



wwPDB X-ray Structure Validation Summary Report ⓘ

May 2, 2026 – 08:06 AM EDT

PDB ID : 9Y3Y / pdb_00009y3y
Title : Crystal structure of hemagglutinin from H1N1 Influenza A virus
A/California/04/2009 bound to the 49_C09 antibody
Authors : Wang, B.; Wilson, I.A.
Deposited on : 2025-09-02
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

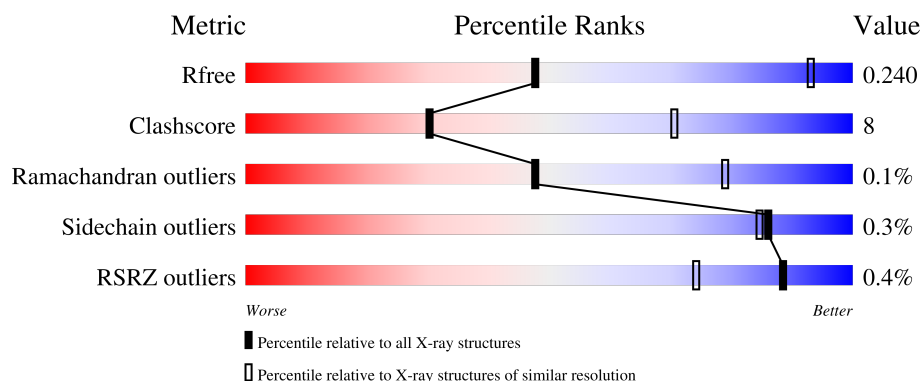
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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	327	<div> <div>75%</div> <div>24%</div> </div>
1	C	327	<div> <div>77%</div> <div>22%</div> </div>
2	B	177	<div> <div>%</div> <div>86%</div> <div>11%</div> <div>.</div> </div>
2	D	177	<div> <div>82%</div> <div>15%</div> <div>.</div> </div>
3	F	214	<div> <div>84%</div> <div>15%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	L	214	 83% 15% .
4	E	228	%  71% 27% .
4	H	228	%  75% 21% .
5	G	3	 67% 33%
5	M	3	 33% 67%
6	P	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14461 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	C	326	Total	C	N	O	S	0	0	0
			2544	1608	438	487	11			
1	A	326	Total	C	N	O	S	0	0	0
			2544	1608	438	487	11			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	7	ALA	-	expression tag	UNP G8EHJ9
C	8	ASP	-	expression tag	UNP G8EHJ9
C	9	PRO	-	expression tag	UNP G8EHJ9
C	10	GLY	-	expression tag	UNP G8EHJ9
C	186	SER	PRO	conflict	UNP G8EHJ9
A	7	ALA	-	expression tag	UNP G8EHJ9
A	8	ASP	-	expression tag	UNP G8EHJ9
A	9	PRO	-	expression tag	UNP G8EHJ9
A	10	GLY	-	expression tag	UNP G8EHJ9
A	186	SER	PRO	conflict	UNP G8EHJ9

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	171	Total	C	N	O	S	0	0	0
			1375	863	234	272	6			
2	B	171	Total	C	N	O	S	0	0	0
			1375	863	234	272	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	175	SER	-	expression tag	UNP I1ZFF9
D	176	GLY	-	expression tag	UNP I1ZFF9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	177	ARG	-	expression tag	UNP I1ZFF9
B	175	SER	-	expression tag	UNP I1ZFF9
B	176	GLY	-	expression tag	UNP I1ZFF9
B	177	ARG	-	expression tag	UNP I1ZFF9

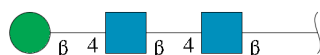
- Molecule 3 is a protein called Antibody 49_C09 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	211	Total	C	N	O	S	0	0	0
			1592	997	274	316	5			
3	F	211	Total	C	N	O	S	0	0	0
			1592	997	274	316	5			

- Molecule 4 is a protein called Antibody 49_C09 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	220	Total	C	N	O	S	0	1	0
			1638	1033	273	324	8			
4	E	222	Total	C	N	O	S	0	1	0
			1653	1042	276	327	8			

- Molecule 5 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
5	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	M	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 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
6	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).

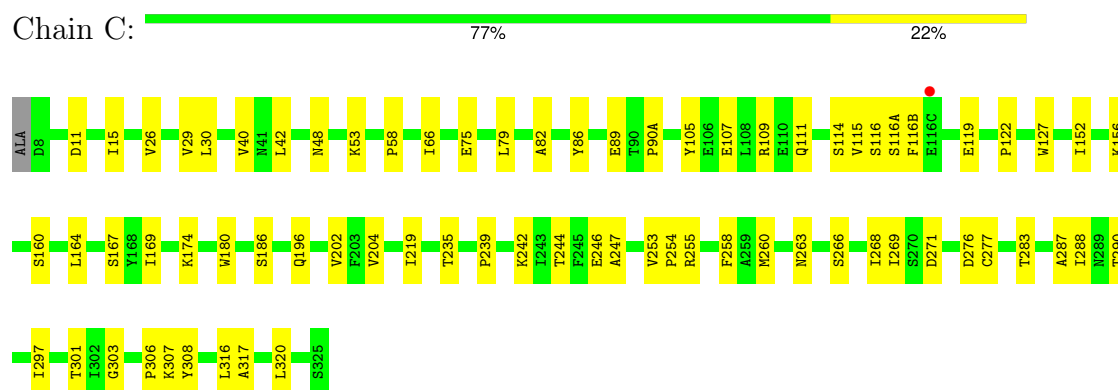


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

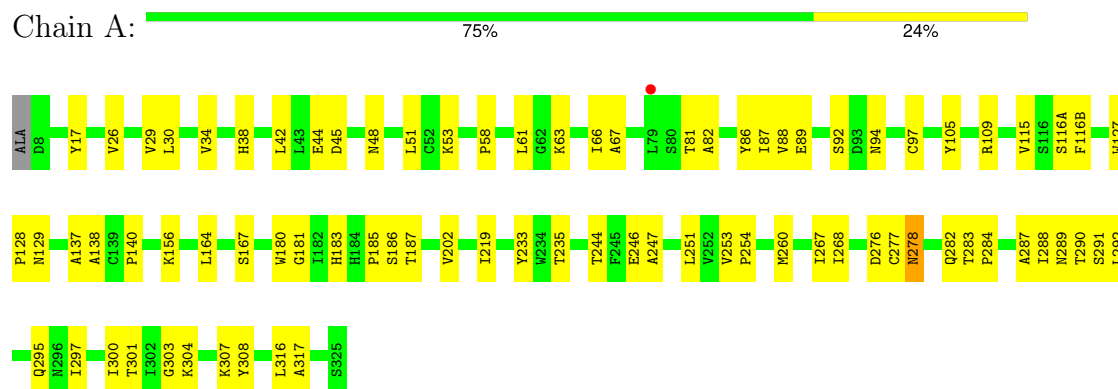
3 Residue-property plots [i](#)

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.

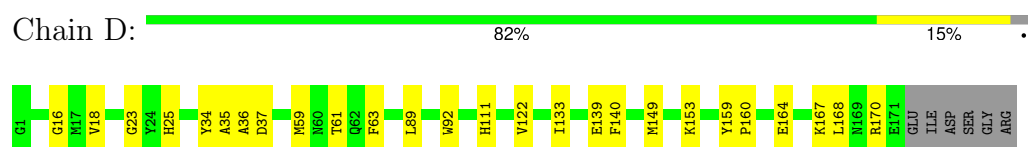
• Molecule 1: Hemagglutinin



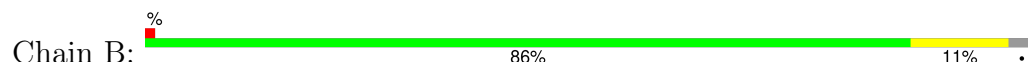
• Molecule 1: Hemagglutinin



• Molecule 2: Hemagglutinin

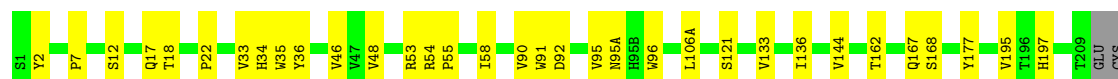
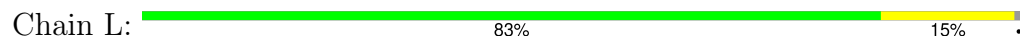


• Molecule 2: Hemagglutinin



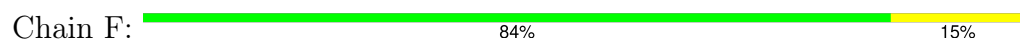


- Molecule 3: Antibody 49_C09 light chain



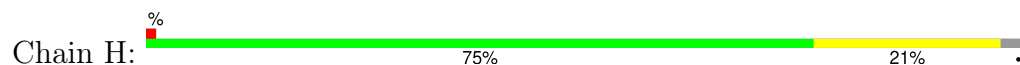
SER

- Molecule 3: Antibody 49_C09 light chain



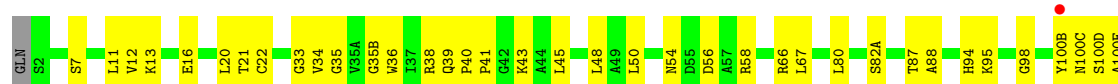
H197
E198
T209
GLU
CYS
SER

- Molecule 4: Antibody 49_C09 heavy chain



T110
P119
P123
P126
S127
SER
LYS
SER
THR
SER
GLY
G134
Y145
F146
P147
E148
P149
V169
L170
L175
Y176
I195
C196
N197
P213
K214
S215
CYS

- Molecule 4: Antibody 49_C09 heavy chain



A100F
F100G
W103
T110
V111
T116
P119
P126
K129
SER
THR
SER
GLY
G134
L138
G139
Y145
T151
L159
G162
V169
S177
V181
V182
T193
Y194
I195
C196
N197
V198
N199
S203
R210
V211
S215
CYS

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





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



- Molecule 6: 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 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.92Å 166.92Å 347.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.71 – 3.80 49.71 – 3.80	Depositor EDS
% Data completeness (in resolution range)	77.3 (49.71-3.80) 77.4 (49.71-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.21	Depositor
R, R_{free}	0.205 , 0.240 0.207 , 0.240	Depositor DCC
R_{free} test set	2006 reflections (3.56%)	wwPDB-VP
Wilson B-factor (Å ²)	64.7	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 92.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.047 for -h,-k,l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	14461	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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: BMA, NAG

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	0.39	0/2609	0.60	0/3547
1	C	0.25	0/2609	0.49	0/3547
2	B	0.31	0/1403	0.53	0/1890
2	D	0.22	0/1403	0.40	0/1890
3	F	0.32	0/1635	0.56	0/2239
3	L	0.22	0/1635	0.45	0/2239
4	E	0.33	0/1695	0.58	0/2314
4	H	0.27	0/1680	0.53	0/2295
All	All	0.30	0/14669	0.53	0/19961

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2544	0	2486	58	0
1	C	2544	0	2488	47	0
2	B	1375	0	1300	16	0
2	D	1375	0	1300	20	0
3	F	1592	0	1539	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	1592	0	1539	23	0
4	E	1653	0	1632	48	0
4	H	1638	0	1614	29	0
5	G	39	0	34	1	0
5	M	39	0	34	3	0
6	P	28	0	25	0	0
7	A	28	0	26	0	0
7	C	14	0	13	0	0
All	All	14461	0	14030	238	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 8.

The worst 5 of 238 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:C:26:VAL:HG21	1:C:317:ALA:HB2	1.55	0.88
4:H:7:SER:HB2	4:H:21:THR:H	1.40	0.87
4:E:7:SER:HB2	4:E:21:THR:H	1.42	0.84
1:C:283:THR:HG22	1:C:301:THR:HG22	1.61	0.80
2:D:133:ILE:HD13	2:D:139:GLU:HB2	1.66	0.76

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	324/327 (99%)	305 (94%)	18 (6%)	1 (0%)	36	67
1	C	324/327 (99%)	309 (95%)	15 (5%)	0	100	100
2	B	169/177 (96%)	163 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	169/177 (96%)	163 (96%)	6 (4%)	0	100	100
3	F	209/214 (98%)	200 (96%)	9 (4%)	0	100	100
3	L	209/214 (98%)	199 (95%)	10 (5%)	0	100	100
4	E	219/228 (96%)	203 (93%)	16 (7%)	0	100	100
4	H	217/228 (95%)	202 (93%)	15 (7%)	0	100	100
All	All	1840/1892 (97%)	1744 (95%)	95 (5%)	1 (0%)	48	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	286/286 (100%)	283 (99%)	3 (1%)	68	74
1	C	286/286 (100%)	285 (100%)	1 (0%)	86	84
2	B	146/151 (97%)	146 (100%)	0	100	100
2	D	146/151 (97%)	146 (100%)	0	100	100
3	F	178/181 (98%)	178 (100%)	0	100	100
3	L	178/181 (98%)	178 (100%)	0	100	100
4	E	190/195 (97%)	190 (100%)	0	100	100
4	H	188/195 (96%)	188 (100%)	0	100	100
All	All	1598/1626 (98%)	1594 (100%)	4 (0%)	86	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	277	CYS
1	A	277	CYS

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Mol	Chain	Res	Type
1	A	278	ASN
1	A	289	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	197	HIS
3	F	95(A)	ASN
4	H	39	GLN
1	A	47	HIS
4	E	199	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 ⓘ

8 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	$\# Z > 2$
5	NAG	G	1	5,1	14,14,15	0.88	1 (7%)	17,19,21	1.04	0
5	NAG	G	2	5	14,14,15	0.70	0	17,19,21	1.35	2 (11%)
5	BMA	G	3	5	11,11,12	0.94	1 (9%)	15,15,17	2.74	4 (26%)
5	NAG	M	1	5,1	14,14,15	0.87	0	17,19,21	1.18	2 (11%)
5	NAG	M	2	5	14,14,15	0.76	0	17,19,21	1.28	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BMA	M	3	5	11,11,12	0.95	0	15,15,17	2.70	6 (40%)
6	NAG	P	1	1,6	14,14,15	0.72	0	17,19,21	1.71	4 (23%)
6	NAG	P	2	6	14,14,15	0.70	0	17,19,21	1.63	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	G	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	G	2	5	-	3/6/23/26	0/1/1/1
5	BMA	G	3	5	-	2/2/19/22	0/1/1/1
5	NAG	M	1	5,1	-	3/6/23/26	0/1/1/1
5	NAG	M	2	5	-	3/6/23/26	0/1/1/1
5	BMA	M	3	5	-	2/2/19/22	0/1/1/1
6	NAG	P	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	P	2	6	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	3	BMA	C2-C3	2.10	1.55	1.52
5	G	1	NAG	C1-C2	2.07	1.55	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	3	BMA	C1-O5-C5	8.26	123.26	112.19
5	M	3	BMA	C1-O5-C5	7.73	122.54	112.19
6	P	2	NAG	C1-O5-C5	5.40	119.42	112.19
6	P	1	NAG	C2-N2-C7	4.21	128.54	122.90
5	M	3	BMA	C3-C4-C5	3.70	116.95	110.23

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	3	BMA	O5-C5-C6-O6

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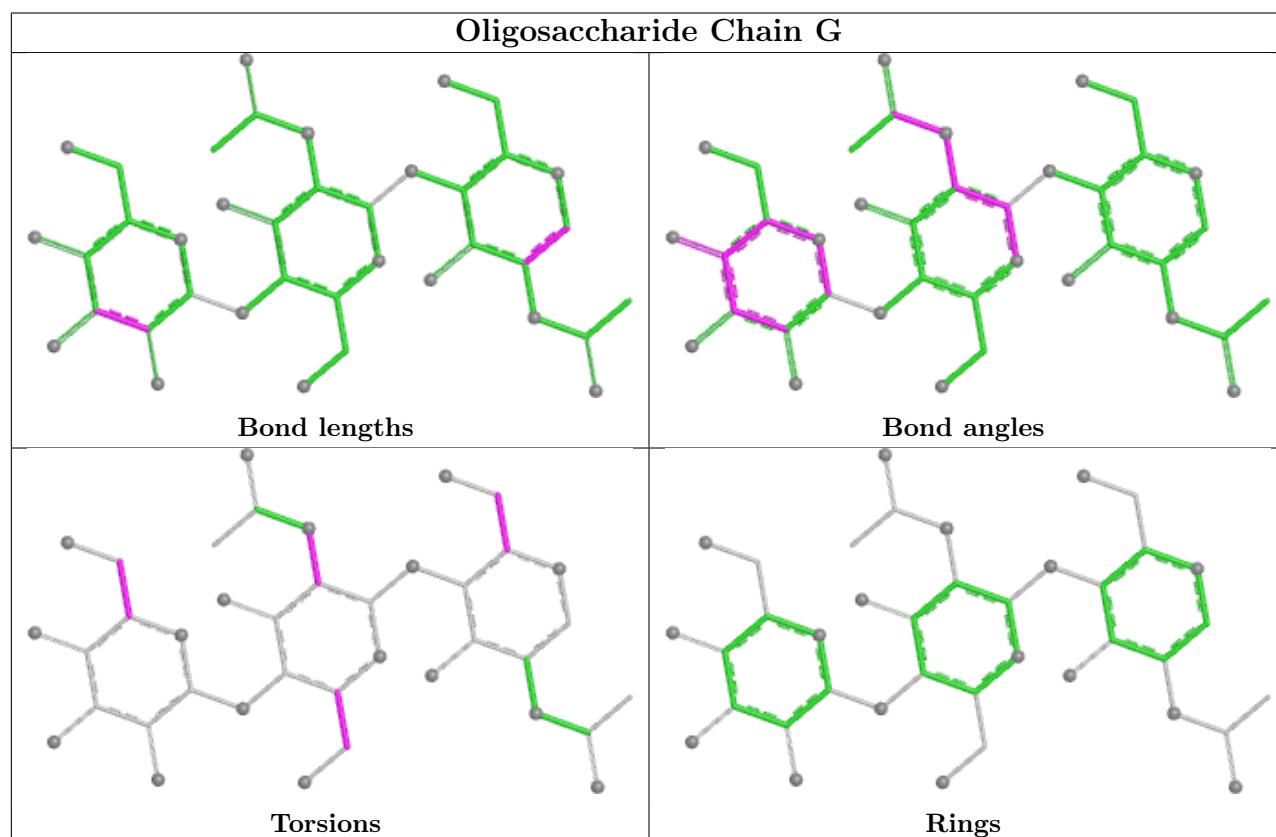
Mol	Chain	Res	Type	Atoms
5	M	3	BMA	O5-C5-C6-O6
6	P	2	NAG	O5-C5-C6-O6
5	M	1	NAG	C8-C7-N2-C2
5	M	1	NAG	O7-C7-N2-C2

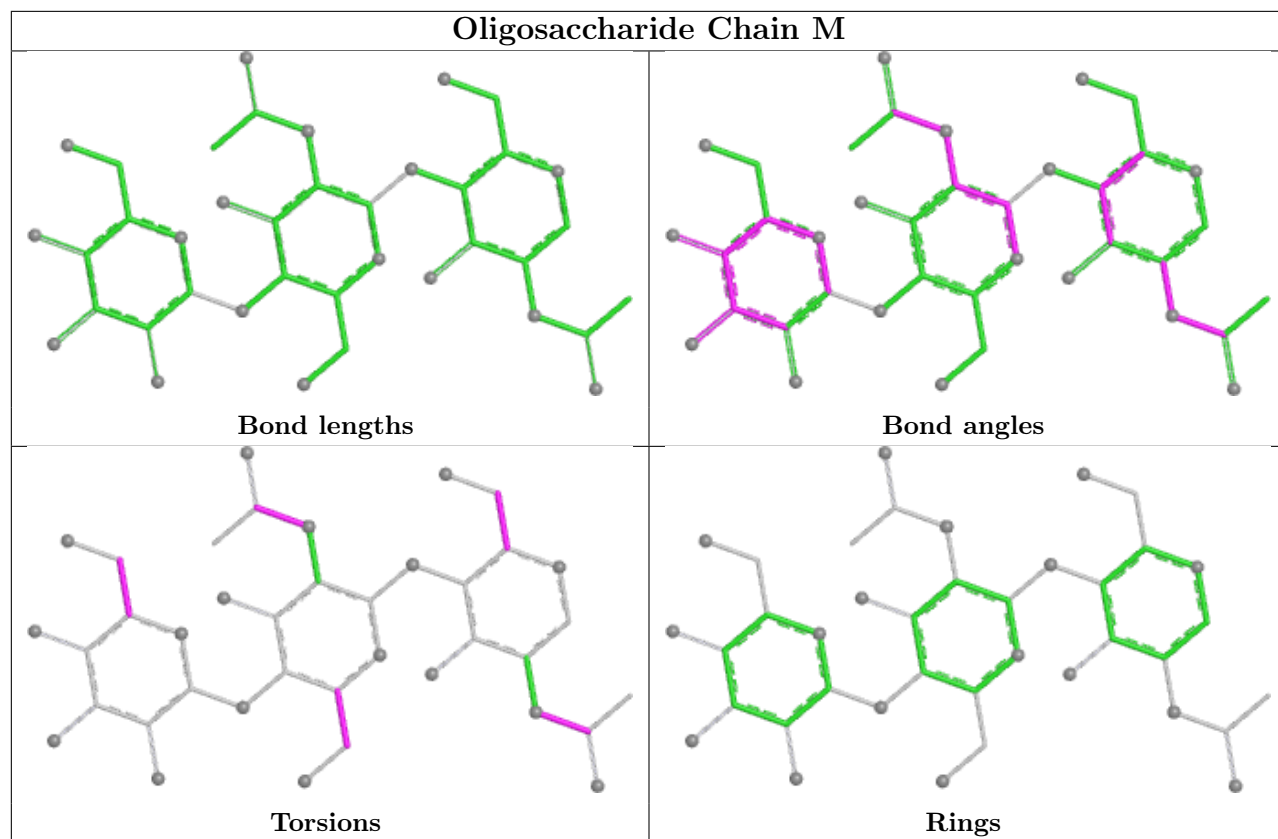
There are no ring outliers.

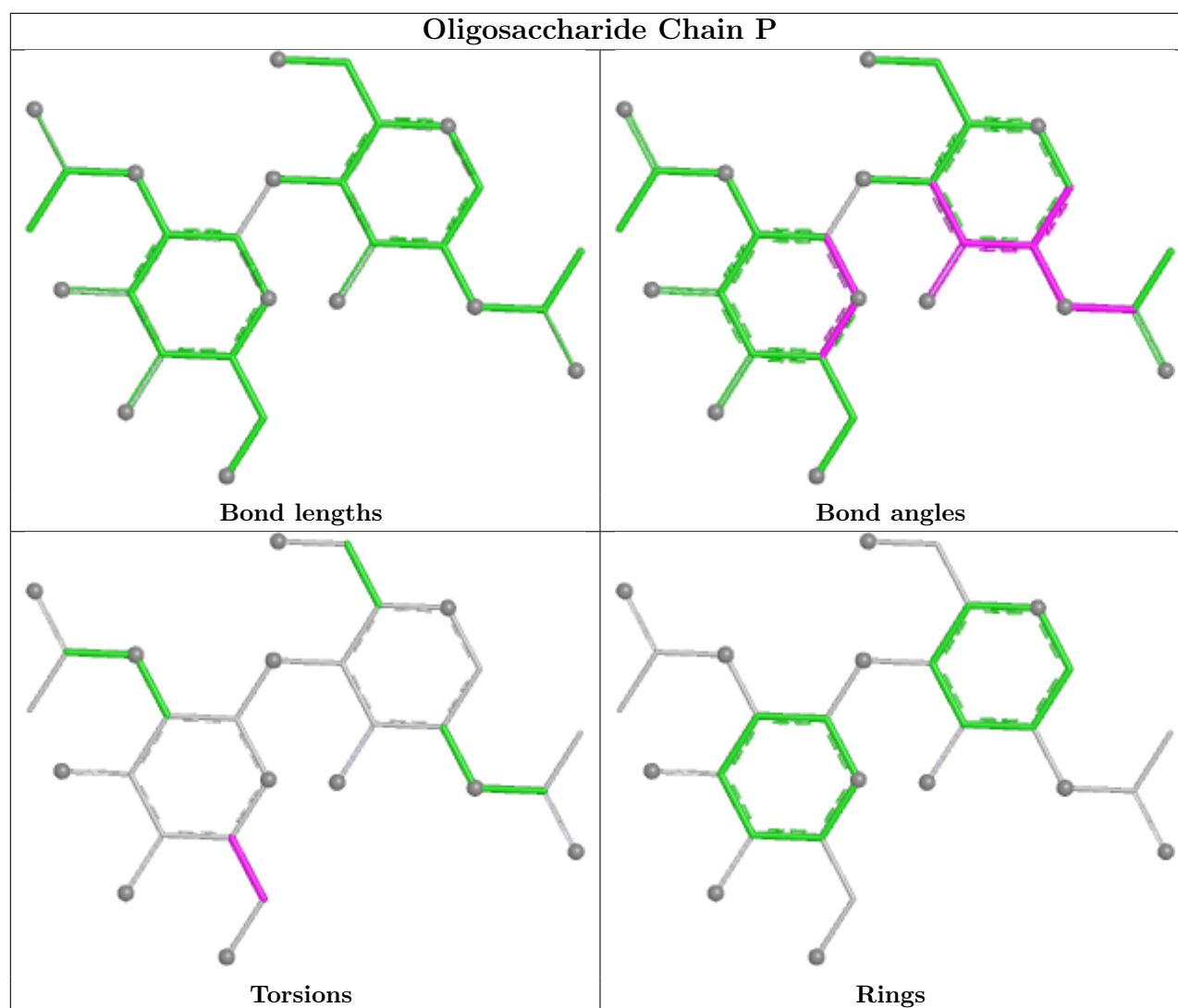
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	1	NAG	1	0
5	M	1	NAG	3	0
5	M	2	NAG	1	0

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







5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
7	NAG	A	701	1	14,14,15	0.81	1 (7%)	17,19,21	1.49	3 (17%)
7	NAG	A	702	1	14,14,15	0.62	0	17,19,21	1.33	2 (11%)
7	NAG	C	401	1	14,14,15	0.75	0	17,19,21	1.20	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	A	701	1	-	1/6/23/26	0/1/1/1
7	NAG	A	702	1	-	0/6/23/26	0/1/1/1
7	NAG	C	401	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)
7	A	701	NAG	C1-C2	2.20	1.55	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	702	NAG	C1-O5-C5	3.89	117.41	112.19
7	A	701	NAG	C1-O5-C5	3.54	116.93	112.19
7	A	701	NAG	C2-N2-C7	3.46	127.54	122.90
7	A	702	NAG	C2-N2-C7	3.03	126.96	122.90
7	C	401	NAG	O5-C1-C2	-2.57	107.31	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

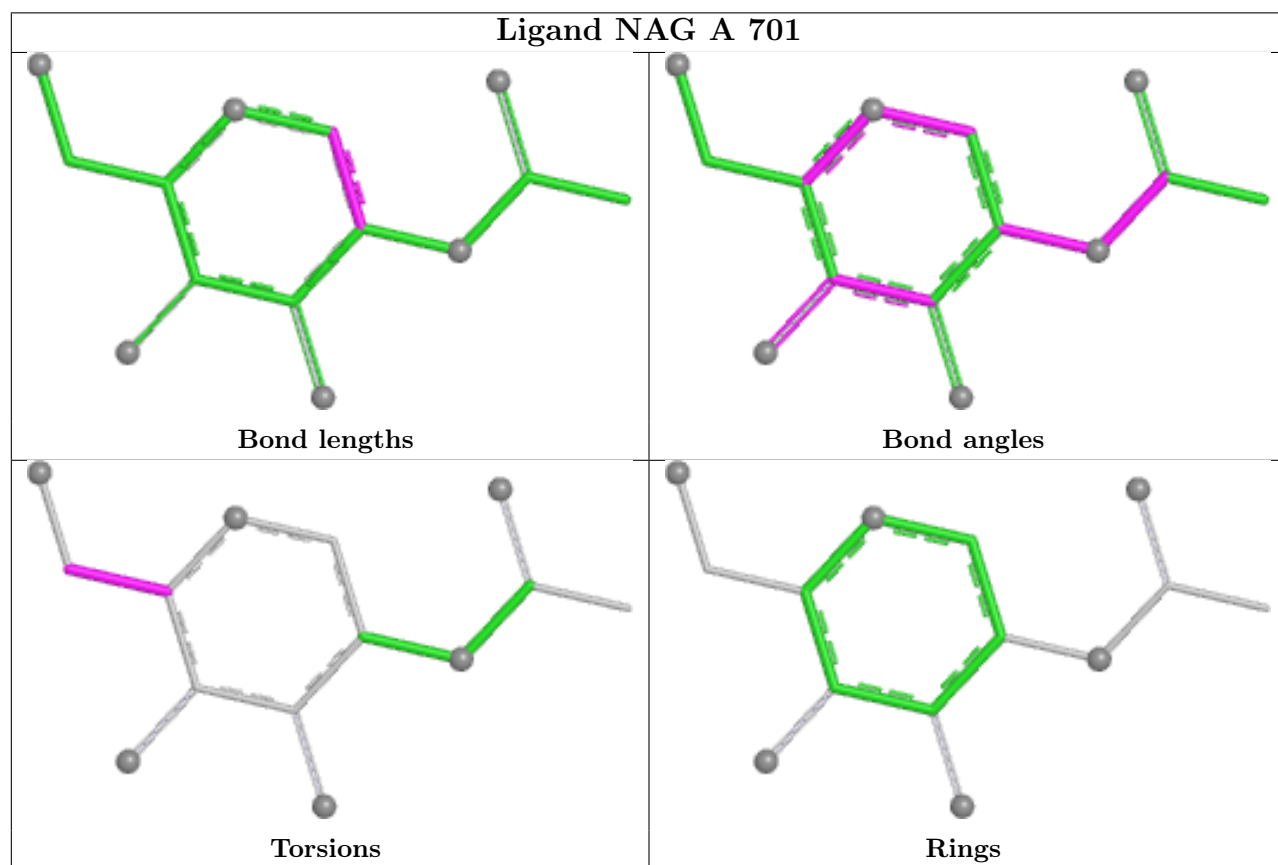
Mol	Chain	Res	Type	Atoms
7	A	701	NAG	O5-C5-C6-O6
7	C	401	NAG	O5-C5-C6-O6

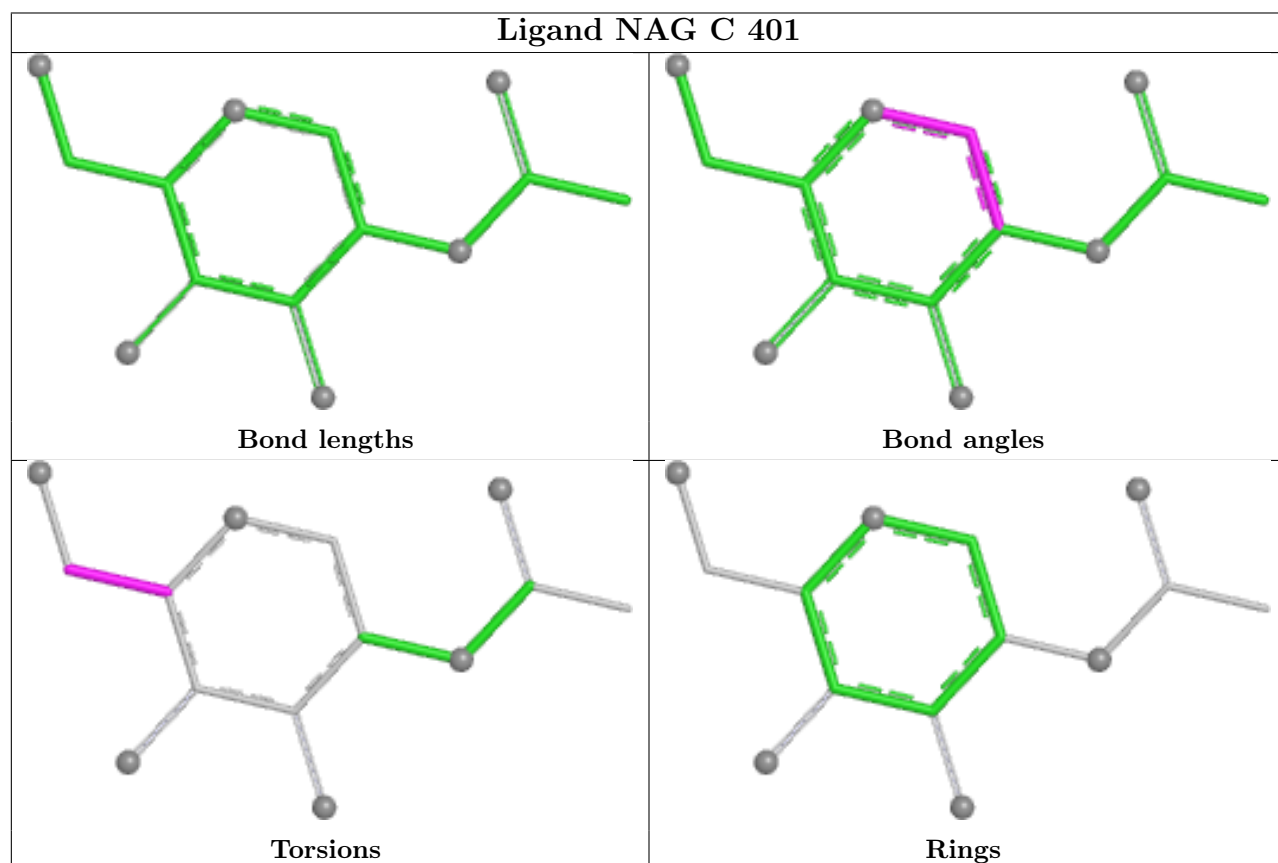
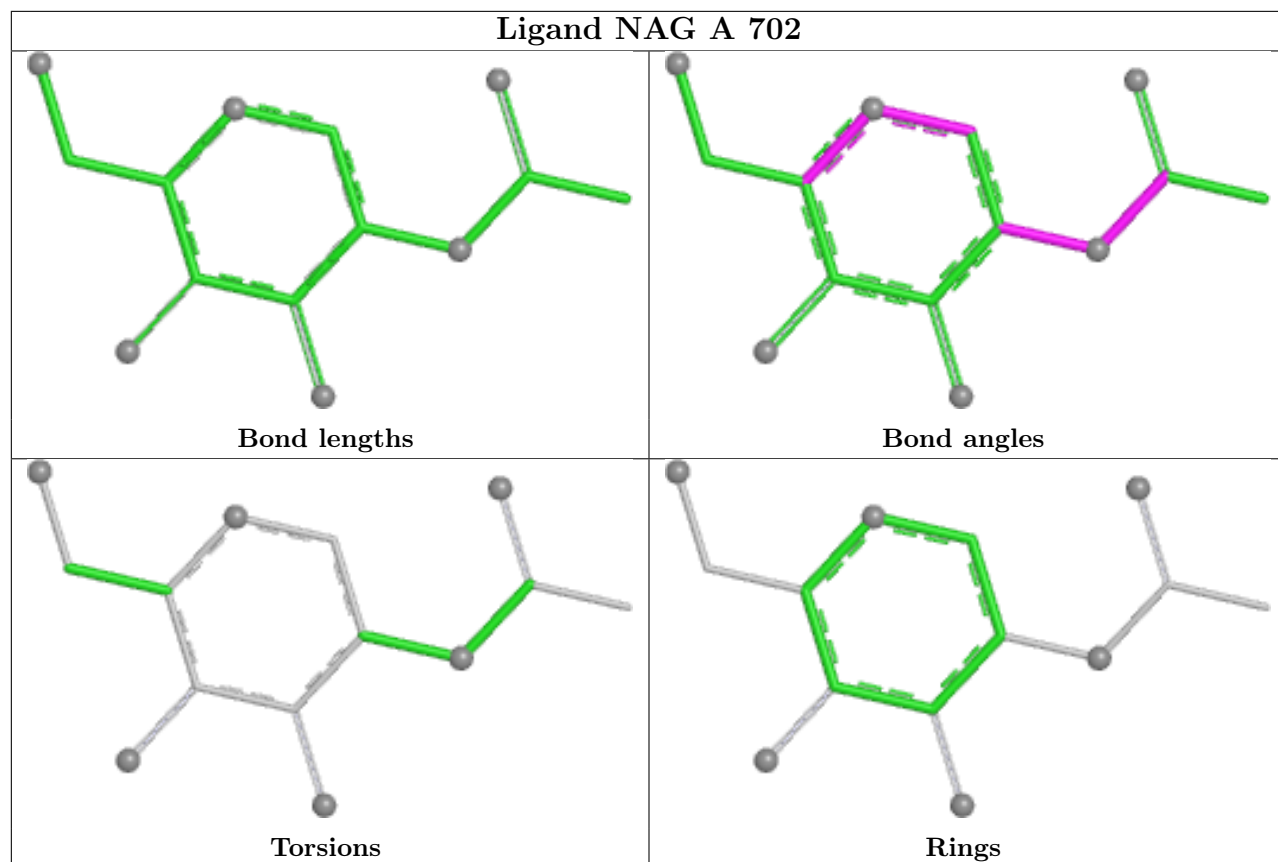
There are no ring outliers.

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	326/327 (99%)	-0.49	1 (0%) 90 78	22, 58, 103, 162	0
1	C	326/327 (99%)	-0.25	1 (0%) 90 78	64, 106, 152, 195	0
2	B	171/177 (96%)	-0.40	1 (0%) 85 68	32, 82, 135, 153	0
2	D	171/177 (96%)	-0.09	0 100 100	75, 128, 171, 197	0
3	F	211/214 (98%)	-0.56	0 100 100	26, 62, 102, 131	0
3	L	211/214 (98%)	-0.22	0 100 100	69, 111, 144, 157	0
4	E	222/228 (97%)	-0.38	2 (0%) 81 60	30, 70, 111, 151	1 (0%)
4	H	220/228 (96%)	-0.22	2 (0%) 81 60	56, 99, 130, 156	1 (0%)
All	All	1858/1892 (98%)	-0.34	7 (0%) 88 74	22, 90, 145, 197	2 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	E	134	GLY	2.8
1	A	79	LEU	2.7
4	H	94	HIS	2.5
1	C	116(C)	GLU	2.4
2	B	164	GLU	2.3

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

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

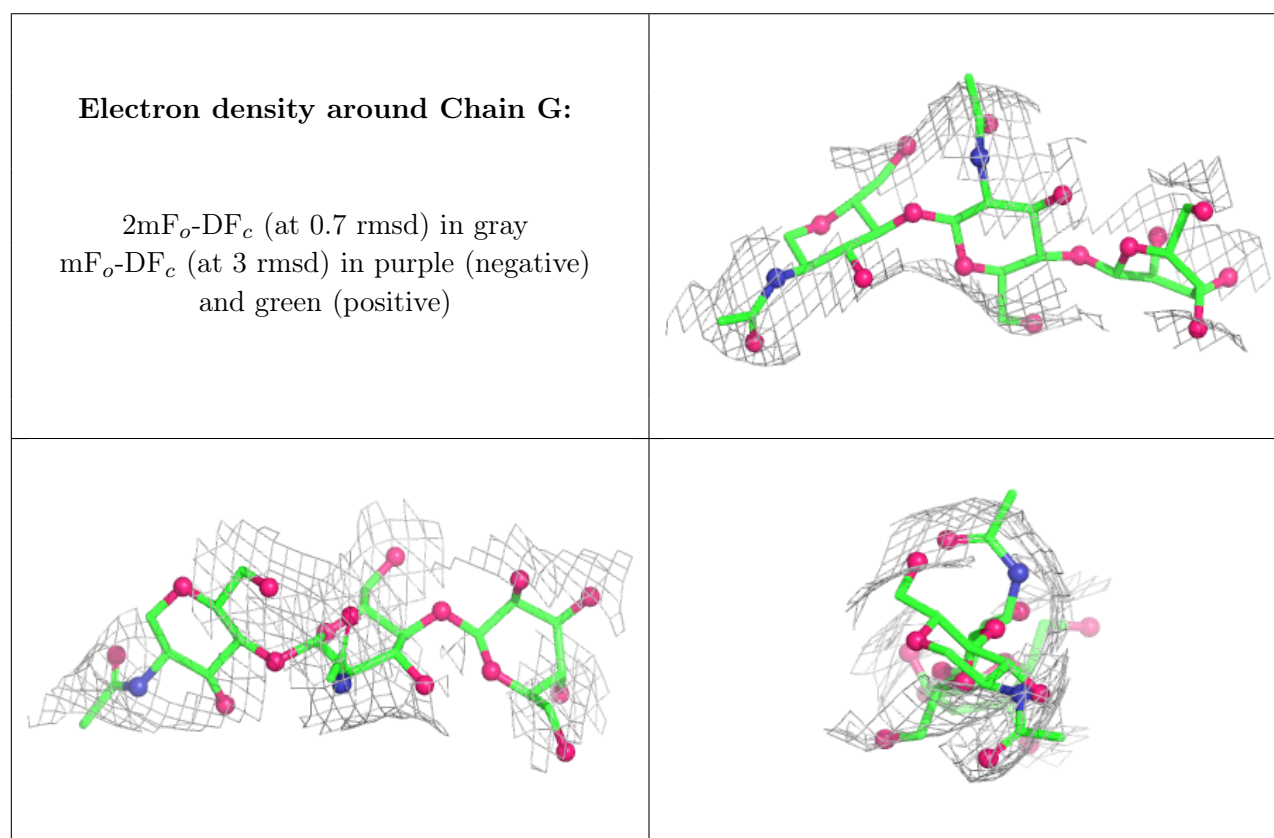
6.3 Carbohydrates [i](#)

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.

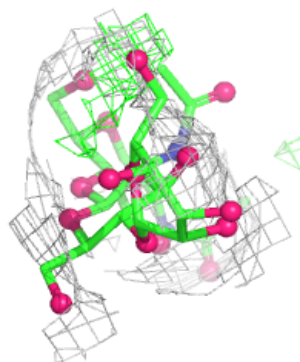
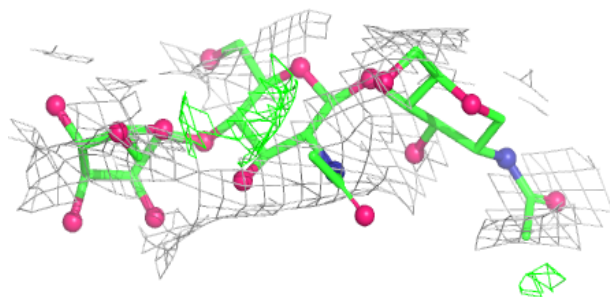
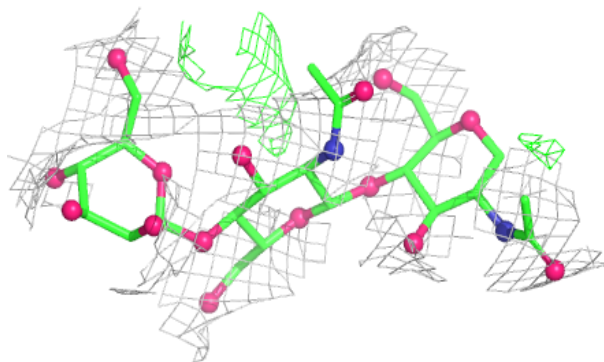
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	G	1	14/15	-	-	89,124,157,158	0
5	NAG	G	2	14/15	-	-	81,147,180,191	0
5	BMA	G	3	11/12	-	-	96,171,189,193	0
5	NAG	M	1	14/15	-	-	69,89,102,105	0
5	NAG	M	2	14/15	-	-	102,146,171,200	0
5	BMA	M	3	11/12	-	-	130,155,170,177	0
6	NAG	P	1	14/15	-	-	112,128,165,170	0
6	NAG	P	2	14/15	-	-	92,179,206,213	0

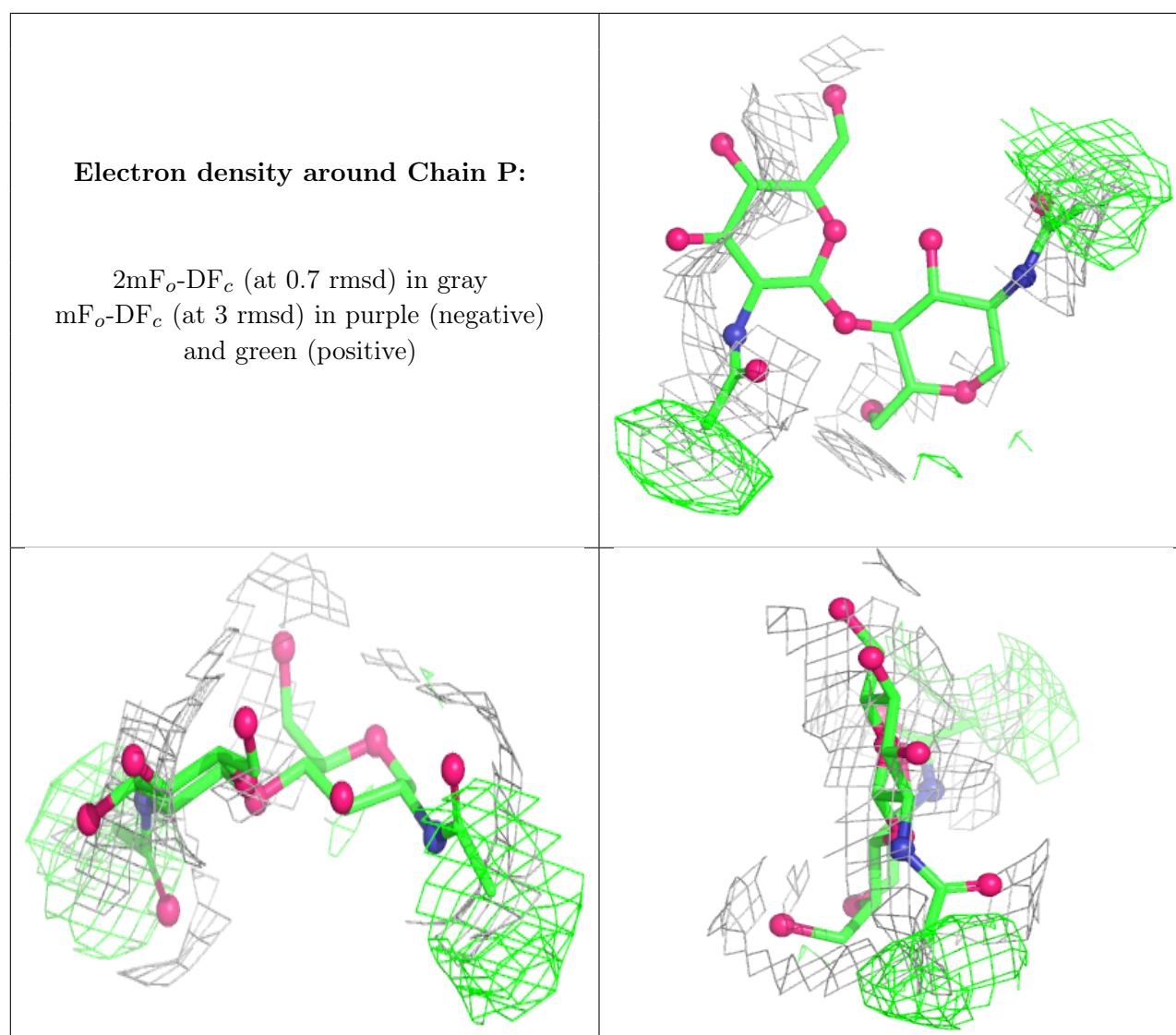
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain M:

$2mF_o - DF_c$ (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.

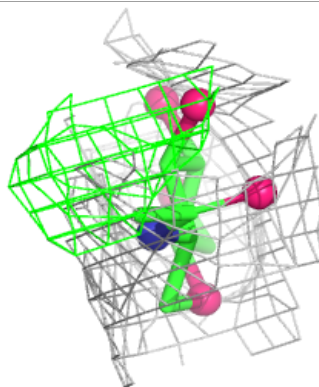
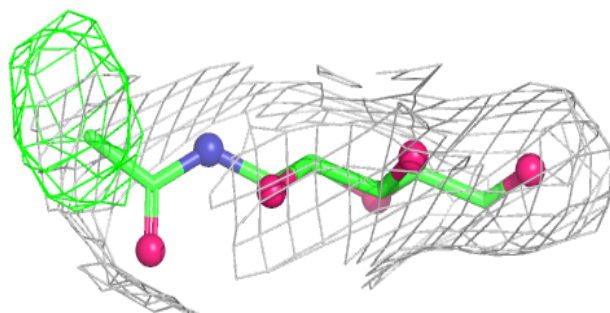
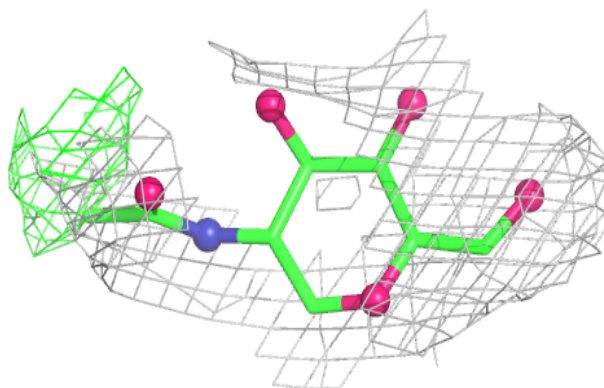
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	C	401	14/15	0.60	0.12	79,161,177,179	0
7	NAG	A	702	14/15	0.69	0.15	77,113,144,153	0
7	NAG	A	701	14/15	0.78	0.11	114,114,114,115	0

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.

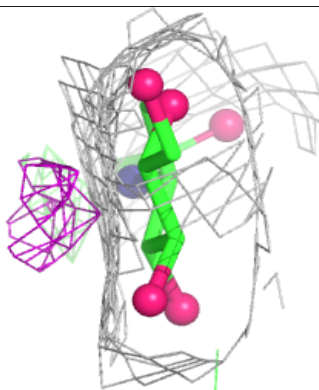
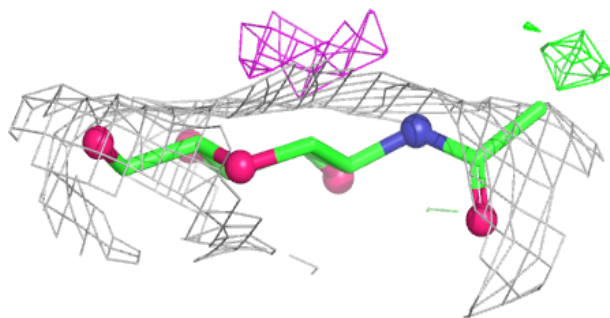
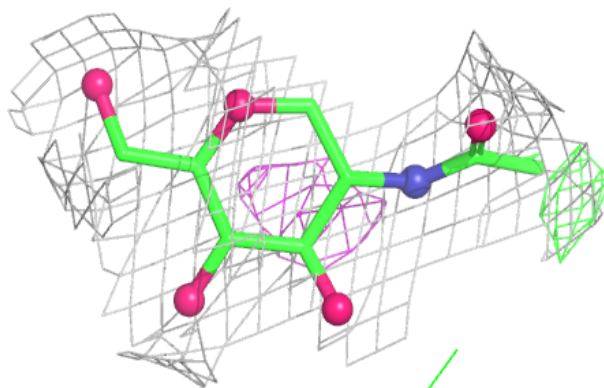
Electron density around NAG C 401:

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



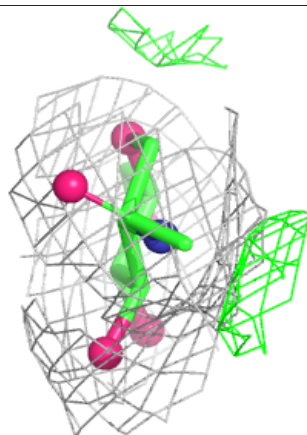
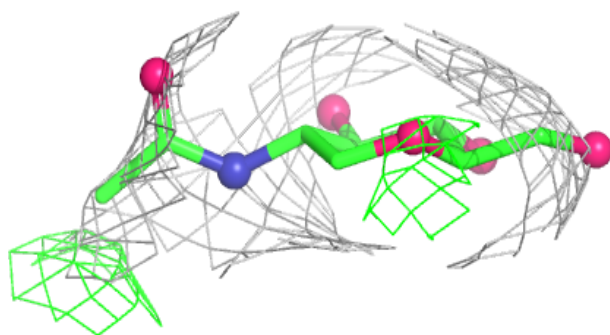
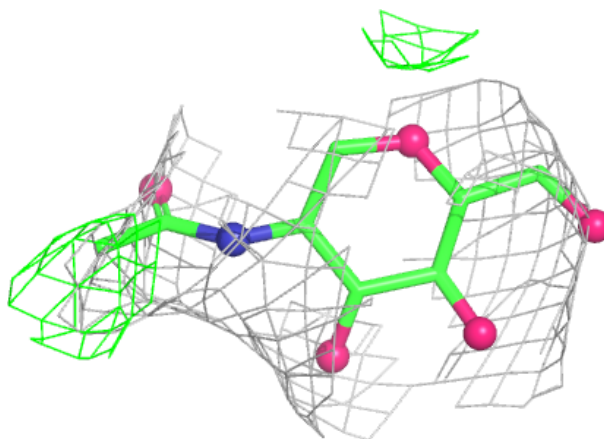
Electron density around NAG A 702:

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



Electron density around NAG A 701:

$2mF_o - DF_c$ (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.