



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 09:34 AM UTC

PDB ID : 1UR4 / pdb_00001ur4
Title : The structure of endo-beta-1,4-galactanase from *Bacillus licheniformis* in complex with two oligosaccharide products.
Authors : Ryttersgaard, C.; Le Nours, J.; Lo Leggio, L.; Jorgensen, C.T.; Christensen, L.L.H.; Bjornvad, M.; Larsen, S.
Deposited on : 2003-10-24
Resolution : 2.20 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

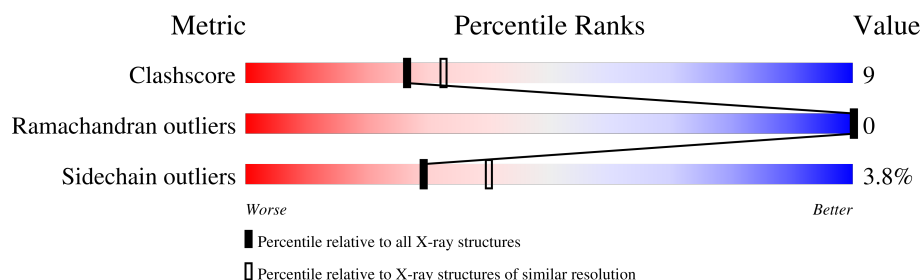
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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	399	
1	B	399	
2	C	2	
2	D	2	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6285 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 GALACTANASE.

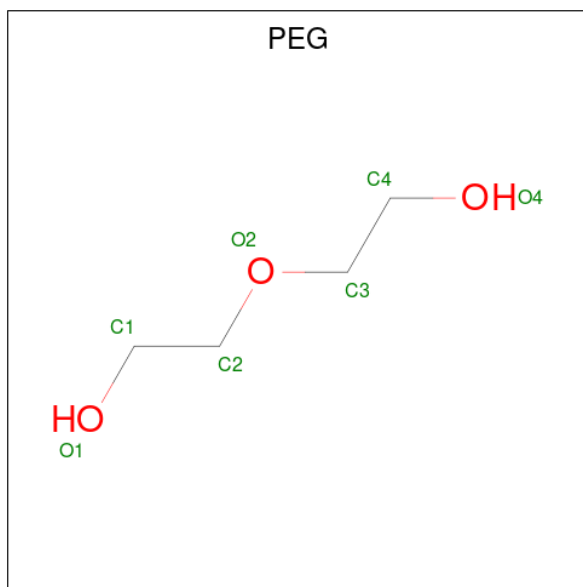
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	0	1
			2998	1905	510	578	5			
1	B	388	Total	C	N	O	S	0	0	1
			3009	1914	511	579	5			

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-4)-beta-D-galactopyranose.



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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	125	Total	O	0	0
			125	125		
6	B	81	Total	O	0	0
			81	81		

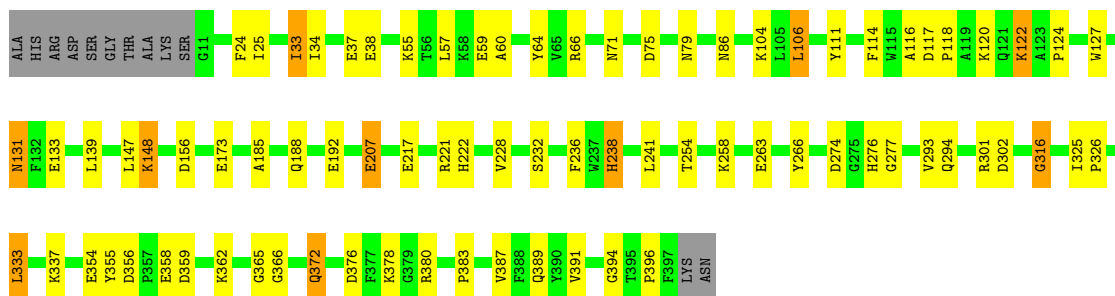
3 Residue-property plots

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.

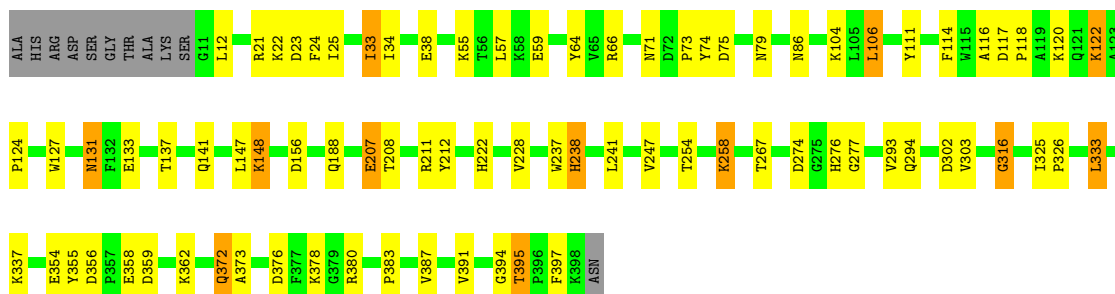
• Molecule 1: GALACTANASE

Chain A: 



• Molecule 1: GALACTANASE

Chain B: 



• Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-galactopyranose

Chain C: 



• Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-galactopyranose

Chain D: 



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	50.33Å 79.52Å 104.89Å 90.00° 100.52° 90.00°	Depositor
Resolution (Å)	19.97 – 2.20	Depositor
% Data completeness (in resolution range)	89.1 (19.97-2.20)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.205 , 0.236	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6285	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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: CA, PEG, PGE, 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	0.53	5/3077 (0.2%)	0.92	10/4183 (0.2%)
1	B	0.55	6/3089 (0.2%)	0.95	12/4199 (0.3%)
All	All	0.54	11/6166 (0.2%)	0.94	22/8382 (0.3%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	222	HIS	CE1-NE2	10.16	1.42	1.32
1	A	222	HIS	CE1-NE2	7.43	1.40	1.32
1	A	372	GLN	CD-OE1	-7.00	1.10	1.23
1	B	372	GLN	CG-CD	6.54	1.68	1.52
1	B	222	HIS	CG-ND1	6.29	1.45	1.38
1	B	372	GLN	CD-OE1	-6.10	1.11	1.23
1	A	372	GLN	CG-CD	5.84	1.66	1.52
1	A	222	HIS	CG-ND1	5.81	1.44	1.38
1	A	396	PRO	C-N	-5.81	1.25	1.33
1	B	397	PHE	C-N	-5.75	1.25	1.33
1	B	222	HIS	CG-CD2	5.51	1.42	1.35

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	238	HIS	N-CA-C	8.76	122.26	112.97
1	B	395	THR	CA-C-N	8.65	128.60	120.03
1	B	395	THR	C-N-CA	8.65	128.60	120.03
1	A	238	HIS	N-CA-C	8.48	122.43	112.93
1	B	394	GLY	N-CA-C	-7.53	103.22	112.33
1	B	258	LYS	N-CA-C	-7.42	100.53	110.55
1	A	258	LYS	N-CA-C	-7.38	100.58	110.55
1	B	33	ILE	N-CA-C	6.63	117.32	110.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	ILE	N-CA-C	6.61	117.31	110.36
1	A	316	GLY	N-CA-C	6.18	119.78	110.75
1	A	394	GLY	N-CA-C	-6.03	105.04	112.33
1	A	131	ASN	N-CA-C	-5.88	102.76	110.53
1	B	316	GLY	N-CA-C	5.82	119.25	110.75
1	B	131	ASN	N-CA-C	-5.62	103.11	110.53
1	A	86	ASN	N-CA-C	5.35	117.19	108.63
1	B	222	HIS	ND1-CG-CD2	5.31	111.41	106.10
1	B	86	ASN	N-CA-C	5.30	117.11	108.63
1	B	254	THR	N-CA-C	5.25	117.08	111.36
1	A	232	SER	N-CA-C	-5.25	102.76	110.52
1	B	228	VAL	N-CA-C	5.16	115.34	108.11
1	A	228	VAL	N-CA-C	5.12	115.28	108.11
1	A	254	THR	N-CA-C	5.06	116.88	111.36

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	2998	0	2860	57	0
1	B	3009	0	2869	54	0
2	C	23	0	21	1	0
2	D	23	0	21	0	0
3	A	7	0	10	1	0
3	B	7	0	10	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	10	0	14	3	0
6	A	125	0	0	2	0
6	B	81	0	0	3	0
All	All	6285	0	5805	111	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 (111) 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:274:ASP:HB3	1:A:326:PRO:HB3	1.55	0.87
1:B:21:ARG:HG2	6:B:2064:HOH:O	1.73	0.86
1:B:293:VAL:HG11	1:B:383:PRO:HG2	1.58	0.85
1:A:293:VAL:HG11	1:A:383:PRO:HG2	1.58	0.83
1:B:274:ASP:HB3	1:B:326:PRO:HB3	1.59	0.83
1:B:66:ARG:HG3	1:B:106:LEU:HD13	1.61	0.83
1:A:276:HIS:HE1	2:C:2:GAL:O6	1.71	0.73
1:A:66:ARG:HG3	1:A:106:LEU:HD13	1.72	0.71
1:A:117:ASP:HB2	1:A:118:PRO:CD	2.22	0.70
1:B:12:LEU:HD22	1:B:383:PRO:O	1.91	0.70
1:B:117:ASP:HB2	1:B:118:PRO:CD	2.22	0.70
1:B:258:LYS:HE2	5:B:1399:PGE:H52	1.73	0.70
1:A:185:ALA:HA	3:A:1397:PEG:H21	1.72	0.69
1:B:325:ILE:HB	1:B:326:PRO:HD2	1.76	0.68
1:B:358:GLU:O	1:B:362:LYS:HE2	1.94	0.68
1:A:33:ILE:HG23	1:A:34:ILE:HD12	1.77	0.67
1:A:333:LEU:HD22	1:A:337:LYS:HE3	1.77	0.67
1:B:137:THR:HG22	1:B:141:GLN:NE2	2.10	0.67
1:A:358:GLU:O	1:A:362:LYS:HE2	1.94	0.66
1:A:325:ILE:HB	1:A:326:PRO:HD2	1.76	0.66
1:B:137:THR:HG22	1:B:141:GLN:HE21	1.60	0.66
1:B:33:ILE:HG23	1:B:34:ILE:HD12	1.78	0.65
1:B:333:LEU:HD22	1:B:337:LYS:HE3	1.79	0.64
1:B:66:ARG:CG	1:B:106:LEU:HD13	2.29	0.63
1:B:55:LYS:O	1:B:59:GLU:HG3	1.98	0.63
1:B:25:ILE:HB	1:B:316:GLY:HA3	1.79	0.63
1:A:55:LYS:O	1:A:59:GLU:HG3	2.00	0.61
1:A:131:ASN:ND2	1:A:133:GLU:OE1	2.34	0.61
1:B:376:ASP:OD2	1:B:380:ARG:HB2	2.04	0.58
1:A:188:GLN:NE2	1:A:192:GLU:OE2	2.30	0.57
1:B:207:GLU:HG2	1:B:238:HIS:HA	1.86	0.57
1:A:207:GLU:HG2	1:A:238:HIS:HA	1.87	0.57
1:A:376:ASP:OD2	1:A:380:ARG:HB2	2.05	0.57
1:B:22:LYS:HG3	1:B:23:ASP:N	2.20	0.57
1:B:212:TYR:HB2	1:B:247:VAL:CG2	2.35	0.56
1:A:66:ARG:NH2	1:A:263:GLU:OE2	2.38	0.56
1:A:333:LEU:CD2	1:A:337:LYS:HE3	2.35	0.56
1:B:303:VAL:HG23	6:B:2062:HOH:O	2.05	0.55
1:B:131:ASN:HD21	1:B:133:GLU:HB3	1.72	0.55
1:B:333:LEU:CD2	1:B:337:LYS:HE3	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:ARG:CG	1:A:106:LEU:HD13	2.36	0.55
1:A:117:ASP:HB2	1:A:118:PRO:HD2	1.88	0.54
1:B:75:ASP:OD2	1:B:79:ASN:HB2	2.08	0.54
1:A:173:GLU:HG3	6:A:2052:HOH:O	2.07	0.54
1:B:117:ASP:HB2	1:B:118:PRO:HD2	1.89	0.54
1:B:378:LYS:HE2	1:B:378:LYS:HA	1.90	0.54
1:A:378:LYS:HA	1:A:378:LYS:HE2	1.90	0.52
1:B:66:ARG:CD	1:B:106:LEU:HD13	2.40	0.52
1:A:276:HIS:CD2	1:A:366:GLY:H	2.26	0.52
1:A:34:ILE:O	1:A:38:GLU:HG3	2.09	0.52
1:A:207:GLU:CG	1:A:238:HIS:HA	2.40	0.51
1:B:207:GLU:CG	1:B:238:HIS:HA	2.40	0.51
1:B:258:LYS:HE2	5:B:1399:PGE:H4	1.92	0.51
1:B:116:ALA:HA	1:B:120:LYS:O	2.11	0.51
1:A:266:TYR:C	1:A:372:GLN:HE21	2.20	0.50
1:A:116:ALA:HA	1:A:120:LYS:O	2.11	0.49
1:A:266:TYR:CA	1:A:372:GLN:HE21	2.25	0.49
1:A:217:GLU:O	1:A:221:ARG:HG3	2.12	0.49
1:B:267:THR:HA	1:B:372:GLN:HG2	1.96	0.48
1:A:274:ASP:HB3	1:A:326:PRO:CB	2.35	0.48
1:A:60:ALA:O	1:A:389:GLN:HG3	2.13	0.48
1:B:373:ALA:HB2	6:B:2069:HOH:O	2.13	0.48
1:A:66:ARG:CD	1:A:106:LEU:HD13	2.44	0.48
1:A:75:ASP:OD2	1:A:79:ASN:HB2	2.13	0.48
1:B:137:THR:O	1:B:141:GLN:HG3	2.15	0.47
1:B:241:LEU:CD1	1:B:302:ASP:HB3	2.45	0.47
1:A:25:ILE:HB	1:A:316:GLY:HA3	1.95	0.47
1:B:104:LYS:HD3	1:B:156:ASP:OD2	2.14	0.47
1:B:34:ILE:O	1:B:38:GLU:HG3	2.15	0.47
1:A:356:ASP:OD2	1:A:359:ASP:HB3	2.16	0.46
1:B:71:ASN:HD21	1:B:111:TYR:HA	1.80	0.46
1:B:211:ARG:HG2	1:B:212:TYR:HD1	1.81	0.46
1:A:104:LYS:HD3	1:A:156:ASP:OD2	2.16	0.46
1:A:354:GLU:HG3	1:A:355:TYR:N	2.32	0.45
1:B:354:GLU:HG3	1:B:355:TYR:N	2.32	0.45
1:B:356:ASP:OD2	1:B:359:ASP:HB3	2.16	0.45
1:B:33:ILE:HG23	1:B:34:ILE:CD1	2.47	0.45
1:A:185:ALA:O	1:A:188:GLN:HB3	2.16	0.45
1:A:71:ASN:HD21	1:A:111:TYR:HA	1.82	0.45
1:A:301:ARG:C	1:A:301:ARG:HD3	2.42	0.45
1:A:241:LEU:CD1	1:A:302:ASP:HB3	2.48	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:VAL:O	1:B:391:VAL:HG13	2.18	0.44
1:A:124:PRO:HD2	1:A:127:TRP:CE3	2.53	0.44
1:A:387:VAL:O	1:A:391:VAL:HG13	2.18	0.43
1:B:124:PRO:HD2	1:B:127:TRP:CE3	2.53	0.43
1:A:24:PHE:CZ	1:A:316:GLY:HA2	2.54	0.43
1:A:131:ASN:HD21	1:A:133:GLU:HB2	1.83	0.43
1:B:208:THR:OG1	1:B:211:ARG:NH1	2.52	0.43
1:B:258:LYS:NZ	5:B:1399:PGE:H22	2.34	0.43
1:A:33:ILE:HG23	1:A:34:ILE:CD1	2.47	0.42
1:B:274:ASP:HB3	1:B:326:PRO:CB	2.39	0.42
1:B:117:ASP:CB	1:B:118:PRO:CD	2.94	0.42
1:A:236:PHE:CZ	1:A:372:GLN:NE2	2.87	0.42
1:B:24:PHE:CZ	1:B:316:GLY:HA2	2.55	0.42
1:A:236:PHE:HZ	1:A:372:GLN:NE2	2.17	0.42
1:A:276:HIS:O	1:A:277:GLY:C	2.63	0.41
1:B:66:ARG:HD2	1:B:106:LEU:HD13	2.02	0.41
1:B:122:LYS:HG2	1:B:355:TYR:CZ	2.55	0.41
1:A:33:ILE:HG23	1:A:34:ILE:N	2.35	0.41
1:A:148:LYS:NZ	1:A:148:LYS:HB3	2.35	0.41
1:B:73:PRO:HG2	1:B:74:TYR:CE1	2.55	0.41
1:A:33:ILE:O	1:A:37:GLU:HG3	2.21	0.41
1:B:33:ILE:HG23	1:B:34:ILE:N	2.35	0.41
1:A:276:HIS:CD2	1:A:365:GLY:HA3	2.56	0.41
1:A:358:GLU:HB2	6:A:2117:HOH:O	2.20	0.41
1:A:66:ARG:HD2	1:A:106:LEU:HD13	2.03	0.41
1:A:117:ASP:CB	1:A:118:PRO:CD	2.95	0.41
1:A:122:LYS:HG2	1:A:355:TYR:CZ	2.56	0.40
1:A:139:LEU:C	1:A:139:LEU:HD23	2.46	0.40
1:B:148:LYS:NZ	1:B:148:LYS:HB3	2.37	0.40
1:B:276:HIS:O	1:B:277:GLY:C	2.64	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	385/399 (96%)	369 (96%)	16 (4%)	0	100	100
1	B	386/399 (97%)	366 (95%)	20 (5%)	0	100	100
All	All	771/798 (97%)	735 (95%)	36 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	305/315 (97%)	295 (97%)	10 (3%)	33	45
1	B	306/315 (97%)	293 (96%)	13 (4%)	26	36
All	All	611/630 (97%)	588 (96%)	23 (4%)	29	40

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

Mol	Chain	Res	Type
1	A	57	LEU
1	A	64	TYR
1	A	106	LEU
1	A	114	PHE
1	A	122	LYS
1	A	147	LEU
1	A	148	LYS
1	A	207	GLU
1	A	294	GLN
1	A	333	LEU
1	B	57	LEU
1	B	64	TYR
1	B	106	LEU
1	B	114	PHE
1	B	122	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	147	LEU
1	B	148	LYS
1	B	188	GLN
1	B	207	GLU
1	B	237	TRP
1	B	294	GLN
1	B	333	LEU
1	B	395	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	86	ASN
1	A	129	ASN
1	A	164	ASN
1	A	181	GLN
1	A	276	HIS
1	A	288	ASN
1	A	289	ASN
1	A	372	GLN
1	B	71	ASN
1	B	86	ASN
1	B	129	ASN
1	B	141	GLN
1	B	164	ASN
1	B	181	GLN
1	B	298	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 ⓘ

4 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	GAL	C	1	2	12,12,12	0.86	0	17,17,17	0.57	0
2	GAL	C	2	2	11,11,12	0.85	0	15,15,17	0.71	0
2	GAL	D	1	2	12,12,12	0.80	0	17,17,17	0.62	0
2	GAL	D	2	2	11,11,12	0.85	0	15,15,17	0.80	1 (6%)

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	GAL	C	1	2	-	1/2/22/22	0/1/1/1
2	GAL	C	2	2	-	1/2/19/22	0/1/1/1
2	GAL	D	1	2	-	0/2/22/22	0/1/1/1
2	GAL	D	2	2	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	GAL	C1-C2-C3	-2.15	106.51	109.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

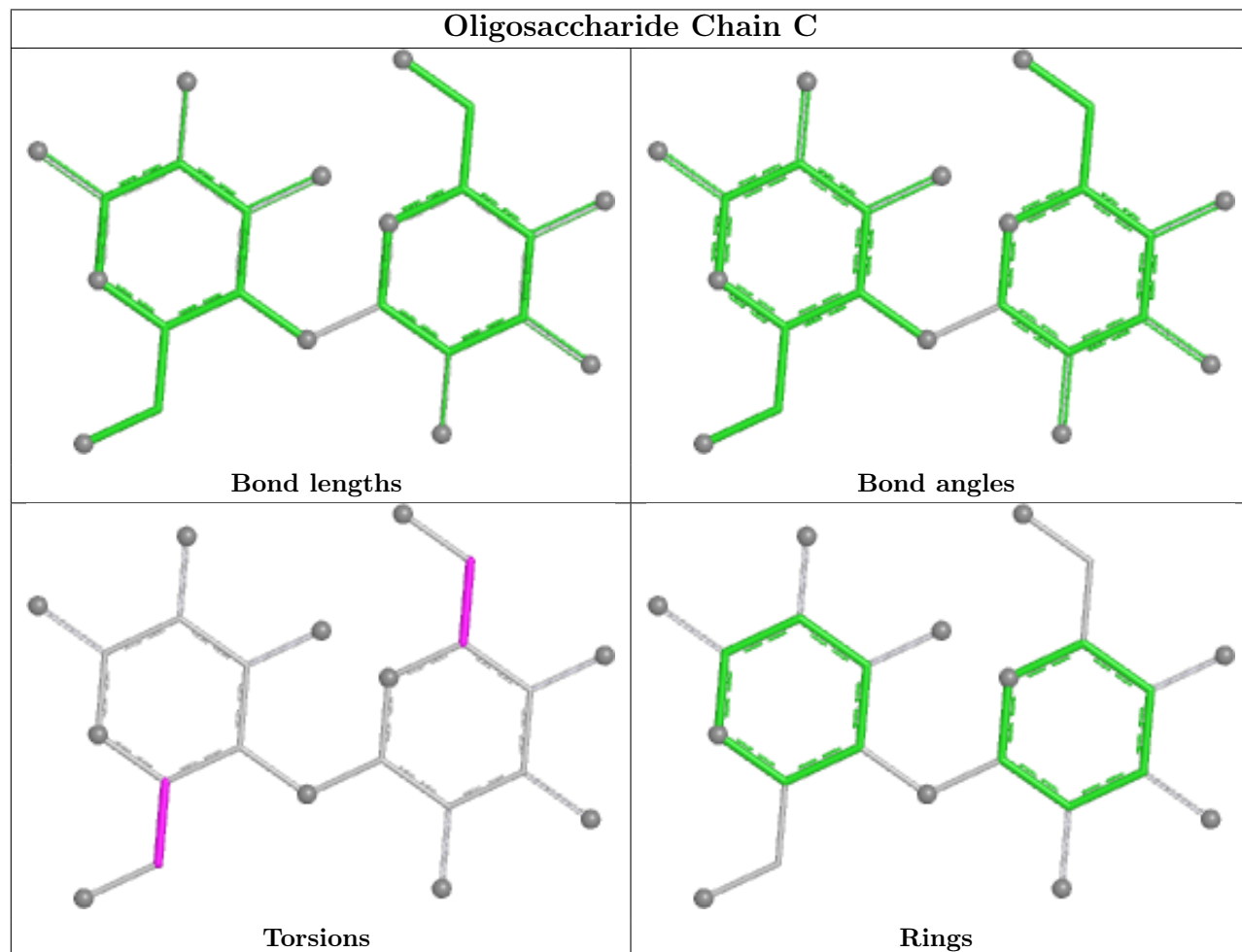
Mol	Chain	Res	Type	Atoms
2	C	2	GAL	O5-C5-C6-O6
2	D	2	GAL	O5-C5-C6-O6
2	C	1	GAL	O5-C5-C6-O6

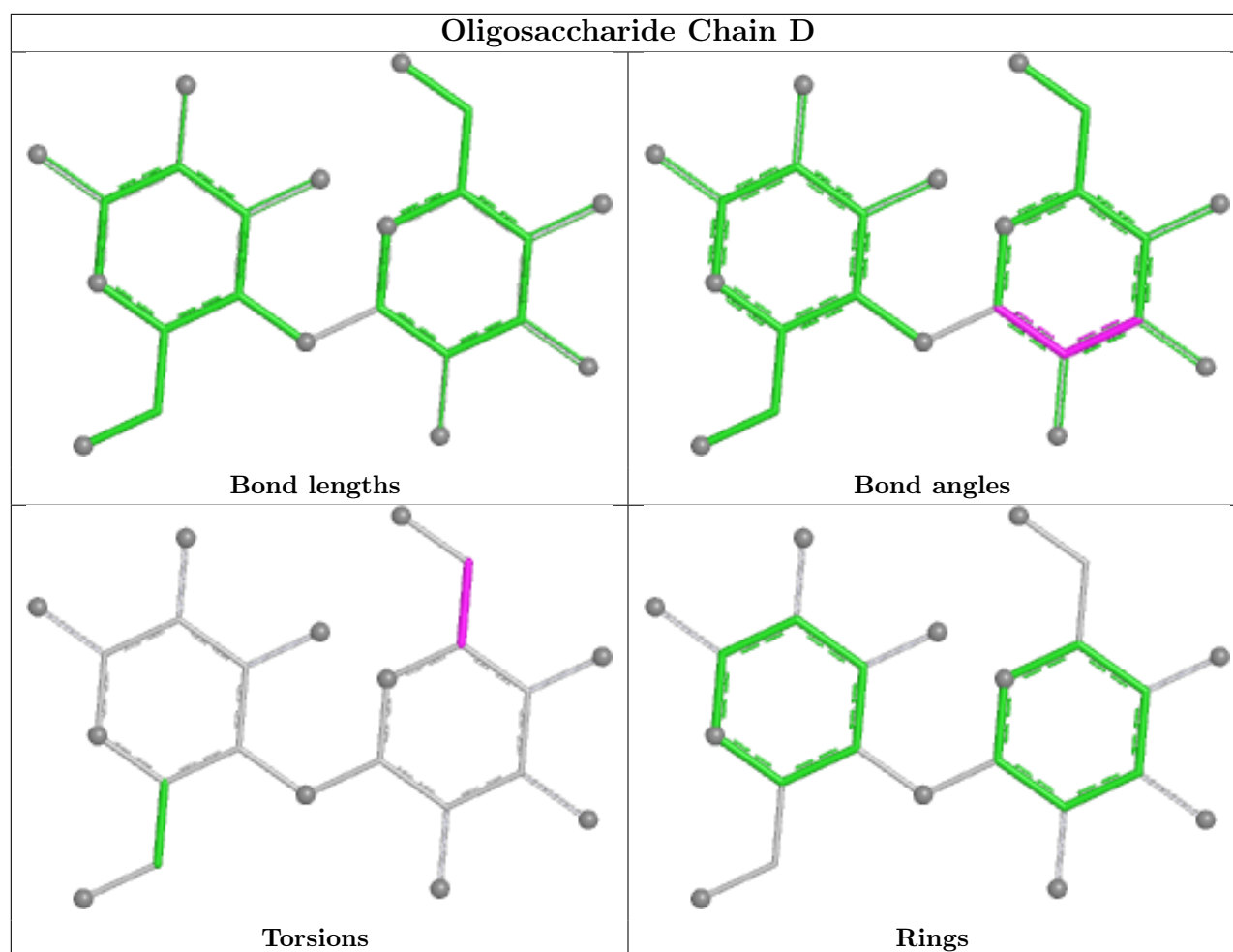
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	GAL	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, 2 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	$\# Z > 2$
5	PGE	B	1399	-	9,9,9	0.85	0	8,8,8	1.60	2 (25%)
3	PEG	B	1398	-	6,6,6	0.80	0	5,5,5	1.44	1 (20%)
3	PEG	A	1397	-	6,6,6	0.59	0	5,5,5	1.62	1 (20%)

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	PGE	B	1399	-	-	6/7/7/7	-
3	PEG	B	1398	-	-	2/4/4/4	-
3	PEG	A	1397	-	-	2/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1397	PEG	O2-C2-C1	3.16	124.02	110.11
5	B	1399	PGE	C5-O3-C4	2.67	124.96	113.26
5	B	1399	PGE	O2-C2-C1	2.56	121.38	110.11
3	B	1398	PEG	O2-C2-C1	2.42	120.76	110.11

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1399	PGE	O2-C3-C4-O3
3	A	1397	PEG	O1-C1-C2-O2
5	B	1399	PGE	O3-C5-C6-O4
5	B	1399	PGE	O1-C1-C2-O2
3	A	1397	PEG	O2-C3-C4-O4
5	B	1399	PGE	C6-C5-O3-C4
5	B	1399	PGE	C3-C4-O3-C5
3	B	1398	PEG	C4-C3-O2-C2
3	B	1398	PEG	O2-C3-C4-O4
5	B	1399	PGE	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1399	PGE	3	0
3	A	1397	PEG	1	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.