



wwPDB X-ray Structure Validation Summary Report

Sep 24, 2023 – 04:16 AM EDT

PDB ID : 5TG9
Title : Crystal structure of H15 hemagglutinin from A/shearwater/WA/2576/1979
H15N9 influenza virus in complex with 3'-SLN
Authors : Wilson, I.A.; Tzarum, N.
Deposited on : 2016-09-27
Resolution : 2.75 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  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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

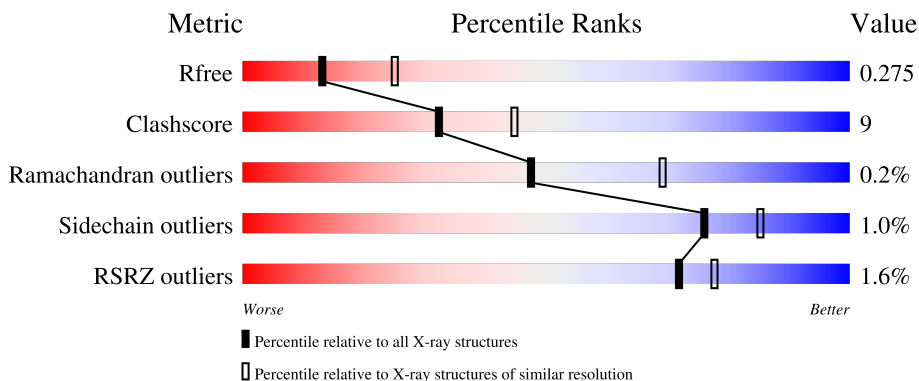
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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.



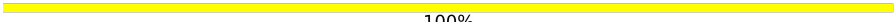

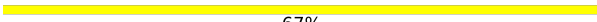

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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 $\leq 5\%$. 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	332	
1	C	332	
2	B	193	
2	D	193	
3	E	2	

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Mol	Chain	Length	Quality of chain
3	G	2	 100%
4	F	2	 100%
5	H	3	 67%  33%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8005 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	325	2497	1557	442	484	14	0	0	0
1	C	325	2497	1557	442	484	14	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ALA	-	expression tag	UNP L0L3X3
A	8	ASP	-	expression tag	UNP L0L3X3
A	9	PRO	-	expression tag	UNP L0L3X3
A	10	GLY	-	expression tag	UNP L0L3X3
C	7	ALA	-	expression tag	UNP L0L3X3
C	8	ASP	-	expression tag	UNP L0L3X3
C	9	PRO	-	expression tag	UNP L0L3X3
C	10	GLY	-	expression tag	UNP L0L3X3

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	168	1372	845	246	274	7	0	0	0
2	D	168	1372	845	246	274	7	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	SER	-	expression tag	UNP L0L3X3
B	178	GLY	-	expression tag	UNP L0L3X3
B	179	GLY	-	expression tag	UNP L0L3X3
B	180	GLY	-	expression tag	UNP L0L3X3

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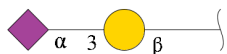
Chain	Residue	Modelled	Actual	Comment	Reference
B	181	GLY	-	expression tag	UNP L0L3X3
B	182	LEU	-	expression tag	UNP L0L3X3
B	183	ASN	-	expression tag	UNP L0L3X3
B	184	ASP	-	expression tag	UNP L0L3X3
B	185	ILE	-	expression tag	UNP L0L3X3
B	186	PHE	-	expression tag	UNP L0L3X3
B	187	GLU	-	expression tag	UNP L0L3X3
B	188	ALA	-	expression tag	UNP L0L3X3
B	189	GLN	-	expression tag	UNP L0L3X3
B	190	LYS	-	expression tag	UNP L0L3X3
D	177	SER	-	expression tag	UNP L0L3X3
D	178	GLY	-	expression tag	UNP L0L3X3
D	179	GLY	-	expression tag	UNP L0L3X3
D	180	GLY	-	expression tag	UNP L0L3X3
D	181	GLY	-	expression tag	UNP L0L3X3
D	182	LEU	-	expression tag	UNP L0L3X3
D	183	ASN	-	expression tag	UNP L0L3X3
D	184	ASP	-	expression tag	UNP L0L3X3
D	185	ILE	-	expression tag	UNP L0L3X3
D	186	PHE	-	expression tag	UNP L0L3X3
D	187	GLU	-	expression tag	UNP L0L3X3
D	188	ALA	-	expression tag	UNP L0L3X3
D	189	GLN	-	expression tag	UNP L0L3X3
D	190	LYS	-	expression tag	UNP L0L3X3

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



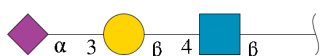
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose.



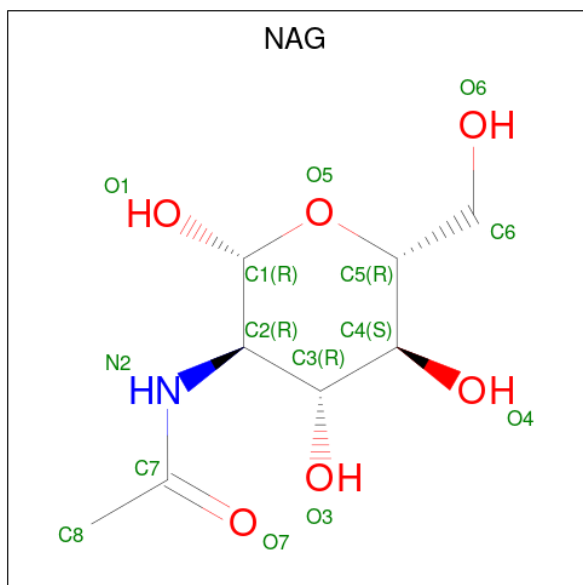
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	F	2	32	17	1	14	0	0	0

- Molecule 5 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	H	3	46	25	2	19	0	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

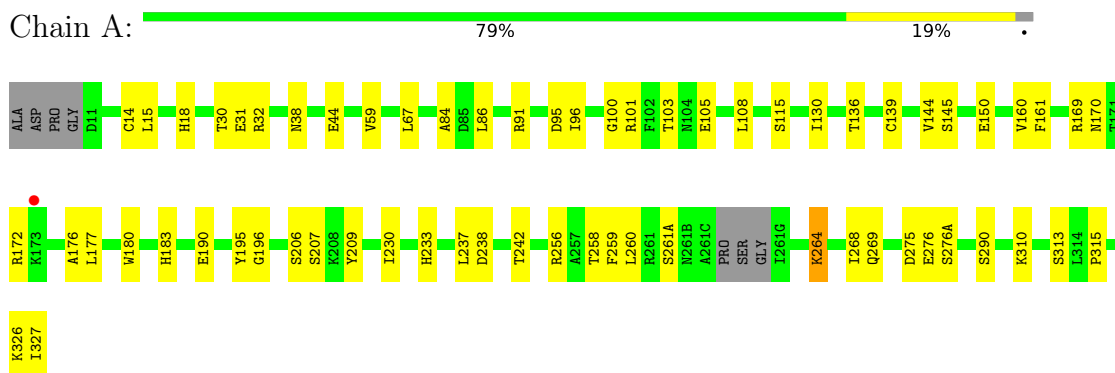
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	24	Total 24	O 24	0	0
7	B	25	Total 25	O 25	0	0
7	C	31	Total 31	O 31	0	0
7	D	25	Total 25	O 25	0	0

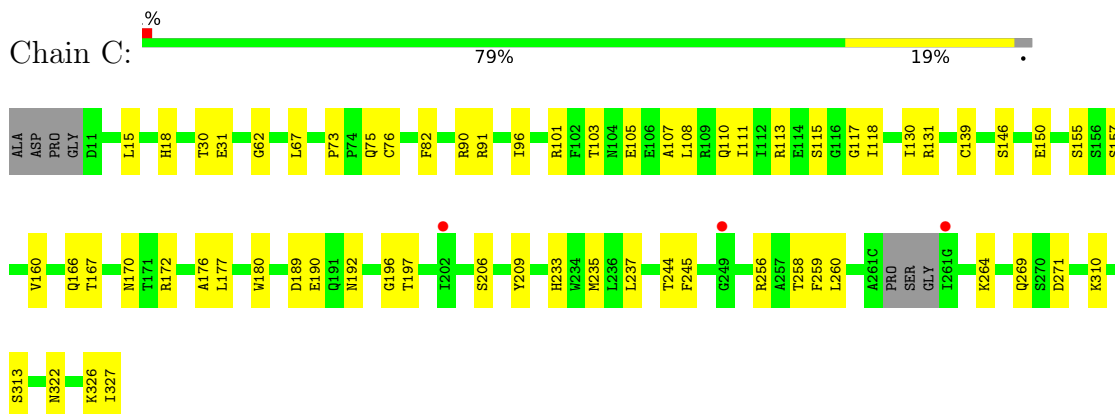
3 Residue-property plots [i](#)

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.

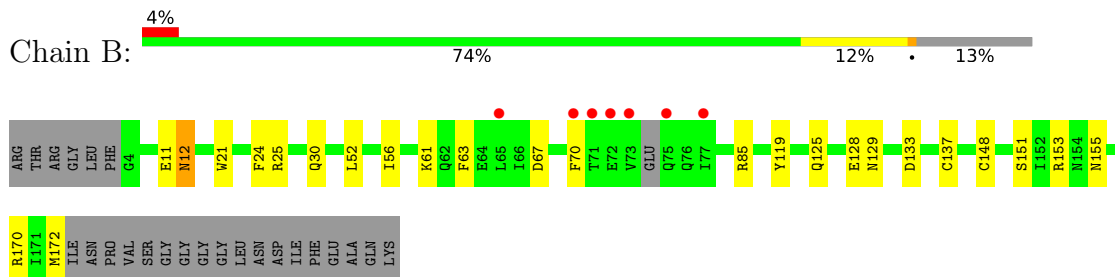
- Molecule 1: Hemagglutinin



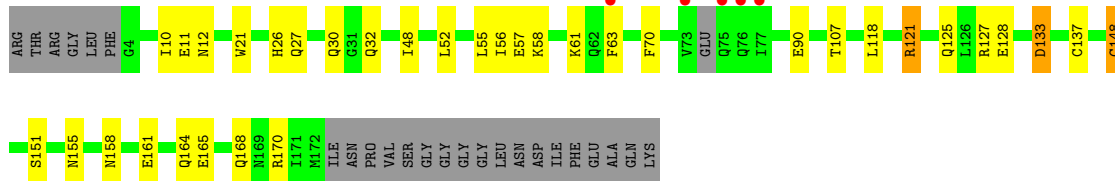
- Molecule 1: Hemagglutinin



- Molecule 2: Hemagglutinin HA2 chain



- Molecule 2: Hemagglutinin HA2 chain

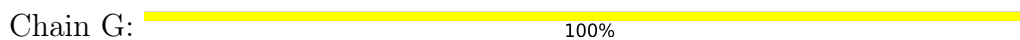


- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



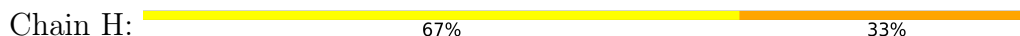
MAG1
MAG2

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose



GAL1
STA2

- Molecule 5: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
GAL2
STA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	116.68Å 116.68Å 129.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.28 – 2.75 43.28 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.3 (43.28-2.75) 89.5 (43.28-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.222 , 0.275 0.222 , 0.275	Depositor DCC
R_{free} test set	2504 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.605	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 11.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.440 for -h,-k,l 0.046 for h,-h-k,-l 0.044 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8005	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	1/2544 (0.0%)	0.68	0/3435
1	C	0.57	0/2544	0.67	0/3435
2	B	0.67	0/1394	0.69	0/1879
2	D	0.69	0/1394	0.73	0/1879
All	All	0.61	1/7876 (0.0%)	0.69	0/10628

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
2	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	CYS	CB-SG	-5.74	1.72	1.81

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	11	GLU	Peptide

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	2497	0	2455	52	0
1	C	2497	0	2455	47	0
2	B	1372	0	1282	19	0
2	D	1372	0	1280	26	0
3	E	28	0	25	2	0
3	G	28	0	25	0	0
4	F	32	0	28	2	0
5	H	46	0	40	2	0
6	B	14	0	13	0	0
6	D	14	0	13	3	0
7	A	24	0	0	6	0
7	B	25	0	0	4	0
7	C	31	0	0	3	0
7	D	25	0	0	6	0
All	All	8005	0	7616	137	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 9.

The worst 5 of 137 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:A:67:LEU:HB2	1:A:95:ASP:OD1	1.64	0.97
2:D:161:GLU:OE1	7:D:401:HOH:O	1.90	0.89
2:B:25:ARG:NH1	7:B:403:HOH:O	2.09	0.85
1:A:91:ARG:NH2	7:A:502:HOH:O	2.09	0.84
2:B:129:ASN:OD1	7:B:401:HOH:O	1.96	0.83

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	321/332 (97%)	307 (96%)	13 (4%)	1 (0%)	41	61
1	C	321/332 (97%)	299 (93%)	21 (6%)	1 (0%)	41	61
2	B	164/193 (85%)	162 (99%)	2 (1%)	0	100	100
2	D	164/193 (85%)	157 (96%)	7 (4%)	0	100	100
All	All	970/1050 (92%)	925 (95%)	43 (4%)	2 (0%)	47	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	264	LYS
1	C	264	LYS

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	276/280 (99%)	275 (100%)	1 (0%)	91	94
1	C	276/280 (99%)	275 (100%)	1 (0%)	91	94
2	B	144/163 (88%)	142 (99%)	2 (1%)	67	80
2	D	144/163 (88%)	140 (97%)	4 (3%)	43	63
All	All	840/886 (95%)	832 (99%)	8 (1%)	76	85

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	164	GLN
2	D	148	CYS
2	D	121	ARG
1	C	75	GLN
2	D	133	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	27	GLN
1	C	75	GLN
2	D	27	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](#)

9 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	E	1	1,3	14,14,15	0.73	1 (7%)	17,19,21	0.92	0
3	NAG	E	2	3	14,14,15	0.83	1 (7%)	17,19,21	1.16	2 (11%)
4	GAL	F	1	4	12,12,12	0.63	0	17,17,17	2.81	7 (41%)
4	SIA	F	2	4	20,20,21	2.36	3 (15%)	24,28,31	1.57	4 (16%)
3	NAG	G	1	1,3	14,14,15	0.80	1 (7%)	17,19,21	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	2	3	14,14,15	0.79	1 (7%)	17,19,21	0.93	1 (5%)
5	NAG	H	1	5	15,15,15	0.69	0	21,21,21	1.99	5 (23%)
5	GAL	H	2	5	11,11,12	0.64	0	15,15,17	2.57	8 (53%)
5	SIA	H	3	5	20,20,21	1.24	1 (5%)	24,28,31	1.82	5 (20%)

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	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1
4	GAL	F	1	4	-	0/2/22/22	0/1/1/1
4	SIA	F	2	4	-	7/18/34/38	0/1/1/1
3	NAG	G	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
5	NAG	H	1	5	-	0/6/26/26	0/1/1/1
5	GAL	H	2	5	-	1/2/19/22	0/1/1/1
5	SIA	H	3	5	-	6/18/34/38	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	2	SIA	C2-C1	-9.10	1.44	1.52
5	H	3	SIA	C5-N5	-3.15	1.40	1.45
4	F	2	SIA	O1B-C1	-2.53	1.22	1.30
4	F	2	SIA	C5-N5	-2.50	1.41	1.45
3	G	1	NAG	O5-C1	-2.40	1.39	1.43

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1	GAL	O1-C1-O5	8.19	134.97	110.38
5	H	3	SIA	C6-C5-N5	-5.66	101.51	110.91
4	F	1	GAL	O4-C4-C3	-5.15	98.44	110.35
5	H	2	GAL	O4-C4-C3	-4.96	98.89	110.35
5	H	1	NAG	O4-C4-C3	-4.85	99.15	110.35

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

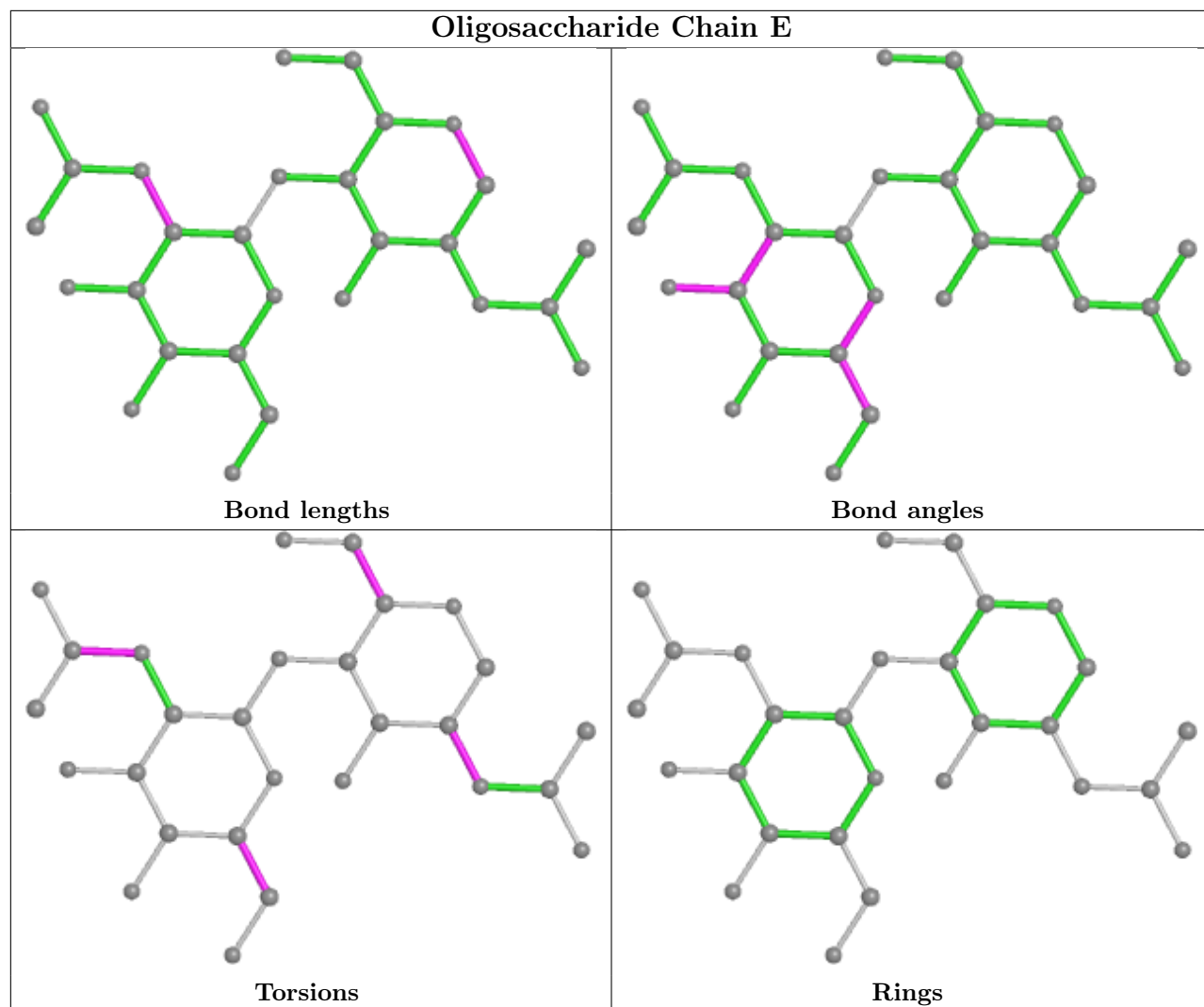
Mol	Chain	Res	Type	Atoms
4	F	2	SIA	O7-C7-C8-C9
5	H	3	SIA	O7-C7-C8-C9
5	H	3	SIA	C11-C10-N5-C5
5	H	3	SIA	O10-C10-N5-C5
3	G	1	NAG	O5-C5-C6-O6

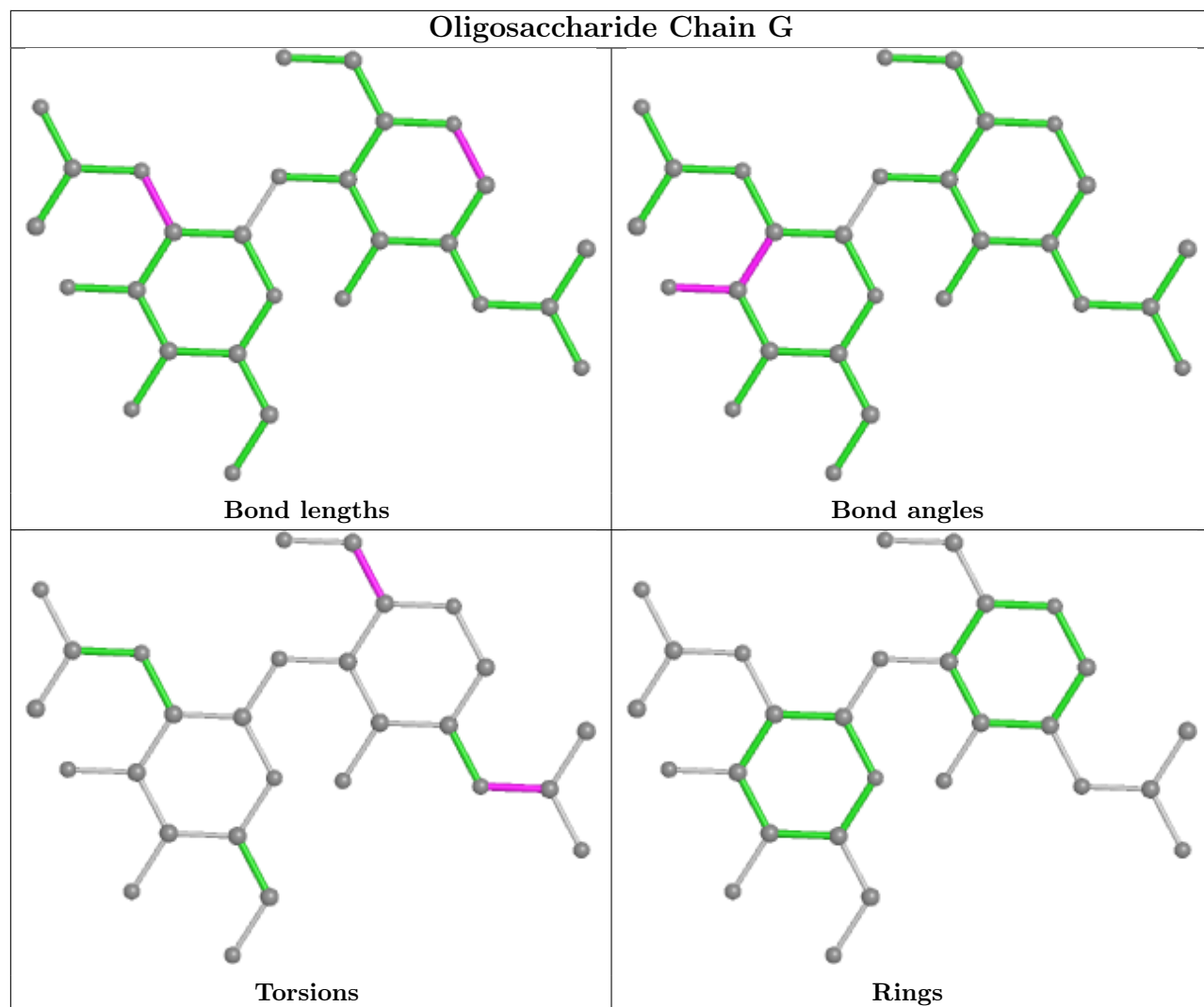
There are no ring outliers.

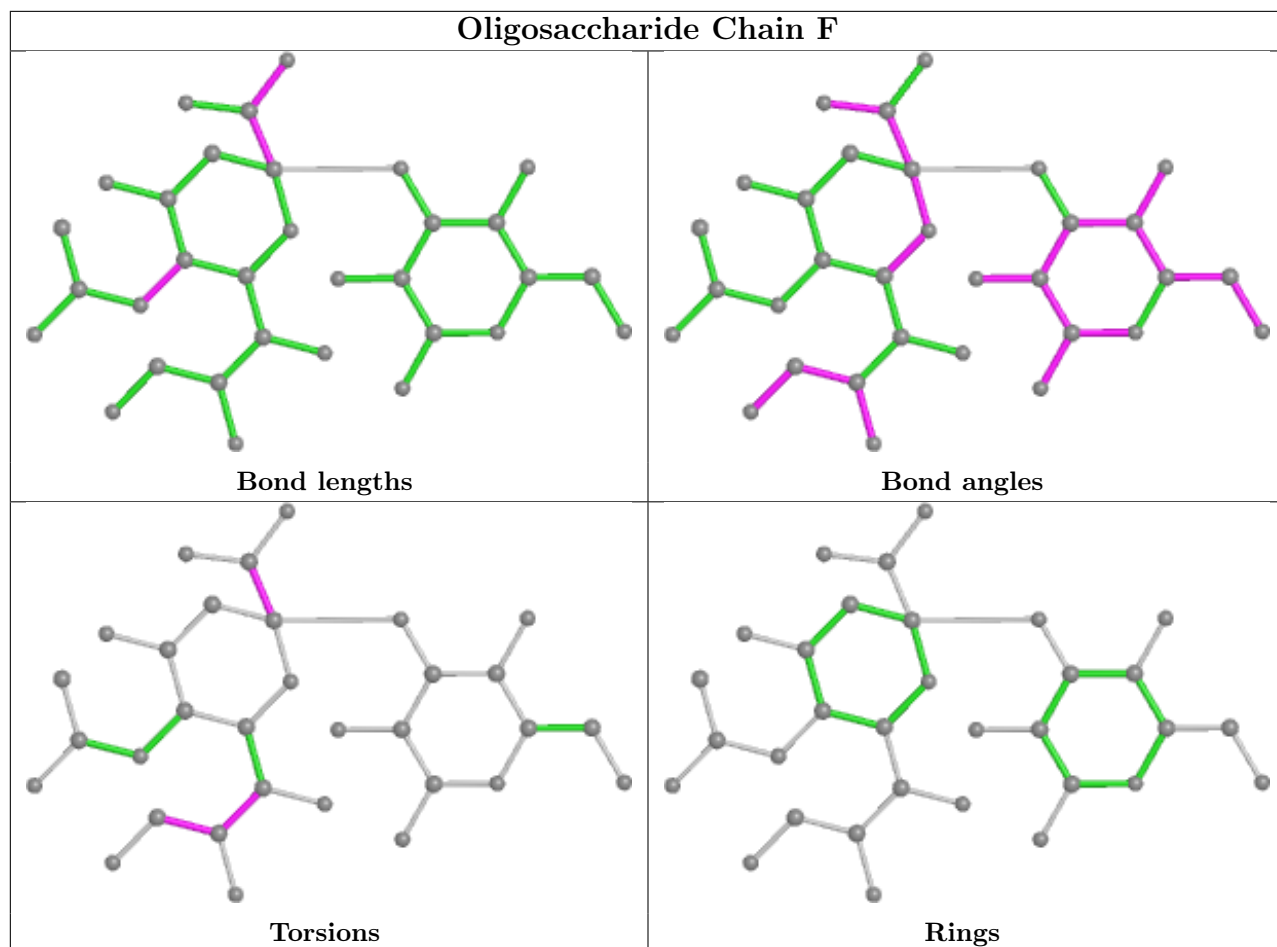
5 monomers are involved in 6 short contacts:

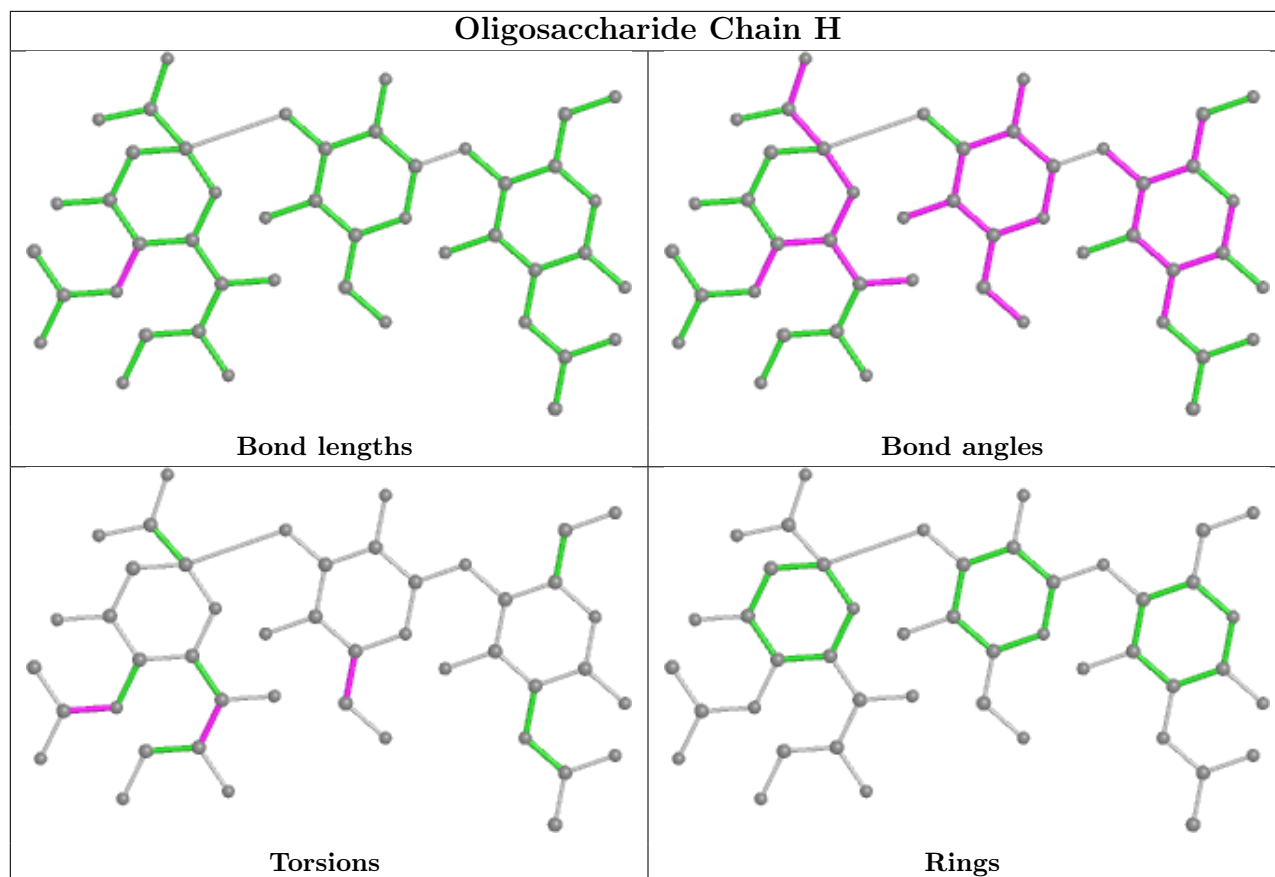
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	2	SIA	1	0
4	F	1	GAL	1	0
3	E	2	NAG	1	0
5	H	3	SIA	2	0
3	E	1	NAG	1	0

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









5.6 Ligand geometry [i](#)

2 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	NAG	D	301	2	14,14,15	0.81	1 (7%)	17,19,21	1.15	1 (5%)
6	NAG	B	301	2	14,14,15	0.89	1 (7%)	17,19,21	1.73	1 (5%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	D	301	2	-	3/6/23/26	0/1/1/1
6	NAG	B	301	2	-	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	B	301	NAG	O5-C1	-2.56	1.39	1.43
6	D	301	NAG	O5-C1	-2.55	1.39	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	301	NAG	C1-C2-N2	5.31	119.55	110.49
6	D	301	NAG	C2-N2-C7	-3.57	117.83	122.90

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	301	NAG	C8-C7-N2-C2
6	D	301	NAG	O7-C7-N2-C2
6	D	301	NAG	O5-C5-C6-O6
6	B	301	NAG	O5-C5-C6-O6
6	B	301	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	301	NAG	3	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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	325/332 (97%)	0.08	1 (0%) 94 96	22, 46, 73, 85	0
1	C	325/332 (97%)	0.07	3 (0%) 84 88	23, 47, 75, 83	0
2	B	168/193 (87%)	0.18	7 (4%) 36 39	21, 35, 75, 106	0
2	D	168/193 (87%)	0.19	5 (2%) 50 57	21, 36, 74, 99	0
All	All	986/1050 (93%)	0.11	16 (1%) 72 78	21, 43, 74, 106	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	249	GLY	4.7
2	B	73	VAL	4.5
2	D	77	ILE	3.8
2	D	73	VAL	3.7
2	D	75	GLN	3.7

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

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, 95th 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.

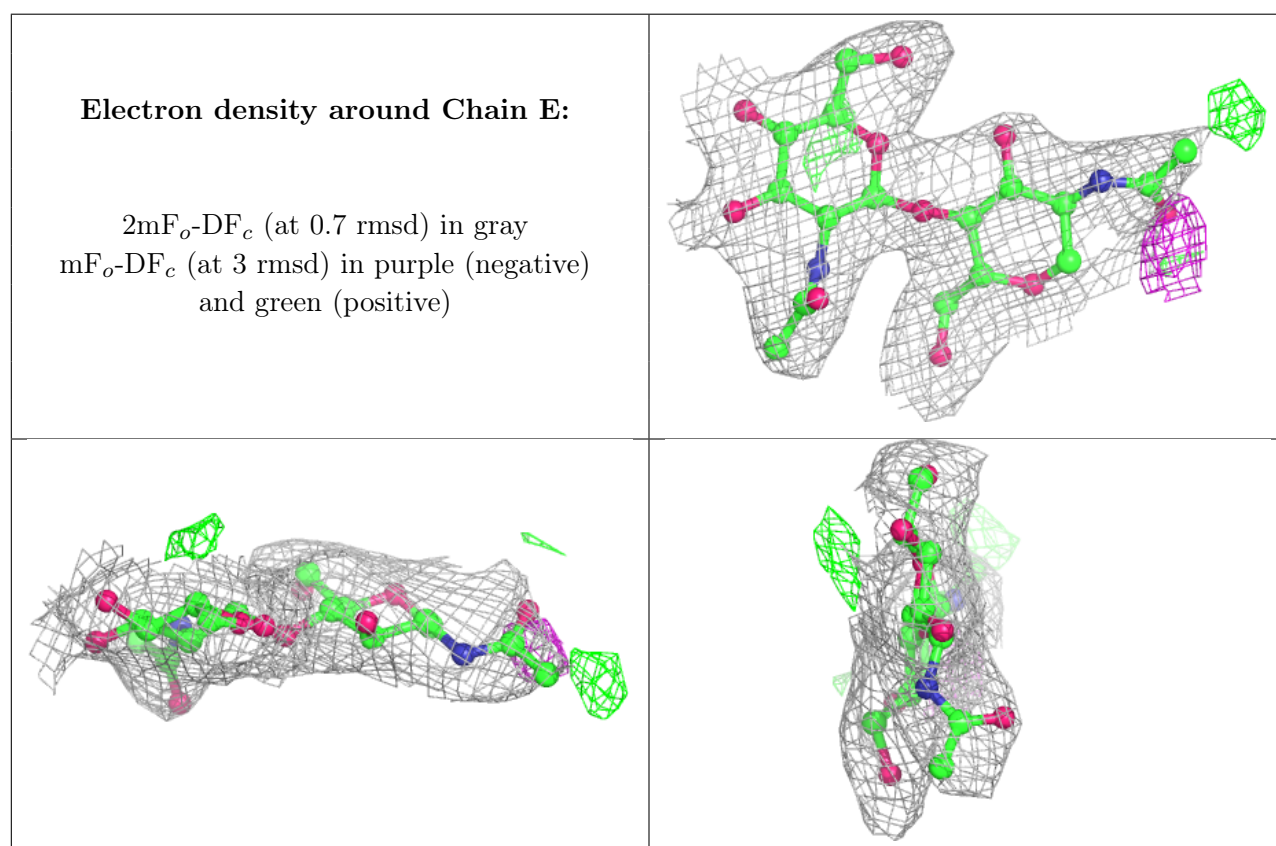
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	H	1	15/15	0.84	0.21	92,105,112,112	0
4	GAL	F	1	12/12	0.85	0.20	63,76,85,85	0

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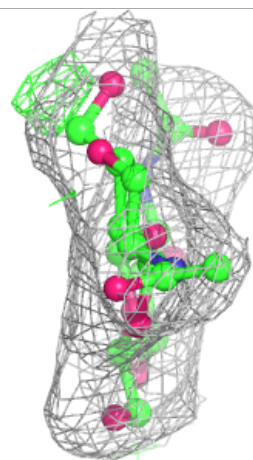
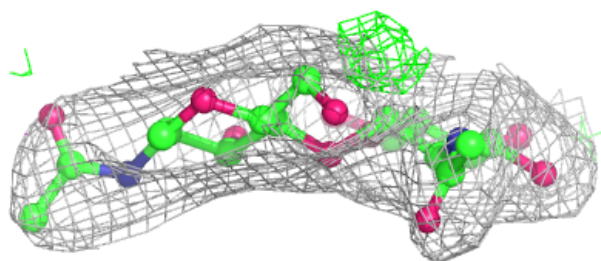
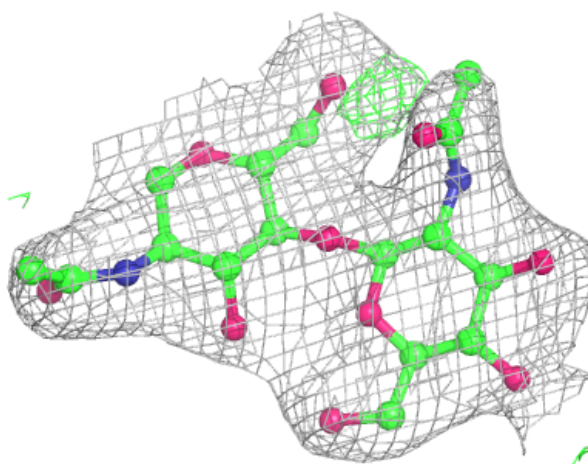
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	GAL	H	2	11/12	0.85	0.17	65,82,96,100	0
3	NAG	E	2	14/15	0.86	0.18	51,75,81,82	0
3	NAG	G	2	14/15	0.87	0.16	58,68,75,75	0
5	SIA	H	3	20/21	0.87	0.20	51,56,64,67	0
3	NAG	E	1	14/15	0.90	0.17	46,58,71,74	0
3	NAG	G	1	14/15	0.93	0.17	43,52,59,65	0
4	SIA	F	2	20/21	0.95	0.20	41,51,58,59	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.



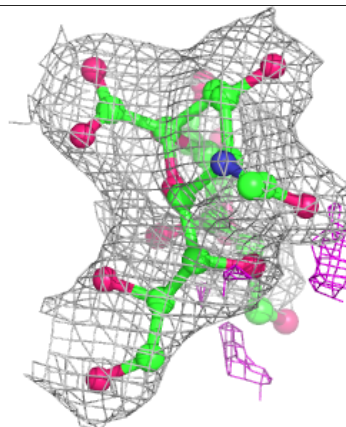
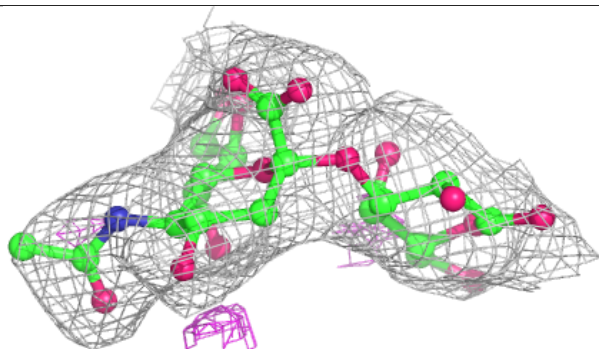
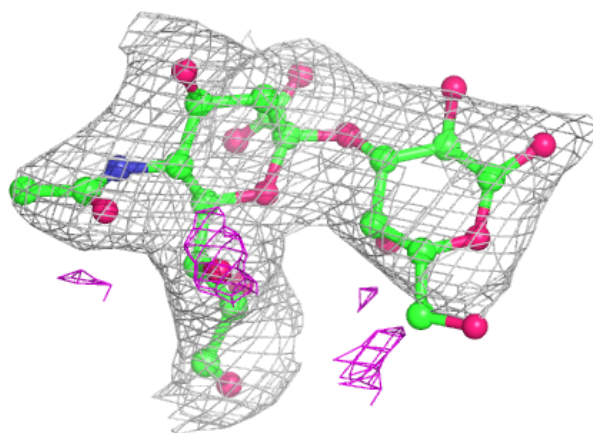
Electron density around Chain G:

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

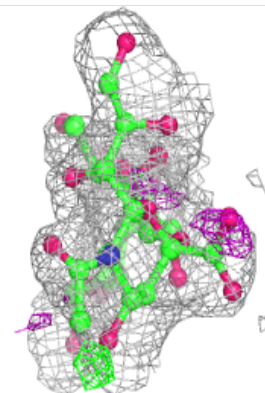
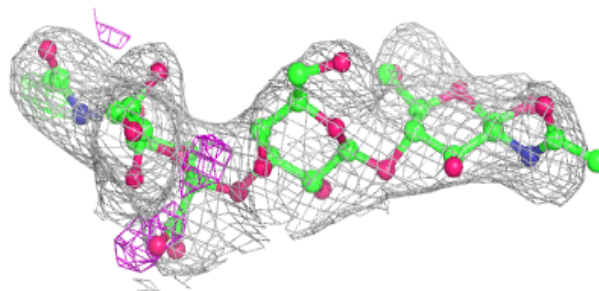
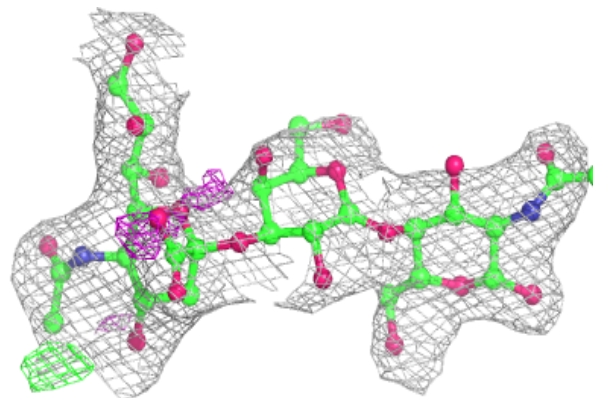


Electron density around Chain F:

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

**Electron density around Chain 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 [i](#)

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, 95th 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
6	NAG	B	301	14/15	0.76	0.27	72,84,89,90	0
6	NAG	D	301	14/15	0.80	0.22	70,79,86,90	0

6.5 Other polymers [i](#)

There are no such residues in this entry.