



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:55 PM UTC

PDB ID : 6CH8 / pdb_00006ch8
Title : Crystal structure of a natively-glycosylated BG505 SOSIP.664 HIV-1 Envelope Trimer in complex with the broadly-neutralizing antibodies BG18 and 35O22
Authors : Barnes, C.O.; Bjorkman, P.J.
Deposited on : 2018-02-22
Resolution : 4.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

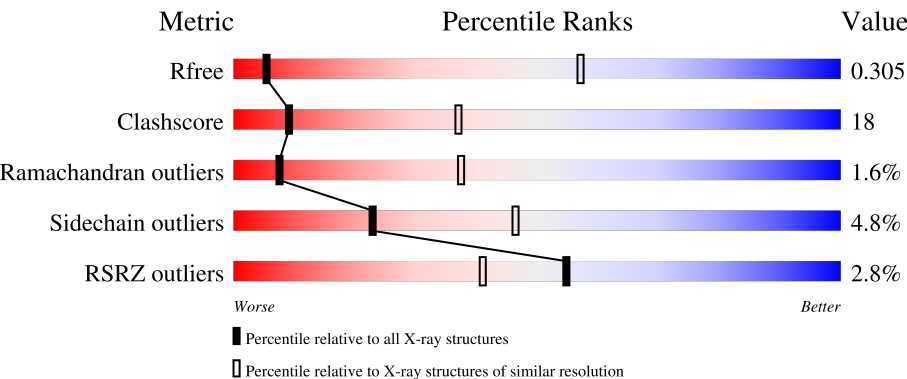
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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	1243 (4.40-3.80)
Clashscore	190562	1293 (4.40-3.80)
Ramachandran outliers	187476	1206 (4.40-3.80)
Sidechain outliers	187428	1193 (4.40-3.80)
RSRZ outliers	180081	1240 (4.40-3.80)

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	B	153	
2	D	243	
3	E	216	
4	G	479	
5	Q	241	

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Mol	Chain	Length	Quality of chain
6	R	215	
7	A	3	
7	O	3	
8	C	5	
8	J	5	
9	F	7	
10	H	5	
10	U	5	
11	I	7	
12	K	4	
12	T	4	
13	L	4	
14	M	7	
15	N	8	
16	P	6	
17	S	8	
18	V	9	

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
17	NAG	S	1	-	-	X	-

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 12325 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 Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	139	Total	C	N	O	S	0	0	0
			1109	700	195	208	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	605	CYS	THR	engineered mutation	UNP Q2N0S7

- Molecule 2 is a protein called 35O22 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	235	Total	C	N	O	S	0	0	0
			1753	1110	295	340	8			

- Molecule 3 is a protein called 35O22 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	210	Total	C	N	O	S	0	0	0
			1592	998	264	322	8			

- Molecule 4 is a protein called Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	451	Total	C	N	O	S	0	0	0
			3537	2220	625	665	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	332	ASN	THR	conflict	UNP Q2N0S6
G	501	CYS	ALA	engineered mutation	UNP Q2N0S6

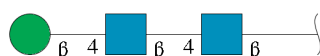
- Molecule 5 is a protein called BG18 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	Q	228	Total	C	N	O	S	0	0	0
			1678	1055	286	329	8			

- Molecule 6 is a protein called BG18 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	R	211	Total	C	N	O	S	0	0	0
			1514	947	253	308	6			

- Molecule 7 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.



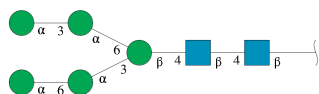
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	A	3	Total	C	N	O		0	0	0
			39	22	2	15				
7	O	3	Total	C	N	O		0	0	0
			39	22	2	15				

- Molecule 8 is an oligosaccharide called 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.



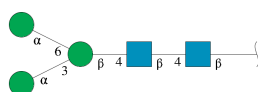
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	C	5	Total	C	N	O		0	0	0
			61	34	2	25				
8	J	5	Total	C	N	O		0	0	0
			61	34	2	25				

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



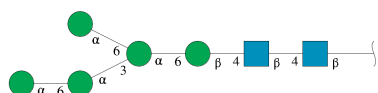
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	F	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	H	5	Total	C	N	O	0	0	0
			61	34	2	25			
10	U	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	I	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 12 is an oligosaccharide called 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.



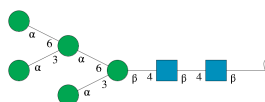
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	K	4	Total	C	N	O	0	0	0
			50	28	2	20			
12	T	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 13 is an oligosaccharide called 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.



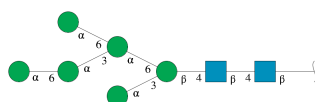
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	L	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 14 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[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.



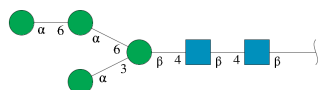
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	M	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 15 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[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.



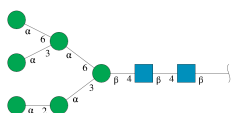
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	N	8	Total	C	N	O	0	0	0
			94	52	2	40			

- Molecule 16 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.



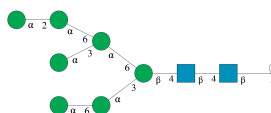
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	P	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 17 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



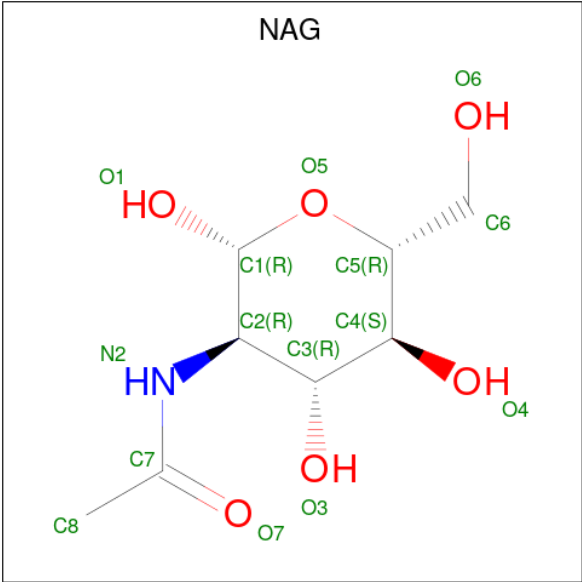
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	S	8	Total	C	N	O	0	0	0
			94	52	2	40			

- Molecule 18 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-6)-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
18	V	9	Total	C	N	O	0	0	0
			105	58	2	45			

- Molecule 19 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

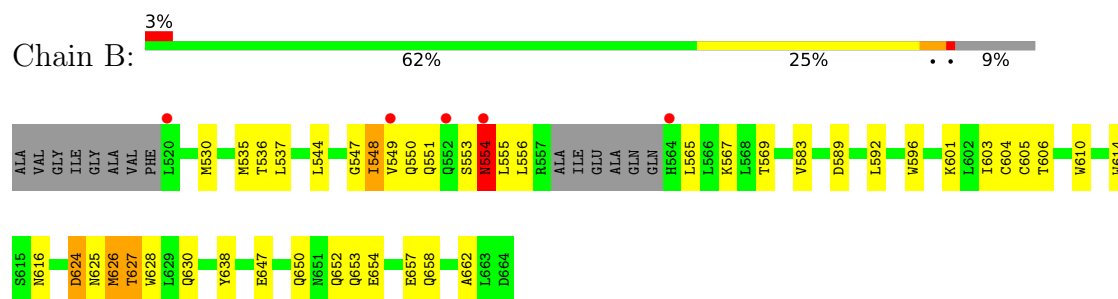


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
19	B	1	Total	C	N	O	0	0
			14	8	1	5		
19	G	1	Total	C	N	O	0	0
			14	8	1	5		
19	G	1	Total	C	N	O	0	0
			14	8	1	5		
19	G	1	Total	C	N	O	0	0
			14	8	1	5		

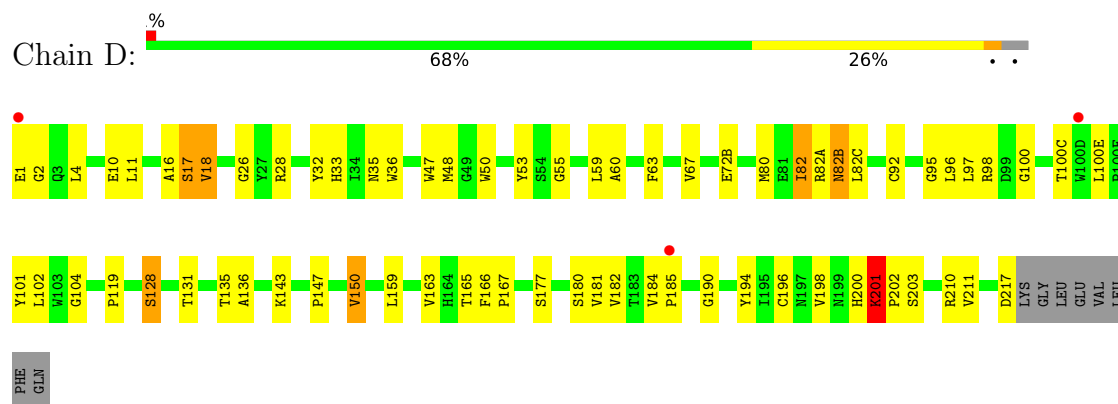
3 Residue-property plots [i](#)

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

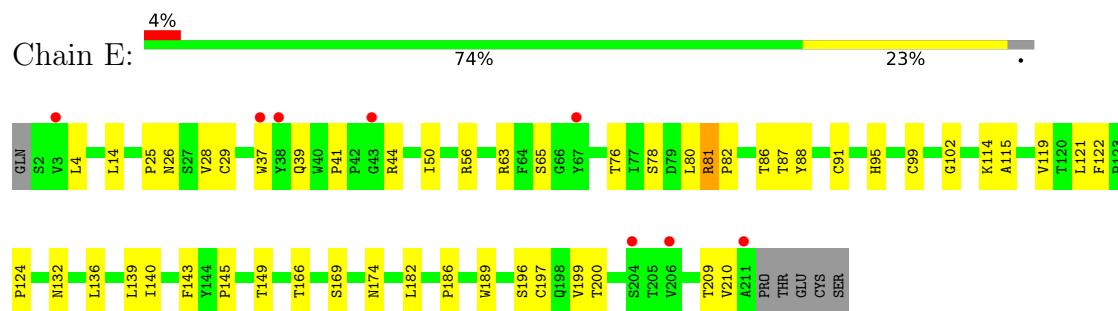
• Molecule 1: Envelope glycoprotein gp41



• Molecule 2: 35O22 Heavy Chain

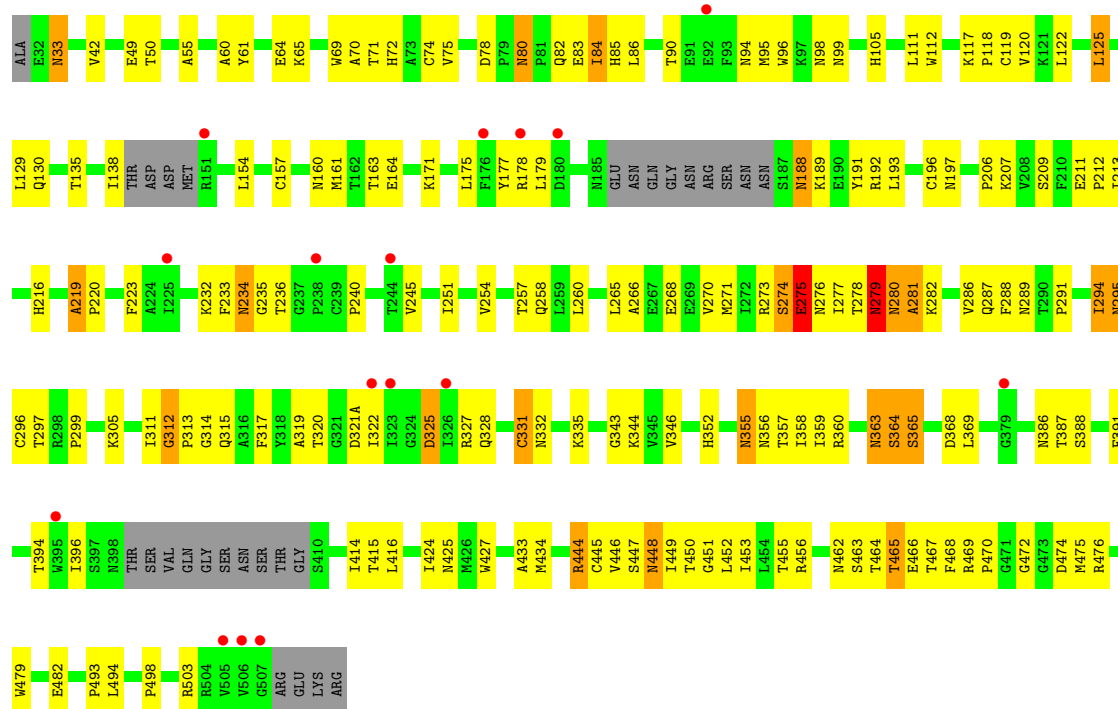


• Molecule 3: 35O22 Light Chain

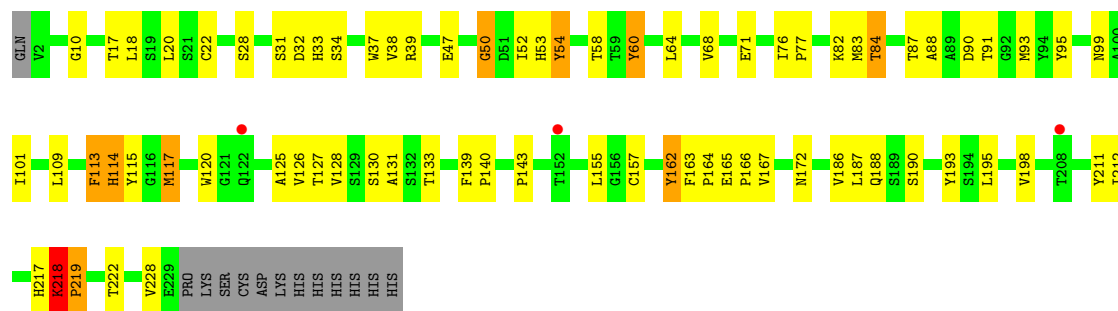


• Molecule 4: Envelope glycoprotein gp120

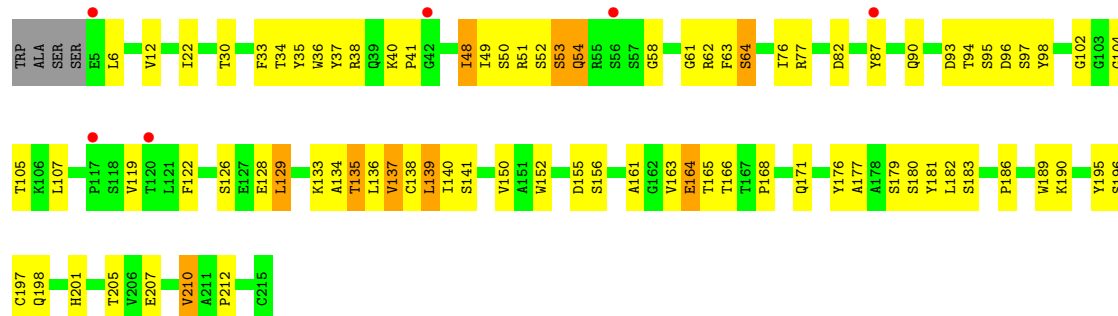




• Molecule 5: BG18 Heavy Chain



• Molecule 6: BG18 Light Chain

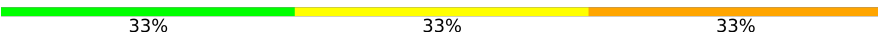


- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain A:  67% 33%

MAG1
MAG2
BMA3

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  33% 33% 33%

MAG1
MAG2
BMA3

- Molecule 8: 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 C:  60% 20% 20%

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 8: 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 J:  60% 20% 20%

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 9: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[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 F:  29% 57% 14%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7

- Molecule 10: 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 H:  40% 40% 20%

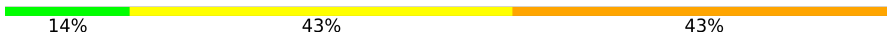
MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 10: 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 U:  40% 60%



- Molecule 11: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  14% 43% 43%



- Molecule 12: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  25% 25% 50%



- Molecule 12: 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 T:  75% 25%

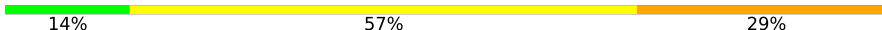


- Molecule 13: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  75% 25%

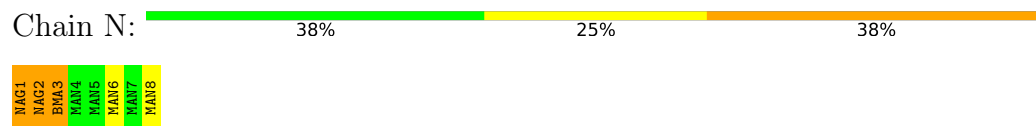


- Molecule 14: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  14% 57% 29%



- Molecule 15: α -D-mannopyranose-(1-6)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose



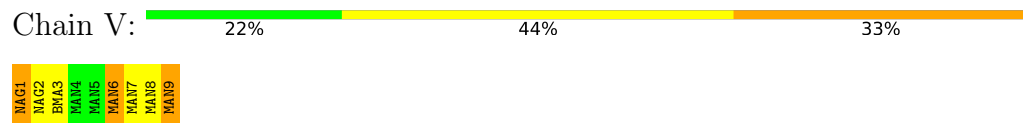
- Molecule 16: α -D-mannopyranose-(1-6)- α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose



- Molecule 17: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-3)] α -D-mannopyranose-(1-6)-[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



- Molecule 18: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-6)- α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	239.22Å 239.22Å 355.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.51 – 4.10 39.51 – 4.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.51-4.10) 99.7 (39.51-4.10)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 4.13Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.229 , 0.274 0.261 , 0.305	Depositor DCC
R_{free} test set	1551 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	163.4	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 189.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	12325	wwPDB-VP
Average B, all atoms (Å ²)	226.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.29	0/1127	0.75	5/1527 (0.3%)
2	D	0.20	0/1798	0.52	2/2450 (0.1%)
3	E	0.14	0/1635	0.32	0/2235
4	G	0.24	0/3610	0.76	15/4901 (0.3%)
5	Q	0.18	0/1721	0.48	0/2353
6	R	0.24	0/1552	0.62	4/2129 (0.2%)
All	All	0.22	0/11443	0.62	26/15595 (0.2%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	219	ALA	CA-C-N	19.29	139.21	120.31
4	G	219	ALA	C-N-CA	19.29	139.21	120.31
4	G	464	THR	N-CA-C	14.82	127.51	111.36
4	G	279	ASN	N-CA-C	-10.24	95.27	109.71
2	D	203	SER	N-CA-C	10.19	124.79	111.75
4	G	312	GLY	CA-C-N	8.84	128.78	119.85
4	G	312	GLY	C-N-CA	8.84	128.78	119.85
6	R	137	VAL	N-CA-C	-7.78	95.60	107.73
1	B	627	THR	N-CA-C	7.74	128.77	113.29
1	B	553	SER	CB-CA-C	-7.52	107.89	116.54
6	R	164	GLU	N-CA-C	7.34	120.22	110.53
4	G	196	CYS	N-CA-C	7.14	121.62	112.34
4	G	188	ASN	N-CA-C	-6.99	96.88	108.34
2	D	100(C)	THR	N-CA-C	-6.58	107.12	114.62
4	G	331	CYS	N-CA-C	6.58	119.62	108.90
4	G	281	ALA	N-CA-C	6.45	118.31	111.28
1	B	554	ASN	N-CA-C	6.33	124.28	110.80
4	G	465	THR	N-CA-C	6.33	118.39	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	61	GLY	CA-C-N	5.67	132.38	121.54
6	R	61	GLY	C-N-CA	5.67	132.38	121.54
1	B	553	SER	N-CA-C	5.67	116.93	108.31
4	G	275	GLU	N-CA-C	-5.43	105.36	111.28
1	B	626	MET	O-C-N	-5.13	116.66	122.10
4	G	61	TYR	CB-CA-C	-5.05	109.26	116.34
4	G	219	ALA	O-C-N	5.03	127.17	121.53
4	G	448	ASN	N-CA-C	-5.00	103.44	110.50

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	B	1109	0	1103	47	1
2	D	1753	0	1713	66	0
3	E	1592	0	1530	35	0
4	G	3537	0	3469	166	0
5	Q	1678	0	1590	58	0
6	R	1514	0	1411	83	0
7	A	39	0	34	2	0
7	O	39	0	34	2	0
8	C	61	0	52	1	0
8	J	61	0	52	1	0
9	F	83	0	70	3	0
10	H	61	0	52	2	0
10	U	61	0	52	3	0
11	I	83	0	70	5	0
12	K	50	0	43	3	0
12	T	50	0	43	0	0
13	L	50	0	43	0	0
14	M	83	0	69	3	0
15	N	94	0	79	3	0
16	P	72	0	61	0	0
17	S	94	0	79	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	V	105	0	87	4	0
19	B	14	0	13	0	0
19	G	42	0	39	0	0
All	All	12325	0	11788	442	1

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 18.

All (442) 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)
4:G:386:ASN:HD21	17:S:1:NAG:C2	1.24	1.48
4:G:386:ASN:ND2	17:S:1:NAG:C1	1.75	1.45
1:B:626:MET:O	1:B:627:THR:CG2	1.79	1.30
1:B:624:ASP:O	2:D:98:ARG:HG3	1.35	1.22
4:G:386:ASN:ND2	17:S:1:NAG:N2	1.86	1.21
2:D:201:LYS:HB2	2:D:202:PRO:CD	1.71	1.20
4:G:386:ASN:HD21	17:S:1:NAG:C1	1.38	1.16
4:G:386:ASN:HD22	17:S:1:NAG:H83	1.04	1.12
6:R:163:VAL:HG11	6:R:182:LEU:HA	1.17	1.12
1:B:626:MET:O	1:B:627:THR:HG22	0.97	1.11
4:G:386:ASN:HD22	17:S:1:NAG:C8	1.63	1.10
1:B:547:GLY:O	1:B:550:GLN:HG3	1.54	1.08
2:D:201:LYS:CB	2:D:202:PRO:HD3	1.84	1.07
6:R:163:VAL:CG1	6:R:182:LEU:HA	1.85	1.06
2:D:119:PRO:HG3	2:D:201:LYS:HZ1	1.20	1.04
6:R:163:VAL:HG11	6:R:182:LEU:CA	1.85	1.04
4:G:386:ASN:CG	17:S:1:NAG:C1	2.29	1.04
4:G:364:SER:O	4:G:365:SER:OG	1.76	1.03
6:R:163:VAL:HG21	6:R:182:LEU:HD12	1.41	1.02
2:D:201:LYS:CB	2:D:202:PRO:CD	2.35	0.99
2:D:201:LYS:HB2	2:D:202:PRO:HD3	0.96	0.96
1:B:624:ASP:O	2:D:98:ARG:CG	2.13	0.96
4:G:365:SER:HB3	4:G:469:ARG:HD2	1.46	0.96
1:B:625:ASN:OD1	2:D:32:TYR:OH	1.81	0.96
1:B:626:MET:C	1:B:627:THR:HG22	1.92	0.94
6:R:163:VAL:HG21	6:R:183:SER:H	1.34	0.93
6:R:139:LEU:HD12	6:R:140:ILE:N	1.86	0.91
2:D:201:LYS:H	2:D:201:LYS:HD3	1.34	0.91
2:D:98:ARG:HD3	9:F:1:NAG:H81	1.50	0.91
2:D:201:LYS:CG	2:D:202:PRO:HD2	2.02	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:386:ASN:ND2	17:S:1:NAG:C8	2.34	0.90
6:R:163:VAL:CG2	6:R:182:LEU:HD12	2.02	0.89
4:G:358:ILE:O	4:G:465:THR:OG1	1.92	0.88
2:D:119:PRO:HG3	2:D:201:LYS:NZ	1.89	0.88
2:D:201:LYS:HG2	2:D:202:PRO:HD2	1.55	0.87
2:D:16:ALA:O	2:D:17:SER:OG	1.91	0.87
4:G:220:PRO:HG2	4:G:223:PHE:CD2	2.12	0.85
6:R:134:ALA:H	6:R:186:PRO:HG3	1.41	0.85
4:G:386:ASN:ND2	17:S:1:NAG:H83	1.90	0.85
1:B:530:MET:HG2	1:B:628:TRP:CD1	2.11	0.84
4:G:386:ASN:ND2	17:S:1:NAG:C7	2.41	0.83
6:R:152:TRP:HE1	6:R:161:ALA:HB3	1.42	0.83
4:G:466:GLU:HG2	4:G:468:PHE:CE1	2.15	0.82
6:R:36:TRP:HB2	6:R:48:ILE:HG21	1.61	0.81
2:D:201:LYS:CG	2:D:202:PRO:CD	2.58	0.81
4:G:49:GLU:HG2	4:G:99:ASN:HB3	1.62	0.79
4:G:295:ASN:HB3	4:G:446:VAL:HG12	1.65	0.79
4:G:219:ALA:HB1	4:G:220:PRO:HD2	1.64	0.79
6:R:163:VAL:HG11	6:R:182:LEU:C	2.08	0.78
4:G:83:GLU:C	4:G:84:ILE:HD12	2.08	0.77
6:R:49:ILE:HD11	6:R:58:GLY:HA2	1.66	0.77
5:Q:17:THR:HG22	5:Q:84:THR:HA	1.66	0.76
4:G:277:ILE:C	4:G:278:THR:HG23	2.09	0.76
4:G:462:ASN:O	4:G:463:SER:OG	2.04	0.75
4:G:295:ASN:OD1	4:G:295:ASN:N	2.17	0.75
5:Q:167:VAL:HA	5:Q:218:LYS:HE2	1.68	0.75
5:Q:167:VAL:HG21	5:Q:195:LEU:HD13	1.69	0.75
1:B:555:LEU:O	1:B:555:LEU:HD23	1.87	0.74
6:R:22:ILE:HD12	6:R:105:THR:HG21	1.69	0.74
2:D:201:LYS:HD3	2:D:201:LYS:N	2.02	0.74
4:G:95:MET:H	4:G:236:THR:HG21	1.51	0.74
4:G:125:LEU:HA	4:G:161:MET:HE1	1.70	0.74
4:G:219:ALA:CB	4:G:220:PRO:HD2	2.18	0.73
1:B:530:MET:HA	1:B:628:TRP:CD1	2.24	0.73
4:G:279:ASN:O	4:G:281:ALA:N	2.21	0.73
5:Q:28:SER:HB2	18:V:6:MAN:H2	1.70	0.73
4:G:277:ILE:HD11	4:G:352:HIS:O	1.89	0.73
5:Q:186:VAL:HG13	5:Q:188:GLN:H	1.55	0.72
4:G:294:ILE:CD1	4:G:296:CYS:SG	2.78	0.72
4:G:356:ASN:O	4:G:357:THR:HG23	1.90	0.71
4:G:358:ILE:HB	4:G:465:THR:OG1	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:233:PHE:HB3	4:G:273:ARG:HH21	1.56	0.70
4:G:364:SER:O	4:G:365:SER:CB	2.39	0.70
1:B:548:ILE:HG21	4:G:78:ASP:OD2	1.92	0.70
5:Q:33:HIS:HA	5:Q:101:ILE:HG22	1.74	0.70
5:Q:117:MET:SD	5:Q:117:MET:N	2.65	0.70
3:E:136:LEU:H	3:E:182:LEU:HB3	1.56	0.70
4:G:84:ILE:HD12	4:G:84:ILE:N	2.06	0.69
1:B:554:ASN:OD1	1:B:567:LYS:NZ	2.19	0.69
6:R:152:TRP:HE1	6:R:161:ALA:CB	2.06	0.69
2:D:47:TRP:HZ2	2:D:50:TRP:HD1	1.41	0.69
6:R:63:PHE:O	6:R:64:SER:HB3	1.92	0.69
3:E:132:ASN:HB3	3:E:186:PRO:HG3	1.74	0.68
4:G:294:ILE:HD11	4:G:296:CYS:SG	2.33	0.68
6:R:40:LYS:HE2	6:R:41:PRO:HD2	1.76	0.68
2:D:96:LEU:HA	2:D:101:TYR:HB2	1.75	0.68
4:G:313:PRO:O	4:G:315:GLN:N	2.25	0.68
5:Q:50:GLY:HA2	5:Q:60:TYR:HA	1.76	0.67
3:E:121:LEU:HD12	3:E:197:CYS:HB2	1.75	0.67
6:R:129:LEU:H	6:R:129:LEU:HD12	1.57	0.67
4:G:277:ILE:O	4:G:278:THR:HG23	1.95	0.67
4:G:328:GLN:HB3	5:Q:109:LEU:HD21	1.76	0.67
2:D:67:VAL:HG22	2:D:82:ILE:HG22	1.74	0.67
4:G:279:ASN:O	4:G:280:ASN:C	2.37	0.66
4:G:466:GLU:HG2	4:G:468:PHE:HE1	1.59	0.66
6:R:152:TRP:NE1	6:R:161:ALA:HB3	2.10	0.66
4:G:50:THR:HG21	4:G:220:PRO:HG3	1.77	0.66
6:R:63:PHE:HD1	6:R:76:ILE:HG13	1.60	0.66
4:G:130:GLN:OE1	4:G:188:ASN:ND2	2.29	0.66
5:Q:88:ALA:HA	5:Q:128:VAL:HG11	1.78	0.66
4:G:386:ASN:ND2	17:S:1:NAG:C2	2.09	0.66
10:U:3:BMA:H61	10:U:5:MAN:H5	1.78	0.66
10:U:3:BMA:H3	10:U:4:MAN:H5	1.76	0.66
6:R:201:HIS:H	6:R:205:THR:HG21	1.61	0.65
11:I:4:MAN:H4	11:I:5:MAN:H5	1.78	0.65
4:G:327:ARG:HH22	18:V:2:NAG:H61	1.61	0.65
4:G:360:ARG:HB3	4:G:467:THR:OG1	1.95	0.65
5:Q:91:THR:HB	5:Q:127:THR:HA	1.76	0.65
3:E:63:ARG:HD3	3:E:81:ARG:CZ	2.29	0.63
5:Q:188:GLN:NE2	6:R:164:GLU:OE2	2.28	0.63
3:E:26:ASN:HA	3:E:29:CYS:HB2	1.79	0.63
6:R:139:LEU:HD12	6:R:140:ILE:CA	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:34:SER:OG	5:Q:99:ASN:ND2	2.31	0.63
2:D:159:LEU:HD21	2:D:184:VAL:HG11	1.81	0.62
6:R:139:LEU:HD12	6:R:139:LEU:C	2.24	0.62
10:H:3:BMA:H3	10:H:4:MAN:H5	1.81	0.62
4:G:279:ASN:ND2	4:G:282:LYS:HG2	2.14	0.62
6:R:119:VAL:O	6:R:140:ILE:HD12	1.99	0.62
1:B:627:THR:O	1:B:628:TRP:HB2	1.98	0.62
4:G:325:ASP:OD2	6:R:54:GLN:NE2	2.31	0.62
4:G:356:ASN:O	4:G:357:THR:CG2	2.48	0.62
4:G:294:ILE:C	4:G:294:ILE:HD12	2.25	0.61
4:G:388:SER:HB3	17:S:1:NAG:HN2	1.65	0.61
2:D:1:GLU:N	2:D:1:GLU:OE1	2.33	0.61
1:B:616:ASN:O	7:A:1:NAG:N2	2.34	0.61
5:Q:162:TYR:HE2	5:Q:195:LEU:H	1.47	0.61
17:S:2:NAG:H5	17:S:3:BMA:H2	1.82	0.61
4:G:331:CYS:HB2	4:G:416:LEU:HB2	1.82	0.61
6:R:63:PHE:HA	6:R:76:ILE:HA	1.81	0.60
6:R:133:LYS:HA	6:R:186:PRO:HD3	1.83	0.60
1:B:627:THR:CG2	1:B:630:GLN:HG3	2.32	0.60
6:R:6:LEU:HG	6:R:102:GLY:HA3	1.83	0.60
6:R:164:GLU:O	6:R:181:TYR:O	2.20	0.59
4:G:358:ILE:HA	4:G:396:ILE:HG21	1.82	0.59
17:S:1:NAG:O3	17:S:2:NAG:N2	2.36	0.59
4:G:60:ALA:HB1	4:G:65:LYS:HA	1.84	0.59
10:U:3:BMA:H5	10:U:5:MAN:H3	1.84	0.59
1:B:625:ASN:HA	2:D:98:ARG:CD	2.33	0.59
1:B:589:ASP:HA	1:B:592:LEU:HD12	1.85	0.59
4:G:286:VAL:HB	4:G:452:LEU:HB2	1.85	0.59
4:G:197:ASN:OD1	12:K:1:NAG:H82	2.03	0.59
4:G:212:PRO:HG3	14:M:1:NAG:H82	1.85	0.59
4:G:275:GLU:OE1	4:G:282:LYS:HE3	2.03	0.59
6:R:37:TYR:H	6:R:48:ILE:HG22	1.67	0.58
6:R:128:GLU:OE2	6:R:135:THR:OG1	2.21	0.58
1:B:628:TRP:CZ3	4:G:42:VAL:HG21	2.37	0.58
6:R:163:VAL:HG11	6:R:183:SER:N	2.17	0.58
4:G:83:GLU:HA	4:G:245:VAL:HG12	1.83	0.58
1:B:658:GLN:HB3	1:B:662:ALA:HB2	1.86	0.58
2:D:28:ARG:NH2	2:D:72(B):GLU:OE1	2.37	0.58
4:G:70:ALA:HB2	4:G:213:ILE:HD11	1.86	0.58
4:G:476:ARG:HA	4:G:479:TRP:CE3	2.39	0.58
3:E:114:LYS:HG2	3:E:145:PRO:HD3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:294:ILE:O	4:G:294:ILE:HG13	2.04	0.58
4:G:291:PRO:HB2	4:G:448:ASN:HB3	1.86	0.57
1:B:596:TRP:HE1	1:B:647:GLU:HG3	1.68	0.57
3:E:41:PRO:HB2	3:E:44:ARG:HB2	1.87	0.57
4:G:386:ASN:OD1	17:S:1:NAG:C1	2.52	0.57
6:R:134:ALA:N	6:R:186:PRO:HG3	2.17	0.57
4:G:265:LEU:HD21	4:G:450:THR:HB	1.85	0.57
4:G:138:ILE:HD13	6:R:30:THR:HG22	1.87	0.57
1:B:627:THR:HG21	1:B:630:GLN:HG3	1.86	0.57
2:D:166:PHE:HE2	3:E:139:LEU:HB3	1.70	0.57
6:R:196:SER:HA	6:R:210:VAL:HG23	1.87	0.57
2:D:119:PRO:CG	2:D:201:LYS:NZ	2.66	0.56
4:G:274:SER:OG	4:G:276:ASN:C	2.49	0.56
4:G:270:VAL:HG12	4:G:288:PHE:HA	1.87	0.56
4:G:273:ARG:NH1	4:G:287:GLN:OE1	2.39	0.56
6:R:93:ASP:OD1	6:R:94:THR:N	2.38	0.56
5:Q:83:MET:HE3	5:Q:87:THR:HG23	1.87	0.56
2:D:59:LEU:HD21	2:D:63:PHE:HB2	1.88	0.56
6:R:95:SER:C	6:R:97:SER:H	2.14	0.56
4:G:276:ASN:C	4:G:276:ASN:OD1	2.49	0.55
6:R:182:LEU:HD12	6:R:183:SER:H	1.71	0.55
1:B:625:ASN:HA	2:D:98:ARG:HD2	1.88	0.55
4:G:258:GLN:HG2	4:G:472:GLY:H	1.70	0.55
6:R:63:PHE:O	6:R:64:SER:CB	2.53	0.55
4:G:95:MET:N	4:G:236:THR:HG21	2.19	0.55
4:G:331:CYS:O	4:G:415:THR:HA	2.05	0.55
6:R:136:LEU:HB2	6:R:182:LEU:HG	1.89	0.55
6:R:163:VAL:HG21	6:R:183:SER:N	2.13	0.55
4:G:80:ASN:OD1	4:G:80:ASN:N	2.40	0.55
4:G:466:GLU:CG	4:G:468:PHE:CE1	2.88	0.55
4:G:119:CYS:SG	4:G:120:VAL:N	2.80	0.55
4:G:311:ILE:HD11	4:G:317:PHE:HB2	1.87	0.55
4:G:425:ASN:HB3	4:G:433:ALA:HA	1.88	0.55
6:R:155:ASP:OD1	6:R:156:SER:N	2.38	0.54
3:E:82:PRO:HB2	3:E:174:ASN:HD22	1.72	0.54
4:G:280:ASN:OD1	4:G:280:ASN:N	2.40	0.54
6:R:129:LEU:HD23	6:R:189:TRP:NE1	2.22	0.54
4:G:281:ALA:HA	4:G:456:ARG:HD3	1.89	0.54
1:B:530:MET:HA	1:B:628:TRP:NE1	2.23	0.54
3:E:124:PRO:HG3	3:E:189:TRP:HZ2	1.73	0.54
4:G:125:LEU:HD23	4:G:193:LEU:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:260:LEU:HD12	4:G:451:GLY:HA3	1.89	0.53
6:R:197:CYS:O	6:R:207:GLU:HG3	2.08	0.53
1:B:555:LEU:HD23	1:B:555:LEU:C	2.33	0.53
2:D:48:MET:HG3	2:D:80:MET:HE1	1.90	0.53
4:G:358:ILE:HG23	4:G:396:ILE:HD13	1.90	0.53
4:G:105:HIS:HD1	4:G:479:TRP:HZ3	1.57	0.53
4:G:90:THR:HG22	4:G:240:PRO:HA	1.91	0.53
3:E:50:ILE:HD13	3:E:56:ARG:HA	1.91	0.53
4:G:94:ASN:O	4:G:98:ASN:HB2	2.09	0.53
5:Q:38:VAL:HG23	5:Q:95:TYR:HB2	1.90	0.53
2:D:100:GLY:HA3	9:F:3:BMA:H61	1.91	0.52
5:Q:164:PRO:HG2	5:Q:218:LYS:HG3	1.91	0.52
4:G:163:THR:OG1	4:G:164:GLU:N	2.42	0.52
1:B:569:THR:HG21	4:G:71:THR:HG21	1.91	0.52
2:D:10:GLU:HG2	2:D:18:VAL:HG11	1.92	0.52
4:G:266:ALA:HB3	4:G:271:MET:HE3	1.91	0.52
4:G:84:ILE:N	4:G:84:ILE:CD1	2.73	0.51
3:E:4:LEU:HD22	3:E:102:GLY:HA2	1.93	0.51
10:H:2:NAG:H61	10:H:3:BMA:H2	1.93	0.51
4:G:50:THR:CG2	4:G:220:PRO:HG3	2.40	0.51
4:G:291:PRO:HB3	4:G:450:THR:HG22	1.92	0.51
2:D:10:GLU:OE2	2:D:18:VAL:HG12	2.11	0.51
4:G:209:SER:HB3	4:G:211:GLU:HG2	1.93	0.51
1:B:548:ILE:O	1:B:551:GLN:OE1	2.29	0.50
2:D:131:THR:HB	2:D:136:ALA:HB2	1.92	0.50
4:G:474:ASP:OD1	4:G:475:MET:N	2.44	0.50
5:Q:10:GLY:HA2	5:Q:126:VAL:HG12	1.93	0.50
2:D:150:VAL:HG11	2:D:200:HIS:HA	1.94	0.50
5:Q:38:VAL:HG21	5:Q:120:TRP:HZ3	1.76	0.50
14:M:4:MAN:O6	14:M:4:MAN:O4	2.26	0.50
4:G:251:ILE:HG23	4:G:482:GLU:HG2	1.94	0.50
4:G:356:ASN:C	4:G:357:THR:HG23	2.36	0.50
5:Q:52:ILE:HD13	5:Q:58:THR:HG22	1.94	0.50
5:Q:115:TYR:CE1	6:R:50:SER:HB2	2.46	0.50
5:Q:167:VAL:HG11	5:Q:195:LEU:HD22	1.94	0.50
6:R:37:TYR:H	6:R:48:ILE:CG2	2.24	0.50
4:G:232:LYS:HE2	4:G:234:ASN:HB3	1.93	0.50
5:Q:64:LEU:O	5:Q:68:VAL:HG22	2.11	0.50
3:E:124:PRO:HG3	3:E:189:TRP:CZ2	2.47	0.50
4:G:360:ARG:HG3	4:G:394:THR:OG1	2.11	0.50
4:G:96:TRP:CZ2	4:G:274:SER:C	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R:53:SER:HB3	18:V:9:MAN:O3	2.12	0.49
4:G:294:ILE:CD1	4:G:294:ILE:C	2.85	0.49
4:G:313:PRO:C	4:G:315:GLN:H	2.19	0.49
4:G:189:LYS:HD3	4:G:191:TYR:OH	2.12	0.49
1:B:601:LYS:HB2	1:B:604:CYS:SG	2.52	0.49
6:R:140:ILE:HG22	6:R:141:SER:N	2.27	0.49
6:R:140:ILE:CG2	6:R:141:SER:N	2.76	0.49
11:I:1:NAG:HO6	11:I:2:NAG:HN2	1.60	0.49
4:G:160:ASN:OD1	4:G:171:LYS:HG2	2.13	0.49
4:G:311:ILE:HD11	4:G:317:PHE:CB	2.43	0.49
4:G:391:PHE:CD2	4:G:470:PRO:HG3	2.47	0.49
4:G:281:ALA:HB2	4:G:456:ARG:HH21	1.77	0.49
1:B:555:LEU:C	1:B:555:LEU:CD2	2.85	0.49
5:Q:38:VAL:HG21	5:Q:120:TRP:CZ3	2.47	0.49
6:R:163:VAL:HG12	6:R:164:GLU:N	2.27	0.49
2:D:100(E):LEU:HD23	2:D:100(E):LEU:H	1.77	0.48
2:D:167:PRO:HG3	3:E:169:SER:HB3	1.95	0.48
4:G:163:THR:O	4:G:312:GLY:N	2.43	0.48
5:Q:186:VAL:HG22	5:Q:187:LEU:HD23	1.95	0.48
6:R:12:VAL:O	6:R:107:LEU:HD12	2.12	0.48
2:D:198:VAL:HB	2:D:200:HIS:NE2	2.28	0.48
5:Q:163:PHE:H	5:Q:164:PRO:HD2	1.78	0.48
6:R:163:VAL:CG2	6:R:182:LEU:CD1	2.86	0.48
3:E:82:PRO:HB2	3:E:174:ASN:ND2	2.28	0.48
6:R:119:VAL:O	6:R:140:ILE:CD1	2.61	0.48
4:G:55:ALA:HB3	4:G:216:HIS:HB2	1.95	0.48
4:G:277:ILE:O	4:G:278:THR:CB	2.62	0.48
6:R:87:TYR:O	6:R:104:GLY:HA3	2.13	0.48
6:R:165:THR:CG2	6:R:166:THR:N	2.76	0.48
1:B:605:CYS:HB2	4:G:503:ARG:HG3	1.96	0.48
1:B:628:TRP:CZ3	4:G:42:VAL:CG2	2.97	0.48
6:R:189:TRP:NE1	6:R:190:LYS:HD3	2.29	0.48
6:R:35:TYR:HB2	6:R:90:GLN:HB3	1.96	0.47
1:B:601:LYS:HE2	1:B:604:CYS:SG	2.54	0.47
2:D:201:LYS:HG2	2:D:202:PRO:CD	2.30	0.47
4:G:277:ILE:O	4:G:278:THR:CG2	2.62	0.47
5:Q:18:LEU:HD13	5:Q:20:LEU:HD13	1.95	0.47
5:Q:218:LYS:HB3	5:Q:218:LYS:HE3	1.66	0.47
1:B:650:GLN:O	1:B:654:GLU:HB3	2.14	0.47
3:E:121:LEU:HD22	3:E:210:VAL:HG23	1.95	0.47
4:G:365:SER:CB	4:G:469:ARG:HD2	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:32:ASP:O	5:Q:53:HIS:NE2	2.44	0.47
1:B:544:LEU:HD21	4:G:493:PRO:HG3	1.97	0.47
4:G:277:ILE:C	4:G:278:THR:CG2	2.80	0.47
6:R:163:VAL:CG1	6:R:164:GLU:N	2.77	0.47
1:B:530:MET:HG2	1:B:628:TRP:CG	2.49	0.47
6:R:122:PHE:O	6:R:137:VAL:O	2.32	0.47
15:N:3:BMA:H61	15:N:6:MAN:H62	1.97	0.47
12:K:1:NAG:H61	12:K:2:NAG:HN2	1.80	0.47
2:D:36:TRP:CZ3	2:D:92:CYS:HB3	2.50	0.47
2:D:150:VAL:HG21	2:D:200:HIS:ND1	2.30	0.47
4:G:55:ALA:HA	4:G:75:VAL:O	2.15	0.47
4:G:274:SER:HG	4:G:276:ASN:C	2.23	0.47
4:G:279:ASN:C	4:G:281:ALA:N	2.72	0.47
5:Q:130:SER:OG	5:Q:131:ALA:N	2.47	0.47
6:R:189:TRP:CD1	6:R:190:LYS:HG2	2.50	0.47
4:G:122:LEU:HD23	4:G:125:LEU:HD22	1.97	0.46
4:G:317:PHE:CE1	4:G:319:ALA:HB2	2.50	0.46
4:G:60:ALA:HB1	4:G:64:GLU:O	2.15	0.46
4:G:277:ILE:HG23	4:G:278:THR:HG23	1.96	0.46
6:R:129:LEU:HD23	6:R:189:TRP:HE1	1.80	0.46
6:R:190:LYS:HD2	6:R:190:LYS:HA	1.69	0.46
2:D:59:LEU:HD23	2:D:60:ALA:N	2.31	0.46
3:E:78:SER:O	3:E:81:ARG:NH2	2.45	0.46
4:G:69:TRP:HA	4:G:111:LEU:HD21	1.96	0.46
4:G:289:ASN:OD1	4:G:344:LYS:NZ	2.45	0.46
11:I:4:MAN:HO2	11:I:5:MAN:C1	2.28	0.46
2:D:4:LEU:O	2:D:104:GLY:HA2	2.14	0.46
5:Q:133:THR:HG21	5:Q:219:PRO:HG2	1.96	0.46
5:Q:117:MET:N	6:R:37:TYR:OH	2.46	0.46
7:A:2:NAG:H4	7:A:3:BMA:H2	1.63	0.46
6:R:38:ARG:HB3	6:R:87:TYR:CE1	2.51	0.46
2:D:210:ARG:HG2	2:D:211:VAL:H	1.81	0.46
1:B:627:THR:HG23	1:B:630:GLN:H	1.81	0.46
4:G:206:PRO:HG2	4:G:207:LYS:HE3	1.97	0.46
4:G:305:LYS:HA	4:G:305:LYS:HD3	1.77	0.46
4:G:368:ASP:OD1	4:G:369:LEU:N	2.49	0.45
6:R:165:THR:HG22	6:R:166:THR:N	2.31	0.45
2:D:163:VAL:HG12	2:D:182:VAL:HG23	1.98	0.45
3:E:14:LEU:HD12	3:E:80:LEU:O	2.15	0.45
1:B:653:GLN:O	1:B:657:GLU:HG2	2.16	0.45
5:Q:113:PHE:CE2	6:R:53:SER:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R:163:VAL:HB	6:R:182:LEU:CD1	2.47	0.45
1:B:610:TRP:CE3	4:G:498:PRO:HB3	2.52	0.45
3:E:119:VAL:HG11	3:E:199:VAL:HG21	1.98	0.45
1:B:625:ASN:HA	2:D:98:ARG:CG	2.47	0.45
4:G:280:ASN:O	4:G:456:ARG:HG2	2.16	0.45
6:R:95:SER:O	6:R:97:SER:N	2.49	0.45
4:G:335:LYS:HD3	4:G:414:ILE:HD11	1.98	0.45
5:Q:172:ASN:HB2	5:Q:211:TYR:HD1	1.81	0.45
6:R:168:PRO:HB3	6:R:176:TYR:HB3	1.99	0.45
8:C:2:NAG:H4	8:C:3:BMA:H2	1.69	0.45
2:D:53:TYR:O	2:D:55:GLY:N	2.47	0.45
5:Q:68:VAL:HA	5:Q:82:LYS:O	2.17	0.45
2:D:201:LYS:N	2:D:201:LYS:CD	2.73	0.45
5:Q:76:ILE:HG13	5:Q:77:PRO:HD2	1.99	0.45
3:E:149:THR:OG1	3:E:200:THR:HB	2.17	0.44
15:N:1:NAG:H62	15:N:2:NAG:HN2	1.80	0.44
1:B:658:GLN:O	1:B:662:ALA:N	2.22	0.44
3:E:56:ARG:H	3:E:56:ARG:HG2	1.63	0.44
4:G:175:LEU:O	4:G:320:THR:OG1	2.31	0.44
5:Q:187:LEU:HD23	5:Q:187:LEU:H	1.83	0.44
5:Q:217:HIS:CB	5:Q:222:THR:H	2.29	0.44
2:D:102:LEU:HA	2:D:102:LEU:HD23	1.77	0.44
4:G:50:THR:HG21	4:G:220:PRO:CG	2.45	0.44
4:G:276:ASN:OD1	4:G:277:ILE:O	2.35	0.44
5:Q:22:CYS:HB2	5:Q:37:TRP:CH2	2.53	0.44
3:E:39:GLN:HG3	3:E:88:TYR:HE2	1.83	0.44
4:G:424:ILE:HD11	4:G:434:MET:HE2	2.00	0.44
2:D:47:TRP:HZ2	2:D:50:TRP:CD1	2.29	0.44
2:D:166:PHE:CD2	3:E:139:LEU:HD22	2.52	0.44
4:G:129:LEU:HB3	4:G:157:CYS:SG	2.58	0.44
3:E:115:ALA:O	3:E:143:PHE:HA	2.18	0.44
3:E:119:VAL:HG22	3:E:140:ILE:HG22	2.00	0.44
2:D:16:ALA:O	2:D:17:SER:CB	2.66	0.43
4:G:220:PRO:HG2	4:G:223:PHE:CG	2.52	0.43
5:Q:91:THR:OG1	5:Q:128:VAL:HG12	2.18	0.43
6:R:138:CYS:O	6:R:180:SER:O	2.35	0.43
4:G:219:ALA:HA	4:G:220:PRO:HD3	1.71	0.43
5:Q:88:ALA:C	5:Q:90:ASP:H	2.27	0.43
6:R:163:VAL:HB	6:R:182:LEU:HD13	1.99	0.43
6:R:163:VAL:CB	6:R:182:LEU:HD12	2.46	0.43
1:B:536:THR:O	1:B:537:LEU:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:135:THR:HB	2:D:185:PRO:HA	2.01	0.43
2:D:181:VAL:HG21	3:E:139:LEU:CD1	2.48	0.43
4:G:112:TRP:CG	4:G:427:TRP:HH2	2.36	0.43
4:G:299:PRO:HB2	4:G:327:ARG:HB2	2.00	0.43
11:I:4:MAN:H61	11:I:7:MAN:H2	1.46	0.43
18:V:1:NAG:H83	18:V:1:NAG:H2	1.79	0.43
4:G:257:THR:HG22	4:G:258:GLN:HG3	2.01	0.43
4:G:343:GLY:O	4:G:346:VAL:HG12	2.19	0.43
1:B:537:LEU:HD22	1:B:603:ILE:HD11	2.00	0.43
3:E:196:SER:HA	3:E:209:THR:HG23	2.00	0.43
4:G:277:ILE:O	4:G:278:THR:OG1	2.33	0.43
4:G:453:ILE:HG21	4:G:472:GLY:HA2	2.01	0.43
6:R:177:ALA:C	6:R:179:SER:H	2.26	0.43
3:E:37:TRP:HB2	3:E:50:ILE:HB	2.01	0.43
3:E:95:HIS:CD2	9:F:6:MAN:H3	2.54	0.43
4:G:197:ASN:CG	12:K:1:NAG:H82	2.43	0.43
4:G:171:LYS:NZ	8:J:2:NAG:O6	2.51	0.43
4:G:355:ASN:HB3	4:G:356:ASN:H	1.52	0.43
2:D:33:HIS:O	2:D:95:GLY:N	2.39	0.43
5:Q:99:ASN:HD21	5:Q:114:HIS:CD2	2.37	0.43
11:I:4:MAN:O2	11:I:5:MAN:O5	2.29	0.43
2:D:11:LEU:HD11	2:D:147:PRO:HG2	2.01	0.42
5:Q:101:ILE:HG23	5:Q:101:ILE:O	2.19	0.42
6:R:126:SER:O	6:R:128:GLU:N	2.45	0.42
1:B:628:TRP:CE3	4:G:42:VAL:CG1	3.02	0.42
2:D:2:GLY:HA3	2:D:26:GLY:HA3	2.01	0.42
4:G:85:HIS:O	4:G:86:LEU:C	2.61	0.42
4:G:332:ASN:HB3	7:O:1:NAG:H82	2.00	0.42
6:R:76:ILE:HG12	6:R:77:ARG:H	1.83	0.42
6:R:129:LEU:H	6:R:129:LEU:CD1	2.27	0.42
5:Q:39:ARG:NH2	5:Q:47:GLU:OE1	2.51	0.42
6:R:198:GLN:HA	6:R:207:GLU:HG3	2.01	0.42
2:D:166:PHE:CE2	3:E:139:LEU:HB3	2.52	0.42
4:G:129:LEU:O	4:G:191:TYR:N	2.35	0.42
4:G:447:SER:HB3	14:M:1:NAG:H3	2.02	0.42
5:Q:155:LEU:O	5:Q:198:VAL:HG23	2.18	0.42
5:Q:33:HIS:HA	5:Q:101:ILE:CG2	2.47	0.42
5:Q:162:TYR:OH	5:Q:195:LEU:HB2	2.18	0.42
5:Q:162:TYR:CZ	5:Q:193:TYR:HB2	2.54	0.42
6:R:33:PHE:CG	6:R:34:THR:N	2.87	0.42
1:B:614:TRP:O	1:B:638:TYR:OH	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:494:LEU:HA	4:G:494:LEU:HD23	1.75	0.42
3:E:65:SER:HB2	3:E:76:THR:HB	2.02	0.42
4:G:275:GLU:OE1	4:G:282:LYS:CE	2.68	0.42
2:D:190:GLY:H	2:D:194:TYR:HE2	1.68	0.41
4:G:135:THR:HG21	6:R:54:GLN:HG3	2.01	0.41
4:G:154:LEU:HG	4:G:177:TYR:HA	2.01	0.41
5:Q:93:MET:HA	5:Q:125:ALA:HA	2.02	0.41
2:D:128:SER:HB3	2:D:217:ASP:OD1	2.20	0.41
5:Q:113:PHE:HZ	6:R:52:SER:C	2.29	0.41
2:D:165:THR:HA	2:D:180:SER:HA	2.02	0.41
4:G:96:TRP:HH2	4:G:235:GLY:HA2	1.85	0.41
5:Q:172:ASN:HA	5:Q:212:ILE:HG22	2.02	0.41
15:N:2:NAG:H61	15:N:3:BMA:H2	2.01	0.41
2:D:200:HIS:HB3	2:D:201:LYS:HD3	2.02	0.41
4:G:444:ARG:NH1	7:O:1:NAG:O6	2.45	0.41
3:E:25:PRO:HD2	3:E:28:VAL:HG12	2.02	0.41
4:G:281:ALA:CA	4:G:456:ARG:HD3	2.50	0.41
4:G:387:THR:HB	4:G:391:PHE:HE2	1.86	0.41
5:Q:188:GLN:O	5:Q:190:SER:N	2.51	0.41
5:Q:186:VAL:HG22	5:Q:187:LEU:H	1.86	0.41
2:D:97:LEU:HD23	2:D:97:LEU:HA	1.72	0.41
5:Q:113:PHE:HD2	6:R:51:ARG:CZ	2.34	0.41
2:D:47:TRP:CZ2	2:D:50:TRP:HD1	2.28	0.41
2:D:119:PRO:CG	2:D:201:LYS:HZ1	2.09	0.41
3:E:86:THR:OG1	3:E:87:THR:N	2.53	0.41
3:E:91:CYS:HB2	3:E:99:CYS:HB3	2.02	0.41
4:G:33:ASN:OD1	4:G:33:ASN:N	2.51	0.41
4:G:359:ILE:O	4:G:394:THR:HG23	2.21	0.41
4:G:363:ASN:O	4:G:364:SER:C	2.64	0.41
1:B:625:ASN:HB2	2:D:97:LEU:HD22	2.03	0.41
4:G:117:LYS:HB3	4:G:118:PRO:HD3	2.03	0.41
5:Q:139:PHE:HE1	6:R:128:GLU:N	2.19	0.41
1:B:627:THR:O	1:B:628:TRP:CB	2.69	0.40
1:B:628:TRP:CE3	4:G:42:VAL:HG11	2.56	0.40
2:D:143:LYS:HD2	2:D:177:SER:OG	2.21	0.40
3:E:121:LEU:HD23	3:E:122:PHE:N	2.35	0.40
4:G:178:ARG:HG2	4:G:179:LEU:N	2.36	0.40
4:G:192:ARG:CZ	4:G:197:ASN:HB2	2.51	0.40
5:Q:31:SER:O	5:Q:54:TYR:HB2	2.20	0.40
2:D:35:ASN:OD1	2:D:50:TRP:HB3	2.21	0.40
5:Q:165:GLU:N	5:Q:166:PRO:HD2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:548:ILE:O	1:B:551:GLN:HB2	2.21	0.40
5:Q:113:PHE:HZ	6:R:52:SER:O	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:535:MET:O	1:B:652:GLN:NE2[2_545]	2.11	0.09

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	B	135/153 (88%)	124 (92%)	10 (7%)	1 (1%)	18	55
2	D	233/243 (96%)	205 (88%)	25 (11%)	3 (1%)	9	41
3	E	208/216 (96%)	185 (89%)	23 (11%)	0	100	100
4	G	443/479 (92%)	386 (87%)	54 (12%)	3 (1%)	18	55
5	Q	226/241 (94%)	184 (81%)	35 (16%)	7 (3%)	3	25
6	R	209/215 (97%)	143 (68%)	57 (27%)	9 (4%)	2	20
All	All	1454/1547 (94%)	1227 (84%)	204 (14%)	23 (2%)	7	37

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	554	ASN
2	D	201	LYS
5	Q	50	GLY
6	R	62	ARG
6	R	212	PRO
4	G	280	ASN

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Mol	Chain	Res	Type
4	G	314	GLY
6	R	64	SER
6	R	98	TYR
4	G	365	SER
5	Q	143	PRO
5	Q	162	TYR
5	Q	218	LYS
6	R	53	SER
6	R	135	THR
2	D	82(B)	ASN
2	D	17	SER
5	Q	84	THR
5	Q	140	PRO
6	R	96	ASP
6	R	195	TYR
5	Q	219	PRO
6	R	210	VAL

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	B	121/129 (94%)	114 (94%)	7 (6%)	18	42
2	D	194/206 (94%)	185 (95%)	9 (5%)	24	47
3	E	183/189 (97%)	181 (99%)	2 (1%)	65	74
4	G	400/426 (94%)	374 (94%)	26 (6%)	15	40
5	Q	181/208 (87%)	172 (95%)	9 (5%)	22	45
6	R	161/182 (88%)	154 (96%)	7 (4%)	26	49
All	All	1240/1340 (92%)	1180 (95%)	60 (5%)	23	46

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	548	ILE

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Mol	Chain	Res	Type
1	B	549	VAL
1	B	556	LEU
1	B	565	LEU
1	B	583	VAL
1	B	606	THR
1	B	624	ASP
2	D	18	VAL
2	D	82	ILE
2	D	82(A)	ARG
2	D	82(B)	ASN
2	D	82(C)	LEU
2	D	128	SER
2	D	150	VAL
2	D	196	CYS
2	D	201	LYS
3	E	81	ARG
3	E	166	THR
4	G	33	ASN
4	G	72	HIS
4	G	74	CYS
4	G	80	ASN
4	G	82	GLN
4	G	84	ILE
4	G	125	LEU
4	G	234	ASN
4	G	254	VAL
4	G	268	GLU
4	G	274	SER
4	G	275	GLU
4	G	279	ASN
4	G	294	ILE
4	G	295	ASN
4	G	297	THR
4	G	321(A)	ASP
4	G	322	ILE
4	G	325	ASP
4	G	355	ASN
4	G	363	ASN
4	G	364	SER
4	G	444	ARG
4	G	445	CYS
4	G	449	ILE

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Mol	Chain	Res	Type
4	G	455	THR
5	Q	54	TYR
5	Q	60	TYR
5	Q	71	GLU
5	Q	113	PHE
5	Q	114	HIS
5	Q	117	MET
5	Q	157	CYS
5	Q	218	LYS
5	Q	228	VAL
6	R	48	ILE
6	R	54	GLN
6	R	82	ASP
6	R	129	LEU
6	R	139	LEU
6	R	150	VAL
6	R	171	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	575	GLN
3	E	174	ASN
4	G	188	ASN
4	G	386	ASN
4	G	422	GLN
4	G	478	ASN
5	Q	40	GLN
5	Q	99	ASN
5	Q	114	HIS
6	R	39	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

90 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
7	NAG	A	1	1,7	14,14,15	0.27	0	17,19,21	1.38	1 (5%)
7	NAG	A	2	7	14,14,15	0.35	0	17,19,21	0.68	0
7	BMA	A	3	7	11,11,12	0.24	0	15,15,17	0.79	0
8	NAG	C	1	1,8	14,14,15	0.29	0	17,19,21	0.83	0
8	NAG	C	2	8	14,14,15	0.32	0	17,19,21	1.15	2 (11%)
8	BMA	C	3	8	11,11,12	0.44	0	15,15,17	0.94	0
8	MAN	C	4	8	11,11,12	0.35	0	15,15,17	0.99	0
8	MAN	C	5	8	11,11,12	0.22	0	15,15,17	0.61	0
9	NAG	F	1	9,4	14,14,15	0.29	0	17,19,21	1.92	6 (35%)
9	NAG	F	2	9	14,14,15	0.26	0	17,19,21	1.65	2 (11%)
9	BMA	F	3	9	11,11,12	0.37	0	15,15,17	1.15	0
9	MAN	F	4	9	11,11,12	0.31	0	15,15,17	0.91	1 (6%)
9	MAN	F	5	9	11,11,12	0.25	0	15,15,17	0.71	0
9	MAN	F	6	9	11,11,12	0.45	0	15,15,17	0.88	0
9	MAN	F	7	9	11,11,12	0.26	0	15,15,17	0.73	0
10	NAG	H	1	10,4	14,14,15	0.28	0	17,19,21	0.90	0
10	NAG	H	2	10	14,14,15	0.31	0	17,19,21	0.59	0
10	BMA	H	3	10	11,11,12	0.31	0	15,15,17	0.82	0
10	MAN	H	4	10	11,11,12	0.94	1 (9%)	15,15,17	1.79	3 (20%)
10	MAN	H	5	10	11,11,12	0.25	0	15,15,17	0.62	0
11	NAG	I	1	11,4	14,14,15	0.28	0	17,19,21	0.92	1 (5%)
11	NAG	I	2	11	14,14,15	0.30	0	17,19,21	0.67	0
11	BMA	I	3	11	11,11,12	0.32	0	15,15,17	0.82	1 (6%)
11	MAN	I	4	11	11,11,12	0.79	0	15,15,17	2.12	4 (26%)
11	MAN	I	5	11	11,11,12	0.49	0	15,15,17	1.09	2 (13%)
11	MAN	I	6	11	11,11,12	0.30	0	15,15,17	0.75	0
11	MAN	I	7	11	11,11,12	0.43	0	15,15,17	0.94	0
8	NAG	J	1	8,4	14,14,15	0.69	0	17,19,21	0.86	1 (5%)
8	NAG	J	2	8	14,14,15	0.42	0	17,19,21	1.06	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	BMA	J	3	8	11,11,12	0.30	0	15,15,17	0.82	0
8	MAN	J	4	8	11,11,12	0.25	0	15,15,17	0.58	0
8	MAN	J	5	8	11,11,12	0.26	0	15,15,17	0.66	0
12	NAG	K	1	12,4	14,14,15	0.47	0	17,19,21	2.25	6 (35%)
12	NAG	K	2	12	14,14,15	0.37	0	17,19,21	0.92	1 (5%)
12	BMA	K	3	12	11,11,12	0.31	0	15,15,17	1.06	0
12	MAN	K	4	12	11,11,12	0.26	0	15,15,17	0.82	1 (6%)
13	NAG	L	1	13,4	14,14,15	0.28	0	17,19,21	0.92	0
13	NAG	L	2	13	14,14,15	0.39	0	17,19,21	1.06	1 (5%)
13	BMA	L	3	13	11,11,12	0.30	0	15,15,17	0.71	0
13	MAN	L	4	13	11,11,12	0.26	0	15,15,17	0.56	0
14	NAG	M	1	14,4	14,14,15	0.31	0	17,19,21	0.90	1 (5%)
14	NAG	M	2	14	14,14,15	0.42	0	17,19,21	0.87	1 (5%)
14	BMA	M	3	14	11,11,12	0.73	0	15,15,17	1.28	2 (13%)
14	MAN	M	4	14	11,11,12	0.36	0	15,15,17	1.82	4 (26%)
14	MAN	M	5	14	11,11,12	0.45	0	15,15,17	1.19	2 (13%)
14	MAN	M	6	14	11,11,12	0.26	0	15,15,17	0.66	0
14	MAN	M	7	14	11,11,12	0.56	0	15,15,17	1.07	2 (13%)
15	NAG	N	1	15	14,14,15	0.94	1 (7%)	17,19,21	3.14	5 (29%)
15	NAG	N	2	15	14,14,15	0.28	0	17,19,21	0.81	1 (5%)
15	BMA	N	3	15	11,11,12	0.31	0	15,15,17	1.37	1 (6%)
15	MAN	N	4	15	11,11,12	0.28	0	15,15,17	0.70	0
15	MAN	N	5	15	11,11,12	0.26	0	15,15,17	0.78	0
15	MAN	N	6	15	11,11,12	0.23	0	15,15,17	0.71	0
15	MAN	N	7	15	11,11,12	0.25	0	15,15,17	0.64	0
15	MAN	N	8	15	11,11,12	0.56	0	15,15,17	1.23	2 (13%)
7	NAG	O	1	7,4	14,14,15	0.31	0	17,19,21	2.31	4 (23%)
7	NAG	O	2	7	14,14,15	0.29	0	17,19,21	0.96	1 (5%)
7	BMA	O	3	7	11,11,12	0.22	0	15,15,17	0.65	0
16	NAG	P	1	16,4	14,14,15	0.26	0	17,19,21	1.12	1 (5%)
16	NAG	P	2	16	14,14,15	0.44	0	17,19,21	1.41	2 (11%)
16	BMA	P	3	16	11,11,12	0.50	0	15,15,17	1.07	1 (6%)
16	MAN	P	4	16	11,11,12	0.31	0	15,15,17	0.62	0
16	MAN	P	5	16	11,11,12	0.27	0	15,15,17	0.73	0
16	MAN	P	6	16	11,11,12	0.27	0	15,15,17	0.70	0
17	NAG	S	1	17	14,14,15	0.27	0	17,19,21	1.54	3 (17%)
17	NAG	S	2	17	14,14,15	0.51	0	17,19,21	1.27	1 (5%)
17	BMA	S	3	17	11,11,12	0.51	0	15,15,17	1.07	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	MAN	S	4	17	11,11,12	0.34	0	15,15,17	0.64	0
17	MAN	S	5	17	11,11,12	0.24	0	15,15,17	0.60	0
17	MAN	S	6	17	11,11,12	0.30	0	15,15,17	0.68	0
17	MAN	S	7	17	11,11,12	0.26	0	15,15,17	0.66	0
17	MAN	S	8	17	11,11,12	0.24	0	15,15,17	0.64	0
12	NAG	T	1	12,4	14,14,15	0.33	0	17,19,21	0.71	0
12	NAG	T	2	12	14,14,15	0.35	0	17,19,21	0.93	1 (5%)
12	BMA	T	3	12	11,11,12	0.25	0	15,15,17	0.78	0
12	MAN	T	4	12	11,11,12	0.32	0	15,15,17	0.84	0
10	NAG	U	1	10,4	14,14,15	0.27	0	17,19,21	1.08	2 (11%)
10	NAG	U	2	10	14,14,15	0.42	0	17,19,21	1.92	4 (23%)
10	BMA	U	3	10	11,11,12	0.46	0	15,15,17	1.83	4 (26%)
10	MAN	U	4	10	11,11,12	1.04	1 (9%)	15,15,17	1.74	3 (20%)
10	MAN	U	5	10	11,11,12	0.90	1 (9%)	15,15,17	1.87	3 (20%)
18	NAG	V	1	18,4	14,14,15	0.28	0	17,19,21	0.96	1 (5%)
18	NAG	V	2	18	14,14,15	0.30	0	17,19,21	0.61	0
18	BMA	V	3	18	11,11,12	0.29	0	15,15,17	1.12	1 (6%)
18	MAN	V	4	18	11,11,12	0.25	0	15,15,17	0.93	0
18	MAN	V	5	18	11,11,12	0.23	0	15,15,17	0.87	0
18	MAN	V	6	18	11,11,12	0.23	0	15,15,17	0.84	1 (6%)
18	MAN	V	7	18	11,11,12	0.54	0	15,15,17	1.16	1 (6%)
18	MAN	V	8	18	11,11,12	0.50	0	15,15,17	1.04	1 (6%)
18	MAN	V	9	18	11,11,12	0.57	0	15,15,17	1.17	2 (13%)

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
7	NAG	A	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	A	2	7	-	3/6/23/26	0/1/1/1
7	BMA	A	3	7	-	1/2/19/22	0/1/1/1
8	NAG	C	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	C	2	8	-	5/6/23/26	0/1/1/1
8	BMA	C	3	8	-	0/2/19/22	0/1/1/1
8	MAN	C	4	8	-	2/2/19/22	0/1/1/1
8	MAN	C	5	8	-	1/2/19/22	0/1/1/1
9	NAG	F	1	9,4	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	F	2	9	-	4/6/23/26	0/1/1/1
9	BMA	F	3	9	-	1/2/19/22	0/1/1/1
9	MAN	F	4	9	-	2/2/19/22	0/1/1/1
9	MAN	F	5	9	-	0/2/19/22	0/1/1/1
9	MAN	F	6	9	-	1/2/19/22	0/1/1/1
9	MAN	F	7	9	-	0/2/19/22	0/1/1/1
10	NAG	H	1	10,4	-	0/6/23/26	0/1/1/1
10	NAG	H	2	10	-	5/6/23/26	0/1/1/1
10	BMA	H	3	10	-	0/2/19/22	0/1/1/1
10	MAN	H	4	10	-	0/2/19/22	0/1/1/1
10	MAN	H	5	10	-	0/2/19/22	0/1/1/1
11	NAG	I	1	11,4	-	4/6/23/26	0/1/1/1
11	NAG	I	2	11	-	3/6/23/26	0/1/1/1
11	BMA	I	3	11	-	0/2/19/22	0/1/1/1
11	MAN	I	4	11	-	2/2/19/22	0/1/1/1
11	MAN	I	5	11	-	1/2/19/22	0/1/1/1
11	MAN	I	6	11	-	0/2/19/22	0/1/1/1
11	MAN	I	7	11	-	1/2/19/22	0/1/1/1
8	NAG	J	1	8,4	-	3/6/23/26	0/1/1/1
8	NAG	J	2	8	-	4/6/23/26	0/1/1/1
8	BMA	J	3	8	-	2/2/19/22	0/1/1/1
8	MAN	J	4	8	-	0/2/19/22	0/1/1/1
8	MAN	J	5	8	-	1/2/19/22	0/1/1/1
12	NAG	K	1	12,4	-	2/6/23/26	0/1/1/1
12	NAG	K	2	12	-	3/6/23/26	0/1/1/1
12	BMA	K	3	12	-	0/2/19/22	0/1/1/1
12	MAN	K	4	12	-	1/2/19/22	0/1/1/1
13	NAG	L	1	13,4	-	2/6/23/26	0/1/1/1
13	NAG	L	2	13	-	3/6/23/26	0/1/1/1
13	BMA	L	3	13	-	2/2/19/22	0/1/1/1
13	MAN	L	4	13	-	0/2/19/22	0/1/1/1
14	NAG	M	1	14,4	-	3/6/23/26	0/1/1/1
14	NAG	M	2	14	-	3/6/23/26	0/1/1/1
14	BMA	M	3	14	-	0/2/19/22	0/1/1/1
14	MAN	M	4	14	-	1/2/19/22	0/1/1/1
14	MAN	M	5	14	-	0/2/19/22	0/1/1/1
14	MAN	M	6	14	-	0/2/19/22	0/1/1/1
14	MAN	M	7	14	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	NAG	N	1	15	-	5/6/23/26	0/1/1/1
15	NAG	N	2	15	-	3/6/23/26	0/1/1/1
15	BMA	N	3	15	-	2/2/19/22	0/1/1/1
15	MAN	N	4	15	-	2/2/19/22	0/1/1/1
15	MAN	N	5	15	-	2/2/19/22	0/1/1/1
15	MAN	N	6	15	-	0/2/19/22	0/1/1/1
15	MAN	N	7	15	-	2/2/19/22	0/1/1/1
15	MAN	N	8	15	-	0/2/19/22	0/1/1/1
7	NAG	O	1	7,4	-	2/6/23/26	0/1/1/1
7	NAG	O	2	7	-	3/6/23/26	0/1/1/1
7	BMA	O	3	7	-	0/2/19/22	0/1/1/1
16	NAG	P	1	16,4	-	2/6/23/26	0/1/1/1
16	NAG	P	2	16	-	1/6/23/26	0/1/1/1
16	BMA	P	3	16	-	1/2/19/22	0/1/1/1
16	MAN	P	4	16	-	2/2/19/22	0/1/1/1
16	MAN	P	5	16	-	0/2/19/22	0/1/1/1
16	MAN	P	6	16	-	0/2/19/22	0/1/1/1
17	NAG	S	1	17	-	5/6/23/26	0/1/1/1
17	NAG	S	2	17	-	4/6/23/26	0/1/1/1
17	BMA	S	3	17	-	2/2/19/22	0/1/1/1
17	MAN	S	4	17	-	1/2/19/22	0/1/1/1
17	MAN	S	5	17	-	1/2/19/22	0/1/1/1
17	MAN	S	6	17	-	2/2/19/22	0/1/1/1
17	MAN	S	7	17	-	1/2/19/22	0/1/1/1
17	MAN	S	8	17	-	1/2/19/22	0/1/1/1
12	NAG	T	1	12,4	-	2/6/23/26	0/1/1/1
12	NAG	T	2	12	-	2/6/23/26	0/1/1/1
12	BMA	T	3	12	-	0/2/19/22	0/1/1/1
12	MAN	T	4	12	-	0/2/19/22	0/1/1/1
10	NAG	U	1	10,4	-	2/6/23/26	0/1/1/1
10	NAG	U	2	10	-	4/6/23/26	0/1/1/1
10	BMA	U	3	10	-	2/2/19/22	0/1/1/1
10	MAN	U	4	10	-	2/2/19/22	0/1/1/1
10	MAN	U	5	10	-	0/2/19/22	0/1/1/1
18	NAG	V	1	18,4	-	4/6/23/26	0/1/1/1
18	NAG	V	2	18	-	0/6/23/26	0/1/1/1
18	BMA	V	3	18	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	MAN	V	4	18	-	2/2/19/22	0/1/1/1
18	MAN	V	5	18	-	0/2/19/22	0/1/1/1
18	MAN	V	6	18	-	0/2/19/22	0/1/1/1
18	MAN	V	7	18	-	0/2/19/22	0/1/1/1
18	MAN	V	8	18	-	2/2/19/22	0/1/1/1
18	MAN	V	9	18	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	N	1	NAG	O5-C1	-2.87	1.38	1.43
10	U	4	MAN	O5-C1	2.73	1.48	1.43
10	H	4	MAN	O5-C1	2.35	1.47	1.43
10	U	5	MAN	O5-C1	2.15	1.47	1.43

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	1	NAG	C1-O5-C5	-9.69	99.20	112.19
7	O	1	NAG	C1-O5-C5	-6.25	103.82	112.19
10	U	2	NAG	O4-C4-C5	-5.73	95.22	109.32
12	K	1	NAG	C1-O5-C5	-5.49	104.83	112.19
10	U	5	MAN	C1-O5-C5	5.24	119.21	112.19
10	U	4	MAN	C1-O5-C5	4.99	118.88	112.19
10	H	4	MAN	C1-O5-C5	4.82	118.65	112.19
15	N	1	NAG	O5-C1-C2	4.73	118.61	111.29
9	F	2	NAG	C2-N2-C7	4.71	129.22	122.90
9	F	1	NAG	C2-N2-C7	4.69	129.18	122.90
11	I	4	MAN	O3-C3-C2	4.62	119.47	110.05
7	A	1	NAG	C1-O5-C5	-4.61	106.01	112.19
14	M	4	MAN	O3-C3-C4	4.50	120.97	110.38
15	N	1	NAG	O4-C4-C5	-4.41	98.47	109.32
7	O	1	NAG	O4-C4-C5	-4.33	98.65	109.32
15	N	1	NAG	C1-C2-N2	4.31	117.23	110.43
12	K	1	NAG	O4-C4-C3	-4.07	100.78	110.38
18	V	7	MAN	O2-C2-C1	4.04	118.46	109.22
10	U	3	BMA	C1-O5-C5	-3.93	106.92	112.19
15	N	3	BMA	O3-C3-C2	-3.89	102.12	110.05
7	O	1	NAG	C1-C2-N2	3.53	116.00	110.43
17	S	2	NAG	O4-C4-C5	3.50	117.94	109.32
10	H	4	MAN	C1-C2-C3	3.45	114.67	109.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	I	4	MAN	O2-C2-C3	3.41	117.21	110.15
7	O	1	NAG	O4-C4-C3	-3.38	102.41	110.38
10	U	5	MAN	C1-C2-C3	3.37	114.55	109.64
10	U	3	BMA	O5-C5-C6	3.37	114.21	107.66
9	F	2	NAG	C1-C2-N2	-3.37	105.13	110.43
15	N	8	MAN	C1-O5-C5	3.31	116.62	112.19
17	S	1	NAG	O4-C4-C3	-3.20	102.83	110.38
14	M	5	MAN	C1-O5-C5	3.16	116.42	112.19
16	P	2	NAG	C2-N2-C7	3.16	127.13	122.90
16	P	2	NAG	O4-C4-C3	3.13	117.74	110.38
11	I	4	MAN	O3-C3-C4	-3.11	103.05	110.38
13	L	2	NAG	O4-C4-C5	3.09	116.93	109.32
17	S	1	NAG	C1-O5-C5	-3.06	108.09	112.19
12	K	1	NAG	C1-C2-N2	3.03	115.20	110.43
17	S	3	BMA	O5-C1-C2	-3.02	103.59	110.79
18	V	3	BMA	O3-C3-C4	2.95	117.33	110.38
14	M	4	MAN	O3-C3-C2	-2.94	104.05	110.05
9	F	1	NAG	C8-C7-N2	-2.92	111.28	116.12
10	U	5	MAN	O5-C1-C2	-2.90	103.87	110.79
10	H	4	MAN	O5-C1-C2	-2.90	103.88	110.79
12	K	1	NAG	C2-N2-C7	-2.90	119.02	122.90
8	C	2	NAG	C2-N2-C7	2.89	126.77	122.90
10	U	4	MAN	C1-C2-C3	2.88	113.84	109.64
12	K	1	NAG	C3-C4-C5	2.85	115.39	110.23
8	J	2	NAG	O5-C1-C2	-2.84	106.90	111.29
14	M	3	BMA	O3-C3-C4	2.80	116.98	110.38
11	I	4	MAN	O2-C2-C1	-2.80	102.81	109.22
17	S	1	NAG	C1-C2-N2	2.78	114.82	110.43
10	U	4	MAN	O5-C1-C2	-2.78	104.16	110.79
9	F	1	NAG	C1-O5-C5	-2.69	108.58	112.19
9	F	1	NAG	C1-C2-N2	-2.69	106.19	110.43
10	U	2	NAG	O4-C4-C3	-2.60	104.25	110.38
10	U	2	NAG	C1-O5-C5	-2.59	108.72	112.19
10	U	1	NAG	C4-C3-C2	-2.54	107.29	111.02
8	C	2	NAG	C1-C2-N2	-2.49	106.51	110.43
11	I	5	MAN	C1-O5-C5	2.48	115.50	112.19
12	K	2	NAG	C4-C3-C2	-2.47	107.39	111.02
16	P	1	NAG	C2-N2-C7	-2.46	119.60	122.90
9	F	4	MAN	O5-C5-C6	2.44	112.41	107.66
12	K	1	NAG	O4-C4-C5	-2.39	103.43	109.32
14	M	5	MAN	O5-C1-C2	-2.39	105.09	110.79
11	I	1	NAG	C1-C2-N2	-2.35	106.73	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	J	1	NAG	O4-C4-C3	2.34	115.89	110.38
11	I	5	MAN	O5-C1-C2	-2.33	105.22	110.79
15	N	2	NAG	O4-C4-C3	-2.32	104.90	110.38
14	M	4	MAN	O5-C1-C2	-2.31	105.27	110.79
12	K	4	MAN	C1-O5-C5	-2.30	109.11	112.19
10	U	1	NAG	C2-N2-C7	-2.30	119.82	122.90
14	M	7	MAN	O3-C3-C4	-2.27	105.02	110.38
15	N	1	NAG	C2-N2-C7	2.24	125.90	122.90
15	N	8	MAN	O5-C1-C2	-2.23	105.47	110.79
7	O	2	NAG	O5-C1-C2	-2.22	107.86	111.29
14	M	2	NAG	O5-C1-C2	-2.22	107.86	111.29
18	V	9	MAN	C1-C2-C3	2.20	112.84	109.64
14	M	1	NAG	C2-N2-C7	2.18	125.82	122.90
18	V	1	NAG	O4-C4-C5	-2.16	104.00	109.32
18	V	8	MAN	C1-O5-C5	-2.15	109.31	112.19
9	F	1	NAG	O4-C4-C3	-2.14	105.33	110.38
14	M	4	MAN	C2-C3-C4	-2.14	107.10	110.86
10	U	3	BMA	C2-C3-C4	-2.10	107.16	110.86
16	P	3	BMA	O5-C1-C2	-2.09	105.80	110.79
11	I	3	BMA	C1-O5-C5	-2.09	109.39	112.19
10	U	3	BMA	O3-C3-C2	-2.08	105.81	110.05
12	T	2	NAG	C2-N2-C7	2.07	125.68	122.90
14	M	3	BMA	O3-C3-C2	2.07	114.27	110.05
9	F	1	NAG	O4-C4-C5	-2.05	104.28	109.32
14	M	7	MAN	C1-C2-C3	2.01	112.58	109.64
18	V	9	MAN	C1-O5-C5	2.01	114.88	112.19
18	V	6	MAN	O5-C1-C2	-2.01	106.01	110.79
10	U	2	NAG	C4-C3-C2	2.00	113.95	111.02

There are no chirality outliers.

All (143) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1	NAG	C8-C7-N2-C2
7	A	1	NAG	O7-C7-N2-C2
7	A	2	NAG	C8-C7-N2-C2
7	A	2	NAG	O7-C7-N2-C2
8	C	2	NAG	C3-C2-N2-C7
8	J	1	NAG	C3-C2-N2-C7
8	J	1	NAG	C8-C7-N2-C2
8	J	1	NAG	O7-C7-N2-C2
8	J	2	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
9	F	1	NAG	C3-C2-N2-C7
10	H	2	NAG	C3-C2-N2-C7
10	H	2	NAG	C8-C7-N2-C2
10	H	2	NAG	O7-C7-N2-C2
10	U	2	NAG	C1-C2-N2-C7
11	I	1	NAG	C8-C7-N2-C2
11	I	1	NAG	O7-C7-N2-C2
11	I	2	NAG	C8-C7-N2-C2
11	I	2	NAG	O7-C7-N2-C2
12	K	1	NAG	C8-C7-N2-C2
12	K	1	NAG	O7-C7-N2-C2
12	K	2	NAG	C8-C7-N2-C2
12	K	2	NAG	O7-C7-N2-C2
13	L	2	NAG	C8-C7-N2-C2
13	L	2	NAG	O7-C7-N2-C2
14	M	1	NAG	C8-C7-N2-C2
14	M	1	NAG	O7-C7-N2-C2
14	M	2	NAG	C3-C2-N2-C7
14	M	2	NAG	C8-C7-N2-C2
14	M	2	NAG	O7-C7-N2-C2
15	N	1	NAG	C1-C2-N2-C7
15	N	1	NAG	C8-C7-N2-C2
15	N	1	NAG	O7-C7-N2-C2
15	N	2	NAG	C3-C2-N2-C7
15	N	2	NAG	C8-C7-N2-C2
15	N	2	NAG	O7-C7-N2-C2
16	P	1	NAG	O7-C7-N2-C2
16	P	2	NAG	C1-C2-N2-C7
17	S	1	NAG	C3-C2-N2-C7
17	S	1	NAG	C8-C7-N2-C2
17	S	1	NAG	O7-C7-N2-C2
17	S	2	NAG	C3-C2-N2-C7
17	S	2	NAG	C8-C7-N2-C2
17	S	2	NAG	O7-C7-N2-C2
18	V	1	NAG	C8-C7-N2-C2
18	V	1	NAG	O7-C7-N2-C2
18	V	4	MAN	C4-C5-C6-O6
7	O	1	NAG	C8-C7-N2-C2
8	J	2	NAG	C8-C7-N2-C2
16	P	1	NAG	C8-C7-N2-C2
15	N	3	BMA	O5-C5-C6-O6
8	J	3	BMA	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
10	U	2	NAG	O5-C5-C6-O6
18	V	9	MAN	C4-C5-C6-O6
18	V	4	MAN	O5-C5-C6-O6
17	S	3	BMA	C4-C5-C6-O6
7	O	1	NAG	O7-C7-N2-C2
8	C	4	MAN	O5-C5-C6-O6
10	U	4	MAN	C4-C5-C6-O6
8	J	3	BMA	C4-C5-C6-O6
14	M	7	MAN	O5-C5-C6-O6
10	U	2	NAG	C4-C5-C6-O6
7	O	2	NAG	C8-C7-N2-C2
10	U	1	NAG	C8-C7-N2-C2
16	P	4	MAN	O5-C5-C6-O6
18	V	1	NAG	O5-C5-C6-O6
14	M	7	MAN	C4-C5-C6-O6
15	N	3	BMA	C4-C5-C6-O6
10	U	4	MAN	O5-C5-C6-O6
18	V	9	MAN	O5-C5-C6-O6
15	N	5	MAN	O5-C5-C6-O6
9	F	4	MAN	O5-C5-C6-O6
8	C	2	NAG	C8-C7-N2-C2
9	F	1	NAG	C8-C7-N2-C2
9	F	2	NAG	C8-C7-N2-C2
15	N	1	NAG	O5-C5-C6-O6
8	C	4	MAN	C4-C5-C6-O6
17	S	3	BMA	O5-C5-C6-O6
16	P	4	MAN	C4-C5-C6-O6
18	V	1	NAG	C4-C5-C6-O6
7	O	2	NAG	O7-C7-N2-C2
8	C	1	NAG	C8-C7-N2-C2
8	C	2	NAG	O7-C7-N2-C2
9	F	1	NAG	O7-C7-N2-C2
9	F	2	NAG	O7-C7-N2-C2
10	U	1	NAG	O7-C7-N2-C2
11	I	7	MAN	O5-C5-C6-O6
15	N	4	MAN	O5-C5-C6-O6
10	U	3	BMA	O5-C5-C6-O6
17	S	2	NAG	O5-C5-C6-O6
8	C	1	NAG	O7-C7-N2-C2
14	M	4	MAN	O5-C5-C6-O6
18	V	8	MAN	C4-C5-C6-O6
11	I	4	MAN	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
18	V	8	MAN	O5-C5-C6-O6
9	F	2	NAG	O5-C5-C6-O6
11	I	2	NAG	O5-C5-C6-O6
13	L	3	BMA	C4-C5-C6-O6
7	A	2	NAG	O5-C5-C6-O6
8	C	5	MAN	O5-C5-C6-O6
17	S	7	MAN	O5-C5-C6-O6
12	K	4	MAN	O5-C5-C6-O6
7	A	3	BMA	O5-C5-C6-O6
15	N	5	MAN	C4-C5-C6-O6
17	S	5	MAN	O5-C5-C6-O6
8	J	5	MAN	O5-C5-C6-O6
17	S	8	MAN	O5-C5-C6-O6
7	O	2	NAG	O5-C5-C6-O6
17	S	4	MAN	O5-C5-C6-O6
11	I	4	MAN	C4-C5-C6-O6
11	I	5	MAN	O5-C5-C6-O6
12	K	2	NAG	O5-C5-C6-O6
9	F	2	NAG	C3-C2-N2-C7
11	I	1	NAG	C3-C2-N2-C7
9	F	3	BMA	O5-C5-C6-O6
11	I	1	NAG	O5-C5-C6-O6
15	N	4	MAN	C4-C5-C6-O6
10	U	3	BMA	C4-C5-C6-O6
17	S	6	MAN	C4-C5-C6-O6
17	S	1	NAG	C4-C5-C6-O6
17	S	1	NAG	O5-C5-C6-O6
9	F	4	MAN	C4-C5-C6-O6
10	H	2	NAG	C4-C5-C6-O6
12	T	2	NAG	C1-C2-N2-C7
13	L	1	NAG	C1-C2-N2-C7
17	S	6	MAN	O5-C5-C6-O6
10	H	2	NAG	O5-C5-C6-O6
8	J	2	NAG	C3-C2-N2-C7
13	L	1	NAG	C3-C2-N2-C7
8	C	2	NAG	C4-C5-C6-O6
15	N	7	MAN	C4-C5-C6-O6
15	N	7	MAN	O5-C5-C6-O6
12	T	1	NAG	C8-C7-N2-C2
9	F	6	MAN	O5-C5-C6-O6
16	P	3	BMA	C4-C5-C6-O6
8	J	2	NAG	C1-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
13	L	2	NAG	O5-C5-C6-O6
13	L	3	BMA	O5-C5-C6-O6
10	U	2	NAG	C3-C2-N2-C7
12	T	2	NAG	C3-C2-N2-C7
14	M	1	NAG	C3-C2-N2-C7
12	T	1	NAG	O7-C7-N2-C2
15	N	1	NAG	C4-C5-C6-O6
8	C	2	NAG	O5-C5-C6-O6

There are no ring outliers.

36 monomers are involved in 47 short contacts:

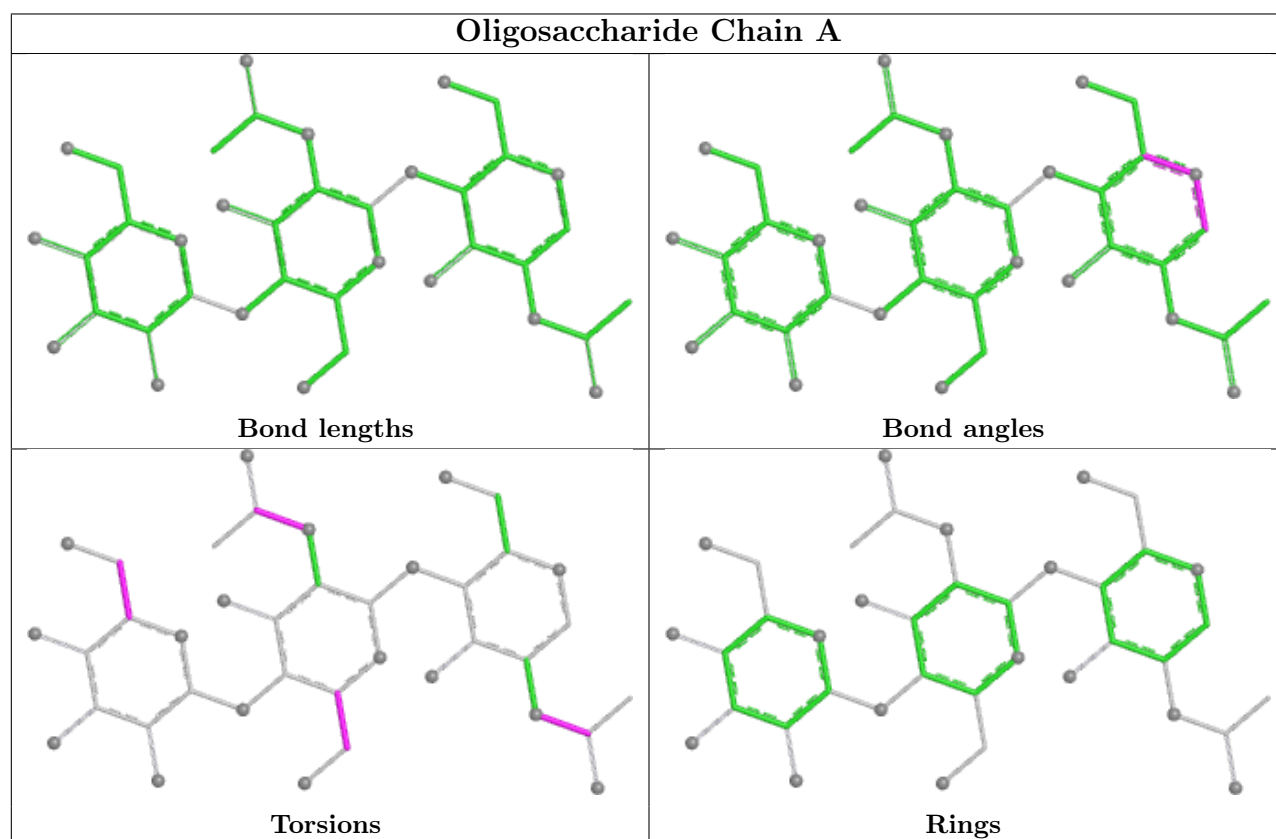
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	N	6	MAN	1	0
10	H	4	MAN	1	0
7	A	1	NAG	1	0
11	I	2	NAG	1	0
15	N	1	NAG	1	0
18	V	6	MAN	1	0
10	U	5	MAN	2	0
9	F	1	NAG	1	0
17	S	1	NAG	14	0
7	A	3	BMA	1	0
12	K	2	NAG	1	0
8	C	2	NAG	1	0
15	N	2	NAG	2	0
11	I	1	NAG	1	0
18	V	2	NAG	1	0
7	O	1	NAG	2	0
18	V	9	MAN	1	0
10	H	3	BMA	2	0
14	M	1	NAG	2	0
14	M	4	MAN	1	0
15	N	3	BMA	2	0
10	U	3	BMA	3	0
12	K	1	NAG	3	0
10	H	2	NAG	1	0
7	A	2	NAG	1	0
11	I	4	MAN	4	0
9	F	6	MAN	1	0
11	I	5	MAN	3	0
11	I	7	MAN	1	0

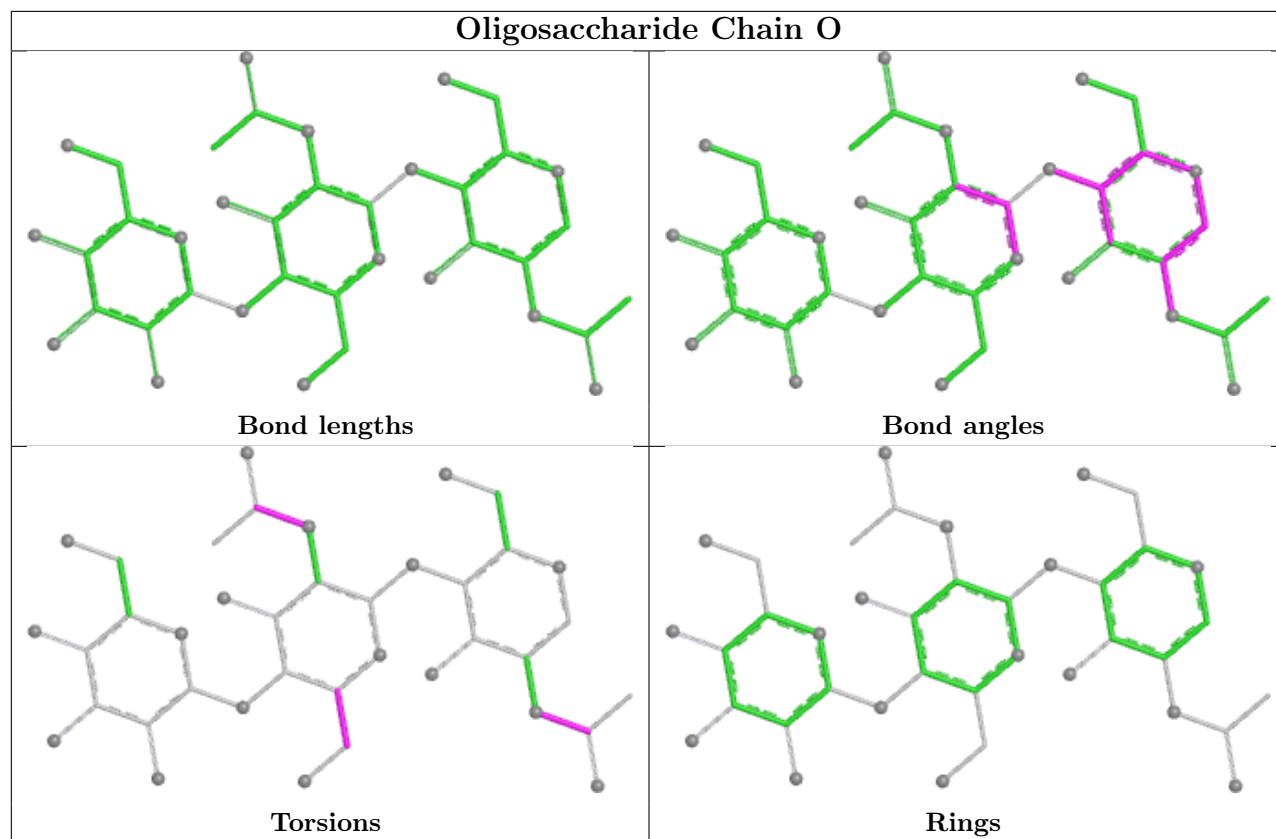
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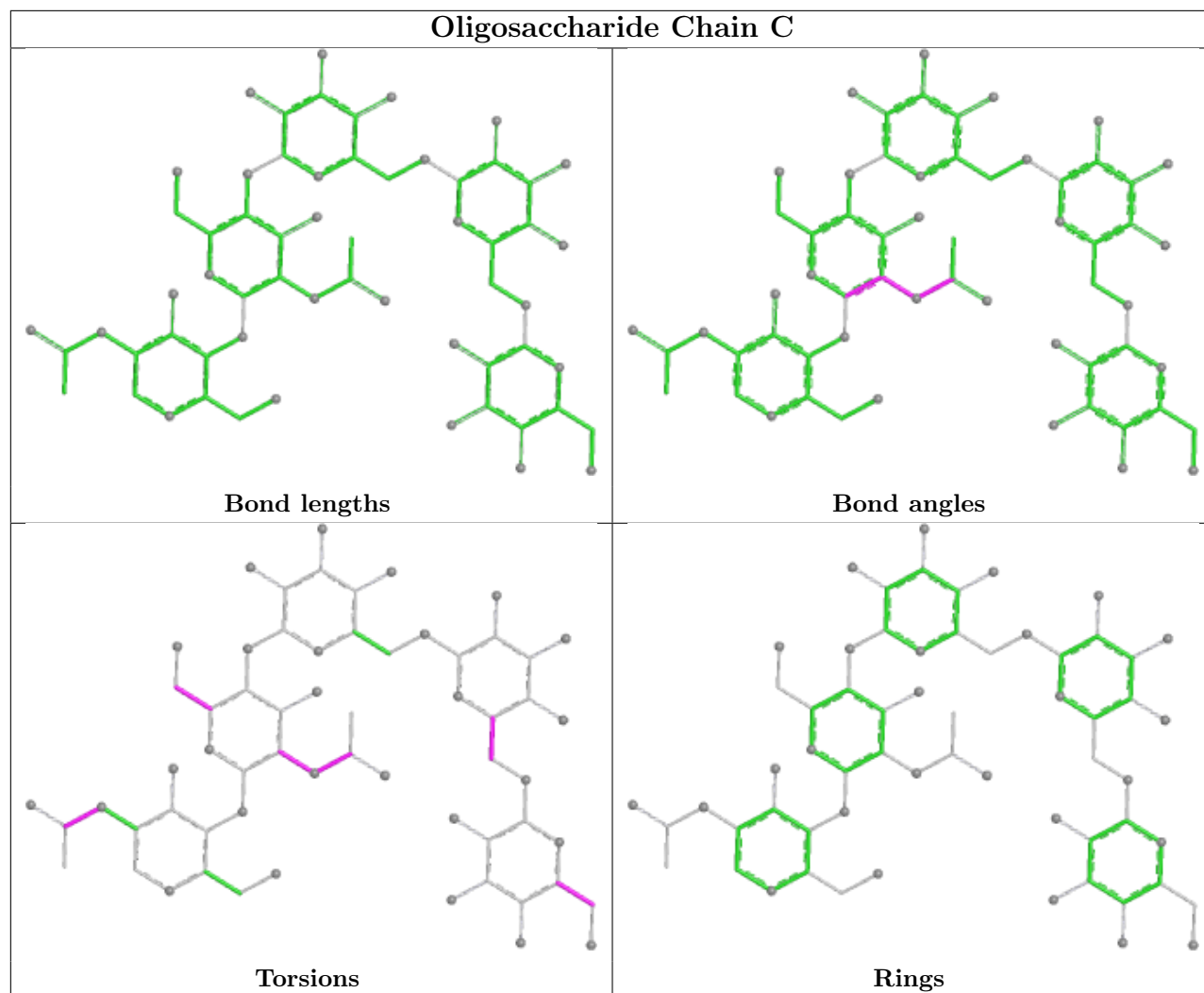
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	3	BMA	1	0
17	S	2	NAG	2	0
10	U	4	MAN	1	0
9	F	3	BMA	1	0
18	V	1	NAG	1	0
17	S	3	BMA	1	0
8	J	2	NAG	1	0

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

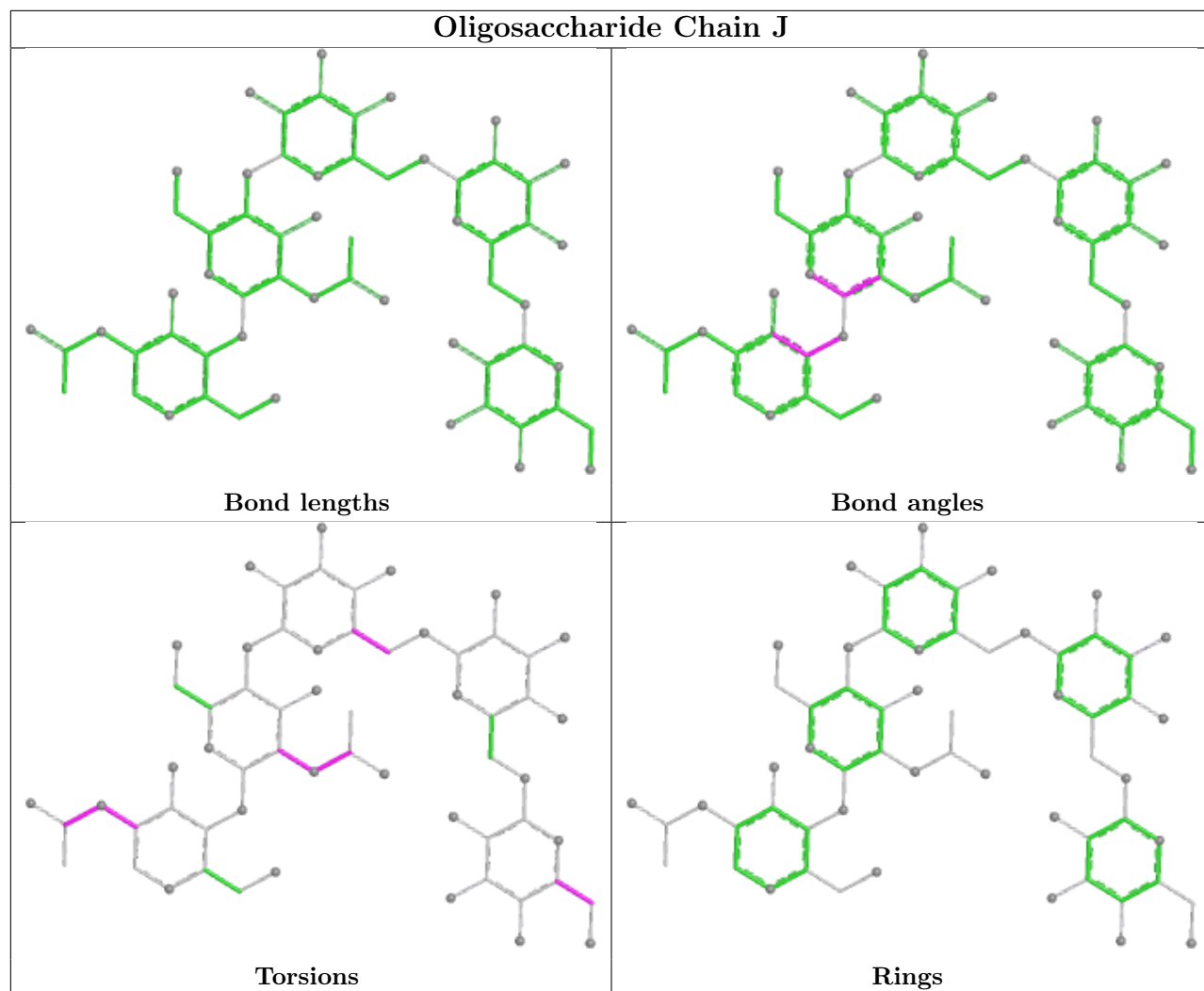


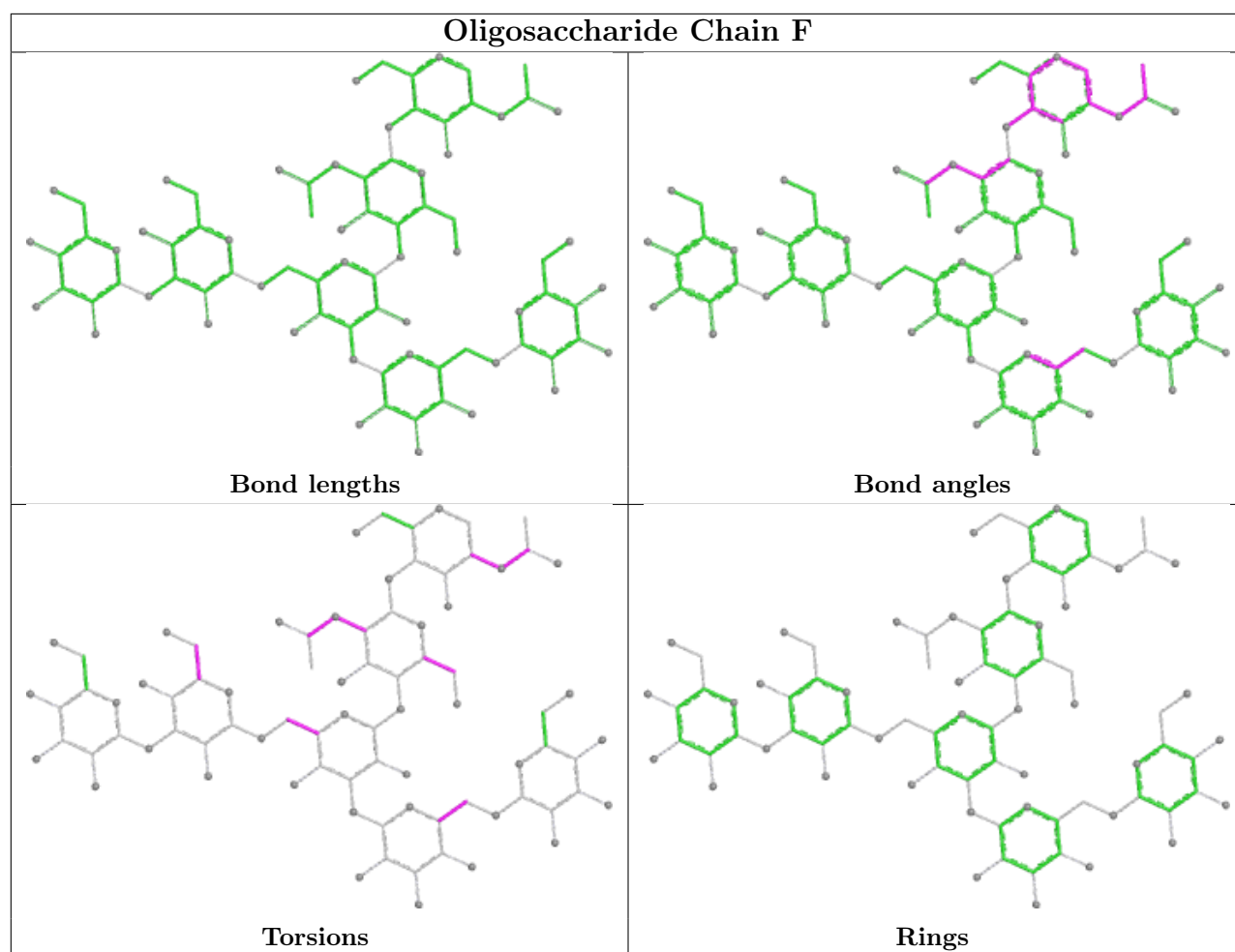


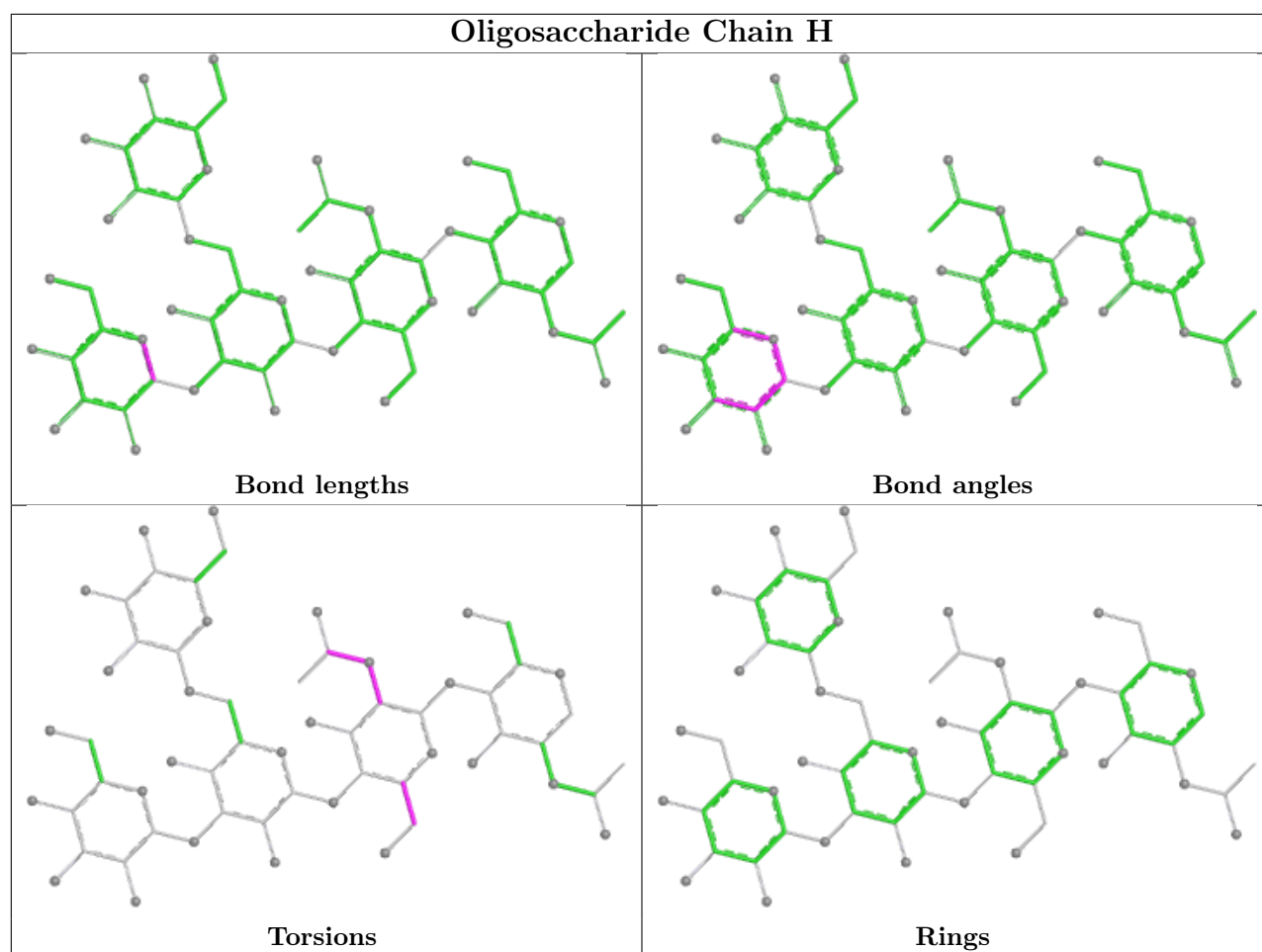
Oligosaccharide Chain C

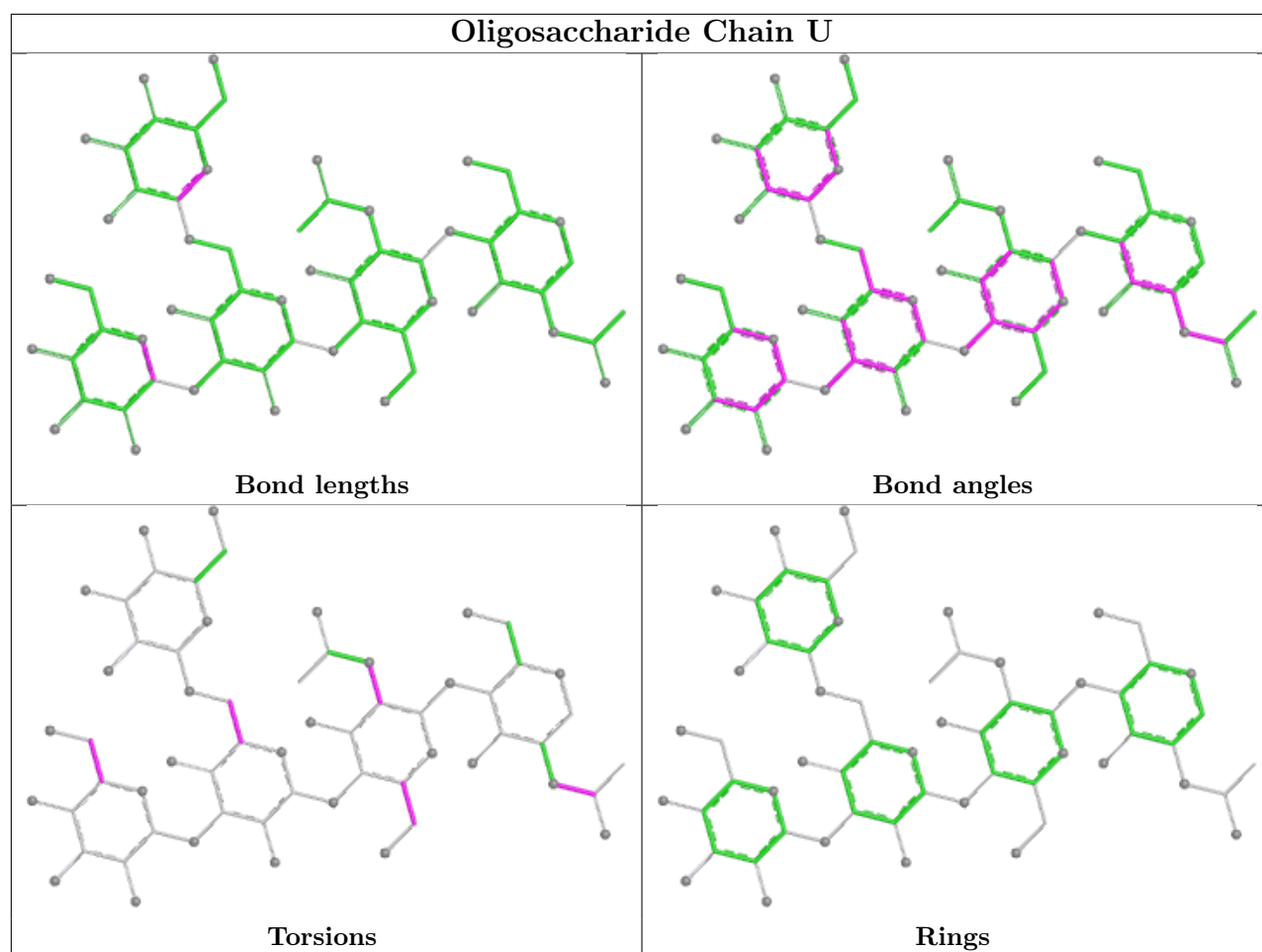


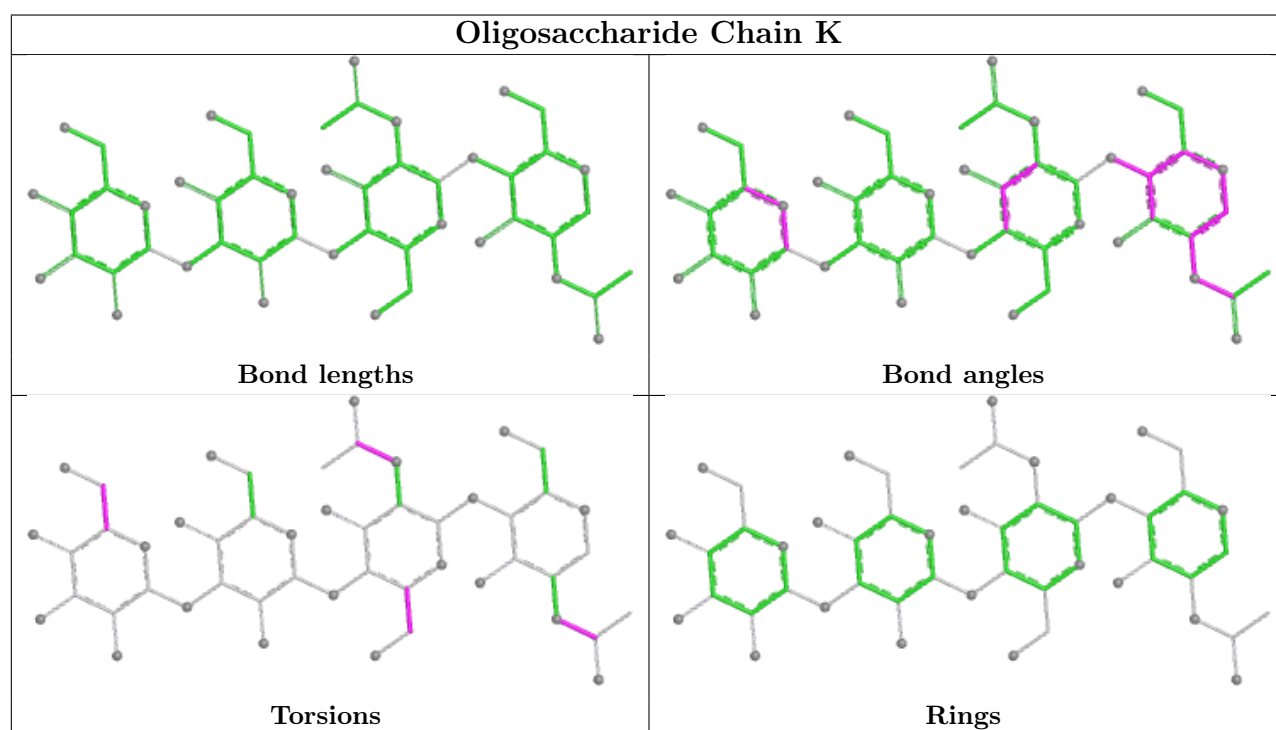
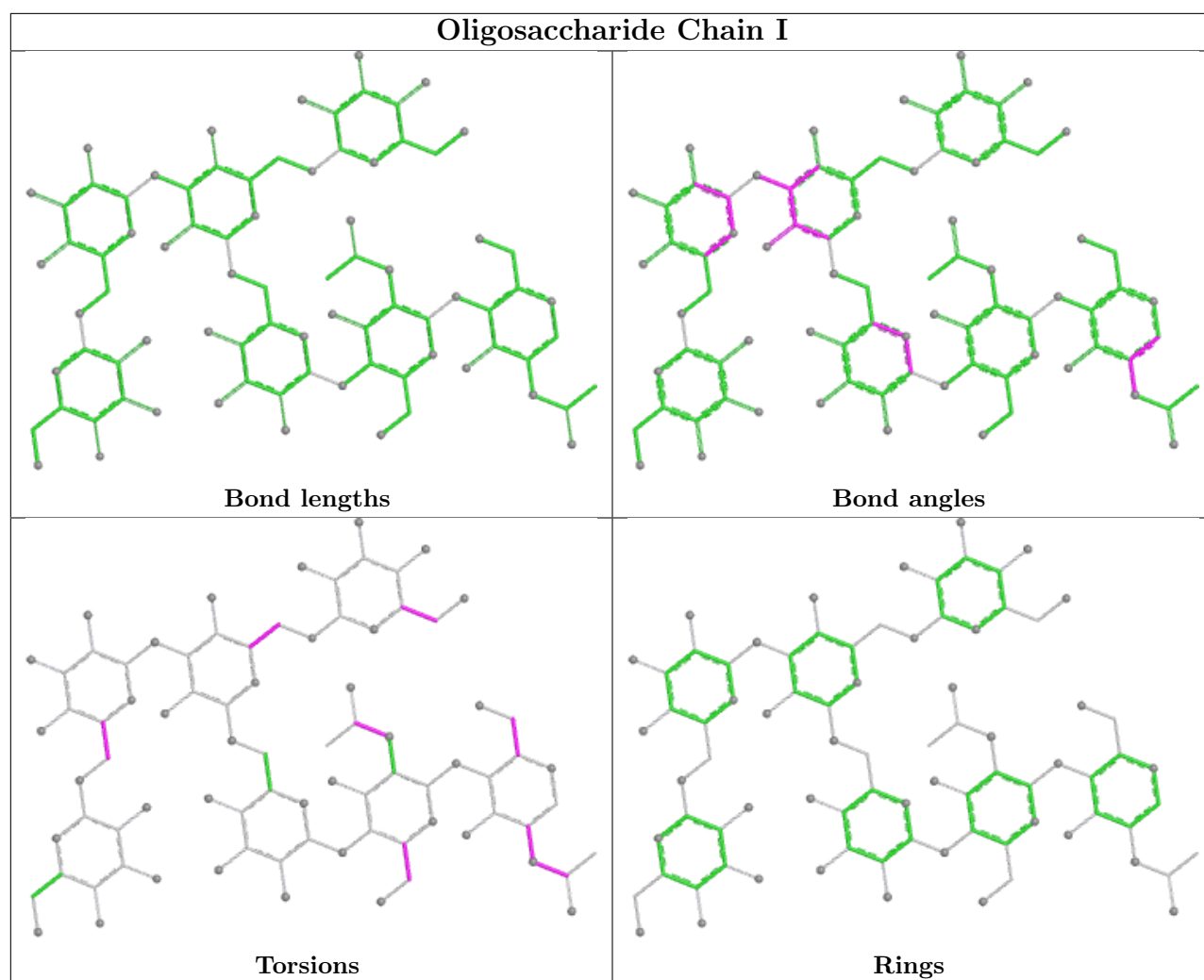
Oligosaccharide Chain J



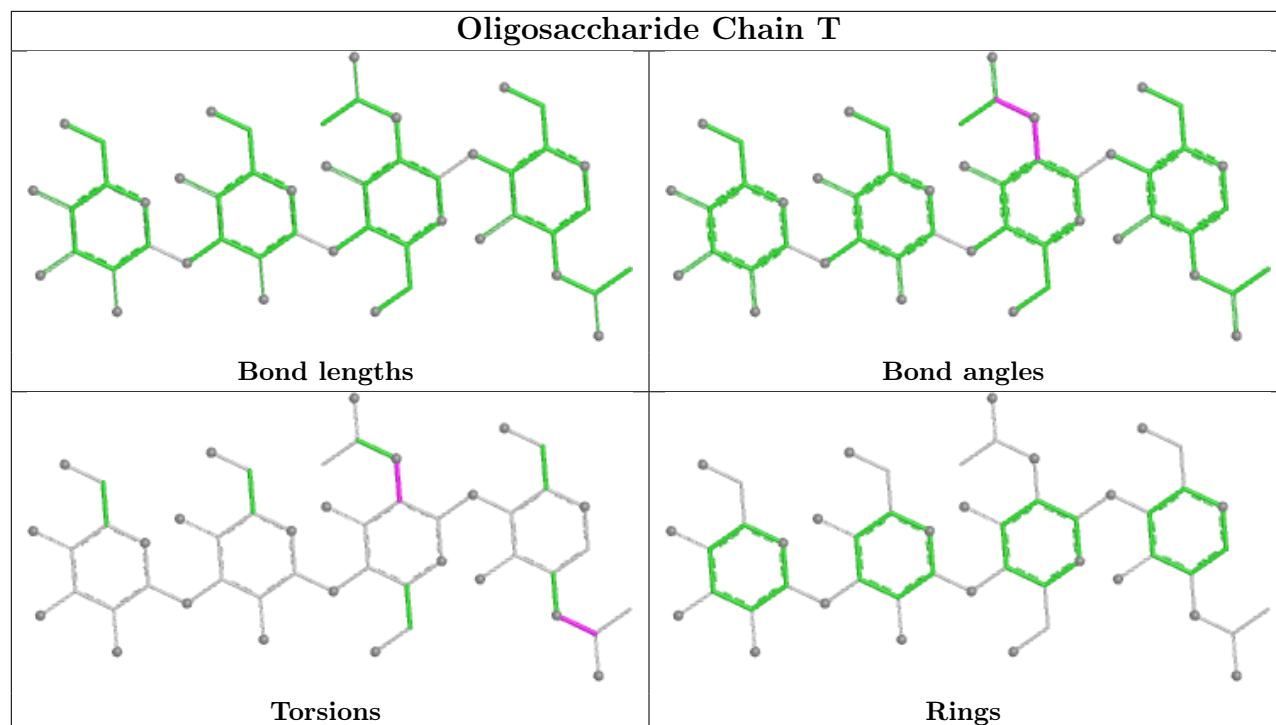




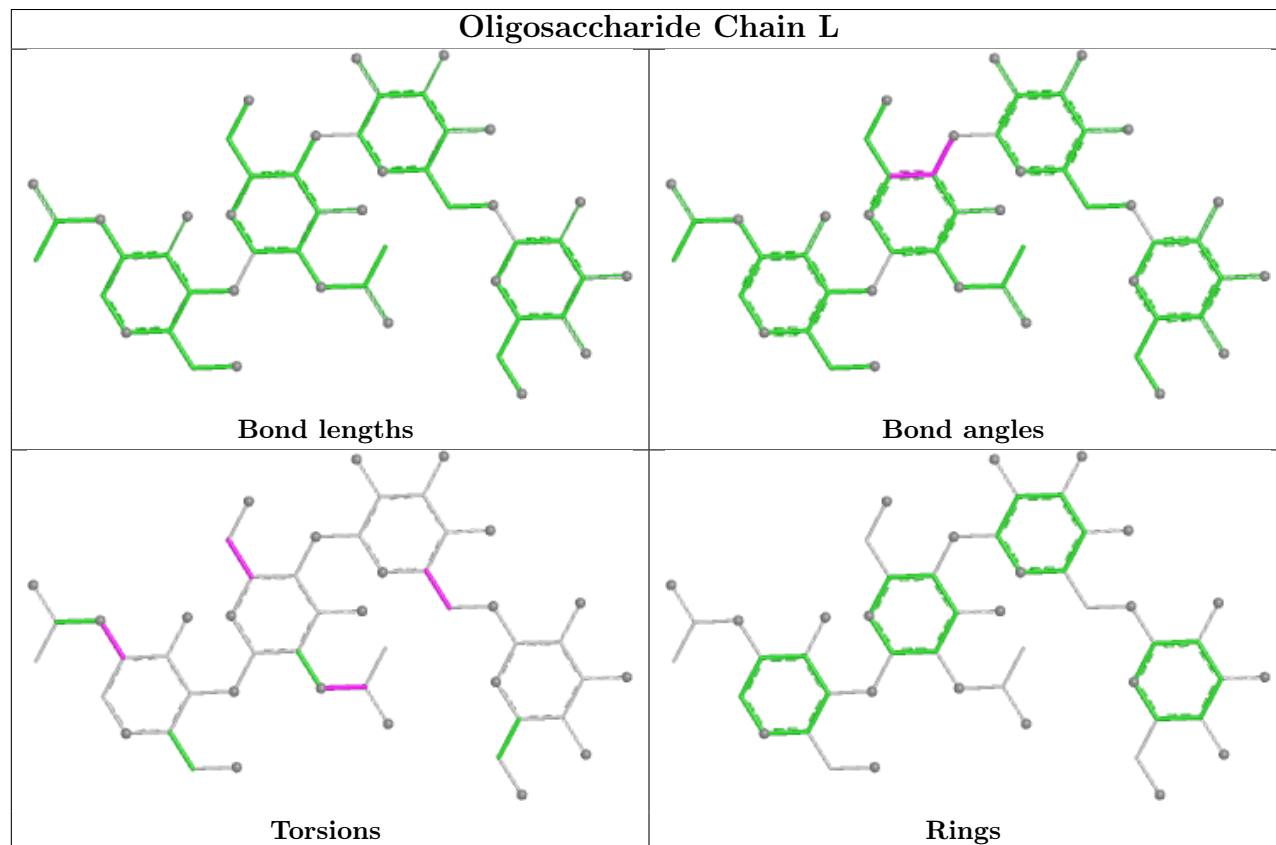


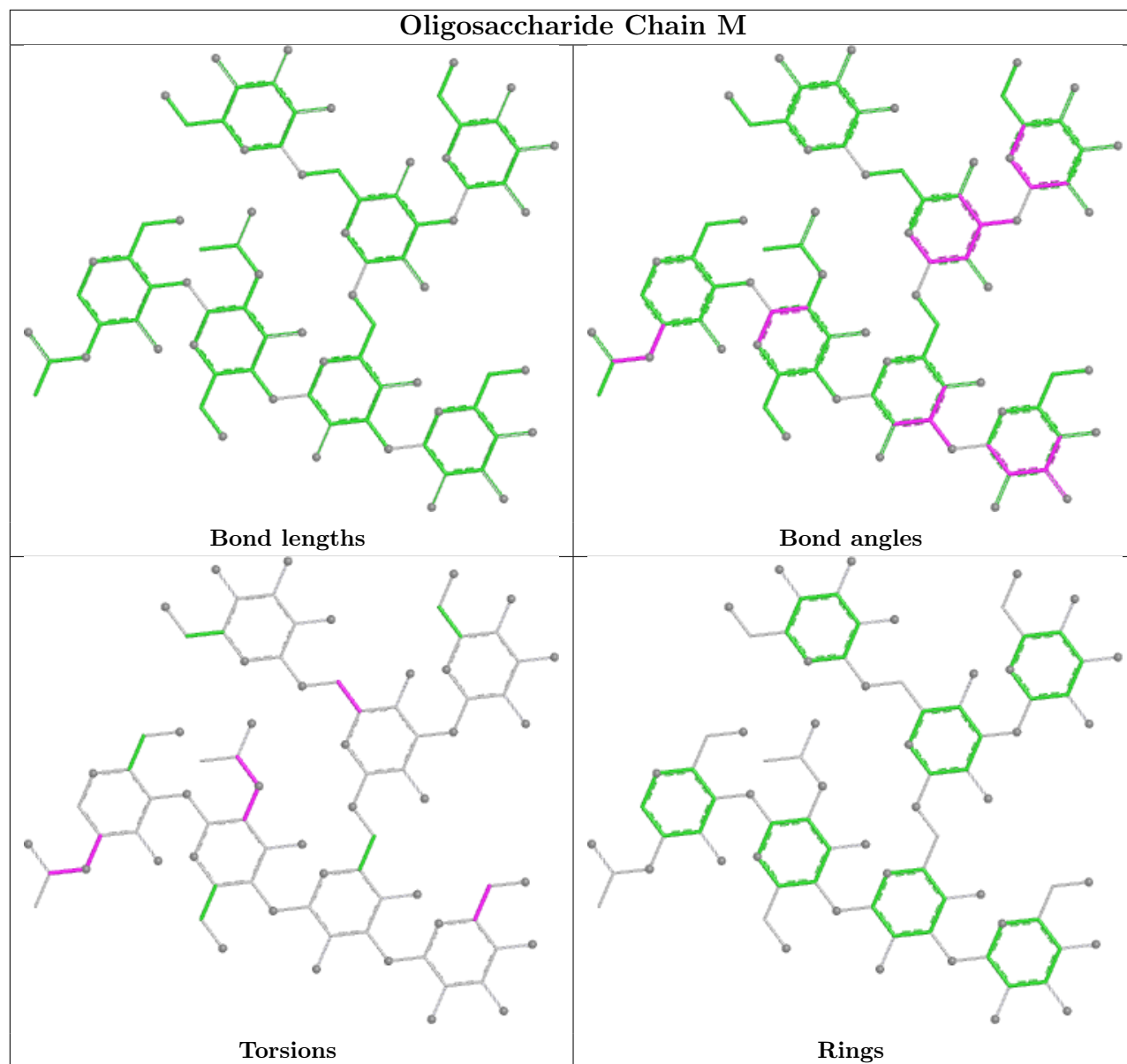


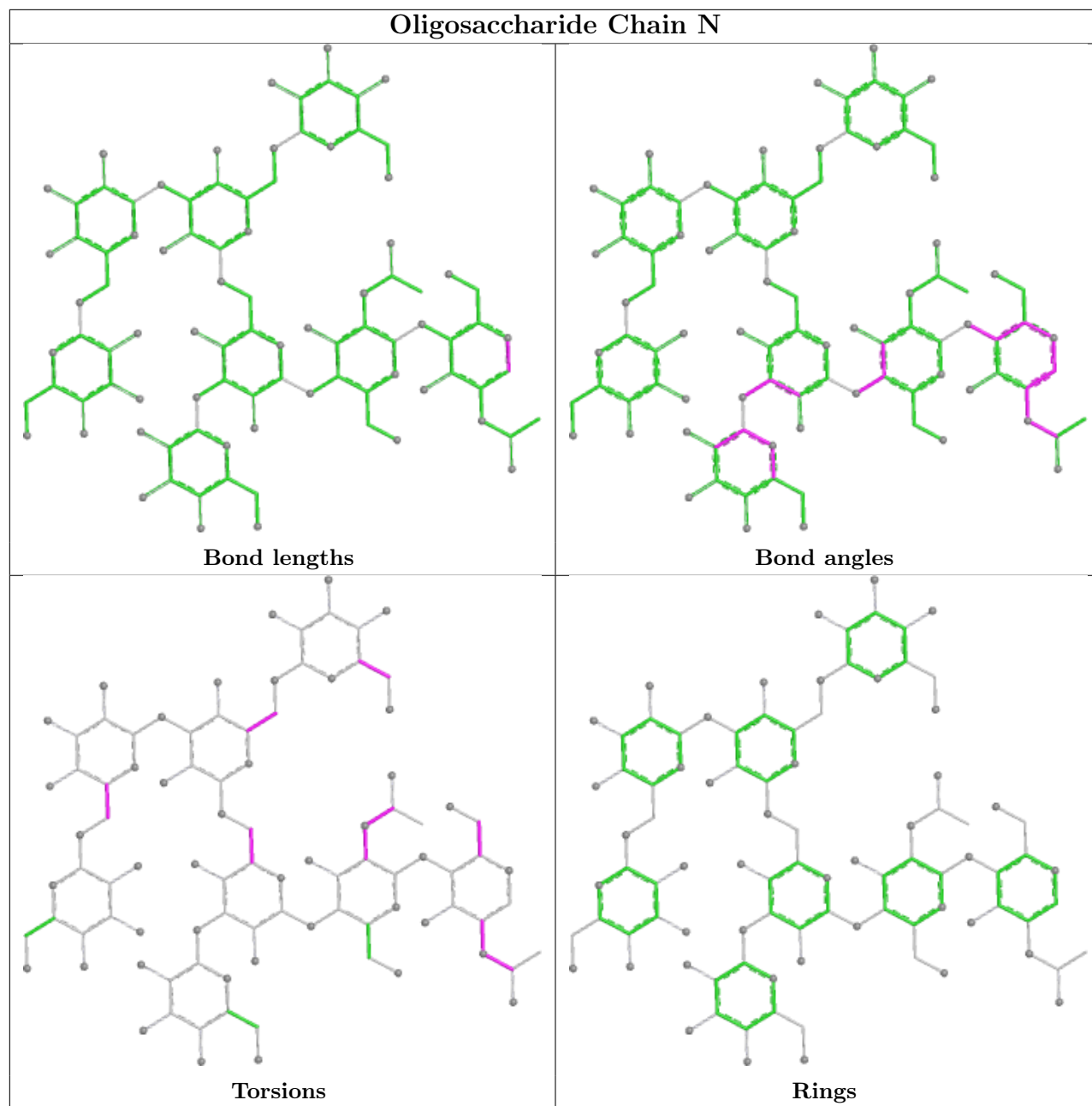
Oligosaccharide Chain T

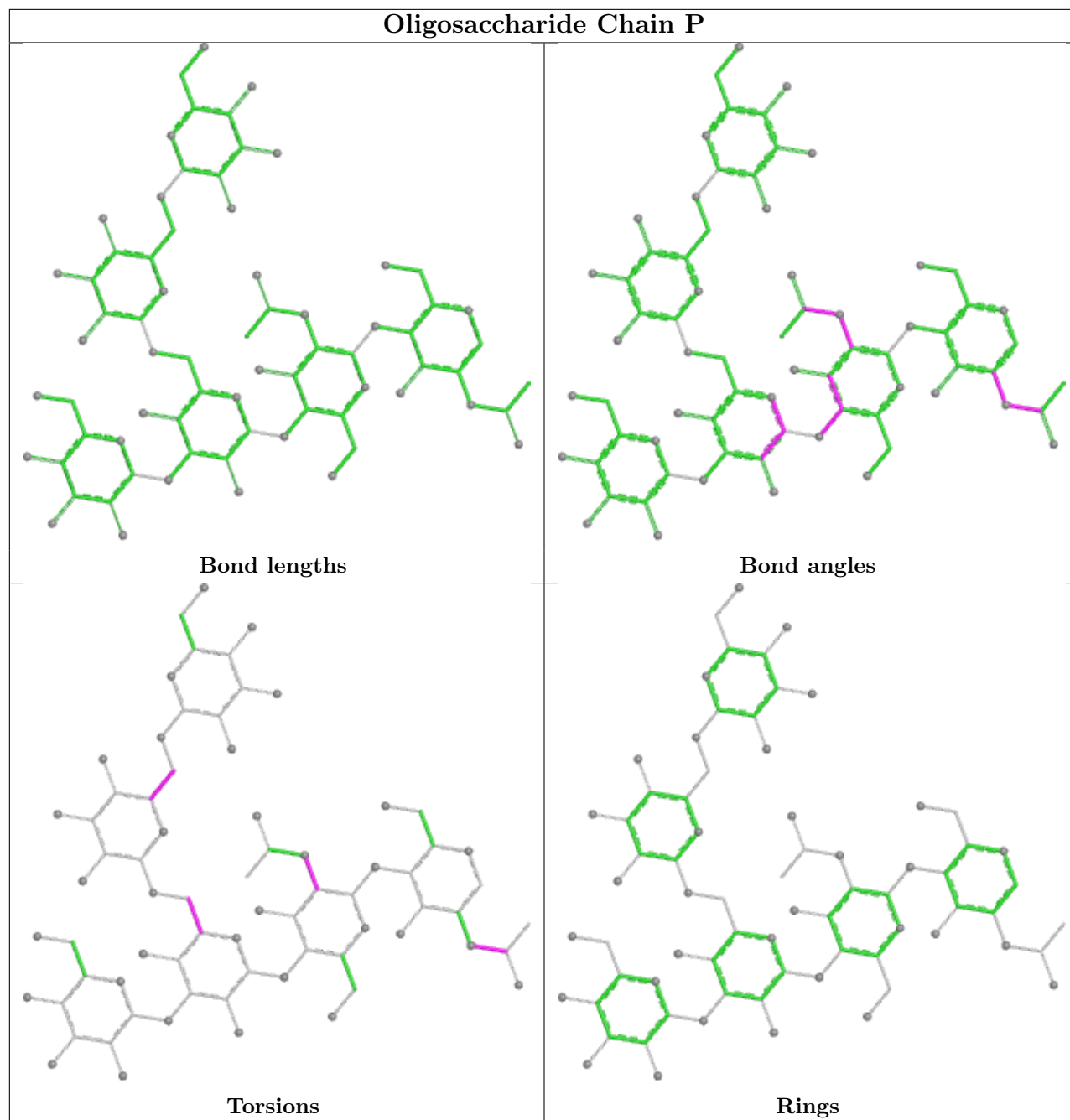


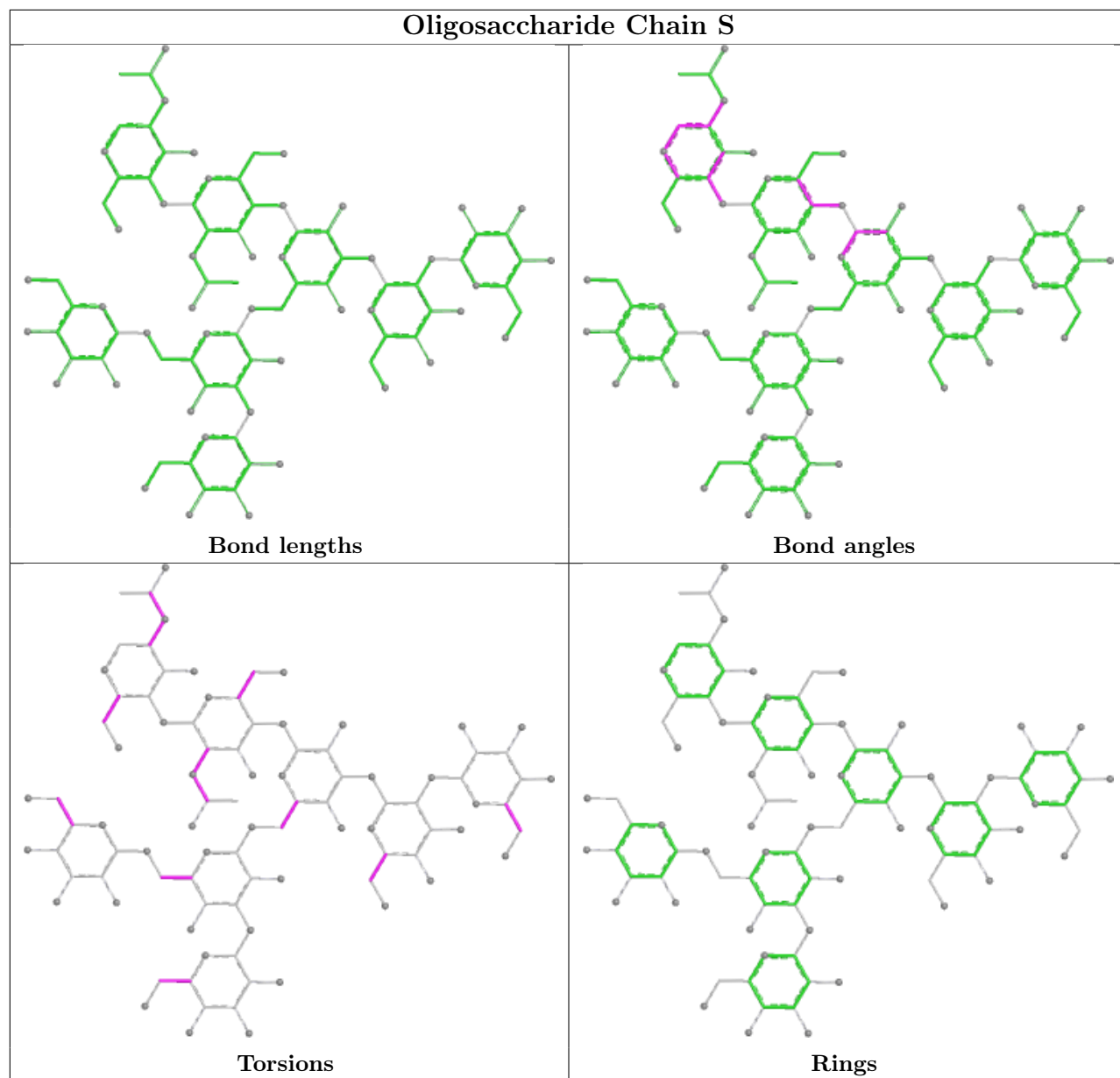
Oligosaccharide Chain L

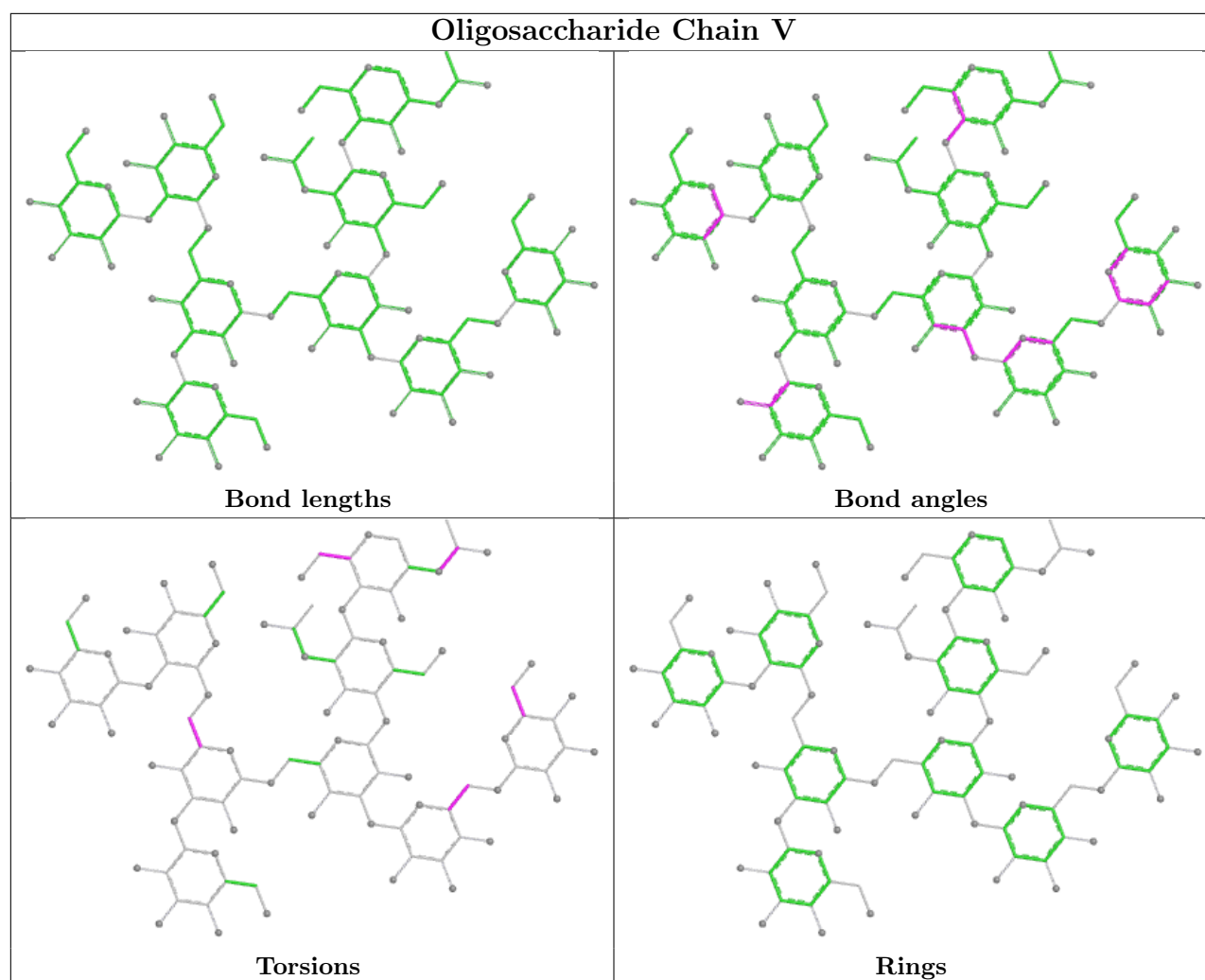












5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
19	NAG	G	603	4	14,14,15	0.32	0	17,19,21	0.83	0
19	NAG	G	601	4	14,14,15	0.30	0	17,19,21	0.74	0
19	NAG	B	701	1	14,14,15	0.29	0	17,19,21	0.61	0
19	NAG	G	602	4	14,14,15	0.36	0	17,19,21	0.89	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
19	NAG	G	603	4	-	3/6/23/26	0/1/1/1
19	NAG	G	601	4	-	4/6/23/26	0/1/1/1
19	NAG	B	701	1	-	2/6/23/26	0/1/1/1
19	NAG	G	602	4	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	B	701	NAG	C8-C7-N2-C2
19	B	701	NAG	O7-C7-N2-C2
19	G	602	NAG	C1-C2-N2-C7
19	G	603	NAG	C3-C2-N2-C7
19	G	603	NAG	C8-C7-N2-C2
19	G	603	NAG	O7-C7-N2-C2
19	G	602	NAG	C8-C7-N2-C2
19	G	602	NAG	O7-C7-N2-C2
19	G	601	NAG	C8-C7-N2-C2
19	G	601	NAG	O7-C7-N2-C2
19	G	601	NAG	O5-C5-C6-O6
19	G	601	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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	B	139/153 (90%)	0.54	5 (3%)	46 35	110, 185, 251, 286	0
2	D	235/243 (96%)	0.19	3 (1%)	75 58	155, 240, 318, 372	0
3	E	210/216 (97%)	0.38	8 (3%)	44 34	150, 223, 312, 352	0
4	G	451/479 (94%)	0.33	16 (3%)	47 35	129, 186, 258, 335	0
5	Q	228/241 (94%)	0.20	3 (1%)	75 58	170, 227, 285, 309	0
6	R	211/215 (98%)	0.42	6 (2%)	55 41	184, 257, 311, 324	0
All	All	1474/1547 (95%)	0.33	41 (2%)	55 41	110, 214, 303, 372	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	G	507	GLY	8.1
4	G	379	GLY	4.1
4	G	151	ARG	3.6
1	B	564	HIS	3.6
4	G	326	ILE	3.4
2	D	1	GLU	3.4
4	G	178	ARG	3.3
6	R	120	THR	3.2
6	R	5	GLU	3.2
6	R	87	TYR	3.1
4	G	322	ILE	2.7
4	G	180	ASP	2.7
1	B	552	GLN	2.7
1	B	554	ASN	2.6
1	B	549	VAL	2.6
2	D	100(D)	TRP	2.6
1	B	520	LEU	2.6
3	E	43	GLY	2.5
4	G	506	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
3	E	206	VAL	2.5
5	Q	208	THR	2.5
3	E	211	ALA	2.3
4	G	505	VAL	2.3
4	G	323	ILE	2.3
4	G	395	TRP	2.2
5	Q	122	GLN	2.2
6	R	42	GLY	2.2
3	E	38	TYR	2.2
3	E	3	VAL	2.2
4	G	225	ILE	2.2
4	G	244	THR	2.1
4	G	238	PRO	2.1
4	G	92	GLU	2.1
3	E	37	TRP	2.1
6	R	56	SER	2.1
4	G	176	PHE	2.1
6	R	117	PRO	2.1
3	E	204	SER	2.1
2	D	185	PRO	2.1
3	E	67	TYR	2.0
5	Q	152	THR	2.0

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	A	1	14/15	-	-	219,264,305,315	0
7	NAG	A	2	14/15	-	-	277,311,319,323	0
7	BMA	A	3	11/12	-	-	291,319,332,336	0
13	MAN	L	4	11/12	-0.35	0.15	303,335,344,344	0
12	BMA	K	3	11/12	-0.11	0.13	312,330,344,345	0
8	MAN	J	4	11/12	-0.11	0.12	319,331,349,350	0

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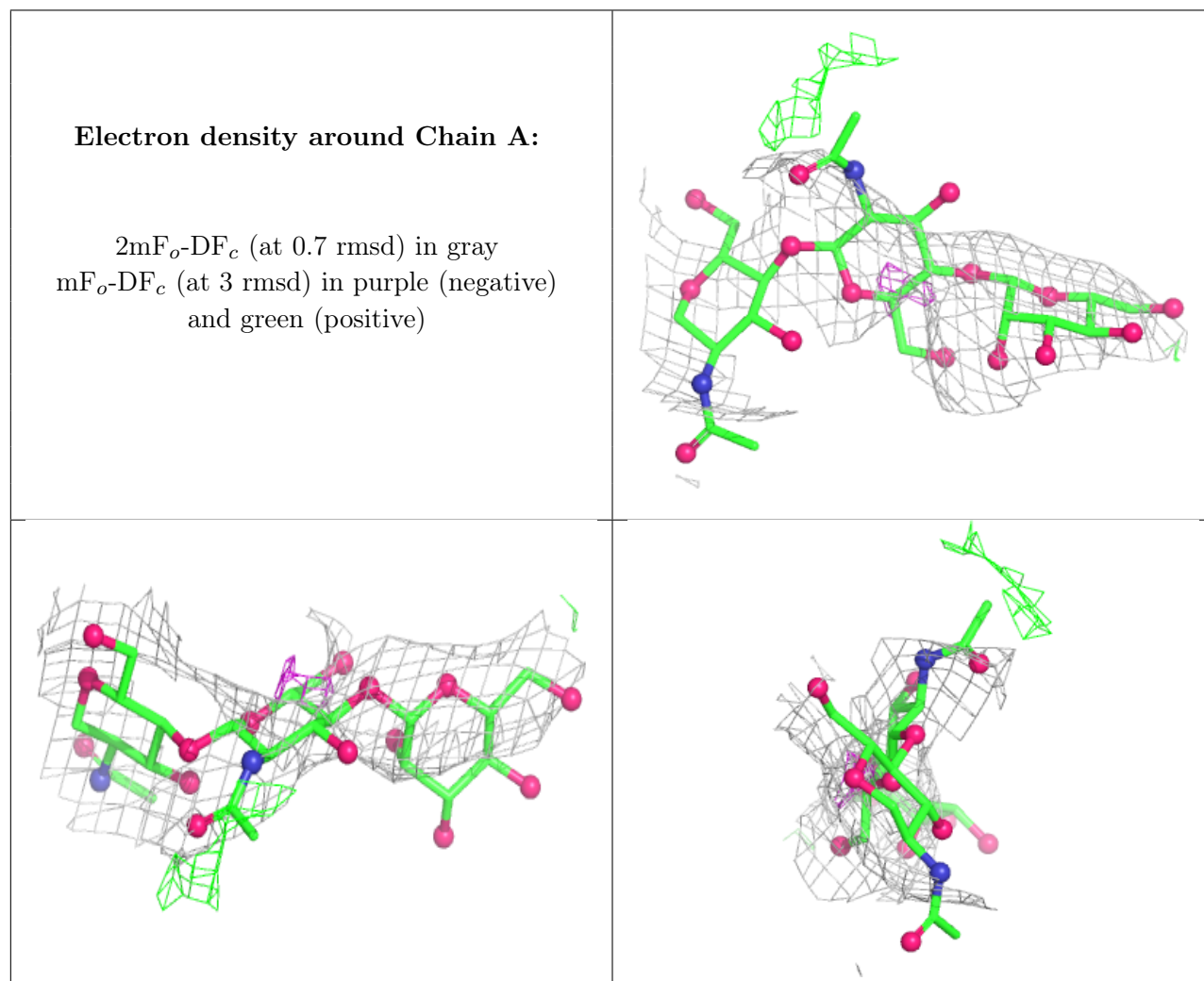
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NAG	C	1	14/15	-	-	215,260,300,306	0
8	NAG	C	2	14/15	-	-	271,316,342,357	0
8	BMA	C	3	11/12	-	-	309,353,369,378	0
8	MAN	C	4	11/12	-	-	373,383,391,392	0
8	MAN	C	5	11/12	-	-	316,356,370,377	0
17	MAN	S	5	11/12	-0.02	0.14	292,310,320,323	0
8	MAN	J	5	11/12	0.00	0.11	317,345,353,355	0
15	MAN	N	4	11/12	0.10	0.10	328,344,348,353	0
17	MAN	S	4	11/12	0.20	0.17	278,315,328,329	0
16	MAN	P	4	11/12	0.30	0.10	337,353,368,374	0
9	NAG	F	1	14/15	-	-	209,229,240,259	0
9	NAG	F	2	14/15	-	-	209,246,269,283	0
9	BMA	F	3	11/12	-	-	209,233,269,291	0
9	MAN	F	4	11/12	-	-	249,256,277,284	0
9	MAN	F	5	11/12	-	-	271,284,296,300	0
9	MAN	F	6	11/12	-	-	209,209,225,242	0
9	MAN	F	7	11/12	-	-	227,243,271,292	0
17	MAN	S	7	11/12	0.34	0.10	329,343,352,353	0
17	MAN	S	6	11/12	0.35	0.09	298,333,339,350	0
16	MAN	P	5	11/12	0.35	0.13	339,350,367,372	0
10	MAN	H	4	11/12	0.36	0.09	307,327,350,352	0
10	BMA	U	3	11/12	0.37	0.12	339,346,356,373	0
12	MAN	K	4	11/12	0.39	0.11	302,342,349,351	0
12	MAN	T	4	11/12	0.41	0.25	223,238,277,286	0
17	MAN	S	8	11/12	0.41	0.13	288,308,326,326	0
15	BMA	N	3	11/12	0.43	0.10	315,321,339,347	0
16	MAN	P	6	11/12	0.44	0.08	331,360,370,372	0
10	BMA	H	3	11/12	0.46	0.13	298,322,334,344	0
8	BMA	J	3	11/12	0.48	0.10	329,340,357,360	0
14	MAN	M	4	11/12	0.49	0.10	286,308,331,339	0
13	BMA	L	3	11/12	0.50	0.12	289,314,339,347	0
10	NAG	H	2	14/15	0.54	0.11	267,303,321,325	0
11	NAG	I	2	14/15	0.55	0.20	249,297,327,348	0
13	NAG	L	2	14/15	0.56	0.13	268,301,316,317	0
10	MAN	U	5	11/12	0.57	0.10	296,344,357,364	0
10	MAN	H	5	11/12	0.58	0.11	272,312,330,333	0
17	BMA	S	3	11/12	0.62	0.08	303,320,323,323	0
14	BMA	M	3	11/12	0.62	0.11	265,271,281,282	0
11	MAN	I	7	11/12	0.63	0.12	327,347,364,367	0
8	NAG	J	2	14/15	0.63	0.10	254,281,315,338	0
10	MAN	U	4	11/12	0.64	0.13	291,317,337,338	0
18	MAN	V	7	11/12	0.69	0.18	275,283,294,298	0

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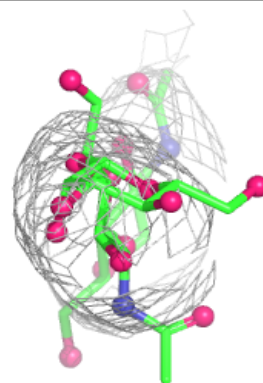
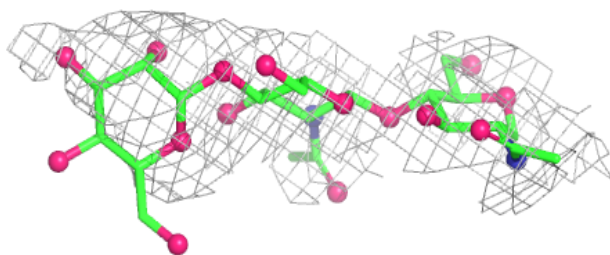
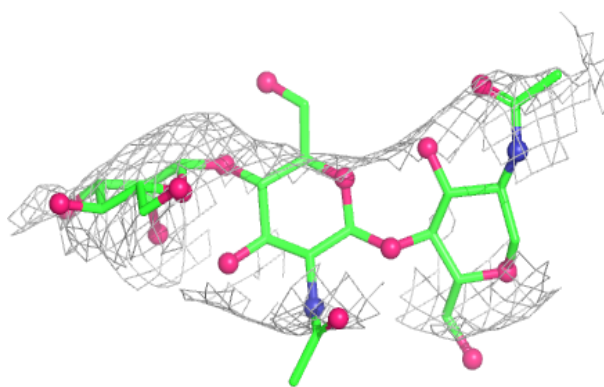
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
16	NAG	P	2	14/15	0.70	0.10	273,300,329,350	0
18	MAN	V	9	11/12	0.70	0.21	213,219,246,253	0
11	MAN	I	5	11/12	0.72	0.15	396,405,410,413	0
8	NAG	J	1	14/15	0.73	0.13	209,241,271,280	0
17	NAG	S	2	14/15	0.77	0.12	263,297,316,319	0
16	BMA	P	3	11/12	0.79	0.07	347,361,374,376	0
15	NAG	N	1	14/15	0.80	0.20	226,256,267,270	0
15	NAG	N	2	14/15	0.80	0.16	265,284,302,318	0
14	MAN	M	5	11/12	-	-	298,313,330,333	0
14	MAN	M	6	11/12	-	-	295,321,330,333	0
14	MAN	M	7	11/12	-	-	213,291,312,322	0
10	NAG	H	1	14/15	0.80	0.10	231,262,279,288	0
12	NAG	K	2	14/15	0.82	0.11	249,281,312,318	0
14	NAG	M	2	14/15	0.83	0.14	211,225,242,251	0
12	NAG	K	1	14/15	0.83	0.15	210,230,261,261	0
15	MAN	N	5	11/12	-	-	327,338,356,364	0
15	MAN	N	6	11/12	-	-	327,338,353,353	0
15	MAN	N	7	11/12	-	-	311,319,334,337	0
15	MAN	N	8	11/12	-	-	277,322,345,346	0
17	NAG	S	1	14/15	0.83	0.14	214,237,276,295	0
11	NAG	I	1	14/15	0.84	0.16	209,225,246,251	0
10	NAG	U	2	14/15	0.84	0.13	252,282,319,327	0
12	BMA	T	3	11/12	0.85	0.13	250,283,301,306	0
16	NAG	P	1	14/15	0.87	0.11	216,241,264,279	0
14	NAG	M	1	14/15	0.88	0.09	211,211,226,257	0
12	NAG	T	1	14/15	0.88	0.09	241,279,310,320	0
11	BMA	I	3	11/12	0.88	0.12	326,350,366,369	0
13	NAG	L	1	14/15	0.89	0.12	212,254,276,290	0
7	BMA	O	3	11/12	0.90	0.10	281,313,324,327	0
18	MAN	V	6	11/12	0.91	0.13	213,228,240,241	0
10	NAG	U	1	14/15	0.91	0.10	215,240,255,265	0
18	MAN	V	8	11/12	0.91	0.13	213,219,260,269	0
18	MAN	V	5	11/12	0.91	0.09	220,227,239,250	0
7	NAG	O	1	14/15	0.92	0.18	211,223,264,274	0
11	MAN	I	6	11/12	0.92	0.12	374,388,396,400	0
12	NAG	T	2	14/15	0.92	0.08	291,311,327,328	0
11	MAN	I	4	11/12	0.92	0.07	372,382,403,404	0
18	MAN	V	4	11/12	0.93	0.10	230,247,262,275	0
7	NAG	O	2	14/15	0.93	0.12	269,288,312,319	0
18	NAG	V	1	14/15	0.95	0.10	213,214,228,234	0
18	BMA	V	3	11/12	0.95	0.06	213,213,228,249	0
18	NAG	V	2	14/15	0.96	0.17	213,224,238,248	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.

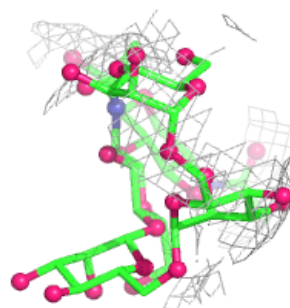
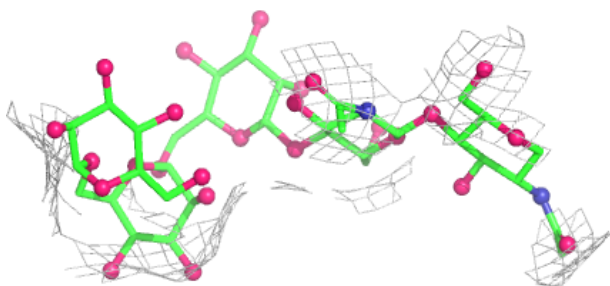
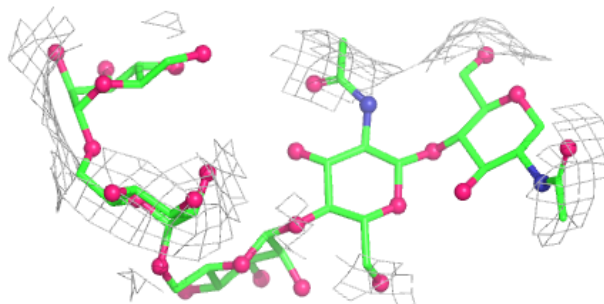


Electron density around Chain O:

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

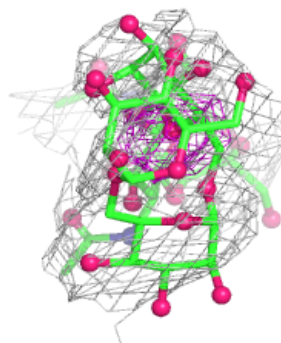
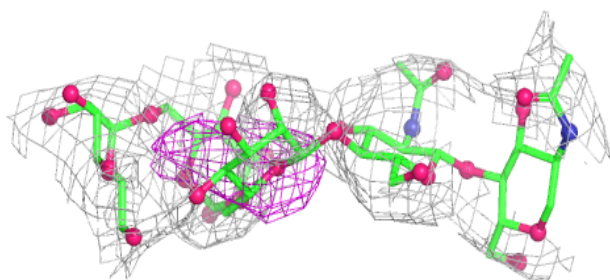
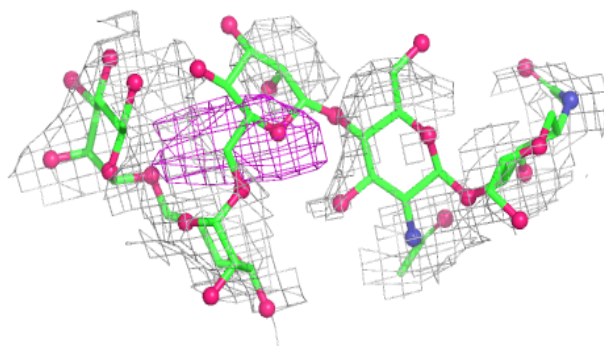
**Electron density around Chain C:**

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

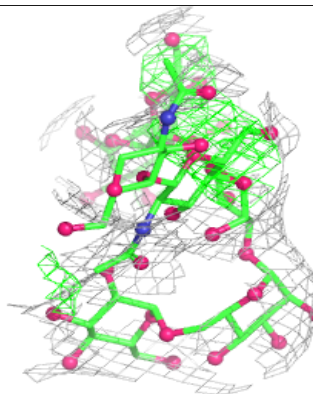
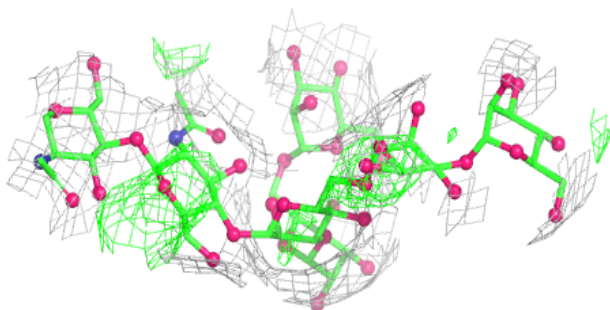
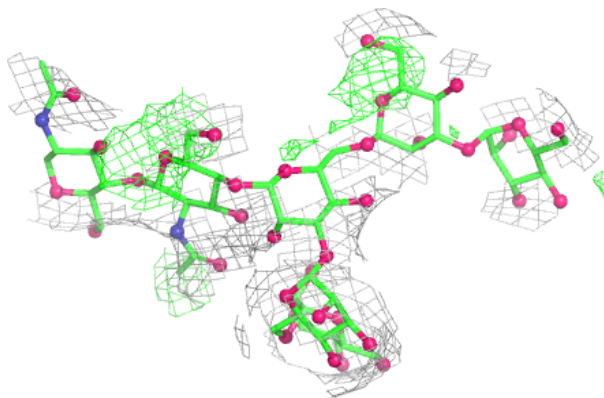


Electron density around Chain J:

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

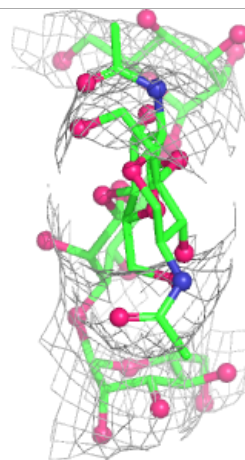
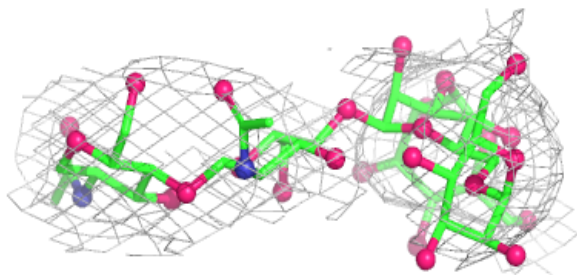
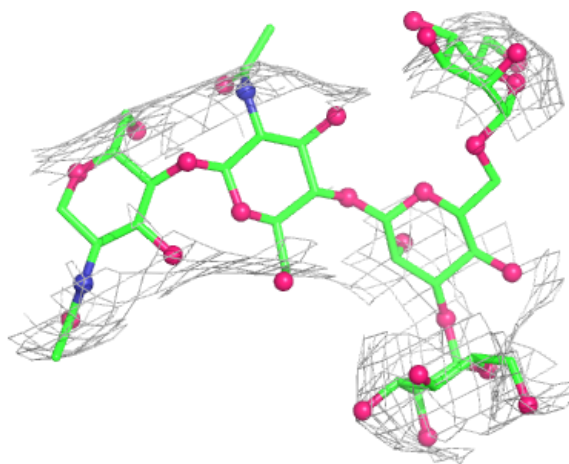
**Electron density around Chain F:**

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



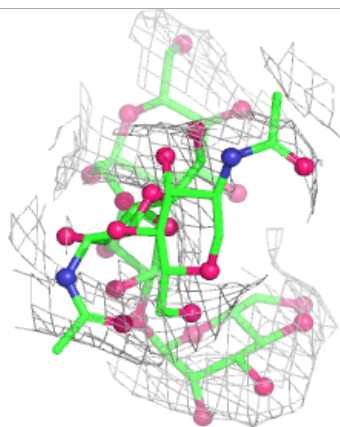
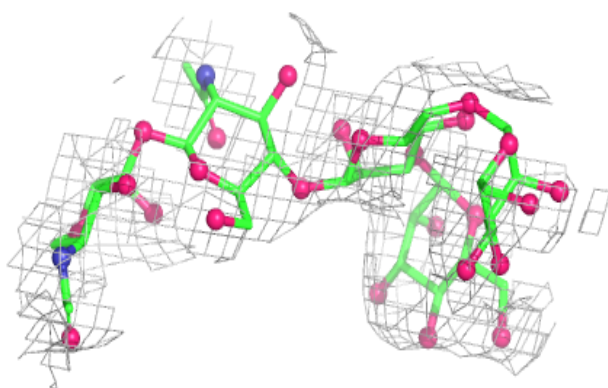
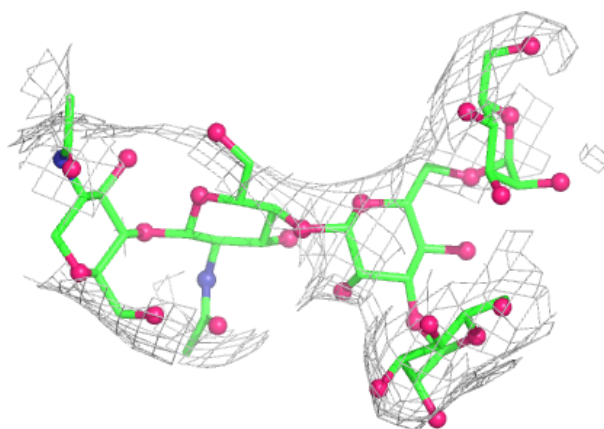
Electron density around Chain H:

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and green (positive)



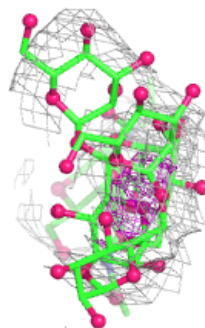
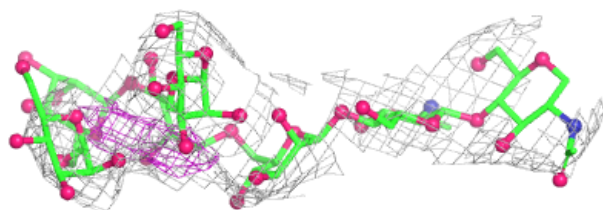
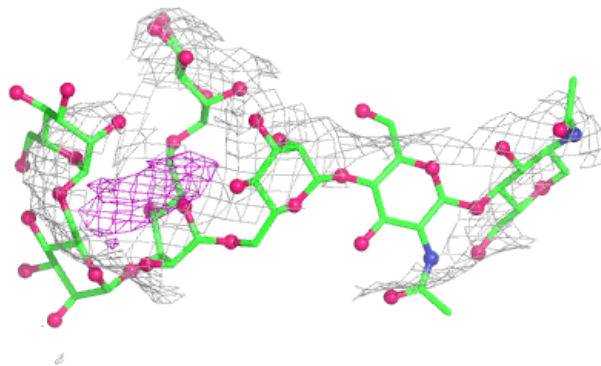
Electron density around Chain U:

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

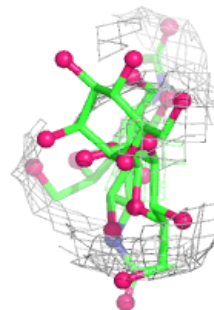
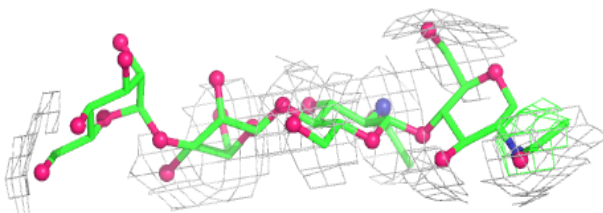
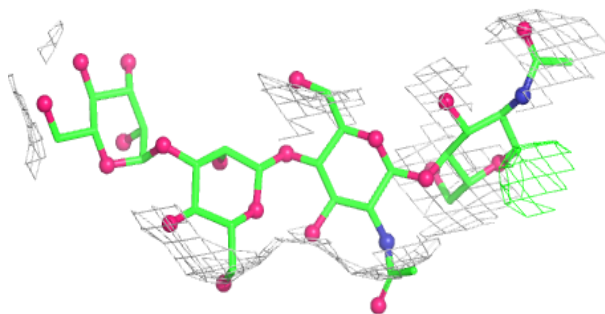


Electron density around Chain I:

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

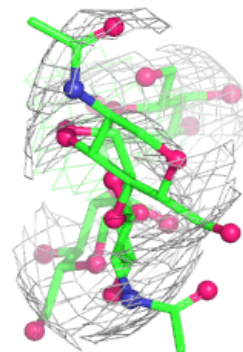
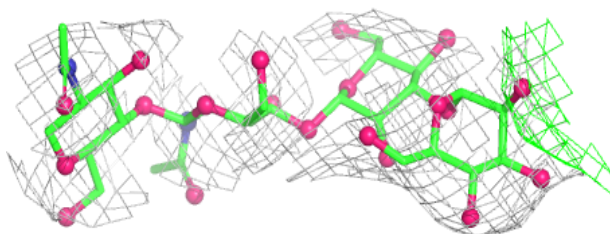
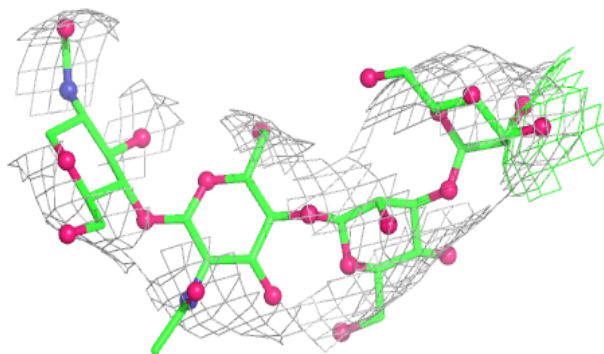
**Electron density around Chain K:**

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

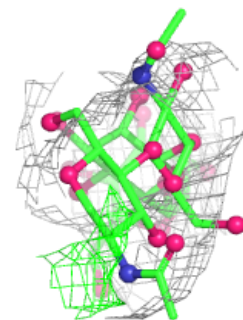
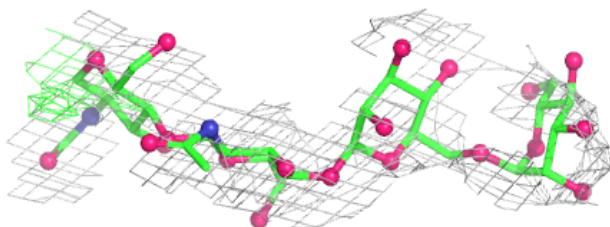
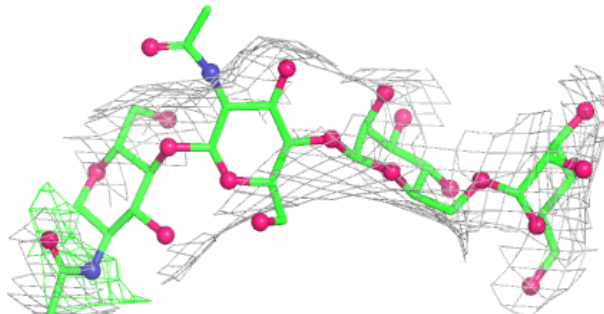


Electron density around Chain T:

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

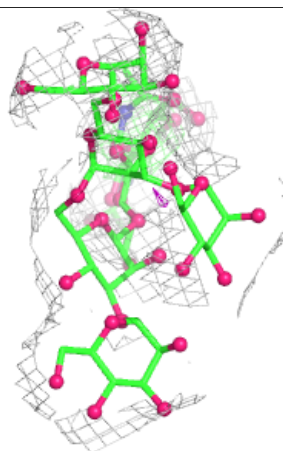
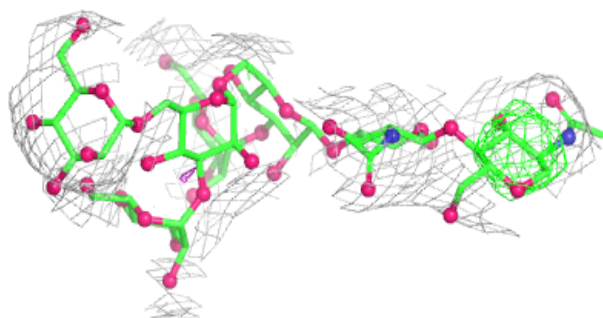
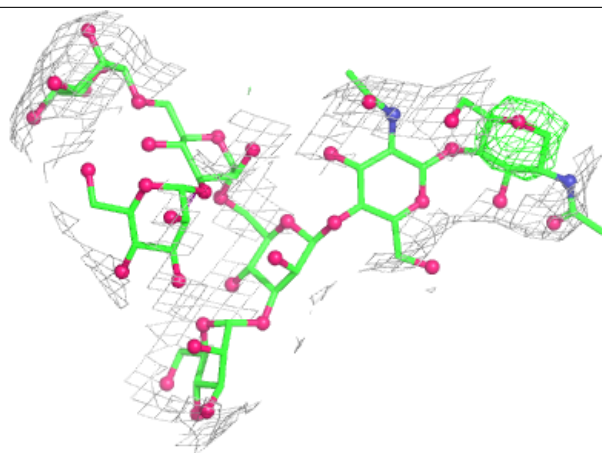
**Electron density around Chain L:**

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

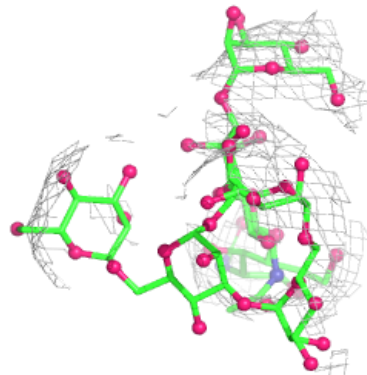
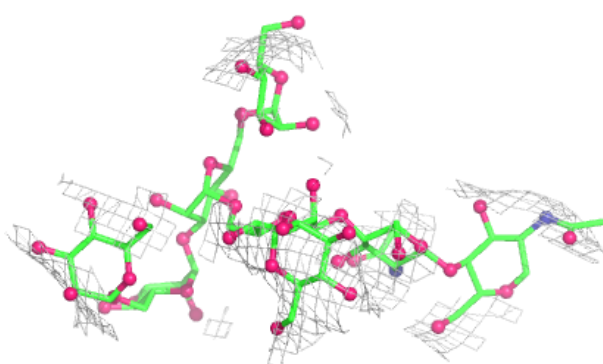
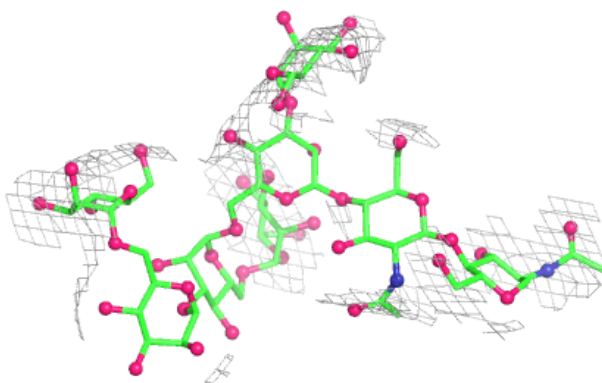


Electron density around Chain M:

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

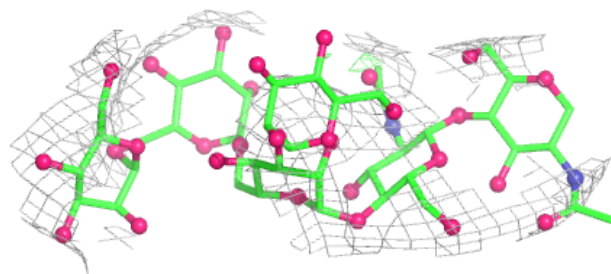
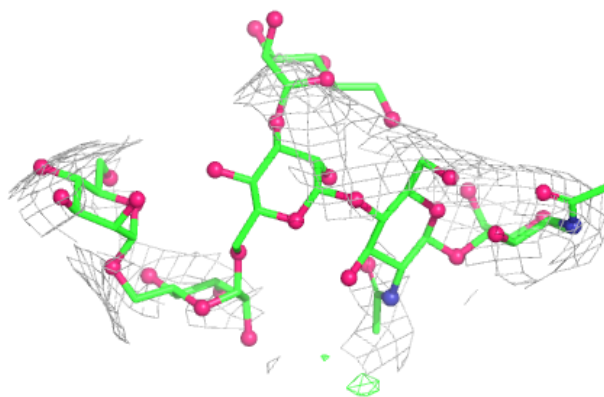
**Electron density around Chain N:**

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



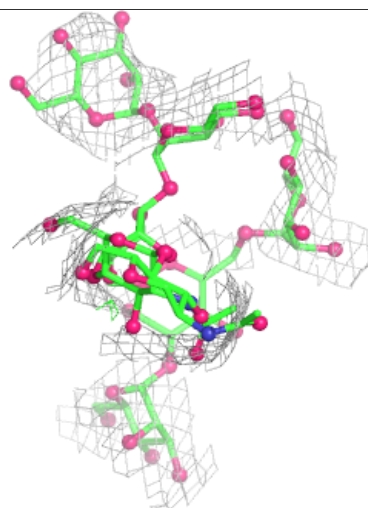
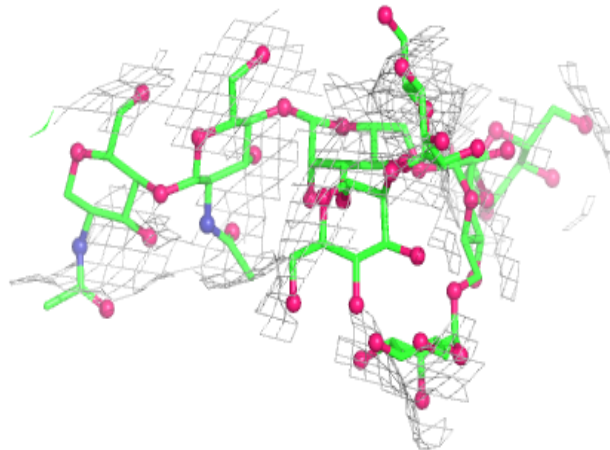
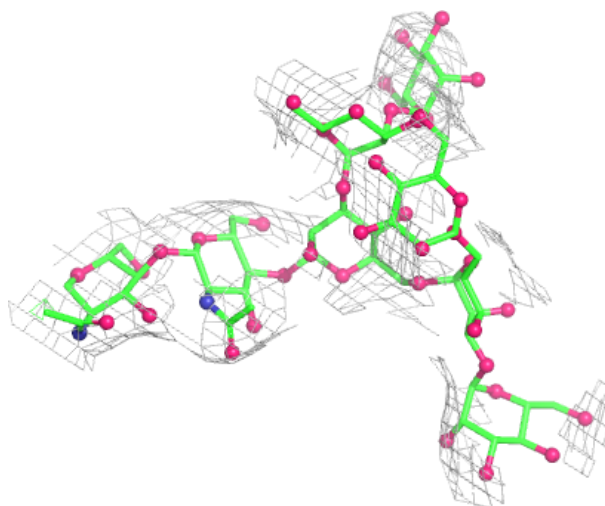
Electron density around Chain P:

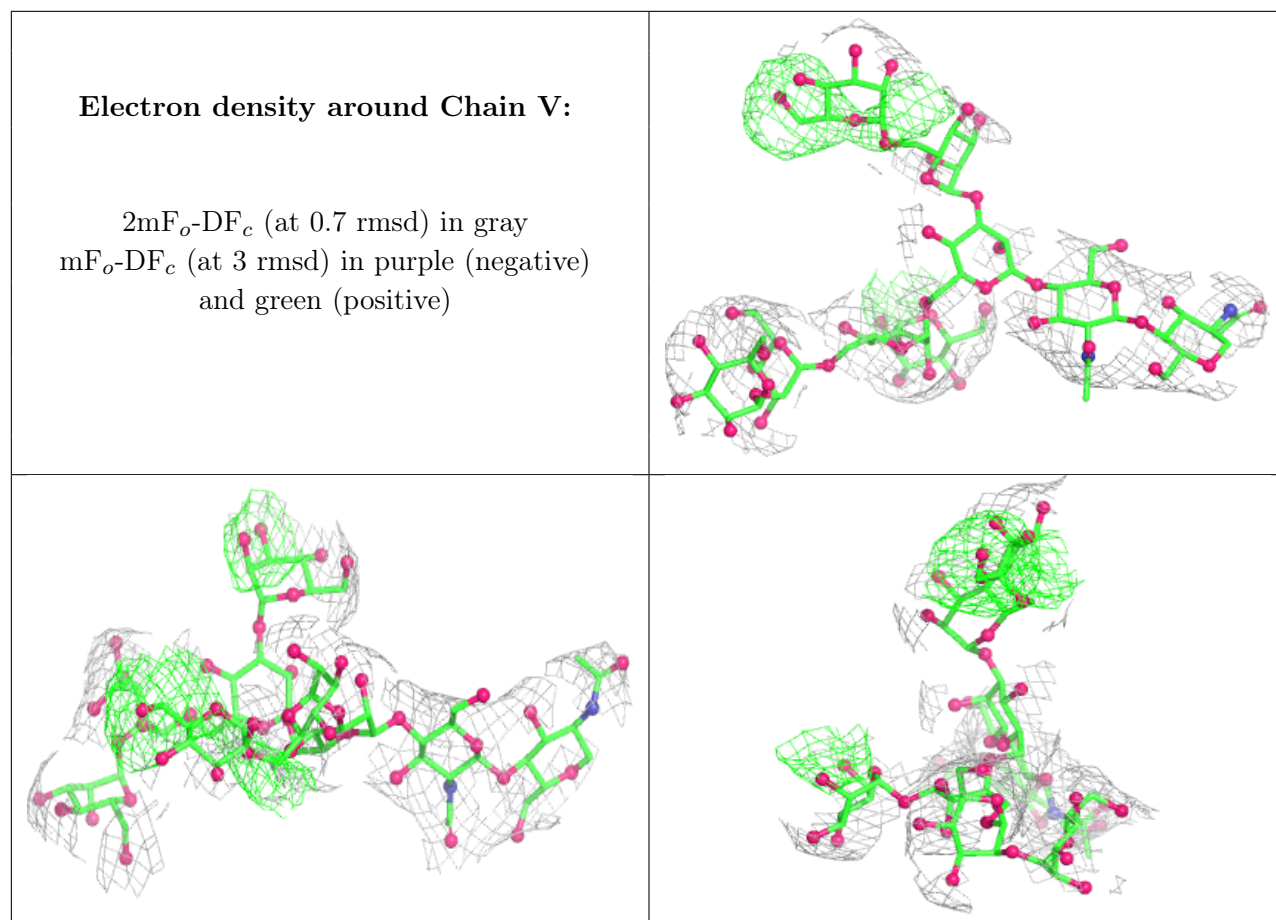
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain S:

$2mF_o-DF_c$ (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
19	NAG	B	701	14/15	0.43	0.16	243,269,290,304	0
19	NAG	G	603	14/15	0.57	0.13	287,309,323,326	0
19	NAG	G	602	14/15	0.63	0.14	213,276,292,301	0
19	NAG	G	601	14/15	0.65	0.11	248,277,292,297	0

6.5 Other polymers [i](#)

There are no such residues in this entry.