



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 3, 2023 – 06:48 am GMT

PDB ID : 2VH9
Title : CRYSTAL STRUCTURE OF NXG1-DELTAYNIIG IN COMPLEX WITH
XLLG, A XYLOGLUCAN DERIVED OLIGOSACCHARIDE
Authors : Czjzek, M.; Mark, P.; Baumann, M.J.; Eklöf, J.M.; Michel, G.; Brumer, H.
Deposited on : 2007-11-20
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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

PERCENTILES INFOmissingINFO

1 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 5013 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 CELLULASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	266	2149	1374	354	414	7	0	0	0
1	B	266	2149	1374	354	414	7	0	0	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	C	3	31	17	14	0	0	0
2	D	3	31	17	14	0	0	0
2	F	3	31	17	14	0	0	0
2	G	3	31	17	14	0	0	0

- Molecule 3 is an oligosaccharide called alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	E	2	20	11	9	0	0	0

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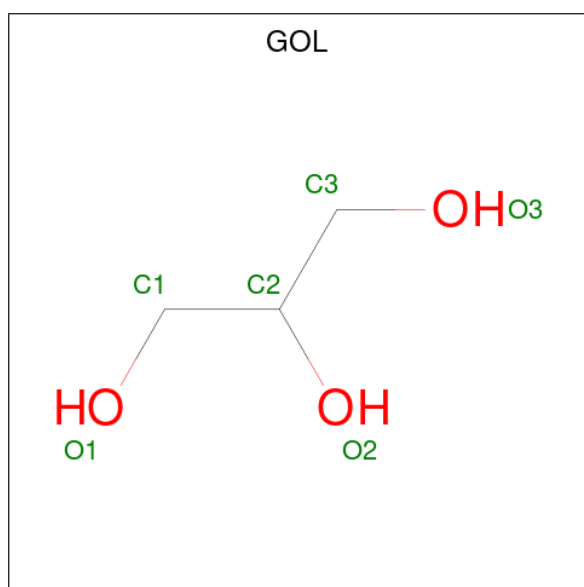
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	H	2	Total	C	O	0	0	0
			20	11	9			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 6 is beta-D-glucopyranose (three-letter code: BGC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 11 6 5	0	0
6	B	1	Total C O 11 6 5	0	0


- Molecule 7 is water.

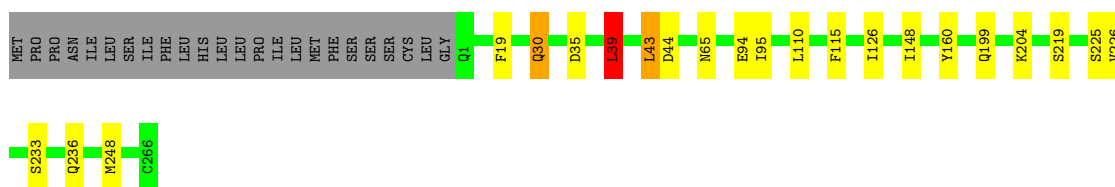
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	256	Total O 256 256	0	0
7	B	259	Total O 259 259	0	0

2 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.

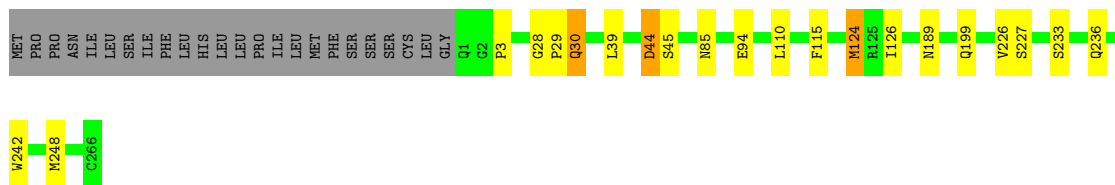
- Molecule 1: CELLULASE

Chain A: 



- Molecule 1: CELLULASE

Chain B: 



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

Chain C: 




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

Chain D: 



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

Chain F:  67% 33%


BGC1
XYS2
GAL3

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

Chain G:  100%


BGC1
XYS2
GAL3

- Molecule 3: alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose

Chain E:  50% 50%

BGC1
XYS2

- Molecule 3: alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose

Chain H:  100%

BGC1
XYS2

3 Data and refinement statistics i

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	100.54Å 100.54Å 61.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 2.10 50.27 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (35.00-2.10) 99.2 (50.27-2.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.148 , 0.203 0.162 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	16.3	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 33.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l 0.478 for h,-h-k,-l 0.030 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5013	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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.

4 Model quality i

4.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: BGC, GAL, ZN, GOL, 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	0.59	0/2222	0.69	1/3031 (0.0%)
1	B	0.57	0/2222	0.67	1/3031 (0.0%)
All	All	0.58	0/4444	0.68	2/6062 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	39	LEU	CA-CB-CG	5.69	128.39	115.30
1	B	44	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

4.2 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	2149	0	1993	18	0
1	B	2149	0	1993	16	0
2	C	31	0	25	6	0
2	D	31	0	25	6	0
2	F	31	0	25	3	0
2	G	31	0	25	0	0
3	E	20	0	17	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	20	0	17	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	6	0	8	0	0
5	B	6	0	8	0	0
6	A	11	0	9	2	0
6	B	11	0	10	3	0
7	A	256	0	0	7	0
7	B	259	0	0	4	0
All	All	5013	0	4155	45	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 5.

The worst 5 of 45 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:303:BGC:O4	2:C:1:BGC:C1	1.64	1.44
2:C:1:BGC:O4	2:D:1:BGC:C1	1.66	1.41
2:D:1:BGC:O4	3:E:1:BGC:C1	1.64	1.41
6:B:303:BGC:O4	2:F:1:BGC:C1	1.72	1.37
6:B:303:BGC:HD	2:F:1:BGC:C1	1.62	0.98

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 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	264/290 (91%)	256 (97%)	8 (3%)	0	100	100
1	B	264/290 (91%)	254 (96%)	10 (4%)	0	100	100
All	All	528/580 (91%)	510 (97%)	18 (3%)	0	100	100

There are no Ramachandran outliers to report.

4.3.2 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	232/255 (91%)	225 (97%)	7 (3%)	41	44
1	B	232/255 (91%)	227 (98%)	5 (2%)	52	57
All	All	464/510 (91%)	452 (97%)	12 (3%)	46	50

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

Mol	Chain	Res	Type
1	B	30	GLN
1	B	39	LEU
1	B	226	VAL
1	B	85	ASN
1	A	43	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	235	GLN
1	B	199	GLN
1	B	25	ASN
1	B	86	GLN
1	A	236	GLN

4.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

4.5 Carbohydrates i

16 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BGC	C	1	2	11,11,12	0.87	0	15,15,17	1.88	4 (26%)
2	XYS	C	2	2	9,9,10	1.07	1 (11%)	10,12,14	1.37	2 (20%)
2	GAL	C	3	2	11,11,12	0.67	0	15,15,17	0.66	0
2	BGC	D	1	2	11,11,12	0.57	0	15,15,17	2.36	5 (33%)
2	XYS	D	2	2	9,9,10	1.38	1 (11%)	10,12,14	0.99	0
2	GAL	D	3	2	11,11,12	0.91	1 (9%)	15,15,17	1.38	3 (20%)
3	BGC	E	1	3	11,11,12	0.57	0	15,15,17	1.48	3 (20%)
3	XYS	E	2	3	9,9,10	1.40	1 (11%)	10,12,14	1.09	0
2	BGC	F	1	2	11,11,12	0.72	0	15,15,17	1.90	5 (33%)
2	XYS	F	2	2	9,9,10	1.34	1 (11%)	10,12,14	1.28	1 (10%)
2	GAL	F	3	2	11,11,12	0.78	1 (9%)	15,15,17	0.93	1 (6%)
2	BGC	G	1	2	11,11,12	0.47	0	15,15,17	2.43	5 (33%)
2	XYS	G	2	2	9,9,10	1.45	1 (11%)	10,12,14	0.72	0
2	GAL	G	3	2	11,11,12	0.57	0	15,15,17	0.97	1 (6%)
3	BGC	H	1	3	11,11,12	0.53	0	15,15,17	1.45	2 (13%)
3	XYS	H	2	3	9,9,10	1.09	1 (11%)	10,12,14	0.72	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
2	BGC	C	1	2	-	0/2/19/22	0/1/1/1
2	XYS	C	2	2	-	-	0/1/1/1
2	GAL	C	3	2	-	0/2/19/22	0/1/1/1
2	BGC	D	1	2	-	0/2/19/22	0/1/1/1
2	XYS	D	2	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GAL	D	3	2	-	1/2/19/22	0/1/1/1
3	BGC	E	1	3	-	0/2/19/22	0/1/1/1
3	XYS	E	2	3	-	-	0/1/1/1
2	BGC	F	1	2	-	0/2/19/22	0/1/1/1
2	XYS	F	2	2	-	-	0/1/1/1
2	GAL	F	3	2	-	0/2/19/22	0/1/1/1
2	BGC	G	1	2	-	0/2/19/22	0/1/1/1
2	XYS	G	2	2	-	-	0/1/1/1
2	GAL	G	3	2	-	0/2/19/22	0/1/1/1
3	BGC	H	1	3	-	0/2/19/22	0/1/1/1
3	XYS	H	2	3	-	-	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2	XYS	O5-C1	-3.99	1.35	1.42
2	D	2	XYS	O5-C1	-3.82	1.35	1.42
3	E	2	XYS	O5-C1	-3.48	1.36	1.42
2	F	2	XYS	O5-C1	-3.23	1.36	1.42
3	H	2	XYS	O5-C1	-2.79	1.37	1.42

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	BGC	O5-C5-C6	5.21	115.37	107.20
2	D	1	BGC	O5-C5-C6	5.09	115.19	107.20
2	G	1	BGC	C1-O5-C5	-4.65	105.89	112.19
2	D	1	BGC	C1-O5-C5	-4.31	106.36	112.19
2	C	1	BGC	O5-C1-C2	3.93	116.84	110.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	3	GAL	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 11 short contacts:

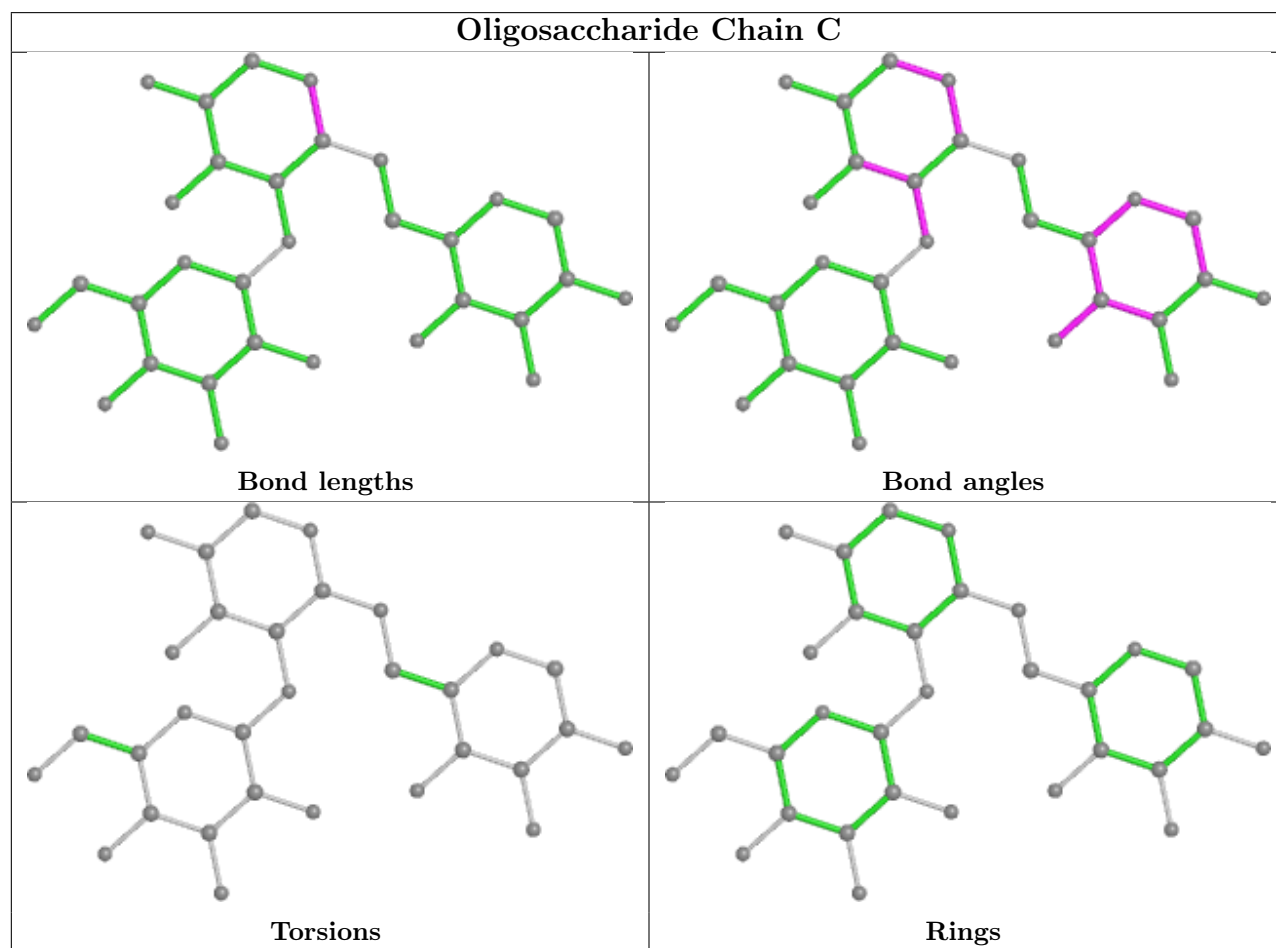
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	BGC	6	0

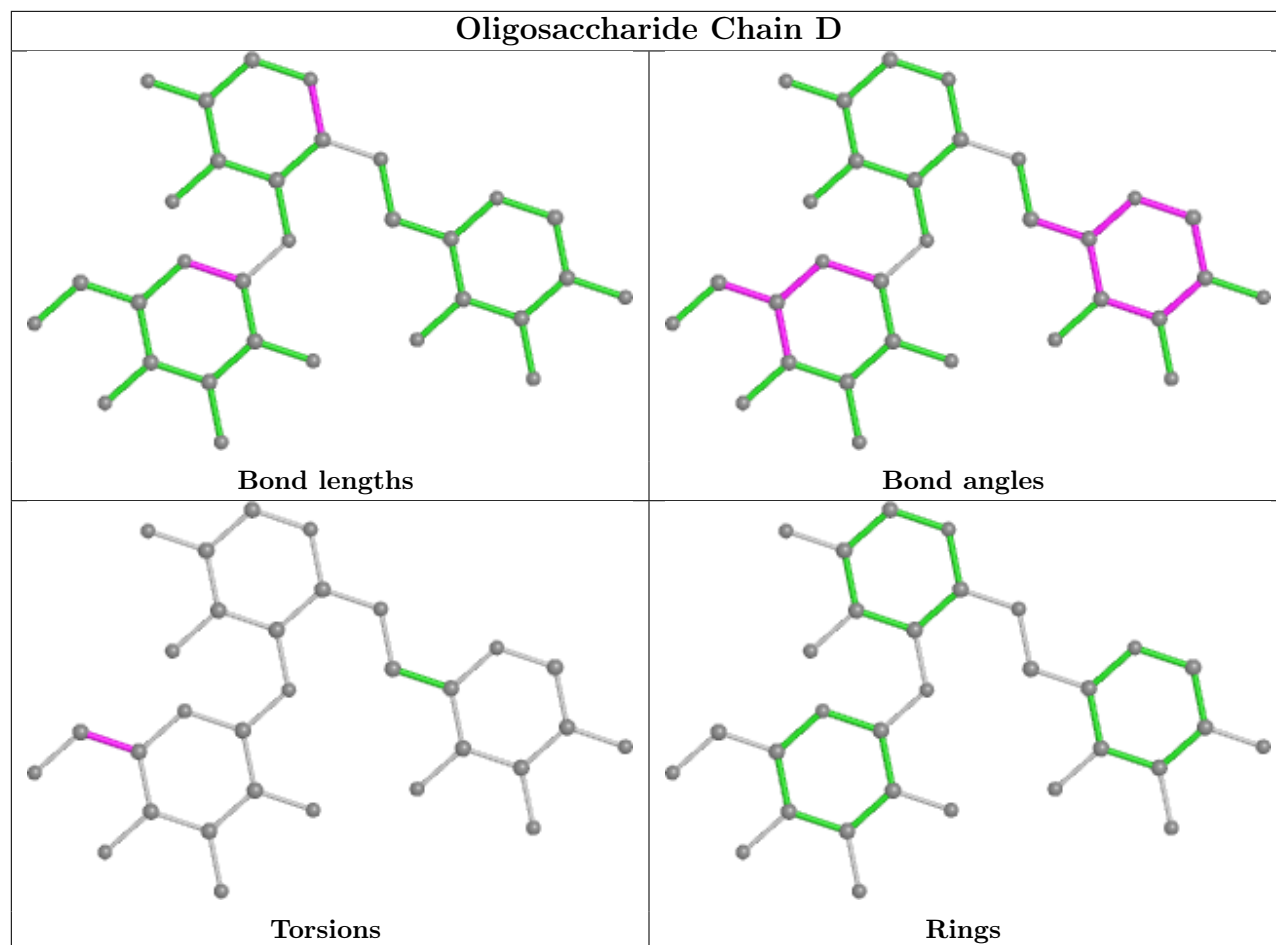
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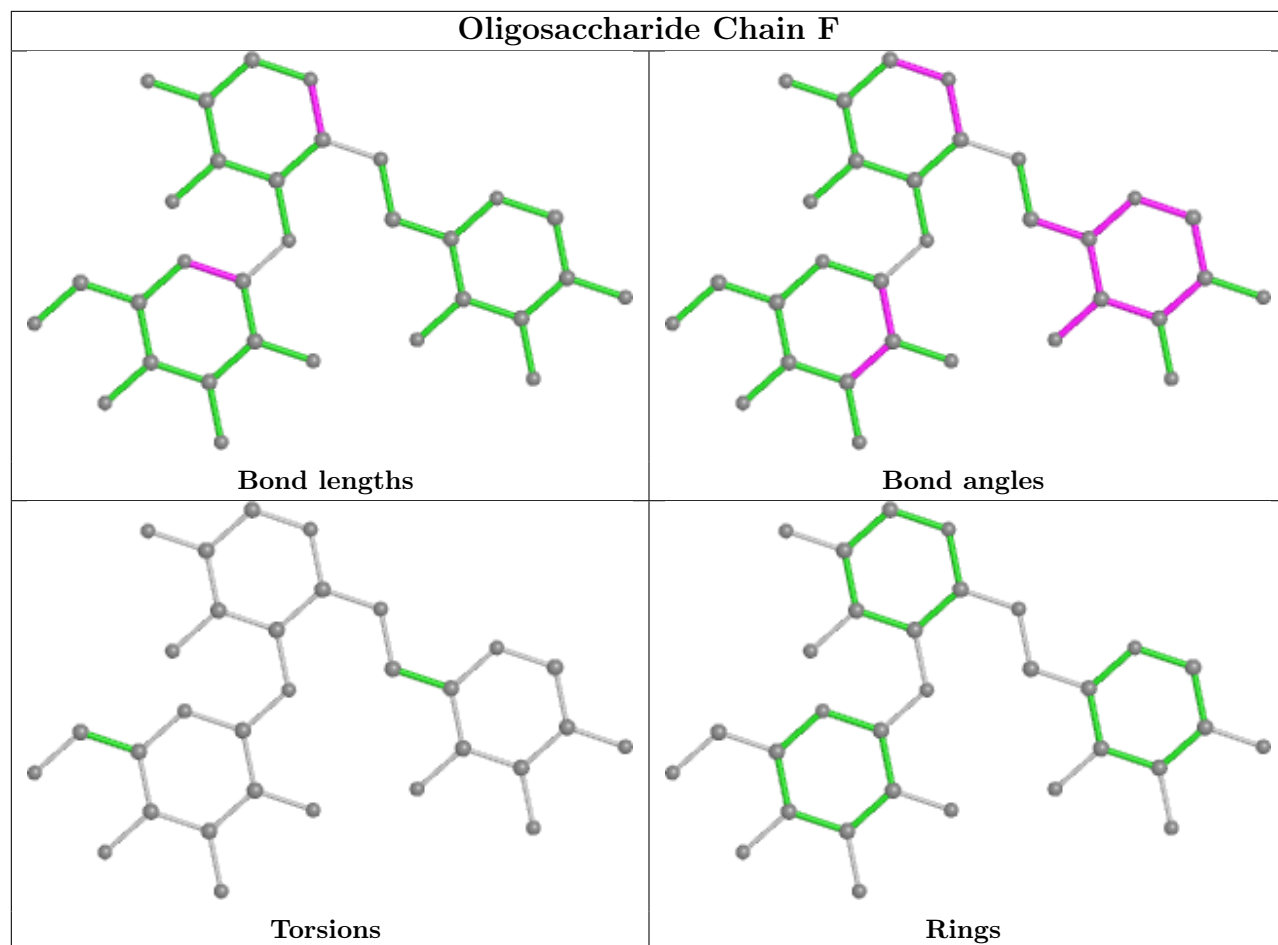
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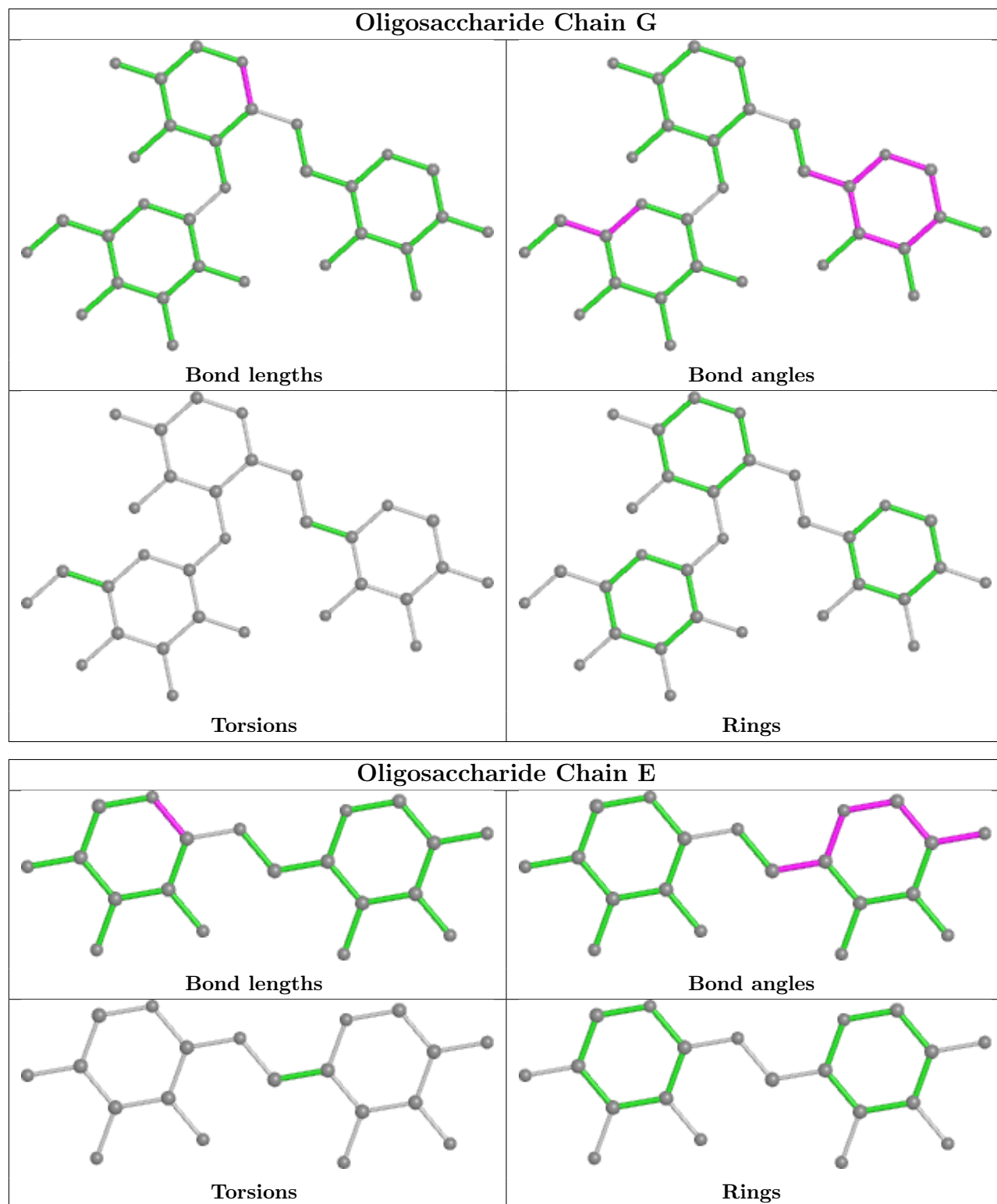
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	BGC	3	0
2	D	1	BGC	6	0
3	E	1	BGC	2	0

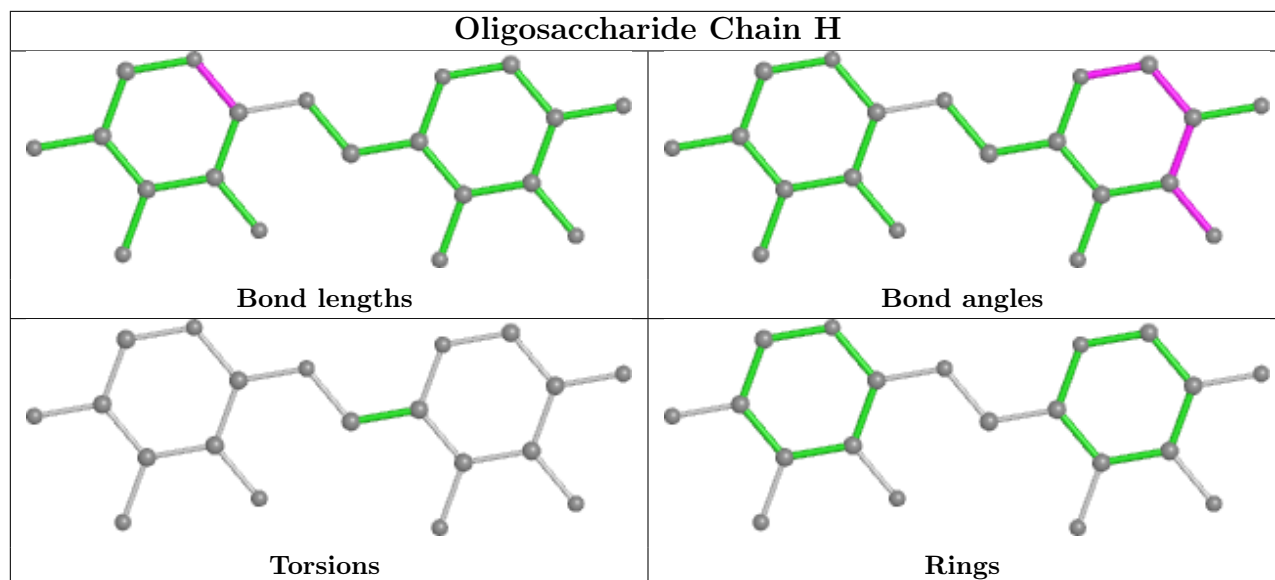
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











4.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
5	GOL	A	302	-	5,5,5	0.52	0	5,5,5	0.57	0
6	BGC	B	303	-	11,11,12	0.46	0	15,15,17	2.44	4 (26%)
5	GOL	B	301	-	5,5,5	0.59	0	5,5,5	0.30	0
6	BGC	A	303	-	11,11,12	0.75	0	15,15,17	2.42	6 (40%)

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
5	GOL	A	302	-	-	2/4/4/4	-
6	BGC	B	303	-	-	0/2/19/22	0/1/1/1
5	GOL	B	301	-	-	4/4/4/4	-
6	BGC	A	303	-	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	303	BGC	C1-C2-C3	5.11	115.94	109.67
6	A	303	BGC	C1-C2-C3	5.08	115.91	109.67
6	B	303	BGC	C1-O5-C5	4.95	118.89	112.19
6	A	303	BGC	C3-C4-C5	3.98	117.33	110.24
6	A	303	BGC	O5-C1-C2	3.86	116.73	110.77

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	302	GOL	C1-C2-C3-O3
5	B	301	GOL	C1-C2-C3-O3
5	B	301	GOL	O2-C2-C3-O3
5	A	302	GOL	O2-C2-C3-O3
5	B	301	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	303	BGC	3	0
6	A	303	BGC	2	0

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 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	266/290 (91%)	-0.76	0 100 100	10, 15, 28, 43	0
1	B	266/290 (91%)	-0.77	0 100 100	9, 15, 28, 44	0
All	All	532/580 (91%)	-0.76	0 100 100	9, 15, 30, 44	0

There are no RSRZ outliers to report.

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

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

5.3 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.

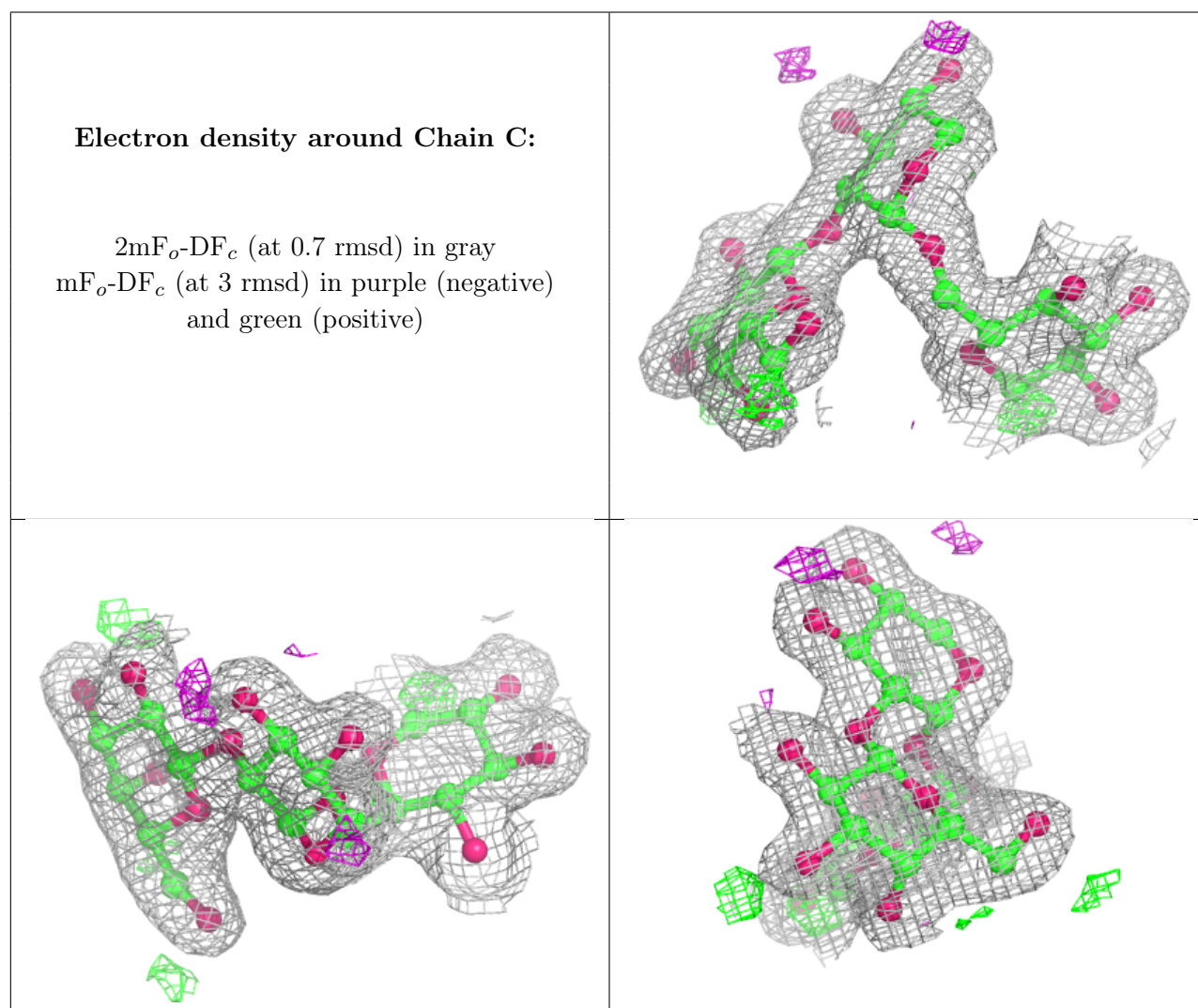
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GAL	G	3	11/12	0.92	0.20	31,34,37,38	0
2	GAL	D	3	11/12	0.93	0.18	28,32,34,36	0
2	GAL	C	3	11/12	0.95	0.12	22,24,26,27	0
2	GAL	F	3	11/12	0.96	0.10	21,23,26,27	0
2	XYS	F	2	9/10	0.97	0.09	14,15,18,18	0
2	BGC	D	1	11/12	0.97	0.09	10,12,13,14	0
2	BGC	G	1	11/12	0.97	0.08	10,11,14,15	0
2	BGC	C	1	11/12	0.97	0.07	8,9,12,14	0
3	BGC	E	1	11/12	0.97	0.08	12,14,16,20	0
3	BGC	H	1	11/12	0.97	0.07	14,15,17,21	0
2	XYS	G	2	9/10	0.98	0.08	19,20,22,26	0

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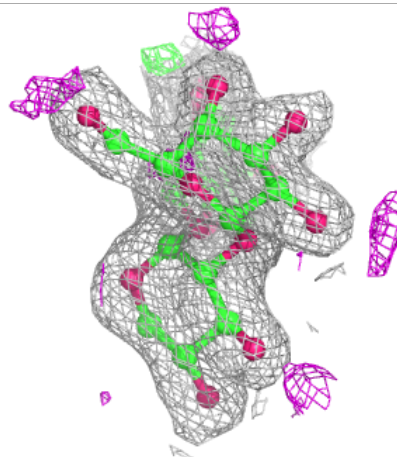
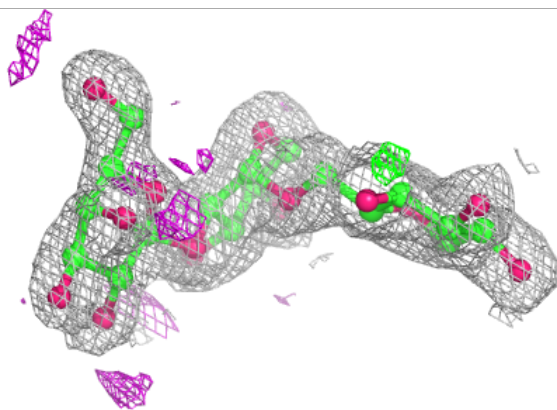
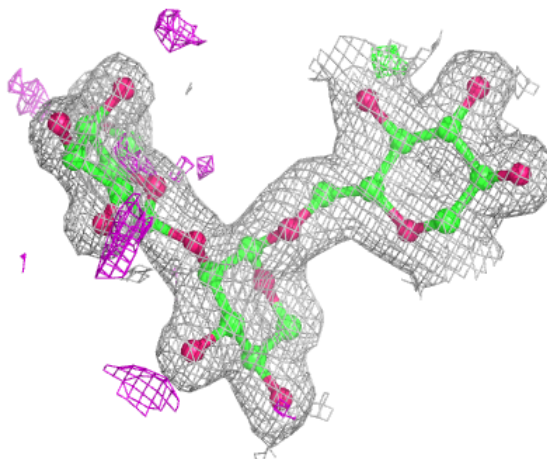
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	XYS	D	2	9/10	0.98	0.07	16,17,20,23	0
2	XYS	C	2	9/10	0.98	0.07	13,15,18,19	0
3	XYS	E	2	9/10	0.98	0.06	13,15,16,17	0
2	BGC	F	1	11/12	0.98	0.07	8,10,12,14	0
3	XYS	H	2	9/10	0.98	0.07	13,14,16,17	0

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.



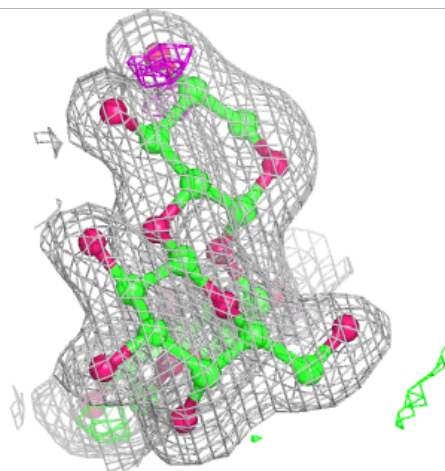
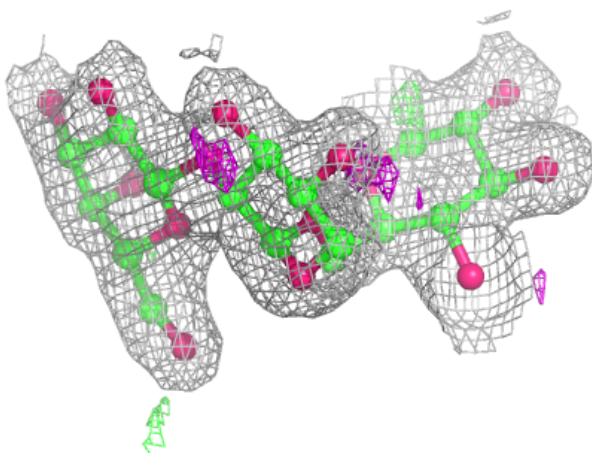
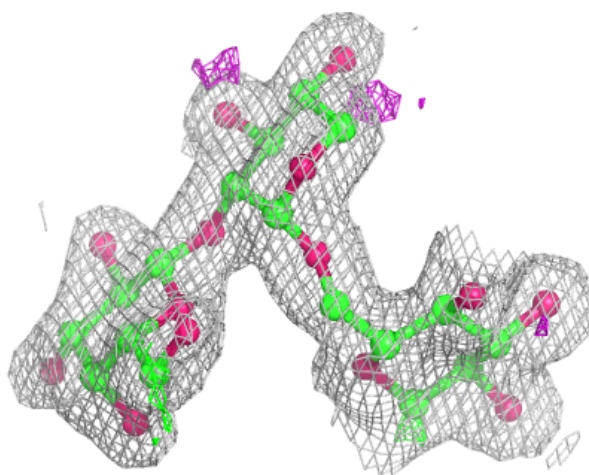
Electron density around Chain D:

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



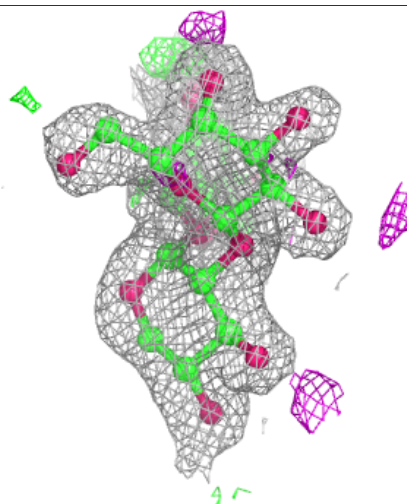
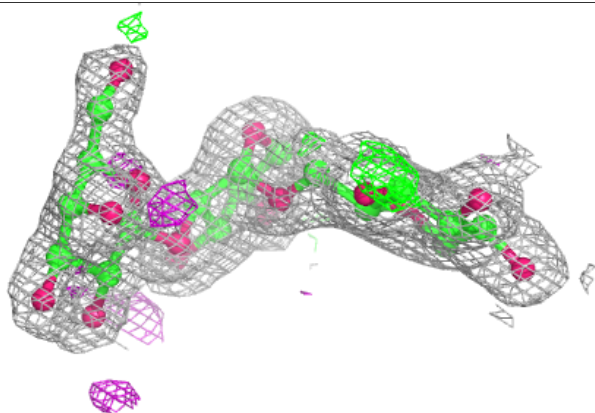
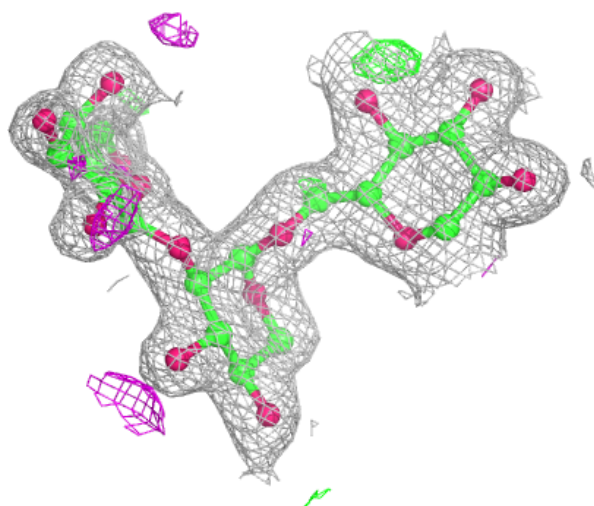
Electron density around Chain F:

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



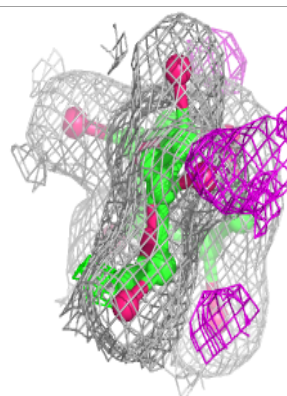
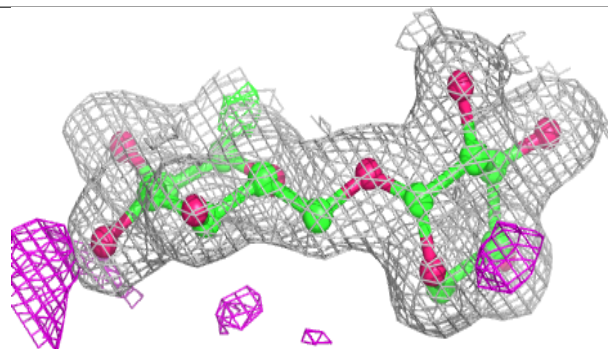
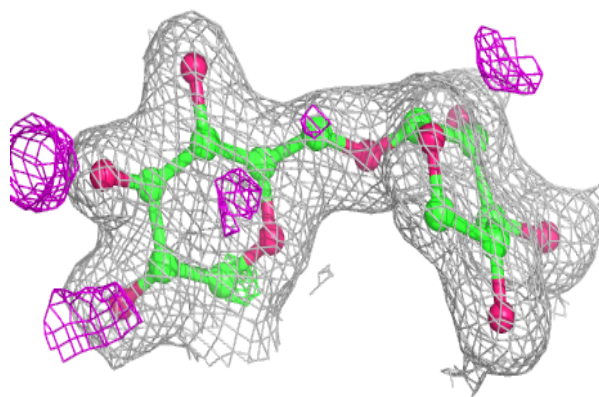
Electron density around Chain G:

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

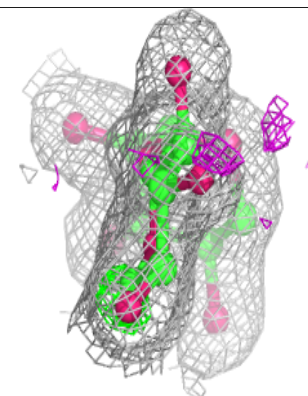
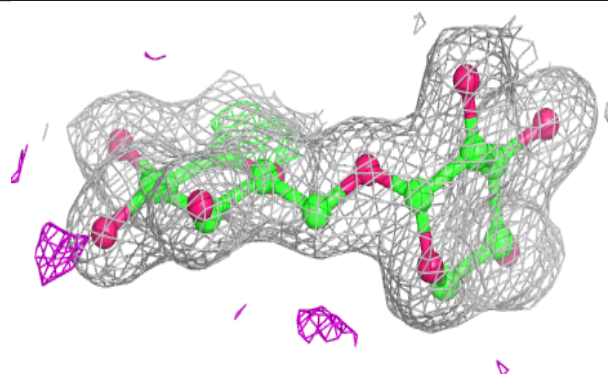
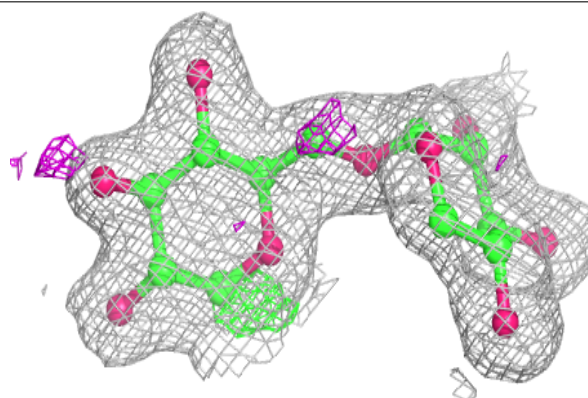


Electron density around Chain E:

$2mF_o-DF_c$ (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)



5.4 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(Å ²)	Q<0.9
5	GOL	B	301	6/6	0.90	0.13	47,48,48,50	0
5	GOL	A	302	6/6	0.93	0.11	39,39,40,40	0
4	ZN	A	301	1/1	0.95	0.04	71,71,71,71	0
6	BGC	A	303	11/12	0.96	0.09	12,18,23,27	0
6	BGC	B	303	11/12	0.96	0.09	11,18,22,26	0
4	ZN	B	302	1/1	0.98	0.05	65,65,65,65	0

5.5 Other polymers [i](#)

There are no such residues in this entry.