



wwPDB X-ray Structure Validation Summary Report (i)

Feb 28, 2014 – 07:08 AM GMT

PDB ID : 3OG2
Title : Native crystal structure of Trichoderma reesei beta-galactosidase
Authors : Maksimainen, M.; Rouvinen, J.
Deposited on : 2010-08-16
Resolution : 1.20 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

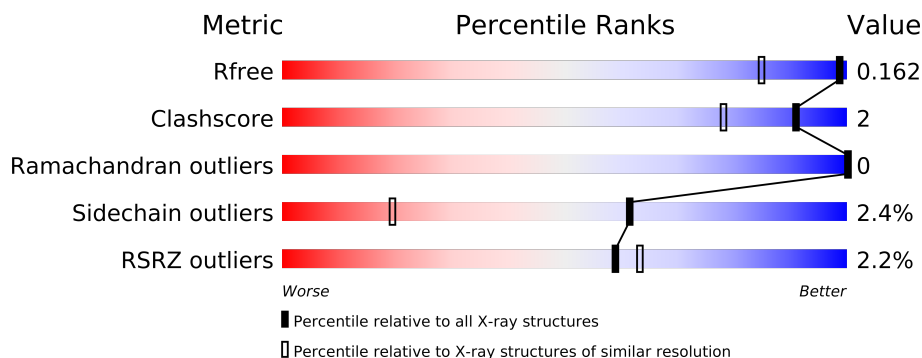
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
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 1.20 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}	66092	1038 (1.26-1.14)
Clashscore	79885	1158 (1.26-1.14)
Ramachandran outliers	78287	1106 (1.26-1.14)
Sidechain outliers	78261	1104 (1.26-1.14)
RSRZ outliers	66119	1038 (1.26-1.14)

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 ≥ 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.

Mol	Chain	Length	Quality of chain
1	A	1003	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	NAG	A	1044	-	X
5	NAG	A	1045	-	X
5	NAG	A	1047	-	X
6	GOL	A	1049	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9055 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 Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	986	Total	C	N	O	S	0	27	0
			7773	5016	1298	1450	9			

- Molecule 2 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 3 is a polymer of unknown type called SUGAR (8-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	8	Total	C	N	O	0	0
			94	52	2	40		

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

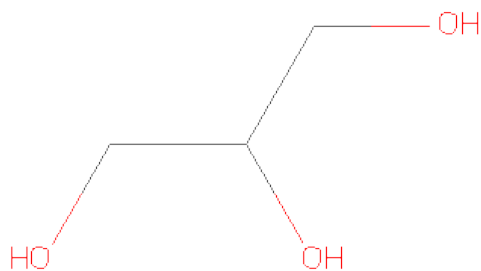
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	4	Total	C	O	0	0
			44	24	20		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	993	Total	O	0	0
			993	993		

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- Molecule 1: Beta-galactosidase

THR	SER	ILE	GLY	LEU	HIS	GLY	GLY	ARG	PRO	ARG	ASP	LEU	ASP	ASP	K39	F63	R71	F90	Y96	V97	D98	R110	F148	L152	D162	S179	K183	E198	F264	D274	N275	R282	F294	F304	R325	F339	V355		
D788	R373	I374	D375	R431	D469	I472	A498	E499	S523	S524	K525	T526	S543	N544	L545	V551	R572	Y576	S586	Y608	R611	N618	K639	G640	I641	V672	Q673	T678	D686	R692	R706	Y722	R736	R742	D766	P767			
R794																																							
D815																																							
R822																																							
N836																																							
R857																																							
E862																																							
H884																																							
G895																																							
P886																																							
S888																																							
S889																																							
S890																																							
S891																																							
A931																																							
T932																																							
A933																																							
Y942																																							

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	67.30Å 69.10Å 81.50Å 109.10° 97.30° 114.50°	Depositor
Resolution (Å)	20.00 – 1.20 47.87 – 1.20	Depositor EDS
% Data completeness (in resolution range)	86.2 (20.00-1.20) 88.4 (47.87-1.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 1.20Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.139 , 0.171 0.133 , 0.162	Depositor DCC
R_{free} test set	16607 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	8.8	Xtriage
Anisotropy	0.453	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 60.0	EDS
Estimated twinning fraction	0.014 for k,h,-h-k-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 719611 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	9055	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, GOL, BMA, NAG, MAN

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	0.71	1/8059 (0.0%)	1.25	66/10981 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1023	TYR	C-OXT	5.92	1.34	1.23

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	942	TYR	CB-CG-CD2	11.84	128.10	121.00
1	A	794	ARG	NE-CZ-NH2	11.22	125.91	120.30
1	A	1007	ARG	CD-NE-CZ	11.22	139.31	123.60
1	A	71	ARG	NE-CZ-NH2	-10.91	114.84	120.30
1	A	1007	ARG	NE-CZ-NH1	10.07	125.34	120.30

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	7773	0	0	16	0
2	A	83	0	0	0	0
3	A	94	0	0	0	0
4	A	44	0	0	0	0
5	A	56	0	0	0	0
6	A	12	0	0	0	0
7	A	993	0	0	7	0
All	All	9055	0	0	16	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 2.

The worst 5 of 16 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:264[B]:PHE:CG	1:A:304[B]:PHE:CE2	2.03	1.44
1:A:264[B]:PHE:CB	1:A:304[B]:PHE:CE2	2.28	1.15
1:A:264[B]:PHE:CB	1:A:304[B]:PHE:CZ	2.42	1.02
1:A:264[B]:PHE:CD1	1:A:304[B]:PHE:CE2	2.52	0.96
1:A:264[B]:PHE:CD2	1:A:304[B]:PHE:CE2	2.62	0.87

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	1012/1003 (101%)	983 (97%)	29 (3%)	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	832/819 (102%)	812 (98%)	20 (2%)	61 19

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	639	LYS
1	A	641	ILE
1	A	947	GLN
1	A	586	SER
1	A	618	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

19 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	NAG	A	1024	1,2	12,14,15	0.83	0	15,19,21	1.45	3 (20%)
2	NAG	A	1025	2	12,14,15	0.71	0	15,19,21	1.11	1 (6%)
2	BMA	A	1026	2	10,11,12	0.62	0	11,15,17	0.94	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	A	1027	2	10,11,12	0.88	0	11,15,17	1.21	2 (18%)
2	MAN	A	1028	2	10,11,12	0.70	0	11,15,17	1.14	1 (9%)
2	MAN	A	1029	2	10,11,12	0.99	0	11,15,17	2.63	5 (45%)
2	MAN	A	1031	2	10,11,12	1.08	0	11,15,17	1.87	3 (27%)
3	NAG	A	1032	1,3	12,14,15	0.86	1 (8%)	15,19,21	0.96	1 (6%)
3	NAG	A	1033	3	12,14,15	0.72	0	15,19,21	2.04	5 (33%)
3	BMA	A	1034	3,4	10,11,12	0.80	0	11,15,17	1.65	2 (18%)
4	MAN	A	1035	3,4	10,11,12	0.62	0	11,15,17	2.08	3 (27%)
4	MAN	A	1036	4	10,11,12	0.86	0	11,15,17	1.19	1 (9%)
4	MAN	A	1037	4	10,11,12	0.84	0	11,15,17	1.35	2 (18%)
4	MAN	A	1038	4	10,11,12	0.95	1 (10%)	11,15,17	2.05	4 (36%)
3	MAN	A	1039	3	10,11,12	0.76	0	11,15,17	1.93	3 (27%)
3	MAN	A	1040	3	10,11,12	0.50	0	11,15,17	0.76	0
3	MAN	A	1041	3	10,11,12	0.86	0	11,15,17	1.97	3 (27%)
3	GLC	A	1042	3	10,11,12	0.86	0	11,15,17	1.47	2 (18%)
3	GLC	A	1043	3	10,11,12	0.92	0	11,15,17	3.89	2 (18%)

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	NAG	A	1024	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1025	2	-	0/6/23/26	0/1/1/1
2	BMA	A	1026	2	-	0/2/19/22	0/1/1/1
2	MAN	A	1027	2	-	0/2/19/22	0/1/1/1
2	MAN	A	1028	2	-	0/2/19/22	0/1/1/1
2	MAN	A	1029	2	-	0/2/19/22	0/1/1/1
2	MAN	A	1031	2	-	0/2/19/22	0/1/1/1
3	NAG	A	1032	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1033	3	-	0/6/23/26	0/1/1/1
3	BMA	A	1034	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1035	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1036	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1037	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1038	4	-	0/2/19/22	0/1/1/1
3	MAN	A	1039	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1040	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	A	1041	3	-	0/2/19/22	0/1/1/1
3	GLC	A	1042	3	-	0/2/19/22	0/1/1/1
3	GLC	A	1043	3	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1038	MAN	O5-C5	-2.13	1.41	1.45
3	A	1032	NAG	O5-C5	-2.00	1.41	1.45

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1043	GLC	O5-C5-C6	11.92	119.49	106.98
2	A	1029	MAN	O5-C5-C4	-6.93	101.86	110.65
3	A	1033	NAG	C3-C2-N2	-5.40	103.55	111.76
4	A	1035	MAN	O5-C5-C6	5.30	112.55	106.98
3	A	1041	MAN	O3-C3-C2	-4.21	102.23	109.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry

6 ligands 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	$\# Z > 2$
5	NAG	A	1044	1	12,14,15	0.75	1 (8%)	15,19,21	1.79	3 (20%)
5	NAG	A	1045	1	12,14,15	0.67	0	15,19,21	1.74	6 (40%)
5	NAG	A	1046	1,5	12,14,15	0.78	1 (8%)	15,19,21	1.95	7 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	1047	5	12,14,15	0.72	0	15,19,21	1.27	2 (13%)
6	GOL	A	1048	-	5,5,5	0.74	0	5,5,5	0.41	0
6	GOL	A	1049	-	5,5,5	0.23	0	5,5,5	1.44	1 (20%)

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
5	NAG	A	1044	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1045	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1046	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1047	5	-	0/6/23/26	0/1/1/1
6	GOL	A	1048	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1049	-	-	0/4/4/4	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1044	NAG	C2-N2	-2.06	1.43	1.46
5	A	1046	NAG	O5-C5	-2.04	1.41	1.45

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1044	NAG	O5-C5-C6	4.84	112.06	106.98
5	A	1046	NAG	O5-C5-C4	-3.62	106.06	110.65
5	A	1047	NAG	O5-C5-C6	3.48	110.63	106.98
5	A	1045	NAG	O7-C7-C8	-3.13	115.93	122.04
5	A	1045	NAG	O5-C5-C4	-3.01	106.84	110.65

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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	986/1003 (98%)	-0.26	21 (2%) 60 65	7, 12, 33, 69	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	888	SER	6.4
1	A	933	ALA	5.9
1	A	932	THR	5.4
1	A	886	PRO	5.2
1	A	525	LYS	4.9

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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, 95th 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MAN	A	1029	11/12	0.26	77.60	20,26,47,52	0
4	MAN	A	1038	11/12	0.31	16.01	32,37,51,59	0
2	MAN	A	1031	11/12	0.12	12.47	18,20,26,27	0
3	GLC	A	1043	11/12	0.31	10.04	66,75,88,91	0
3	MAN	A	1039	11/12	0.14	8.33	18,25,38,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MAN	A	1041	11/12	0.16	5.44	19,25,36,36	0
3	GLC	A	1042	11/12	0.17	4.37	35,50,55,66	0
3	NAG	A	1033	14/15	0.10	2.72	12,19,45,46	0
3	MAN	A	1040	11/12	0.12	2.10	17,20,25,30	0
3	BMA	A	1034	11/12	0.08	0.82	14,15,17,18	0
2	MAN	A	1028	11/12	0.06	0.80	11,11,17,28	0
3	NAG	A	1032	14/15	0.08	0.08	11,14,28,37	0
2	MAN	A	1027	11/12	0.04	-0.35	9,10,14,22	0
2	NAG	A	1025	14/15	0.04	-0.91	8,10,13,15	0
2	NAG	A	1024	14/15	0.04	-1.36	9,11,22,24	0
4	MAN	A	1037	11/12	0.33	-	34,40,66,76	0
4	MAN	A	1036	11/12	0.37	-	41,55,72,74	0
4	MAN	A	1035	11/12	0.18	-	21,26,34,39	0
2	BMA	A	1026	11/12	0.07	-	10,12,15,17	0

6.4 Ligands

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, 95th 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	NAG	A	1047	14/15	0.25	16.38	55,86,102,108	0
5	NAG	A	1045	14/15	0.21	9.07	27,42,59,65	0
5	NAG	A	1044	14/15	0.14	7.64	23,35,50,55	0
6	GOL	A	1049	6/6	0.20	7.61	23,48,51,59	0
5	NAG	A	1046	14/15	0.12	0.70	29,43,58,68	0
6	GOL	A	1048	6/6	0.05	-0.93	11,12,12,14	0

6.5 Other polymers

There are no such residues in this entry.