Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2023 – 05:44 AM EDT

PDB ID	:	6UQC
Title	:	Mouse IgG2a Bispecific Fc
Authors	:	Wang, F.; Tsai, J.C.; Davis, J.H.; West, S.M.; Strop, P.
Deposited on	:	2019-10-18
Resolution	:	1.87 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

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

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

MolProbity	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.87 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8155 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 Ig gamma-2A chain C region, membrane-bound form.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	207	Total	C	N	O	S	0	8	0
			1733	1096	292	335	10			
1	D	207	Total	C	N	O	S	0	8	0
			1733	1096	292	335	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	356	LYS	GLU	microheterogeneity	UNP P01865
C	364	SER	THR	microheterogeneity	UNP P01865
C	409	ASP	LYS	microheterogeneity	UNP P01865
C	411	THR	ARG	microheterogeneity	UNP P01865
D	356	LYS	GLU	microheterogeneity	UNP P01865
D	364	SER	THR	microheterogeneity	UNP P01865
D	409	ASP	LYS	microheterogeneity	UNP P01865
D	411	THR	ARG	microheterogeneity	UNP P01865

- Molecule 2 is a protein called Ig gamma-2A chain C region, membrane-bound form.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	207	Total	C	N	O	S	0	8	0
			1733	1096	292	335	10			
2	F	207	Total	C	N	O	S	0	8	0
			1733	1096	292	335	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	368	LEU	MET	microheterogeneity	UNP P01865
E	370	LYS	THR	microheterogeneity	UNP P01865
E	399	LYS	ASP	microheterogeneity	UNP P01865
E	439	GLU	LYS	microheterogeneity	UNP P01865

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Chain	Residue	Modelled	Actual	Comment	Reference
F	368	LEU	MET	microheterogeneity	UNP P01865
F	370	LYS	THR	microheterogeneity	UNP P01865
F	399	LYS	ASP	microheterogeneity	UNP P01865
F	439	GLU	LYS	microheterogeneity	UNP P01865

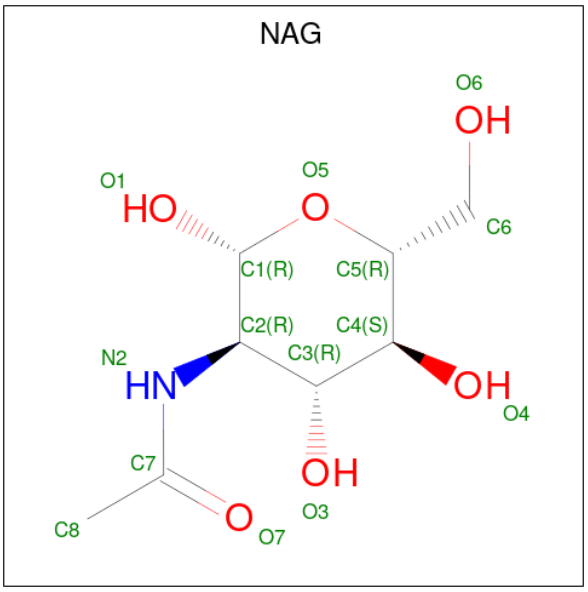
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	A	6	Total	C	N	O	0	0	0
			75	42	3	30			
3	B	6	Total	C	N	O	0	0	0
			75	42	3	30			

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

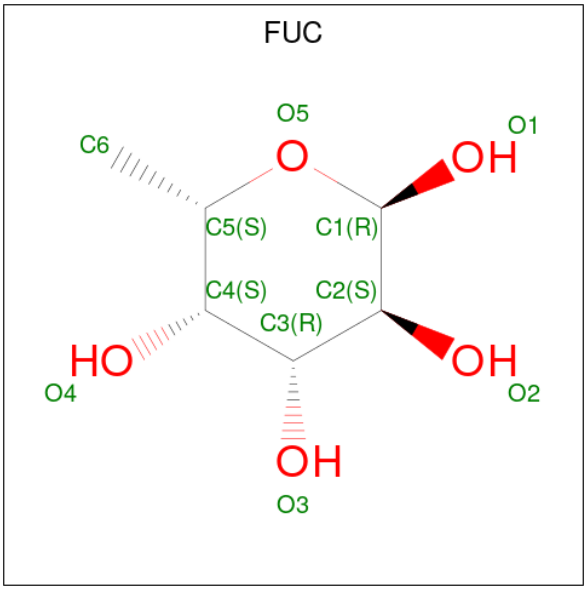
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	7	Total	C	N	O	0	0	0
			89	50	4	35			
4	H	7	Total	C	N	O	0	0	0
			89	50	4	35			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is alpha-L-fucopyranose (three-letter code: FUC) (formula: $C_6H_{12}O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	O		0	0
			10	6	4			
6	D	1	Total	C	O		0	0
			10	6	4			

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	F	1	Total C O 10 6 4	0	0
6	F	1	Total C O 10 6 4	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	192	Total O 192 192	0	0
7	D	190	Total O 190 190	0	0
7	E	205	Total O 205 205	0	0
7	F	240	Total O 240 240	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	64.27Å 64.40Å 88.98Å 76.19° 72.17° 61.48°	Depositor
Resolution (Å)	35.65 – 1.87	Depositor
% Data completeness (in resolution range)	84.8 (35.65-1.87)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.11 (at 1.87Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.194 , 0.229	Depositor
Wilson B-factor (Å^2)	30.1	Xtriage
Anisotropy	0.542	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8155	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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.

4 Model quality

4.1 Standard geometry

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles

4.3.1 Protein backbone

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates

26 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	$\#\|Z\|>2$
3	NAG	A	1	1,3	14,14,15	0.26	0	17,19,21	0.43	0
3	NAG	A	2	3	14,14,15	0.45	0	17,19,21	0.54	0
3	BMA	A	3	3	11,11,12	0.78	0	15,15,17	0.95	2 (13%)
3	MAN	A	4	3	11,11,12	0.81	0	15,15,17	1.29	2 (13%)
3	NAG	A	5	3	14,14,15	0.49	0	17,19,21	0.51	0
3	MAN	A	6	3	11,11,12	0.84	0	15,15,17	1.00	1 (6%)
3	NAG	B	1	1,3	14,14,15	0.22	0	17,19,21	0.46	0
3	NAG	B	2	3	14,14,15	0.39	0	17,19,21	0.56	0
3	BMA	B	3	3	11,11,12	0.63	0	15,15,17	0.93	1 (6%)
3	MAN	B	4	3	11,11,12	0.90	0	15,15,17	1.18	2 (13%)
3	NAG	B	5	3	14,14,15	0.40	0	17,19,21	0.46	0
3	MAN	B	6	3	11,11,12	0.79	0	15,15,17	0.94	1 (6%)
4	NAG	G	1	2,4	14,14,15	0.30	0	17,19,21	0.48	0
4	NAG	G	2	4	14,14,15	0.55	0	17,19,21	0.65	0
4	BMA	G	3	4	11,11,12	0.84	0	15,15,17	0.93	0
4	MAN	G	4	4	11,11,12	1.02	1 (9%)	15,15,17	1.24	2 (13%)
4	NAG	G	5	4	14,14,15	0.29	0	17,19,21	0.49	0
4	MAN	G	6	4	11,11,12	0.87	0	15,15,17	1.03	2 (13%)
4	NAG	G	7	4	14,14,15	0.38	0	17,19,21	0.44	0
4	NAG	H	1	2,4	14,14,15	0.19	0	17,19,21	0.55	0
4	NAG	H	2	4	14,14,15	0.57	0	17,19,21	0.66	0
4	BMA	H	3	4	11,11,12	0.95	1 (9%)	15,15,17	0.81	1 (6%)
4	MAN	H	4	4	11,11,12	0.94	0	15,15,17	1.11	2 (13%)
4	NAG	H	5	4	14,14,15	0.37	0	17,19,21	0.48	0
4	MAN	H	6	4	11,11,12	0.75	0	15,15,17	1.13	2 (13%)
4	NAG	H	7	4	14,14,15	0.33	0	17,19,21	0.43	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
3	NAG	A	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2	3	-	0/6/23/26	0/1/1/1
3	BMA	A	3	3	-	0/2/19/22	0/1/1/1
3	MAN	A	4	3	-	1/2/19/22	0/1/1/1
3	NAG	A	5	3	-	0/6/23/26	0/1/1/1
3	MAN	A	6	3	-	0/2/19/22	0/1/1/1
3	NAG	B	1	1,3	-	0/6/23/26	0/1/1/1

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	4	MAN	O5-C1	-2.34	1.40	1.43
4	H	3	BMA	O5-C1	-2.30	1.40	1.43

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	4	MAN	C1-O5-C5	3.28	116.63	112.19
4	H	4	MAN	C1-O5-C5	3.10	116.39	112.19
4	G	4	MAN	O2-C2-C3	-3.07	103.98	110.14
4	H	6	MAN	O2-C2-C3	-2.99	104.14	110.14
3	A	4	MAN	O2-C2-C3	-2.94	104.25	110.14
4	G	4	MAN	C1-O5-C5	2.87	116.08	112.19
3	B	4	MAN	C1-O5-C5	2.84	116.05	112.19
4	G	6	MAN	C1-O5-C5	2.80	115.98	112.19
3	B	4	MAN	O2-C2-C3	-2.75	104.64	110.14
3	A	6	MAN	C1-O5-C5	2.52	115.61	112.19
3	B	6	MAN	C1-O5-C5	2.48	115.55	112.19
3	A	3	BMA	C1-O5-C5	2.33	115.35	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	3	BMA	C1-O5-C5	2.29	115.30	112.19
4	H	6	MAN	C1-O5-C5	2.18	115.15	112.19
4	H	3	BMA	C1-O5-C5	2.14	115.09	112.19
4	H	4	MAN	O2-C2-C3	-2.08	105.98	110.14
4	G	6	MAN	O2-C2-C3	-2.06	106.01	110.14
3	A	3	BMA	O2-C2-C3	-2.02	106.08	110.14

There are no chirality outliers.

All (12) torsion outliers are listed below:

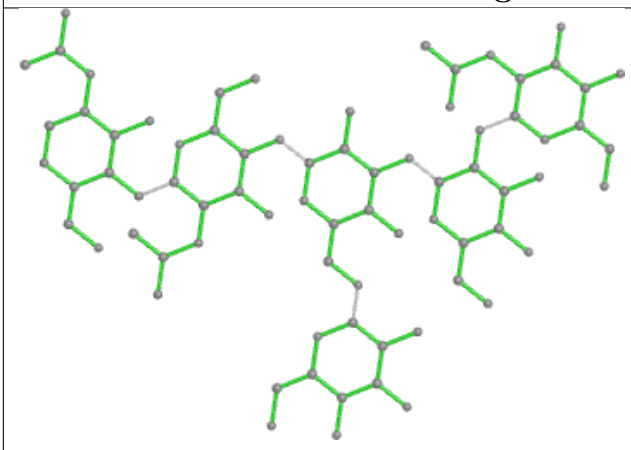
Mol	Chain	Res	Type	Atoms
4	G	5	NAG	O5-C5-C6-O6
4	G	5	NAG	C4-C5-C6-O6
4	H	7	NAG	O5-C5-C6-O6
4	H	7	NAG	C4-C5-C6-O6
4	G	7	NAG	O5-C5-C6-O6
4	G	7	NAG	C4-C5-C6-O6
4	H	4	MAN	C4-C5-C6-O6
3	B	4	MAN	C4-C5-C6-O6
3	A	4	MAN	C4-C5-C6-O6
4	G	4	MAN	C4-C5-C6-O6
4	H	4	MAN	O5-C5-C6-O6
4	G	6	MAN	O5-C5-C6-O6

There are no ring outliers.

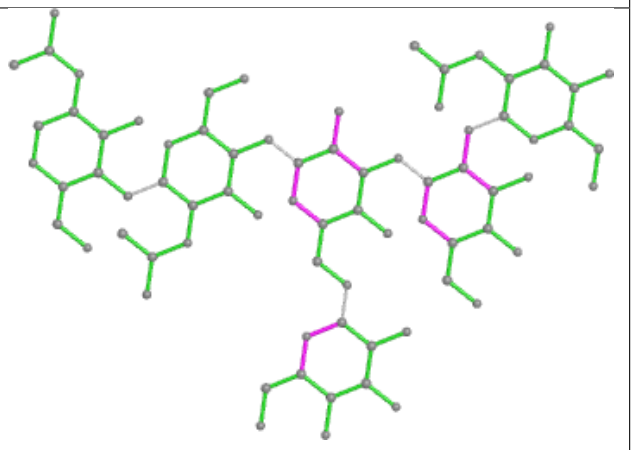
No monomer is involved in short contacts.

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

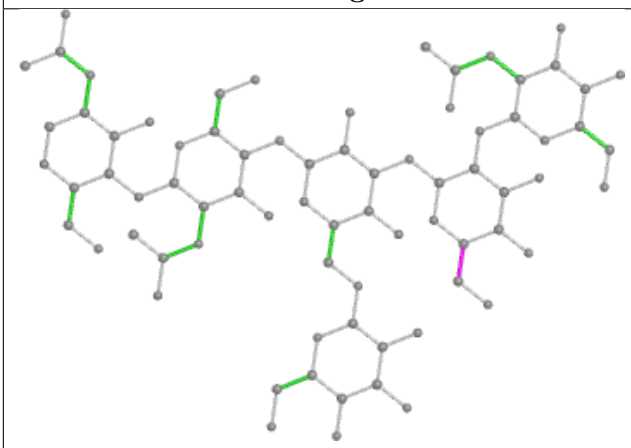
Oligosaccharide Chain A



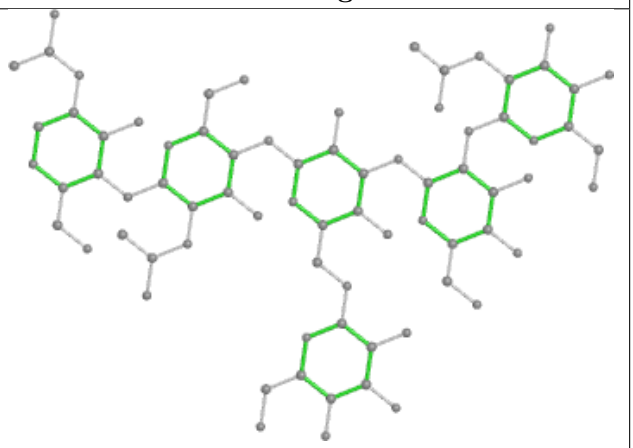
Bond lengths



Bond angles

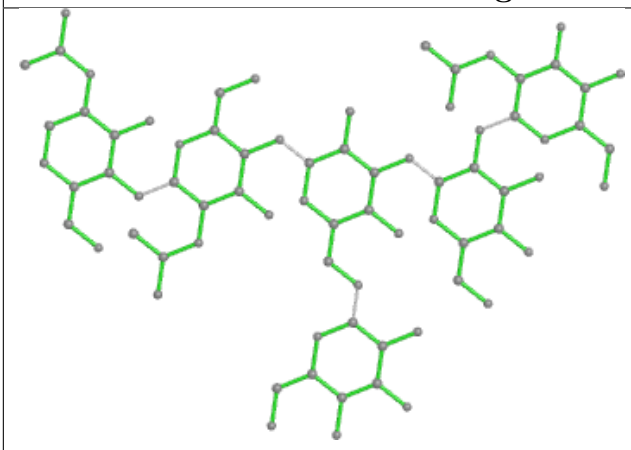


Torsions

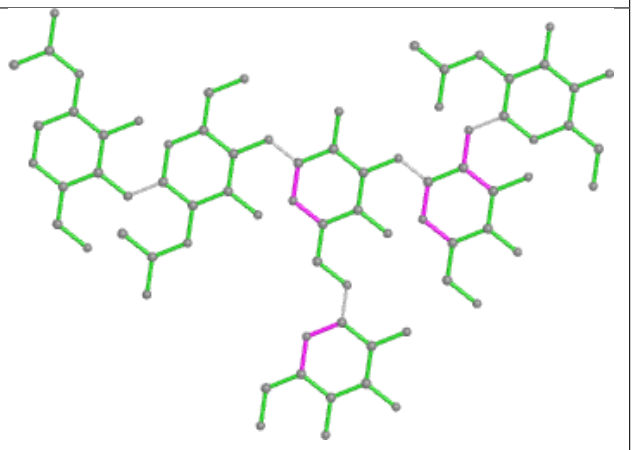


Rings

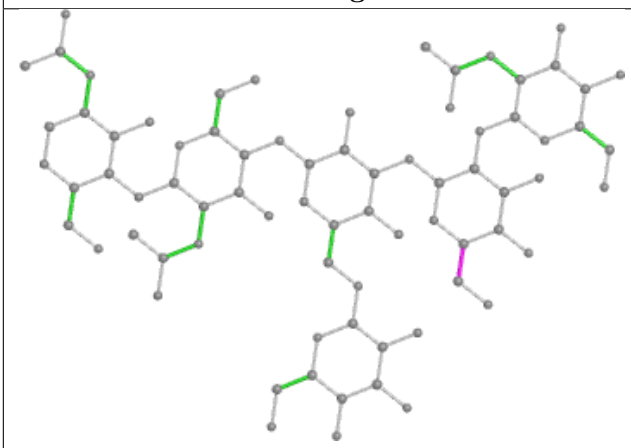
Oligosaccharide Chain B



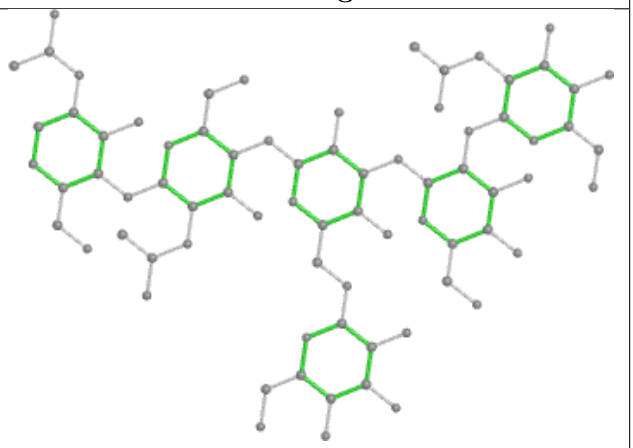
Bond lengths



Bond angles

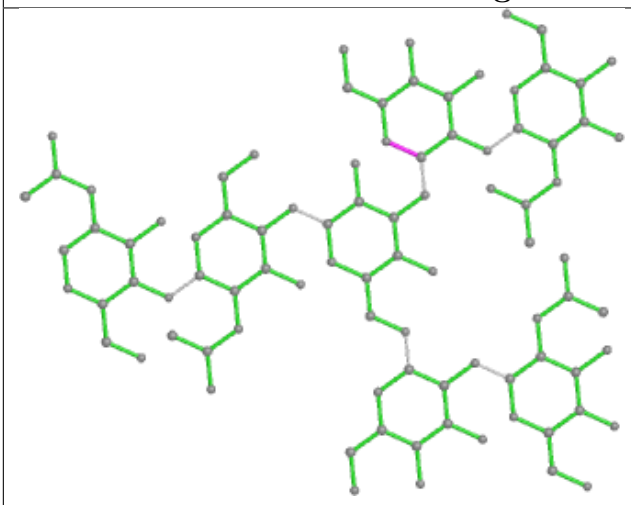


Torsions

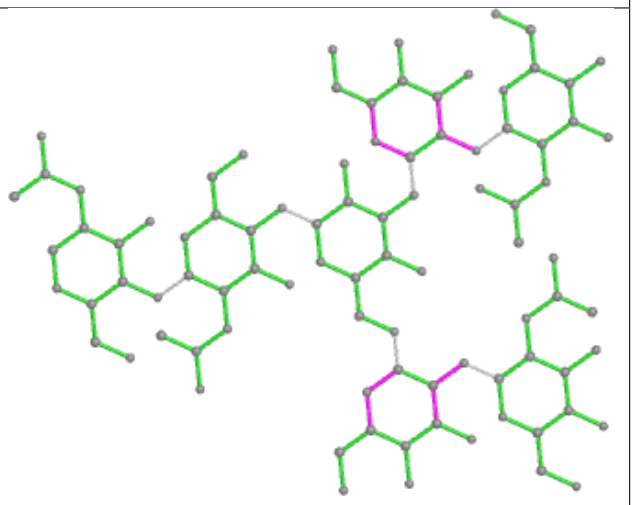


Rings

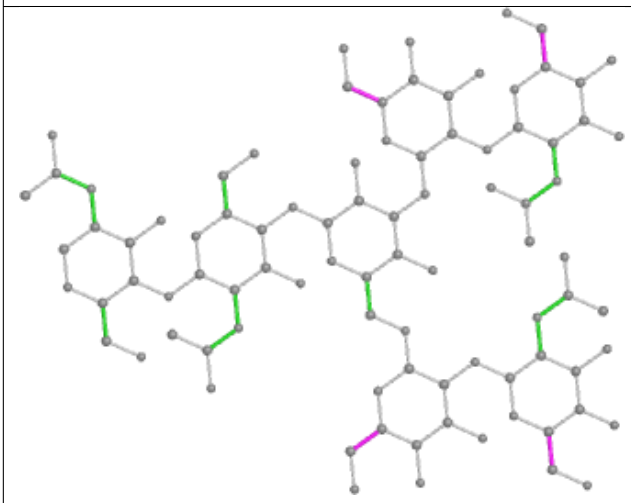
Oligosaccharide Chain G



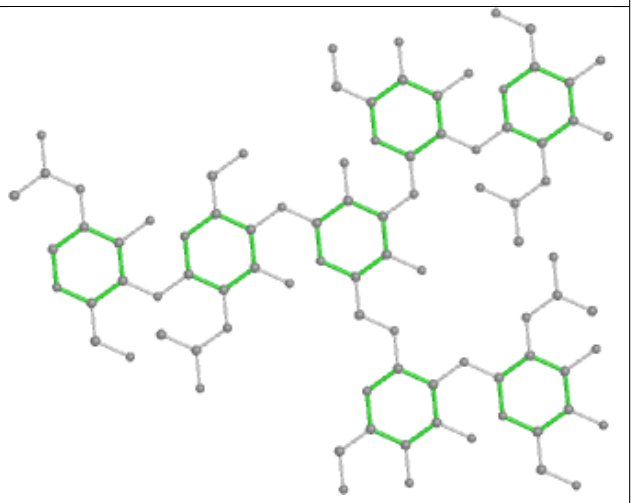
Bond lengths



Bond angles

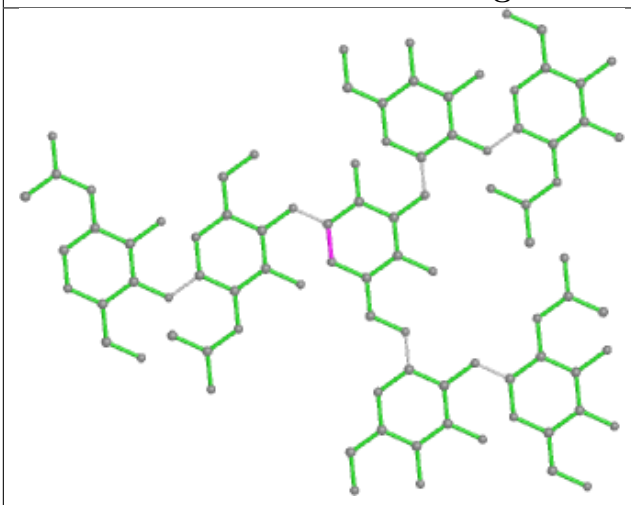


Torsions

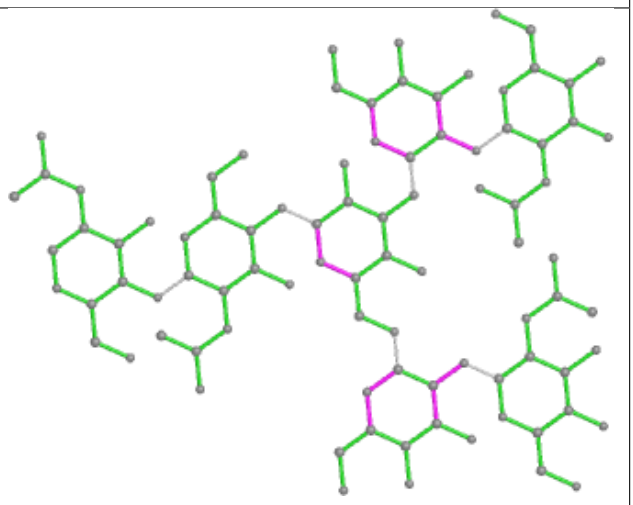


Rings

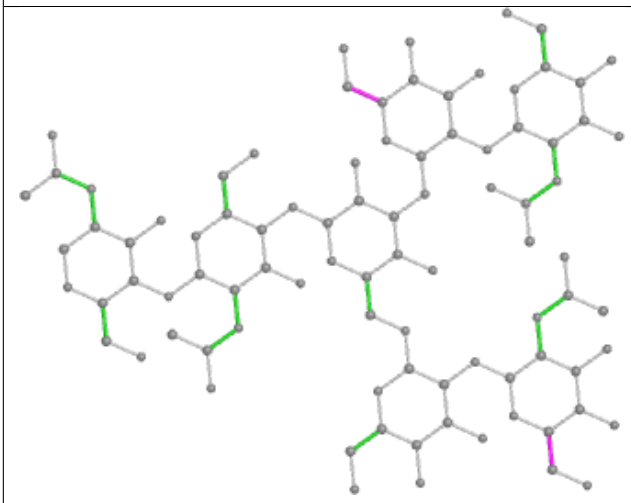
Oligosaccharide Chain H



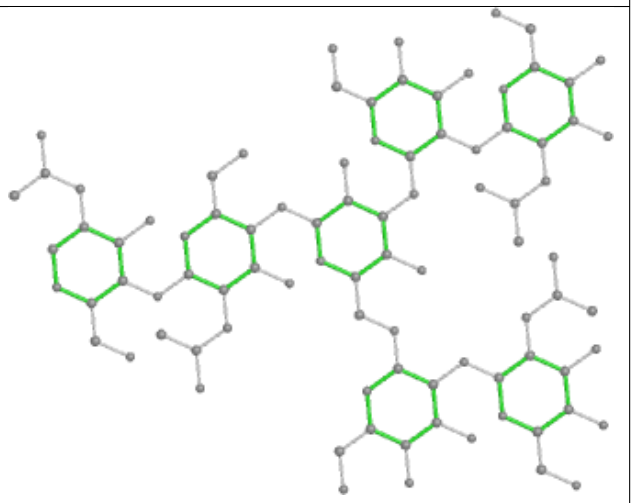
Bond lengths



Bond angles



Torsions



Rings

4.6 Ligand geometry

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	FUC	F	501	-	10,10,11	1.08	2 (20%)	14,14,16	1.94	4 (28%)
5	NAG	C	507	-	14,14,15	0.40	0	17,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	FUC	C	508	-	10,10,11	0.78	0	14,14,16	1.90	3 (21%)
6	FUC	D	508	-	10,10,11	0.85	0	14,14,16	1.91	4 (28%)
6	FUC	F	509	-	10,10,11	0.79	0	14,14,16	1.91	3 (21%)
5	NAG	D	507	-	14,14,15	0.35	0	17,19,21	0.47	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
6	FUC	F	501	-	-	-	0/1/1/1
5	NAG	C	507	-	-	2/6/23/26	0/1/1/1
6	FUC	C	508	-	-	-	0/1/1/1
6	FUC	D	508	-	-	-	0/1/1/1
6	FUC	F	509	-	-	-	0/1/1/1
5	NAG	D	507	-	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	501	FUC	O5-C5	2.21	1.48	1.43
6	F	501	FUC	C1-C2	2.08	1.56	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	D	508	FUC	O5-C1-C2	4.25	117.33	110.77
6	F	509	FUC	O5-C1-C2	4.24	117.31	110.77
6	C	508	FUC	O5-C1-C2	4.20	117.26	110.77
6	F	501	FUC	O5-C1-C2	3.80	116.63	110.77
6	C	508	FUC	C1-O5-C5	3.73	121.23	112.78
6	F	509	FUC	C1-O5-C5	3.67	121.10	112.78
6	F	501	FUC	C1-C2-C3	3.64	114.14	109.67
6	D	508	FUC	C1-O5-C5	3.63	121.00	112.78
6	F	501	FUC	C1-O5-C5	3.59	120.91	112.78
6	F	509	FUC	C1-C2-C3	3.16	113.55	109.67
6	D	508	FUC	C1-C2-C3	3.08	113.46	109.67
6	C	508	FUC	C1-C2-C3	3.04	113.40	109.67
6	F	501	FUC	O5-C5-C4	2.20	113.47	109.52
6	D	508	FUC	O5-C5-C4	2.14	113.36	109.52

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	507	NAG	O5-C5-C6-O6
5	C	507	NAG	O5-C5-C6-O6
5	D	507	NAG	C4-C5-C6-O6
5	C	507	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.