



# Full wwPDB X-ray Structure Validation Report i

Feb 26, 2014 – 09:36 PM GMT

PDB ID : 1O7Q  
Title : ROLES OF INDIVIDUAL RESIDUES OF ALPHA-1,3 GALACTOSYLTRANSFERASESIN SUBSTRATE BINDING AND CATALYSIS  
Authors : Zhang, Y.; Swaminathan, G.J.; Deshpande, A.; Natesh, R.; Xie, X.; Acharya, K.R.; Brew, K.  
Deposited on : 2002-11-12  
Resolution : 1.30 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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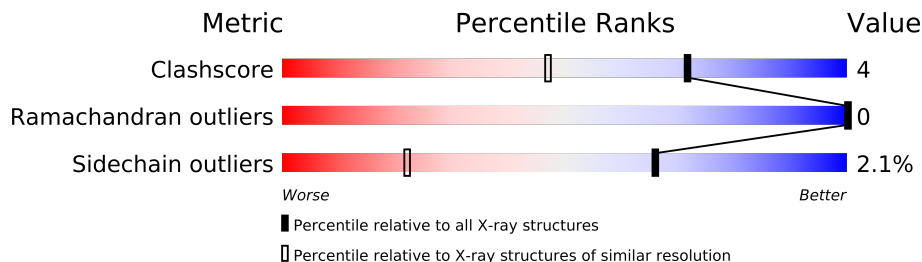
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.30 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))
Clashscore	79885	1140 (1.34-1.26)
Ramachandran outliers	78287	1093 (1.34-1.26)
Sidechain outliers	78261	1092 (1.34-1.26)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	289	
1	B	289	

## 2 Entry composition i

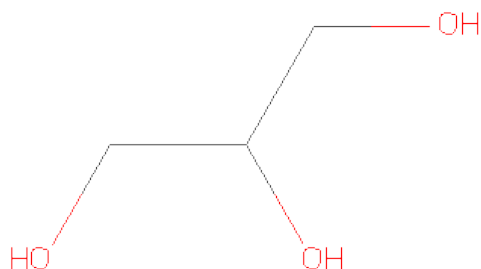
There are 6 unique types of molecules in this entry. The entry contains 10790 atoms, of which 4791 are hydrogens and 0 are deuterium.

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 N-ACETYLLACTOSAMINIDEALPHA-1,3-GALACTOSYL TRANSFERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	287	Total	C	H	N	O	S	0	10	0
			4823	1592	2394	397	424	16			
1	B	287	Total	C	H	N	O	S	0	11	0
			4831	1596	2397	395	427	16			

- Molecule 2 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
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

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

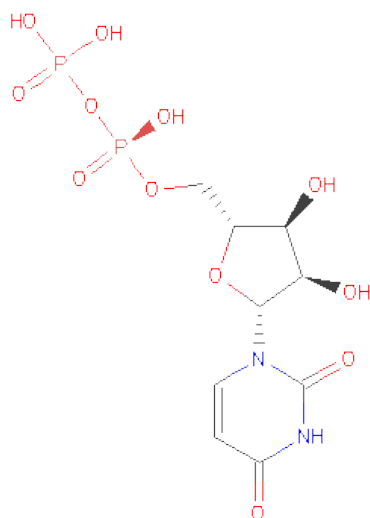
- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			26	14	1	11		
4	B	2	Total	C	N	O	0	0
			26	14	1	11		

- Molecule 5 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C<sub>9</sub>H<sub>14</sub>N<sub>2</sub>O<sub>12</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
5	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
5	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 6 is water.

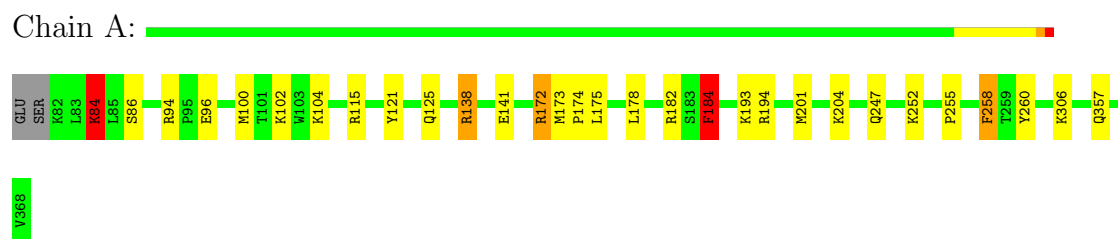
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	468	Total	O	0	0
			468	468		
6	B	484	Total	O	0	0
			484	484		

### 3 Residue-property plots

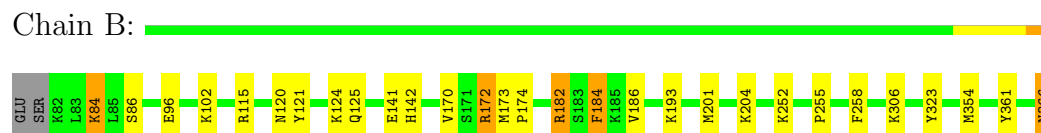
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

- Molecule 1: N-ACETYLLACTOSAMINIDEALPHA-1,3-GALACTOSYLTRANSFERASE



- Molecule 1: N-ACETYLLACTOSAMINIDEALPHA-1,3-GALACTOSYLTRANSFERASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.33Å 94.68Å 95.01Å 90.00° 99.03° 90.00°	Depositor
Resolution (Å)	40.00 – 1.30	Depositor
% Data completeness (in resolution range)	94.9 (40.00-1.30)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.116 , 0.154	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10790	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, GOL, UDP, MN, NAG

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	0.64	2/2544 (0.1%)	1.10	17/3444 (0.5%)
1	B	0.59	0/2554	1.09	9/3457 (0.3%)
All	All	0.62	2/5098 (0.0%)	1.10	26/6901 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	96	GLU	CD-OE1	-9.08	1.15	1.25
1	A	96	GLU	CD-OE2	-6.41	1.18	1.25

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	182	ARG	NE-CZ-NH2	9.31	124.95	120.30
1	B	184[A]	PHE	CB-CG-CD1	-9.20	114.36	120.80
1	B	184[B]	PHE	CB-CG-CD1	-9.20	114.36	120.80
1	A	96	GLU	OE1-CD-OE2	-8.86	112.67	123.30
1	B	323	TYR	CB-CG-CD1	8.73	126.24	121.00
1	A	260	TYR	CB-CG-CD2	6.93	125.16	121.00
1	A	184[A]	PHE	CB-CG-CD1	-6.89	115.98	120.80
1	A	184[B]	PHE	CB-CG-CD1	-6.89	115.98	120.80
1	A	138[A]	ARG	CD-NE-CZ	6.57	132.80	123.60
1	A	138[B]	ARG	CD-NE-CZ	6.57	132.80	123.60
1	A	94	ARG	NE-CZ-NH2	-6.54	117.03	120.30
1	A	96	GLU	CG-CD-OE2	6.44	131.19	118.30
1	A	115	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	A	141	GLU	OE1-CD-OE2	-6.28	115.76	123.30
1	A	84	LYS	CD-CE-NZ	6.22	126.00	111.70
1	B	96	GLU	CB-CG-CD	6.05	130.55	114.20
1	B	115	ARG	NE-CZ-NH1	5.82	123.21	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	194	ARG	CD-NE-CZ	5.54	131.35	123.60
1	A	258	PHE	CB-CG-CD2	5.49	124.64	120.80
1	B	361	TYR	CB-CG-CD2	5.39	124.23	121.00
1	A	138[A]	ARG	NE-CZ-NH2	5.18	122.89	120.30
1	A	138[B]	ARG	NE-CZ-NH2	5.18	122.89	120.30
1	A	172	ARG	CA-CB-CG	-5.15	102.08	113.40
1	B	366	ASN	CA-CB-CG	-5.12	102.13	113.40
1	B	172	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	172	ARG	CD-NE-CZ	5.05	130.67	123.60

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2429	2394	0	18	0
1	B	2434	2397	0	18	0
2	A	12	0	0	0	0
2	B	18	0	0	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	26	0	0	0	0
4	B	26	0	0	1	0
5	A	50	0	0	6	0
5	B	50	0	0	2	0
6	A	468	0	0	8	0
6	B	484	0	0	5	0
All	All	5999	4791	0	43	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (43) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:A:1375:UDP:O5'	5:A:1375:UDP:C6	2.34	0.80
5:A:1375:UDP:C5'	5:A:1375:UDP:C6	2.68	0.77
1:A:100[A]:MET:HG3	6:A:2045:HOH:O	1.91	0.70
1:A:102:LYS:HE3	6:A:2333:HOH:O	1.92	0.69
5:A:1375:UDP:C6	5:A:1375:UDP:C3'	2.76	0.69
1:B:141:GLU:OE2	1:B:172:ARG:HD2	1.94	0.68
1:A:84:LYS:HD3	1:A:86[A]:SER:OG	1.94	0.67
1:A:175:LEU:HB2	6:A:2170:HOH:O	1.95	0.65
1:A:100[B]:MET:SD	1:A:104:LYS:HA	2.40	0.61
5:A:1375:UDP:C6	5:A:1375:UDP:C4'	2.89	0.56
1:A:178:LEU:HD13	1:A:184[A]:PHE:CD1	2.41	0.56
1:B:86:SER:HB3	2:B:1378:GOL:C1	2.36	0.55
1:B:306:LYS:HB3	5:B:1377:UDP:O3'	2.07	0.54
1:A:138[B]:ARG:HD3	6:A:2165:HOH:O	2.08	0.53
1:B:84:LYS:HG3	6:B:2002:HOH:O	2.10	0.52
1:A:193:LYS:HD2	1:A:193:LYS:N	2.25	0.52
1:A:306:LYS:O	5:A:1375:UDP:O2'	2.29	0.51
1:A:255:PRO:HA	1:A:258:PHE:CD1	2.46	0.50
1:B:173[B]:MET:SD	1:B:186:VAL:HG22	2.50	0.50
1:B:120:ASN:O	1:B:124:LYS:HG3	2.11	0.50
4:B:1374:NAG:O6	2:B:1379:GOL:O3	2.31	0.48
1:B:84:LYS:HD3	1:B:86:SER:OG	2.14	0.47
1:A:201[A]:MET:HE1	6:A:2222:HOH:O	2.14	0.47
1:A:172:ARG:NH2	6:A:2165:HOH:O	2.48	0.46
1:B:142:HIS:HD2	6:B:2100:HOH:O	1.97	0.46
1:B:252:LYS:NZ	6:B:2291:HOH:O	2.48	0.46
1:B:121:TYR:O	1:B:125:GLN:HG3	2.16	0.46
1:A:121:TYR:O	1:A:125:GLN:HG3	2.16	0.45
1:B:173[B]:MET:HE1	1:B:174:PRO:O	2.17	0.45
1:B:255:PRO:HA	1:B:258:PHE:CE1	2.51	0.45
1:B:193:LYS:NZ	6:B:2221:HOH:O	2.49	0.45
1:B:255:PRO:HA	1:B:258:PHE:CD1	2.52	0.45
5:A:1375:UDP:O5'	5:A:1375:UDP:C5	2.70	0.44
5:B:1377:UDP:C3'	5:B:1377:UDP:C6	3.01	0.44
1:A:204:LYS:HE2	6:A:2241:HOH:O	2.17	0.43
1:A:173[A]:MET:HE2	1:A:174:PRO:O	2.18	0.43
1:B:170:VAL:O	1:B:170:VAL:HG11	2.18	0.43
1:A:138[A]:ARG:HG2	6:A:2443:HOH:O	2.17	0.43
1:A:255:PRO:HA	1:A:258:PHE:CE1	2.53	0.43
1:B:120:ASN:ND2	6:B:2059:HOH:O	2.51	0.42
1:B:354[B]:MET:HE3	1:B:354[B]:MET:HB3	1.99	0.41
1:A:201[B]:MET:HE3	1:A:204:LYS:CD	2.51	0.41
1:B:201[B]:MET:HE2	1:B:204:LYS:CD	2.51	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	295/289 (102%)	289 (98%)	6 (2%)	0	100	100
1	B	296/289 (102%)	290 (98%)	6 (2%)	0	100	100
All	All	591/578 (102%)	579 (98%)	12 (2%)	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	267/260 (103%)	260 (97%)	7 (3%)	59	14
1	B	268/260 (103%)	262 (98%)	6 (2%)	64	21
All	All	535/520 (103%)	522 (98%)	13 (2%)	66	17

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	LYS
1	A	182	ARG
1	A	184[A]	PHE
1	A	184[B]	PHE
1	A	247	GLN
1	A	252	LYS
1	A	357	GLN
1	B	84	LYS

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Mol	Chain	Res	Type
1	B	102	LYS
1	B	182	ARG
1	B	184[A]	PHE
1	B	184[B]	PHE
1	B	366	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	GLN
1	A	231	GLN
1	A	245	GLN
1	A	293	ASN
1	A	313	GLN
1	A	327	ASN
1	A	357	GLN
1	A	366	ASN
1	B	215	GLN
1	B	245	GLN
1	B	293	ASN
1	B	296	GLN
1	B	313	GLN
1	B	327	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

4 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	GAL	A	1372	4	10,11,12	0.72	0	11,15,17	1.07	1 (9%)
4	NAG	A	1373	4	15,15,15	1.02	1 (6%)	21,21,21	1.36	1 (4%)
4	GAL	B	1373	4	10,11,12	0.66	0	11,15,17	0.99	1 (9%)
4	NAG	B	1374	4	15,15,15	1.42	3 (20%)	21,21,21	1.58	3 (14%)

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	GAL	A	1372	4	-	0/2/19/22	0/1/1/1
4	NAG	A	1373	4	-	0/6/26/26	0/1/1/1
4	GAL	B	1373	4	-	0/2/19/22	0/1/1/1
4	NAG	B	1374	4	-	0/6/26/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1374	NAG	C1-C2	3.20	1.56	1.53
4	B	1374	NAG	C2-N2	2.62	1.50	1.45
4	A	1373	NAG	O5-C1	2.12	1.47	1.43
4	B	1374	NAG	O5-C1	2.06	1.47	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1374	NAG	C1-C2-N2	-5.48	104.48	110.85
4	A	1373	NAG	C1-C2-N2	-5.24	104.76	110.85
4	A	1372	GAL	O5-C5-C4	-3.11	106.71	110.65
4	B	1373	GAL	O5-C5-C4	-2.52	107.45	110.65
4	B	1374	NAG	C4-C3-C2	-2.16	107.38	110.44
4	B	1374	NAG	O5-C5-C4	-2.07	105.92	109.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	$\# Z  > 2$
2	GOL	A	1369	-	5,5,5	0.42	0	5,5,5	0.78	0
2	GOL	A	1370	-	5,5,5	1.16	0	5,5,5	1.89	2 (40%)
5	UDP	A	1374	3	26,26,26	1.86	5 (19%)	36,40,40	1.13	4 (11%)
5	UDP	A	1375	-	26,26,26	2.91	8 (30%)	36,40,40	2.10	8 (22%)
2	GOL	B	1372	-	5,5,5	0.30	0	5,5,5	0.83	0
5	UDP	B	1376	3	26,26,26	2.01	6 (23%)	36,40,40	1.06	3 (8%)
5	UDP	B	1377	-	26,26,26	3.27	8 (30%)	36,40,40	1.52	7 (19%)
2	GOL	B	1378	-	5,5,5	2.15	3 (60%)	5,5,5	3.51	2 (40%)
2	GOL	B	1379	-	5,5,5	1.96	2 (40%)	5,5,5	3.58	2 (40%)

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	GOL	A	1369	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1370	-	-	0/4/4/4	0/0/0/0
5	UDP	A	1374	3	-	0/14/32/32	0/2/2/2
5	UDP	A	1375	-	-	0/14/32/32	0/2/2/2
2	GOL	B	1372	-	-	0/4/4/4	0/0/0/0
5	UDP	B	1376	3	-	0/14/32/32	0/2/2/2
5	UDP	B	1377	-	-	0/14/32/32	0/2/2/2
2	GOL	B	1378	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1379	-	-	0/4/4/4	0/0/0/0

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1377	UDP	C6-C5	12.33	1.56	1.36
5	A	1375	UDP	C6-C5	10.20	1.52	1.36
5	B	1376	UDP	C6-C5	6.64	1.46	1.36
5	B	1377	UDP	C5-C4	6.27	1.56	1.40
5	B	1377	UDP	C6-N1	5.88	1.45	1.35
5	A	1374	UDP	C6-C5	5.80	1.45	1.36
5	A	1375	UDP	C5-C4	5.68	1.55	1.40
5	A	1375	UDP	C6-N1	4.29	1.42	1.35
5	B	1376	UDP	C5-C4	4.24	1.51	1.40
5	A	1374	UDP	C5-C4	4.22	1.51	1.40
5	A	1375	UDP	PB-O1B	3.55	1.63	1.51
5	B	1377	UDP	PB-O1B	3.53	1.63	1.51
5	A	1375	UDP	C4-N3	3.48	1.43	1.37
5	A	1375	UDP	C2-N1	3.42	1.42	1.38
5	A	1374	UDP	C6-N1	3.18	1.41	1.35
5	B	1376	UDP	C4-N3	3.13	1.42	1.37
2	B	1379	GOL	C3-C2	-3.01	1.39	1.52
2	B	1378	GOL	C3-C2	-2.94	1.40	1.52
5	A	1374	UDP	PB-O3A	2.78	1.65	1.60
2	B	1378	GOL	O2-C2	-2.75	1.35	1.43
2	B	1379	GOL	O3-C3	-2.71	1.30	1.42
5	B	1376	UDP	O4'-C1'	2.61	1.45	1.41
5	B	1377	UDP	C4-N3	2.60	1.41	1.37
2	B	1378	GOL	O3-C3	-2.59	1.31	1.42
5	B	1377	UDP	C5'-C4'	2.36	1.59	1.51
5	B	1376	UDP	C6-N1	2.27	1.39	1.35
5	A	1375	UDP	O4'-C1'	2.25	1.44	1.41
5	B	1377	UDP	O4'-C1'	2.25	1.44	1.41
5	A	1374	UDP	C4-N3	2.21	1.40	1.37
5	B	1376	UDP	PB-O3A	2.19	1.64	1.60
5	B	1377	UDP	C2-N1	2.10	1.40	1.38
5	A	1375	UDP	C5'-C4'	2.05	1.58	1.51

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1375	UDP	C2-N1-C1'	-9.57	112.20	118.21
2	B	1379	GOL	O3-C3-C2	6.61	141.96	109.71
2	B	1378	GOL	O3-C3-C2	6.07	139.34	109.71
2	B	1378	GOL	O2-C2-C3	4.45	128.50	108.22
2	B	1379	GOL	O2-C2-C3	4.01	126.49	108.22
5	B	1376	UDP	C2-N1-C1'	-3.61	115.94	118.21
5	A	1374	UDP	C2-N1-C1'	-3.57	115.97	118.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1377	UDP	C2-N1-C1'	-3.40	116.07	118.21
5	A	1374	UDP	PA-O3A-PB	-2.96	123.01	131.68
5	A	1375	UDP	C5-C6-N1	2.93	124.53	121.21
2	A	1370	GOL	O2-C2-C3	2.93	121.55	108.22
5	B	1377	UDP	O4'-C1'-N1	2.89	114.17	108.06
5	B	1376	UDP	C6-N1-C2	2.72	123.30	119.51
5	A	1375	UDP	PA-O3A-PB	2.71	139.62	131.68
5	B	1377	UDP	O3B-PB-O2B	2.66	117.99	107.61
5	B	1377	UDP	O2A-PA-O3A	2.57	117.32	105.14
5	A	1375	UDP	O2A-PA-O3A	2.49	116.95	105.14
5	B	1377	UDP	O4'-C4'-C3'	-2.44	100.23	105.17
5	A	1375	UDP	O3B-PB-O2B	2.39	116.92	107.61
5	A	1375	UDP	O4'-C1'-C2'	-2.38	103.12	106.77
5	B	1376	UDP	PA-O3A-PB	-2.33	124.86	131.68
2	A	1370	GOL	O2-C2-C1	2.32	118.79	108.22
5	A	1374	UDP	C6-N1-C2	2.31	122.73	119.51
5	A	1374	UDP	O3B-PB-O2B	2.20	116.19	107.61
5	B	1377	UDP	O4'-C1'-C2'	-2.17	103.44	106.77
5	B	1377	UDP	C2'-C3'-C4'	-2.13	98.41	102.65
5	A	1375	UDP	O3B-PB-O1B	-2.13	103.49	110.44
5	A	1375	UDP	O2'-C2'-C3'	2.06	118.54	111.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.