



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 10:04 PM BST

PDB ID : 5F93
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 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	:	2.13.1
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)	:	2.13.1

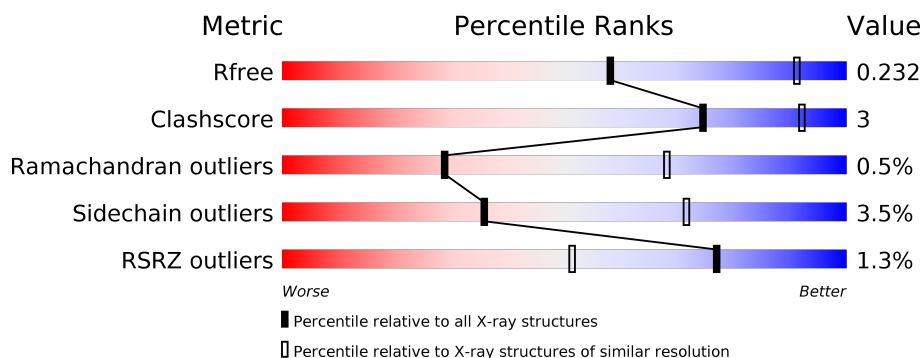
1 Overall quality at a glance

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.




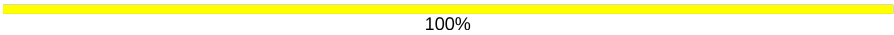
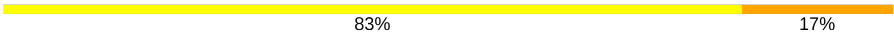
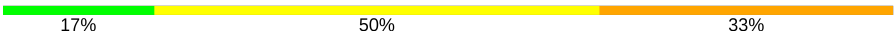
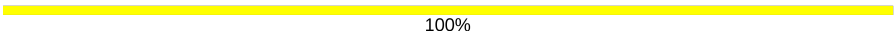
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 on 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	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>10%</div> </div> </div>
1	B	469	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>9%</div> <div>9%</div> </div> </div>
1	E	469	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>8%</div> <div>10%</div> </div> </div>
1	G	469	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>10%</div> <div>10%</div> </div> </div>
2	C	120	<div> <div></div> <div> <div>80%</div> <div>15%</div> <div>5%</div> </div> </div>
2	D	120	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	F	120	 88% 8% 5%
2	H	120	 84% 10% 5%
3	I	6	 100%
3	J	6	 83% 17%
3	K	6	 17% 50% 33%
3	L	6	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GLC	J	1	-	-	-	X

2 Entry composition

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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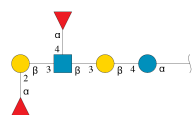
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Chain	Residue	Modelled	Actual	Comment	Reference
G	17	GLY	-	expression tag	UNP O52269
G	18	GLY	-	expression tag	UNP O52269
G	19	LEU	-	expression tag	UNP O52269
G	20	VAL	-	expression tag	UNP O52269
G	21	PRO	-	expression tag	UNP O52269
G	22	ARG	-	expression 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
2	C	114	Total 873	C 546	N 158	O 164	S 5	0	0	0
2	D	114	Total 873	C 546	N 158	O 164	S 5	0	0	0
2	F	114	Total 873	C 546	N 158	O 164	S 5	0	0	0
2	H	114	Total 873	C 546	N 158	O 164	S 5	0	0	0

- 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
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
3	K	6	Total	C	N	O	0	0	0
			68	38	1	29			
3	L	6	Total	C	N	O	0	0	0
			68	38	1	29			

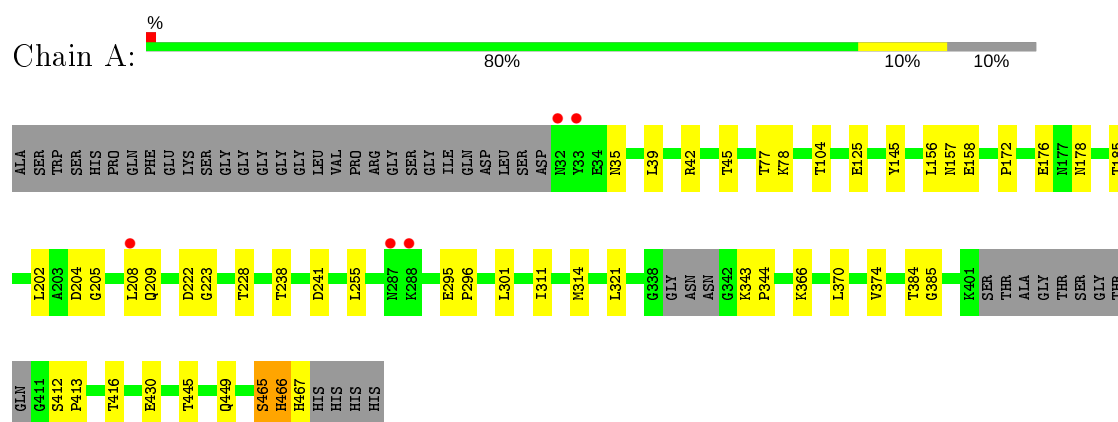
- Molecule 4 is water.

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		

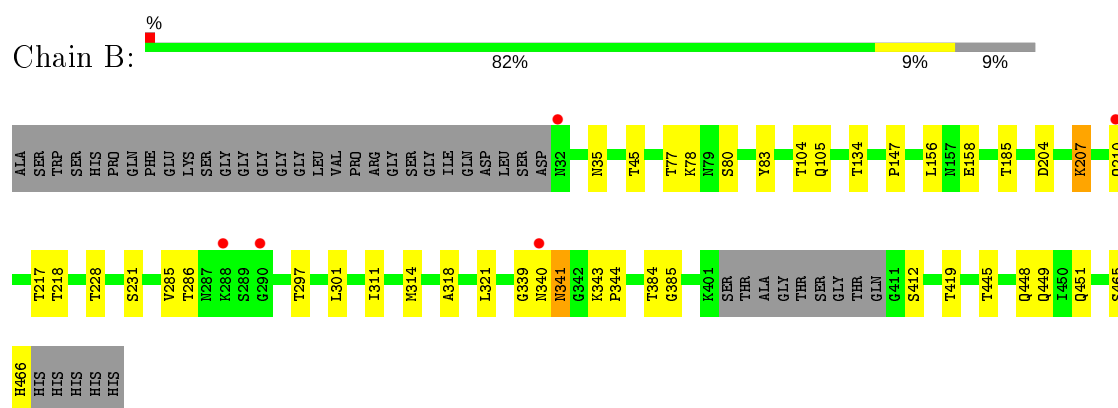
3 Residue-property plots

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.

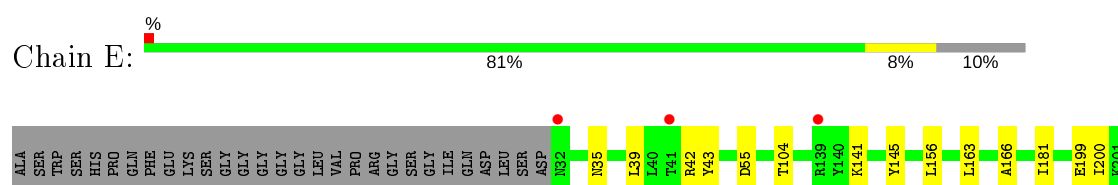
- Molecule 1: Adhesin binding fucosylated histo-blood group antigen,Adhesin,Adhesin binding fucosylated histo-blood group antigen




- 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 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%


GLC1
GAL2
NAG3
GAL4
FUC5
FUC6

- 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%

GLC1
GAL2
NAG3
GAL4
FUC5
FUC6

- 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%

GLC1
GAL2
NAG3
GAL4
FUC5
FUC6

- 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%

GLC1
GAL2
NAG3
GAL4
FUC5
FUC6

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)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.181 , 0.234 0.185 , 0.232	Depositor DCC
R_{free} test set	3241 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	67.2	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 49.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
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

Xtriage'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.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

5.1 Standard geometry

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

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	0.62	0/3234	0.74	0/4395
1	B	0.63	0/3261	0.75	0/4433
1	E	0.55	0/3198	0.70	0/4347
1	G	0.54	0/3217	0.70	0/4373
2	C	0.62	0/893	0.82	0/1210
2	D	0.60	0/893	0.78	0/1210
2	F	0.69	0/893	0.86	0/1210
2	H	0.71	0/893	0.82	0/1210
All	All	0.60	0/16482	0.74	0/22388

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

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

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	20	0
1	B	3205	0	3106	23	0
1	E	3149	0	3047	20	0
1	G	3165	0	3063	20	0
2	C	873	0	852	7	0
2	D	873	0	852	5	0
2	F	873	0	852	3	0
2	H	873	0	852	6	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	102	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 102 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)
2:F:3:VAL:N	2:F:26:SER:HG	1.86	0.74
1:G:202:LEU:HD23	1:G:206:GLN:O	1.90	0.71
1:B:339:GLY:O	1:B:341:ASN:N	2.30	0.64
1:A:35:ASN:OD1	1:A:35:ASN:C	2.38	0.62
1:B:465:SER:O	1:B:466:HIS:HB2	2.01	0.61

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	47	82
1	B	424/469 (90%)	401 (95%)	22 (5%)	1 (0%)	47	82
1	E	414/469 (88%)	383 (92%)	30 (7%)	1 (0%)	47	82
1	G	417/469 (89%)	385 (92%)	28 (7%)	4 (1%)	15	53
2	C	112/120 (93%)	107 (96%)	4 (4%)	1 (1%)	17	55
2	D	112/120 (93%)	109 (97%)	2 (2%)	1 (1%)	17	55
2	F	112/120 (93%)	108 (96%)	3 (3%)	1 (1%)	17	55
2	H	112/120 (93%)	104 (93%)	7 (6%)	1 (1%)	17	55
All	All	2121/2356 (90%)	1991 (94%)	119 (6%)	11 (0%)	29	68

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	340	ASN
1	E	341	ASN
2	C	115	SER
2	D	115	SER
1	A	465	SER

5.3.2 Protein sidechains

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%)	337 (96%)	13 (4%)	34	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	353/384 (92%)	342 (97%)	11 (3%)	40	75
1	E	346/384 (90%)	334 (96%)	12 (4%)	36	71
1	G	348/384 (91%)	336 (97%)	12 (3%)	37	72
2	C	93/99 (94%)	89 (96%)	4 (4%)	29	66
2	D	93/99 (94%)	90 (97%)	3 (3%)	39	74
2	F	93/99 (94%)	90 (97%)	3 (3%)	39	74
2	H	93/99 (94%)	90 (97%)	3 (3%)	39	74
All	All	1769/1932 (92%)	1708 (97%)	61 (3%)	36	72

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	202	LEU
1	E	419	THR
2	F	85	SER
1	E	227	SER
1	E	334	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	124	ASN
1	G	161	GLN
2	D	77	ASN
1	G	109	ASN
2	F	55	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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	1.41	3 (17%)
3	GAL	I	2	3	11,11,12	0.58	0	15,15,17	1.32	2 (13%)
3	NAG	I	3	3	14,14,15	0.56	0	17,19,21	1.68	4 (23%)
3	GAL	I	4	3	11,11,12	0.85	0	15,15,17	1.20	2 (13%)
3	FUC	I	5	3	10,10,11	0.70	0	14,14,16	1.37	2 (14%)
3	FUC	I	6	3	10,10,11	0.62	0	14,14,16	1.15	1 (7%)
3	GLC	J	1	3	12,12,12	0.54	0	17,17,17	1.95	5 (29%)
3	GAL	J	2	3	11,11,12	0.61	0	15,15,17	1.63	3 (20%)
3	NAG	J	3	3	14,14,15	0.84	0	17,19,21	2.37	8 (47%)
3	GAL	J	4	3	11,11,12	0.64	0	15,15,17	1.38	3 (20%)
3	FUC	J	5	3	10,10,11	0.81	0	14,14,16	1.42	2 (14%)
3	FUC	J	6	3	10,10,11	0.83	0	14,14,16	2.00	6 (42%)
3	GLC	K	1	3	12,12,12	0.45	0	17,17,17	0.52	0
3	GAL	K	2	3	11,11,12	0.48	0	15,15,17	1.53	2 (13%)
3	NAG	K	3	3	14,14,15	0.54	0	17,19,21	1.18	0
3	GAL	K	4	3	11,11,12	0.82	0	15,15,17	1.67	4 (26%)
3	FUC	K	5	3	10,10,11	0.77	0	14,14,16	1.25	2 (14%)
3	FUC	K	6	3	10,10,11	0.76	0	14,14,16	1.50	3 (21%)
3	GLC	L	1	3	12,12,12	0.59	0	17,17,17	1.03	2 (11%)
3	GAL	L	2	3	11,11,12	0.65	0	15,15,17	1.50	2 (13%)
3	NAG	L	3	3	14,14,15	0.46	0	17,19,21	1.53	4 (23%)
3	GAL	L	4	3	11,11,12	0.99	1 (9%)	15,15,17	1.45	3 (20%)
3	FUC	L	5	3	10,10,11	0.78	0	14,14,16	1.66	3 (21%)
3	FUC	L	6	3	10,10,11	0.60	0	14,14,16	1.36	3 (21%)

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
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	L	4	GAL	C1-C2	2.09	1.57	1.52

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	3	NAG	O7-C7-N2	5.09	131.30	121.95
3	J	1	GLC	C1-O5-C5	4.82	122.76	113.66
3	K	2	GAL	O5-C5-C6	4.49	114.24	107.20
3	J	3	NAG	C1-C2-N2	4.38	117.98	110.49
3	K	4	GAL	C1-O5-C5	4.24	117.94	112.19

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

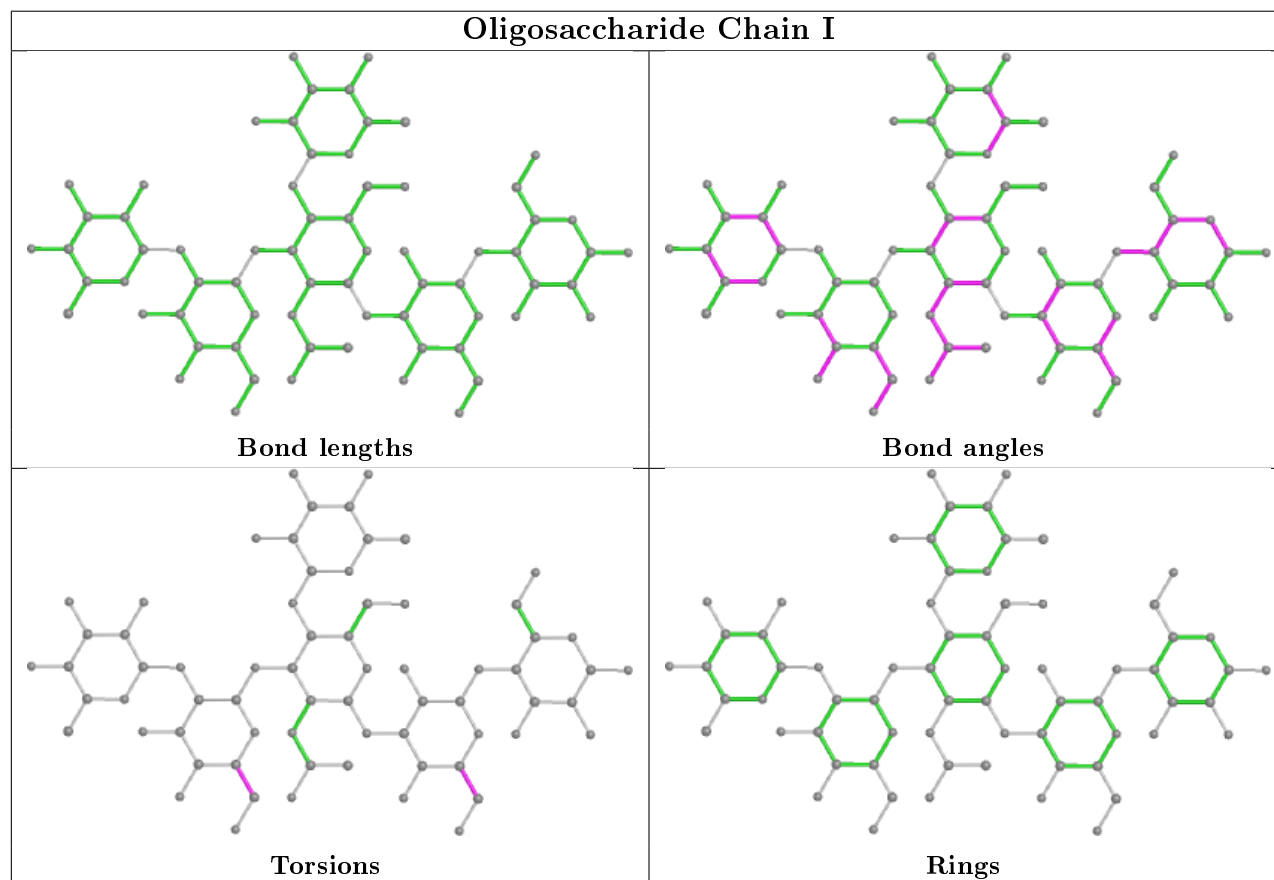
Mol	Chain	Res	Type	Atoms
3	J	2	GAL	O5-C5-C6-O6
3	K	2	GAL	O5-C5-C6-O6
3	I	2	GAL	O5-C5-C6-O6
3	I	4	GAL	O5-C5-C6-O6
3	I	2	GAL	C4-C5-C6-O6

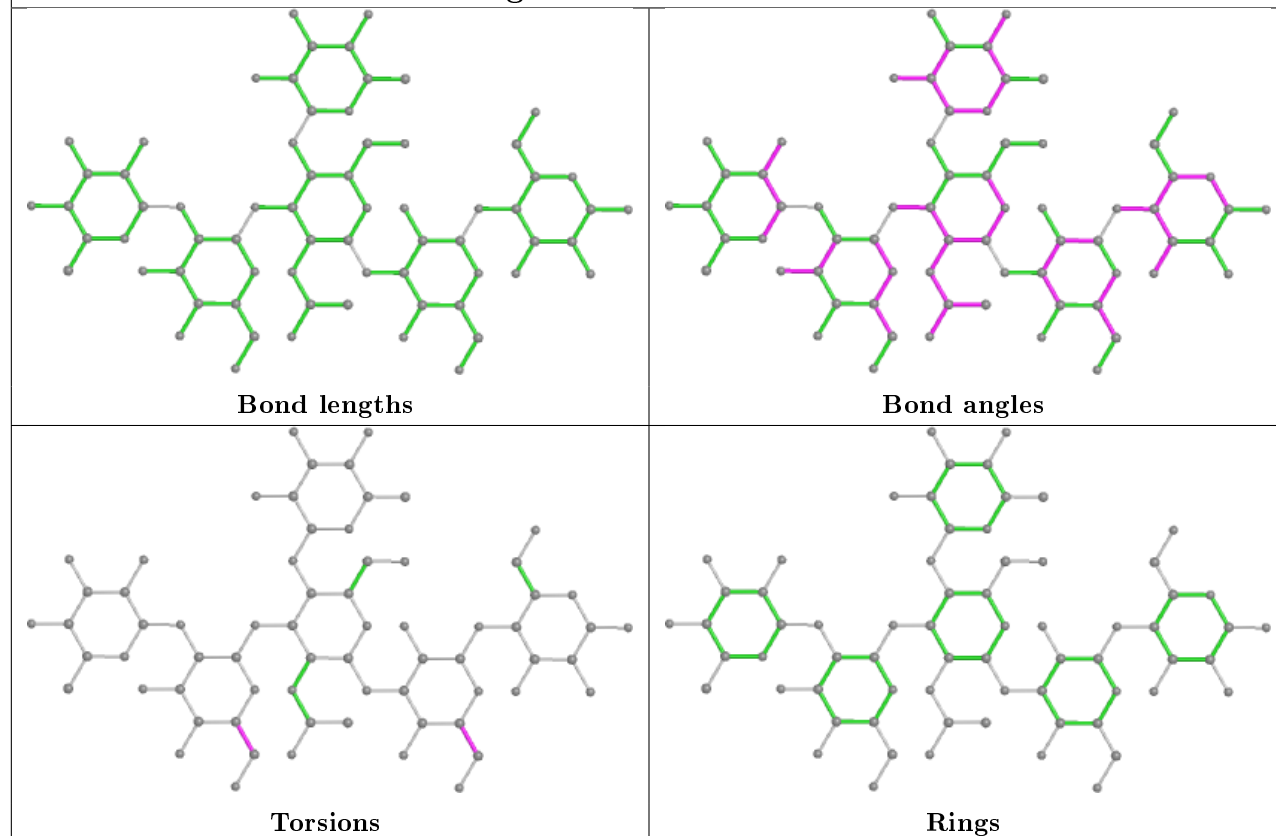
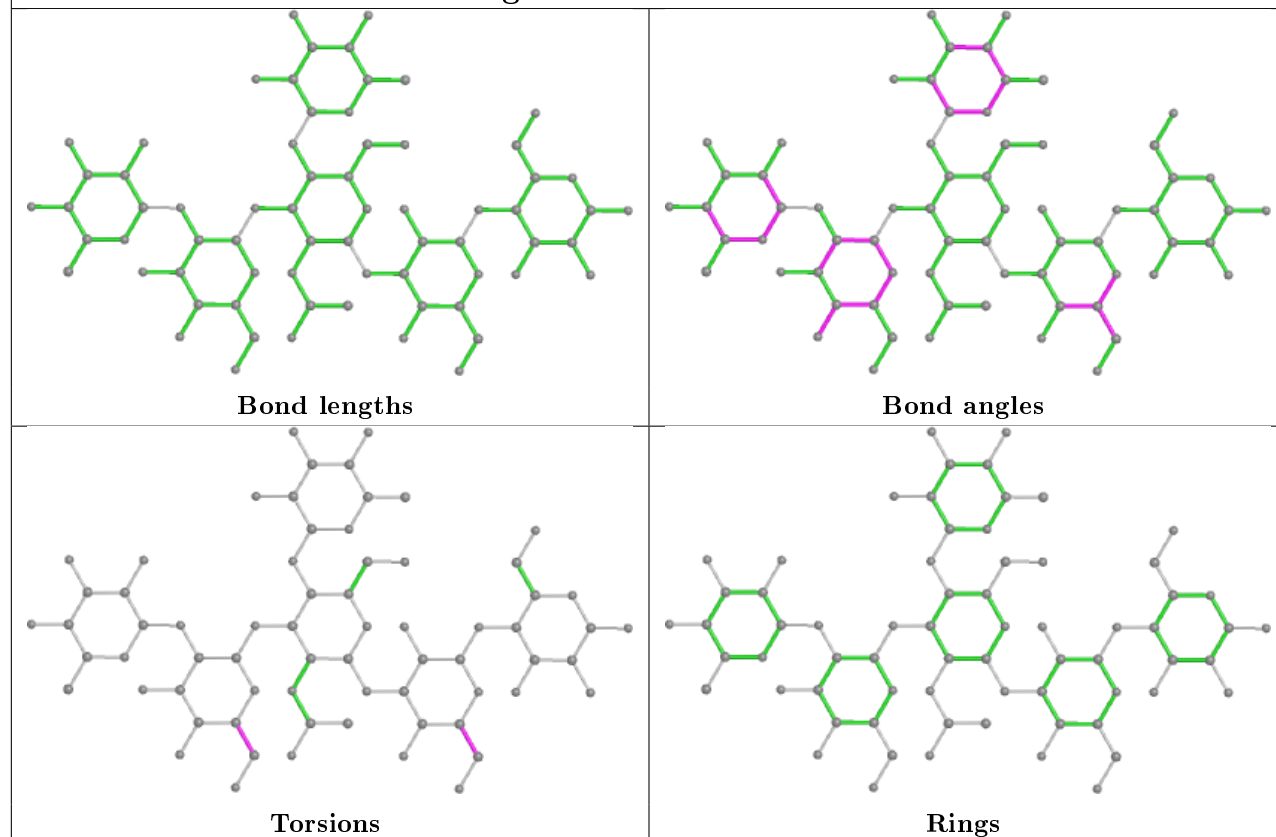
There are no ring outliers.

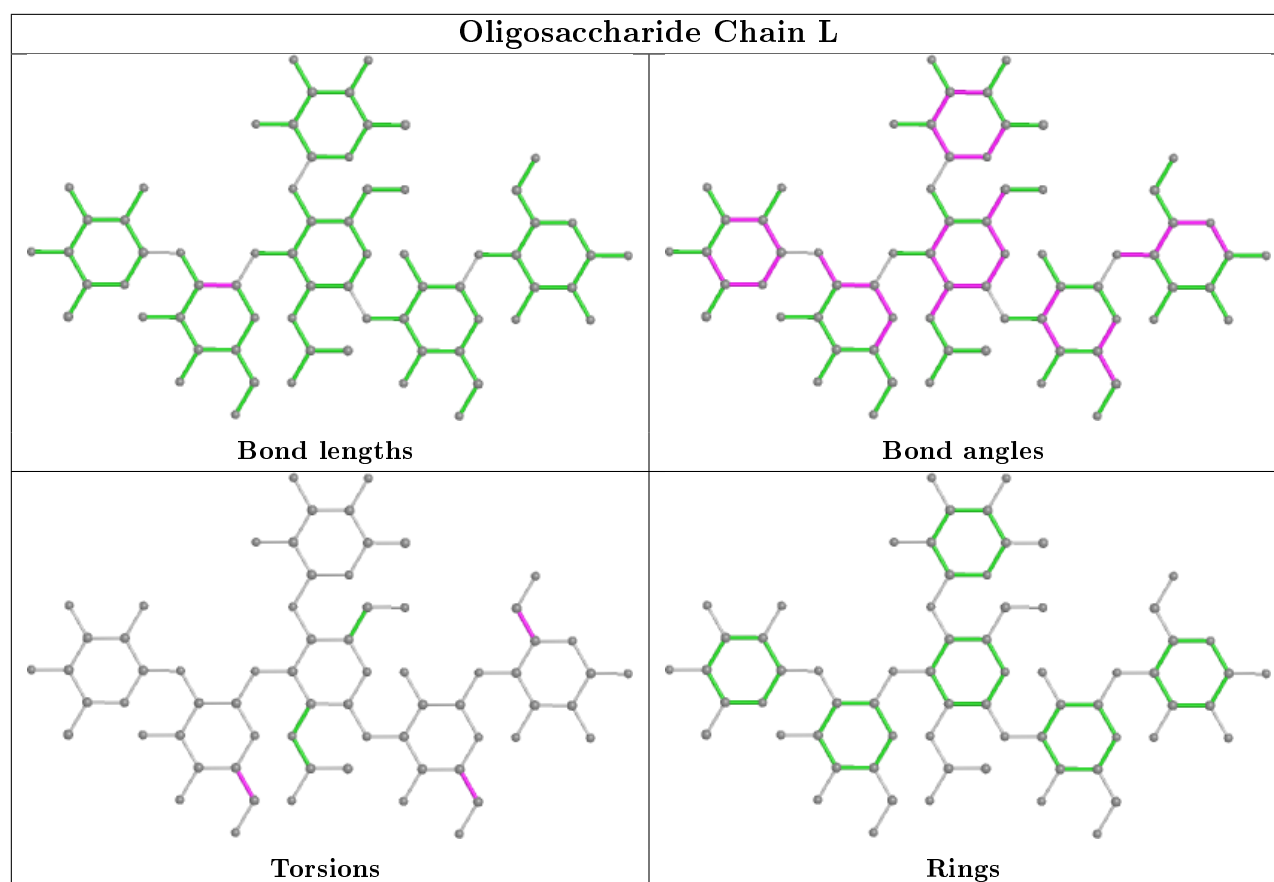
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	5	FUC	1	0
3	K	1	GLC	2	0
3	J	6	FUC	1	0
3	K	2	GAL	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.



Oligosaccharide Chain J**Oligosaccharide Chain K**



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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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%)	-0.15	5 (1%) 79 54	39, 62, 113, 136	0
1	B	426/469 (90%)	-0.21	5 (1%) 79 54	38, 61, 106, 142	0
1	E	420/469 (89%)	-0.11	6 (1%) 75 49	41, 69, 123, 146	0
1	G	422/469 (89%)	-0.03	10 (2%) 59 30	41, 71, 127, 146	0
2	C	114/120 (95%)	-0.19	0 100 100	45, 69, 96, 135	0
2	D	114/120 (95%)	-0.26	1 (0%) 84 63	44, 66, 90, 127	0
2	F	114/120 (95%)	-0.26	0 100 100	38, 56, 78, 116	0
2	H	114/120 (95%)	-0.29	1 (0%) 84 63	41, 59, 80, 119	0
All	All	2148/2356 (91%)	-0.15	28 (1%) 77 51	38, 65, 119, 146	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	32	ASN	4.9
1	B	32	ASN	4.4
1	G	290	GLY	4.2
1	E	32	ASN	3.6
2	H	3	VAL	3.5

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

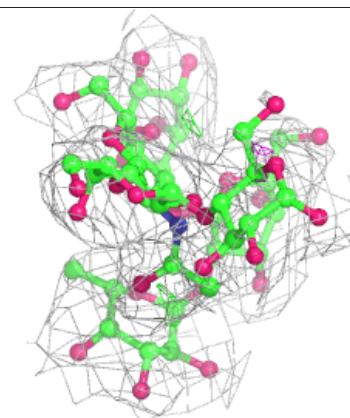
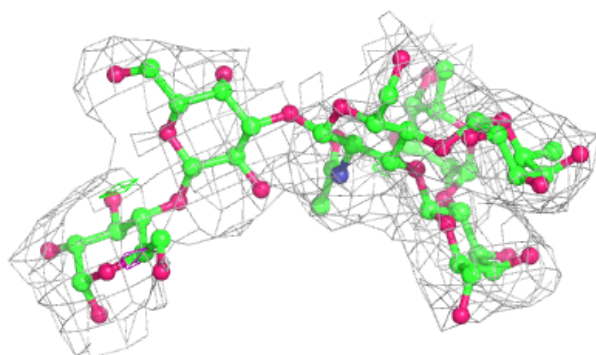
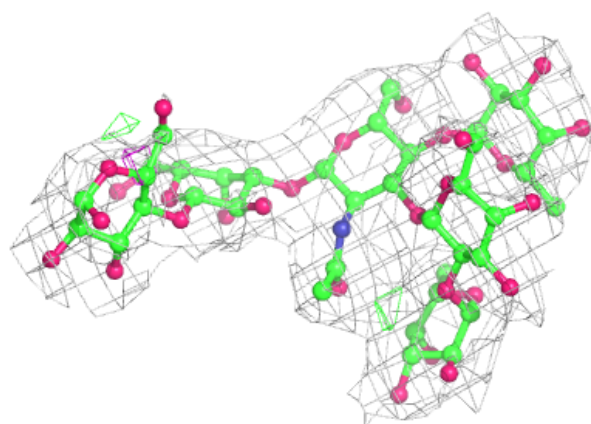
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GLC	K	1	12/12	0.77	0.31	89,110,130,135	0
3	GLC	J	1	12/12	0.79	0.54	103,118,124,124	0
3	GAL	L	2	11/12	0.84	0.32	96,113,123,125	0
3	GLC	I	1	12/12	0.84	0.35	92,98,104,107	0
3	GLC	L	1	12/12	0.85	0.39	93,104,117,122	0
3	GAL	K	2	11/12	0.85	0.27	85,112,123,125	0
3	GAL	J	2	11/12	0.87	0.21	68,93,107,110	0
3	GAL	K	4	11/12	0.88	0.19	71,83,89,91	0
3	GAL	L	4	11/12	0.89	0.34	73,90,95,95	0
3	FUC	L	6	10/11	0.89	0.34	100,102,105,109	0
3	FUC	K	6	10/11	0.91	0.33	83,91,102,108	0
3	NAG	J	3	14/15	0.93	0.16	48,65,68,68	0
3	NAG	L	3	14/15	0.94	0.25	78,90,101,101	0
3	GAL	I	2	11/12	0.94	0.23	74,87,91,94	0
3	FUC	I	6	10/11	0.94	0.26	72,77,79,81	0
3	FUC	L	5	10/11	0.94	0.26	78,85,90,91	0
3	GAL	J	4	11/12	0.95	0.17	57,62,67,69	0
3	FUC	K	5	10/11	0.95	0.25	69,79,83,85	0
3	FUC	J	5	10/11	0.95	0.30	58,63,68,73	0
3	NAG	K	3	14/15	0.95	0.19	80,88,93,95	0
3	GAL	I	4	11/12	0.95	0.17	54,59,65,71	0
3	NAG	I	3	14/15	0.96	0.15	55,63,64,67	0
3	FUC	J	6	10/11	0.96	0.21	67,72,81,82	0
3	FUC	I	5	10/11	0.98	0.18	46,48,50,50	0

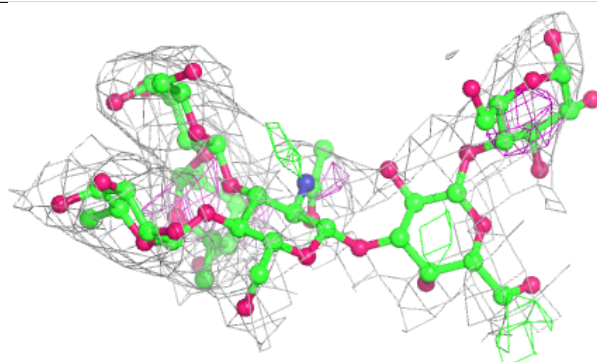
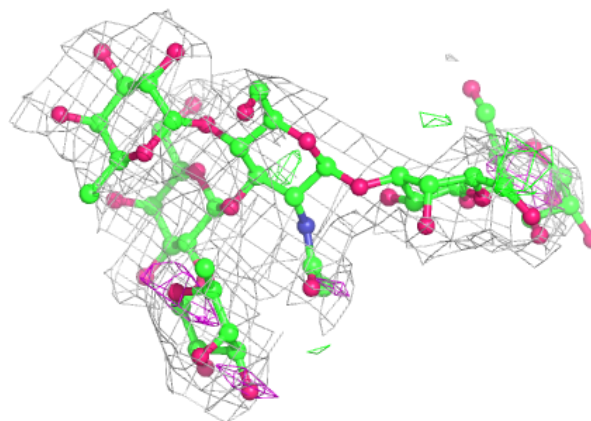
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

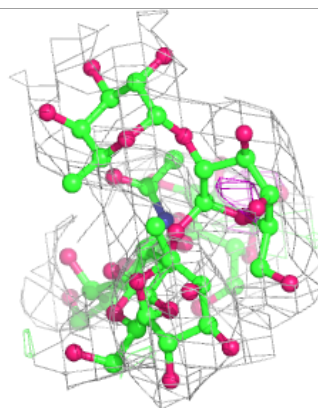
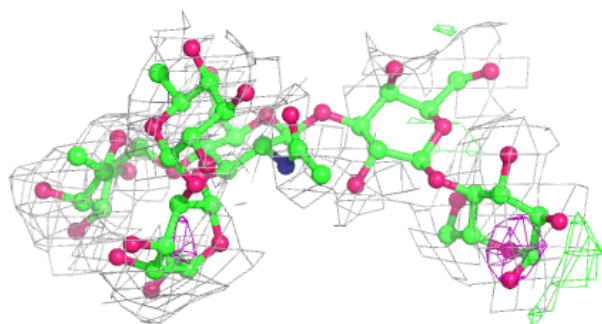
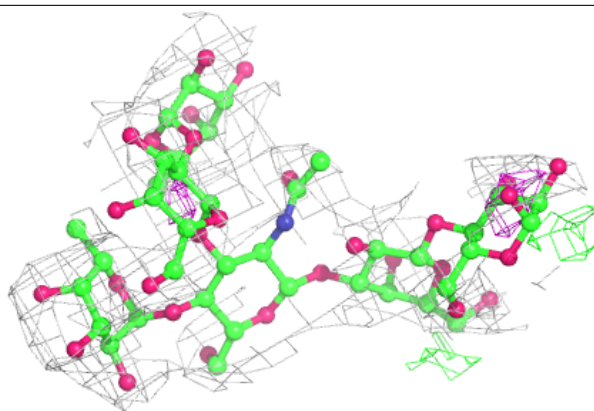
**Electron density around Chain J:**

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

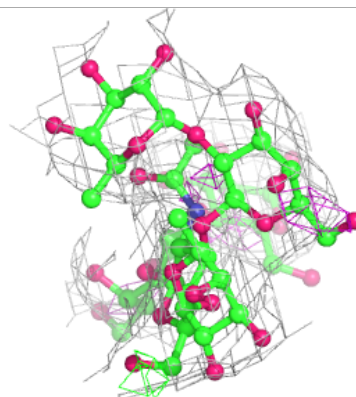
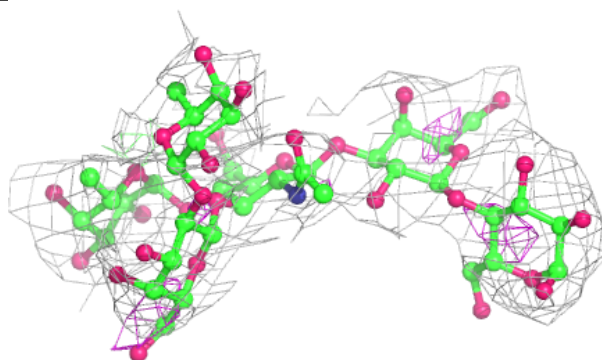
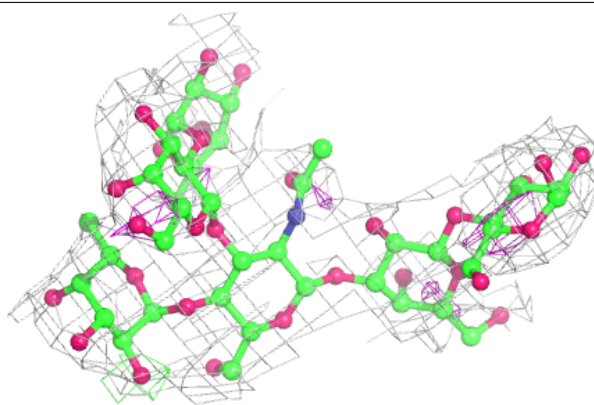


Electron density around Chain K:

$2mF_o-DF_c$ (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.