



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 26, 2022 – 12:10 PM JST

PDB ID : 6JG1  
Title : Crystal structure of barley exohydrolaseI wildtype in complex with 4I,4III,4V  
-S-trithiocellohexaose  
Authors : Luang, S.; Streltsov, V.A.; Hrmova, M.  
Deposited on : 2019-02-13  
Resolution : 1.78 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>.

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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	:	2.31.2
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)	:	2.31.2

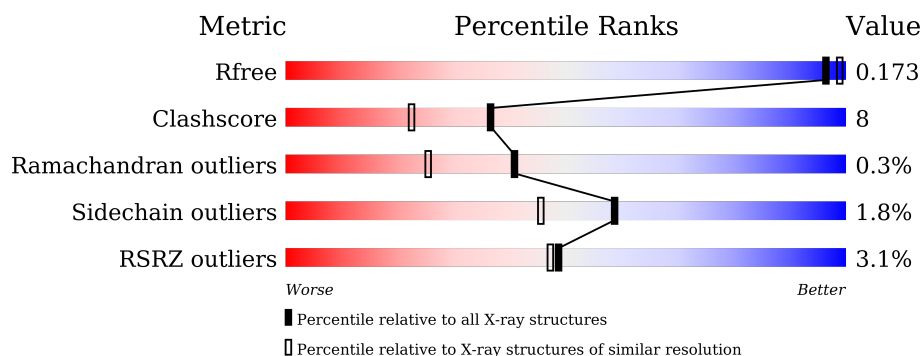
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.78 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	609	<div> <div>3%</div> <div> <div></div> <div>84%</div> <div>13%</div> <div>.</div> </div> </div>
2	B	3	<div> <div>100%</div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5347 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 Barley exohydrolase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	606	4628	2929	801	870	28	0	11	0

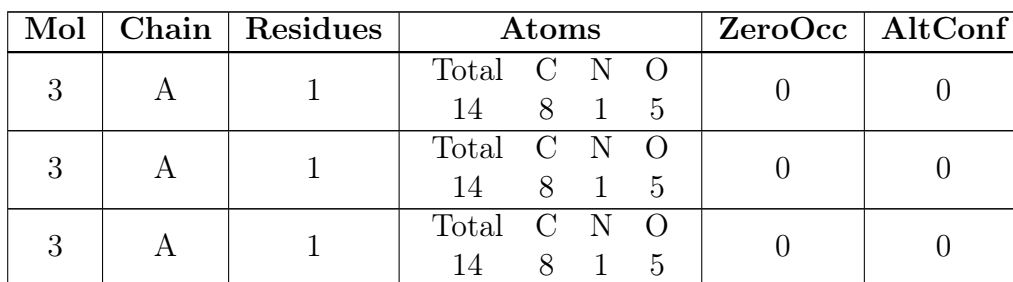
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	HIS	-	expression tag	UNP A0A287SCR5
A	-2	HIS	-	expression tag	UNP A0A287SCR5
A	-1	ALA	-	expression tag	UNP A0A287SCR5
A	0	ALA	-	expression tag	UNP A0A287SCR5
A	320	LYS	ASN	See sequence details	UNP A0A287SCR5

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	O	S			
2	B	3	35	18	15	2	0	1	0

- 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>).



- # 1PE
- 
- Chemical structure of 1PE (1,3,5,7-tetrahydroxyheptane) showing a zigzag chain of seven carbon atoms (C12 to C18) with hydroxyl groups (OH) attached to each. The carbons are labeled C12, C22, C23, C13, C24, C14, C25, C15, C26, and C16. The hydroxyl groups are labeled OH2, OH3, OH4, OH5, and OH7. The structure is drawn in a zigzag pattern with red oxygen atoms and black carbon atoms.

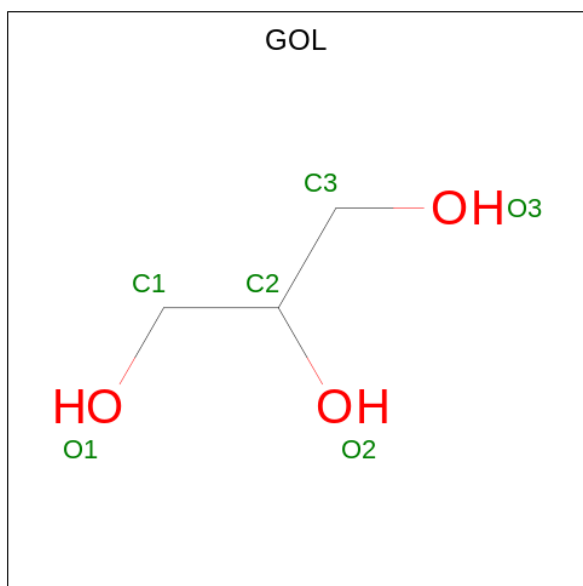
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		



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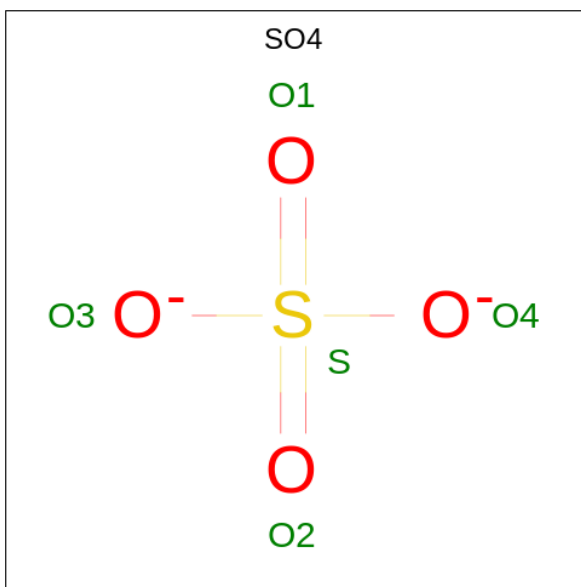
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			5	3	2		
4	A	1	Total	C	O	0	0
			5	3	2		
4	A	1	Total	C	O	0	0
			7	4	3		
4	A	1	Total	C	O	0	1
			11	6	5		
4	A	1	Total	C	O	0	0
			5	3	2		
4	A	1	Total	C	O	0	0
			5	3	2		
4	A	1	Total	C	O	0	1
			19	12	7		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

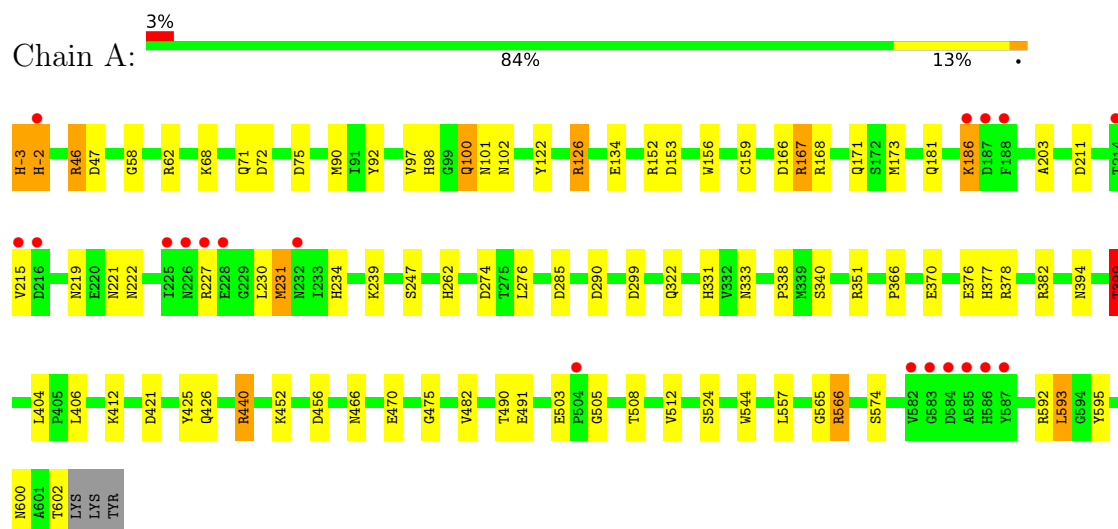
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	545	Total	O	0	0
			545	545		

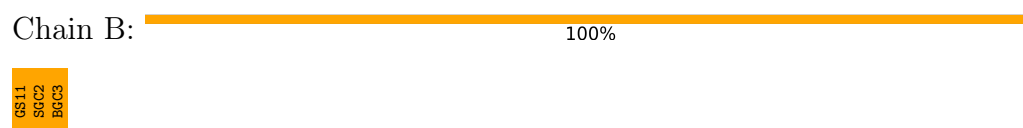
### 3 Residue-property plots

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: Barley exohydrolase I



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.76Å 99.76Å 183.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.17 – 1.78 48.13 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.17-1.78) 99.9 (48.13-1.78)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.96 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.136 , 0.164 0.148 , 0.173	Depositor DCC
$R_{free}$ test set	4447 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.7	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 50.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5347	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: SGC, GS1, GOL, SO4, BGC, NAG, 1PE

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	1.17	8/4784 (0.2%)	1.26	47/6496 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	503	GLU	CD-OE2	12.22	1.39	1.25
1	A	426	GLN	CB-CG	-7.02	1.33	1.52
1	A	126	ARG	CD-NE	-6.69	1.35	1.46
1	A	399	THR	CB-CG2	-6.32	1.31	1.52
1	A	333	ASN	CG-ND2	5.69	1.47	1.32

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	ARG	NE-CZ-NH1	20.76	130.68	120.30
1	A	126	ARG	NE-CZ-NH2	-20.00	110.30	120.30
1	A	68	LYS	CD-CE-NZ	11.57	138.32	111.70
1	A	46	ARG	NE-CZ-NH2	10.20	125.40	120.30
1	A	452	LYS	CD-CE-NZ	-9.96	88.80	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	-3	HIS	Peptide

## 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	4628	0	4621	64	0
2	B	35	0	27	7	0
3	A	42	0	39	8	0
4	A	64	0	54	7	0
5	A	18	0	24	4	0
6	A	15	0	0	0	0
7	A	545	0	0	22	0
All	All	5347	0	4765	75	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 8.

The worst 5 of 75 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:600:ASN:HD21	3:A:703:NAG:C1	1.10	1.58
1:A:221:ASN:ND2	3:A:702:NAG:C1	1.72	1.48
1:A:600:ASN:ND2	3:A:703:NAG:C1	1.94	1.30
7:A:805:HOH:O	2:B:1:GS1:H5	0.98	1.14
1:A:394:ASN:HD21	1:A:404:LEU:H	1.17	0.91

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	615/609 (101%)	597 (97%)	16 (3%)	2 (0%)	41	25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-2	HIS
1	A	505	GLY

### 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	498/490 (102%)	489 (98%)	9 (2%)	59	45

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

Mol	Chain	Res	Type
1	A	440	ARG
1	A	593	LEU
1	A	186	LYS
1	A	227	ARG
1	A	290	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	377	HIS
1	A	600	ASN
1	A	181	GLN
1	A	199	ASN
1	A	219	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues 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$
3	NAG	A	702	-	14,14,15	0.56	0	17,19,21	2.81	5 (29%)
3	NAG	A	703	-	14,14,15	0.89	0	17,19,21	1.03	0
3	NAG	A	701	-	14,14,15	0.79	0	17,19,21	1.66	3 (17%)

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
3	NAG	A	702	-	-	0/6/23/26	0/1/1/1
3	NAG	A	703	-	-	0/6/23/26	0/1/1/1
3	NAG	A	701	-	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	NAG	O5-C1-C2	7.39	122.96	111.29
3	A	702	NAG	C1-O5-C5	4.76	118.64	112.19
3	A	701	NAG	O5-C5-C6	4.31	113.96	107.20
3	A	702	NAG	C1-C2-N2	3.65	116.73	110.49
3	A	702	NAG	C3-C4-C5	3.44	116.38	110.24

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	NAG	3	0
3	A	703	NAG	5	0

## 5.5 Carbohydrates [i](#)

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	GS1	B	1	2	11,12,12	0.75	0	15,17,17	1.30	1 (6%)
2	SGC	B	2[A]	-	10,11,12	2.38	4 (40%)	12,15,17	2.24	4 (33%)
2	SGC	B	2[B]	-	10,11,12	2.34	4 (40%)	12,15,17	2.41	5 (41%)
2	BGC	B	3	2	11,11,12	0.89	0	15,15,17	3.44	7 (46%)

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	GS1	B	1	2	-	1/2/22/22	0/1/1/1
2	SGC	B	2[A]	-	-	0/2/19/22	0/1/1/1
2	SGC	B	2[B]	-	-	2/2/19/22	0/1/1/1
2	BGC	B	3	2	-	0/2/19/22	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2[A]	SGC	C5-C4	4.49	1.56	1.53
2	B	2[B]	SGC	C5-C4	4.49	1.56	1.53
2	B	2[A]	SGC	O5-C5	3.64	1.50	1.43
2	B	2[B]	SGC	O5-C5	3.64	1.50	1.43
2	B	2[A]	SGC	C6-C5	3.20	1.62	1.51

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	BGC	C1-O5-C5	9.06	124.47	112.19
2	B	3	BGC	O5-C1-C2	5.63	119.46	110.77
2	B	2[A]	SGC	O5-C5-C6	5.41	115.68	107.20
2	B	2[B]	SGC	O5-C5-C6	5.41	115.68	107.20
2	B	3	BGC	C1-C2-C3	4.47	115.16	109.67

There are no chirality outliers.

All (3) torsion outliers are listed below:

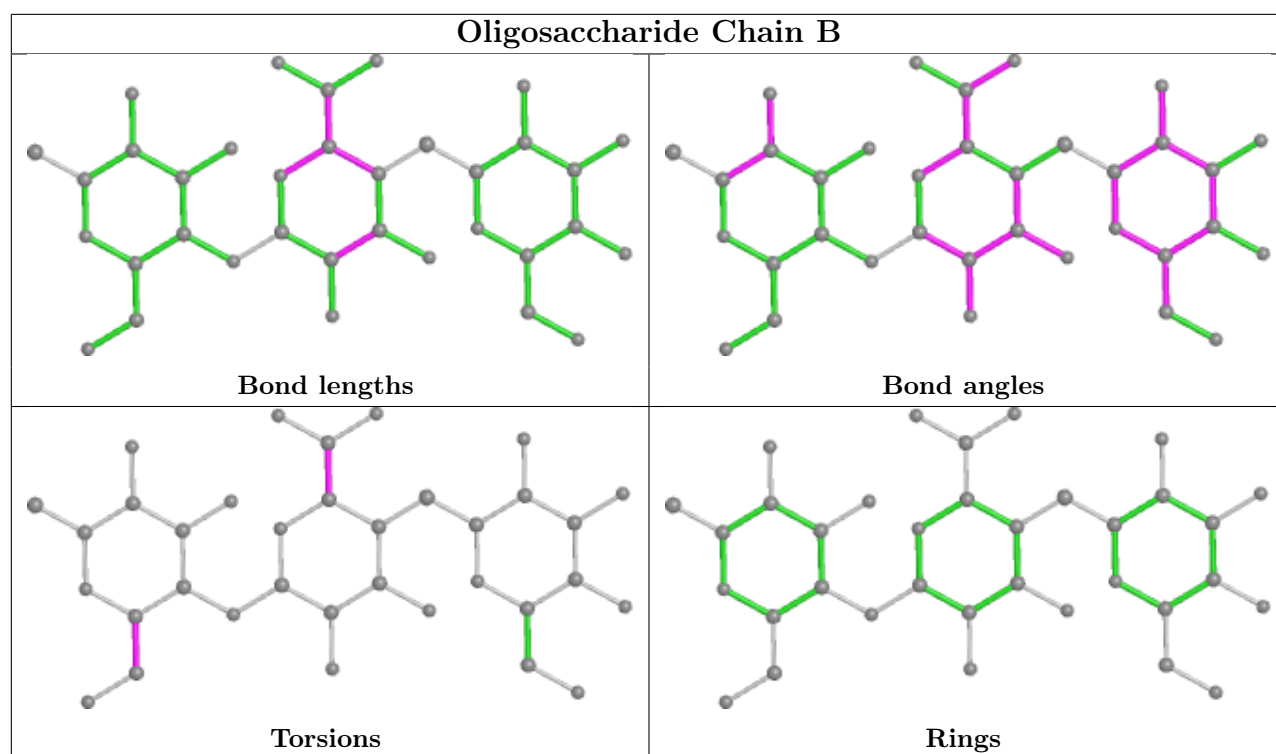
Mol	Chain	Res	Type	Atoms
2	B	2[B]	SGC	O5-C5-C6-O6
2	B	2[B]	SGC	C4-C5-C6-O6
2	B	1	GS1	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2[B]	SGC	2	0
2	B	1	GS1	5	0
2	B	3	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.



## 5.6 Ligand geometry [i](#)

19 ligands 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	$\# Z  > 2$
4	1PE	A	707	-	6,6,15	0.83	0	5,5,14	0.66	0
4	1PE	A	710	-	4,4,15	1.38	1 (25%)	3,3,14	0.76	0
4	1PE	A	711[A]	-	15,15,15	1.22	0	14,14,14	1.63	4 (28%)
5	GOL	A	712	-	5,5,5	0.64	0	5,5,5	0.90	0
6	SO4	A	716	-	4,4,4	0.55	0	6,6,6	0.75	0
3	NAG	A	701	-	14,14,15	0.79	0	17,19,21	1.66	3 (17%)
4	1PE	A	708[B]	-	9,9,15	0.47	0	8,8,14	1.55	1 (12%)
3	NAG	A	702	-	14,14,15	0.56	0	17,19,21	2.81	5 (29%)
4	1PE	A	711[B]	-	15,15,15	1.19	0	14,14,14	1.57	3 (21%)
5	GOL	A	713	-	5,5,5	0.35	0	5,5,5	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GOL	A	714	-	5,5,5	0.18	0	5,5,5	0.96	0
4	1PE	A	709	-	4,4,15	0.63	0	3,3,14	0.33	0
4	1PE	A	704	-	6,6,15	0.46	0	5,5,14	0.68	0
6	SO4	A	715	-	4,4,4	0.44	0	6,6,6	0.84	0
4	1PE	A	706	-	4,4,15	0.68	0	3,3,14	0.35	0
3	NAG	A	703	-	14,14,15	0.89	0	17,19,21	1.03	0
6	SO4	A	717	-	4,4,4	0.39	0	6,6,6	0.94	0
4	1PE	A	708[A]	-	9,9,15	0.49	0	8,8,14	1.26	1 (12%)
4	1PE	A	705	-	4,4,15	1.04	0	3,3,14	0.89	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
5	GOL	A	713	-	-	2/4/4/4	-
4	1PE	A	704	-	-	1/4/4/13	-
4	1PE	A	707	-	-	1/4/4/13	-
4	1PE	A	710	-	-	1/2/2/13	-
4	1PE	A	711[A]	-	-	9/13/13/13	-
4	1PE	A	708[B]	-	-	4/7/7/13	-
4	1PE	A	706	-	-	1/2/2/13	-
3	NAG	A	703	-	-	0/6/23/26	0/1/1/1
5	GOL	A	714	-	-	2/4/4/4	-
4	1PE	A	709	-	-	0/2/2/13	-
3	NAG	A	702	-	-	0/6/23/26	0/1/1/1
5	GOL	A	712	-	-	2/4/4/4	-
4	1PE	A	711[B]	-	-	10/13/13/13	-
4	1PE	A	708[A]	-	-	4/7/7/13	-
4	1PE	A	705	-	-	0/2/2/13	-
3	NAG	A	701	-	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	710	1PE	OH3-C22	2.24	1.53	1.40

The worst 5 of 17 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	NAG	O5-C1-C2	7.39	122.96	111.29
3	A	702	NAG	C1-O5-C5	4.76	118.64	112.19
3	A	701	NAG	O5-C5-C6	4.31	113.96	107.20
4	A	708[B]	1PE	OH2-C12-C22	-3.79	89.84	111.81
3	A	702	NAG	C1-C2-N2	3.65	116.73	110.49

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	712	GOL	C1-C2-C3-O3
4	A	711[A]	1PE	C13-C23-OH3-C22
4	A	711[B]	1PE	C13-C23-OH3-C22
4	A	711[A]	1PE	C14-C24-OH4-C13
4	A	711[B]	1PE	C14-C24-OH4-C13

There are no ring outliers.

7 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	710	1PE	5	0
5	A	712	GOL	1	0
3	A	702	NAG	3	0
5	A	713	GOL	3	0
4	A	709	1PE	1	0
3	A	703	NAG	5	0
4	A	705	1PE	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	606/609 (99%)	-0.23	19 (3%)	49 47	12, 19, 36, 62	4 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	585	ALA	5.7
1	A	187	ASP	4.3
1	A	186	LYS	4.0
1	A	582	VAL	3.9
1	A	586	HIS	3.7

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

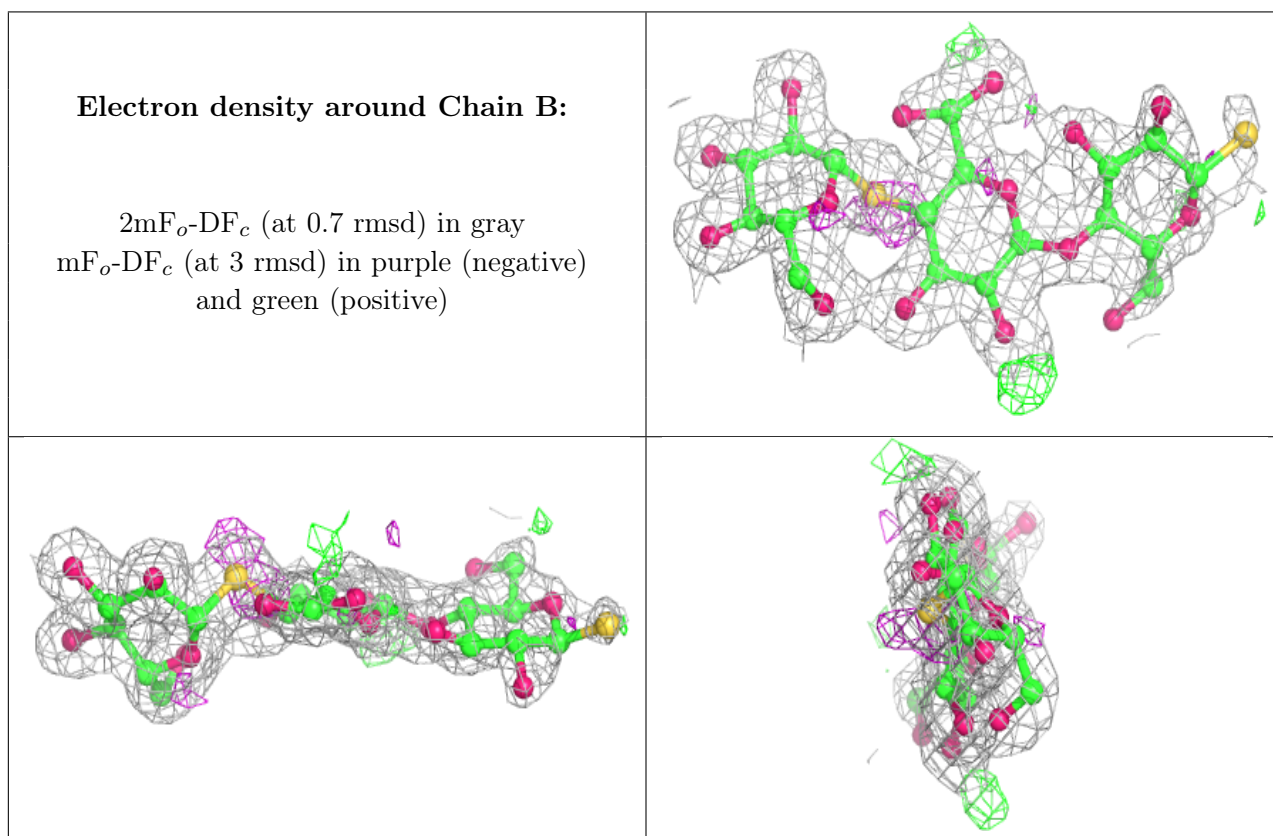
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
3	NAG	A	703	14/15	0.78	0.19	52,60,64,70	0
3	NAG	A	702	14/15	0.79	0.20	46,54,68,77	14
3	NAG	A	701	14/15	0.90	0.29	43,50,60,60	0

### 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( $\text{\AA}^2$ )	Q<0.9
2	GS1	B	1	12/12	0.83	0.15	39,52,58,69	11
2	SGC	B	2[A]	11/12	0.92	0.12	21,29,31,34	1
2	SGC	B	2[B]	11/12	0.92	0.12	21,28,31,34	1
2	BGC	B	3	11/12	0.96	0.08	20,23,26,28	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 ⓘ

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( $\text{\AA}^2$ )	Q<0.9
4	1PE	A	706	5/16	0.73	0.15	56,57,66,71	0
4	1PE	A	707	7/16	0.76	0.16	44,50,64,68	0
4	1PE	A	711[A]	16/16	0.76	0.23	27,49,65,67	3
4	1PE	A	711[B]	16/16	0.76	0.23	36,49,65,67	3
3	NAG	A	703	14/15	0.78	0.19	52,60,64,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	A	702	14/15	0.79	0.20	46,54,68,77	14
5	GOL	A	712	6/6	0.79	0.30	50,53,65,66	0
5	GOL	A	713	6/6	0.85	0.28	62,69,75,81	0
4	1PE	A	709	5/16	0.86	0.15	54,59,63,70	0
4	1PE	A	710	5/16	0.86	0.17	24,26,43,49	0
4	1PE	A	704	7/16	0.87	0.15	49,53,57,59	0
6	SO4	A	717	5/5	0.87	0.16	36,42,45,45	5
4	1PE	A	705	5/16	0.88	0.17	35,36,55,64	0
4	1PE	A	708[B]	10/16	0.89	0.12	35,40,48,49	1
5	GOL	A	714	6/6	0.89	0.28	54,61,67,68	0
4	1PE	A	708[A]	10/16	0.89	0.12	34,40,48,49	1
3	NAG	A	701	14/15	0.90	0.29	43,50,60,60	0
6	SO4	A	716	5/5	0.92	0.13	31,35,44,45	5
6	SO4	A	715	5/5	0.94	0.13	32,33,40,41	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.