



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:51 AM UTC

PDB ID : 1O7O / pdb\_00001o7o  
Title : Roles of Individual Residues of Alpha-1,3 Galactosyltransferases in Substrate Binding and Catalysis  
Authors : Zhang, Y.; Swaminathan, G.J.; Deshpande, A.; Natesh, R.; Xie, Z.; Acharya, K.R.; Brew, K.  
Deposited on : 2002-11-11  
Resolution : 1.97 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 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	<b>NOT EXECUTED</b>
EDS	:	<b>NOT EXECUTED</b>
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

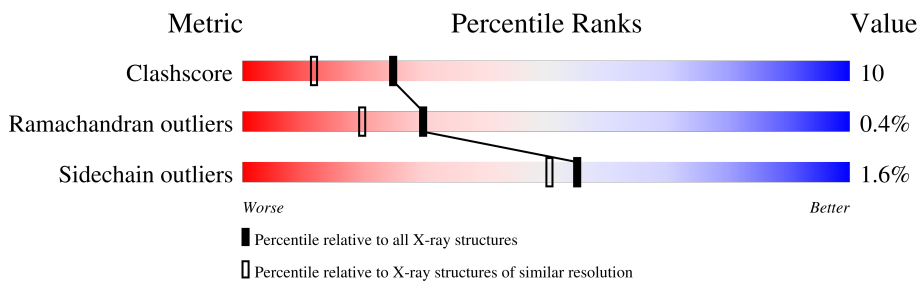
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)

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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	289	
1	B	289	
2	C	2	
2	D	2	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5478 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 N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYL TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	0	0
			2393	1564	396	421	12			
1	B	287	Total	C	N	O	S	0	0	0
			2393	1564	396	421	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	317	GLN	GLU	engineered mutation	UNP P14769
B	1317	GLN	GLU	engineered mutation	UNP P14769

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

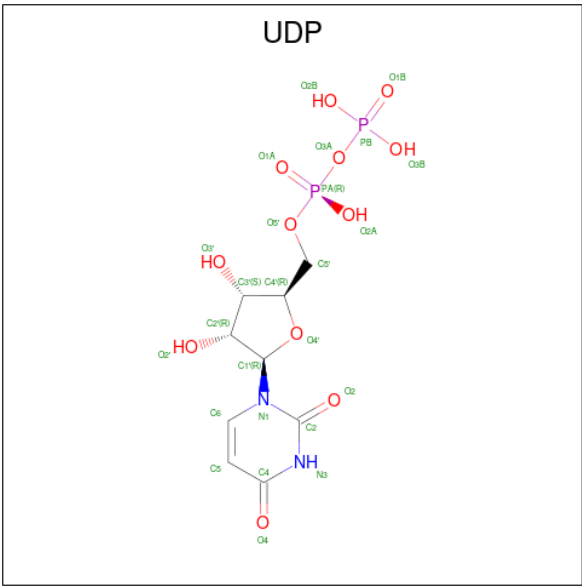


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	0	0	0
			23	12	11			
2	D	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 4 is URIDINE-5'-DIPHOSPHATE (CCD ID: 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
4	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
4	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 5 is water.

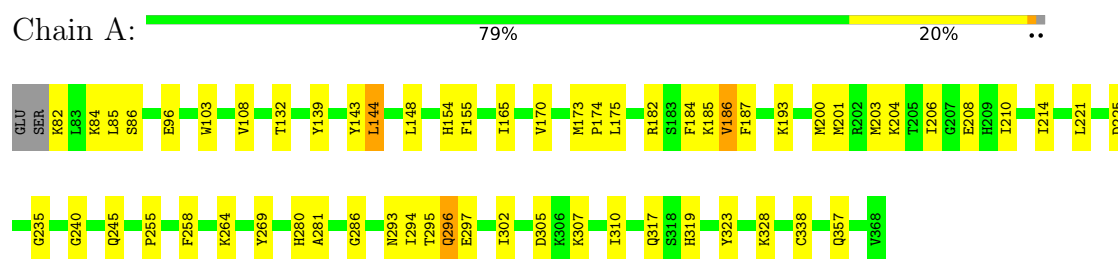
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	291	Total	O	0	0
			291	291		
5	B	303	Total	O	0	0
			303	303		

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

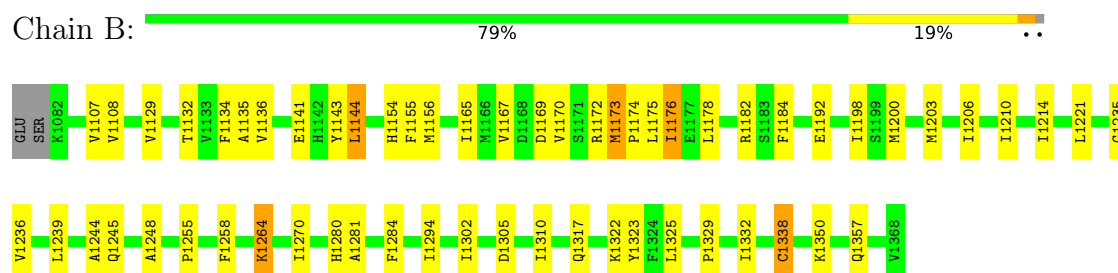
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

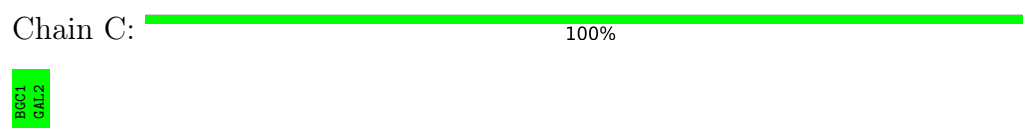
- Molecule 1: N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE



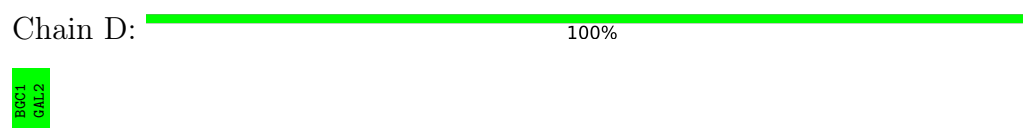
- Molecule 1: N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYLTRANSFERASE



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



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



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.20 Å   94.29 Å   94.67 Å 90.00°   99.10°   90.00°	Depositor
Resolution (Å)	50.00 – 1.97	Depositor
% Data completeness (in resolution range)	0.0 (50.00-1.97)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.181 , 0.206	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5478	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	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, MN, BGC, UDP

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	0.34	0/2466	0.91	9/3340 (0.3%)
1	B	0.34	0/2466	0.89	10/3340 (0.3%)
All	All	0.34	0/4932	0.90	19/6680 (0.3%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	GLN	N-CA-C	-10.53	96.34	110.55
1	A	235	GLY	N-CA-C	7.22	122.92	112.60
1	B	1143	TYR	N-CA-C	7.17	122.93	114.04
1	B	1235	GLY	N-CA-C	6.55	121.97	112.60
1	B	1248	ALA	N-CA-C	6.39	119.06	111.33
1	A	144	LEU	N-CA-C	6.37	117.88	111.07
1	A	143	TYR	N-CA-C	5.80	121.92	114.56
1	A	108	VAL	N-CA-C	5.69	116.57	107.98
1	A	155	PHE	N-CA-C	5.58	117.32	108.67
1	B	1357	GLN	N-CA-C	-5.46	101.64	110.32
1	B	1108	VAL	N-CA-C	5.44	116.19	107.98
1	B	1107	VAL	N-CA-C	-5.40	99.38	107.37
1	B	1154	HIS	N-CA-C	5.36	121.22	114.31
1	B	1350	LYS	N-CA-C	5.35	117.20	111.36
1	B	1155	PHE	N-CA-C	5.28	116.86	108.67
1	A	139	TYR	N-CA-C	-5.27	105.70	111.82
1	A	225	ASP	N-CA-C	-5.27	103.57	110.53
1	A	154	HIS	N-CA-C	5.06	120.83	114.31
1	B	1144	LEU	N-CA-C	5.01	117.12	111.11

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	2393	0	2354	43	0
1	B	2393	0	2354	54	0
2	C	23	0	21	0	0
2	D	23	0	21	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	25	0	11	0	0
4	B	25	0	11	0	0
5	A	291	0	0	2	0
5	B	303	0	0	0	0
All	All	5478	0	4772	95	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 10.

All (95) 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:1129:VAL:HG21	1:B:1156:MET:HE2	1.35	1.04
1:A:206:ILE:O	1:A:210:ILE:HD13	1.75	0.87
1:A:84:LYS:HD3	1:A:85:LEU:N	1.93	0.84
1:B:1281:ALA:H	1:B:1317:GLN:HE21	1.28	0.80
1:B:1329:PRO:CG	1:B:1332:ILE:HD11	2.19	0.72
1:A:296:GLN:O	1:A:297:GLU:HB2	1.87	0.72
1:A:281:ALA:H	1:A:317:GLN:HE21	1.38	0.72
1:A:200:MET:SD	1:A:302:ILE:HD12	2.29	0.71
1:A:210:ILE:HD12	1:A:214:ILE:HD12	1.70	0.71
1:B:1329:PRO:HG3	1:B:1332:ILE:HD11	1.75	0.69
1:B:1141:GLU:OE2	1:B:1172:ARG:HD2	1.94	0.67
1:B:1156:MET:HE1	1:B:1239:LEU:HD11	1.76	0.66
1:B:1210:ILE:HA	1:B:1214:ILE:HB	1.77	0.65
1:A:338:CYS:O	1:A:338:CYS:SG	2.55	0.64
1:B:1200:MET:HB3	1:B:1302:ILE:HD13	1.79	0.64
1:B:1129:VAL:HG21	1:B:1156:MET:CE	2.21	0.63
1:B:1173:MET:HE3	1:B:1174:PRO:HD2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1270:ILE:HD12	1:B:1325:LEU:CD2	2.30	0.60
1:B:1255:PRO:HA	1:B:1258:PHE:CD1	2.37	0.60
1:A:255:PRO:HA	1:A:258:PHE:CD1	2.37	0.60
1:A:280:HIS:HD2	1:A:317:GLN:NE2	2.01	0.59
1:B:1338:CYS:SG	1:B:1338:CYS:O	2.60	0.59
1:B:1280:HIS:HD2	1:B:1317:GLN:NE2	2.01	0.59
1:B:1134:PHE:HE1	1:B:1206:ILE:HD11	1.69	0.58
1:A:293:ASN:O	1:A:296:GLN:O	2.21	0.58
1:B:1156:MET:HE1	1:B:1236:VAL:HG12	1.87	0.56
1:B:1270:ILE:HD12	1:B:1325:LEU:HD23	1.87	0.56
1:B:1245:GLN:CD	1:B:1338:CYS:SG	2.88	0.55
1:B:1244:ALA:HB3	1:B:1332:ILE:CD1	2.37	0.55
1:A:296:GLN:O	1:A:297:GLU:CB	2.55	0.55
1:B:1192:GLU:O	1:B:1198:ILE:HD11	2.06	0.55
1:B:1245:GLN:NE2	1:B:1338:CYS:SG	2.80	0.55
1:A:210:ILE:HA	1:A:214:ILE:HB	1.87	0.54
1:A:245:GLN:NE2	1:A:338:CYS:SG	2.80	0.54
1:A:132:THR:HG23	1:A:221:LEU:HD11	1.90	0.54
1:A:184:PHE:CD1	1:A:186:VAL:HG23	2.43	0.53
1:A:193:LYS:N	1:A:193:LYS:HD2	2.24	0.53
1:A:294:ILE:HG12	1:A:323:TYR:CE1	2.43	0.53
1:B:1132:THR:HG23	1:B:1221:LEU:HD11	1.90	0.53
1:B:1280:HIS:HD2	1:B:1317:GLN:HE22	1.56	0.53
1:B:1270:ILE:CD1	1:B:1322:LYS:HD3	2.39	0.52
1:B:1329:PRO:HG2	1:B:1332:ILE:HD11	1.91	0.51
1:A:201:MET:HE1	1:A:204:LYS:HD3	1.93	0.51
1:B:1173:MET:HE2	1:B:1174:PRO:O	2.11	0.50
1:B:1245:GLN:CG	1:B:1338:CYS:SG	3.00	0.50
1:A:280:HIS:HD2	1:A:317:GLN:HE22	1.60	0.50
1:B:1173:MET:HE3	1:B:1174:PRO:CD	2.42	0.50
1:B:1255:PRO:HA	1:B:1258:PHE:CE1	2.46	0.50
1:A:84:LYS:HD3	1:A:84:LYS:C	2.37	0.49
1:A:165:ILE:HB	1:A:186:VAL:HG22	1.93	0.49
1:A:144:LEU:HD23	1:A:174:PRO:HD2	1.95	0.48
1:B:1144:LEU:HD23	1:B:1174:PRO:HD2	1.96	0.48
1:B:1169:ASP:HB3	1:B:1172:ARG:HE	1.79	0.48
1:B:1178:LEU:HD11	1:B:1184:PHE:HD2	1.77	0.48
1:A:305:ASP:HB3	1:A:310:ILE:O	2.14	0.48
1:B:1176:ILE:H	1:B:1176:ILE:HD13	1.79	0.48
1:A:173:MET:HE3	1:A:174:PRO:O	2.13	0.47
1:A:175:LEU:HD11	1:B:1175:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:LYS:O	1:A:208:GLU:HG3	2.15	0.47
1:A:245:GLN:CD	1:A:338:CYS:SG	2.98	0.47
1:A:302:ILE:HD13	1:A:319:HIS:CD2	2.50	0.47
1:A:245:GLN:CG	1:A:338:CYS:SG	3.03	0.47
1:B:1270:ILE:HD11	1:B:1322:LYS:HD3	1.96	0.46
1:B:1294:ILE:HG12	1:B:1323:TYR:CE1	2.51	0.46
1:A:148:LEU:HD21	1:A:165:ILE:CD1	2.46	0.46
1:B:1156:MET:CE	1:B:1239:LEU:HD11	2.45	0.46
1:A:103:TRP:CE2	1:A:328:LYS:HB3	2.52	0.45
1:A:148:LEU:HD21	1:A:165:ILE:HD11	1.99	0.45
1:B:1135:ALA:HB3	1:B:1167:VAL:HG12	1.99	0.45
1:B:1203:MET:HE1	1:B:1284:PHE:CZ	2.52	0.45
1:A:193:LYS:HD3	5:A:2119:HOH:O	2.17	0.45
1:A:184:PHE:CE1	1:A:186:VAL:HG23	2.52	0.45
1:B:1264:LYS:HB2	1:B:1264:LYS:NZ	2.31	0.45
1:B:1280:HIS:CD2	1:B:1317:GLN:HE22	2.34	0.45
1:B:1192:GLU:H	1:B:1198:ILE:HD13	1.81	0.45
1:B:1192:GLU:HB2	1:B:1198:ILE:HD13	1.99	0.44
1:A:240:GLY:O	1:A:286:GLY:HA2	2.16	0.44
1:A:84:LYS:HD2	1:A:86:SER:OG	2.18	0.43
1:A:280:HIS:CD2	1:A:317:GLN:HE22	2.36	0.43
1:B:1165:ILE:HD12	1:B:1165:ILE:N	2.32	0.43
1:B:1305:ASP:HB3	1:B:1310:ILE:O	2.19	0.43
1:A:185:LYS:HD3	1:A:187:PHE:CZ	2.54	0.43
1:B:1270:ILE:HD11	1:B:1322:LYS:HA	2.01	0.43
1:B:1176:ILE:HD13	1:B:1176:ILE:N	2.35	0.42
1:A:203:MET:O	1:A:295:THR:HB	2.19	0.42
1:B:1244:ALA:HB3	1:B:1332:ILE:HD13	2.02	0.41
1:B:1192:GLU:H	1:B:1198:ILE:CD1	2.33	0.41
1:B:1170:VAL:O	1:B:1173:MET:HB3	2.20	0.41
1:A:307:LYS:HE2	5:A:2222:HOH:O	2.20	0.41
1:B:1270:ILE:HD12	1:B:1325:LEU:HD22	1.99	0.41
1:A:264:LYS:HA	1:A:269:TYR:CG	2.56	0.41
1:B:1136:VAL:HG11	1:B:1198:ILE:HD12	2.03	0.41
1:A:170:VAL:O	1:A:173:MET:HB3	2.21	0.40
1:A:184:PHE:CZ	1:B:1184:PHE:CZ	3.09	0.40
1:B:1270:ILE:HD13	1:B:1322:LYS:HD3	2.03	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	285/289 (99%)	273 (96%)	11 (4%)	1 (0%)	30	20
1	B	285/289 (99%)	278 (98%)	6 (2%)	1 (0%)	30	20
All	All	570/578 (99%)	551 (97%)	17 (3%)	2 (0%)	30	20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	VAL
1	B	1338	CYS

### 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	258/260 (99%)	254 (98%)	4 (2%)	55	50
1	B	258/260 (99%)	254 (98%)	4 (2%)	55	50
All	All	516/520 (99%)	508 (98%)	8 (2%)	55	50

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	LYS
1	A	96	GLU
1	A	182	ARG
1	A	357	GLN

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Mol	Chain	Res	Type
1	B	1173	MET
1	B	1176	ILE
1	B	1182	ARG
1	B	1264	LYS

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

Mol	Chain	Res	Type
1	A	245	GLN
1	A	290	GLN
1	A	296	GLN
1	A	313	GLN
1	A	317	GLN
1	A	357	GLN
1	A	366	ASN
1	B	1120	ASN
1	B	1125	GLN
1	B	1231	GLN
1	B	1245	GLN
1	B	1296	GLN
1	B	1313	GLN
1	B	1317	GLN

### 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](#)

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	BGC	C	1	2	12,12,12	0.81	0	17,17,17	0.71	0
2	GAL	C	2	2	11,11,12	0.87	0	15,15,17	0.67	0
2	BGC	D	1	2	12,12,12	0.77	0	17,17,17	0.72	0
2	GAL	D	2	2	11,11,12	0.84	0	15,15,17	0.73	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
2	BGC	C	1	2	-	2/2/22/22	0/1/1/1
2	GAL	C	2	2	-	0/2/19/22	0/1/1/1
2	BGC	D	1	2	-	0/2/22/22	0/1/1/1
2	GAL	D	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

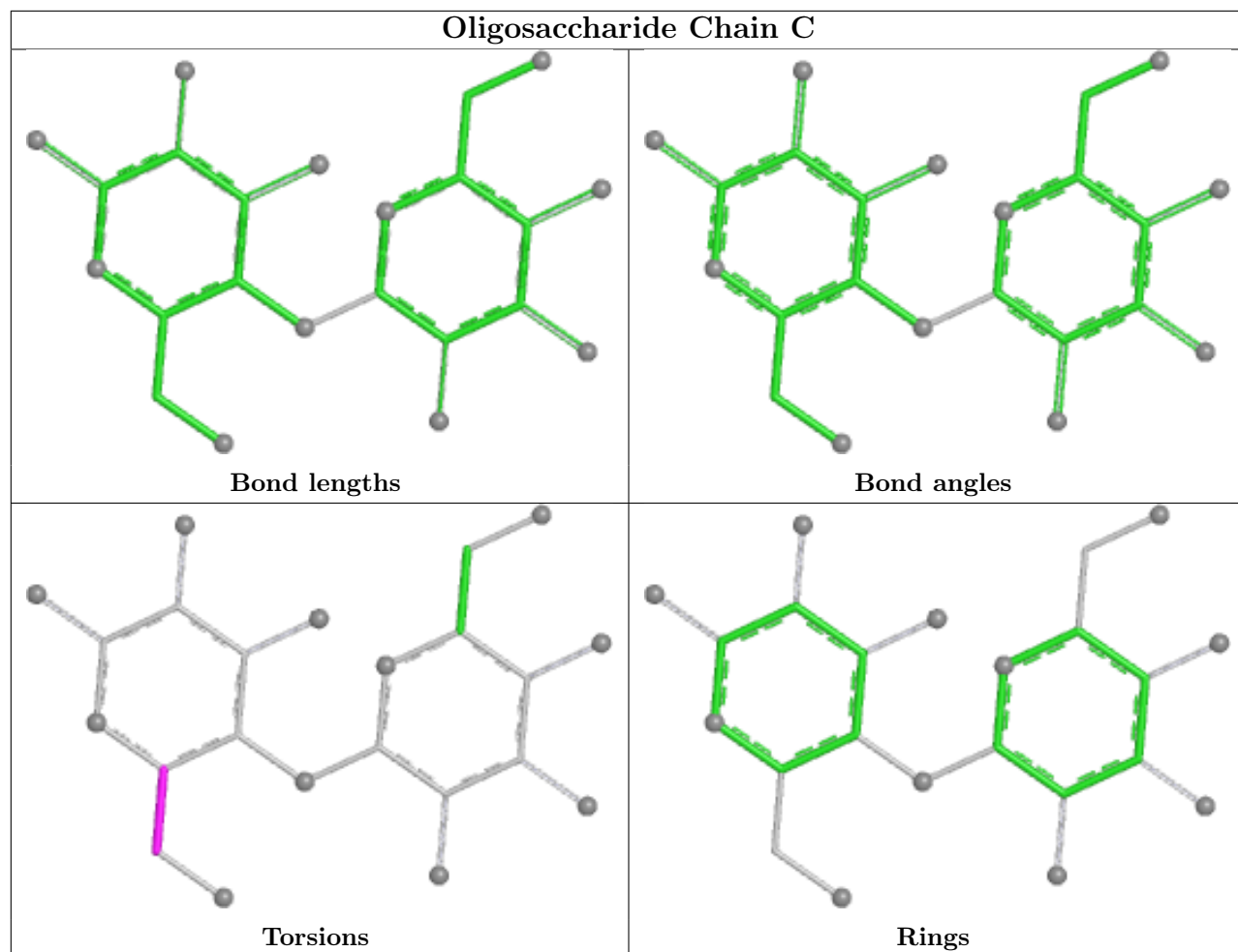
All (2) torsion outliers are listed below:

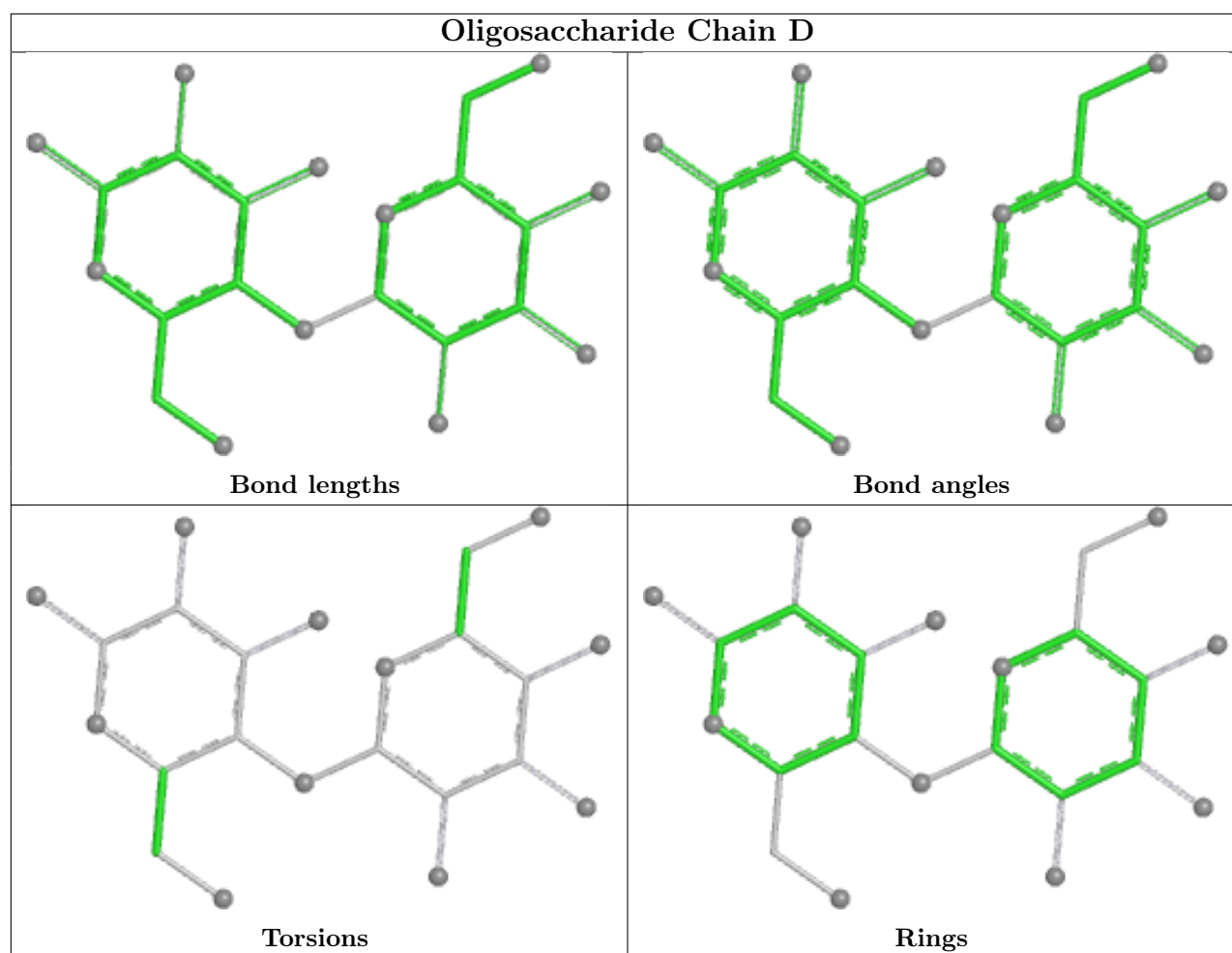
Mol	Chain	Res	Type	Atoms
2	C	1	BGC	C4-C5-C6-O6
2	C	1	BGC	O5-C5-C6-O6

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, 2 are monoatomic - leaving 2 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	UDP	B	2371	3	25,26,26	1.24	1 (4%)	38,40,40	1.09	3 (7%)
4	UDP	A	1371	3	25,26,26	1.26	2 (8%)	38,40,40	1.09	4 (10%)

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	UDP	B	2371	3	-	3/16/32/32	0/2/2/2
4	UDP	A	1371	3	-	3/16/32/32	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2371	UDP	PB-O1B	3.56	1.61	1.50
4	A	1371	UDP	PB-O1B	3.48	1.61	1.50
4	A	1371	UDP	C4-N3	2.14	1.42	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2371	UDP	O3B-PB-O2B	3.38	120.46	107.80
4	A	1371	UDP	O3B-PB-O2B	3.34	120.34	107.80
4	A	1371	UDP	O3B-PB-O3A	2.28	112.27	104.64
4	A	1371	UDP	O2A-PA-O3A	2.22	113.27	107.27
4	B	2371	UDP	O3B-PB-O3A	2.21	112.05	104.64
4	B	2371	UDP	O2A-PA-O3A	2.06	112.85	107.27
4	A	1371	UDP	PA-O5'-C5'	2.05	133.08	121.35

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1371	UDP	C3'-C4'-C5'-O5'
4	A	1371	UDP	O4'-C4'-C5'-O5'
4	B	2371	UDP	C3'-C4'-C5'-O5'
4	A	1371	UDP	C4'-C5'-O5'-PA
4	B	2371	UDP	C4'-C5'-O5'-PA
4	B	2371	UDP	O4'-C4'-C5'-O5'

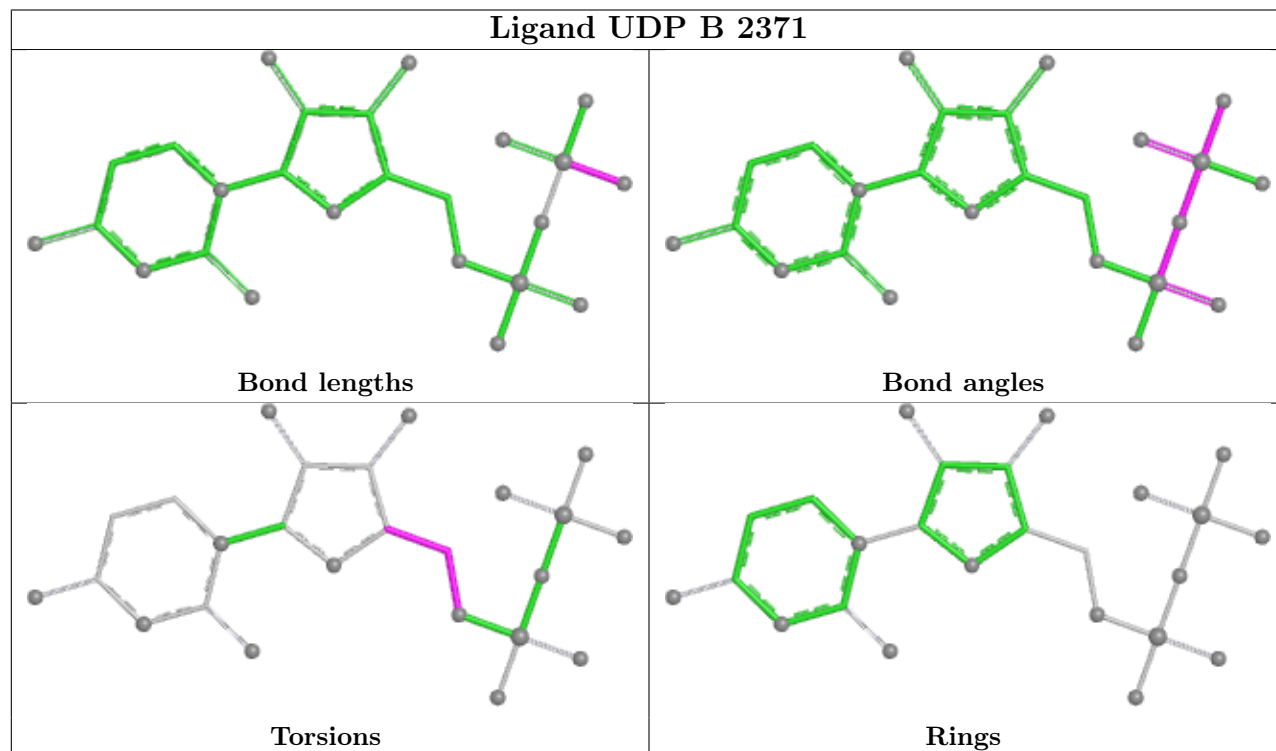
There are no ring outliers.

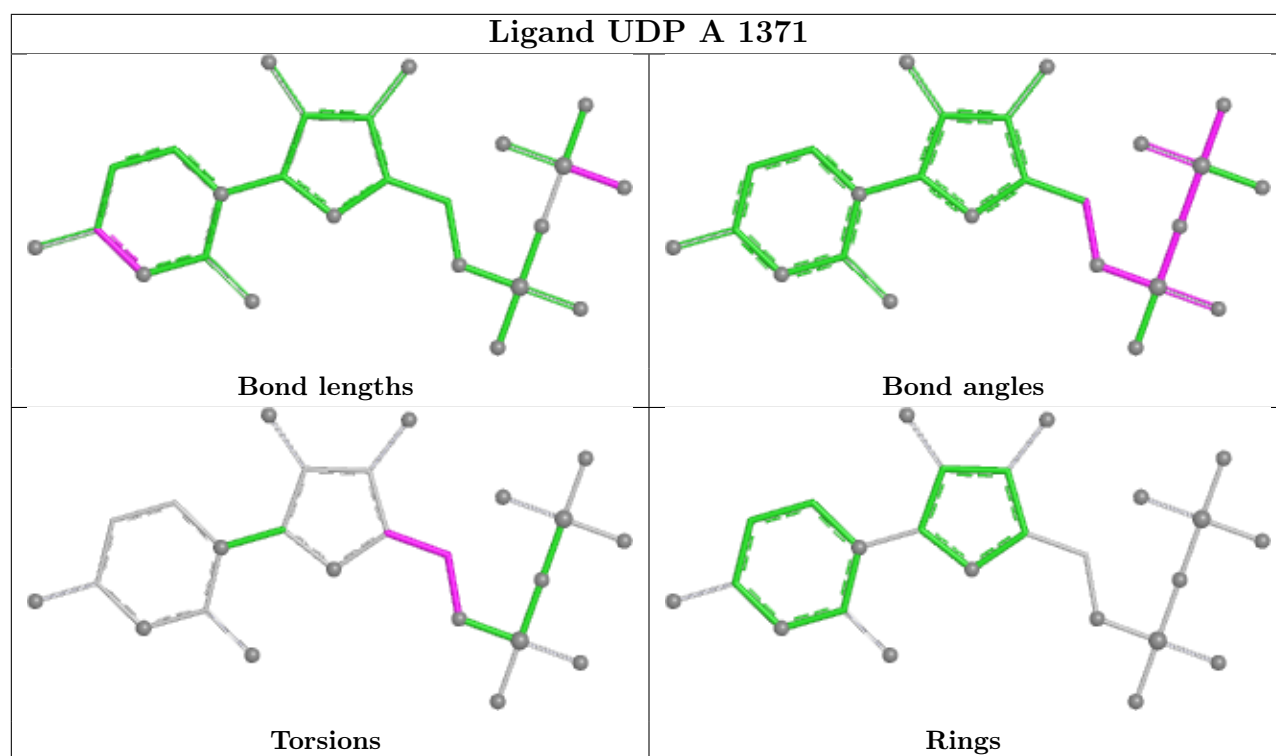
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is



within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.