wwPDB EM Validation Summary Report

Oct 16, 2024 – 12:59 AM JST

PDB ID	:	8ZDW
EMDB ID	:	EMD-60015
Title	:	The cryoEM structure of H5N1 HA split from symmetric filament in conformation A
Authors	:	Li, R.; Gao, J.; Wang, L.; Gui, M.; Xiang, Y.
Deposited on	:	2024-05-03
Resolution	:	3.45 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp
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:

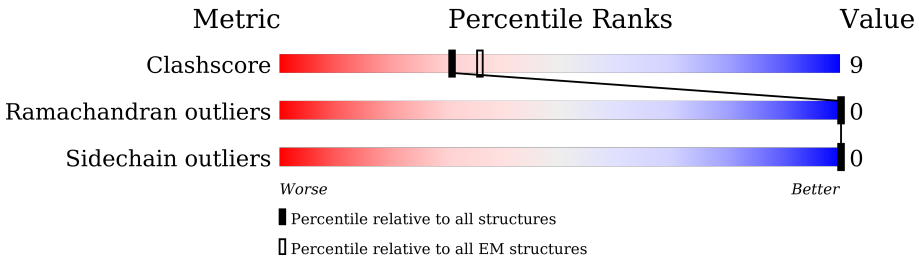
EMDB validation analysis	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.45 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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%

Mol	Chain	Length	Quality of chain
1	A	337	78% 17% 5%
1	C	337	77% 18% 5%
1	H	337	77% 18% 5%
2	B	228	58% 18% 24%
2	D	228	59% 18% 24%
2	I	228	58% 18% 24%
3	E	217	83% 17%
3	J	217	83% 17%
3	R	217	82% 18%

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Mol	Chain	Length	Quality of chain
4	F	222	80% 20%
4	L	222	80% 20%
4	U	222	82% 18%
5	G	2	100%
5	N	2	100%
5	Q	2	100%
6	K	3	67% 33%
6	M	3	100%
6	O	3	67% 33%
6	P	3	100%
6	S	3	67% 33%
6	T	3	100%
7	V	3	33% 67%
7	W	3	33% 67%
7	X	3	33% 67%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 22602 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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					AltConf	Trace
1	A	321	Total	C	N	O	S	0	0
			2549	1611	440	483	15		
1	C	321	Total	C	N	O	S	0	0
			2549	1611	440	483	15		
1	H	321	Total	C	N	O	S	0	0
			2549	1611	440	483	15		

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	174	Total	C	N	O	S	0	0
			1412	878	245	281	8		
2	D	174	Total	C	N	O	S	0	0
			1412	878	245	281	8		
2	I	174	Total	C	N	O	S	0	0
			1412	878	245	281	8		

- Molecule 3 is a protein called H5M9 Fab, light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	217	Total	C	N	O	S	0	0
			1683	1044	291	342	6		
3	E	217	Total	C	N	O	S	0	0
			1683	1044	291	342	6		
3	J	217	Total	C	N	O	S	0	0
			1683	1044	291	342	6		

- Molecule 4 is a protein called Anti-H5N1 hemagglutinin monoclonal anitbody H5M9 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	222	Total	C	N	O	S	0	0
			1682	1062	277	334	9		

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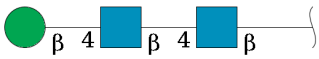
Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	222	Total	C	N	O	S	0	0
			1682	1062	277	334	9		
4	L	222	Total	C	N	O	S	0	0
			1682	1062	277	334	9		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	2	Total	C	N	O	0	0
			28	16	2	10		
5	N	2	Total	C	N	O	0	0
			28	16	2	10		
5	Q	2	Total	C	N	O	0	0
			28	16	2	10		

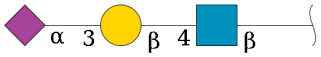
- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
6	K	3	Total	C	N	O	0	0
			39	22	2	15		
6	M	3	Total	C	N	O	0	0
			39	22	2	15		
6	O	3	Total	C	N	O	0	0
			39	22	2	15		
6	P	3	Total	C	N	O	0	0
			39	22	2	15		
6	S	3	Total	C	N	O	0	0
			39	22	2	15		
6	T	3	Total	C	N	O	0	0
			39	22	2	15		

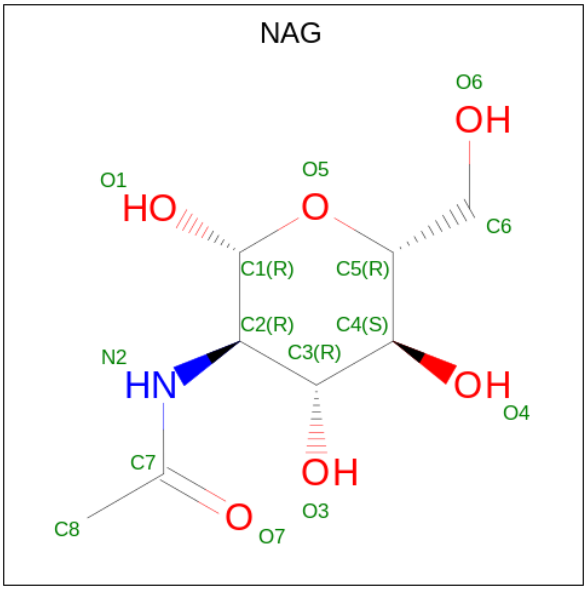
- Molecule 7 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galacto

pyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	AltConf	Trace
7	V	3	Total C N O 46 25 2 19	0	0
7	W	3	Total C N O 46 25 2 19	0	0
7	X	3	Total C N O 46 25 2 19	0	0

- Molecule 8 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	AltConf
8	A	1	Total C N O 14 8 1 5	0
8	A	1	Total C N O 14 8 1 5	0
8	B	1	Total C N O 14 8 1 5	0
8	R	1	Total C N O 14 8 1 5	0
8	D	1	Total C N O 14 8 1 5	0

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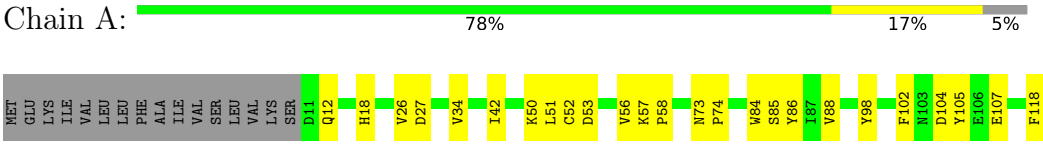
Mol	Chain	Residues	Atoms				AltConf
8	I	1	Total	C	N	O	0
			14	8	1	5	
8	E	1	Total	C	N	O	0
			14	8	1	5	
8	J	1	Total	C	N	O	0
			14	8	1	5	
8	C	1	Total	C	N	O	0
			14	8	1	5	
8	C	1	Total	C	N	O	0
			14	8	1	5	
8	H	1	Total	C	N	O	0
			14	8	1	5	
8	H	1	Total	C	N	O	0
			14	8	1	5	

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. 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. 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.

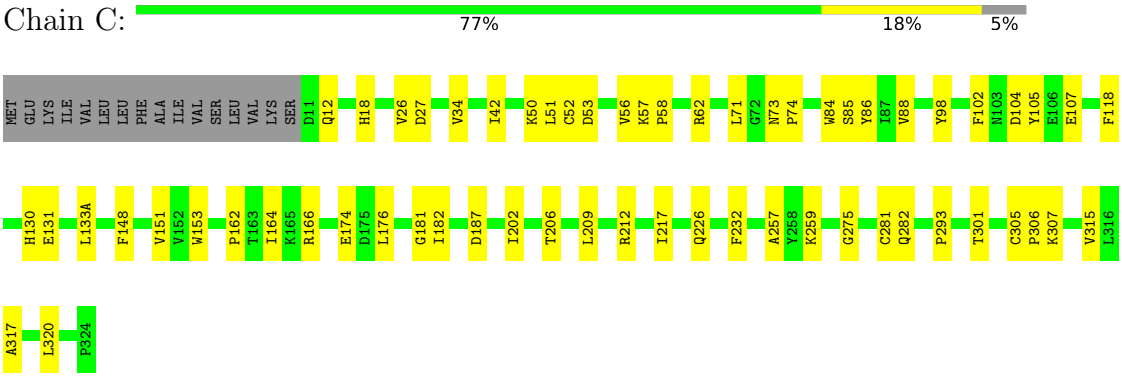
• Molecule 1: Hemagglutinin

Chain A:



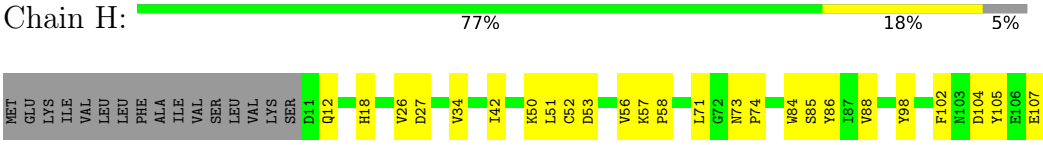
• Molecule 1: Hemagglutinin

Chain C:



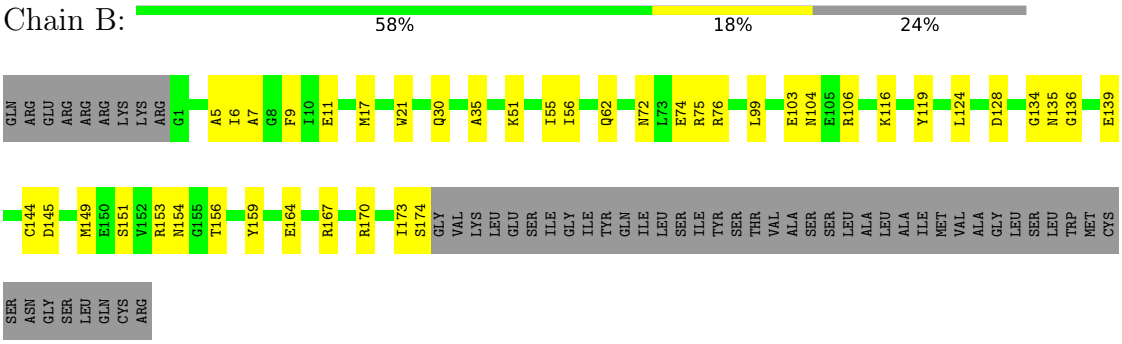
• Molecule 1: Hemagglutinin

Chain H:



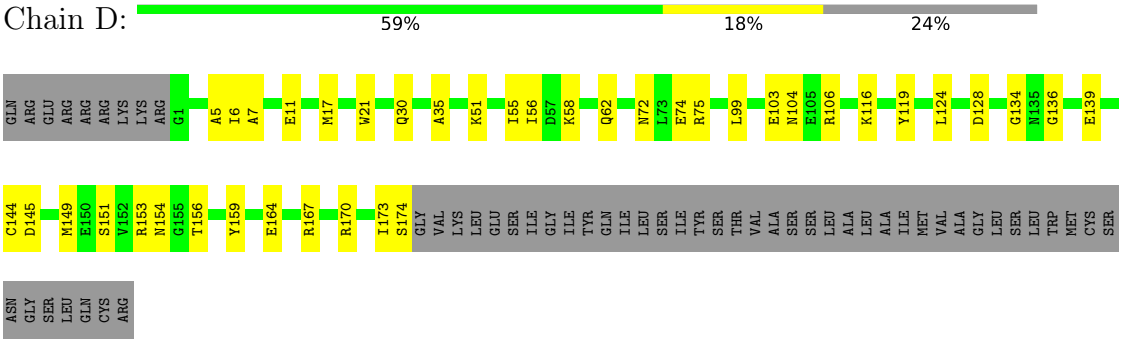
• Molecule 2: Hemagglutinin

Chain B:



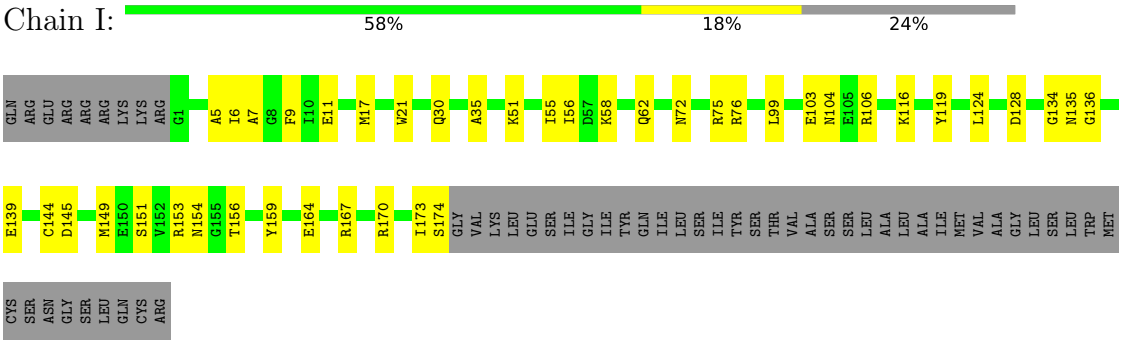
• Molecule 2: Hemagglutinin

Chain D:



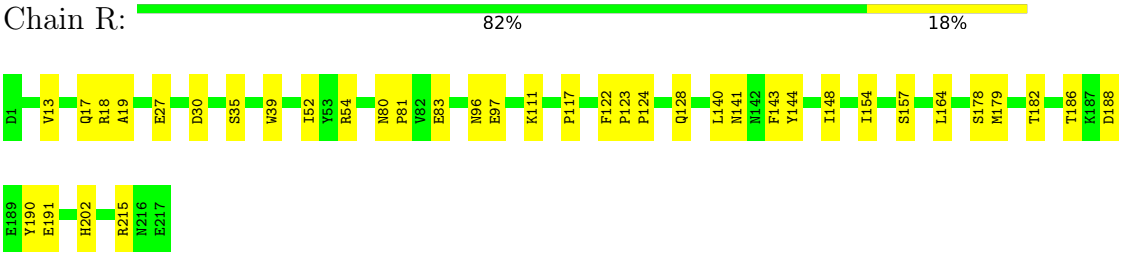
• Molecule 2: Hemagglutinin

Chain I:



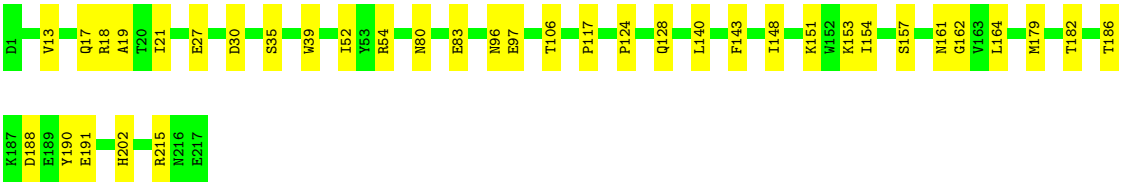
• Molecule 3: H5M9 Fab, light chain

Chain R:



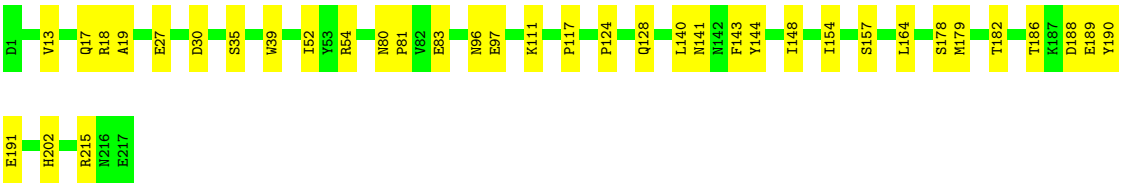
• Molecule 3: H5M9 Fab, light chain

Chain E:



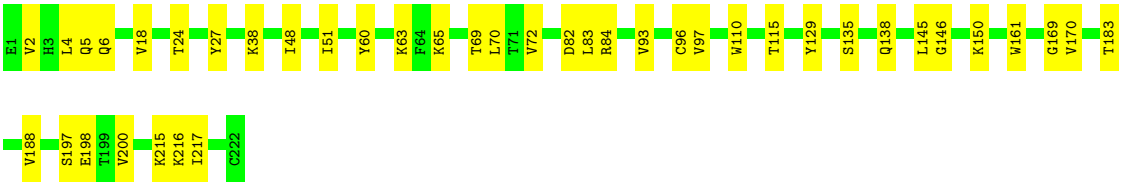
• Molecule 3: H5M9 Fab, light chain

Chain J:



• Molecule 4: Anti-H5N1 hemagglutinin monoclonal anitbody H5M9 heavy chain

Chain U:

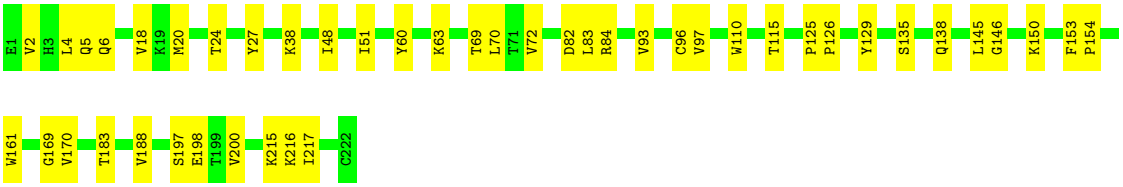


• Molecule 4: Anti-H5N1 hemagglutinin monoclonal anitbody H5M9 heavy chain

Chain F:

• Molecule 4: Anti-H5N1 hemagglutinin monoclonal anitbody H5M9 heavy chain

Chain L:

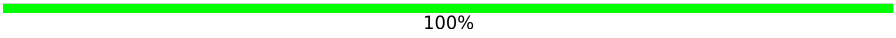


• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:

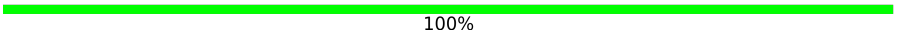
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:



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

Chain Q:

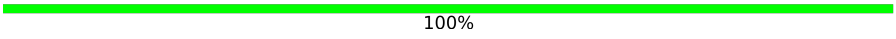


• Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:

• Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

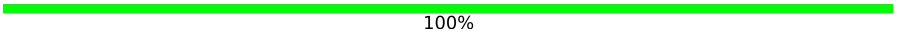


• Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

• Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:

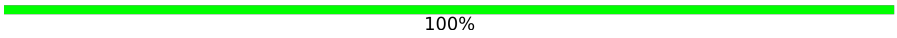


• Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:

• Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:



• Molecule 7: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:

• Molecule 7: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:

• Molecule 7: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	216514	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SIA, NAG, GAL, 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	0.30	0/2611	0.52	0/3546
1	C	0.30	0/2611	0.52	0/3546
1	H	0.30	0/2611	0.52	0/3546
2	B	0.27	0/1439	0.48	0/1934
2	D	0.27	0/1439	0.48	0/1934
2	I	0.27	0/1439	0.48	0/1934
3	E	0.28	0/1720	0.52	0/2332
3	J	0.28	0/1720	0.52	0/2332
3	R	0.27	0/1720	0.52	0/2332
4	F	0.27	0/1728	0.51	0/2361
4	L	0.27	0/1728	0.51	0/2361
4	U	0.26	0/1728	0.51	0/2361
All	All	0.28	0/22494	0.51	0/30519

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	2549	0	2491	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2549	0	2491	47	0
1	H	2549	0	2491	47	0
2	B	1412	0	1319	43	0
2	D	1412	0	1319	42	0
2	I	1412	0	1319	43	0
3	E	1683	0	1606	24	0
3	J	1683	0	1606	24	0
3	R	1683	0	1606	25	0
4	F	1682	0	1632	28	0
4	L	1682	0	1632	28	0
4	U	1682	0	1632	26	0
5	G	28	0	25	0	0
5	N	28	0	25	0	0
5	Q	28	0	25	0	0
6	K	39	0	34	0	0
6	M	39	0	34	0	0
6	O	39	0	34	0	0
6	P	39	0	34	0	0
6	S	39	0	34	0	0
6	T	39	0	34	0	0
7	V	46	0	40	5	0
7	W	46	0	40	5	0
7	X	46	0	40	5	0
8	A	28	0	26	0	0
8	B	14	0	13	1	0
8	C	28	0	26	0	0
8	D	14	0	13	1	0
8	E	14	0	13	0	0
8	H	28	0	26	0	0
8	I	14	0	13	1	0
8	J	14	0	13	0	0
8	R	14	0	13	0	0
All	All	22602	0	21699	383	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 9.

The worst 5 of 383 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:56:VAL:HG23	1:C:85:SER:HB2	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:56:VAL:HG23	1:H:85:SER:HB2	1.65	0.78
1:A:56:VAL:HG23	1:A:85:SER:HB2	1.65	0.77
2:D:144:CYS:SG	2:D:145:ASP:N	2.67	0.67
2:B:144:CYS:SG	2:B:145:ASP:N	2.67	0.67

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 PDB entries followed by that with respect to all EM entries.

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	319/337 (95%)	306 (96%)	13 (4%)	0	100	100
1	C	319/337 (95%)	306 (96%)	13 (4%)	0	100	100
1	H	319/337 (95%)	306 (96%)	13 (4%)	0	100	100
2	B	172/228 (75%)	167 (97%)	5 (3%)	0	100	100
2	D	172/228 (75%)	167 (97%)	5 (3%)	0	100	100
2	I	172/228 (75%)	167 (97%)	5 (3%)	0	100	100
3	E	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
3	J	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
3	R	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
4	F	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
4	L	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
4	U	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
All	All	2778/3012 (92%)	2668 (96%)	110 (4%)	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 PDB entries followed by that with respect to all EM entries.

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	289/304 (95%)	289 (100%)	0	100	100
1	C	289/304 (95%)	289 (100%)	0	100	100
1	H	289/304 (95%)	289 (100%)	0	100	100
2	B	149/195 (76%)	149 (100%)	0	100	100
2	D	149/195 (76%)	149 (100%)	0	100	100
2	I	149/195 (76%)	149 (100%)	0	100	100
3	E	190/190 (100%)	190 (100%)	0	100	100
3	J	190/190 (100%)	190 (100%)	0	100	100
3	R	190/190 (100%)	190 (100%)	0	100	100
4	F	193/193 (100%)	193 (100%)	0	100	100
4	L	193/193 (100%)	193 (100%)	0	100	100
4	U	193/193 (100%)	193 (100%)	0	100	100
All	All	2463/2646 (93%)	2463 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	HIS
1	C	130	HIS
1	H	130	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

33 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	0.29	0	17,19,21	0.56	0
5	NAG	G	2	5	14,14,15	0.22	0	17,19,21	0.42	0
6	NAG	K	1	1,6	14,14,15	0.28	0	17,19,21	0.46	0
6	NAG	K	2	6	14,14,15	0.45	0	17,19,21	0.64	1 (5%)
6	BMA	K	3	6	11,11,12	0.57	0	15,15,17	0.81	0
6	NAG	M	1	1,6	14,14,15	0.36	0	17,19,21	0.54	0
6	NAG	M	2	6	14,14,15	0.33	0	17,19,21	0.58	0
6	BMA	M	3	6	11,11,12	0.59	0	15,15,17	0.74	0
5	NAG	N	1	5,1	14,14,15	0.29	0	17,19,21	0.56	0
5	NAG	N	2	5	14,14,15	0.22	0	17,19,21	0.43	0
6	NAG	O	1	1,6	14,14,15	0.28	0	17,19,21	0.46	0
6	NAG	O	2	6	14,14,15	0.45	0	17,19,21	0.63	1 (5%)
6	BMA	O	3	6	11,11,12	0.57	0	15,15,17	0.82	0
6	NAG	P	1	1,6	14,14,15	0.34	0	17,19,21	0.54	0
6	NAG	P	2	6	14,14,15	0.33	0	17,19,21	0.58	0
6	BMA	P	3	6	11,11,12	0.59	0	15,15,17	0.74	0
5	NAG	Q	1	5,1	14,14,15	0.29	0	17,19,21	0.56	0
5	NAG	Q	2	5	14,14,15	0.22	0	17,19,21	0.42	0
6	NAG	S	1	1,6	14,14,15	0.28	0	17,19,21	0.45	0
6	NAG	S	2	6	14,14,15	0.45	0	17,19,21	0.63	1 (5%)
6	BMA	S	3	6	11,11,12	0.57	0	15,15,17	0.81	0
6	NAG	T	1	1,6	14,14,15	0.34	0	17,19,21	0.54	0
6	NAG	T	2	6	14,14,15	0.33	0	17,19,21	0.58	0
6	BMA	T	3	6	11,11,12	0.59	0	15,15,17	0.74	0
7	NAG	V	1	7	15,15,15	0.41	0	21,21,21	0.87	1 (4%)
7	GAL	V	2	7	11,11,12	0.53	0	15,15,17	1.52	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	SIA	V	3	7	20,20,21	0.92	1 (5%)	24,28,31	1.12	3 (12%)
7	NAG	W	1	7	15,15,15	0.41	0	21,21,21	0.87	1 (4%)
7	GAL	W	2	7	11,11,12	0.53	0	15,15,17	1.53	4 (26%)
7	SIA	W	3	7	20,20,21	0.91	1 (5%)	24,28,31	1.12	3 (12%)
7	NAG	X	1	7	15,15,15	0.41	0	21,21,21	0.89	1 (4%)
7	GAL	X	2	7	11,11,12	0.53	0	15,15,17	1.53	4 (26%)
7	SIA	X	3	7	20,20,21	0.91	1 (5%)	24,28,31	1.12	3 (12%)

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	-	0/6/23/26	0/1/1/1
6	NAG	K	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	K	2	6	-	2/6/23/26	0/1/1/1
6	BMA	K	3	6	-	0/2/19/22	0/1/1/1
6	NAG	M	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	M	2	6	-	1/6/23/26	0/1/1/1
6	BMA	M	3	6	-	0/2/19/22	0/1/1/1
5	NAG	N	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
6	NAG	O	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	O	2	6	-	2/6/23/26	0/1/1/1
6	BMA	O	3	6	-	0/2/19/22	0/1/1/1
6	NAG	P	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	P	2	6	-	1/6/23/26	0/1/1/1
6	BMA	P	3	6	-	0/2/19/22	0/1/1/1
5	NAG	Q	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	0/6/23/26	0/1/1/1
6	NAG	S	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	S	2	6	-	2/6/23/26	0/1/1/1
6	BMA	S	3	6	-	0/2/19/22	0/1/1/1
6	NAG	T	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	T	2	6	-	1/6/23/26	0/1/1/1
6	BMA	T	3	6	-	0/2/19/22	0/1/1/1
7	NAG	V	1	7	-	4/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GAL	V	2	7	-	1/2/19/22	0/1/1/1
7	SIA	V	3	7	-	4/18/34/38	0/1/1/1
7	NAG	W	1	7	-	4/6/26/26	0/1/1/1
7	GAL	W	2	7	-	1/2/19/22	0/1/1/1
7	SIA	W	3	7	-	4/18/34/38	0/1/1/1
7	NAG	X	1	7	-	4/6/26/26	0/1/1/1
7	GAL	X	2	7	-	1/2/19/22	0/1/1/1
7	SIA	X	3	7	-	4/18/34/38	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	X	3	SIA	O1B-C1	-3.23	1.20	1.30
7	V	3	SIA	O1B-C1	-3.23	1.20	1.30
7	W	3	SIA	O1B-C1	-3.21	1.20	1.30

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	2	GAL	O5-C5-C6	3.02	111.93	107.20
7	X	2	GAL	O5-C5-C6	2.99	111.90	107.20
7	V	2	GAL	O5-C5-C6	2.97	111.86	107.20
7	V	3	SIA	O1B-C1-C2	2.96	121.49	113.03
7	X	3	SIA	O1B-C1-C2	2.96	121.48	113.03

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	V	1	NAG	C1-C2-N2-C7
7	V	1	NAG	C3-C2-N2-C7
7	V	1	NAG	C8-C7-N2-C2
7	V	1	NAG	O7-C7-N2-C2
7	V	3	SIA	C7-C8-C9-O9

There are no ring outliers.

6 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	V	3	SIA	4	0

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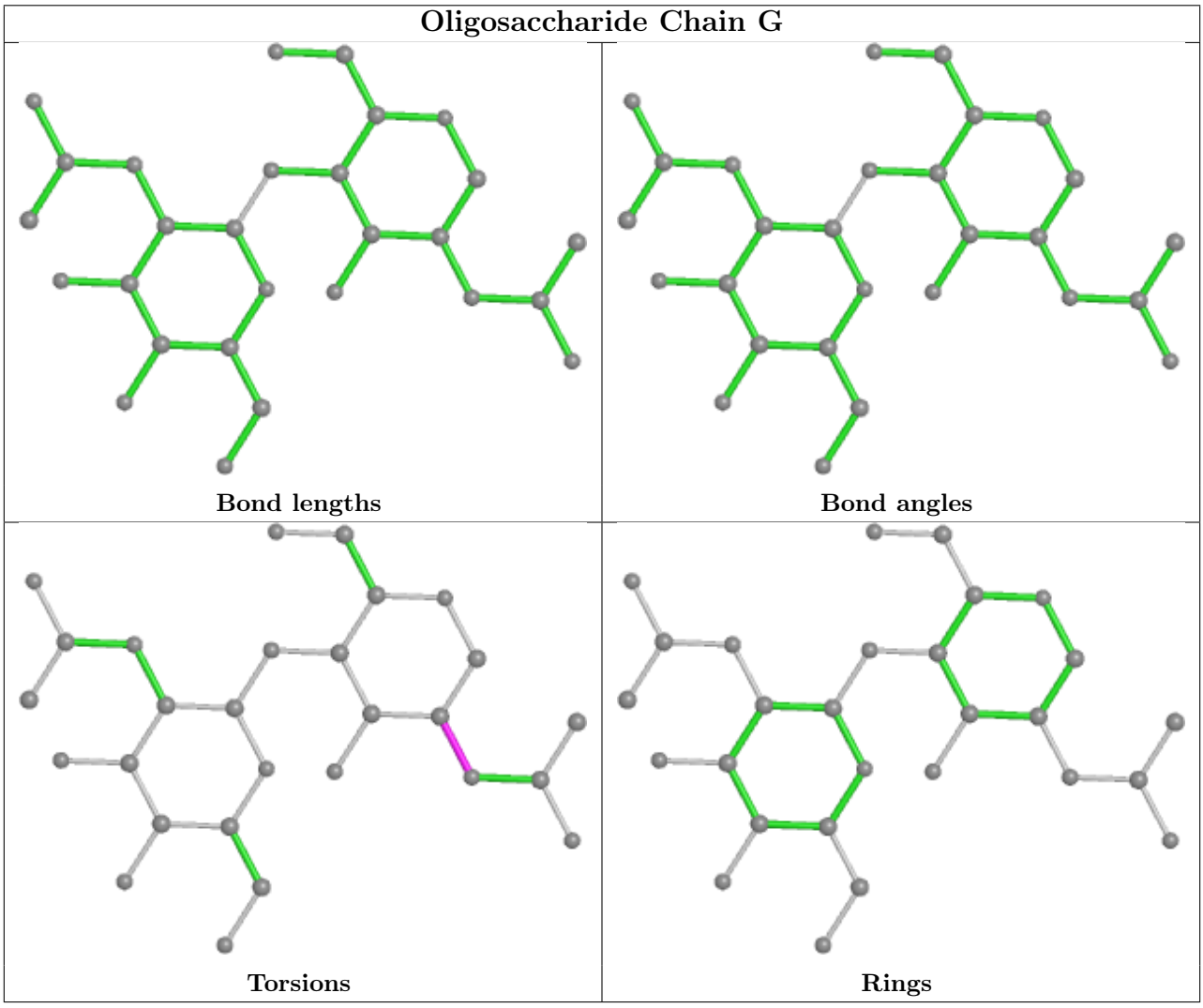
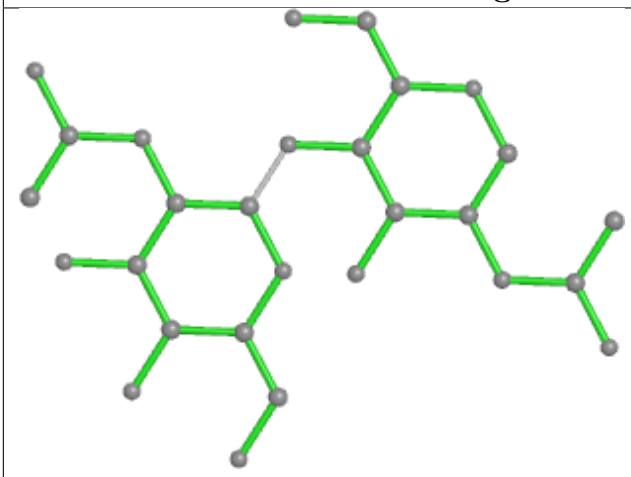
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	X	1	NAG	1	0
7	X	3	SIA	4	0
7	W	1	NAG	1	0
7	W	3	SIA	4	0
7	V	1	NAG	1	0

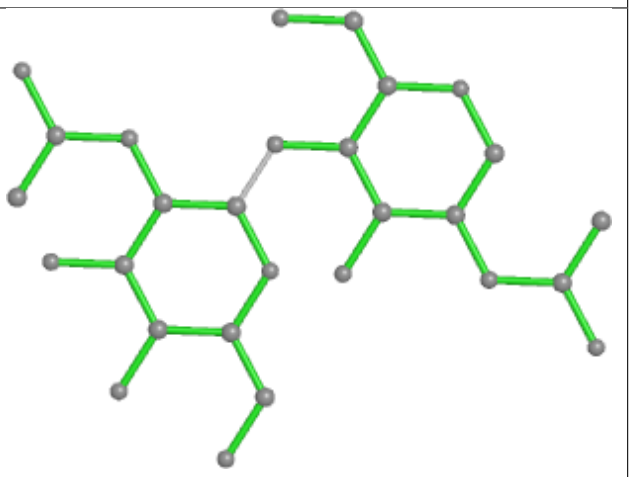
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



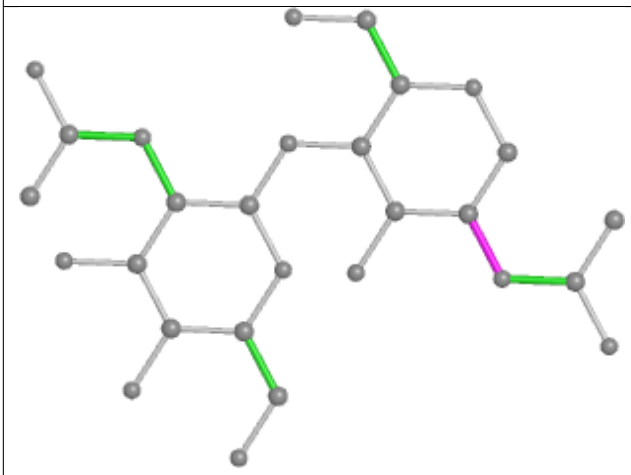
Oligosaccharide Chain N



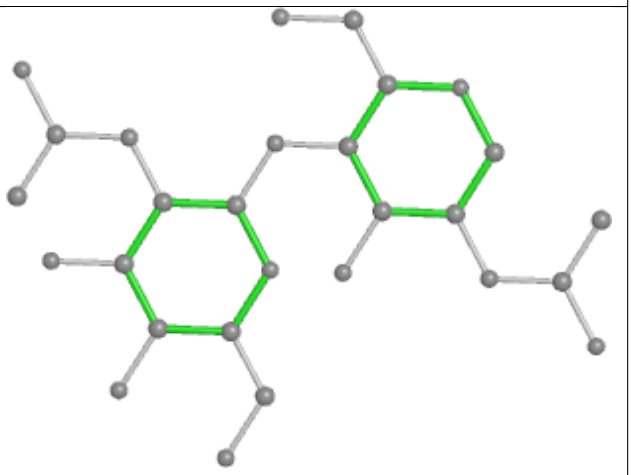
Bond lengths



Bond angles

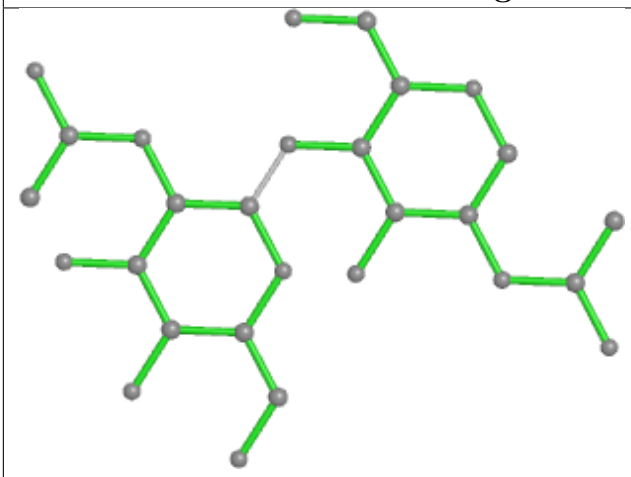


Torsions

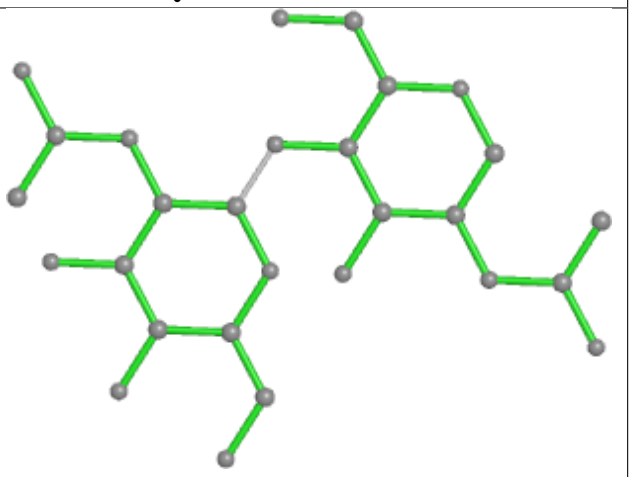


Rings

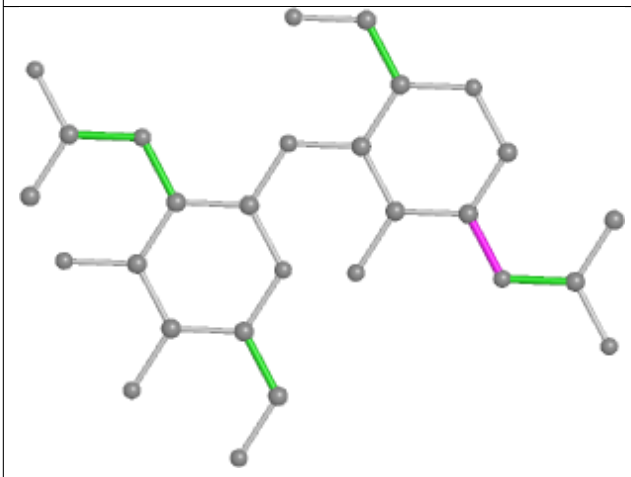
Oligosaccharide Chain Q



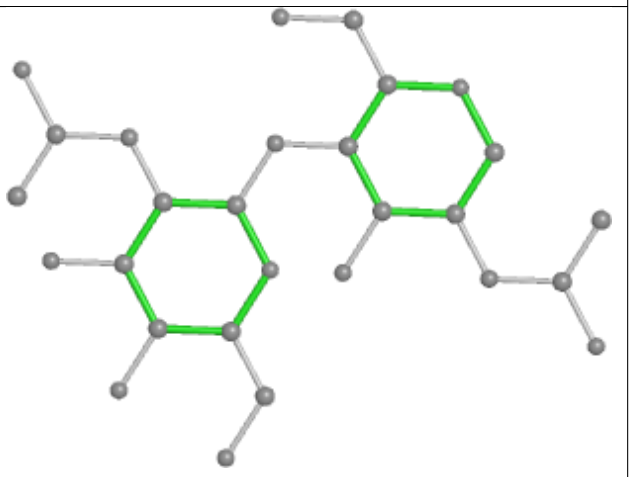
Bond lengths



Bond angles

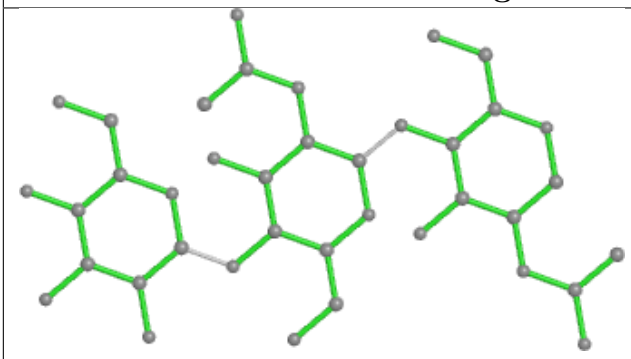


Torsions

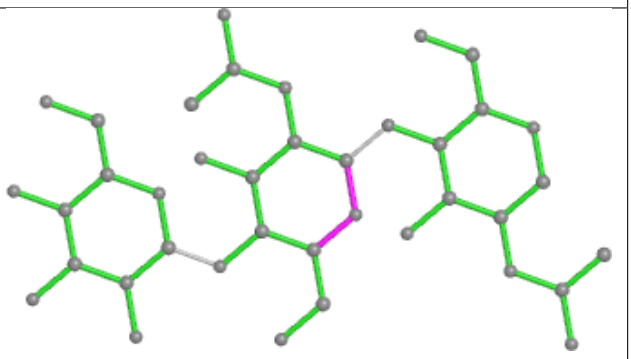


Rings

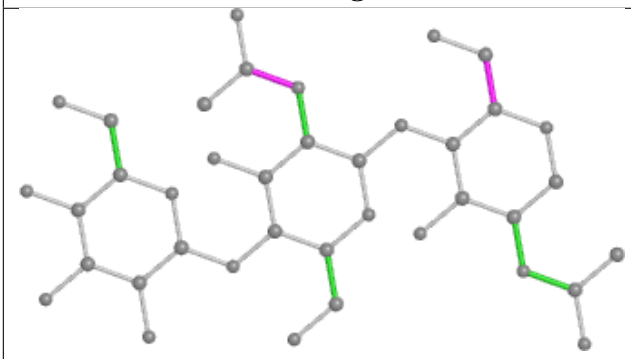
Oligosaccharide Chain K



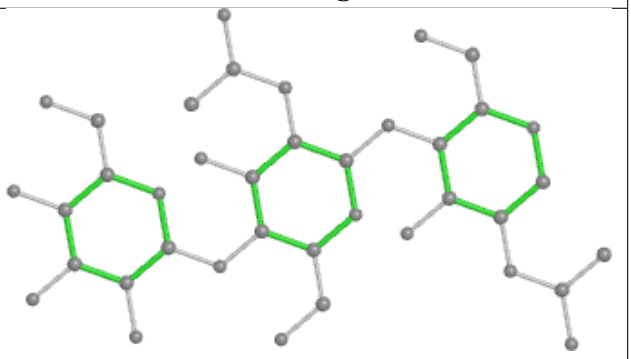
Bond lengths



Bond angles

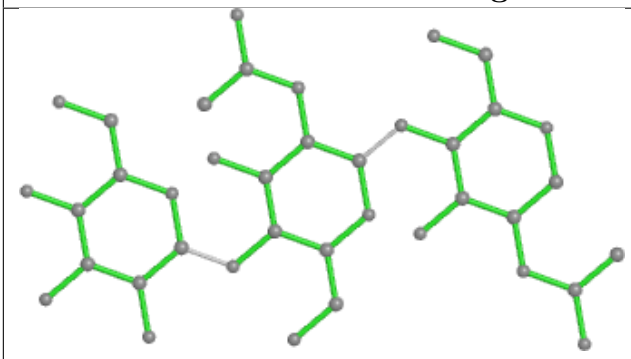


Torsions

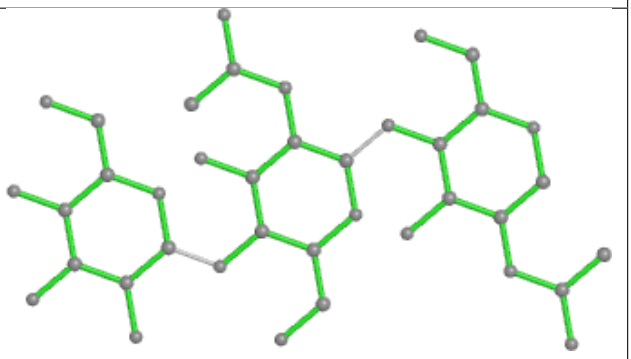


Rings

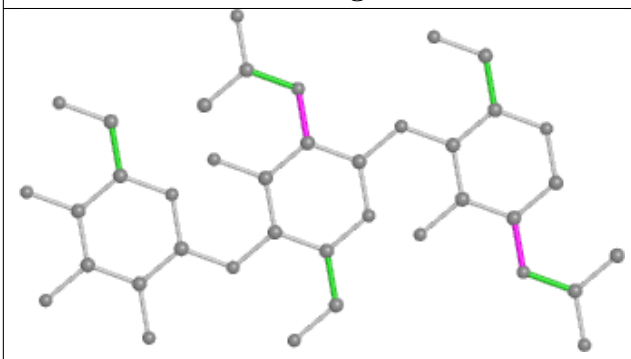
Oligosaccharide Chain M



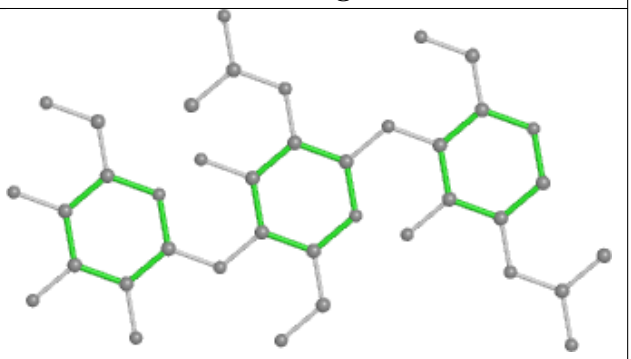
Bond lengths



Bond angles

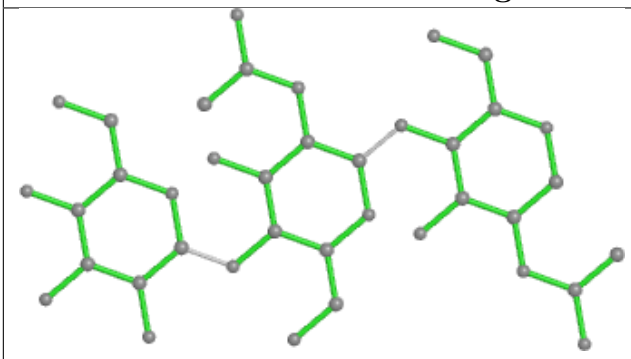


Torsions

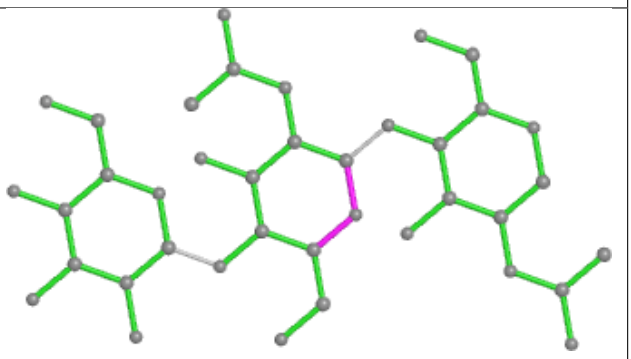


Rings

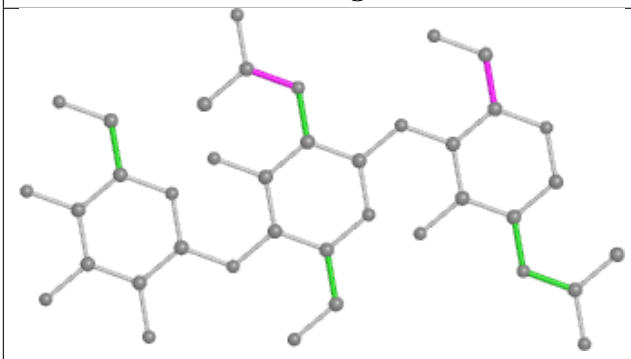
Oligosaccharide Chain O



Bond lengths



Bond angles



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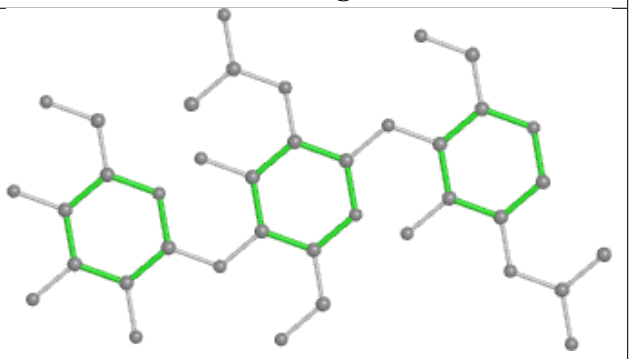
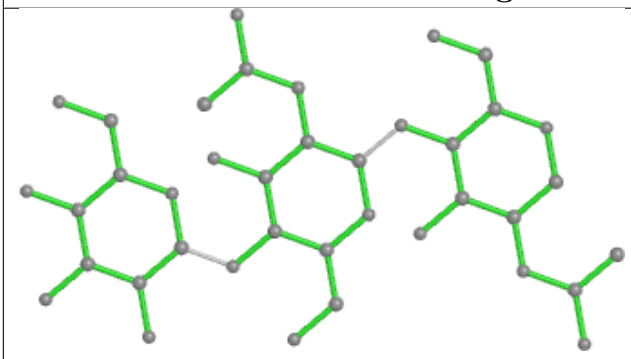
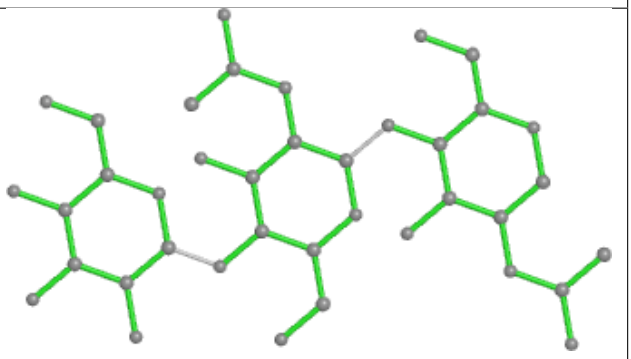


Rings

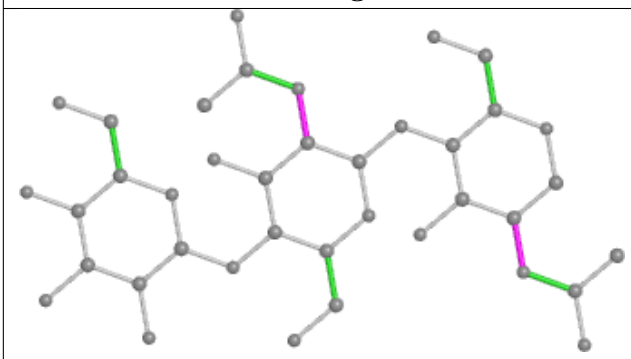
Oligosaccharide Chain P



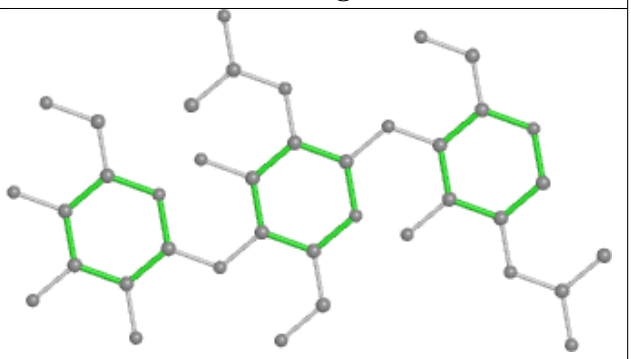
Bond lengths



Bond angles

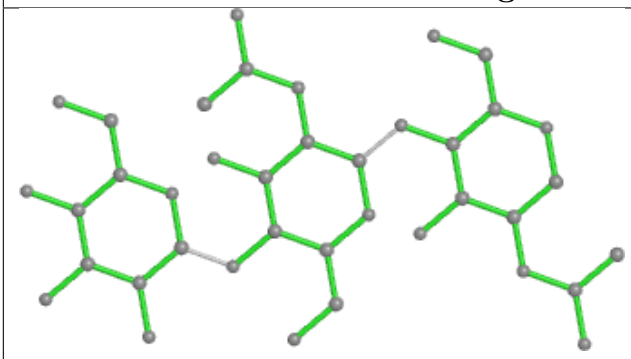


Torsions

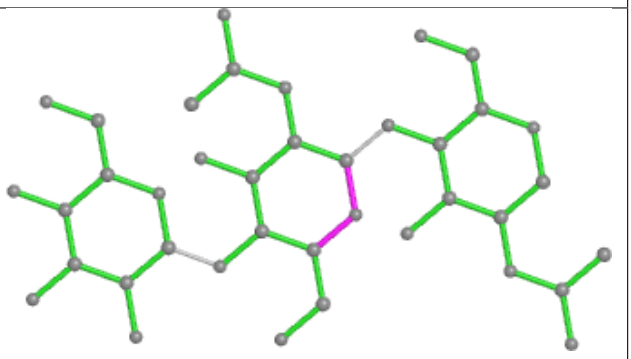


Rings

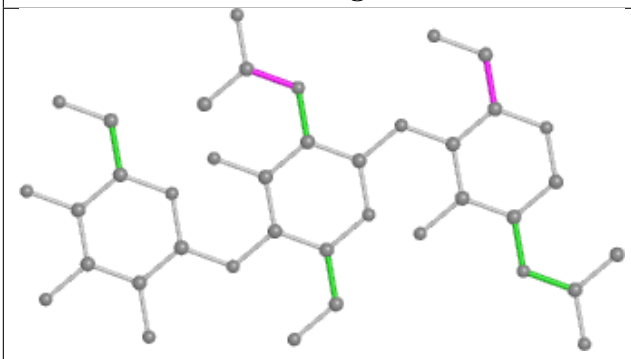
Oligosaccharide Chain S



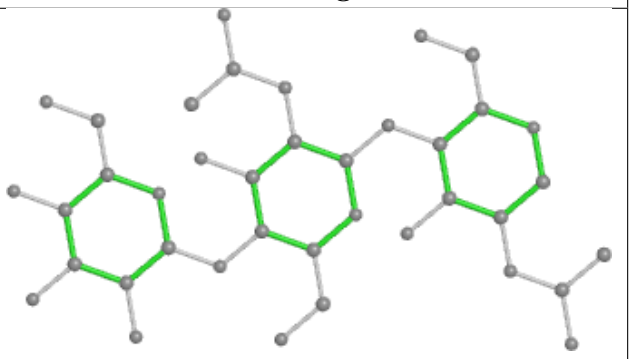
Bond lengths



Bond angles

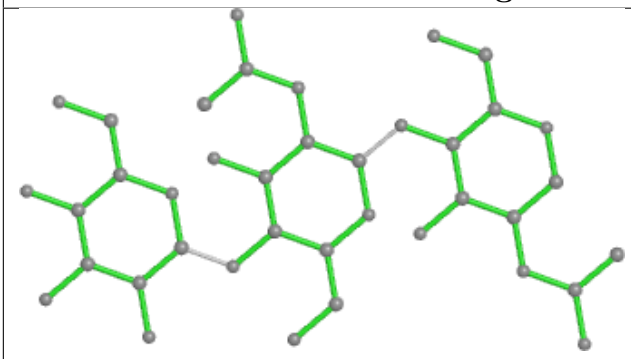


Torsions

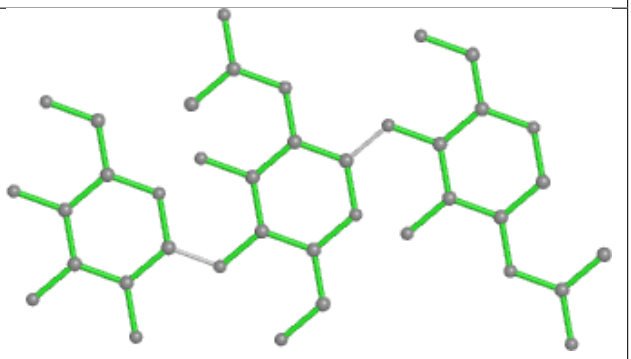


Rings

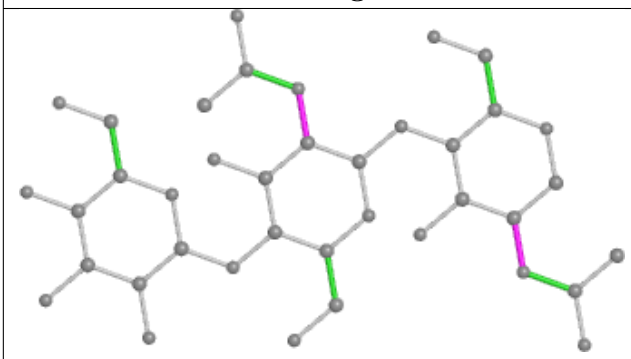
Oligosaccharide Chain T



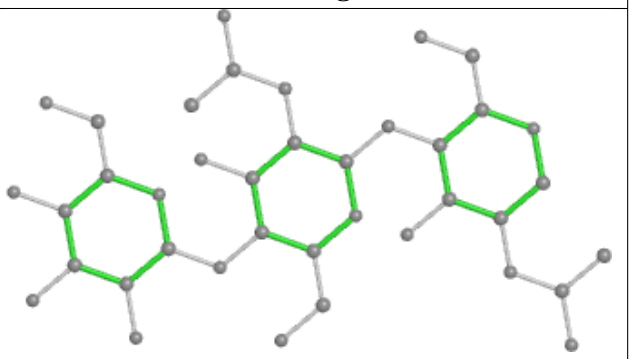
Bond lengths



Bond angles

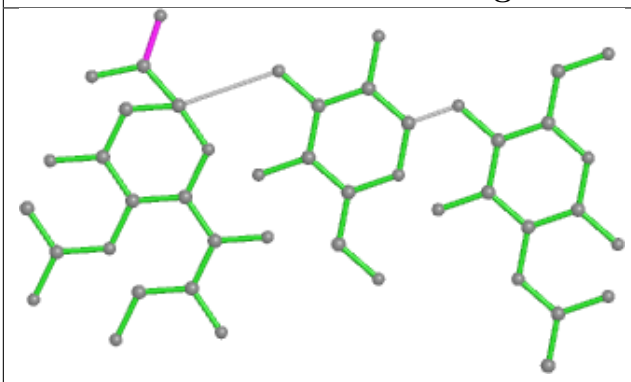


Torsions

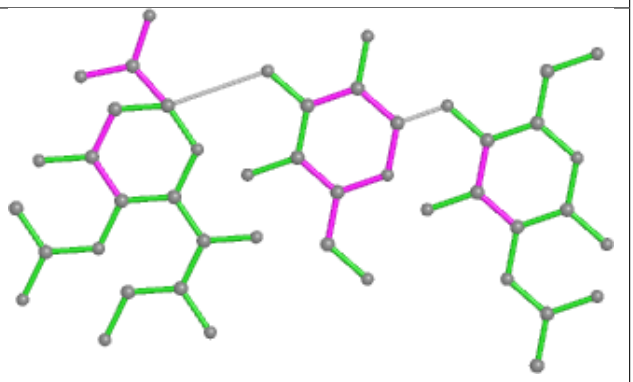


Rings

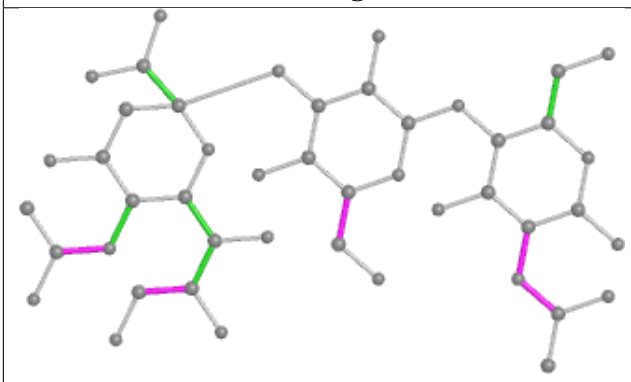
Oligosaccharide Chain V



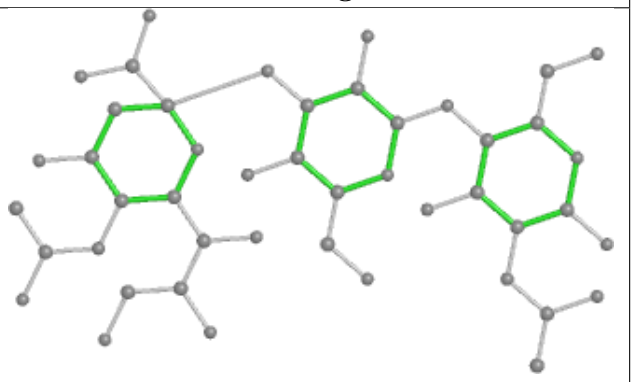
Bond lengths



Bond angles

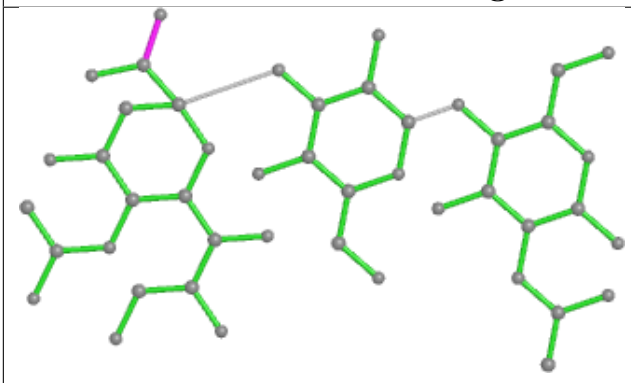


Torsions

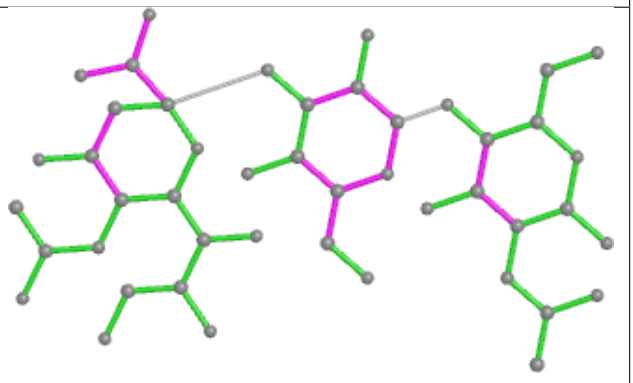


Rings

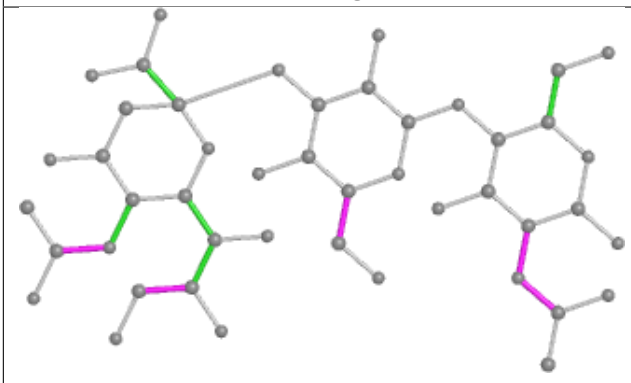
Oligosaccharide Chain W



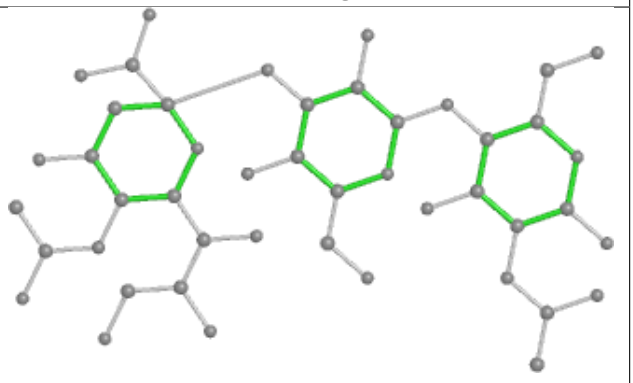
Bond lengths



Bond angles

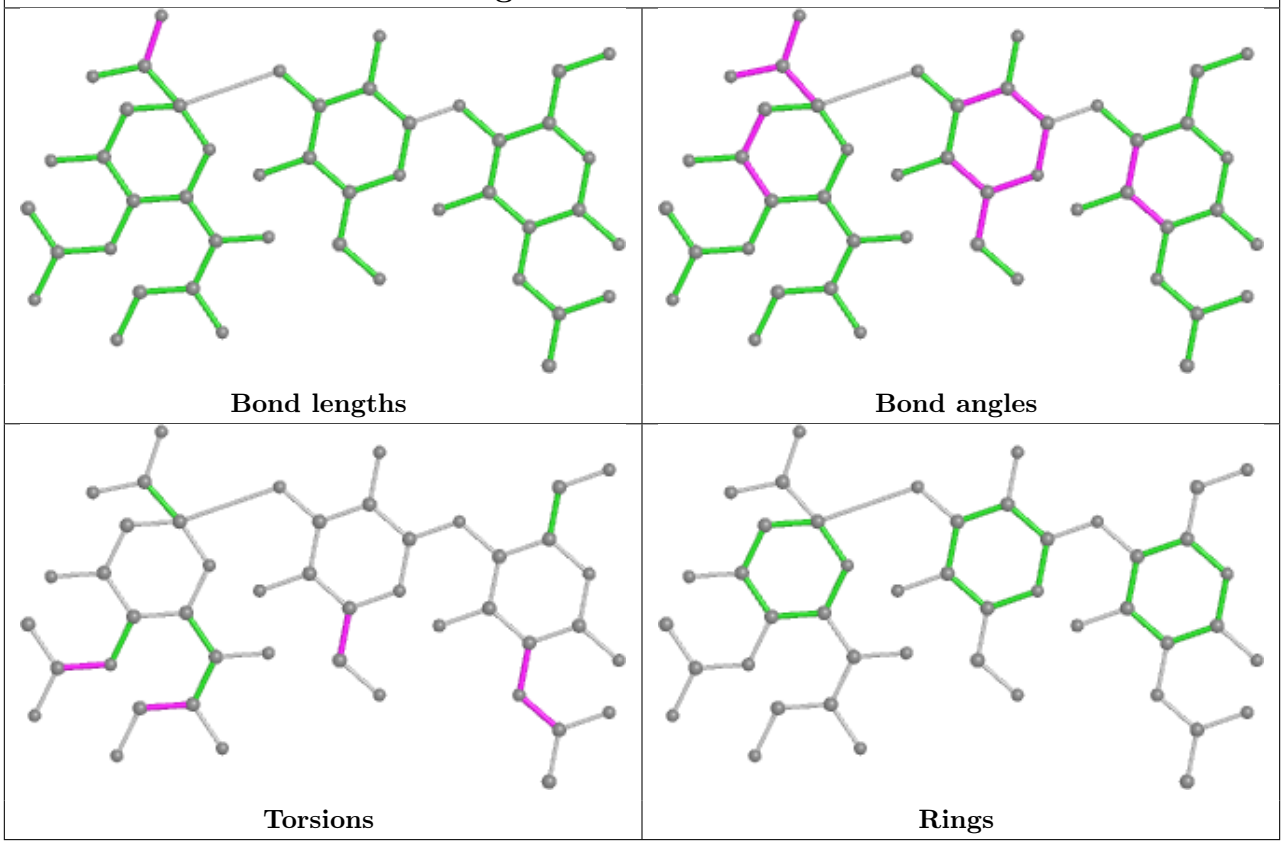


Torsions



Rings

Oligosaccharide Chain X



5.6 Ligand geometry (i)

12 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	$\#\|Z\| > 2$
8	NAG	A	401	1	14,14,15	0.22	0	17,19,21	0.40	0
8	NAG	C	401	1	14,14,15	0.22	0	17,19,21	0.41	0
8	NAG	A	402	1	14,14,15	0.23	0	17,19,21	0.42	0
8	NAG	B	301	2	14,14,15	0.25	0	17,19,21	0.49	0
8	NAG	J	301	3	14,14,15	0.37	0	17,19,21	0.46	0
8	NAG	C	402	1	14,14,15	0.23	0	17,19,21	0.42	0
8	NAG	R	301	3	14,14,15	0.38	0	17,19,21	0.45	0
8	NAG	H	401	1	14,14,15	0.22	0	17,19,21	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	NAG	E	301	3	14,14,15	0.38	0	17,19,21	0.45	0
8	NAG	I	301	2	14,14,15	0.25	0	17,19,21	0.49	0
8	NAG	H	402	1	14,14,15	0.23	0	17,19,21	0.41	0
8	NAG	D	301	2	14,14,15	0.25	0	17,19,21	0.48	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	A	401	1	-	1/6/23/26	0/1/1/1
8	NAG	C	401	1	-	1/6/23/26	0/1/1/1
8	NAG	A	402	1	-	0/6/23/26	0/1/1/1
8	NAG	B	301	2	-	1/6/23/26	0/1/1/1
8	NAG	J	301	3	-	2/6/23/26	0/1/1/1
8	NAG	C	402	1	-	0/6/23/26	0/1/1/1
8	NAG	R	301	3	-	2/6/23/26	0/1/1/1
8	NAG	H	401	1	-	1/6/23/26	0/1/1/1
8	NAG	E	301	3	-	2/6/23/26	0/1/1/1
8	NAG	I	301	2	-	1/6/23/26	0/1/1/1
8	NAG	H	402	1	-	0/6/23/26	0/1/1/1
8	NAG	D	301	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	R	301	NAG	O5-C5-C6-O6
8	E	301	NAG	O5-C5-C6-O6
8	J	301	NAG	O5-C5-C6-O6
8	R	301	NAG	C4-C5-C6-O6
8	E	301	NAG	C4-C5-C6-O6

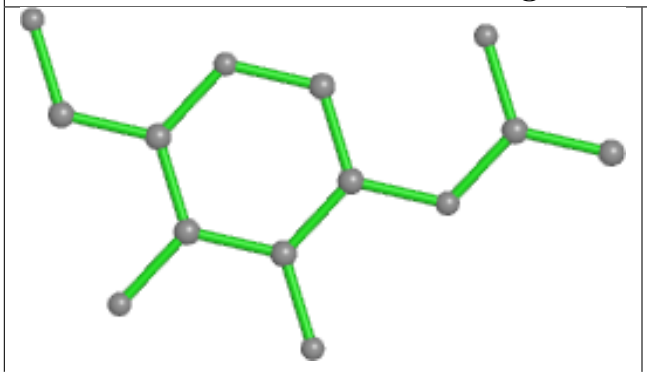
There are no ring outliers.

3 monomers are involved in 3 short contacts:

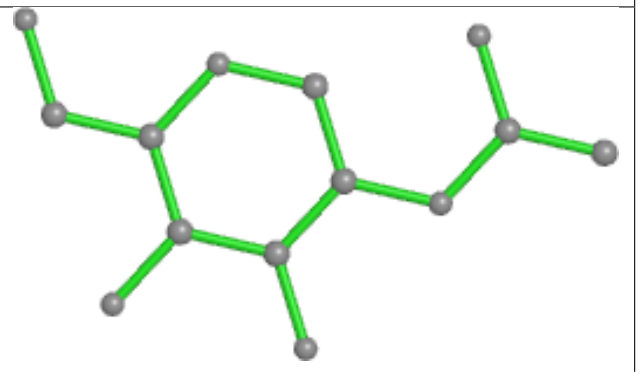
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	301	NAG	1	0
8	I	301	NAG	1	0
8	D	301	NAG	1	0

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.

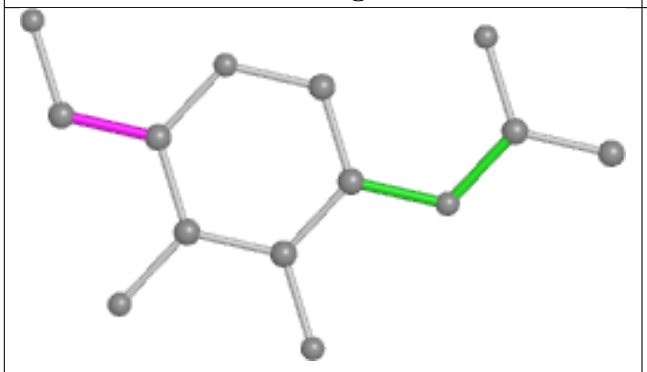
Ligand NAG A 401



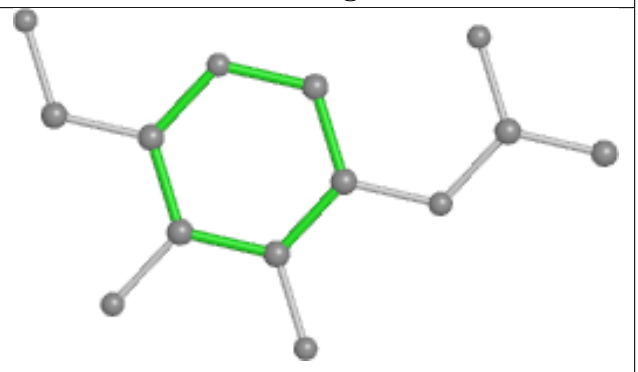
Bond lengths



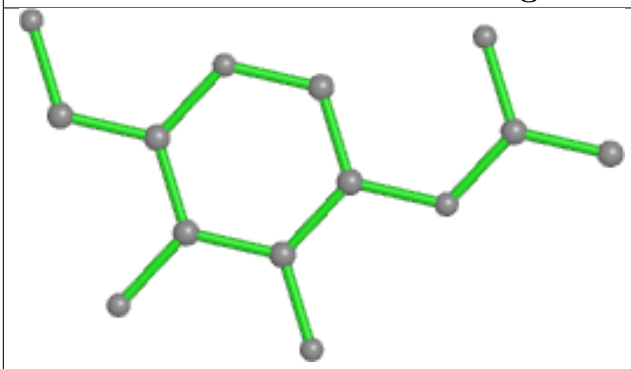
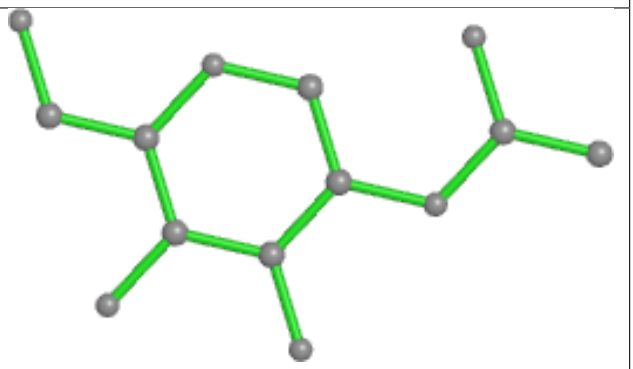
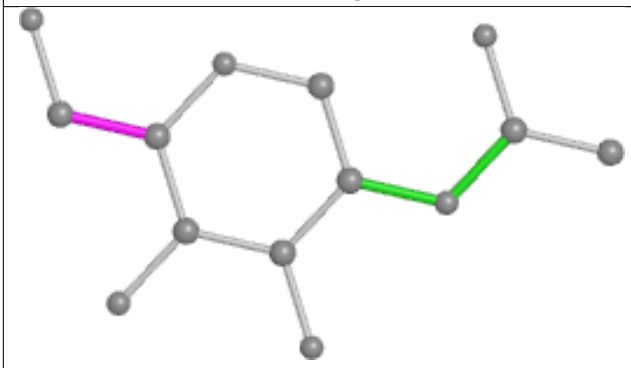
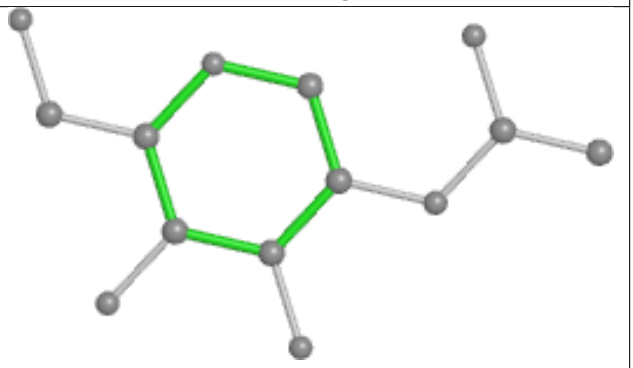
Bond angles

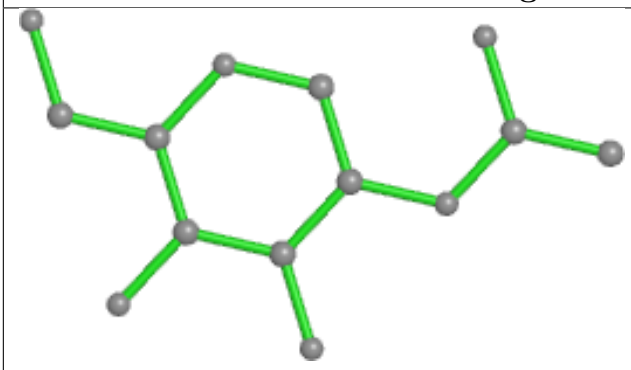
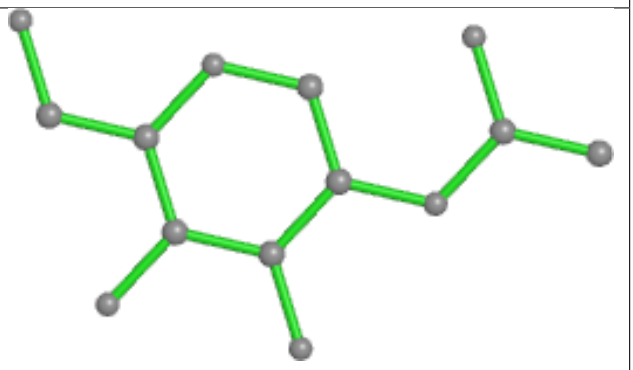
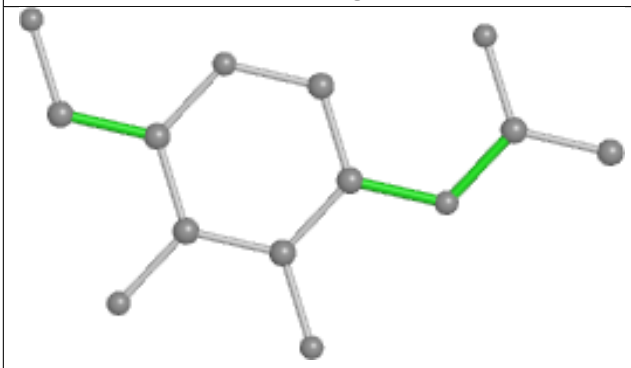
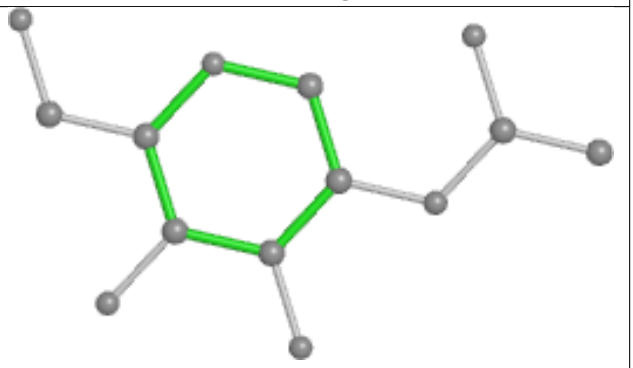


Torsions

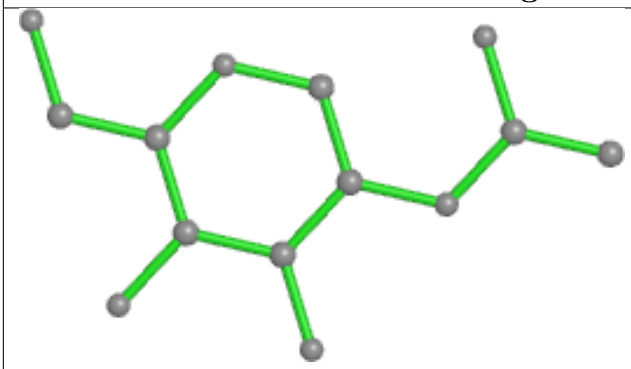


Rings

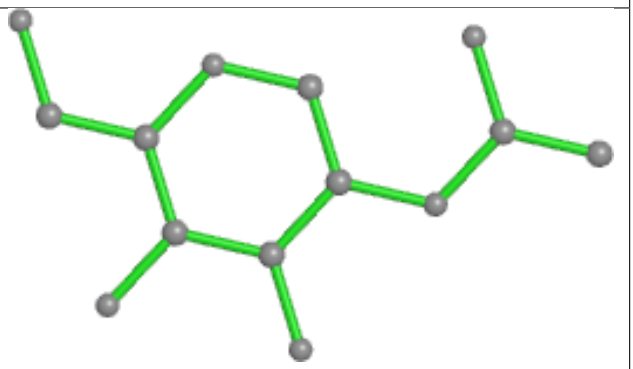
Ligand NAG C 401	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand NAG A 402	
	
Bond lengths	Bond angles
	
Torsions	Rings

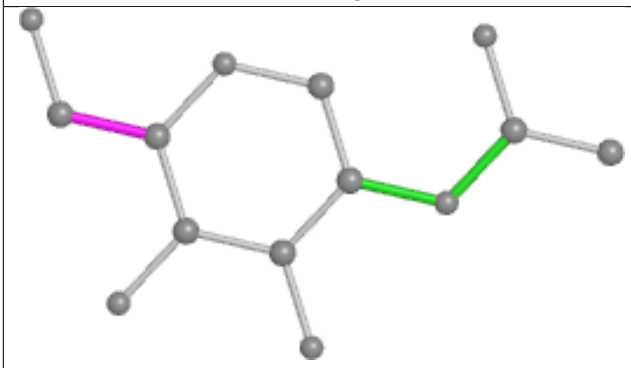
Ligand NAG B 301



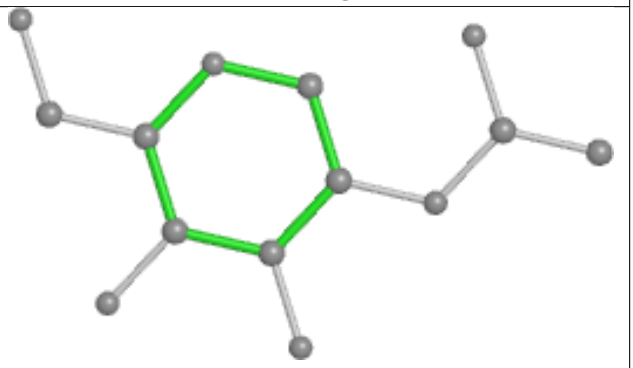
Bond lengths



Bond angles

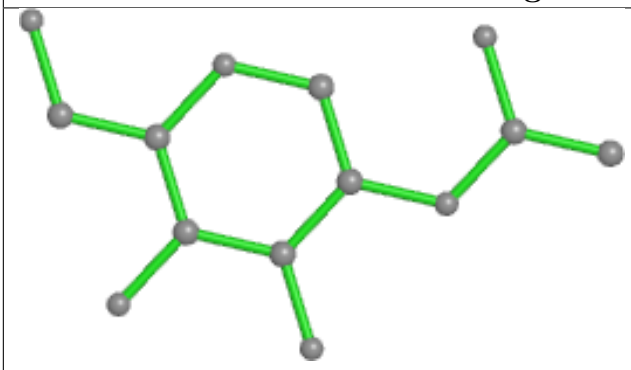


Torsions

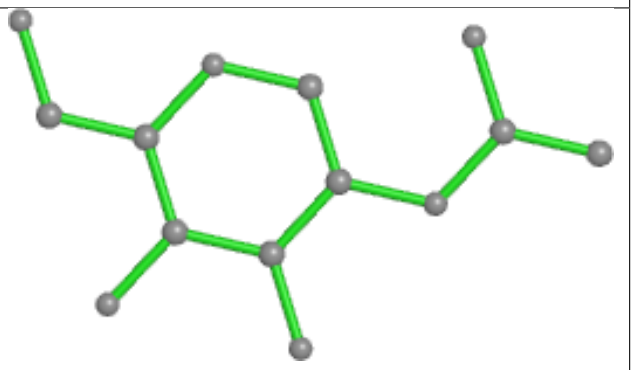


Rings

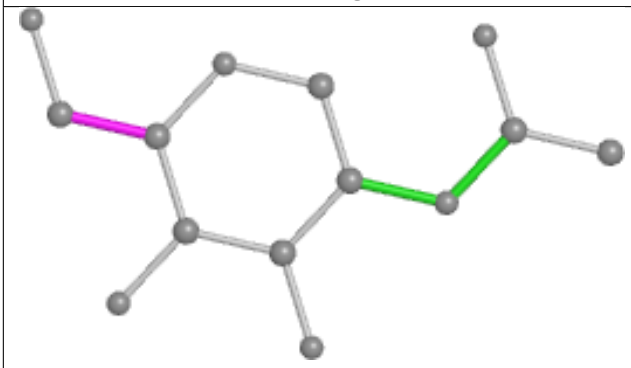
Ligand NAG J 301



Bond lengths



Bond angles



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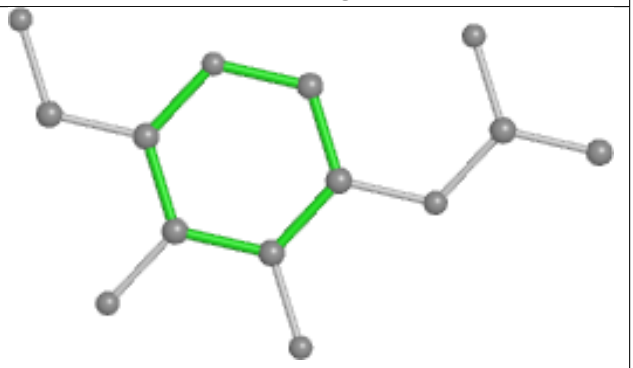
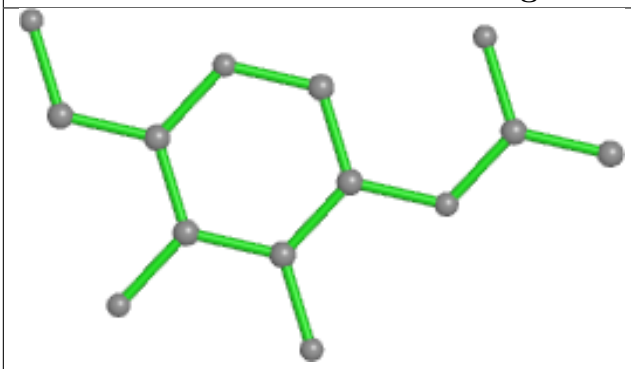
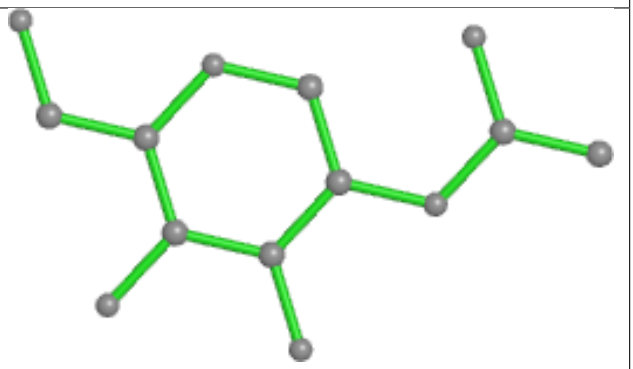


Rings

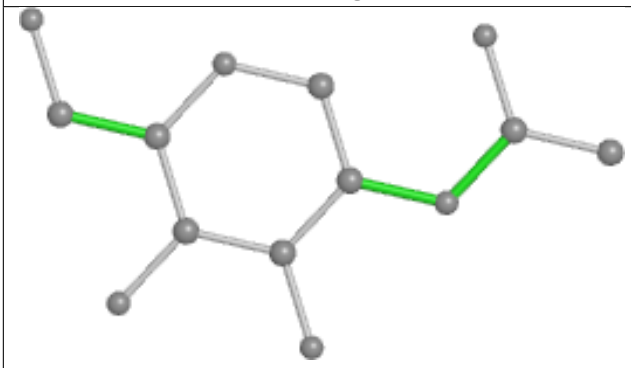
Ligand NAG C 402



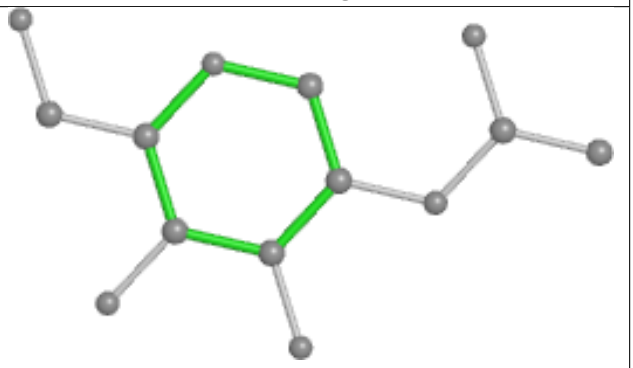
Bond lengths



Bond angles

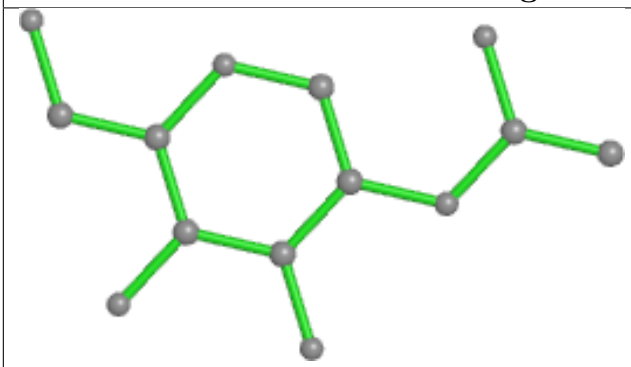


Torsions

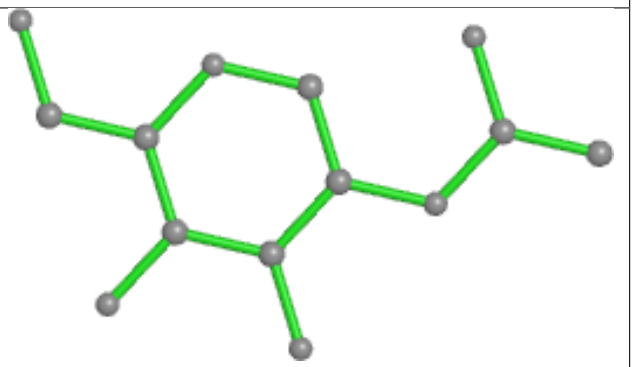


Rings

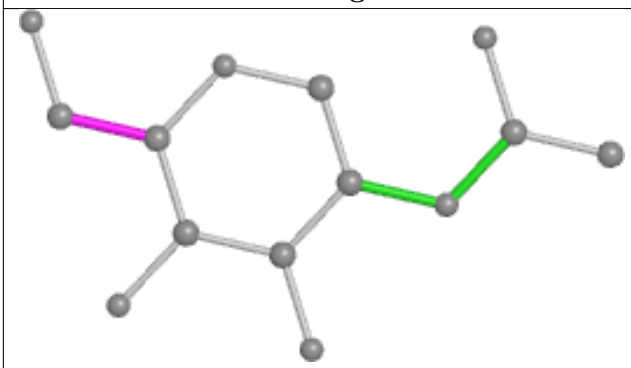
Ligand NAG R 301



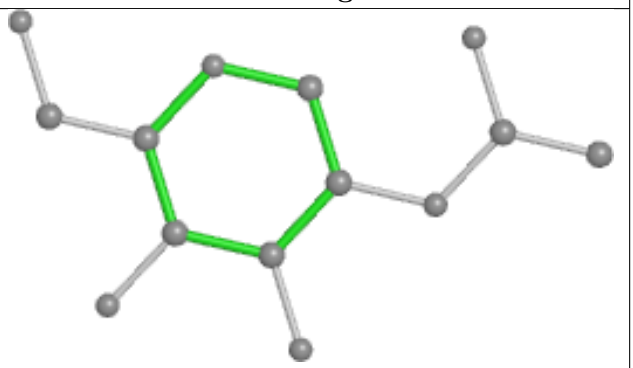
Bond lengths



Bond angles

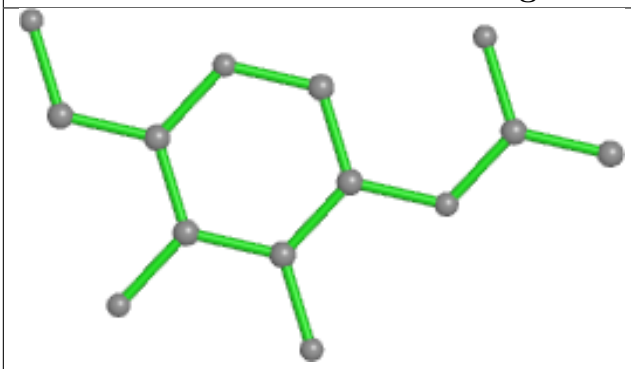


Torsions

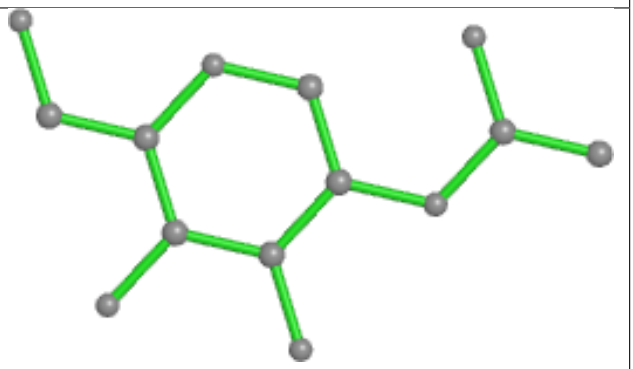


Rings

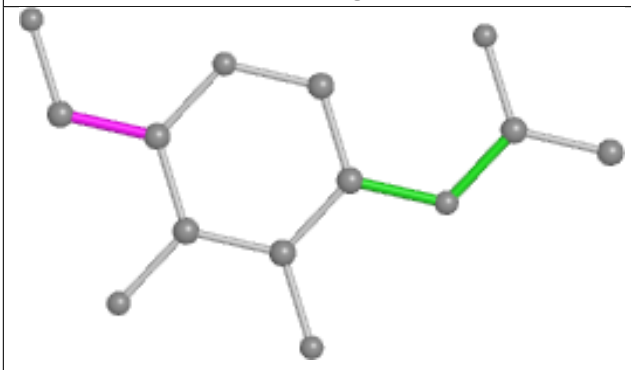
Ligand NAG H 401



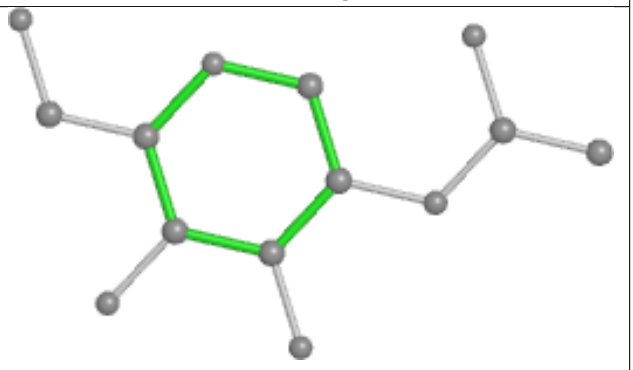
Bond lengths



Bond angles

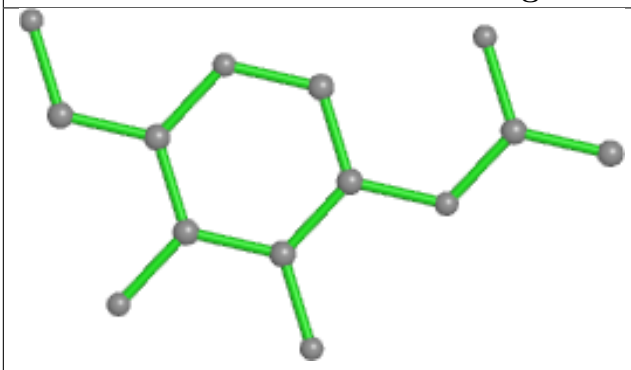


Torsions

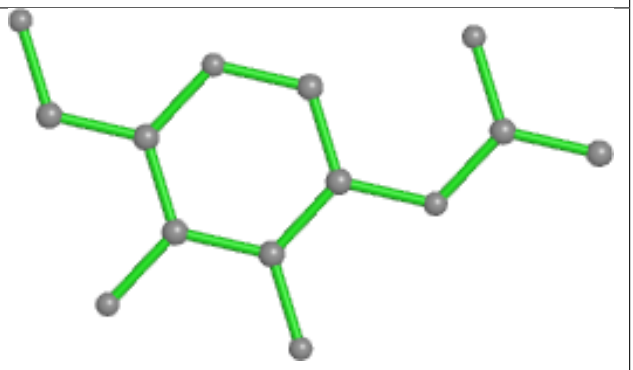


Rings

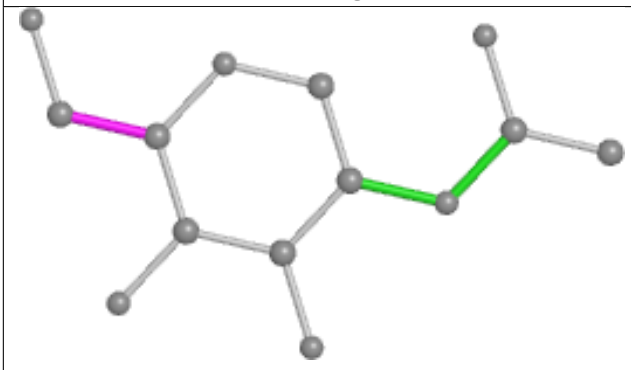
Ligand NAG E 301



Bond lengths



Bond angles



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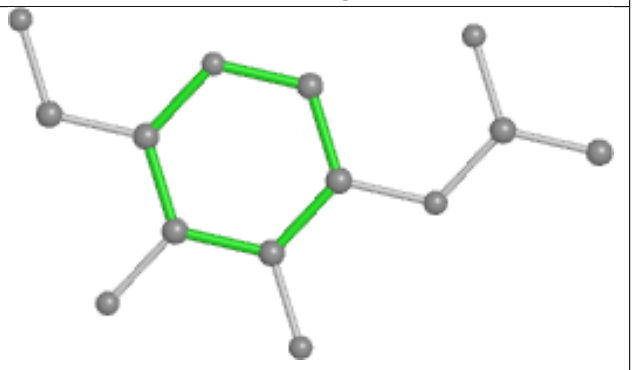
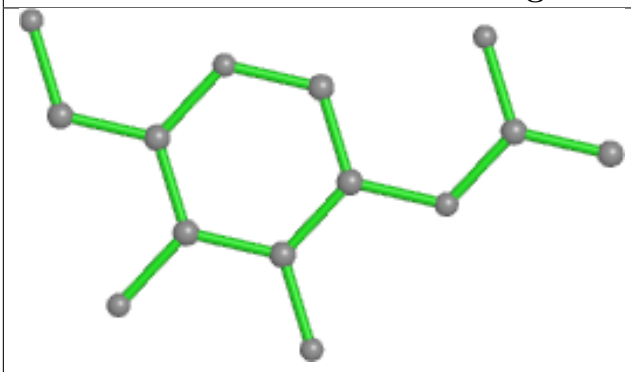


Rings

Ligand NAG I 301



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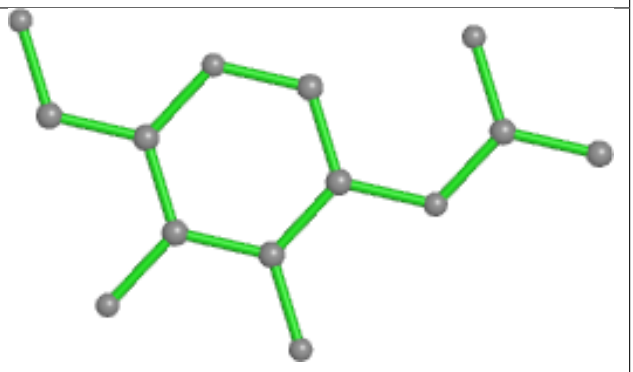
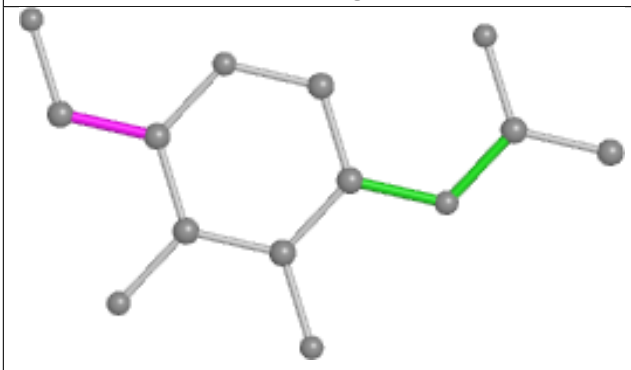
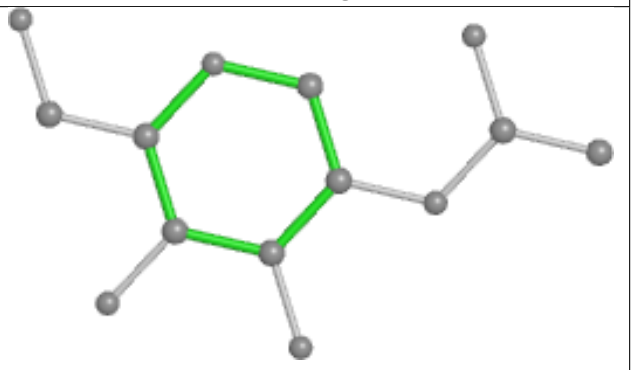


Bond angles

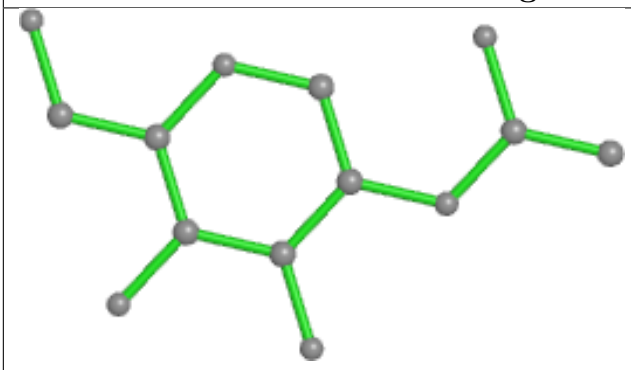


Torsions

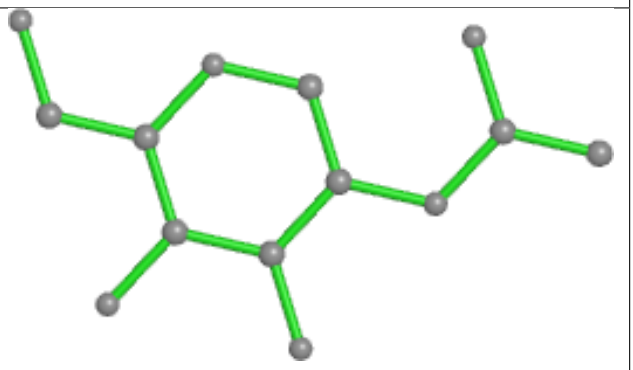


Rings

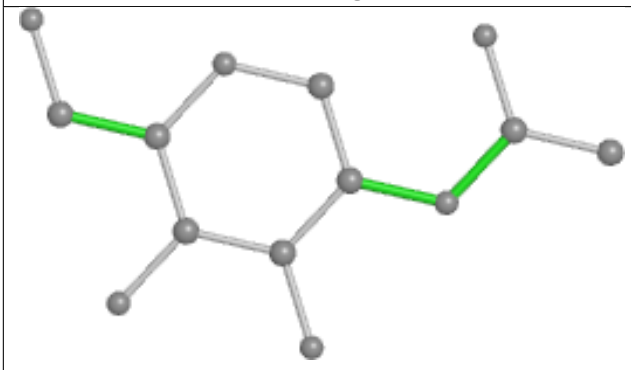
Ligand NAG H 402



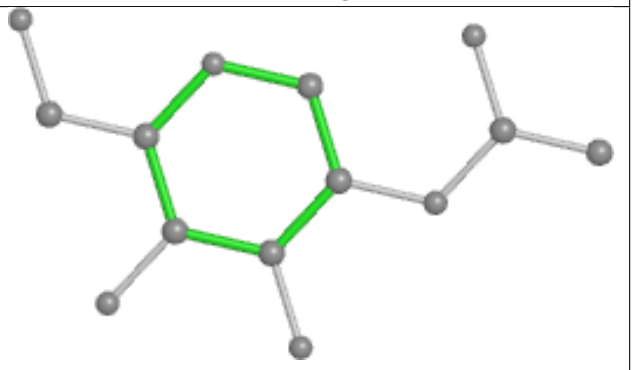
Bond lengths



Bond angles

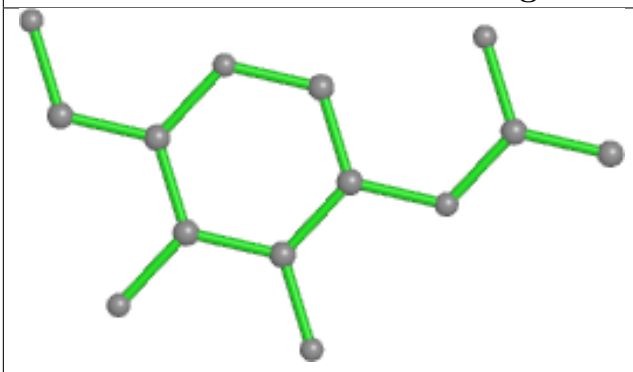


Torsions

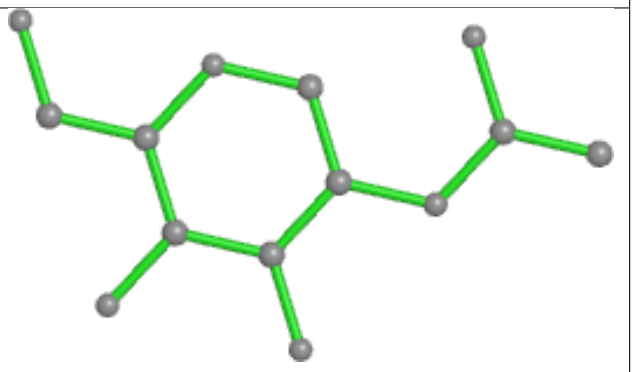


Rings

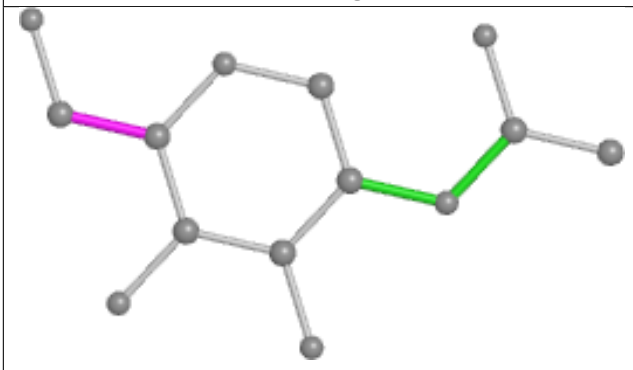
Ligand NAG D 301



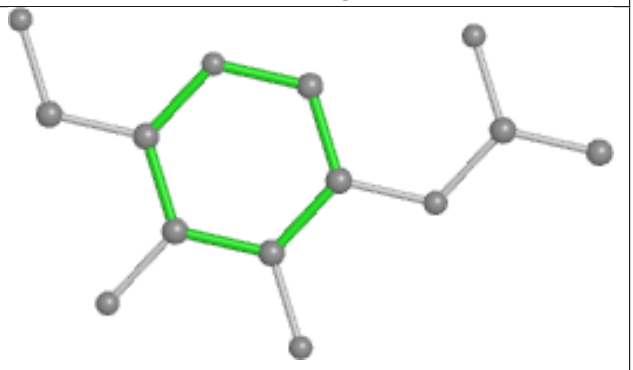
Bond lengths



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.