



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:29 AM UTC

PDB ID : 4WA2 / pdb_00004wa2
Title : The crystal structure of hemagglutinin from a H3N8 influenza virus isolated from New England harbor seals in complex with 3'SLN
Authors : Yang, H.; Villanueva, J.M.; Gubareva, L.V.; Stevens, J.
Deposited on : 2014-08-28
Resolution : 2.50 Å(reported)

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

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

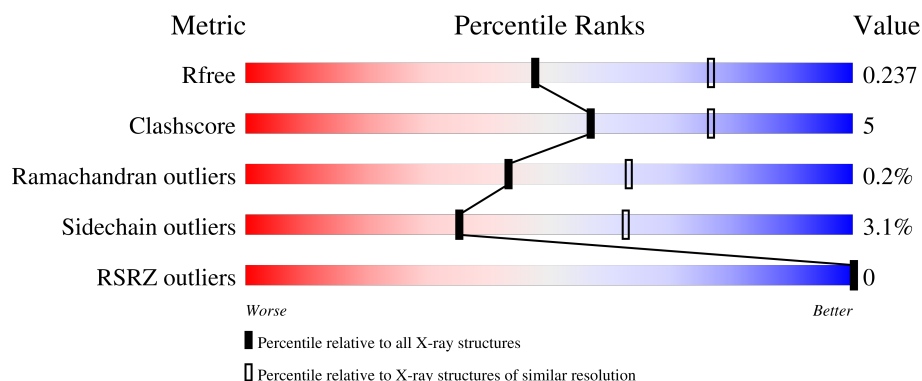
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



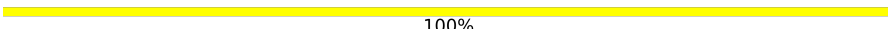
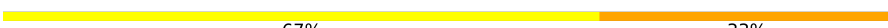
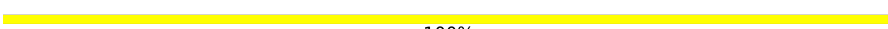
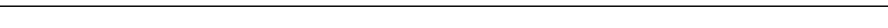
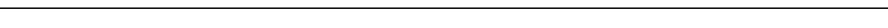
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	496	89% 10% .
1	B	496	87% 11% ..
1	C	496	86% 11% ..
1	D	496	87% 11% ..
1	E	496	85% 13% ..

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Mol	Chain	Length	Quality of chain
1	F	496	 87% 10% ..
2	G	3	 100%
2	I	3	 67% 33%
2	K	3	 67% 33%
2	P	3	 100%
3	H	2	 50% 50%
3	J	2	 50% 50%
3	L	2	 100%
3	M	2	 100%
3	O	2	 50% 50%
3	Q	2	 50% 50%
3	R	2	 100%
3	T	2	 100%
4	N	3	 100%
4	S	3	 100%

2 Entry composition [i](#)

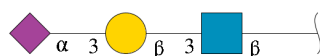
There are 6 unique types of molecules in this entry. The entry contains 24811 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	0	0
			3860	2404	683	752	21			
1	B	491	Total	C	N	O	S	0	0	0
			3860	2404	683	752	21			
1	C	491	Total	C	N	O	S	0	0	0
			3860	2404	683	752	21			
1	D	491	Total	C	N	O	S	0	0	0
			3860	2404	683	752	21			
1	E	491	Total	C	N	O	S	0	0	0
			3860	2404	683	752	21			
1	F	491	Total	C	N	O	S	0	0	0
			3860	2404	683	752	21			

- Molecule 2 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose.



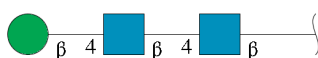
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	3	Total	C	N	O	0	0	0
			46	25	2	19			
2	I	3	Total	C	N	O	0	0	0
			46	25	2	19			
2	K	3	Total	C	N	O	0	0	0
			46	25	2	19			
2	P	3	Total	C	N	O	0	0	0
			46	25	2	19			

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



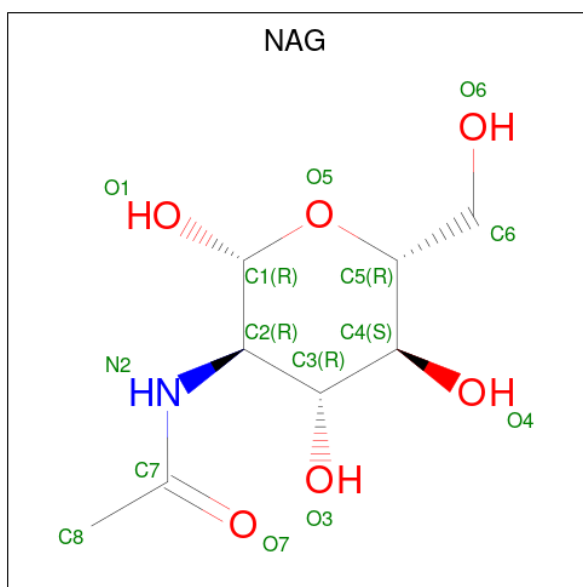
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	O	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	Q	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	R	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	T	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	188	Total	O	0	0
			188	188		
6	B	171	Total	O	0	0
			171	171		
6	C	187	Total	O	0	0
			187	187		
6	D	174	Total	O	0	0
			174	174		

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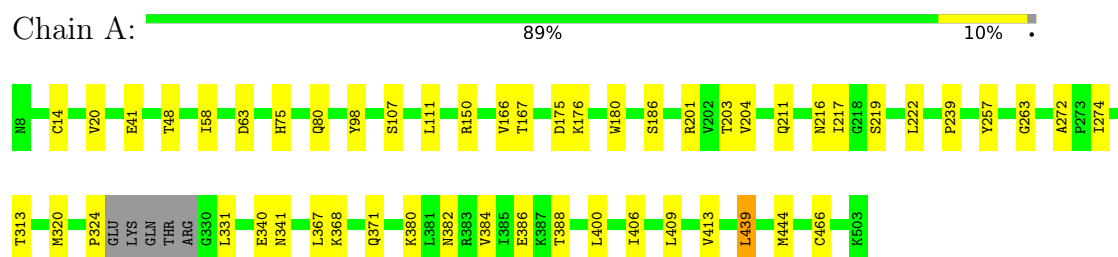
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	163	Total 163	O 163	0	0
6	F	170	Total 170	O 170	0	0

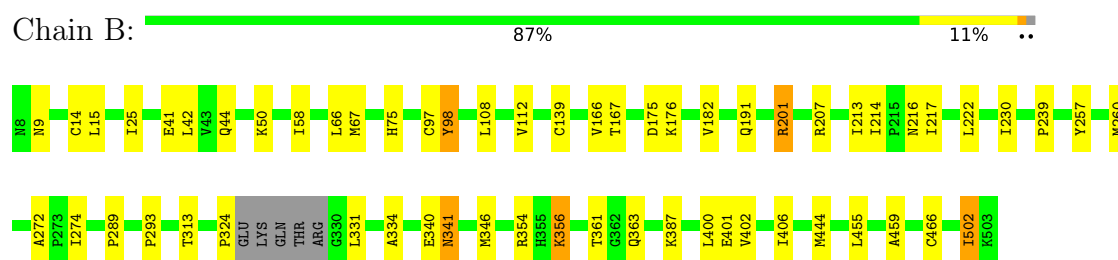
3 Residue-property plots [i](#)

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

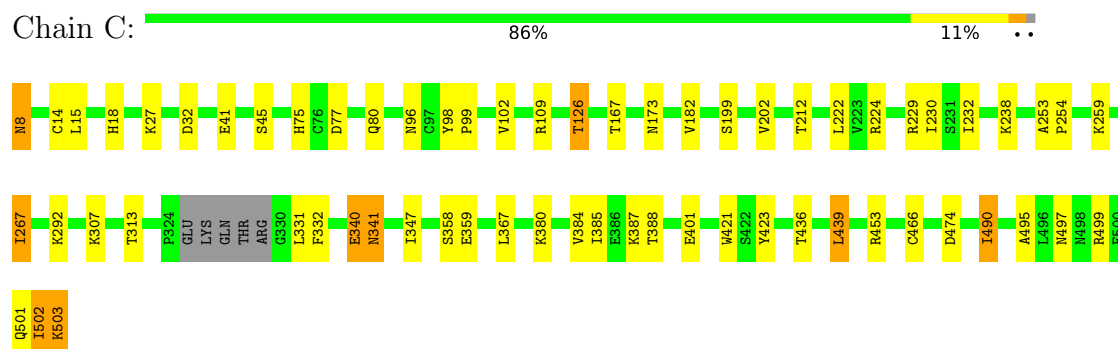
• Molecule 1: Hemagglutinin



• Molecule 1: Hemagglutinin

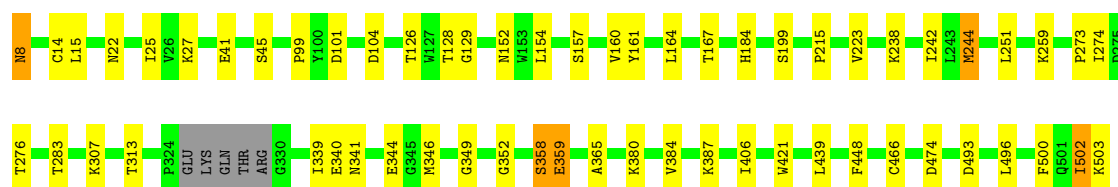


• Molecule 1: Hemagglutinin



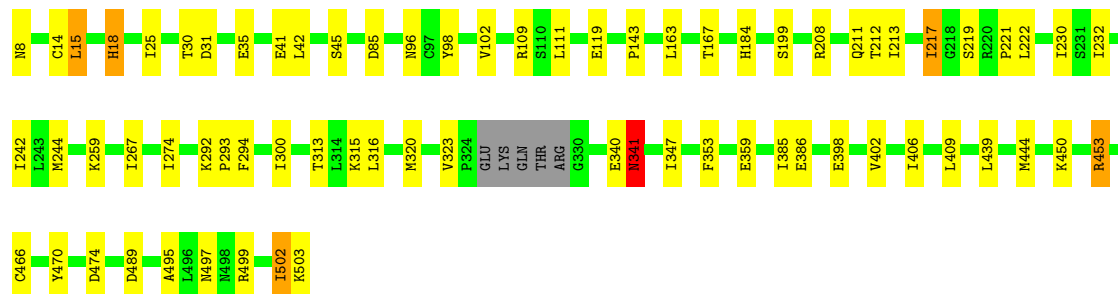
• Molecule 1: Hemagglutinin





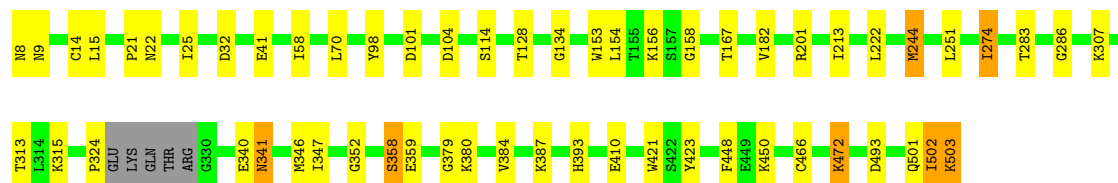
- Molecule 1: Hemagglutinin

Chain E: 85% 13% ..



- Molecule 1: Hemagglutinin

Chain F: 87% 10% ..



- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 100%



- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I: 67% 33%



- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K: 67% 33%



- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:

100%



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

Chain H:

50%

50%



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

Chain J:

50%

50%



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

Chain L:

100%



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

Chain M:

100%



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

Chain O:

50%

50%

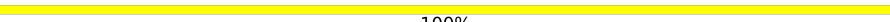


- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  50% 50%

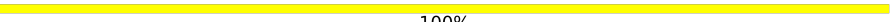
MAG1
MAG2

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

Chain R:  100%

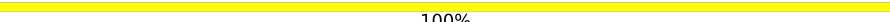
MAG1
MAG2

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

Chain T:  100%

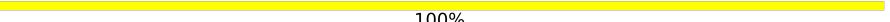
MAG1
MAG2

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

Chain N:  100%

MAG1
MAG2
EMA3

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

Chain S:  100%

MAG1
MAG2
EMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	79.54Å 102.33Å 109.67Å 90.02° 90.02° 89.51°	Depositor
Resolution (Å)	45.19 – 2.50 45.19 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.5 (45.19-2.50) 96.4 (45.19-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.184 , 0.236 0.187 , 0.237	Depositor DCC
R_{free} test set	5793 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	35.1	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 9.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.011 for h,-k,-l 0.011 for -h,k,-l 0.457 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	24811	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.63% 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, GAL, BMA, SIA

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	0.98	0/3937	1.02	6/5333 (0.1%)
1	B	1.00	1/3937 (0.0%)	1.03	6/5333 (0.1%)
1	C	0.99	0/3937	1.02	3/5333 (0.1%)
1	D	0.99	4/3937 (0.1%)	1.05	10/5333 (0.2%)
1	E	0.99	1/3937 (0.0%)	1.03	7/5333 (0.1%)
1	F	1.00	0/3937	1.03	8/5333 (0.2%)
All	All	0.99	6/23622 (0.0%)	1.03	40/31998 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
All	All	0	6

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	152	ASN	N-CA	-5.92	1.39	1.46
1	D	273	PRO	C-O	-5.30	1.17	1.23
1	B	334	ALA	C-O	5.29	1.28	1.23
1	E	453	ARG	C-O	-5.18	1.17	1.24
1	D	244	MET	CA-C	-5.17	1.46	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	341	ASN	N-CA-CB	-8.19	96.65	110.49
1	D	341	ASN	N-CA-CB	-7.59	97.66	110.49
1	A	341	ASN	N-CA-CB	-7.50	97.81	110.49
1	D	25	ILE	CB-CA-C	-7.49	101.63	110.91
1	A	272	ALA	CA-C-N	-7.21	112.89	120.03

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	340	GLU	Peptide
1	B	340	GLU	Peptide
1	C	340	GLU	Peptide
1	D	340	GLU	Peptide
1	E	340	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3860	0	3739	37	0
1	B	3860	0	3739	36	0
1	C	3860	0	3739	47	0
1	D	3860	0	3739	35	0
1	E	3860	0	3739	45	0
1	F	3860	0	3739	39	0
2	G	46	0	40	0	0
2	I	46	0	40	1	0
2	K	46	0	40	1	0
2	P	46	0	40	0	0
3	H	28	0	25	1	0
3	J	28	0	25	1	0
3	L	28	0	25	0	0
3	M	28	0	25	0	0
3	O	28	0	25	1	0
3	Q	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	R	28	0	25	0	0
3	T	28	0	25	0	0
4	N	39	0	34	0	0
4	S	39	0	34	0	0
5	A	28	0	26	0	0
5	B	28	0	26	0	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
5	E	14	0	13	1	0
5	F	14	0	13	0	0
6	A	188	0	0	12	0
6	B	171	0	0	7	0
6	C	187	0	0	14	0
6	D	174	0	0	9	0
6	E	163	0	0	11	0
6	F	170	0	0	7	0
All	All	24811	0	22966	216	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 5.

The worst 5 of 216 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:ILE:HG22	6:B:1260:HOH:O	1.58	1.02
1:D:22:ASN:HB3	6:D:712:HOH:O	1.68	0.93
1:A:48:THR:HA	6:A:1120:HOH:O	1.79	0.83
1:A:75:HIS:CB	6:A:1228:HOH:O	2.27	0.82
1:F:22:ASN:HA	6:F:870:HOH:O	1.82	0.80

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	487/496 (98%)	469 (96%)	17 (4%)	1 (0%)	43	63
1	B	487/496 (98%)	468 (96%)	18 (4%)	1 (0%)	43	63
1	C	487/496 (98%)	469 (96%)	16 (3%)	2 (0%)	30	49
1	D	487/496 (98%)	464 (95%)	23 (5%)	0	100	100
1	E	487/496 (98%)	470 (96%)	16 (3%)	1 (0%)	43	63
1	F	487/496 (98%)	466 (96%)	19 (4%)	2 (0%)	30	49
All	All	2922/2976 (98%)	2806 (96%)	109 (4%)	7 (0%)	43	63

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	ARG
1	F	341	ASN
1	F	501	GLN
1	B	201	ARG
1	C	224	ARG

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	427/432 (99%)	420 (98%)	7 (2%)	55	79
1	B	427/432 (99%)	417 (98%)	10 (2%)	44	72
1	C	427/432 (99%)	411 (96%)	16 (4%)	30	57
1	D	427/432 (99%)	413 (97%)	14 (3%)	33	61
1	E	427/432 (99%)	410 (96%)	17 (4%)	28	54
1	F	427/432 (99%)	412 (96%)	15 (4%)	32	58
All	All	2562/2592 (99%)	2483 (97%)	79 (3%)	35	62

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	315	LYS
1	F	244	MET
1	E	385	ILE
1	F	32	ASP
1	F	387	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	18	HIS
1	F	44	GLN
1	C	341	ASN
1	F	497	ASN
1	E	296	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

36 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	S	1	4,1	14,14,15	0.88	0	17,19,21	1.43	4 (23%)
3	NAG	Q	2	3	14,14,15	0.75	0	17,19,21	1.64	6 (35%)
4	NAG	S	2	4	14,14,15	0.61	0	17,19,21	1.78	6 (35%)
3	NAG	M	2	3	14,14,15	0.57	0	17,19,21	2.79	5 (29%)
5	NAG	A	1007	1	14,14,15	1.00	1 (7%)	17,19,21	1.66	4 (23%)
5	NAG	A	1004	1	14,14,15	0.96	1 (7%)	17,19,21	2.68	6 (35%)
5	NAG	E	1008	1	14,14,15	0.86	0	17,19,21	1.98	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	D	606	1	14,14,15	1.13	1 (7%)	17,19,21	1.87	5 (29%)
5	NAG	F	606	1	14,14,15	1.12	1 (7%)	17,19,21	1.62	3 (17%)
3	NAG	T	2	3	14,14,15	0.84	1 (7%)	17,19,21	1.91	3 (17%)
3	NAG	O	1	3,1	14,14,15	0.78	0	17,19,21	1.59	3 (17%)
3	NAG	H	1	3,1	14,14,15	0.85	0	17,19,21	2.13	3 (17%)
3	NAG	O	2	3	14,14,15	0.86	1 (7%)	17,19,21	2.20	6 (35%)
2	NAG	K	1	2	15,15,15	0.60	0	21,21,21	2.22	6 (28%)
3	NAG	L	1	3,1	14,14,15	1.04	1 (7%)	17,19,21	1.70	6 (35%)
3	NAG	L	2	3	14,14,15	0.64	0	17,19,21	1.17	2 (11%)
4	NAG	N	1	4,1	14,14,15	1.10	2 (14%)	17,19,21	1.37	2 (11%)
3	NAG	R	2	3	14,14,15	0.63	0	17,19,21	1.57	2 (11%)
4	NAG	N	2	4	14,14,15	0.54	0	17,19,21	1.60	3 (17%)
2	GAL	G	2	2	11,11,12	0.76	0	15,15,17	1.81	4 (26%)
2	GAL	P	2	2	11,11,12	0.79	0	15,15,17	2.00	4 (26%)
2	NAG	I	1	2	15,15,15	0.72	0	21,21,21	2.17	7 (33%)
2	NAG	P	1	2	15,15,15	0.45	0	21,21,21	1.96	6 (28%)
2	GAL	I	2	2	11,11,12	0.88	0	15,15,17	2.06	6 (40%)
5	NAG	C	1008	1	14,14,15	0.87	1 (7%)	17,19,21	2.35	5 (29%)
5	NAG	B	1004	1	14,14,15	0.74	0	17,19,21	2.26	5 (29%)
3	NAG	T	1	3,1	14,14,15	1.09	2 (14%)	17,19,21	1.78	3 (17%)
3	NAG	H	2	3	14,14,15	0.54	0	17,19,21	1.64	3 (17%)
3	NAG	R	1	3,1	14,14,15	0.85	1 (7%)	17,19,21	1.00	0
3	NAG	J	1	3,1	14,14,15	0.71	0	17,19,21	1.97	5 (29%)
3	NAG	J	2	3	14,14,15	0.54	0	17,19,21	2.65	8 (47%)
2	GAL	K	2	2	11,11,12	0.96	0	15,15,17	2.04	5 (33%)
5	NAG	B	1007	1	14,14,15	1.03	1 (7%)	17,19,21	1.56	3 (17%)
2	NAG	G	1	2	15,15,15	0.75	0	21,21,21	3.03	9 (42%)
3	NAG	M	1	3,1	14,14,15	1.18	1 (7%)	17,19,21	2.28	7 (41%)
3	NAG	Q	1	3,1	14,14,15	0.47	0	17,19,21	1.49	3 (17%)

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
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	0/6/23/26	0/1/1/1
5	NAG	A	1007	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1004	1	-	0/6/23/26	0/1/1/1
5	NAG	E	1008	1	-	1/6/23/26	0/1/1/1
5	NAG	D	606	1	-	2/6/23/26	0/1/1/1
5	NAG	F	606	1	-	2/6/23/26	0/1/1/1
3	NAG	T	2	3	-	0/6/23/26	0/1/1/1
3	NAG	O	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	O	2	3	-	2/6/23/26	0/1/1/1
2	NAG	K	1	2	-	0/6/26/26	0/1/1/1
3	NAG	L	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
3	NAG	R	2	3	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
2	GAL	G	2	2	-	2/2/19/22	0/1/1/1
2	GAL	P	2	2	-	0/2/19/22	0/1/1/1
2	NAG	I	1	2	-	0/6/26/26	0/1/1/1
2	NAG	P	1	2	-	2/6/26/26	0/1/1/1
2	GAL	I	2	2	-	2/2/19/22	0/1/1/1
5	NAG	C	1008	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1004	1	-	0/6/23/26	0/1/1/1
3	NAG	T	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	NAG	R	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	J	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
2	GAL	K	2	2	-	0/2/19/22	0/1/1/1
5	NAG	B	1007	1	-	2/6/23/26	0/1/1/1
2	NAG	G	1	2	-	2/6/26/26	0/1/1/1
3	NAG	M	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	Q	1	3,1	-	0/6/23/26	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	606	NAG	C1-C2	3.13	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	606	NAG	C1-C2	3.02	1.56	1.52
3	M	1	NAG	O5-C1	-2.97	1.38	1.43
4	N	1	NAG	O5-C1	-2.89	1.38	1.43
5	B	1007	NAG	C1-C2	2.68	1.56	1.52

The worst 5 of 163 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	2	NAG	O5-C1-C2	-9.26	96.96	111.29
2	G	1	NAG	C1-C2-C3	-8.22	99.33	110.54
5	A	1004	NAG	C1-O5-C5	7.60	122.38	112.19
5	B	1004	NAG	C1-O5-C5	6.97	121.53	112.19
5	C	1008	NAG	C1-O5-C5	6.56	120.98	112.19

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	1	NAG	C1-C2-N2-C7
5	F	606	NAG	O5-C5-C6-O6
5	D	606	NAG	O5-C5-C6-O6
2	I	2	GAL	O5-C5-C6-O6
2	I	2	GAL	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Q	2	NAG	1	0
5	E	1008	NAG	1	0
3	H	1	NAG	1	0
3	O	2	NAG	1	0
2	I	1	NAG	1	0
3	J	1	NAG	1	0

5.5 Carbohydrates

34 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	G	1	2	15,15,15	0.75	0	21,21,21	3.03	9 (42%)
2	GAL	G	2	2	11,11,12	0.76	0	15,15,17	1.81	4 (26%)
2	SIA	G	3	2	20,20,21	1.19	2 (10%)	21,28,31	1.38	4 (19%)
3	NAG	H	1	3,1	14,14,15	0.85	0	17,19,21	2.13	3 (17%)
3	NAG	H	2	3	14,14,15	0.54	0	17,19,21	1.64	3 (17%)
2	NAG	I	1	2	15,15,15	0.72	0	21,21,21	2.17	7 (33%)
2	GAL	I	2	2	11,11,12	0.88	0	15,15,17	2.06	6 (40%)
2	SIA	I	3	2	20,20,21	1.06	2 (10%)	21,28,31	1.58	4 (19%)
3	NAG	J	1	3,1	14,14,15	0.71	0	17,19,21	1.97	5 (29%)
3	NAG	J	2	3	14,14,15	0.54	0	17,19,21	2.65	8 (47%)
2	NAG	K	1	2	15,15,15	0.60	0	21,21,21	2.22	6 (28%)
2	GAL	K	2	2	11,11,12	0.96	0	15,15,17	2.04	5 (33%)
2	SIA	K	3	2	20,20,21	0.83	1 (5%)	21,28,31	1.49	3 (14%)
3	NAG	L	1	3,1	14,14,15	1.04	1 (7%)	17,19,21	1.70	6 (35%)
3	NAG	L	2	3	14,14,15	0.64	0	17,19,21	1.17	2 (11%)
3	NAG	M	1	3,1	14,14,15	1.18	1 (7%)	17,19,21	2.28	7 (41%)
3	NAG	M	2	3	14,14,15	0.57	0	17,19,21	2.79	5 (29%)
4	NAG	N	1	4,1	14,14,15	1.10	2 (14%)	17,19,21	1.37	2 (11%)
4	NAG	N	2	4	14,14,15	0.54	0	17,19,21	1.60	3 (17%)
4	BMA	N	3	4	11,11,12	0.74	0	15,15,17	2.56	5 (33%)
3	NAG	O	1	3,1	14,14,15	0.78	0	17,19,21	1.59	3 (17%)
3	NAG	O	2	3	14,14,15	0.86	1 (7%)	17,19,21	2.20	6 (35%)
2	NAG	P	1	2	15,15,15	0.45	0	21,21,21	1.96	6 (28%)
2	GAL	P	2	2	11,11,12	0.79	0	15,15,17	2.00	4 (26%)
2	SIA	P	3	2	20,20,21	1.16	1 (5%)	21,28,31	1.70	3 (14%)
3	NAG	Q	1	3,1	14,14,15	0.47	0	17,19,21	1.49	3 (17%)
3	NAG	Q	2	3	14,14,15	0.75	0	17,19,21	1.64	6 (35%)
3	NAG	R	1	3,1	14,14,15	0.85	1 (7%)	17,19,21	1.00	0
3	NAG	R	2	3	14,14,15	0.63	0	17,19,21	1.57	2 (11%)
4	NAG	S	1	4,1	14,14,15	0.88	0	17,19,21	1.43	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	S	2	4	14,14,15	0.61	0	17,19,21	1.78	6 (35%)
4	BMA	S	3	4	11,11,12	0.88	0	15,15,17	2.37	5 (33%)
3	NAG	T	1	3,1	14,14,15	1.09	2 (14%)	17,19,21	1.78	3 (17%)
3	NAG	T	2	3	14,14,15	0.84	1 (7%)	17,19,21	1.91	3 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	G	1	2	-	2/6/26/26	0/1/1/1
2	GAL	G	2	2	-	2/2/19/22	0/1/1/1
2	SIA	G	3	2	-	0/18/34/38	0/1/1/1
3	NAG	H	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
2	NAG	I	1	2	-	0/6/26/26	0/1/1/1
2	GAL	I	2	2	-	2/2/19/22	0/1/1/1
2	SIA	I	3	2	-	0/18/34/38	0/1/1/1
3	NAG	J	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
2	NAG	K	1	2	-	0/6/26/26	0/1/1/1
2	GAL	K	2	2	-	0/2/19/22	0/1/1/1
2	SIA	K	3	2	-	0/18/34/38	0/1/1/1
3	NAG	L	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
3	NAG	M	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	0/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	BMA	N	3	4	-	2/2/19/22	0/1/1/1
3	NAG	O	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	2/6/23/26	0/1/1/1
2	NAG	P	1	2	-	2/6/26/26	0/1/1/1
2	GAL	P	2	2	-	0/2/19/22	0/1/1/1
2	SIA	P	3	2	-	0/18/34/38	0/1/1/1
3	NAG	Q	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	0/6/23/26	0/1/1/1
3	NAG	R	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	R	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	0/6/23/26	0/1/1/1
4	BMA	S	3	4	-	1/2/19/22	0/1/1/1
3	NAG	T	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	T	2	3	-	0/6/23/26	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	1	NAG	O5-C1	-2.97	1.38	1.43
4	N	1	NAG	O5-C1	-2.89	1.38	1.43
2	G	3	SIA	C4-C5	-2.88	1.50	1.53
2	P	3	SIA	C3-C2	2.79	1.56	1.52
2	G	3	SIA	C7-C6	2.73	1.56	1.52

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	2	NAG	O5-C1-C2	-9.26	96.96	111.29
2	G	1	NAG	C1-C2-C3	-8.22	99.33	110.54
4	N	3	BMA	C1-O5-C5	8.14	123.09	112.19
3	J	2	NAG	C1-O5-C5	-6.18	103.90	112.19
3	H	1	NAG	C1-C2-N2	6.12	120.08	110.43

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	1	NAG	C1-C2-N2-C7
2	I	2	GAL	O5-C5-C6-O6
2	I	2	GAL	C4-C5-C6-O6
2	P	1	NAG	O5-C5-C6-O6
2	G	2	GAL	O5-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 6 short contacts:

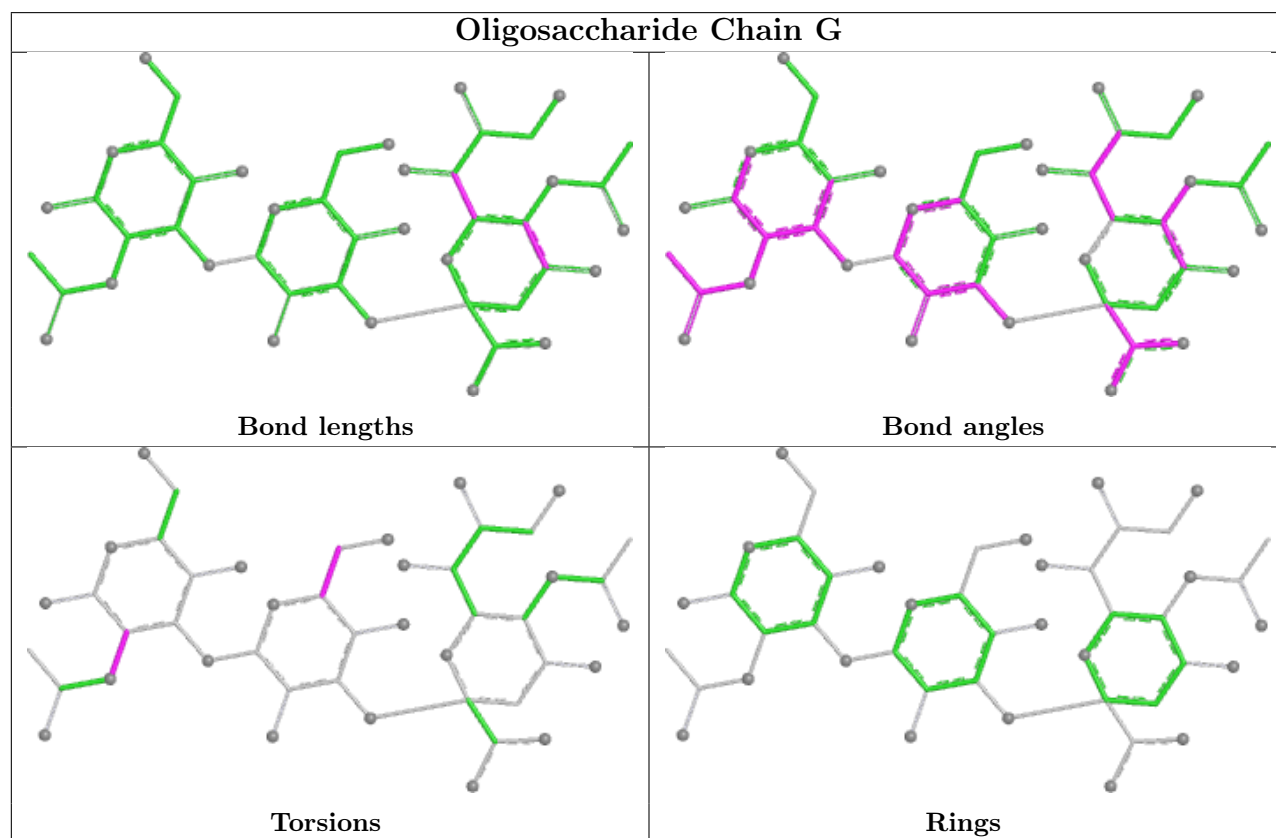
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Q	2	NAG	1	0
3	H	1	NAG	1	0
3	O	2	NAG	1	0

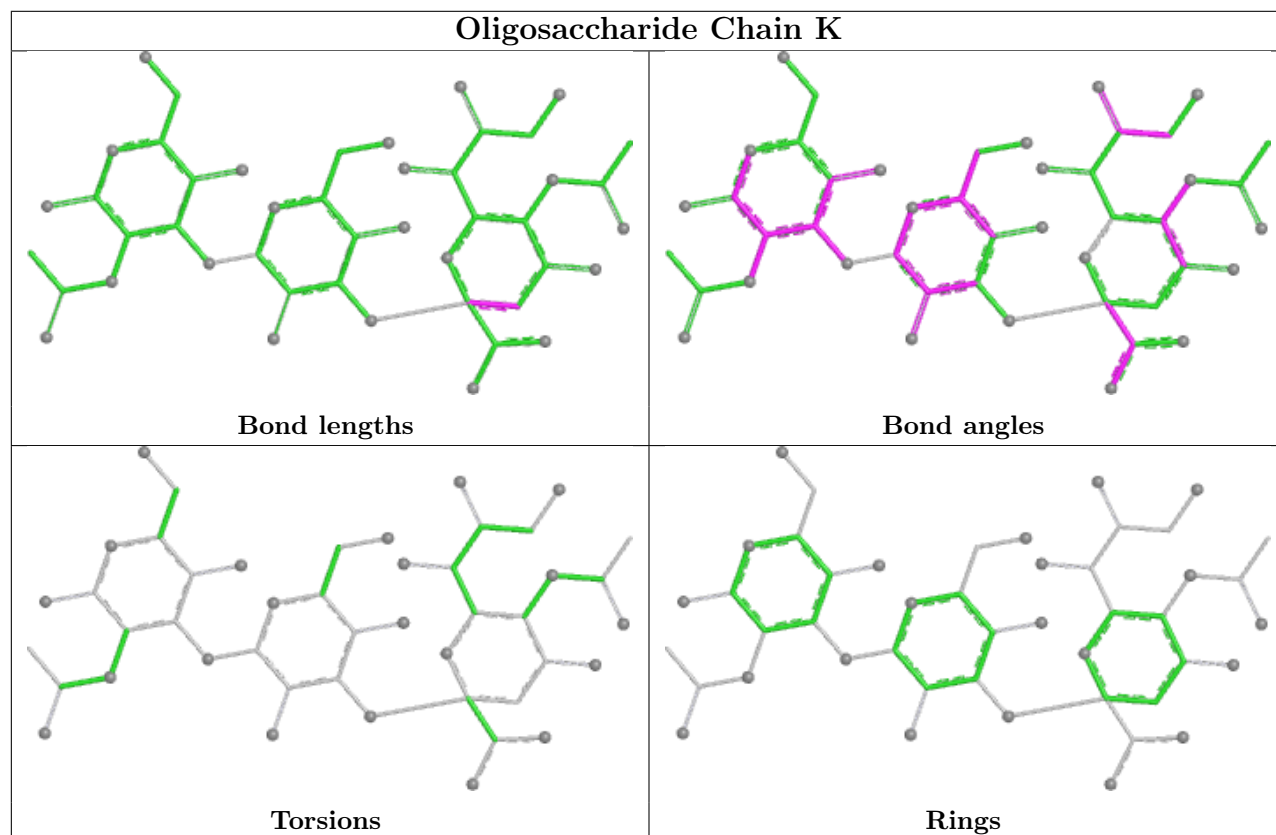
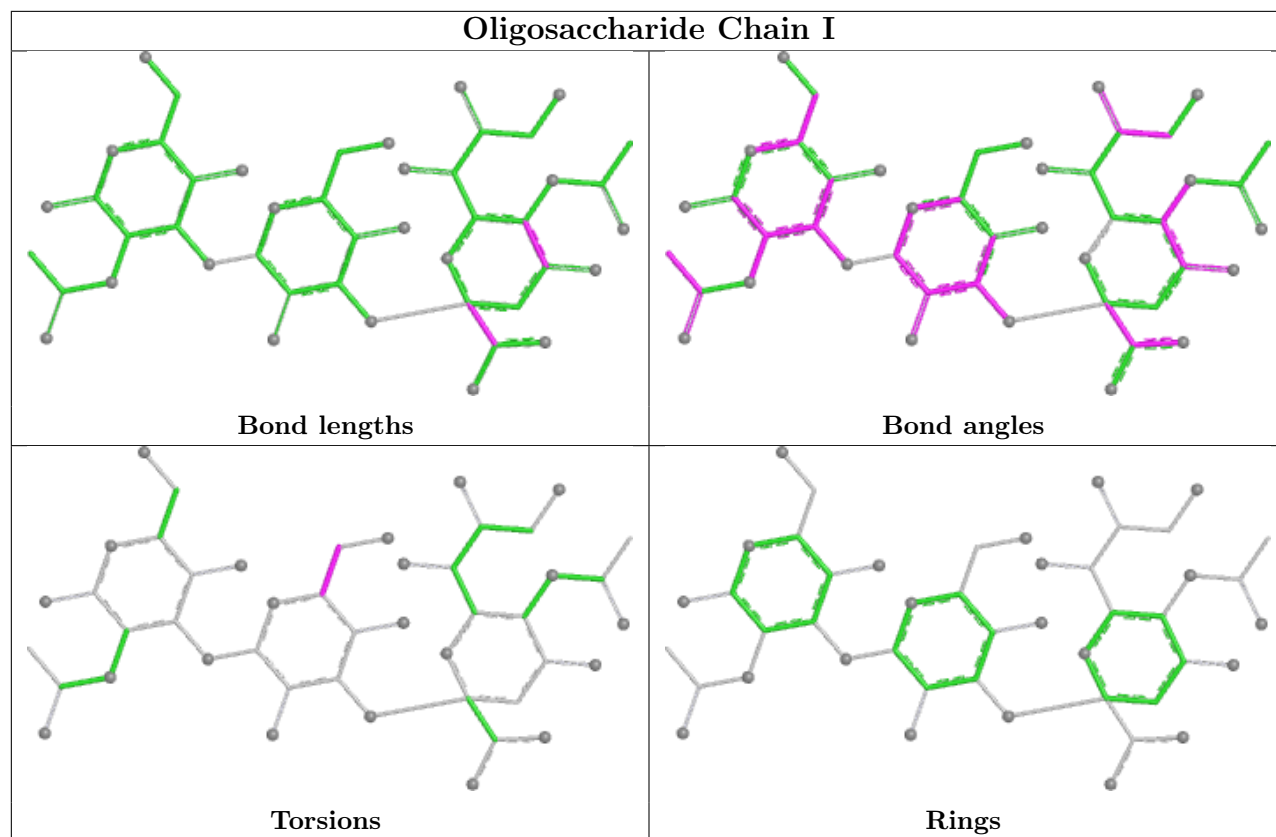
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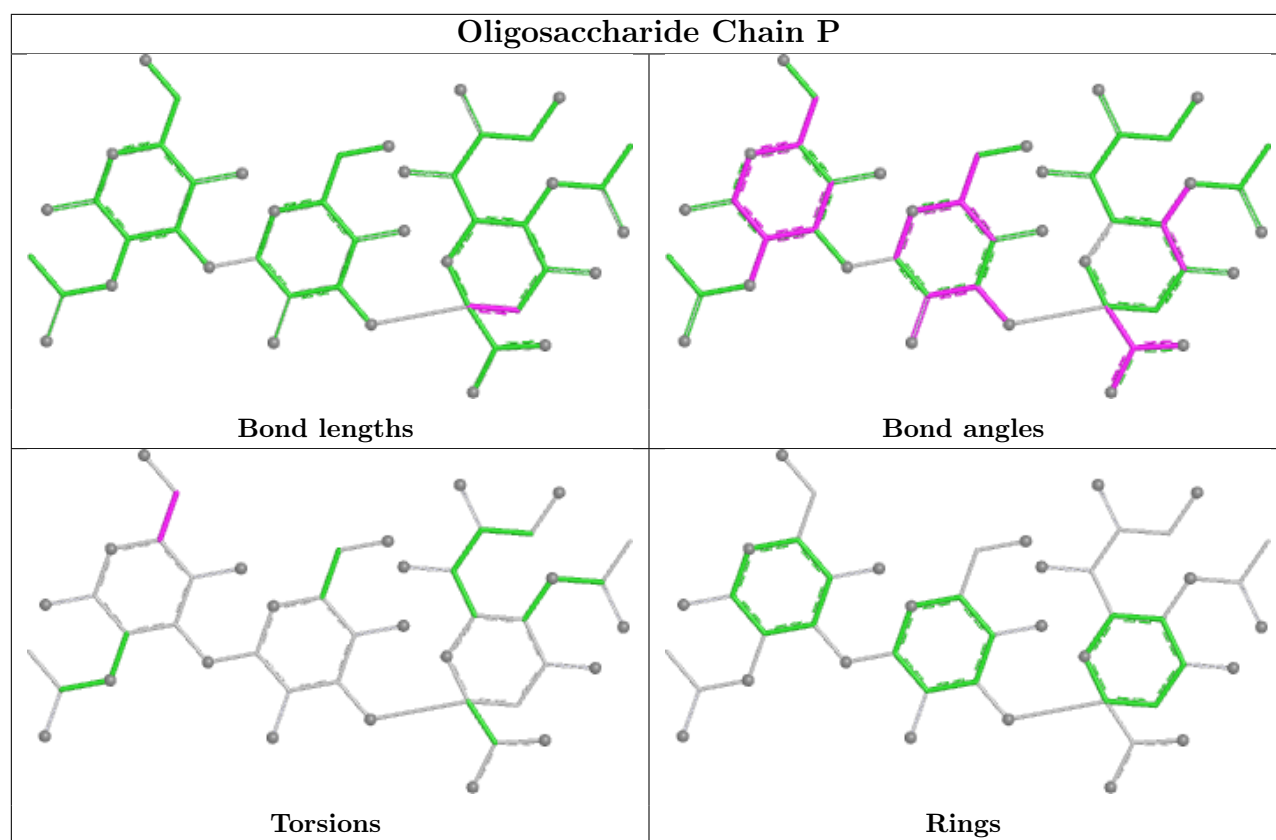
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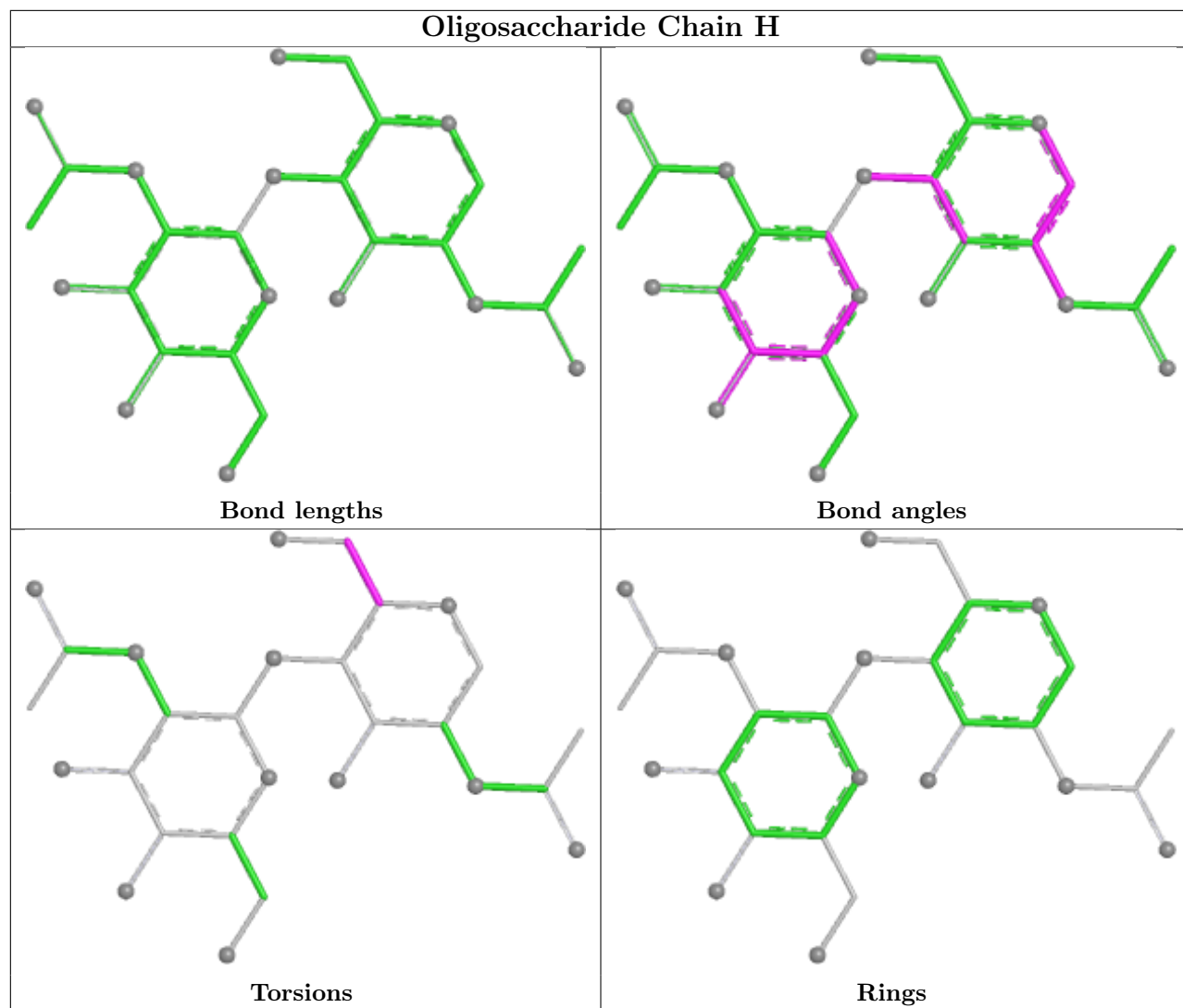
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	1	NAG	1	0
2	K	3	SIA	1	0
3	J	1	NAG	1	0

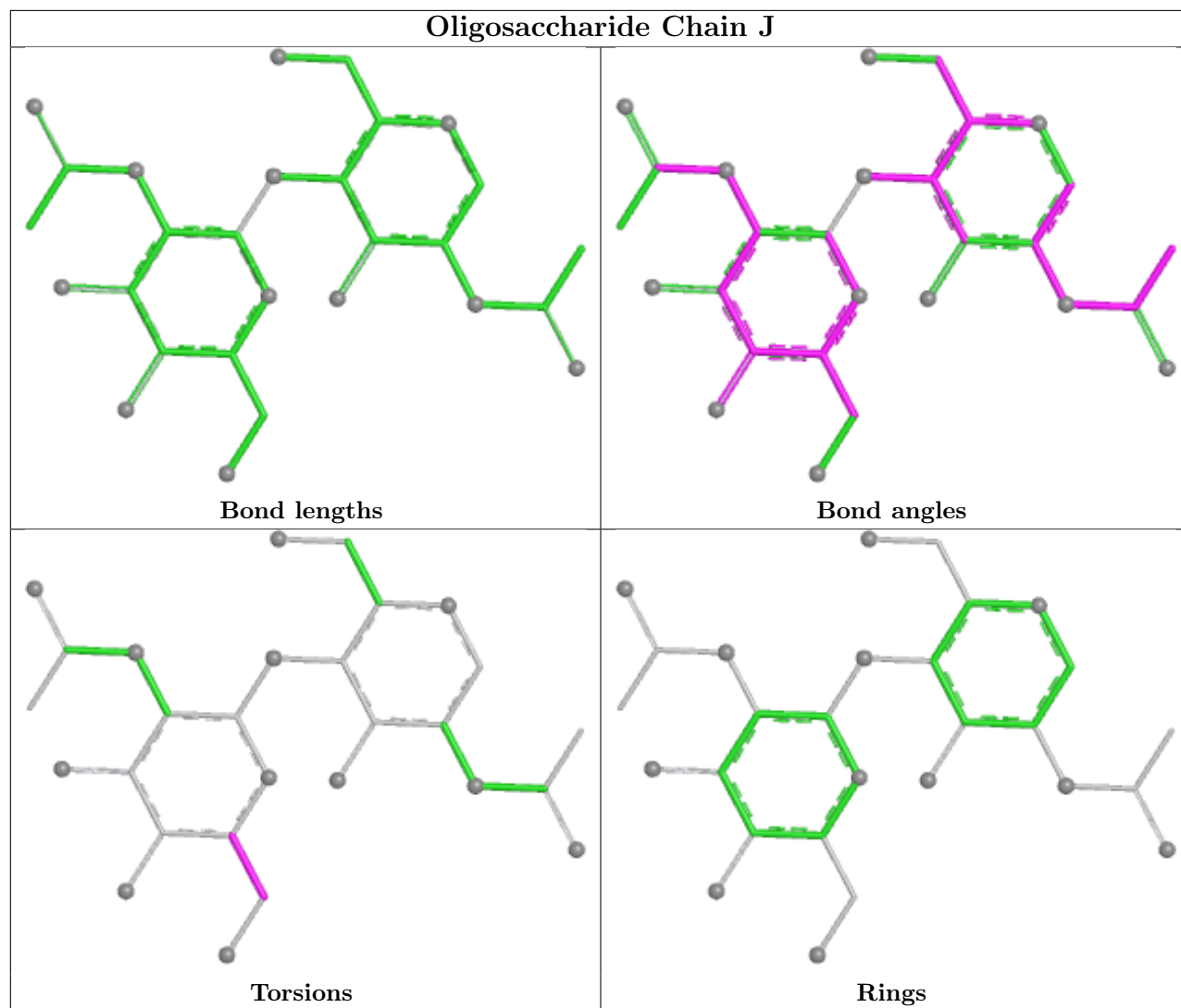
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

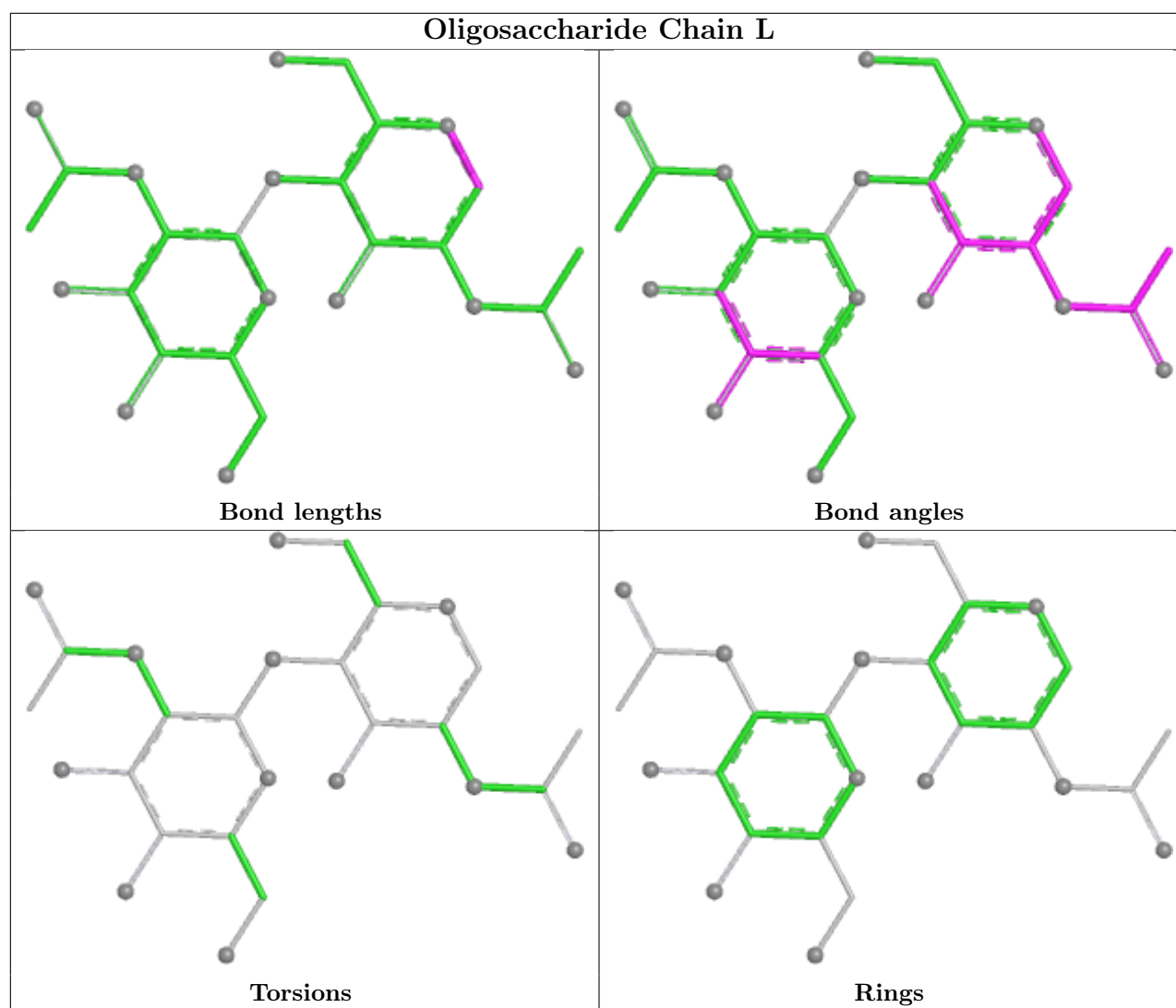


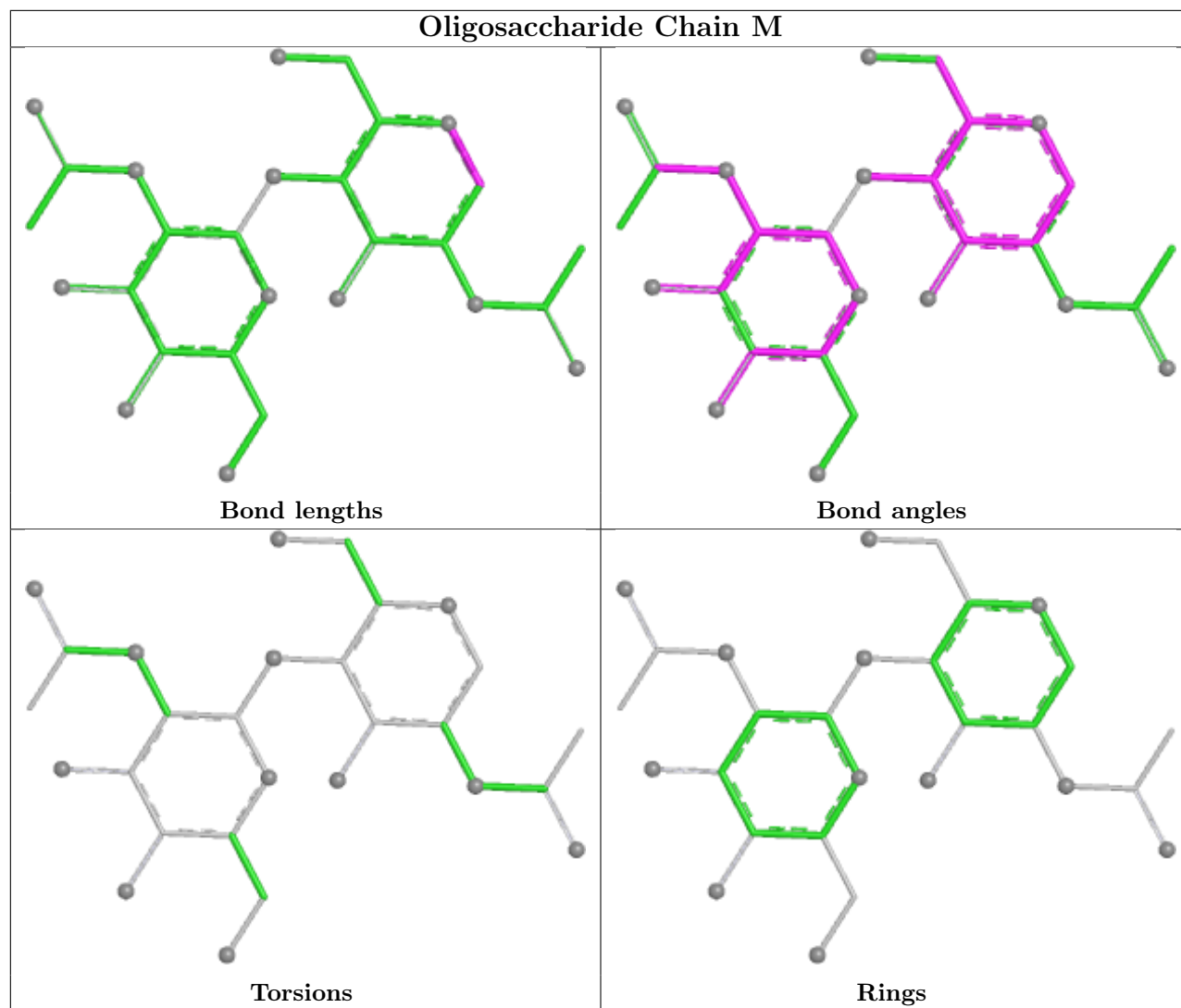


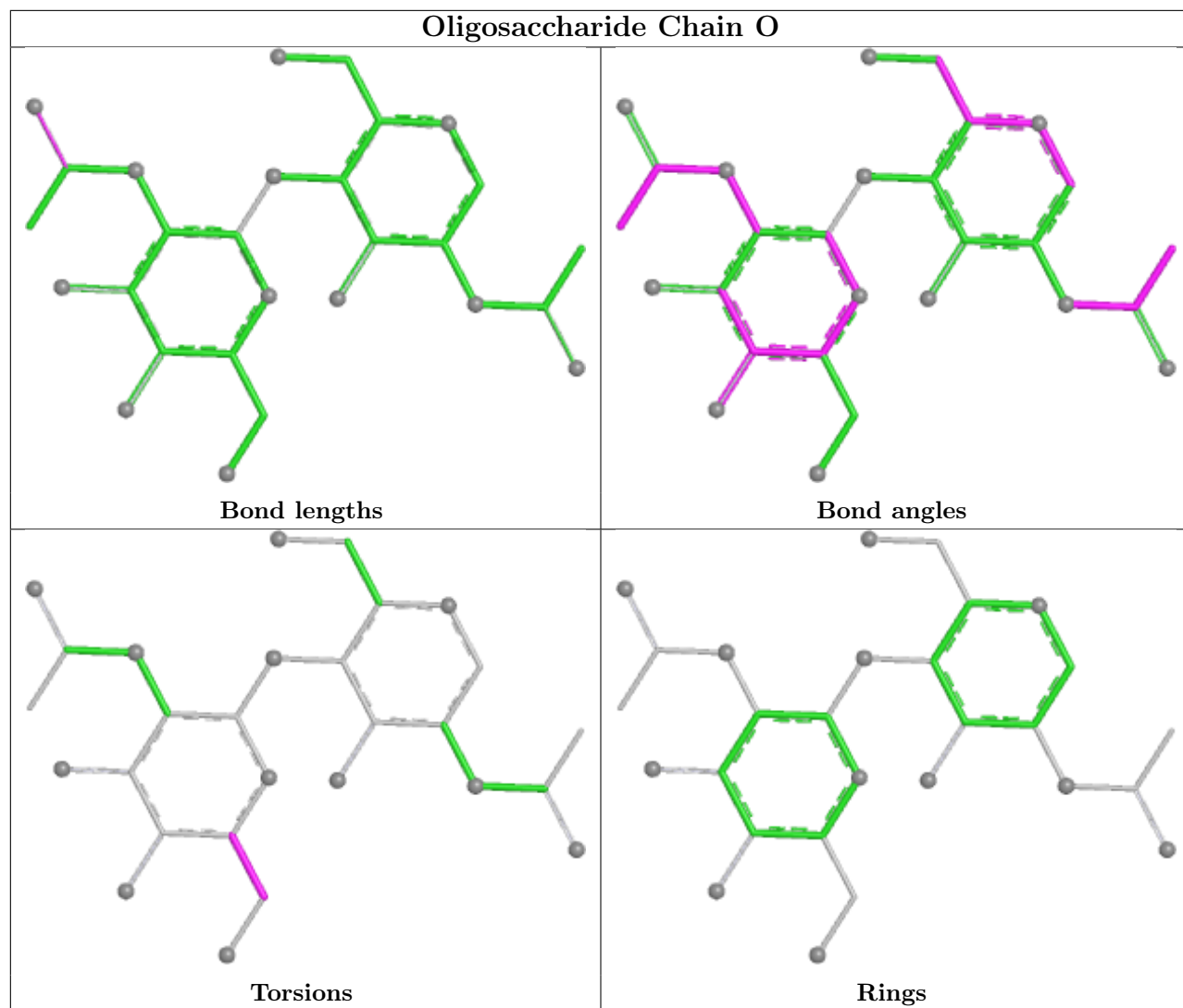


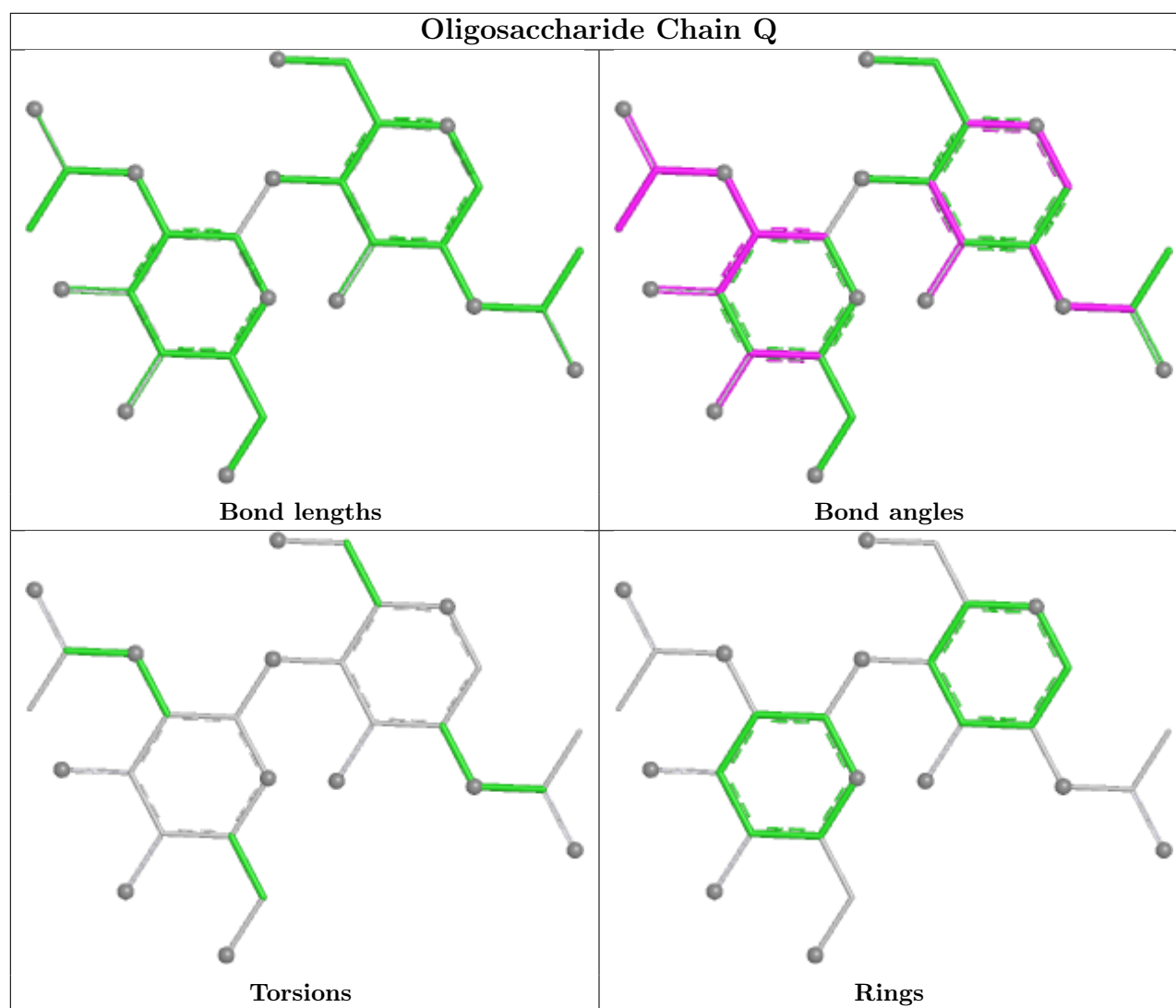


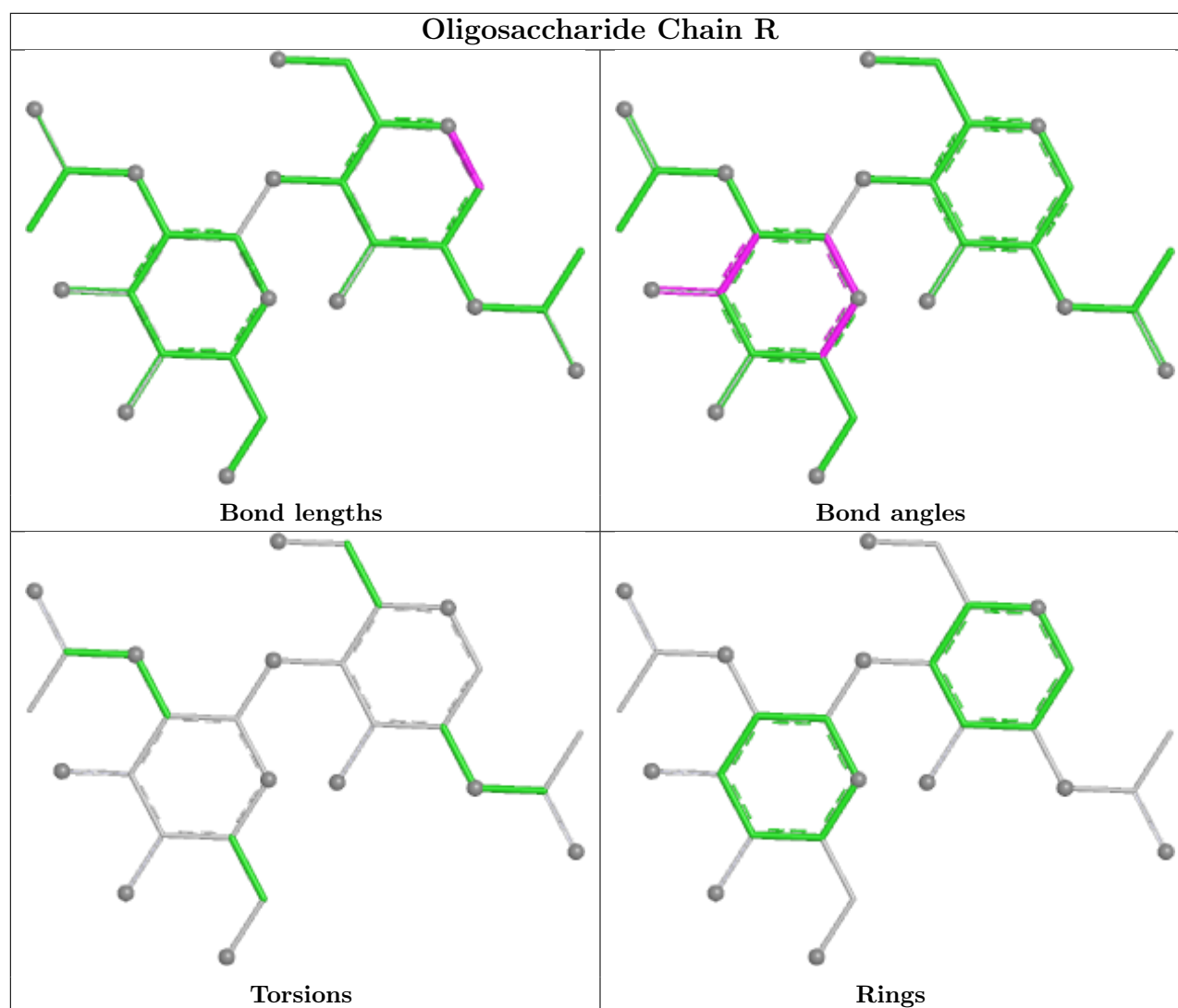


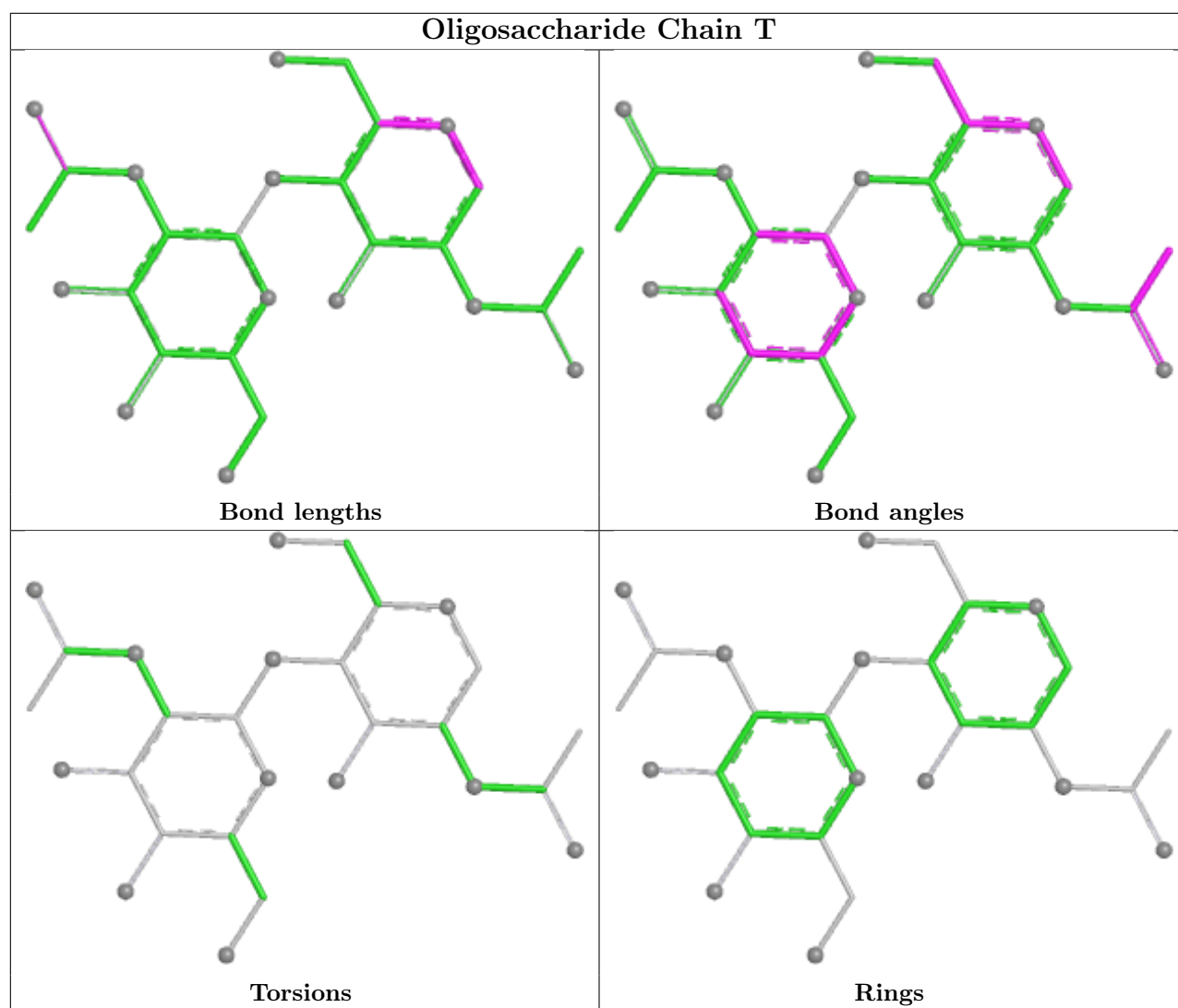


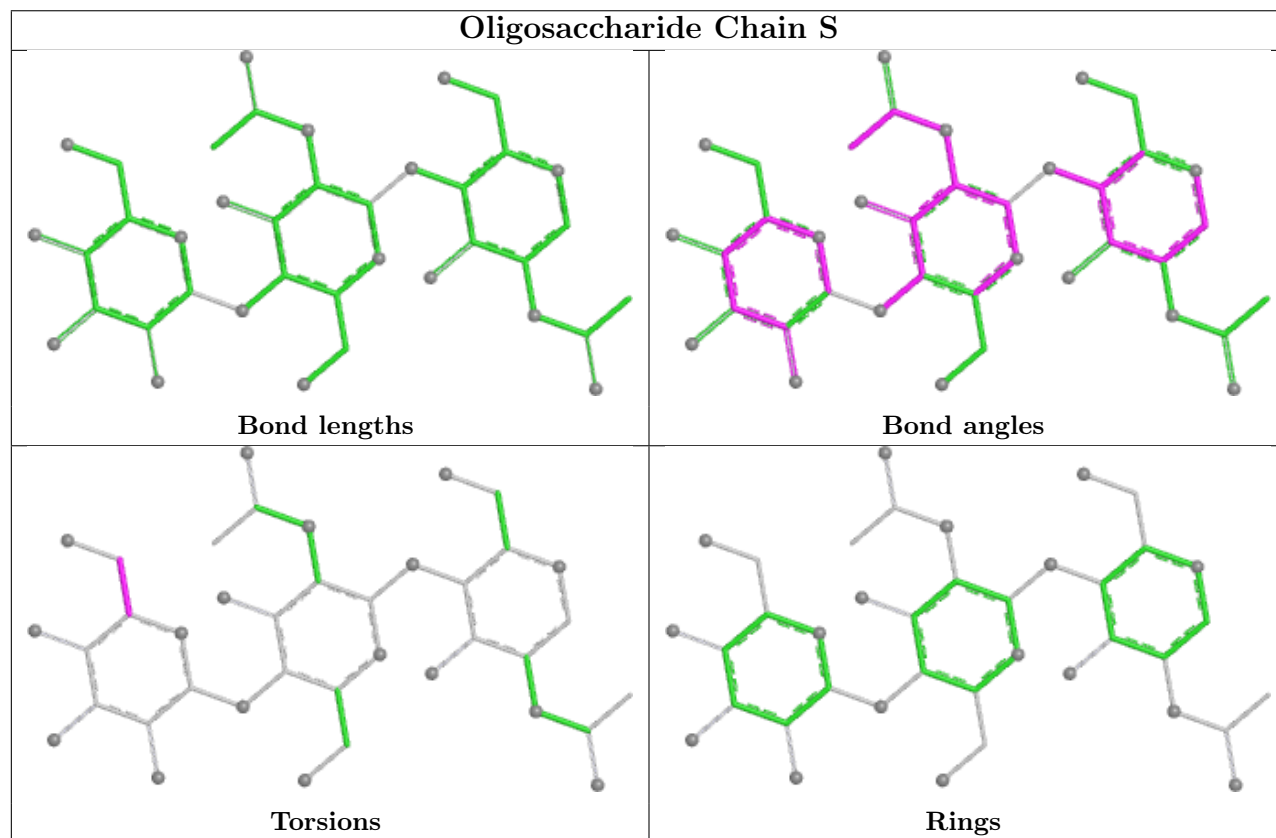
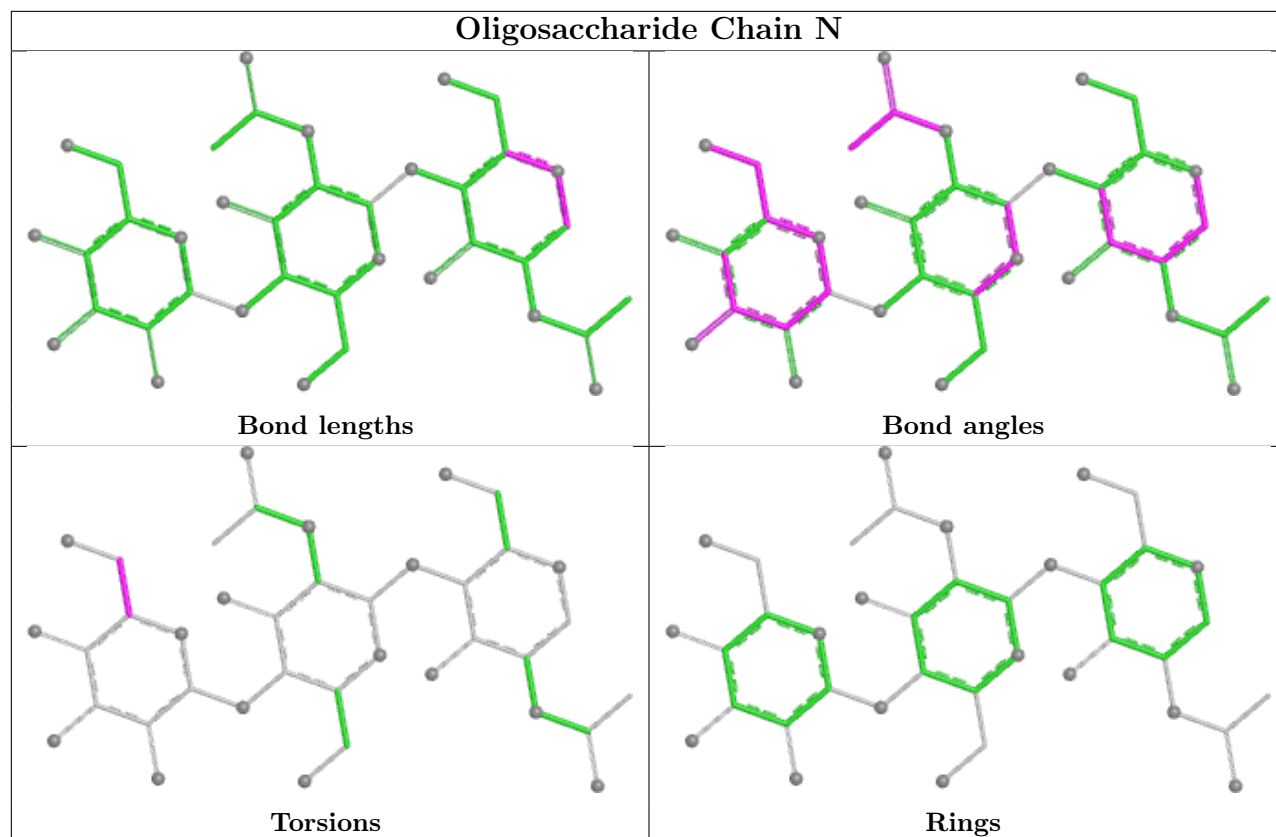












5.6 Ligand geometry

8 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
5	NAG	A	1007	1	14,14,15	1.00	1 (7%)	17,19,21	1.66	4 (23%)
5	NAG	A	1004	1	14,14,15	0.96	1 (7%)	17,19,21	2.68	6 (35%)
5	NAG	C	1008	1	14,14,15	0.87	1 (7%)	17,19,21	2.35	5 (29%)
5	NAG	B	1004	1	14,14,15	0.74	0	17,19,21	2.26	5 (29%)
5	NAG	B	1007	1	14,14,15	1.03	1 (7%)	17,19,21	1.56	3 (17%)
5	NAG	D	606	1	14,14,15	1.13	1 (7%)	17,19,21	1.87	5 (29%)
5	NAG	F	606	1	14,14,15	1.12	1 (7%)	17,19,21	1.62	3 (17%)
5	NAG	E	1008	1	14,14,15	0.86	0	17,19,21	1.98	5 (29%)

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
5	NAG	A	1007	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1004	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1008	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1004	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1007	1	-	2/6/23/26	0/1/1/1
5	NAG	D	606	1	-	2/6/23/26	0/1/1/1
5	NAG	F	606	1	-	2/6/23/26	0/1/1/1
5	NAG	E	1008	1	-	1/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	606	NAG	C1-C2	3.13	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	606	NAG	C1-C2	3.02	1.56	1.52
5	B	1007	NAG	C1-C2	2.68	1.56	1.52
5	C	1008	NAG	C1-C2	2.56	1.55	1.52
5	A	1007	NAG	C1-C2	2.51	1.55	1.52

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1004	NAG	C1-O5-C5	7.60	122.38	112.19
5	B	1004	NAG	C1-O5-C5	6.97	121.53	112.19
5	C	1008	NAG	C1-O5-C5	6.56	120.98	112.19
5	E	1008	NAG	C1-O5-C5	5.02	118.92	112.19
5	A	1004	NAG	C1-C2-N2	-4.41	103.48	110.43

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	606	NAG	O5-C5-C6-O6
5	D	606	NAG	O5-C5-C6-O6
5	F	606	NAG	C4-C5-C6-O6
5	A	1007	NAG	O5-C5-C6-O6
5	A	1007	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1008	NAG	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	491/496 (98%)	-1.53	0 100 100	20, 34, 52, 84	0
1	B	491/496 (98%)	-1.53	0 100 100	21, 33, 52, 90	0
1	C	491/496 (98%)	-1.53	0 100 100	23, 35, 53, 95	0
1	D	491/496 (98%)	-1.51	0 100 100	21, 34, 56, 119	0
1	E	491/496 (98%)	-1.52	0 100 100	20, 35, 53, 90	0
1	F	491/496 (98%)	-1.52	0 100 100	22, 33, 54, 136	0
All	All	2946/2976 (98%)	-1.53	0 100 100	20, 34, 53, 136	0

There are no RSRZ outliers to report.

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	L	2	14/15	0.96	0.07	53,64,74,76	0
2	NAG	I	1	15/15	0.96	0.07	67,88,106,108	0
2	NAG	G	1	15/15	0.97	0.05	58,79,87,89	0
5	NAG	E	1008	14/15	0.97	0.05	53,64,75,79	0
2	NAG	K	1	15/15	0.97	0.06	50,66,80,82	0
2	NAG	P	1	15/15	0.97	0.06	53,67,85,97	0
3	NAG	Q	2	14/15	0.98	0.05	55,61,67,72	0
3	NAG	H	2	14/15	0.98	0.05	41,54,64,66	0
4	NAG	S	2	14/15	0.98	0.06	46,55,62,66	0
3	NAG	T	2	14/15	0.98	0.04	37,44,53,54	0
5	NAG	F	606	14/15	0.98	0.04	52,61,66,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	A	1004	14/15	0.98	0.04	46,55,62,64	0
5	NAG	C	1008	14/15	0.98	0.05	49,60,66,69	0
4	NAG	N	2	14/15	0.98	0.05	50,55,64,68	0
5	NAG	D	606	14/15	0.98	0.04	57,64,73,76	0
3	NAG	O	2	14/15	0.99	0.03	35,40,45,48	0
3	NAG	J	2	14/15	0.99	0.04	37,49,59,67	0
3	NAG	Q	1	14/15	0.99	0.03	57,60,65,69	0
5	NAG	B	1007	14/15	0.99	0.03	43,50,59,60	0
3	NAG	R	1	14/15	0.99	0.03	39,43,56,60	0
3	NAG	R	2	14/15	0.99	0.03	33,42,49,54	0
3	NAG	L	1	14/15	0.99	0.04	47,53,59,60	0
4	NAG	S	1	14/15	0.99	0.03	37,46,53,54	0
3	NAG	M	1	14/15	0.99	0.02	42,47,54,54	0
3	NAG	T	1	14/15	0.99	0.02	34,38,44,44	0
5	NAG	A	1007	14/15	0.99	0.04	49,56,60,64	0
3	NAG	M	2	14/15	0.99	0.03	37,47,50,50	0
2	GAL	G	2	11/12	0.99	0.03	45,52,58,60	0
5	NAG	B	1004	14/15	0.99	0.05	51,59,68,69	0
2	GAL	I	2	11/12	0.99	0.02	42,50,60,64	0
4	NAG	N	1	14/15	0.99	0.03	36,41,46,48	0
2	GAL	K	2	11/12	0.99	0.04	29,32,38,42	0
3	NAG	J	1	14/15	0.99	0.03	35,39,43,46	0
2	GAL	P	2	11/12	0.99	0.04	30,38,44,46	0
3	NAG	O	1	14/15	0.99	0.03	38,42,47,49	0
3	NAG	H	1	14/15	1.00	0.02	35,40,43,43	0

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($\text{\AA}^2$)	Q<0.9
2	NAG	I	1	15/15	0.96	0.07	67,88,106,108	0
3	NAG	L	2	14/15	0.96	0.07	53,64,74,76	0
4	BMA	N	3	11/12	0.96	0.05	63,77,81,81	0
2	NAG	P	1	15/15	0.97	0.06	53,67,85,97	0
2	NAG	G	1	15/15	0.97	0.05	58,79,87,89	0
2	NAG	K	1	15/15	0.97	0.06	50,66,80,82	0
3	NAG	Q	2	14/15	0.98	0.05	55,61,67,72	0
3	NAG	T	2	14/15	0.98	0.04	37,44,53,54	0

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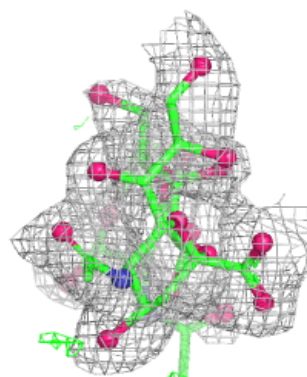
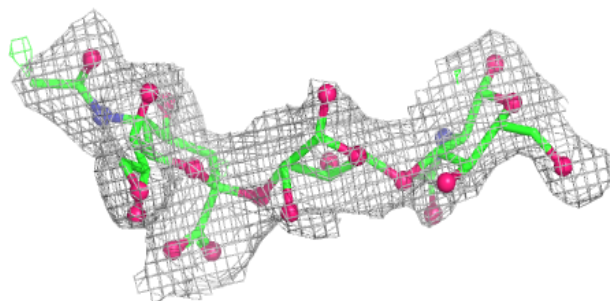
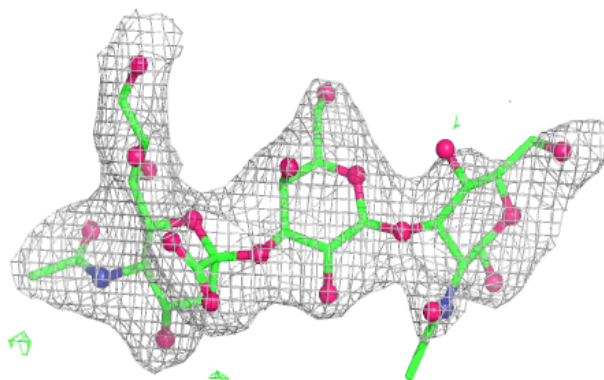
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	N	2	14/15	0.98	0.05	50,55,64,68	0
3	NAG	H	2	14/15	0.98	0.05	41,54,64,66	0
4	NAG	S	2	14/15	0.98	0.06	46,55,62,66	0
4	BMA	S	3	11/12	0.98	0.06	71,73,78,79	0
2	GAL	I	2	11/12	0.99	0.02	42,50,60,64	0
3	NAG	J	1	14/15	0.99	0.03	35,39,43,46	0
3	NAG	J	2	14/15	0.99	0.04	37,49,59,67	0
3	NAG	L	1	14/15	0.99	0.04	47,53,59,60	0
2	SIA	I	3	20/21	0.99	0.03	30,35,38,38	0
3	NAG	M	1	14/15	0.99	0.02	42,47,54,54	0
3	NAG	M	2	14/15	0.99	0.03	37,47,50,50	0
3	NAG	O	1	14/15	0.99	0.03	38,42,47,49	0
3	NAG	O	2	14/15	0.99	0.03	35,40,45,48	0
3	NAG	Q	1	14/15	0.99	0.03	57,60,65,69	0
2	SIA	G	3	20/21	0.99	0.03	30,35,40,41	0
3	NAG	R	1	14/15	0.99	0.03	39,43,56,60	0
3	NAG	R	2	14/15	0.99	0.03	33,42,49,54	0
3	NAG	T	1	14/15	0.99	0.02	34,38,44,44	0
2	GAL	K	2	11/12	0.99	0.04	29,32,38,42	0
4	NAG	N	1	14/15	0.99	0.03	36,41,46,48	0
2	SIA	K	3	20/21	0.99	0.03	25,27,29,32	0
2	GAL	G	2	11/12	0.99	0.03	45,52,58,60	0
4	NAG	S	1	14/15	0.99	0.03	37,46,53,54	0
2	GAL	P	2	11/12	0.99	0.04	30,38,44,46	0
2	SIA	P	3	20/21	0.99	0.03	24,28,31,31	0
3	NAG	H	1	14/15	1.00	0.02	35,40,43,43	0

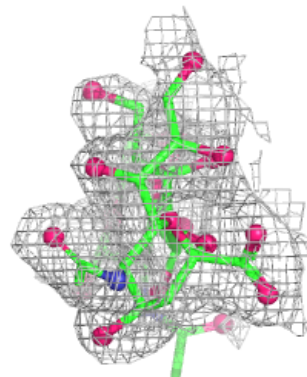
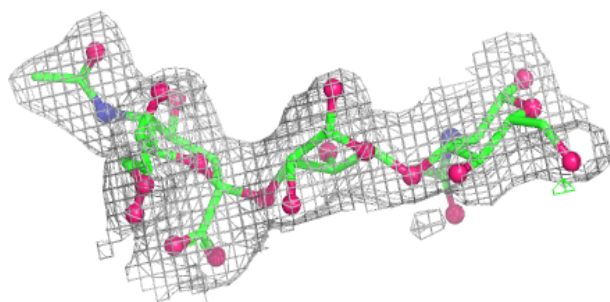
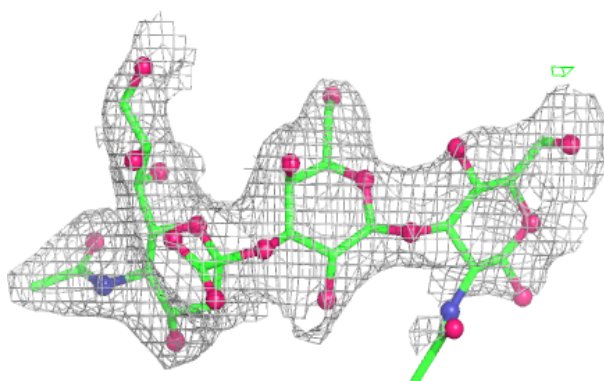
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain G:

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

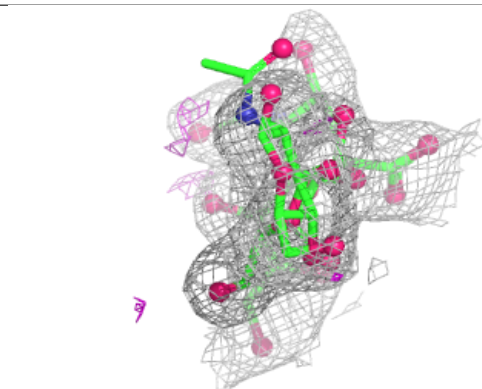
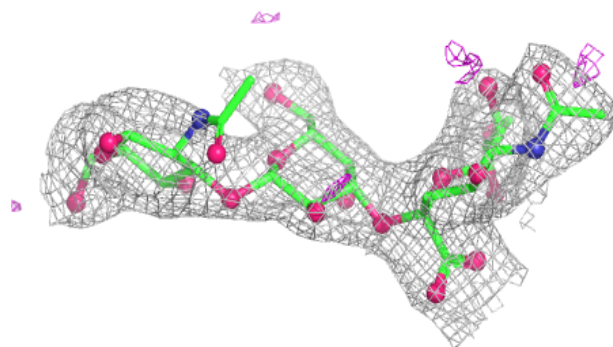
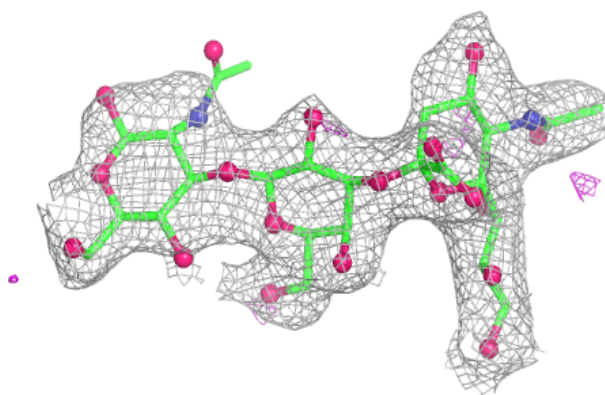
**Electron density around Chain I:**

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

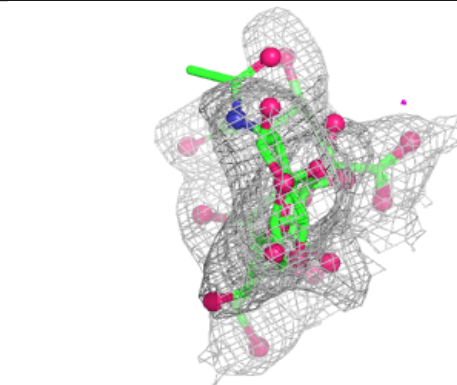
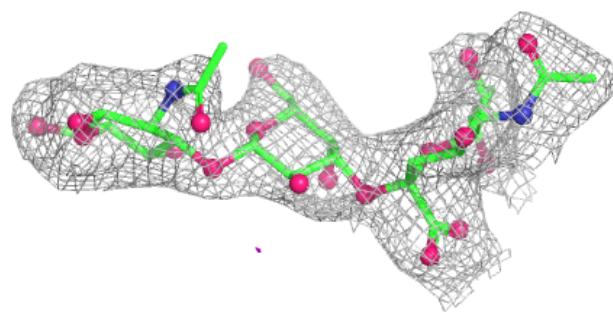
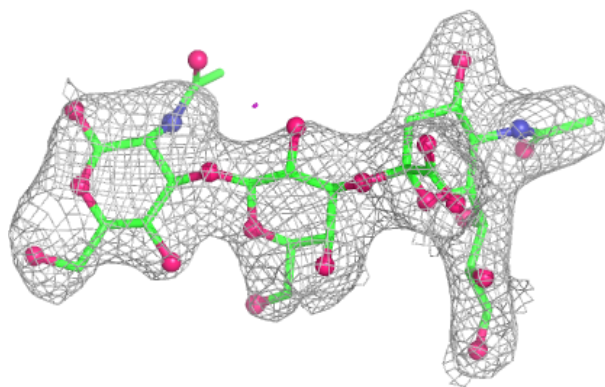


Electron density around Chain K:

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and green (positive)

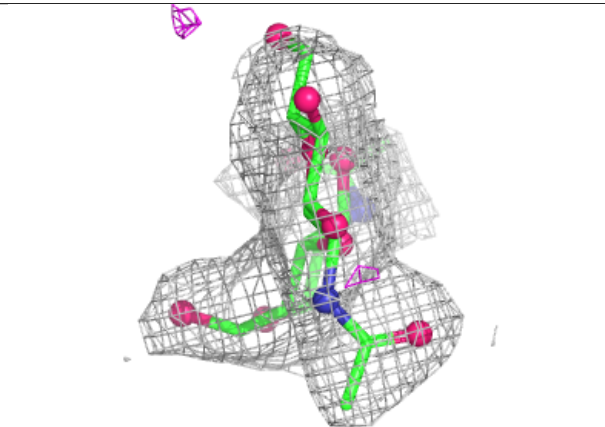
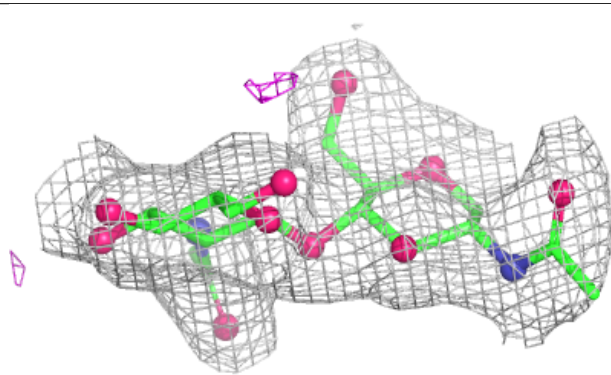
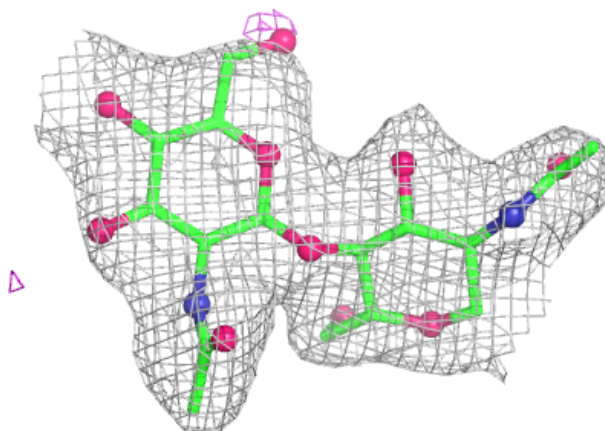
**Electron density around Chain P:**

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

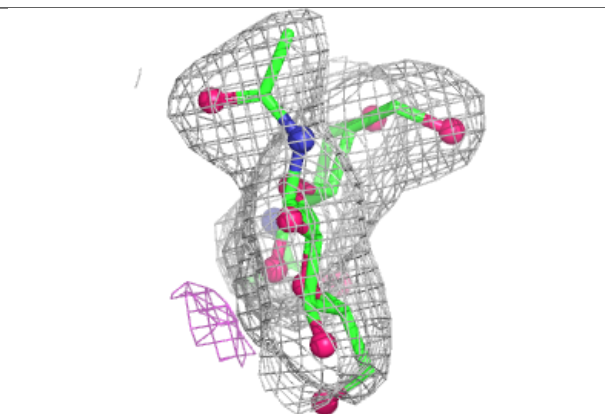
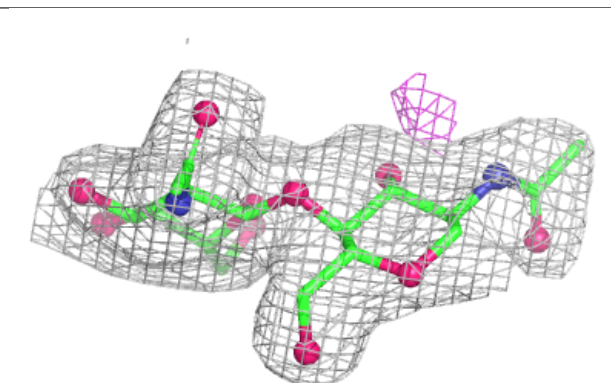
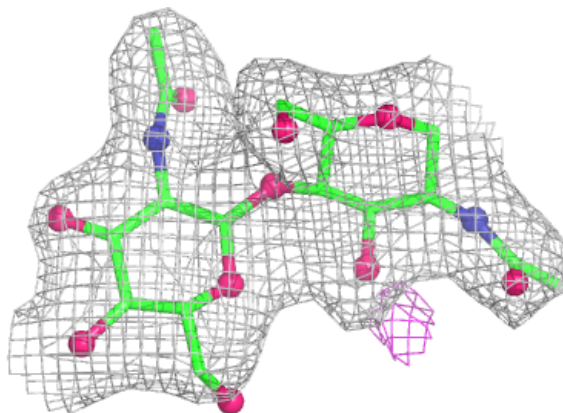


Electron density around Chain H:

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

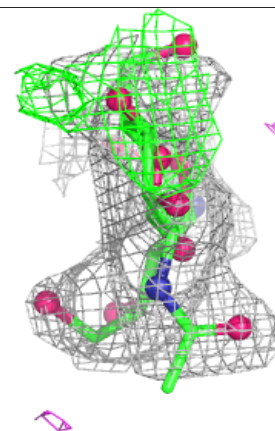
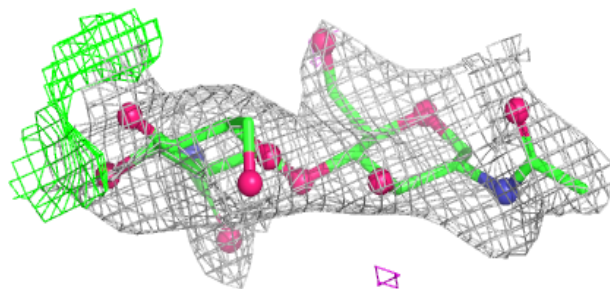
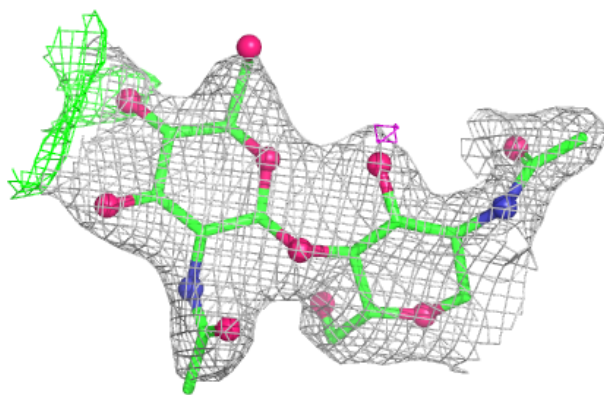
**Electron density around Chain J:**

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



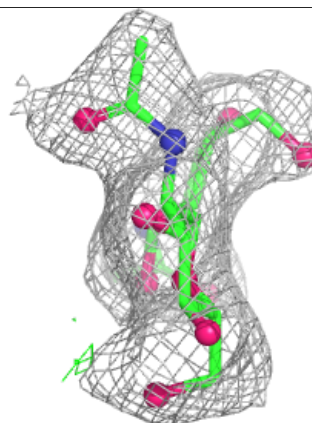
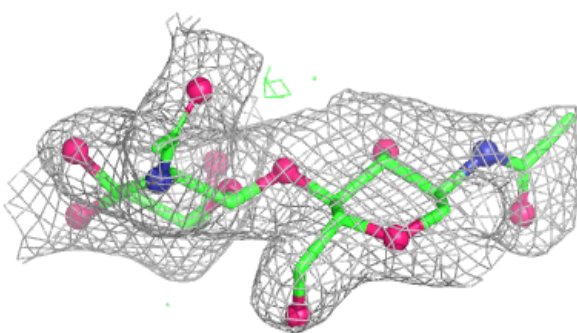
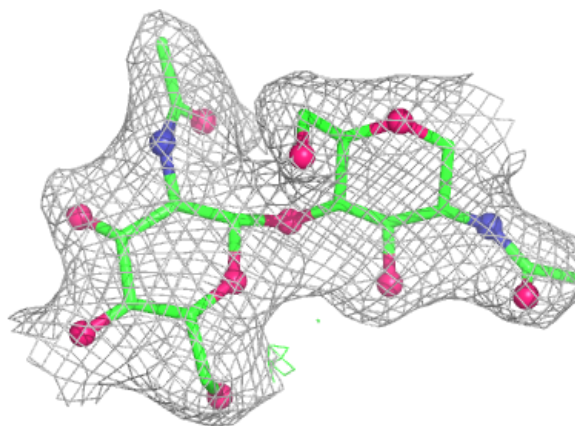
Electron density around Chain L:

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

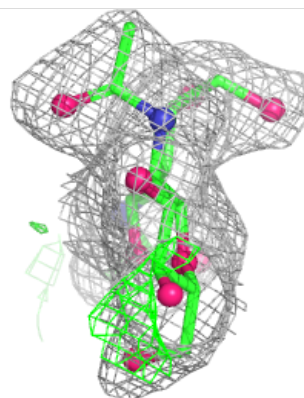
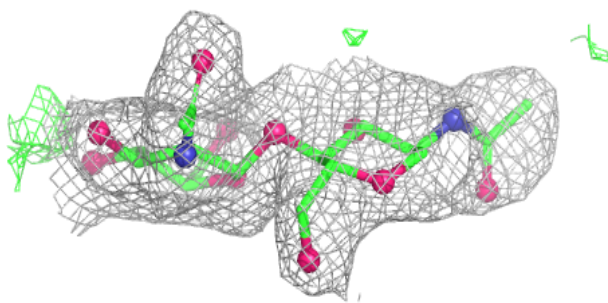
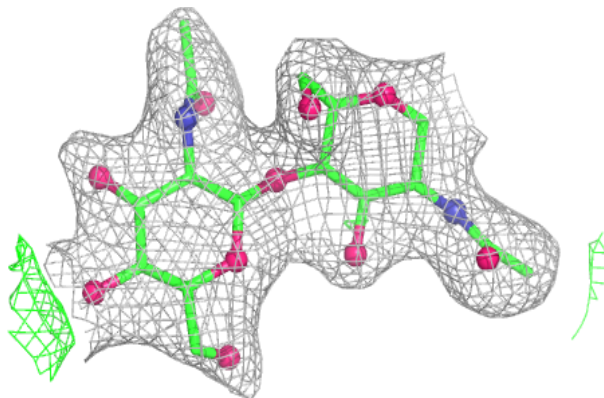


Electron density around Chain M:

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

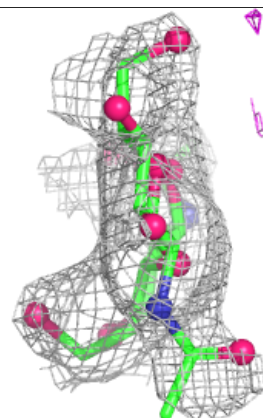
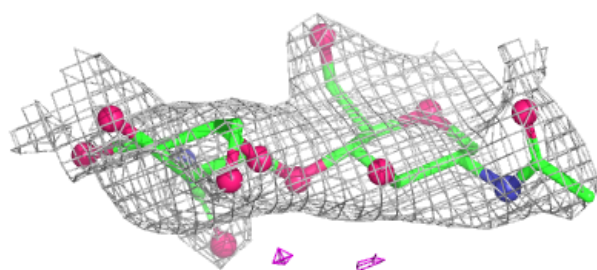
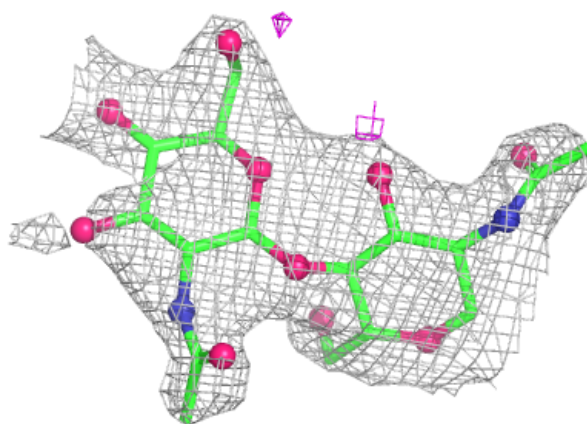
**Electron density around Chain O:**

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



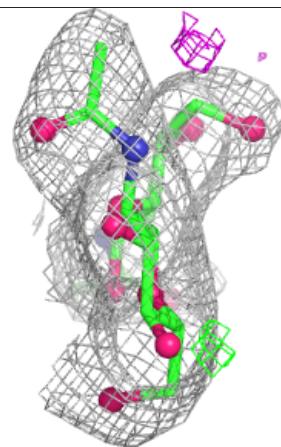
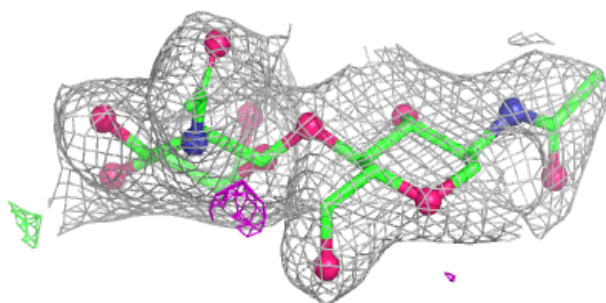
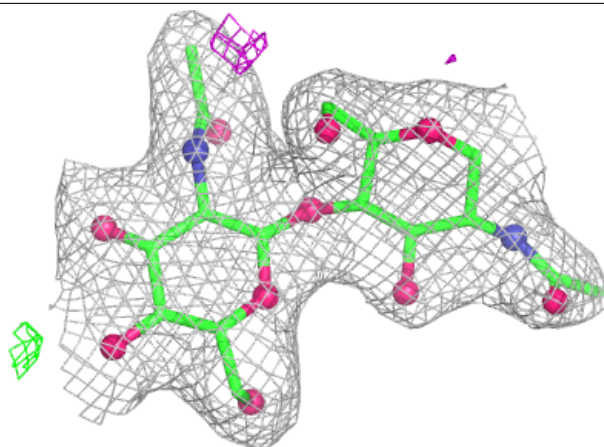
Electron density around Chain Q:

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

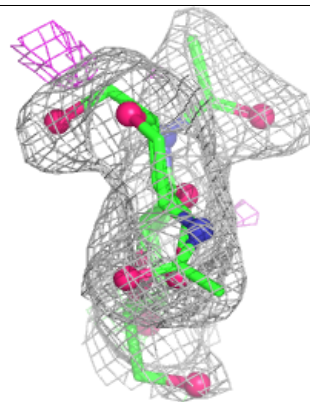
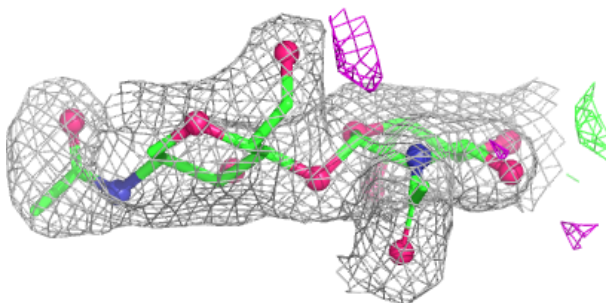
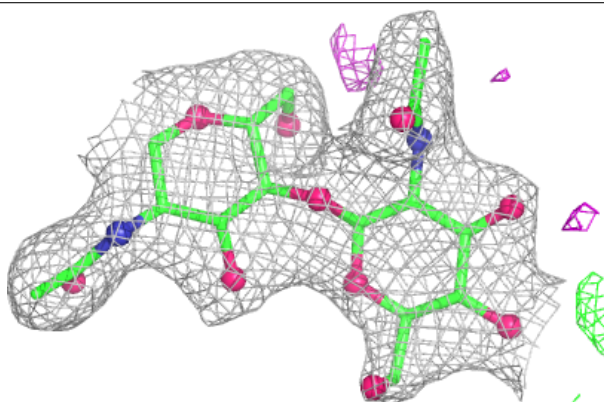


Electron density around Chain R:

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

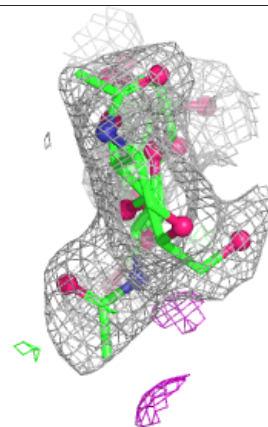
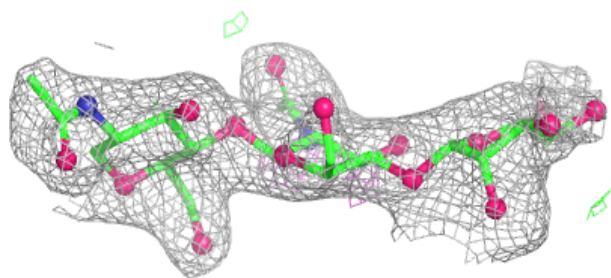
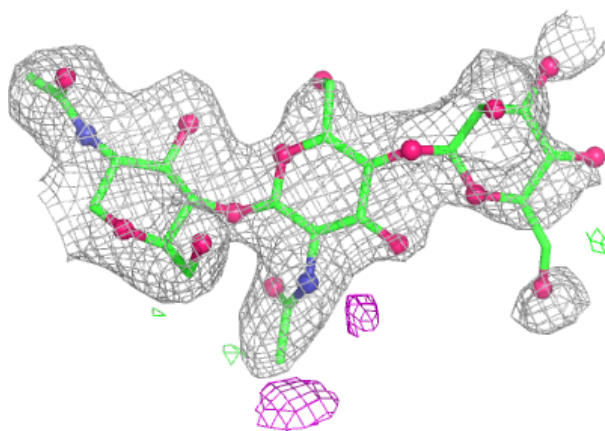
**Electron density around Chain T:**

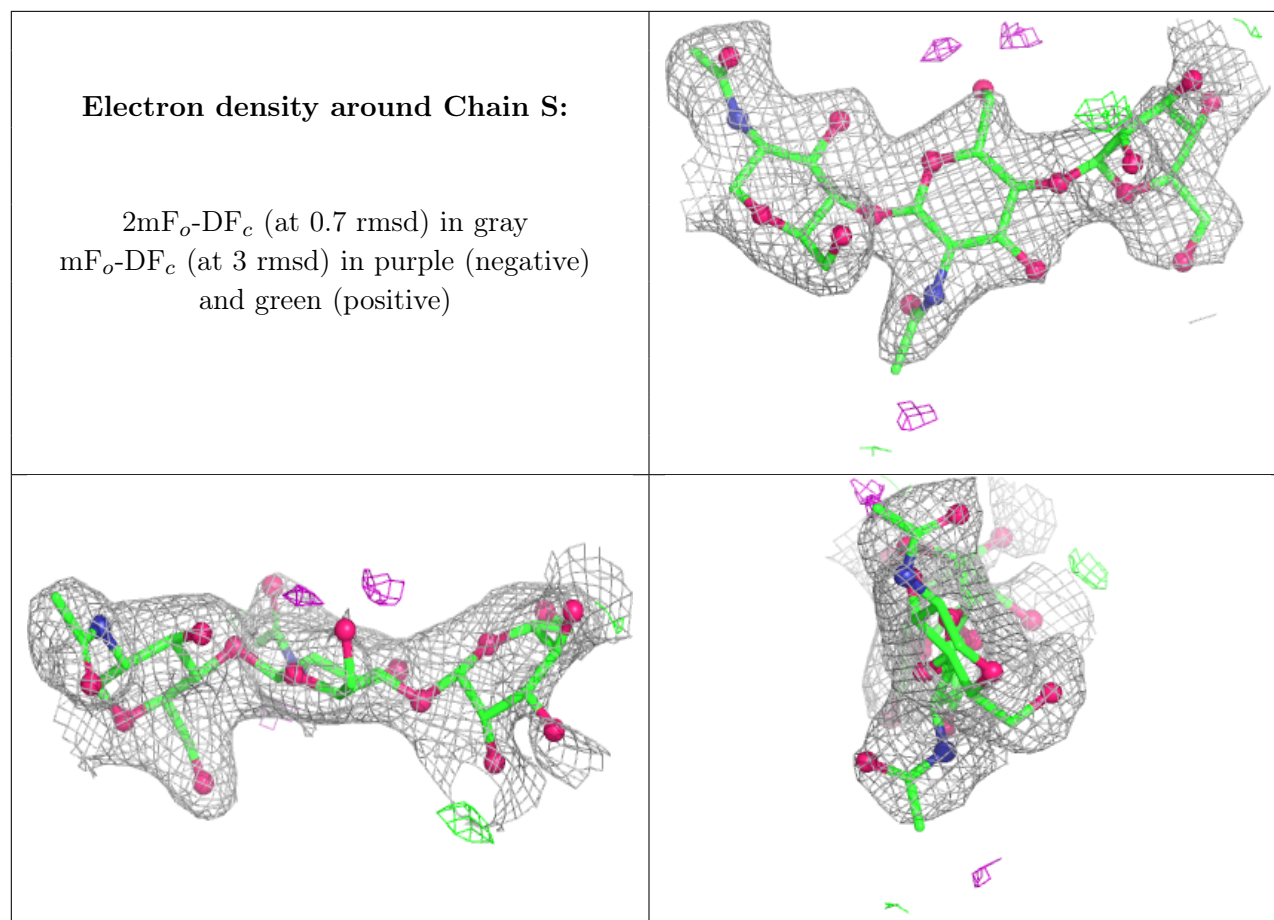
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain N:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	E	1008	14/15	0.97	0.05	53,64,75,79	0
5	NAG	C	1008	14/15	0.98	0.05	49,60,66,69	0
5	NAG	D	606	14/15	0.98	0.04	57,64,73,76	0
5	NAG	A	1004	14/15	0.98	0.04	46,55,62,64	0
5	NAG	F	606	14/15	0.98	0.04	52,61,66,72	0
5	NAG	B	1004	14/15	0.99	0.05	51,59,68,69	0
5	NAG	B	1007	14/15	0.99	0.03	43,50,59,60	0
5	NAG	A	1007	14/15	0.99	0.04	49,56,60,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.