



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 05:19 PM UTC

PDB ID : 7JPD / pdb_00007jpd
Title : Crystal structure of the trimeric full length mature hemagglutinin from influenza A virus A/Fort Monmouth/1/1947
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2020-08-07
Resolution : 2.95 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

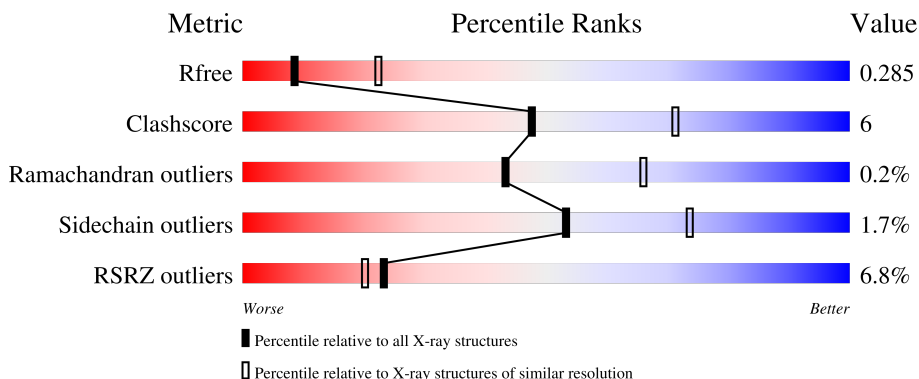
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	329	 7% 85% 13% .
1	B	329	 6% 84% 14% ..
1	C	329	 3% 83% 15% .
1	D	329	 5% 82% 16% .
1	E	329	 4% 82% 16% .

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Mol	Chain	Length	Quality of chain
1	F	329	 6% 83% 14% 6%
2	a	170	 10% 84% 10% 6%
2	b	170	 6% 82% 11% 6%
2	c	170	 5% 81% 12% 6%
2	d	170	 6% 79% 14% 6%
2	e	170	 15% 82% 11% 6%
2	f	170	 12% 85% 8% 6%
3	G	3	 33% 67%
4	H	2	 100%
4	I	2	 100%
4	K	2	 50% 50%
4	M	2	 50% 50%
4	O	2	 100%
4	Q	2	 100%
5	J	5	 40% 60%
5	L	5	 40% 40% 20%
5	N	5	 40% 60%
5	P	5	 40% 60%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 22983 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 HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	323	2478	1555	429	482	12	0	0	0
1	B	323	2467	1546	427	482	12	0	0	0
1	C	323	2478	1556	434	476	12	0	0	0
1	D	323	2460	1544	427	477	12	0	0	0
1	E	323	2475	1552	429	482	12	0	0	0
1	F	320	2441	1539	424	466	12	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q20MG8
A	2	SER	-	expression tag	UNP Q20MG8
B	1	GLY	-	expression tag	UNP Q20MG8
B	2	SER	-	expression tag	UNP Q20MG8
C	1	GLY	-	expression tag	UNP Q20MG8
C	2	SER	-	expression tag	UNP Q20MG8
D	1	GLY	-	expression tag	UNP Q20MG8
D	2	SER	-	expression tag	UNP Q20MG8
E	1	GLY	-	expression tag	UNP Q20MG8
E	2	SER	-	expression tag	UNP Q20MG8
F	1	GLY	-	expression tag	UNP Q20MG8
F	2	SER	-	expression tag	UNP Q20MG8

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	a	160	1222	767	210	238	7	0	0	0
2	b	160	1221	765	211	239	6	0	0	0
2	c	160	1239	774	214	244	7	0	0	0
2	d	160	1233	772	213	241	7	0	0	0
2	e	160	1211	760	208	237	6	0	0	0
2	f	160	1203	757	206	233	7	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

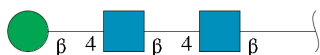
Chain	Residue	Modelled	Actual	Comment	Reference
a	495	PHE	-	expression tag	UNP Q20MG8
a	496	LEU	-	expression tag	UNP Q20MG8
a	497	VAL	-	expression tag	UNP Q20MG8
a	498	PRO	-	expression tag	UNP Q20MG8
a	499	ARG	-	expression tag	UNP Q20MG8
b	495	PHE	-	expression tag	UNP Q20MG8
b	496	LEU	-	expression tag	UNP Q20MG8
b	497	VAL	-	expression tag	UNP Q20MG8
b	498	PRO	-	expression tag	UNP Q20MG8
b	499	ARG	-	expression tag	UNP Q20MG8
c	495	PHE	-	expression tag	UNP Q20MG8
c	496	LEU	-	expression tag	UNP Q20MG8
c	497	VAL	-	expression tag	UNP Q20MG8
c	498	PRO	-	expression tag	UNP Q20MG8
c	499	ARG	-	expression tag	UNP Q20MG8
d	495	PHE	-	expression tag	UNP Q20MG8
d	496	LEU	-	expression tag	UNP Q20MG8
d	497	VAL	-	expression tag	UNP Q20MG8
d	498	PRO	-	expression tag	UNP Q20MG8
d	499	ARG	-	expression tag	UNP Q20MG8
e	495	PHE	-	expression tag	UNP Q20MG8
e	496	LEU	-	expression tag	UNP Q20MG8
e	497	VAL	-	expression tag	UNP Q20MG8
e	498	PRO	-	expression tag	UNP Q20MG8
e	499	ARG	-	expression tag	UNP Q20MG8
f	495	PHE	-	expression tag	UNP Q20MG8
f	496	LEU	-	expression tag	UNP Q20MG8
f	497	VAL	-	expression tag	UNP Q20MG8

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Chain	Residue	Modelled	Actual	Comment	Reference
f	498	PRO	-	expression tag	UNP Q20MG8
f	499	ARG	-	expression tag	UNP Q20MG8

- Molecule 3 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.



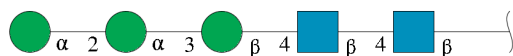
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	3	39	22	2	15	0	0	0

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



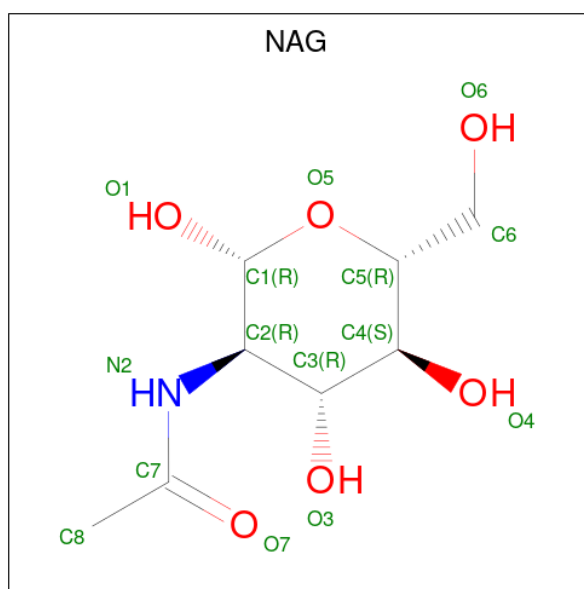
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	H	2	28	16	2	10	0	0	0
4	I	2	28	16	2	10	0	0	0
4	K	2	28	16	2	10	0	0	0
4	M	2	28	16	2	10	0	0	0
4	O	2	28	16	2	10	0	0	0
4	Q	2	28	16	2	10	0	0	0

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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
			Total	C	N	O			
5	J	5	61	34	2	25	0	0	0
5	L	5	61	34	2	25	0	0	0
5	N	5	61	34	2	25	0	0	0
5	P	5	61	34	2	25	0	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



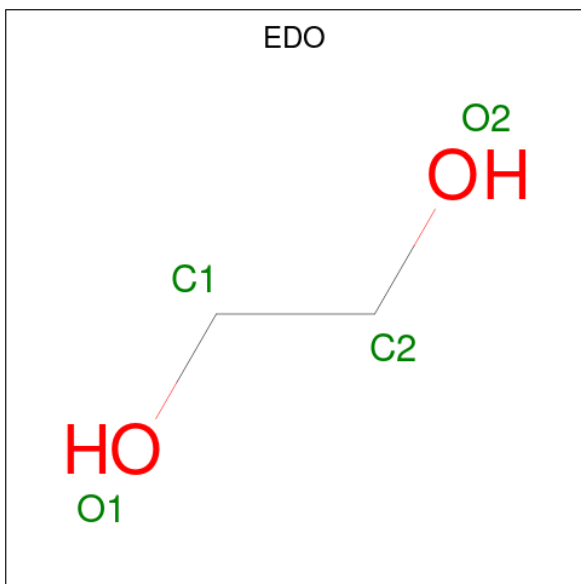
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	A	1	14	8	1	5	0	0
6	B	1	14	8	1	5	0	0
6	B	1	14	8	1	5	0	0
6	B	1	14	8	1	5	0	0
6	C	1	14	8	1	5	0	0

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

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	Total 4	C 2	O 2	0	0

- Molecule 8 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	I		
8	A	13	Total 13	I 13	0	0
8	B	9	Total 9	I 9	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	b	1	Total I 1 1	0	0
8	C	10	Total I 10 10	0	0
8	c	3	Total I 3 3	0	0
8	D	12	Total I 12 12	0	0
8	d	1	Total I 1 1	0	0
8	E	12	Total I 12 12	0	0
8	e	2	Total I 2 2	0	0
8	F	13	Total I 13 13	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	21	Total O 21 21	0	0
9	a	10	Total O 10 10	0	0
9	B	22	Total O 22 22	0	0
9	b	7	Total O 7 7	0	0
9	C	19	Total O 19 19	0	0
9	c	3	Total O 3 3	0	0
9	D	20	Total O 20 20	0	0
9	d	7	Total O 7 7	0	0
9	E	31	Total O 31 31	0	0
9	e	12	Total O 12 12	0	0
9	F	11	Total O 11 11	0	0

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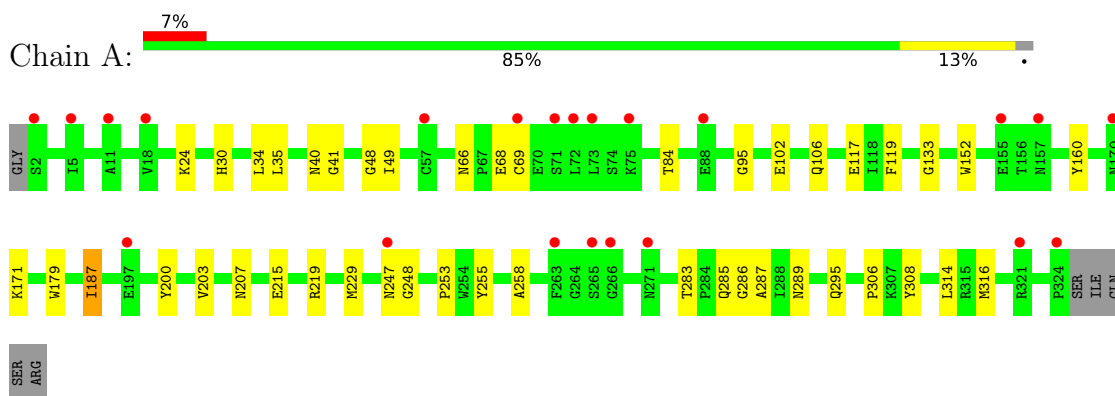
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	f	7	Total	O	0	0
			7	7		

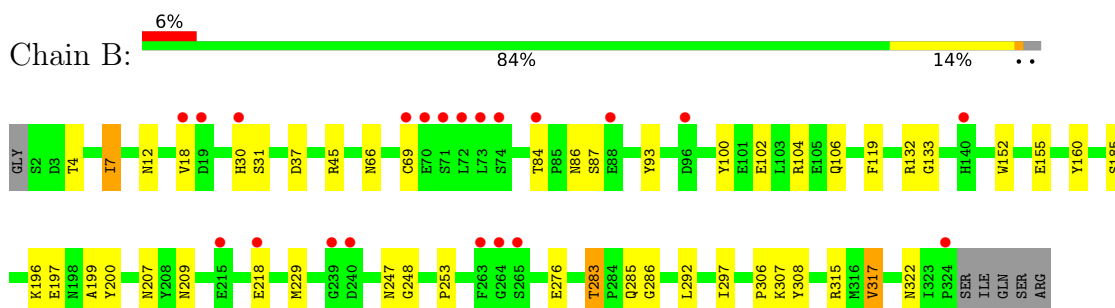
3 Residue-property plots

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

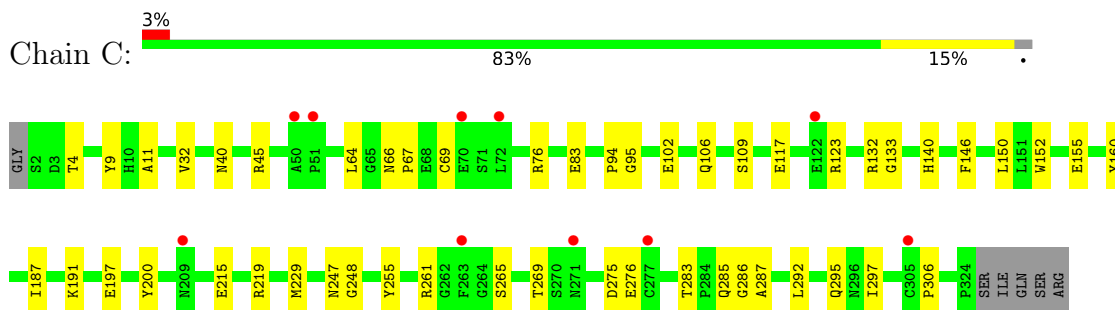
- Molecule 1: Hemagglutinin HA1 chain



- Molecule 1: Hemagglutinin HA1 chain

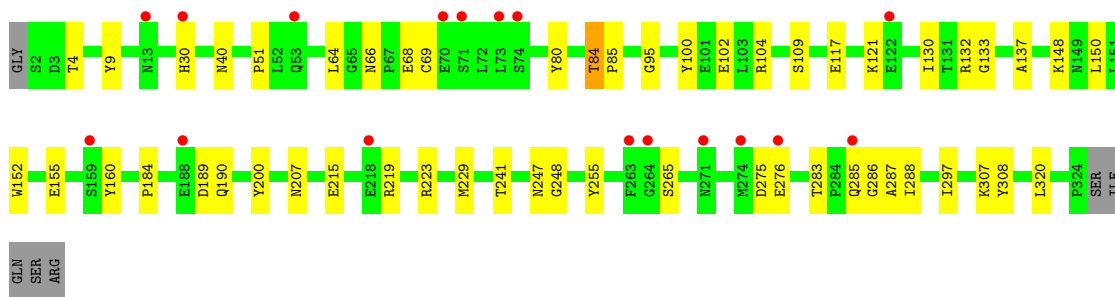


- Molecule 1: Hemagglutinin HA1 chain

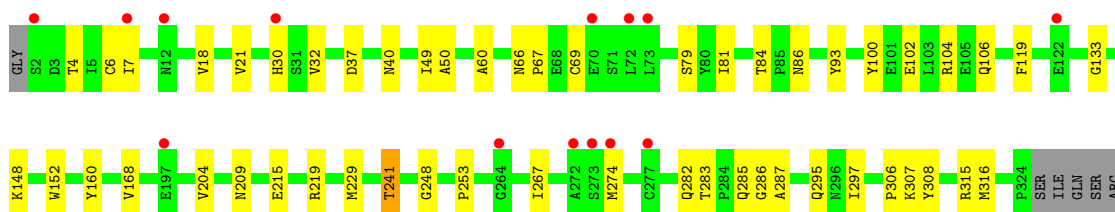
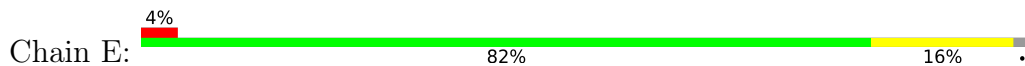


- Molecule 1: Hemagglutinin HA1 chain

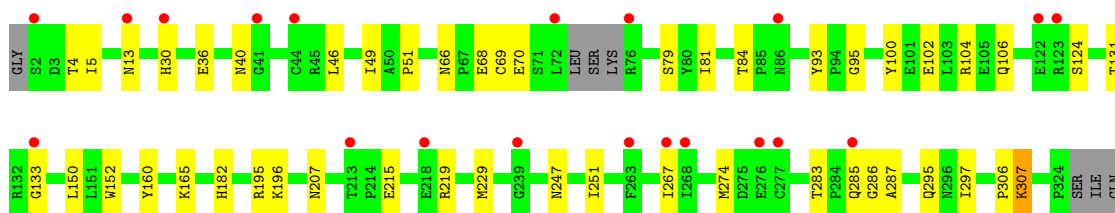
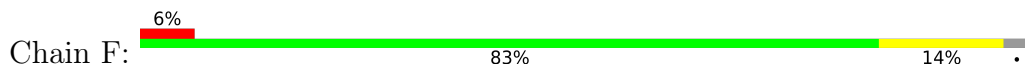




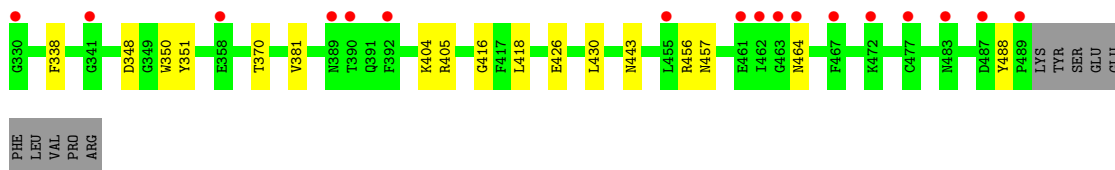
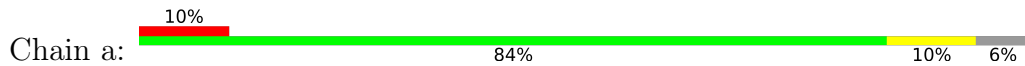
• Molecule 1: Hemagglutinin HA1 chain



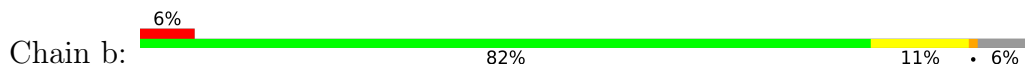
• Molecule 1: Hemagglutinin HA1 chain



• Molecule 2: Hemagglutinin HA2 chain

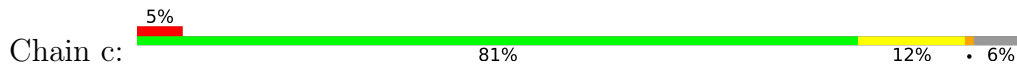


• Molecule 2: Hemagglutinin HA2 chain

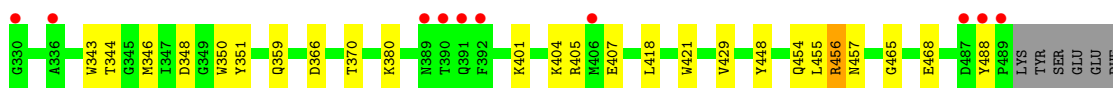
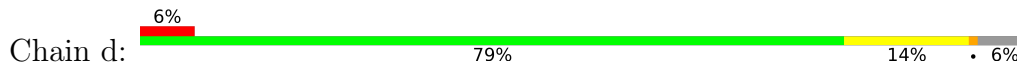


PHE
LEU
VAL
PRO
ARG

• Molecule 2: Hemagglutinin HA2 chain

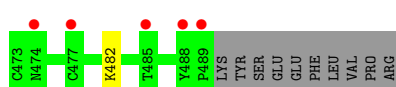
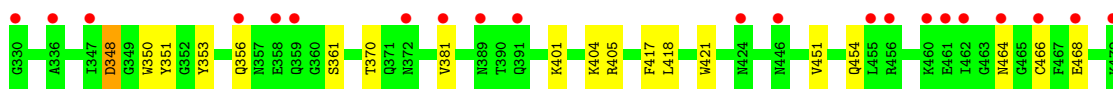
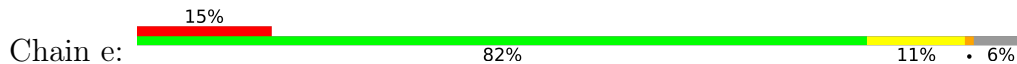


• Molecule 2: Hemagglutinin HA2 chain

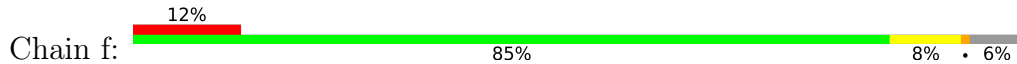


LEU
VAL
PRO
ARG

• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



TYR
SER
GLU
PHE
LEU
VAL
PRO
ARG

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



MAG1
MAG2
BMA3

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

Chain H:  100%

NAG1
NAG2

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

Chain I:  100%

NAG1
NAG2

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

Chain K:  50% 50%

NAG1
NAG2

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

Chain M:  50% 50%

NAG1
NAG2

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

Chain O:  100%

NAG1
NAG2

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

Chain Q:  100%

NAG1
NAG2

- Molecule 5: alpha-D-mannopyranose-(1-2)-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 J:  40% 60%



- Molecule 5: alpha-D-mannopyranose-(1-2)-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



- Molecule 5: alpha-D-mannopyranose-(1-2)-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



- Molecule 5: alpha-D-mannopyranose-(1-2)-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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	131.79Å 142.36Å 234.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.85 – 2.95 48.85 – 2.95	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.85-2.95) 98.2 (48.85-2.95)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.96Å)	Xtrriage
Refinement program	PHENIX dev-4274	Depositor
R, R_{free}	0.254 , 0.286 0.253 , 0.285	Depositor DCC
R_{free} test set	4463 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	57.4	Xtrriage
Anisotropy	0.284	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 28.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	22983	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.92% 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, EDO, MAN, IOD, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.14	0/2539	0.36	0/3464
1	B	0.17	0/2528	0.42	0/3452
1	C	0.14	0/2539	0.37	0/3463
1	D	0.15	0/2521	0.39	0/3442
1	E	0.15	0/2536	0.38	0/3460
1	F	0.16	0/2501	0.38	0/3412
2	a	0.14	0/1248	0.35	0/1689
2	b	0.16	0/1246	0.38	0/1686
2	c	0.14	0/1265	0.35	0/1711
2	d	0.14	0/1259	0.36	0/1703
2	e	0.16	0/1237	0.35	0/1677
2	f	0.14	0/1229	0.34	0/1666
All	All	0.15	0/22648	0.37	0/30825

There are no bond length outliers.

There are no bond angle outliers.

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	2478	0	2323	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2467	0	2291	34	0
1	C	2478	0	2333	34	0
1	D	2460	0	2291	34	0
1	E	2475	0	2313	37	0
1	F	2441	0	2301	32	0
2	a	1222	0	1093	13	0
2	b	1221	0	1086	14	0
2	c	1239	0	1111	13	0
2	d	1233	0	1105	16	0
2	e	1211	0	1069	16	0
2	f	1203	0	1056	12	0
3	G	39	0	34	1	0
4	H	28	0	25	0	0
4	I	28	0	25	0	0
4	K	28	0	25	1	0
4	M	28	0	25	1	0
4	O	28	0	25	0	0
4	Q	28	0	25	0	0
5	J	61	0	52	0	0
5	L	61	0	52	1	0
5	N	61	0	52	0	0
5	P	61	0	52	1	0
6	A	14	0	13	0	0
6	B	42	0	39	0	0
6	C	28	0	26	0	0
6	D	14	0	13	0	0
6	E	28	0	26	0	0
6	F	28	0	26	0	0
7	A	4	0	6	0	0
8	A	13	0	0	0	0
8	B	9	0	0	0	0
8	C	10	0	0	4	0
8	D	12	0	0	2	0
8	E	12	0	0	0	0
8	F	13	0	0	1	0
8	b	1	0	0	0	0
8	c	3	0	0	1	0
8	d	1	0	0	0	0
8	e	2	0	0	0	0
9	A	21	0	0	1	0
9	B	22	0	0	1	0
9	C	19	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	D	20	0	0	0	0
9	E	31	0	0	1	0
9	F	11	0	0	0	0
9	a	10	0	0	1	0
9	b	7	0	0	0	0
9	c	3	0	0	0	0
9	d	7	0	0	0	0
9	e	12	0	0	0	0
9	f	7	0	0	0	0
All	All	22983	0	20913	244	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 6.

The worst 5 of 244 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:50:ALA:HB1	1:E:274:MET:HE1	1.54	0.87
1:B:18:VAL:HG21	1:B:317:VAL:HG22	1.56	0.86
1:C:283:THR:HG22	1:C:285:GLN:H	1.48	0.79
2:f:348:ASP:OD1	2:f:348:ASP:N	2.15	0.78
1:D:283:THR:HG22	1:D:285:GLN:H	1.49	0.78

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	321/329 (98%)	313 (98%)	8 (2%)	0	100 100
1	B	321/329 (98%)	312 (97%)	9 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	321/329 (98%)	313 (98%)	8 (2%)	0	100	100
1	D	321/329 (98%)	312 (97%)	9 (3%)	0	100	100
1	E	321/329 (98%)	312 (97%)	9 (3%)	0	100	100
1	F	316/329 (96%)	308 (98%)	8 (2%)	0	100	100
2	a	158/170 (93%)	152 (96%)	5 (3%)	1 (1%)	21	45
2	b	158/170 (93%)	155 (98%)	2 (1%)	1 (1%)	21	45
2	c	158/170 (93%)	154 (98%)	3 (2%)	1 (1%)	21	45
2	d	158/170 (93%)	154 (98%)	3 (2%)	1 (1%)	21	45
2	e	158/170 (93%)	153 (97%)	5 (3%)	0	100	100
2	f	158/170 (93%)	153 (97%)	4 (2%)	1 (1%)	21	45
All	All	2869/2994 (96%)	2791 (97%)	73 (2%)	5 (0%)	43	66

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	a	456	ARG
2	b	456	ARG
2	c	456	ARG
2	d	456	ARG
2	f	456	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	267/289 (92%)	264 (99%)	3 (1%)	65	80
1	B	264/289 (91%)	257 (97%)	7 (3%)	39	64
1	C	266/289 (92%)	263 (99%)	3 (1%)	65	80
1	D	262/289 (91%)	259 (99%)	3 (1%)	65	80
1	E	266/289 (92%)	264 (99%)	2 (1%)	73	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	261/289 (90%)	257 (98%)	4 (2%)	57	76
2	a	120/146 (82%)	119 (99%)	1 (1%)	73	85
2	b	119/146 (82%)	117 (98%)	2 (2%)	53	73
2	c	124/146 (85%)	120 (97%)	4 (3%)	34	59
2	d	122/146 (84%)	117 (96%)	5 (4%)	27	53
2	e	117/146 (80%)	115 (98%)	2 (2%)	53	73
2	f	114/146 (78%)	112 (98%)	2 (2%)	51	72
All	All	2302/2610 (88%)	2264 (98%)	38 (2%)	53	73

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	32	VAL
1	F	307	LYS
1	E	241	THR
1	F	84	THR
2	f	369	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	d	371	GLN
2	e	354	HIS
2	f	354	HIS
2	e	355	HIS
1	D	30	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates i

35 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	1	3,1	14,14,15	0.29	0	17,19,21	0.61	0
3	NAG	G	2	3	14,14,15	0.28	0	17,19,21	0.42	0
3	BMA	G	3	3	11,11,12	1.10	2 (18%)	15,15,17	0.84	0
4	NAG	H	1	4,1	14,14,15	0.24	0	17,19,21	0.57	0
4	NAG	H	2	4	14,14,15	0.35	0	17,19,21	0.37	0
4	NAG	I	1	4,1	14,14,15	0.24	0	17,19,21	0.65	0
4	NAG	I	2	4	14,14,15	0.47	0	17,19,21	0.45	0
5	NAG	J	1	5,1	14,14,15	0.32	0	17,19,21	0.64	1 (5%)
5	NAG	J	2	5	14,14,15	0.21	0	17,19,21	0.48	0
5	BMA	J	3	5	11,11,12	0.99	0	15,15,17	0.67	0
5	MAN	J	4	5	11,11,12	1.18	1 (9%)	15,15,17	1.47	2 (13%)
5	MAN	J	5	5	11,11,12	1.47	2 (18%)	15,15,17	2.15	3 (20%)
4	NAG	K	1	4,1	14,14,15	0.30	0	17,19,21	0.71	0
4	NAG	K	2	4	14,14,15	0.27	0	17,19,21	0.54	0
5	NAG	L	1	5,1	14,14,15	0.33	0	17,19,21	0.65	1 (5%)
5	NAG	L	2	5	14,14,15	0.39	0	17,19,21	0.54	0
5	BMA	L	3	5	11,11,12	0.85	0	15,15,17	0.75	0
5	MAN	L	4	5	11,11,12	1.16	2 (18%)	15,15,17	1.09	1 (6%)
5	MAN	L	5	5	11,11,12	0.89	1 (9%)	15,15,17	2.09	3 (20%)
4	NAG	M	1	4,1	14,14,15	0.23	0	17,19,21	0.58	0
4	NAG	M	2	4	14,14,15	0.24	0	17,19,21	0.43	0
5	NAG	N	1	5,1	14,14,15	0.46	0	17,19,21	0.61	0
5	NAG	N	2	5	14,14,15	0.27	0	17,19,21	0.65	0
5	BMA	N	3	5	11,11,12	0.97	1 (9%)	15,15,17	0.78	0
5	MAN	N	4	5	11,11,12	1.15	1 (9%)	15,15,17	0.99	1 (6%)
5	MAN	N	5	5	11,11,12	1.59	2 (18%)	15,15,17	1.92	3 (20%)
4	NAG	O	1	4,1	14,14,15	0.24	0	17,19,21	0.49	0
4	NAG	O	2	4	14,14,15	0.35	0	17,19,21	0.43	0
5	NAG	P	1	5,1	14,14,15	0.35	0	17,19,21	0.60	0
5	NAG	P	2	5	14,14,15	0.28	0	17,19,21	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BMA	P	3	5	11,11,12	0.60	0	15,15,17	0.71	0
5	MAN	P	4	5	11,11,12	0.95	0	15,15,17	1.08	2 (13%)
5	MAN	P	5	5	11,11,12	2.26	3 (27%)	15,15,17	2.43	2 (13%)
4	NAG	Q	1	4,1	14,14,15	0.26	0	17,19,21	0.42	0
4	NAG	Q	2	4	14,14,15	0.26	0	17,19,21	0.43	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	1/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	3/6/23/26	0/1/1/1
5	NAG	J	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	J	2	5	-	1/6/23/26	0/1/1/1
5	BMA	J	3	5	-	2/2/19/22	0/1/1/1
5	MAN	J	4	5	-	0/2/19/22	0/1/1/1
5	MAN	J	5	5	-	2/2/19/22	0/1/1/1
4	NAG	K	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	K	2	4	-	4/6/23/26	0/1/1/1
5	NAG	L	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	L	2	5	-	0/6/23/26	0/1/1/1
5	BMA	L	3	5	-	0/2/19/22	0/1/1/1
5	MAN	L	4	5	-	2/2/19/22	0/1/1/1
5	MAN	L	5	5	-	0/2/19/22	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1
5	NAG	N	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	N	2	5	-	3/6/23/26	0/1/1/1
5	BMA	N	3	5	-	0/2/19/22	0/1/1/1
5	MAN	N	4	5	-	2/2/19/22	0/1/1/1
5	MAN	N	5	5	-	1/2/19/22	0/1/1/1
4	NAG	O	1	4,1	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
5	NAG	P	1	5,1	-	3/6/23/26	0/1/1/1
5	NAG	P	2	5	-	2/6/23/26	0/1/1/1
5	BMA	P	3	5	-	0/2/19/22	0/1/1/1
5	MAN	P	4	5	-	2/2/19/22	0/1/1/1
5	MAN	P	5	5	-	0/2/19/22	0/1/1/1
4	NAG	Q	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	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	P	5	MAN	C1-C2	4.71	1.63	1.52
5	P	5	MAN	O5-C1	4.15	1.50	1.43
5	N	5	MAN	O5-C5	3.51	1.50	1.43
5	J	5	MAN	O5-C1	-3.51	1.37	1.43
5	P	5	MAN	O5-C5	3.49	1.50	1.43

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	P	5	MAN	C1-O5-C5	7.55	122.30	112.19
5	L	5	MAN	C1-O5-C5	5.85	120.03	112.19
5	J	5	MAN	C1-O5-C5	5.75	119.89	112.19
5	N	5	MAN	C1-O5-C5	5.50	119.56	112.19
5	J	4	MAN	O2-C2-C3	-4.78	100.26	110.15

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

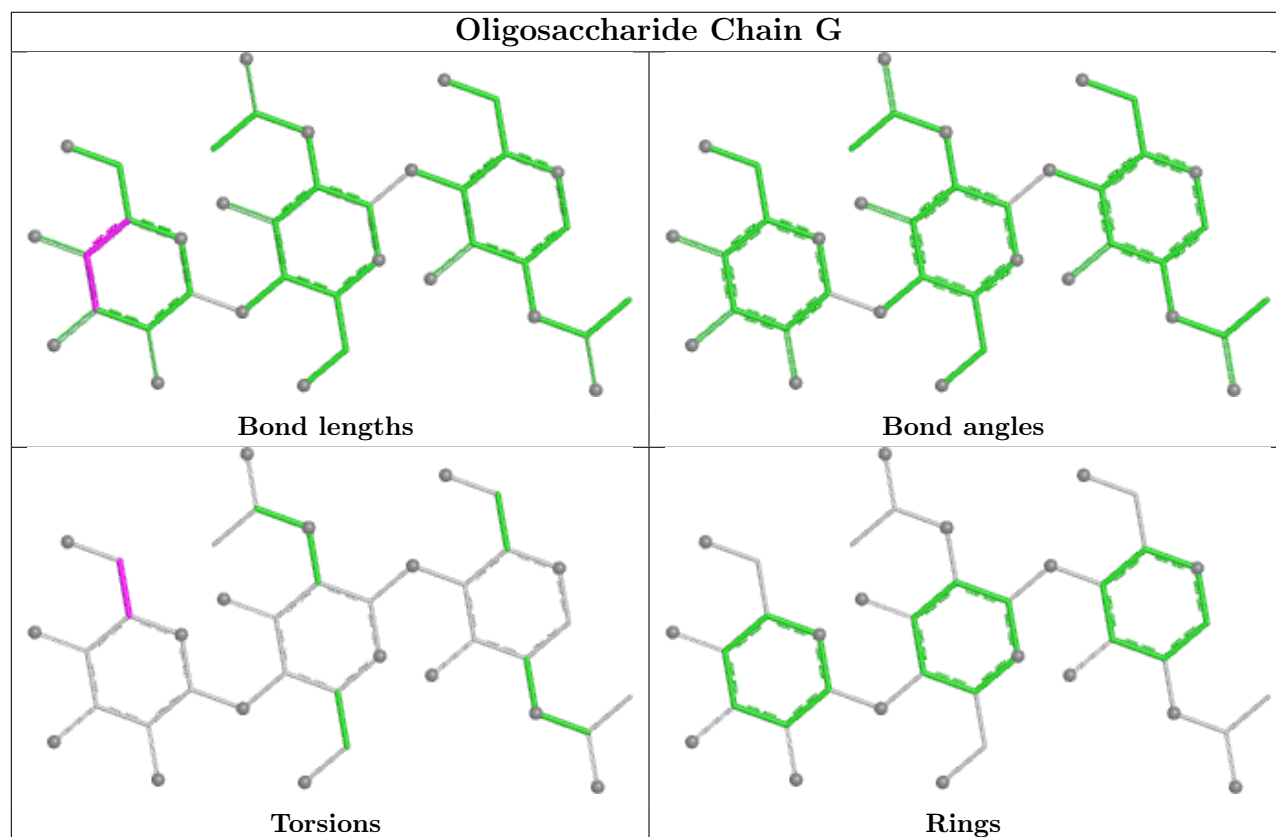
Mol	Chain	Res	Type	Atoms
4	O	1	NAG	O5-C5-C6-O6
4	O	2	NAG	O5-C5-C6-O6
5	N	2	NAG	O5-C5-C6-O6
5	N	2	NAG	C4-C5-C6-O6
4	I	2	NAG	O5-C5-C6-O6

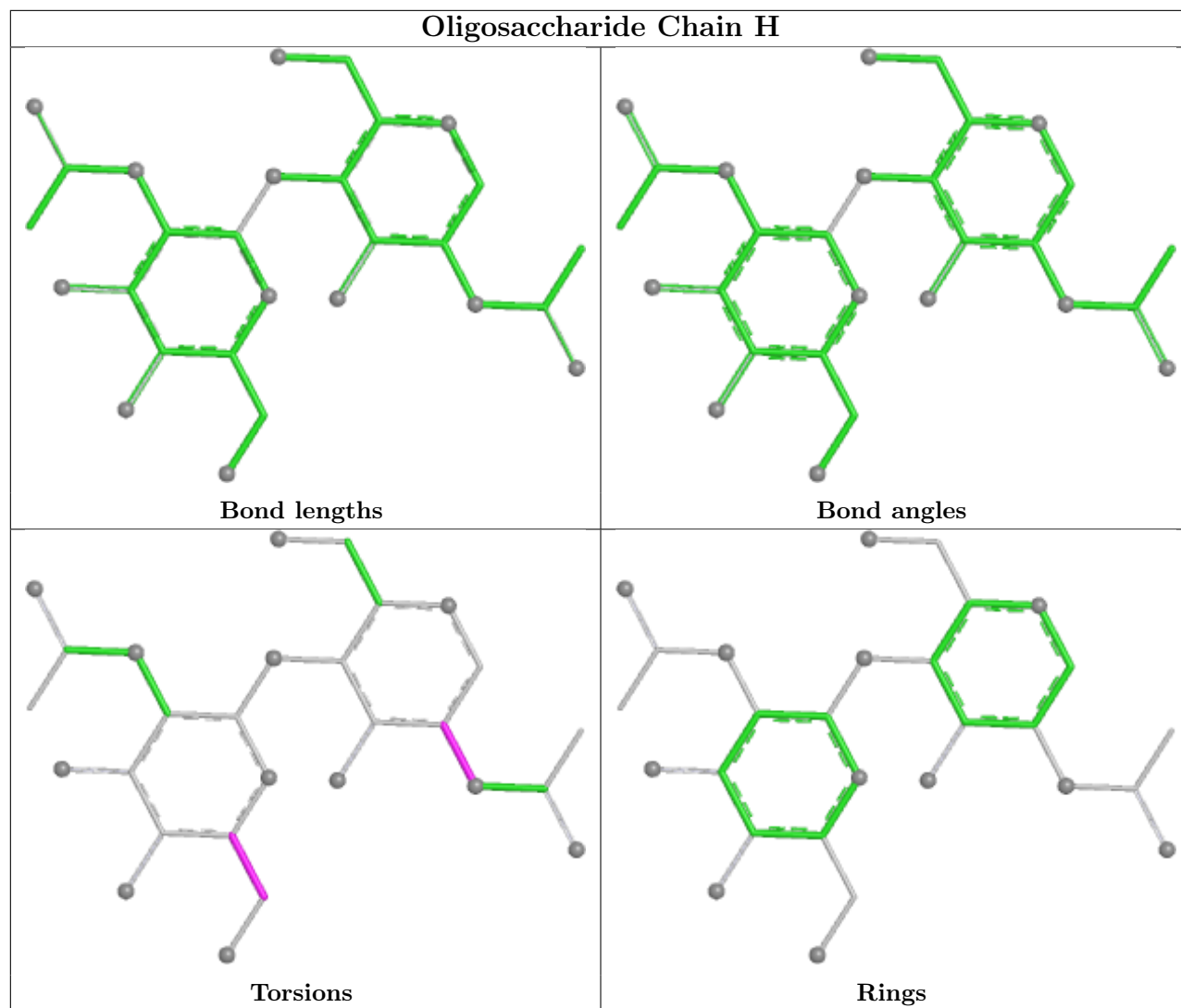
There are no ring outliers.

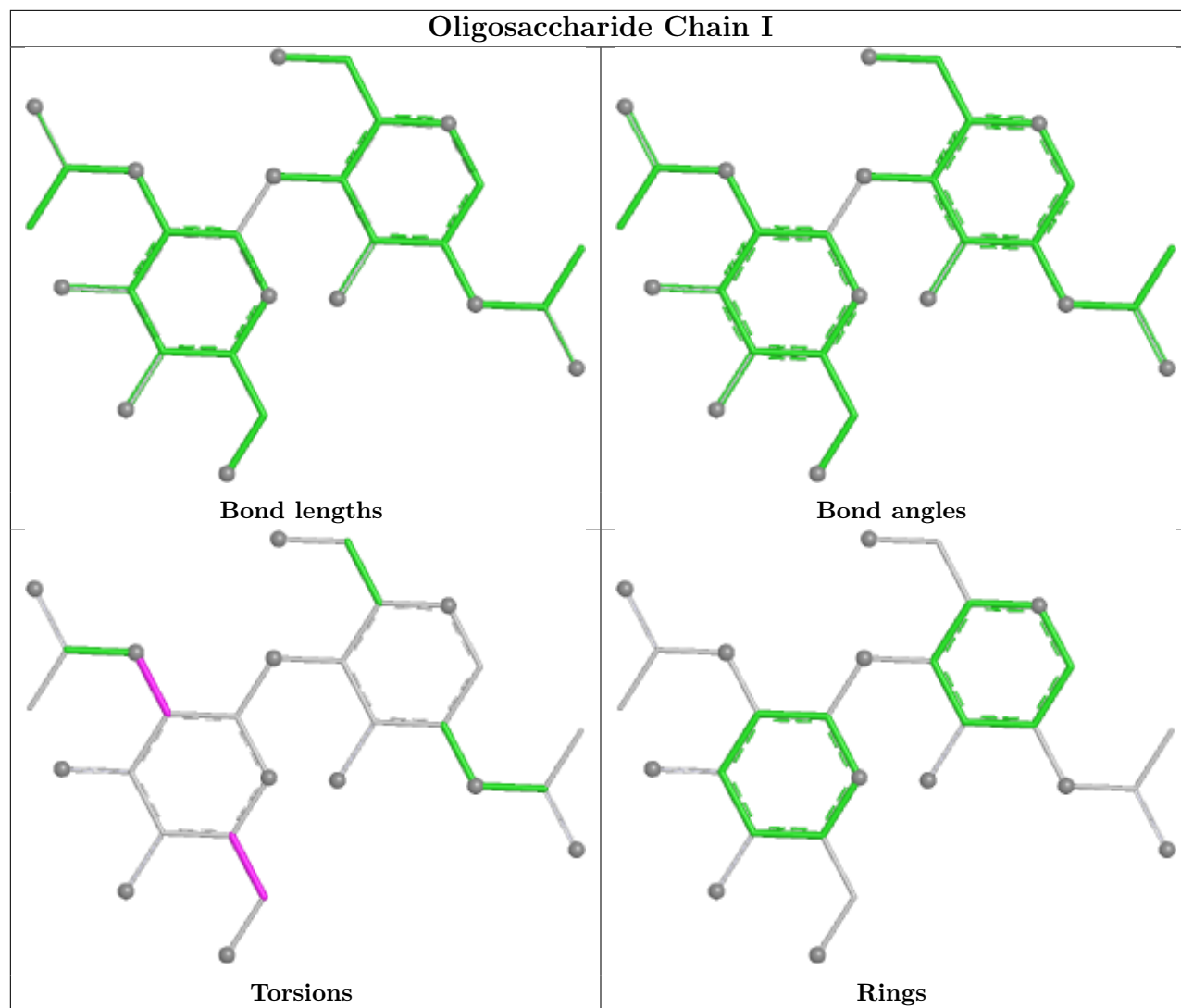
5 monomers are involved in 5 short contacts:

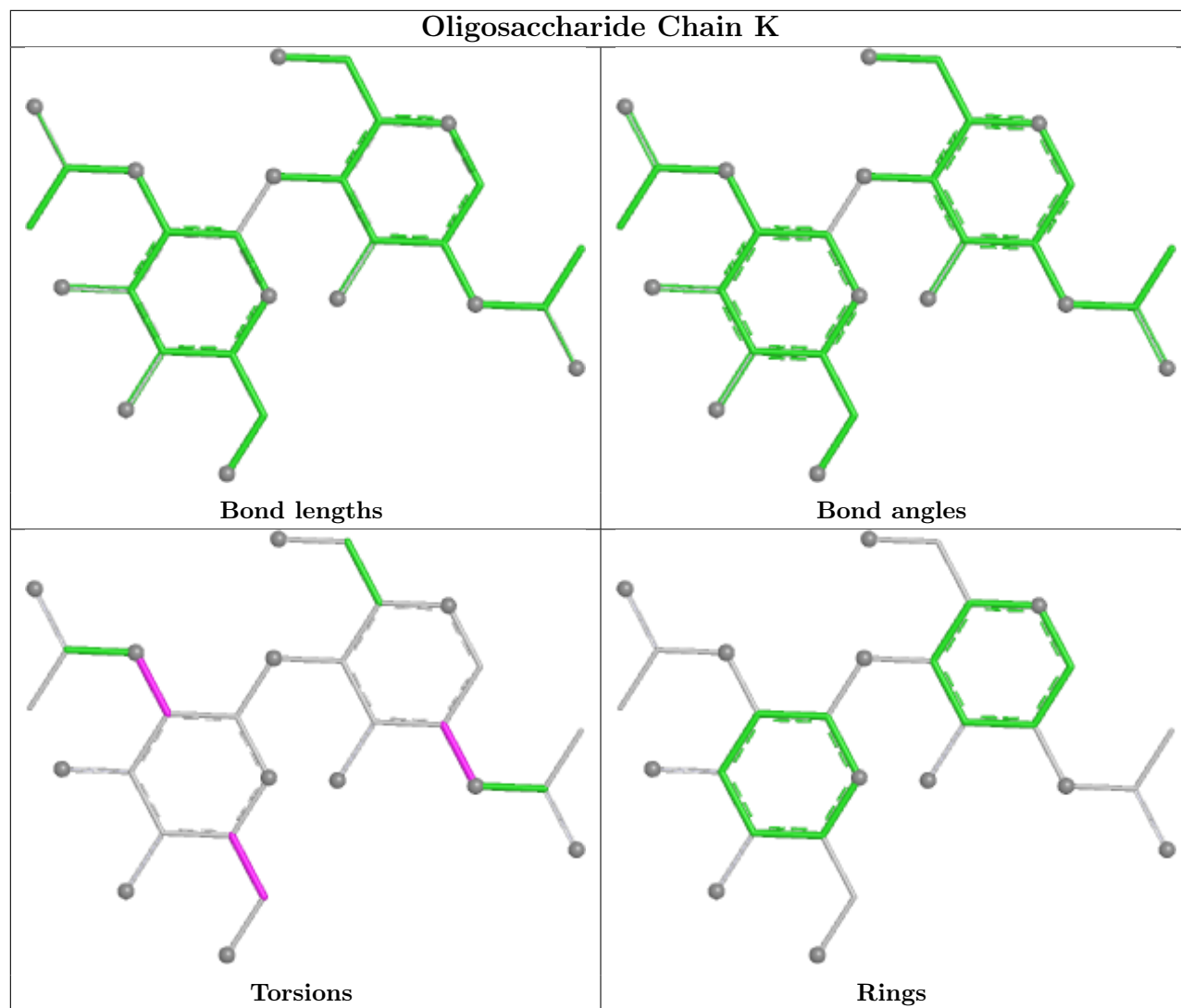
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	1	NAG	1	0
3	G	1	NAG	1	0
4	K	1	NAG	1	0
4	M	1	NAG	1	0
5	P	1	NAG	1	0

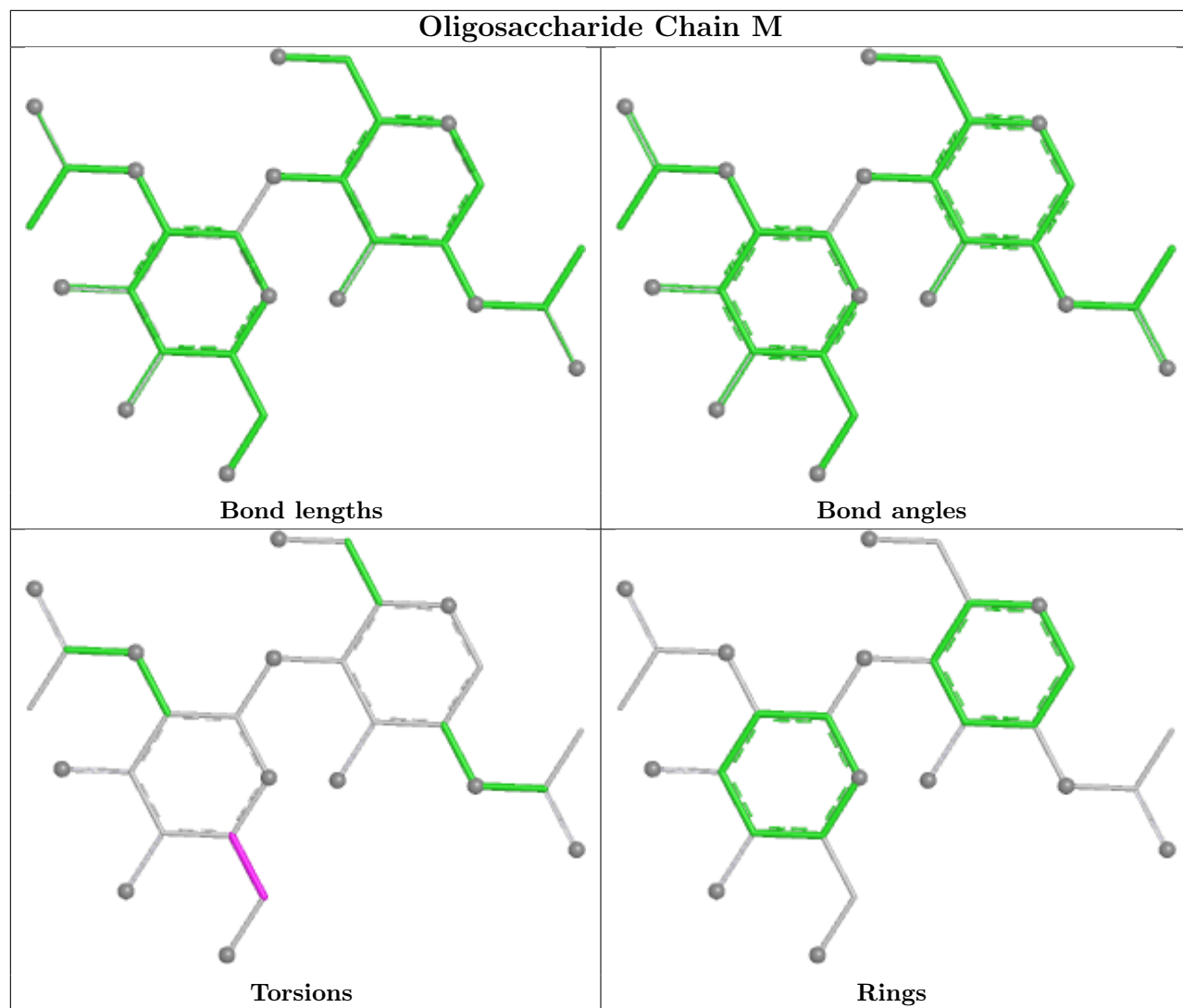
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

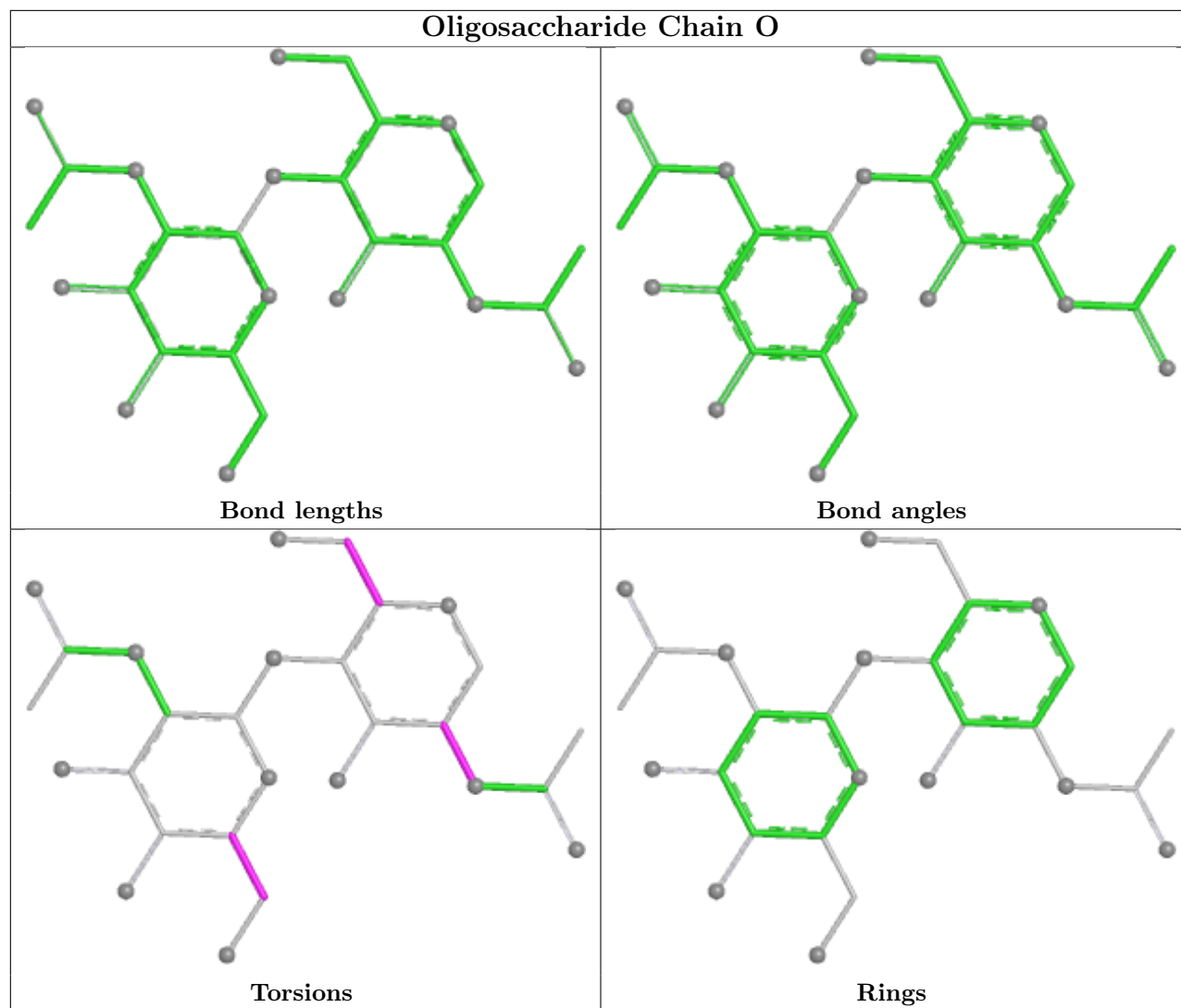


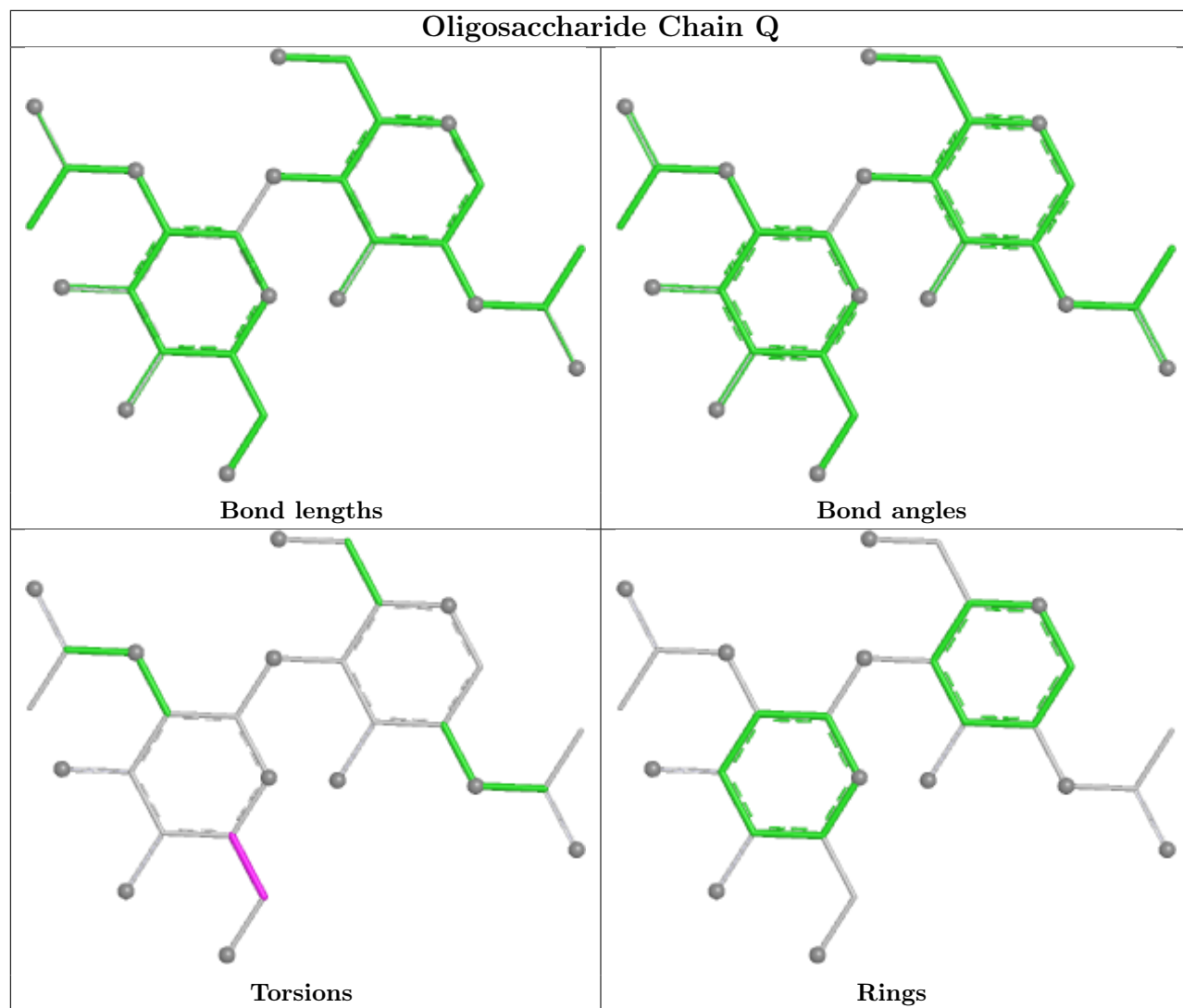


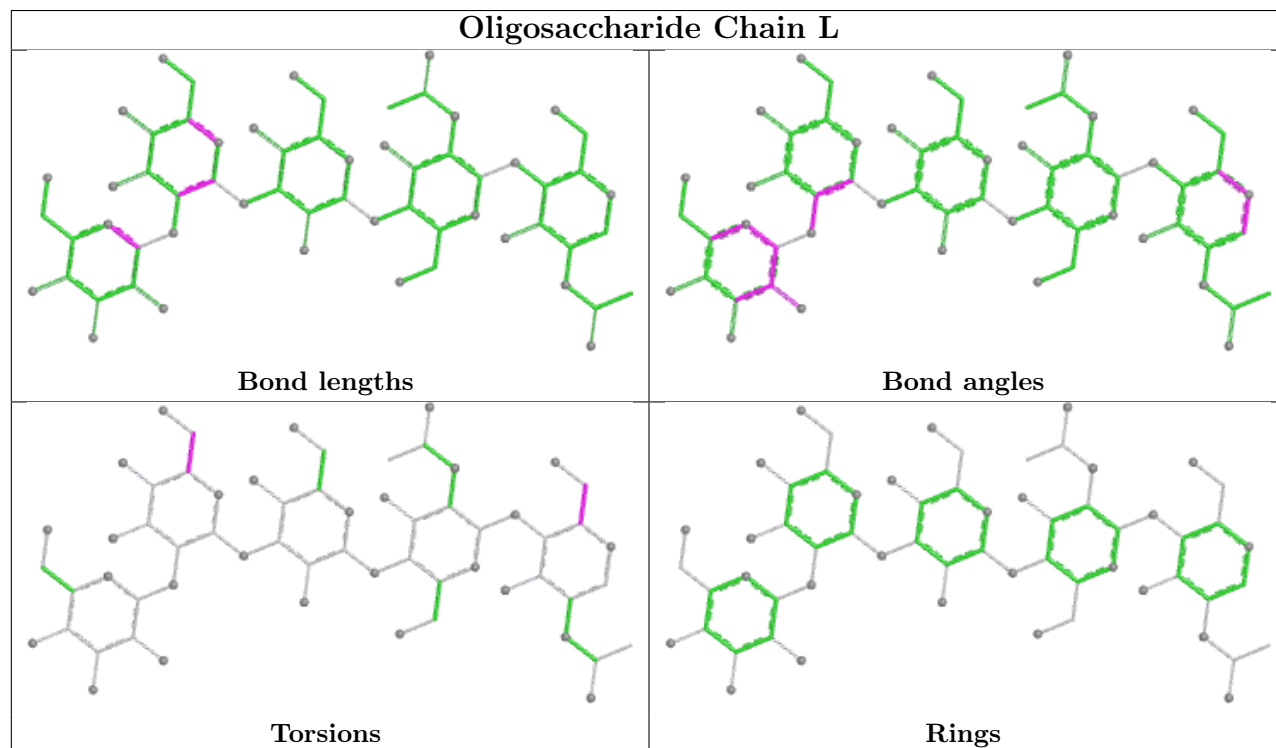
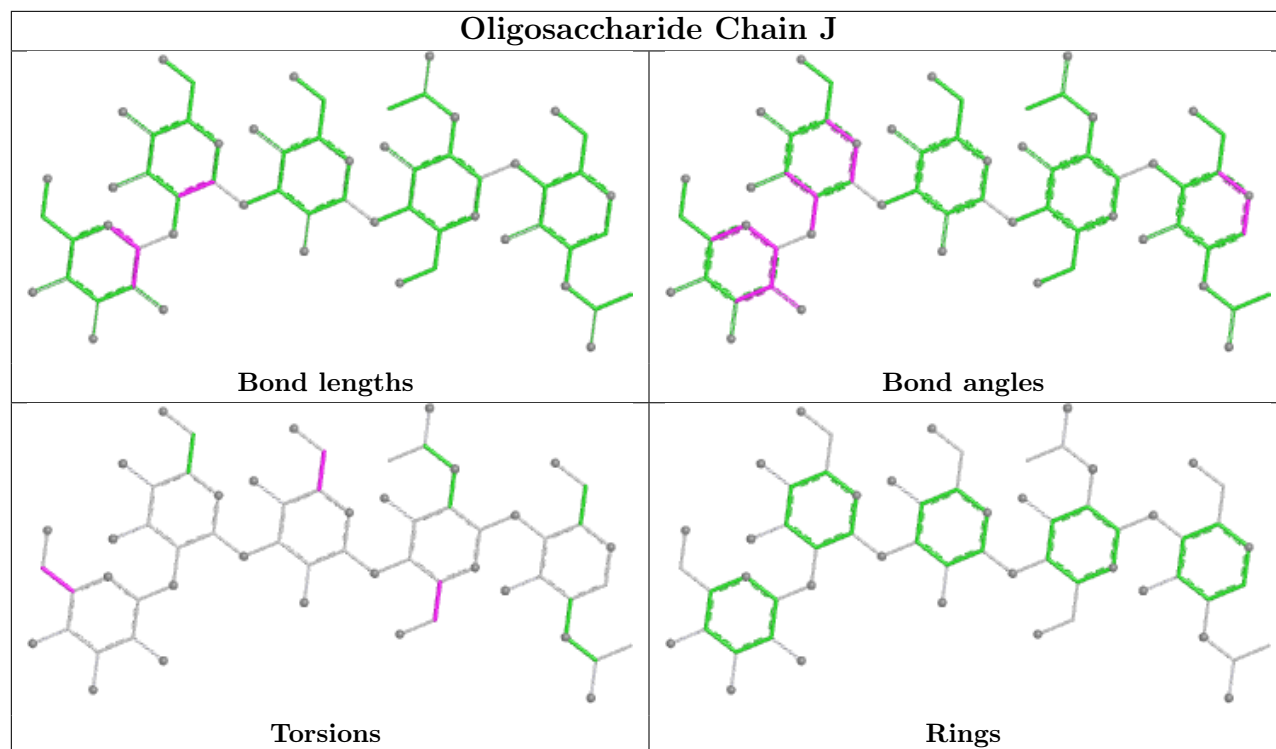


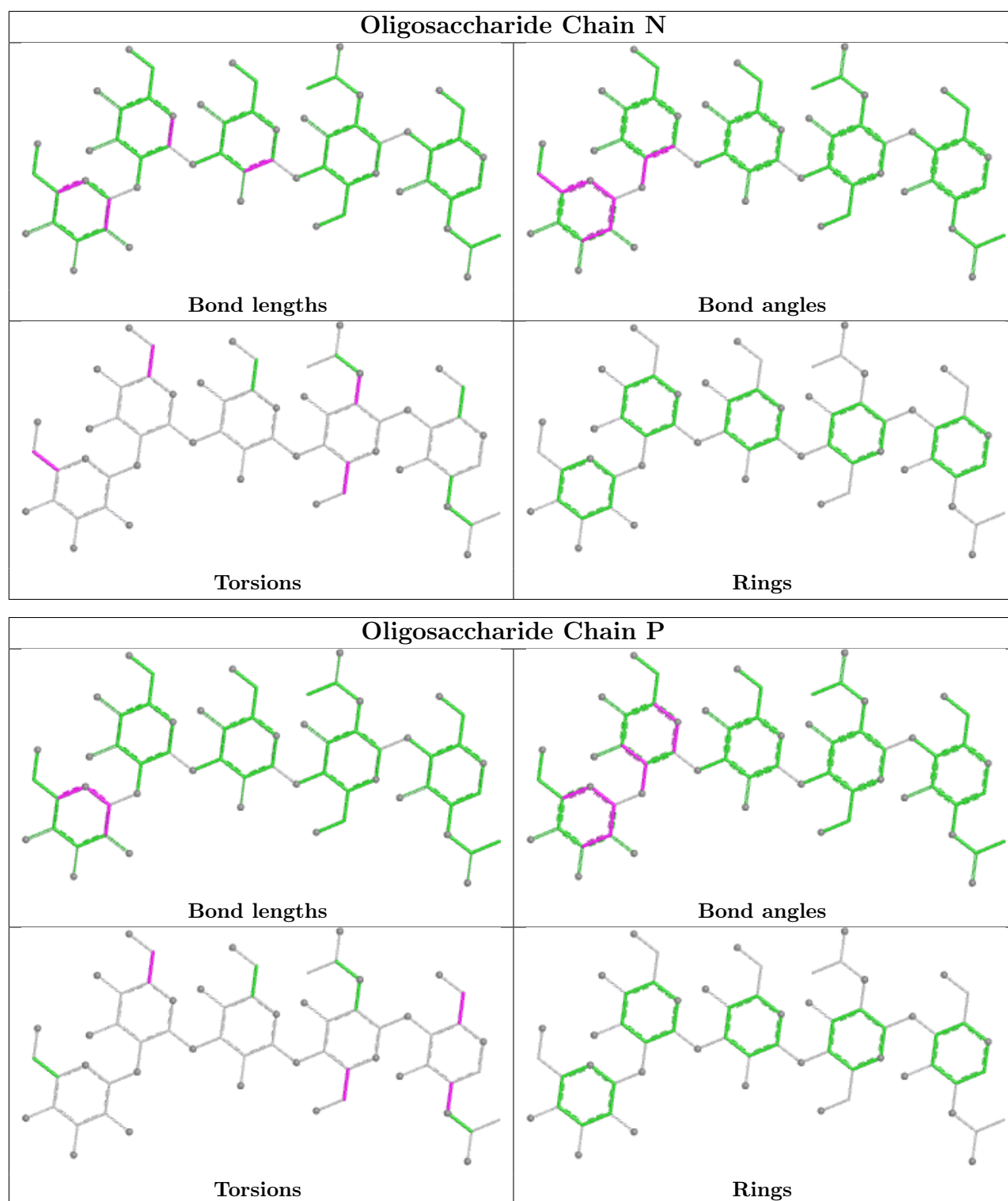












5.6 Ligand geometry [i](#)

Of 88 ligands modelled in this entry, 76 are monoatomic - leaving 12 for Mogul analysis.

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
6	NAG	B	602	1	14,14,15	0.47	0	17,19,21	0.45	0
6	NAG	E	602	1	14,14,15	0.27	0	17,19,21	0.36	0
6	NAG	A	601	1	14,14,15	0.60	1 (7%)	17,19,21	0.73	1 (5%)
6	NAG	C	602	1	14,14,15	0.34	0	17,19,21	0.63	0
6	NAG	F	602	1	14,14,15	0.33	0	17,19,21	0.38	0
6	NAG	B	601	1	14,14,15	0.48	0	17,19,21	0.42	0
6	NAG	F	601	1	14,14,15	0.44	0	17,19,21	0.56	0
6	NAG	B	603	1	14,14,15	0.44	0	17,19,21	0.51	0
7	EDO	A	602	-	3,3,3	0.44	0	2,2,2	0.36	0
6	NAG	C	601	1	14,14,15	0.47	0	17,19,21	0.58	0
6	NAG	D	601	1	14,14,15	0.47	0	17,19,21	0.55	0
6	NAG	E	601	1	14,14,15	0.37	0	17,19,21	0.48	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
6	NAG	B	602	1	-	0/6/23/26	0/1/1/1
6	NAG	E	602	1	-	1/6/23/26	0/1/1/1
6	NAG	A	601	1	-	2/6/23/26	0/1/1/1
6	NAG	C	602	1	-	4/6/23/26	0/1/1/1
6	NAG	F	602	1	-	2/6/23/26	0/1/1/1
6	NAG	B	601	1	-	2/6/23/26	0/1/1/1
6	NAG	F	601	1	-	2/6/23/26	0/1/1/1
6	NAG	B	603	1	-	0/6/23/26	0/1/1/1
7	EDO	A	602	-	-	0/1/1/1	-
6	NAG	C	601	1	-	3/6/23/26	0/1/1/1
6	NAG	D	601	1	-	1/6/23/26	0/1/1/1
6	NAG	E	601	1	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	601	NAG	C1-C2	2.10	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	601	NAG	C1-O5-C5	2.35	115.33	112.19

There are no chirality outliers.

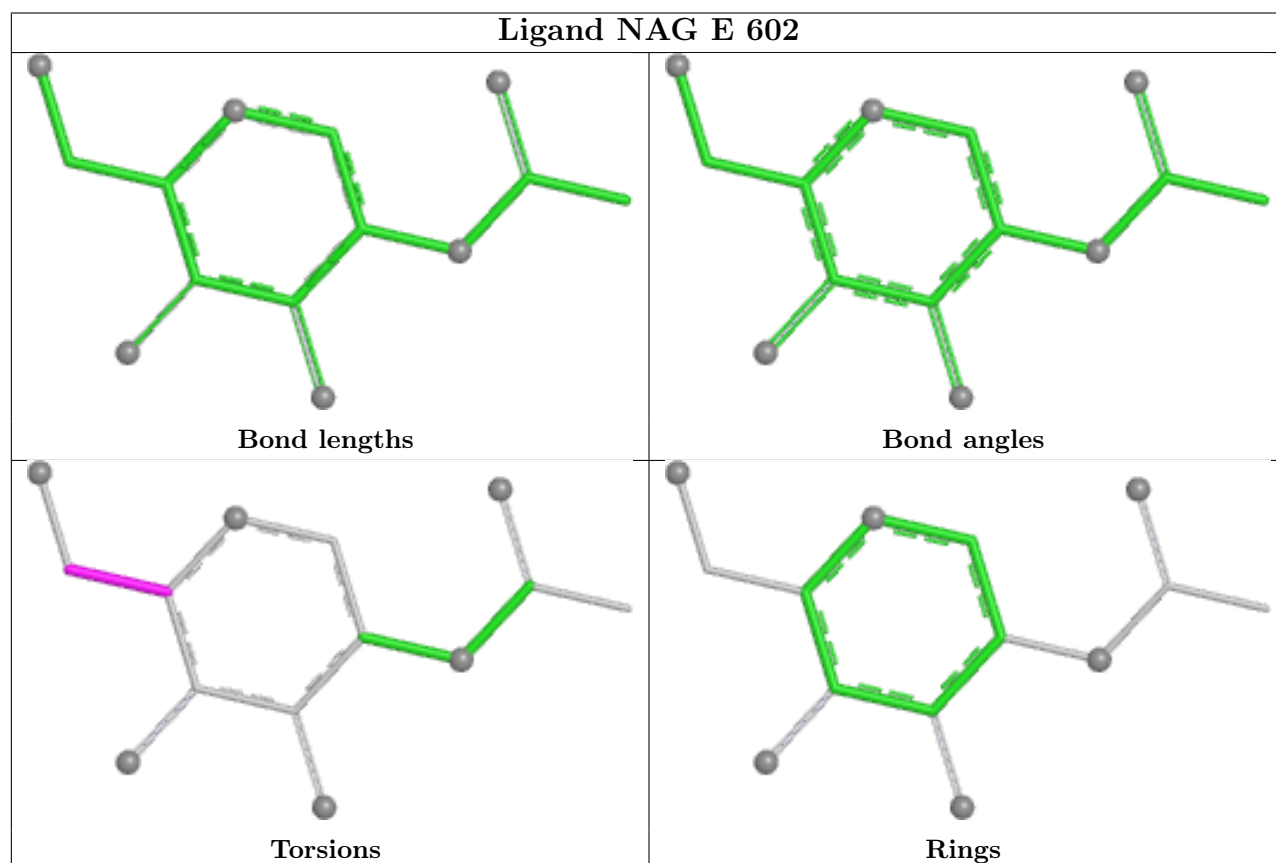
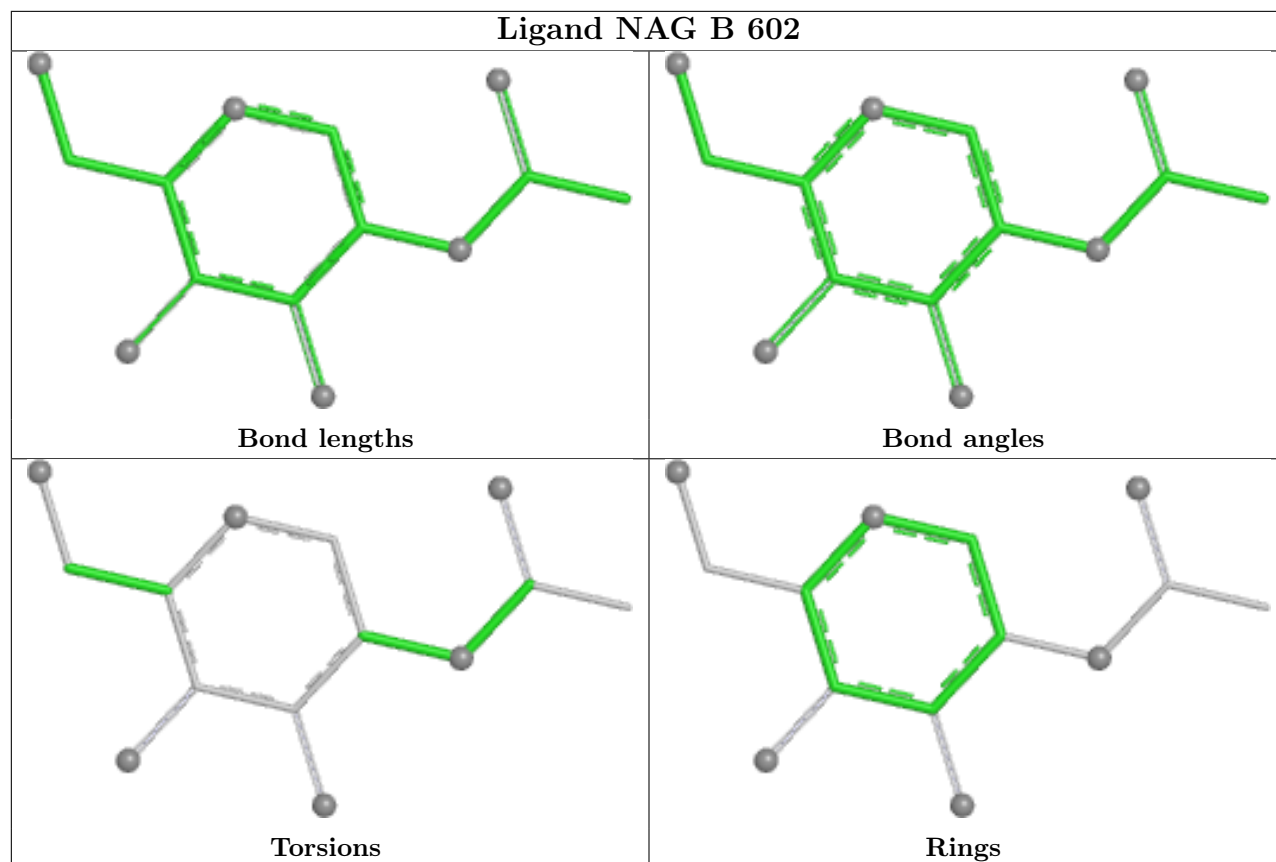
5 of 18 torsion outliers are listed below:

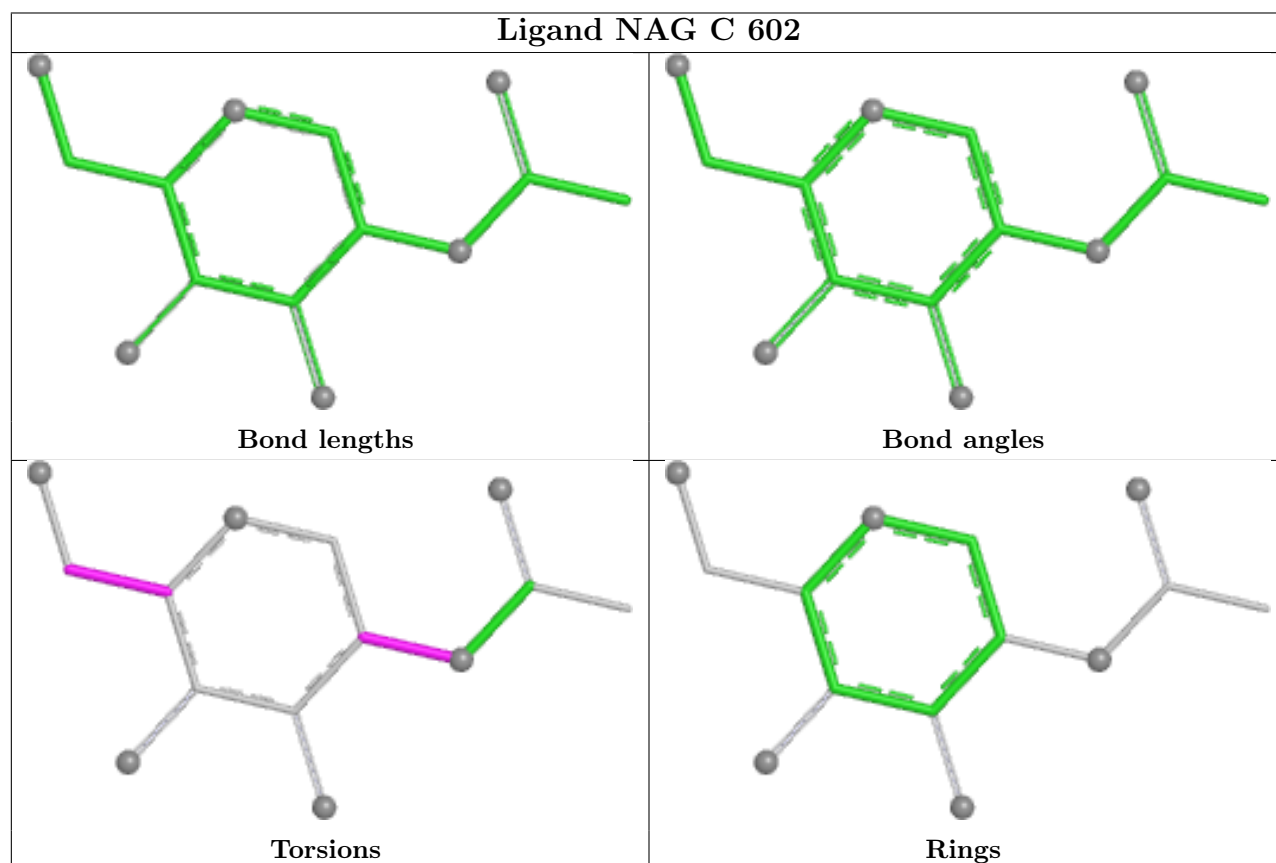
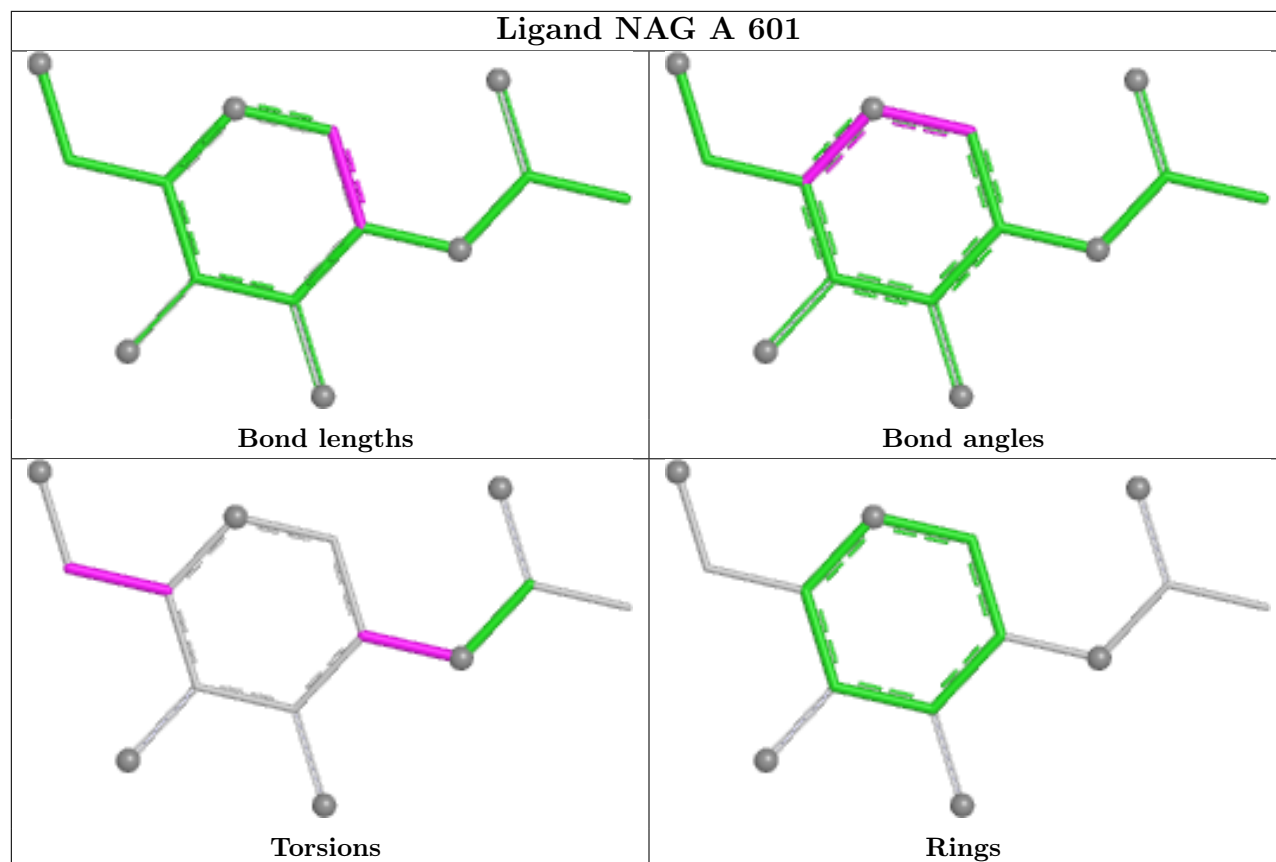
Mol	Chain	Res	Type	Atoms
6	F	601	NAG	O5-C5-C6-O6
6	C	601	NAG	O5-C5-C6-O6
6	F	602	NAG	O5-C5-C6-O6
6	C	601	NAG	C4-C5-C6-O6
6	B	601	NAG	O5-C5-C6-O6

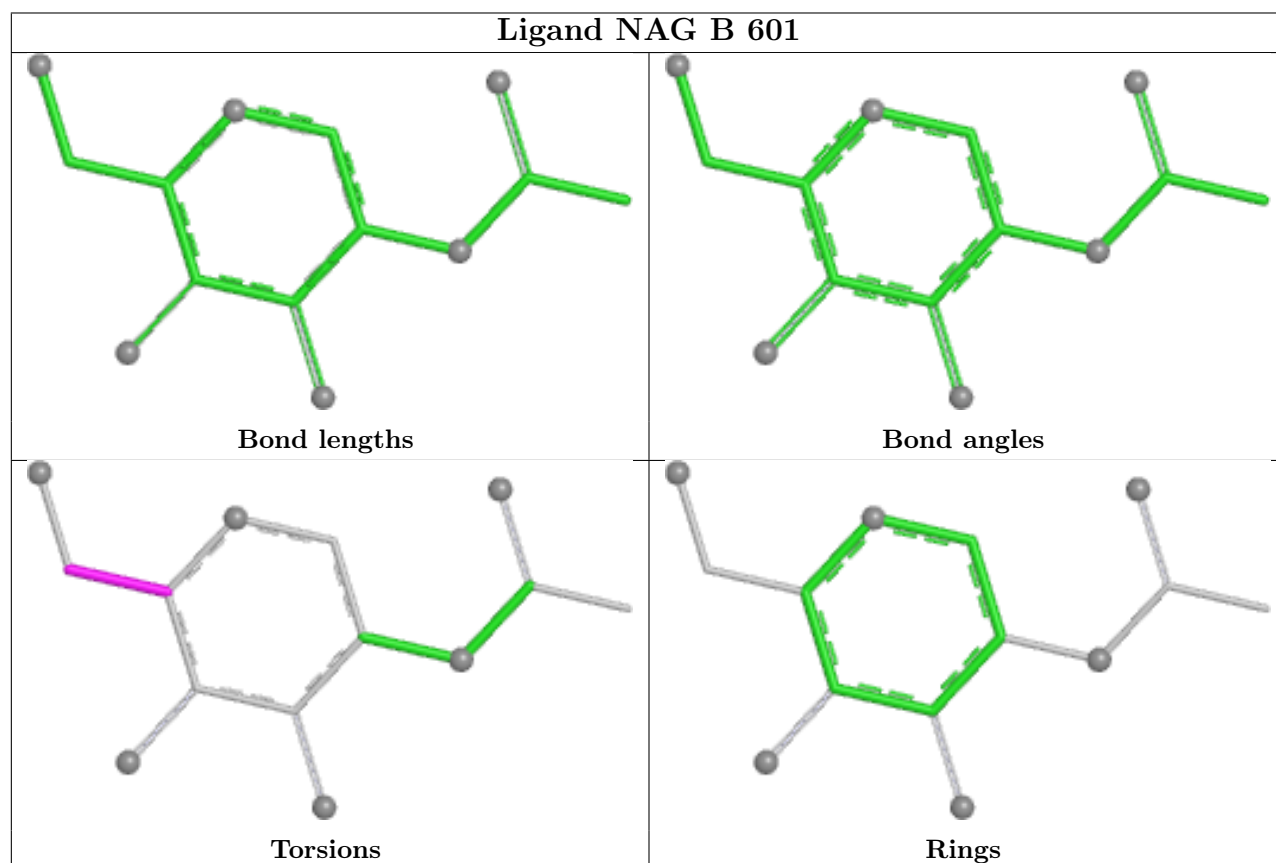
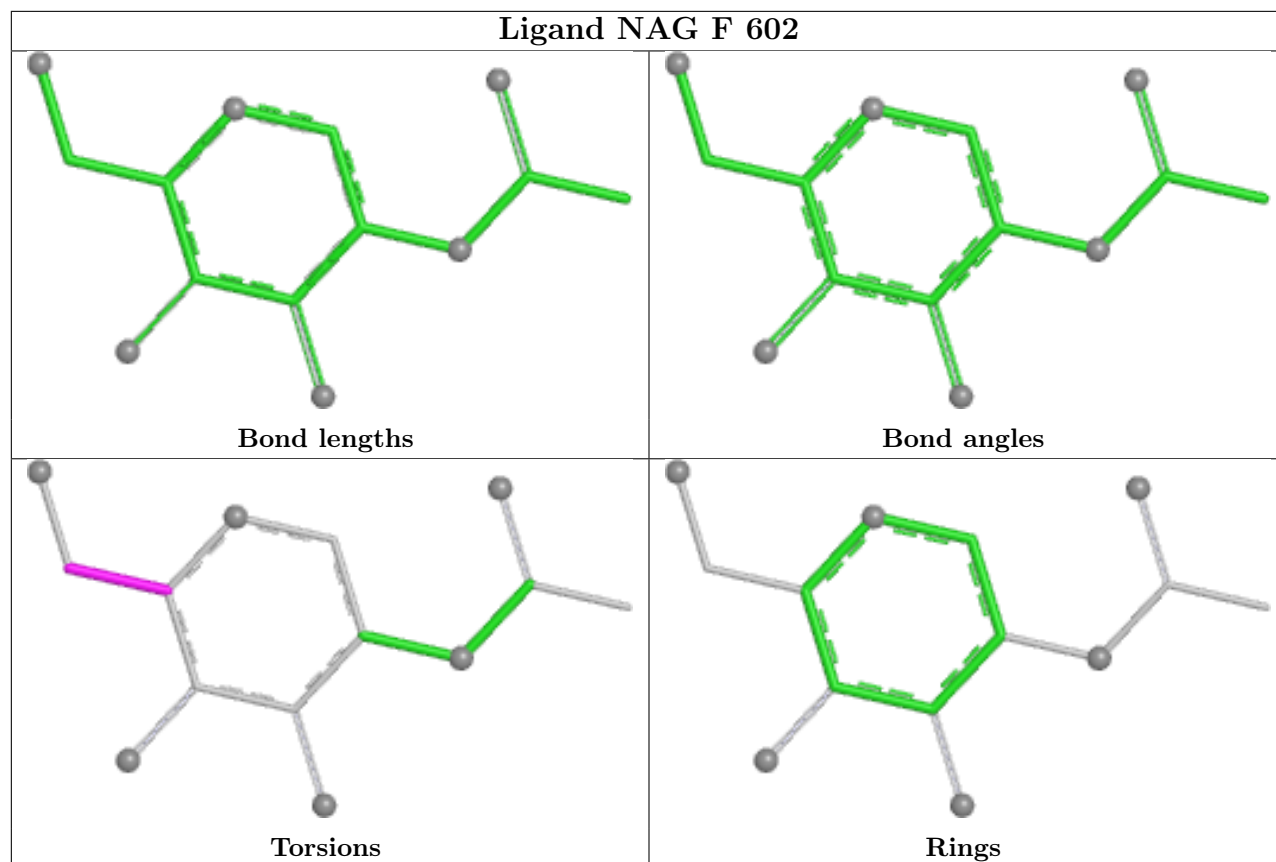
There are no ring outliers.

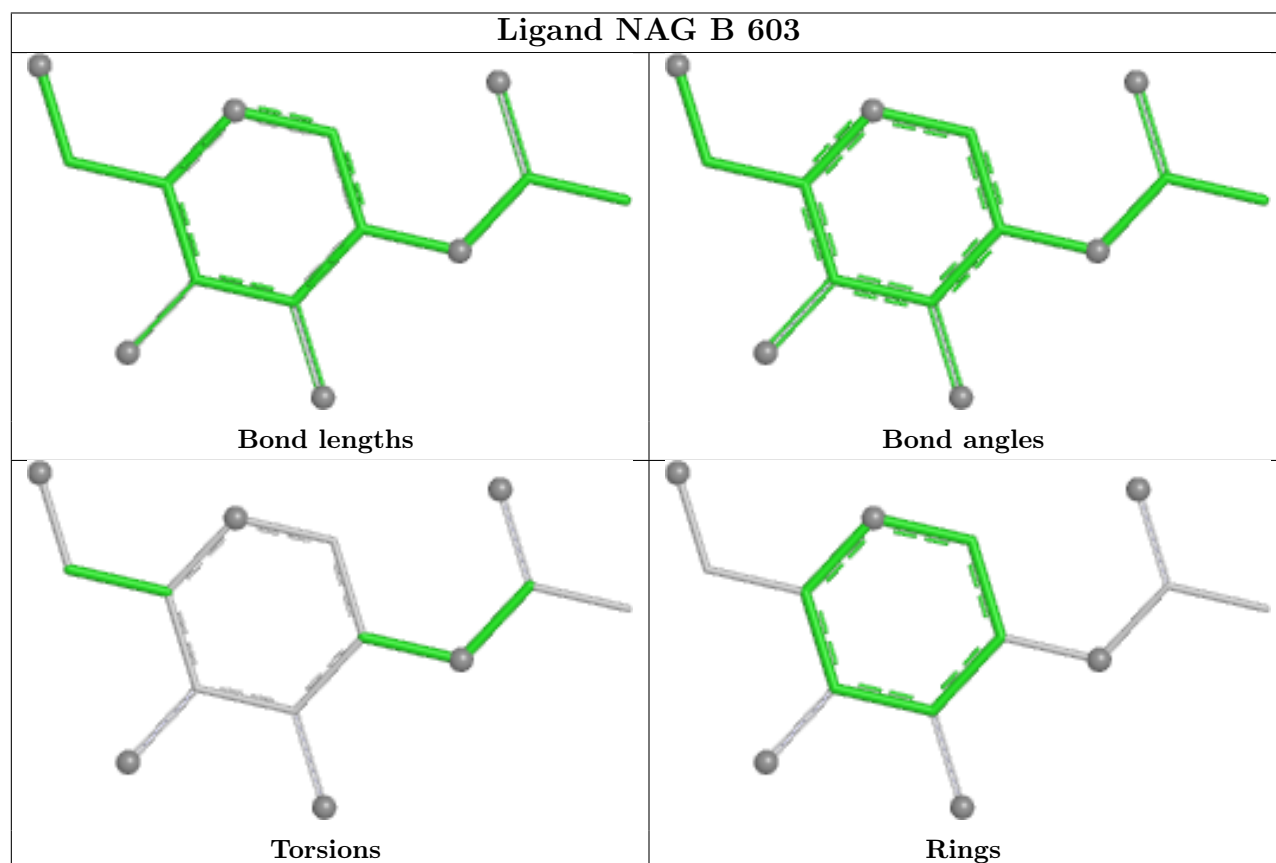
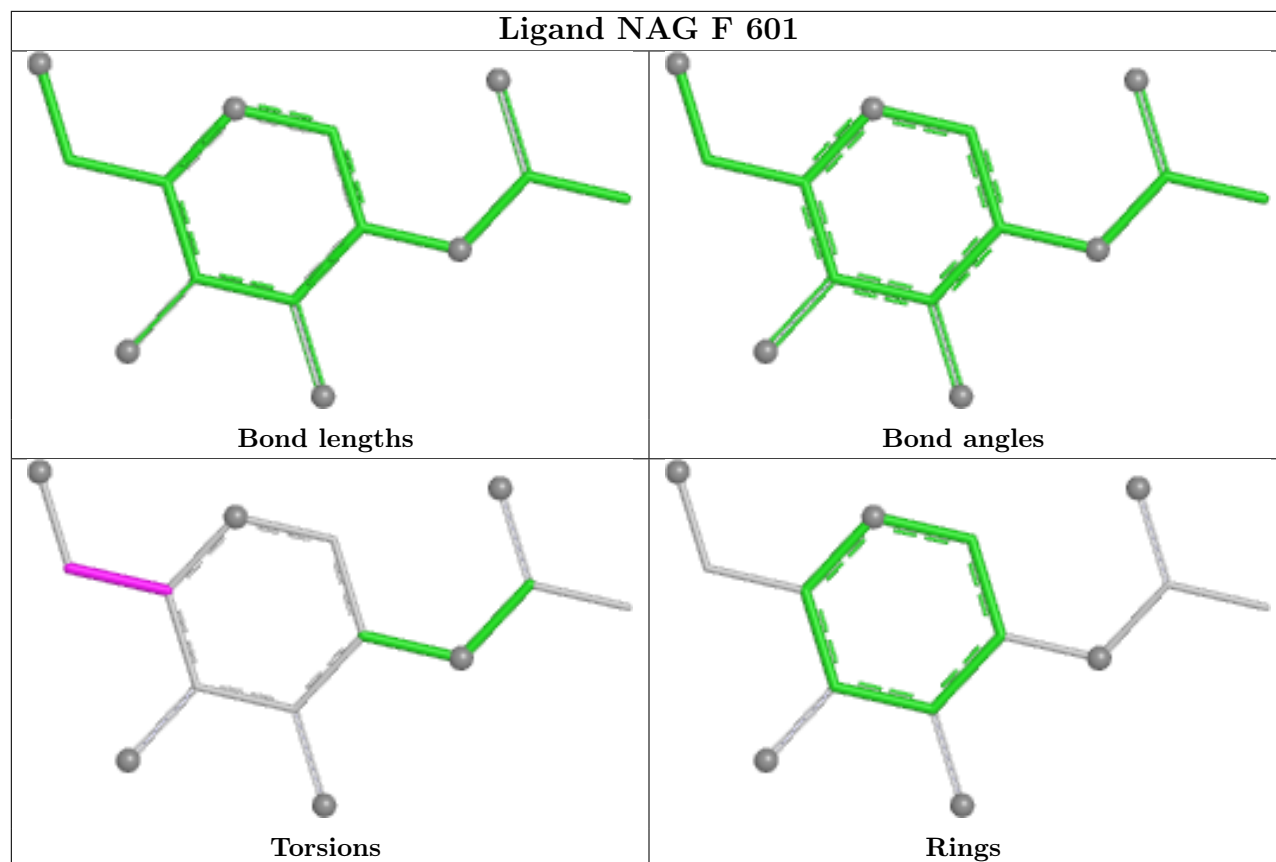
No monomer is involved in short contacts.

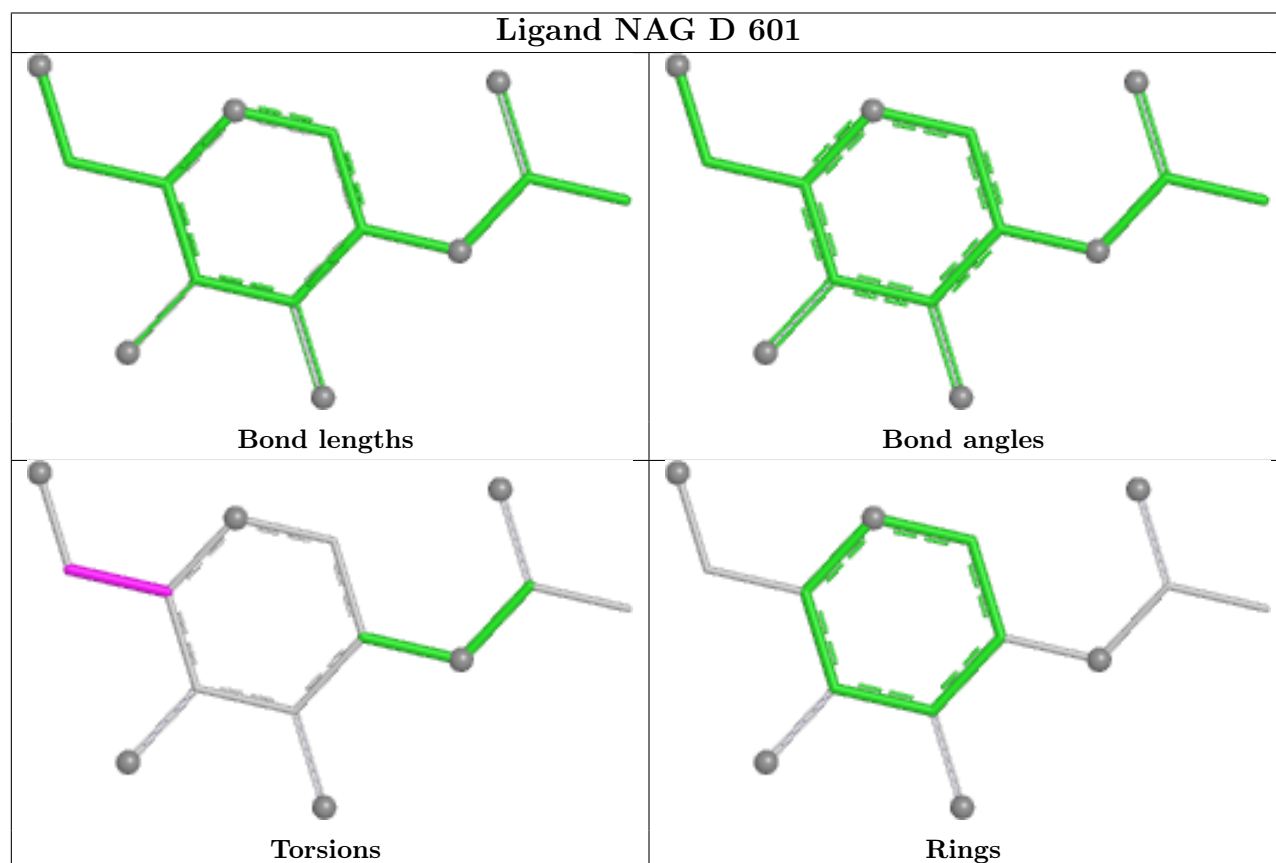
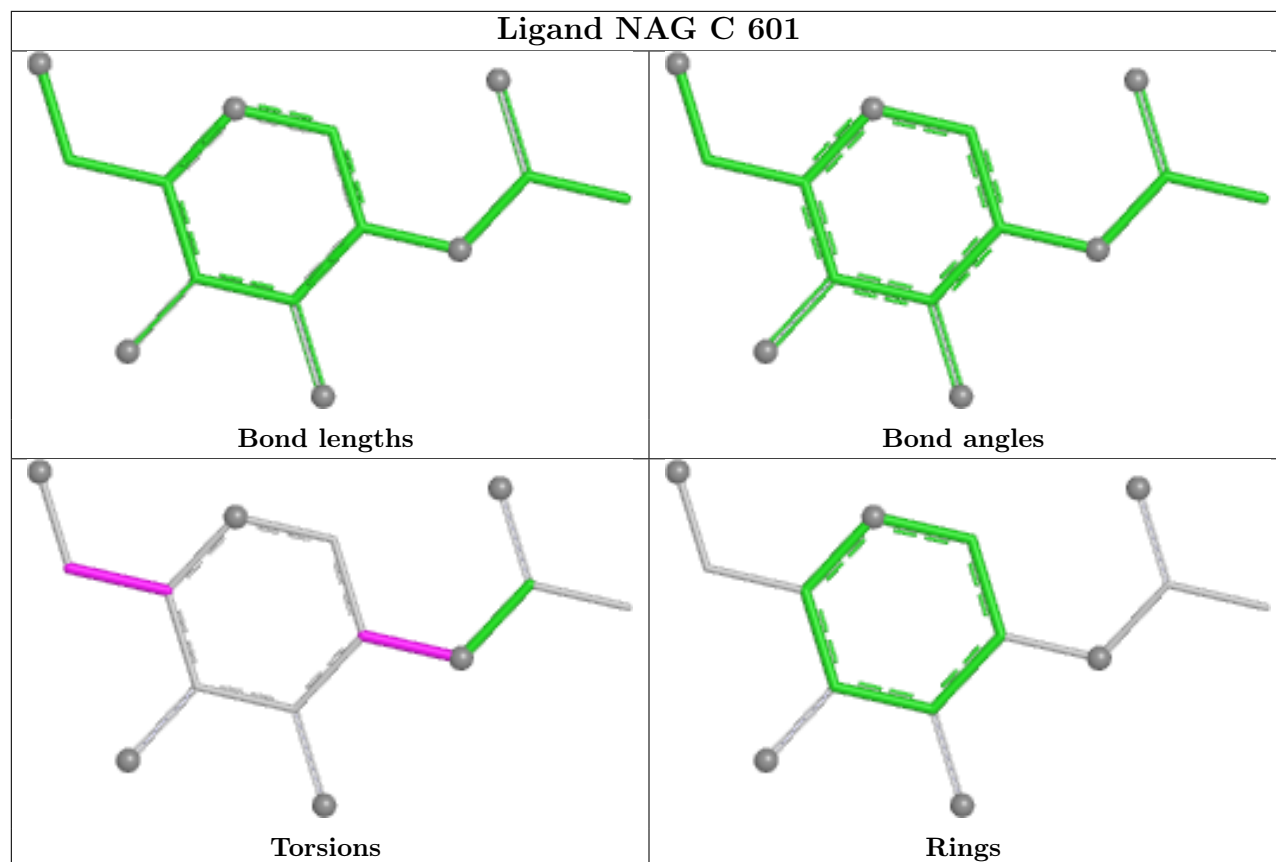
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

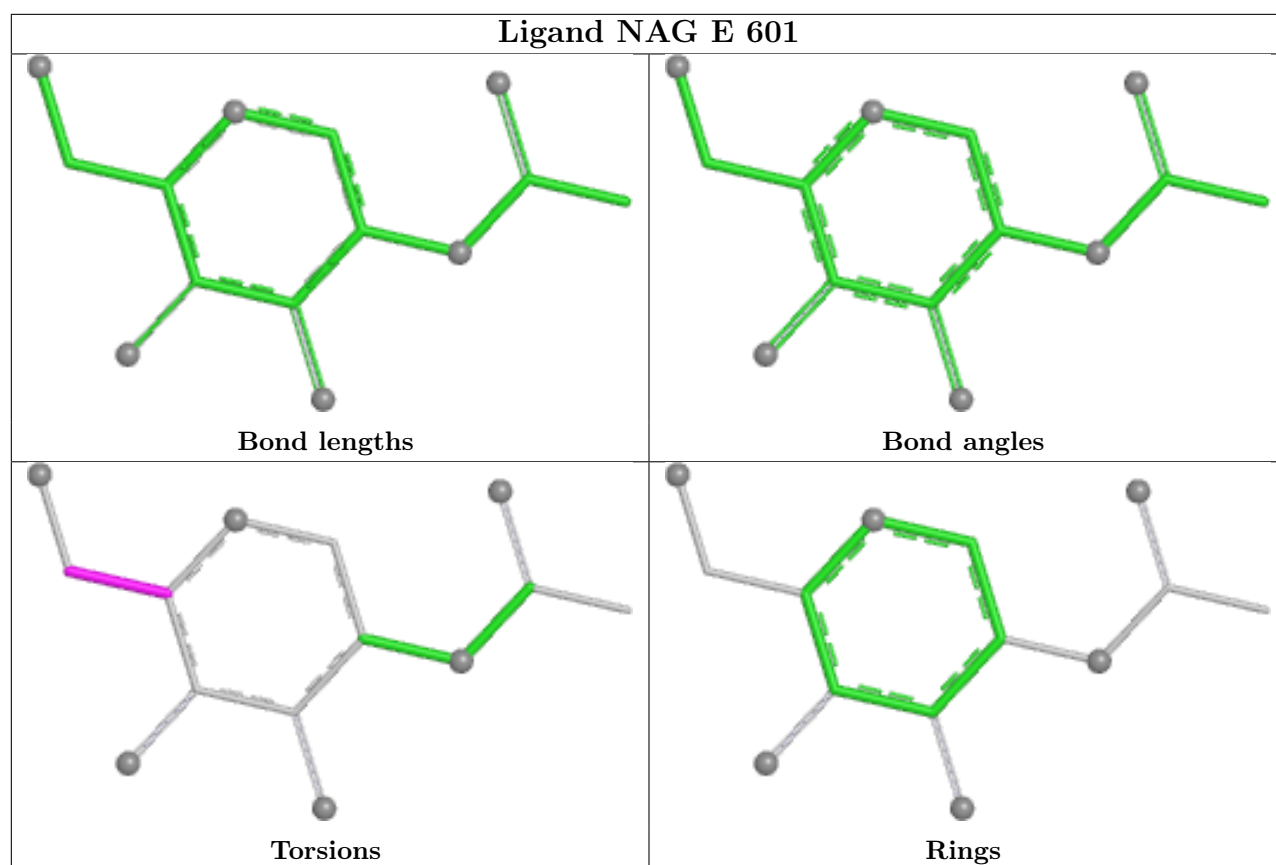












5.7 Other polymers [i](#)

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	323/329 (98%)	0.69	22 (6%) 23 20	31, 49, 77, 99	0
1	B	323/329 (98%)	0.61	21 (6%) 25 21	29, 46, 72, 92	0
1	C	323/329 (98%)	0.62	10 (3%) 51 44	32, 48, 68, 98	0
1	D	323/329 (98%)	0.59	17 (5%) 32 27	32, 50, 79, 107	0
1	E	323/329 (98%)	0.69	14 (4%) 40 32	34, 50, 83, 111	0
1	F	320/329 (97%)	0.76	20 (6%) 26 22	36, 54, 78, 107	0
2	a	160/170 (94%)	0.85	17 (10%) 11 10	34, 56, 85, 96	0
2	b	160/170 (94%)	0.85	11 (6%) 23 19	37, 62, 90, 113	0
2	c	160/170 (94%)	0.70	8 (5%) 34 28	35, 51, 71, 104	0
2	d	160/170 (94%)	0.69	10 (6%) 26 22	34, 49, 71, 110	0
2	e	160/170 (94%)	1.04	26 (16%) 4 4	36, 57, 92, 100	0
2	f	160/170 (94%)	1.05	21 (13%) 7 7	36, 61, 92, 107	0
All	All	2895/2994 (96%)	0.73	197 (6%) 23 20	29, 51, 84, 113	0

The worst 5 of 197 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	72	LEU	5.9
1	E	264	GLY	5.2
2	b	489	PRO	5.1
2	b	330	GLY	5.0
2	e	389	ASN	5.0

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

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

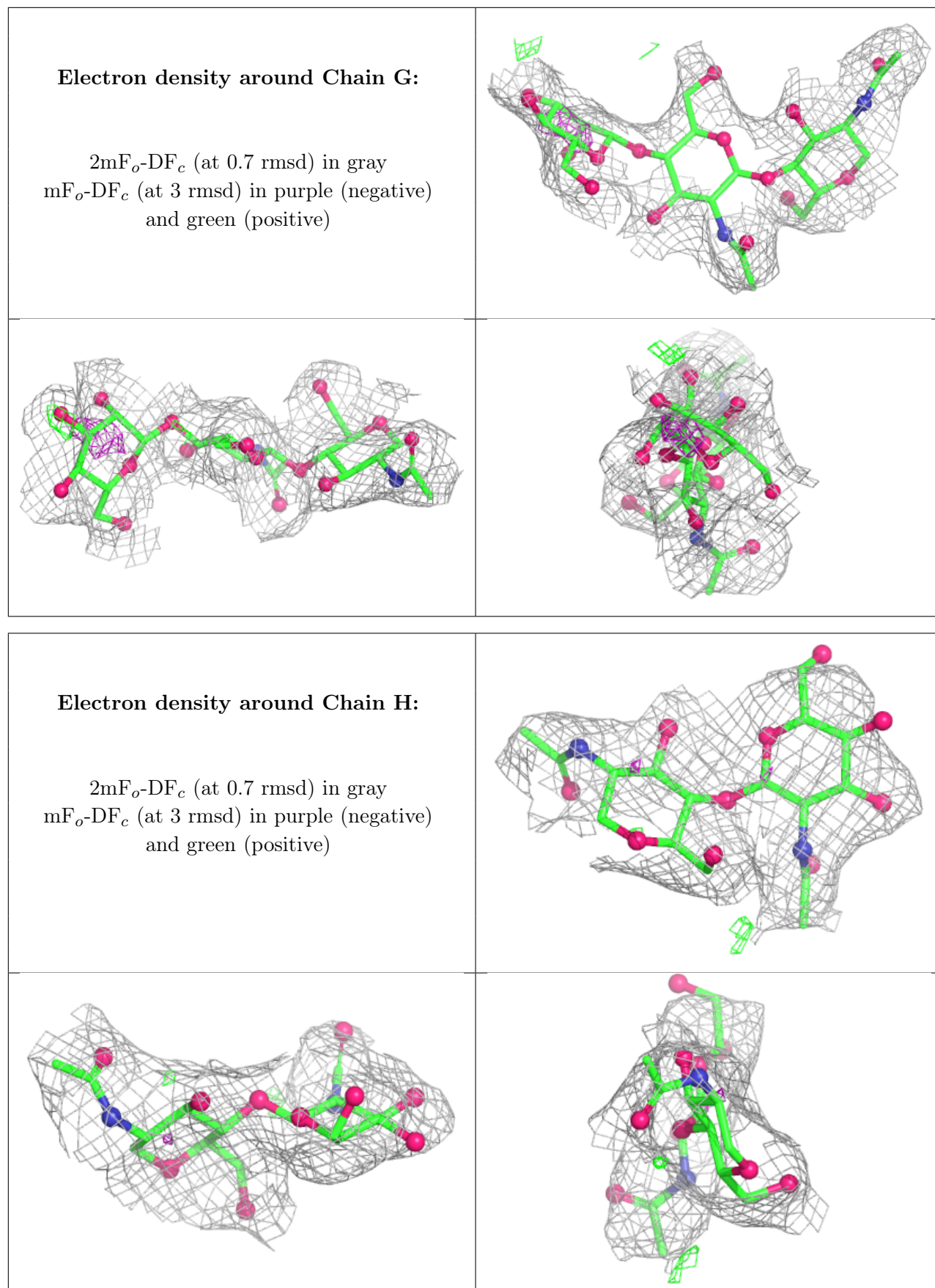
6.3 Carbohydrates i

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
3	NAG	G	1	14/15	-	-	53,55,58,59	0
3	NAG	G	2	14/15	-	-	58,60,62,64	0
3	BMA	G	3	11/12	-	-	65,66,67,68	0
4	NAG	H	1	14/15	-	-	56,59,61,63	0
4	NAG	H	2	14/15	-	-	63,64,66,67	0
4	NAG	I	1	14/15	-	-	52,54,56,56	0
4	NAG	I	2	14/15	-	-	53,54,55,55	0
4	NAG	K	1	14/15	-	-	48,49,51,52	0
4	NAG	K	2	14/15	-	-	50,52,52,53	0
5	BMA	P	3	11/12	0.40	0.19	70,72,74,76	0
5	MAN	P	4	11/12	0.59	0.17	77,79,82,82	0
5	NAG	N	2	14/15	0.62	0.13	58,60,65,68	0
5	MAN	P	5	11/12	0.66	0.16	63,73,75,75	0
4	NAG	Q	2	14/15	0.72	0.13	64,64,65,66	0
4	NAG	O	2	14/15	0.75	0.13	63,65,66,66	0
5	NAG	J	1	14/15	-	-	48,50,52,52	0
5	NAG	J	2	14/15	-	-	52,53,57,58	0
5	BMA	J	3	11/12	-	-	61,63,66,69	0
5	MAN	J	4	11/12	-	-	67,69,72,74	0
5	MAN	J	5	11/12	-	-	58,60,65,66	0
5	NAG	L	1	14/15	-	-	52,54,57,57	0
5	NAG	L	2	14/15	-	-	50,52,53,54	0
5	BMA	L	3	11/12	-	-	55,56,57,57	0
5	MAN	L	4	11/12	-	-	56,56,57,58	0
5	MAN	L	5	11/12	-	-	50,54,56,56	0
5	NAG	N	1	14/15	0.76	0.13	53,55,57,58	0
4	NAG	M	2	14/15	0.77	0.12	56,58,59,60	0
5	BMA	N	3	11/12	-	-	71,75,79,80	0
5	MAN	N	4	11/12	-	-	82,85,86,86	0
5	MAN	N	5	11/12	-	-	83,87,88,89	0
5	NAG	P	2	14/15	0.82	0.11	62,63,67,69	0
4	NAG	Q	1	14/15	0.84	0.11	58,61,62,63	0
4	NAG	M	1	14/15	0.86	0.10	55,57,59,61	0
4	NAG	O	1	14/15	0.87	0.10	61,63,65,65	0
5	NAG	P	1	14/15	0.87	0.12	56,59,61,63	0

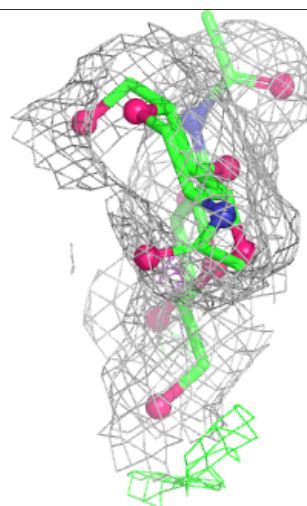
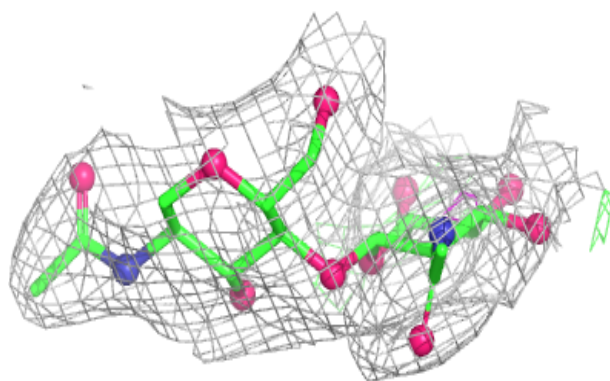
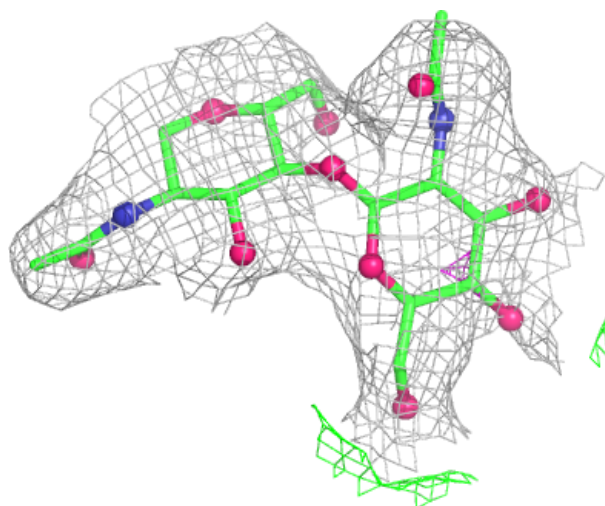
The following is a graphical depiction of the model fit to experimental electron density for oligosac-

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



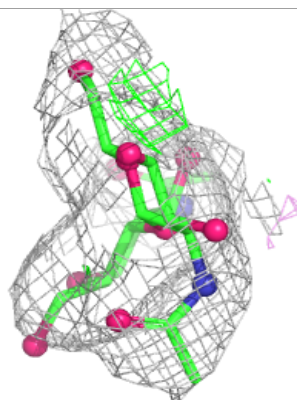
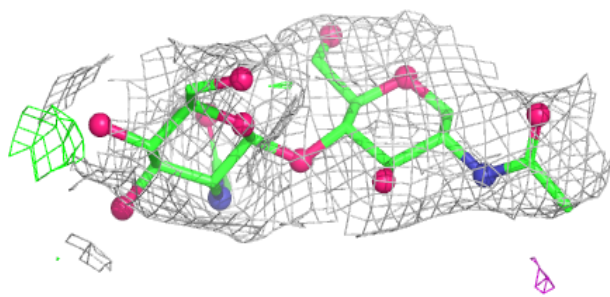
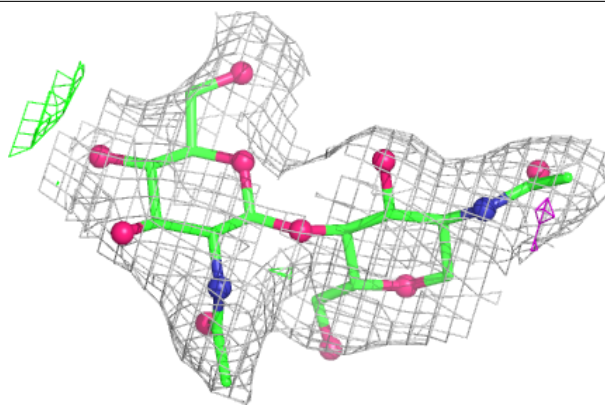
Electron density around Chain I:

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

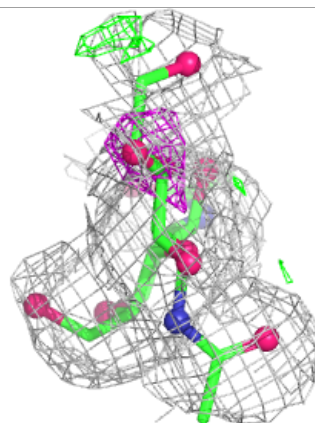
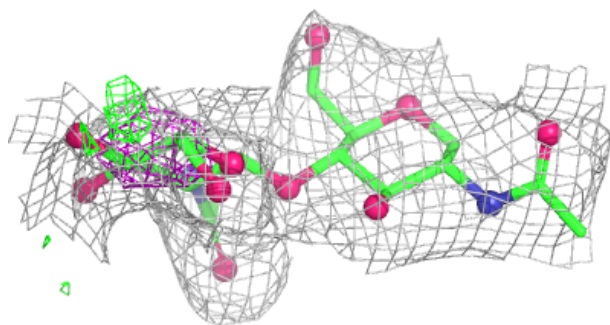
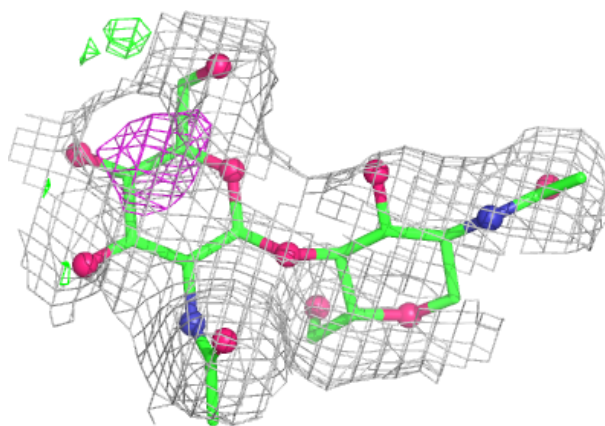


Electron density around Chain K:

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

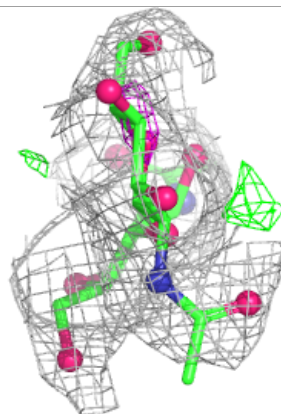
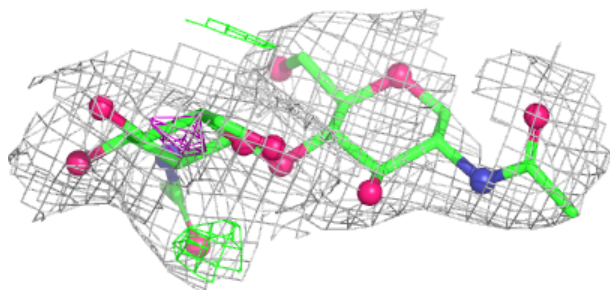
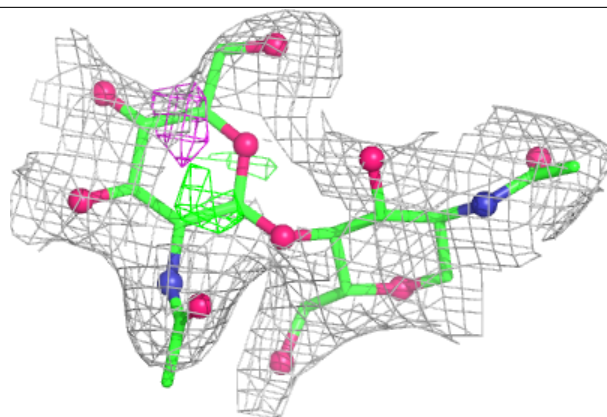
**Electron density around Chain M:**

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

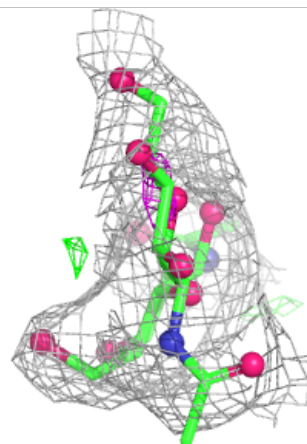
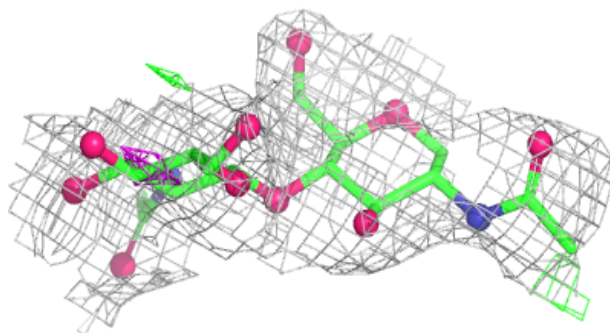
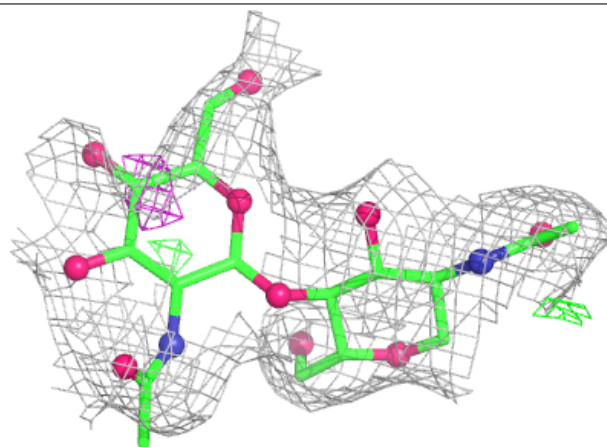


Electron density around Chain O:

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

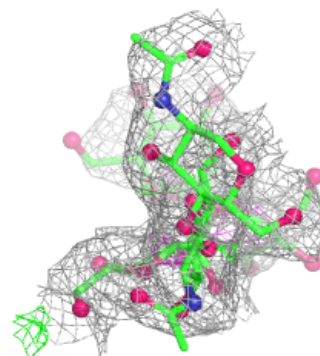
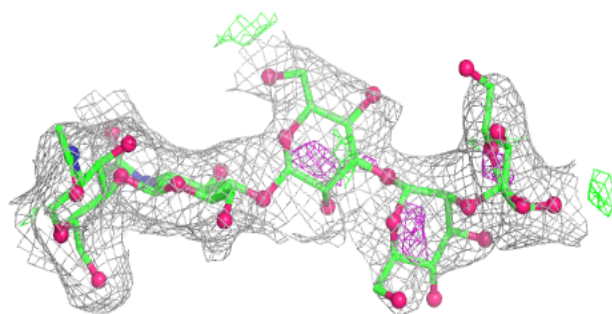
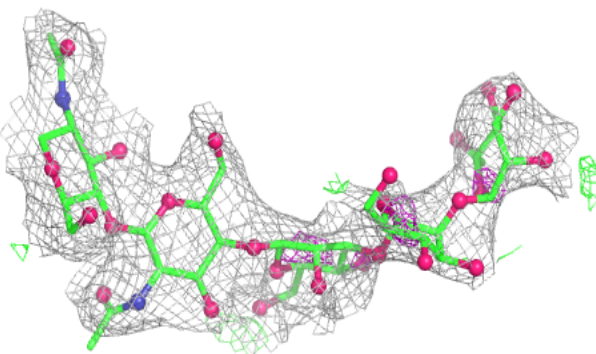
**Electron density around Chain Q:**

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

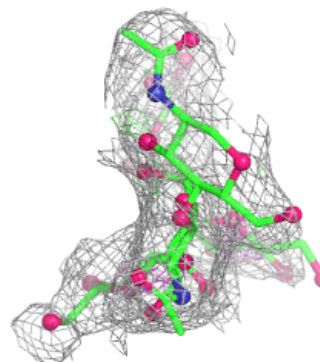
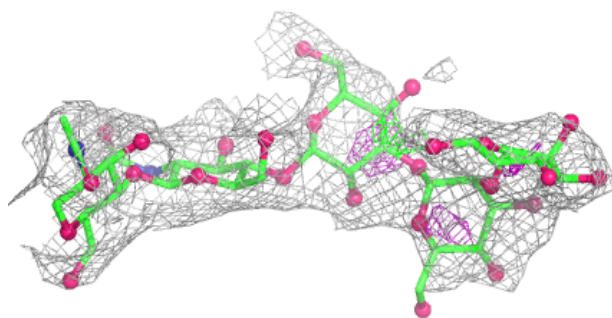
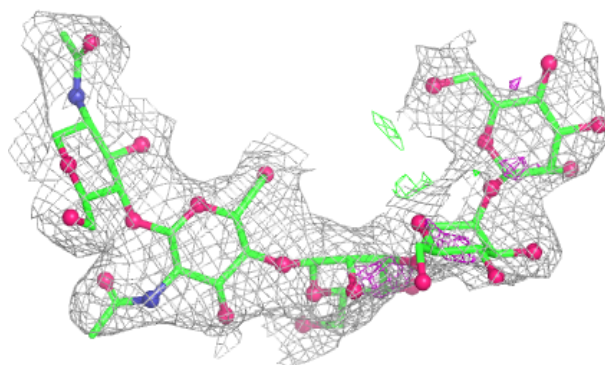


Electron density around Chain J:

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

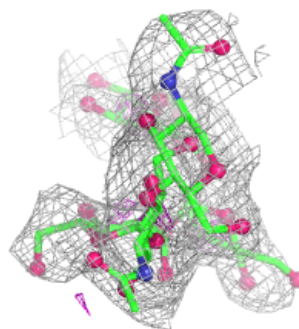
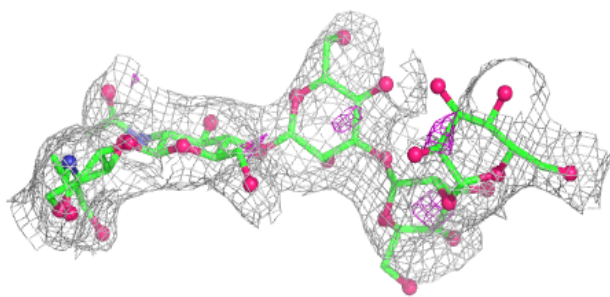
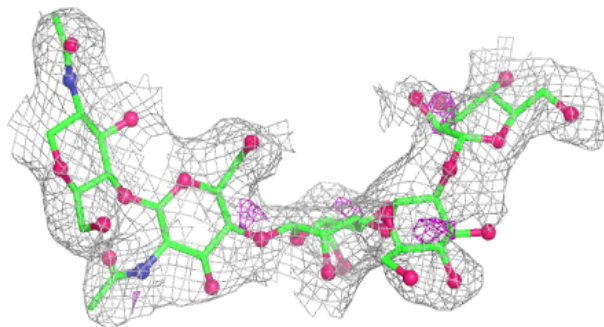
**Electron density around Chain L:**

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

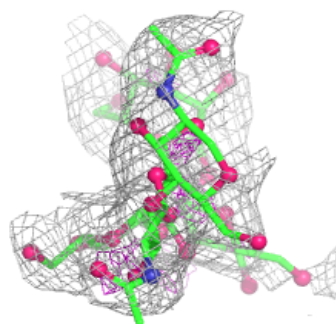
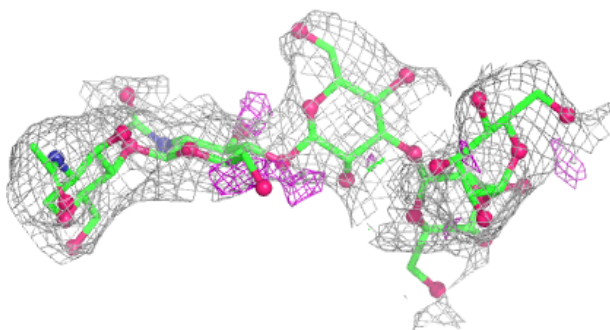
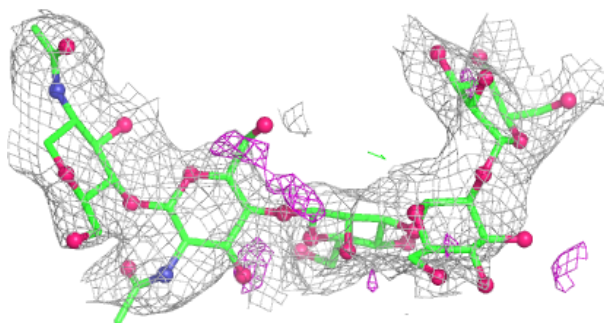


Electron density around Chain N:

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

**Electron density around Chain P:**

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



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
6	NAG	A	601	14/15	0.42	0.17	87,89,91,91	0
6	NAG	B	601	14/15	0.44	0.18	68,70,71,71	0
6	NAG	E	601	14/15	0.45	0.16	62,63,64,64	0
6	NAG	E	602	14/15	0.48	0.18	68,70,72,74	0
6	NAG	F	601	14/15	0.51	0.16	54,56,58,58	0
6	NAG	F	602	14/15	0.51	0.16	81,84,84,84	0
6	NAG	C	601	14/15	0.57	0.15	55,57,59,59	0
6	NAG	B	603	14/15	0.58	0.15	72,73,74,75	0
7	EDO	A	602	4/4	0.60	0.17	50,51,51,52	0
6	NAG	D	601	14/15	0.65	0.14	55,57,58,61	0
6	NAG	C	602	14/15	0.72	0.13	51,52,53,53	0
8	IOD	e	502	1/1	0.73	0.17	174,174,174,174	0
8	IOD	E	605	1/1	0.80	0.14	142,142,142,142	1
8	IOD	F	607	1/1	0.81	0.18	131,131,131,131	1
8	IOD	A	614	1/1	0.83	0.18	98,98,98,98	1
8	IOD	A	608	1/1	0.83	0.18	150,150,150,150	0
6	NAG	B	602	14/15	0.84	0.10	50,51,52,53	0
8	IOD	D	606	1/1	0.86	0.20	104,104,104,104	0
8	IOD	A	607	1/1	0.86	0.08	61,61,61,61	1
8	IOD	F	611	1/1	0.86	0.16	102,102,102,102	1
8	IOD	D	604	1/1	0.87	0.07	48,48,48,48	1
8	IOD	A	606	1/1	0.88	0.08	81,81,81,81	1
8	IOD	F	606	1/1	0.89	0.07	48,48,48,48	1
8	IOD	B	605	1/1	0.89	0.09	59,59,59,59	1
8	IOD	b	501	1/1	0.89	0.13	141,141,141,141	1
8	IOD	F	614	1/1	0.90	0.20	141,141,141,141	1
8	IOD	A	613	1/1	0.91	0.23	127,127,127,127	1
8	IOD	c	501	1/1	0.91	0.14	52,52,52,52	1
8	IOD	E	610	1/1	0.92	0.09	51,51,51,51	1
8	IOD	F	610	1/1	0.92	0.07	67,67,67,67	1
8	IOD	D	605	1/1	0.92	0.10	99,99,99,99	1
8	IOD	E	609	1/1	0.92	0.06	54,54,54,54	1
8	IOD	B	606	1/1	0.93	0.07	81,81,81,81	1
8	IOD	C	611	1/1	0.93	0.08	43,43,43,43	1
8	IOD	B	610	1/1	0.93	0.07	53,53,53,53	1
8	IOD	F	615	1/1	0.93	0.05	60,60,60,60	1
8	IOD	C	605	1/1	0.94	0.04	38,38,38,38	1

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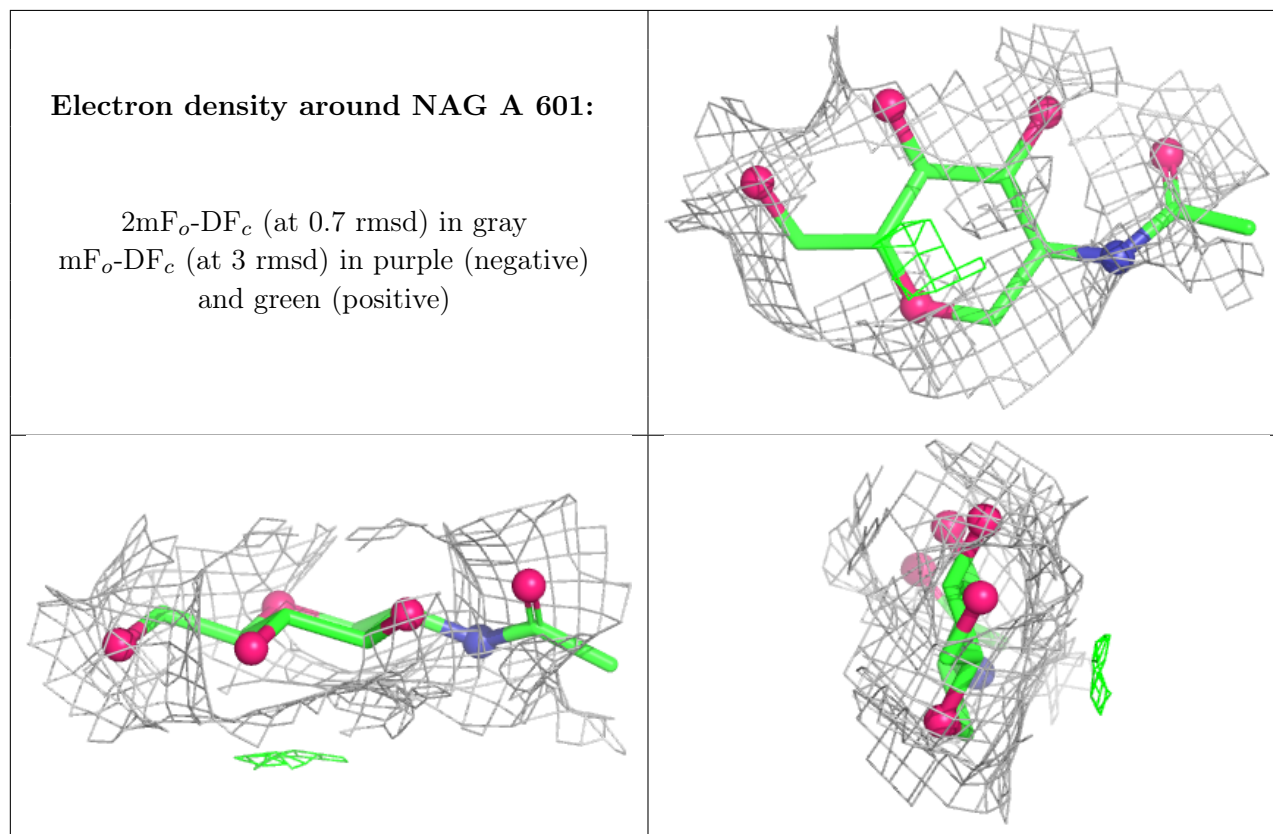
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	IOD	B	612	1/1	0.94	0.06	80,80,80,80	1
8	IOD	C	612	1/1	0.94	0.10	81,81,81,81	1
8	IOD	D	609	1/1	0.94	0.09	98,98,98,98	1
8	IOD	D	610	1/1	0.94	0.15	97,97,97,97	1
8	IOD	A	612	1/1	0.94	0.06	52,52,52,52	1
8	IOD	F	613	1/1	0.94	0.07	95,95,95,95	1
8	IOD	E	608	1/1	0.94	0.06	55,55,55,55	1
8	IOD	c	503	1/1	0.94	0.13	44,44,44,44	1
8	IOD	E	613	1/1	0.95	0.06	59,59,59,59	1
8	IOD	C	607	1/1	0.95	0.05	68,68,68,68	1
8	IOD	F	603	1/1	0.95	0.06	64,64,64,64	1
8	IOD	A	605	1/1	0.95	0.06	53,53,53,53	1
8	IOD	E	612	1/1	0.95	0.05	58,58,58,58	1
8	IOD	E	614	1/1	0.96	0.08	64,64,64,64	1
8	IOD	D	611	1/1	0.96	0.05	44,44,44,44	1
8	IOD	D	613	1/1	0.96	0.07	80,80,80,80	1
8	IOD	C	610	1/1	0.96	0.06	47,47,47,47	1
8	IOD	E	606	1/1	0.96	0.04	49,49,49,49	1
8	IOD	F	608	1/1	0.96	0.07	67,67,67,67	1
8	IOD	A	615	1/1	0.96	0.05	50,50,50,50	1
8	IOD	D	607	1/1	0.96	0.04	58,58,58,58	1
8	IOD	D	608	1/1	0.96	0.06	48,48,48,48	1
8	IOD	D	603	1/1	0.96	0.06	51,51,51,51	1
8	IOD	A	610	1/1	0.96	0.08	43,43,43,43	1
8	IOD	E	607	1/1	0.97	0.04	50,50,50,50	1
8	IOD	F	604	1/1	0.97	0.23	82,82,82,82	0
8	IOD	F	605	1/1	0.97	0.07	50,50,50,50	1
8	IOD	C	608	1/1	0.97	0.04	51,51,51,51	1
8	IOD	B	607	1/1	0.97	0.09	75,75,75,75	0
8	IOD	B	608	1/1	0.97	0.04	41,41,41,41	1
8	IOD	B	609	1/1	0.97	0.07	54,54,54,54	1
8	IOD	E	603	1/1	0.97	0.04	48,48,48,48	1
8	IOD	C	606	1/1	0.97	0.04	63,63,63,63	1
8	IOD	e	501	1/1	0.97	0.05	70,70,70,70	1
8	IOD	A	611	1/1	0.97	0.06	57,57,57,57	1
8	IOD	A	609	1/1	0.98	0.04	46,46,46,46	1
8	IOD	C	603	1/1	0.98	0.05	54,54,54,54	1
8	IOD	D	602	1/1	0.98	0.03	57,57,57,57	1
8	IOD	A	604	1/1	0.98	0.03	47,47,47,47	1
8	IOD	C	604	1/1	0.99	0.11	46,46,46,46	1
8	IOD	D	612	1/1	0.99	0.02	33,33,33,33	1
8	IOD	c	502	1/1	0.99	0.15	88,88,88,88	0

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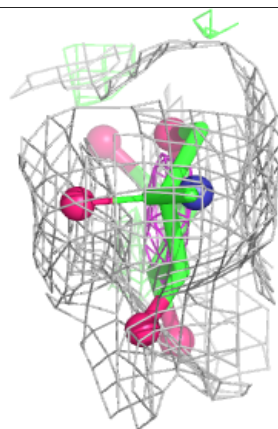
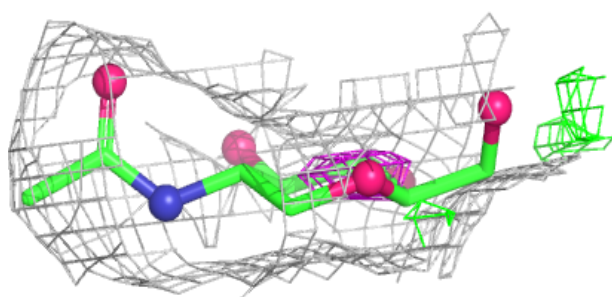
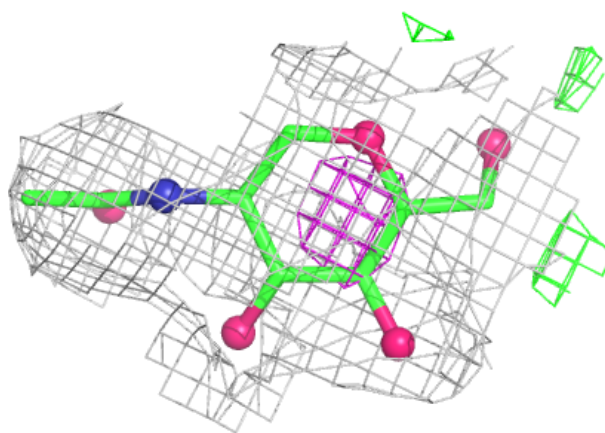
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	IOD	E	611	1/1	0.99	0.04	42,42,42,42	1
8	IOD	d	501	1/1	0.99	0.02	42,42,42,42	1
8	IOD	F	609	1/1	0.99	0.04	57,57,57,57	1
8	IOD	C	609	1/1	0.99	0.02	39,39,39,39	1
8	IOD	E	604	1/1	0.99	0.03	43,43,43,43	1
8	IOD	F	612	1/1	0.99	0.04	36,36,36,36	1
8	IOD	A	603	1/1	0.99	0.03	45,45,45,45	1
8	IOD	B	604	1/1	0.99	0.02	40,40,40,40	1
8	IOD	B	611	1/1	0.99	0.02	33,33,33,33	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

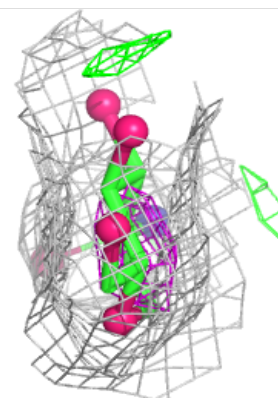
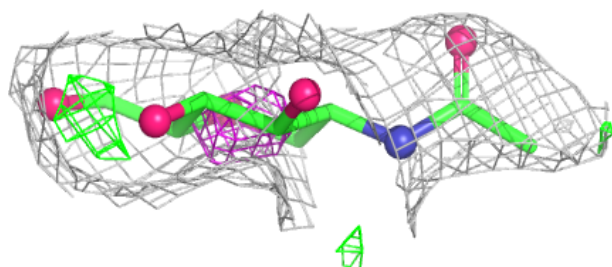
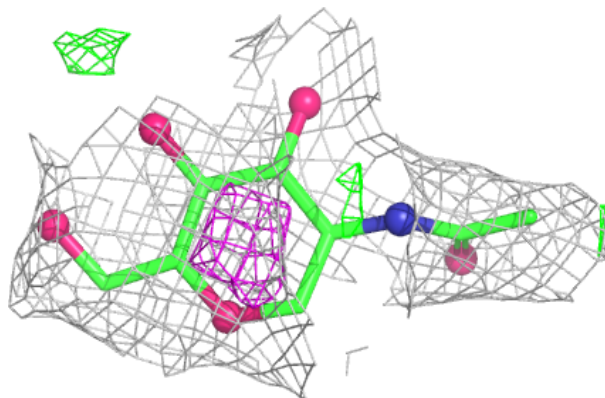


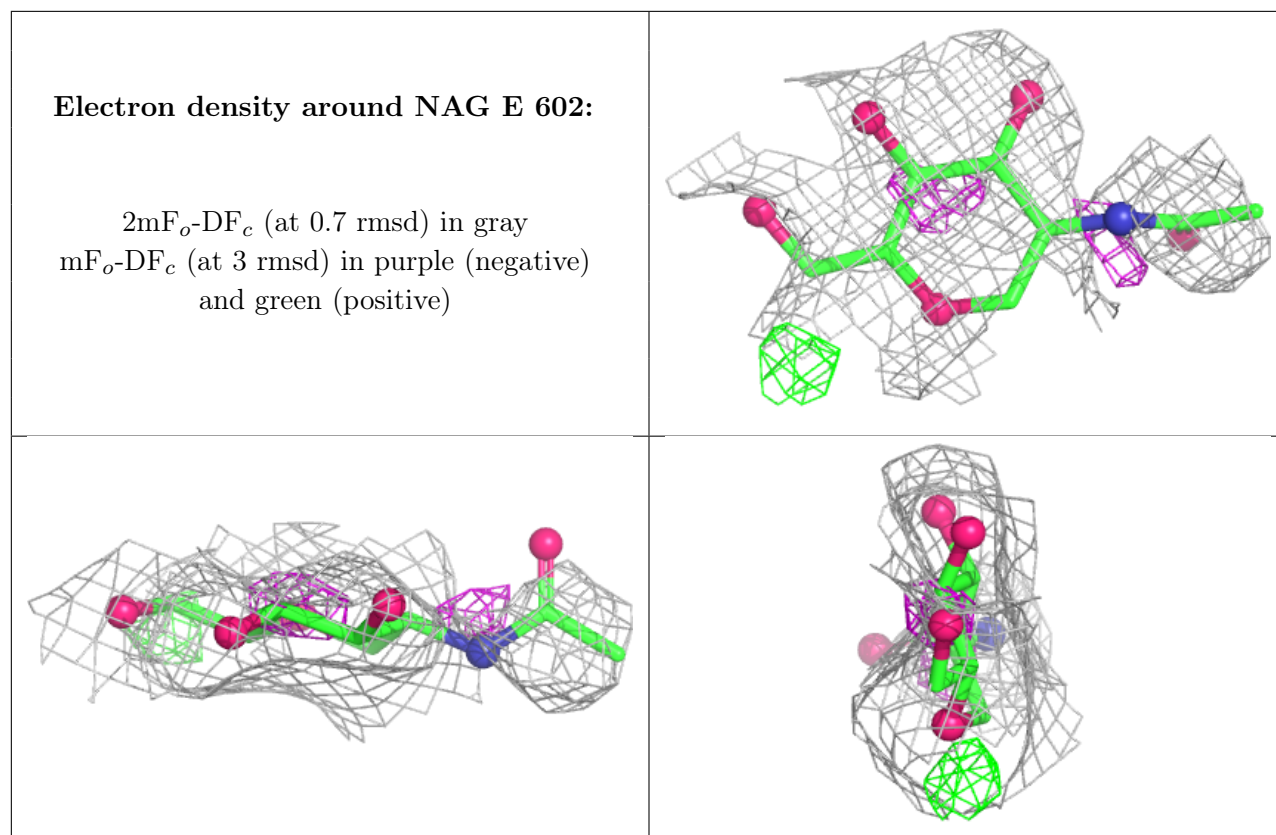
Electron density around NAG B 601:

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

**Electron density around NAG E 601:**

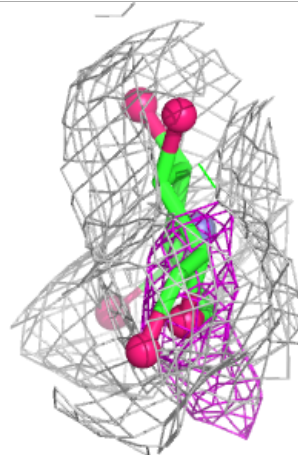
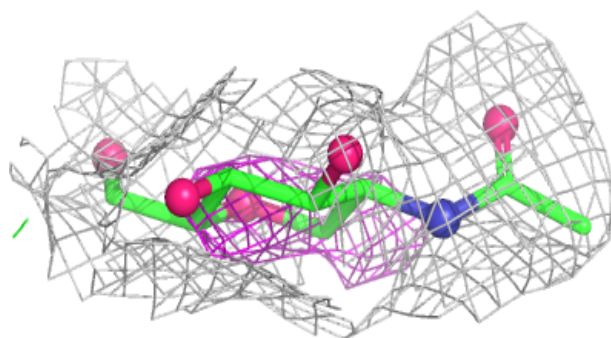
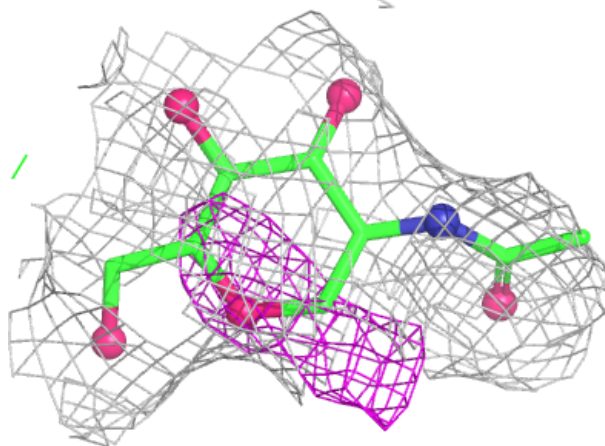
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





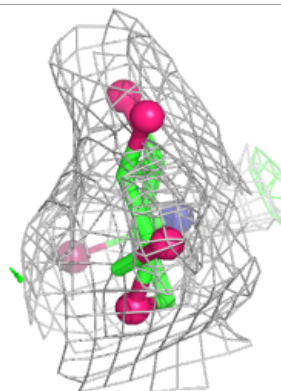
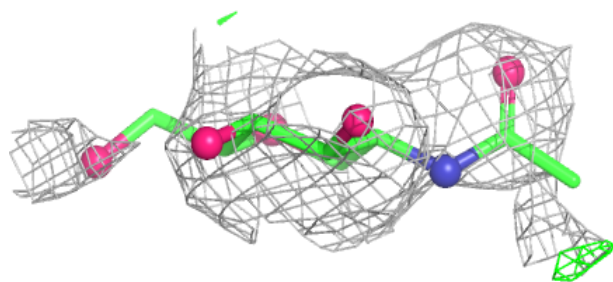
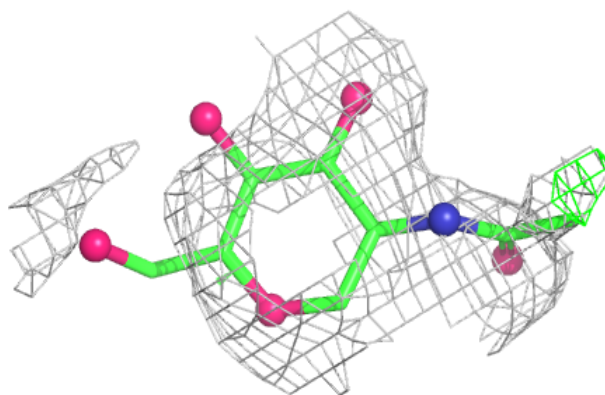
Electron density around NAG F 601:

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

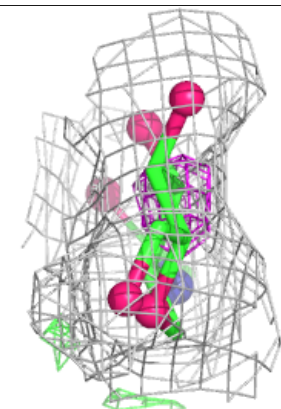
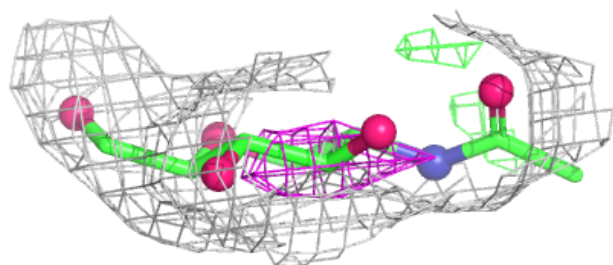
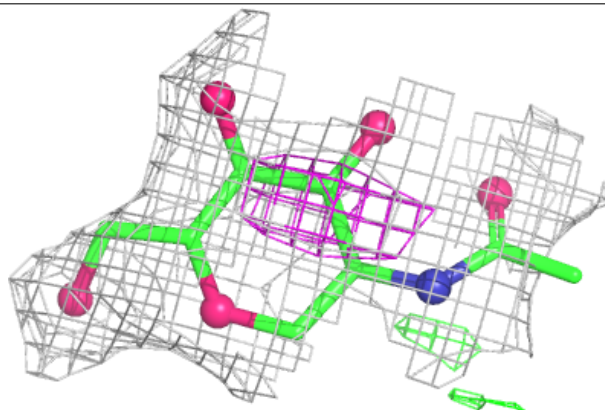


Electron density around NAG F 602:

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

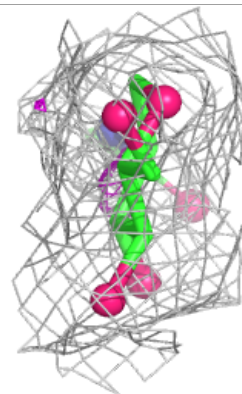
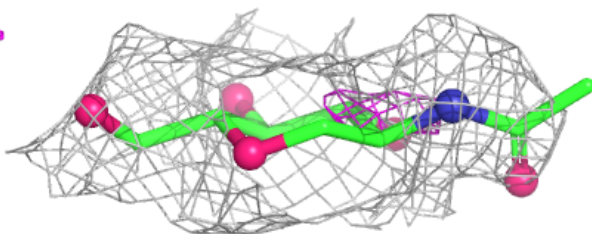
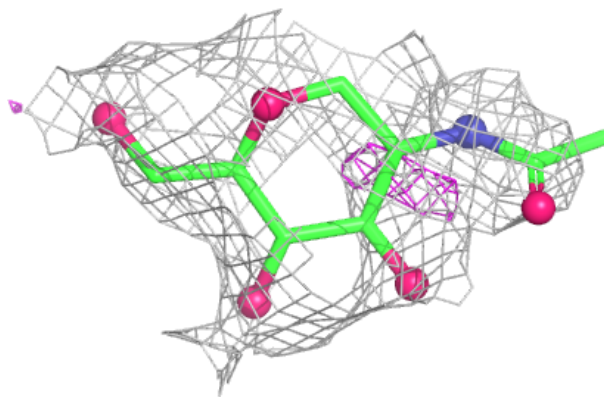
**Electron density around NAG C 601:**

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

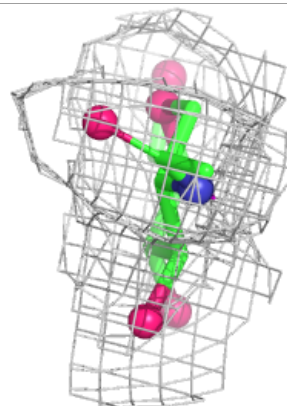
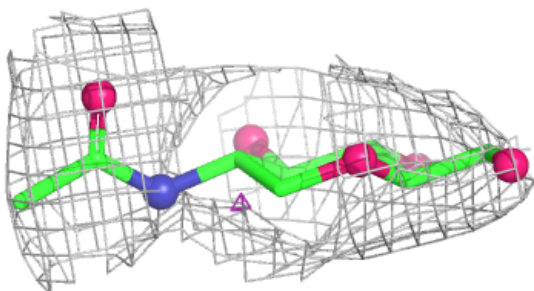
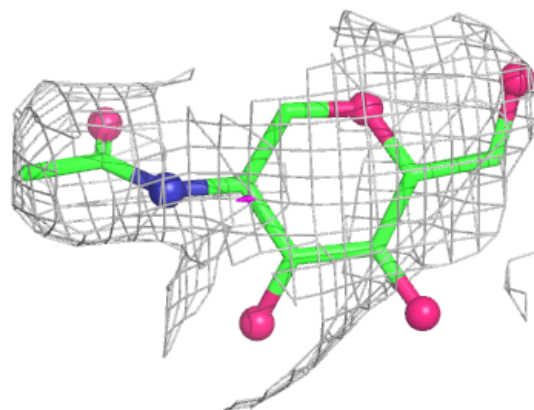


Electron density around NAG B 603:

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

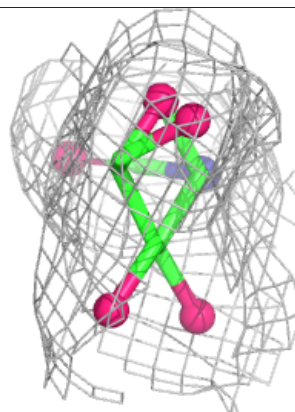
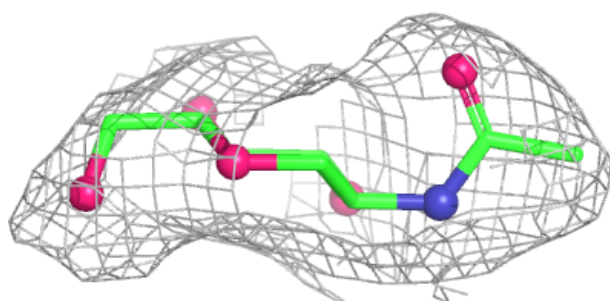
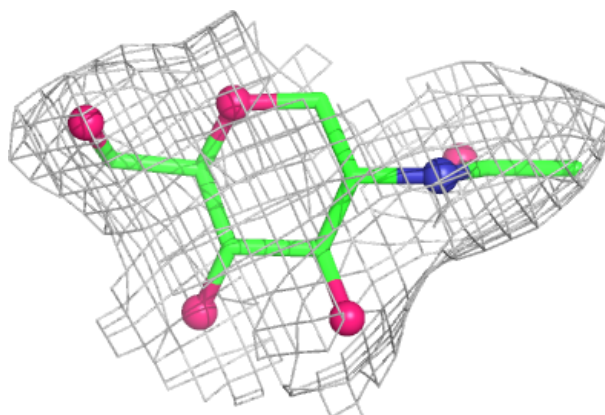
**Electron density around NAG D 601:**

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

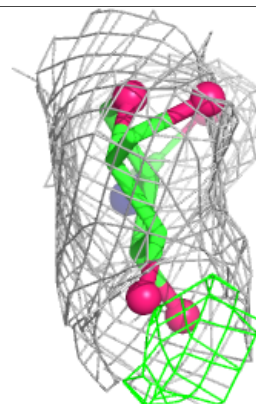
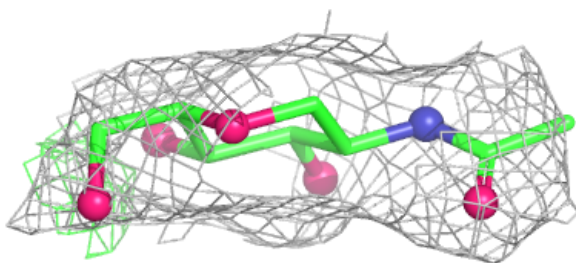
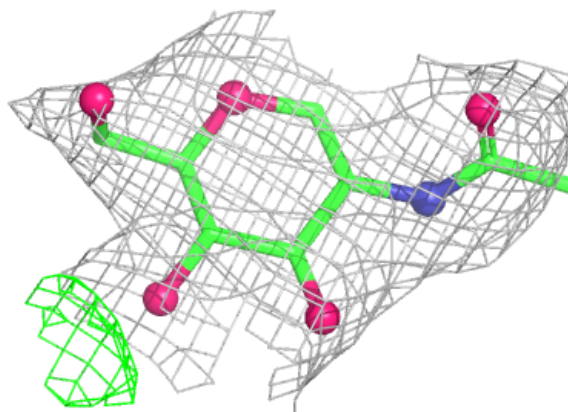


Electron density around NAG C 602:

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

**Electron density around NAG B 602:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.