



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 07:44 AM EDT

PDB ID : 9S90 / pdb_00009s90
Title : Crystal structure of the BRL3 ectodomain from Arabidopsis thaliana in complex with castasterone.
Authors : Caregnato, A.; Hothorn, M.
Deposited on : 2025-08-05
Resolution : 2.61 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

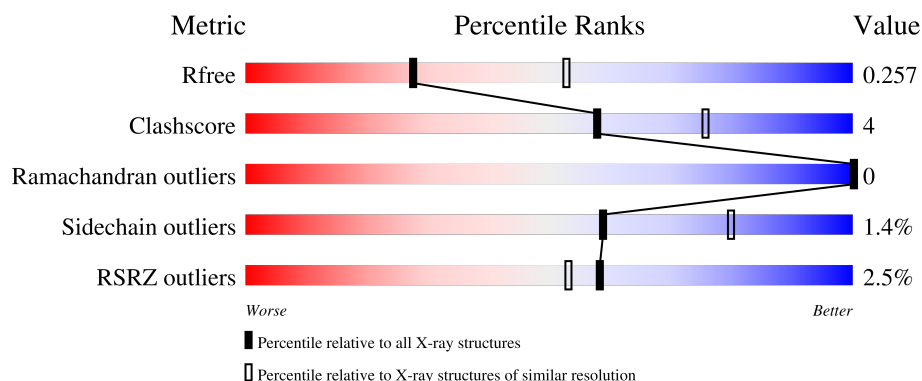
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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.



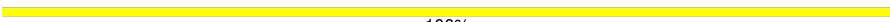
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	779	2% 85% 8% 8%
1	B	779	2% 82% 11% 7%
2	C	2	50% 50%
2	D	2	50% 50%
2	G	2	50% 50%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	I	2	 100%
2	J	2	 100%
2	K	2	 100%
2	L	2	 100%
2	O	2	 100%
2	Q	2	 100%
2	R	2	 50% 50%
3	E	11	 9% 82% 9%
4	F	3	 33% 67%
4	N	3	 67% 33%
5	H	3	 33% 67%
5	P	3	 67% 33%
6	M	10	 10% 80% 10%

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
10	ACT	B	808	-	-	X	-
9	SO4	B	809	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 23159 atoms, of which 11485 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 Receptor-like protein kinase BRI1-like 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	720	Total	C	H	N	O	S	0	0	0
			10732	3382	5348	906	1069	27			
1	B	726	Total	C	H	N	O	S	0	0	0
			10813	3409	5382	915	1080	27			

There are 18 discrepancies between the modelled and reference sequences:

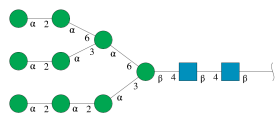
Chain	Residue	Modelled	Actual	Comment	Reference
A	771	ALA	-	expression tag	UNP Q9LJF3
A	772	ALA	-	expression tag	UNP Q9LJF3
A	773	ALA	-	expression tag	UNP Q9LJF3
A	774	GLU	-	expression tag	UNP Q9LJF3
A	775	ASN	-	expression tag	UNP Q9LJF3
A	776	LEU	-	expression tag	UNP Q9LJF3
A	777	TYR	-	expression tag	UNP Q9LJF3
A	778	PHE	-	expression tag	UNP Q9LJF3
A	779	GLN	-	expression tag	UNP Q9LJF3
B	771	ALA	-	expression tag	UNP Q9LJF3
B	772	ALA	-	expression tag	UNP Q9LJF3
B	773	ALA	-	expression tag	UNP Q9LJF3
B	774	GLU	-	expression tag	UNP Q9LJF3
B	775	ASN	-	expression tag	UNP Q9LJF3
B	776	LEU	-	expression tag	UNP Q9LJF3
B	777	TYR	-	expression tag	UNP Q9LJF3
B	778	PHE	-	expression tag	UNP Q9LJF3
B	779	GLN	-	expression tag	UNP Q9LJF3

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



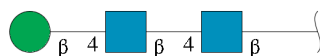
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	D	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	G	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	I	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	J	2	Total 52	C 16	H 24	N 2	O 10	0	0	0
2	K	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	L	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	O	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	Q	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	R	2	Total 53	C 16	H 25	N 2	O 10	0	0	0

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



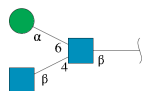
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	11	Total	C	H	N	O	0	0	0
			233	70	106	2	55			

- Molecule 4 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.



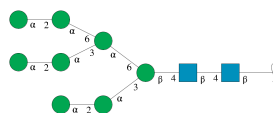
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	3	Total	C	H	N	O	0	0	0
			73	22	34	2	15			
4	N	3	Total	C	H	N	O	0	0	0
			73	22	34	2	15			

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



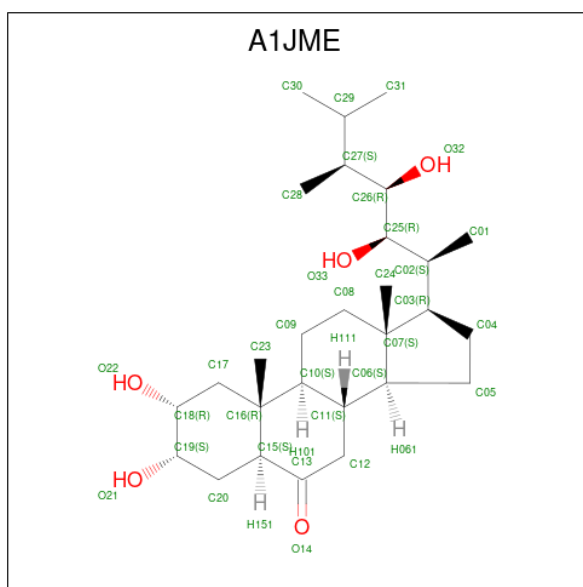
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	H	3	Total	C	H	N	O	0	0	0
			73	22	34	2	15			
5	P	3	Total	C	H	N	O	0	0	0
			73	22	34	2	15			

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



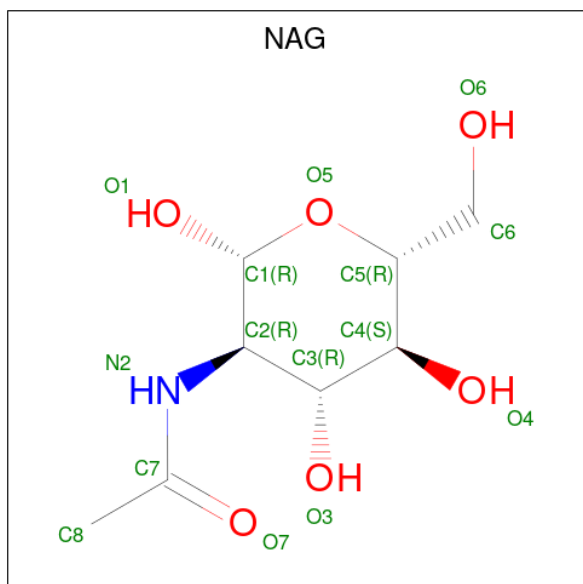
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	M	10	Total	C	H	N	O	0	0	0
			213	64	97	2	50			

- Molecule 7 is Castasterone (CCD ID: A1JME) (formula: C₂₈H₄₈O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			81	28	48	5		
7	B	1	Total	C	H	O	0	0
			81	28	48	5		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



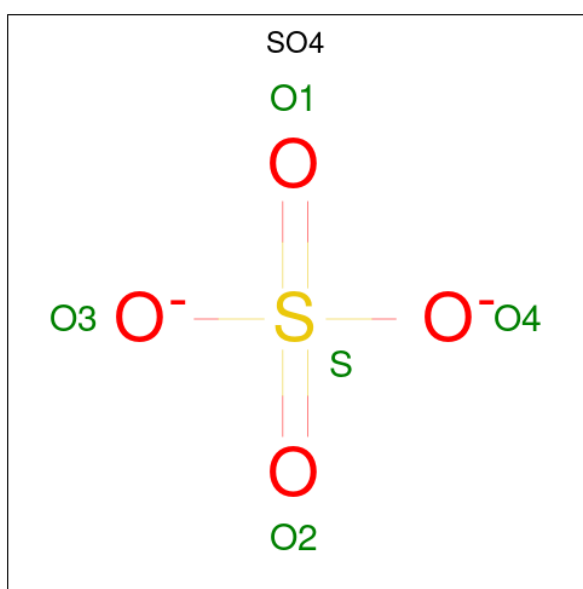
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

Continued on next page...

Continued from previous page...

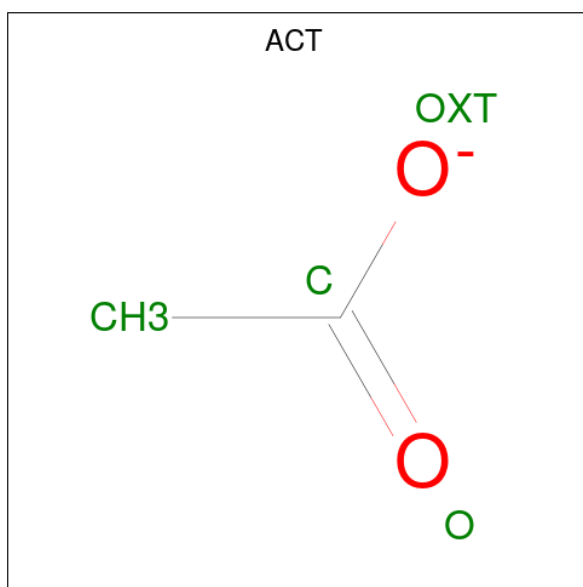
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	
			27	8	13	1	5	
8	B	1	Total	C	H	N	O	
			27	8	13	1	5	
8	B	1	Total	C	H	N	O	
			27	8	13	1	5	
8	B	1	Total	C	H	N	O	
			27	8	13	1	5	

- Molecule 9 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 10 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	H	O	0	0
			7	2	3	2		
10	B	1	Total	C	H	O	0	0
			7	2	3	2		

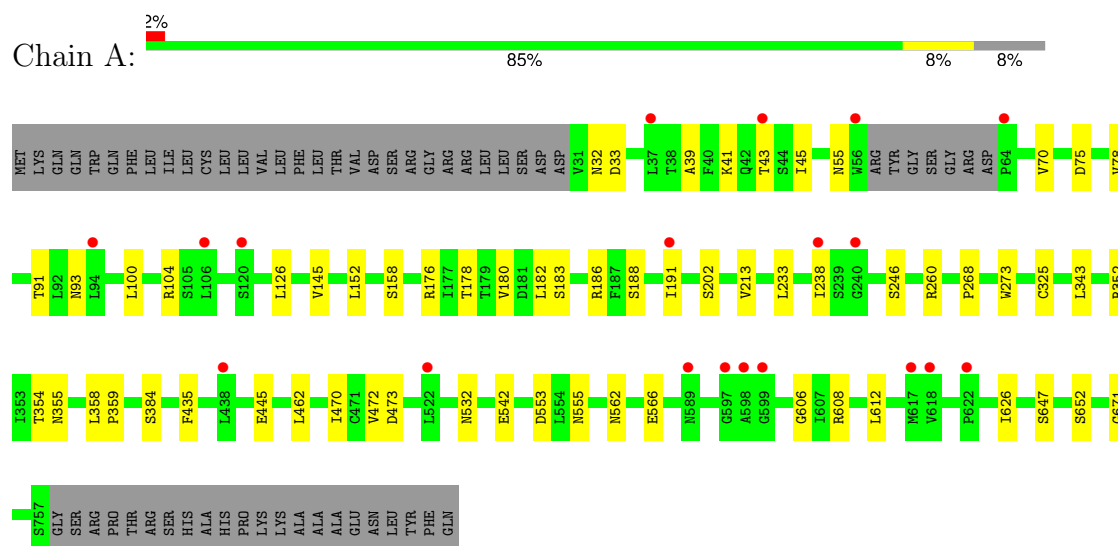
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	4	Total	O	0	0
			4	4		
11	B	7	Total	O	0	0
			7	7		

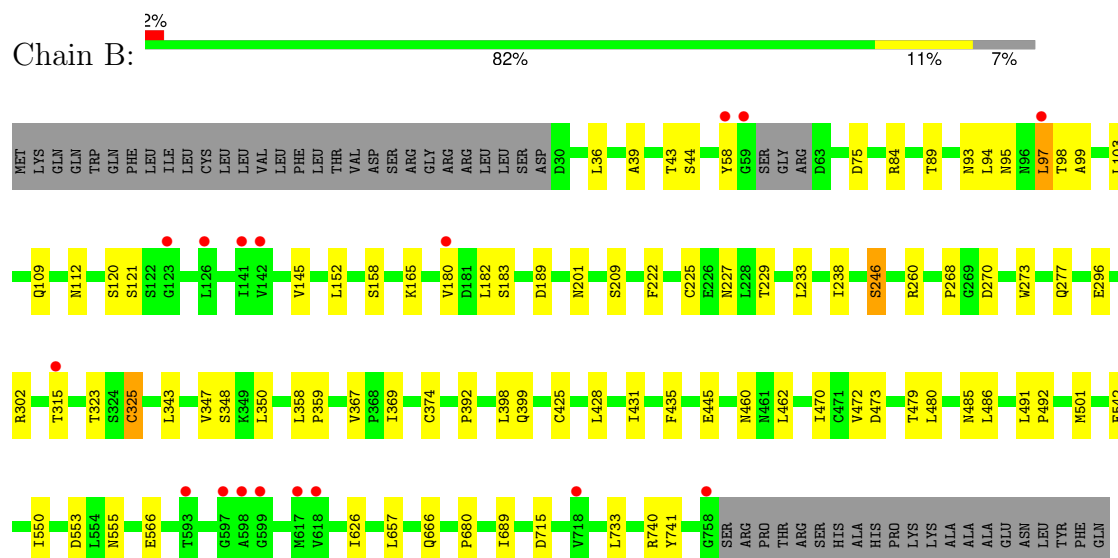
3 Residue-property plots [i](#)

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: Receptor-like protein kinase BRI1-like 3



- Molecule 1: Receptor-like protein kinase BRI1-like 3



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

Chain C:  50% 50%

MAG1
MAG2

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

Chain D:  50% 50%

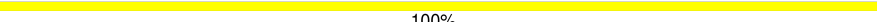
MAG1
MAG2

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

Chain G:  50% 50%

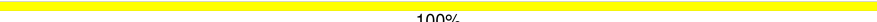
MAG1
MAG2

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

Chain I:  100%

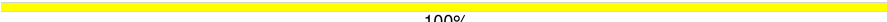
MAG1
MAG2

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

Chain J:  100%

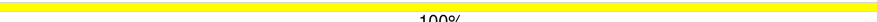
MAG1
MAG2

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

Chain K:  100%

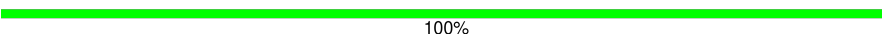
MAG1
MAG2

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

Chain L:  100%

MAG1
MAG2

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

Chain O:  100%

MAG1
MAG2

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

Chain Q:  100%

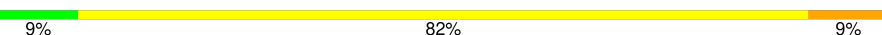
MAG1
MAG2

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

Chain R:  50% 50%

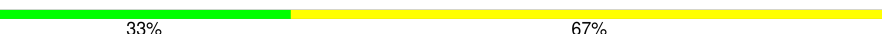
MAG1
MAG2

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

Chain E:  9% 82% 9%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10
MAN11

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

Chain F:  33% 67%

MAG1
MAG2
BMA3

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

Chain N:  67% 33%

MAG1
MAG2
BMA3

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

Chain H:  33% 67%

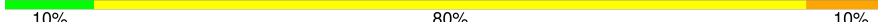
MAG1
MAG2
MAN3

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

Chain P:  67% 33%

MAG1
MAG2
MAN3

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

Chain M:  10% 80% 10%

MAG1
MAG2
MAN3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	62.26Å 81.94Å 122.48Å 107.02° 91.50° 112.53°	Depositor
Resolution (Å)	49.35 – 2.61 49.35 – 2.61	Depositor EDS
% Data completeness (in resolution range)	91.4 (49.35-2.61) 77.7 (49.35-2.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.44 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.223 , 0.258 0.226 , 0.257	Depositor DCC
R_{free} test set	2936 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	58.4	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.014 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23159	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: NAG, A1JME, BMA, SO4, ACT, MAN

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	0.13	0/5478	0.34	0/7442
1	B	0.14	0/5526	0.35	0/7507
All	All	0.14	0/11004	0.35	0/14949

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	5384	5348	5347	41	0
1	B	5431	5382	5381	56	0
2	C	28	25	25	3	0
2	D	28	25	25	0	0
2	G	28	25	25	2	0
2	I	28	25	25	0	0
2	J	28	24	25	0	0
2	K	28	25	25	0	0
2	L	28	25	25	0	0
2	O	28	25	25	0	0
2	Q	28	25	25	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	28	25	25	0	0
3	E	127	106	106	1	0
4	F	39	34	34	0	0
4	N	39	34	34	0	0
5	H	39	34	34	1	0
5	P	39	34	34	0	0
6	M	116	97	97	1	0
7	A	33	48	0	0	0
7	B	33	48	0	0	0
8	A	28	26	26	2	0
8	B	42	39	39	1	0
9	A	10	0	0	0	0
9	B	15	0	0	2	0
10	B	8	6	6	2	0
11	A	4	0	0	0	0
11	B	7	0	0	0	0
All	All	11674	11485	11388	103	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 4.

The worst 5 of 103 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:612:LEU:HD23	1:A:626:ILE:HD11	1.43	0.98
1:A:612:LEU:HD23	1:A:626:ILE:CD1	2.12	0.80
1:B:733:LEU:O	1:B:741:TYR:OH	2.02	0.75
1:A:93:ASN:HB3	2:C:1:NAG:H82	1.71	0.72
1:B:277:GLN:OE1	1:B:302:ARG:NH1	2.24	0.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	716/779 (92%)	654 (91%)	62 (9%)	0	100	100
1	B	722/779 (93%)	659 (91%)	63 (9%)	0	100	100
All	All	1438/1558 (92%)	1313 (91%)	125 (9%)	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	628/679 (92%)	620 (99%)	8 (1%)	61	81
1	B	632/679 (93%)	622 (98%)	10 (2%)	55	78
All	All	1260/1358 (93%)	1242 (99%)	18 (1%)	59	80

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	325	CYS
1	B	550	ILE
1	B	479	THR
1	B	58	TYR
1	B	323	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	95	ASN
1	B	562	ASN
1	B	102	ASN
1	B	732	GLN
1	B	483	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 ⓘ

53 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	2,1	14,14,15	0.62	0	17,19,21	1.11	1 (5%)
2	NAG	C	2	2	14,14,15	0.69	0	17,19,21	1.63	3 (17%)
2	NAG	D	1	2,1	14,14,15	0.75	0	17,19,21	1.44	2 (11%)
2	NAG	D	2	2	14,14,15	0.70	0	17,19,21	0.84	0
3	NAG	E	1	1,3	14,14,15	0.69	0	17,19,21	1.47	2 (11%)
3	MAN	E	10	3	11,11,12	0.76	0	15,15,17	1.17	1 (6%)
3	MAN	E	11	3	11,11,12	0.72	0	15,15,17	1.10	1 (6%)
3	NAG	E	2	3	14,14,15	0.78	0	17,19,21	1.10	1 (5%)
3	BMA	E	3	3	11,11,12	0.81	0	15,15,17	2.58	6 (40%)
3	MAN	E	4	3	11,11,12	0.69	0	15,15,17	1.19	1 (6%)
3	MAN	E	5	3	11,11,12	0.87	1 (9%)	15,15,17	0.92	0
3	MAN	E	6	3	11,11,12	0.74	0	15,15,17	0.88	0
3	MAN	E	7	3	11,11,12	0.96	1 (9%)	15,15,17	0.83	0
3	MAN	E	8	3	11,11,12	0.87	1 (9%)	15,15,17	0.94	0
3	MAN	E	9	3	11,11,12	0.80	1 (9%)	15,15,17	0.91	0
4	NAG	F	1	4,1	14,14,15	0.78	0	17,19,21	0.84	0
4	NAG	F	2	4	14,14,15	0.73	0	17,19,21	0.99	1 (5%)
4	BMA	F	3	4	11,11,12	0.77	0	15,15,17	2.90	6 (40%)
2	NAG	G	1	2,1	14,14,15	0.74	0	17,19,21	1.73	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	G	2	2	14,14,15	0.74	0	17,19,21	0.84	0
5	NAG	H	1	1,5	14,14,15	0.76	0	17,19,21	1.11	0
5	NAG	H	2	5	14,14,15	0.70	0	17,19,21	0.90	1 (5%)
5	MAN	H	3	5	11,11,12	0.80	1 (9%)	15,15,17	1.05	1 (6%)
2	NAG	I	1	2,1	14,14,15	0.69	0	17,19,21	1.22	2 (11%)
2	NAG	I	2	2	14,14,15	0.70	0	17,19,21	1.46	2 (11%)
2	NAG	J	1	2,1	14,14,15	0.72	0	17,19,21	1.01	2 (11%)
2	NAG	J	2	2	14,14,15	0.74	0	17,19,21	0.99	1 (5%)
2	NAG	K	1	2,1	14,14,15	0.67	0	17,19,21	1.63	2 (11%)
2	NAG	K	2	2	14,14,15	0.68	0	17,19,21	0.93	1 (5%)
2	NAG	L	1	2,1	14,14,15	0.69	0	17,19,21	1.17	2 (11%)
2	NAG	L	2	2	14,14,15	0.69	0	17,19,21	1.48	2 (11%)
6	NAG	M	1	6,1	14,14,15	0.70	0	17,19,21	0.97	2 (11%)
6	MAN	M	10	6	11,11,12	0.76	0	15,15,17	0.88	0
6	NAG	M	2	6	14,14,15	0.69	0	17,19,21	1.09	2 (11%)
6	BMA	M	3	6	11,11,12	0.86	0	15,15,17	2.31	5 (33%)
6	MAN	M	4	6	11,11,12	0.94	1 (9%)	15,15,17	0.87	0
6	MAN	M	5	6	11,11,12	0.74	0	15,15,17	1.12	1 (6%)
6	MAN	M	6	6	11,11,12	0.80	1 (9%)	15,15,17	0.83	0
6	MAN	M	7	6	11,11,12	0.76	0	15,15,17	0.98	1 (6%)
6	MAN	M	8	6	11,11,12	0.82	1 (9%)	15,15,17	0.82	0
6	MAN	M	9	6	11,11,12	0.78	0	15,15,17	1.12	1 (6%)
4	NAG	N	1	4,1	14,14,15	0.81	0	17,19,21	0.80	0
4	NAG	N	2	4	14,14,15	0.76	0	17,19,21	0.80	0
4	BMA	N	3	4	11,11,12	0.77	0	15,15,17	2.09	3 (20%)
2	NAG	O	1	2,1	14,14,15	0.73	0	17,19,21	0.92	0
2	NAG	O	2	2	14,14,15	0.71	0	17,19,21	0.84	0
5	NAG	P	1	1,5	14,14,15	0.76	0	17,19,21	0.87	0
5	NAG	P	2	5	14,14,15	0.72	0	17,19,21	1.27	1 (5%)
5	MAN	P	3	5	11,11,12	0.79	0	15,15,17	0.81	0
2	NAG	Q	1	2,1	14,14,15	0.71	0	17,19,21	1.76	4 (23%)
2	NAG	Q	2	2	14,14,15	0.71	0	17,19,21	1.74	3 (17%)
2	NAG	R	1	2,1	14,14,15	0.70	0	17,19,21	0.95	1 (5%)
2	NAG	R	2	2	14,14,15	0.72	0	17,19,21	0.83	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	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	4/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	MAN	E	10	3	-	2/2/19/22	0/1/1/1
3	MAN	E	11	3	-	0/2/19/22	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	2/2/19/22	0/1/1/1
3	MAN	E	6	3	-	0/2/19/22	0/1/1/1
3	MAN	E	7	3	-	0/2/19/22	0/1/1/1
3	MAN	E	8	3	-	2/2/19/22	0/1/1/1
3	MAN	E	9	3	-	0/2/19/22	0/1/1/1
4	NAG	F	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	1/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
2	NAG	G	1	2,1	-	5/6/23/26	0/1/1/1
2	NAG	G	2	2	-	1/6/23/26	0/1/1/1
5	NAG	H	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	H	2	5	-	3/6/23/26	0/1/1/1
5	MAN	H	3	5	-	0/2/19/22	0/1/1/1
2	NAG	I	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	NAG	J	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	J	2	2	-	2/6/23/26	0/1/1/1
2	NAG	K	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	1/6/23/26	0/1/1/1
2	NAG	L	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	L	2	2	-	2/6/23/26	0/1/1/1
6	NAG	M	1	6,1	-	0/6/23/26	0/1/1/1
6	MAN	M	10	6	-	2/2/19/22	0/1/1/1
6	NAG	M	2	6	-	0/6/23/26	0/1/1/1
6	BMA	M	3	6	-	0/2/19/22	0/1/1/1
6	MAN	M	4	6	-	0/2/19/22	0/1/1/1
6	MAN	M	5	6	-	2/2/19/22	0/1/1/1
6	MAN	M	6	6	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	M	7	6	-	2/2/19/22	0/1/1/1
6	MAN	M	8	6	-	0/2/19/22	0/1/1/1
6	MAN	M	9	6	-	2/2/19/22	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	1/6/23/26	0/1/1/1
4	BMA	N	3	4	-	0/2/19/22	0/1/1/1
2	NAG	O	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	O	2	2	-	1/6/23/26	0/1/1/1
5	NAG	P	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	P	2	5	-	2/6/23/26	0/1/1/1
5	MAN	P	3	5	-	2/2/19/22	0/1/1/1
2	NAG	Q	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	Q	2	2	-	2/6/23/26	0/1/1/1
2	NAG	R	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	R	2	2	-	1/6/23/26	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)
3	E	7	MAN	O5-C1	-2.67	1.39	1.43
6	M	4	MAN	O5-C1	-2.55	1.39	1.43
3	E	5	MAN	O5-C1	-2.44	1.39	1.43
3	E	8	MAN	O5-C1	-2.29	1.39	1.43
6	M	8	MAN	O5-C1	-2.08	1.40	1.43

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	3	BMA	C1-O5-C5	9.04	124.30	112.19
3	E	3	BMA	C1-O5-C5	7.22	121.87	112.19
4	N	3	BMA	C1-O5-C5	6.55	120.97	112.19
6	M	3	BMA	C1-O5-C5	6.38	120.73	112.19
2	Q	2	NAG	C2-N2-C7	5.35	130.07	122.90

There are no chirality outliers.

5 of 58 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	P	2	NAG	C3-C2-N2-C7
2	J	2	NAG	O5-C5-C6-O6

Continued on next page...

Continued from previous page...

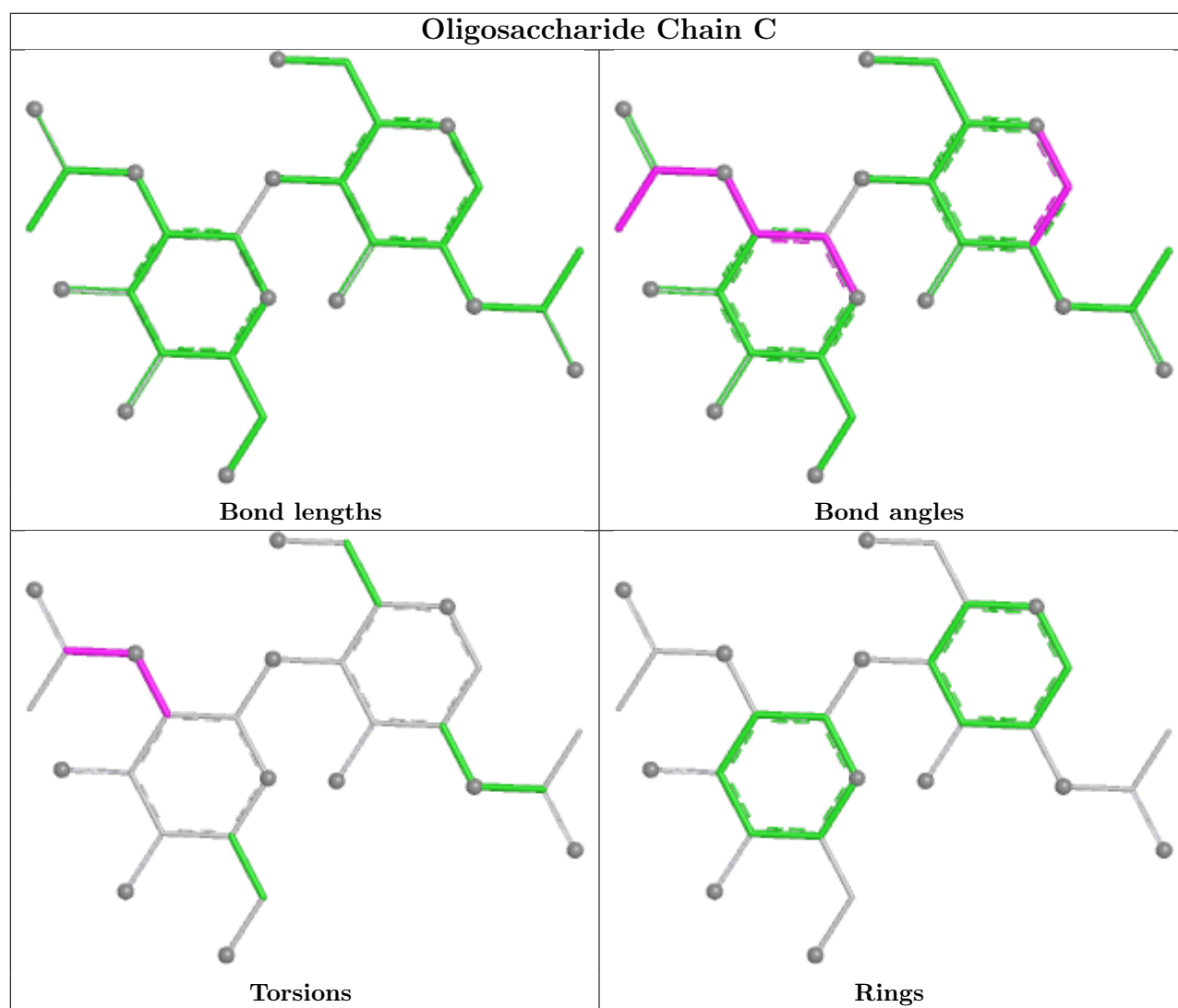
Mol	Chain	Res	Type	Atoms
6	M	9	MAN	O5-C5-C6-O6
3	E	10	MAN	O5-C5-C6-O6
6	M	7	MAN	O5-C5-C6-O6

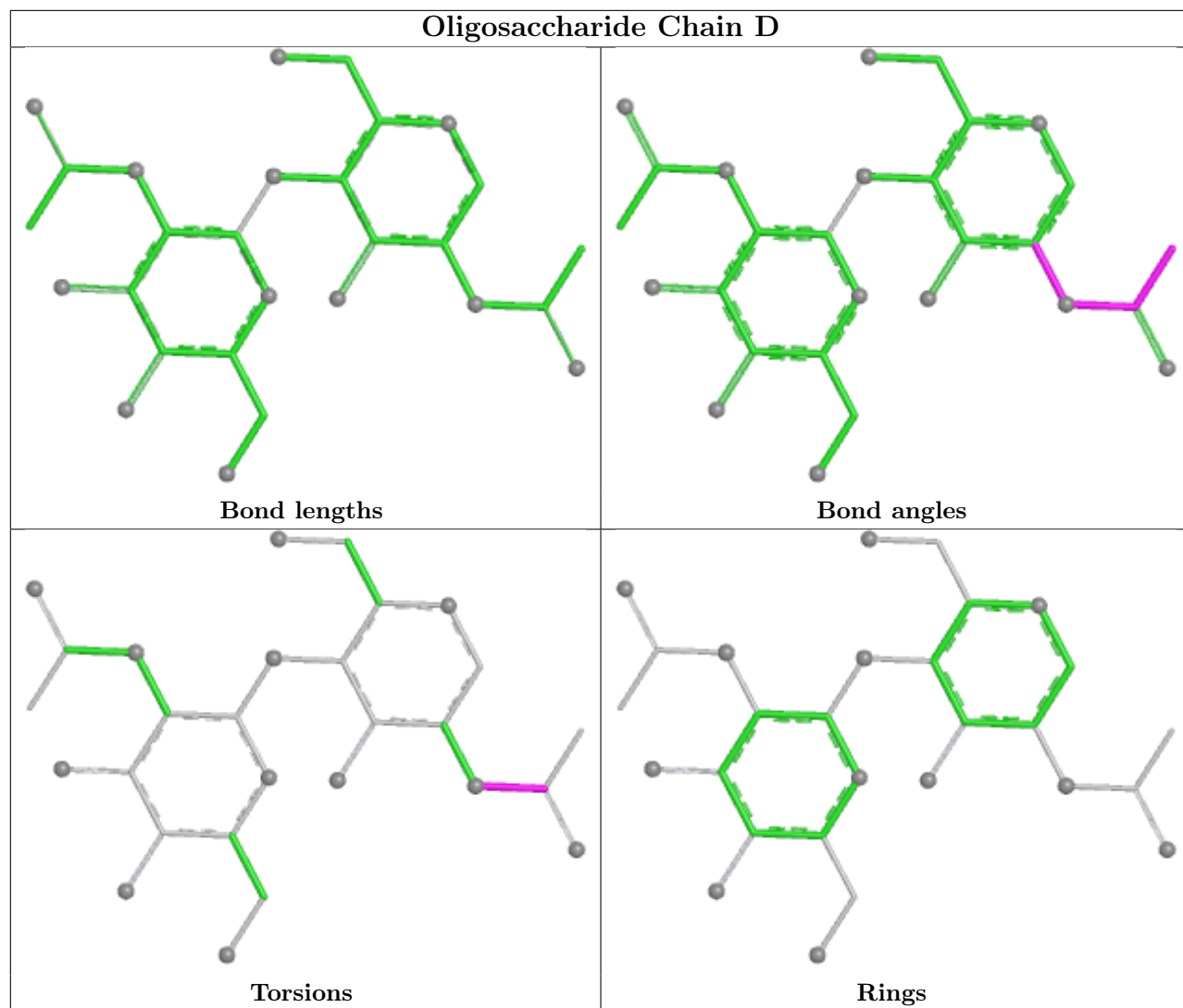
There are no ring outliers.

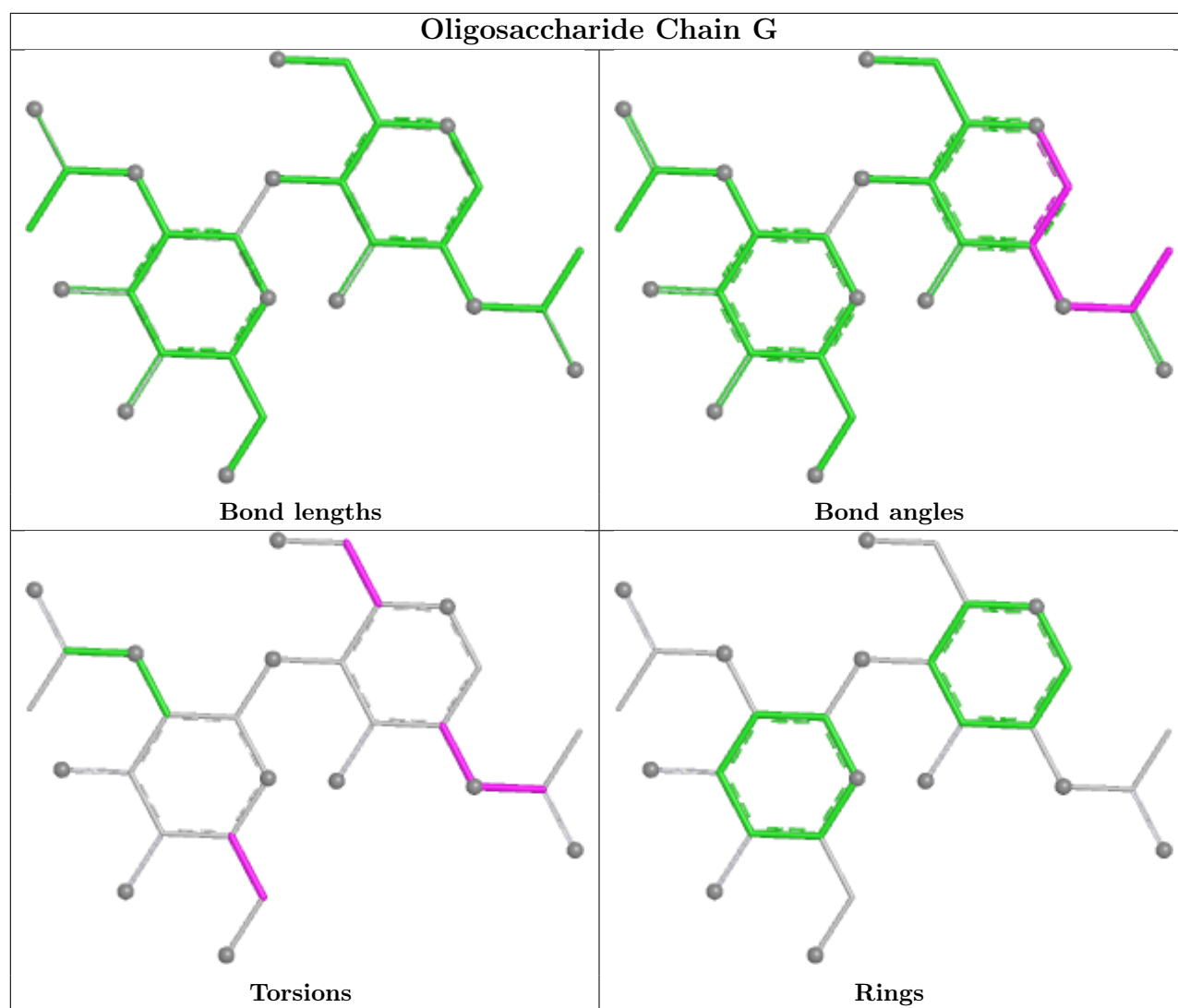
8 monomers are involved in 10 short contacts:

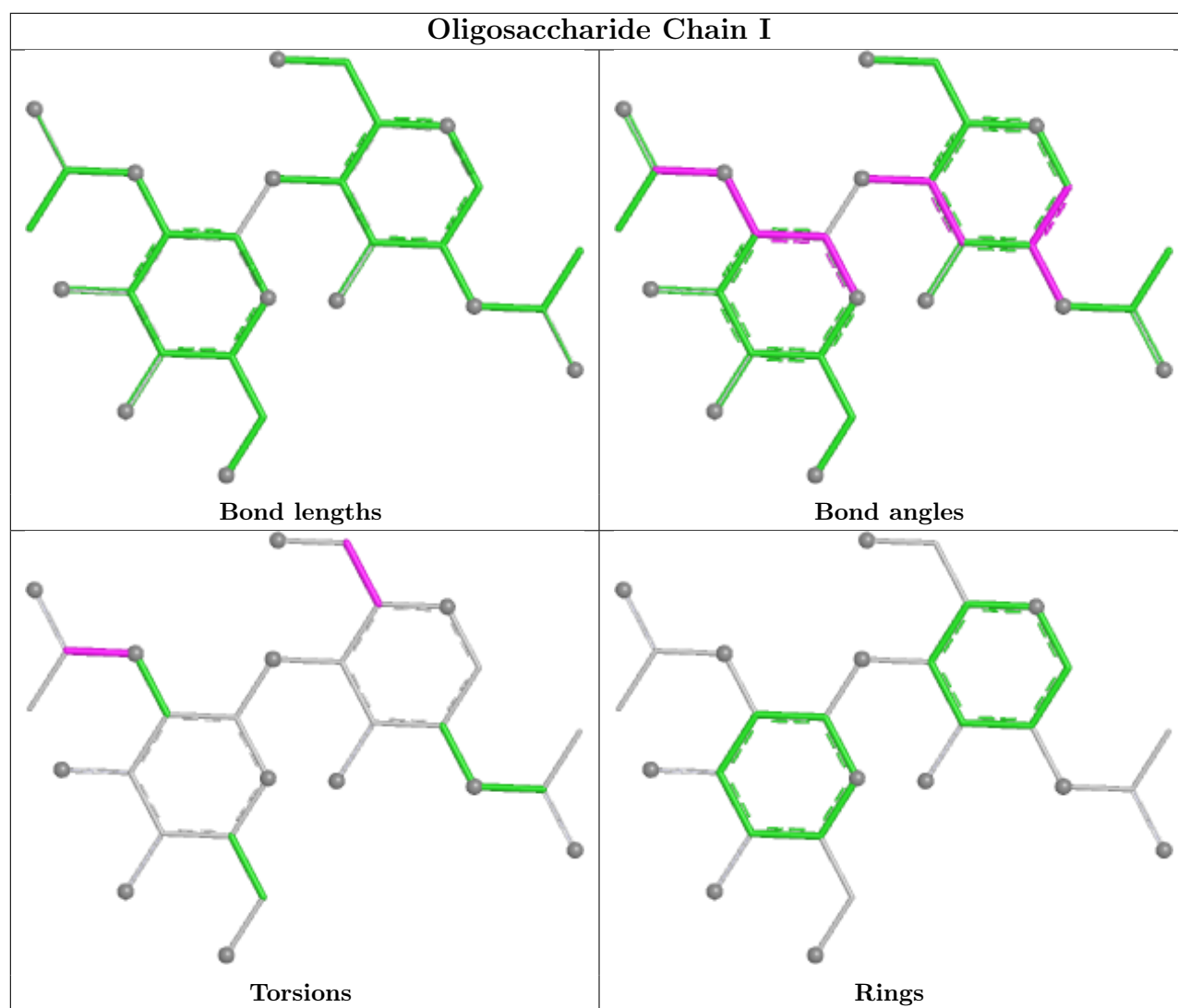
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	NAG	2	0
5	H	3	MAN	1	0
3	E	2	NAG	1	0
2	C	1	NAG	3	0
2	Q	1	NAG	2	0
2	Q	2	NAG	2	0
6	M	2	NAG	1	0
5	H	2	NAG	1	0

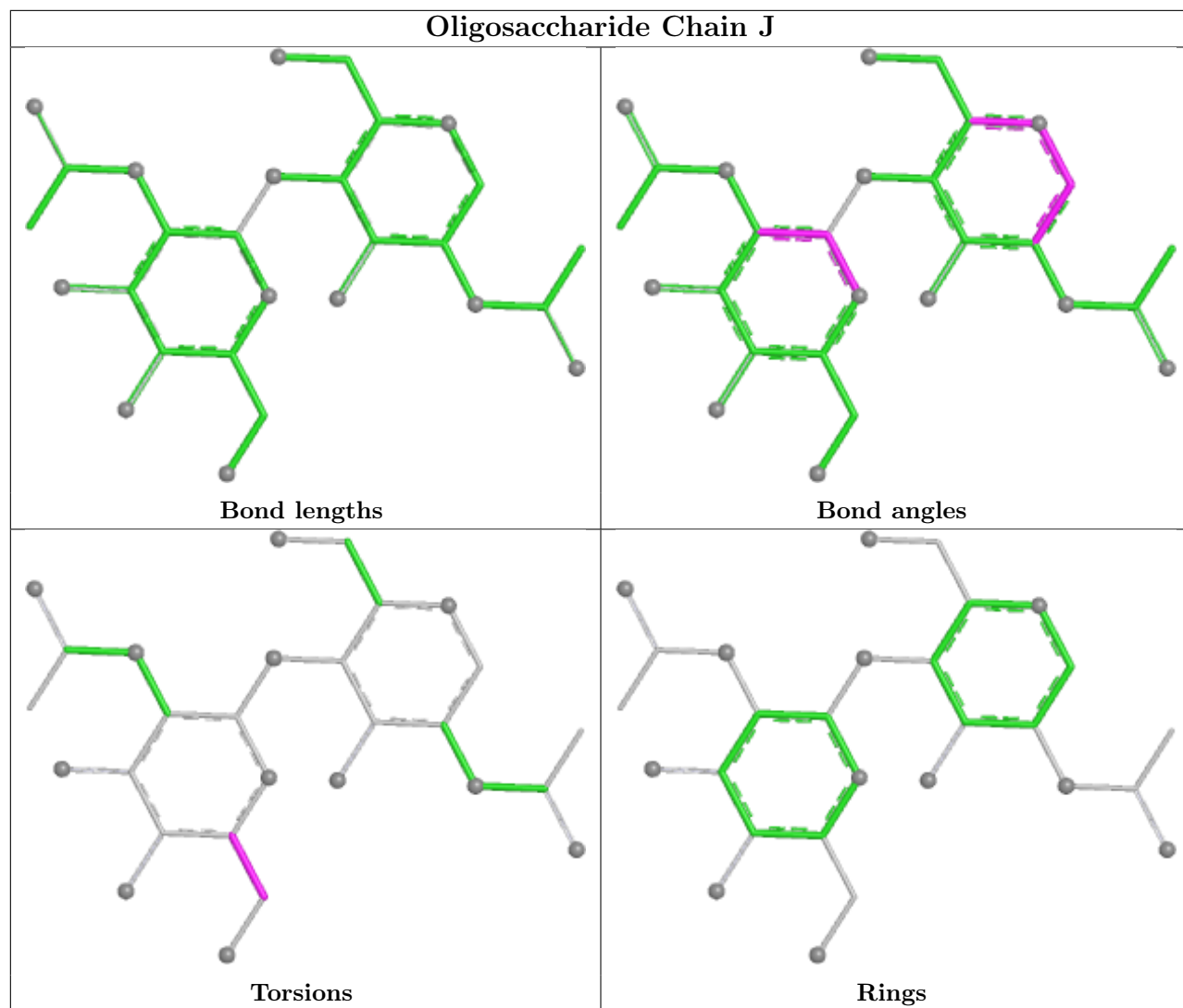
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

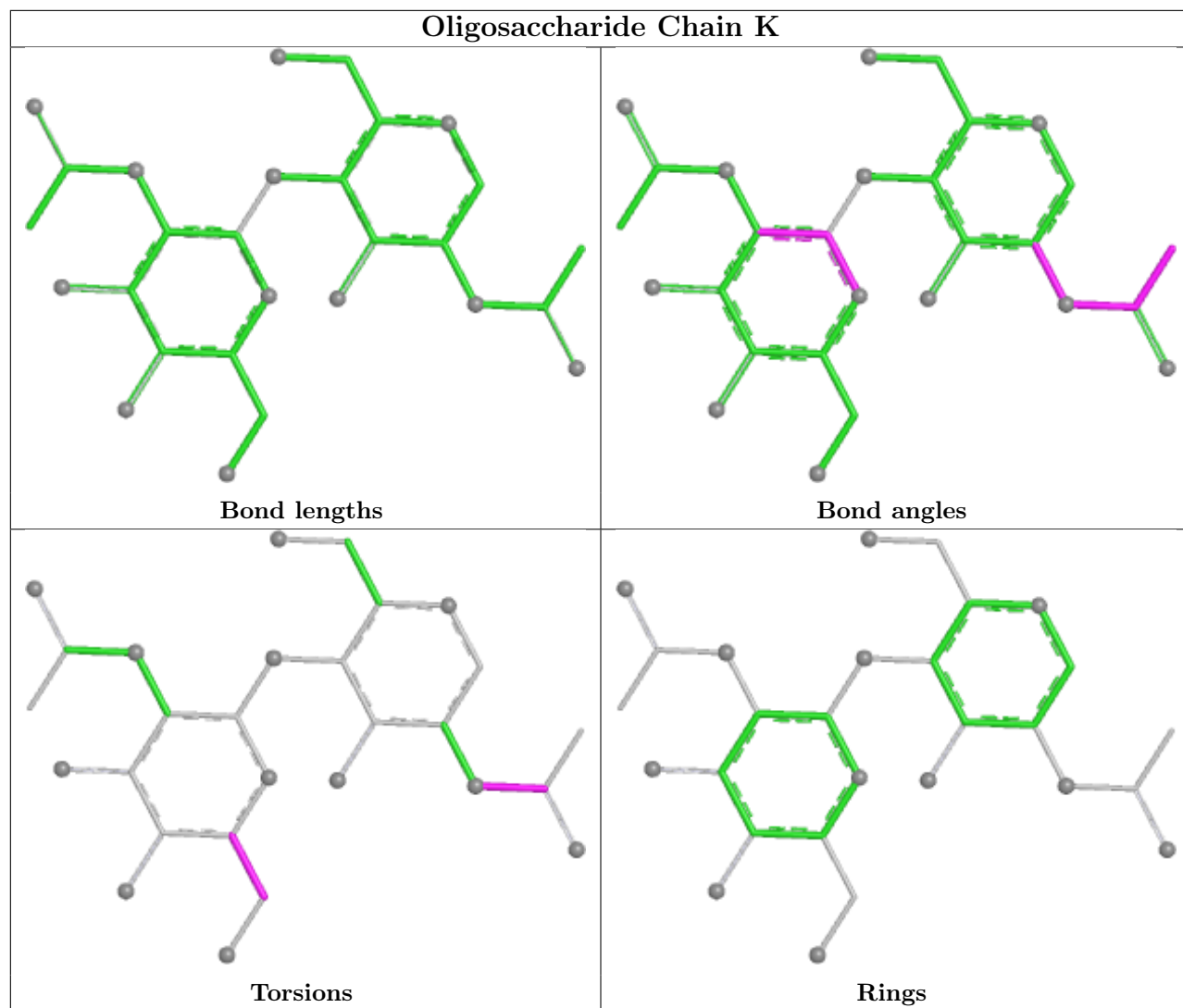


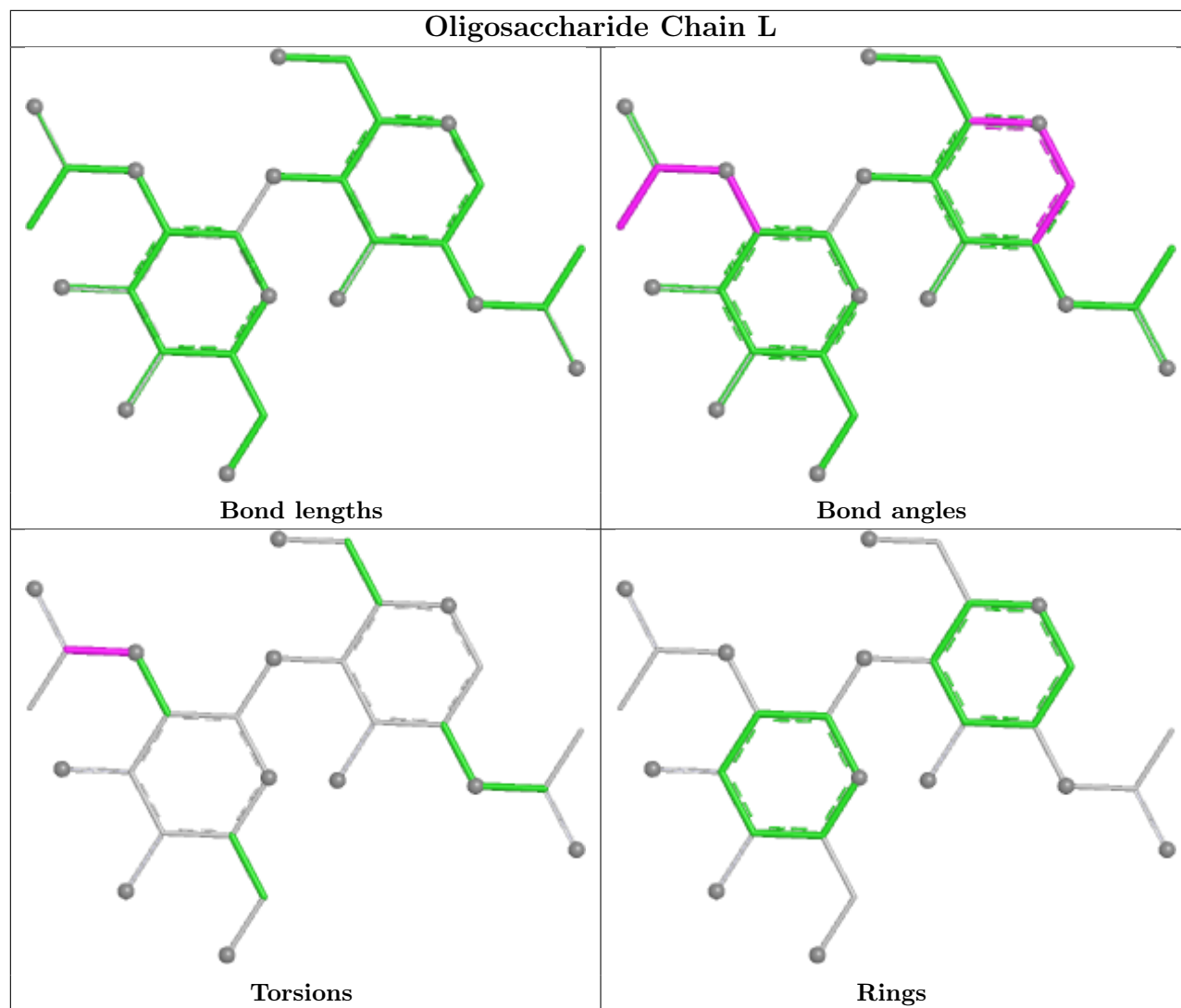


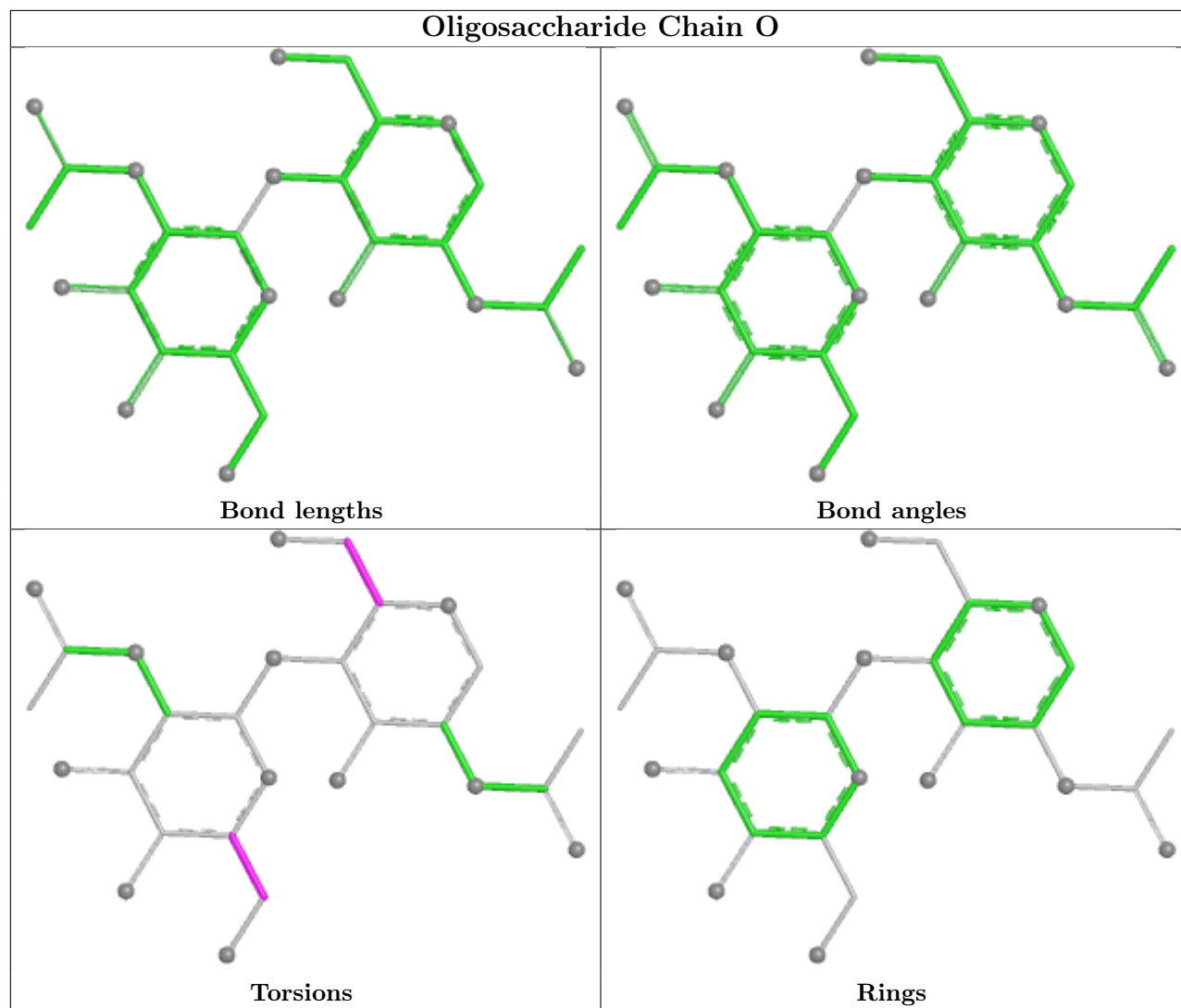


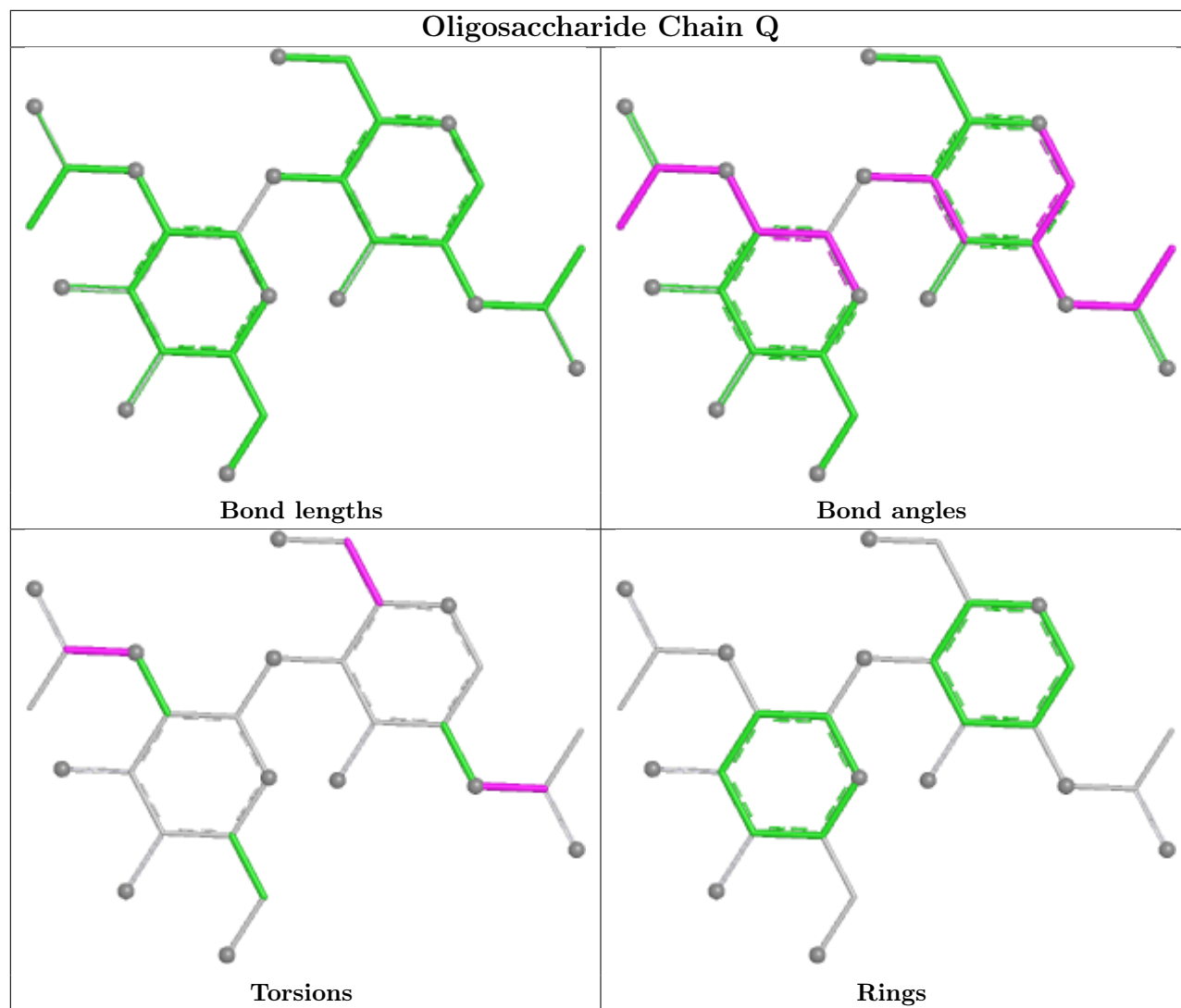


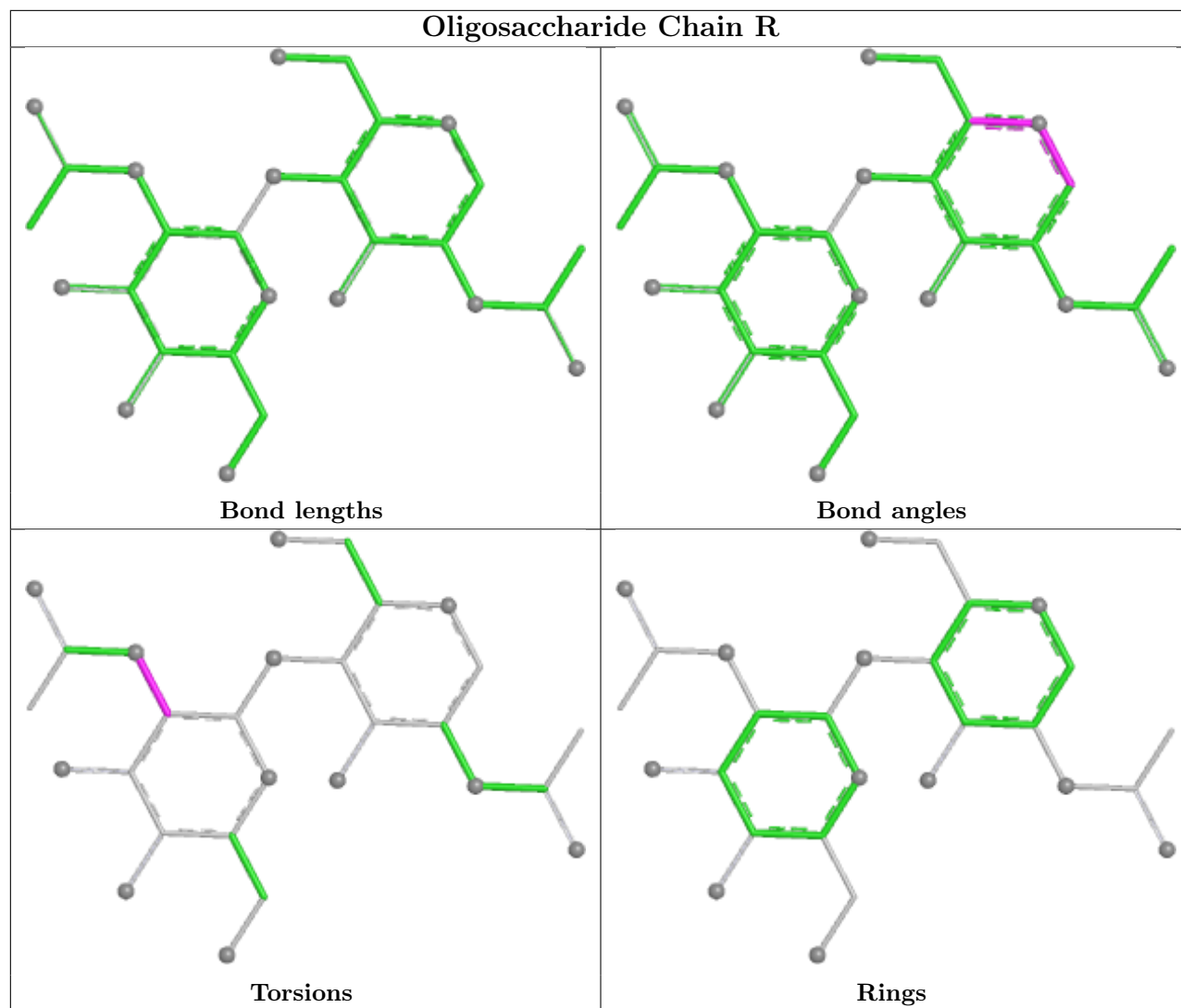


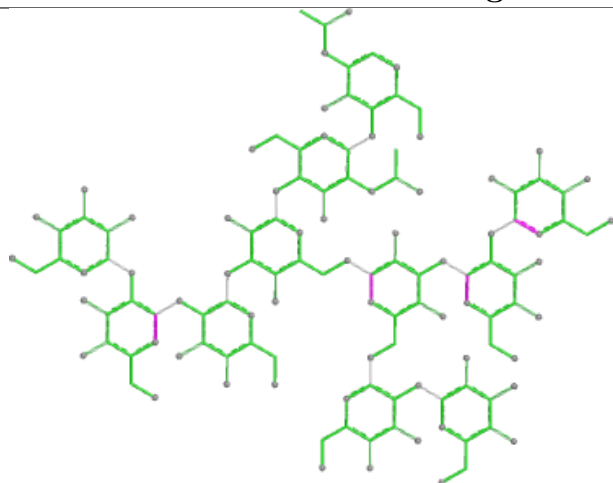
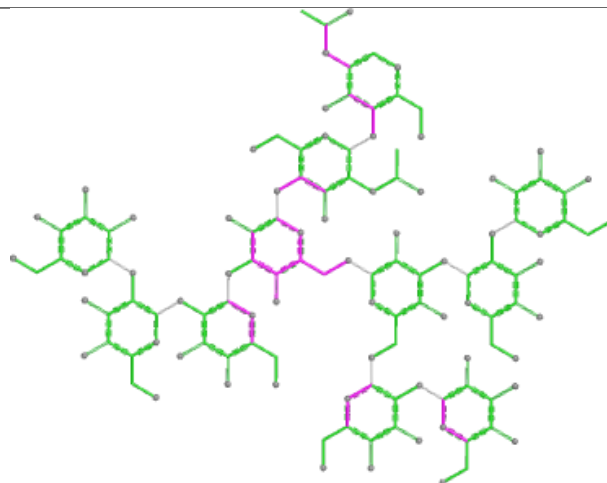
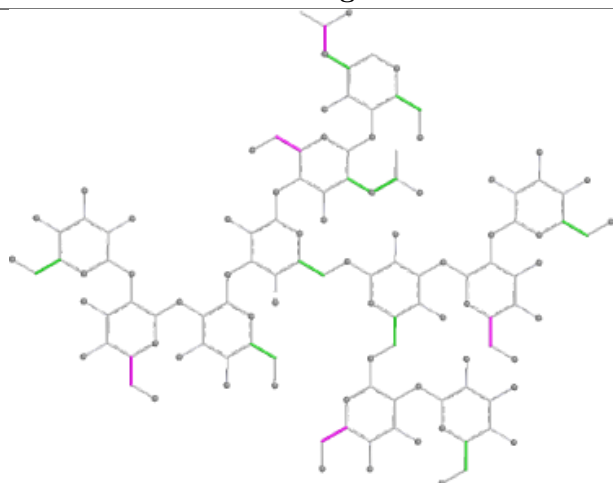
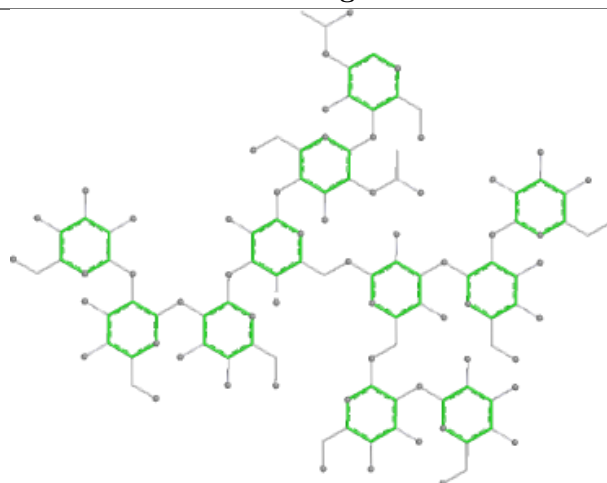


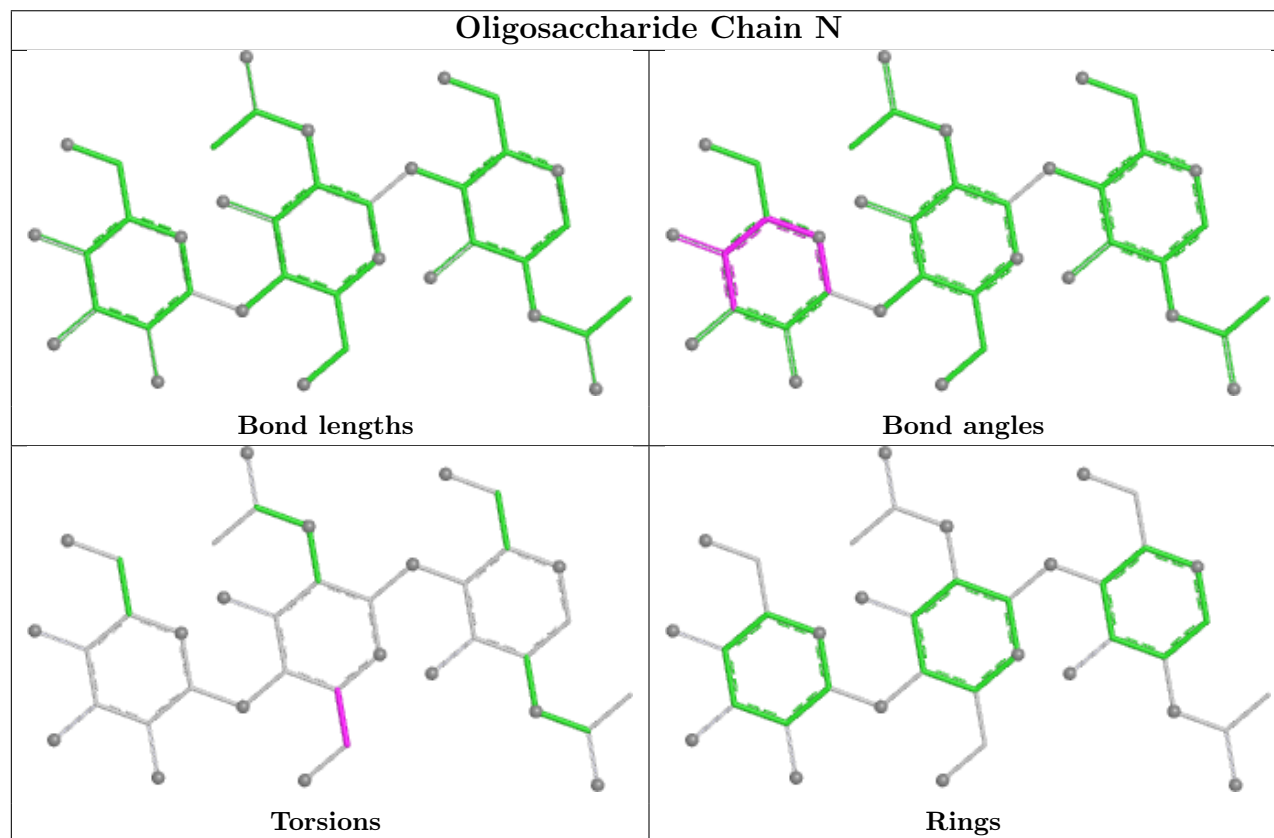
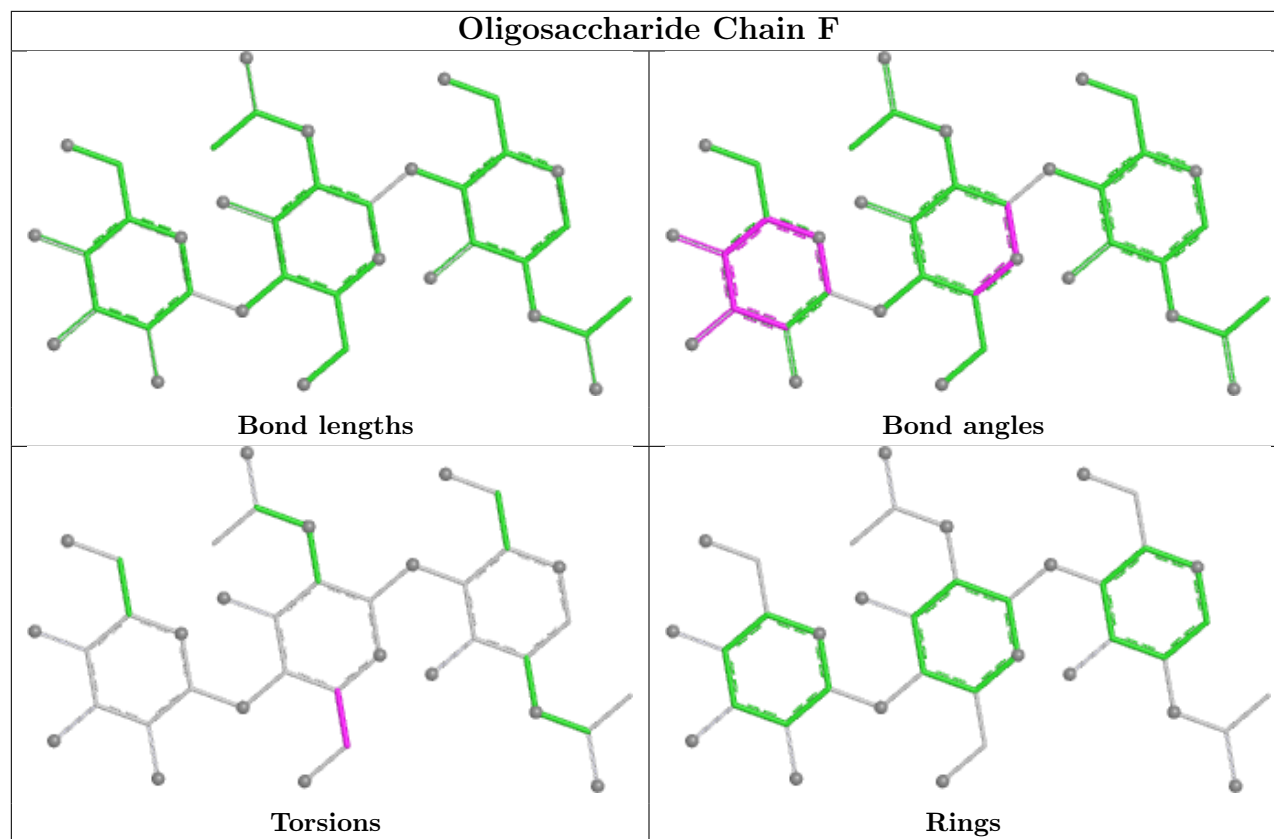




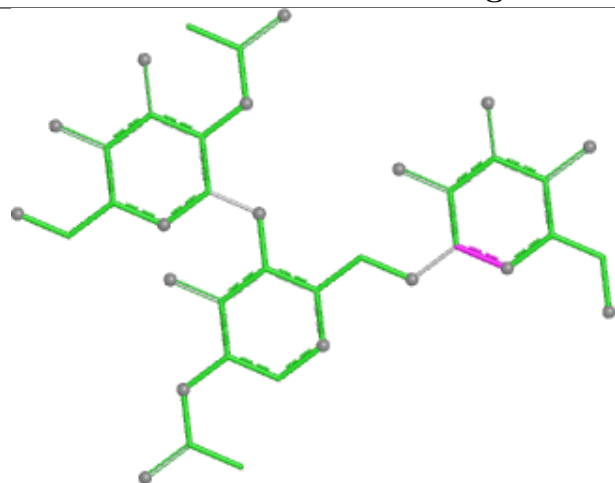




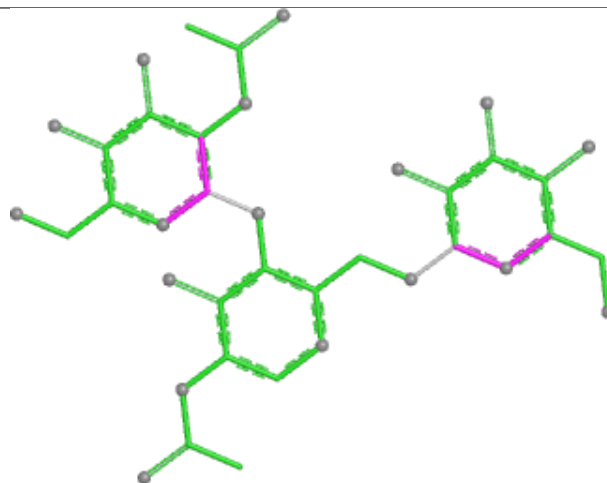
Oligosaccharide Chain E**Bond lengths****Bond angles****Torsions****Rings**



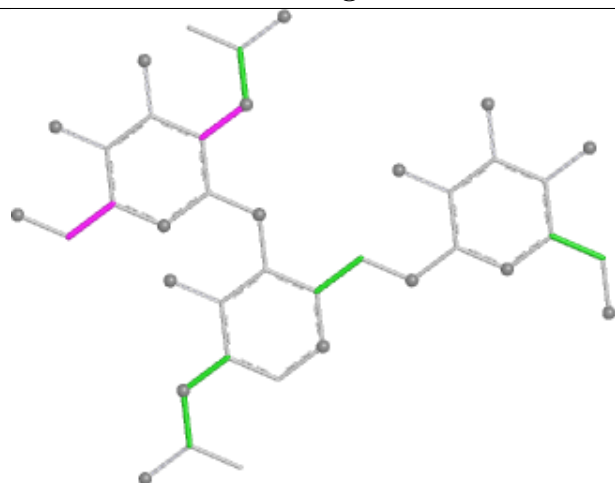
Oligosaccharide Chain H



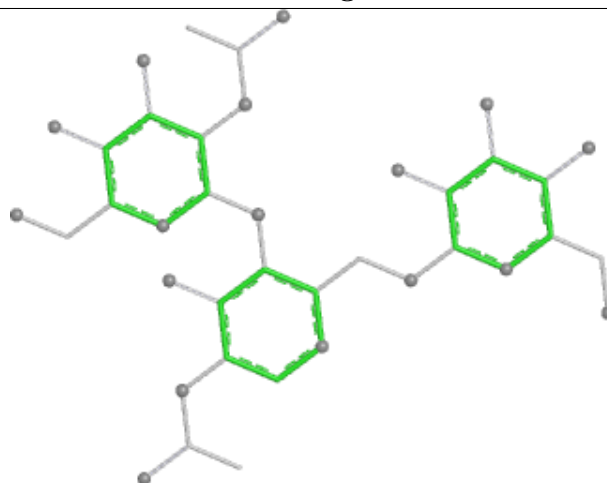
Bond lengths



Bond angles

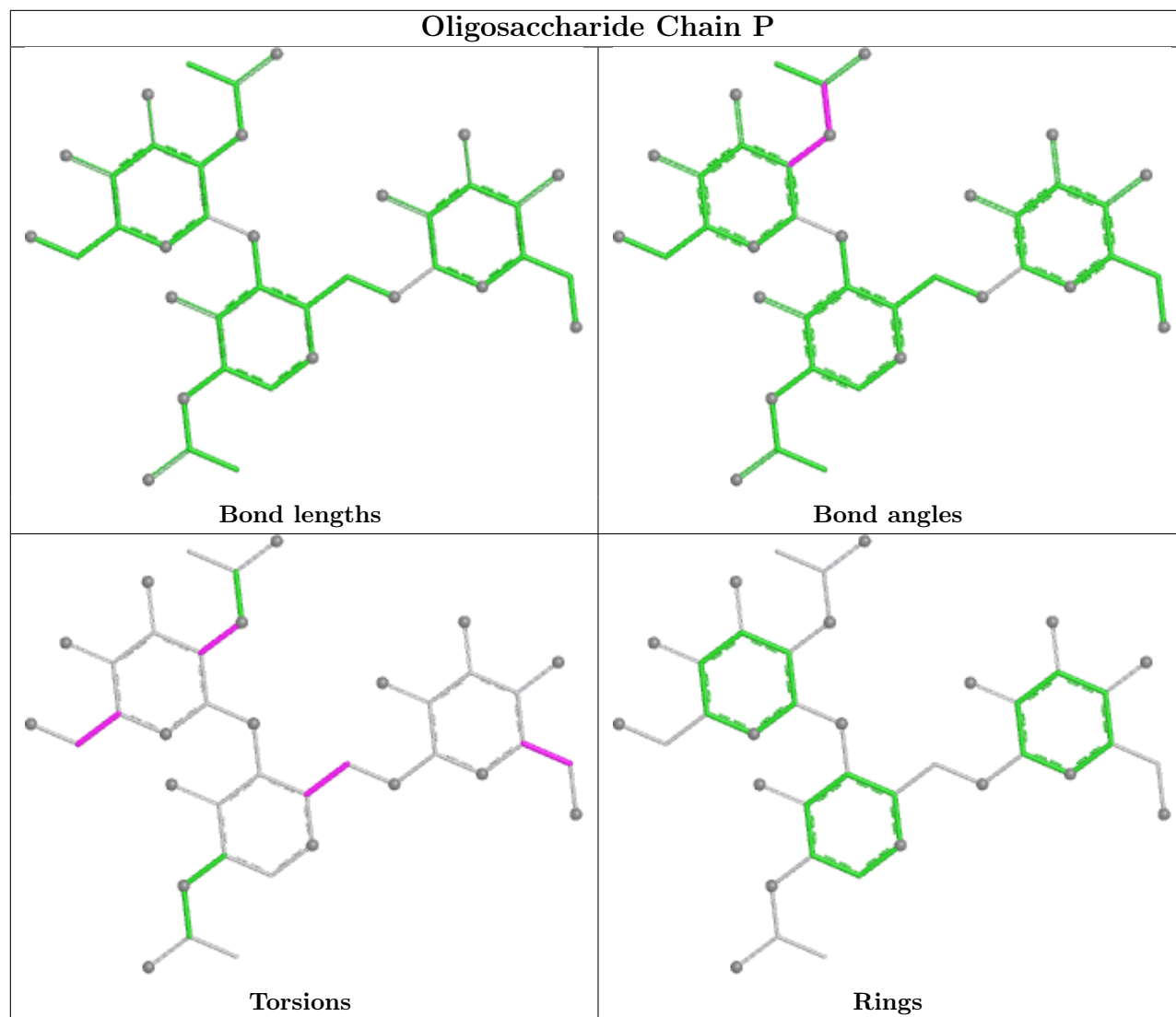


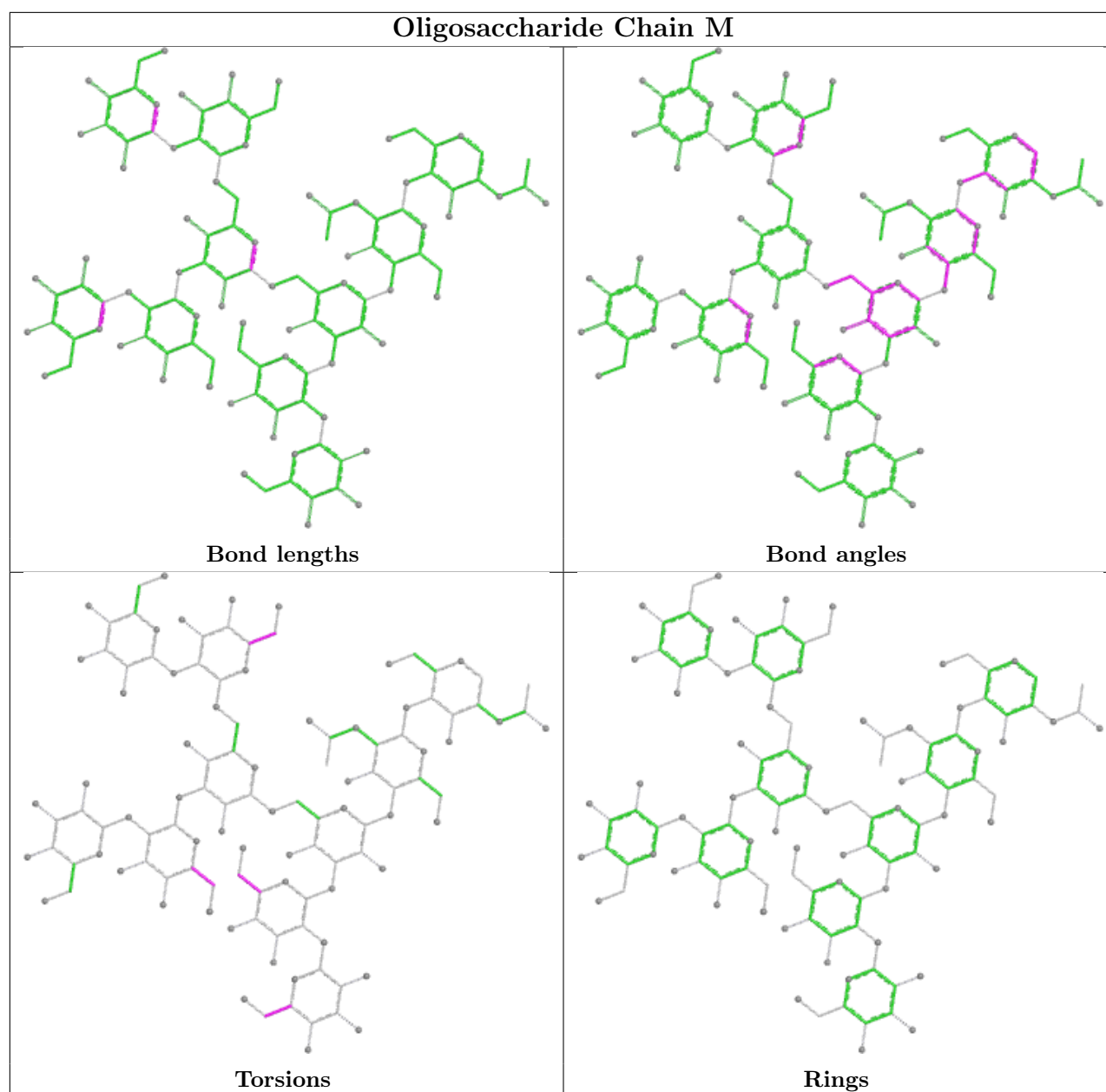
Torsions



Rings

Oligosaccharide Chain P





5.6 Ligand geometry [i](#)

14 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	A	803	1	14,14,15	0.82	0	17,19,21	1.57	2 (11%)
9	SO4	B	806	-	4,4,4	0.70	0	6,6,6	0.06	0
8	NAG	A	802	1	14,14,15	0.70	0	17,19,21	0.82	0
7	A1JME	B	801	-	36,36,36	1.81	11 (30%)	57,58,58	2.13	14 (24%)
7	A1JME	A	801	-	36,36,36	1.67	10 (27%)	57,58,58	2.13	12 (21%)
8	NAG	B	804	1	14,14,15	0.68	0	17,19,21	1.28	1 (5%)
9	SO4	A	804	-	4,4,4	0.69	0	6,6,6	0.11	0
10	ACT	B	805	-	3,3,3	1.15	0	3,3,3	1.19	0
9	SO4	B	809	-	4,4,4	0.68	0	6,6,6	0.14	0
9	SO4	A	805	-	4,4,4	0.65	0	6,6,6	0.11	0
10	ACT	B	808	-	3,3,3	1.13	0	3,3,3	1.23	0
8	NAG	B	803	1	14,14,15	0.64	0	17,19,21	2.13	5 (29%)
9	SO4	B	807	-	4,4,4	0.70	0	6,6,6	0.07	0
8	NAG	B	802	1	14,14,15	0.74	0	17,19,21	0.98	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	A	803	1	-	3/6/23/26	0/1/1/1
8	NAG	A	802	1	-	2/6/23/26	0/1/1/1
7	A1JME	B	801	-	-	3/20/84/84	0/4/4/4
7	A1JME	A	801	-	-	4/20/84/84	0/4/4/4
8	NAG	B	804	1	-	2/6/23/26	0/1/1/1
8	NAG	B	803	1	-	3/6/23/26	0/1/1/1
8	NAG	B	802	1	-	0/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	801	A1JME	C16-C10	5.01	1.64	1.56
7	A	801	A1JME	C16-C10	3.96	1.63	1.56
7	B	801	A1JME	C26-C25	3.17	1.59	1.53
7	B	801	A1JME	C20-C19	2.91	1.58	1.52
7	A	801	A1JME	C19-C18	2.79	1.56	1.52

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	801	A1JME	C09-C10-C16	8.27	123.23	113.91
7	A	801	A1JME	C09-C10-C16	8.06	122.99	113.91
7	A	801	A1JME	C12-C11-C06	-7.01	102.56	111.22
7	B	801	A1JME	C12-C11-C06	-6.18	103.58	111.22
8	B	803	NAG	C2-N2-C7	6.07	131.04	122.90

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

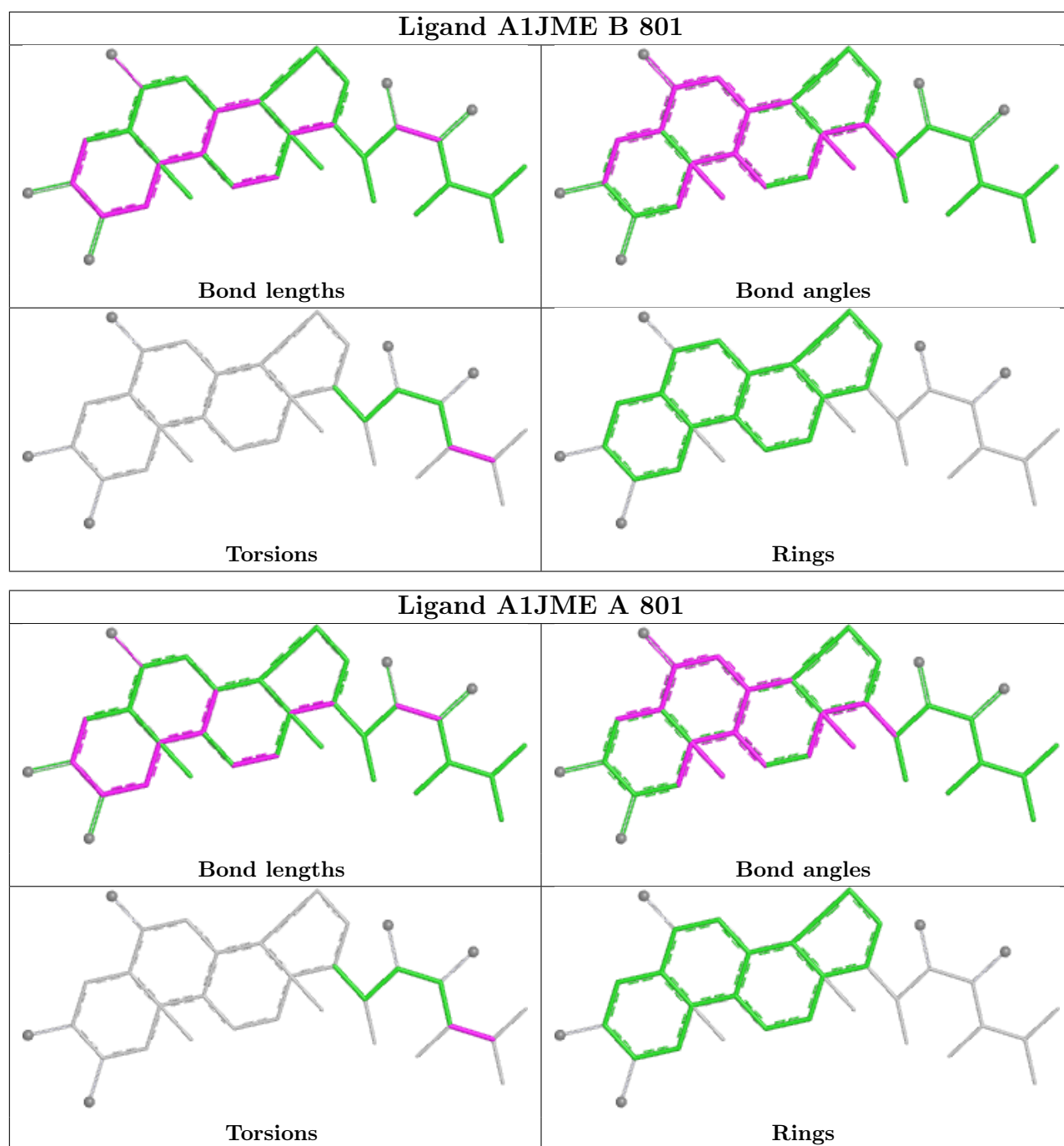
Mol	Chain	Res	Type	Atoms
7	A	801	A1JME	C26-C27-C29-C31
7	A	801	A1JME	C28-C27-C29-C30
7	A	801	A1JME	C28-C27-C29-C31
7	B	801	A1JME	C26-C27-C29-C31
8	B	803	NAG	C1-C2-N2-C7

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	803	NAG	1	0
8	A	802	NAG	1	0
8	B	804	NAG	1	0
9	B	809	SO4	2	0
10	B	808	ACT	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	720/779 (92%)	0.18	19 (2%) 57 52	68, 95, 160, 205	0
1	B	726/779 (93%)	0.13	17 (2%) 61 56	64, 87, 146, 231	0
All	All	1446/1558 (92%)	0.16	36 (2%) 58 53	64, 91, 155, 231	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	59	GLY	5.2
1	A	240	GLY	4.7
1	A	598	ALA	4.4
1	B	618	VAL	3.1
1	B	758	GLY	3.0

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	F	3	11/12	0.38	0.11	140,157,178,189	0
2	NAG	D	2	14/15	0.53	0.11	136,155,180,191	0
2	NAG	C	2	14/15	0.53	0.11	136,144,173,174	0
2	NAG	Q	2	14/15	0.56	0.13	123,147,163,172	0
2	NAG	I	2	14/15	0.56	0.11	134,159,188,192	0

Continued on next page...

Continued from previous page...

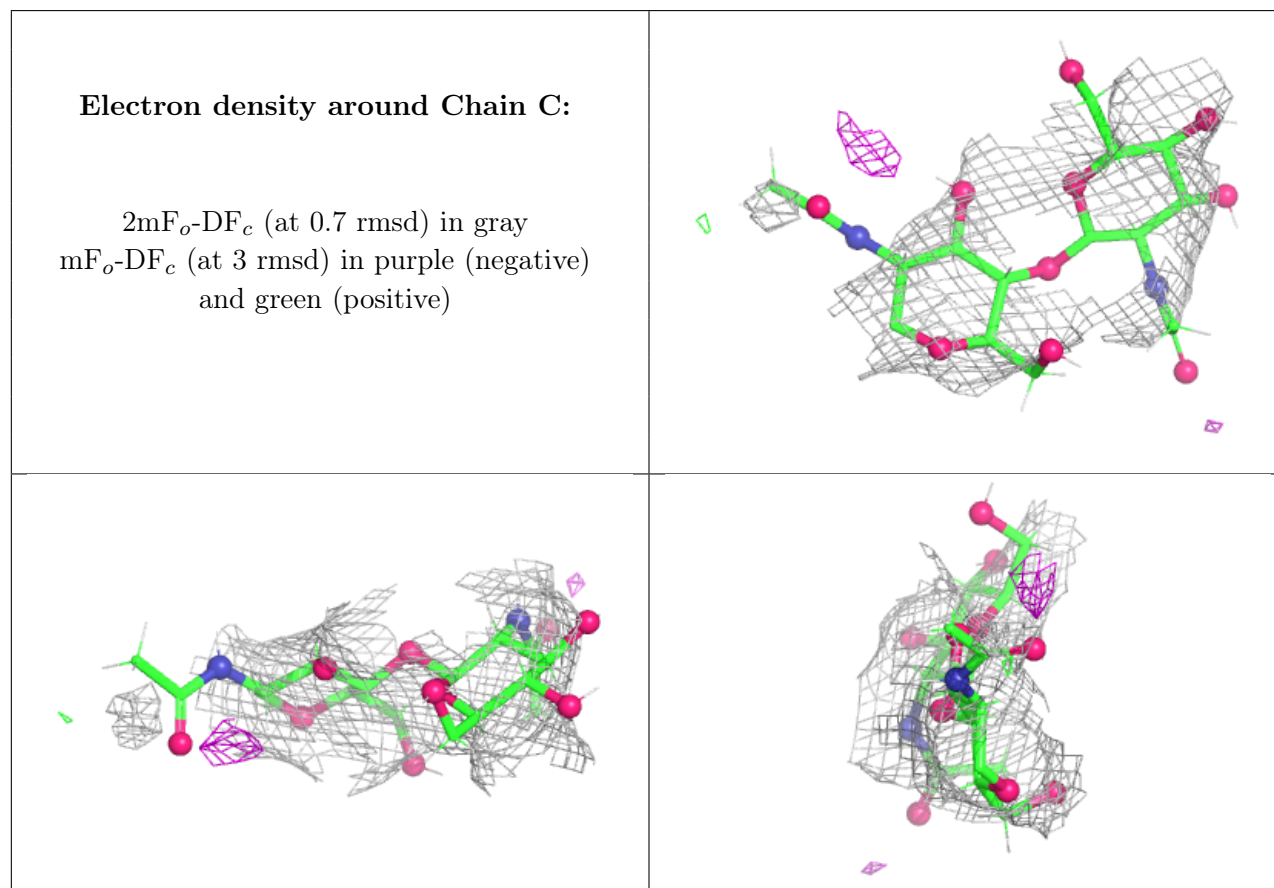
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	E	6	11/12	0.57	0.21	128,148,175,186	0
4	BMA	N	3	11/12	0.59	0.12	134,148,173,174	0
2	NAG	J	2	14/15	0.60	0.12	121,137,164,170	0
2	NAG	G	1	14/15	0.60	0.15	101,130,150,164	0
3	MAN	E	5	11/12	0.60	0.10	113,127,153,154	0
2	NAG	L	1	14/15	0.61	0.13	117,142,168,173	0
2	NAG	L	2	14/15	0.66	0.10	125,142,165,171	0
5	MAN	H	3	11/12	0.66	0.11	122,136,165,165	0
5	NAG	P	2	14/15	0.67	0.11	123,141,168,170	0
2	NAG	I	1	14/15	0.68	0.12	102,131,168,189	0
2	NAG	R	2	14/15	0.70	0.11	108,130,149,163	0
5	MAN	P	3	11/12	0.71	0.12	126,151,179,185	0
2	NAG	K	2	14/15	0.73	0.09	129,141,171,181	0
2	NAG	C	1	14/15	0.73	0.10	136,146,176,182	0
2	NAG	K	1	14/15	0.74	0.10	107,129,151,164	0
3	MAN	E	4	11/12	0.76	0.08	83,101,122,124	0
2	NAG	D	1	14/15	0.76	0.10	116,138,163,165	0
2	NAG	O	2	14/15	0.77	0.10	128,152,181,187	0
5	NAG	H	2	14/15	0.78	0.10	115,138,163,174	0
6	MAN	M	10	11/12	0.78	0.09	114,130,155,167	0
2	NAG	O	1	14/15	0.79	0.10	101,125,155,160	0
2	NAG	G	2	14/15	0.79	0.10	133,145,170,187	0
2	NAG	Q	1	14/15	0.80	0.10	103,125,152,161	0
4	NAG	N	2	14/15	0.80	0.12	106,125,147,151	0
6	MAN	M	9	11/12	0.82	0.10	101,114,135,138	0
2	NAG	J	1	14/15	0.83	0.10	91,114,139,144	0
2	NAG	R	1	14/15	0.83	0.09	84,105,128,130	0
4	NAG	F	2	14/15	0.83	0.10	115,140,169,180	0
3	NAG	E	1	14/15	0.84	0.12	71,79,106,106	0
6	MAN	M	8	11/12	0.85	0.09	71,79,96,101	0
5	NAG	H	1	14/15	0.86	0.11	95,115,138,143	0
3	NAG	E	2	14/15	0.86	0.12	69,77,94,135	0
5	NAG	P	1	14/15	0.87	0.10	96,117,140,145	0
3	BMA	E	3	11/12	0.87	0.08	66,75,91,94	0
4	NAG	N	1	14/15	0.89	0.10	81,93,110,113	0
3	MAN	E	7	11/12	0.89	0.08	66,67,82,82	0
6	MAN	M	4	11/12	0.90	0.10	65,69,84,89	0
4	NAG	F	1	14/15	0.90	0.10	88,107,125,135	0
6	NAG	M	2	14/15	0.91	0.08	66,74,90,110	0
3	MAN	E	9	11/12	0.91	0.08	69,75,86,102	0
6	MAN	M	5	11/12	0.91	0.09	60,66,79,87	0
3	MAN	E	10	11/12	0.91	0.07	69,72,86,87	0

Continued on next page...

Continued from previous page...

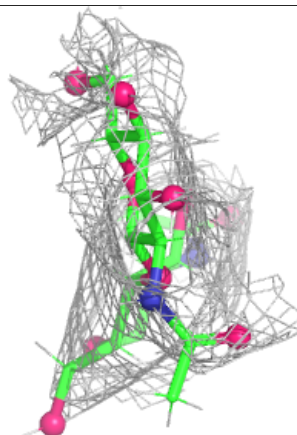
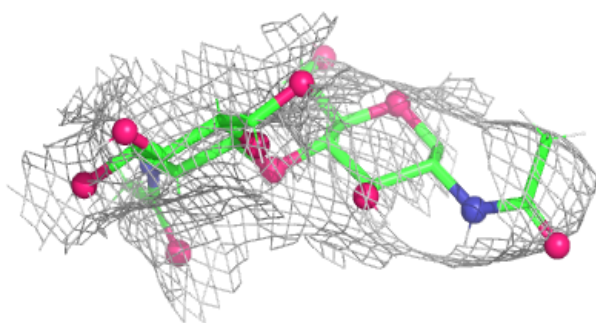
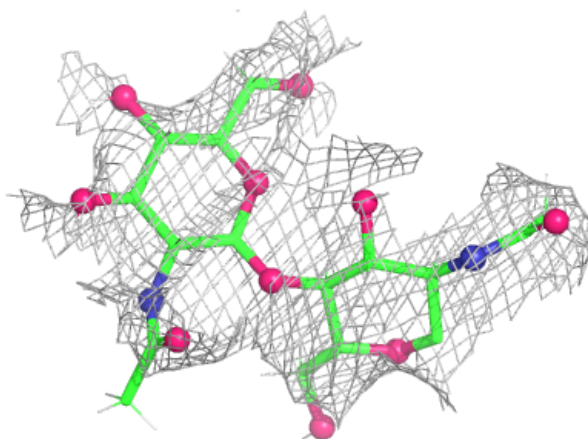
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	E	11	11/12	0.91	0.09	74,88,107,107	0
6	NAG	M	1	14/15	0.91	0.09	62,67,81,83	0
6	MAN	M	7	11/12	0.92	0.08	70,73,88,90	0
3	MAN	E	8	11/12	0.93	0.08	62,68,82,84	0
6	BMA	M	3	11/12	0.93	0.09	68,80,97,102	0
6	MAN	M	6	11/12	0.94	0.07	64,69,80,84	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.



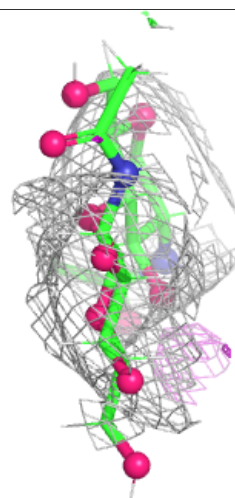
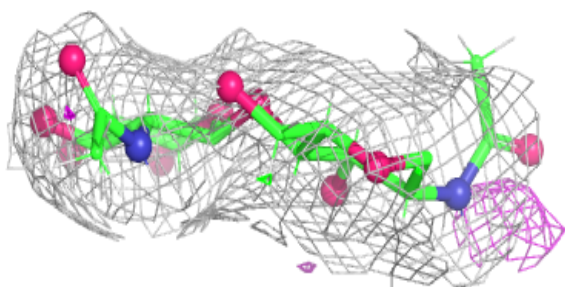
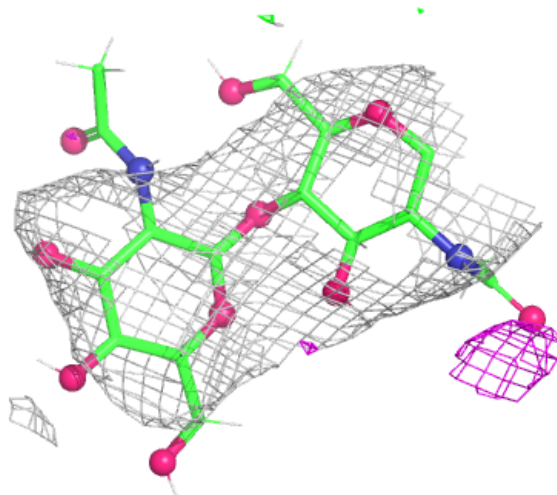
Electron density around Chain D:

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



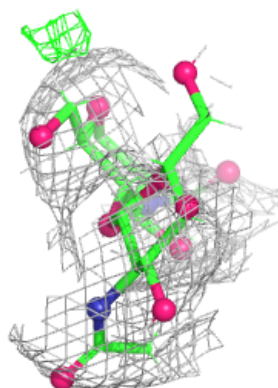
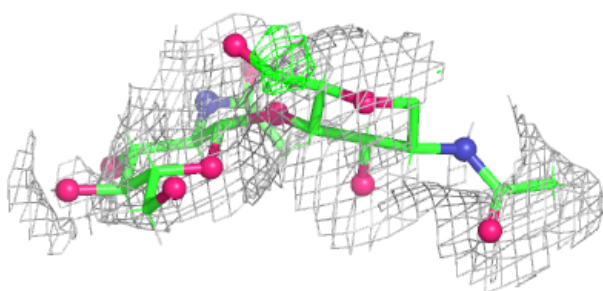
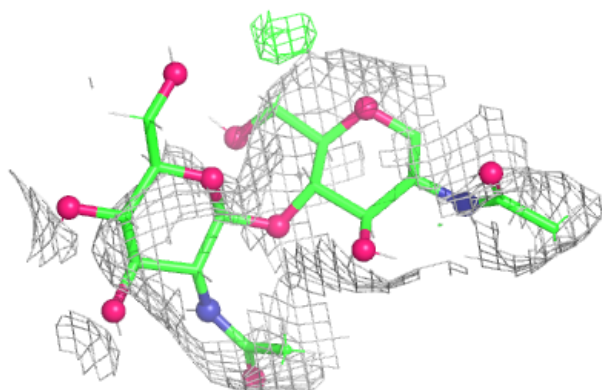
Electron density around Chain G:

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

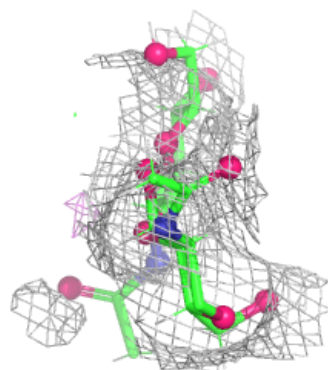
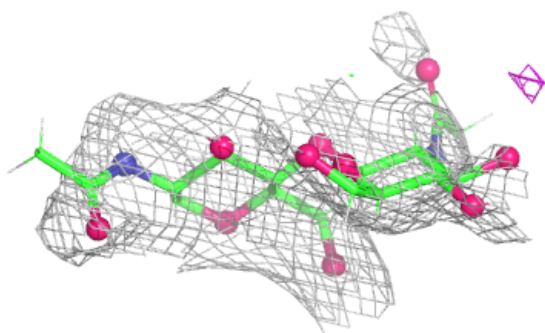
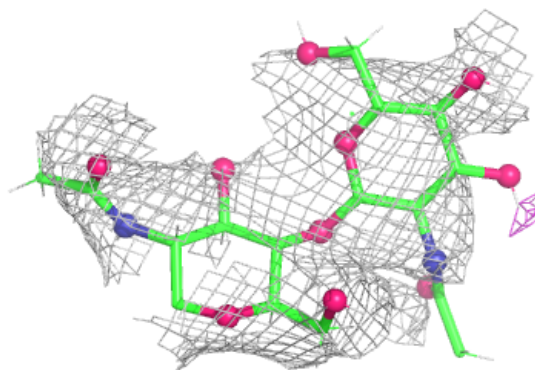


Electron density around Chain I:

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

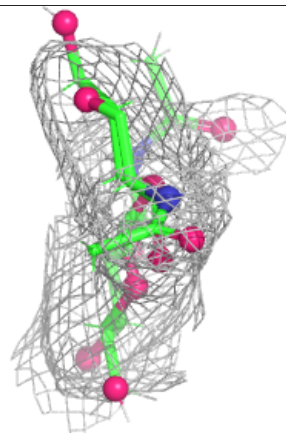
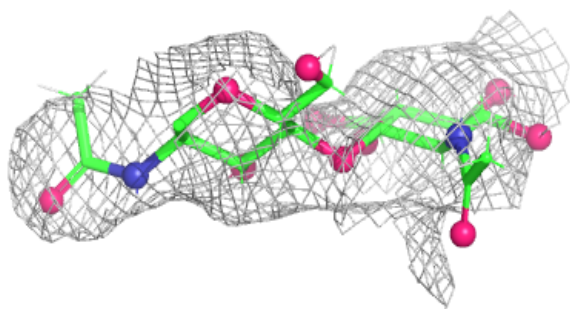
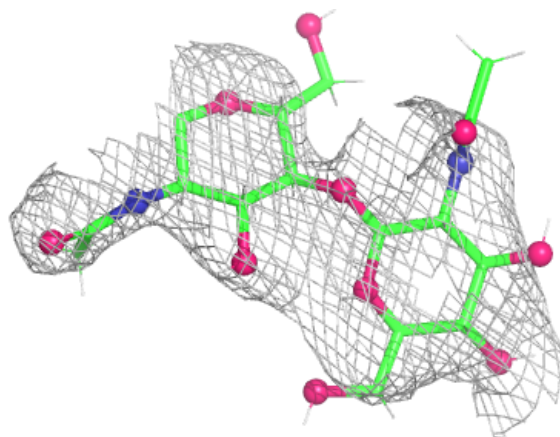
**Electron density around Chain J:**

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



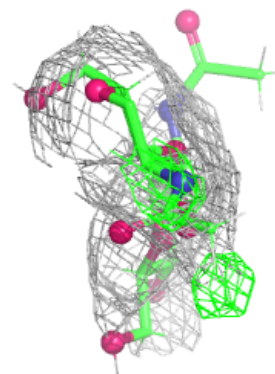
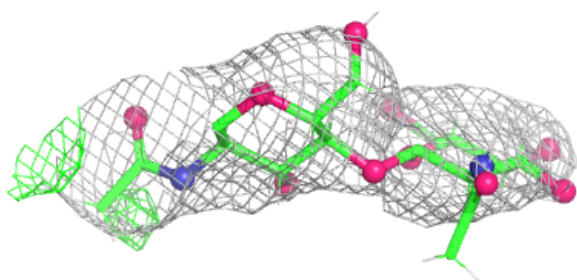
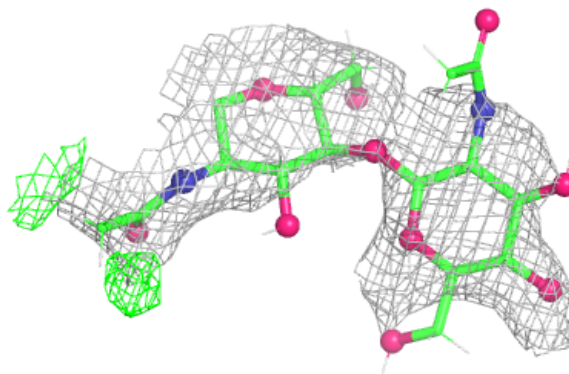
Electron density around Chain K:

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

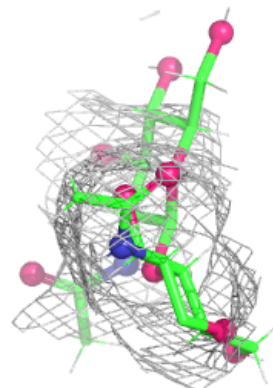
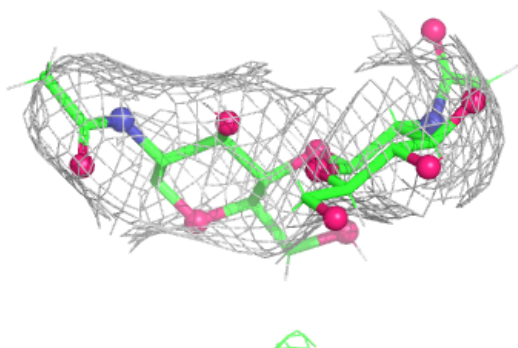
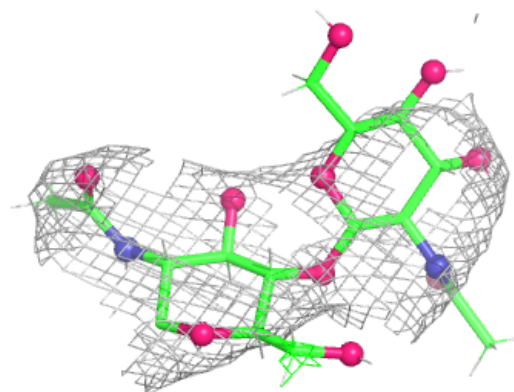


Electron density around Chain L:

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

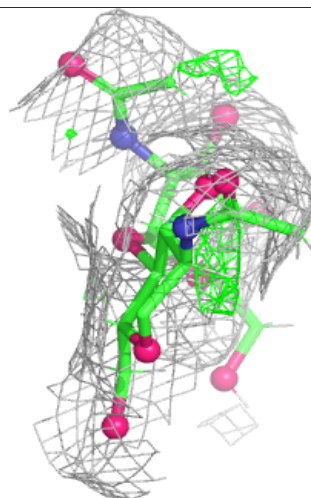
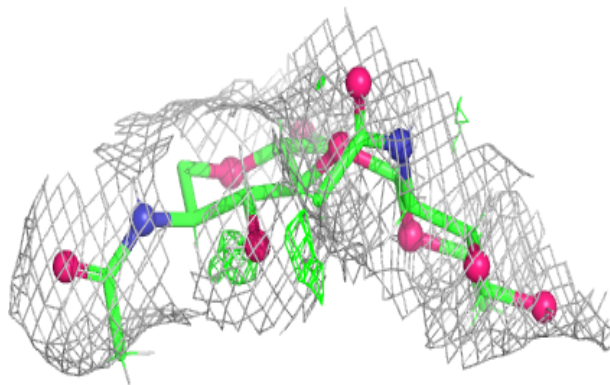
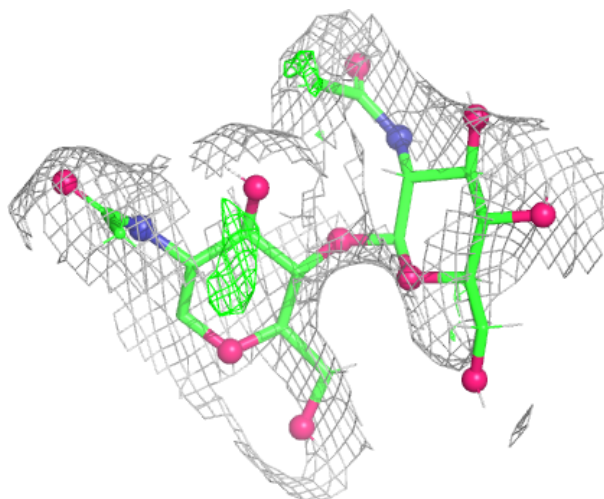
**Electron density around Chain O:**

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



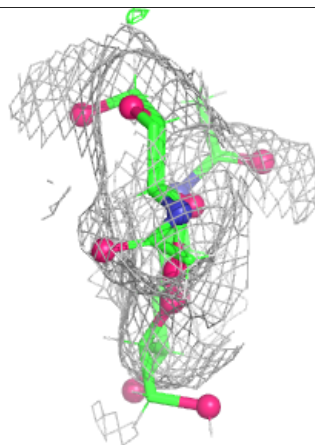
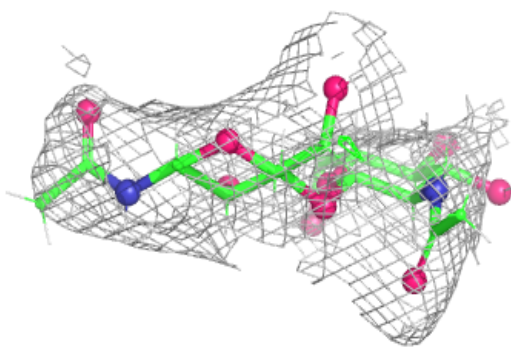
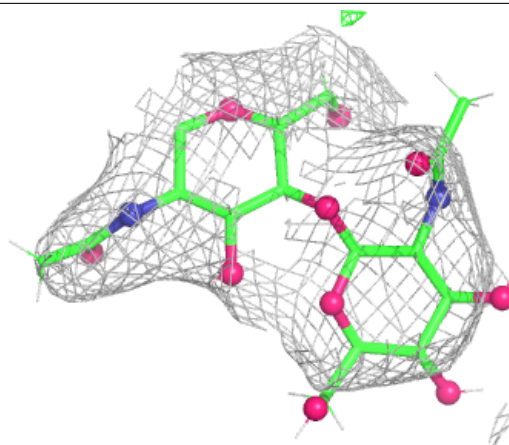
Electron density around Chain Q:

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



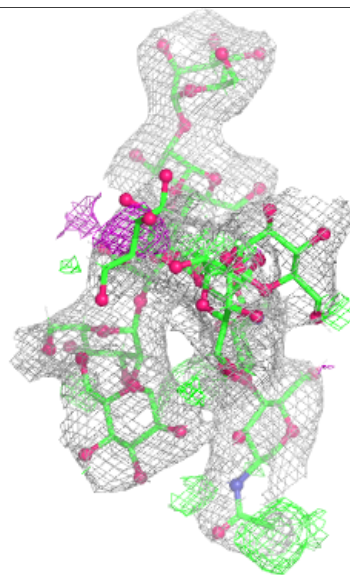
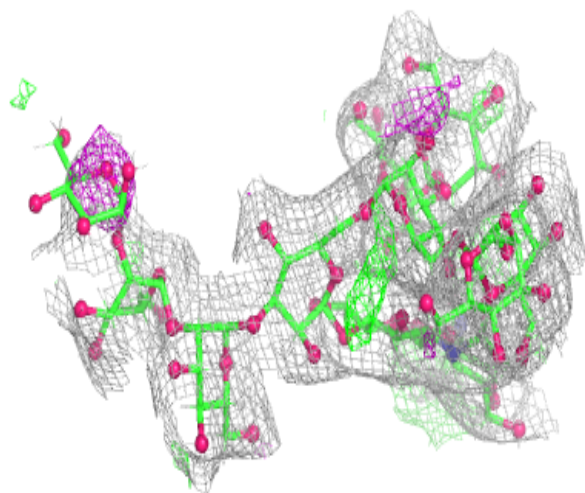
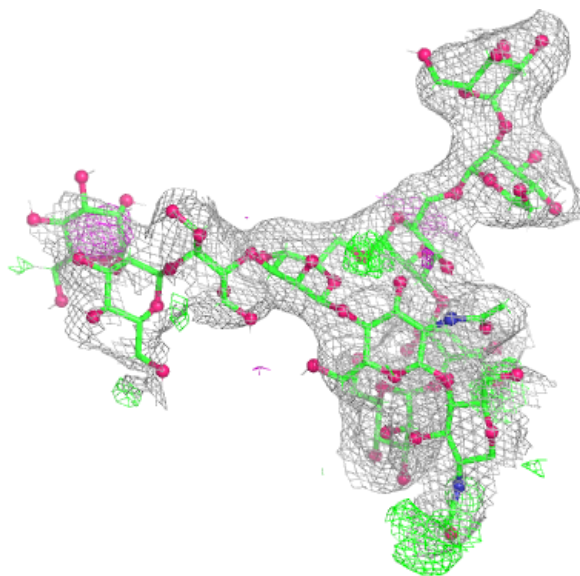
Electron density around Chain R:

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



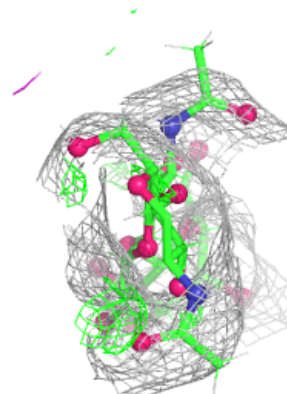
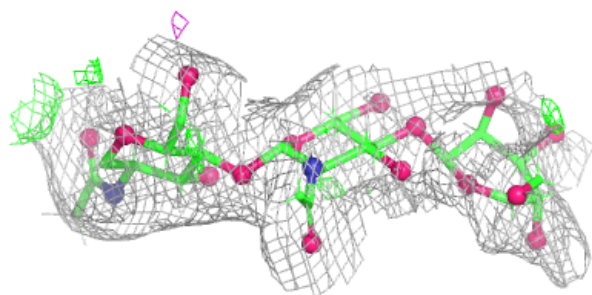
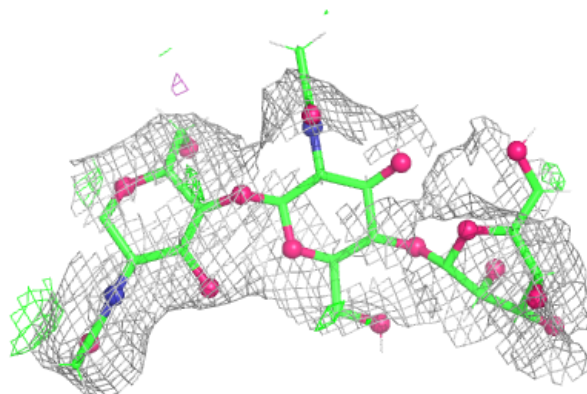
Electron density around Chain E:

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

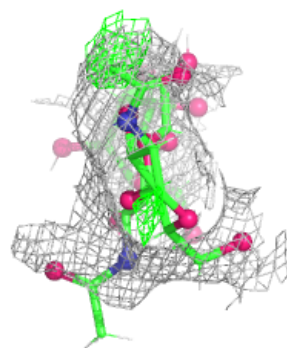
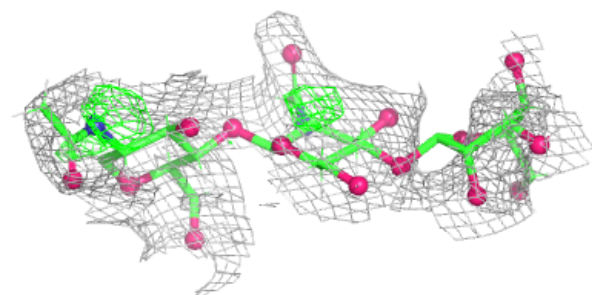
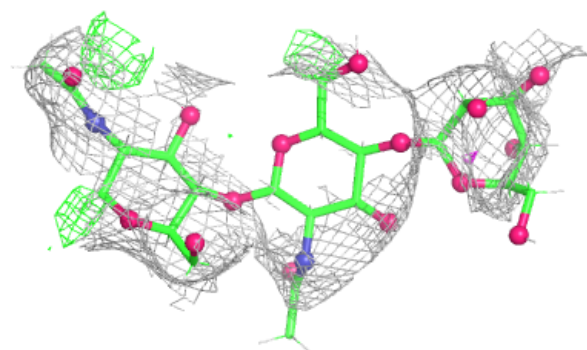


Electron density around Chain F:

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

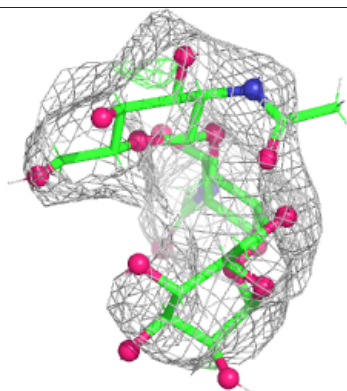
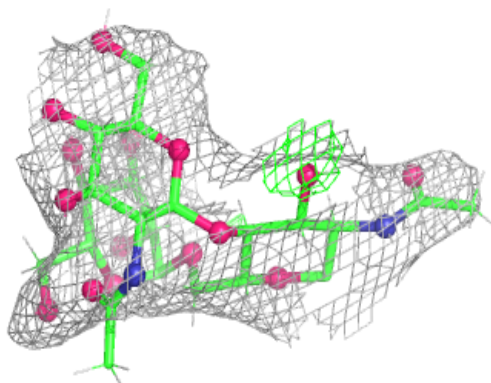
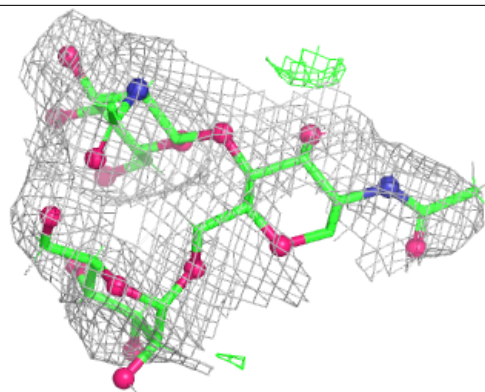
**Electron density around Chain N:**

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



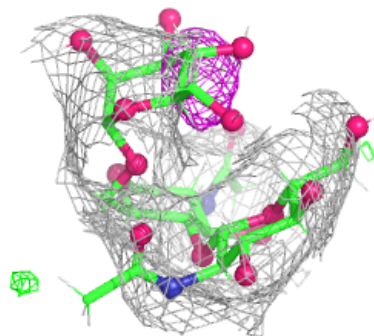
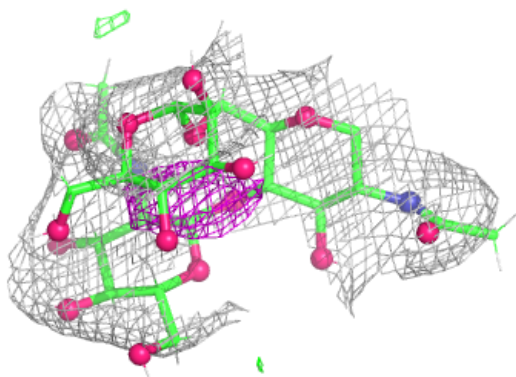
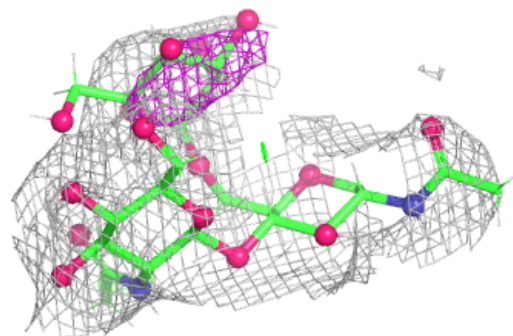
Electron density around Chain H:

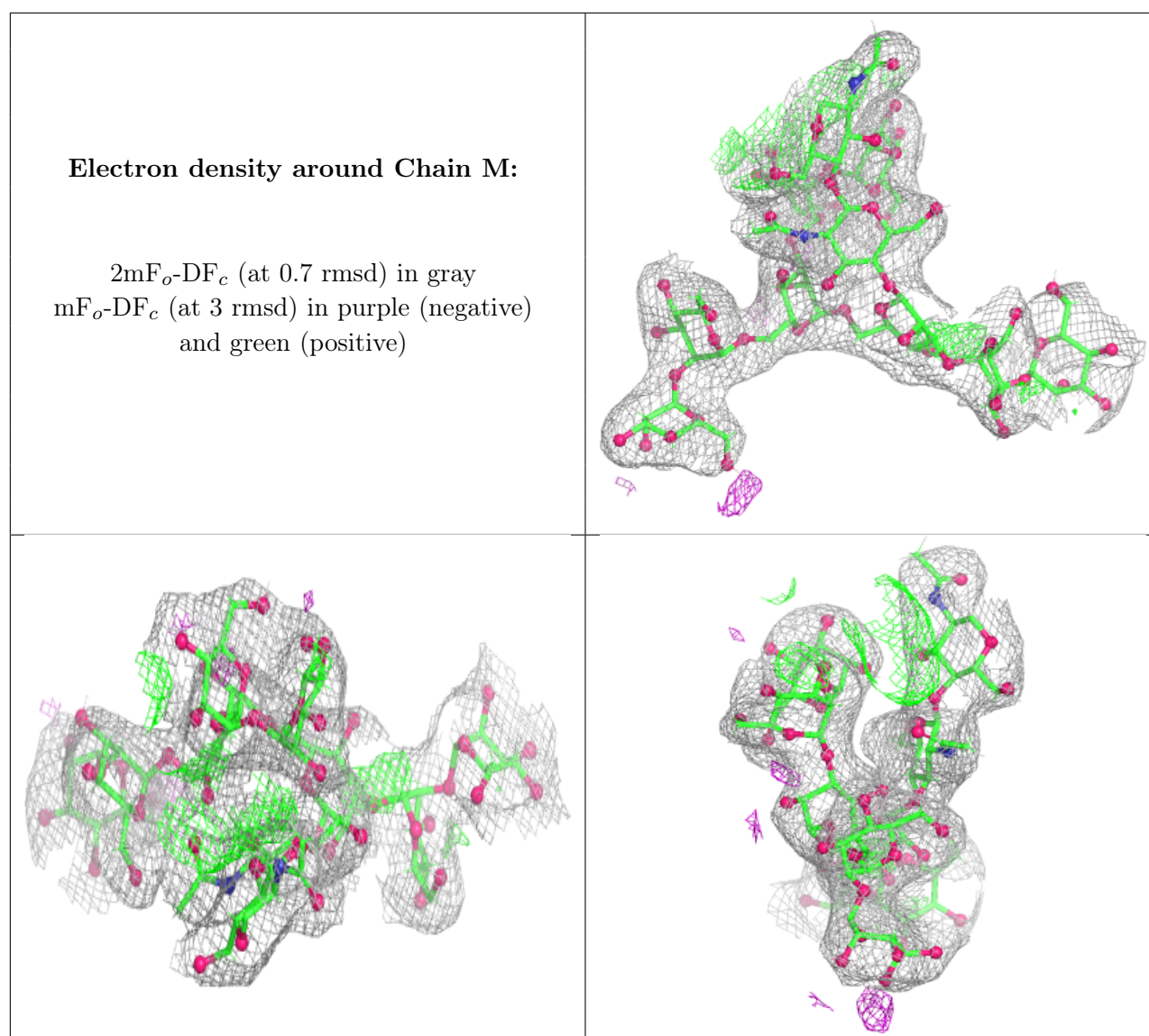
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain P:

$2mF_o-DF_c$ (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(Å ²)	Q<0.9
8	NAG	B	803	14/15	0.30	0.17	114,138,164,169	0
8	NAG	B	804	14/15	0.62	0.13	112,136,162,174	0
8	NAG	A	803	14/15	0.64	0.11	97,123,149,155	0
10	ACT	B	805	4/4	0.71	0.20	79,86,96,96	0
10	ACT	B	808	4/4	0.76	0.29	79,81,102,102	0
9	SO4	B	809	5/5	0.77	0.08	107,118,132,134	0

Continued on next page...

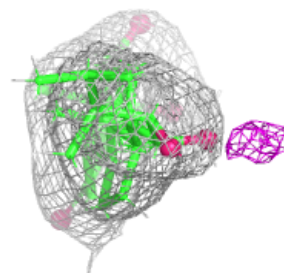
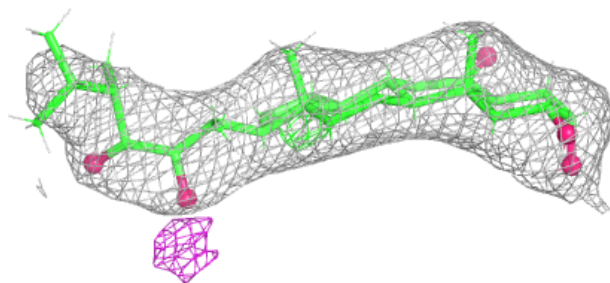
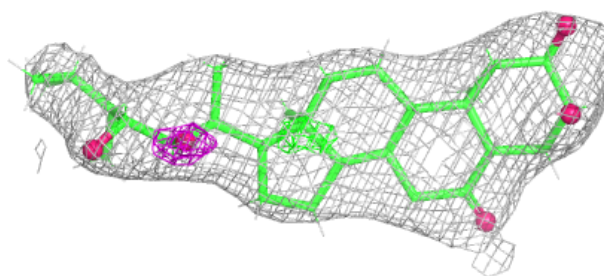
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NAG	A	802	14/15	0.77	0.12	113,125,149,157	0
8	NAG	B	802	14/15	0.77	0.12	114,137,158,166	0
9	SO4	A	804	5/5	0.79	0.10	93,107,118,126	0
9	SO4	B	806	5/5	0.81	0.10	98,99,112,123	0
9	SO4	A	805	5/5	0.88	0.12	73,73,75,91	0
9	SO4	B	807	5/5	0.93	0.09	74,77,89,89	0
7	A1JME	B	801	33/33	0.95	0.11	57,72,86,87	0
7	A1JME	A	801	33/33	0.96	0.10	57,72,90,92	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

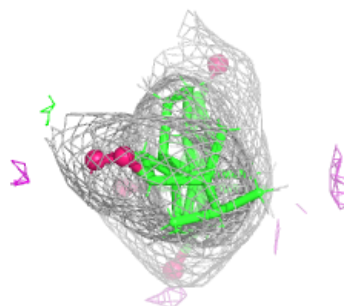
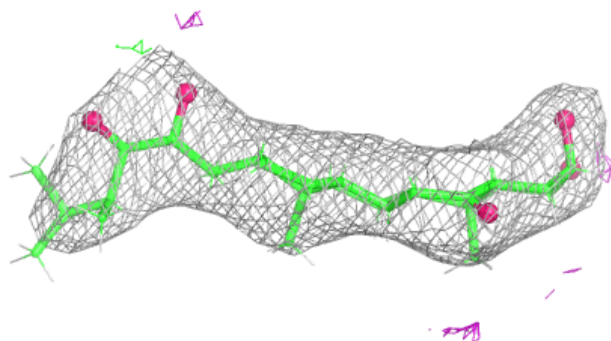
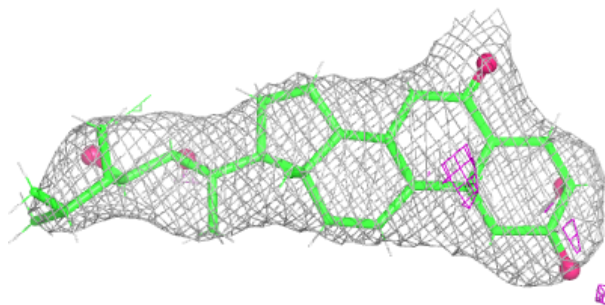
Electron density around A1JME B 801:

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 A1JME A 801:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.