



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 05:01 PM UTC

PDB ID : 3WO3 / pdb_00003wo3
Title : Crystal structure of IL-18 in complex with IL-18 receptor alpha
Authors : Tsutsumi, N.; Kimura, T.; Arita, K.; Ariyoshi, M.; Ohnishi, H.; Kondo, N.; Shirakawa, M.; Kato, Z.; Tochio, H.
Deposited on : 2013-12-19
Resolution : 3.10 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

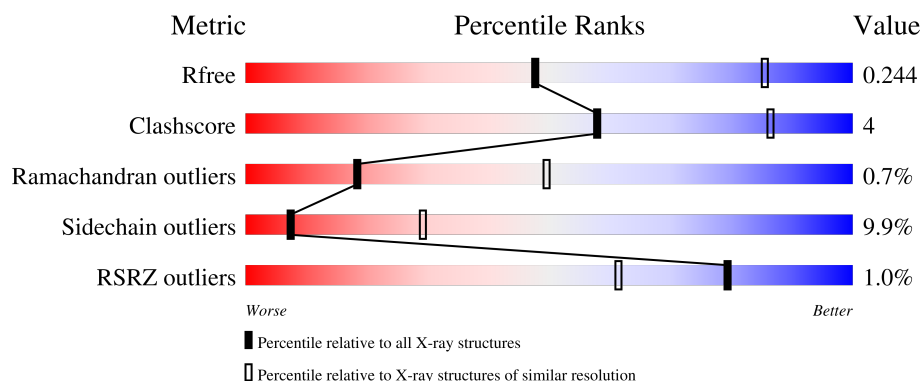
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



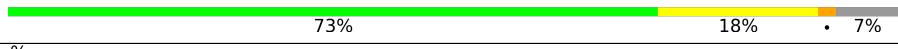
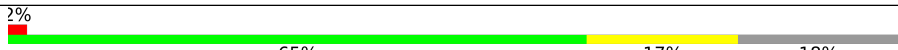
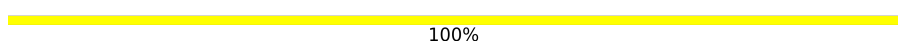
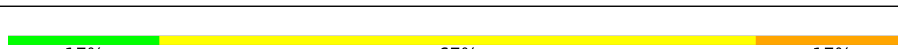
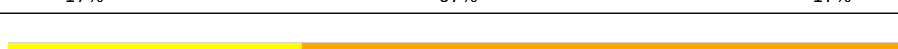
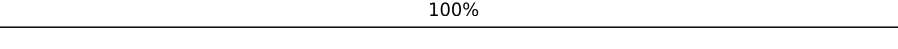
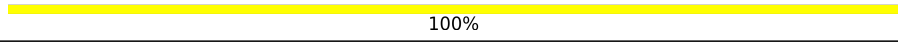
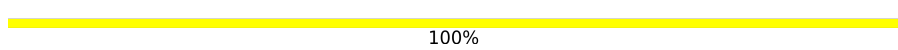
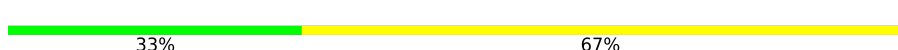
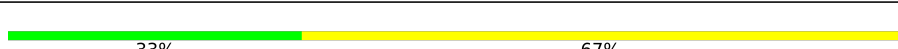
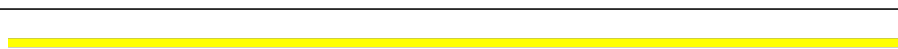
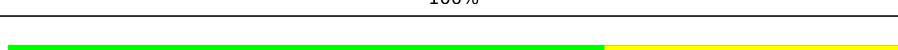
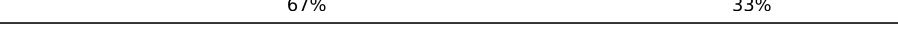
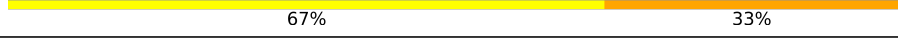
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	157	% 79% 17% ..
1	C	157	83% 13% ..
1	E	157	% 82% 15% .
1	G	157	80% 17% ...
1	I	157	81% 15% ...

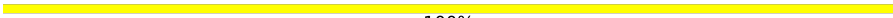
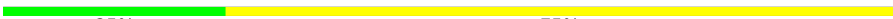
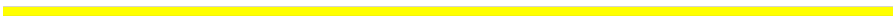
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Mol	Chain	Length	Quality of chain
1	K	157	% 
2	B	312	% 
2	D	312	
2	F	312	% 
2	H	312	% 
2	J	312	3% 
2	L	312	2% 
3	M	3	
3	Q	3	
3	h	3	
4	N	6	
4	W	6	
5	O	2	
5	b	2	
5	g	2	
5	j	2	
5	k	2	
6	P	3	
6	T	3	
6	U	3	
6	X	3	
6	c	3	
6	e	3	
6	f	3	
6	i	3	

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Mol	Chain	Length	Quality of chain
7	R	2	 100%
8	S	5	 100%
8	a	5	 80% 20%
9	V	4	 50% 50%
9	d	4	 25% 75%
9	l	4	 50% 50%
10	Y	4	 100%
11	Z	5	 40% 60%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 22047 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 Interleukin-18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1245	783	207	245	10			
1	C	156	Total	C	N	O	S	0	0	0
			1258	791	209	248	10			
1	E	157	Total	C	N	O	S	0	1	0
			1255	787	208	250	10			
1	G	156	Total	C	N	O	S	0	0	0
			1240	782	208	240	10			
1	I	156	Total	C	N	O	S	0	0	0
			1179	739	195	235	10			
1	K	156	Total	C	N	O	S	0	0	0
			1180	737	197	236	10			

- Molecule 2 is a protein called Interleukin-18 receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	294	Total	C	N	O	S	0	1	0
			2336	1477	403	442	14			
2	D	290	Total	C	N	O	S	0	0	0
			2316	1470	395	437	14			
2	F	288	Total	C	N	O	S	0	1	0
			2280	1445	392	429	14			
2	H	288	Total	C	N	O	S	0	0	0
			2284	1445	391	434	14			
2	J	272	Total	C	N	O	S	0	0	0
			2037	1286	341	397	13			
2	L	255	Total	C	N	O	S	0	0	0
			1923	1213	327	370	13			

There are 12 discrepancies between the modelled and reference sequences:

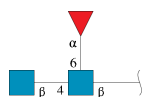
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP Q13478

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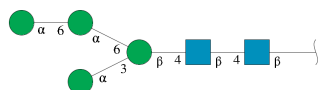
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	PRO	-	expression tag	UNP Q13478
D	-2	GLY	-	expression tag	UNP Q13478
D	-1	PRO	-	expression tag	UNP Q13478
F	-2	GLY	-	expression tag	UNP Q13478
F	-1	PRO	-	expression tag	UNP Q13478
H	-2	GLY	-	expression tag	UNP Q13478
H	-1	PRO	-	expression tag	UNP Q13478
J	-2	GLY	-	expression tag	UNP Q13478
J	-1	PRO	-	expression tag	UNP Q13478
L	-2	GLY	-	expression tag	UNP Q13478
L	-1	PRO	-	expression tag	UNP Q13478

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	M	3	Total	C	N	O	0	0	0
			38	22	2	14			
3	Q	3	Total	C	N	O	0	0	0
			38	22	2	14			
3	h	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-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	N	6	Total	C	N	O	0	0	0
			72	40	2	30			
4	W	6	Total	C	N	O	0	0	0
			72	40	2	30			

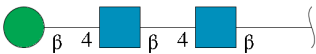
- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a

cetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	O	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	b	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	g	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	j	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	k	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	P	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	T	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	U	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	X	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	c	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	e	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	f	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	i	3	Total	C	N	O	0	0	0
			39	22	2	15			

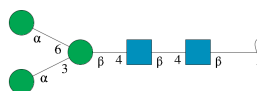
- Molecule 7 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-bet

α -D-glucopyranose.



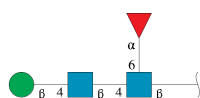
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	R	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 8 is an oligosaccharide called α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose.



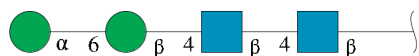
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	S	5	Total	C	N	O	0	0	0
			61	34	2	25			
8	a	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 9 is an oligosaccharide called β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-[α -L-fucopyranose-(1-6)]2-acetamido-2-deoxy- β -D-glucopyranose.



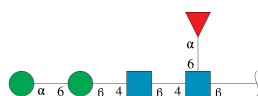
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	V	4	Total	C	N	O	0	0	0
			49	28	2	19			
9	d	4	Total	C	N	O	0	0	0
			49	28	2	19			
9	l	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 10 is an oligosaccharide called α -D-mannopyranose-(1-6)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose.



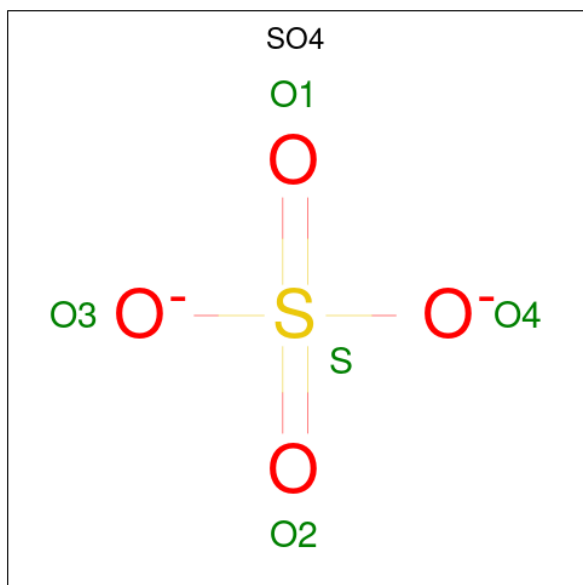
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	Y	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 12 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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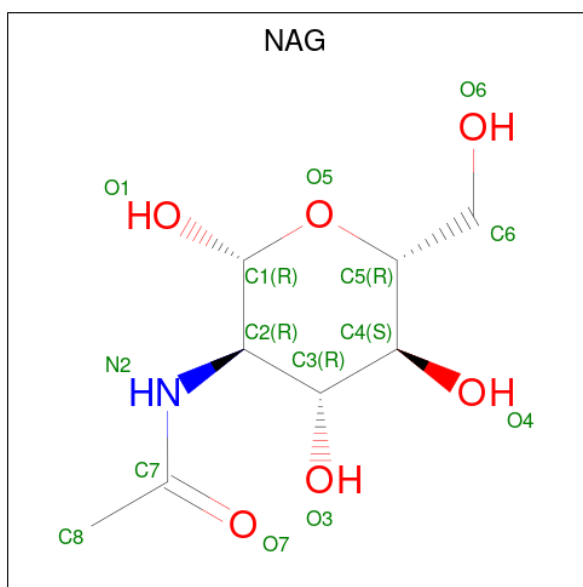
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	O	S	0	0
			5	4	1		
12	B	1	Total	O	S	0	0
			5	4	1		
12	B	1	Total	O	S	0	0
			5	4	1		
12	B	1	Total	O	S	0	0
			5	4	1		
12	B	1	Total	O	S	0	0
			5	4	1		
12	C	1	Total	O	S	0	0
			5	4	1		
12	C	1	Total	O	S	0	0
			5	4	1		
12	C	1	Total	O	S	0	0
			5	4	1		
12	C	1	Total	O	S	0	0
			5	4	1		
12	C	1	Total	O	S	0	0
			5	4	1		
12	D	1	Total	O	S	0	0
			5	4	1		
12	D	1	Total	O	S	0	0
			5	4	1		
12	D	1	Total	O	S	0	0
			5	4	1		
12	D	1	Total	O	S	0	0
			5	4	1		
12	D	1	Total	O	S	0	0
			5	4	1		
12	D	1	Total	O	S	0	0
			5	4	1		
12	E	1	Total	O	S	0	0
			5	4	1		
12	E	1	Total	O	S	0	0
			5	4	1		
12	E	1	Total	O	S	0	0
			5	4	1		
12	F	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	F	1	Total	O	S	0	0
			5	4	1		
12	F	1	Total	O	S	0	0
			5	4	1		
12	F	1	Total	O	S	0	0
			5	4	1		
12	F	1	Total	O	S	0	0
			5	4	1		
12	G	1	Total	O	S	0	0
			5	4	1		
12	G	1	Total	O	S	0	0
			5	4	1		
12	H	1	Total	O	S	0	0
			5	4	1		
12	H	1	Total	O	S	0	0
			5	4	1		
12	H	1	Total	O	S	0	0
			5	4	1		
12	H	1	Total	O	S	0	0
			5	4	1		
12	H	1	Total	O	S	0	0
			5	4	1		
12	I	1	Total	O	S	0	0
			5	4	1		
12	J	1	Total	O	S	0	0
			5	4	1		
12	K	1	Total	O	S	0	0
			5	4	1		
12	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	15	Total	O	0	0
			15	15		
14	B	10	Total	O	0	0
			10	10		
14	C	9	Total	O	0	0
			9	9		
14	D	18	Total	O	0	0
			18	18		

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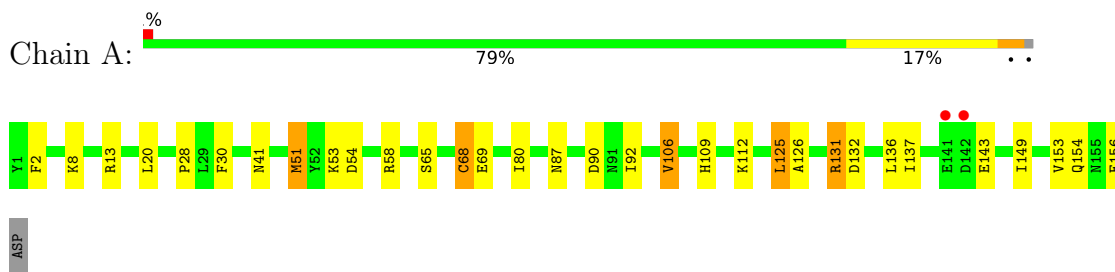
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	E	5	Total 5	O 5	0	0
14	F	12	Total 12	O 12	0	0
14	G	3	Total 3	O 3	0	0
14	H	11	Total 11	O 11	0	0
14	I	6	Total 6	O 6	0	0
14	J	3	Total 3	O 3	0	0
14	K	1	Total 1	O 1	0	0
14	L	6	Total 6	O 6	0	0

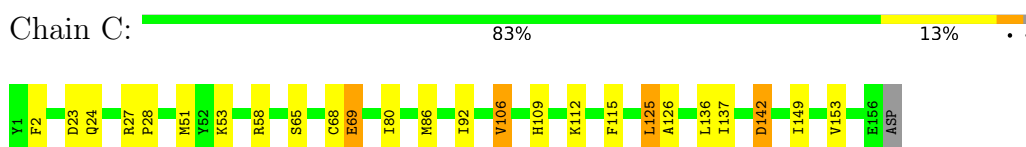
3 Residue-property plots

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.

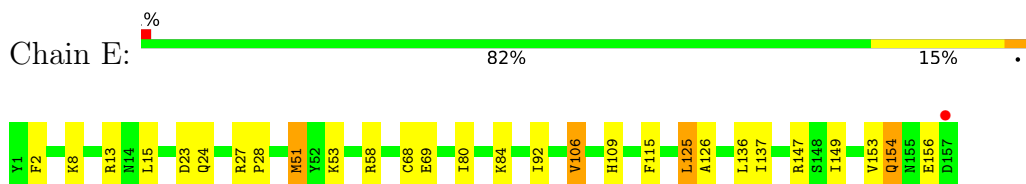
- Molecule 1: Interleukin-18



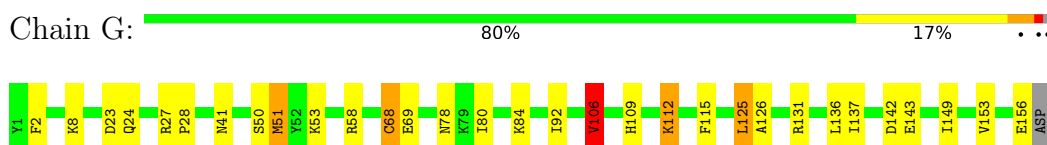
- Molecule 1: Interleukin-18



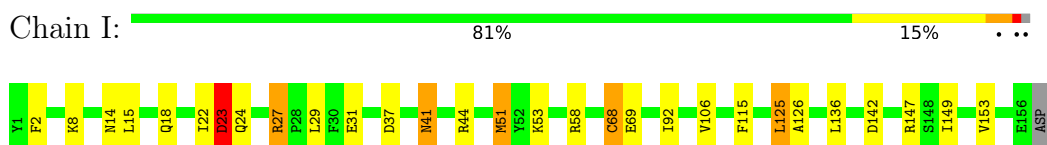
- Molecule 1: Interleukin-18



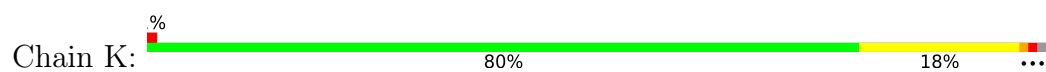
- Molecule 1: Interleukin-18



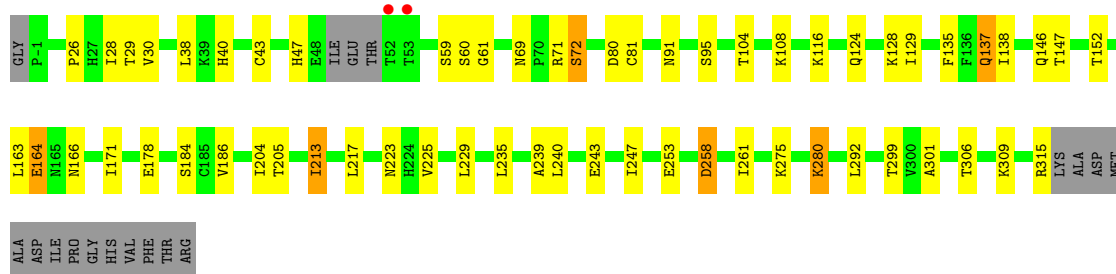
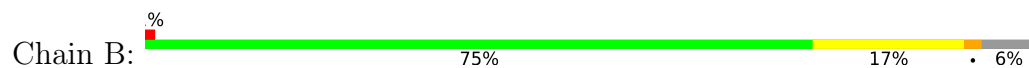
- Molecule 1: Interleukin-18



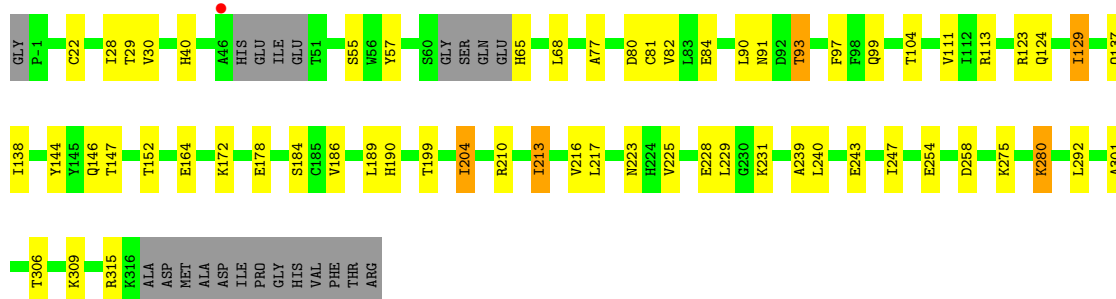
- Molecule 1: Interleukin-18



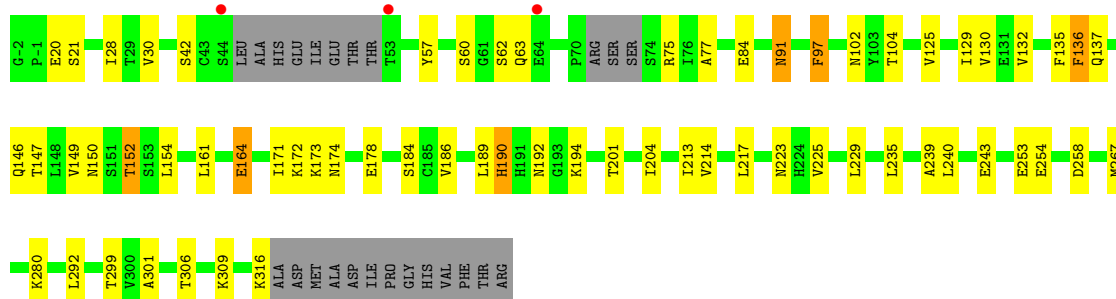
• Molecule 2: Interleukin-18 receptor 1



• Molecule 2: Interleukin-18 receptor 1

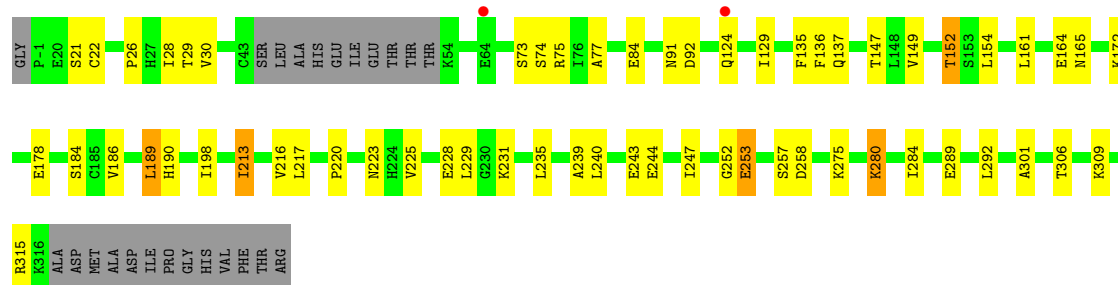


• Molecule 2: Interleukin-18 receptor 1

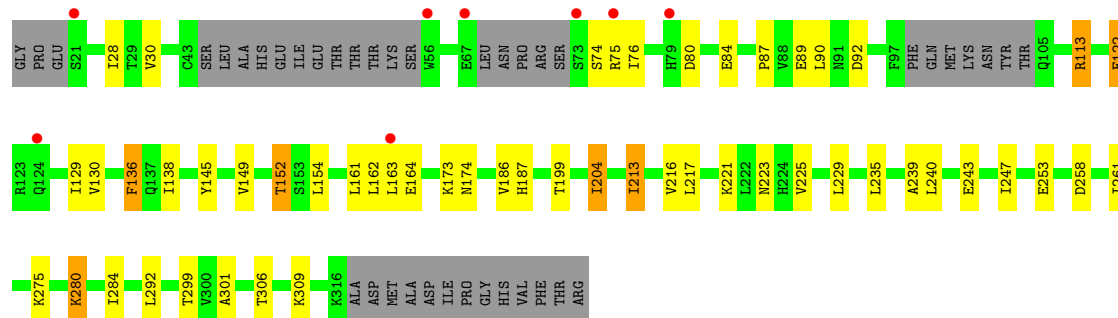


• Molecule 2: Interleukin-18 receptor 1

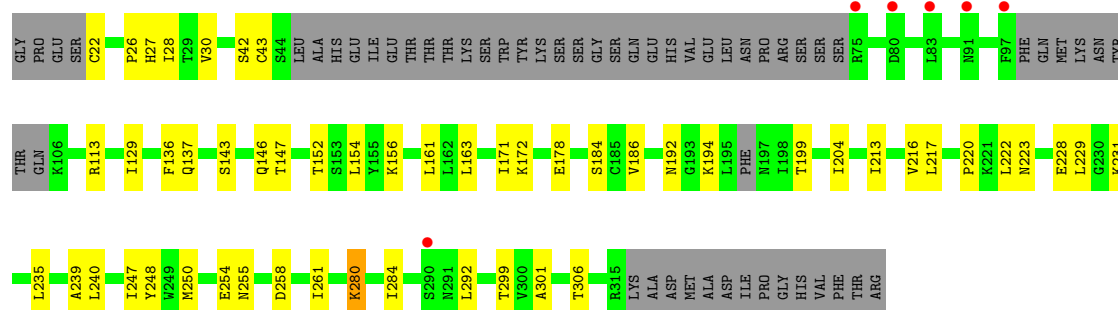




• Molecule 2: Interleukin-18 receptor 1



• Molecule 2: Interleukin-18 receptor 1



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



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





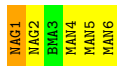
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h:



- Molecule 4: alpha-D-mannopyranose-(1-6)-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 N:



- Molecule 4: alpha-D-mannopyranose-(1-6)-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 W:



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b:



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:

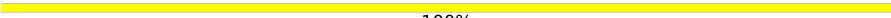


- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:  50% 50%

MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain k:  100%

MAG1
MAG2

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

Chain P:  33% 67%

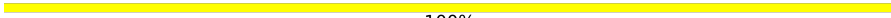
MAG1
MAG2
EMA3

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

Chain T:  33% 67%

MAG1
MAG2
EMA3

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

Chain U:  100%

MAG1
MAG2
EMA3

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

Chain X:  67% 33%

MAG1
MAG2
EMA3

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

Chain c:  67% 33%



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

Chain e:



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

Chain f:



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

Chain i:



- Molecule 7: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:



- Molecule 8: 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 S:



- Molecule 8: 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 a:

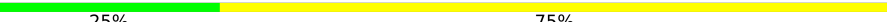


- Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:  50% 50%

NAG1
NAG2
BMA3
FUC4

- Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:  25% 75%

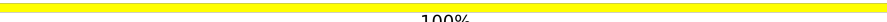
NAG1
NAG2
BMA3
FUC4

- Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain l:  50% 50%

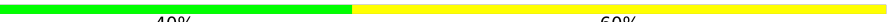
NAG1
NAG2
BMA3
FUC4

- Molecule 10: 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 Y:  100%

NAG1
NAG2
BMA3
MAN4

- Molecule 11: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:  40% 60%

NAG1
NAG2
BMA3
MAN4
FUC5

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.49Å 174.81Å 183.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.25 – 3.10 31.25 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (31.25-3.10) 99.3 (31.25-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 3.12Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.191 , 0.222 0.210 , 0.244	Depositor DCC
R_{free} test set	3974 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	69.6	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 94.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.028 for -h,l,k	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	22047	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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: FUC, NAG, MAN, SO4, 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	0.84	0/1266	1.14	2/1701 (0.1%)
1	C	0.87	0/1279	1.16	1/1717 (0.1%)
1	E	0.79	0/1279	1.14	0/1719
1	G	0.88	0/1261	1.14	2/1695 (0.1%)
1	I	0.79	0/1200	1.13	2/1625 (0.1%)
1	K	0.81	0/1200	1.15	4/1622 (0.2%)
2	B	0.79	0/2390	1.17	2/3244 (0.1%)
2	D	0.79	0/2368	1.17	3/3209 (0.1%)
2	F	0.78	1/2335 (0.0%)	1.17	5/3166 (0.2%)
2	H	0.79	0/2337	1.13	7/3174 (0.2%)
2	J	0.78	0/2077	1.22	10/2830 (0.4%)
2	L	0.76	0/1964	1.14	4/2677 (0.1%)
All	All	0.80	1/20956 (0.0%)	1.16	42/28379 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	267	MET	SD-CE	7.06	1.97	1.79

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	142	ASP	CA-CB-CG	7.22	119.83	112.60
1	A	54	ASP	CA-CB-CG	6.64	119.24	112.60
2	J	92	ASP	CA-C-N	6.61	130.53	120.82
2	J	92	ASP	C-N-CA	6.61	130.53	120.82
2	B	72	SER	N-CA-C	-6.56	104.06	111.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1245	0	1207	14	0
1	C	1258	0	1233	11	0
1	E	1255	0	1206	12	0
1	G	1240	0	1210	15	0
1	I	1179	0	1066	14	0
1	K	1180	0	1074	16	0
2	B	2336	0	2208	18	0
2	D	2316	0	2233	22	0
2	F	2280	0	2166	16	0
2	H	2284	0	2154	22	0
2	J	2037	0	1832	19	0
2	L	1923	0	1715	17	0
3	M	38	0	34	0	0
3	Q	38	0	34	0	0
3	h	38	0	34	0	0
4	N	72	0	61	1	0
4	W	72	0	61	3	0
5	O	28	0	25	0	0
5	b	28	0	25	0	0
5	g	28	0	25	0	0
5	j	28	0	25	0	0
5	k	28	0	25	0	0
6	P	39	0	34	0	0
6	T	39	0	34	0	0
6	U	39	0	34	0	0
6	X	39	0	34	0	0
6	c	39	0	34	0	0
6	e	39	0	34	1	0
6	f	39	0	34	0	0
6	i	39	0	34	1	0
7	R	24	0	22	1	0
8	S	61	0	52	0	0
8	a	61	0	52	1	0
9	V	49	0	43	0	0
9	d	49	0	43	0	0
9	l	49	0	43	2	0
10	Y	50	0	43	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Z	60	0	52	1	0
12	A	10	0	0	0	0
12	B	25	0	0	0	0
12	C	25	0	0	0	0
12	D	35	0	0	0	0
12	E	15	0	0	0	0
12	F	25	0	0	1	0
12	G	10	0	0	0	0
12	H	25	0	0	1	0
12	I	5	0	0	0	0
12	J	5	0	0	0	0
12	K	5	0	0	0	0
12	L	5	0	0	0	0
13	B	28	0	26	0	0
13	D	14	0	13	0	0
13	F	28	0	26	0	0
13	H	28	0	26	0	0
13	J	14	0	13	0	0
14	A	15	0	0	1	0
14	B	10	0	0	0	0
14	C	9	0	0	0	0
14	D	18	0	0	0	0
14	E	5	0	0	0	0
14	F	12	0	0	0	0
14	G	3	0	0	0	0
14	H	11	0	0	0	0
14	I	6	0	0	0	0
14	J	3	0	0	0	0
14	K	1	0	0	0	0
14	L	6	0	0	0	0
All	All	22047	0	20379	190	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 190 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:221:LYS:HG2	11:Z:2:NAG:H83	1.73	0.70
2:D:90:LEU:O	2:D:93:THR:HG23	1.92	0.70
1:G:106:VAL:HG22	1:G:109:HIS:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:106:VAL:HG22	1:E:109:HIS:HB2	1.76	0.68
1:K:41:ASN:HD21	2:L:27:HIS:H	1.41	0.67

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	154/157 (98%)	145 (94%)	9 (6%)	0	100	100
1	C	154/157 (98%)	145 (94%)	8 (5%)	1 (1%)	21	52
1	E	156/157 (99%)	148 (95%)	8 (5%)	0	100	100
1	G	154/157 (98%)	144 (94%)	10 (6%)	0	100	100
1	I	154/157 (98%)	143 (93%)	11 (7%)	0	100	100
1	K	154/157 (98%)	143 (93%)	11 (7%)	0	100	100
2	B	291/312 (93%)	278 (96%)	10 (3%)	3 (1%)	12	41
2	D	284/312 (91%)	274 (96%)	9 (3%)	1 (0%)	30	61
2	F	283/312 (91%)	266 (94%)	13 (5%)	4 (1%)	9	34
2	H	284/312 (91%)	270 (95%)	12 (4%)	2 (1%)	18	49
2	J	264/312 (85%)	240 (91%)	21 (8%)	3 (1%)	11	39
2	L	247/312 (79%)	237 (96%)	6 (2%)	4 (2%)	7	30
All	All	2579/2814 (92%)	2433 (94%)	128 (5%)	18 (1%)	18	49

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	61	GLY
2	B	164	GLU
2	F	42	SER

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Mol	Chain	Res	Type
1	C	142	ASP
2	F	20	GLU

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	141/148 (95%)	129 (92%)	12 (8%)	10	35
1	C	145/148 (98%)	134 (92%)	11 (8%)	12	39
1	E	142/148 (96%)	130 (92%)	12 (8%)	10	35
1	G	140/148 (95%)	126 (90%)	14 (10%)	7	29
1	I	124/148 (84%)	114 (92%)	10 (8%)	11	36
1	K	125/148 (84%)	115 (92%)	10 (8%)	11	37
2	B	259/288 (90%)	228 (88%)	31 (12%)	5	21
2	D	262/288 (91%)	235 (90%)	27 (10%)	7	27
2	F	253/288 (88%)	219 (87%)	34 (13%)	4	17
2	H	254/288 (88%)	233 (92%)	21 (8%)	10	35
2	J	212/288 (74%)	192 (91%)	20 (9%)	8	31
2	L	199/288 (69%)	178 (89%)	21 (11%)	6	26
All	All	2256/2616 (86%)	2033 (90%)	223 (10%)	7	29

5 of 223 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	201	THR
2	L	280	LYS
2	H	28	ILE
2	L	240	LEU
1	K	133	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	102	ASN
1	I	114	GLN
2	L	224	HIS
2	H	124	GLN
2	H	192	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 ⓘ

88 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	M	1	2,3	14,14,15	0.32	0	17,19,21	0.71	1 (5%)
3	NAG	M	2	3	14,14,15	0.35	0	17,19,21	1.18	2 (11%)
3	FUC	M	3	3	10,10,11	0.46	0	14,14,16	0.78	1 (7%)
4	NAG	N	1	2,4	14,14,15	0.28	0	17,19,21	0.86	1 (5%)
4	NAG	N	2	4	14,14,15	0.27	0	17,19,21	1.05	2 (11%)
4	BMA	N	3	4	11,11,12	0.34	0	15,15,17	0.56	0
4	MAN	N	4	4	11,11,12	0.45	0	15,15,17	1.01	1 (6%)
4	MAN	N	5	4	11,11,12	0.37	0	15,15,17	0.84	1 (6%)
4	MAN	N	6	4	11,11,12	0.45	0	15,15,17	0.85	1 (6%)
5	NAG	O	1	2,5	14,14,15	0.27	0	17,19,21	0.77	1 (5%)
5	NAG	O	2	5	14,14,15	0.30	0	17,19,21	0.76	1 (5%)
6	NAG	P	1	2,6	14,14,15	0.34	0	17,19,21	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	P	2	6	14,14,15	0.32	0	17,19,21	1.34	2 (11%)
6	BMA	P	3	6	11,11,12	0.49	0	15,15,17	1.06	2 (13%)
3	NAG	Q	1	2,3	14,14,15	0.29	0	17,19,21	0.90	1 (5%)
3	NAG	Q	2	3	14,14,15	0.29	0	17,19,21	0.57	0
3	FUC	Q	3	3	10,10,11	0.43	0	14,14,16	0.59	0
7	NAG	R	1	2,7	14,14,15	0.31	0	17,19,21	0.72	1 (5%)
7	FUC	R	2	7	10,10,11	0.43	0	14,14,16	0.67	0
8	NAG	S	1	2,8	14,14,15	0.23	0	17,19,21	0.91	1 (5%)
8	NAG	S	2	8	14,14,15	0.25	0	17,19,21	1.05	2 (11%)
8	BMA	S	3	8	11,11,12	0.32	0	15,15,17	0.76	1 (6%)
8	MAN	S	4	8	11,11,12	0.40	0	15,15,17	0.86	1 (6%)
8	MAN	S	5	8	11,11,12	0.42	0	15,15,17	0.87	1 (6%)
6	NAG	T	1	2,6	14,14,15	0.28	0	17,19,21	0.76	1 (5%)
6	NAG	T	2	6	14,14,15	0.31	0	17,19,21	0.70	0
6	BMA	T	3	6	11,11,12	0.36	0	15,15,17	0.60	1 (6%)
6	NAG	U	1	2,6	14,14,15	0.32	0	17,19,21	0.92	1 (5%)
6	NAG	U	2	6	14,14,15	0.29	0	17,19,21	1.46	2 (11%)
6	BMA	U	3	6	11,11,12	0.39	0	15,15,17	0.90	1 (6%)
9	NAG	V	1	2,9	14,14,15	0.32	0	17,19,21	1.03	1 (5%)
9	NAG	V	2	9	14,14,15	0.33	0	17,19,21	0.57	0
9	BMA	V	3	9	11,11,12	0.37	0	15,15,17	0.72	1 (6%)
9	FUC	V	4	9	10,10,11	0.43	0	14,14,16	0.52	0
4	NAG	W	1	2,4	14,14,15	0.26	0	17,19,21	0.86	1 (5%)
4	NAG	W	2	4	14,14,15	0.28	0	17,19,21	1.06	2 (11%)
4	BMA	W	3	4	11,11,12	0.33	0	15,15,17	0.83	1 (6%)
4	MAN	W	4	4	11,11,12	0.32	0	15,15,17	0.87	1 (6%)
4	MAN	W	5	4	11,11,12	0.41	0	15,15,17	0.84	1 (6%)
4	MAN	W	6	4	11,11,12	0.51	0	15,15,17	1.21	1 (6%)
6	NAG	X	1	2,6	14,14,15	0.22	0	17,19,21	0.73	1 (5%)
6	NAG	X	2	6	14,14,15	0.28	0	17,19,21	0.69	0
6	BMA	X	3	6	11,11,12	0.32	0	15,15,17	0.48	0
10	NAG	Y	1	2,10	14,14,15	0.31	0	17,19,21	0.95	1 (5%)
10	NAG	Y	2	10	14,14,15	0.28	0	17,19,21	1.13	2 (11%)
10	BMA	Y	3	10	11,11,12	0.40	0	15,15,17	0.83	1 (6%)
10	MAN	Y	4	10	11,11,12	0.38	0	15,15,17	0.95	1 (6%)
11	NAG	Z	1	2,11	14,14,15	0.29	0	17,19,21	1.02	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	NAG	Z	2	11	14,14,15	0.33	0	17,19,21	0.55	0
11	BMA	Z	3	11	11,11,12	0.42	0	15,15,17	0.77	1 (6%)
11	MAN	Z	4	11	11,11,12	0.51	0	15,15,17	0.78	0
11	FUC	Z	5	11	10,10,11	0.38	0	14,14,16	0.57	0
8	NAG	a	1	2,8	14,14,15	0.27	0	17,19,21	0.86	1 (5%)
8	NAG	a	2	8	14,14,15	0.25	0	17,19,21	1.03	2 (11%)
8	BMA	a	3	8	11,11,12	0.28	0	15,15,17	0.95	1 (6%)
8	MAN	a	4	8	11,11,12	0.42	0	15,15,17	0.87	1 (6%)
8	MAN	a	5	8	11,11,12	0.41	0	15,15,17	0.92	1 (6%)
5	NAG	b	1	2,5	14,14,15	0.27	0	17,19,21	0.66	0
5	NAG	b	2	5	14,14,15	0.30	0	17,19,21	0.72	1 (5%)
6	NAG	c	1	2,6	14,14,15	0.36	0	17,19,21	0.86	0
6	NAG	c	2	6	14,14,15	0.35	0	17,19,21	1.33	1 (5%)
6	BMA	c	3	6	11,11,12	0.47	0	15,15,17	0.77	0
9	NAG	d	1	2,9	14,14,15	0.32	0	17,19,21	1.05	1 (5%)
9	NAG	d	2	9	14,14,15	0.31	0	17,19,21	0.67	1 (5%)
9	BMA	d	3	9	11,11,12	0.47	0	15,15,17	0.90	1 (6%)
9	FUC	d	4	9	10,10,11	0.40	0	14,14,16	0.55	0
6	NAG	e	1	2,6	14,14,15	0.27	0	17,19,21	0.77	1 (5%)
6	NAG	e	2	6	14,14,15	0.32	0	17,19,21	2.01	4 (23%)
6	BMA	e	3	6	11,11,12	0.32	0	15,15,17	0.77	1 (6%)
6	NAG	f	1	2,6	14,14,15	0.27	0	17,19,21	0.54	0
6	NAG	f	2	6	14,14,15	0.29	0	17,19,21	0.72	0
6	BMA	f	3	6	11,11,12	0.35	0	15,15,17	0.53	0
5	NAG	g	1	2,5	14,14,15	0.32	0	17,19,21	0.86	1 (5%)
5	NAG	g	2	5	14,14,15	0.29	0	17,19,21	1.28	2 (11%)
3	NAG	h	1	2,3	14,14,15	0.29	0	17,19,21	0.99	2 (11%)
3	NAG	h	2	3	14,14,15	0.31	0	17,19,21	0.55	0
3	FUC	h	3	3	10,10,11	0.41	0	14,14,16	0.54	0
6	NAG	i	1	2,6	14,14,15	0.27	0	17,19,21	0.79	1 (5%)
6	NAG	i	2	6	14,14,15	0.26	0	17,19,21	1.07	2 (11%)
6	BMA	i	3	6	11,11,12	0.33	0	15,15,17	0.51	0
5	NAG	j	1	2,5	14,14,15	0.30	0	17,19,21	0.79	1 (5%)
5	NAG	j	2	5	14,14,15	0.29	0	17,19,21	0.61	0
5	NAG	k	1	2,5	14,14,15	0.32	0	17,19,21	0.89	1 (5%)
5	NAG	k	2	5	14,14,15	0.30	0	17,19,21	0.97	1 (5%)
9	NAG	l	1	2,9	14,14,15	0.31	0	17,19,21	0.94	1 (5%)
9	NAG	l	2	9	14,14,15	0.35	0	17,19,21	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	BMA	1	3	9	11,11,12	0.36	0	15,15,17	0.57	0
9	FUC	1	4	9	10,10,11	0.38	0	14,14,16	0.54	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	M	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	1/6/23/26	0/1/1/1
3	FUC	M	3	3	-	-	0/1/1/1
4	NAG	N	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	1/6/23/26	0/1/1/1
4	BMA	N	3	4	-	2/2/19/22	0/1/1/1
4	MAN	N	4	4	-	1/2/19/22	0/1/1/1
4	MAN	N	5	4	-	0/2/19/22	0/1/1/1
4	MAN	N	6	4	-	0/2/19/22	0/1/1/1
5	NAG	O	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1
6	NAG	P	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	P	2	6	-	1/6/23/26	0/1/1/1
6	BMA	P	3	6	-	2/2/19/22	0/1/1/1
3	NAG	Q	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	2/6/23/26	0/1/1/1
3	FUC	Q	3	3	-	-	0/1/1/1
7	NAG	R	1	2,7	-	0/6/23/26	0/1/1/1
7	FUC	R	2	7	-	-	0/1/1/1
8	NAG	S	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	S	2	8	-	1/6/23/26	0/1/1/1
8	BMA	S	3	8	-	2/2/19/22	0/1/1/1
8	MAN	S	4	8	-	0/2/19/22	0/1/1/1
8	MAN	S	5	8	-	1/2/19/22	1/1/1/1
6	NAG	T	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	T	2	6	-	0/6/23/26	0/1/1/1
6	BMA	T	3	6	-	0/2/19/22	0/1/1/1
6	NAG	U	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	U	2	6	-	1/6/23/26	0/1/1/1
6	BMA	U	3	6	-	2/2/19/22	0/1/1/1
9	NAG	V	1	2,9	-	0/6/23/26	0/1/1/1
9	NAG	V	2	9	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	BMA	V	3	9	-	0/2/19/22	0/1/1/1
9	FUC	V	4	9	-	-	0/1/1/1
4	NAG	W	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	W	2	4	-	1/6/23/26	0/1/1/1
4	BMA	W	3	4	-	0/2/19/22	0/1/1/1
4	MAN	W	4	4	-	2/2/19/22	0/1/1/1
4	MAN	W	5	4	-	0/2/19/22	0/1/1/1
4	MAN	W	6	4	-	0/2/19/22	1/1/1/1
6	NAG	X	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	X	2	6	-	0/6/23/26	0/1/1/1
6	BMA	X	3	6	-	0/2/19/22	0/1/1/1
10	NAG	Y	1	2,10	-	1/6/23/26	0/1/1/1
10	NAG	Y	2	10	-	0/6/23/26	0/1/1/1
10	BMA	Y	3	10	-	2/2/19/22	0/1/1/1
10	MAN	Y	4	10	-	2/2/19/22	0/1/1/1
11	NAG	Z	1	2,11	-	0/6/23/26	0/1/1/1
11	NAG	Z	2	11	-	2/6/23/26	0/1/1/1
11	BMA	Z	3	11	-	0/2/19/22	0/1/1/1
11	MAN	Z	4	11	-	0/2/19/22	0/1/1/1
11	FUC	Z	5	11	-	-	0/1/1/1
8	NAG	a	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	a	2	8	-	1/6/23/26	0/1/1/1
8	BMA	a	3	8	-	2/2/19/22	0/1/1/1
8	MAN	a	4	8	-	0/2/19/22	0/1/1/1
8	MAN	a	5	8	-	0/2/19/22	0/1/1/1
5	NAG	b	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	b	2	5	-	0/6/23/26	0/1/1/1
6	NAG	c	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	c	2	6	-	1/6/23/26	0/1/1/1
6	BMA	c	3	6	-	0/2/19/22	0/1/1/1
9	NAG	d	1	2,9	-	0/6/23/26	0/1/1/1
9	NAG	d	2	9	-	2/6/23/26	0/1/1/1
9	BMA	d	3	9	-	0/2/19/22	0/1/1/1
9	FUC	d	4	9	-	-	0/1/1/1
6	NAG	e	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	e	2	6	-	2/6/23/26	0/1/1/1
6	BMA	e	3	6	-	0/2/19/22	0/1/1/1
6	NAG	f	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	f	2	6	-	0/6/23/26	0/1/1/1
6	BMA	f	3	6	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	g	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	g	2	5	-	0/6/23/26	0/1/1/1
3	NAG	h	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	h	2	3	-	2/6/23/26	0/1/1/1
3	FUC	h	3	3	-	-	0/1/1/1
6	NAG	i	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	i	2	6	-	0/6/23/26	0/1/1/1
6	BMA	i	3	6	-	0/2/19/22	0/1/1/1
5	NAG	j	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	j	2	5	-	0/6/23/26	0/1/1/1
5	NAG	k	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	k	2	5	-	0/6/23/26	0/1/1/1
9	NAG	l	1	2,9	-	0/6/23/26	0/1/1/1
9	NAG	l	2	9	-	2/6/23/26	0/1/1/1
9	BMA	l	3	9	-	0/2/19/22	0/1/1/1
9	FUC	l	4	9	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	e	2	NAG	C1-C2-N2	6.02	119.92	110.43
6	P	2	NAG	O5-C1-C2	-4.51	104.31	111.29
5	g	2	NAG	O5-C1-C2	-4.39	104.50	111.29
4	W	6	MAN	C1-O5-C5	4.38	118.06	112.19
6	c	2	NAG	O5-C1-C2	-4.37	104.53	111.29

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	e	2	NAG	C1-C2-N2-C7
4	W	4	MAN	O5-C5-C6-O6
6	f	3	BMA	C4-C5-C6-O6
4	W	4	MAN	C4-C5-C6-O6
6	f	3	BMA	O5-C5-C6-O6

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	S	5	MAN	C1-C2-C3-C4-C5-O5

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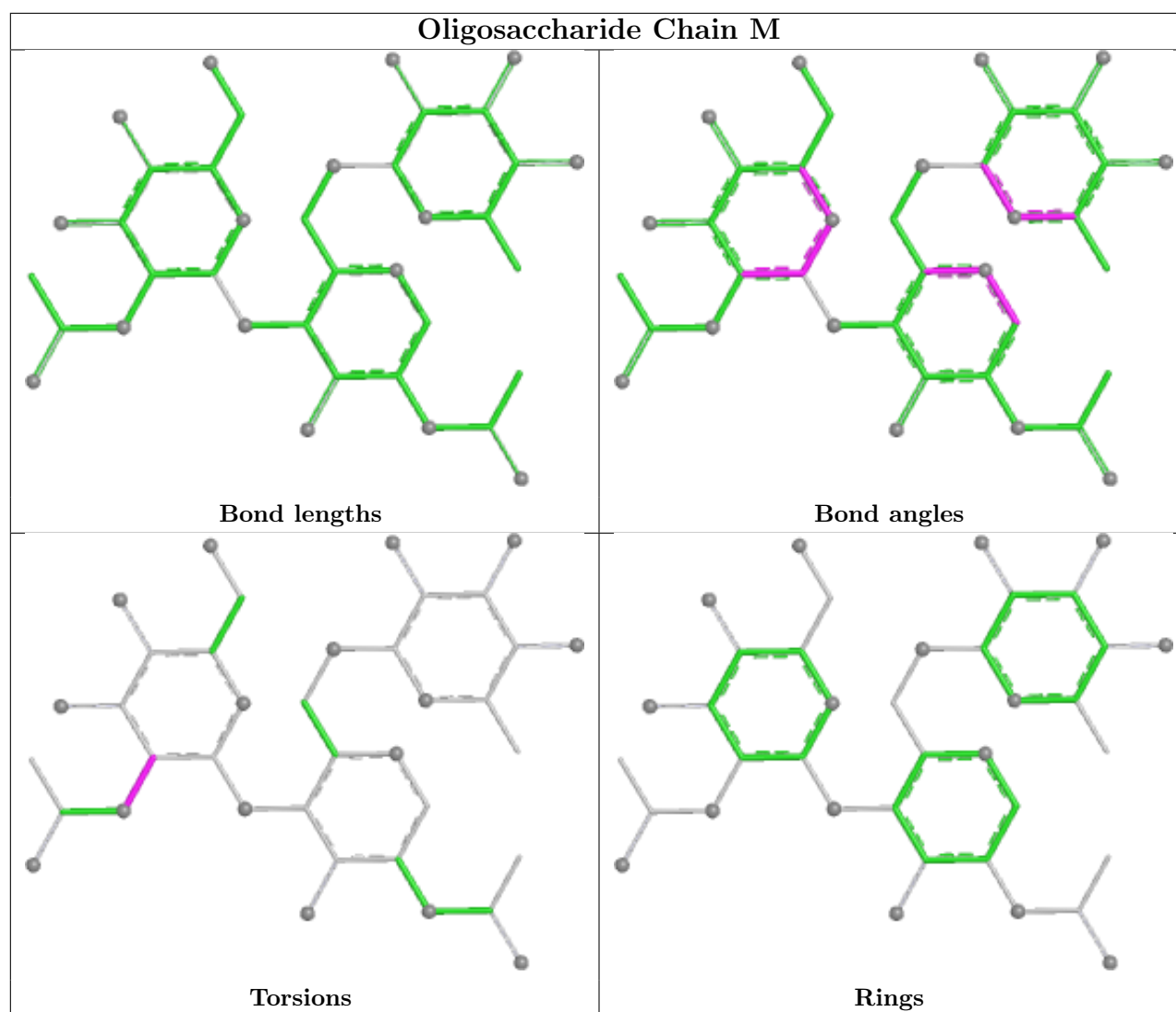
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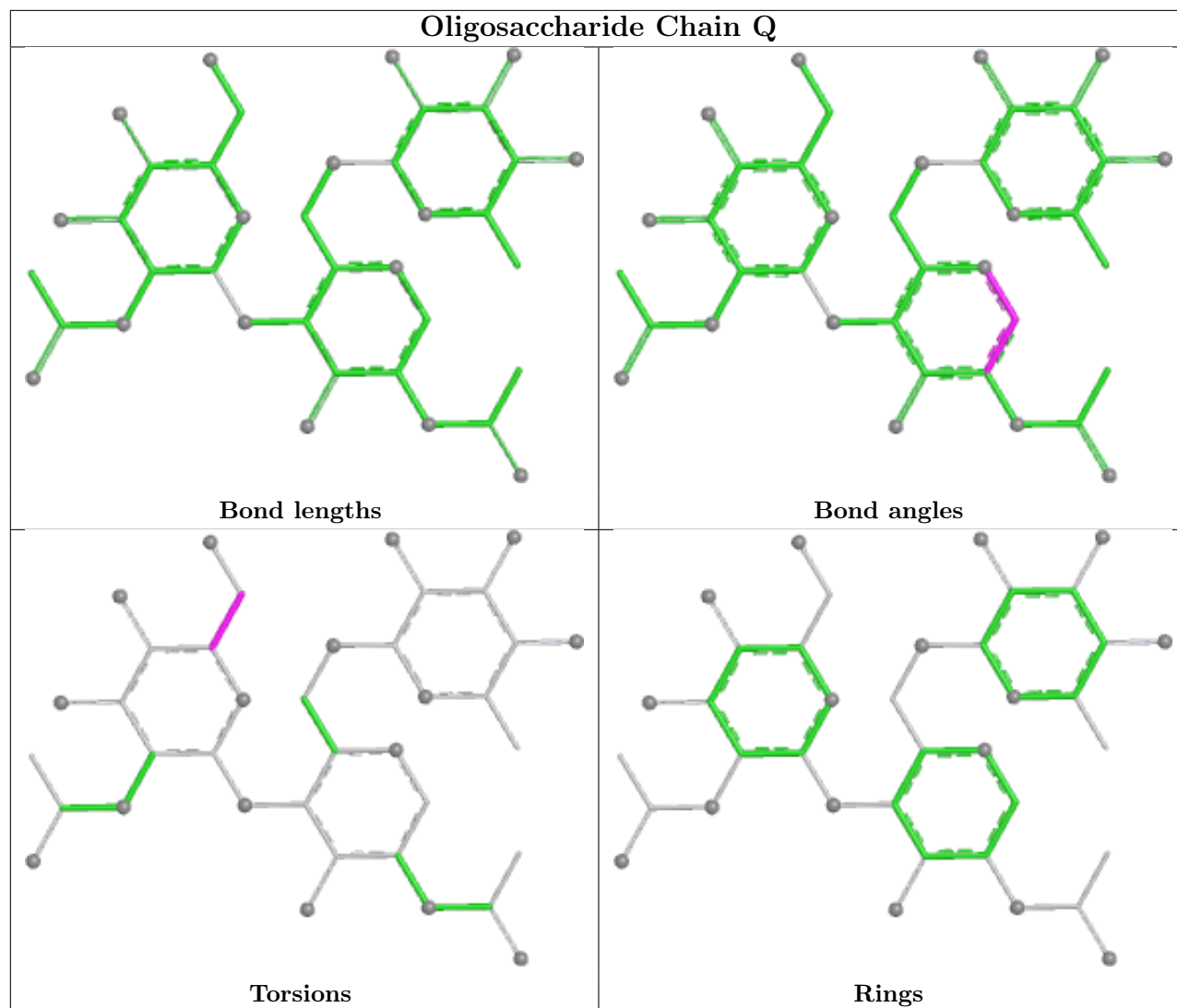
Mol	Chain	Res	Type	Atoms
4	W	6	MAN	C1-C2-C3-C4-C5-O5

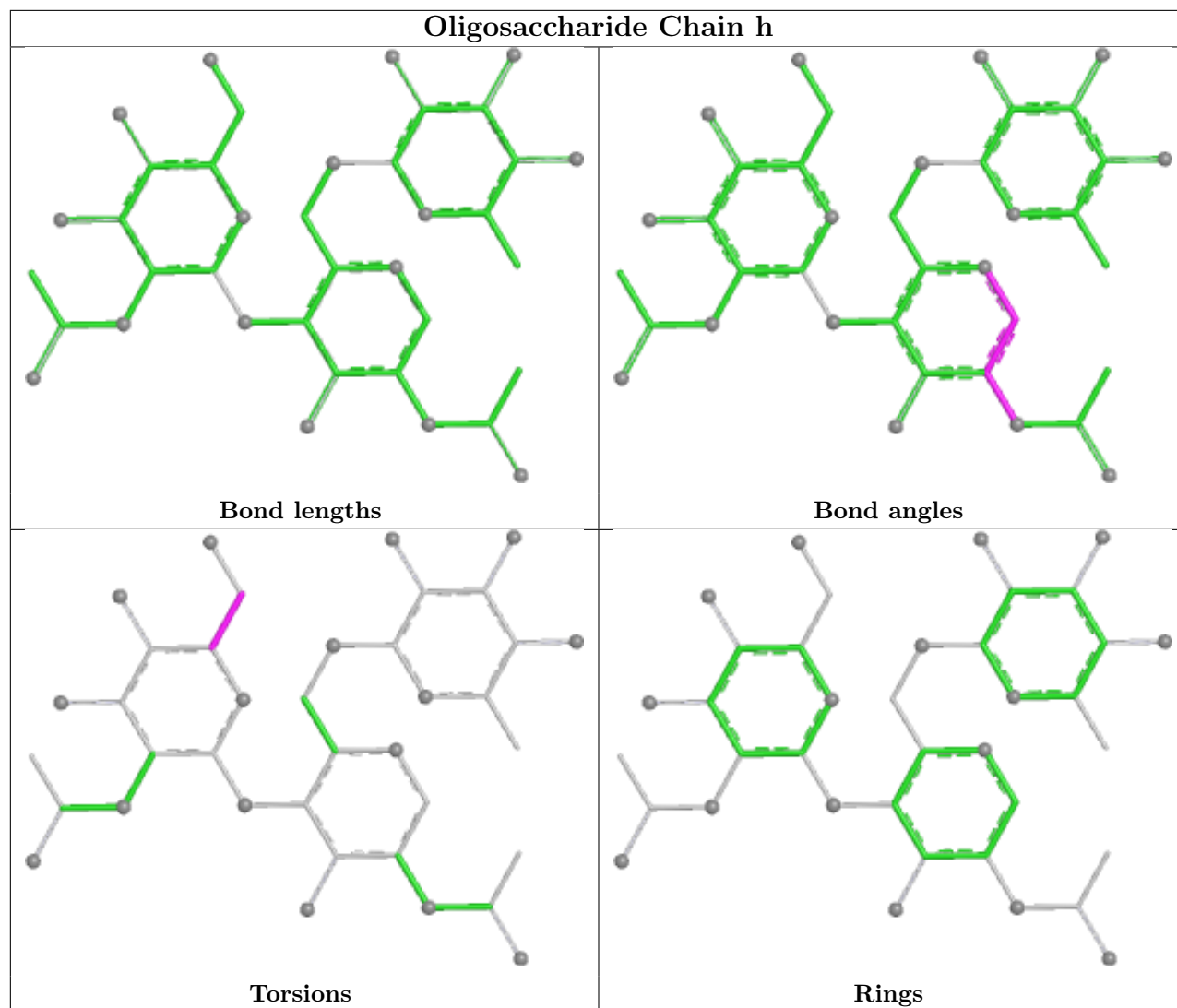
11 monomers are involved in 11 short contacts:

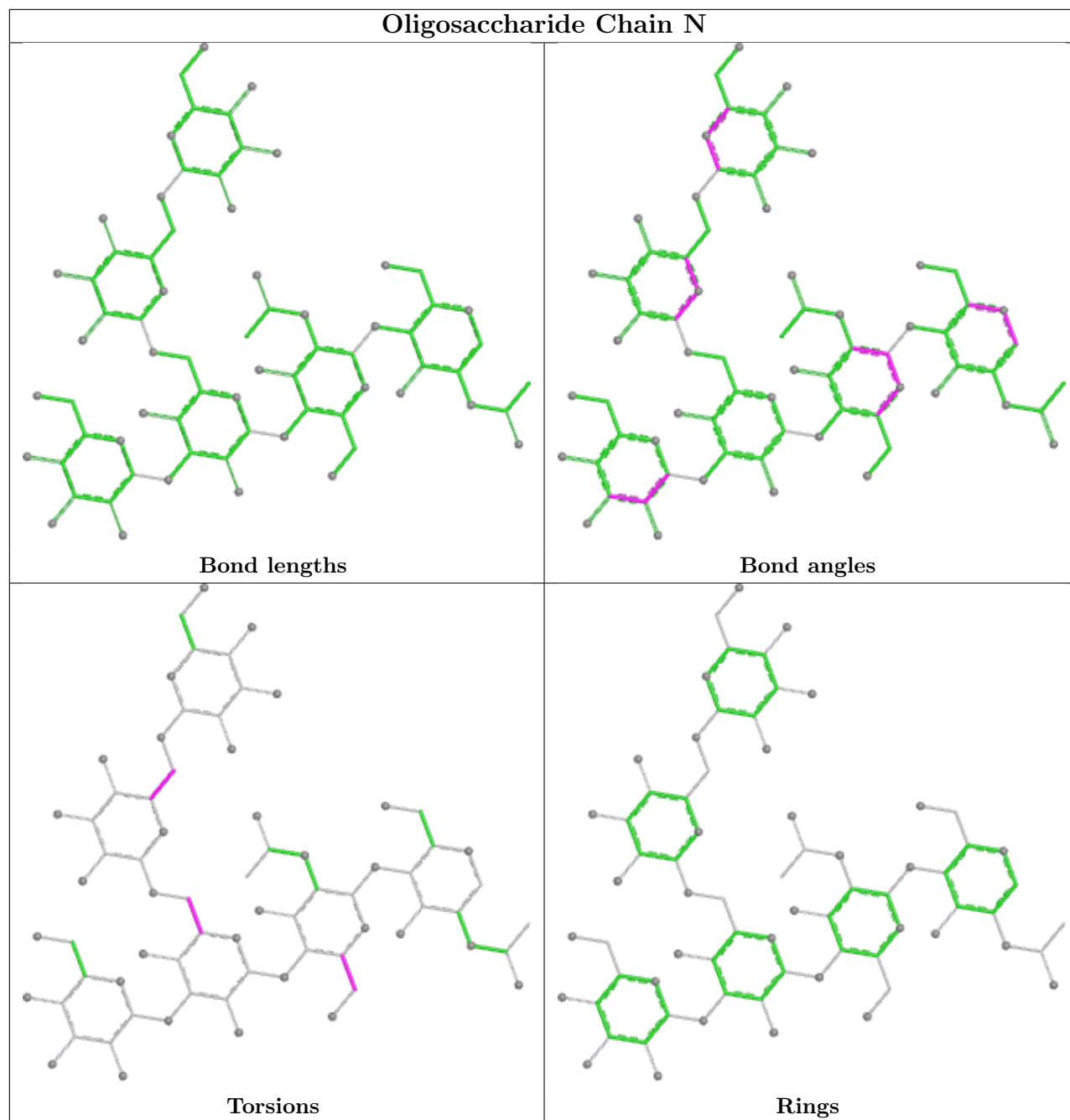
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	e	1	NAG	1	0
4	W	5	MAN	1	0
4	W	1	NAG	1	0
4	W	6	MAN	1	0
4	N	1	NAG	1	0
4	W	3	BMA	1	0
6	i	1	NAG	1	0
7	R	2	FUC	1	0
9	l	4	FUC	2	0
11	Z	2	NAG	1	0
8	a	1	NAG	1	0

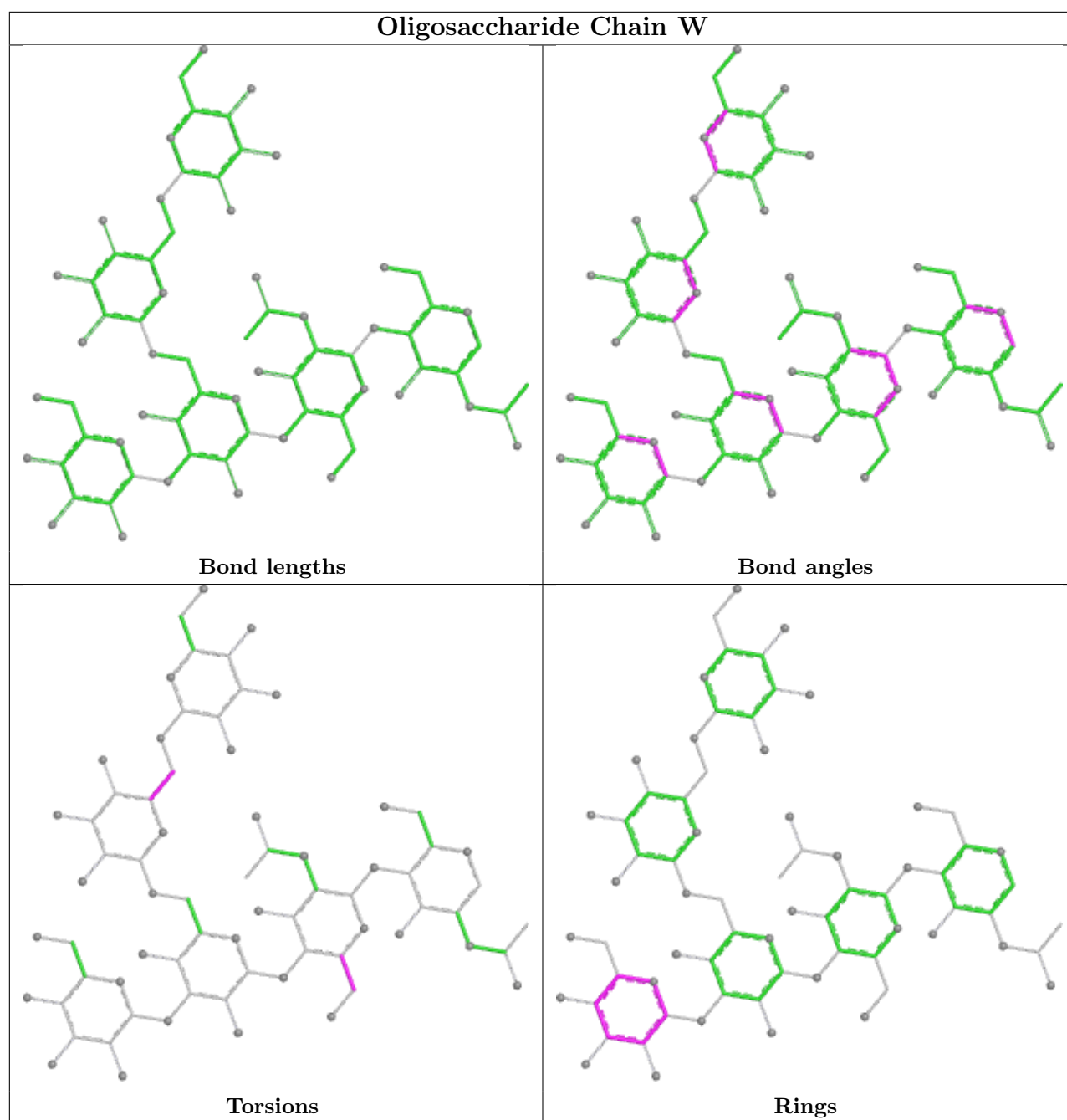
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

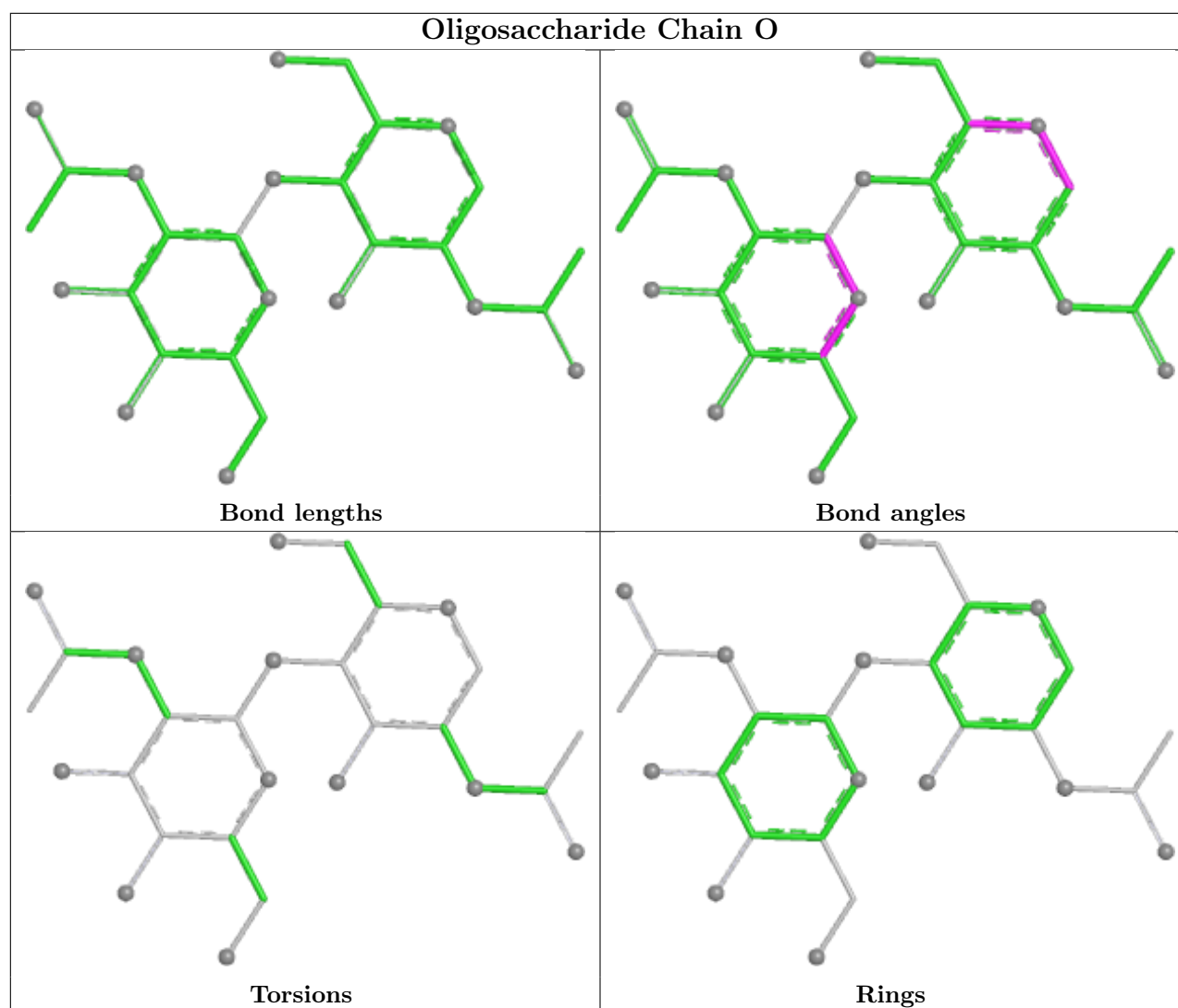


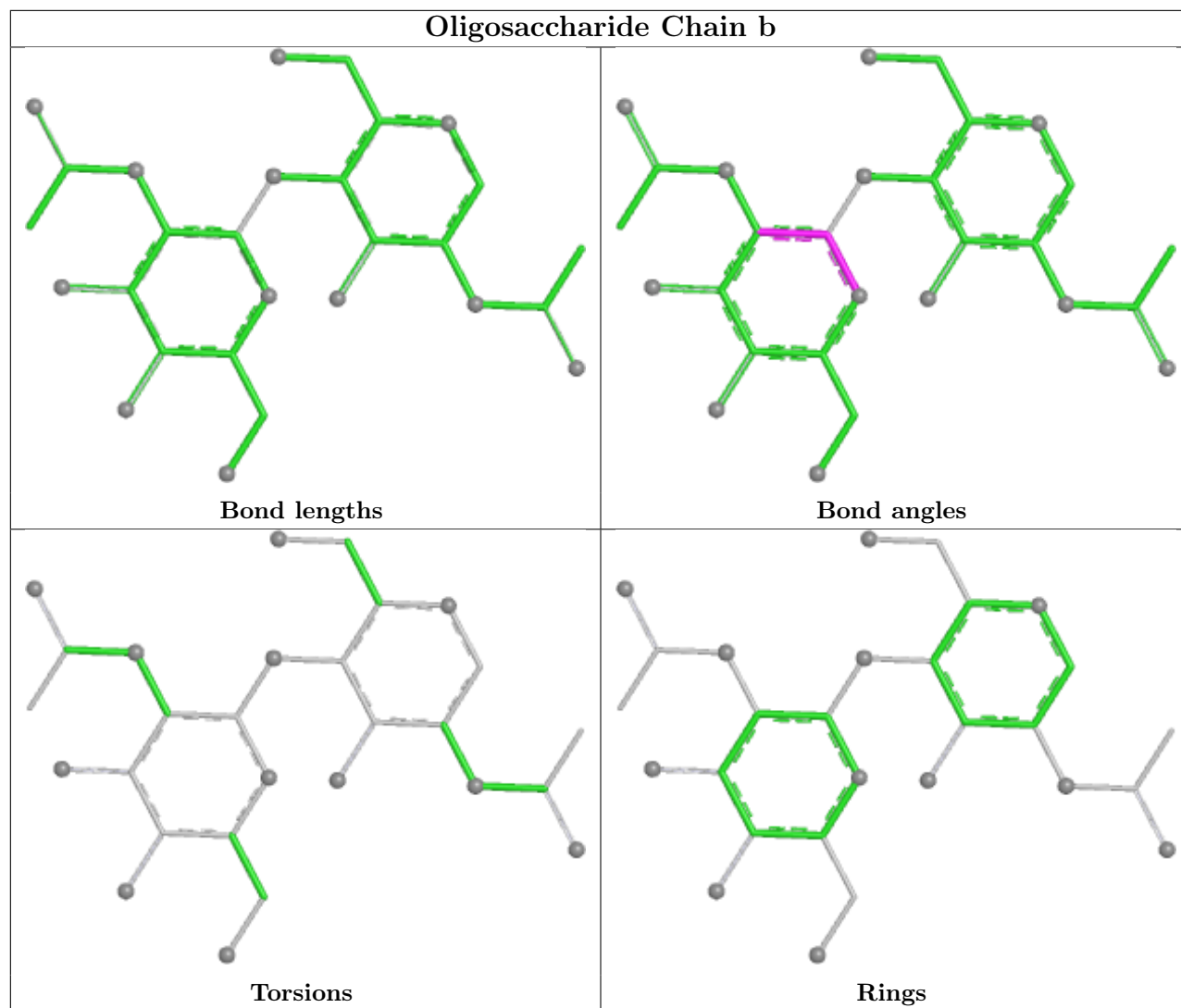


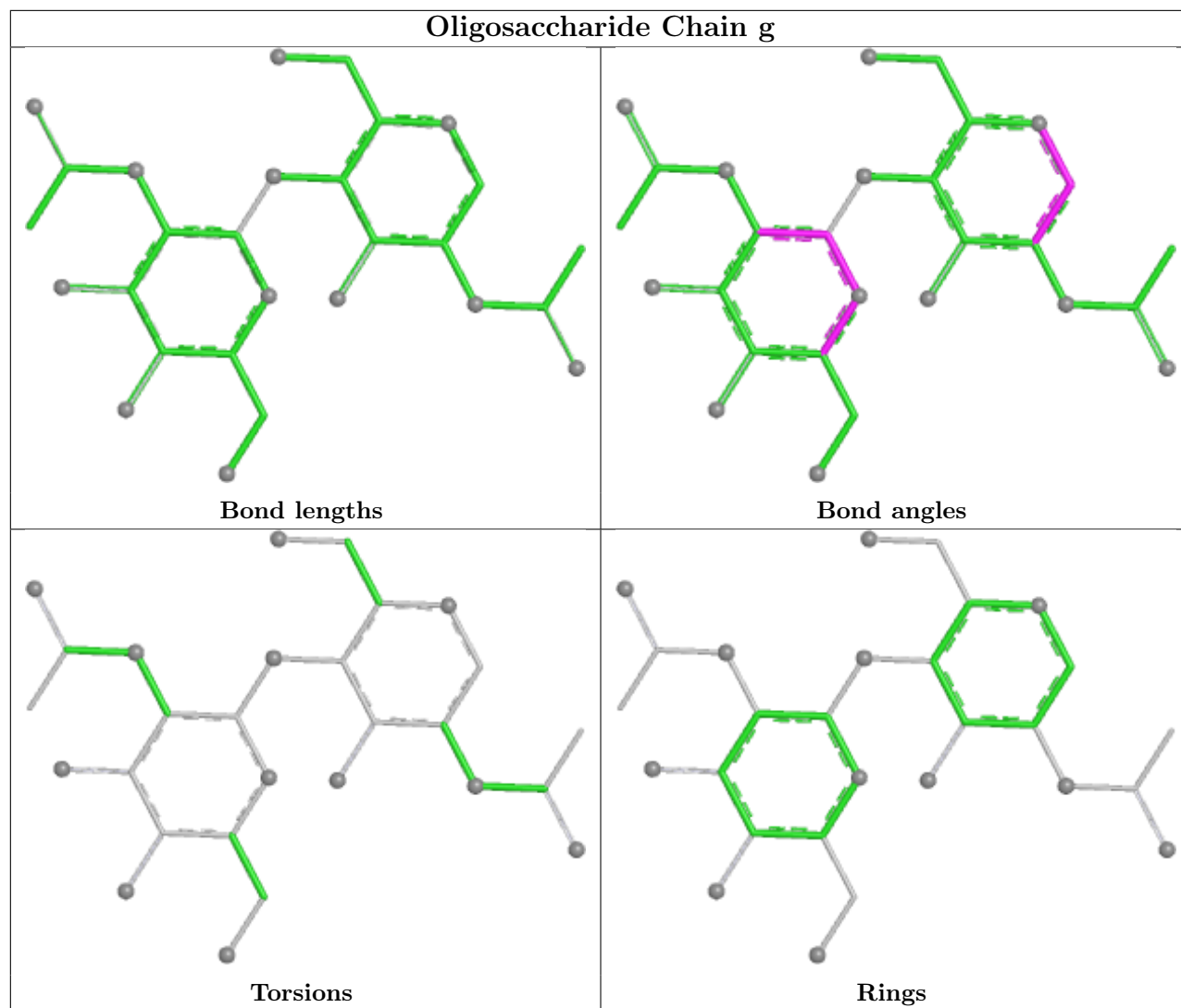


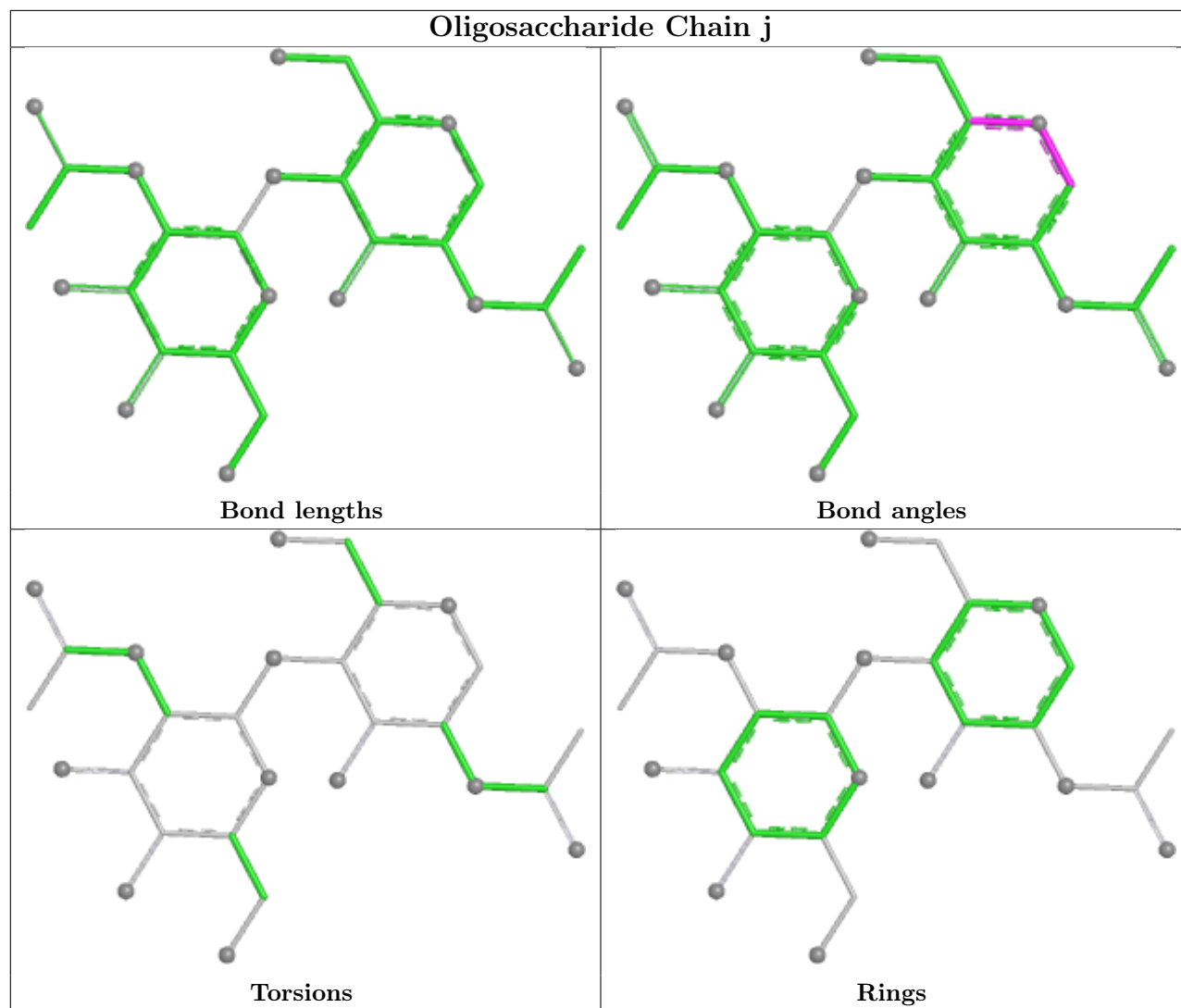


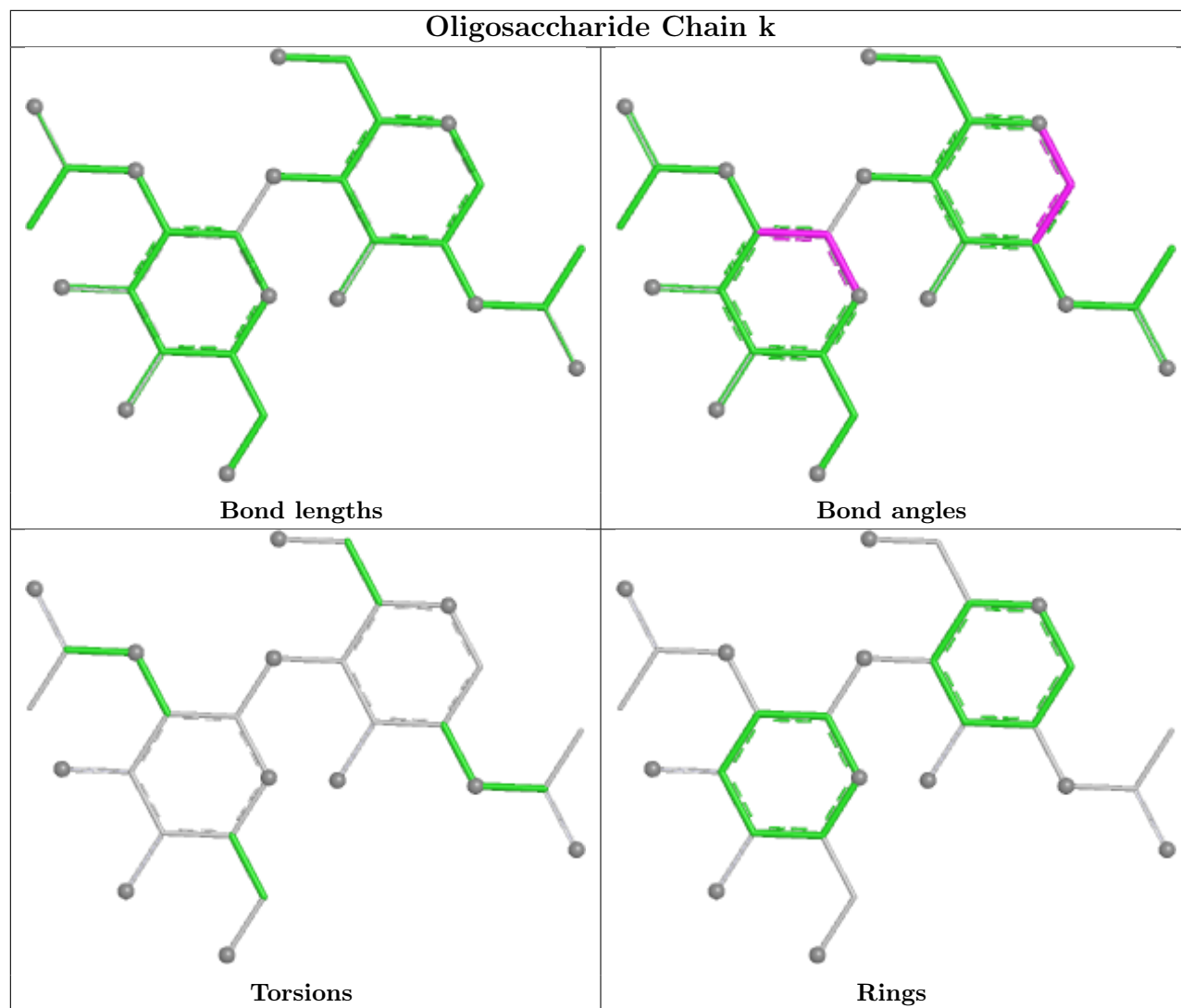


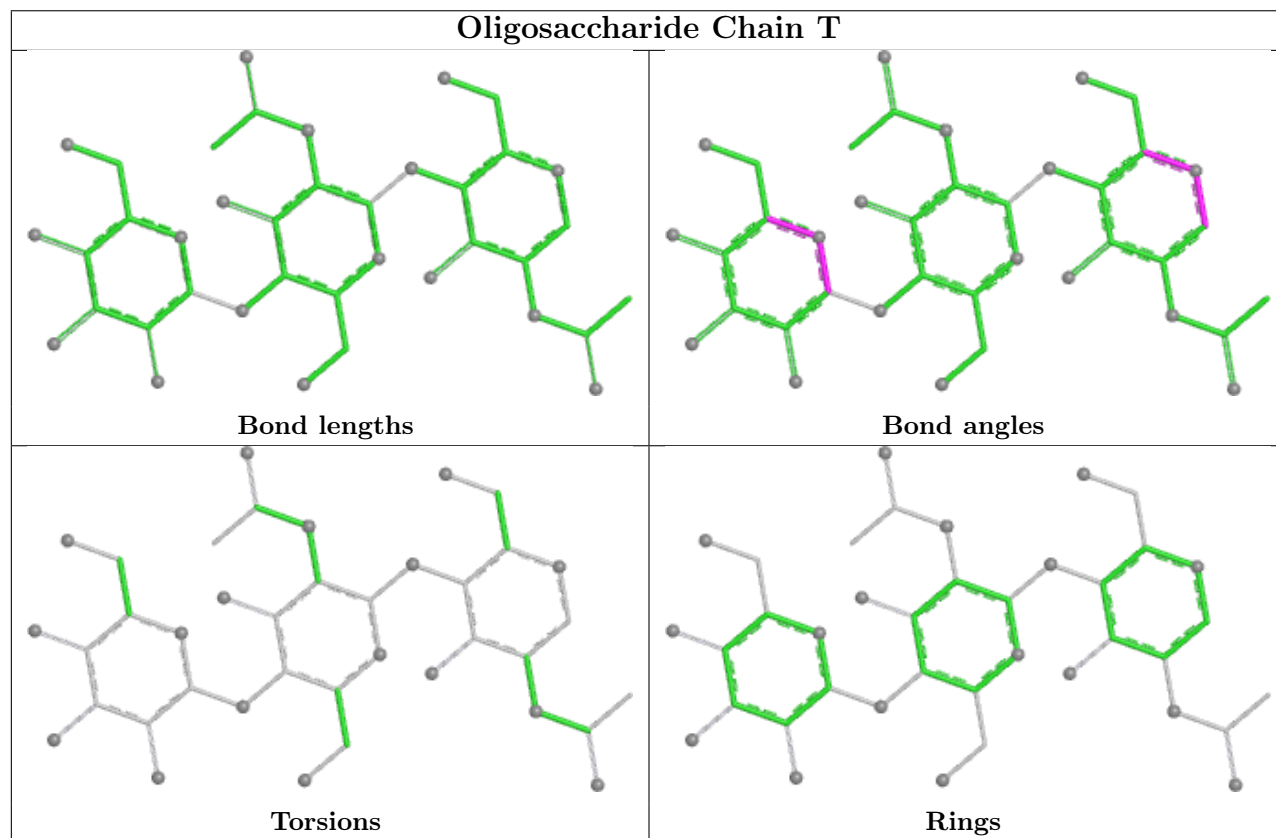
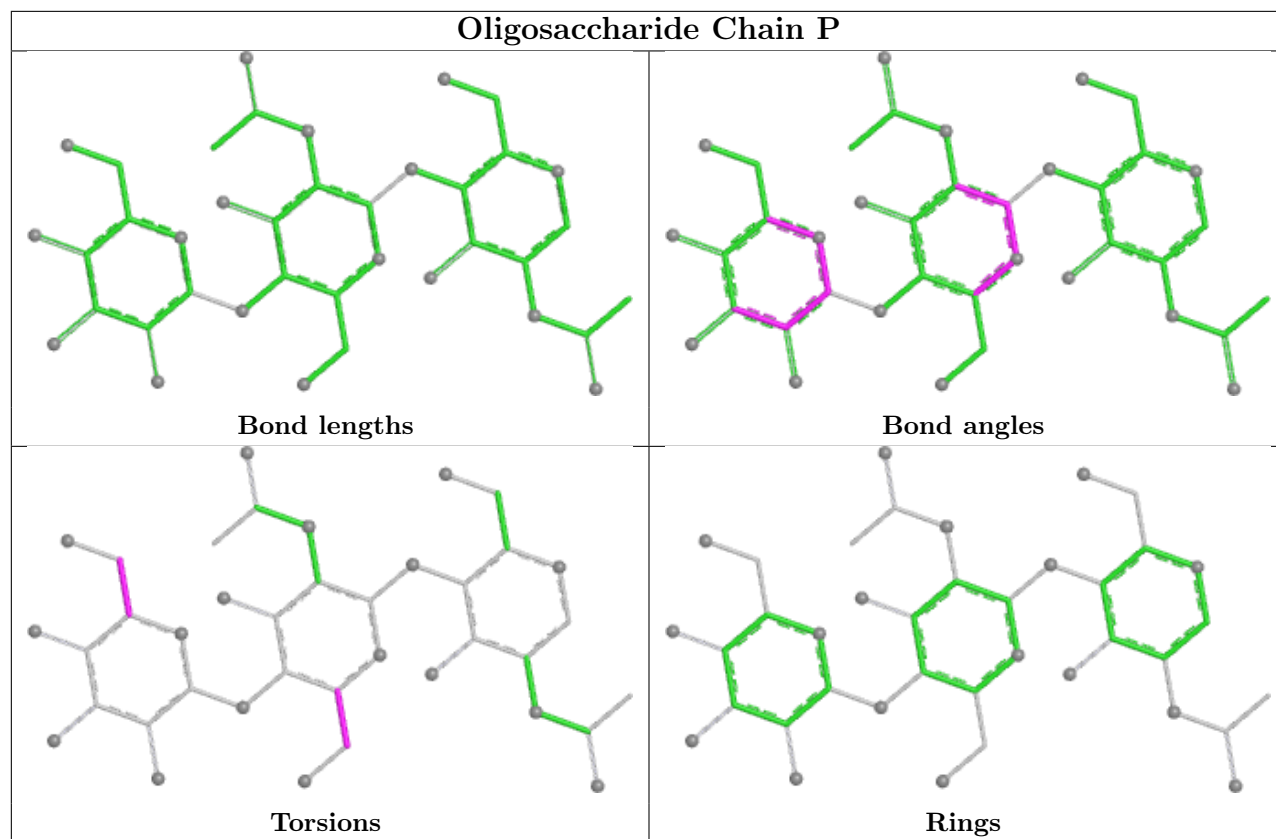


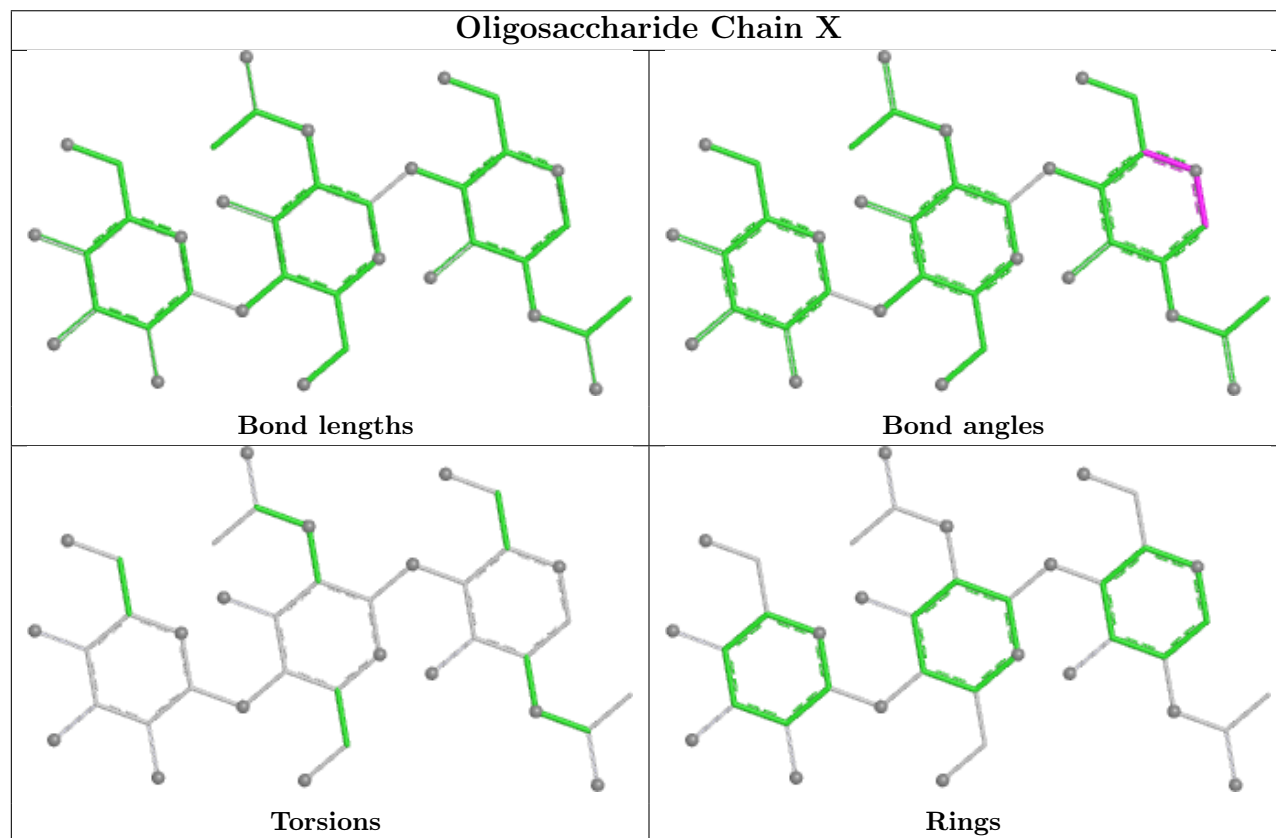
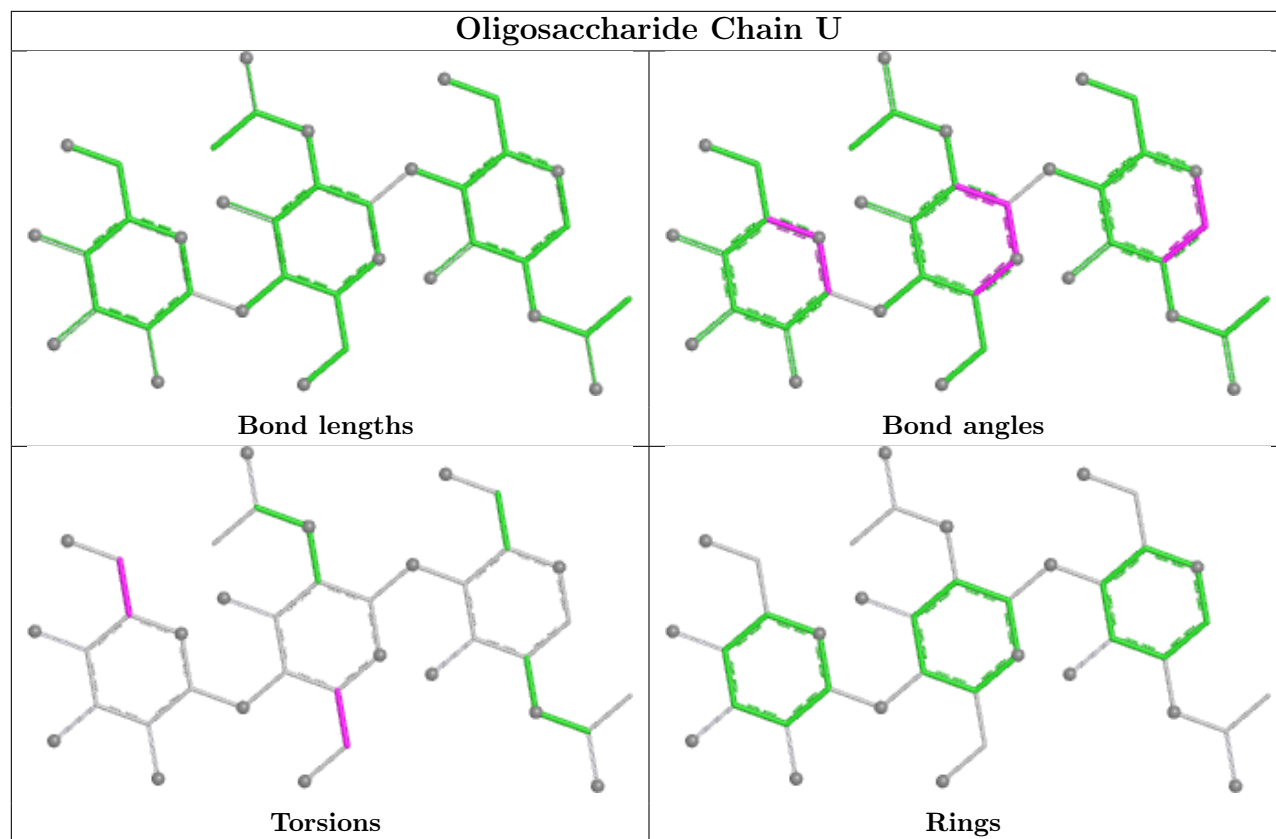


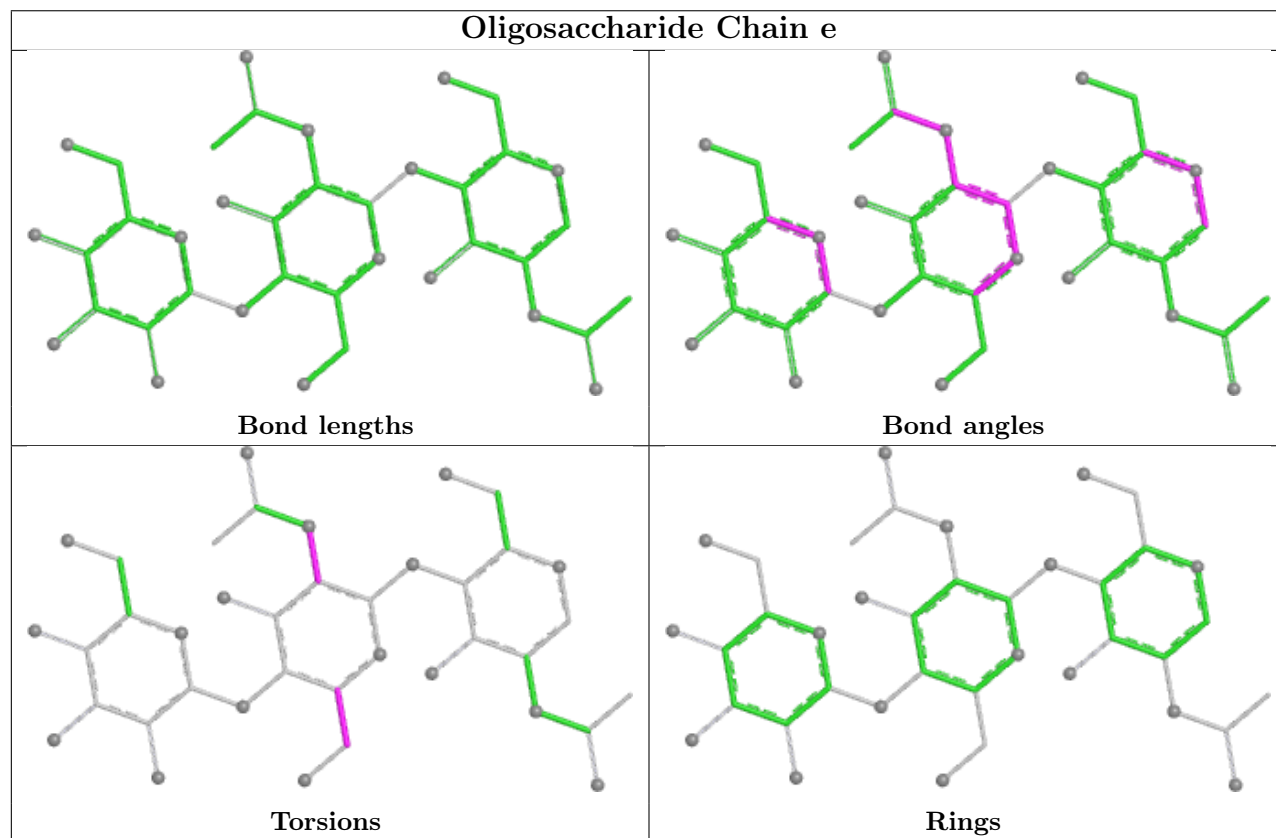
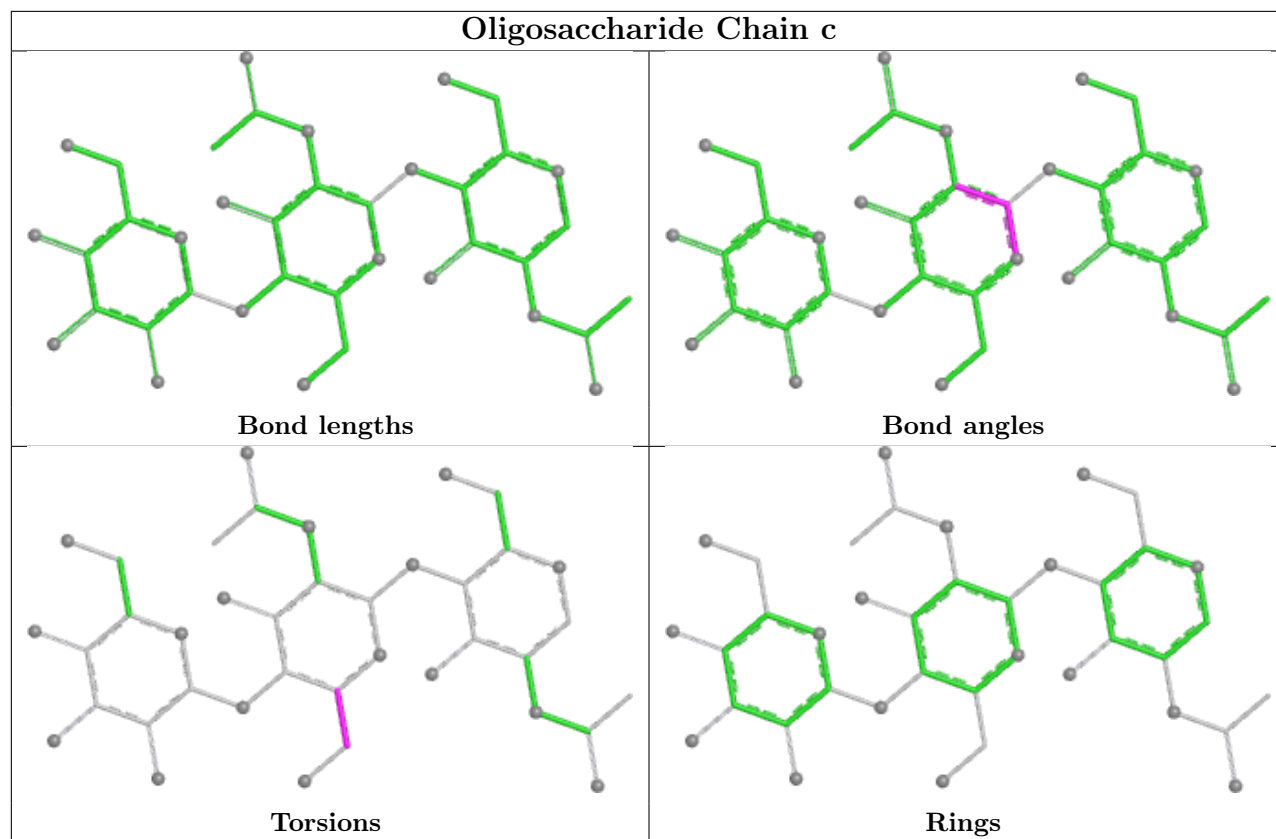


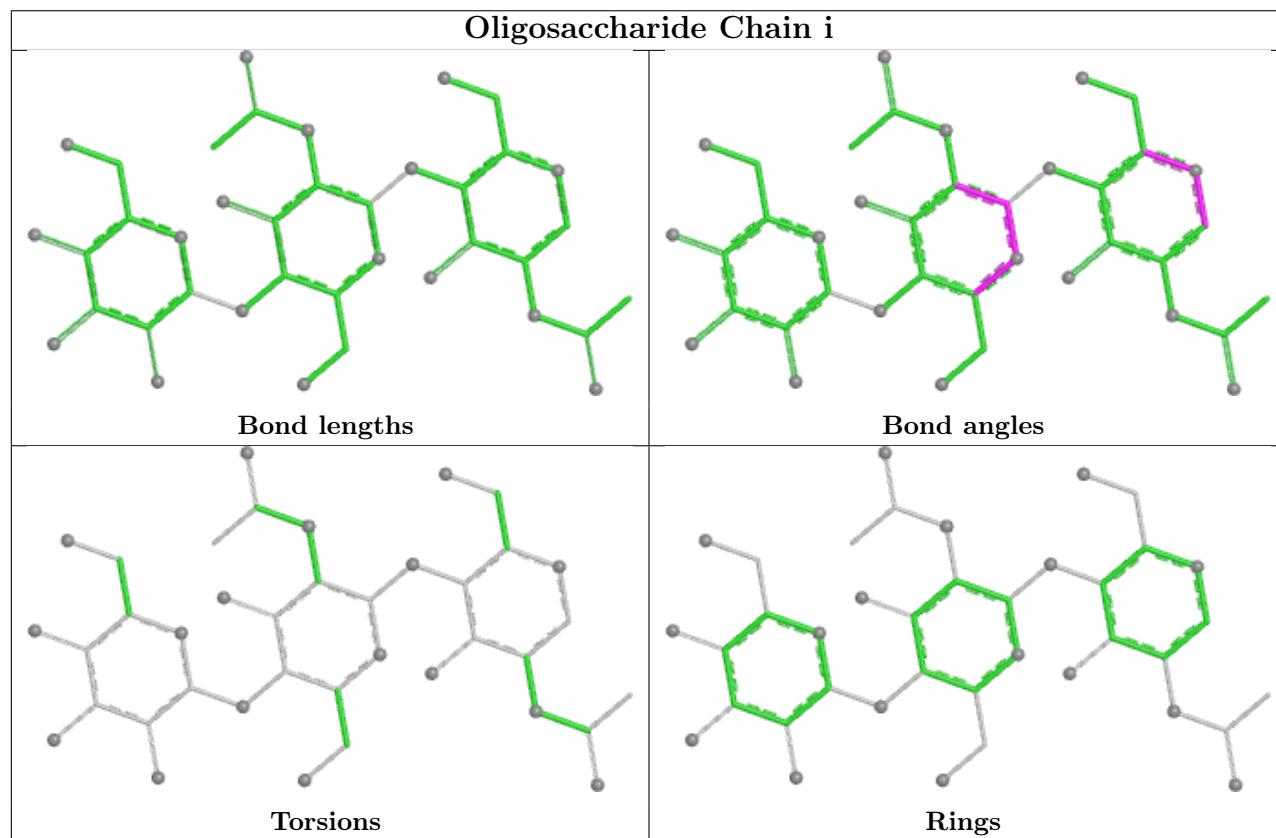
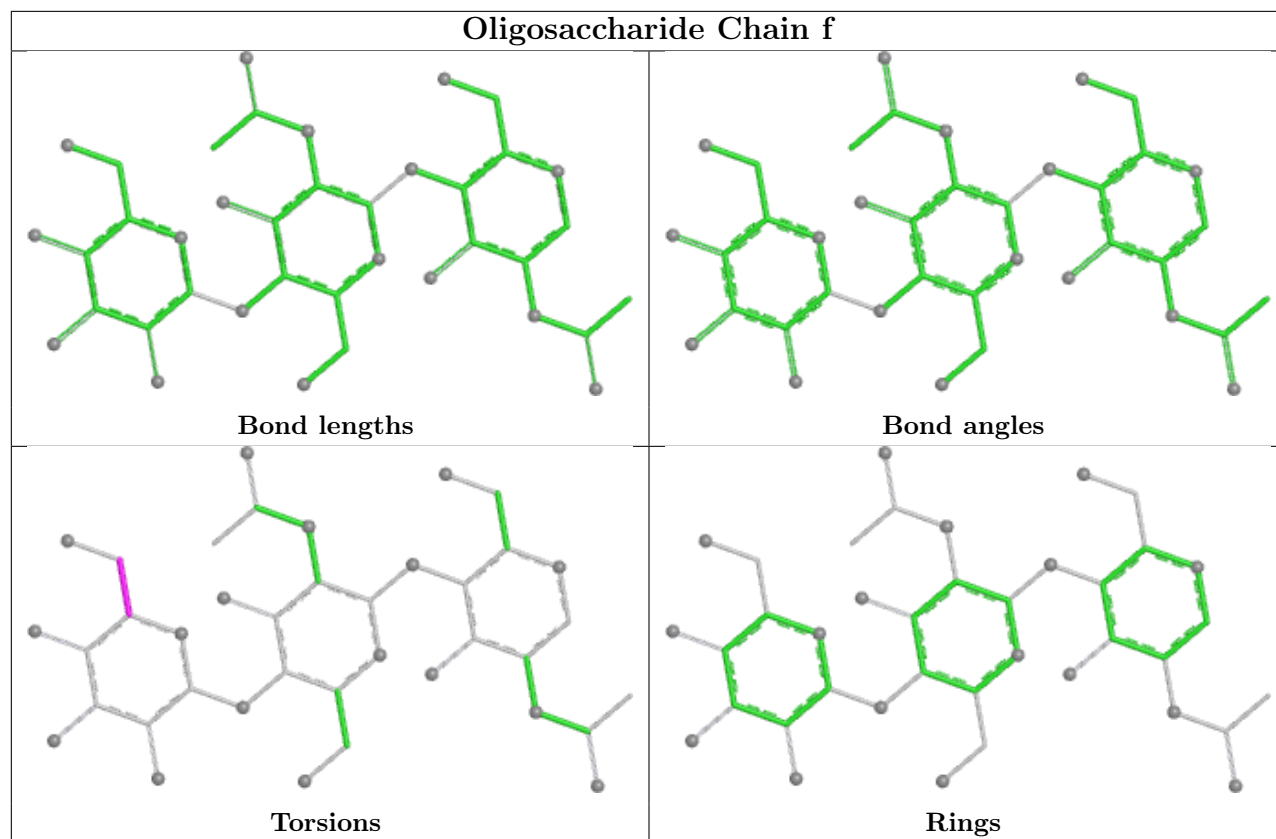


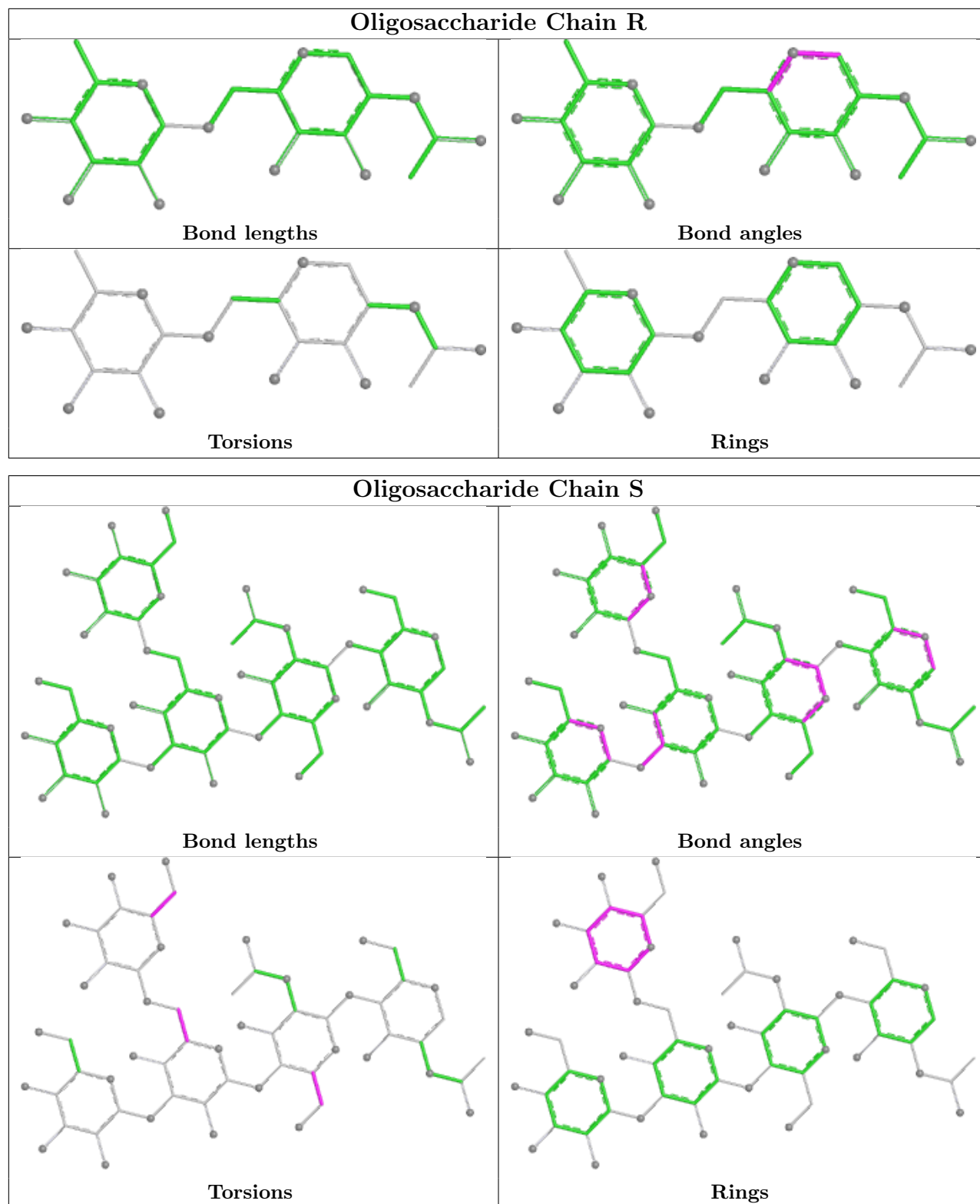


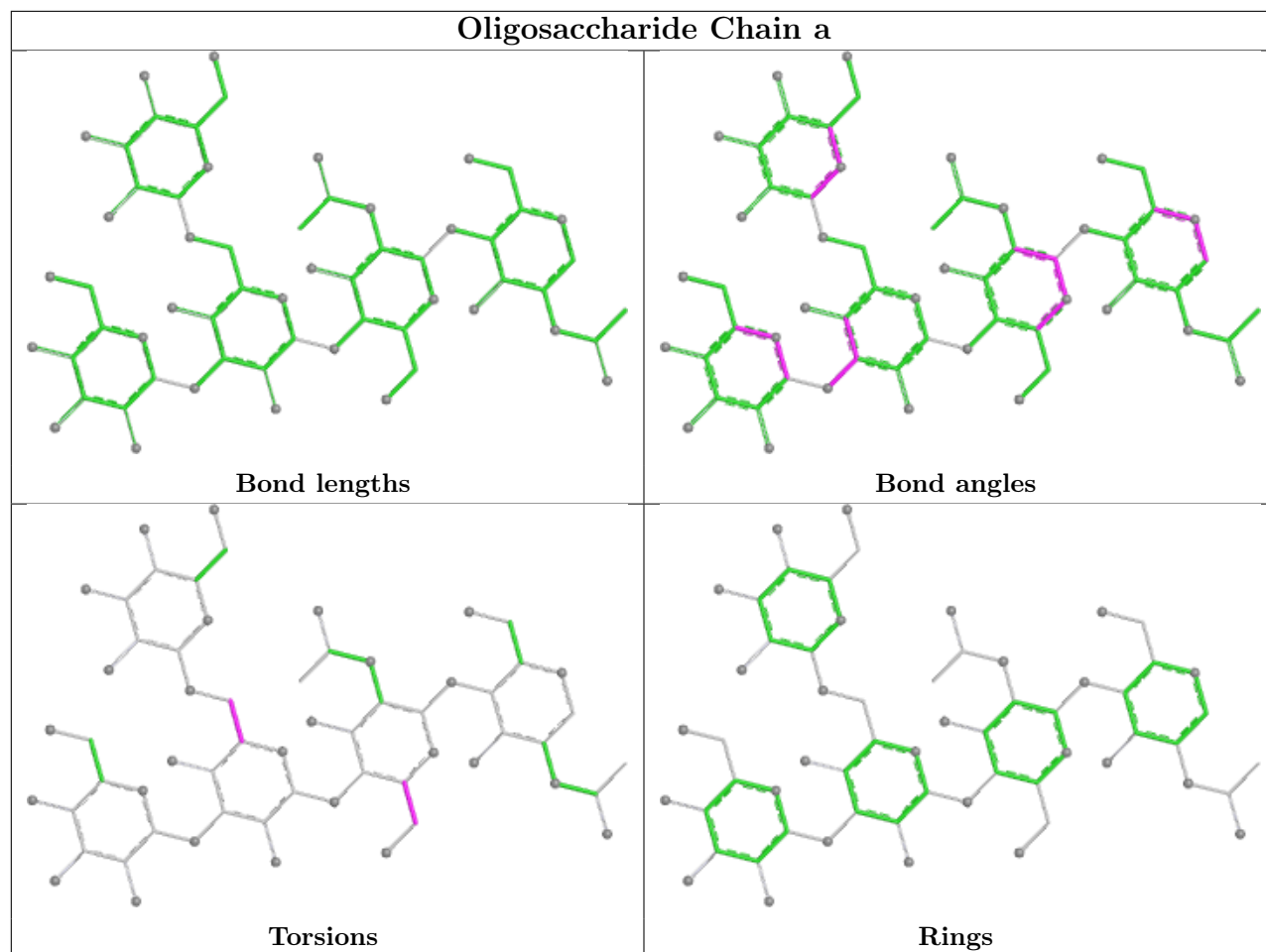


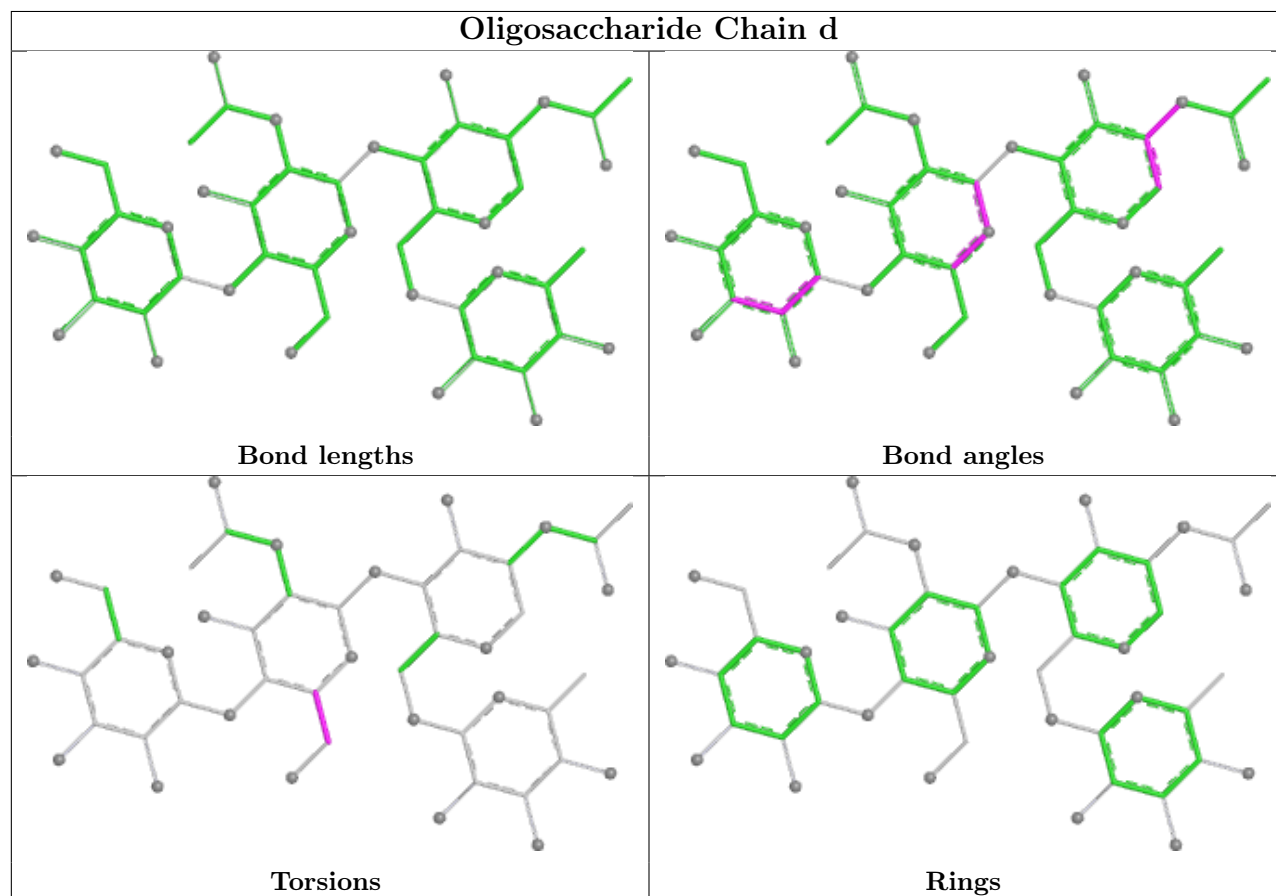
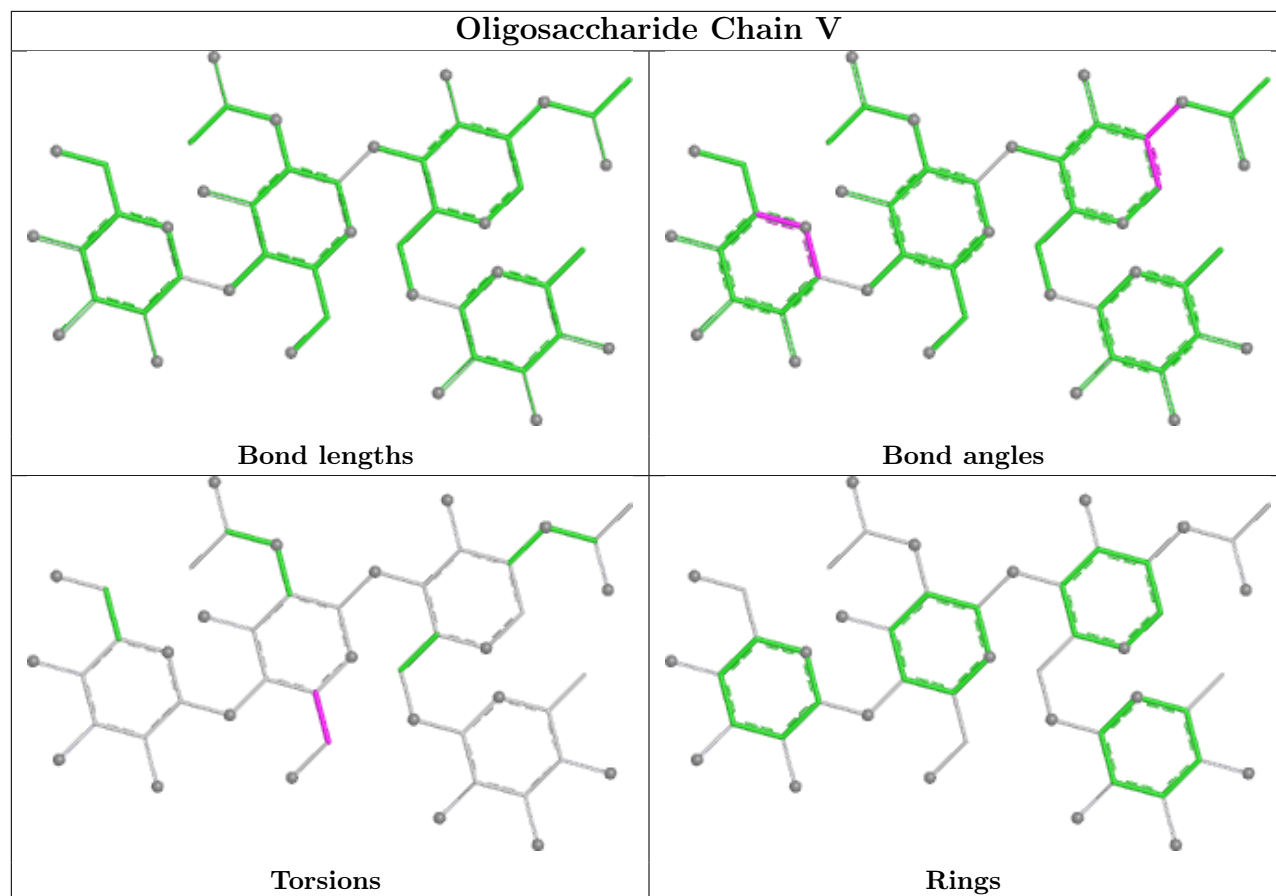


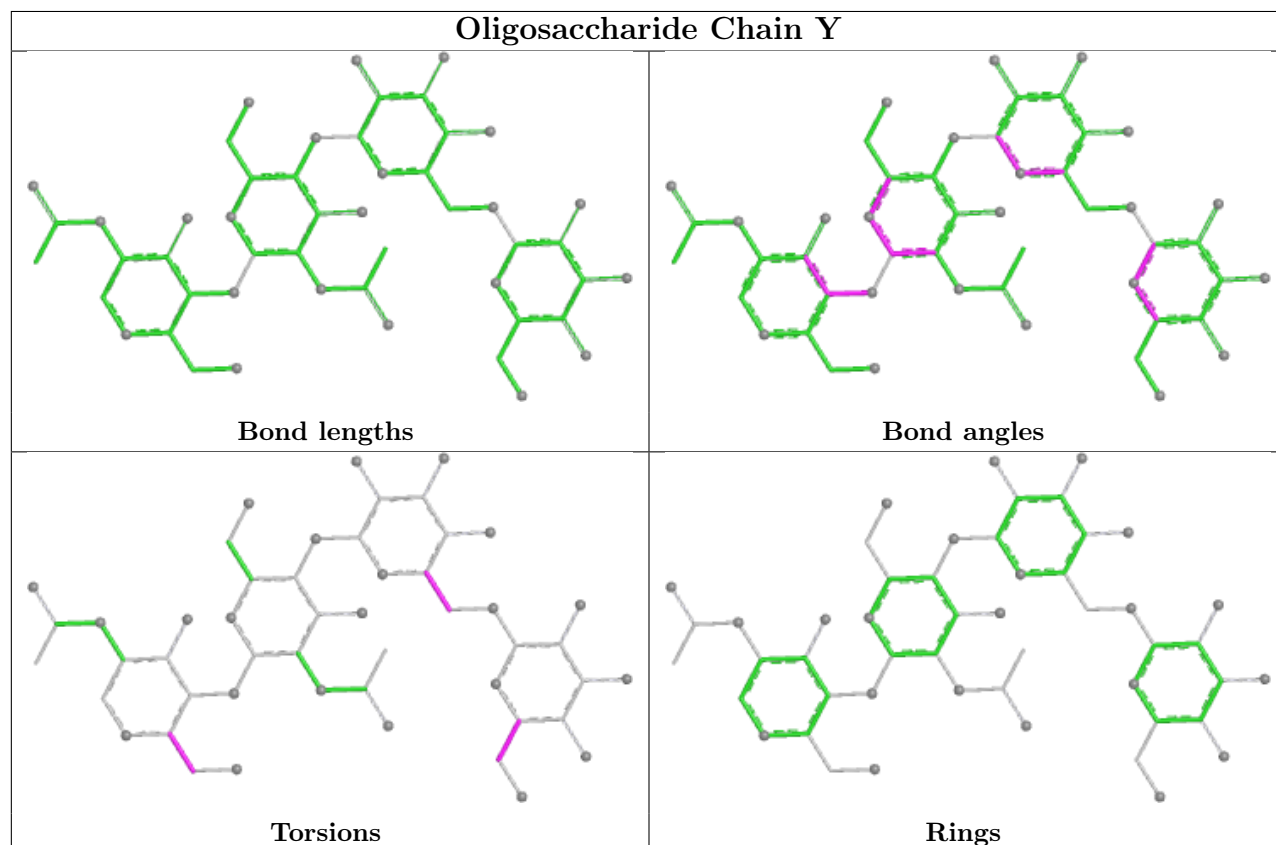
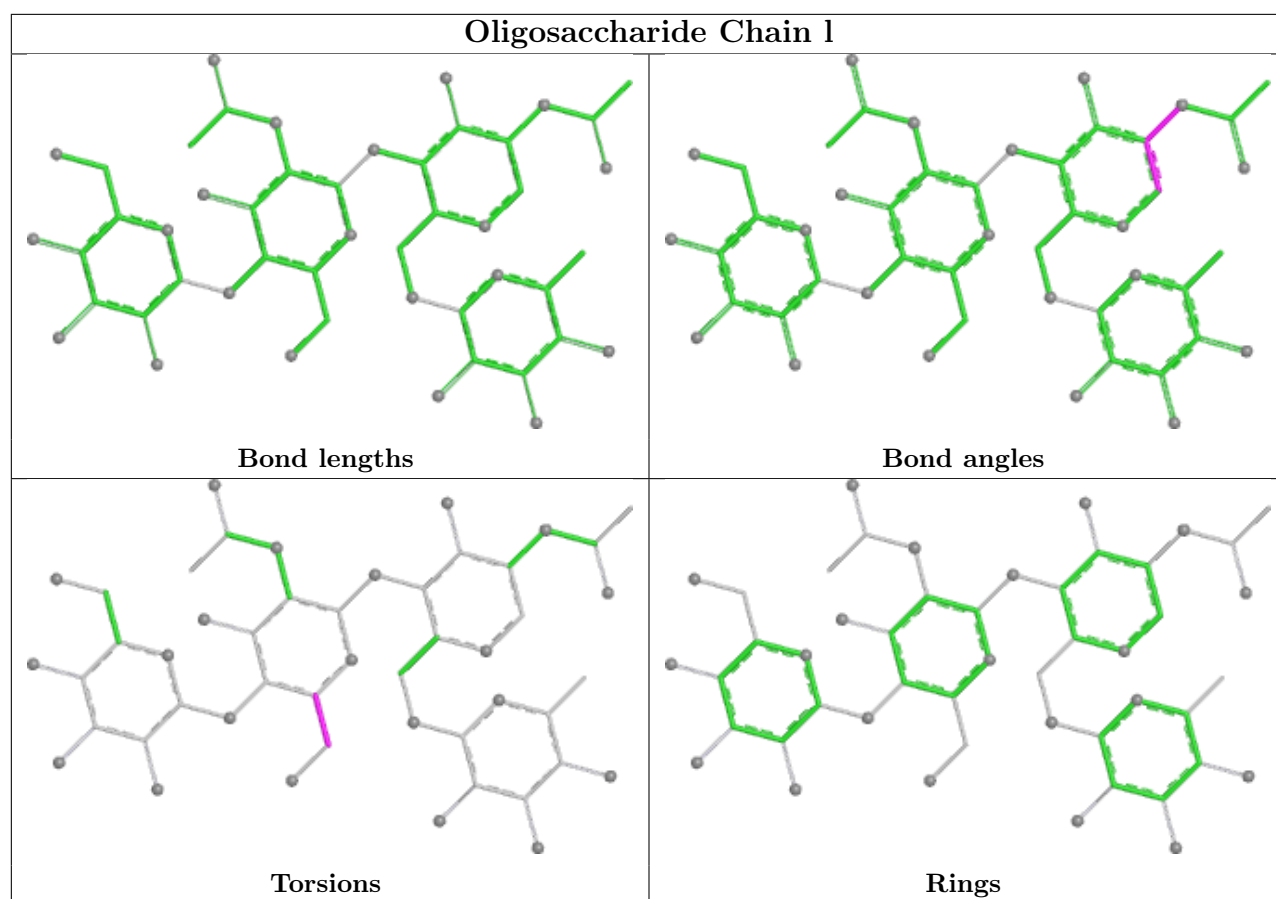


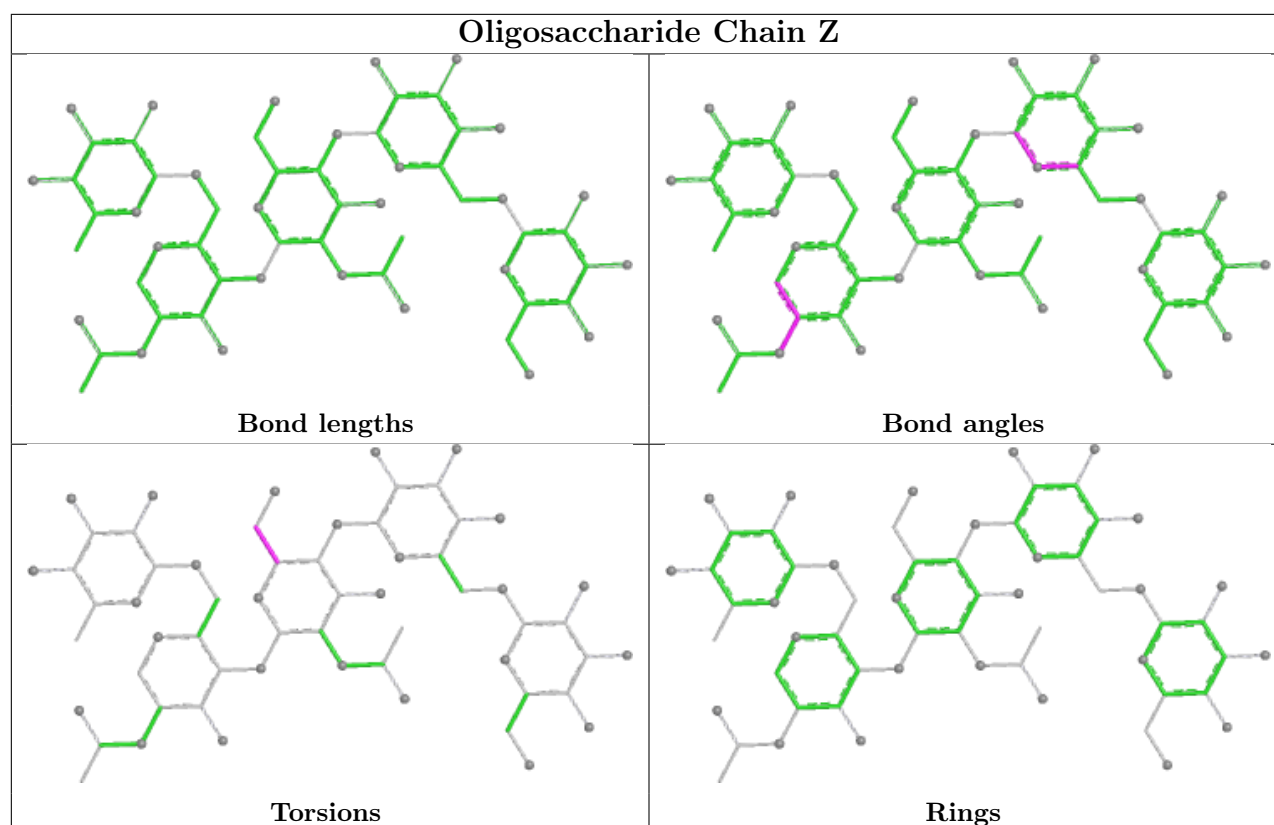












5.6 Ligand geometry [i](#)

46 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	$\# Z > 2$
12	SO4	B	822	-	4,4,4	0.21	0	6,6,6	0.14	0
12	SO4	B	824	-	4,4,4	0.25	0	6,6,6	0.15	0
13	NAG	H	901	2	14,14,15	0.30	0	17,19,21	0.91	2 (11%)
13	NAG	H	903	2	14,14,15	0.28	0	17,19,21	0.74	1 (5%)
12	SO4	F	823	-	4,4,4	0.26	0	6,6,6	0.29	0
12	SO4	J	413	-	4,4,4	0.26	0	6,6,6	0.25	0
12	SO4	D	420	-	4,4,4	0.26	0	6,6,6	0.12	0
12	SO4	A	201	-	4,4,4	0.32	0	6,6,6	0.14	0
12	SO4	D	425	-	4,4,4	0.30	0	6,6,6	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	SO4	E	203	-	4,4,4	0.35	0	6,6,6	0.20	0
12	SO4	C	203	-	4,4,4	0.29	0	6,6,6	0.08	0
12	SO4	G	202	-	4,4,4	0.37	0	6,6,6	0.15	0
12	SO4	E	201	-	4,4,4	0.23	0	6,6,6	0.19	0
12	SO4	H	820	-	4,4,4	0.34	0	6,6,6	0.15	0
13	NAG	D	902	2	14,14,15	0.41	0	17,19,21	0.91	1 (5%)
12	SO4	A	202	-	4,4,4	0.26	0	6,6,6	0.16	0
12	SO4	G	201	-	4,4,4	0.24	0	6,6,6	0.27	0
12	SO4	F	821	-	4,4,4	0.31	0	6,6,6	0.14	0
12	SO4	F	822	-	4,4,4	0.28	0	6,6,6	0.10	0
12	SO4	C	204	-	4,4,4	0.27	0	6,6,6	0.30	0
12	SO4	D	423	-	4,4,4	0.31	0	6,6,6	0.08	0
12	SO4	B	820	-	4,4,4	0.24	0	6,6,6	0.11	0
12	SO4	C	202	-	4,4,4	0.25	0	6,6,6	0.13	0
12	SO4	D	422	-	4,4,4	0.29	0	6,6,6	0.09	0
12	SO4	B	821	-	4,4,4	0.34	0	6,6,6	0.16	0
12	SO4	D	424	-	4,4,4	0.23	0	6,6,6	0.16	0
13	NAG	B	902	2	14,14,15	0.32	0	17,19,21	0.88	1 (5%)
12	SO4	H	818	-	4,4,4	0.21	0	6,6,6	0.26	0
12	SO4	D	419	-	4,4,4	0.24	0	6,6,6	0.24	0
12	SO4	H	821	-	4,4,4	0.21	0	6,6,6	0.25	0
12	SO4	B	823	-	4,4,4	0.22	0	6,6,6	0.21	0
12	SO4	F	825	-	4,4,4	0.34	0	6,6,6	0.10	0
13	NAG	J	903	2	14,14,15	0.30	0	17,19,21	0.52	0
12	SO4	D	421	-	4,4,4	0.25	0	6,6,6	0.21	0
12	SO4	E	202	-	4,4,4	0.32	0	6,6,6	0.12	0
12	SO4	C	205	-	4,4,4	0.29	0	6,6,6	0.13	0
12	SO4	L	412	-	4,4,4	0.23	0	6,6,6	0.10	0
12	SO4	H	819	-	4,4,4	0.19	0	6,6,6	0.16	0
12	SO4	K	201	-	4,4,4	0.28	0	6,6,6	0.11	0
12	SO4	I	201	-	4,4,4	0.23	0	6,6,6	0.16	0
12	SO4	H	817	-	4,4,4	0.30	0	6,6,6	0.10	0
12	SO4	C	201	-	4,4,4	0.26	0	6,6,6	0.13	0
13	NAG	F	903	2	14,14,15	0.33	0	17,19,21	0.76	1 (5%)
13	NAG	B	901	2	14,14,15	0.29	0	17,19,21	0.68	1 (5%)
12	SO4	F	824	-	4,4,4	0.27	0	6,6,6	0.10	0
13	NAG	F	901	2	14,14,15	0.29	0	17,19,21	0.76	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
13	NAG	H	901	2	-	1/6/23/26	0/1/1/1
13	NAG	H	903	2	-	0/6/23/26	0/1/1/1
13	NAG	D	902	2	-	0/6/23/26	0/1/1/1
13	NAG	F	903	2	-	0/6/23/26	0/1/1/1
13	NAG	B	901	2	-	0/6/23/26	0/1/1/1
13	NAG	B	902	2	-	0/6/23/26	0/1/1/1
13	NAG	J	903	2	-	0/6/23/26	0/1/1/1
13	NAG	F	901	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	902	NAG	C1-O5-C5	3.20	116.48	112.19
13	F	903	NAG	C1-O5-C5	2.84	116.00	112.19
13	H	903	NAG	C1-O5-C5	2.72	115.83	112.19
13	H	901	NAG	C1-O5-C5	2.58	115.64	112.19
13	B	901	NAG	C1-O5-C5	2.18	115.11	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	H	901	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	F	821	SO4	1	0
12	H	817	SO4	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	156/157 (99%)	-0.46	2 (1%) 75 56	38, 57, 90, 110	0
1	C	156/157 (99%)	-0.41	0 100 100	32, 58, 85, 109	0
1	E	157/157 (100%)	-0.28	1 (0%) 85 70	35, 64, 92, 129	1 (0%)
1	G	156/157 (99%)	-0.46	0 100 100	34, 53, 80, 95	0
1	I	156/157 (99%)	0.23	0 100 100	75, 99, 132, 145	0
1	K	156/157 (99%)	0.17	1 (0%) 85 70	71, 96, 121, 130	0
2	B	294/312 (94%)	-0.10	2 (0%) 84 68	29, 68, 111, 139	1 (0%)
2	D	290/312 (92%)	-0.15	1 (0%) 90 80	36, 67, 102, 136	0
2	F	288/312 (92%)	-0.07	3 (1%) 79 61	36, 72, 129, 152	1 (0%)
2	H	288/312 (92%)	-0.15	2 (0%) 84 68	35, 68, 121, 161	0
2	J	272/312 (87%)	0.36	8 (2%) 53 32	54, 94, 165, 191	0
2	L	255/312 (81%)	0.33	6 (2%) 59 38	69, 101, 137, 163	0
All	All	2624/2814 (93%)	-0.06	26 (0%) 79 61	29, 76, 128, 191	3 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	44	SER	3.9
2	J	67	GLU	3.6
2	L	97	PHE	3.3
2	F	53	THR	3.3
2	L	80	ASP	3.2

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	N	5	11/12	0.23	0.13	163,166,172,174	0
4	MAN	N	4	11/12	0.30	0.18	149,151,159,161	0
6	BMA	T	3	11/12	0.33	0.14	121,125,128,131	0
6	BMA	U	3	11/12	0.34	0.14	123,130,134,134	0
10	BMA	Y	3	11/12	0.36	0.15	140,148,154,157	0
11	BMA	Z	3	11/12	0.36	0.17	122,130,137,138	0
3	NAG	h	1	14/15	-	-	99,105,109,115	0
3	NAG	h	2	14/15	-	-	120,125,130,133	0
3	FUC	h	3	10/11	-	-	106,111,114,115	0
4	MAN	W	5	11/12	0.38	0.16	155,162,169,172	0
3	NAG	M	2	14/15	0.41	0.15	164,166,172,174	0
6	BMA	X	3	11/12	0.51	0.13	138,145,147,150	0
4	MAN	W	6	11/12	0.52	0.13	150,151,157,157	0
8	MAN	S	4	11/12	0.52	0.11	137,142,144,144	0
4	MAN	N	6	11/12	0.54	0.11	146,151,153,154	0
8	MAN	S	5	11/12	0.57	0.13	138,140,143,143	0
10	MAN	Y	4	11/12	0.58	0.21	160,163,165,166	0
9	BMA	V	3	11/12	0.60	0.15	127,130,132,134	0
11	MAN	Z	4	11/12	0.60	0.15	138,143,148,152	0
4	MAN	W	4	11/12	0.62	0.13	139,144,155,159	0
6	NAG	P	2	14/15	0.65	0.12	93,100,104,110	0
6	BMA	P	3	11/12	0.66	0.12	108,114,117,118	0
6	NAG	X	2	14/15	0.71	0.13	106,115,124,131	0
5	NAG	b	1	14/15	-	-	69,83,99,111	0
5	NAG	b	2	14/15	-	-	120,125,132,133	0
5	NAG	g	1	14/15	-	-	86,90,96,103	0
5	NAG	g	2	14/15	-	-	113,121,124,126	0
5	NAG	j	1	14/15	-	-	110,113,119,124	0
5	NAG	j	2	14/15	-	-	126,128,129,130	0
5	NAG	k	1	14/15	-	-	100,104,110,115	0
5	NAG	k	2	14/15	-	-	116,125,132,133	0
5	NAG	O	2	14/15	0.73	0.12	119,125,131,131	0
10	NAG	Y	2	14/15	0.73	0.14	111,118,125,133	0
7	NAG	R	1	14/15	0.74	0.14	124,128,137,138	0
3	FUC	M	3	10/11	0.77	0.13	152,154,157,158	0
3	NAG	Q	2	14/15	0.77	0.14	96,104,111,111	0
9	NAG	V	2	14/15	0.79	0.12	105,111,124,125	0

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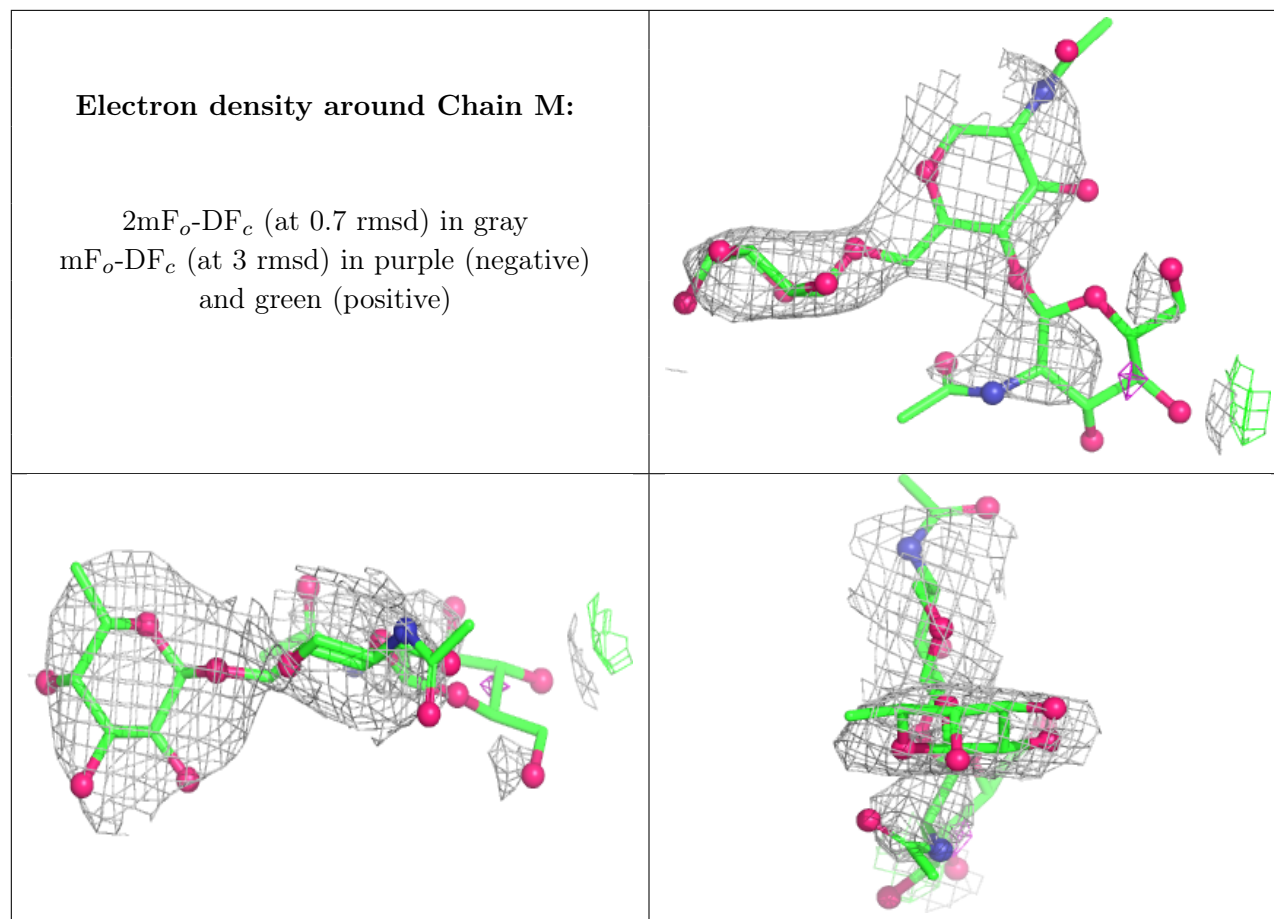
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	M	1	14/15	0.81	0.12	149,154,157,161	0
6	NAG	T	2	14/15	0.81	0.10	93,98,109,114	0
8	BMA	S	3	11/12	0.82	0.12	122,130,136,137	0
6	NAG	U	2	14/15	0.82	0.10	91,96,105,114	0
4	BMA	N	3	11/12	0.83	0.08	129,136,144,145	0
8	NAG	S	2	14/15	0.84	0.14	94,98,107,116	0
6	NAG	c	1	14/15	-	-	68,76,81,88	0
6	NAG	c	2	14/15	-	-	92,101,110,118	0
6	BMA	c	3	11/12	-	-	119,125,132,135	0
6	NAG	e	1	14/15	-	-	107,109,115,116	0
6	NAG	e	2	14/15	-	-	116,125,130,132	0
6	BMA	e	3	11/12	-	-	132,135,138,139	0
6	NAG	f	1	14/15	-	-	109,114,121,129	0
6	NAG	f	2	14/15	-	-	133,142,147,153	0
6	BMA	f	3	11/12	-	-	158,159,163,163	0
6	NAG	i	1	14/15	-	-	142,147,151,152	0
6	NAG	i	2	14/15	-	-	149,155,161,163	0
6	BMA	i	3	11/12	-	-	165,169,171,172	0
11	NAG	Z	2	14/15	0.86	0.13	83,94,108,114	0
7	FUC	R	2	10/11	0.86	0.15	126,129,131,131	0
4	BMA	W	3	11/12	0.86	0.11	131,137,143,148	0
4	NAG	W	2	14/15	0.87	0.13	109,111,120,127	0
3	FUC	Q	3	10/11	0.88	0.12	74,80,83,89	0
4	NAG	N	2	14/15	0.89	0.12	104,107,117,123	0
10	NAG	Y	1	14/15	0.89	0.14	74,84,91,100	0
8	NAG	a	1	14/15	-	-	96,105,111,116	0
8	NAG	a	2	14/15	-	-	121,126,133,139	0
8	BMA	a	3	11/12	-	-	145,152,156,156	0
8	MAN	a	4	11/12	-	-	158,163,168,169	0
8	MAN	a	5	11/12	-	-	157,159,161,163	0
11	FUC	Z	5	10/11	0.90	0.11	81,87,93,97	0
9	FUC	V	4	10/11	0.91	0.11	96,99,102,105	0
6	NAG	P	1	14/15	0.91	0.12	67,73,79,84	0
6	NAG	X	1	14/15	0.91	0.12	87,90,96,104	0
9	NAG	d	1	14/15	-	-	65,70,80,91	0
9	NAG	d	2	14/15	-	-	92,100,111,118	0
9	BMA	d	3	11/12	-	-	123,127,131,135	0
9	FUC	d	4	10/11	-	-	79,82,85,85	0
9	NAG	l	1	14/15	-	-	120,128,136,145	0
9	NAG	l	2	14/15	-	-	150,155,161,164	0
9	BMA	l	3	11/12	-	-	161,165,170,171	0
9	FUC	l	4	10/11	-	-	130,135,140,143	0

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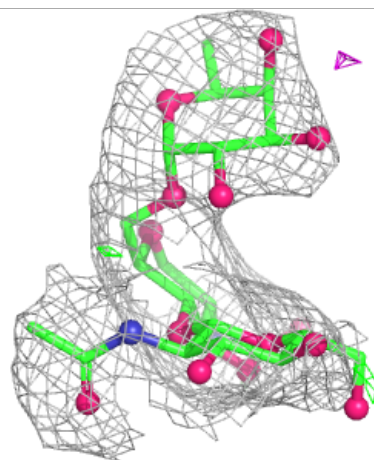
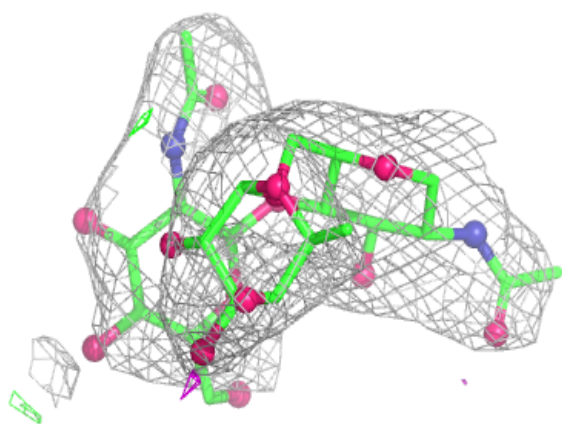
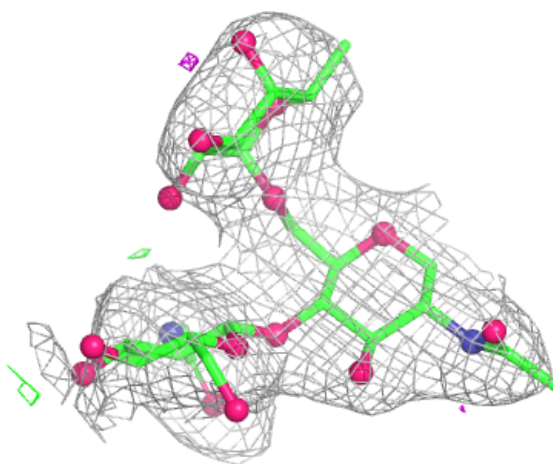
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	NAG	V	1	14/15	0.92	0.11	78,82,96,101	0
8	NAG	S	1	14/15	0.92	0.10	64,74,85,89	0
11	NAG	Z	1	14/15	0.94	0.09	55,66,81,82	0
6	NAG	T	1	14/15	0.94	0.08	62,71,77,86	0
4	NAG	W	1	14/15	0.94	0.09	88,94,105,105	0
4	NAG	N	1	14/15	0.94	0.09	91,97,102,103	0
6	NAG	U	1	14/15	0.94	0.09	63,67,74,81	0
5	NAG	O	1	14/15	0.95	0.08	81,88,99,110	0
3	NAG	Q	1	14/15	0.95	0.09	68,76,84,94	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.



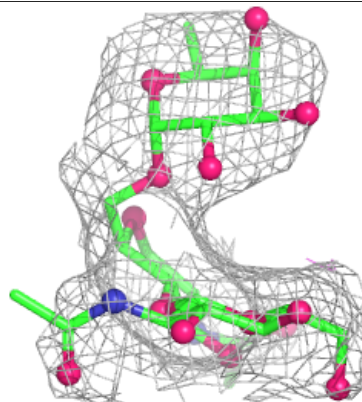
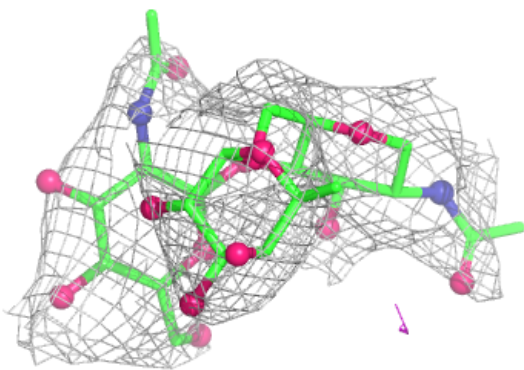
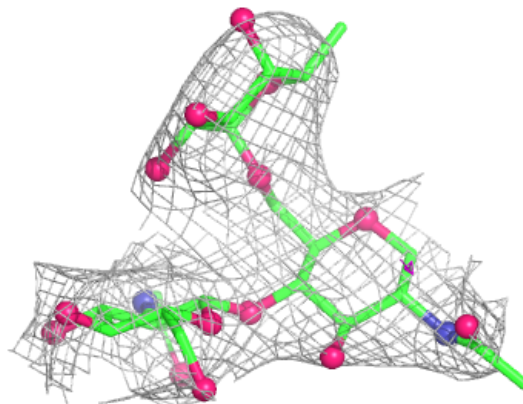
Electron density around Chain Q:

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



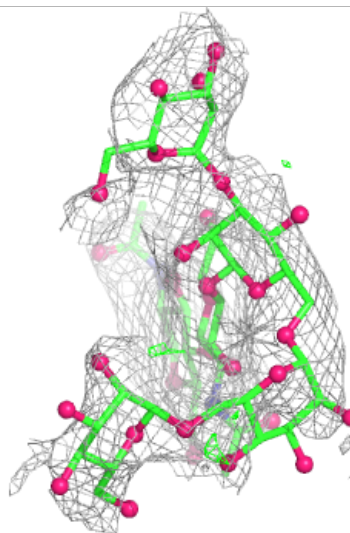
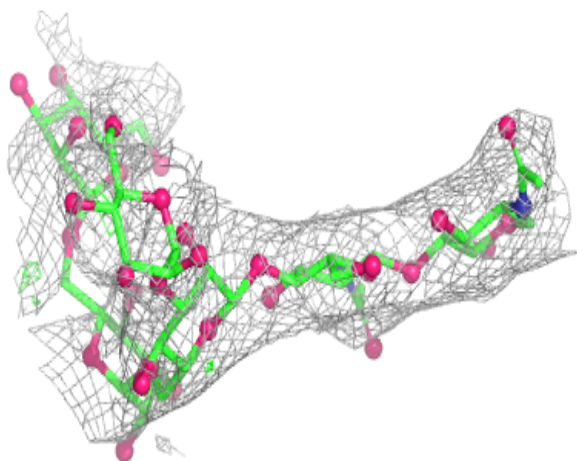
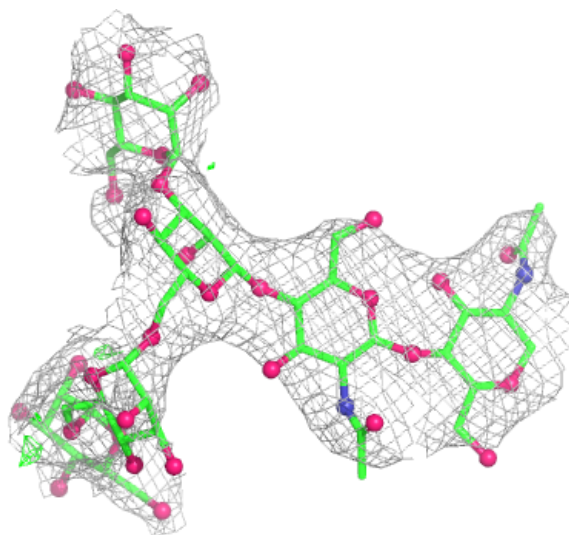
Electron density around Chain h:

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



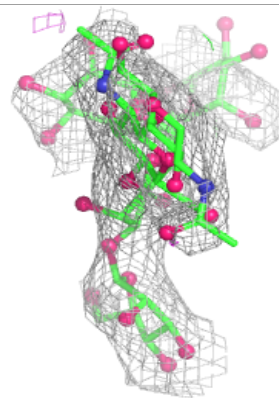
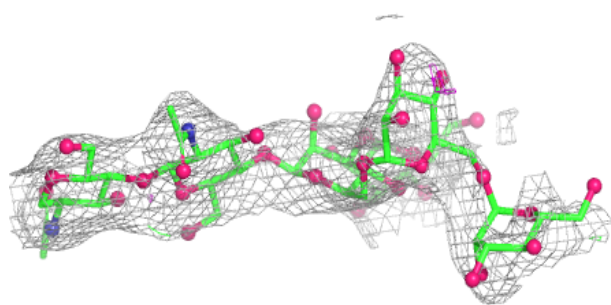
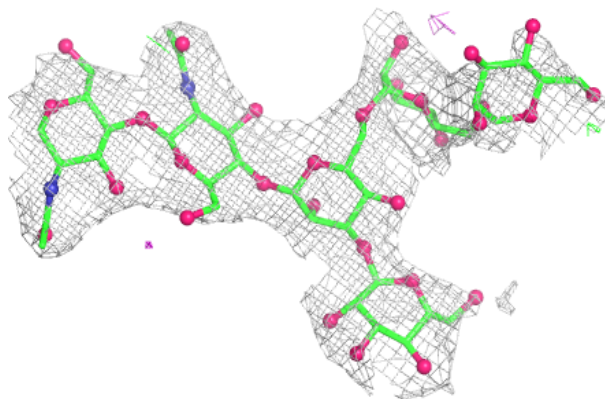
Electron density around Chain N:

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

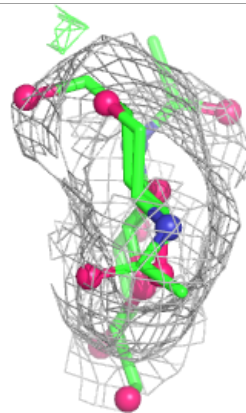
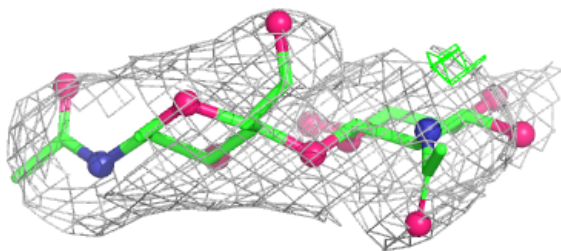
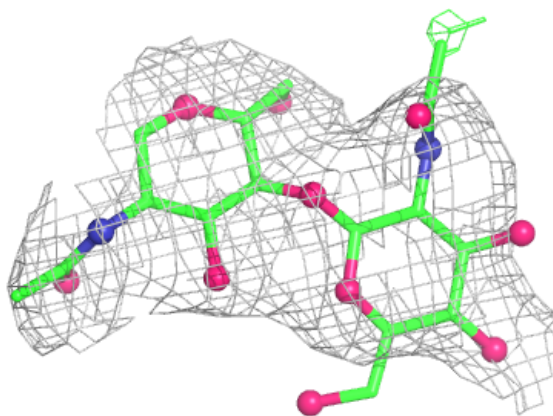


Electron density around Chain W:

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

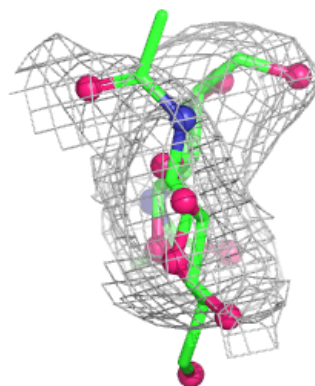
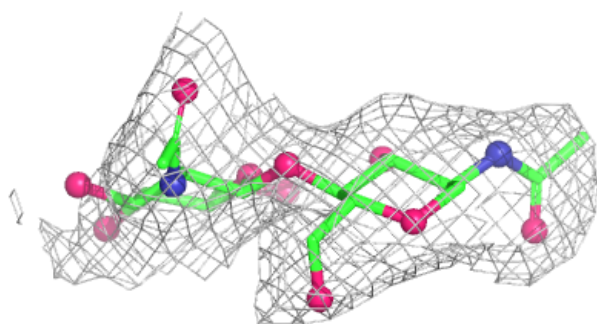
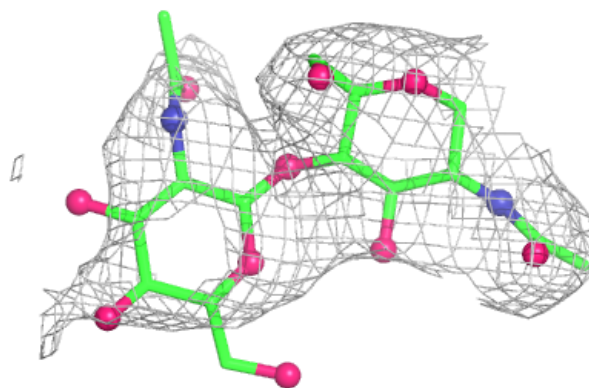
**Electron density around Chain O:**

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



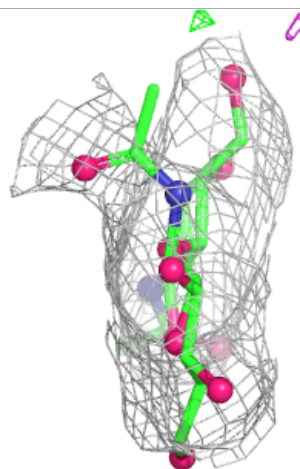
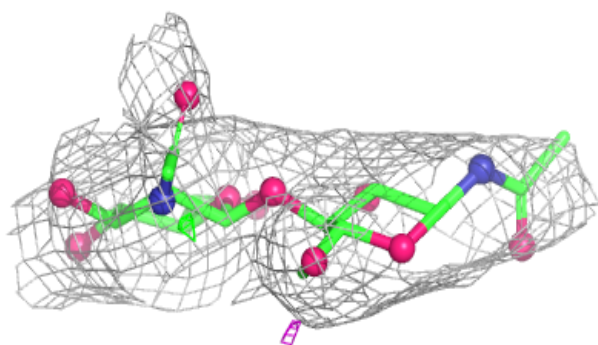
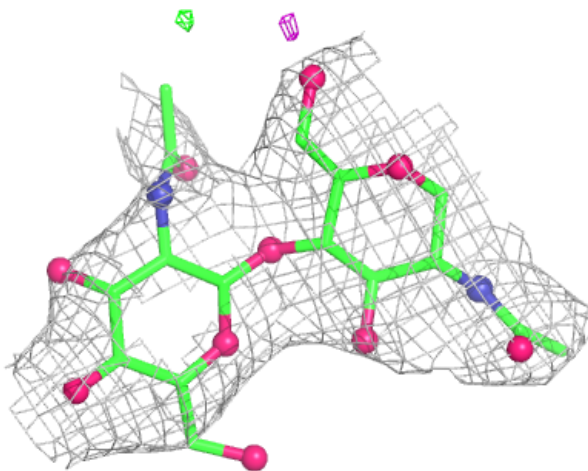
Electron density around Chain b:

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



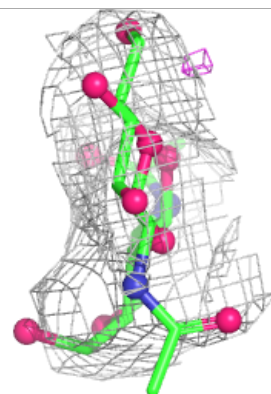
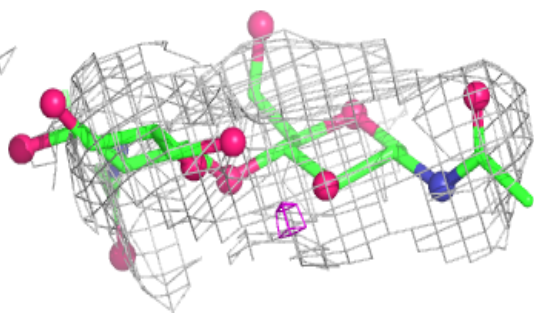
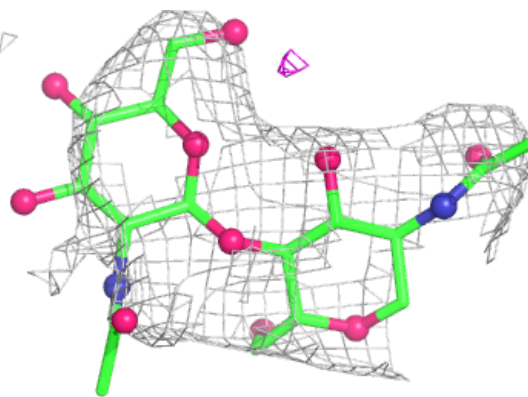
Electron density around Chain g:

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



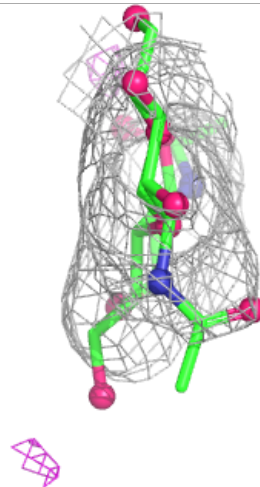
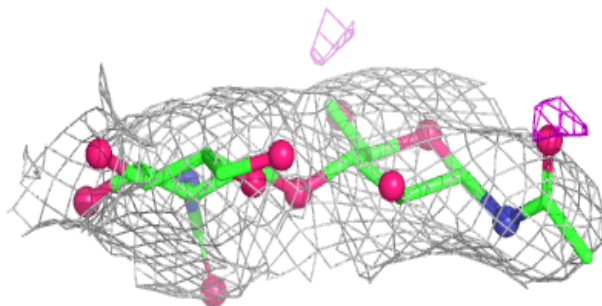
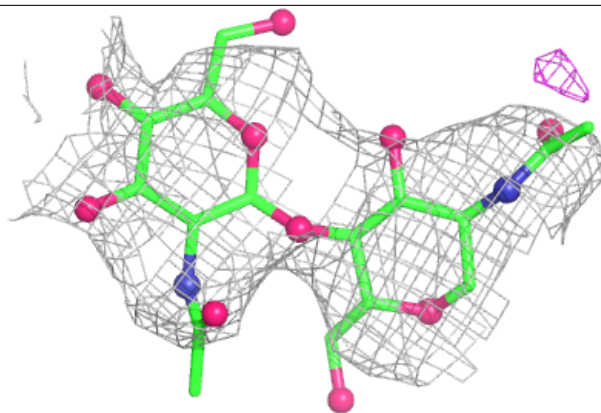
Electron density around Chain j:

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



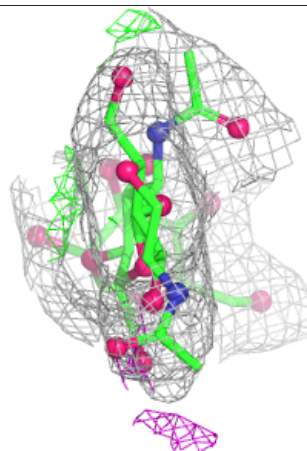
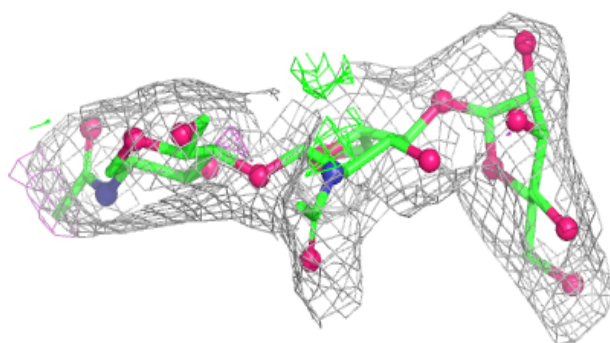
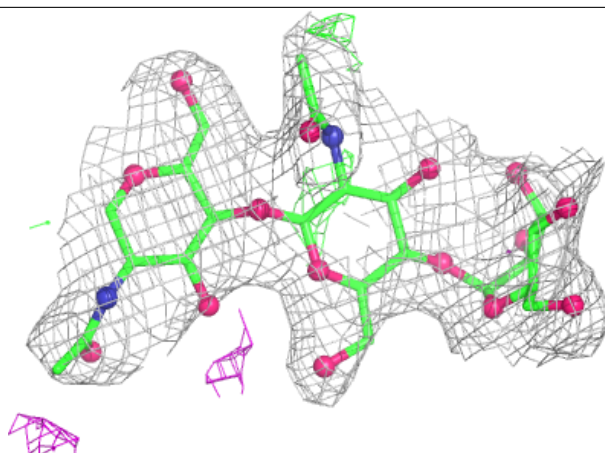
Electron density around Chain k:

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

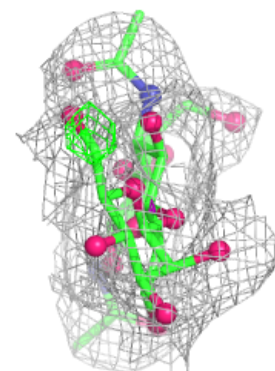
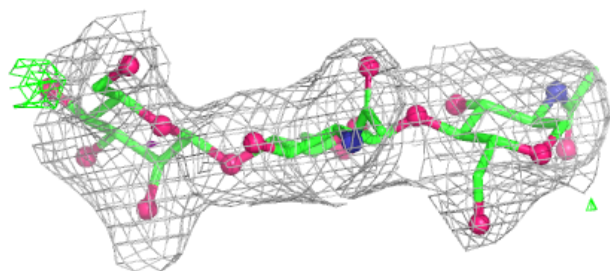
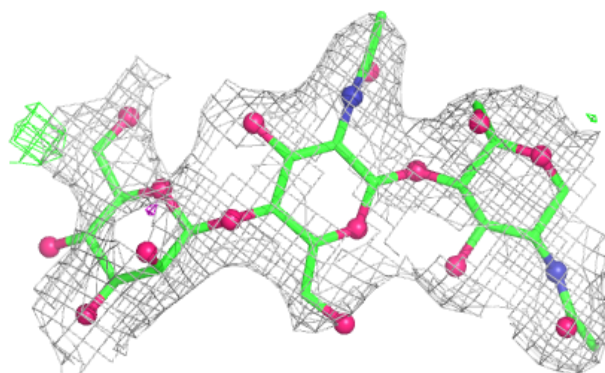


Electron density around Chain P:

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

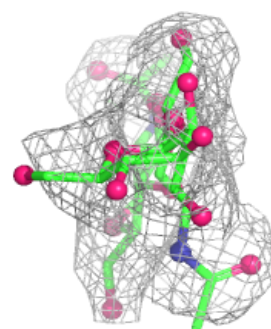
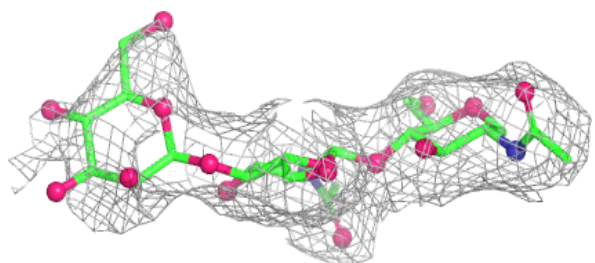
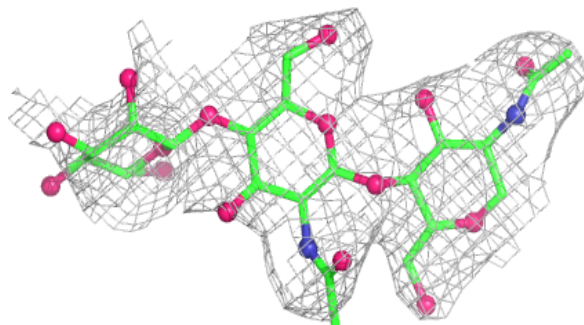
**Electron density around Chain T:**

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

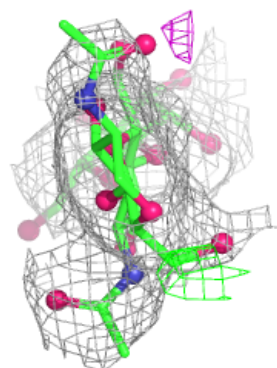
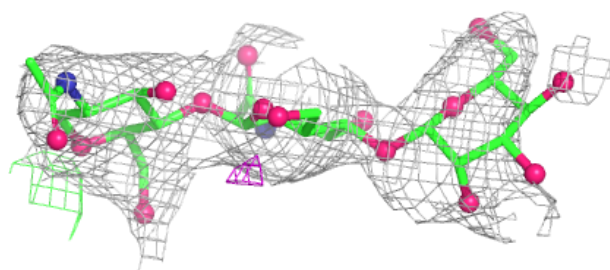
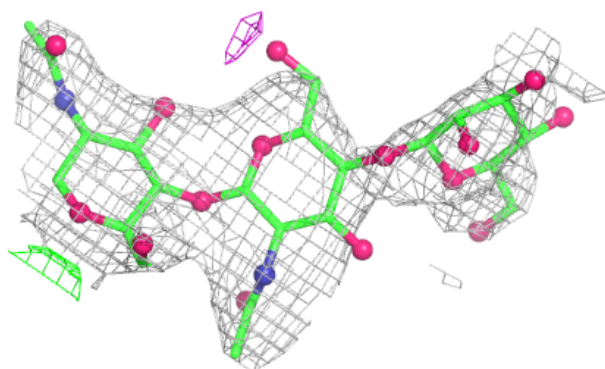


Electron density around Chain U:

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

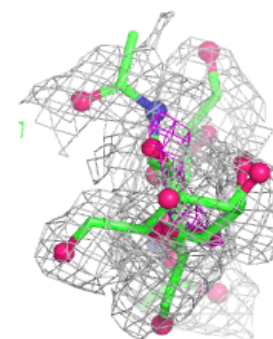
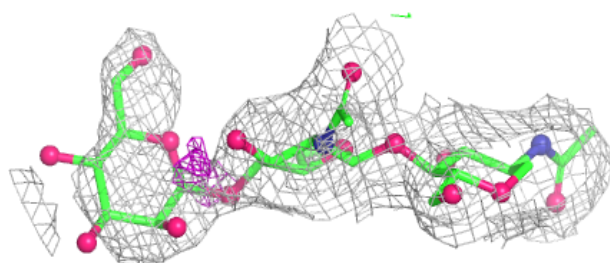
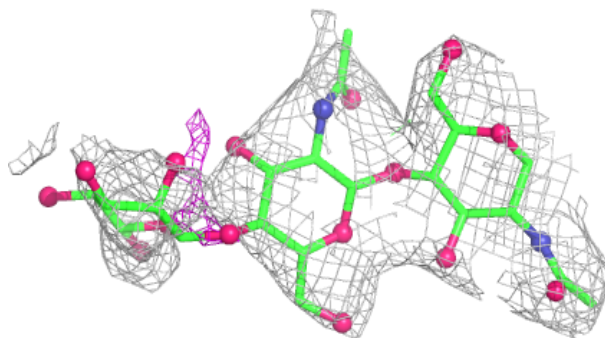
**Electron density around Chain X:**

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

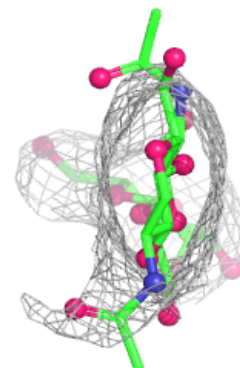
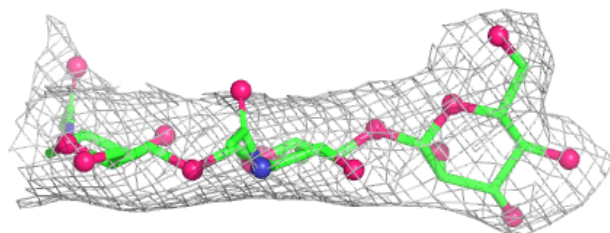
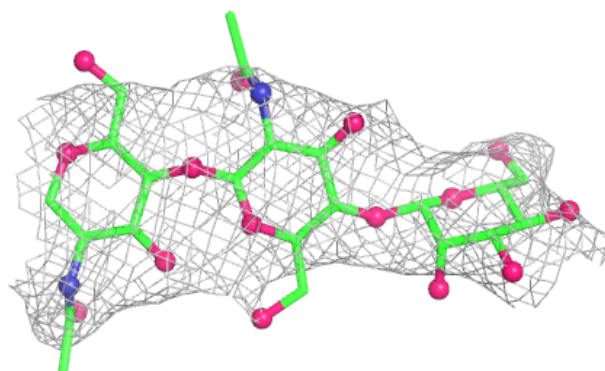


Electron density around Chain c:

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

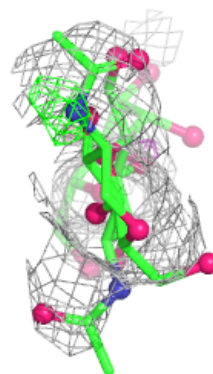
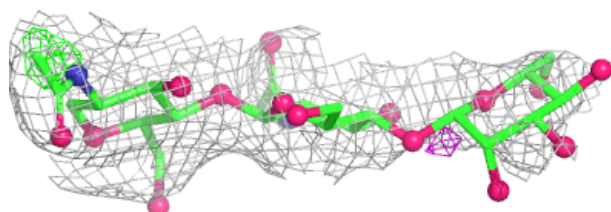
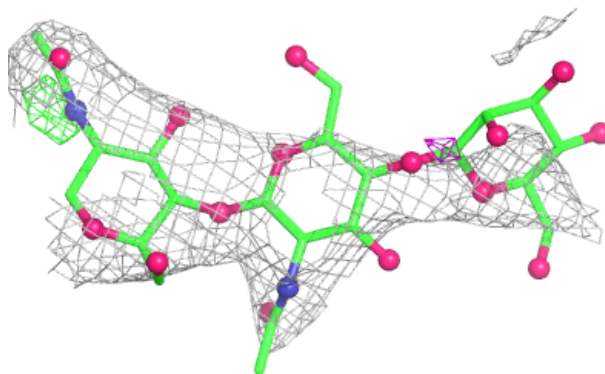
**Electron density around Chain e:**

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

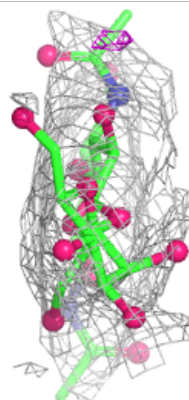
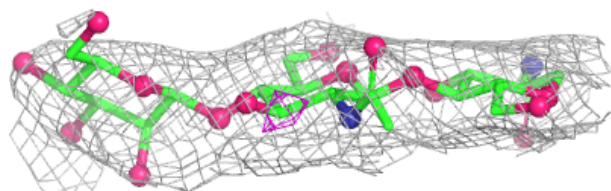
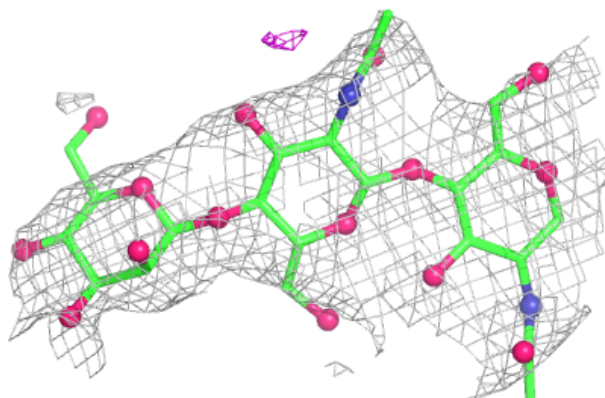


Electron density around Chain f:

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

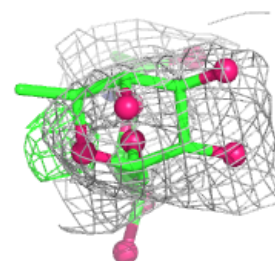
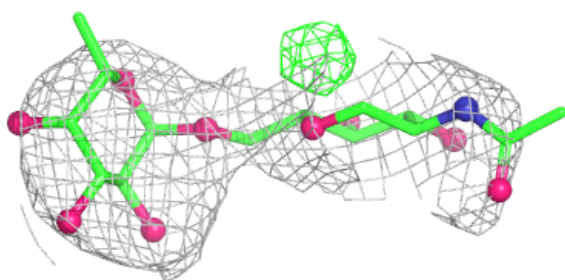
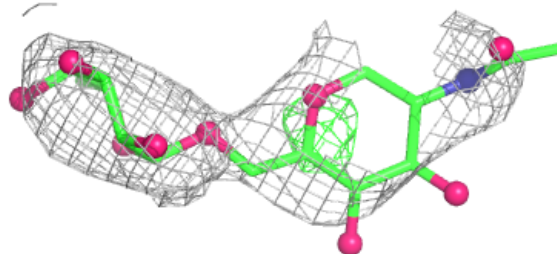
**Electron density around Chain i:**

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



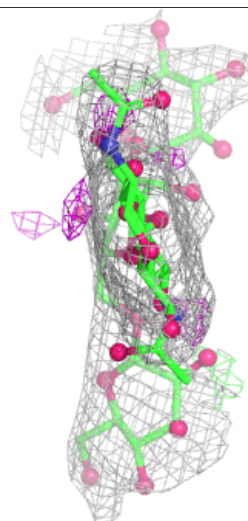
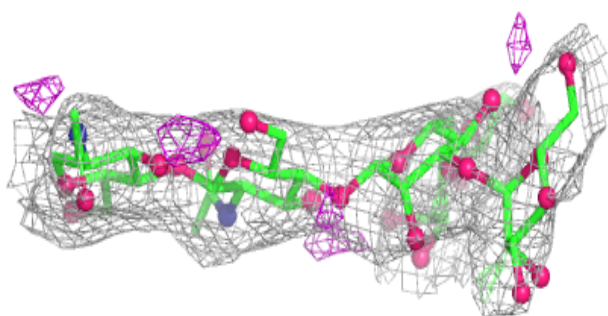
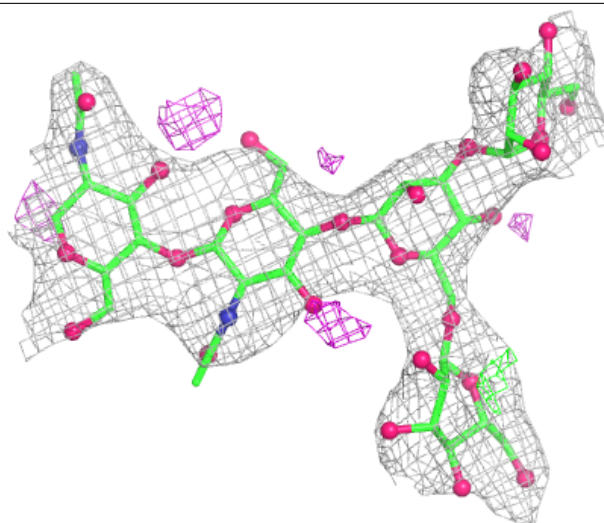
Electron density around Chain R:

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



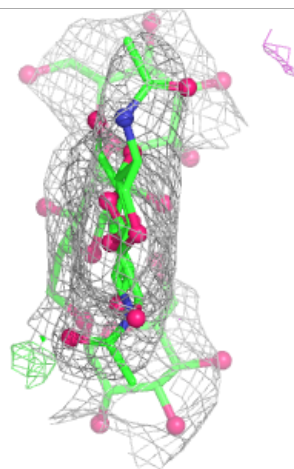
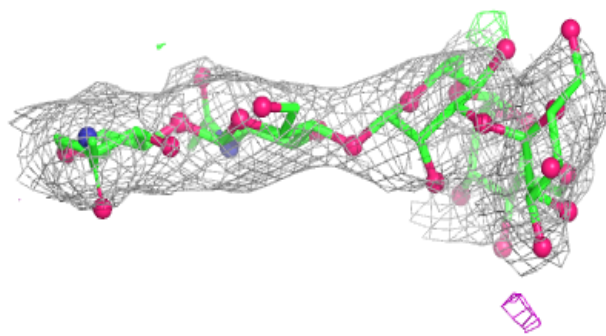
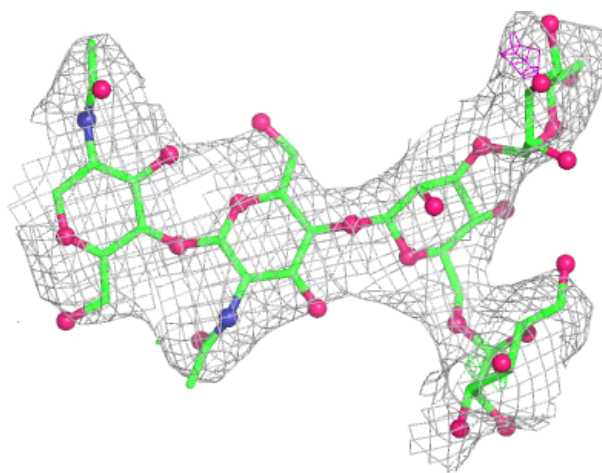
Electron density around Chain S:

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



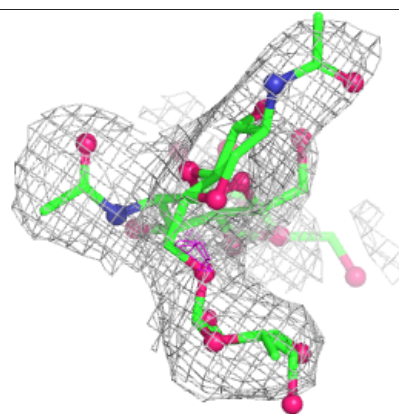
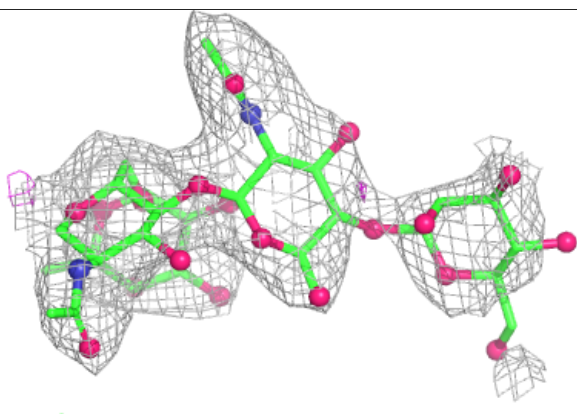
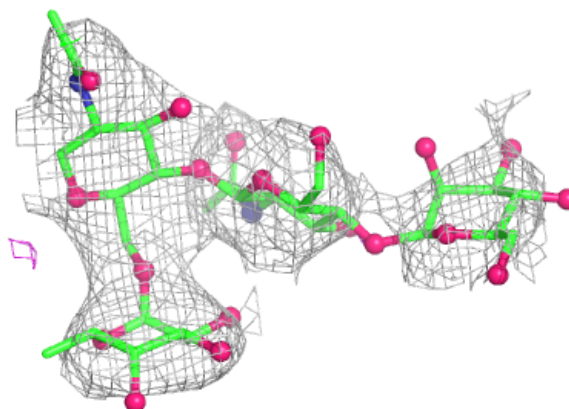
Electron density around Chain a:

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

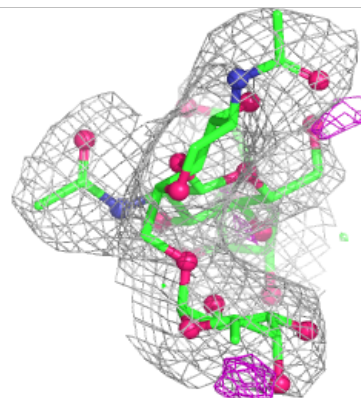
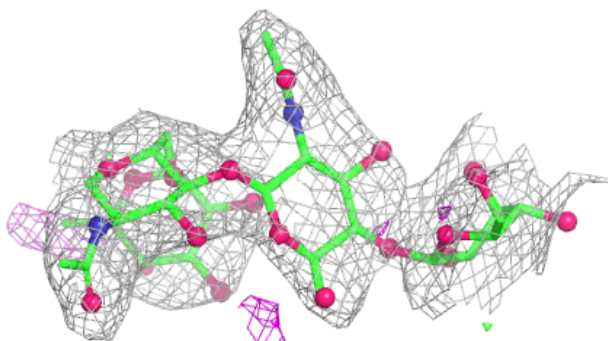
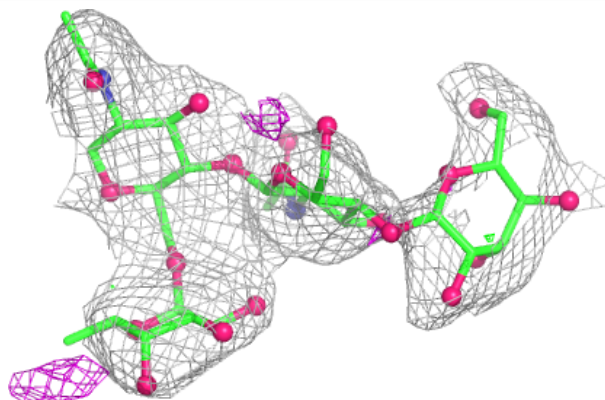


Electron density around Chain V:

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

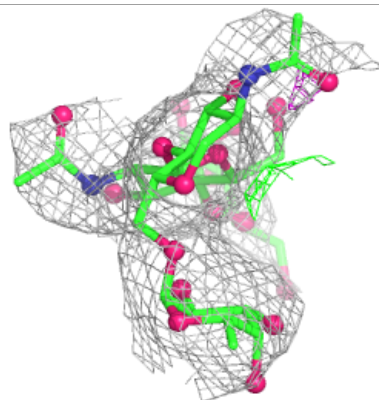
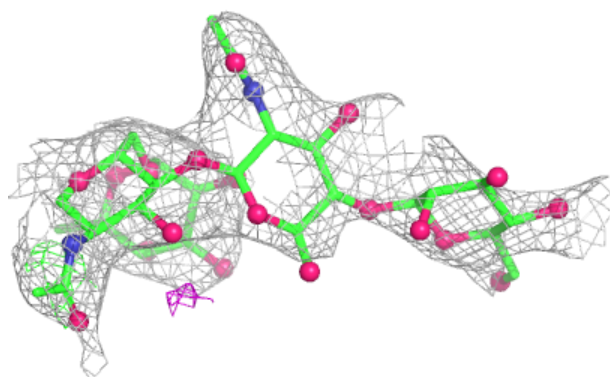
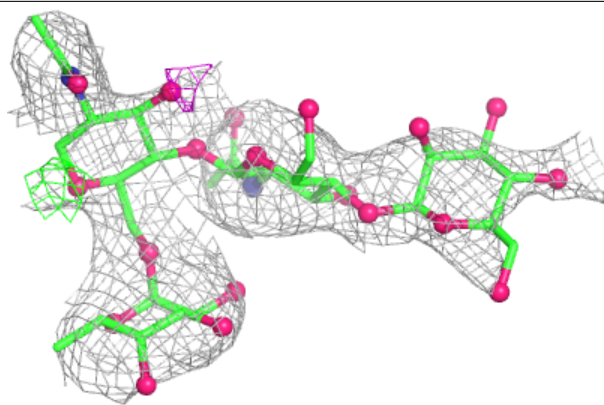
**Electron density around Chain d:**

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

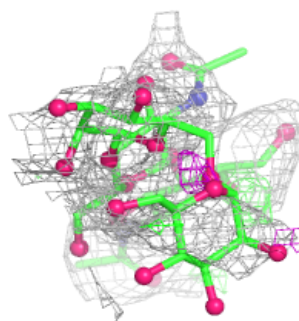
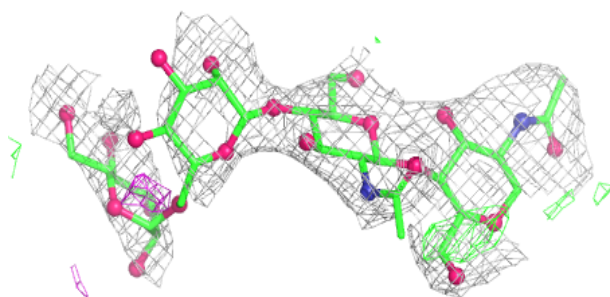
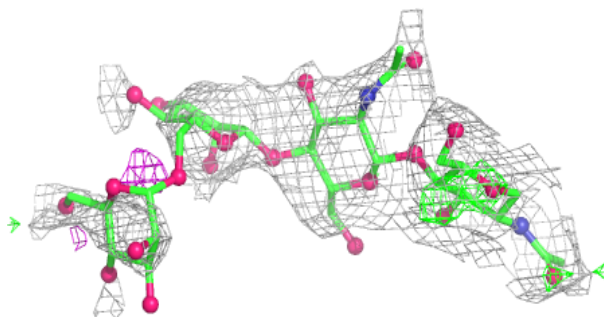


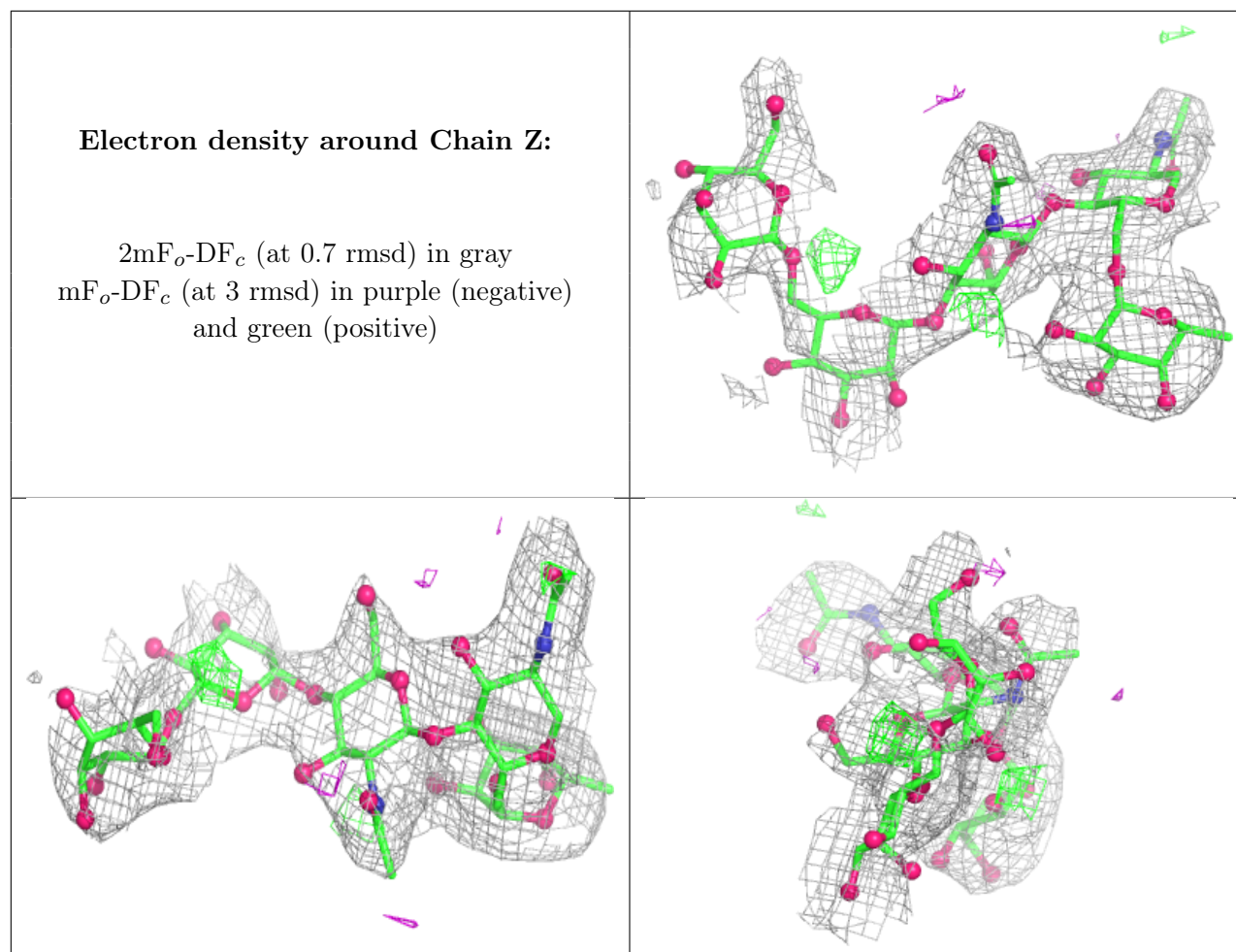
Electron density around Chain I:

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

**Electron density around Chain Y:**

$2mF_o-DF_c$ (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
13	NAG	F	901	14/15	0.35	0.20	151,155,162,163	0
12	SO4	C	205	5/5	0.47	0.11	191,191,192,192	0
13	NAG	J	903	14/15	0.49	0.17	144,150,154,156	0
12	SO4	B	822	5/5	0.53	0.19	162,163,163,163	0
12	SO4	E	202	5/5	0.55	0.14	185,186,186,187	0
13	NAG	B	902	14/15	0.55	0.15	128,137,143,144	0
12	SO4	D	422	5/5	0.56	0.14	171,172,173,174	0
13	NAG	H	903	14/15	0.57	0.13	127,135,140,144	0
12	SO4	H	821	5/5	0.61	0.15	166,169,169,171	0
13	NAG	B	901	14/15	0.63	0.13	145,152,156,156	0
13	NAG	H	901	14/15	0.63	0.12	124,131,134,135	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
12	SO4	F	825	5/5	0.63	0.12	158,159,161,161	0
13	NAG	D	902	14/15	0.63	0.17	119,125,137,138	0
12	SO4	L	412	5/5	0.66	0.11	157,159,159,160	0
12	SO4	J	413	5/5	0.66	0.12	125,126,126,127	0
12	SO4	D	425	5/5	0.73	0.10	144,146,147,147	0
13	NAG	F	903	14/15	0.74	0.18	123,127,133,137	0
12	SO4	C	202	5/5	0.75	0.17	142,143,143,144	0
12	SO4	H	820	5/5	0.76	0.21	142,143,144,147	0
12	SO4	D	419	5/5	0.76	0.31	144,145,146,146	0
12	SO4	D	423	5/5	0.77	0.10	158,159,159,159	0
12	SO4	D	421	5/5	0.78	0.22	129,129,132,133	0
12	SO4	E	203	5/5	0.78	0.18	121,121,122,123	0
12	SO4	C	203	5/5	0.78	0.15	174,175,176,176	0
12	SO4	H	819	5/5	0.79	0.12	159,159,159,160	0
12	SO4	D	424	5/5	0.80	0.12	130,130,132,133	0
12	SO4	D	420	5/5	0.80	0.14	146,147,147,148	0
12	SO4	B	823	5/5	0.82	0.11	155,157,159,160	0
12	SO4	I	201	5/5	0.82	0.09	124,125,125,126	0
12	SO4	G	202	5/5	0.83	0.14	160,160,160,160	0
12	SO4	H	817	5/5	0.84	0.31	142,143,143,144	0
12	SO4	F	822	5/5	0.88	0.17	119,120,121,121	0
12	SO4	A	202	5/5	0.88	0.16	147,148,148,150	0
12	SO4	F	821	5/5	0.88	0.20	112,114,115,116	0
12	SO4	F	824	5/5	0.89	0.22	163,163,163,163	0
12	SO4	B	821	5/5	0.89	0.23	144,145,145,147	0
12	SO4	C	204	5/5	0.89	0.21	126,129,129,131	0
12	SO4	H	818	5/5	0.90	0.20	147,148,148,149	0
12	SO4	B	820	5/5	0.90	0.21	126,127,129,129	0
12	SO4	K	201	5/5	0.90	0.11	123,124,124,125	0
12	SO4	C	201	5/5	0.91	0.09	118,118,119,119	0
12	SO4	B	824	5/5	0.91	0.12	155,155,156,156	0
12	SO4	F	823	5/5	0.94	0.13	121,122,123,123	0
12	SO4	E	201	5/5	0.95	0.10	81,82,82,83	0
12	SO4	G	201	5/5	0.95	0.06	63,68,68,70	0
12	SO4	A	201	5/5	0.98	0.06	76,77,78,78	0

6.5 Other polymers

There are no such residues in this entry.