



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 12:31 PM BST

PDB ID : 5GQF
Title : Crystal structure of lacto-N-biosidase LnbX from Bifidobacterium longum subsp. longum, lacto-N-biose complex
Authors : Yamada, C.; Arakawa, T.; Katayama, T.; Fushinobu, S.
Deposited on : 2016-08-07
Resolution : 1.82 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

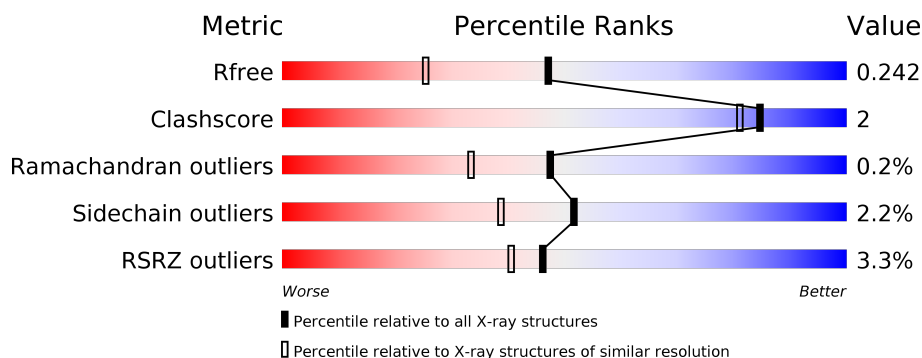
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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	606	<div> <div>5%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>• •</div> </div> </div>
1	B	606	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>9%</div> <div>•</div> </div> </div>
2	C	2	<div> <div>50%</div> <div>50%</div> </div>
2	D	2	<div> <div>50%</div> <div>50%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10102 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 Lacto-N-biosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	0	0	0
			4468	2760	772	924	12			
1	B	582	Total	C	N	O	S	0	0	0
			4468	2760	772	924	12			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	expression tag	UNP A0A024QYS6
A	626	ALA	-	expression tag	UNP A0A024QYS6
A	627	ALA	-	expression tag	UNP A0A024QYS6
A	628	LEU	-	expression tag	UNP A0A024QYS6
A	629	GLU	-	expression tag	UNP A0A024QYS6
A	630	HIS	-	expression tag	UNP A0A024QYS6
A	631	HIS	-	expression tag	UNP A0A024QYS6
A	632	HIS	-	expression tag	UNP A0A024QYS6
A	633	HIS	-	expression tag	UNP A0A024QYS6
A	634	HIS	-	expression tag	UNP A0A024QYS6
A	635	HIS	-	expression tag	UNP A0A024QYS6
B	30	MET	-	expression tag	UNP A0A024QYS6
B	626	ALA	-	expression tag	UNP A0A024QYS6
B	627	ALA	-	expression tag	UNP A0A024QYS6
B	628	LEU	-	expression tag	UNP A0A024QYS6
B	629	GLU	-	expression tag	UNP A0A024QYS6
B	630	HIS	-	expression tag	UNP A0A024QYS6
B	631	HIS	-	expression tag	UNP A0A024QYS6
B	632	HIS	-	expression tag	UNP A0A024QYS6
B	633	HIS	-	expression tag	UNP A0A024QYS6
B	634	HIS	-	expression tag	UNP A0A024QYS6
B	635	HIS	-	expression tag	UNP A0A024QYS6

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			26	14	1	11			
2	D	2	Total	C	N	O	0	0	0
			26	14	1	11			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		
3	A	2	Total	Ca	0	0
			2	2		

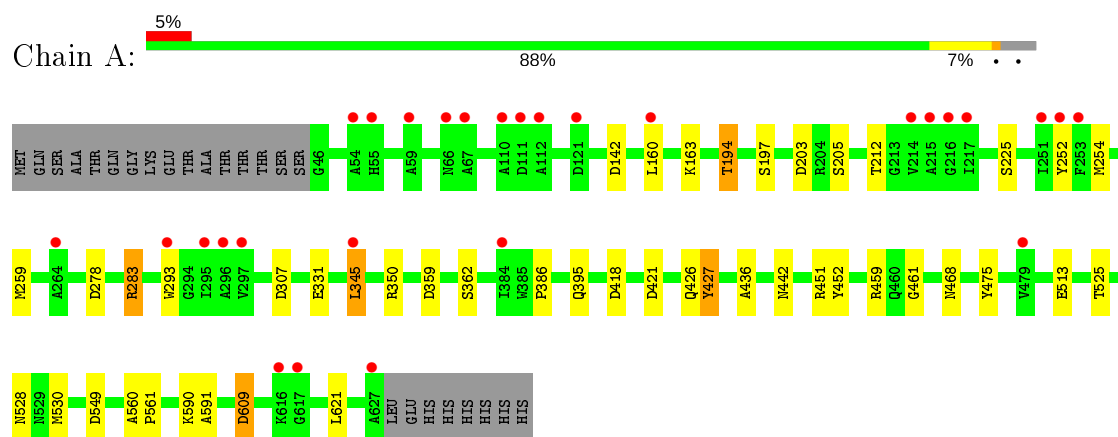
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	530	Total	O	0	0
			530	530		
4	B	580	Total	O	0	0
			580	580		

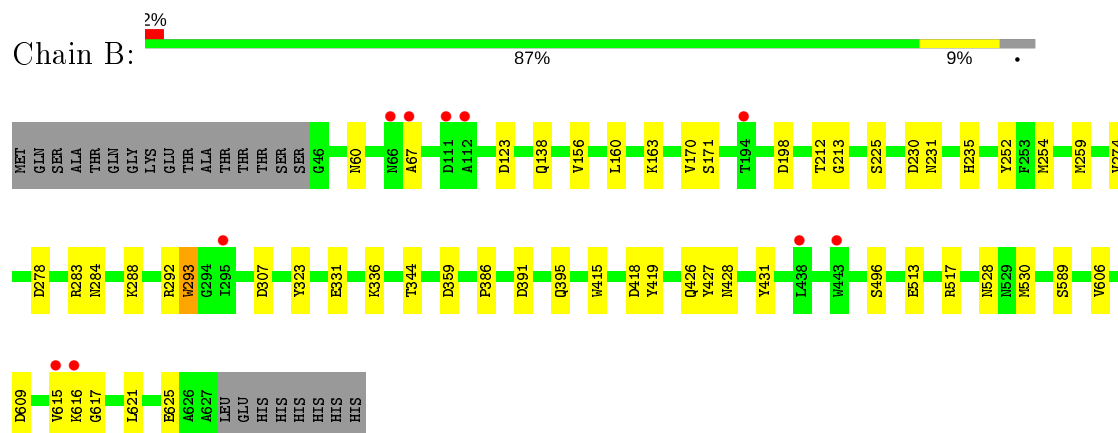
3 Residue-property plots [i](#)

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: Lacto-N-biosidase



- Molecule 1: Lacto-N-biosidase



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



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





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.03Å 143.62Å 146.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	102.45 – 1.82 31.28 – 1.82	Depositor EDS
% Data completeness (in resolution range)	96.3 (102.45-1.82) 96.3 (31.28-1.82)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.181 , 0.236 0.193 , 0.242	Depositor DCC
R_{free} test set	1991 reflections (1.70%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.009 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10102	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, GAL, 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	1.01	3/4567 (0.1%)	0.97	13/6224 (0.2%)
1	B	1.06	5/4567 (0.1%)	0.98	7/6224 (0.1%)
All	All	1.04	8/9134 (0.1%)	0.98	20/12448 (0.2%)

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	B	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	513	GLU	CD-OE2	6.88	1.33	1.25
1	A	362	SER	CA-CB	6.31	1.62	1.52
1	B	513	GLU	CD-OE2	5.80	1.32	1.25
1	B	419	TYR	CE1-CZ	-5.62	1.31	1.38
1	B	213	GLY	N-CA	5.37	1.54	1.46
1	A	205	SER	CA-CB	5.36	1.60	1.52
1	B	589	SER	CA-CB	5.19	1.60	1.52
1	B	431	TYR	CB-CG	5.13	1.59	1.51

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	ASP	CB-CG-OD1	7.92	125.43	118.30
1	A	350	ARG	NE-CZ-NH1	7.59	124.09	120.30
1	A	350	ARG	NE-CZ-NH2	-7.45	116.57	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	307	ASP	CB-CG-OD1	7.17	124.75	118.30
1	B	292	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	A	359	ASP	CB-CG-OD1	6.36	124.03	118.30
1	A	459	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	B	609	ASP	CB-CG-OD1	6.14	123.82	118.30
1	A	609	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	283	ARG	NE-CZ-NH2	-5.81	117.40	120.30
1	A	203	ASP	CB-CG-OD1	5.55	123.30	118.30
1	A	549	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	421	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	B	391	ASP	CB-CG-OD1	5.25	123.03	118.30
1	B	307	ASP	CB-CG-OD1	5.22	123.00	118.30
1	B	198	ASP	CB-CG-OD2	5.21	122.99	118.30
1	B	123	ASP	CB-CG-OD2	-5.14	113.67	118.30
1	B	517	ARG	NE-CZ-NH1	5.11	122.85	120.30
1	A	345	LEU	CB-CG-CD2	5.10	119.67	111.00
1	A	283	ARG	NE-CZ-NH1	5.09	122.84	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	617	GLY	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	4468	0	4135	18	0
1	B	4468	0	4135	21	0
2	C	26	0	24	1	0
2	D	26	0	24	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	530	0	0	4	0
4	B	580	0	0	1	0
All	All	10102	0	8318	39	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 2.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:590:LYS:HD2	4:A:1315:HOH:O	1.78	0.82
1:A:194:THR:HG22	4:A:994:HOH:O	1.84	0.77
1:A:194:THR:HG23	1:A:197:SER:HB3	1.84	0.58
1:A:418:ASP:OD2	2:C:1:NAG:H1	2.04	0.57
1:B:336:LYS:NZ	4:B:803:HOH:O	2.37	0.53
1:A:283:ARG:HA	1:A:331:GLU:O	2.09	0.52
1:B:606:VAL:HG12	1:B:615:VAL:CG2	2.39	0.52
1:B:606:VAL:HG12	1:B:615:VAL:HG21	1.92	0.52
1:A:525:THR:HG23	4:A:927:HOH:O	2.09	0.51
1:B:606:VAL:CG1	1:B:615:VAL:HG21	2.41	0.51
1:B:395:GLN:HA	1:B:426:GLN:O	2.12	0.50
1:A:194:THR:CG2	4:A:994:HOH:O	2.51	0.49
1:B:293:TRP:HZ2	1:B:344:THR:HG1	1.59	0.49
1:B:283:ARG:HA	1:B:331:GLU:O	2.12	0.49
1:B:615:VAL:HG12	1:B:625:GLU:HG3	1.95	0.48
1:B:225:SER:HA	1:B:278:ASP:O	2.14	0.47
1:A:436:ALA:HA	1:A:461:GLY:O	2.14	0.47
1:B:415:TRP:CZ2	1:B:428:ASN:HB3	2.50	0.46
1:B:418:ASP:OD2	2:D:1:NAG:H1	2.16	0.46
1:A:442:ASN:O	1:A:468:ASN:HA	2.16	0.46
1:A:427:TYR:HA	1:A:452:TYR:O	2.17	0.45
1:B:530:MET:HB2	1:B:621:LEU:HD13	1.99	0.45
1:A:530:MET:HB2	1:A:621:LEU:HD13	1.97	0.45
1:B:60:ASN:OD1	1:B:67:ALA:HB1	2.16	0.44
1:A:225:SER:HA	1:A:278:ASP:O	2.17	0.44
1:A:426:GLN:HA	1:A:451:ARG:O	2.17	0.44
1:B:615:VAL:O	1:B:615:VAL:HG23	2.18	0.44
1:A:395:GLN:HA	1:A:426:GLN:O	2.17	0.43
1:B:336:LYS:HA	1:B:359:ASP:O	2.16	0.43
1:A:591:ALA:HA	1:A:621:LEU:HD12	2.01	0.43
1:B:160:LEU:HD21	1:B:170:VAL:HG11	2.01	0.43
1:B:138:GLN:HA	1:B:156:VAL:O	2.18	0.42
1:B:274:VAL:HG11	1:B:323:TYR:HA	2.01	0.42
1:A:451:ARG:HA	1:A:475:TYR:O	2.20	0.42
1:B:171:SER:HA	1:B:230:ASP:O	2.20	0.42
1:A:452:TYR:CD1	1:A:609:ASP:HA	2.55	0.41
1:A:560:ALA:HB1	1:A:561:PRO:CD	2.51	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:ASN:HA	1:B:284:ASN:O	2.21	0.40
1:B:235:HIS:HA	1:B:288:LYS:O	2.21	0.40

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	580/606 (96%)	547 (94%)	32 (6%)	1 (0%)	47 33
1	B	580/606 (96%)	553 (95%)	26 (4%)	1 (0%)	47 33
All	All	1160/1212 (96%)	1100 (95%)	58 (5%)	2 (0%)	47 33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	386	PRO
1	B	386	PRO

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	470/491 (96%)	459 (98%)	11 (2%)	50 37
1	B	470/491 (96%)	460 (98%)	10 (2%)	53 41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	940/982 (96%)	919 (98%)	21 (2%)	52 39

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	160	LEU
1	A	163	LYS
1	A	194	THR
1	A	212	THR
1	A	252	TYR
1	A	254	MET
1	A	259	MET
1	A	293	TRP
1	A	345	LEU
1	A	427	TYR
1	A	528	ASN
1	B	163	LYS
1	B	212	THR
1	B	252	TYR
1	B	254	MET
1	B	259	MET
1	B	293	TRP
1	B	427	TYR
1	B	496	SER
1	B	528	ASN
1	B	616	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

4 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$
2	NAG	C	1	2	15,15,15	1.12	2 (13%)	21,21,21	1.64	4 (19%)
2	GAL	C	2	2	11,11,12	1.27	1 (9%)	15,15,17	1.56	3 (20%)
2	NAG	D	1	2	15,15,15	1.12	1 (6%)	21,21,21	2.34	6 (28%)
2	GAL	D	2	2	11,11,12	0.97	1 (9%)	15,15,17	1.58	3 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2	-	0/6/26/26	0/1/1/1
2	GAL	C	2	2	-	1/2/19/22	0/1/1/1
2	NAG	D	1	2	-	0/6/26/26	0/1/1/1
2	GAL	D	2	2	-	1/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	GAL	O5-C1	-3.18	1.38	1.43
2	D	1	NAG	C3-C2	2.68	1.58	1.53
2	C	1	NAG	O1-C1	2.44	1.47	1.39
2	C	1	NAG	O4-C4	2.37	1.48	1.43
2	D	2	GAL	O3-C3	2.22	1.48	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	O5-C1-C2	7.07	116.62	109.52
2	C	1	NAG	C1-C2-N2	-3.85	106.27	110.73

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	C1-C2-N2	-3.82	106.30	110.73
2	D	2	GAL	O5-C1-C2	3.81	116.65	110.77
2	D	1	NAG	C6-C5-C4	3.65	121.55	113.00
2	C	2	GAL	O5-C1-C2	3.19	115.69	110.77
2	C	1	NAG	C3-C4-C5	-3.12	104.68	110.24
2	C	2	GAL	C1-C2-C3	3.04	113.40	109.67
2	D	1	NAG	C1-C2-C3	2.99	114.62	110.54
2	D	1	NAG	C3-C2-N2	2.95	116.18	110.62
2	C	1	NAG	O5-C1-C2	2.90	112.43	109.52
2	D	2	GAL	C6-C5-C4	2.26	118.30	113.00
2	D	2	GAL	O3-C3-C4	2.23	115.50	110.35
2	C	2	GAL	O2-C2-C1	2.08	113.40	109.15
2	C	1	NAG	O3-C3-C4	-2.04	105.63	110.35
2	D	1	NAG	O5-C5-C6	-2.03	101.38	106.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

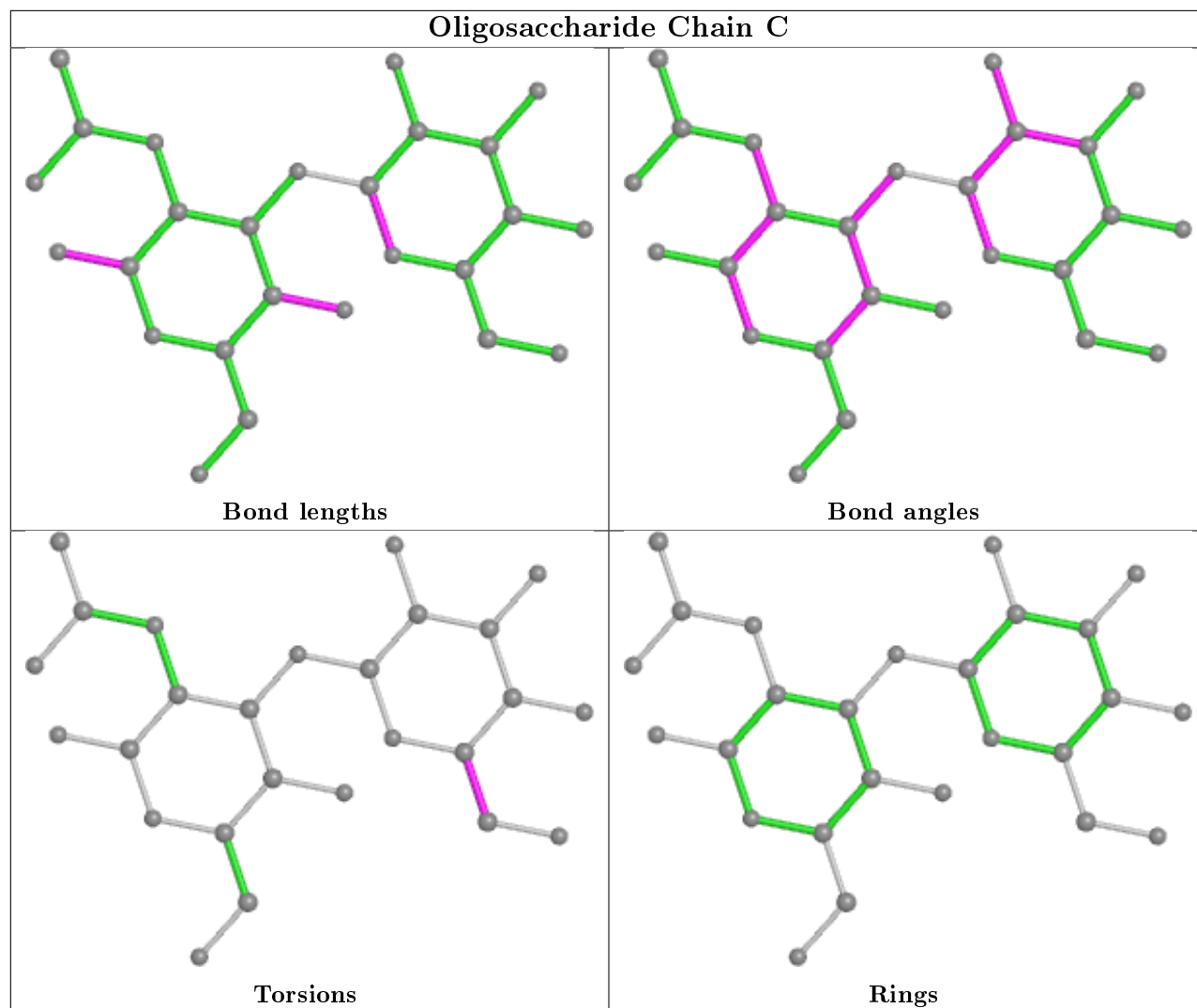
Mol	Chain	Res	Type	Atoms
2	C	2	GAL	O5-C5-C6-O6
2	D	2	GAL	O5-C5-C6-O6

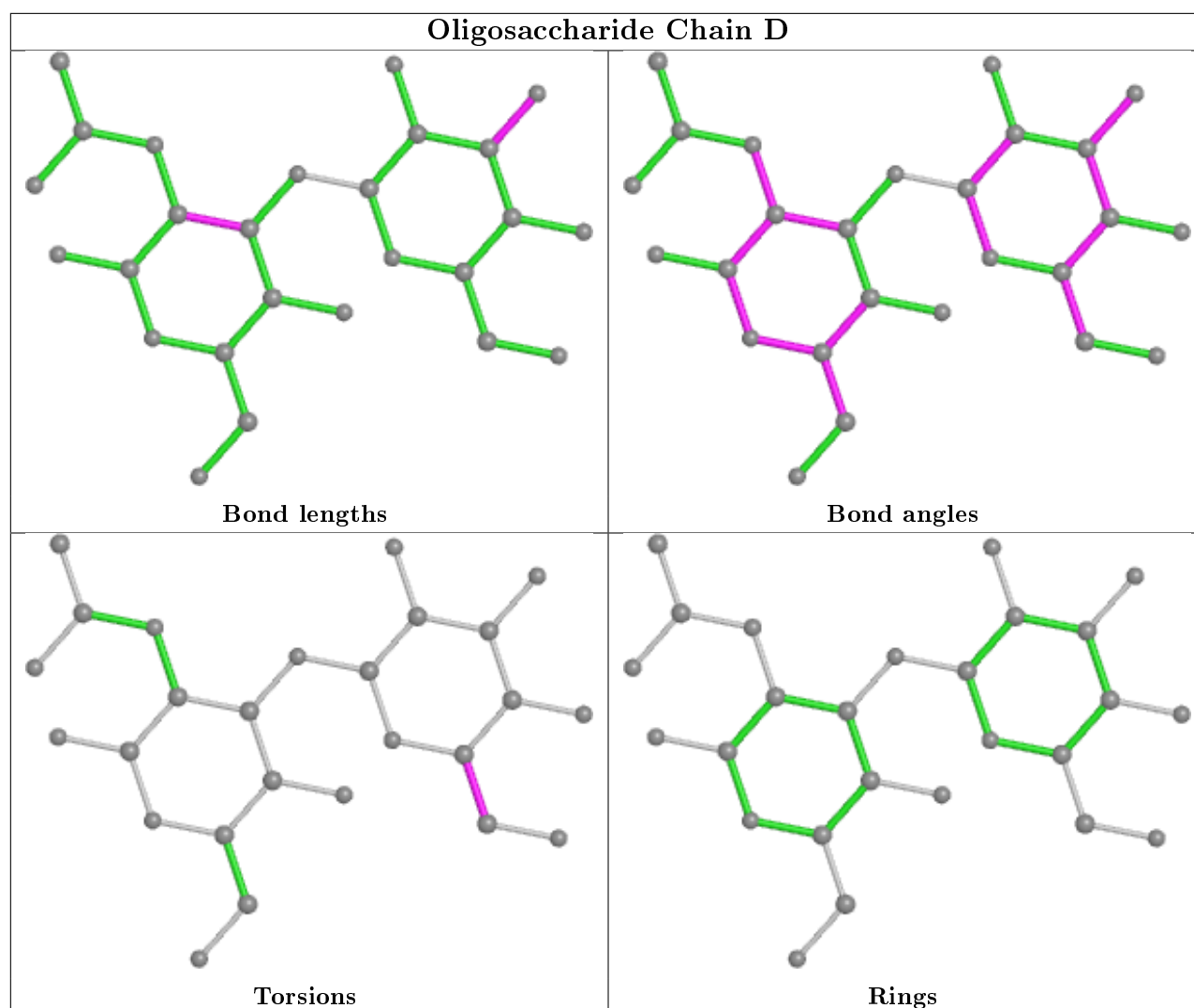
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	1	0
2	D	1	NAG	1	0

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





5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

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	582/606 (96%)	0.05	28 (4%) 30 25	22, 33, 55, 79	0
1	B	582/606 (96%)	-0.07	10 (1%) 70 66	22, 34, 49, 90	0
All	All	1164/1212 (96%)	-0.01	38 (3%) 46 40	22, 34, 52, 90	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	616	LYS	4.6
1	A	616	LYS	3.8
1	A	67	ALA	3.7
1	B	67	ALA	3.5
1	A	55	HIS	3.5
1	A	112	ALA	3.2
1	A	297	VAL	3.2
1	A	251	ILE	3.1
1	A	59	ALA	3.0
1	A	253	PHE	3.0
1	A	295	ILE	3.0
1	B	443	TRP	2.9
1	A	66	ASN	2.9
1	A	214	VAL	2.9
1	A	54	ALA	2.8
1	A	111	ASP	2.7
1	A	384	ILE	2.7
1	A	617	GLY	2.7
1	A	110	ALA	2.6
1	B	112	ALA	2.5
1	A	217	ILE	2.4
1	A	345	LEU	2.4
1	A	252	TYR	2.4
1	A	215	ALA	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	296	ALA	2.3
1	A	264	ALA	2.3
1	A	479	VAL	2.3
1	A	627	ALA	2.3
1	A	160	LEU	2.3
1	B	438	LEU	2.3
1	B	615	VAL	2.3
1	B	111	ASP	2.3
1	B	295	ILE	2.2
1	A	293	TRP	2.2
1	A	216	GLY	2.1
1	A	121	ASP	2.1
1	B	66	ASN	2.1
1	B	194	THR	2.0

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](#)

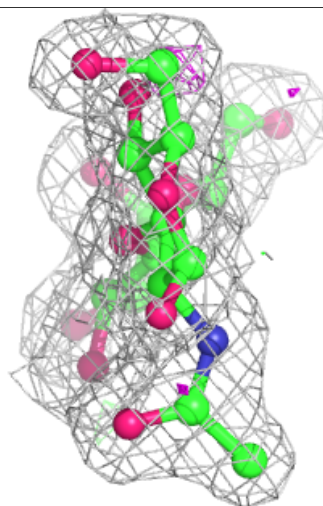
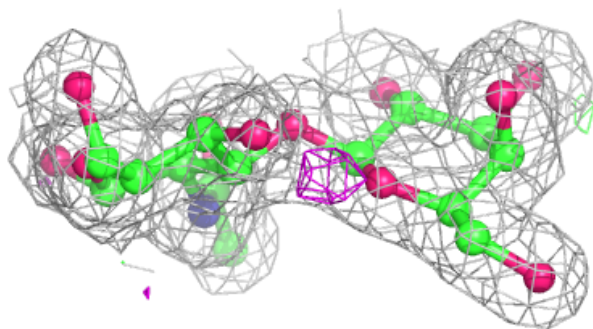
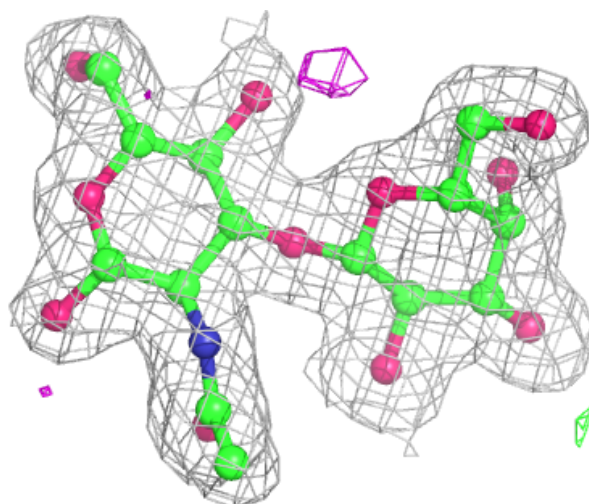
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

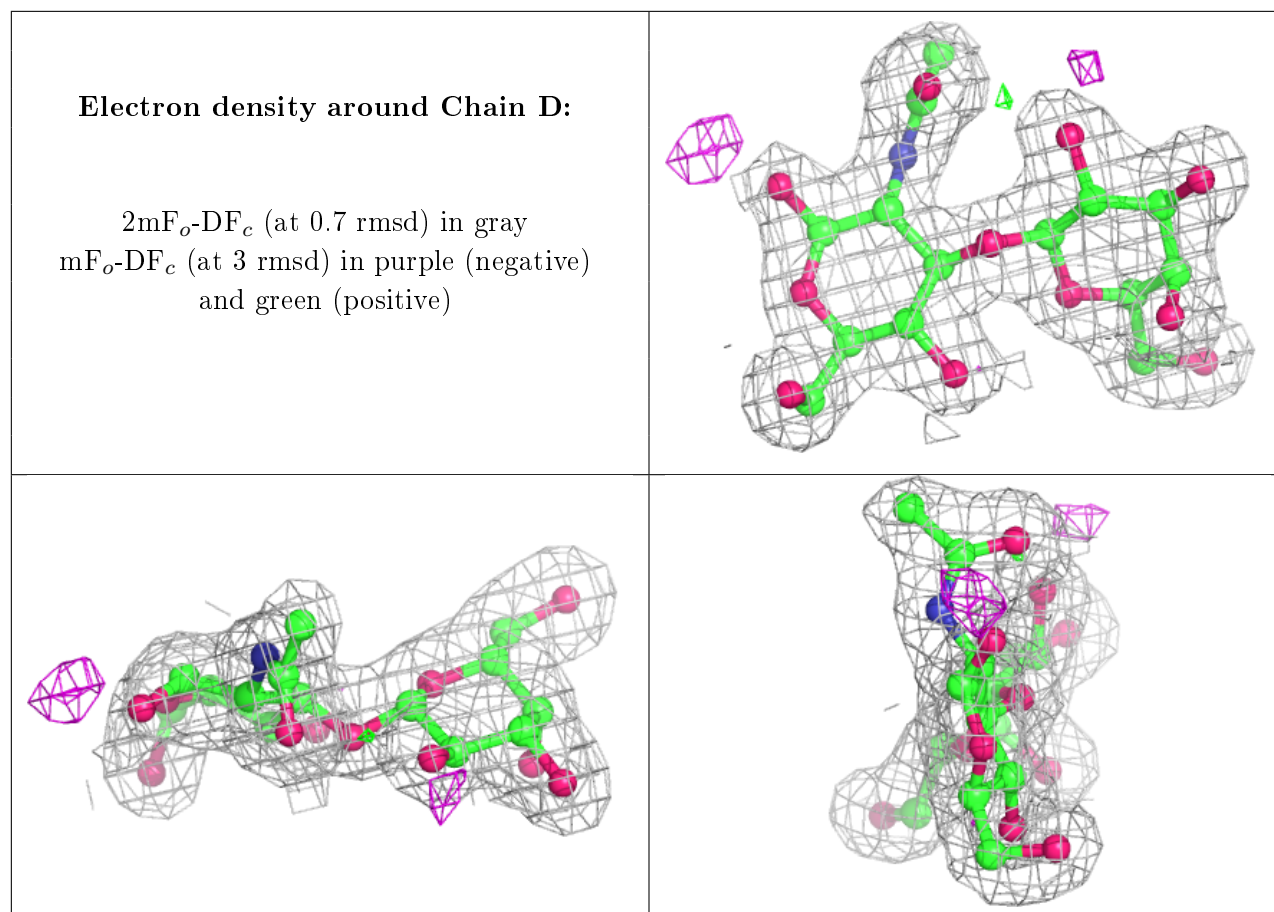
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	1	15/15	0.95	0.08	27,30,37,39	0
2	GAL	D	2	11/12	0.95	0.10	27,29,33,34	0
2	NAG	C	1	15/15	0.96	0.07	24,28,33,33	0
2	GAL	C	2	11/12	0.97	0.09	24,25,27,28	0

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 C:

$2mF_o-DF_c$ (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
3	CA	B	702	1/1	0.97	0.04	35,35,35,35	0
3	CA	A	701	1/1	0.98	0.07	37,37,37,37	0
3	CA	B	701	1/1	0.99	0.03	33,33,33,33	0
3	CA	A	702	1/1	0.99	0.09	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.