Full wwPDB X-ray Structure Validation Report (i)

Aug 9, 2020 – 12:50 PM BST

PDB ID	:	1LED
Title	:	STRUCTURES OF THE LECTIN IV OF GRIFFONIA SIMPLICIFOLIA AND ITS COMPLEX WITH THE LEWIS B HUMAN BLOOD GROUP DETERMINANT AT 2.0 ANGSTROMS RESOLUTION
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Deposited on	:	1992-12-17
Resolution	:	2.00 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

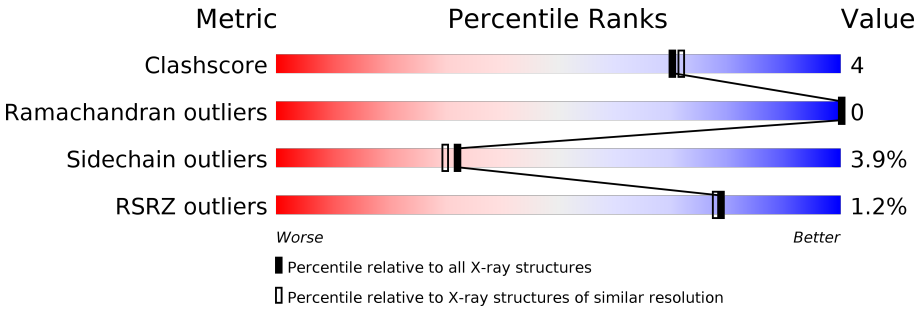
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	243	% 84% 14% .
2	B	4	25% 50% 25%
3	C	3	33% 67%

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
6	SO4	A	500	-	-	-	X

2 Entry composition

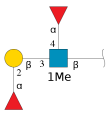
There are 7 unique types of molecules in this entry. The entry contains 2140 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 WEST-CENTRAL AFRICAN LEGUME LECTIN IV.

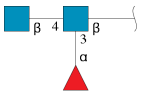
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	0	0	0
			1904	1226	309	369			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	4	Total	C	N	O	0	0	0
			47	27	1	19			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O	0	0	0
			38	22	2	14			

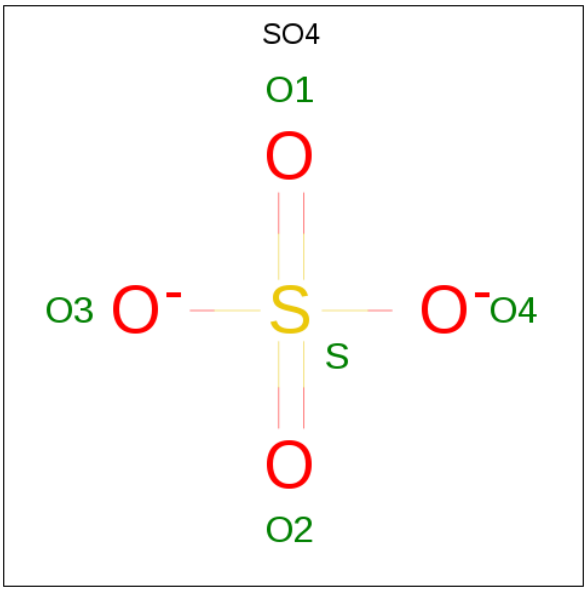
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mn	0	0
			1	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Ca 1 1	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0

- Molecule 7 is water.

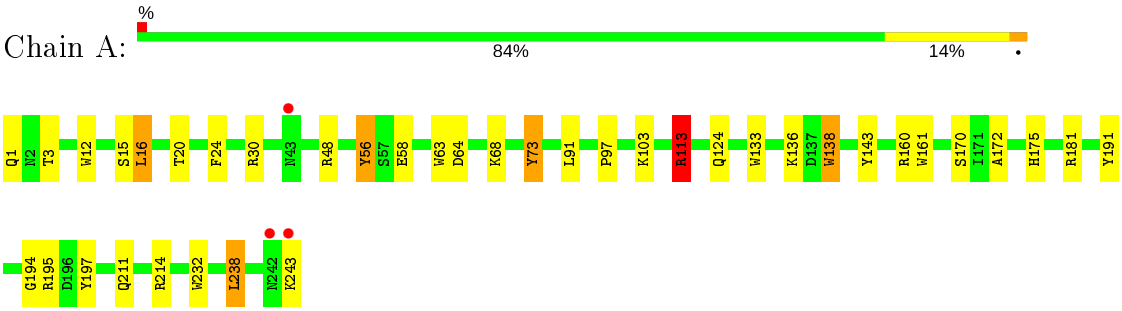
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	144	Total O 144 144	0	0

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.

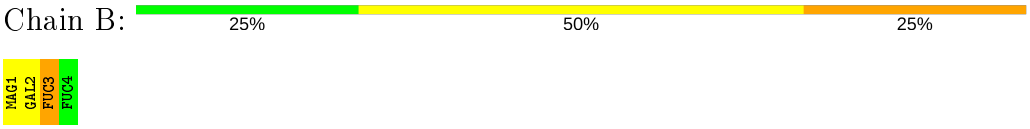
• Molecule 1: WEST-CENTRAL AFRICAN LEGUME LECTIN IV

Chain A:



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

Chain B:



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

Chain C:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	78.90Å 78.90Å 89.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00 39.45 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00) 99.8 (39.45-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.84 (at 2.00Å)	Xtriage
Refinement program	PROLSQ, X-PLOR	Depositor
R, R_{free}	0.181 , (Not available) 0.174 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	27.1	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 78.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	2140	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.32% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, CA, MN, GAL, FUC, MAG, PCA, SO4

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	0.86	1/1953 (0.1%)	1.64	26/2670 (1.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	TYR	CE2-CZ	-5.04	1.31	1.38

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	214	ARG	NE-CZ-NH2	-10.86	114.87	120.30
1	A	214	ARG	NE-CZ-NH1	9.76	125.18	120.30
1	A	133	TRP	CD1-CG-CD2	9.39	113.81	106.30
1	A	73	TYR	CB-CG-CD2	-8.97	115.62	121.00
1	A	195	ARG	NE-CZ-NH1	8.08	124.34	120.30
1	A	143	TYR	CB-CG-CD2	-7.80	116.32	121.00
1	A	138	TRP	CD1-CG-CD2	7.68	112.44	106.30
1	A	133	TRP	CE2-CD2-CG	-7.51	101.29	107.30
1	A	138	TRP	CE2-CD2-CG	-7.45	101.34	107.30
1	A	197	TYR	CB-CG-CD1	-7.21	116.67	121.00
1	A	12	TRP	CE2-CD2-CG	-7.17	101.56	107.30
1	A	12	TRP	CD1-CG-CD2	7.11	111.99	106.30
1	A	63	TRP	CE2-CD2-CG	-6.44	102.15	107.30
1	A	161	TRP	CD1-CG-CD2	6.38	111.40	106.30
1	A	12	TRP	CG-CD2-CE3	6.30	139.57	133.90
1	A	63	TRP	CD1-CG-CD2	6.23	111.28	106.30
1	A	12	TRP	CB-CG-CD1	-6.12	119.04	127.00
1	A	48	ARG	NE-CZ-NH1	6.11	123.35	120.30
1	A	161	TRP	CE2-CD2-CG	-6.08	102.44	107.30
1	A	133	TRP	CG-CD1-NE1	-6.06	104.04	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	170	SER	CB-CA-C	-5.67	99.33	110.10
1	A	232	TRP	CE2-CD2-CG	-5.50	102.90	107.30
1	A	113	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	56	TYR	CB-CG-CD2	-5.19	117.89	121.00
1	A	73	TYR	CB-CG-CD1	5.06	124.04	121.00
1	A	138	TRP	CB-CG-CD1	-5.03	120.46	127.00

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	1904	0	1811	14	0
2	B	47	0	44	1	0
3	C	38	0	34	0	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	A	5	0	0	0	0
7	A	144	0	0	3	0
All	All	2140	0	1889	14	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 4.

All (14) 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:103:LYS:HD3	1:A:113:ARG:HG2	1.85	0.56
1:A:138:TRP:HE1	2:B:3:FUC:HO2	1.53	0.56
1:A:238:LEU:HD23	1:A:243:LYS:HD2	1.91	0.53
1:A:175:HIS:HD2	7:A:351:HOH:O	1.93	0.51
1:A:56:TYR:CE2	1:A:58:GLU:HB2	2.47	0.49
1:A:73:TYR:OH	1:A:175:HIS:ND1	2.45	0.49
1:A:16:LEU:HD23	1:A:20:THR:OG1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:GLY:HA3	7:A:341:HOH:O	2.17	0.45
1:A:172:ALA:HB2	1:A:191:TYR:CE2	2.54	0.43
1:A:136:LYS:HA	7:A:410:HOH:O	2.18	0.43
1:A:64:ASP:HA	1:A:211:GLN:HE21	1.84	0.42
1:A:24:PHE:CZ	1:A:30:ARG:HB2	2.55	0.42
1:A:97:PRO:HD3	1:A:124:GLN:O	2.20	0.42
1:A:3:THR:HG22	1:A:238:LEU:HD13	2.04	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	241/243 (99%)	229 (95%)	12 (5%)	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	203/203 (100%)	195 (96%)	8 (4%)	32 30

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	SER
1	A	16	LEU
1	A	68	LYS
1	A	91	LEU
1	A	113	ARG
1	A	160	ARG
1	A	181	ARG
1	A	238	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	163	ASN
1	A	211	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)

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	PCA	A	1	1	7,8,9	0.83	0	9,10,12	2.77	4 (44%)

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
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1	PCA	OE-CD-N	5.77	138.32	124.86
1	A	1	PCA	OE-CD-CG	-3.91	119.95	126.76
1	A	1	PCA	CB-CG-CD	2.87	109.03	104.40
1	A	1	PCA	CG-CD-N	-2.57	101.73	108.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

7 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	MAG	B	1	2	16,16,16	2.04	6 (37%)	22,22,22	2.82	7 (31%)
2	GAL	B	2	2	11,11,12	1.12	1 (9%)	15,15,17	1.35	1 (6%)
2	FUC	B	3	2	10,10,11	1.73	4 (40%)	14,14,16	1.24	1 (7%)
2	FUC	B	4	2	10,10,11	0.85	0	14,14,16	0.54	0
3	NAG	C	1	1,3	14,14,15	1.09	2 (14%)	17,19,21	1.23	2 (11%)
3	FUC	C	2	3	10,10,11	0.74	0	14,14,16	0.89	0
3	NAG	C	3	3	14,14,15	0.94	0	17,19,21	0.91	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
2	MAG	B	1	2	-	0/8/28/28	0/1/1/1
2	GAL	B	2	2	-	0/2/19/22	0/1/1/1
2	FUC	B	3	2	-	-	0/1/1/1
2	FUC	B	4	2	-	-	0/1/1/1
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	FUC	C	2	3	-	-	0/1/1/1
3	NAG	C	3	3	-	0/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	MAG	O1-C1	4.36	1.47	1.40
2	B	1	MAG	C4-C5	4.16	1.61	1.53
2	B	1	MAG	C6-C5	2.82	1.61	1.51
2	B	3	FUC	C2-C3	2.58	1.56	1.52
2	B	2	GAL	C2-C3	2.57	1.56	1.52
2	B	3	FUC	C1-C2	2.55	1.58	1.52
2	B	3	FUC	C4-C5	2.50	1.58	1.52
2	B	1	MAG	C1-C2	2.38	1.57	1.53
2	B	1	MAG	C4-C3	2.33	1.58	1.52
2	B	1	MAG	C2-N2	2.10	1.49	1.45
3	C	1	NAG	C4-C3	-2.08	1.47	1.52
2	B	3	FUC	O2-C2	2.02	1.47	1.43
3	C	1	NAG	C1-C2	-2.01	1.49	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	MAG	O1-C1-C2	-10.67	91.77	108.14
2	B	2	GAL	C1-O5-C5	3.96	117.55	112.19
2	B	3	FUC	O5-C1-C2	3.65	116.41	110.77
2	B	1	MAG	C3-C4-C5	3.53	116.54	110.24
2	B	1	MAG	O5-C1-O1	-3.34	103.22	110.97
2	B	1	MAG	O4-C4-C3	-2.75	103.99	110.35
3	C	1	NAG	C8-C7-N2	2.73	120.73	116.10
3	C	3	NAG	C1-O5-C5	2.45	115.51	112.19
2	B	1	MAG	C8-C7-N2	2.38	120.13	116.10
2	B	1	MAG	O7-C7-C8	-2.22	117.94	122.06
2	B	1	MAG	C1-O5-C5	2.15	117.91	113.69
3	C	1	NAG	C1-O5-C5	2.14	115.10	112.19

There are no chirality outliers.

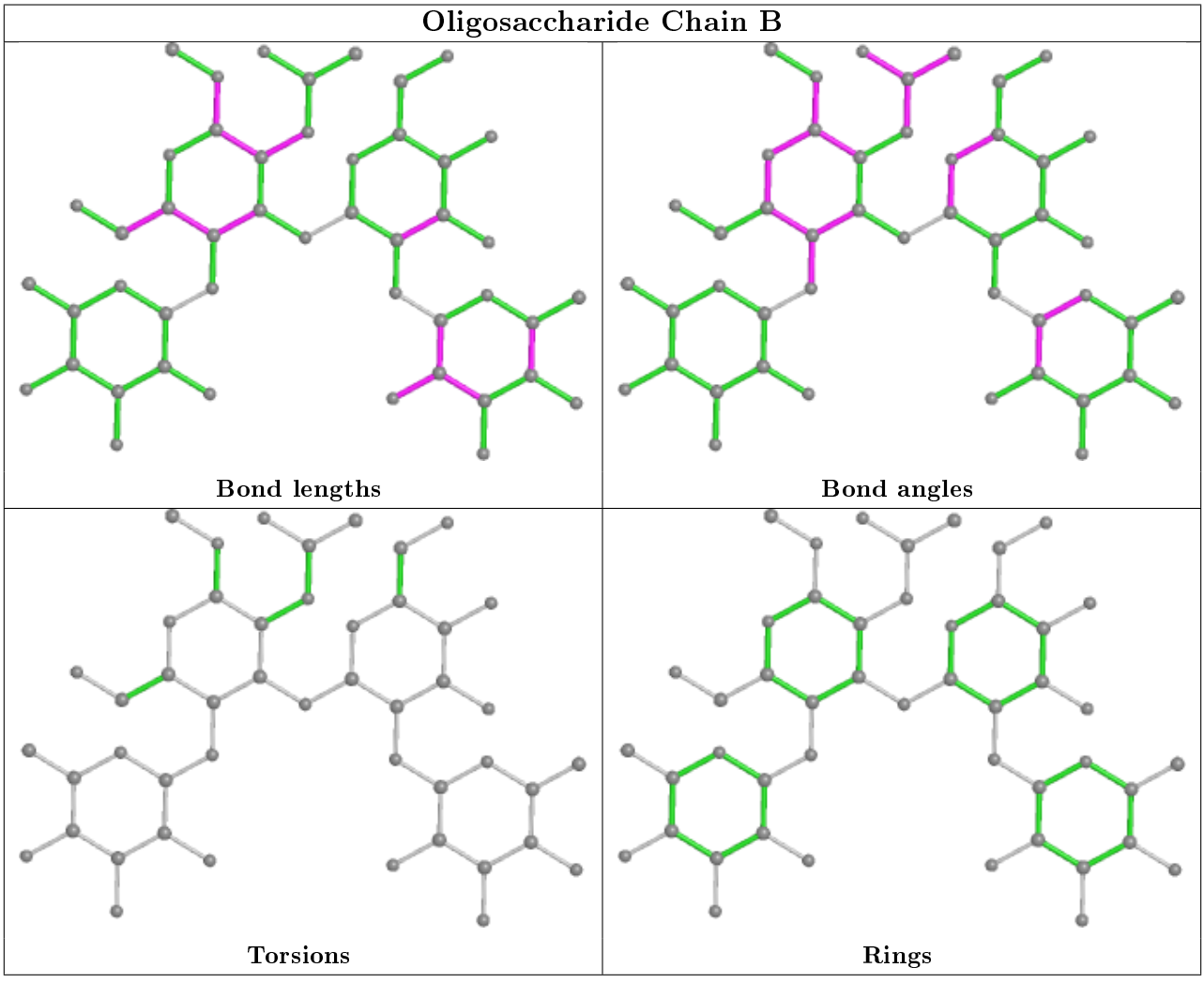
There are no torsion outliers.

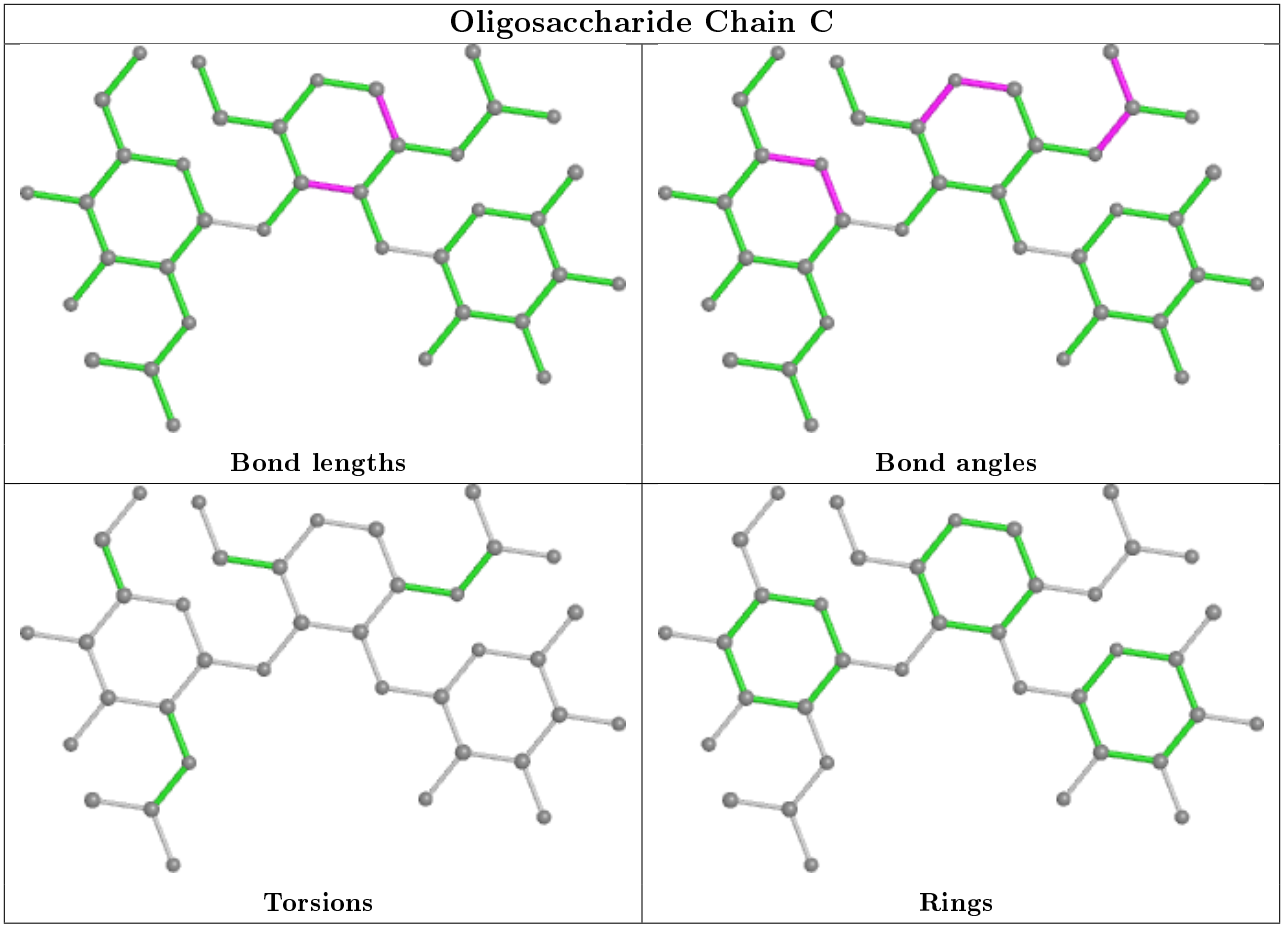
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	3	FUC	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 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	$\#\|Z\| > 2$
6	SO4	A	500	-	4,4,4	0.42	0	6,6,6	0.25	0

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

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, 95^{th} 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	242/243 (99%)	-0.39	3 (1%)	79	78	12, 23, 48, 89	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	LYS	5.1
1	A	242	ASN	4.3
1	A	43	ASN	2.5

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

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, 95^{th} 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
1	PCA	A	1	8/9	0.69	0.35	71,79,83,84	0

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, 95^{th} 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
2	MAG	B	1	16/16	0.81	0.21	35,40,50,54	0
3	NAG	C	3	14/15	0.91	0.13	29,43,49,53	0
2	FUC	B	4	10/11	0.92	0.16	27,32,36,39	0

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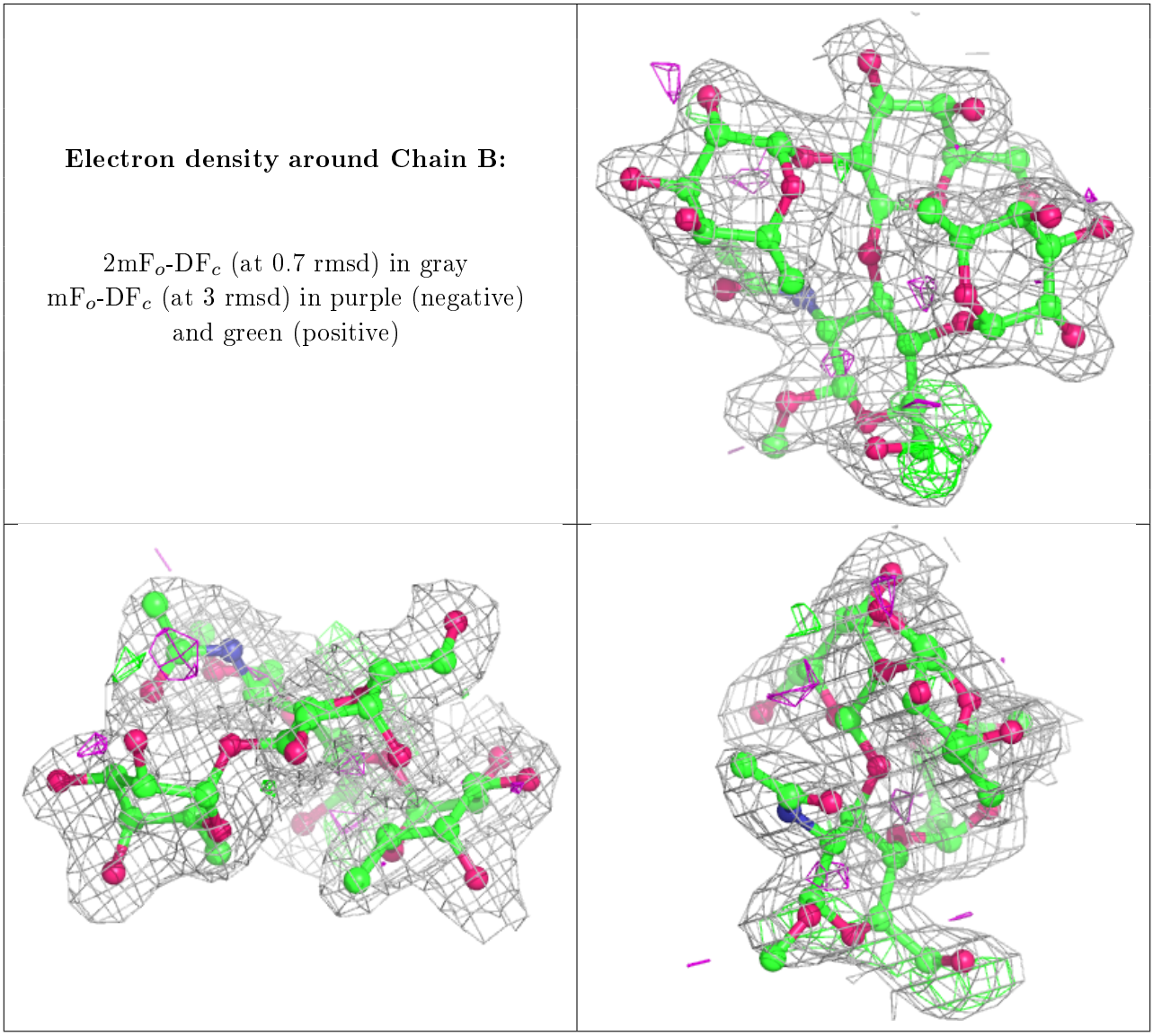
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	FUC	B	3	10/11	0.93	0.13	27,29,31,33	0
3	NAG	C	1	14/15	0.93	0.11	30,35,40,52	0
2	GAL	B	2	11/12	0.94	0.10	26,30,32,34	0
3	FUC	C	2	10/11	0.95	0.14	33,35,36,41	0

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.

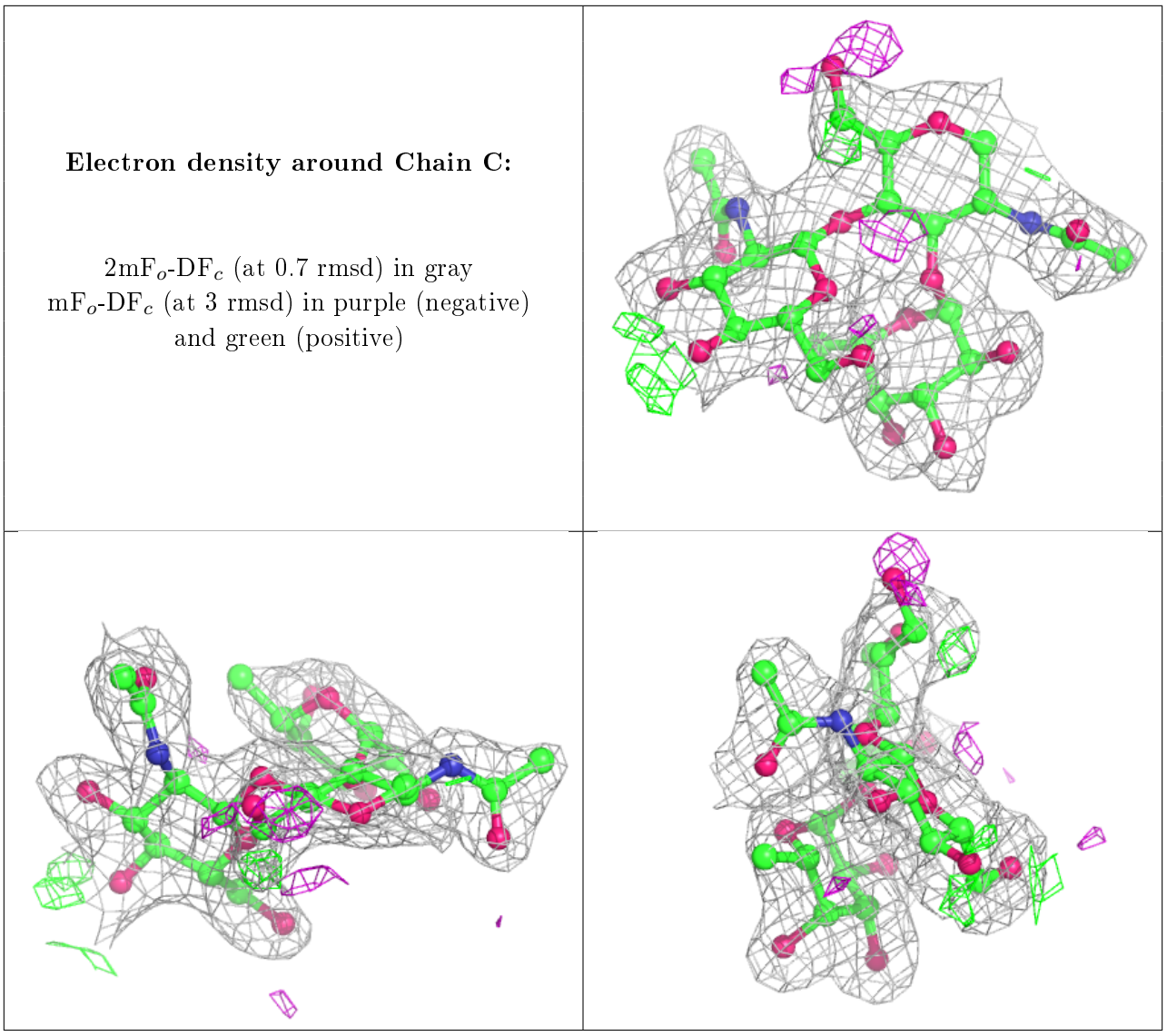
Electron density around Chain B:

$2mF_o$-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 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

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, 95^{th} 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
6	SO4	A	500	5/5	0.49	0.48	58,60,61,63	5
4	MN	A	250	1/1	0.99	0.06	21,21,21,21	0
5	CA	A	251	1/1	0.99	0.05	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.