wwPDB X-ray Structure Validation Summary Report (i)

Aug 10, 2020 – 08:43 AM BST

PDB ID	:	1ZPU
Title	:	Crystal Structure of Fet3p, a Multicopper Oxidase that Functions in Iron Import
Authors	:	Taylor, A.B.; Stoj, C.S.; Ziegler, L.; Kosman, D.J.; Hart, P.J.
Deposited on	:	2005-05-17
Resolution	:	2.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

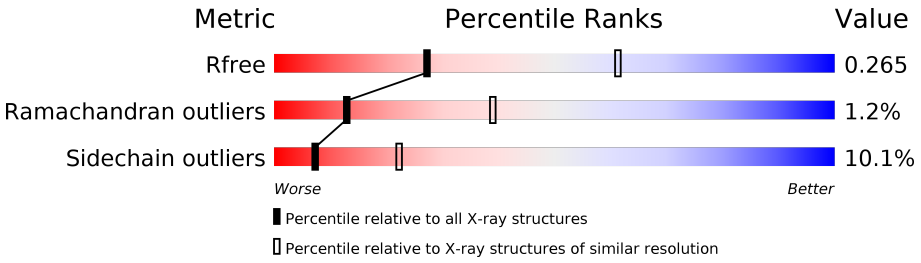
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	534	89% 9% ••
1	B	534	88% 10% •
1	C	534	89% 10% •
1	D	534	88% 10% •
1	E	534	90% 9% •
1	F	534	87% 11% •
2	G	5	100%
2	J	5	100%
2	M	5	20% 80%

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Mol	Chain	Length	Quality of chain
2	O	5	100%
2	S	5	100%
2	U	5	100%
2	Y	5	100%
2	a	5	100%
2	d	5	40% 60%
2	f	5	20% 80%
2	i	5	20% 80%
2	k	5	100%
3	H	6	17% 83%
3	N	6	17% 83%
3	Z	6	100%
3	j	6	100%
4	I	2	100%
4	P	2	50% 50%
4	Q	2	100%
4	V	2	100%
4	b	2	50% 50%
4	g	2	100%
5	K	3	100%
5	L	3	100%
5	W	3	100%
5	X	3	100%
5	c	3	33% 67%
5	h	3	100%

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Mol	Chain	Length	Quality of chain
5	l	3	100%
6	R	4	100%
7	T	7	14% 86%
7	e	7	100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	a	1	X	-	-	-
2	NAG	f	1	X	-	-	-
3	NAG	H	1	X	-	-	-
3	NAG	N	1	X	-	-	-
3	NAG	Z	1	X	-	-	-
3	NAG	j	1	X	-	-	-
4	NAG	b	1	X	-	-	-
5	NAG	L	1	X	-	-	-
5	NAG	X	1	X	-	-	-
5	NAG	c	1	X	-	-	-
5	NAG	h	1	X	-	-	-
5	NAG	l	1	X	-	-	-
6	NAG	R	1	X	-	-	-
7	NAG	T	1	X	-	-	-
7	NAG	e	1	X	-	-	-
8	NAG	A	2006	X	-	-	-
8	NAG	A	2012	X	-	-	-
8	NAG	A	2018	X	-	-	-
8	NAG	B	2006	X	-	-	-
8	NAG	B	2012	X	-	-	-
8	NAG	B	2018	X	-	-	-
8	NAG	C	2012	X	-	-	-
8	NAG	C	2018	X	-	-	-
8	NAG	D	2006	X	-	-	-
8	NAG	E	2012	X	-	-	-
8	NAG	F	2005	X	-	-	-
8	NAG	F	2006	X	-	-	-
8	NAG	F	2009	X	-	-	-
8	NAG	F	2012	X	-	-	-

2 Entry composition

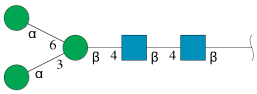
There are 9 unique types of molecules in this entry. The entry contains 27659 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Iron transport multicopper oxidase FET3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	0	0
			4254	2701	695	838	20			
1	B	529	Total	C	N	O	S	0	0	0
			4254	2701	695	838	20			
1	C	529	Total	C	N	O	S	0	0	0
			4254	2701	695	838	20			
1	D	529	Total	C	N	O	S	0	0	0
			4254	2701	695	838	20			
1	E	529	Total	C	N	O	S	0	0	0
			4254	2701	695	838	20			
1	F	529	Total	C	N	O	S	0	0	0
			4254	2701	695	838	20			

- Molecule 2 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				ZeroOcc	AltConf	Trace
2	G	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	J	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	M	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	O	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	S	5	Total	C	N	O	0	0	0
			61	34	2	25			

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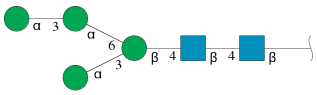
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	U	5	Total C N O 61 34 2 25	0	0	0
2	Y	5	Total C N O 61 34 2 25	0	0	0
2	a	5	Total C N O 61 34 2 25	0	0	0
2	d	5	Total C N O 61 34 2 25	0	0	0
2	f	5	Total C N O 61 34 2 25	0	0	0
2	i	5	Total C N O 61 34 2 25	0	0	0
2	k	5	Total C N O 61 34 2 25	0	0	0

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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.

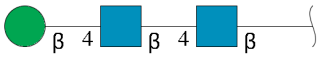


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	H	6	Total C N O 72 40 2 30	0	0	0
3	N	6	Total C N O 72 40 2 30	0	0	0
3	Z	6	Total C N O 72 40 2 30	0	0	0
3	j	6	Total C N O 72 40 2 30	0	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	I	2	Total C N O 28 16 2 10	0	0	0
4	P	2	Total C N O 28 16 2 10	0	0	0
4	Q	2	Total C N O 28 16 2 10	0	0	0
4	V	2	Total C N O 28 16 2 10	0	0	0
4	b	2	Total C N O 28 16 2 10	0	0	0
4	g	2	Total C N O 28 16 2 10	0	0	0

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

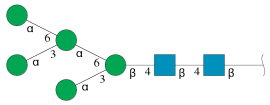


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	K	3	Total C N O 39 22 2 15	0	0	0
5	L	3	Total C N O 39 22 2 15	0	0	0
5	W	3	Total C N O 39 22 2 15	0	0	0
5	X	3	Total C N O 39 22 2 15	0	0	0
5	c	3	Total C N O 39 22 2 15	0	0	0
5	h	3	Total C N O 39 22 2 15	0	0	0
5	l	3	Total C N O 39 22 2 15	0	0	0

- Molecule 6 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.

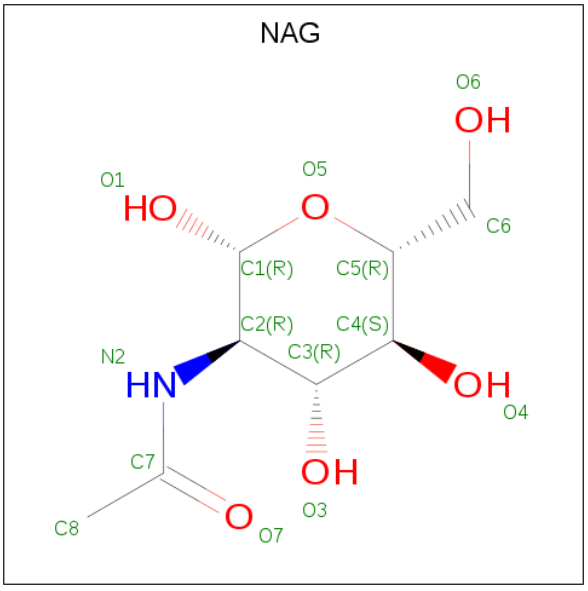
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	R	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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				ZeroOcc	AltConf	Trace
7	T	7	Total	C	N	O	0	0	0
			83	46	2	35			
7	e	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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

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

- Molecule 9 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

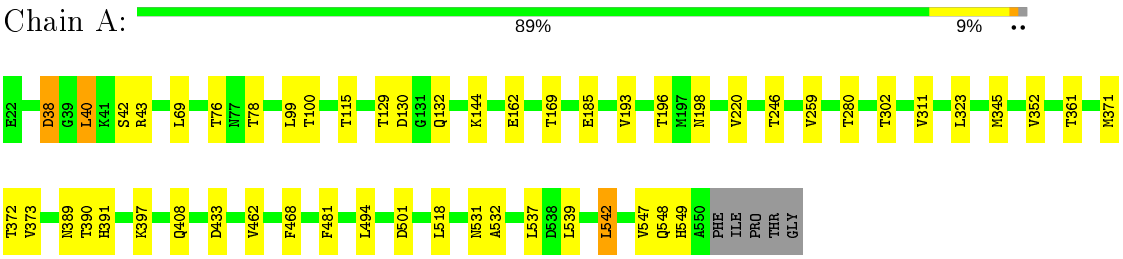
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	D	4	Total Cu 4 4	0	0
9	E	4	Total Cu 4 4	0	0
9	B	4	Total Cu 4 4	0	0
9	C	4	Total Cu 4 4	0	0
9	A	4	Total Cu 4 4	0	0
9	F	4	Total Cu 4 4	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

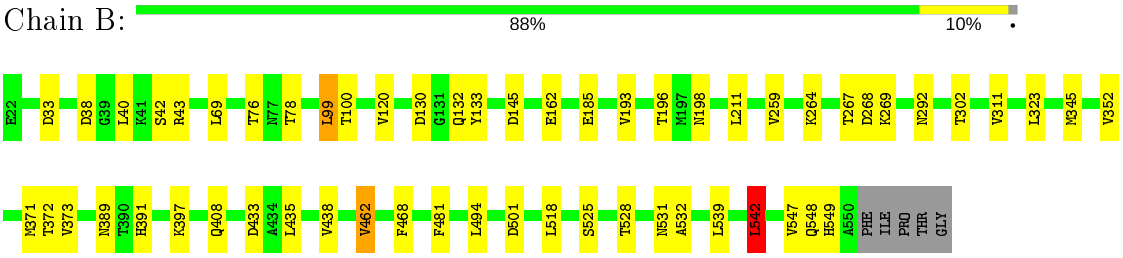
- Molecule 1: Iron transport multicopper oxidase FET3

Chain A:



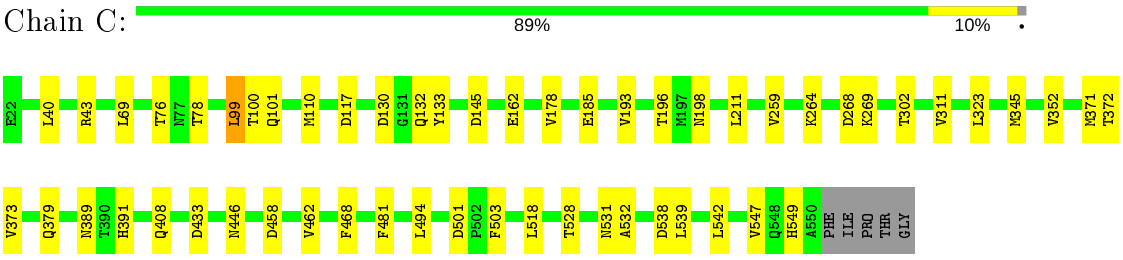
- Molecule 1: Iron transport multicopper oxidase FET3

Chain B:



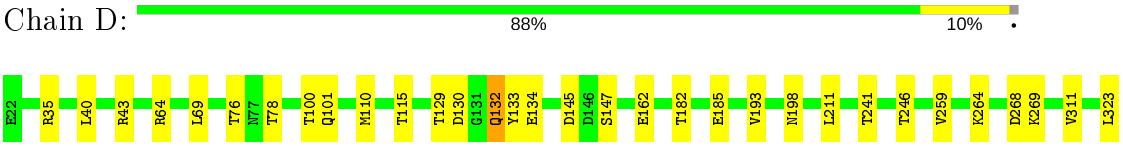
- Molecule 1: Iron transport multicopper oxidase FET3

Chain C:



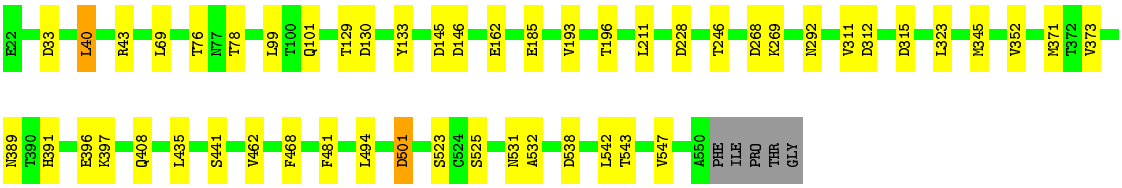
- Molecule 1: Iron transport multicopper oxidase FET3

Chain D:



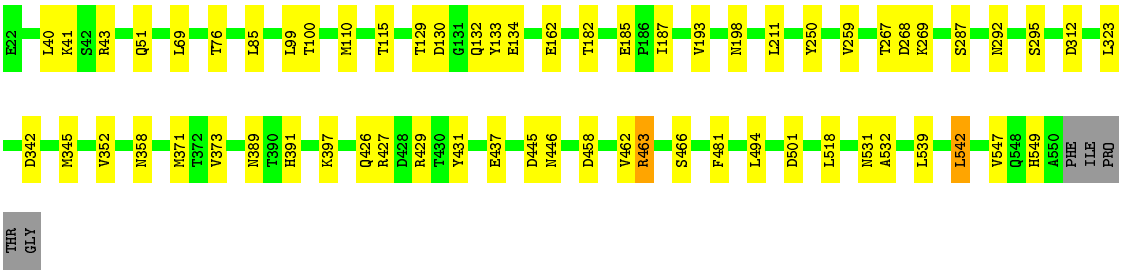
• Molecule 1: Iron transport multicopper oxidase FET3

Chain E:



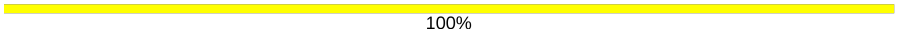
• Molecule 1: Iron transport multicopper oxidase FET3

Chain F:



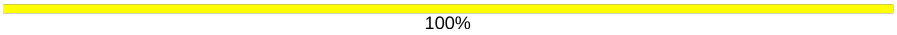
• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



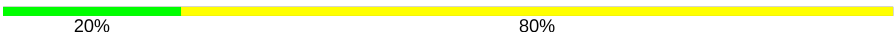
• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:



• Molecule 2: 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 M:

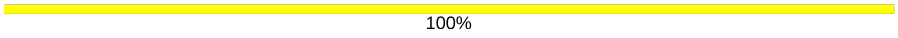


• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

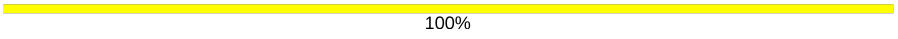
• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:



• Molecule 2: 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:

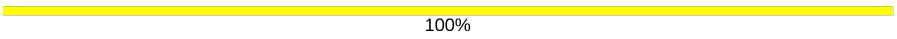


• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:

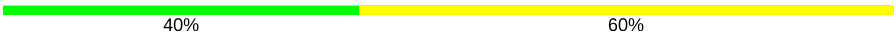
• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:



• Molecule 2: 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 d:



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

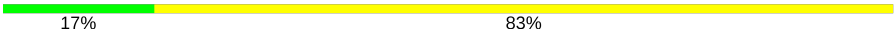
Chain i:

• Molecule 2: 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 k:

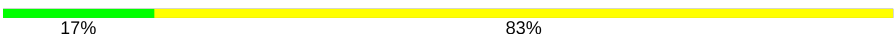
• Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

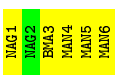
Chain H:



• Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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 N:

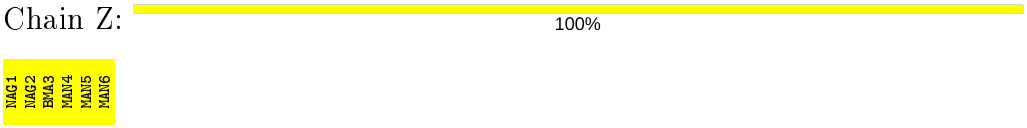




• Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetam

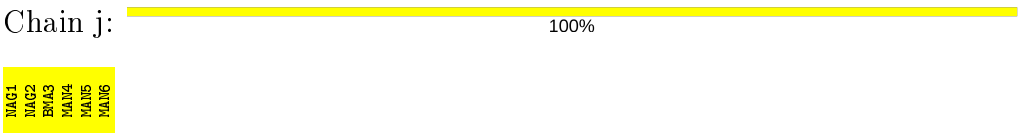
ido-2-deoxy-beta-D-glucopyranose

Chain Z:



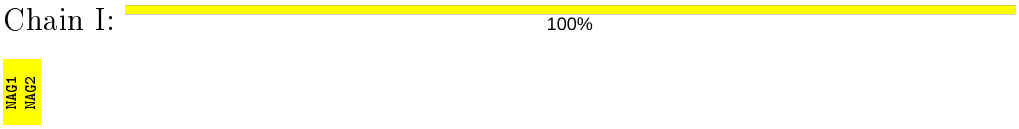
• Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:



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

Chain I:

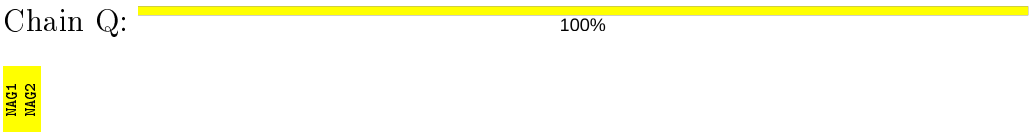


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:

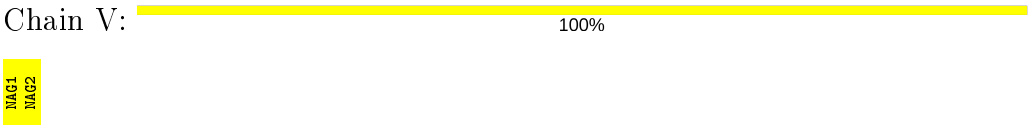
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:



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

Chain V:



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

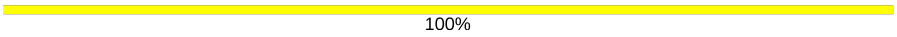
Chain b:

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

Chain g:

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

Chain K:



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

Chain L:

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

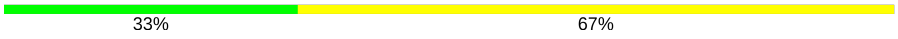
Chain W:

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

Chain X:

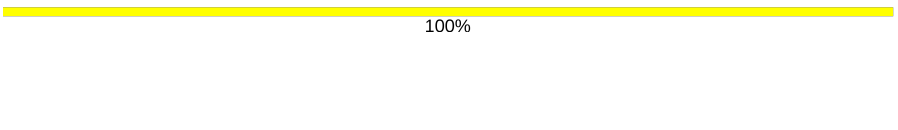
• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:



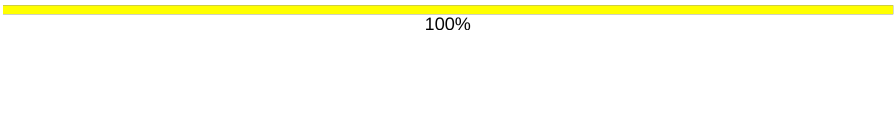
• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h:



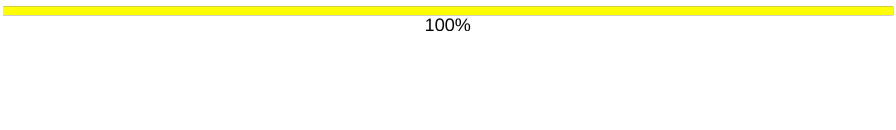
• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain l:



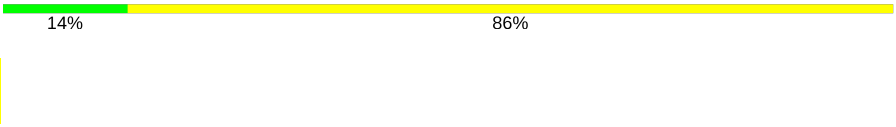
• Molecule 6: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:



• Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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 T:



• Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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 e:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	168.53Å 168.53Å 174.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.80 36.72 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.2 (50.00-2.80) 98.2 (36.72-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.09 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.226 , 0.257 0.235 , 0.265	Depositor DCC
R_{free} test set	6726 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	62.6	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 67.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.010 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	27659	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.19 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3641e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, CU1, MAN

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	0.50	0/4373	0.66	2/5981 (0.0%)
1	B	0.50	0/4373	0.66	3/5981 (0.1%)
1	C	0.55	5/4373 (0.1%)	0.64	2/5981 (0.0%)
1	D	0.51	3/4373 (0.1%)	0.60	2/5981 (0.0%)
1	E	0.44	1/4373 (0.0%)	0.58	1/5981 (0.0%)
1	F	0.99	20/4373 (0.5%)	0.77	11/5981 (0.2%)
All	All	0.61	29/26238 (0.1%)	0.65	21/35886 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	463	ARG	CZ-NH1	40.06	1.85	1.33
1	F	250	TYR	CE2-CZ	15.67	1.58	1.38
1	F	250	TYR	CG-CD2	15.35	1.59	1.39
1	D	515	GLU	CD-OE1	13.48	1.40	1.25
1	F	250	TYR	CE1-CZ	13.27	1.55	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	463	ARG	NE-CZ-NH2	-25.91	107.34	120.30
1	F	463	ARG	NE-CZ-NH1	10.71	125.66	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	445	ASP	CB-CG-OD2	-9.31	109.92	118.30
1	F	429	ARG	NE-CZ-NH2	-8.88	115.86	120.30
1	F	463	ARG	NH1-CZ-NH2	-8.13	110.46	119.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	463	ARG	Sidechain

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	527/534 (99%)	497 (94%)	23 (4%)	7 (1%)	12	36
1	B	527/534 (99%)	498 (94%)	23 (4%)	6 (1%)	14	41
1	C	527/534 (99%)	495 (94%)	27 (5%)	5 (1%)	17	46
1	D	527/534 (99%)	497 (94%)	22 (4%)	8 (2%)	10	33
1	E	527/534 (99%)	497 (94%)	24 (5%)	6 (1%)	14	41
1	F	527/534 (99%)	498 (94%)	23 (4%)	6 (1%)	14	41
All	All	3162/3204 (99%)	2982 (94%)	142 (4%)	38 (1%)	13	39

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	ASP

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Mol	Chain	Res	Type
1	B	531	ASN
1	C	130	ASP
1	D	130	ASP
1	E	130	ASP

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	477/481 (99%)	430 (90%)	47 (10%)	8	23
1	B	477/481 (99%)	425 (89%)	52 (11%)	6	19
1	C	477/481 (99%)	431 (90%)	46 (10%)	8	24
1	D	477/481 (99%)	425 (89%)	52 (11%)	6	19
1	E	477/481 (99%)	432 (91%)	45 (9%)	8	26
1	F	477/481 (99%)	429 (90%)	48 (10%)	7	22
All	All	2862/2886 (99%)	2572 (90%)	290 (10%)	7	22

5 of 290 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	389	ASN
1	D	185	GLU
1	F	292	ASN
1	C	446	ASN
1	D	64	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	517	HIS
1	C	51	GLN
1	E	382	ASN
1	B	324	GLN

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Mol	Chain	Res	Type
1	E	195	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

135 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	G	1	1,2	14,14,15	0.72	0	17,19,21	1.36	3 (17%)
2	NAG	G	2	2	14,14,15	0.55	0	17,19,21	1.06	2 (11%)
2	BMA	G	3	2	11,11,12	0.83	0	15,15,17	1.88	3 (20%)
2	MAN	G	4	2	11,11,12	0.60	0	15,15,17	1.37	1 (6%)
2	MAN	G	5	2	11,11,12	0.74	0	15,15,17	2.18	2 (13%)
3	NAG	H	1	1,3	14,14,15	0.79	0	17,19,21	2.04	4 (23%)
3	NAG	H	2	3	14,14,15	0.63	0	17,19,21	0.85	0
3	BMA	H	3	3	11,11,12	0.76	0	15,15,17	1.95	3 (20%)
3	MAN	H	4	3	11,11,12	0.61	0	15,15,17	1.10	1 (6%)
3	MAN	H	5	3	11,11,12	0.72	0	15,15,17	1.13	1 (6%)
3	MAN	H	6	3	11,11,12	0.68	0	15,15,17	1.75	3 (20%)
4	NAG	I	1	1,4	14,14,15	0.64	0	17,19,21	2.13	5 (29%)
4	NAG	I	2	4	14,14,15	1.05	1 (7%)	17,19,21	1.35	3 (17%)
2	NAG	J	1	1,2	14,14,15	0.71	0	17,19,21	1.80	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	J	2	2	14,14,15	0.63	0	17,19,21	1.99	3 (17%)
2	BMA	J	3	2	11,11,12	0.73	0	15,15,17	1.51	3 (20%)
2	MAN	J	4	2	11,11,12	0.73	0	15,15,17	1.85	3 (20%)
2	MAN	J	5	2	11,11,12	0.70	0	15,15,17	1.76	1 (6%)
5	NAG	K	1	1,5	14,14,15	0.51	0	17,19,21	1.95	4 (23%)
5	NAG	K	2	5	14,14,15	0.48	0	17,19,21	1.00	1 (5%)
5	BMA	K	3	5	11,11,12	0.94	0	15,15,17	1.19	1 (6%)
5	NAG	L	1	1,5	14,14,15	0.50	0	17,19,21	1.88	4 (23%)
5	NAG	L	2	5	14,14,15	0.54	0	17,19,21	1.15	2 (11%)
5	BMA	L	3	5	11,11,12	0.64	0	15,15,17	2.08	2 (13%)
2	NAG	M	1	1,2	14,14,15	0.73	0	17,19,21	1.01	0
2	NAG	M	2	2	14,14,15	0.62	0	17,19,21	1.10	1 (5%)
2	BMA	M	3	2	11,11,12	0.77	0	15,15,17	1.00	2 (13%)
2	MAN	M	4	2	11,11,12	0.71	0	15,15,17	2.81	7 (46%)
2	MAN	M	5	2	11,11,12	0.45	0	15,15,17	1.47	3 (20%)
3	NAG	N	1	1,3	14,14,15	0.68	0	17,19,21	1.50	4 (23%)
3	NAG	N	2	3	14,14,15	0.57	0	17,19,21	1.04	0
3	BMA	N	3	3	11,11,12	0.78	0	15,15,17	1.51	3 (20%)
3	MAN	N	4	3	11,11,12	0.62	0	15,15,17	2.07	2 (13%)
3	MAN	N	5	3	11,11,12	0.56	0	15,15,17	1.27	1 (6%)
3	MAN	N	6	3	11,11,12	0.57	0	15,15,17	1.19	2 (13%)
2	NAG	O	1	1,2	14,14,15	0.55	0	17,19,21	1.73	3 (17%)
2	NAG	O	2	2	14,14,15	0.74	0	17,19,21	1.27	2 (11%)
2	BMA	O	3	2	11,11,12	0.76	0	15,15,17	1.70	5 (33%)
2	MAN	O	4	2	11,11,12	0.62	0	15,15,17	2.11	5 (33%)
2	MAN	O	5	2	11,11,12	1.69	2 (18%)	15,15,17	2.30	4 (26%)
4	NAG	P	1	1,4	14,14,15	0.56	0	17,19,21	1.00	0
4	NAG	P	2	4	14,14,15	0.51	0	17,19,21	0.99	1 (5%)
4	NAG	Q	1	1,4	14,14,15	0.47	0	17,19,21	1.79	3 (17%)
4	NAG	Q	2	4	14,14,15	0.48	0	17,19,21	1.19	1 (5%)
6	NAG	R	1	1,6	14,14,15	0.74	0	17,19,21	1.61	1 (5%)
6	NAG	R	2	6	14,14,15	0.64	0	17,19,21	1.26	3 (17%)
6	BMA	R	3	6	11,11,12	0.55	0	15,15,17	1.13	2 (13%)
6	MAN	R	4	6	11,11,12	0.55	0	15,15,17	2.23	5 (33%)
2	NAG	S	1	1,2	14,14,15	0.73	0	17,19,21	1.34	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	S	2	2	14,14,15	0.63	0	17,19,21	1.34	3 (17%)
2	BMA	S	3	2	11,11,12	0.57	0	15,15,17	2.13	4 (26%)
2	MAN	S	4	2	11,11,12	0.57	0	15,15,17	1.52	3 (20%)
2	MAN	S	5	2	11,11,12	0.63	0	15,15,17	1.48	4 (26%)
7	NAG	T	1	1,7	14,14,15	0.91	1 (7%)	17,19,21	2.07	7 (41%)
7	NAG	T	2	7	14,14,15	0.45	0	17,19,21	1.01	1 (5%)
7	BMA	T	3	7	11,11,12	0.59	0	15,15,17	1.91	3 (20%)
7	MAN	T	4	7	11,11,12	0.61	0	15,15,17	1.29	1 (6%)
7	MAN	T	5	7	11,11,12	0.72	0	15,15,17	0.78	0
7	MAN	T	6	7	11,11,12	0.57	0	15,15,17	2.15	3 (20%)
7	MAN	T	7	7	11,11,12	0.77	0	15,15,17	2.01	4 (26%)
2	NAG	U	1	1,2	14,14,15	0.48	0	17,19,21	1.96	2 (11%)
2	NAG	U	2	2	14,14,15	0.74	1 (7%)	17,19,21	1.25	4 (23%)
2	BMA	U	3	2	11,11,12	0.70	0	15,15,17	1.31	2 (13%)
2	MAN	U	4	2	11,11,12	0.78	0	15,15,17	1.68	3 (20%)
2	MAN	U	5	2	11,11,12	0.60	0	15,15,17	1.65	2 (13%)
4	NAG	V	1	1,4	14,14,15	0.52	0	17,19,21	1.14	1 (5%)
4	NAG	V	2	4	14,14,15	1.20	2 (14%)	17,19,21	1.48	2 (11%)
5	NAG	W	1	1,5	14,14,15	1.98	3 (21%)	17,19,21	0.93	0
5	NAG	W	2	5	14,14,15	1.75	3 (21%)	17,19,21	2.18	4 (23%)
5	BMA	W	3	5	11,11,12	2.47	1 (9%)	15,15,17	1.82	4 (26%)
5	NAG	X	1	1,5	14,14,15	0.49	0	17,19,21	1.79	5 (29%)
5	NAG	X	2	5	14,14,15	0.43	0	17,19,21	1.20	2 (11%)
5	BMA	X	3	5	11,11,12	0.68	0	15,15,17	1.03	1 (6%)
2	NAG	Y	1	1,2	14,14,15	0.55	0	17,19,21	0.94	1 (5%)
2	NAG	Y	2	2	14,14,15	0.59	0	17,19,21	1.23	3 (17%)
2	BMA	Y	3	2	11,11,12	0.59	0	15,15,17	1.50	3 (20%)
2	MAN	Y	4	2	11,11,12	0.58	0	15,15,17	1.38	2 (13%)
2	MAN	Y	5	2	11,11,12	0.64	0	15,15,17	1.24	1 (6%)
3	NAG	Z	1	1,3	14,14,15	0.63	0	17,19,21	1.70	3 (17%)
3	NAG	Z	2	3	14,14,15	0.70	0	17,19,21	0.94	1 (5%)
3	BMA	Z	3	3	11,11,12	0.73	0	15,15,17	1.85	4 (26%)
3	MAN	Z	4	3	11,11,12	0.60	0	15,15,17	1.17	2 (13%)
3	MAN	Z	5	3	11,11,12	0.63	0	15,15,17	0.96	1 (6%)
3	MAN	Z	6	3	11,11,12	1.07	1 (9%)	15,15,17	2.06	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	a	1	1,2	14,14,15	0.41	0	17,19,21	1.26	2 (11%)
2	NAG	a	2	2	14,14,15	0.59	0	17,19,21	1.00	2 (11%)
2	BMA	a	3	2	11,11,12	0.68	0	15,15,17	1.22	2 (13%)
2	MAN	a	4	2	11,11,12	0.55	0	15,15,17	1.75	4 (26%)
2	MAN	a	5	2	11,11,12	0.62	0	15,15,17	1.54	2 (13%)
4	NAG	b	1	1,4	14,14,15	1.38	2 (14%)	17,19,21	1.59	3 (17%)
4	NAG	b	2	4	14,14,15	0.51	0	17,19,21	0.72	0
5	NAG	c	1	1,5	14,14,15	0.53	0	17,19,21	1.36	2 (11%)
5	NAG	c	2	5	14,14,15	0.55	0	17,19,21	0.85	0
5	BMA	c	3	5	11,11,12	0.56	0	15,15,17	0.98	2 (13%)
2	NAG	d	1	1,2	14,14,15	0.60	0	17,19,21	1.15	1 (5%)
2	NAG	d	2	2	14,14,15	0.56	0	17,19,21	0.82	0
2	BMA	d	3	2	11,11,12	0.78	0	15,15,17	2.15	4 (26%)
2	MAN	d	4	2	11,11,12	0.60	0	15,15,17	0.69	0
2	MAN	d	5	2	11,11,12	0.55	0	15,15,17	1.40	1 (6%)
7	NAG	e	1	1,7	14,14,15	0.58	0	17,19,21	1.05	1 (5%)
7	NAG	e	2	7	14,14,15	0.50	0	17,19,21	1.26	2 (11%)
7	BMA	e	3	7	11,11,12	0.63	0	15,15,17	1.53	3 (20%)
7	MAN	e	4	7	11,11,12	0.63	0	15,15,17	1.55	4 (26%)
7	MAN	e	5	7	11,11,12	0.56	0	15,15,17	1.06	1 (6%)
7	MAN	e	6	7	11,11,12	0.71	0	15,15,17	1.61	2 (13%)
7	MAN	e	7	7	11,11,12	0.53	0	15,15,17	1.56	1 (6%)
2	NAG	f	1	1,2	14,14,15	0.55	0	17,19,21	1.47	3 (17%)
2	NAG	f	2	2	14,14,15	0.51	0	17,19,21	0.94	0
2	BMA	f	3	2	11,11,12	0.64	0	15,15,17	1.09	1 (6%)
2	MAN	f	4	2	11,11,12	0.57	0	15,15,17	1.44	3 (20%)
2	MAN	f	5	2	11,11,12	0.58	0	15,15,17	1.48	3 (20%)
4	NAG	g	1	1,4	14,14,15	0.54	0	17,19,21	1.22	2 (11%)
4	NAG	g	2	4	14,14,15	0.59	0	17,19,21	1.06	1 (5%)
5	NAG	h	1	1,5	14,14,15	0.59	0	17,19,21	1.64	4 (23%)
5	NAG	h	2	5	14,14,15	0.61	0	17,19,21	1.10	1 (5%)
5	BMA	h	3	5	11,11,12	0.88	0	15,15,17	1.98	5 (33%)
2	NAG	i	1	1,2	14,14,15	0.62	0	17,19,21	0.94	0
2	NAG	i	2	2	14,14,15	0.61	0	17,19,21	1.17	1 (5%)
2	BMA	i	3	2	11,11,12	0.66	0	15,15,17	1.41	3 (20%)
2	MAN	i	4	2	11,11,12	0.65	0	15,15,17	1.87	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	MAN	i	5	2	11,11,12	0.49	0	15,15,17	1.63	2 (13%)
3	NAG	j	1	1,3	14,14,15	0.63	0	17,19,21	1.45	3 (17%)
3	NAG	j	2	3	14,14,15	0.73	0	17,19,21	1.52	3 (17%)
3	BMA	j	3	3	11,11,12	0.80	0	15,15,17	0.97	2 (13%)
3	MAN	j	4	3	11,11,12	1.18	1 (9%)	15,15,17	1.45	2 (13%)
3	MAN	j	5	3	11,11,12	0.95	1 (9%)	15,15,17	0.94	1 (6%)
3	MAN	j	6	3	11,11,12	0.60	0	15,15,17	1.68	2 (13%)
2	NAG	k	1	1,2	14,14,15	0.51	0	17,19,21	1.31	2 (11%)
2	NAG	k	2	2	14,14,15	0.56	0	17,19,21	1.06	2 (11%)
2	BMA	k	3	2	11,11,12	0.71	0	15,15,17	1.34	1 (6%)
2	MAN	k	4	2	11,11,12	0.67	0	15,15,17	1.03	1 (6%)
2	MAN	k	5	2	11,11,12	1.57	1 (9%)	15,15,17	1.81	2 (13%)
5	NAG	l	1	1,5	14,14,15	0.50	0	17,19,21	1.10	1 (5%)
5	NAG	l	2	5	14,14,15	0.58	0	17,19,21	1.48	4 (23%)
5	BMA	l	3	5	11,11,12	1.85	2 (18%)	15,15,17	1.07	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
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
2	MAN	G	4	2	-	2/2/19/22	0/1/1/1
2	MAN	G	5	2	-	2/2/19/22	1/1/1/1
3	NAG	H	1	1,3	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	1/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
3	MAN	H	4	3	-	2/2/19/22	0/1/1/1
3	MAN	H	5	3	-	0/2/19/22	0/1/1/1
3	MAN	H	6	3	-	2/2/19/22	0/1/1/1
4	NAG	I	1	1,4	-	4/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
2	NAG	J	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	J	2	2	-	5/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMA	J	3	2	-	2/2/19/22	0/1/1/1
2	MAN	J	4	2	-	2/2/19/22	0/1/1/1
2	MAN	J	5	2	-	1/2/19/22	0/1/1/1
5	NAG	K	1	1,5	-	5/6/23/26	0/1/1/1
5	NAG	K	2	5	-	4/6/23/26	0/1/1/1
5	BMA	K	3	5	-	0/2/19/22	0/1/1/1
5	NAG	L	1	1,5	1/1/5/7	2/6/23/26	0/1/1/1
5	NAG	L	2	5	-	2/6/23/26	0/1/1/1
5	BMA	L	3	5	-	2/2/19/22	0/1/1/1
2	NAG	M	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	M	2	2	-	1/6/23/26	0/1/1/1
2	BMA	M	3	2	-	0/2/19/22	0/1/1/1
2	MAN	M	4	2	-	1/2/19/22	0/1/1/1
2	MAN	M	5	2	-	1/2/19/22	1/1/1/1
3	NAG	N	1	1,3	1/1/5/7	4/6/23/26	0/1/1/1
3	NAG	N	2	3	-	2/6/23/26	0/1/1/1
3	BMA	N	3	3	-	0/2/19/22	0/1/1/1
3	MAN	N	4	3	-	1/2/19/22	0/1/1/1
3	MAN	N	5	3	-	0/2/19/22	0/1/1/1
3	MAN	N	6	3	-	2/2/19/22	0/1/1/1
2	NAG	O	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	O	2	2	-	2/6/23/26	0/1/1/1
2	BMA	O	3	2	-	2/2/19/22	0/1/1/1
2	MAN	O	4	2	-	2/2/19/22	0/1/1/1
2	MAN	O	5	2	-	2/2/19/22	0/1/1/1
4	NAG	P	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	4/6/23/26	0/1/1/1
4	NAG	Q	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	0/6/23/26	0/1/1/1
6	NAG	R	1	1,6	1/1/5/7	4/6/23/26	0/1/1/1
6	NAG	R	2	6	-	1/6/23/26	0/1/1/1
6	BMA	R	3	6	-	0/2/19/22	0/1/1/1
6	MAN	R	4	6	-	1/2/19/22	0/1/1/1
2	NAG	S	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	S	2	2	-	0/6/23/26	0/1/1/1
2	BMA	S	3	2	-	2/2/19/22	0/1/1/1
2	MAN	S	4	2	-	1/2/19/22	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	a	5	2	-	2/2/19/22	0/1/1/1
4	NAG	b	1	1,4	1/1/5/7	5/6/23/26	0/1/1/1
4	NAG	b	2	4	-	0/6/23/26	0/1/1/1
5	NAG	c	1	1,5	1/1/5/7	2/6/23/26	0/1/1/1
5	NAG	c	2	5	-	2/6/23/26	0/1/1/1
5	BMA	c	3	5	-	0/2/19/22	0/1/1/1
2	NAG	d	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	d	2	2	-	4/6/23/26	0/1/1/1
2	BMA	d	3	2	-	2/2/19/22	0/1/1/1
2	MAN	d	4	2	-	2/2/19/22	0/1/1/1
2	MAN	d	5	2	-	2/2/19/22	0/1/1/1
7	NAG	e	1	1,7	1/1/5/7	3/6/23/26	0/1/1/1
7	NAG	e	2	7	-	4/6/23/26	0/1/1/1
7	BMA	e	3	7	-	2/2/19/22	0/1/1/1
7	MAN	e	4	7	-	2/2/19/22	0/1/1/1
7	MAN	e	5	7	-	0/2/19/22	0/1/1/1
7	MAN	e	6	7	-	2/2/19/22	0/1/1/1
7	MAN	e	7	7	-	2/2/19/22	0/1/1/1
2	NAG	f	1	1,2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	f	2	2	-	2/6/23/26	0/1/1/1
2	BMA	f	3	2	-	2/2/19/22	0/1/1/1
2	MAN	f	4	2	-	1/2/19/22	1/1/1/1
2	MAN	f	5	2	-	2/2/19/22	0/1/1/1
4	NAG	g	1	1,4	-	5/6/23/26	0/1/1/1
4	NAG	g	2	4	-	0/6/23/26	0/1/1/1
5	NAG	h	1	1,5	1/1/5/7	2/6/23/26	0/1/1/1
5	NAG	h	2	5	-	2/6/23/26	0/1/1/1
5	BMA	h	3	5	-	2/2/19/22	0/1/1/1
2	NAG	i	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	i	2	2	-	4/6/23/26	0/1/1/1
2	BMA	i	3	2	-	0/2/19/22	0/1/1/1
2	MAN	i	4	2	-	1/2/19/22	0/1/1/1
2	MAN	i	5	2	-	1/2/19/22	1/1/1/1
3	NAG	j	1	1,3	1/1/5/7	4/6/23/26	0/1/1/1
3	NAG	j	2	3	-	5/6/23/26	0/1/1/1
3	BMA	j	3	3	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	j	4	3	-	2/2/19/22	0/1/1/1
3	MAN	j	5	3	-	1/2/19/22	0/1/1/1
3	MAN	j	6	3	-	2/2/19/22	0/1/1/1
2	NAG	k	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	k	2	2	-	5/6/23/26	0/1/1/1
2	BMA	k	3	2	-	0/2/19/22	0/1/1/1
2	MAN	k	4	2	-	2/2/19/22	0/1/1/1
2	MAN	k	5	2	-	0/2/19/22	1/1/1/1
5	NAG	l	1	1,5	1/1/5/7	2/6/23/26	0/1/1/1
5	NAG	l	2	5	-	2/6/23/26	0/1/1/1
5	BMA	l	3	5	-	2/2/19/22	0/1/1/1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	W	3	BMA	O6-C6	7.74	1.75	1.42
2	k	5	MAN	O6-C6	4.87	1.63	1.42
5	l	3	BMA	O6-C6	4.79	1.62	1.42
5	W	1	NAG	C8-C7	4.59	1.60	1.50
5	W	2	NAG	C8-C7	4.54	1.60	1.50

The worst 5 of 311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	5	MAN	C1-O5-C5	7.19	121.93	112.19
2	M	4	MAN	C1-O5-C5	7.07	121.77	112.19
2	O	5	MAN	C1-O5-C5	6.76	121.35	112.19
2	U	1	NAG	C1-O5-C5	6.66	121.22	112.19
7	T	6	MAN	C1-O5-C5	6.53	121.04	112.19

5 of 15 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	T	1	NAG	C1
5	L	1	NAG	C1
3	N	1	NAG	C1
2	a	1	NAG	C1
5	h	1	NAG	C1

5 of 247 torsion outliers are listed below:

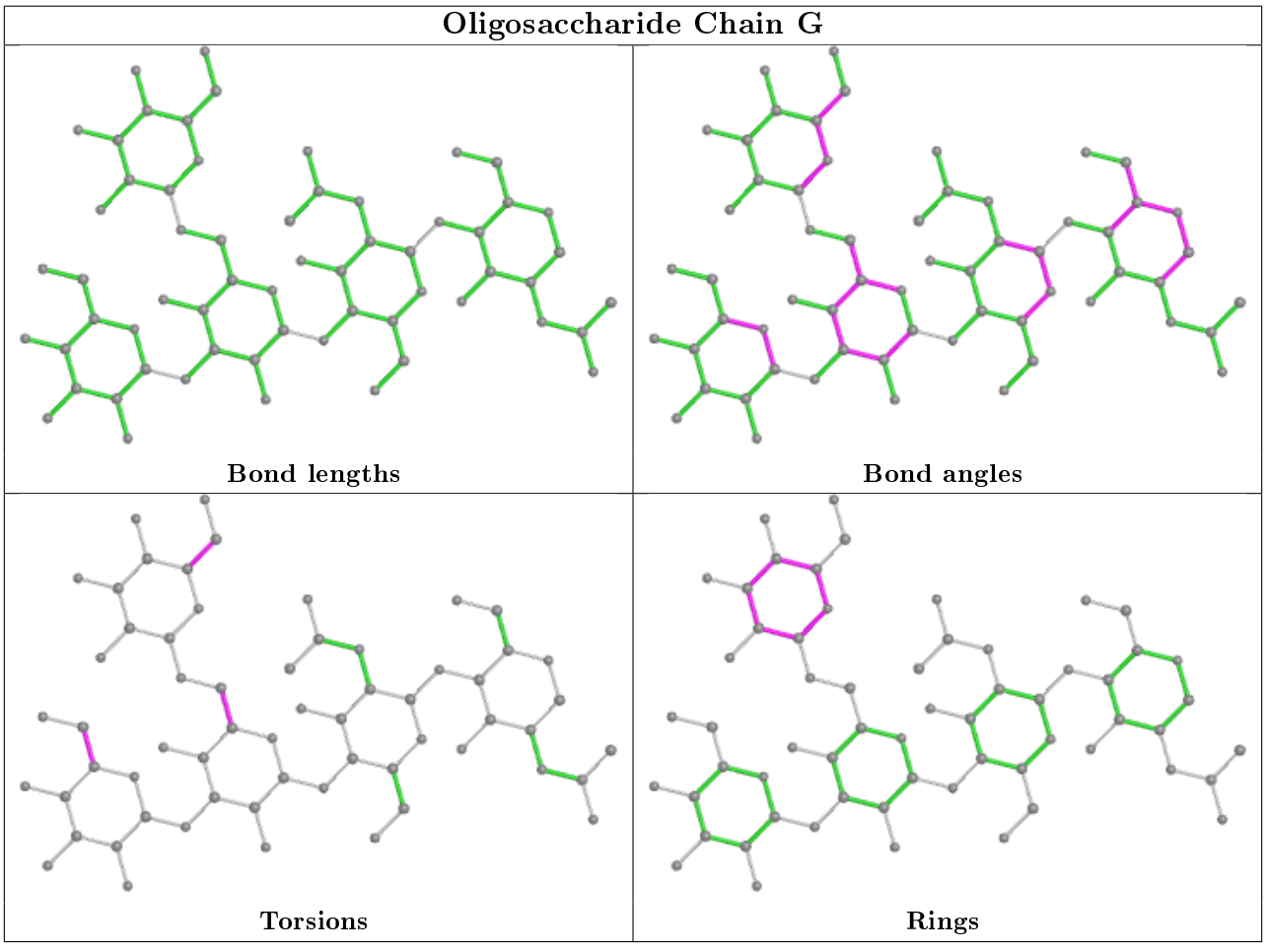
Mol	Chain	Res	Type	Atoms
5	K	1	NAG	C8-C7-N2-C2
5	K	1	NAG	O7-C7-N2-C2
7	e	2	NAG	C8-C7-N2-C2
7	e	2	NAG	O7-C7-N2-C2
4	Q	1	NAG	C3-C2-N2-C7

All (5) ring outliers are listed below:

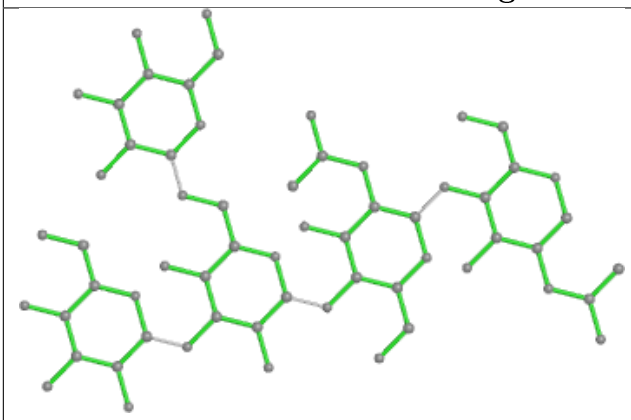
Mol	Chain	Res	Type	Atoms
2	G	5	MAN	C1-C2-C3-C4-C5-O5
2	k	5	MAN	C1-C2-C3-C4-C5-O5
2	f	4	MAN	C1-C2-C3-C4-C5-O5
2	i	5	MAN	C1-C2-C3-C4-C5-O5
2	M	5	MAN	C1-C2-C3-C4-C5-O5

No monomer is involved in short contacts.

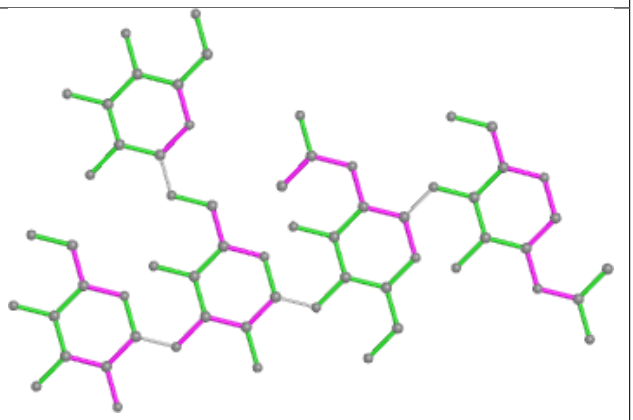
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



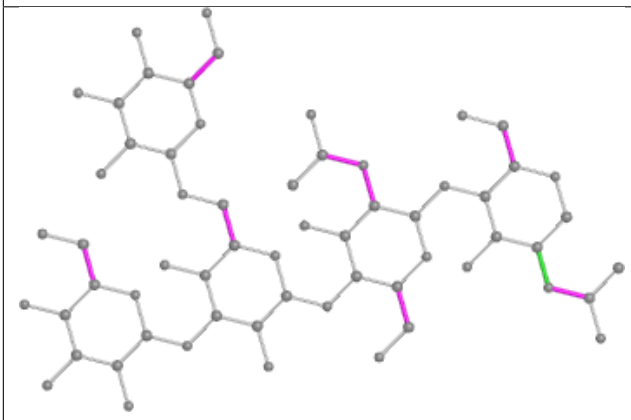
Oligosaccharide Chain J



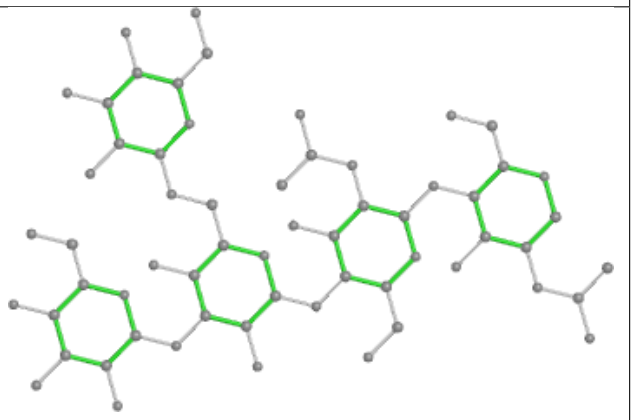
Bond lengths



Bond angles

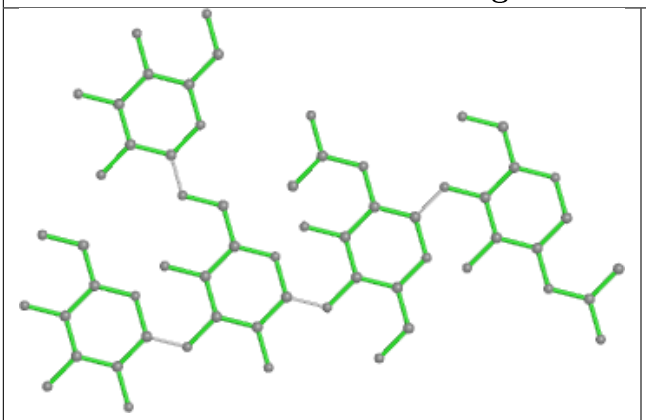


Torsions

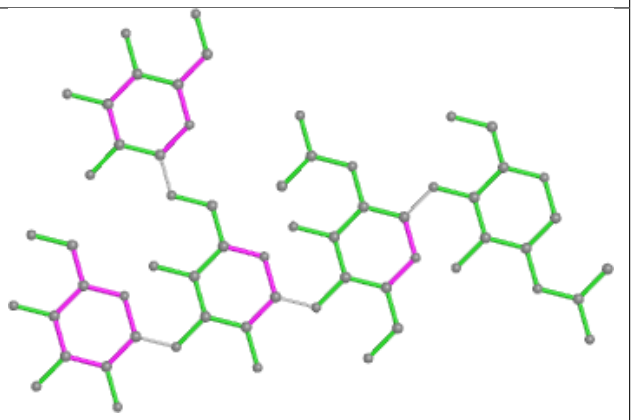


Rings

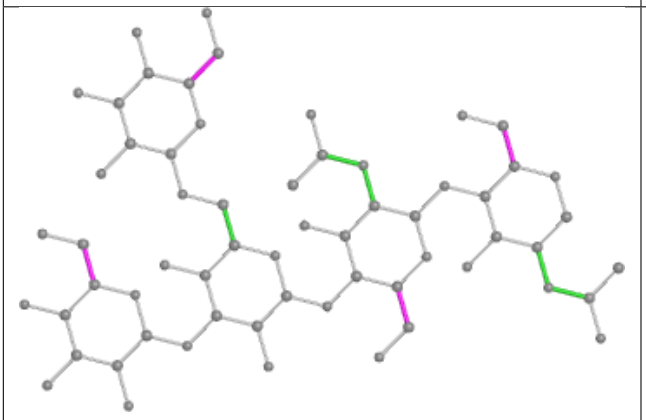
Oligosaccharide Chain M



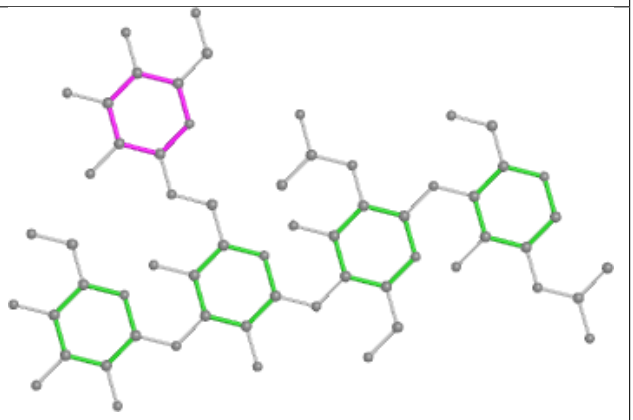
Bond lengths



Bond angles

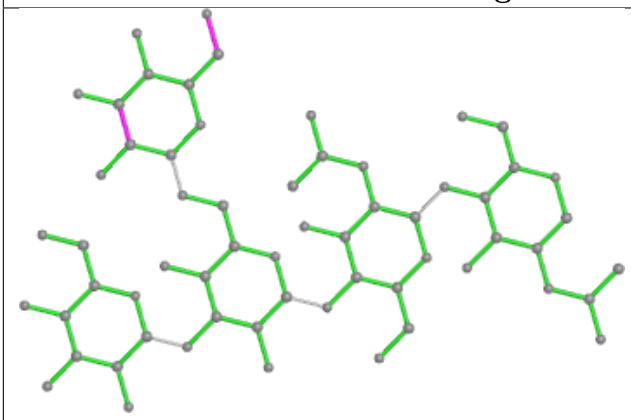


Torsions

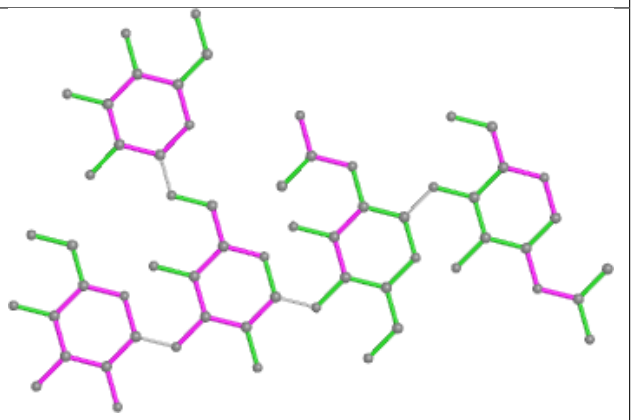


Rings

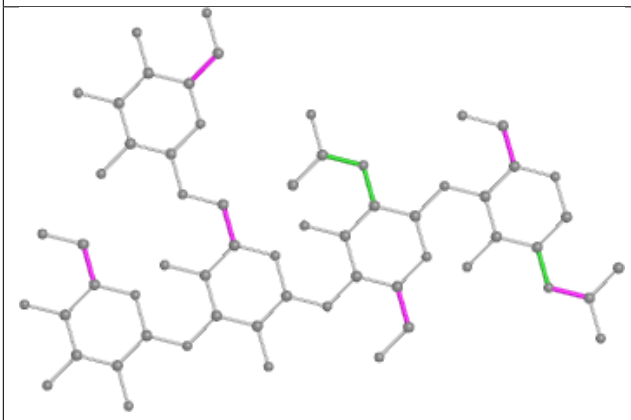
Oligosaccharide Chain O



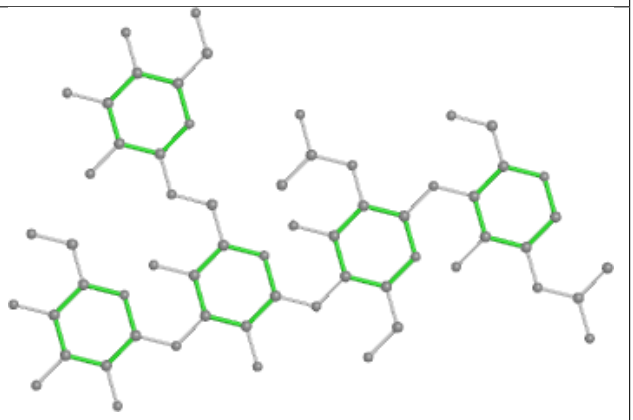
Bond lengths



Bond angles

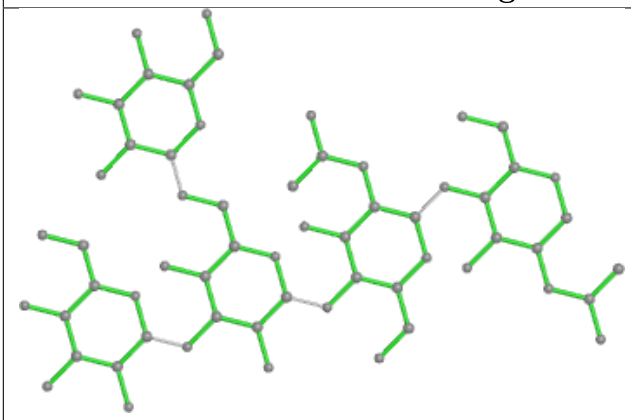


Torsions

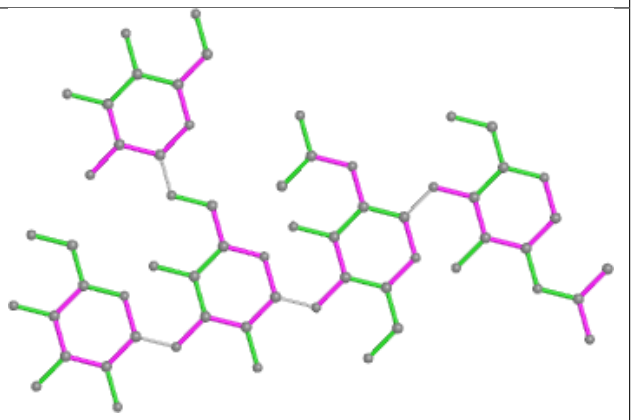


Rings

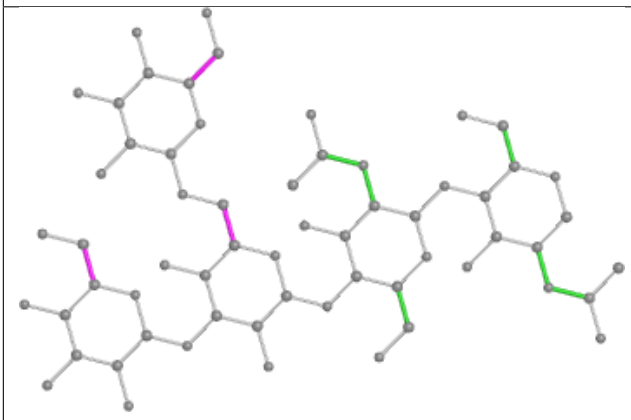
Oligosaccharide Chain S



Bond lengths



Bond angles



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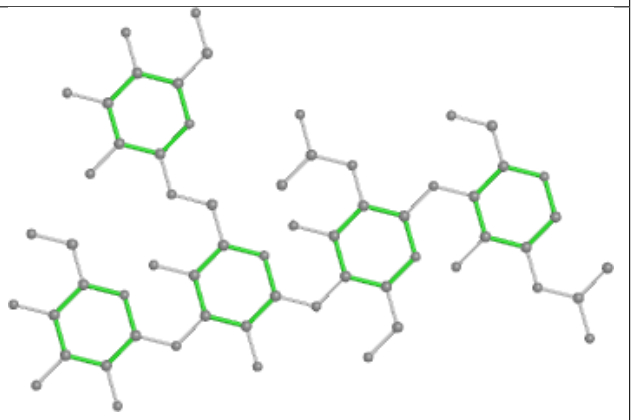
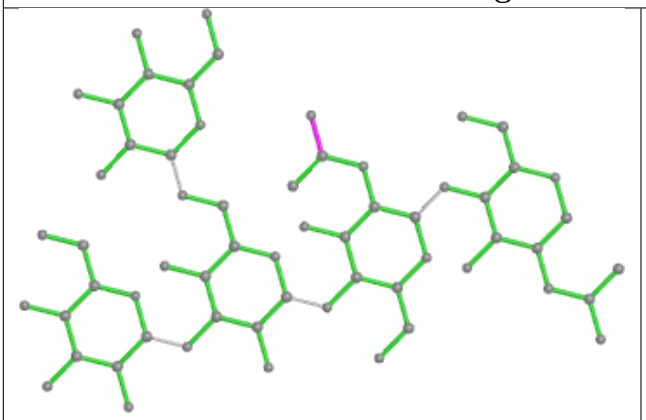
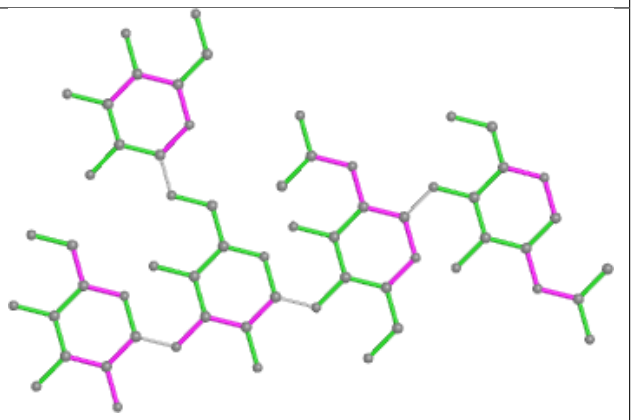


Rings

Oligosaccharide Chain U



Bond lengths



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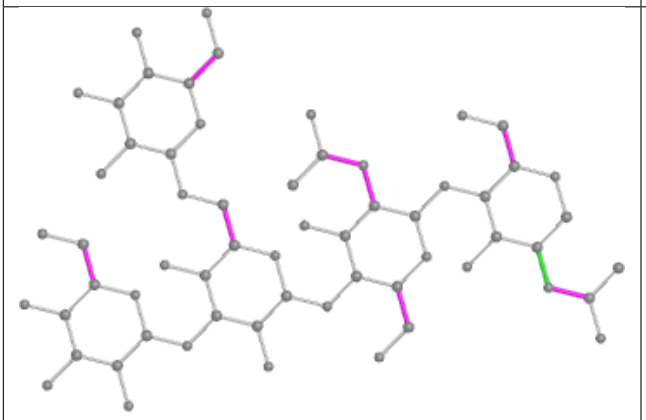

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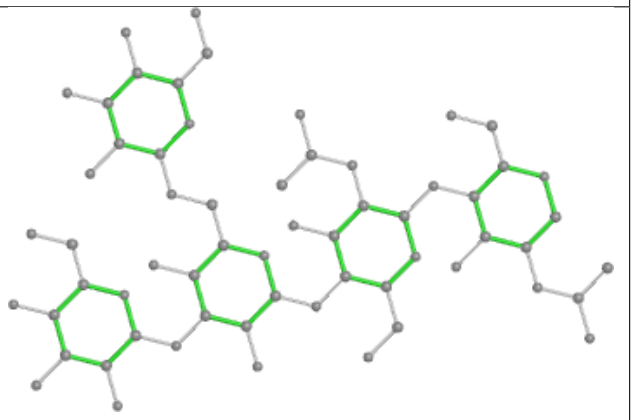
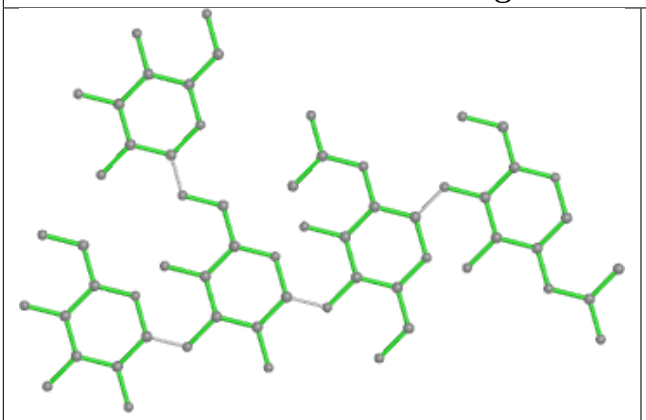


Rings

Oligosaccharide Chain Y



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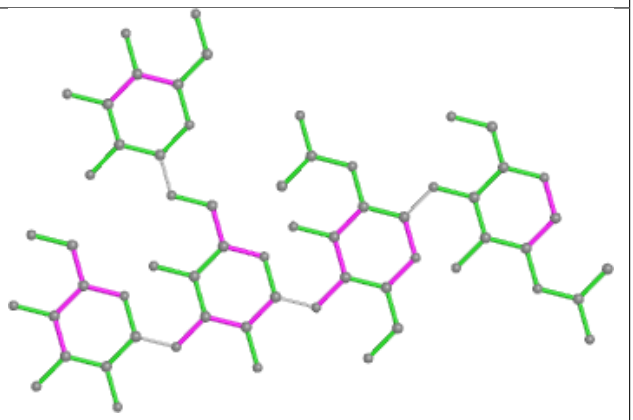
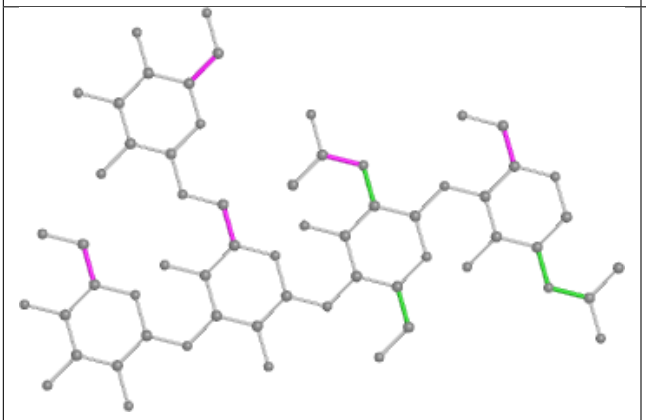
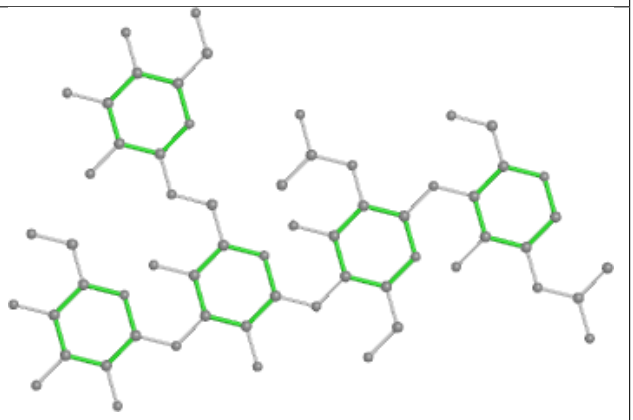


Bond angles

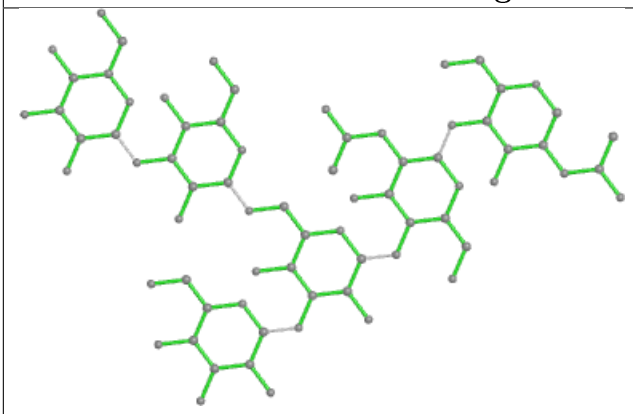


Torsions

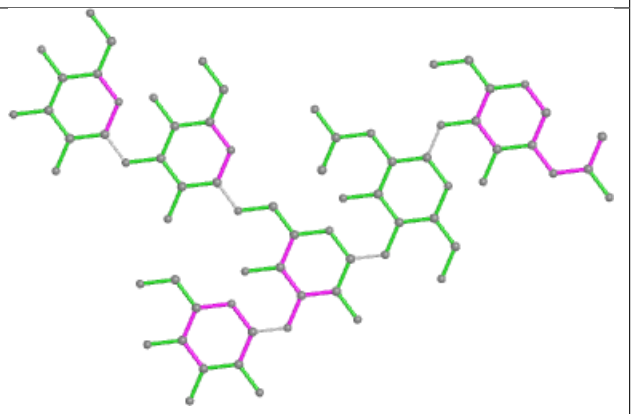


Rings

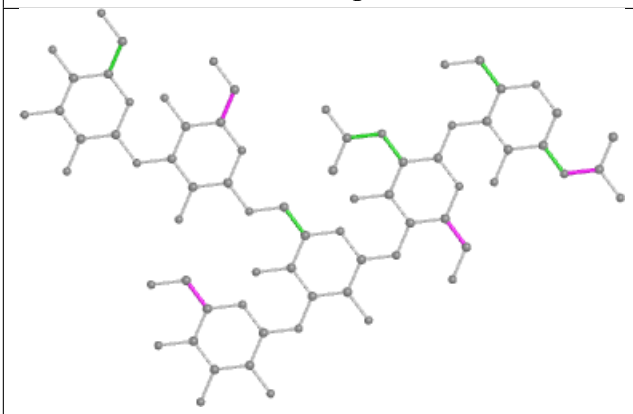
Oligosaccharide Chain H



Bond lengths



Bond angles



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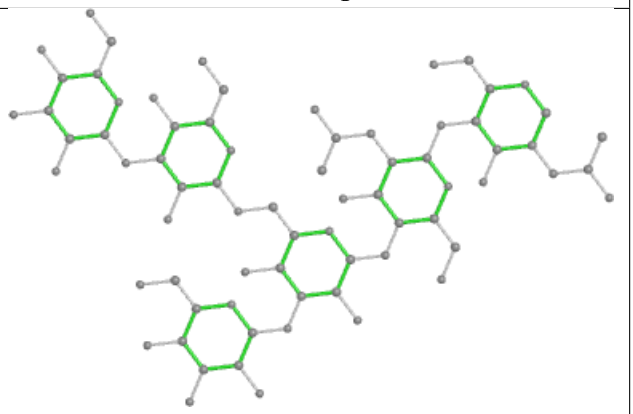
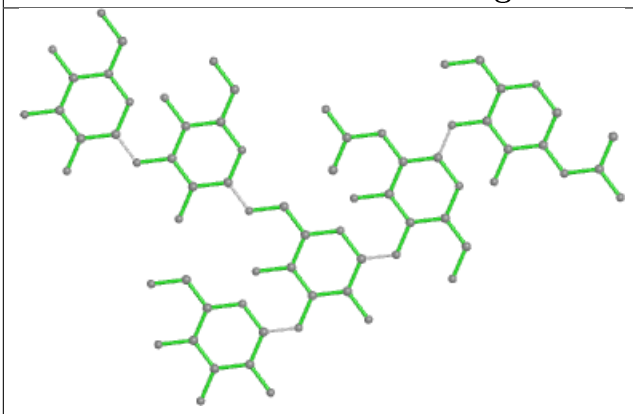
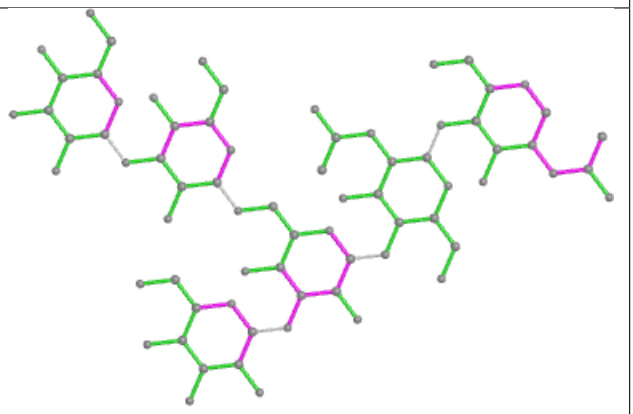


Rings

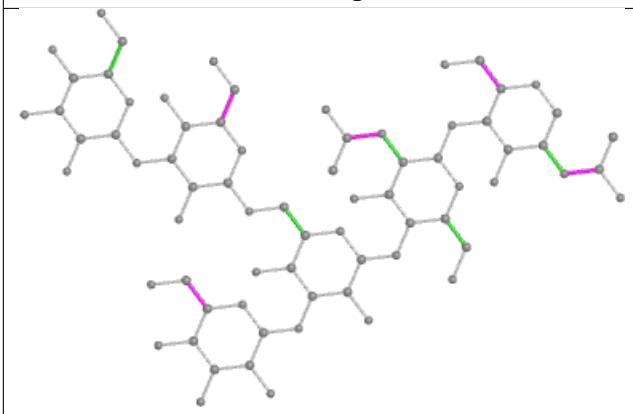
Oligosaccharide Chain N



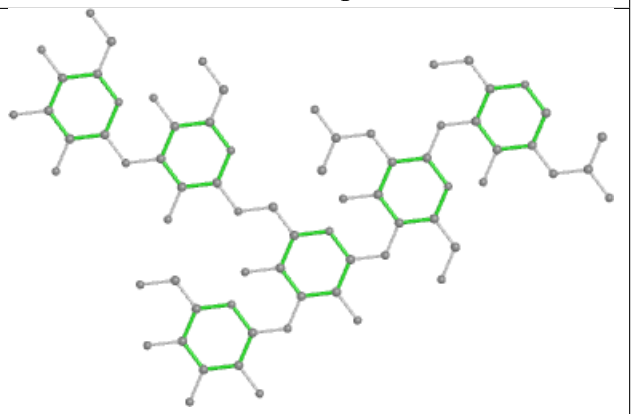
Bond lengths



Bond angles

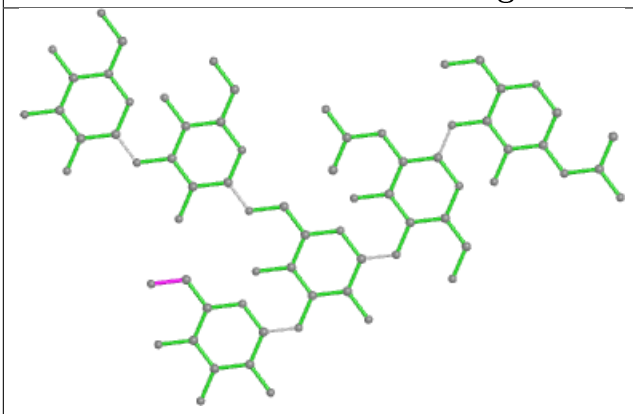


Torsions

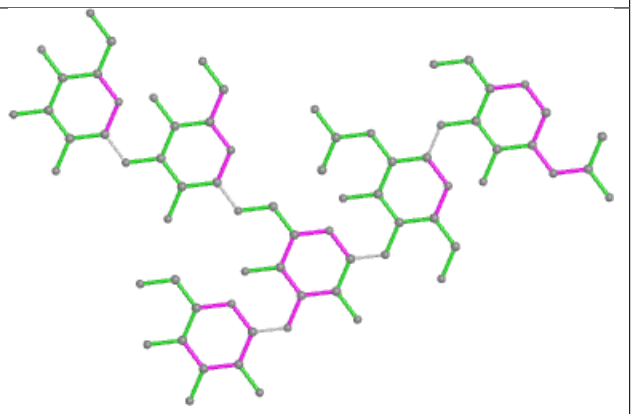


Rings

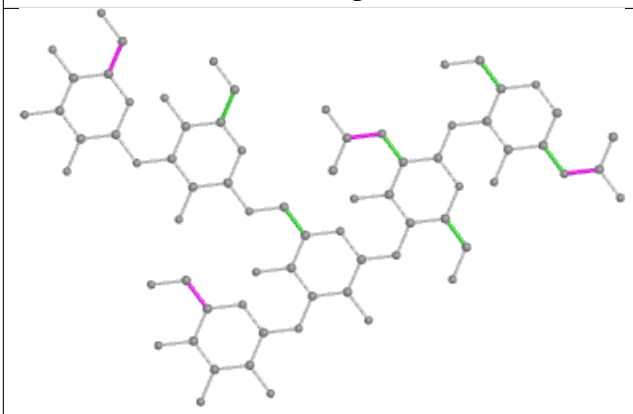
Oligosaccharide Chain Z



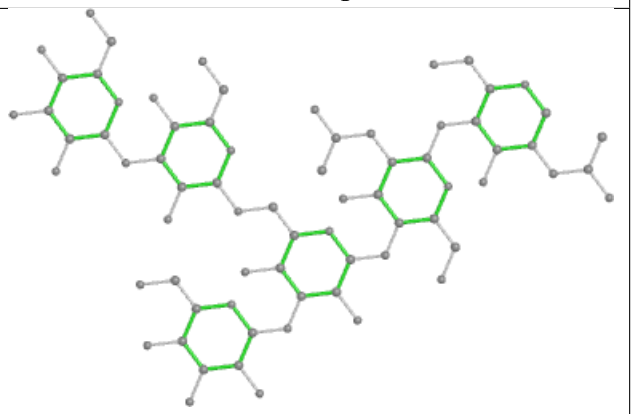
Bond lengths



Bond angles

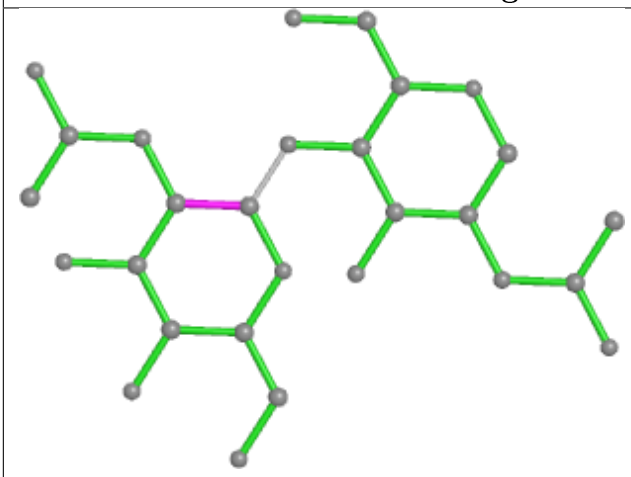


Torsions

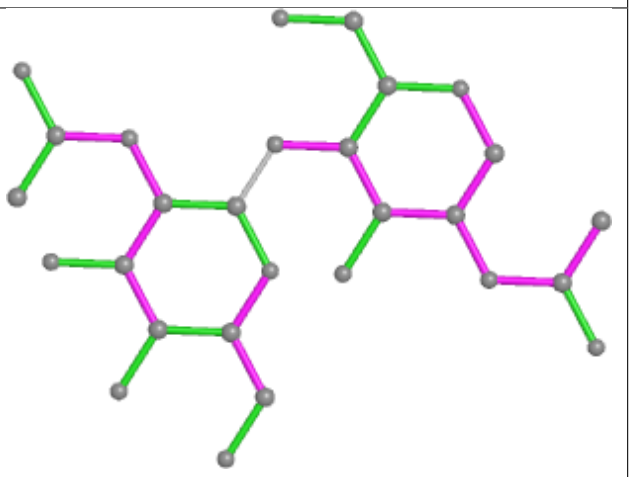


Rings

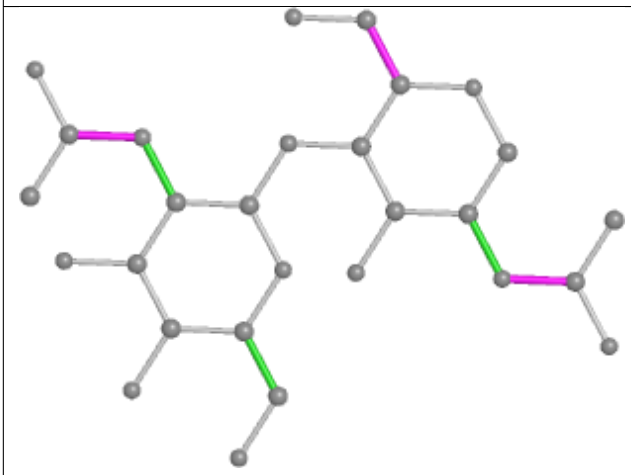
Oligosaccharide Chain I



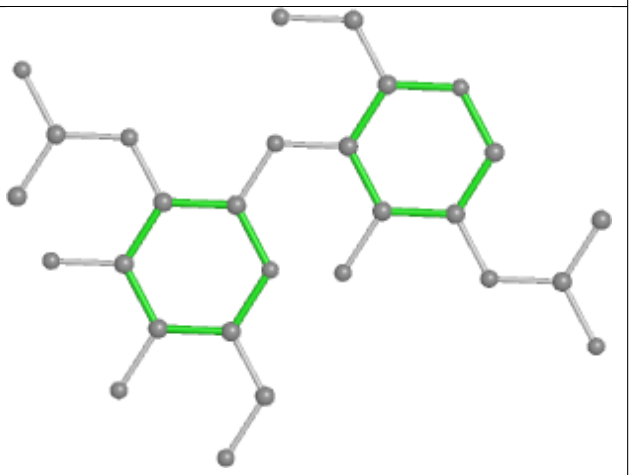
Bond lengths



Bond angles

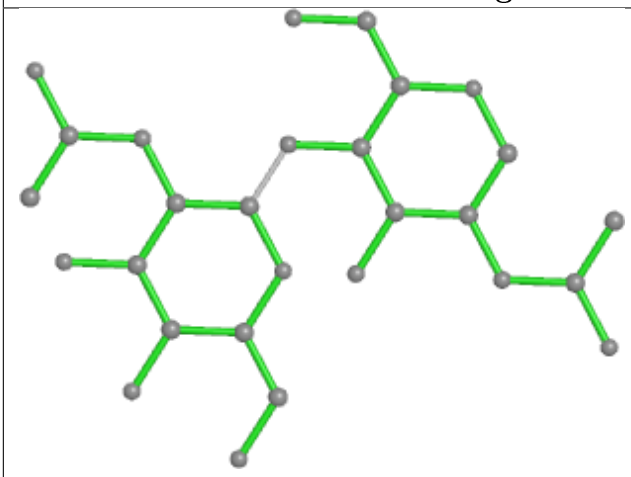


Torsions

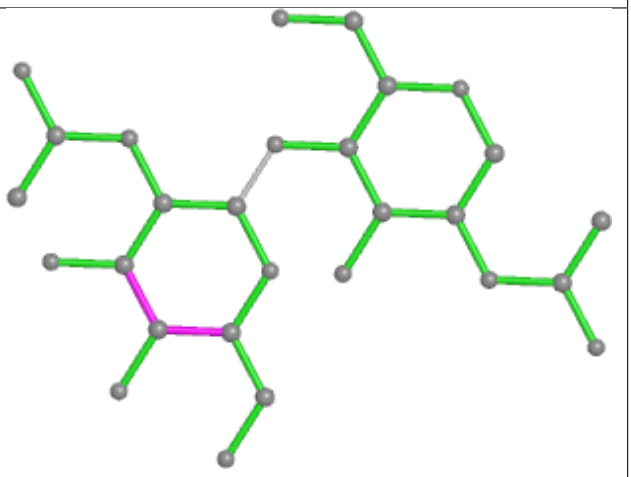


Rings

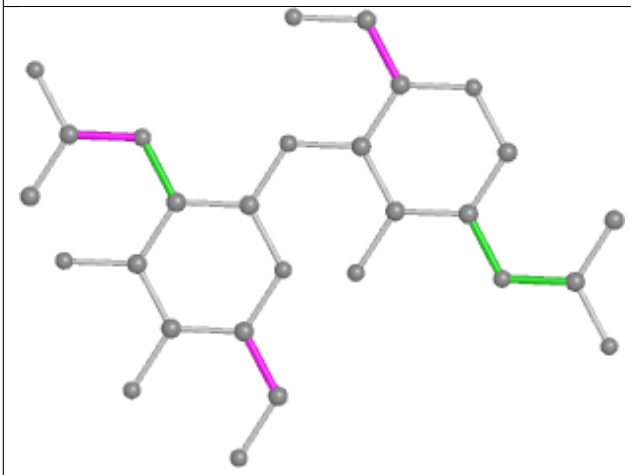
Oligosaccharide Chain P



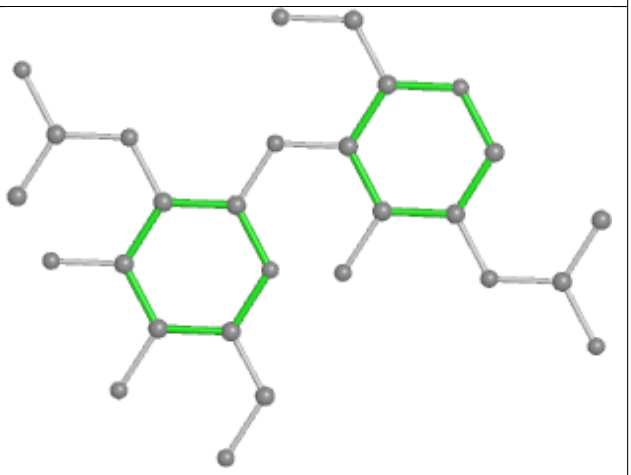
Bond lengths



Bond angles

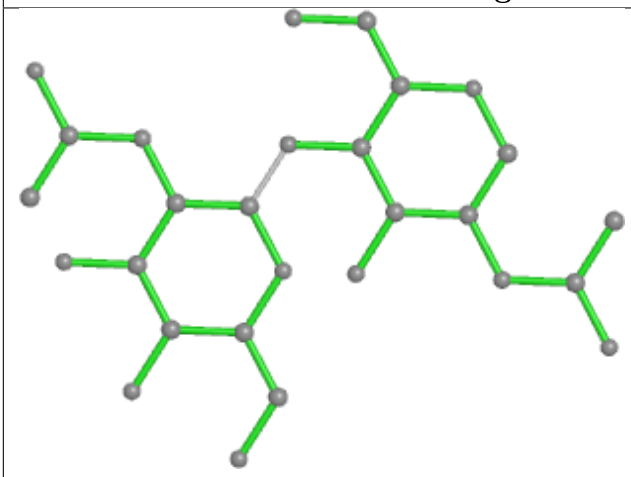


Torsions

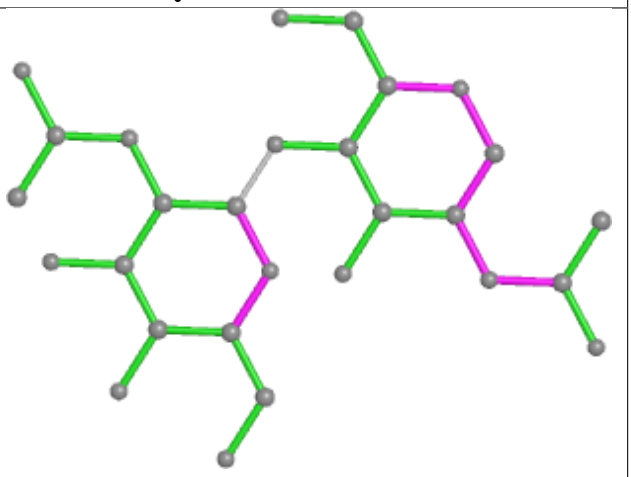


Rings

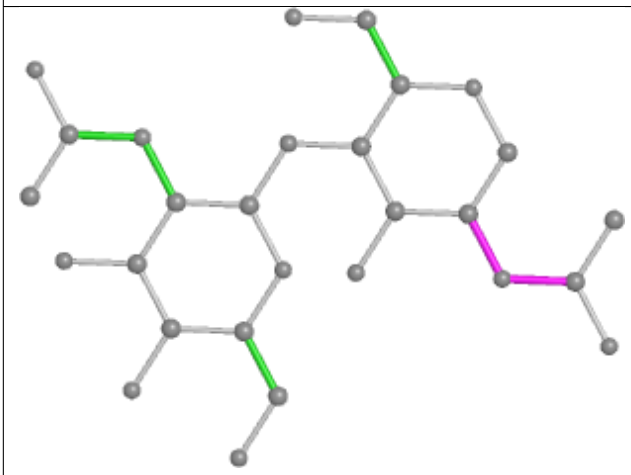
Oligosaccharide Chain Q



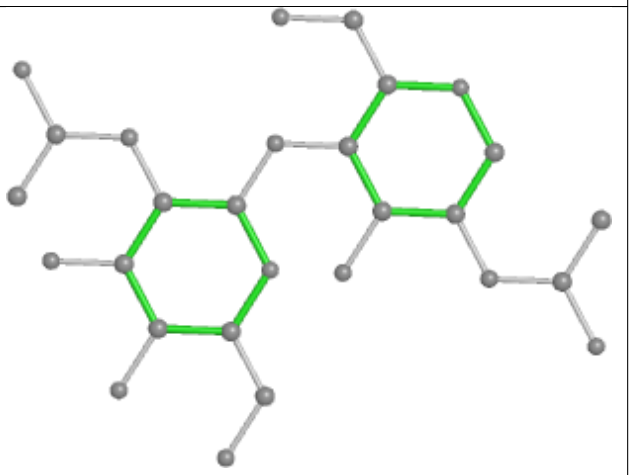
Bond lengths



Bond angles

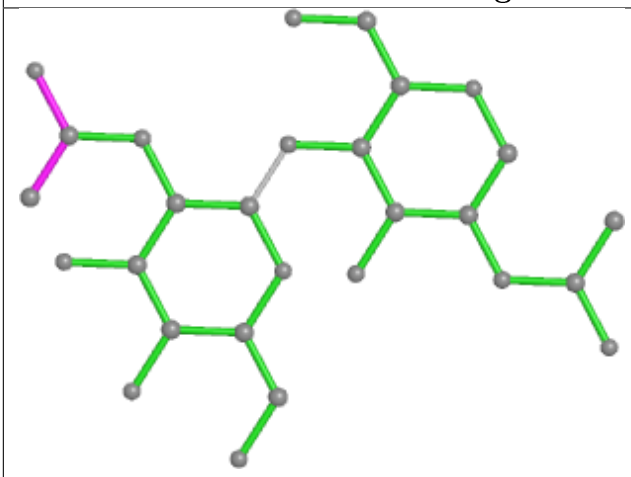


Torsions

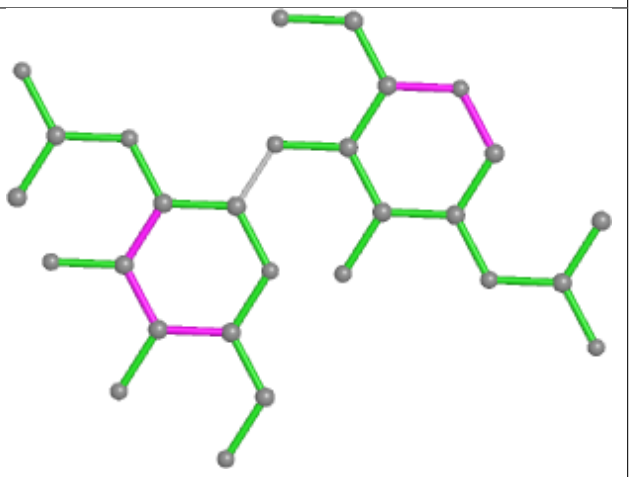


Rings

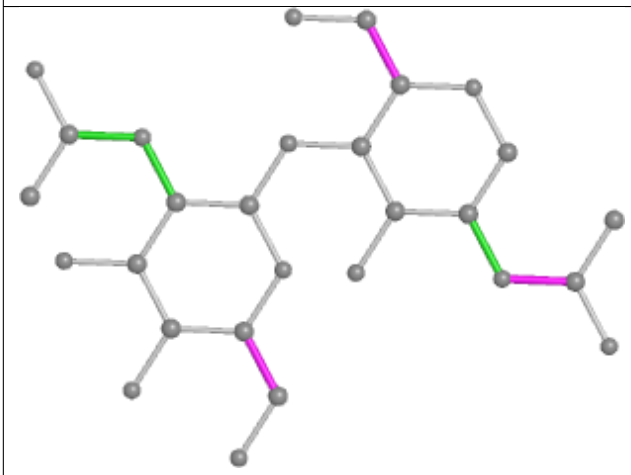
Oligosaccharide Chain V



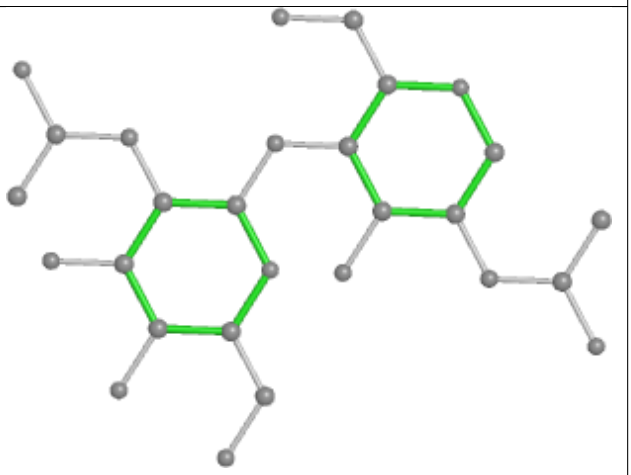
Bond lengths



Bond angles

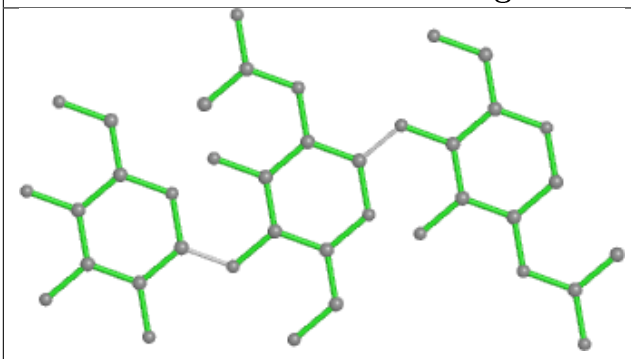


Torsions

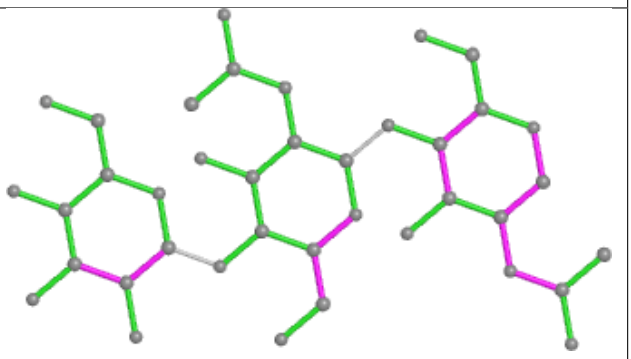


Rings

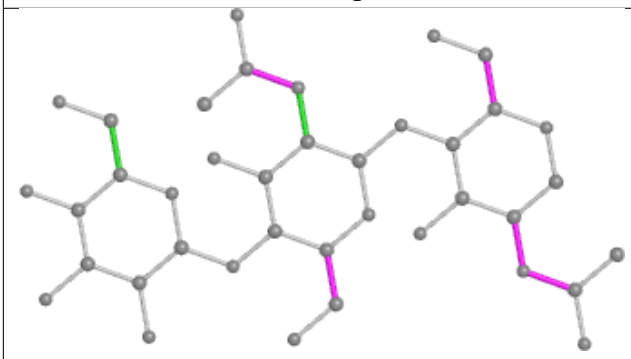
Oligosaccharide Chain K



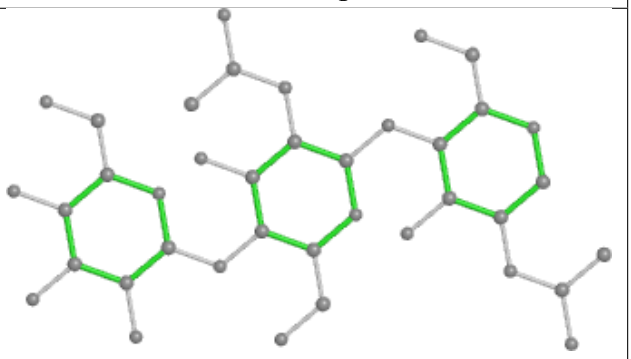
Bond lengths



Bond angles

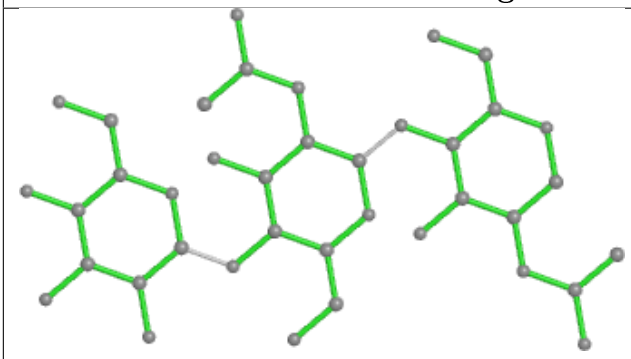


Torsions

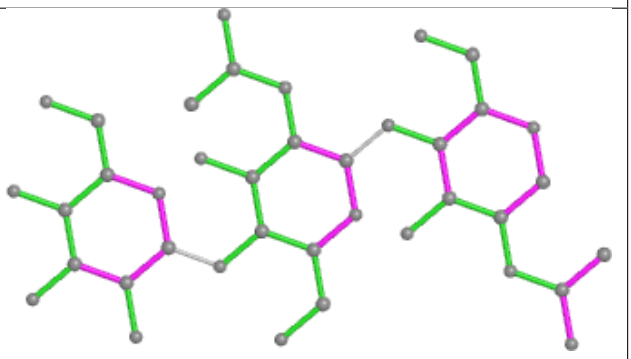


Rings

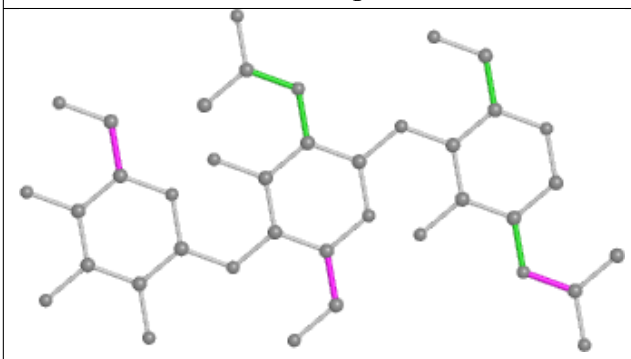
Oligosaccharide Chain L



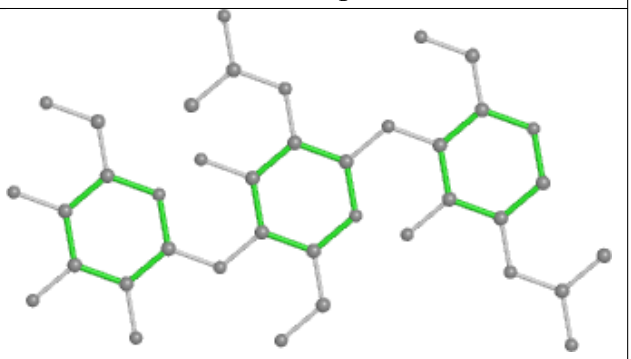
Bond lengths



Bond angles

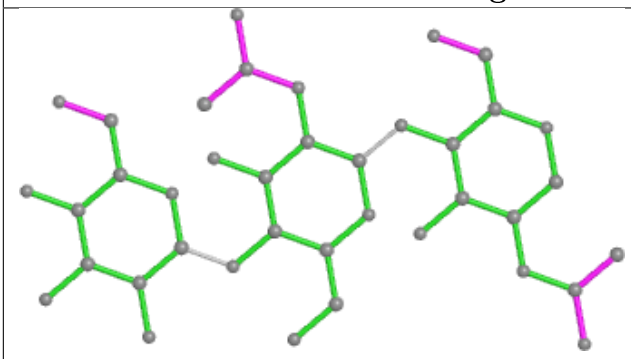


Torsions

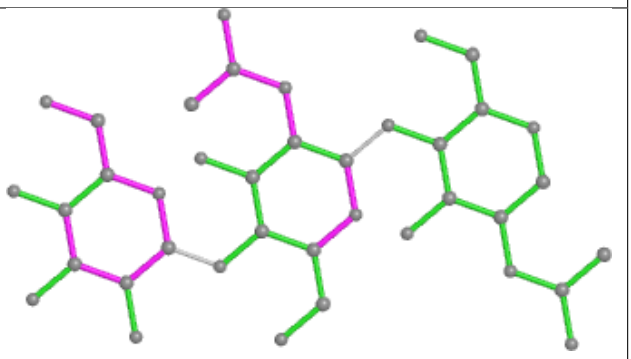


Rings

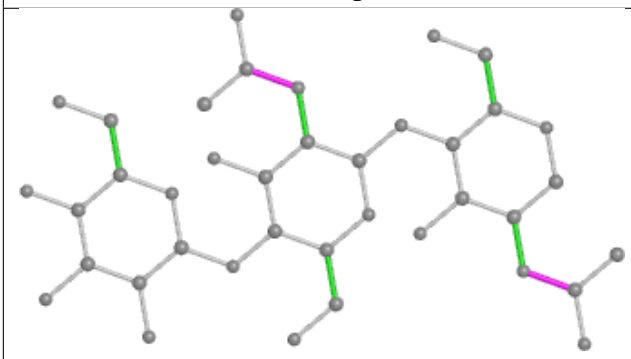
Oligosaccharide Chain W



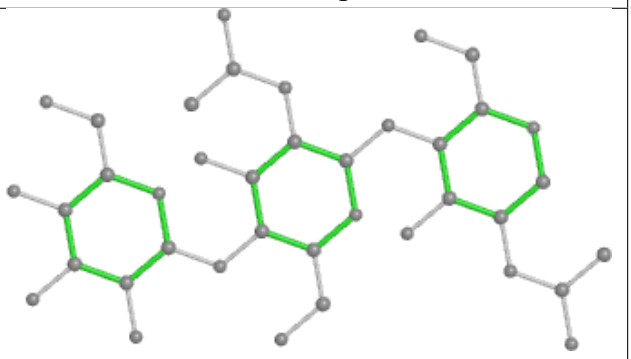
Bond lengths



Bond angles

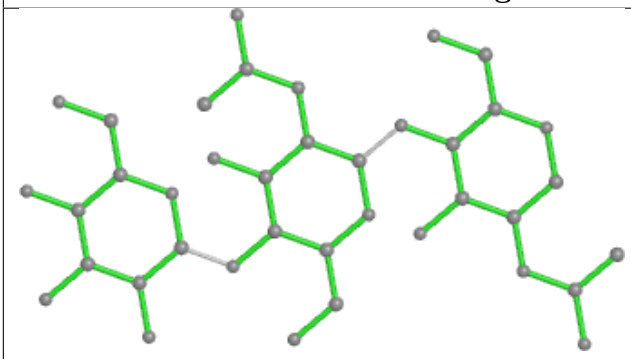


Torsions

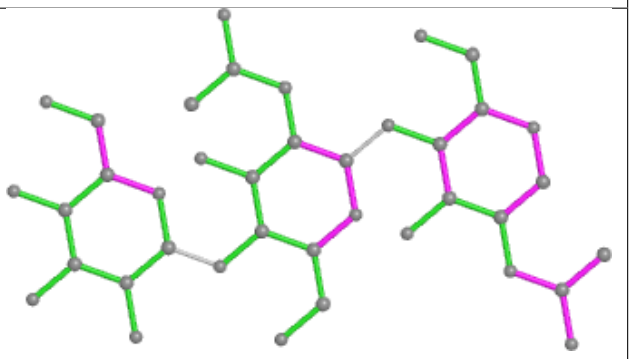


Rings

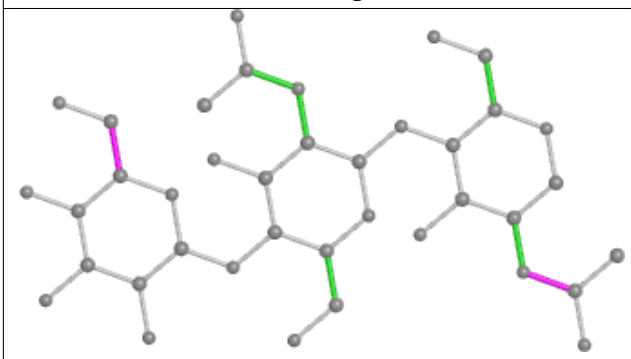
Oligosaccharide Chain X



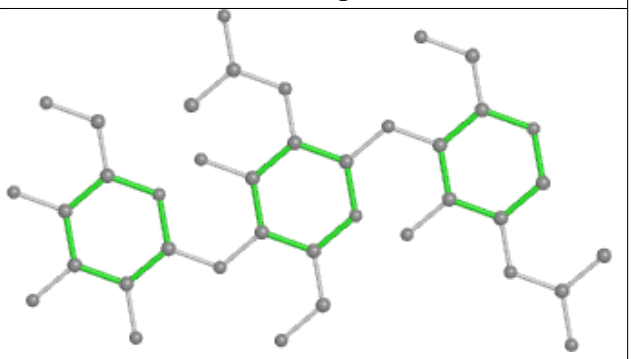
Bond lengths



Bond angles

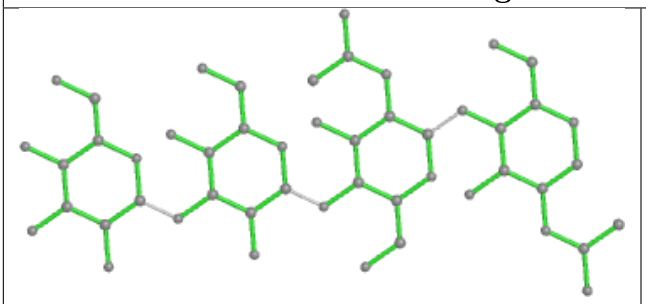


Torsions

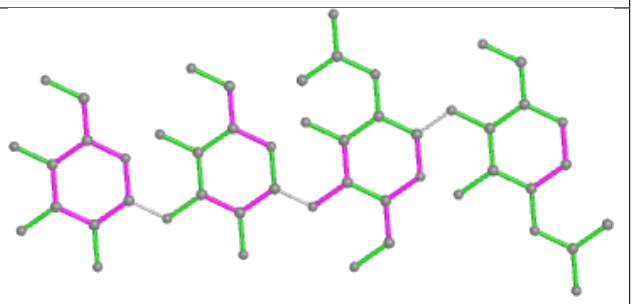


Rings

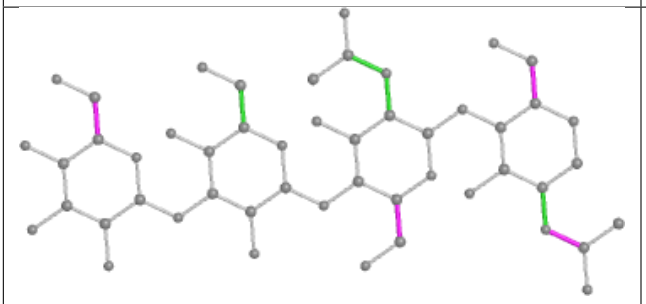
Oligosaccharide Chain R



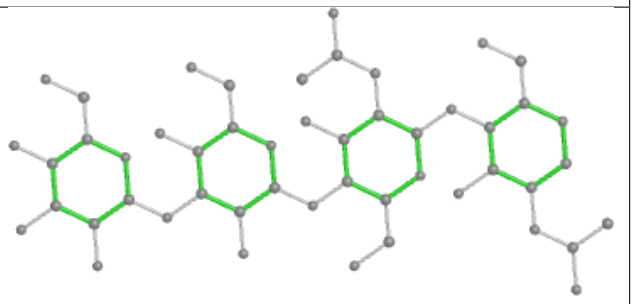
Bond lengths



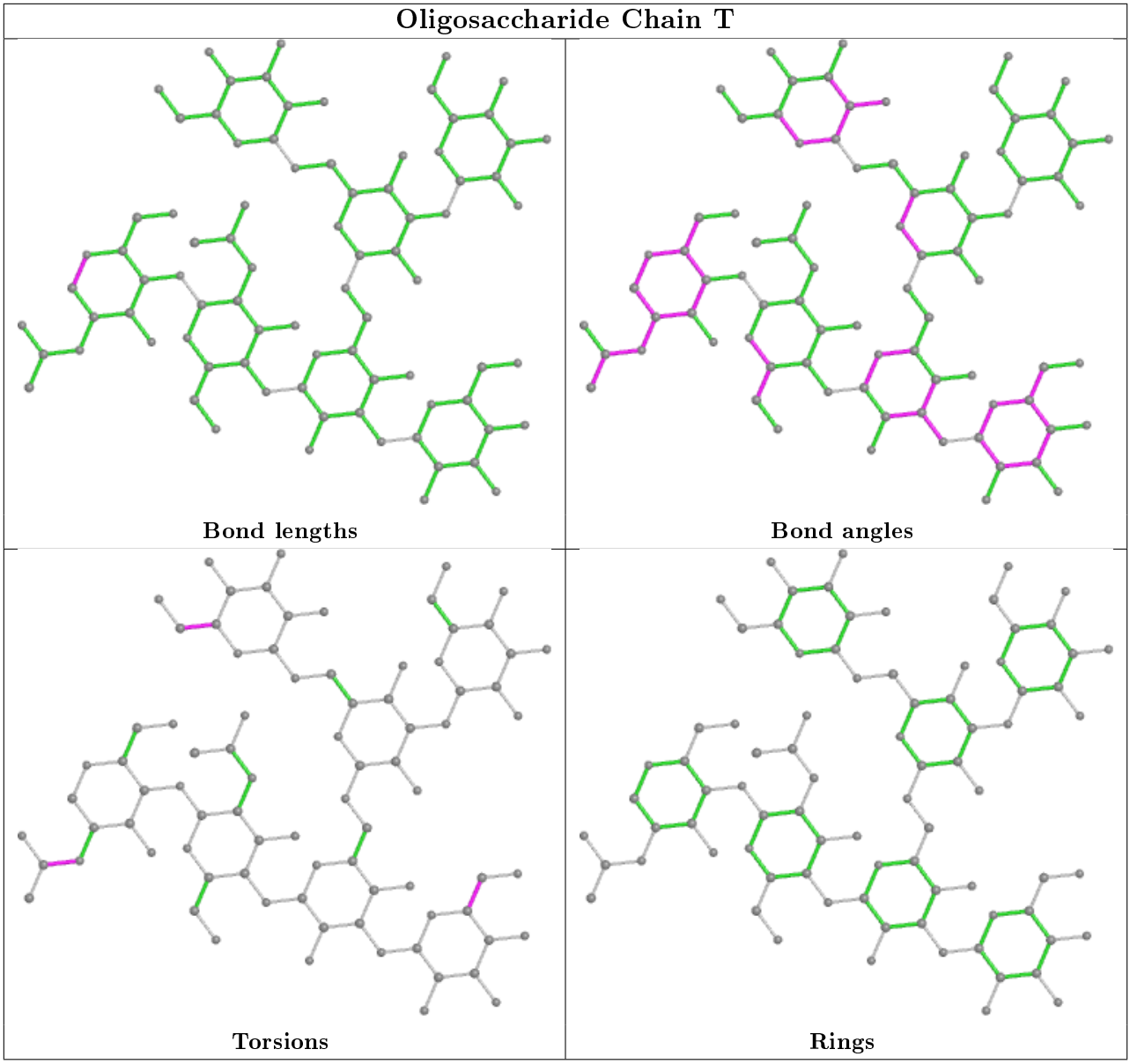
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 55 ligands modelled in this entry, 24 are monoatomic - leaving 31 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	NAG	A	2012	1	14,14,15	0.55	0	17,19,21	1.22	1 (5%)
8	NAG	B	2012	1	14,14,15	0.54	0	17,19,21	1.23	1 (5%)
8	NAG	F	2012	1	14,14,15	0.49	0	17,19,21	1.39	2 (11%)
8	NAG	A	2008	1	14,14,15	0.48	0	17,19,21	0.92	1 (5%)
8	NAG	E	2005	1	14,14,15	0.56	0	17,19,21	0.87	1 (5%)
8	NAG	A	2014	1	14,14,15	0.65	0	17,19,21	1.06	0
8	NAG	B	2018	1	14,14,15	0.76	1 (7%)	17,19,21	1.33	2 (11%)
8	NAG	C	2014	1	14,14,15	0.55	0	17,19,21	1.81	3 (17%)
8	NAG	F	2014	1	14,14,15	0.46	0	17,19,21	1.29	2 (11%)
8	NAG	B	2006	1	14,14,15	0.69	0	17,19,21	1.03	1 (5%)
8	NAG	F	2009	1	14,14,15	0.85	0	17,19,21	1.53	4 (23%)
8	NAG	E	2012	1	14,14,15	3.41	2 (14%)	17,19,21	1.52	4 (23%)
8	NAG	C	2006	1	14,14,15	0.46	0	17,19,21	1.45	1 (5%)
8	NAG	D	2005	1	14,14,15	0.54	0	17,19,21	1.21	3 (17%)
8	NAG	C	2018	1	14,14,15	5.03	3 (21%)	17,19,21	2.16	4 (23%)
8	NAG	D	2006	1	14,14,15	3.82	3 (21%)	17,19,21	2.05	5 (29%)
8	NAG	F	2006	1	14,14,15	4.09	4 (28%)	17,19,21	1.92	4 (23%)
8	NAG	E	2014	1	14,14,15	0.48	0	17,19,21	1.84	2 (11%)
8	NAG	B	2014	1	14,14,15	0.47	0	17,19,21	1.97	3 (17%)
8	NAG	D	2014	1	14,14,15	0.53	0	17,19,21	0.90	0
8	NAG	E	2008	1	14,14,15	0.52	0	17,19,21	0.95	0
8	NAG	F	2008	1	14,14,15	0.54	0	17,19,21	1.11	1 (5%)
8	NAG	D	2008	1	14,14,15	0.48	0	17,19,21	1.08	1 (5%)
8	NAG	F	2005	1	14,14,15	4.14	4 (28%)	17,19,21	1.96	5 (29%)
8	NAG	D	2012	1	14,14,15	0.66	0	17,19,21	1.05	0
8	NAG	A	2006	1	14,14,15	0.88	1 (7%)	17,19,21	1.21	3 (17%)
8	NAG	E	2006	1	14,14,15	0.65	0	17,19,21	1.84	4 (23%)
8	NAG	C	2005	1	14,14,15	0.54	0	17,19,21	1.67	4 (23%)
8	NAG	A	2018	1	14,14,15	0.70	0	17,19,21	1.56	2 (11%)
8	NAG	B	2005	1	14,14,15	0.58	0	17,19,21	0.99	2 (11%)
8	NAG	C	2012	1	14,14,15	0.54	0	17,19,21	1.63	3 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	A	2012	1	1/1/5/7	3/6/23/26	0/1/1/1
8	NAG	B	2012	1	1/1/5/7	4/6/23/26	0/1/1/1
8	NAG	F	2012	1	1/1/5/7	5/6/23/26	0/1/1/1
8	NAG	A	2008	1	-	0/6/23/26	0/1/1/1
8	NAG	E	2005	1	-	2/6/23/26	0/1/1/1
8	NAG	A	2014	1	-	2/6/23/26	0/1/1/1
8	NAG	B	2018	1	1/1/5/7	4/6/23/26	0/1/1/1
8	NAG	C	2014	1	-	4/6/23/26	0/1/1/1
8	NAG	F	2014	1	-	2/6/23/26	0/1/1/1
8	NAG	B	2006	1	1/1/5/7	3/6/23/26	0/1/1/1
8	NAG	F	2009	1	1/1/5/7	5/6/23/26	0/1/1/1
8	NAG	E	2012	1	1/1/5/7	5/6/23/26	0/1/1/1
8	NAG	C	2006	1	-	2/6/23/26	0/1/1/1
8	NAG	D	2005	1	-	4/6/23/26	0/1/1/1
8	NAG	C	2018	1	1/1/5/7	4/6/23/26	0/1/1/1
8	NAG	D	2006	1	1/1/5/7	2/6/23/26	0/1/1/1
8	NAG	F	2006	1	1/1/5/7	4/6/23/26	0/1/1/1
8	NAG	F	2008	1	-	0/6/23/26	0/1/1/1
8	NAG	E	2014	1	-	2/6/23/26	0/1/1/1
8	NAG	B	2014	1	-	4/6/23/26	0/1/1/1
8	NAG	D	2014	1	-	4/6/23/26	0/1/1/1
8	NAG	E	2008	1	-	2/6/23/26	0/1/1/1
8	NAG	A	2018	1	1/1/5/7	3/6/23/26	0/1/1/1
8	NAG	D	2008	1	-	0/6/23/26	0/1/1/1
8	NAG	F	2005	1	1/1/5/7	4/6/23/26	0/1/1/1
8	NAG	D	2012	1	-	6/6/23/26	0/1/1/1
8	NAG	A	2006	1	1/1/5/7	4/6/23/26	0/1/1/1
8	NAG	E	2006	1	-	3/6/23/26	0/1/1/1
8	NAG	C	2005	1	-	4/6/23/26	0/1/1/1
8	NAG	B	2005	1	-	4/6/23/26	0/1/1/1
8	NAG	C	2012	1	1/1/5/7	2/6/23/26	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	2018	NAG	O7-C7	14.37	1.55	1.23
8	F	2006	NAG	C8-C7	14.35	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	2006	NAG	O7-C7	11.78	1.49	1.23
8	C	2018	NAG	C8-C7	11.44	1.74	1.50
8	E	2012	NAG	C8-C7	10.36	1.72	1.50

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	E	2014	NAG	C1-O5-C5	6.29	120.71	112.19
8	C	2014	NAG	C1-O5-C5	5.90	120.19	112.19
8	F	2005	NAG	C1-O5-C5	5.40	119.51	112.19
8	D	2006	NAG	C8-C7-N2	-5.19	107.31	116.10
8	B	2014	NAG	C1-O5-C5	5.19	119.22	112.19

5 of 14 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	A	2012	NAG	C1
8	B	2012	NAG	C1
8	B	2018	NAG	C1
8	F	2012	NAG	C1
8	B	2006	NAG	C1

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	2012	NAG	C8-C7-N2-C2
8	A	2012	NAG	O7-C7-N2-C2
8	B	2012	NAG	O7-C7-N2-C2
8	E	2005	NAG	C8-C7-N2-C2
8	E	2005	NAG	O7-C7-N2-C2

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

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

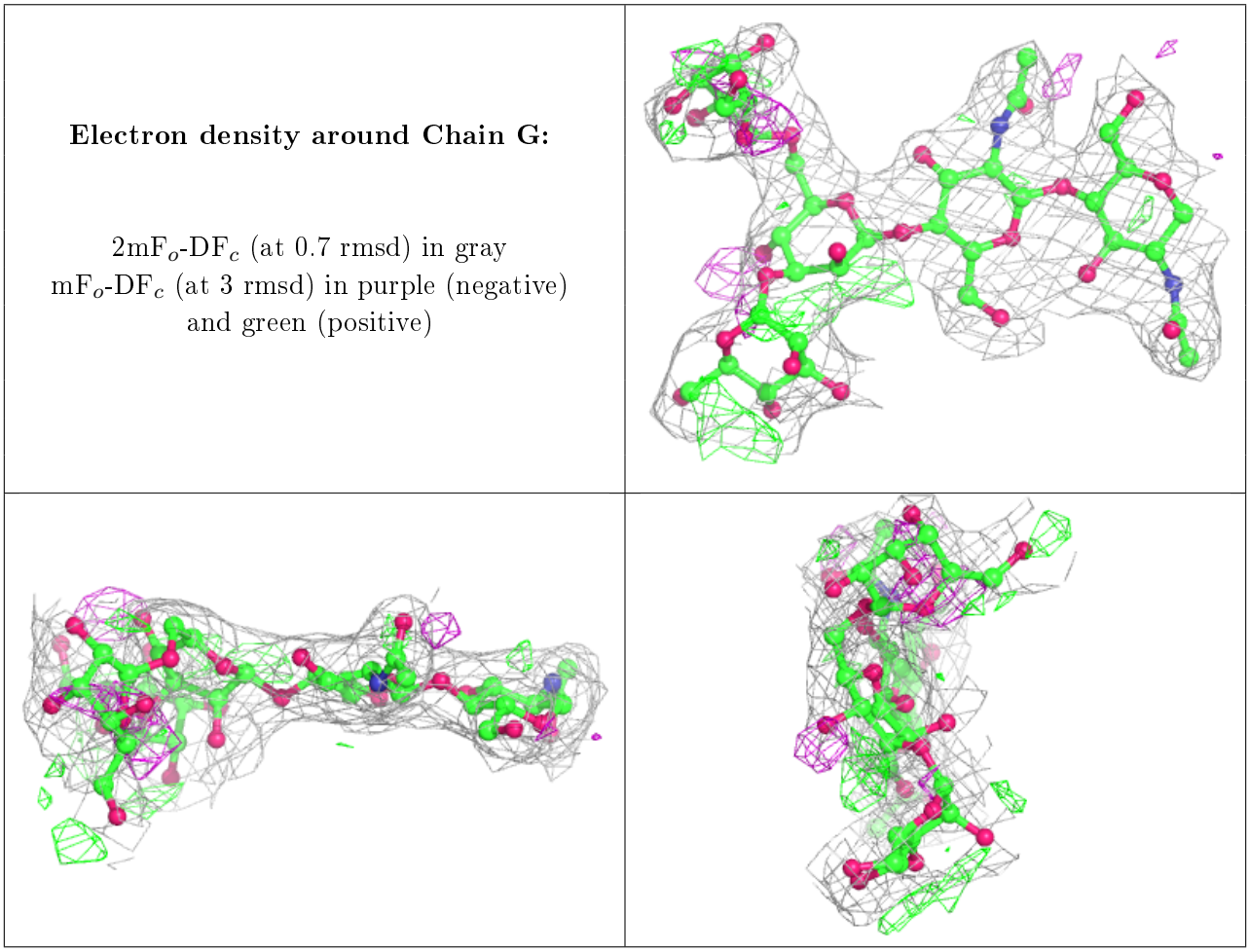
6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

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

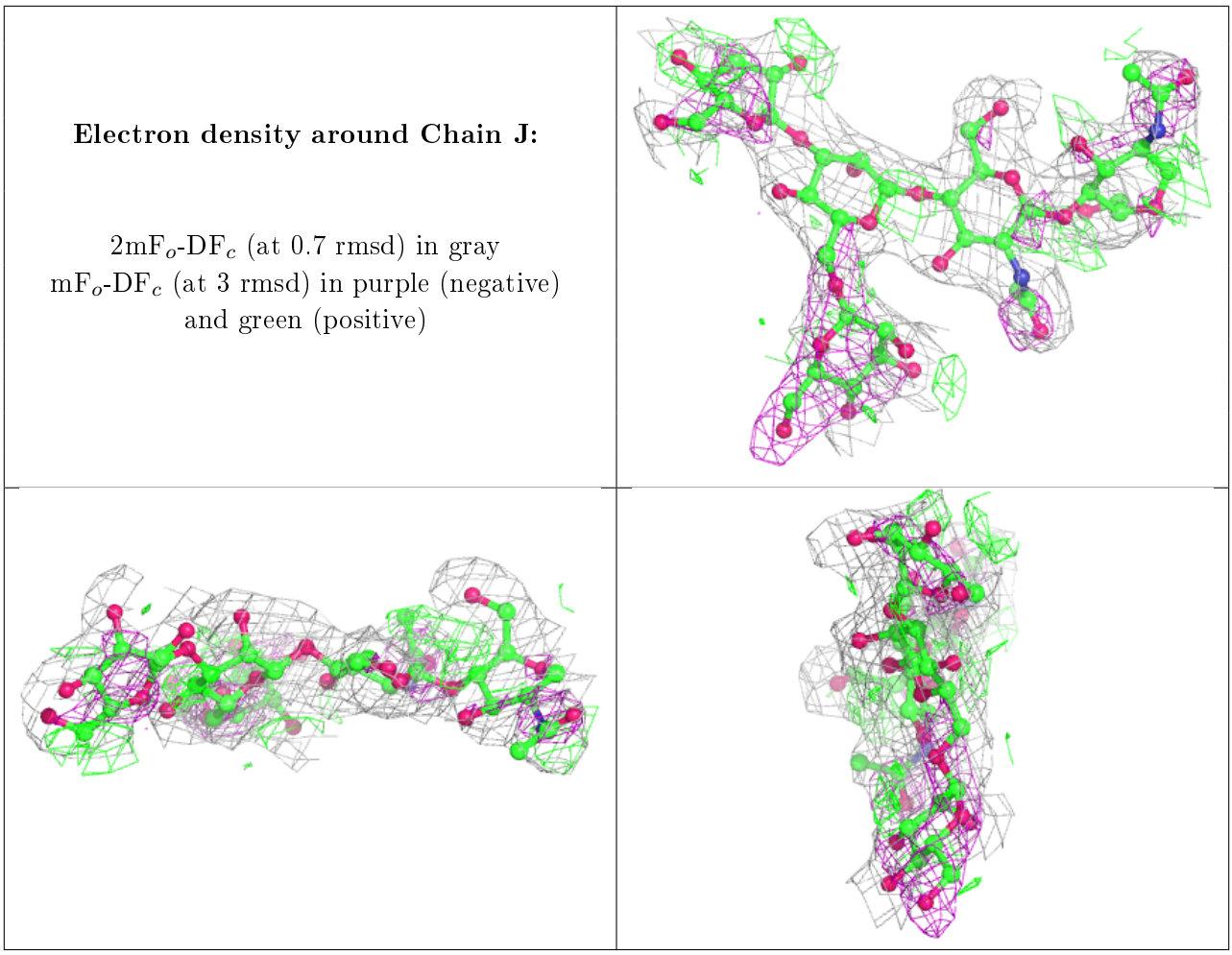
Electron density around Chain G:

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



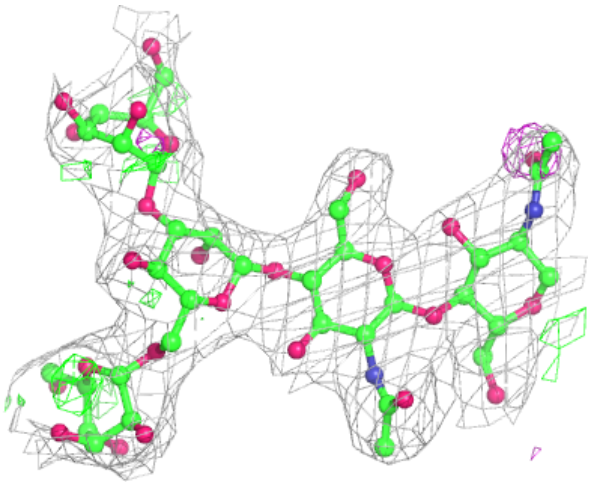
Electron density around Chain J:

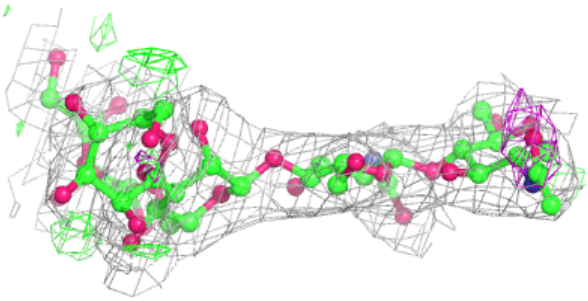
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around Chain M:

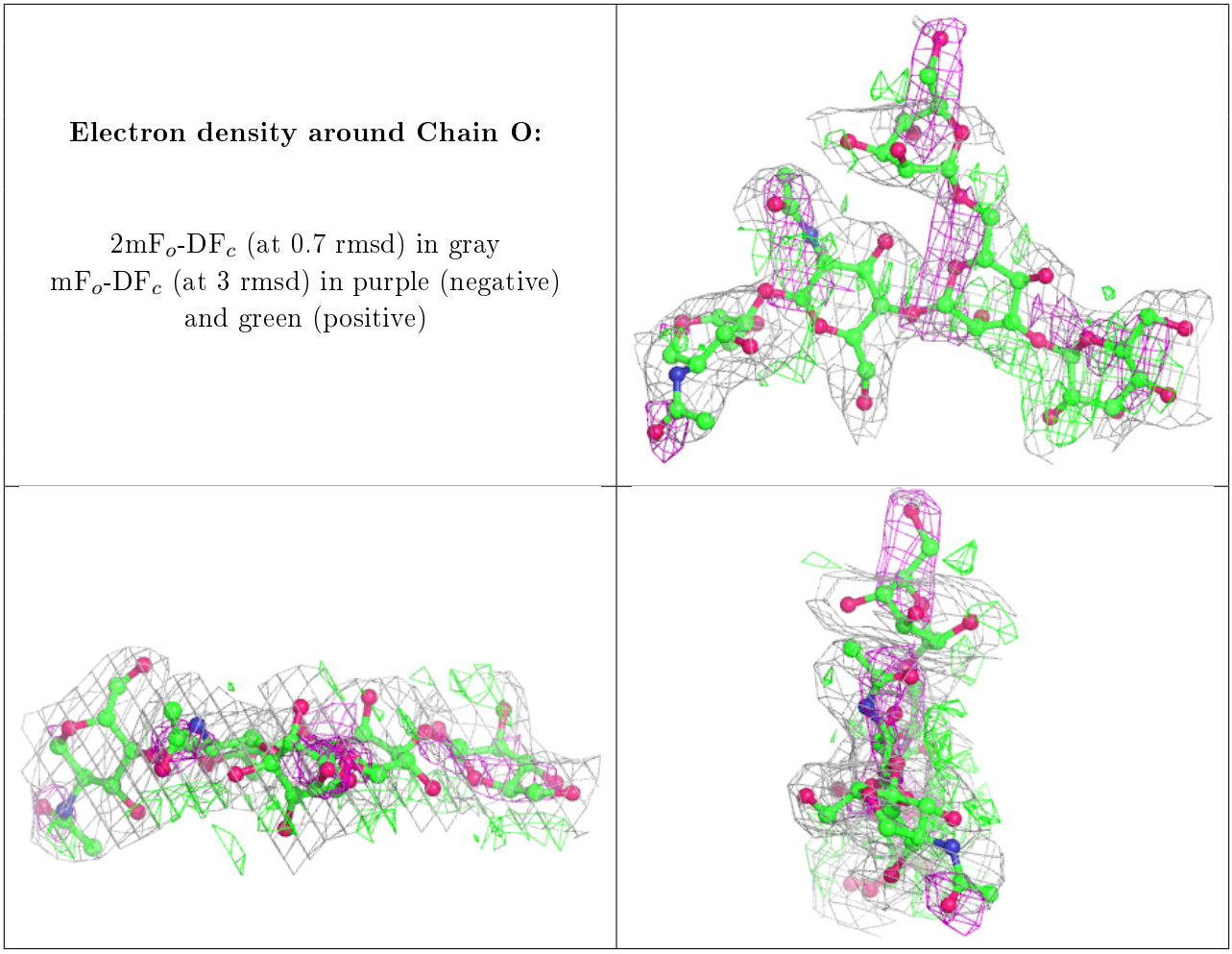
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





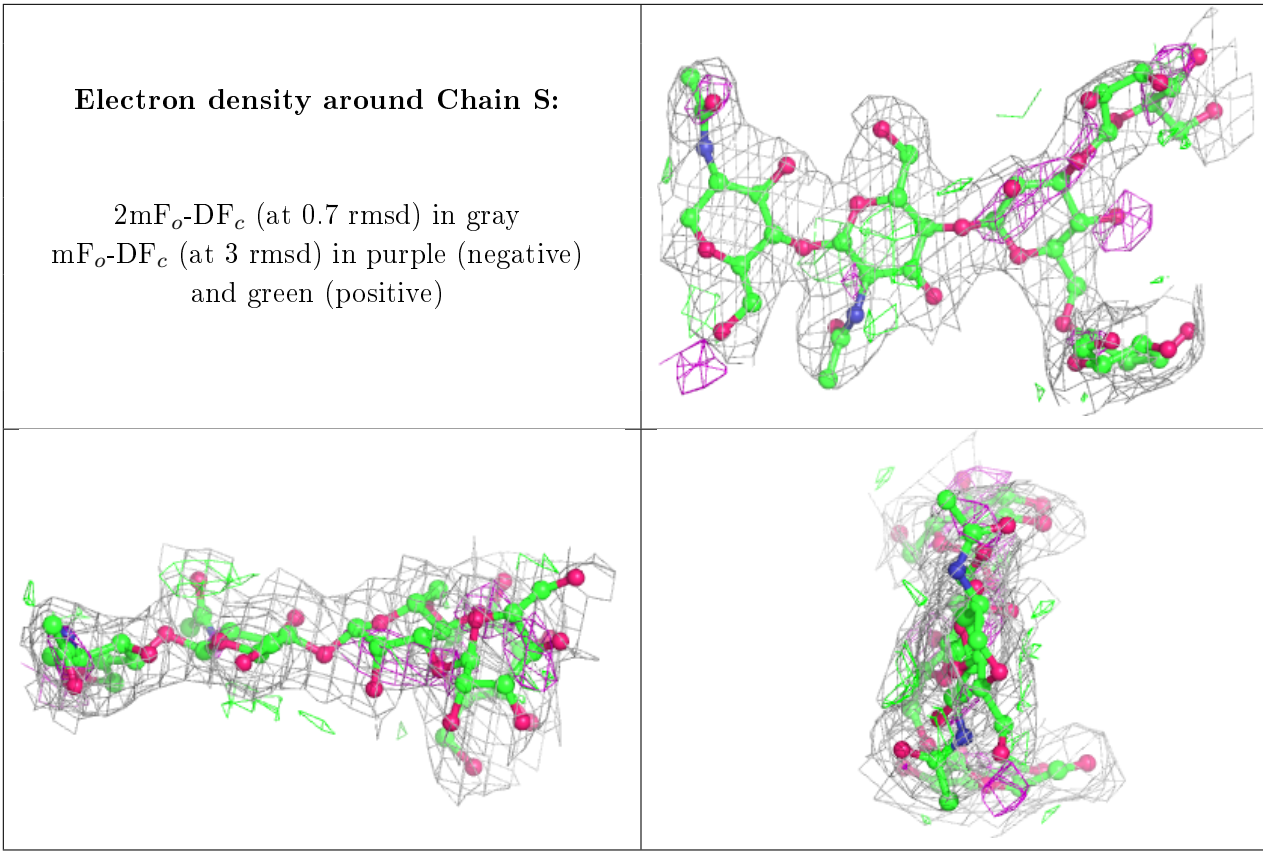
Electron density around Chain O:

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



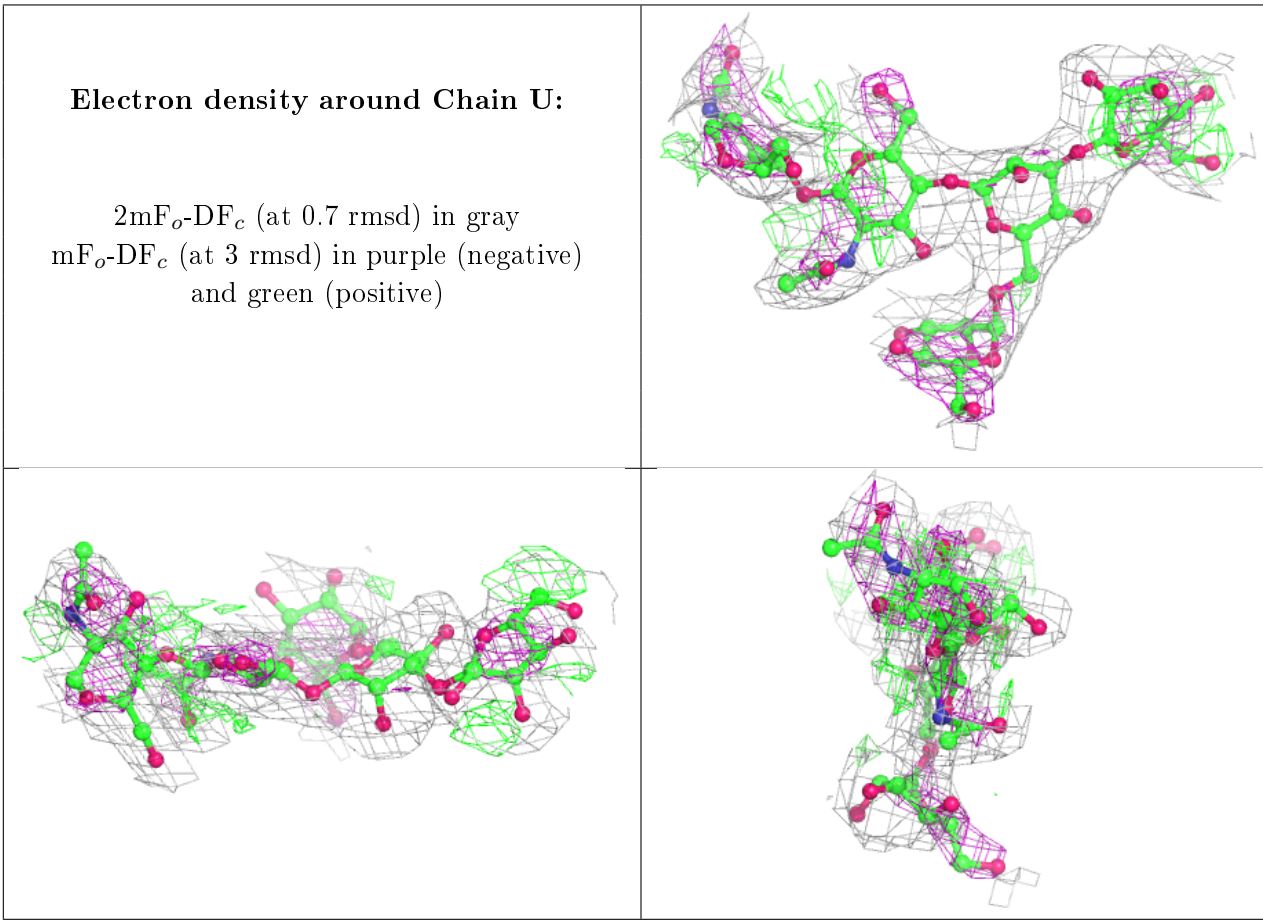
Electron density around Chain S:

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



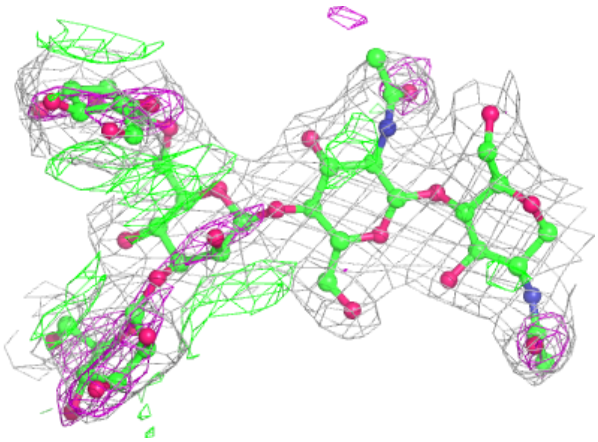
Electron density around Chain U:

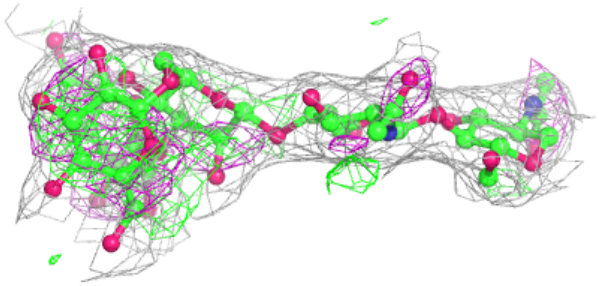
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

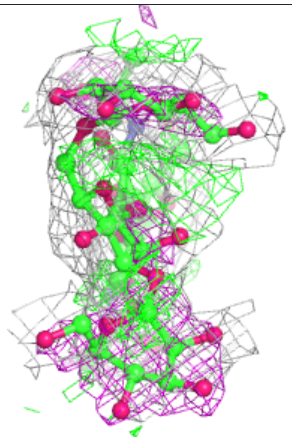


Electron density around Chain Y:

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

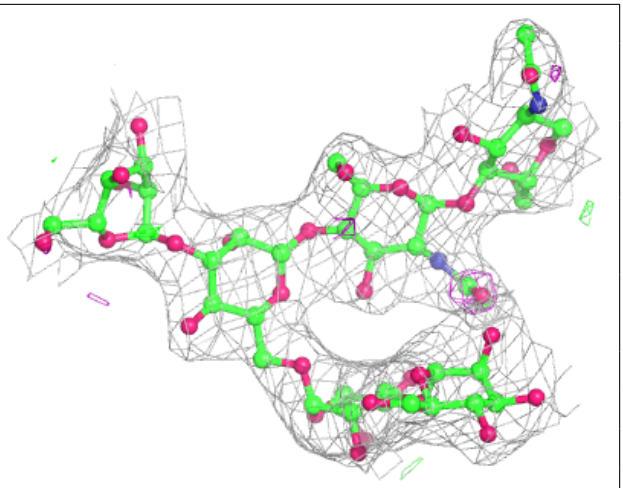


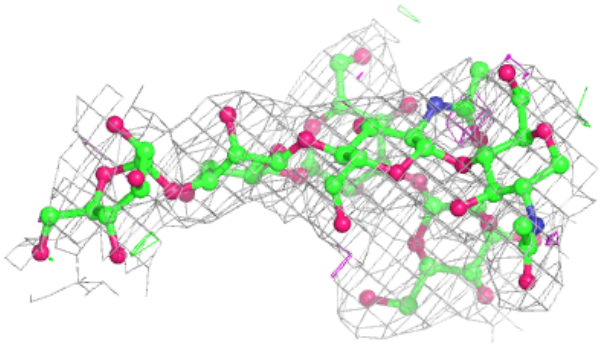


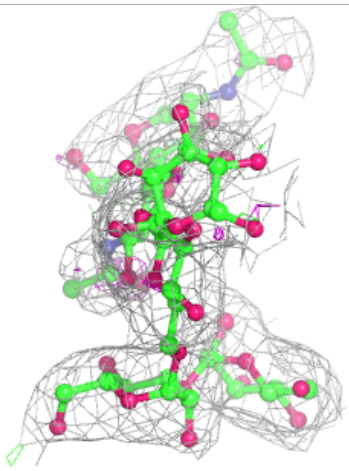


Electron density around Chain H:

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

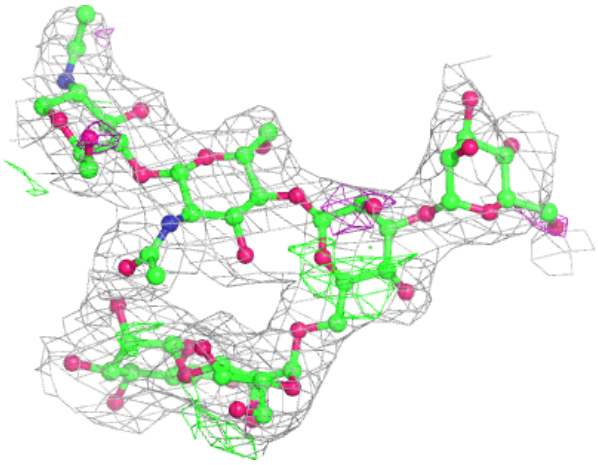


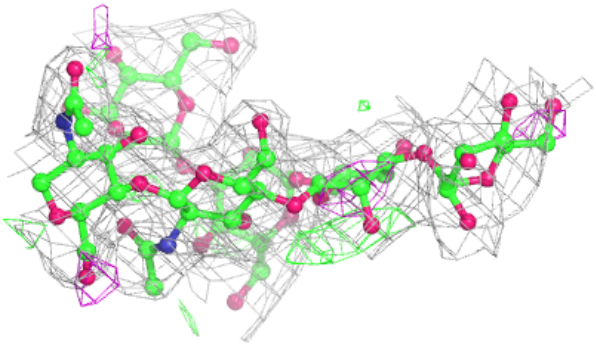


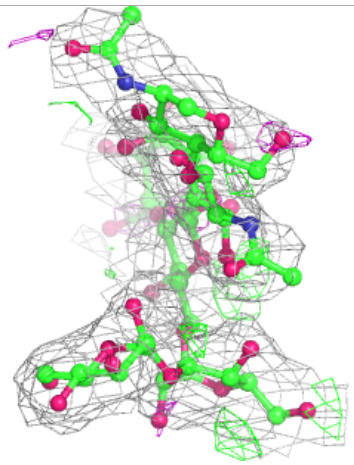


Electron density around Chain N:

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

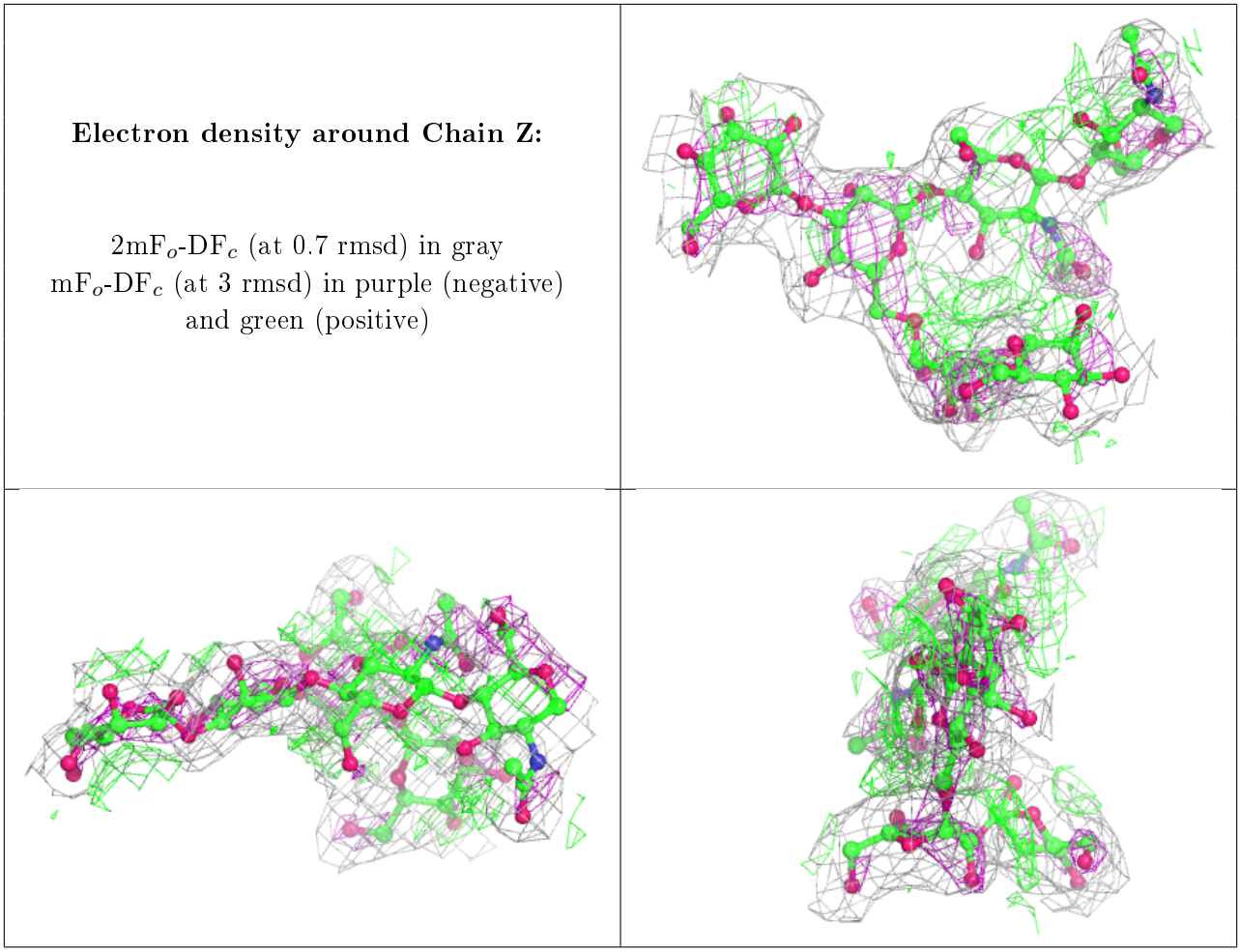






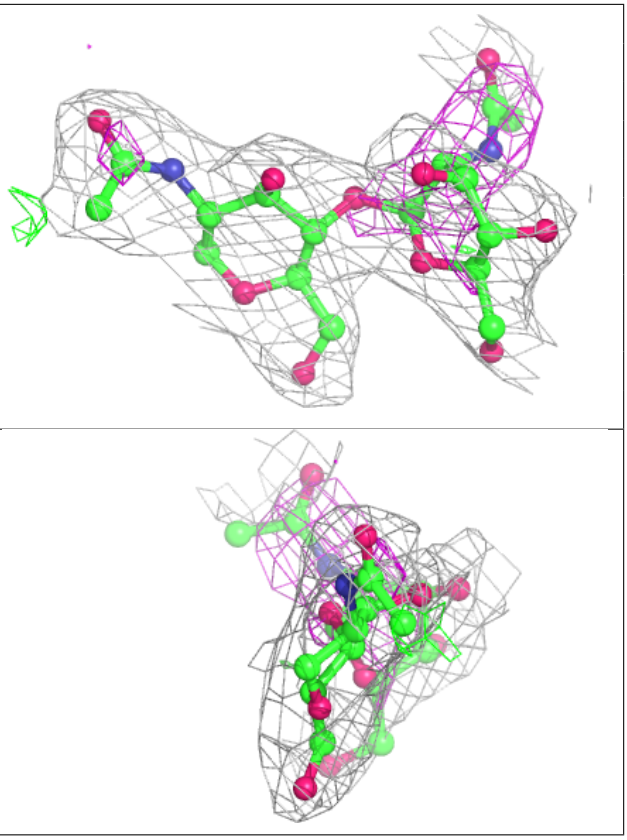
Electron density around Chain Z:

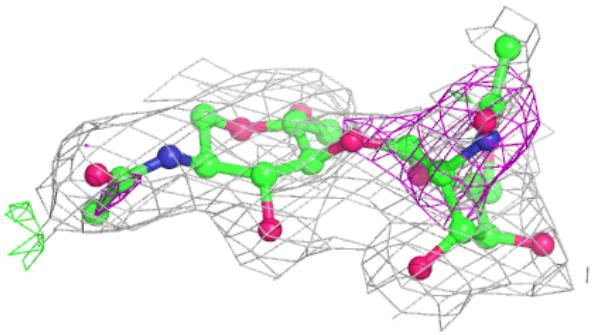
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around Chain I:

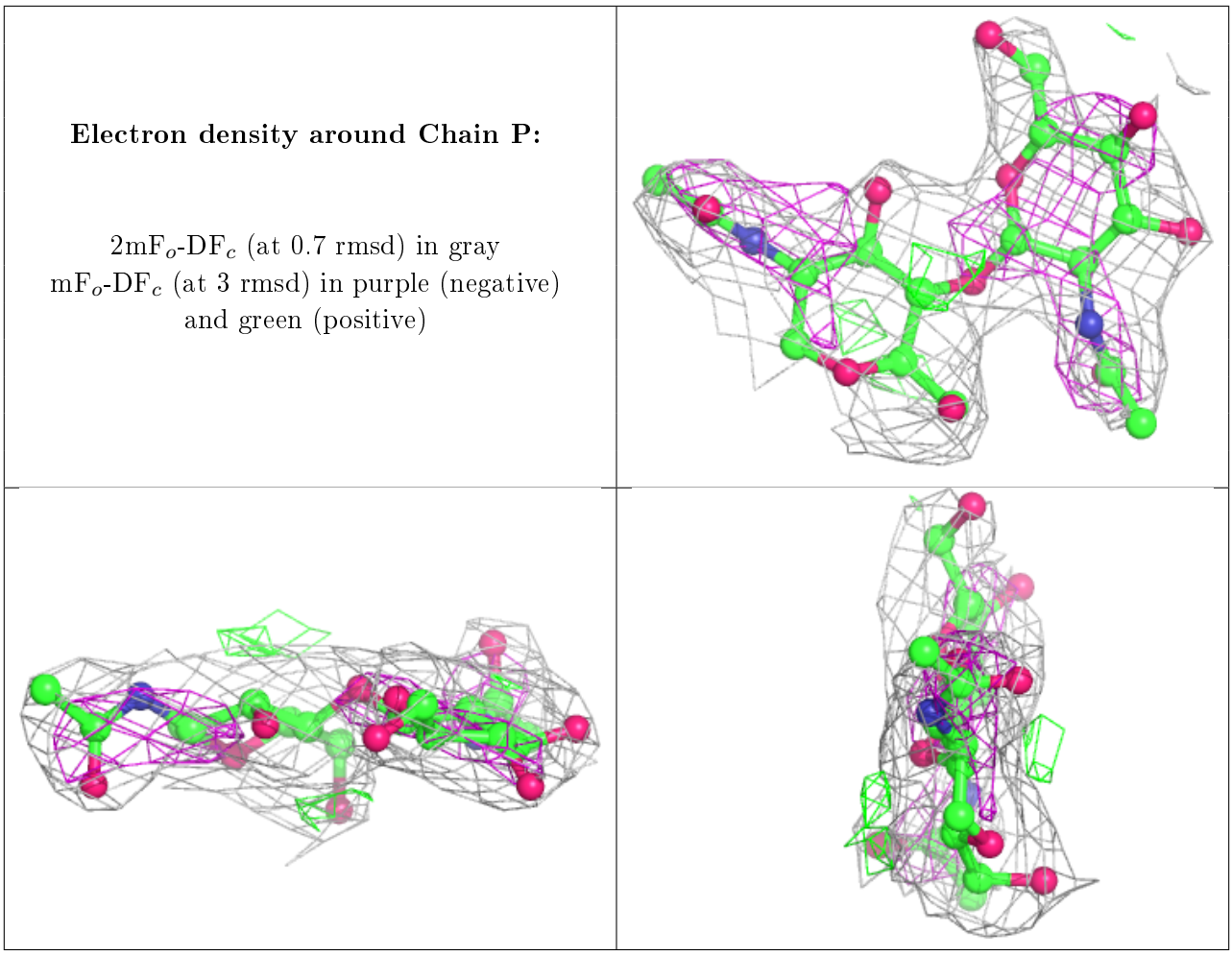
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





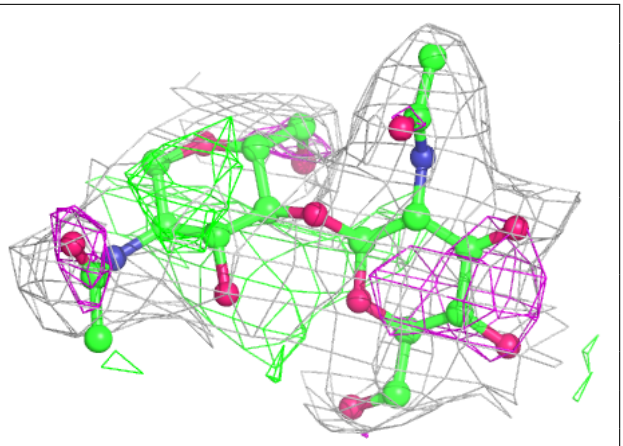
Electron density around Chain P:

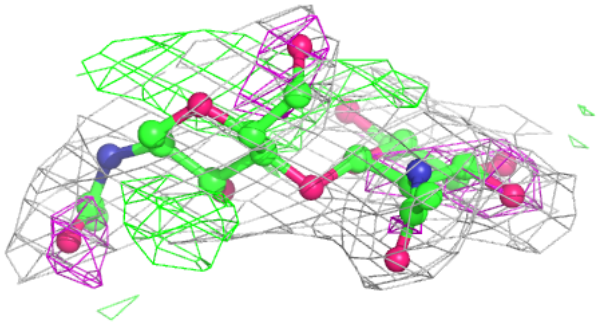
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

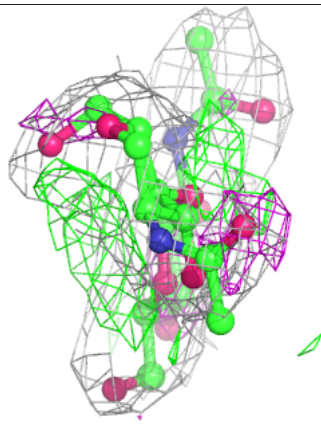


Electron density around Chain Q:

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

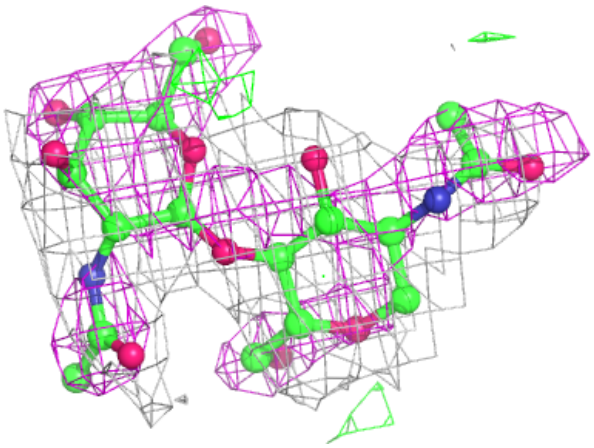


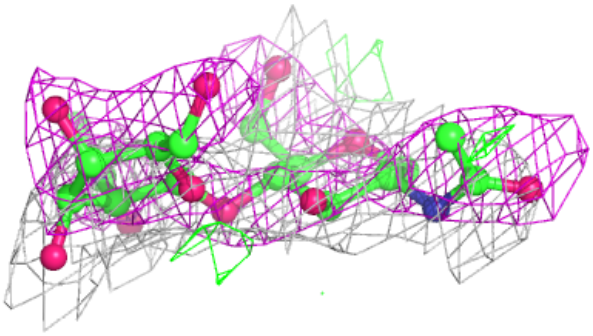


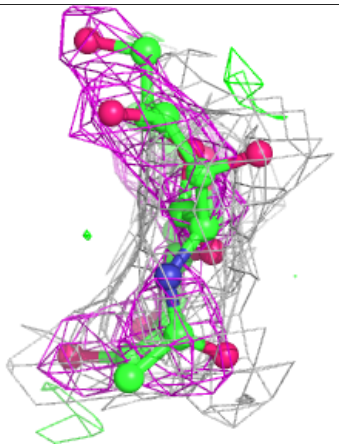


Electron density around Chain V:

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

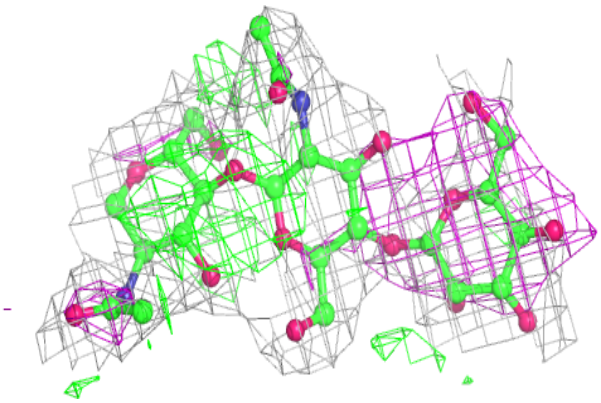


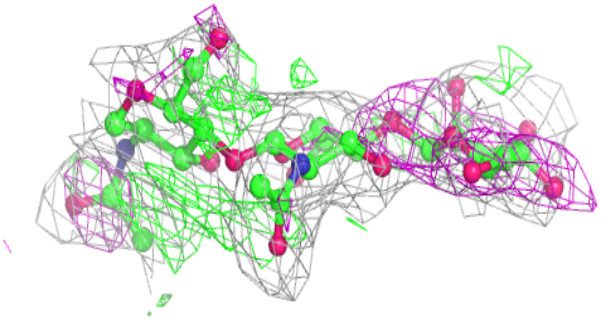


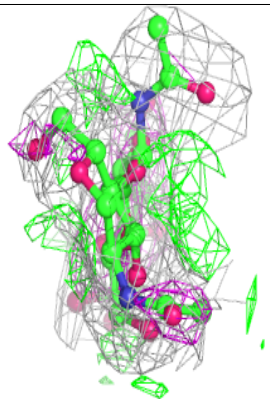


Electron density around Chain K:

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

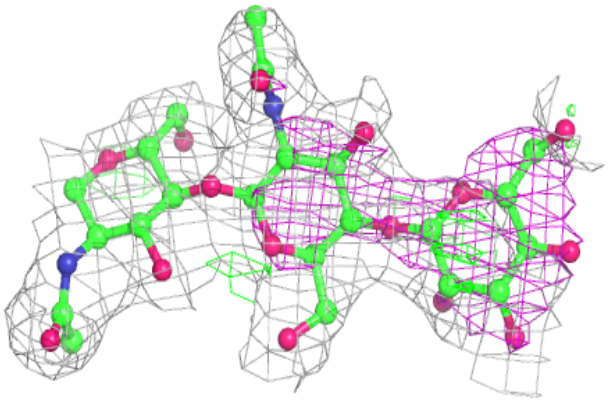


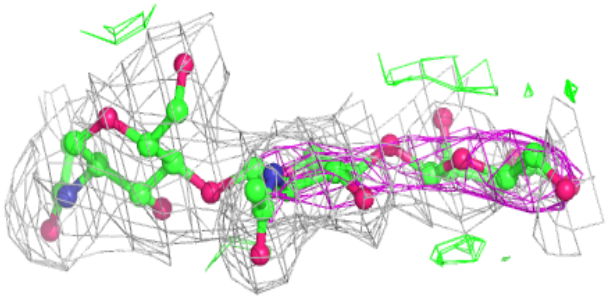


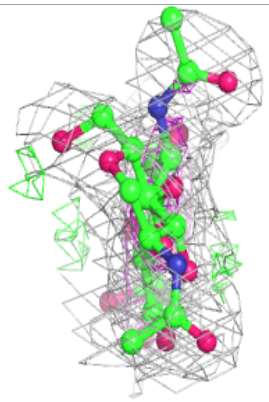


Electron density around Chain L:

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

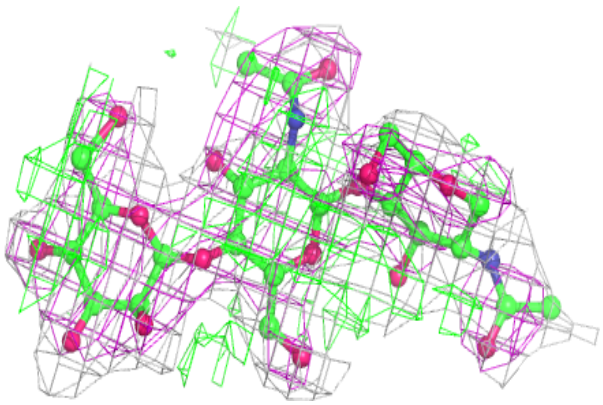


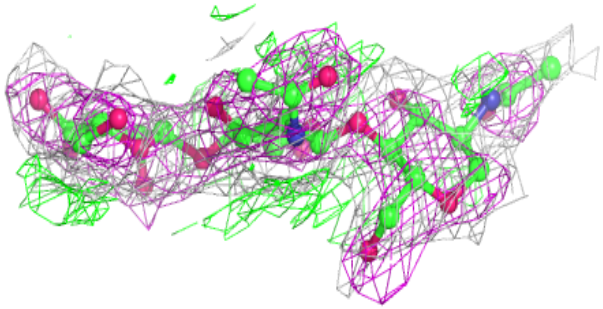


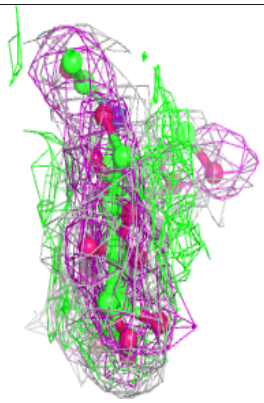


Electron density around Chain W:

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

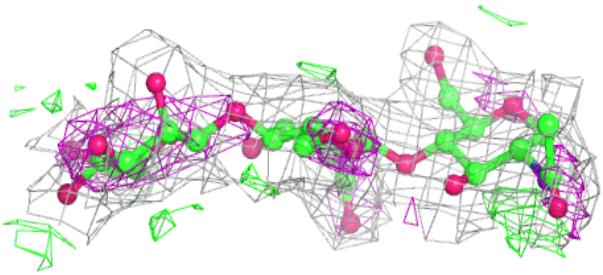


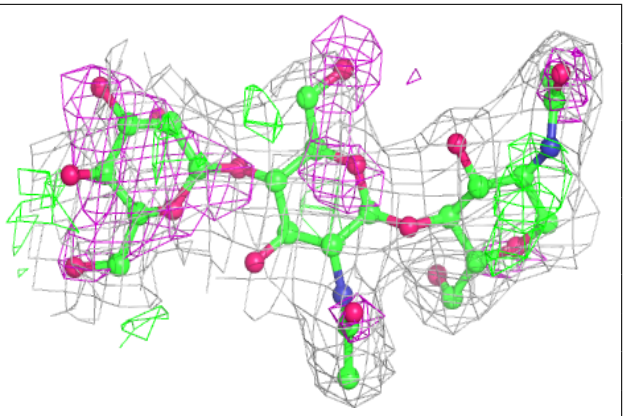


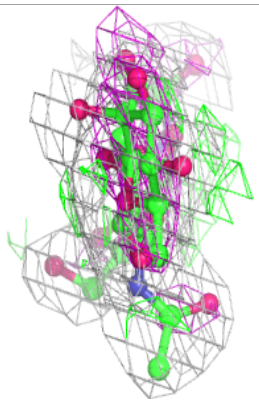


Electron density around Chain X:

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

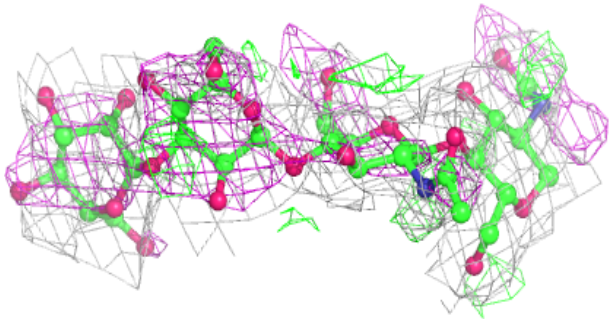


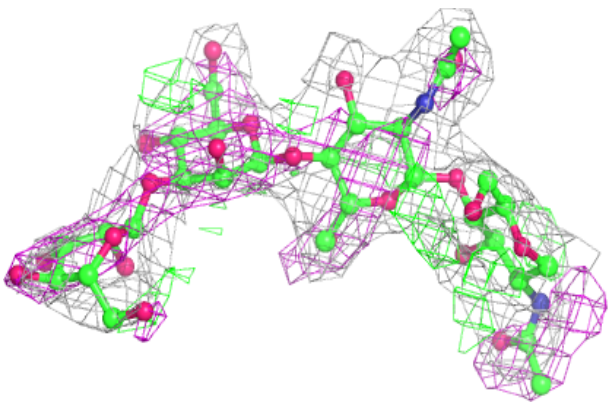


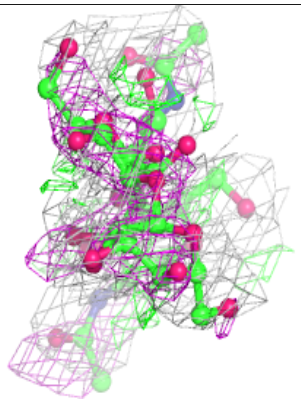


Electron density around Chain R:

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

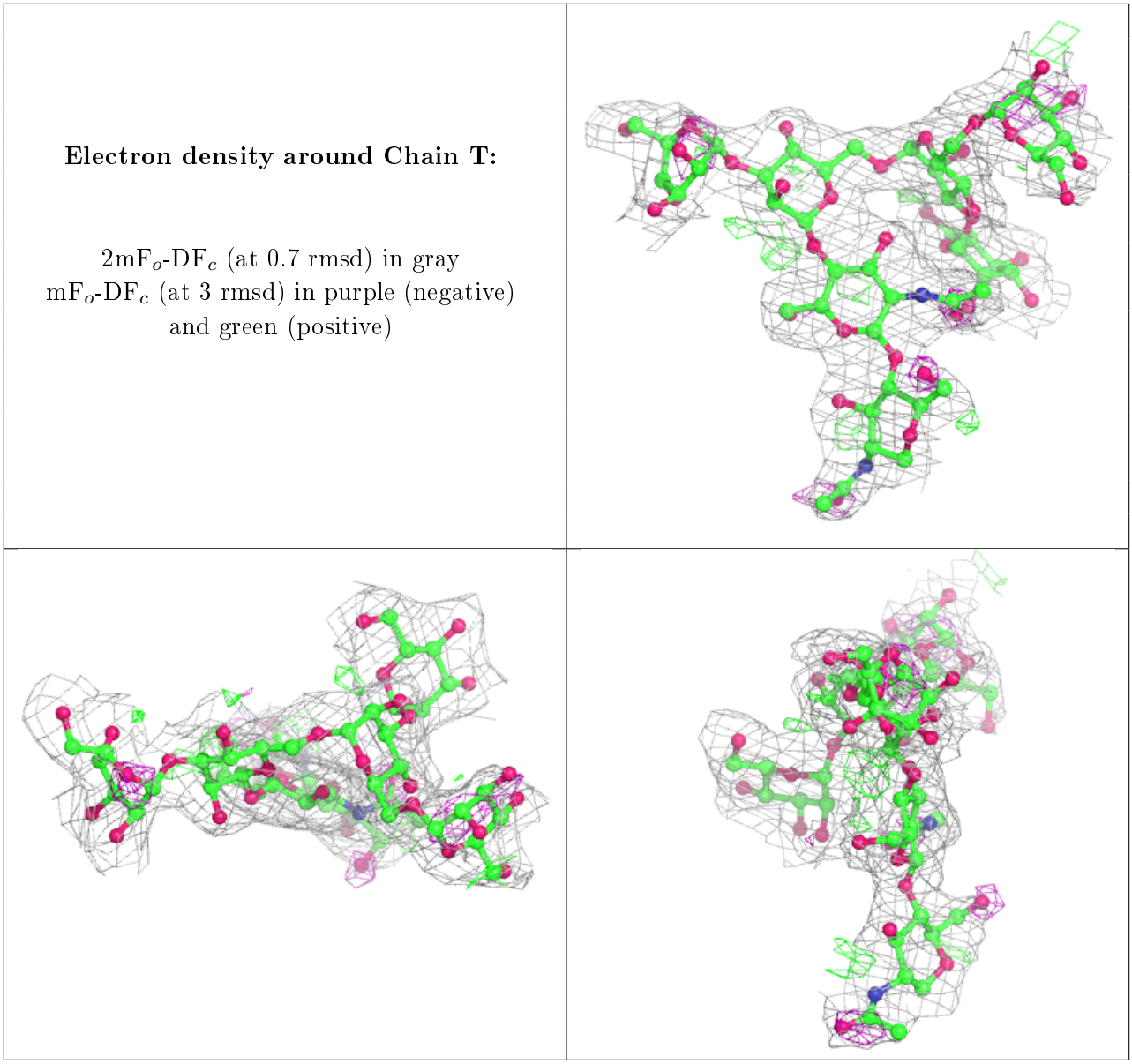






Electron density around Chain T:

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



6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.