



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 11:11 AM UTC

PDB ID : 1LGB / pdb_00001lgb
Title : INTERACTION OF A LEGUME LECTIN WITH THE N2 FRAGMENT OF HUMAN LACTOTRANSFERRIN OR WITH THE ISOLATED BIAN-TEN-NARY GLYCOPEPTIDE: ROLE OF THE FUCOSE MOIETY
Authors : Bourne, Y.; Cambillau, C.
Deposited on : 1994-01-07
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

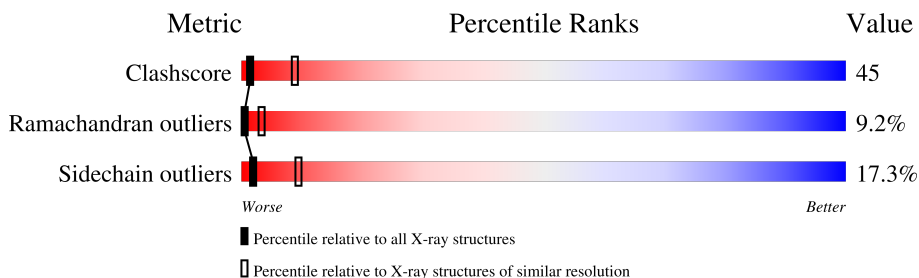
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	181	23% 51% 22% .
2	B	53	34% 45% 6% . 11%
3	C	159	33% 49% 15% .
4	D	9	33% 56% 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3119 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 LEGUME ISOLECTIN II (ALPHA CHAIN).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	0	0	0
			1403	893	231	279			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	PRO	GLN	conflict	UNP P04122
A	153	ALA	LYS	conflict	UNP P04122
A	168	GLY	ALA	conflict	UNP P04122

- Molecule 2 is a protein called LEGUME ISOLECTIN II (BETA CHAIN).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	47	Total	C	N	O	0	0	1
			371	244	57	70			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	47	ALA	SER	conflict	UNP P12307

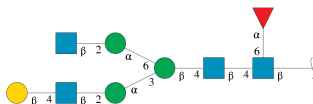
- Molecule 3 is a protein called LACTOTRANSFERRIN (N2 FRAGMENT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	159	Total	C	N	O	S	0	0	0
			1233	779	214	232	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	200	LYS	ARG	conflict	UNP P02788

- Molecule 4 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	9	Total	C	N	O	0	0	0
			110	62	4	44			

- Molecule 5 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

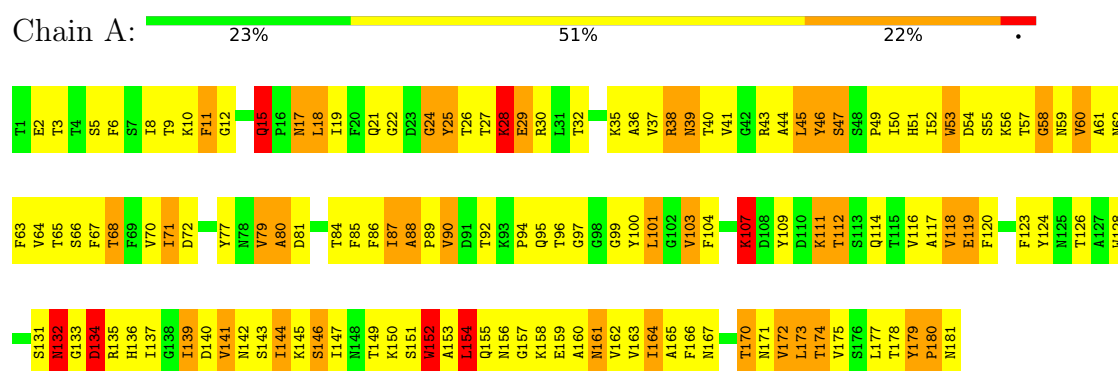
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		

3 Residue-property plots

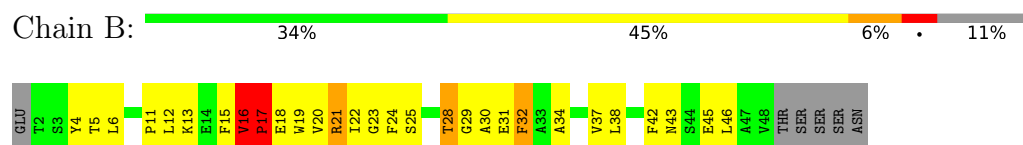
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

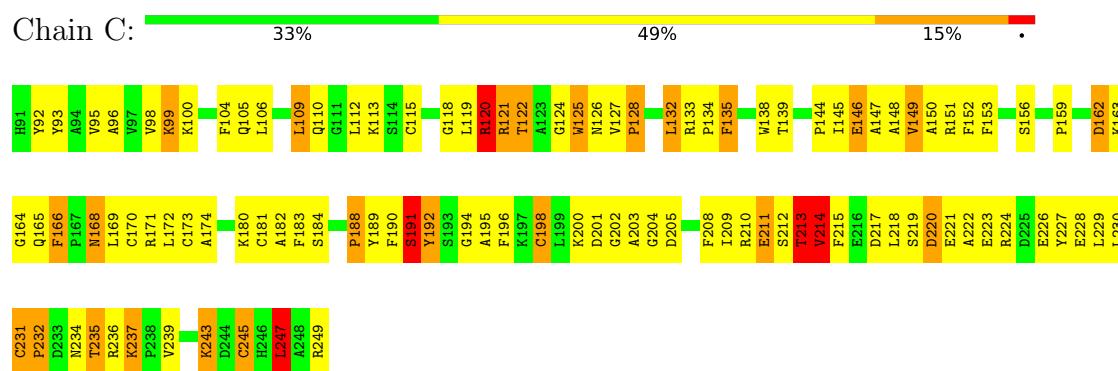
• Molecule 1: LEGUME ISOLECTIN II (ALPHA CHAIN)



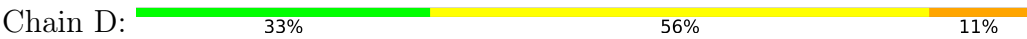
• Molecule 2: LEGUME ISOLECTIN II (BETA CHAIN)



• Molecule 3: LACTOTRANSFERRIN (N2 FRAGMENT)



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



MAN1
MAN2
MAN3
MAN4
MAN5
MAN6
MAN7
MAN8
FUC9

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.50Å 63.50Å 251.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 3.30	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-3.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.210 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3119	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.56	0/1438	1.27	23/1963 (1.2%)
2	B	0.62	1/383 (0.3%)	1.07	6/525 (1.1%)
3	C	0.74	5/1265 (0.4%)	1.16	11/1710 (0.6%)
All	All	0.65	6/3086 (0.2%)	1.20	40/4198 (1.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	121	ARG	C-N	-9.82	1.20	1.33
3	C	121	ARG	C-O	-7.32	1.14	1.23
3	C	202	GLY	C-O	-5.45	1.16	1.23
3	C	191	SER	CA-C	5.44	1.60	1.52
3	C	201	ASP	C-N	-5.43	1.25	1.33

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	121	ARG	O-C-N	-12.12	106.00	122.48
3	C	121	ARG	CA-C-O	11.01	133.68	121.02
1	A	47	SER	N-CA-C	10.41	122.70	111.36
1	A	15	GLN	CA-C-N	9.09	128.76	118.85
1	A	15	GLN	C-N-CA	9.09	128.76	118.85

There are no chirality outliers.

There are no planarity outliers.

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	1403	0	1349	157	0
2	B	371	0	347	46	0
3	C	1233	0	1175	106	0
4	D	110	0	94	3	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
All	All	3119	0	2965	271	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 45.

The worst 5 of 271 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)
3:C:229:LEU:HD22	3:C:245:CYS:SG	2.14	0.87
1:A:43:ARG:HB3	2:B:25:SER:HB2	1.58	0.83
3:C:122:THR:HA	3:C:126:ASN:HB2	1.65	0.79
1:A:6:PHE:CE1	2:B:42:PHE:HB3	2.20	0.77
3:C:221:GLU:HA	3:C:224:ARG:HE	1.49	0.76

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	179/181 (99%)	137 (76%)	26 (14%)	16 (9%)	0 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	45/53 (85%)	38 (84%)	6 (13%)	1 (2%)	5	26
3	C	157/159 (99%)	119 (76%)	20 (13%)	18 (12%)	0	2
All	All	381/393 (97%)	294 (77%)	52 (14%)	35 (9%)	0	3

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	GLY
1	A	28	LYS
1	A	36	ALA
1	A	132	ASN
1	A	144	ILE

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	155/155 (100%)	123 (79%)	32 (21%)	1	6
2	B	39/46 (85%)	34 (87%)	5 (13%)	4	18
3	C	130/130 (100%)	111 (85%)	19 (15%)	3	14
All	All	324/331 (98%)	268 (83%)	56 (17%)	2	9

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	173	LEU
3	C	247	LEU
2	B	28	THR
3	C	243	LYS
3	C	219	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	110	GLN
3	C	168	ASN
3	C	179	ASN
1	A	59	ASN
1	A	132	ASN

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 ⓘ

9 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	$\# Z > 2$
4	NAG	D	1	3,4	14,14,15	0.70	0	17,19,21	1.33	2 (11%)
4	NAG	D	2	4	14,14,15	0.55	0	17,19,21	0.82	1 (5%)
4	BMA	D	3	4	11,11,12	0.53	0	15,15,17	0.71	0
4	MAN	D	4	4	11,11,12	0.53	0	15,15,17	0.93	1 (6%)
4	NAG	D	5	4	14,14,15	0.57	0	17,19,21	0.87	0
4	GAL	D	6	4	11,11,12	0.48	0	15,15,17	0.46	0
4	MAN	D	7	4	11,11,12	0.57	0	15,15,17	0.76	1 (6%)
4	NAG	D	8	4	14,14,15	0.52	0	17,19,21	0.55	0
4	FUC	D	9	4	10,10,11	0.73	0	14,14,16	1.04	1 (7%)

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
4	NAG	D	1	3,4	-	1/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
4	NAG	D	5	4	-	0/6/23/26	0/1/1/1
4	GAL	D	6	4	-	1/2/19/22	0/1/1/1
4	MAN	D	7	4	-	0/2/19/22	0/1/1/1
4	NAG	D	8	4	-	1/6/23/26	0/1/1/1
4	FUC	D	9	4	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	NAG	C4-C3-C2	-3.58	105.77	111.02
4	D	1	NAG	C1-C2-N2	3.09	115.31	110.43
4	D	2	NAG	C2-N2-C7	-2.86	119.06	122.90
4	D	4	MAN	C3-C4-C5	2.30	114.40	110.23
4	D	9	FUC	C1-C2-C3	2.16	112.78	109.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

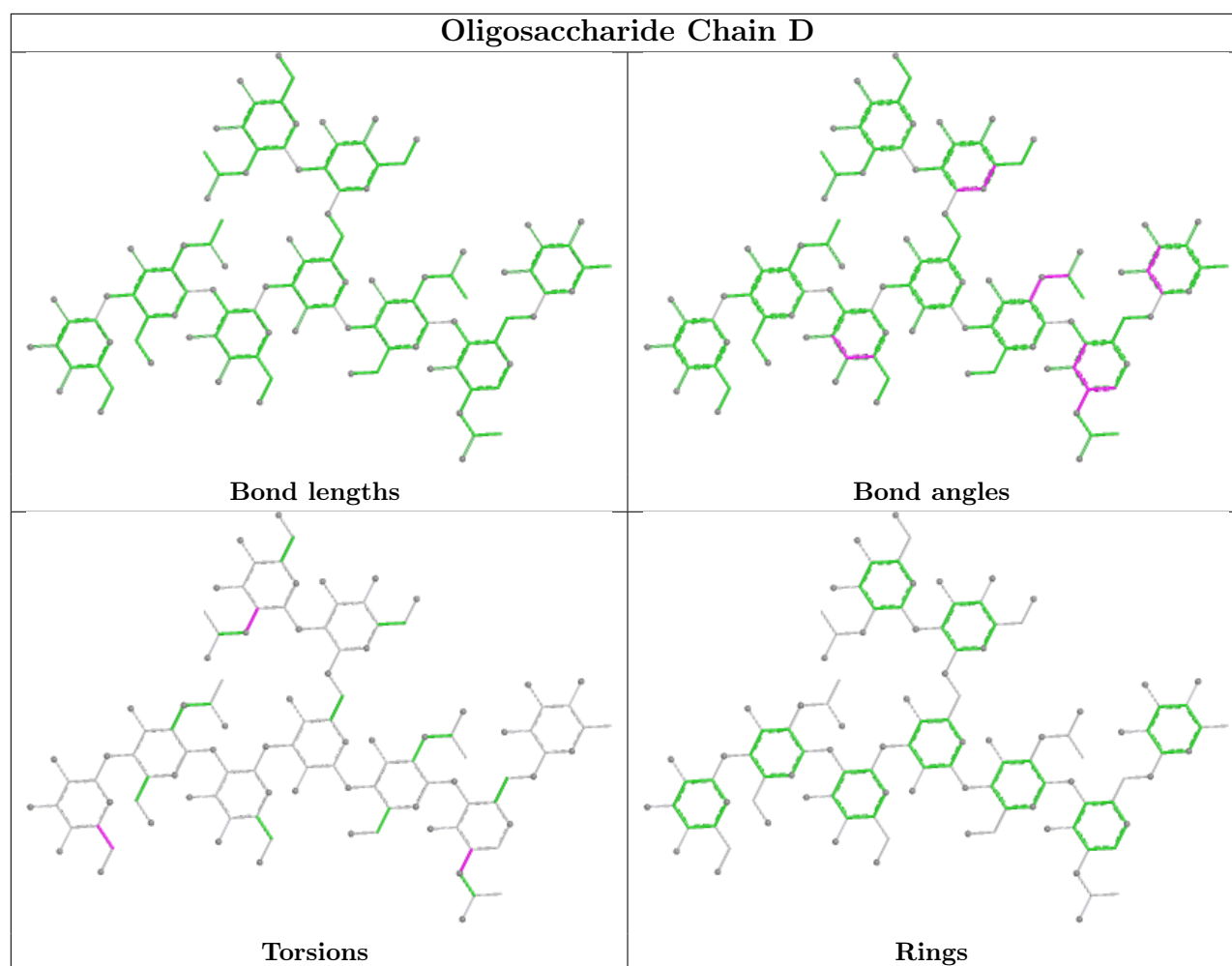
Mol	Chain	Res	Type	Atoms
4	D	1	NAG	C1-C2-N2-C7
4	D	6	GAL	O5-C5-C6-O6
4	D	8	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	4	MAN	2	0
4	D	8	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 2 ligands modelled in this entry, 2 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	121:ARG	C	122:THR	N	1.19

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.