



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:43 PM UTC

PDB ID : 1IEQ / pdb_00001ieq
Title : CRYSTAL STRUCTURE OF BARLEY BETA-D-GLUCAN GLUCOHYDROLASE ISOENZYME EXO1
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Deposited on : 2001-04-11
Resolution : 2.70 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

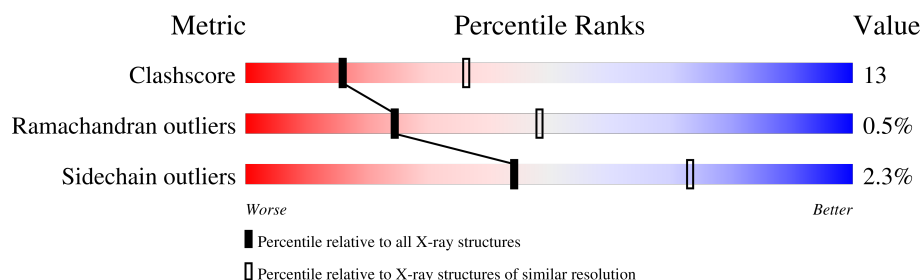
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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	605	 74% 23% .
2	B	3	 67% 33%
3	C	6	 83% 17%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4911 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.

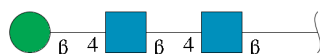
- Molecule 1 is a protein called BETA-D-GLUCAN GLUCOHYDROLASE ISOENZYME EXO1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	602	Total	C	N	O	S	0	0	0
			4566	2891	787	862	26			

There is a discrepancy between the modelled and reference sequences:

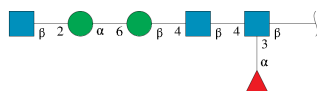
Chain	Residue	Modelled	Actual	Comment	Reference
A	320	LYS	ASN	SEE REMARK 999	GB 4566505

- Molecule 2 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.



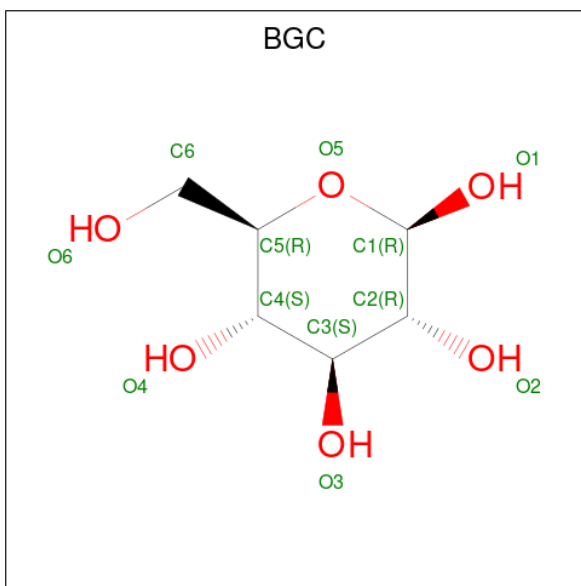
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	6	Total	C	N	O	0	0	0
			74	42	3	29			

- Molecule 4 is beta-D-glucopyranose (CCD ID: BGC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is water.

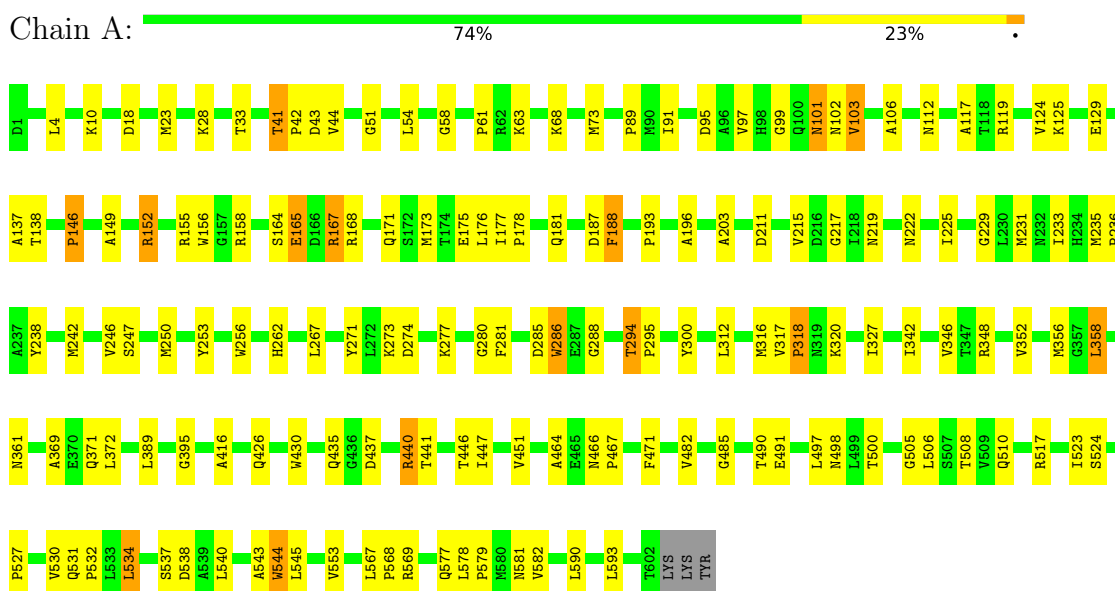
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	220	Total	O	0	0
			220	220		

3 Residue-property plots

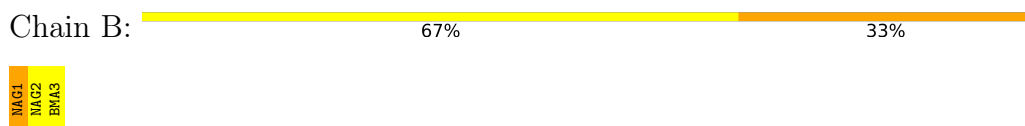
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

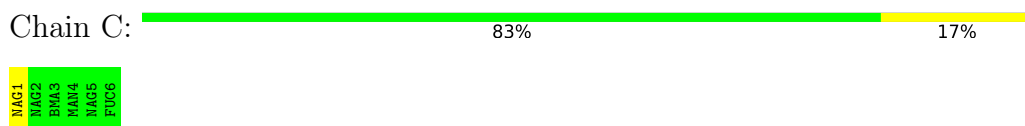
• Molecule 1: BETA-D-GLUCAN GLUCOHYDROLASE ISOENZYME EXO1



• Molecule 2: 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-(1-2)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]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 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.95Å 100.95Å 181.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.70)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.189 , 0.228	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4911	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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: NAG, BMA, BGC, FUC, 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	0.40	0/4663	0.96	20/6334 (0.3%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	545	LEU	CA-C-N	8.05	129.91	119.84
1	A	545	LEU	C-N-CA	8.05	129.91	119.84
1	A	101	ASN	N-CA-C	7.48	122.06	112.34
1	A	590	LEU	N-CA-C	-6.77	103.36	111.69
1	A	112	ASN	N-CA-C	6.73	119.47	111.33
1	A	99	GLY	N-CA-C	-6.71	105.20	112.04
1	A	233	ILE	N-CA-C	6.20	117.31	111.48
1	A	103	VAL	N-CA-C	6.05	116.88	108.89
1	A	577	GLN	N-CA-C	-5.93	105.88	113.23
1	A	233	ILE	CB-CA-C	-5.90	106.70	111.71
1	A	165	GLU	N-CA-C	-5.68	106.35	113.28
1	A	196	ALA	N-CA-C	5.55	117.01	111.07
1	A	23	MET	N-CA-C	5.55	118.49	110.28
1	A	361	ASN	CA-C-N	5.48	125.09	119.56
1	A	361	ASN	C-N-CA	5.48	125.09	119.56
1	A	537	SER	N-CA-C	5.39	118.89	110.32
1	A	274	ASP	N-CA-C	5.32	117.16	111.36
1	A	63	LYS	N-CA-C	-5.25	102.52	110.28
1	A	33	THR	N-CA-C	5.18	116.96	108.52
1	A	544	TRP	CB-CA-C	-5.06	110.76	116.63

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	4566	0	4551	122	0
2	B	39	0	34	2	0
3	C	74	0	64	0	0
4	A	12	0	12	3	0
5	A	220	0	0	7	0
All	All	4911	0	4661	123	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 13.

All (123) 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:181:GLN:HE21	1:A:203:ALA:H	1.09	0.96
1:A:181:GLN:NE2	1:A:203:ALA:H	1.79	0.80
1:A:440:ARG:HB2	1:A:440:ARG:HH11	1.47	0.79
1:A:231:MET:HE1	1:A:271:TYR:CZ	2.18	0.78
1:A:285:ASP:OD1	4:A:619:BGC:H1	1.86	0.76
1:A:181:GLN:HE22	1:A:247:SER:H	1.34	0.73
1:A:41:THR:HG22	1:A:43:ASP:H	1.53	0.72
1:A:517:ARG:HG2	5:A:817:HOH:O	1.91	0.71
1:A:286:TRP:CA	1:A:316:MET:HE2	2.22	0.70
1:A:181:GLN:HE21	1:A:203:ALA:N	1.88	0.70
1:A:464:ALA:CB	1:A:467:PRO:HG3	2.23	0.69
1:A:97:VAL:H	1:A:101:ASN:HD21	1.43	0.66
1:A:41:THR:HG22	1:A:43:ASP:N	2.11	0.66
1:A:286:TRP:HE3	1:A:316:MET:HE3	1.60	0.66
1:A:352:VAL:HG12	1:A:356:MET:CE	2.25	0.66
1:A:167:ARG:O	1:A:171:GLN:HG3	1.95	0.65
1:A:231:MET:HE1	1:A:271:TYR:CE1	2.31	0.65
1:A:437:ASP:HB3	1:A:441:THR:HG21	1.77	0.65
1:A:91:ILE:HD12	1:A:356:MET:HE1	1.78	0.64
1:A:490:THR:HG22	1:A:491:GLU:HG3	1.80	0.63
1:A:175:GLU:O	1:A:178:PRO:HD2	2.00	0.62
1:A:273:LYS:O	1:A:277:LYS:HA	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:ARG:HD3	5:A:871:HOH:O	1.99	0.62
1:A:156:TRP:HE1	1:A:219:ASN:HD22	1.47	0.62
1:A:524:SER:O	1:A:544:TRP:HA	2.01	0.61
1:A:4:LEU:HD21	1:A:10:LYS:HE2	1.82	0.61
1:A:146:PRO:HB3	1:A:176:LEU:HD23	1.83	0.60
1:A:177:ILE:HB	1:A:178:PRO:HD3	1.83	0.60
1:A:464:ALA:HB3	1:A:467:PRO:HG3	1.83	0.60
1:A:4:LEU:HB3	1:A:18:ASP:CG	2.27	0.60
1:A:146:PRO:HB3	1:A:176:LEU:CD2	2.31	0.60
1:A:124:VAL:HG21	1:A:173:MET:SD	2.42	0.60
1:A:58:GLY:H	1:A:102:ASN:ND2	2.00	0.59
1:A:155:ARG:HD2	1:A:497:LEU:HD23	1.85	0.59
1:A:222:ASN:HB2	2:B:1:NAG:H82	1.85	0.58
1:A:286:TRP:HA	1:A:316:MET:HE2	1.85	0.58
1:A:530:VAL:O	1:A:530:VAL:HG22	2.04	0.58
1:A:534:LEU:HD13	1:A:540:LEU:HD13	1.86	0.57
1:A:156:TRP:HE1	1:A:219:ASN:ND2	2.03	0.57
1:A:464:ALA:HB1	1:A:467:PRO:HG3	1.86	0.57
1:A:238:TYR:O	1:A:242:MET:HG2	2.06	0.56
1:A:352:VAL:HG12	1:A:356:MET:HE2	1.87	0.56
1:A:582:VAL:HG21	1:A:593:LEU:HD13	1.85	0.56
1:A:41:THR:HG23	1:A:42:PRO:HD2	1.87	0.56
1:A:578:LEU:HA	1:A:579:PRO:C	2.31	0.56
1:A:58:GLY:H	1:A:102:ASN:HD21	1.54	0.55
1:A:181:GLN:HE22	1:A:247:SER:N	2.04	0.54
1:A:320:LYS:HB3	5:A:830:HOH:O	2.07	0.54
1:A:175:GLU:C	1:A:178:PRO:HD2	2.33	0.54
1:A:286:TRP:CB	1:A:316:MET:HE2	2.39	0.53
1:A:91:ILE:CD1	1:A:356:MET:HE1	2.37	0.53
1:A:286:TRP:HB2	1:A:316:MET:HE2	1.90	0.53
1:A:125:LYS:O	1:A:129:GLU:HG3	2.09	0.53
1:A:4:LEU:CD2	1:A:10:LYS:HE2	2.39	0.52
1:A:225:ILE:HD11	1:A:229:GLY:HA3	1.93	0.51
1:A:167:ARG:HD3	1:A:168:ARG:N	2.26	0.50
1:A:256:TRP:CE3	1:A:267:LEU:HD11	2.47	0.50
1:A:262:HIS:HE1	1:A:285:ASP:H	1.58	0.50
1:A:103:VAL:HG21	1:A:138:THR:HG21	1.93	0.49
1:A:117:ALA:CA	1:A:568:PRO:HG3	2.42	0.49
1:A:342:ILE:O	1:A:346:VAL:HG23	2.12	0.49
2:B:2:NAG:H4	2:B:3:BMA:O2	2.12	0.49
1:A:286:TRP:HB2	1:A:316:MET:CE	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:LEU:C	1:A:4:LEU:HD13	2.38	0.49
1:A:193:PRO:HG3	1:A:280:GLY:HA2	1.94	0.49
1:A:294:THR:HA	1:A:295:PRO:C	2.37	0.49
1:A:165:GLU:HB2	1:A:581:ASN:HD22	1.77	0.49
1:A:466:ASN:OD1	1:A:508:THR:OG1	2.28	0.49
1:A:517:ARG:HA	1:A:538:ASP:OD2	2.12	0.49
1:A:579:PRO:HG3	5:A:911:HOH:O	2.12	0.49
1:A:51:GLY:HA2	5:A:721:HOH:O	2.12	0.49
1:A:177:ILE:HD13	1:A:246:VAL:HB	1.95	0.49
1:A:300:TYR:HD2	1:A:327:ILE:HD12	1.78	0.48
1:A:531:GLN:HB2	1:A:532:PRO:HD3	1.95	0.48
1:A:193:PRO:HG3	1:A:280:GLY:CA	2.43	0.48
1:A:593:LEU:C	1:A:593:LEU:HD23	2.39	0.48
1:A:149:ALA:HB2	1:A:211:ASP:OD2	2.13	0.48
1:A:137:ALA:HB2	1:A:371:GLN:HB2	1.95	0.47
1:A:281:PHE:CD2	1:A:352:VAL:HG21	2.50	0.47
1:A:95:ASP:OD2	4:A:619:BGC:H6C1	2.15	0.47
1:A:506:LEU:O	1:A:510:GLN:HG3	2.15	0.47
1:A:156:TRP:CZ2	1:A:158:ARG:HB2	2.51	0.46
1:A:312:LEU:HD12	1:A:312:LEU:N	2.30	0.46
1:A:250:MET:HE2	5:A:869:HOH:O	2.16	0.45
1:A:262:HIS:CE1	1:A:288:GLY:HA3	2.51	0.45
1:A:61:PRO:HG3	1:A:73:MET:SD	2.57	0.45
1:A:235:MET:N	1:A:236:PRO:CD	2.80	0.45
1:A:41:THR:HB	1:A:44:VAL:HG23	1.99	0.44
1:A:286:TRP:CE3	1:A:316:MET:HE3	2.48	0.43
1:A:467:PRO:HB3	1:A:471:PHE:CD1	2.52	0.43
1:A:317:VAL:HB	1:A:318:PRO:HA	2.00	0.43
1:A:440:ARG:HH11	1:A:440:ARG:CB	2.24	0.43
1:A:89:PRO:HB2	1:A:358:LEU:HD13	1.99	0.43
1:A:316:MET:HE1	4:A:619:BGC:H6C2	2.01	0.43
1:A:101:ASN:HB2	1:A:430:TRP:O	2.19	0.43
1:A:389:LEU:HD11	1:A:553:VAL:HA	2.01	0.43
1:A:485:GLY:HA3	1:A:523:ILE:O	2.19	0.43
1:A:348:ARG:O	1:A:352:VAL:HG23	2.18	0.43
1:A:523:ILE:HD13	1:A:543:ALA:HB3	1.99	0.43
1:A:164:SER:OG	1:A:165:GLU:N	2.52	0.42
1:A:187:ASP:OD1	1:A:188:PHE:N	2.52	0.42
1:A:447:ILE:O	1:A:451:VAL:HG23	2.19	0.42
1:A:527:PRO:HD3	1:A:569:ARG:HD3	2.01	0.42
1:A:211:ASP:N	1:A:211:ASP:OD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:TRP:HE3	1:A:316:MET:CE	2.30	0.42
1:A:320:LYS:HE3	5:A:826:HOH:O	2.20	0.42
1:A:119:ARG:HH11	1:A:119:ARG:HG2	1.85	0.42
1:A:426:GLN:OE1	1:A:446:THR:HA	2.20	0.42
1:A:91:ILE:HD12	1:A:356:MET:CE	2.48	0.41
1:A:106:ALA:HB2	1:A:372:LEU:HD11	2.02	0.41
1:A:435:GLN:NE2	1:A:490:THR:HB	2.35	0.41
1:A:498:ASN:O	1:A:500:THR:HG23	2.21	0.41
1:A:28:LYS:HB3	1:A:346:VAL:HG21	2.01	0.41
1:A:395:GLY:N	1:A:538:ASP:O	2.51	0.41
1:A:156:TRP:HA	1:A:217:GLY:O	2.21	0.41
1:A:253:TYR:OH	1:A:286:TRP:HB3	2.21	0.41
1:A:125:LYS:HB2	1:A:175:GLU:HB3	2.01	0.41
1:A:146:PRO:HB3	1:A:176:LEU:HD22	2.02	0.41
1:A:416:ALA:O	1:A:482:VAL:HA	2.21	0.41
1:A:567:LEU:HA	1:A:568:PRO:HD3	1.74	0.40
1:A:68:LYS:HE3	1:A:369:ALA:HB2	2.02	0.40
1:A:117:ALA:HA	1:A:568:PRO:HG3	2.01	0.40
1:A:155:ARG:HD2	1:A:497:LEU:CD2	2.51	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	600/605 (99%)	573 (96%)	24 (4%)	3 (0%)	24 48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	188	PHE
1	A	505	GLY

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Mol	Chain	Res	Type
1	A	286	TRP

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	485/488 (99%)	474 (98%)	11 (2%)	44 73

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	54	LEU
1	A	146	PRO
1	A	152	ARG
1	A	167	ARG
1	A	215	VAL
1	A	294	THR
1	A	318	PRO
1	A	358	LEU
1	A	440	ARG
1	A	534	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	102	ASN
1	A	171	GLN
1	A	181	GLN
1	A	199	ASN
1	A	219	ASN
1	A	262	HIS
1	A	319	ASN
1	A	323	GLN

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Mol	Chain	Res	Type
1	A	331	HIS
1	A	377	HIS
1	A	581	ASN
1	A	600	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	1,2	14,14,15	0.67	0	17,19,21	0.93	1 (5%)
2	NAG	B	2	2	14,14,15	0.66	0	17,19,21	0.94	0
2	BMA	B	3	2	11,11,12	0.76	0	15,15,17	0.55	0
3	NAG	C	1	1,3	14,14,15	0.60	0	17,19,21	0.92	1 (5%)
3	NAG	C	2	3	14,14,15	0.69	0	17,19,21	0.66	0
3	BMA	C	3	3	11,11,12	0.66	0	15,15,17	0.45	0
3	MAN	C	4	3	11,11,12	0.52	0	15,15,17	0.60	0
3	NAG	C	5	3	14,14,15	0.64	0	17,19,21	0.73	0
3	FUC	C	6	3	10,10,11	0.58	0	14,14,16	0.40	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	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	4/6/23/26	0/1/1/1
2	BMA	B	3	2	-	2/2/19/22	0/1/1/1
3	NAG	C	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	C	2	3	-	3/6/23/26	0/1/1/1
3	BMA	C	3	3	-	1/2/19/22	0/1/1/1
3	MAN	C	4	3	-	2/2/19/22	0/1/1/1
3	NAG	C	5	3	-	2/6/23/26	0/1/1/1
3	FUC	C	6	3	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C2-N2-C7	-2.52	119.52	122.90
2	B	1	NAG	C2-N2-C7	-2.45	119.62	122.90

There are no chirality outliers.

All (18) torsion outliers are listed below:

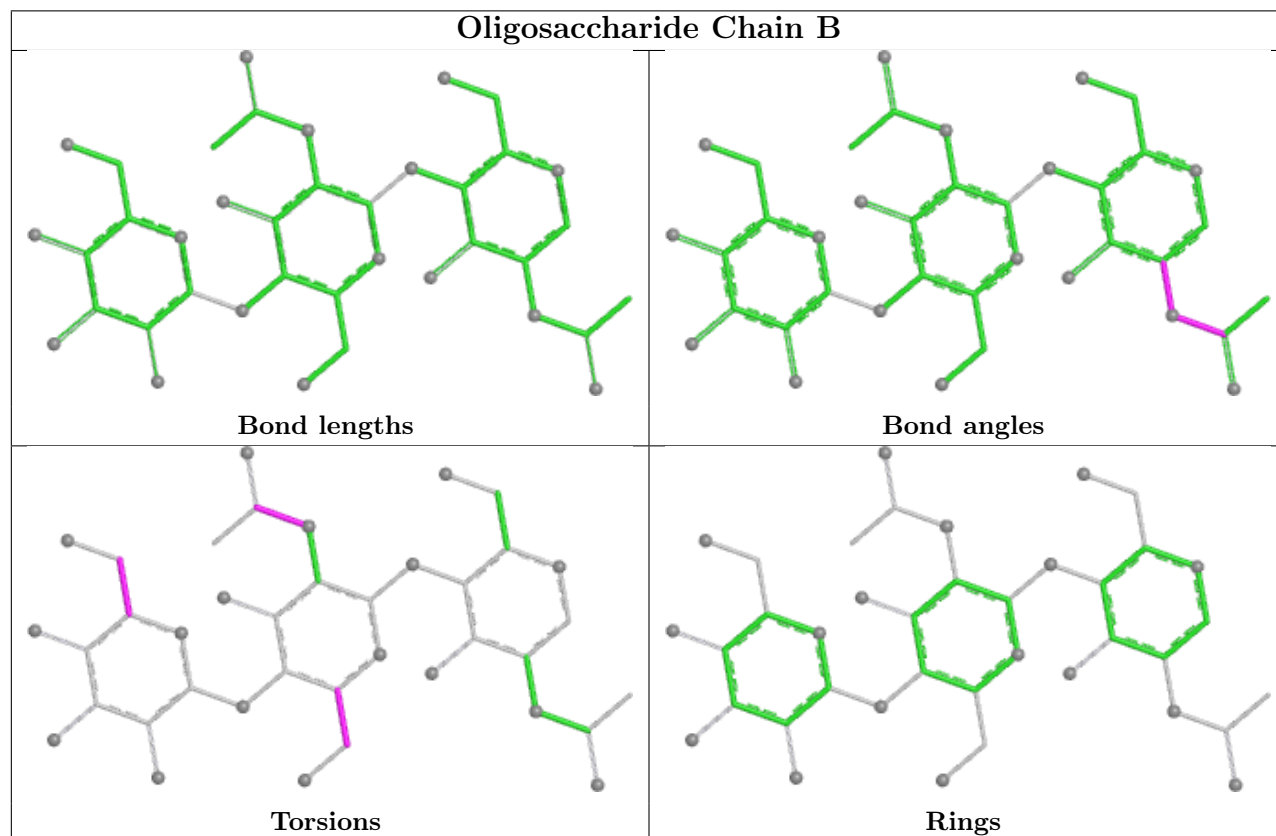
Mol	Chain	Res	Type	Atoms
3	C	5	NAG	C8-C7-N2-C2
3	C	5	NAG	O7-C7-N2-C2
2	B	3	BMA	C4-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
2	B	3	BMA	O5-C5-C6-O6
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
3	C	1	NAG	C4-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O5-C5-C6-O6
2	B	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
3	C	4	MAN	C4-C5-C6-O6
2	B	2	NAG	O7-C7-N2-C2
3	C	4	MAN	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	3	BMA	O5-C5-C6-O6

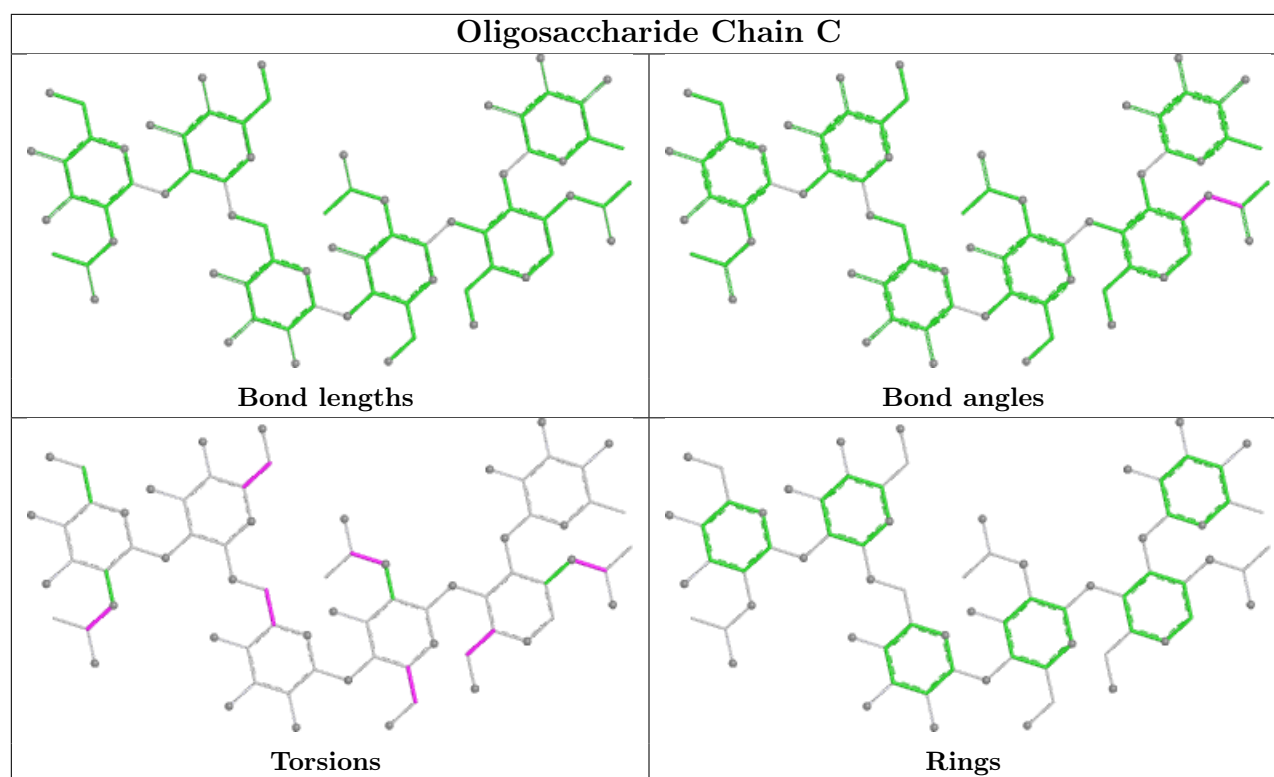
There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	1	0
2	B	2	NAG	1	0
2	B	3	BMA	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](#)

1 ligand 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	$\# Z > 2$
4	BGC	A	619	-	12,12,12	0.47	0	17,17,17	0.35	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
4	BGC	A	619	-	-	2/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	619	BGC	O5-C5-C6-O6
4	A	619	BGC	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	619	BGC	3	0

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.