wwPDB EM Validation Summary Report

Oct 31, 2022 – 10:25 AM EDT

PDB ID	:	7UGQ
EMDB ID	:	EMD-26496
Title	:	Cryo-EM structure of BG24 Fabs with an inferred germline CDRL1 and 10-1074 Fabs in complex with HIV-1 Env 6405-SOSIP.664
Authors	:	Dam, K.A.; Bjorkman, P.J.
Deposited on	:	2022-03-25
Resolution	:	3.40 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:

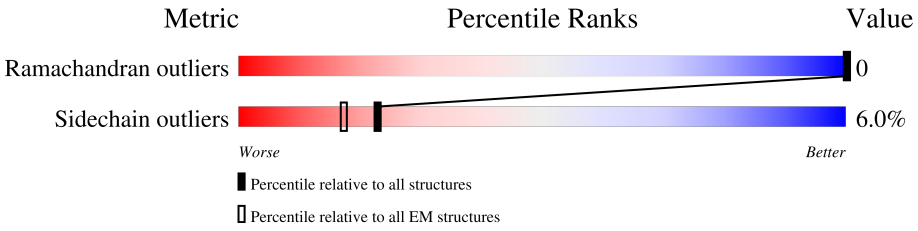
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.40 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	447	94% 6%
1	B	447	94% 6%
1	C	447	93% 7%
2	D	129	95% 5%
2	E	129	95% 5%
2	F	129	95% 5%
3	G	125	96%
3	H	125	94% 6%
3	I	125	95% 5%

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Mol	Chain	Length	Quality of chain
4	J	105	97%
4	K	105	98%
4	L	105	97%
5	M	133	20% 92% 8%
5	N	133	19% 95% 5%
5	O	133	17% 95% 5%
6	P	107	8% 98%
6	Q	107	7% 97%
6	R	107	9% 97%
7	0	3	100%
7	S	3	100%
7	V	3	33% 33% 67%
7	c	3	100%
7	e	3	100%
7	h	3	100%
7	o	3	100%
7	q	3	100%
7	t	3	67% 33%
8	T	2	100%
8	U	2	100%
8	X	2	100%
8	Y	2	100%
8	Z	2	50% 50% 50%
8	a	2	50% 50%
8	b	2	100%

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Mol	Chain	Length	Quality of chain
8	f	2	100%
8	g	2	100%
8	j	2	100%
8	k	2	50% 50%
8	l	2	50% 50% 50%
8	m	2	50% 50%
8	n	2	100%
8	r	2	100%
8	s	2	100%
8	v	2	100%
8	w	2	50% 50%
8	x	2	50% 50% 50%
8	y	2	50% 50%
8	z	2	100%
9	W	5	100%
9	i	5	100%
9	u	5	100%
10	1	9	11% 89%
10	d	9	11% 89%
11	p	8	12% 88%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	NAG	0	1	X	-	-	-
7	NAG	c	1	X	-	-	-
7	NAG	o	1	X	-	-	-

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 26113 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 Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	447	Total	C	N	O	S	0	0
			3498	2191	616	662	29		
1	B	447	Total	C	N	O	S	0	0
			3498	2191	616	662	29		
1	C	447	Total	C	N	O	S	0	0
			3498	2191	616	662	29		

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	ASN	ASP	conflict	UNP D7S1H2
A	?	-	GLU	deletion	UNP D7S1H2
A	?	-	THR	deletion	UNP D7S1H2
A	?	-	GLU	deletion	UNP D7S1H2
A	?	-	ARG	deletion	UNP D7S1H2
A	?	-	GLY	deletion	UNP D7S1H2
A	?	-	ALA	deletion	UNP D7S1H2
A	?	-	SER	deletion	UNP D7S1H2
A	?	-	ASN	deletion	UNP D7S1H2
A	?	-	SER	deletion	UNP D7S1H2
A	?	-	THR	deletion	UNP D7S1H2
A	?	-	GLY	deletion	UNP D7S1H2
A	?	-	THR	deletion	UNP D7S1H2
A	?	-	ASN	deletion	UNP D7S1H2
A	?	-	ASN	deletion	UNP D7S1H2
A	?	-	GLY	deletion	UNP D7S1H2
A	?	-	THR	deletion	UNP D7S1H2
A	?	-	ILE	deletion	UNP D7S1H2
A	?	-	SER	deletion	UNP D7S1H2
A	?	-	SER	deletion	UNP D7S1H2
A	?	-	THR	deletion	UNP D7S1H2
A	?	-	GLY	deletion	UNP D7S1H2
A	?	-	PRO	deletion	UNP D7S1H2
A	?	-	GLY	deletion	UNP D7S1H2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP D7S1H2
A	?	-	ALA	deletion	UNP D7S1H2
A	?	-	ILE	deletion	UNP D7S1H2
A	?	-	TRP	deletion	UNP D7S1H2
A	496	VAL	ILE	conflict	UNP D7S1H2
A	500	ARG	LYS	conflict	UNP D7S1H2
A	501	CYS	ALA	conflict	UNP D7S1H2
A	502	LYS	ARG	conflict	UNP D7S1H2
B	33	ASN	ASP	conflict	UNP D7S1H2
B	?	-	GLU	deletion	UNP D7S1H2
B	?	-	THR	deletion	UNP D7S1H2
B	?	-	GLU	deletion	UNP D7S1H2
B	?	-	ARG	deletion	UNP D7S1H2
B	?	-	GLY	deletion	UNP D7S1H2
B	?	-	ALA	deletion	UNP D7S1H2
B	?	-	SER	deletion	UNP D7S1H2
B	?	-	ASN	deletion	UNP D7S1H2
B	?	-	SER	deletion	UNP D7S1H2
B	?	-	THR	deletion	UNP D7S1H2
B	?	-	GLY	deletion	UNP D7S1H2
B	?	-	THR	deletion	UNP D7S1H2
B	?	-	ASN	deletion	UNP D7S1H2
B	?	-	ASN	deletion	UNP D7S1H2
B	?	-	GLY	deletion	UNP D7S1H2
B	?	-	THR	deletion	UNP D7S1H2
B	?	-	ILE	deletion	UNP D7S1H2
B	?	-	SER	deletion	UNP D7S1H2
B	?	-	SER	deletion	UNP D7S1H2
B	?	-	THR	deletion	UNP D7S1H2
B	?	-	GLY	deletion	UNP D7S1H2
B	?	-	PRO	deletion	UNP D7S1H2
B	?	-	GLY	deletion	UNP D7S1H2
B	?	-	GLN	deletion	UNP D7S1H2
B	?	-	ALA	deletion	UNP D7S1H2
B	?	-	ILE	deletion	UNP D7S1H2
B	?	-	TRP	deletion	UNP D7S1H2
B	496	VAL	ILE	conflict	UNP D7S1H2
B	500	ARG	LYS	conflict	UNP D7S1H2
B	501	CYS	ALA	conflict	UNP D7S1H2
B	502	LYS	ARG	conflict	UNP D7S1H2
C	33	ASN	ASP	conflict	UNP D7S1H2
C	?	-	GLU	deletion	UNP D7S1H2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	THR	deletion	UNP D7S1H2
C	?	-	GLU	deletion	UNP D7S1H2
C	?	-	ARG	deletion	UNP D7S1H2
C	?	-	GLY	deletion	UNP D7S1H2
C	?	-	ALA	deletion	UNP D7S1H2
C	?	-	SER	deletion	UNP D7S1H2
C	?	-	ASN	deletion	UNP D7S1H2
C	?	-	SER	deletion	UNP D7S1H2
C	?	-	THR	deletion	UNP D7S1H2
C	?	-	GLY	deletion	UNP D7S1H2
C	?	-	THR	deletion	UNP D7S1H2
C	?	-	ASN	deletion	UNP D7S1H2
C	?	-	ASN	deletion	UNP D7S1H2
C	?	-	GLY	deletion	UNP D7S1H2
C	?	-	THR	deletion	UNP D7S1H2
C	?	-	ILE	deletion	UNP D7S1H2
C	?	-	SER	deletion	UNP D7S1H2
C	?	-	SER	deletion	UNP D7S1H2
C	?	-	THR	deletion	UNP D7S1H2
C	?	-	GLY	deletion	UNP D7S1H2
C	?	-	PRO	deletion	UNP D7S1H2
C	?	-	GLY	deletion	UNP D7S1H2
C	?	-	GLN	deletion	UNP D7S1H2
C	?	-	ALA	deletion	UNP D7S1H2
C	?	-	ILE	deletion	UNP D7S1H2
C	?	-	TRP	deletion	UNP D7S1H2
C	496	VAL	ILE	conflict	UNP D7S1H2
C	500	ARG	LYS	conflict	UNP D7S1H2
C	501	CYS	ALA	conflict	UNP D7S1H2
C	502	LYS	ARG	conflict	UNP D7S1H2

- Molecule 2 is a protein called Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	129	Total	C	N	O	S	0	0
			1030	655	176	193	6		
2	E	129	Total	C	N	O	S	0	0
			1030	655	176	193	6		
2	F	129	Total	C	N	O	S	0	0
			1030	655	176	193	6		

- Molecule 3 is a protein called BG24 with an inferred germline CDRL1 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	125	Total	C	N	O	S	0	0
			966	605	172	183	6		
3	H	125	Total	C	N	O	S	0	0
			966	605	172	183	6		
3	I	125	Total	C	N	O	S	0	0
			966	605	172	183	6		

- Molecule 4 is a protein called BG24 with an inferred germline CDRL1 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	105	Total	C	N	O	S	0	0
			758	468	135	153	2		
4	K	105	Total	C	N	O	S	0	0
			758	468	135	153	2		
4	L	105	Total	C	N	O	S	0	0
			758	468	135	153	2		

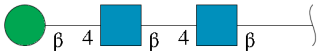
- Molecule 5 is a protein called 10-1074 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	133	Total	C	N	O	S	0	0
			1041	657	175	205	4		
5	N	133	Total	C	N	O	S	0	0
			1041	657	175	205	4		
5	O	133	Total	C	N	O	S	0	0
			1041	657	175	205	4		

- Molecule 6 is a protein called 10-1074 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	107	Total	C	N	O	S	0	0
			824	515	152	154	3		
6	Q	107	Total	C	N	O	S	0	0
			824	515	152	154	3		
6	R	107	Total	C	N	O	S	0	0
			824	515	152	154	3		

- Molecule 7 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
7	S	3	Total	C	N	O	0	0
			39	22	2	15		
7	V	3	Total	C	N	O	0	0
			39	22	2	15		
7	c	3	Total	C	N	O	0	0
			39	22	2	15		
7	e	3	Total	C	N	O	0	0
			39	22	2	15		
7	h	3	Total	C	N	O	0	0
			39	22	2	15		
7	o	3	Total	C	N	O	0	0
			39	22	2	15		
7	q	3	Total	C	N	O	0	0
			39	22	2	15		
7	t	3	Total	C	N	O	0	0
			39	22	2	15		
7	0	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 8 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
8	T	2	Total	C	N	O	0	0
			28	16	2	10		
8	U	2	Total	C	N	O	0	0
			28	16	2	10		
8	X	2	Total	C	N	O	0	0
			28	16	2	10		
8	Y	2	Total	C	N	O	0	0
			28	16	2	10		
8	Z	2	Total	C	N	O	0	0
			28	16	2	10		
8	a	2	Total	C	N	O	0	0
			28	16	2	10		
8	b	2	Total	C	N	O	0	0
			28	16	2	10		
8	f	2	Total	C	N	O	0	0
			28	16	2	10		

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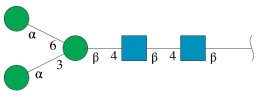
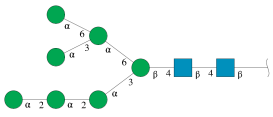
Mol	Chain	Residues	Atoms				AltConf	Trace
8	g	2	Total	C	N	O	0	0
			28	16	2	10		
8	j	2	Total	C	N	O	0	0
			28	16	2	10		
8	k	2	Total	C	N	O	0	0
			28	16	2	10		
8	l	2	Total	C	N	O	0	0
			28	16	2	10		
8	m	2	Total	C	N	O	0	0
			28	16	2	10		
8	n	2	Total	C	N	O	0	0
			28	16	2	10		
8	r	2	Total	C	N	O	0	0
			28	16	2	10		
8	s	2	Total	C	N	O	0	0
			28	16	2	10		
8	v	2	Total	C	N	O	0	0
			28	16	2	10		
8	w	2	Total	C	N	O	0	0
			28	16	2	10		
8	x	2	Total	C	N	O	0	0
			28	16	2	10		
8	y	2	Total	C	N	O	0	0
			28	16	2	10		
8	z	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



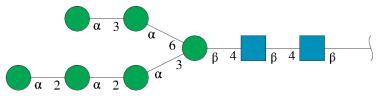
Mol	Chain	Residues	Atoms				AltConf	Trace
9	W	5	Total	C	N	O	0	0
			61	34	2	25		
9	i	5	Total	C	N	O	0	0
			61	34	2	25		
9	u	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



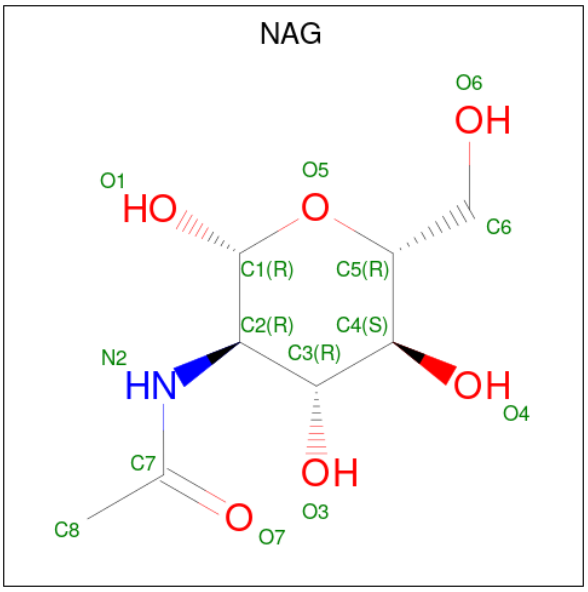
Mol	Chain	Residues	Atoms				AltConf	Trace
10	d	9	Total	C	N	O	0	0
			105	58	2	45		
10	1	9	Total	C	N	O	0	0
			105	58	2	45		

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]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
11	p	8	Total	C	N	O	0	0
			94	52	2	40		

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	A	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	
12	B	1	Total	C	N	O	0
			98	56	7	35	

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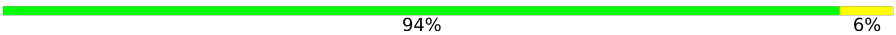
Mol	Chain	Residues	Atoms				AltConf
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	C	1	Total	C	N	O	0
			98	56	7	35	
12	D	1	Total	C	N	O	0
			14	8	1	5	
12	E	1	Total	C	N	O	0
			14	8	1	5	
12	F	1	Total	C	N	O	0
			14	8	1	5	

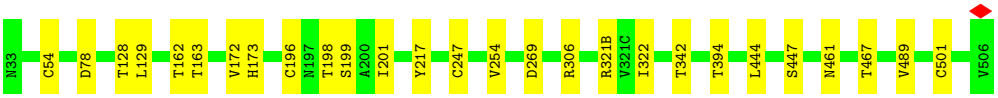
3 Residue-property plots (i)

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 and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Envelope glycoprotein gp120

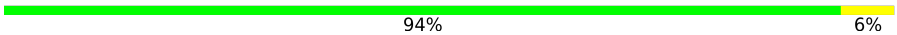
Chain A:

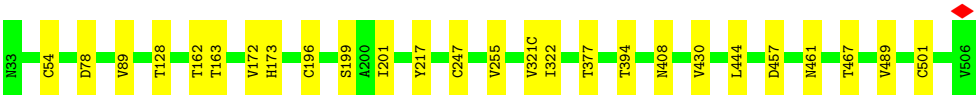




- Molecule 1: Envelope glycoprotein gp120

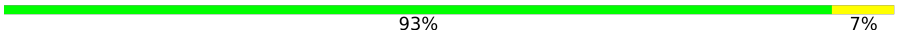
Chain B:

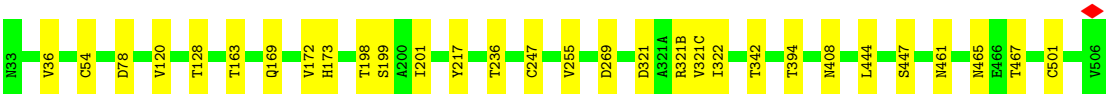




- Molecule 1: Envelope glycoprotein gp120

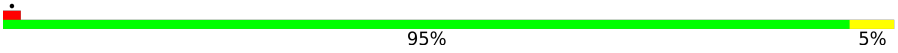
Chain C:





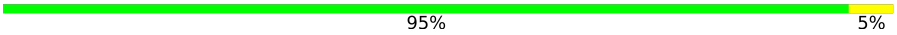
- Molecule 2: Envelope glycoprotein gp41

Chain D:



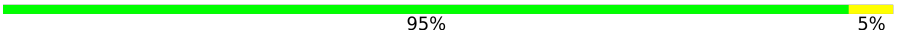
- Molecule 2: Envelope glycoprotein gp41

Chain E:



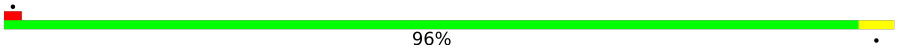
• Molecule 2: Envelope glycoprotein gp41

Chain F:



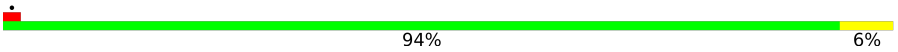
• Molecule 3: BG24 with an inferred germline CDRL1 Fab heavy chain

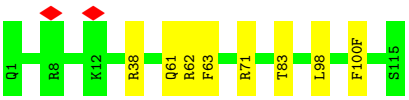
Chain G:



• Molecule 3: BG24 with an inferred germline CDRL1 Fab heavy chain

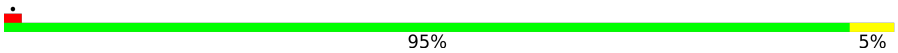
Chain H:

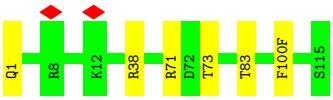




• Molecule 3: BG24 with an inferred germline CDRL1 Fab heavy chain

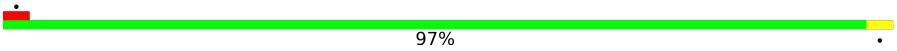
Chain I:

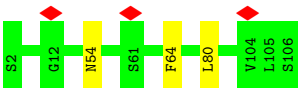




• Molecule 4: BG24 with an inferred germline CDRL1 Fab light chain

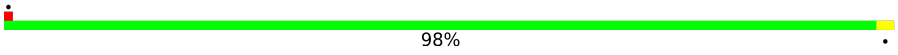
Chain J:

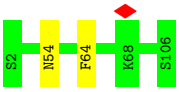




• Molecule 4: BG24 with an inferred germline CDRL1 Fab light chain

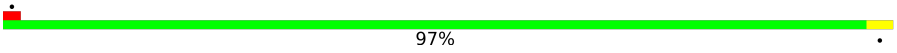
Chain K:

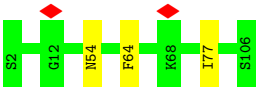




• Molecule 4: BG24 with an inferred germline CDRL1 Fab light chain

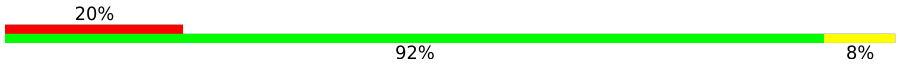
Chain L:

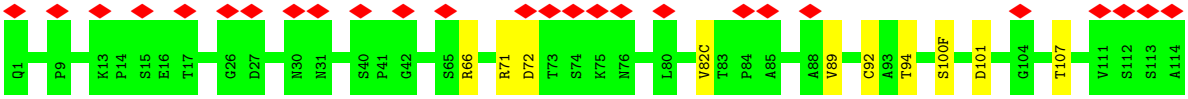




• Molecule 5: 10-1074 Fab heavy chain

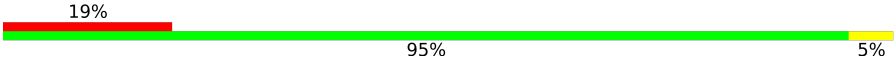
Chain M:

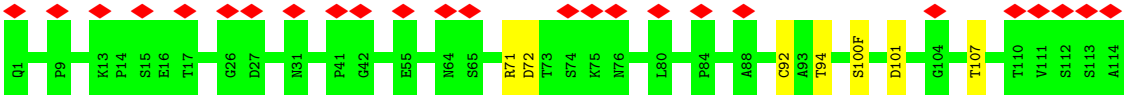




• Molecule 5: 10-1074 Fab heavy chain

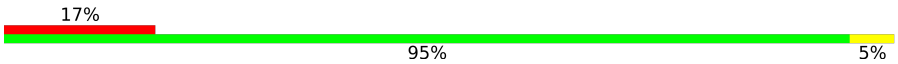
Chain N:

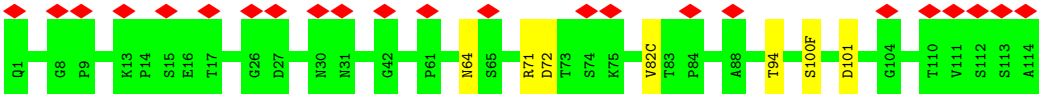




• Molecule 5: 10-1074 Fab heavy chain

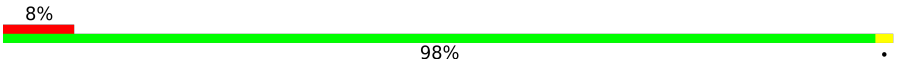
Chain O:

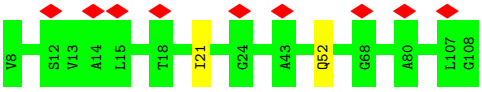




• Molecule 6: 10-1074 Fab light chain

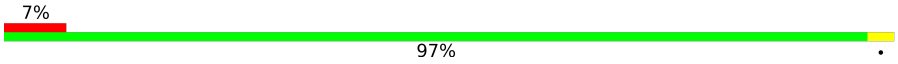
Chain P:

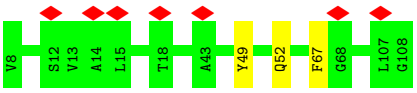




• Molecule 6: 10-1074 Fab light chain

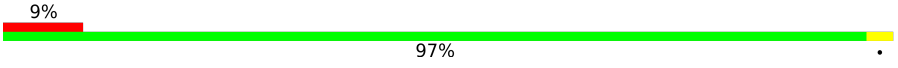
Chain Q:

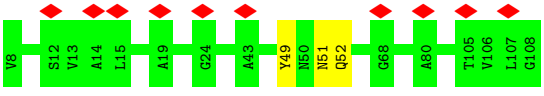




• Molecule 6: 10-1074 Fab light chain

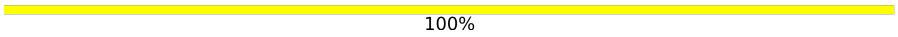
Chain R:





• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:

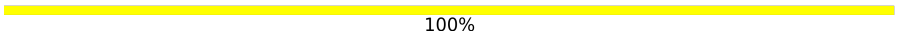


• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:

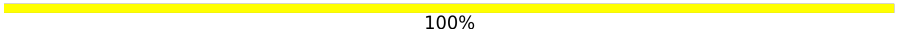
• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:



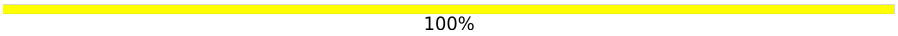
• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e:



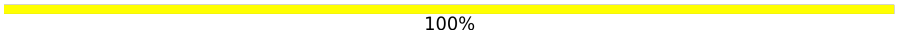
• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h:



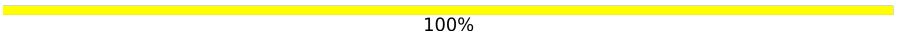
• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain o:



• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain q:

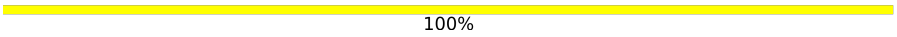


• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain t:

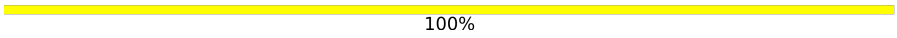
• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain 0:



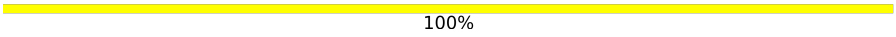
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:



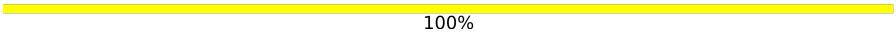
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:



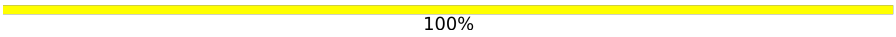
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:



• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:



• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

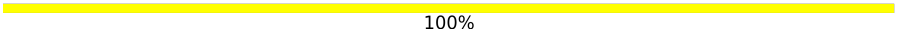
Chain Z:

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:

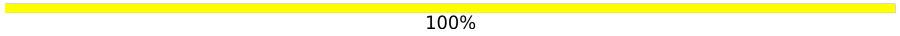
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b:



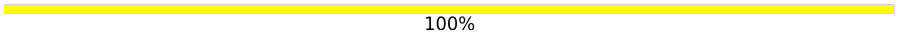
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:



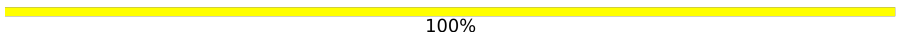
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:



• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:



• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain k:

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

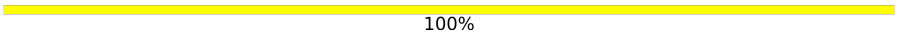
Chain l:

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain m:

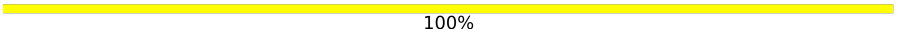
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain n:



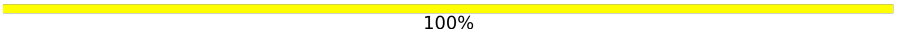
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain r:



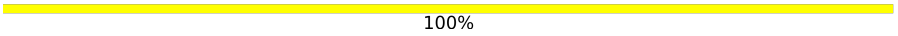
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain s:



• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain v:



• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain w:

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

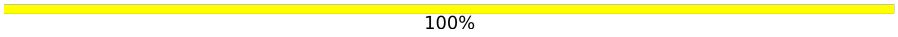
Chain x:

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain y:

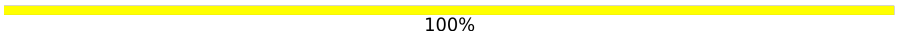
• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain z:



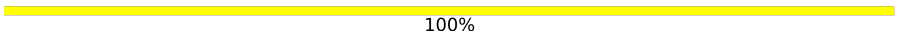
• Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:



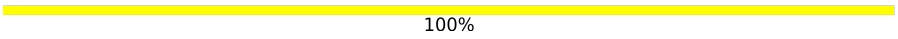
• Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain i:



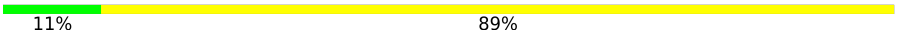
• Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain u:



• Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:



• Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain 1:

• Molecule 11: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain p:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	170897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.119	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0115	Depositor
Map size (Å)	312.84, 312.84, 312.84	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.869, 0.869, 0.869	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, MAN, 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	0.31	0/3572	0.55	0/4859
1	B	0.31	0/3572	0.55	0/4859
1	C	0.31	0/3572	0.55	0/4859
2	D	0.27	0/1048	0.54	0/1421
2	E	0.33	0/1048	0.54	0/1421
2	F	0.27	0/1048	0.54	0/1421
3	G	0.30	0/990	0.53	0/1346
3	H	0.30	0/990	0.54	0/1346
3	I	0.29	0/990	0.52	0/1346
4	J	0.28	0/773	0.54	0/1047
4	K	0.28	0/773	0.55	0/1047
4	L	0.29	0/773	0.56	0/1047
5	M	0.28	0/1066	0.54	0/1451
5	N	0.27	0/1066	0.55	0/1451
5	O	0.27	0/1066	0.55	0/1451
6	P	0.27	0/845	0.50	0/1148
6	Q	0.28	0/845	0.55	0/1148
6	R	0.28	0/845	0.53	0/1148
All	All	0.29	0/24882	0.54	0/33816

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	439/447 (98%)	405 (92%)	34 (8%)	0	100	100
1	B	439/447 (98%)	404 (92%)	35 (8%)	0	100	100
1	C	439/447 (98%)	407 (93%)	32 (7%)	0	100	100
2	D	125/129 (97%)	116 (93%)	9 (7%)	0	100	100
2	E	125/129 (97%)	118 (94%)	7 (6%)	0	100	100
2	F	125/129 (97%)	115 (92%)	10 (8%)	0	100	100
3	G	123/125 (98%)	113 (92%)	10 (8%)	0	100	100
3	H	123/125 (98%)	112 (91%)	11 (9%)	0	100	100
3	I	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
4	J	103/105 (98%)	91 (88%)	12 (12%)	0	100	100
4	K	103/105 (98%)	91 (88%)	12 (12%)	0	100	100
4	L	103/105 (98%)	91 (88%)	12 (12%)	0	100	100
5	M	131/133 (98%)	129 (98%)	2 (2%)	0	100	100
5	N	131/133 (98%)	127 (97%)	4 (3%)	0	100	100
5	O	131/133 (98%)	126 (96%)	5 (4%)	0	100	100
6	P	105/107 (98%)	99 (94%)	6 (6%)	0	100	100
6	Q	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
6	R	105/107 (98%)	94 (90%)	11 (10%)	0	100	100
All	All	3078/3138 (98%)	2852 (93%)	226 (7%)	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	397/397 (100%)	370 (93%)	27 (7%)	16	45
1	B	397/397 (100%)	371 (94%)	26 (6%)	17	46
1	C	397/397 (100%)	367 (92%)	30 (8%)	13	41
2	D	112/112 (100%)	106 (95%)	6 (5%)	22	52
2	E	112/112 (100%)	106 (95%)	6 (5%)	22	52
2	F	112/112 (100%)	106 (95%)	6 (5%)	22	52
3	G	102/102 (100%)	97 (95%)	5 (5%)	25	55
3	H	102/102 (100%)	94 (92%)	8 (8%)	12	39
3	I	102/102 (100%)	96 (94%)	6 (6%)	19	49
4	J	79/87 (91%)	76 (96%)	3 (4%)	33	61
4	K	79/87 (91%)	77 (98%)	2 (2%)	47	72
4	L	79/87 (91%)	76 (96%)	3 (4%)	33	61
5	M	116/116 (100%)	106 (91%)	10 (9%)	10	35
5	N	116/116 (100%)	109 (94%)	7 (6%)	19	49
5	O	116/116 (100%)	109 (94%)	7 (6%)	19	49
6	P	85/85 (100%)	83 (98%)	2 (2%)	49	74
6	Q	85/85 (100%)	82 (96%)	3 (4%)	36	65
6	R	85/85 (100%)	82 (96%)	3 (4%)	36	65
All	All	2673/2697 (99%)	2513 (94%)	160 (6%)	23	49

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	38	ARG
5	N	101	ASP
3	I	100(F)	PHE
5	M	72	ASP
5	O	100(F)	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
5	N	30	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	O	5	GLN
6	R	50	ASN
2	D	651	ASN
1	C	408	ASN

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)

110 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	$\#\|Z\| > 2$
7	NAG	0	1	1,7	14,14,15	2.05	1 (7%)	17,19,21	1.90	3 (17%)
7	NAG	0	2	7	14,14,15	0.43	0	17,19,21	1.42	4 (23%)
7	BMA	0	3	7	11,11,12	0.24	0	15,15,17	0.95	1 (6%)
10	NAG	1	1	1,10	14,14,15	0.27	0	17,19,21	0.74	0
10	NAG	1	2	10	14,14,15	0.28	0	17,19,21	0.82	1 (5%)
10	BMA	1	3	10	11,11,12	1.38	3 (27%)	15,15,17	1.86	3 (20%)
10	MAN	1	4	10	11,11,12	0.85	0	15,15,17	1.38	1 (6%)
10	MAN	1	5	10	11,11,12	0.85	0	15,15,17	1.29	1 (6%)
10	MAN	1	6	10	11,11,12	0.97	0	15,15,17	1.17	2 (13%)
10	MAN	1	7	10	11,11,12	1.61	3 (27%)	15,15,17	2.24	3 (20%)
10	MAN	1	8	10	11,11,12	1.06	1 (9%)	15,15,17	1.31	2 (13%)
10	MAN	1	9	10	11,11,12	1.11	1 (9%)	15,15,17	1.17	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	NAG	S	1	1,7	14,14,15	0.55	0	17,19,21	0.82	1 (5%)
7	NAG	S	2	7	14,14,15	1.09	1 (7%)	17,19,21	2.60	3 (17%)
7	BMA	S	3	7	11,11,12	1.05	0	15,15,17	1.05	1 (6%)
8	NAG	T	1	1,8	14,14,15	0.95	1 (7%)	17,19,21	2.58	3 (17%)
8	NAG	T	2	8	14,14,15	0.62	0	17,19,21	0.63	1 (5%)
8	NAG	U	1	1,8	14,14,15	0.97	1 (7%)	17,19,21	2.62	3 (17%)
8	NAG	U	2	8	14,14,15	0.51	0	17,19,21	0.62	1 (5%)
7	NAG	V	1	1,7	14,14,15	0.42	0	17,19,21	0.75	0
7	NAG	V	2	7	14,14,15	0.73	1 (7%)	17,19,21	1.35	3 (17%)
7	BMA	V	3	7	11,11,12	1.05	1 (9%)	15,15,17	1.16	1 (6%)
9	NAG	W	1	1,9	14,14,15	0.73	0	17,19,21	2.73	4 (23%)
9	NAG	W	2	9	14,14,15	0.46	0	17,19,21	0.62	1 (5%)
9	BMA	W	3	9	11,11,12	0.91	0	15,15,17	1.08	1 (6%)
9	MAN	W	4	9	11,11,12	1.29	3 (27%)	15,15,17	1.80	1 (6%)
9	MAN	W	5	9	11,11,12	1.15	0	15,15,17	1.05	2 (13%)
8	NAG	X	1	1,8	14,14,15	0.37	0	17,19,21	0.67	1 (5%)
8	NAG	X	2	8	14,14,15	1.06	1 (7%)	17,19,21	2.59	3 (17%)
8	NAG	Y	1	1,8	14,14,15	0.92	1 (7%)	17,19,21	1.30	3 (17%)
8	NAG	Y	2	8	14,14,15	0.53	0	17,19,21	0.60	1 (5%)
8	NAG	Z	1	1,8	14,14,15	0.33	0	17,19,21	0.63	0
8	NAG	Z	2	8	14,14,15	0.54	0	17,19,21	0.84	1 (5%)
8	NAG	a	1	1,8	14,14,15	0.46	0	17,19,21	0.61	0
8	NAG	a	2	8	14,14,15	0.64	1 (7%)	17,19,21	0.59	1 (5%)
8	NAG	b	1	1,8	14,14,15	0.39	0	17,19,21	0.66	1 (5%)
8	NAG	b	2	8	14,14,15	0.54	0	17,19,21	0.88	1 (5%)
7	NAG	c	1	1,7	14,14,15	2.11	1 (7%)	17,19,21	2.27	5 (29%)
7	NAG	c	2	7	14,14,15	0.39	0	17,19,21	1.48	3 (17%)
7	BMA	c	3	7	11,11,12	0.24	0	15,15,17	1.01	1 (6%)
10	NAG	d	1	1,10	14,14,15	0.28	0	17,19,21	0.77	0
10	NAG	d	2	10	14,14,15	0.27	0	17,19,21	0.82	1 (5%)
10	BMA	d	3	10	11,11,12	1.34	3 (27%)	15,15,17	1.91	4 (26%)
10	MAN	d	4	10	11,11,12	0.84	0	15,15,17	1.43	1 (6%)
10	MAN	d	5	10	11,11,12	0.88	0	15,15,17	1.27	1 (6%)
10	MAN	d	6	10	11,11,12	0.91	0	15,15,17	1.17	2 (13%)
10	MAN	d	7	10	11,11,12	1.52	3 (27%)	15,15,17	2.13	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
10	MAN	d	8	10	11,11,12	1.06	1 (9%)	15,15,17	1.34	2 (13%)
10	MAN	d	9	10	11,11,12	1.07	0	15,15,17	1.20	2 (13%)
7	NAG	e	1	1,7	14,14,15	0.56	0	17,19,21	0.81	1 (5%)
7	NAG	e	2	7	14,14,15	1.08	1 (7%)	17,19,21	2.60	3 (17%)
7	BMA	e	3	7	11,11,12	1.05	1 (9%)	15,15,17	1.07	1 (6%)
8	NAG	f	1	1,8	14,14,15	0.95	1 (7%)	17,19,21	2.58	3 (17%)
8	NAG	f	2	8	14,14,15	0.61	0	17,19,21	0.62	1 (5%)
8	NAG	g	1	1,8	14,14,15	0.97	1 (7%)	17,19,21	2.62	3 (17%)
8	NAG	g	2	8	14,14,15	0.49	0	17,19,21	0.80	1 (5%)
7	NAG	h	1	1,7	14,14,15	0.33	0	17,19,21	1.06	1 (5%)
7	NAG	h	2	7	14,14,15	0.65	0	17,19,21	0.73	1 (5%)
7	BMA	h	3	7	11,11,12	1.03	1 (9%)	15,15,17	1.17	1 (6%)
9	NAG	i	1	1,9	14,14,15	0.78	1 (7%)	17,19,21	2.71	4 (23%)
9	NAG	i	2	9	14,14,15	0.49	0	17,19,21	0.64	1 (5%)
9	BMA	i	3	9	11,11,12	0.86	0	15,15,17	1.11	1 (6%)
9	MAN	i	4	9	11,11,12	1.17	1 (9%)	15,15,17	1.79	1 (6%)
9	MAN	i	5	9	11,11,12	1.02	0	15,15,17	1.12	2 (13%)
8	NAG	j	1	1,8	14,14,15	0.37	0	17,19,21	0.66	1 (5%)
8	NAG	j	2	8	14,14,15	1.05	1 (7%)	17,19,21	2.59	3 (17%)
8	NAG	k	1	1,8	14,14,15	1.03	1 (7%)	17,19,21	1.40	4 (23%)
8	NAG	k	2	8	14,14,15	0.60	0	17,19,21	0.54	0
8	NAG	l	1	1,8	14,14,15	0.32	0	17,19,21	0.61	0
8	NAG	l	2	8	14,14,15	0.54	0	17,19,21	0.84	1 (5%)
8	NAG	m	1	1,8	14,14,15	0.31	0	17,19,21	0.81	0
8	NAG	m	2	8	14,14,15	0.72	1 (7%)	17,19,21	0.51	0
8	NAG	n	1	1,8	14,14,15	0.40	0	17,19,21	0.67	1 (5%)
8	NAG	n	2	8	14,14,15	0.54	0	17,19,21	0.86	1 (5%)
7	NAG	o	1	1,7	14,14,15	2.10	1 (7%)	17,19,21	1.90	2 (11%)
7	NAG	o	2	7	14,14,15	0.46	0	17,19,21	1.82	4 (23%)
7	BMA	o	3	7	11,11,12	0.24	0	15,15,17	0.95	1 (6%)
11	NAG	p	1	1,11	14,14,15	0.28	0	17,19,21	0.78	0
11	NAG	p	2	11	14,14,15	0.28	0	17,19,21	0.85	2 (11%)
11	BMA	p	3	11	11,11,12	1.45	3 (27%)	15,15,17	1.94	4 (26%)
11	MAN	p	4	11	11,11,12	0.90	0	15,15,17	1.34	1 (6%)
11	MAN	p	5	11	11,11,12	0.82	0	15,15,17	1.26	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
11	MAN	p	6	11	11,11,12	0.97	0	15,15,17	1.18	2 (13%)
11	MAN	p	7	11	11,11,12	1.37	3 (27%)	15,15,17	1.94	2 (13%)
11	MAN	p	8	11	11,11,12	1.06	1 (9%)	15,15,17	1.35	2 (13%)
7	NAG	q	1	1,7	14,14,15	0.58	0	17,19,21	0.81	1 (5%)
7	NAG	q	2	7	14,14,15	1.09	1 (7%)	17,19,21	2.60	3 (17%)
7	BMA	q	3	7	11,11,12	1.06	1 (9%)	15,15,17	1.05	1 (6%)
8	NAG	r	1	1,8	14,14,15	0.96	1 (7%)	17,19,21	2.58	3 (17%)
8	NAG	r	2	8	14,14,15	0.61	0	17,19,21	0.63	1 (5%)
8	NAG	s	1	1,8	14,14,15	0.97	1 (7%)	17,19,21	2.62	4 (23%)
8	NAG	s	2	8	14,14,15	0.52	0	17,19,21	0.62	1 (5%)
7	NAG	t	1	1,7	14,14,15	0.38	0	17,19,21	0.85	0
7	NAG	t	2	7	14,14,15	0.48	0	17,19,21	0.74	0
7	BMA	t	3	7	11,11,12	1.06	1 (9%)	15,15,17	1.12	1 (6%)
9	NAG	u	1	1,9	14,14,15	0.75	0	17,19,21	2.72	4 (23%)
9	NAG	u	2	9	14,14,15	0.48	0	17,19,21	0.64	1 (5%)
9	BMA	u	3	9	11,11,12	1.00	0	15,15,17	0.96	1 (6%)
9	MAN	u	4	9	11,11,12	1.11	1 (9%)	15,15,17	1.59	2 (13%)
9	MAN	u	5	9	11,11,12	1.00	0	15,15,17	1.18	2 (13%)
8	NAG	v	1	1,8	14,14,15	0.39	0	17,19,21	0.64	1 (5%)
8	NAG	v	2	8	14,14,15	1.07	1 (7%)	17,19,21	2.59	3 (17%)
8	NAG	w	1	1,8	14,14,15	1.03	1 (7%)	17,19,21	1.38	4 (23%)
8	NAG	w	2	8	14,14,15	0.57	0	17,19,21	0.55	0
8	NAG	x	1	1,8	14,14,15	0.34	0	17,19,21	0.62	0
8	NAG	x	2	8	14,14,15	0.55	0	17,19,21	0.84	1 (5%)
8	NAG	y	1	1,8	14,14,15	0.46	0	17,19,21	0.60	0
8	NAG	y	2	8	14,14,15	0.63	0	17,19,21	0.59	1 (5%)
8	NAG	z	1	1,8	14,14,15	0.40	0	17,19,21	0.67	1 (5%)
8	NAG	z	2	8	14,14,15	0.52	0	17,19,21	0.87	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	0	1	1,7	1/1/5/7	5/6/23/26	0/1/1/1
7	NAG	0	2	7	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BMA	0	3	7	-	1/2/19/22	0/1/1/1
10	NAG	1	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	1	2	10	-	0/6/23/26	0/1/1/1
10	BMA	1	3	10	-	1/2/19/22	0/1/1/1
10	MAN	1	4	10	-	2/2/19/22	0/1/1/1
10	MAN	1	5	10	-	2/2/19/22	0/1/1/1
10	MAN	1	6	10	-	0/2/19/22	0/1/1/1
10	MAN	1	7	10	-	2/2/19/22	0/1/1/1
10	MAN	1	8	10	-	0/2/19/22	0/1/1/1
10	MAN	1	9	10	-	0/2/19/22	0/1/1/1
7	NAG	S	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	S	2	7	-	5/6/23/26	0/1/1/1
7	BMA	S	3	7	-	0/2/19/22	0/1/1/1
8	NAG	T	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	T	2	8	-	2/6/23/26	0/1/1/1
8	NAG	U	1	1,8	-	5/6/23/26	0/1/1/1
8	NAG	U	2	8	-	0/6/23/26	0/1/1/1
7	NAG	V	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	V	2	7	-	3/6/23/26	0/1/1/1
7	BMA	V	3	7	-	2/2/19/22	0/1/1/1
9	NAG	W	1	1,9	-	3/6/23/26	0/1/1/1
9	NAG	W	2	9	-	0/6/23/26	0/1/1/1
9	BMA	W	3	9	-	0/2/19/22	0/1/1/1
9	MAN	W	4	9	-	0/2/19/22	0/1/1/1
9	MAN	W	5	9	-	1/2/19/22	0/1/1/1
8	NAG	X	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	X	2	8	-	5/6/23/26	0/1/1/1
8	NAG	Y	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	Y	2	8	-	2/6/23/26	0/1/1/1
8	NAG	Z	1	1,8	-	0/6/23/26	0/1/1/1
8	NAG	Z	2	8	-	4/6/23/26	0/1/1/1
8	NAG	a	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	a	2	8	-	0/6/23/26	0/1/1/1
8	NAG	b	1	1,8	-	0/6/23/26	0/1/1/1
8	NAG	b	2	8	-	2/6/23/26	0/1/1/1
7	NAG	c	1	1,7	1/1/5/7	3/6/23/26	0/1/1/1
7	NAG	c	2	7	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BMA	c	3	7	-	2/2/19/22	0/1/1/1
10	NAG	d	1	1,10	-	1/6/23/26	0/1/1/1
10	NAG	d	2	10	-	0/6/23/26	0/1/1/1
10	BMA	d	3	10	-	1/2/19/22	0/1/1/1
10	MAN	d	4	10	-	0/2/19/22	0/1/1/1
10	MAN	d	5	10	-	2/2/19/22	0/1/1/1
10	MAN	d	6	10	-	0/2/19/22	0/1/1/1
10	MAN	d	7	10	-	2/2/19/22	0/1/1/1
10	MAN	d	8	10	-	0/2/19/22	0/1/1/1
10	MAN	d	9	10	-	0/2/19/22	0/1/1/1
7	NAG	e	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	e	2	7	-	5/6/23/26	0/1/1/1
7	BMA	e	3	7	-	0/2/19/22	0/1/1/1
8	NAG	f	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	f	2	8	-	2/6/23/26	0/1/1/1
8	NAG	g	1	1,8	-	5/6/23/26	0/1/1/1
8	NAG	g	2	8	-	2/6/23/26	0/1/1/1
7	NAG	h	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	h	2	7	-	2/6/23/26	0/1/1/1
7	BMA	h	3	7	-	2/2/19/22	0/1/1/1
9	NAG	i	1	1,9	-	3/6/23/26	0/1/1/1
9	NAG	i	2	9	-	1/6/23/26	0/1/1/1
9	BMA	i	3	9	-	0/2/19/22	0/1/1/1
9	MAN	i	4	9	-	0/2/19/22	0/1/1/1
9	MAN	i	5	9	-	0/2/19/22	0/1/1/1
8	NAG	j	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	j	2	8	-	5/6/23/26	0/1/1/1
8	NAG	k	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	k	2	8	-	2/6/23/26	0/1/1/1
8	NAG	l	1	1,8	-	0/6/23/26	0/1/1/1
8	NAG	l	2	8	-	4/6/23/26	0/1/1/1
8	NAG	m	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	m	2	8	-	1/6/23/26	0/1/1/1
8	NAG	n	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	n	2	8	-	2/6/23/26	0/1/1/1
7	NAG	o	1	1,7	1/1/5/7	4/6/23/26	0/1/1/1
7	NAG	o	2	7	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BMA	o	3	7	-	2/2/19/22	0/1/1/1
11	NAG	p	1	1,11	-	1/6/23/26	0/1/1/1
11	NAG	p	2	11	-	0/6/23/26	0/1/1/1
11	BMA	p	3	11	-	1/2/19/22	0/1/1/1
11	MAN	p	4	11	-	0/2/19/22	0/1/1/1
11	MAN	p	5	11	-	2/2/19/22	0/1/1/1
11	MAN	p	6	11	-	0/2/19/22	0/1/1/1
11	MAN	p	7	11	-	2/2/19/22	0/1/1/1
11	MAN	p	8	11	-	0/2/19/22	0/1/1/1
7	NAG	q	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	q	2	7	-	5/6/23/26	0/1/1/1
7	BMA	q	3	7	-	0/2/19/22	0/1/1/1
8	NAG	r	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	r	2	8	-	2/6/23/26	0/1/1/1
8	NAG	s	1	1,8	-	5/6/23/26	0/1/1/1
8	NAG	s	2	8	-	0/6/23/26	0/1/1/1
7	NAG	t	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	t	2	7	-	2/6/23/26	0/1/1/1
7	BMA	t	3	7	-	2/2/19/22	0/1/1/1
9	NAG	u	1	1,9	-	3/6/23/26	0/1/1/1
9	NAG	u	2	9	-	2/6/23/26	0/1/1/1
9	BMA	u	3	9	-	2/2/19/22	0/1/1/1
9	MAN	u	4	9	-	0/2/19/22	0/1/1/1
9	MAN	u	5	9	-	0/2/19/22	0/1/1/1
8	NAG	v	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	v	2	8	-	5/6/23/26	0/1/1/1
8	NAG	w	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	w	2	8	-	2/6/23/26	0/1/1/1
8	NAG	x	1	1,8	-	0/6/23/26	0/1/1/1
8	NAG	x	2	8	-	4/6/23/26	0/1/1/1
8	NAG	y	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	y	2	8	-	0/6/23/26	0/1/1/1
8	NAG	z	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	z	2	8	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	c	1	NAG	C1-C2	7.82	1.64	1.52
7	o	1	NAG	C1-C2	7.76	1.63	1.52
7	0	1	NAG	C1-C2	7.58	1.63	1.52
8	k	1	NAG	O5-C1	-3.40	1.38	1.43
8	w	1	NAG	O5-C1	-3.37	1.38	1.43

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	r	1	NAG	C2-N2-C7	9.10	135.86	122.90
8	f	1	NAG	C2-N2-C7	9.09	135.84	122.90
9	W	1	NAG	C2-N2-C7	9.09	135.84	122.90
9	u	1	NAG	C2-N2-C7	9.08	135.84	122.90
9	i	1	NAG	C2-N2-C7	9.08	135.83	122.90

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	c	1	NAG	C1
7	o	1	NAG	C1
7	0	1	NAG	C1

5 of 188 torsion outliers are listed below:

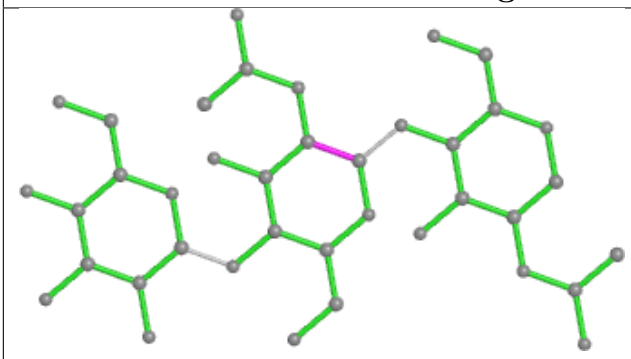
Mol	Chain	Res	Type	Atoms
7	c	1	NAG	C8-C7-N2-C2
7	c	1	NAG	O7-C7-N2-C2
7	c	2	NAG	C8-C7-N2-C2
7	c	2	NAG	O7-C7-N2-C2
7	o	1	NAG	C8-C7-N2-C2

There are no ring outliers.

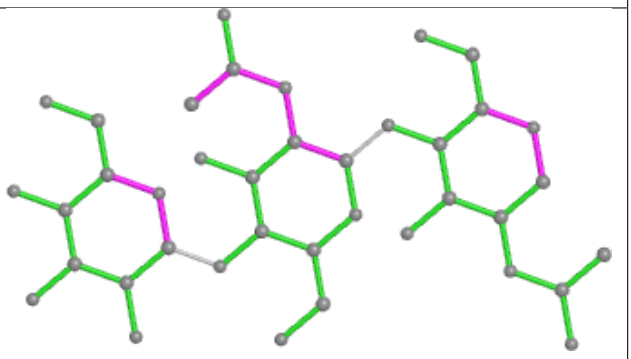
No monomer is involved in short contacts.

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

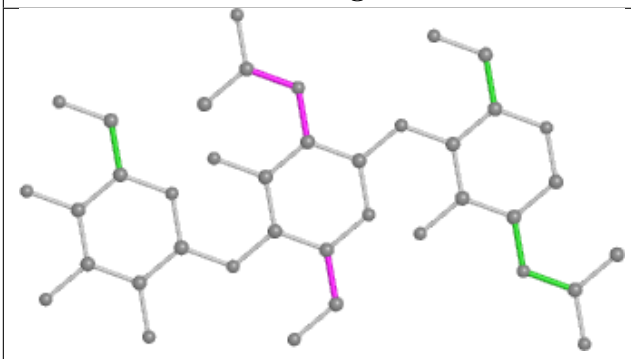
Oligosaccharide Chain S



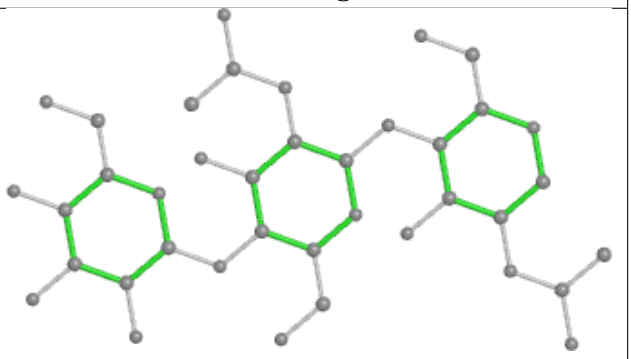
Bond lengths



Bond angles

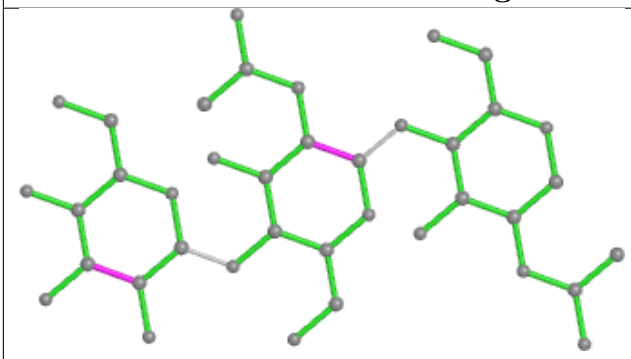


Torsions

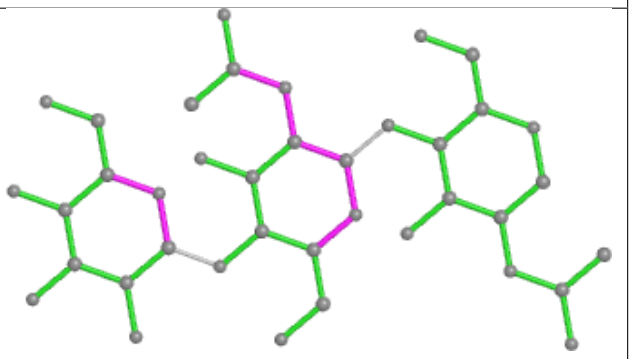


Rings

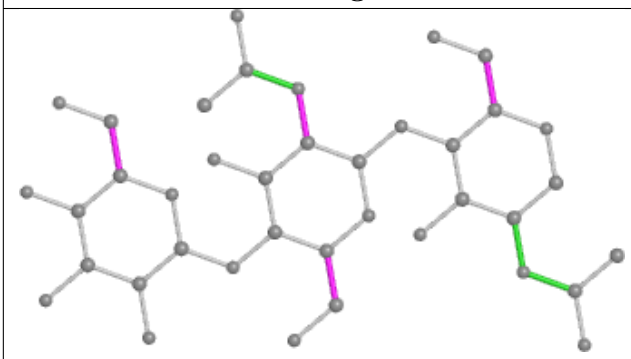
Oligosaccharide Chain V



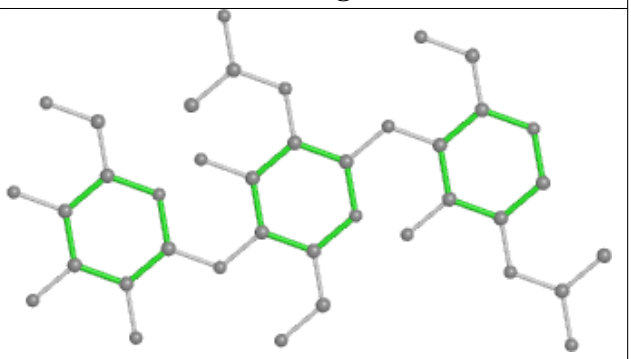
Bond lengths



Bond angles

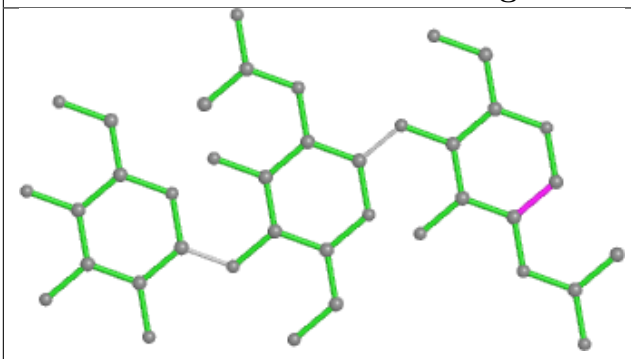


Torsions

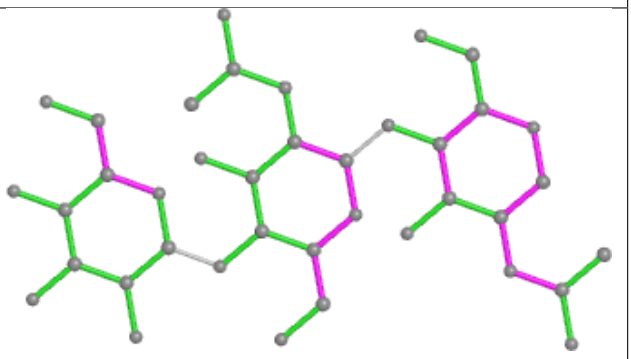


Rings

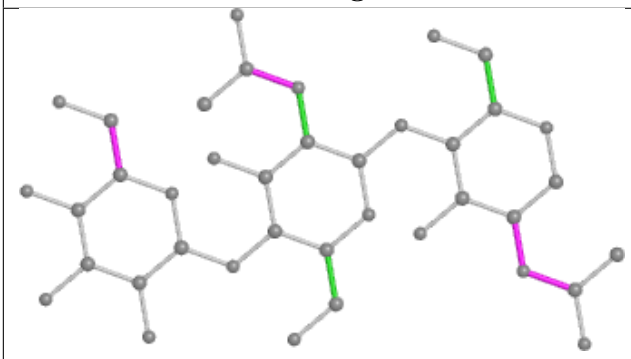
Oligosaccharide Chain c



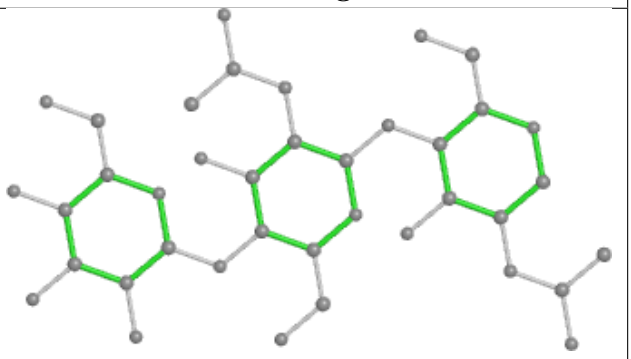
Bond lengths



Bond angles

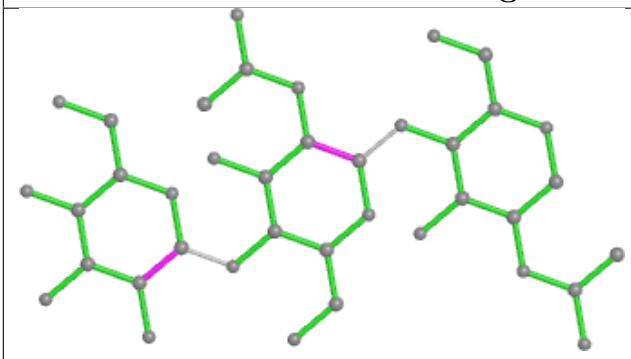


Torsions



Rings

Oligosaccharide Chain e



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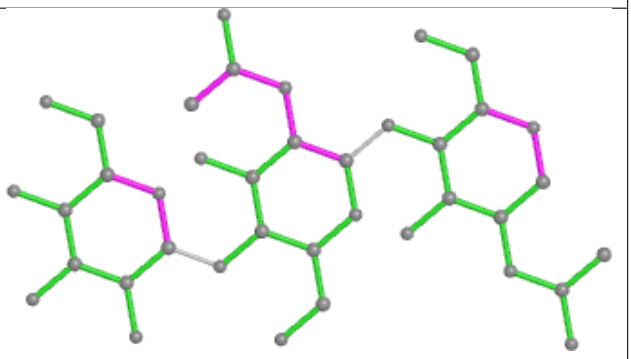

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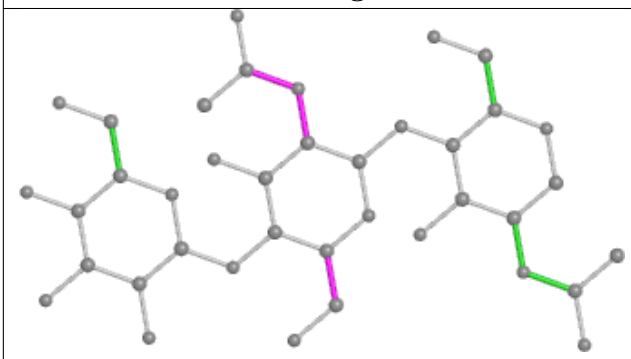
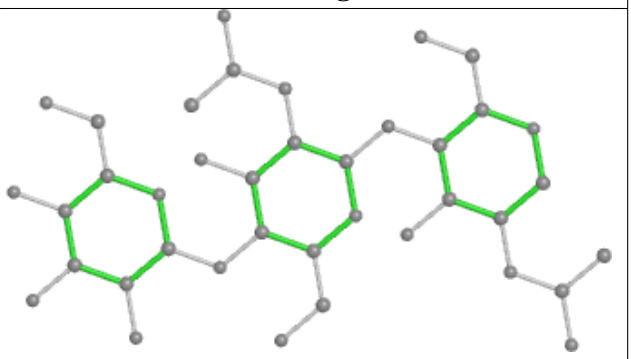
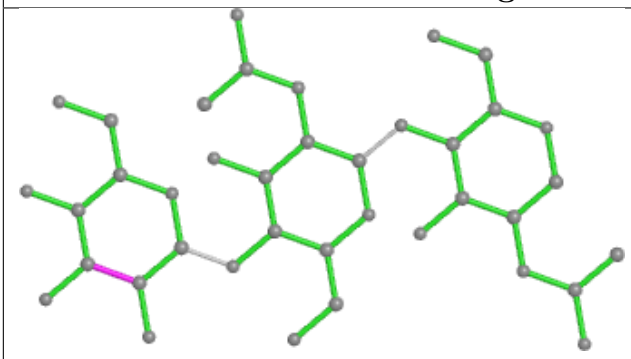


Torsions



Rings

Oligosaccharide Chain h



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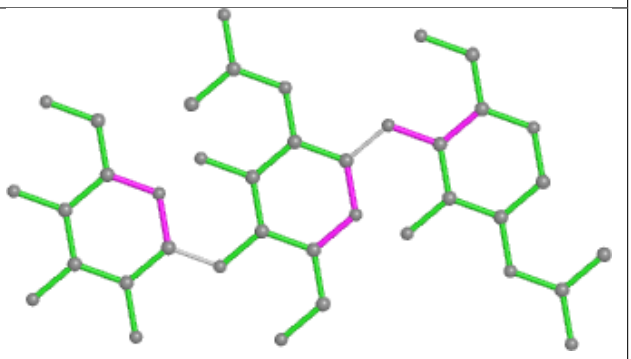

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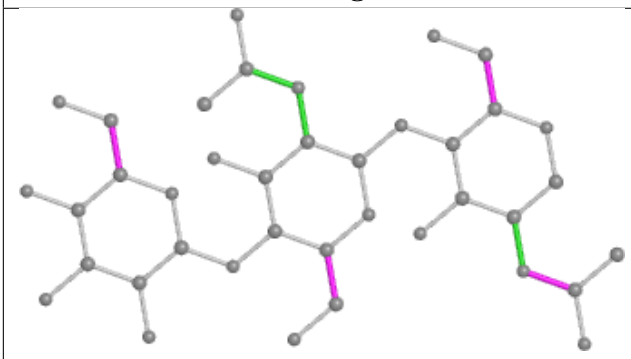

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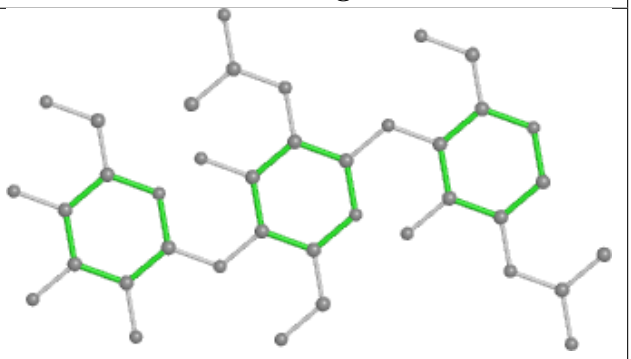
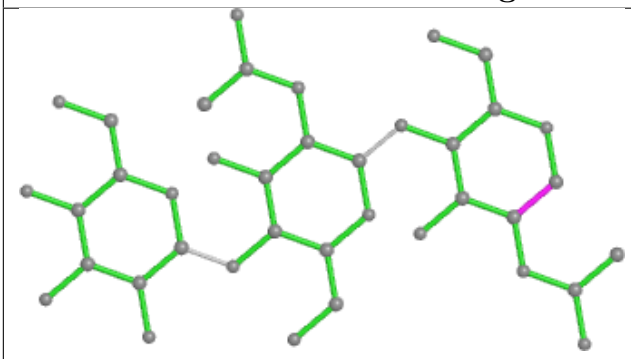


Rings

Oligosaccharide Chain o



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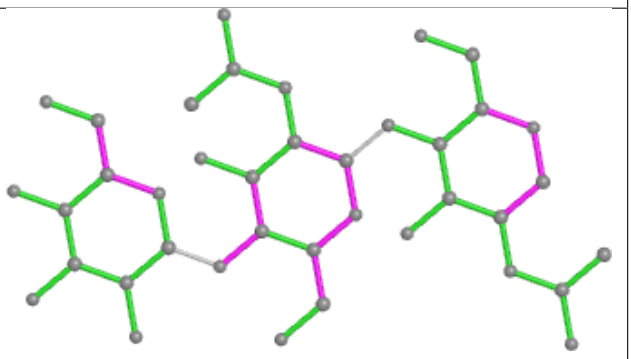

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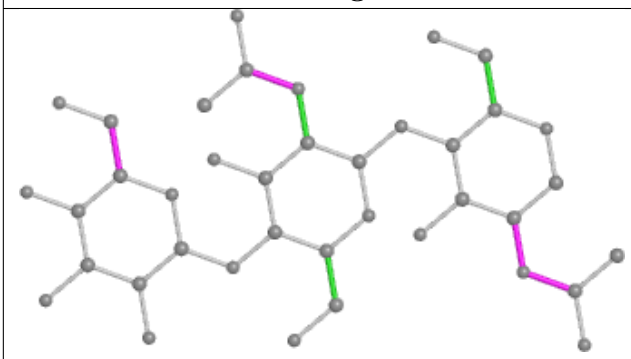

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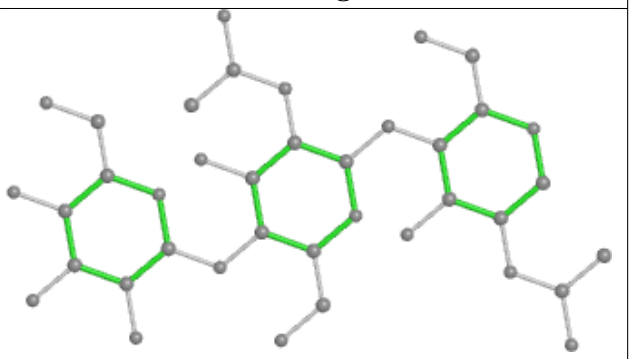
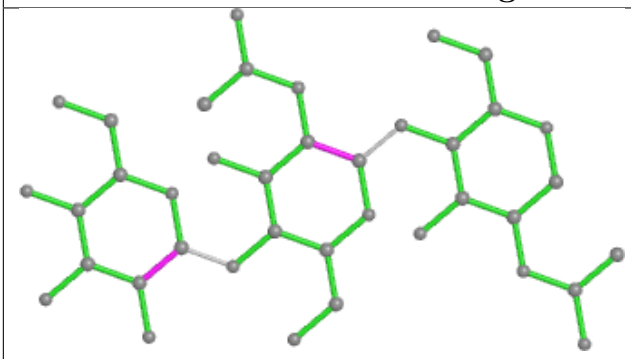


Rings

Oligosaccharide Chain q



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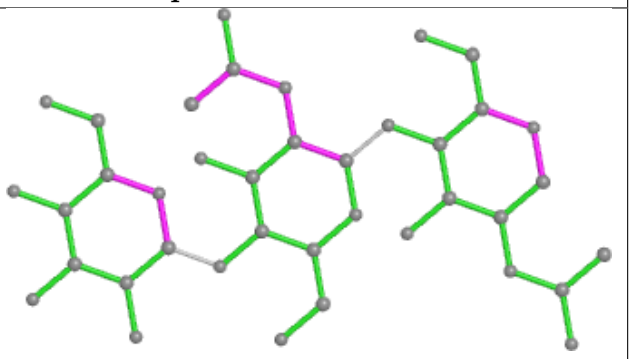

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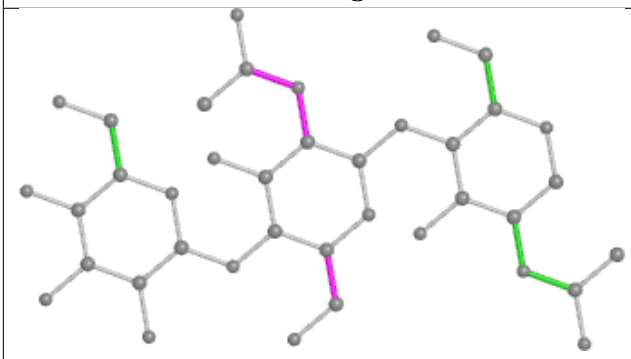

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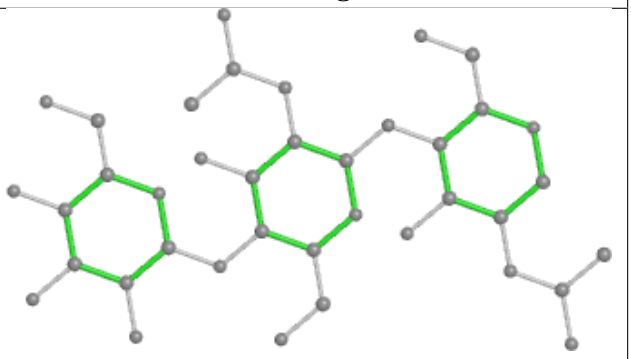
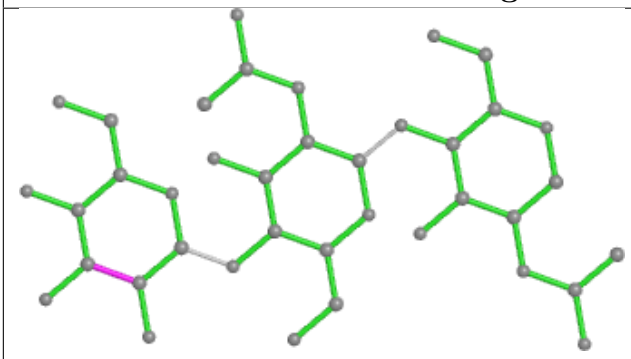


Rings

Oligosaccharide Chain t



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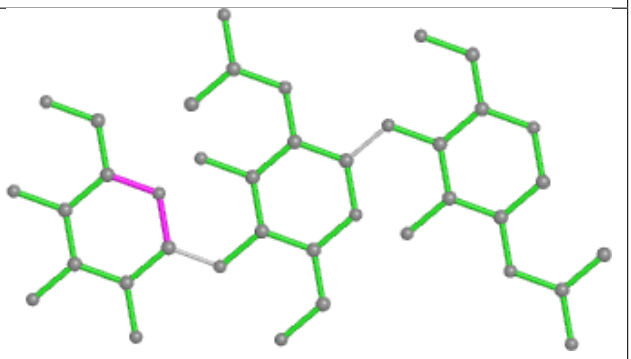

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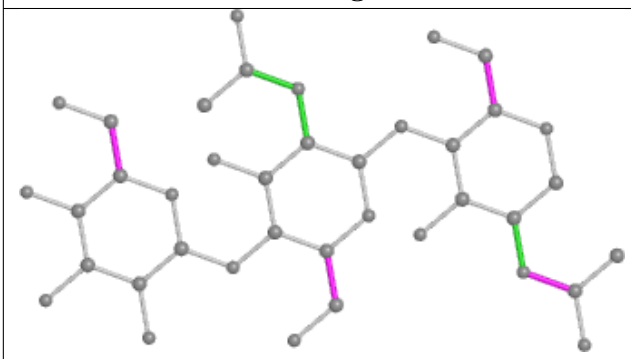

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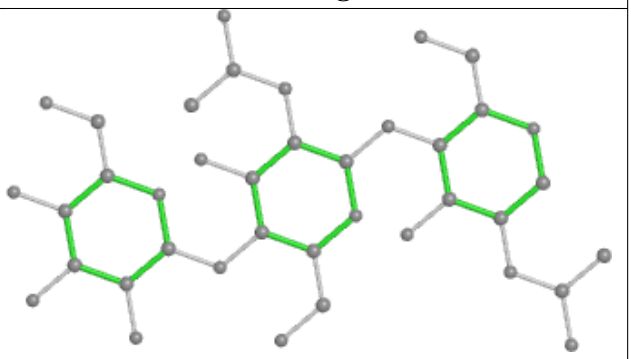
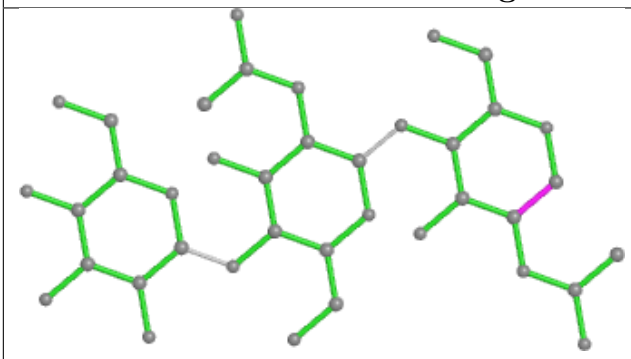


Rings

Oligosaccharide Chain 0



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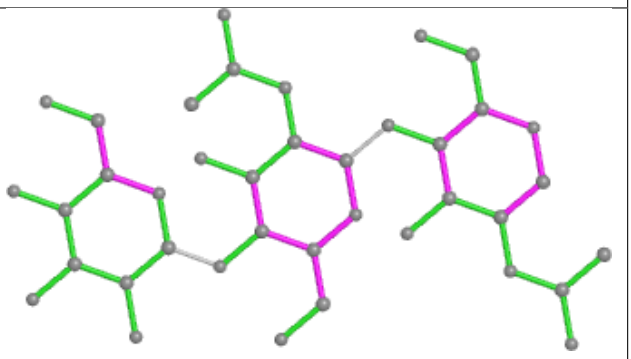

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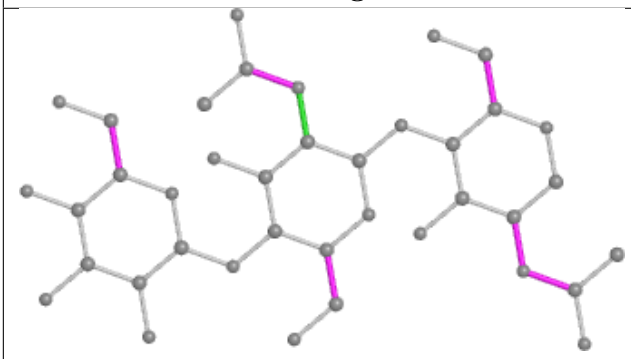

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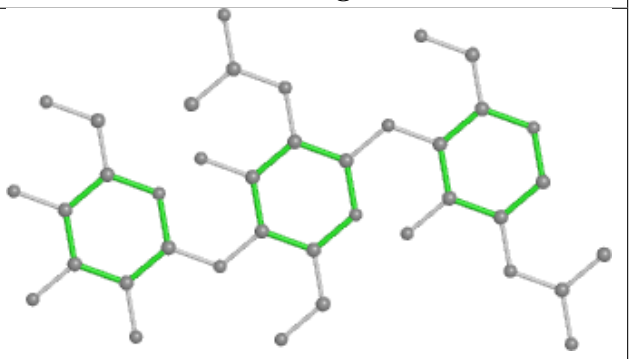
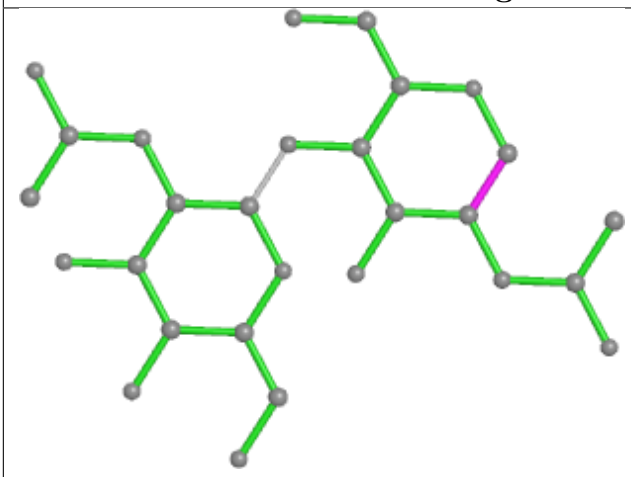


Rings

Oligosaccharide Chain T



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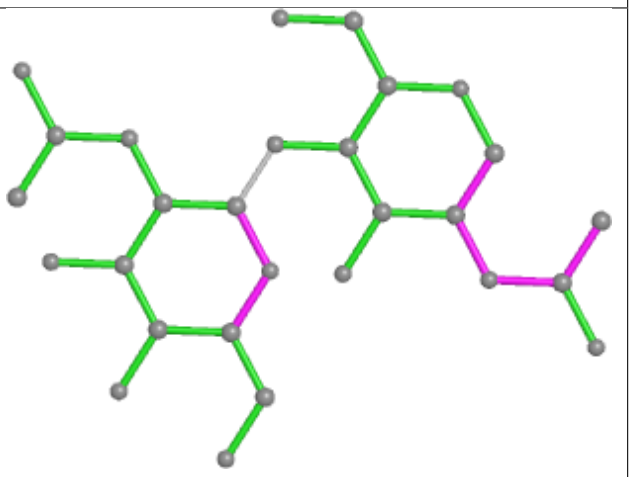

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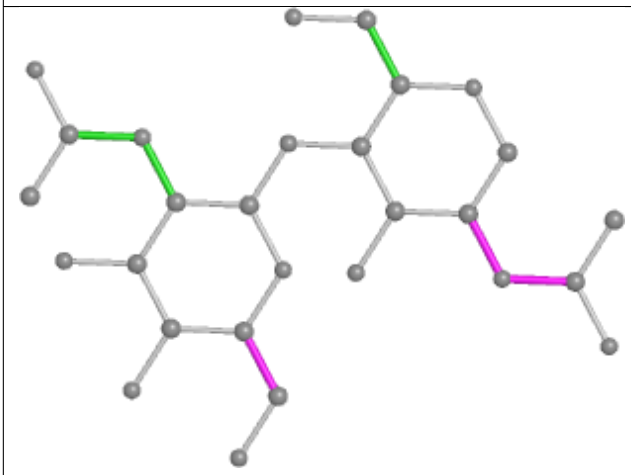

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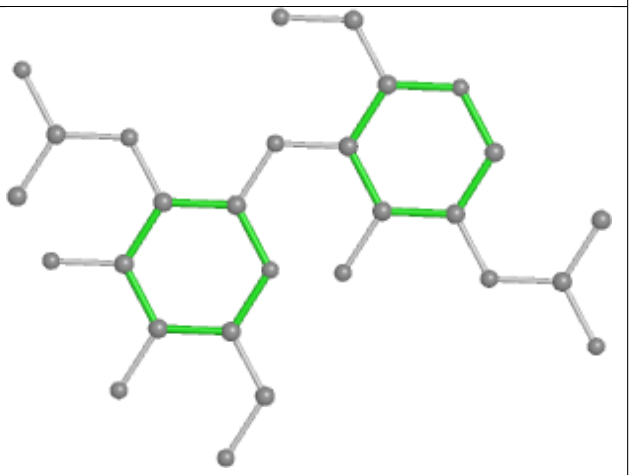
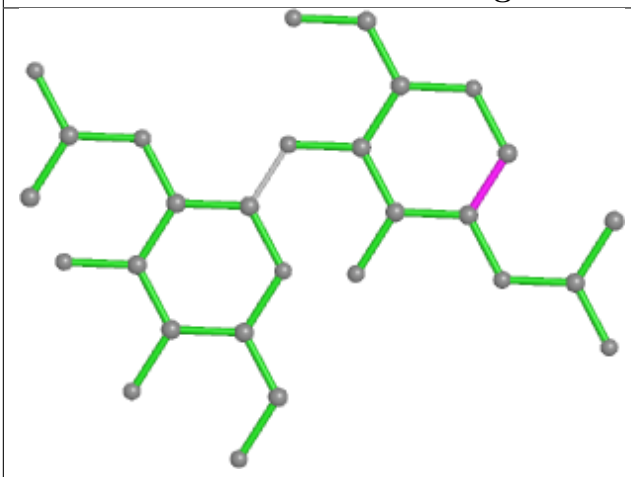


Rings

Oligosaccharide Chain U



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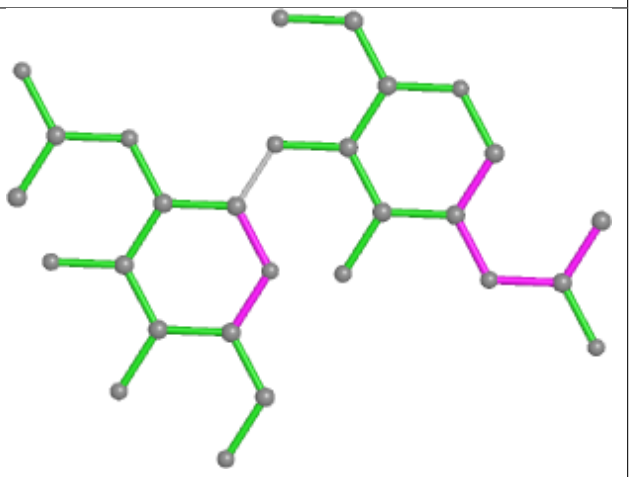

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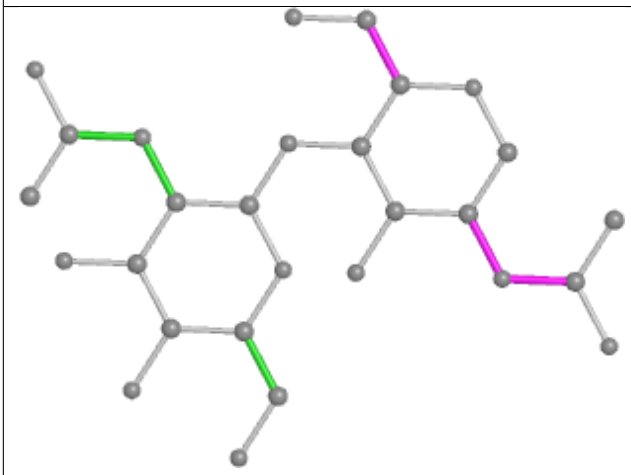

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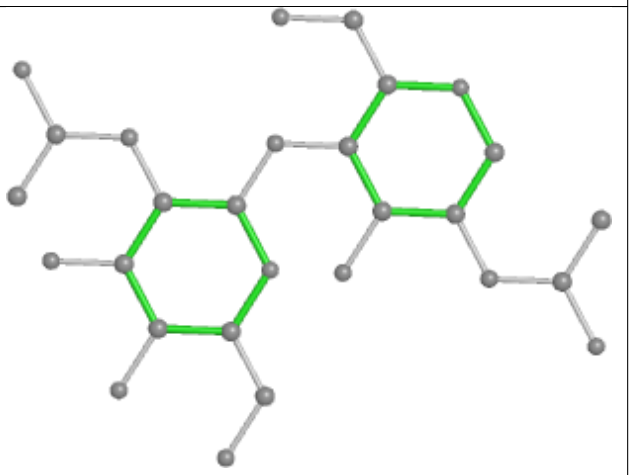

Rings

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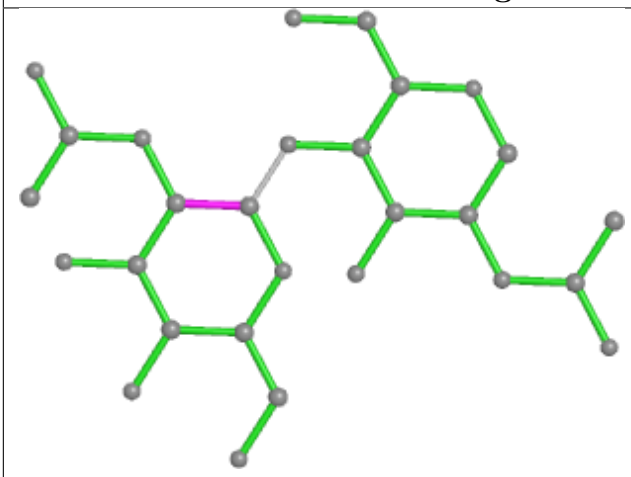

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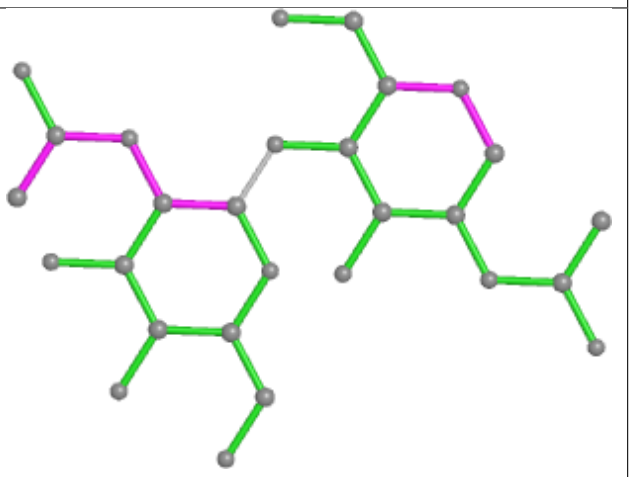

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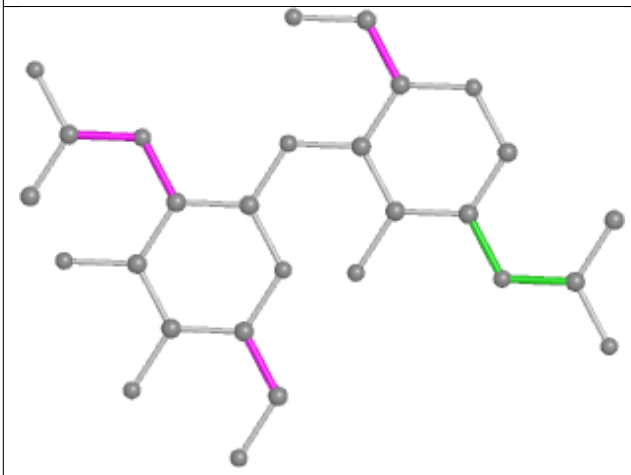

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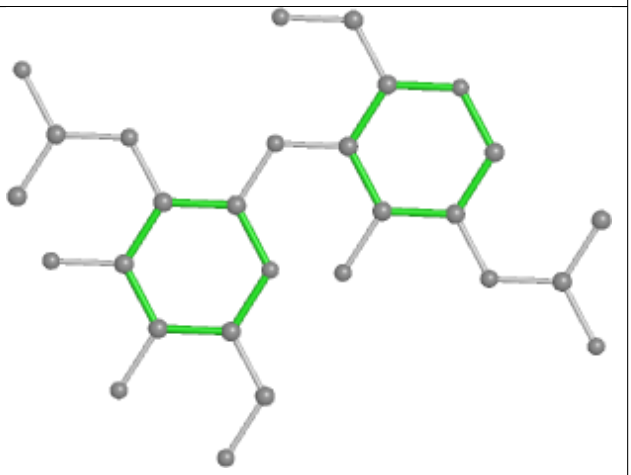
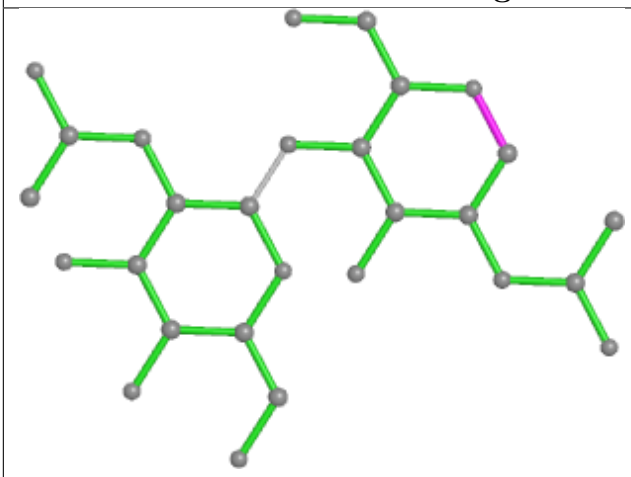


Rings

Oligosaccharide Chain Y



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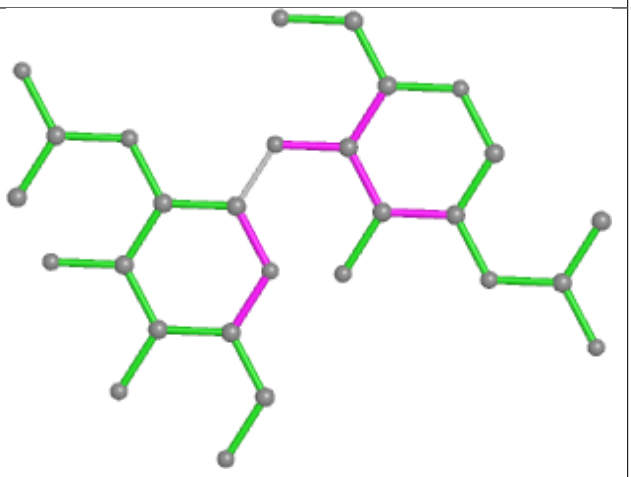

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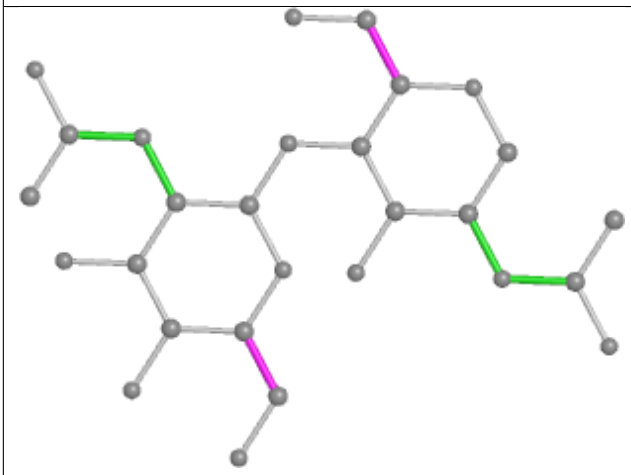

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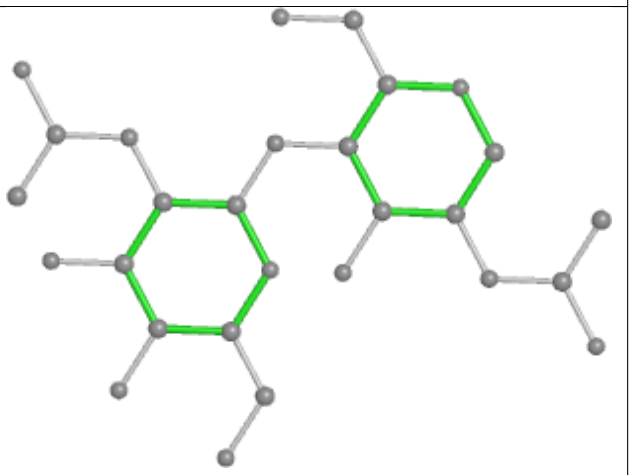
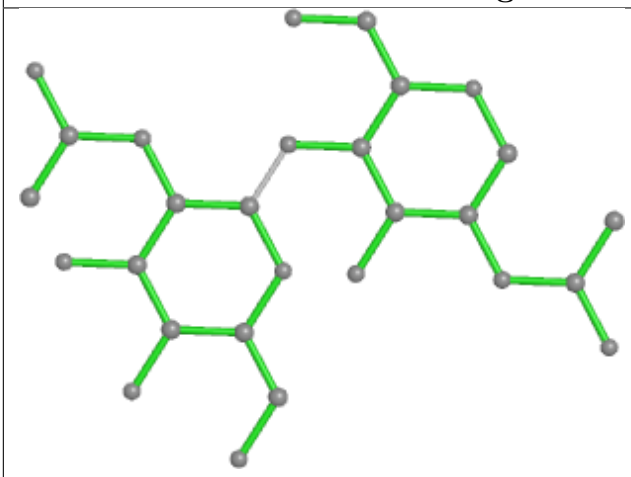


Rings

Oligosaccharide Chain Z



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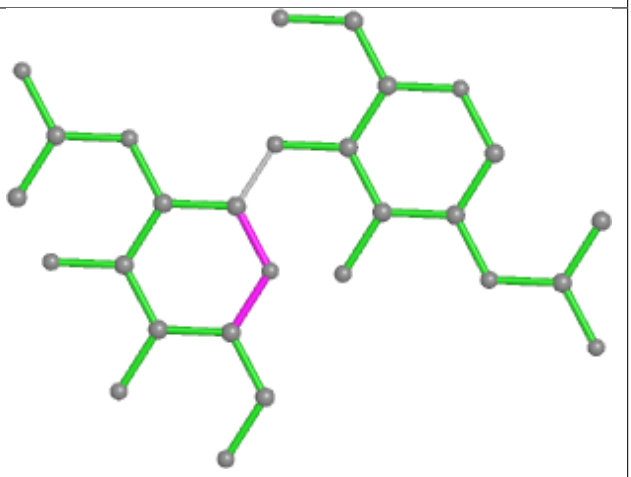

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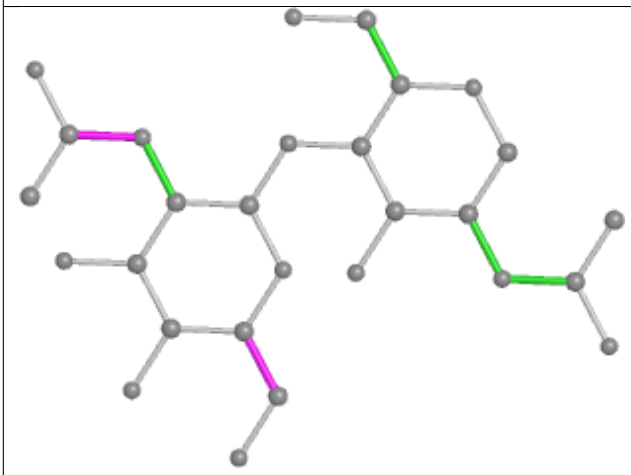

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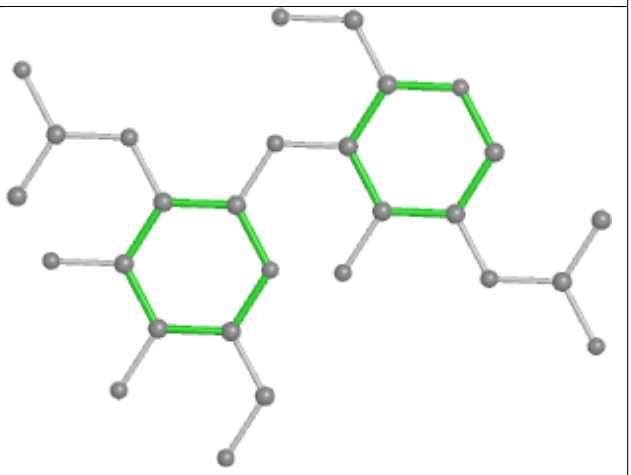
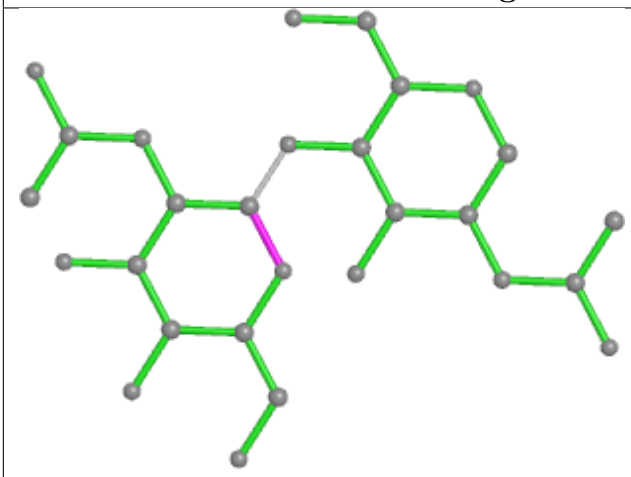


Rings

Oligosaccharide Chain a



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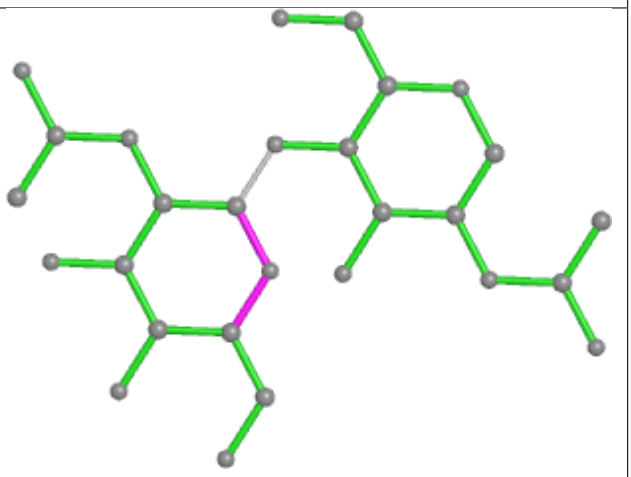
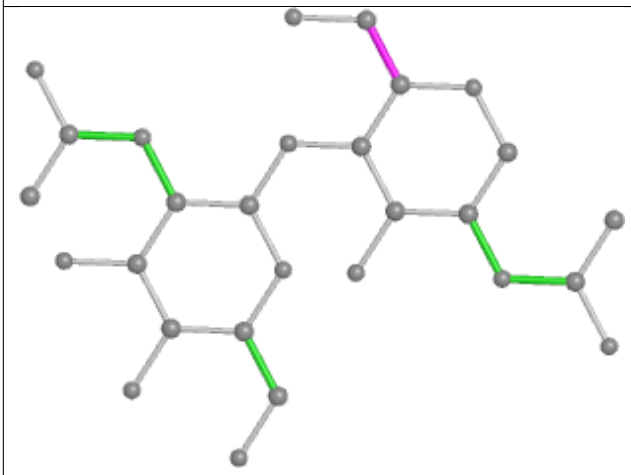


Bond angles



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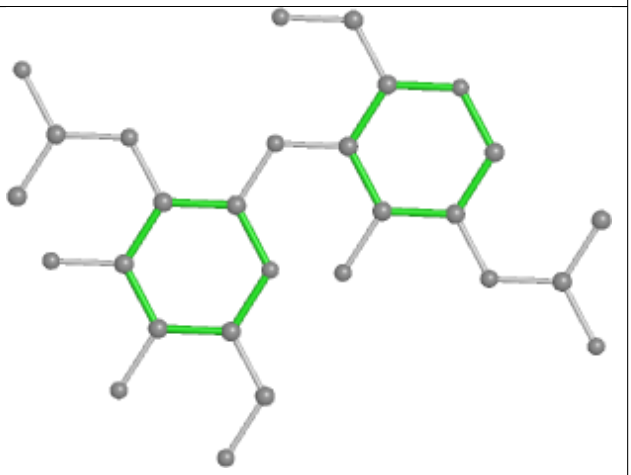
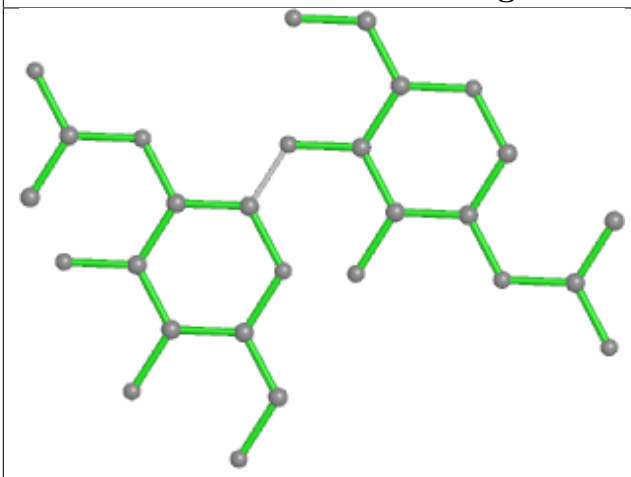


Rings

Oligosaccharide Chain b



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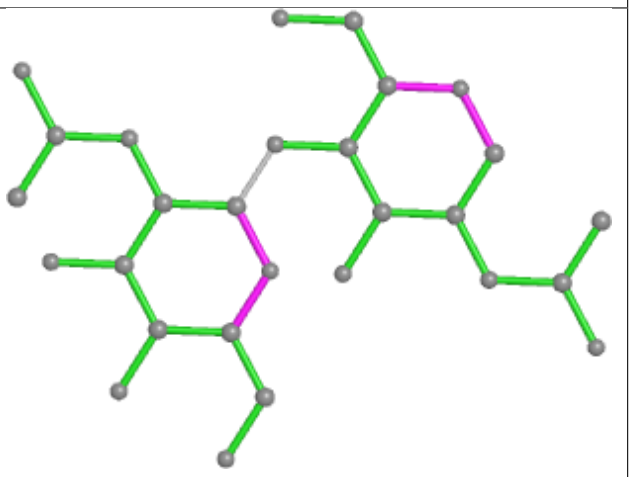
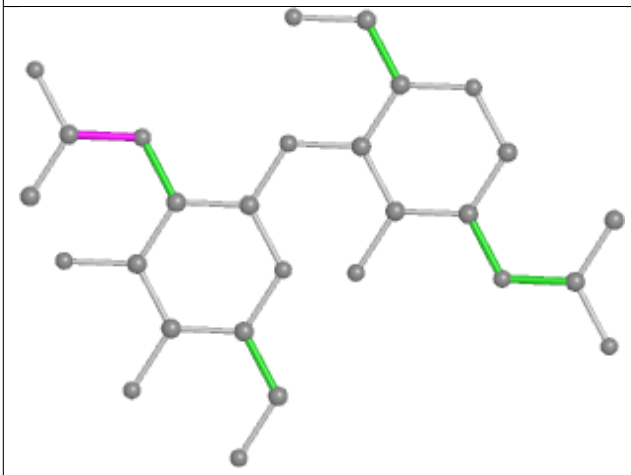


Bond angles



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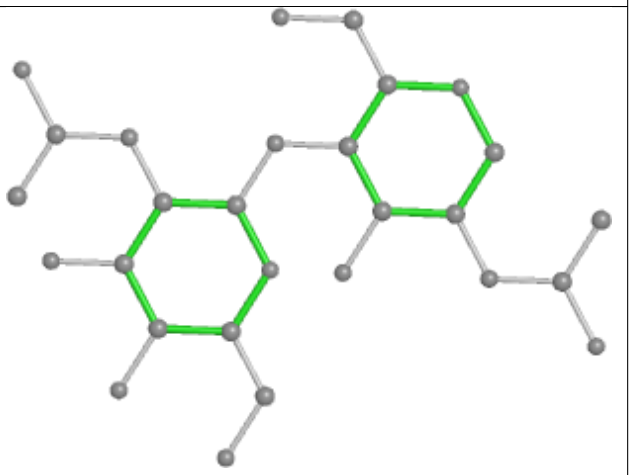
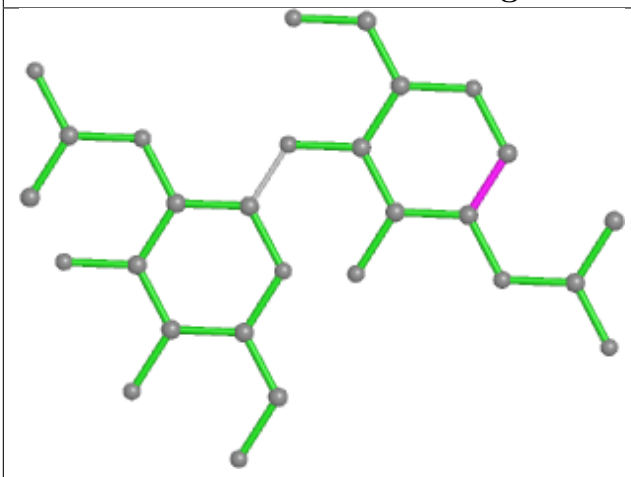


Rings

Oligosaccharide Chain f



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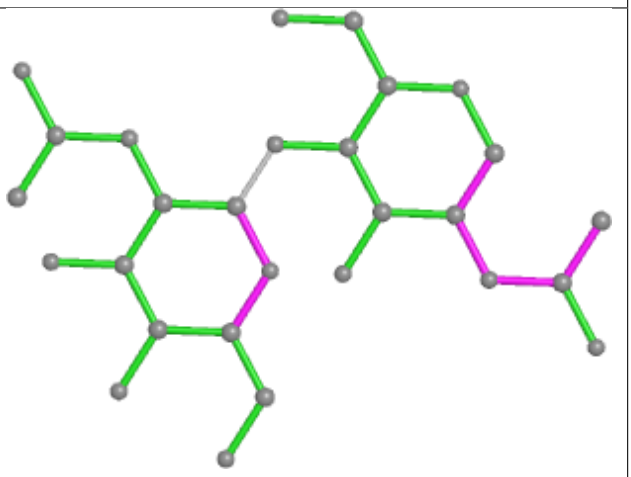
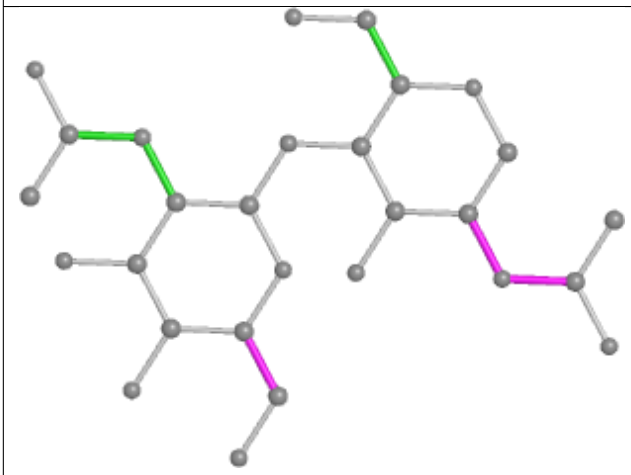
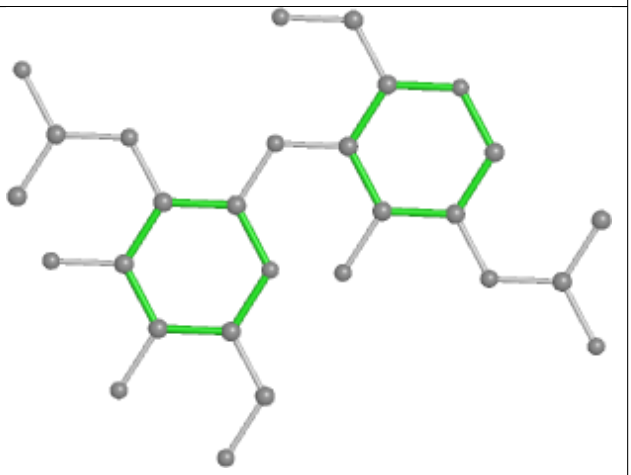


Bond angles

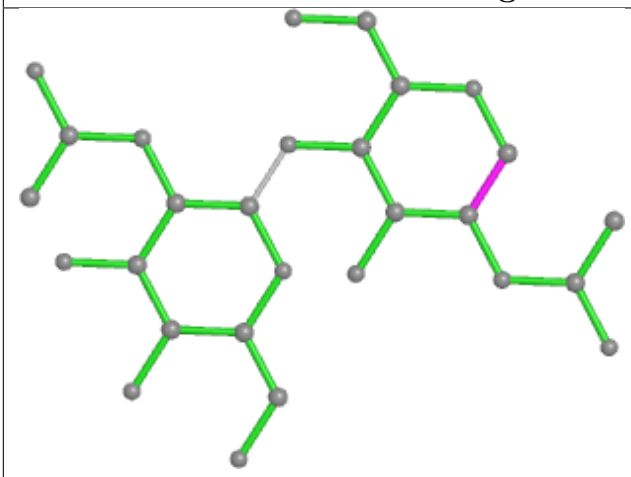


Torsions

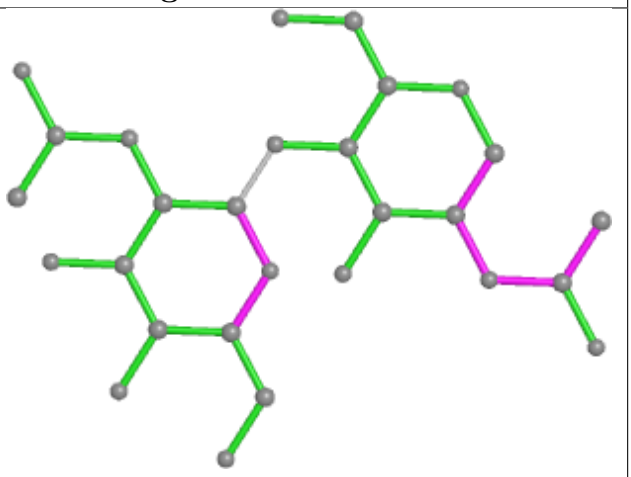


Rings

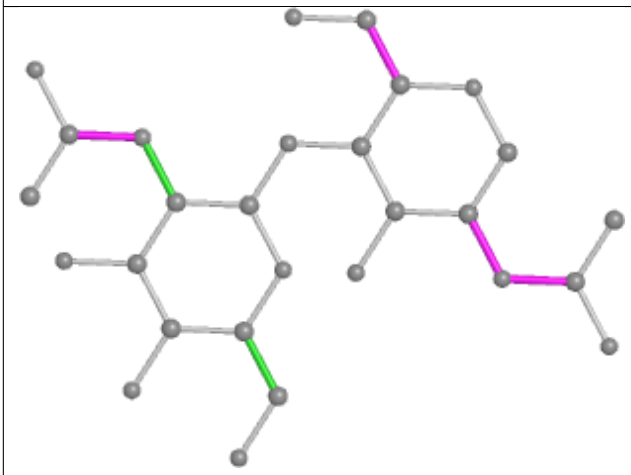
Oligosaccharide Chain g



Bond lengths



Bond angles



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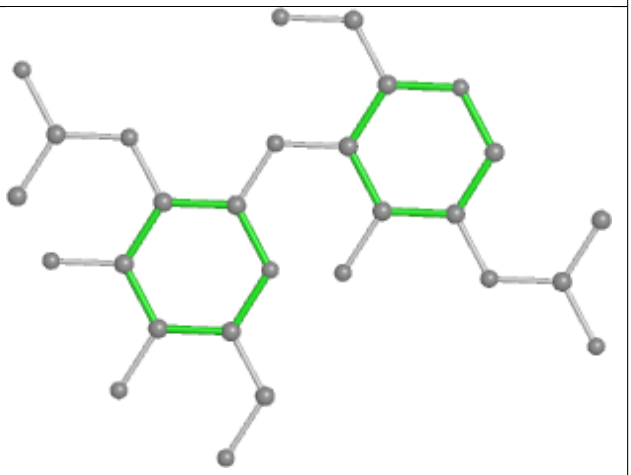
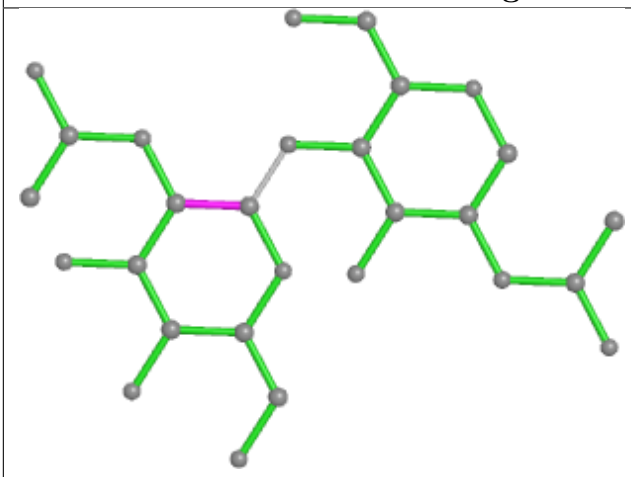


Rings

Oligosaccharide Chain j



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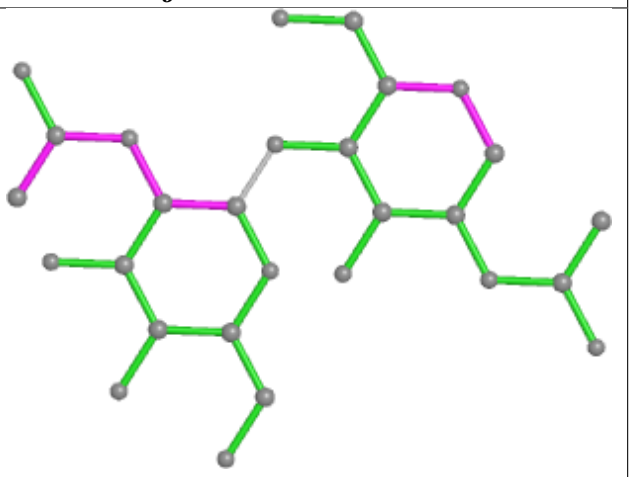
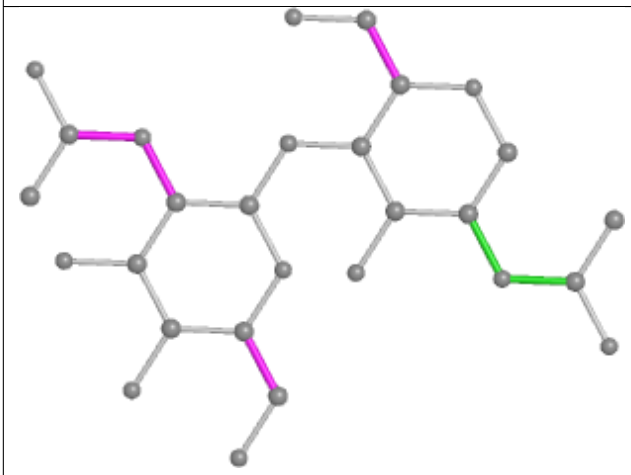


Bond angles



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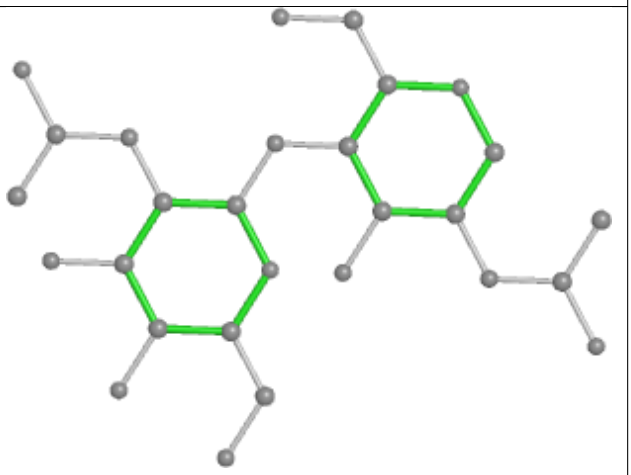
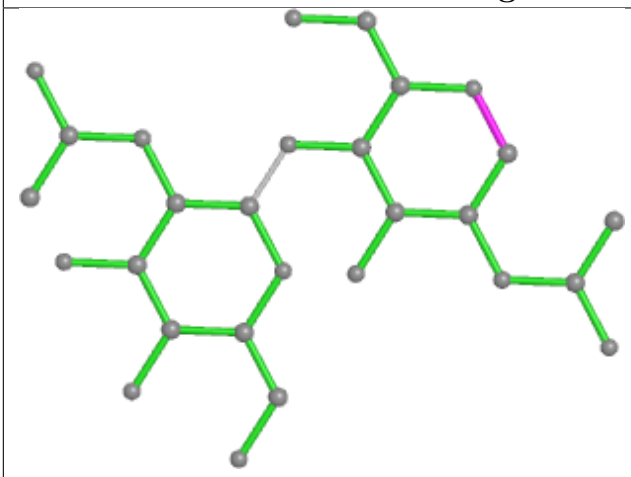


Rings

Oligosaccharide Chain k



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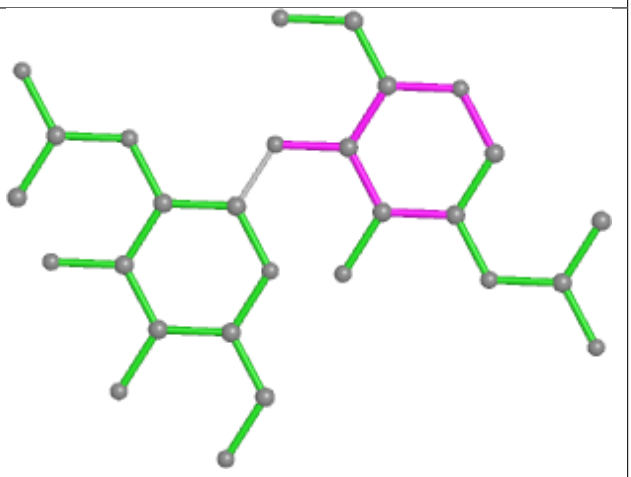
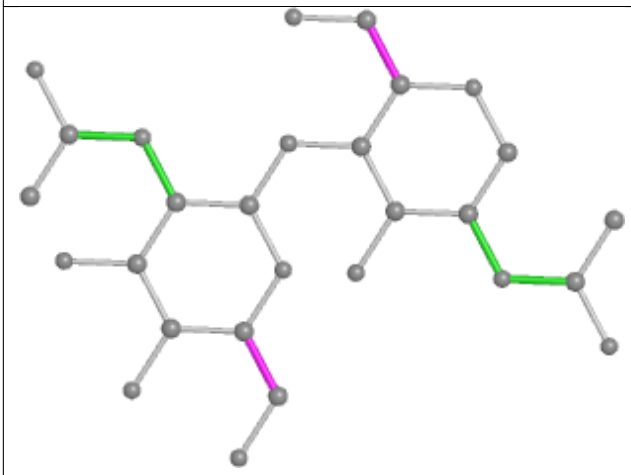


Bond angles



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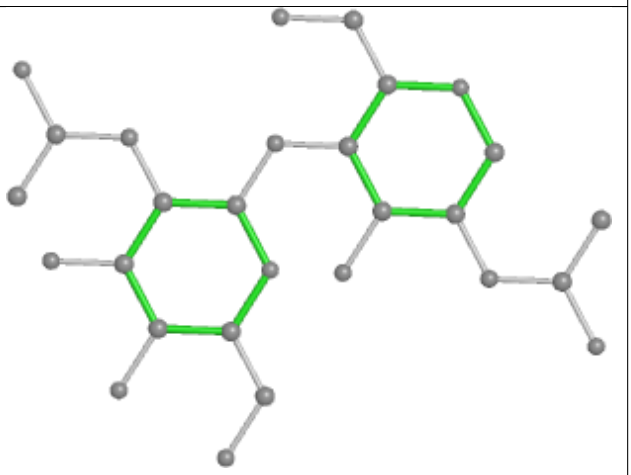
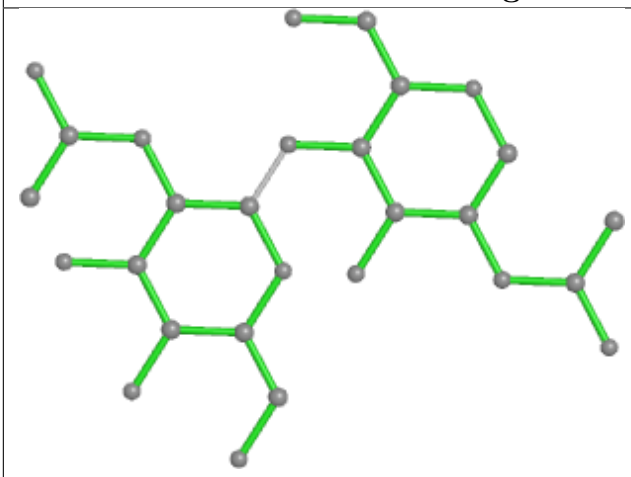


Rings

Oligosaccharide Chain l



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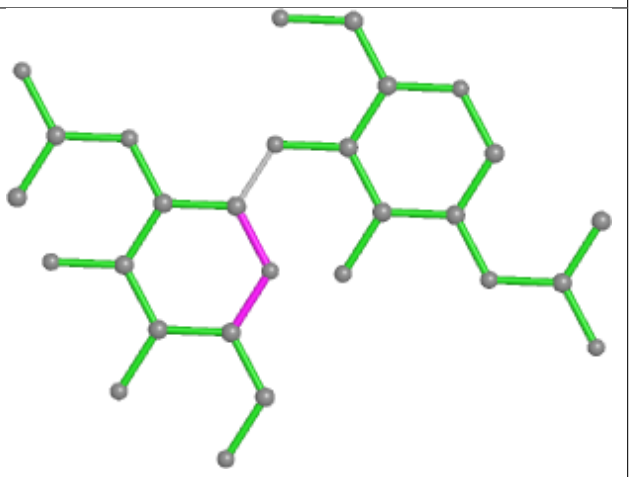
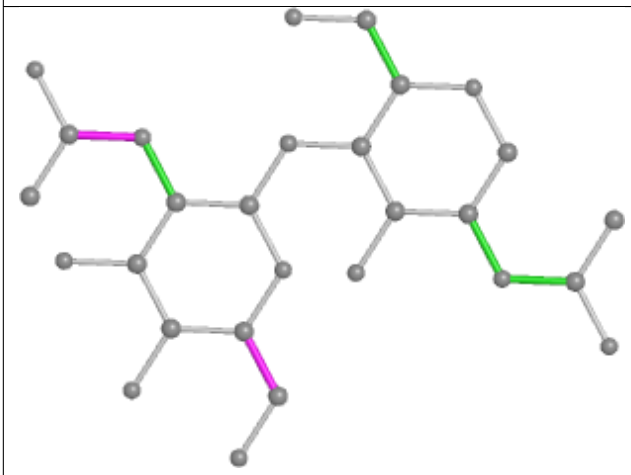


Bond angles



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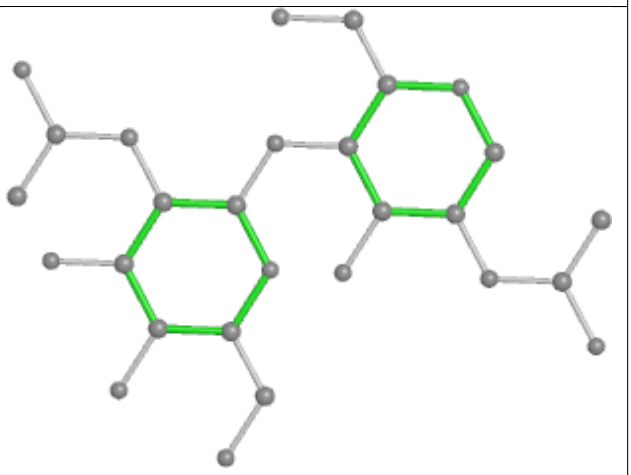
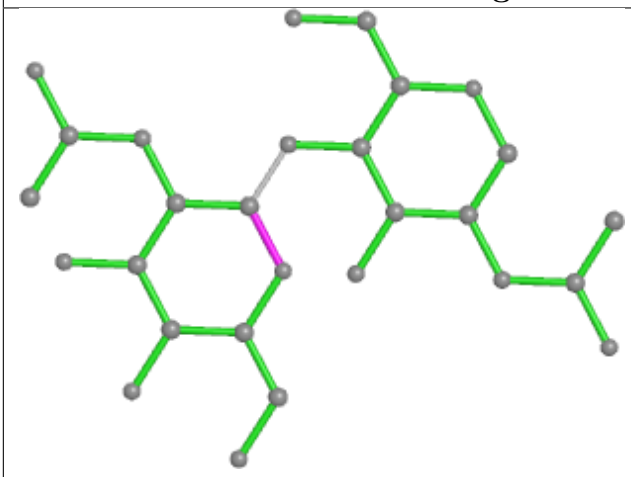


Rings

Oligosaccharide Chain m



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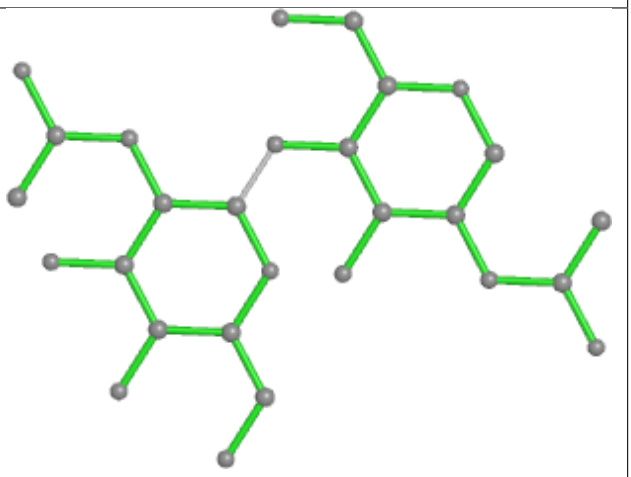

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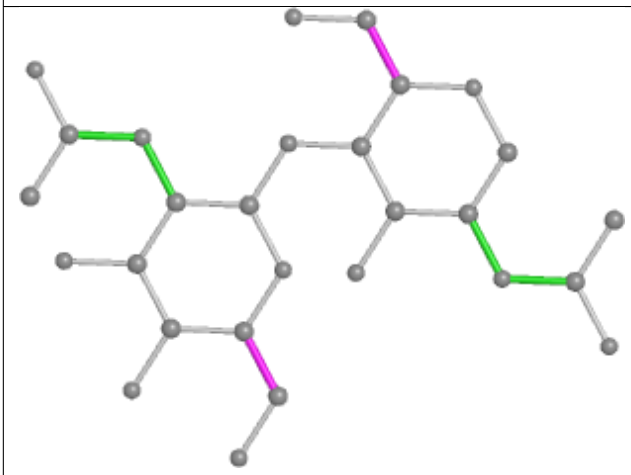

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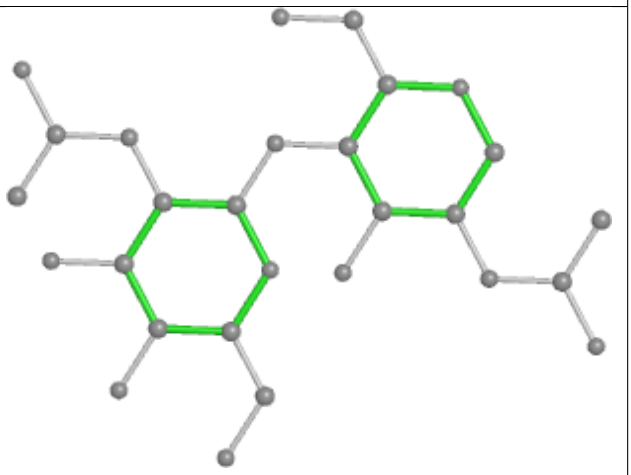
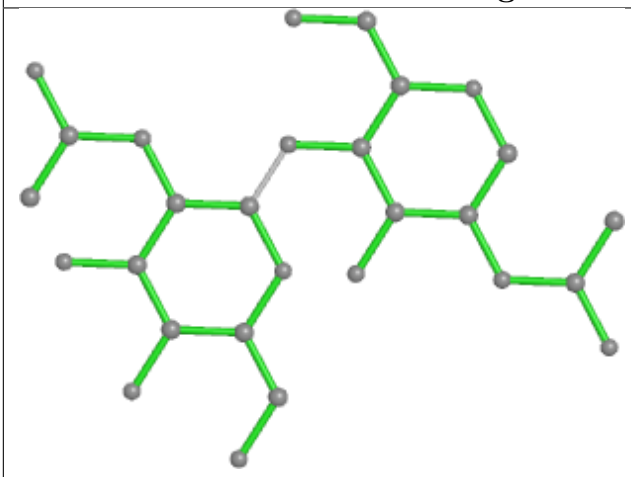
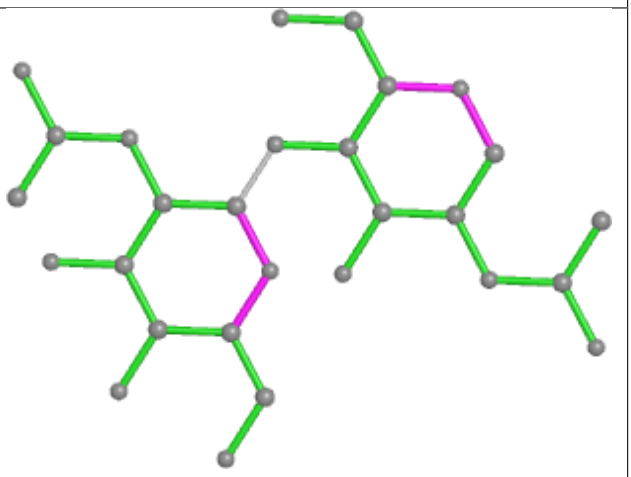
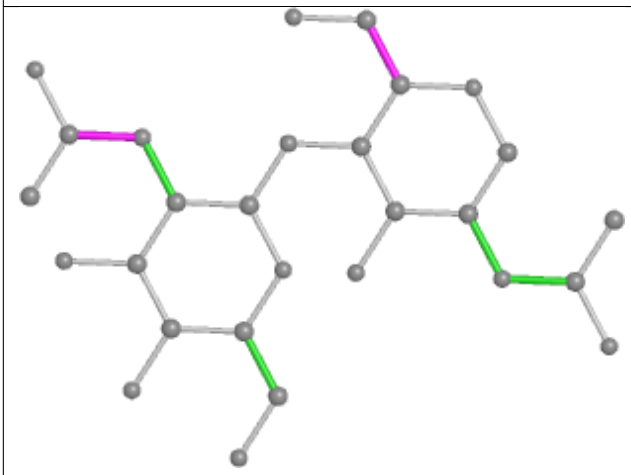
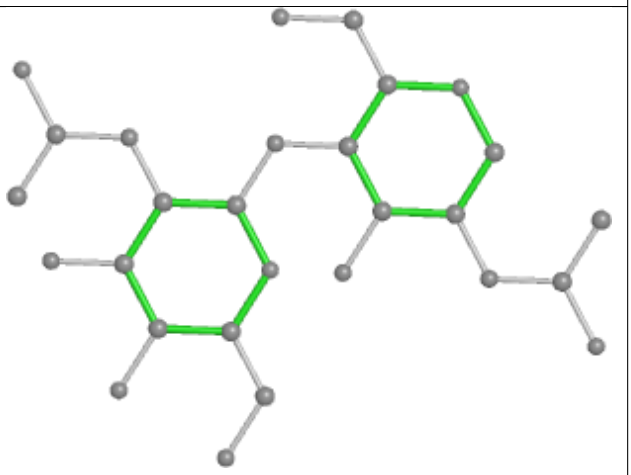
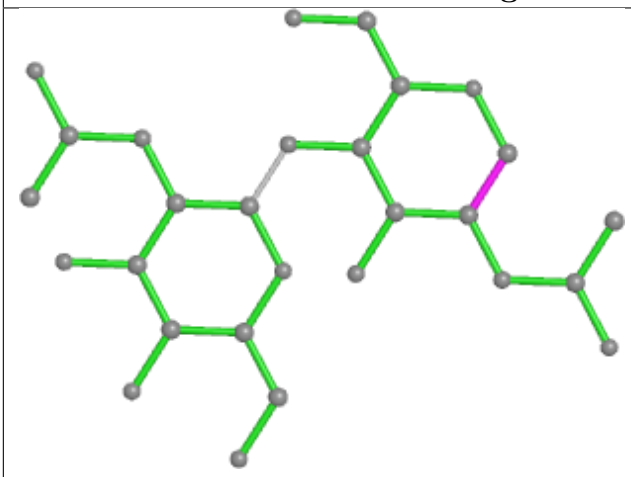


Rings

Oligosaccharide Chain n	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

Oligosaccharide Chain r



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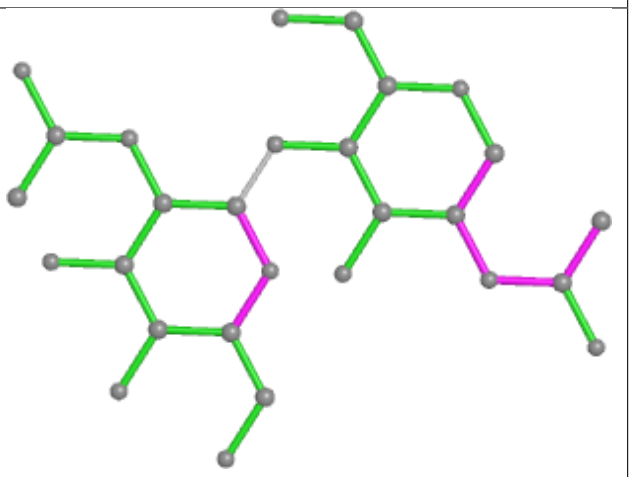

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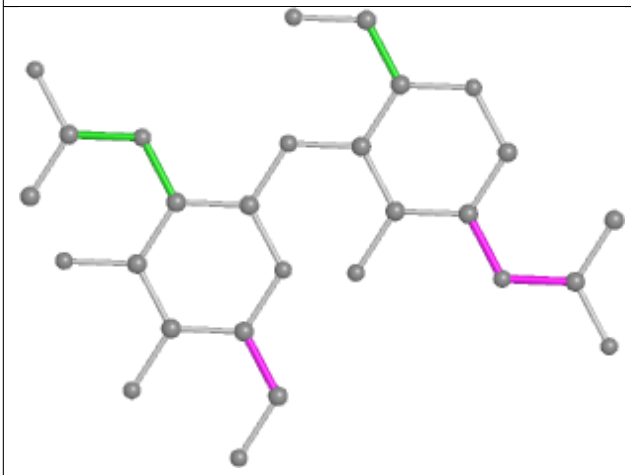

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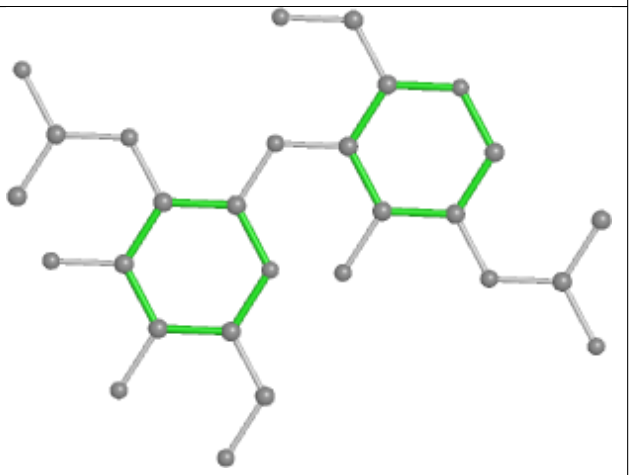
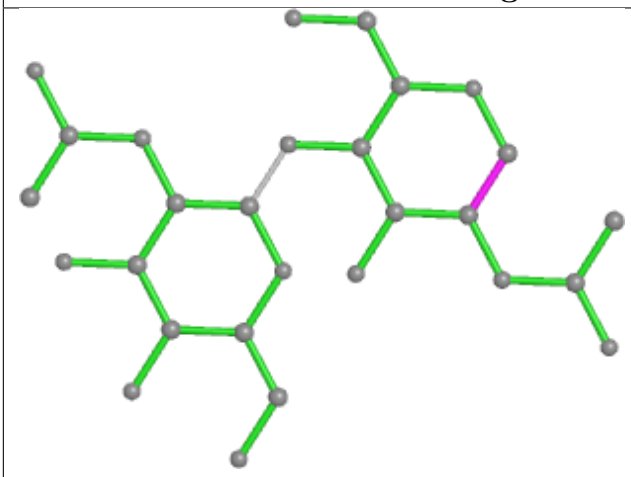


Rings

Oligosaccharide Chain s



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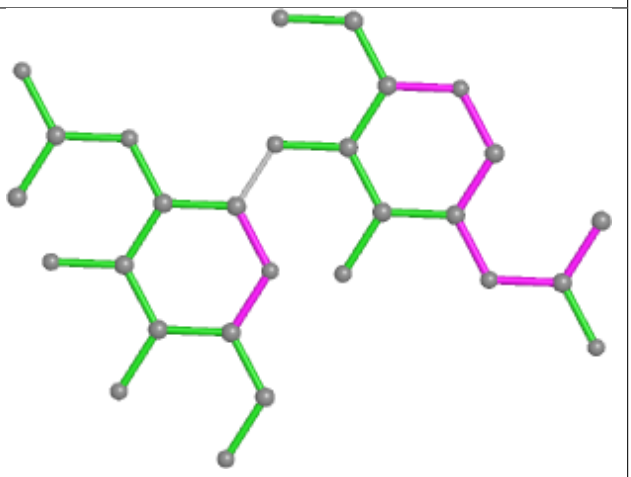

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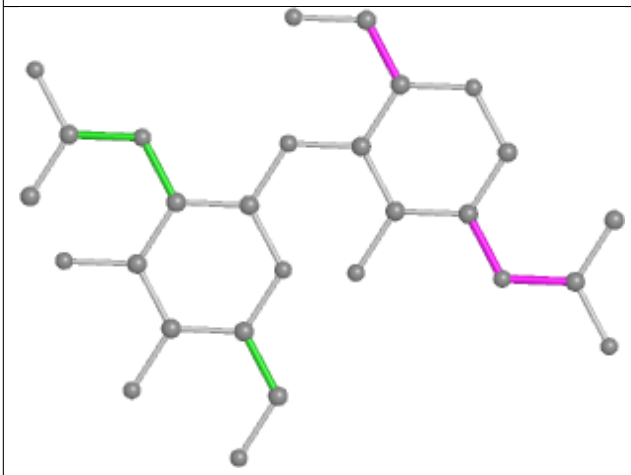

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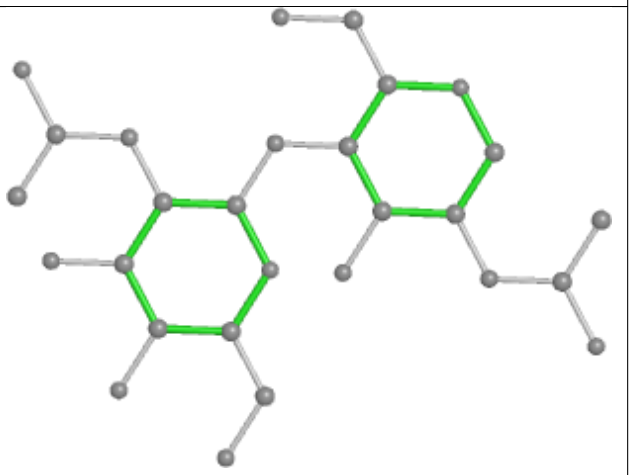
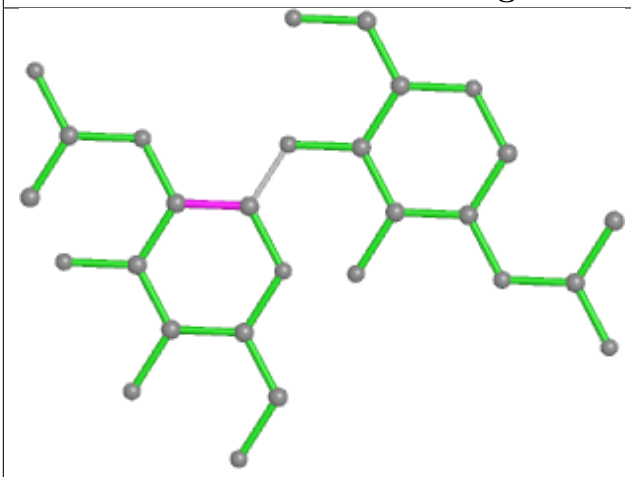


Rings

Oligosaccharide Chain v



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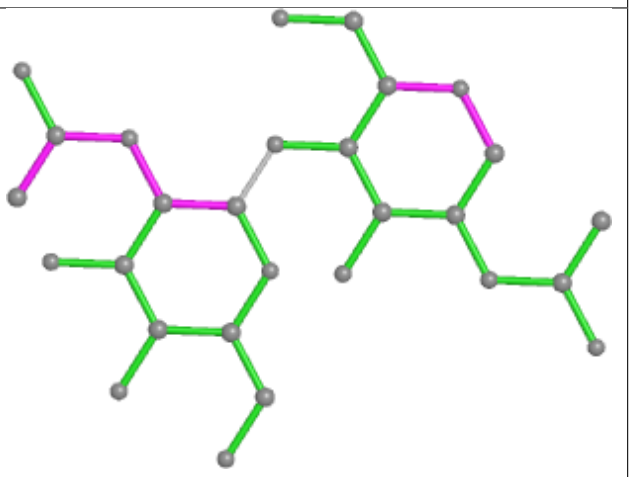

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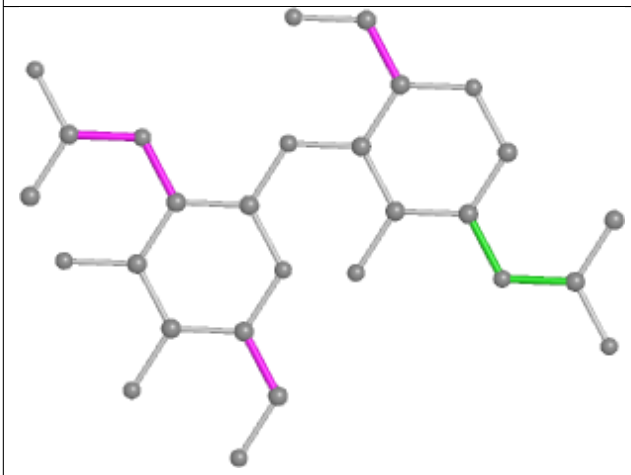

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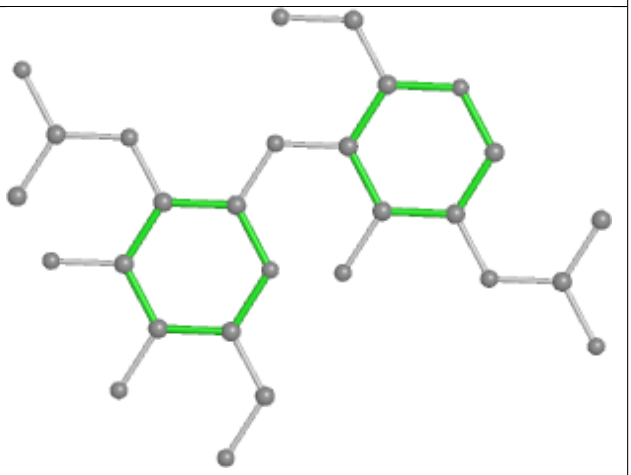
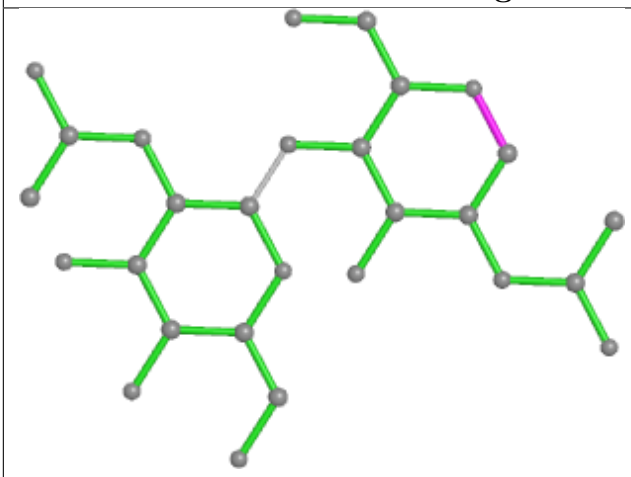


Rings

Oligosaccharide Chain w



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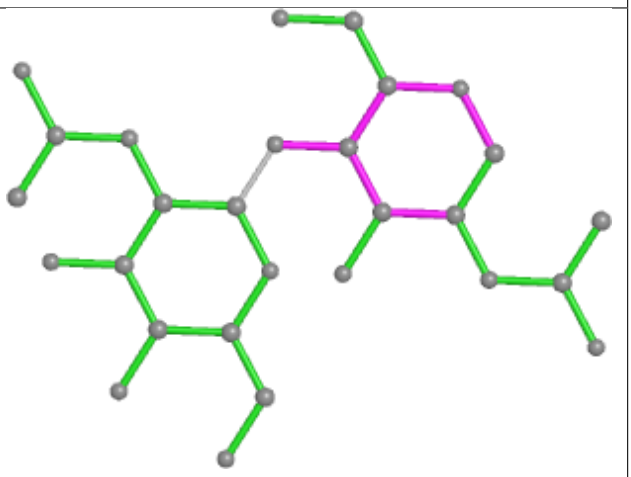
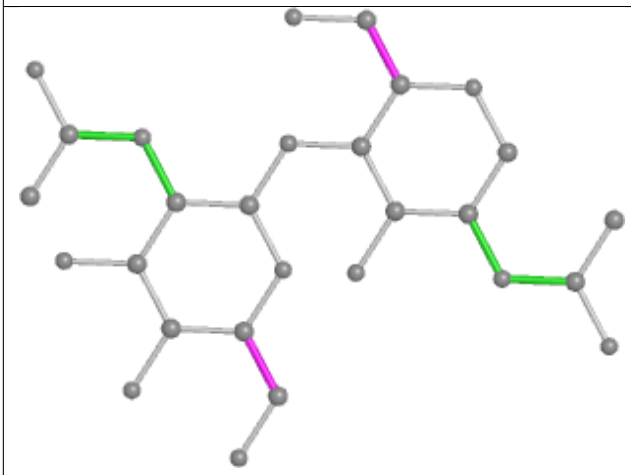


Bond angles



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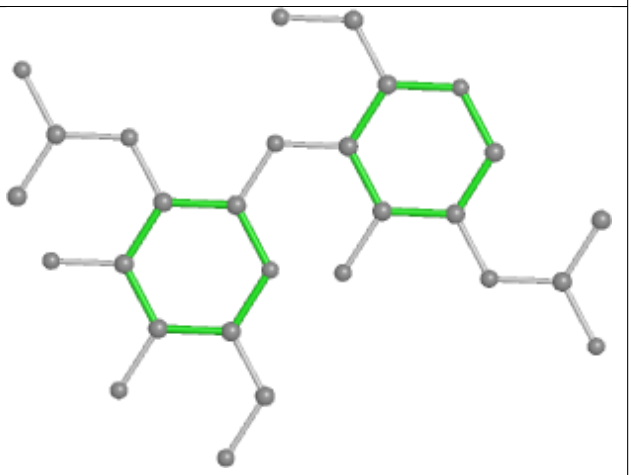
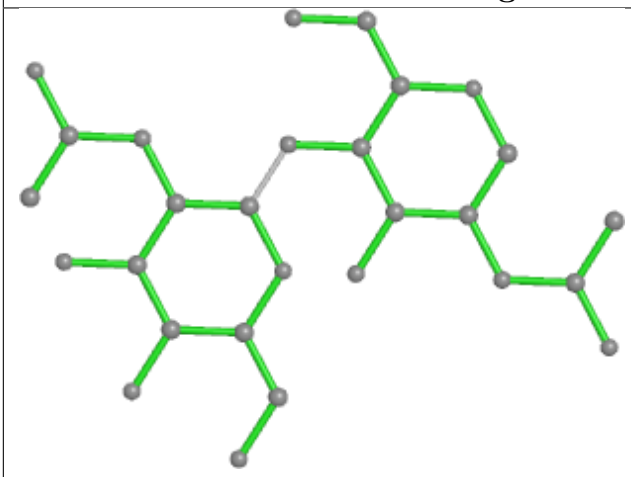


Rings

Oligosaccharide Chain x



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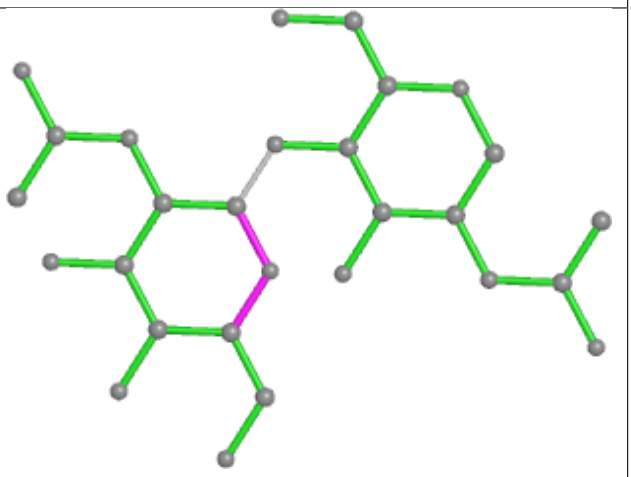
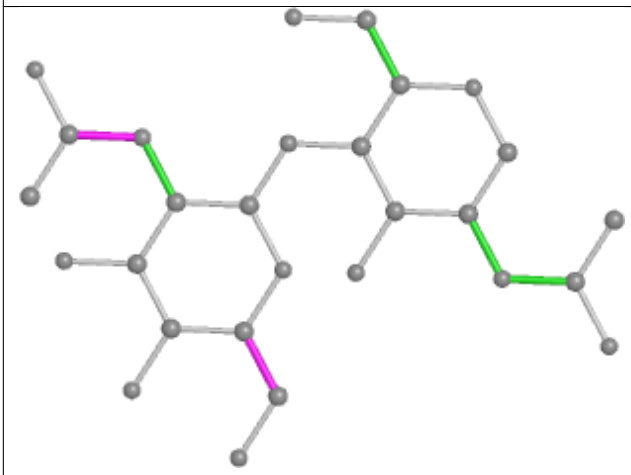


Bond angles



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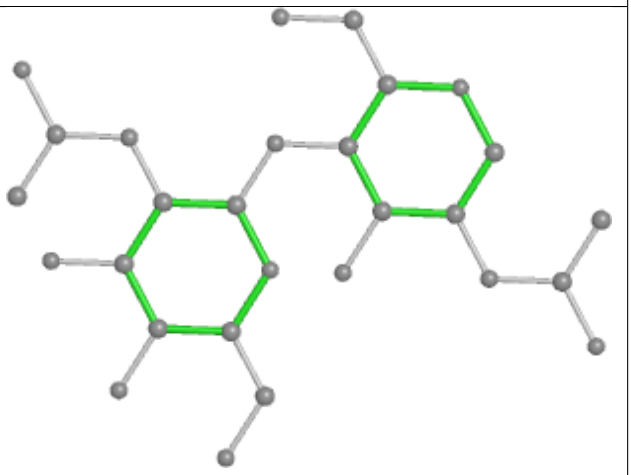
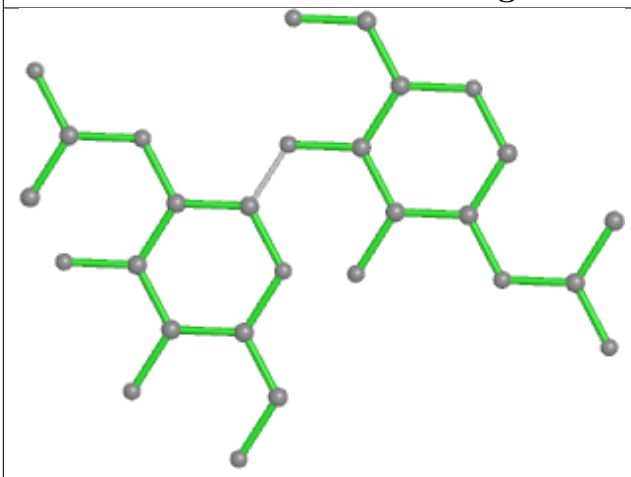


Rings

Oligosaccharide Chain y



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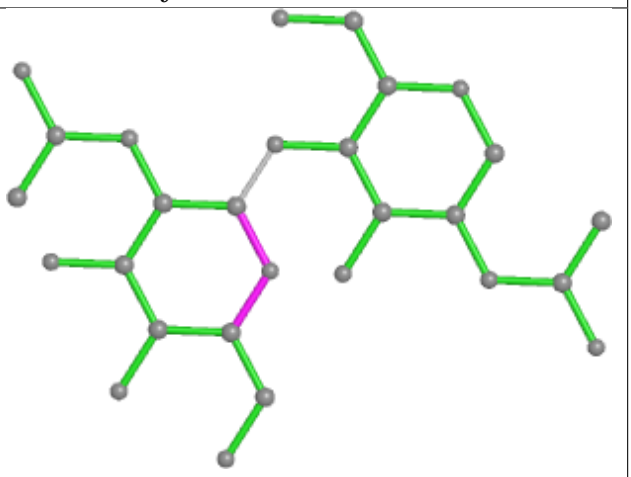
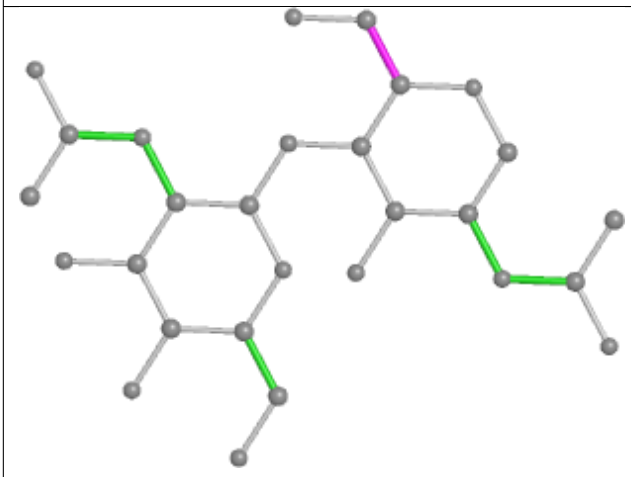


Bond angles



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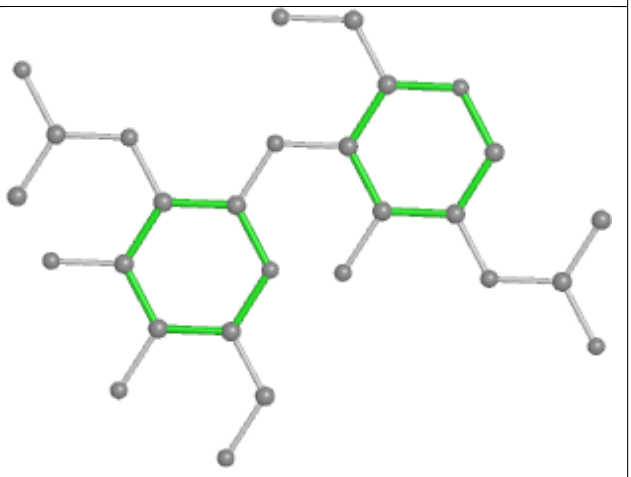
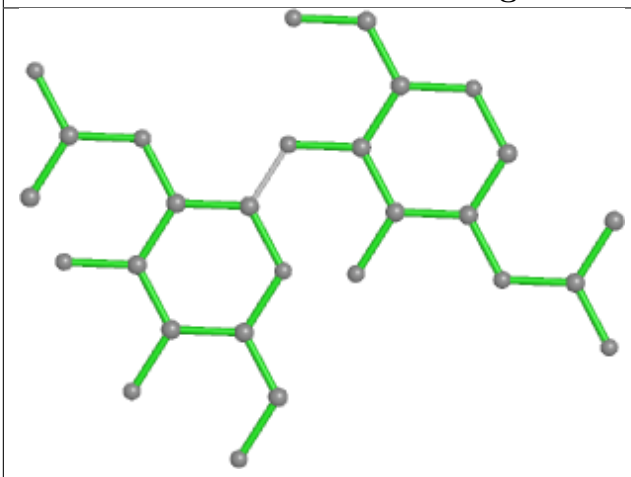


Rings

Oligosaccharide Chain z



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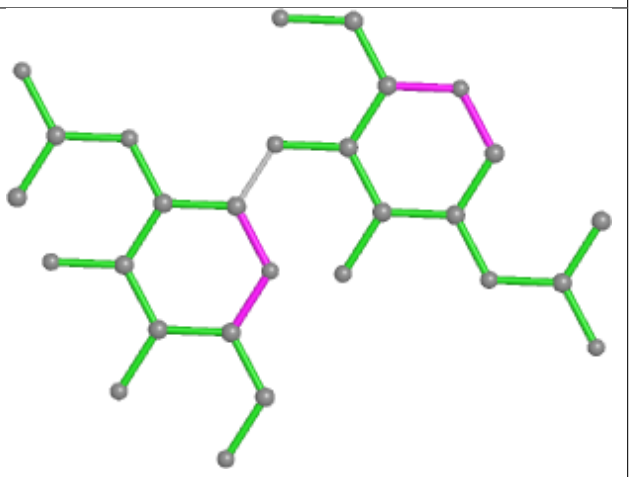
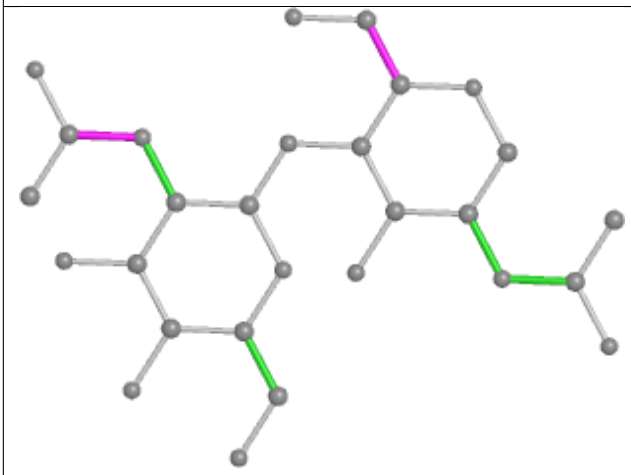


Bond angles



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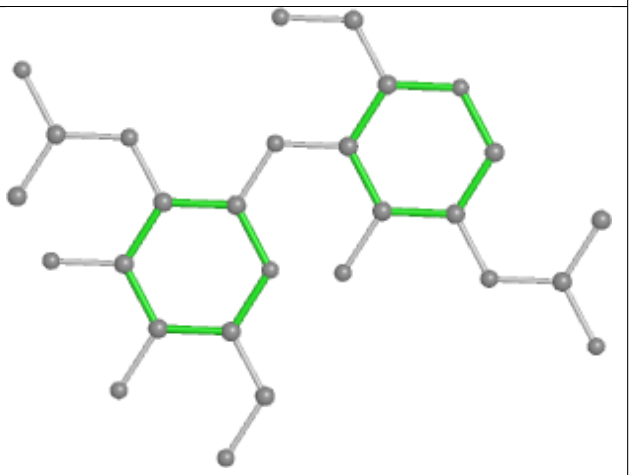
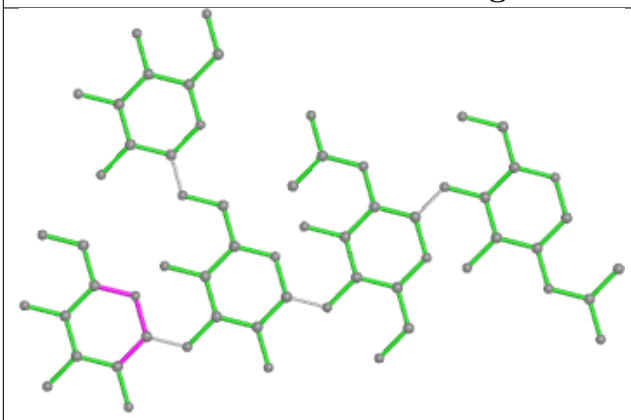
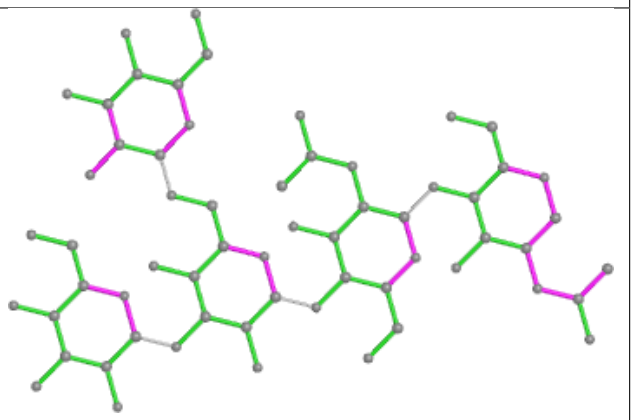


Rings

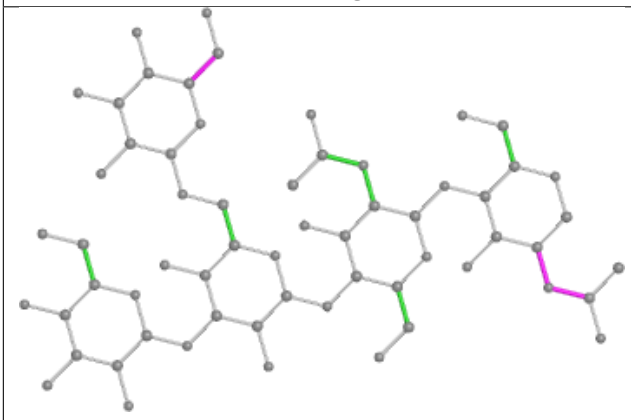
Oligosaccharide Chain W



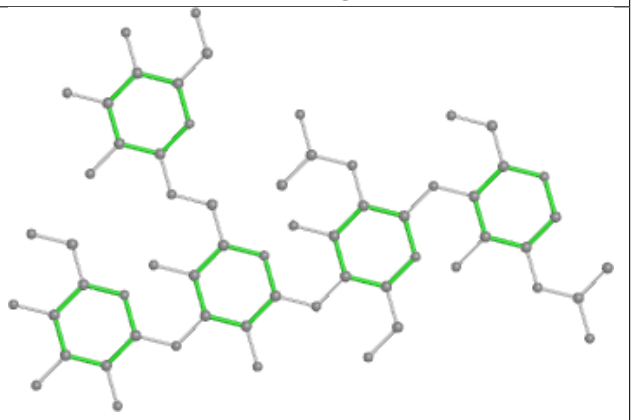
Bond lengths



Bond angles

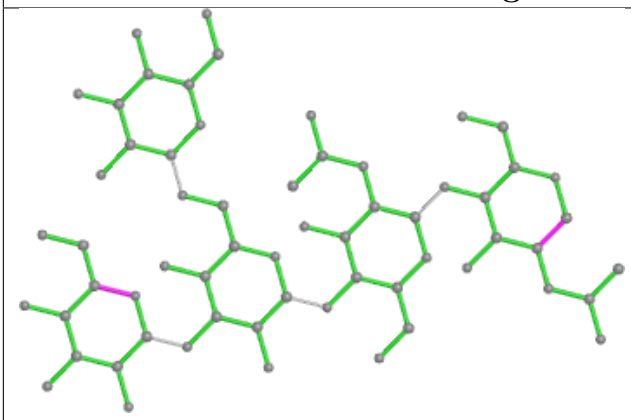


Torsions

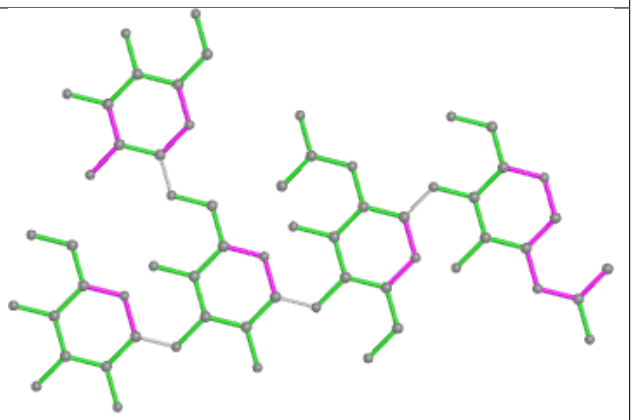


Rings

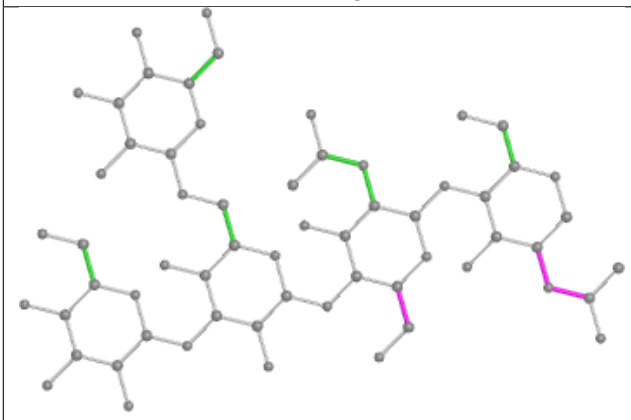
Oligosaccharide Chain i



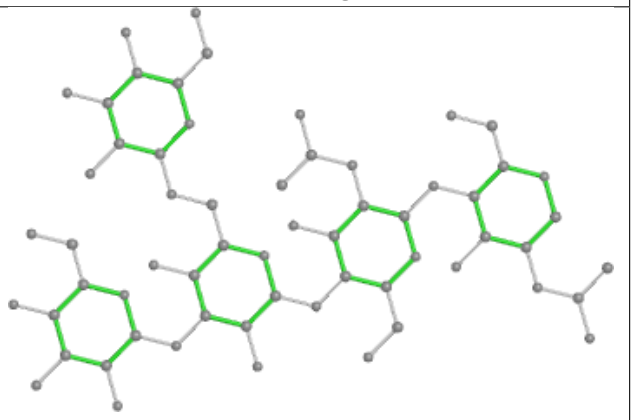
Bond lengths



Bond angles

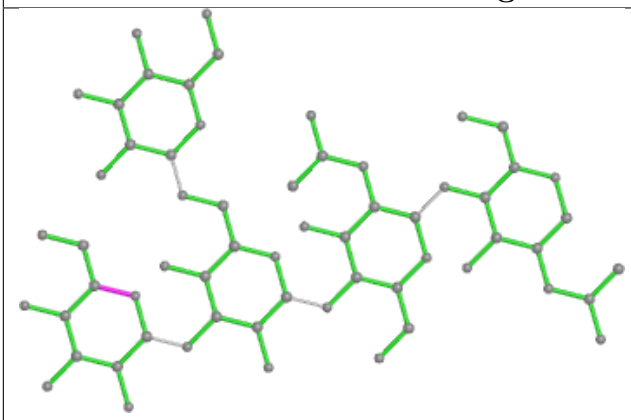


Torsions

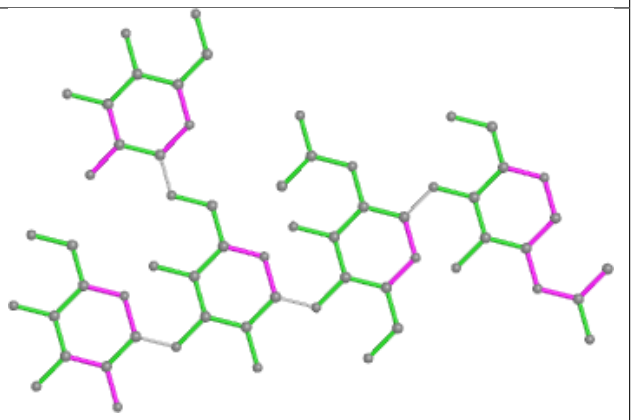


Rings

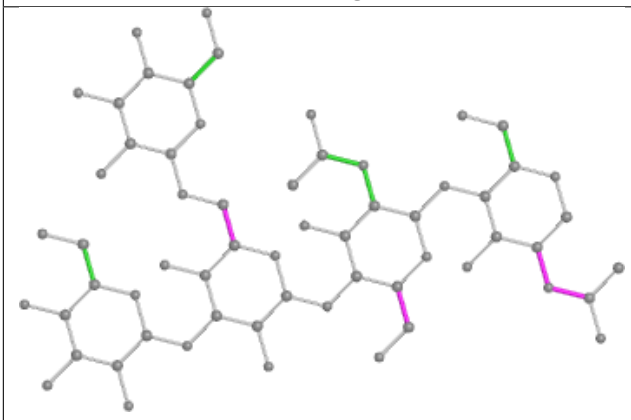
Oligosaccharide Chain u



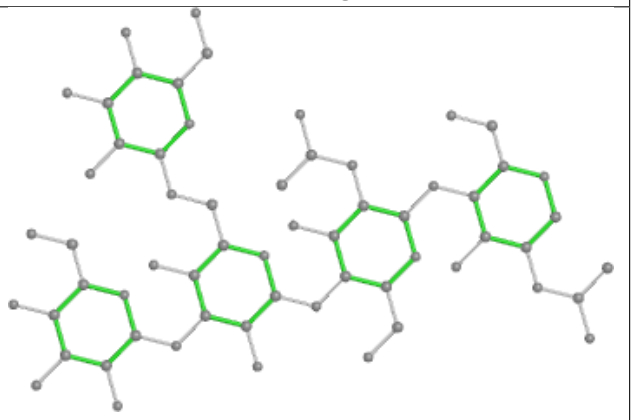
Bond lengths



Bond angles

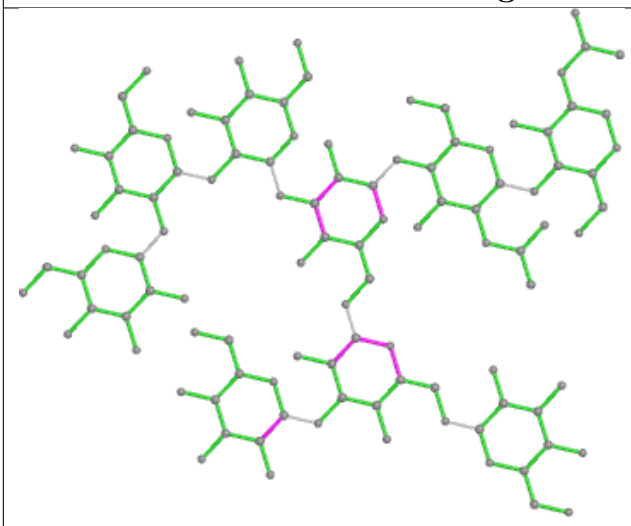


Torsions

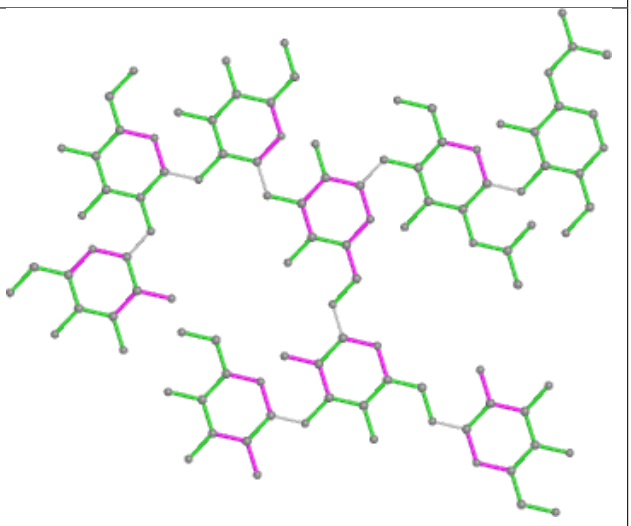


Rings

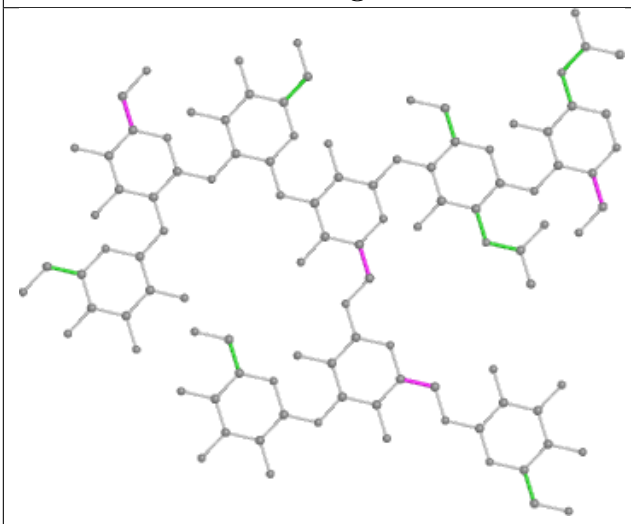
Oligosaccharide Chain d



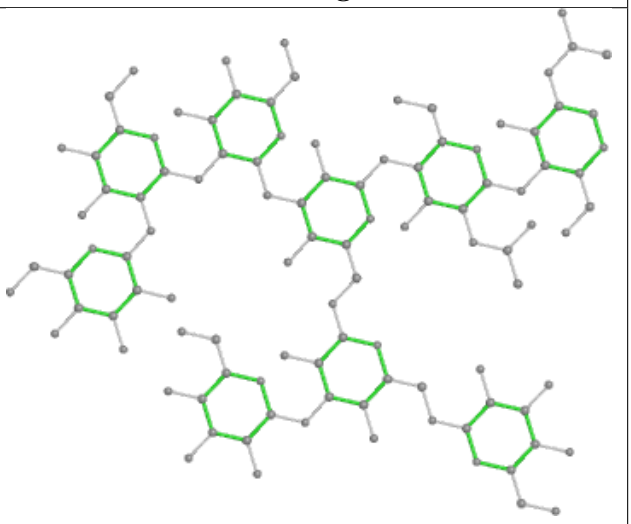
Bond lengths



Bond angles

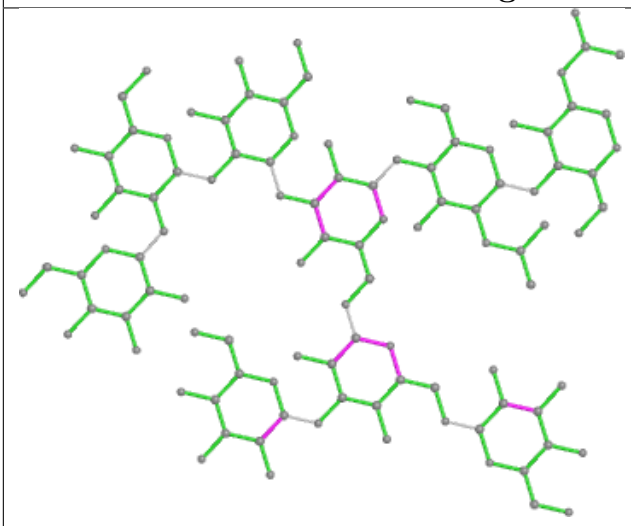


Torsions

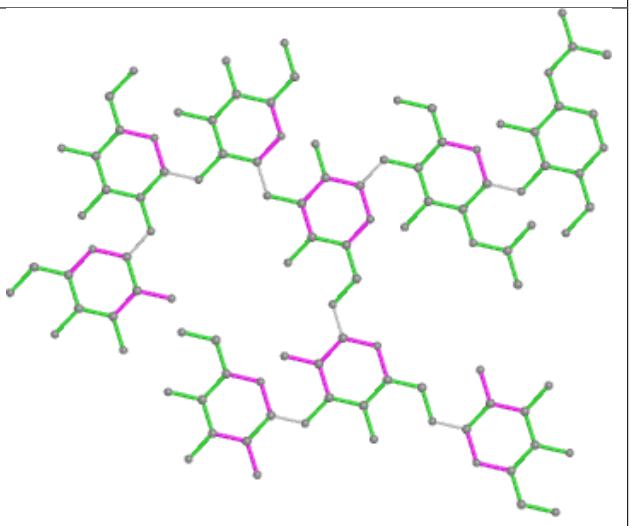


Rings

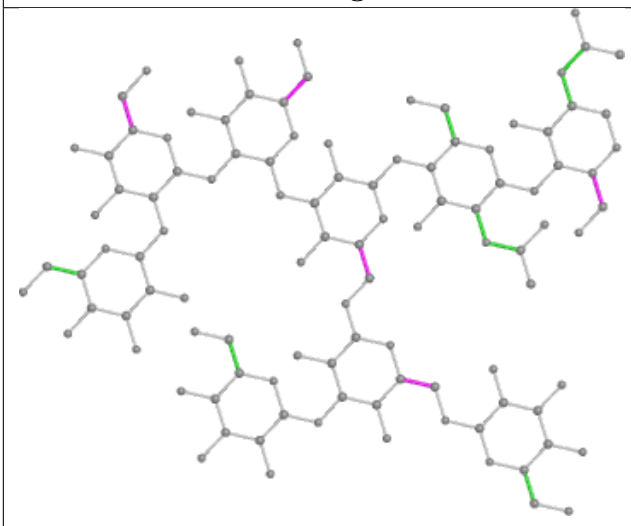
Oligosaccharide Chain 1



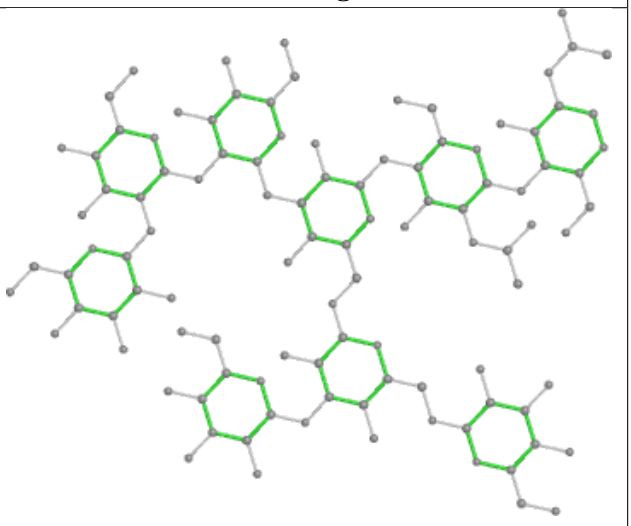
Bond lengths



Bond angles

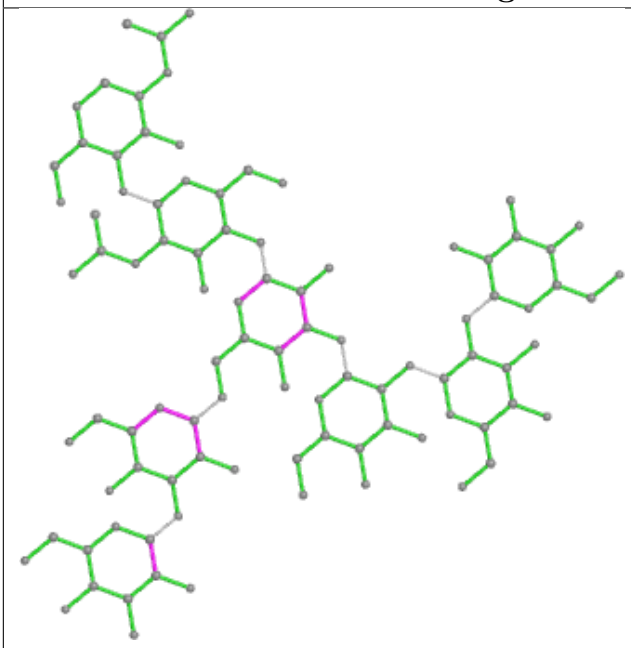


Torsions

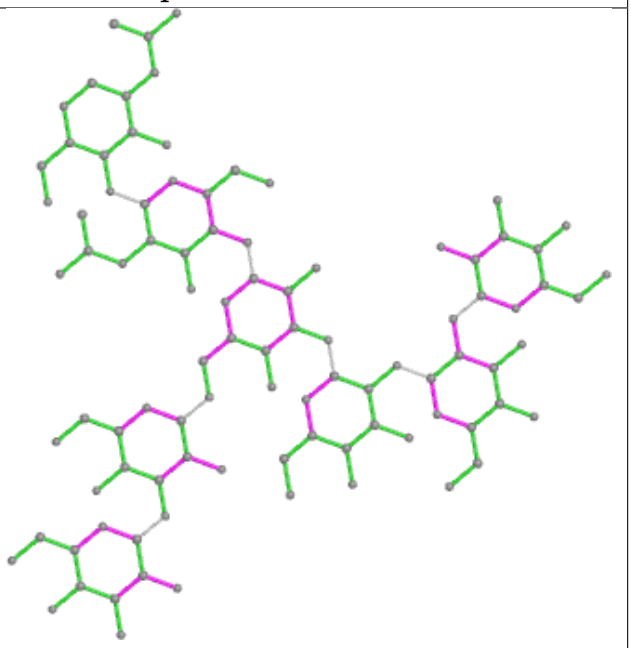


Rings

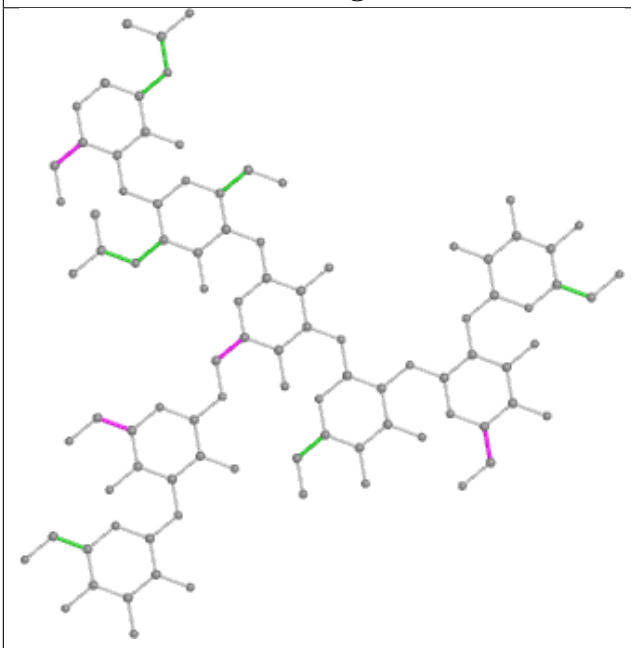
Oligosaccharide Chain p



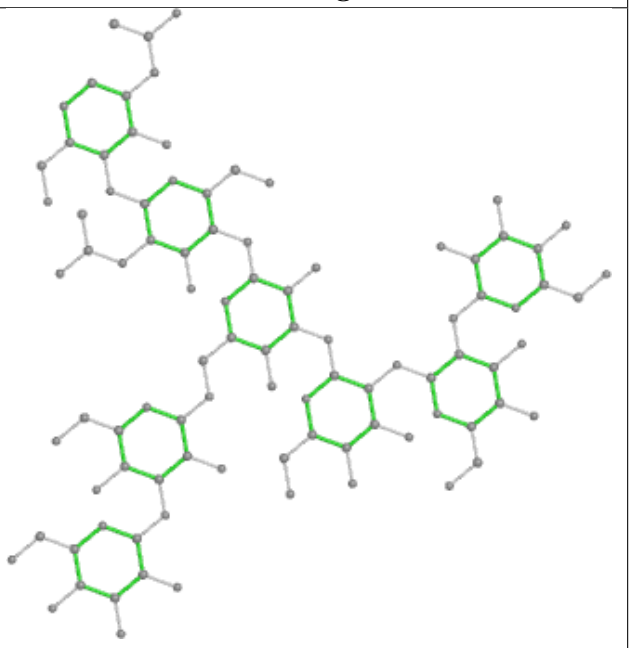
Bond lengths



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	$\#\|Z\| > 2$
12	NAG	E	701	2	14,14,15	0.86	1 (7%)	17,19,21	1.22	2 (11%)
12	NAG	B	606	1	14,14,15	1.06	1 (7%)	17,19,21	2.60	4 (23%)
12	NAG	F	701	2	14,14,15	0.85	1 (7%)	17,19,21	1.22	2 (11%)
12	NAG	C	605	1	14,14,15	0.57	0	17,19,21	0.71	1 (5%)
12	NAG	A	603	1	14,14,15	0.60	0	17,19,21	0.64	1 (5%)
12	NAG	B	602	1	14,14,15	0.62	0	17,19,21	0.60	1 (5%)
12	NAG	C	607	1	14,14,15	0.63	0	17,19,21	0.69	1 (5%)
12	NAG	C	601	1	14,14,15	0.74	0	17,19,21	1.32	3 (17%)
12	NAG	B	603	1	14,14,15	0.57	0	17,19,21	0.54	0
12	NAG	C	603	1	14,14,15	0.57	0	17,19,21	0.55	0
12	NAG	D	701	2	14,14,15	0.83	1 (7%)	17,19,21	1.21	2 (11%)
12	NAG	B	605	1	14,14,15	0.58	0	17,19,21	0.71	1 (5%)
12	NAG	C	606	1	14,14,15	1.15	1 (7%)	17,19,21	2.59	3 (17%)
12	NAG	A	606	1	14,14,15	0.63	0	17,19,21	0.69	1 (5%)
12	NAG	C	602	1	14,14,15	0.62	0	17,19,21	0.58	1 (5%)
12	NAG	A	604	1	14,14,15	0.69	0	17,19,21	1.28	2 (11%)
12	NAG	B	607	1	14,14,15	0.62	0	17,19,21	0.69	1 (5%)
12	NAG	A	605	1	14,14,15	0.59	0	17,19,21	0.71	1 (5%)
12	NAG	B	601	1	14,14,15	0.74	0	17,19,21	1.32	3 (17%)
12	NAG	C	604	1	14,14,15	0.69	0	17,19,21	1.29	2 (11%)
12	NAG	B	604	1	14,14,15	0.70	0	17,19,21	1.28	2 (11%)
12	NAG	A	601	1	14,14,15	0.74	0	17,19,21	1.29	3 (17%)
12	NAG	A	607	1	14,14,15	0.82	1 (7%)	17,19,21	0.66	1 (5%)
12	NAG	A	602	1	14,14,15	0.63	0	17,19,21	0.60	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	E	701	2	-	1/6/23/26	0/1/1/1
12	NAG	B	606	1	-	5/6/23/26	0/1/1/1
12	NAG	F	701	2	-	1/6/23/26	0/1/1/1

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	C	605	1	-	2/6/23/26	0/1/1/1
12	NAG	A	603	1	-	2/6/23/26	0/1/1/1
12	NAG	B	602	1	-	1/6/23/26	0/1/1/1
12	NAG	C	607	1	-	2/6/23/26	0/1/1/1
12	NAG	C	601	1	-	3/6/23/26	0/1/1/1
12	NAG	B	603	1	-	0/6/23/26	0/1/1/1
12	NAG	C	603	1	-	0/6/23/26	0/1/1/1
12	NAG	D	701	2	-	1/6/23/26	0/1/1/1
12	NAG	B	605	1	-	2/6/23/26	0/1/1/1
12	NAG	C	606	1	-	4/6/23/26	0/1/1/1
12	NAG	A	606	1	-	2/6/23/26	0/1/1/1
12	NAG	C	602	1	-	1/6/23/26	0/1/1/1
12	NAG	A	604	1	-	3/6/23/26	0/1/1/1
12	NAG	B	607	1	-	2/6/23/26	0/1/1/1
12	NAG	A	605	1	-	2/6/23/26	0/1/1/1
12	NAG	B	601	1	-	3/6/23/26	0/1/1/1
12	NAG	C	604	1	-	3/6/23/26	0/1/1/1
12	NAG	B	604	1	-	3/6/23/26	0/1/1/1
12	NAG	A	601	1	-	3/6/23/26	0/1/1/1
12	NAG	A	607	1	-	0/6/23/26	0/1/1/1
12	NAG	A	602	1	-	1/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	C	606	NAG	C1-C2	3.14	1.57	1.52
12	B	606	NAG	C1-C2	2.76	1.56	1.52
12	A	607	NAG	O5-C1	2.43	1.47	1.43
12	E	701	NAG	C1-C2	2.29	1.55	1.52
12	F	701	NAG	C1-C2	2.25	1.55	1.52

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	B	606	NAG	C2-N2-C7	9.04	135.77	122.90
12	C	606	NAG	C2-N2-C7	8.97	135.68	122.90
12	C	606	NAG	C1-C2-N2	4.50	118.18	110.49
12	B	606	NAG	C1-C2-N2	4.33	117.88	110.49
12	C	604	NAG	C2-N2-C7	4.00	128.60	122.90

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	601	NAG	O5-C5-C6-O6
12	B	606	NAG	O5-C5-C6-O6
12	B	601	NAG	O5-C5-C6-O6
12	C	601	NAG	O5-C5-C6-O6
12	A	603	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	3
1	B	3
1	A	3
2	E	1
2	F	1
2	D	1

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	546:SER	C	565:LEU	N	25.08
1	F	546:SER	C	565:LEU	N	25.01
1	D	546:SER	C	565:LEU	N	24.75
1	C	137:GLY	C	152:THR	N	13.35
1	B	137:GLY	C	152:THR	N	13.34

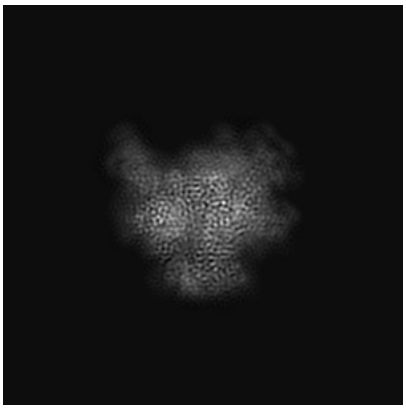
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26496. These allow visual inspection of the internal detail of the map and identification of artifacts.

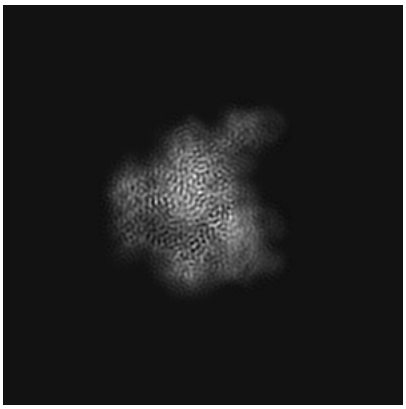
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

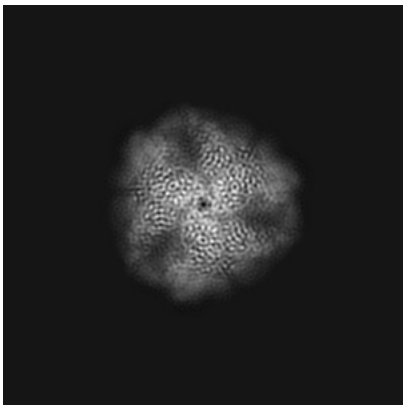
6.1.1 Primary map



X

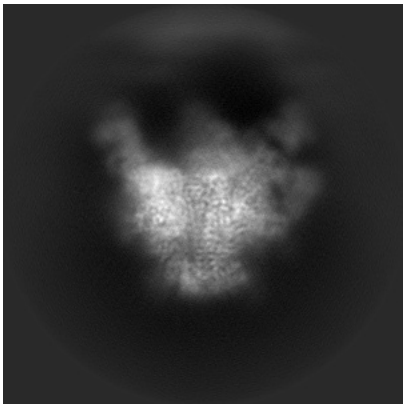


Y

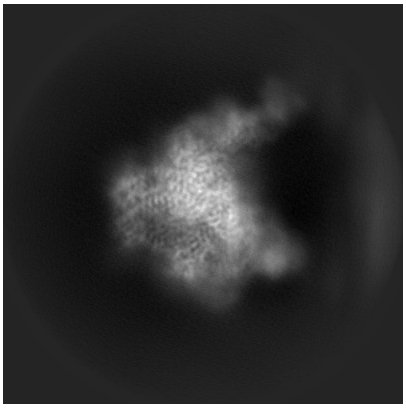


Z

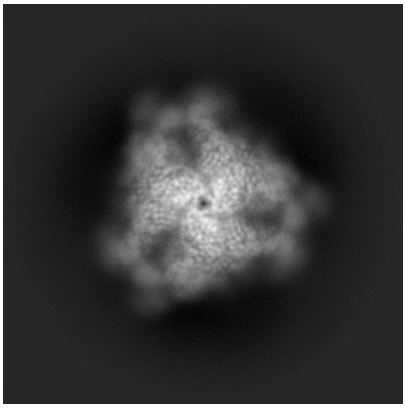
6.1.2 Raw map



X



Y

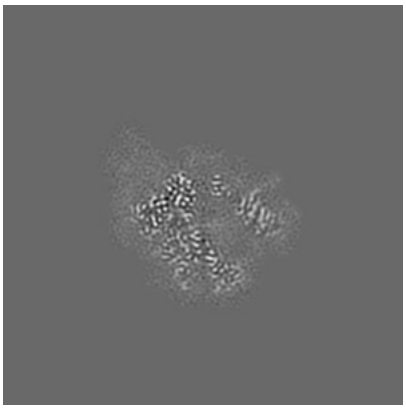


Z

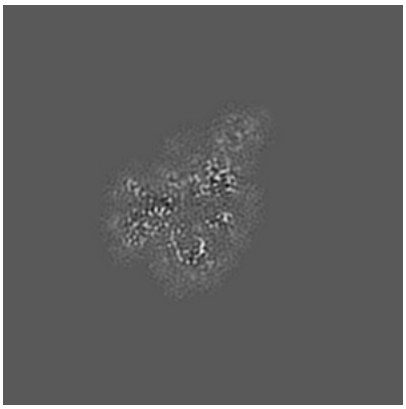
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

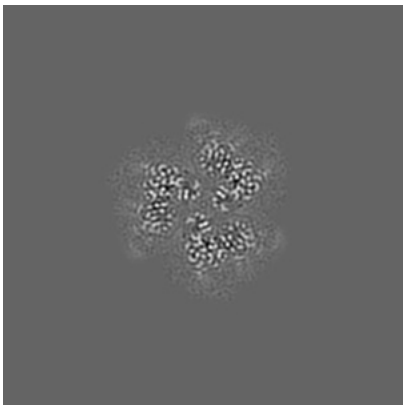
6.2.1 Primary map



X Index: 180

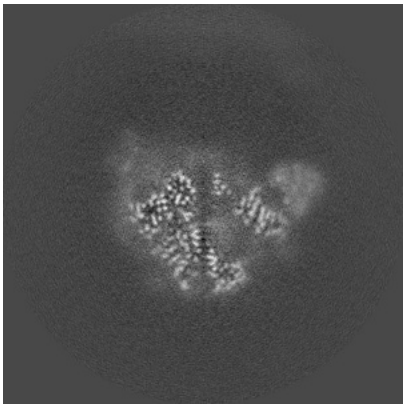


Y Index: 180

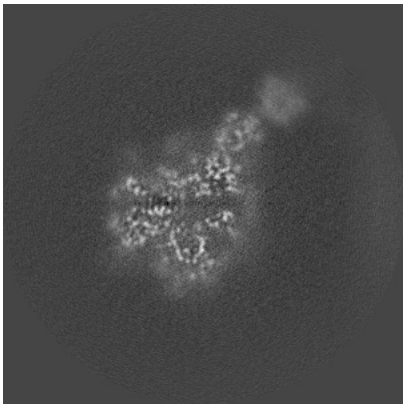


Z Index: 180

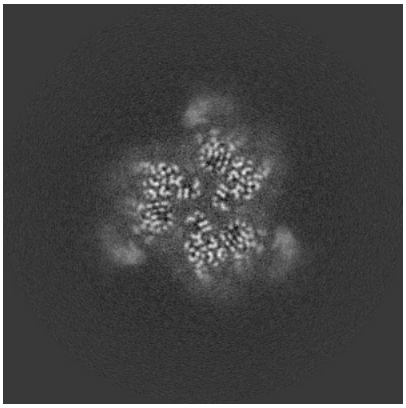
6.2.2 Raw map



X Index: 180



Y Index: 180

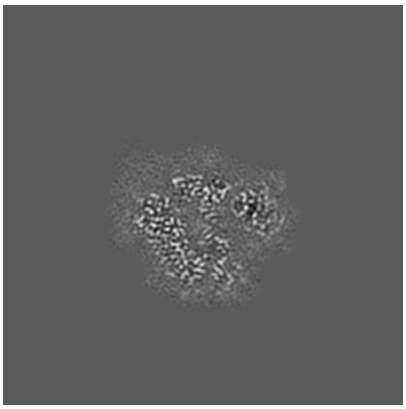


Z Index: 180

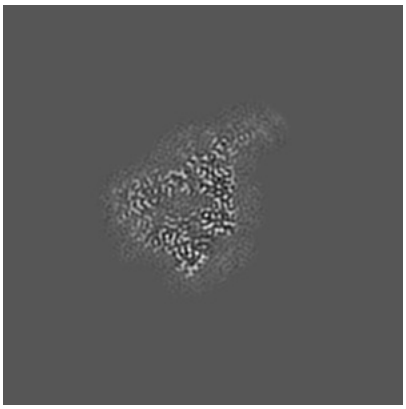
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

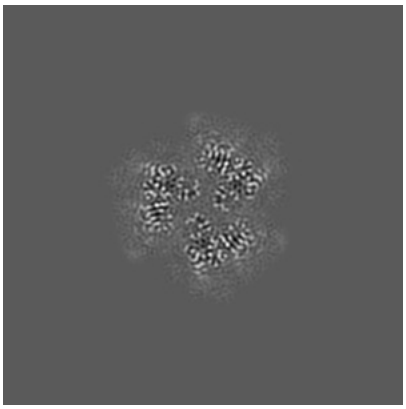
6.3.1 Primary map



X Index: 189

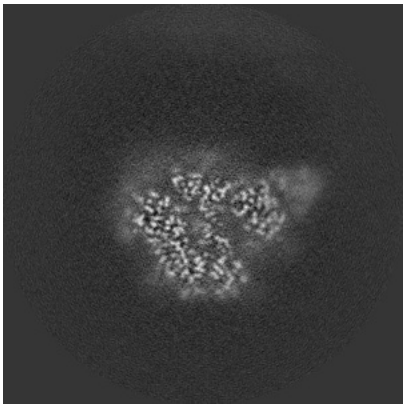


Y Index: 191

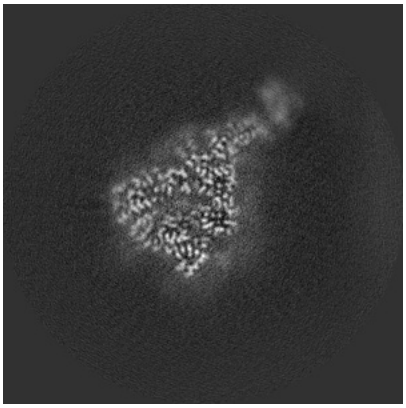


Z Index: 179

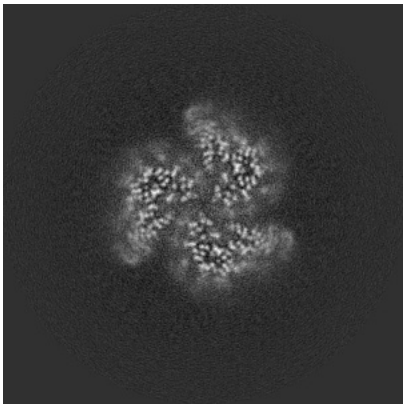
6.3.2 Raw map



X Index: 189



Y Index: 191

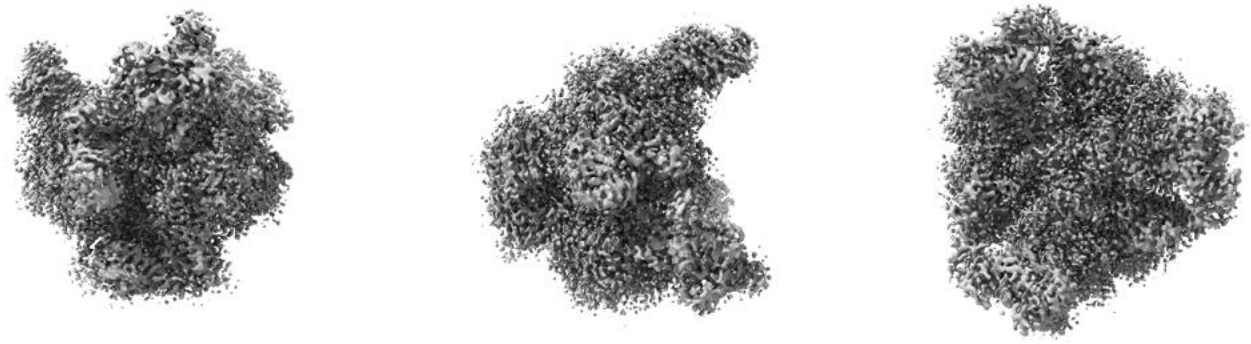


Z Index: 168

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0115. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

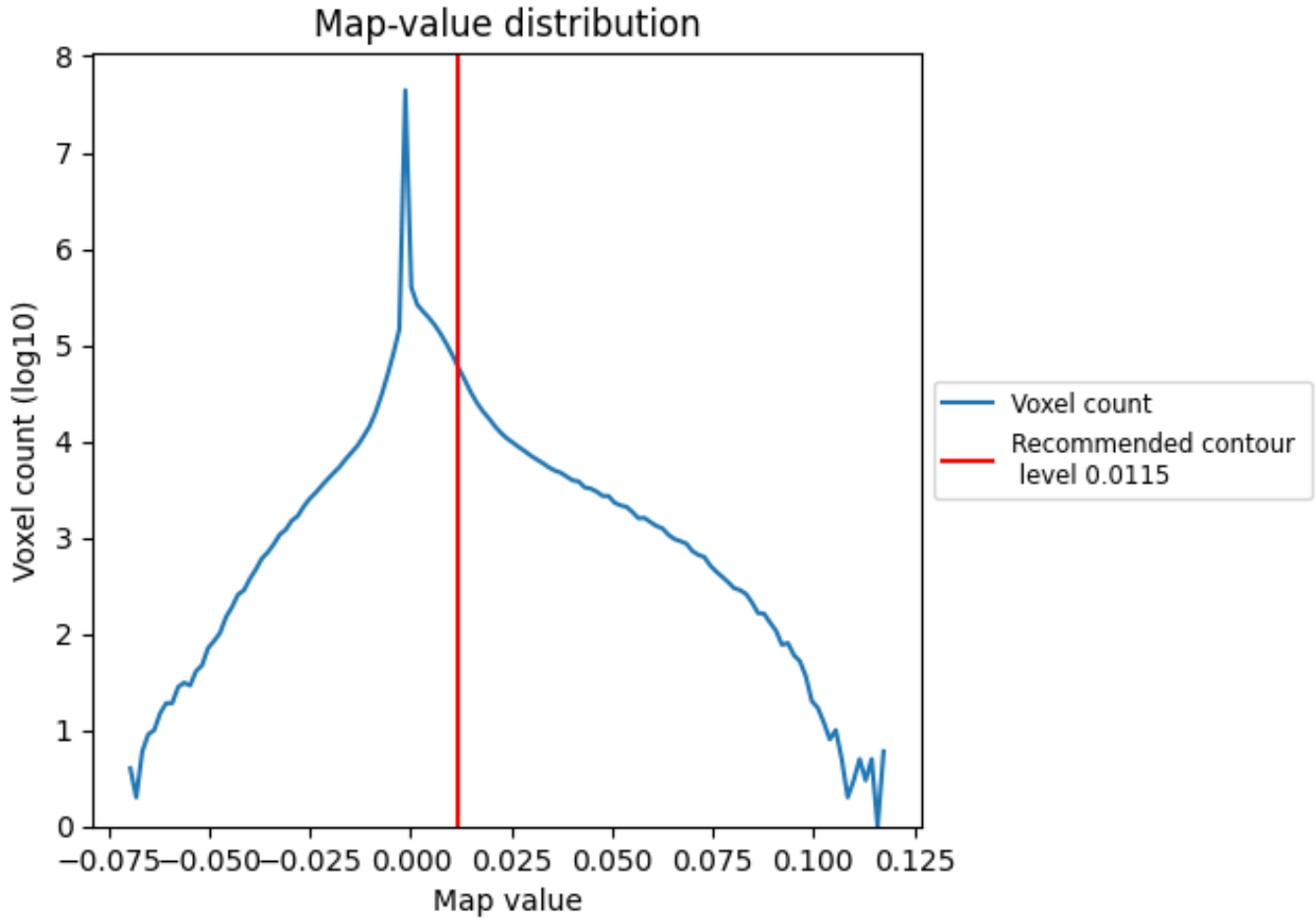
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

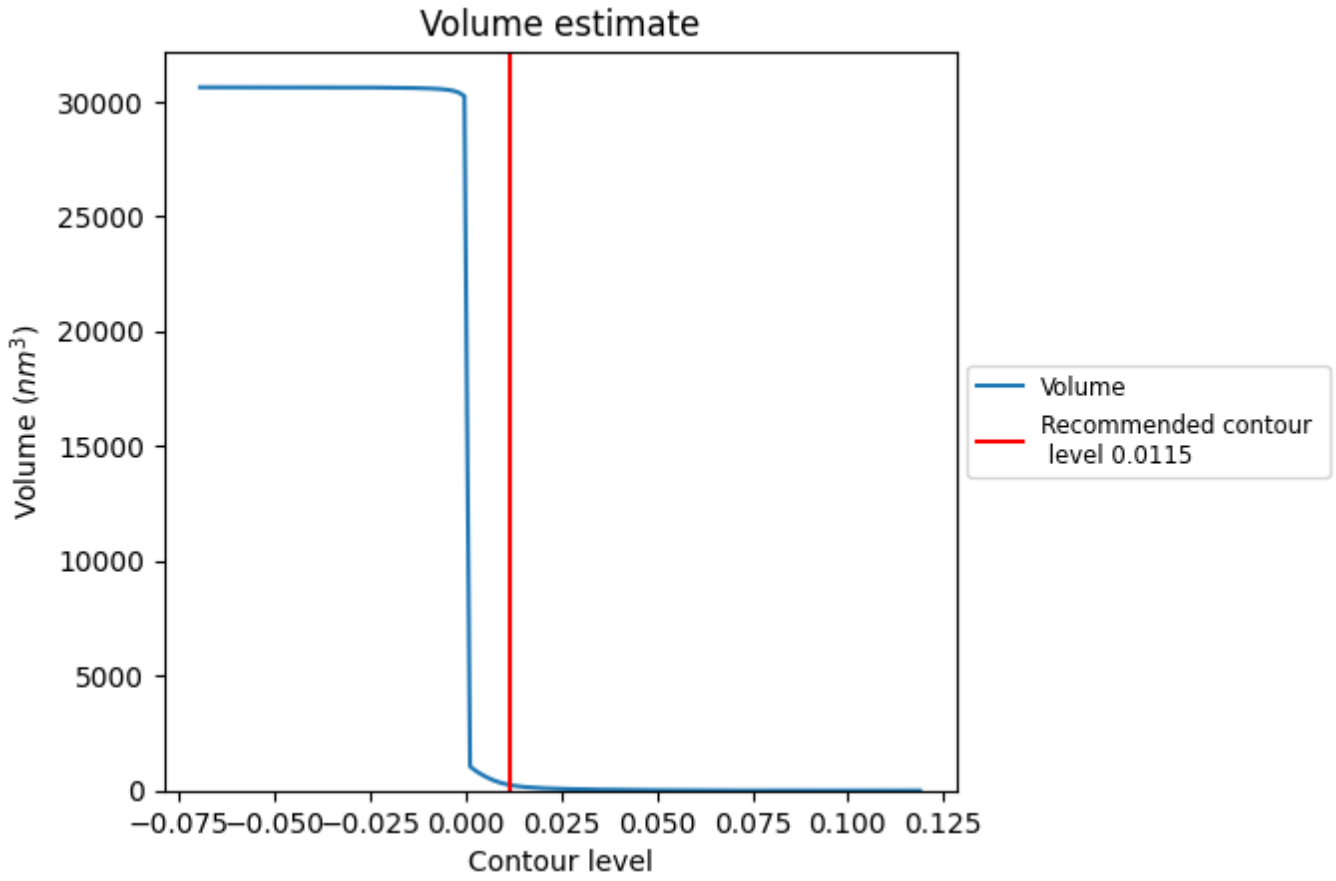
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

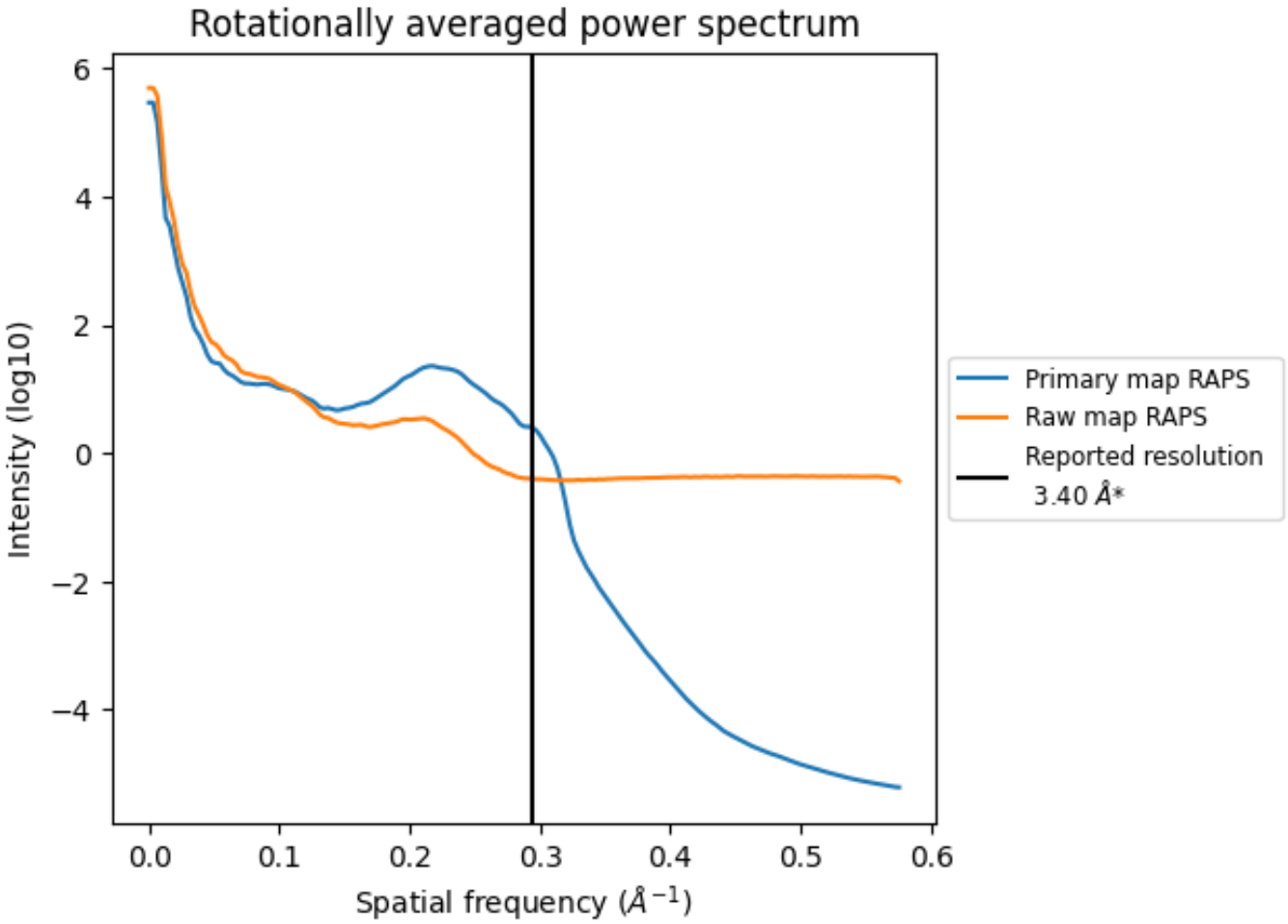
7.2 Volume estimate (i)



The volume at the recommended contour level is 243 nm^3; this corresponds to an approximate mass of 219 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

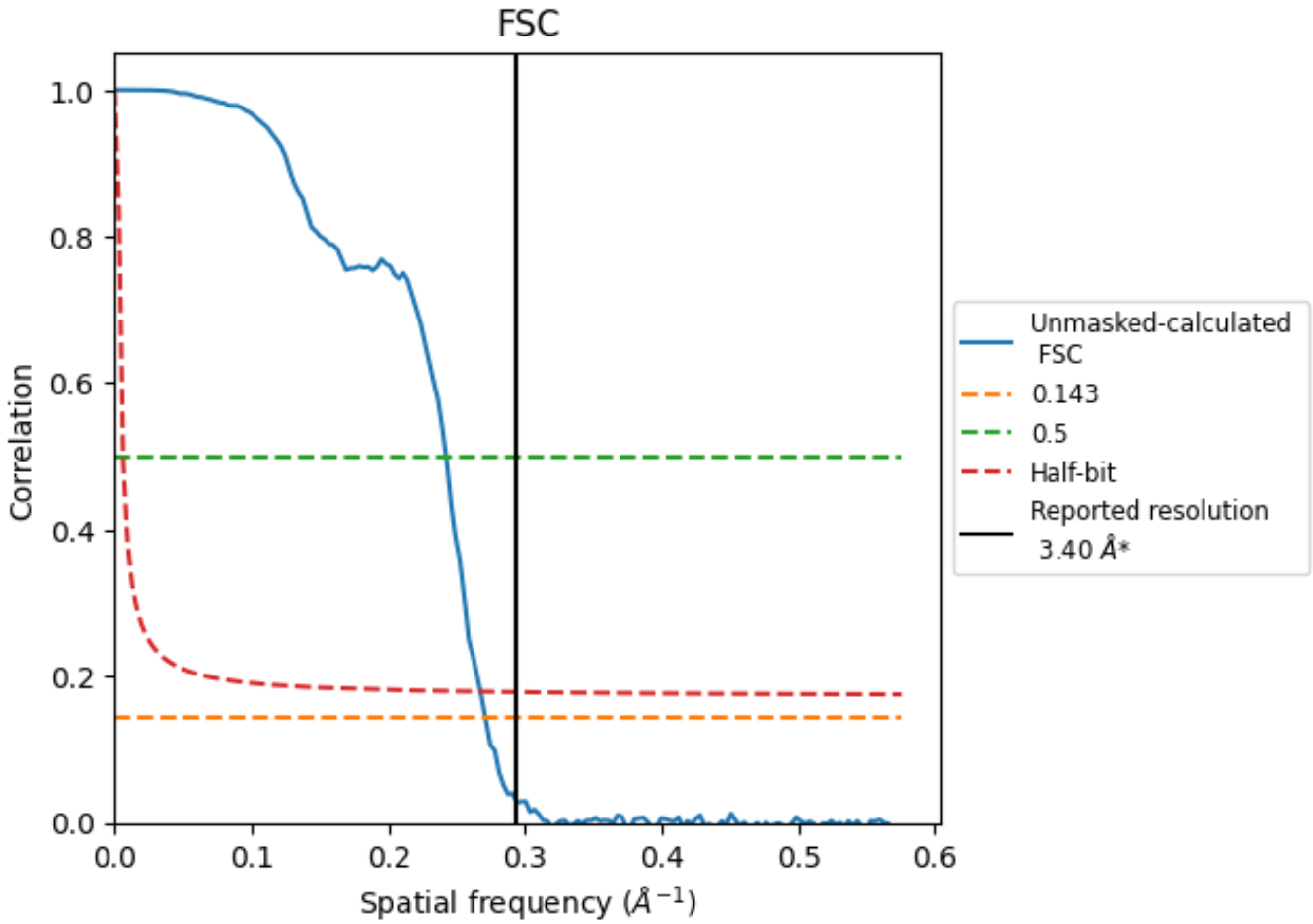


*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.294 $Å^{-1}$

8.2 Resolution estimates (i)

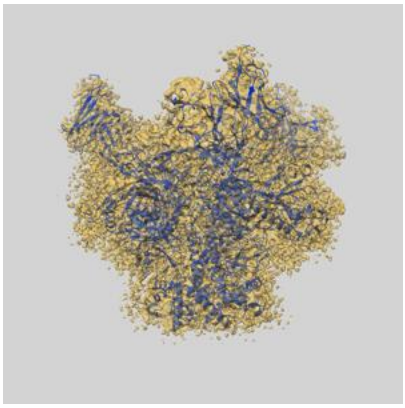
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.69	4.13	3.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

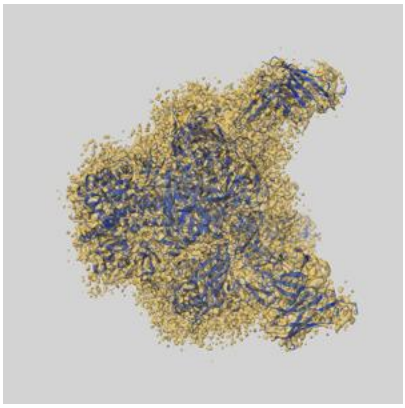
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26496 and PDB model 7UGQ. Per-residue inclusion information can be found in section 3 on page 14.

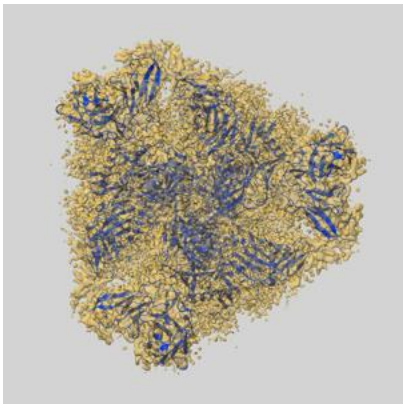
9.1 Map-model overlay



X



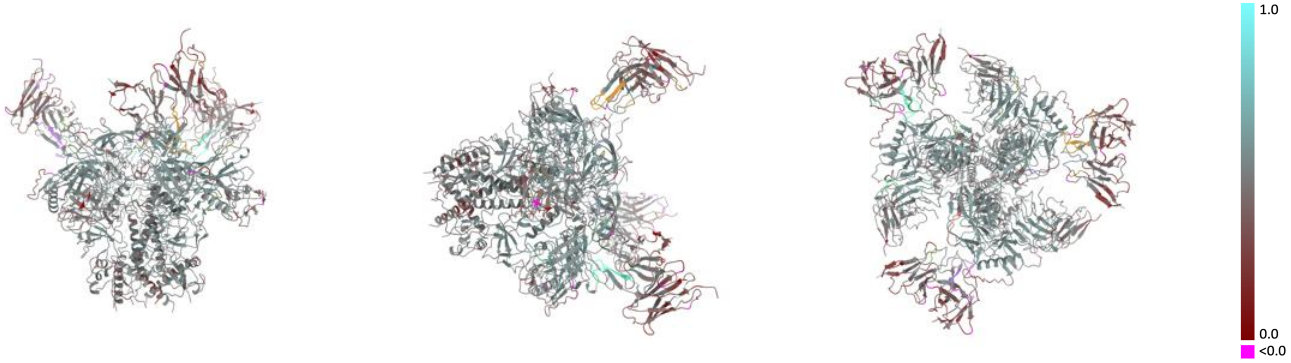
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0115 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

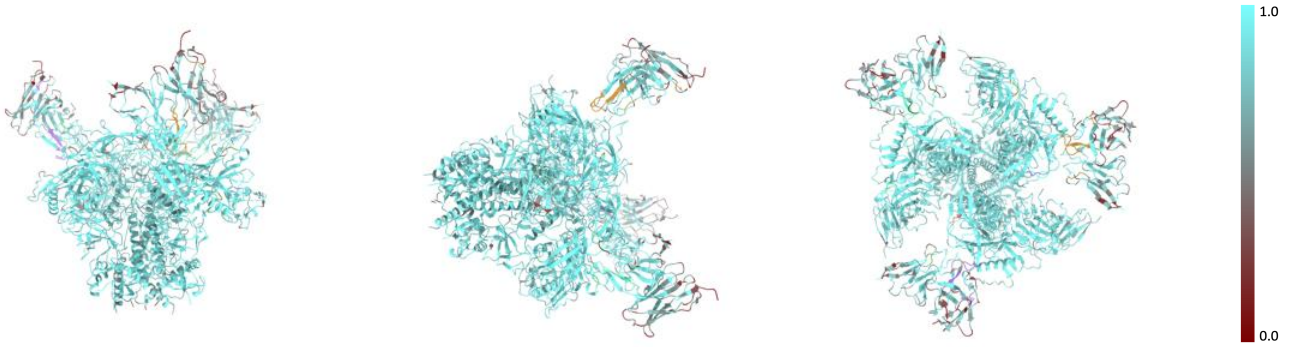
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

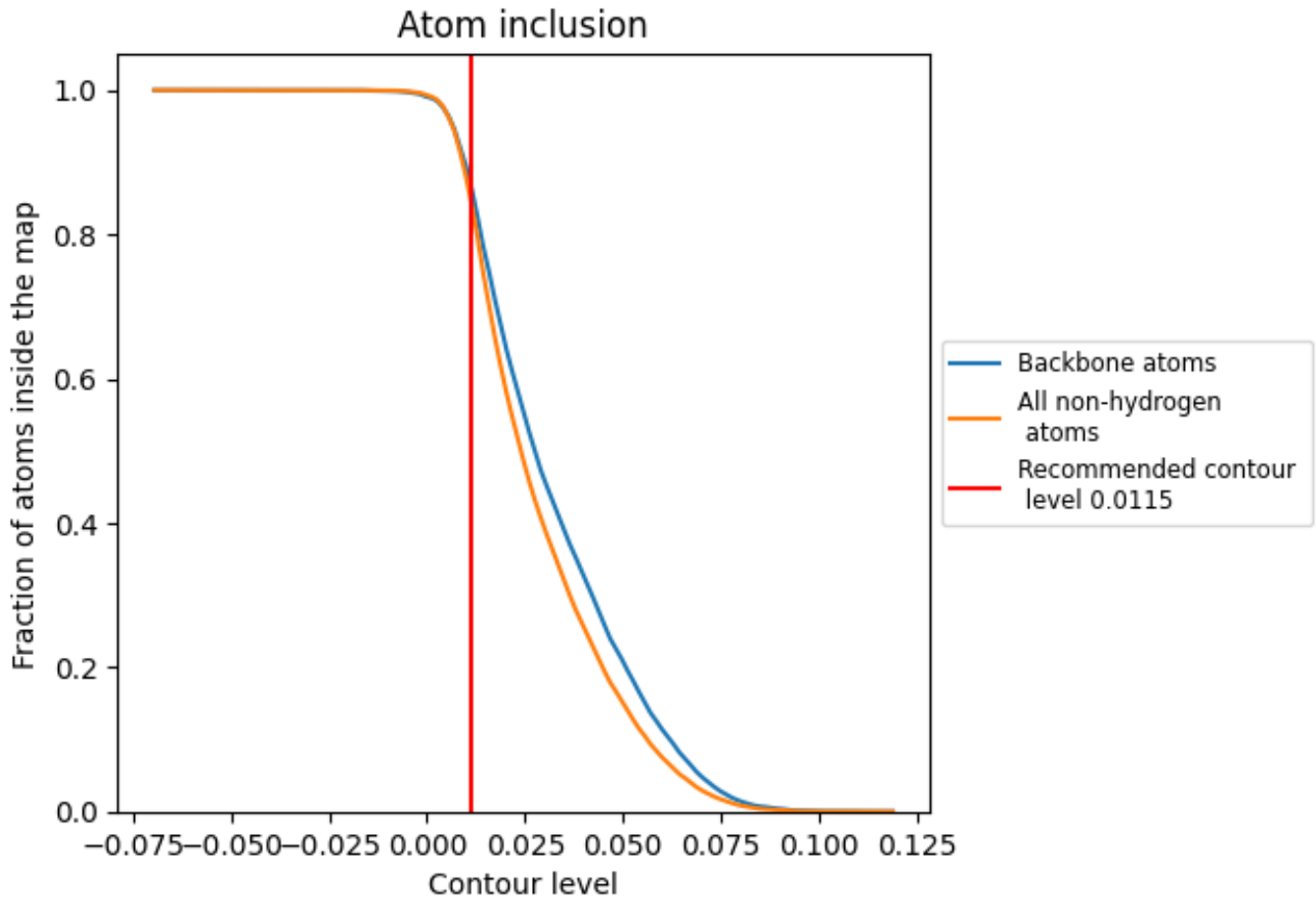
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0115).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8388	0.4700
0	0.6154	0.3230
1	0.8000	0.4520
A	0.8889	0.5090
B	0.8923	0.5090
C	0.8914	0.5100
D	0.8516	0.4660
E	0.8564	0.4690
F	0.8525	0.4680
G	0.9001	0.5280
H	0.8990	0.5230
I	0.8959	0.5230
J	0.8354	0.4460
K	0.8394	0.4470
L	0.8435	0.4460
M	0.6584	0.3690
N	0.6515	0.3690
O	0.6535	0.3640
P	0.7905	0.4220
Q	0.7930	0.4170
R	0.7905	0.4170
S	0.8205	0.4340
T	0.8571	0.4680
U	0.7857	0.4400
V	0.6667	0.3180
W	0.8197	0.4360
X	0.8214	0.4790
Y	0.7857	0.3310
Z	0.5000	0.3260
a	0.7143	0.3840
b	0.8929	0.4870
c	0.7179	0.3190
d	0.8000	0.4460
e	0.8205	0.4350
f	0.8571	0.4600

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Chain	Atom inclusion	Q-score
g	0.7857	0.4220
h	0.7436	0.3850
i	0.8525	0.4370
j	0.7857	0.4660
k	0.7500	0.3370
l	0.5000	0.3130
m	0.8571	0.4290
n	0.8571	0.4750
o	0.6667	0.3470
p	0.8298	0.4660
q	0.8205	0.4400
r	0.8571	0.4590
s	0.7857	0.4300
t	0.6667	0.3360
u	0.8525	0.4360
v	0.7857	0.4850
w	0.7500	0.3560
x	0.5357	0.3360
y	0.7143	0.3920
z	0.8571	0.4750