



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 03:51 PM EDT

PDB ID : 6PDL / pdb_00006pdl
Title : Crystal Structure of Hendra Virus Attachment G Glycoprotein in Complex with Receptor Ephrin-B2
Authors : Xu, K.; Nikolov, D.B.
Deposited on : 2019-06-19
Resolution : 2.70 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

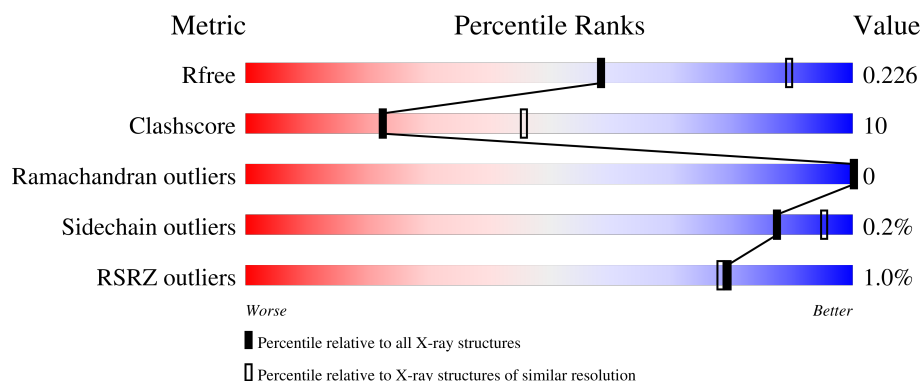
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	441	 73% 21% • 5%
1	C	441	 77% 16% • 5%
1	E	441	 77% 17% • 5%
1	G	441	 68% 25% • 5%
2	B	141	 65% 28% • 6%

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Mol	Chain	Length	Quality of chain
2	D	141	
2	F	141	
2	H	141	
3	I	2	
3	J	2	
3	L	2	
3	M	2	
3	P	2	
3	S	2	
4	K	7	
4	T	7	
5	N	7	
6	O	3	
6	R	3	
7	Q	5	

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
4	BMA	K	3	X	-	-	-
4	MAN	K	4	X	-	-	-
4	FUC	K	6	X	-	-	-
4	BMA	T	3	X	-	-	-
4	MAN	T	4	X	-	-	-
5	MAN	N	3	X	-	-	-
5	BMA	N	4	X	-	-	-

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 18707 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 Attachment glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3309	2107	555	628	19			
1	C	418	Total	C	N	O	S	0	0	0
			3286	2093	551	623	19			
1	E	421	Total	C	N	O	S	0	0	0
			3309	2107	555	628	19			
1	G	418	Total	C	N	O	S	0	0	0
			3286	2093	551	623	19			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	605	GLY	-	expression tag	UNP F4YH71
A	606	ARG	-	expression tag	UNP F4YH71
A	607	GLY	-	expression tag	UNP F4YH71
A	608	LEU	-	expression tag	UNP F4YH71
A	609	VAL	-	expression tag	UNP F4YH71
A	610	PRO	-	expression tag	UNP F4YH71
A	611	ARG	-	expression tag	UNP F4YH71
C	605	GLY	-	expression tag	UNP F4YH71
C	606	ARG	-	expression tag	UNP F4YH71
C	607	GLY	-	expression tag	UNP F4YH71
C	608	LEU	-	expression tag	UNP F4YH71
C	609	VAL	-	expression tag	UNP F4YH71
C	610	PRO	-	expression tag	UNP F4YH71
C	611	ARG	-	expression tag	UNP F4YH71
E	605	GLY	-	expression tag	UNP F4YH71
E	606	ARG	-	expression tag	UNP F4YH71
E	607	GLY	-	expression tag	UNP F4YH71
E	608	LEU	-	expression tag	UNP F4YH71
E	609	VAL	-	expression tag	UNP F4YH71
E	610	PRO	-	expression tag	UNP F4YH71
E	611	ARG	-	expression tag	UNP F4YH71

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Chain	Residue	Modelled	Actual	Comment	Reference
G	605	GLY	-	expression tag	UNP F4YH71
G	606	ARG	-	expression tag	UNP F4YH71
G	607	GLY	-	expression tag	UNP F4YH71
G	608	LEU	-	expression tag	UNP F4YH71
G	609	VAL	-	expression tag	UNP F4YH71
G	610	PRO	-	expression tag	UNP F4YH71
G	611	ARG	-	expression tag	UNP F4YH71

- Molecule 2 is a protein called Ephrin-B2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	133	Total	C	N	O	S	0	0	0
			1070	687	172	204	7			
2	D	139	Total	C	N	O	S	0	0	0
			1111	711	179	214	7			
2	F	133	Total	C	N	O	S	0	0	0
			1070	687	172	204	7			
2	H	139	Total	C	N	O	S	0	0	0
			1111	711	179	214	7			

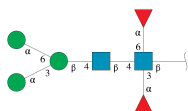
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	P	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	S	2	Total	C	N	O	0	0	0
			28	16	2	10			

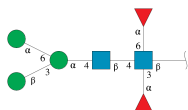
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyran

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



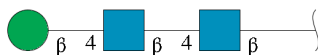
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	K	7	Total	C	N	O	0	0	0
			81	46	2	33			
4	T	7	Total	C	N	O	0	0	0
			81	46	2	33			

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



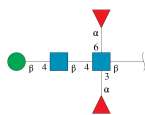
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	N	7	Total	C	N	O	0	0	0
			81	46	2	33			

- Molecule 6 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.



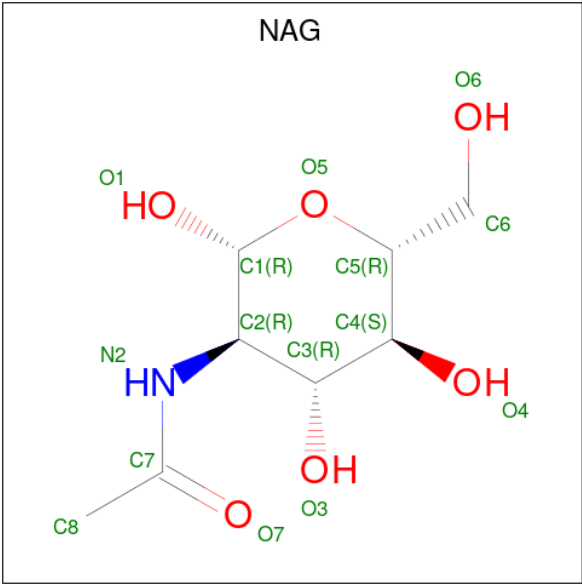
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	O	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	R	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	Q	5	Total	C	N	O	0	0	0
			59	34	2	23			

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	F	1	Total	C	N	O	0	0
			14	8	1	5		
8	G	1	Total	C	N	O	0	0
			14	8	1	5		
8	G	1	Total	C	N	O	0	0
			14	8	1	5		
8	H	1	Total	C	N	O	0	0
			14	8	1	5		
8	H	1	Total	C	N	O	0	0
			14	8	1	5		

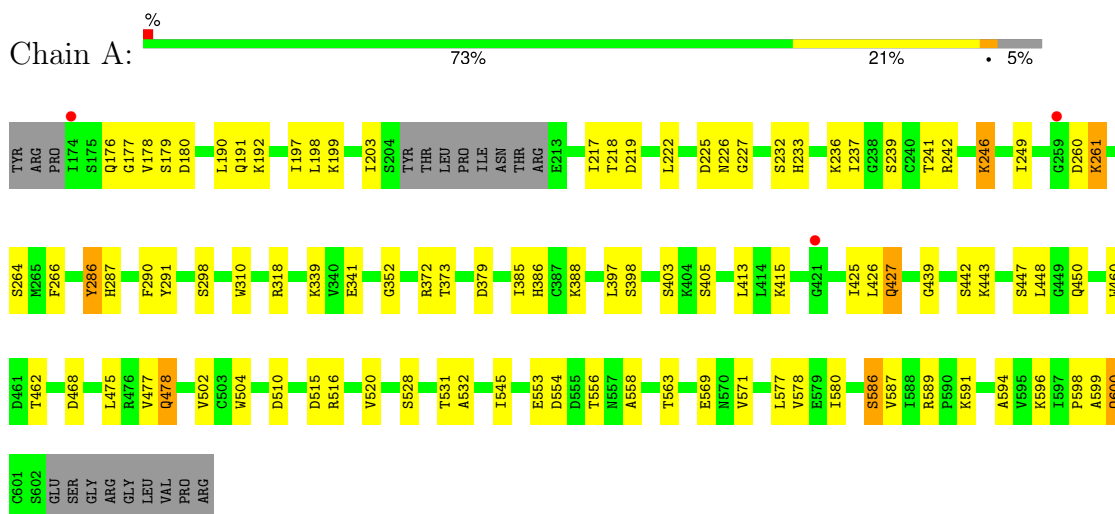
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	75	Total	O	0	0
			75	75		
9	B	21	Total	O	0	0
			21	21		
9	C	104	Total	O	0	0
			104	104		
9	D	11	Total	O	0	0
			11	11		
9	E	127	Total	O	0	0
			127	127		
9	F	22	Total	O	0	0
			22	22		
9	G	47	Total	O	0	0
			47	47		
9	H	18	Total	O	0	0
			18	18		

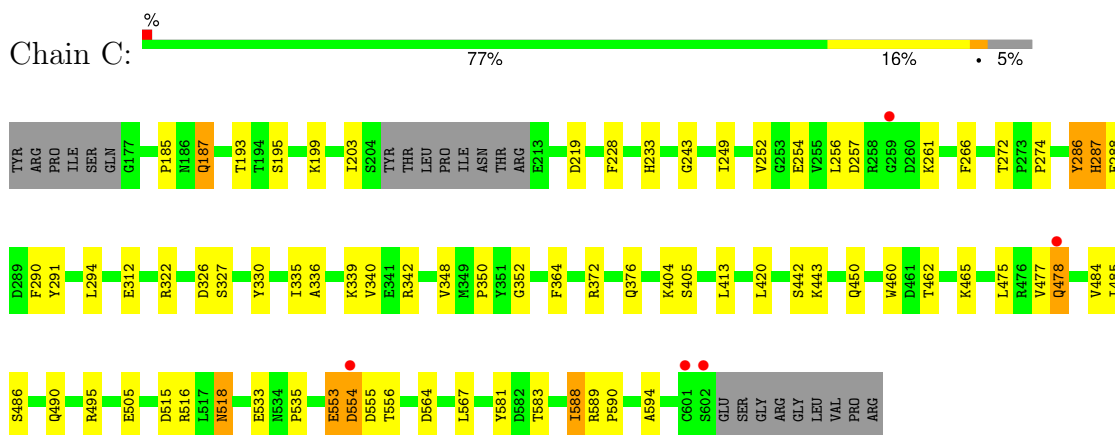
3 Residue-property plots

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.

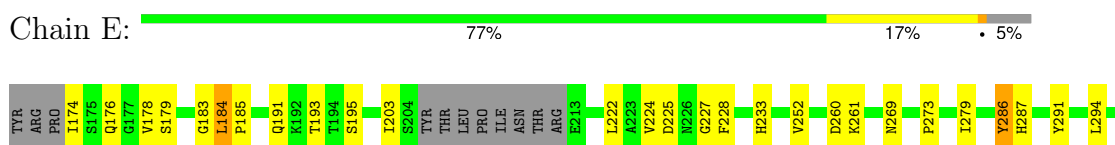
• Molecule 1: Attachment glycoprotein

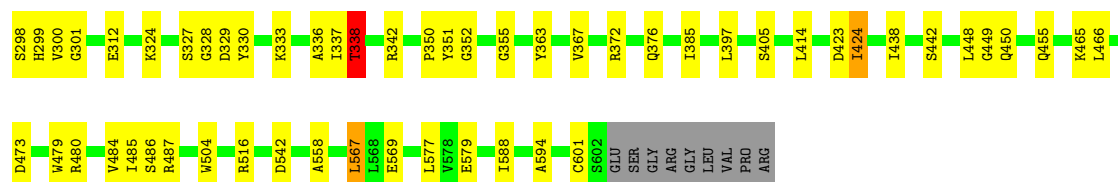


• Molecule 1: Attachment glycoprotein

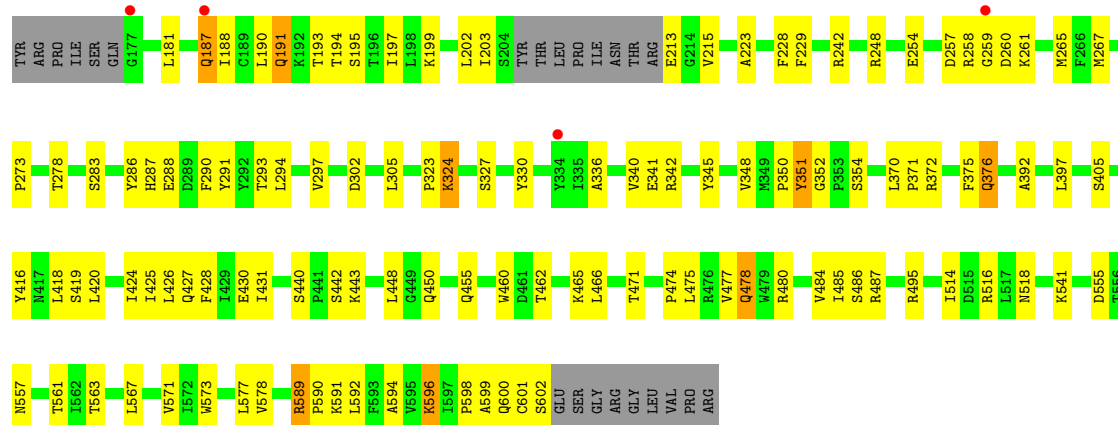


• Molecule 1: Attachment glycoprotein

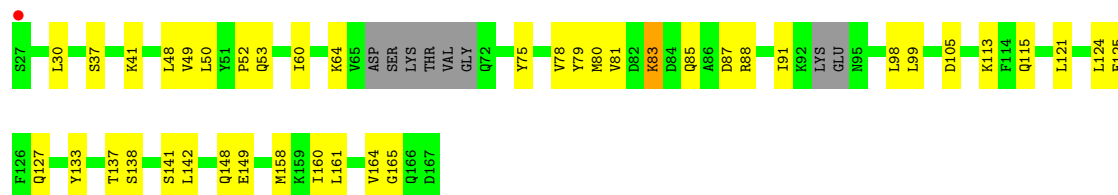




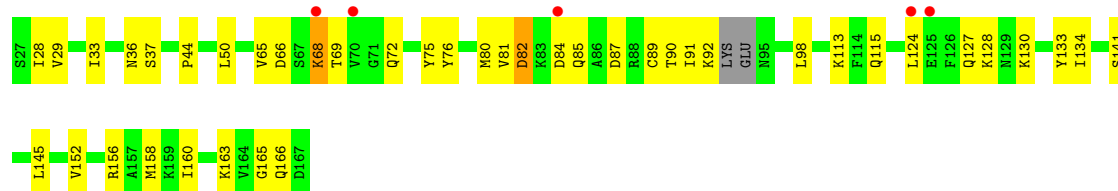
• Molecule 1: Attachment glycoprotein



• Molecule 2: Ephrin-B2

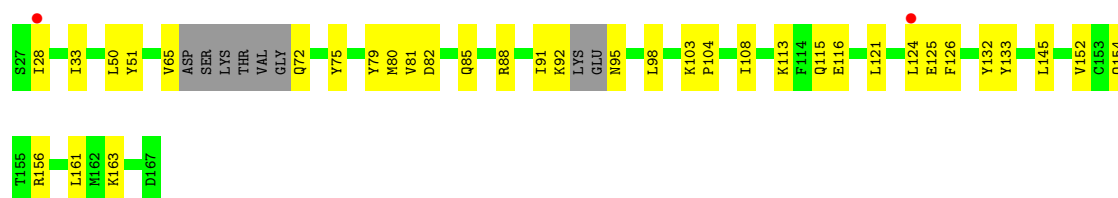


• Molecule 2: Ephrin-B2



• Molecule 2: Ephrin-B2





- Molecule 2: Ephrin-B2



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



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



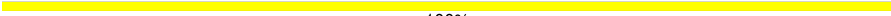
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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

Chain P:  100%

MAG1
MAG2

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

Chain S:  50% 50%

MAG1
MAG2

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

Chain K:  57% 29% 14%

MAG1
MAG2
BMA3
MAN4
MAN5
FUC6
FUC7

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

Chain T:  57% 43%

MAG1
MAG2
BMA3
MAN4
MAN5
FUC6
FUC7

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

Chain N:  43% 57%

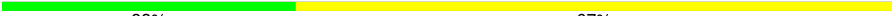
MAG1
MAG2
MAN3
BMA4
MAN5
FUC6
FUC7

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

Chain O:  67% 33%

MAG1
MAG2
BMA3

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

Chain R:  33% 67%

NAG1
NAG2
BMA3

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

Chain Q:  80% 20%

NAG1
NAG2
BMA3
FUC4
FUC5

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.76Å 94.64Å 102.52Å 112.86° 97.44° 97.56°	Depositor
Resolution (Å)	37.56 – 2.70 37.56 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.5 (37.56-2.70) 93.8 (37.56-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.172 , 0.227 0.174 , 0.226	Depositor DCC
R_{free} test set	3225 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.1	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	0.94	EDS
Total number of atoms	18707	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.49 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6099e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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, MAN, FUC, 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	0.53	7/3387 (0.2%)	0.78	15/4610 (0.3%)
1	C	0.46	2/3364 (0.1%)	0.80	14/4579 (0.3%)
1	E	0.68	14/3387 (0.4%)	0.66	8/4610 (0.2%)
1	G	0.49	3/3364 (0.1%)	0.87	22/4579 (0.5%)
2	B	0.50	0/1091	0.91	2/1471 (0.1%)
2	D	0.54	3/1133 (0.3%)	0.74	4/1529 (0.3%)
2	F	0.33	0/1091	0.69	1/1471 (0.1%)
2	H	0.46	1/1133 (0.1%)	0.82	5/1529 (0.3%)
All	All	0.53	30/17950 (0.2%)	0.78	71/24378 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	G	0	1
2	D	0	1
2	H	0	1
All	All	0	5

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	225	ASP	C-O	-10.30	1.12	1.23
1	A	225	ASP	C-O	-9.41	1.12	1.23
1	E	423	ASP	CA-C	-9.24	1.41	1.52
1	A	179	SER	C-O	-7.94	1.14	1.23
1	E	184	LEU	C-O	-7.81	1.17	1.24

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	258	ARG	CA-CB-CG	12.09	138.27	114.10
1	G	376	GLN	CA-CB-CG	-10.62	92.87	114.10
1	C	477	VAL	CA-C-N	-10.31	108.47	123.11
1	C	477	VAL	C-N-CA	-10.31	108.47	123.11
1	G	478	GLN	CB-CG-CD	-9.17	97.01	112.60

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	287	HIS	Peptide
2	D	82	ASP	Sidechain
1	E	287	HIS	Peptide
1	G	478	GLN	Sidechain
2	H	149	GLU	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3309	0	3248	60	1
1	C	3286	0	3224	54	0
1	E	3309	0	3248	51	3
1	G	3286	0	3224	93	1
2	B	1070	0	1057	31	0
2	D	1111	0	1099	28	3
2	F	1070	0	1057	23	1
2	H	1111	0	1098	43	1
3	I	28	0	25	0	0
3	J	28	0	25	2	0
3	L	28	0	25	1	0
3	M	28	0	25	0	0
3	P	28	0	25	1	0
3	S	28	0	25	1	1
4	K	81	0	70	1	1
4	T	81	0	70	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	N	81	0	70	0	0
6	O	39	0	34	0	0
6	R	39	0	34	0	0
7	Q	59	0	52	0	0
8	A	28	0	26	0	0
8	B	14	0	13	1	0
8	C	28	0	26	0	0
8	D	14	0	13	1	0
8	E	28	0	26	1	0
8	F	14	0	13	0	0
8	G	28	0	26	0	0
8	H	28	0	26	4	0
9	A	75	0	0	9	1
9	B	21	0	0	4	0
9	C	104	0	0	11	0
9	D	11	0	0	2	0
9	E	127	0	0	8	0
9	F	22	0	0	2	0
9	G	47	0	0	8	1
9	H	18	0	0	6	0
All	All	18707	0	17904	380	7

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 10.

The worst 5 of 380 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)
2:H:152:VAL:HG21	2:H:158:MET:HE2	1.21	1.13
2:H:95:ASN:ND2	9:H:302:HOH:O	1.84	1.08
1:C:553:GLU:HG2	1:C:555:ASP:OD1	1.52	1.08
2:H:27:SER:N	9:H:303:HOH:O	1.86	1.08
2:H:152:VAL:CG2	2:H:158:MET:HE2	1.83	1.07

The worst 5 of 7 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)
9:A:859:HOH:O	9:G:844:HOH:O[1_556]	1.87	0.33
2:D:68:LYS:NZ	1:E:183:GLY:O[1_665]	1.94	0.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:288:GLU:OE1	4:K:4:MAN:O4[1_444]	1.97	0.23
2:D:68:LYS:CD	1:E:183:GLY:N[1_665]	2.01	0.19
2:F:88:ARG:NH1	3:S:2:NAG:O6[1_656]	2.02	0.18

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	417/441 (95%)	405 (97%)	12 (3%)	0	100	100
1	C	414/441 (94%)	404 (98%)	10 (2%)	0	100	100
1	E	417/441 (95%)	407 (98%)	10 (2%)	0	100	100
1	G	414/441 (94%)	402 (97%)	12 (3%)	0	100	100
2	B	127/141 (90%)	125 (98%)	2 (2%)	0	100	100
2	D	135/141 (96%)	133 (98%)	2 (2%)	0	100	100
2	F	127/141 (90%)	125 (98%)	2 (2%)	0	100	100
2	H	135/141 (96%)	132 (98%)	3 (2%)	0	100	100
All	All	2186/2328 (94%)	2133 (98%)	53 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	376/394 (95%)	376 (100%)	0	100	100
1	C	373/394 (95%)	373 (100%)	0	100	100
1	E	376/394 (95%)	374 (100%)	2 (0%)	81	92
1	G	373/394 (95%)	372 (100%)	1 (0%)	86	94
2	B	121/128 (94%)	121 (100%)	0	100	100
2	D	126/128 (98%)	126 (100%)	0	100	100
2	F	121/128 (94%)	121 (100%)	0	100	100
2	H	126/128 (98%)	126 (100%)	0	100	100
All	All	1992/2088 (95%)	1989 (100%)	3 (0%)	87	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	184	LEU
1	E	338	THR
1	G	351	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	406	HIS
2	F	95	ASN
1	G	446	ASN
2	F	85	GLN
2	F	106	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 ⓘ

44 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	$\# Z > 2$
3	NAG	I	1	1,3	14,14,15	0.21	0	17,19,21	0.59	0
3	NAG	I	2	3	14,14,15	1.12	1 (7%)	17,19,21	2.57	1 (5%)
3	NAG	J	1	1,3	14,14,15	0.26	0	17,19,21	0.64	1 (5%)
3	NAG	J	2	3	14,14,15	0.40	0	17,19,21	1.34	2 (11%)
4	NAG	K	1	1,4	14,14,15	0.36	0	17,19,21	0.46	0
4	NAG	K	2	4	14,14,15	0.33	0	17,19,21	0.40	0
4	BMA	K	3	4	11,11,12	0.84	0	15,15,17	1.02	0
4	MAN	K	4	4	11,11,12	0.93	0	15,15,17	1.18	1 (6%)
4	MAN	K	5	4	11,11,12	0.83	0	15,15,17	1.10	1 (6%)
4	FUC	K	6	4	10,10,11	0.99	0	14,14,16	1.08	1 (7%)
4	FUC	K	7	4	10,10,11	0.88	0	14,14,16	0.83	0
3	NAG	L	1	1,3	14,14,15	0.26	0	17,19,21	0.64	1 (5%)
3	NAG	L	2	3	14,14,15	0.48	0	17,19,21	0.90	1 (5%)
3	NAG	M	1	1,3	14,14,15	0.38	0	17,19,21	0.37	0
3	NAG	M	2	3	14,14,15	0.34	0	17,19,21	0.64	0
5	NAG	N	1	1,5	14,14,15	0.35	0	17,19,21	0.44	0
5	NAG	N	2	5	14,14,15	0.39	0	17,19,21	0.48	0
5	MAN	N	3	5	11,11,12	0.90	1 (9%)	15,15,17	0.91	1 (6%)
5	BMA	N	4	5	11,11,12	0.65	0	15,15,17	0.97	1 (6%)
5	MAN	N	5	5	11,11,12	0.69	0	15,15,17	1.18	1 (6%)
5	FUC	N	6	5	10,10,11	0.88	1 (10%)	14,14,16	0.75	0
5	FUC	N	7	5	10,10,11	0.84	0	14,14,16	0.94	0
6	NAG	O	1	6,1	14,14,15	0.24	0	17,19,21	0.71	0
6	NAG	O	2	6	14,14,15	0.19	0	17,19,21	0.95	1 (5%)
6	BMA	O	3	6	11,11,12	0.52	0	15,15,17	0.95	0
3	NAG	P	1	1,3	14,14,15	0.35	0	17,19,21	0.49	0
3	NAG	P	2	3	14,14,15	0.21	0	17,19,21	0.53	0
7	NAG	Q	1	7,1	14,14,15	0.25	0	17,19,21	0.50	0
7	NAG	Q	2	7	14,14,15	0.38	0	17,19,21	0.42	0
7	BMA	Q	3	7	11,11,12	0.69	0	15,15,17	0.91	0
7	FUC	Q	4	7	10,10,11	0.81	0	14,14,16	0.82	0
7	FUC	Q	5	7	10,10,11	0.79	1 (10%)	14,14,16	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	R	1	6,1	14,14,15	0.17	0	17,19,21	0.72	1 (5%)
6	NAG	R	2	6	14,14,15	0.45	0	17,19,21	0.77	1 (5%)
6	BMA	R	3	6	11,11,12	0.95	0	15,15,17	0.88	0
3	NAG	S	1	1,3	14,14,15	0.42	0	17,19,21	0.48	0
3	NAG	S	2	3	14,14,15	0.40	0	17,19,21	0.45	0
4	NAG	T	1	1,4	14,14,15	0.27	0	17,19,21	0.47	0
4	NAG	T	2	4	14,14,15	0.17	0	17,19,21	0.54	0
4	BMA	T	3	4	11,11,12	0.92	0	15,15,17	1.31	3 (20%)
4	MAN	T	4	4	11,11,12	0.88	0	15,15,17	1.17	2 (13%)
4	MAN	T	5	4	11,11,12	0.70	0	15,15,17	1.36	1 (6%)
4	FUC	T	6	4	10,10,11	0.89	0	14,14,16	0.82	0
4	FUC	T	7	4	10,10,11	0.63	0	14,14,16	0.73	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
3	NAG	I	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	I	2	3	-	1/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	6/6/23/26	0/1/1/1
4	NAG	K	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	0/6/23/26	0/1/1/1
4	BMA	K	3	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	K	4	4	1/1/4/5	2/2/19/22	0/1/1/1
4	MAN	K	5	4	-	2/2/19/22	0/1/1/1
4	FUC	K	6	4	1/1/4/5	-	0/1/1/1
4	FUC	K	7	4	-	-	0/1/1/1
3	NAG	L	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
3	NAG	M	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	M	2	3	-	1/6/23/26	0/1/1/1
5	NAG	N	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
5	MAN	N	3	5	1/1/4/5	0/2/19/22	0/1/1/1
5	BMA	N	4	5	1/1/4/5	2/2/19/22	0/1/1/1
5	MAN	N	5	5	-	0/2/19/22	0/1/1/1
5	FUC	N	6	5	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FUC	N	7	5	-	-	0/1/1/1
6	NAG	O	1	6,1	-	1/6/23/26	0/1/1/1
6	NAG	O	2	6	-	2/6/23/26	0/1/1/1
6	BMA	O	3	6	-	2/2/19/22	0/1/1/1
3	NAG	P	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	P	2	3	-	3/6/23/26	0/1/1/1
7	NAG	Q	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	Q	2	7	-	0/6/23/26	0/1/1/1
7	BMA	Q	3	7	-	0/2/19/22	0/1/1/1
7	FUC	Q	4	7	-	-	0/1/1/1
7	FUC	Q	5	7	-	-	0/1/1/1
6	NAG	R	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	R	2	6	-	2/6/23/26	0/1/1/1
6	BMA	R	3	6	-	2/2/19/22	0/1/1/1
3	NAG	S	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	S	2	3	-	2/6/23/26	0/1/1/1
4	NAG	T	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	T	2	4	-	0/6/23/26	0/1/1/1
4	BMA	T	3	4	1/1/4/5	2/2/19/22	1/1/1/1
4	MAN	T	4	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	T	5	4	-	2/2/19/22	0/1/1/1
4	FUC	T	6	4	-	-	0/1/1/1
4	FUC	T	7	4	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	2	NAG	O5-C1	3.94	1.50	1.43
5	N	3	MAN	O5-C1	-2.60	1.39	1.43
5	N	6	FUC	O5-C1	-2.30	1.39	1.43
7	Q	5	FUC	O5-C1	-2.07	1.40	1.43

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	2	NAG	C1-O5-C5	10.41	126.14	112.19
3	J	2	NAG	C2-N2-C7	4.58	129.04	122.90
6	O	2	NAG	C1-O5-C5	3.65	117.07	112.19
4	T	5	MAN	C1-O5-C5	3.44	116.80	112.19
3	L	2	NAG	C1-O5-C5	3.39	116.73	112.19

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	K	3	BMA	C1
4	K	4	MAN	C1
4	K	6	FUC	C1
4	T	3	BMA	C1
4	T	4	MAN	C1

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	S	2	NAG	O5-C5-C6-O6
6	R	2	NAG	O5-C5-C6-O6
4	K	4	MAN	O5-C5-C6-O6
3	P	2	NAG	O5-C5-C6-O6
3	P	1	NAG	O5-C5-C6-O6

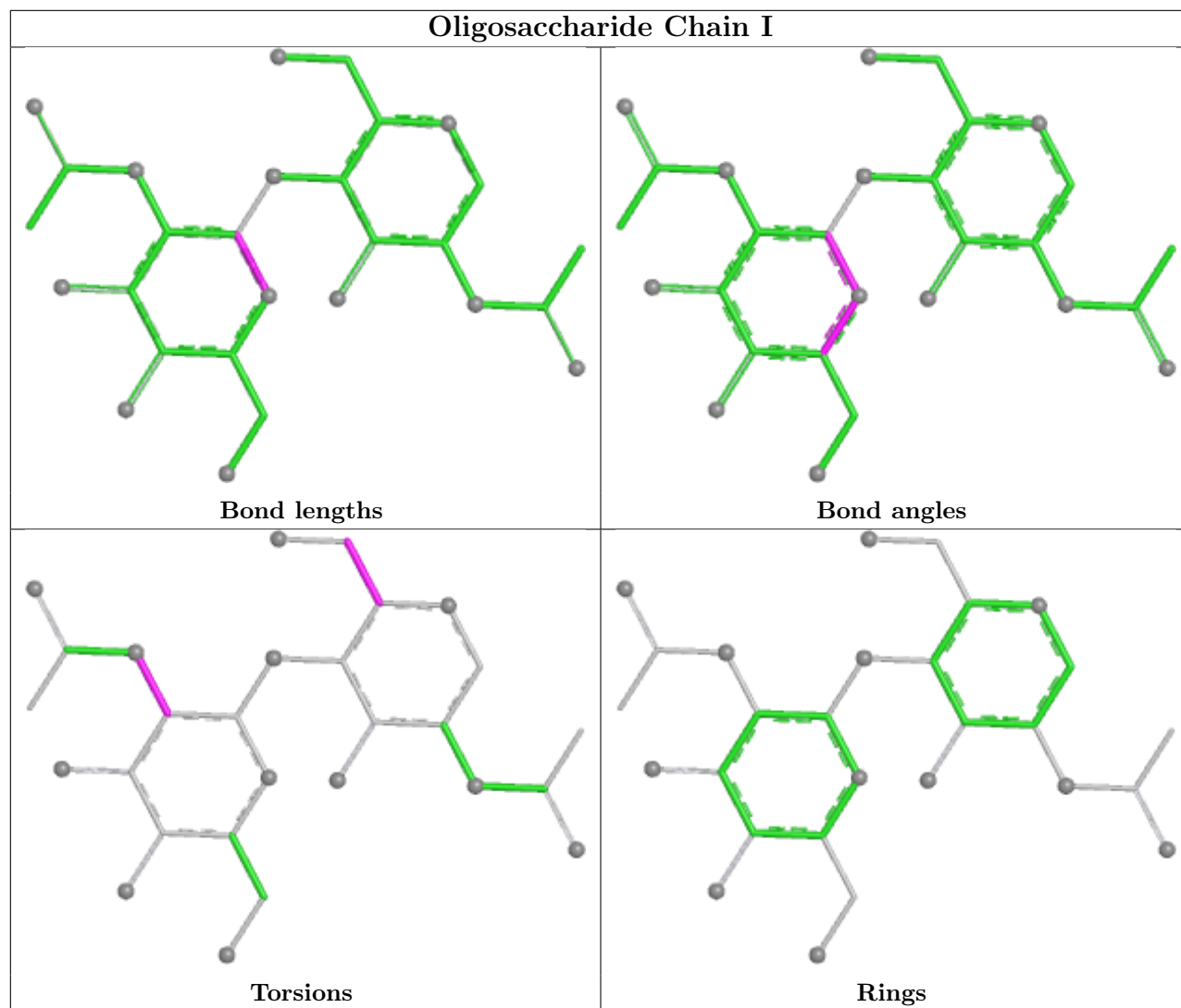
All (1) ring outliers are listed below:

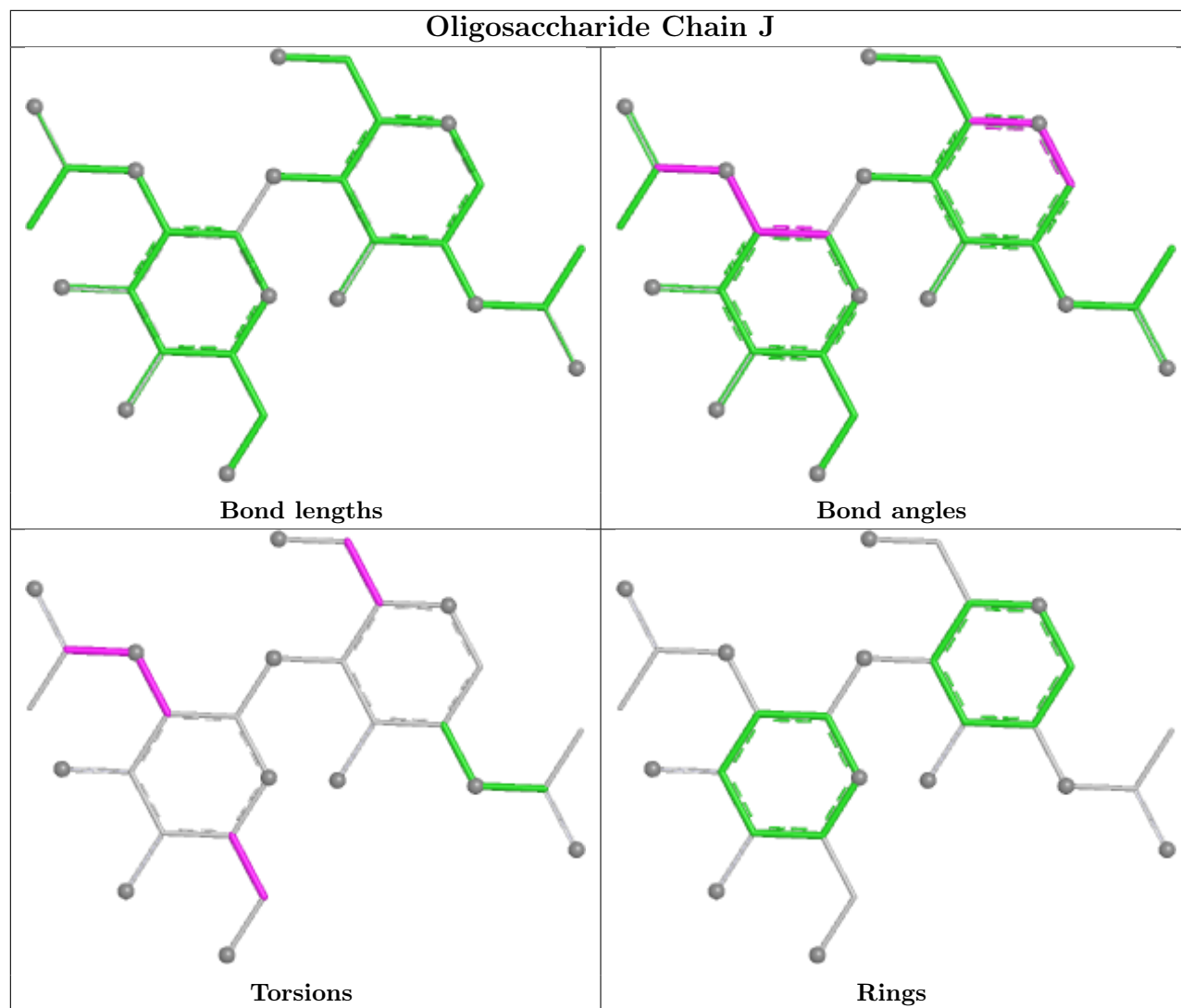
Mol	Chain	Res	Type	Atoms
4	T	3	BMA	C1-C2-C3-C4-C5-O5

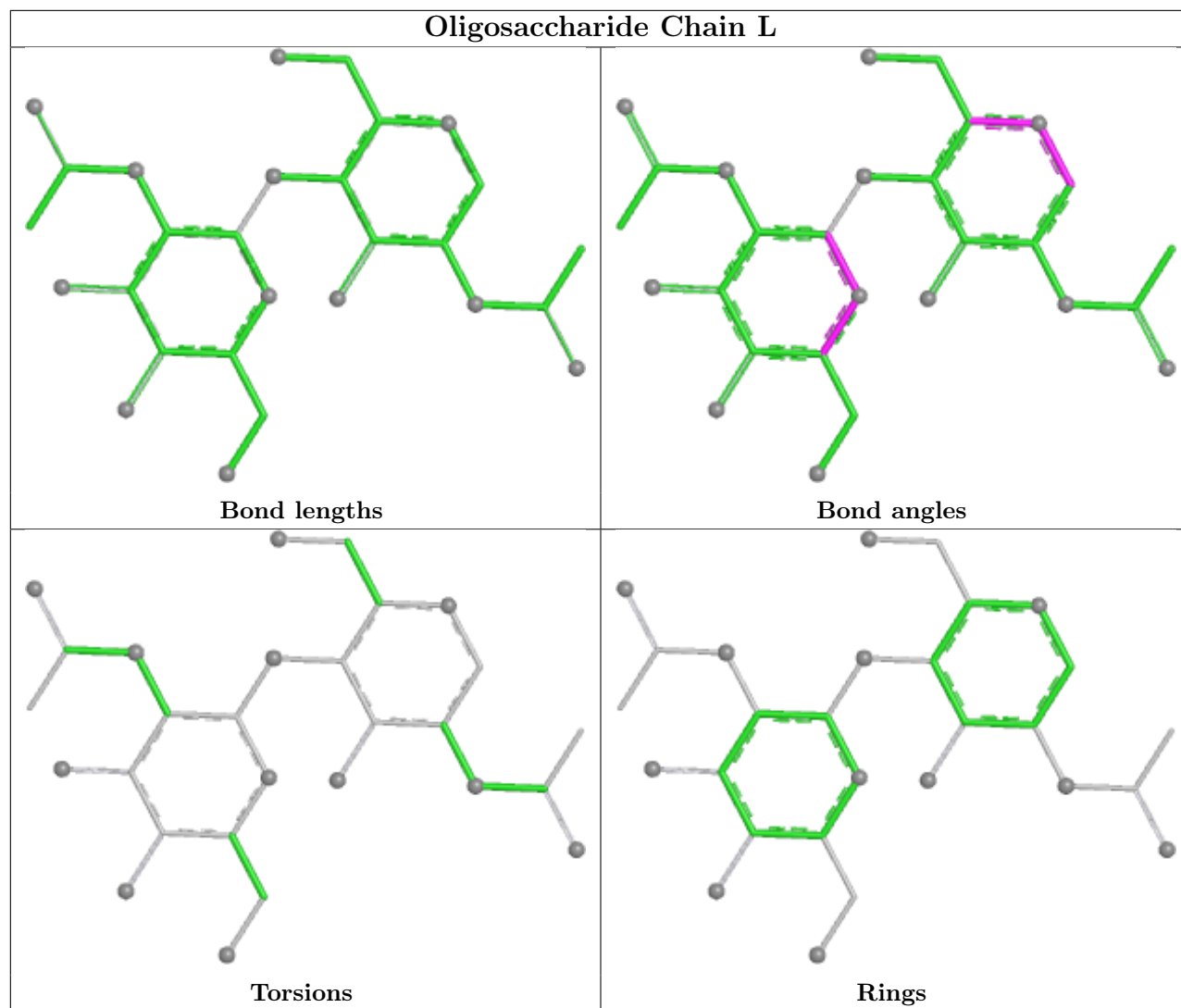
7 monomers are involved in 8 short contacts:

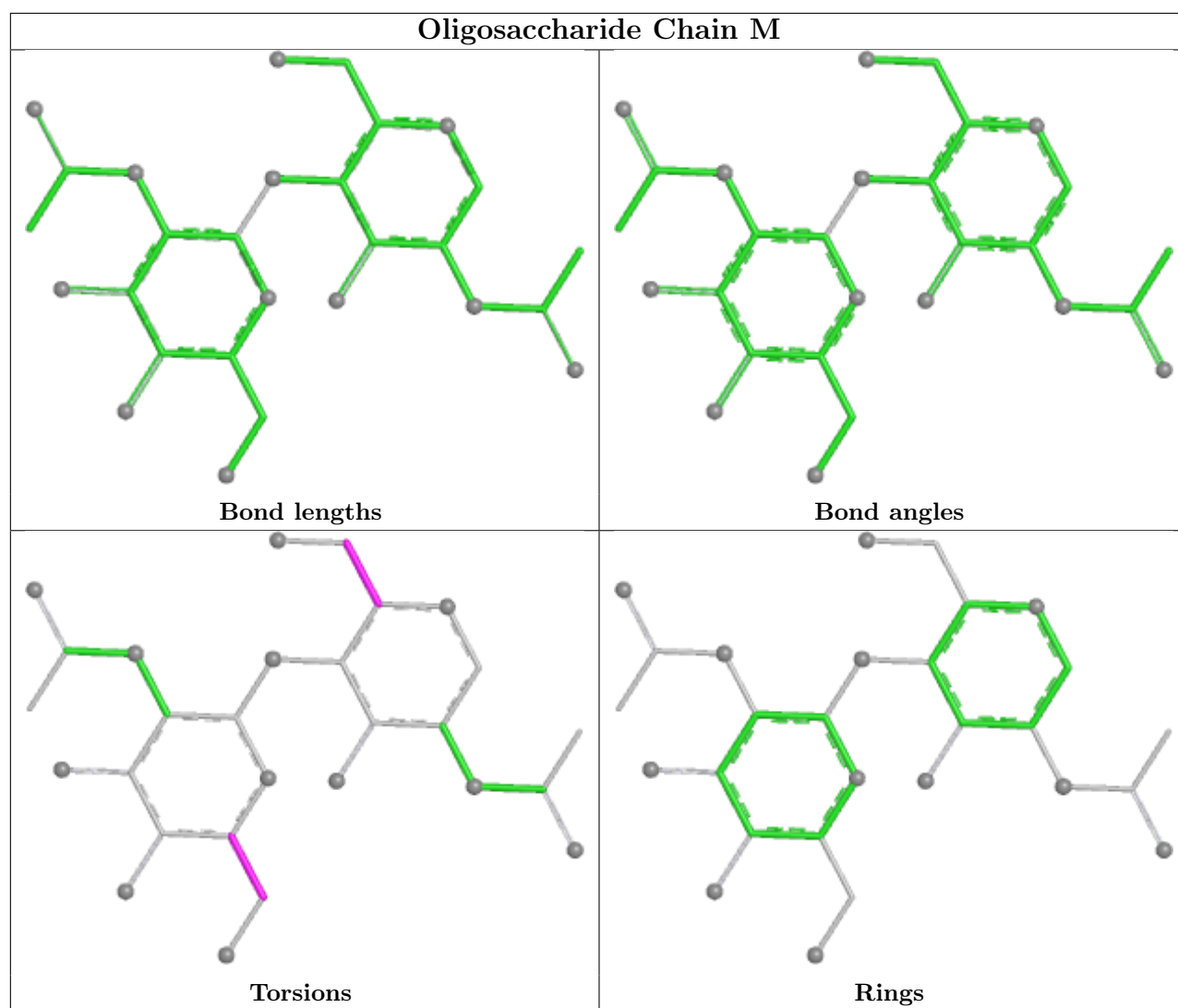
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	1	NAG	1	0
3	J	1	NAG	1	0
3	S	2	NAG	1	1
3	J	2	NAG	2	0
3	L	1	NAG	1	0
3	P	2	NAG	1	0
4	K	4	MAN	1	1

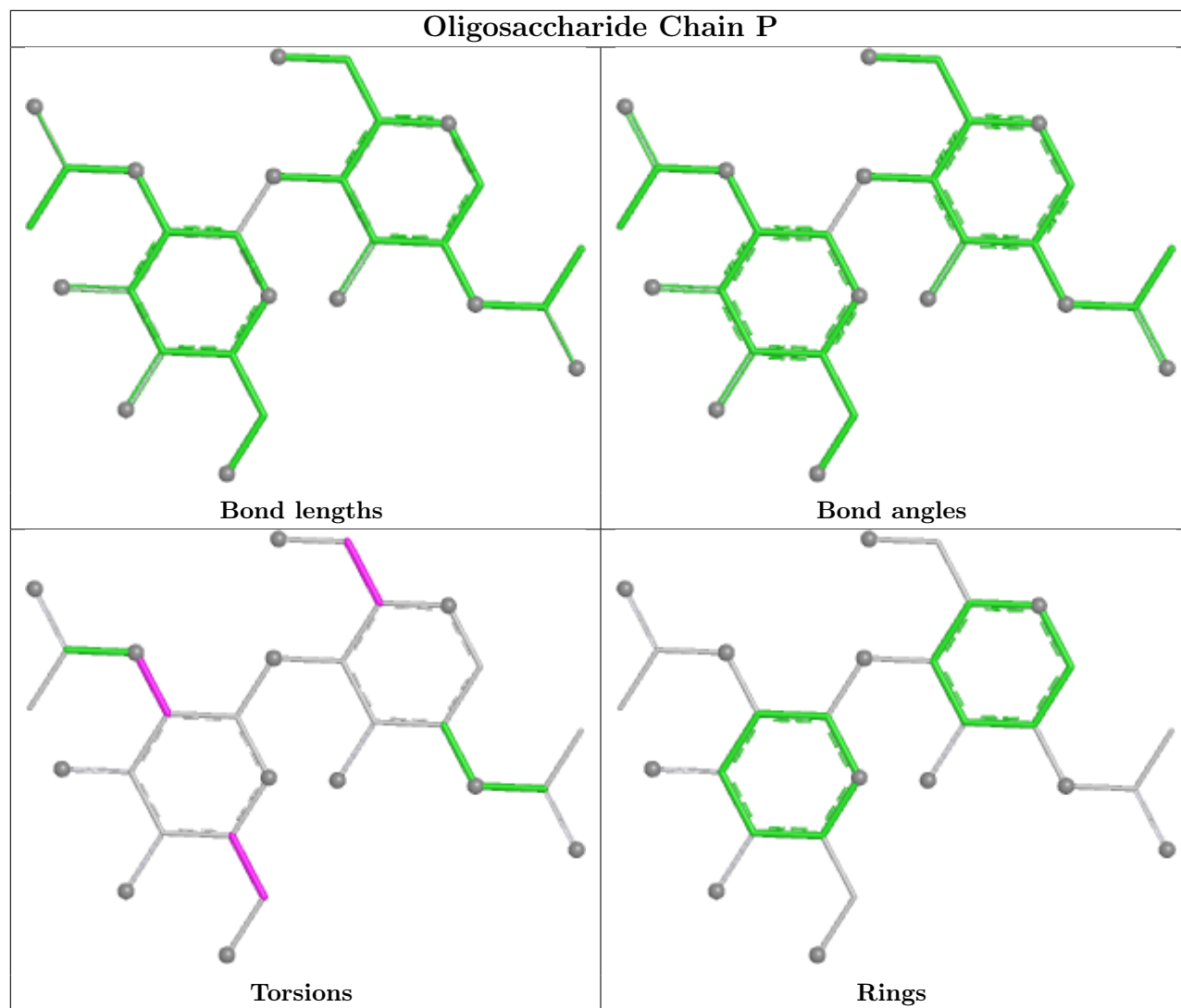
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

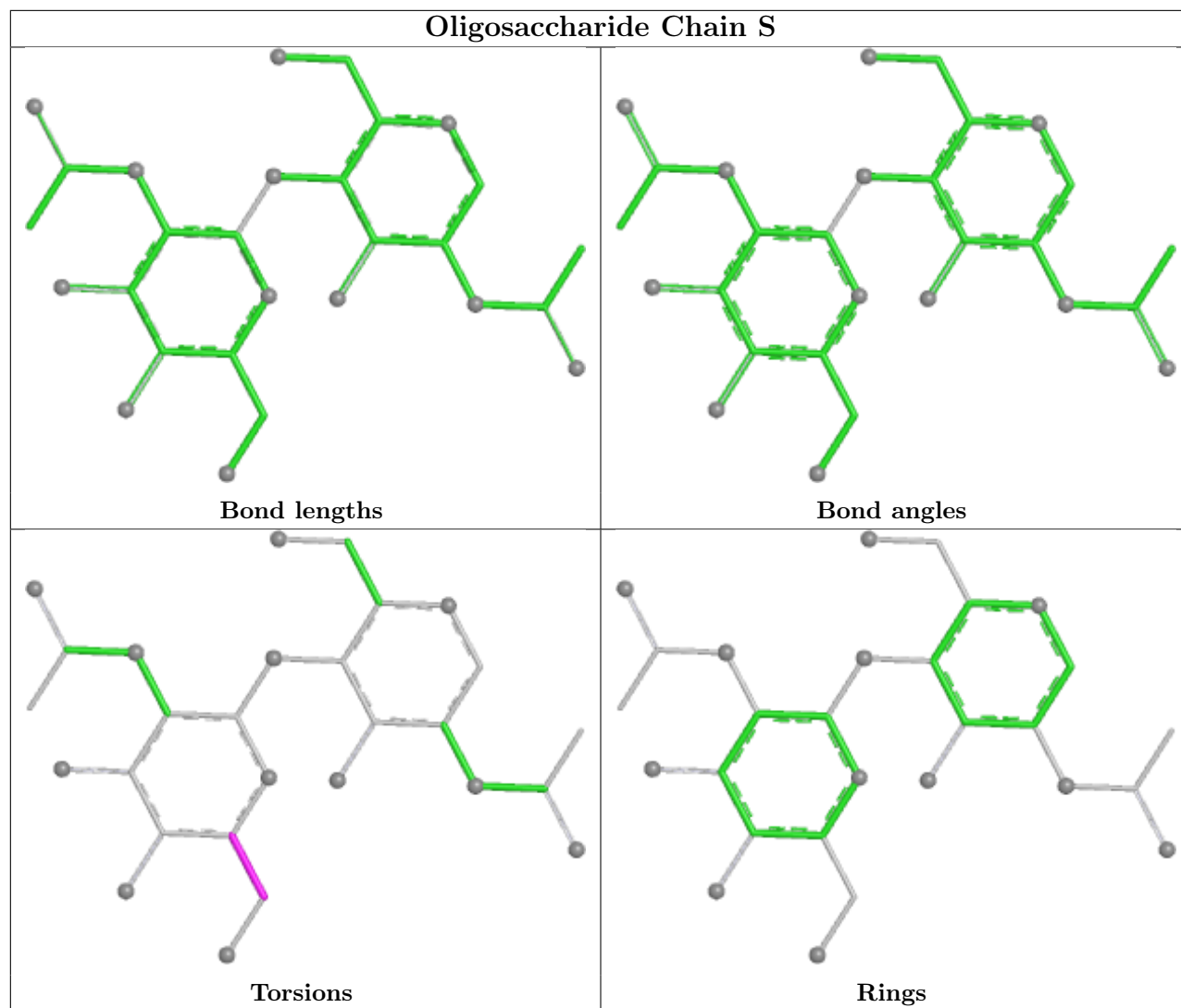


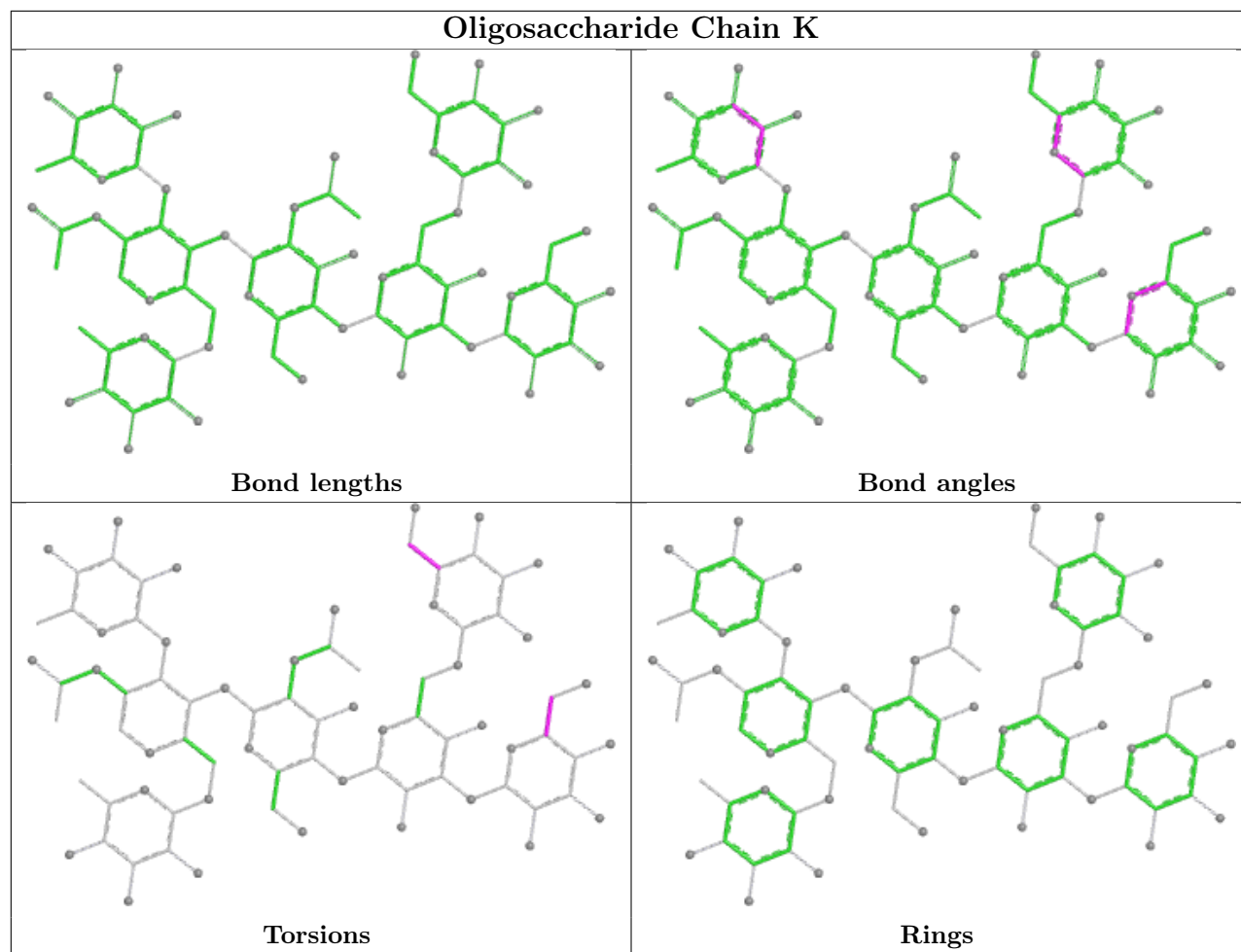


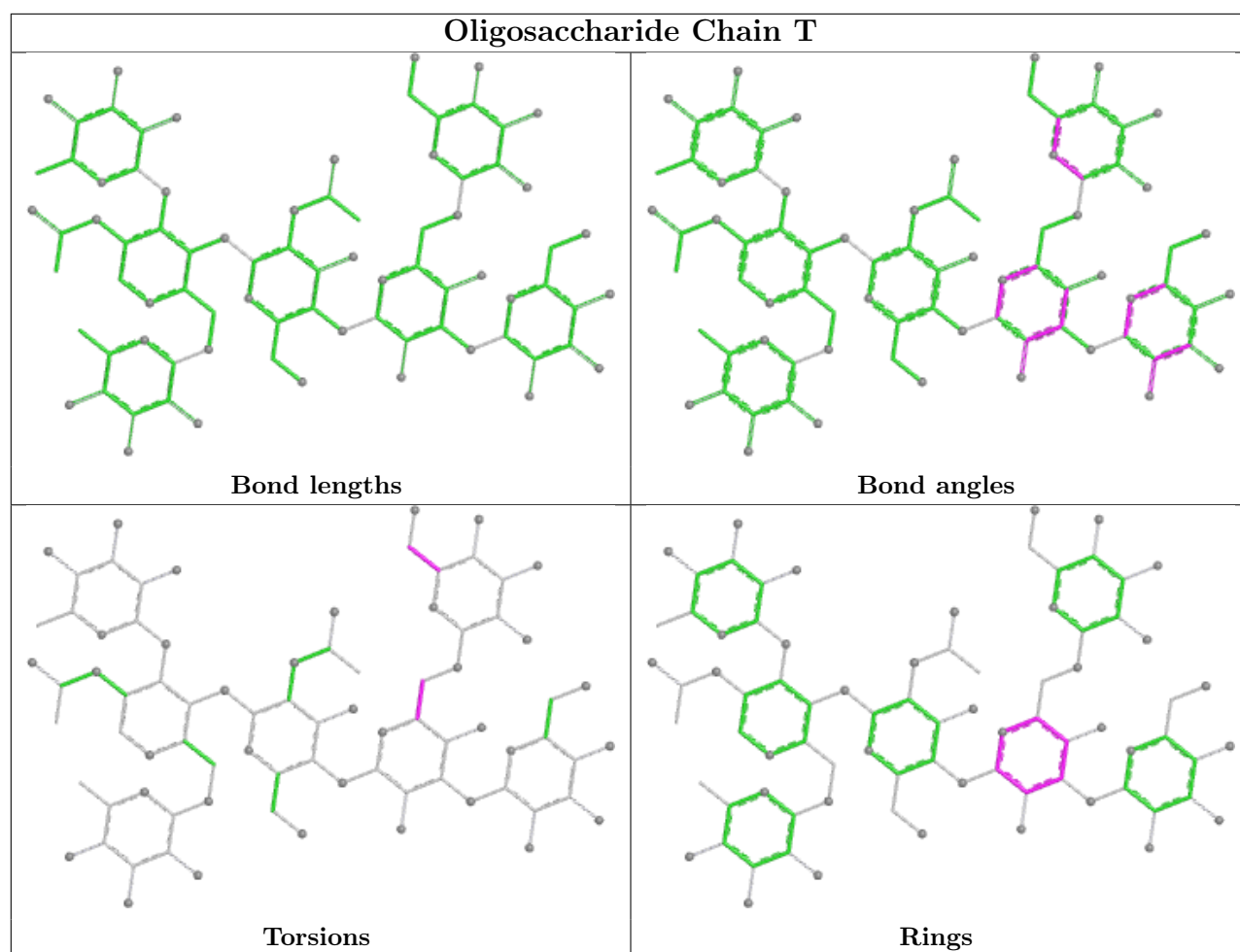


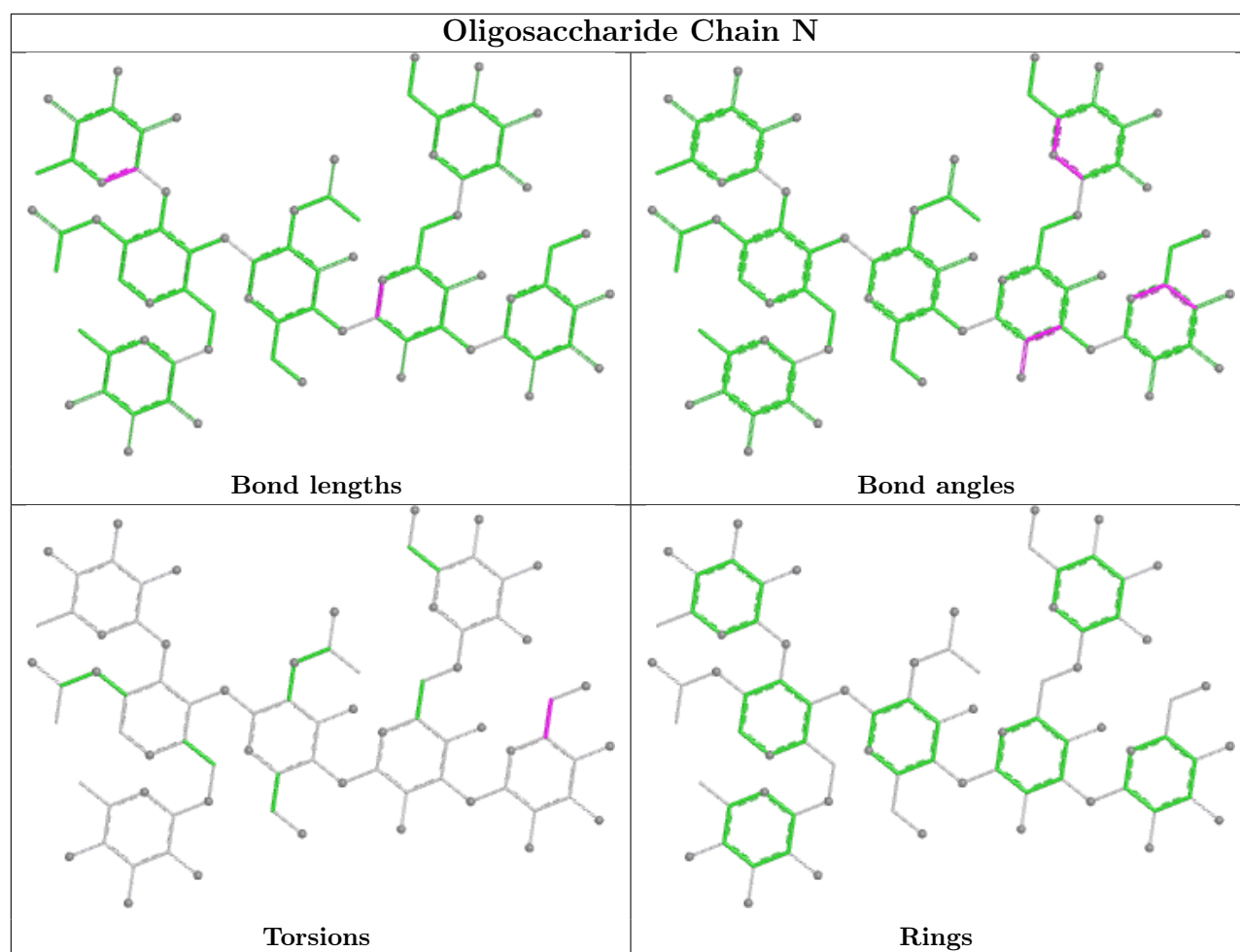


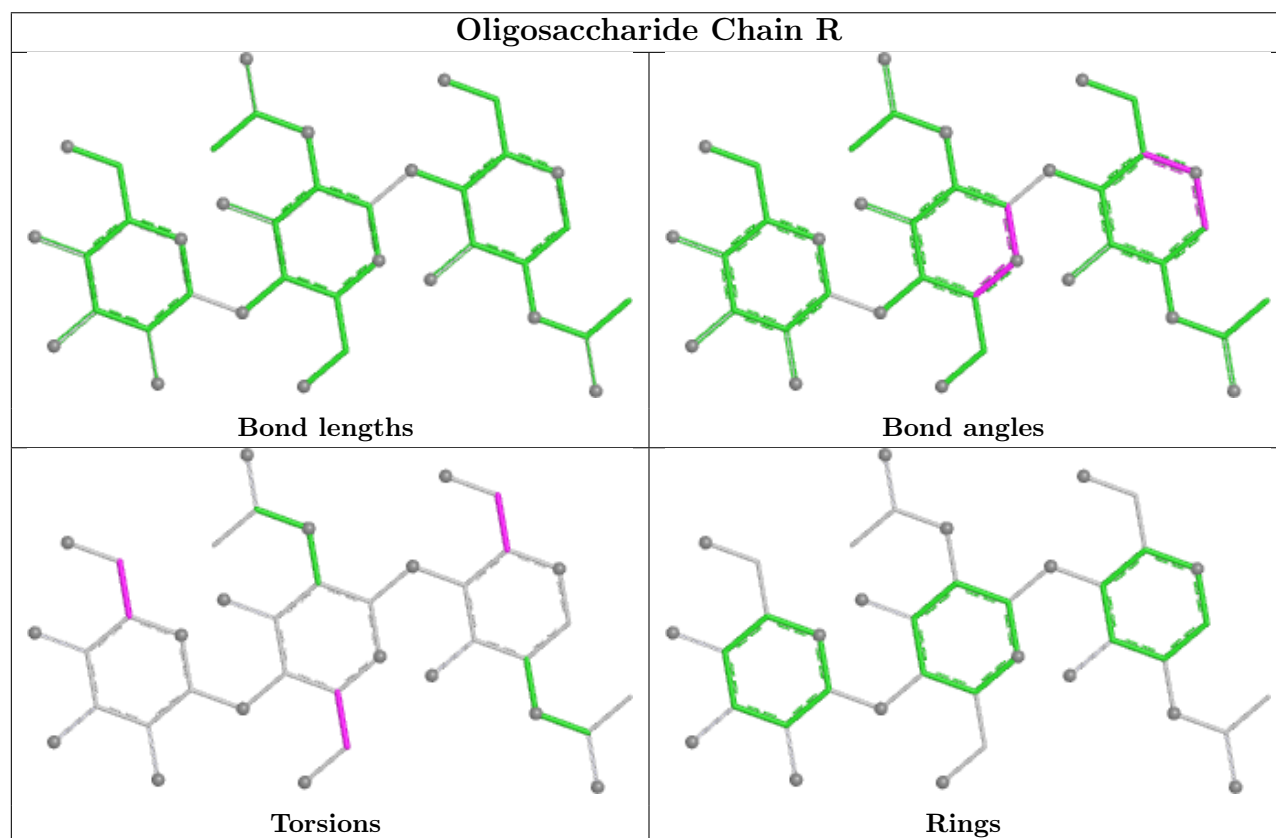
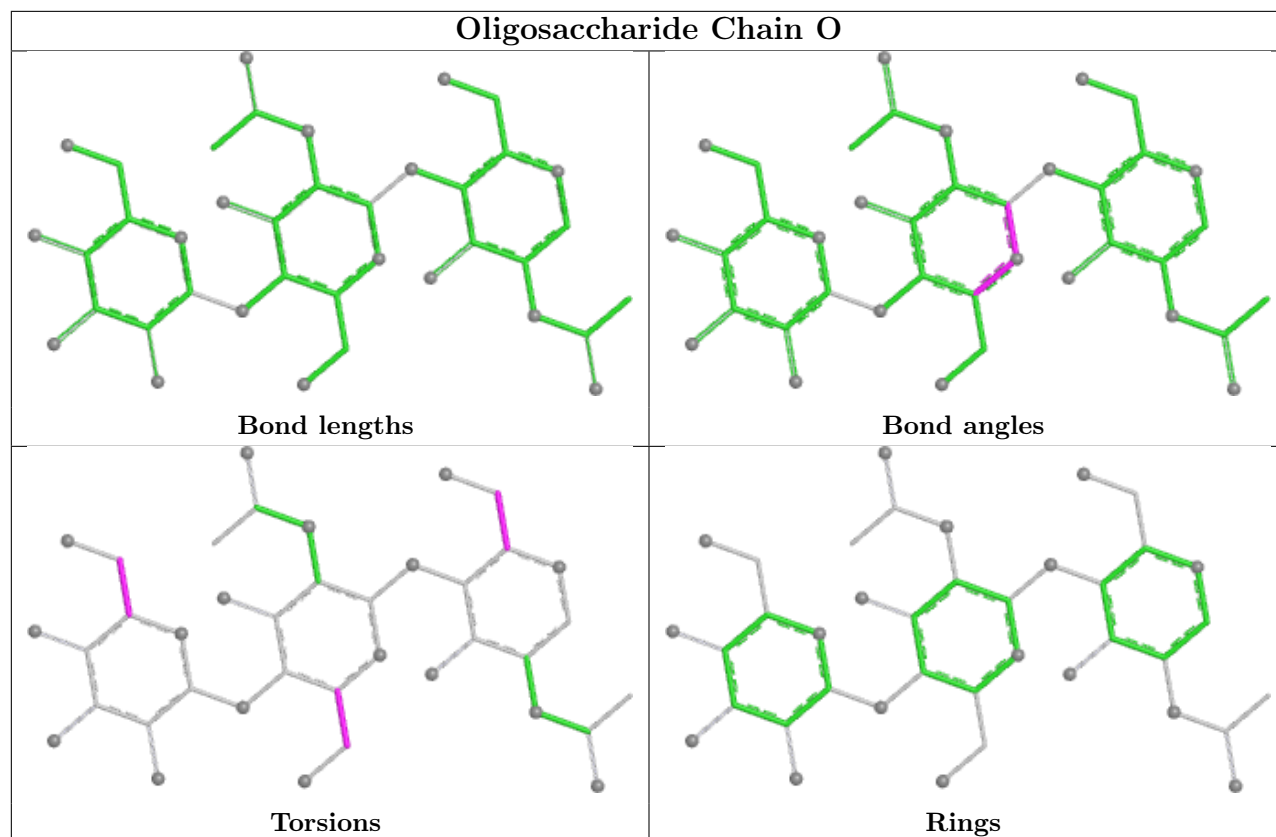


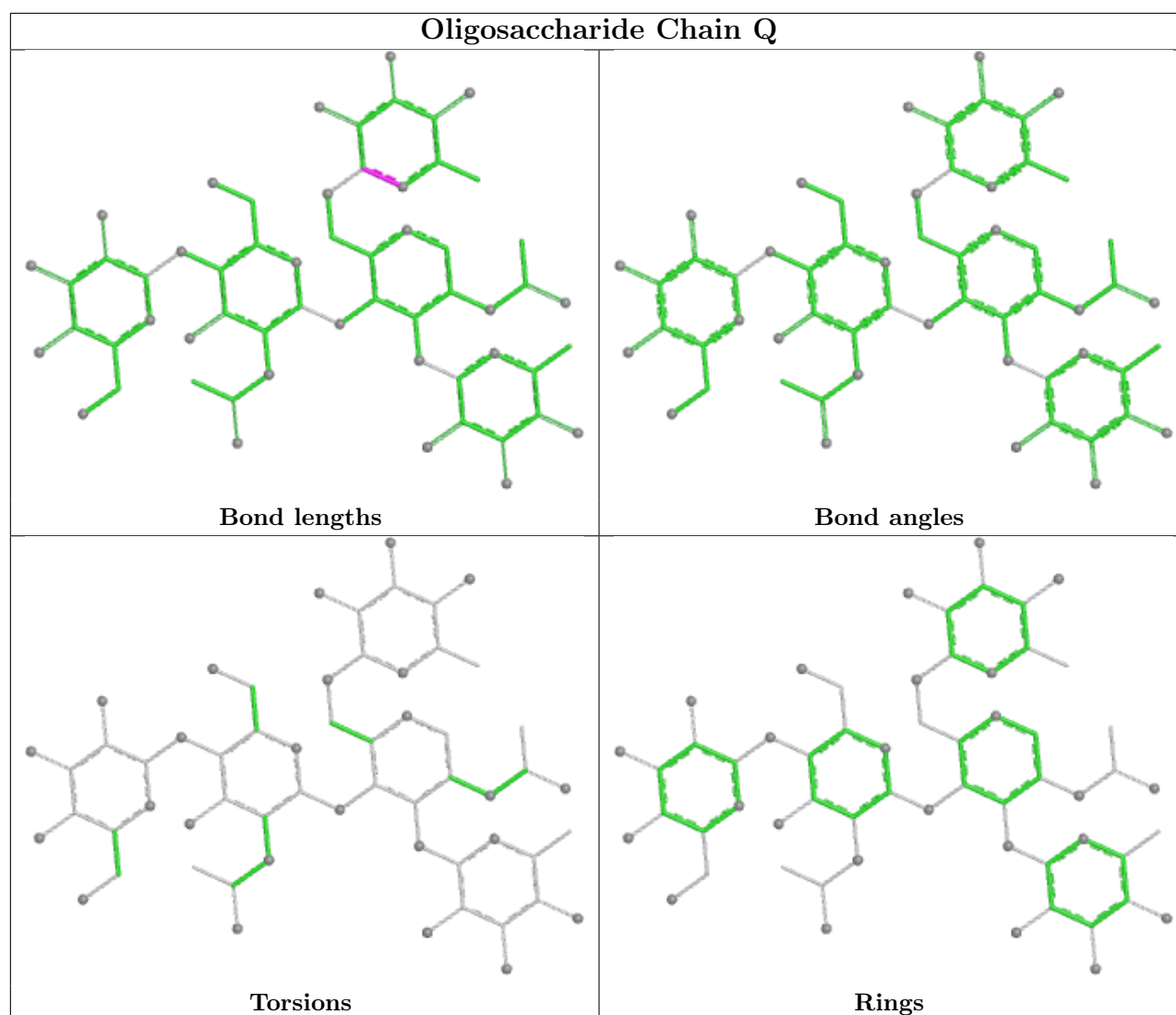












5.6 Ligand geometry [i](#)

13 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	$\# Z > 2$
8	NAG	H	201	2	14,14,15	0.67	0	17,19,21	0.91	1 (5%)
8	NAG	E	702	1	14,14,15	0.55	0	17,19,21	0.88	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	F	201	2	14,14,15	0.58	0	17,19,21	1.06	1 (5%)
8	NAG	C	702	1	14,14,15	0.48	0	17,19,21	0.75	1 (5%)
8	NAG	A	702	1	14,14,15	0.78	1 (7%)	17,19,21	0.69	0
8	NAG	G	702	1	14,14,15	0.72	1 (7%)	17,19,21	0.60	0
8	NAG	G	701	1	14,14,15	0.73	1 (7%)	17,19,21	0.58	0
8	NAG	D	201	2	14,14,15	0.62	0	17,19,21	0.80	1 (5%)
8	NAG	A	701	1	14,14,15	0.58	0	17,19,21	0.68	1 (5%)
8	NAG	H	202	2	14,14,15	1.33	2 (14%)	17,19,21	0.71	0
8	NAG	C	701	1	14,14,15	0.67	1 (7%)	17,19,21	0.67	1 (5%)
8	NAG	B	201	2	14,14,15	0.72	1 (7%)	17,19,21	0.87	1 (5%)
8	NAG	E	701	1	14,14,15	0.46	0	17,19,21	0.80	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	H	201	2	-	1/6/23/26	0/1/1/1
8	NAG	E	702	1	-	2/6/23/26	0/1/1/1
8	NAG	F	201	2	-	1/6/23/26	0/1/1/1
8	NAG	C	702	1	-	2/6/23/26	0/1/1/1
8	NAG	A	702	1	-	2/6/23/26	0/1/1/1
8	NAG	G	702	1	-	0/6/23/26	0/1/1/1
8	NAG	G	701	1	-	0/6/23/26	0/1/1/1
8	NAG	D	201	2	-	1/6/23/26	0/1/1/1
8	NAG	A	701	1	-	0/6/23/26	0/1/1/1
8	NAG	H	202	2	-	2/6/23/26	0/1/1/1
8	NAG	C	701	1	-	0/6/23/26	0/1/1/1
8	NAG	B	201	2	-	1/6/23/26	0/1/1/1
8	NAG	E	701	1	-	2/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	202	NAG	C1-C2	4.01	1.57	1.52
8	H	202	NAG	O5-C1	2.58	1.48	1.43
8	G	701	NAG	O5-C1	2.48	1.47	1.43
8	B	201	NAG	O5-C1	2.37	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	702	NAG	O5-C1	2.11	1.47	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	201	NAG	C1-O5-C5	3.38	116.72	112.19
8	F	201	NAG	C1-O5-C5	2.91	116.09	112.19
8	B	201	NAG	C1-O5-C5	2.89	116.06	112.19
8	D	201	NAG	C1-O5-C5	2.82	115.97	112.19
8	E	702	NAG	C1-O5-C5	2.65	115.73	112.19

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	702	NAG	O5-C5-C6-O6
8	H	202	NAG	O5-C5-C6-O6
8	A	702	NAG	C4-C5-C6-O6
8	E	701	NAG	C8-C7-N2-C2
8	E	701	NAG	O7-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	H	201	NAG	1	0
8	D	201	NAG	1	0
8	H	202	NAG	3	0
8	B	201	NAG	1	0
8	E	701	NAG	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	421/441 (95%)	-0.38	3 (0%) 84 83	12, 29, 57, 84	0
1	C	418/441 (94%)	-0.45	5 (1%) 76 75	14, 27, 58, 82	0
1	E	421/441 (95%)	-0.56	0 100 100	12, 23, 46, 74	0
1	G	418/441 (94%)	-0.16	4 (0%) 79 78	17, 36, 68, 97	0
2	B	133/141 (94%)	-0.09	1 (0%) 82 81	20, 40, 70, 76	0
2	D	139/141 (98%)	0.13	5 (3%) 46 42	22, 46, 82, 93	0
2	F	133/141 (94%)	-0.23	2 (1%) 72 70	18, 35, 60, 71	0
2	H	139/141 (98%)	-0.16	2 (1%) 73 72	17, 36, 64, 80	0
All	All	2222/2328 (95%)	-0.31	22 (0%) 79 78	12, 31, 64, 97	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	554	ASP	4.1
1	G	177	GLY	3.3
1	A	421	GLY	3.3
2	D	124	LEU	3.2
2	D	70	VAL	2.9

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.

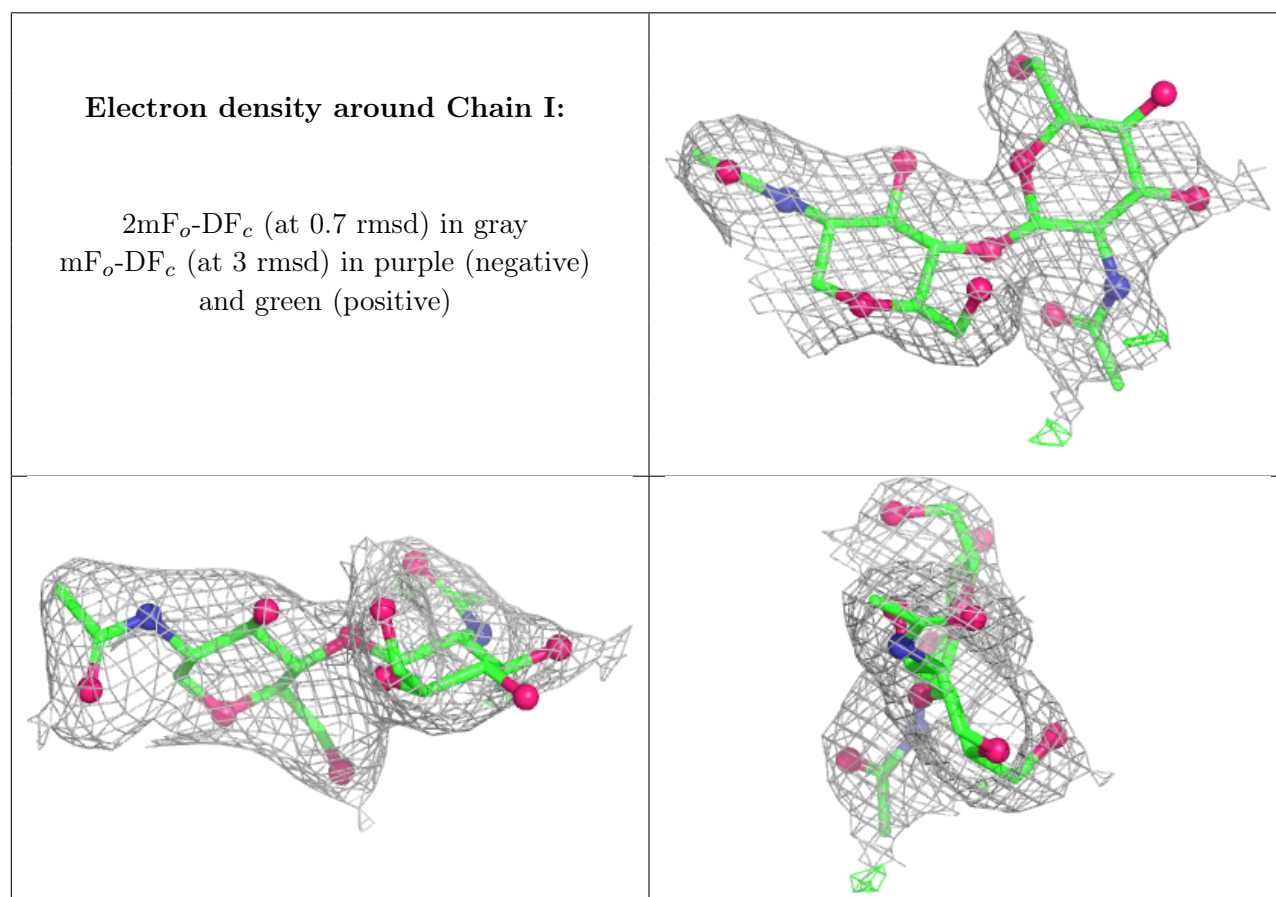
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	K	5	11/12	0.38	0.20	92,103,113,116	0
4	BMA	K	3	11/12	0.62	0.12	85,95,101,103	0
7	BMA	Q	3	11/12	0.63	0.12	74,84,90,91	0
3	NAG	L	2	14/15	0.66	0.12	55,79,90,93	0
6	BMA	O	3	11/12	0.68	0.12	75,83,92,94	0
3	NAG	M	2	14/15	0.68	0.14	60,77,89,98	0
6	NAG	R	2	14/15	0.69	0.11	74,87,93,102	0
3	NAG	I	2	14/15	0.70	0.12	53,71,85,87	0
6	BMA	R	3	11/12	0.72	0.13	65,80,91,93	0
3	NAG	P	2	14/15	0.74	0.13	50,63,73,81	0
6	NAG	R	1	14/15	0.75	0.12	56,77,90,103	0
6	NAG	O	2	14/15	0.78	0.11	40,65,83,90	0
3	NAG	J	2	14/15	0.78	0.12	52,82,87,88	0
3	NAG	S	2	14/15	0.79	0.13	65,76,80,81	0
3	NAG	J	1	14/15	0.81	0.11	30,62,85,91	0
4	MAN	K	4	11/12	0.84	0.11	74,93,102,105	0
4	FUC	K	6	10/11	0.85	0.10	43,51,61,72	0
4	BMA	T	3	11/12	0.85	0.11	29,42,58,68	0
3	NAG	L	1	14/15	0.88	0.09	28,55,69,83	0
7	NAG	Q	2	14/15	0.89	0.11	42,53,74,83	0
3	NAG	I	1	14/15	0.89	0.10	28,46,53,67	0
6	NAG	O	1	14/15	0.90	0.08	30,40,58,61	0
7	FUC	Q	4	10/11	0.90	0.09	34,47,51,55	0
4	FUC	K	7	10/11	0.91	0.08	33,36,45,46	0
4	NAG	K	2	14/15	0.91	0.09	38,57,82,86	0
4	FUC	T	6	10/11	0.91	0.09	26,36,41,57	0
3	NAG	P	1	14/15	0.92	0.09	21,39,56,68	0
5	BMA	N	4	11/12	0.93	0.07	27,31,43,44	0
4	MAN	T	4	11/12	0.93	0.07	25,32,40,48	0
7	FUC	Q	5	10/11	0.93	0.07	20,28,46,48	0
5	NAG	N	2	14/15	0.94	0.09	16,29,38,42	0
4	MAN	T	5	11/12	0.94	0.07	36,44,51,57	0
3	NAG	M	1	14/15	0.94	0.08	24,38,60,70	0
4	FUC	T	7	10/11	0.94	0.08	23,28,40,53	0
4	NAG	T	2	14/15	0.95	0.06	20,29,37,41	0
3	NAG	S	1	14/15	0.95	0.08	24,38,60,75	0
5	MAN	N	5	11/12	0.95	0.06	18,25,32,35	0
5	FUC	N	6	10/11	0.95	0.07	21,28,33,42	0
5	FUC	N	7	10/11	0.95	0.06	15,27,32,32	0
5	MAN	N	3	11/12	0.96	0.05	27,33,41,44	0
7	NAG	Q	1	14/15	0.96	0.06	18,34,43,50	0

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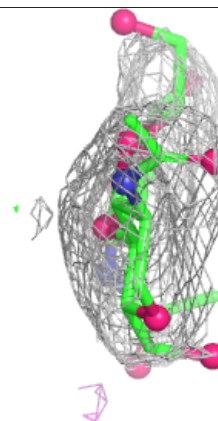
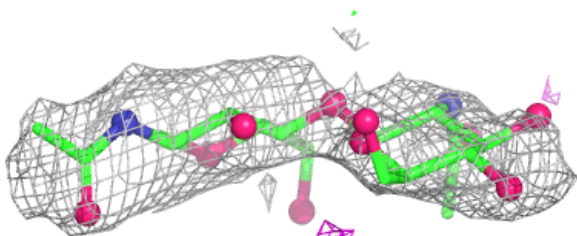
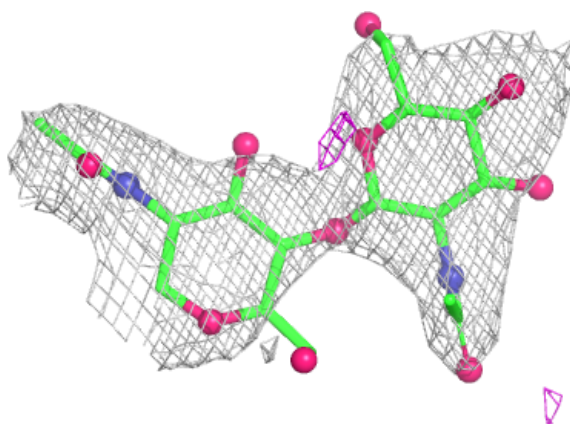
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	K	1	14/15	0.96	0.06	30,39,51,56	0
5	NAG	N	1	14/15	0.97	0.05	15,20,28,31	0
4	NAG	T	1	14/15	0.97	0.05	18,23,29,33	0

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.

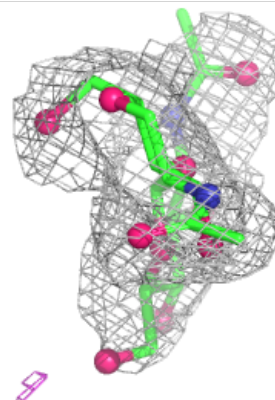
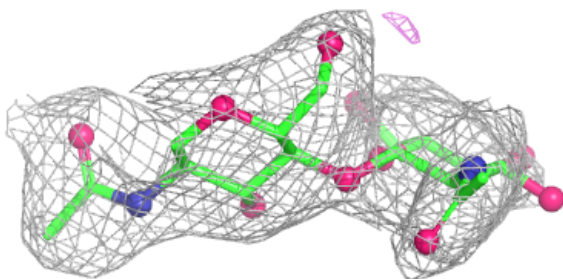
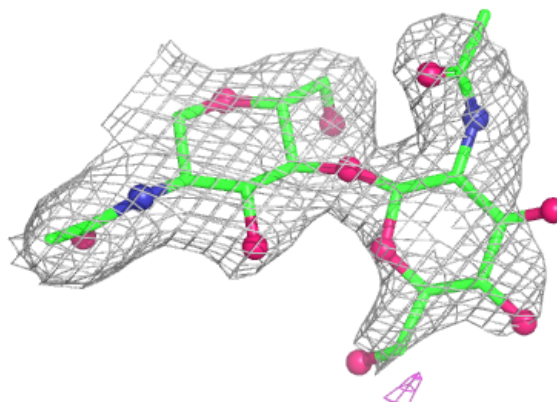


Electron density around Chain J:

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

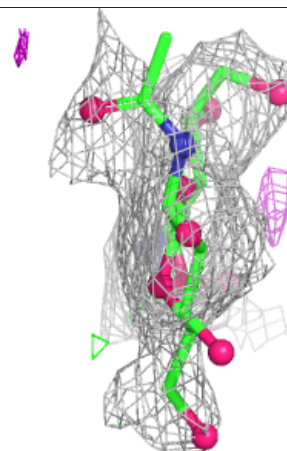
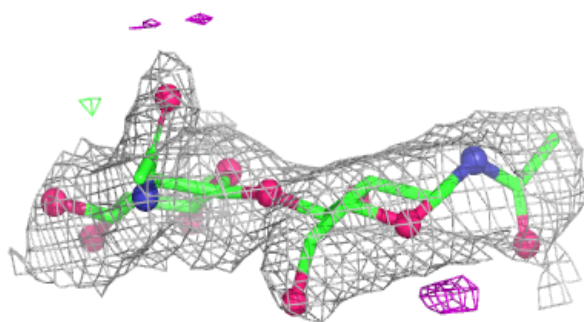
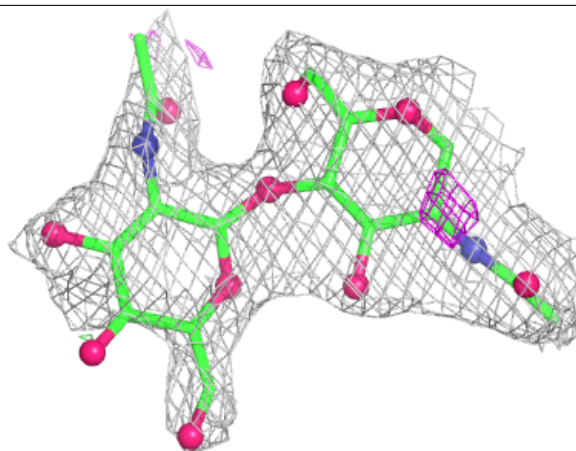
**Electron density around Chain L:**

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



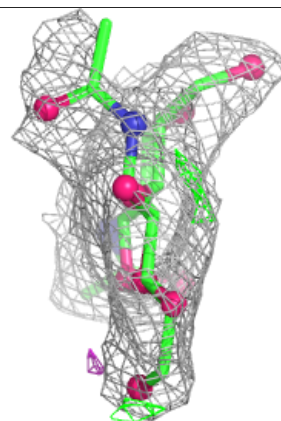
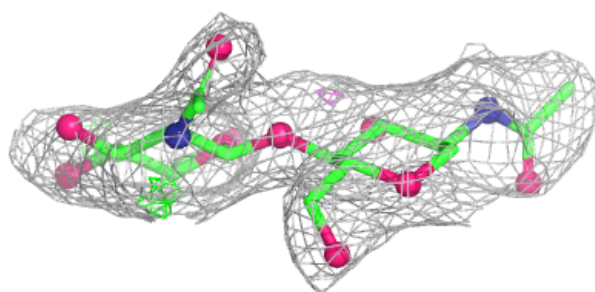
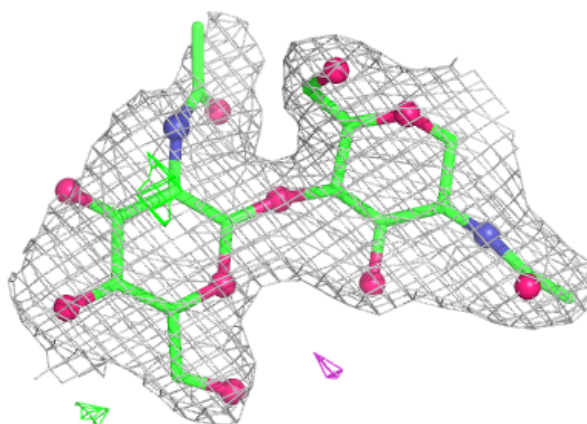
Electron density around Chain M:

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



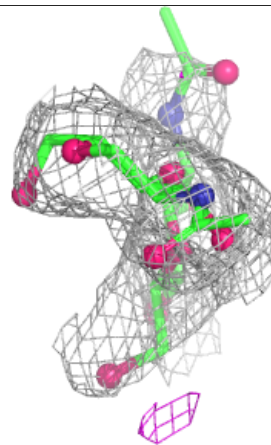
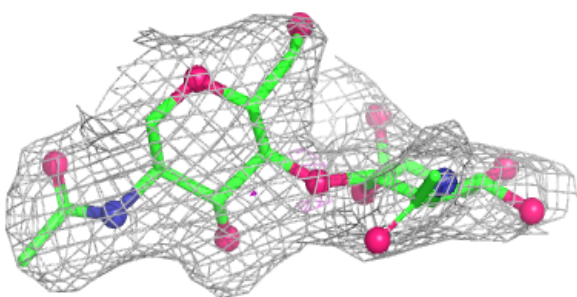
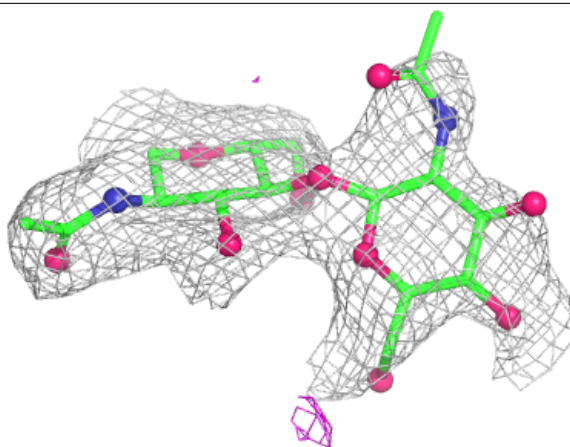
Electron density around Chain P:

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



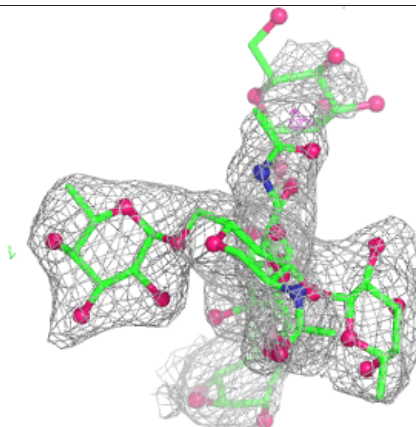
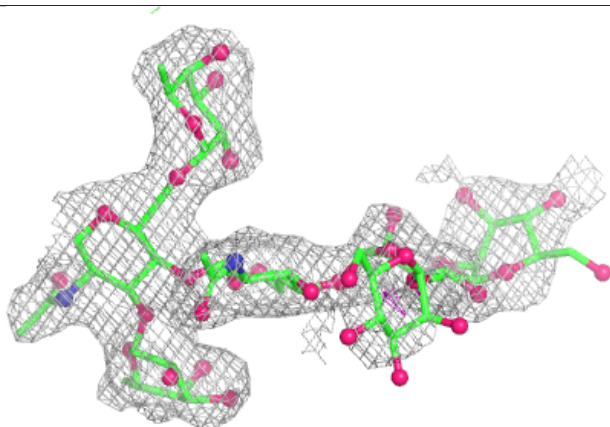
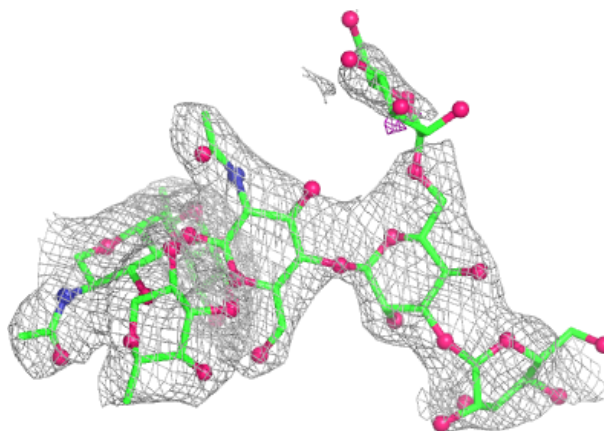
Electron density around Chain S:

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

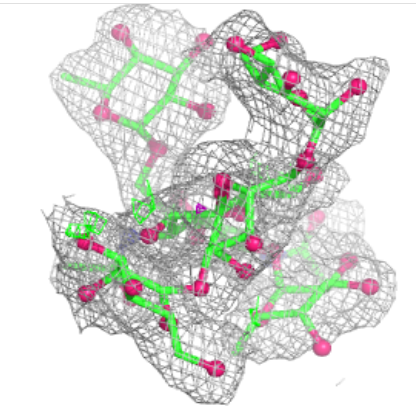
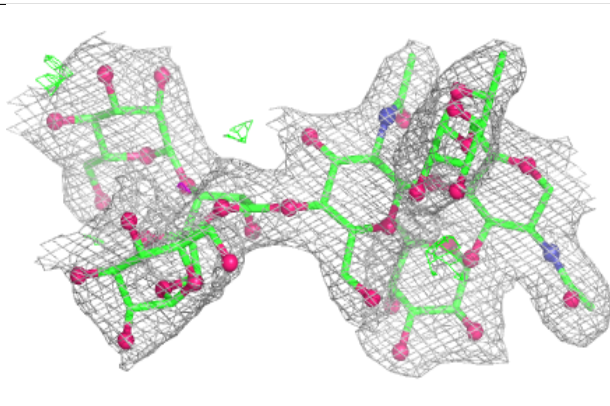
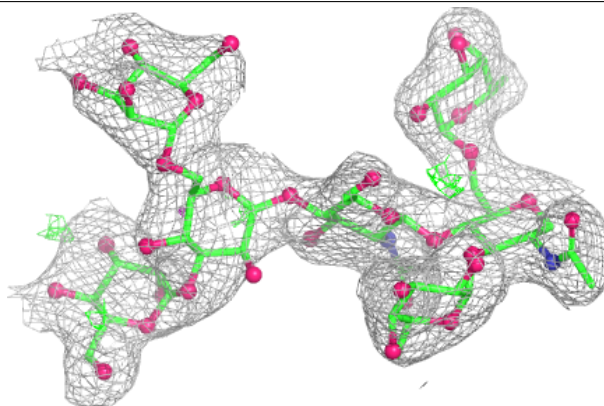


Electron density around Chain K:

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

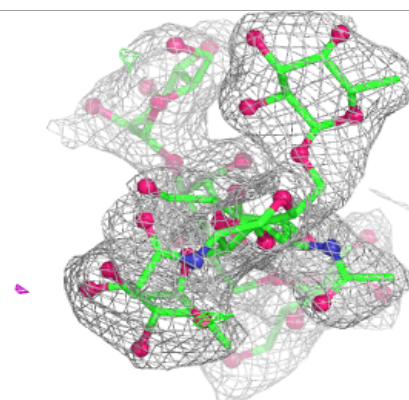
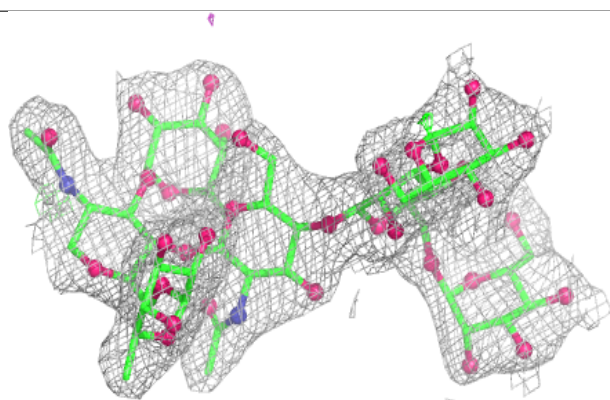
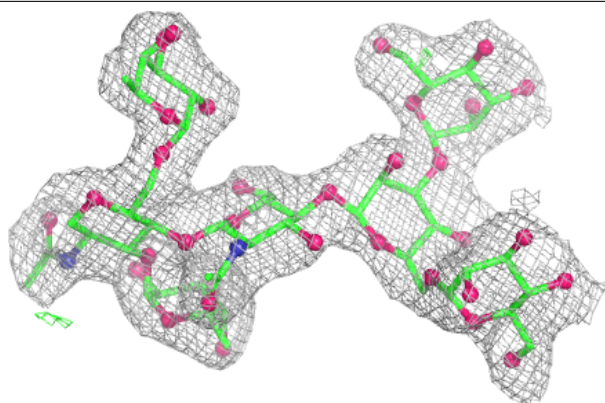
**Electron density around Chain T:**

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

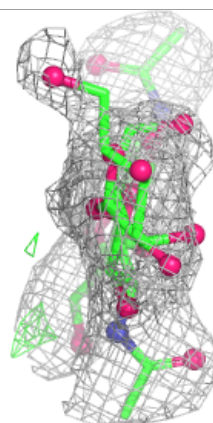
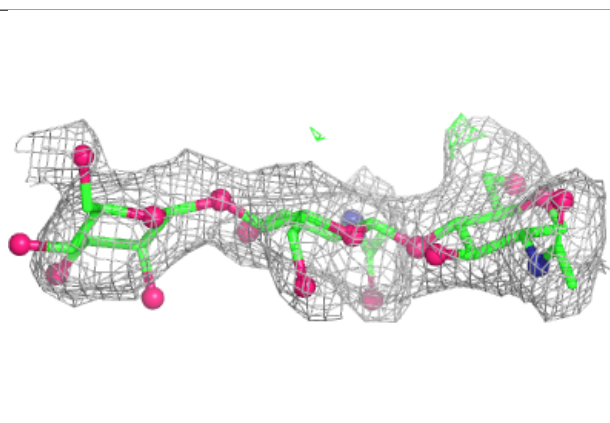
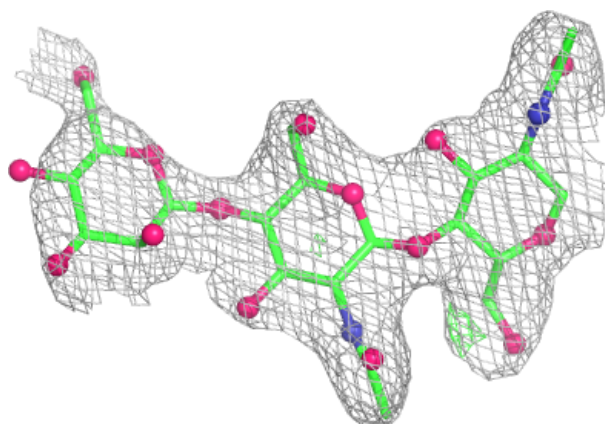


Electron density around Chain N:

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

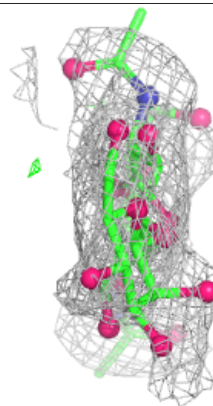
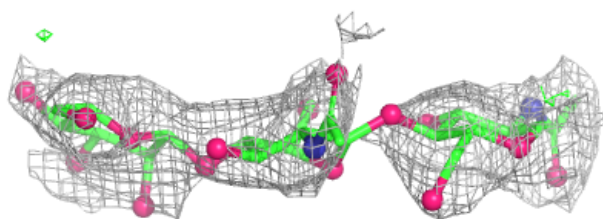
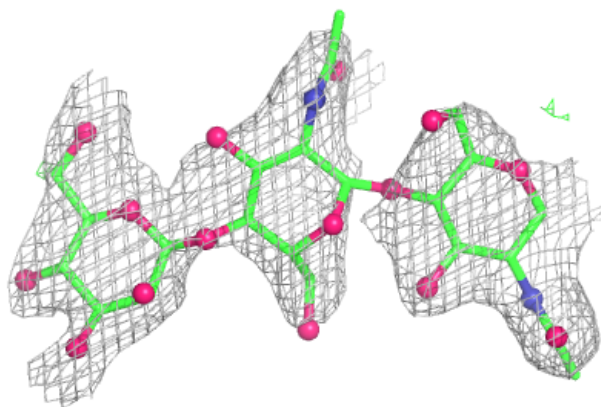
**Electron density around Chain O:**

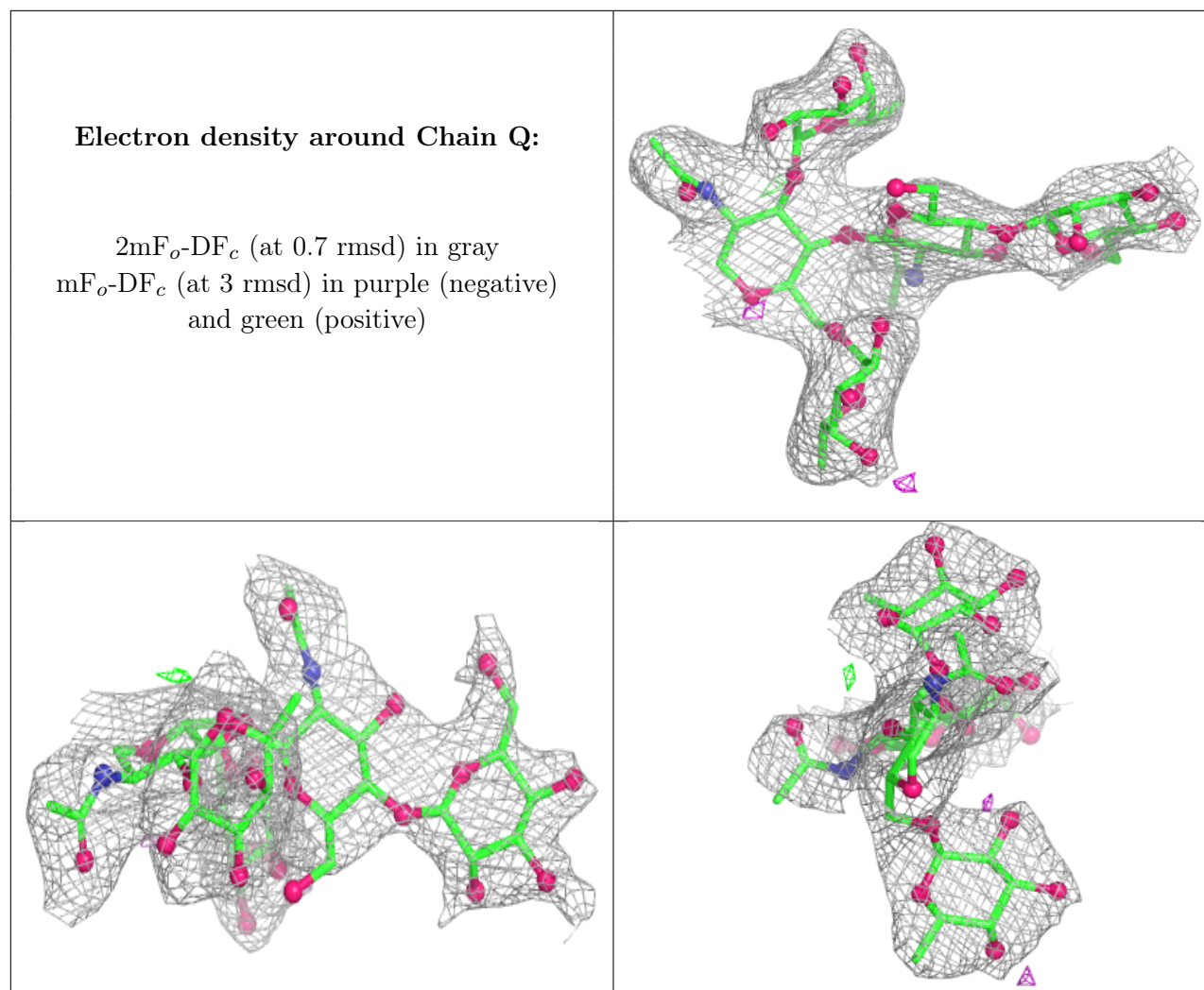
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain R:

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





6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	NAG	F	201	14/15	0.50	0.15	60,88,103,105	0
8	NAG	C	702	14/15	0.54	0.14	46,73,89,89	0
8	NAG	G	701	14/15	0.54	0.18	70,78,100,102	0
8	NAG	G	702	14/15	0.57	0.15	42,81,91,94	0
8	NAG	H	202	14/15	0.62	0.16	41,75,88,92	0
8	NAG	E	702	14/15	0.63	0.15	47,67,81,83	0
8	NAG	E	701	14/15	0.65	0.15	44,70,79,86	0
8	NAG	A	702	14/15	0.66	0.15	58,81,91,95	0
8	NAG	B	201	14/15	0.67	0.14	52,69,93,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NAG	H	201	14/15	0.68	0.13	56,70,87,95	0
8	NAG	C	701	14/15	0.73	0.14	55,62,81,102	0
8	NAG	A	701	14/15	0.76	0.13	47,71,82,83	0
8	NAG	D	201	14/15	0.80	0.10	55,61,68,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.