



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:35 PM UTC

PDB ID : 5GY0 / pdb_00005gy0
Title : Crystal structure of endoglucanase CelQ from Clostridium thermocellum complexed with cellotetraose
Authors : Jeng, W.Y.; Liu, C.I.; Wang, A.H.J.
Deposited on : 2016-09-21
Resolution : 1.74 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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

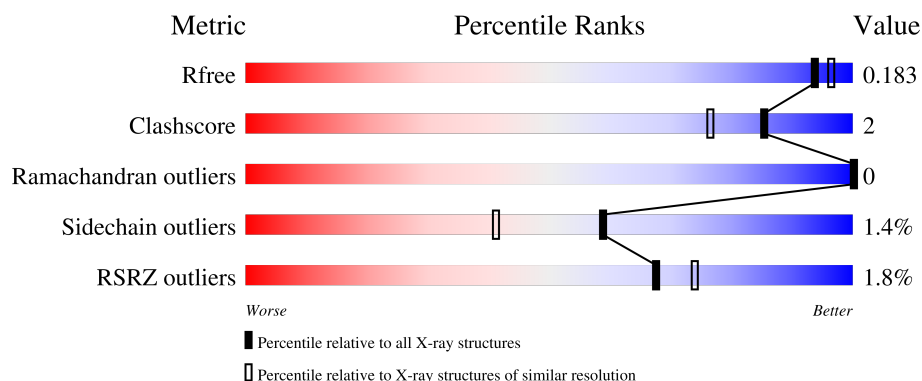
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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))
R_{free}	180053	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	610	% 92% 6%
1	B	610	3% 93% 5%
2	C	4	75% 25%
2	D	4	25% 75%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11148 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 Glucanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	599	Total	C	N	O	S	0	2	0
			4804	3072	799	915	18			
1	B	599	Total	C	N	O	S	0	6	0
			4823	3084	802	919	18			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	initiating methionine	UNP Q9AJF8
A	251	THR	ILE	engineered mutation	UNP Q9AJF8
A	435	ALA	GLU	engineered mutation	UNP Q9AJF8
A	629	LEU	-	expression tag	UNP Q9AJF8
A	630	GLU	-	expression tag	UNP Q9AJF8
A	631	HIS	-	expression tag	UNP Q9AJF8
A	632	HIS	-	expression tag	UNP Q9AJF8
A	633	HIS	-	expression tag	UNP Q9AJF8
A	634	HIS	-	expression tag	UNP Q9AJF8
A	635	HIS	-	expression tag	UNP Q9AJF8
A	636	HIS	-	expression tag	UNP Q9AJF8
B	27	MET	-	initiating methionine	UNP Q9AJF8
B	251	THR	ILE	engineered mutation	UNP Q9AJF8
B	435	ALA	GLU	engineered mutation	UNP Q9AJF8
B	629	LEU	-	expression tag	UNP Q9AJF8
B	630	GLU	-	expression tag	UNP Q9AJF8
B	631	HIS	-	expression tag	UNP Q9AJF8
B	632	HIS	-	expression tag	UNP Q9AJF8
B	633	HIS	-	expression tag	UNP Q9AJF8
B	634	HIS	-	expression tag	UNP Q9AJF8
B	635	HIS	-	expression tag	UNP Q9AJF8
B	636	HIS	-	expression tag	UNP Q9AJF8

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	4	Total	C	O	0	0	0
			45	24	21			
2	D	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		
3	B	2	Total	Ca	0	0
			2	2		

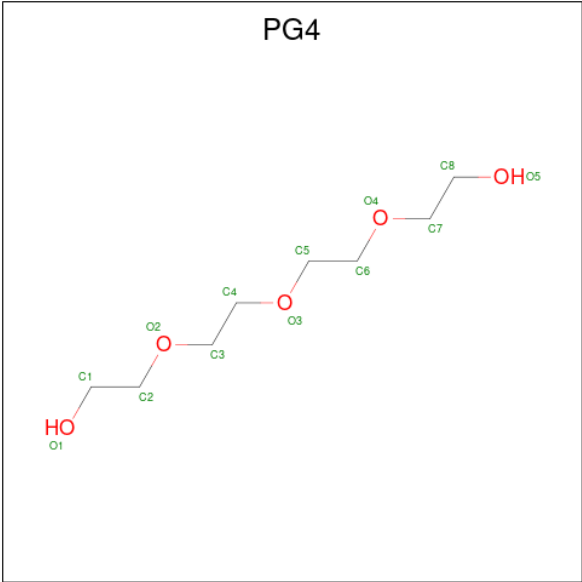
- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Cl	0	0
			4	4		
4	B	3	Total	Cl	0	0
			3	3		

- Molecule 5 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Br	0	0
			1	1		

- Molecule 6 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			13	8	5		

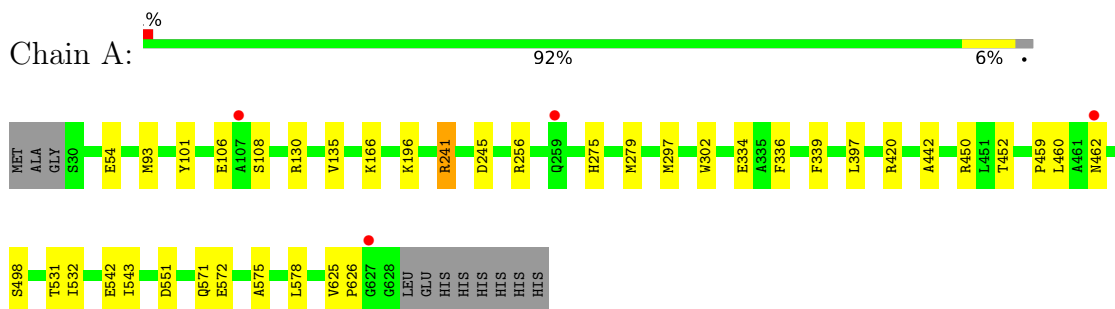
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	662	Total	O	0	0
			662	662		
7	B	744	Total	O	0	0
			744	744		

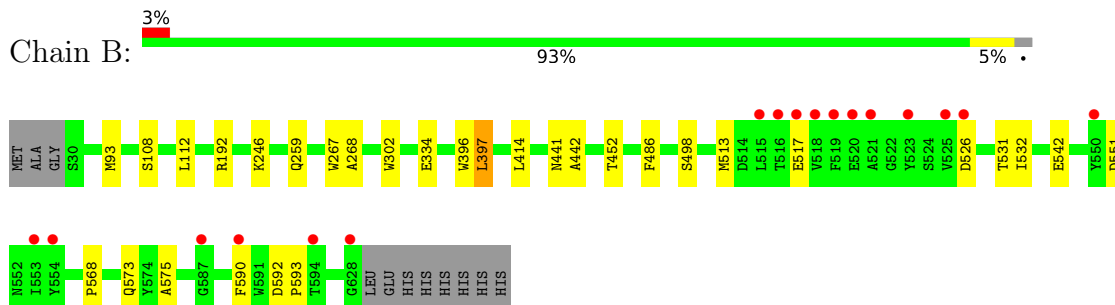
3 Residue-property plots

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

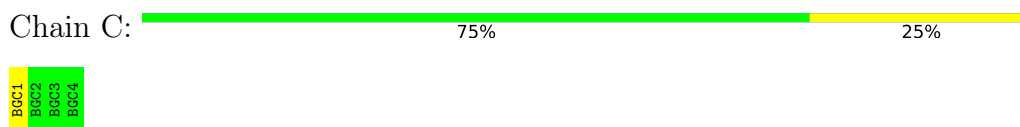
- Molecule 1: Glucanase



- Molecule 1: Glucanase



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.02Å 108.80Å 139.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.94 – 1.74 22.94 – 1.74	Depositor EDS
% Data completeness (in resolution range)	98.3 (22.94-1.74) 98.9 (22.94-1.74)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.81 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.157 , 0.183 0.157 , 0.183	Depositor DCC
R_{free} test set	8375 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11148	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, BR, CA, BGC, PG4

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	0.41	0/4955	0.83	2/6748 (0.0%)
1	B	0.45	0/4986	0.84	3/6790 (0.0%)
All	All	0.43	0/9941	0.84	5/13538 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	486	PHE	N-CA-C	7.21	119.81	108.79
1	B	551	ASP	CB-CA-C	-6.07	109.56	116.54
1	A	551	ASP	CB-CA-C	-5.58	110.12	116.54
1	A	135	VAL	N-CA-C	-5.29	102.69	109.30
1	B	397	LEU	N-CA-C	5.13	118.59	111.71

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	4804	0	4496	27	0
1	B	4823	0	4521	17	0
2	C	45	0	39	0	0
2	D	45	0	39	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	4	0	0	1	0
4	B	3	0	0	0	0
5	B	1	0	0	0	0
6	B	13	0	18	1	0
7	A	662	0	0	9	0
7	B	744	0	0	4	0
All	All	11148	0	9113	42	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 2.

All (42) 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:532:ILE:HD11	1:A:543[B]:ILE:HD12	1.55	0.88
1:A:241:ARG:NH1	1:A:245:ASP:OD1	2.11	0.83
1:B:414:LEU:H	1:B:441:ASN:HD21	1.30	0.78
1:A:532:ILE:HD11	1:A:543[B]:ILE:CD1	2.15	0.77
1:B:192:ARG:HD2	6:B:711:PG4:H42	1.73	0.71
1:A:256:ARG:N	1:A:256:ARG:HD2	2.12	0.65
1:A:420:ARG:NE	7:A:806:HOH:O	2.32	0.63
1:A:542:GLU:HB3	1:B:531:THR:HG22	1.81	0.62
1:A:575:ALA:O	7:A:802:HOH:O	2.17	0.58
1:B:452[A]:THR:HG22	7:B:1339:HOH:O	2.04	0.58
1:A:625:VAL:HG13	1:A:626:PRO:HD2	1.86	0.57
1:B:573[B]:GLN:HE21	1:B:573[B]:GLN:H	1.53	0.57
1:A:543[B]:ILE:HD11	1:A:578:LEU:HD21	1.88	0.56
1:B:575:ALA:O	7:B:801:HOH:O	2.18	0.55
1:A:571:GLN:NE2	7:A:808:HOH:O	2.38	0.54
1:B:93:MET:HB2	1:B:442:ALA:HB1	1.94	0.50
1:B:108:SER:HB3	1:B:452[A]:THR:HG21	1.94	0.50
1:A:625:VAL:CG1	1:A:626:PRO:HD2	2.42	0.49
1:A:572:GLU:O	7:A:802:HOH:O	2.20	0.49
1:A:462:ASN:OD1	7:A:803:HOH:O	2.20	0.48
1:B:414:LEU:H	1:B:441:ASN:ND2	2.07	0.47
1:B:302:TRP:CE2	1:B:334:GLU:HG3	2.50	0.47
1:A:93:MET:HB2	1:A:442:ALA:HB1	1.96	0.47
1:B:573[B]:GLN:NE2	7:B:812:HOH:O	2.49	0.46
1:B:575:ALA:O	7:B:802:HOH:O	2.21	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:ARG:CZ	7:A:806:HOH:O	2.63	0.46
1:A:130:ARG:NH2	7:A:805:HOH:O	2.28	0.45
1:A:297:MET:HE1	7:A:1346:HOH:O	2.18	0.44
1:A:108:SER:O	1:A:459:PRO:HG3	2.18	0.43
1:B:517:GLU:HG3	1:B:590:PHE:O	2.19	0.43
1:A:54:GLU:CG	7:A:811:HOH:O	2.66	0.43
1:A:108:SER:HB3	1:A:452[B]:THR:HG21	2.01	0.43
1:A:275:HIS:O	1:A:279:MET:HG2	2.18	0.42
1:A:302:TRP:CE2	1:A:334:GLU:HG3	2.54	0.42
1:A:101:TYR:HE2	1:A:336:PHE:HE1	1.66	0.42
1:B:396:TRP:HA	1:B:568:PRO:HB2	2.02	0.42
1:A:339:PHE:CG	1:A:450:ARG:HG2	2.56	0.41
1:A:531:THR:HG22	1:B:542:GLU:HB3	2.01	0.41
1:B:267:TRP:CD1	1:B:268:ALA:H	2.39	0.41
1:A:460:LEU:HD13	4:A:705:CL:CL	2.58	0.40
1:B:592:ASP:HA	1:B:593:PRO:HD2	1.85	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	599/610 (98%)	586 (98%)	13 (2%)	0	100	100
1	B	603/610 (99%)	588 (98%)	15 (2%)	0	100	100
All	All	1202/1220 (98%)	1174 (98%)	28 (2%)	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	488/495 (99%)	482 (99%)	6 (1%)	63	47
1	B	492/495 (99%)	484 (98%)	8 (2%)	55	35
All	All	980/990 (99%)	966 (99%)	14 (1%)	59	41

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	GLU
1	A	166	LYS
1	A	196	LYS
1	A	241	ARG
1	A	397	LEU
1	A	498	SER
1	B	112	LEU
1	B	246	LYS
1	B	259	GLN
1	B	397	LEU
1	B	498	SER
1	B	513	MET
1	B	526	ASP
1	B	532	ILE

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	255	ASN
1	A	352	GLN
1	A	385	GLN
1	A	462	ASN
1	A	565	ASN
1	A	600	GLN
1	B	67	ASN
1	B	137	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	220	HIS
1	B	258	ASN
1	B	296	GLN
1	B	305	GLN
1	B	346	ASN
1	B	372	ASN
1	B	441	ASN
1	B	600	GLN

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](#)

8 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	BGC	C	1	2	12,12,12	0.56	0	17,17,17	1.20	1 (5%)
2	BGC	C	2	2	11,11,12	0.41	0	15,15,17	0.87	0
2	BGC	C	3	2	11,11,12	0.32	0	15,15,17	0.71	0
2	BGC	C	4	2	11,11,12	0.29	0	15,15,17	0.62	0
2	BGC	D	1	2	12,12,12	0.57	0	17,17,17	1.28	1 (5%)
2	BGC	D	2	2	11,11,12	0.51	0	15,15,17	1.10	1 (6%)
2	BGC	D	3	2	11,11,12	0.45	0	15,15,17	0.81	0
2	BGC	D	4	2	11,11,12	0.33	0	15,15,17	1.22	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	BGC	C	1	2	-	0/2/22/22	0/1/1/1
2	BGC	C	2	2	-	0/2/19/22	0/1/1/1
2	BGC	C	3	2	-	0/2/19/22	0/1/1/1
2	BGC	C	4	2	-	0/2/19/22	0/1/1/1
2	BGC	D	1	2	-	2/2/22/22	0/1/1/1
2	BGC	D	2	2	-	0/2/19/22	0/1/1/1
2	BGC	D	3	2	-	0/2/19/22	0/1/1/1
2	BGC	D	4	2	-	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	D	1	BGC	O6-C6-C5	-3.83	98.31	111.33
2	C	1	BGC	O5-C5-C6	2.30	112.13	106.44
2	D	2	BGC	C1-C2-C3	2.23	112.90	109.64
2	D	4	BGC	O4-C4-C3	2.17	115.50	110.38

There are no chirality outliers.

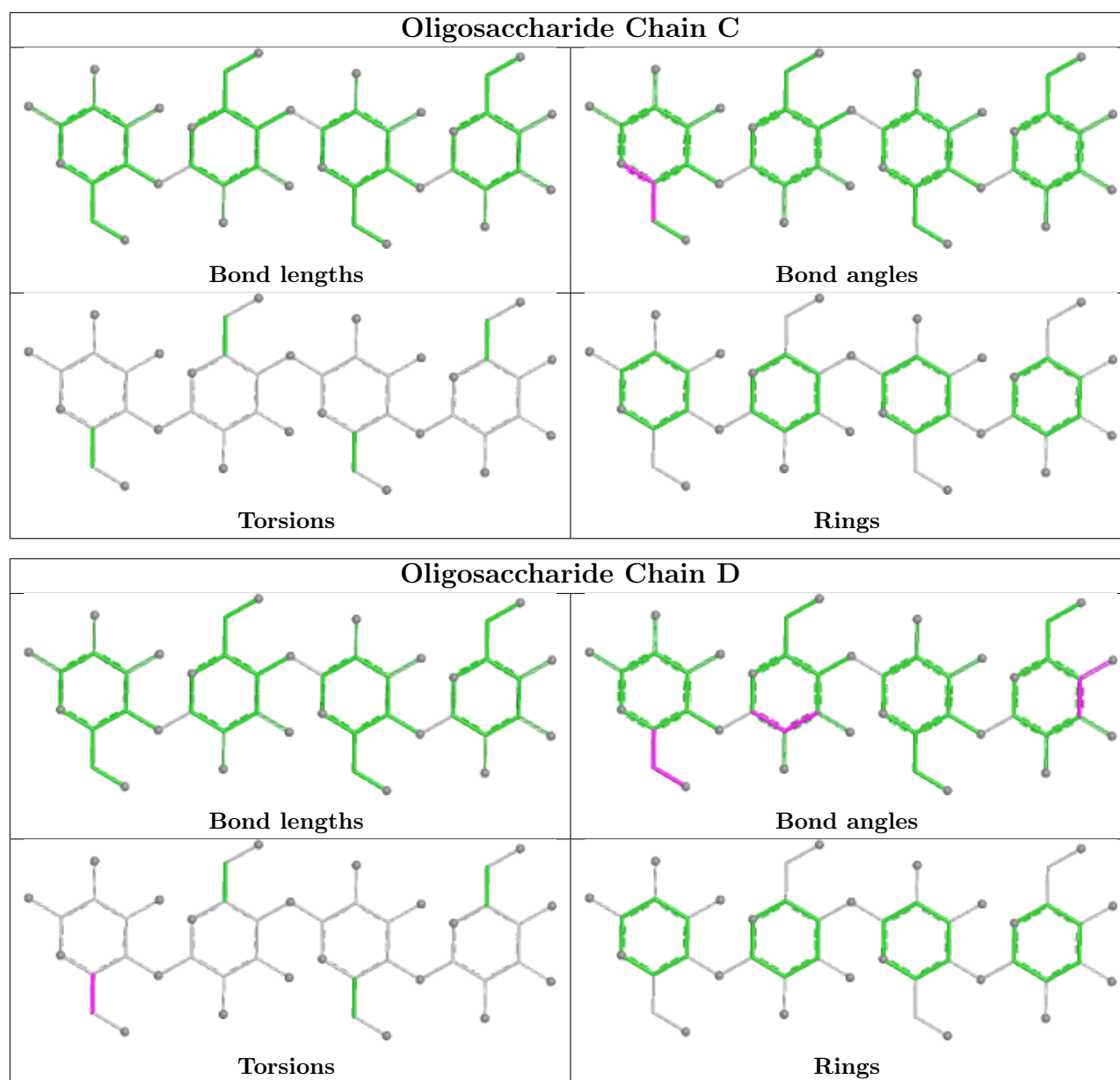
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	BGC	O5-C5-C6-O6
2	D	1	BGC	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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 13 ligands modelled in this entry, 12 are monoatomic - leaving 1 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
6	PG4	B	711	-	12,12,12	0.47	0	11,11,11	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
6	PG4	B	711	-	-	6/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	711	PG4	O2-C3-C4-O3
6	B	711	PG4	O4-C7-C8-O5
6	B	711	PG4	O1-C1-C2-O2
6	B	711	PG4	C3-C4-O3-C5
6	B	711	PG4	C6-C5-O3-C4
6	B	711	PG4	O3-C5-C6-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	711	PG4	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	599/610 (98%)	-0.40	4 (0%) 84 89	13, 20, 35, 50	2 (0%)
1	B	599/610 (98%)	-0.40	17 (2%) 55 63	9, 17, 39, 55	6 (1%)
All	All	1198/1220 (98%)	-0.40	21 (1%) 67 74	9, 19, 36, 55	8 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	518	VAL	4.3
1	B	519	PHE	3.2
1	B	521	ALA	3.2
1	B	590	PHE	3.1
1	B	516	THR	3.1
1	B	587	GLY	2.9
1	B	526	ASP	2.7
1	B	523	TYR	2.7
1	B	515	LEU	2.6
1	B	525	VAL	2.6
1	B	517	GLU	2.5
1	B	628	GLY	2.4
1	A	462	ASN	2.4
1	B	594	THR	2.3
1	A	107	ALA	2.3
1	B	553	ILE	2.2
1	A	259	GLN	2.1
1	B	520	GLU	2.1
1	B	550	TYR	2.1
1	B	554	TYR	2.1
1	A	627	GLY	2.0

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

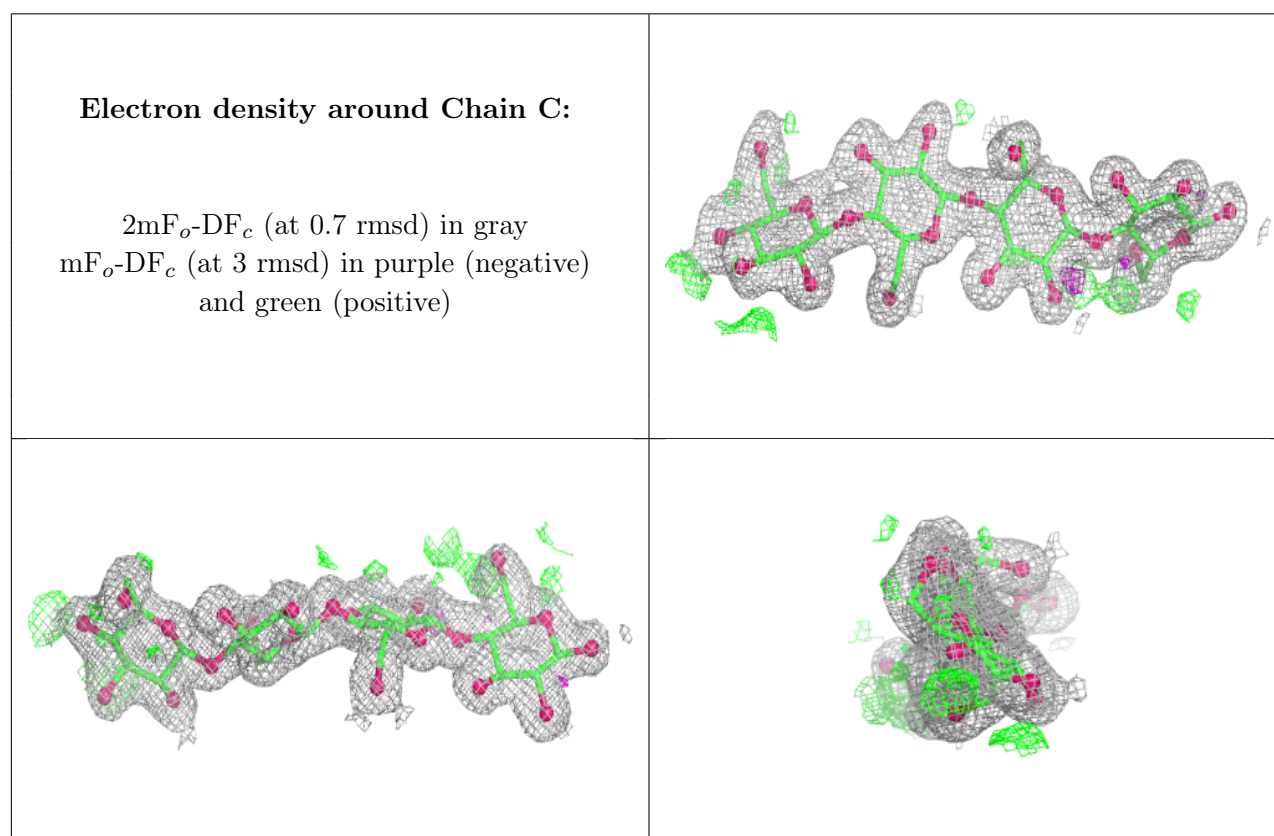
There are no non-standard protein/DNA/RNA residues in this entry.

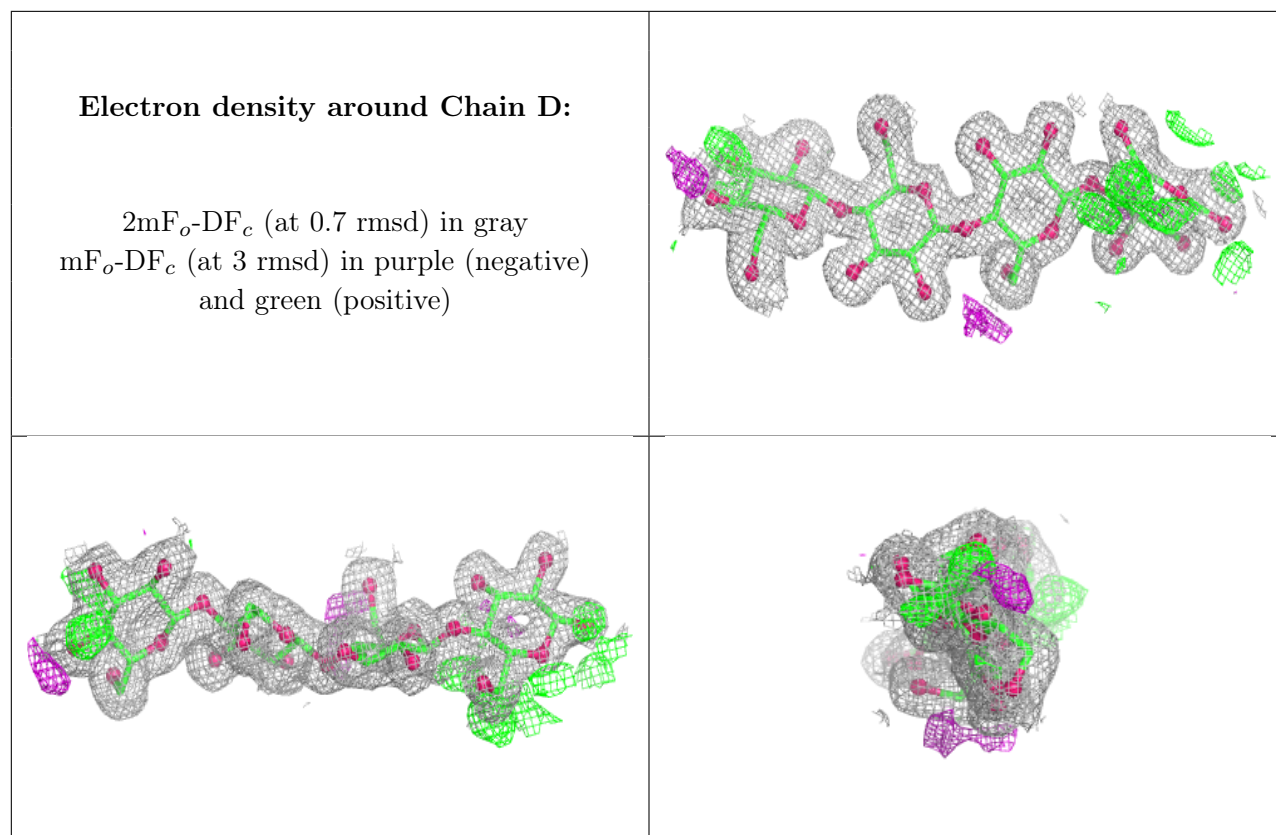
6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BGC	D	1	12/12	0.91	0.11	19,24,29,29	1
2	BGC	C	4	11/12	0.92	0.10	23,30,38,40	0
2	BGC	C	1	12/12	0.92	0.09	22,27,30,32	1
2	BGC	D	4	11/12	0.95	0.07	14,24,31,33	0
2	BGC	D	2	11/12	0.97	0.05	14,16,18,20	0
2	BGC	C	2	11/12	0.97	0.05	17,19,23,26	0
2	BGC	D	3	11/12	0.98	0.04	13,15,19,19	0
2	BGC	C	3	11/12	0.98	0.05	19,21,24,25	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	PG4	B	711	13/13	0.84	0.15	38,47,50,50	0
4	CL	B	704	1/1	0.88	0.13	49,49,49,49	0
4	CL	A	704	1/1	0.94	0.10	47,47,47,47	0
3	CA	B	702	1/1	0.95	0.09	34,34,34,34	0
4	CL	B	706	1/1	0.97	0.08	29,29,29,29	0
4	CL	A	706	1/1	0.97	0.05	36,36,36,36	0
3	CA	A	701	1/1	0.99	0.03	20,20,20,20	0
4	CL	A	703	1/1	0.99	0.09	28,28,28,28	0
4	CL	B	705	1/1	0.99	0.04	28,28,28,28	0
3	CA	A	702	1/1	0.99	0.04	24,24,24,24	0
4	CL	A	705	1/1	0.99	0.02	25,25,25,25	0
5	BR	B	703	1/1	1.00	0.04	30,30,30,30	0
3	CA	B	701	1/1	1.00	0.02	14,14,14,14	0

6.5 Other polymers ⓘ

There are no such residues in this entry.