



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 5, 2024 – 01:33 pm BST

PDB ID : 1QJW  
Title : CEL6A (Y169F) WITH A NON-HYDROLYSABLE CELLOTETRAOSE  
Authors : Zou, J.-Y.; Jones, T.A.  
Deposited on : 1999-07-06  
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

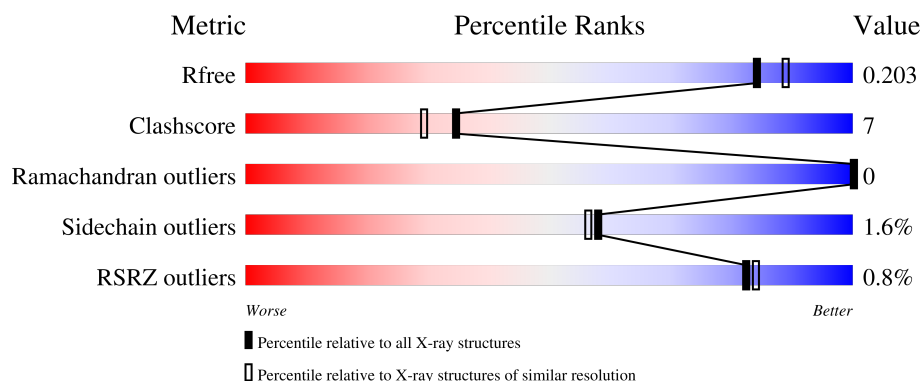
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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  $\geq 3$ , 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	365	<div> <div></div> <div>82% 16% ..</div> </div>
1	B	365	<div> <div></div> <div>84% 14% ..</div> </div>
2	C	4	<div> <div></div> <div>75% 25%</div> </div>
2	D	4	<div> <div></div> <div>75% 25%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLC	C	3	X	-	-	-
2	GLC	C	4	X	-	-	-
2	GLC	D	3	X	-	-	-
2	GLC	D	4	X	-	-	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6528 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 CELLOBIOHYDROLASE CEL6A (FORMERLY CALLED CBH II).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	0	0
			2739	1739	462	528	10			
1	B	362	Total	C	N	O	S	0	0	0
			2739	1739	462	528	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	PHE	TYR	engineered mutation	UNP P07987
B	169	PHE	TYR	engineered mutation	UNP P07987

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-4-thio-beta-D-glucopyranose-(1-4)-methyl beta-D-glucopyranoside.

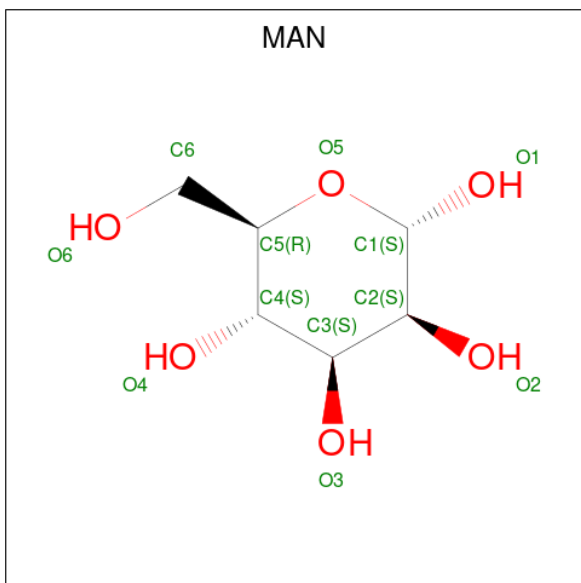
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	O	S	0	0	0
			46	25	20	1			
2	D	4	Total	C	O	S	0	0	0
			46	25	20	1			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 11 6 5	0	0
4	A	1	Total C O 11 6 5	0	0
4	A	1	Total C O 11 6 5	0	0
4	A	1	Total C O 11 6 5	0	0
4	A	1	Total C O 11 6 5	0	0
4	A	1	Total C O 11 6 5	0	0
4	A	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0
4	B	1	Total C O 11 6 5	0	0

- Molecule 5 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Cd 2 2	0	0
5	B	2	Total Cd 2 2	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

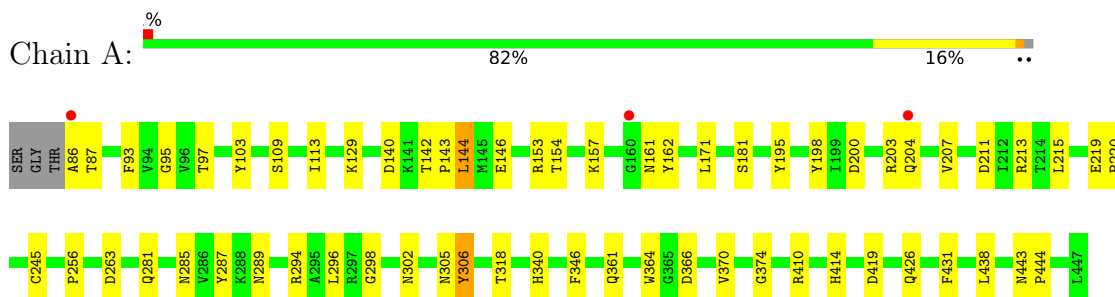
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	373	Total	O	0	0
			373	373		
7	B	359	Total	O	0	0
			359	359		

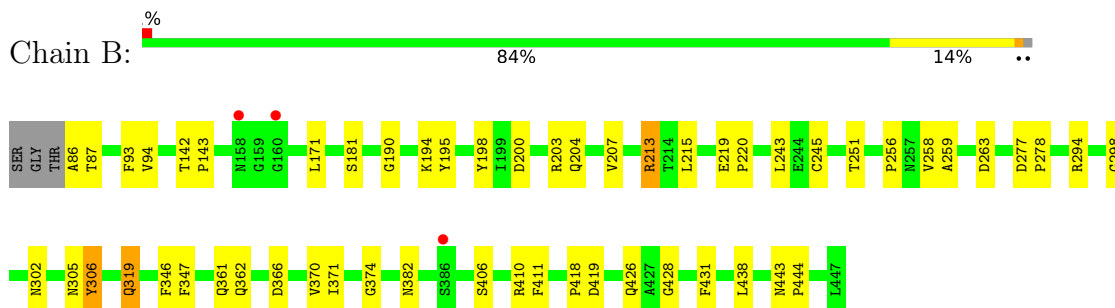
### 3 Residue-property plots

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.

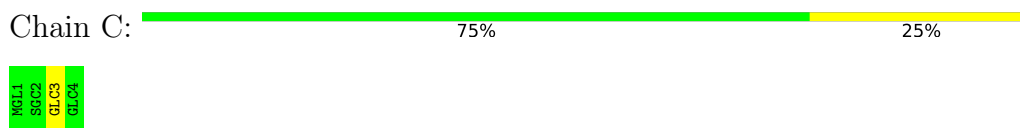
- Molecule 1: CELLOBIOHYDROLASE CEL6A (FORMERLY CALLED CBH II)



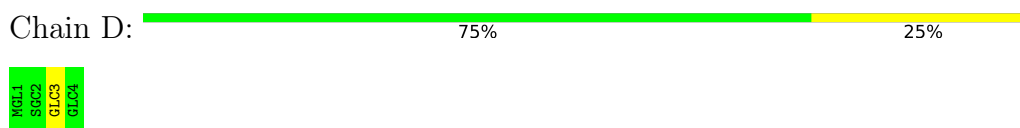
- Molecule 1: CELLOBIOHYDROLASE CEL6A (FORMERLY CALLED CBH II)



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-4-thio-beta-D-glucopyranose-(1-4)-methyl beta-D-glucopyranoside



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-4-thio-beta-D-glucopyranose-(1-4)-methyl beta-D-glucopyranoside





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.49Å 74.31Å 90.71Å 90.00° 103.82° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 20.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	90.1 (20.00-1.90) 90.2 (20.00-1.90)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.18 (at 1.91Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, $R_{free}$	0.179 , 0.208 0.174 , 0.203	Depositor DCC
$R_{free}$ test set	1321 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	11.6	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 55.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6528	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.34 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.5607e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MGL, GLC, MAN, CD, SGC, NAG, GOL

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	0/2815	0.59	0/3858
1	B	0.30	0/2815	0.59	0/3858
All	All	0.31	0/5630	0.59	0/7716

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 [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	2739	0	2599	40	0
1	B	2739	0	2599	44	0
2	C	46	0	41	0	0
2	D	46	0	41	0	0
3	A	28	0	26	0	0
3	B	28	0	26	1	0
4	A	77	0	70	1	0
4	B	77	0	70	1	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	6	0	8	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	6	0	8	1	0
7	A	373	0	0	6	0
7	B	359	0	0	5	0
All	All	6528	0	5488	84	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 7.

The worst 5 of 84 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:B:200:ASP:O	1:B:204:GLN:HG2	1.76	0.86
1:B:410:ARG:HD2	7:B:2314:HOH:O	1.81	0.79
1:B:319:GLN:HE21	1:B:319:GLN:HA	1.50	0.76
1:A:200:ASP:O	1:A:204:GLN:HG3	1.92	0.69
1:A:129:LYS:NZ	7:A:2037:HOH:O	2.17	0.68

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	360/365 (99%)	346 (96%)	14 (4%)	0	100	100
1	B	360/365 (99%)	346 (96%)	14 (4%)	0	100	100
All	All	720/730 (99%)	692 (96%)	28 (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	283/285 (99%)	279 (99%)	4 (1%)	62	62
1	B	283/285 (99%)	278 (98%)	5 (2%)	54	52
All	All	566/570 (99%)	557 (98%)	9 (2%)	58	56

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	382	ASN
1	B	431	PHE
1	A	431	PHE
1	B	213	ARG
1	B	306	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	426	GLN
1	B	158	ASN
1	B	426	GLN
1	B	305	ASN
1	A	305	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 ⓘ

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	MGL	C	1	2	13,13,13	0.64	0	18,18,18	0.60	0
2	SGC	C	2	2	10,11,12	0.67	0	12,15,17	0.71	0
2	GLC	C	3	2	11,11,12	0.58	0	15,15,17	1.37	3 (20%)
2	GLC	C	4	2	11,11,12	0.46	0	15,15,17	0.70	0
2	MGL	D	1	2	13,13,13	0.69	0	18,18,18	0.59	0
2	SGC	D	2	2	10,11,12	0.63	0	12,15,17	0.77	0
2	GLC	D	3	2	11,11,12	0.57	0	15,15,17	1.34	3 (20%)
2	GLC	D	4	2	11,11,12	0.49	0	15,15,17	0.75	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	MGL	C	1	2	-	0/4/24/24	0/1/1/1
2	SGC	C	2	2	-	0/2/19/22	0/1/1/1
2	GLC	C	3	2	1/1/4/5	0/2/19/22	0/1/1/1
2	GLC	C	4	2	1/1/4/5	0/2/19/22	0/1/1/1
2	MGL	D	1	2	-	0/4/24/24	0/1/1/1
2	SGC	D	2	2	-	0/2/19/22	0/1/1/1
2	GLC	D	3	2	1/1/4/5	0/2/19/22	0/1/1/1
2	GLC	D	4	2	1/1/4/5	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	GLC	C1-O5-C5	3.24	116.58	112.19
2	D	3	GLC	C1-O5-C5	3.05	116.33	112.19

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3	GLC	O5-C5-C6	2.68	111.41	107.20
2	C	3	GLC	O5-C5-C6	2.66	111.37	107.20
2	C	3	GLC	C1-C2-C3	2.34	112.55	109.67

All (4) chirality outliers are listed below:

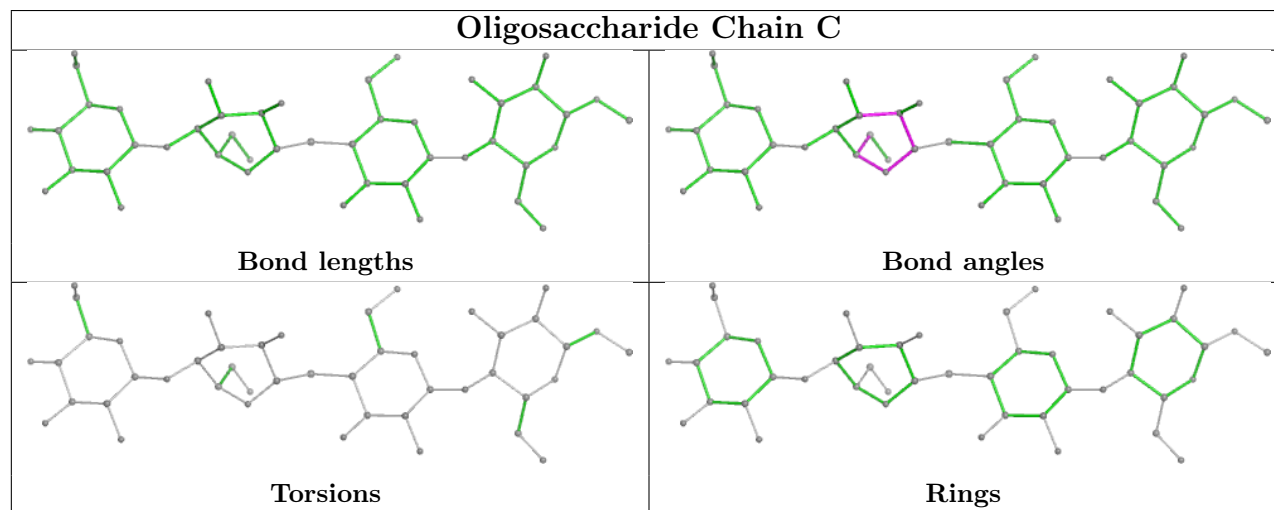
Mol	Chain	Res	Type	Atom
2	C	3	GLC	C1
2	C	4	GLC	C1
2	D	3	GLC	C1
2	D	4	GLC	C1

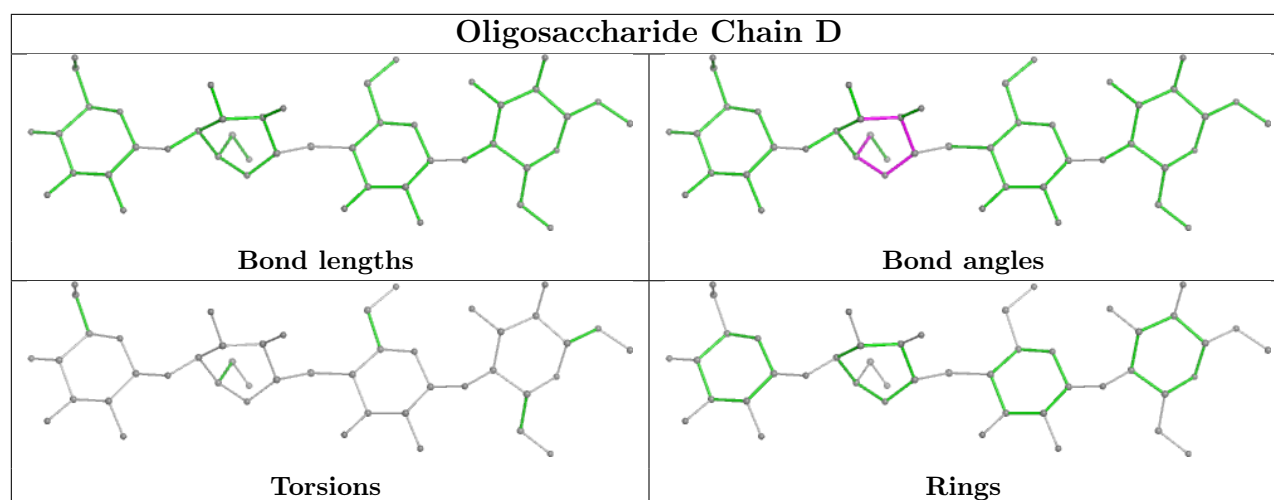
There are no torsion outliers.

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 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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	$\# Z  > 2$
4	MAN	B	503	1	11,11,12	0.49	0	15,15,17	0.73	0
4	MAN	A	503	1	11,11,12	0.44	0	15,15,17	0.69	0
4	MAN	A	505	1	11,11,12	0.46	0	15,15,17	0.77	1 (6%)
4	MAN	B	505	1	11,11,12	0.46	0	15,15,17	0.82	1 (6%)
3	NAG	A	502	1	14,14,15	0.45	0	17,19,21	0.84	0
6	GOL	A	910	-	5,5,5	0.31	0	5,5,5	0.19	0
4	MAN	A	504	1	11,11,12	0.50	0	15,15,17	0.73	0
4	MAN	A	506	1	11,11,12	0.54	0	15,15,17	0.70	0
4	MAN	B	509	1	11,11,12	0.51	0	15,15,17	0.66	0
6	GOL	B	910	-	5,5,5	0.19	0	5,5,5	0.38	0
3	NAG	A	501	1	14,14,15	0.44	0	17,19,21	0.84	1 (5%)
4	MAN	A	509	1	11,11,12	0.55	0	15,15,17	0.78	1 (6%)
4	MAN	B	508	1	11,11,12	0.48	0	15,15,17	0.68	0
4	MAN	A	508	1	11,11,12	0.45	0	15,15,17	0.71	0
3	NAG	B	501	1	14,14,15	0.44	0	17,19,21	0.81	0
4	MAN	B	504	1	11,11,12	0.46	0	15,15,17	0.69	0
4	MAN	A	507	1	11,11,12	0.47	0	15,15,17	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	B	507	1	11,11,12	0.46	0	15,15,17	0.67	0
3	NAG	B	502	1	14,14,15	0.43	0	17,19,21	0.80	0
4	MAN	B	506	1	11,11,12	0.51	0	15,15,17	0.76	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
4	MAN	B	503	1	-	1/2/19/22	0/1/1/1
4	MAN	A	503	1	-	0/2/19/22	0/1/1/1
4	MAN	A	505	1	-	0/2/19/22	0/1/1/1
4	MAN	B	505	1	-	0/2/19/22	0/1/1/1
3	NAG	A	502	1	-	0/6/23/26	0/1/1/1
6	GOL	A	910	-	-	4/4/4/4	-
4	MAN	A	504	1	-	2/2/19/22	0/1/1/1
4	MAN	A	506	1	-	0/2/19/22	0/1/1/1
4	MAN	B	509	1	-	1/2/19/22	0/1/1/1
6	GOL	B	910	-	-	2/4/4/4	-
3	NAG	A	501	1	-	1/6/23/26	0/1/1/1
4	MAN	A	509	1	-	0/2/19/22	0/1/1/1
4	MAN	B	508	1	-	0/2/19/22	0/1/1/1
4	MAN	A	508	1	-	0/2/19/22	0/1/1/1
3	NAG	B	501	1	-	2/6/23/26	0/1/1/1
4	MAN	B	504	1	-	2/2/19/22	0/1/1/1
4	MAN	A	507	1	-	0/2/19/22	0/1/1/1
4	MAN	B	507	1	-	0/2/19/22	0/1/1/1
3	NAG	B	502	1	-	0/6/23/26	0/1/1/1
4	MAN	B	506	1	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	505	MAN	C1-O5-C5	2.52	115.61	112.19
4	A	505	MAN	C1-O5-C5	2.30	115.30	112.19
4	A	509	MAN	C1-O5-C5	2.27	115.27	112.19
3	A	501	NAG	C1-O5-C5	2.24	115.23	112.19
4	B	506	MAN	C1-O5-C5	2.00	114.90	112.19



There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	910	GOL	C1-C2-C3-O3
6	B	910	GOL	C1-C2-C3-O3
4	A	504	MAN	O5-C5-C6-O6
4	B	504	MAN	O5-C5-C6-O6
4	A	504	MAN	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	MAN	1	0
4	A	503	MAN	1	0
6	B	910	GOL	1	0
3	B	501	NAG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	362/365 (99%)	-0.41	3 (0%) 82 84	5, 10, 16, 22	0
1	B	362/365 (99%)	-0.36	3 (0%) 82 84	5, 10, 17, 33	0
All	All	724/730 (99%)	-0.39	6 (0%) 82 84	5, 10, 17, 33	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	160	GLY	3.8
1	B	158	ASN	3.6
1	B	160	GLY	3.0
1	A	86	ALA	2.2
1	B	386	SER	2.1

### 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, 95<sup>th</sup> 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.

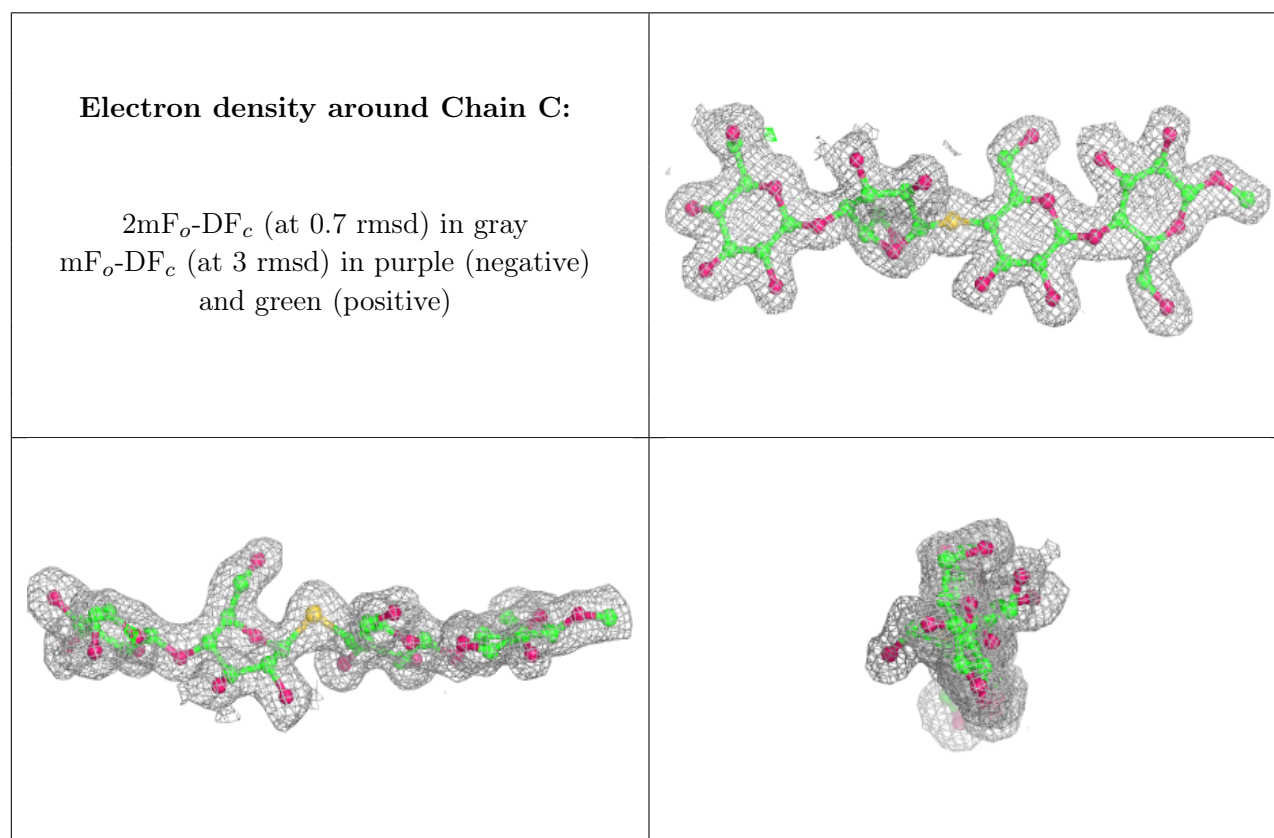
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MGL	C	1	13/13	0.94	0.07	8,10,11,12	0
2	GLC	D	3	11/12	0.95	0.06	6,8,10,13	0
2	MGL	D	1	13/13	0.96	0.06	8,10,13,13	0
2	GLC	C	3	11/12	0.97	0.05	7,7,8,9	0
2	GLC	C	4	11/12	0.97	0.05	6,8,8,8	0

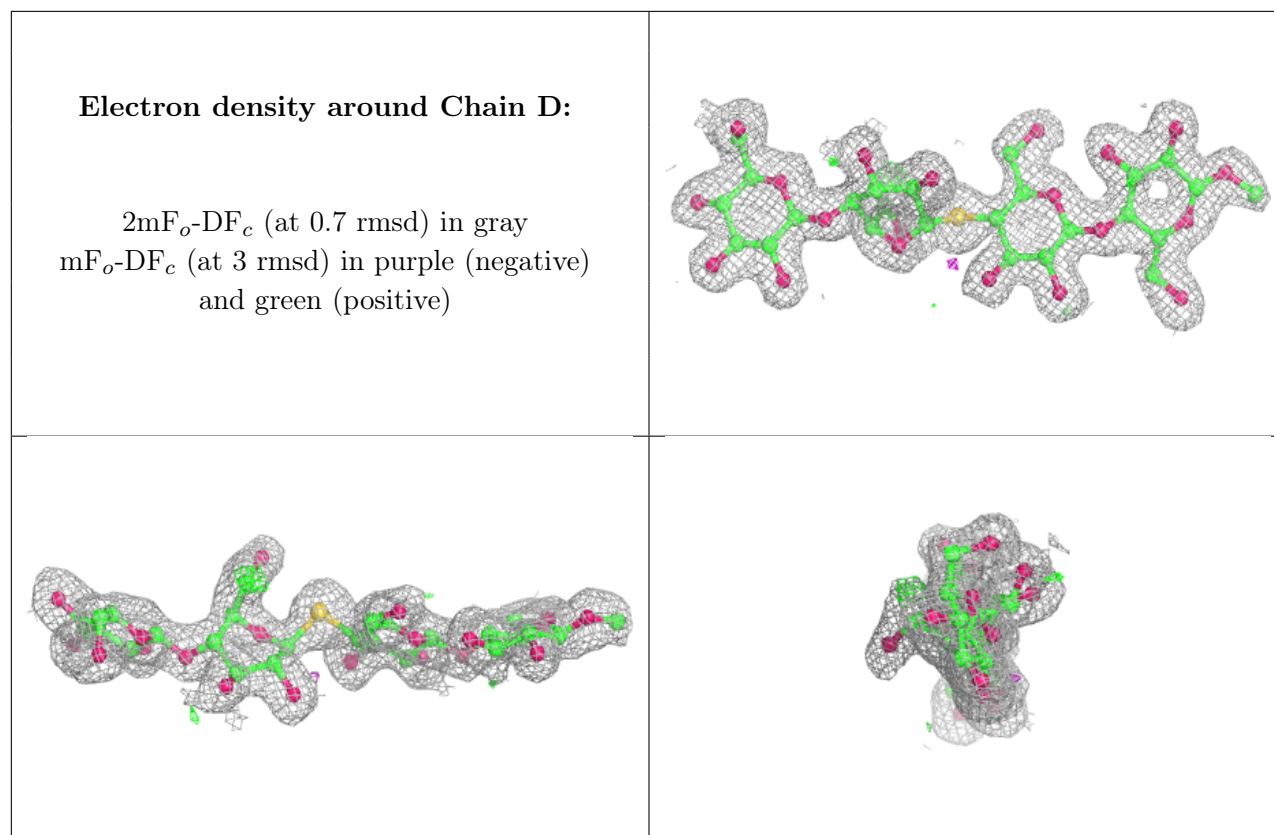
*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLC	D	4	11/12	0.97	0.04	5,6,7,7	0
2	SGC	C	2	11/12	0.98	0.04	6,7,8,11	0
2	SGC	D	2	11/12	0.98	0.05	5,8,9,12	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	MAN	A	503	11/12	0.28	0.22	32,35,36,37	0
4	MAN	B	503	11/12	0.37	0.18	31,34,36,37	0
3	NAG	B	501	14/15	0.56	0.18	31,34,35,35	0
4	MAN	B	504	11/12	0.58	0.16	24,28,29,31	0
3	NAG	A	501	14/15	0.61	0.17	33,35,36,37	0
4	MAN	B	509	11/12	0.67	0.13	27,30,31,32	0
4	MAN	A	504	11/12	0.75	0.12	23,26,27,29	0
6	GOL	B	910	6/6	0.77	0.20	20,21,23,26	0
6	GOL	A	910	6/6	0.82	0.12	16,18,20,23	0
4	MAN	B	506	11/12	0.84	0.10	14,16,18,20	0
4	MAN	A	507	11/12	0.86	0.09	17,19,20,20	0
4	MAN	B	507	11/12	0.87	0.08	16,18,19,20	0
4	MAN	A	509	11/12	0.91	0.08	18,19,20,21	0
3	NAG	B	502	14/15	0.92	0.07	13,15,16,16	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MAN	A	505	11/12	0.93	0.08	16,18,19,19	0
4	MAN	A	506	11/12	0.93	0.07	14,16,17,19	0
4	MAN	B	508	11/12	0.93	0.07	10,11,11,11	0
3	NAG	A	502	14/15	0.94	0.06	13,14,15,15	0
4	MAN	B	505	11/12	0.94	0.06	14,15,16,16	0
4	MAN	A	508	11/12	0.95	0.06	9,10,10,11	0
5	CD	B	895	1/1	0.99	0.03	21,21,21,21	0
5	CD	A	895	1/1	0.99	0.02	20,20,20,20	0
5	CD	A	896	1/1	0.99	0.08	32,32,32,32	0
5	CD	B	896	1/1	1.00	0.06	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.