



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 03:50 PM GMT

PDB ID : 1KFG  
Title : The X-ray Crystal Structure of Cel9G from Clostridium cellulolyticum complexed with a Thio-Oligosaccharide Inhibitor  
Authors : Mandelman, D.; Belaich, A.; Belaich, J.-P.; Driguez, H.; Haser, R.  
Deposited on : 2001-11-20  
Resolution : 1.90 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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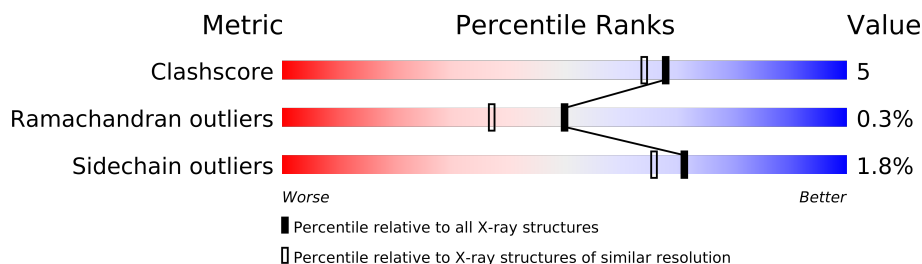
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.90 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	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)

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. 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	614	
1	B	614	

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 10341 atoms, of which 0 are hydrogen 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 ENDOGLUCANASE G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	612	Total	C	N	O	S	0	0	0
			4781	3041	783	938	19			
1	B	613	Total	C	N	O	S	0	0	0
			4762	3028	780	935	19			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	574	THR	ARG	CONFLICT	UNP P37700
A	575	THR	ARG	CONFLICT	UNP P37700
B	574	THR	ARG	CONFLICT	UNP P37700
B	575	THR	ARG	CONFLICT	UNP P37700

- Molecule 2 is a polymer of unknown type called SUGAR (GS4-GLC).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	O	S	0	0
			22	12	9	1		
2	B	2	Total	C	O	S	0	0
			22	12	9	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	574	THR	ARG	CONFLICT	UNP P37700
A	575	THR	ARG	CONFLICT	UNP P37700
B	574	THR	ARG	CONFLICT	UNP P37700
B	575	THR	ARG	CONFLICT	UNP P37700

- Molecule 3 is a polymer of unknown type called SUGAR (GS4-GS1).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	O	S	0	0
			23	12	9	2		
3	B	2	Total	C	O	S	0	0
			23	12	9	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	574	THR	ARG	CONFLICT	UNP P37700
A	575	THR	ARG	CONFLICT	UNP P37700
B	574	THR	ARG	CONFLICT	UNP P37700
B	575	THR	ARG	CONFLICT	UNP P37700

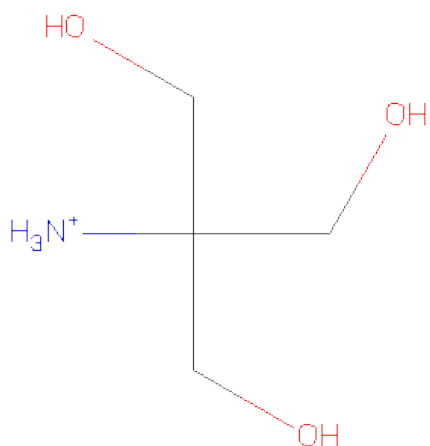
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Ca	0	0
			2	2		
4	A	2	Total	Ca	0	0
			2	2		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

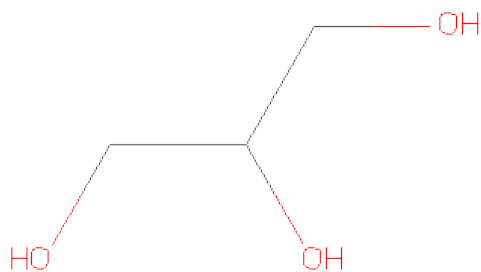
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Mg	0	0
			2	2		
5	A	3	Total	Mg	0	0
			3	3		

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

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

- Molecule 8 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ni	0	0
			1	1		

- Molecule 9 is water.

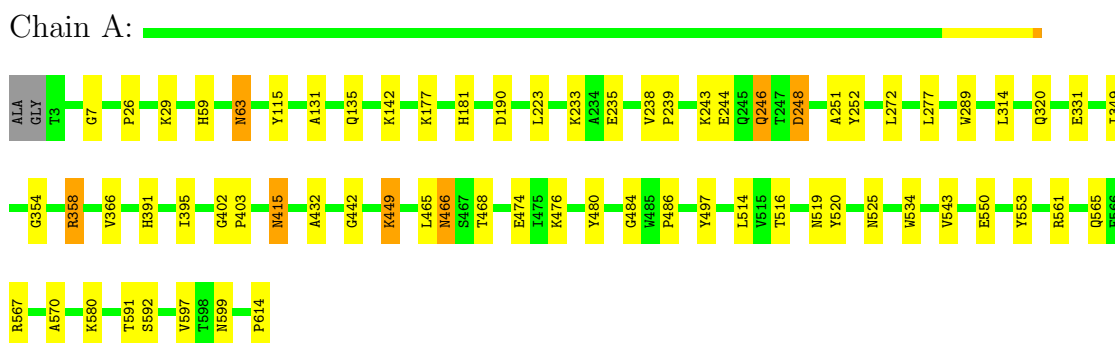
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	312	Total	O	0	0
			312	312		
9	B	354	Total	O	0	0
			354	354		

### 3 Residue-property plots

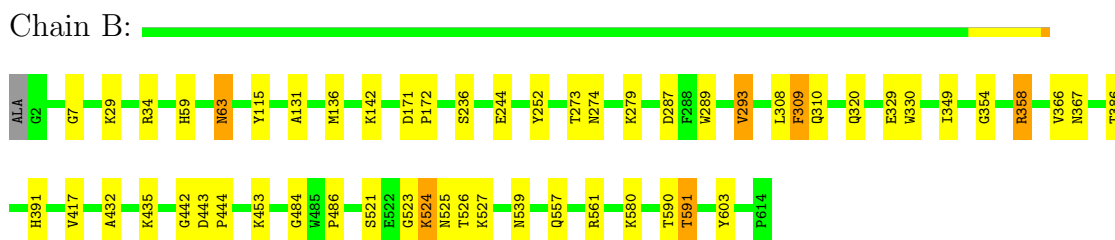
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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



#### • Molecule 1: ENDOGLUCANASE G



## 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	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.04Å 57.73Å 86.63Å 93.86° 100.83° 99.54°	Depositor
Resolution (Å)	42.42 – 1.90	Depositor
% Data completeness (in resolution range)	93.2 (42.42-1.90)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.167 , 0.204	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10341	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	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: GS1, GOL, MG, BGC, NI, CA, TRS, SGC

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	0.42	0/4922	0.62	0/6710
1	B	0.43	0/4901	0.65	0/6682
All	All	0.43	0/9823	0.63	0/13392

There are no bond length outliers.

There are no bond angle outliers.

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	4781	0	4475	55	0
1	B	4762	0	4447	35	1
2	A	22	0	19	0	0
2	B	22	0	19	0	0
3	A	23	0	20	1	0
3	B	23	0	20	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	8	0	12	0	0
7	A	12	0	16	0	0
7	B	12	0	16	1	0
8	B	1	0	0	0	0
9	A	312	0	0	3	1
9	B	354	0	0	6	0
All	All	10341	0	9044	92	1

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 5.

All (92) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:465:LEU:HD11	1:A:468:THR:HG23	1.43	0.97
1:A:497:TYR:HB3	1:A:543:VAL:HG22	1.65	0.76
1:B:236:SER:OG	7:B:5012:GOL:H32	1.87	0.73
1:A:314:LEU:HD13	1:A:402:GLY:HA3	1.71	0.70
3:A:618:GS1:H1	9:A:9052:HOH:O	1.91	0.70
1:A:238:VAL:HG13	1:A:239:PRO:HD3	1.73	0.69
1:B:523:GLY:O	1:B:526:THR:HG22	1.95	0.67
1:A:277:LEU:C	1:A:277:LEU:HD23	2.15	0.66
1:A:235:GLU:O	1:A:238:VAL:HG12	1.95	0.66
1:B:287:ASP:HB3	1:B:293:VAL:HG13	1.78	0.66
1:A:358:ARG:HA	1:A:366:VAL:HG23	1.81	0.62
1:A:331:GLU:H	1:A:331:GLU:CD	2.03	0.62
1:A:449:LYS:N	1:A:449:LYS:HD3	2.14	0.62
1:B:310:GLN:HE21	1:B:417:VAL:HG11	1.67	0.60
1:B:244:GLU:HG3	1:B:252:TYR:CE1	2.38	0.58
1:A:534:TRP:CZ3	1:A:614:PRO:HG2	2.38	0.58
3:B:618:GS1:H1	9:B:9080:HOH:O	2.04	0.57
1:A:465:LEU:CD1	1:A:468:THR:HG23	2.28	0.56
1:B:358:ARG:HA	1:B:366:VAL:HG23	1.89	0.55
1:A:277:LEU:O	1:A:277:LEU:HD23	2.06	0.55
1:A:497:TYR:HB3	1:A:543:VAL:CG2	2.33	0.55
1:A:597:VAL:CG2	1:A:599:ASN:OD1	2.55	0.55
1:B:557:GLN:O	1:B:561:ARG:HG2	2.06	0.55
1:A:238:VAL:CG1	1:A:239:PRO:HD3	2.38	0.53
1:B:525:ASN:O	1:B:527:LYS:HG3	2.09	0.53
1:B:329:GLU:OE1	1:B:435:LYS:HD2	2.08	0.53
1:A:63:ASN:HD22	1:A:63:ASN:N	2.06	0.53
1:A:331:GLU:N	1:A:331:GLU:CD	2.63	0.52
1:A:223:LEU:HD21	1:A:272:LEU:HD21	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:591:THR:HG22	1:A:592:SER:N	2.24	0.52
1:B:63:ASN:N	1:B:63:ASN:HD22	2.07	0.52
1:A:580:LYS:HE3	9:A:9218:HOH:O	2.10	0.51
1:A:516:THR:HA	1:A:567:ARG:O	2.11	0.51
1:A:465:LEU:HD21	1:A:468:THR:HG22	1.92	0.51
1:A:449:LYS:H	1:A:449:LYS:HD3	1.74	0.51
1:A:244:GLU:HG3	1:A:252:TYR:CE1	2.45	0.51
1:B:29:LYS:HE2	1:B:34:ARG:O	2.11	0.51
1:A:465:LEU:HD21	1:A:468:THR:CG2	2.41	0.50
1:A:238:VAL:HG13	1:A:239:PRO:CD	2.40	0.50
1:A:480:TYR:CE2	1:A:561:ARG:HD3	2.46	0.50
1:B:367:ASN:ND2	9:B:9256:HOH:O	2.43	0.50
1:B:524:LYS:H	1:B:524:LYS:CD	2.24	0.50
1:A:597:VAL:HG22	1:A:599:ASN:H	1.76	0.50
1:A:465:LEU:HD13	1:A:465:LEU:C	2.33	0.50
1:B:524:LYS:HD2	1:B:524:LYS:H	1.76	0.49
1:A:476:LYS:HG2	1:A:565:GLN:HG2	1.94	0.49
1:B:590:THR:C	1:B:591:THR:HG23	2.32	0.49
1:A:277:LEU:C	1:A:277:LEU:CD2	2.82	0.48
1:B:349:ILE:HD11	1:B:432:ALA:HB3	1.94	0.48
1:B:453:LYS:HG2	9:B:9227:HOH:O	2.12	0.48
1:B:279:LYS:HD3	1:B:330:TRP:CH2	2.49	0.48
1:A:115:TYR:CD1	1:A:142:LYS:HB3	2.48	0.48
1:B:358:ARG:HA	1:B:366:VAL:CG2	2.43	0.48
1:B:580:LYS:HE3	9:B:9290:HOH:O	2.13	0.48
1:B:524:LYS:HD3	9:B:9316:HOH:O	2.14	0.47
1:A:349:ILE:HD11	1:A:432:ALA:HB3	1.95	0.47
1:A:243:LYS:HD3	1:A:248:ASP:HA	1.97	0.47
1:A:525:ASN:HB2	1:A:550:GLU:OE1	2.15	0.46
1:B:279:LYS:HD3	1:B:330:TRP:HH2	1.80	0.46
1:A:520:TYR:HB3	1:A:565:GLN:HE21	1.81	0.46
1:A:7:GLY:HA3	1:A:442:GLY:O	2.15	0.46
1:A:289:TRP:CE2	1:A:320:GLN:HG3	2.51	0.45
1:A:514:LEU:HD22	1:A:570:ALA:HA	1.98	0.45
1:A:358:ARG:HA	1:A:366:VAL:CG2	2.46	0.45
1:A:244:GLU:HG2	1:A:251:ALA:HA	1.98	0.45
1:B:443:ASP:HA	1:B:444:PRO:HD3	1.86	0.45
1:B:171:ASP:HA	1:B:172:PRO:HD2	1.61	0.45
1:A:415:ASN:C	1:A:415:ASN:HD22	2.19	0.44
1:B:590:THR:HG22	1:B:591:THR:N	2.32	0.44
1:A:366:VAL:HG23	1:A:366:VAL:O	2.17	0.44
1:B:7:GLY:HA3	1:B:442:GLY:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:466:ASN:OD1	1:A:565:GLN:OE1	2.35	0.44
1:B:521:SER:OG	1:B:526:THR:HG21	2.18	0.43
1:A:190:ASP:OD2	1:A:233:LYS:HE2	2.17	0.43
1:B:273:THR:O	1:B:274:ASN:HB2	2.19	0.43
1:A:246:GLN:HG3	9:A:9222:HOH:O	2.19	0.43
1:A:314:LEU:CD1	1:A:403:PRO:HD2	2.48	0.43
1:A:26:PRO:O	1:A:29:LYS:HB2	2.19	0.43
1:A:474:GLU:OE1	1:A:519:ASN:ND2	2.52	0.42
1:B:603:TYR:N	1:B:603:TYR:CD1	2.86	0.42
1:B:308:LEU:O	1:B:309:PHE:HB3	2.19	0.42
1:B:366:VAL:HG23	1:B:366:VAL:O	2.19	0.42
1:A:591:THR:HG22	1:A:592:SER:H	1.84	0.42
1:A:135:GLN:HG3	1:A:553:TYR:CZ	2.55	0.42
1:B:289:TRP:CE2	1:B:320:GLN:HG3	2.55	0.41
1:B:59:HIS:CE1	1:B:131:ALA:HB2	2.55	0.41
1:A:177:LYS:NZ	1:A:181:HIS:HE1	2.17	0.41
1:A:395:ILE:O	1:A:395:ILE:HG23	2.19	0.41
1:B:115:TYR:CD1	1:B:142:LYS:HB3	2.56	0.41
1:A:59:HIS:CD2	1:A:131:ALA:HB2	2.56	0.41
1:A:520:TYR:HB3	1:A:565:GLN:NE2	2.36	0.40
1:B:539:ASN:ND2	9:B:9146:HOH:O	2.54	0.40

All (1) 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	Distance(Å)	Clash(Å)
1:B:386:THR:O	9:A:9068:HOH:O[1_454]	2.17	0.03

## 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	610/614 (99%)	591 (97%)	17 (3%)	2 (0%)	50	37
1	B	611/614 (100%)	589 (96%)	20 (3%)	2 (0%)	50	37
All	All	1221/1228 (99%)	1180 (97%)	37 (3%)	4 (0%)	50	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	354	GLY
1	A	354	GLY
1	B	484	GLY
1	A	484	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	503/507 (99%)	494 (98%)	9 (2%)	71	66
1	B	498/507 (98%)	489 (98%)	9 (2%)	71	66
All	All	1001/1014 (99%)	983 (98%)	18 (2%)	71	66

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	246	GLN
1	A	248	ASP
1	A	358	ARG
1	A	391	HIS
1	A	415	ASN
1	A	449	LYS
1	A	466	ASN
1	A	486	PRO
1	B	63	ASN
1	B	136	MET
1	B	293	VAL
1	B	309	PHE
1	B	358	ARG
1	B	391	HIS
1	B	486	PRO
1	B	524	LYS
1	B	591	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	117	GLN
1	A	135	GLN
1	A	181	HIS
1	A	240	ASN
1	A	245	GLN
1	A	246	GLN
1	A	276	GLN
1	A	294	ASN
1	A	415	ASN
1	A	466	ASN
1	A	519	ASN
1	A	525	ASN
1	A	544	ASN
1	A	551	ASN
1	A	605	ASN
1	B	59	HIS
1	B	63	ASN
1	B	117	GLN
1	B	181	HIS
1	B	240	ASN
1	B	276	GLN
1	B	294	ASN
1	B	310	GLN
1	B	367	ASN
1	B	466	ASN
1	B	539	ASN
1	B	557	GLN
1	B	595	ASN
1	B	605	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 ⓘ

8 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	$\# Z  > 2$
2	SGC	A	615	2	10,11,12	0.72	0	11,15,17	0.74	0
2	BGC	A	616	3,2	10,11,12	0.72	0	11,15,17	0.51	0
3	SGC	A	617	3,2	10,11,12	0.75	0	11,15,17	0.54	0
3	GS1	A	618	3	12,12,12	0.62	0	17,17,17	0.36	0
2	SGC	B	615	2	10,11,12	0.77	0	11,15,17	0.54	0
2	BGC	B	616	3,2	10,11,12	0.70	0	11,15,17	0.36	0
3	SGC	B	617	3,2	10,11,12	0.87	0	11,15,17	0.44	0
3	GS1	B	618	3	12,12,12	0.63	0	17,17,17	0.25	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	SGC	A	615	2	-	0/2/19/22	0/1/1/1
2	BGC	A	616	3,2	-	0/2/19/22	0/1/1/1
3	SGC	A	617	3,2	-	0/2/19/22	0/1/1/1
3	GS1	A	618	3	-	0/2/22/22	0/1/1/1
2	SGC	B	615	2	-	0/2/19/22	0/1/1/1
2	BGC	B	616	3,2	-	0/2/19/22	0/1/1/1
3	SGC	B	617	3,2	-	0/2/19/22	0/1/1/1
3	GS1	B	618	3	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry

Of 15 ligands modelled in this entry, 10 are monoatomic - leaving 5 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
7	GOL	A	5010	-	5,5,5	0.96	0	5,5,5	0.78	0
7	GOL	A	5011	-	5,5,5	0.98	0	5,5,5	0.74	0
6	TRS	A	5013	-	7,7,7	2.26	1 (14%)	9,9,9	3.27	7 (77%)
7	GOL	B	5009	-	5,5,5	0.93	0	5,5,5	0.78	0
7	GOL	B	5012	-	5,5,5	0.83	0	5,5,5	0.84	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
7	GOL	A	5010	-	-	0/4/4/4	0/0/0/0
7	GOL	A	5011	-	-	0/4/4/4	0/0/0/0
6	TRS	A	5013	-	-	0/9/9/9	0/0/0/0
7	GOL	B	5009	-	-	0/4/4/4	0/0/0/0
7	GOL	B	5012	-	-	0/4/4/4	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	5013	TRS	C-N	-4.99	1.43	1.50

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	5013	TRS	C2-C-C1	-6.40	100.19	110.70
6	A	5013	TRS	O1-C1-C	-4.53	101.62	111.55
6	A	5013	TRS	C2-C-N	2.74	115.75	108.30
6	A	5013	TRS	C3-C-C2	-2.48	106.63	110.70
6	A	5013	TRS	C3-C-N	2.39	114.80	108.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	5013	TRS	C3-C-C1	2.35	114.57	110.70
6	A	5013	TRS	O2-C2-C	-2.05	107.06	111.55

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.