



wwPDB X-ray Structure Validation Summary Report ⓘ

May 7, 2025 – 12:26 AM JST

PDB ID : 8X26 / pdb_00008x26
Title : Crystal structure of H5 hemagglutinin from human-infecting H5N8 influenza virus in complex with LSTa
Authors : Jin, X.Y.; Song, H.; Han, P.; Qi, J.X.
Deposited on : 2023-11-09
Resolution : 3.12 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

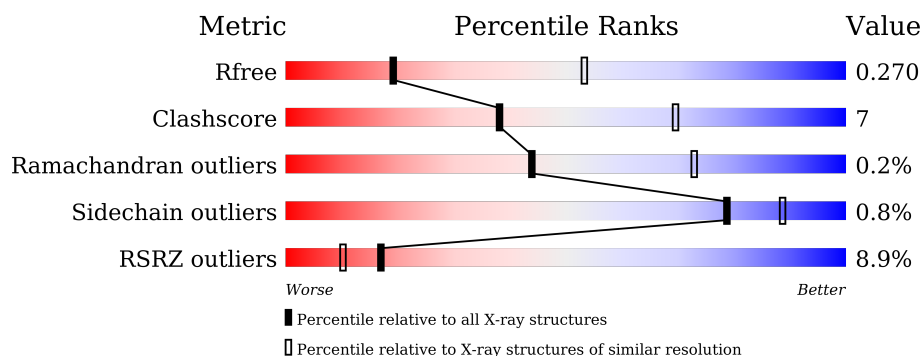
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.12 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.




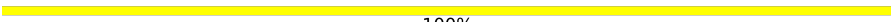







Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1668 (3.14-3.10)
Clashscore	180529	1788 (3.14-3.10)
Ramachandran outliers	177936	1696 (3.14-3.10)
Sidechain outliers	177891	1696 (3.14-3.10)
RSRZ outliers	164620	1668 (3.14-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	506	<div> <div>9%</div> <div>78%</div> <div>17%</div> <div>•</div> </div>
1	B	506	<div> <div>10%</div> <div>78%</div> <div>18%</div> <div>•</div> </div>
1	C	506	<div> <div>5%</div> <div>80%</div> <div>15%</div> <div>• 5%</div> </div>
1	D	506	<div> <div>6%</div> <div>79%</div> <div>16%</div> <div>•</div> </div>
1	E	506	<div> <div>7%</div> <div>81%</div> <div>14%</div> <div>•</div> </div>
1	F	506	<div> <div>13%</div> <div>79%</div> <div>17%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 100%
2	I	2	 100%
3	J	4	 25% 25% 50%
3	K	4	 50% 50%
3	L	4	 50% 50%
3	M	4	 25% 50% 25%
3	N	4	 50% 50%
3	O	4	 25% 25% 50%

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
3	SIA	N	4	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 23778 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.

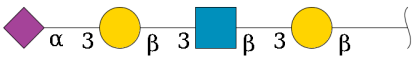
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	S	0	0	0
			3877	2437	675	743	22			
1	B	485	Total	C	N	O	S	0	0	0
			3883	2441	676	744	22			
1	C	483	Total	C	N	O	S	0	0	0
			3873	2435	674	742	22			
1	D	484	Total	C	N	O	S	0	0	0
			3877	2437	675	743	22			
1	E	485	Total	C	N	O	S	0	0	0
			3882	2440	676	744	22			
1	F	486	Total	C	N	O	S	0	0	0
			3890	2446	677	745	22			

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



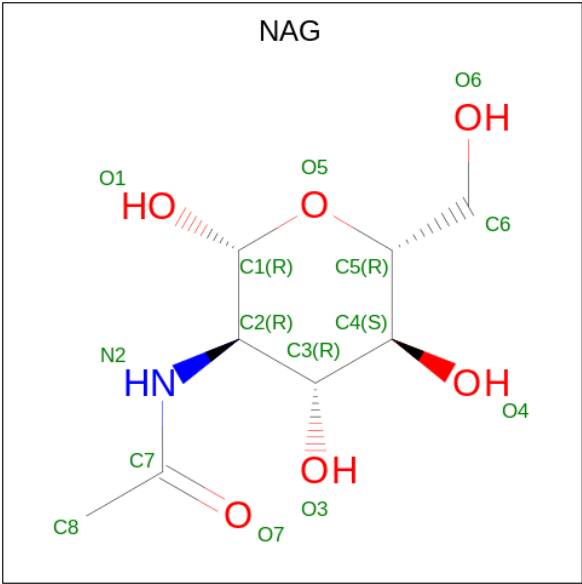
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	J	4	Total	C	N	O	0	0	0
			57	31	2	24			
3	K	4	Total	C	N	O	0	0	0
			57	31	2	24			
3	L	4	Total	C	N	O	0	0	0
			57	31	2	24			
3	M	4	Total	C	N	O	0	0	0
			57	31	2	24			
3	N	4	Total	C	N	O	0	0	0
			57	31	2	24			
3	O	4	Total	C	N	O	0	0	0
			57	31	2	24			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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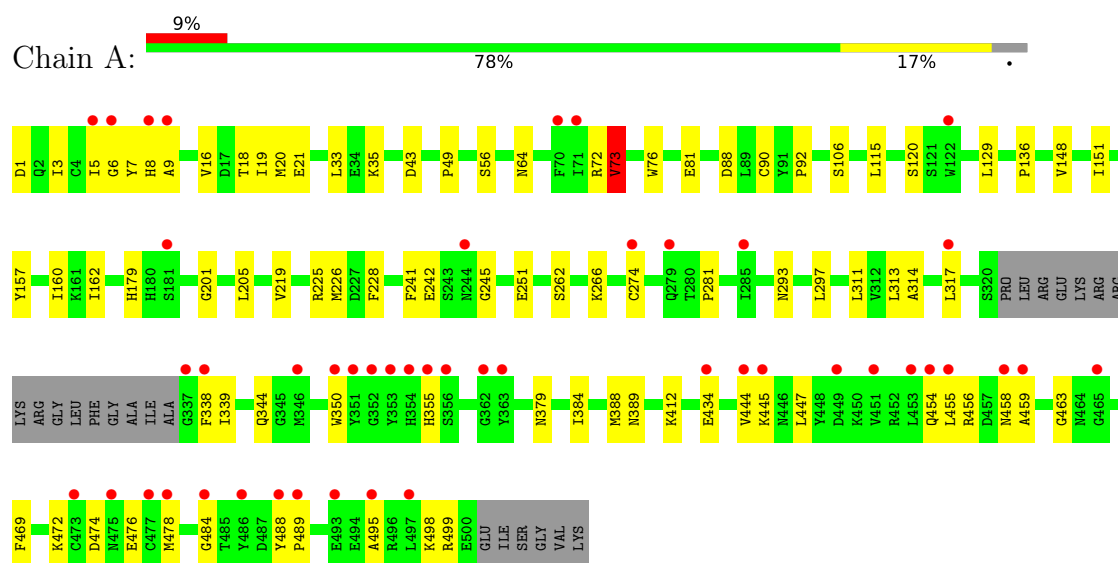
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

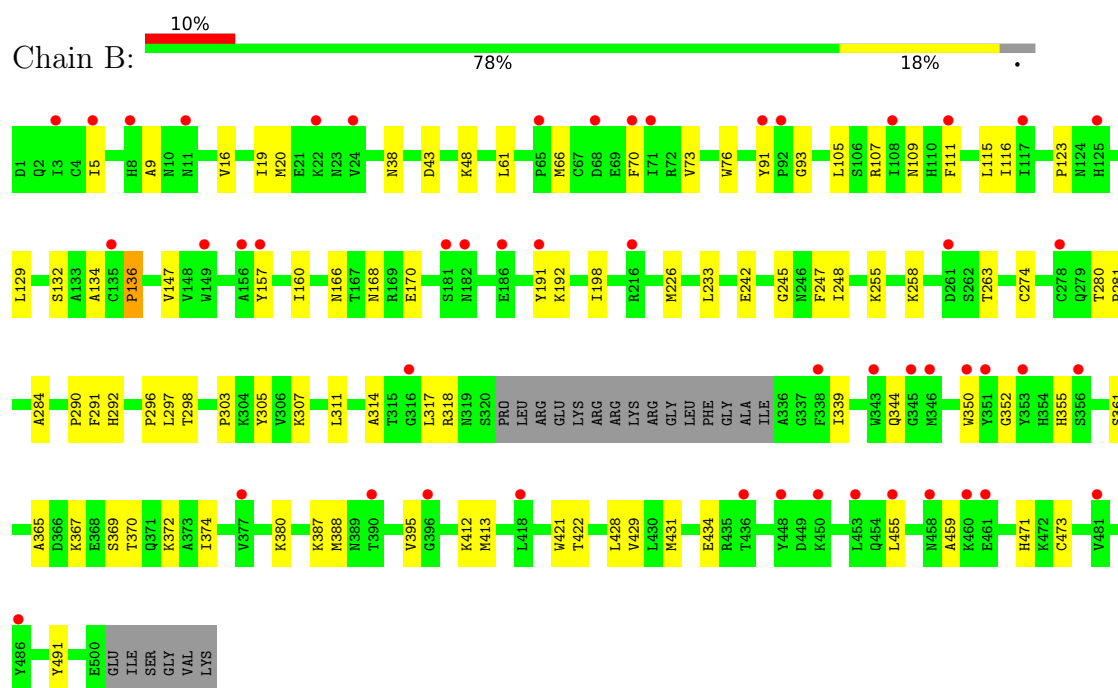
3 Residue-property plots [i](#)

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.

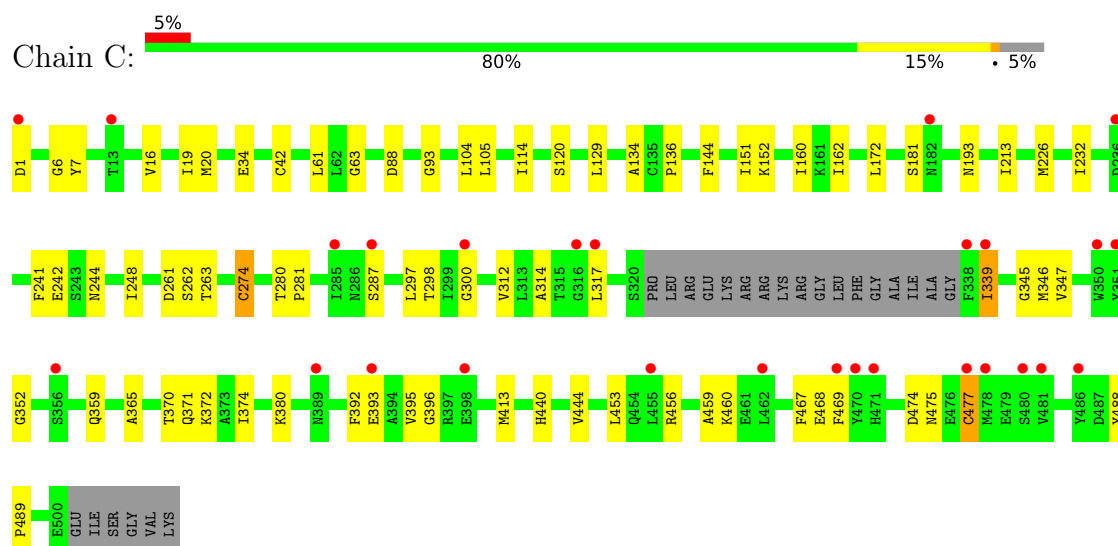
• Molecule 1: Hemagglutinin



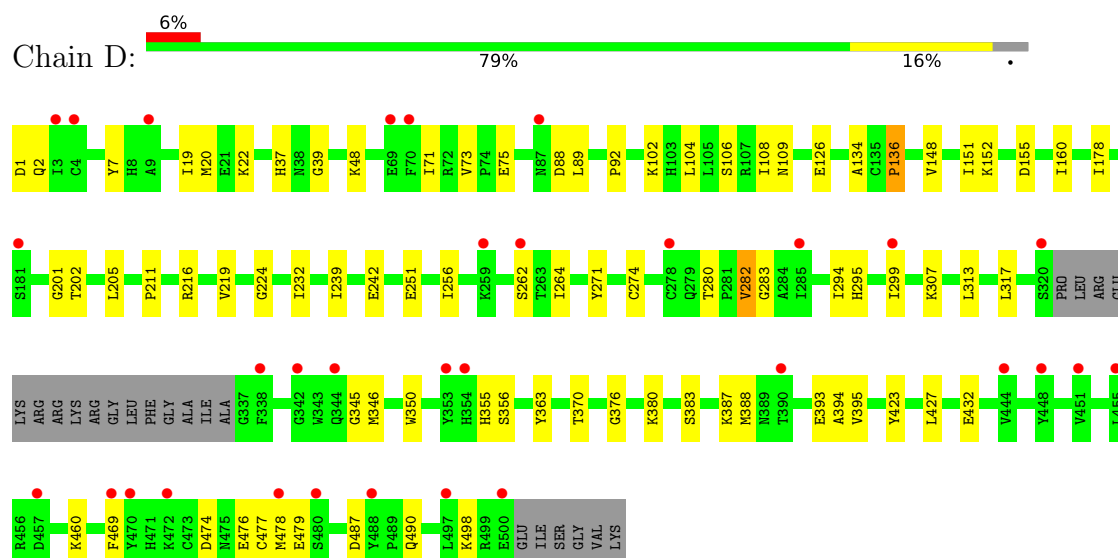
• Molecule 1: Hemagglutinin



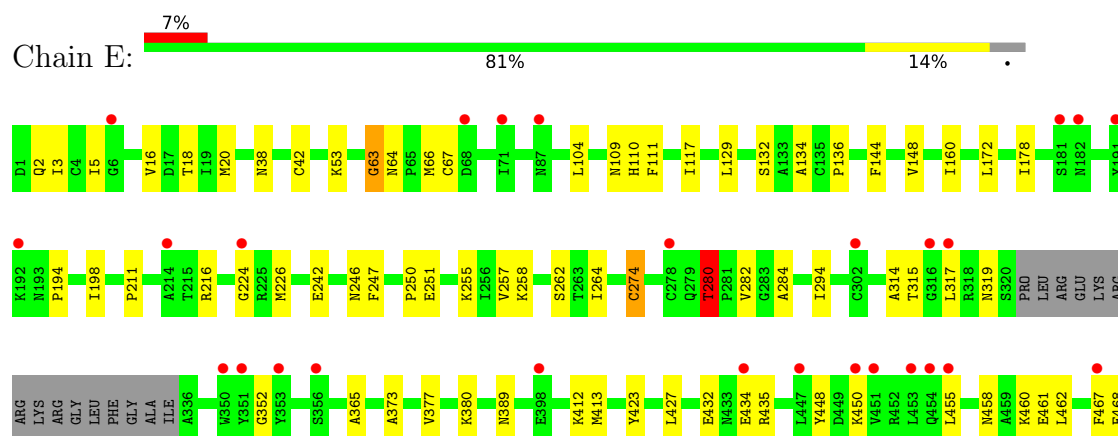
• Molecule 1: Hemagglutinin

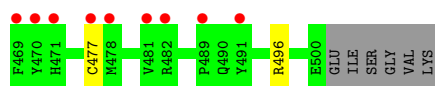


• Molecule 1: Hemagglutinin

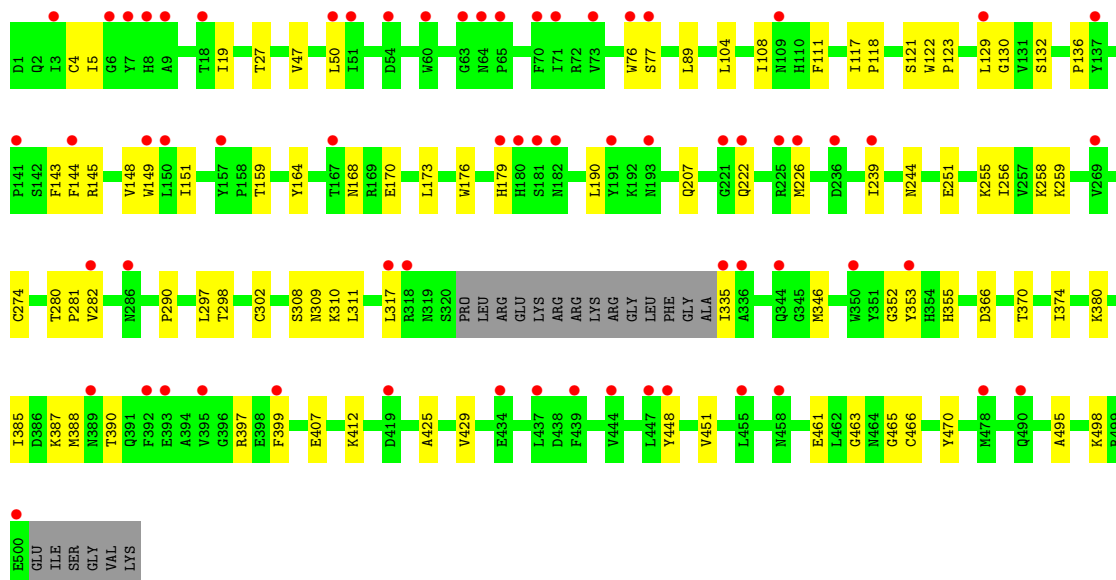
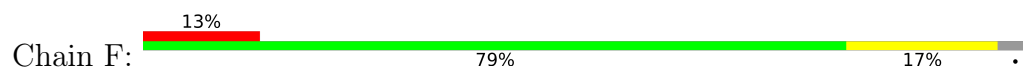


• Molecule 1: Hemagglutinin





- Molecule 1: Hemagglutinin



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




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



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



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

Chain J:  25% 25% 50%



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

Chain K:  50% 50%



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

Chain L:  50% 50%



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

Chain M:  25% 50% 25%

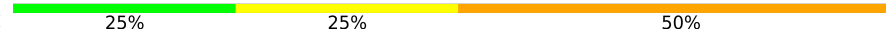


- Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose

Chain N:  50% 50%



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

Chain O:  25% 25% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.98Å 263.81Å 131.62Å 90.00° 101.64° 90.00°	Depositor
Resolution (Å)	48.28 – 3.12 48.28 – 3.12	Depositor EDS
% Data completeness (in resolution range)	90.8 (48.28-3.12) 90.8 (48.28-3.12)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.265 , 0.271 0.264 , 0.270	Depositor DCC
R_{free} test set	82630 reflections (2.34%)	wwPDB-VP
Wilson B-factor (Å ²)	67.0	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 86.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	23778	wwPDB-VP
Average B, all atoms (Å ²)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.53% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.32	0/3966	0.62	4/5370 (0.1%)
1	B	0.38	0/3972	0.64	3/5379 (0.1%)
1	C	0.34	1/3962 (0.0%)	0.61	3/5365 (0.1%)
1	D	0.22	0/3966	0.49	0/5370
1	E	0.40	1/3971 (0.0%)	0.70	3/5377 (0.1%)
1	F	0.28	0/3979	0.54	2/5388 (0.0%)
All	All	0.33	2/23816 (0.0%)	0.61	15/32249 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	262	SER	CA-CB	-6.73	1.45	1.54
1	E	262	SER	CA-CB	-5.11	1.46	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	72	ARG	CA-C-N	-7.26	117.02	123.33
1	A	72	ARG	C-N-CA	-7.26	117.02	123.33
1	C	88	ASP	CB-CA-C	-7.14	108.32	116.54
1	F	222	GLN	N-CA-C	6.34	117.80	108.86
1	B	116	ILE	N-CA-C	-5.96	107.00	112.96

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3877	0	3734	61	0
1	B	3883	0	3739	57	0
1	C	3873	0	3726	52	0
1	D	3877	0	3731	55	0
1	E	3882	0	3735	49	0
1	F	3890	0	3746	54	0
2	G	28	0	25	1	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
3	J	57	0	49	2	0
3	K	57	0	49	3	0
3	L	57	0	49	0	0
3	M	57	0	49	2	0
3	N	57	0	49	9	0
3	O	57	0	49	3	0
4	B	14	0	13	0	0
4	C	28	0	26	0	0
4	D	14	0	13	0	0
4	F	14	0	13	0	0
All	All	23778	0	22845	315	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 7.

The worst 5 of 315 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:E:178:ILE:HD12	1:E:246:ASN:O	1.80	0.82
1:C:7:TYR:HB2	1:C:317:LEU:HD13	1.63	0.81
1:D:476:GLU:O	1:D:479:GLU:HG3	1.80	0.81
1:B:132:SER:OG	3:O:4:SIA:O1B	1.99	0.80
1:B:129:LEU:O	3:O:4:SIA:H113	1.81	0.79

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	480/506 (95%)	455 (95%)	24 (5%)	1 (0%)	44	73
1	B	481/506 (95%)	456 (95%)	24 (5%)	1 (0%)	44	73
1	C	479/506 (95%)	466 (97%)	13 (3%)	0	100	100
1	D	480/506 (95%)	458 (95%)	21 (4%)	1 (0%)	44	73
1	E	481/506 (95%)	468 (97%)	12 (2%)	1 (0%)	44	73
1	F	482/506 (95%)	456 (95%)	25 (5%)	1 (0%)	44	73
All	All	2883/3036 (95%)	2759 (96%)	119 (4%)	5 (0%)	44	73

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	136	PRO
1	B	136	PRO
1	E	194	PRO
1	D	136	PRO
1	A	136	PRO

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	427/445 (96%)	425 (100%)	2 (0%)	86	92
1	B	428/445 (96%)	425 (99%)	3 (1%)	81	90
1	C	428/445 (96%)	424 (99%)	4 (1%)	75	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	428/445 (96%)	426 (100%)	2 (0%)	86	92
1	E	427/445 (96%)	421 (99%)	6 (1%)	62	79
1	F	429/445 (96%)	426 (99%)	3 (1%)	81	90
All	All	2567/2670 (96%)	2547 (99%)	20 (1%)	79	89

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	317	LEU
1	F	274	CYS
1	F	355	HIS
1	F	282	VAL
1	C	274	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	168	ASN
1	F	189	ASN
1	F	475	ASN
1	C	222	GLN
1	C	146	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

30 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	1,2	14,14,15	0.73	0	17,19,21	1.11	1 (5%)
2	NAG	G	2	2	14,14,15	0.57	0	17,19,21	1.20	2 (11%)
2	NAG	H	1	1,2	14,14,15	0.92	1 (7%)	17,19,21	1.91	4 (23%)
2	NAG	H	2	2	14,14,15	0.80	1 (7%)	17,19,21	1.60	2 (11%)
2	NAG	I	1	1,2	14,14,15	0.80	0	17,19,21	1.04	1 (5%)
2	NAG	I	2	2	14,14,15	2.10	4 (28%)	17,19,21	1.00	0
3	GAL	J	1	3	12,12,12	0.23	0	17,17,17	0.67	0
3	NAG	J	2	3	14,14,15	0.42	0	17,19,21	1.60	3 (17%)
3	GAL	J	3	3	11,11,12	0.70	0	15,15,17	1.27	2 (13%)
3	SIA	J	4	3	20,20,21	2.04	2 (10%)	24,28,31	1.92	7 (29%)
3	GAL	K	1	3	12,12,12	0.22	0	17,17,17	0.53	0
3	NAG	K	2	3	14,14,15	0.40	0	17,19,21	0.81	0
3	GAL	K	3	3	11,11,12	0.69	0	15,15,17	1.28	2 (13%)
3	SIA	K	4	3	20,20,21	2.04	2 (10%)	24,28,31	1.92	7 (29%)
3	GAL	L	1	3	12,12,12	0.17	0	17,17,17	0.46	0
3	NAG	L	2	3	14,14,15	0.40	0	17,19,21	0.77	0
3	GAL	L	3	3	11,11,12	0.71	0	15,15,17	1.27	2 (13%)
3	SIA	L	4	3	20,20,21	2.05	2 (10%)	24,28,31	1.93	7 (29%)
3	GAL	M	1	3	12,12,12	0.19	0	17,17,17	0.60	0
3	NAG	M	2	3	14,14,15	0.38	0	17,19,21	1.09	1 (5%)
3	GAL	M	3	3	11,11,12	0.68	0	15,15,17	1.29	2 (13%)
3	SIA	M	4	3	20,20,21	2.04	2 (10%)	24,28,31	1.92	7 (29%)
3	GAL	N	1	3	12,12,12	0.24	0	17,17,17	0.52	0
3	NAG	N	2	3	14,14,15	0.41	0	17,19,21	0.49	0
3	GAL	N	3	3	11,11,12	0.69	0	15,15,17	1.27	2 (13%)
3	SIA	N	4	3	20,20,21	2.05	2 (10%)	24,28,31	1.92	7 (29%)
3	GAL	O	1	3	12,12,12	0.13	0	17,17,17	0.48	0
3	NAG	O	2	3	14,14,15	0.41	0	17,19,21	0.87	1 (5%)
3	GAL	O	3	3	11,11,12	0.69	0	15,15,17	1.28	2 (13%)
3	SIA	O	4	3	20,20,21	2.02	2 (10%)	24,28,31	1.91	7 (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
2	NAG	G	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	3/6/23/26	0/1/1/1
3	GAL	J	1	3	-	0/2/22/22	0/1/1/1
3	NAG	J	2	3	-	1/6/23/26	0/1/1/1
3	GAL	J	3	3	-	1/2/19/22	0/1/1/1
3	SIA	J	4	3	-	3/18/34/38	0/1/1/1
3	GAL	K	1	3	-	0/2/22/22	0/1/1/1
3	NAG	K	2	3	-	1/6/23/26	0/1/1/1
3	GAL	K	3	3	-	1/2/19/22	0/1/1/1
3	SIA	K	4	3	-	3/18/34/38	0/1/1/1
3	GAL	L	1	3	-	0/2/22/22	0/1/1/1
3	NAG	L	2	3	-	1/6/23/26	0/1/1/1
3	GAL	L	3	3	-	1/2/19/22	0/1/1/1
3	SIA	L	4	3	-	3/18/34/38	0/1/1/1
3	GAL	M	1	3	-	0/2/22/22	0/1/1/1
3	NAG	M	2	3	-	3/6/23/26	0/1/1/1
3	GAL	M	3	3	-	1/2/19/22	0/1/1/1
3	SIA	M	4	3	-	3/18/34/38	0/1/1/1
3	GAL	N	1	3	-	1/2/22/22	0/1/1/1
3	NAG	N	2	3	-	3/6/23/26	0/1/1/1
3	GAL	N	3	3	-	1/2/19/22	0/1/1/1
3	SIA	N	4	3	-	3/18/34/38	0/1/1/1
3	GAL	O	1	3	-	0/2/22/22	0/1/1/1
3	NAG	O	2	3	-	1/6/23/26	0/1/1/1
3	GAL	O	3	3	-	1/2/19/22	0/1/1/1
3	SIA	O	4	3	-	3/18/34/38	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	4	SIA	C2-C1	7.79	1.59	1.52
3	L	4	SIA	C2-C1	7.77	1.59	1.52
3	M	4	SIA	C2-C1	7.76	1.59	1.52
3	J	4	SIA	C2-C1	7.74	1.59	1.52
3	K	4	SIA	C2-C1	7.73	1.59	1.52

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	2	NAG	O5-C1-C2	-5.33	102.87	111.29
2	H	2	NAG	C2-N2-C7	5.08	130.14	122.90
3	L	4	SIA	O1A-C1-C2	-4.66	111.57	122.57
3	N	4	SIA	O1A-C1-C2	-4.65	111.58	122.57
3	M	4	SIA	O1A-C1-C2	-4.64	111.62	122.57

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

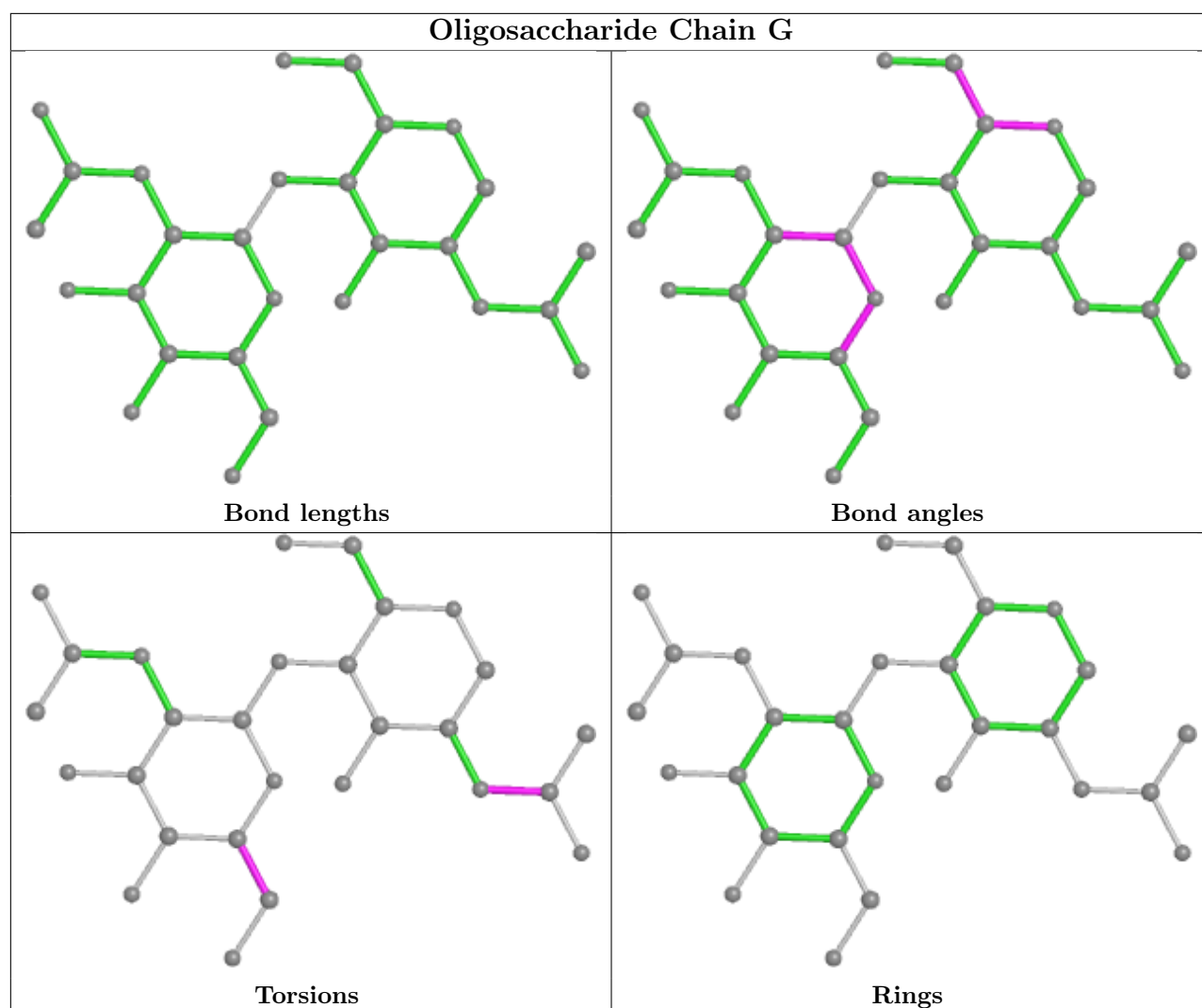
Mol	Chain	Res	Type	Atoms
2	G	1	NAG	C8-C7-N2-C2
2	G	1	NAG	O7-C7-N2-C2
2	H	1	NAG	C8-C7-N2-C2
2	H	1	NAG	O7-C7-N2-C2
2	I	2	NAG	O5-C5-C6-O6

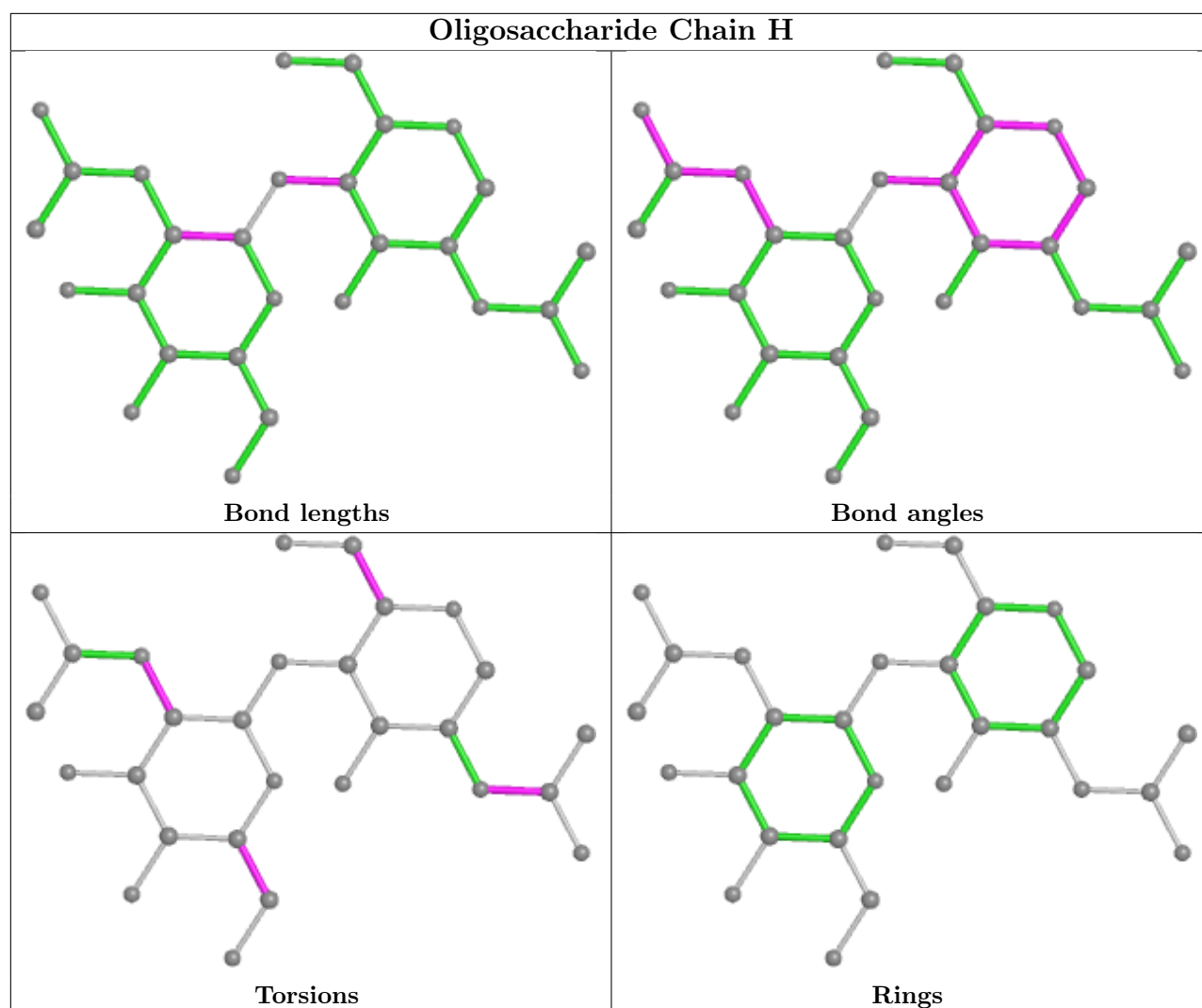
There are no ring outliers.

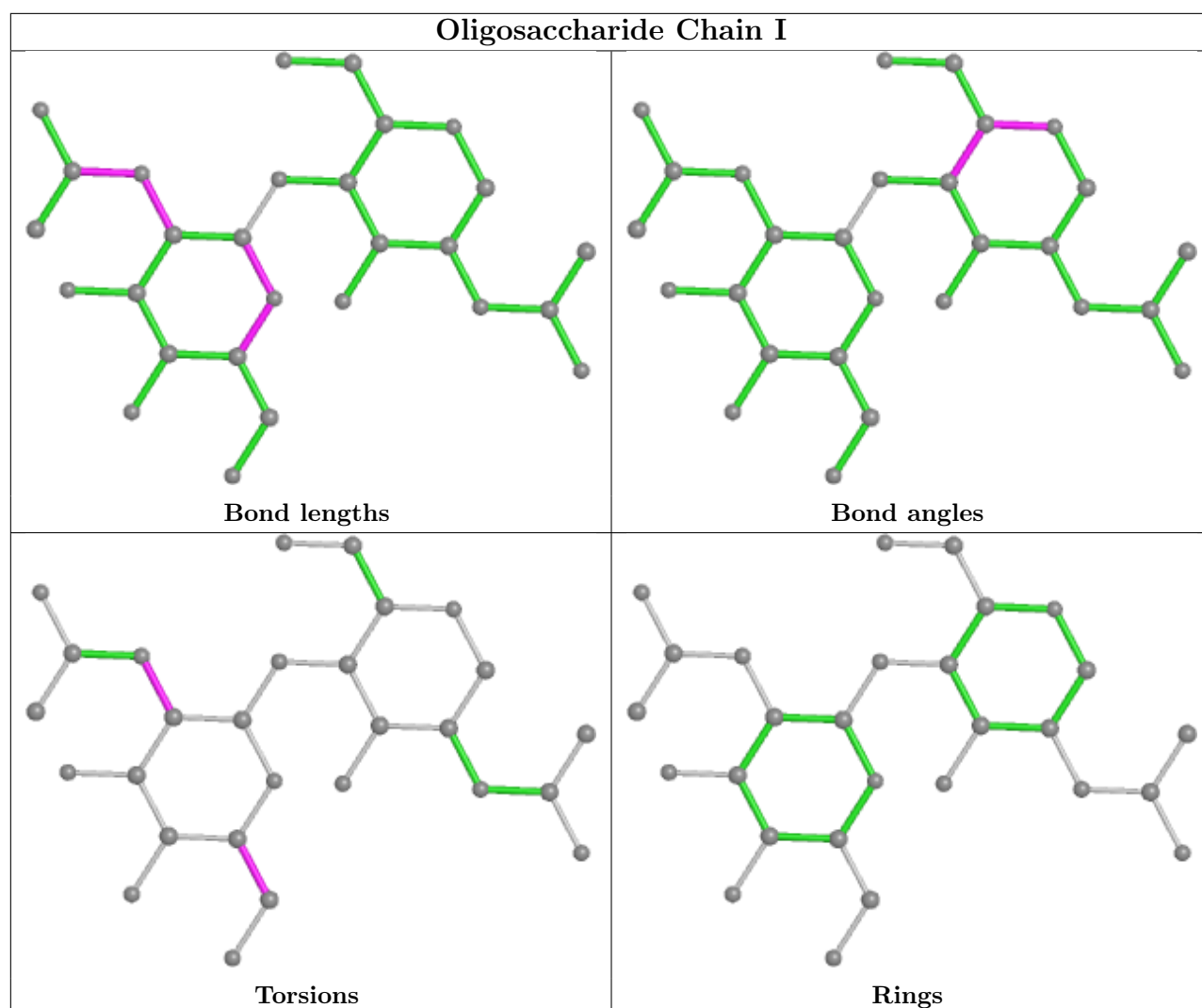
11 monomers are involved in 20 short contacts:

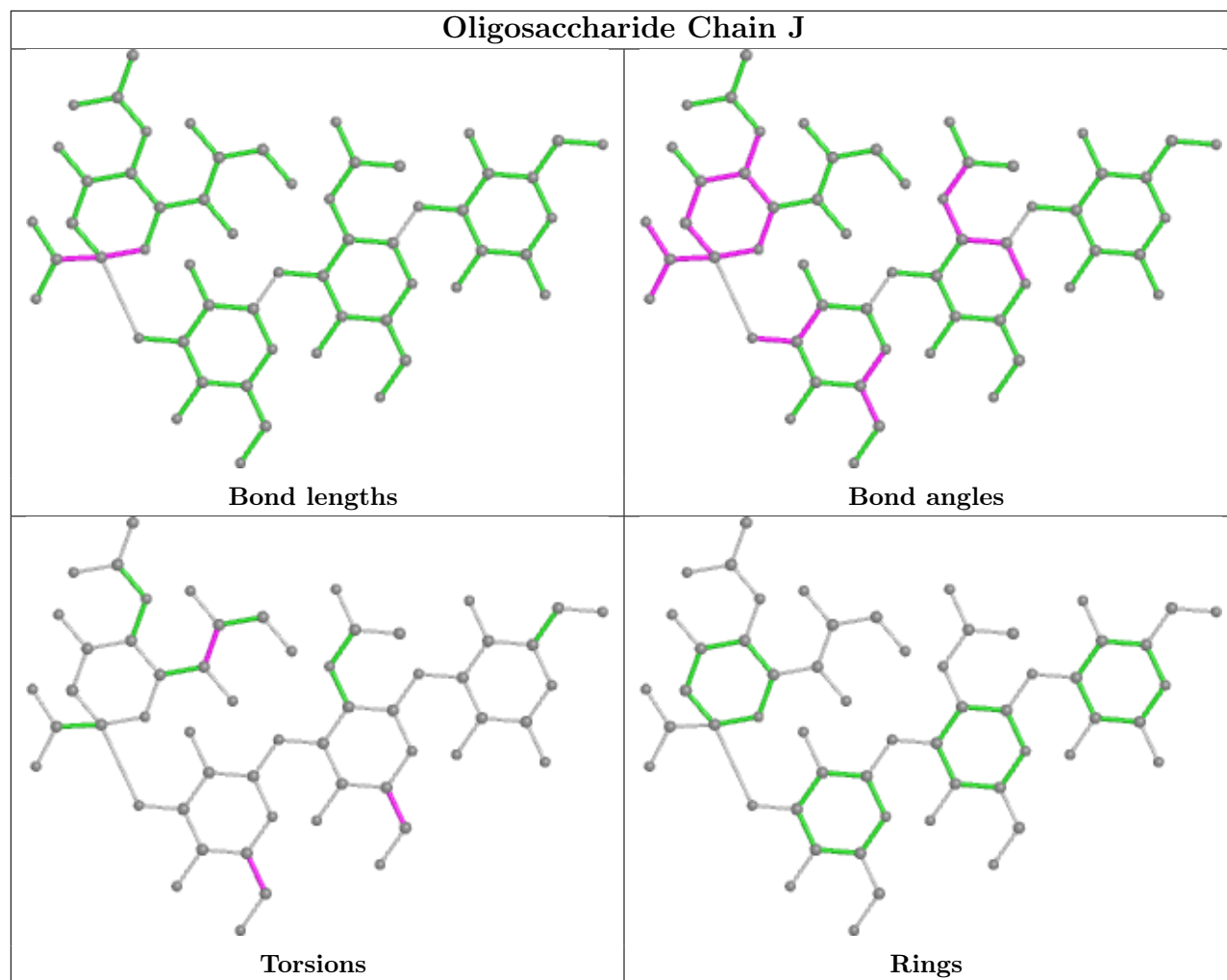
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	NAG	1	0
2	G	2	NAG	1	0
3	K	3	GAL	1	0
3	N	3	GAL	1	0
3	O	3	GAL	1	0
3	K	4	SIA	3	0
3	N	4	SIA	9	0
3	O	4	SIA	3	0
3	J	3	GAL	1	0
3	M	4	SIA	2	0
3	J	4	SIA	2	0

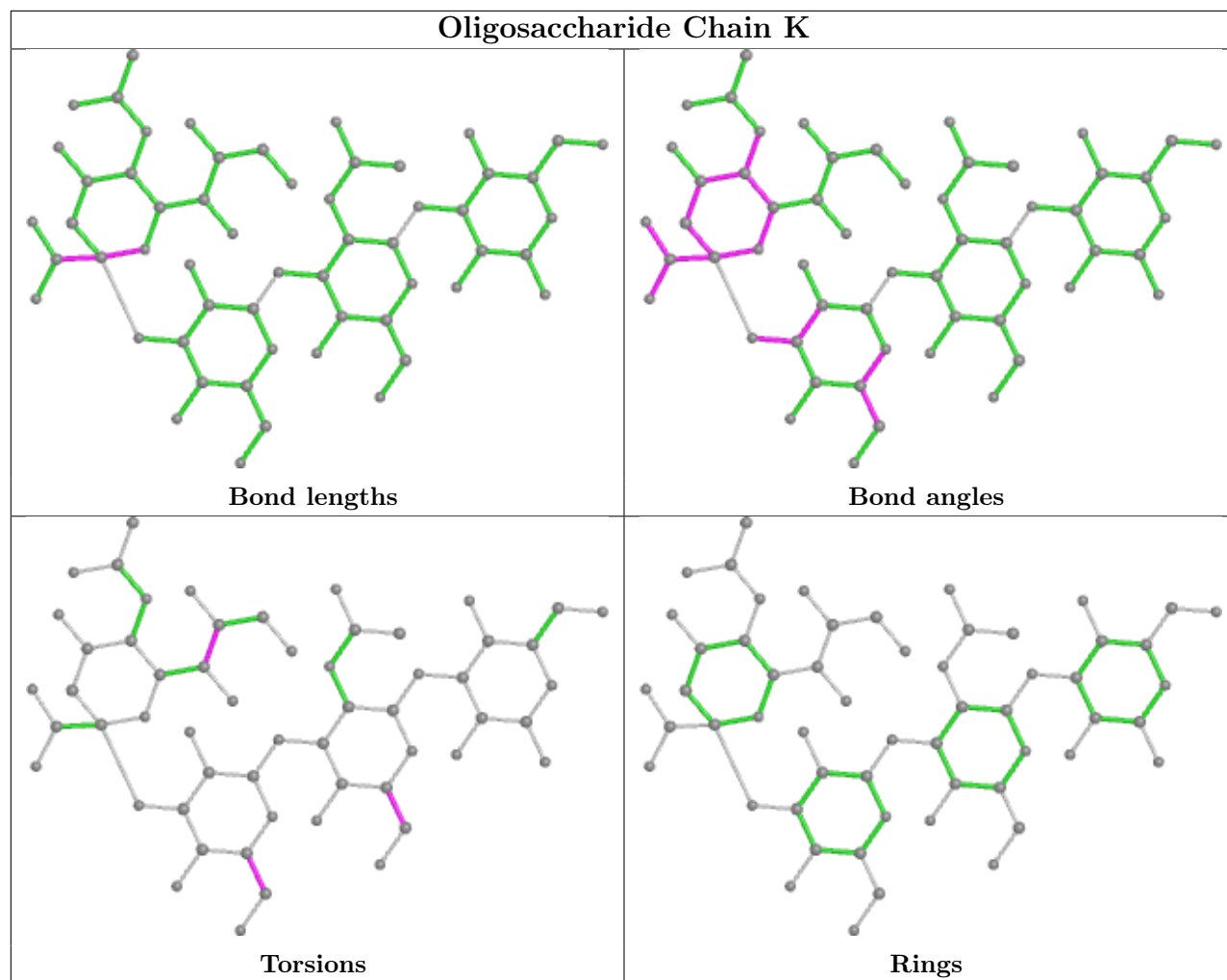
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

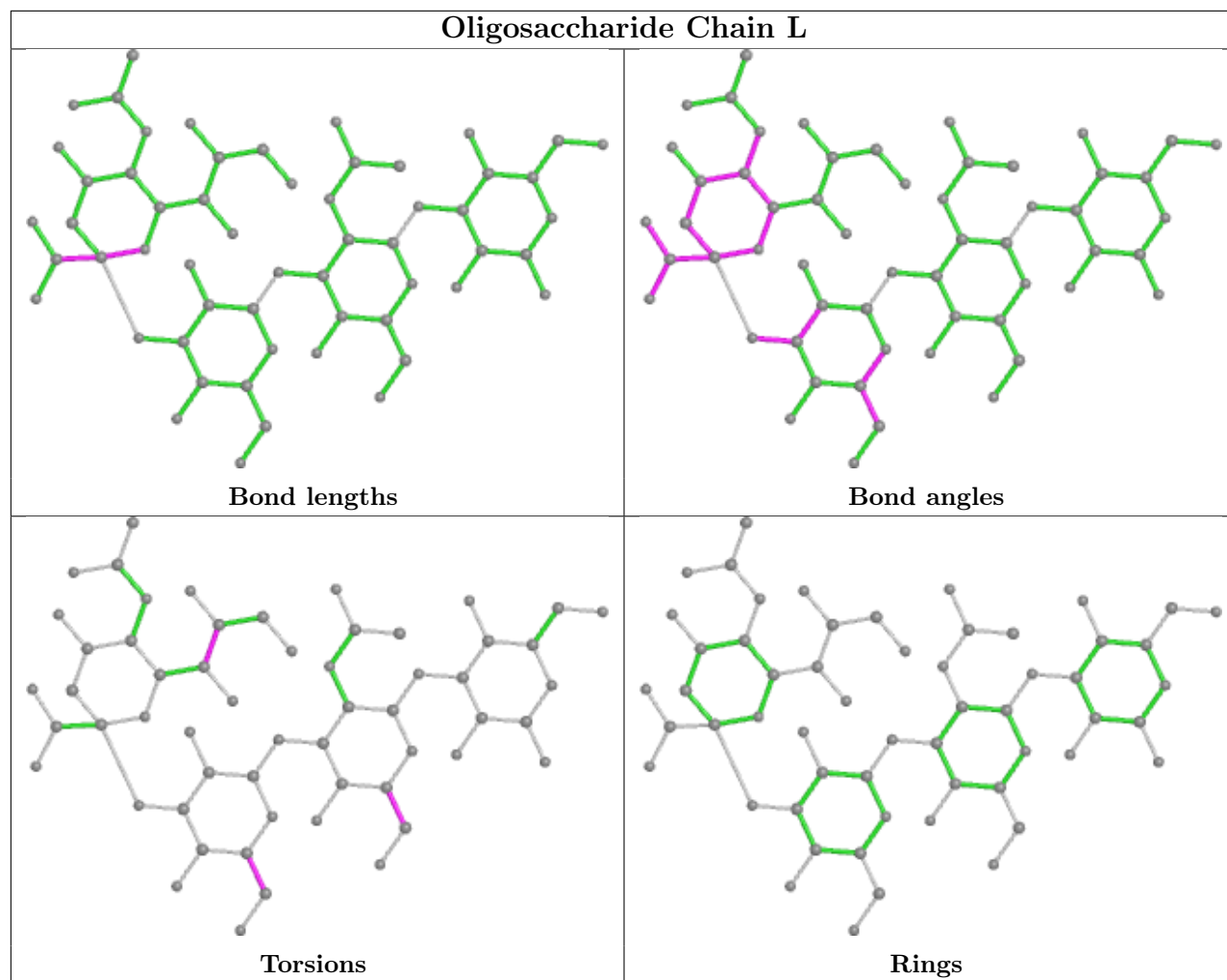


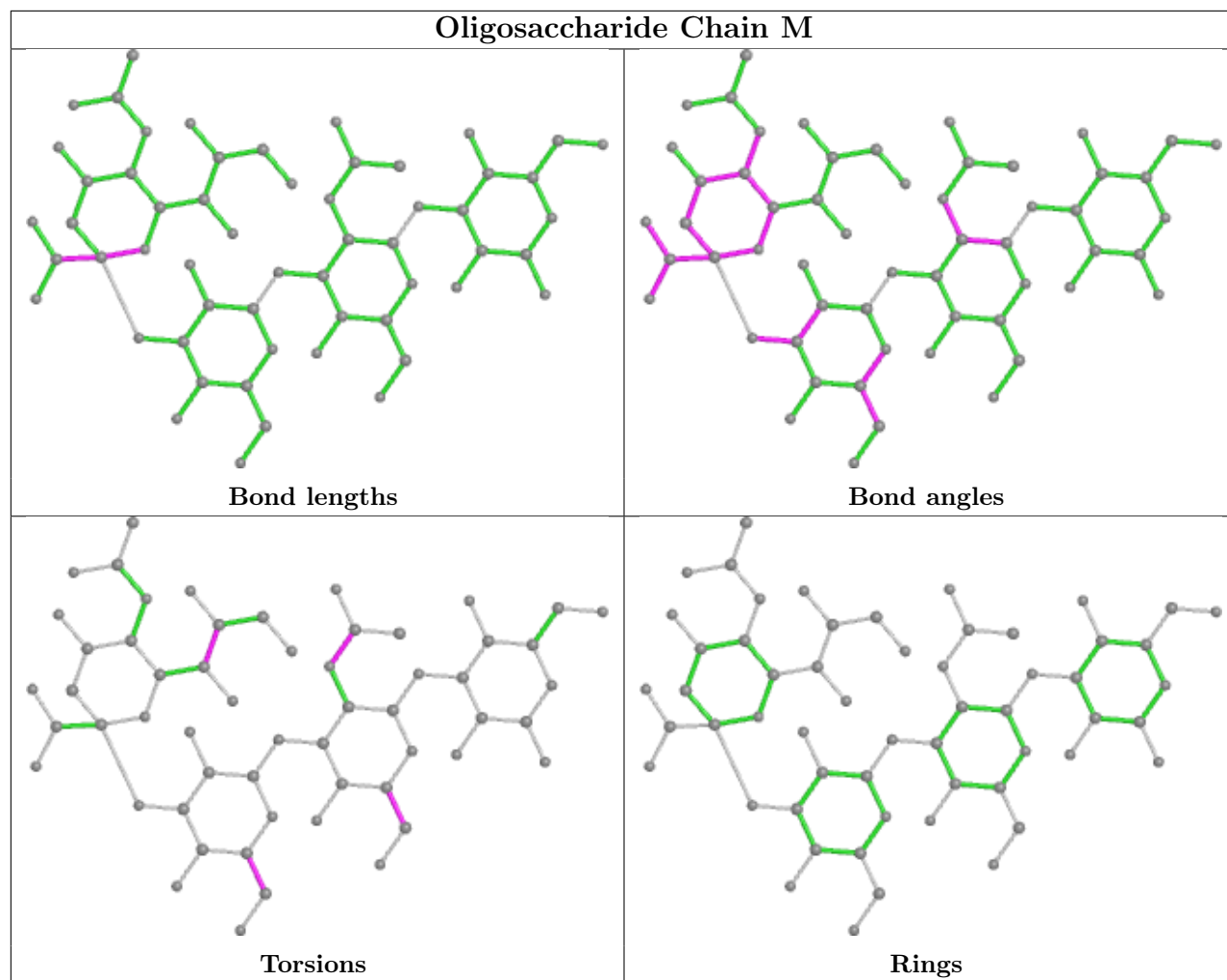


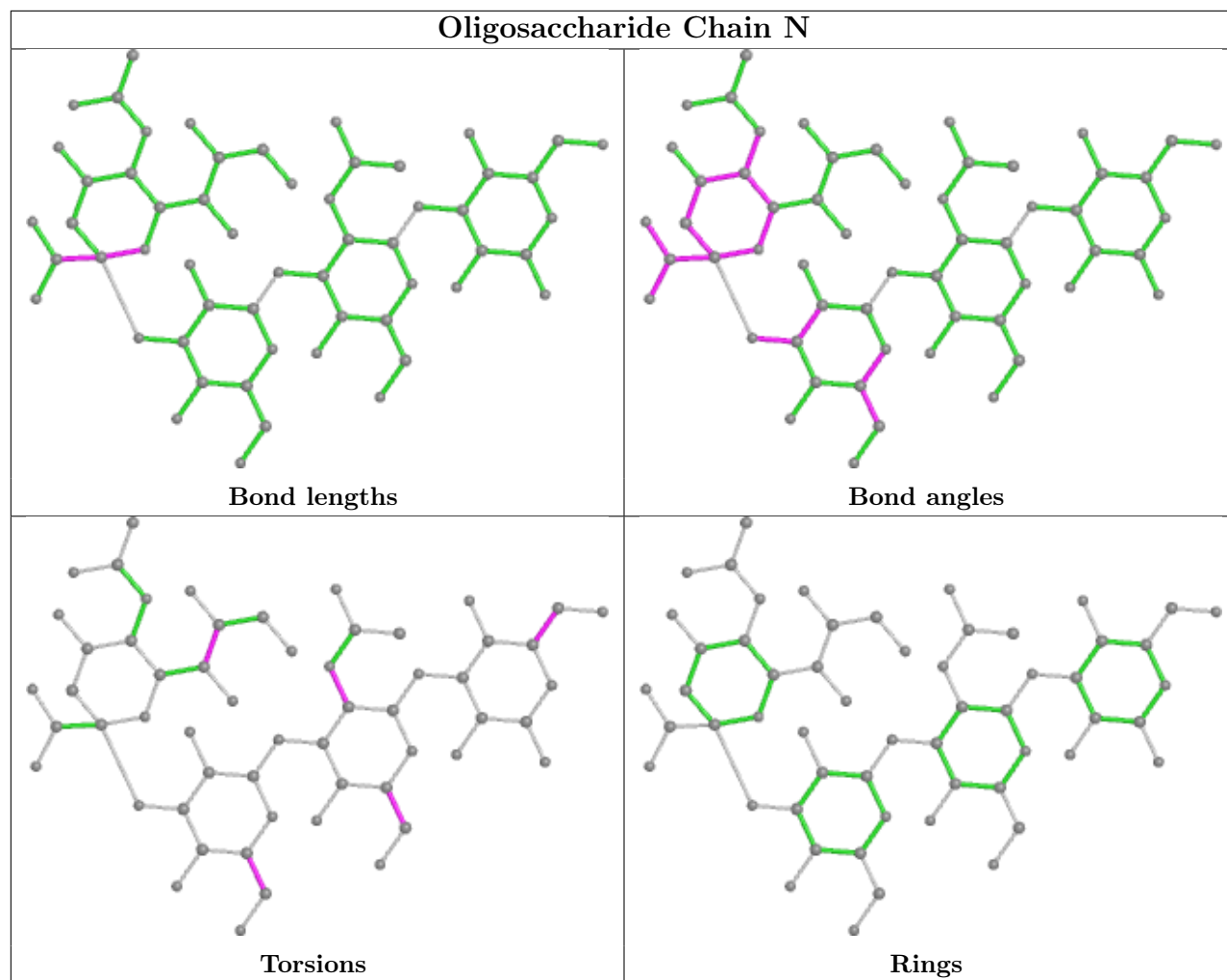


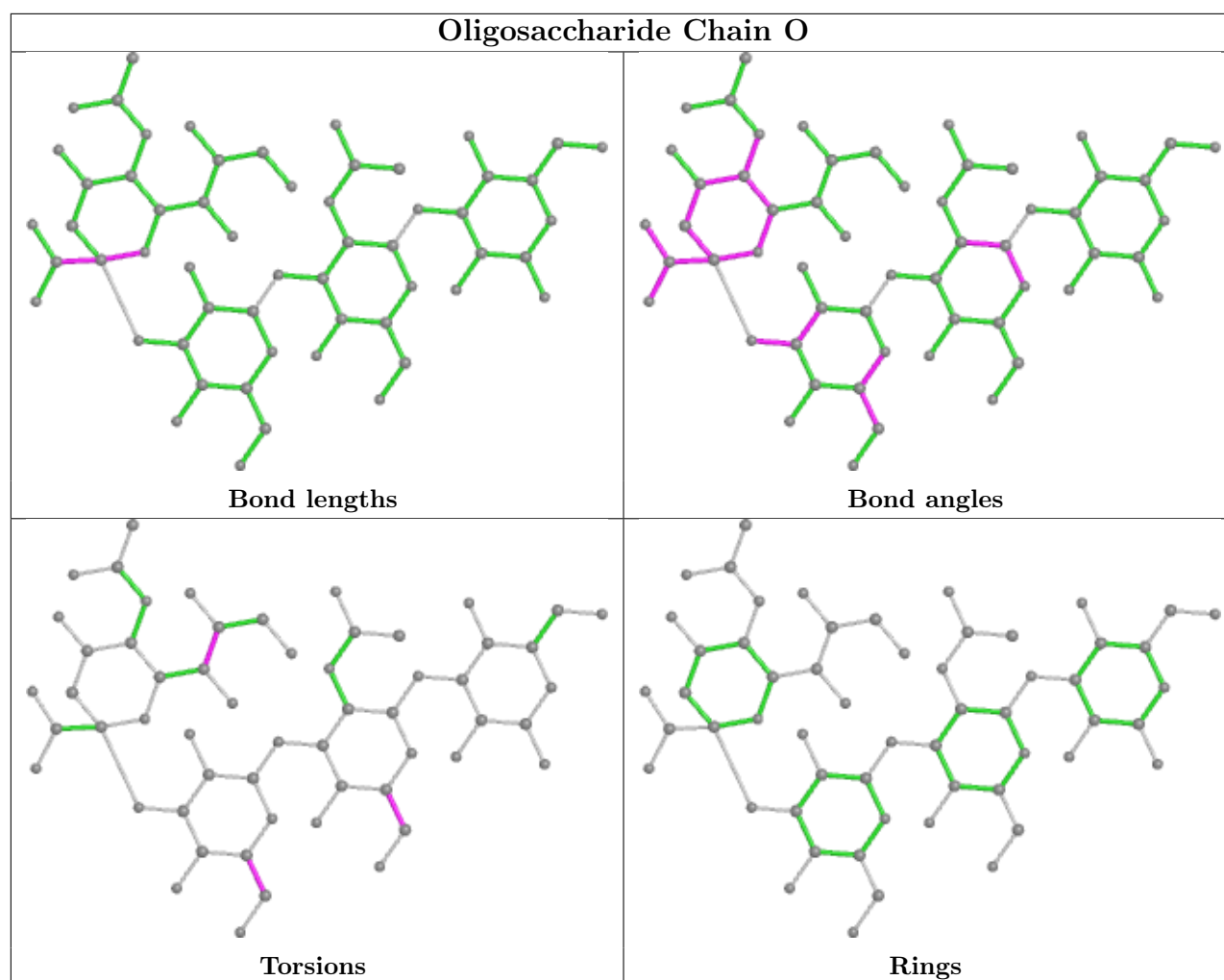












5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	702	1	14,14,15	1.99	4 (28%)	17,19,21	1.17	2 (11%)
4	NAG	B	701	1	14,14,15	0.39	0	17,19,21	1.58	3 (17%)
4	NAG	F	601	1	14,14,15	0.40	0	17,19,21	1.21	1 (5%)
4	NAG	D	601	1	14,14,15	2.00	4 (28%)	17,19,21	1.23	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	C	701	1	14,14,15	0.71	0	17,19,21	1.09	2 (11%)

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	C	702	1	-	2/6/23/26	0/1/1/1
4	NAG	B	701	1	-	2/6/23/26	0/1/1/1
4	NAG	F	601	1	-	5/6/23/26	0/1/1/1
4	NAG	D	601	1	-	0/6/23/26	0/1/1/1
4	NAG	C	701	1	-	2/6/23/26	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	601	NAG	O5-C1	4.57	1.51	1.43
4	C	702	NAG	O5-C1	4.48	1.50	1.43
4	D	601	NAG	C7-N2	3.65	1.46	1.34
4	C	702	NAG	C7-N2	3.59	1.46	1.34
4	D	601	NAG	C2-N2	2.42	1.50	1.46

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	701	NAG	O5-C1-C2	-3.90	105.13	111.29
4	B	701	NAG	C2-N2-C7	-3.22	118.31	122.90
4	B	701	NAG	C1-O5-C5	2.75	115.92	112.19
4	C	702	NAG	C2-N2-C7	-2.57	119.24	122.90
4	C	702	NAG	C8-C7-N2	2.44	120.23	116.10

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	601	NAG	C8-C7-N2-C2
4	F	601	NAG	O7-C7-N2-C2
4	C	701	NAG	C8-C7-N2-C2
4	C	701	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	C	702	NAG	O5-C5-C6-O6

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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	484/506 (95%)	0.72	47 (9%) 15 9	47, 77, 206, 236	0
1	B	485/506 (95%)	0.90	50 (10%) 13 8	64, 107, 214, 256	0
1	C	483/506 (95%)	0.43	27 (5%) 31 19	31, 64, 184, 205	0
1	D	484/506 (95%)	0.54	32 (6%) 26 15	38, 77, 174, 220	0
1	E	485/506 (95%)	0.73	36 (7%) 22 13	45, 86, 220, 240	0
1	F	486/506 (96%)	1.11	66 (13%) 8 5	75, 127, 231, 259	0
All	All	2907/3036 (95%)	0.74	258 (8%) 17 10	31, 93, 212, 259	0

The worst 5 of 258 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	111	PHE	5.4
1	A	356	SER	5.3
1	A	6	GLY	5.2
1	F	478	MET	4.8
1	C	316	GLY	4.5

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](#)

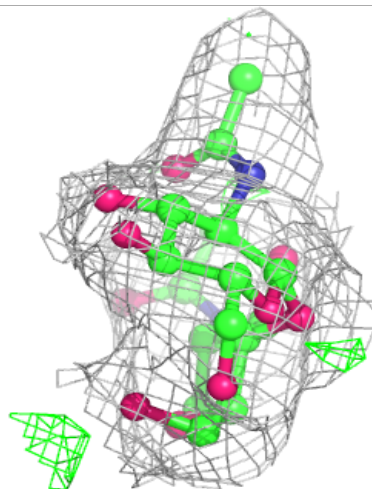
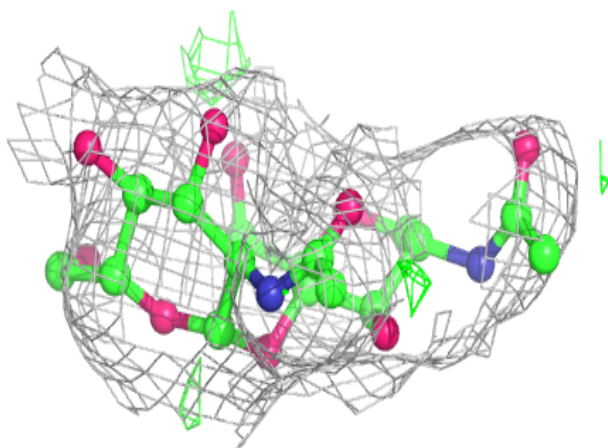
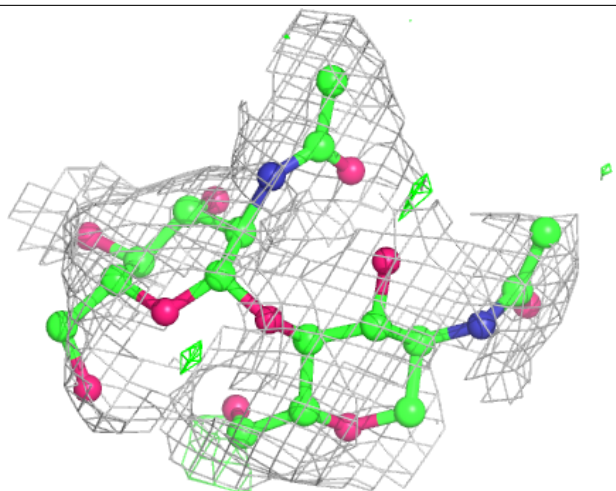
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GAL	N	1	12/12	0.28	0.15	119,128,135,137	0
3	GAL	O	1	12/12	0.32	0.13	119,128,135,137	0
3	NAG	O	2	14/15	0.42	0.16	106,114,122,126	0
3	GAL	L	1	12/12	0.50	0.10	119,128,135,137	0
3	NAG	N	2	14/15	0.51	0.14	106,114,122,126	0
3	GAL	M	1	12/12	0.54	0.12	119,128,135,137	0
3	GAL	K	1	12/12	0.57	0.11	119,128,135,137	0
2	NAG	G	2	14/15	0.58	0.15	64,122,139,144	0
2	NAG	H	2	14/15	0.61	0.15	82,107,124,124	0
2	NAG	I	2	14/15	0.63	0.15	99,140,169,174	0
3	GAL	J	1	12/12	0.66	0.12	119,128,135,137	0
3	NAG	L	2	14/15	0.68	0.12	106,114,122,126	0
3	GAL	O	3	11/12	0.68	0.15	68,76,87,90	0
3	GAL	N	3	11/12	0.69	0.12	68,76,87,90	0
3	NAG	K	2	14/15	0.69	0.13	106,114,122,126	0
3	NAG	J	2	14/15	0.76	0.13	106,114,122,126	0
3	NAG	M	2	14/15	0.78	0.12	106,114,122,126	0
3	SIA	N	4	20/21	0.79	0.12	49,64,82,83	0
2	NAG	I	1	14/15	0.81	0.12	80,105,140,142	0
3	SIA	O	4	20/21	0.83	0.14	49,64,82,83	0
2	NAG	G	1	14/15	0.84	0.14	83,99,123,137	0
3	GAL	J	3	11/12	0.86	0.12	68,76,87,90	0
2	NAG	H	1	14/15	0.87	0.15	51,85,109,110	0
3	GAL	M	3	11/12	0.87	0.10	68,76,87,90	0
3	GAL	L	3	11/12	0.88	0.09	68,76,87,90	0
3	SIA	M	4	20/21	0.92	0.09	49,64,82,83	0
3	GAL	K	3	11/12	0.93	0.09	68,76,87,90	0
3	SIA	J	4	20/21	0.93	0.11	49,64,82,83	0
3	SIA	L	4	20/21	0.93	0.12	49,64,82,83	0
3	SIA	K	4	20/21	0.95	0.09	49,64,82,83	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.

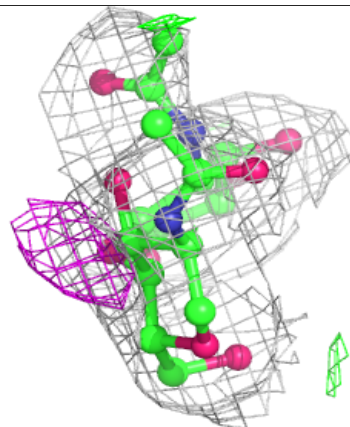
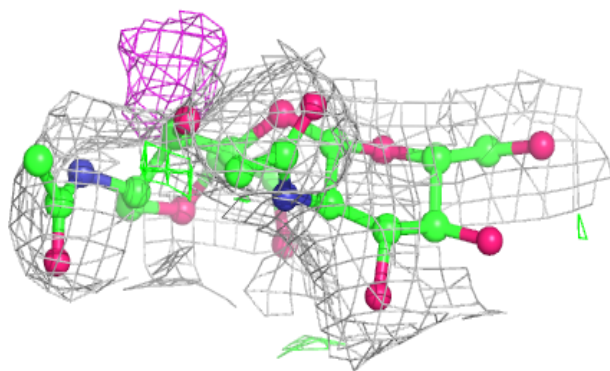
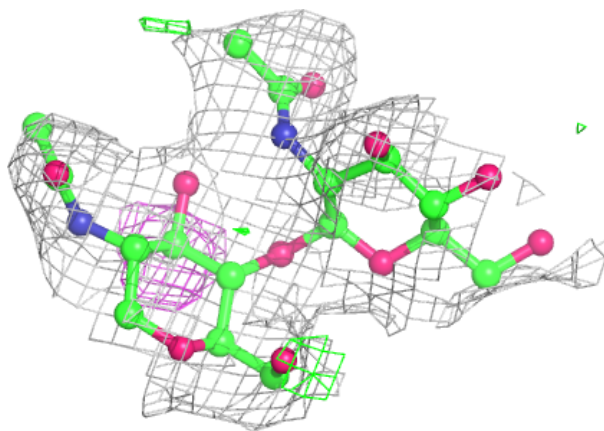
Electron density around Chain G:

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

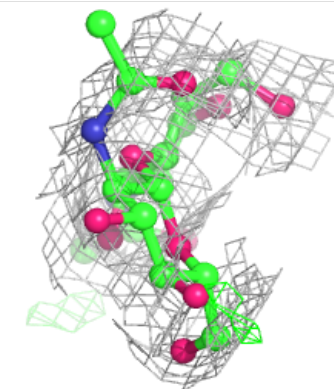
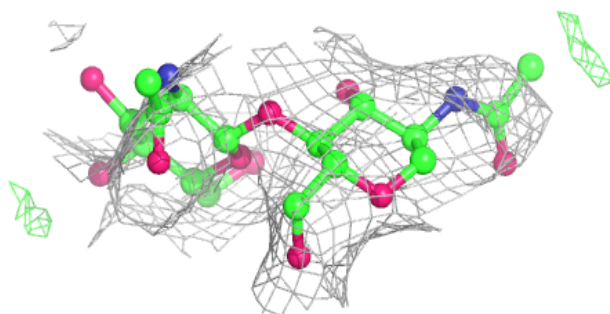
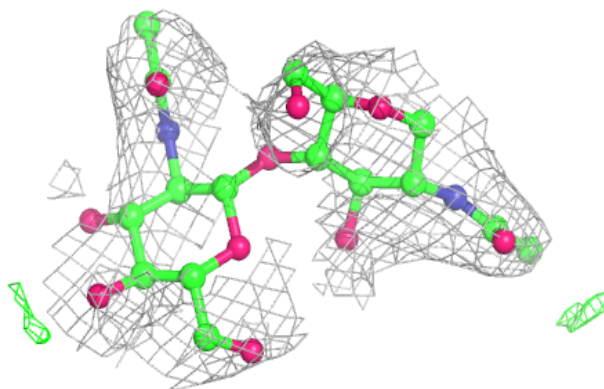


Electron density around Chain H:

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

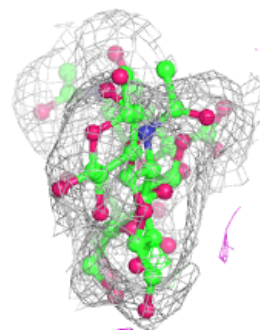
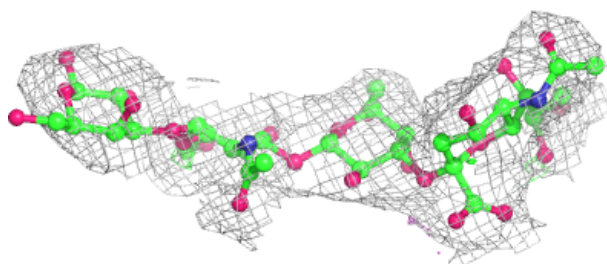
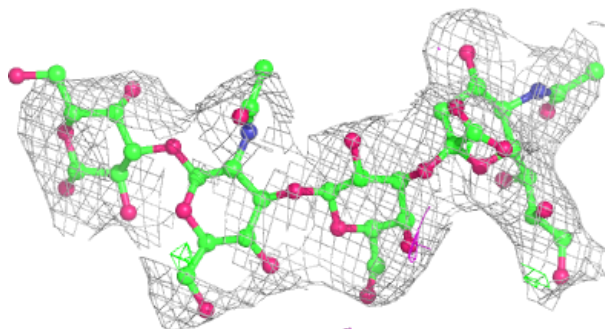
**Electron density around Chain I:**

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and green (positive)

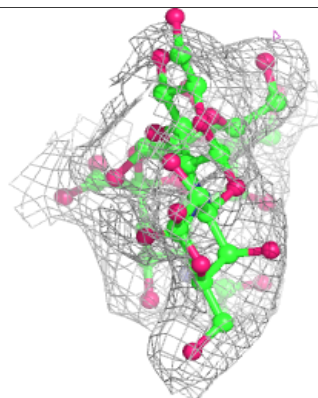
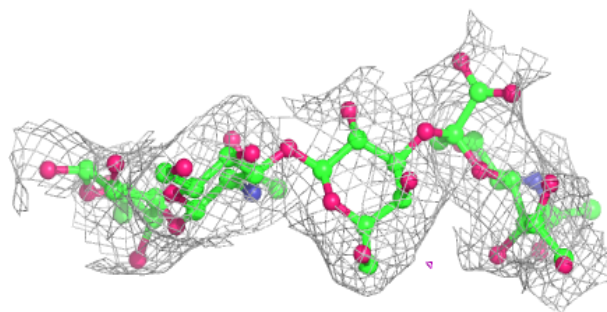
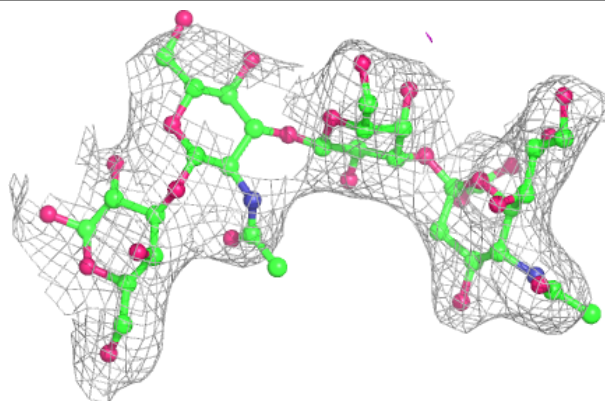


Electron density around Chain J:

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and green (positive)

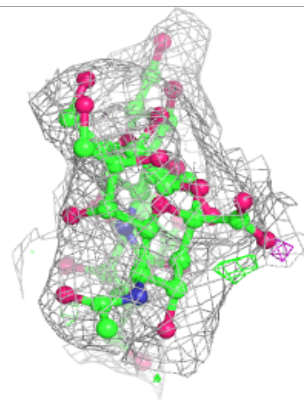
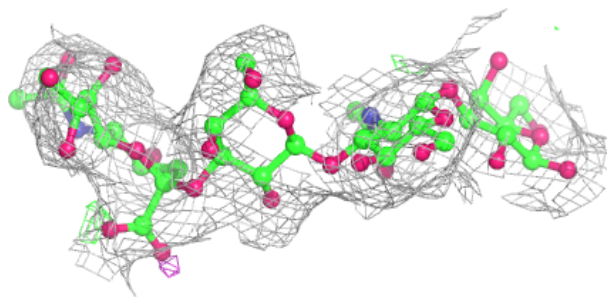
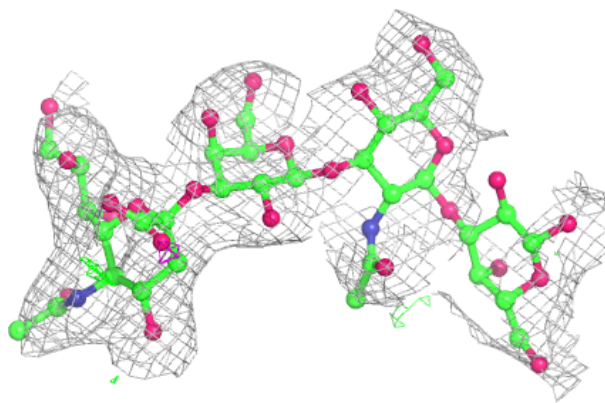
**Electron density around Chain K:**

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and green (positive)

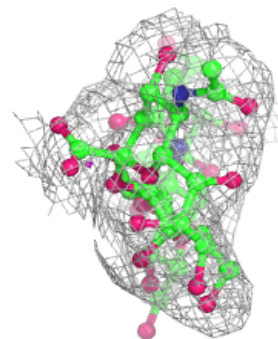
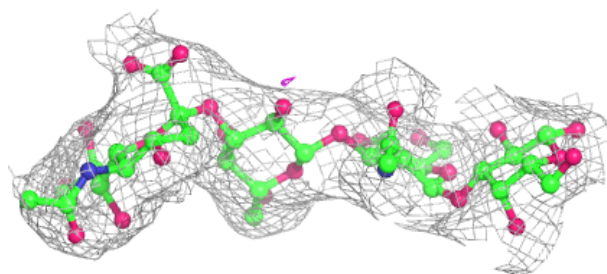
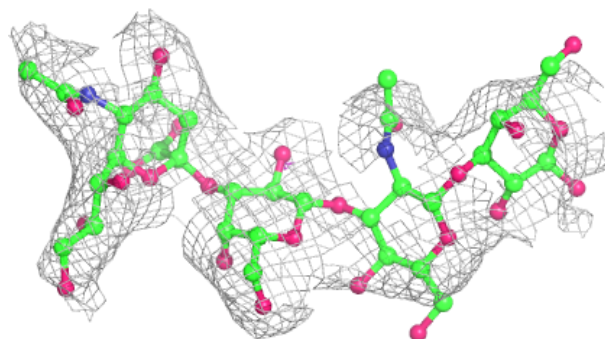


Electron density around Chain L:

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

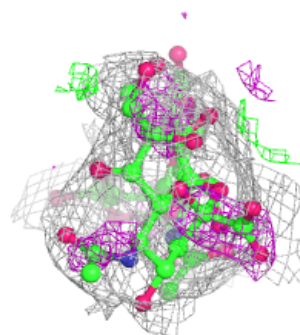
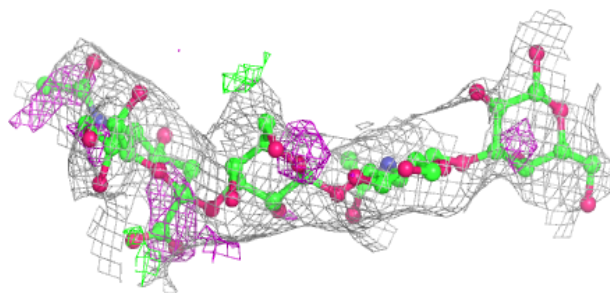
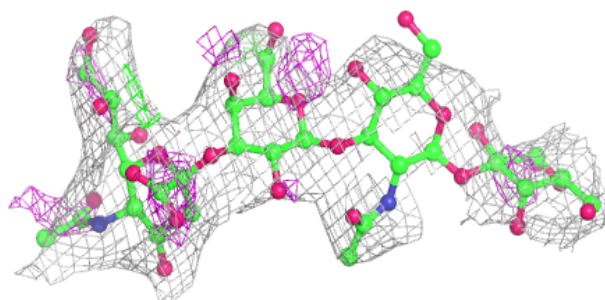
**Electron density around Chain M:**

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

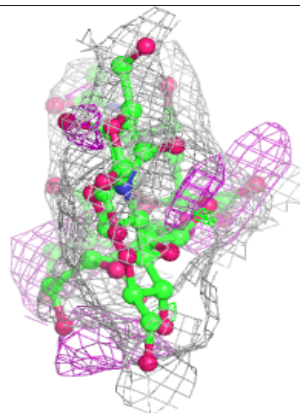
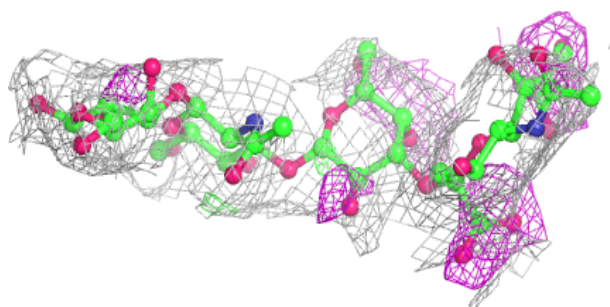
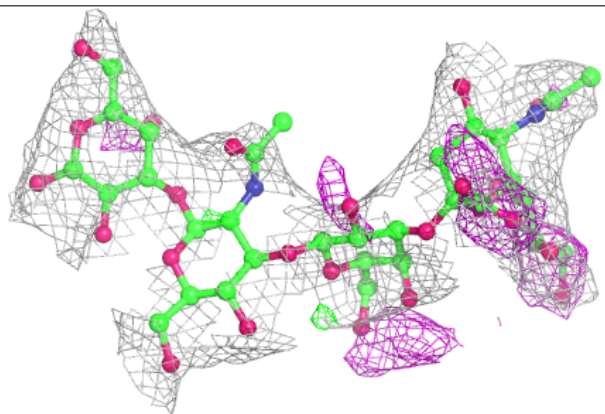


Electron density around Chain N:

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

**Electron density around Chain O:**

$2mF_o-DF_c$ (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
4	NAG	D	601	14/15	0.26	0.15	126,154,178,179	0
4	NAG	C	702	14/15	0.66	0.14	125,142,158,166	0
4	NAG	B	701	14/15	0.76	0.17	107,142,155,156	0
4	NAG	F	601	14/15	0.81	0.15	98,115,132,140	0
4	NAG	C	701	14/15	0.88	0.11	76,91,103,110	0

6.5 Other polymers [i](#)

There are no such residues in this entry.