



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:21 AM UTC

PDB ID : 2DWH / pdb_00002dwh
Title : Crystal structure of N-acetylglucosamine complex of bovine lactoferrin C-lobe at 2.8 Å resolution
Authors : Mir, R.; Ethayathulla, A.S.; Singh, N.; Sharma, S.; Bhushan, A.; Kaur, P.; Singh, T.P.
Deposited on : 2006-08-12
Resolution : 2.80 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 ⓘ 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

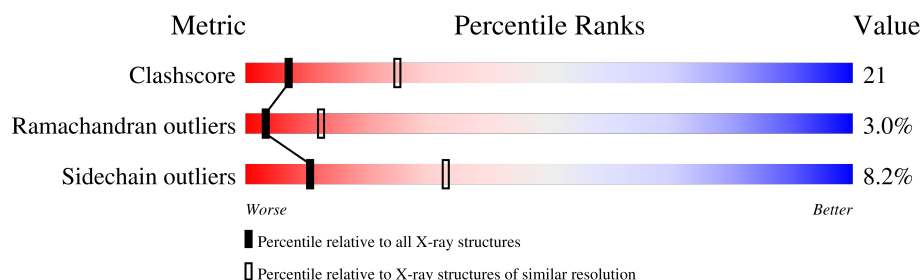
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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	345	
2	B	2	
3	C	3	
4	D	4	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 2899 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	340	Total	C	N	O	S	0	0	0
			2593	1613	453	506	21			

There are 2 discrepancies between the modelled and reference sequences:

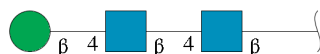
Chain	Residue	Modelled	Actual	Comment	Reference
A	565	LYS	ASN	SEE REMARK 999	UNP P24627
A	608	GLU	LYS	SEE REMARK 999	UNP P24627

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



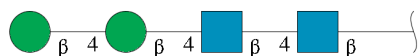
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



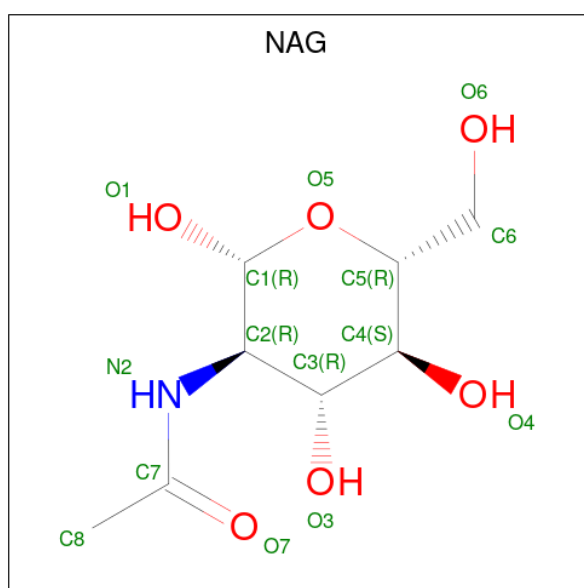
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is an oligosaccharide called 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
4	D	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			15	8	1	6		

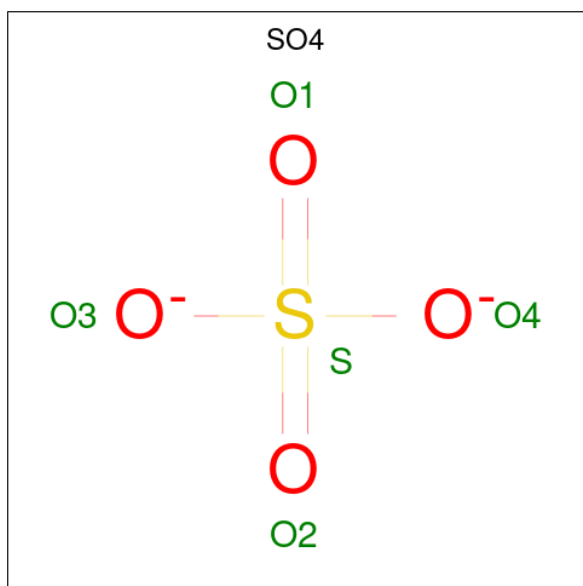
- Molecule 6 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

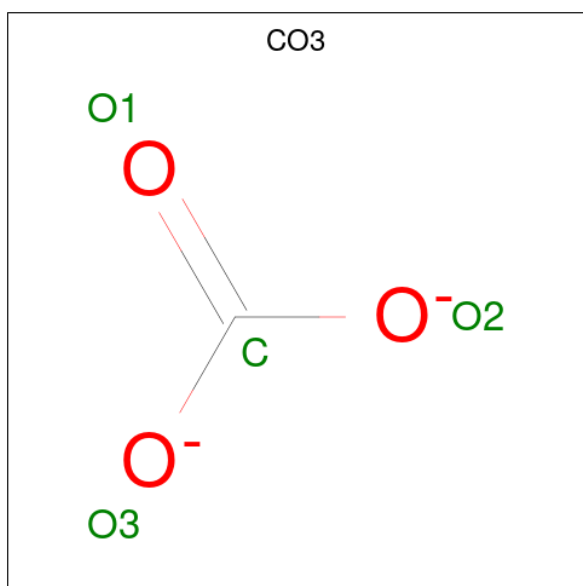
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	Zn	0	0
			2	2		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 9 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).



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

- Molecule 10 is water.

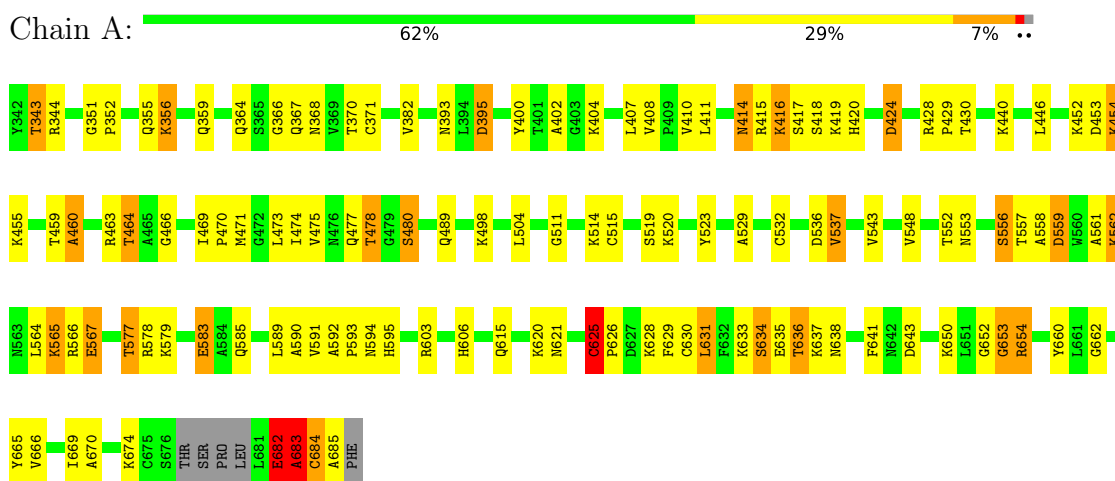
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	162	Total	O	0	0
			162	162		

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.

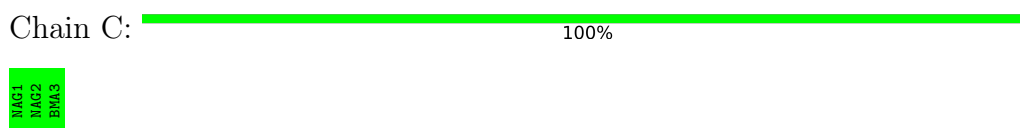
- Molecule 1: Lactotransferrin



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



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



- Molecule 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



MAG1
MAG2
BMA3
BMA4

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, α , β , γ	63.58Å 50.49Å 66.03Å 90.00° 107.73° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	96.8 (20.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.194 , 0.228	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2899	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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: NAG, SO4, ZN, BMA, FE, CO3

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	0.46	0/2640	1.03	14/3575 (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	654	ARG	CA-C-N	9.28	129.34	119.78
1	A	654	ARG	C-N-CA	9.28	129.34	119.78
1	A	683	ALA	N-CA-C	-7.77	94.26	110.80
1	A	653	GLY	N-CA-C	-7.56	104.11	115.00
1	A	351	GLY	CA-C-N	7.03	126.86	119.05
1	A	351	GLY	C-N-CA	7.03	126.86	119.05
1	A	537	VAL	N-CA-C	-6.53	104.49	110.82
1	A	682	GLU	N-CA-C	-6.38	97.21	110.80
1	A	408	VAL	N-CA-C	6.16	114.24	109.19
1	A	371	CYS	N-CA-C	6.12	119.68	109.95
1	A	650	LYS	N-CA-C	-5.78	102.90	110.53
1	A	556	SER	N-CA-C	5.28	119.82	112.90
1	A	523	TYR	N-CA-C	5.11	118.35	112.57
1	A	343	THR	N-CA-C	-5.01	106.48	112.59

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	2593	0	2510	107	0
2	B	28	0	25	3	0
3	C	39	0	34	0	0
4	D	50	0	43	5	0
5	A	15	0	15	3	0
6	A	1	0	0	0	0
7	A	2	0	0	0	0
8	A	5	0	0	0	0
9	A	4	0	0	0	0
10	A	162	0	0	13	0
All	All	2899	0	2627	112	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 21.

All (112) 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:638:ASN:HD22	1:A:643:ASP:H	1.17	0.92
1:A:638:ASN:ND2	1:A:643:ASP:H	1.70	0.88
1:A:474:ILE:O	1:A:478:THR:HB	1.74	0.88
1:A:395:ASP:HA	1:A:595:HIS:CD2	2.10	0.86
1:A:478:THR:HG22	1:A:480:SER:H	1.41	0.84
1:A:625:CYS:HA	1:A:629:PHE:O	1.77	0.83
1:A:430:THR:HB	1:A:594:ASN:ND2	1.97	0.80
1:A:660:TYR:O	5:A:3001:NAG:H62	1.83	0.79
1:A:593:PRO:HB3	5:A:3001:NAG:H5	1.63	0.79
1:A:559:ASP:HA	1:A:562:LYS:HD3	1.65	0.77
10:A:3154:HOH:O	2:B:1:NAG:H4	1.88	0.74
1:A:635:GLU:O	1:A:636:THR:HG22	1.88	0.73
1:A:367:GLN:HB3	10:A:3107:HOH:O	1.89	0.72
1:A:430:THR:HB	1:A:594:ASN:HD22	1.54	0.71
1:A:473:LEU:O	1:A:477:GLN:HG3	1.90	0.71
1:A:416:LYS:NZ	1:A:416:LYS:HB3	2.11	0.66
1:A:577:THR:HG21	1:A:579:LYS:HZ3	1.62	0.64
1:A:662:GLY:O	1:A:666:VAL:HG23	1.98	0.64
1:A:424:ASP:HB2	10:A:3117:HOH:O	1.96	0.64
1:A:603:ARG:NH2	1:A:606:HIS:HD1	1.96	0.62
1:A:471:MET:CE	1:A:474:ILE:HD12	2.28	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:THR:HG21	1:A:592:ALA:CB	2.31	0.61
1:A:478:THR:CG2	1:A:480:SER:H	2.14	0.60
1:A:684:CYS:O	1:A:685:ALA:CB	2.49	0.60
2:B:1:NAG:H61	2:B:2:NAG:HN2	1.65	0.60
1:A:356:LYS:NZ	1:A:356:LYS:HB2	2.17	0.60
1:A:359:GLN:HG2	10:A:3092:HOH:O	2.01	0.60
1:A:464:THR:HG21	1:A:592:ALA:HB1	1.83	0.60
1:A:585:GLN:NE2	4:D:1:NAG:H81	2.16	0.59
1:A:683:ALA:HA	10:A:3118:HOH:O	2.01	0.58
1:A:532:CYS:O	1:A:537:VAL:HB	2.03	0.58
1:A:585:GLN:HE21	4:D:1:NAG:H81	1.68	0.58
1:A:460:ALA:HB3	1:A:463:ARG:HD3	1.86	0.56
1:A:556:SER:C	1:A:558:ALA:H	2.14	0.56
1:A:585:GLN:HG2	10:A:3051:HOH:O	2.05	0.55
1:A:410:VAL:HG12	1:A:411:LEU:HG	1.89	0.55
1:A:620:LYS:C	1:A:621:ASN:HD22	2.14	0.55
1:A:625:CYS:C	1:A:630:CYS:SG	2.88	0.55
1:A:415:ARG:HG2	1:A:415:ARG:HH11	1.70	0.55
1:A:561:ALA:HA	1:A:564:LEU:HG	1.89	0.55
1:A:653:GLY:O	1:A:654:ARG:C	2.49	0.55
1:A:577:THR:CG2	1:A:578:ARG:N	2.69	0.54
1:A:553:ASN:HD21	1:A:565:LYS:HE2	1.72	0.54
1:A:684:CYS:O	1:A:685:ALA:HB2	2.08	0.54
1:A:638:ASN:HD22	1:A:643:ASP:N	1.97	0.54
1:A:471:MET:HE2	1:A:474:ILE:HD12	1.89	0.53
1:A:634:SER:O	1:A:635:GLU:HG3	2.09	0.53
1:A:637:LYS:HG2	10:A:3136:HOH:O	2.09	0.53
1:A:471:MET:HE1	1:A:474:ILE:HD12	1.90	0.53
1:A:364:GLN:OE1	1:A:628:LYS:HE2	2.07	0.53
1:A:682:GLU:O	1:A:683:ALA:CB	2.57	0.53
1:A:352:PRO:HG3	1:A:520:LYS:HD2	1.92	0.51
1:A:471:MET:HE2	1:A:471:MET:HA	1.93	0.51
1:A:552:THR:OG1	1:A:566:ARG:HG3	2.11	0.51
1:A:565:LYS:HD3	1:A:567:GLU:H	1.76	0.51
1:A:683:ALA:O	1:A:685:ALA:N	2.38	0.50
1:A:343:THR:HA	1:A:606:HIS:NE2	2.26	0.50
1:A:625:CYS:CB	1:A:626:PRO:HD3	2.41	0.50
1:A:469:ILE:N	1:A:470:PRO:HD2	2.27	0.50
1:A:416:LYS:HB3	1:A:416:LYS:HZ2	1.75	0.50
1:A:414:ASN:HD21	1:A:430:THR:HA	1.76	0.49
1:A:415:ARG:HG2	1:A:415:ARG:NH1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:583:GLU:HG3	10:A:3128:HOH:O	2.11	0.49
1:A:670:ALA:O	1:A:674:LYS:HG3	2.12	0.49
4:D:2:NAG:O3	4:D:3:BMA:C1	2.61	0.49
1:A:366:GLY:O	1:A:367:GLN:HB2	2.11	0.48
1:A:553:ASN:HD21	1:A:565:LYS:CE	2.27	0.48
1:A:489:GLN:HB3	1:A:504:LEU:HD13	1.95	0.48
1:A:459:THR:O	1:A:460:ALA:HB2	2.15	0.47
1:A:417:SER:HB3	10:A:3065:HOH:O	2.14	0.47
1:A:356:LYS:HB2	1:A:356:LYS:HZ2	1.80	0.47
4:D:2:NAG:H3	4:D:3:BMA:O5	2.14	0.47
1:A:416:LYS:NZ	10:A:3134:HOH:O	2.41	0.47
1:A:548:VAL:O	1:A:552:THR:HG23	2.15	0.47
1:A:452:LYS:O	1:A:453:ASP:HB2	2.13	0.47
1:A:625:CYS:HB3	1:A:626:PRO:HD3	1.96	0.47
1:A:419:LYS:O	1:A:420:HIS:HB2	2.16	0.46
1:A:660:TYR:O	5:A:3001:NAG:C6	2.60	0.46
1:A:577:THR:HG21	1:A:579:LYS:NZ	2.28	0.46
1:A:393:ASN:ND2	10:A:3067:HOH:O	2.49	0.45
4:D:2:NAG:C3	4:D:3:BMA:O5	2.63	0.45
1:A:478:THR:HG22	1:A:480:SER:N	2.20	0.45
1:A:470:PRO:O	1:A:474:ILE:HG13	2.17	0.45
1:A:556:SER:C	1:A:558:ALA:N	2.75	0.45
1:A:344:ARG:HD2	1:A:370:THR:HG23	1.98	0.45
1:A:498:LYS:HB2	1:A:498:LYS:HE2	1.73	0.45
1:A:529:ALA:O	1:A:532:CYS:HB3	2.18	0.44
1:A:355:GLN:O	1:A:359:GLN:HG3	2.17	0.44
1:A:478:THR:HG23	1:A:480:SER:HB3	1.99	0.44
1:A:589:LEU:O	1:A:590:ALA:HB2	2.18	0.44
1:A:514:LYS:HD2	10:A:3082:HOH:O	2.17	0.43
1:A:455:LYS:HB3	1:A:504:LEU:HD21	2.00	0.43
1:A:634:SER:O	1:A:637:LYS:HD3	2.18	0.43
1:A:511:GLY:HA2	10:A:3157:HOH:O	2.19	0.43
1:A:478:THR:CG2	1:A:480:SER:HB3	2.47	0.43
1:A:382:VAL:HG22	1:A:682:GLU:HG2	2.01	0.42
1:A:400:TYR:CZ	1:A:404:LYS:HE2	2.54	0.42
1:A:553:ASN:ND2	1:A:565:LYS:HE2	2.33	0.42
1:A:368:ASN:HD22	2:B:1:NAG:C7	2.32	0.42
1:A:428:ARG:HA	1:A:429:PRO:HD3	1.94	0.42
1:A:459:THR:OG1	1:A:466:GLY:HA3	2.19	0.42
1:A:469:ILE:HB	1:A:470:PRO:CD	2.50	0.42
1:A:402:ALA:HB1	1:A:407:LEU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:LEU:HD11	1:A:454:LYS:HG3	2.02	0.41
1:A:471:MET:O	1:A:475:VAL:HG23	2.19	0.41
1:A:556:SER:C	1:A:557:THR:HG23	2.45	0.41
1:A:343:THR:O	1:A:343:THR:HG23	2.21	0.41
1:A:440:LYS:NZ	1:A:536:ASP:OD1	2.54	0.41
1:A:464:THR:HG21	1:A:592:ALA:HB2	2.01	0.41
1:A:625:CYS:SG	1:A:626:PRO:N	2.93	0.41
1:A:631:LEU:HD22	1:A:641:PHE:CE2	2.56	0.41
1:A:665:TYR:CZ	1:A:669:ILE:HD11	2.56	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	336/345 (97%)	308 (92%)	18 (5%)	10 (3%)	3 12

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	683	ALA
1	A	684	CYS
1	A	519	SER
1	A	464	THR
1	A	460	ALA
1	A	634	SER
1	A	652	GLY
1	A	682	GLU
1	A	625	CYS
1	A	543	VAL

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	281/286 (98%)	258 (92%)	23 (8%)	10	33

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	356	LYS
1	A	395	ASP
1	A	414	ASN
1	A	416	LYS
1	A	418	SER
1	A	424	ASP
1	A	454	LYS
1	A	478	THR
1	A	480	SER
1	A	515	CYS
1	A	559	ASP
1	A	562	LYS
1	A	565	LYS
1	A	567	GLU
1	A	577	THR
1	A	583	GLU
1	A	591	VAL
1	A	615	GLN
1	A	625	CYS
1	A	631	LEU
1	A	633	LYS
1	A	636	THR
1	A	682	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	393	ASN
1	A	414	ASN

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Mol	Chain	Res	Type
1	A	585	GLN
1	A	594	ASN
1	A	613	HIS
1	A	621	ASN
1	A	638	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	$\# Z > 2$
2	NAG	B	1	2,1	14,14,15	0.68	0	17,19,21	0.88	0
2	NAG	B	2	2	14,14,15	0.59	0	17,19,21	1.08	1 (5%)
3	NAG	C	1	3,1	14,14,15	0.58	0	17,19,21	0.69	0
3	NAG	C	2	3	14,14,15	0.53	0	17,19,21	0.66	0
3	BMA	C	3	3	11,11,12	0.54	0	15,15,17	0.22	0
4	NAG	D	1	1,4	14,14,15	0.46	0	17,19,21	0.79	1 (5%)
4	NAG	D	2	4	14,14,15	0.81	0	17,19,21	0.94	1 (5%)
4	BMA	D	3	4	11,11,12	1.01	0	15,15,17	1.10	1 (6%)
4	BMA	D	4	4	11,11,12	0.62	0	15,15,17	0.46	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	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
3	NAG	C	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	4/6/23/26	0/1/1/1
3	BMA	C	3	3	-	1/2/19/22	0/1/1/1
4	NAG	D	1	1,4	-	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	-	0/2/19/22	0/1/1/1
4	BMA	D	4	4	-	0/2/19/22	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(°)	Ideal(°)
2	B	2	NAG	C2-N2-C7	-3.34	118.43	122.90
4	D	3	BMA	C2-C3-C4	2.92	116.00	110.86
4	D	1	NAG	C2-N2-C7	-2.50	119.54	122.90
4	D	2	NAG	C3-C4-C5	-2.27	106.12	110.23

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
3	C	1	NAG	C4-C5-C6-O6
3	C	3	BMA	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 8 short contacts:

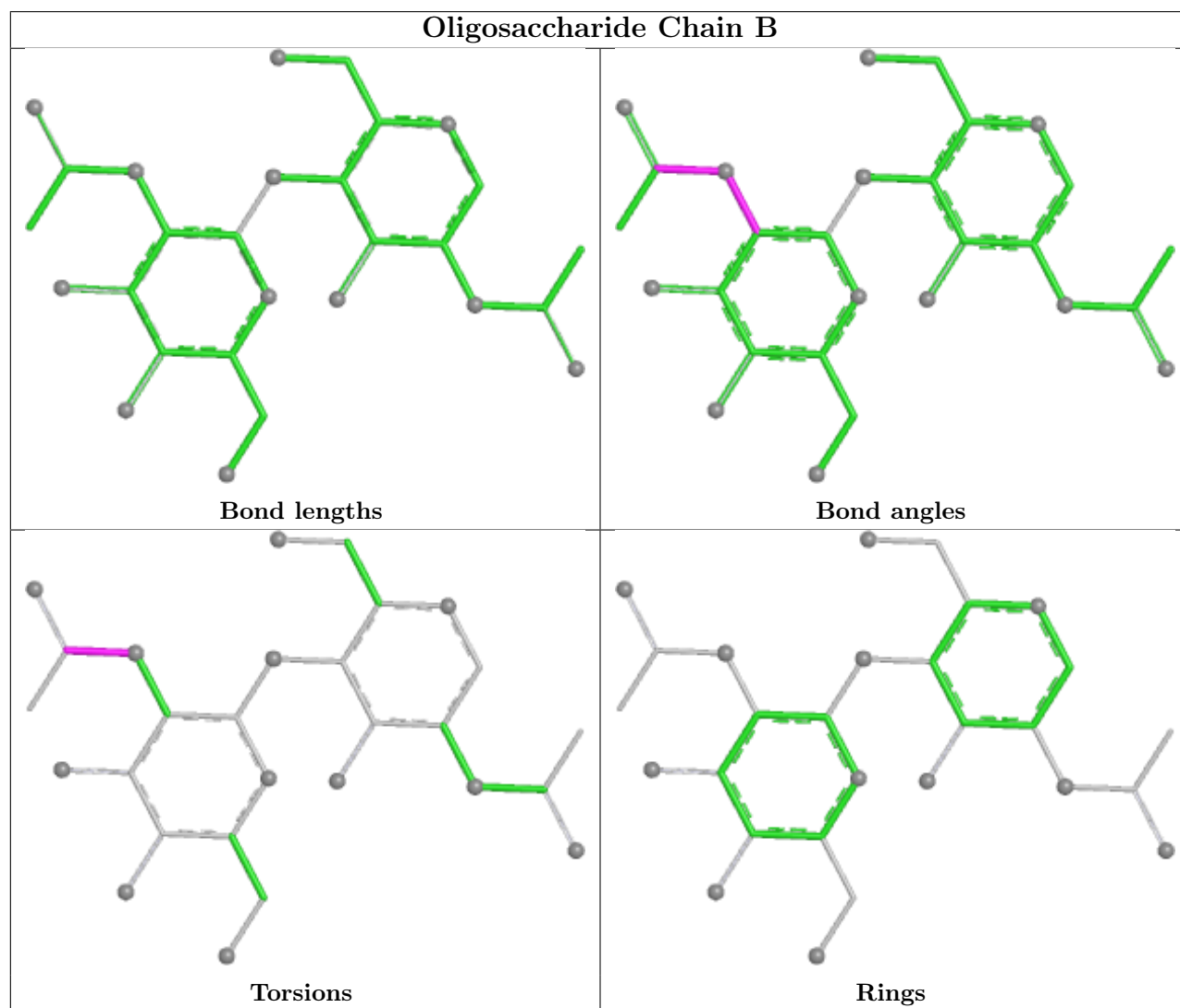
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1	NAG	2	0
2	B	2	NAG	1	0

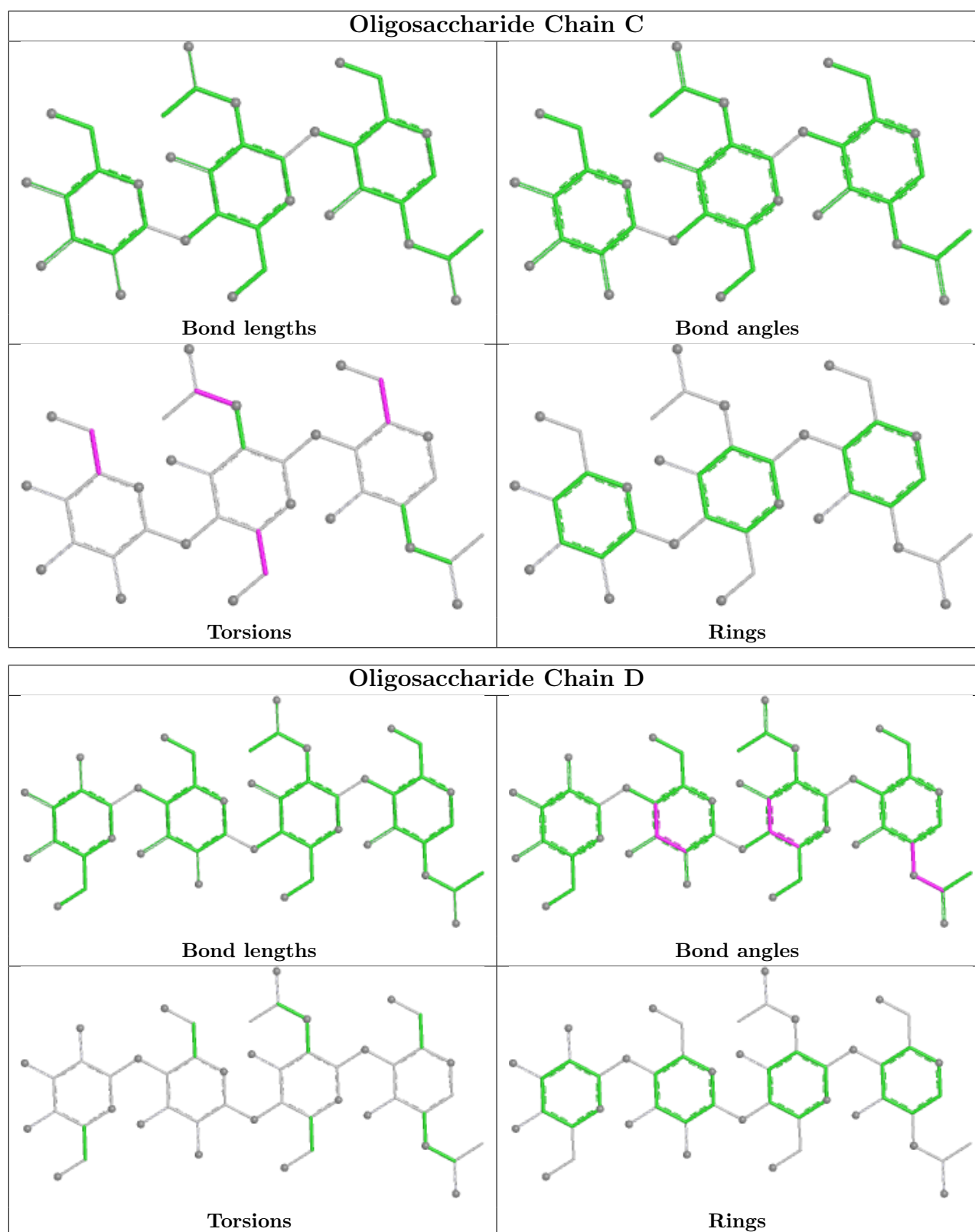
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	NAG	3	0
4	D	3	BMA	3	0
2	B	1	NAG	3	0

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 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	$\# Z > 2$
9	CO3	A	2001	6	3,3,3	0.69	0	2,3,3	0.15	0
5	NAG	A	3001	-	15,15,15	0.36	0	21,21,21	0.68	0
8	SO4	A	1001	-	4,4,4	0.20	0	6,6,6	0.23	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
5	NAG	A	3001	-	-	4/6/26/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	3001	NAG	C8-C7-N2-C2
5	A	3001	NAG	O7-C7-N2-C2
5	A	3001	NAG	C4-C5-C6-O6
5	A	3001	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	3001	NAG	3	0

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

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.