



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:39 AM GMT

PDB ID : 3MKK  
Title : The crystal structure of the D307A mutant of glycoside HYDROLASE (FAMILY 31) from Ruminococcus obeum ATCC 29174 in complex with isomaltose  
Authors : Tan, K.; Tesar, C.; Freeman, L.; Babnigg, G.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2010-04-15  
Resolution : 1.91 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

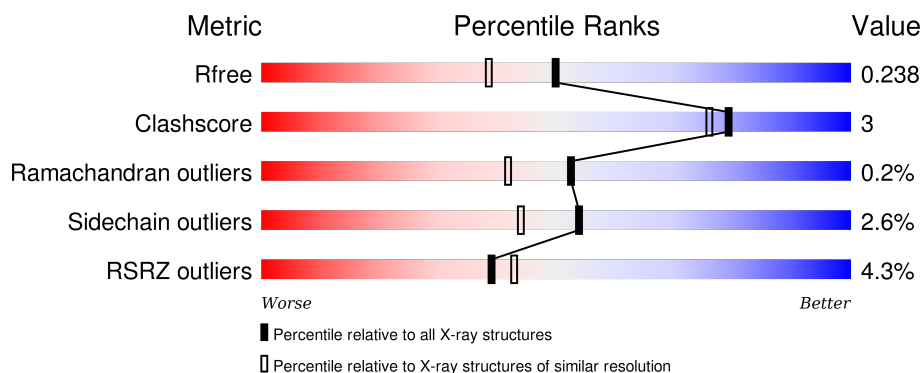
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.91 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))
$R_{free}$	91344	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	666	<div> <div>5%</div> <div>89%</div> <div>10%</div> </div>
1	B	666	<div> <div>4%</div> <div>92%</div> <div>7%</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	A	801	-	-	-	X
4	GLC	B	801	-	-	-	X
4	BGC	B	802	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11896 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.

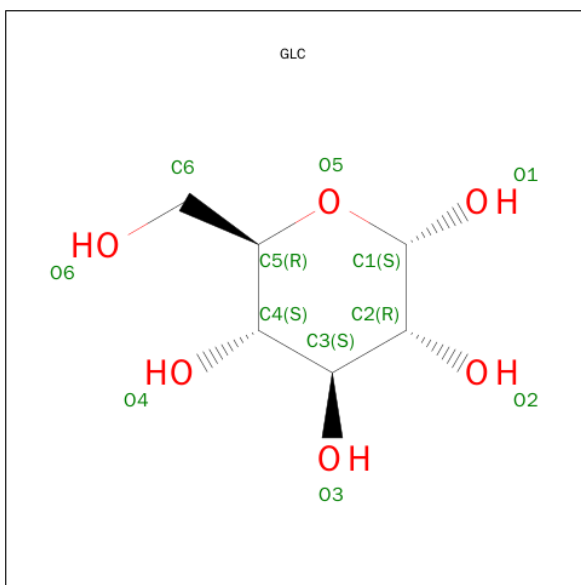
- Molecule 1 is a protein called alpha-glucosidase GH31 family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	664	Total	C	N	O	S	3	6	0
			5468	3510	895	1028	35			
1	B	664	Total	C	N	O	S	0	8	0
			5475	3518	897	1025	35			

There are 8 discrepancies between the modelled and reference sequences:

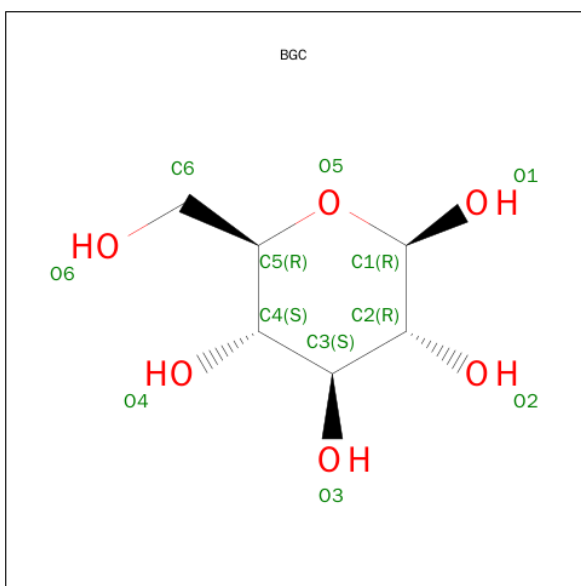
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A5ZY13
A	-1	ASN	-	expression tag	UNP A5ZY13
A	0	ALA	-	expression tag	UNP A5ZY13
A	307	ALA	ASP	engineered	UNP A5ZY13
B	-2	SER	-	expression tag	UNP A5ZY13
B	-1	ASN	-	expression tag	UNP A5ZY13
B	0	ALA	-	expression tag	UNP A5ZY13
B	307	ALA	ASP	engineered	UNP A5ZY13

- Molecule 2 is SUGAR (ALPHA-D-GLUCOSE) (three-letter code: GLC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



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

- Molecule 3 is SUGAR (BETA-D-GLUCOSE) (three-letter code: BGC) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	2	Total	C	O	0	0
			23	12	11		

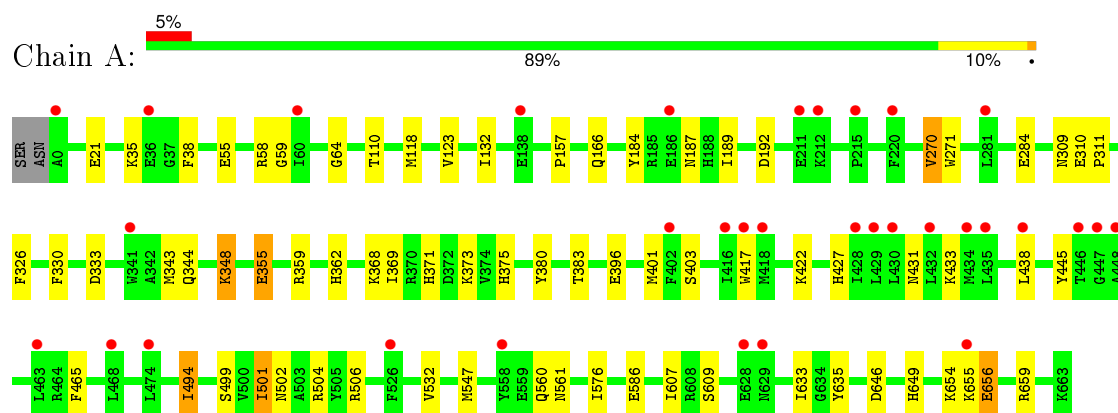
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	439	Total	O	0	0
			439	439		
5	B	468	Total	O	0	0
			468	468		

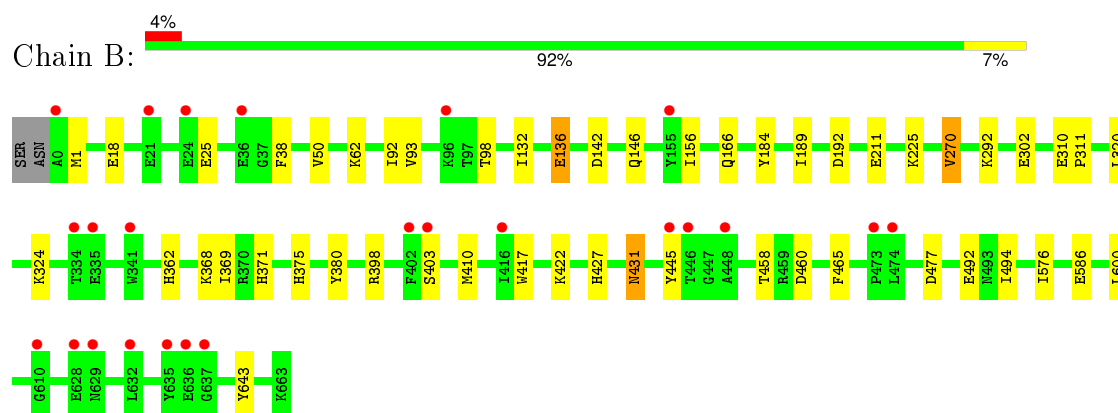
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: alpha-glucosidase GH31 family



- Molecule 1: alpha-glucosidase GH31 family



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.45Å 125.51Å 87.87Å 90.00° 107.85° 90.00°	Depositor
Resolution (Å)	41.44 – 1.91 41.44 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.0 (41.44-1.91) 99.0 (41.44-1.91)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.170 , 0.218 0.197 , 0.238	Depositor DCC
$R_{free}$ test set	5381 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtriage
Anisotropy	0.621	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 31.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 107640 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11896	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GLC, 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	0.68	0/5626	0.68	1/7585 (0.0%)
1	B	0.73	1/5642 (0.0%)	0.71	1/7603 (0.0%)
All	All	0.71	1/11268 (0.0%)	0.70	2/15188 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	445	TYR	CD1-CE1	6.79	1.49	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	646	ASP	CB-CG-OD1	5.42	123.18	118.30
1	B	477	ASP	CB-CG-OD1	5.21	122.99	118.30

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	5468	0	5247	48	0
1	B	5475	0	5277	28	0
2	A	11	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	12	0	11	0	0
4	B	23	0	19	1	0
5	A	439	0	0	3	0
5	B	468	0	0	4	0
All	All	11896	0	10564	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 3.

All (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:B:422:LYS:H	1:B:427:HIS:HD2	1.21	0.84
1:A:330:PHE:HB2	1:A:343:MET:HE3	1.59	0.83
1:A:422:LYS:H	1:A:427:HIS:HD2	1.28	0.80
1:A:326:PHE:CD2	1:A:343:MET:HE2	2.19	0.77
1:B:136:GLU:HG3	5:B:857:HOH:O	1.83	0.77
1:A:330:PHE:HB2	1:A:343:MET:CE	2.20	0.72
1:A:189:ILE:HD11	1:A:494:ILE:HD12	1.71	0.72
1:A:21:GLU:HG2	5:A:993:HOH:O	1.89	0.71
1:A:326:PHE:CE2	1:A:343:MET:HE2	2.30	0.67
1:A:330:PHE:CB	1:A:343:MET:HE3	2.26	0.65
1:A:333:ASP:O	1:B:324:LYS:NZ	2.30	0.63
1:B:371:HIS:HE1	1:B:375:HIS:ND1	1.97	0.63
1:A:187:ASN:CB	1:A:494:ILE:HD11	2.30	0.62
1:A:362:HIS:NE2	1:A:371:HIS:HD2	1.97	0.62
1:A:38:PHE:CZ	1:A:132:ILE:HD11	2.37	0.60
1:A:166:GLN:NE2	1:A:184:TYR:OH	2.35	0.59
1:A:310:GLU:N	1:A:311:PRO:HA	2.18	0.58
1:B:362:HIS:NE2	1:B:371:HIS:HD2	2.02	0.57
1:B:422:LYS:N	1:B:427:HIS:HD2	1.99	0.57
1:A:494:ILE:HG23	5:A:887:HOH:O	2.03	0.56
1:A:371:HIS:HE1	1:A:375:HIS:ND1	2.03	0.56
1:A:187:ASN:HB3	1:A:494:ILE:HD11	1.87	0.56
1:A:659[B]:ARG:HB2	1:A:659[B]:ARG:HH21	1.71	0.55
1:B:371:HIS:CE1	1:B:375:HIS:ND1	2.75	0.55
1:A:118:MET:HG2	5:B:1061:HOH:O	2.07	0.55
1:A:309:ASN:ND2	1:A:403:SER:OG	2.40	0.54
1:A:422:LYS:N	1:A:427:HIS:HD2	2.02	0.54
1:A:383:THR:HG23	1:A:401:MET:HE2	1.90	0.54
1:A:189:ILE:HD11	1:A:494:ILE:CD1	2.36	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:ILE:CD1	1:A:633:ILE:HG22	2.39	0.53
1:B:225:LYS:HE2	1:B:302:GLU:OE2	2.10	0.52
1:B:38:PHE:CZ	1:B:132:ILE:HD11	2.46	0.50
1:A:502:ASN:O	1:A:506:ARG:HG3	2.11	0.50
1:A:656:GLU:HB2	5:A:904:HOH:O	2.11	0.49
1:B:292:LYS:HE2	5:B:1083:HOH:O	2.12	0.49
1:B:576:ILE:HD12	1:B:586:GLU:HG2	1.96	0.47
1:A:576:ILE:CD1	1:A:586:GLU:HG3	2.45	0.47
1:A:157:PRO:HG3	1:A:445:TYR:CD1	2.50	0.46
1:A:330:PHE:CB	1:A:343:MET:CE	2.90	0.46
1:B:189:ILE:HD11	1:B:494:ILE:CG2	2.45	0.46
1:B:431:ASN:HD22	1:B:431:ASN:C	2.20	0.45
1:B:576:ILE:CD1	1:B:586:GLU:HG2	2.47	0.45
1:B:422:LYS:H	1:B:427:HIS:CD2	2.14	0.45
1:B:93:VAL:O	1:B:98:THR:HA	2.16	0.45
1:A:371:HIS:CE1	1:A:375:HIS:ND1	2.84	0.45
1:B:142:ASP:O	1:B:146:GLN:HG3	2.17	0.45
1:A:422:LYS:H	1:A:427:HIS:CD2	2.19	0.44
1:A:59:GLY:HA2	1:A:433:LYS:HD3	1.99	0.44
1:B:460:ASP:HB3	1:B:600:LEU:HD11	2.00	0.44
1:B:92:ILE:HD12	1:B:92:ILE:N	2.32	0.43
1:A:501:ILE:O	1:A:504:ARG:HB3	2.18	0.43
1:B:50:VAL:O	1:B:62:LYS:HG2	2.18	0.43
1:A:609:SER:HA	1:A:635:TYR:CE2	2.54	0.43
4:B:801:GLC:C5	4:B:802:BGC:H6C1	2.49	0.43
1:A:348:LYS:HB3	1:A:348:LYS:HE2	1.83	0.43
1:A:38:PHE:HZ	1:A:132:ILE:HD11	1.82	0.43
1:B:310:GLU:N	1:B:311:PRO:HA	2.34	0.43
1:B:166:GLN:NE2	1:B:184:TYR:OH	2.52	0.42
1:A:270:VAL:HG12	1:A:271:TRP:H	1.84	0.42
1:A:560:GLN:O	1:A:561:ASN:HB2	2.19	0.42
1:B:643:TYR:C	1:B:643:TYR:CD2	2.91	0.42
1:A:355:GLU:O	1:A:359:ARG:HG3	2.19	0.42
1:B:156:ILE:HG22	1:B:398:ARG:HD3	2.01	0.42
1:A:110:THR:O	1:A:123:VAL:HA	2.20	0.41
1:A:326:PHE:CD2	1:A:343:MET:CE	2.98	0.41
1:A:659[B]:ARG:HB2	1:A:659[B]:ARG:NH2	2.35	0.41
1:B:403[A]:SER:HB3	1:B:410:MET:HE1	2.03	0.41
1:B:403[A]:SER:HB3	1:B:410:MET:CE	2.50	0.41
1:A:396:GLU:O	1:A:649:HIS:HA	2.21	0.41
1:A:55:GLU:HB2	1:A:438:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:LYS:O	1:A:369:ILE:HD13	2.21	0.41
1:A:344:GLN:HG3	5:B:1074:HOH:O	2.22	0.40
1:A:64:GLY:O	1:B:458:THR:HG21	2.22	0.40
1:B:1:MET:HB3	1:B:146:GLN:OE1	2.21	0.40
1:A:532:VAL:HG21	1:A:547:MET:HG3	2.03	0.40

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	668/666 (100%)	639 (96%)	27 (4%)	2 (0%)	46	34
1	B	670/666 (101%)	649 (97%)	20 (3%)	1 (0%)	56	46
All	All	1338/1332 (100%)	1288 (96%)	47 (4%)	3 (0%)	52	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	ARG
1	A	270	VAL
1	B	270	VAL

### 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	577/574 (100%)	560 (97%)	17 (3%)	50	39
1	B	579/574 (101%)	565 (98%)	14 (2%)	57	48
All	All	1156/1148 (101%)	1125 (97%)	31 (3%)	54	42

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LYS
1	A	192	ASP
1	A	284	GLU
1	A	348	LYS
1	A	355	GLU
1	A	373	LYS
1	A	380	TYR
1	A	417	TRP
1	A	431	ASN
1	A	465	PHE
1	A	494	ILE
1	A	499[A]	SER
1	A	499[B]	SER
1	A	501	ILE
1	A	654	LYS
1	A	655	LYS
1	A	656	GLU
1	B	18	GLU
1	B	25	GLU
1	B	136	GLU
1	B	192	ASP
1	B	211	GLU
1	B	270	VAL
1	B	320	LEU
1	B	368	LYS
1	B	369	ILE
1	B	380	TYR
1	B	417	TRP
1	B	431	ASN
1	B	465	PHE
1	B	492	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	166	GLN
1	A	339	HIS
1	A	344	GLN
1	A	371	HIS
1	A	427	HIS
1	A	431	ASN
1	A	550	ASN
1	B	166	GLN
1	B	371	HIS
1	B	427	HIS
1	B	550	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

2 carbohydrates 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	GLC	B	801	4	11,11,12	0.67	0	14,15,17	0.89	0
4	BGC	B	802	4	12,12,12	0.62	0	17,17,17	3.21	8 (47%)

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	GLC	B	801	4	-	0/2/19/22	0/1/1/1
4	BGC	B	802	4	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	B	802	BGC	O1-C1-O5	2.20	116.27	110.25
4	B	802	BGC	C6-C5-C4	2.46	119.08	113.02
4	B	802	BGC	O4-C4-C5	2.89	116.90	109.24
4	B	802	BGC	O5-C5-C6	3.96	116.36	106.36
4	B	802	BGC	O1-C1-C2	4.11	120.23	109.21
4	B	802	BGC	O4-C4-C3	5.57	122.87	110.34
4	B	802	BGC	O5-C5-C4	5.98	120.91	109.68
4	B	802	BGC	O5-C1-C2	6.48	120.14	109.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	801	GLC	1	0
4	B	802	BGC	1	0

## 5.6 Ligand geometry

2 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	$\# Z  > 2$
2	GLC	A	801	-	11,11,12	0.65	0	14,15,17	1.37	2 (14%)
3	BGC	A	802	-	12,12,12	0.71	0	17,17,17	1.61	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
2	GLC	A	801	-	-	0/2/19/22	0/1/1/1
3	BGC	A	802	-	-	0/2/22/22	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(°)
3	A	802	BGC	C4-C3-C2	-3.51	104.24	110.79
2	A	801	GLC	C2-C3-C4	-2.04	107.58	111.04
3	A	802	BGC	O4-C4-C3	2.66	116.32	110.34
3	A	802	BGC	O2-C2-C3	2.82	116.69	110.34
2	A	801	GLC	C1-O5-C5	3.95	117.27	112.25

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 [i](#)

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	664/666 (99%)	0.12	33 (4%) 32 36	3, 9, 17, 28	4 (0%)
1	B	664/666 (99%)	0.04	24 (3%) 46 50	2, 7, 17, 28	2 (0%)
All	All	1328/1332 (99%)	0.08	57 (4%) 39 43	2, 8, 17, 28	6 (0%)

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	0	ALA	5.3
1	B	629	ASN	4.4
1	A	0	ALA	4.2
1	B	637	GLY	4.0
1	A	432[A]	LEU	3.9
1	A	463	LEU	3.7
1	A	435	LEU	3.4
1	A	211	GLU	3.4
1	A	629	ASN	3.3
1	A	430	LEU	3.2
1	B	402	PHE	3.1
1	B	341	TRP	3.1
1	B	474	LEU	3.0
1	A	416	ILE	3.0
1	A	428	ILE	3.0
1	A	429	LEU	2.9
1	B	628	GLU	2.9
1	A	138	GLU	2.8
1	A	215	PRO	2.8
1	A	341	TRP	2.8
1	B	334	THR	2.7
1	A	438	LEU	2.7
1	A	446[A]	THR	2.6
1	B	416	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	446	THR	2.6
1	B	445	TYR	2.6
1	A	402	PHE	2.6
1	B	21	GLU	2.5
1	A	448	ALA	2.5
1	B	473	PRO	2.5
1	A	468	LEU	2.4
1	A	220	PHE	2.4
1	A	417	TRP	2.4
1	A	60	ILE	2.4
1	B	335	GLU	2.4
1	A	526	PHE	2.4
1	B	96	LYS	2.4
1	A	447	GLY	2.3
1	A	281	LEU	2.3
1	B	403[A]	SER	2.3
1	B	636	GLU	2.3
1	A	474	LEU	2.3
1	A	186	GLU	2.3
1	A	655	LYS	2.2
1	B	24	GLU	2.2
1	B	632	LEU	2.2
1	A	434	MET	2.2
1	B	448	ALA	2.1
1	A	628	GLU	2.1
1	A	418	MET	2.1
1	B	610	GLY	2.1
1	B	36	GLU	2.1
1	A	212	LYS	2.1
1	B	635	TYR	2.1
1	A	36	GLU	2.1
1	A	558	TYR	2.0
1	B	155	TYR	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 [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	BGC	B	802	12/12	0.75	0.23	3.87	26,40,43,43	0
4	GLC	B	801	11/12	0.95	0.23	3.14	15,19,22,22	0

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	GLC	A	801	11/12	0.93	0.32	4.73	21,23,26,28	0
3	BGC	A	802	12/12	0.70	0.21	1.73	28,43,45,48	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.