



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 09:55 pm GMT

PDB ID : 1CXE  
Title : COMPLEX OF CGTASE WITH MALTOTETRAOSE AT ROOM TEMPERATURE AND PH 9.1 BASED ON DIFFRACTION DATA OF A CRYSTAL SOAKED WITH ALPHA-CYCLODEXTRIN  
Authors : Knegt, R.M.A.; Strokopytov, B.V.; Dijkstra, B.W.  
Deposited on : 1995-07-28  
Resolution : 2.10 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

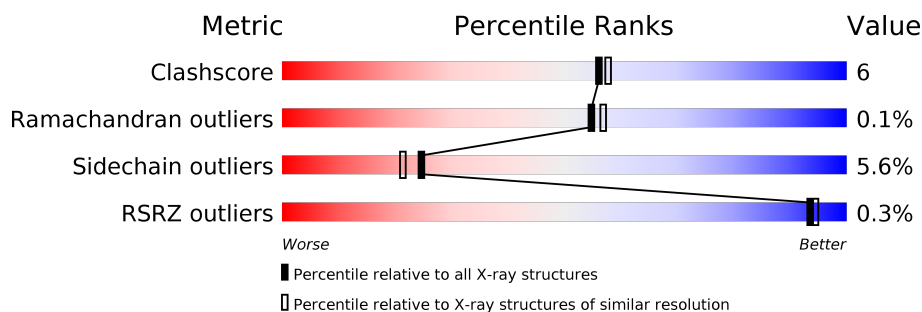
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 2.10 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	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	686	

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	MAL	A	688	-	-	-	X
2	MAL	A	691	-	-	-	X
3	GLC	A	692	-	-	-	X
3	GLC	A	693	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GLC	A	694	-	-	-	X
3	GLC	A	695	-	-	-	X

## 2 Entry composition [i](#)

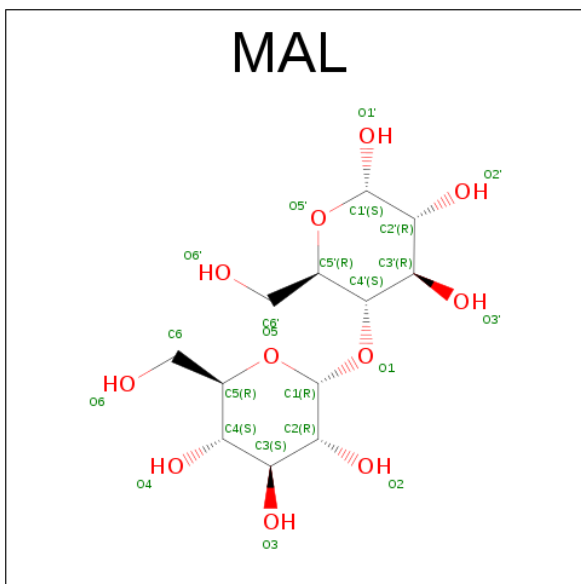
There are 5 unique types of molecules in this entry. The entry contains 5797 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CYCLODEXTRIN GLYCOSYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	686	Total	C	N	O	S	0	0	0
			5264	3321	900	1027	16			

- Molecule 2 is SUGAR (MALTOSE) (three-letter code: MAL) (formula: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			23	12	11		
2	A	1	Total	C	O	0	0
			23	12	11		
2	A	1	Total	C	O	0	0
			23	12	11		

- Molecule 3 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	4	Total	C	O	0	0
			45	24	21		

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

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

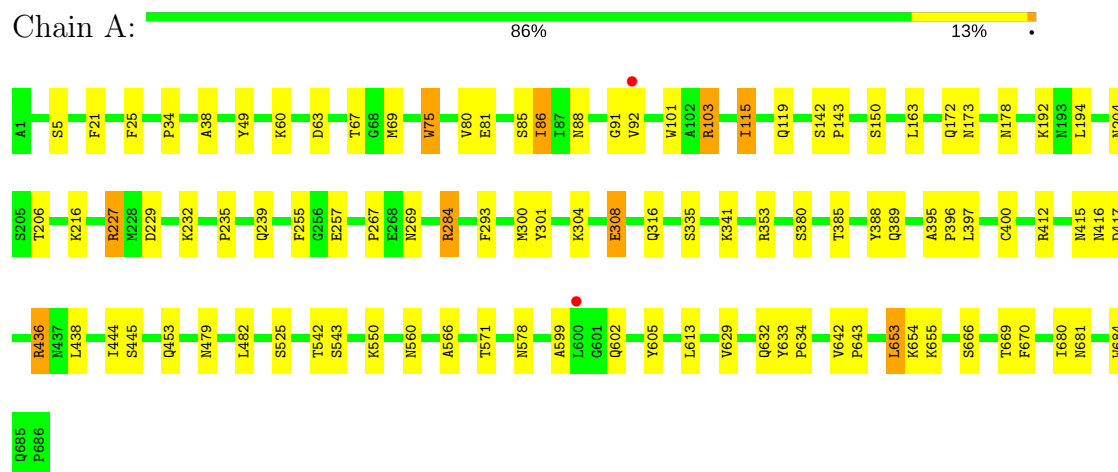
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	417	Total	O	0	0
			417	417		

### 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 the various outlier classes 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: CYCLODEXTRIN GLYCOSYLTRANSFERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.39Å 111.60Å 66.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.10 40.29 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.10) 82.9 (40.29-2.10)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 2.10Å)	Xtriage
Refinement program	TNT	Depositor
R, $R_{free}$	0.153 , 0.100 0.148 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	22.4	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 91.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5797	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, GLC, MAL

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	0.43	0/5394	0.66	0/7352

There are no bond length outliers.

There are no bond angle outliers.

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	5264	0	5025	60	0
2	A	69	0	66	0	0
3	A	45	0	39	6	0
4	A	2	0	0	0	0
5	A	417	0	0	8	0
All	All	5797	0	5130	61	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 6.

All (61) 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:A:75:TRP:CZ2	1:A:227:ARG:HD3	2.06	0.91
1:A:227:ARG:HG3	1:A:255:PHE:CE2	2.09	0.87
1:A:670:PHE:CE2	1:A:680:ILE:HD11	2.13	0.83
1:A:101:TRP:HE1	3:A:692:GLC:H62	1.44	0.82
1:A:560:ASN:HD21	1:A:578:ASN:HA	1.48	0.77
1:A:88:ASN:HD21	1:A:91:GLY:H	1.32	0.77
1:A:38:ALA:HB2	1:A:86:ILE:HD11	1.71	0.71
1:A:267:PRO:HD2	5:A:983:HOH:O	1.88	0.71
1:A:304:LYS:O	1:A:308:GLU:HG2	1.89	0.71
1:A:101:TRP:HZ2	3:A:692:GLC:HO6	1.37	0.70
1:A:227:ARG:HH21	1:A:229:ASP:HB2	1.62	0.64
1:A:142:SER:HB2	1:A:143:PRO:HD2	1.79	0.64
1:A:417:ASP:O	1:A:436:ARG:HG3	1.98	0.63
1:A:257:GLU:OE1	3:A:693:GLC:H1	2.00	0.60
1:A:380:SER:HB2	5:A:875:HOH:O	2.01	0.60
1:A:142:SER:HB2	1:A:143:PRO:CD	2.30	0.59
1:A:395:ALA:HB3	1:A:396:PRO:HD3	1.84	0.59
1:A:115:ILE:O	1:A:119:GLN:HG3	2.04	0.57
1:A:60:LYS:HE3	1:A:60:LYS:HA	1.87	0.57
1:A:293:PHE:O	1:A:341:LYS:HD2	2.03	0.57
1:A:670:PHE:CD2	1:A:680:ILE:HD11	2.40	0.56
1:A:232:LYS:HE3	5:A:1080:HOH:O	2.03	0.56
1:A:542:THR:HG21	5:A:919:HOH:O	2.06	0.54
1:A:229:ASP:OD1	3:A:693:GLC:H2	2.09	0.53
1:A:284:ARG:HD3	5:A:931:HOH:O	2.09	0.53
1:A:670:PHE:CZ	1:A:680:ILE:HD11	2.44	0.52
1:A:60:LYS:HE3	1:A:63:ASP:OD1	2.12	0.50
1:A:101:TRP:HZ2	3:A:692:GLC:O6	1.94	0.49
1:A:397:LEU:HA	1:A:400:CYS:SG	2.53	0.49
1:A:599:ALA:O	1:A:602:GLN:HB3	2.12	0.48
1:A:178:ASN:O	1:A:192:LYS:HD3	2.14	0.48
1:A:654:LYS:HE3	1:A:684:TRP:CZ2	2.49	0.48
1:A:605:TYR:CE1	1:A:655:LYS:HB2	2.51	0.46
1:A:69:MET:HG3	1:A:388:TYR:CE2	2.50	0.46
1:A:642:VAL:HB	1:A:643:PRO:HD2	1.98	0.46
1:A:670:PHE:CD2	1:A:680:ILE:CD1	2.99	0.46
3:A:693:GLC:H5	3:A:694:GLC:O6	2.15	0.46
1:A:301:TYR:HE2	1:A:416:ASN:HD22	1.64	0.45
1:A:227:ARG:NH2	1:A:229:ASP:HB2	2.30	0.45
1:A:235:PRO:O	1:A:239:GLN:HG3	2.16	0.45
1:A:204:ASN:OD1	1:A:206:THR:HB	2.17	0.45
1:A:88:ASN:ND2	1:A:91:GLY:H	2.07	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ARG:HB2	5:A:724:HOH:O	2.17	0.44
1:A:300:MET:HB2	1:A:415:ASN:O	2.19	0.43
1:A:444:ILE:CD1	1:A:482:LEU:HB2	2.49	0.43
1:A:81:GLU:OE1	1:A:103:ARG:HD3	2.18	0.43
1:A:25:PHE:HB3	5:A:732:HOH:O	2.18	0.43
1:A:34:PRO:HG2	1:A:49:TYR:CG	2.54	0.43
1:A:227:ARG:HG3	1:A:255:PHE:HE2	1.78	0.42
1:A:444:ILE:HD12	1:A:482:LEU:HB2	2.01	0.42
1:A:194:LEU:HA	1:A:194:LEU:HD23	1.84	0.42
1:A:566:ALA:HA	1:A:571:THR:O	2.19	0.42
1:A:633:TYR:CG	1:A:634:PRO:HA	2.55	0.42
1:A:385:THR:O	1:A:389:GLN:HG3	2.20	0.41
1:A:669:THR:HG22	1:A:670:PHE:N	2.35	0.41
1:A:308:GLU:HG2	1:A:308:GLU:H	1.76	0.41
1:A:445:SER:CB	1:A:479:ASN:ND2	2.84	0.41
1:A:670:PHE:CG	1:A:680:ILE:HD13	2.55	0.41
1:A:67:THR:HG23	5:A:860:HOH:O	2.19	0.40
1:A:653:LEU:N	1:A:653:LEU:HD23	2.37	0.40
1:A:543:SER:OG	1:A:550:LYS:HB2	2.21	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	684/686 (100%)	665 (97%)	18 (3%)	1 (0%)	55 57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	629	VAL

### 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	556/556 (100%)	525 (94%)	31 (6%)	25	21

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

Mol	Chain	Res	Type
1	A	5	SER
1	A	21	PHE
1	A	75	TRP
1	A	80	VAL
1	A	85	SER
1	A	86	ILE
1	A	92	VAL
1	A	103	ARG
1	A	115	ILE
1	A	150	SER
1	A	163	LEU
1	A	172	GLN
1	A	173	ASN
1	A	216	LYS
1	A	227	ARG
1	A	269	ASN
1	A	284	ARG
1	A	308	GLU
1	A	316	GLN
1	A	335	SER
1	A	353	ARG
1	A	412	ARG
1	A	436	ARG
1	A	438	LEU
1	A	453	GLN
1	A	525	SER
1	A	613	LEU
1	A	632	GLN
1	A	653	LEU
1	A	666	SER

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Mol	Chain	Res	Type
1	A	681	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	62	ASN
1	A	88	ASN
1	A	120	ASN
1	A	269	ASN
1	A	410	GLN
1	A	416	ASN
1	A	479	ASN
1	A	560	ASN
1	A	685	GLN

### 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 ⓘ

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	$\# Z  > 2$
3	GLC	A	692	3	12,12,12	0.52	0	17,17,17	1.73	5 (29%)
3	GLC	A	693	3	11,11,12	0.66	0	15,15,17	1.83	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLC	A	694	3	11,11,12	0.49	0	15,15,17	1.29	2 (13%)
3	GLC	A	695	3	11,11,12	0.45	0	15,15,17	1.19	1 (6%)

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	GLC	A	692	3	-	0/2/22/22	0/1/1/1
3	GLC	A	693	3	-	0/2/18/22	0/1/1/1
3	GLC	A	694	3	-	0/2/18/22	0/1/1/1
3	GLC	A	695	3	-	0/2/18/22	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	694	GLC	C3-C4-C5	-2.57	106.97	111.26
3	A	695	GLC	C3-C4-C5	-2.57	106.98	111.26
3	A	692	GLC	O2-C2-C3	-2.51	104.89	110.36
3	A	693	GLC	C4-C3-C2	-2.35	107.52	110.59
3	A	693	GLC	O6-C6-C5	-2.15	105.82	111.76
3	A	693	GLC	O3-C3-C2	-2.04	106.16	110.17
3	A	692	GLC	O5-C5-C4	2.03	113.40	109.66
3	A	692	GLC	C4-C3-C2	2.08	114.50	110.84
3	A	693	GLC	C1-O5-C5	2.53	117.90	113.39
3	A	694	GLC	O5-C1-C2	2.73	114.57	110.04
3	A	693	GLC	O3-C3-C4	2.82	116.86	110.02
3	A	692	GLC	O5-C1-C2	3.09	115.17	110.04
3	A	692	GLC	C1-O5-C5	3.13	119.04	113.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	692	GLC	3	0
3	A	693	GLC	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	694	GLC	1	0

## 5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	MAL	A	687	-	24,24,24	0.35	0	35,35,35	0.76	1 (2%)
2	MAL	A	688	-	24,24,24	0.31	0	35,35,35	0.82	0
2	MAL	A	691	-	24,24,24	0.35	0	35,35,35	1.29	5 (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
2	MAL	A	687	-	-	0/8/48/48	0/2/2/2
2	MAL	A	688	-	-	0/8/48/48	0/2/2/2
2	MAL	A	691	-	-	0/8/48/48	0/2/2/2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	691	MAL	O3'-C3'-C2'	-2.97	103.90	110.36
2	A	691	MAL	O1-C1-C2	-2.30	102.93	108.11
2	A	691	MAL	O2-C2-C3	-2.13	105.73	110.36
2	A	687	MAL	O4-C4-C5	-2.01	104.22	109.28
2	A	691	MAL	O5'-C1'-C2'	2.07	113.47	110.04
2	A	691	MAL	C1'-O5'-C5'	2.58	118.05	113.39

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

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	686/686 (100%)	-0.78	2 (0%) 93 94	11, 20, 41, 72	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	600	LEU	2.7
1	A	92	VAL	2.0

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

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
3	GLC	A	695	11/12	0.57	0.39	19.88	62,65,69,73	11
3	GLC	A	693	11/12	0.53	0.50	11.08	54,56,60,64	11
3	GLC	A	692	12/12	0.59	0.38	7.20	61,63,68,73	12
3	GLC	A	694	11/12	0.73	0.21	5.11	53,54,62,62	11



## 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	MAL	A	688	23/23	0.79	0.26	25.17	50,57,64,69	0
2	MAL	A	691	23/23	0.70	0.31	3.85	64,68,73,78	0
2	MAL	A	687	23/23	0.96	0.09	1.36	16,23,28,31	0
4	CA	A	690	1/1	0.99	0.09	1.01	17,17,17,17	0
4	CA	A	689	1/1	0.99	0.03	-3.65	23,23,23,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.