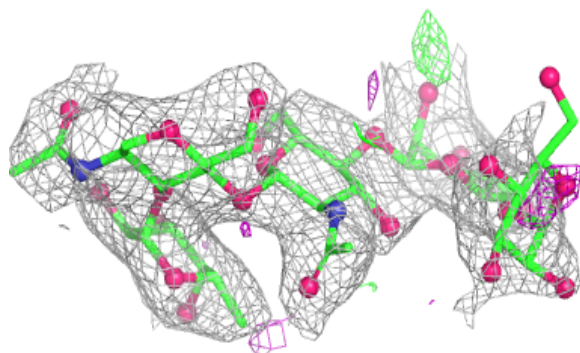
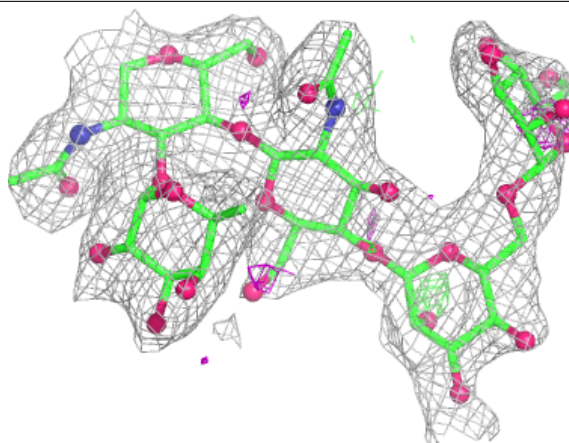
Electron density around Chain E:

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

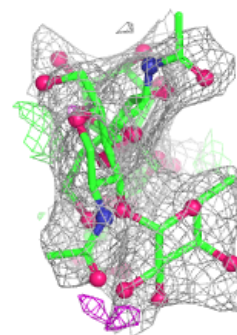
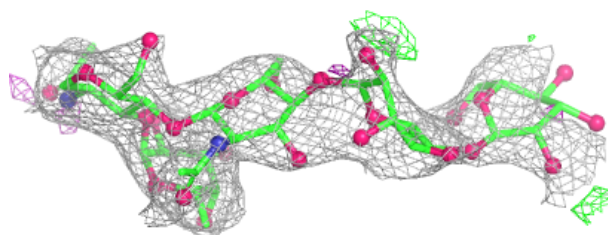
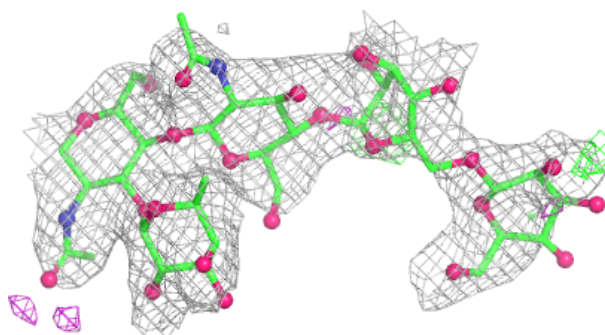


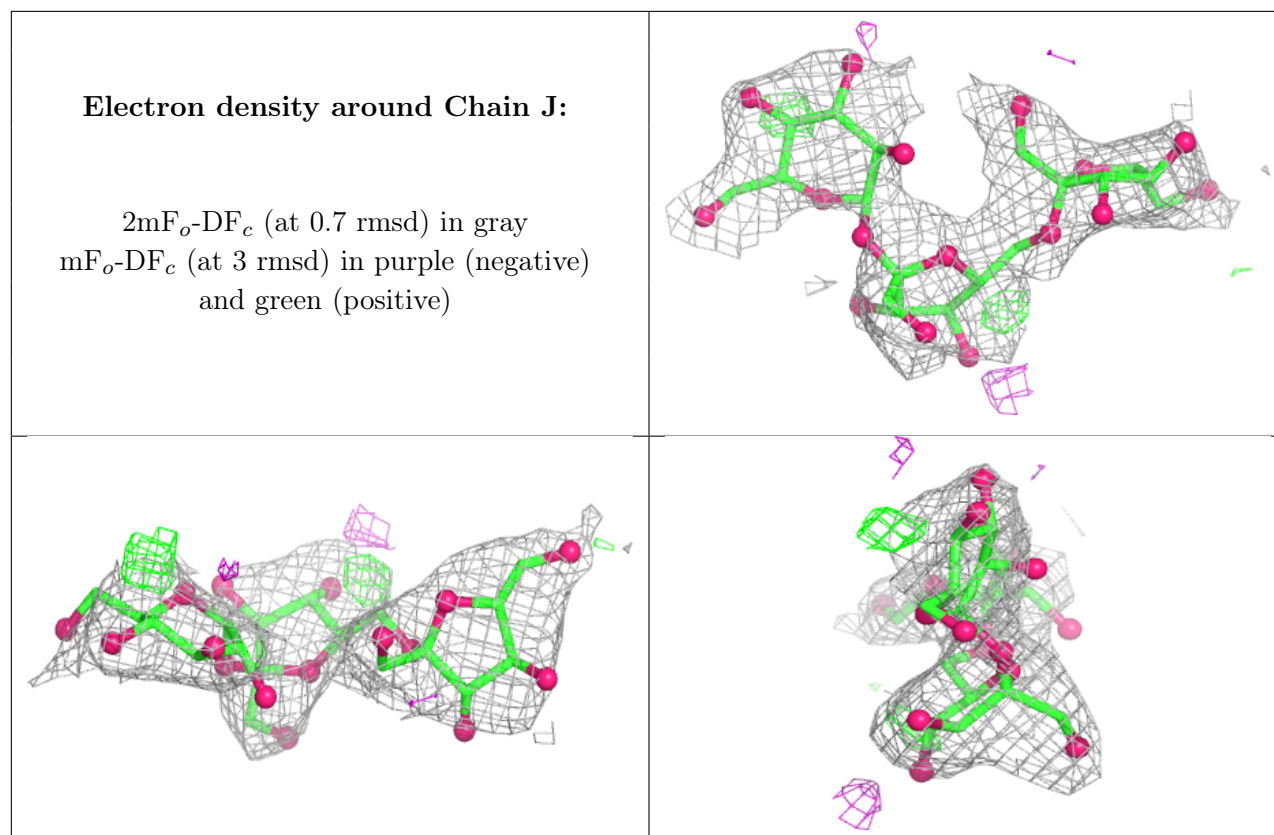
Electron density around Chain H:

$2mF_o-DF_c$ (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)





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, 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($\text{\AA}^2$)	Q<0.9
7	NAG	A	547	14/15	0.84	0.12	23,25,26,27	0
9	GOL	A	562	6/6	0.86	0.31	40,42,42,42	0
8	SO4	A	561	5/5	0.88	0.12	58,58,58,58	0
9	GOL	B	564	6/6	0.93	0.17	25,26,27,27	0
8	SO4	B	563	5/5	0.94	0.10	47,47,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.