



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:15 AM UTC

PDB ID : 3GWJ / pdb_00003gwj
Title : Crystal structure of Antheraea pernyi arylphorin
Authors : Ryu, K.S.; Lee, J.O.; Kwon, T.H.; Kim, S.
Deposited on : 2009-04-01
Resolution : 2.43 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

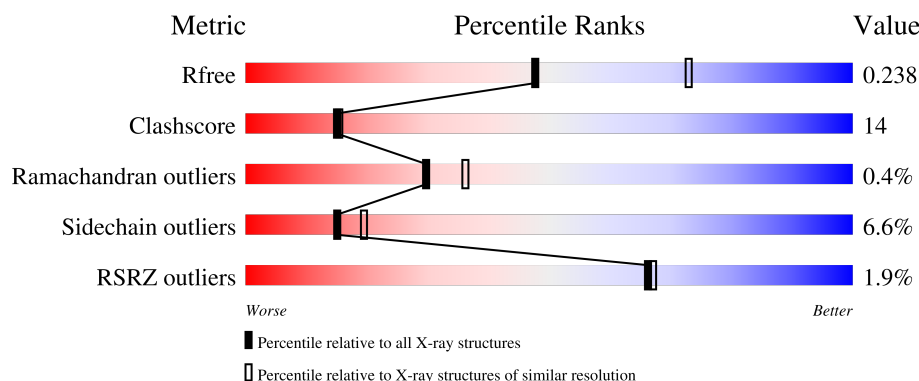
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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.



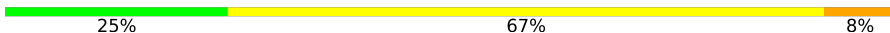
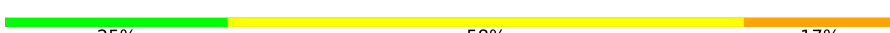
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	674	2% 69% 26% .
1	B	674	2% 69% 27% .
1	C	674	% 69% 28% .
1	D	674	% 70% 26% .
1	E	674	2% 70% 26% .

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Mol	Chain	Length	Quality of chain
1	F	674	
2	G	12	
2	I	12	
2	K	12	
2	M	12	
2	O	12	
2	Q	12	
3	H	2	
3	J	2	
3	L	2	
3	N	2	
3	P	2	
3	R	2	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FMT	B	2002	-	-	X	-

2 Entry composition [i](#)

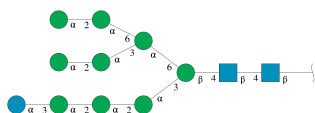
There are 5 unique types of molecules in this entry. The entry contains 36702 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Arylphorin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	674	Total	C	N	O	S	0	0	0
			5718	3752	906	1047	13			
1	B	674	Total	C	N	O	S	0	0	0
			5718	3752	906	1047	13			
1	C	674	Total	C	N	O	S	0	0	0
			5718	3752	906	1047	13			
1	D	674	Total	C	N	O	S	0	0	0
			5718	3752	906	1047	13			
1	E	674	Total	C	N	O	S	0	0	0
			5718	3752	906	1047	13			
1	F	674	Total	C	N	O	S	0	0	0
			5718	3752	906	1047	13			

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-3)-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-(1-2)-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.



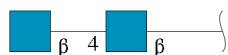
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	12	Total	C	N	O	0	0	0
			138	76	2	60			
2	I	12	Total	C	N	O	0	0	0
			138	76	2	60			
2	K	12	Total	C	N	O	0	0	0
			138	76	2	60			
2	M	12	Total	C	N	O	0	0	0
			138	76	2	60			

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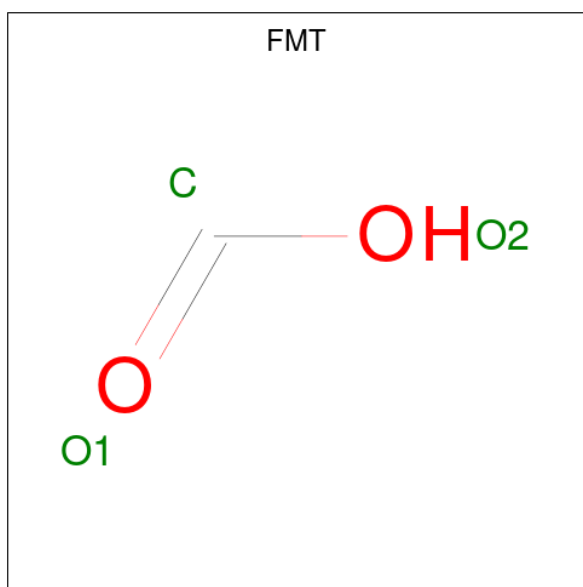
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	O	12	Total	C	N	O	0	0	0
			138	76	2	60			
2	Q	12	Total	C	N	O	0	0	0
			138	76	2	60			

- 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	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	P	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	R	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			3	1	2		
4	B	1	Total	C	O	0	0
			3	1	2		
4	C	1	Total	C	O	0	0
			3	1	2		
4	D	1	Total	C	O	0	0
			3	1	2		
4	E	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		

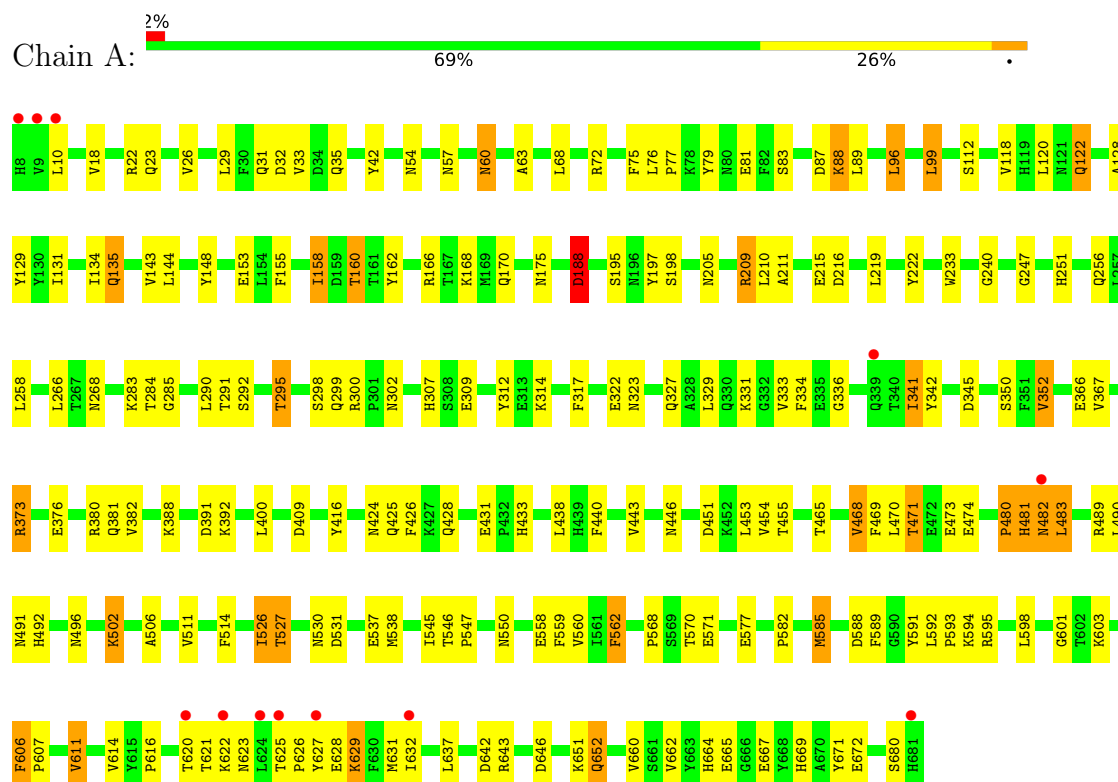
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	225	Total	O	0	0
			225	225		
5	B	241	Total	O	0	0
			241	241		
5	C	200	Total	O	0	0
			200	200		
5	D	243	Total	O	0	0
			243	243		
5	E	218	Total	O	0	0
			218	218		
5	F	253	Total	O	0	0
			253	253		

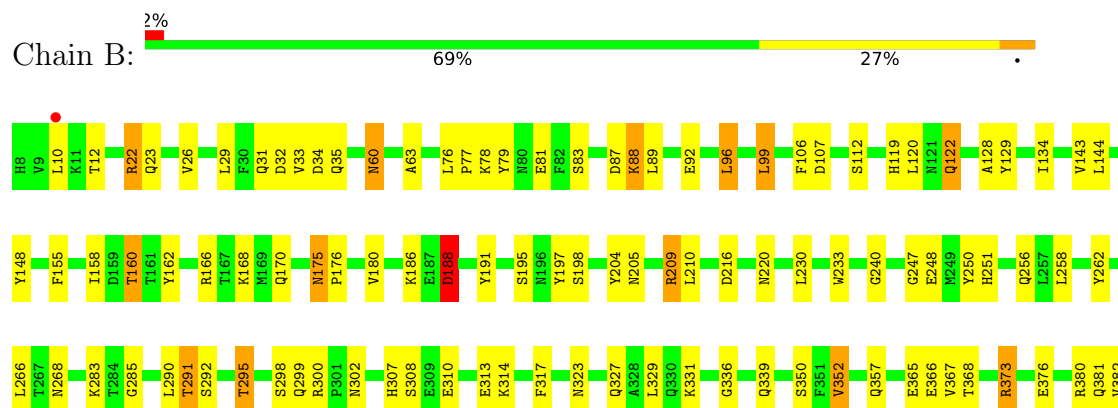
3 Residue-property plots

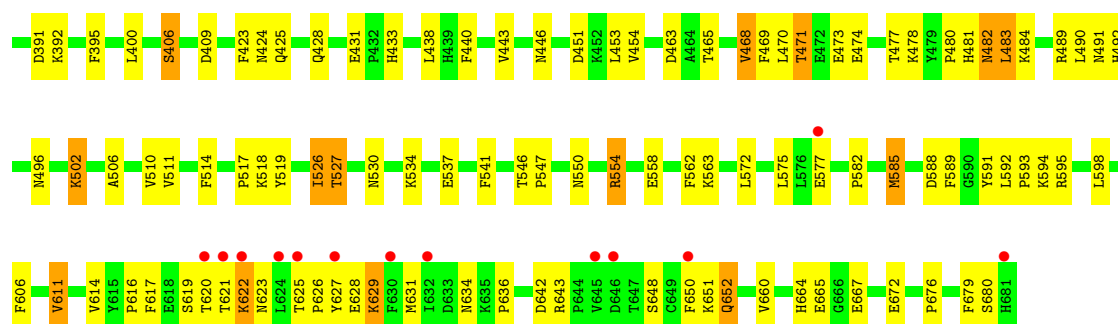
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Arylphorin

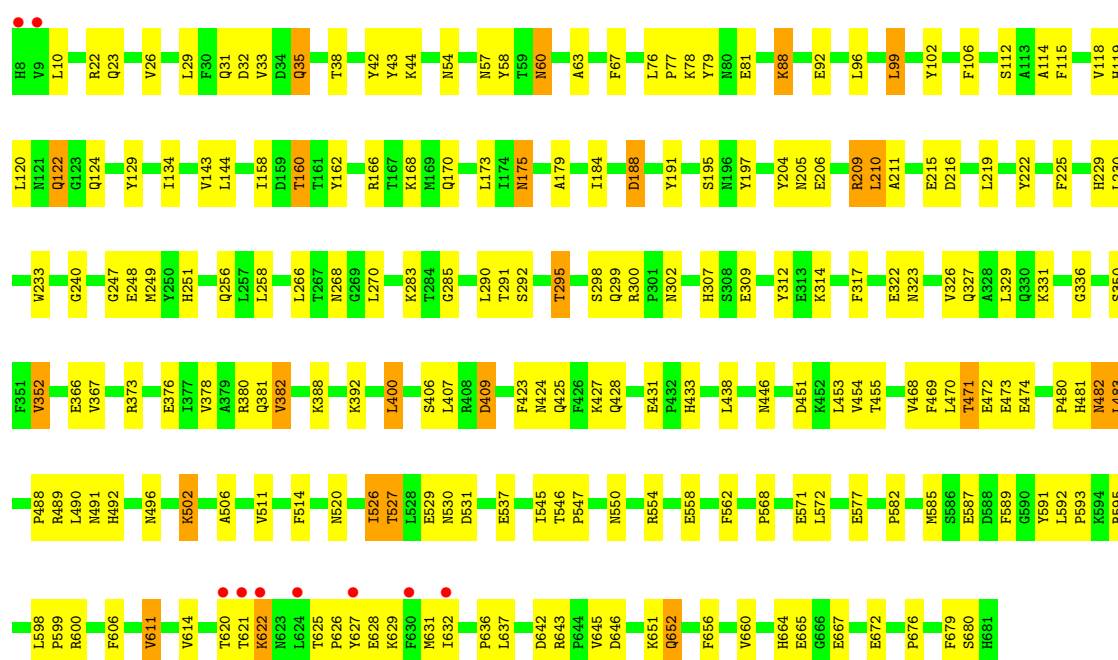


• Molecule 1: Arylphorin

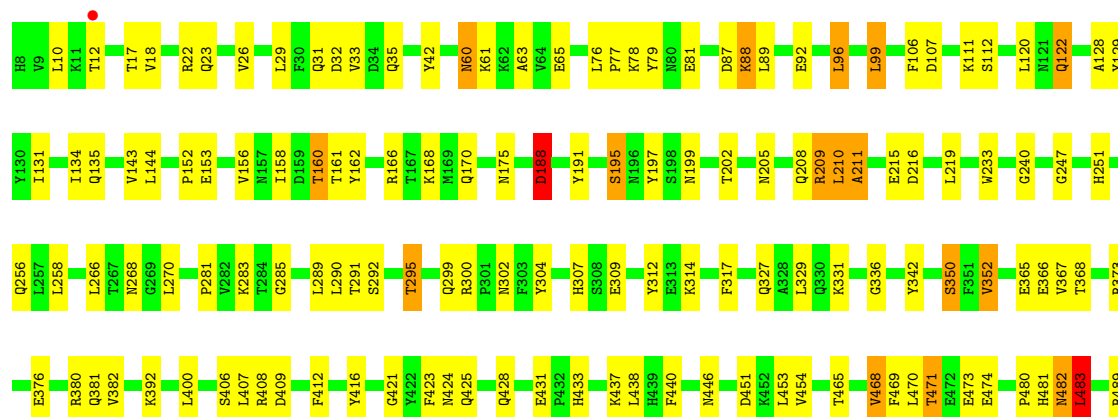


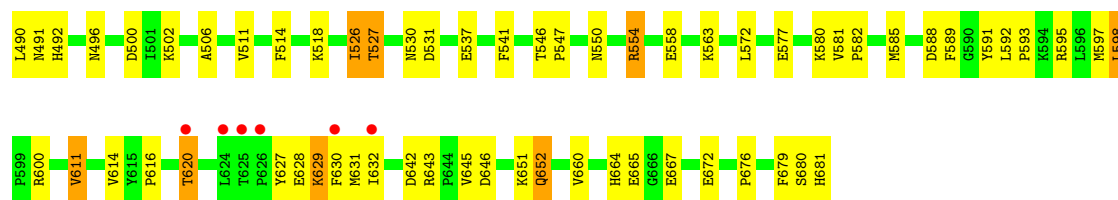


• Molecule 1: Arylphorin

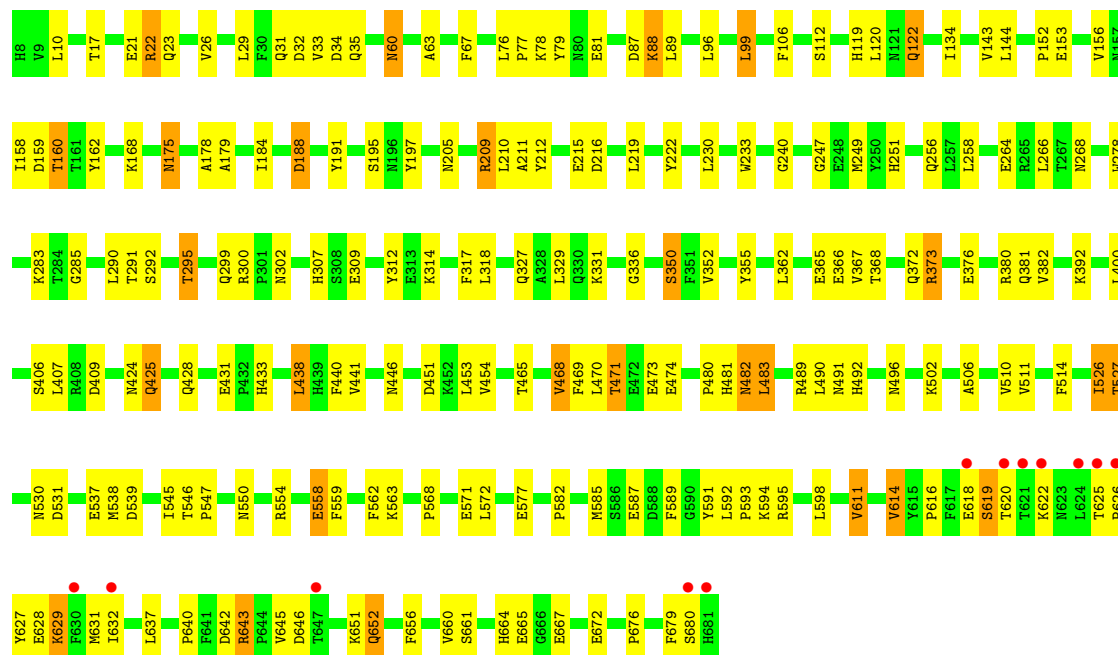


• Molecule 1: Arylphorin

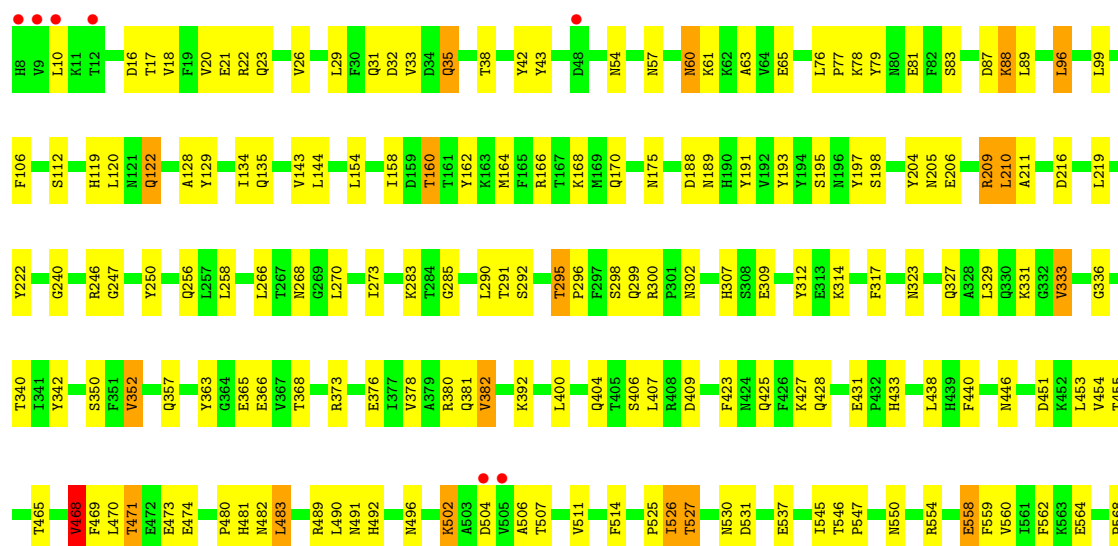


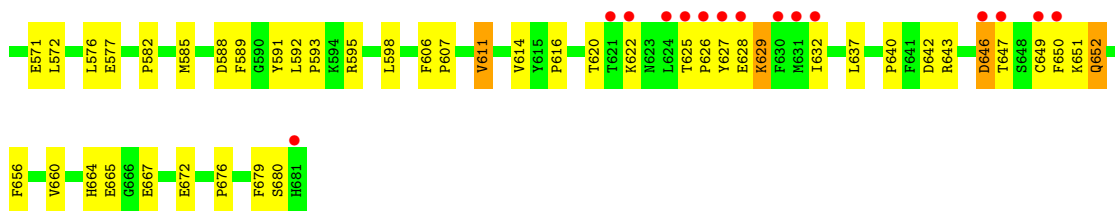


• Molecule 1: Arylphorin



• Molecule 1: Arylphorin





- Molecule 2: alpha-D-glucopyranose-(1-3)-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-(1-2)-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

Chain G: 33% 67%



- Molecule 2: alpha-D-glucopyranose-(1-3)-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-(1-2)-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

Chain I: 25% 67% 8%



- Molecule 2: alpha-D-glucopyranose-(1-3)-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-(1-2)-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

Chain K: 42% 50% 8%



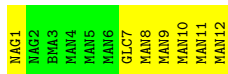
- Molecule 2: alpha-D-glucopyranose-(1-3)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-be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

Chain M: 33% 67%



- Molecule 2: alpha-D-glucopyranose-(1-3)-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-(1-2)-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

Chain O: 42% 58%



- Molecule 2: alpha-D-glucopyranose-(1-3)-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-(1-2)-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

Chain Q: 25% 58% 17%



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

Chain H: 100%



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

Chain J: 100%



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

Chain L: 100%



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

Chain N:  100%

MAG1
MAG2

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

Chain P:  50% 50%

MAG1
MAG2

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

Chain R:  50% 50%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	121.20Å 119.47Å 319.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 2.43 48.80 – 2.43	Depositor EDS
% Data completeness (in resolution range)	95.7 (48.80-2.43) 96.0 (48.80-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.10 (at 2.42Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.182 , 0.229 0.197 , 0.238	Depositor DCC
R_{free} test set	8410 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.276	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	36702	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.12% 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: FMT, GLC, MAN, NAG, BMA

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	0.43	0/5907	0.90	23/8017 (0.3%)
1	B	0.44	0/5907	0.89	22/8017 (0.3%)
1	C	0.43	0/5907	0.89	21/8017 (0.3%)
1	D	0.43	0/5907	0.89	20/8017 (0.2%)
1	E	0.43	0/5907	0.88	16/8017 (0.2%)
1	F	0.45	0/5907	0.89	23/8017 (0.3%)
All	All	0.43	0/35442	0.89	125/48102 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

There are no bond length outliers.

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	482	ASN	N-CA-C	8.37	120.48	111.36
1	E	283	LYS	N-CA-C	7.84	119.46	111.07
1	C	283	LYS	N-CA-C	7.77	119.39	111.07
1	B	33	VAL	N-CA-C	7.71	121.81	111.17
1	B	283	LYS	N-CA-C	7.66	119.41	111.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	342	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5718	0	5424	157	0
1	B	5718	0	5424	162	0
1	C	5718	0	5424	160	0
1	D	5718	0	5424	165	0
1	E	5718	0	5424	167	0
1	F	5718	0	5424	167	0
2	G	138	0	115	0	0
2	I	138	0	115	1	0
2	K	138	0	115	1	0
2	M	138	0	115	0	0
2	O	138	0	115	0	0
2	Q	138	0	115	2	0
3	H	28	0	25	0	0
3	J	28	0	25	0	0
3	L	28	0	25	0	0
3	N	28	0	25	0	0
3	P	28	0	25	0	0
3	R	28	0	25	0	0
4	A	3	0	1	1	0
4	B	3	0	1	2	0
4	C	3	0	1	1	0
4	D	3	0	1	1	0
4	E	3	0	1	1	0
4	F	3	0	1	1	0
5	A	225	0	0	7	0
5	B	241	0	0	11	0
5	C	200	0	0	12	0
5	D	243	0	0	11	0
5	E	218	0	0	14	0
5	F	253	0	0	11	0
All	All	36702	0	33390	940	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 14.

The worst 5 of 940 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:D:134:ILE:HD11	1:D:144:LEU:HD11	1.38	1.06
1:C:134:ILE:HD11	1:C:144:LEU:HD11	1.41	1.02
1:C:23:GLN:HE22	1:C:143:VAL:H	1.06	1.00
1:B:134:ILE:HD11	1:B:144:LEU:HD11	1.48	0.96
1:B:35:GLN:HE22	1:B:470:LEU:H	1.12	0.96

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	672/674 (100%)	649 (97%)	20 (3%)	3 (0%)	30	36
1	B	672/674 (100%)	649 (97%)	21 (3%)	2 (0%)	36	44
1	C	672/674 (100%)	653 (97%)	17 (2%)	2 (0%)	36	44
1	D	672/674 (100%)	655 (98%)	13 (2%)	4 (1%)	21	25
1	E	672/674 (100%)	651 (97%)	18 (3%)	3 (0%)	30	36
1	F	672/674 (100%)	649 (97%)	20 (3%)	3 (0%)	30	36
All	All	4032/4044 (100%)	3906 (97%)	109 (3%)	17 (0%)	30	36

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	87	ASP
1	C	646	ASP
1	E	240	GLY
1	F	240	GLY
1	F	646	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	613/613 (100%)	574 (94%)	39 (6%)	16	21
1	B	613/613 (100%)	569 (93%)	44 (7%)	13	16
1	C	613/613 (100%)	573 (94%)	40 (6%)	15	20
1	D	613/613 (100%)	575 (94%)	38 (6%)	16	22
1	E	613/613 (100%)	571 (93%)	42 (7%)	14	18
1	F	613/613 (100%)	574 (94%)	39 (6%)	16	21
All	All	3678/3678 (100%)	3436 (93%)	242 (7%)	15	19

5 of 242 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	577	GLU
1	F	431	GLU
1	D	431	GLU
1	F	382	VAL
1	F	598	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 207 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	307	HIS
1	E	119	HIS
1	F	493	GLN
1	D	359	ASN
1	D	543	HIS

5.3.3 RNA [i](#)

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 ⓘ

84 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	G	1	2,1	14,14,15	0.52	0	17,19,21	0.74	1 (5%)
2	MAN	G	10	2	11,11,12	0.53	0	15,15,17	0.65	1 (6%)
2	MAN	G	11	2	11,11,12	0.61	0	15,15,17	0.64	1 (6%)
2	MAN	G	12	2	11,11,12	0.57	0	15,15,17	0.74	1 (6%)
2	NAG	G	2	2	14,14,15	0.59	0	17,19,21	0.81	0
2	BMA	G	3	2	11,11,12	0.42	0	15,15,17	0.38	0
2	MAN	G	4	2	11,11,12	0.37	0	15,15,17	0.71	1 (6%)
2	MAN	G	5	2	11,11,12	0.52	0	15,15,17	0.60	0
2	MAN	G	6	2	11,11,12	0.58	0	15,15,17	0.66	1 (6%)
2	GLC	G	7	2	11,11,12	0.44	0	15,15,17	1.33	1 (6%)
2	MAN	G	8	2	11,11,12	0.55	0	15,15,17	0.72	1 (6%)
2	MAN	G	9	2	11,11,12	0.70	0	15,15,17	0.83	0
3	NAG	H	1	3,1	14,14,15	0.46	0	17,19,21	0.68	0
3	NAG	H	2	3	14,14,15	0.57	0	17,19,21	0.69	0
2	NAG	I	1	2,1	14,14,15	0.51	0	17,19,21	0.62	0
2	MAN	I	10	2	11,11,12	0.77	0	15,15,17	1.42	1 (6%)
2	MAN	I	11	2	11,11,12	0.66	0	15,15,17	0.66	1 (6%)
2	MAN	I	12	2	11,11,12	0.56	0	15,15,17	0.99	1 (6%)
2	NAG	I	2	2	14,14,15	0.61	0	17,19,21	0.83	0
2	BMA	I	3	2	11,11,12	0.46	0	15,15,17	0.28	0
2	MAN	I	4	2	11,11,12	0.55	0	15,15,17	0.61	1 (6%)
2	MAN	I	5	2	11,11,12	0.55	0	15,15,17	0.70	1 (6%)
2	MAN	I	6	2	11,11,12	0.45	0	15,15,17	0.59	1 (6%)
2	GLC	I	7	2	11,11,12	0.48	0	15,15,17	0.67	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	I	8	2	11,11,12	0.61	0	15,15,17	0.67	1 (6%)
2	MAN	I	9	2	11,11,12	0.61	0	15,15,17	1.17	2 (13%)
3	NAG	J	1	3,1	14,14,15	0.69	0	17,19,21	0.68	0
3	NAG	J	2	3	14,14,15	0.58	0	17,19,21	0.65	0
2	NAG	K	1	2,1	14,14,15	0.46	0	17,19,21	0.86	1 (5%)
2	MAN	K	10	2	11,11,12	0.62	0	15,15,17	0.71	1 (6%)
2	MAN	K	11	2	11,11,12	0.54	0	15,15,17	0.69	1 (6%)
2	MAN	K	12	2	11,11,12	0.56	0	15,15,17	0.73	1 (6%)
2	NAG	K	2	2	14,14,15	0.43	0	17,19,21	0.91	1 (5%)
2	BMA	K	3	2	11,11,12	0.52	0	15,15,17	0.36	0
2	MAN	K	4	2	11,11,12	0.52	0	15,15,17	0.72	1 (6%)
2	MAN	K	5	2	11,11,12	0.49	0	15,15,17	0.64	0
2	MAN	K	6	2	11,11,12	0.45	0	15,15,17	0.56	0
2	GLC	K	7	2	11,11,12	0.50	0	15,15,17	0.73	1 (6%)
2	MAN	K	8	2	11,11,12	0.56	0	15,15,17	0.64	0
2	MAN	K	9	2	11,11,12	0.69	0	15,15,17	0.82	0
3	NAG	L	1	3,1	14,14,15	0.77	0	17,19,21	0.68	0
3	NAG	L	2	3	14,14,15	0.68	0	17,19,21	0.60	0
2	NAG	M	1	2,1	14,14,15	0.50	0	17,19,21	0.78	1 (5%)
2	MAN	M	10	2	11,11,12	0.60	0	15,15,17	1.26	1 (6%)
2	MAN	M	11	2	11,11,12	0.71	0	15,15,17	0.72	1 (6%)
2	MAN	M	12	2	11,11,12	0.60	0	15,15,17	1.01	1 (6%)
2	NAG	M	2	2	14,14,15	0.53	0	17,19,21	0.86	0
2	BMA	M	3	2	11,11,12	0.54	0	15,15,17	0.35	0
2	MAN	M	4	2	11,11,12	0.36	0	15,15,17	0.72	1 (6%)
2	MAN	M	5	2	11,11,12	0.51	0	15,15,17	0.62	0
2	MAN	M	6	2	11,11,12	0.48	0	15,15,17	0.51	0
2	GLC	M	7	2	11,11,12	0.42	0	15,15,17	0.77	1 (6%)
2	MAN	M	8	2	11,11,12	0.55	0	15,15,17	0.67	1 (6%)
2	MAN	M	9	2	11,11,12	0.70	0	15,15,17	1.12	2 (13%)
3	NAG	N	1	3,1	14,14,15	0.69	0	17,19,21	0.65	0
3	NAG	N	2	3	14,14,15	0.70	0	17,19,21	0.58	0
2	NAG	O	1	2,1	14,14,15	0.45	0	17,19,21	0.76	1 (5%)
2	MAN	O	10	2	11,11,12	0.66	0	15,15,17	1.27	1 (6%)
2	MAN	O	11	2	11,11,12	0.55	0	15,15,17	0.59	1 (6%)
2	MAN	O	12	2	11,11,12	0.57	0	15,15,17	0.74	1 (6%)
2	NAG	O	2	2	14,14,15	0.52	0	17,19,21	0.78	0
2	BMA	O	3	2	11,11,12	0.59	0	15,15,17	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	O	4	2	11,11,12	0.46	0	15,15,17	0.71	0
2	MAN	O	5	2	11,11,12	0.55	0	15,15,17	0.56	0
2	MAN	O	6	2	11,11,12	0.65	0	15,15,17	0.64	0
2	GLC	O	7	2	11,11,12	0.52	0	15,15,17	1.22	1 (6%)
2	MAN	O	8	2	11,11,12	0.55	0	15,15,17	0.75	1 (6%)
2	MAN	O	9	2	11,11,12	0.77	0	15,15,17	1.12	1 (6%)
3	NAG	P	1	3,1	14,14,15	0.66	0	17,19,21	0.64	0
3	NAG	P	2	3	14,14,15	0.53	0	17,19,21	0.73	1 (5%)
2	NAG	Q	1	2,1	14,14,15	0.49	0	17,19,21	0.70	1 (5%)
2	MAN	Q	10	2	11,11,12	0.52	0	15,15,17	0.72	1 (6%)
2	MAN	Q	11	2	11,11,12	0.49	0	15,15,17	0.58	1 (6%)
2	MAN	Q	12	2	11,11,12	0.59	0	15,15,17	0.70	1 (6%)
2	NAG	Q	2	2	14,14,15	0.52	0	17,19,21	0.93	1 (5%)
2	BMA	Q	3	2	11,11,12	0.40	0	15,15,17	0.32	0
2	MAN	Q	4	2	11,11,12	0.55	0	15,15,17	0.60	0
2	MAN	Q	5	2	11,11,12	0.51	0	15,15,17	0.80	1 (6%)
2	MAN	Q	6	2	11,11,12	0.46	0	15,15,17	0.65	1 (6%)
2	GLC	Q	7	2	11,11,12	0.42	0	15,15,17	0.62	1 (6%)
2	MAN	Q	8	2	11,11,12	0.51	0	15,15,17	0.59	0
2	MAN	Q	9	2	11,11,12	0.72	0	15,15,17	0.86	1 (6%)
3	NAG	R	1	3,1	14,14,15	0.51	0	17,19,21	0.74	1 (5%)
3	NAG	R	2	3	14,14,15	0.61	0	17,19,21	0.66	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	G	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	G	10	2	-	0/2/19/22	1/1/1/1
2	MAN	G	11	2	-	0/2/19/22	0/1/1/1
2	MAN	G	12	2	-	2/2/19/22	1/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	0/2/19/22	0/1/1/1
2	MAN	G	4	2	-	0/2/19/22	0/1/1/1
2	MAN	G	5	2	-	0/2/19/22	0/1/1/1
2	MAN	G	6	2	-	0/2/19/22	0/1/1/1
2	GLC	G	7	2	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	G	8	2	-	0/2/19/22	0/1/1/1
2	MAN	G	9	2	-	0/2/19/22	0/1/1/1
3	NAG	H	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
2	NAG	I	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	I	10	2	-	2/2/19/22	0/1/1/1
2	MAN	I	11	2	-	0/2/19/22	0/1/1/1
2	MAN	I	12	2	-	1/2/19/22	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1
2	BMA	I	3	2	-	0/2/19/22	0/1/1/1
2	MAN	I	4	2	-	0/2/19/22	0/1/1/1
2	MAN	I	5	2	-	0/2/19/22	0/1/1/1
2	MAN	I	6	2	-	1/2/19/22	0/1/1/1
2	GLC	I	7	2	-	0/2/19/22	0/1/1/1
2	MAN	I	8	2	-	0/2/19/22	0/1/1/1
2	MAN	I	9	2	-	0/2/19/22	0/1/1/1
3	NAG	J	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
2	NAG	K	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	K	10	2	-	0/2/19/22	1/1/1/1
2	MAN	K	11	2	-	1/2/19/22	0/1/1/1
2	MAN	K	12	2	-	2/2/19/22	1/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1
2	BMA	K	3	2	-	0/2/19/22	0/1/1/1
2	MAN	K	4	2	-	0/2/19/22	0/1/1/1
2	MAN	K	5	2	-	0/2/19/22	0/1/1/1
2	MAN	K	6	2	-	1/2/19/22	0/1/1/1
2	GLC	K	7	2	-	0/2/19/22	0/1/1/1
2	MAN	K	8	2	-	0/2/19/22	0/1/1/1
2	MAN	K	9	2	-	1/2/19/22	0/1/1/1
3	NAG	L	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
2	NAG	M	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	M	10	2	-	2/2/19/22	0/1/1/1
2	MAN	M	11	2	-	2/2/19/22	0/1/1/1
2	MAN	M	12	2	-	1/2/19/22	0/1/1/1
2	NAG	M	2	2	-	0/6/23/26	0/1/1/1
2	BMA	M	3	2	-	0/2/19/22	0/1/1/1
2	MAN	M	4	2	-	0/2/19/22	0/1/1/1
2	MAN	M	5	2	-	0/2/19/22	0/1/1/1
2	MAN	M	6	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	M	7	2	-	0/2/19/22	0/1/1/1
2	MAN	M	8	2	-	0/2/19/22	0/1/1/1
2	MAN	M	9	2	-	0/2/19/22	0/1/1/1
3	NAG	N	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	N	2	3	-	2/6/23/26	0/1/1/1
2	NAG	O	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	O	10	2	-	2/2/19/22	0/1/1/1
2	MAN	O	11	2	-	0/2/19/22	0/1/1/1
2	MAN	O	12	2	-	2/2/19/22	1/1/1/1
2	NAG	O	2	2	-	0/6/23/26	0/1/1/1
2	BMA	O	3	2	-	0/2/19/22	0/1/1/1
2	MAN	O	4	2	-	0/2/19/22	0/1/1/1
2	MAN	O	5	2	-	0/2/19/22	0/1/1/1
2	MAN	O	6	2	-	0/2/19/22	0/1/1/1
2	GLC	O	7	2	-	0/2/19/22	0/1/1/1
2	MAN	O	8	2	-	0/2/19/22	0/1/1/1
2	MAN	O	9	2	-	0/2/19/22	0/1/1/1
3	NAG	P	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	P	2	3	-	0/6/23/26	0/1/1/1
2	NAG	Q	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	Q	10	2	-	0/2/19/22	1/1/1/1
2	MAN	Q	11	2	-	0/2/19/22	0/1/1/1
2	MAN	Q	12	2	-	0/2/19/22	1/1/1/1
2	NAG	Q	2	2	-	0/6/23/26	0/1/1/1
2	BMA	Q	3	2	-	0/2/19/22	0/1/1/1
2	MAN	Q	4	2	-	0/2/19/22	0/1/1/1
2	MAN	Q	5	2	-	1/2/19/22	0/1/1/1
2	MAN	Q	6	2	-	0/2/19/22	0/1/1/1
2	GLC	Q	7	2	-	0/2/19/22	0/1/1/1
2	MAN	Q	8	2	-	0/2/19/22	0/1/1/1
2	MAN	Q	9	2	-	0/2/19/22	0/1/1/1
3	NAG	R	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	R	2	3	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	10	MAN	C1-C2-C3	-4.98	102.39	109.64
2	G	7	GLC	C1-O5-C5	4.62	118.38	112.19
2	M	10	MAN	C1-O5-C5	4.44	118.14	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	10	MAN	C1-O5-C5	4.37	118.04	112.19
2	O	7	GLC	C1-O5-C5	4.19	117.80	112.19

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	2	NAG	O5-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
3	N	1	NAG	O5-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
2	M	10	MAN	O5-C5-C6-O6

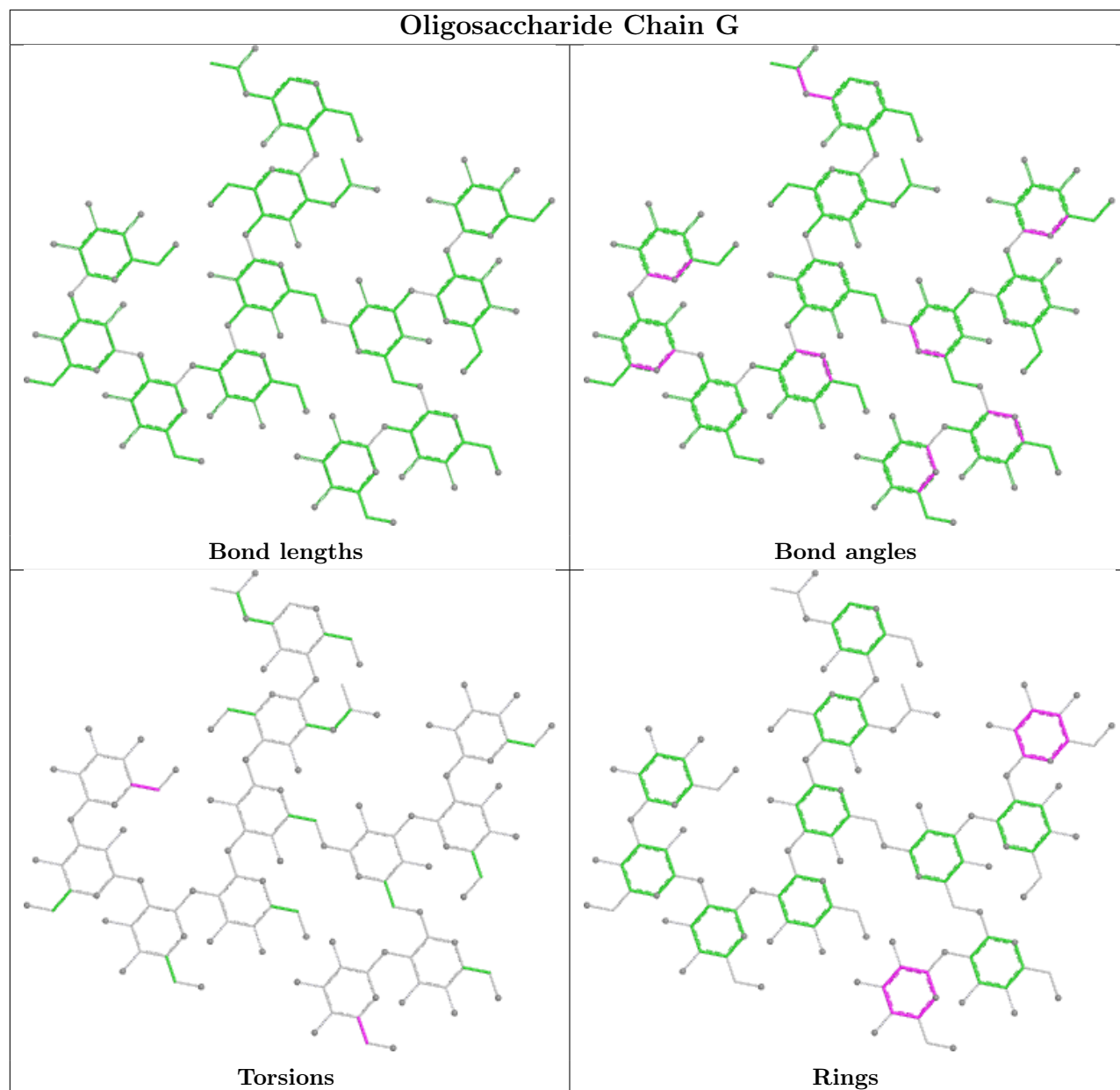
5 of 7 ring outliers are listed below:

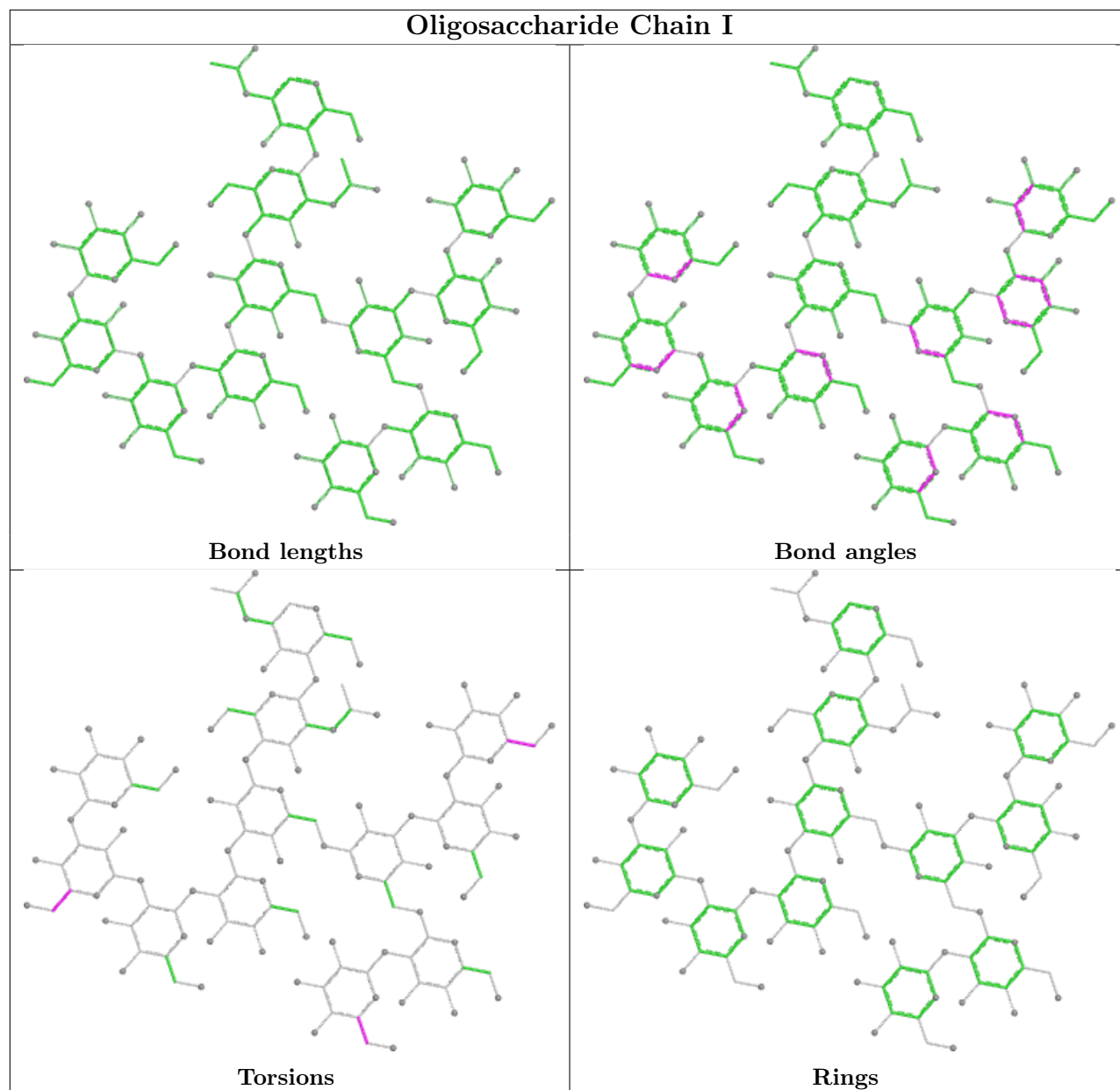
Mol	Chain	Res	Type	Atoms
2	Q	12	MAN	C1-C2-C3-C4-C5-O5
2	K	10	MAN	C1-C2-C3-C4-C5-O5
2	G	12	MAN	C1-C2-C3-C4-C5-O5
2	Q	10	MAN	C1-C2-C3-C4-C5-O5
2	K	12	MAN	C1-C2-C3-C4-C5-O5

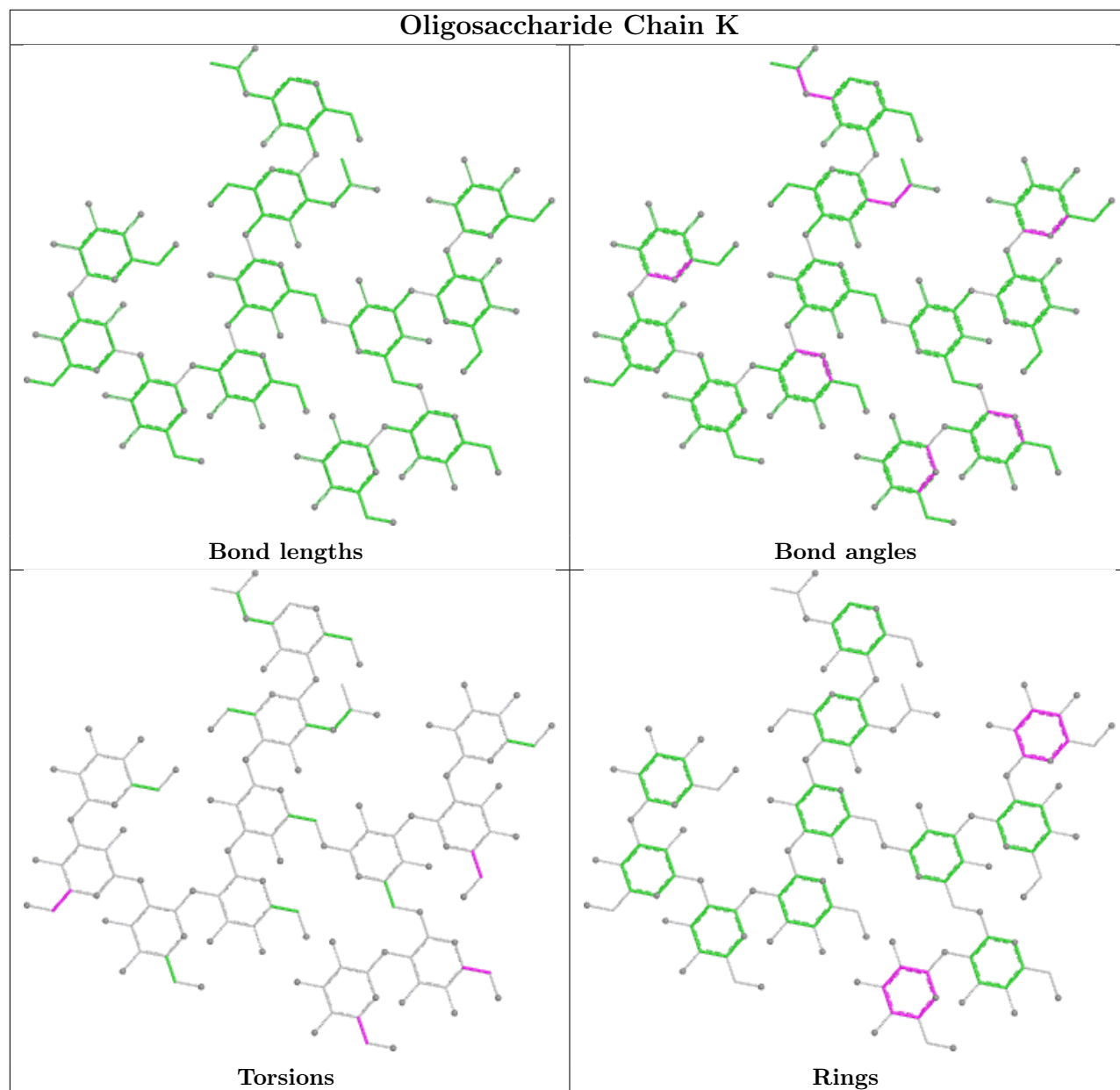
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Q	9	MAN	1	0
2	Q	10	MAN	1	0
2	K	4	MAN	1	0
2	I	10	MAN	1	0

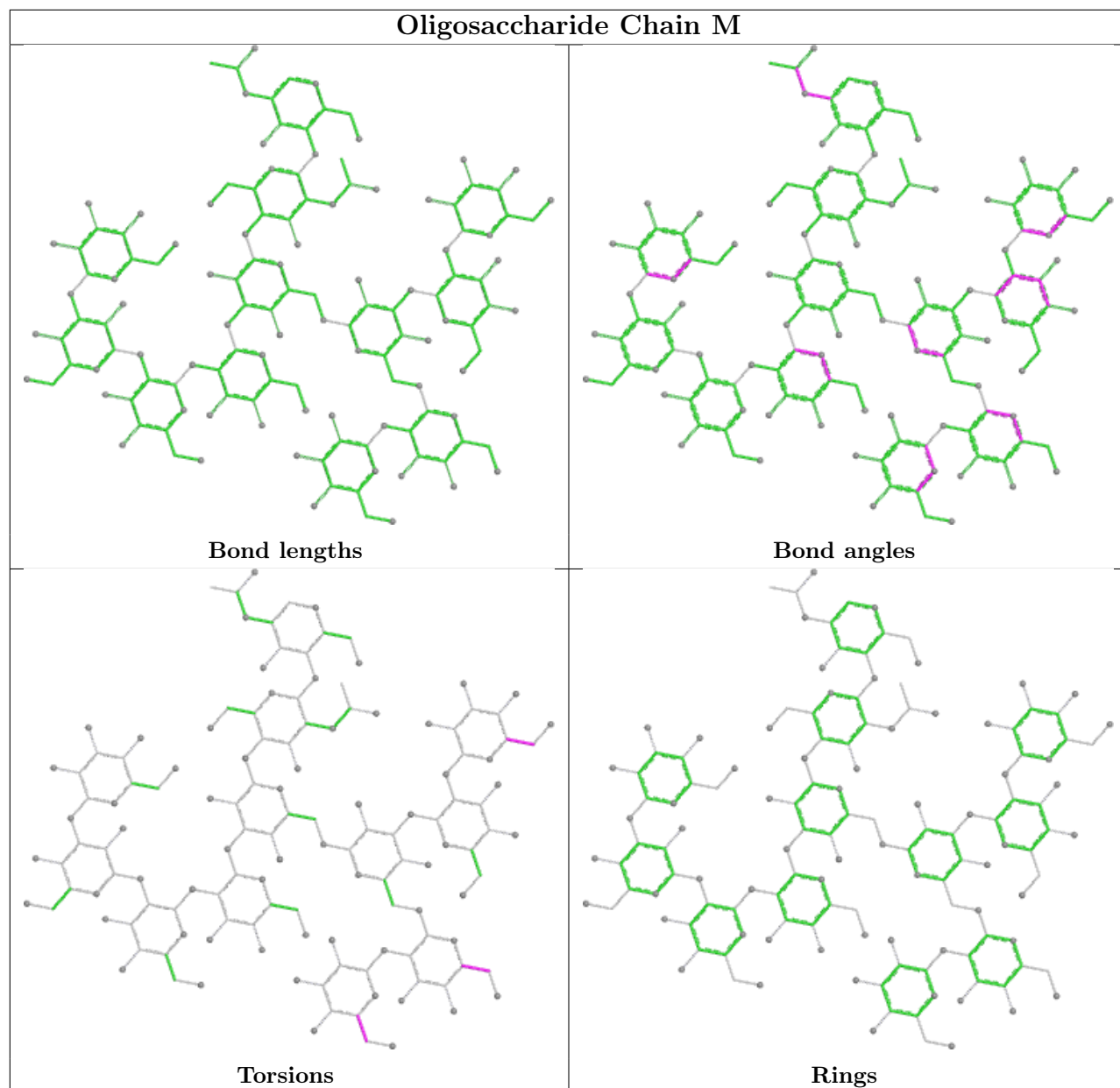
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

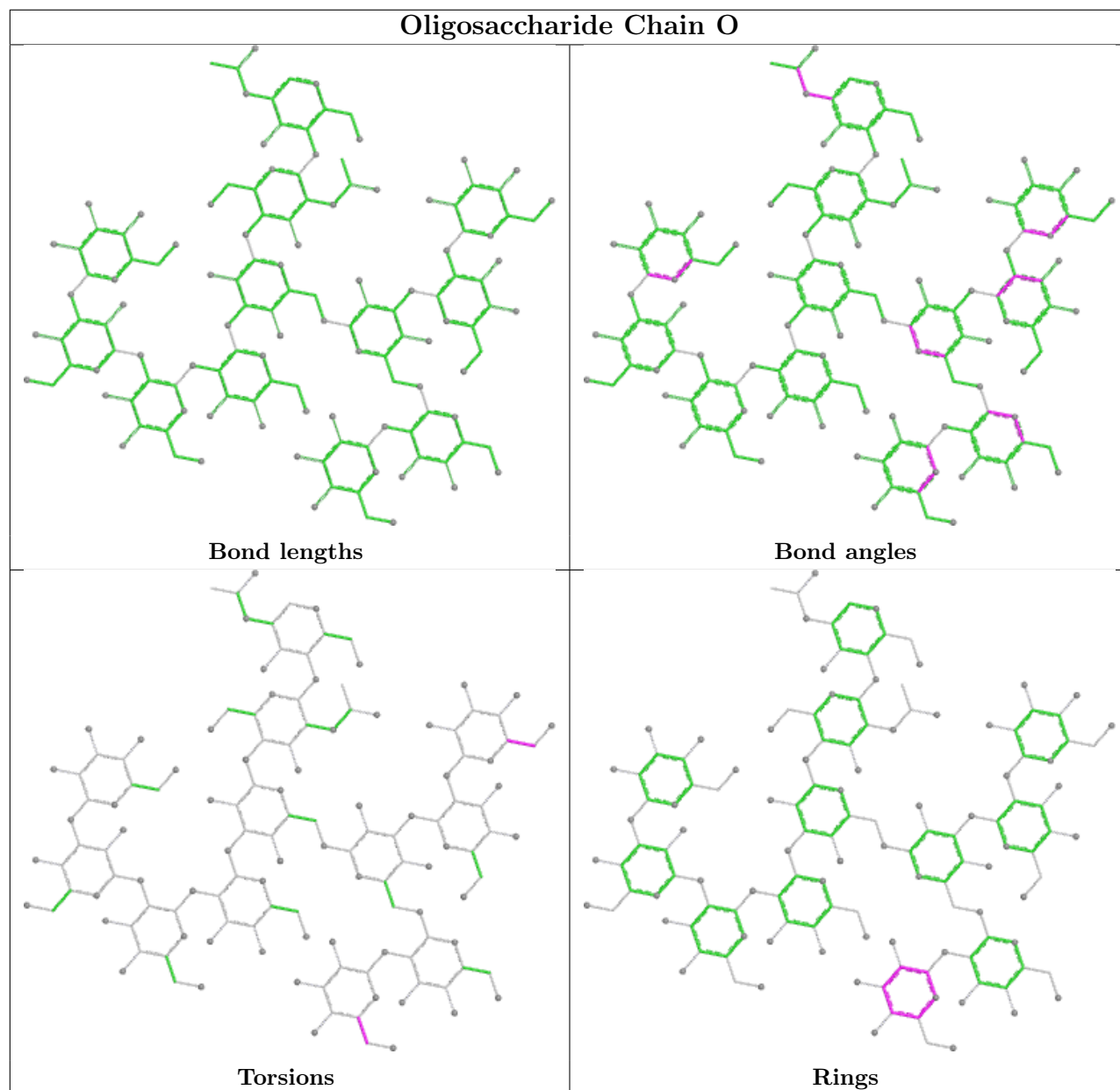


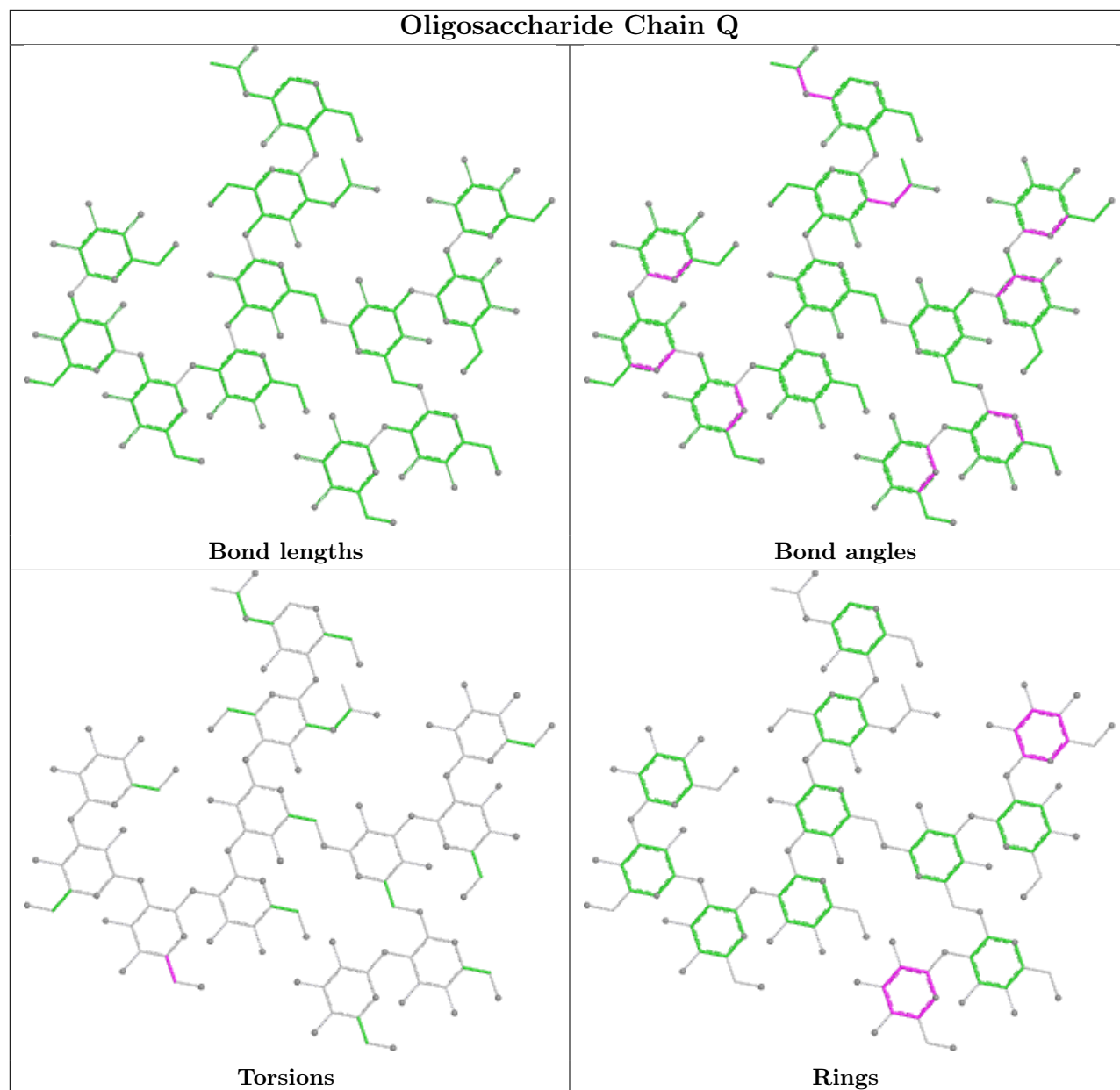


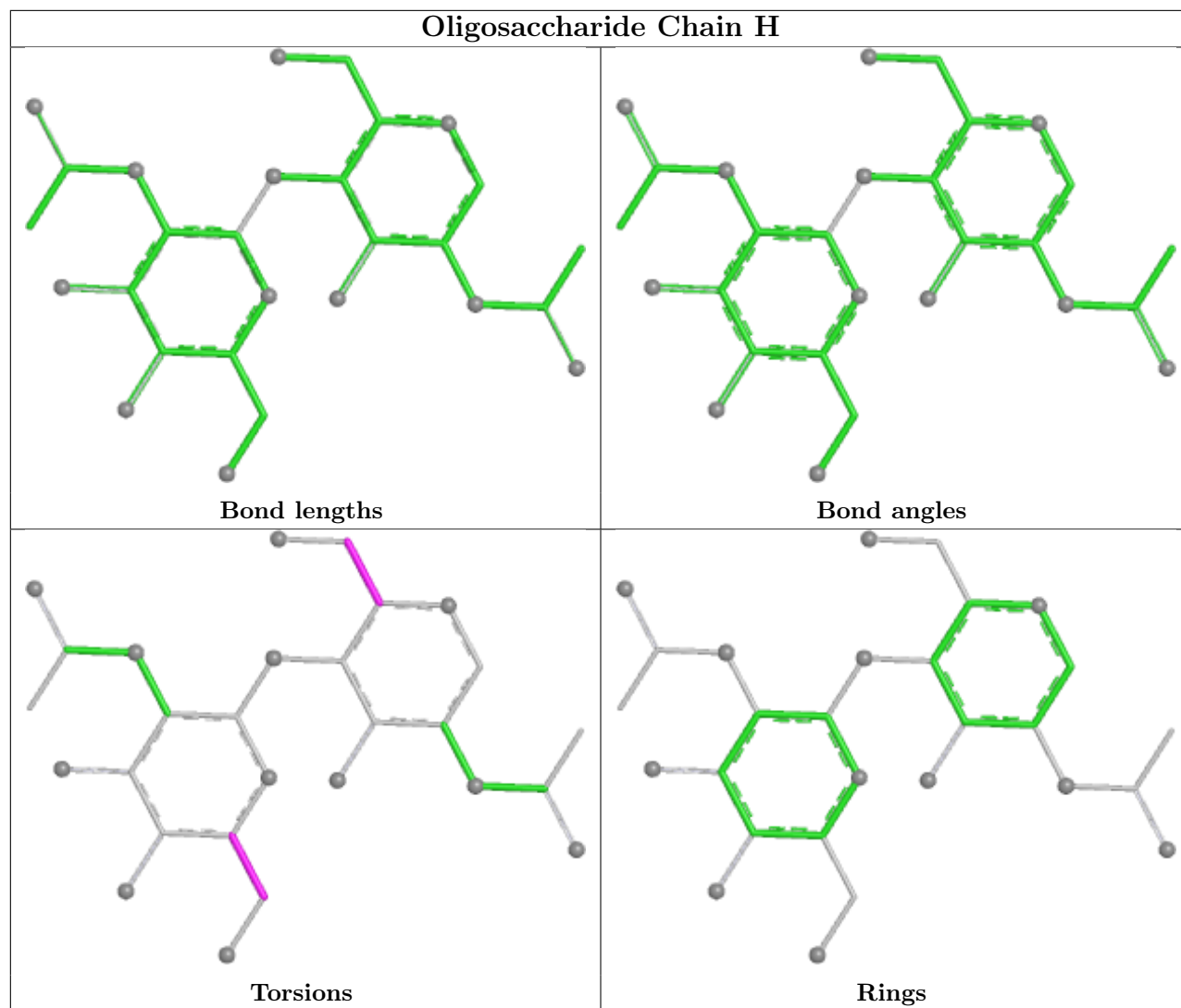


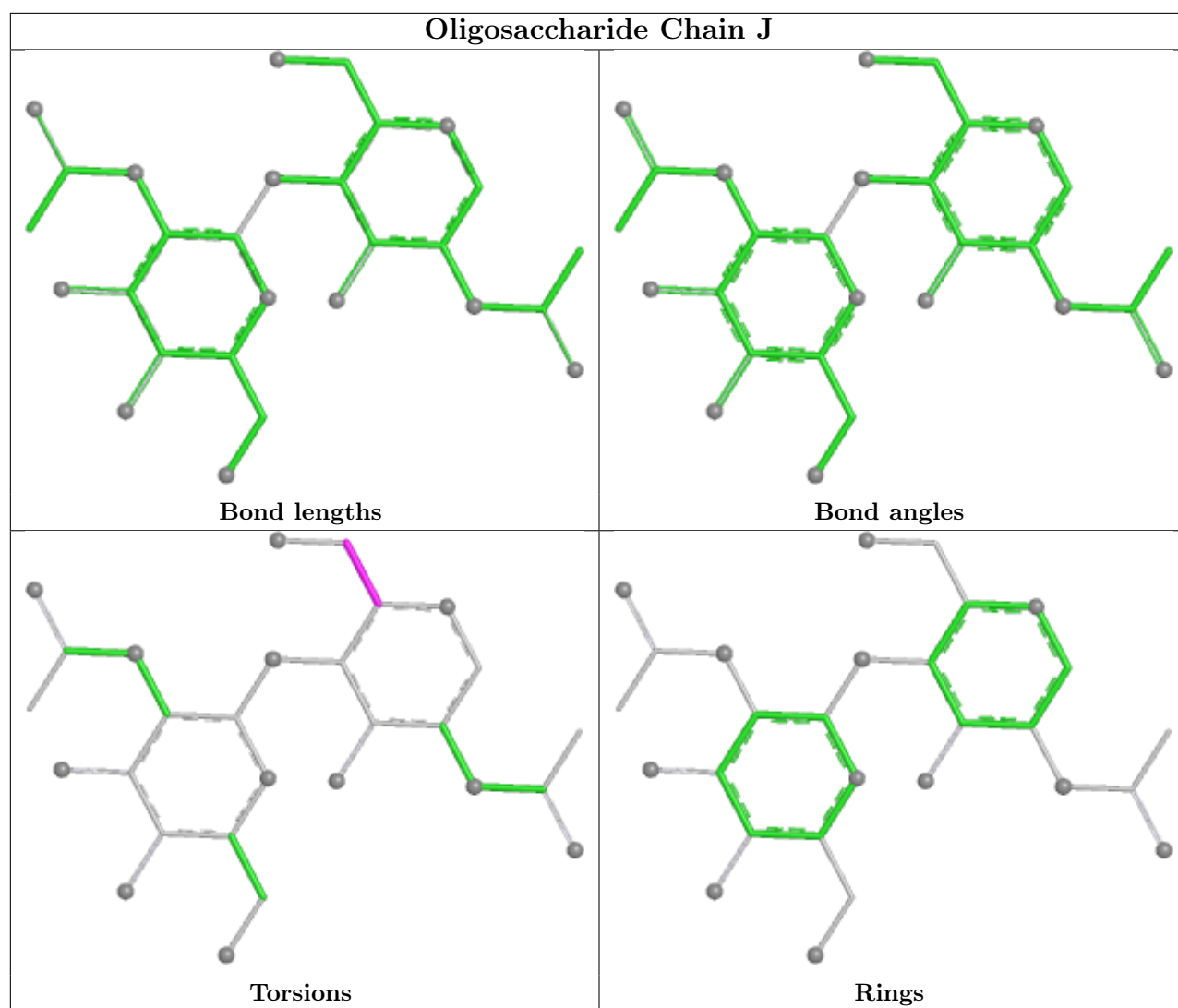
Oligosaccharide Chain M

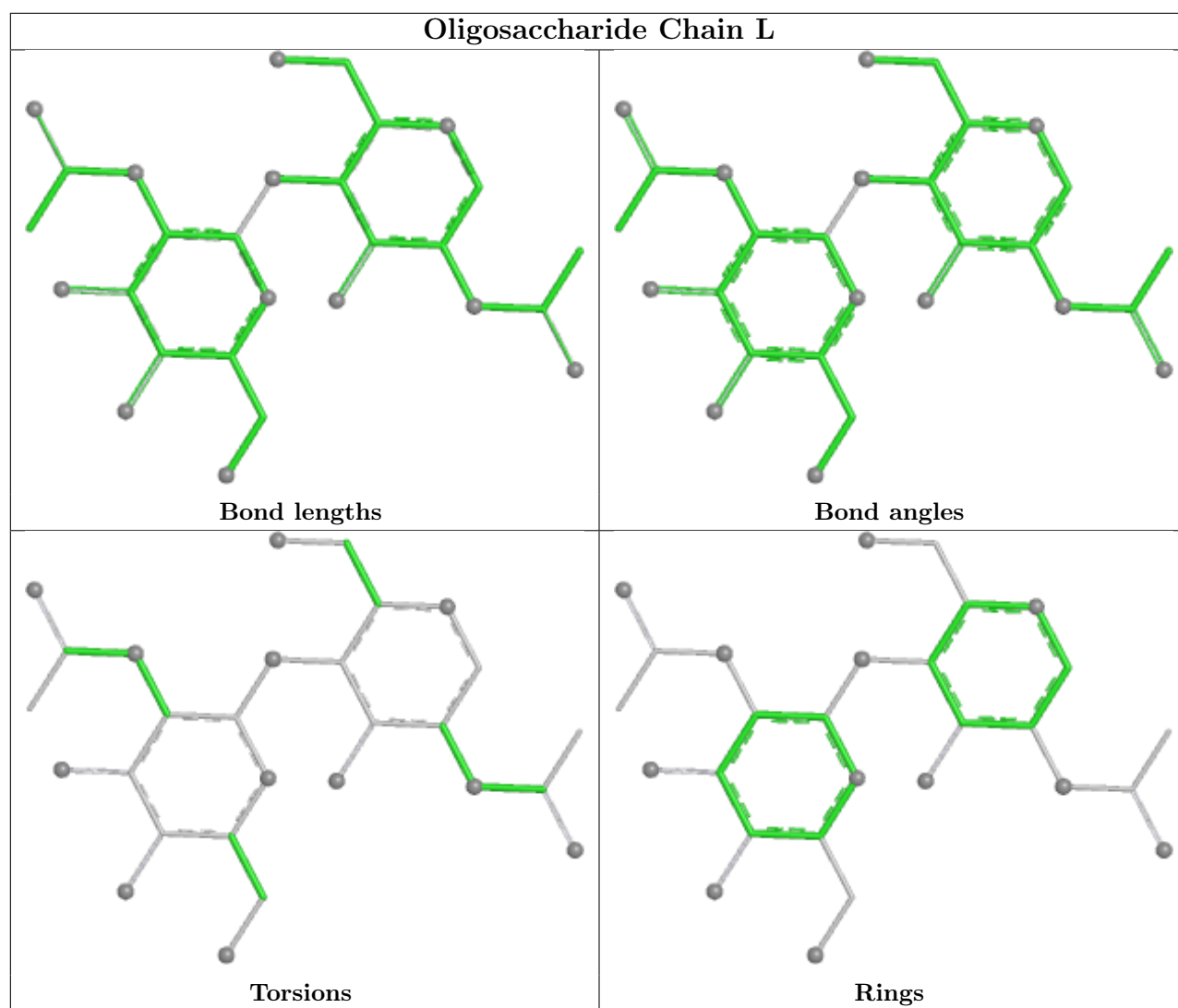


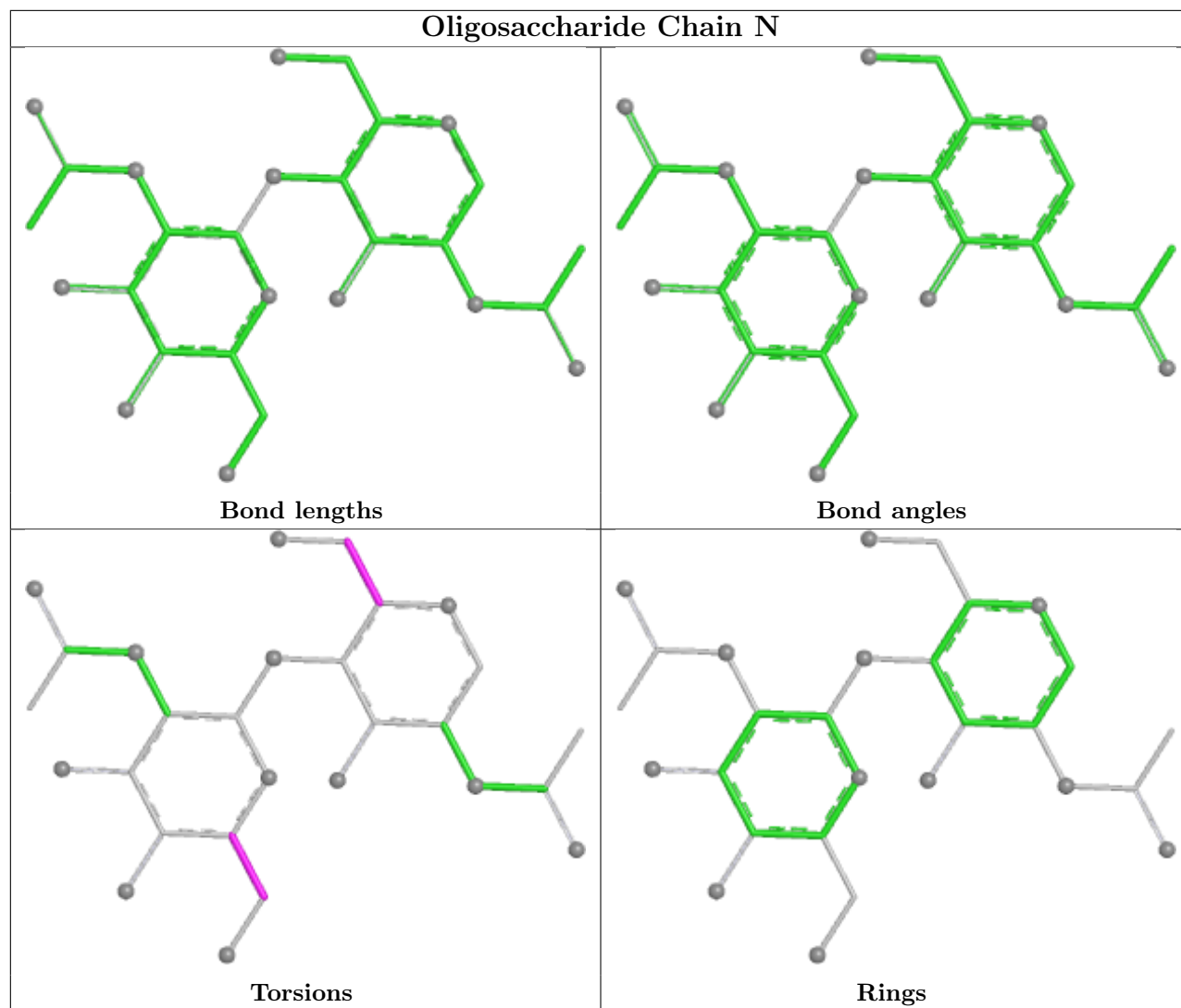


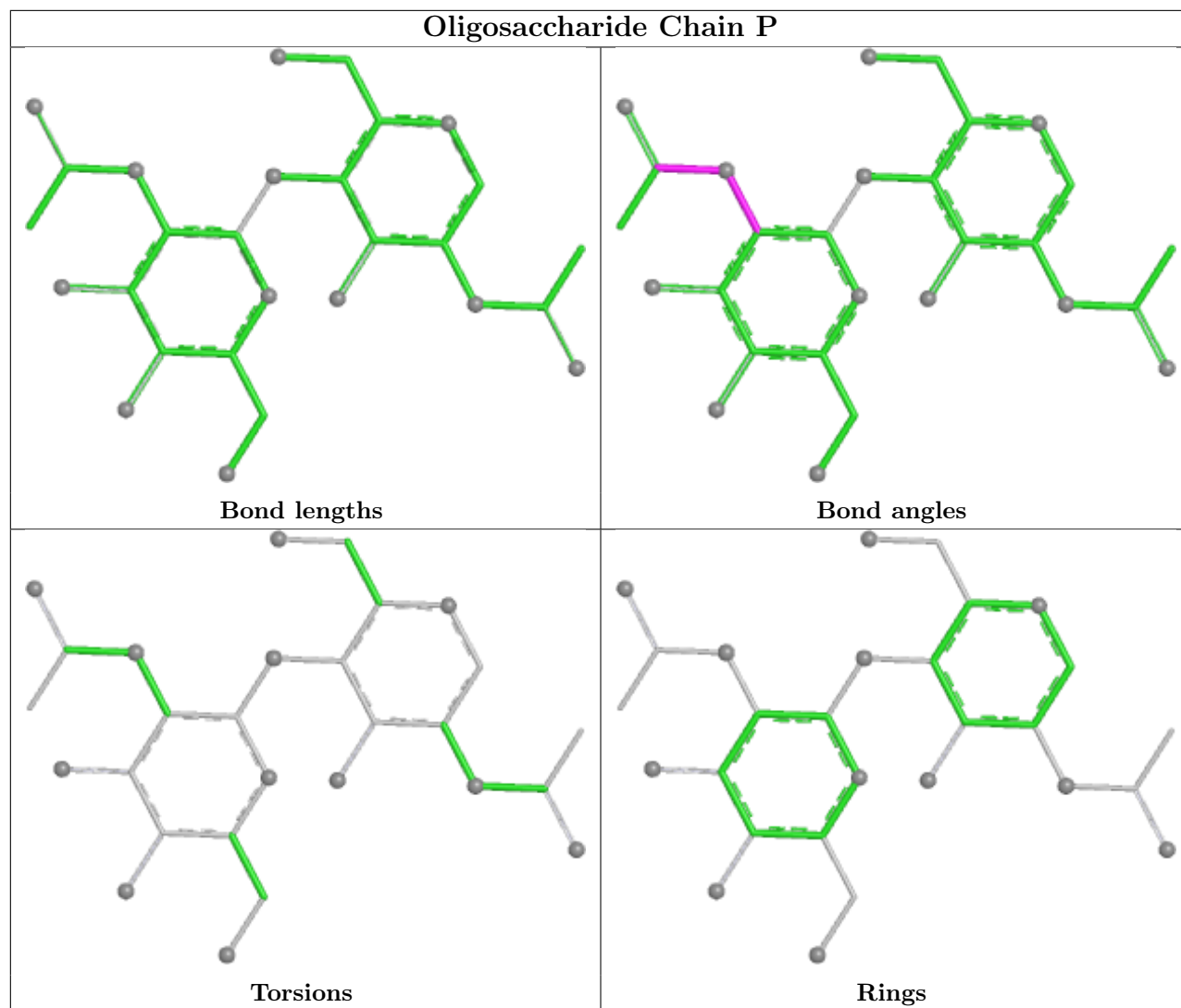


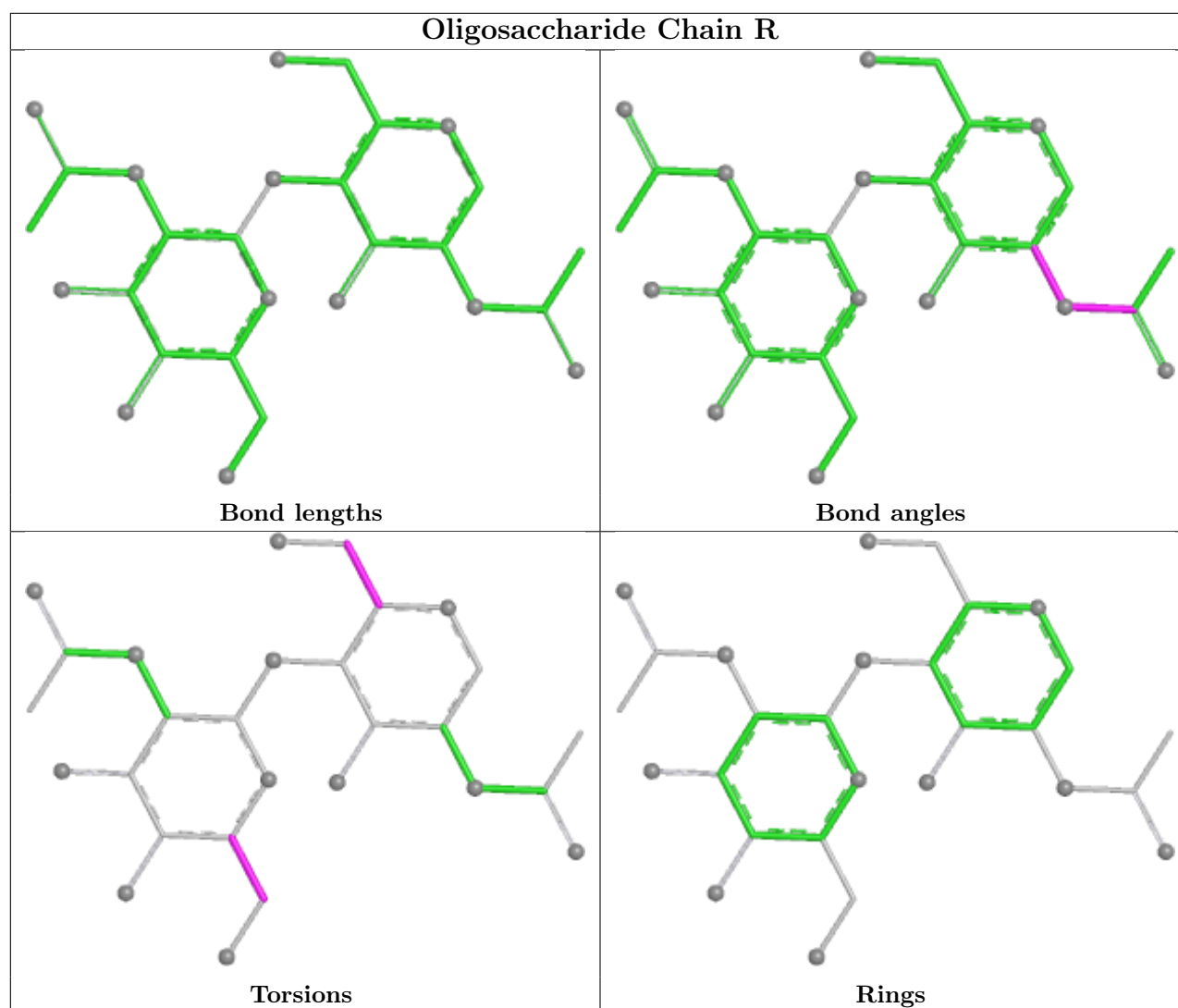












5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
4	FMT	C	2004	-	2,2,2	0.62	0	1,1,1	0.08	0
4	FMT	F	2006	-	2,2,2	0.58	0	1,1,1	0.06	0
4	FMT	B	2002	-	2,2,2	0.63	0	1,1,1	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	FMT	A	2003	-	2,2,2	0.57	0	1,1,1	0.05	0
4	FMT	D	2001	-	2,2,2	0.61	0	1,1,1	0.06	0
4	FMT	E	2005	-	2,2,2	0.62	0	1,1,1	0.07	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	2004	FMT	1	0
4	F	2006	FMT	1	0
4	B	2002	FMT	2	0
4	A	2003	FMT	1	0
4	D	2001	FMT	1	0
4	E	2005	FMT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	674/674 (100%)	-0.38	12 (1%) 67 68	18, 33, 64, 96	0
1	B	674/674 (100%)	-0.34	14 (2%) 63 64	16, 32, 63, 94	0
1	C	674/674 (100%)	-0.32	9 (1%) 75 77	17, 34, 65, 97	0
1	D	674/674 (100%)	-0.40	7 (1%) 79 81	17, 33, 63, 96	0
1	E	674/674 (100%)	-0.31	12 (1%) 67 68	17, 34, 65, 97	0
1	F	674/674 (100%)	-0.29	22 (3%) 49 48	17, 33, 66, 96	0
All	All	4044/4044 (100%)	-0.34	76 (1%) 66 67	16, 33, 65, 97	0

The worst 5 of 76 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	650	PHE	4.4
1	F	649	CYS	4.2
1	A	624	LEU	4.0
1	F	505	VAL	3.7
1	E	681	HIS	3.6

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($\text{\AA}^2$)	Q<0.9
2	MAN	K	12	11/12	0.37	0.19	97,99,101,101	0
2	MAN	Q	12	11/12	0.40	0.16	97,99,100,100	0
3	NAG	N	2	14/15	0.41	0.21	98,102,104,105	0
2	MAN	I	12	11/12	0.43	0.17	95,99,101,103	0
2	MAN	M	12	11/12	0.43	0.18	97,100,101,102	0
2	MAN	G	12	11/12	0.47	0.15	96,98,100,100	0
2	MAN	O	12	11/12	0.48	0.17	96,99,100,101	0
3	NAG	J	2	14/15	0.54	0.17	88,90,91,91	0
3	NAG	N	1	14/15	0.56	0.18	79,86,90,95	0
2	MAN	K	10	11/12	0.56	0.23	86,91,92,92	0
2	MAN	M	10	11/12	0.63	0.20	87,91,93,93	0
3	NAG	R	2	14/15	0.63	0.16	86,89,92,92	0
2	MAN	M	11	11/12	0.64	0.15	88,90,91,96	0
2	MAN	Q	10	11/12	0.65	0.18	85,90,91,91	0
2	MAN	I	10	11/12	0.66	0.17	88,89,91,91	0
2	MAN	G	11	11/12	0.66	0.15	84,88,90,94	0
2	MAN	O	10	11/12	0.67	0.20	87,89,91,92	0
2	MAN	G	10	11/12	0.67	0.18	86,90,92,93	0
2	MAN	M	9	11/12	0.68	0.15	81,83,85,87	0
3	NAG	L	2	14/15	0.70	0.15	79,82,84,85	0
2	MAN	K	9	11/12	0.71	0.15	79,80,83,86	0
2	MAN	K	11	11/12	0.72	0.13	85,87,89,94	0
2	MAN	Q	11	11/12	0.74	0.14	86,87,90,94	0
3	NAG	R	1	14/15	0.76	0.13	67,74,79,81	0
2	MAN	I	11	11/12	0.76	0.12	83,87,90,94	0
3	NAG	P	2	14/15	0.77	0.12	72,74,76,76	0
2	MAN	G	9	11/12	0.77	0.11	79,82,83,86	0
2	MAN	I	9	11/12	0.77	0.12	78,79,81,86	0
3	NAG	J	1	14/15	0.78	0.13	67,72,77,81	0
2	MAN	O	11	11/12	0.79	0.13	86,88,90,95	0
3	NAG	H	2	14/15	0.79	0.13	63,68,70,71	0
2	MAN	O	9	11/12	0.80	0.12	78,81,82,85	0
2	MAN	M	8	11/12	0.80	0.11	63,70,76,83	0
3	NAG	L	1	14/15	0.80	0.11	63,68,72,76	0
2	MAN	G	8	11/12	0.81	0.12	66,70,77,85	0
2	MAN	Q	9	11/12	0.82	0.11	79,80,82,84	0
2	GLC	I	7	11/12	0.83	0.12	56,57,59,61	0
2	GLC	K	7	11/12	0.84	0.11	53,55,58,58	0
2	MAN	K	8	11/12	0.85	0.11	62,66,75,83	0
2	GLC	G	7	11/12	0.85	0.10	53,57,59,60	0
2	MAN	O	8	11/12	0.85	0.12	61,65,75,84	0
3	NAG	P	1	14/15	0.86	0.10	60,65,68,70	0
2	GLC	O	7	11/12	0.87	0.10	57,60,62,62	0

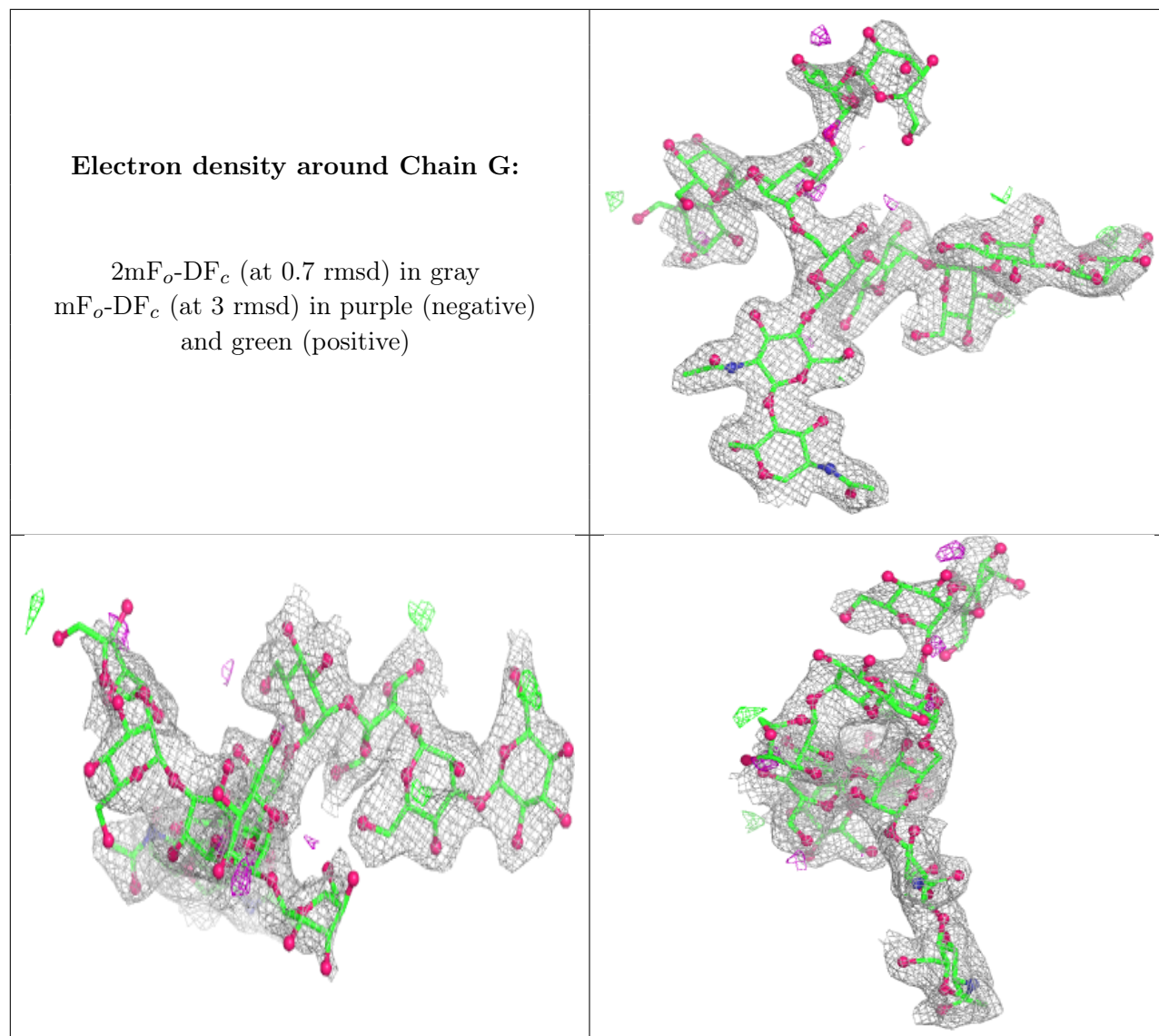
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MAN	O	6	11/12	0.89	0.09	44,45,50,54	0
2	MAN	I	8	11/12	0.91	0.10	63,69,77,84	0
2	MAN	M	6	11/12	0.91	0.09	39,43,45,49	0
2	GLC	M	7	11/12	0.91	0.09	51,55,59,60	0
2	MAN	Q	8	11/12	0.92	0.08	63,67,76,84	0
2	BMA	G	3	11/12	0.92	0.08	36,39,48,59	0
2	BMA	Q	3	11/12	0.92	0.08	33,35,42,53	0
2	GLC	Q	7	11/12	0.92	0.08	50,53,55,58	0
2	MAN	K	6	11/12	0.93	0.08	40,41,43,50	0
2	BMA	O	3	11/12	0.93	0.07	31,39,44,55	0
2	NAG	M	2	14/15	0.93	0.08	24,32,39,40	0
2	MAN	G	6	11/12	0.94	0.07	40,42,45,49	0
2	BMA	I	3	11/12	0.94	0.07	36,39,48,57	0
2	BMA	M	3	11/12	0.94	0.09	35,38,47,56	0
2	MAN	I	6	11/12	0.94	0.06	40,42,46,50	0
2	NAG	G	2	14/15	0.94	0.07	29,33,37,43	0
2	MAN	O	5	11/12	0.94	0.06	29,34,38,44	0
3	NAG	H	1	14/15	0.94	0.07	39,49,52,56	0
2	MAN	G	4	11/12	0.94	0.07	36,37,39,40	0
2	MAN	Q	6	11/12	0.94	0.07	40,40,43,46	0
2	NAG	I	2	14/15	0.95	0.06	28,32,37,38	0
2	MAN	O	4	11/12	0.95	0.07	34,36,39,41	0
2	MAN	M	4	11/12	0.95	0.07	34,36,39,40	0
2	MAN	M	5	11/12	0.95	0.06	33,35,36,40	0
2	MAN	Q	4	11/12	0.95	0.06	34,35,37,38	0
2	MAN	G	5	11/12	0.95	0.07	33,35,39,42	0
2	MAN	I	5	11/12	0.95	0.06	32,35,38,41	0
2	NAG	O	2	14/15	0.95	0.07	29,32,34,37	0
2	NAG	G	1	14/15	0.96	0.06	20,26,31,31	0
2	NAG	Q	2	14/15	0.96	0.06	29,31,33,39	0
2	MAN	I	4	11/12	0.96	0.06	34,36,37,38	0
2	NAG	M	1	14/15	0.96	0.06	22,24,29,30	0
2	MAN	Q	5	11/12	0.96	0.06	28,32,36,37	0
2	NAG	K	1	14/15	0.96	0.06	20,25,28,30	0
2	NAG	K	2	14/15	0.96	0.06	25,31,37,40	0
2	BMA	K	3	11/12	0.96	0.07	32,37,46,55	0
2	NAG	I	1	14/15	0.97	0.06	22,24,29,32	0
2	NAG	O	1	14/15	0.97	0.05	24,27,29,29	0
2	MAN	K	4	11/12	0.97	0.06	32,32,34,35	0
2	MAN	K	5	11/12	0.97	0.05	32,33,36,38	0
2	NAG	Q	1	14/15	0.98	0.05	21,24,26,27	0

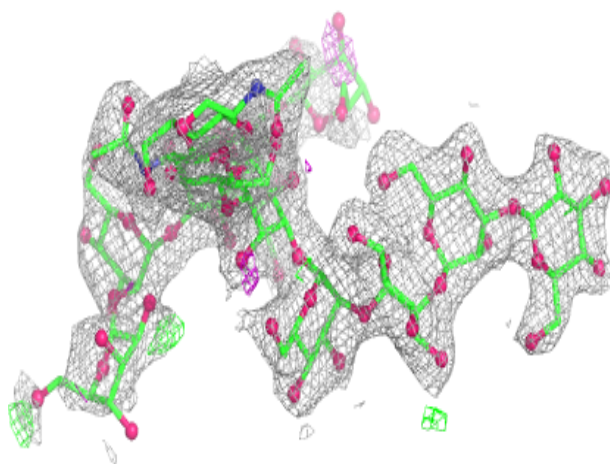
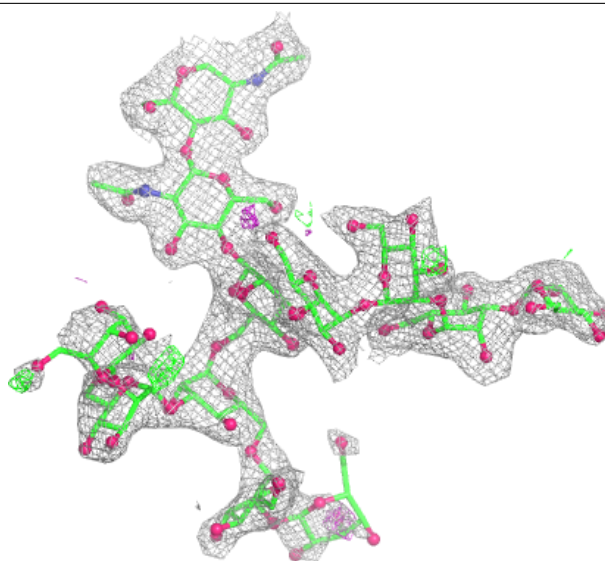
The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.



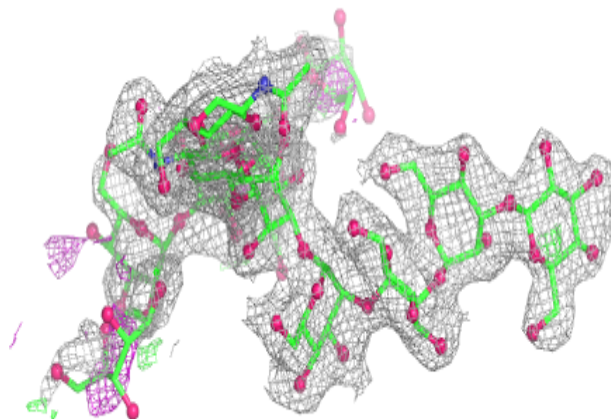
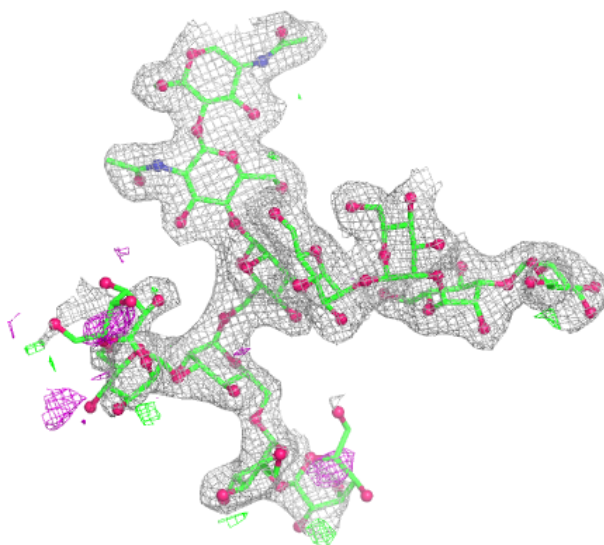
Electron density around Chain I:

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



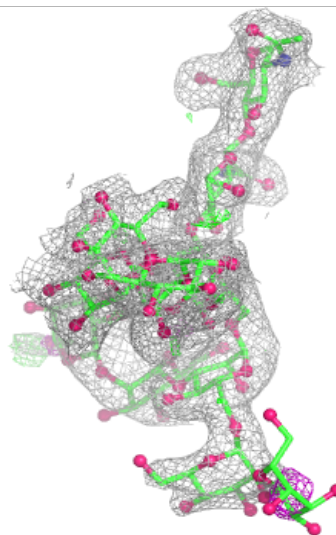
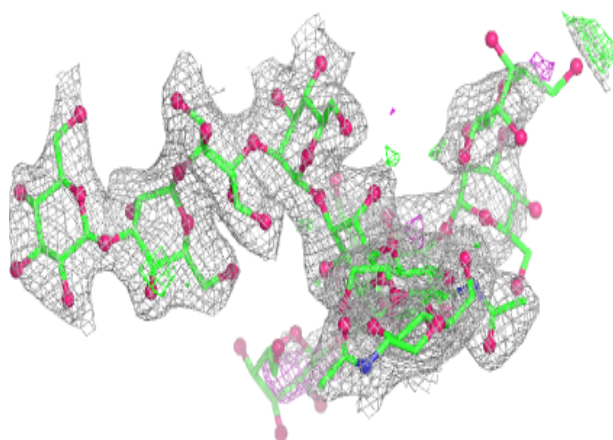
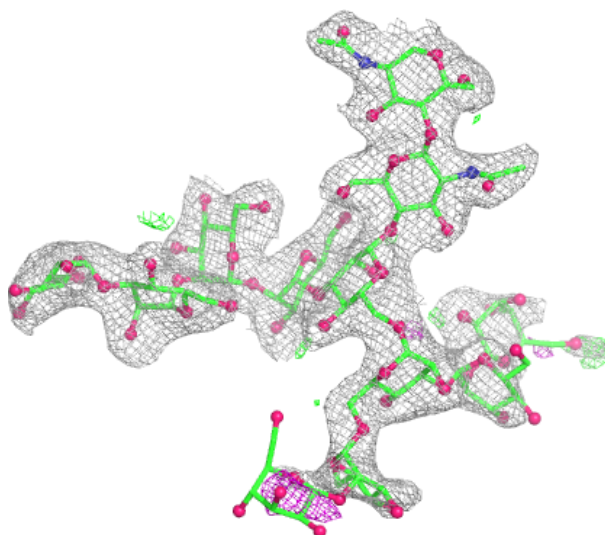
Electron density around Chain K:

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



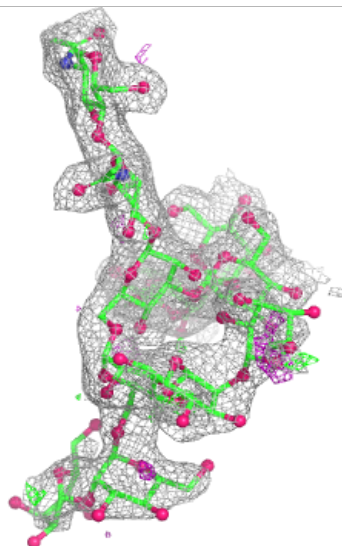
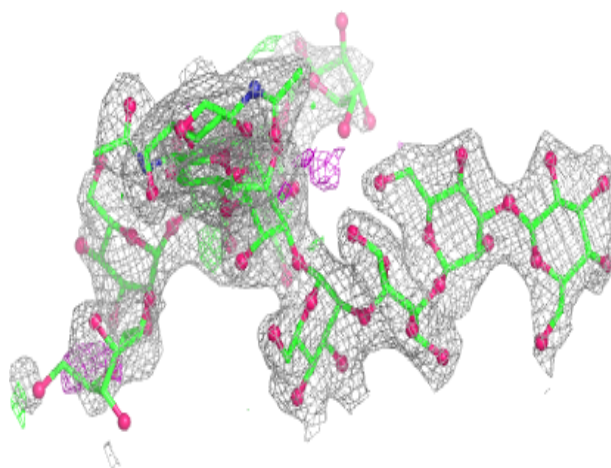
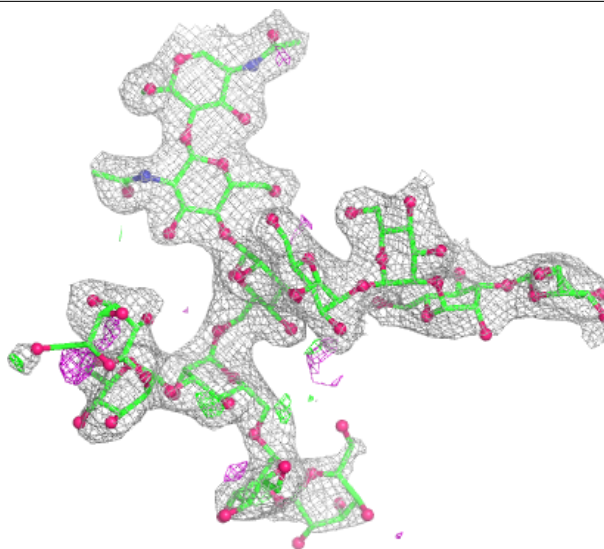
Electron density around Chain M:

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



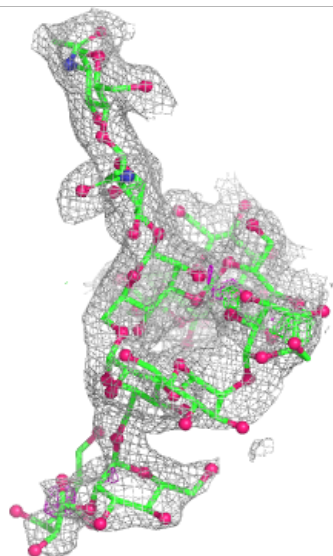
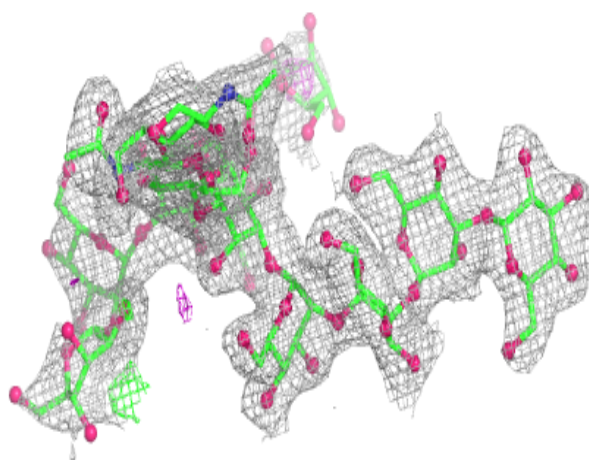
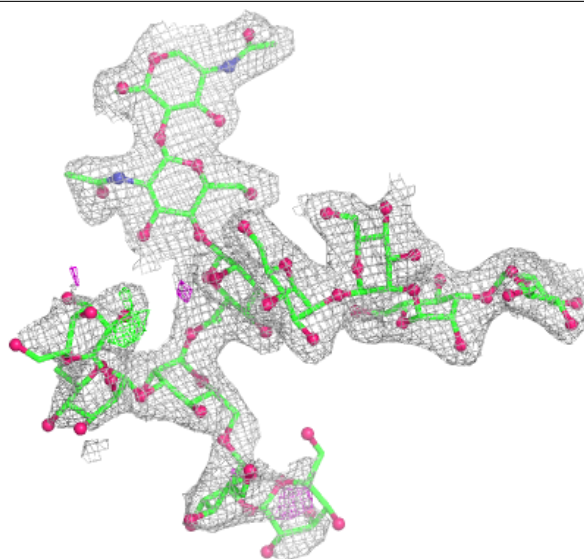
Electron density around Chain O:

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



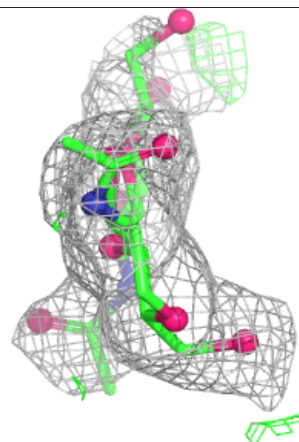
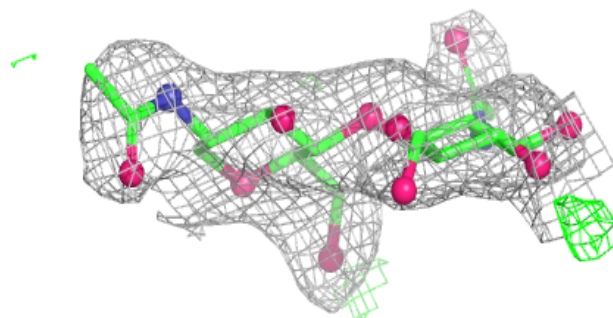
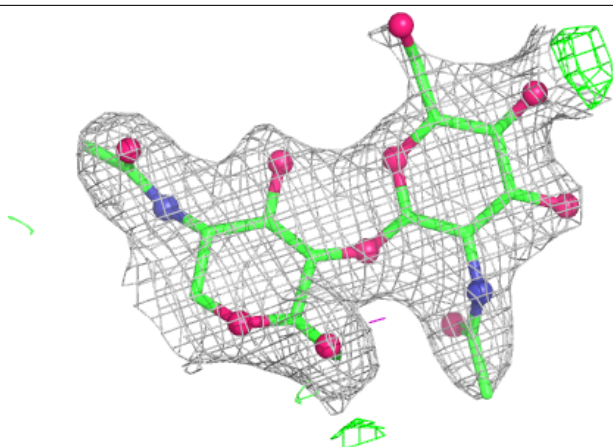
Electron density around Chain Q:

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

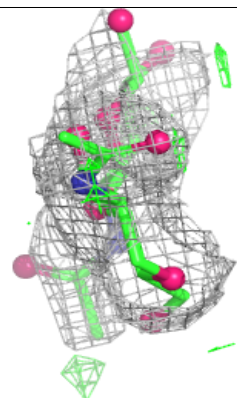
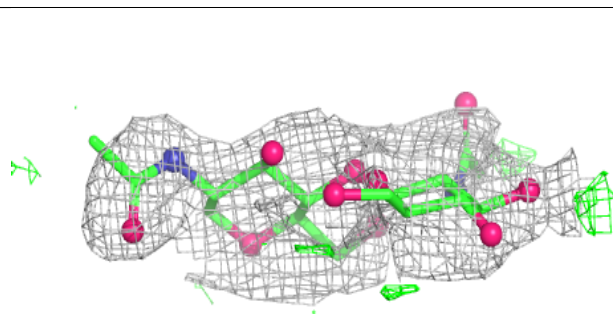
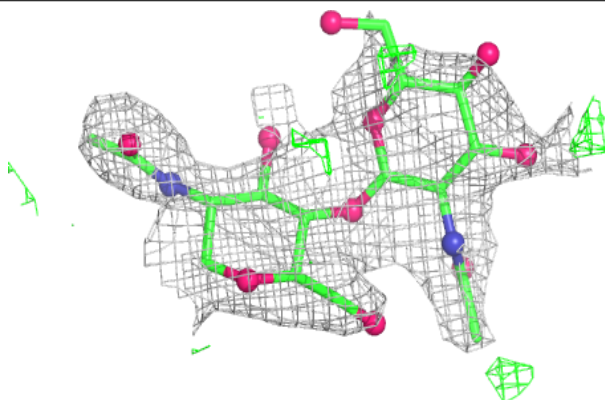


Electron density around Chain H:

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

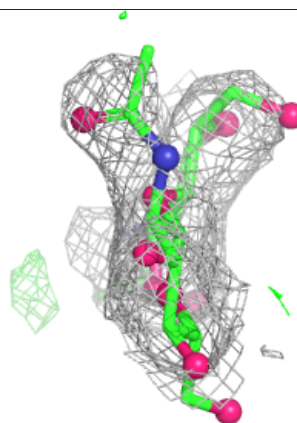
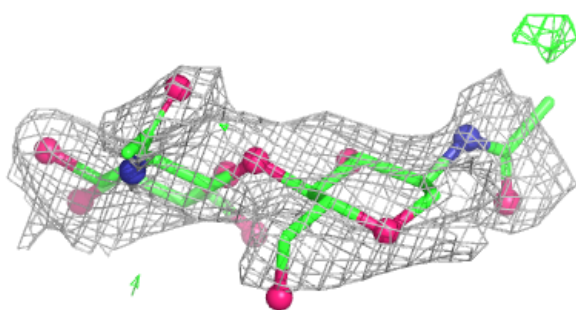
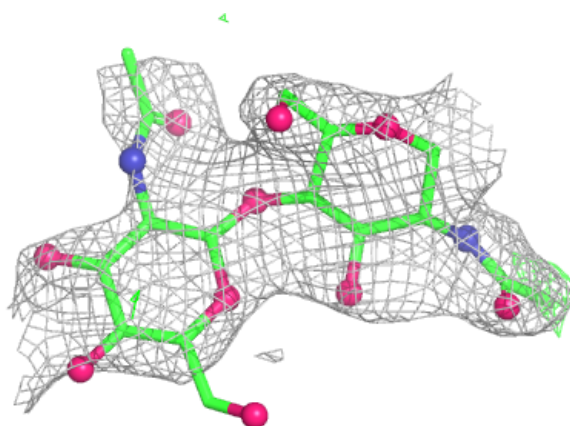
**Electron density around Chain J:**

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



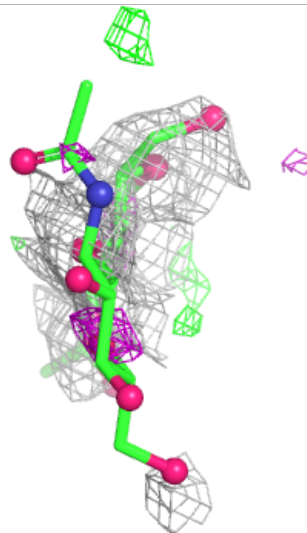
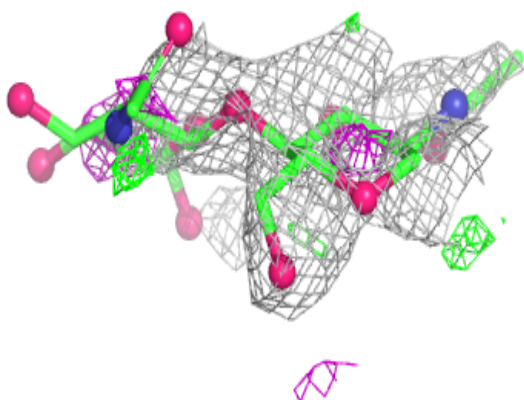
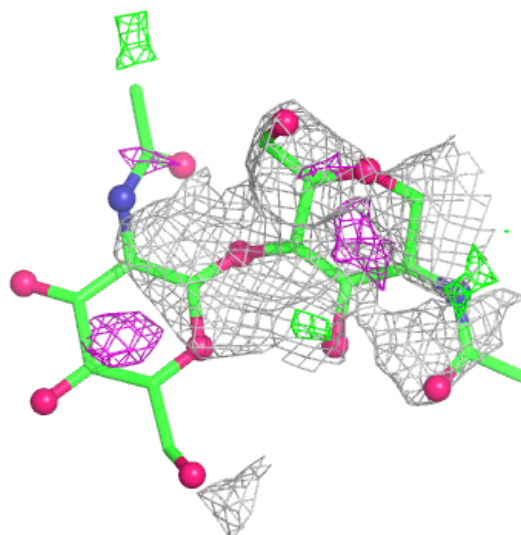
Electron density around Chain L:

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



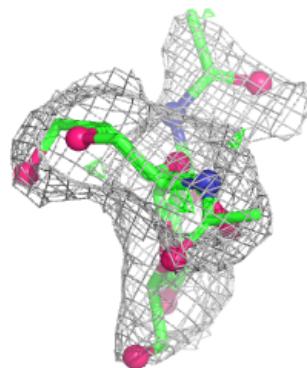
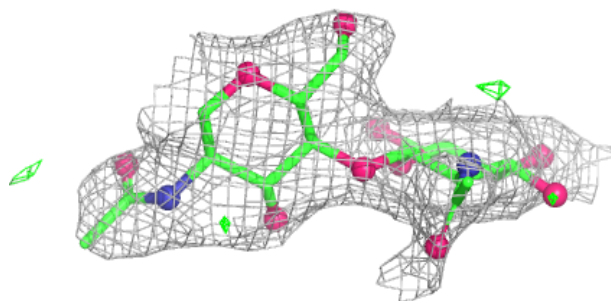
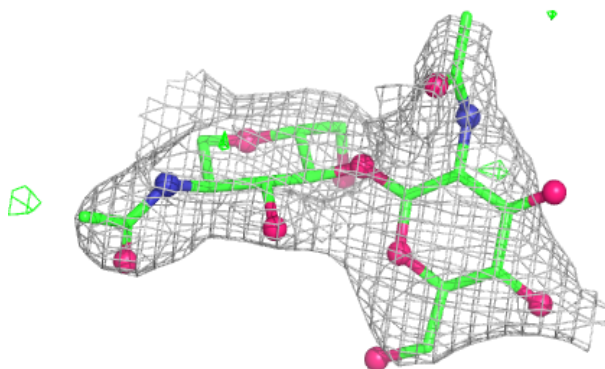
Electron density around Chain N:

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

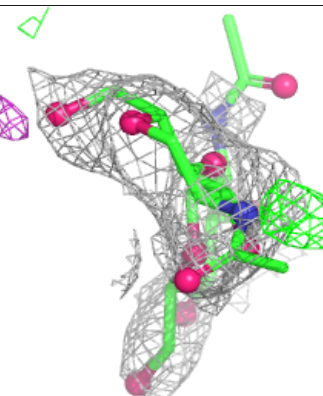
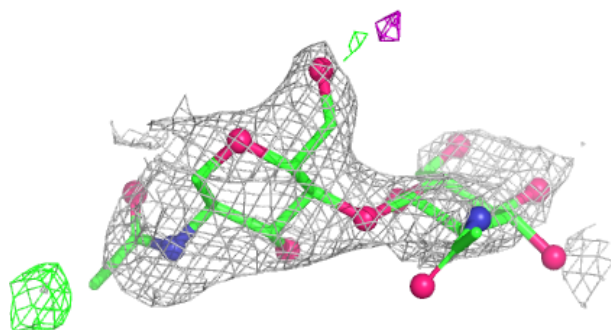
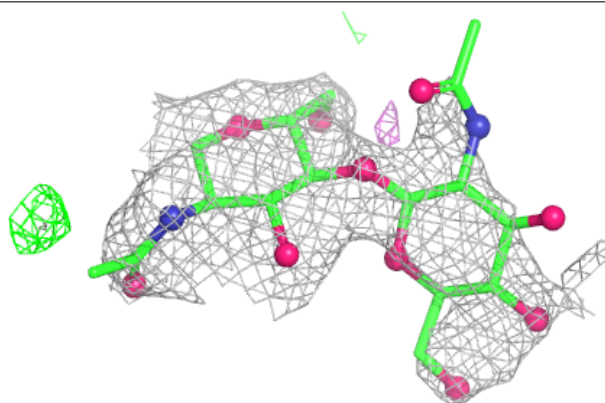


Electron density around Chain P:

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

**Electron density around Chain R:**

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



6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	FMT	C	2004	3/3	0.96	0.06	23,23,25,28	0
4	FMT	F	2006	3/3	0.97	0.04	23,23,26,26	0
4	FMT	D	2001	3/3	0.98	0.05	30,30,31,33	0
4	FMT	E	2005	3/3	0.98	0.04	12,12,16,18	0
4	FMT	B	2002	3/3	0.98	0.07	21,21,22,23	0
4	FMT	A	2003	3/3	0.99	0.03	22,22,29,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.