



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:42 PM UTC

PDB ID : 5F93 / pdb_00005f93
Title : Blood group antigen binding adhesin BabA of Helicobacter pylori strain A730
in complex with blood group H Lewis b hexasaccharide
Authors : Moonens, K.; Gideonsson, P.; Subedi, S.; Romao, E.; Oscarson, S.; Muylder-
mans, S.; Boren, T.; Remaut, H.
Deposited on : 2015-12-09
Resolution : 2.99 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

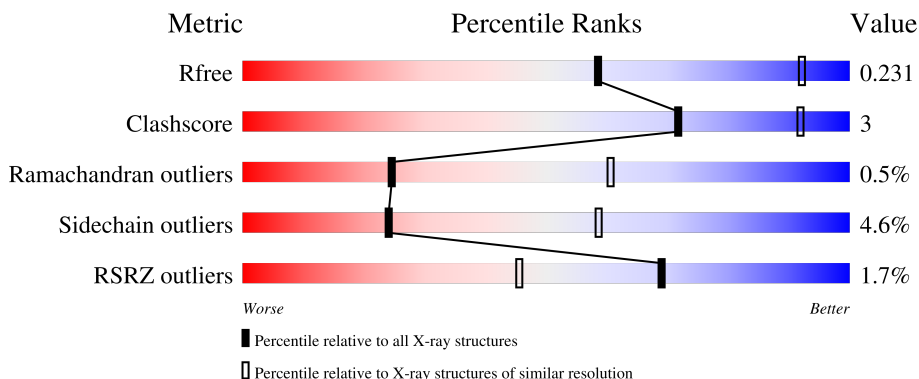
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	469	 78% 11% 10% 2%
1	B	469	 79% 11% 9% 1%
1	E	469	 80% 9% 10% 2%
1	G	469	 77% 13% 10% 1%
2	C	120	 81% 13% 5% 2%

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Mol	Chain	Length	Quality of chain
2	D	120	<p>2% 85% 10% 5%</p>
2	F	120	<p>2% 86% 9% 5%</p>
2	H	120	<p>2% 82% 12% 5%</p>
3	I	6	<p>100%</p>
3	J	6	<p>83% 17%</p>
3	K	6	<p>17% 50% 33%</p>
3	L	6	<p>100%</p>

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 16509 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 Adhesin binding fucosylated histo-blood group antigen, Adhesin, Adhesin binding fucosylated histo-blood group antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3184	1970	544	657	13			
1	B	426	Total	C	N	O	S	0	2	0
			3205	1981	547	664	13			
1	E	420	Total	C	N	O	S	0	0	0
			3149	1947	538	651	13			
1	G	422	Total	C	N	O	S	0	1	0
			3165	1956	541	655	13			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	ALA	-	expression tag	UNP O52269
A	4	SER	-	expression tag	UNP O52269
A	5	TRP	-	expression tag	UNP O52269
A	6	SER	-	expression tag	UNP O52269
A	7	HIS	-	expression tag	UNP O52269
A	8	PRO	-	expression tag	UNP O52269
A	9	GLN	-	expression tag	UNP O52269
A	10	PHE	-	expression tag	UNP O52269
A	11	GLU	-	expression tag	UNP O52269
A	12	LYS	-	expression tag	UNP O52269
A	13	SER	-	expression tag	UNP O52269
A	14	GLY	-	expression tag	UNP O52269
A	15	GLY	-	expression tag	UNP O52269
A	16	GLY	-	expression tag	UNP O52269
A	17	GLY	-	expression tag	UNP O52269
A	18	GLY	-	expression tag	UNP O52269
A	19	LEU	-	expression tag	UNP O52269
A	20	VAL	-	expression tag	UNP O52269
A	21	PRO	-	expression tag	UNP O52269
A	22	ARG	-	expression tag	UNP O52269

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Chain	Residue	Modelled	Actual	Comment	Reference
A	23	GLY	-	expression tag	UNP O52269
A	24	SER	-	expression tag	UNP O52269
A	464	GLY	-	expression tag	UNP O52269
A	465	SER	-	expression tag	UNP O52269
A	466	HIS	-	expression tag	UNP O52269
A	467	HIS	-	expression tag	UNP O52269
A	468	HIS	-	expression tag	UNP O52269
A	469	HIS	-	expression tag	UNP O52269
A	470	HIS	-	expression tag	UNP O52269
A	471	HIS	-	expression tag	UNP O52269
B	3	ALA	-	expression tag	UNP O52269
B	4	SER	-	expression tag	UNP O52269
B	5	TRP	-	expression tag	UNP O52269
B	6	SER	-	expression tag	UNP O52269
B	7	HIS	-	expression tag	UNP O52269
B	8	PRO	-	expression tag	UNP O52269
B	9	GLN	-	expression tag	UNP O52269
B	10	PHE	-	expression tag	UNP O52269
B	11	GLU	-	expression tag	UNP O52269
B	12	LYS	-	expression tag	UNP O52269
B	13	SER	-	expression tag	UNP O52269
B	14	GLY	-	expression tag	UNP O52269
B	15	GLY	-	expression tag	UNP O52269
B	16	GLY	-	expression tag	UNP O52269
B	17	GLY	-	expression tag	UNP O52269
B	18	GLY	-	expression tag	UNP O52269
B	19	LEU	-	expression tag	UNP O52269
B	20	VAL	-	expression tag	UNP O52269
B	21	PRO	-	expression tag	UNP O52269
B	22	ARG	-	expression tag	UNP O52269
B	23	GLY	-	expression tag	UNP O52269
B	24	SER	-	expression tag	UNP O52269
B	464	GLY	-	expression tag	UNP O52269
B	465	SER	-	expression tag	UNP O52269
B	466	HIS	-	expression tag	UNP O52269
B	467	HIS	-	expression tag	UNP O52269
B	468	HIS	-	expression tag	UNP O52269
B	469	HIS	-	expression tag	UNP O52269
B	470	HIS	-	expression tag	UNP O52269
B	471	HIS	-	expression tag	UNP O52269
E	3	ALA	-	expression tag	UNP O52269
E	4	SER	-	expression tag	UNP O52269

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Chain	Residue	Modelled	Actual	Comment	Reference
E	5	TRP	-	expression tag	UNP O52269
E	6	SER	-	expression tag	UNP O52269
E	7	HIS	-	expression tag	UNP O52269
E	8	PRO	-	expression tag	UNP O52269
E	9	GLN	-	expression tag	UNP O52269
E	10	PHE	-	expression tag	UNP O52269
E	11	GLU	-	expression tag	UNP O52269
E	12	LYS	-	expression tag	UNP O52269
E	13	SER	-	expression tag	UNP O52269
E	14	GLY	-	expression tag	UNP O52269
E	15	GLY	-	expression tag	UNP O52269
E	16	GLY	-	expression tag	UNP O52269
E	17	GLY	-	expression tag	UNP O52269
E	18	GLY	-	expression tag	UNP O52269
E	19	LEU	-	expression tag	UNP O52269
E	20	VAL	-	expression tag	UNP O52269
E	21	PRO	-	expression tag	UNP O52269
E	22	ARG	-	expression tag	UNP O52269
E	23	GLY	-	expression tag	UNP O52269
E	24	SER	-	expression tag	UNP O52269
E	464	GLY	-	expression tag	UNP O52269
E	465	SER	-	expression tag	UNP O52269
E	466	HIS	-	expression tag	UNP O52269
E	467	HIS	-	expression tag	UNP O52269
E	468	HIS	-	expression tag	UNP O52269
E	469	HIS	-	expression tag	UNP O52269
E	470	HIS	-	expression tag	UNP O52269
E	471	HIS	-	expression tag	UNP O52269
G	3	ALA	-	expression tag	UNP O52269
G	4	SER	-	expression tag	UNP O52269
G	5	TRP	-	expression tag	UNP O52269
G	6	SER	-	expression tag	UNP O52269
G	7	HIS	-	expression tag	UNP O52269
G	8	PRO	-	expression tag	UNP O52269
G	9	GLN	-	expression tag	UNP O52269
G	10	PHE	-	expression tag	UNP O52269
G	11	GLU	-	expression tag	UNP O52269
G	12	LYS	-	expression tag	UNP O52269
G	13	SER	-	expression tag	UNP O52269
G	14	GLY	-	expression tag	UNP O52269
G	15	GLY	-	expression tag	UNP O52269
G	16	GLY	-	expression tag	UNP O52269

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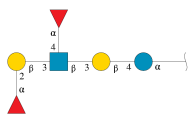
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Chain	Residue	Modelled	Actual	Comment	Reference
G	17	GLY	-	expression tag	UNP O52269
G	18	GLY	-	expression tag	UNP O52269
G	19	LEU	-	expression tag	UNP O52269
G	20	VAL	-	expression tag	UNP O52269
G	21	PRO	-	expression tag	UNP O52269
G	22	ARG	-	expression tag	UNP O52269
G	23	GLY	-	expression tag	UNP O52269
G	24	SER	-	expression tag	UNP O52269
G	464	GLY	-	expression tag	UNP O52269
G	465	SER	-	expression tag	UNP O52269
G	466	HIS	-	expression tag	UNP O52269
G	467	HIS	-	expression tag	UNP O52269
G	468	HIS	-	expression tag	UNP O52269
G	469	HIS	-	expression tag	UNP O52269
G	470	HIS	-	expression tag	UNP O52269
G	471	HIS	-	expression tag	UNP O52269

- Molecule 2 is a protein called Nanobody Nb-ER19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	114	Total	C	N	O	S	0	0	0
			873	546	158	164	5			
2	D	114	Total	C	N	O	S	0	0	0
			873	546	158	164	5			
2	F	114	Total	C	N	O	S	0	0	0
			873	546	158	164	5			
2	H	114	Total	C	N	O	S	0	0	0
			873	546	158	164	5			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	I	6	Total	C	N	O	0	0	0
			68	38	1	29			
3	J	6	Total	C	N	O	0	0	0
			68	38	1	29			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	K	6	68	38	1	29	0	0	0
3	L	6	68	38	1	29	0	0	0

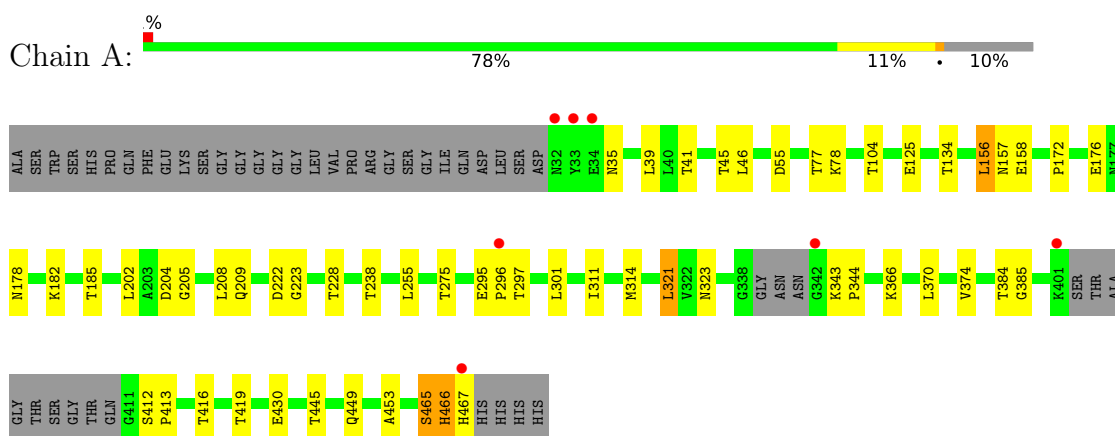
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	13	Total	O	0	0
			13	13		
4	E	6	Total	O	0	0
			6	6		
4	G	7	Total	O	0	0
			7	7		
4	C	2	Total	O	0	0
			2	2		
4	F	3	Total	O	0	0
			3	3		
4	H	3	Total	O	0	0
			3	3		

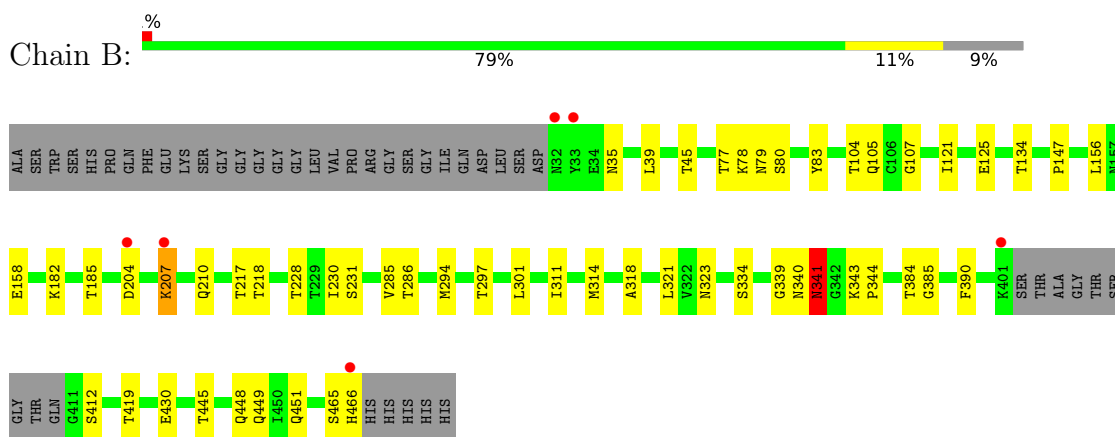
3 Residue-property plots [i](#)

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.

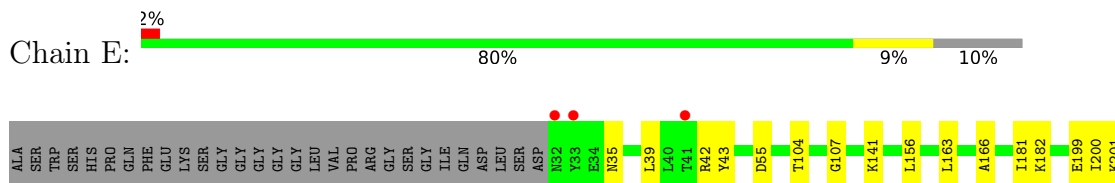
- Molecule 1: Adhesin binding fucosylated histo-blood group antigen,Adhesin,Adhesin binding fucosylated histo-blood group antigen

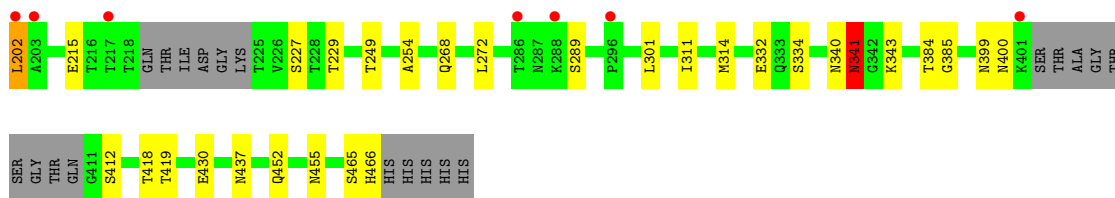


- Molecule 1: Adhesin binding fucosylated histo-blood group antigen,Adhesin,Adhesin binding fucosylated histo-blood group antigen

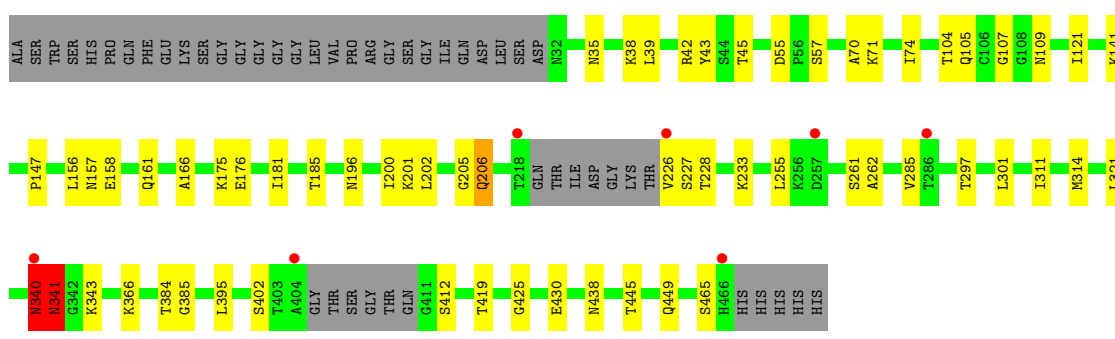
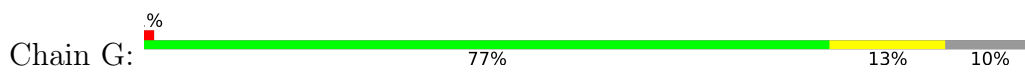


- Molecule 1: Adhesin binding fucosylated histo-blood group antigen,Adhesin,Adhesin binding fucosylated histo-blood group antigen

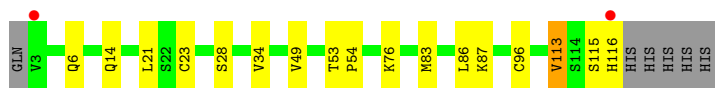
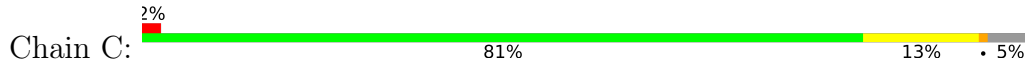




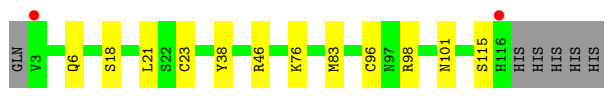
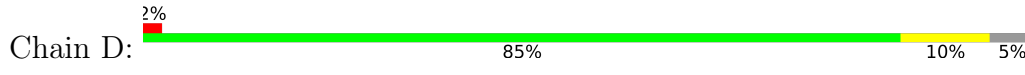
● Molecule 1: Adhesin binding fucosylated histo-blood group antigen,Adhesin,Adhesin binding fucosylated histo-blood group antigen



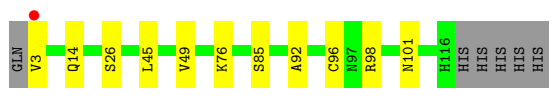
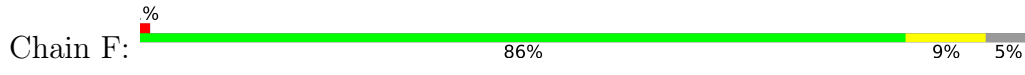
● Molecule 2: Nanobody Nb-ER19



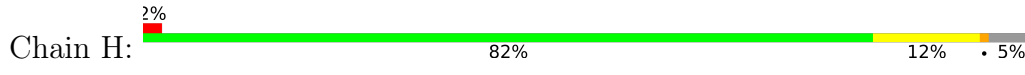
● Molecule 2: Nanobody Nb-ER19



● Molecule 2: Nanobody Nb-ER19



● Molecule 2: Nanobody Nb-ER19





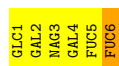
- Molecule 3: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain I: 100%



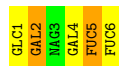
- Molecule 3: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain J: 83% 17%



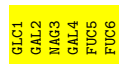
- Molecule 3: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain K: 17% 50% 33%



- Molecule 3: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain L: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.17Å 134.47Å 123.98Å 90.00° 102.30° 90.00°	Depositor
Resolution (Å)	48.64 – 2.99 48.64 – 2.99	Depositor EDS
% Data completeness (in resolution range)	97.9 (48.64-2.99) 97.9 (48.64-2.99)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.181 , 0.234 0.185 , 0.231	Depositor DCC
R_{free} test set	3241 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	67.2	Xtrriage
Anisotropy	0.367	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16509	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.54 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.7101e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GAL, GLC, FUC, NAG

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	0.87	0/3234	1.03	4/4395 (0.1%)
1	B	0.89	0/3261	1.03	7/4433 (0.2%)
1	E	0.79	1/3198 (0.0%)	0.98	4/4347 (0.1%)
1	G	0.77	0/3217	0.98	3/4373 (0.1%)
2	C	0.84	0/893	0.96	1/1210 (0.1%)
2	D	0.81	0/893	0.94	0/1210
2	F	0.93	0/893	1.01	0/1210
2	H	0.94	0/893	1.00	0/1210
All	All	0.84	1/16482 (0.0%)	1.00	19/22388 (0.1%)

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	1
1	G	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	437	ASN	CA-C	-5.52	1.45	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	227	SER	N-CA-C	6.92	120.86	110.14
1	B	107	GLY	N-CA-C	6.25	119.88	110.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	323	ASN	N-CA-C	6.07	118.69	111.71
1	E	400	ASN	N-CA-C	5.92	120.66	113.38
1	G	121	ILE	N-CA-C	5.81	116.49	108.12

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	466	HIS	Peptide
1	G	226	VAL	Peptide
1	G	340	ASN	Peptide

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	3184	0	3085	21	0
1	B	3205	0	3106	24	0
1	E	3149	0	3047	20	0
1	G	3165	0	3063	22	0
2	C	873	0	852	6	0
2	D	873	0	852	5	0
2	F	873	0	852	3	0
2	H	873	0	852	7	0
3	I	68	0	60	0	0
3	J	68	0	60	1	0
3	K	68	0	60	3	0
3	L	68	0	60	0	0
4	A	8	0	0	0	0
4	B	13	0	0	0	0
4	C	2	0	0	0	0
4	E	6	0	0	0	0
4	F	3	0	0	0	0
4	G	7	0	0	0	0
4	H	3	0	0	0	0
All	All	16509	0	15949	106	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 3.

The worst 5 of 106 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:G:202:LEU:HD23	1:G:206:GLN:O	1.90	0.71
1:A:35:ASN:OD1	1:A:35:ASN:C	2.38	0.67
1:B:339:GLY:O	1:B:341:ASN:N	2.30	0.64
2:F:3:VAL:N	2:F:26:SER:HG	1.96	0.64
1:B:465:SER:O	1:B:466:HIS:HB2	2.01	0.61

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	418/469 (89%)	394 (94%)	23 (6%)	1 (0%)	43 76
1	B	424/469 (90%)	401 (95%)	22 (5%)	1 (0%)	43 76
1	E	414/469 (88%)	383 (92%)	30 (7%)	1 (0%)	43 76
1	G	417/469 (89%)	385 (92%)	28 (7%)	4 (1%)	12 45
2	C	112/120 (93%)	107 (96%)	4 (4%)	1 (1%)	14 48
2	D	112/120 (93%)	109 (97%)	2 (2%)	1 (1%)	14 48
2	F	112/120 (93%)	108 (96%)	3 (3%)	1 (1%)	14 48
2	H	112/120 (93%)	104 (93%)	7 (6%)	1 (1%)	14 48
All	All	2121/2356 (90%)	1991 (94%)	119 (6%)	11 (0%)	24 60

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	340	ASN

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Mol	Chain	Res	Type
1	E	341	ASN
2	C	115	SER
2	D	115	SER
1	A	465	SER

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	350/384 (91%)	333 (95%)	17 (5%)	22	56
1	B	353/384 (92%)	337 (96%)	16 (4%)	24	59
1	E	346/384 (90%)	332 (96%)	14 (4%)	28	62
1	G	348/384 (91%)	331 (95%)	17 (5%)	22	56
2	C	93/99 (94%)	88 (95%)	5 (5%)	20	53
2	D	93/99 (94%)	90 (97%)	3 (3%)	34	67
2	F	93/99 (94%)	88 (95%)	5 (5%)	20	53
2	H	93/99 (94%)	88 (95%)	5 (5%)	20	53
All	All	1769/1932 (92%)	1687 (95%)	82 (5%)	24	58

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	341	ASN
2	D	96	CYS
1	G	366	LYS
2	C	49	VAL
2	F	85	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	206	GLN

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Mol	Chain	Res	Type
2	D	77	ASN
1	G	324	GLN
2	C	55	GLN
2	F	40	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](#)

24 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	GLC	I	1	3	12,12,12	0.59	0	17,17,17	1.40	3 (17%)
3	GAL	I	2	3	11,11,12	0.57	0	15,15,17	1.15	2 (13%)
3	NAG	I	3	3	14,14,15	0.55	0	17,19,21	1.71	5 (29%)
3	GAL	I	4	3	11,11,12	0.84	0	15,15,17	1.17	2 (13%)
3	FUC	I	5	3	10,10,11	0.69	0	14,14,16	1.28	2 (14%)
3	FUC	I	6	3	10,10,11	0.61	0	14,14,16	1.09	1 (7%)
3	GLC	J	1	3	12,12,12	0.55	0	17,17,17	1.92	5 (29%)
3	GAL	J	2	3	11,11,12	0.60	0	15,15,17	1.43	3 (20%)
3	NAG	J	3	3	14,14,15	0.87	1 (7%)	17,19,21	2.46	7 (41%)
3	GAL	J	4	3	11,11,12	0.62	0	15,15,17	1.26	2 (13%)
3	FUC	J	5	3	10,10,11	0.80	0	14,14,16	1.23	1 (7%)
3	FUC	J	6	3	10,10,11	0.83	0	14,14,16	1.81	4 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GLC	K	1	3	12,12,12	0.46	0	17,17,17	0.52	0
3	GAL	K	2	3	11,11,12	0.47	0	15,15,17	1.30	2 (13%)
3	NAG	K	3	3	14,14,15	0.53	0	17,19,21	1.20	0
3	GAL	K	4	3	11,11,12	0.79	0	15,15,17	1.58	3 (20%)
3	FUC	K	5	3	10,10,11	0.76	0	14,14,16	1.06	1 (7%)
3	FUC	K	6	3	10,10,11	0.75	0	14,14,16	1.36	2 (14%)
3	GLC	L	1	3	12,12,12	0.58	0	17,17,17	1.03	2 (11%)
3	GAL	L	2	3	11,11,12	0.64	0	15,15,17	1.33	2 (13%)
3	NAG	L	3	3	14,14,15	0.45	0	17,19,21	1.49	3 (17%)
3	GAL	L	4	3	11,11,12	0.95	0	15,15,17	1.33	2 (13%)
3	FUC	L	5	3	10,10,11	0.77	0	14,14,16	1.36	3 (21%)
3	FUC	L	6	3	10,10,11	0.59	0	14,14,16	1.27	2 (14%)

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	GLC	I	1	3	-	0/2/22/22	0/1/1/1
3	GAL	I	2	3	-	2/2/19/22	0/1/1/1
3	NAG	I	3	3	-	0/6/23/26	0/1/1/1
3	GAL	I	4	3	-	2/2/19/22	0/1/1/1
3	FUC	I	5	3	-	-	0/1/1/1
3	FUC	I	6	3	-	-	0/1/1/1
3	GLC	J	1	3	-	0/2/22/22	0/1/1/1
3	GAL	J	2	3	-	2/2/19/22	0/1/1/1
3	NAG	J	3	3	-	0/6/23/26	0/1/1/1
3	GAL	J	4	3	-	1/2/19/22	0/1/1/1
3	FUC	J	5	3	-	-	0/1/1/1
3	FUC	J	6	3	-	-	0/1/1/1
3	GLC	K	1	3	-	0/2/22/22	0/1/1/1
3	GAL	K	2	3	-	2/2/19/22	0/1/1/1
3	NAG	K	3	3	-	0/6/23/26	0/1/1/1
3	GAL	K	4	3	-	1/2/19/22	0/1/1/1
3	FUC	K	5	3	-	-	0/1/1/1
3	FUC	K	6	3	-	-	0/1/1/1
3	GLC	L	1	3	-	1/2/22/22	0/1/1/1
3	GAL	L	2	3	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	L	3	3	-	0/6/23/26	0/1/1/1
3	GAL	L	4	3	-	2/2/19/22	0/1/1/1
3	FUC	L	5	3	-	-	0/1/1/1
3	FUC	L	6	3	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	3	NAG	C1-C2	2.15	1.55	1.52

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	3	NAG	O7-C7-N2	5.27	131.30	121.98
3	J	3	NAG	C1-C2-N2	4.79	117.98	110.43
3	J	1	GLC	C1-O5-C5	4.71	122.76	113.65
3	K	4	GAL	C1-O5-C5	4.29	117.94	112.19
3	J	6	FUC	O5-C5-C4	3.98	116.72	109.55

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

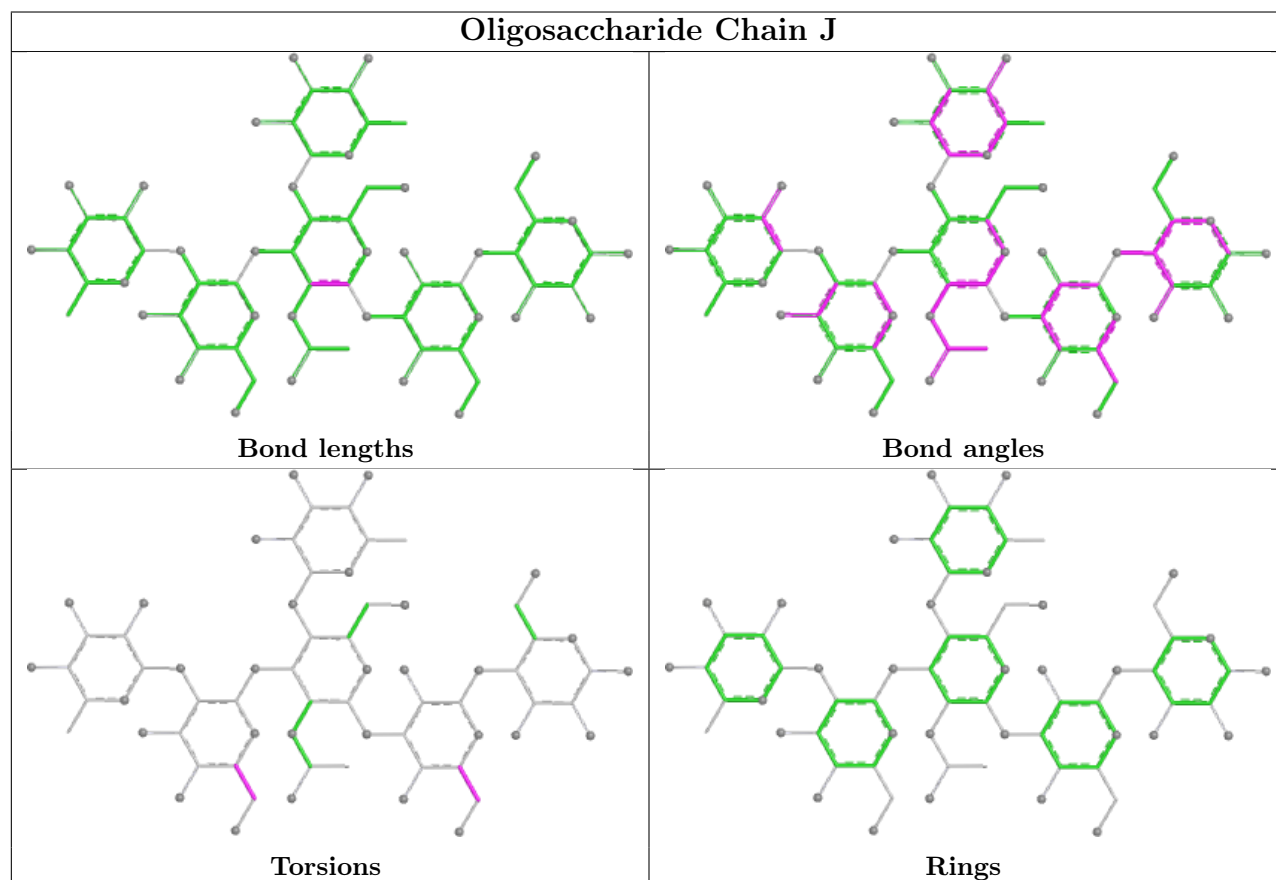
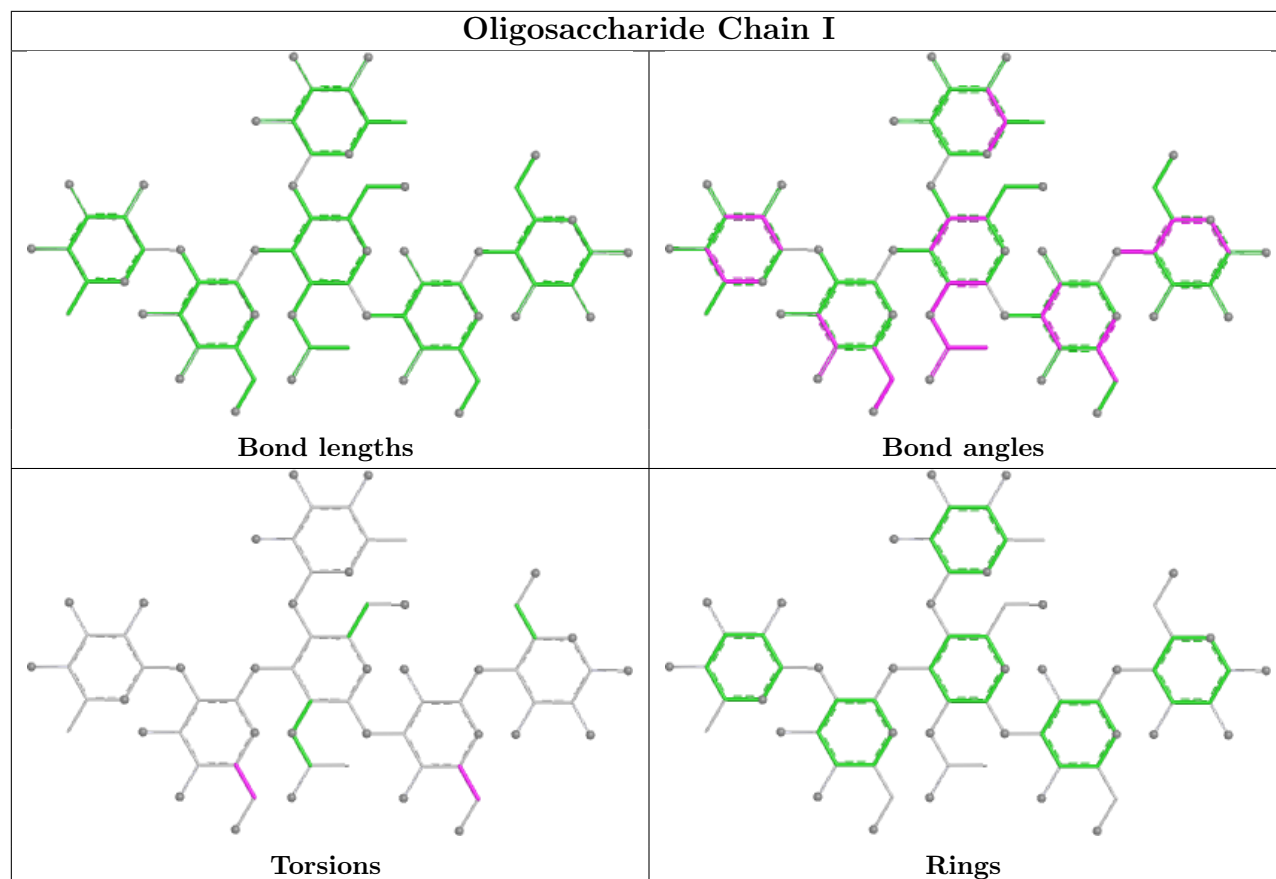
Mol	Chain	Res	Type	Atoms
3	J	2	GAL	O5-C5-C6-O6
3	K	2	GAL	O5-C5-C6-O6
3	I	2	GAL	O5-C5-C6-O6
3	I	4	GAL	O5-C5-C6-O6
3	I	2	GAL	C4-C5-C6-O6

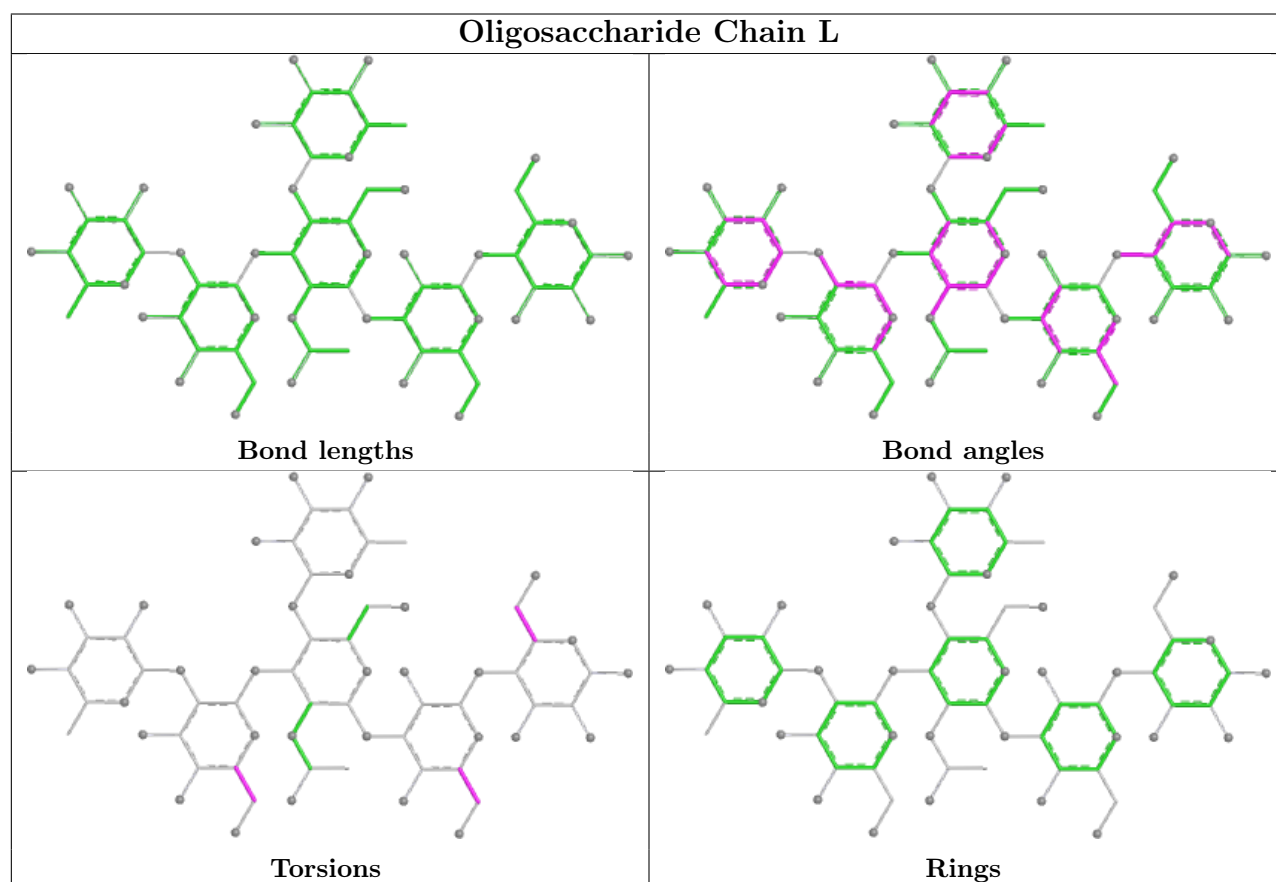
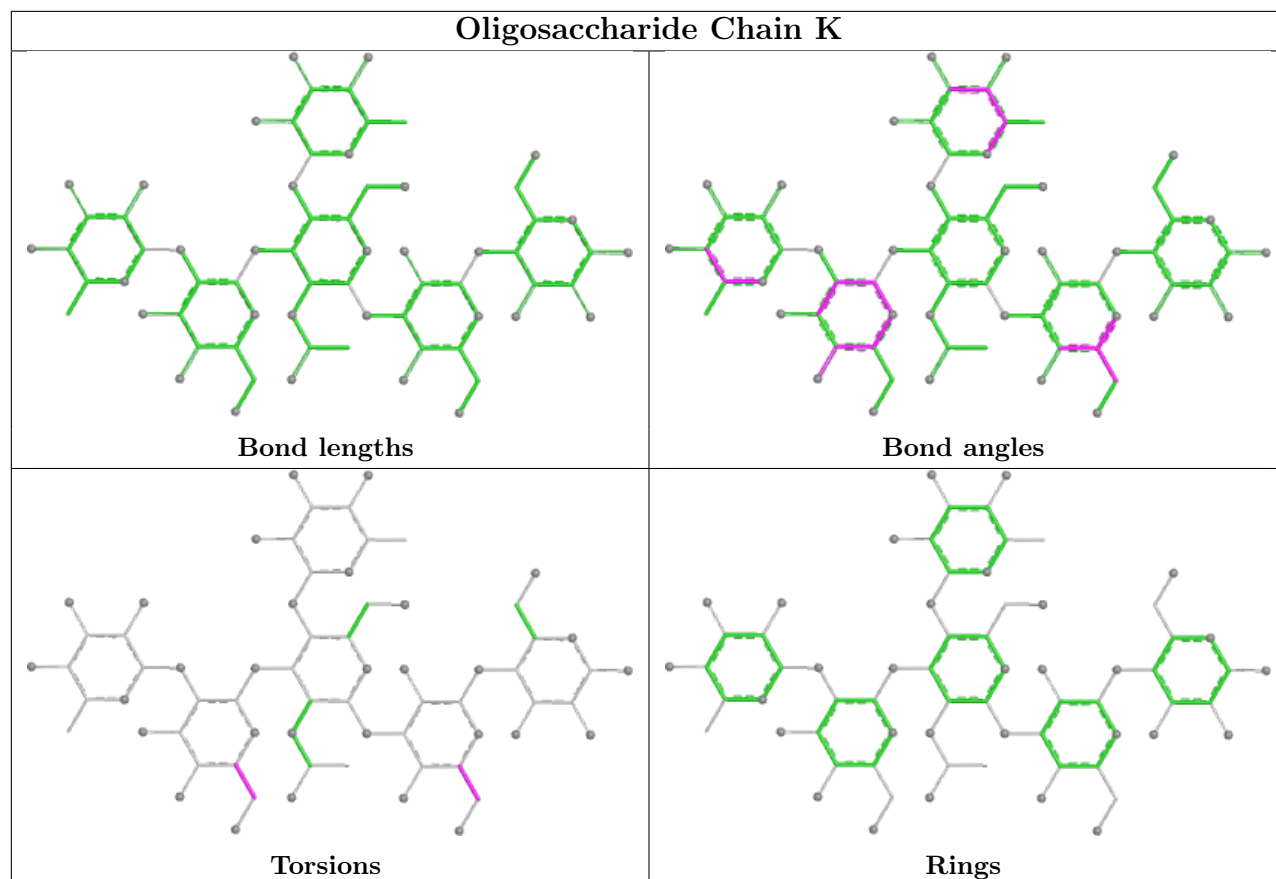
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	5	FUC	1	0
3	K	2	GAL	2	0
3	J	6	FUC	1	0
3	K	1	GLC	2	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](#)

There are no ligands in this entry.

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	424/469 (90%)	-0.37	7 (1%) 69 45	39, 62, 113, 136	0
1	B	426/469 (90%)	-0.30	6 (1%) 73 51	29, 61, 106, 142	2 (0%)
1	E	420/469 (89%)	-0.21	10 (2%) 59 36	41, 69, 123, 146	0
1	G	422/469 (89%)	-0.17	7 (1%) 69 45	41, 71, 127, 146	1 (0%)
2	C	114/120 (95%)	-0.36	2 (1%) 67 44	45, 69, 96, 135	0
2	D	114/120 (95%)	-0.46	2 (1%) 67 44	44, 66, 90, 127	0
2	F	114/120 (95%)	-0.39	1 (0%) 81 61	38, 56, 78, 116	0
2	H	114/120 (95%)	-0.39	2 (1%) 67 44	41, 59, 80, 119	0
All	All	2148/2356 (91%)	-0.29	37 (1%) 69 45	29, 65, 119, 146	3 (0%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	3	VAL	4.3
2	D	116	HIS	4.0
1	G	226	VAL	3.6
1	G	404	ALA	3.6
1	A	401	LYS	3.6

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,

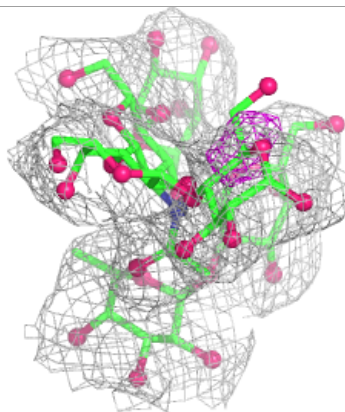
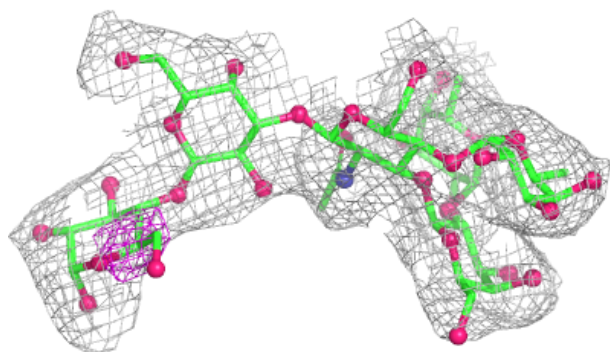
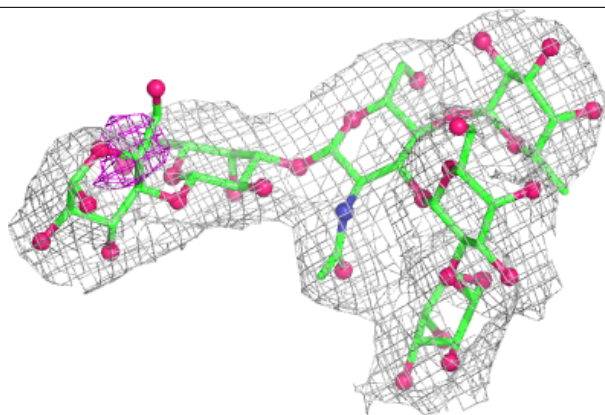
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GLC	K	1	12/12	0.39	0.15	89,110,130,135	0
3	GLC	J	1	12/12	0.51	0.13	103,118,124,124	0
3	GAL	J	2	11/12	0.62	0.14	68,93,107,110	0
3	GAL	L	2	11/12	0.64	0.12	96,113,123,125	0
3	FUC	L	6	10/11	0.64	0.12	100,102,105,109	0
3	GAL	K	2	11/12	0.65	0.12	85,112,123,125	0
3	GLC	I	1	12/12	0.68	0.10	92,98,104,107	0
3	GAL	K	4	11/12	0.74	0.11	71,83,89,91	0
3	GAL	L	4	11/12	0.76	0.11	73,90,95,95	0
3	GLC	L	1	12/12	0.76	0.09	93,104,117,122	0
3	FUC	K	6	10/11	0.86	0.10	83,91,102,108	0
3	GAL	I	2	11/12	0.87	0.08	74,87,91,94	0
3	NAG	L	3	14/15	0.87	0.09	78,90,101,101	0
3	FUC	J	5	10/11	0.90	0.11	58,63,68,73	0
3	FUC	I	6	10/11	0.90	0.09	72,77,79,81	0
3	GAL	I	4	11/12	0.91	0.07	54,59,65,71	0
3	NAG	J	3	14/15	0.91	0.09	48,65,68,68	0
3	NAG	K	3	14/15	0.92	0.08	80,88,93,95	0
3	FUC	J	6	10/11	0.92	0.08	67,72,81,82	0
3	FUC	L	5	10/11	0.92	0.08	78,85,90,91	0
3	FUC	K	5	10/11	0.92	0.08	69,79,83,85	0
3	GAL	J	4	11/12	0.93	0.06	57,62,67,69	0
3	NAG	I	3	14/15	0.94	0.07	55,63,64,67	0
3	FUC	I	5	10/11	0.95	0.06	46,48,50,50	0

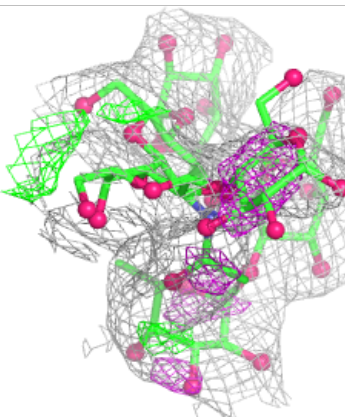
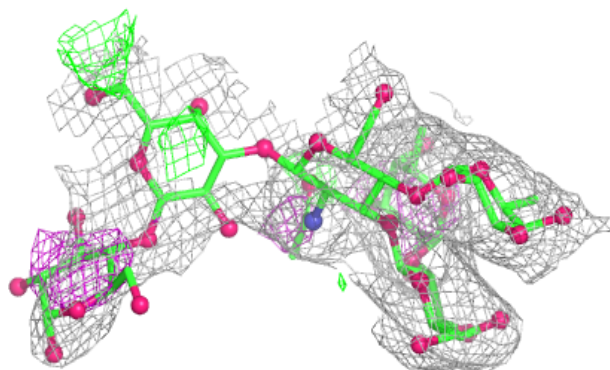
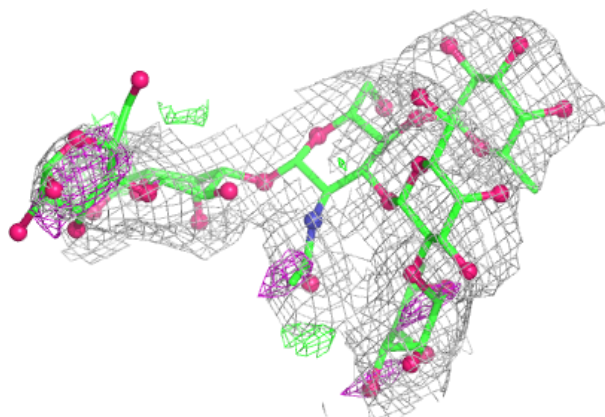
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain I:

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

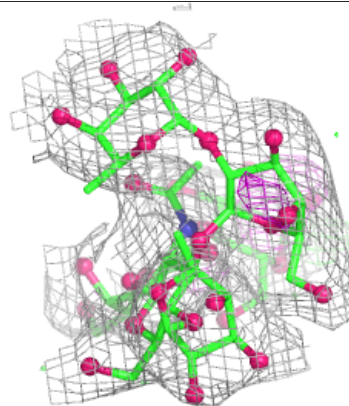
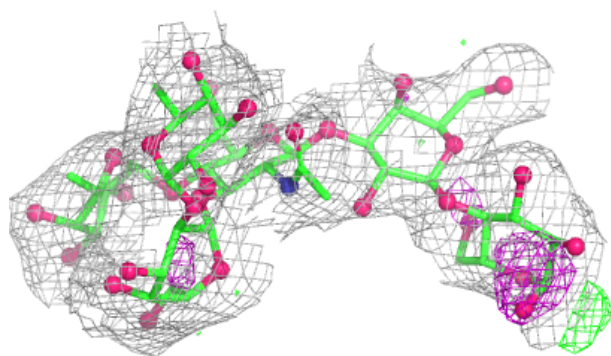
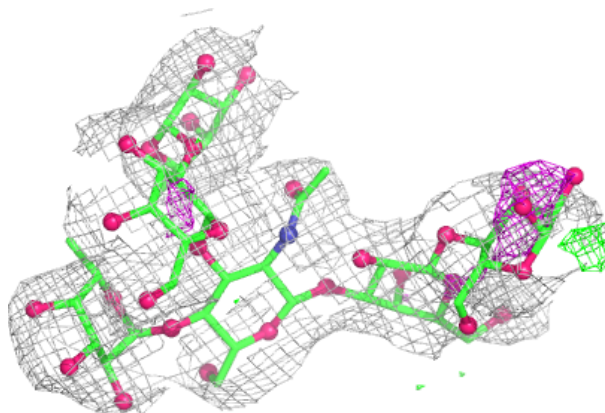
**Electron density around Chain J:**

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

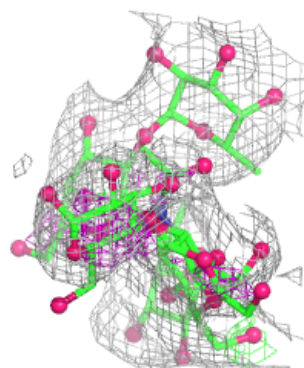
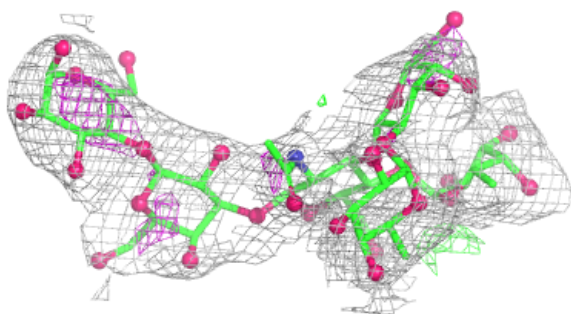
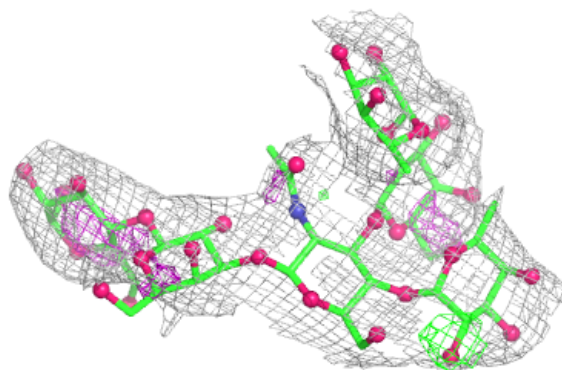


Electron density around Chain K:

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

**Electron density around Chain L:**

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



6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.