wwPDB EM Validation Summary Report

Oct 6, 2024 – 11:20 AM EDT

PDB ID	:	7UOJ
EMDB ID	:	EMD-26648
Title	:	The CryoEM structure of N49-P9.6-FR3 and PGT121 Fabs in complex with BG505 SOSIP.664
Authors	:	Nguyen, D.N.; Tolbert, W.D.; Pazgier, M.
Deposited on	:	2022-04-13
Resolution	:	4.02 Å(reported)
Based on initial models	:	7SX7, 6CDI, 5CEZ

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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

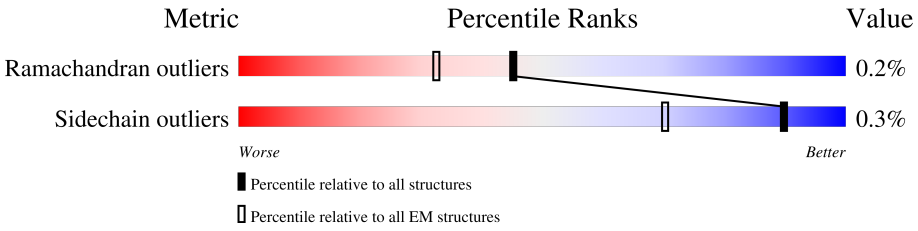
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.02 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	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% 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	481	94% 6%
1	G	481	5% 94% 6%
1	I	481	5% 94% 6%
2	B	153	13% 85% 14%
2	C	153	11% 86% 14%
2	J	153	12% 86% 14%
3	D	230	54% 45%
3	H	230	54% 45%
3	K	230	54% 45%

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Mol	Chain	Length	Quality of chain
4	E	203	6% 47% 52%
4	L	203	47% 52%
4	M	203	48% 52%
5	e	213	17% 51% 49%
5	l	213	17% 51% 49%
5	m	213	17% 51% 49%
6	d	235	18% 56% 43%
6	h	235	20% 56% 43%
6	k	235	18% 56% 43%
7	F	2	100%
7	N	2	50% 100%
7	P	2	100%
7	Q	2	100%
7	T	2	100%
7	V	2	50% 50%
7	W	2	100%
7	X	2	100%
7	Y	2	50% 100%
7	a	2	100%
7	b	2	50% 100%
7	g	2	50% 50% 50%
7	j	2	100%
7	n	2	50% 50%
7	o	2	100%
7	p	2	50% 100%

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Mol	Chain	Length	Quality of chain
7	r	2	50% 50%
7	s	2	100%
7	v	2	100%
7	x	2	100%
7	y	2	50% 50%
8	O	4	50% 50%
8	Z	4	50% 50%
8	q	4	50% 50%
9	R	3	100%
9	c	3	100%
9	t	3	100%
10	S	5	20% 60% 40%
10	f	5	20% 60% 40%
10	u	5	40% 60% 40%
11	U	9	33% 67%
11	i	9	33% 67%
11	w	9	22% 33% 67%

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 26133 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	G	452	Total	C	N	O	S	0	0
			3559	2233	629	669	28		
1	A	452	Total	C	N	O	S	0	0
			3559	2233	629	669	28		
1	I	452	Total	C	N	O	S	0	0
			3559	2233	629	669	28		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	332	ASN	THR	engineered mutation	UNP Q2N0S6
G	501	CYS	ALA	engineered mutation	UNP Q2N0S6
G	509	ARG	-	expression tag	UNP Q2N0S6
G	510	ARG	-	expression tag	UNP Q2N0S6
G	511	ARG	-	expression tag	UNP Q2N0S6
G	512	ARG	-	expression tag	UNP Q2N0S6
G	513	ARG	-	expression tag	UNP Q2N0S6
A	332	ASN	THR	engineered mutation	UNP Q2N0S6
A	501	CYS	ALA	engineered mutation	UNP Q2N0S6
A	509	ARG	-	expression tag	UNP Q2N0S6
A	510	ARG	-	expression tag	UNP Q2N0S6
A	511	ARG	-	expression tag	UNP Q2N0S6
A	512	ARG	-	expression tag	UNP Q2N0S6
A	513	ARG	-	expression tag	UNP Q2N0S6
I	332	ASN	THR	engineered mutation	UNP Q2N0S6
I	501	CYS	ALA	engineered mutation	UNP Q2N0S6
I	509	ARG	-	expression tag	UNP Q2N0S6
I	510	ARG	-	expression tag	UNP Q2N0S6
I	511	ARG	-	expression tag	UNP Q2N0S6
I	512	ARG	-	expression tag	UNP Q2N0S6
I	513	ARG	-	expression tag	UNP Q2N0S6

- Molecule 2 is a protein called Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	131	Total	C	N	O	S	0	0
			1029	651	177	195	6		
2	C	131	Total	C	N	O	S	0	0
			1029	651	177	195	6		
2	J	131	Total	C	N	O	S	0	0
			1029	651	177	195	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S6
B	605	CYS	THR	engineered mutation	UNP Q2N0S6
C	559	PRO	ILE	engineered mutation	UNP Q2N0S6
C	605	CYS	THR	engineered mutation	UNP Q2N0S6
J	559	PRO	ILE	engineered mutation	UNP Q2N0S6
J	605	CYS	THR	engineered mutation	UNP Q2N0S6

- Molecule 3 is a protein called N49-P9.6-FR3 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	126	Total	C	N	O	S	0	0
			1010	642	180	181	7		
3	D	126	Total	C	N	O	S	0	0
			1010	642	180	181	7		
3	K	126	Total	C	N	O	S	0	0
			1010	642	180	181	7		

- Molecule 4 is a protein called N49-P9.6-FR3 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	98	Total	C	N	O	S	0	0
			737	464	124	146	3		
4	E	98	Total	C	N	O	S	0	0
			737	464	124	146	3		
4	M	98	Total	C	N	O	S	0	0
			737	464	124	146	3		

- Molecule 5 is a protein called PGT121 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	l	108	Total	C	N	O	S	0	0
			824	516	143	163	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	108	Total	C	N	O	S	0	0
			824	516	143	163	2		
5	m	108	Total	C	N	O	S	0	0
			824	516	143	163	2		

- Molecule 6 is a protein called PGT121 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	133	Total	C	N	O	S	0	0
			1031	652	176	199	4		
6	d	133	Total	C	N	O	S	0	0
			1031	652	176	199	4		
6	k	133	Total	C	N	O	S	0	0
			1031	652	176	199	4		

- Molecule 7 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
7	F	2	Total	C	N	O	0	0
			28	16	2	10		
7	N	2	Total	C	N	O	0	0
			28	16	2	10		
7	P	2	Total	C	N	O	0	0
			28	16	2	10		
7	Q	2	Total	C	N	O	0	0
			28	16	2	10		
7	T	2	Total	C	N	O	0	0
			28	16	2	10		
7	V	2	Total	C	N	O	0	0
			28	16	2	10		
7	W	2	Total	C	N	O	0	0
			28	16	2	10		
7	X	2	Total	C	N	O	0	0
			28	16	2	10		
7	Y	2	Total	C	N	O	0	0
			28	16	2	10		

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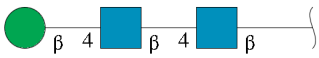
Mol	Chain	Residues	Atoms				AltConf	Trace
7	a	2	Total	C	N	O	0	0
			28	16	2	10		
7	b	2	Total	C	N	O	0	0
			28	16	2	10		
7	g	2	Total	C	N	O	0	0
			28	16	2	10		
7	j	2	Total	C	N	O	0	0
			28	16	2	10		
7	n	2	Total	C	N	O	0	0
			28	16	2	10		
7	o	2	Total	C	N	O	0	0
			28	16	2	10		
7	p	2	Total	C	N	O	0	0
			28	16	2	10		
7	r	2	Total	C	N	O	0	0
			28	16	2	10		
7	s	2	Total	C	N	O	0	0
			28	16	2	10		
7	v	2	Total	C	N	O	0	0
			28	16	2	10		
7	x	2	Total	C	N	O	0	0
			28	16	2	10		
7	y	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

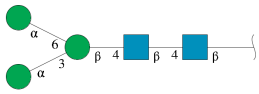
Mol	Chain	Residues	Atoms				AltConf	Trace
8	O	4	Total	C	N	O	0	0
			50	28	2	20		
8	Z	4	Total	C	N	O	0	0
			50	28	2	20		
8	q	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 9 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.



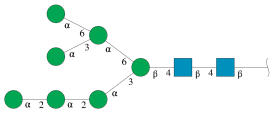
Mol	Chain	Residues	Atoms				AltConf	Trace
9	R	3	Total	C	N	O	0	0
			39	22	2	15		
9	c	3	Total	C	N	O	0	0
			39	22	2	15		
9	t	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 10 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
10	S	5	Total	C	N	O	0	0
			61	34	2	25		
10	f	5	Total	C	N	O	0	0
			61	34	2	25		
10	u	5	Total	C	N	O	0	0
			61	34	2	25		

- 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)]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	U	9	Total	C	N	O	0	0
			105	58	2	45		
11	i	9	Total	C	N	O	0	0
			105	58	2	45		

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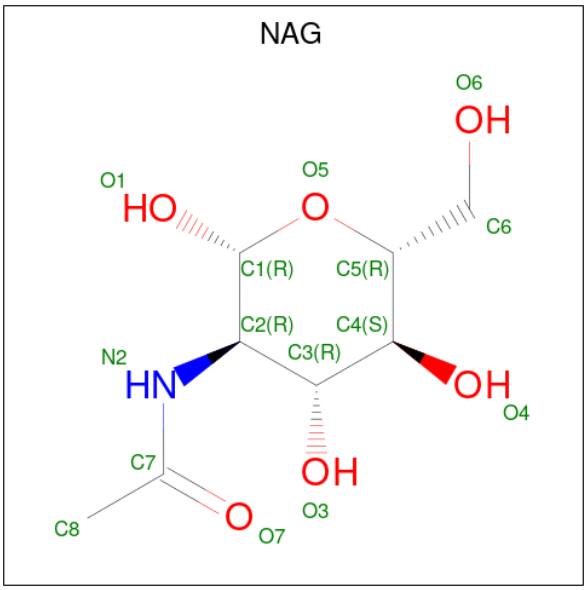
Mol	Chain	Residues	Atoms				AltConf	Trace
11	w	9	Total	C	N	O	0	0
			105	58	2	45		

- 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	G	1	Total	C	N	O	0
			14	8	1	5	
12	G	1	Total	C	N	O	0
			14	8	1	5	
12	G	1	Total	C	N	O	0
			14	8	1	5	
12	G	1	Total	C	N	O	0
			14	8	1	5	
12	G	1	Total	C	N	O	0
			14	8	1	5	
12	A	1	Total	C	N	O	0
			14	8	1	5	
12	A	1	Total	C	N	O	0
			14	8	1	5	
12	A	1	Total	C	N	O	0
			14	8	1	5	
12	A	1	Total	C	N	O	0
			14	8	1	5	
12	A	1	Total	C	N	O	0
			14	8	1	5	

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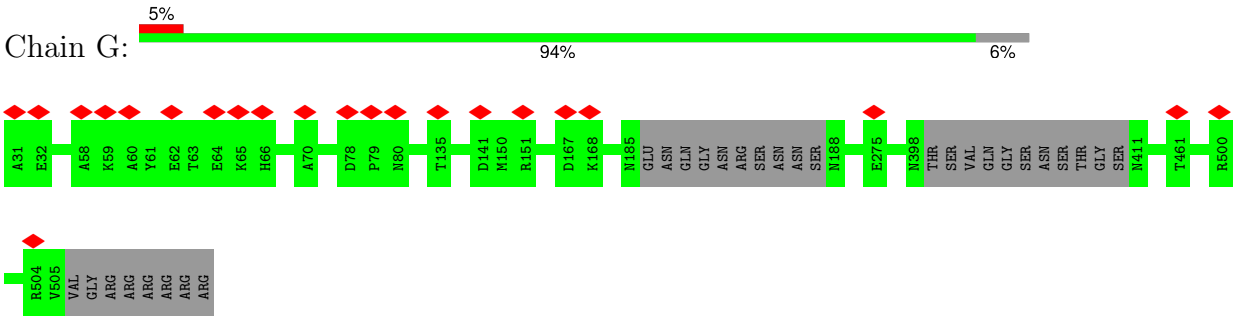
Mol	Chain	Residues	Atoms				AltConf
12	I	1	Total	C	N	O	0
			14	8	1	5	
12	I	1	Total	C	N	O	0
			14	8	1	5	
12	I	1	Total	C	N	O	0
			14	8	1	5	
12	I	1	Total	C	N	O	0
			14	8	1	5	
12	I	1	Total	C	N	O	0
			14	8	1	5	

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.

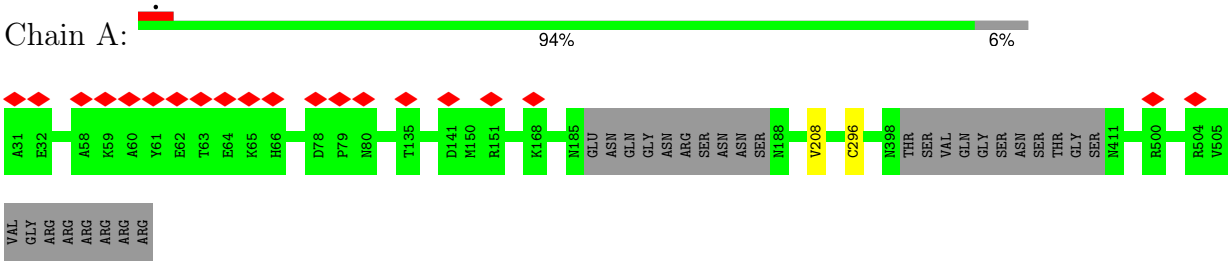
• Molecule 1: Envelope glycoprotein gp120

Chain G:



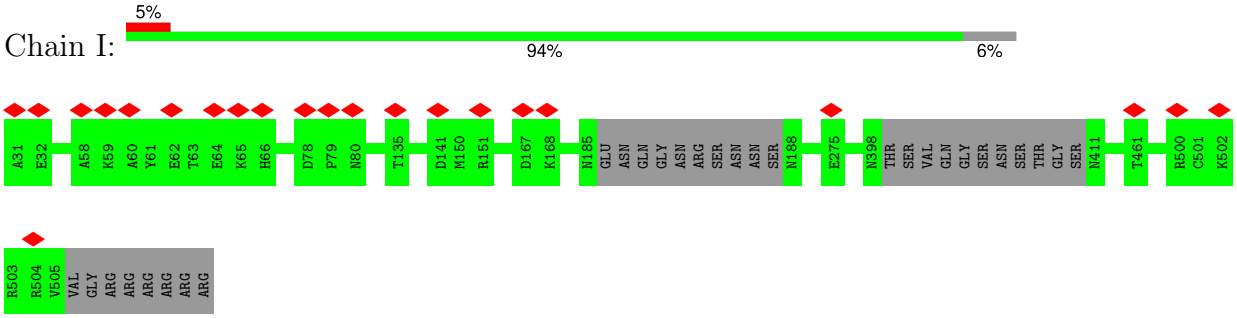
• Molecule 1: Envelope glycoprotein gp120

Chain A:



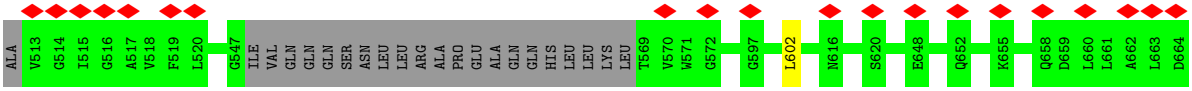
• Molecule 1: Envelope glycoprotein gp120

Chain I:

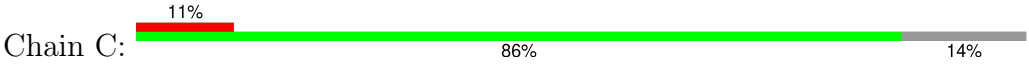


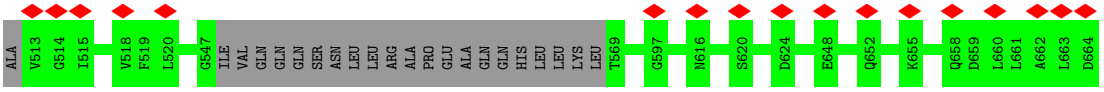
• Molecule 2: Envelope glycoprotein gp41

Chain B:

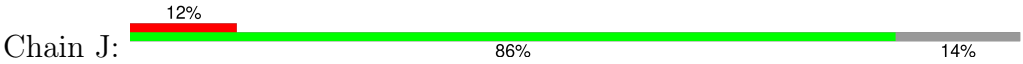


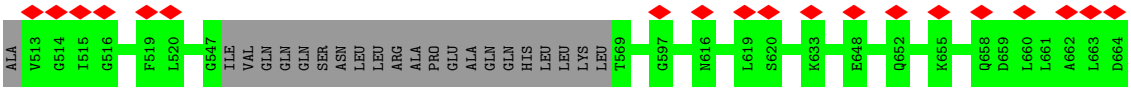
• Molecule 2: Envelope glycoprotein gp41



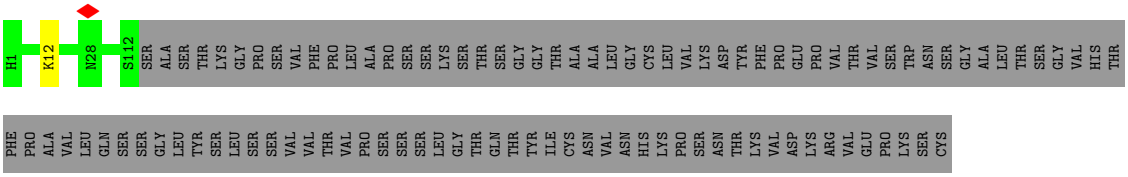


• Molecule 2: Envelope glycoprotein gp41

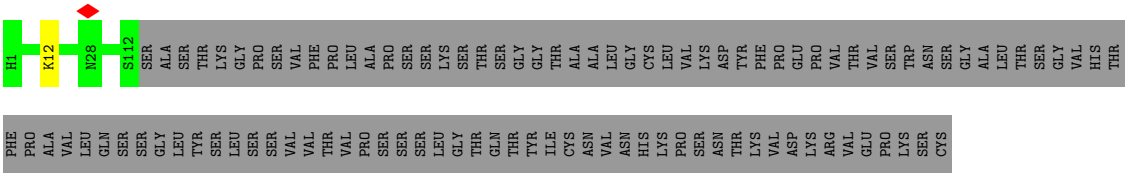




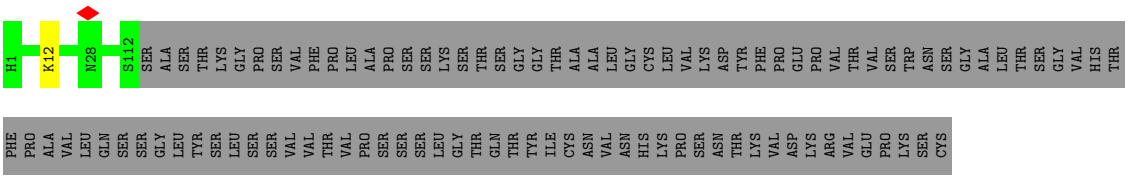
• Molecule 3: N49-P9.6-FR3 Fab heavy chain



• Molecule 3: N49-P9.6-FR3 Fab heavy chain

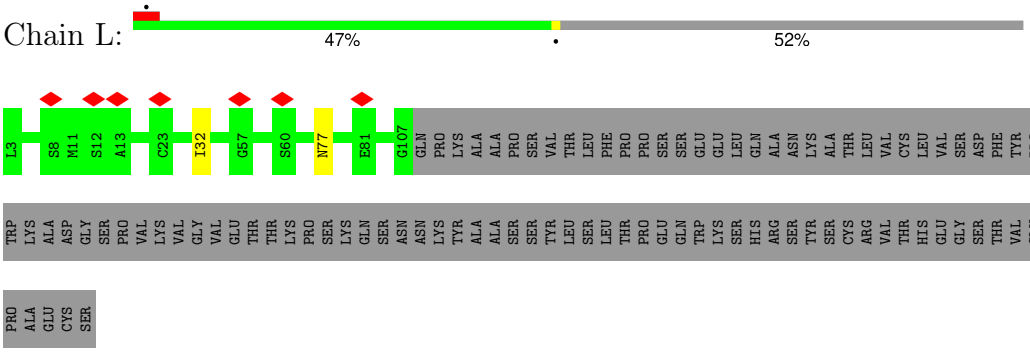


• Molecule 3: N49-P9.6-FR3 Fab heavy chain



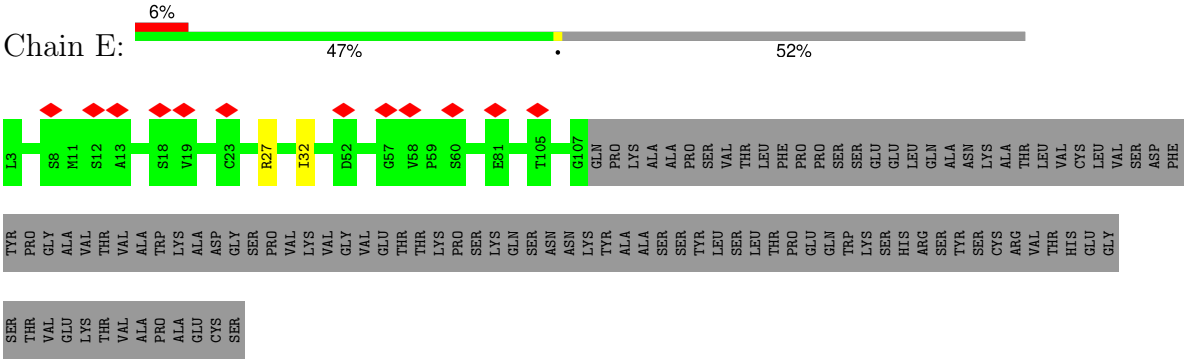
• Molecule 4: N49-P9.6-FR3 Fab light chain

Chain L:



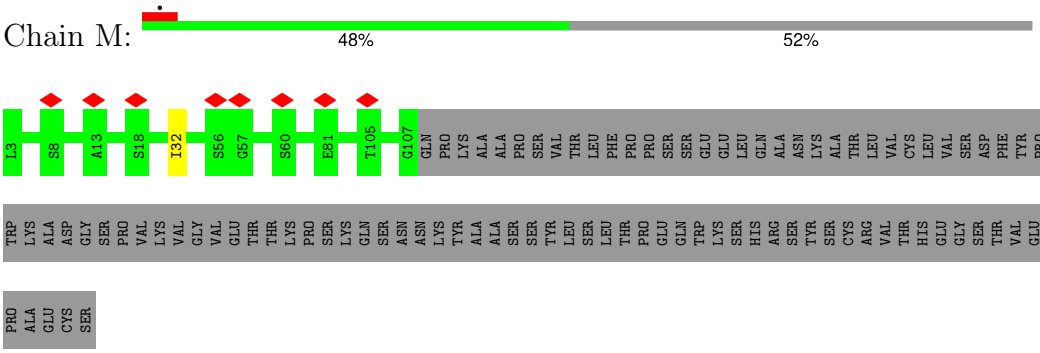
• Molecule 4: N49-P9.6-FR3 Fab light chain

Chain E:



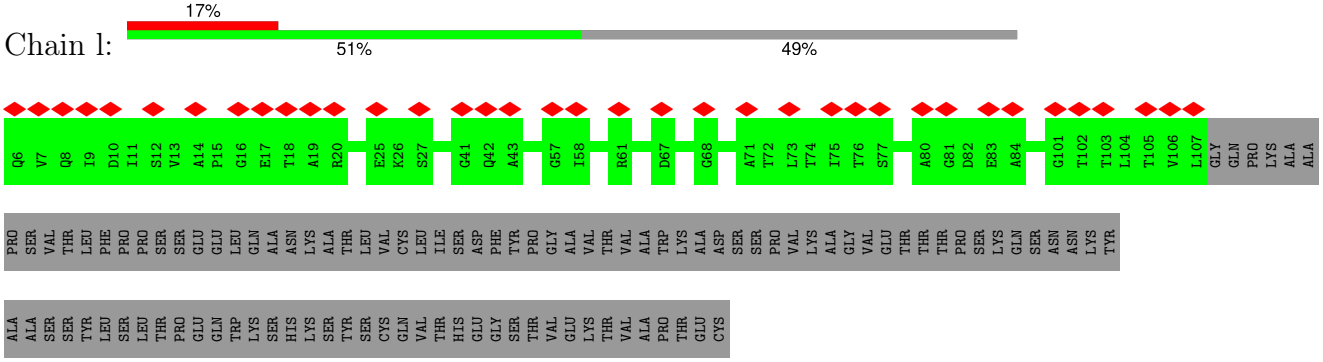
• Molecule 4: N49-P9.6-FR3 Fab light chain

Chain M:



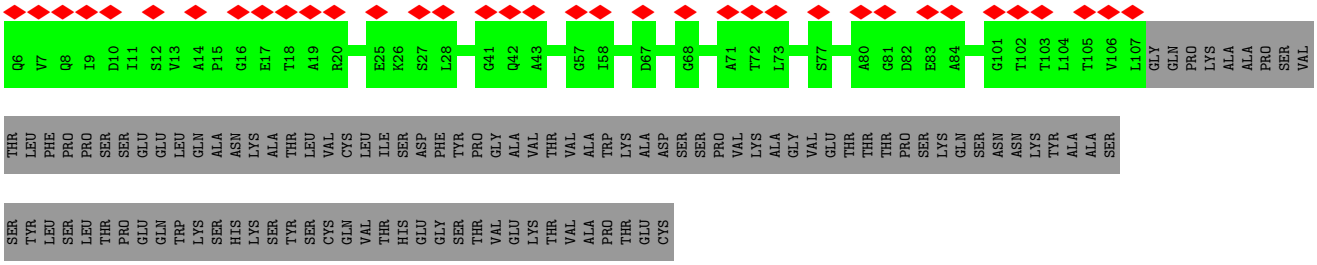
• Molecule 5: PGT121 Fab light chain

Chain l:



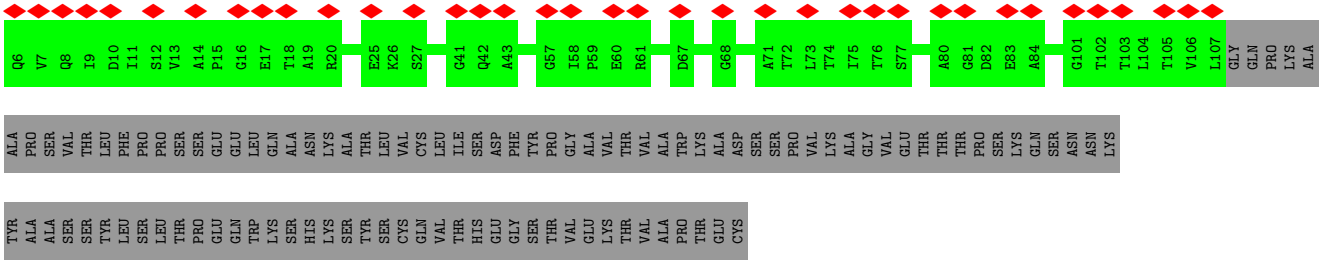
• Molecule 5: PGT121 Fab light chain

Chain e:



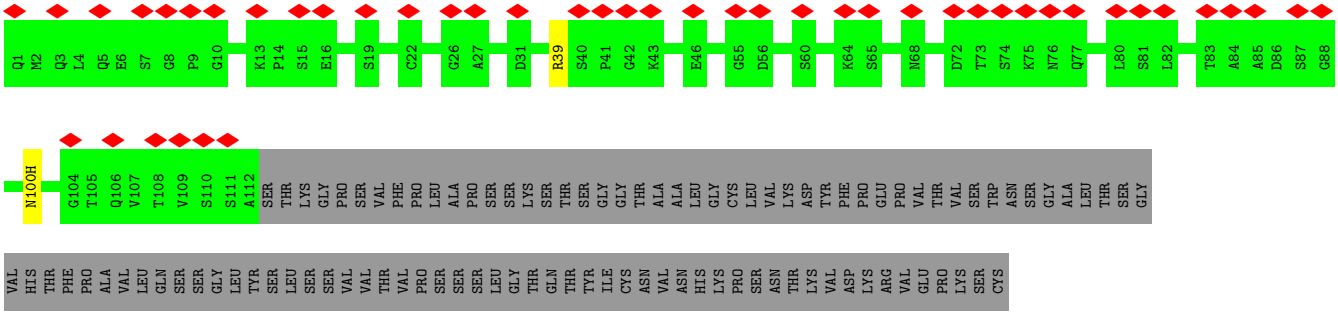
• Molecule 5: PGT121 Fab light chain

Chain m:



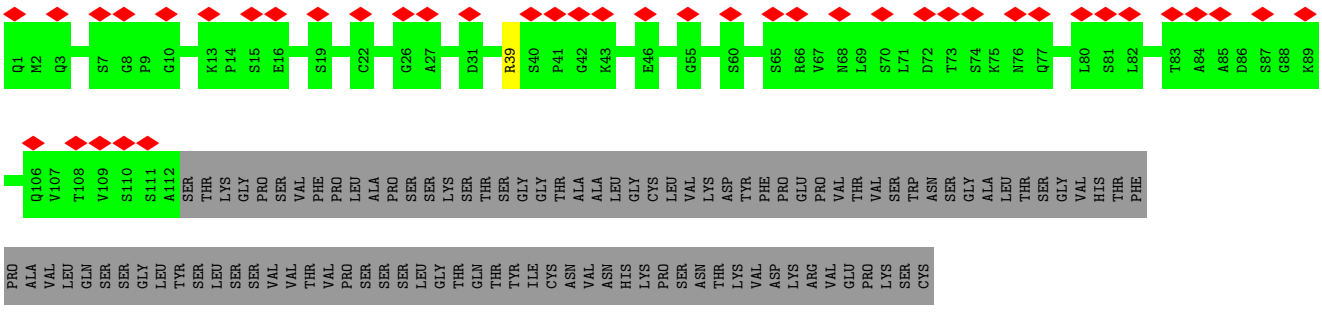
• Molecule 6: PGT121 Fab heavy chain

Chain h:



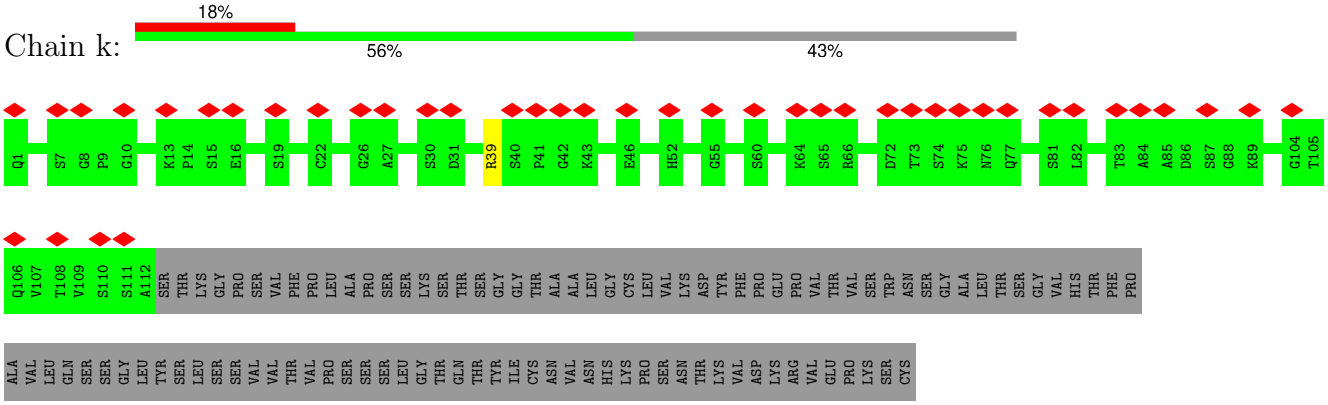
• Molecule 6: PGT121 Fab heavy chain

Chain d:



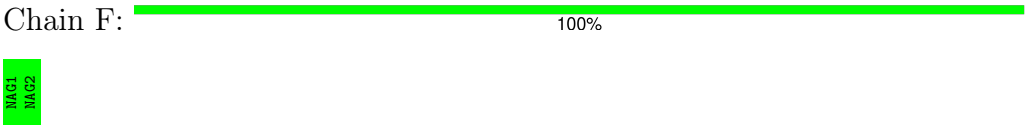
• Molecule 6: PGT121 Fab heavy chain

Chain k:



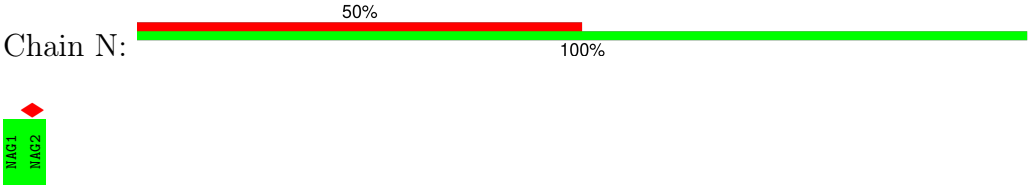
• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:



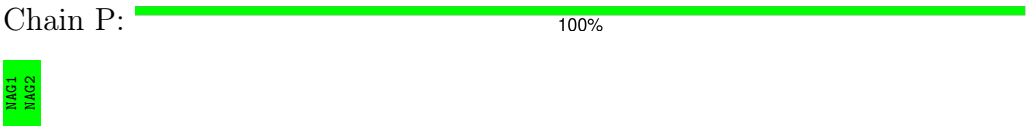
• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:



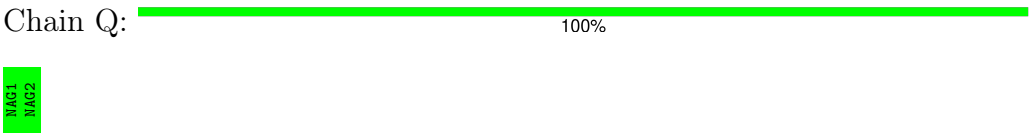
• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:



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

Chain Q:



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

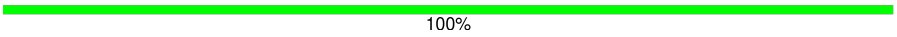
Chain T:

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

Chain V:

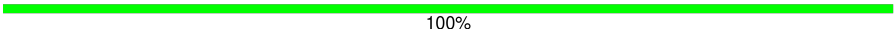
• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:



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

Chain X:

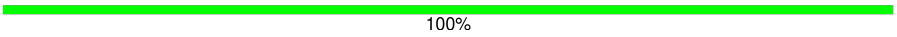


• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:

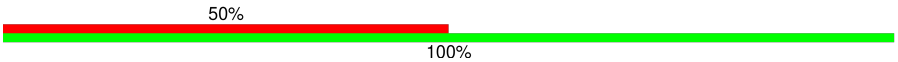
• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:



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

Chain b:

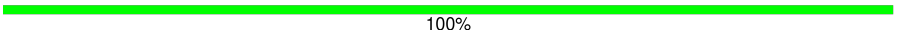


• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:

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

Chain j:

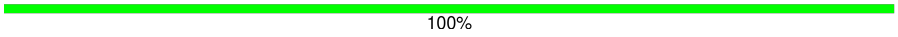


• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain n:

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

Chain o:



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

Chain p:

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

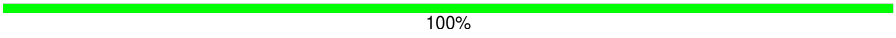
Chain r:

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

Chain s:

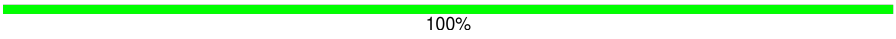
• Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain v:



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

Chain x:



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

Chain y:

• Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

• Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

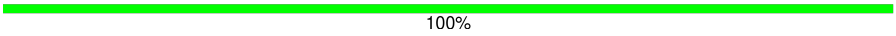
Chain Z:

• Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain q:

• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:



• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

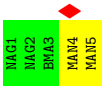
Chain c:

• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain t:

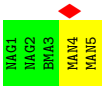
• Molecule 10: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:



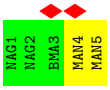
• Molecule 10: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:



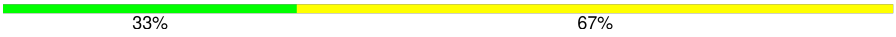
• Molecule 10: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain u:



• Molecule 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)]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 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)]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 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)]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:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	132055	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	58.8	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	49.328	Depositor
Minimum map value	-48.408	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.8	Depositor
Map size (Å)	355.72, 355.72, 355.72	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3895313, 1.3895313, 1.3895313	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.28	0/3633	0.55	0/4933
1	G	0.29	0/3633	0.56	0/4933
1	I	0.28	0/3633	0.54	0/4933
2	B	0.25	0/1047	0.50	0/1420
2	C	0.25	0/1047	0.52	0/1420
2	J	0.24	0/1047	0.51	0/1420
3	D	0.29	0/1041	0.56	0/1414
3	H	0.29	0/1041	0.57	0/1414
3	K	0.29	0/1041	0.57	0/1414
4	E	0.26	0/756	0.53	0/1029
4	L	0.26	0/756	0.52	0/1029
4	M	0.27	0/756	0.52	0/1029
5	e	0.26	0/845	0.53	0/1154
5	l	0.26	0/845	0.53	0/1154
5	m	0.26	0/845	0.54	0/1154
6	d	0.27	0/1057	0.53	0/1436
6	h	0.27	0/1057	0.53	0/1436
6	k	0.26	0/1057	0.53	0/1436
All	All	0.27	0/25137	0.54	0/34158

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	446/481 (93%)	407 (91%)	38 (8%)	1 (0%)	44 76
1	G	446/481 (93%)	411 (92%)	35 (8%)	0	100 100
1	I	446/481 (93%)	403 (90%)	43 (10%)	0	100 100
2	B	127/153 (83%)	119 (94%)	7 (6%)	1 (1%)	16 53
2	C	127/153 (83%)	118 (93%)	9 (7%)	0	100 100
2	J	127/153 (83%)	119 (94%)	8 (6%)	0	100 100
3	D	124/230 (54%)	116 (94%)	8 (6%)	0	100 100
3	H	124/230 (54%)	117 (94%)	7 (6%)	0	100 100
3	K	124/230 (54%)	116 (94%)	8 (6%)	0	100 100
4	E	96/203 (47%)	82 (85%)	13 (14%)	1 (1%)	13 47
4	L	96/203 (47%)	86 (90%)	9 (9%)	1 (1%)	13 47
4	M	96/203 (47%)	84 (88%)	11 (12%)	1 (1%)	13 47
5	e	106/213 (50%)	97 (92%)	9 (8%)	0	100 100
5	l	106/213 (50%)	98 (92%)	8 (8%)	0	100 100
5	m	106/213 (50%)	98 (92%)	8 (8%)	0	100 100
6	d	131/235 (56%)	127 (97%)	4 (3%)	0	100 100
6	h	131/235 (56%)	126 (96%)	4 (3%)	1 (1%)	16 53
6	k	131/235 (56%)	127 (97%)	4 (3%)	0	100 100
All	All	3090/4545 (68%)	2851 (92%)	233 (8%)	6 (0%)	45 76

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	602	LEU
1	A	208	VAL
4	L	32	ILE
4	E	32	ILE

Continued on next page...

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Mol	Chain	Res	Type
4	M	32	ILE

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	403/428 (94%)	402 (100%)	1 (0%)	92 94
1	G	403/428 (94%)	403 (100%)	0	100 100
1	I	403/428 (94%)	403 (100%)	0	100 100
2	B	110/129 (85%)	110 (100%)	0	100 100
2	C	110/129 (85%)	110 (100%)	0	100 100
2	J	110/129 (85%)	110 (100%)	0	100 100
3	D	104/194 (54%)	103 (99%)	1 (1%)	73 81
3	H	104/194 (54%)	103 (99%)	1 (1%)	73 81
3	K	104/194 (54%)	103 (99%)	1 (1%)	73 81
4	E	83/173 (48%)	82 (99%)	1 (1%)	67 79
4	L	83/173 (48%)	82 (99%)	1 (1%)	67 79
4	M	83/173 (48%)	83 (100%)	0	100 100
5	e	89/179 (50%)	89 (100%)	0	100 100
5	l	89/179 (50%)	89 (100%)	0	100 100
5	m	89/179 (50%)	89 (100%)	0	100 100
6	d	113/202 (56%)	112 (99%)	1 (1%)	75 83
6	h	113/202 (56%)	112 (99%)	1 (1%)	75 83
6	k	113/202 (56%)	112 (99%)	1 (1%)	75 83
All	All	2706/3915 (69%)	2697 (100%)	9 (0%)	90 92

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	K	12	LYS

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Mol	Chain	Res	Type
6	k	39	ARG
1	A	296	CYS
3	D	12	LYS
4	E	27	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	100	ASN
5	e	37	GLN
2	J	591	GLN
1	I	425	ASN
2	C	640	GLN

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)

105 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	F	1	1,7	14,14,15	0.21	0	17,19,21	0.40	0
7	NAG	F	2	7	14,14,15	0.23	0	17,19,21	0.44	0
7	NAG	N	1	1,7	14,14,15	0.32	0	17,19,21	0.50	0
7	NAG	N	2	7	14,14,15	0.21	0	17,19,21	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	NAG	O	1	1,8	14,14,15	0.63	1 (7%)	17,19,21	0.67	1 (5%)
8	NAG	O	2	8	14,14,15	0.25	0	17,19,21	0.50	0
8	BMA	O	3	8	11,11,12	0.45	0	15,15,17	0.80	0
8	MAN	O	4	8	11,11,12	0.59	0	15,15,17	0.94	2 (13%)
7	NAG	P	1	1,7	14,14,15	0.43	0	17,19,21	0.49	0
7	NAG	P	2	7	14,14,15	0.22	0	17,19,21	0.43	0
7	NAG	Q	1	1,7	14,14,15	0.32	0	17,19,21	0.53	0
7	NAG	Q	2	7	14,14,15	0.23	0	17,19,21	0.46	0
9	NAG	R	1	1,9	14,14,15	0.17	0	17,19,21	0.41	0
9	NAG	R	2	9	14,14,15	0.19	0	17,19,21	0.53	0
9	BMA	R	3	9	11,11,12	0.58	0	15,15,17	0.69	0
10	NAG	S	1	1,10	14,14,15	0.20	0	17,19,21	0.49	0
10	NAG	S	2	10	14,14,15	0.38	0	17,19,21	0.38	0
10	BMA	S	3	10	11,11,12	0.61	0	15,15,17	0.76	0
10	MAN	S	4	10	11,11,12	0.82	0	15,15,17	1.16	2 (13%)
10	MAN	S	5	10	11,11,12	0.66	0	15,15,17	1.02	2 (13%)
7	NAG	T	1	1,7	14,14,15	0.44	0	17,19,21	0.38	0
7	NAG	T	2	7	14,14,15	0.25	0	17,19,21	0.52	0
11	NAG	U	1	11,1	14,14,15	0.24	0	17,19,21	0.41	0
11	NAG	U	2	11	14,14,15	0.27	0	17,19,21	0.64	0
11	BMA	U	3	11	11,11,12	0.96	0	15,15,17	0.91	0
11	MAN	U	4	11	11,11,12	0.65	0	15,15,17	1.09	2 (13%)
11	MAN	U	5	11	11,11,12	0.70	0	15,15,17	0.97	1 (6%)
11	MAN	U	6	11	11,11,12	0.80	0	15,15,17	1.30	2 (13%)
11	MAN	U	7	11	11,11,12	0.72	0	15,15,17	1.03	2 (13%)
11	MAN	U	8	11	11,11,12	0.64	0	15,15,17	0.92	1 (6%)
11	MAN	U	9	11	11,11,12	0.83	1 (9%)	15,15,17	1.32	2 (13%)
7	NAG	V	1	1,7	14,14,15	0.25	0	17,19,21	0.75	1 (5%)
7	NAG	V	2	7	14,14,15	0.30	0	17,19,21	0.41	0
7	NAG	W	1	1,7	14,14,15	0.31	0	17,19,21	0.52	0
7	NAG	W	2	7	14,14,15	0.31	0	17,19,21	0.55	0
7	NAG	X	1	1,7	14,14,15	0.20	0	17,19,21	0.44	0
7	NAG	X	2	7	14,14,15	0.24	0	17,19,21	0.43	0
7	NAG	Y	1	1,7	14,14,15	0.28	0	17,19,21	0.50	0
7	NAG	Y	2	7	14,14,15	0.19	0	17,19,21	0.43	0
8	NAG	Z	1	1,8	14,14,15	0.63	1 (7%)	17,19,21	0.69	1 (5%)
8	NAG	Z	2	8	14,14,15	0.26	0	17,19,21	0.49	0
8	BMA	Z	3	8	11,11,12	0.48	0	15,15,17	0.81	0
8	MAN	Z	4	8	11,11,12	0.65	0	15,15,17	1.03	2 (13%)
7	NAG	a	1	1,7	14,14,15	0.37	0	17,19,21	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	NAG	a	2	7	14,14,15	0.32	0	17,19,21	0.40	0
7	NAG	b	1	1,7	14,14,15	0.32	0	17,19,21	0.53	0
7	NAG	b	2	7	14,14,15	0.24	0	17,19,21	0.41	0
9	NAG	c	1	1,9	14,14,15	0.19	0	17,19,21	0.40	0
9	NAG	c	2	9	14,14,15	0.20	0	17,19,21	0.50	0
9	BMA	c	3	9	11,11,12	0.57	0	15,15,17	0.66	0
10	NAG	f	1	1,10	14,14,15	0.26	0	17,19,21	0.51	0
10	NAG	f	2	10	14,14,15	0.24	0	17,19,21	0.56	0
10	BMA	f	3	10	11,11,12	0.66	0	15,15,17	0.75	0
10	MAN	f	4	10	11,11,12	0.81	1 (9%)	15,15,17	1.08	2 (13%)
10	MAN	f	5	10	11,11,12	0.58	0	15,15,17	0.92	2 (13%)
7	NAG	g	1	1,7	14,14,15	0.58	1 (7%)	17,19,21	0.48	0
7	NAG	g	2	7	14,14,15	0.38	0	17,19,21	0.59	0
11	NAG	i	1	11,1	14,14,15	0.25	0	17,19,21	0.63	0
11	NAG	i	2	11	14,14,15	0.41	0	17,19,21	0.71	0
11	BMA	i	3	11	11,11,12	0.92	0	15,15,17	1.00	0
11	MAN	i	4	11	11,11,12	0.66	0	15,15,17	1.14	2 (13%)
11	MAN	i	5	11	11,11,12	0.72	0	15,15,17	0.93	1 (6%)
11	MAN	i	6	11	11,11,12	0.79	1 (9%)	15,15,17	1.34	2 (13%)
11	MAN	i	7	11	11,11,12	0.67	0	15,15,17	0.89	2 (13%)
11	MAN	i	8	11	11,11,12	0.64	0	15,15,17	1.00	2 (13%)
11	MAN	i	9	11	11,11,12	0.78	1 (9%)	15,15,17	1.17	2 (13%)
7	NAG	j	1	1,7	14,14,15	0.29	0	17,19,21	0.69	0
7	NAG	j	2	7	14,14,15	0.32	0	17,19,21	0.42	0
7	NAG	n	1	1,7	14,14,15	0.78	1 (7%)	17,19,21	0.68	0
7	NAG	n	2	7	14,14,15	0.47	0	17,19,21	0.54	0
7	NAG	o	1	1,7	14,14,15	0.15	0	17,19,21	0.45	0
7	NAG	o	2	7	14,14,15	0.25	0	17,19,21	0.44	0
7	NAG	p	1	1,7	14,14,15	0.28	0	17,19,21	0.56	0
7	NAG	p	2	7	14,14,15	0.26	0	17,19,21	0.44	0
8	NAG	q	1	1,8	14,14,15	0.62	1 (7%)	17,19,21	0.69	1 (5%)
8	NAG	q	2	8	14,14,15	0.26	0	17,19,21	0.48	0
8	BMA	q	3	8	11,11,12	0.48	0	15,15,17	0.82	0
8	MAN	q	4	8	11,11,12	0.64	0	15,15,17	1.04	2 (13%)
7	NAG	r	1	1,7	14,14,15	0.64	1 (7%)	17,19,21	0.84	1 (5%)
7	NAG	r	2	7	14,14,15	0.47	0	17,19,21	0.47	0
7	NAG	s	1	1,7	14,14,15	0.27	0	17,19,21	0.52	0
7	NAG	s	2	7	14,14,15	0.26	0	17,19,21	0.53	0
9	NAG	t	1	1,9	14,14,15	0.22	0	17,19,21	0.37	0
9	NAG	t	2	9	14,14,15	0.19	0	17,19,21	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
9	BMA	t	3	9	11,11,12	0.61	0	15,15,17	0.67	0
10	NAG	u	1	1,10	14,14,15	0.31	0	17,19,21	0.62	0
10	NAG	u	2	10	14,14,15	0.33	0	17,19,21	0.37	0
10	BMA	u	3	10	11,11,12	0.65	0	15,15,17	0.80	0
10	MAN	u	4	10	11,11,12	0.75	0	15,15,17	1.20	2 (13%)
10	MAN	u	5	10	11,11,12	0.67	0	15,15,17	1.08	2 (13%)
7	NAG	v	1	1,7	14,14,15	0.52	0	17,19,21	0.42	0
7	NAG	v	2	7	14,14,15	0.27	0	17,19,21	0.55	0
11	NAG	w	1	11,1	14,14,15	0.20	0	17,19,21	0.51	0
11	NAG	w	2	11	14,14,15	0.29	0	17,19,21	0.69	0
11	BMA	w	3	11	11,11,12	0.97	0	15,15,17	0.96	0
11	MAN	w	4	11	11,11,12	0.72	0	15,15,17	1.11	1 (6%)
11	MAN	w	5	11	11,11,12	0.67	0	15,15,17	1.02	2 (13%)
11	MAN	w	6	11	11,11,12	0.83	0	15,15,17	1.32	2 (13%)
11	MAN	w	7	11	11,11,12	0.64	0	15,15,17	0.96	1 (6%)
11	MAN	w	8	11	11,11,12	0.92	1 (9%)	15,15,17	1.50	2 (13%)
11	MAN	w	9	11	11,11,12	0.94	1 (9%)	15,15,17	0.97	1 (6%)
7	NAG	x	1	1,7	14,14,15	0.30	0	17,19,21	0.69	0
7	NAG	x	2	7	14,14,15	0.29	0	17,19,21	0.42	0
7	NAG	y	1	1,7	14,14,15	0.69	1 (7%)	17,19,21	1.77	1 (5%)
7	NAG	y	2	7	14,14,15	0.51	0	17,19,21	0.44	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	F	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	F	2	7	-	0/6/23/26	0/1/1/1
7	NAG	N	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	N	2	7	-	0/6/23/26	0/1/1/1
8	NAG	O	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	O	2	8	-	0/6/23/26	0/1/1/1
8	BMA	O	3	8	-	0/2/19/22	0/1/1/1
8	MAN	O	4	8	-	0/2/19/22	0/1/1/1
7	NAG	P	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	P	2	7	-	2/6/23/26	0/1/1/1
7	NAG	Q	1	1,7	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	Q	2	7	-	2/6/23/26	0/1/1/1
9	NAG	R	1	1,9	-	2/6/23/26	0/1/1/1
9	NAG	R	2	9	-	2/6/23/26	0/1/1/1
9	BMA	R	3	9	-	2/2/19/22	0/1/1/1
10	NAG	S	1	1,10	-	1/6/23/26	0/1/1/1
10	NAG	S	2	10	-	2/6/23/26	0/1/1/1
10	BMA	S	3	10	-	1/2/19/22	0/1/1/1
10	MAN	S	4	10	-	0/2/19/22	1/1/1/1
10	MAN	S	5	10	-	1/2/19/22	0/1/1/1
7	NAG	T	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	T	2	7	-	2/6/23/26	0/1/1/1
11	NAG	U	1	11,1	-	0/6/23/26	0/1/1/1
11	NAG	U	2	11	-	4/6/23/26	0/1/1/1
11	BMA	U	3	11	-	1/2/19/22	0/1/1/1
11	MAN	U	4	11	-	2/2/19/22	0/1/1/1
11	MAN	U	5	11	-	1/2/19/22	0/1/1/1
11	MAN	U	6	11	-	2/2/19/22	1/1/1/1
11	MAN	U	7	11	-	2/2/19/22	0/1/1/1
11	MAN	U	8	11	-	2/2/19/22	0/1/1/1
11	MAN	U	9	11	-	0/2/19/22	0/1/1/1
7	NAG	V	1	1,7	-	3/6/23/26	0/1/1/1
7	NAG	V	2	7	-	0/6/23/26	0/1/1/1
7	NAG	W	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	W	2	7	-	3/6/23/26	0/1/1/1
7	NAG	X	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	X	2	7	-	2/6/23/26	0/1/1/1
7	NAG	Y	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	Y	2	7	-	2/6/23/26	0/1/1/1
8	NAG	Z	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	Z	2	8	-	0/6/23/26	0/1/1/1
8	BMA	Z	3	8	-	0/2/19/22	0/1/1/1
8	MAN	Z	4	8	-	2/2/19/22	0/1/1/1
7	NAG	a	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	a	2	7	-	2/6/23/26	0/1/1/1
7	NAG	b	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	b	2	7	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	c	1	1,9	-	1/6/23/26	0/1/1/1
9	NAG	c	2	9	-	0/6/23/26	0/1/1/1
9	BMA	c	3	9	-	2/2/19/22	0/1/1/1
10	NAG	f	1	1,10	-	1/6/23/26	0/1/1/1
10	NAG	f	2	10	-	2/6/23/26	0/1/1/1
10	BMA	f	3	10	-	1/2/19/22	0/1/1/1
10	MAN	f	4	10	-	0/2/19/22	0/1/1/1
10	MAN	f	5	10	-	1/2/19/22	0/1/1/1
7	NAG	g	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	g	2	7	-	4/6/23/26	0/1/1/1
11	NAG	i	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	i	2	11	-	4/6/23/26	0/1/1/1
11	BMA	i	3	11	-	2/2/19/22	0/1/1/1
11	MAN	i	4	11	-	0/2/19/22	0/1/1/1
11	MAN	i	5	11	-	1/2/19/22	0/1/1/1
11	MAN	i	6	11	-	0/2/19/22	0/1/1/1
11	MAN	i	7	11	-	2/2/19/22	0/1/1/1
11	MAN	i	8	11	-	1/2/19/22	0/1/1/1
11	MAN	i	9	11	-	0/2/19/22	0/1/1/1
7	NAG	j	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	j	2	7	-	0/6/23/26	0/1/1/1
7	NAG	n	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	n	2	7	-	3/6/23/26	0/1/1/1
7	NAG	o	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	o	2	7	-	2/6/23/26	0/1/1/1
7	NAG	p	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	p	2	7	-	2/6/23/26	0/1/1/1
8	NAG	q	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	q	2	8	-	0/6/23/26	0/1/1/1
8	BMA	q	3	8	-	0/2/19/22	0/1/1/1
8	MAN	q	4	8	-	1/2/19/22	0/1/1/1
7	NAG	r	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	r	2	7	-	2/6/23/26	0/1/1/1
7	NAG	s	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	s	2	7	-	2/6/23/26	0/1/1/1
9	NAG	t	1	1,9	-	1/6/23/26	0/1/1/1
9	NAG	t	2	9	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	BMA	t	3	9	-	2/2/19/22	0/1/1/1
10	NAG	u	1	1,10	-	1/6/23/26	0/1/1/1
10	NAG	u	2	10	-	2/6/23/26	0/1/1/1
10	BMA	u	3	10	-	2/2/19/22	0/1/1/1
10	MAN	u	4	10	-	1/2/19/22	1/1/1/1
10	MAN	u	5	10	-	2/2/19/22	0/1/1/1
7	NAG	v	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	v	2	7	-	4/6/23/26	0/1/1/1
11	NAG	w	1	11,1	-	1/6/23/26	0/1/1/1
11	NAG	w	2	11	-	4/6/23/26	0/1/1/1
11	BMA	w	3	11	-	1/2/19/22	0/1/1/1
11	MAN	w	4	11	-	0/2/19/22	0/1/1/1
11	MAN	w	5	11	-	1/2/19/22	0/1/1/1
11	MAN	w	6	11	-	1/2/19/22	1/1/1/1
11	MAN	w	7	11	-	1/2/19/22	0/1/1/1
11	MAN	w	8	11	-	1/2/19/22	0/1/1/1
11	MAN	w	9	11	-	2/2/19/22	0/1/1/1
7	NAG	x	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	x	2	7	-	2/6/23/26	0/1/1/1
7	NAG	y	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	y	2	7	-	4/6/23/26	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	n	1	NAG	O5-C1	-2.74	1.39	1.43
7	y	1	NAG	O5-C1	2.46	1.47	1.43
11	w	8	MAN	C1-C2	2.43	1.58	1.52
11	i	9	MAN	C1-C2	2.41	1.57	1.52
10	f	4	MAN	C1-C2	2.38	1.57	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	y	1	NAG	C1-O5-C5	6.71	121.19	112.19
11	w	8	MAN	C1-O5-C5	4.25	117.89	112.19
11	i	6	MAN	C1-O5-C5	4.05	117.61	112.19
11	U	6	MAN	C1-O5-C5	3.97	117.51	112.19
11	w	6	MAN	C1-O5-C5	3.97	117.50	112.19

There are no chirality outliers.

5 of 175 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	g	1	NAG	O5-C5-C6-O6
7	T	1	NAG	C4-C5-C6-O6
7	Q	1	NAG	O5-C5-C6-O6
7	o	2	NAG	C4-C5-C6-O6
7	N	1	NAG	O5-C5-C6-O6

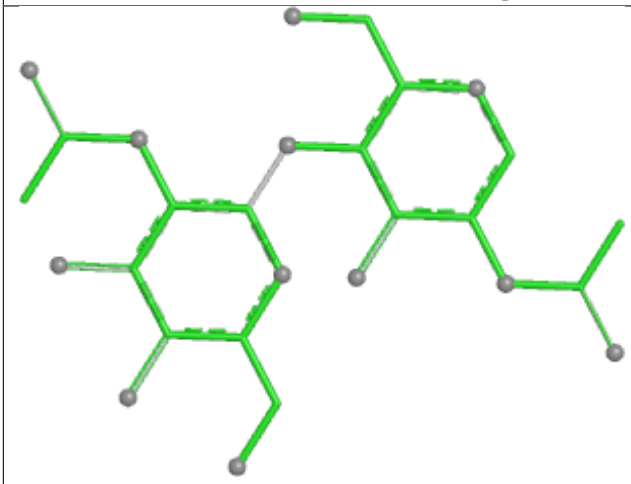
All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	S	4	MAN	C1-C2-C3-C4-C5-O5
11	w	6	MAN	C1-C2-C3-C4-C5-O5
11	U	6	MAN	C1-C2-C3-C4-C5-O5
10	u	4	MAN	C1-C2-C3-C4-C5-O5

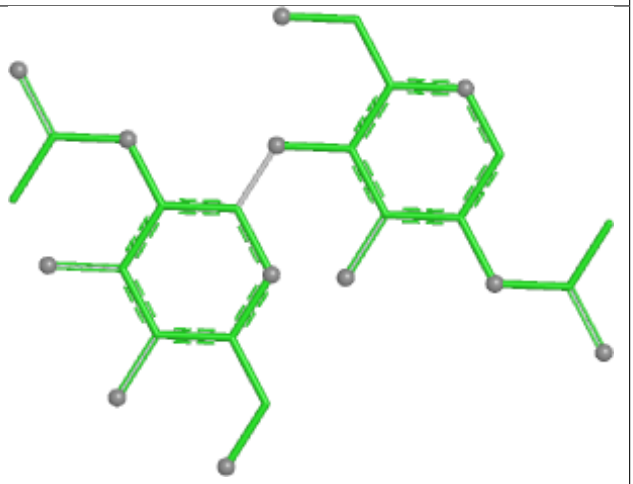
No monomer is involved in short contacts.

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

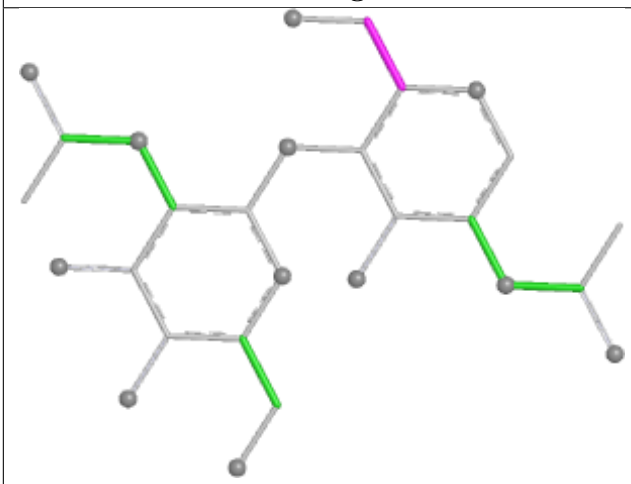
Oligosaccharide Chain F



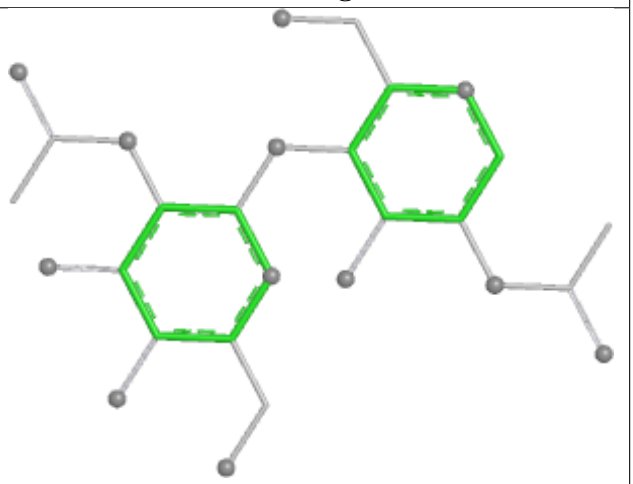
Bond lengths



Bond angles

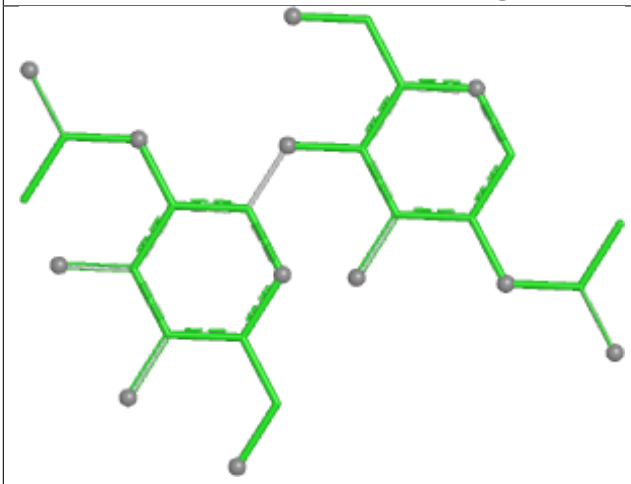


Torsions

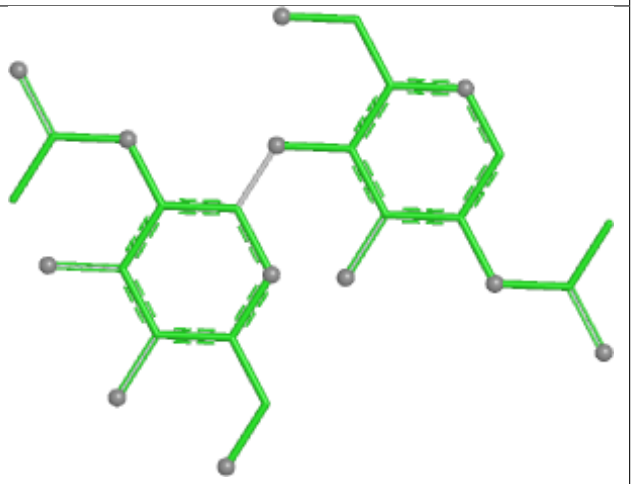


Rings

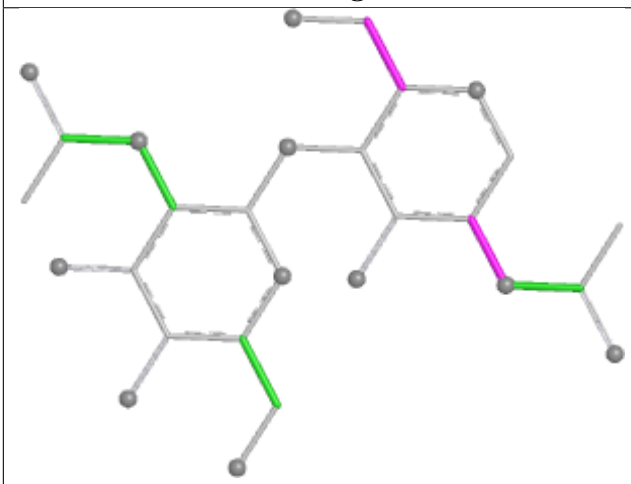
Oligosaccharide Chain N



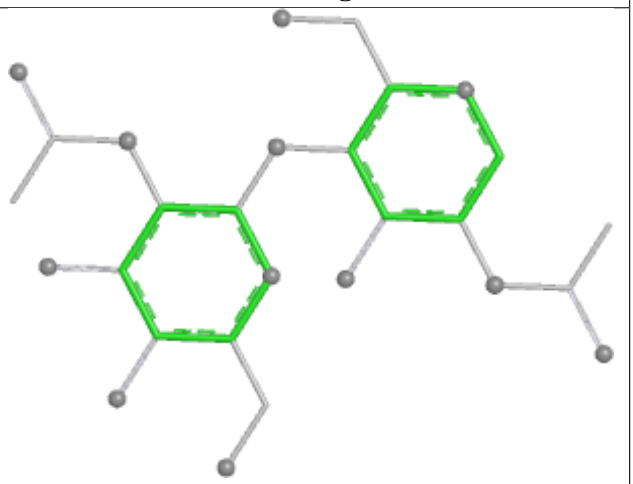
Bond lengths



Bond angles

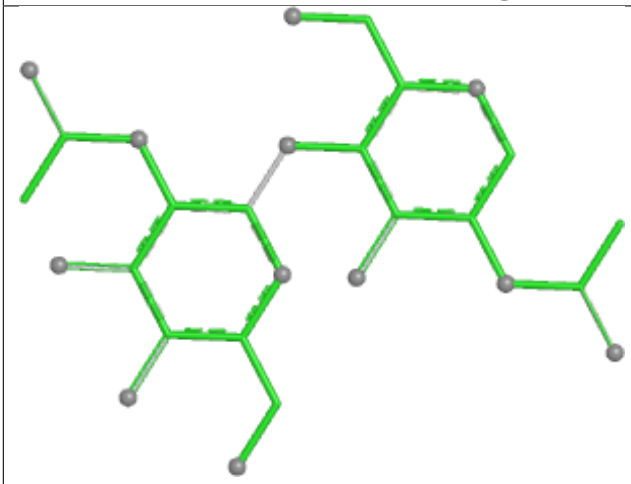


Torsions

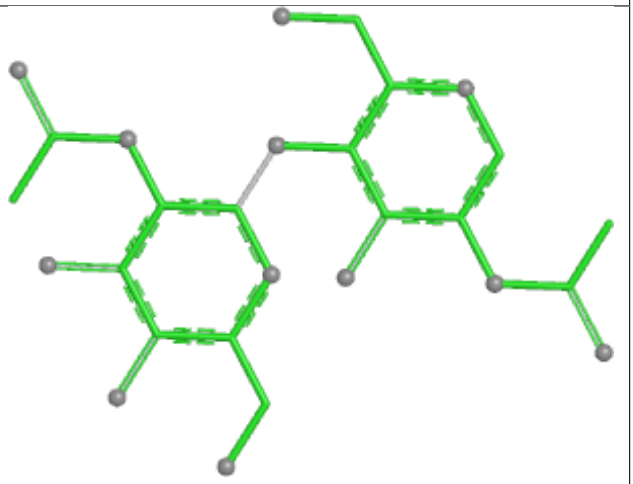


Rings

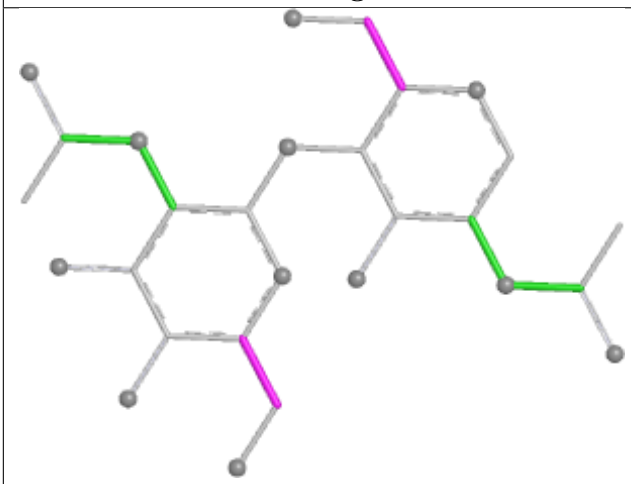
Oligosaccharide Chain P



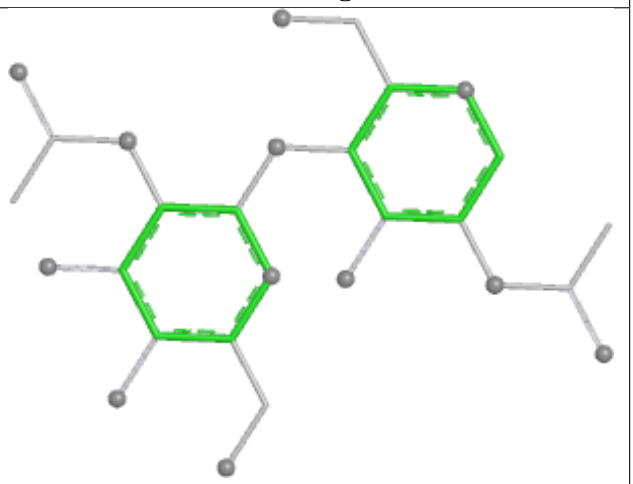
Bond lengths



Bond angles

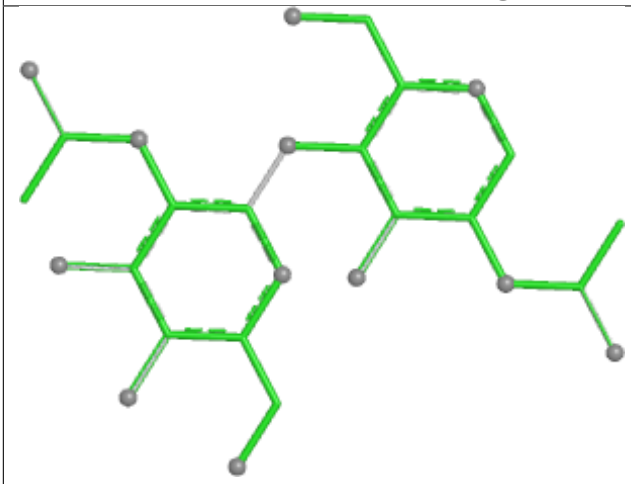


Torsions

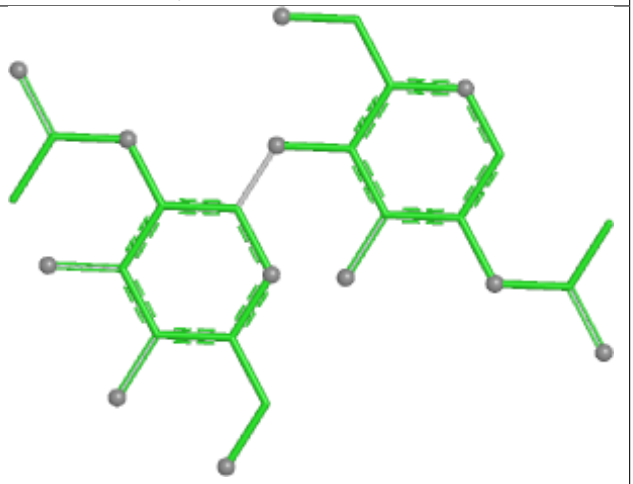


Rings

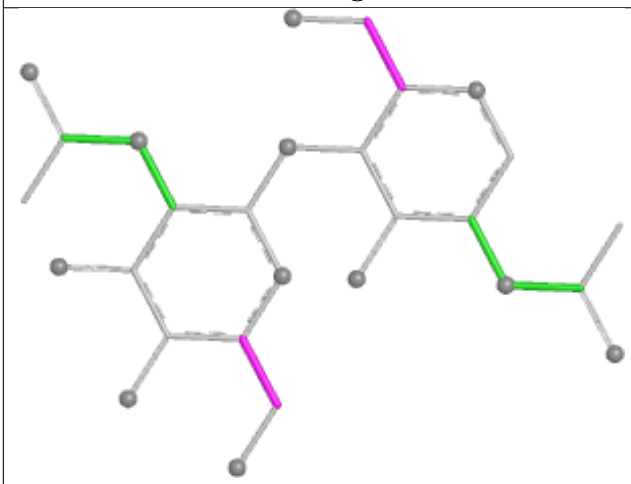
Oligosaccharide Chain Q



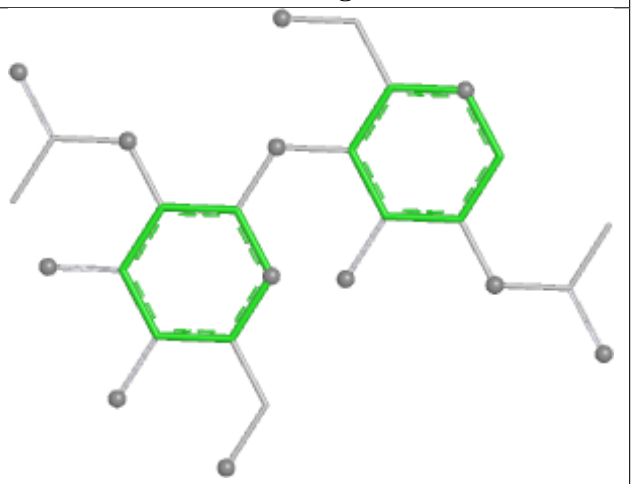
Bond lengths



Bond angles

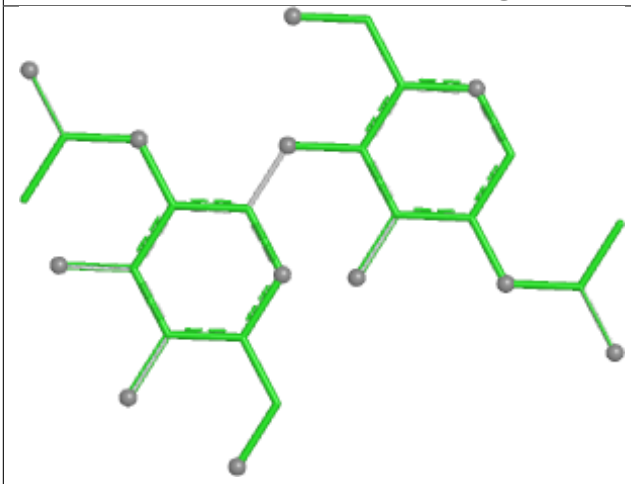


Torsions

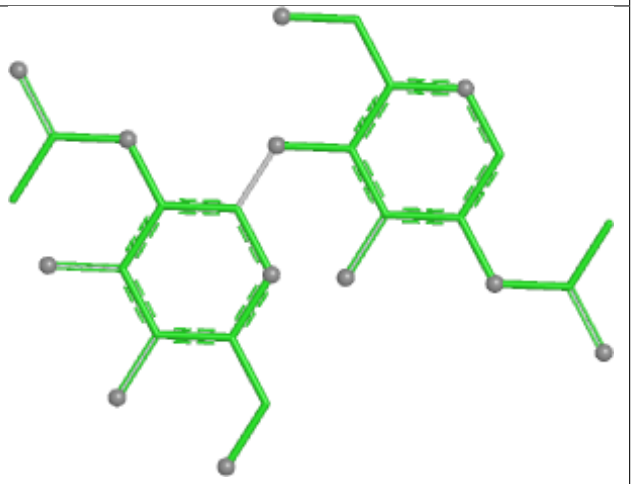


Rings

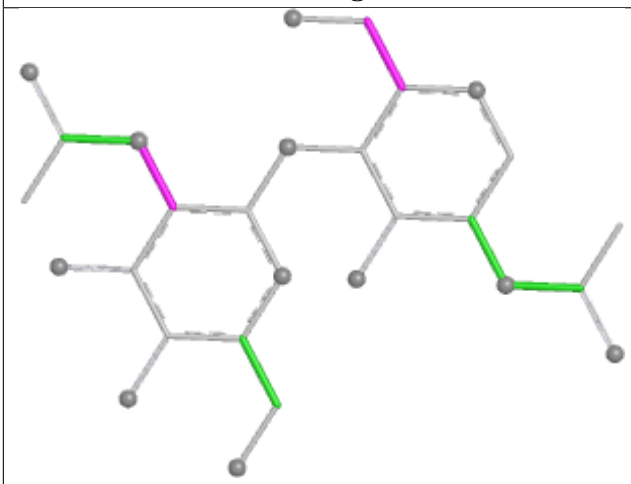
Oligosaccharide Chain T



Bond lengths



Bond angles



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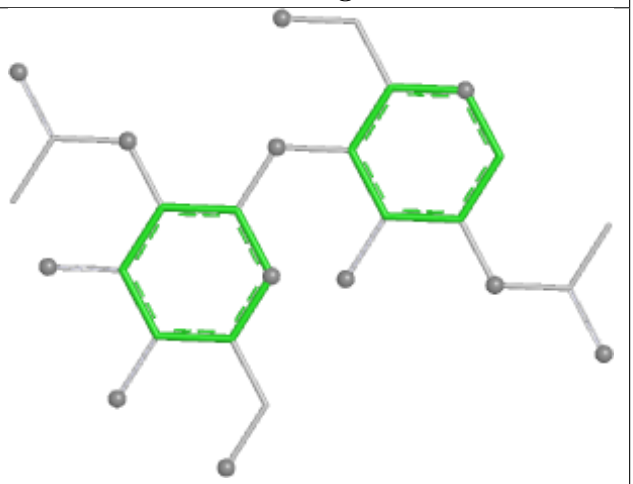
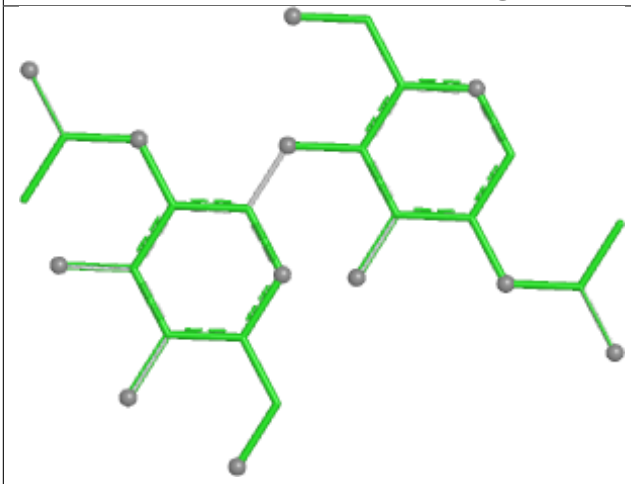
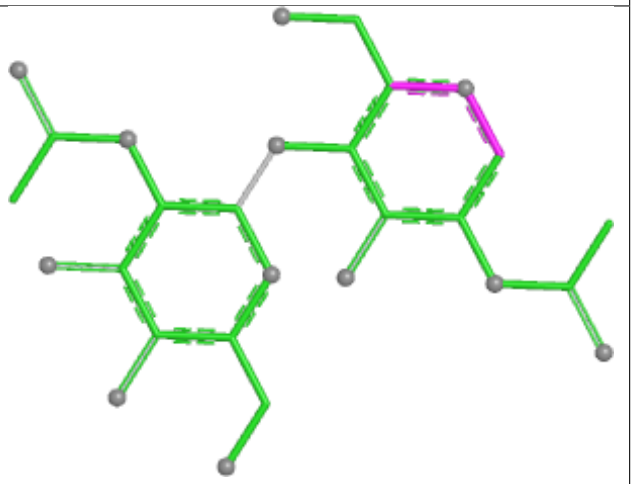


Rings

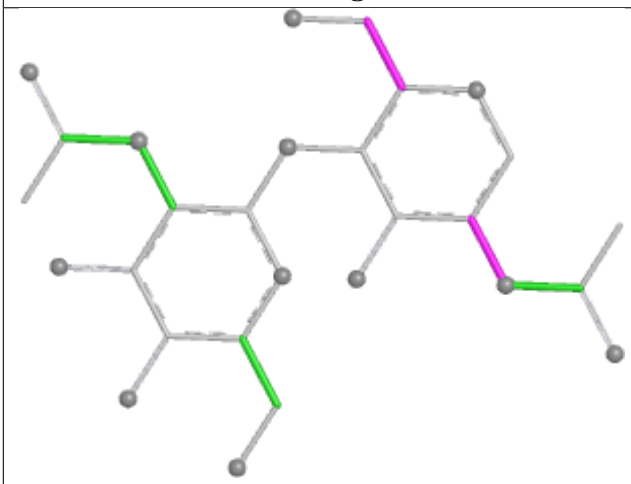
Oligosaccharide Chain V



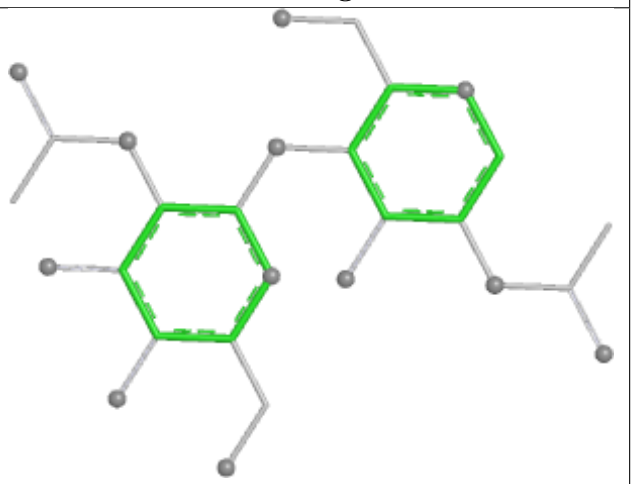
Bond lengths



Bond angles

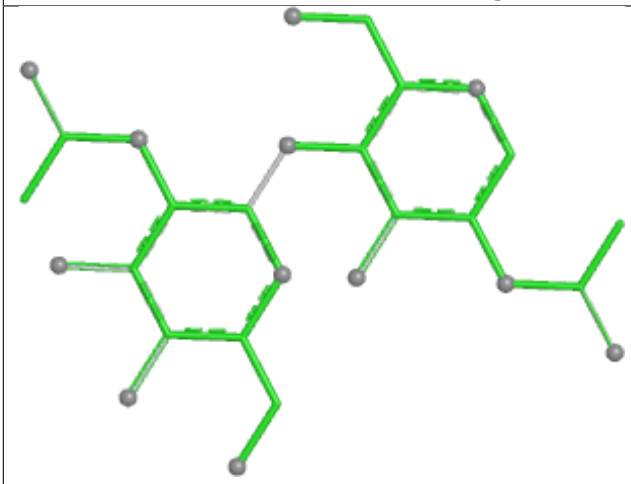


Torsions

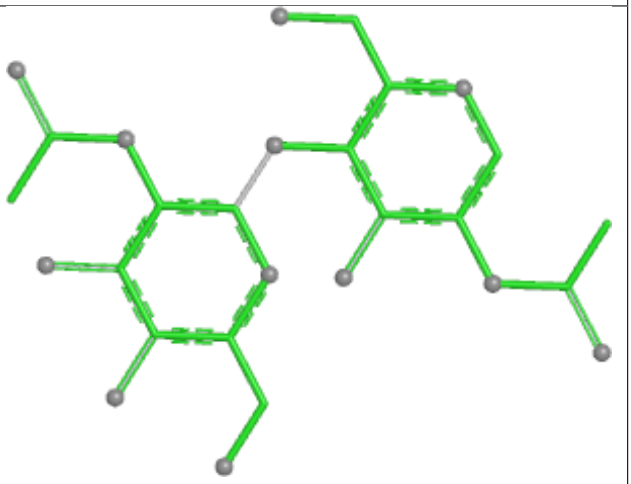


Rings

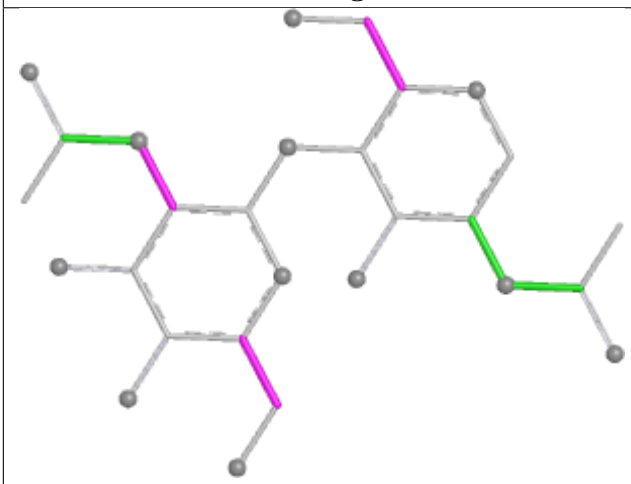
Oligosaccharide Chain W



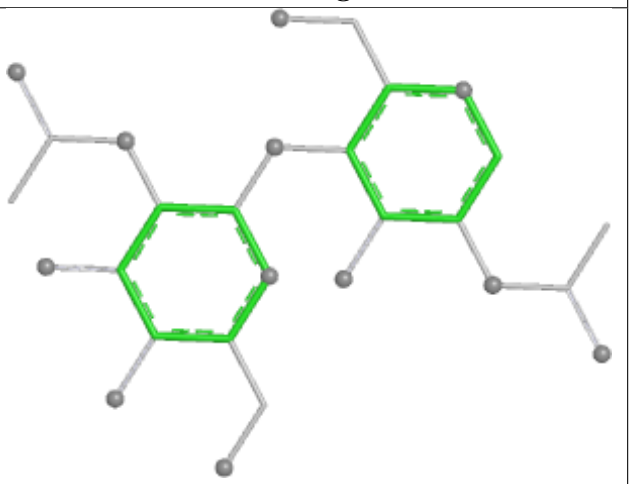
Bond lengths



Bond angles

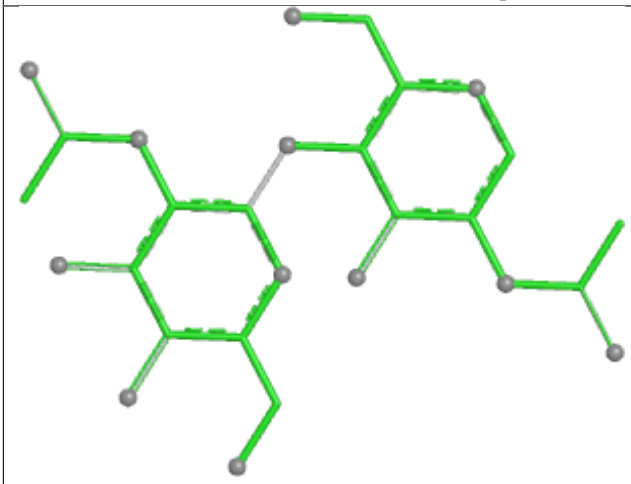


Torsions

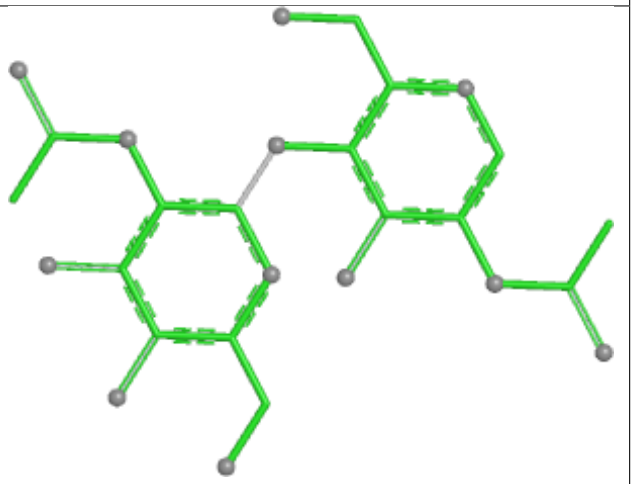


Rings

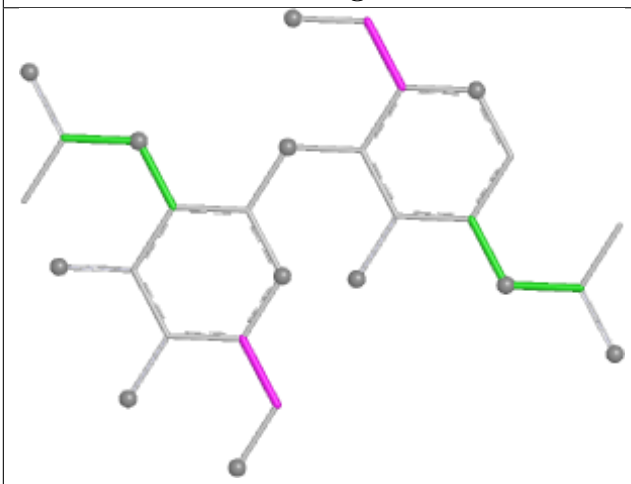
Oligosaccharide Chain X



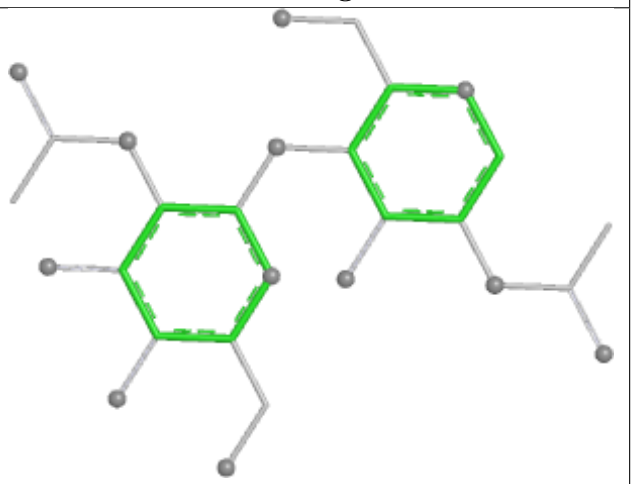
Bond lengths



Bond angles

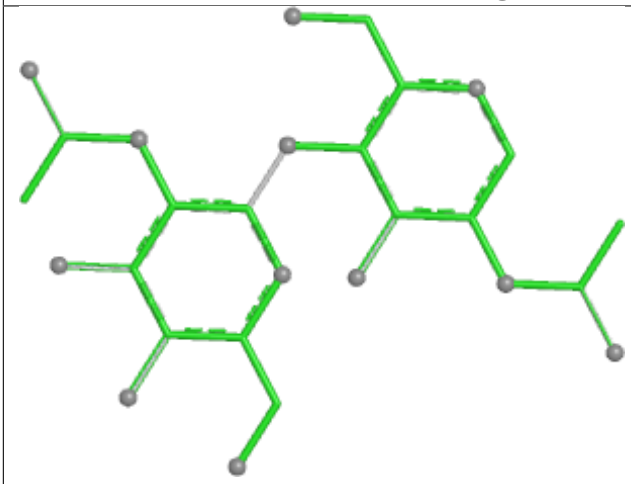


Torsions

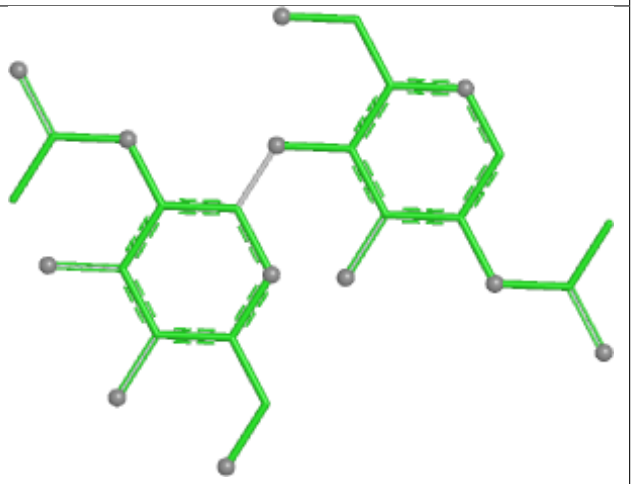


Rings

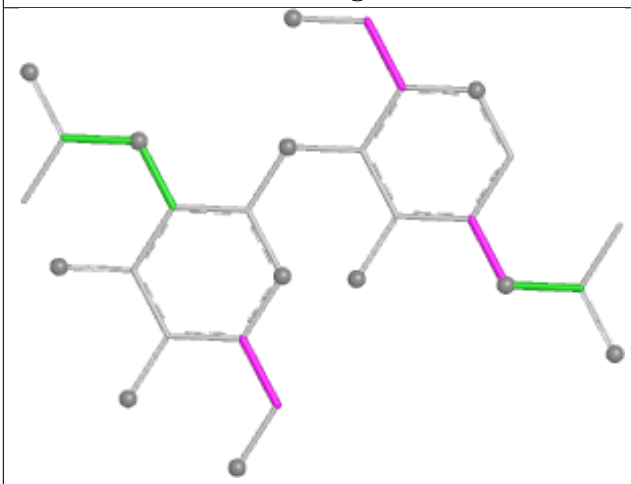
Oligosaccharide Chain Y



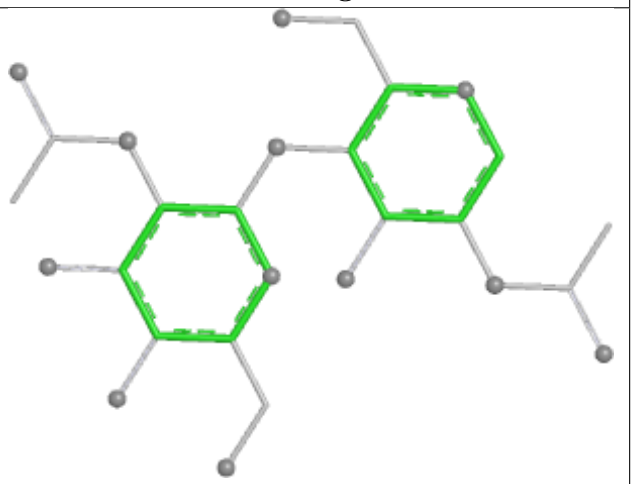
Bond lengths



Bond angles

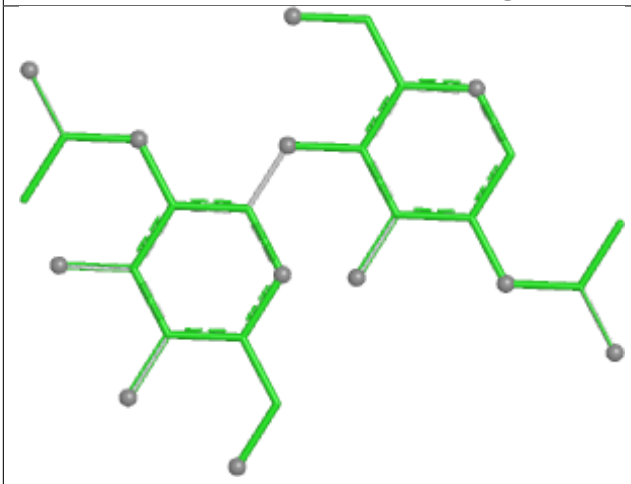


Torsions



Rings

Oligosaccharide Chain a



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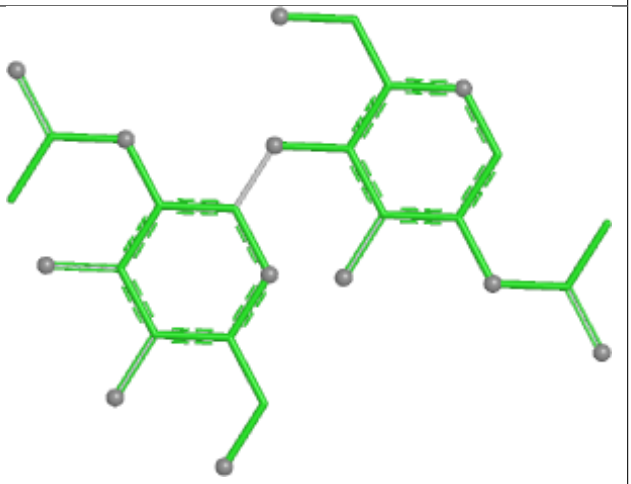

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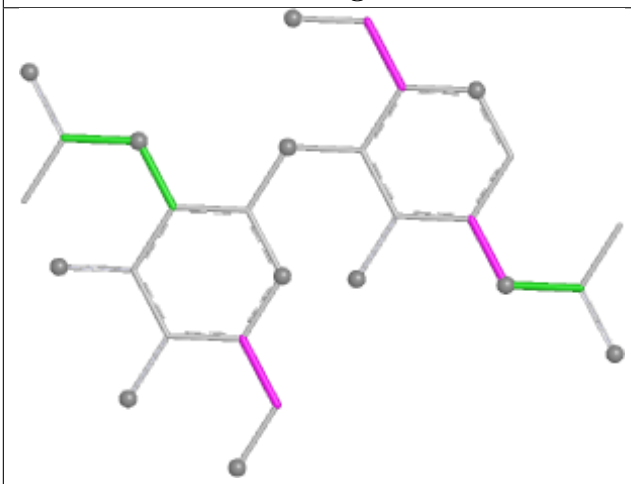
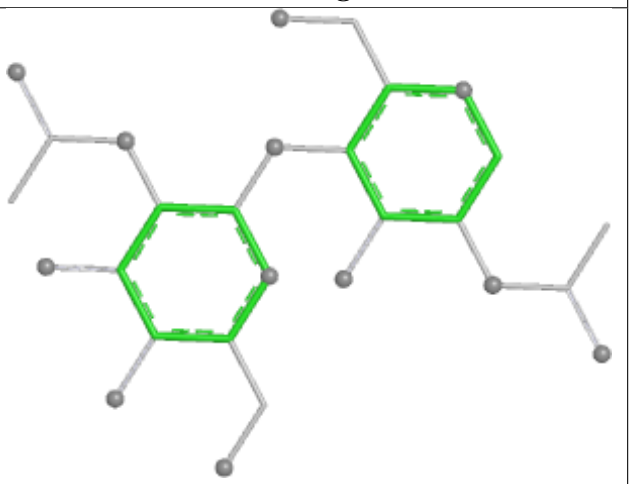
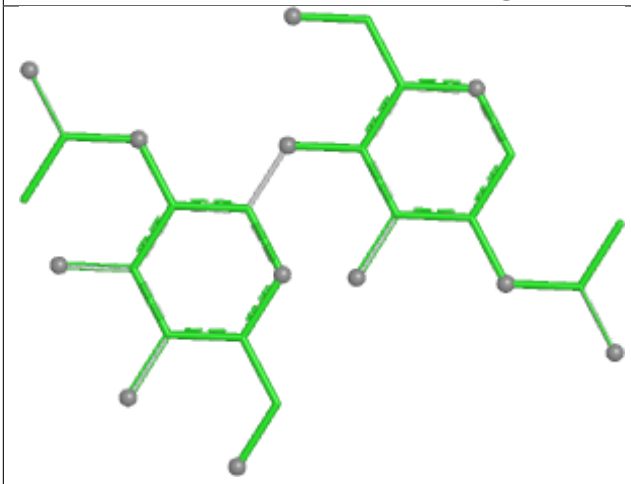


Torsions

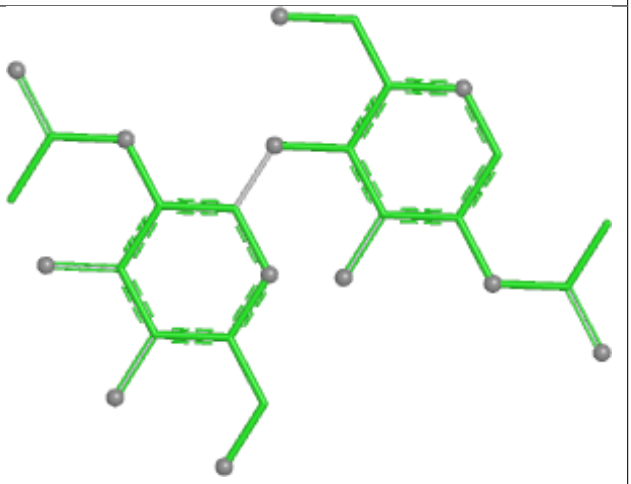


Rings

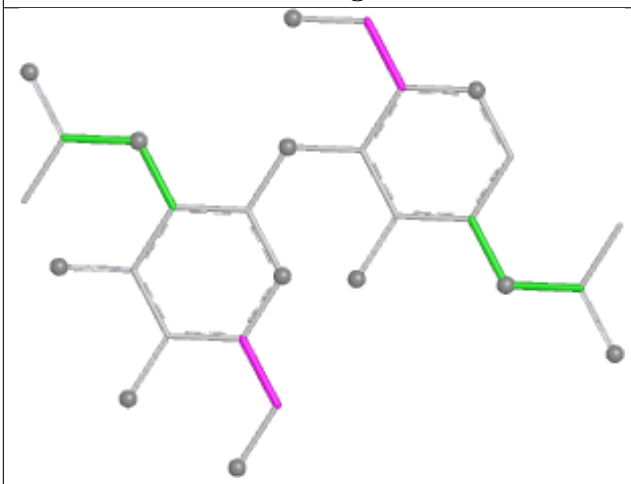
Oligosaccharide Chain b



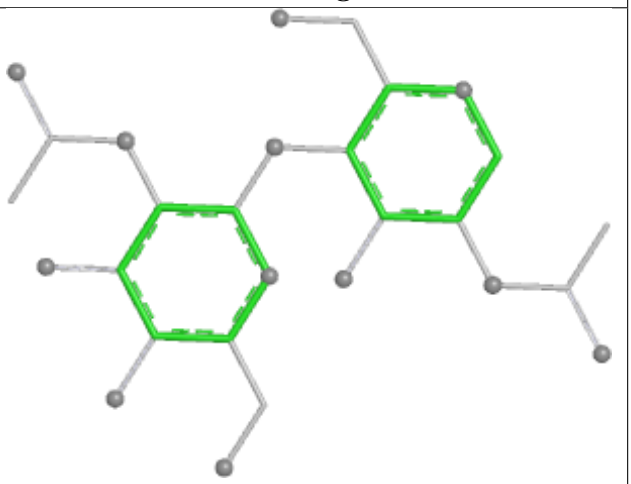
Bond lengths



Bond angles

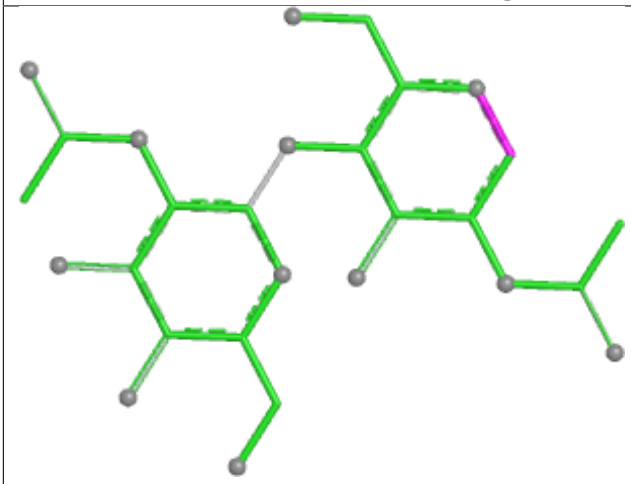


Torsions

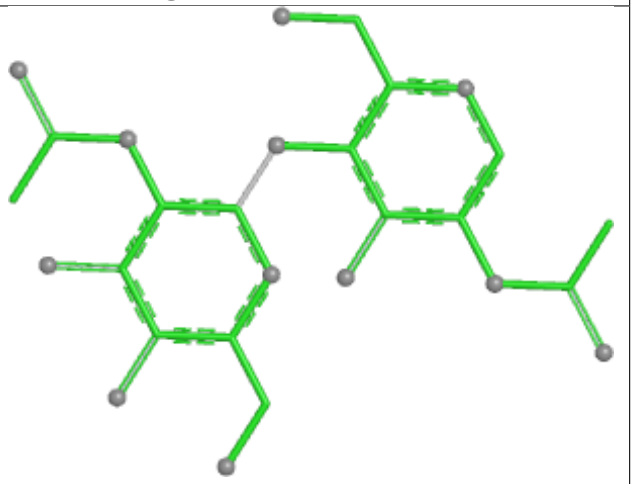


Rings

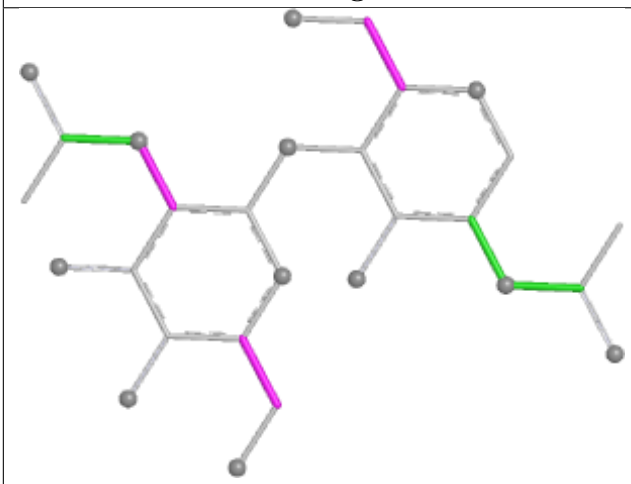
Oligosaccharide Chain g



Bond lengths



Bond angles



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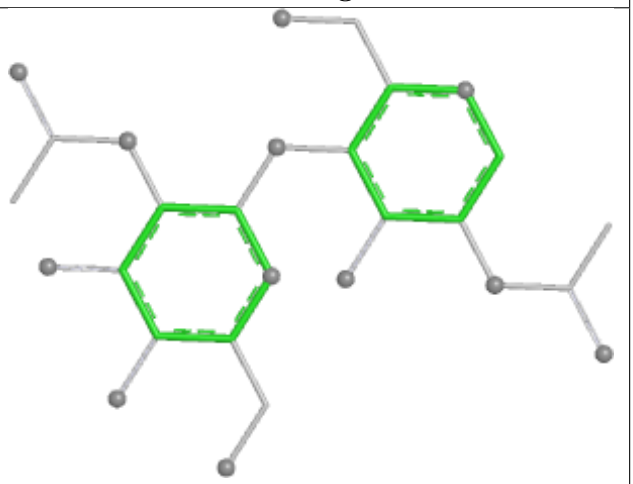
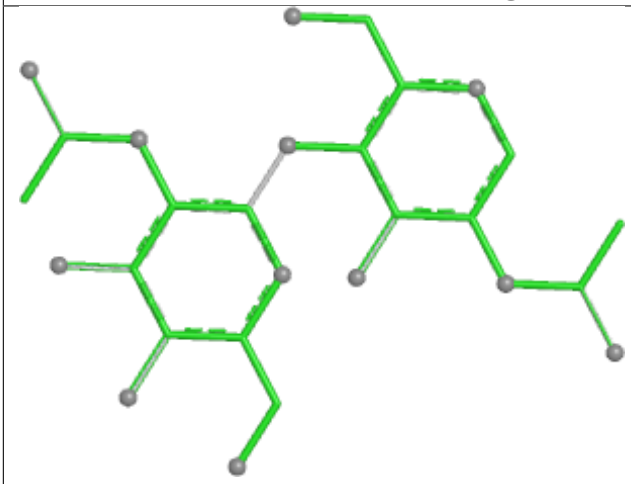
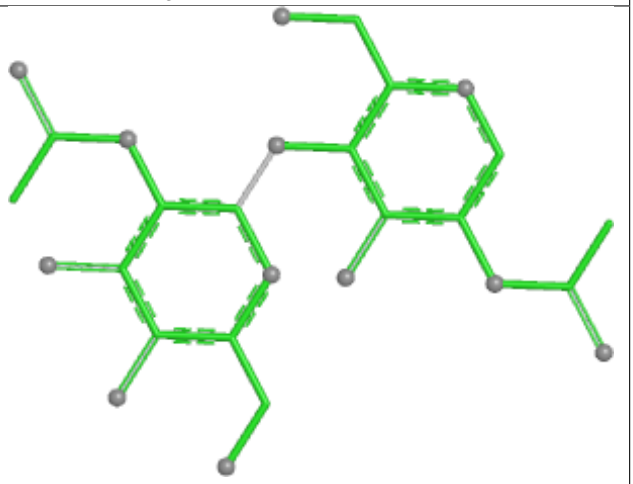


Rings

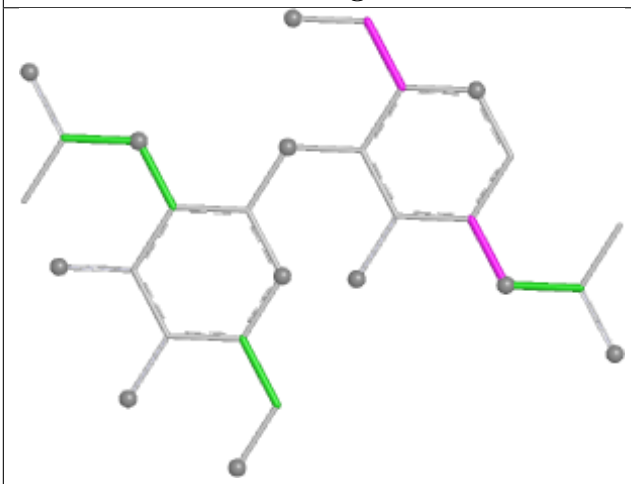
Oligosaccharide Chain j



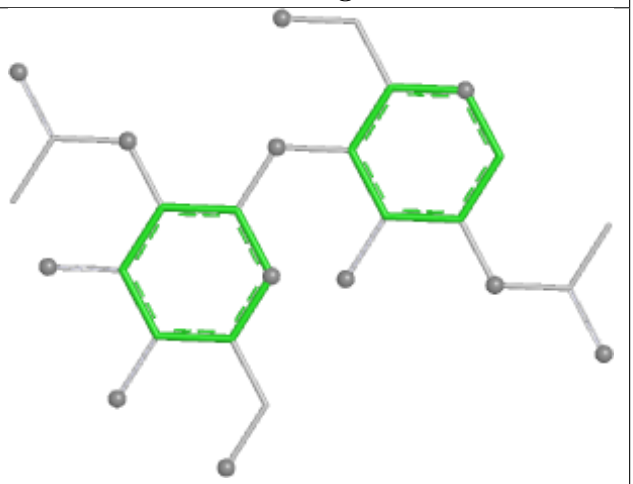
Bond lengths



Bond angles

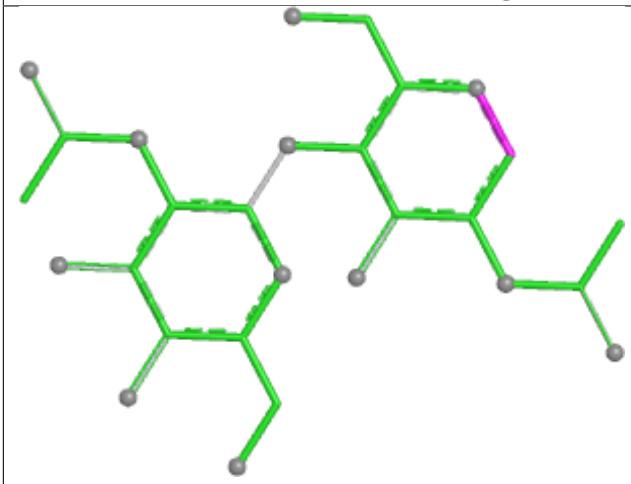


Torsions

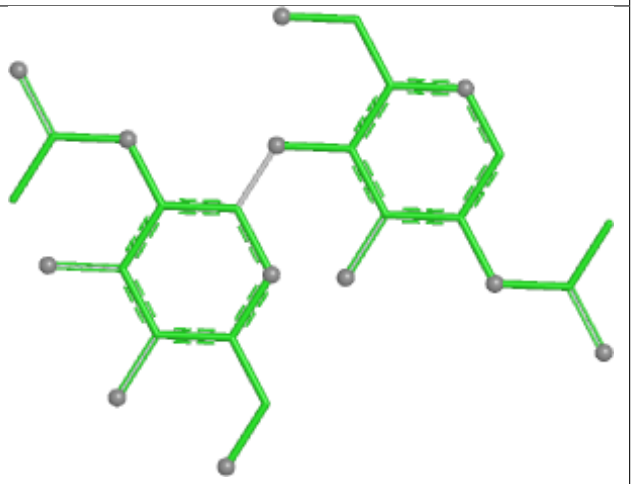


Rings

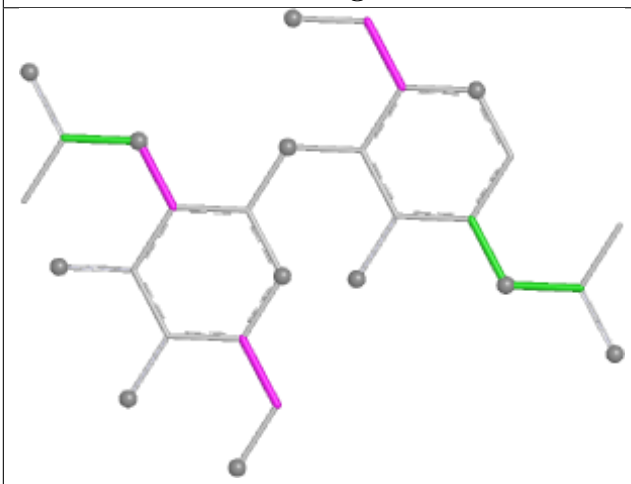
Oligosaccharide Chain n



Bond lengths



Bond angles



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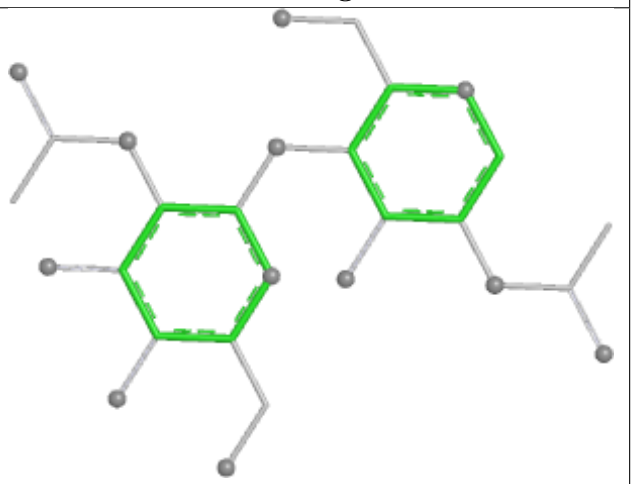
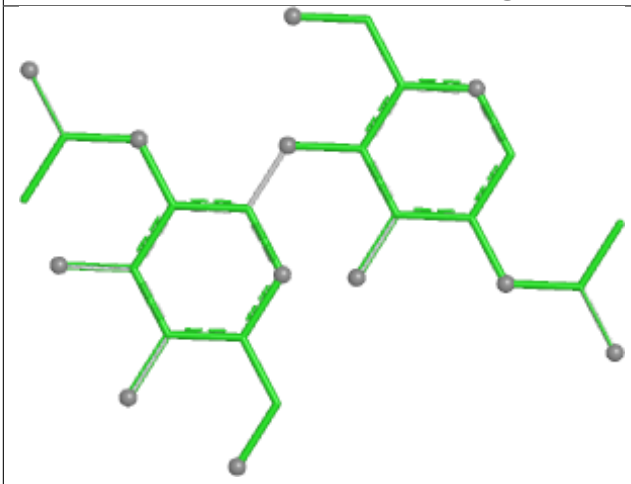
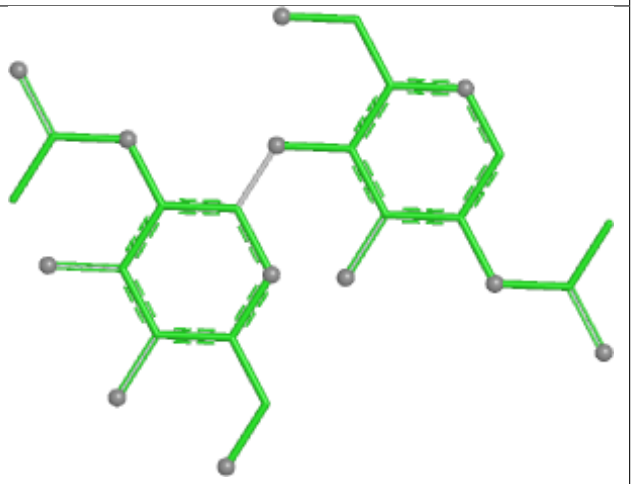


Rings

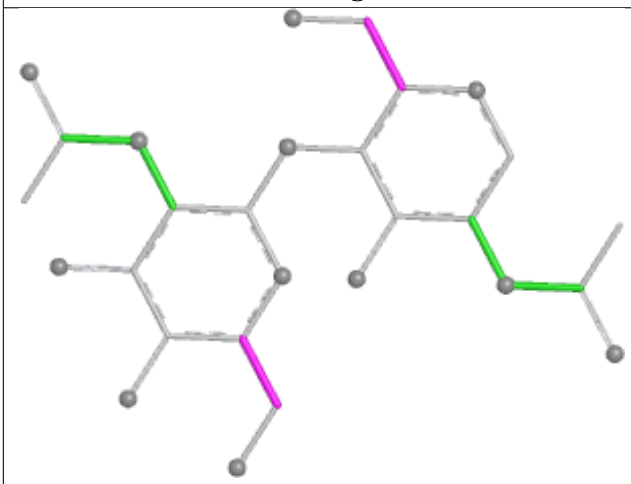
Oligosaccharide Chain o



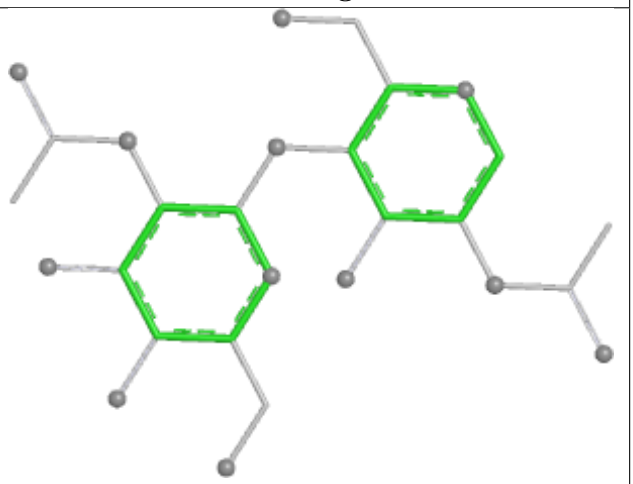
Bond lengths



Bond angles

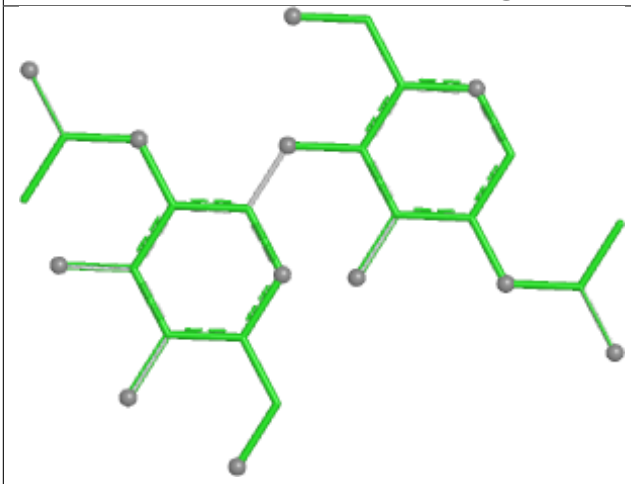


Torsions



Rings

Oligosaccharide Chain p



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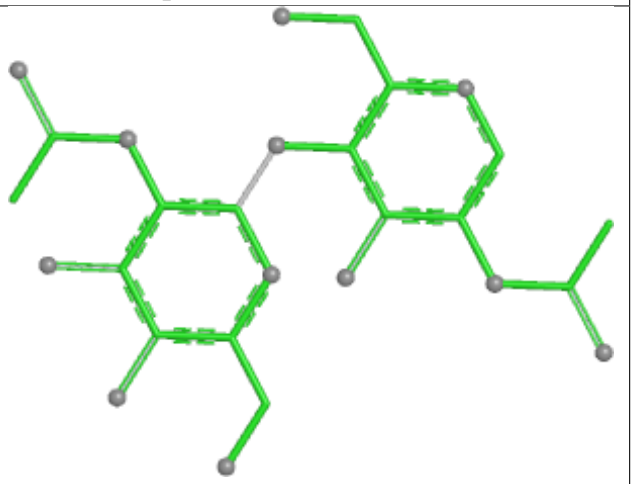
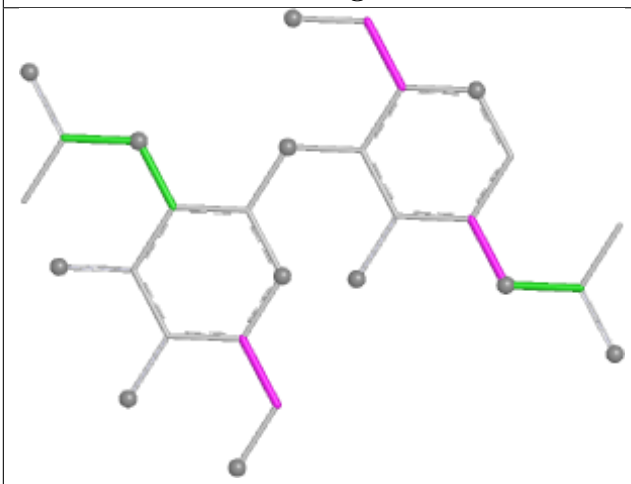


Bond angles



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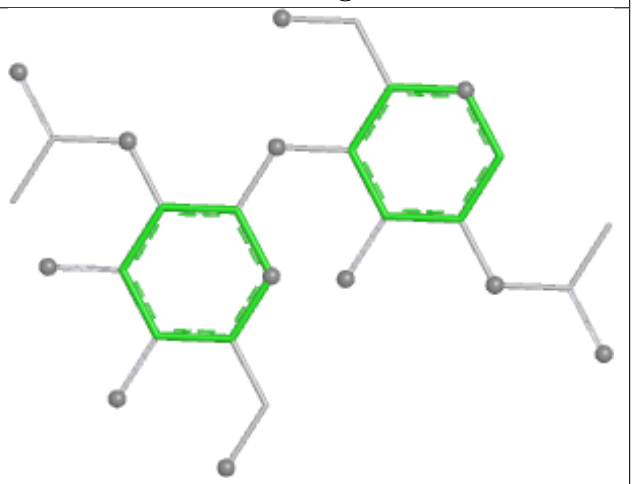
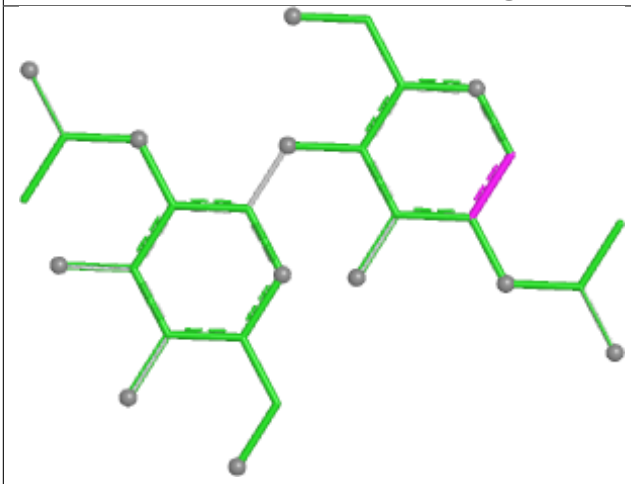


Rings

Oligosaccharide Chain r



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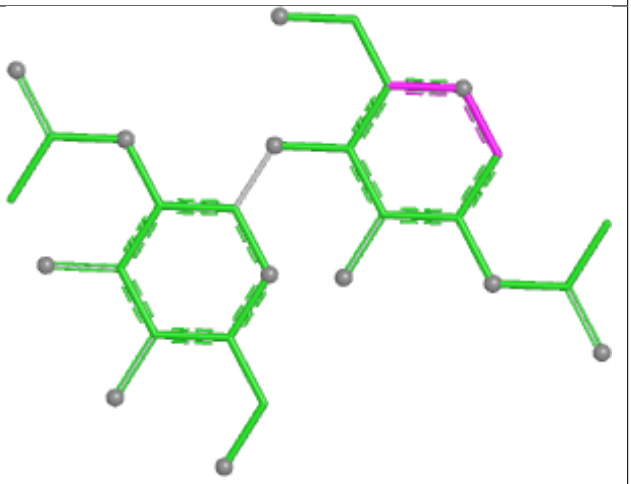
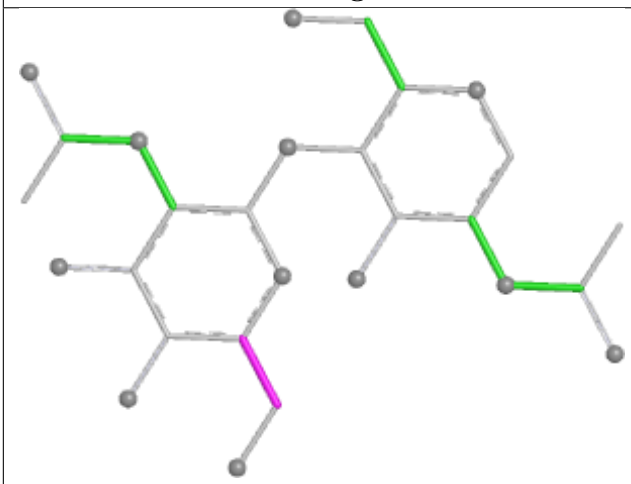
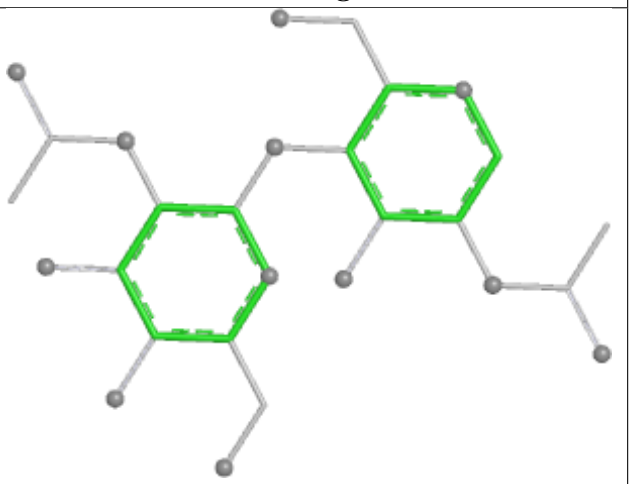


Bond angles

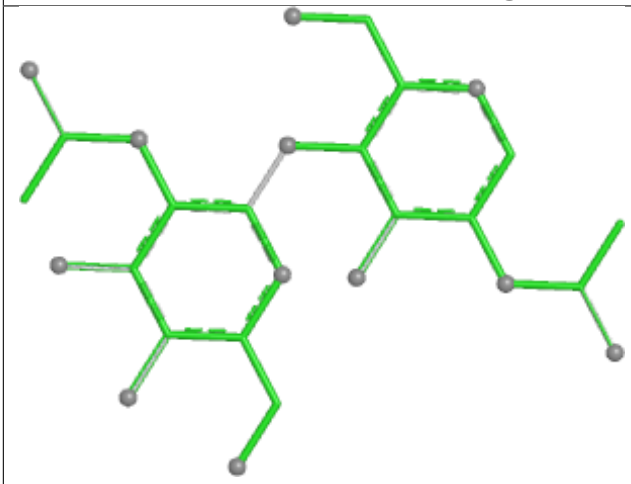


Torsions



Rings

Oligosaccharide Chain s



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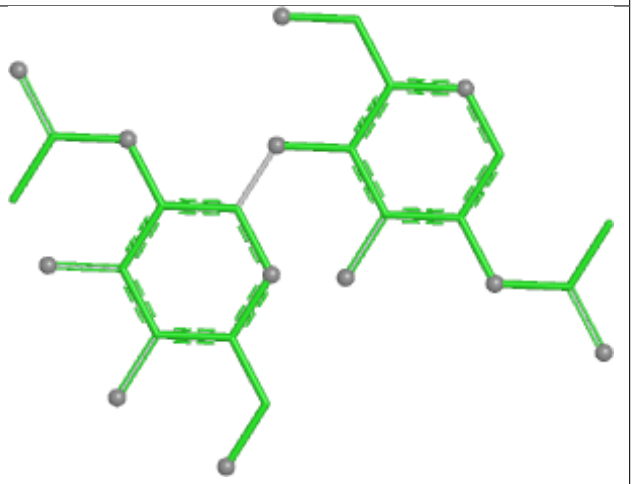

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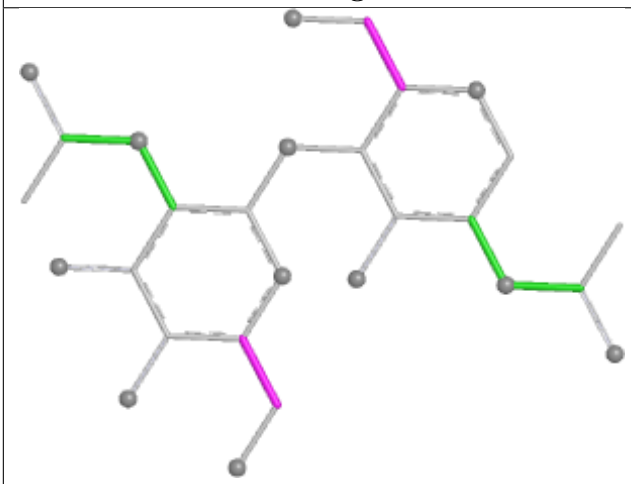
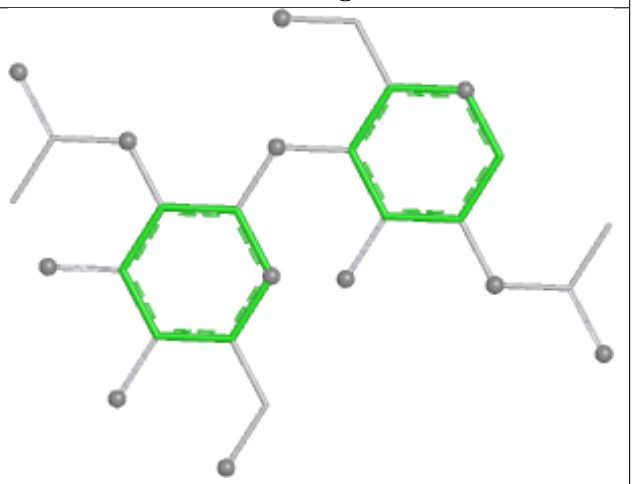
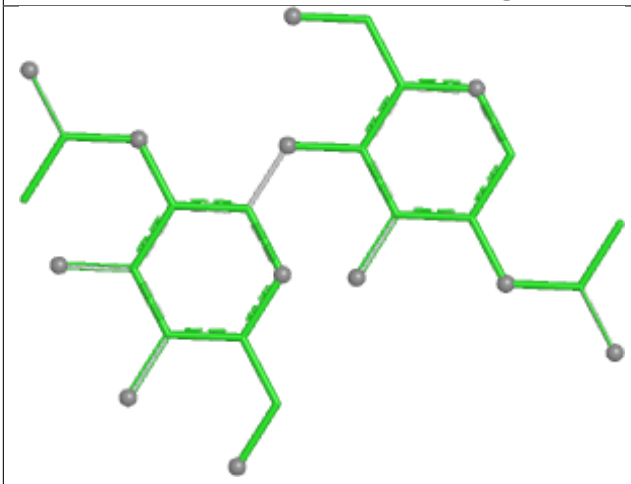


Torsions



Rings

Oligosaccharide Chain v



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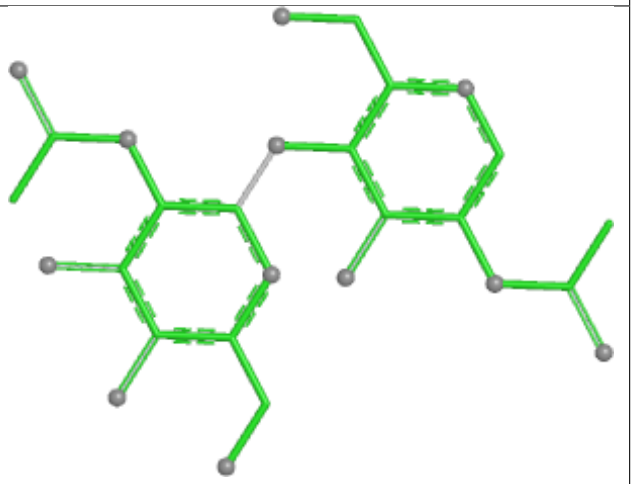
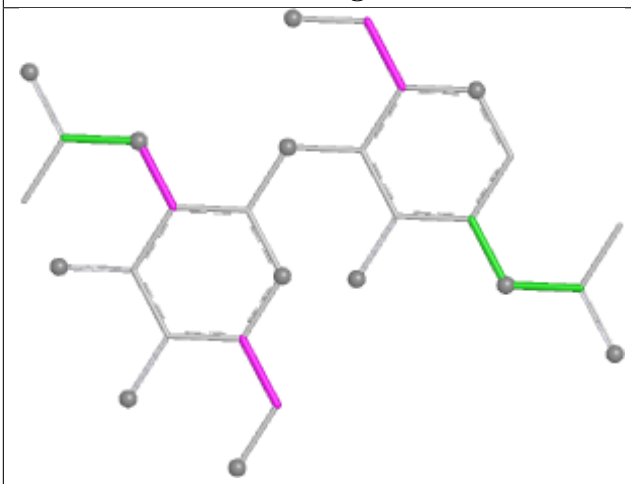
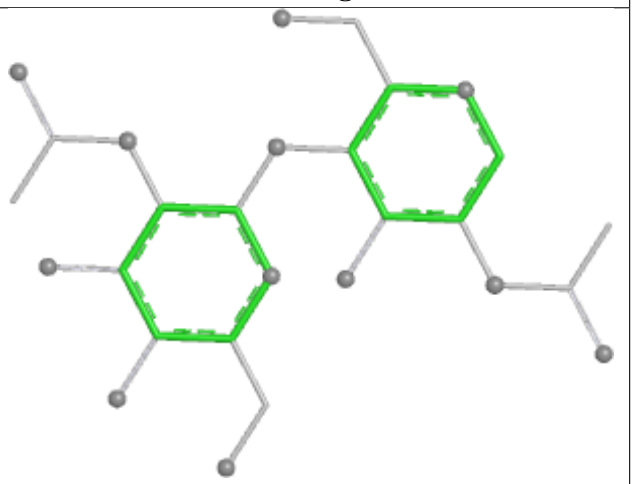


Bond angles

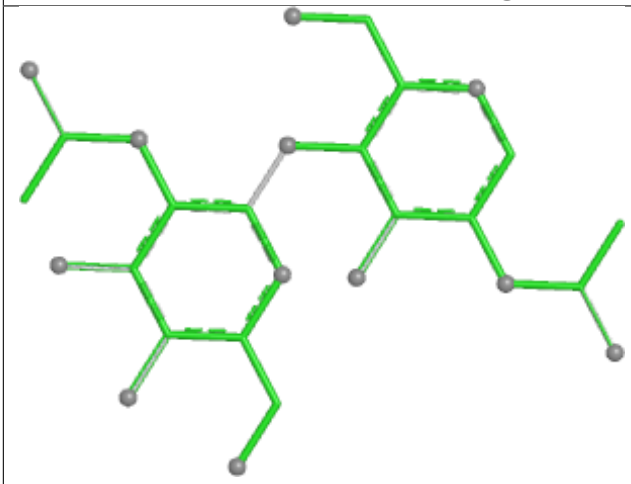


Torsions

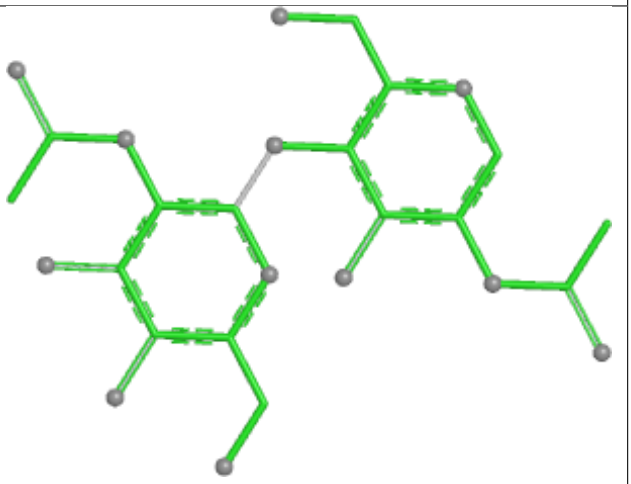


Rings

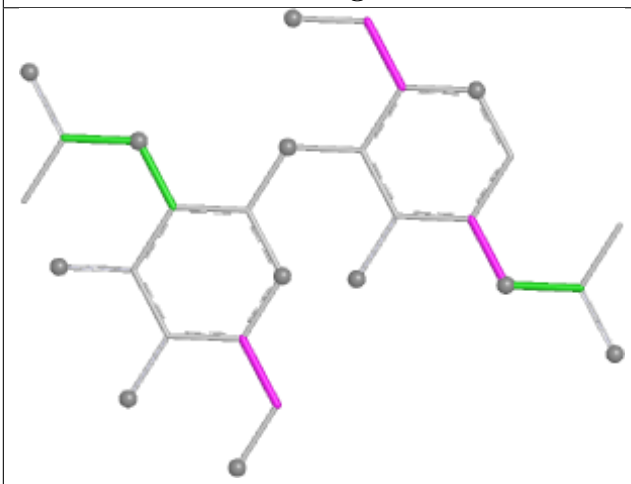
Oligosaccharide Chain x



Bond lengths



Bond angles



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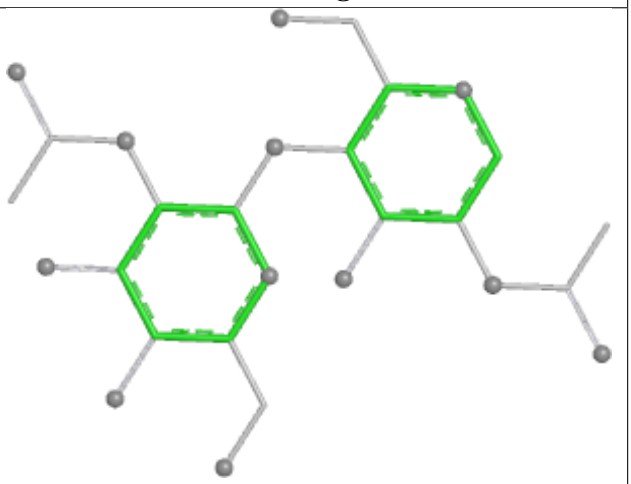
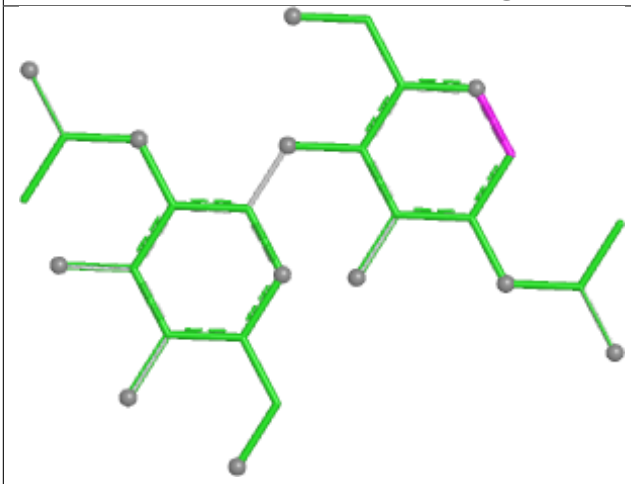


Rings

Oligosaccharide Chain y



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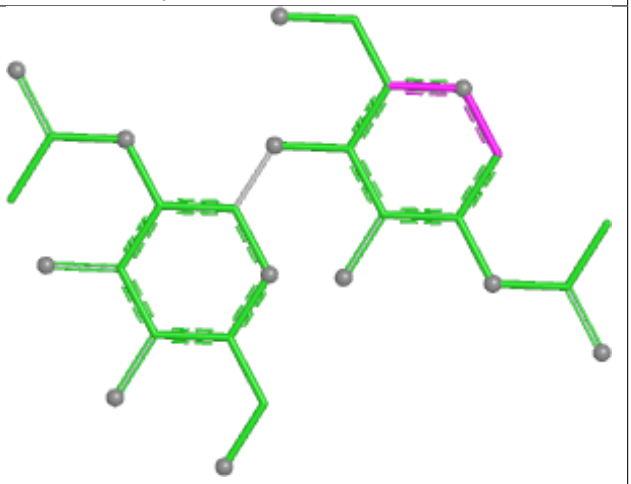
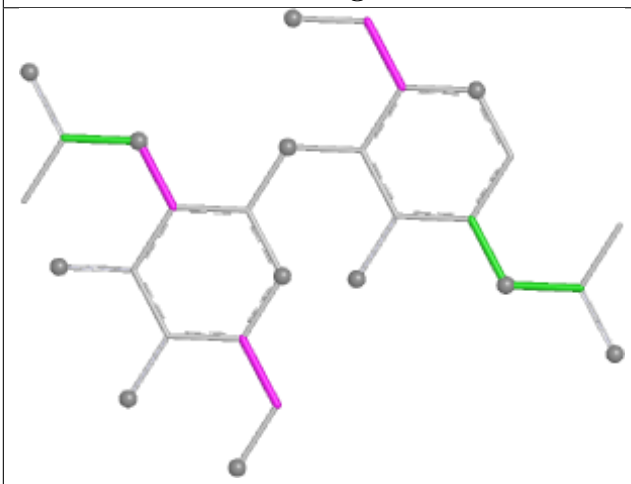


Bond angles



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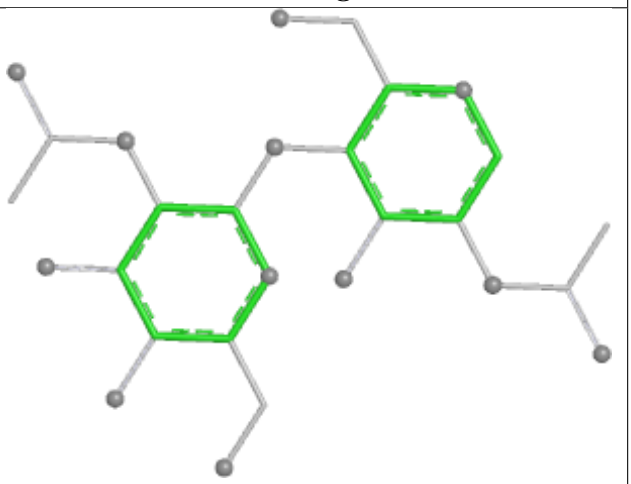
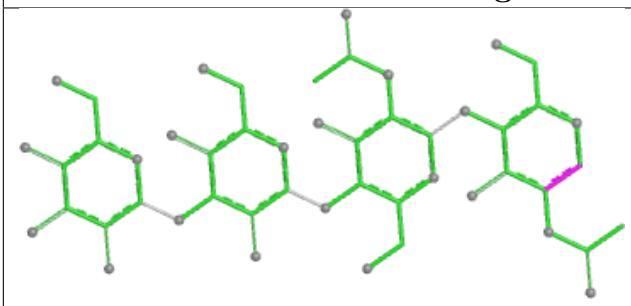
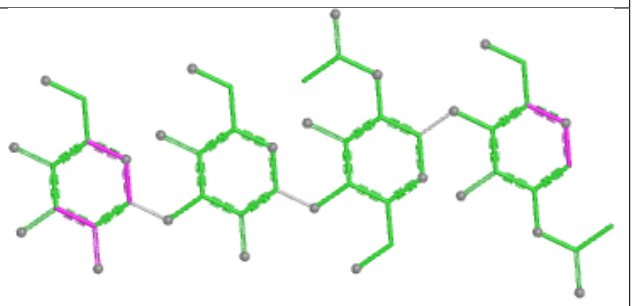
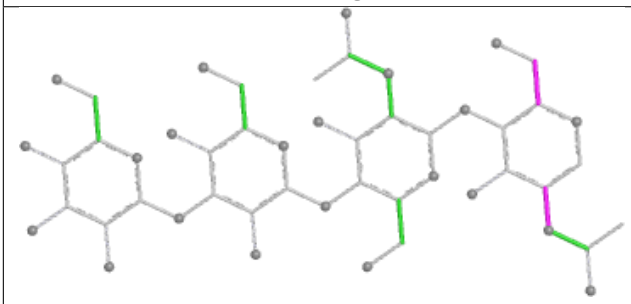
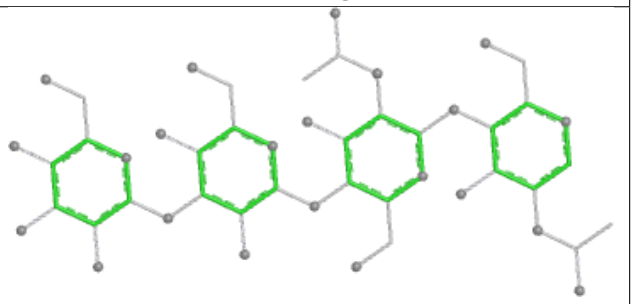
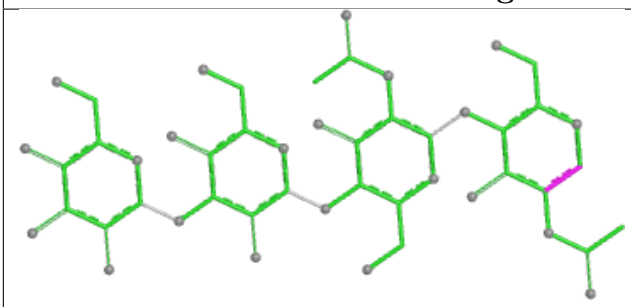
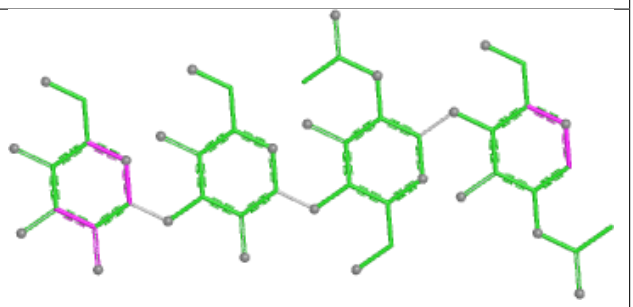
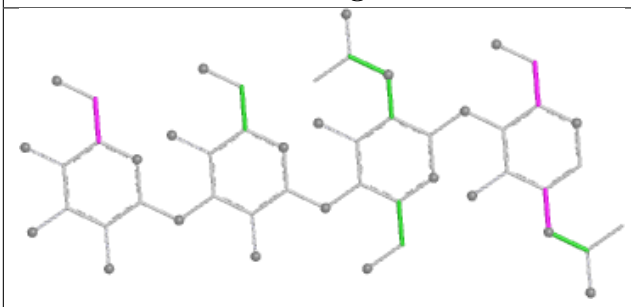
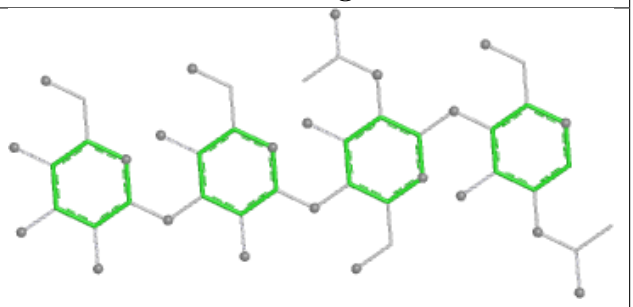
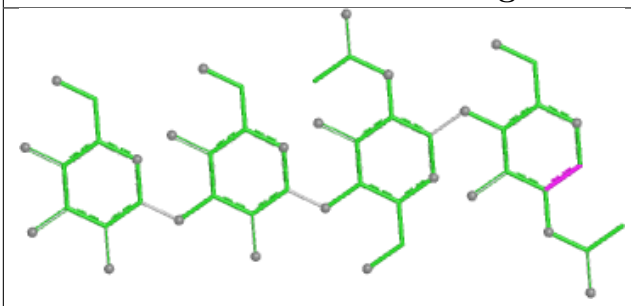


Rings

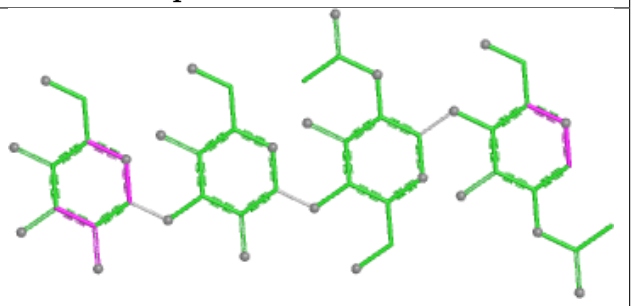
Oligosaccharide Chain O	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

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

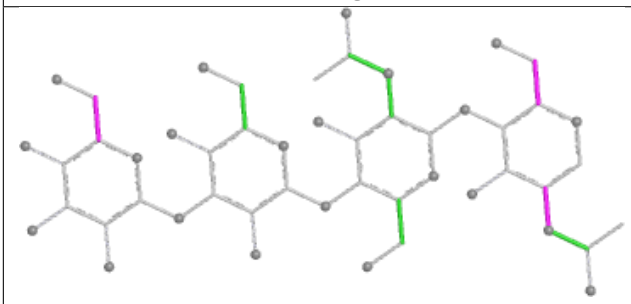
Oligosaccharide Chain q



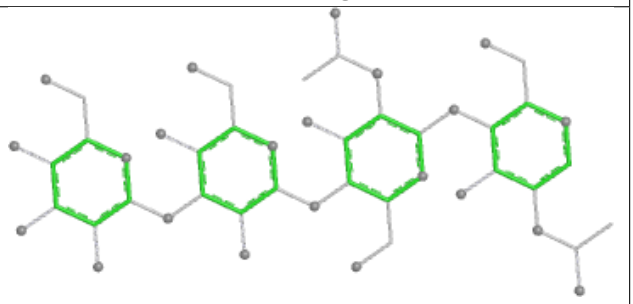
Bond lengths



Bond angles

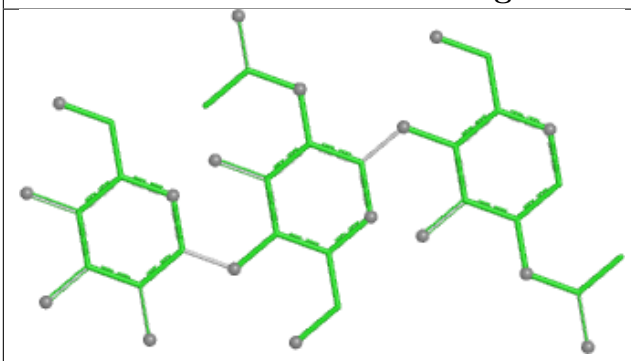


Torsions

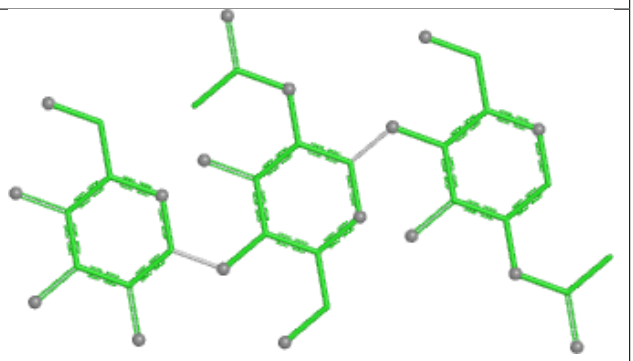


Rings

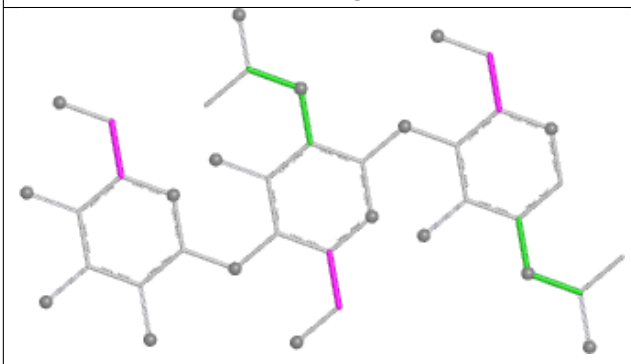
Oligosaccharide Chain R



Bond lengths



Bond angles



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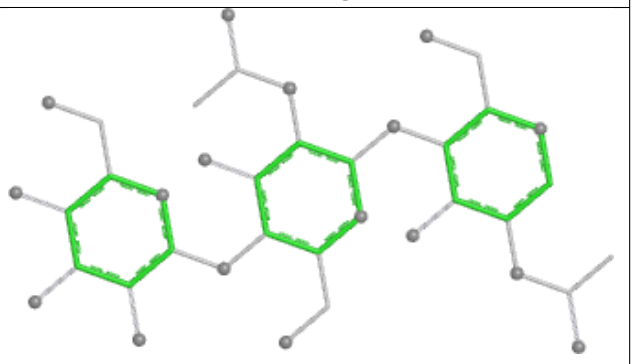
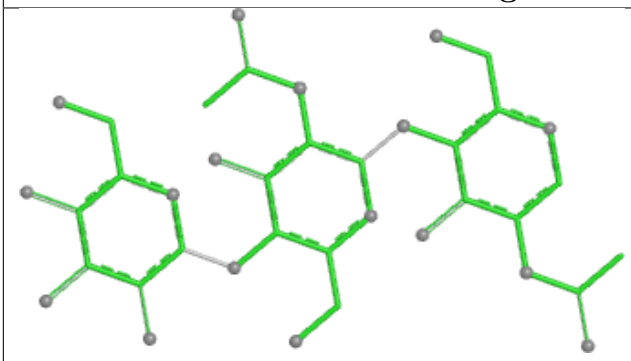


Rings

Oligosaccharide Chain c



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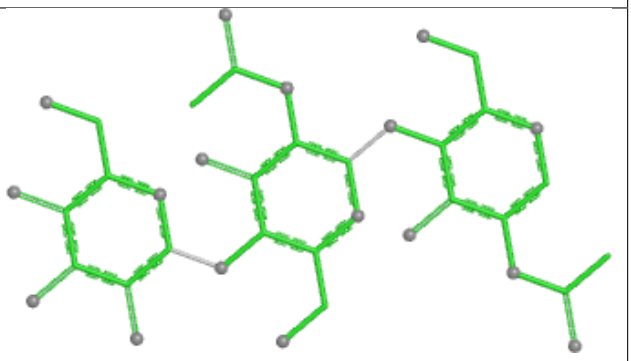
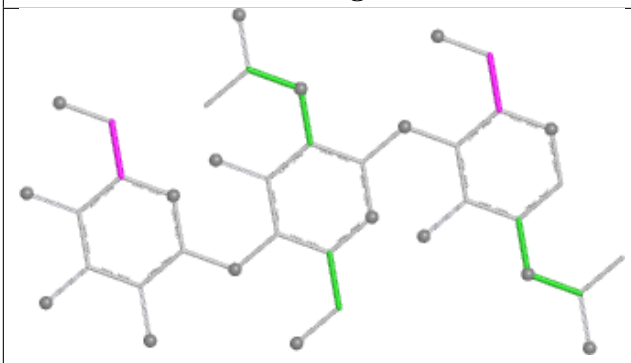
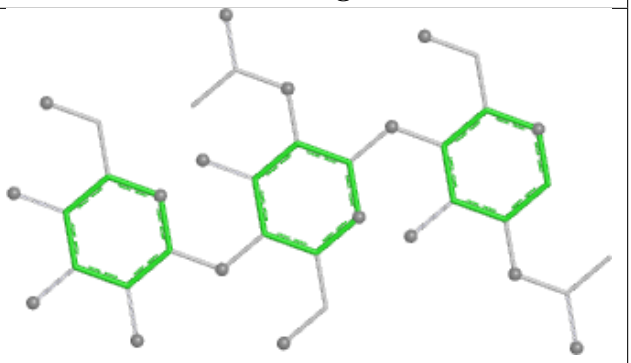


Bond angles

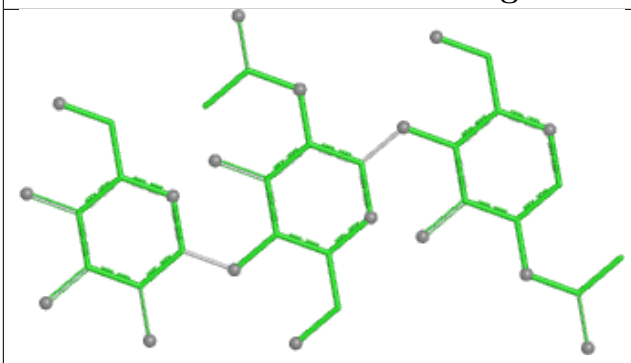


Torsions

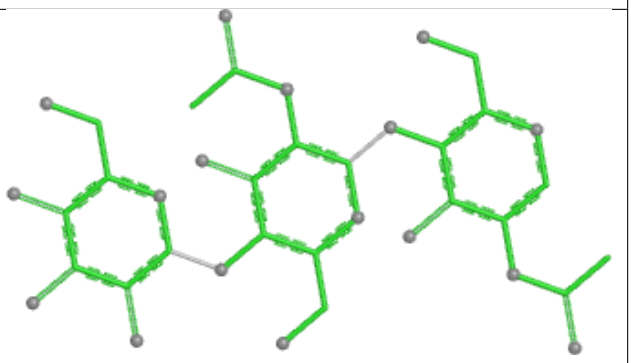


Rings

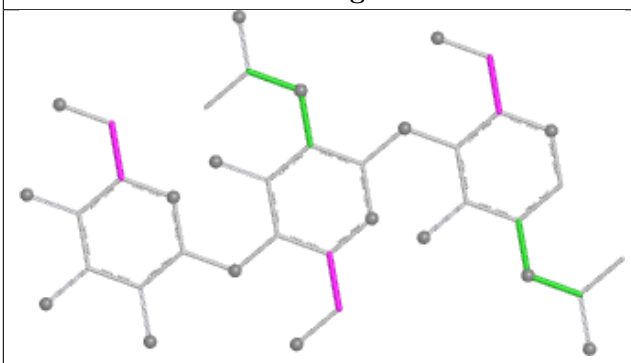
Oligosaccharide Chain t



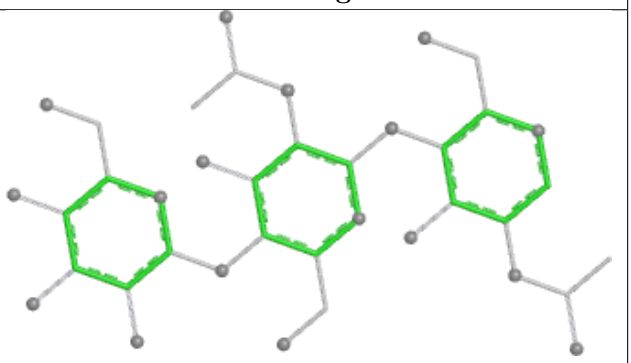
Bond lengths



Bond angles

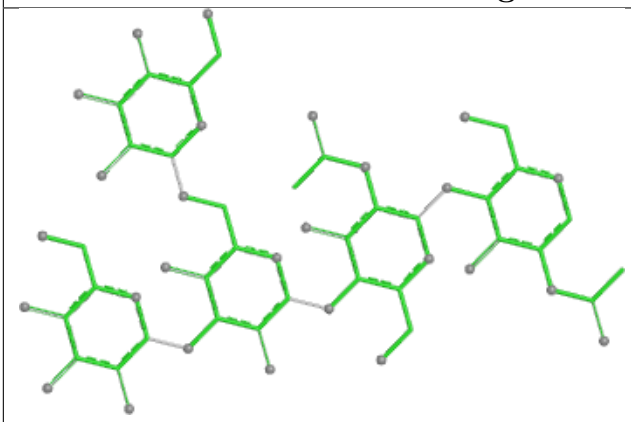


Torsions

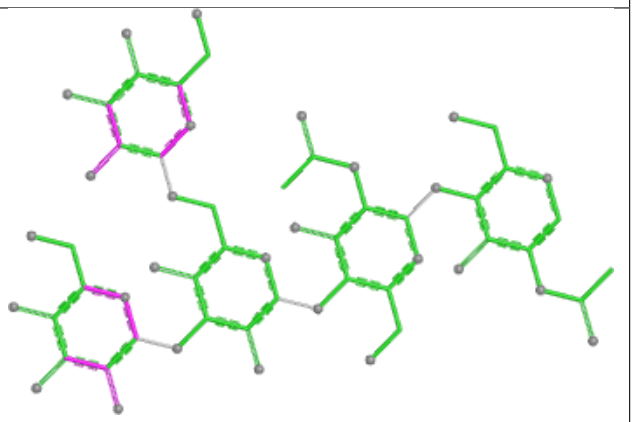


Rings

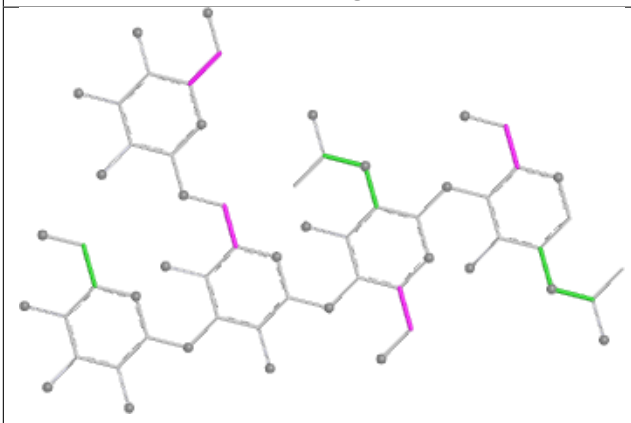
Oligosaccharide Chain S



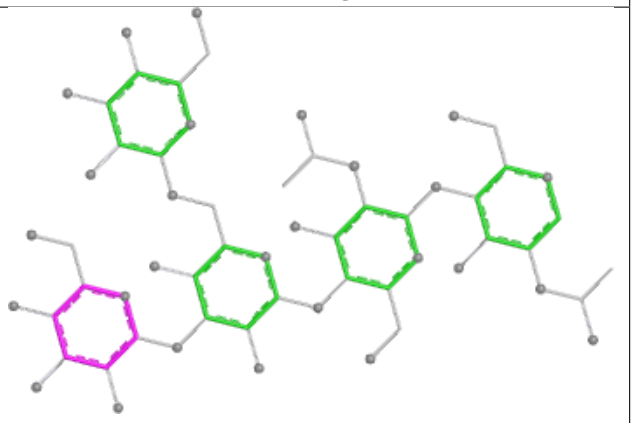
Bond lengths



Bond angles

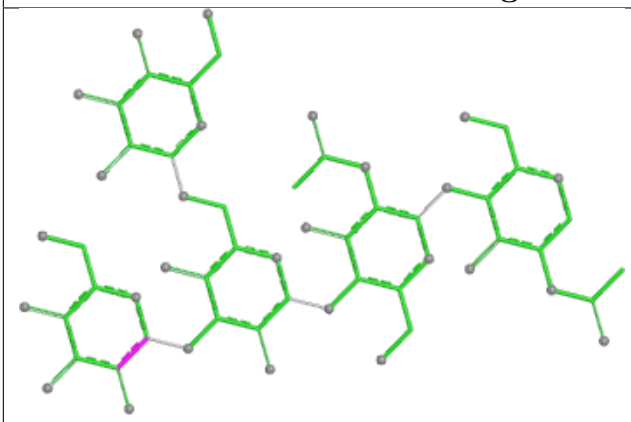


Torsions

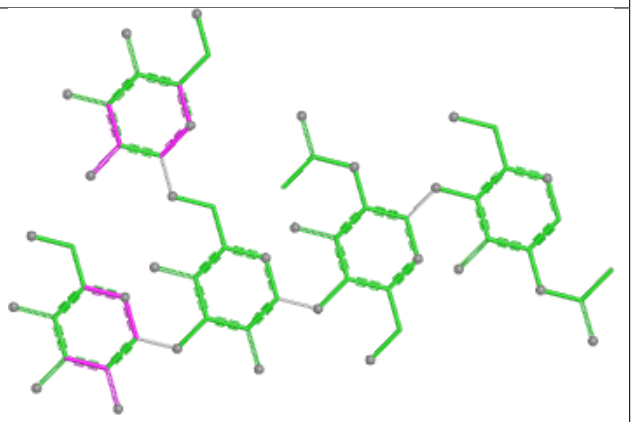


Rings

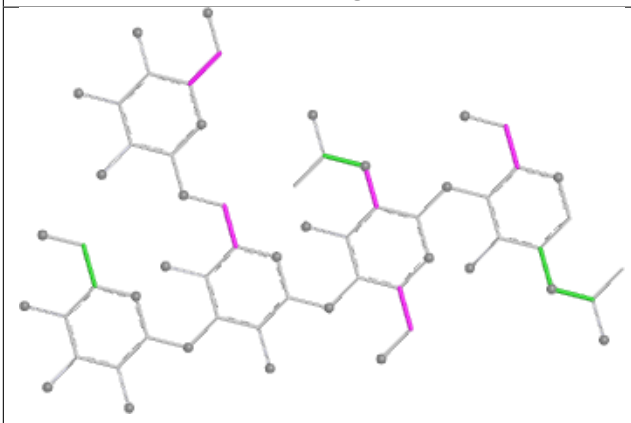
Oligosaccharide Chain f



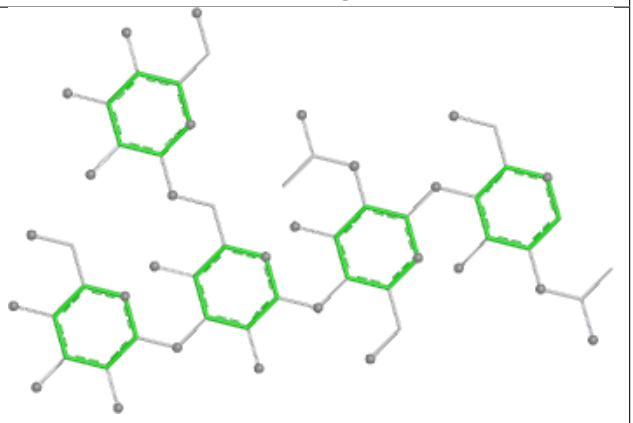
Bond lengths



Bond angles

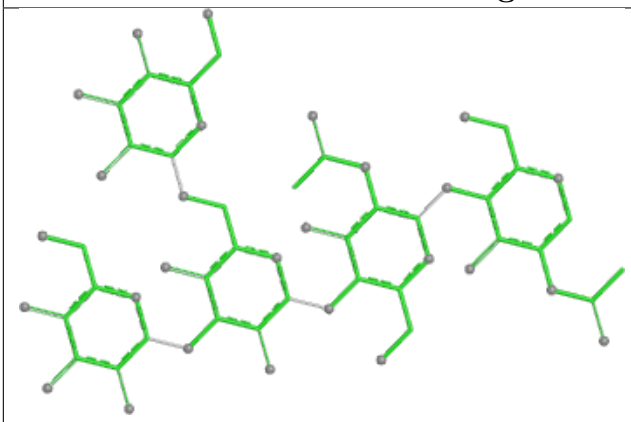


Torsions

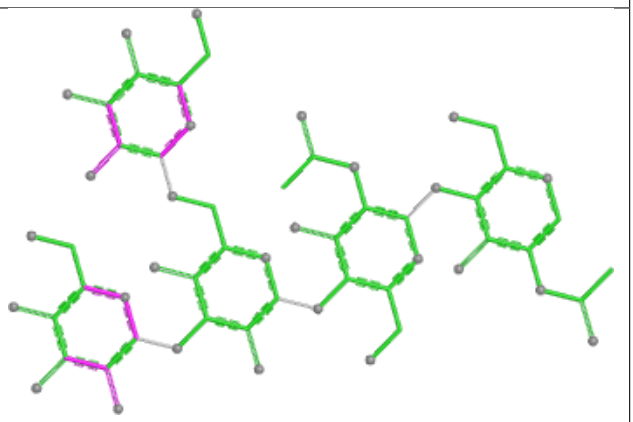


Rings

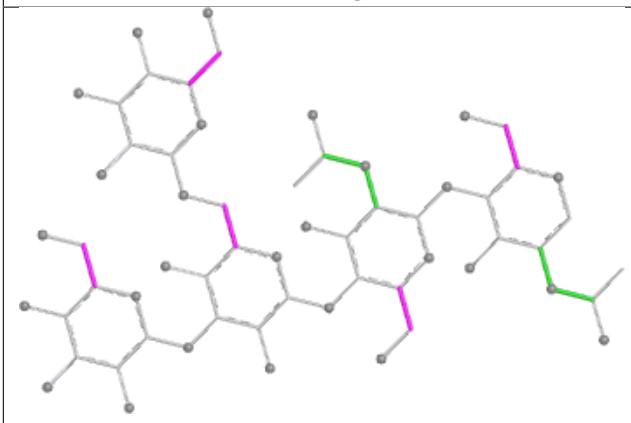
Oligosaccharide Chain u



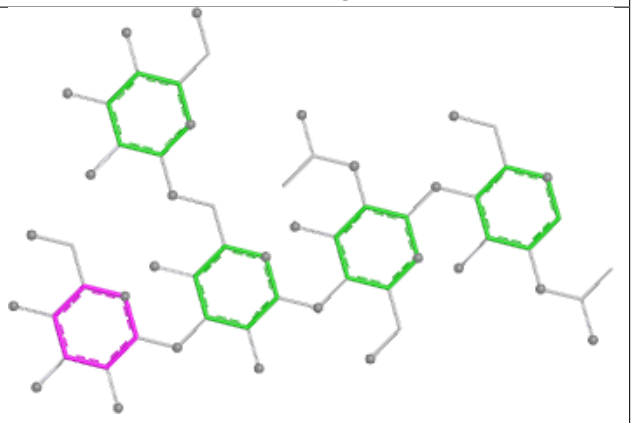
Bond lengths



Bond angles

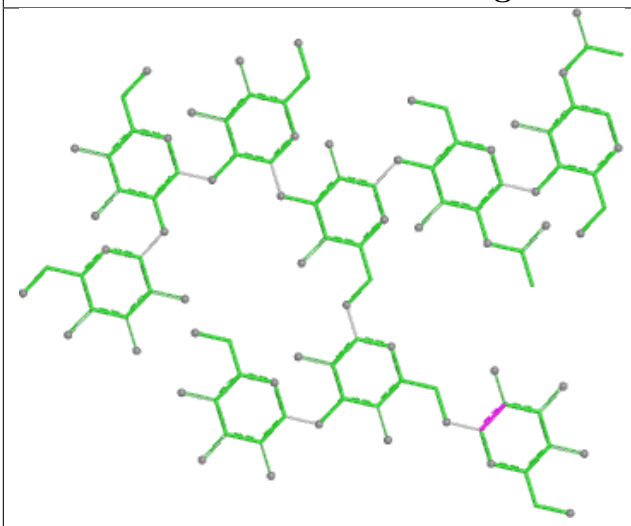


Torsions

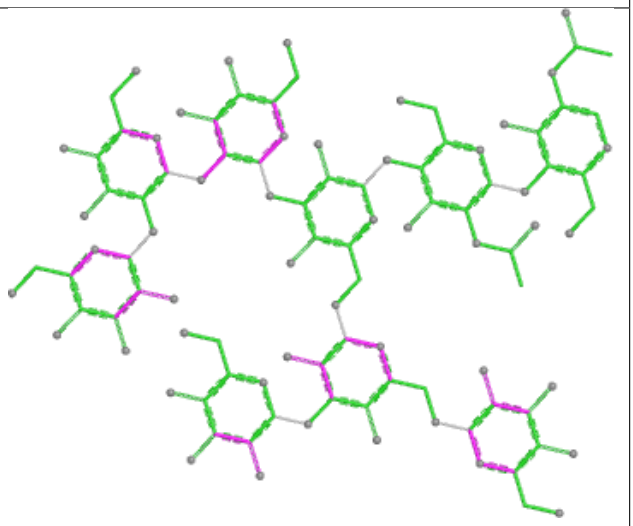


Rings

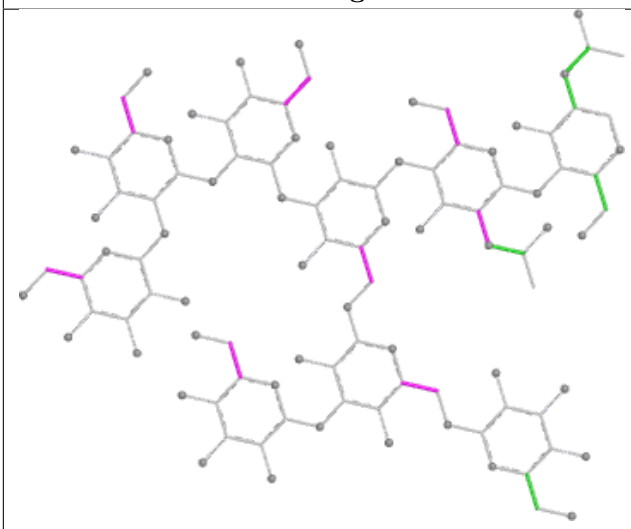
Oligosaccharide Chain U



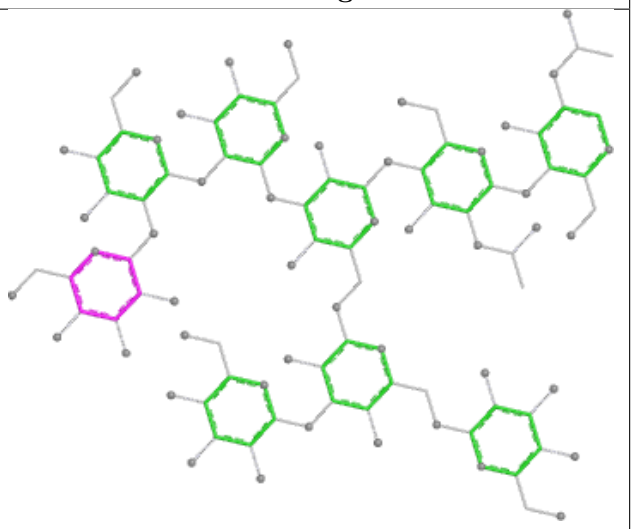
Bond lengths



Bond angles

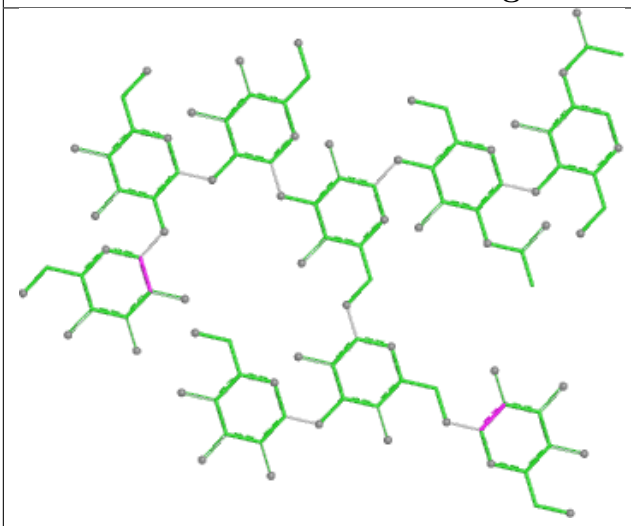


Torsions

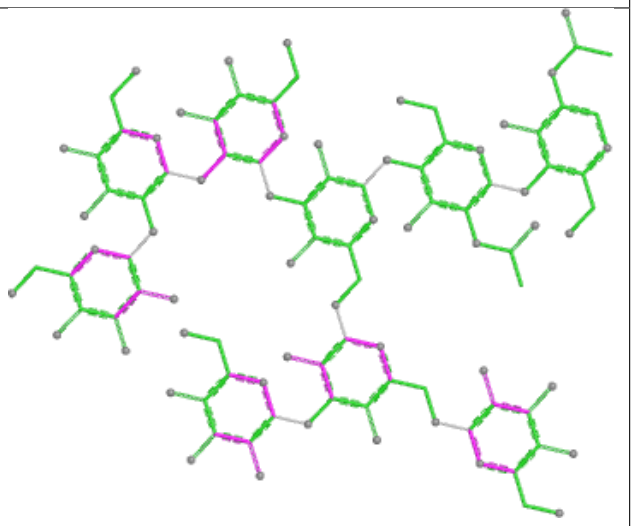


Rings

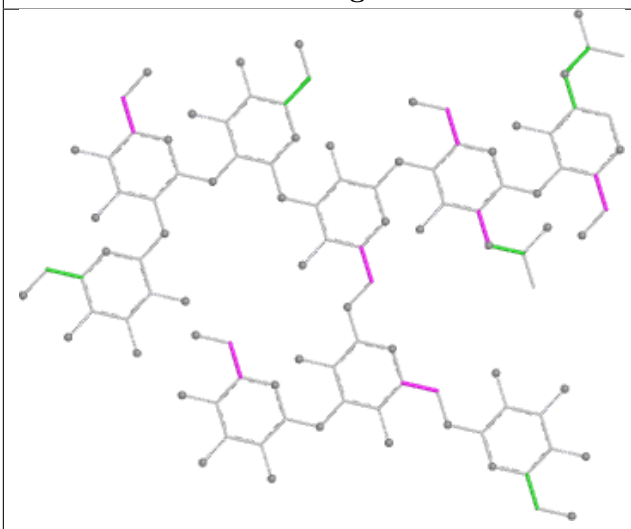
Oligosaccharide Chain i



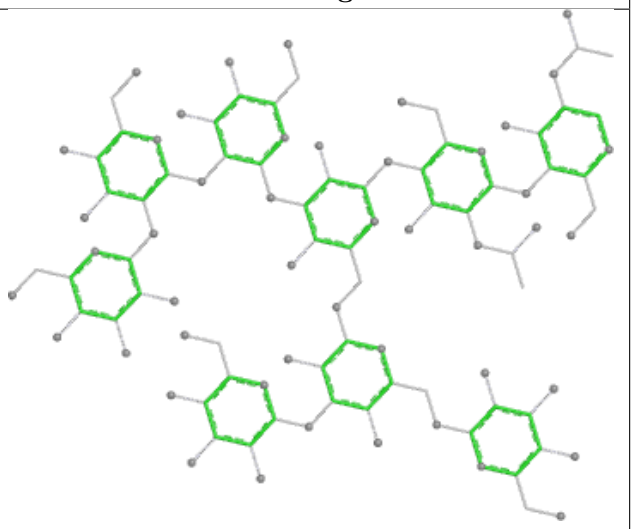
Bond lengths



Bond angles

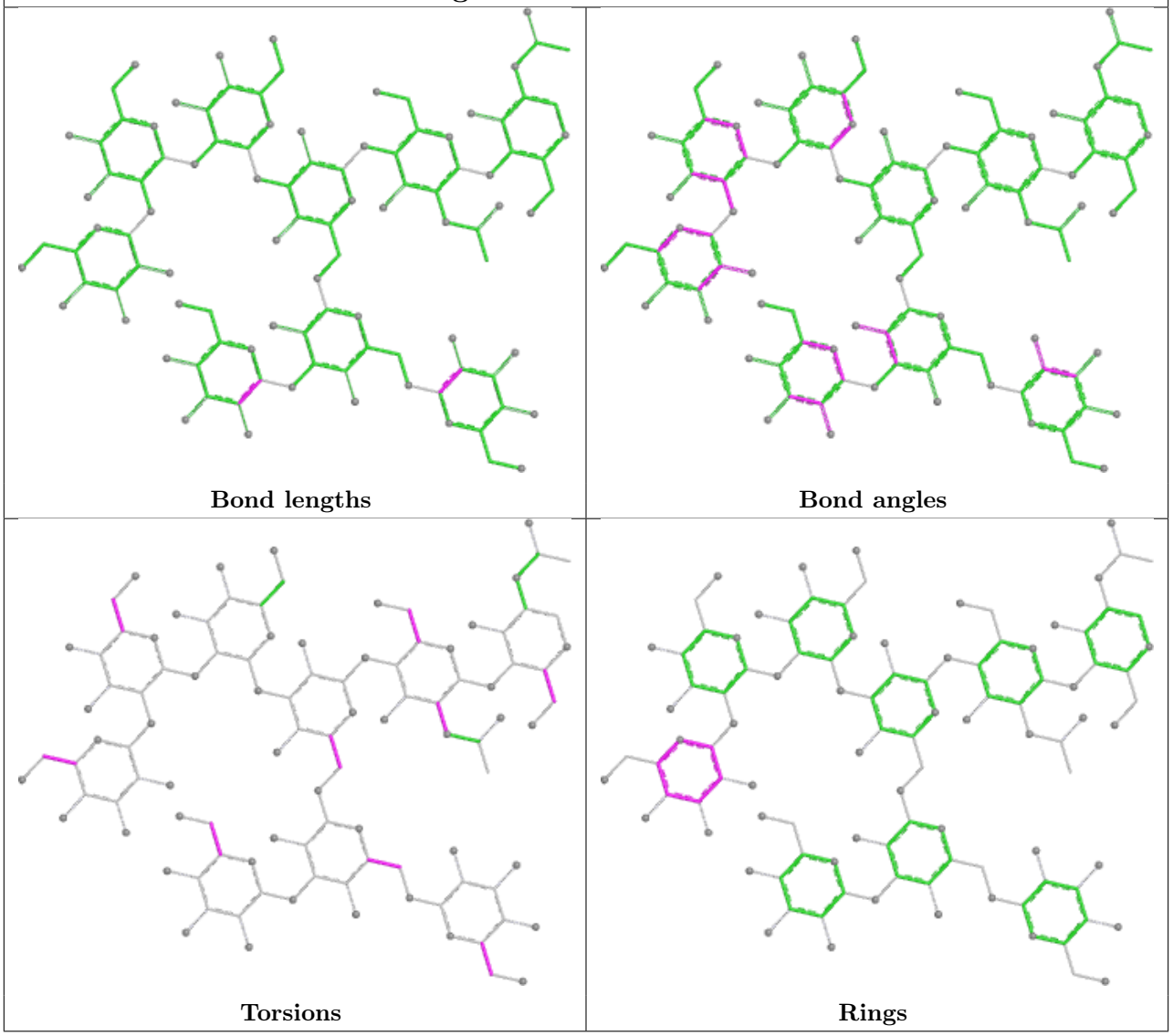


Torsions



Rings

Oligosaccharide Chain w



5.6 Ligand geometry (i)

15 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	G	601	1	14,14,15	0.24	0	17,19,21	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
12	NAG	A	603	1	14,14,15	0.44	0	17,19,21	0.65	1 (5%)
12	NAG	I	604	1	14,14,15	0.27	0	17,19,21	0.38	0
12	NAG	A	601	1	14,14,15	0.27	0	17,19,21	0.41	0
12	NAG	A	605	1	14,14,15	0.37	0	17,19,21	0.54	0
12	NAG	I	602	1	14,14,15	0.44	0	17,19,21	0.63	0
12	NAG	I	605	1	14,14,15	0.27	0	17,19,21	0.46	0
12	NAG	A	604	1	14,14,15	0.41	0	17,19,21	0.61	1 (5%)
12	NAG	I	601	1	14,14,15	0.30	0	17,19,21	0.40	0
12	NAG	G	602	1	14,14,15	0.42	0	17,19,21	0.59	0
12	NAG	G	603	1	14,14,15	0.33	0	17,19,21	0.59	0
12	NAG	I	603	1	14,14,15	0.35	0	17,19,21	0.59	0
12	NAG	G	604	1	14,14,15	0.38	0	17,19,21	0.56	0
12	NAG	G	605	1	14,14,15	0.23	0	17,19,21	0.45	0
12	NAG	A	602	1	14,14,15	0.44	0	17,19,21	0.62	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	G	601	1	-	2/6/23/26	0/1/1/1
12	NAG	A	603	1	-	0/6/23/26	0/1/1/1
12	NAG	I	604	1	-	2/6/23/26	0/1/1/1
12	NAG	A	601	1	-	1/6/23/26	0/1/1/1
12	NAG	A	605	1	-	3/6/23/26	0/1/1/1
12	NAG	I	602	1	-	3/6/23/26	0/1/1/1
12	NAG	I	605	1	-	1/6/23/26	0/1/1/1
12	NAG	A	604	1	-	0/6/23/26	0/1/1/1
12	NAG	I	601	1	-	1/6/23/26	0/1/1/1
12	NAG	G	602	1	-	4/6/23/26	0/1/1/1
12	NAG	G	603	1	-	1/6/23/26	0/1/1/1
12	NAG	I	603	1	-	1/6/23/26	0/1/1/1
12	NAG	G	604	1	-	0/6/23/26	0/1/1/1
12	NAG	G	605	1	-	2/6/23/26	0/1/1/1
12	NAG	A	602	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	A	603	NAG	C1-O5-C5	2.26	115.21	112.19
12	A	604	NAG	C1-O5-C5	2.05	114.93	112.19

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	G	601	NAG	C4-C5-C6-O6
12	G	602	NAG	C4-C5-C6-O6
12	G	605	NAG	O5-C5-C6-O6
12	A	602	NAG	O5-C5-C6-O6
12	G	601	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)

There are no chain breaks in this entry.

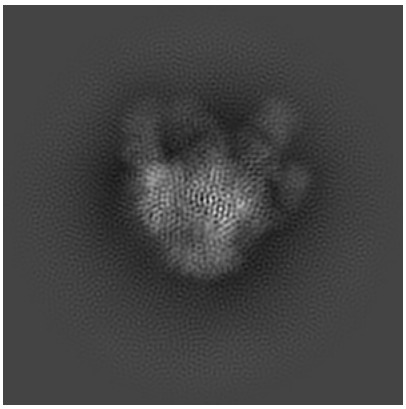
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26648. These allow visual inspection of the internal detail of the map and identification of artifacts.

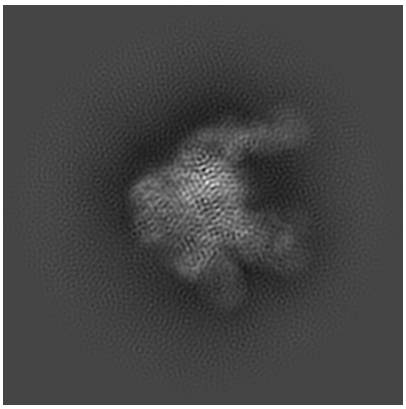
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

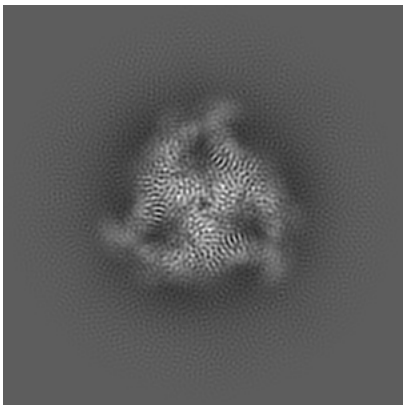
6.1.1 Primary map



X

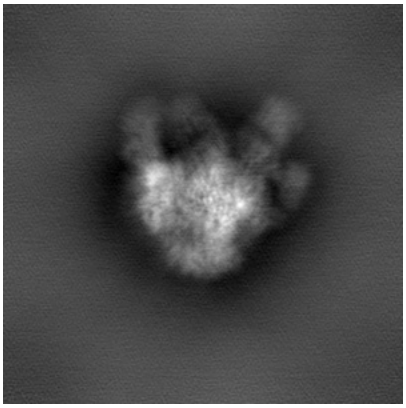


Y

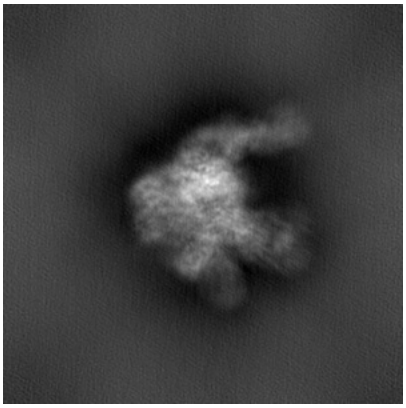


Z

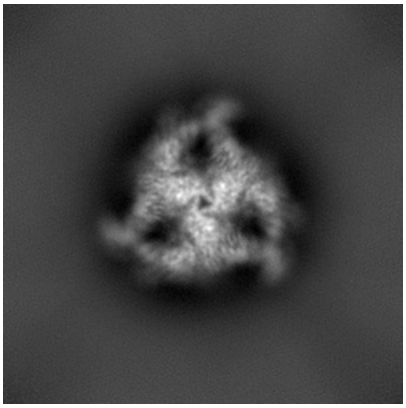
6.1.2 Raw map



X



Y

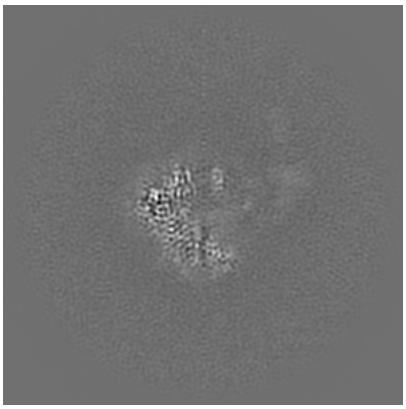


Z

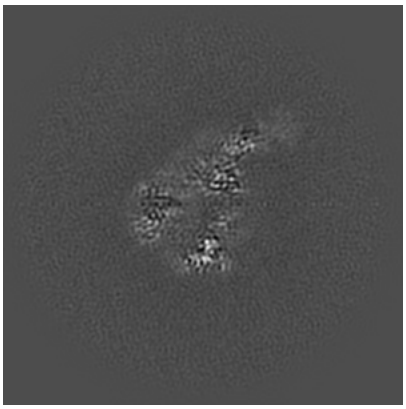
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

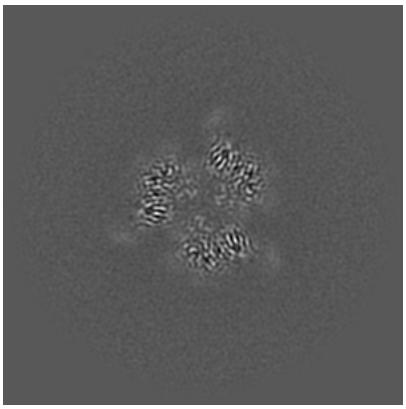
6.2.1 Primary map



X Index: 128

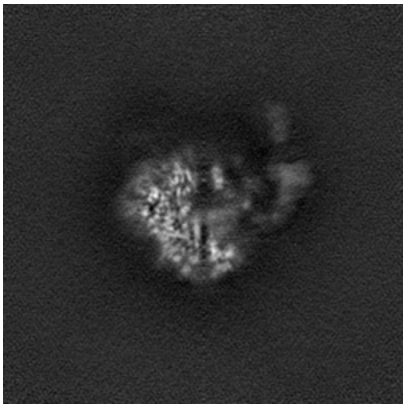


Y Index: 128

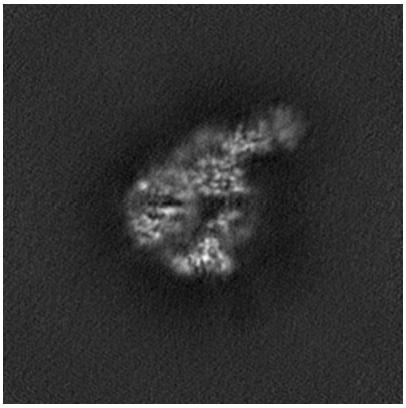


Z Index: 128

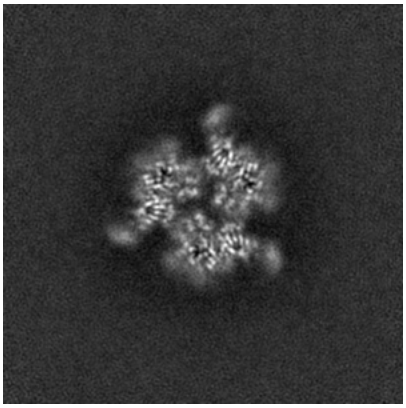
6.2.2 Raw map



X Index: 128



Y Index: 128

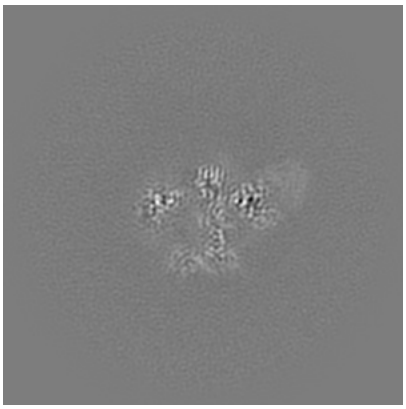


Z Index: 128

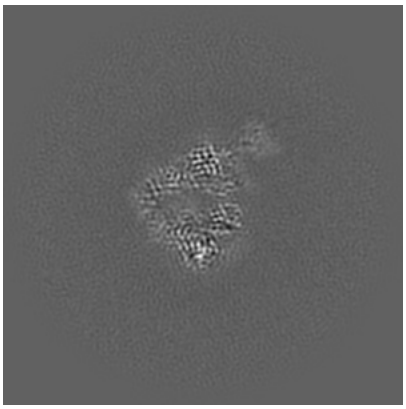
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

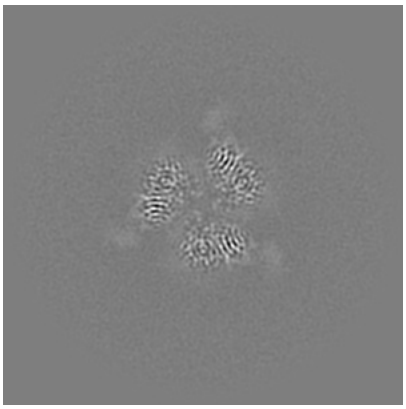
6.3.1 Primary map



X Index: 140

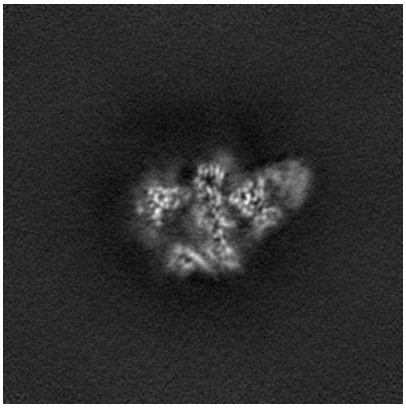


Y Index: 139

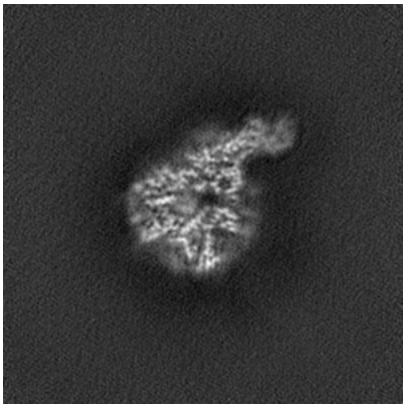


Z Index: 131

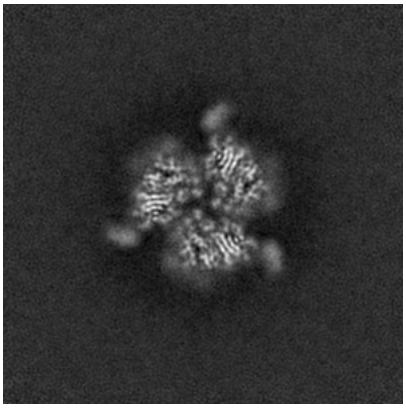
6.3.2 Raw map



X Index: 141



Y Index: 133

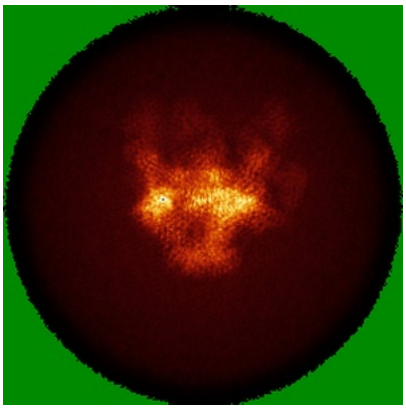


Z Index: 130

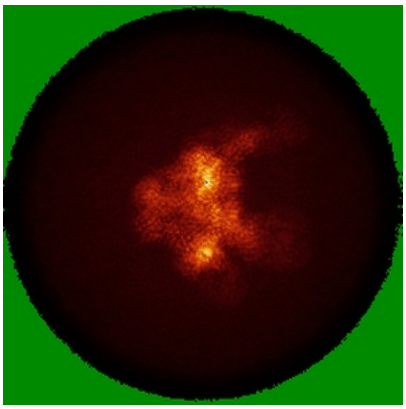
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

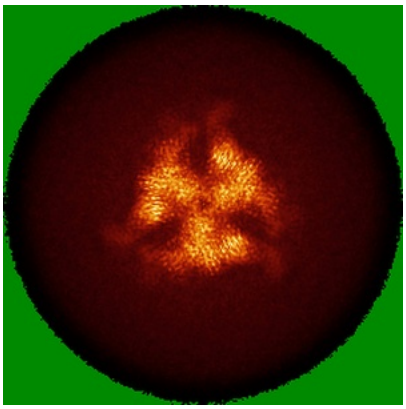
6.4.1 Primary map



X

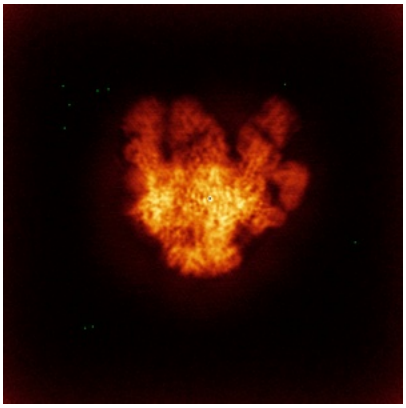


Y

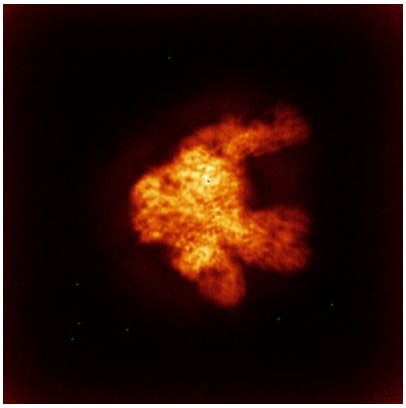


Z

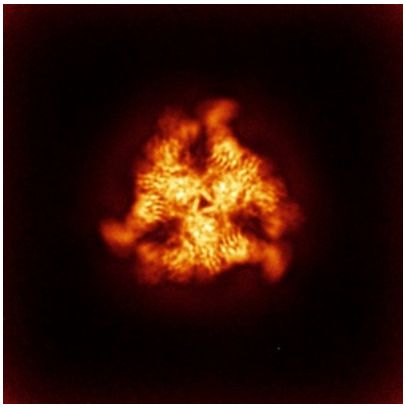
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

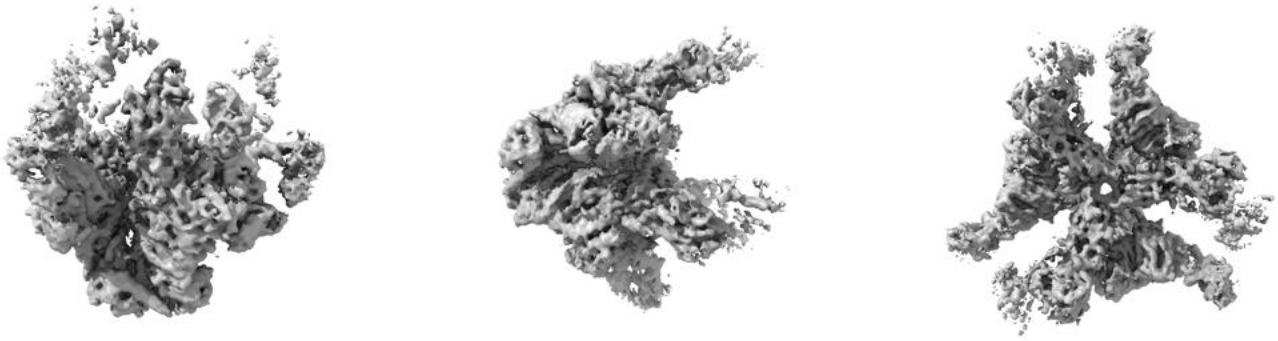
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 3.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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.

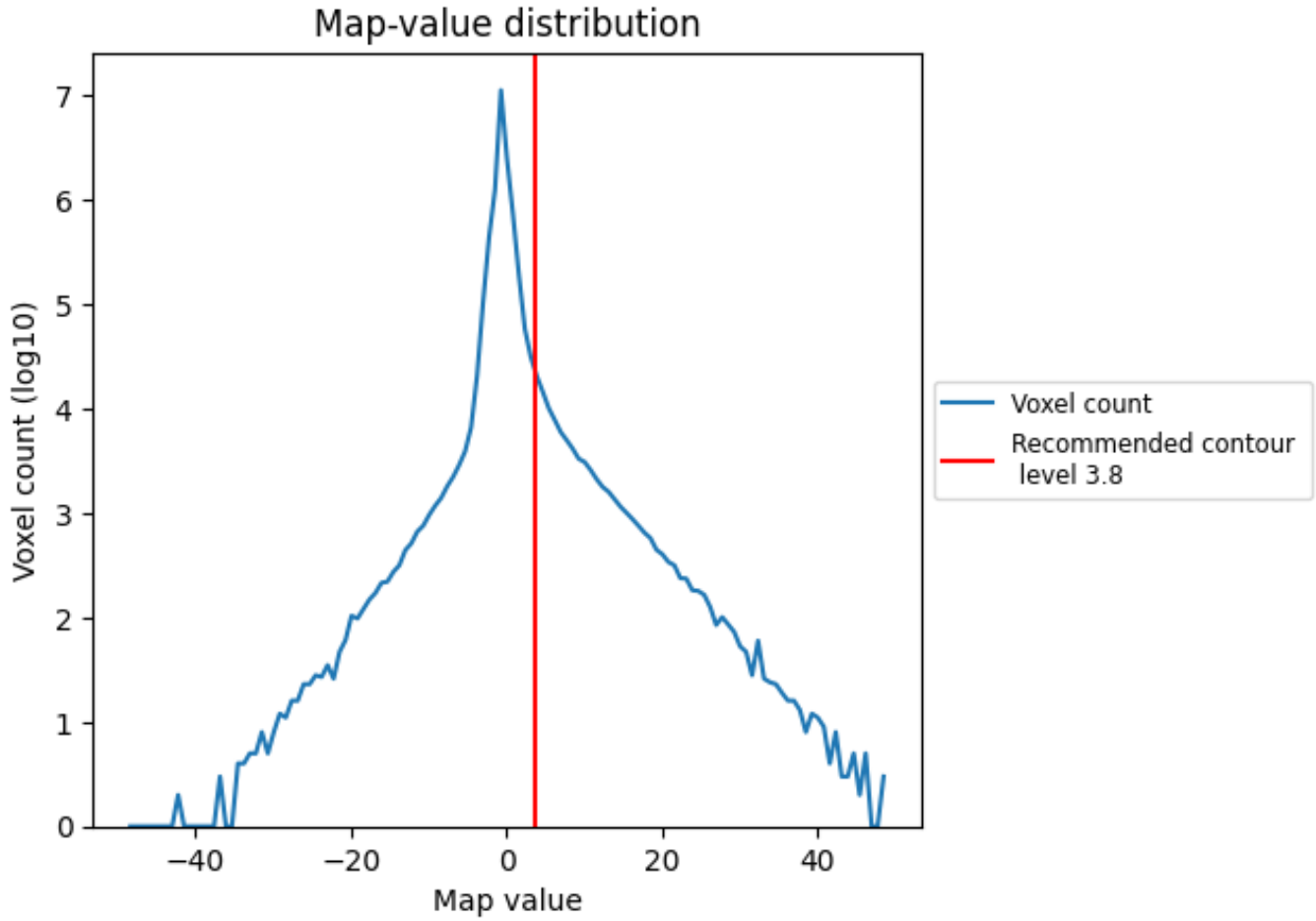
6.6 Mask visualisation (i)

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

7 Map analysis

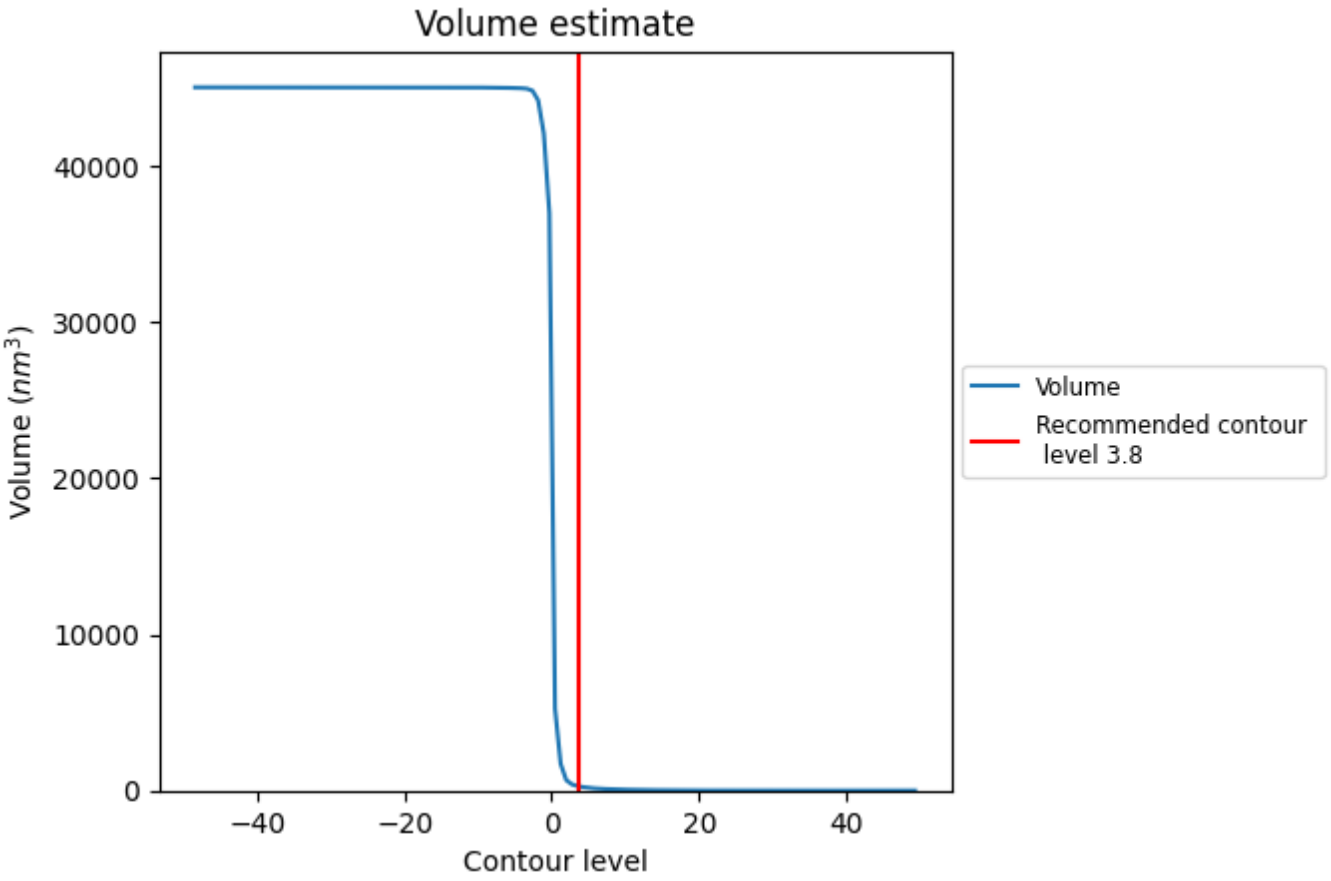
This section contains the results of statistical analysis of the map.

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.

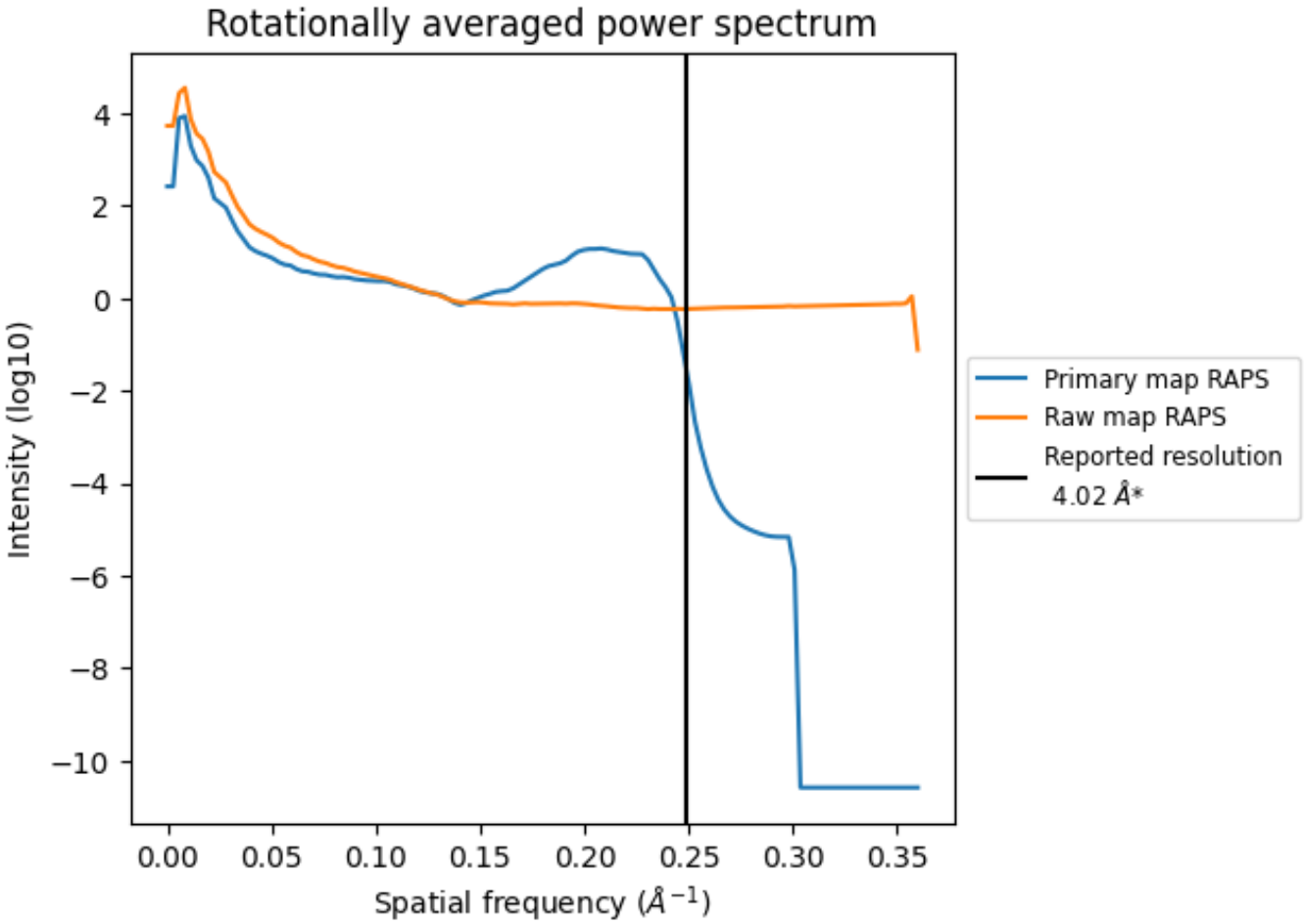
7.2 Volume estimate (i)



The volume at the recommended contour level is 262 nm^3; this corresponds to an approximate mass of 237 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)

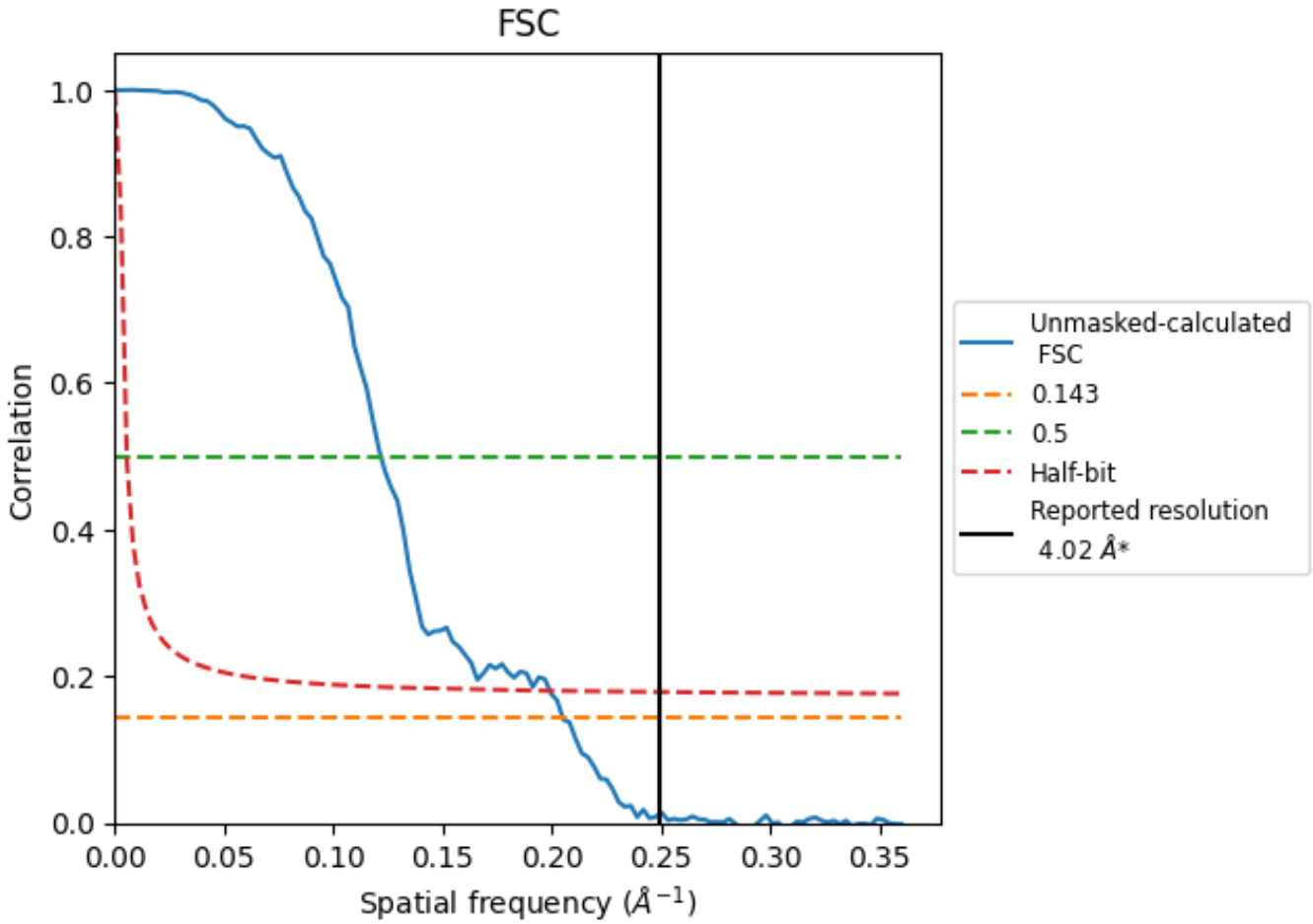


*Reported resolution corresponds to spatial frequency of 0.249 Å^{-1}

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 0.249 Å^{-1}

8.2 Resolution estimates (i)

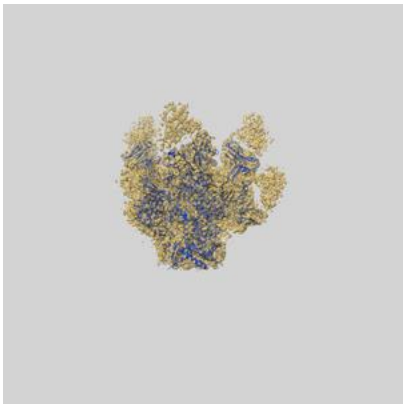
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.02	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.88	8.22	5.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.88 differs from the reported value 4.02 by more than 10 %

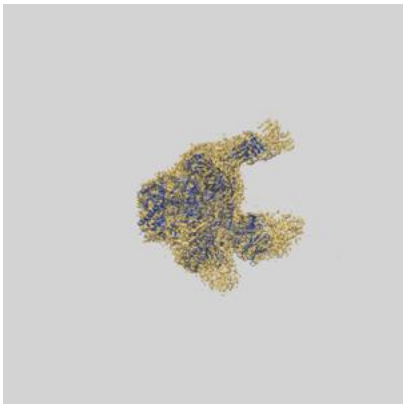
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26648 and PDB model 7UOJ. Per-residue inclusion information can be found in section 3 on page 12.

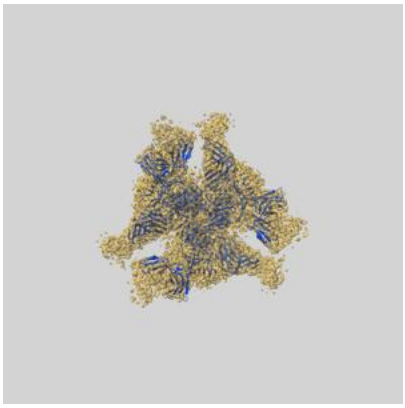
9.1 Map-model overlay



X



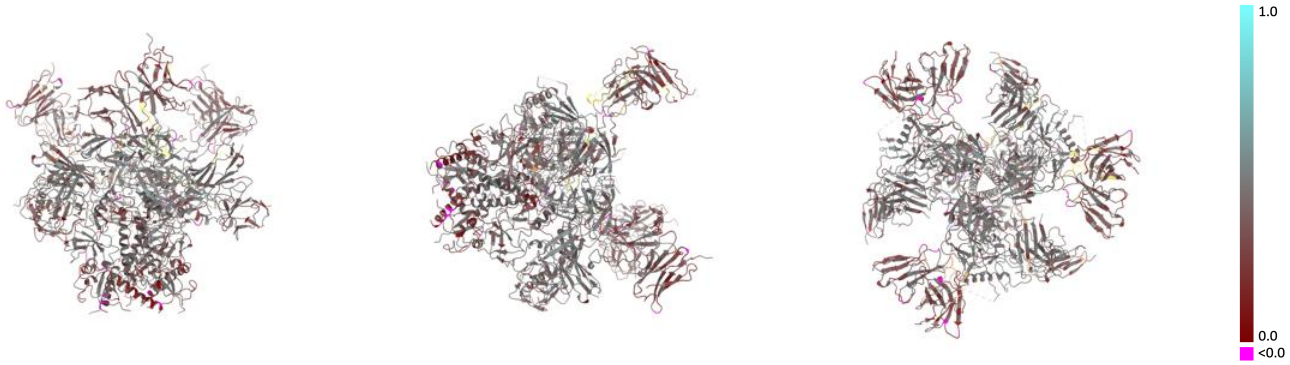
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.8 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.

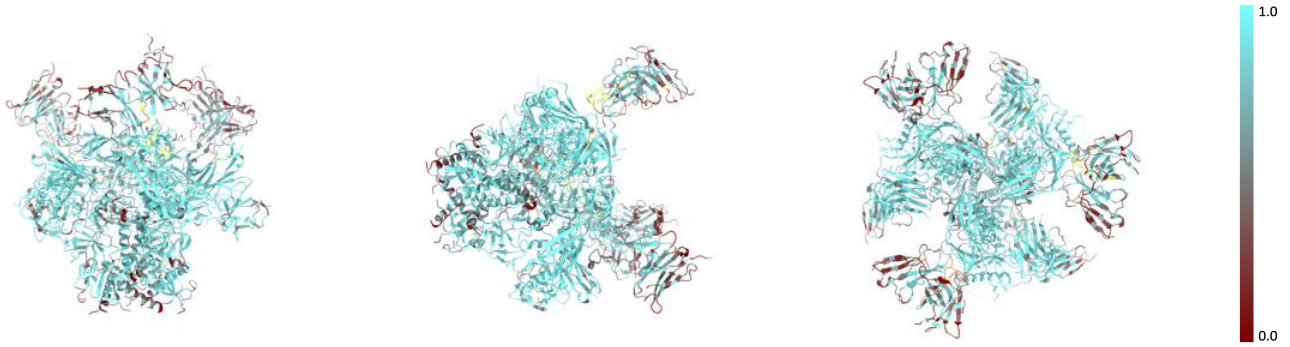
9.2 Q-score mapped to coordinate model (i)



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.

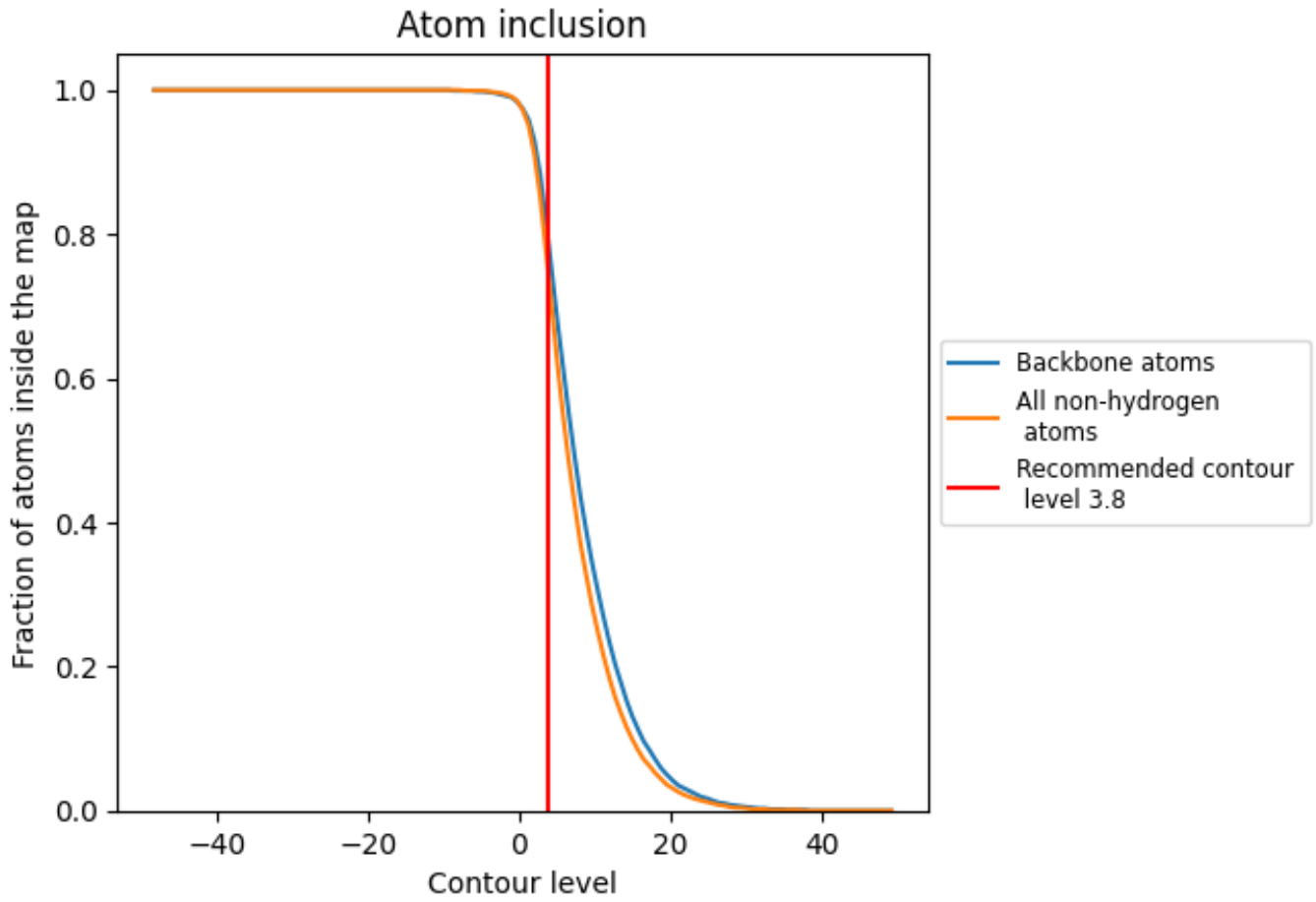
9.3 Atom inclusion mapped to coordinate model (i)



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 (3.8).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (3.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7500	0.3900
A	0.8320	0.4230
B	0.7240	0.3320
C	0.7080	0.3290
D	0.8550	0.4290
E	0.7260	0.3730
F	0.7140	0.4710
G	0.8340	0.4260
H	0.8580	0.4310
I	0.8380	0.4260
J	0.7070	0.3250
K	0.8580	0.4310
L	0.7350	0.3820
M	0.7380	0.3840
N	0.3570	0.3610
O	0.7800	0.3940
P	0.6430	0.3130
Q	0.5710	0.3670
R	0.8970	0.4820
S	0.6890	0.3280
T	0.6790	0.4100
U	0.7620	0.4210
V	0.7500	0.3900
W	0.7500	0.3420
X	0.7140	0.4900
Y	0.4640	0.3580
Z	0.7600	0.4300
a	0.6430	0.3070
b	0.4640	0.3260
c	0.8460	0.4520
d	0.5710	0.3290
e	0.5560	0.3490
f	0.6560	0.3470
g	0.5000	0.3970
h	0.5600	0.3300

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Chain	Atom inclusion	Q-score
i	0.8190	0.4370
j	0.7500	0.4280
k	0.5650	0.3310
l	0.5750	0.3520
m	0.5650	0.3470
n	0.7140	0.3230
o	0.6790	0.4710
p	0.3930	0.3410
q	0.7800	0.4090
r	0.7860	0.3730
s	0.5360	0.2630
t	0.9230	0.4750
u	0.5740	0.3110
v	0.7500	0.3810
w	0.6670	0.3810
x	0.7500	0.4480
y	0.6790	0.2990