



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 12, 2022 – 12:10 AM JST

PDB ID : 7X87  
Title : The complex structure of beta-1,2-glucosyltransferase from Ignavibacterium album with sophotetraose observed as sophorose  
Authors : Kobayashi, K.; Shimizu, H.; Tanaka, N.; Kuramochi, K.; Nakai, H.; Nakajima, M.; Taguchi, H.  
Deposited on : 2022-03-11  
Resolution : 1.79 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](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 following versions of software and data (see [references ⓘ](#)) 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 : 2.27  
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) : 2.27

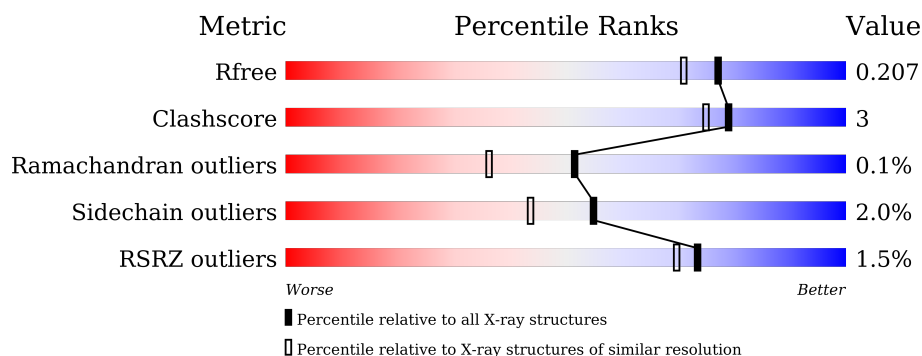
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.79 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))
$R_{free}$	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  $\geq 3$ , 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	724	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>90%</span> <span>7%</span> <span>.</span> </div> </div>
1	B	724	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>2%</span> <span>88%</span> <span>9%</span> <span>.</span> </div> </div>
2	F	2	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span></span> <span>100%</span> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12583 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-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	707	Total	C	N	O	S	0	0	0
			5845	3799	959	1071	16			
1	B	706	Total	C	N	O	S	0	1	0
			5848	3802	960	1070	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	343	GLN	GLU	engineered mutation	UNP I0AIT9
A	717	LEU	-	expression tag	UNP I0AIT9
A	718	GLU	-	expression tag	UNP I0AIT9
A	719	HIS	-	expression tag	UNP I0AIT9
A	720	HIS	-	expression tag	UNP I0AIT9
A	721	HIS	-	expression tag	UNP I0AIT9
A	722	HIS	-	expression tag	UNP I0AIT9
A	723	HIS	-	expression tag	UNP I0AIT9
A	724	HIS	-	expression tag	UNP I0AIT9
B	343	GLN	GLU	engineered mutation	UNP I0AIT9
B	717	LEU	-	expression tag	UNP I0AIT9
B	718	GLU	-	expression tag	UNP I0AIT9
B	719	HIS	-	expression tag	UNP I0AIT9
B	720	HIS	-	expression tag	UNP I0AIT9
B	721	HIS	-	expression tag	UNP I0AIT9
B	722	HIS	-	expression tag	UNP I0AIT9
B	723	HIS	-	expression tag	UNP I0AIT9
B	724	HIS	-	expression tag	UNP I0AIT9

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



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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	B	3	Total	Ca	0	0
			3	3		

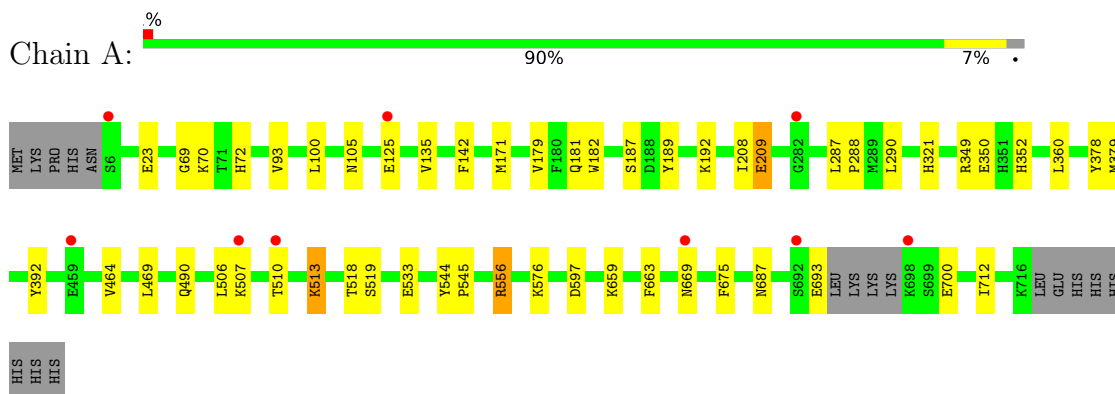
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	453	Total	O	0	0
			453	453		
4	B	410	Total	O	0	0
			410	410		

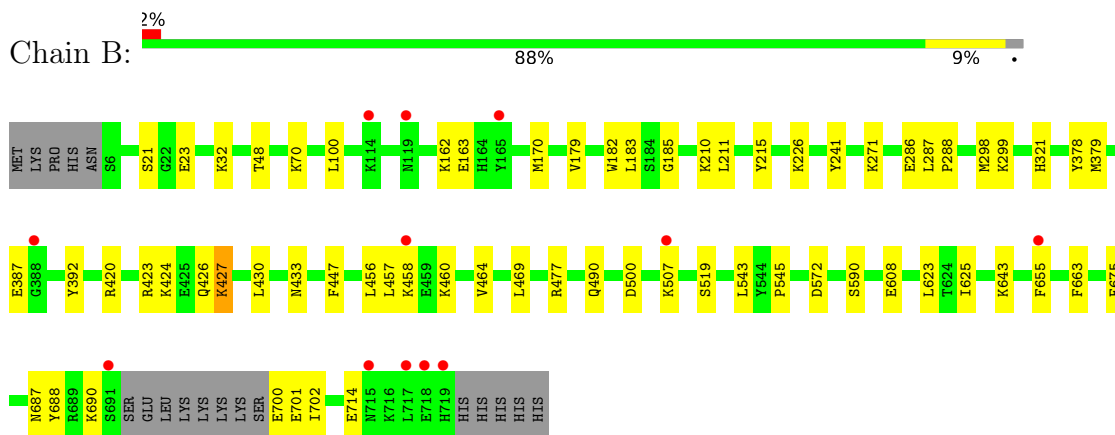
### 3 Residue-property plots

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.

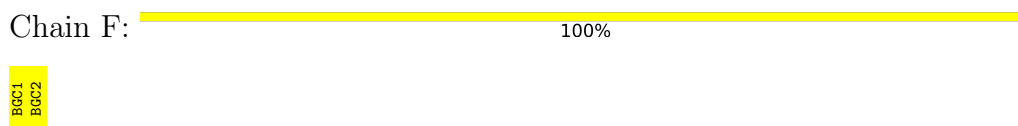
#### • Molecule 1: Beta-galactosidase



#### • Molecule 1: Beta-galactosidase



#### • Molecule 2: beta-D-glucopyranose-(1-2)-beta-D-glucopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	165.13Å 71.61Å 130.31Å 90.00° 104.89° 90.00°	Depositor
Resolution (Å)	47.91 – 1.79 44.21 – 1.79	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.91-1.79) 100.0 (44.21-1.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.97 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.166 , 0.201 0.177 , 0.207	Depositor DCC
$R_{free}$ test set	6808 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.3	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 44.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12583	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.76	3/5995 (0.1%)	0.83	1/8094 (0.0%)
1	B	0.74	0/5999	0.84	4/8101 (0.0%)
All	All	0.75	3/11994 (0.0%)	0.84	5/16195 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	209	GLU	CD-OE1	8.41	1.34	1.25
1	A	209	GLU	CD-OE2	6.40	1.32	1.25
1	A	181	GLN	C-O	5.33	1.33	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	423	ARG	NE-CZ-NH2	-6.95	116.82	120.30
1	B	215	TYR	CB-CG-CD1	5.42	124.25	121.00
1	A	392	TYR	CB-CA-C	-5.34	99.72	110.40
1	B	423	ARG	CG-CD-NE	-5.22	100.83	111.80
1	B	423	ARG	NE-CZ-NH1	5.05	122.82	120.30

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	5845	0	5782	31	0
1	B	5848	0	5780	35	0
2	F	23	0	21	0	0
3	A	1	0	0	0	0
3	B	3	0	0	0	0
4	A	453	0	0	7	0
4	B	410	0	0	6	0
All	All	12583	0	11583	65	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 3.

All (65) 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:623:LEU:HD11	1:B:625:ILE:HD11	1.45	0.95
1:A:105:ASN:OD1	4:A:901:HOH:O	2.01	0.77
1:A:187:SER:HB2	4:A:907:HOH:O	1.87	0.75
1:B:170:MET:HG2	1:B:271:LYS:HB3	1.76	0.66
1:B:182:TRP:CE2	1:B:456:LEU:HD22	2.33	0.64
1:A:187:SER:CB	4:A:907:HOH:O	2.44	0.60
1:B:500:ASP:OD2	4:B:901:HOH:O	2.16	0.60
1:B:543:LEU:HD23	1:B:625:ILE:HD12	1.82	0.60
1:A:576:LYS:HD3	1:B:392:TYR:O	2.02	0.59
1:A:70:LYS:HE2	1:A:70:LYS:HA	1.85	0.59
1:A:513:LYS:CE	4:A:1048:HOH:O	2.51	0.58
1:A:100:LEU:HD21	1:A:179:VAL:HG11	1.88	0.55
1:B:424:LYS:HE2	4:B:1132:HOH:O	2.06	0.53
1:B:100:LEU:HD21	1:B:179:VAL:HG11	1.90	0.53
1:A:349:ARG:HG3	1:A:350:GLU:HG3	1.91	0.53
1:B:623:LEU:HD11	1:B:625:ILE:CD1	2.27	0.52
1:B:211:LEU:C	1:B:211:LEU:HD23	2.29	0.52
1:B:663:PHE:HA	1:B:675:PHE:O	2.12	0.50
1:A:209:GLU:HG3	4:A:1263:HOH:O	2.13	0.49
1:A:519:SER:O	1:A:545:PRO:HD2	2.13	0.48
1:B:183:LEU:HA	1:B:456:LEU:HD23	1.94	0.48
1:B:163:GLU:HB2	4:B:941:HOH:O	2.13	0.48
1:B:185:GLY:HA3	1:B:457:LEU:HD13	1.96	0.48
1:A:464:VAL:HB	1:A:469:LEU:HB2	1.96	0.47
1:B:420:ARG:NH1	4:B:908:HOH:O	2.32	0.47
1:B:21:SER:HA	1:B:48:THR:O	2.15	0.47
1:A:23:GLU:HG2	1:A:379:MET:SD	2.55	0.47

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:GLU:HG3	1:A:189:TYR:CE2	2.51	0.46
1:B:464:VAL:HB	1:B:469:LEU:HB2	1.97	0.46
1:A:518:THR:HA	1:A:544:TYR:O	2.16	0.46
1:B:321:HIS:HA	1:B:490:GLN:OE1	2.16	0.46
1:A:687:ASN:HA	1:A:700:GLU:O	2.16	0.46
1:B:23:GLU:HG2	1:B:379:MET:SD	2.57	0.45
1:B:543:LEU:HB3	1:B:625:ILE:HD13	1.98	0.45
1:B:298:MET:O	4:B:902:HOH:O	2.21	0.45
1:B:519:SER:O	1:B:545:PRO:HD2	2.17	0.45
1:A:350:GLU:HB3	1:A:352:HIS:CE1	2.52	0.44
1:A:663:PHE:HA	1:A:675:PHE:O	2.16	0.44
1:A:69:GLY:HA2	1:A:72:HIS:O	2.18	0.44
1:B:426:GLN:HE21	1:B:427:LYS:NZ	2.15	0.44
1:B:690:LYS:NZ	1:B:714:GLU:OE2	2.36	0.44
1:A:321:HIS:HA	1:A:490:GLN:OE1	2.18	0.44
1:A:287:LEU:N	1:A:288:PRO:CD	2.81	0.43
1:B:299:LYS:HE3	1:B:299:LYS:HB2	1.81	0.43
1:B:543:LEU:HD23	1:B:625:ILE:CD1	2.49	0.43
1:B:433:ASN:HB3	4:B:943:HOH:O	2.19	0.42
1:B:655:PHE:O	1:B:688:TYR:HA	2.19	0.42
1:B:378:TYR:HA	1:B:379:MET:HA	1.83	0.42
1:B:608:GLU:HA	1:B:608:GLU:OE1	2.19	0.42
1:A:506:LEU:O	1:A:510:THR:HG23	2.19	0.42
1:B:287:LEU:N	1:B:288:PRO:CD	2.82	0.42
1:A:135:VAL:HG21	1:A:142:PHE:CE1	2.54	0.42
1:A:513:LYS:HE2	4:A:1048:HOH:O	2.19	0.42
1:A:93:VAL:O	1:A:171:MET:HA	2.19	0.41
1:A:182:TRP:CD2	1:A:290:LEU:HD11	2.55	0.41
1:A:556:ARG:HG2	4:A:990:HOH:O	2.19	0.41
1:B:182:TRP:NE1	1:B:456:LEU:HD22	2.35	0.41
1:B:572:ASP:OD1	1:B:590[A]:SER:OG	2.32	0.41
1:A:208:ILE:HD12	1:A:208:ILE:HA	1.96	0.41
1:B:430:LEU:HD23	1:B:430:LEU:HA	1.95	0.41
1:A:360:LEU:HD23	1:A:360:LEU:HA	1.93	0.41
1:A:378:TYR:HA	1:A:379:MET:HA	1.79	0.40
1:A:712:ILE:HD12	1:A:712:ILE:N	2.35	0.40
1:B:447:PHE:CD2	1:B:477:ARG:HD2	2.57	0.40
1:A:70:LYS:HA	1:A:70:LYS:CE	2.49	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	703/724 (97%)	681 (97%)	22 (3%)	0	100	100
1	B	703/724 (97%)	681 (97%)	21 (3%)	1 (0%)	51	36
All	All	1406/1448 (97%)	1362 (97%)	43 (3%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	387	GLU

### 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	640/657 (97%)	631 (99%)	9 (1%)	67	59
1	B	640/657 (97%)	624 (98%)	16 (2%)	47	34
All	All	1280/1314 (97%)	1255 (98%)	25 (2%)	55	44

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	192	LYS
1	A	507	LYS
1	A	513	LYS
1	A	533	GLU
1	A	556	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	597	ASP
1	A	659	LYS
1	A	669	ASN
1	A	693	GLU
1	B	32	LYS
1	B	70	LYS
1	B	162	LYS
1	B	210	LYS
1	B	226	LYS
1	B	241	TYR
1	B	286	GLU
1	B	427	LYS
1	B	458	LYS
1	B	460	LYS
1	B	507	LYS
1	B	643	LYS
1	B	687	ASN
1	B	700	GLU
1	B	701	GLU
1	B	702	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	599	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 ⓘ

2 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	F	1	2	12,12,12	1.10	1 (8%)	17,17,17	1.37	4 (23%)
2	BGC	F	2	2	11,11,12	0.74	0	15,15,17	1.23	2 (13%)

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	F	1	2	-	0/2/22/22	0/1/1/1
2	BGC	F	2	2	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1	BGC	O1-C1	2.16	1.46	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	BGC	O5-C5-C6	-3.27	102.07	107.20
2	F	1	BGC	O2-C2-C3	-2.40	104.79	110.35
2	F	1	BGC	O4-C4-C5	2.26	114.90	109.30
2	F	2	BGC	C1-C2-C3	2.14	112.29	109.67
2	F	1	BGC	O3-C3-C2	-2.08	105.53	110.35
2	F	1	BGC	O1-C1-C2	2.02	114.73	109.03

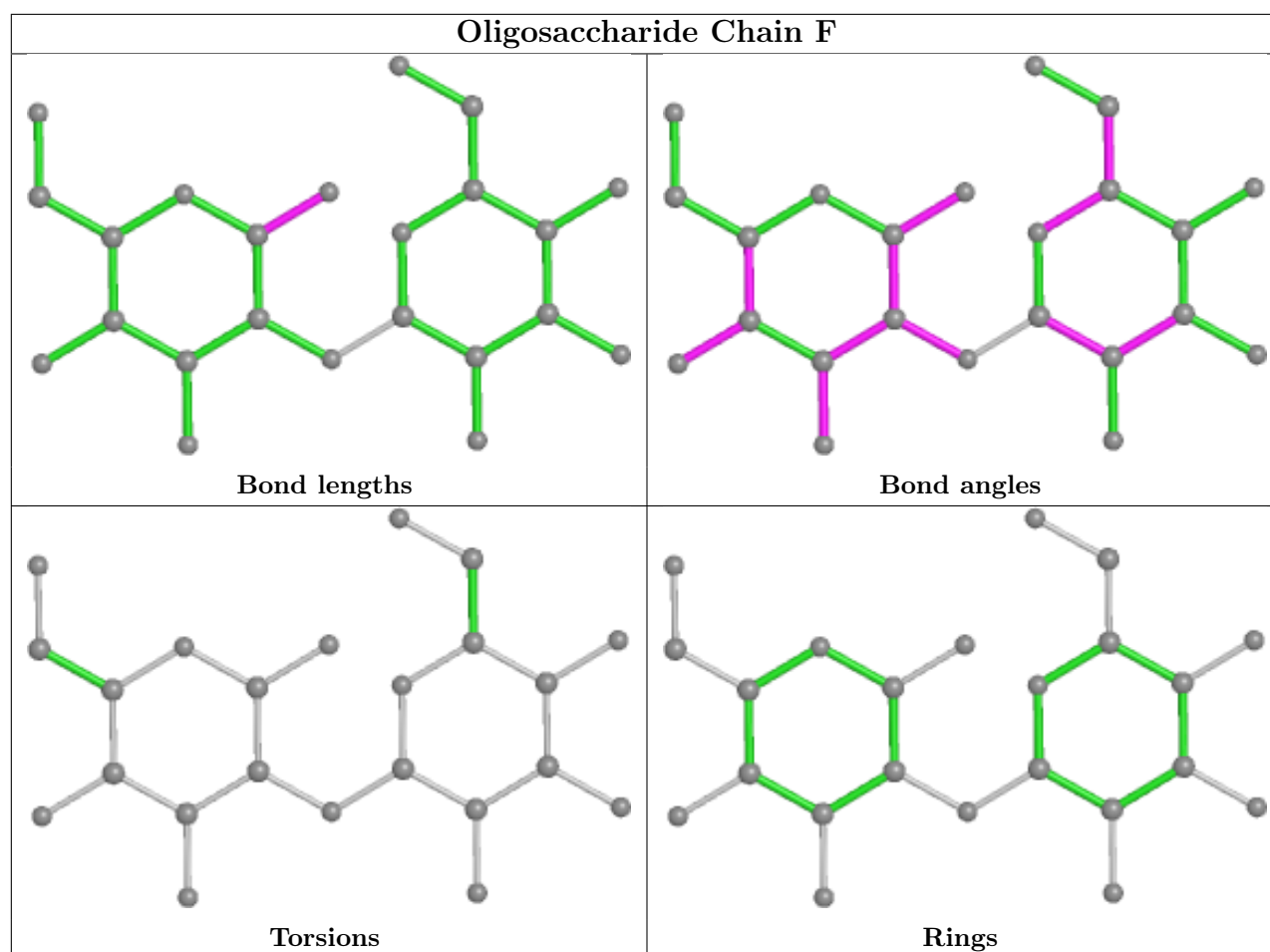
There are no chirality outliers.

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

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, 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	707/724 (97%)	-0.20	9 (1%) 77 74	8, 15, 34, 59	0
1	B	706/724 (97%)	-0.18	12 (1%) 70 66	9, 17, 35, 59	0
All	All	1413/1448 (97%)	-0.19	21 (1%) 73 70	8, 16, 34, 59	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	717	LEU	5.8
1	B	165	TYR	3.8
1	A	692	SER	3.2
1	B	718	GLU	3.2
1	B	719	HIS	3.0
1	A	507	LYS	2.9
1	A	698	LYS	2.5
1	B	715	ASN	2.5
1	B	388	GLY	2.4
1	A	669	ASN	2.4
1	A	510	THR	2.4
1	B	507	LYS	2.3
1	A	459	GLU	2.3
1	A	125	GLU	2.3
1	B	114	LYS	2.3
1	A	6	SER	2.3
1	B	458	LYS	2.2
1	B	119	ASN	2.2
1	B	691	SER	2.1
1	B	655	PHE	2.1
1	A	282	GLY	2.0

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

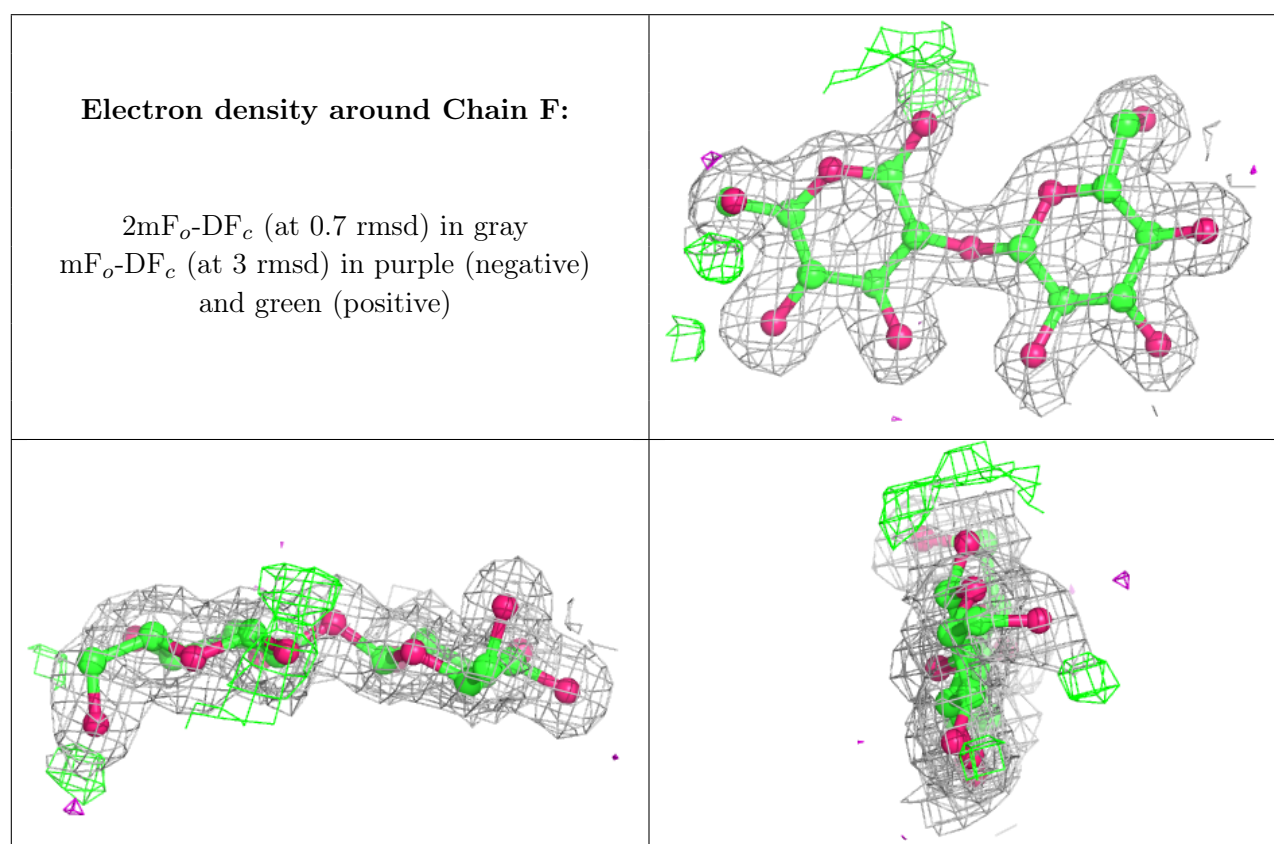
There are no non-standard protein/DNA/RNA residues in this entry.

## 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, 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	BGC	F	1	12/12	0.92	0.10	18,20,26,34	0
2	BGC	F	2	11/12	0.96	0.08	13,14,16,17	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
3	CA	B	802	1/1	0.89	0.20	69,69,69,69	0
3	CA	B	803	1/1	0.97	0.18	42,42,42,42	0
3	CA	A	801	1/1	0.99	0.05	22,22,22,22	0
3	CA	B	801	1/1	0.99	0.05	14,14,14,14	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.