wwPDB X-ray Structure Validation Summary Report (i)

Oct 4, 2023 – 03:47 PM EDT

PDB ID	:	6P6P
Title	:	Crystal structure of hemagglutinin from influenza virus A/Sichuan/2/1987 (H3N2)
Authors	:	Dai, Y.N.; Fremont, D.H.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2019-06-04
Resolution	:	2.31 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 (i) 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 (i)) were used in the production of this report:

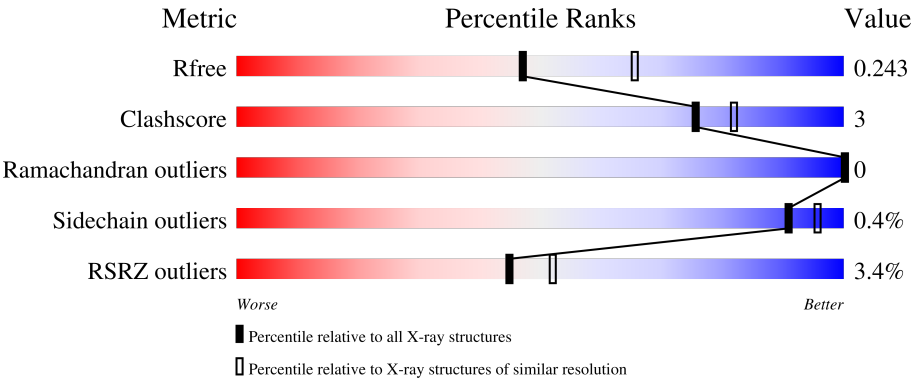
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.31 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.



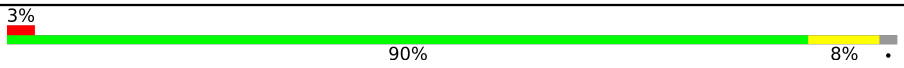
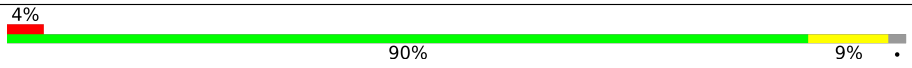
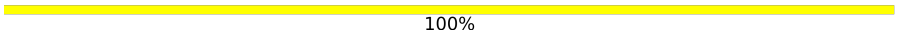
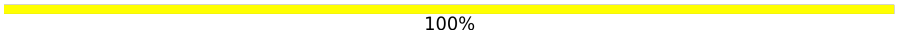
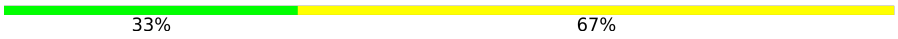
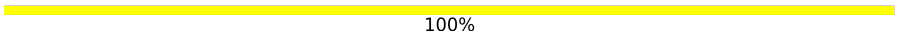
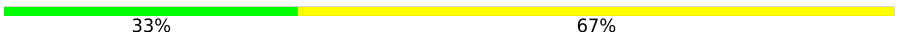
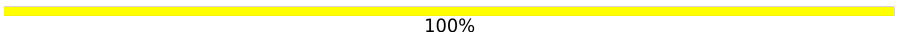
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 <=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	497	3% 92% 6% ·
1	B	497	4% 89% 9% ·
1	C	497	3% 90% 8% ·
1	D	497	2% 92% 6% ·

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	497	
1	F	497	
2	G	3	
2	H	3	
2	I	3	
2	J	3	
2	K	3	
2	L	3	

2 Entry composition (i)

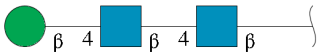
There are 4 unique types of molecules in this entry. The entry contains 24621 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Hemagglutinin.

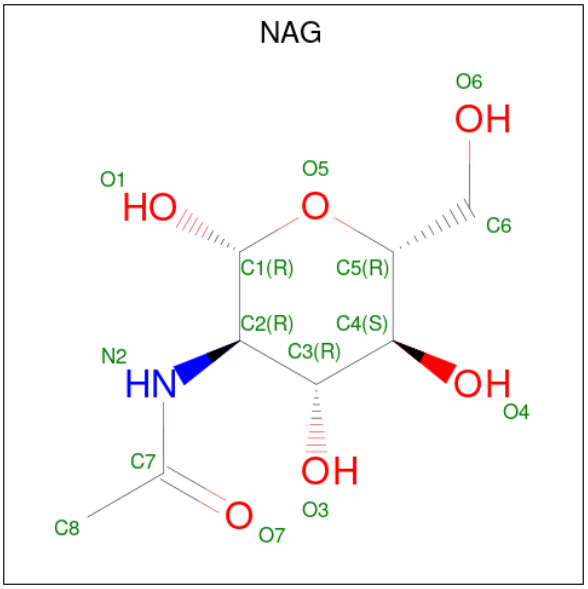
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	487	Total	C	N	O	S	0	1	0
			3849	2401	685	744	19			
1	B	488	Total	C	N	O	S	0	3	0
			3873	2418	688	748	19			
1	C	489	Total	C	N	O	S	0	3	0
			3878	2421	689	749	19			
1	D	489	Total	C	N	O	S	0	4	0
			3883	2424	690	750	19			
1	E	489	Total	C	N	O	S	0	4	0
			3883	2424	690	750	19			
1	F	489	Total	C	N	O	S	0	4	0
			3883	2424	690	750	19			

- Molecule 2 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
2	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	I	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	K	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	L	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



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

Continued on next page...

Continued from previous page...

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

- Molecule 4 is water.

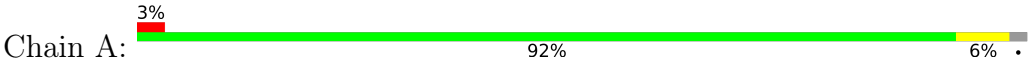
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	134	Total	O	0	0
			134	134		
4	B	126	Total	O	0	0
			126	126		
4	C	120	Total	O	0	0
			120	120		
4	D	141	Total	O	0	0
			141	141		
4	E	142	Total	O	0	0
			142	142		
4	F	139	Total	O	0	0
			139	139		

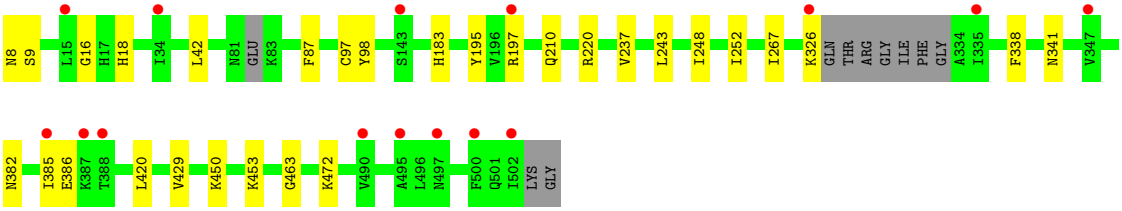
3 Residue-property plots (i)

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

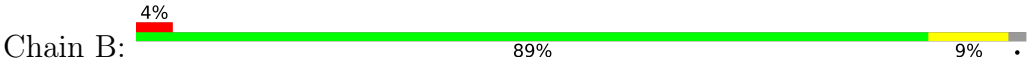
Chain A:

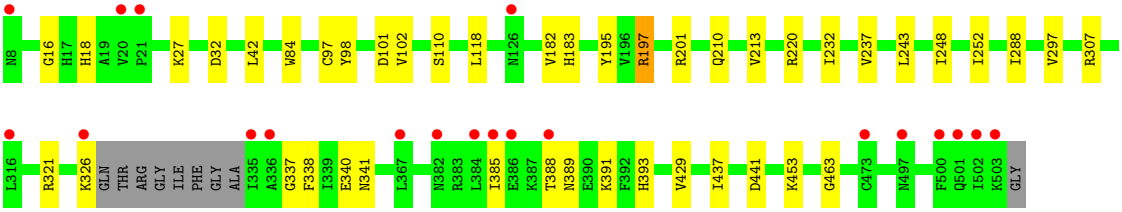




- Molecule 1: Hemagglutinin

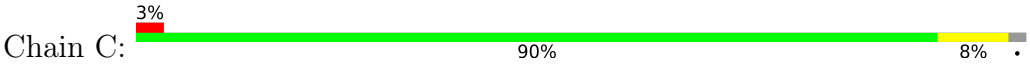
Chain B:

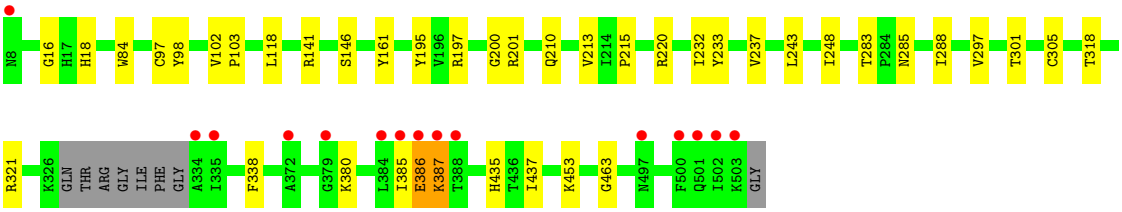




- Molecule 1: Hemagglutinin

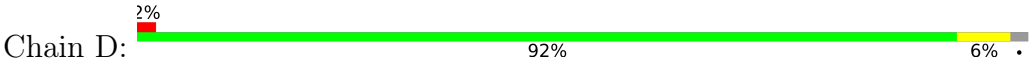
Chain C:

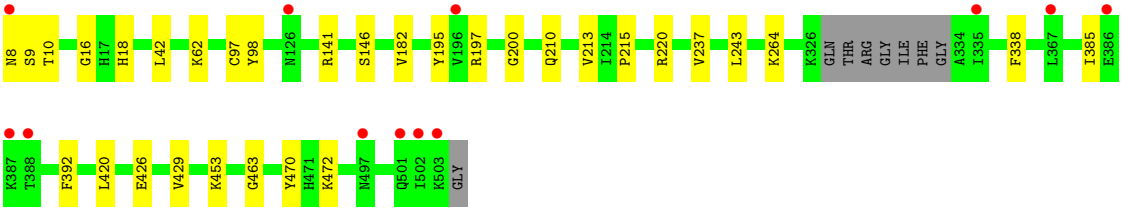




- Molecule 1: Hemagglutinin

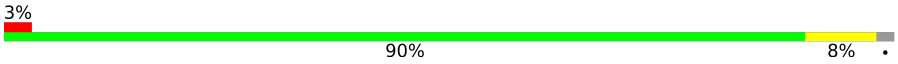
Chain D:

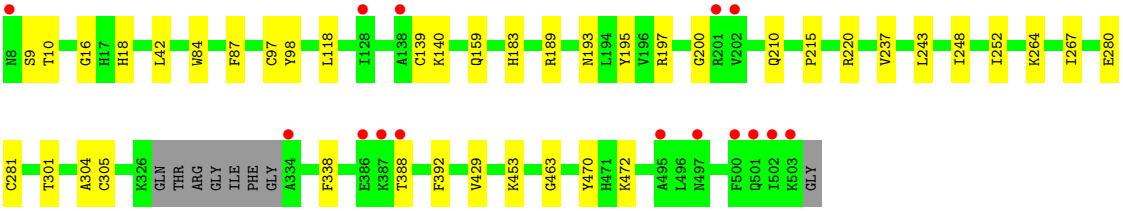




• Molecule 1: Hemagglutinin

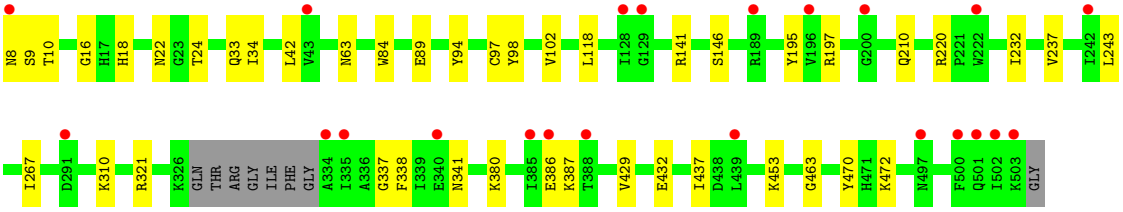
Chain E:





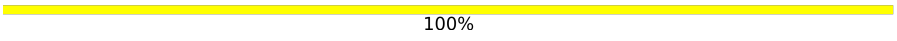
• Molecule 1: Hemagglutinin

Chain F:



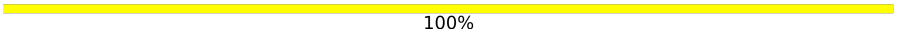
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



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

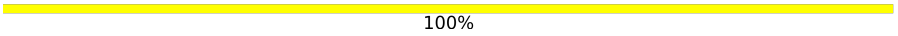
Chain H:



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

Chain I:

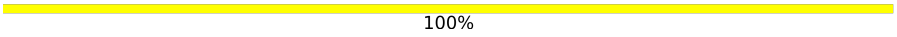
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J: 

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

Chain K:

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

Chain L: 

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	211.94Å 149.94Å 150.09Å 90.00° 135.01° 90.00°	Depositor
Resolution (Å)	47.47 – 2.31 47.47 – 2.31	Depositor EDS
% Data completeness (in resolution range)	98.8 (47.47-2.31) 98.8 (47.47-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.54 (at 2.32Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.221 , 0.251 0.224 , 0.243	Depositor DCC
R_{free} test set	7163 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	34.9	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 21.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.014 for -h-2*l,k,h+l 0.014 for -h-k-l,l,k 0.017 for -h+k-l,-l,-k 0.022 for -k+l,-h-l,-l 0.021 for k+l,h+l,-l 0.418 for k-l,h+l,-k 0.410 for h+k+l,-l,-h-l 0.408 for -k-l,-h-l,k 0.409 for h-k+l,l,-h-l 0.015 for h,-k,-h-l 0.439 for h+2*l,-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	24621	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.25	0/3930	0.45	0/5319
1	B	0.26	0/3961	0.45	0/5361
1	C	0.26	0/3966	0.45	0/5368
1	D	0.25	0/3974	0.44	0/5379
1	E	0.30	0/3974	0.45	0/5379
1	F	0.26	0/3974	0.44	0/5379
All	All	0.26	0/23779	0.45	0/32185

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	3849	0	3733	20	0
1	B	3873	0	3767	30	0
1	C	3878	0	3772	31	0
1	D	3883	0	3778	20	0
1	E	3883	0	3780	29	0
1	F	3883	0	3778	28	0
2	G	39	0	34	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	39	0	34	0	0
2	I	39	0	34	0	0
2	J	39	0	34	0	0
2	K	39	0	34	0	0
2	L	39	0	34	0	0
3	A	56	0	52	0	0
3	B	56	0	52	1	0
3	C	56	0	52	2	0
3	D	56	0	52	1	0
3	E	56	0	52	0	0
3	F	56	0	52	2	0
4	A	134	0	0	1	0
4	B	126	0	0	1	0
4	C	120	0	0	1	0
4	D	141	0	0	0	0
4	E	142	0	0	1	0
4	F	139	0	0	2	0
All	All	24621	0	23124	142	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 3.

The worst 5 of 142 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:326:LYS:NZ	1:B:341:ASN:HB2	1.86	0.90
1:B:326:LYS:HZ3	1:B:341:ASN:HB2	1.41	0.85
1:B:463:GLY:HA2	1:F:453:LYS:HD2	1.70	0.72
1:B:453:LYS:HD2	1:E:463:GLY:HA2	1.73	0.70
1:C:318:THR:HG21	3:C:701:NAG:H62	1.73	0.70

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	482/497 (97%)	460 (95%)	22 (5%)	0	100	100
1	B	487/497 (98%)	463 (95%)	24 (5%)	0	100	100
1	C	488/497 (98%)	465 (95%)	23 (5%)	0	100	100
1	D	489/497 (98%)	466 (95%)	23 (5%)	0	100	100
1	E	489/497 (98%)	467 (96%)	22 (4%)	0	100	100
1	F	489/497 (98%)	466 (95%)	23 (5%)	0	100	100
All	All	2924/2982 (98%)	2787 (95%)	137 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	426/432 (99%)	425 (100%)	1 (0%)	93	97
1	B	430/432 (100%)	428 (100%)	2 (0%)	88	95
1	C	430/432 (100%)	427 (99%)	3 (1%)	84	92
1	D	431/432 (100%)	430 (100%)	1 (0%)	93	97
1	E	431/432 (100%)	429 (100%)	2 (0%)	88	95
1	F	431/432 (100%)	430 (100%)	1 (0%)	93	97
All	All	2579/2592 (100%)	2569 (100%)	10 (0%)	91	96

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	18	HIS
1	E	140	LYS
1	F	18	HIS
1	C	18	HIS
1	C	386	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	33	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

18 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	G	1	2,1	14,14,15	1.19	2 (14%)	17,19,21	1.03	1 (5%)
2	NAG	G	2	2	14,14,15	0.29	0	17,19,21	1.05	2 (11%)
2	BMA	G	3	2	11,11,12	0.97	1 (9%)	15,15,17	0.94	0
2	NAG	H	1	2,1	14,14,15	0.74	0	17,19,21	0.98	1 (5%)
2	NAG	H	2	2	14,14,15	0.58	0	17,19,21	1.14	2 (11%)
2	BMA	H	3	2	11,11,12	1.03	1 (9%)	15,15,17	1.34	2 (13%)
2	NAG	I	1	2,1	14,14,15	0.46	0	17,19,21	1.06	1 (5%)
2	NAG	I	2	2	14,14,15	0.25	0	17,19,21	0.66	0
2	BMA	I	3	2	11,11,12	1.56	1 (9%)	15,15,17	1.37	4 (26%)
2	NAG	J	1	2,1	14,14,15	0.61	0	17,19,21	1.16	2 (11%)
2	NAG	J	2	2	14,14,15	0.51	0	17,19,21	0.84	1 (5%)
2	BMA	J	3	2	11,11,12	1.40	1 (9%)	15,15,17	1.45	3 (20%)
2	NAG	K	1	2,1	14,14,15	0.34	0	17,19,21	1.26	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	K	2	2	14,14,15	0.23	0	17,19,21	0.65	0
2	BMA	K	3	2	11,11,12	1.09	2 (18%)	15,15,17	1.35	2 (13%)
2	NAG	L	1	2,1	14,14,15	0.54	0	17,19,21	1.12	2 (11%)
2	NAG	L	2	2	14,14,15	0.30	0	17,19,21	0.83	1 (5%)
2	BMA	L	3	2	11,11,12	0.64	0	15,15,17	1.66	4 (26%)

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

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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	3	BMA	O5-C1	-4.41	1.36	1.43
2	G	1	NAG	O5-C1	3.30	1.49	1.43
2	H	3	BMA	O5-C1	-3.07	1.38	1.43
2	G	1	NAG	C1-C2	2.65	1.56	1.52
2	G	3	BMA	O5-C1	-2.63	1.39	1.43

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	L	3	BMA	O5-C5-C6	4.03	113.53	107.20
2	K	1	NAG	C1-O5-C5	3.87	117.44	112.19
2	H	3	BMA	O5-C5-C6	3.86	113.26	107.20
2	I	1	NAG	C1-O5-C5	3.21	116.54	112.19
2	G	1	NAG	C1-O5-C5	3.17	116.49	112.19

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

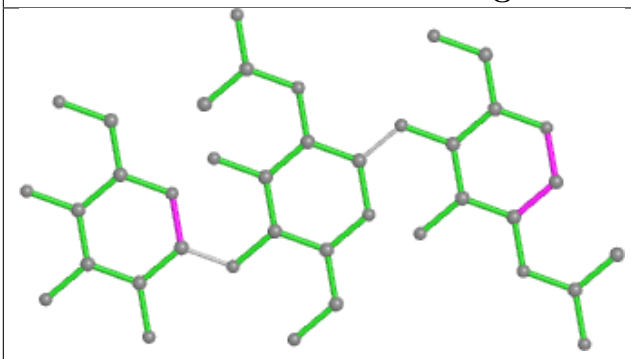
Mol	Chain	Res	Type	Atoms
2	G	3	BMA	O5-C5-C6-O6
2	K	2	NAG	O5-C5-C6-O6
2	L	3	BMA	O5-C5-C6-O6
2	H	3	BMA	O5-C5-C6-O6
2	H	3	BMA	C4-C5-C6-O6

There are no ring outliers.

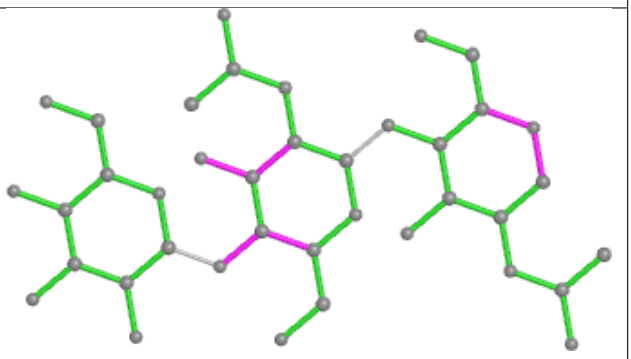
No monomer is involved in short contacts.

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

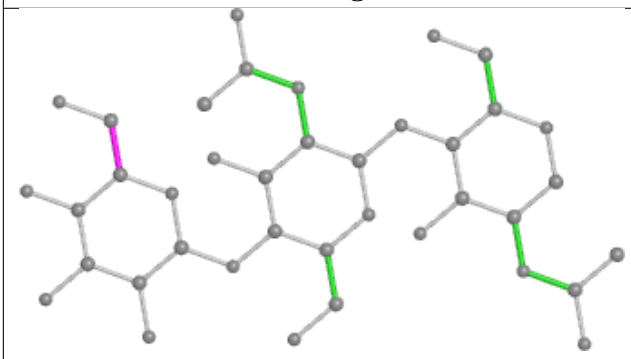
Oligosaccharide Chain G



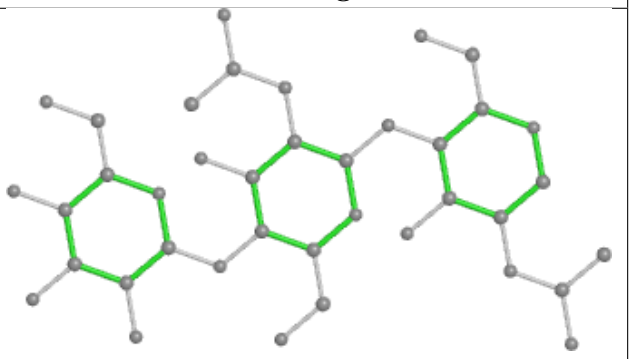
Bond lengths



Bond angles

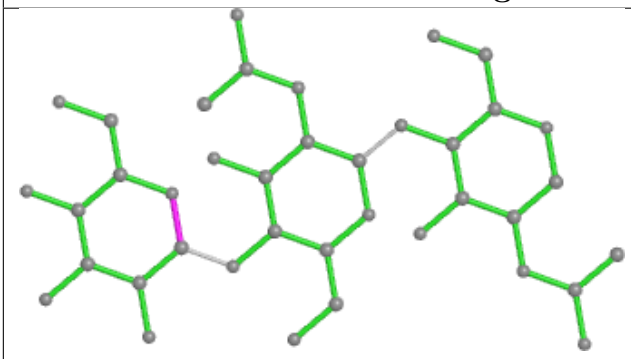


Torsions

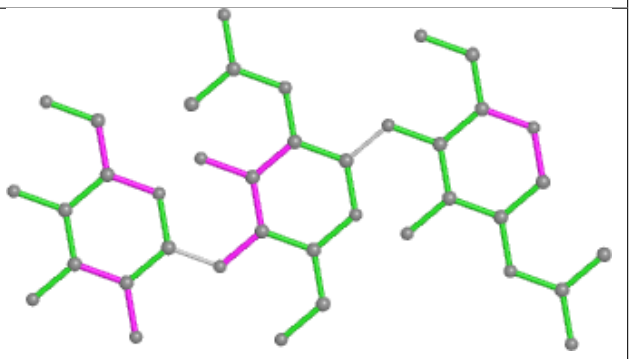


Rings

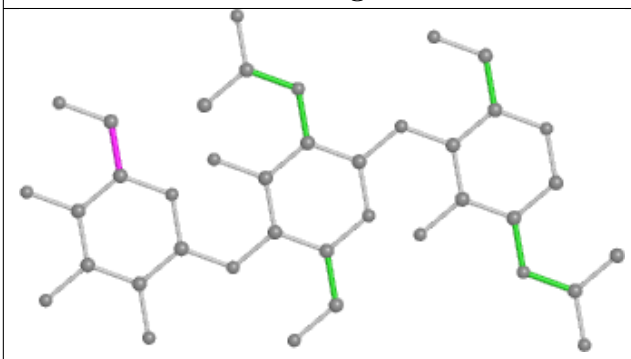
Oligosaccharide Chain H



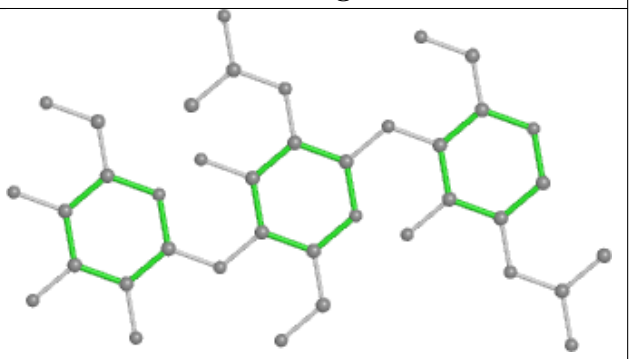
Bond lengths



Bond angles

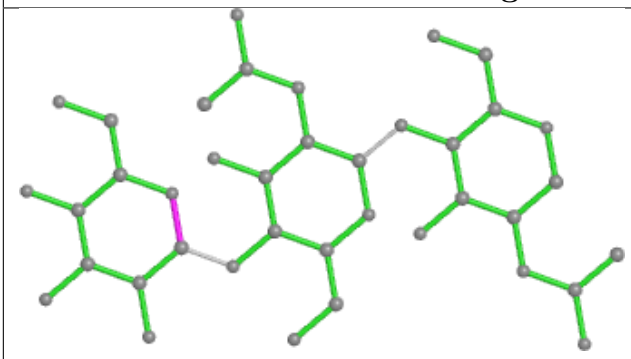


Torsions

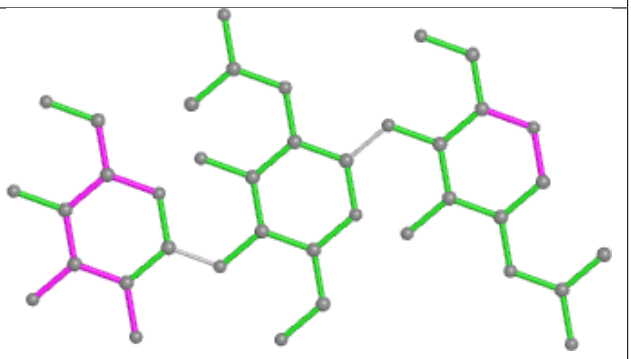


Rings

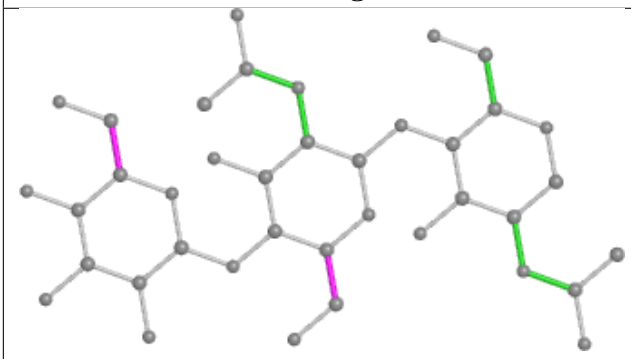
Oligosaccharide Chain I



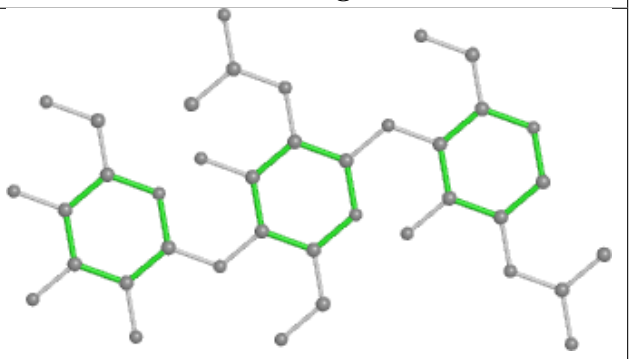
Bond lengths



Bond angles

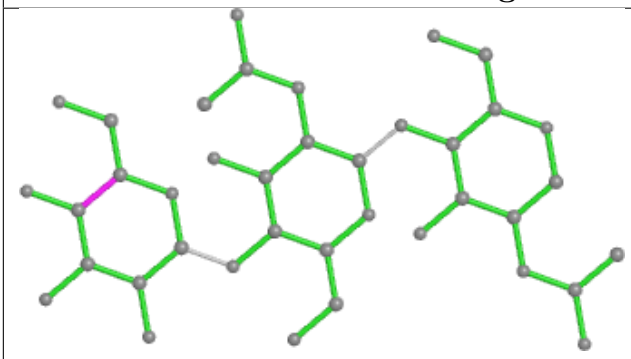


Torsions

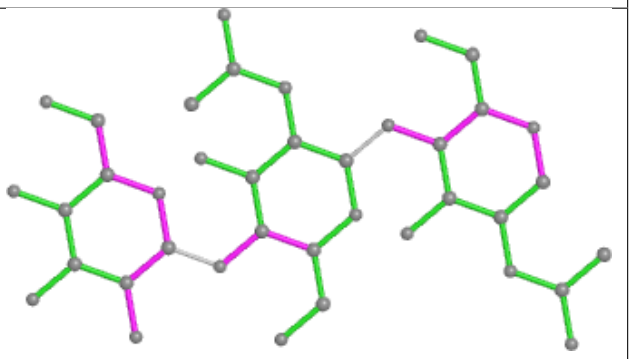


Rings

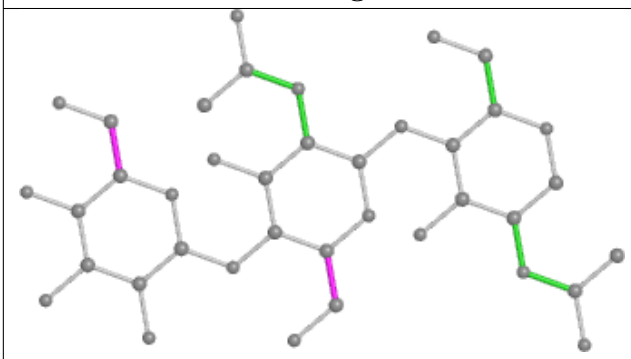
Oligosaccharide Chain J



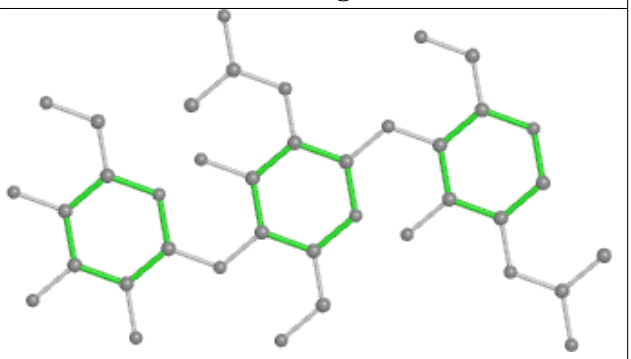
Bond lengths



Bond angles

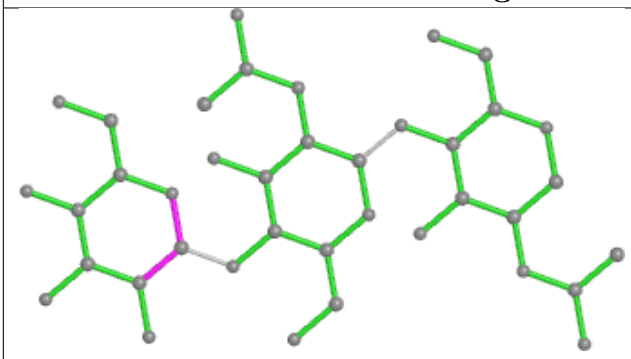


Torsions

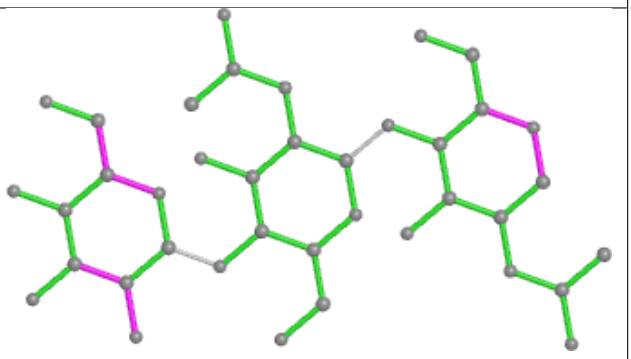


Rings

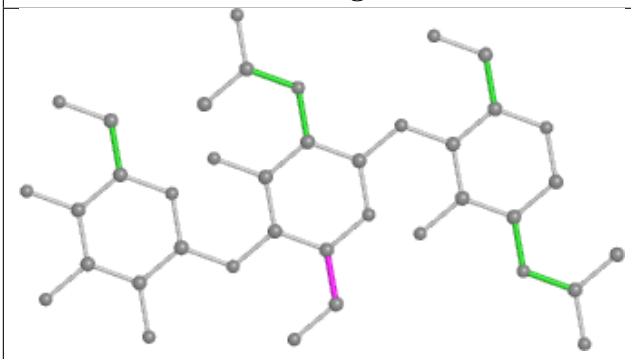
Oligosaccharide Chain K



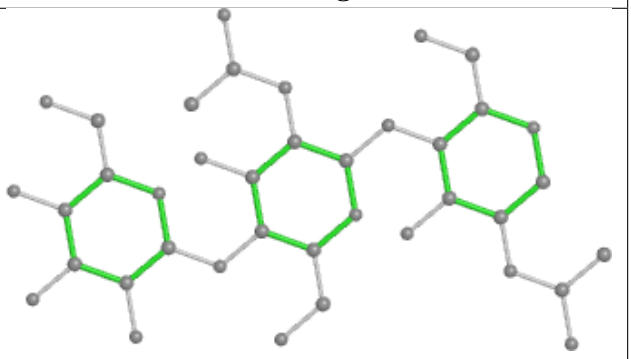
Bond lengths



Bond angles

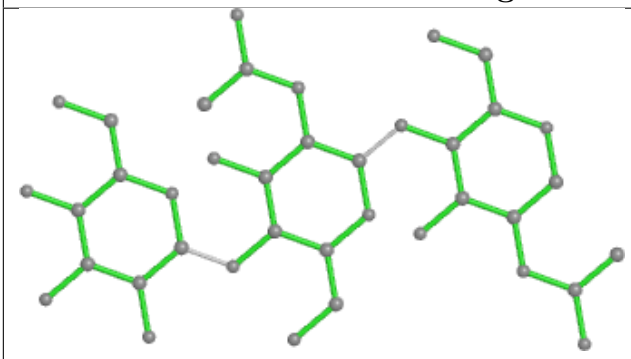


Torsions

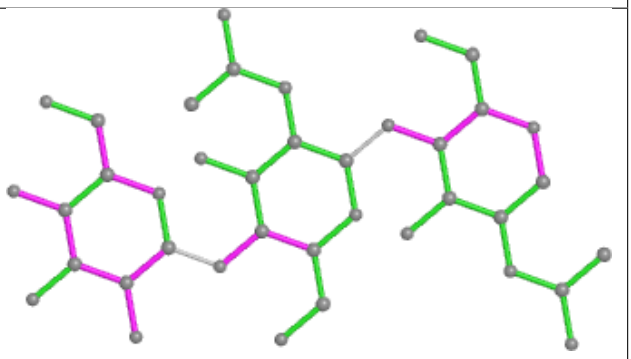


Rings

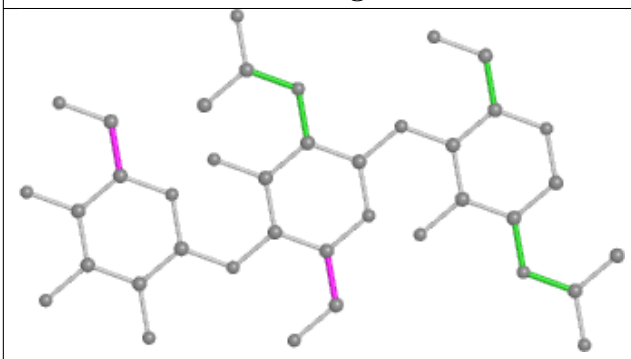
Oligosaccharide Chain L



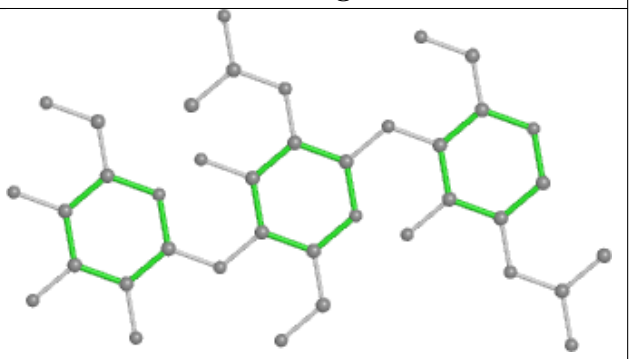
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

24 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	$\#\|Z\| > 2$
3	NAG	A	700	1	14,14,15	0.94	2 (14%)	17,19,21	0.90	1 (5%)
3	NAG	E	700	1	14,14,15	0.90	2 (14%)	17,19,21	1.34	3 (17%)
3	NAG	C	700	1	14,14,15	2.72	2 (14%)	17,19,21	1.97	4 (23%)
3	NAG	B	702	1	14,14,15	0.40	0	17,19,21	1.09	2 (11%)
3	NAG	F	700	1	14,14,15	0.87	1 (7%)	17,19,21	1.16	2 (11%)
3	NAG	B	700	1	14,14,15	0.79	1 (7%)	17,19,21	0.97	0
3	NAG	E	701	1	14,14,15	1.30	3 (21%)	17,19,21	2.66	4 (23%)
3	NAG	D	706	1	14,14,15	0.82	1 (7%)	17,19,21	1.36	2 (11%)
3	NAG	A	701	1	14,14,15	1.41	2 (14%)	17,19,21	1.20	2 (11%)
3	NAG	A	702	1	14,14,15	0.90	1 (7%)	17,19,21	2.00	4 (23%)
3	NAG	A	706	1	14,14,15	1.58	2 (14%)	17,19,21	1.94	1 (5%)
3	NAG	D	700	1	14,14,15	0.45	0	17,19,21	0.76	1 (5%)
3	NAG	F	701	1	14,14,15	0.76	1 (7%)	17,19,21	1.21	1 (5%)
3	NAG	E	706	1	14,14,15	2.19	2 (14%)	17,19,21	1.50	2 (11%)
3	NAG	F	702	1	14,14,15	0.70	0	17,19,21	1.31	1 (5%)
3	NAG	B	701	1	14,14,15	1.00	1 (7%)	17,19,21	1.94	5 (29%)
3	NAG	C	702	1	14,14,15	1.10	2 (14%)	17,19,21	0.83	0
3	NAG	C	706	1	14,14,15	0.59	0	17,19,21	1.79	3 (17%)
3	NAG	F	706	1	14,14,15	0.65	0	17,19,21	1.61	5 (29%)
3	NAG	D	702	1	14,14,15	1.09	2 (14%)	17,19,21	0.90	1 (5%)
3	NAG	E	702	1	14,14,15	0.84	1 (7%)	17,19,21	1.19	1 (5%)
3	NAG	D	701	1	14,14,15	0.51	0	17,19,21	1.14	1 (5%)
3	NAG	C	701	1	14,14,15	0.83	1 (7%)	17,19,21	2.72	4 (23%)
3	NAG	B	706	1	14,14,15	3.01	3 (21%)	17,19,21	3.95	4 (23%)

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	A	700	1	-	0/6/23/26	0/1/1/1
3	NAG	E	700	1	-	4/6/23/26	0/1/1/1
3	NAG	C	700	1	-	4/6/23/26	0/1/1/1
3	NAG	B	702	1	-	0/6/23/26	0/1/1/1
3	NAG	F	700	1	-	4/6/23/26	0/1/1/1
3	NAG	B	700	1	-	2/6/23/26	0/1/1/1
3	NAG	E	701	1	-	3/6/23/26	0/1/1/1
3	NAG	D	706	1	-	0/6/23/26	0/1/1/1
3	NAG	A	701	1	-	2/6/23/26	0/1/1/1
3	NAG	A	702	1	-	3/6/23/26	0/1/1/1
3	NAG	A	706	1	-	2/6/23/26	0/1/1/1
3	NAG	D	700	1	-	2/6/23/26	0/1/1/1
3	NAG	F	701	1	-	2/6/23/26	0/1/1/1
3	NAG	E	706	1	-	3/6/23/26	0/1/1/1
3	NAG	F	702	1	-	2/6/23/26	0/1/1/1
3	NAG	B	701	1	-	2/6/23/26	0/1/1/1
3	NAG	C	702	1	-	0/6/23/26	0/1/1/1
3	NAG	C	706	1	-	3/6/23/26	0/1/1/1
3	NAG	F	706	1	-	2/6/23/26	0/1/1/1
3	NAG	D	702	1	-	0/6/23/26	0/1/1/1
3	NAG	E	702	1	-	0/6/23/26	0/1/1/1
3	NAG	D	701	1	-	0/6/23/26	0/1/1/1
3	NAG	C	701	1	-	2/6/23/26	0/1/1/1
3	NAG	B	706	1	-	4/6/23/26	0/1/1/1

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	706	NAG	O5-C1	9.80	1.59	1.43
3	C	700	NAG	O5-C1	9.05	1.58	1.43
3	E	706	NAG	O5-C1	-7.54	1.31	1.43
3	A	706	NAG	O5-C1	5.30	1.52	1.43
3	B	706	NAG	C1-C2	4.94	1.59	1.52

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	706	NAG	C1-O5-C5	12.78	129.51	112.19
3	C	701	NAG	C2-N2-C7	8.32	134.75	122.90
3	A	706	NAG	C1-O5-C5	7.26	122.03	112.19
3	E	701	NAG	C2-N2-C7	7.23	133.19	122.90
3	B	706	NAG	C4-C3-C2	6.75	120.91	111.02

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	706	NAG	C3-C2-N2-C7
3	C	700	NAG	C3-C2-N2-C7
3	C	701	NAG	O7-C7-N2-C2
3	E	700	NAG	C3-C2-N2-C7
3	E	701	NAG	C1-C2-N2-C7

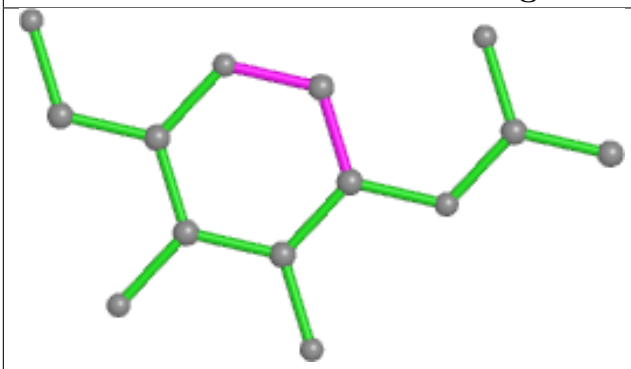
There are no ring outliers.

5 monomers are involved in 6 short contacts:

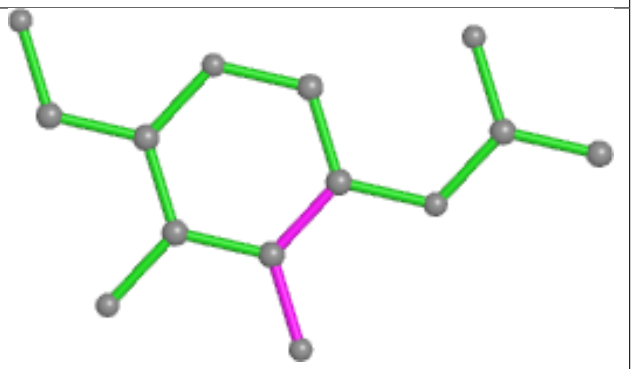
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	700	NAG	2	0
3	C	706	NAG	1	0
3	D	702	NAG	1	0
3	C	701	NAG	1	0
3	B	706	NAG	1	0

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

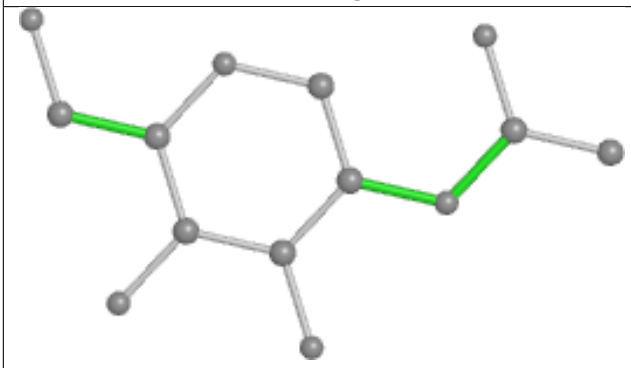
Ligand NAG A 700



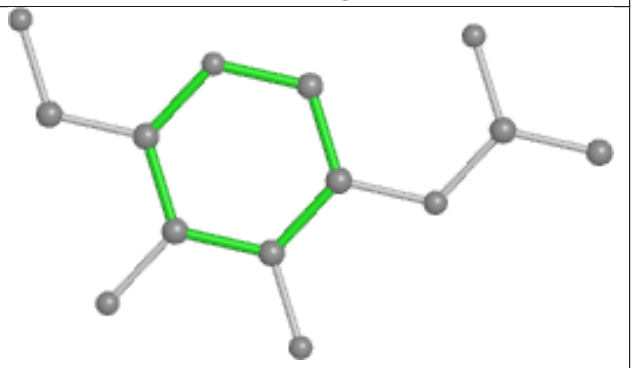
Bond lengths



Bond angles

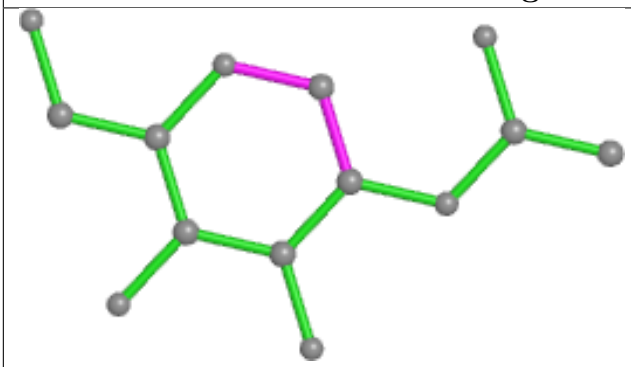


Torsions

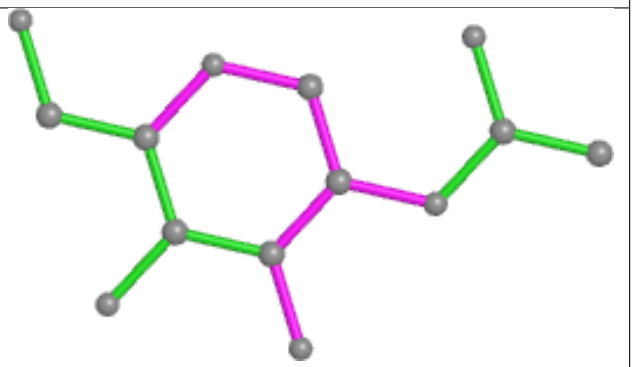


Rings

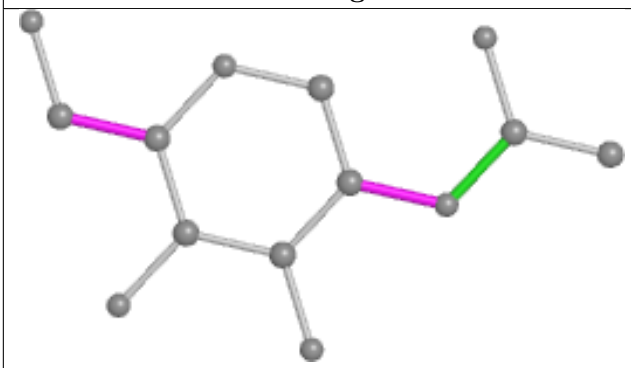
Ligand NAG E 700



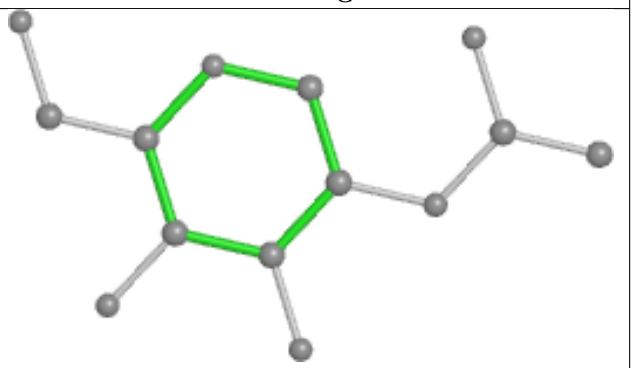
Bond lengths



Bond angles

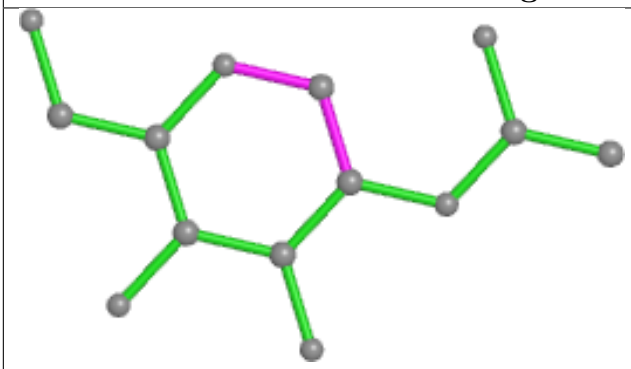


Torsions

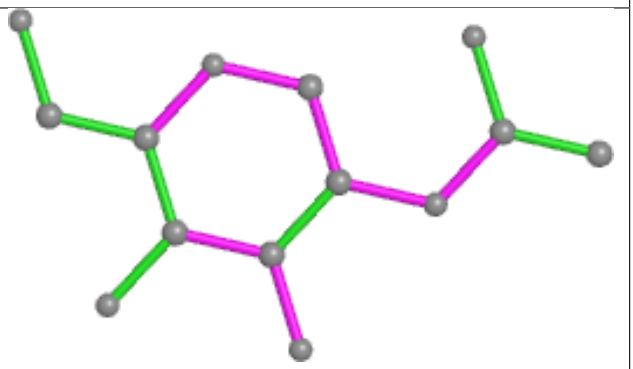


Rings

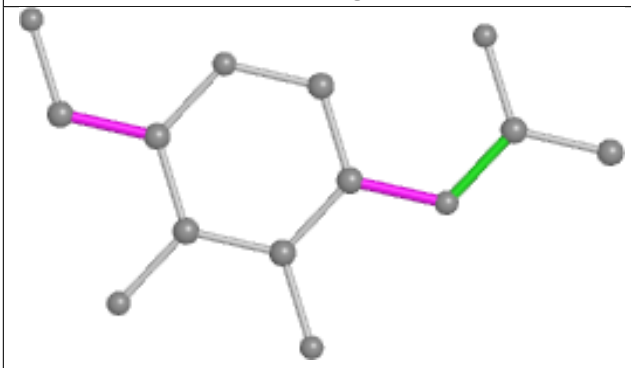
Ligand NAG C 700



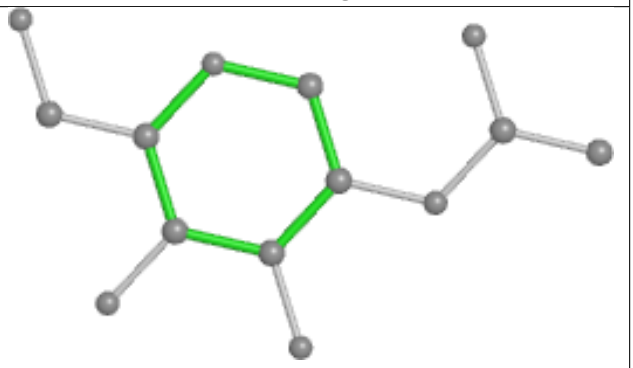
Bond lengths



Bond angles

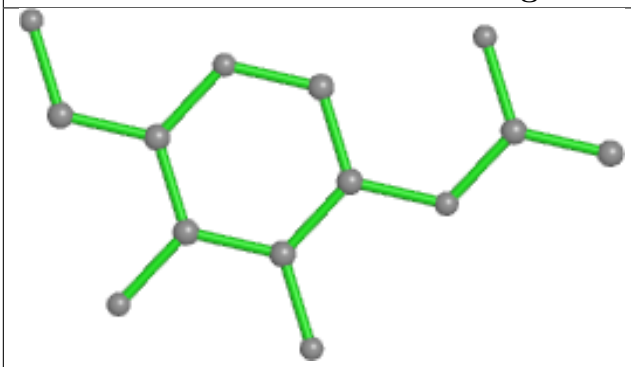


Torsions

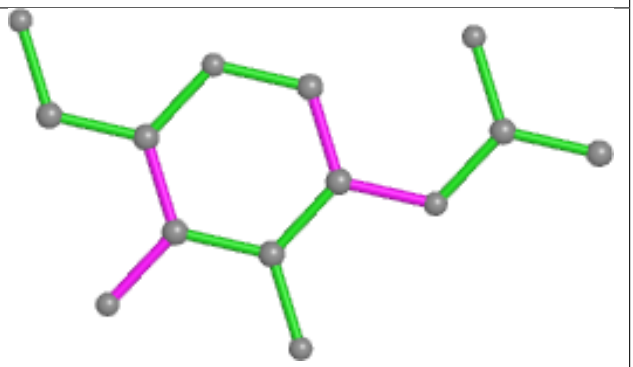


Rings

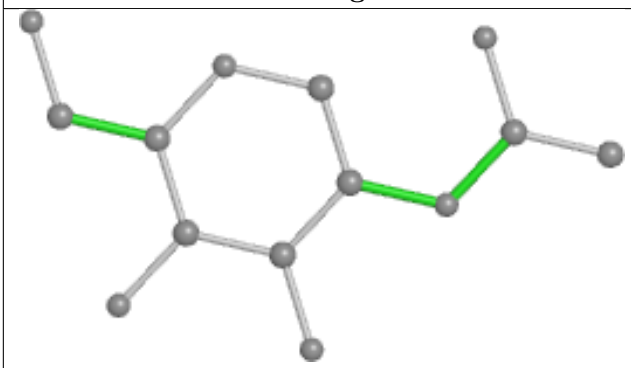
Ligand NAG B 702



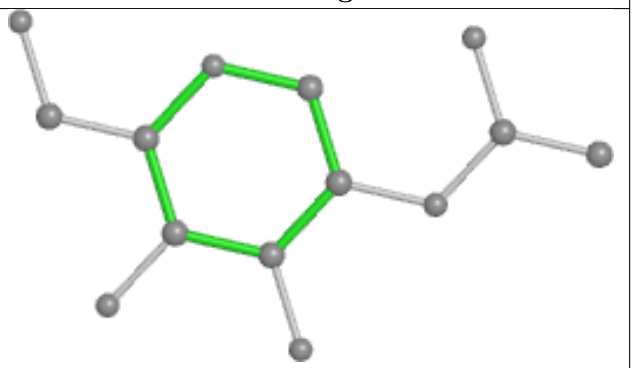
Bond lengths



Bond angles

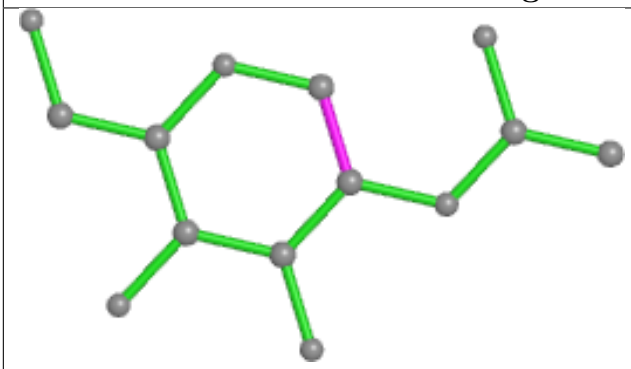


Torsions

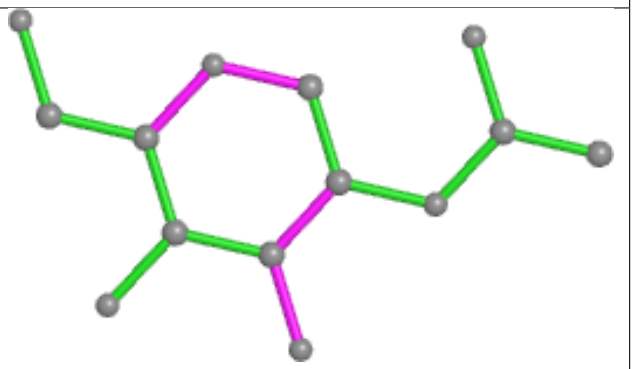


Rings

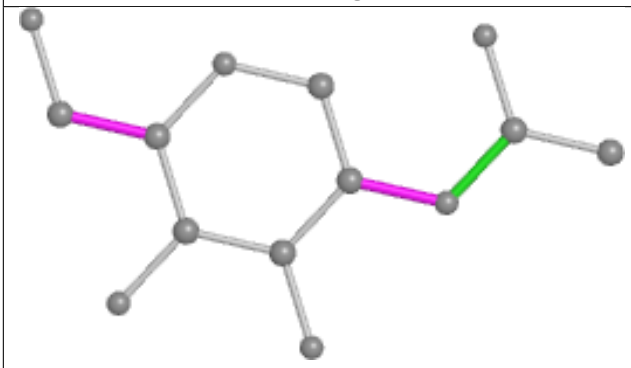
Ligand NAG F 700



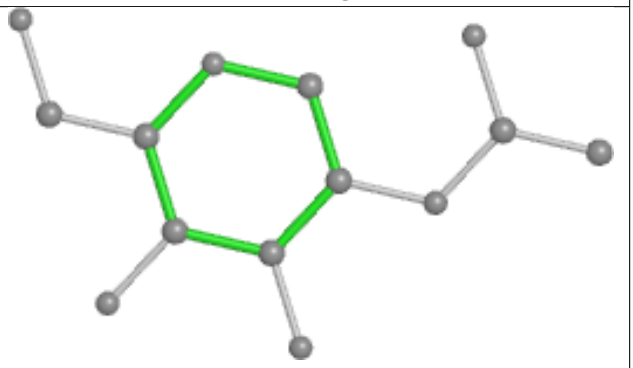
Bond lengths



Bond angles

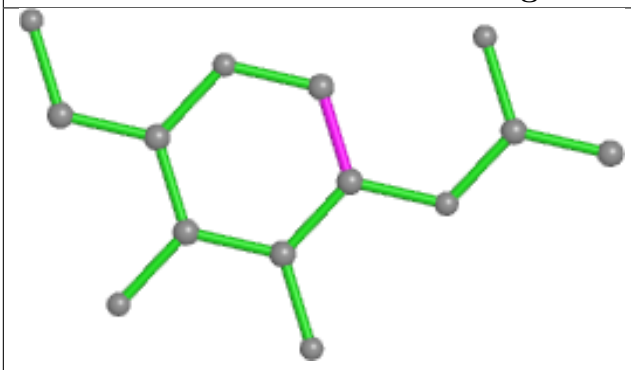


Torsions

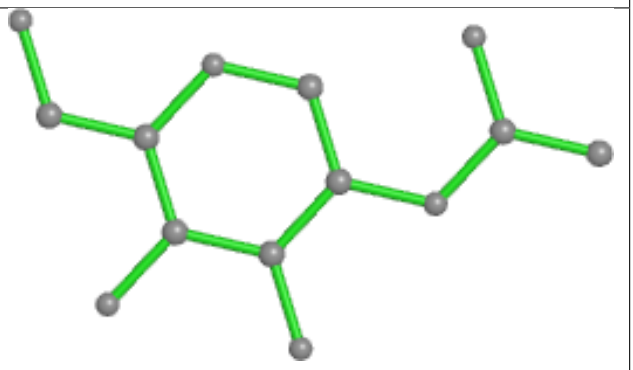


Rings

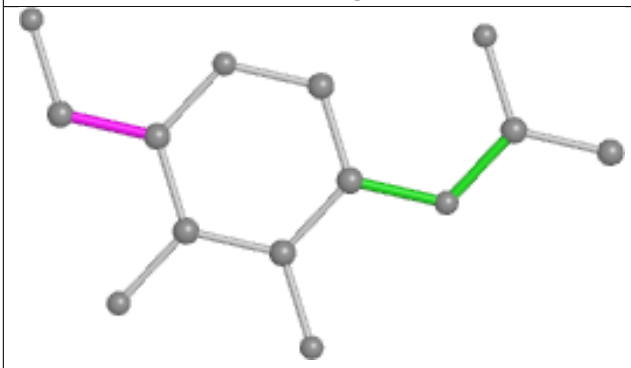
Ligand NAG B 700



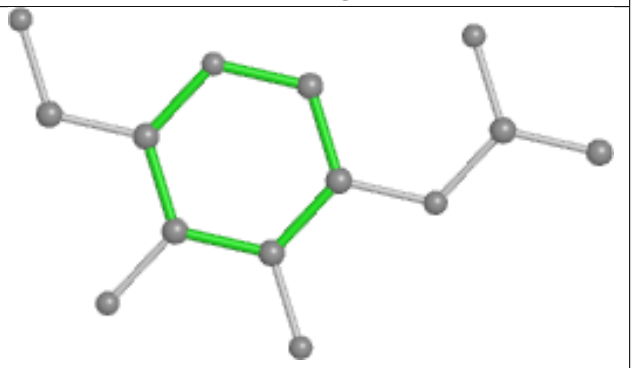
Bond lengths



Bond angles

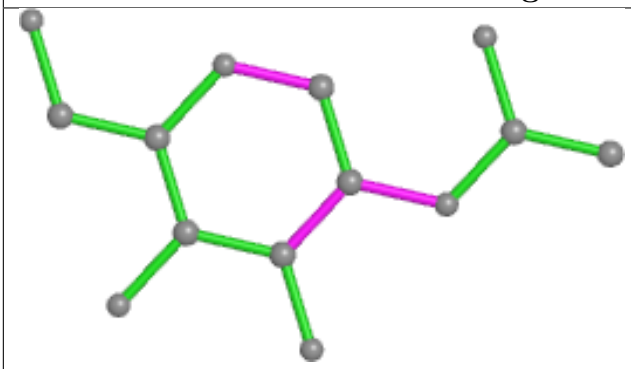


Torsions

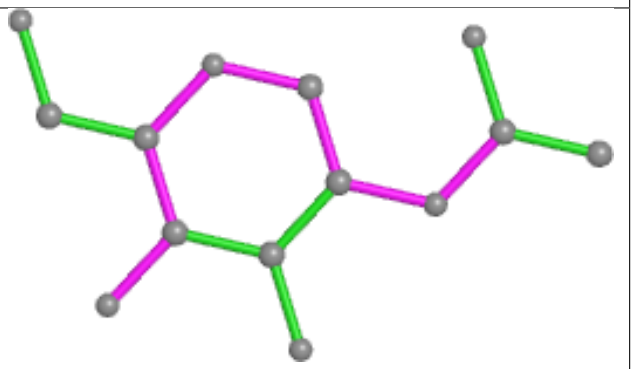


Rings

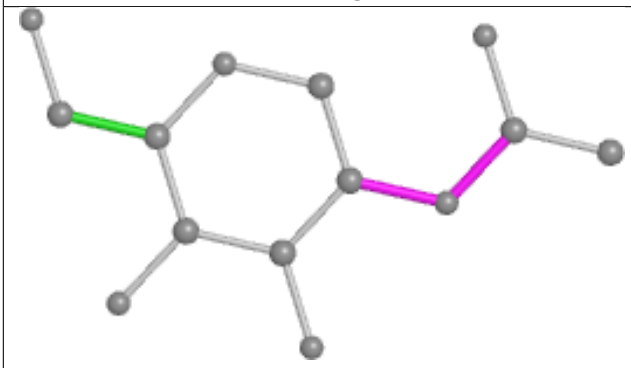
Ligand NAG E 701



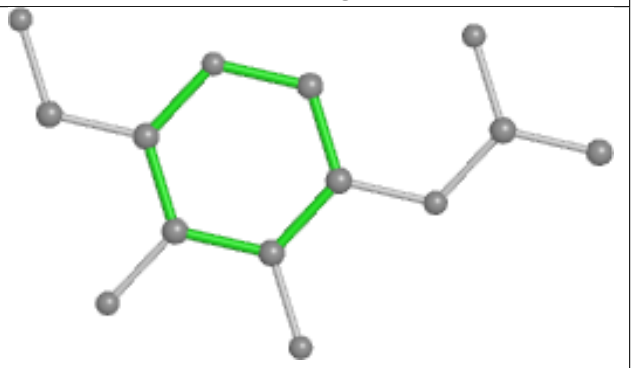
Bond lengths



Bond angles

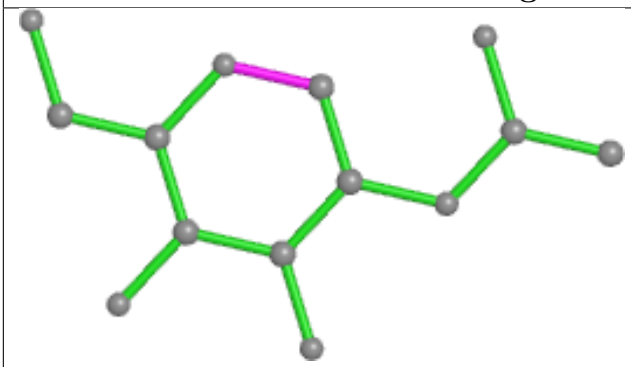


Torsions

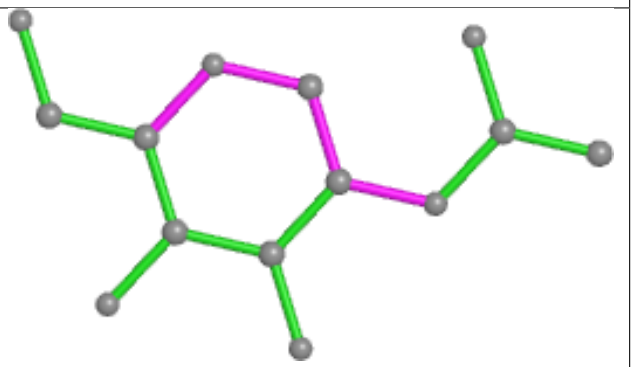


Rings

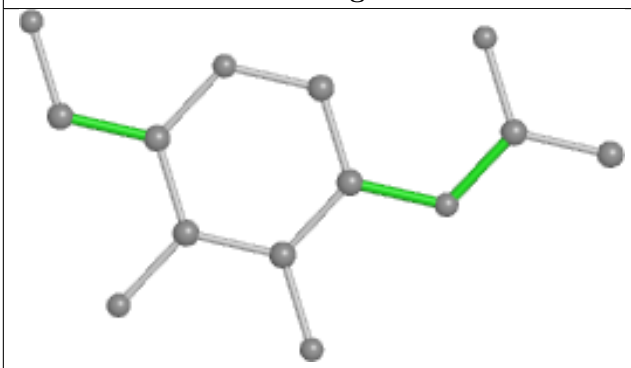
Ligand NAG D 706



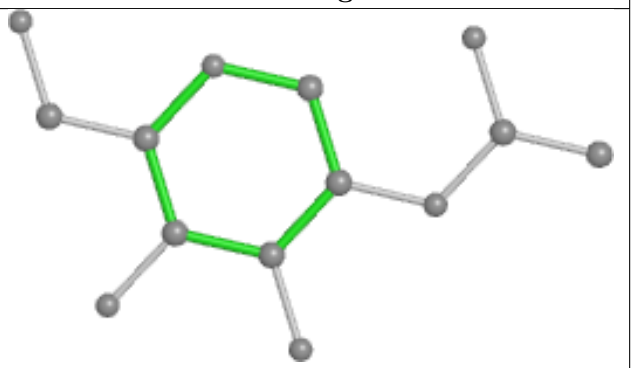
Bond lengths



Bond angles

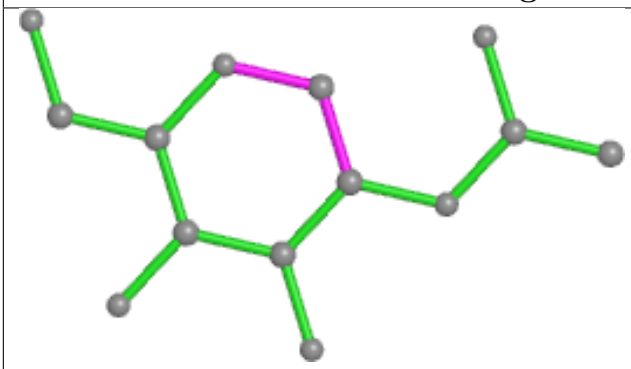


Torsions

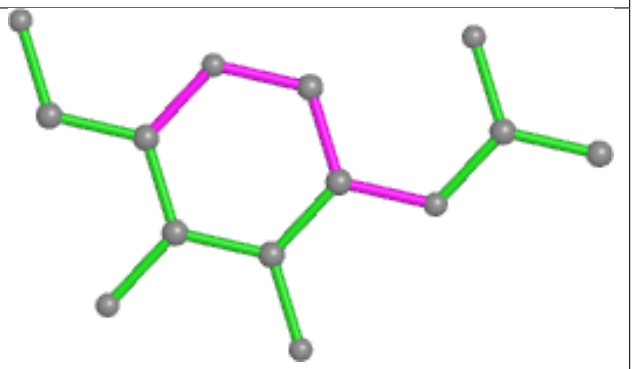


Rings

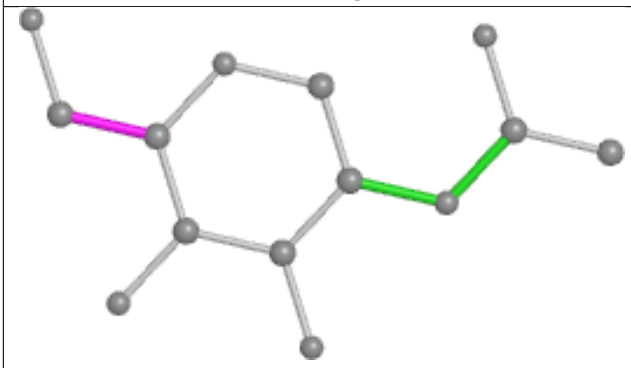
Ligand NAG A 701



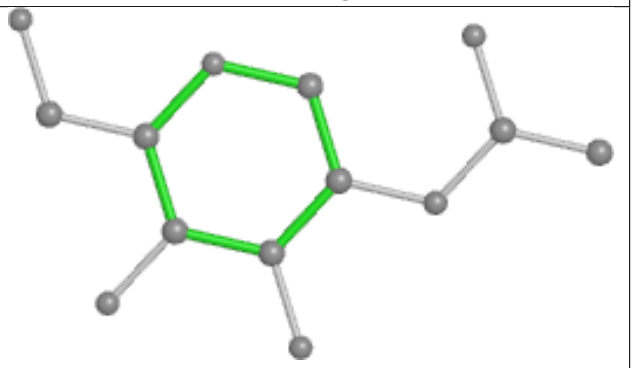
Bond lengths



Bond angles

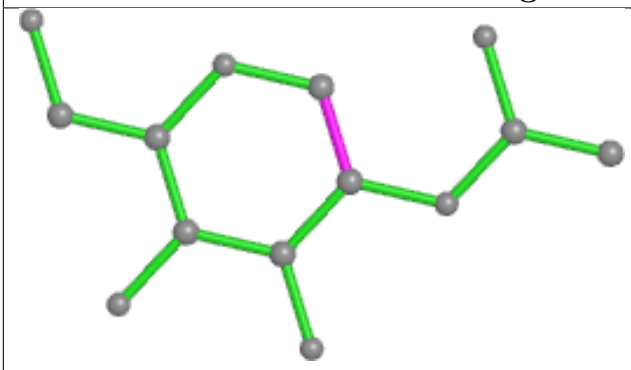


Torsions

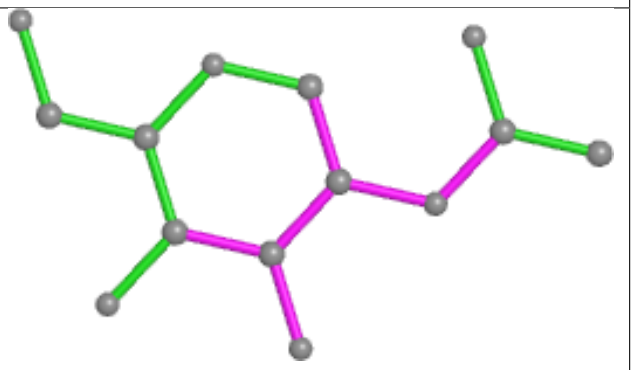


Rings

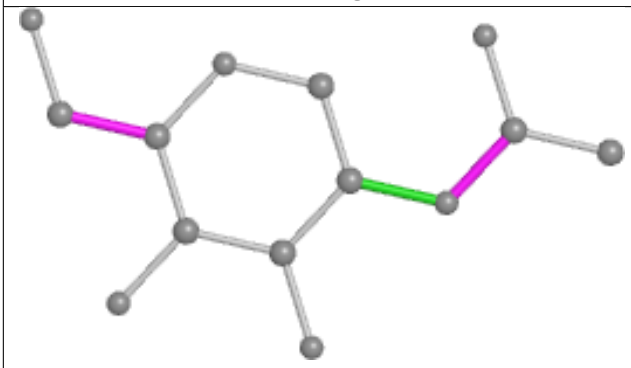
Ligand NAG A 702



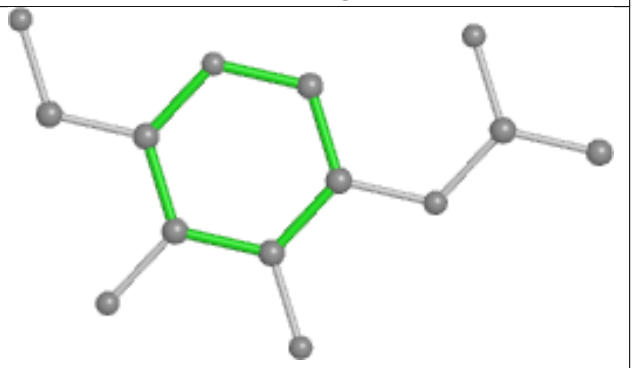
Bond lengths



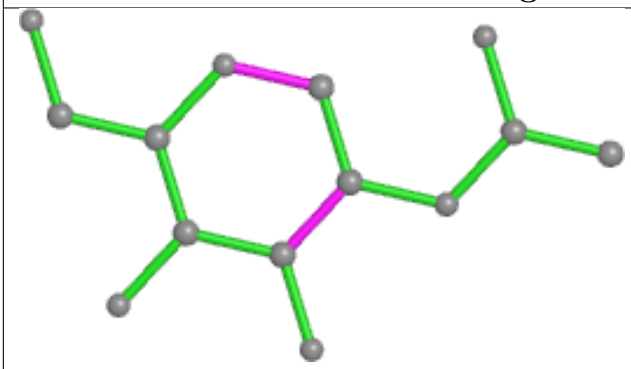
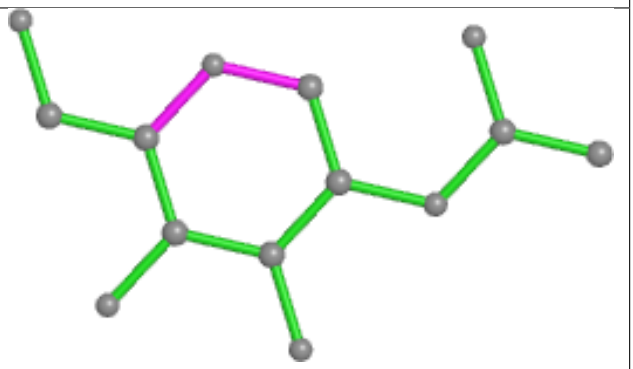
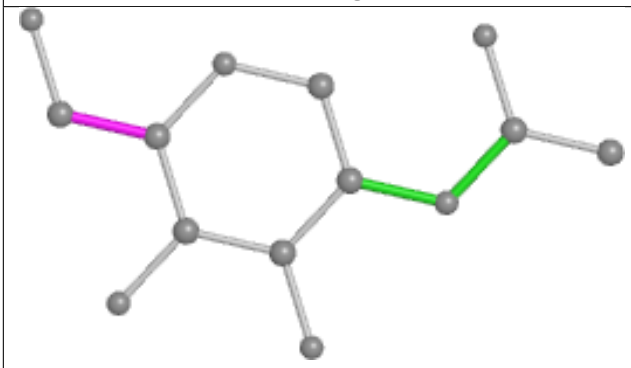
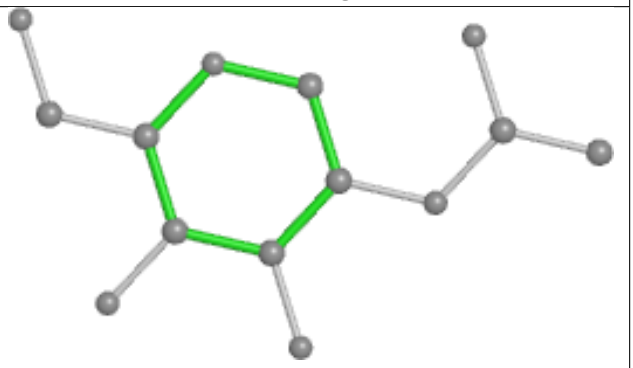
Bond angles

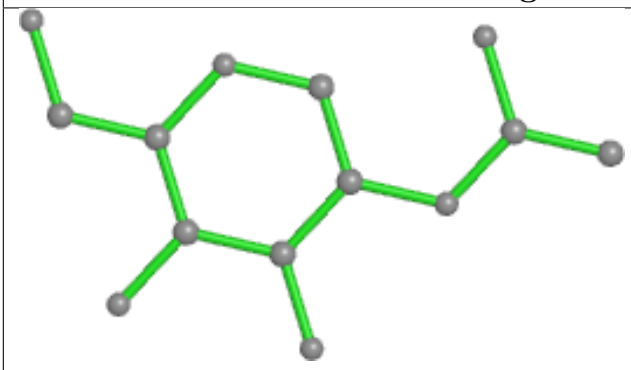
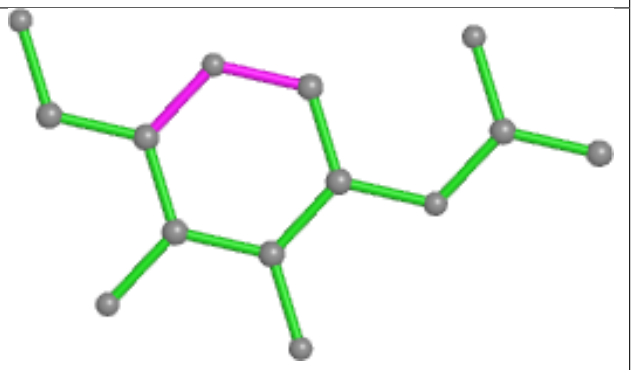
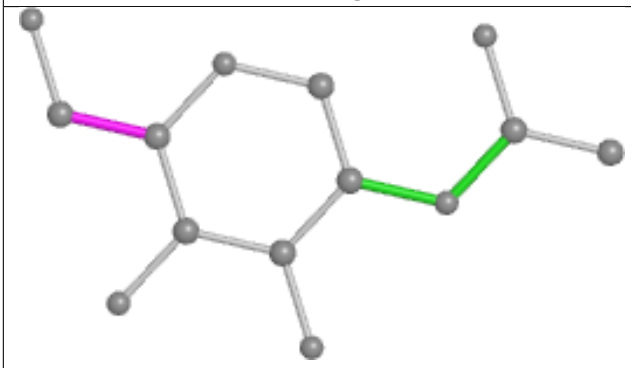
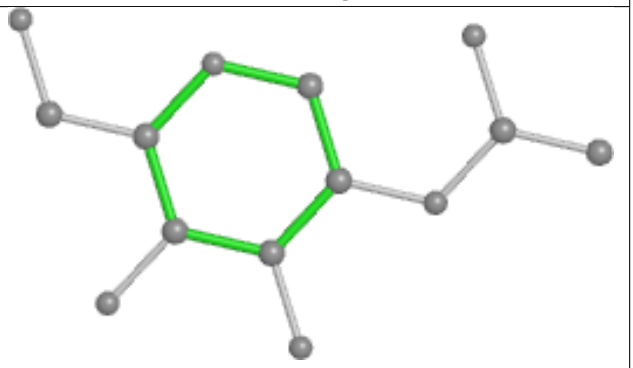


Torsions

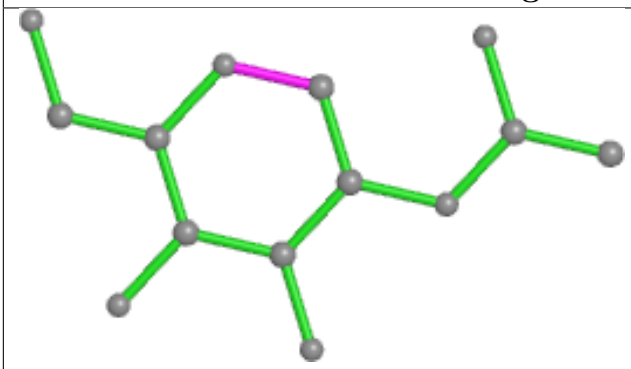


Rings

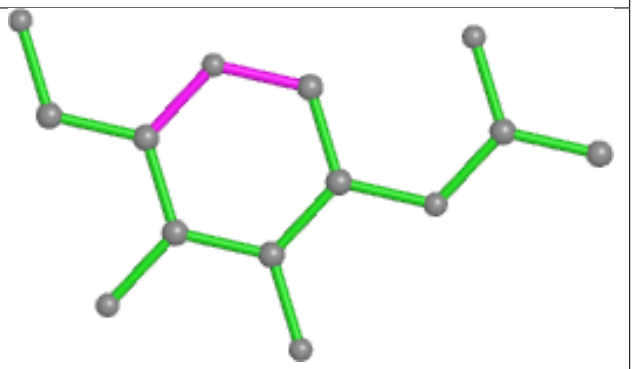
Ligand NAG A 706	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand NAG D 700	
	
Bond lengths	Bond angles
	
Torsions	Rings

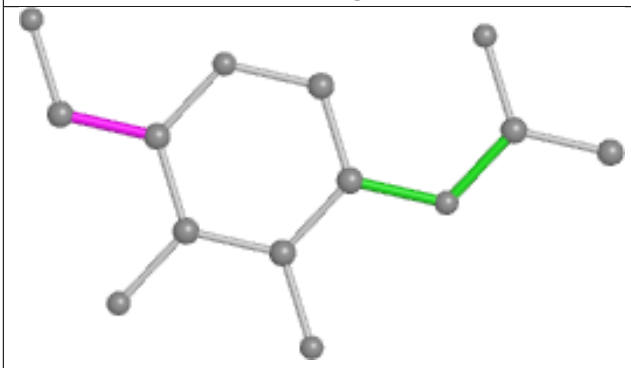
Ligand NAG F 701



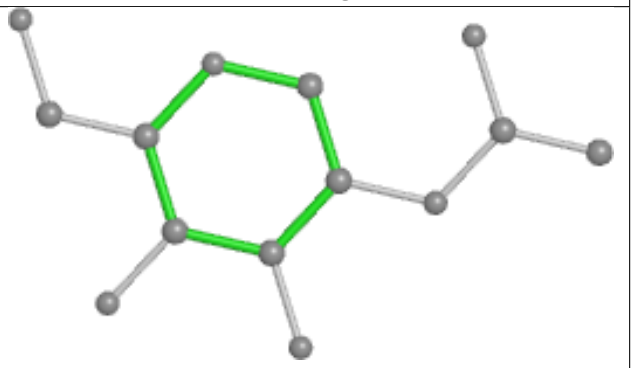
Bond lengths



Bond angles

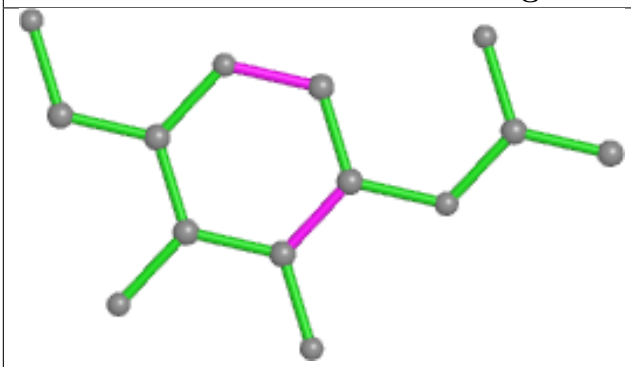


Torsions

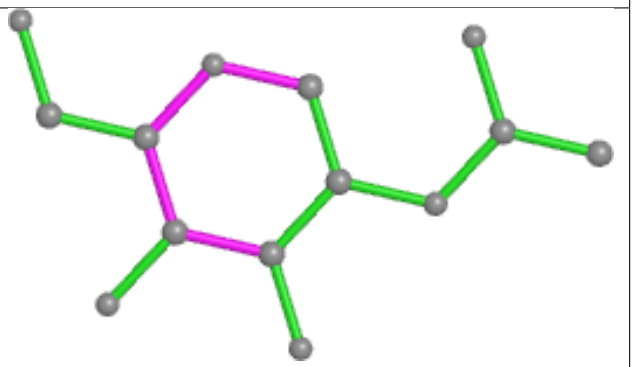


Rings

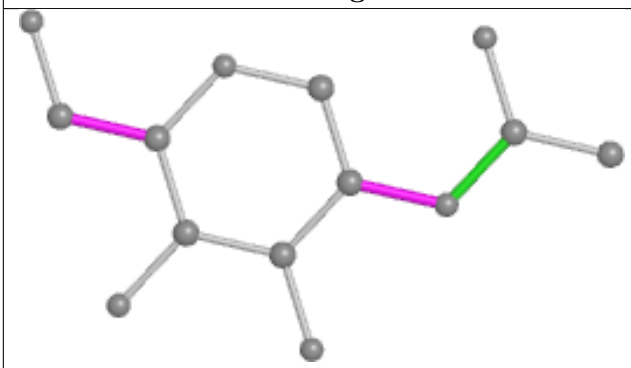
Ligand NAG E 706



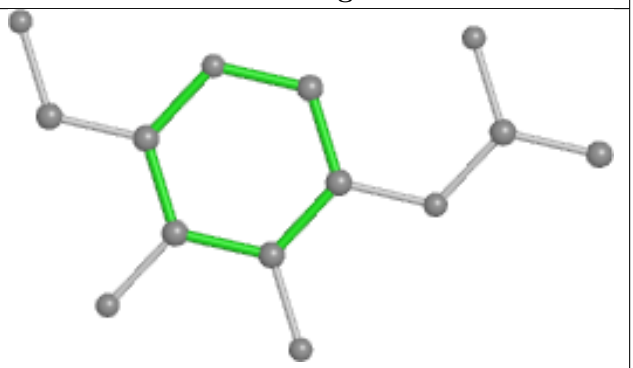
Bond lengths



Bond angles

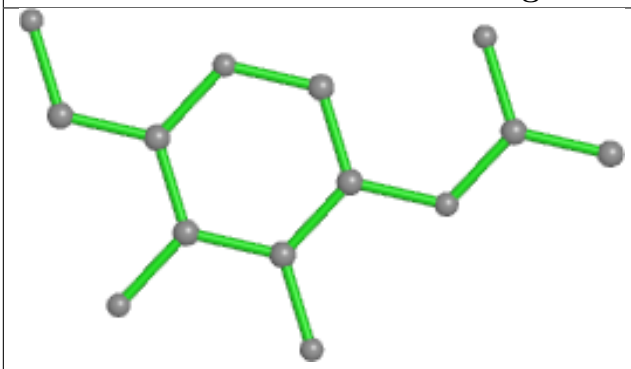


Torsions

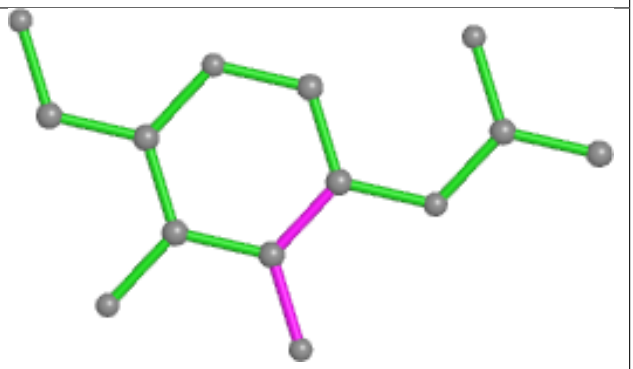


Rings

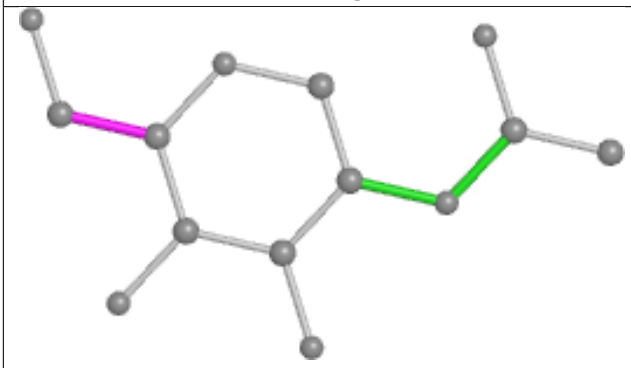
Ligand NAG F 702



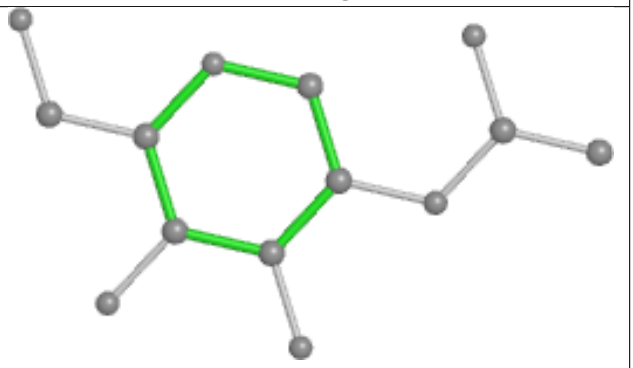
Bond lengths



Bond angles

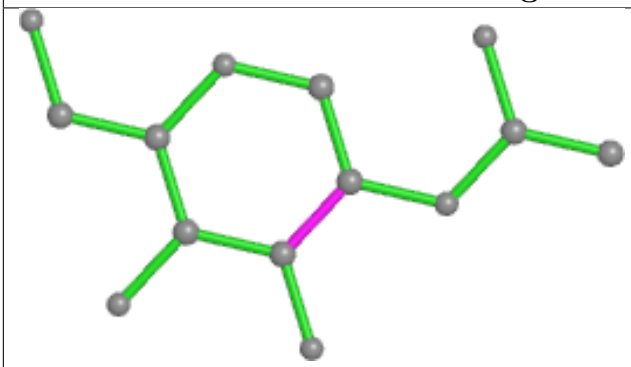


Torsions

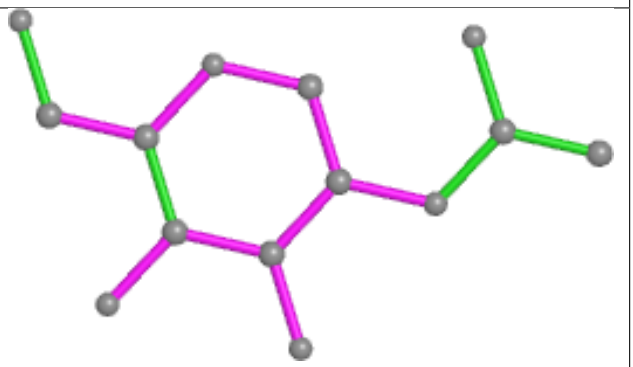


Rings

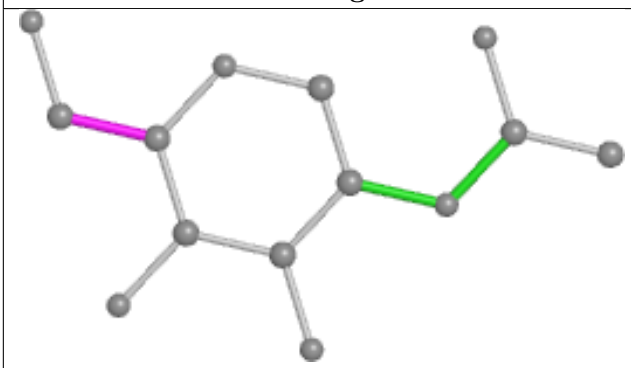
Ligand NAG B 701



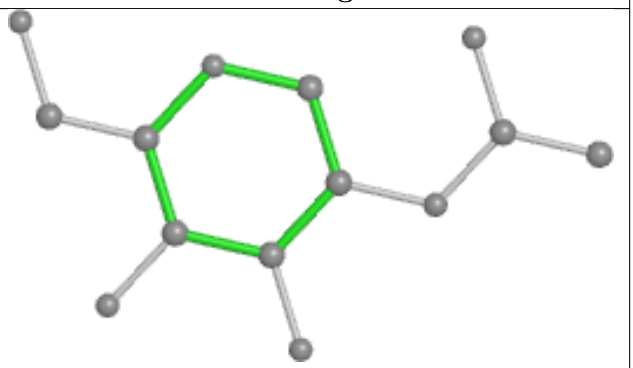
Bond lengths



Bond angles

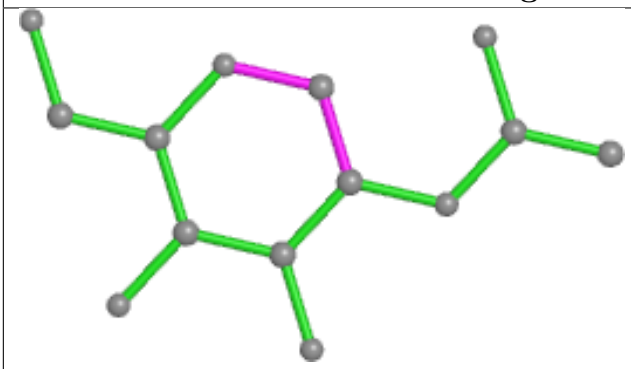


Torsions

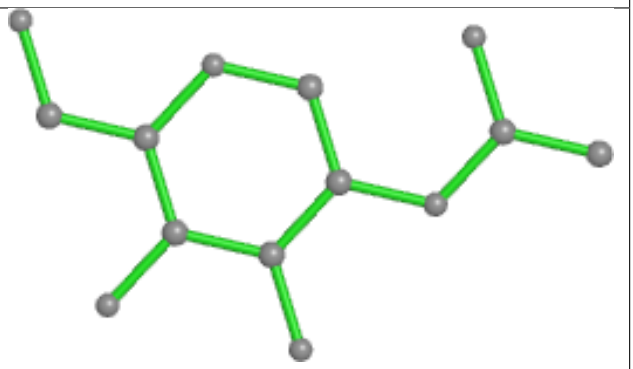


Rings

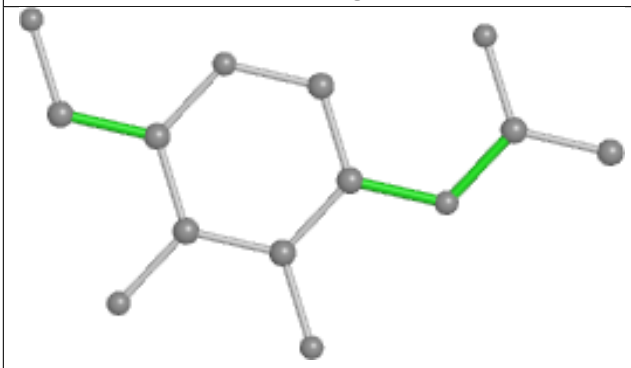
Ligand NAG C 702



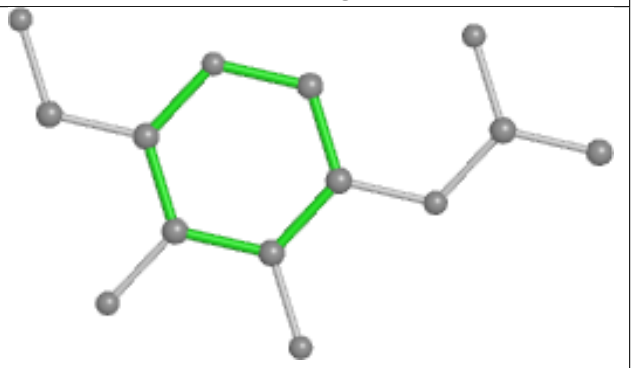
Bond lengths



Bond angles

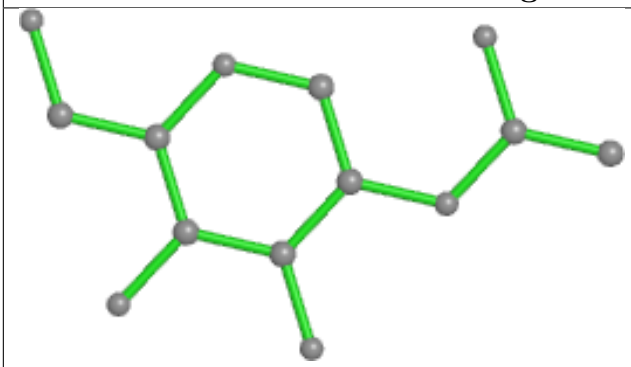


Torsions

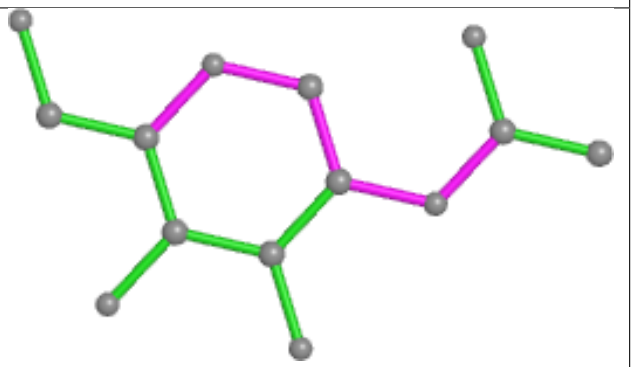


Rings

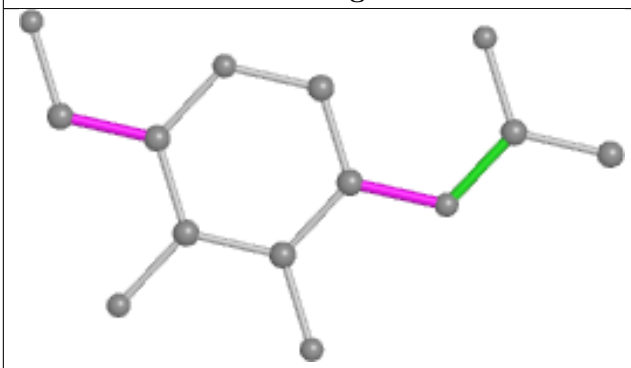
Ligand NAG C 706



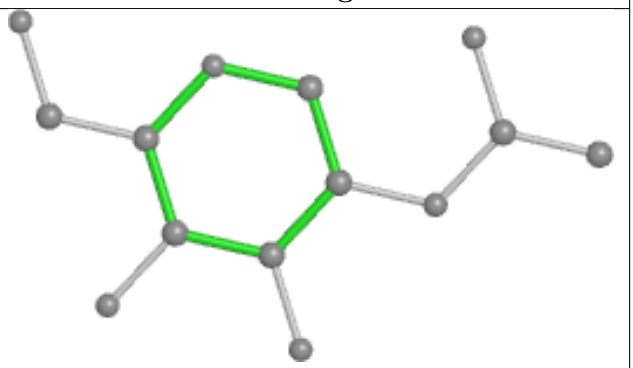
Bond lengths



Bond angles

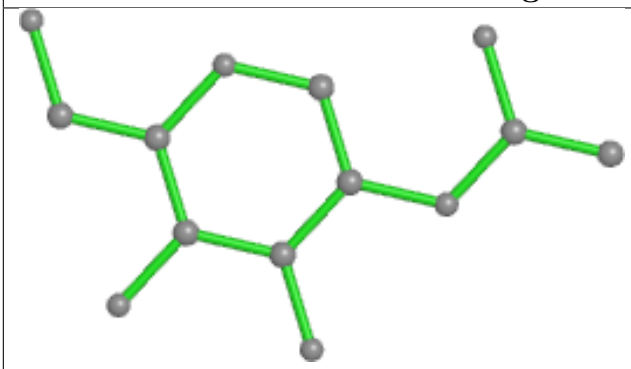


Torsions

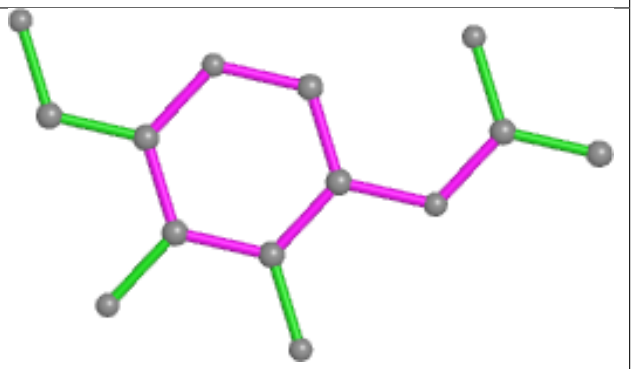


Rings

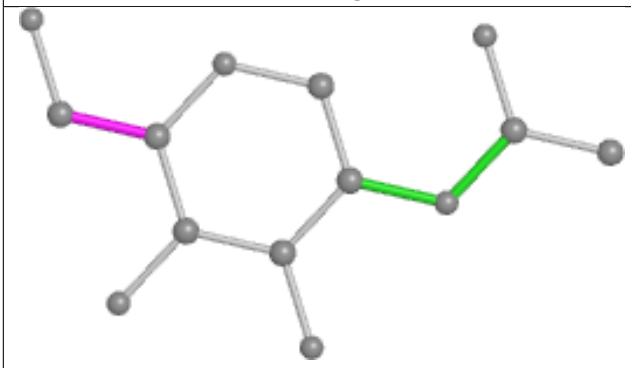
Ligand NAG F 706



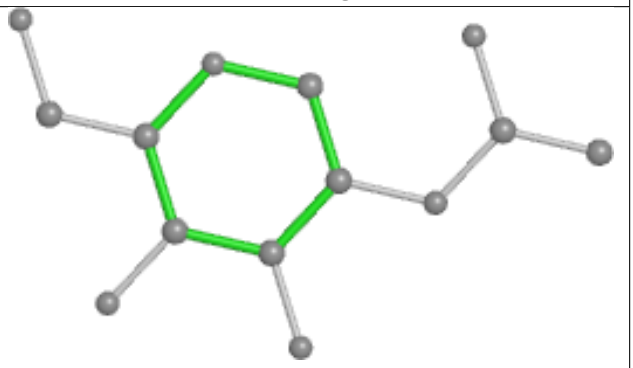
Bond lengths



Bond angles

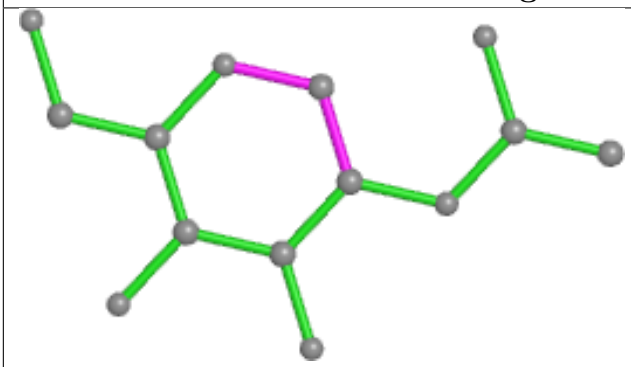


Torsions

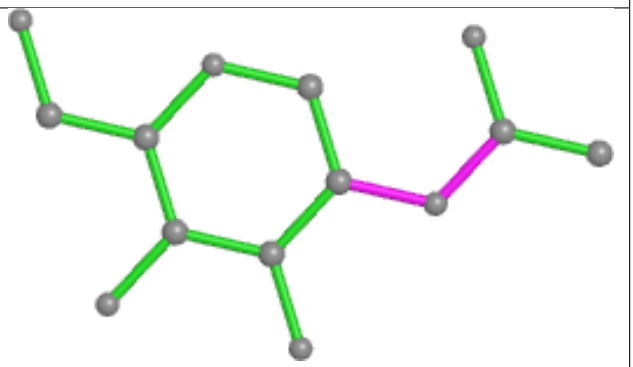


Rings

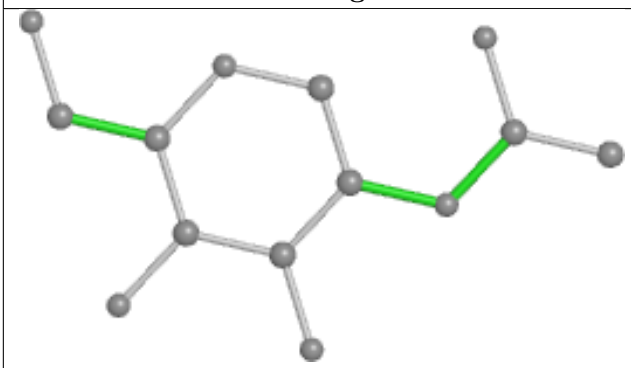
Ligand NAG D 702



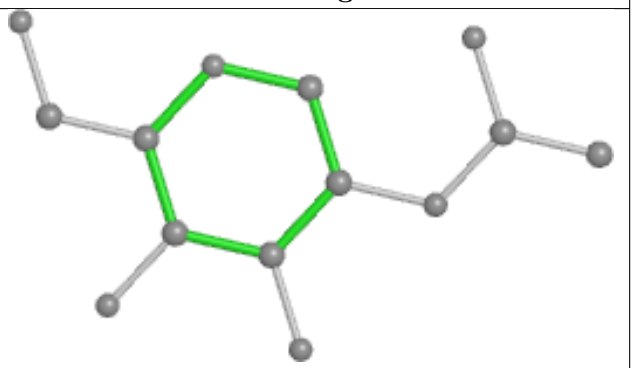
Bond lengths



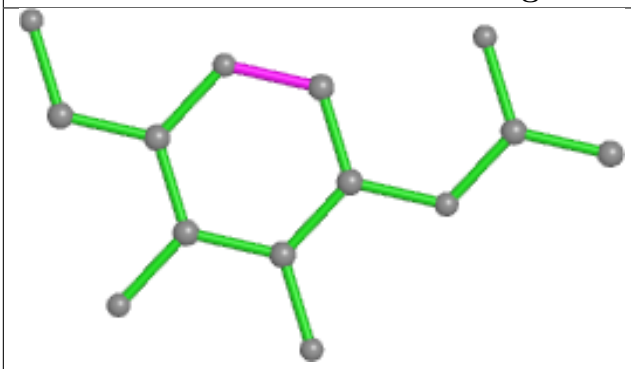
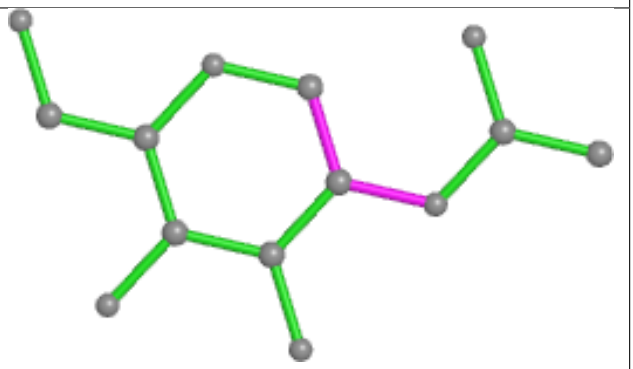
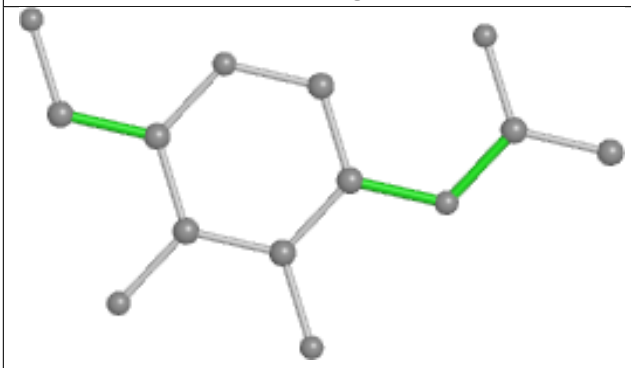
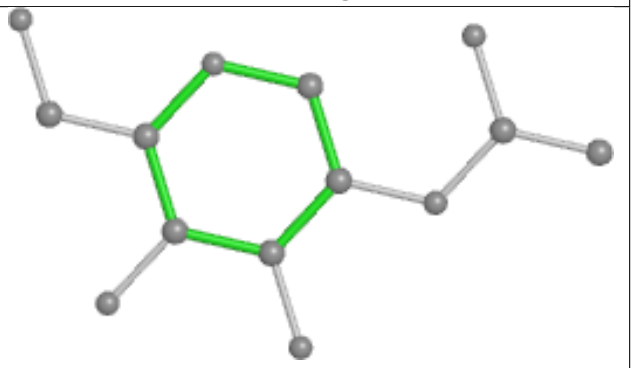
Bond angles

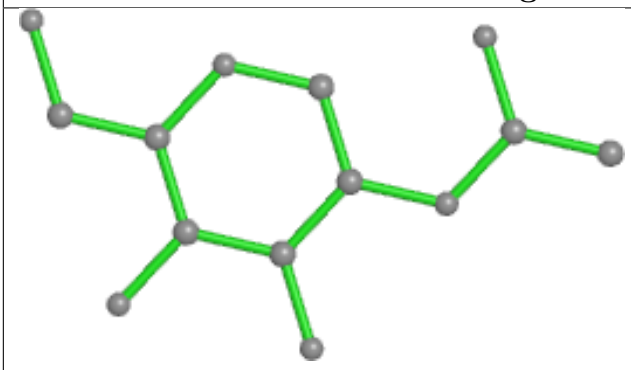
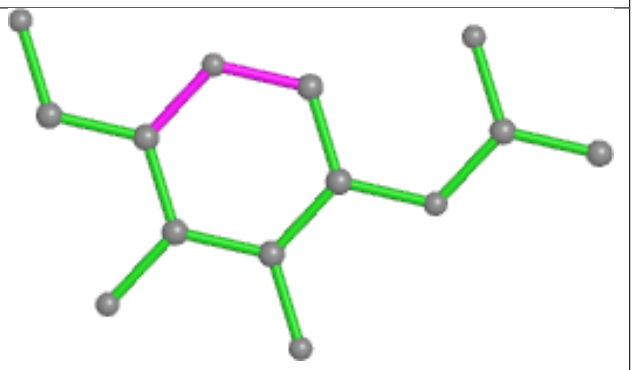
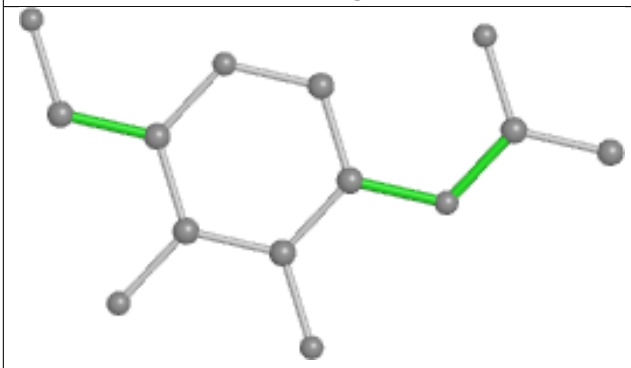
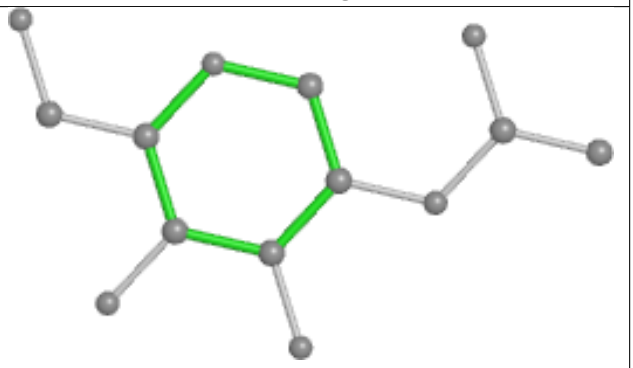


Torsions

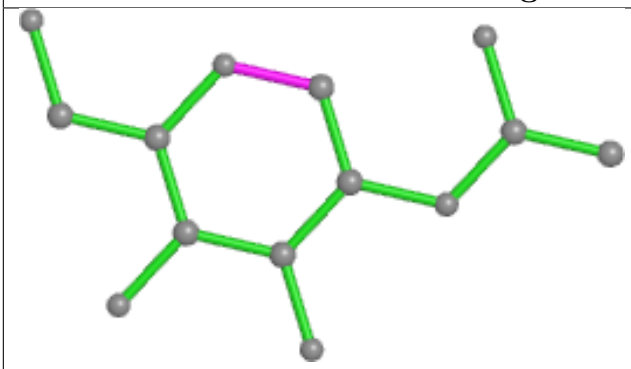


Rings

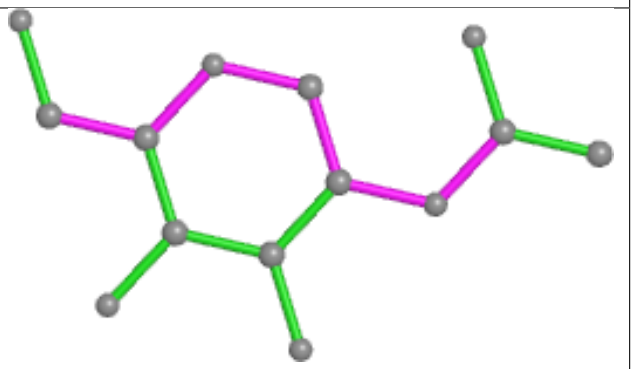
Ligand NAG E 702	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NAG D 701	
 Bond lengths	 Bond angles
 Torsions	 Rings

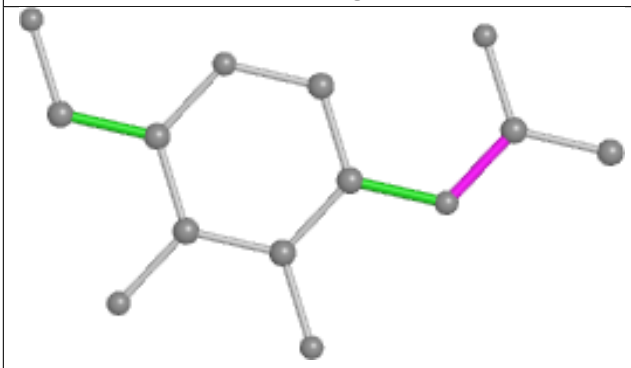
Ligand NAG C 701



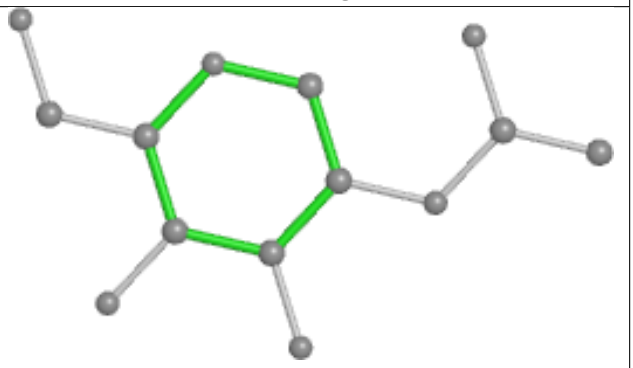
Bond lengths



Bond angles

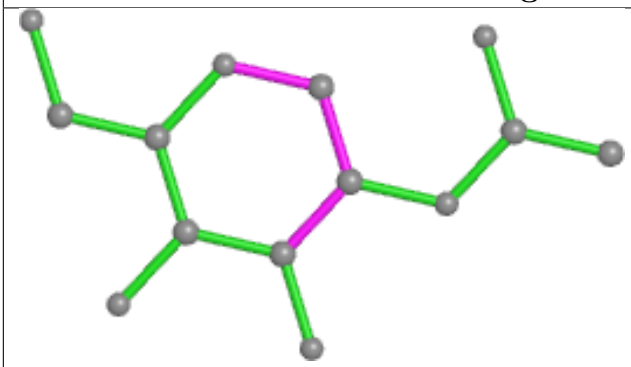


Torsions

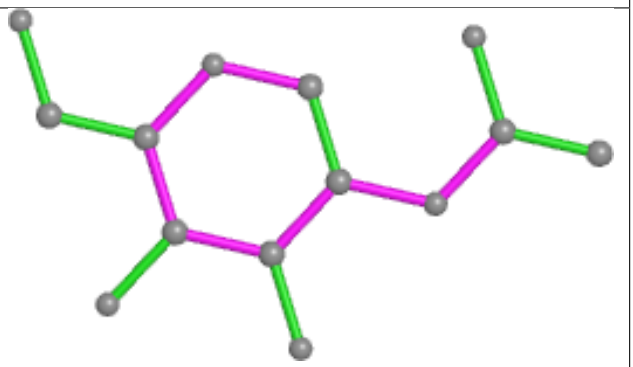


Rings

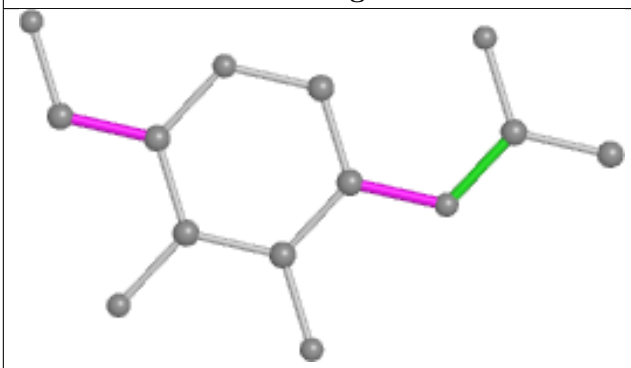
Ligand NAG B 706



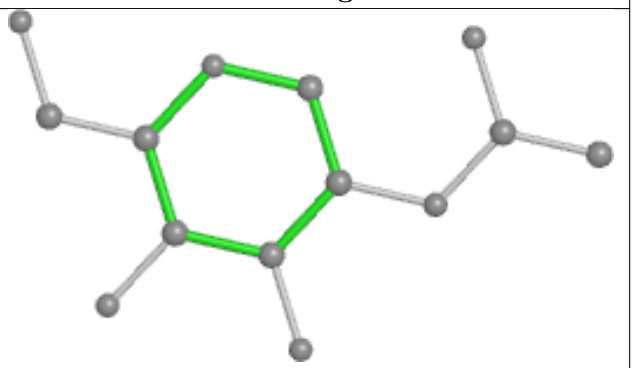
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	487/497 (97%)	0.39	15 (3%)	49	56	22, 39, 64, 119	0
1	B	488/497 (98%)	0.42	20 (4%)	37	44	15, 39, 67, 130	0
1	C	489/497 (98%)	0.34	15 (3%)	49	56	21, 37, 64, 135	0
1	D	489/497 (98%)	0.32	12 (2%)	57	64	19, 36, 62, 125	0
1	E	489/497 (98%)	0.40	15 (3%)	49	56	20, 38, 65, 108	0
1	F	489/497 (98%)	0.45	22 (4%)	33	40	21, 40, 73, 128	0
All	All	2931/2982 (98%)	0.39	99 (3%)	45	52	15, 38, 66, 135	0

The worst 5 of 99 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	503	LYS	8.2
1	A	502	ILE	7.4
1	D	502	ILE	5.7
1	F	502	ILE	5.6
1	C	502	ILE	5.5

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

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

6.3 Carbohydrates

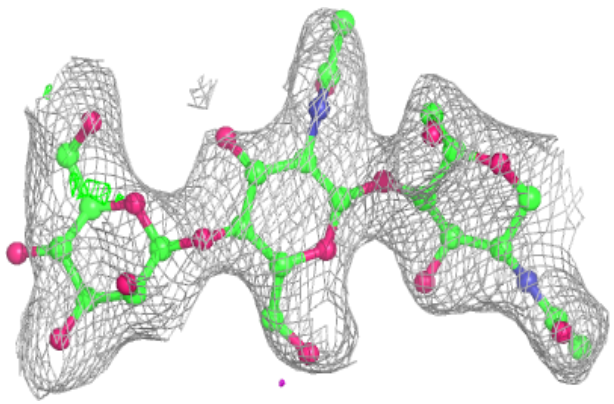
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

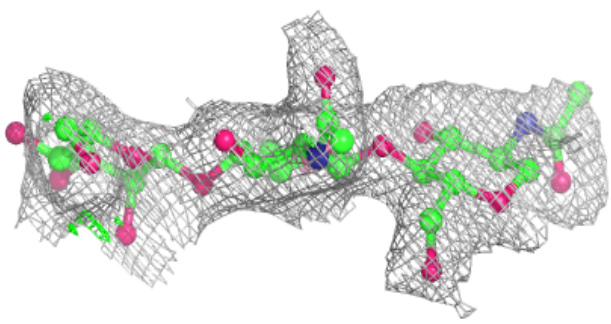
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	BMA	G	3	11/12	0.81	0.18	36,49,60,79	0
2	BMA	I	3	11/12	0.81	0.12	43,51,65,67	0
2	NAG	G	2	14/15	0.85	0.15	31,35,43,57	0
2	BMA	K	3	11/12	0.87	0.14	36,54,67,78	0
2	BMA	J	3	11/12	0.88	0.13	46,54,59,62	0
2	NAG	J	1	14/15	0.88	0.16	17,30,39,42	0
2	NAG	L	1	14/15	0.88	0.16	26,40,46,52	0
2	NAG	K	2	14/15	0.89	0.14	15,41,60,61	0
2	BMA	H	3	11/12	0.89	0.14	42,50,60,63	0
2	NAG	G	1	14/15	0.89	0.14	30,45,52,55	0
2	NAG	L	2	14/15	0.90	0.14	35,46,57,59	0
2	BMA	L	3	11/12	0.90	0.11	41,53,66,68	0
2	NAG	H	2	14/15	0.91	0.14	27,37,56,63	0
2	NAG	H	1	14/15	0.91	0.14	25,36,51,52	0
2	NAG	I	1	14/15	0.91	0.12	21,35,45,49	0
2	NAG	I	2	14/15	0.91	0.14	27,37,43,65	0
2	NAG	K	1	14/15	0.92	0.16	21,39,64,66	0
2	NAG	J	2	14/15	0.92	0.19	24,35,49,67	0

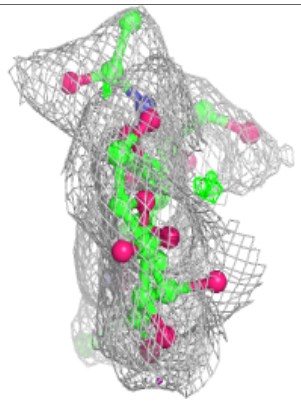
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain G:

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

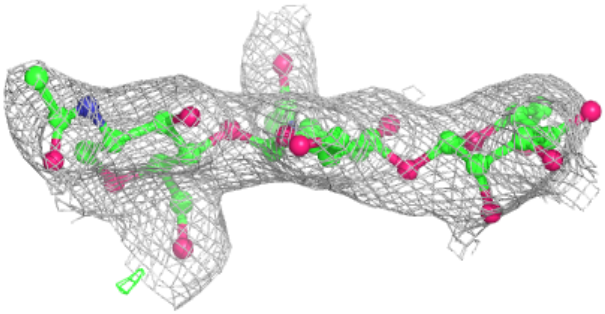


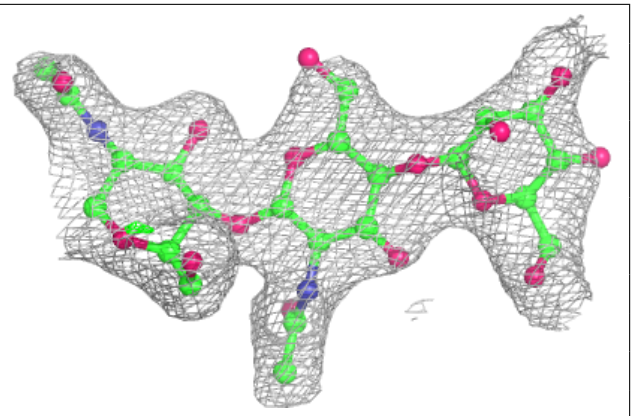


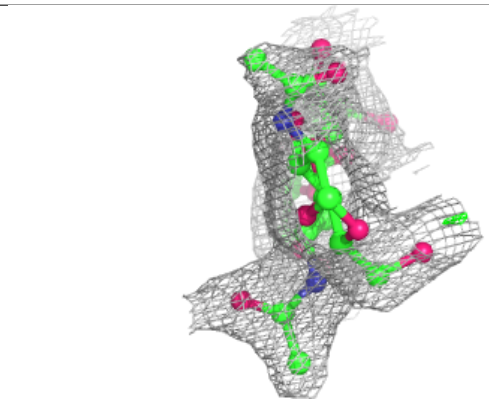


Electron density around Chain H:

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

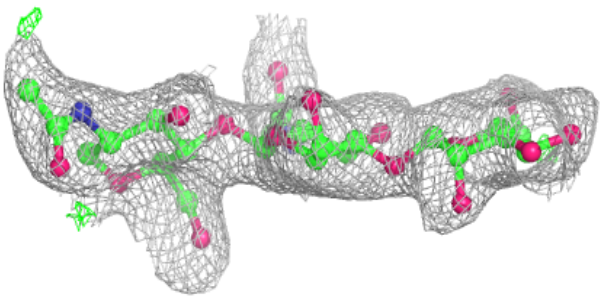


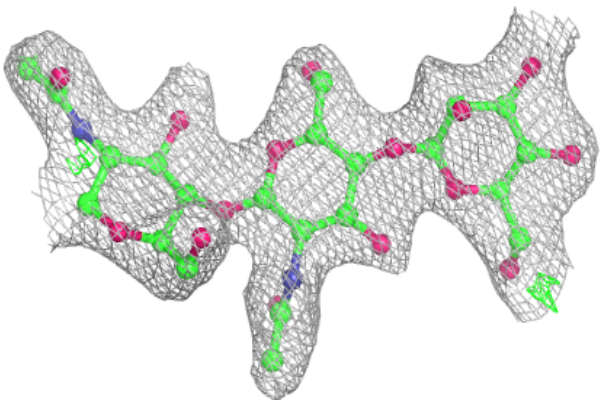


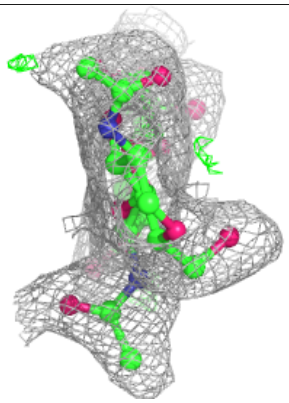


Electron density around Chain I:

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

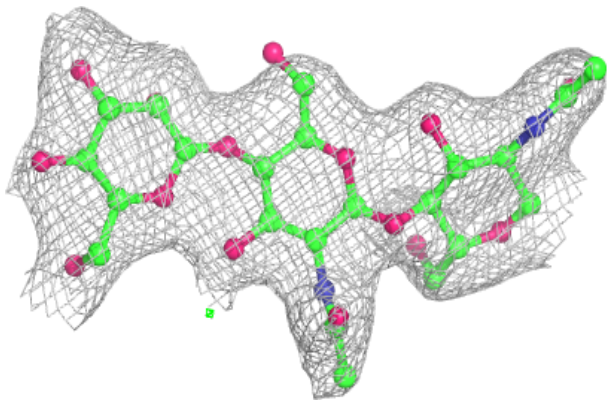


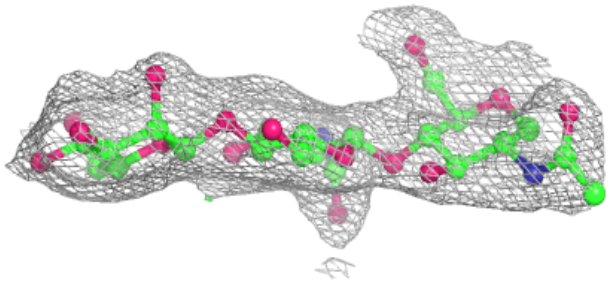


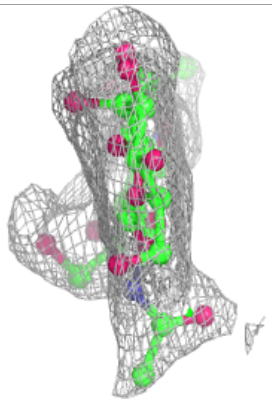


Electron density around Chain J:

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

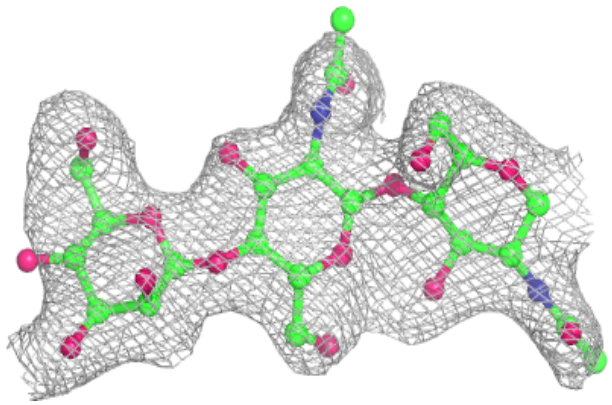


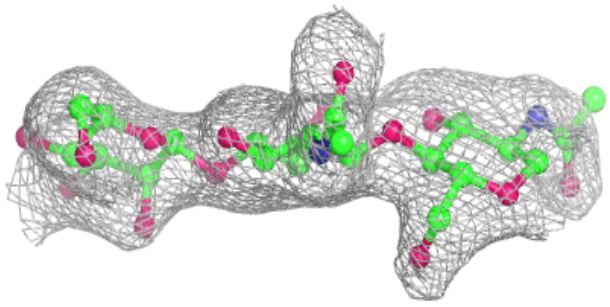




Electron density around Chain K:

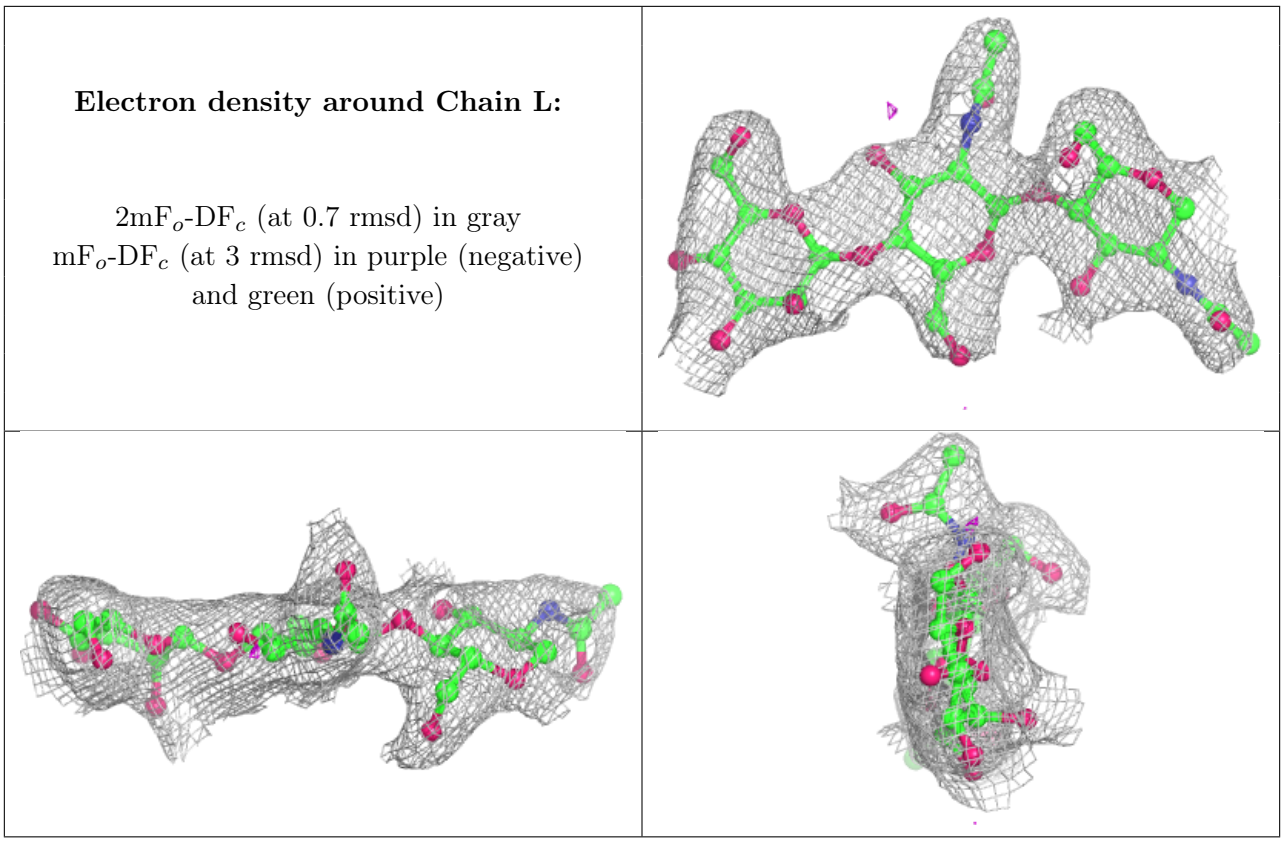
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around Chain L:

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



6.4 Ligands

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, 95^{th} 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	B	706	14/15	0.54	0.40	45,63,71,75	0
3	NAG	A	706	14/15	0.63	0.34	39,60,69,70	0
3	NAG	E	701	14/15	0.66	0.28	39,60,79,81	0
3	NAG	A	702	14/15	0.68	0.37	65,74,84,86	0
3	NAG	F	702	14/15	0.68	0.32	39,58,70,76	0
3	NAG	B	701	14/15	0.69	0.24	58,66,77,79	0
3	NAG	D	706	14/15	0.70	0.29	35,54,66,72	0
3	NAG	A	700	14/15	0.71	0.21	35,41,62,64	0
3	NAG	F	706	14/15	0.71	0.30	50,57,70,76	0
3	NAG	C	702	14/15	0.72	0.28	49,76,102,106	0
3	NAG	D	700	14/15	0.72	0.23	36,60,71,72	0
3	NAG	C	700	14/15	0.72	0.22	45,63,73,82	0
3	NAG	D	702	14/15	0.73	0.29	26,75,92,102	0
3	NAG	E	702	14/15	0.76	0.22	31,45,58,60	0

Continued on next page...

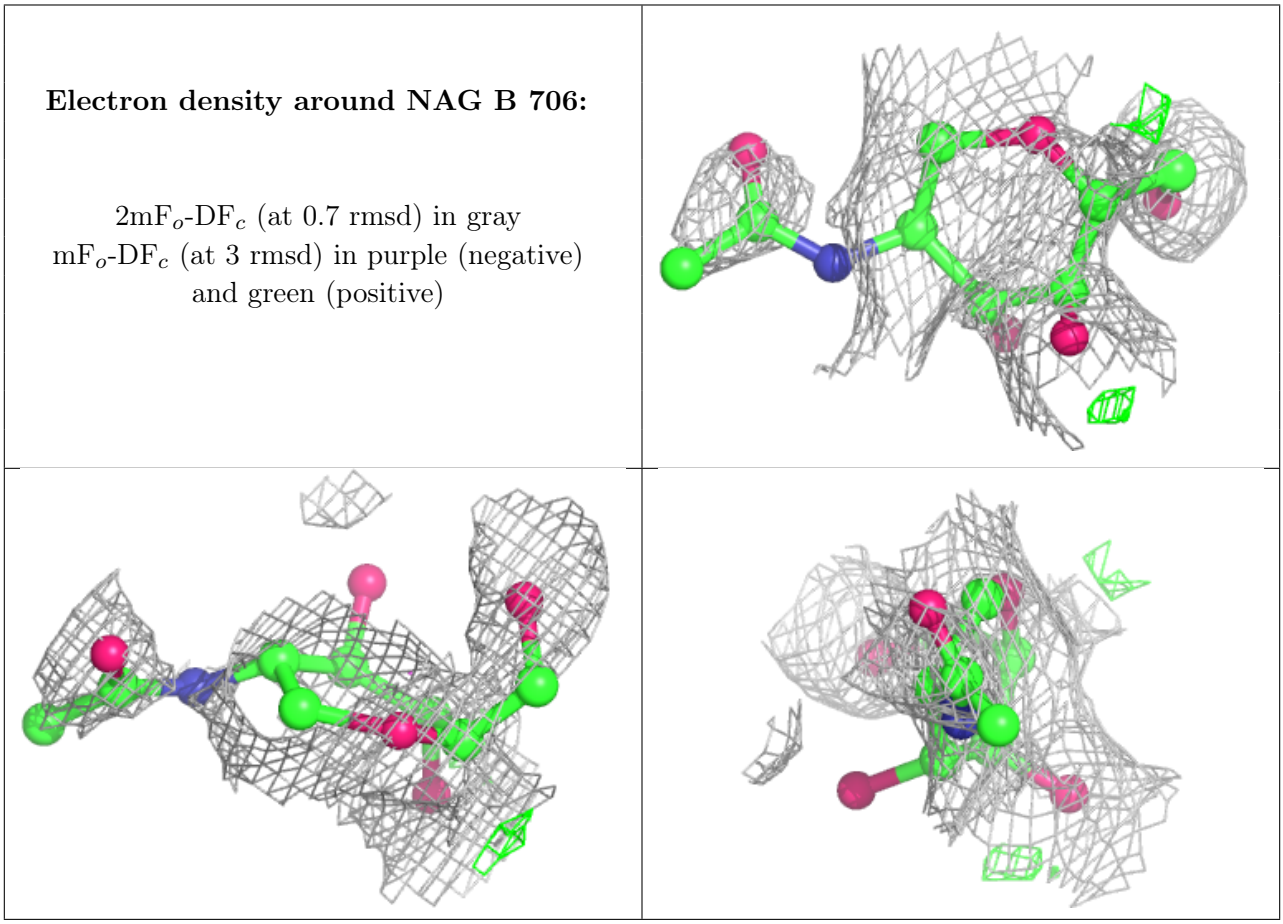
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	E	700	14/15	0.76	0.23	47,57,79,79	0
3	NAG	D	701	14/15	0.76	0.24	30,63,74,79	0
3	NAG	B	700	14/15	0.77	0.25	43,54,64,71	0
3	NAG	C	701	14/15	0.78	0.20	32,53,67,76	0
3	NAG	F	700	14/15	0.78	0.22	30,46,62,63	0
3	NAG	A	701	14/15	0.80	0.26	27,45,59,76	0
3	NAG	B	702	14/15	0.81	0.17	46,56,76,78	0
3	NAG	E	706	14/15	0.83	0.24	23,47,74,75	0
3	NAG	C	706	14/15	0.83	0.19	37,46,65,66	0
3	NAG	F	701	14/15	0.86	0.18	38,44,61,65	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.

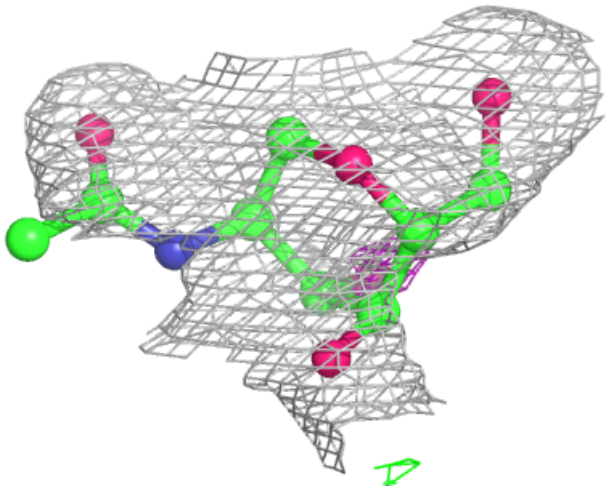
Electron density around NAG B 706:

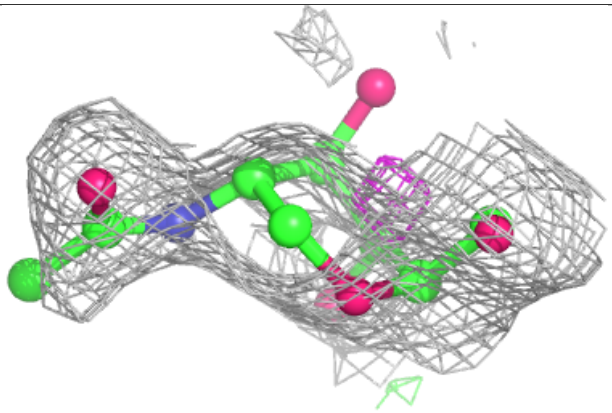
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

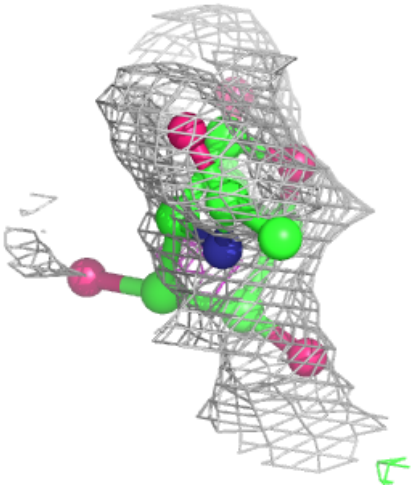


Electron density around NAG A 706:

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

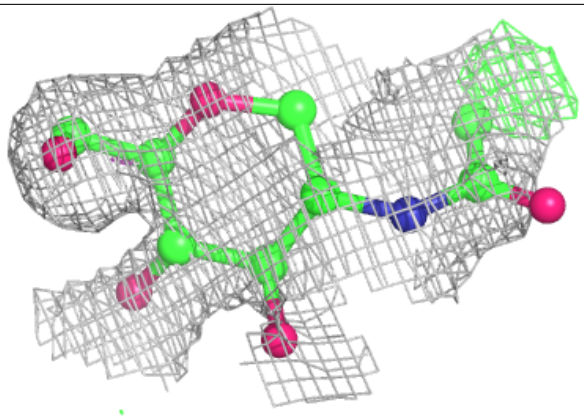


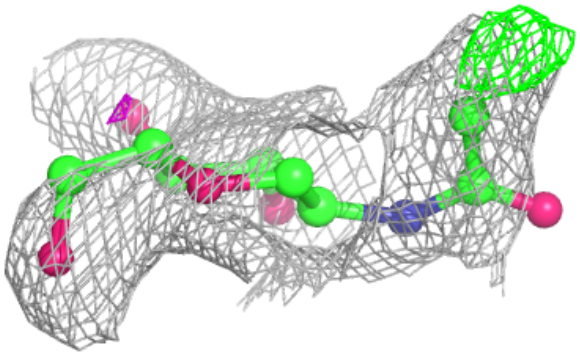


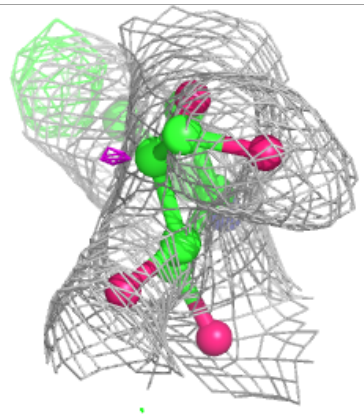


Electron density around NAG E 701:

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

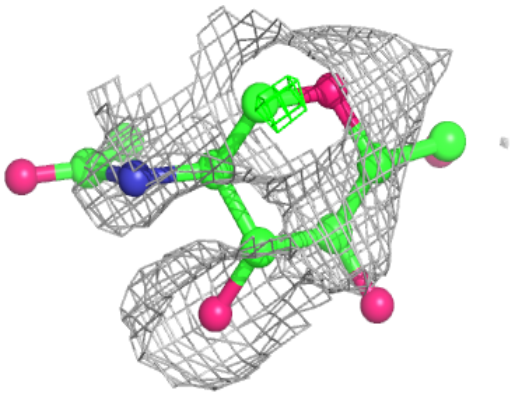


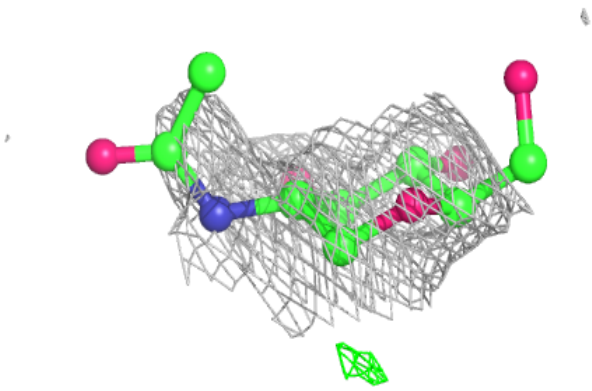


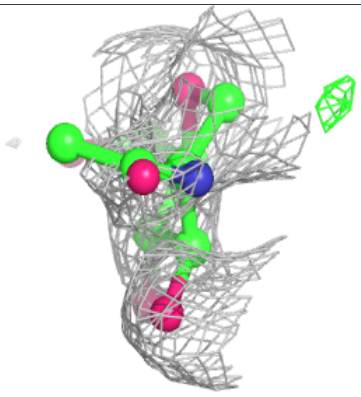


Electron density around NAG A 702:

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

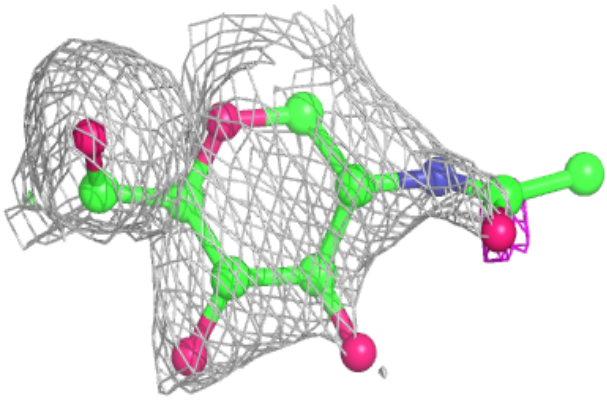


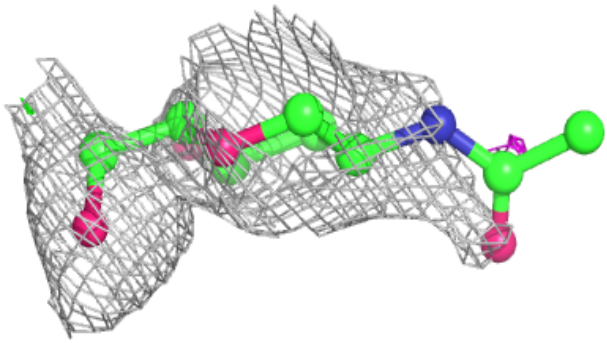


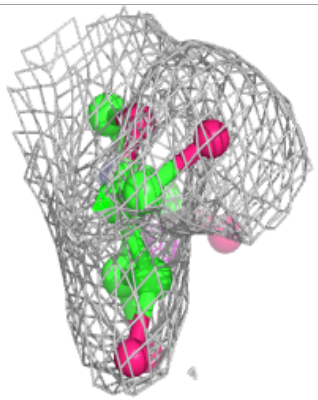


Electron density around NAG F 702:

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

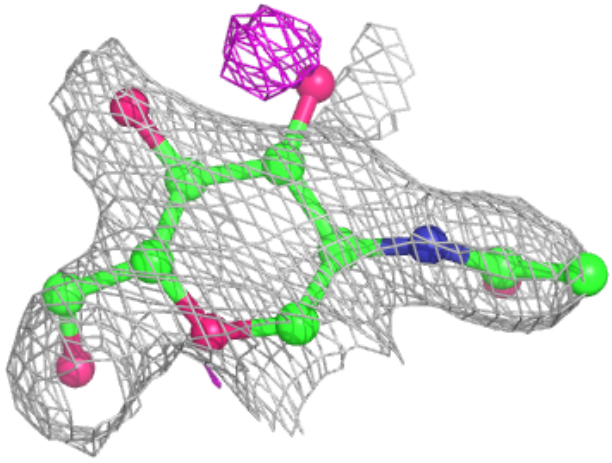


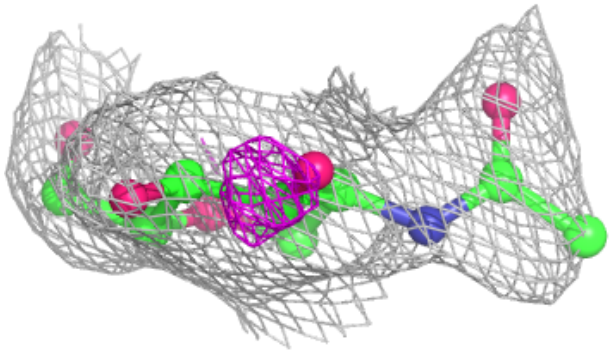


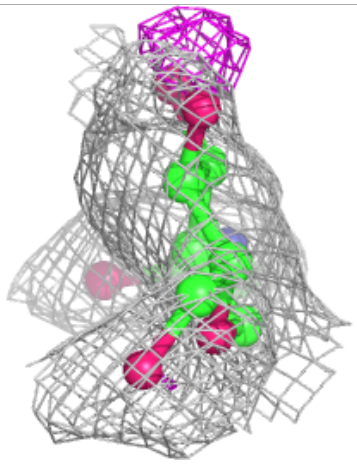


Electron density around NAG B 701:

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

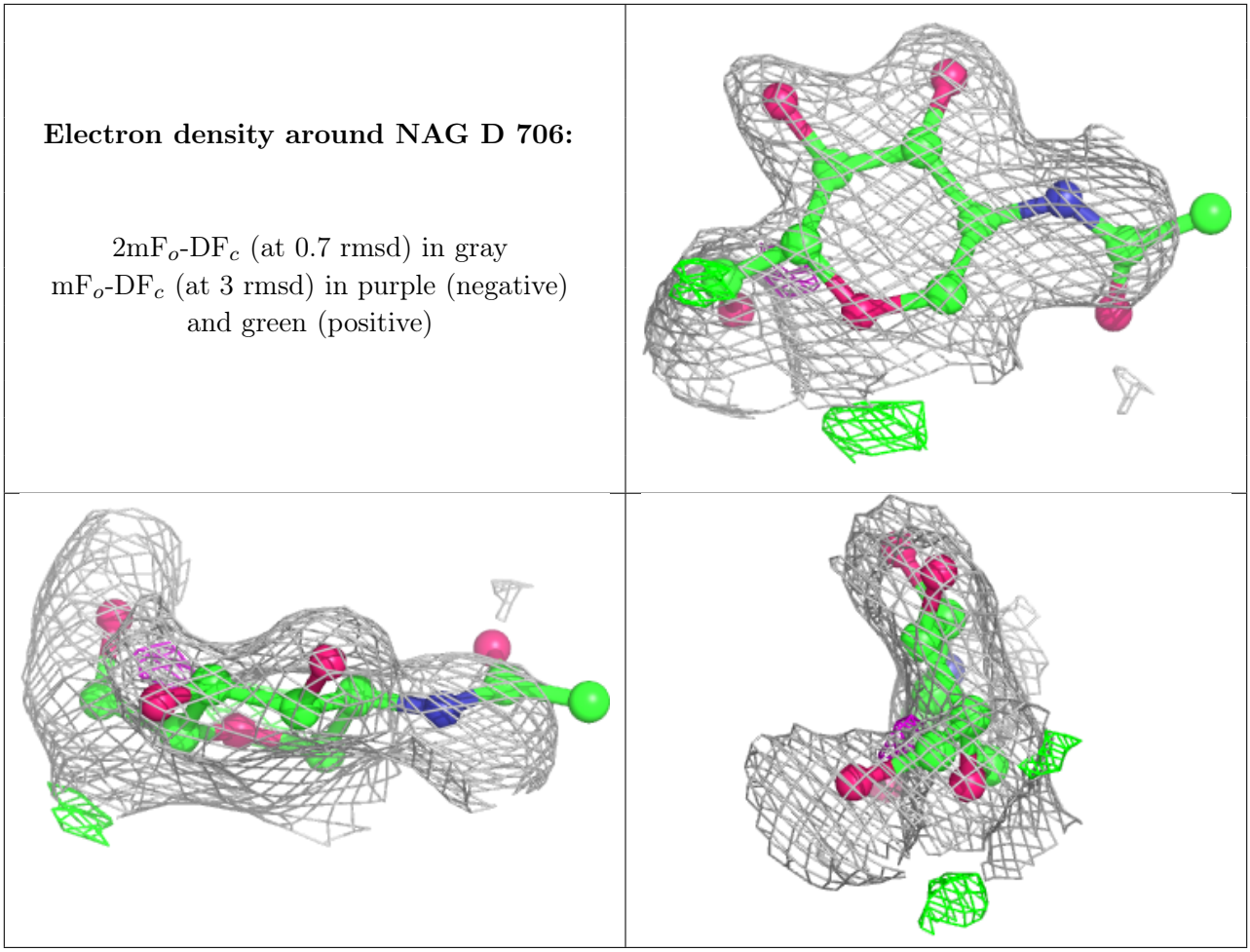






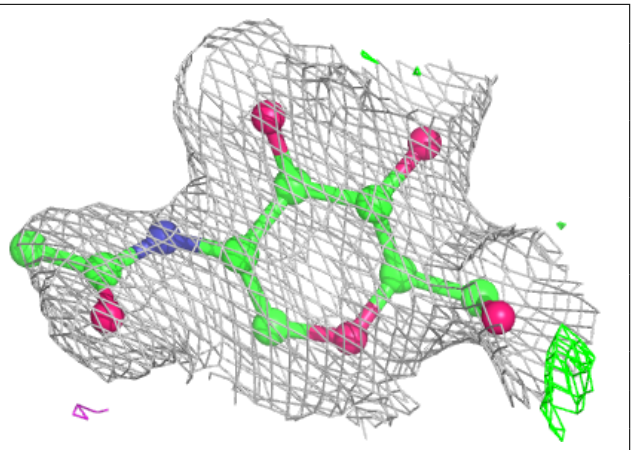
Electron density around NAG D 706:

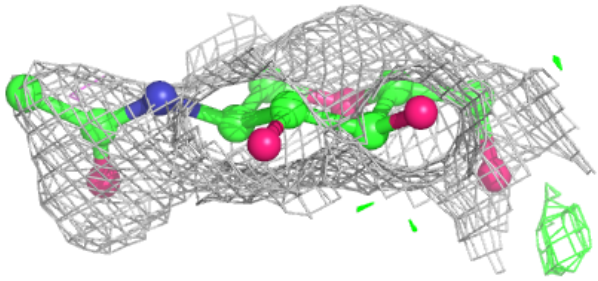
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

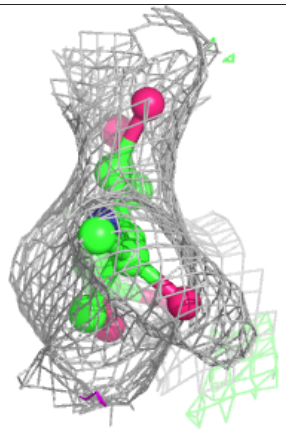


Electron density around NAG A 700:

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

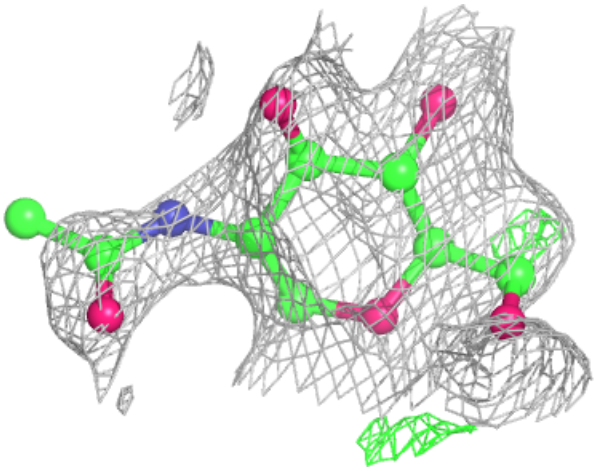


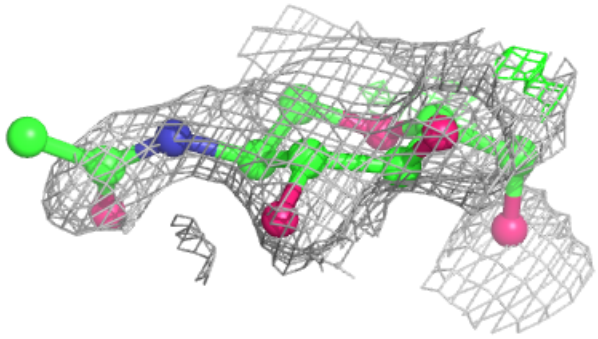


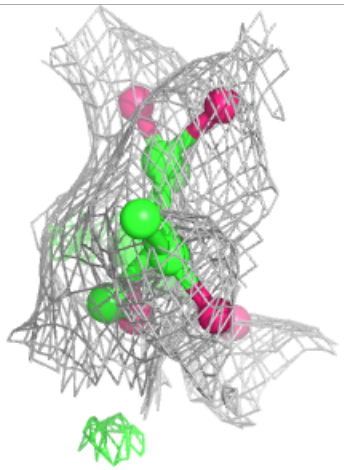


Electron density around NAG F 706:

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

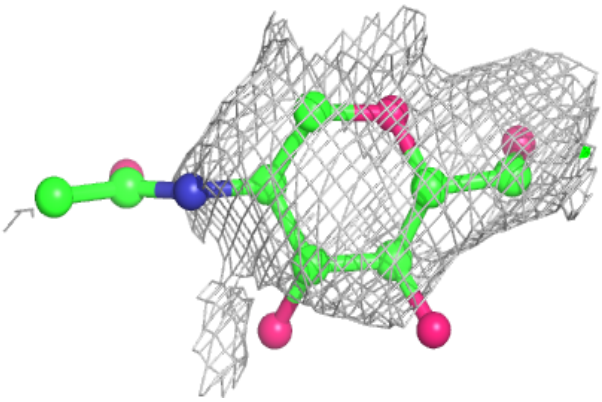


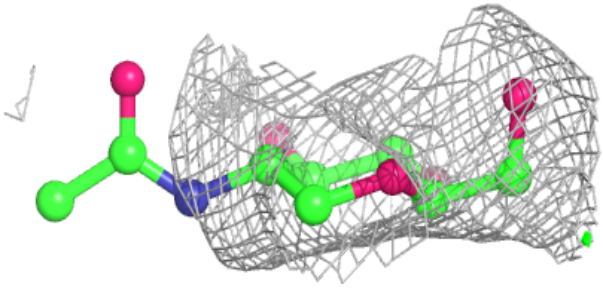


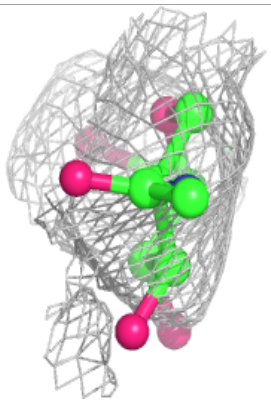


Electron density around NAG C 702:

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

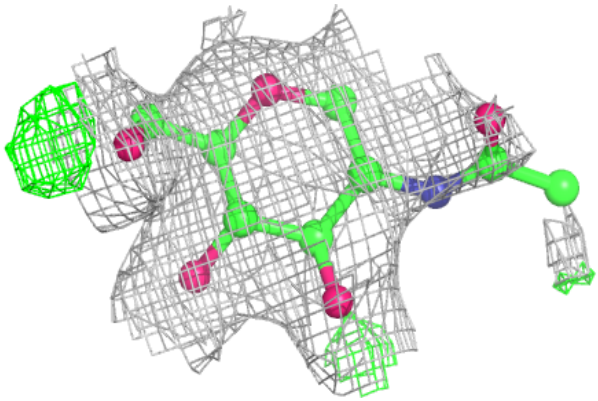


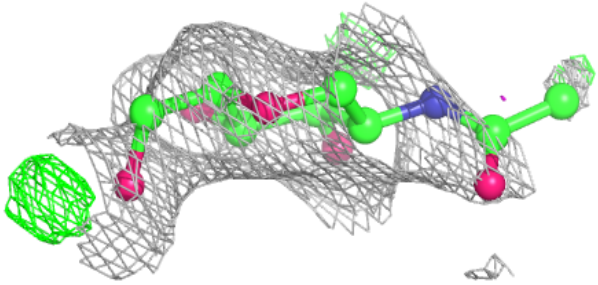


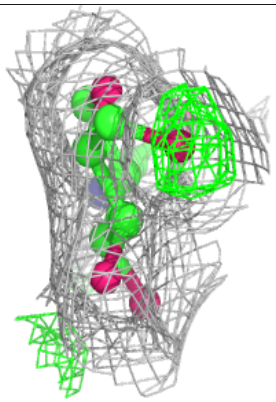


Electron density around NAG D 700:

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

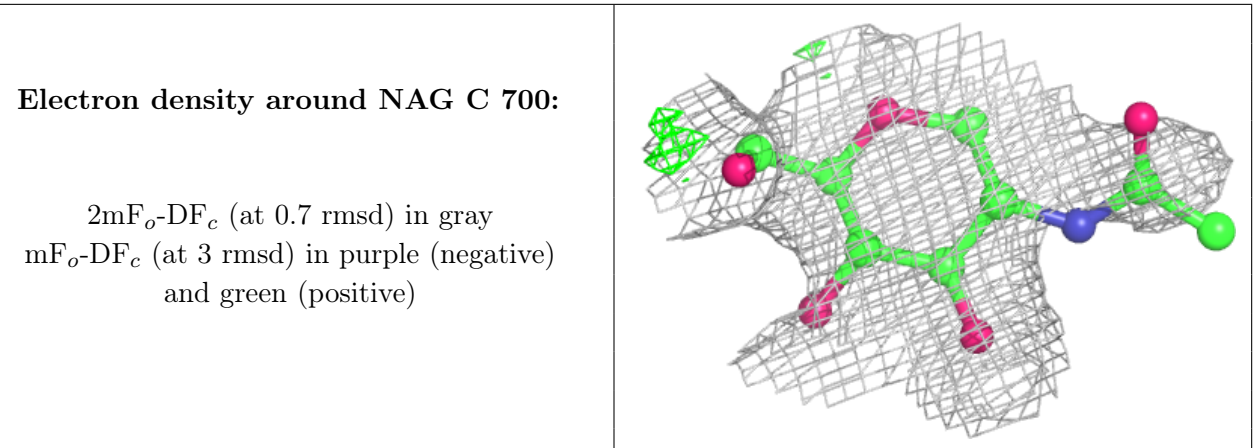






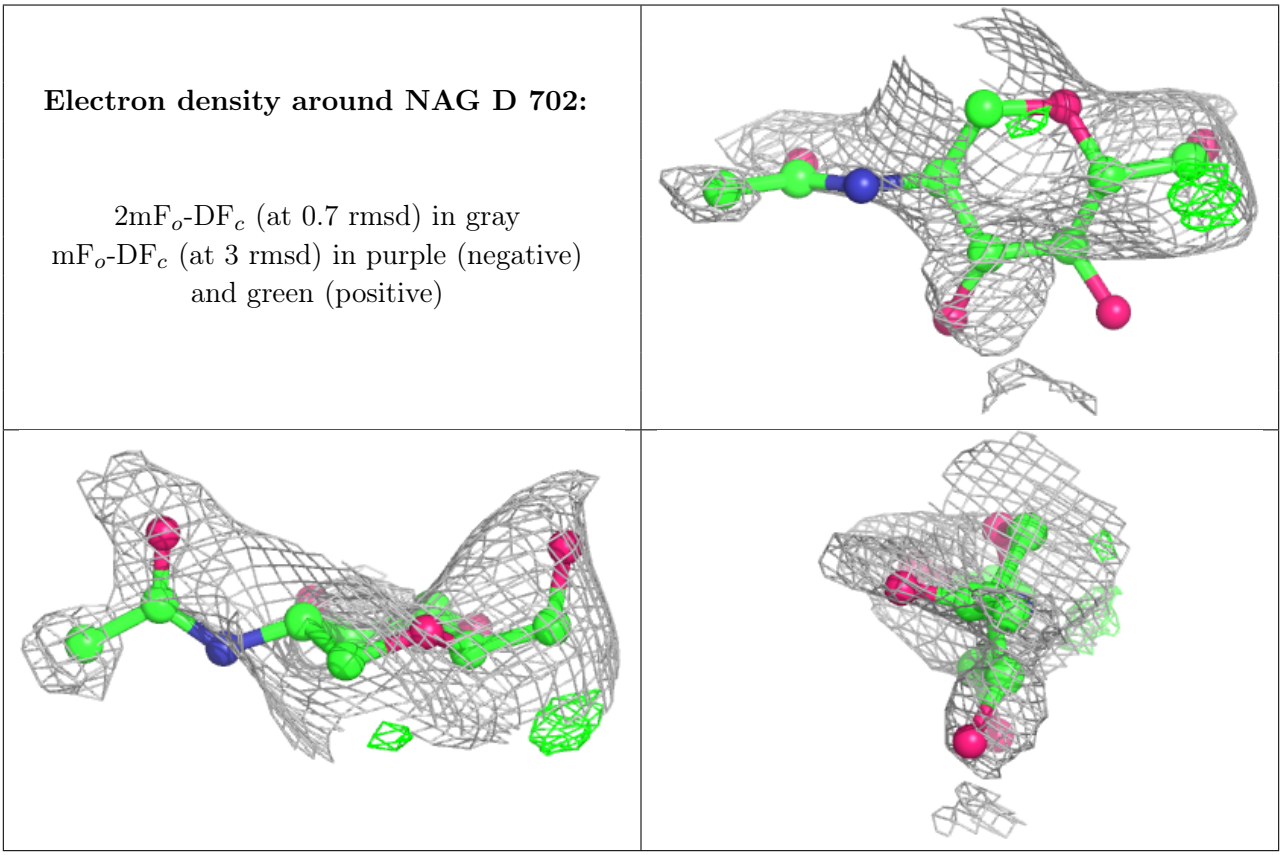
Electron density around NAG C 700:

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



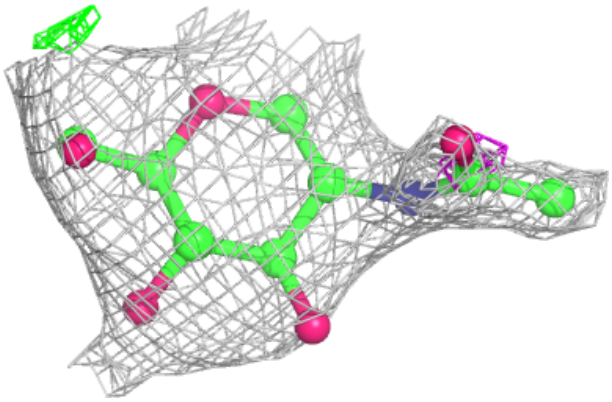
Electron density around NAG D 702:

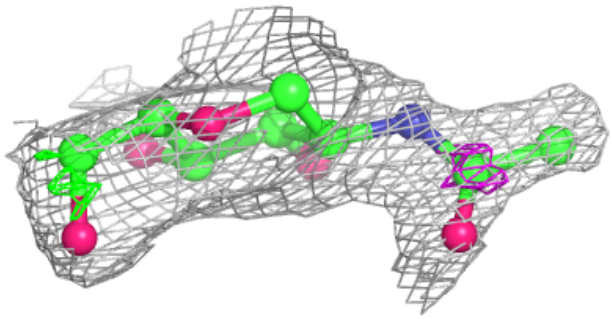
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

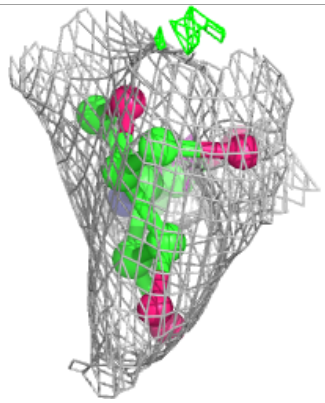


Electron density around NAG E 702:

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

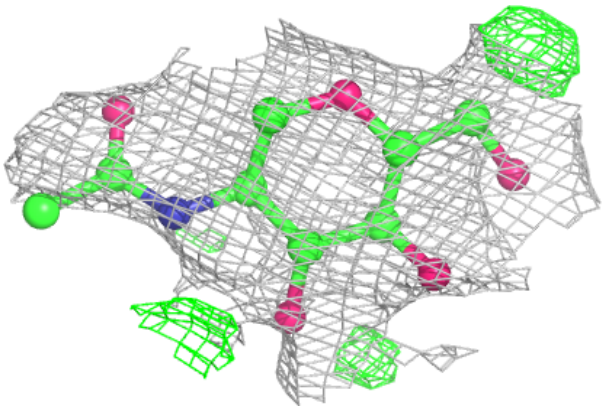


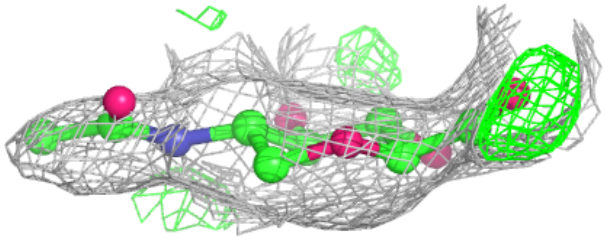


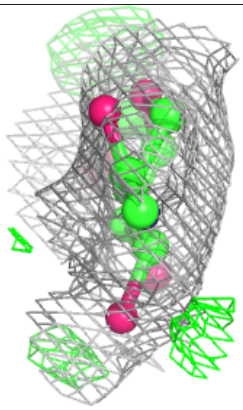


Electron density around NAG E 700:

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

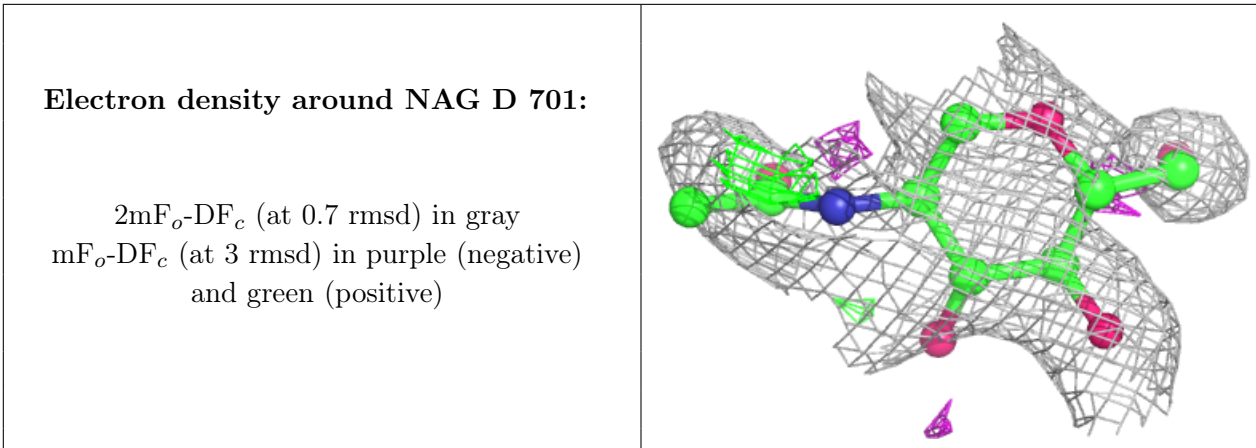






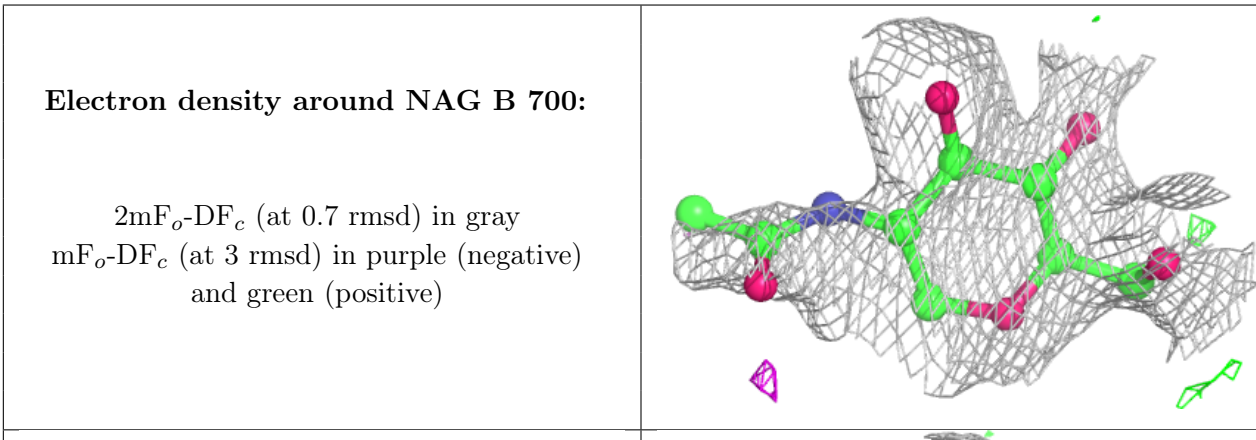
Electron density around NAG D 701:

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



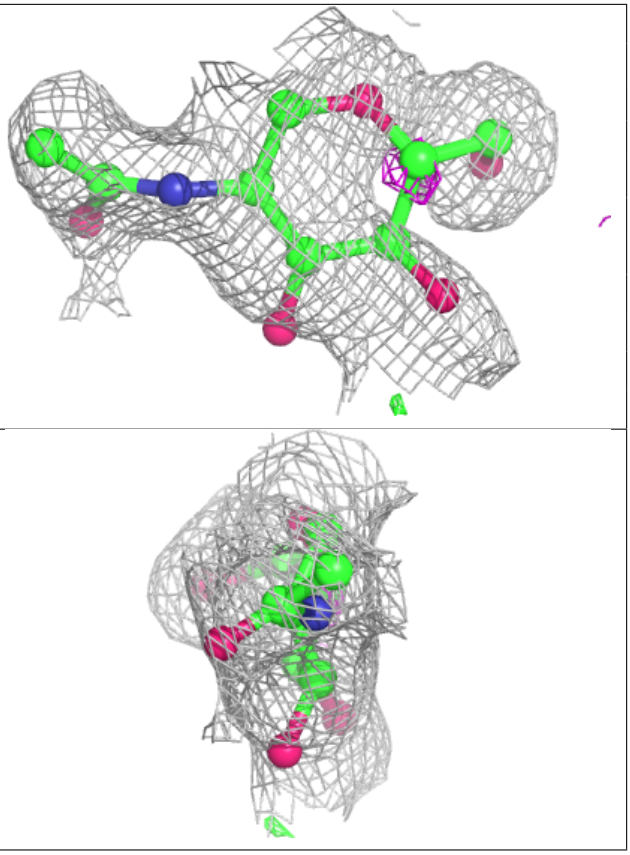
Electron density around NAG B 700:

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



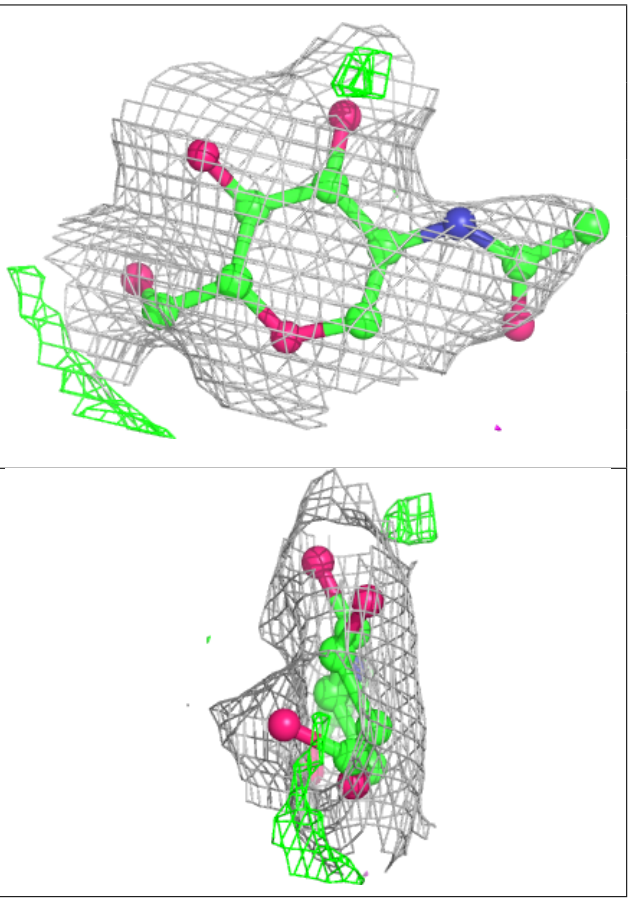
Electron density around NAG C 701:

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



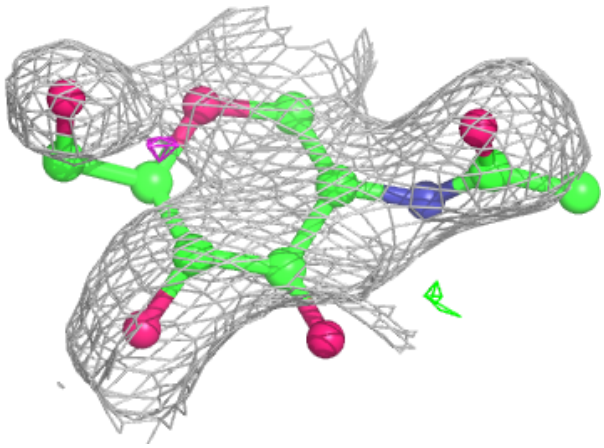
Electron density around NAG F 700:

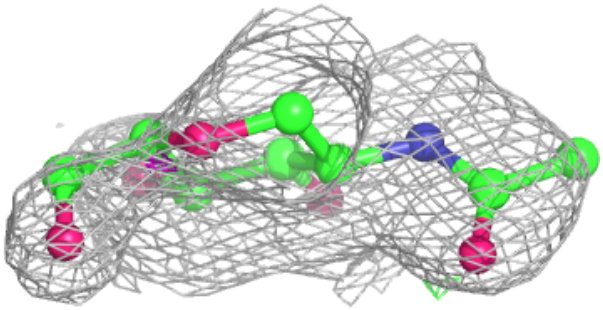
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

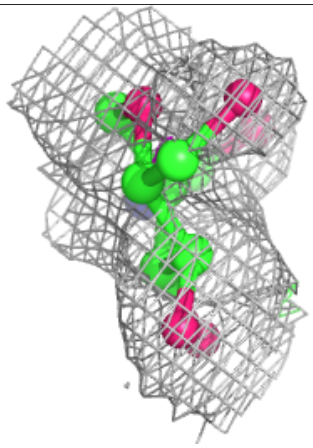


Electron density around NAG A 701:

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

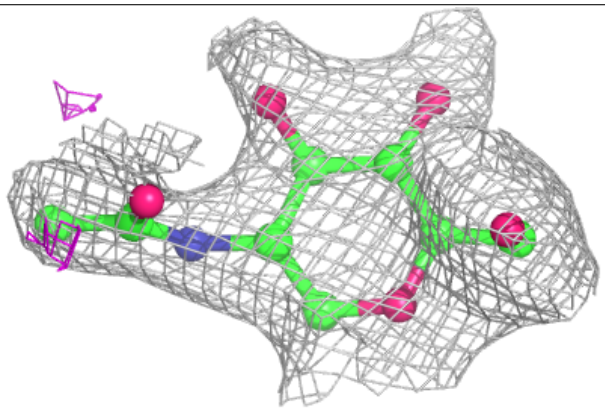


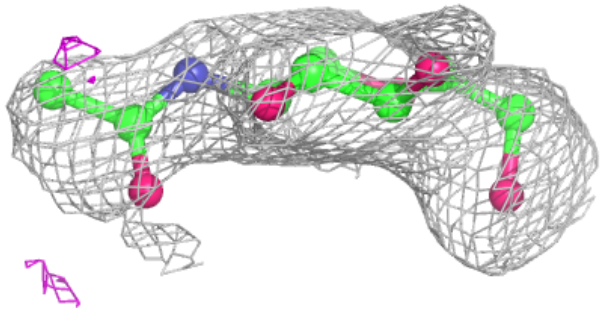


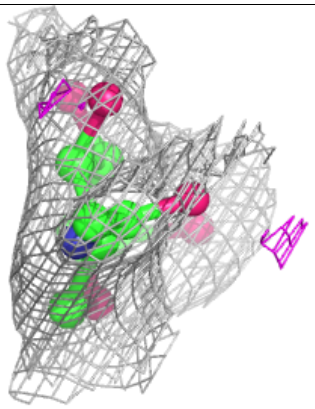


Electron density around NAG B 702:

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

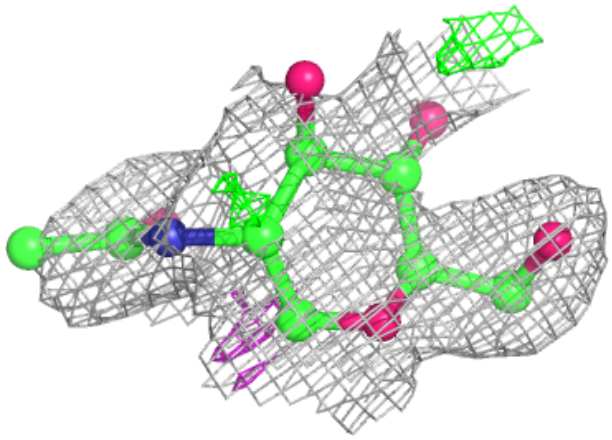


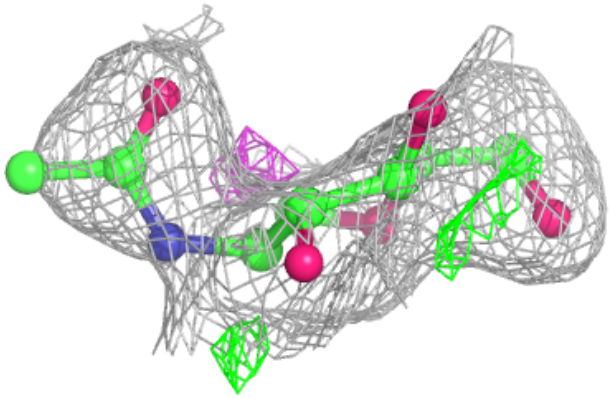


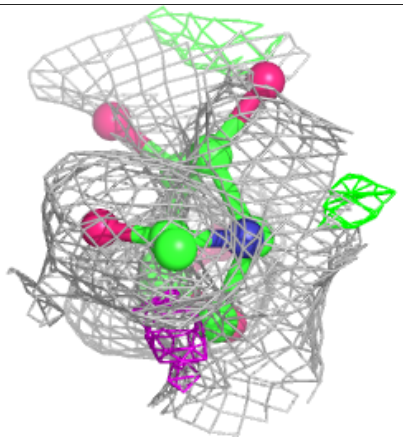


Electron density around NAG E 706:

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

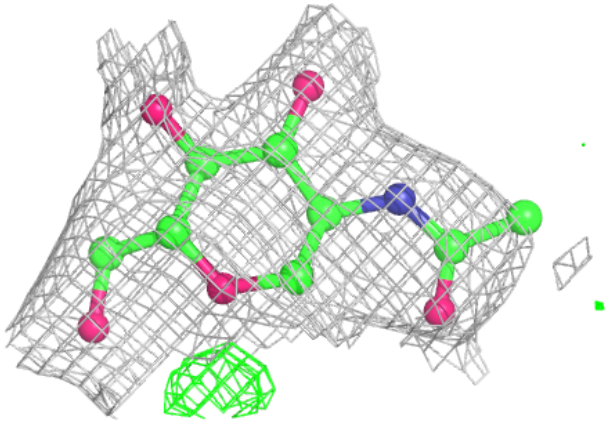


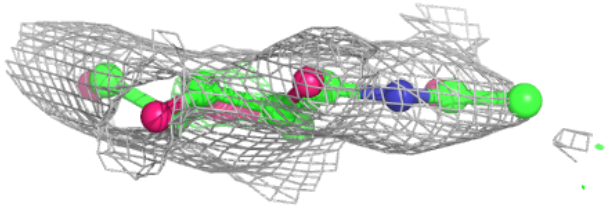


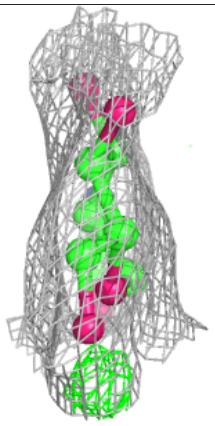


Electron density around NAG C 706:

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

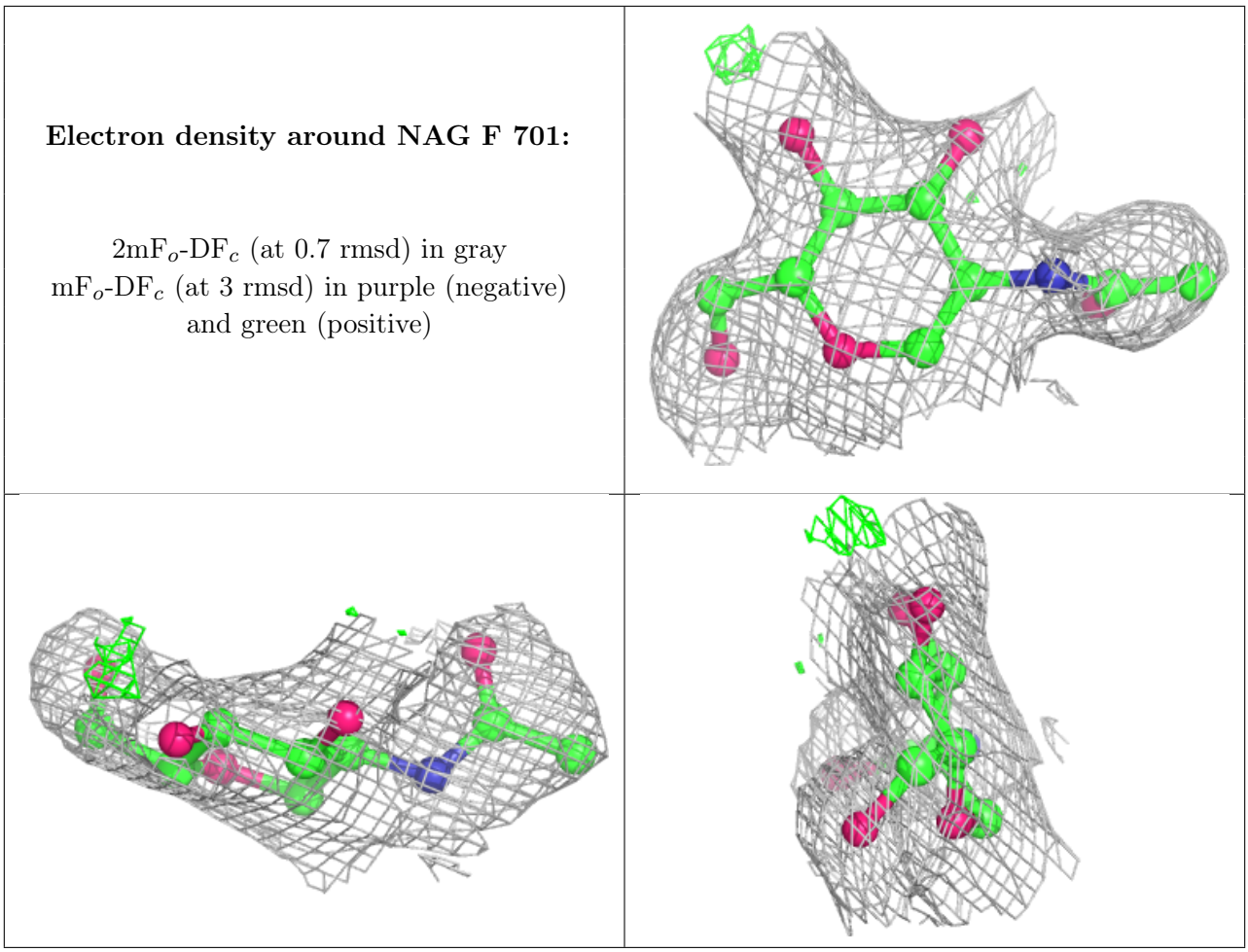






Electron density around NAG F 701:

$2mF_o$-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

There are no such residues in this entry.