



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 12:59 PM BST

PDB ID : 2O1L  
Title : Structure of a complex of C-terminal lobe of bovine lactoferrin with disaccharide at 1.97 Å resolution  
Authors : Singh, N.; Sharma, S.; Perbandt, M.; Kaur, P.; Betzel, C.; Singh, T.P.  
Deposited on : 2006-11-29  
Resolution : 1.97 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.

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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)  
Xtriage (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) : 2.13.1

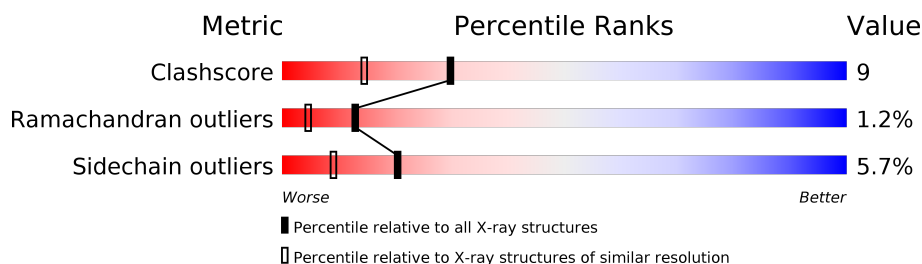
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)

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  $\geq 3$ , 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	2	
2	E	2	
3	C	3	
4	D	4	

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
3	NAG	C	1	X	-	-	-
4	MAN	D	4	X	-	-	-

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 3086 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
1	A	341	Total	C	N	O	S	0	0	0
			2605	1622	454	508	21			

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 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			29	16	2	11			

- Molecule 3 is an oligosaccharide called alpha-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
3	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-alpha-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
4	D	4	Total	C	N	O	0	0	0
			50	28	2	20			

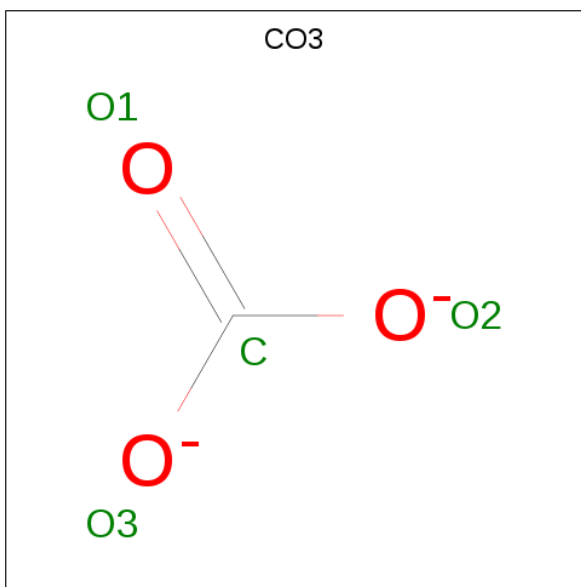
- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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

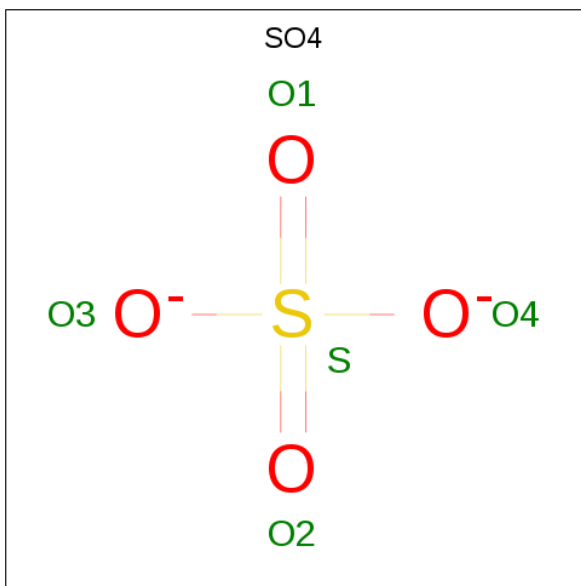
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Fe	0	0
			1	1		

- 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 SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

- Molecule 9 is water.

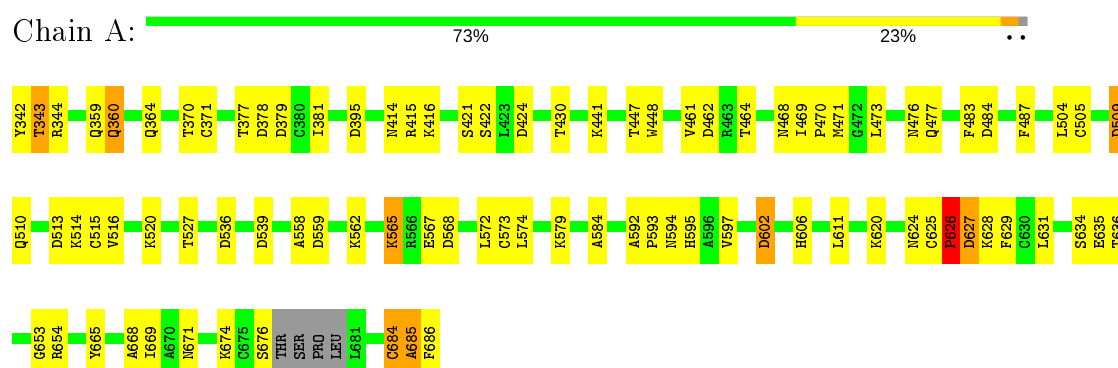
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	318	Total 318	O 318	0	0

### 3 Residue-property plots

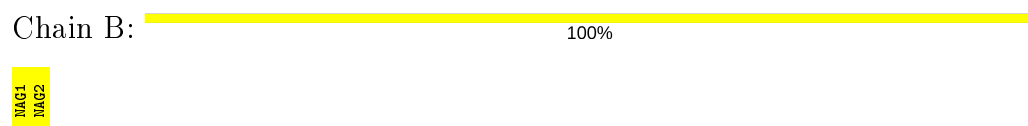
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

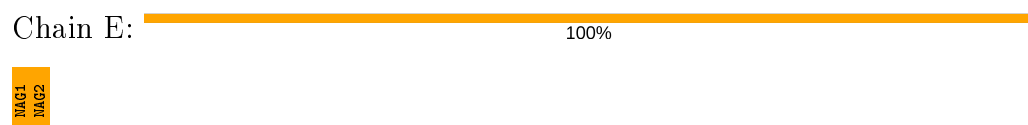
- Molecule 1: Lactotransferrin



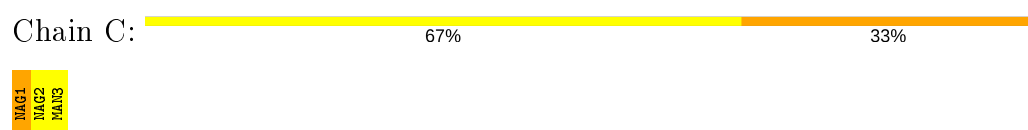
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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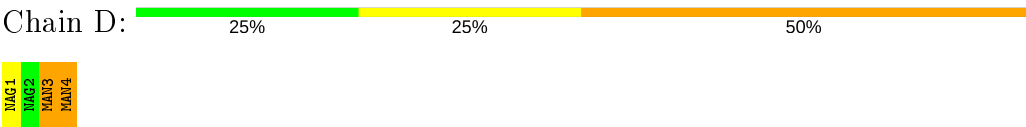


- Molecule 3: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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





## 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, $\alpha$ , $\beta$ , $\gamma$	61.61Å 50.02Å 65.39Å 90.00° 107.11° 90.00°	Depositor
Resolution (Å)	62.02 – 1.97	Depositor
% Data completeness (in resolution range)	88.8 (62.02-1.97)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC 5.0	Depositor
R, $R_{free}$	0.214 , 0.231	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3086	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	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: ZN, NAG, SO4, CO3, FE, 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	0.49	0/2653	0.99	14/3591 (0.4%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	625	CYS	C-N-CD	-27.15	60.86	120.60
1	A	625	CYS	C-N-CA	8.80	158.95	122.00
1	A	626	PRO	CA-N-CD	-8.49	99.61	111.50
1	A	536	ASP	CB-CG-OD2	6.96	124.56	118.30
1	A	509	ASP	CB-CG-OD2	6.28	123.95	118.30
1	A	627	ASP	CB-CG-OD2	6.27	123.94	118.30
1	A	539	ASP	CB-CG-OD2	6.22	123.90	118.30
1	A	379	ASP	CB-CG-OD2	5.61	123.34	118.30
1	A	602	ASP	CB-CG-OD2	5.59	123.34	118.30
1	A	568	ASP	CB-CG-OD2	5.54	123.28	118.30
1	A	484	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	378	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	421	SER	N-CA-C	5.30	125.32	111.00
1	A	424	ASP	CB-CG-OD2	5.05	122.85	118.30

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	2605	0	2519	49	0
2	B	28	0	25	0	0
2	E	29	0	27	1	0
3	C	39	0	34	1	0
4	D	50	0	43	2	0
5	A	2	0	0	0	0
6	A	1	0	0	0	0
7	A	4	0	0	0	0
8	A	10	0	0	0	0
9	A	318	0	0	8	0
All	All	3086	0	2648	51	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 9.

All (51) 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:514:LYS:HB2	9:A:2098:HOH:O	1.77	0.83
1:A:685:ALA:HB3	9:A:2127:HOH:O	1.81	0.80
1:A:371:CYS:HB3	9:A:2045:HOH:O	1.82	0.80
1:A:359:GLN:HG2	9:A:2256:HOH:O	1.81	0.80
4:D:3:MAN:H5	4:D:4:MAN:H2	1.70	0.73
1:A:629:PHE:HA	9:A:2055:HOH:O	1.93	0.68
1:A:565:LYS:HD3	1:A:567:GLU:H	1.63	0.64
1:A:448:TRP:HE1	1:A:477:GLN:HE22	1.45	0.63
1:A:370:THR:HG22	1:A:371:CYS:N	2.17	0.59
1:A:527:THR:HG21	1:A:636:THR:O	2.02	0.59
1:A:665:TYR:CE1	1:A:669:ILE:HD11	2.37	0.59
1:A:461:VAL:O	1:A:462:ASP:HB2	2.02	0.58
1:A:370:THR:CG2	1:A:371:CYS:N	2.68	0.57
1:A:416:LYS:HE3	1:A:620:LYS:HE3	1.88	0.54
1:A:447:THR:HA	1:A:572:LEU:HD22	1.90	0.54
1:A:584:ALA:HB3	4:D:1:NAG:H82	1.90	0.54
1:A:624:ASN:HB3	1:A:628:LYS:HB2	1.90	0.53
1:A:513:ASP:OD2	1:A:520:LYS:NZ	2.39	0.53
1:A:430:THR:HB	1:A:594:ASN:ND2	2.26	0.51
1:A:395:ASP:HA	1:A:595:HIS:CD2	2.47	0.49
1:A:370:THR:CG2	1:A:371:CYS:H	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:LYS:HE2	1:A:567:GLU:O	2.12	0.48
1:A:415:ARG:HG2	1:A:416:LYS:N	2.30	0.47
1:A:505:CYS:O	1:A:514:LYS:HE2	2.15	0.47
1:A:343:THR:O	1:A:343:THR:HG23	2.14	0.47
1:A:471:MET:HE1	1:A:487:PHE:HE2	1.79	0.47
1:A:416:LYS:CE	1:A:620:LYS:HE3	2.45	0.47
1:A:513:ASP:OD2	1:A:520:LYS:HD3	2.15	0.46
1:A:469:ILE:HB	1:A:470:PRO:HD3	1.98	0.46
1:A:668:ALA:HB1	3:C:1:NAG:H83	1.98	0.46
1:A:509:ASP:OD1	1:A:510:GLN:HG3	2.15	0.45
1:A:573:CYS:SG	1:A:579:LYS:HG3	2.56	0.45
1:A:653:GLY:O	1:A:654:ARG:C	2.55	0.45
2:E:1:NAG:H5	2:E:2:NAG:O5	2.14	0.45
1:A:360:GLN:NE2	9:A:2198:HOH:O	2.49	0.45
1:A:635:GLU:N	9:A:2089:HOH:O	2.49	0.45
1:A:468:ASN:HB3	1:A:669:ILE:CD1	2.46	0.44
1:A:364:GLN:HG3	1:A:629:PHE:HB2	1.99	0.44
1:A:343:THR:OG1	1:A:606:HIS:CE1	2.72	0.43
1:A:684:CYS:C	1:A:686:PHE:H	2.21	0.43
1:A:448:TRP:HE1	1:A:477:GLN:NE2	2.16	0.42
1:A:377:THR:O	1:A:381:ILE:HG12	2.19	0.42
1:A:671:ASN:HA	1:A:674:LYS:HD2	2.01	0.42
1:A:558:ALA:O	1:A:562:LYS:HG3	2.20	0.42
1:A:483:PHE:C	1:A:483:PHE:CD2	2.93	0.42
1:A:516:VAL:O	1:A:516:VAL:HG23	2.20	0.42
1:A:473:LEU:HD13	1:A:574:LEU:HD21	2.02	0.42
1:A:597:VAL:HG11	1:A:611:LEU:HD21	2.02	0.41
1:A:464:THR:HG21	1:A:592:ALA:HB1	2.02	0.41
1:A:469:ILE:HB	1:A:470:PRO:CD	2.51	0.41
1:A:559:ASP:HB2	9:A:2234:HOH:O	2.20	0.41

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	337/345 (98%)	315 (94%)	18 (5%)	4 (1%)	13 4

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	626	PRO
1	A	634	SER
1	A	684	CYS
1	A	685	ALA

### 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	282/286 (99%)	266 (94%)	16 (6%)	20 9

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

Mol	Chain	Res	Type
1	A	342	TYR
1	A	343	THR
1	A	344	ARG
1	A	360	GLN
1	A	414	ASN
1	A	422	SER
1	A	476	ASN
1	A	504	LEU
1	A	515	CYS
1	A	565	LYS
1	A	593	PRO
1	A	602	ASP
1	A	626	PRO
1	A	627	ASP
1	A	631	LEU

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Mol	Chain	Res	Type
1	A	676	SER

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

Mol	Chain	Res	Type
1	A	359	GLN
1	A	414	ASN
1	A	477	GLN
1	A	606	HIS
1	A	624	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 ⓘ

11 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	1,2	14,14,15	0.69	0	17,19,21	1.29	2 (11%)
2	NAG	B	2	2	14,14,15	0.55	0	17,19,21	0.98	2 (11%)
3	NAG	C	1	1,3	14,14,15	0.50	0	17,19,21	1.51	2 (11%)
3	NAG	C	2	3	14,14,15	0.60	0	17,19,21	1.11	1 (5%)
3	MAN	C	3	3	11,11,12	0.62	0	15,15,17	1.85	4 (26%)
4	NAG	D	1	1,4	14,14,15	0.70	0	17,19,21	0.95	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	D	2	4	14,14,15	0.59	0	17,19,21	0.76	0
4	MAN	D	3	4	11,11,12	0.62	0	15,15,17	1.85	4 (26%)
4	MAN	D	4	4	11,11,12	0.76	0	15,15,17	2.00	3 (20%)
2	NAG	E	1	2	15,15,15	0.49	0	21,21,21	1.65	5 (23%)
2	NAG	E	2	2	14,14,15	0.60	0	17,19,21	1.69	4 (23%)

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	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
3	NAG	C	1	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	MAN	C	3	3	-	0/2/19/22	0/1/1/1
4	NAG	D	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	MAN	D	3	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4	4	1/1/4/5	2/2/19/22	1/1/1/1
2	NAG	E	1	2	-	2/6/26/26	0/1/1/1
2	NAG	E	2	2	-	6/6/23/26	0/1/1/1

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	4	MAN	C1-O5-C5	5.71	119.93	112.19
4	D	3	MAN	C1-O5-C5	4.39	118.14	112.19
3	C	3	MAN	C1-O5-C5	4.38	118.13	112.19
3	C	1	NAG	C1-O5-C5	4.06	117.70	112.19
3	C	1	NAG	O5-C5-C6	3.93	113.36	107.20
2	E	1	NAG	C3-C4-C5	3.77	116.96	110.24
2	E	1	NAG	C4-C3-C2	3.60	115.61	110.34
2	B	1	NAG	C4-C3-C2	3.23	115.75	111.02
3	C	2	NAG	C4-C3-C2	3.16	115.66	111.02
2	E	2	NAG	C2-N2-C7	3.13	127.36	122.90
3	C	3	MAN	O5-C5-C6	2.94	111.81	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	3	MAN	O5-C5-C6	2.93	111.80	107.20
4	D	4	MAN	O5-C5-C6	2.85	111.67	107.20
4	D	3	MAN	C1-C2-C3	2.78	113.08	109.67
3	C	3	MAN	C1-C2-C3	2.77	113.08	109.67
2	E	1	NAG	C1-C2-C3	2.73	114.27	110.54
2	E	1	NAG	C1-O5-C5	-2.60	108.75	113.66
2	B	1	NAG	O5-C1-C2	-2.50	107.34	111.29
2	E	2	NAG	C3-C4-C5	2.46	114.62	110.24
2	E	2	NAG	C6-C5-C4	-2.43	107.32	113.00
4	D	4	MAN	O5-C1-C2	2.39	114.46	110.77
2	E	1	NAG	C1-C2-N2	-2.28	108.09	110.73
2	B	2	NAG	O5-C1-C2	-2.20	107.81	111.29
4	D	3	MAN	C3-C4-C5	2.19	114.15	110.24
3	C	3	MAN	C3-C4-C5	2.19	114.15	110.24
2	E	2	NAG	O7-C7-N2	2.17	125.93	121.95
2	B	2	NAG	C3-C4-C5	2.10	113.98	110.24

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	1	NAG	C1
4	D	4	MAN	C1

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
4	D	4	MAN	O5-C5-C6-O6
4	D	4	MAN	C4-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6
4	D	2	NAG	C8-C7-N2-C2
2	E	2	NAG	C8-C7-N2-C2
2	E	2	NAG	C1-C2-N2-C7
2	E	2	NAG	O7-C7-N2-C2
2	B	1	NAG	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O7-C7-N2-C2
4	D	1	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
2	E	2	NAG	C3-C2-N2-C7

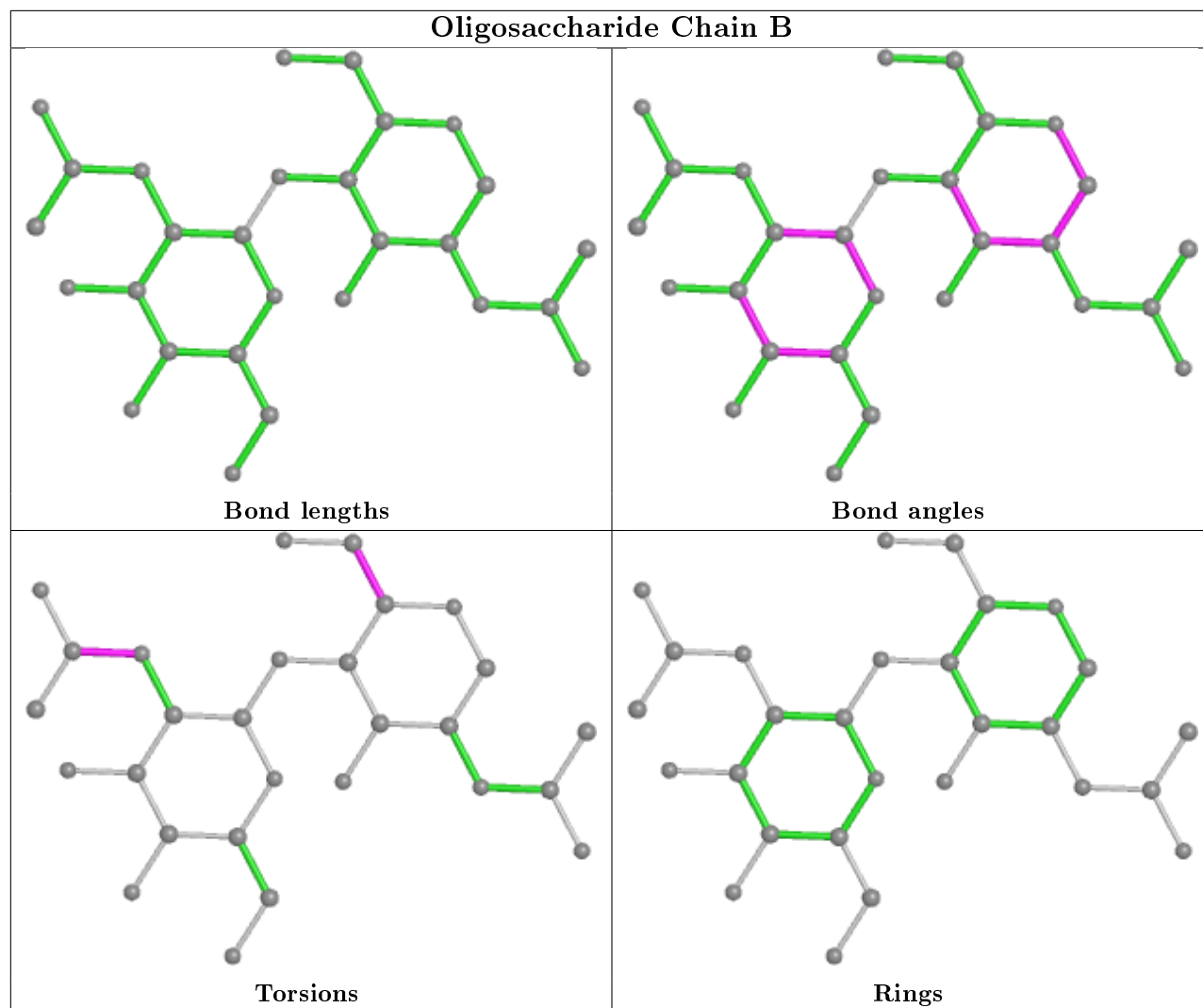
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	4	MAN	C1-C2-C3-C4-C5-O5

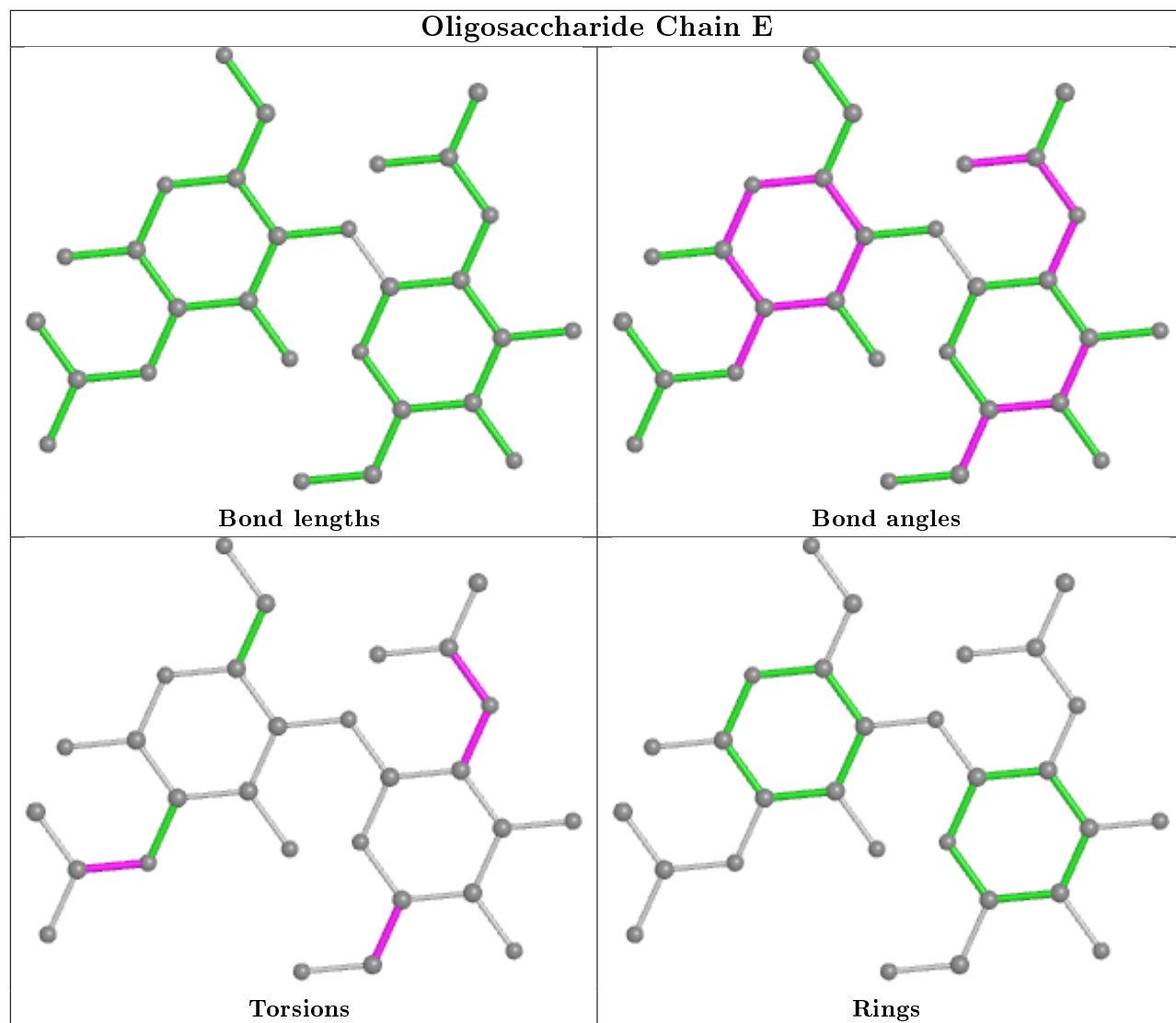
6 monomers are involved in 4 short contacts:

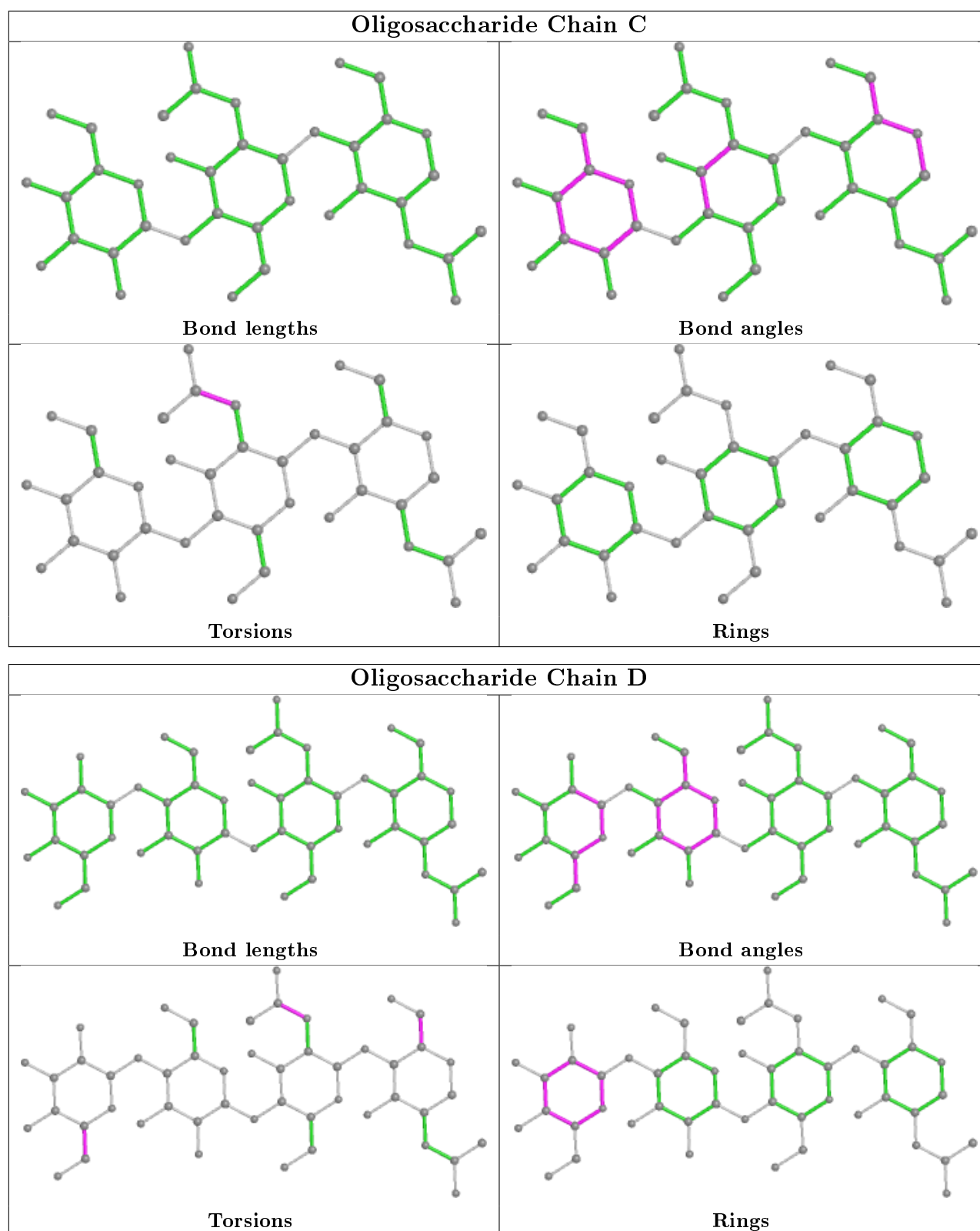
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0
3	C	1	NAG	1	0
4	D	1	NAG	1	0
2	E	2	NAG	1	0
4	D	3	MAN	1	0
4	D	4	MAN	1	0

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



## Oligosaccharide Chain E





## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	1999	6	0,3,3	0.00	-	0,3,3	0.00	-
8	SO4	A	2000	-	4,4,4	0.14	0	6,6,6	0.11	0
8	SO4	A	2001	-	4,4,4	0.13	0	6,6,6	0.08	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 [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 ⓘ

### 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.