



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 19, 2024 – 02:37 AM EDT

PDB ID : 4ARN
Title : Crystal structure of the N-terminal domain of Drosophila Toll receptor
Authors : Gangloff, M.; Gay, N.J.
Deposited on : 2012-04-25
Resolution : 2.41 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

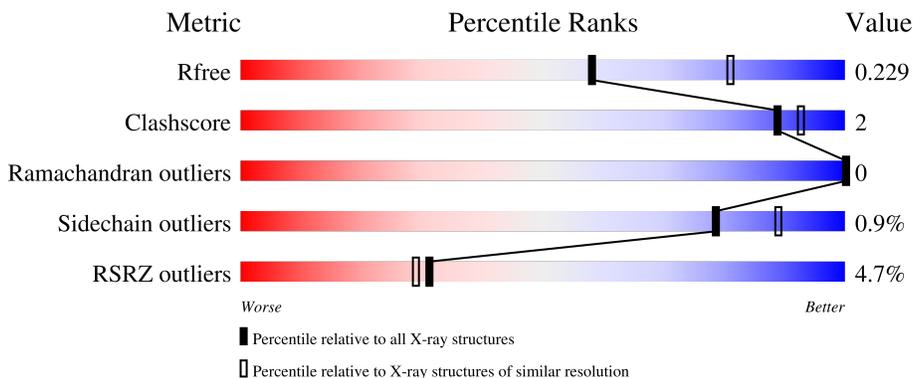
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

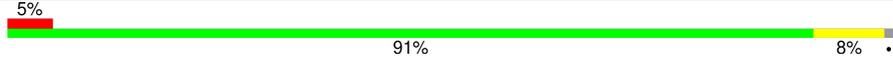
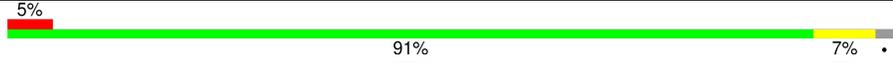
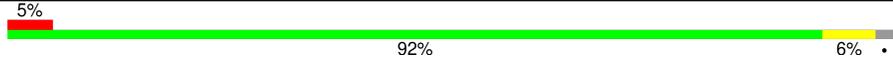
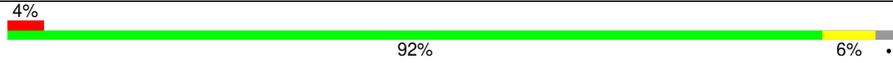
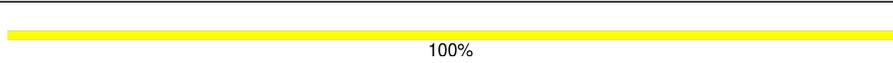
The reported resolution of this entry is 2.41 Å.

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	4647 (2.44-2.40)
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)
RSRZ outliers	127900	4543 (2.44-2.40)

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	279	
1	B	279	
1	C	279	
1	D	279	
2	E	2	

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Mol	Chain	Length	Quality of chain
3	F	2	 100%
3	H	2	 100%
4	G	7	 29% 71%

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
2	FUC	E	2	-	-	-	X
4	BMA	G	3	-	-	-	X
4	BMA	G	5	-	-	-	X

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 9283 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 TOLL RECEPTOR, VARIABLE LYMPHOCYTE RECEPTOR B.61 CHIMERA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	277	2217	1389	399	408	21	0	2	0
1	B	273	2162	1354	388	399	21	0	1	0
1	C	273	2172	1360	392	399	21	0	1	0
1	D	272	2164	1355	391	397	21	0	1	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	229	ALA	ASP	cloning artifact	UNP Q4G1L2
A	230	SER	THR	cloning artifact	UNP Q4G1L2
A	300	GLY	-	expression tag	UNP Q4G1L2
A	301	GLU	-	expression tag	UNP Q4G1L2
A	302	ASN	-	expression tag	UNP Q4G1L2
A	303	LEU	-	expression tag	UNP Q4G1L2
A	304	TYR	-	expression tag	UNP Q4G1L2
A	305	PHE	-	expression tag	UNP Q4G1L2
A	306	GLN	-	expression tag	UNP Q4G1L2
B	229	ALA	ASP	cloning artifact	UNP Q4G1L2
B	230	SER	THR	cloning artifact	UNP Q4G1L2
B	300	GLY	-	expression tag	UNP Q4G1L2
B	301	GLU	-	expression tag	UNP Q4G1L2
B	302	ASN	-	expression tag	UNP Q4G1L2
B	303	LEU	-	expression tag	UNP Q4G1L2
B	304	TYR	-	expression tag	UNP Q4G1L2
B	305	PHE	-	expression tag	UNP Q4G1L2
B	306	GLN	-	expression tag	UNP Q4G1L2
C	229	ALA	ASP	cloning artifact	UNP Q4G1L2
C	230	SER	THR	cloning artifact	UNP Q4G1L2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	300	GLY	-	expression tag	UNP Q4G1L2
C	301	GLU	-	expression tag	UNP Q4G1L2
C	302	ASN	-	expression tag	UNP Q4G1L2
C	303	LEU	-	expression tag	UNP Q4G1L2
C	304	TYR	-	expression tag	UNP Q4G1L2
C	305	PHE	-	expression tag	UNP Q4G1L2
C	306	GLN	-	expression tag	UNP Q4G1L2
D	229	ALA	ASP	cloning artifact	UNP Q4G1L2
D	230	SER	THR	cloning artifact	UNP Q4G1L2
D	300	GLY	-	expression tag	UNP Q4G1L2
D	301	GLU	-	expression tag	UNP Q4G1L2
D	302	ASN	-	expression tag	UNP Q4G1L2
D	303	LEU	-	expression tag	UNP Q4G1L2
D	304	TYR	-	expression tag	UNP Q4G1L2
D	305	PHE	-	expression tag	UNP Q4G1L2
D	306	GLN	-	expression tag	UNP Q4G1L2

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	2	24	14	1	9	0	0	0

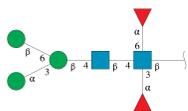
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

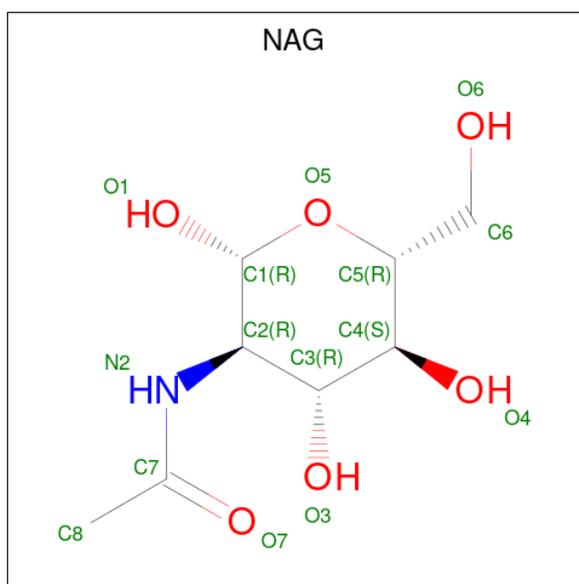
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[beta-D-mannopyranose]

se-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



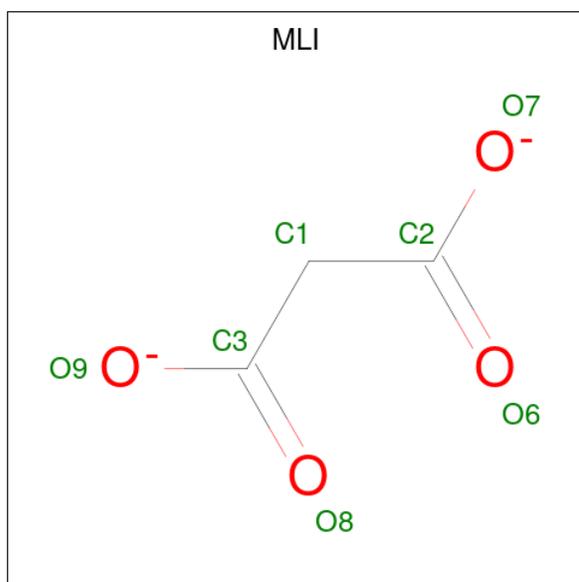
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	G	7	81	46	2	33	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 3 4	0	0
6	B	1	Total C O 7 3 4	0	0

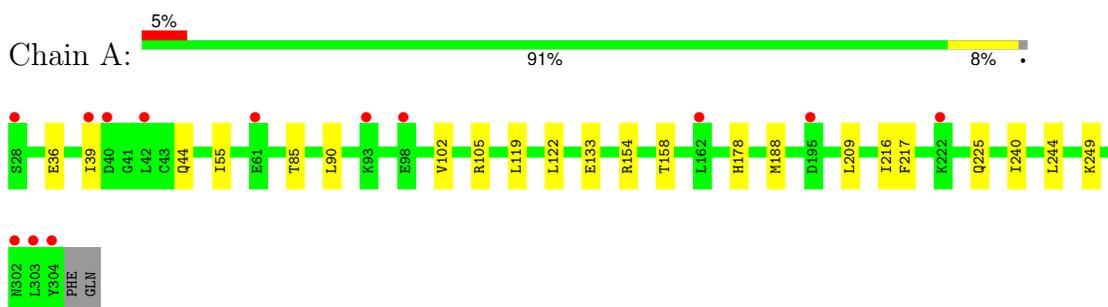
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	107	Total O 107 107	0	0
7	B	90	Total O 90 90	0	0
7	C	68	Total O 68 68	0	0
7	D	58	Total O 58 58	0	0

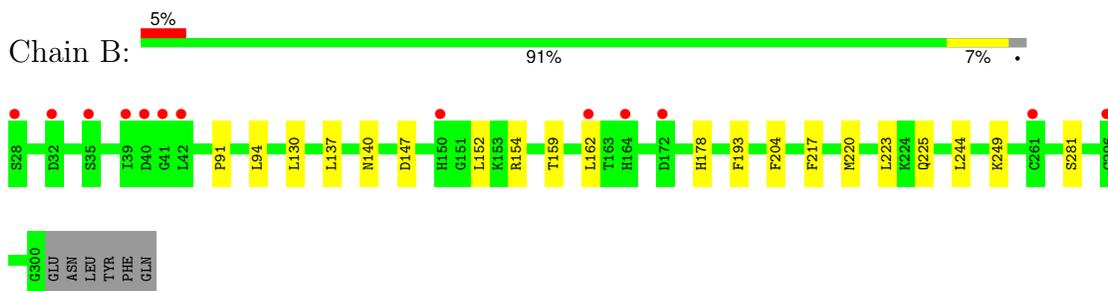
3 Residue-property plots [i](#)

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

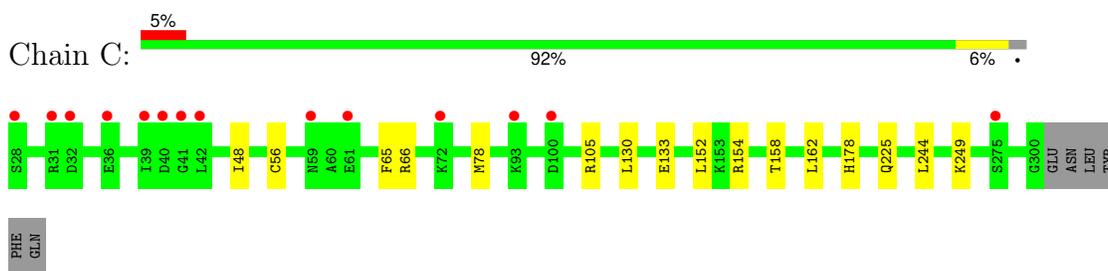
- Molecule 1: TOLL RECEPTOR, VARIABLE LYMPHOCYTE RECEPTOR B.61 CHIMERA



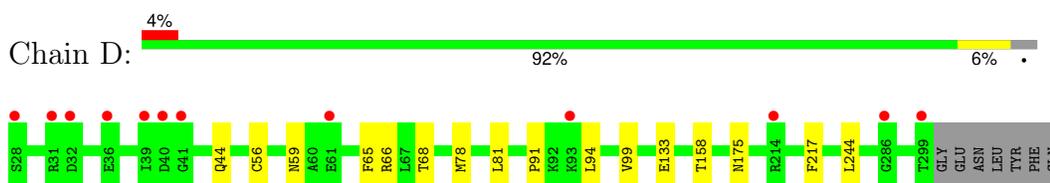
- Molecule 1: TOLL RECEPTOR, VARIABLE LYMPHOCYTE RECEPTOR B.61 CHIMERA



- Molecule 1: TOLL RECEPTOR, VARIABLE LYMPHOCYTE RECEPTOR B.61 CHIMERA



- Molecule 1: TOLL RECEPTOR, VARIABLE LYMPHOCYTE RECEPTOR B.61 CHIMERA



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1
FUC2

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

Chain F:  100%

MAG1
MAG2

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

Chain H:  100%

MAG1
MAG2

- Molecule 4: alpha-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  29% 71%

MAG1
MAG2
BMA3
MAN4
BMA5
FUC6
FUC7

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.79Å 93.28Å 225.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.95 – 2.41 29.34 – 2.41	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.95-2.41) 99.6 (29.34-2.41)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.42Å)	Xtrriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.201 , 0.216 0.211 , 0.229	Depositor DCC
R_{free} test set	3668 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	51.8	Xtrriage
Anisotropy	0.551	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.027 for k,h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9283	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, BMA, MLI, NAG, MAN

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	0.39	0/2268	0.58	0/3065
1	B	0.41	1/2208 (0.0%)	0.59	0/2986
1	C	0.40	0/2218	0.58	0/2997
1	D	0.39	0/2210	0.58	0/2987
All	All	0.40	1/8904 (0.0%)	0.58	0/12035

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	140	ASN	CG-ND2	-5.52	1.19	1.32

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2217	0	2217	11	0
1	B	2162	0	2152	8	0
1	C	2172	0	2175	8	0
1	D	2164	0	2160	7	0
2	E	24	0	22	0	0
3	F	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	28	0	25	0	0
4	G	81	0	70	0	0
5	A	14	0	13	0	0
5	B	42	0	39	0	0
5	D	14	0	13	1	0
6	A	7	0	2	0	0
6	B	7	0	2	0	0
7	A	107	0	0	0	0
7	B	90	0	0	0	0
7	C	68	0	0	0	0
7	D	58	0	0	0	0
All	All	9283	0	8915	33	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.

The worst 5 of 33 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:44:GLN:HG2	1:A:55:ILE:HB	1.84	0.60
1:C:225:GLN:HG2	1:C:249:LYS:HB2	1.86	0.57
1:D:44:GLN:HE21	1:D:59:ASN:H	1.53	0.56
1:A:217:PHE:HB3	1:A:244:LEU:HD21	1.87	0.56
1:C:66:ARG:HB3	1:C:78:MET:HB3	1.88	0.56

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	277/279 (99%)	264 (95%)	13 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	272/279 (98%)	254 (93%)	18 (7%)	0	100	100
1	C	272/279 (98%)	257 (94%)	15 (6%)	0	100	100
1	D	271/279 (97%)	257 (95%)	14 (5%)	0	100	100
All	All	1092/1116 (98%)	1032 (94%)	60 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	253/255 (99%)	252 (100%)	1 (0%)	91	96
1	B	245/255 (96%)	242 (99%)	3 (1%)	71	84
1	C	247/255 (97%)	245 (99%)	2 (1%)	81	91
1	D	245/255 (96%)	242 (99%)	3 (1%)	71	84
All	All	990/1020 (97%)	981 (99%)	9 (1%)	78	89

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	81	LEU
1	D	99	VAL
1	B	281	SER
1	C	162	LEU
1	C	244	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	144	GLN
1	C	232	GLN
1	D	44	GLN

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Mol	Chain	Res	Type
1	D	76	GLN
1	D	232	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](#)

13 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	E	1	2,1	14,14,15	0.29	0	17,19,21	0.73	1 (5%)
2	FUC	E	2	2	10,10,11	2.06	4 (40%)	14,14,16	1.49	2 (14%)
3	NAG	F	1	3,1	14,14,15	0.32	0	17,19,21	0.68	0
3	NAG	F	2	3	14,14,15	0.28	0	17,19,21	0.52	0
4	NAG	G	1	4,1	14,14,15	0.27	0	17,19,21	0.86	0
4	NAG	G	2	4	14,14,15	0.28	0	17,19,21	0.48	0
4	BMA	G	3	4	11,11,12	2.09	3 (27%)	15,15,17	2.04	2 (13%)
4	MAN	G	4	4	11,11,12	1.67	3 (27%)	15,15,17	2.74	2 (13%)
4	BMA	G	5	4	11,11,12	1.90	4 (36%)	15,15,17	1.34	1 (6%)
4	FUC	G	6	4	10,10,11	2.00	4 (40%)	14,14,16	1.39	2 (14%)
4	FUC	G	7	4	10,10,11	2.04	4 (40%)	14,14,16	1.33	2 (14%)
3	NAG	H	1	3,1	14,14,15	0.29	0	17,19,21	0.59	0
3	NAG	H	2	3	14,14,15	0.28	0	17,19,21	0.45	0

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	E	1	2,1	-	0/6/23/26	0/1/1/1
2	FUC	E	2	2	-	-	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
4	NAG	G	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	2/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	0/1/1/1
4	BMA	G	5	4	-	2/2/19/22	0/1/1/1
4	FUC	G	6	4	-	-	0/1/1/1
4	FUC	G	7	4	-	-	0/1/1/1
3	NAG	H	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	3	BMA	C2-C3	4.51	1.59	1.52
2	E	2	FUC	C2-C3	3.92	1.58	1.52
4	G	7	FUC	C2-C3	3.80	1.58	1.52
4	G	6	FUC	C2-C3	3.70	1.58	1.52
4	G	5	BMA	C2-C3	3.48	1.57	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	4	MAN	C1-O5-C5	8.84	124.04	112.19
4	G	3	BMA	O3-C3-C2	6.89	124.11	110.05
4	G	4	MAN	O5-C1-C2	4.00	120.34	110.79
4	G	3	BMA	C1-C2-C3	-3.05	105.20	109.64
2	E	2	FUC	C1-O5-C5	2.95	119.91	112.97

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	3	BMA	O5-C5-C6-O6
4	G	3	BMA	C4-C5-C6-O6

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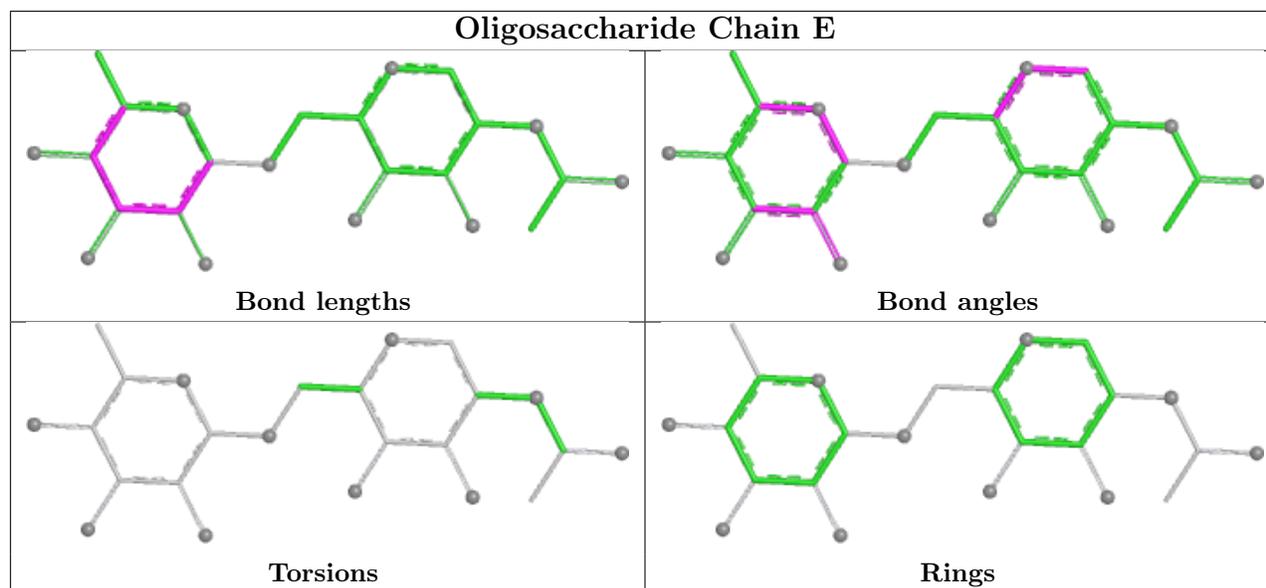
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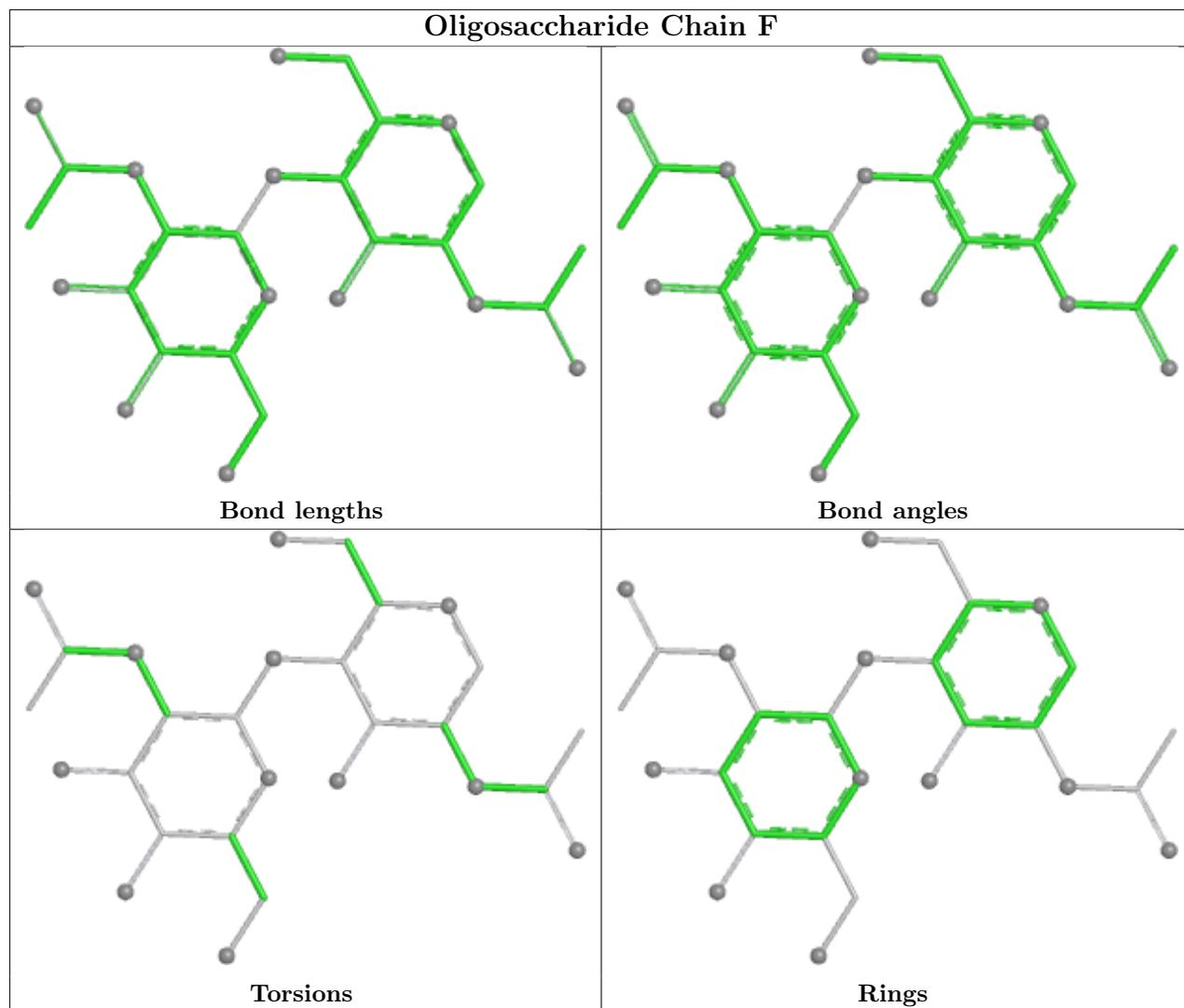
Mol	Chain	Res	Type	Atoms
4	G	5	BMA	O5-C5-C6-O6
4	G	5	BMA	C4-C5-C6-O6

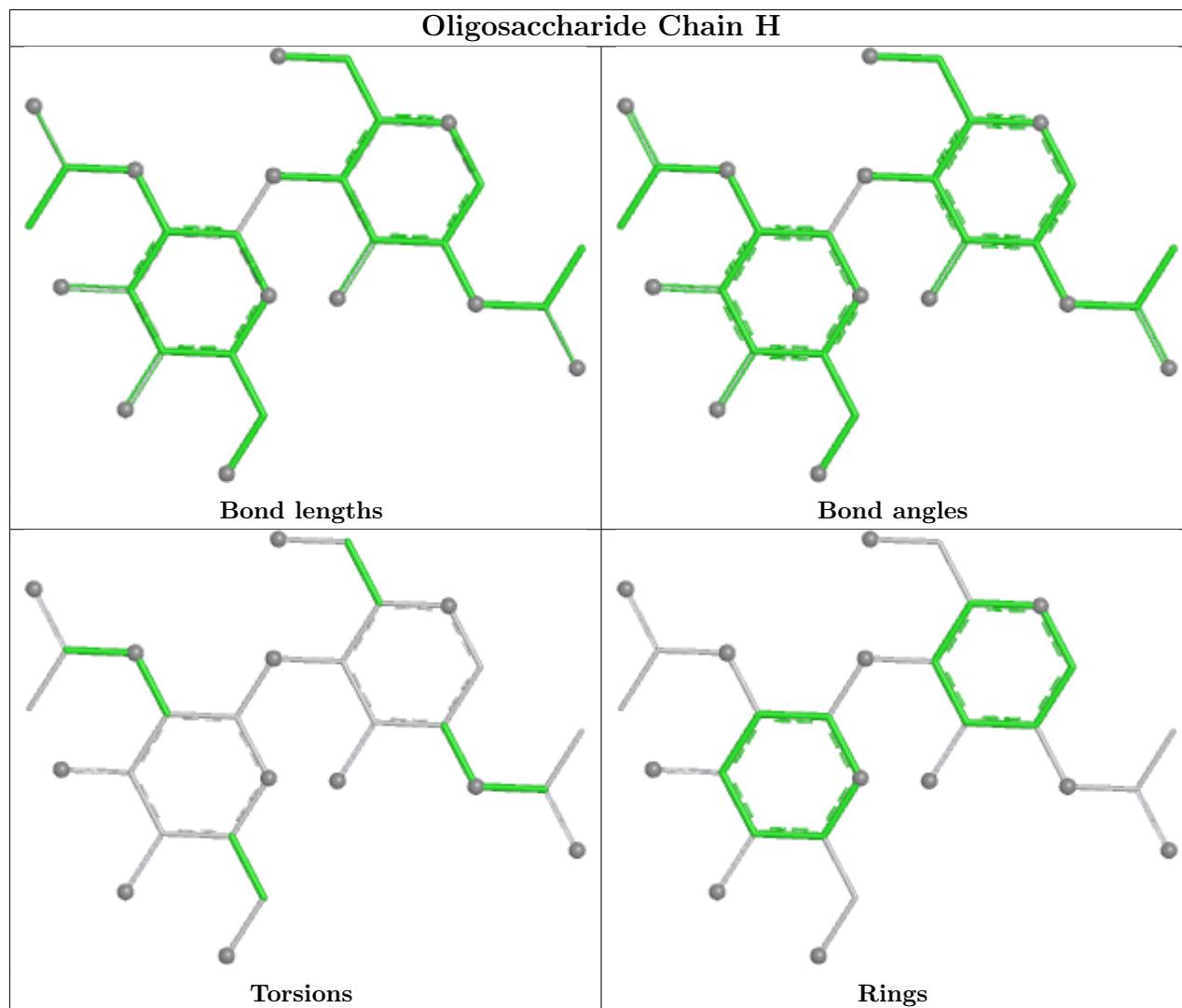
There are no ring outliers.

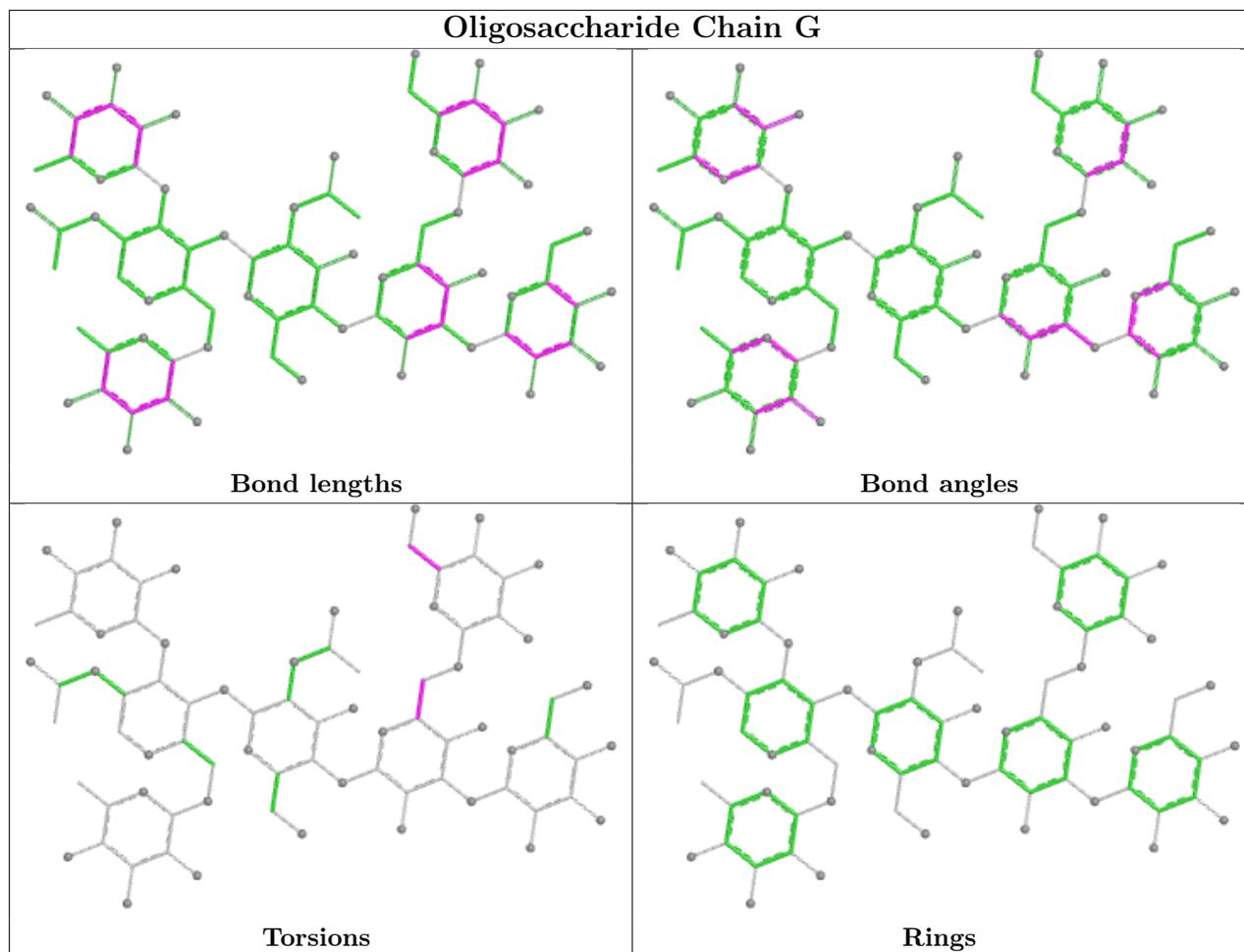
No monomer is involved in short contacts.

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









5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	401	1	14,14,15	0.29	0	17,19,21	0.59	0
6	MLI	A	601	-	6,6,6	1.35	1 (16%)	7,7,7	1.00	1 (14%)
6	MLI	B	602	-	6,6,6	1.31	0	7,7,7	1.25	1 (14%)
5	NAG	B	501	-	14,14,15	0.29	0	17,19,21	0.69	0
5	NAG	B	401	1	14,14,15	0.27	0	17,19,21	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	D	601	-	14,14,15	0.38	0	17,19,21	0.87	1 (5%)
5	NAG	B	601	1	14,14,15	0.29	0	17,19,21	0.61	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	401	1	-	0/6/23/26	0/1/1/1
6	MLI	A	601	-	-	4/4/4/4	-
6	MLI	B	602	-	-	2/4/4/4	-
5	NAG	B	501	-	-	0/6/23/26	0/1/1/1
5	NAG	B	401	1	-	0/6/23/26	0/1/1/1
5	NAG	D	601	-	-	0/6/23/26	0/1/1/1
5	NAG	B	601	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	601	MLI	C1-C3	2.06	1.54	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	601	NAG	C1-O5-C5	3.01	116.21	112.19
6	B	602	MLI	C3-C1-C2	3.00	123.54	112.95
6	A	601	MLI	C3-C1-C2	2.26	120.93	112.95
5	B	601	NAG	C1-O5-C5	2.12	115.03	112.19

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	601	MLI	C3-C1-C2-O7
6	A	601	MLI	C3-C1-C2-O6
6	A	601	MLI	C2-C1-C3-O9
6	B	602	MLI	C3-C1-C2-O7
6	A	601	MLI	C2-C1-C3-O8

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	601	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	277/279 (99%)	0.01	13 (4%) 31 29	38, 59, 93, 110	3 (1%)
1	B	273/279 (97%)	0.02	13 (4%) 30 28	37, 59, 90, 103	5 (1%)
1	C	273/279 (97%)	0.10	14 (5%) 28 26	45, 68, 98, 116	5 (1%)
1	D	272/279 (97%)	-0.01	12 (4%) 34 32	47, 67, 96, 131	3 (1%)
All	All	1095/1116 (98%)	0.03	52 (4%) 31 29	37, 64, 95, 131	16 (1%)

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	40	ASP	5.6
1	D	28	SER	5.6
1	C	41	GLY	5.5
1	A	42	LEU	5.1
1	D	299	THR	4.4

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.

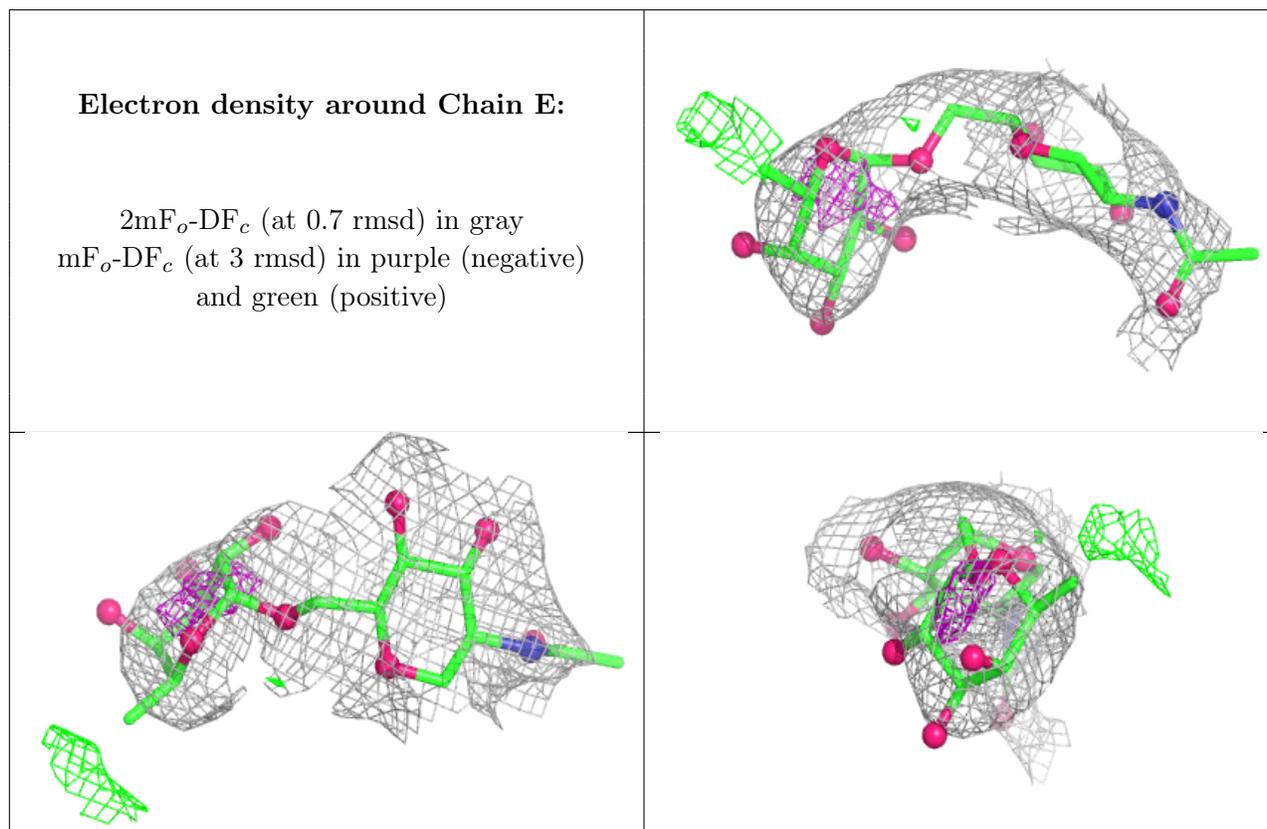
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	G	5	11/12	0.62	0.74	92,96,101,103	11
4	MAN	G	4	11/12	0.67	0.38	114,118,126,127	0

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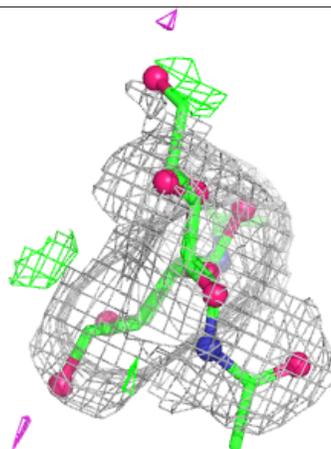
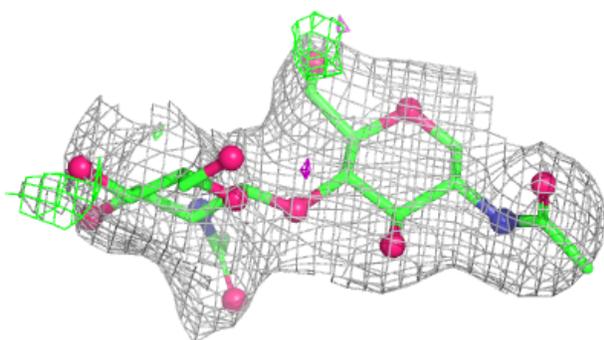
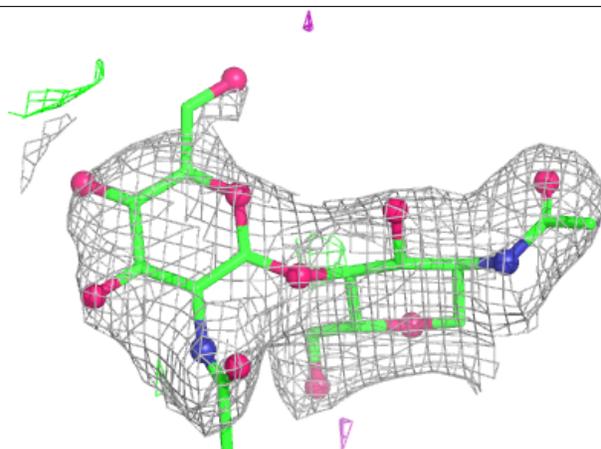
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	BMA	G	3	11/12	0.67	0.43	101,105,110,114	11
4	FUC	G	7	10/11	0.73	0.33	97,102,107,108	10
2	FUC	E	2	10/11	0.79	0.45	113,116,118,119	0
3	NAG	H	2	14/15	0.80	0.45	98,102,109,111	14
3	NAG	H	1	14/15	0.81	0.31	81,91,97,97	0
2	NAG	E	1	14/15	0.88	0.32	103,108,110,111	0
3	NAG	F	2	14/15	0.89	0.51	100,103,109,110	0
4	NAG	G	2	14/15	0.91	0.20	83,89,94,98	0
4	NAG	G	1	14/15	0.92	0.14	76,81,87,92	0
3	NAG	F	1	14/15	0.93	0.24	80,88,94,96	0
4	FUC	G	6	10/11	0.94	0.25	78,80,82,84	10

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.

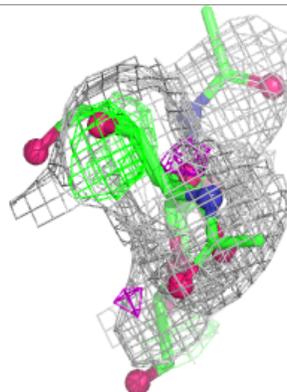
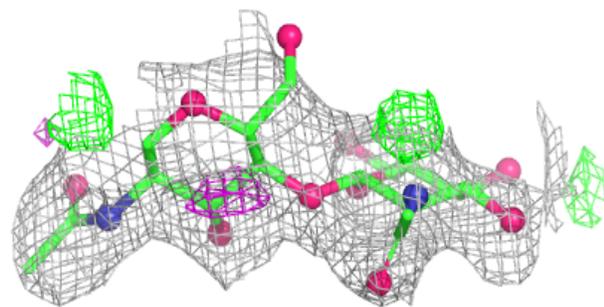
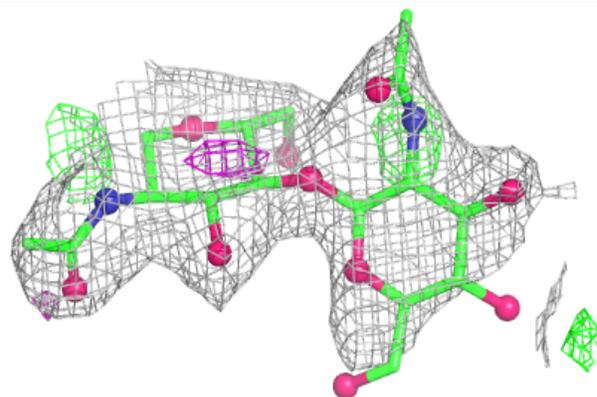


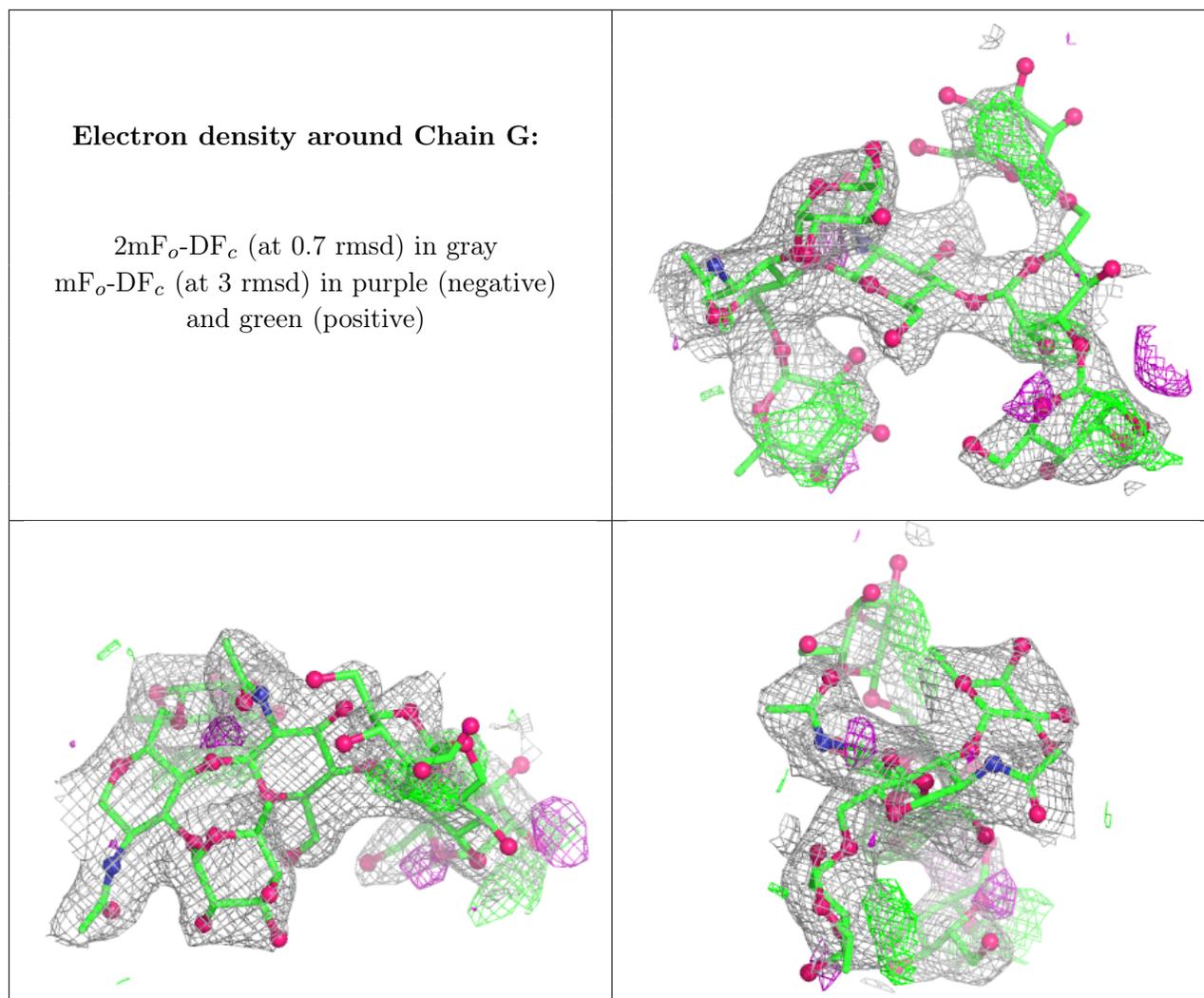
Electron density around Chain F:

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

**Electron density around Chain H:**

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	D	601	14/15	0.65	0.38	108,111,113,115	14
5	NAG	B	501	14/15	0.71	0.34	88,90,93,94	14
5	NAG	B	601	14/15	0.84	0.41	102,104,109,112	0
6	MLI	B	602	7/7	0.88	0.19	80,80,82,83	0
5	NAG	A	401	14/15	0.92	0.23	87,91,94,96	0
5	NAG	B	401	14/15	0.94	0.23	81,85,88,88	0
6	MLI	A	601	7/7	0.97	0.15	40,41,43,44	0

6.5 Other polymers

There are no such residues in this entry.