



wwPDB X-ray Structure Validation Summary Report

Dec 2, 2024 – 06:31 PM EST

PDB ID : 4BH1
Title : H5 (tyTy) Influenza Virus Haemagglutinin in Complex with Avian Receptor Analogue 3'-SLN
Authors : Xiong, X.; Coombs, P.J.; Martin, S.R.; Liu, J.; Xiao, H.; McCauley, J.W.; Locher, K.; Walker, P.A.; Collins, P.J.; Kawaoka, Y.; Skehel, J.J.; Gamblin, S.J.
Deposited on : 2013-03-29
Resolution : 2.15 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 : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 1.21
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

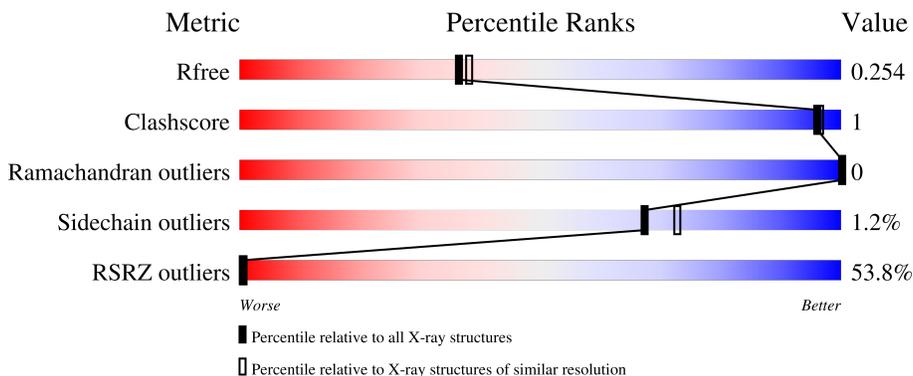
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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.



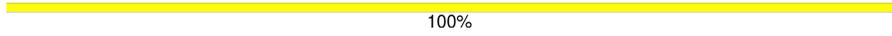
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1881 (2.16-2.16)
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (2.16-2.16)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	326	
1	C	326	
1	E	326	
2	B	166	
2	D	166	

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Mol	Chain	Length	Quality of chain
2	F	166	
3	G	3	
3	H	3	
3	I	3	

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 11980 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	319	Total 2526	C 1592	N 439	O 481	S 14	0	0	0
1	C	319	Total 2519	C 1587	N 439	O 479	S 14	0	0	0
1	E	319	Total 2519	C 1587	N 439	O 479	S 14	0	0	0

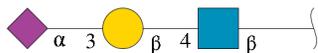
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	323	ARG	-	expression tag	UNP Q207Z6
A	324	GLU	-	expression tag	UNP Q207Z6
A	325	THR	-	expression tag	UNP Q207Z6
A	326	ARG	-	expression tag	UNP Q207Z6
C	323	ARG	-	expression tag	UNP Q207Z6
C	324	GLU	-	expression tag	UNP Q207Z6
C	325	THR	-	expression tag	UNP Q207Z6
C	326	ARG	-	expression tag	UNP Q207Z6
E	323	ARG	-	expression tag	UNP Q207Z6
E	324	GLU	-	expression tag	UNP Q207Z6
E	325	THR	-	expression tag	UNP Q207Z6
E	326	ARG	-	expression tag	UNP Q207Z6

- Molecule 2 is a protein called HEMAGGLUTININ.

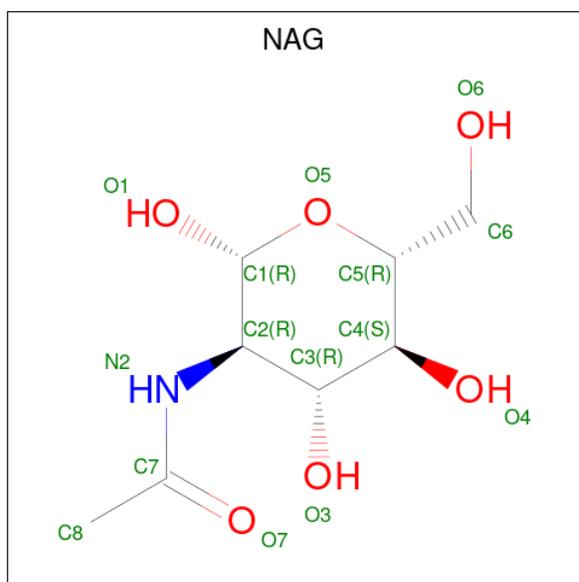
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	145	Total 1129	C 697	N 200	O 224	S 8	0	0	0
2	D	146	Total 1130	C 698	N 201	O 223	S 8	0	0	0
2	F	145	Total 1129	C 697	N 200	O 224	S 8	0	0	0

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



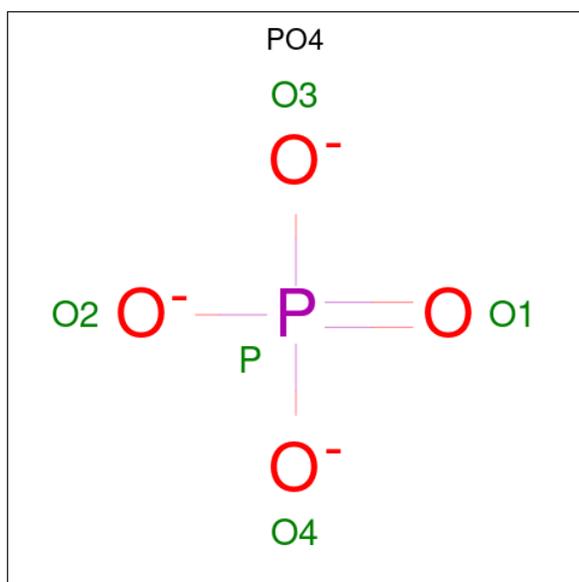
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	3	Total	C	N	O	0	0	0
			46	25	2	19			
3	H	3	Total	C	N	O	0	0	0
			46	25	2	19			
3	I	3	Total	C	N	O	0	0	0
			46	25	2	19			

- Molecule 4 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		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O P 5 4 1	0	0
5	A	1	Total O P 5 4 1	0	0
5	C	1	Total O P 5 4 1	0	0
5	E	1	Total O P 5 4 1	0	0

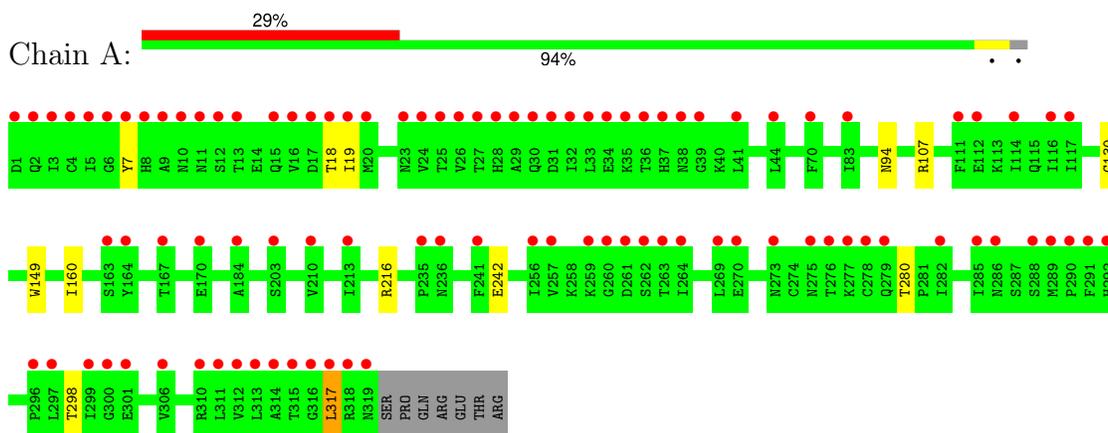
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	266	Total O 266 266	0	0
6	B	36	Total O 36 36	0	0
6	C	243	Total O 243 243	0	0
6	D	35	Total O 35 35	0	0
6	E	218	Total O 218 218	0	0
6	F	30	Total O 30 30	0	0

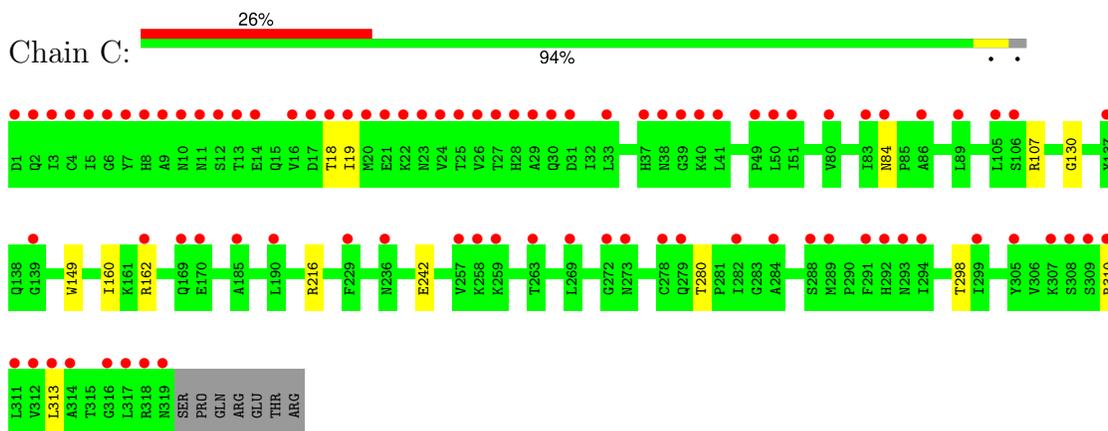
3 Residue-property plots [i](#)

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

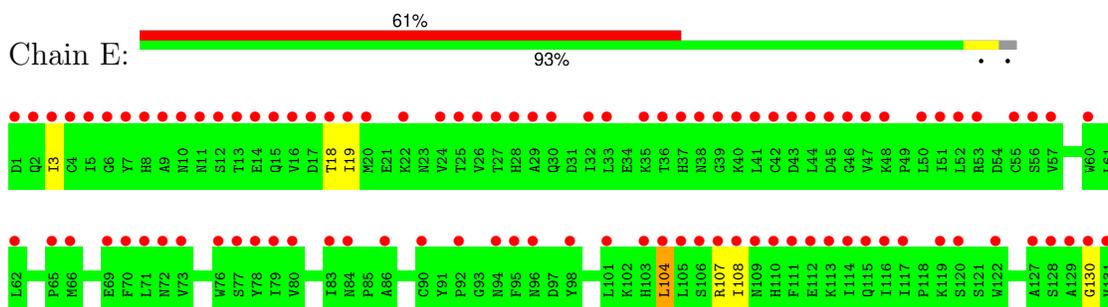
- Molecule 1: HEMAGGLUTININ

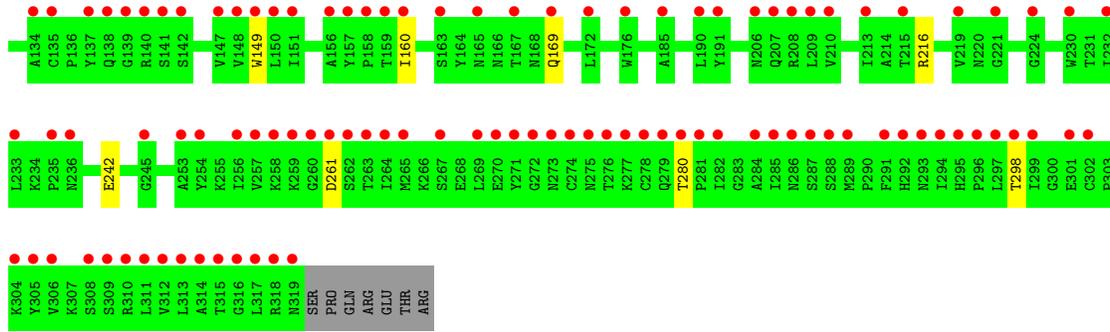


- Molecule 1: HEMAGGLUTININ

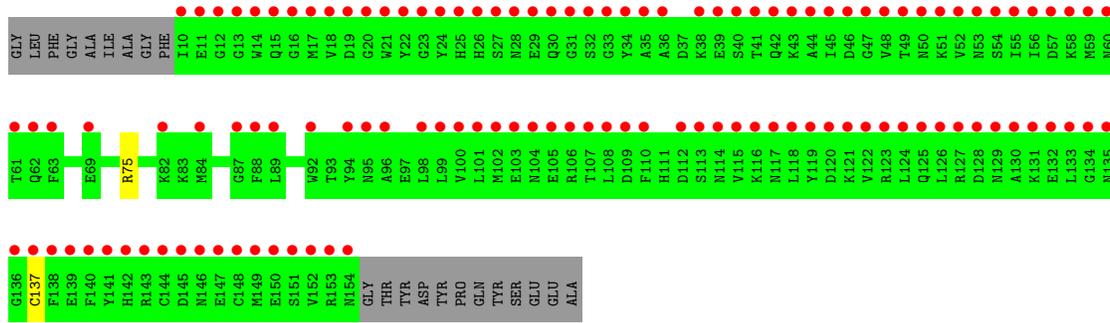
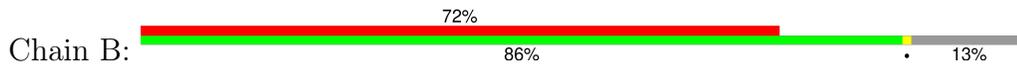


- Molecule 1: HEMAGGLUTININ

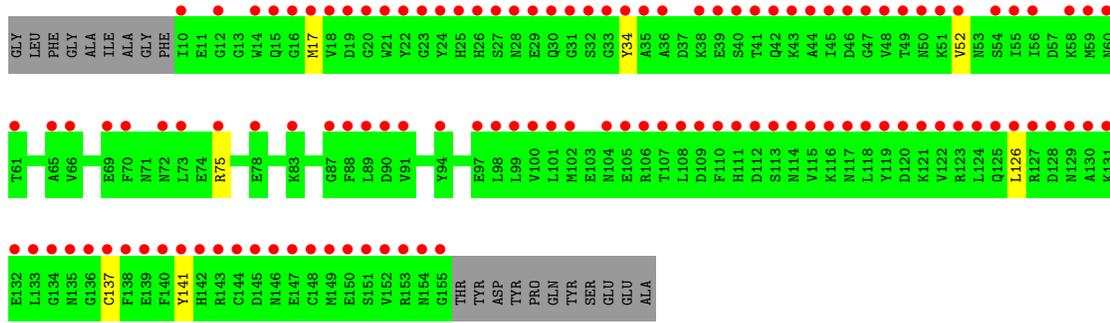
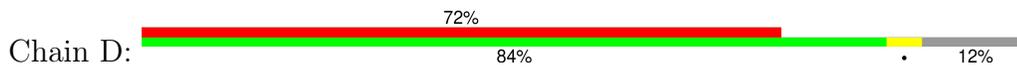




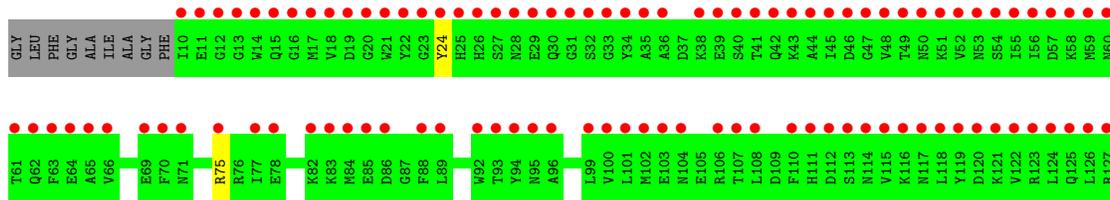
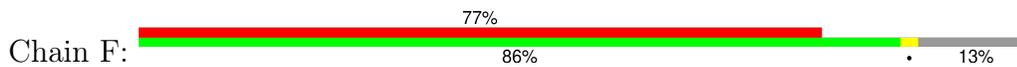
● Molecule 2: HEMAGGLUTININ

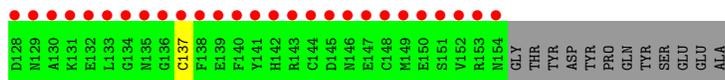


● Molecule 2: HEMAGGLUTININ



● Molecule 2: HEMAGGLUTININ





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



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



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



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.86Å 228.29Å 71.92Å 90.00° 113.71° 90.00°	Depositor
Resolution (Å)	62.48 – 2.15 62.48 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.0 (62.48-2.15) 98.6 (62.48-2.15)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.16Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.205 , 0.224 0.261 , 0.254	Depositor DCC
R_{free} test set	5489 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	35.4	Xtrriage
Anisotropy	0.700	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.035 for l,-k,h	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	11980	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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: PO4, 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	0.32	0/2586	0.55	2/3515 (0.1%)
1	C	0.32	0/2579	0.55	2/3506 (0.1%)
1	E	0.31	0/2579	0.55	1/3506 (0.0%)
2	B	0.29	0/1149	0.44	0/1551
2	D	0.30	0/1150	0.44	0/1552
2	F	0.29	0/1149	0.43	0/1551
All	All	0.31	0/11192	0.52	5/15181 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	C	216	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	C	216	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	E	216	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	216	ARG	NE-CZ-NH2	-5.18	117.71	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2526	0	2460	7	0
1	C	2519	0	2447	7	0
1	E	2519	0	2447	6	1
2	B	1129	0	1007	1	0
2	D	1130	0	1008	2	0
2	F	1129	0	1007	1	0
3	G	46	0	40	0	0
3	H	46	0	40	0	0
3	I	46	0	40	0	0
4	A	14	0	13	0	0
4	C	14	0	13	0	0
4	E	14	0	13	0	0
5	A	10	0	0	0	0
5	C	5	0	0	0	0
5	E	5	0	0	0	0
6	A	266	0	0	2	1
6	B	36	0	0	0	0
6	C	243	0	0	3	0
6	D	35	0	0	0	0
6	E	218	0	0	0	0
6	F	30	0	0	0	0
All	All	11980	0	10535	22	1

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 1.

The worst 5 of 22 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:C:162:ARG:HD2	6:C:2149:HOH:O	2.03	0.58
1:C:84:ASN:ND2	6:C:2069:HOH:O	2.36	0.57
1:A:7:TYR:HB2	1:A:317:LEU:CD2	2.43	0.48
1:A:130:GLY:HA3	1:A:149:TRP:HB3	1.96	0.47
1:E:130:GLY:HA3	1:E:149:TRP:HB3	1.95	0.47

All (1) 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:E:169:GLN:NE2	6:A:2135:HOH:O[1_655]	2.09	0.11

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	317/326 (97%)	309 (98%)	8 (2%)	0	100	100
1	C	317/326 (97%)	309 (98%)	8 (2%)	0	100	100
1	E	317/326 (97%)	309 (98%)	8 (2%)	0	100	100
2	B	143/166 (86%)	137 (96%)	6 (4%)	0	100	100
2	D	144/166 (87%)	137 (95%)	7 (5%)	0	100	100
2	F	143/166 (86%)	137 (96%)	6 (4%)	0	100	100
All	All	1381/1476 (94%)	1338 (97%)	43 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	284/292 (97%)	282 (99%)	2 (1%)	81	86
1	C	282/292 (97%)	280 (99%)	2 (1%)	81	86
1	E	282/292 (97%)	279 (99%)	3 (1%)	70	75
2	B	113/141 (80%)	112 (99%)	1 (1%)	75	81
2	D	112/141 (79%)	108 (96%)	4 (4%)	30	29
2	F	113/141 (80%)	111 (98%)	2 (2%)	54	59
All	All	1186/1299 (91%)	1172 (99%)	14 (1%)	67	73

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	137	CYS
2	D	141	TYR
2	F	137	CYS
1	E	261	ASP
2	F	75	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	2	GLN
1	E	87	ASN
1	E	110	HIS
1	C	2	GLN
1	A	2	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	G	1	3	15,15,15	0.38	0	21,21,21	1.37	4 (19%)
3	GAL	G	2	3	11,11,12	0.41	0	15,15,17	0.88	0
3	SIA	G	3	3	20,20,21	0.73	0	21,28,31	1.51	4 (19%)
3	NAG	H	1	3	15,15,15	0.45	0	21,21,21	1.24	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GAL	H	2	3	11,11,12	0.33	0	15,15,17	1.07	2 (13%)
3	SIA	H	3	3	20,20,21	0.70	0	21,28,31	1.19	2 (9%)
3	NAG	I	1	3	15,15,15	0.40	0	21,21,21	1.27	2 (9%)
3	GAL	I	2	3	11,11,12	0.26	0	15,15,17	0.77	0
3	SIA	I	3	3	20,20,21	0.63	0	21,28,31	1.11	2 (9%)

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	G	1	3	-	0/6/26/26	0/1/1/1
3	GAL	G	2	3	-	1/2/19/22	0/1/1/1
3	SIA	G	3	3	-	0/18/34/38	0/1/1/1
3	NAG	H	1	3	-	0/6/26/26	0/1/1/1
3	GAL	H	2	3	-	1/2/19/22	0/1/1/1
3	SIA	H	3	3	-	0/18/34/38	0/1/1/1
3	NAG	I	1	3	-	0/6/26/26	0/1/1/1
3	GAL	I	2	3	-	0/2/19/22	0/1/1/1
3	SIA	I	3	3	-	0/18/34/38	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	1	NAG	C1-C2-N2	-4.25	105.80	110.73
3	G	3	SIA	O6-C2-C1	3.62	114.55	107.72
3	G	1	NAG	C1-C2-N2	-3.61	106.55	110.73
3	I	1	NAG	C1-C2-N2	-3.52	106.65	110.73
3	G	3	SIA	C6-C5-N5	-2.77	106.48	110.91

There are no chirality outliers.

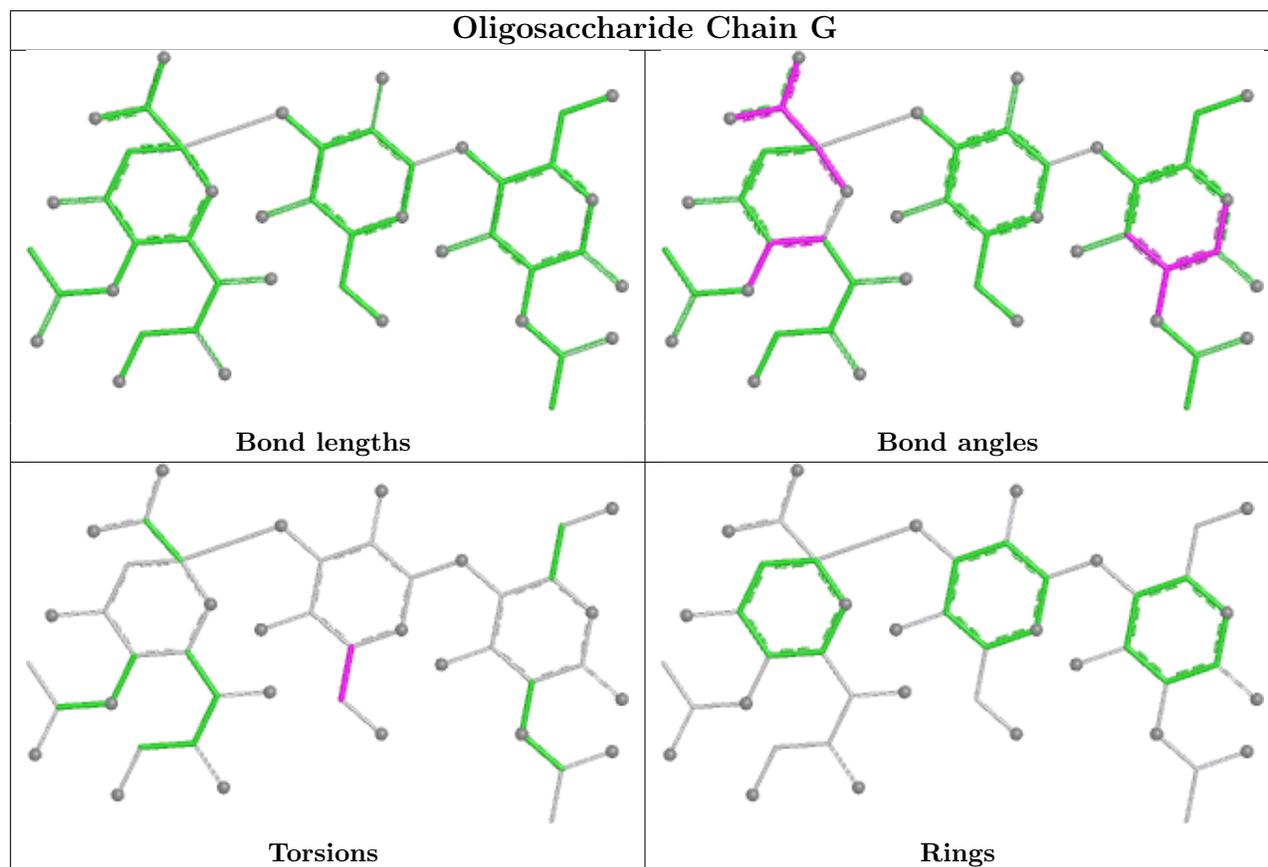
All (2) torsion outliers are listed below:

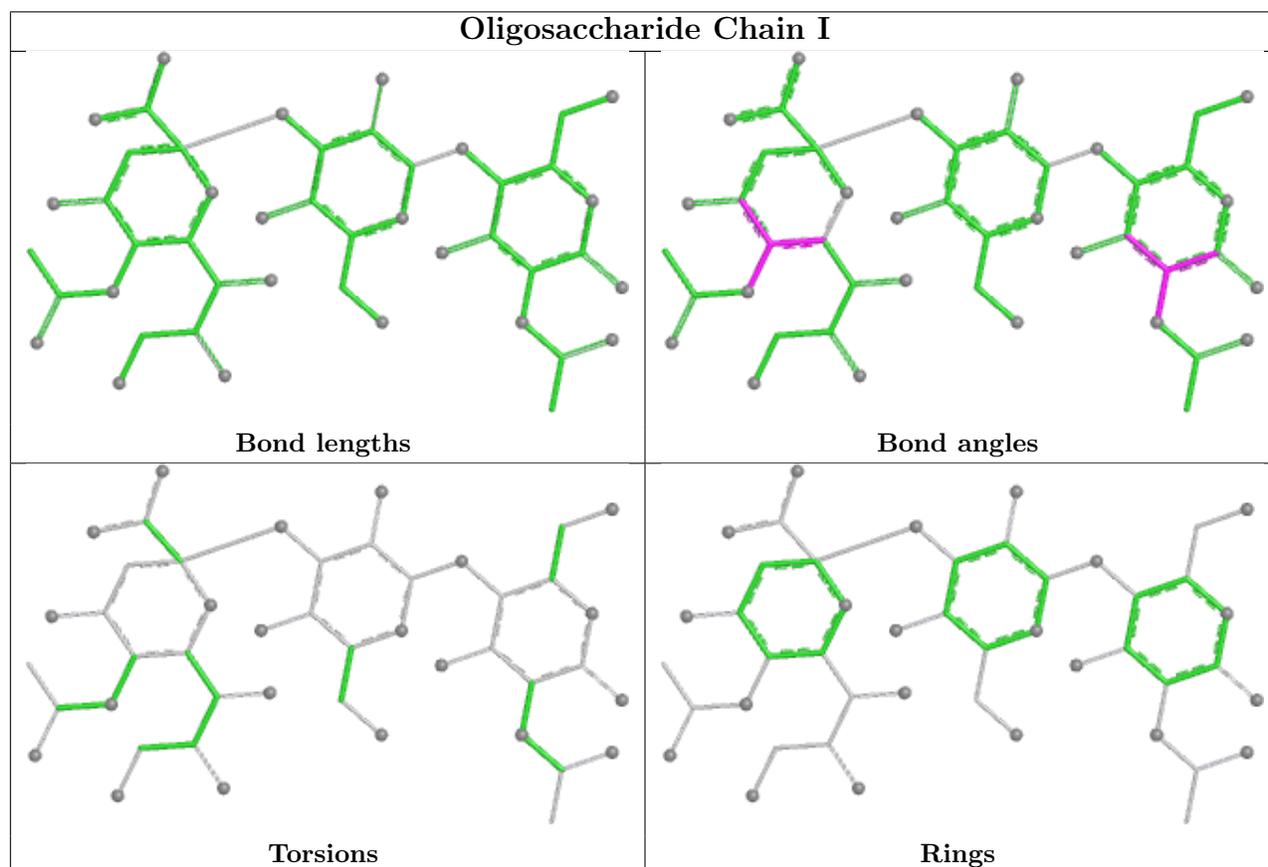
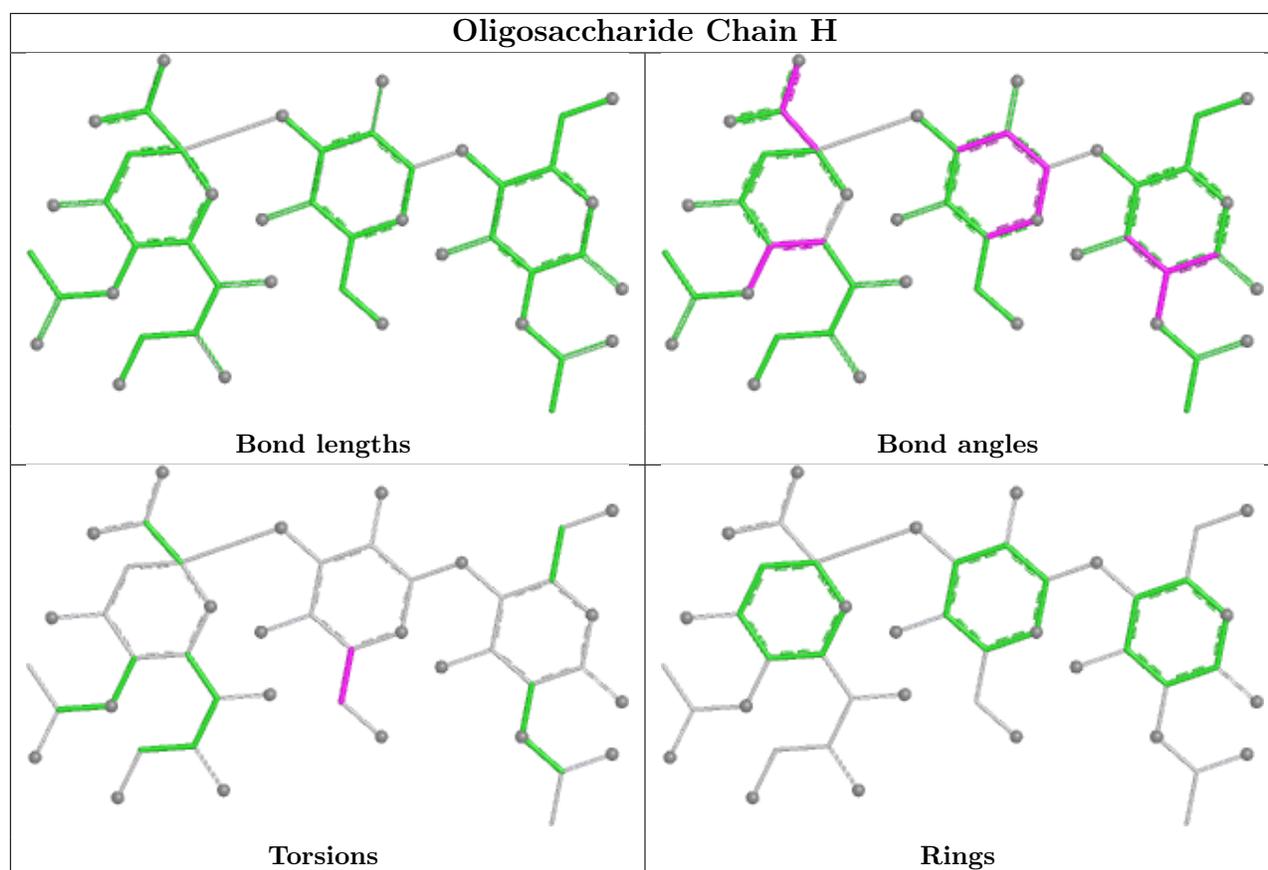
Mol	Chain	Res	Type	Atoms
3	H	2	GAL	C4-C5-C6-O6
3	G	2	GAL	C4-C5-C6-O6

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.





5.6 Ligand geometry

7 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
5	PO4	C	1324	-	4,4,4	0.99	0	6,6,6	0.53	0
4	NAG	C	1320	1	14,14,15	0.55	0	17,19,21	1.38	3 (17%)
5	PO4	A	1325	-	4,4,4	0.82	0	6,6,6	0.60	0
5	PO4	E	1324	-	4,4,4	1.00	0	6,6,6	0.56	0
5	PO4	A	1324	-	4,4,4	0.92	0	6,6,6	0.57	0
4	NAG	A	1320	1	14,14,15	0.47	0	17,19,21	1.33	2 (11%)
4	NAG	E	1320	1	14,14,15	0.37	0	17,19,21	1.06	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1320	1	-	2/6/23/26	0/1/1/1
4	NAG	E	1320	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1320	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1320	NAG	C1-O5-C5	3.70	117.14	112.19
4	A	1320	NAG	C1-O5-C5	3.54	116.93	112.19
4	E	1320	NAG	C1-O5-C5	2.61	115.68	112.19
4	C	1320	NAG	C1-C2-N2	2.25	113.98	110.43
4	A	1320	NAG	C3-C4-C5	-2.09	106.44	110.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1320	NAG	C4-C5-C6-O6
4	A	1320	NAG	O5-C5-C6-O6

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 [i](#)

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

Warning: The R factor obtained from EDS is 0.3001, which does not match the depositor's R factor of 0.20518. Please interpret the results in this section carefully.

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	319/326 (97%)	1.73	96 (30%)	1 2	23, 38, 124, 285	0
1	C	319/326 (97%)	1.54	86 (26%)	2 2	22, 40, 101, 147	0
1	E	319/326 (97%)	2.47	200 (62%)	0 0	24, 41, 129, 233	0
2	B	145/166 (87%)	3.58	119 (82%)	0 0	25, 172, 220, 245	0
2	D	146/166 (87%)	3.73	120 (82%)	0 0	29, 126, 188, 208	0
2	F	145/166 (87%)	3.79	128 (88%)	0 0	24, 166, 204, 226	0
All	All	1393/1476 (94%)	2.47	749 (53%)	0 1	22, 47, 193, 285	0

The worst 5 of 749 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	138	PHE	12.6
1	E	3	ILE	9.4
2	B	21	TRP	8.8
2	D	140	PHE	8.8
2	B	141	TYR	8.8

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

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

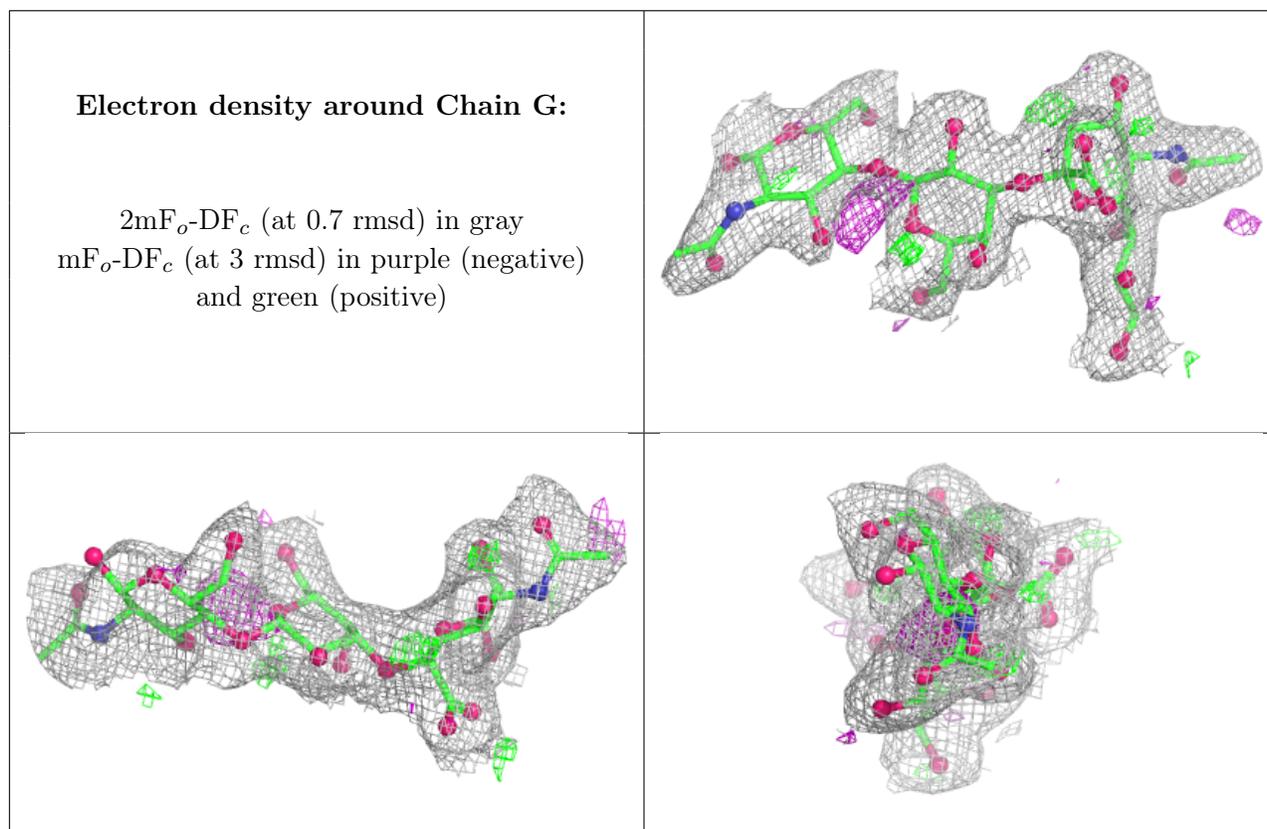
6.3 Carbohydrates [i](#)

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.

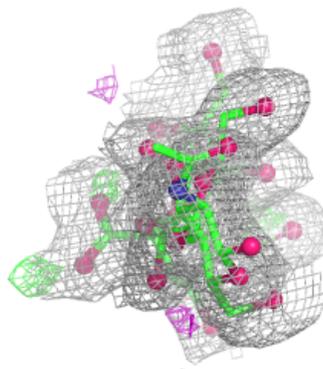
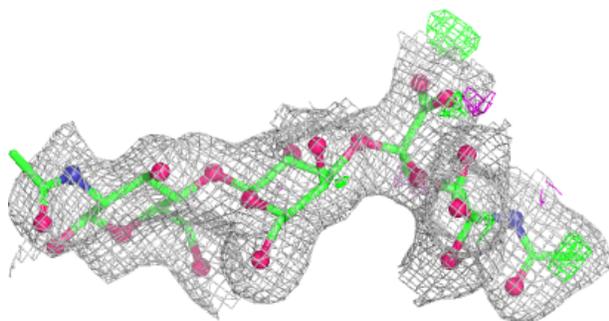
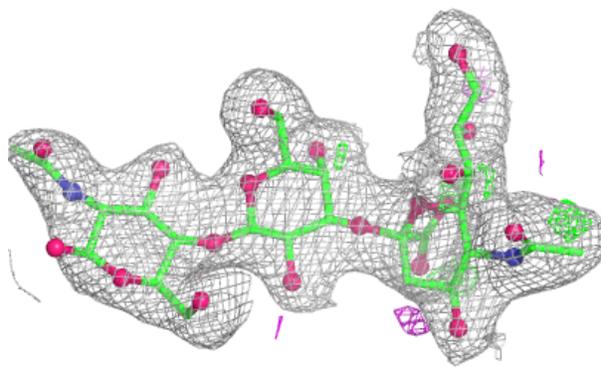
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	G	1	15/15	0.71	0.18	46,56,64,66	0
3	NAG	H	1	15/15	0.81	0.14	43,56,66,68	0
3	GAL	I	2	11/12	0.82	0.12	47,50,54,56	0
3	SIA	I	3	20/21	0.82	0.13	34,40,46,46	0
3	NAG	I	1	15/15	0.83	0.13	62,73,76,78	0
3	GAL	G	2	11/12	0.86	0.12	30,36,37,40	0
3	SIA	H	3	20/21	0.87	0.11	23,25,29,30	0
3	SIA	G	3	20/21	0.88	0.10	26,31,33,34	0
3	GAL	H	2	11/12	0.90	0.09	28,32,34,36	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.

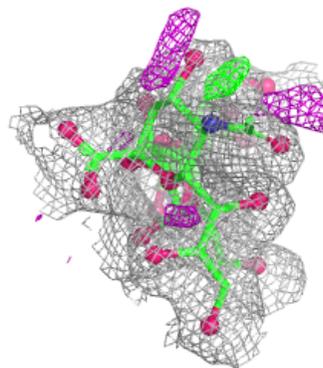
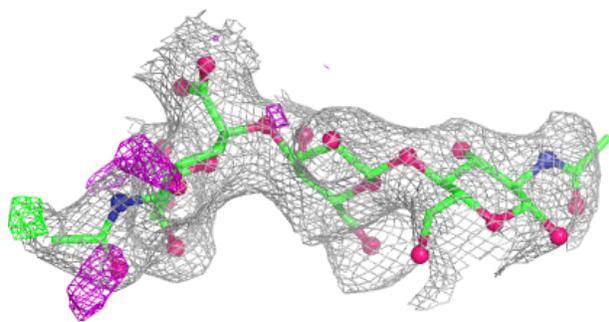
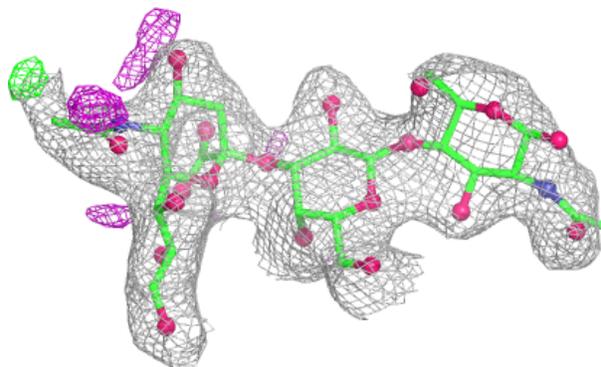


Electron density around Chain H:

$2mF_o-DF_c$ (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)



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(\AA^2)	Q<0.9
5	PO4	E	1324	5/5	0.58	0.17	64,71,74,75	0
5	PO4	A	1325	5/5	0.59	0.21	66,71,78,80	0
5	PO4	C	1324	5/5	0.67	0.18	53,65,67,67	0
4	NAG	C	1320	14/15	0.79	0.13	37,40,47,49	0
4	NAG	E	1320	14/15	0.84	0.12	35,37,46,50	0
5	PO4	A	1324	5/5	0.86	0.16	63,63,67,68	0
4	NAG	A	1320	14/15	0.86	0.10	36,39,47,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.