WORLDWIDE PDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Aug 21, 2023 – 03:28 PM EDT

PDB ID	:	8GHY
Title	:	Crystal Structure of the E154D mutant CelD Cellulase from the Anaerobic Fungus Piromyces finnis in the complex with cellotriose.
Authors	:	Dementieve, A.; Kim, Y.; Jedrzejczak, R.; Michalska, K.; Joachimiak, A.
Deposited on	:	2023-03-13
Resolution	:	1.80 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

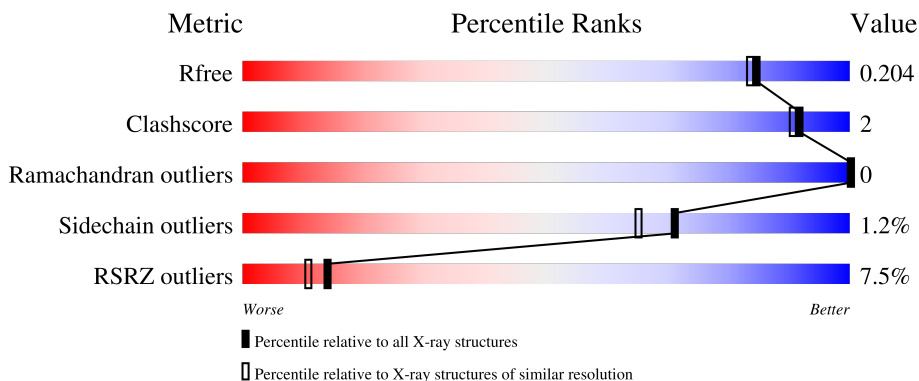|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1   Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
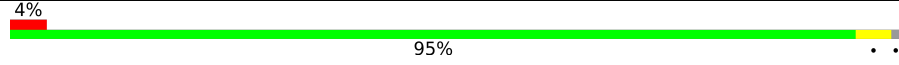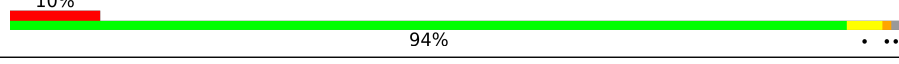*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	Percentile Ranks	Value
Rfree		0.204
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		1.2%
RSRZ outliers		7.5%

Worse ——— *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 <=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	365	4% ... 95% ...
1	B	365	10% ... 94% ...
2	C	3	67% ... 33%
2	E	3	67% ... 33%

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 6391 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 Cellulase CelD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	2	0
			2918	1853	496	555	14			
1	B	362	Total	C	N	O	S	0	2	0
			2916	1855	497	550	14			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A0A1Y1V643
A	-1	ASN	-	expression tag	UNP A0A1Y1V643
A	0	ALA	-	expression tag	UNP A0A1Y1V643
A	154	ALA	GLU	engineered mutation	UNP A0A1Y1V643
A	361	GLU	THR	conflict	UNP A0A1Y1V643
B	-2	SER	-	expression tag	UNP A0A1Y1V643
B	-1	ASN	-	expression tag	UNP A0A1Y1V643
B	0	ALA	-	expression tag	UNP A0A1Y1V643
B	154	ALA	GLU	engineered mutation	UNP A0A1Y1V643
B	361	GLU	THR	conflict	UNP A0A1Y1V643

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1 -4)-beta-D-glucopyranose.
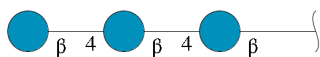
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	3	Total	C	O	0	0	0
			34	18	16			
2	E	3	Total	C	O	0	0	0
			34	18	16			

• Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	302	Total O 302 302		0	0
3	B	187	Total O 187 187		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 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 = 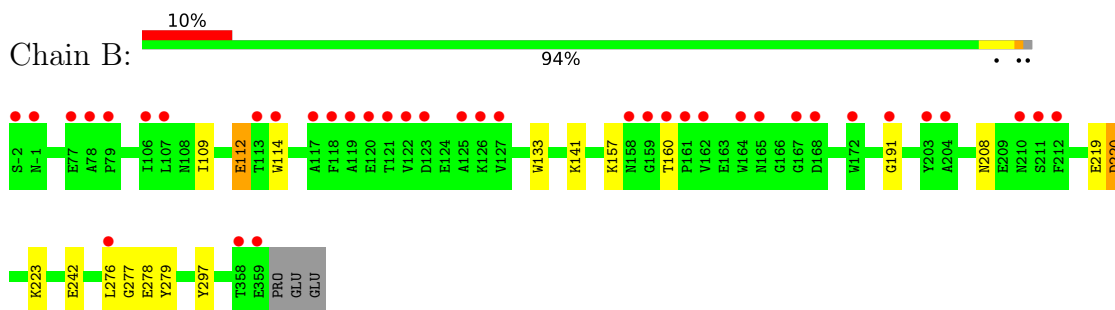3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Cellulase CelD
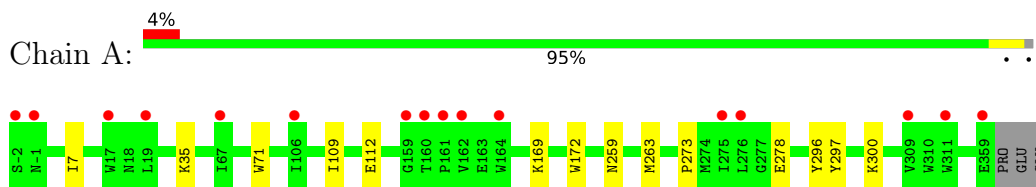
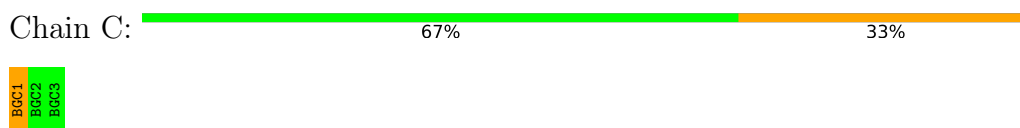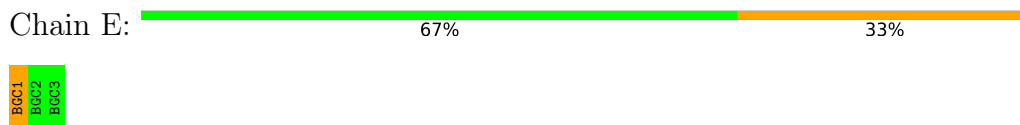Chain A:

- Molecule 1: Cellulase CelD

Chain B:

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

Chain C:

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

Chain E:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	69.50Å 81.01Å 131.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.78 – 1.80 33.78 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (33.78-1.80) 98.8 (33.78-1.80)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.50 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.176 , 0.205 0.176 , 0.204	Depositor DCC
R_{free} test set	3395 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	25.9	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 46.5	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	6391	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: BGC

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	0.31	0/2999	0.51	0/4066
1	B	0.28	0/2997	0.49	0/4063
All	All	0.30	0/5996	0.50	0/8129

There are no bond length outliers.

There are no bond angle outliers.

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	2918	0	2767	8	0
1	B	2916	0	2776	10	0
2	C	34	0	30	1	0
2	E	34	0	30	1	0
3	A	302	0	0	0	0
3	B	187	0	0	2	0
All	All	6391	0	5603	18	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 (18) 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:71:TRP:CD1	1:A:109:ILE:HG13	2.43	0.54
1:A:7:ILE:HG12	1:A:273:PRO:HG3	1.90	0.53
1:B:219:GLU:O	1:B:220:ASP:HB2	2.12	0.50
1:A:169:LYS:HA	1:A:172:TRP:CE3	2.47	0.49
1:A:109:ILE:HG23	1:A:112:GLU:CG	2.43	0.49
1:B:278:GLU:OE1	2:E:1:BGC:H1	2.13	0.48
1:B:223:LYS:NZ	3:B:409:HOH:O	2.47	0.48
1:A:109:ILE:HG23	1:A:112:GLU:HG3	1.97	0.47
1:B:157:LYS:HB3	1:B:160:THR:HG21	1.96	0.46
1:B:276[B]:LEU:CD2	1:B:279:TYR:HB3	2.47	0.45
1:B:141:LYS:HB2	1:B:191:GLY:HA3	1.98	0.44
1:B:112:GLU:HG3	1:B:114:TRP:NE1	2.33	0.44
1:B:277:GLY:HA3	3:B:414:HOH:O	2.18	0.44
1:A:278:GLU:OE1	2:C:1:BGC:H1	2.19	0.43
1:B:112:GLU:HG3	1:B:114:TRP:CE2	2.54	0.42
1:A:296:TYR:CE1	1:A:300:LYS:HE3	2.55	0.41
1:B:109:ILE:HD13	1:B:133:TRP:CZ2	2.56	0.41
1:A:259:ASN:O	1:A:263:MET:HG3	2.21	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	362/365 (99%)	350 (97%)	12 (3%)	0	100	100
1	B	362/365 (99%)	344 (95%)	18 (5%)	0	100	100
All	All	724/730 (99%)	694 (96%)	30 (4%)	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	304/307 (99%)	302 (99%)	2 (1%)	84	81
1	B	303/307 (99%)	298 (98%)	5 (2%)	60	51
All	All	607/614 (99%)	600 (99%)	7 (1%)	71	65

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LYS
1	A	297	TYR
1	B	112	GLU
1	B	208	ASN
1	B	220	ASP
1	B	242	GLU
1	B	297	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

6 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	0.51	0	17,17,17	1.07	1 (5%)
2	BGC	C	2	2	11,11,12	0.41	0	15,15,17	0.56	0
2	BGC	C	3	2	11,11,12	0.31	0	15,15,17	0.64	0
2	BGC	E	1	2	12,12,12	0.54	0	17,17,17	1.06	1 (5%)
2	BGC	E	2	2	11,11,12	0.33	0	15,15,17	0.58	0
2	BGC	E	3	2	11,11,12	0.29	0	15,15,17	0.95	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	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	E	1	2	-	0/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	3	2	-	1/2/19/22	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(^{o})	Ideal(^{o})
2	E	1	BGC	C3-C4-C5	-2.65	105.50	110.24
2	C	1	BGC	C3-C4-C5	-2.01	106.64	110.24

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	3	BGC	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	BGC	1	0
2	E	1	BGC	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 C

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain E

Bond lengths

Bond angles

Torsions

Rings
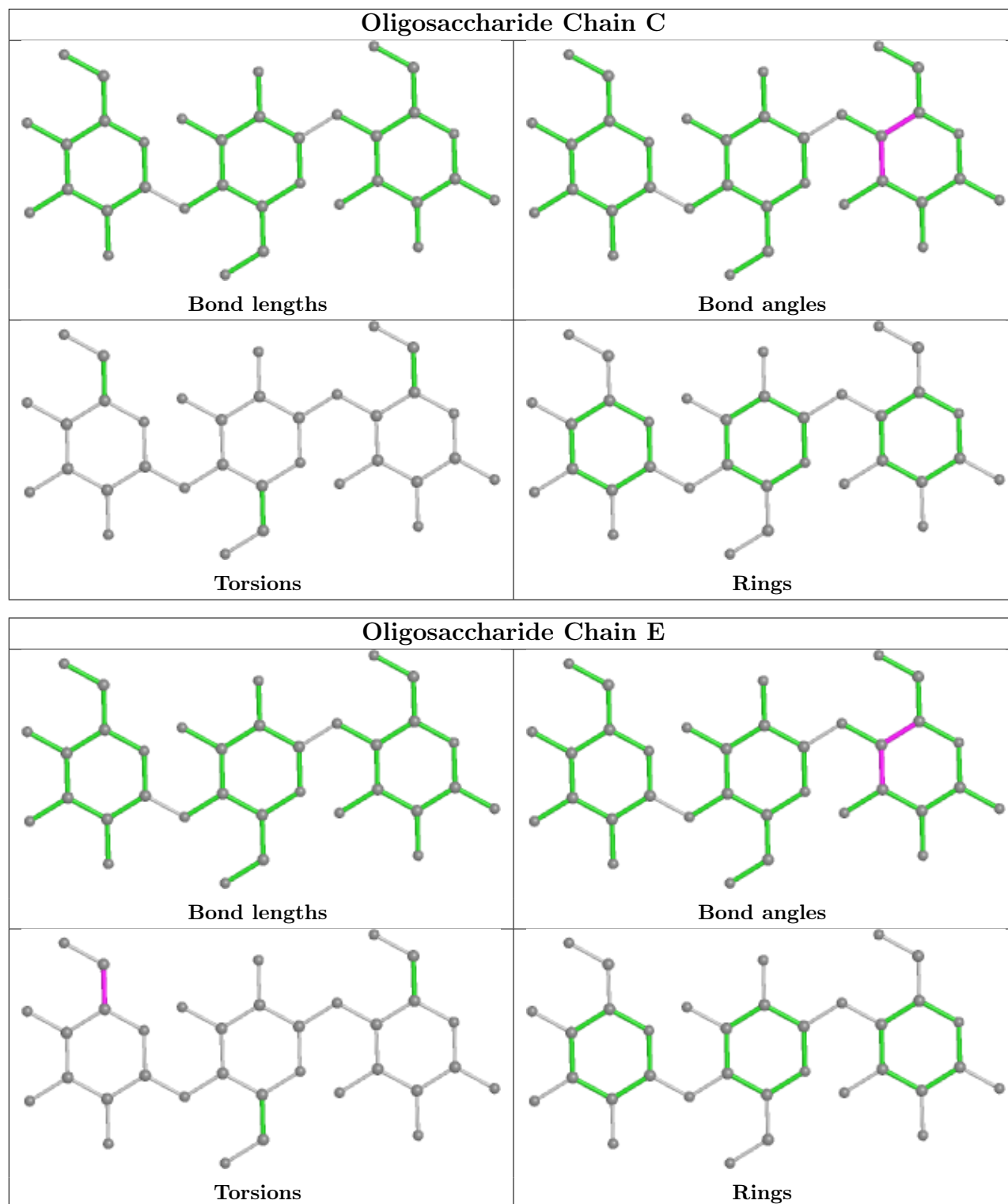
5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

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	362/365 (99%)	0.04	16 (4%)	34	28	15, 26, 44, 89	0
1	B	362/365 (99%)	0.32	38 (10%)	6	4	20, 35, 74, 91	0
All	All	724/730 (99%)	0.18	54 (7%)	14	11	15, 30, 67, 91	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-2	SER	7.4
1	B	122	VAL	5.6
1	B	118	PHE	5.6
1	B	-2	SER	5.2
1	B	121	THR	4.9
1	B	167	GLY	4.6
1	B	117	ALA	4.5
1	B	161	PRO	4.3
1	B	114	TRP	4.2
1	B	165	ASN	4.1
1	B	358	THR	4.0
1	B	160	THR	3.8
1	B	211	SER	3.8
1	A	-1	ASN	3.7
1	B	119	ALA	3.7
1	A	162	VAL	3.5
1	B	123	ASP	3.5
1	B	-1	ASN	3.4
1	B	204	ALA	3.4
1	B	79	PRO	3.4
1	B	78	ALA	3.4
1	A	359	GLU	3.4
1	B	210	ASN	3.3
1	B	359	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	159	GLY	3.2
1	A	161	PRO	3.0
1	A	160	THR	2.9
1	B	212	PHE	2.9
1	A	106	ILE	2.9
1	A	275	ILE	2.9
1	B	125	ALA	2.7
1	A	159	GLY	2.7
1	B	158	ASN	2.7
1	A	164	TRP	2.7
1	B	172	TRP	2.7
1	B	113	THR	2.6
1	B	164	TRP	2.5
1	B	106	ILE	2.5
1	A	276	LEU	2.5
1	A	67	ILE	2.5
1	B	77	GLU	2.4
1	B	120	GLU	2.4
1	B	168	ASP	2.3
1	A	309	VAL	2.3
1	A	311	TRP	2.2
1	B	191	GLY	2.2
1	A	19	LEU	2.1
1	B	203	TYR	2.1
1	B	127	VAL	2.1
1	B	276[A]	LEU	2.1
1	B	162	VAL	2.0
1	B	126	LYS	2.0
1	A	17	TRP	2.0
1	B	107	LEU	2.0

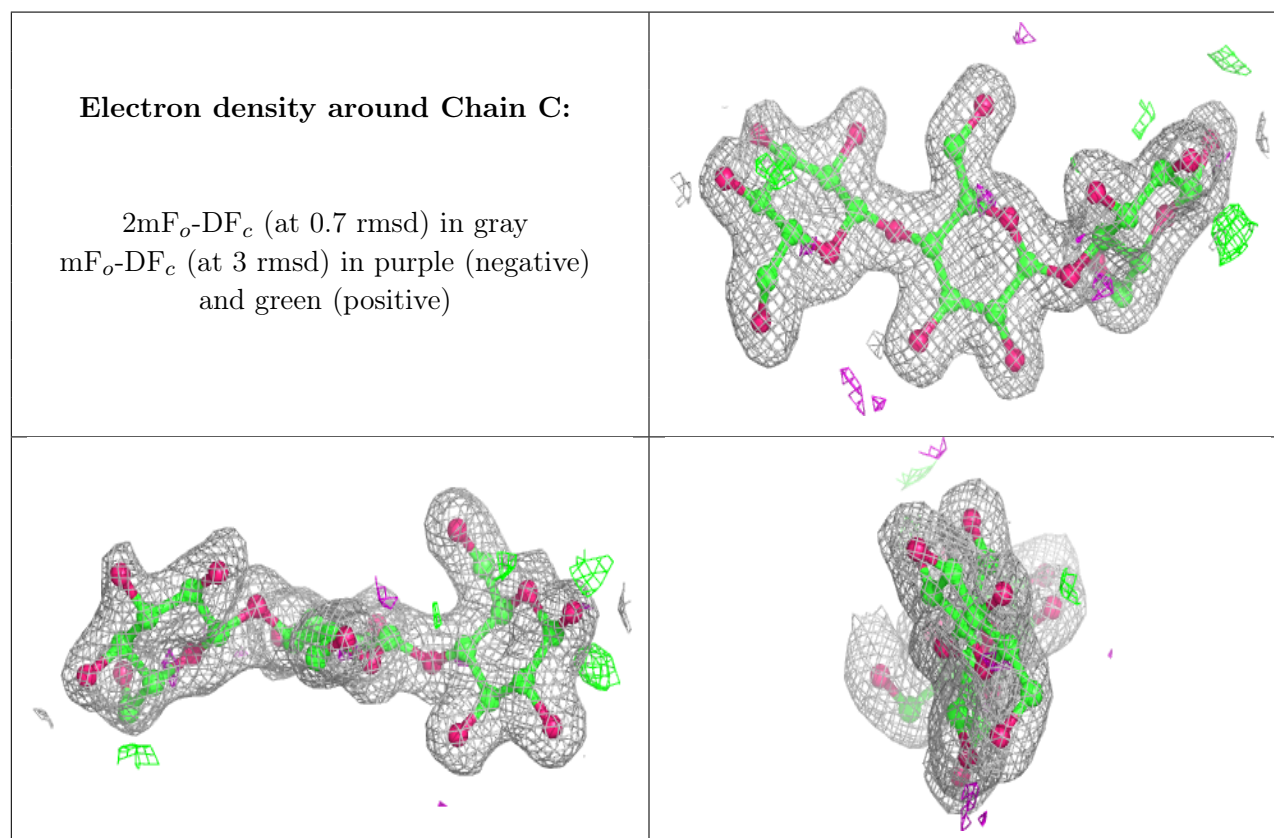## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

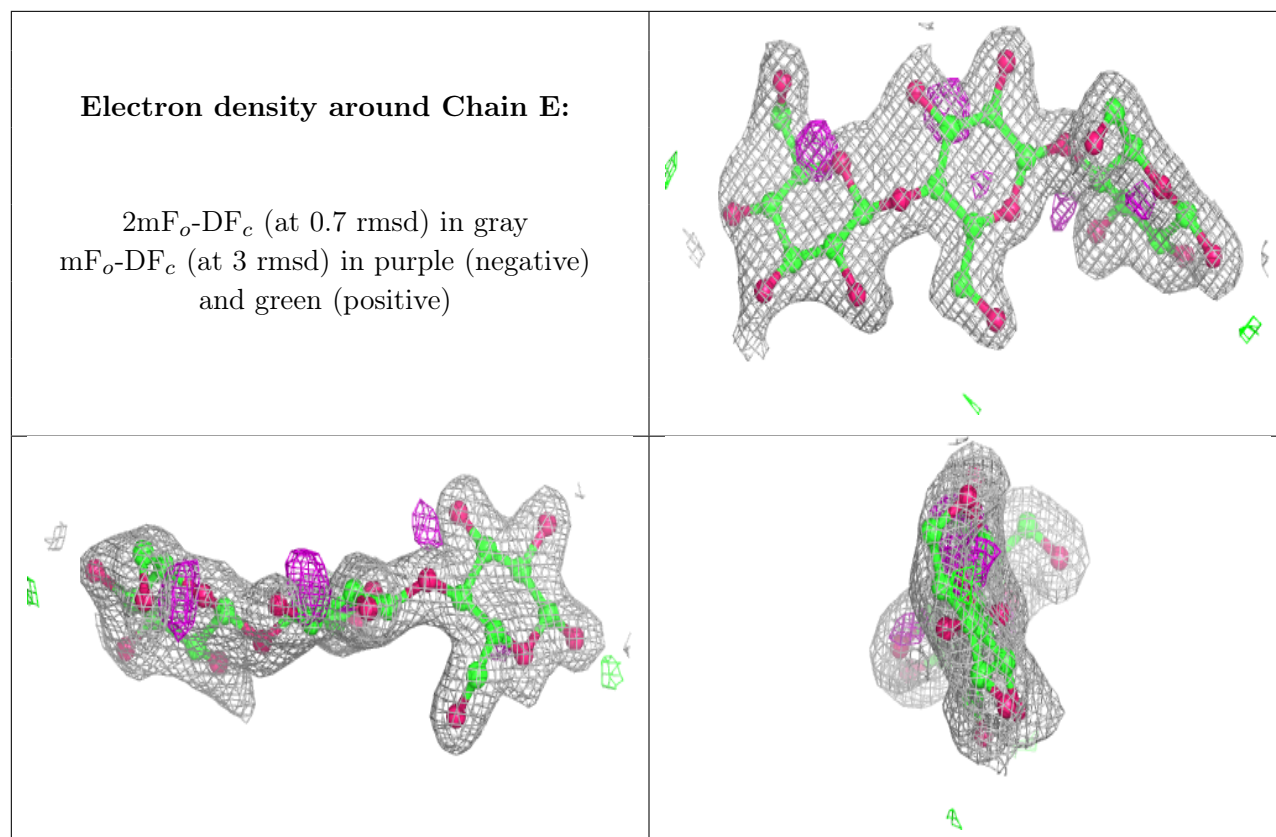There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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
2	BGC	E	3	11/12	0.88	0.13	37,44,49,55	0
2	BGC	E	2	11/12	0.89	0.15	27,35,42,42	0
2	BGC	E	1	12/12	0.89	0.11	30,34,42,46	0
2	BGC	C	3	11/12	0.92	0.11	30,35,44,48	0
2	BGC	C	1	12/12	0.94	0.09	22,24,26,33	0
2	BGC	C	2	11/12	0.96	0.08	19,23,30,33	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.

Electron density around Chain C:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around Chain E:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.