



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 08:54 AM BST

PDB ID : 3EII  
Title : Zinc-bound glycoside hydrolase 61 E from Thielavia terrestris  
Authors : Salbo, R.; Welner, D.; Lo Leggio, L.; Harris, P.; McFarland, K.  
Deposited on : 2008-09-16  
Resolution : 2.25 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.

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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 : 2.13.1  
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) : 2.13.1

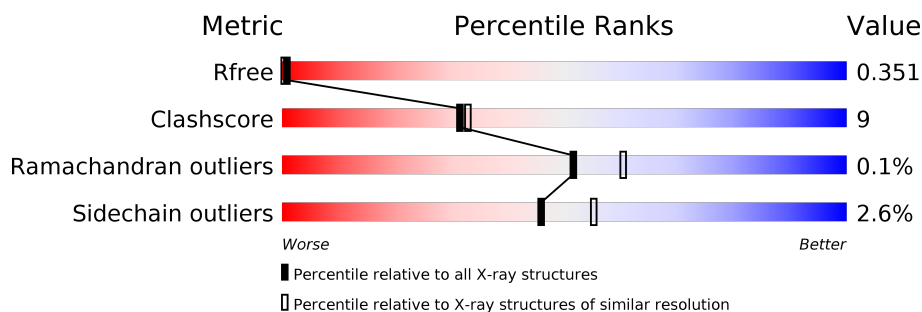
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)

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 on 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	208	<div> <div style="width: 83%;"></div> <div style="width: 17%;"></div> </div> <div>83%17%</div>
1	B	208	<div> <div style="width: 78%;"></div> <div style="width: 21%;"></div> </div> <div>78%21%</div>
1	C	208	<div> <div style="width: 84%;"></div> <div style="width: 15%;"></div> </div> <div>84%15%</div>
1	D	208	<div> <div style="width: 82%;"></div> <div style="width: 18%;"></div> </div> <div>82%18%</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
5	GOL	C	2647	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7221 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 protein GH61E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1599	1025	265	304	5			
1	B	208	Total	C	N	O	S	0	0	0
			1599	1025	265	304	5			
1	C	208	Total	C	N	O	S	0	0	0
			1599	1025	265	304	5			
1	D	208	Total	C	N	O	S	0	0	0
			1599	1025	265	304	5			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

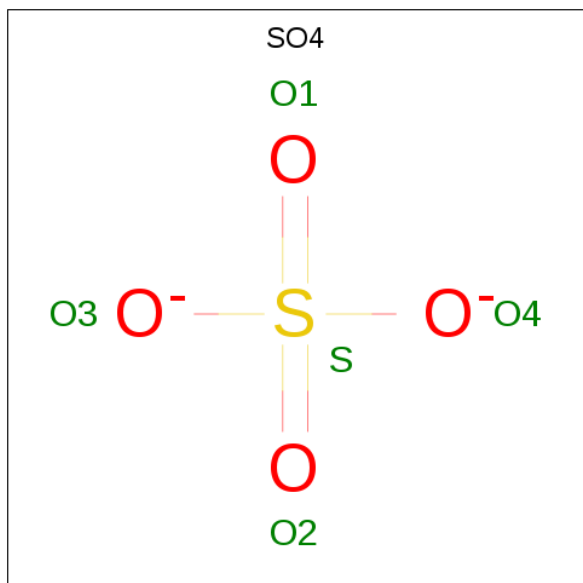
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	C	2	Total	Zn	0	0
			2	2		

- 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>).



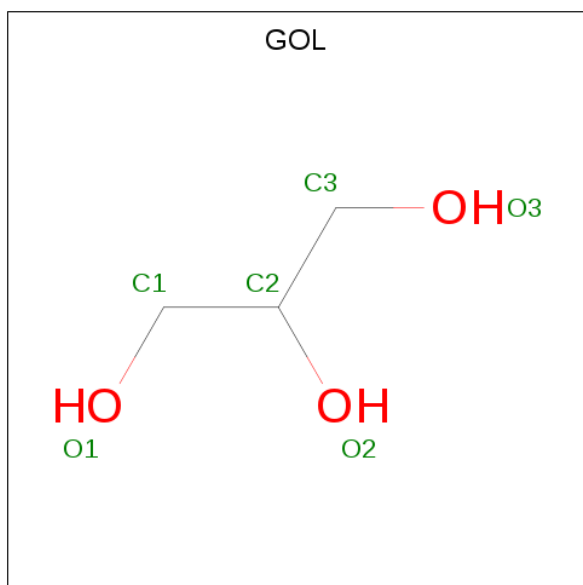
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

- Molecule 5 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
5	C	1	Total C O 6 3 3	0	0

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

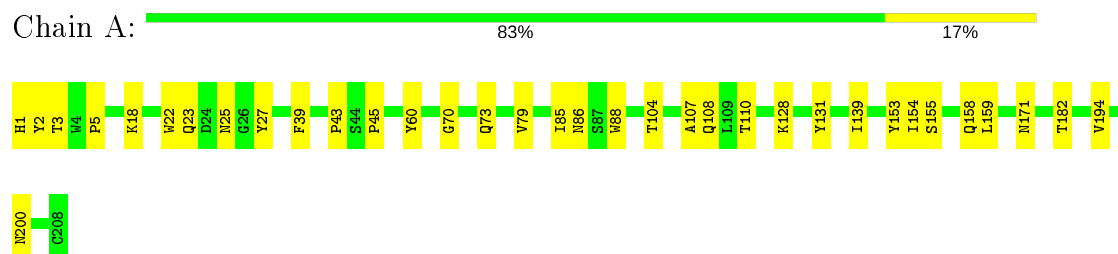
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	183	Total	O	0	0
			183	183		
6	B	151	Total	O	0	0
			151	151		
6	C	192	Total	O	0	0
			192	192		
6	D	170	Total	O	0	0
			170	170		

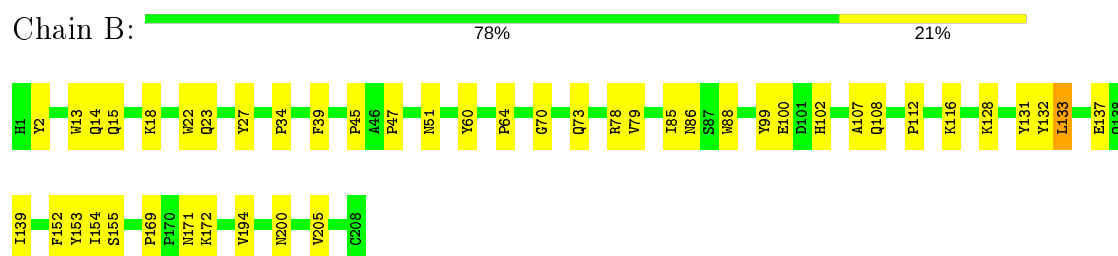
### 3 Residue-property plots [i](#)

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. 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. 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.

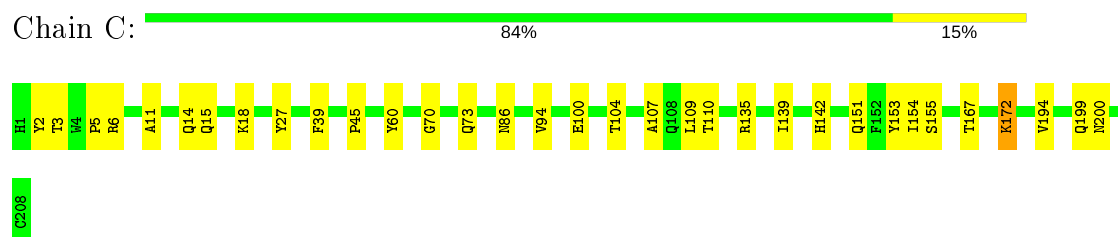
- Molecule 1: protein GH61E



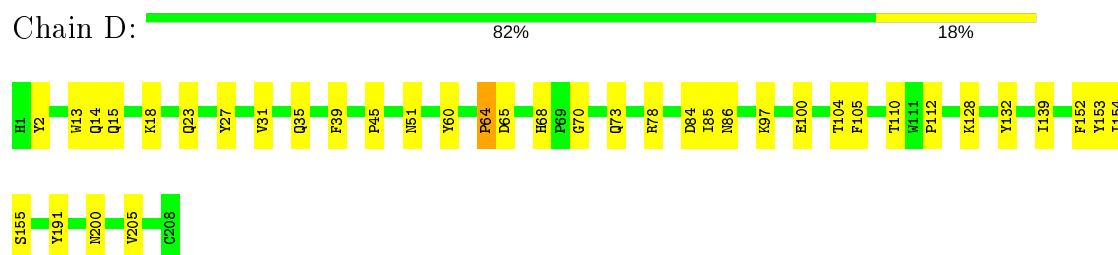
- Molecule 1: protein GH61E



- Molecule 1: protein GH61E



- Molecule 1: protein GH61E





## 4 Data and refinement statistics

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	220.92Å 220.92Å 220.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.25 19.92 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.2 (20.00-2.25) 98.8 (19.92-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 2.01Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.217 , 0.251 0.349 , 0.351	Depositor DCC
$R_{free}$ test set	2989 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.045 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.79	EDS
Total number of atoms	7221	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	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 24.85 % 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 3.5412e-03.*

<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: GOL, ZN, NAG, SO4

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	0.54	0/1659	0.69	0/2284
1	B	0.52	0/1659	0.68	0/2284
1	C	0.54	0/1659	0.69	0/2284
1	D	0.52	0/1659	0.67	0/2284
All	All	0.53	0/6636	0.68	0/9136

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	64	PRO	Mainchain

### 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	1599	0	1487	22	1
1	B	1599	0	1487	34	0
1	C	1599	0	1487	25	1
1	D	1599	0	1487	32	1
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	A	14	0	13	0	0
3	B	14	0	13	1	0
3	C	14	0	13	0	1
3	D	14	0	13	4	0
4	A	15	0	0	0	0
4	B	20	0	0	0	0
4	C	10	0	0	0	0
4	D	10	0	0	0	0
5	C	6	0	8	6	0
5	D	6	0	8	1	0
6	A	183	0	0	5	0
6	B	151	0	0	5	0
6	C	192	0	0	5	3
6	D	170	0	0	10	2
All	All	7221	0	6016	113	5

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 9.

The worst 5 of 113 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:D:51:ASN:HD22	3:D:601:NAG:H82	1.34	0.93
1:C:135:ARG:HG2	6:C:4615:HOH:O	1.69	0.90
1:C:107:ALA:O	1:C:194:VAL:HG21	1.89	0.72
1:D:35:GLN:HG3	6:D:4228:HOH:O	1.90	0.72
1:B:34:PRO:HD2	6:B:4250:HOH:O	1.92	0.70

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:191:TYR:O	6:C:4120:HOH:O[12_665]	1.95	0.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:601:NAG:O4	6:C:4202:HOH:O[16_556]	2.09	0.11
1:C:172:LYS:O	6:D:4223:HOH:O[6_566]	2.10	0.10
1:A:182:THR:OG1	6:C:4323:HOH:O[45_545]	2.16	0.04
6:D:4287:HOH:O	6:D:4495:HOH:O[12_665]	2.19	0.01

## 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	206/208 (99%)	198 (96%)	8 (4%)	0	100	100
1	B	206/208 (99%)	200 (97%)	6 (3%)	0	100	100
1	C	206/208 (99%)	200 (97%)	6 (3%)	0	100	100
1	D	206/208 (99%)	200 (97%)	5 (2%)	1 (0%)	29	29
All	All	824/832 (99%)	798 (97%)	25 (3%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	64	PRO

### 5.3.2 Protein sidechains [i](#)

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	170/170 (100%)	166 (98%)	4 (2%)	49	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	170/170 (100%)	166 (98%)	4 (2%)	49	58
1	C	170/170 (100%)	165 (97%)	5 (3%)	42	51
1	D	170/170 (100%)	165 (97%)	5 (3%)	42	51
All	All	680/680 (100%)	662 (97%)	18 (3%)	46	55

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2	TYR
1	C	39	PHE
1	D	39	PHE
1	B	60	TYR
1	B	133	LEU

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

Mol	Chain	Res	Type
1	B	14	GLN
1	B	108	GLN
1	D	14	GLN
1	A	199	GLN
1	C	171	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 ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 23 ligands modelled in this entry, 6 are monoatomic - leaving 17 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	SO4	B	3403	-	4,4,4	0.15	0	6,6,6	0.14	0
4	SO4	C	4849	-	4,4,4	1.05	0	6,6,6	1.56	1 (16%)
5	GOL	D	2647	2	5,5,5	0.26	0	5,5,5	0.25	0
4	SO4	A	4849	-	4,4,4	0.98	0	6,6,6	1.54	1 (16%)
4	SO4	D	3402	-	4,4,4	0.21	0	6,6,6	0.10	0
4	SO4	D	4849	-	4,4,4	1.01	0	6,6,6	1.56	1 (16%)
4	SO4	B	4851	-	4,4,4	1.07	0	6,6,6	1.56	1 (16%)
3	NAG	C	601	1	14,14,15	0.60	0	17,19,21	0.84	1 (5%)
3	NAG	B	601	1	14,14,15	1.09	2 (14%)	17,19,21	0.62	0
3	NAG	D	601	1	14,14,15	1.05	2 (14%)	17,19,21	0.95	1 (5%)
4	SO4	B	3405	-	4,4,4	0.19	0	6,6,6	0.16	0
4	SO4	A	3404	-	4,4,4	0.28	0	6,6,6	0.11	0
4	SO4	B	4849	-	4,4,4	1.00	0	6,6,6	1.58	1 (16%)
3	NAG	A	601	1	14,14,15	0.64	0	17,19,21	0.68	1 (5%)
4	SO4	A	4851	-	4,4,4	1.02	0	6,6,6	1.57	1 (16%)
5	GOL	C	2647	-	5,5,5	0.64	0	5,5,5	2.06	1 (20%)
4	SO4	C	3401	-	4,4,4	0.19	0	6,6,6	0.08	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
3	NAG	C	601	1	-	4/6/23/26	0/1/1/1
3	NAG	B	601	1	-	2/6/23/26	0/1/1/1
5	GOL	D	2647	2	-	0/4/4/4	-
3	NAG	D	601	1	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	C	2647	-	-	2/4/4/4	-
3	NAG	A	601	1	-	4/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	601	NAG	C1-C2	2.79	1.56	1.52
3	D	601	NAG	C8-C7	2.08	1.54	1.50
3	B	601	NAG	O7-C7	-2.03	1.18	1.23
3	B	601	NAG	C8-C7	-2.00	1.46	1.50

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	4849	SO4	O4-S-O3	3.62	124.52	109.06
4	A	4851	SO4	O4-S-O3	3.61	124.49	109.06
5	C	2647	GOL	C3-C2-C1	-3.59	97.76	111.70
4	C	4849	SO4	O4-S-O3	3.58	124.35	109.06
4	B	4851	SO4	O4-S-O3	3.57	124.30	109.06

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	601	NAG	C8-C7-N2-C2
3	D	601	NAG	O7-C7-N2-C2
3	A	601	NAG	C8-C7-N2-C2
3	A	601	NAG	O7-C7-N2-C2
3	B	601	NAG	C8-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	2647	GOL	1	0
3	C	601	NAG	0	1
3	B	601	NAG	1	0
3	D	601	NAG	4	0
5	C	2647	GOL	6	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.