wwPDB X-ray Structure Validation Summary Report (i)

Oct 19, 2024 – 04:39 PM EDT

PDB ID	:	1IVE
Title	:	STRUCTURES OF AROMATIC INHIBITORS OF INFLUENZA VIRUS NEURAMINIDASE
Authors	:	Jedrzejas, M.J.; Luo, M.
Deposited on	:	1994-12-12
Resolution	:	2.40 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 (1)) were used in the production of this report:

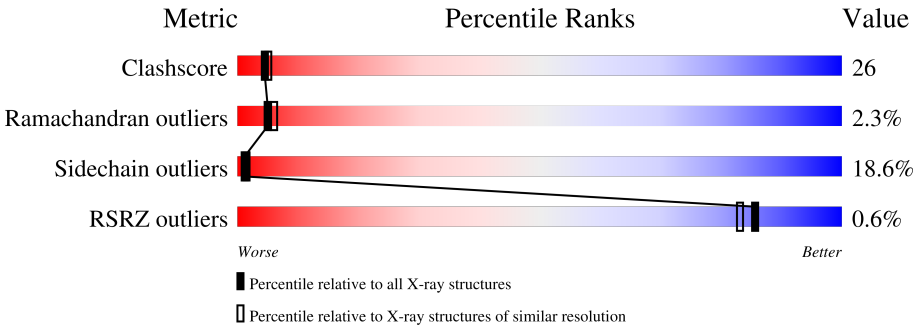
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)

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	388	% 52% 38% 9% •
1	B	388	% 52% 38% 8% •
2	C	2	100%
2	G	2	100%
3	D	4	25% 75%
4	E	6	17% 83%
4	I	6	17% 83%

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Mol	Chain	Length	Quality of chain
5	F	2	
5	J	2	
6	H	4	

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
3	BMA	D	3	-	-	X	-
3	FUL	D	4	-	-	X	-
4	NAG	E	1	-	-	X	-
4	NAG	E	2	-	-	X	-
4	MAN	E	4	-	-	X	-
4	MAN	E	5	X	-	-	-
4	MAN	I	5	X	-	-	-
6	FUC	H	4	X	-	-	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 8216 atoms, of which 1788 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.

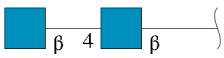
- Molecule 1 is a protein called INFLUENZA A SUBTYPE N2 NEURAMINIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	388	Total	C	H	N	O	S	0	0	0
			3745	1866	723	545	588	23			
1	B	388	Total	C	H	N	O	S	0	0	0
			3745	1866	723	545	588	23			

There are 2 discrepancies between the modelled and reference sequences:

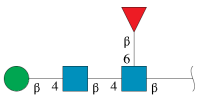
Chain	Residue	Modelled	Actual	Comment	Reference
A	339	ASP	ASN	conflict	UNP P06820
B	339	ASP	ASN	conflict	UNP P06820

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



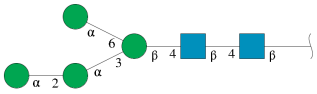
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
2	G	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	4	Total	C	H	N	O	0	0	0
			96	28	47	2	19			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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.

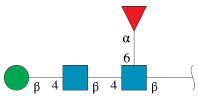


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	6	Total	C	H	N	O	0	0	0
			139	40	67	2	30			
4	I	6	Total	C	H	N	O	0	0	0
			139	40	67	2	30			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
5	J	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

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

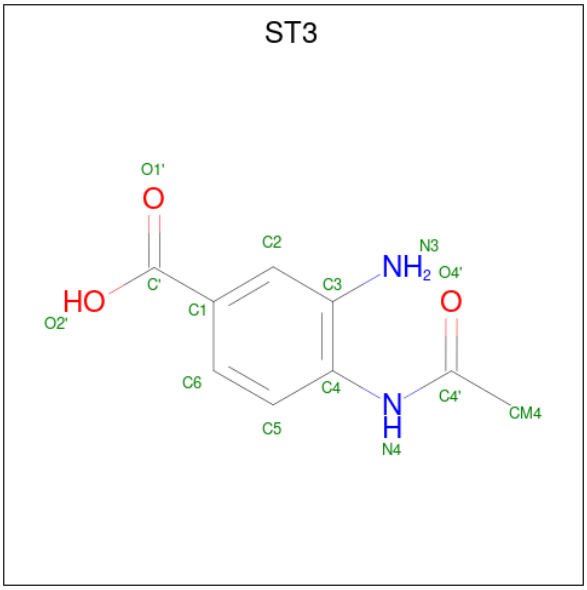


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	4	Total	C	H	N	O	0	0	0
			96	28	47	2	19			

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0
7	B	1	Total Ca 1 1	0	0

- Molecule 8 is 4-(ACETYLAMINO)-3-AMINO BENZOIC ACID (three-letter code: ST3) (formula: $C_9H_{10}N_2O_3$).



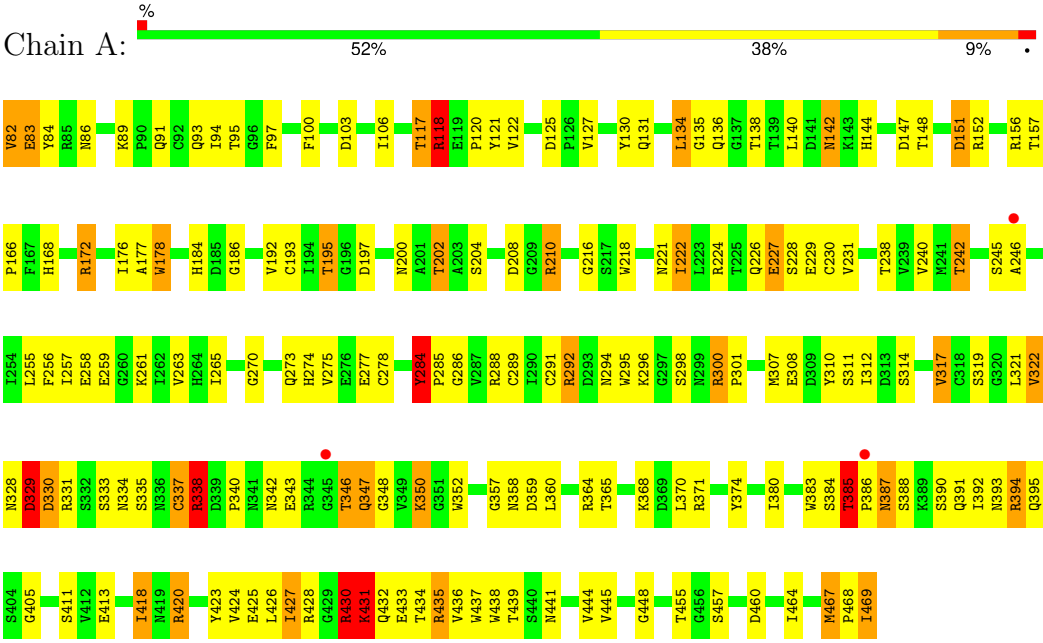
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C H N O 17 9 3 2 3	0	0
8	B	1	Total C H N O 17 9 3 2 3	0	0

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.

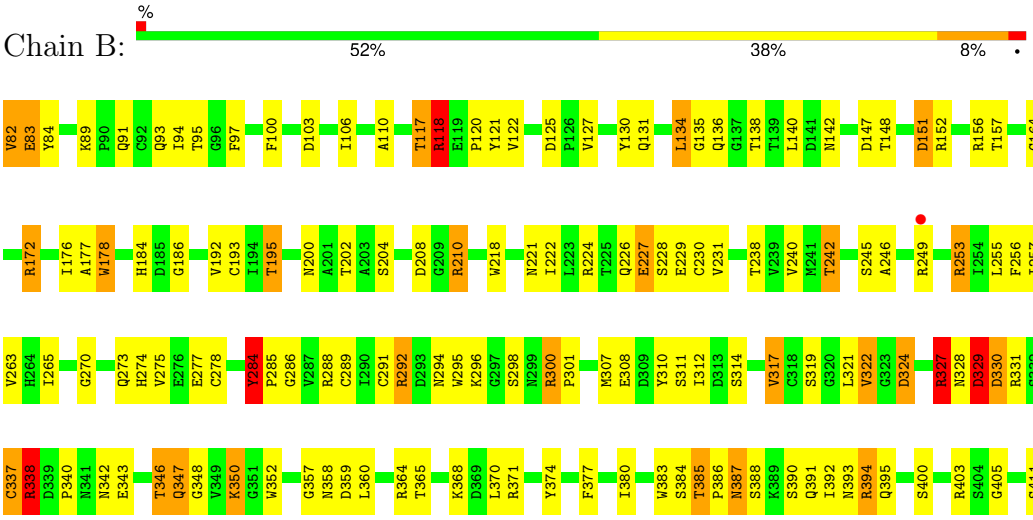
• Molecule 1: INFLUENZA A SUBTYPE N2 NEURAMINIDASE

Chain A:



• Molecule 1: INFLUENZA A SUBTYPE N2 NEURAMINIDASE

Chain B:



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

Chain C:

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

Chain G:

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

Chain D:

• Molecule 4: alpha-D-mannopyranose-(1-2)-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 E:

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

Chain F:

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

Chain J:

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

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	121.88Å 140.88Å 141.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.50 – 2.40 6.50 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.50-2.40) 49.9 (6.50-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 2.42Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.217 , (Not available) 0.221 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	18.4	Xtriage
Anisotropy	1.296	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 65.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	8216	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: ST3, NAG, NDG, FUL, FUC, MAN, CA, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.69	0/3092	0.77	1/4194 (0.0%)
1	B	0.69	0/3092	0.77	1/4194 (0.0%)
All	All	0.69	0/6184	0.77	2/8388 (0.0%)

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	A	0	18
1	B	0	18
All	All	0	36

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	103	ASP	CB-CG-OD1	5.67	123.40	118.30
1	B	103	ASP	CB-CG-OD1	5.67	123.40	118.30

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	THR	Mainchain
1	A	118	ARG	Sidechain
1	A	121	TYR	Sidechain
1	A	122	VAL	Mainchain

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Mol	Chain	Res	Type	Group
1	A	84	TYR	Sidechain

5.2 Too-close contacts (i)

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	3022	723	2851	145	3
1	B	3022	723	2852	158	4
2	C	28	27	25	4	0
2	G	28	27	25	5	0
3	D	49	47	43	4	18
4	E	72	67	61	25	20
4	I	72	67	61	7	1
5	F	28	27	23	2	0
5	J	28	27	23	2	0
6	H	49	47	43	4	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	14	3	9	2	0
8	B	14	3	9	1	0
All	All	6428	1788	6025	320	23

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 26.

The worst 5 of 320 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:455:THR:CG2	4:E:2:NAG:H82	1.74	1.18
1:B:455:THR:HB	4:E:1:NAG:O5	1.49	1.11
1:B:455:THR:OG1	4:E:2:NAG:H82	1.59	1.02
1:B:455:THR:HG21	4:E:2:NAG:H82	1.46	0.97
1:A:437:TRP:H	1:A:469:ILE:HG21	1.33	0.93

The worst 5 of 23 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LEU:O	1:B:172:ARG:NH1[4_555]	1.32	0.88
1:A:163:LEU:O	1:B:172:ARG:HH12[4_555]	0.74	0.86
3:D:3:BMA:H61	4:E:2:NAG:HO6[3_654]	0.99	0.61
3:D:3:BMA:H4	4:E:2:NAG:H62[3_654]	1.00	0.60
3:D:4:FUL:H5	4:E:4:MAN:H62[3_654]	1.01	0.59

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	386/388 (100%)	326 (84%)	51 (13%)	9 (2%)	5	6
1	B	386/388 (100%)	326 (84%)	51 (13%)	9 (2%)	5	6
All	All	772/776 (100%)	652 (84%)	102 (13%)	18 (2%)	5	6

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	ILE
1	A	284	TYR
1	A	347	GLN
1	A	387	ASN
1	B	222	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	338/338 (100%)	275 (81%)	63 (19%)	1 1
1	B	338/338 (100%)	275 (81%)	63 (19%)	1 1
All	All	676/676 (100%)	550 (81%)	126 (19%)	1 1

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	431	LYS
1	B	388	SER
1	B	142	ASN
1	B	385	THR
1	B	427	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	142	ASN
1	B	184	HIS
1	B	419	ASN
1	B	168	HIS
1	B	220	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

28 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	C	1	1,2	14,14,15	1.90	3 (21%)	17,19,21	4.02	10 (58%)
2	NAG	C	2	2	14,14,15	2.60	6 (42%)	17,19,21	3.08	8 (47%)
3	NAG	D	1	3,1	14,14,15	1.57	4 (28%)	17,19,21	4.08	9 (52%)
3	NAG	D	2	3	14,14,15	3.14	10 (71%)	17,19,21	2.37	7 (41%)
3	BMA	D	3	3	11,11,12	4.99	9 (81%)	15,15,17	2.10	5 (33%)
3	FUL	D	4	3	10,10,11	2.61	5 (50%)	14,14,16	2.72	5 (35%)
4	NAG	E	1	1,4	14,14,15	2.27	5 (35%)	17,19,21	4.58	10 (58%)
4	NAG	E	2	4	14,14,15	3.88	9 (64%)	17,19,21	4.33	9 (52%)
4	BMA	E	3	4	11,11,12	4.62	10 (90%)	15,15,17	2.70	6 (40%)
4	MAN	E	4	4	11,11,12	3.50	6 (54%)	15,15,17	2.05	6 (40%)
4	MAN	E	5	4	11,11,12	5.54	10 (90%)	15,15,17	2.27	5 (33%)
4	MAN	E	6	4	11,11,12	4.25	5 (45%)	15,15,17	1.97	3 (20%)
5	NAG	F	1	5,1	14,14,15	2.10	6 (42%)	17,19,21	2.92	4 (23%)
5	NDG	F	2	5	14,14,15	2.37	5 (35%)	17,19,21	3.79	10 (58%)
2	NAG	G	1	1,2	14,14,15	1.90	3 (21%)	17,19,21	4.02	10 (58%)
2	NAG	G	2	2	14,14,15	2.60	6 (42%)	17,19,21	3.08	8 (47%)
6	NAG	H	1	6,1	14,14,15	1.57	4 (28%)	17,19,21	4.08	9 (52%)
6	NAG	H	2	6	14,14,15	3.14	10 (71%)	17,19,21	2.37	7 (41%)
6	BMA	H	3	6	11,11,12	4.99	9 (81%)	15,15,17	2.10	5 (33%)
6	FUC	H	4	6	10,10,11	2.61	5 (50%)	14,14,16	2.72	5 (35%)
4	NAG	I	1	1,4	14,14,15	2.27	5 (35%)	17,19,21	4.58	10 (58%)
4	NAG	I	2	4	14,14,15	3.88	9 (64%)	17,19,21	4.33	9 (52%)
4	BMA	I	3	4	11,11,12	4.62	10 (90%)	15,15,17	2.70	6 (40%)
4	MAN	I	4	4	11,11,12	3.50	6 (54%)	15,15,17	2.05	6 (40%)
4	MAN	I	5	4	11,11,12	5.54	10 (90%)	15,15,17	2.27	5 (33%)
4	MAN	I	6	4	11,11,12	4.25	5 (45%)	15,15,17	1.97	3 (20%)
5	NAG	J	1	5,1	14,14,15	2.10	6 (42%)	17,19,21	2.92	4 (23%)
5	NDG	J	2	5	14,14,15	2.37	5 (35%)	17,19,21	3.79	10 (58%)

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	C	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
3	NAG	D	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	1/1/1/1
3	FUL	D	4	3	-	-	0/1/1/1
4	NAG	E	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	E	2	4	-	1/6/23/26	0/1/1/1
4	BMA	E	3	4	-	1/2/19/22	0/1/1/1
4	MAN	E	4	4	-	0/2/19/22	0/1/1/1
4	MAN	E	5	4	1/1/5/5	0/2/19/22	0/1/1/1
4	MAN	E	6	4	-	1/2/19/22	1/1/1/1
5	NAG	F	1	5,1	-	1/6/23/26	0/1/1/1
5	NDG	F	2	5	-	3/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
6	NAG	H	1	6,1	-	3/6/23/26	0/1/1/1
6	NAG	H	2	6	-	2/6/23/26	0/1/1/1
6	BMA	H	3	6	-	2/2/19/22	1/1/1/1
6	FUC	H	4	6	1/1/5/5	-	0/1/1/1
4	NAG	I	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	I	2	4	-	1/6/23/26	0/1/1/1
4	BMA	I	3	4	-	1/2/19/22	0/1/1/1
4	MAN	I	4	4	-	0/2/19/22	0/1/1/1
4	MAN	I	5	4	1/1/5/5	0/2/19/22	0/1/1/1
4	MAN	I	6	4	-	1/2/19/22	1/1/1/1
5	NAG	J	1	5,1	-	1/6/23/26	0/1/1/1
5	NDG	J	2	5	-	3/6/23/26	0/1/1/1

The worst 5 of 186 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	5	MAN	C2-C3	10.42	1.68	1.52
4	I	5	MAN	C2-C3	10.42	1.68	1.52
4	E	6	MAN	C2-C3	10.07	1.67	1.52
4	I	6	MAN	C2-C3	10.07	1.67	1.52
3	D	3	BMA	C2-C3	9.81	1.67	1.52

The worst 5 of 194 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1	NAG	C1-O5-C5	11.03	126.97	112.19
2	G	1	NAG	C1-O5-C5	11.03	126.97	112.19
3	D	1	NAG	C2-N2-C7	10.89	137.49	122.90
6	H	1	NAG	C2-N2-C7	10.89	137.49	122.90
4	E	1	NAG	C2-N2-C7	10.80	137.37	122.90

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	E	5	MAN	C1
4	I	5	MAN	C1
6	H	4	FUC	C1

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	NAG	C1-C2-N2-C7
4	E	1	NAG	C1-C2-N2-C7
4	I	1	NAG	C1-C2-N2-C7
6	H	1	NAG	C1-C2-N2-C7
2	C	2	NAG	O5-C5-C6-O6

All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	6	MAN	C1-C2-C3-C4-C5-O5
4	I	6	MAN	C1-C2-C3-C4-C5-O5
3	D	3	BMA	C1-C2-C3-C4-C5-O5
6	H	3	BMA	C1-C2-C3-C4-C5-O5

22 monomers are involved in 70 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1	NAG	10	0
2	G	1	NAG	2	0
6	H	3	BMA	1	0
3	D	4	FUL	3	9
5	F	2	NDG	2	0
5	J	2	NDG	2	0
4	E	3	BMA	2	0
4	E	4	MAN	1	8
4	E	5	MAN	1	4
2	C	2	NAG	2	0

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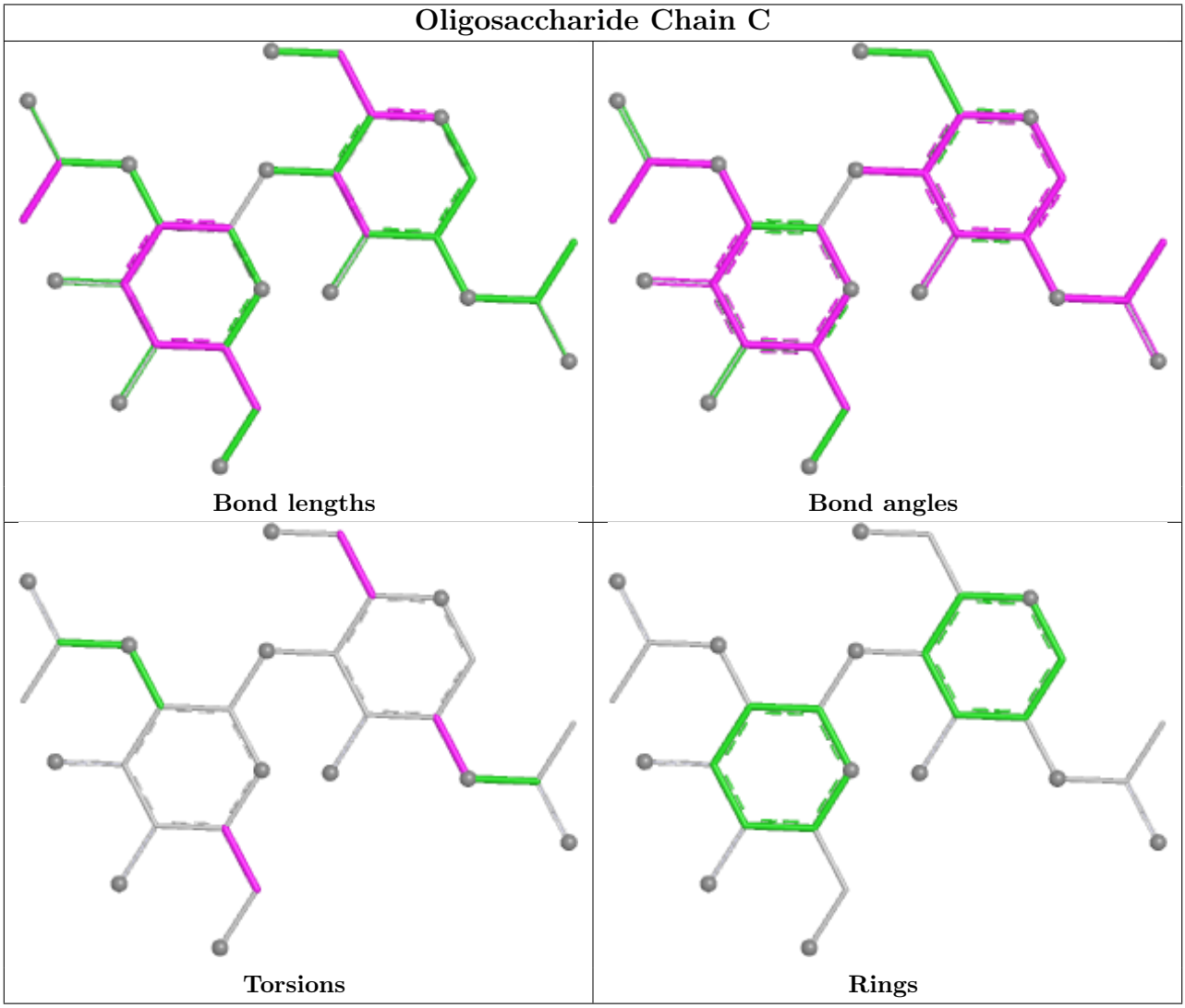
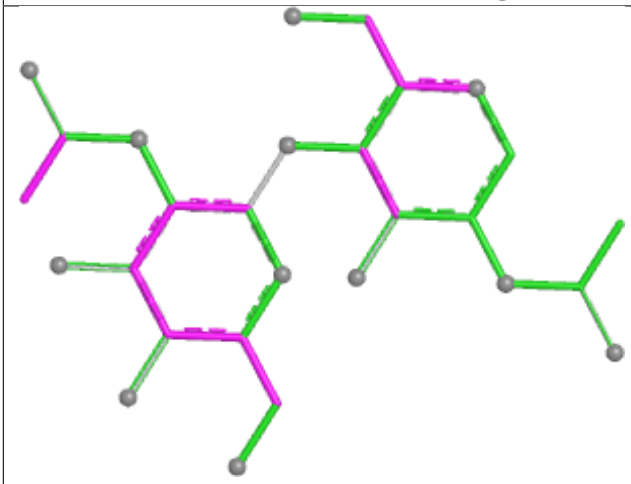
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	2	NAG	16	8
2	G	2	NAG	3	0
6	H	2	NAG	4	0
4	I	1	NAG	4	0
6	H	4	FUC	3	0
4	I	4	MAN	1	0
3	D	2	NAG	4	0
4	I	3	BMA	2	0
2	C	1	NAG	2	0
3	D	3	BMA	1	9
4	I	5	MAN	1	0
4	I	2	NAG	4	1

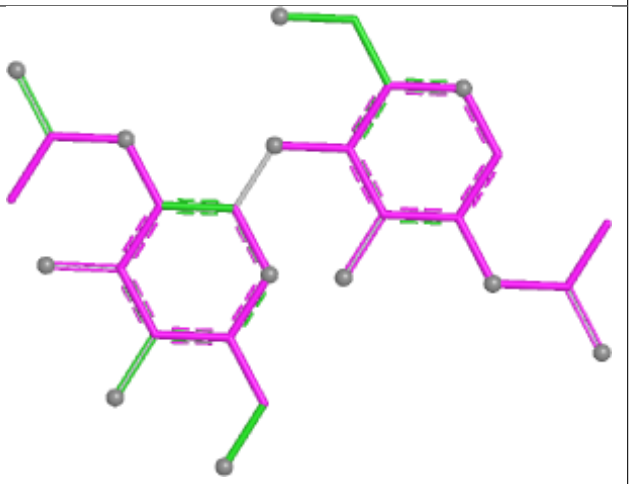
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



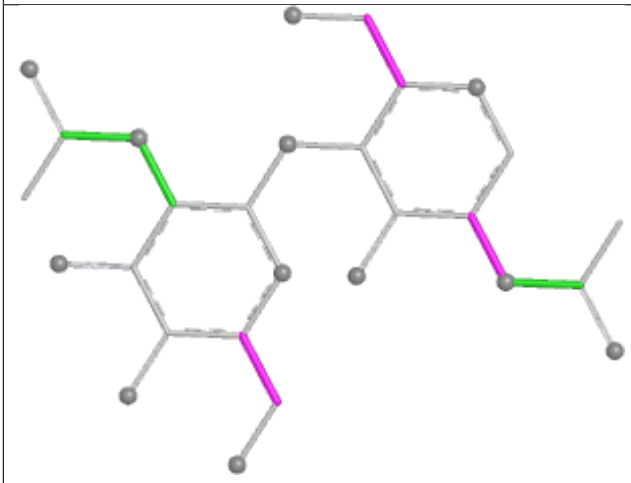
Oligosaccharide Chain G



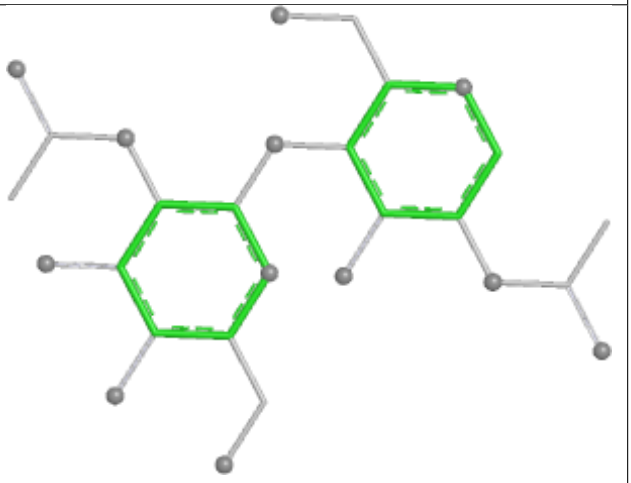
Bond lengths



Bond angles

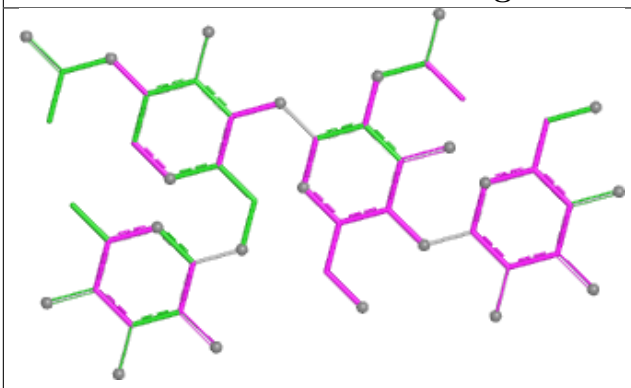


Torsions

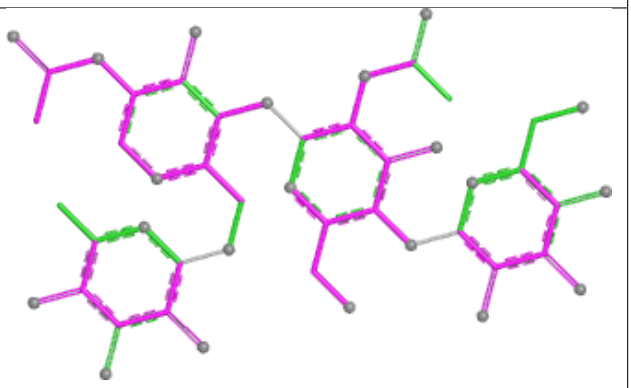


Rings

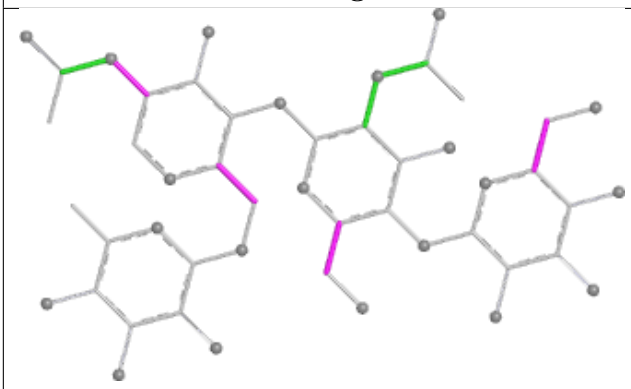
Oligosaccharide Chain D



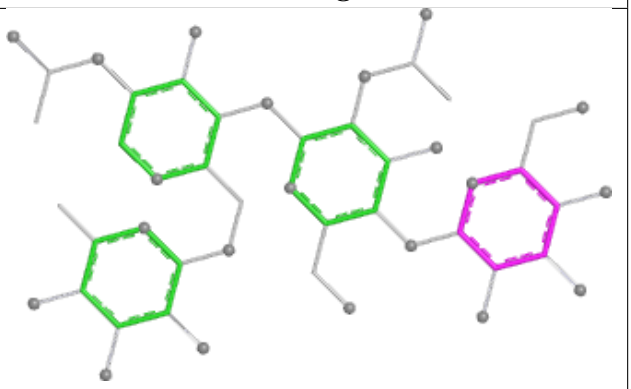
Bond lengths



Bond angles

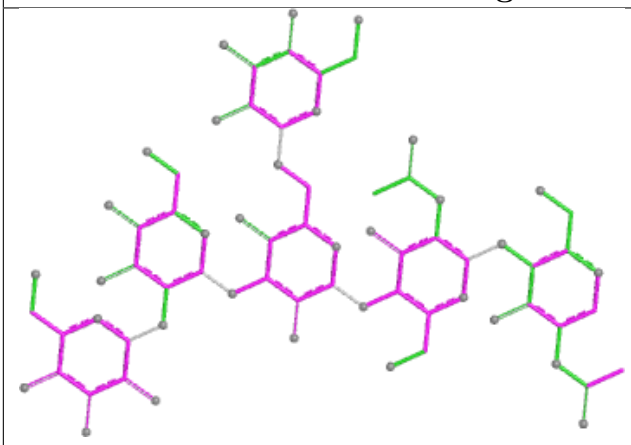


Torsions

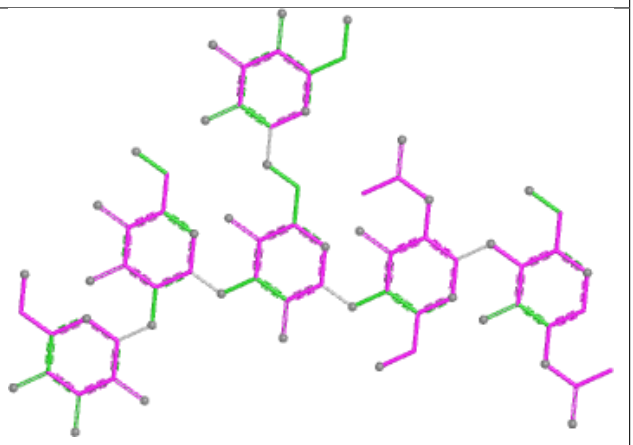


Rings

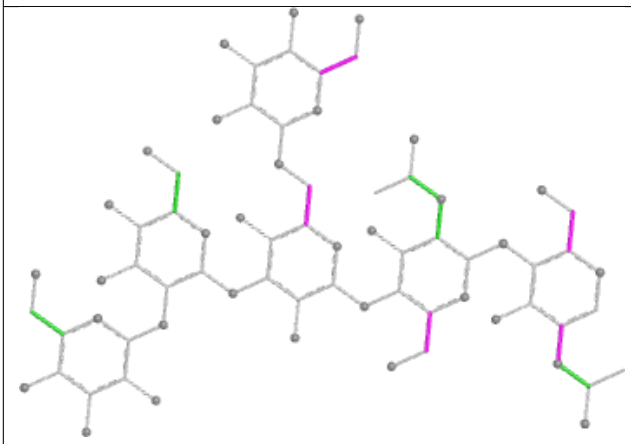
Oligosaccharide Chain E



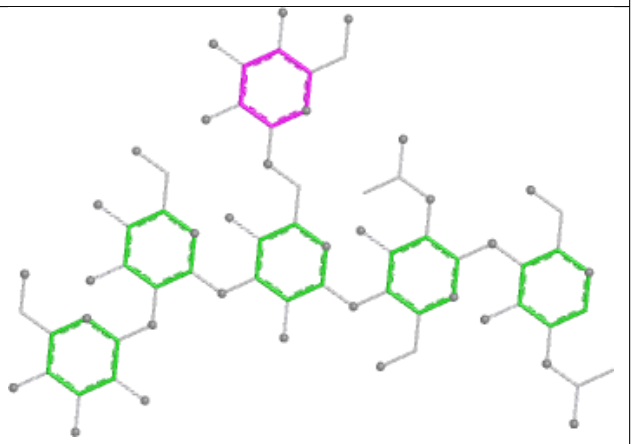
Bond lengths



Bond angles

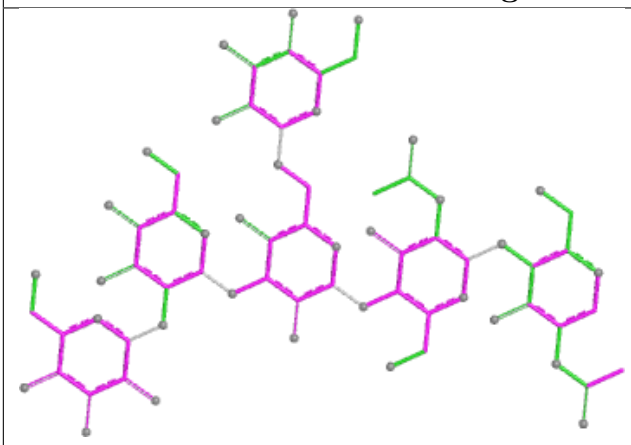


Torsions

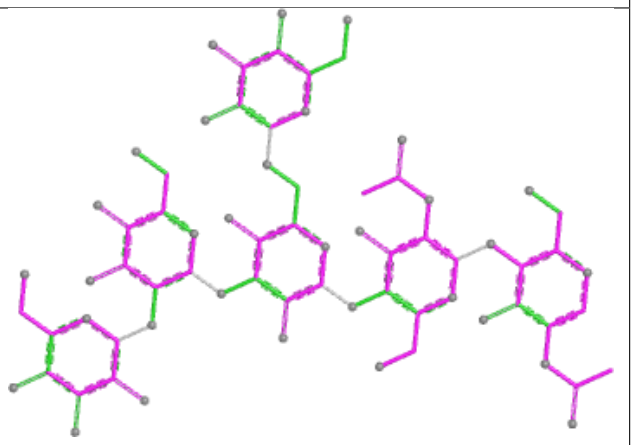


Rings

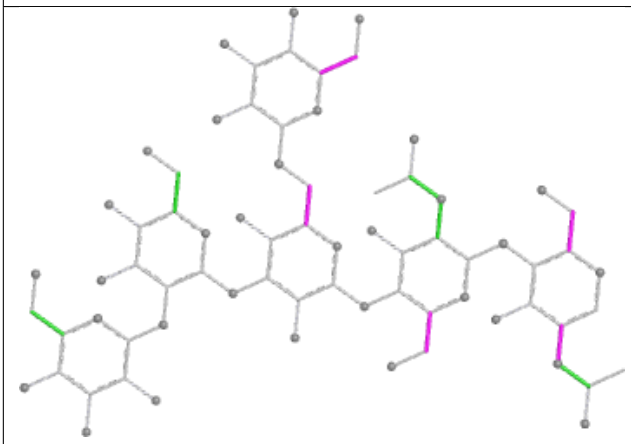
Oligosaccharide Chain I



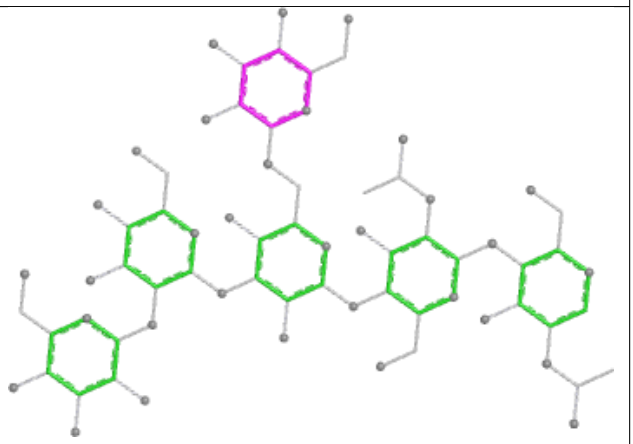
Bond lengths



Bond angles

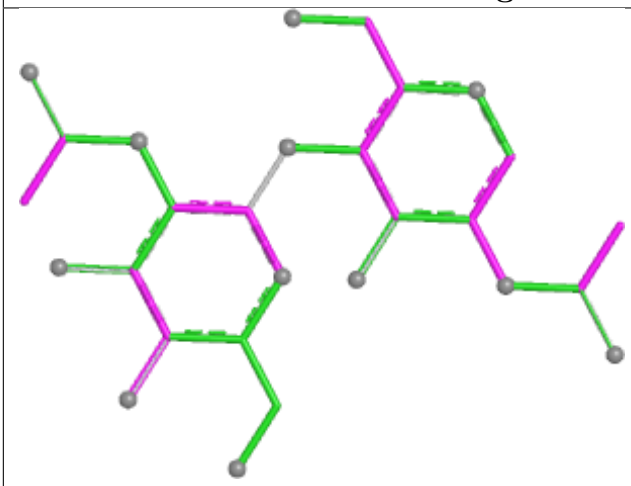


Torsions

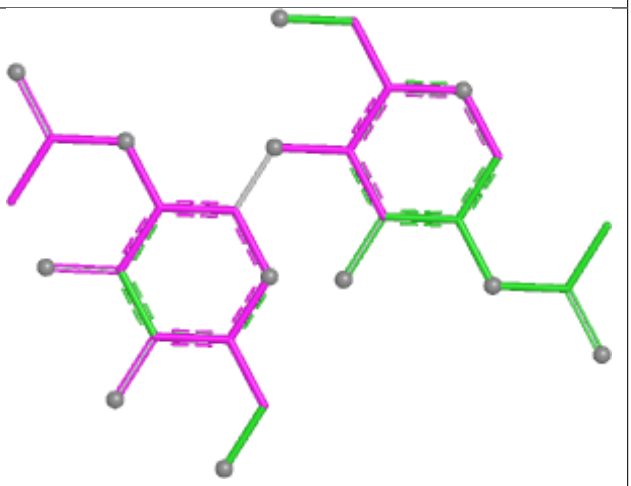


Rings

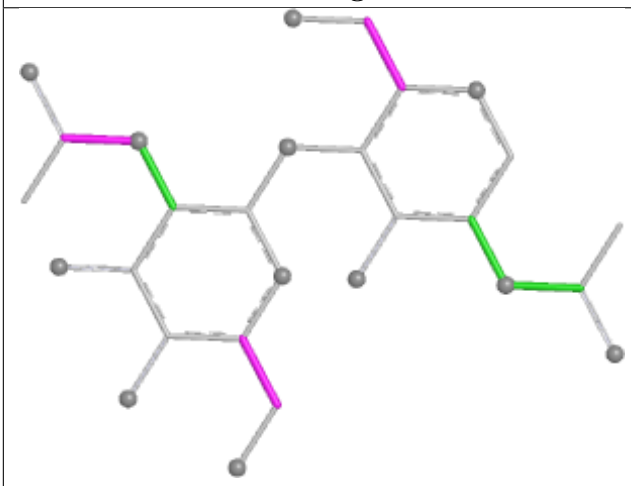
Oligosaccharide Chain F



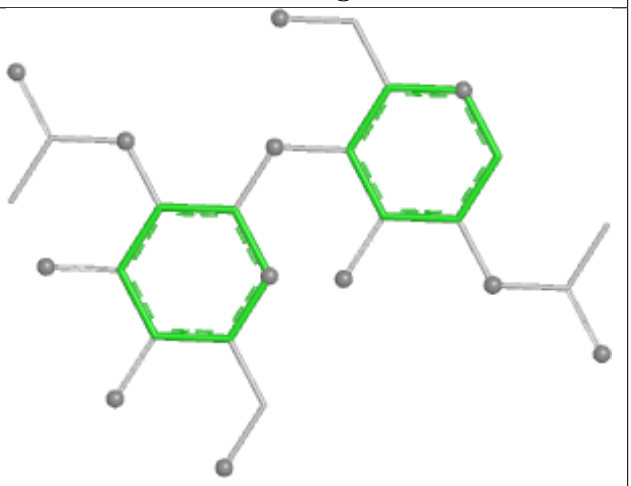
Bond lengths



Bond angles

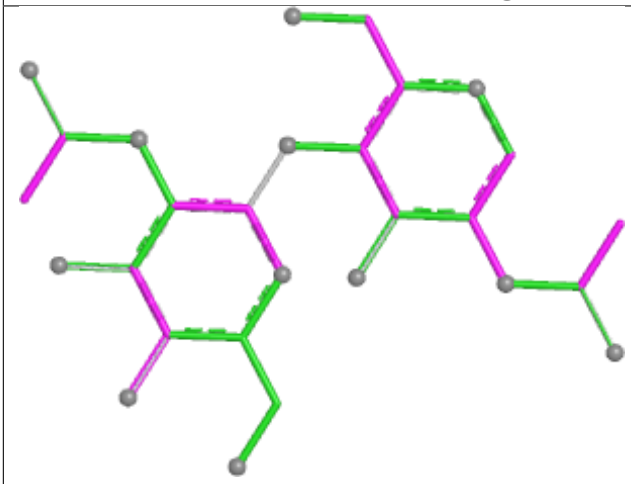


Torsions

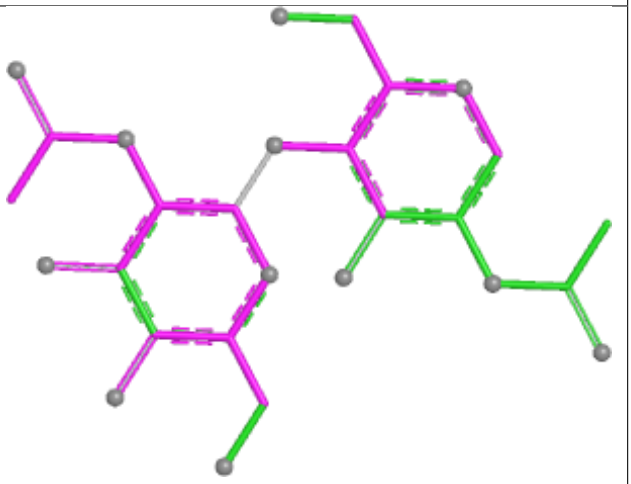


Rings

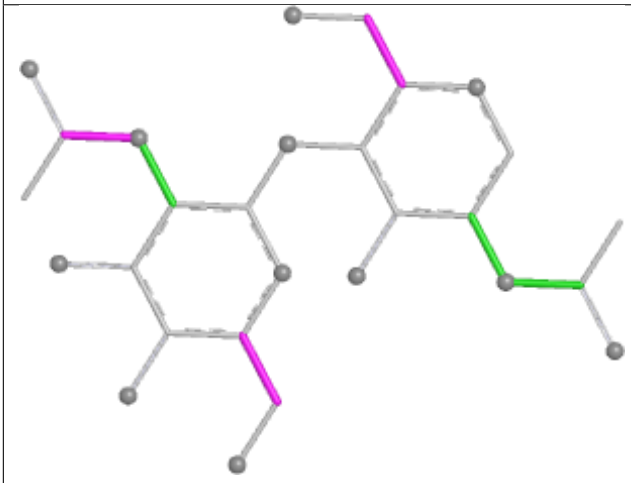
Oligosaccharide Chain J



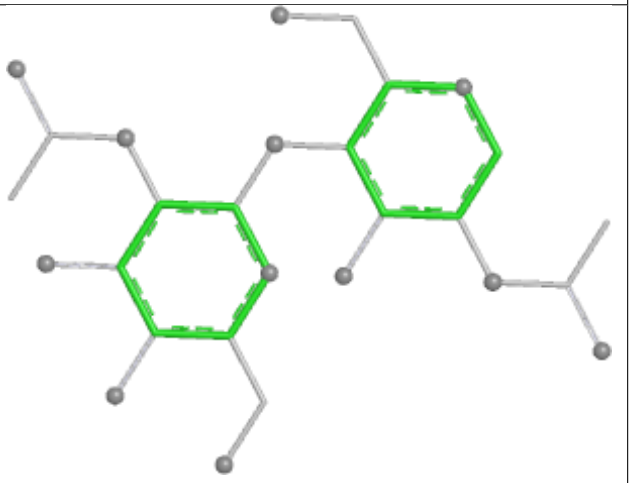
Bond lengths



Bond angles

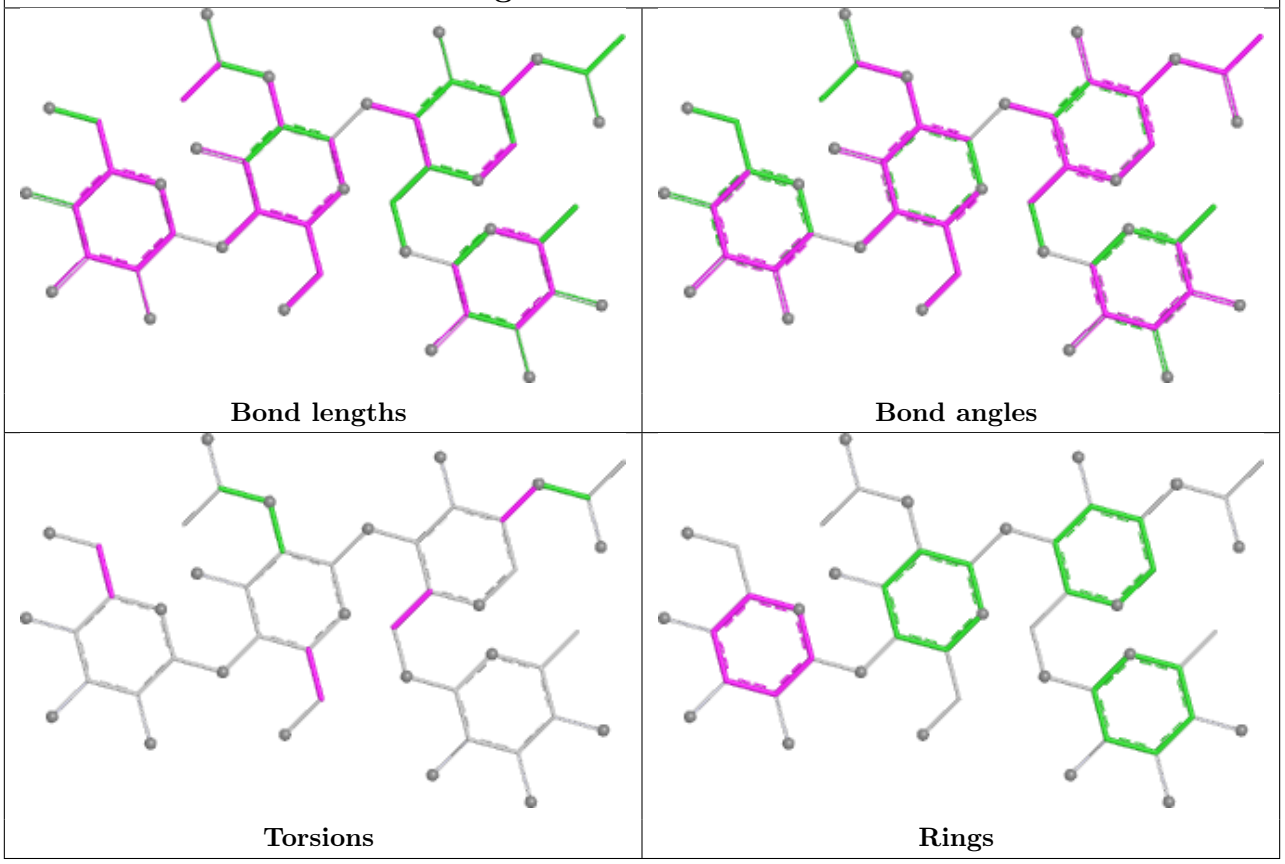


Torsions



Rings

Oligosaccharide Chain H



5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	ST3	A	471	-	14,14,14	1.49	1 (7%)	19,19,19	1.95	2 (10%)
8	ST3	B	471	-	14,14,14	1.49	1 (7%)	19,19,19	1.95	2 (10%)

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	ST3	A	471	-	-	7/8/8/8	0/1/1/1
8	ST3	B	471	-	-	7/8/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	471	ST3	C1-C'	-4.53	1.39	1.49
8	B	471	ST3	C1-C'	-4.53	1.39	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	471	ST3	C4-N4-C4'	-7.06	110.46	127.50
8	B	471	ST3	C4-N4-C4'	-7.06	110.46	127.50
8	A	471	ST3	CM4-C4'-N4	3.16	119.70	114.95
8	B	471	ST3	CM4-C4'-N4	3.16	119.70	114.95

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	471	ST3	O2'-C'-C1-C6
8	A	471	ST3	O4'-C4'-N4-C4
8	A	471	ST3	CM4-C4'-N4-C4
8	B	471	ST3	O2'-C'-C1-C6
8	B	471	ST3	O4'-C4'-N4-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	471	ST3	2	0
8	B	471	ST3	1	0

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

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	388/388 (100%)	-0.25	3 (0%)	82	80	4, 11, 18, 25	0
1	B	388/388 (100%)	-0.20	2 (0%)	87	85	4, 11, 18, 25	0
All	All	776/776 (100%)	-0.23	5 (0%)	85	83	4, 11, 18, 25	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	386	PRO	3.0
1	A	246	ALA	2.6
1	A	345	GLY	2.4
1	B	455	THR	2.1
1	B	249	ARG	2.0

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
4	MAN	I	5	11/12	0.29	0.17	15,15,31,33	0
3	BMA	D	3	11/12	0.52	0.19	15,15,32,33	0
6	BMA	H	3	11/12	0.57	0.16	15,15,32,33	0
4	MAN	E	5	11/12	0.65	0.20	15,15,31,33	0

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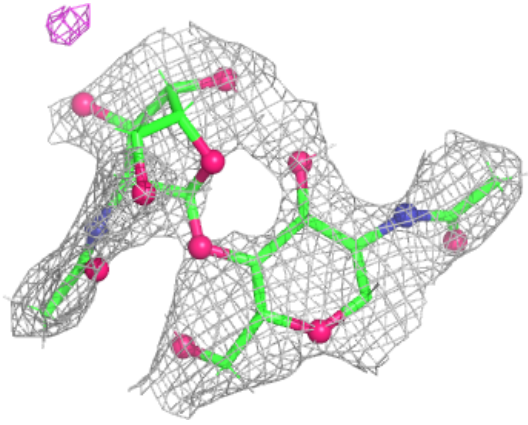
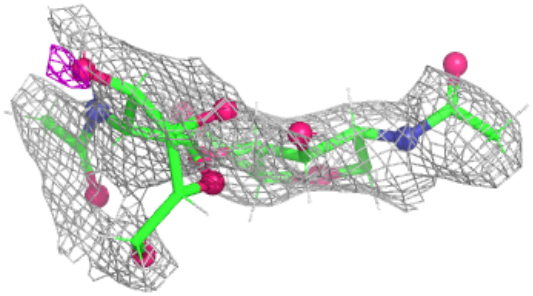
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	BMA	E	3	11/12	0.65	0.14	15,26,30,31	0
4	MAN	E	4	11/12	0.65	0.17	15,15,29,29	0
5	NDG	F	2	14/15	0.66	0.16	15,15,35,37	0
4	NAG	I	2	14/15	0.66	0.13	15,15,27,28	0
6	FUC	H	4	10/11	0.68	0.17	15,15,25,27	0
2	NAG	G	2	14/15	0.69	0.17	15,15,30,31	0
4	NAG	E	1	14/15	0.70	0.19	11,15,22,24	0
4	MAN	I	4	11/12	0.77	0.12	15,15,29,29	0
4	MAN	E	6	11/12	0.78	0.12	15,15,29,32	0
3	NAG	D	2	14/15	0.80	0.12	15,15,32,34	0
4	NAG	E	2	14/15	0.80	0.13	15,15,27,28	0
6	NAG	H	1	14/15	0.81	0.11	15,16,24,29	0
4	MAN	I	6	11/12	0.82	0.12	15,15,29,32	0
4	BMA	I	3	11/12	0.83	0.10	15,26,30,31	0
3	NAG	D	1	14/15	0.83	0.12	15,16,24,29	0
3	FUL	D	4	10/11	0.84	0.10	15,15,25,27	0
6	NAG	H	2	14/15	0.84	0.16	15,15,32,34	0
2	NAG	C	2	14/15	0.85	0.11	15,15,30,31	0
5	NDG	J	2	14/15	0.85	0.17	15,15,35,37	0
4	NAG	I	1	14/15	0.88	0.12	11,15,22,24	0
2	NAG	G	1	14/15	0.88	0.09	15,15,26,27	0
5	NAG	F	1	14/15	0.88	0.08	15,15,25,26	0
5	NAG	J	1	14/15	0.89	0.08	15,15,25,26	0
2	NAG	C	1	14/15	0.90	0.09	15,15,26,27	0

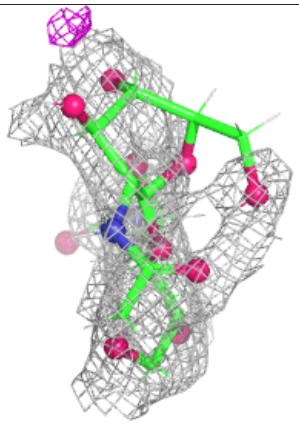
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

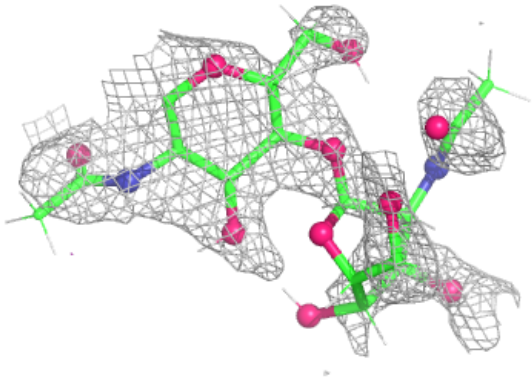


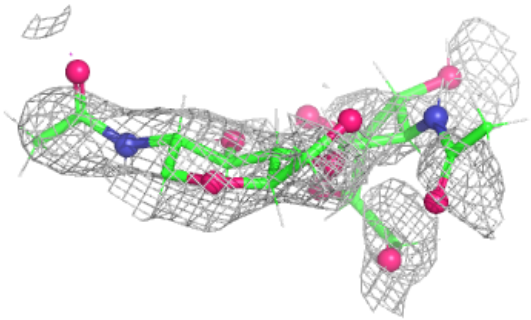


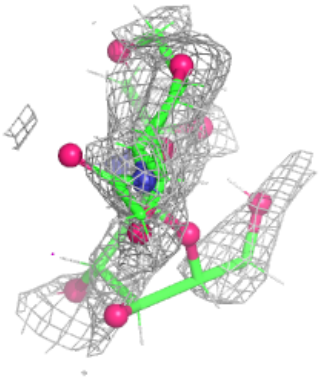


Electron density around Chain G:

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

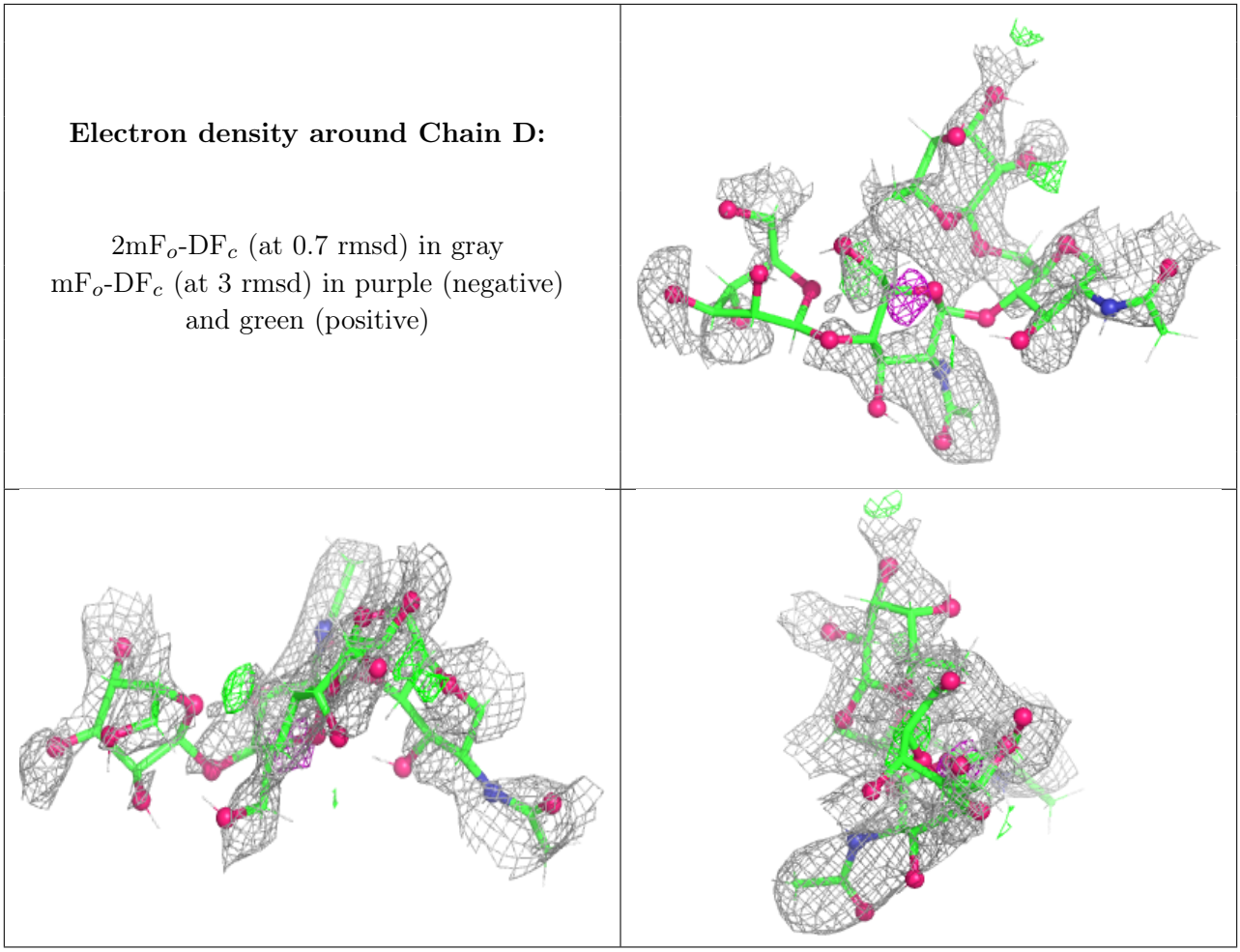






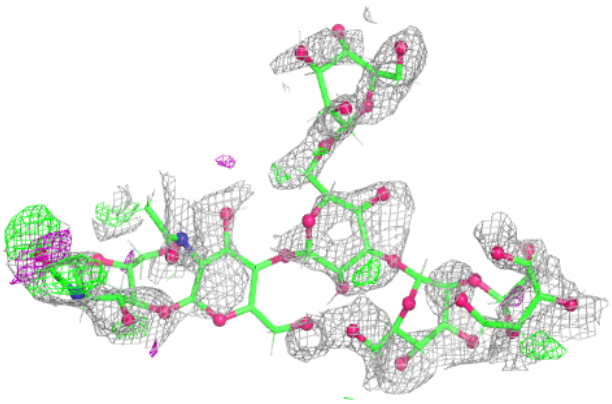
Electron density around Chain D:

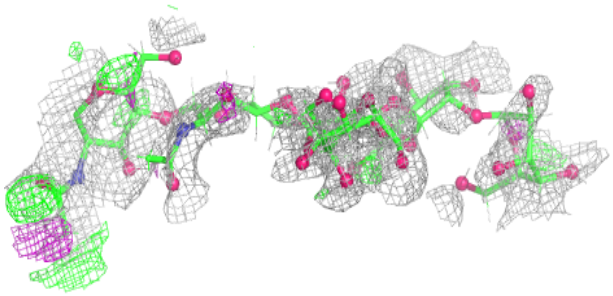
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

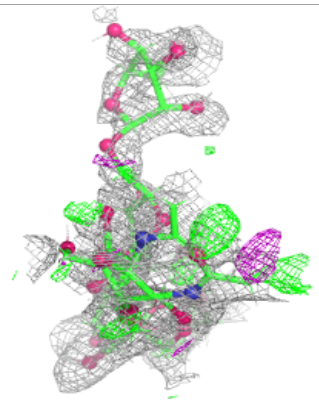


Electron density around Chain E:

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

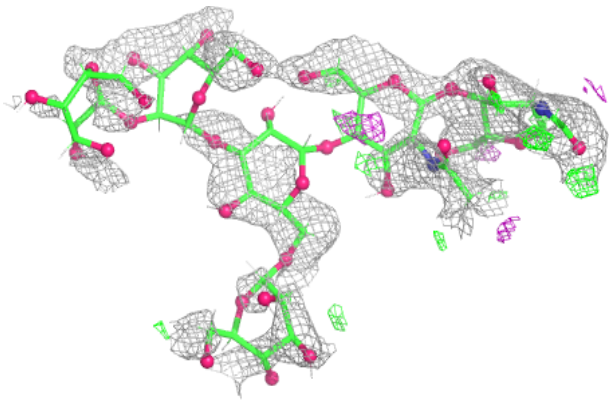


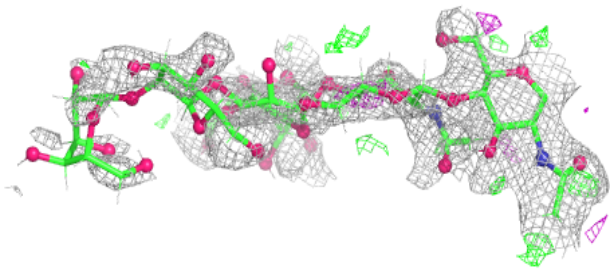


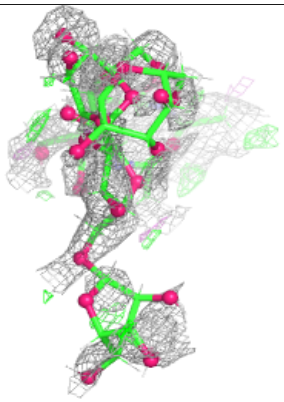


Electron density around Chain I:

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

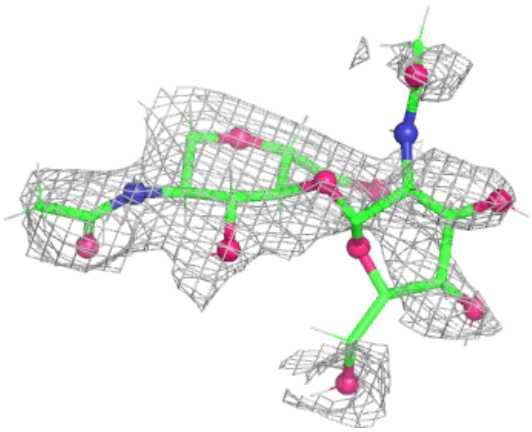


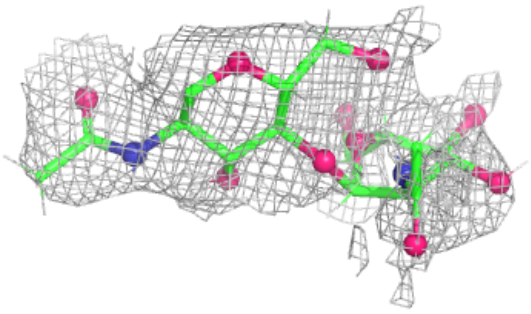


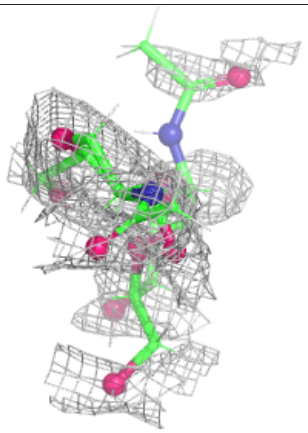


Electron density around Chain F:

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

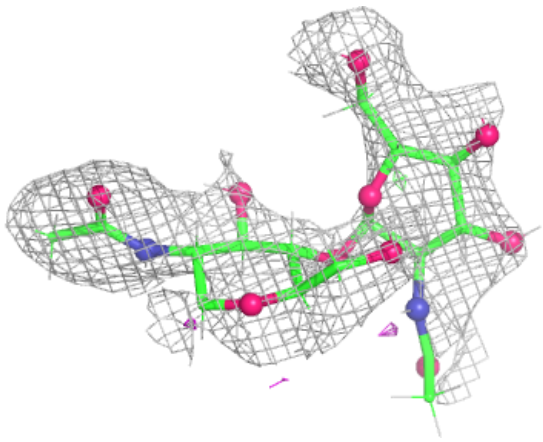


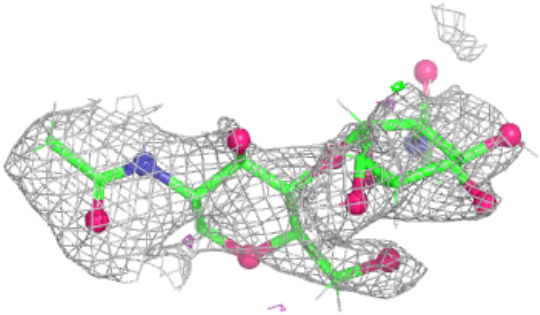


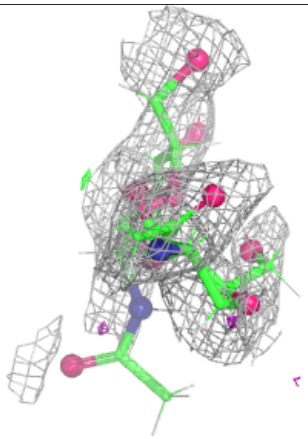


Electron density around Chain J:

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

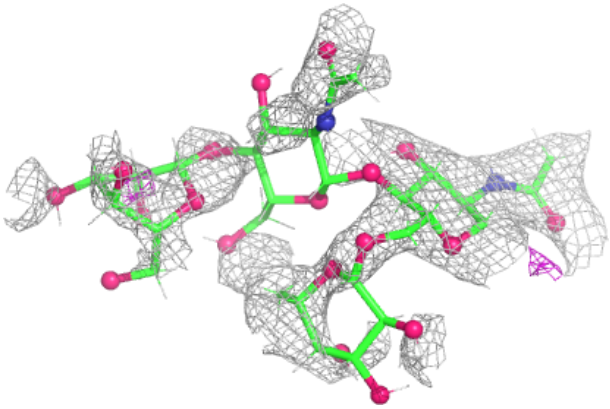


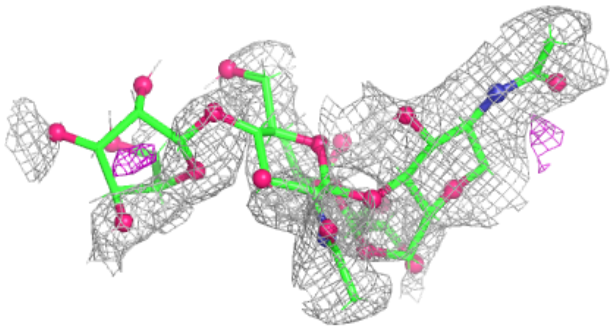


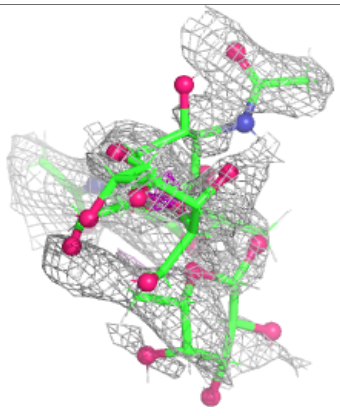


Electron density around Chain H:

$2mF_o$-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
8	ST3	B	471	14/14	0.86	0.14	12,18,22,24	0
8	ST3	A	471	14/14	0.91	0.12	12,18,22,24	0
7	CA	A	470	1/1	0.91	0.06	14,14,14,14	0
7	CA	B	470	1/1	0.98	0.06	14,14,14,14	0

6.5 Other polymers

There are no such residues in this entry.