



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2023 – 09:12 PM EDT

PDB ID : 2DYX  
Title : Structure of the complex of lactoferrin C-lobe with melibiose at 2.0 Å resolution  
Authors : Mir, R.; Prem kumar, R.; Sinha, M.; Singh, N.; Sharma, S.; Kaur, P.; Bhushan, A.; Singh, T.P.  
Deposited on : 2006-09-19  
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](mailto: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>.

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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)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

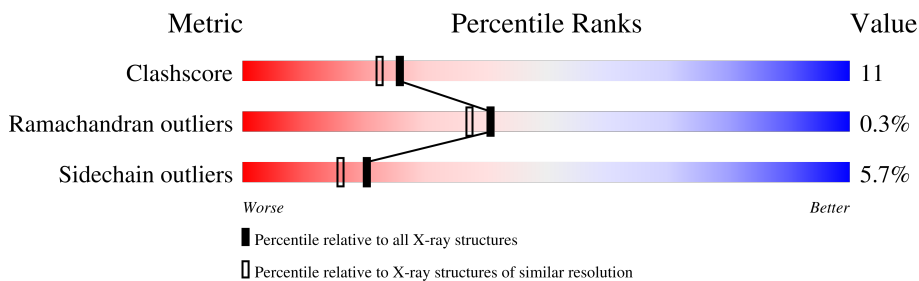
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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)

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  $\geq 3$ , 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	345	
2	B	5	
3	C	2	
4	D	6	
5	E	2	

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
5	BGC	E	1	X	-	-	-

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 3113 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.

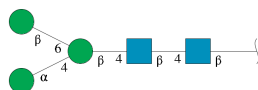
- Molecule 1 is a protein called Lactotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	341	2624	1632	459	512	21	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	565	LYS	ASN	SEE REMARK 999	UNP P24627
A	608	GLU	LYS	SEE REMARK 999	UNP P24627

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



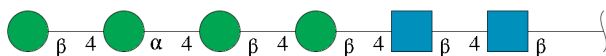
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	5	61	34	2	25	0	0	0

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



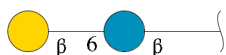
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	2	28	16	2	10	0	0	0

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-alpha-D-mannopyranos e-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-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			
4	D	6	72	40	2	30	0	0	0

- Molecule 5 is an oligosaccharide called beta-D-galactopyranose-(1-6)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
5	E	2	23	12	11	0	0	0

- Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

- Molecule 7 is CARBONATE ION (three-letter code: CO3) (formula: CO<sub>3</sub>).

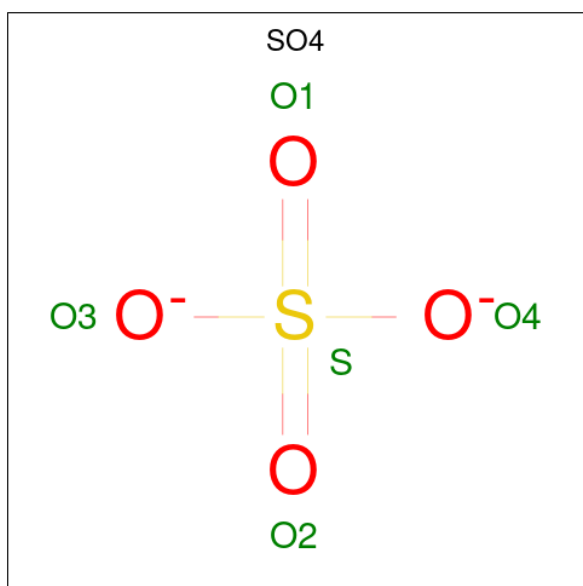


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	1	3		

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	2	Total	Zn	0	0
			2	2		

- Molecule 9 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 10 is water.

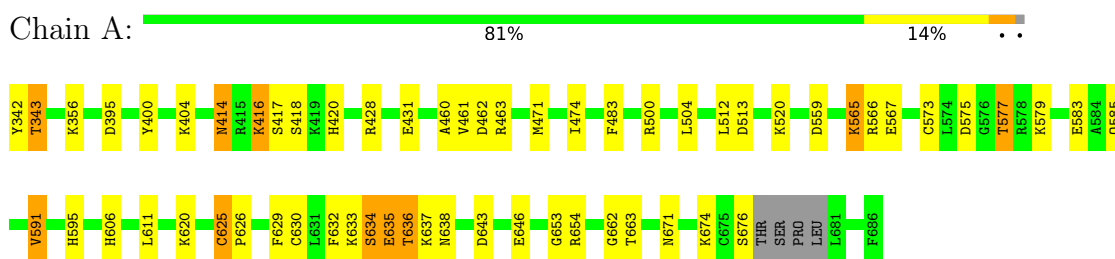
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	293	Total	O	0	0
			293	293		

### 3 Residue-property plots [i](#)

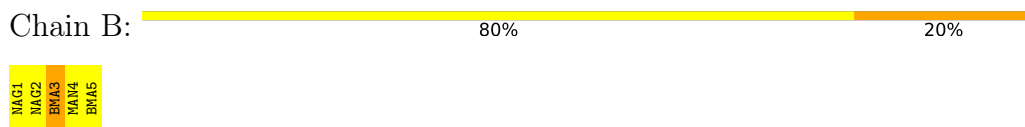
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



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



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



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



- Molecule 5: beta-D-galactopyranose-(1-6)-beta-D-glucopyranose





BGCI  
GALZ

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.59Å 50.40Å 65.93Å 90.00° 107.86° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	96.2 (20.00-2.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.172 , 0.201	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3113	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

## 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: MAN, FE, BGC, SO4, ZN, CO3, NAG, BMA, GAL

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	0.60	0/2672	0.66	0/3616

There are no bond length outliers.

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	2624	0	2534	52	0
2	B	61	0	52	2	0
3	C	28	0	25	0	0
4	D	72	0	61	5	0
5	E	23	0	21	5	0
6	A	1	0	0	0	0
7	A	4	0	0	0	0
8	A	2	0	0	0	0
9	A	5	0	0	0	0
10	A	293	0	0	6	0
All	All	3113	0	2693	58	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 11.

All (58) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3:BMA:H4	2:B:5:BMA:H2	1.31	1.06
4:D:3:BMA:H3	4:D:4:BMA:O5	1.60	1.02
1:A:634:SER:O	1:A:637:LYS:HD3	1.64	0.97
1:A:343:THR:HA	1:A:606:HIS:NE2	1.85	0.91
1:A:416:LYS:HG2	10:A:1218:HOH:O	1.71	0.90
1:A:663:THR:H	5:E:2:GAL:H4	1.40	0.84
1:A:638:ASN:HD22	1:A:643:ASP:H	1.24	0.82
1:A:635:GLU:O	1:A:636:THR:HG22	1.79	0.81
1:A:577:THR:HG21	1:A:579:LYS:NZ	1.96	0.81
1:A:565:LYS:CD	1:A:567:GLU:H	1.97	0.78
1:A:565:LYS:HD3	1:A:566:ARG:N	2.00	0.76
1:A:565:LYS:HD2	1:A:567:GLU:H	1.53	0.73
1:A:625:CYS:HA	1:A:629:PHE:O	1.88	0.73
1:A:638:ASN:ND2	1:A:643:ASP:H	1.88	0.70
4:D:5:MAN:H3	4:D:6:BMA:O5	1.92	0.69
1:A:662:GLY:CA	5:E:2:GAL:H5	2.21	0.69
1:A:565:LYS:HD2	1:A:567:GLU:HB2	1.73	0.69
1:A:577:THR:HG21	1:A:579:LYS:HZ3	1.59	0.68
1:A:635:GLU:N	10:A:1185:HOH:O	2.28	0.67
2:B:3:BMA:H4	2:B:5:BMA:C2	2.16	0.67
1:A:625:CYS:C	1:A:630:CYS:SG	2.77	0.62
1:A:662:GLY:HA3	5:E:2:GAL:H5	1.80	0.62
1:A:565:LYS:HD3	1:A:565:LYS:C	2.20	0.61
1:A:632:PHE:C	1:A:633:LYS:HD2	2.22	0.60
4:D:4:BMA:O3	4:D:5:MAN:H2	2.04	0.56
1:A:395:ASP:HA	1:A:595:HIS:CD2	2.40	0.56
1:A:400:TYR:CZ	1:A:404:LYS:HE2	2.41	0.56
1:A:471:MET:HE2	1:A:474:ILE:HD12	1.89	0.55
1:A:565:LYS:HD3	1:A:567:GLU:H	1.72	0.55
1:A:577:THR:HG21	1:A:579:LYS:HZ2	1.70	0.55
4:D:3:BMA:H2	4:D:4:BMA:O2	2.07	0.55
1:A:591:VAL:CG1	10:A:1284:HOH:O	2.56	0.52
1:A:662:GLY:HA2	5:E:2:GAL:H5	1.91	0.51
1:A:460:ALA:HB3	1:A:463:ARG:HD3	1.91	0.51
1:A:625:CYS:O	1:A:630:CYS:SG	2.69	0.51
1:A:662:GLY:HA2	5:E:2:GAL:H3	1.91	0.50
1:A:653:GLY:O	1:A:654:ARG:C	2.49	0.50
1:A:671:ASN:O	1:A:674:LYS:HG2	2.12	0.49
1:A:625:CYS:HB3	1:A:626:PRO:HD3	1.94	0.49
1:A:636:THR:HG21	10:A:1131:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:ASP:OD1	1:A:577:THR:HB	2.13	0.49
1:A:342:TYR:O	1:A:606:HIS:CE1	2.67	0.48
1:A:633:LYS:HD2	1:A:633:LYS:N	2.30	0.47
1:A:343:THR:HG23	1:A:343:THR:O	2.16	0.46
1:A:620:LYS:HD3	1:A:646:GLU:HG3	1.98	0.45
1:A:676:SER:OG	10:A:1199:HOH:O	2.21	0.45
1:A:573:CYS:SG	1:A:577:THR:HG22	2.58	0.43
1:A:585:GLN:NE2	4:D:1:NAG:H81	2.34	0.43
1:A:483:PHE:CD2	1:A:483:PHE:C	2.91	0.42
1:A:625:CYS:CB	1:A:626:PRO:HD3	2.48	0.42
1:A:565:LYS:HD2	1:A:567:GLU:N	2.29	0.42
1:A:420:HIS:HB3	1:A:428:ARG:HG3	2.02	0.42
1:A:654:ARG:HG2	10:A:1196:HOH:O	2.20	0.41
1:A:512:LEU:O	1:A:513:ASP:HB2	2.21	0.41
1:A:461:VAL:O	1:A:462:ASP:HB2	2.21	0.41
1:A:513:ASP:OD2	1:A:520:LYS:HD3	2.21	0.41
1:A:417:SER:CB	1:A:431:GLU:OE2	2.69	0.41
1:A:414:ASN:HD22	1:A:414:ASN:HA	1.63	0.40

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	339/345 (98%)	323 (95%)	15 (4%)	1 (0%)	41 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	634	SER

### 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	284/286 (99%)	268 (94%)	16 (6%)	<b>21</b> <b>17</b>

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	343	THR
1	A	356	LYS
1	A	414	ASN
1	A	416	LYS
1	A	418	SER
1	A	500	ARG
1	A	504	LEU
1	A	559	ASP
1	A	565	LYS
1	A	577	THR
1	A	583	GLU
1	A	591	VAL
1	A	611	LEU
1	A	625	CYS
1	A	635	GLU
1	A	636	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	355	GLN
1	A	414	ASN
1	A	585	GLN
1	A	638	ASN

### 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](#)

15 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	B	1	2,1	14,14,15	0.57	0	17,19,21	1.01	1 (5%)
2	NAG	B	2	2	14,14,15	0.59	0	17,19,21	1.11	1 (5%)
2	BMA	B	3	2	11,11,12	0.65	0	15,15,17	1.63	3 (20%)
2	MAN	B	4	2	11,11,12	0.52	0	15,15,17	1.39	2 (13%)
2	BMA	B	5	2	11,11,12	0.53	0	15,15,17	0.92	0
3	NAG	C	1	3,1	14,14,15	0.68	0	17,19,21	1.35	4 (23%)
3	NAG	C	2	3	14,14,15	0.68	0	17,19,21	1.28	1 (5%)
4	NAG	D	1	4,1	14,14,15	0.68	0	17,19,21	1.44	1 (5%)
4	NAG	D	2	4	14,14,15	0.68	0	17,19,21	1.23	2 (11%)
4	BMA	D	3	4	11,11,12	0.84	0	15,15,17	1.67	1 (6%)
4	BMA	D	4	4	11,11,12	0.59	0	15,15,17	1.02	1 (6%)
4	MAN	D	5	4	11,11,12	0.63	0	15,15,17	1.10	2 (13%)
4	BMA	D	6	4	11,11,12	0.72	0	15,15,17	1.47	2 (13%)
5	BGC	E	1	5	12,12,12	0.61	0	17,17,17	1.44	3 (17%)
5	GAL	E	2	5	11,11,12	0.42	0	15,15,17	1.90	5 (33%)

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	B	1	2,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
2	MAN	B	4	2	-	2/2/19/22	0/1/1/1
2	BMA	B	5	2	-	2/2/19/22	0/1/1/1
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
4	NAG	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	2/2/19/22	0/1/1/1
4	BMA	D	4	4	-	0/2/19/22	0/1/1/1
4	MAN	D	5	4	-	2/2/19/22	0/1/1/1
4	BMA	D	6	4	-	0/2/19/22	0/1/1/1
5	BGC	E	1	5	1/1/5/5	2/2/22/22	0/1/1/1
5	GAL	E	2	5	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	3	BMA	C1-C2-C3	5.07	115.90	109.67
4	D	1	NAG	C1-O5-C5	4.90	118.83	112.19
2	B	3	BMA	C1-O5-C5	4.12	117.77	112.19
5	E	2	GAL	O5-C1-C2	-4.00	104.60	110.77
2	B	4	MAN	C1-O5-C5	3.90	117.47	112.19
4	D	6	BMA	O5-C5-C6	3.66	112.94	107.20
5	E	2	GAL	C1-C2-C3	-3.64	105.19	109.67
3	C	2	NAG	O5-C5-C6	3.56	112.79	107.20
3	C	1	NAG	C1-O5-C5	2.92	116.15	112.19
4	D	6	BMA	C1-C2-C3	2.88	113.21	109.67
4	D	4	BMA	O5-C5-C6	2.85	111.67	107.20
5	E	1	BGC	O5-C5-C4	2.80	114.77	109.69
2	B	3	BMA	C3-C4-C5	2.76	115.16	110.24
3	C	1	NAG	O5-C1-C2	-2.59	107.20	111.29
5	E	2	GAL	C1-O5-C5	-2.52	108.77	112.19
5	E	2	GAL	O2-C2-C1	2.52	114.30	109.15
4	D	5	MAN	C1-C2-C3	2.38	112.59	109.67
2	B	2	NAG	C1-O5-C5	2.37	115.40	112.19
2	B	3	BMA	O5-C1-C2	-2.37	107.12	110.77
3	C	1	NAG	C2-N2-C7	2.31	126.19	122.90
2	B	4	MAN	C1-C2-C3	2.23	112.41	109.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	5	MAN	C1-O5-C5	2.21	115.19	112.19
4	D	2	NAG	C1-O5-C5	2.21	115.19	112.19
5	E	2	GAL	O5-C5-C6	2.15	110.57	107.20
2	B	1	NAG	C3-C4-C5	-2.12	106.45	110.24
5	E	1	BGC	C3-C4-C5	2.12	114.03	110.24
5	E	1	BGC	C1-C2-C3	-2.10	105.95	110.31
4	D	2	NAG	O7-C7-N2	2.04	125.70	121.95
3	C	1	NAG	O7-C7-N2	2.01	125.66	121.95

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	E	1	BGC	C1

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	O5-C5-C6-O6
2	B	5	BMA	O5-C5-C6-O6
5	E	1	BGC	O5-C5-C6-O6
5	E	2	GAL	O5-C5-C6-O6
2	B	5	BMA	C4-C5-C6-O6
5	E	1	BGC	C4-C5-C6-O6
4	D	5	MAN	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
2	B	4	MAN	O5-C5-C6-O6
5	E	2	GAL	C4-C5-C6-O6
4	D	5	MAN	C4-C5-C6-O6
2	B	4	MAN	C4-C5-C6-O6
4	D	3	BMA	C4-C5-C6-O6
4	D	3	BMA	O5-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 12 short contacts:

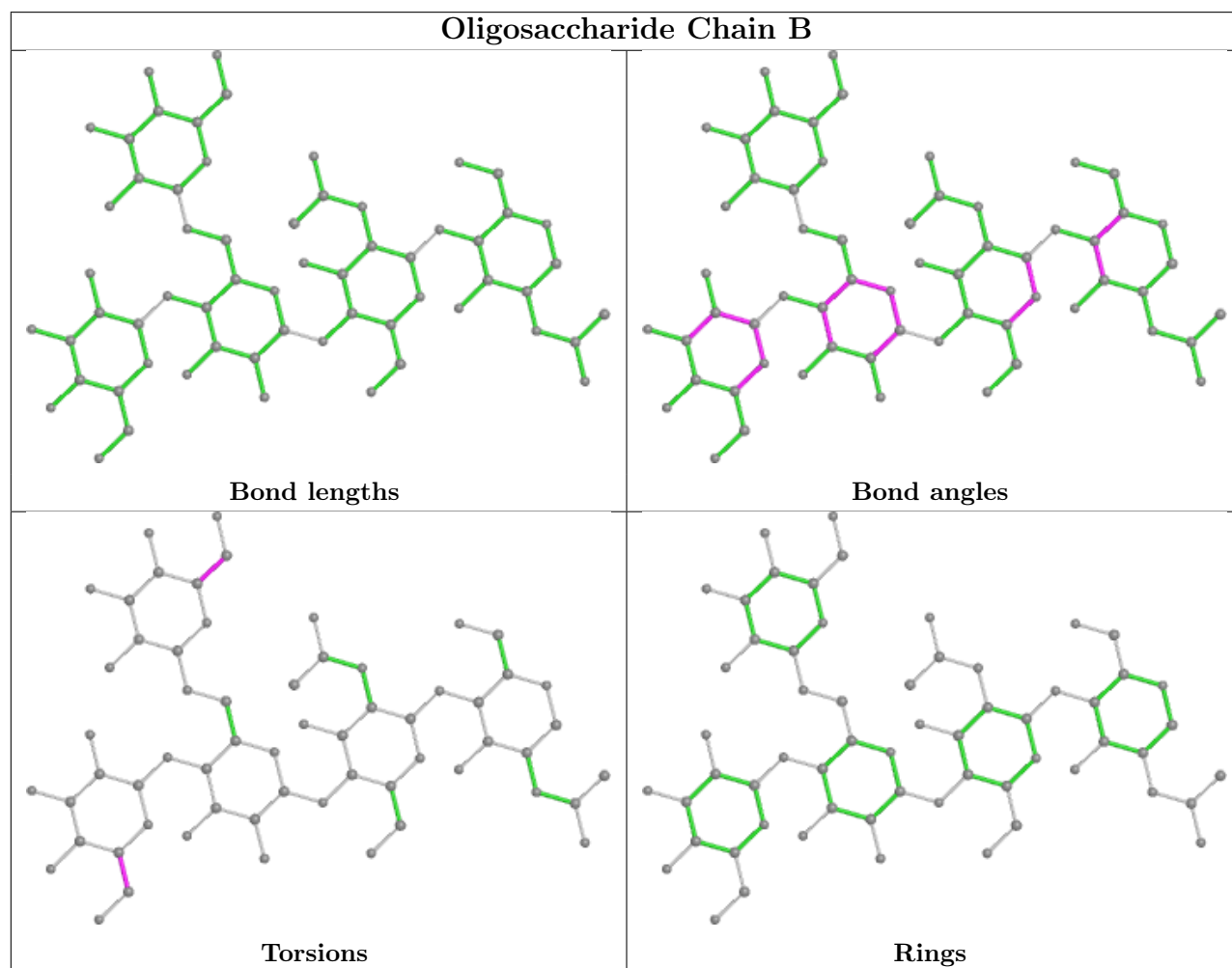
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	4	BMA	3	0
5	E	2	GAL	5	0
2	B	5	BMA	2	0
4	D	6	BMA	1	0
4	D	3	BMA	2	0

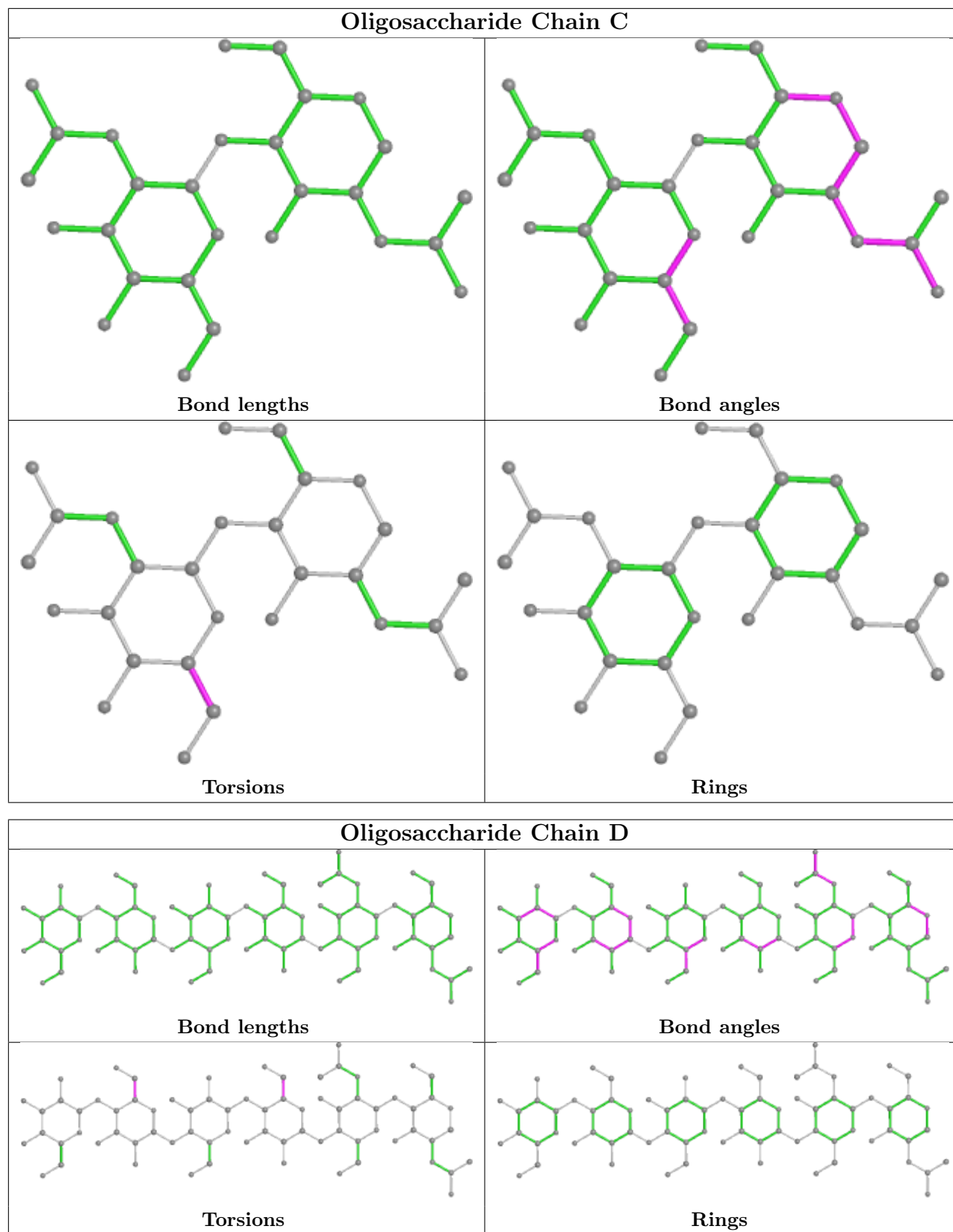
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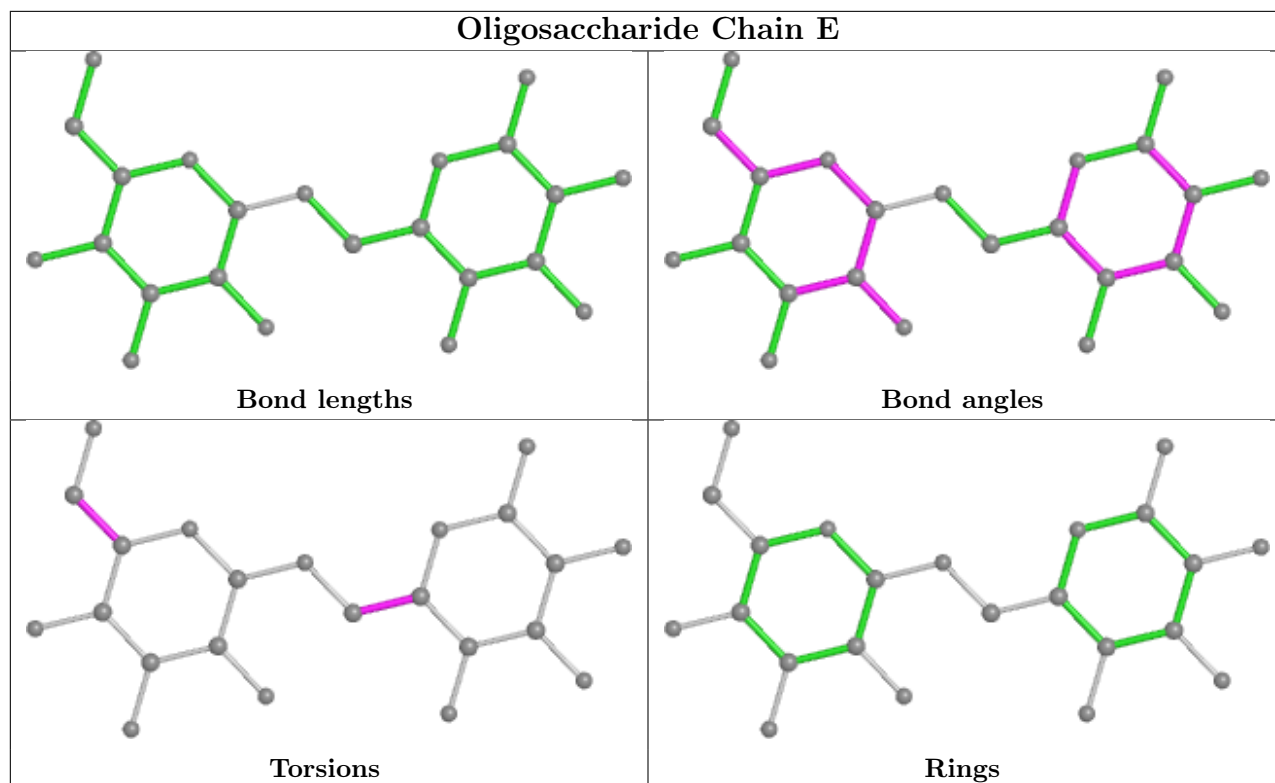
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	3	BMA	2	0
4	D	5	MAN	2	0
4	D	1	NAG	1	0

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 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\# Z  > 2$
7	CO3	A	1003	6	2,3,3	0.67	0	2,3,3	0.97	0
9	SO4	A	1006	-	4,4,4	0.17	0	6,6,6	0.15	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 [i](#)

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

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.