



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:26 PM UTC

PDB ID : 8IDQ / pdb_00008idq
Title : Crystal structure of reducing-end xylose-releasing exoxylanase in GH30 from
Talaromyces cellulolyticus with xylose
Authors : Nakamichi, Y.; Watanabe, M.; Fujii, T.; Inoue, H.; Morita, T.
Deposited on : 2023-02-14
Resolution : 1.70 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
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

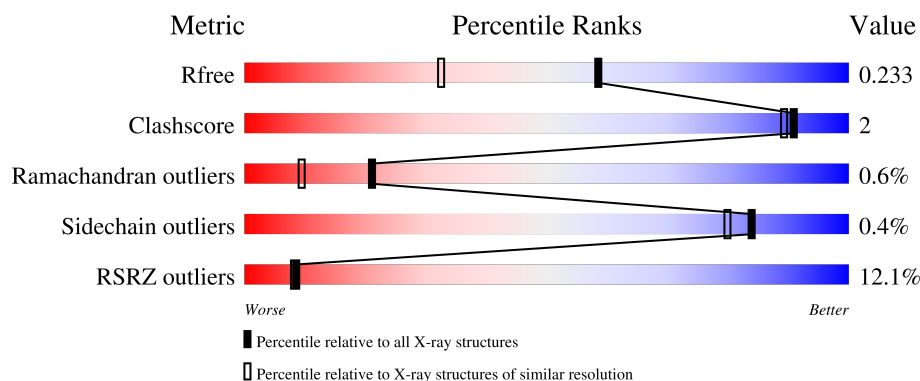
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	462	11% 93% • •
1	B	462	14% 91% 5% •
1	C	462	12% 92% 5% •
1	D	462	10% 93% • •
2	E	11	27% 64% 9%

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Mol	Chain	Length	Quality of chain
2	N	11	
3	F	2	
3	J	2	
3	M	2	
3	O	2	
4	G	6	
4	I	6	
4	P	6	
5	H	10	
6	K	9	
7	L	5	

2 Entry composition [i](#)

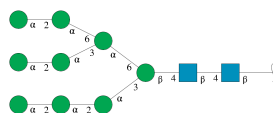
There are 12 unique types of molecules in this entry. The entry contains 16775 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Reducing-end xylose-releasing exoxylanase Xyn30A.

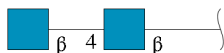
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	4	0
			3511	2221	588	686	16			
1	B	444	Total	C	N	O	S	0	5	0
			3508	2223	586	683	16			
1	C	446	Total	C	N	O	S	0	5	0
			3522	2229	588	689	16			
1	D	446	Total	C	N	O	S	0	7	0
			3537	2237	590	694	16			

- Molecule 2 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.



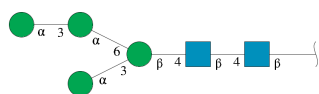
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	11	Total	C	N	O	0	0	0
			127	70	2	55			
2	N	11	Total	C	N	O	0	0	0
			127	70	2	55			

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



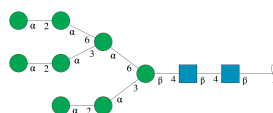
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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.



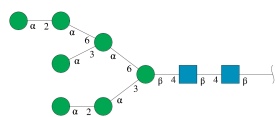
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	6	Total	C	N	O	0	0	0
			72	40	2	30			
4	I	6	Total	C	N	O	0	0	0
			72	40	2	30			
4	P	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 5 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.



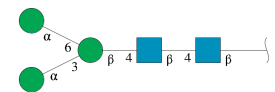
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	10	Total	C	N	O	0	0	0
			116	64	2	50			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]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.



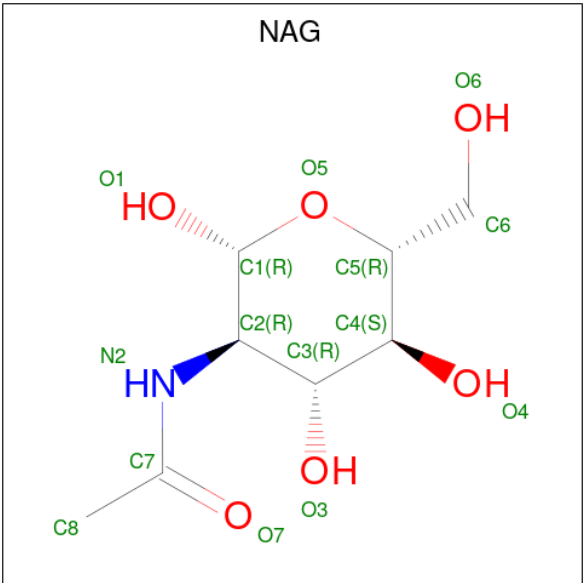
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	K	9	Total	C	N	O	0	0	0
			105	58	2	45			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[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
7	L	5	Total	C	N	O	0	0	0
			61	34	2	25			

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



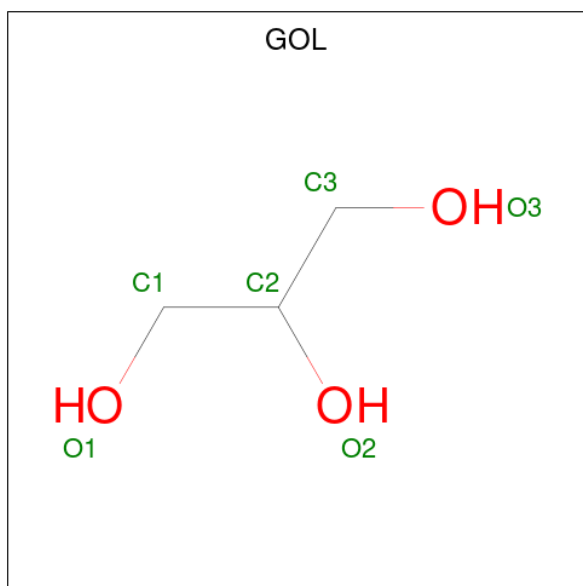
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

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



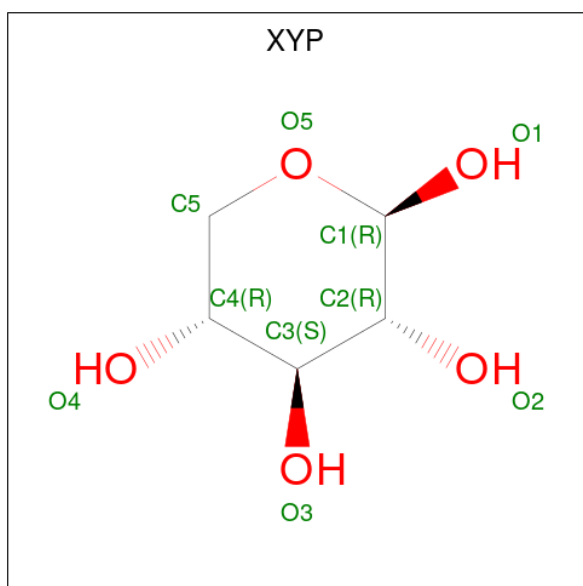
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			6	3	3		
9	B	1	Total	C	O	0	0
			6	3	3		
9	B	1	Total	C	O	0	0
			6	3	3		
9	B	1	Total	C	O	0	0
			6	3	3		
9	C	1	Total	C	O	0	1
			12	6	6		

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

- Molecule 10 is beta-D-xylopyranose (CCD ID: XYP) (formula: C₅H₁₀O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			10	5	5		
10	B	1	Total	C	O	0	0
			10	5	5		
10	C	1	Total	C	O	0	0
			10	5	5		
10	D	1	Total	C	O	0	0
			10	5	5		

- Molecule 11 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	1	Total	Cl	0	0
			1	1		
11	C	1	Total	Cl	0	0
			1	1		

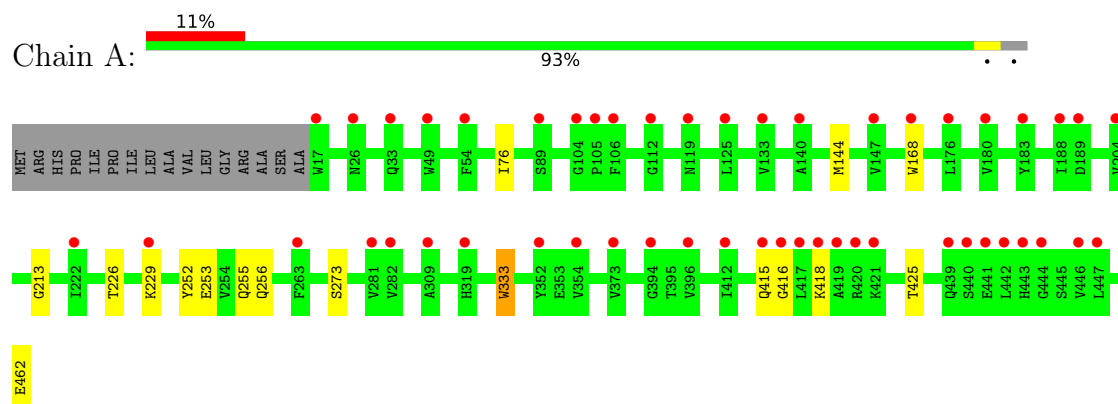
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	398	Total 398	O 398	0	0
12	B	399	Total 399	O 399	0	0
12	C	401	Total 401	O 401	0	0
12	D	427	Total 427	O 427	0	0

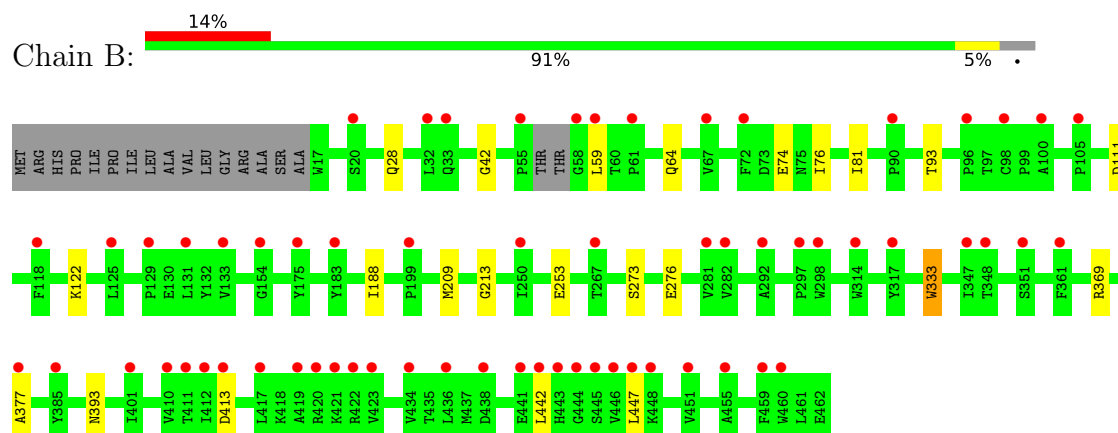
3 Residue-property plots [i](#)

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

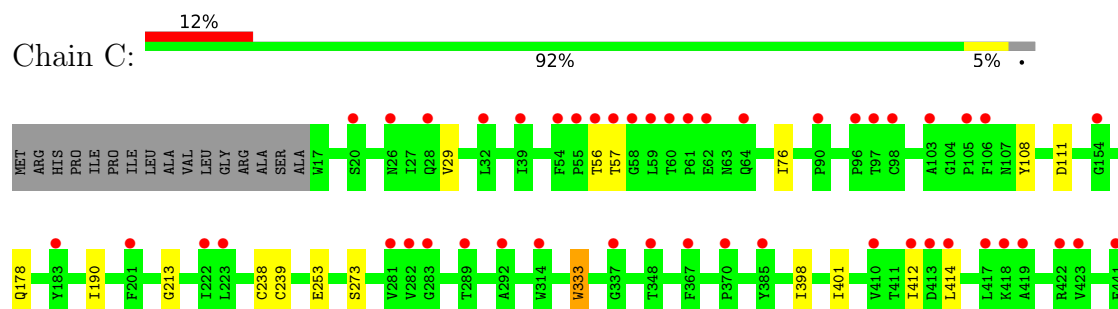
- Molecule 1: Reducing-end xylose-releasing exoxylanase Xyn30A

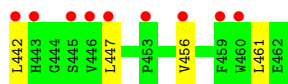


- Molecule 1: Reducing-end xylose-releasing exoxylanase Xyn30A

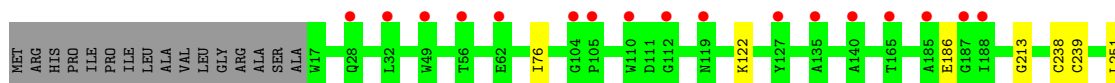
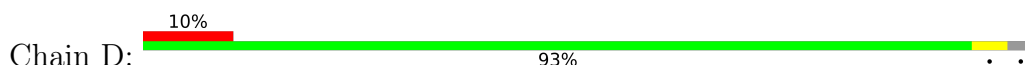


- Molecule 1: Reducing-end xylose-releasing exoxylanase Xyn30A





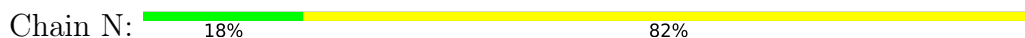
- Molecule 1: Reducing-end xylose-releasing exoxylanase Xyn30A



- Molecule 2: 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



- Molecule 2: alpha-D-mannopyranose-(1-2)-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



- 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 M:  50% 50%

MAG1
MAG2

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

Chain O:  50% 50%

MAG1
MAG2

- Molecule 4: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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

Chain G:  67% 33%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

- Molecule 4: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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

Chain I:  50% 33% 17%

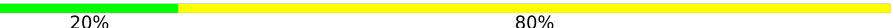
MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

- Molecule 4: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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

Chain P:  50% 50%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

- Molecule 5: 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

Chain H:  20% 80%

NAG1	NAG2	EMA3	MAN4	MAN5	MAN6	MAN7	MAN8	MAN9	MAN10
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- Molecule 6: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]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

Chain K:  33% 67%

NAG1	NAG2	EMA3	MAN4	MAN5	MAN6	MAN7	MAN8	MAN9
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- Molecule 7: alpha-D-mannopyranose-(1-3)-[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 L:  60% 20% 20%

NAG1	NAG2	EMA3	MAN4	MAN5
------	------	------	------	------

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	138.25Å 120.16Å 122.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.35 – 1.70 45.35 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.1 (45.35-1.70) 99.1 (45.35-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 1.70Å)	Xtriage
Refinement program	PHENIX 11.2	Depositor
R, R_{free}	0.199 , 0.233 0.199 , 0.233	Depositor DCC
R_{free} test set	11115 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.782	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.021 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16775	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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 49.09 % 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 7.8401e-05. 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: MAN, NAG, GOL, CL, BMA, XYP

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	0.31	0/3611	0.54	0/4930
1	B	0.31	0/3607	0.53	0/4922
1	C	0.32	0/3622	0.54	0/4945
1	D	0.31	0/3637	0.53	0/4965
All	All	0.31	0/14477	0.53	0/19762

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3511	0	3264	14	0
1	B	3508	0	3265	15	0
1	C	3522	0	3273	10	0
1	D	3537	0	3283	10	0
2	E	127	0	106	1	0
2	N	127	0	106	0	0
3	F	28	0	25	0	0
3	J	28	0	25	1	0
3	M	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	O	28	0	25	0	0
4	G	72	0	61	0	0
4	I	72	0	61	1	0
4	P	72	0	61	0	0
5	H	116	0	97	1	0
6	K	105	0	88	0	0
7	L	61	0	52	1	0
8	A	28	0	26	0	0
8	B	28	0	26	0	0
8	C	28	0	26	0	0
8	D	28	0	26	0	0
9	A	6	0	8	0	0
9	B	18	0	24	2	0
9	C	12	0	16	1	0
9	D	18	0	24	1	0
10	A	10	0	0	0	0
10	B	10	0	0	0	0
10	C	10	0	0	0	0
10	D	10	0	0	0	0
11	B	1	0	0	0	0
11	C	1	0	0	0	0
12	A	398	0	0	4	0
12	B	399	0	0	2	0
12	C	401	0	0	1	0
12	D	427	0	0	0	0
All	All	16775	0	13993	50	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 50 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:442:LEU:HD21	1:B:447:LEU:HD21	1.74	0.70
7:L:5:MAN:O2	3:M:2:NAG:O3	2.11	0.69
1:B:393:ASN:HD22	5:H:1:NAG:H83	1.71	0.55
1:B:28:GLN:NE2	1:B:413:ASP:OD2	2.32	0.54
1:A:415:GLN:HG2	12:A:2024:HOH:O	2.08	0.53

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	448/462 (97%)	430 (96%)	14 (3%)	4 (1%)	14	4
1	B	445/462 (96%)	427 (96%)	14 (3%)	4 (1%)	14	4
1	C	449/462 (97%)	430 (96%)	15 (3%)	4 (1%)	14	4
1	D	451/462 (98%)	433 (96%)	17 (4%)	1 (0%)	43	28
All	All	1793/1848 (97%)	1720 (96%)	60 (3%)	13 (1%)	21	7

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	333	TRP
1	C	333	TRP
1	A	273[A]	SER
1	A	273[B]	SER
1	B	333	TRP

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	375/383 (98%)	374 (100%)	1 (0%)	86	83
1	B	374/383 (98%)	373 (100%)	1 (0%)	86	83
1	C	376/383 (98%)	373 (99%)	3 (1%)	73	65
1	D	378/383 (99%)	377 (100%)	1 (0%)	86	83
All	All	1503/1532 (98%)	1497 (100%)	6 (0%)	84	80

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	57	THR
1	C	333	TRP
1	D	333	TRP
1	B	333	TRP
1	A	333	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	255	GLN
1	D	151	ASN
1	D	415	GLN
1	D	178	GLN
1	B	26	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 ⓘ

72 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	E	1	2,1	14,14,15	0.57	0	17,19,21	0.60	0
2	MAN	E	10	2	11,11,12	0.53	0	15,15,17	1.18	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	E	11	2	11,11,12	1.01	1 (9%)	15,15,17	0.79	0
2	NAG	E	2	2	14,14,15	0.25	0	17,19,21	0.54	0
2	BMA	E	3	2	11,11,12	0.82	0	15,15,17	0.84	0
2	MAN	E	4	2	11,11,12	0.80	0	15,15,17	1.21	2 (13%)
2	MAN	E	5	2	11,11,12	0.90	0	15,15,17	1.01	1 (6%)
2	MAN	E	6	2	11,11,12	0.70	0	15,15,17	0.88	1 (6%)
2	MAN	E	7	2	11,11,12	0.81	1 (9%)	15,15,17	0.92	1 (6%)
2	MAN	E	8	2	11,11,12	0.84	0	15,15,17	0.95	1 (6%)
2	MAN	E	9	2	11,11,12	0.96	1 (9%)	15,15,17	1.17	1 (6%)
3	NAG	F	1	3,1	14,14,15	0.43	0	17,19,21	0.67	0
3	NAG	F	2	3	14,14,15	0.27	0	17,19,21	0.61	1 (5%)
4	NAG	G	1	1,4	14,14,15	0.30	0	17,19,21	0.74	0
4	NAG	G	2	4	14,14,15	0.45	0	17,19,21	0.46	0
4	BMA	G	3	4	11,11,12	0.84	0	15,15,17	0.74	0
4	MAN	G	4	4	11,11,12	0.70	0	15,15,17	0.86	1 (6%)
4	MAN	G	5	4	11,11,12	0.93	0	15,15,17	0.93	1 (6%)
4	MAN	G	6	4	11,11,12	0.89	0	15,15,17	0.90	0
5	NAG	H	1	5,1	14,14,15	0.43	0	17,19,21	0.59	0
5	MAN	H	10	5	11,11,12	0.62	0	15,15,17	1.05	1 (6%)
5	NAG	H	2	5	14,14,15	0.27	0	17,19,21	0.64	0
5	BMA	H	3	5	11,11,12	1.07	1 (9%)	15,15,17	0.67	0
5	MAN	H	4	5	11,11,12	0.61	0	15,15,17	1.06	1 (6%)
5	MAN	H	5	5	11,11,12	1.10	1 (9%)	15,15,17	1.09	2 (13%)
5	MAN	H	6	5	11,11,12	0.85	0	15,15,17	0.86	1 (6%)
5	MAN	H	7	5	11,11,12	1.10	1 (9%)	15,15,17	1.04	2 (13%)
5	MAN	H	8	5	11,11,12	0.77	0	15,15,17	0.88	0
5	MAN	H	9	5	11,11,12	0.68	0	15,15,17	1.14	2 (13%)
4	NAG	I	1	1,4	14,14,15	0.31	0	17,19,21	0.57	0
4	NAG	I	2	4	14,14,15	0.49	0	17,19,21	0.46	0
4	BMA	I	3	4	11,11,12	0.71	0	15,15,17	0.56	0
4	MAN	I	4	4	11,11,12	0.72	0	15,15,17	1.31	3 (20%)
4	MAN	I	5	4	11,11,12	0.96	1 (9%)	15,15,17	1.70	1 (6%)
4	MAN	I	6	4	11,11,12	1.16	2 (18%)	15,15,17	0.79	0
3	NAG	J	1	3,1	14,14,15	0.43	0	17,19,21	0.65	0
3	NAG	J	2	3	14,14,15	0.36	0	17,19,21	0.62	1 (5%)
6	NAG	K	1	6,1	14,14,15	0.44	0	17,19,21	0.62	0
6	NAG	K	2	6	14,14,15	0.37	0	17,19,21	0.56	0
6	BMA	K	3	6	11,11,12	0.78	0	15,15,17	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	MAN	K	4	6	11,11,12	0.85	0	15,15,17	1.31	1 (6%)
6	MAN	K	5	6	11,11,12	0.63	0	15,15,17	1.10	2 (13%)
6	MAN	K	6	6	11,11,12	0.59	0	15,15,17	0.90	1 (6%)
6	MAN	K	7	6	11,11,12	0.83	0	15,15,17	1.15	1 (6%)
6	MAN	K	8	6	11,11,12	0.60	0	15,15,17	1.10	2 (13%)
6	MAN	K	9	6	11,11,12	0.71	0	15,15,17	1.05	2 (13%)
7	NAG	L	1	1,7	14,14,15	0.43	0	17,19,21	0.68	0
7	NAG	L	2	7	14,14,15	0.41	0	17,19,21	0.52	0
7	BMA	L	3	7	11,11,12	0.80	0	15,15,17	0.90	0
7	MAN	L	4	7	11,11,12	0.95	1 (9%)	15,15,17	0.84	0
7	MAN	L	5	7	11,11,12	0.58	0	15,15,17	1.05	2 (13%)
3	NAG	M	1	3,1	14,14,15	0.49	0	17,19,21	0.61	0
3	NAG	M	2	3	14,14,15	0.37	0	17,19,21	0.56	0
2	NAG	N	1	2,1	14,14,15	0.57	0	17,19,21	0.70	0
2	MAN	N	10	2	11,11,12	0.68	0	15,15,17	1.20	2 (13%)
2	MAN	N	11	2	11,11,12	0.85	1 (9%)	15,15,17	1.01	2 (13%)
2	NAG	N	2	2	14,14,15	0.41	0	17,19,21	0.62	0
2	BMA	N	3	2	11,11,12	0.74	1 (9%)	15,15,17	0.88	1 (6%)
2	MAN	N	4	2	11,11,12	0.64	0	15,15,17	1.01	2 (13%)
2	MAN	N	5	2	11,11,12	0.93	1 (9%)	15,15,17	1.29	2 (13%)
2	MAN	N	6	2	11,11,12	0.56	0	15,15,17	1.04	1 (6%)
2	MAN	N	7	2	11,11,12	0.69	0	15,15,17	1.06	1 (6%)
2	MAN	N	8	2	11,11,12	0.74	0	15,15,17	0.97	1 (6%)
2	MAN	N	9	2	11,11,12	0.50	0	15,15,17	1.25	2 (13%)
3	NAG	O	1	3,1	14,14,15	0.30	0	17,19,21	0.62	0
3	NAG	O	2	3	14,14,15	0.24	0	17,19,21	0.60	1 (5%)
4	NAG	P	1	1,4	14,14,15	0.26	0	17,19,21	0.66	0
4	NAG	P	2	4	14,14,15	0.41	0	17,19,21	0.56	0
4	BMA	P	3	4	11,11,12	0.72	0	15,15,17	0.72	0
4	MAN	P	4	4	11,11,12	0.57	0	15,15,17	1.15	2 (13%)
4	MAN	P	5	4	11,11,12	0.67	0	15,15,17	1.05	2 (13%)
4	MAN	P	6	4	11,11,12	1.10	1 (9%)	15,15,17	0.85	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	E	10	2	-	0/2/19/22	0/1/1/1
2	MAN	E	11	2	-	0/2/19/22	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4	2	-	0/2/19/22	0/1/1/1
2	MAN	E	5	2	-	1/2/19/22	0/1/1/1
2	MAN	E	6	2	-	0/2/19/22	0/1/1/1
2	MAN	E	7	2	-	0/2/19/22	0/1/1/1
2	MAN	E	8	2	-	2/2/19/22	0/1/1/1
2	MAN	E	9	2	-	0/2/19/22	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
4	NAG	G	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	0/1/1/1
4	MAN	G	5	4	-	0/2/19/22	0/1/1/1
4	MAN	G	6	4	-	0/2/19/22	0/1/1/1
5	NAG	H	1	5,1	-	2/6/23/26	0/1/1/1
5	MAN	H	10	5	-	2/2/19/22	0/1/1/1
5	NAG	H	2	5	-	0/6/23/26	0/1/1/1
5	BMA	H	3	5	-	0/2/19/22	0/1/1/1
5	MAN	H	4	5	-	0/2/19/22	0/1/1/1
5	MAN	H	5	5	-	0/2/19/22	0/1/1/1
5	MAN	H	6	5	-	0/2/19/22	0/1/1/1
5	MAN	H	7	5	-	0/2/19/22	0/1/1/1
5	MAN	H	8	5	-	0/2/19/22	0/1/1/1
5	MAN	H	9	5	-	0/2/19/22	0/1/1/1
4	NAG	I	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	MAN	I	4	4	-	1/2/19/22	0/1/1/1
4	MAN	I	5	4	-	2/2/19/22	0/1/1/1
4	MAN	I	6	4	-	0/2/19/22	0/1/1/1
3	NAG	J	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
6	NAG	K	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	0/6/23/26	0/1/1/1
6	BMA	K	3	6	-	0/2/19/22	0/1/1/1
6	MAN	K	4	6	-	0/2/19/22	0/1/1/1
6	MAN	K	5	6	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	K	6	6	-	0/2/19/22	0/1/1/1
6	MAN	K	7	6	-	1/2/19/22	0/1/1/1
6	MAN	K	8	6	-	0/2/19/22	0/1/1/1
6	MAN	K	9	6	-	0/2/19/22	0/1/1/1
7	NAG	L	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	L	2	7	-	0/6/23/26	0/1/1/1
7	BMA	L	3	7	-	0/2/19/22	0/1/1/1
7	MAN	L	4	7	-	0/2/19/22	0/1/1/1
7	MAN	L	5	7	-	0/2/19/22	0/1/1/1
3	NAG	M	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	2/6/23/26	0/1/1/1
2	NAG	N	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	N	10	2	-	0/2/19/22	0/1/1/1
2	MAN	N	11	2	-	0/2/19/22	0/1/1/1
2	NAG	N	2	2	-	0/6/23/26	0/1/1/1
2	BMA	N	3	2	-	0/2/19/22	0/1/1/1
2	MAN	N	4	2	-	0/2/19/22	0/1/1/1
2	MAN	N	5	2	-	1/2/19/22	0/1/1/1
2	MAN	N	6	2	-	0/2/19/22	0/1/1/1
2	MAN	N	7	2	-	0/2/19/22	0/1/1/1
2	MAN	N	8	2	-	0/2/19/22	0/1/1/1
2	MAN	N	9	2	-	0/2/19/22	0/1/1/1
3	NAG	O	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	1/6/23/26	0/1/1/1
4	NAG	P	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	BMA	P	3	4	-	0/2/19/22	0/1/1/1
4	MAN	P	4	4	-	0/2/19/22	0/1/1/1
4	MAN	P	5	4	-	0/2/19/22	0/1/1/1
4	MAN	P	6	4	-	0/2/19/22	0/1/1/1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	3	BMA	O5-C1	-2.71	1.39	1.43
2	E	7	MAN	O5-C5	2.53	1.48	1.43
4	I	6	MAN	O5-C1	-2.50	1.39	1.43
5	H	5	MAN	O5-C5	2.40	1.48	1.43
2	N	5	MAN	O5-C5	2.36	1.48	1.43

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	5	MAN	C1-O5-C5	5.76	119.91	112.19
2	N	9	MAN	C1-O5-C5	3.79	117.26	112.19
2	E	9	MAN	C1-O5-C5	3.32	116.63	112.19
2	E	10	MAN	O2-C2-C3	-3.27	103.39	110.15
2	N	6	MAN	C1-O5-C5	3.16	116.42	112.19

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

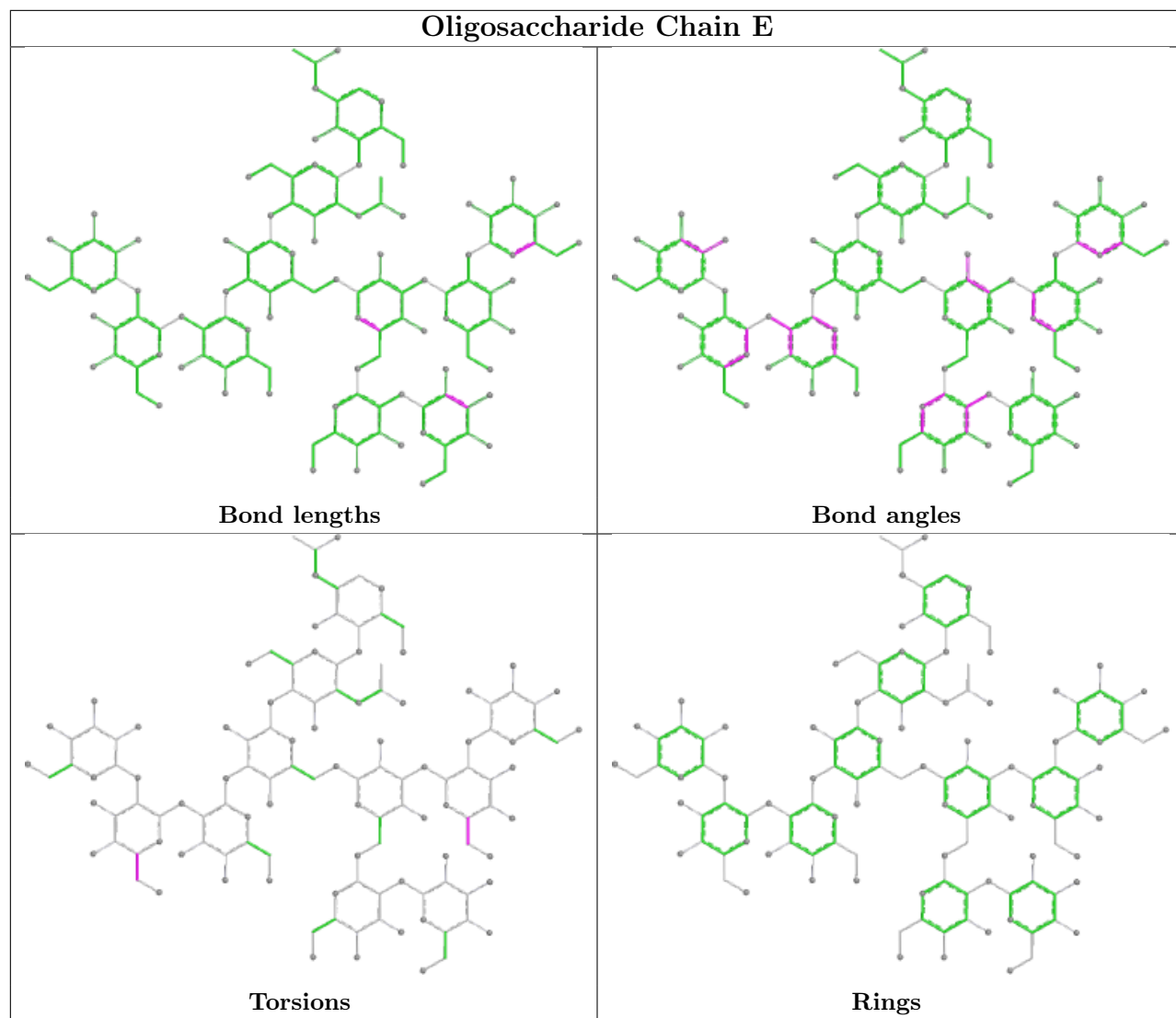
Mol	Chain	Res	Type	Atoms
4	I	5	MAN	C4-C5-C6-O6
5	H	1	NAG	C8-C7-N2-C2
5	H	1	NAG	O7-C7-N2-C2
4	I	5	MAN	O5-C5-C6-O6
3	M	2	NAG	O5-C5-C6-O6

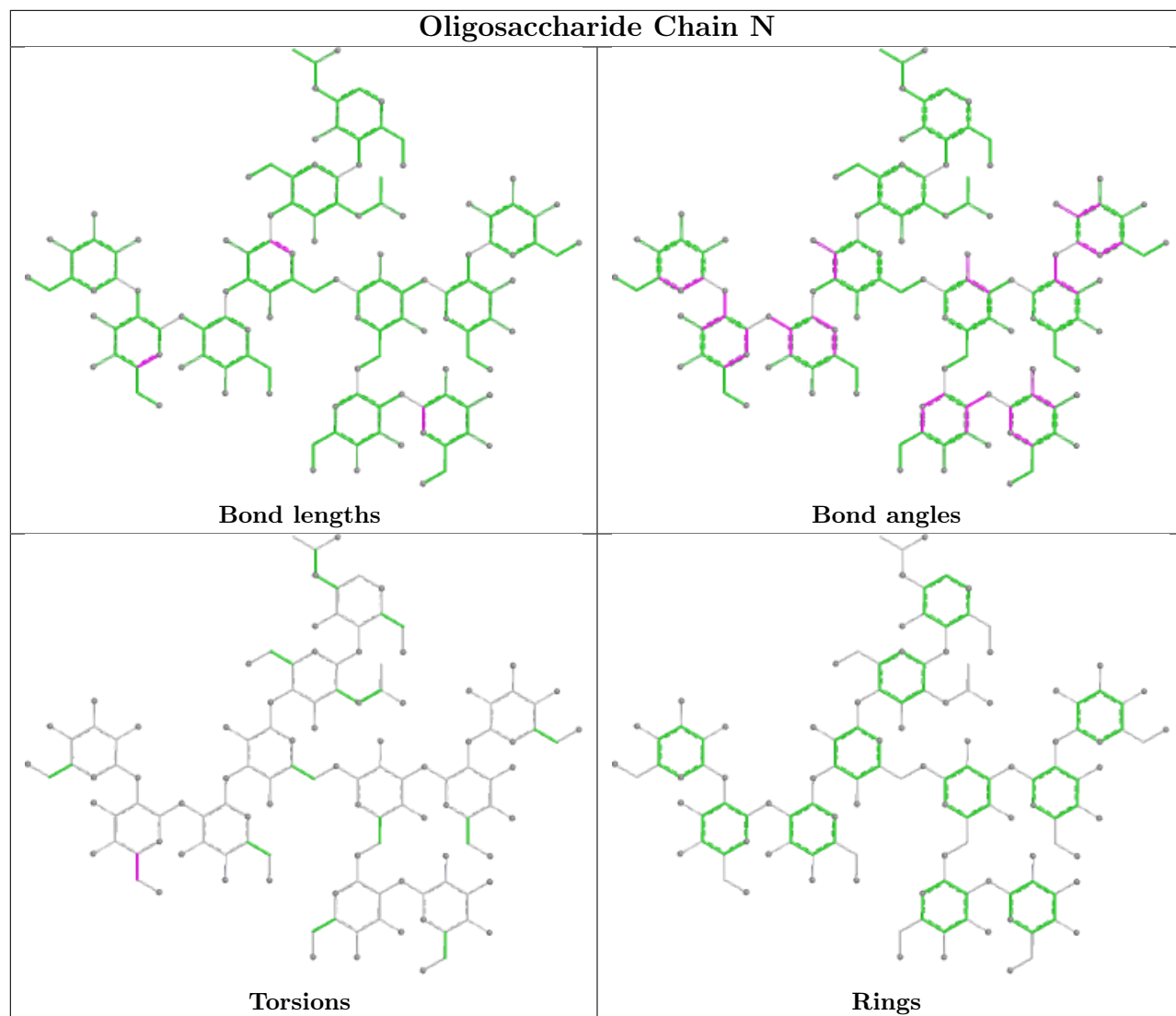
There are no ring outliers.

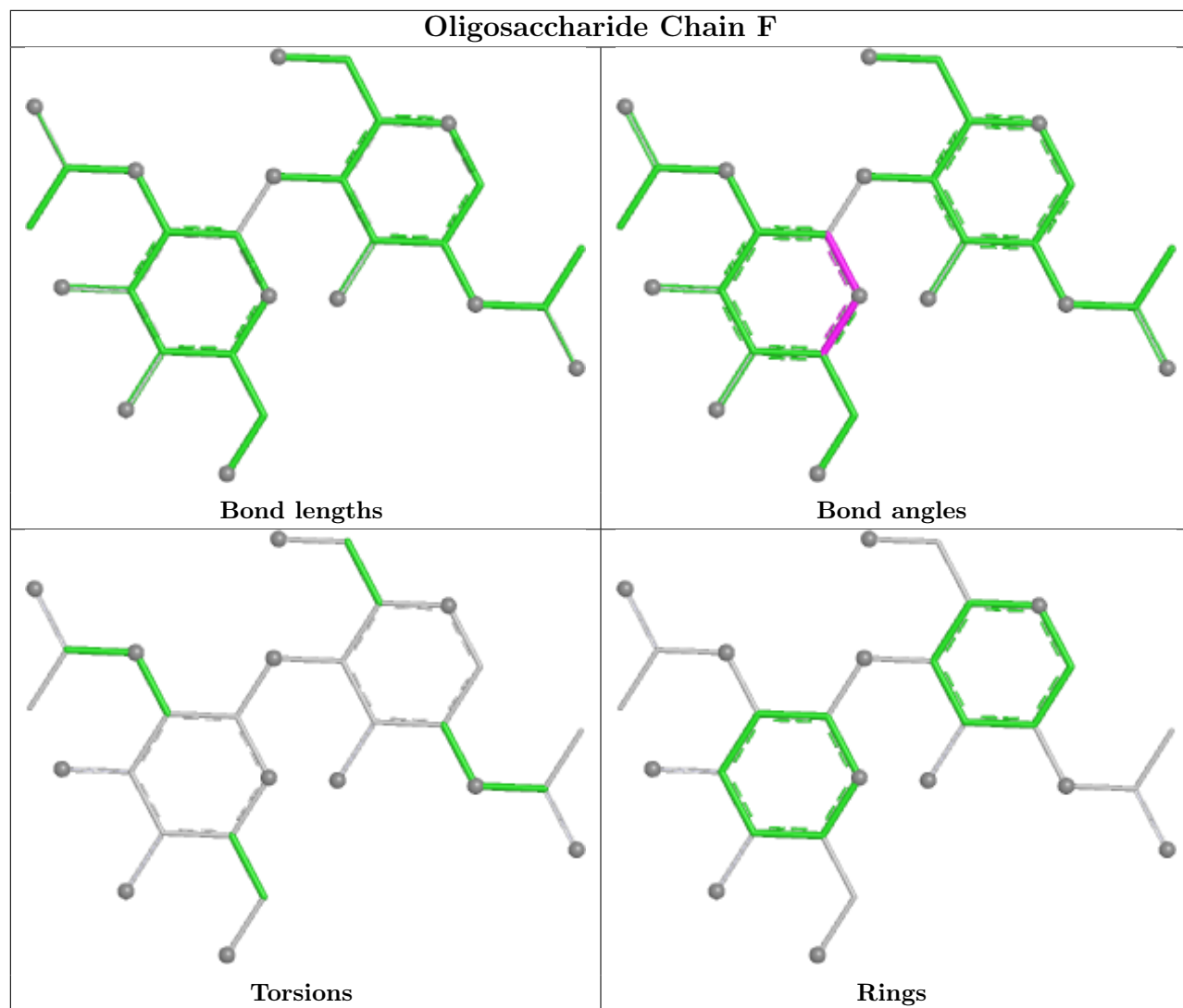
6 monomers are involved in 4 short contacts:

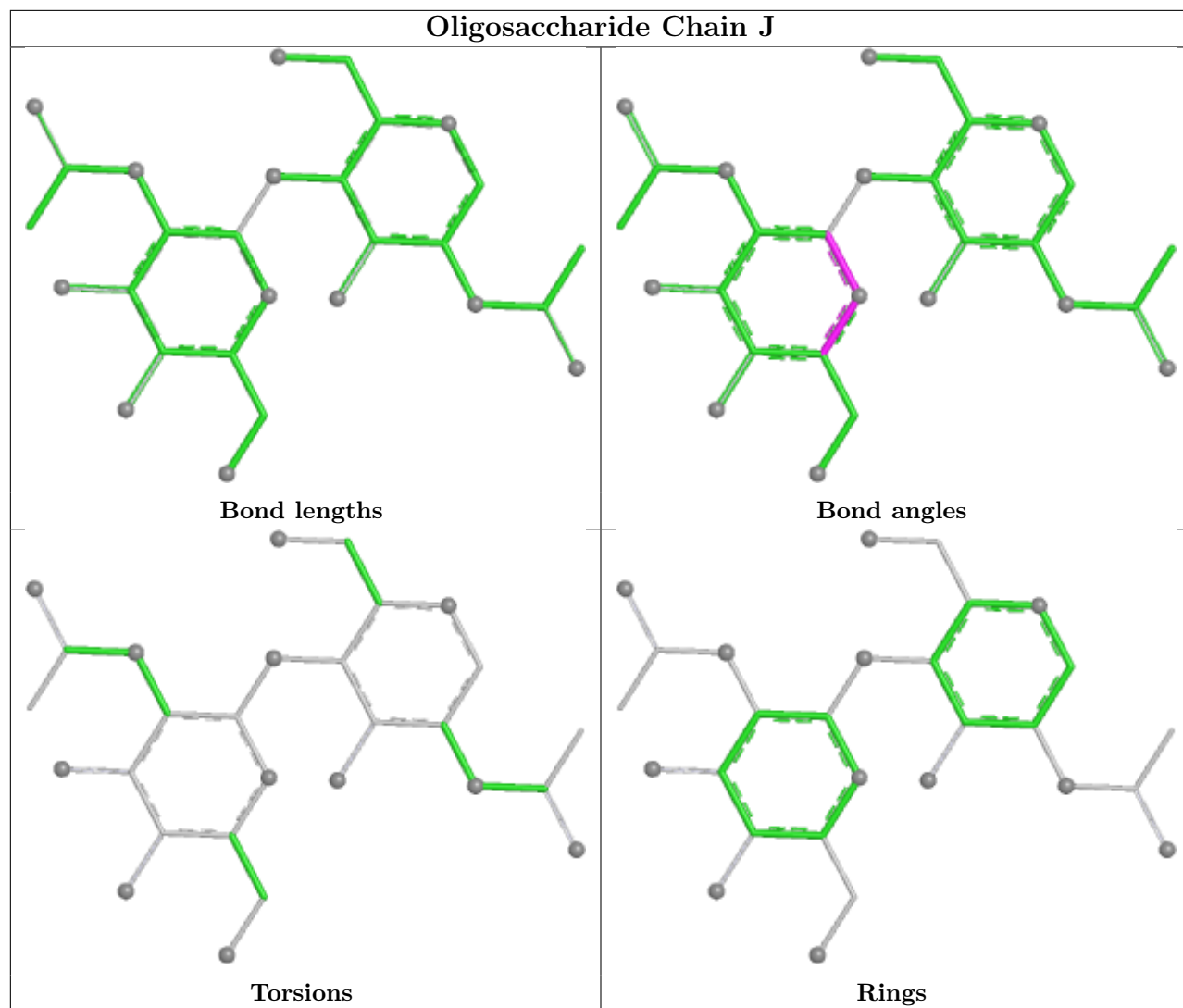
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	1	NAG	1	0
2	E	9	MAN	1	0
4	I	4	MAN	1	0
7	L	5	MAN	1	0
3	J	2	NAG	1	0
3	M	2	NAG	1	0

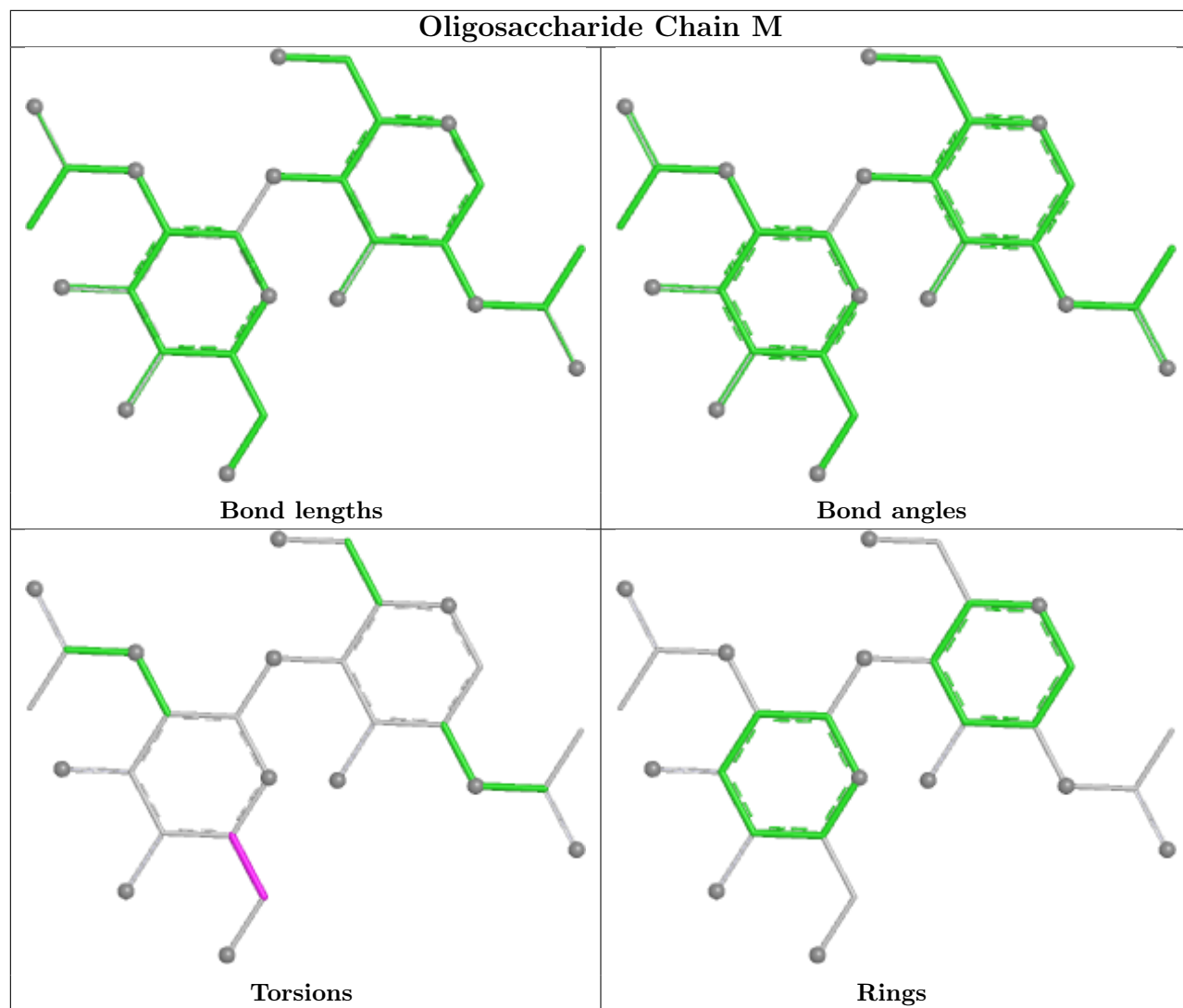
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

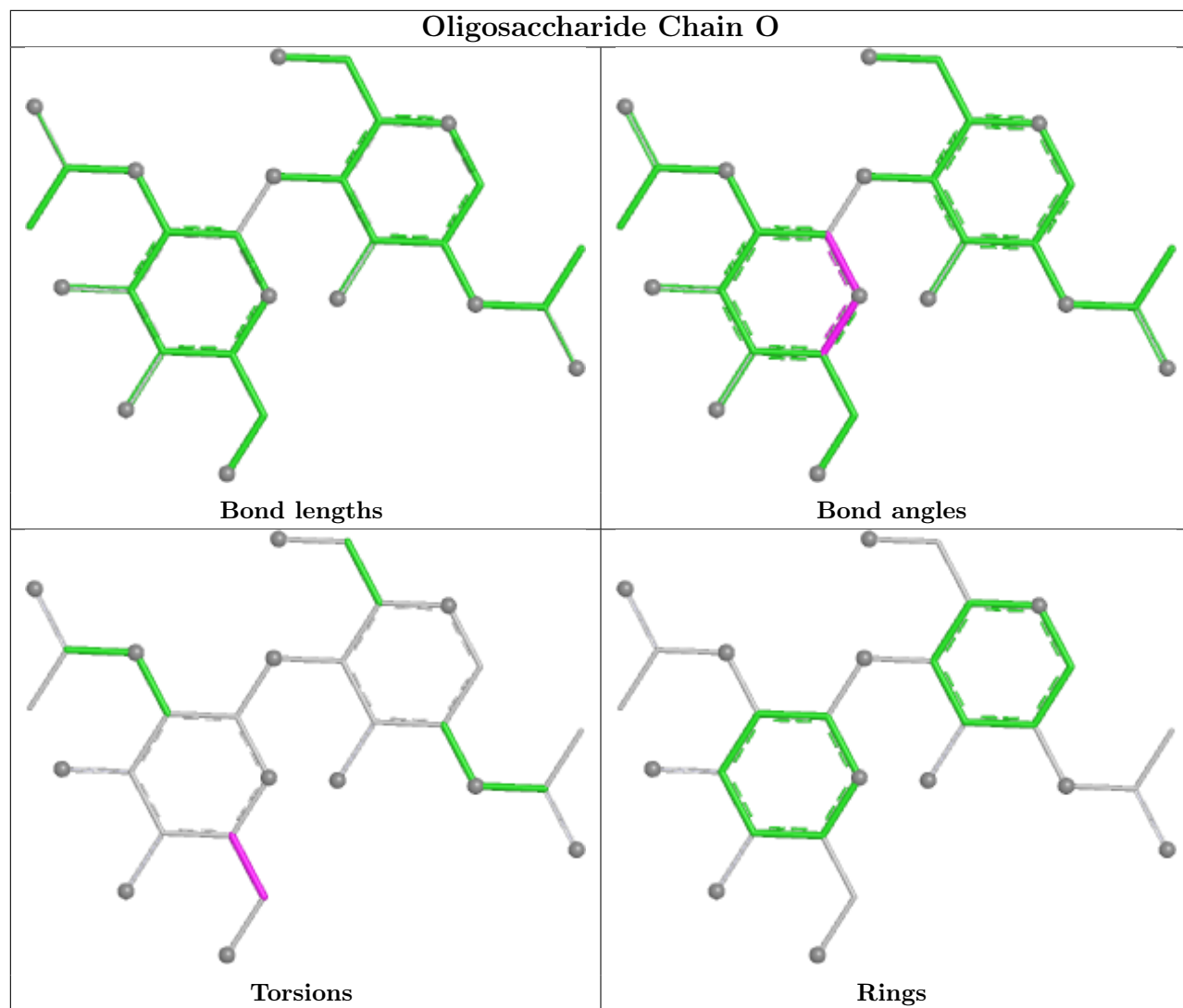


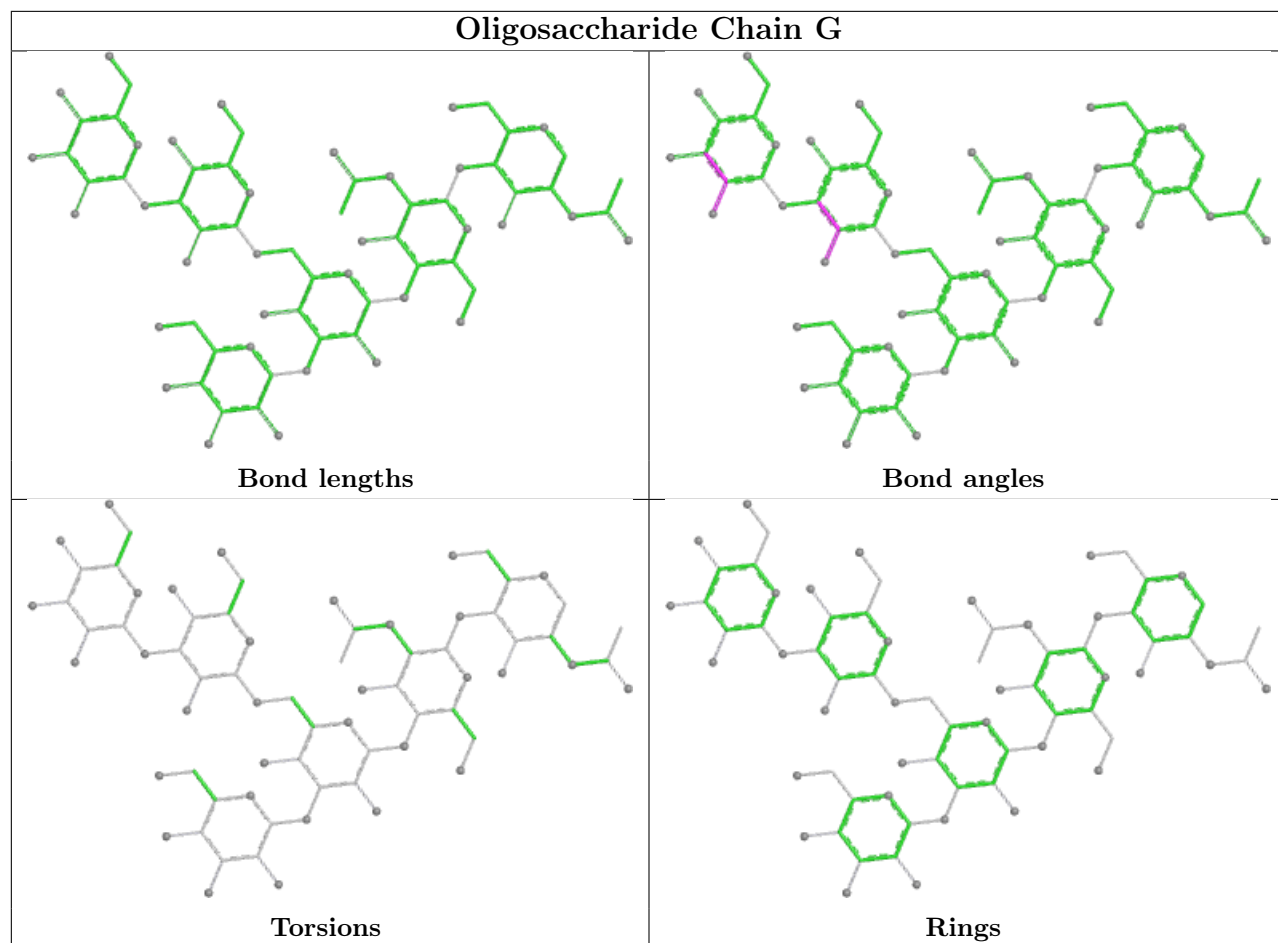


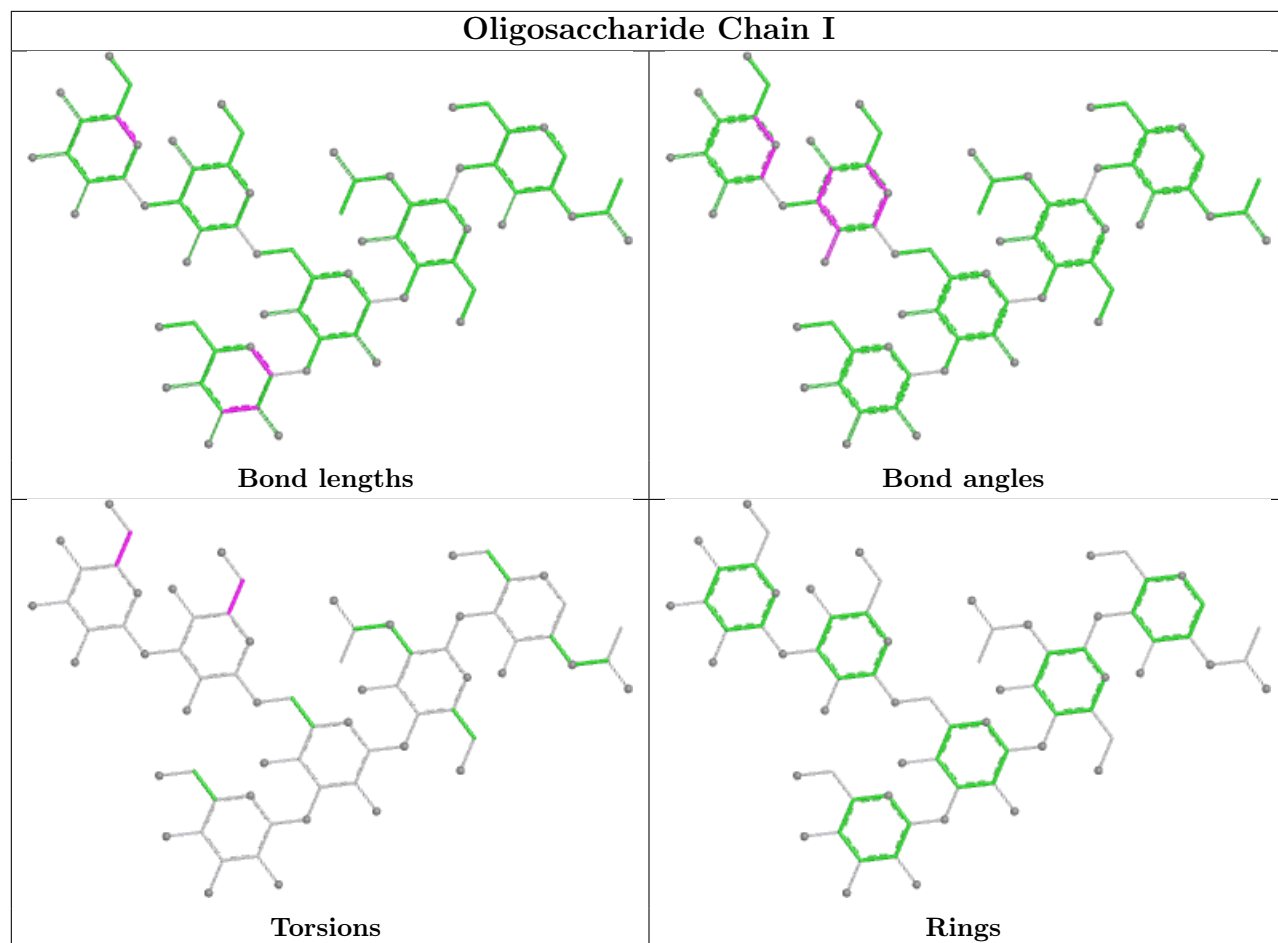


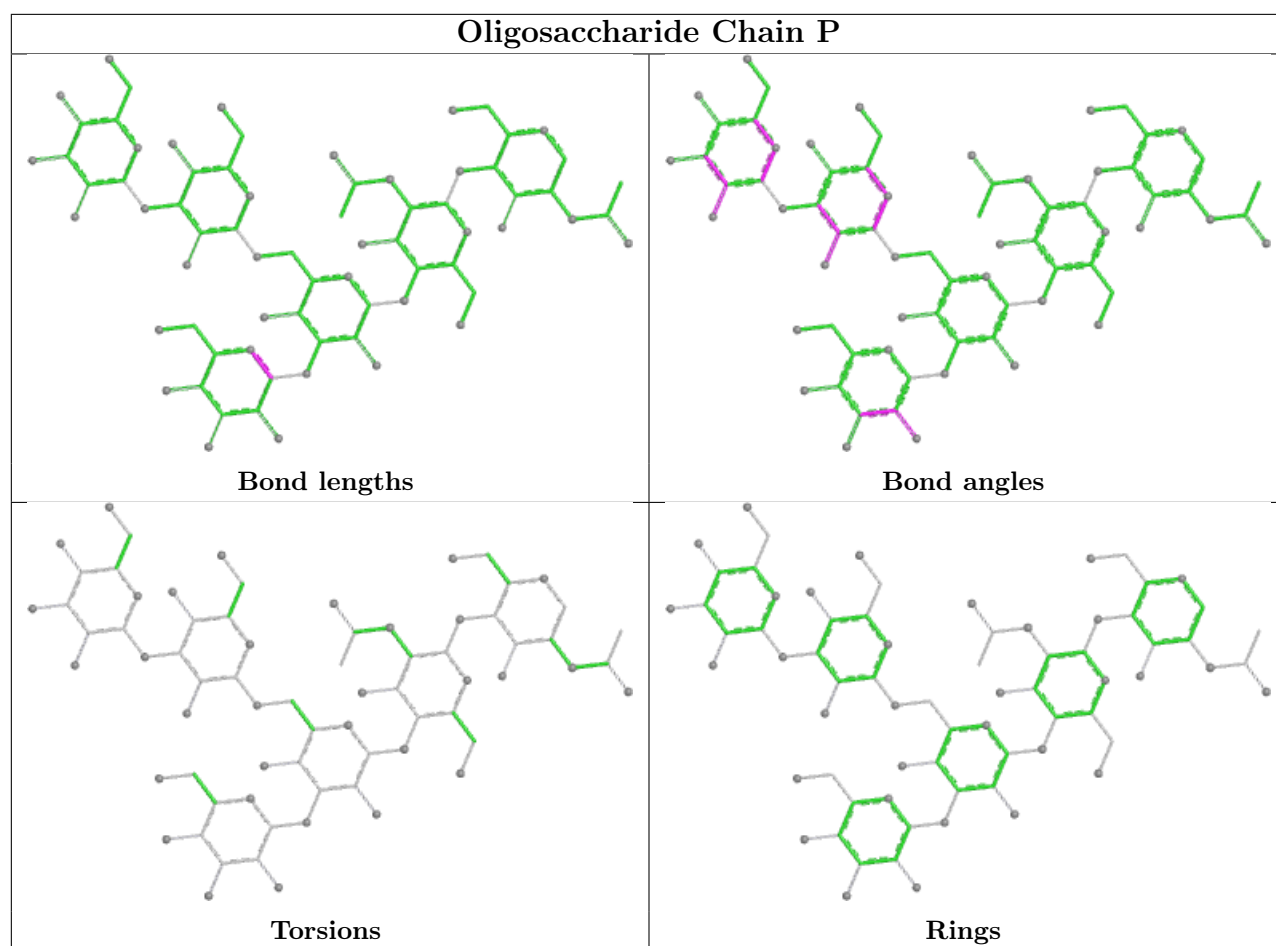


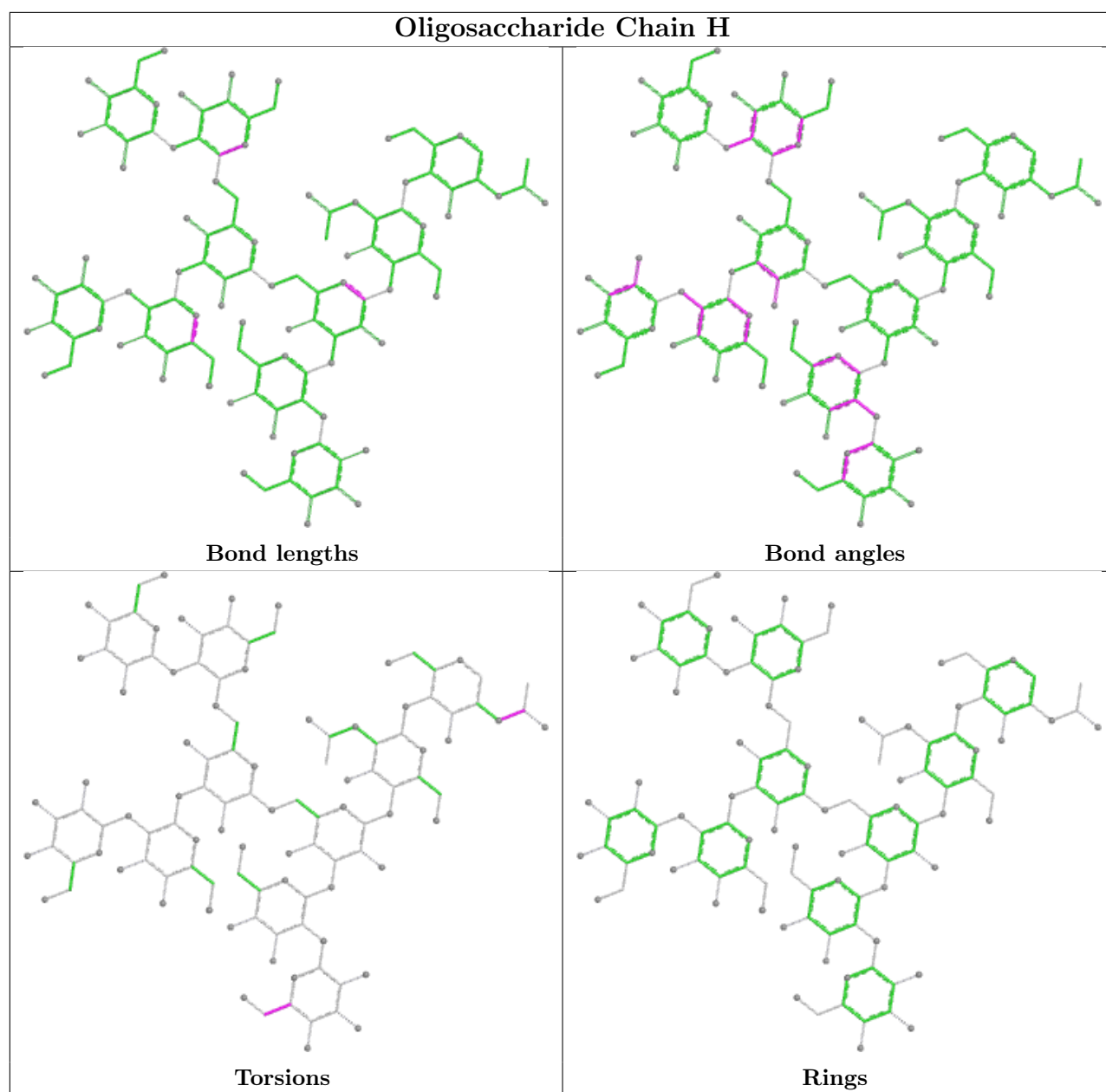


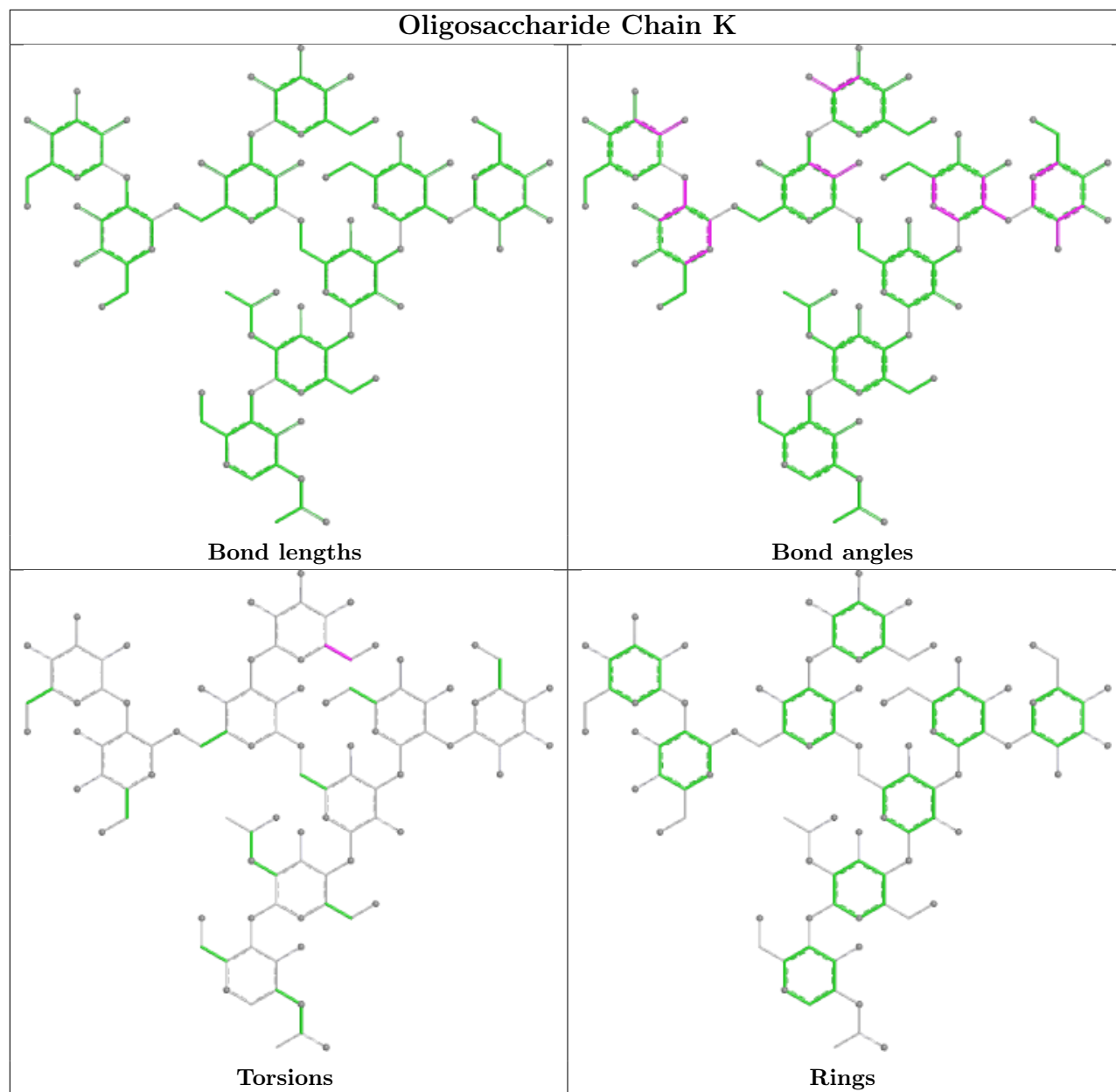


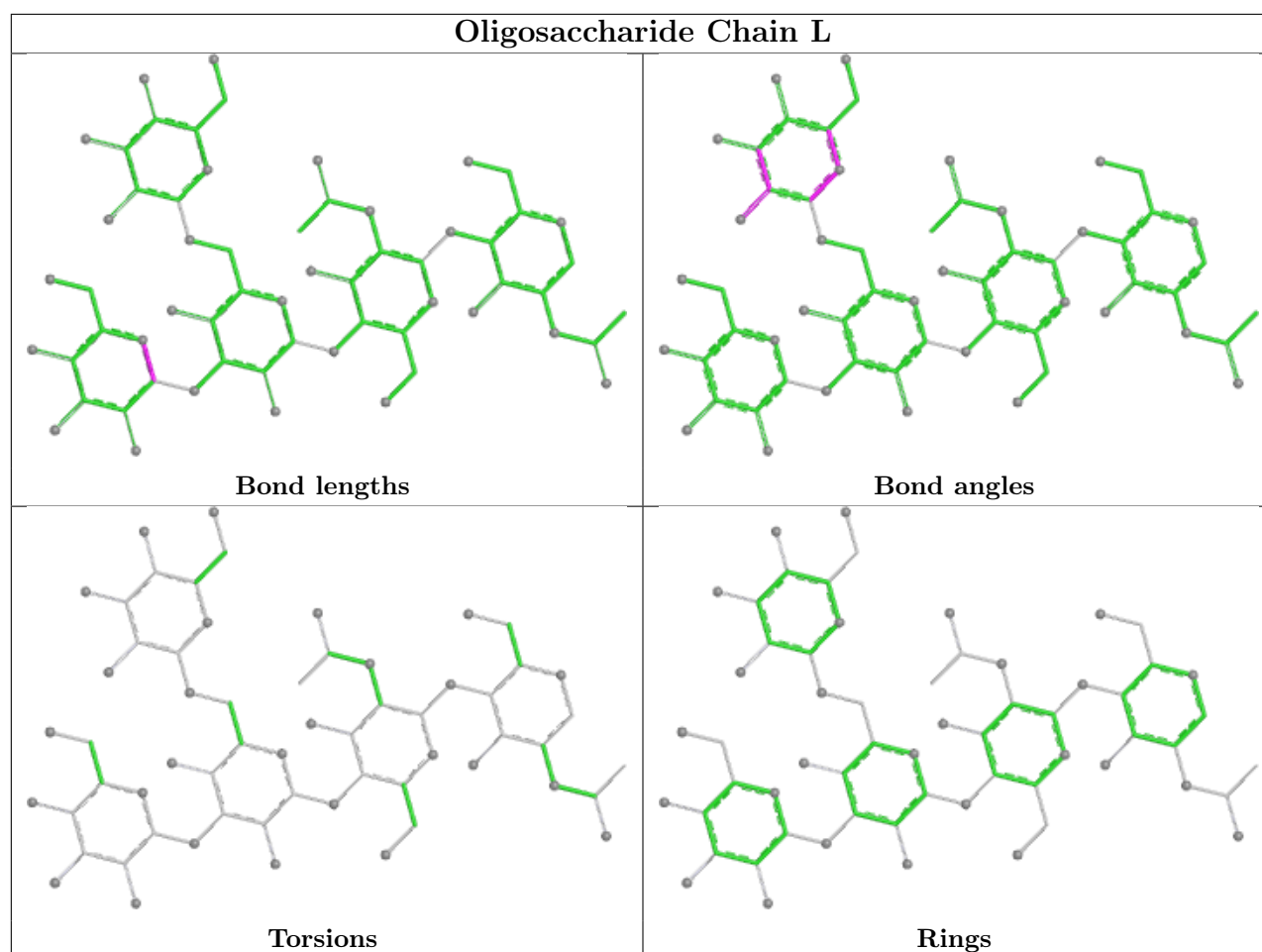












5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 2 are monoatomic - leaving 21 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	GOL	D	1304	-	5,5,5	1.11	0	5,5,5	1.05	0
9	GOL	B	1302	-	5,5,5	0.85	0	5,5,5	1.06	0
8	NAG	B	1303	1	14,14,15	0.33	0	17,19,21	0.61	1 (5%)
9	GOL	A	1803	-	5,5,5	0.80	0	5,5,5	1.02	0
10	XYP	D	1306	-	10,10,10	1.62	2 (20%)	14,14,14	0.80	0
9	GOL	C	1203[A]	-	5,5,5	0.94	0	5,5,5	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	D	1301	1	14,14,15	0.42	0	17,19,21	0.74	1 (5%)
8	NAG	B	1301	1	14,14,15	0.45	0	17,19,21	0.56	0
9	GOL	B	1305	-	5,5,5	1.02	0	5,5,5	1.11	0
10	XYP	C	1204	-	10,10,10	1.77	2 (20%)	14,14,14	0.70	0
8	NAG	D	1303	1	14,14,15	0.30	0	17,19,21	0.49	0
8	NAG	C	1201	1	14,14,15	0.44	0	17,19,21	0.44	0
8	NAG	A	1801	1	14,14,15	0.39	0	17,19,21	0.49	0
10	XYP	B	1306	-	10,10,10	1.65	2 (20%)	14,14,14	0.64	0
9	GOL	B	1304	-	5,5,5	0.84	0	5,5,5	1.13	1 (20%)
10	XYP	A	1804	-	10,10,10	1.82	2 (20%)	14,14,14	0.69	0
9	GOL	C	1203[B]	-	5,5,5	1.02	0	5,5,5	1.06	0
9	GOL	D	1305	-	5,5,5	0.72	0	5,5,5	1.16	1 (20%)
8	NAG	A	1802	1	14,14,15	0.34	0	17,19,21	0.85	1 (5%)
9	GOL	D	1302	-	5,5,5	0.79	0	5,5,5	1.29	1 (20%)
8	NAG	C	1202	1	14,14,15	0.16	0	17,19,21	0.59	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GOL	D	1304	-	-	2/4/4/4	-
9	GOL	B	1302	-	-	2/4/4/4	-
8	NAG	B	1303	1	-	1/6/23/26	0/1/1/1
9	GOL	A	1803	-	-	0/4/4/4	-
10	XYP	D	1306	-	-	-	0/1/1/1
9	GOL	C	1203[A]	-	-	2/4/4/4	-
8	NAG	D	1301	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
9	GOL	B	1305	-	-	0/4/4/4	-
10	XYP	C	1204	-	-	-	0/1/1/1
8	NAG	D	1303	1	-	2/6/23/26	0/1/1/1
8	NAG	C	1201	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1801	1	-	0/6/23/26	0/1/1/1
10	XYP	B	1306	-	-	-	0/1/1/1
9	GOL	B	1304	-	-	1/4/4/4	-
10	XYP	A	1804	-	-	-	0/1/1/1
9	GOL	C	1203[B]	-	-	2/4/4/4	-
9	GOL	D	1305	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	A	1802	1	-	1/6/23/26	0/1/1/1
9	GOL	D	1302	-	-	0/4/4/4	-
8	NAG	C	1202	1	-	2/6/23/26	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)
10	A	1804	XYP	O5-C1	4.26	1.50	1.43
10	C	1204	XYP	O5-C1	4.19	1.50	1.43
10	B	1306	XYP	O5-C1	3.89	1.49	1.43
10	D	1306	XYP	O5-C1	3.76	1.49	1.43
10	A	1804	XYP	O5-C5	2.66	1.48	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1802	NAG	C1-O5-C5	2.87	116.04	112.19
8	D	1301	NAG	C1-O5-C5	2.47	115.49	112.19
9	D	1302	GOL	C3-C2-C1	-2.16	103.87	111.80
9	D	1305	GOL	C3-C2-C1	-2.16	103.88	111.80
9	B	1304	GOL	C3-C2-C1	-2.06	104.23	111.80

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	1302	GOL	O1-C1-C2-C3
9	C	1203[A]	GOL	O1-C1-C2-C3
9	D	1304	GOL	O1-C1-C2-C3
8	C	1202	NAG	O5-C5-C6-O6
8	C	1202	NAG	C4-C5-C6-O6

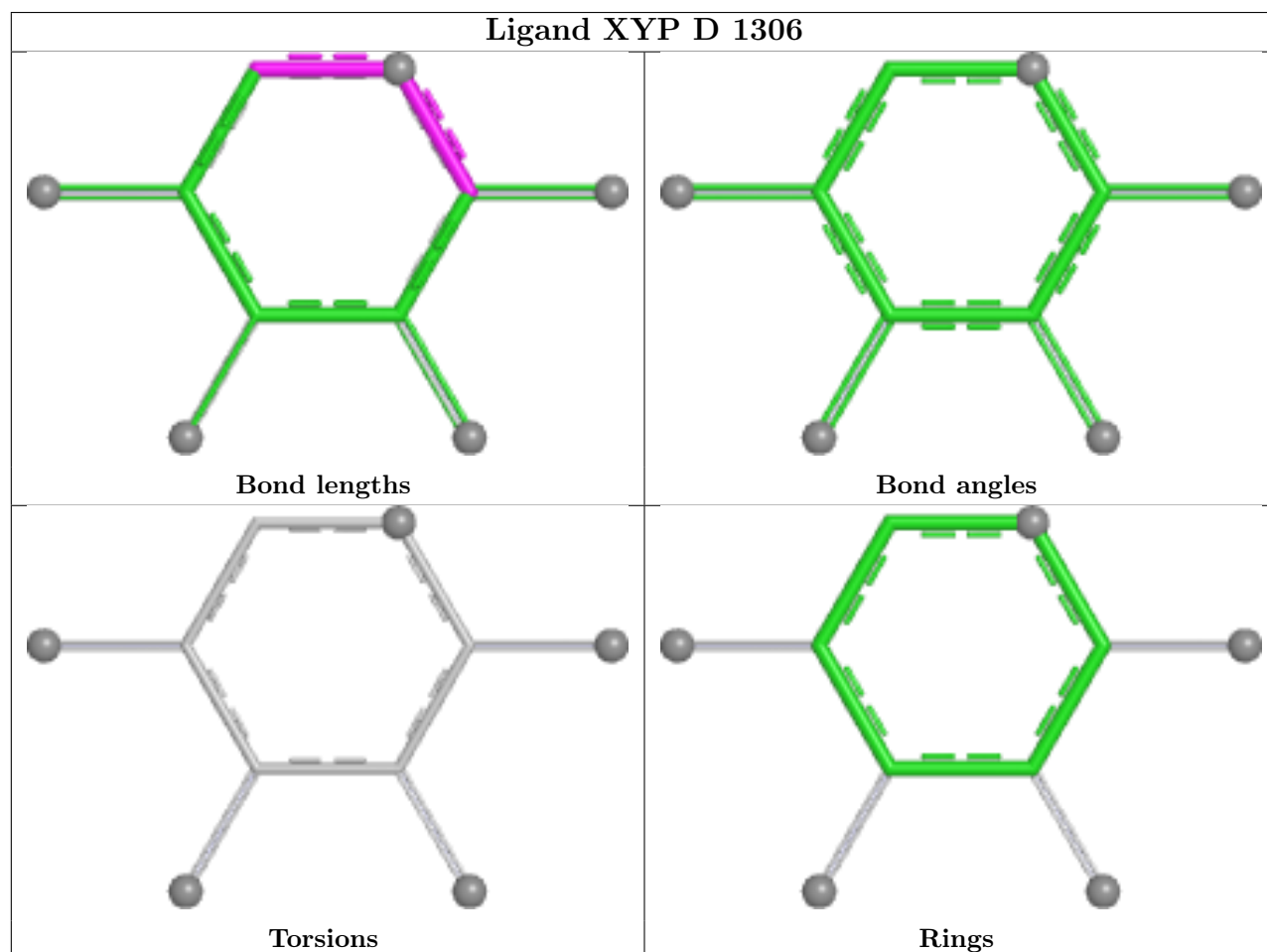
There are no ring outliers.

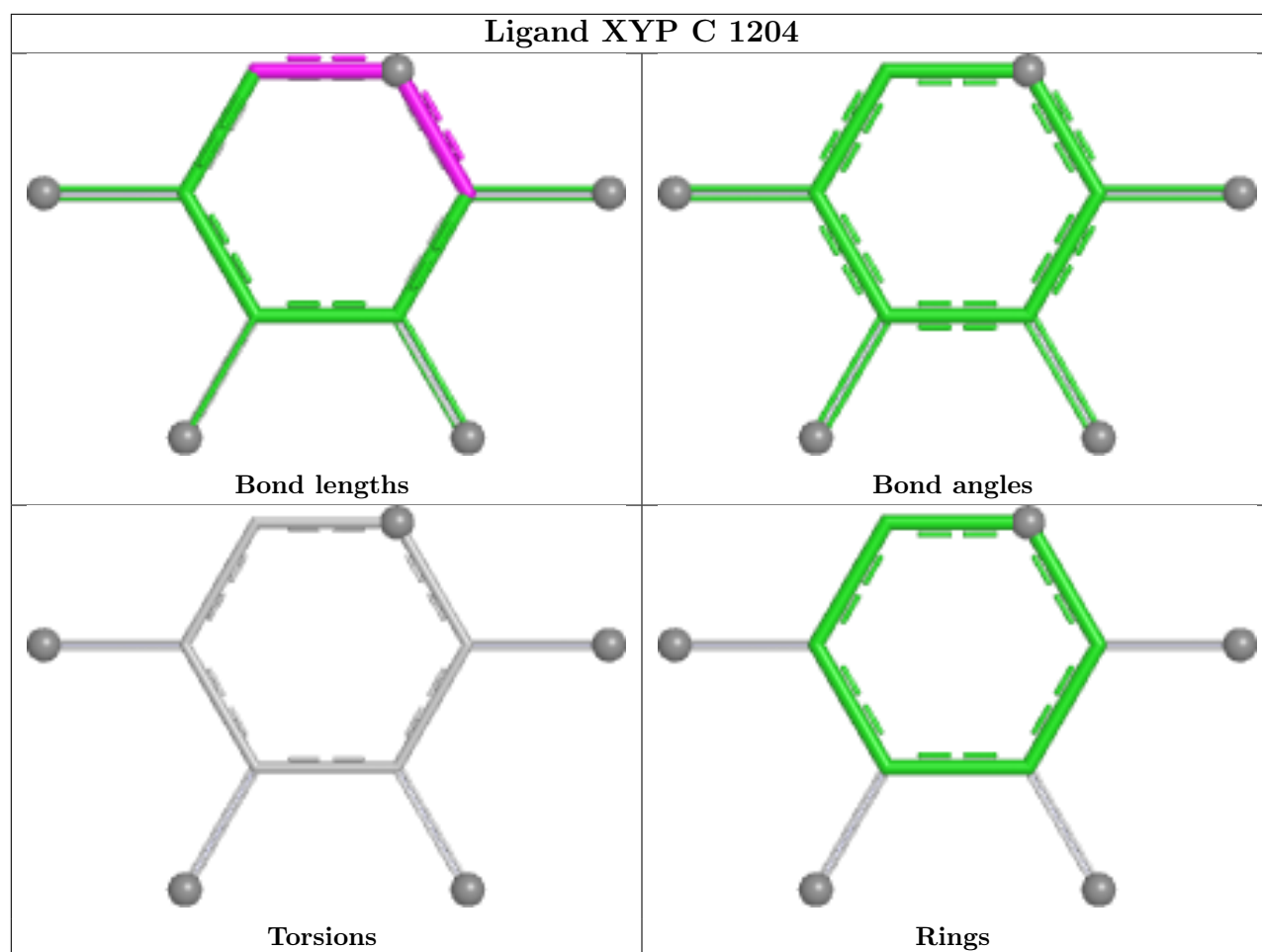
3 monomers are involved in 4 short contacts:

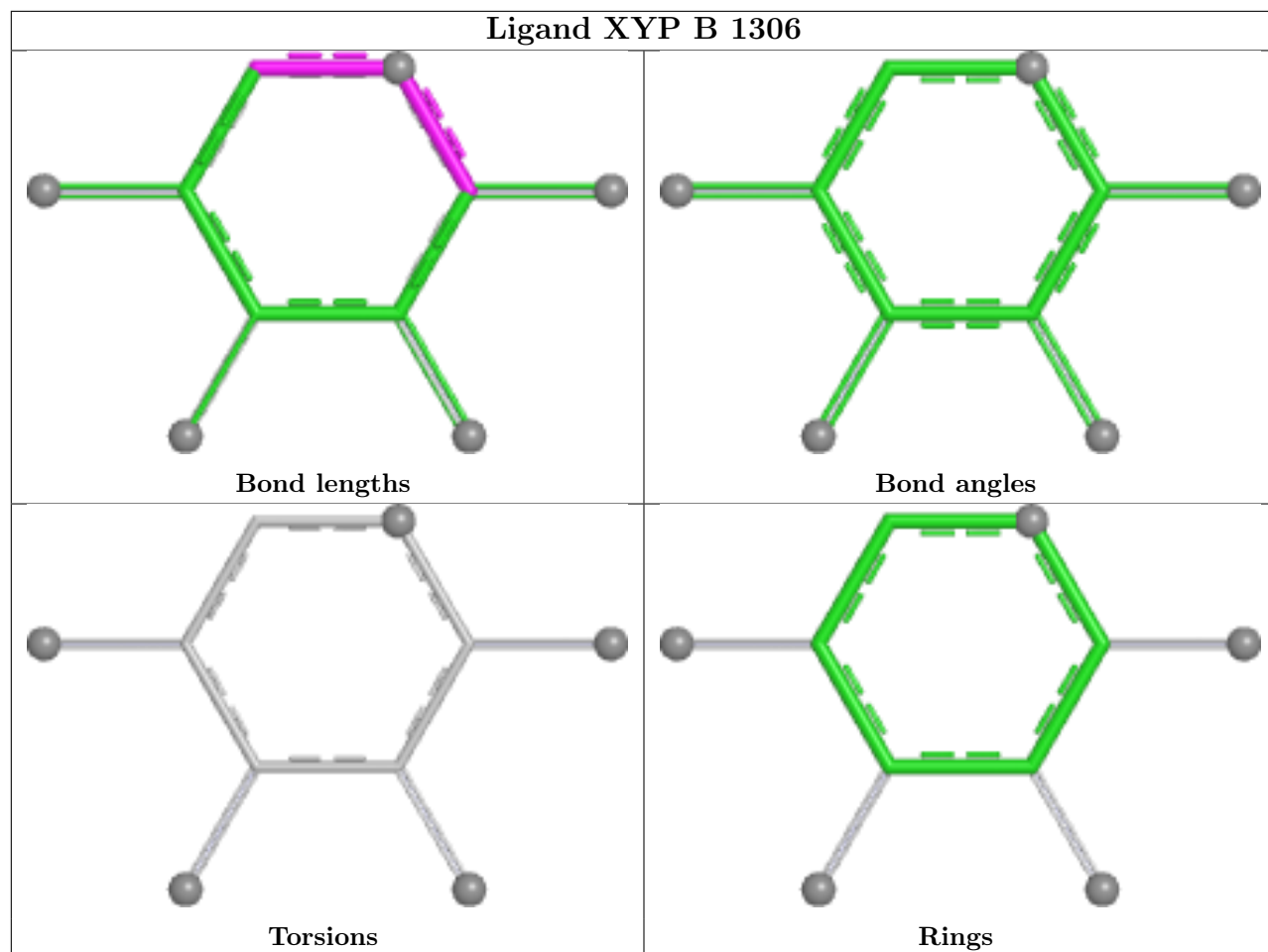
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	1304	GOL	1	0
9	C	1203[A]	GOL	1	0
9	B	1305	GOL	2	0

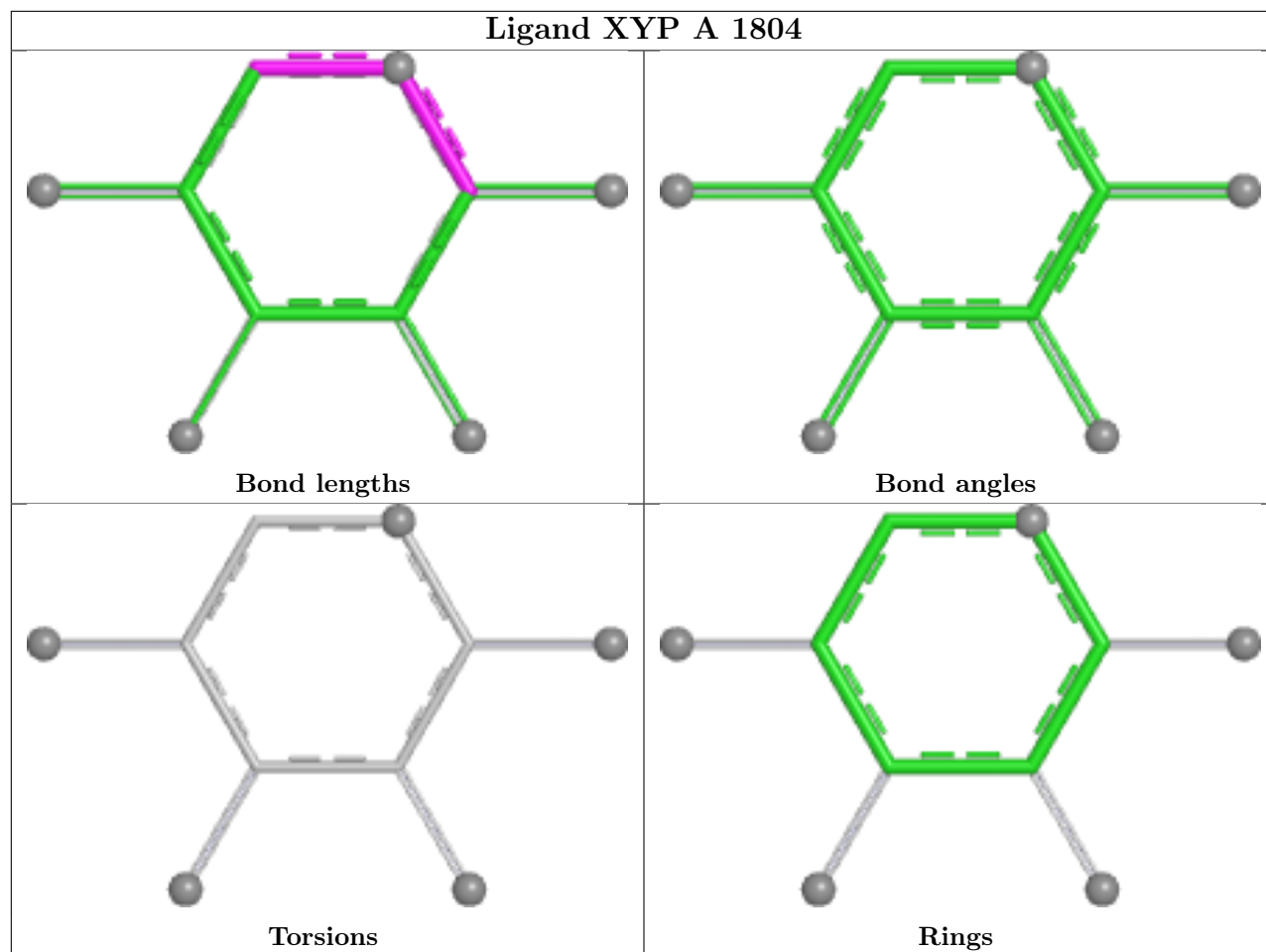
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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	446/462 (96%)	0.95	50 (11%)	10 10	6, 14, 25, 49	4 (0%)
1	B	444/462 (96%)	1.07	64 (14%)	6 5	6, 13, 26, 48	5 (1%)
1	C	446/462 (96%)	1.10	57 (12%)	7 7	6, 13, 28, 48	5 (1%)
1	D	446/462 (96%)	0.91	44 (9%)	13 13	5, 13, 25, 47	7 (1%)
All	All	1782/1848 (96%)	1.01	215 (12%)	8 8	5, 13, 27, 49	21 (1%)

The worst 5 of 215 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	56	THR	15.0
1	B	446	VAL	6.7
1	D	419	ALA	5.4
1	C	412	ILE	5.4
1	B	419	ALA	5.3

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
3	NAG	J	2	14/15	0.46	0.22	25,31,37,43	0
2	MAN	N	5	11/12	0.50	0.25	36,41,46,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	M	2	14/15	0.50	0.21	25,31,37,40	0
4	MAN	I	5	11/12	0.56	0.20	35,47,49,55	0
7	MAN	L	4	11/12	0.57	0.20	31,43,49,52	0
5	MAN	H	10	11/12	0.58	0.22	42,43,52,55	0
4	MAN	G	4	11/12	0.62	0.18	35,39,47,51	0
4	MAN	G	6	11/12	0.65	0.17	31,34,40,40	0
4	MAN	G	5	11/12	0.65	0.16	37,43,51,54	0
4	MAN	P	5	11/12	0.66	0.17	36,42,45,48	0
2	MAN	E	6	11/12	0.66	0.17	34,39,43,47	0
4	MAN	P	4	11/12	0.66	0.17	35,42,47,47	0
2	MAN	E	5	11/12	0.67	0.16	28,34,37,37	0
4	MAN	I	6	11/12	0.68	0.19	29,36,40,43	0
2	MAN	N	6	11/12	0.70	0.16	38,40,43,46	0
6	MAN	K	9	11/12	0.70	0.18	31,37,47,49	0
4	MAN	I	4	11/12	0.70	0.16	34,39,45,45	0
4	MAN	P	6	11/12	0.73	0.15	27,33,36,36	0
3	NAG	O	2	14/15	0.73	0.17	23,30,35,39	0
7	MAN	L	5	11/12	0.73	0.17	32,38,45,47	0
6	MAN	K	6	11/12	0.75	0.17	19,26,31,32	0
3	NAG	F	2	14/15	0.77	0.15	24,29,38,42	0
2	MAN	N	4	11/12	0.77	0.14	27,28,32,36	0
2	MAN	E	8	11/12	0.78	0.13	18,21,26,30	0
2	MAN	N	9	11/12	0.78	0.13	24,29,34,36	0
2	MAN	E	9	11/12	0.79	0.14	24,28,29,30	0
5	MAN	H	9	11/12	0.80	0.15	32,35,39,40	0
2	MAN	N	8	11/12	0.80	0.13	21,27,29,31	0
6	MAN	K	7	11/12	0.81	0.13	24,27,30,31	0
4	NAG	G	2	14/15	0.81	0.12	15,19,23,27	0
6	MAN	K	4	11/12	0.82	0.13	23,27,33,34	0
2	NAG	E	2	14/15	0.82	0.13	14,17,20,25	0
4	BMA	I	3	11/12	0.83	0.13	22,26,28,32	0
6	NAG	K	2	14/15	0.83	0.14	20,23,28,28	0
7	NAG	L	2	14/15	0.84	0.12	19,23,29,35	0
5	MAN	H	7	11/12	0.84	0.12	18,20,25,25	0
2	MAN	E	10	11/12	0.84	0.12	17,21,25,25	0
5	MAN	H	6	11/12	0.85	0.12	25,26,29,30	0
2	MAN	N	11	11/12	0.85	0.13	20,21,27,28	0
2	BMA	N	3	11/12	0.85	0.12	18,20,23,25	0
3	NAG	M	1	14/15	0.86	0.12	10,14,18,19	0
4	NAG	I	1	14/15	0.86	0.13	15,19,25,25	0
2	MAN	E	7	11/12	0.86	0.12	16,20,22,22	0
5	MAN	H	5	11/12	0.86	0.11	20,22,24,26	0

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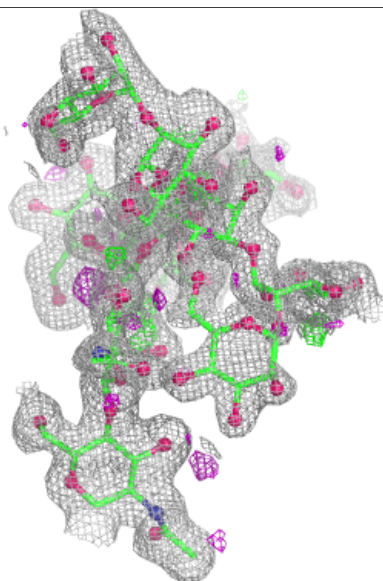
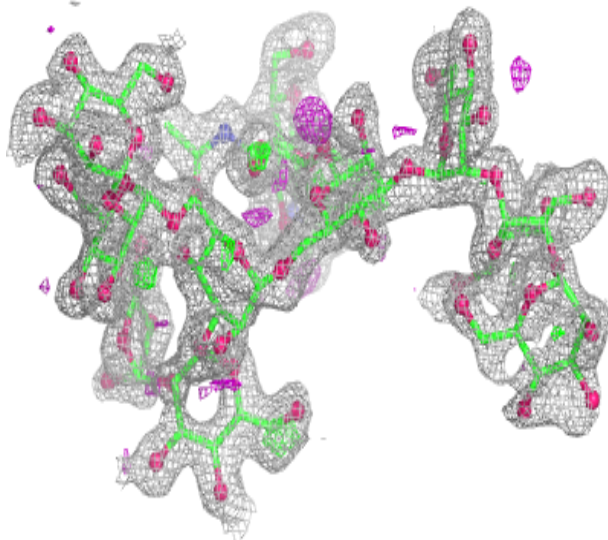
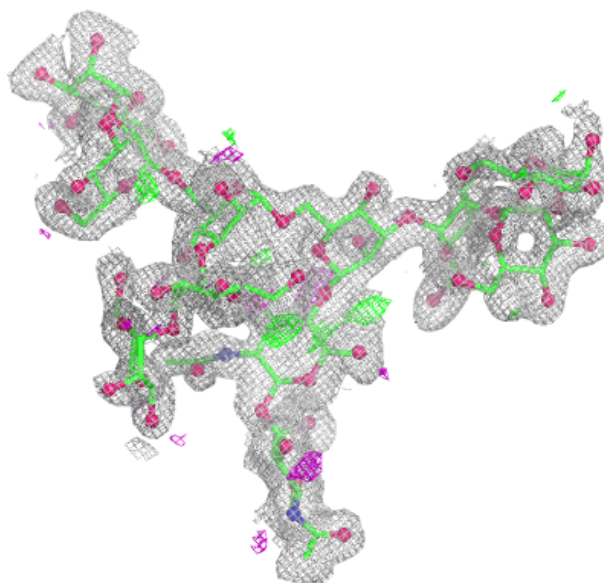
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	K	1	14/15	0.87	0.11	20,21,23,23	0
2	MAN	E	11	11/12	0.87	0.10	20,24,27,28	0
5	NAG	H	2	14/15	0.87	0.12	15,17,20,22	0
6	MAN	K	5	11/12	0.87	0.12	24,25,30,32	0
4	NAG	G	1	14/15	0.87	0.12	14,19,23,26	0
2	NAG	N	2	14/15	0.87	0.12	18,19,25,25	0
6	MAN	K	8	11/12	0.87	0.10	24,26,28,29	0
4	BMA	P	3	11/12	0.87	0.12	20,26,30,30	0
7	NAG	L	1	14/15	0.87	0.12	18,22,27,30	0
5	MAN	H	8	11/12	0.87	0.11	18,22,24,30	0
4	NAG	I	2	14/15	0.87	0.12	17,21,27,34	0
3	NAG	J	1	14/15	0.87	0.12	10,13,18,18	0
2	MAN	N	7	11/12	0.88	0.10	20,21,23,27	0
6	BMA	K	3	11/12	0.88	0.11	19,23,26,26	0
2	NAG	E	1	14/15	0.88	0.13	13,17,24,24	0
2	BMA	E	3	11/12	0.88	0.12	15,17,19,20	0
7	BMA	L	3	11/12	0.88	0.10	23,26,30,34	0
4	BMA	G	3	11/12	0.88	0.12	19,27,31,31	0
3	NAG	O	1	14/15	0.88	0.10	12,12,17,18	0
4	NAG	P	1	14/15	0.89	0.10	13,18,23,25	0
2	NAG	N	1	14/15	0.89	0.13	14,19,26,26	0
5	NAG	H	1	14/15	0.89	0.10	14,17,25,29	0
2	MAN	N	10	11/12	0.89	0.11	18,20,23,24	0
5	MAN	H	4	11/12	0.90	0.10	19,20,22,23	0
3	NAG	F	1	14/15	0.90	0.10	10,12,17,19	0
4	NAG	P	2	14/15	0.90	0.09	15,18,22,29	0
5	BMA	H	3	11/12	0.91	0.11	16,20,24,27	0
2	MAN	E	4	11/12	0.92	0.08	18,20,22,24	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.

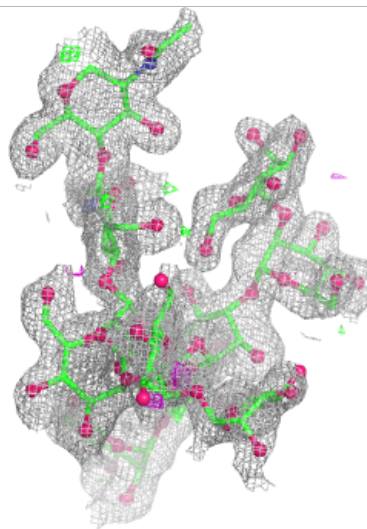
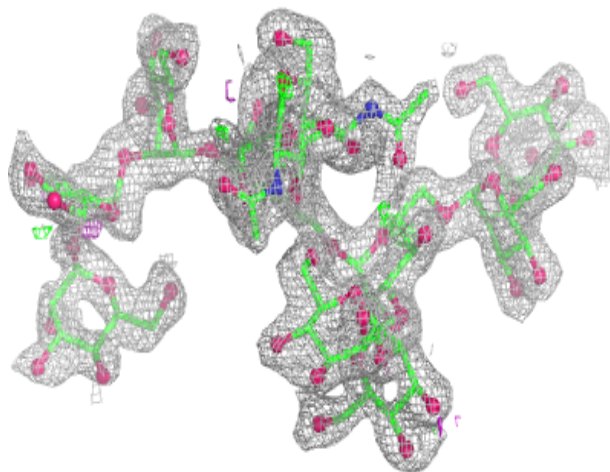
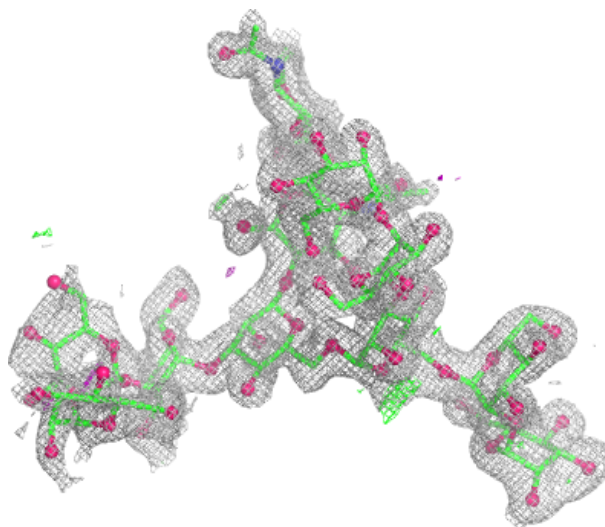
Electron density around Chain E:

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



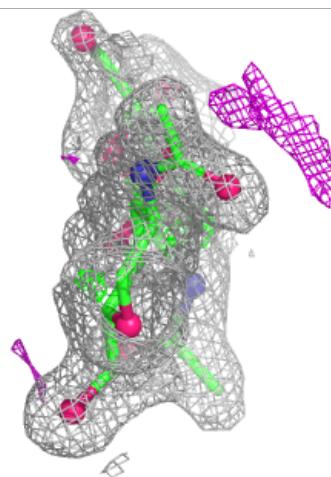
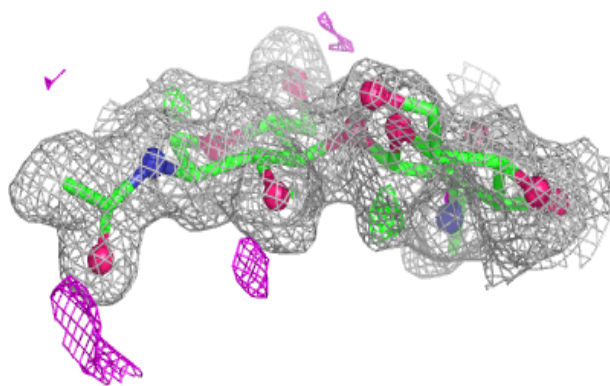
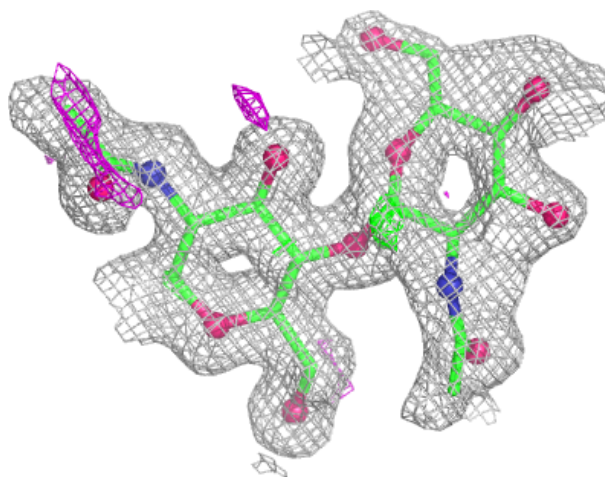
Electron density around Chain N:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



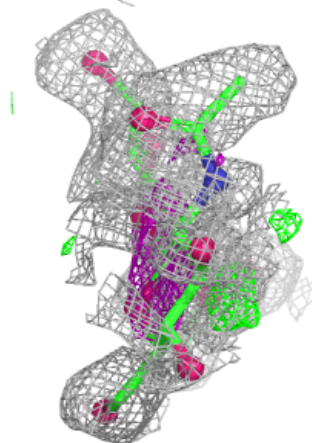
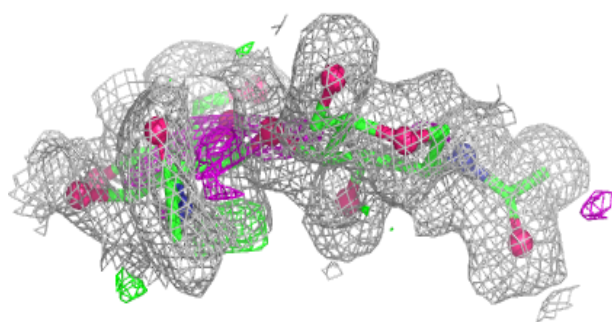
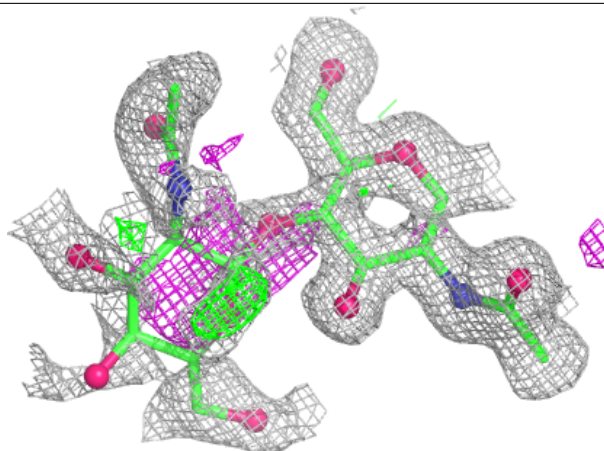
Electron density around Chain F:

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and green (positive)



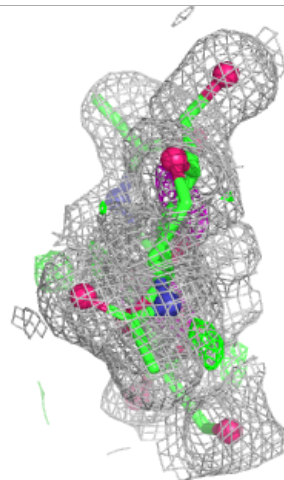
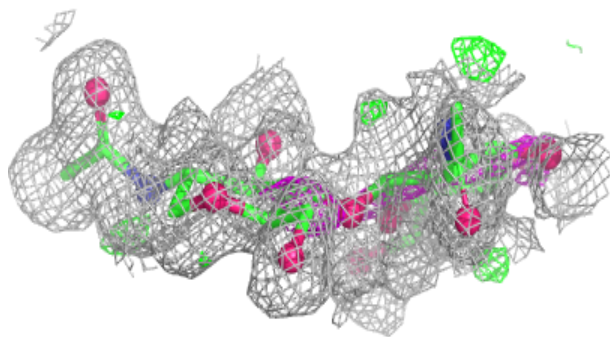
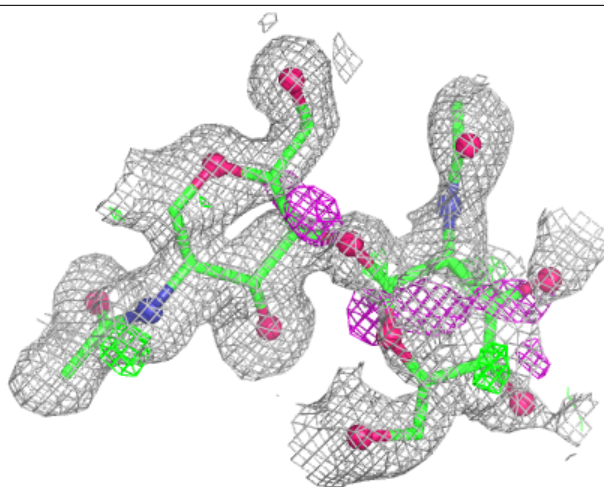
Electron density around Chain J:

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



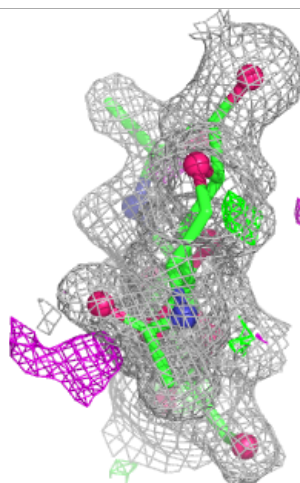
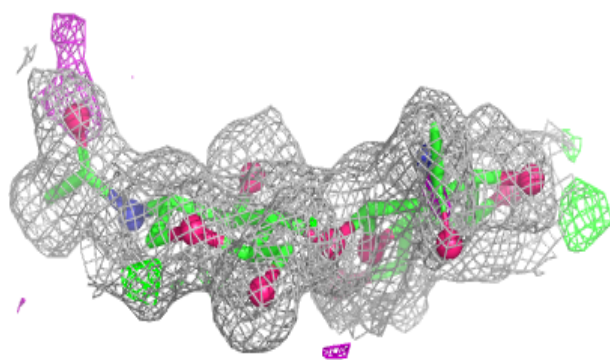
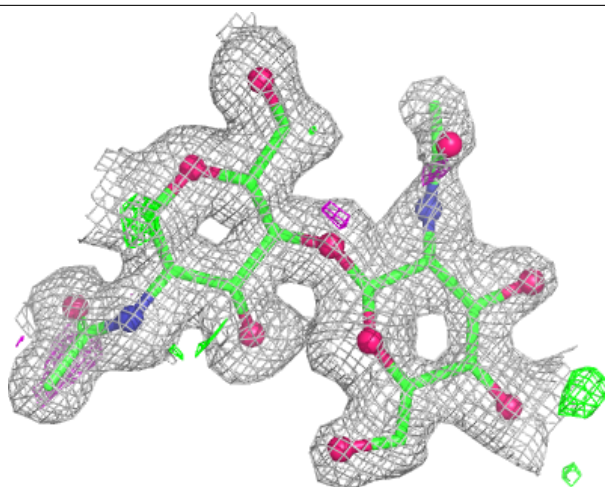
Electron density around Chain M:

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



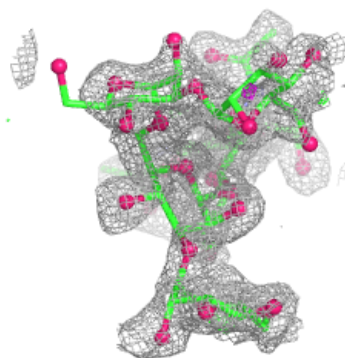
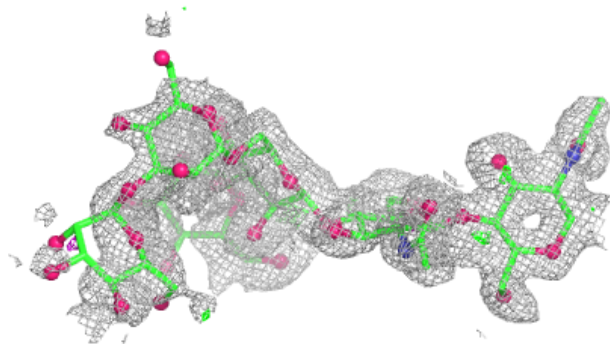
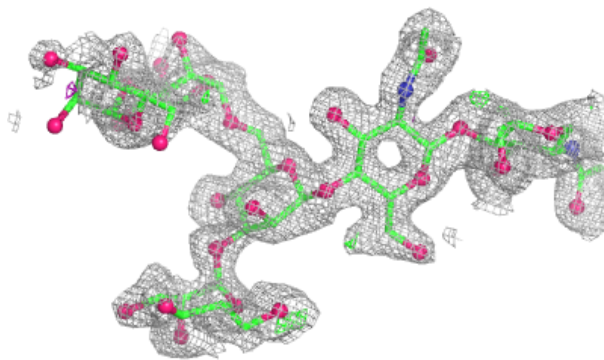
Electron density around Chain O:

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

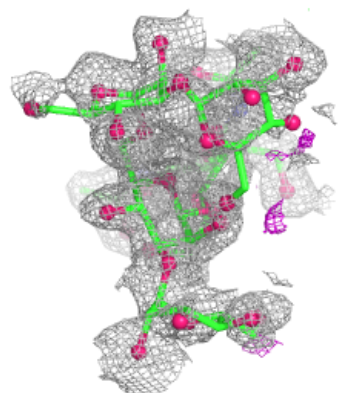
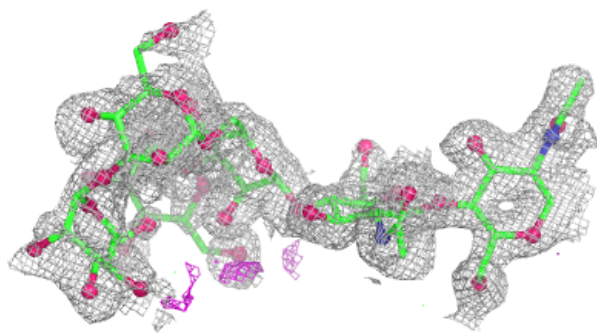
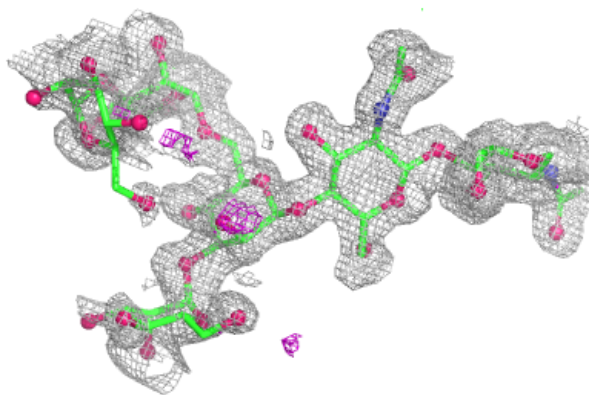


Electron density around Chain G:

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

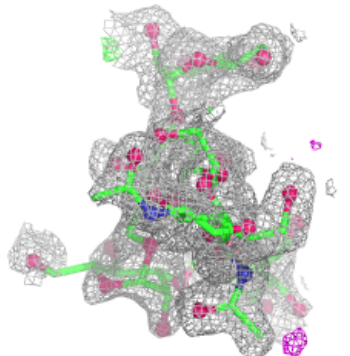
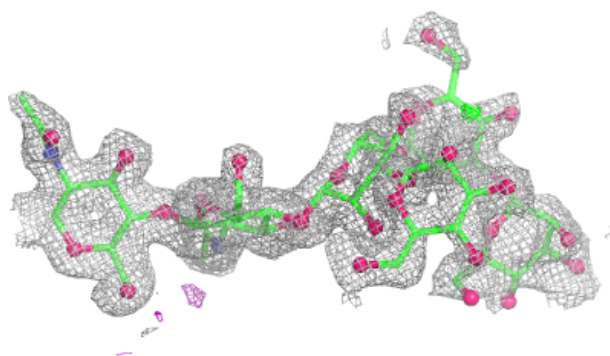
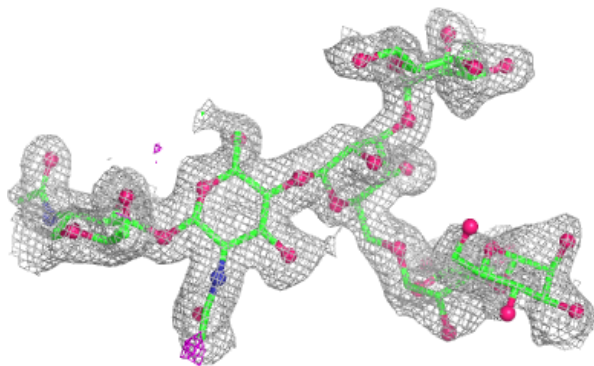
**Electron density around Chain I:**

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



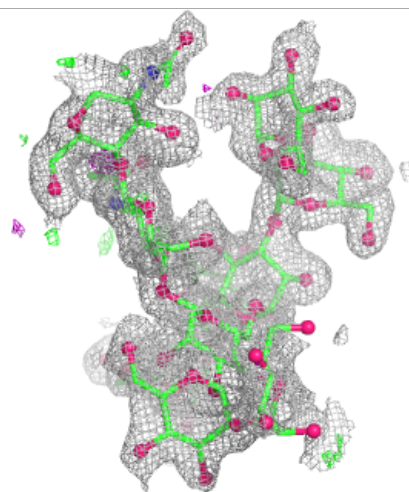
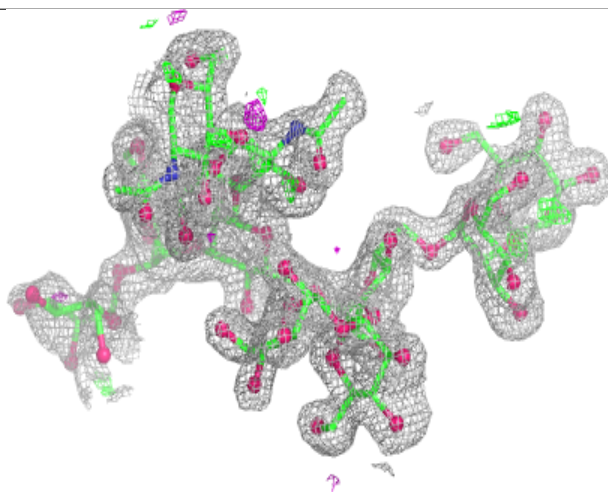
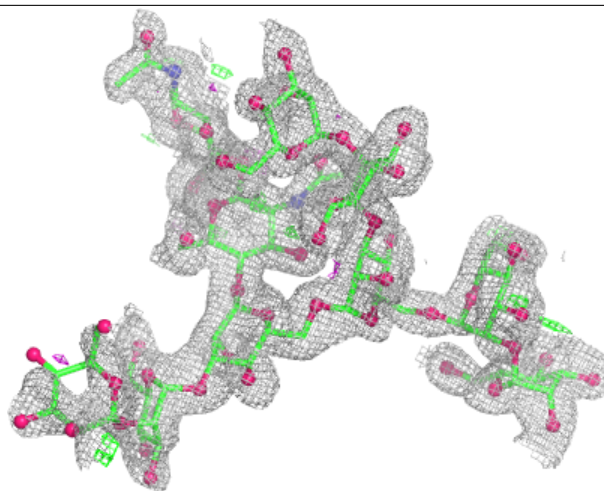
Electron density around Chain P:

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



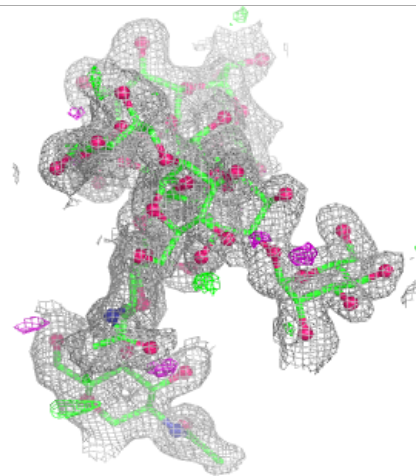
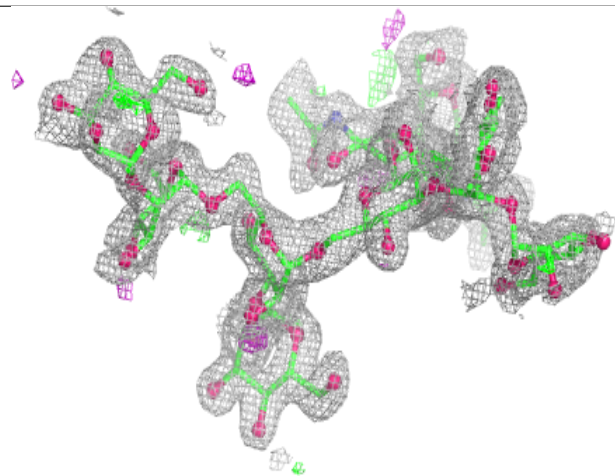
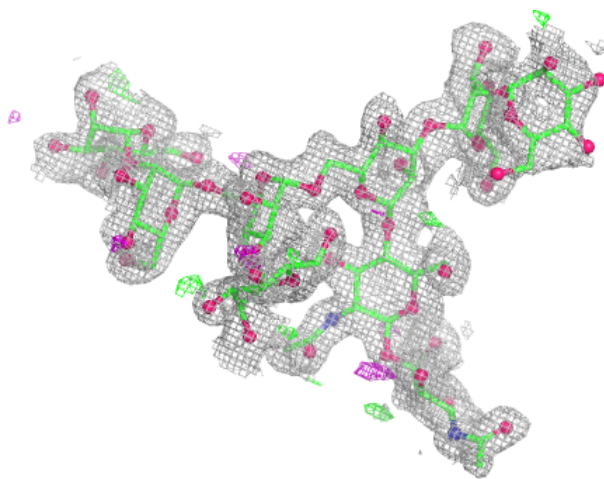
Electron density around Chain H:

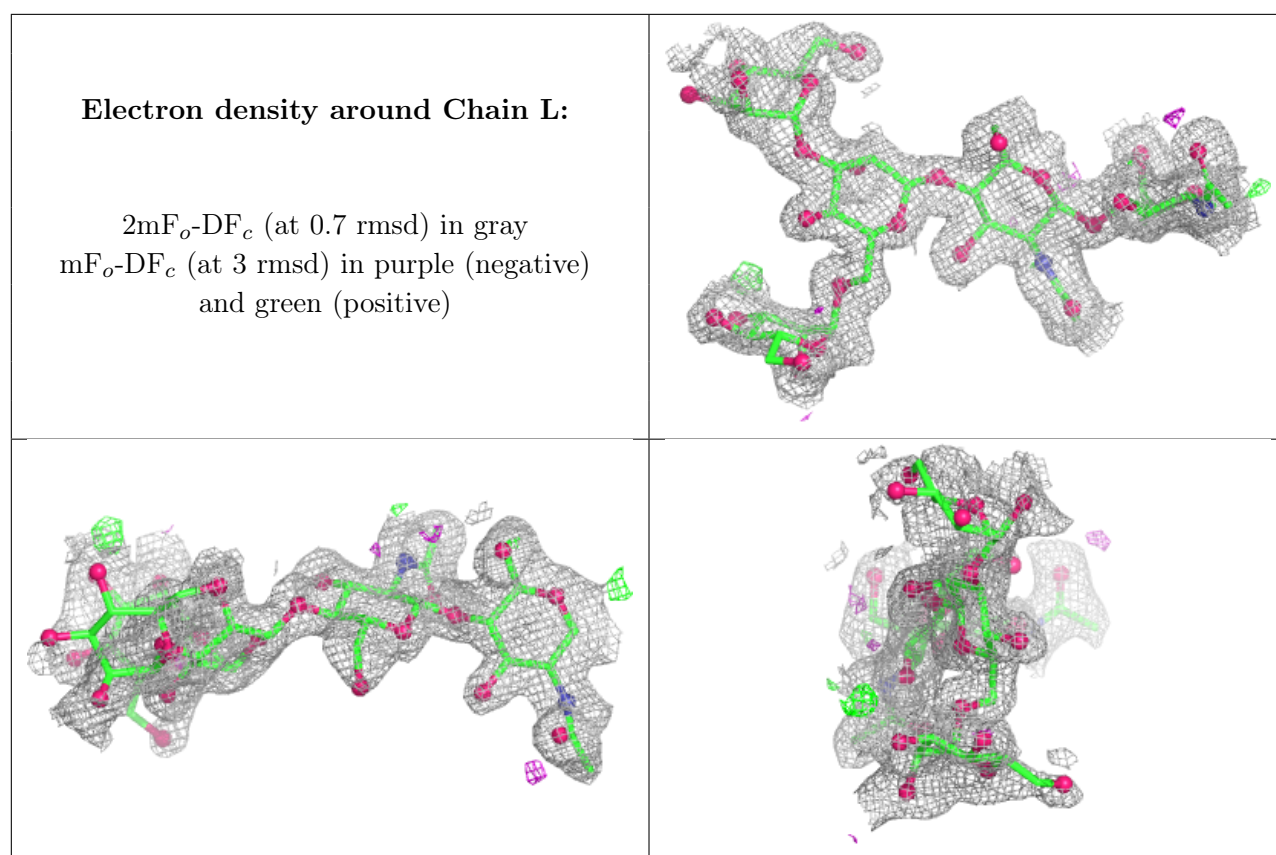
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

$2mF_o-DF_c$ (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
9	GOL	C	1203[A]	6/6	0.55	0.17	18,22,23,26	6
9	GOL	C	1203[B]	6/6	0.55	0.17	18,22,23,27	6
8	NAG	A	1802	14/15	0.58	0.20	35,42,47,50	0
8	NAG	D	1303	14/15	0.59	0.20	29,36,41,46	0
8	NAG	C	1202	14/15	0.60	0.19	34,38,43,45	0
8	NAG	B	1303	14/15	0.61	0.18	36,42,47,49	0
8	NAG	A	1801	14/15	0.65	0.17	24,26,32,34	0
9	GOL	D	1302	6/6	0.71	0.23	21,24,26,27	0
9	GOL	B	1302	6/6	0.74	0.17	22,28,30,31	0
8	NAG	D	1301	14/15	0.77	0.13	13,15,19,27	0
10	XYP	C	1204	10/10	0.77	0.13	14,19,23,24	0
9	GOL	A	1803	6/6	0.78	0.14	21,25,30,40	0
10	XYP	A	1804	10/10	0.80	0.12	16,21,23,24	0
9	GOL	D	1305	6/6	0.80	0.16	21,25,31,37	0

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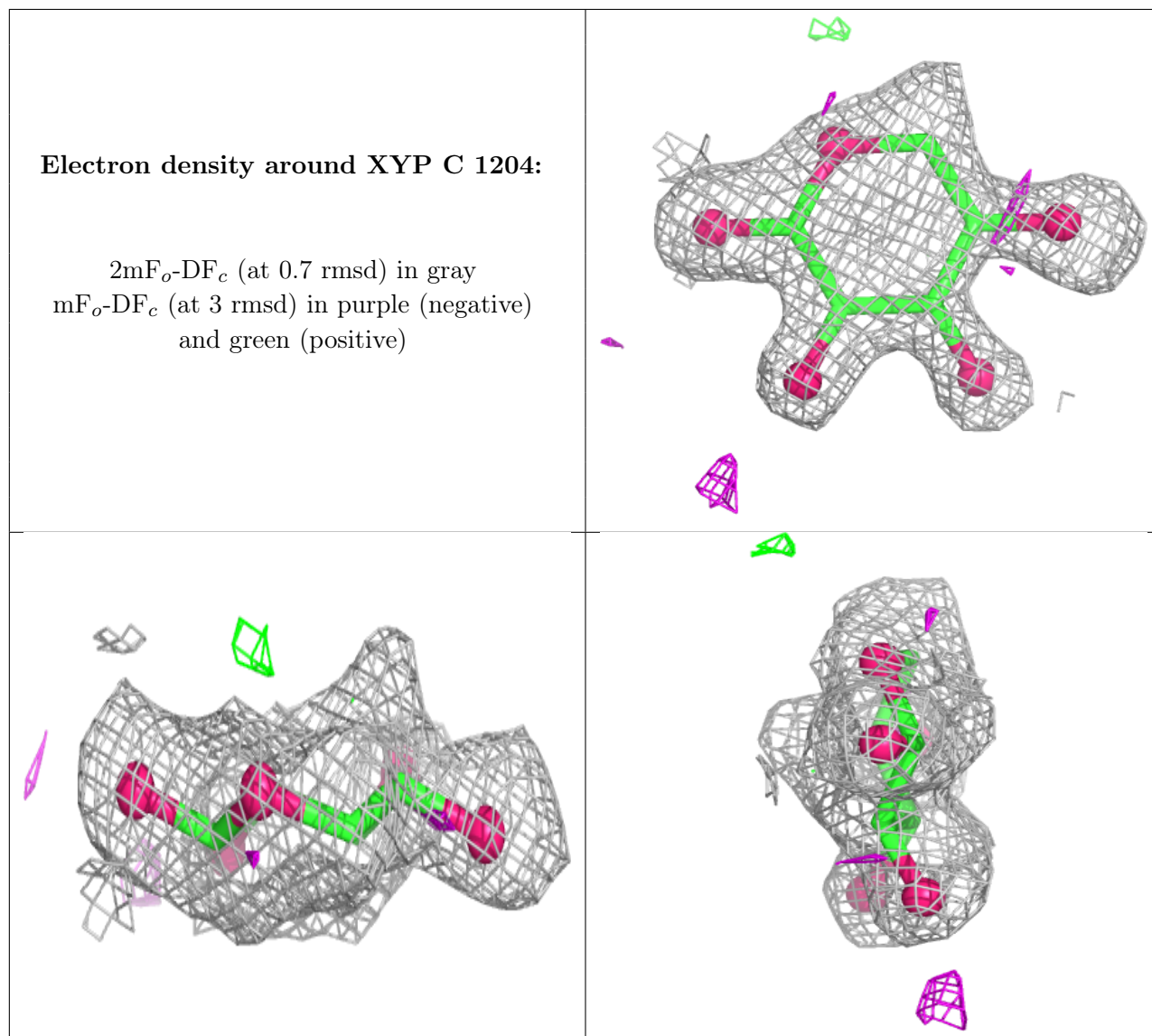
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	XYP	B	1306	10/10	0.81	0.12	13,18,24,26	0
9	GOL	B	1305	6/6	0.81	0.17	20,25,30,35	0
10	XYP	D	1306	10/10	0.82	0.12	14,19,24,27	0
8	NAG	B	1301	14/15	0.84	0.14	13,15,27,33	0
11	CL	C	1205	1/1	0.86	0.14	31,31,31,31	0
8	NAG	C	1201	14/15	0.88	0.10	15,18,19,27	0
9	GOL	B	1304	6/6	0.88	0.11	23,24,31,32	0
9	GOL	D	1304	6/6	0.90	0.13	14,21,23,25	0
11	CL	B	1307	1/1	0.98	0.07	18,18,18,18	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.

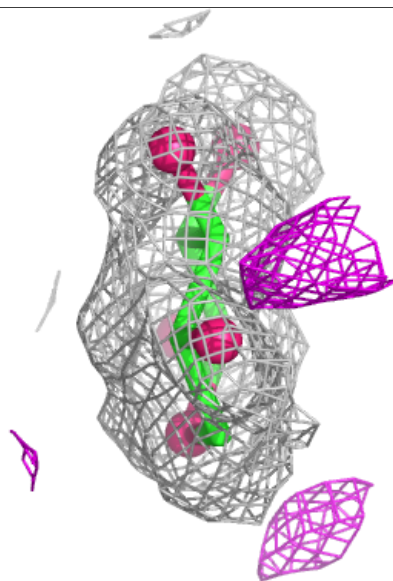
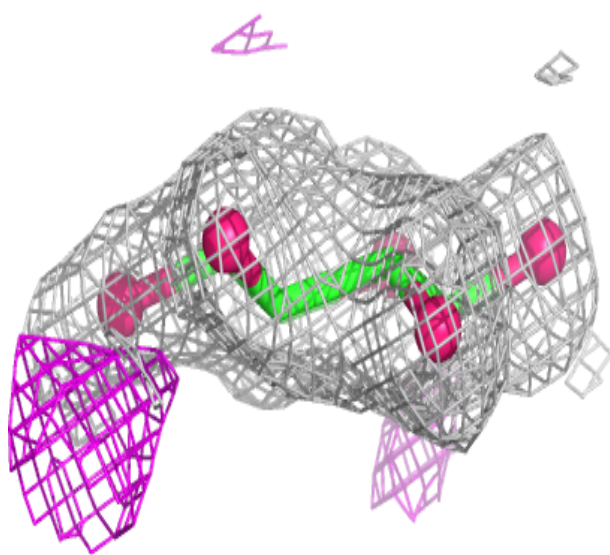
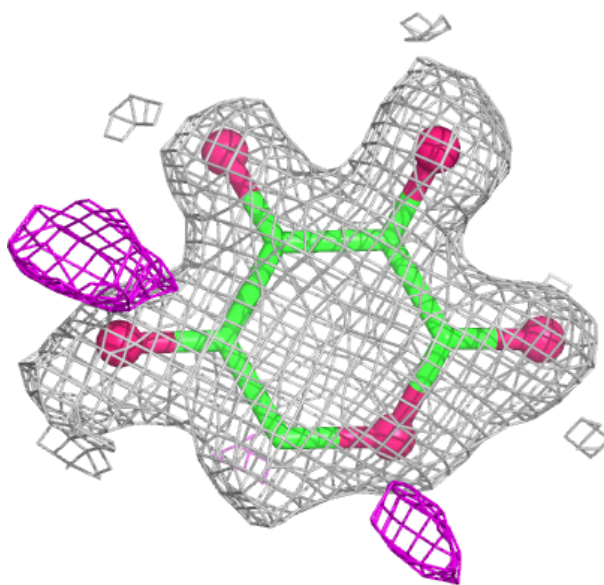
Electron density around XYP C 1204:

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



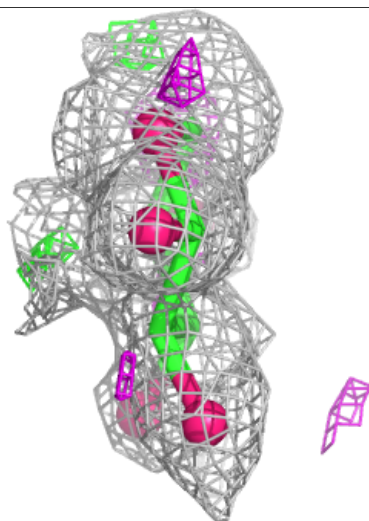
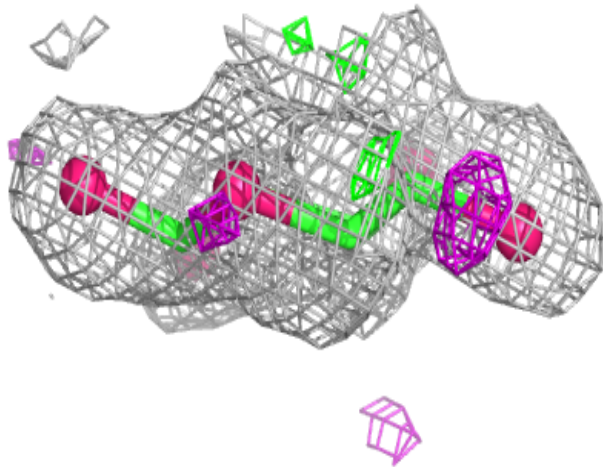
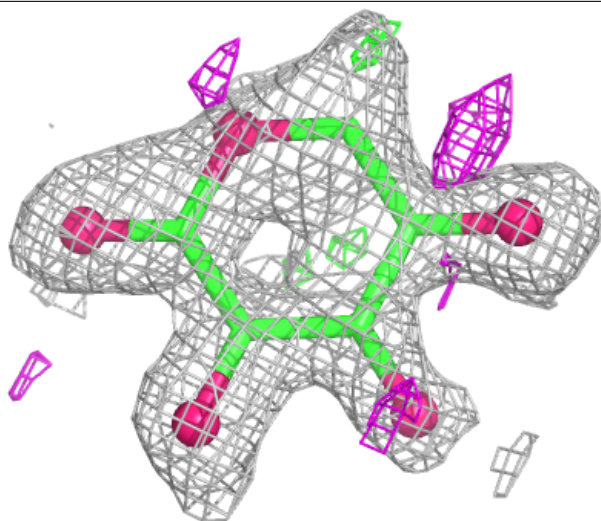
Electron density around XYP A 1804:

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



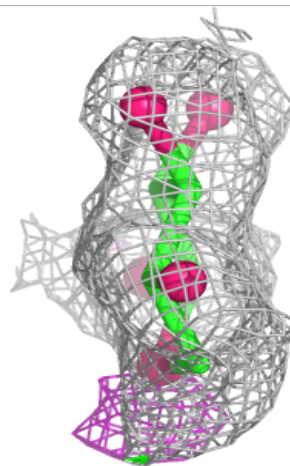
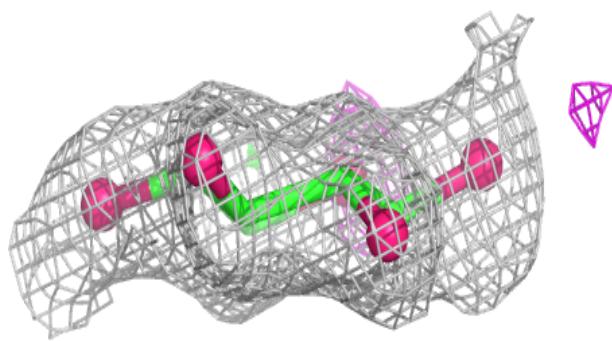
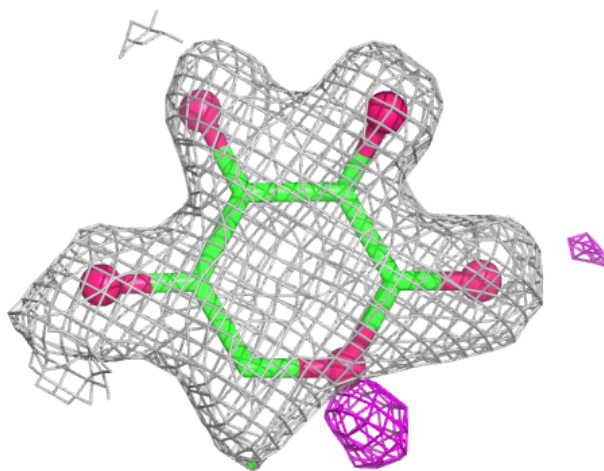
Electron density around XYP B 1306:

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



Electron density around XYP D 1306:

$2mF_o-DF_c$ (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.