



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 12:42 AM UTC

PDB ID : 7AMK / pdb_00007amk
Title : Zebrafish RET Cadherin Like Domains 1 to 4.
Authors : Purkiss, A.G.; McDonald, N.Q.; Goodman, K.M.; Narowtek, A.; Knowles, P.P.
Deposited on : 2020-10-09
Resolution : 2.20 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

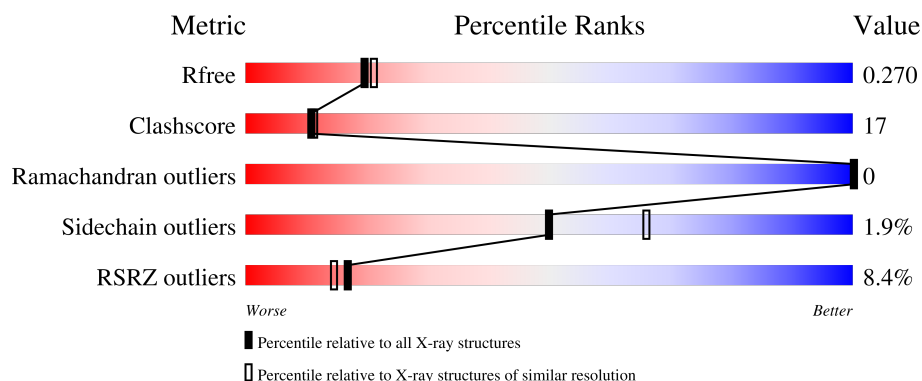
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	480	11% 73% 26% ..
1	B	480	6% 74% 24% ..
2	C	7	14% 57% 29%
3	D	2	100%
3	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
3	I	2	 100%
4	F	3	 100%
4	G	3	 33% 67%
5	H	5	 20% 20% 60%
6	J	4	 25% 75%
7	K	5	 80% 20%

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
12	PEG	A	611	-	-	X	-
12	PEG	A	612	-	-	X	-
12	PEG	A	615	-	-	X	-
12	PEG	B	607	-	-	X	-
12	PEG	B	611	-	-	X	-

2 Entry composition i

There are 14 unique types of molecules in this entry. The entry contains 8199 atoms, of which 13 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.

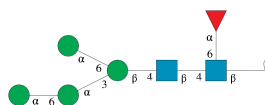
- Molecule 1 is a protein called Proto-oncogene tyrosine-protein kinase receptor Ret.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	2	0
			3680	2351	601	712	16			
1	B	472	Total	C	N	O	S	0	1	0
			3678	2346	604	713	15			

There are 8 discrepancies between the modelled and reference sequences:

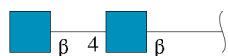
Chain	Residue	Modelled	Actual	Comment	Reference
A	259	GLN	ASN	engineered mutation	UNP A8E7C6
A	308	GLN	ASN	engineered mutation	UNP A8E7C6
A	390	GLN	ASN	engineered mutation	UNP A8E7C6
A	433	GLN	ASN	engineered mutation	UNP A8E7C6
B	259	GLN	ASN	engineered mutation	UNP A8E7C6
B	308	GLN	ASN	engineered mutation	UNP A8E7C6
B	390	GLN	ASN	engineered mutation	UNP A8E7C6
B	433	GLN	ASN	engineered mutation	UNP A8E7C6

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



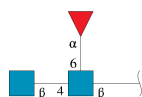
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			82	46	2	34			

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



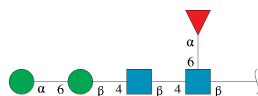
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



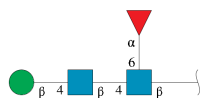
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	3	Total	C	N	O	0	0	0
			38	22	2	14			
4	G	3	Total	C	N	O	0	0	0
			38	22	2	14			

- 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-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



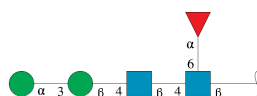
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	5	Total	C	N	O	0	0	0
			60	34	2	24			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	J	4	Total	C	N	O	0	0	0
			49	28	2	19			

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

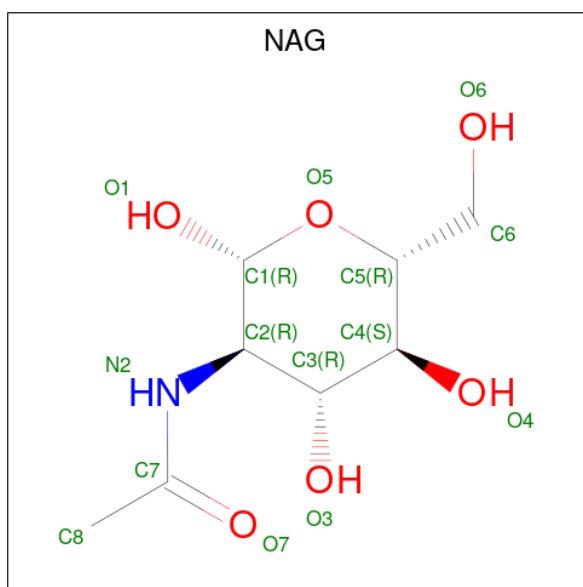


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	K	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

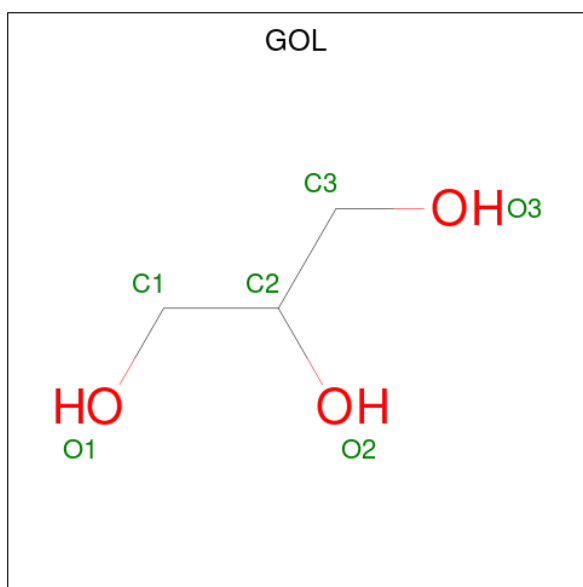
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	3	Total	Ca	0	0
			3	3		
8	B	3	Total	Ca	0	0
			3	3		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



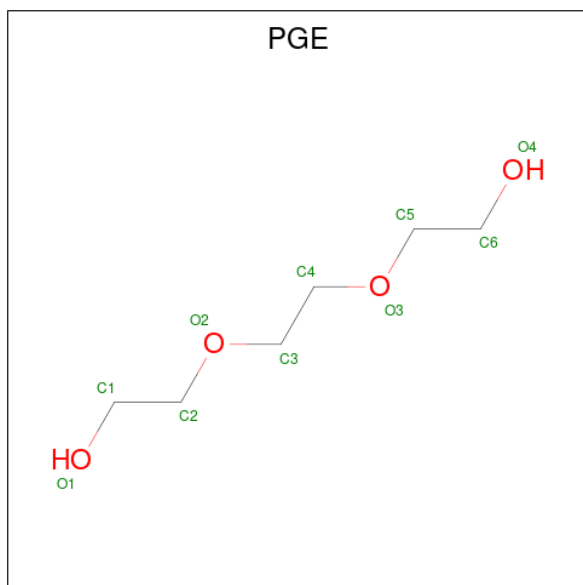
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			6	3	3		

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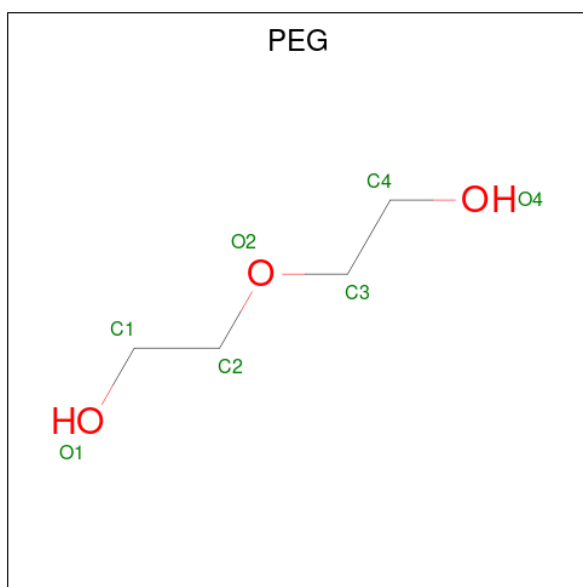
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			6	3	3		
10	B	1	Total	C	O	0	0
			6	3	3		
10	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 11 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



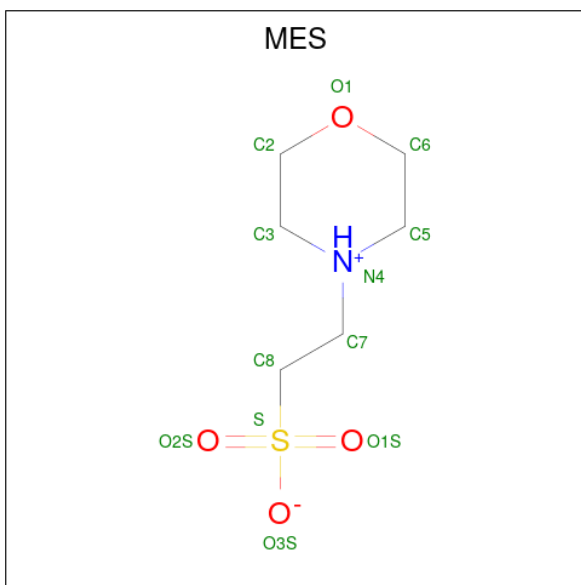
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			10	6	4		
11	A	1	Total	C	O	0	0
			10	6	4		
11	B	1	Total	C	O	0	0
			10	6	4		
11	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 12 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	0	0
			7	4	3		
12	A	1	Total	C	O	0	0
			7	4	3		
12	A	1	Total	C	O	0	0
			7	4	3		
12	A	1	Total	C	O	0	0
			7	4	3		
12	A	1	Total	C	O	0	0
			7	4	3		
12	B	1	Total	C	O	0	0
			7	4	3		
12	B	1	Total	C	O	0	0
			7	4	3		
12	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 13 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	B	1	Total	C	H	N	O	S	
			25	6	13	1	4	1	0

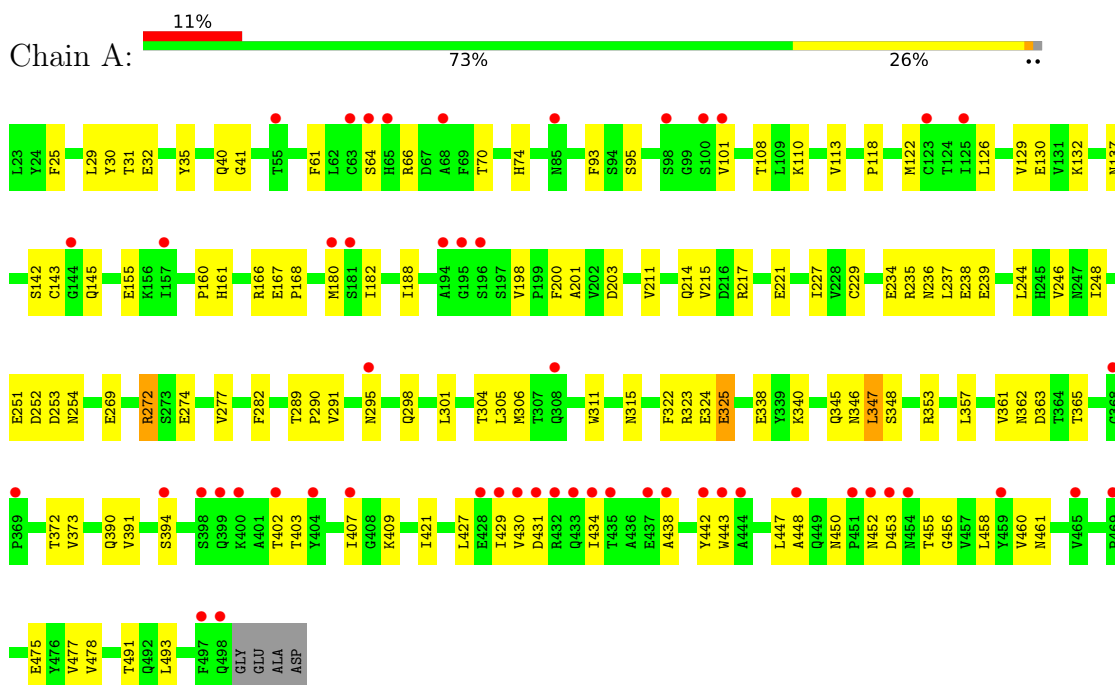
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	102	Total	O		
			102	102	0	0
14	B	117	Total	O		
			117	117	0	0

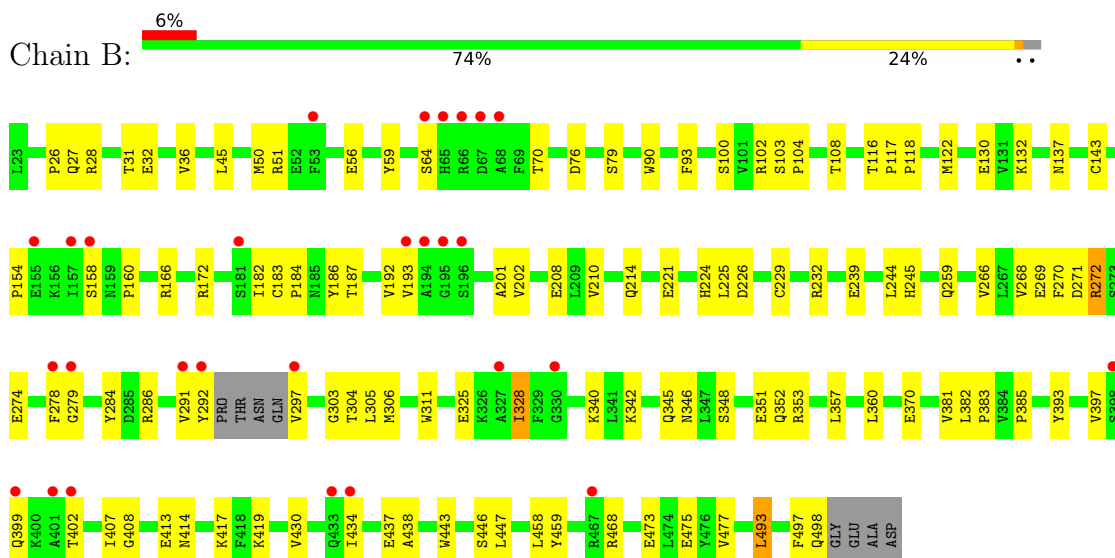
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Proto-oncogene tyrosine-protein kinase receptor Ret



• Molecule 1: Proto-oncogene tyrosine-protein kinase receptor Ret

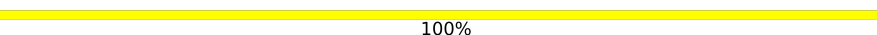


- Molecule 2: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  14% 57% 29%

MAG1
MAG2
MAN3
MAN4
MAN5
MAN6
FUC7

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

Chain D:  100%

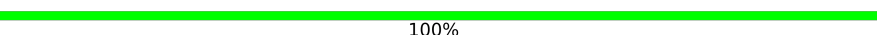
MAG1
MAG2

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

Chain E:  50% 50%

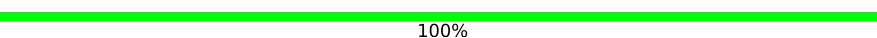
MAG1
MAG2

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

Chain I:  100%

MAG1
MAG2

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

Chain F:  100%

MAG1
MAG2
FUC3

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

Chain G:  33% 67%

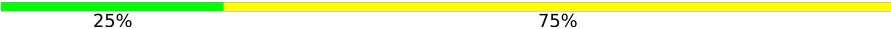
MAG1
MAG2
FUC3

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

Chain H:  20% 20% 60%

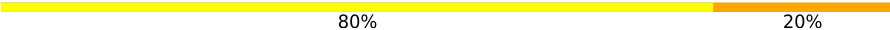
MAG1
MAG2
BMA3
MAN4
FUC5

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

Chain J:  25% 75%

MAG1
MAG2
BMA3
FUC4

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

Chain K:  80% 20%

MAG1
MAG2
BMA3
MAN4
FUC5

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.17Å 70.50Å 105.44Å 105.41° 100.93° 100.25°	Depositor
Resolution (Å)	65.96 – 2.20 65.96 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.3 (65.96-2.20) 91.2 (65.96-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.20Å)	Xtriage
Refinement program	PHENIX dev_3965	Depositor
R, R_{free}	0.225 , 0.269 0.225 , 0.270	Depositor DCC
R_{free} test set	3445 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8199	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.47% 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: MAN, FUC, PGE, BMA, MES, GOL, CA, PEG, NAG

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	0.34	0/3770	0.51	0/5155
1	B	0.36	0/3761	0.53	0/5134
All	All	0.35	0/7531	0.52	0/10289

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3680	0	3466	125	1
1	B	3678	0	3501	109	0
2	C	82	0	70	10	0
3	D	28	0	25	3	0
3	E	28	0	25	5	0
3	I	28	0	25	0	0
4	F	38	0	34	0	0
4	G	38	0	32	4	0
5	H	60	0	52	8	0
6	J	49	0	43	1	0
7	K	60	0	52	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	3	0	0	0	0
8	B	3	0	0	0	0
9	A	28	0	26	1	0
9	B	14	0	13	3	0
10	A	12	0	16	1	0
10	B	12	0	16	1	0
11	A	24	0	32	4	0
11	B	20	0	28	6	0
12	A	42	0	60	34	0
12	B	28	0	40	18	0
13	B	12	13	12	1	0
14	A	102	0	0	6	0
14	B	117	0	0	5	0
All	All	8186	13	7568	258	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 258 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:291:VAL:HA	12:A:612:PEG:H12	1.26	1.17
1:B:413:GLU:HG2	12:B:611:PEG:H32	1.33	1.05
2:C:3:BMA:H3	2:C:4:MAN:H5	1.42	0.98
11:A:614:PGE:H6	11:A:614:PGE:H1	1.51	0.91
2:C:3:BMA:H3	2:C:4:MAN:C5	2.02	0.90

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ARG:NH2	1:A:491:THR:OG1[1_666]	2.14	0.06

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	476/480 (99%)	462 (97%)	14 (3%)	0	100	100
1	B	469/480 (98%)	459 (98%)	10 (2%)	0	100	100
All	All	945/960 (98%)	921 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	398/441 (90%)	391 (98%)	7 (2%)	51	68
1	B	404/441 (92%)	396 (98%)	8 (2%)	48	64
All	All	802/882 (91%)	787 (98%)	15 (2%)	50	66

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	27	GLN
1	B	402	THR
1	B	32	GLU
1	B	493	LEU
1	B	328	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	74	HIS
1	B	214	GLN
1	B	414	ASN
1	A	224	HIS

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Mol	Chain	Res	Type
1	A	159	ASN

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 ⓘ

33 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	0.40	0	17,19,21	0.45	0
2	NAG	C	2	2	14,14,15	0.32	0	17,19,21	0.47	0
2	BMA	C	3	2	11,11,12	0.85	0	15,15,17	0.79	0
2	MAN	C	4	2	11,11,12	1.18	1 (9%)	15,15,17	1.53	2 (13%)
2	MAN	C	5	2	11,11,12	0.95	1 (9%)	15,15,17	0.99	0
2	MAN	C	6	2	11,11,12	0.93	0	15,15,17	1.12	1 (6%)
2	FUC	C	7	2	10,10,11	0.82	0	14,14,16	0.87	0
3	NAG	D	1	1,3	14,14,15	0.27	0	17,19,21	0.62	0
3	NAG	D	2	3	14,14,15	0.47	0	17,19,21	0.53	0
3	NAG	E	1	1,3	14,14,15	0.34	0	17,19,21	0.66	0
3	NAG	E	2	3	14,14,15	0.21	0	17,19,21	0.59	0
4	NAG	F	1	1,4	14,14,15	0.42	0	17,19,21	0.45	0
4	NAG	F	2	4	14,14,15	0.28	0	17,19,21	0.35	0
4	FUC	F	3	4	10,10,11	0.85	0	14,14,16	0.80	0
4	NAG	G	1	1,4	14,14,15	0.27	0	17,19,21	0.53	0
4	NAG	G	2	4	14,14,15	0.20	0	17,19,21	0.62	1 (5%)
4	FUC	G	3	4	10,10,11	1.06	0	14,14,16	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	H	1	1,5	14,14,15	0.57	0	17,19,21	0.90	1 (5%)
5	NAG	H	2	5	14,14,15	0.17	0	17,19,21	0.81	1 (5%)
5	BMA	H	3	5	11,11,12	1.10	1 (9%)	15,15,17	1.03	0
5	MAN	H	4	5	11,11,12	0.96	0	15,15,17	0.82	0
5	FUC	H	5	5	10,10,11	1.88	3 (30%)	14,14,16	1.32	2 (14%)
3	NAG	I	1	1,3	14,14,15	0.63	0	17,19,21	0.60	0
3	NAG	I	2	3	14,14,15	0.36	0	17,19,21	0.51	0
6	NAG	J	1	1,6	14,14,15	0.28	0	17,19,21	0.54	0
6	NAG	J	2	6	14,14,15	0.29	0	17,19,21	0.50	0
6	BMA	J	3	6	11,11,12	0.91	0	15,15,17	0.84	0
6	FUC	J	4	6	10,10,11	1.38	2 (20%)	14,14,16	1.16	1 (7%)
7	NAG	K	1	1,7	14,14,15	0.25	0	17,19,21	0.71	1 (5%)
7	NAG	K	2	7	14,14,15	0.27	0	17,19,21	0.53	0
7	BMA	K	3	7	11,11,12	0.70	0	15,15,17	0.79	1 (6%)
7	MAN	K	4	7	11,11,12	1.33	1 (9%)	15,15,17	1.24	2 (13%)
7	FUC	K	5	7	10,10,11	1.63	2 (20%)	14,14,16	0.92	0

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

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

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

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	5	FUC	C1-C2	3.86	1.61	1.52
7	K	5	FUC	C2-C3	3.50	1.57	1.52
5	H	5	FUC	C2-C3	2.96	1.57	1.52
7	K	5	FUC	O5-C5	2.48	1.48	1.43
6	J	4	FUC	C2-C3	2.44	1.56	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	MAN	C1-O5-C5	4.99	118.88	112.19
2	C	6	MAN	O2-C2-C3	-3.62	102.64	110.15
6	J	4	FUC	O5-C5-C4	2.89	114.75	109.55
5	H	1	NAG	C1-O5-C5	2.88	116.04	112.19
7	K	4	MAN	C1-O5-C5	2.81	115.95	112.19

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

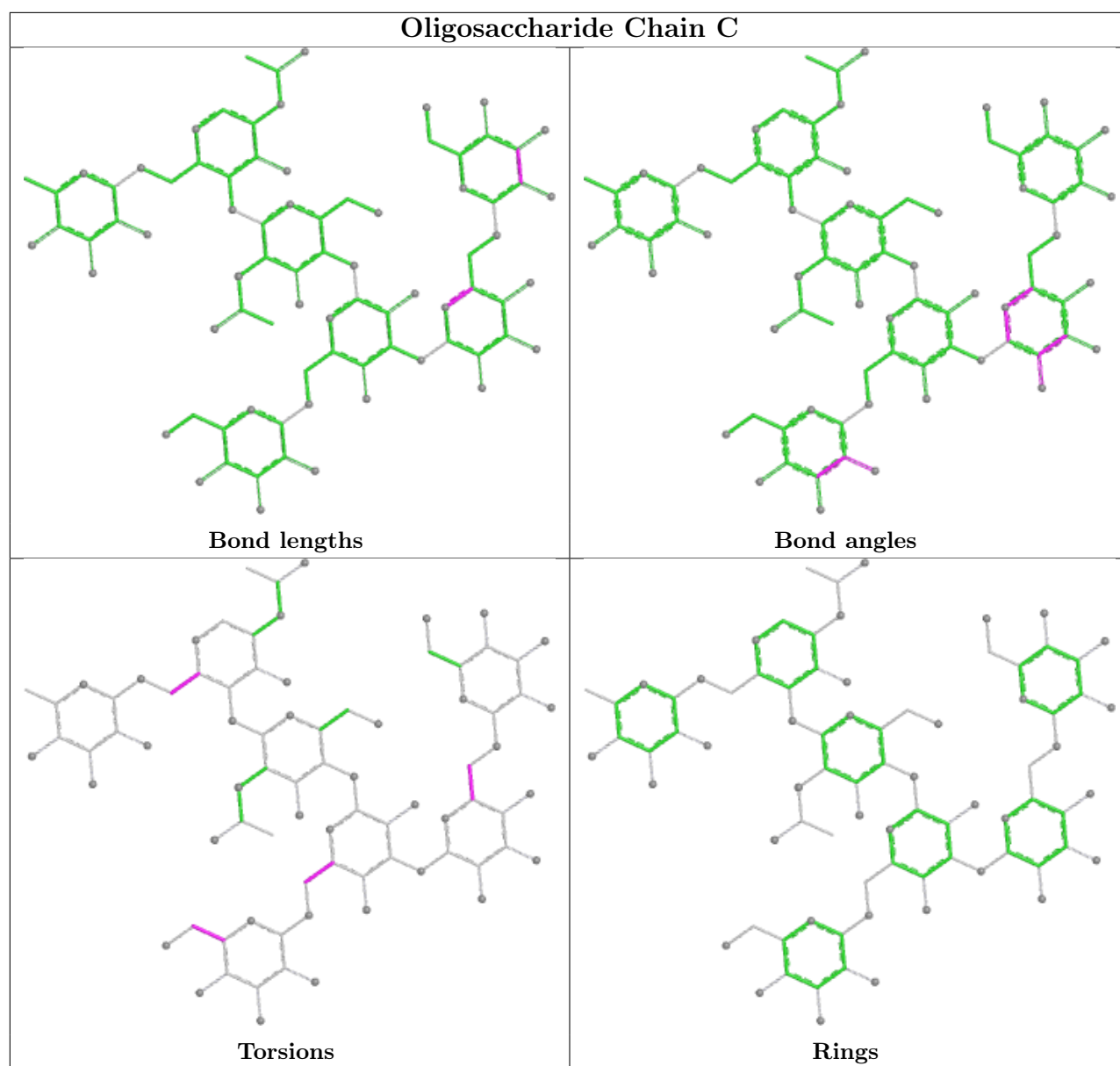
Mol	Chain	Res	Type	Atoms
3	D	1	NAG	C3-C2-N2-C7
5	H	2	NAG	C3-C2-N2-C7
2	C	6	MAN	O5-C5-C6-O6
6	J	3	BMA	O5-C5-C6-O6
2	C	4	MAN	O5-C5-C6-O6

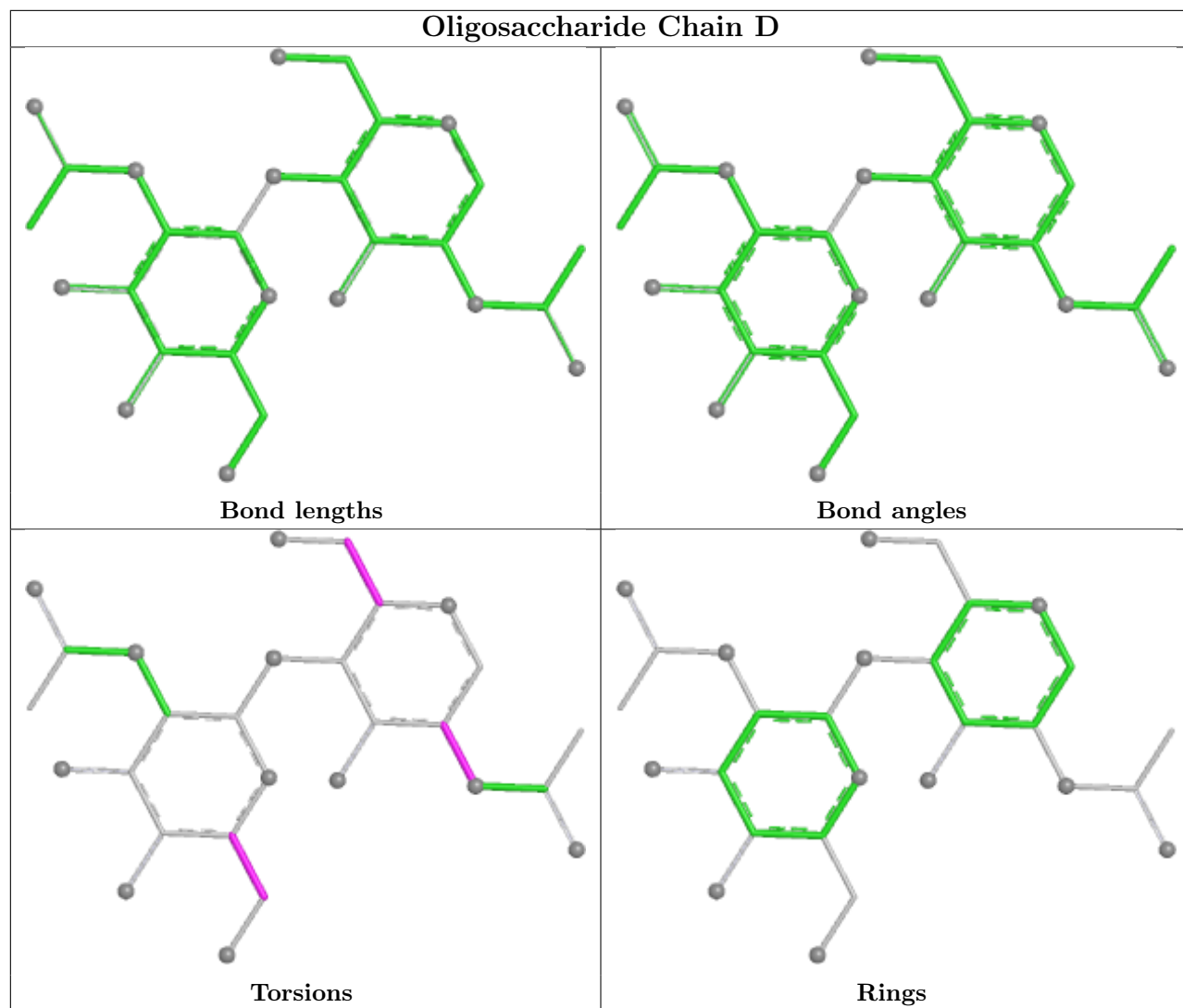
There are no ring outliers.

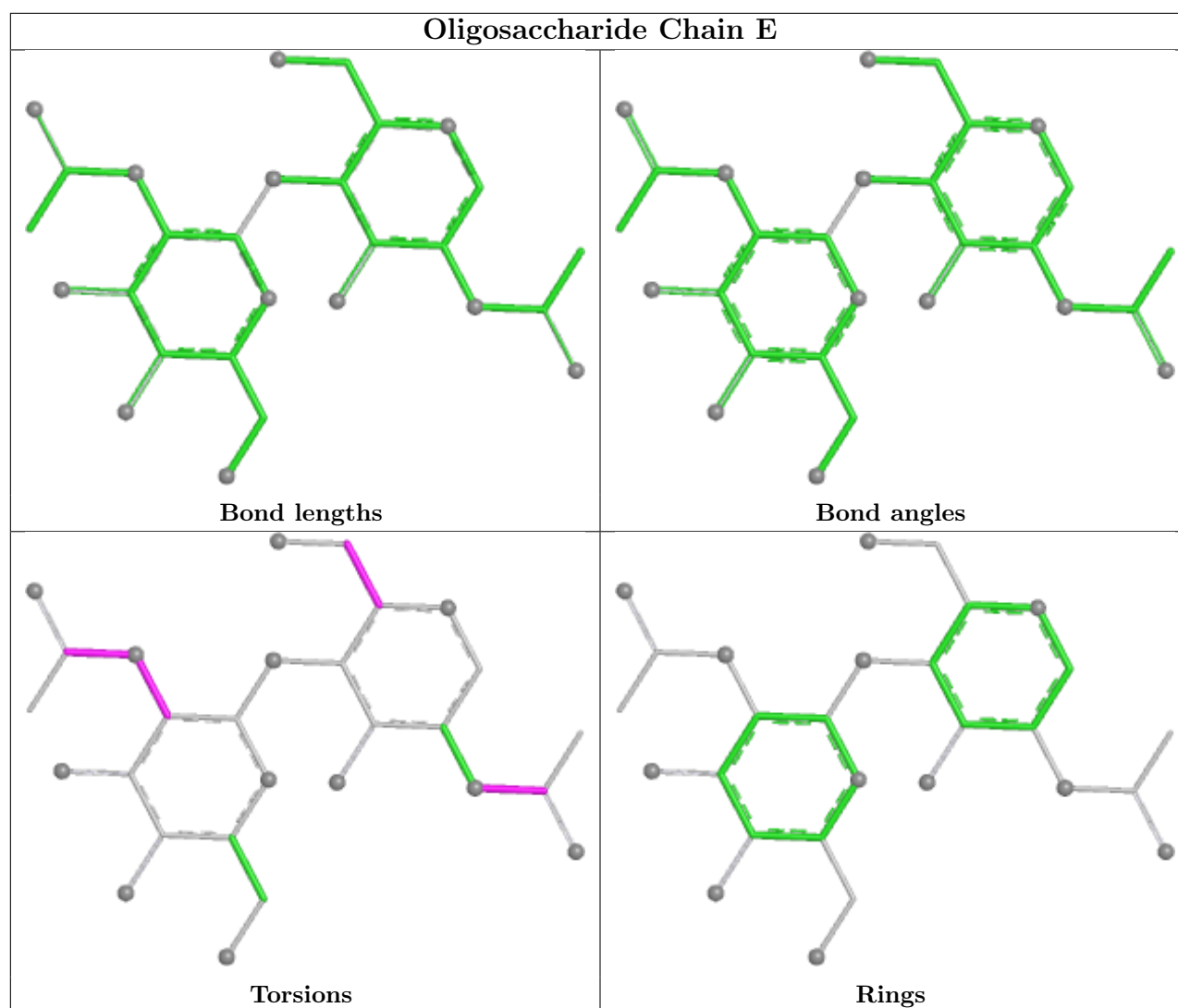
16 monomers are involved in 34 short contacts:

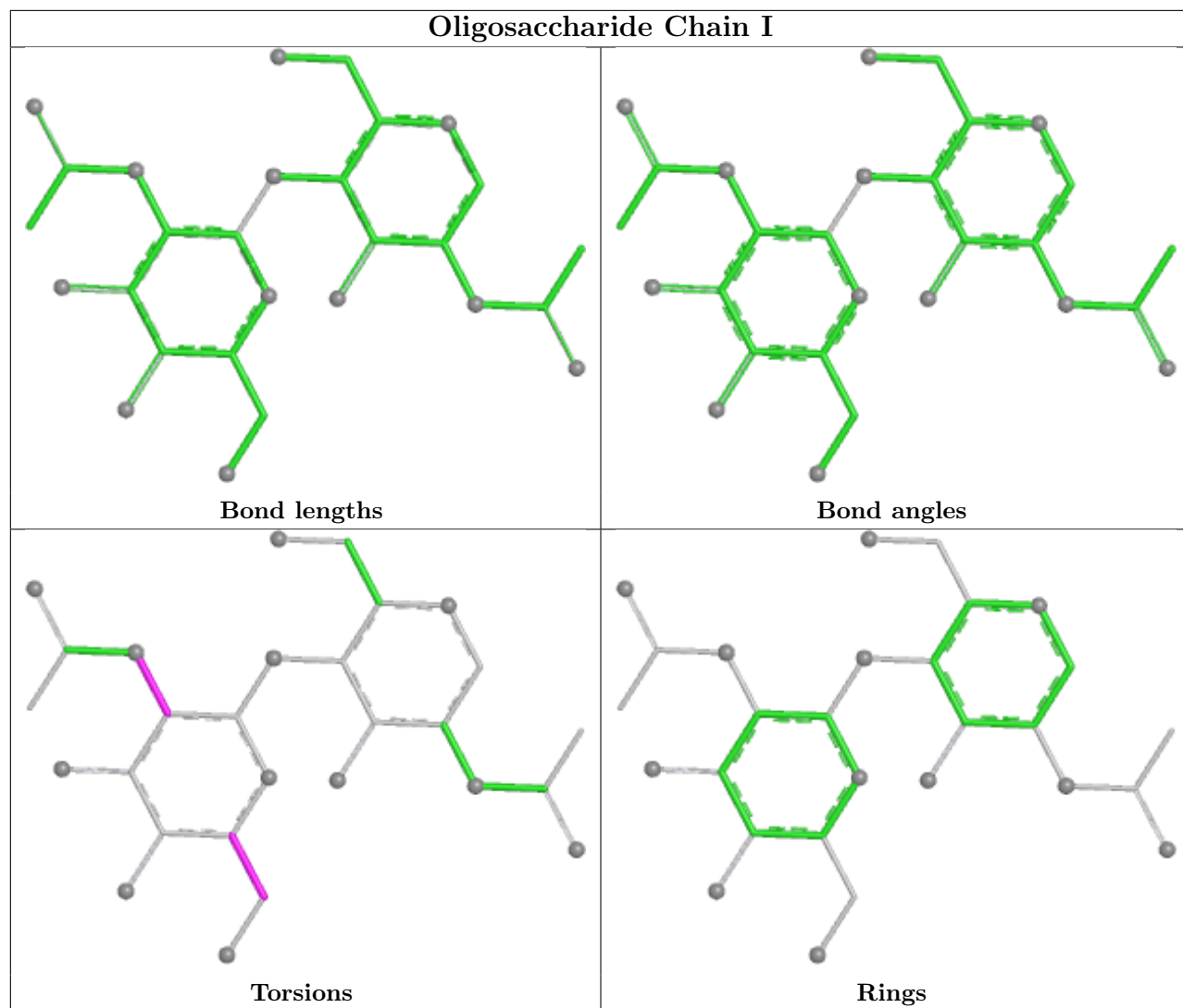
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	5	0
3	E	2	NAG	5	0
7	K	1	NAG	2	0
5	H	1	NAG	6	0
5	H	2	NAG	3	0
2	C	3	BMA	5	0
6	J	2	NAG	1	0
2	C	6	MAN	3	0
2	C	1	NAG	4	0
2	C	4	MAN	3	0
6	J	3	BMA	1	0
5	H	5	FUC	4	0
3	D	2	NAG	1	0
3	D	1	NAG	3	0
7	K	2	NAG	1	0
4	G	1	NAG	4	0

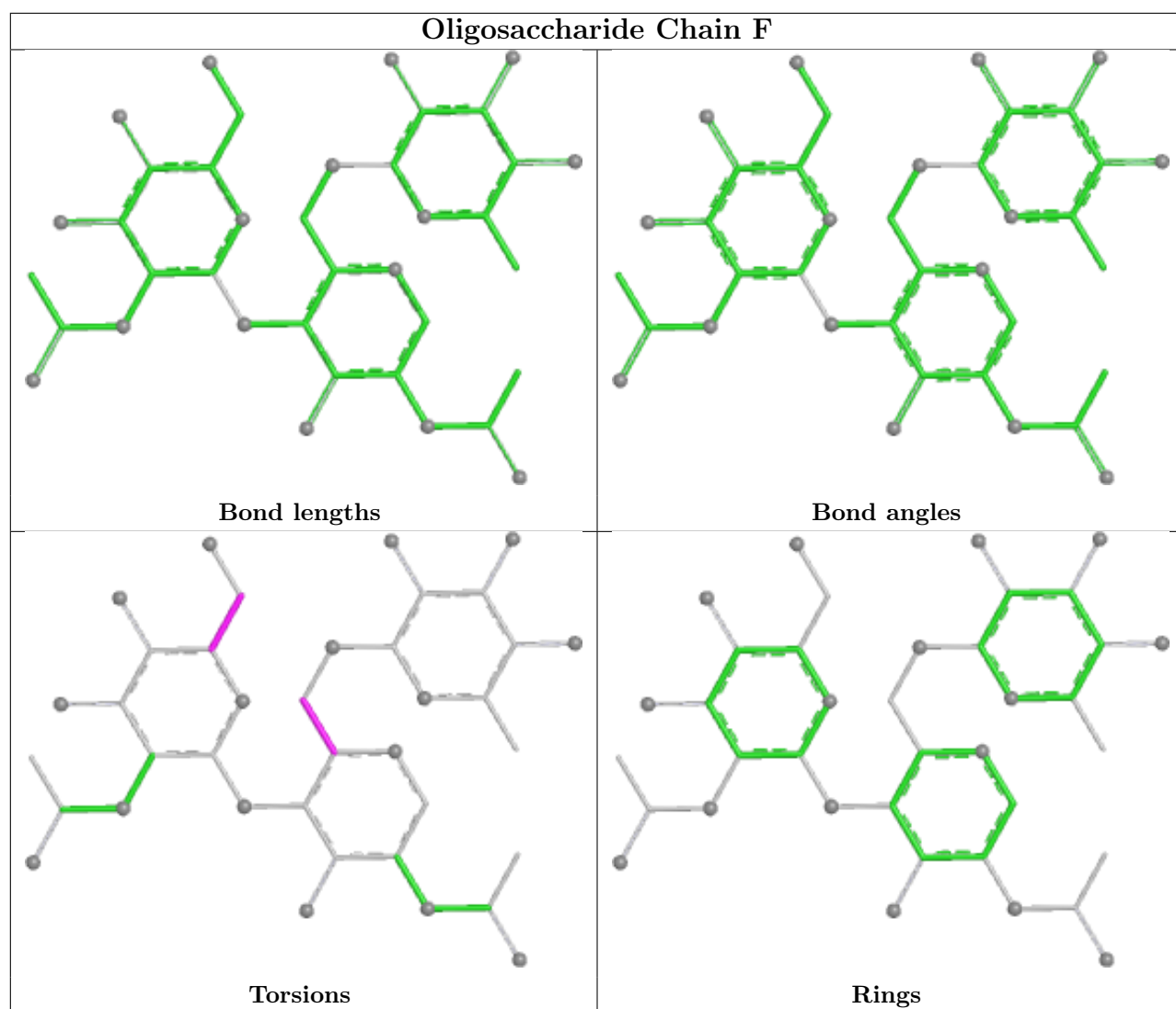
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

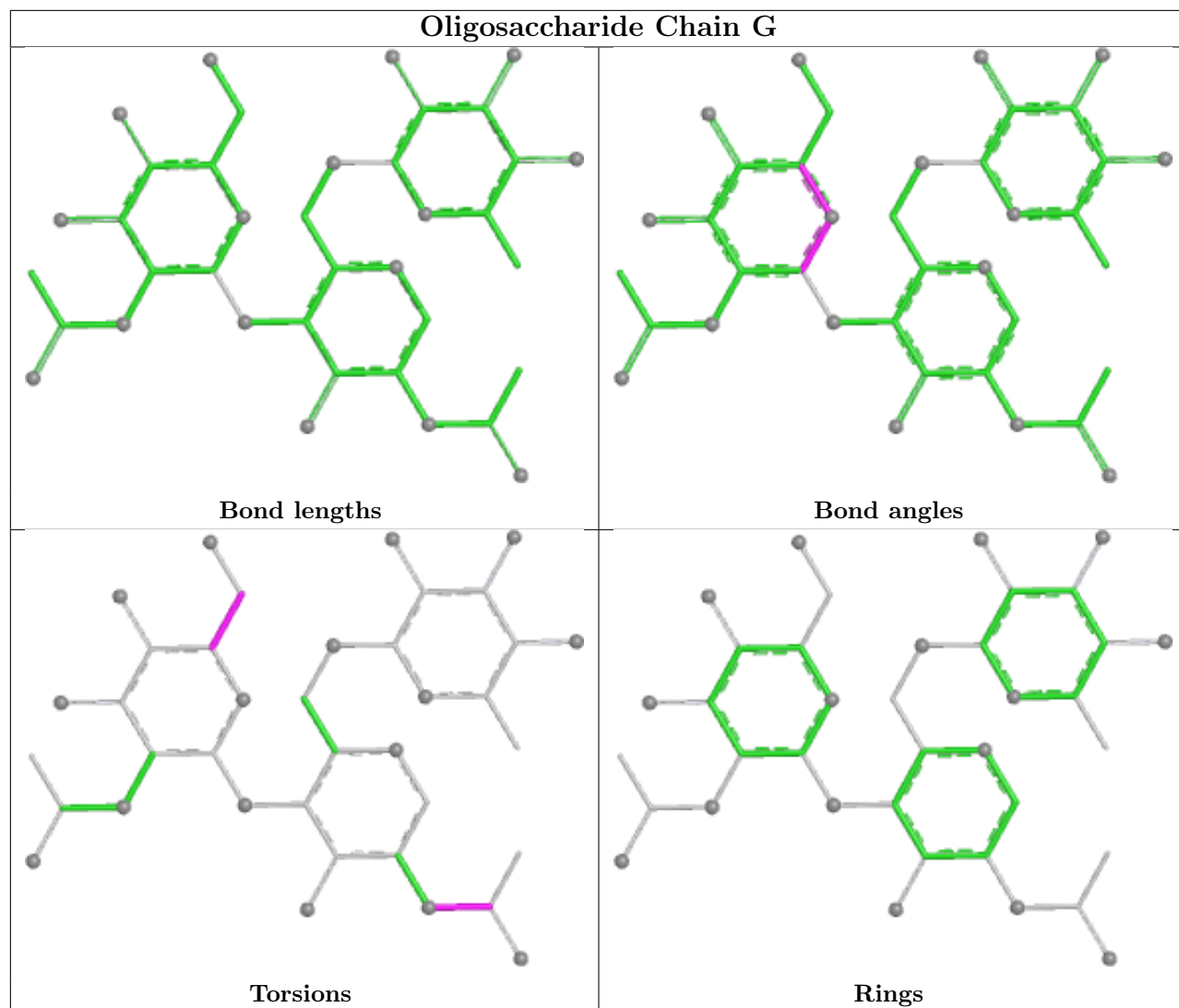


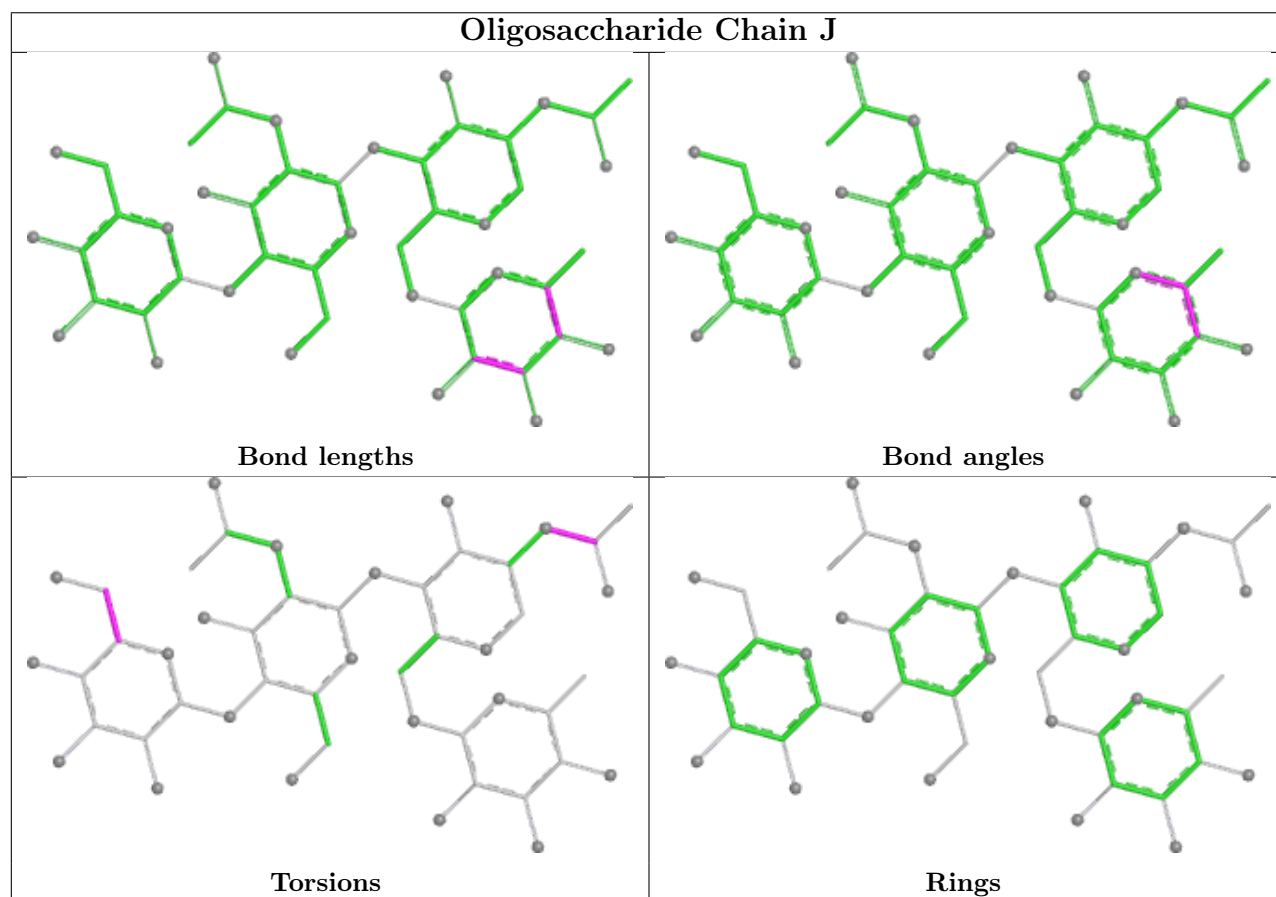
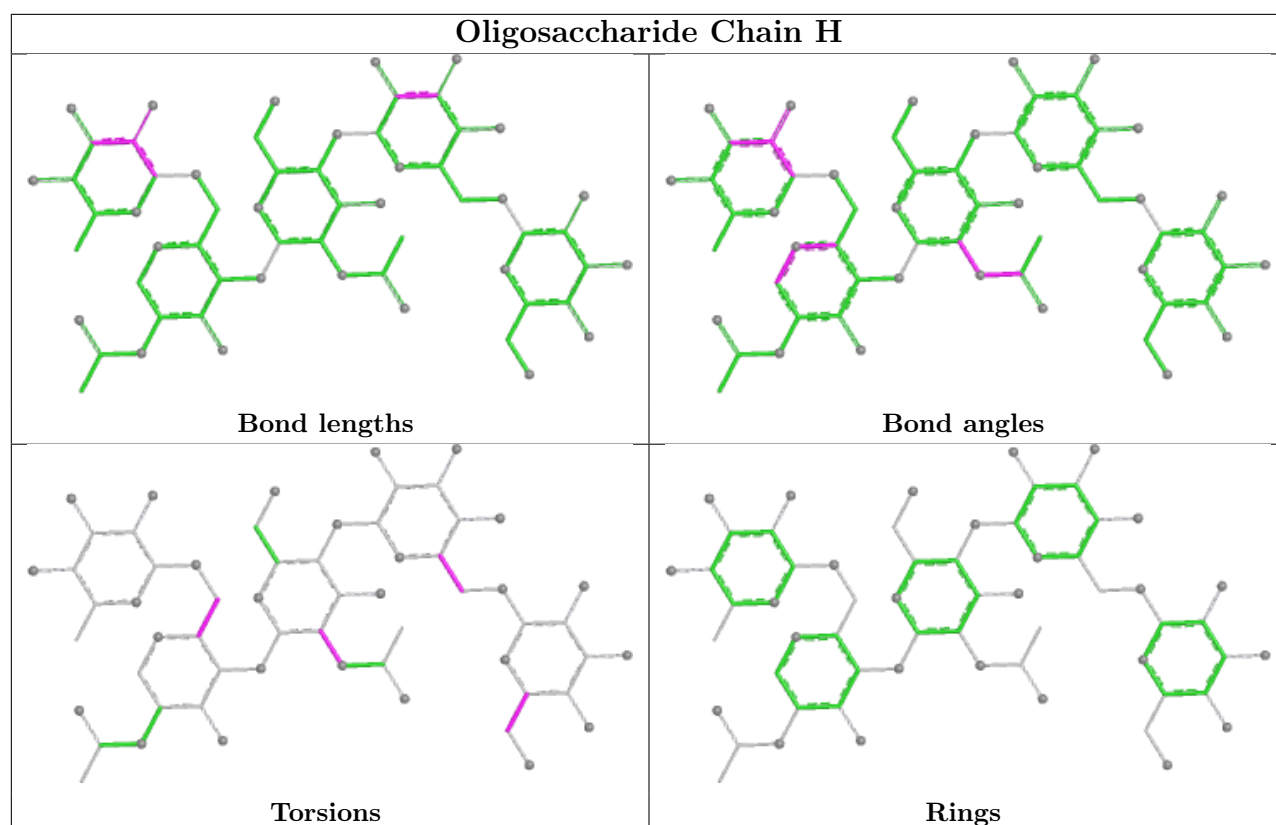


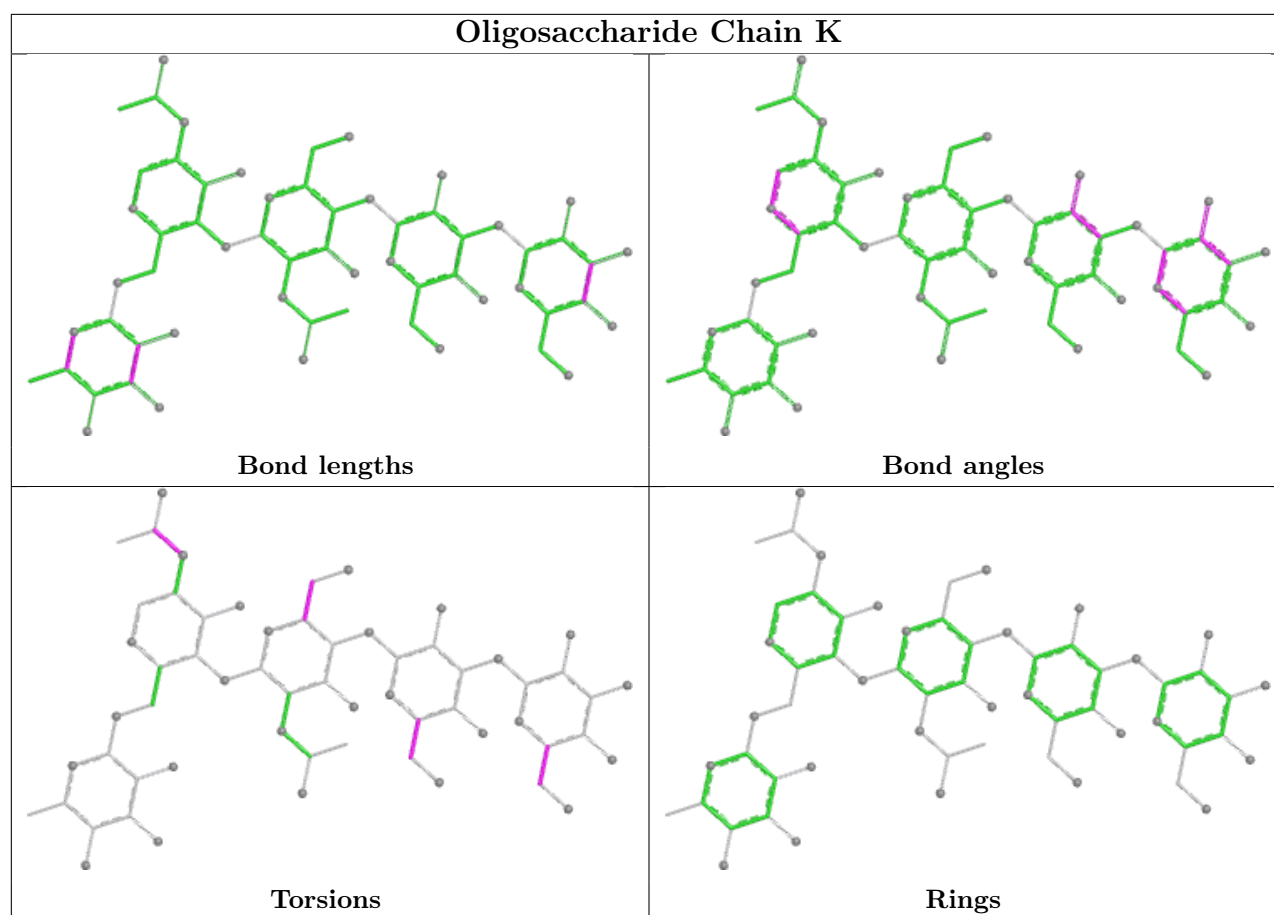












5.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 6 are monoatomic - leaving 23 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	$\# Z > 2$
11	PGE	B	609	-	9,9,9	0.65	0	8,8,8	0.30	0
12	PEG	B	607	-	6,6,6	0.72	0	5,5,5	0.59	0
12	PEG	A	616	-	6,6,6	0.48	0	5,5,5	0.35	0
10	GOL	B	605	-	5,5,5	0.88	0	5,5,5	1.06	0
11	PGE	A	614	-	9,9,9	0.62	0	8,8,8	0.25	0
12	PEG	A	611	-	6,6,6	0.56	0	5,5,5	0.26	0
11	PGE	A	610	-	9,9,9	0.61	0	8,8,8	0.31	0
11	PGE	A	608	-	3,3,9	0.58	0	2,2,8	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	A	604	1	14,14,15	0.34	0	17,19,21	0.68	1 (5%)
12	PEG	A	609	-	6,6,6	0.52	0	5,5,5	0.34	0
13	MES	B	613	-	12,12,12	2.05	1 (8%)	15,16,16	2.00	5 (33%)
10	GOL	B	606	-	5,5,5	1.05	0	5,5,5	0.89	0
12	PEG	B	612	-	6,6,6	0.53	0	5,5,5	0.22	0
12	PEG	A	613	-	6,6,6	0.63	0	5,5,5	0.46	0
11	PGE	B	610	-	9,9,9	0.57	0	8,8,8	0.37	0
12	PEG	B	611	-	6,6,6	0.43	0	5,5,5	0.61	0
10	GOL	A	607	-	5,5,5	1.12	0	5,5,5	0.92	0
12	PEG	A	615	-	6,6,6	0.51	0	5,5,5	0.33	0
9	NAG	B	604	1	14,14,15	0.37	0	17,19,21	0.61	0
12	PEG	A	612	-	6,6,6	0.48	0	5,5,5	0.60	0
12	PEG	B	608	-	6,6,6	0.50	0	5,5,5	0.42	0
10	GOL	A	606	-	5,5,5	1.03	0	5,5,5	0.97	0
9	NAG	A	605	1	14,14,15	0.45	0	17,19,21	0.44	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
11	PGE	B	609	-	-	4/7/7/7	-
12	PEG	B	607	-	-	2/4/4/4	-
12	PEG	A	616	-	-	1/4/4/4	-
10	GOL	B	605	-	-	3/4/4/4	-
11	PGE	A	614	-	-	6/7/7/7	-
12	PEG	A	611	-	-	1/4/4/4	-
11	PGE	A	610	-	-	1/7/7/7	-
11	PGE	A	608	-	-	1/1/1/7	-
9	NAG	A	604	1	-	2/6/23/26	0/1/1/1
12	PEG	A	609	-	-	2/4/4/4	-
13	MES	B	613	-	-	1/6/14/14	0/1/1/1
10	GOL	B	606	-	-	4/4/4/4	-
12	PEG	B	612	-	-	1/4/4/4	-
12	PEG	A	613	-	-	3/4/4/4	-
11	PGE	B	610	-	-	3/7/7/7	-
12	PEG	B	611	-	-	3/4/4/4	-
10	GOL	A	607	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	PEG	A	615	-	-	2/4/4/4	-
9	NAG	B	604	1	-	1/6/23/26	0/1/1/1
12	PEG	A	612	-	-	2/4/4/4	-
12	PEG	B	608	-	-	1/4/4/4	-
10	GOL	A	606	-	-	2/4/4/4	-
9	NAG	A	605	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	B	613	MES	C8-S	-6.76	1.68	1.77

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	613	MES	O1S-S-C8	4.00	112.77	106.73
13	B	613	MES	C6-C5-N4	-3.65	104.57	110.12
13	B	613	MES	C5-N4-C3	3.24	115.81	108.84
13	B	613	MES	O3S-S-C8	2.38	110.66	106.00
13	B	613	MES	C7-N4-C5	2.14	116.94	111.24

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	B	610	PGE	C4-C3-O2-C2
11	B	610	PGE	O3-C5-C6-O4
12	B	612	PEG	O2-C3-C4-O4
11	A	614	PGE	O2-C3-C4-O3
10	A	607	GOL	O1-C1-C2-C3

There are no ring outliers.

16 monomers are involved in 68 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	B	609	PGE	1	0
12	B	607	PEG	4	0
12	A	616	PEG	3	0
11	A	614	PGE	3	0
12	A	611	PEG	10	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	610	PGE	1	0
9	A	604	NAG	1	0
13	B	613	MES	1	0
10	B	606	GOL	1	0
12	A	613	PEG	3	0
11	B	610	PGE	5	0
12	B	611	PEG	14	0
12	A	615	PEG	5	0
9	B	604	NAG	3	0
12	A	612	PEG	13	0
10	A	606	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	476/480 (99%)	0.68	52 (10%) 10 8	13, 38, 69, 99	3 (0%)
1	B	472/480 (98%)	0.41	28 (5%) 28 25	12, 34, 57, 84	1 (0%)
All	All	948/960 (98%)	0.55	80 (8%) 17 14	12, 36, 62, 99	4 (0%)

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	430	VAL	5.4
1	A	431	ASP	4.7
1	A	438	ALA	4.6
1	A	194	ALA	4.1
1	A	157	ILE	3.9

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
6	BMA	J	3	11/12	0.30	0.20	92,104,107,108	0
2	MAN	C	4	11/12	0.34	0.24	89,106,111,114	0
3	NAG	D	2	14/15	0.46	0.17	95,113,117,120	0
3	NAG	D	1	14/15	0.53	0.19	102,112,119,123	0
5	MAN	H	4	11/12	0.58	0.18	73,85,92,93	0

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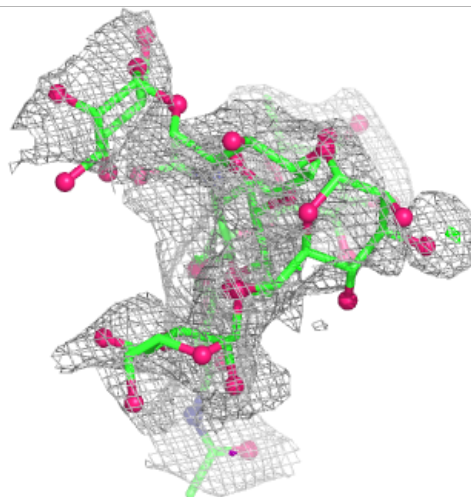
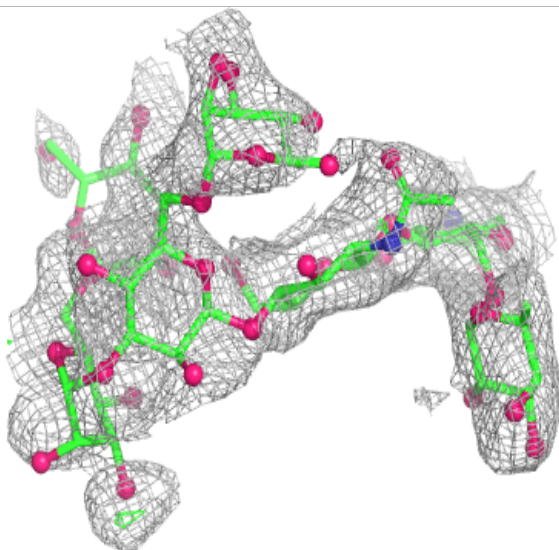
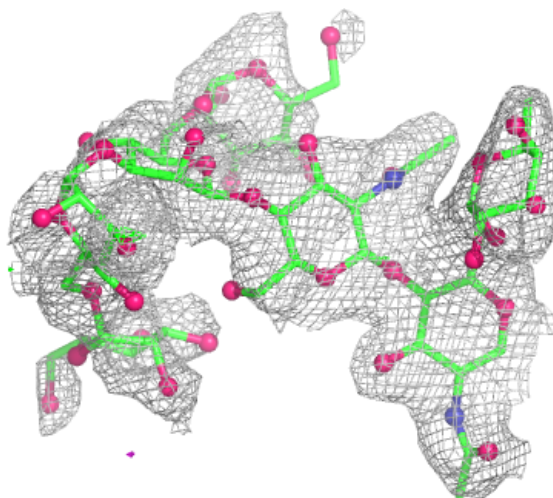
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MAN	C	5	11/12	0.60	0.23	82,94,103,111	0
4	FUC	G	3	10/11	0.62	0.19	90,94,100,103	0
5	BMA	H	3	11/12	0.63	0.20	64,81,89,92	0
5	NAG	H	2	14/15	0.66	0.19	68,79,87,91	0
4	NAG	F	2	14/15	0.66	0.16	82,90,98,99	0
3	NAG	E	2	14/15	0.67	0.18	54,69,79,79	0
2	BMA	C	3	11/12	0.68	0.16	88,97,104,107	0
6	NAG	J	2	14/15	0.71	0.16	74,88,98,102	0
3	NAG	I	2	14/15	0.72	0.18	68,79,85,92	0
2	MAN	C	6	11/12	0.72	0.22	89,95,101,107	0
4	NAG	G	2	14/15	0.73	0.19	66,82,89,90	0
7	MAN	K	4	11/12	0.73	0.18	50,60,66,68	0
4	NAG	F	1	14/15	0.74	0.14	65,73,86,87	0
7	FUC	K	5	10/11	0.74	0.18	45,51,60,67	0
7	BMA	K	3	11/12	0.76	0.14	54,57,62,63	0
2	FUC	C	7	10/11	0.77	0.17	63,73,80,87	0
4	NAG	G	1	14/15	0.78	0.15	58,68,77,81	0
3	NAG	E	1	14/15	0.81	0.14	34,47,59,63	0
2	NAG	C	2	14/15	0.81	0.14	62,73,86,91	0
4	FUC	F	3	10/11	0.82	0.14	50,68,74,76	0
6	NAG	J	1	14/15	0.84	0.11	47,59,67,76	0
5	NAG	H	1	14/15	0.84	0.14	40,51,59,61	0
3	NAG	I	1	14/15	0.85	0.14	42,53,68,70	0
7	NAG	K	1	14/15	0.86	0.12	30,39,51,52	0
6	FUC	J	4	10/11	0.86	0.13	49,57,62,66	0
7	NAG	K	2	14/15	0.88	0.12	39,44,59,60	0
2	NAG	C	1	14/15	0.88	0.11	45,55,62,69	0
5	FUC	H	5	10/11	0.90	0.12	38,48,55,55	0

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

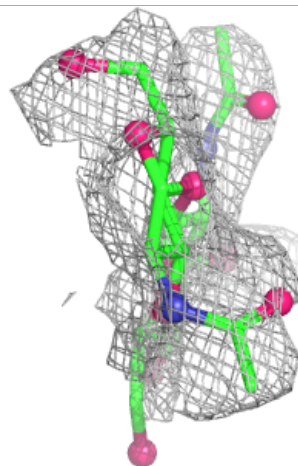
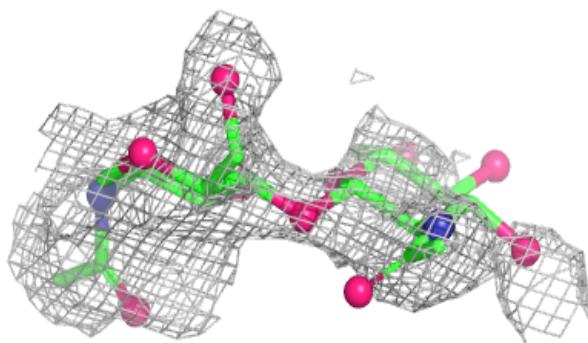
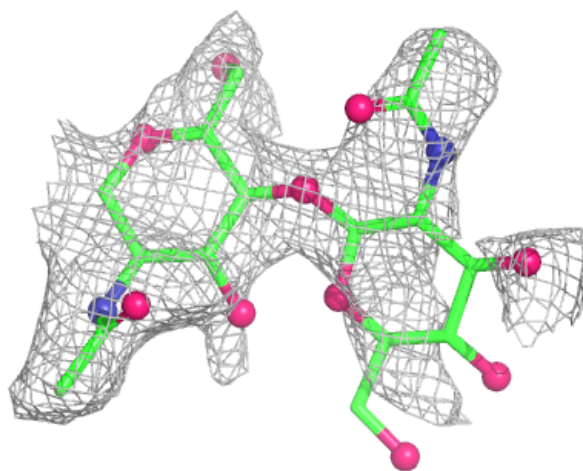
Electron density around Chain C:

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



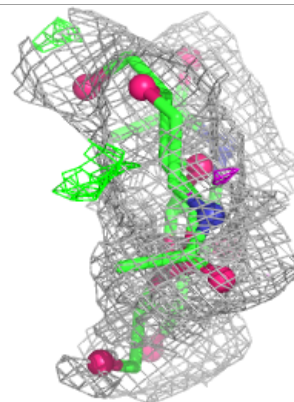
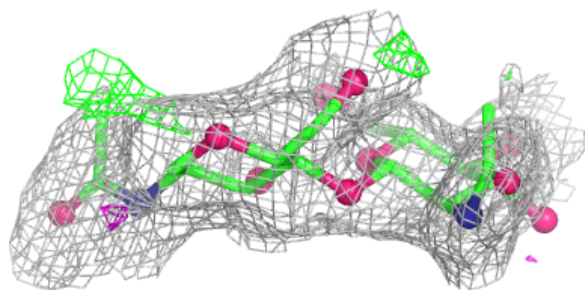
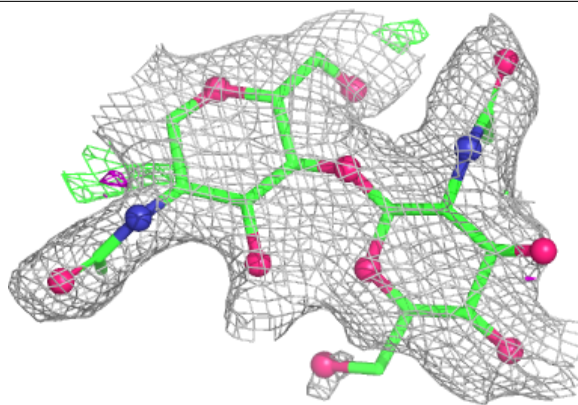
Electron density around Chain D:

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

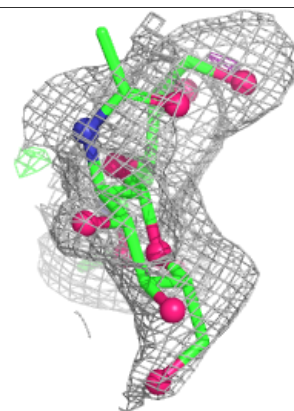
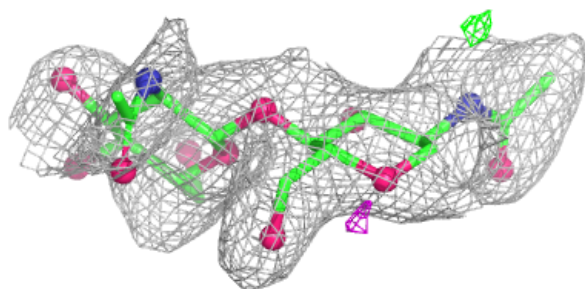
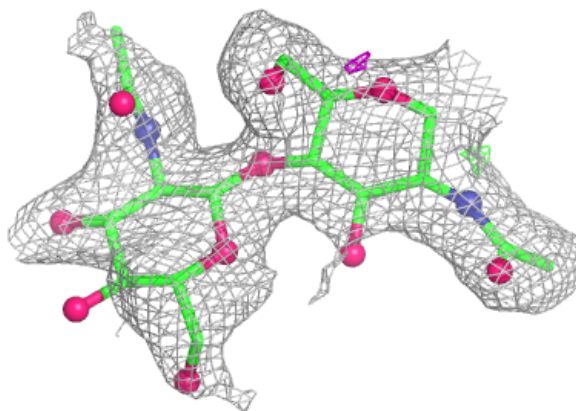


Electron density around Chain E:

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

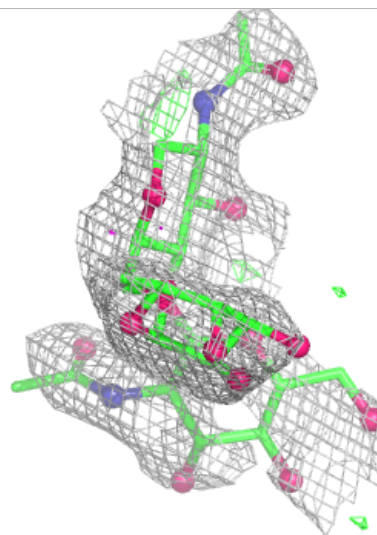
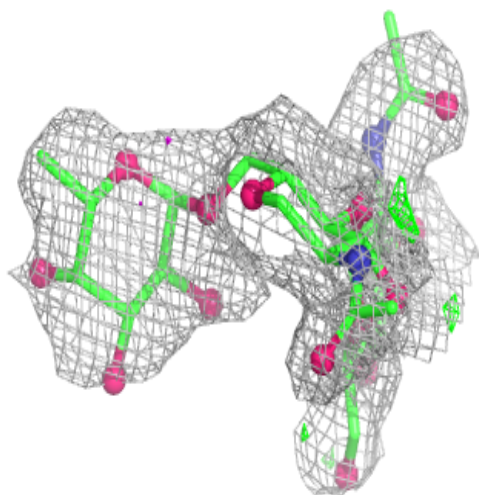
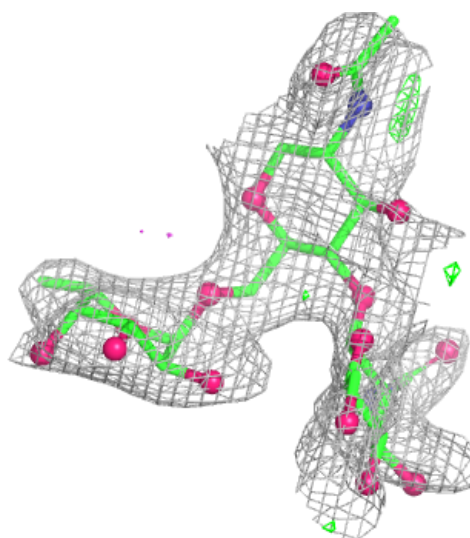
**Electron density around Chain I:**

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



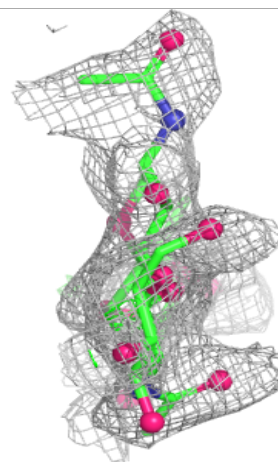
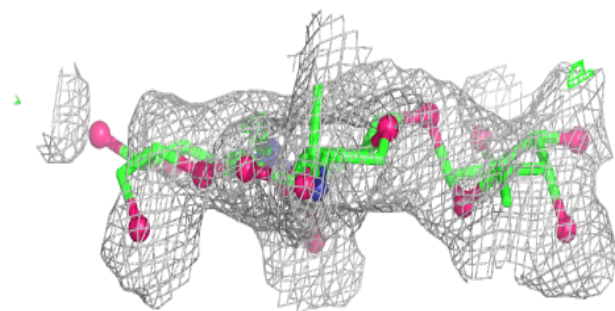
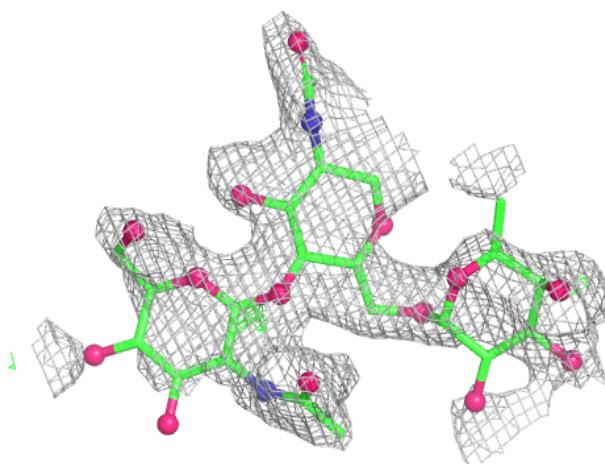
Electron density around Chain F:

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



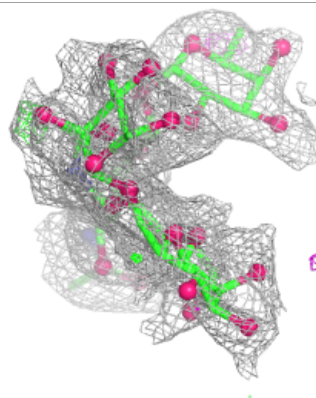
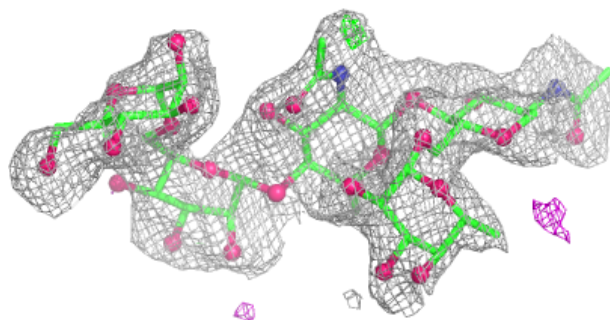
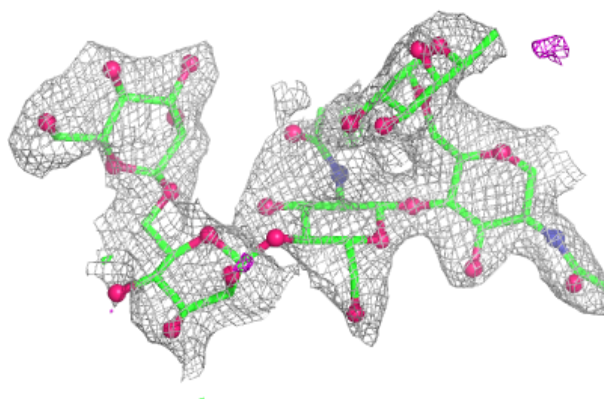
Electron density around Chain G:

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

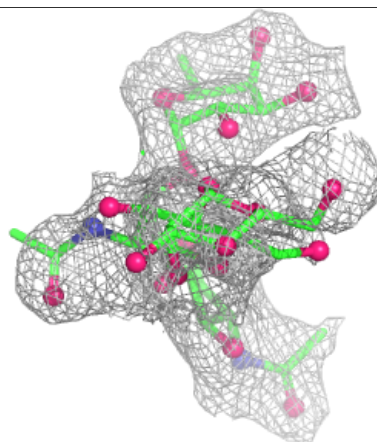
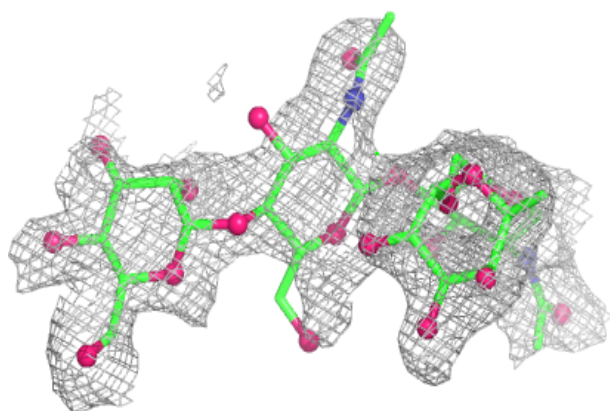
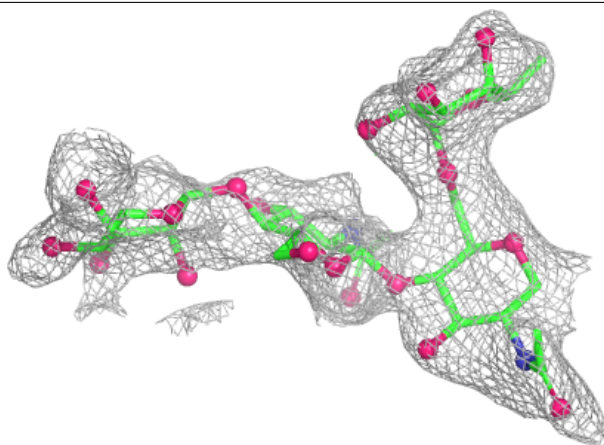


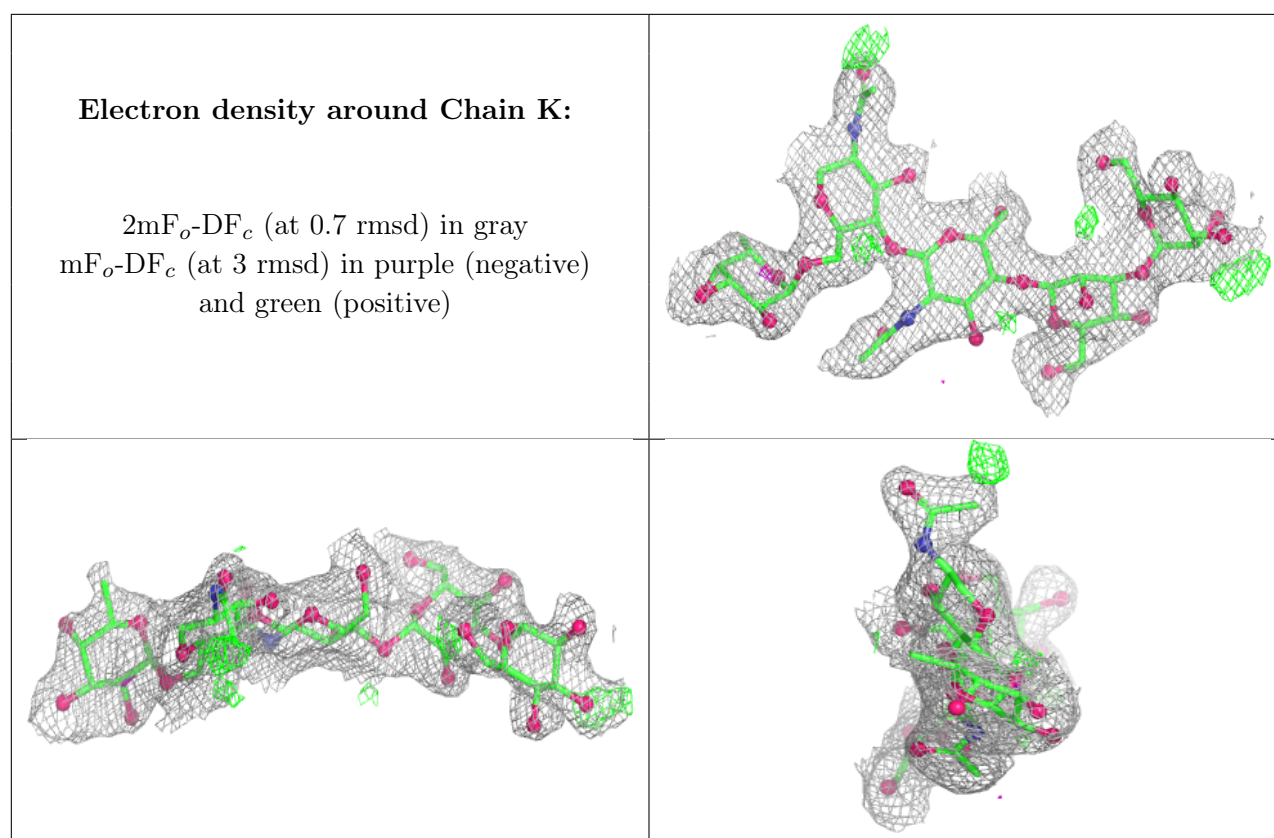
Electron density around Chain H:

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

**Electron density around Chain J:**

$2mF_o - DF_c$ (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
9	NAG	B	604	14/15	0.56	0.19	60,75,82,90	0
9	NAG	A	604	14/15	0.63	0.18	54,74,91,97	0
9	NAG	A	605	14/15	0.68	0.19	57,74,79,93	0
10	GOL	A	607	6/6	0.73	0.19	43,52,56,59	0
12	PEG	A	616	7/7	0.73	0.19	58,58,60,63	0
11	PGE	B	609	10/10	0.75	0.20	38,47,51,62	0
10	GOL	B	605	6/6	0.81	0.18	42,45,52,53	0
11	PGE	A	614	10/10	0.81	0.15	49,53,58,60	0
12	PEG	B	612	7/7	0.82	0.15	45,46,51,51	0
11	PGE	A	610	10/10	0.83	0.15	34,40,54,61	0
13	MES	B	613	12/12	0.83	0.16	36,51,58,69	25
12	PEG	B	608	7/7	0.84	0.14	29,41,43,45	0
10	GOL	B	606	6/6	0.86	0.20	40,45,49,52	0
12	PEG	B	611	7/7	0.86	0.28	26,31,39,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	PGE	B	610	10/10	0.86	0.13	31,50,58,65	0
11	PGE	A	608	4/10	0.86	0.14	31,35,38,42	0
12	PEG	A	615	7/7	0.88	0.12	43,48,50,54	0
12	PEG	A	611	7/7	0.88	0.14	35,36,47,57	0
12	PEG	A	613	7/7	0.88	0.15	18,36,45,45	0
12	PEG	A	612	7/7	0.90	0.18	25,30,32,34	0
10	GOL	A	606	6/6	0.90	0.15	29,39,42,42	0
12	PEG	A	609	7/7	0.91	0.10	31,40,47,50	0
12	PEG	B	607	7/7	0.91	0.18	28,34,37,38	0
8	CA	B	602	1/1	0.98	0.03	22,22,22,22	0
8	CA	B	603	1/1	0.99	0.02	22,22,22,22	0
8	CA	B	601	1/1	0.99	0.02	20,20,20,20	0
8	CA	A	603	1/1	1.00	0.03	13,13,13,13	0
8	CA	A	601	1/1	1.00	0.02	22,22,22,22	0
8	CA	A	602	1/1	1.00	0.03	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.