wwPDB X-ray Structure Validation Summary Report (i)

Dec 16, 2023 – 08:13 pm GMT

PDB ID	:	2WW3
Title	:	Structure of the Family GH92 Inverting Mannosidase BT3990 from Bacteroides thetaiotaomicron VPI-5482 in complex with thiomannobioside
Authors	:	Suits, M.D.L.; Zhu, Y.; Thompson, A.J.; Gilbert, H.J.; Davies, G.J.
Deposited on	:	2009-10-21
Resolution	:	2.10 Å(reported)

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

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

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

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

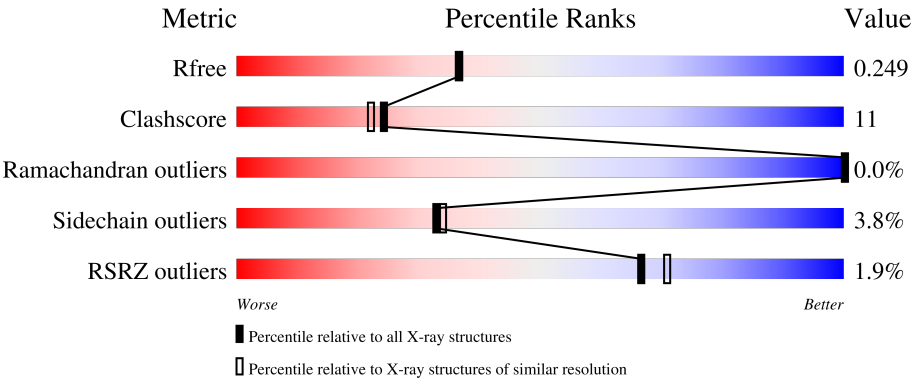
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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

Mol	Chain	Length	Quality of chain
1	A	744	82% 15%
1	B	744	6% 72% 25%
1	C	744	84% 14%
1	D	744	2% 78% 19%
1	E	744	84% 13%

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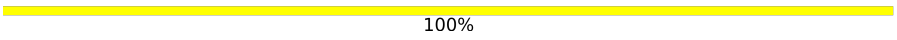
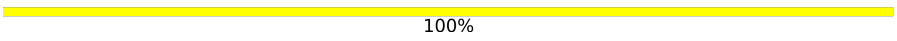
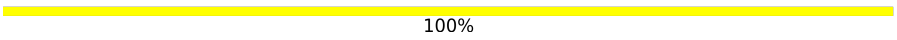
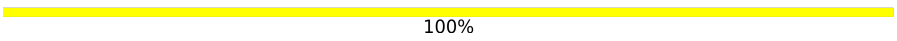
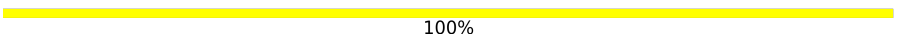
Mol	Chain	Length	Quality of chain
1	F	744	
2	G	2	
2	H	2	
2	I	2	
2	J	2	
2	K	2	
2	L	2	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 37131 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 PUTATIVE ALPHA-1,2-MANNOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	736	Total	C	N	O	S	0	0	0
			5957	3818	981	1125	33			
1	B	736	Total	C	N	O	S	0	0	0
			5937	3806	979	1119	33			
1	C	736	Total	C	N	O	S	0	0	0
			5949	3814	980	1122	33			
1	D	738	Total	C	N	O	S	0	0	0
			5946	3809	977	1127	33			
1	E	736	Total	C	N	O	S	0	1	0
			5945	3811	975	1126	33			
1	F	738	Total	C	N	O	S	0	0	0
			5948	3814	978	1123	33			

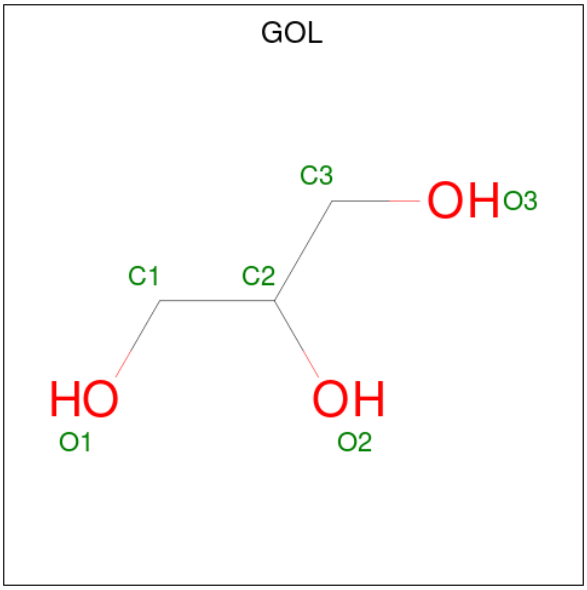
- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	2	Total	C	O	S	0	0	0
			24	13	10	1			
2	H	2	Total	C	O	S	0	0	0
			24	13	10	1			
2	I	2	Total	C	O	S	0	0	0
			24	13	10	1			
2	J	2	Total	C	O	S	0	0	0
			24	13	10	1			
2	K	2	Total	C	O	S	0	0	0
			24	13	10	1			
2	L	2	Total	C	O	S	0	0	0
			24	13	10	1			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	D	1	Total Ca 1 1	0	0
3	E	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	230	Total O 230 230	0	0

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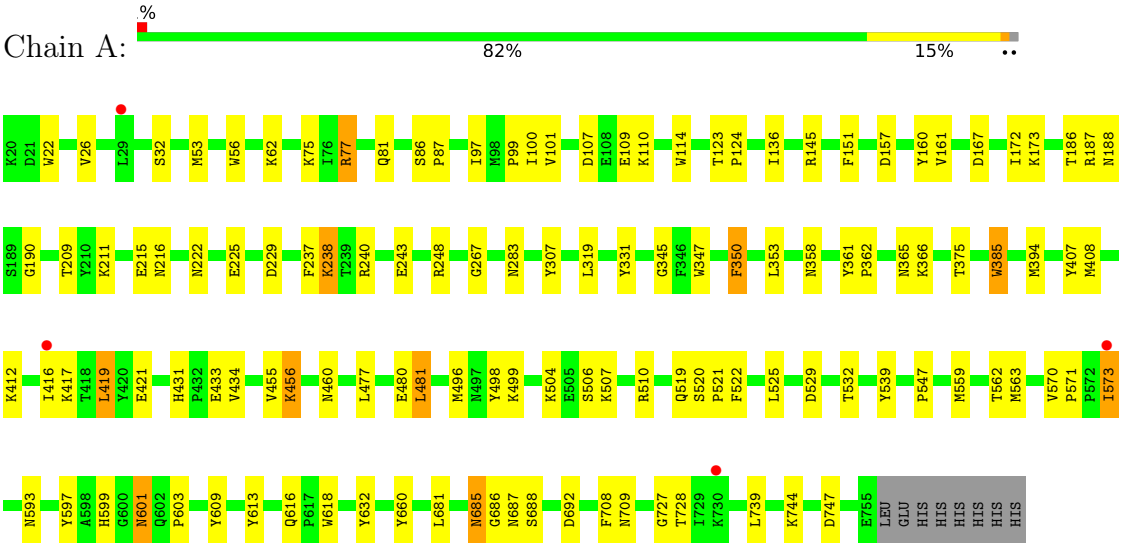
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	162	Total O 162 162	0	0
5	C	322	Total O 322 322	0	0
5	D	155	Total O 155 155	0	0
5	E	217	Total O 217 217	0	0
5	F	195	Total O 195 195	0	0

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

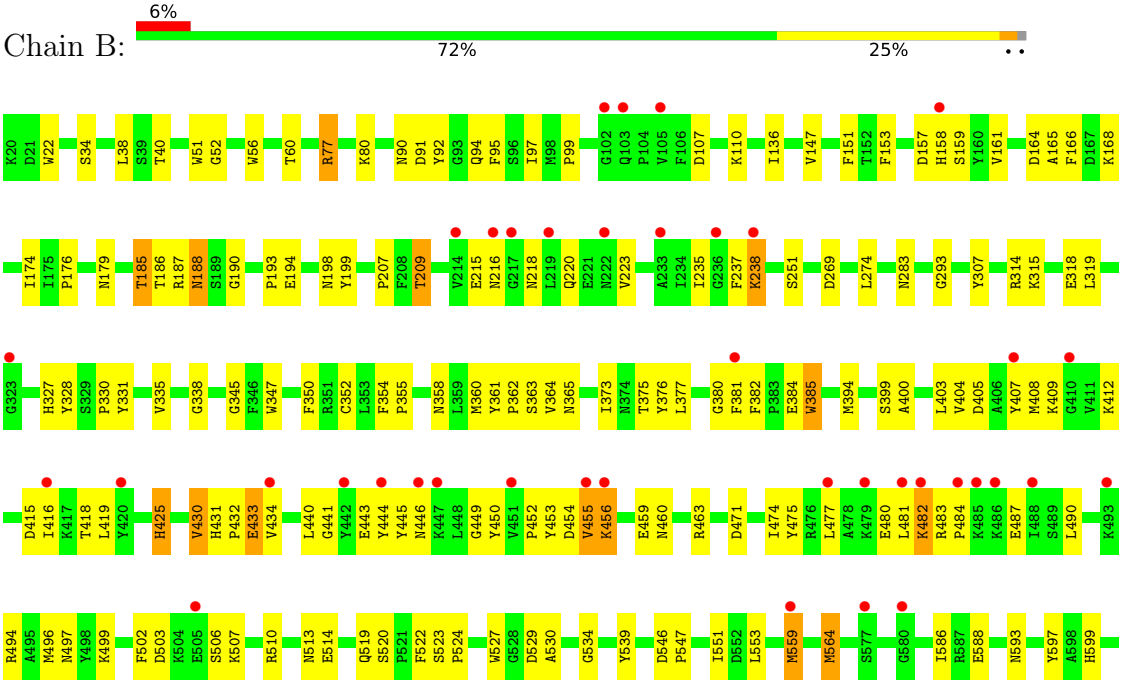
• Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

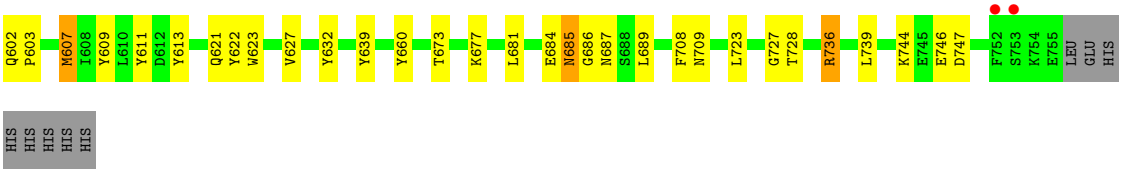
Chain A:



• Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

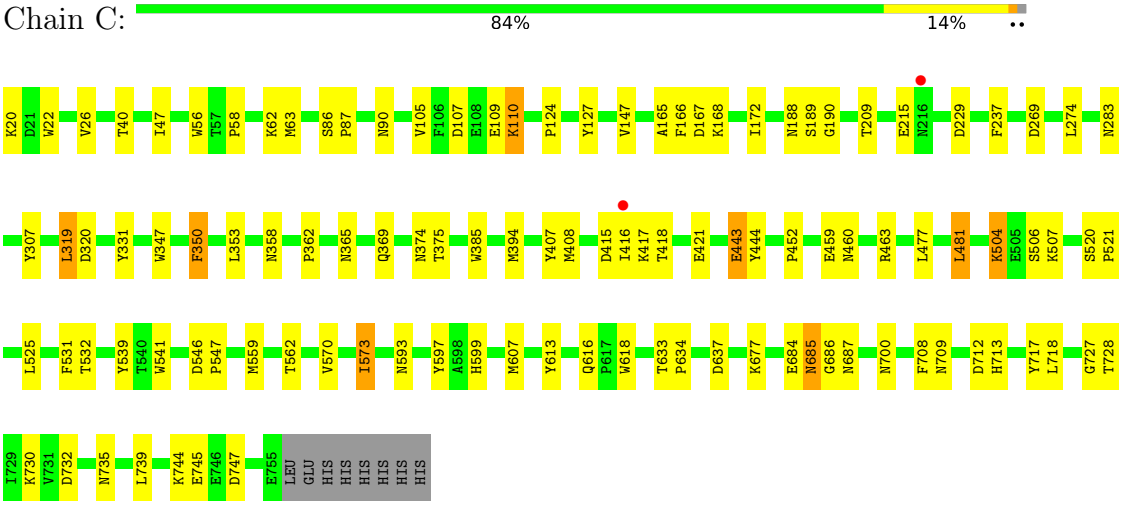
Chain B:





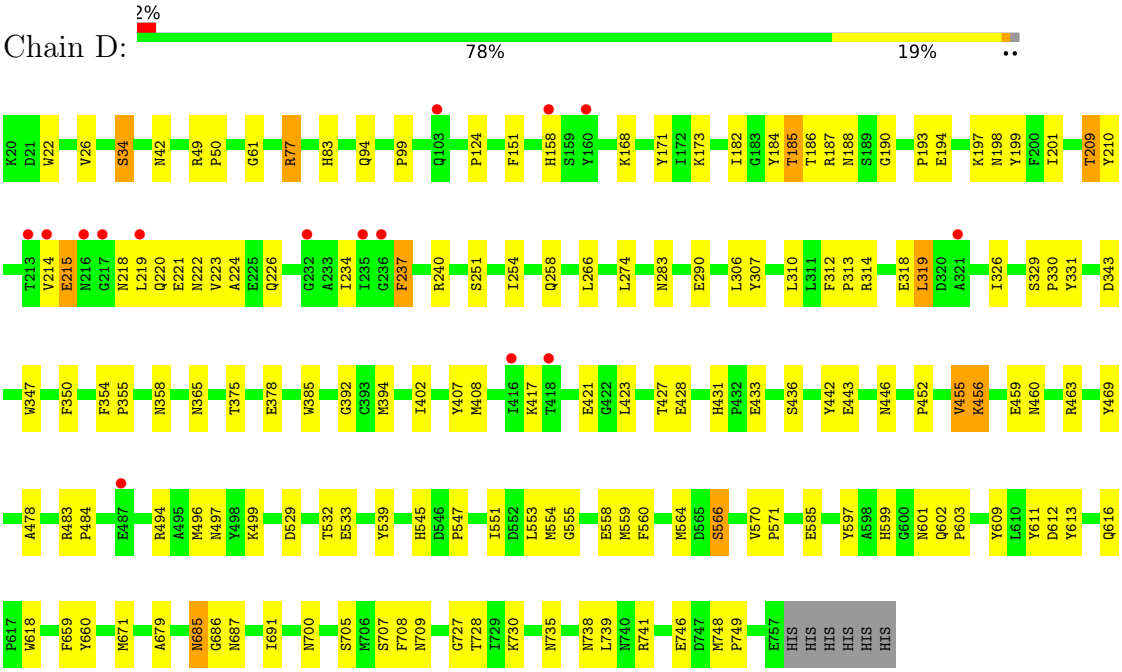
• Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

Chain C:



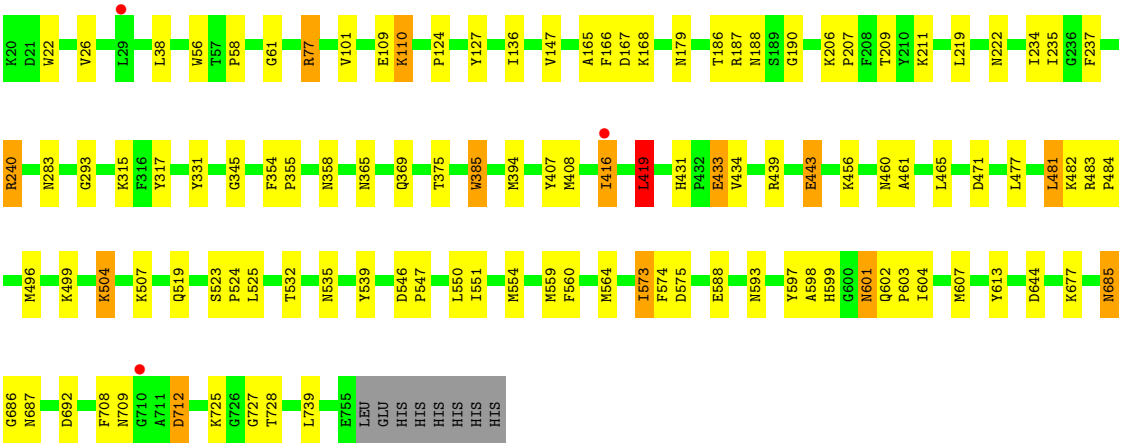
• Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

Chain D:



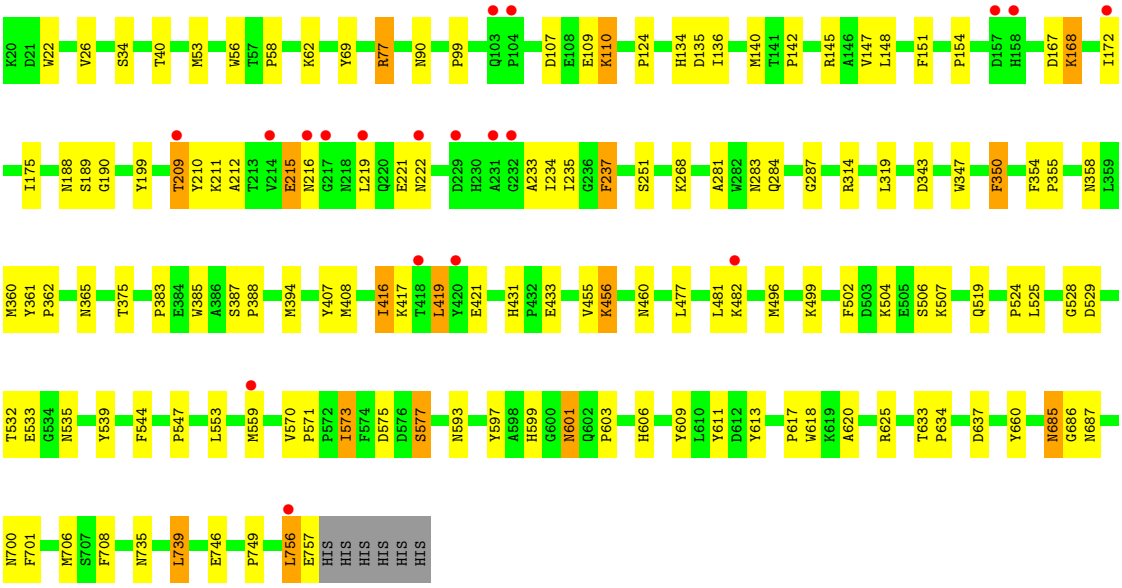
• Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

Chain E:



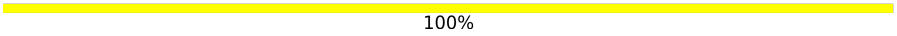
• Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

Chain F:



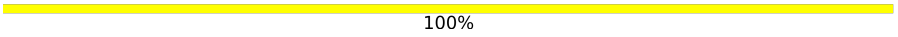
• Molecule 2: alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside

Chain G:



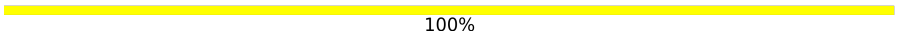
• Molecule 2: alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside

Chain H:



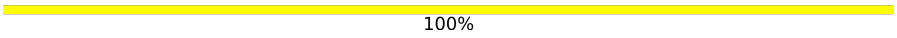
• Molecule 2: alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside

Chain I:



- Molecule 2: alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside

Chain J:

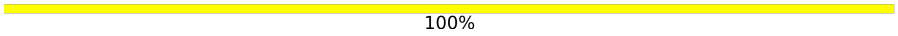


- Molecule 2: alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside

Chain K:

- Molecule 2: alpha-D-mannopyranose-(1-2)-methyl 2-thio-alpha-D-mannopyranoside

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	161.26Å 68.59Å 204.01Å 90.00° 94.66° 90.00°	Depositor
Resolution (Å)	203.33 – 2.10 49.90 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.3 (203.33-2.10) 97.3 (49.90-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.46 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, R_{free}	0.190 , 0.244 0.195 , 0.249	Depositor DCC
R_{free} test set	12627 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 41.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	37131	wwPDB-VP
Average B, all atoms (Å^2)	27.0	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 29.05 % 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 1.6577e-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: CA, Z5L, GOL, 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	0.56	0/6138	0.62	0/8330
1	B	0.56	0/6118	0.62	0/8307
1	C	0.57	1/6130 (0.0%)	0.63	0/8320
1	D	0.52	0/6127	0.60	0/8324
1	E	0.55	1/6129 (0.0%)	0.62	1/8322 (0.0%)
1	F	0.48	0/6129	0.59	0/8323
All	All	0.54	2/36771 (0.0%)	0.61	1/49926 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	443	GLU	CB-CG	7.00	1.65	1.52
1	E	443	GLU	CB-CG	5.51	1.62	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	419	LEU	CA-CB-CG	5.40	127.72	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5957	0	5610	116	0
1	B	5937	0	5576	218	0
1	C	5949	0	5600	79	0
1	D	5946	0	5557	143	0
1	E	5945	0	5577	83	0
1	F	5948	0	5582	122	0
2	G	24	0	9	0	0
2	H	24	0	9	0	0
2	I	24	0	8	0	0
2	J	24	0	8	0	0
2	K	24	0	8	0	0
2	L	24	0	8	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	6	0	8	0	0
4	C	6	0	8	0	0
4	E	6	0	8	0	0
5	A	230	0	0	4	0
5	B	162	0	0	5	0
5	C	322	0	0	3	0
5	D	155	0	0	3	0
5	E	217	0	0	1	0
5	F	195	0	0	4	0
All	All	37131	0	33576	760	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 760 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:444:TYR:CZ	1:B:455:VAL:HG11	1.50	1.44
1:F:211:LYS:NZ	1:F:222:ASN:OD1	1.63	1.31
1:D:554:MET:O	1:D:559:MET:CE	1.81	1.26
1:D:318:GLU:C	1:D:319:LEU:HD23	1.55	1.26
1:B:446:ASN:HD21	1:B:494:ARG:NH1	1.39	1.21

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	734/744 (99%)	710 (97%)	23 (3%)	1 (0%)	51	54
1	B	734/744 (99%)	693 (94%)	41 (6%)	0	100	100
1	C	734/744 (99%)	711 (97%)	23 (3%)	0	100	100
1	D	736/744 (99%)	700 (95%)	35 (5%)	1 (0%)	51	54
1	E	735/744 (99%)	705 (96%)	30 (4%)	0	100	100
1	F	736/744 (99%)	701 (95%)	35 (5%)	0	100	100
All	All	4409/4464 (99%)	4220 (96%)	187 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	529	ASP
1	A	529	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	632/643 (98%)	610 (96%)	22 (4%)	36	38
1	B	627/643 (98%)	599 (96%)	28 (4%)	27	27
1	C	630/643 (98%)	609 (97%)	21 (3%)	38	40
1	D	627/643 (98%)	605 (96%)	22 (4%)	36	38
1	E	629/643 (98%)	604 (96%)	25 (4%)	31	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	F	628/643 (98%)	603 (96%)	25 (4%)	31 32
All	All	3773/3858 (98%)	3630 (96%)	143 (4%)	33 34

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	708	PHE
1	F	77	ARG
1	F	456	LYS
1	B	739	LEU
1	B	736	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	59	GLN
1	F	709	ASN
1	D	685	ASN
1	F	700	ASN
1	F	374	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

12 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	Z5L	G	1	2	12,13,13	0.85	1 (8%)	14,18,18	0.74	0
2	MAN	G	2	2,3	11,11,12	0.45	0	15,15,17	1.35	1 (6%)
2	Z5L	H	1	2	12,13,13	0.77	1 (8%)	14,18,18	0.79	0
2	MAN	H	2	2,3	11,11,12	0.62	0	15,15,17	1.74	2 (13%)
2	Z5L	I	1	2	12,13,13	0.79	1 (8%)	14,18,18	1.07	1 (7%)
2	MAN	I	2	2,3	11,11,12	0.61	0	15,15,17	1.57	2 (13%)
2	Z5L	J	1	2	12,13,13	0.91	1 (8%)	14,18,18	0.62	0
2	MAN	J	2	2,3	11,11,12	0.38	0	15,15,17	1.30	1 (6%)
2	Z5L	K	1	2	12,13,13	0.67	0	14,18,18	0.83	0
2	MAN	K	2	2,3	11,11,12	0.59	0	15,15,17	1.25	2 (13%)
2	Z5L	L	1	2	12,13,13	0.73	1 (8%)	14,18,18	0.87	0
2	MAN	L	2	2,3	11,11,12	0.55	0	15,15,17	1.38	2 (13%)

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	Z5L	G	1	2	-	2/4/24/24	0/1/1/1
2	MAN	G	2	2,3	-	1/2/19/22	0/1/1/1
2	Z5L	H	1	2	-	0/4/24/24	0/1/1/1
2	MAN	H	2	2,3	-	0/2/19/22	0/1/1/1
2	Z5L	I	1	2	-	2/4/24/24	0/1/1/1
2	MAN	I	2	2,3	-	0/2/19/22	0/1/1/1
2	Z5L	J	1	2	-	0/4/24/24	0/1/1/1
2	MAN	J	2	2,3	-	0/2/19/22	0/1/1/1
2	Z5L	K	1	2	-	2/4/24/24	0/1/1/1
2	MAN	K	2	2,3	-	0/2/19/22	0/1/1/1
2	Z5L	L	1	2	-	0/4/24/24	0/1/1/1
2	MAN	L	2	2,3	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1	Z5L	O1-C1	2.63	1.44	1.40
2	L	1	Z5L	O1-C1	2.29	1.44	1.40
2	I	1	Z5L	O1-C1	2.23	1.44	1.40
2	J	1	Z5L	O1-C1	2.23	1.44	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	Z5L	O1-C1	2.21	1.43	1.40

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	2	MAN	C1-C2-C3	4.59	115.31	109.67
2	L	2	MAN	C1-C2-C3	4.11	114.72	109.67
2	I	2	MAN	C1-C2-C3	4.08	114.68	109.67
2	H	2	MAN	O5-C1-C2	3.77	116.60	110.77
2	J	2	MAN	C1-C2-C3	3.72	114.24	109.67

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

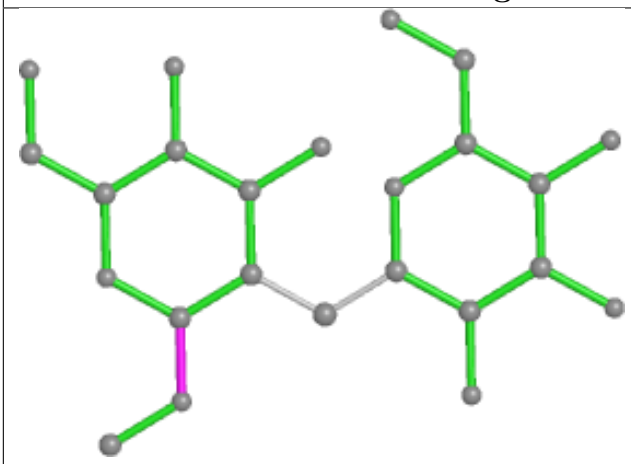
Mol	Chain	Res	Type	Atoms
2	I	1	Z5L	O5-C5-C6-O6
2	I	1	Z5L	C4-C5-C6-O6
2	K	1	Z5L	O5-C5-C6-O6
2	G	1	Z5L	O5-C5-C6-O6
2	K	1	Z5L	C4-C5-C6-O6

There are no ring outliers.

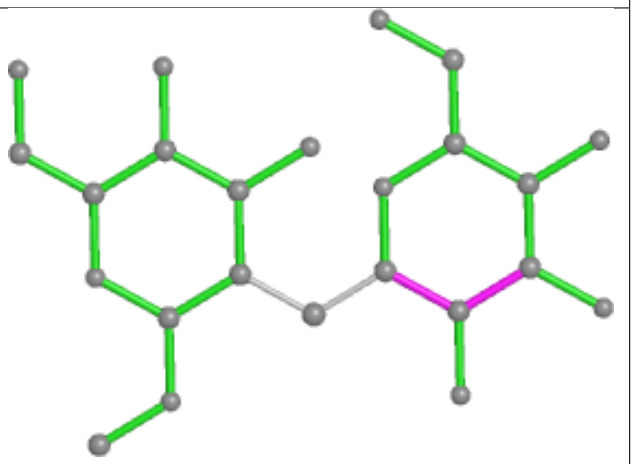
No monomer is involved in short contacts.

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

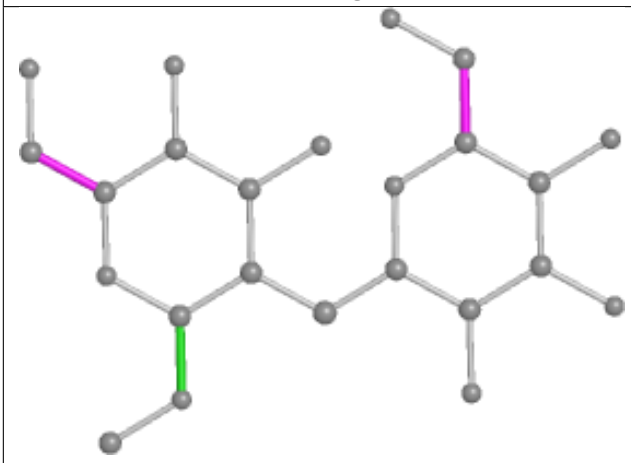
Oligosaccharide Chain G



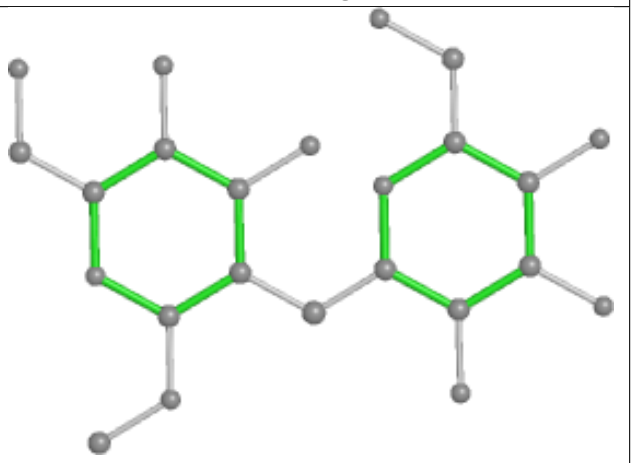
Bond lengths



Bond angles

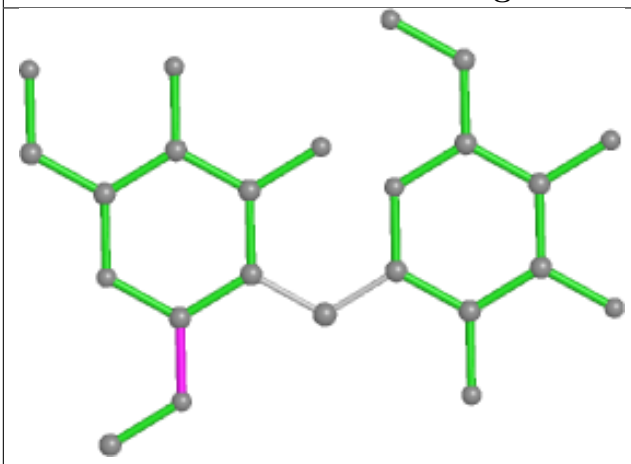


Torsions

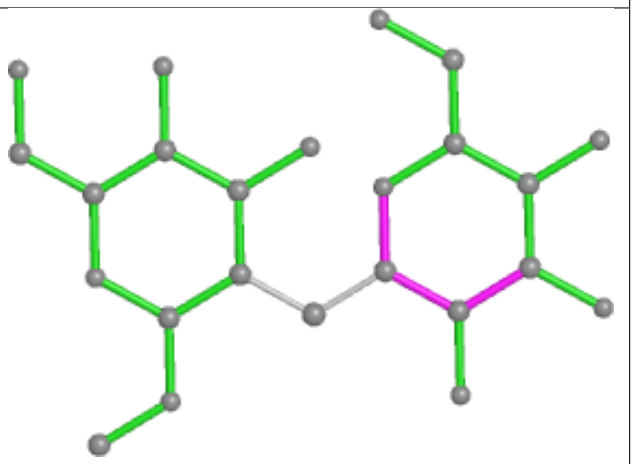


Rings

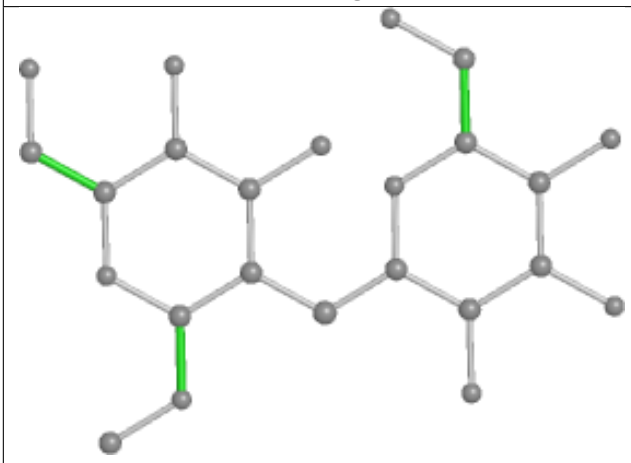
Oligosaccharide Chain H



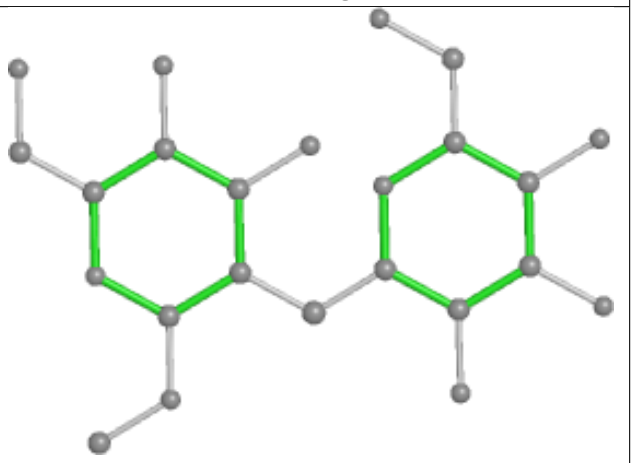
Bond lengths



Bond angles

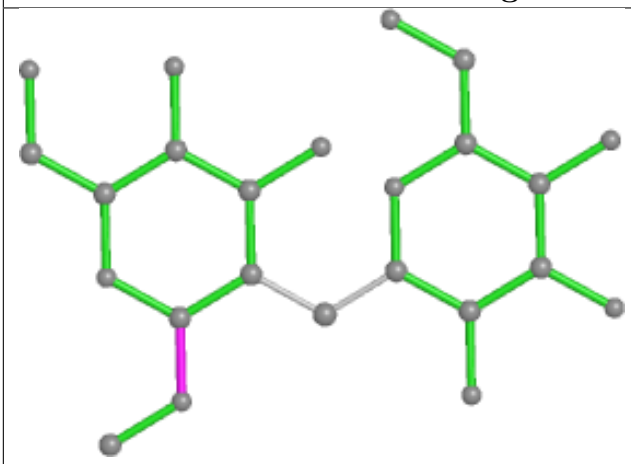


Torsions

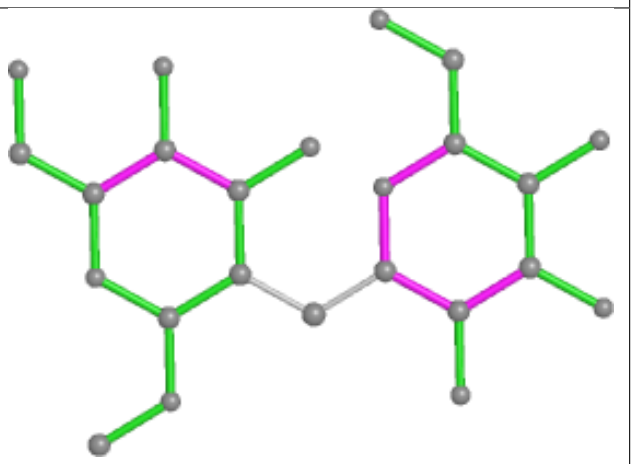


Rings

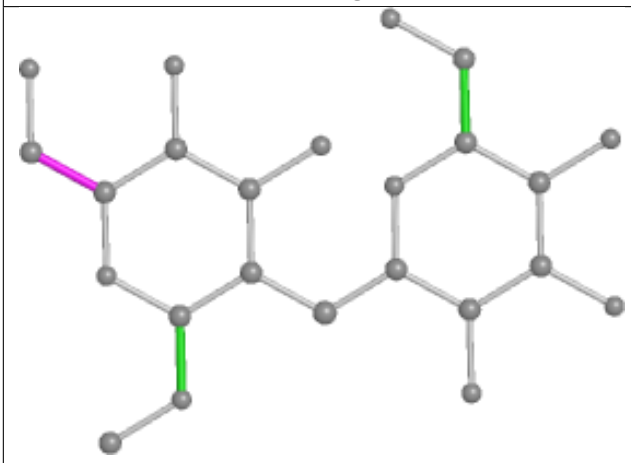
Oligosaccharide Chain I



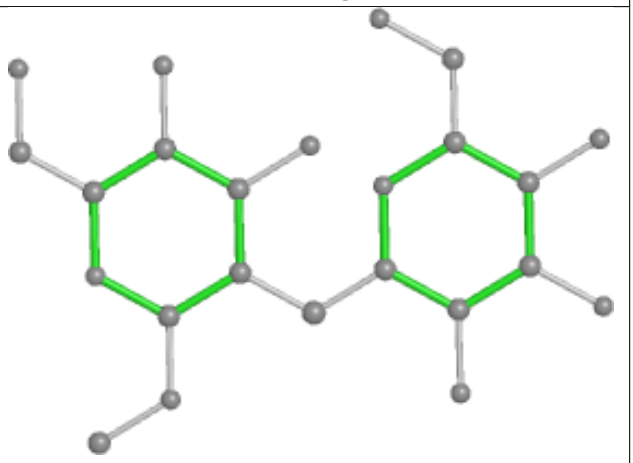
Bond lengths



Bond angles

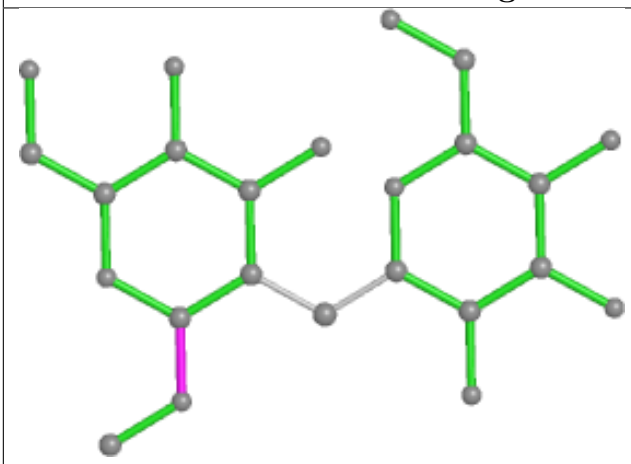


Torsions

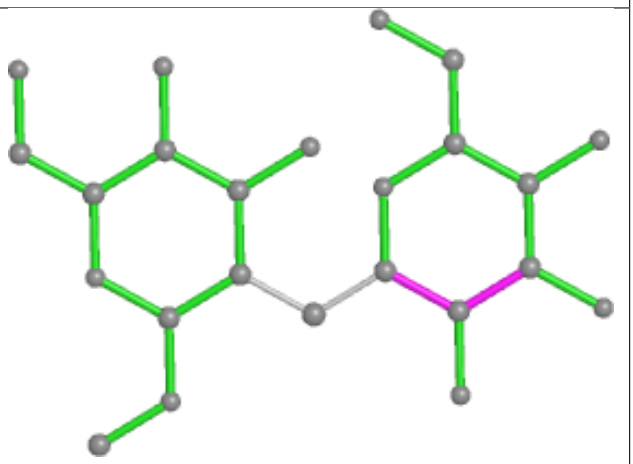


Rings

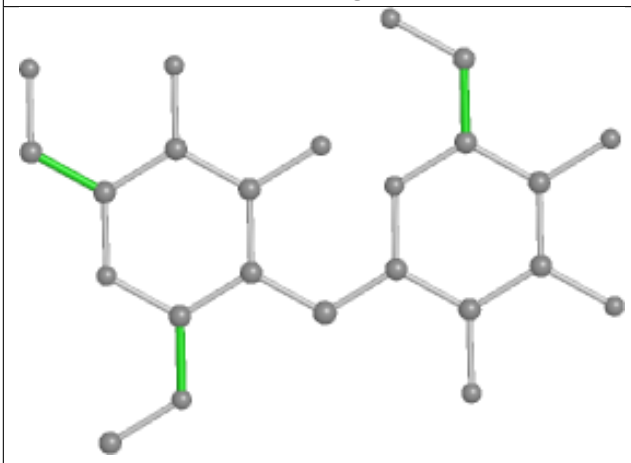
Oligosaccharide Chain J



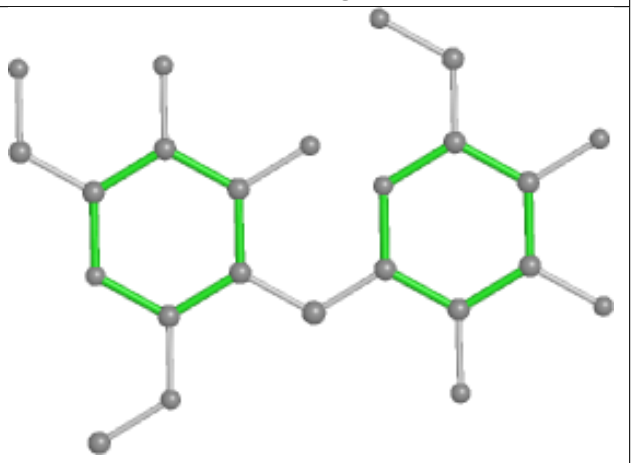
Bond lengths



Bond angles

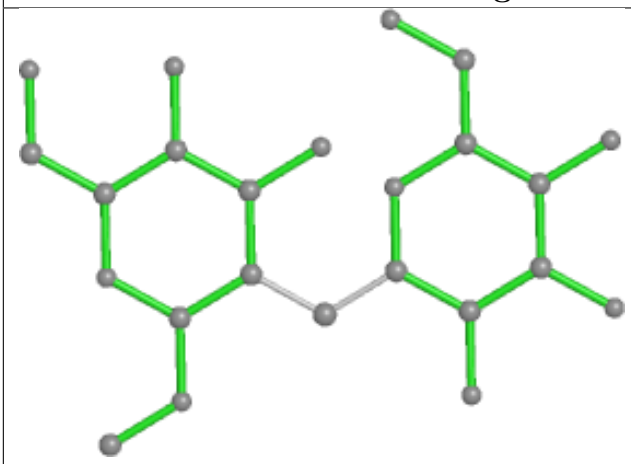


Torsions

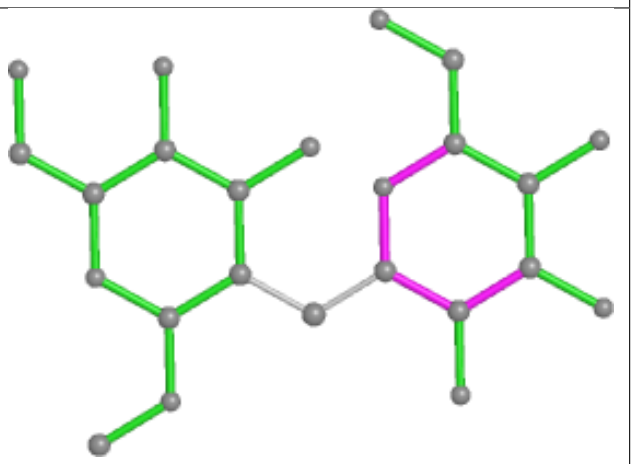


Rings

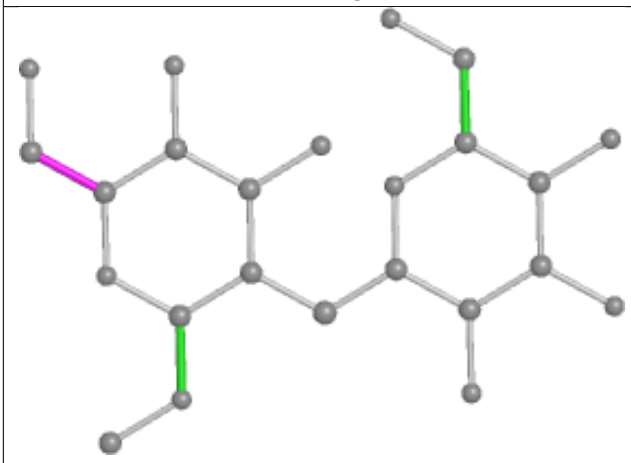
Oligosaccharide Chain K



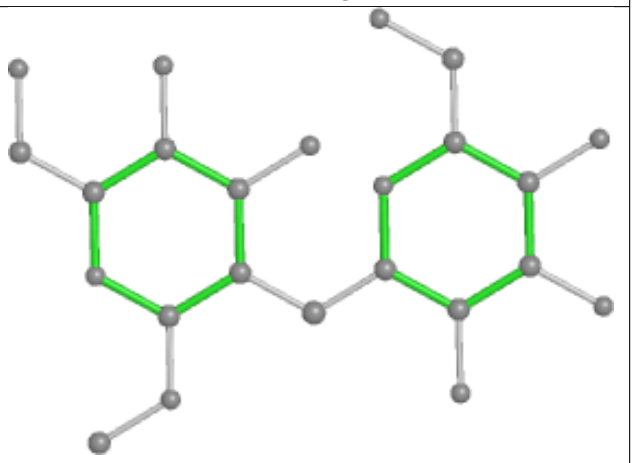
Bond lengths



Bond angles

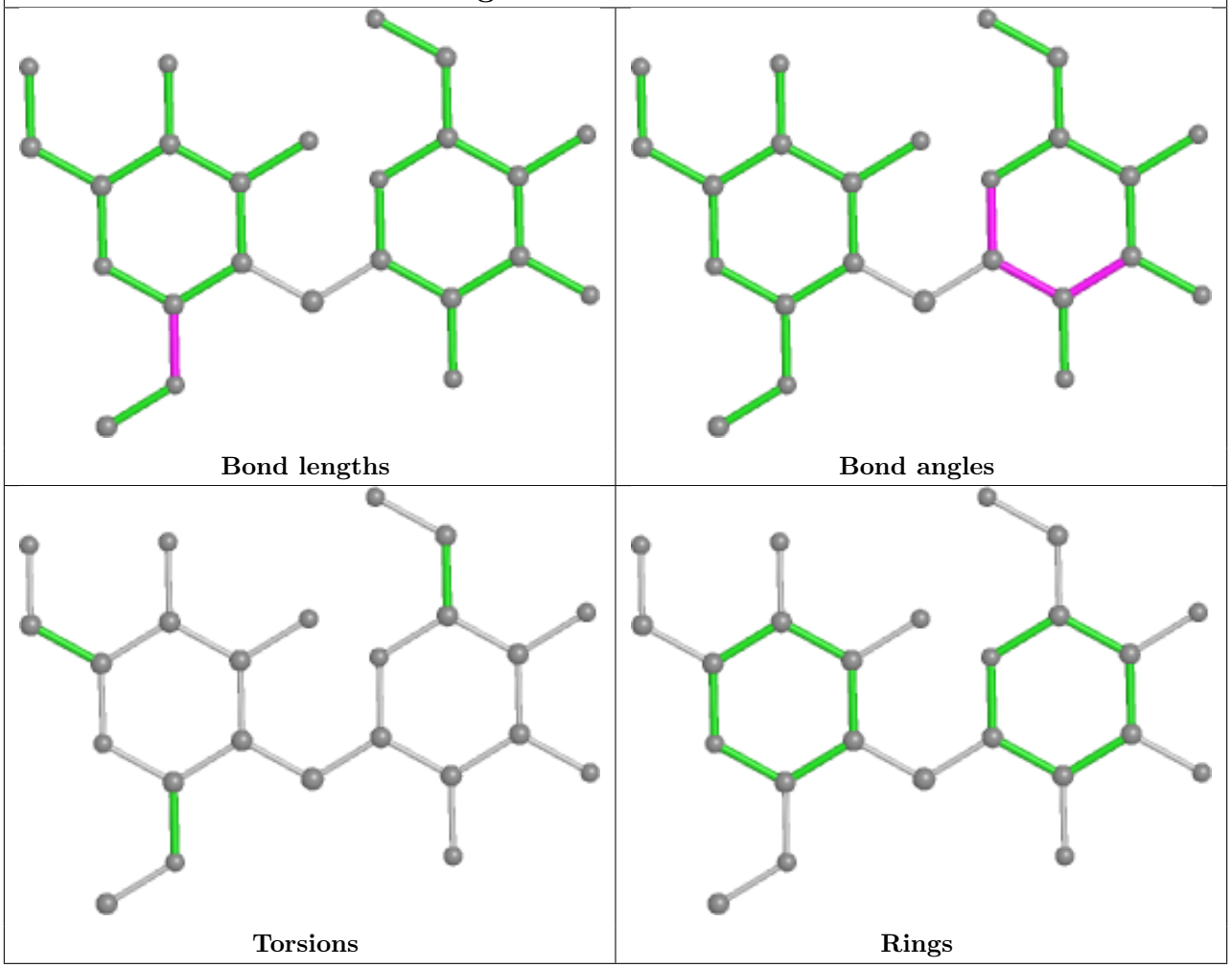


Torsions



Rings

Oligosaccharide Chain L



5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
4	GOL	A	802	-	5,5,5	0.39	0	5,5,5	0.30	0
4	GOL	C	802	-	5,5,5	0.29	0	5,5,5	0.41	0
4	GOL	E	802	-	5,5,5	0.30	0	5,5,5	0.54	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
4	GOL	A	802	-	-	4/4/4/4	-
4	GOL	C	802	-	-	2/4/4/4	-
4	GOL	E	802	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	802	GOL	O1-C1-C2-C3
4	A	802	GOL	C1-C2-C3-O3
4	A	802	GOL	O2-C2-C3-O3
4	E	802	GOL	C1-C2-C3-O3
4	C	802	GOL	O1-C1-C2-C3

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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	736/744 (98%)	-0.02	4 (0%) 91 92	17, 23, 33, 40	0
1	B	736/744 (98%)	0.51	41 (5%) 24 29	21, 33, 44, 55	0
1	C	736/744 (98%)	0.01	2 (0%) 94 94	15, 21, 32, 39	0
1	D	738/744 (99%)	0.19	15 (2%) 65 69	18, 28, 38, 45	0
1	E	736/744 (98%)	-0.05	3 (0%) 92 93	17, 23, 33, 40	0
1	F	738/744 (99%)	0.20	19 (2%) 56 61	21, 30, 41, 46	0
All	All	4420/4464 (99%)	0.14	84 (1%) 66 71	15, 26, 40, 55	0

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	442	TYR	4.8
1	B	444	TYR	4.2
1	B	420	TYR	4.1
1	F	217	GLY	4.0
1	F	172	ILE	3.7

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

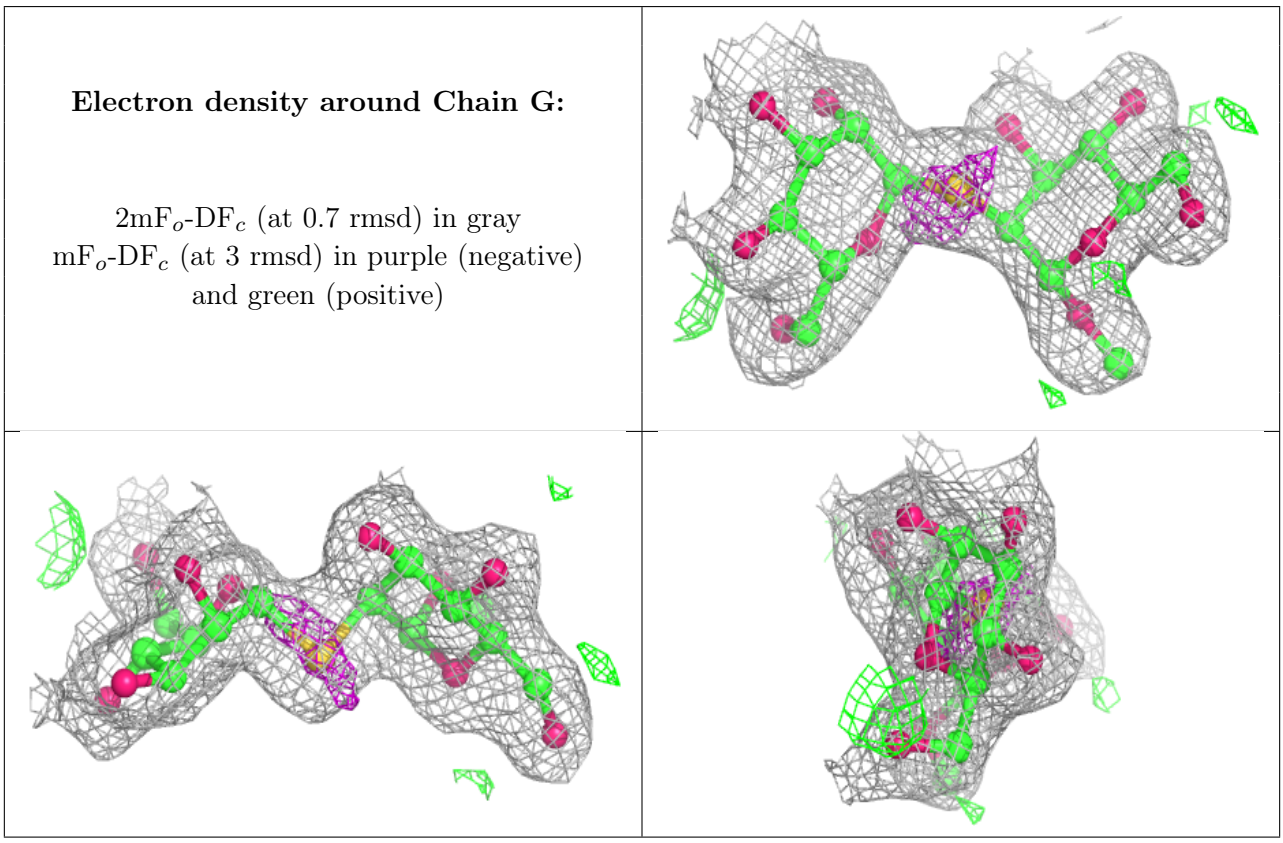
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

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

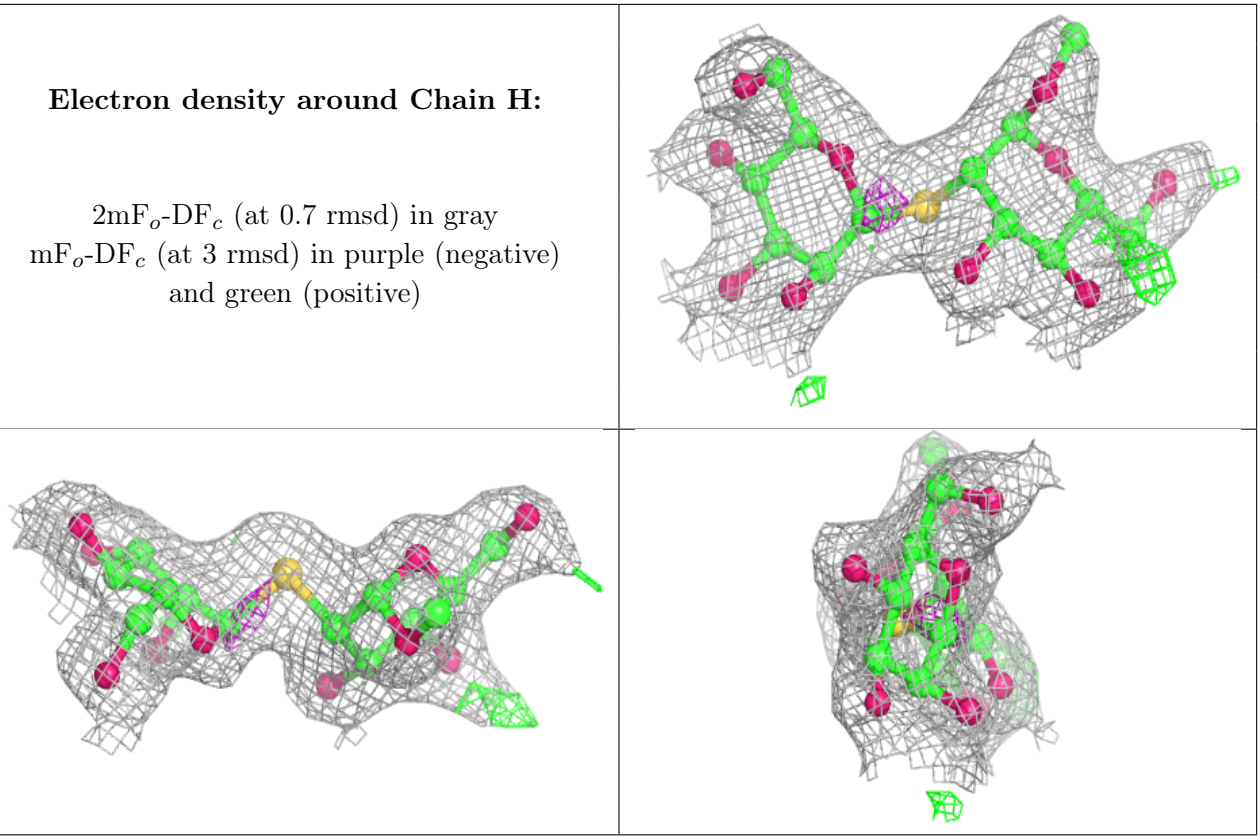
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MAN	H	2	11/12	0.92	0.12	34,37,39,40	0
2	MAN	I	2	11/12	0.92	0.13	20,24,26,27	0
2	MAN	J	2	11/12	0.93	0.10	30,31,32,32	0
2	Z5L	H	1	13/13	0.94	0.11	36,37,39,39	0
2	Z5L	J	1	13/13	0.95	0.13	28,29,34,35	0
2	MAN	G	2	11/12	0.95	0.09	22,27,29,29	0
2	MAN	L	2	11/12	0.95	0.10	31,33,34,34	0
2	Z5L	L	1	13/13	0.96	0.10	32,34,37,38	0
2	Z5L	G	1	13/13	0.96	0.08	25,27,29,31	0
2	Z5L	K	1	13/13	0.97	0.07	25,28,31,31	0
2	MAN	K	2	11/12	0.97	0.07	22,26,27,28	0
2	Z5L	I	1	13/13	0.98	0.08	22,25,30,31	0

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



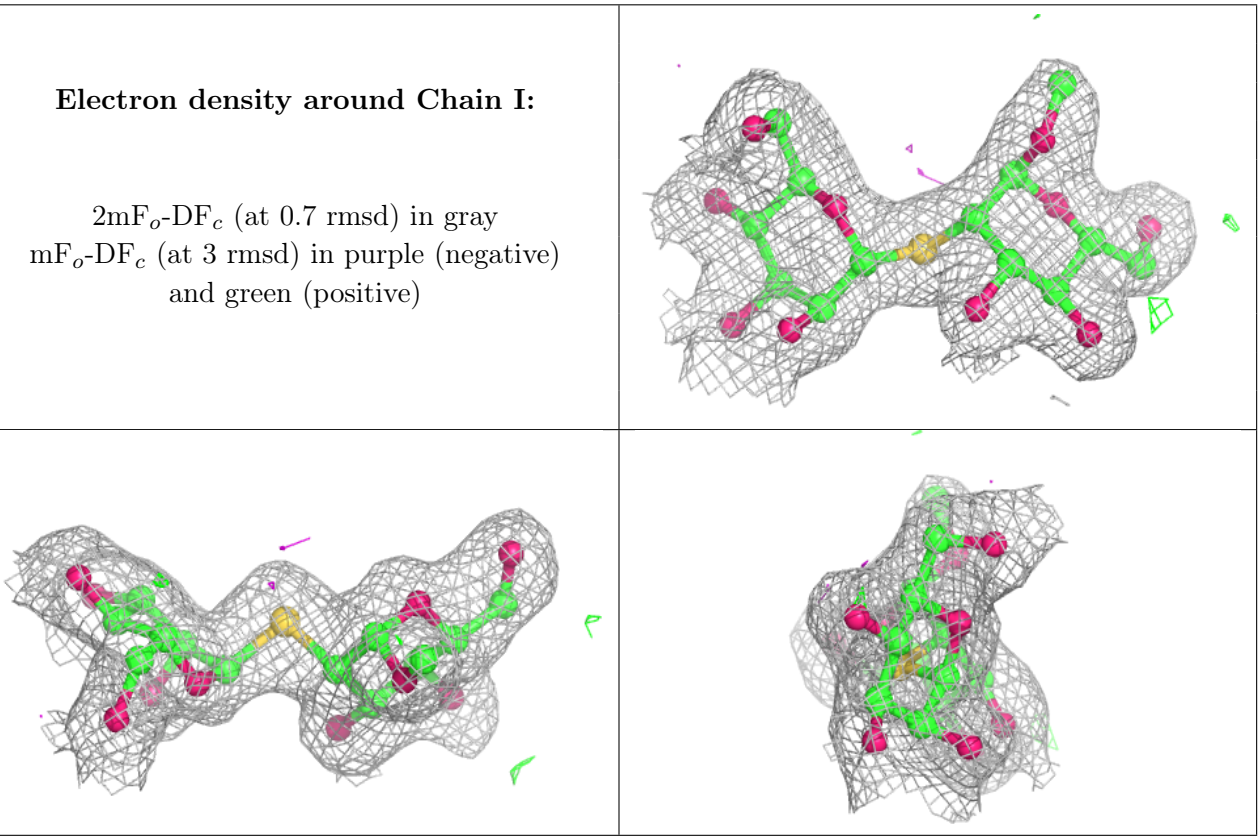
Electron density around Chain H:

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



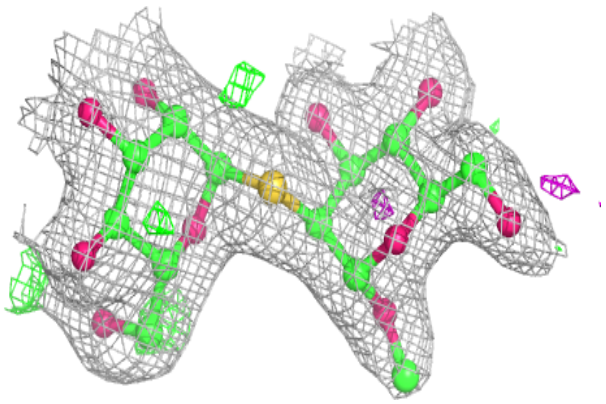
Electron density around Chain I:

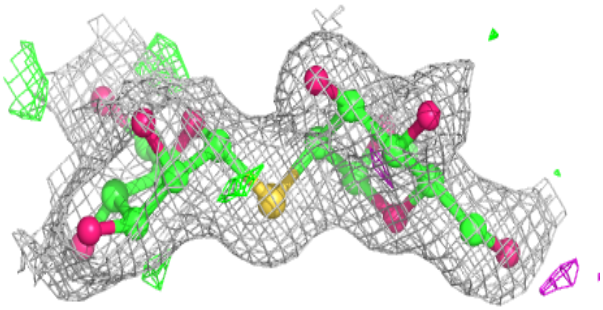
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

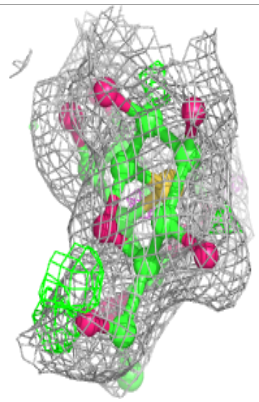


Electron density around Chain J:

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

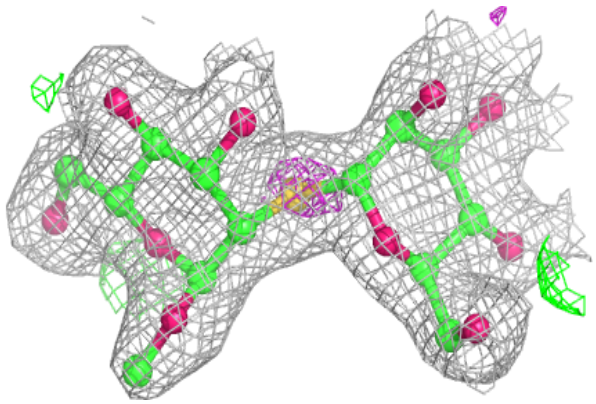


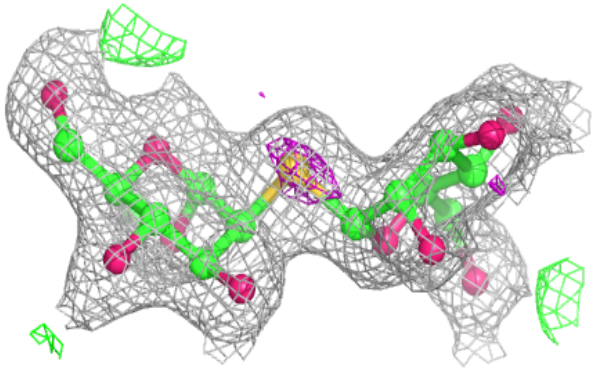


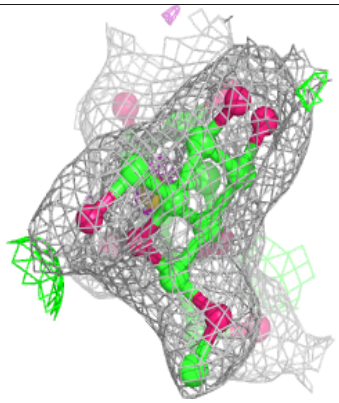


Electron density around Chain K:

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

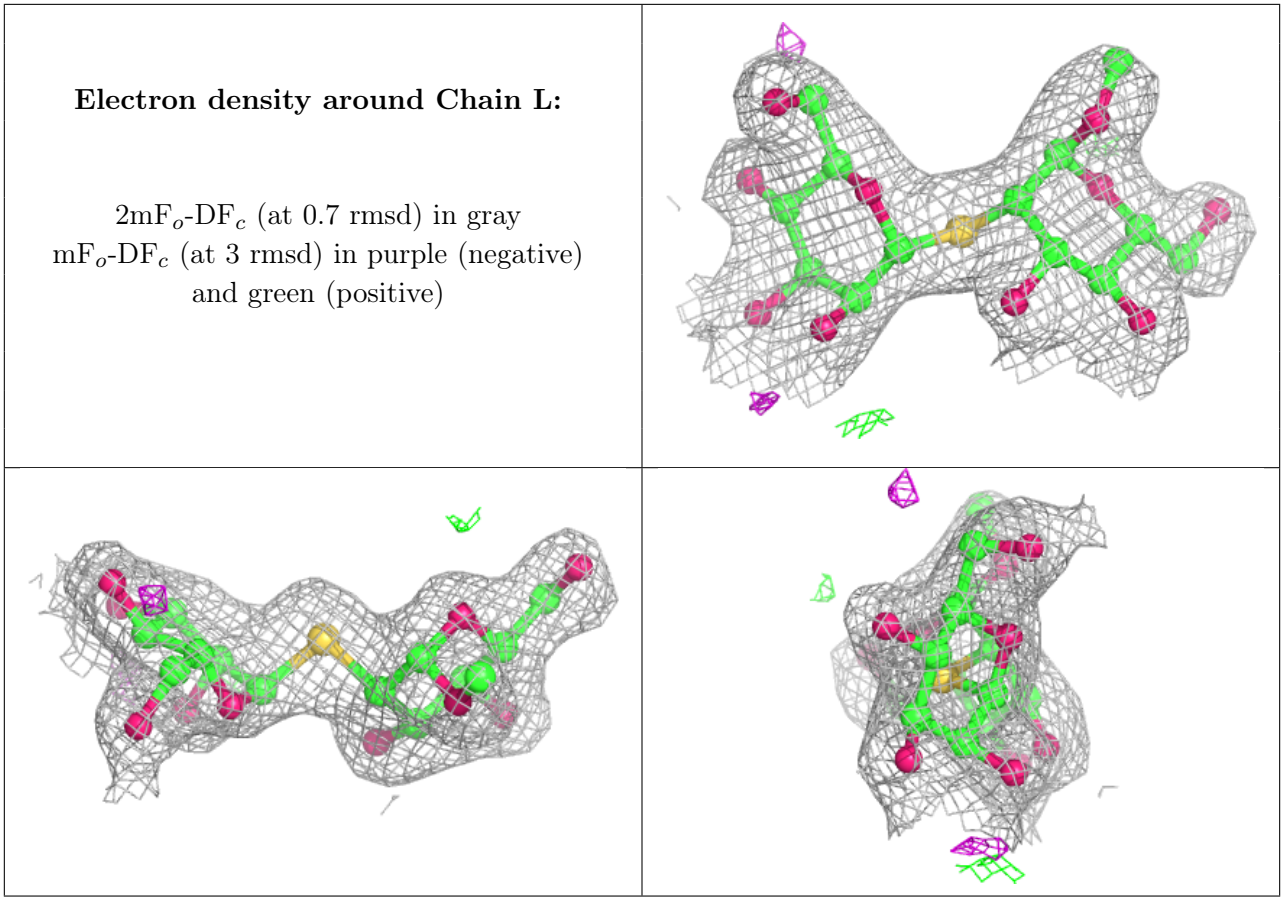






Electron density around Chain L:

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



6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	A	802	6/6	0.90	0.16	48,49,49,50	0
4	GOL	E	802	6/6	0.91	0.17	40,41,42,46	0
4	GOL	C	802	6/6	0.95	0.15	30,33,34,34	0
3	CA	F	800	1/1	0.97	0.06	31,31,31,31	0
3	CA	D	800	1/1	0.98	0.09	29,29,29,29	0
3	CA	E	800	1/1	0.98	0.06	24,24,24,24	0
3	CA	A	800	1/1	0.99	0.06	25,25,25,25	0
3	CA	B	800	1/1	0.99	0.05	36,36,36,36	0
3	CA	C	800	1/1	0.99	0.09	26,26,26,26	0

6.5 Other polymers (i)

There are no such residues in this entry.