



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2024 – 08:23 PM EST

PDB ID : 3VM7  
Title : Structure of an Alpha-Amylase from Malbranchea cinnamomea  
Authors : Zhou, P.; Hu, S.Q.; Zhou, Y.; Han, P.; Yang, S.Q.; Jiang, Z.Q.  
Deposited on : 2011-12-09  
Resolution : 2.25 Å(reported)

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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 : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

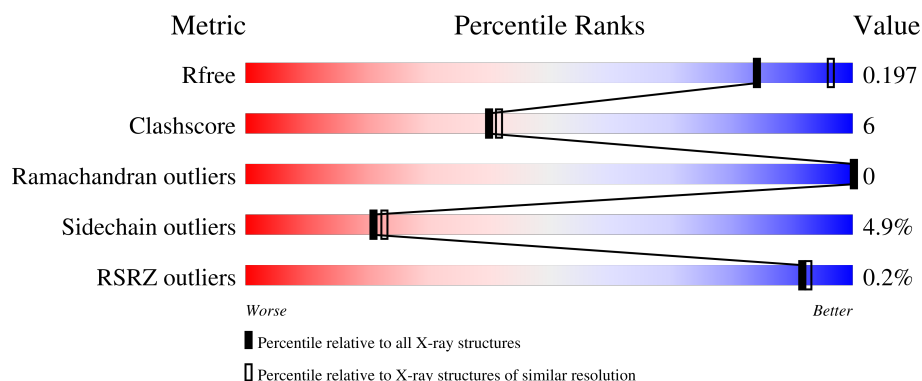
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	164625	1763 (2.26-2.26)
Clashscore	180529	1919 (2.26-2.26)
Ramachandran outliers	177936	1884 (2.26-2.26)
Sidechain outliers	177891	1885 (2.26-2.26)
RSRZ outliers	164620	1763 (2.26-2.26)

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 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  $\leq 5\%$ . 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	492	 83% 11% . .

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4091 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-amylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	0	0
			3660	2310	607	730	13			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

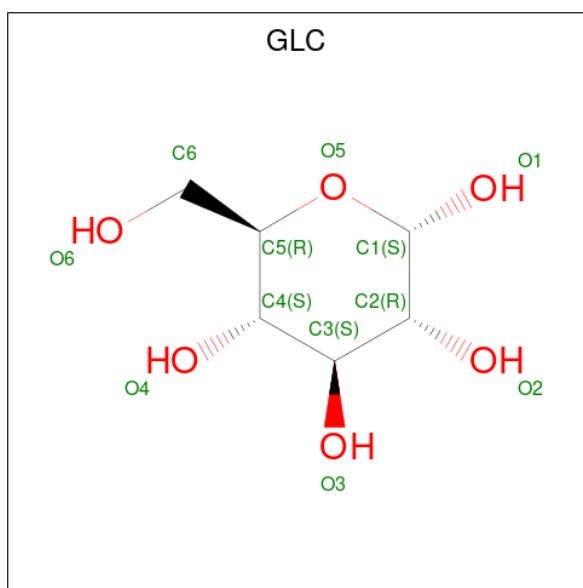
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



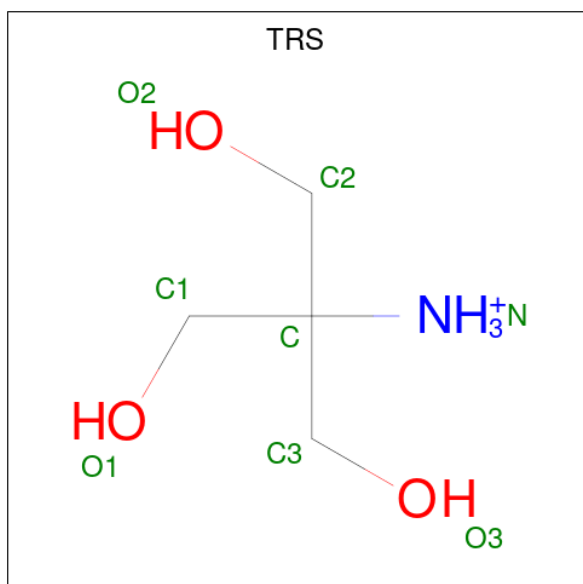
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is alpha-D-glucopyranose (three-letter code: GLC) (formula:  $C_6H_{12}O_6$ ).



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

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	396	Total 396	O 396	0	0



- Molecule 1: Alpha-amylase

G432	D153	THR	T178	LEU	E198	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425
VAL	H167	ALA	M190	D194	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425	
THR	T178	LEU	E198	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425		
LEU	M190	D194	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425			
PHE	D194	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425				
LEU	E198	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425				
ALA	H206	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425					
ALA	N239	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425						
ALA	Y245	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425							
ALA	Q252	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425								
ALA	V265	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425									
ALA	D266	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425										
ALA	F271	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425											
ALA	P272	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425												
ALA	V273	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425													
ALA	T287	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425														
ALA	N288	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425															
ALA	W299	D304	N314	H315	D316	I317	N332	V333	L339	Q353	Y361	L366	W367	L368	Y378	S393	L413	T425																
ALA	D304	N314	H315																															

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.90Å 84.94Å 56.41Å 90.00° 105.61° 90.00°	Depositor
Resolution (Å)	49.99 – 2.25 49.99 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.99-2.25) 100.0 (49.99-2.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	12.13 (at 2.25Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.143 , 0.191 0.148 , 0.197	Depositor DCC
$R_{free}$ test set	2003 reflections (8.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.8	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 34.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4091	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.40% 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: TRS, NAG, GLC, CA

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	0.52	0/3762	0.66	0/5147

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	3660	0	3391	46	0
2	A	1	0	0	0	0
3	A	14	0	13	0	0
4	A	12	0	11	0	0
5	A	8	0	12	1	0
6	A	396	0	0	8	0
All	All	4091	0	3427	46	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 (46) 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:287:THR:HG22	6:A:682:HOH:O	1.68	0.91
1:A:89:GLN:HE22	1:A:103:TRP:H	1.17	0.85
1:A:74:GLN:HE21	1:A:130:ARG:HH11	1.23	0.83
1:A:53:THR:HG21	1:A:361:TYR:HA	1.60	0.82
1:A:458:ILE:HA	6:A:932:HOH:O	1.79	0.81
1:A:153:ASP:HB2	6:A:856:HOH:O	1.79	0.80
1:A:332:ASN:ND2	1:A:425:THR:H	1.84	0.74
1:A:167:HIS:HD2	1:A:194:ASP:OD2	1.71	0.72
1:A:484:LEU:O	1:A:487:SER:HB2	1.97	0.65
1:A:239:ASN:HD22	1:A:265:VAL:HA	1.62	0.65
1:A:153:ASP:CB	6:A:856:HOH:O	2.43	0.63
1:A:53:THR:CG2	1:A:361:TYR:HA	2.27	0.62
1:A:62:ASN:ND2	1:A:65:GLY:H	1.98	0.62
1:A:74:GLN:NE2	1:A:130:ARG:HH11	1.97	0.61
1:A:314:ASN:HD22	1:A:316:ASP:H	1.47	0.61
1:A:67:ILE:HA	1:A:70:LEU:HD22	1.83	0.60
1:A:266:ASP:OD1	5:A:504:TRS:H12	2.02	0.59
1:A:206:HIS:HE1	6:A:746:HOH:O	1.85	0.58
1:A:89:GLN:HE22	1:A:103:TRP:N	1.96	0.58
1:A:471:ASN:ND2	1:A:472:GLN:HG3	2.19	0.57
1:A:89:GLN:HE21	1:A:98:PRO:HB2	1.71	0.55
1:A:353:GLN:HG2	6:A:917:HOH:O	2.07	0.54
1:A:153:ASP:CG	6:A:856:HOH:O	2.46	0.54
1:A:332:ASN:HD21	1:A:425:THR:H	1.55	0.54
1:A:167:HIS:HE1	1:A:198:GLU:OE2	1.91	0.53
1:A:287:THR:HG23	1:A:289:TRP:H	1.75	0.52
1:A:239:ASN:HD21	1:A:266:ASP:H	1.58	0.51
1:A:62:ASN:HD22	1:A:65:GLY:H	1.57	0.51
1:A:314:ASN:ND2	1:A:316:ASP:H	2.08	0.51
1:A:167:HIS:CD2	1:A:194:ASP:OD2	2.60	0.50
1:A:74:GLN:HE21	1:A:130:ARG:NH1	2.00	0.50
1:A:274:TYR:CZ	1:A:317:ILE:HD12	2.48	0.48
1:A:89:GLN:NE2	1:A:103:TRP:H	1.99	0.46
1:A:62:ASN:HD22	1:A:62:ASN:C	2.19	0.45
1:A:262:GLN:NE2	1:A:304:ASP:H	2.16	0.44
1:A:314:ASN:HD22	1:A:314:ASN:C	2.20	0.44
1:A:58:TYR:CE1	1:A:99:TYR:HA	2.52	0.44
1:A:487:SER:HB3	1:A:489:LEU:H	1.83	0.44
1:A:262:GLN:HE22	1:A:304:ASP:H	1.67	0.42
1:A:27:TRP:CD1	1:A:245:TYR:HB3	2.54	0.42
1:A:146:PRO:HA	1:A:190:ASN:ND2	2.34	0.42
1:A:239:ASN:ND2	1:A:266:ASP:H	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:GLY:HA2	6:A:780:HOH:O	2.20	0.40
1:A:76:MET:HG3	1:A:378:TYR:CE2	2.56	0.40
1:A:82:TRP:HA	1:A:135:MET:O	2.21	0.40
1:A:271:PHE:N	1:A:272:PRO:CD	2.84	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	468/492 (95%)	462 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	391/404 (97%)	372 (95%)	19 (5%)	21	23

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	THR
1	A	62	ASN

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Mol	Chain	Res	Type
1	A	70	LEU
1	A	82	TRP
1	A	123	LEU
1	A	178	THR
1	A	265	VAL
1	A	287	THR
1	A	314	ASN
1	A	333	VAL
1	A	339	LEU
1	A	366	LEU
1	A	368	LEU
1	A	393	SER
1	A	413	LEU
1	A	436	VAL
1	A	437	THR
1	A	469	THR
1	A	487	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	74	GLN
1	A	89	GLN
1	A	113	HIS
1	A	143	ASN
1	A	167	HIS
1	A	177	GLN
1	A	190	ASN
1	A	206	HIS
1	A	207	ASN
1	A	239	ASN
1	A	262	GLN
1	A	300	GLN
1	A	303	ASN
1	A	314	ASN
1	A	332	ASN
1	A	411	HIS
1	A	471	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](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is 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	$\# Z  > 2$
3	NAG	A	502	1	14,14,15	0.49	0	17,19,21	1.00	2 (11%)
5	TRS	A	504	-	7,7,7	0.68	0	9,9,9	0.36	0
4	GLC	A	503	-	12,12,12	1.27	1 (8%)	17,17,17	2.64	4 (23%)

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	NAG	A	502	1	-	0/6/23/26	0/1/1/1
5	TRS	A	504	-	-	8/9/9/9	-
4	GLC	A	503	-	-	1/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	GLC	O5-C1	-3.28	1.34	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	GLC	C1-O5-C5	-6.72	100.65	113.65
4	A	503	GLC	O1-C1-C2	6.63	128.24	108.98
4	A	503	GLC	O5-C1-C2	3.36	116.21	110.30
3	A	502	NAG	C2-N2-C7	-2.81	119.13	122.90
3	A	502	NAG	C1-O5-C5	2.32	115.30	112.19
4	A	503	GLC	O6-C6-C5	-2.02	104.45	111.33

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	504	TRS	C2-C-C1-O1
5	A	504	TRS	C3-C-C1-O1
5	A	504	TRS	N-C-C1-O1
5	A	504	TRS	N-C-C3-O3
5	A	504	TRS	C3-C-C2-O2
5	A	504	TRS	C1-C-C2-O2
4	A	503	GLC	C4-C5-C6-O6
5	A	504	TRS	N-C-C2-O2
5	A	504	TRS	C1-C-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	TRS	1	0

## 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 [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	470/492 (95%)	-0.61	1 (0%) 92 93	14, 20, 30, 42	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	432	GLY	2.4

### 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](#)

There are no monosaccharides in this entry.

### 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
4	GLC	A	503	12/12	0.74	0.27	15,19,21,23	12
3	NAG	A	502	14/15	0.81	0.13	36,40,42,44	0
5	TRS	A	504	8/8	0.81	0.13	34,34,36,36	0
2	CA	A	501	1/1	0.99	0.02	19,19,19,19	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.