



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:39 PM GMT

PDB ID : 4CVU
Title : Structure of Fungal beta-mannosidase from Glycoside Hydrolase Family 2 of *Trichoderma harzianum*
Authors : Muniz, J.R.C.; Aparicio, R.; Santos, J.C.; Nascimento, A.S.; Golubev, A.M.; Polikarpov, I.
Deposited on : 2014-03-31
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure 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/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

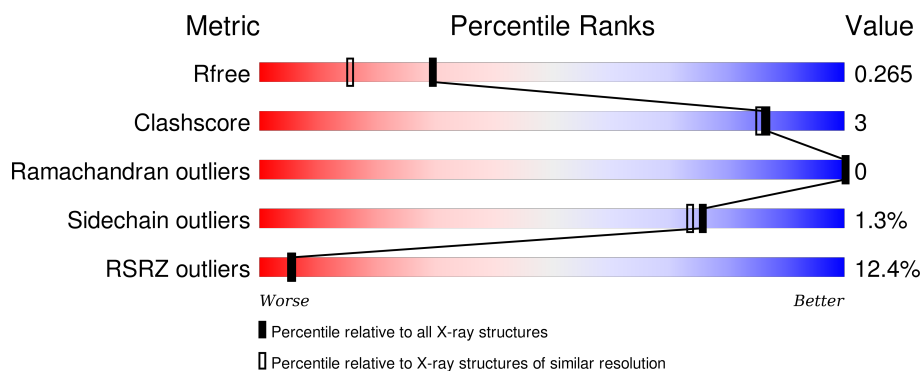
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
R_{free}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (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 ≥ 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	942	

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
3	NAG	A	1974	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	A	1950	-	-	-	X
4	MAN	A	1954	-	-	-	X
5	NAG	A	1956	-	-	-	X
5	MAN	A	1958	-	-	-	X
7	NAG	A	1977	X	-	-	-

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 8456 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 BETA-MANNOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	913	Total	C	N	O	S	0	6	0
			7241	4645	1208	1371	17			

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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

- Molecule 4 is a polymer of unknown type called SUGAR (8-MER).

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

- Molecule 5 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 6 is a polymer of unknown type called SUGAR (11-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	11	Total	C	N	O	0	0
			127	70	2	55		

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	2	Total	C	N	O	0	0
			28	16	2	10		

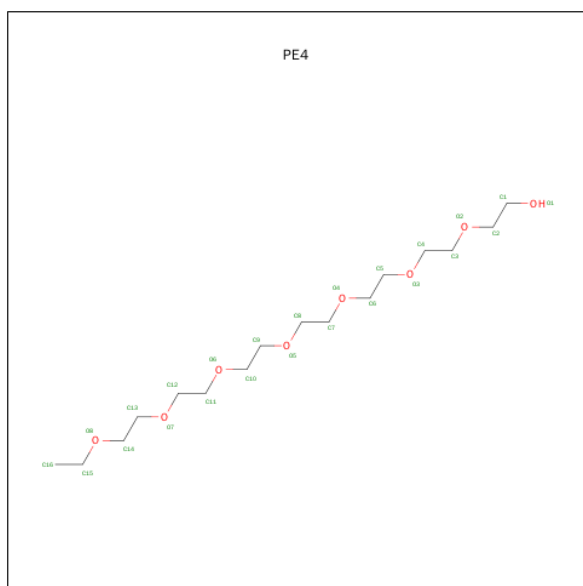
- Molecule 8 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	17	Total	Cd	0	0
			17	17		

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

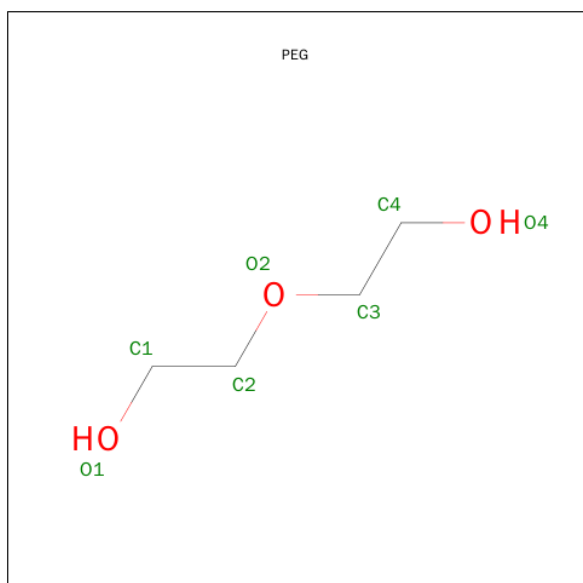
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	6	Total	Na	0	0
			6	6		

- Molecule 10 is 2-{2-[2-(2-{2-[2-(2-ETHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (three-letter code: PE4) (formula: C₁₆H₃₄O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			12	8	4		

- Molecule 11 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 12 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 13 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	1	Total	Cl	0	0
			1	1		

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	741	Total	O	0	0
			741	741		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	166.46Å 166.46Å 121.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	117.70 – 1.90 48.30 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (117.70-1.90) 98.8 (48.30-1.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.234 , 0.263 0.239 , 0.265	Depositor DCC
R_{free} test set	6641 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.511	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 131627 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8456	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, CL, PE4, NA, CA, CD, PEG, 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	0.67	0/7479	0.72	4/10243 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
7	A	1	0
All	All	1	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	723	ASP	CB-CG-OD1	6.79	124.41	118.30
1	A	409	ASP	CB-CG-OD1	6.43	124.09	118.30
1	A	723	ASP	CB-CG-OD2	-6.22	112.70	118.30
1	A	188	ARG	NE-CZ-NH2	5.04	122.82	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	1977	NAG	C3

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	424	SER	Peptide

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	7241	0	6832	39	0
2	A	39	0	34	1	0
3	A	70	0	65	0	0
4	A	94	0	79	1	0
5	A	72	0	61	0	0
6	A	127	0	105	0	0
7	A	28	0	23	0	0
8	A	17	0	0	0	0
9	A	6	0	0	0	0
10	A	12	0	14	0	0
11	A	7	0	10	0	0
12	A	1	0	0	0	0
13	A	1	0	0	1	0
14	A	741	0	0	7	0
All	All	8456	0	7223	40	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 3.

The worst 5 of 40 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)
4:A:1948:NAG:H81	4:A:1953:MAN:O6	1.81	0.80
1:A:194:GLU:HG3	1:A:425:GLY:HA2	1.67	0.75
1:A:597:PHE:HB2	1:A:682:MET:CE	2.26	0.66
1:A:565:HIS:NE2	13:A:2003:CL:CL	2.58	0.65
1:A:597:PHE:HB2	1:A:682:MET:HE1	1.80	0.64

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	915/942 (97%)	891 (97%)	24 (3%)	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	777/811 (96%)	766 (99%)	11 (1%)	74	71

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	349[B]	ARG
1	A	444	TRP
1	A	699	ARG
1	A	349[A]	ARG
1	A	559	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	HIS
1	A	243	ASN

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 ⓘ

30 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	1943	1,2	14,14,15	0.64	0	15,19,21	1.16	1 (6%)
2	NAG	A	1944	2	14,14,15	0.62	0	15,19,21	0.94	1 (6%)
2	BMA	A	1945	2	11,11,12	0.50	0	14,15,17	0.76	0
4	NAG	A	1947	1,4	14,14,15	0.79	1 (7%)	15,19,21	0.94	0
4	NAG	A	1948	4	14,14,15	0.65	0	15,19,21	1.37	2 (13%)
4	BMA	A	1949	4	11,11,12	0.76	0	14,15,17	1.17	2 (14%)
4	MAN	A	1950	4	11,11,12	0.58	0	14,15,17	0.87	0
4	MAN	A	1951	4	11,11,12	0.51	0	14,15,17	1.07	1 (7%)
4	MAN	A	1952	4	11,11,12	0.59	0	14,15,17	1.97	1 (7%)
4	MAN	A	1953	4	11,11,12	0.74	0	14,15,17	1.59	2 (14%)
4	MAN	A	1954	4	11,11,12	0.66	0	14,15,17	0.91	1 (7%)
5	NAG	A	1955	1,5	14,14,15	0.50	0	15,19,21	0.88	1 (6%)
5	NAG	A	1956	5	14,14,15	0.72	0	15,19,21	1.30	1 (6%)
5	BMA	A	1957	5	11,11,12	0.58	0	14,15,17	1.15	1 (7%)
5	MAN	A	1958	5	11,11,12	0.60	0	14,15,17	1.25	2 (14%)
5	MAN	A	1959	5	11,11,12	0.59	0	14,15,17	0.97	0
5	MAN	A	1960	5	11,11,12	0.97	0	15,15,17	5.63	3 (20%)
6	NAG	A	1961	1,6	14,14,15	0.64	0	15,19,21	1.01	1 (6%)
6	NAG	A	1962	6	14,14,15	0.75	0	15,19,21	0.97	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BMA	A	1963	6	11,11,12	0.52	0	14,15,17	0.93	1 (7%)
6	MAN	A	1964	6	11,11,12	0.59	0	14,15,17	1.19	3 (21%)
6	MAN	A	1965	6	11,11,12	1.00	0	14,15,17	1.16	1 (7%)
6	MAN	A	1966	6	11,11,12	0.60	0	14,15,17	1.13	2 (14%)
6	MAN	A	1967	6	11,11,12	1.37	1 (9%)	14,15,17	3.50	3 (21%)
6	MAN	A	1968	6	11,11,12	0.73	1 (9%)	14,15,17	0.82	0
6	MAN	A	1969	6	11,11,12	0.62	0	14,15,17	0.76	1 (7%)
6	MAN	A	1970	6	11,11,12	0.72	0	14,15,17	1.57	4 (28%)
6	MAN	A	1971	6	11,11,12	0.69	0	14,15,17	1.38	1 (7%)
7	NAG	A	1976	1,7	14,14,15	0.93	1 (7%)	15,19,21	1.16	1 (6%)
7	NAG	A	1977	7	14,14,15	25.93	1 (7%)	15,19,21	11.78	8 (53%)

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	1943	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1944	2	-	0/6/23/26	0/1/1/1
2	BMA	A	1945	2	-	0/2/19/22	0/1/1/1
4	NAG	A	1947	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1948	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1949	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1950	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1951	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1952	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1953	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1954	4	-	0/2/19/22	0/1/1/1
5	NAG	A	1955	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1956	5	-	0/6/23/26	0/1/1/1
5	BMA	A	1957	5	-	0/2/19/22	0/1/1/1
5	MAN	A	1958	5	-	0/2/19/22	0/1/1/1
5	MAN	A	1959	5	-	0/2/19/22	0/1/1/1
5	MAN	A	1960	5	-	0/2/18/22	0/1/1/1
6	NAG	A	1961	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	1962	6	-	0/6/23/26	0/1/1/1
6	BMA	A	1963	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1964	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1965	6	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	A	1966	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1967	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1968	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1969	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1970	6	-	0/2/19/22	0/1/1/1
6	MAN	A	1971	6	-	0/2/19/22	0/1/1/1
7	NAG	A	1976	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	1977	7	1/1/5/7	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1967	MAN	O3-C3	-3.95	1.33	1.43
7	A	1976	NAG	O5-C1	-2.06	1.40	1.43
6	A	1968	MAN	O5-C5	-2.01	1.39	1.43
4	A	1947	NAG	C1-C2	2.15	1.55	1.52
7	A	1977	NAG	O3-C3	97.00	3.75	1.43

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1977	NAG	O3-C3-C2	-44.35	21.26	109.11
7	A	1977	NAG	O3-C3-C4	-6.80	95.03	110.34
5	A	1960	MAN	C1-C2-C3	-6.23	100.55	111.23
5	A	1958	MAN	O2-C2-C3	-2.80	104.49	110.12
6	A	1966	MAN	C2-C3-C4	-2.79	106.30	111.04

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	1977	NAG	C3

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1943	NAG	1	0
4	A	1948	NAG	1	0
4	A	1953	MAN	1	0

5.6 Ligand geometry

Of 32 ligands modelled in this entry, 25 are monoatomic - leaving 7 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	1946	1	14,14,15	0.90	0	15,19,21	1.46	1 (6%)
3	NAG	A	1972	1	14,14,15	0.46	0	15,19,21	1.26	1 (6%)
3	NAG	A	1973	1	14,14,15	0.43	0	15,19,21	1.33	1 (6%)
3	NAG	A	1974	1	14,14,15	0.52	0	15,19,21	1.05	1 (6%)
3	NAG	A	1975	1	14,14,15	0.51	0	15,19,21	1.05	1 (6%)
10	PE4	A	2000	-	11,11,23	0.55	0	10,10,22	0.43	0
11	PEG	A	2001	-	6,6,6	0.52	0	5,5,5	0.24	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
3	NAG	A	1946	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1972	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1973	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1974	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1975	1	-	0/6/23/26	0/1/1/1
10	PE4	A	2000	-	-	0/9/9/21	0/0/0/0
11	PEG	A	2001	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1975	NAG	O7-C7-C8	-2.03	118.34	122.06
3	A	1974	NAG	C1-O5-C5	2.54	115.47	112.25
3	A	1973	NAG	C1-O5-C5	2.95	116.00	112.25
3	A	1972	NAG	C1-O5-C5	3.71	116.95	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1946	NAG	C1-O5-C5	4.93	118.51	112.25

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 [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, 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	913/942 (96%)	0.79	113 (12%) 5 5	28, 45, 69, 105	1 (0%)

The worst 5 of 113 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	749	THR	7.3
1	A	839	LYS	6.5
1	A	750	ALA	6.4
1	A	334	GLY	6.1
1	A	838	SER	5.7

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, 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	MAN	A	1950	11/12	0.88	0.27	7.60	57,60,64,64	0
4	MAN	A	1954	11/12	0.85	0.26	3.22	52,60,62,64	0
5	MAN	A	1958	11/12	0.91	0.16	3.07	43,46,47,48	0
5	NAG	A	1956	14/15	0.87	0.15	2.44	44,48,50,58	0
4	NAG	A	1947	14/15	0.85	0.18	1.92	40,43,47,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	MAN	A	1959	11/12	0.89	0.17	1.77	43,47,53,56	0
2	NAG	A	1943	14/15	0.92	0.12	1.44	35,38,42,45	0
6	MAN	A	1966	11/12	0.83	0.21	1.44	52,57,61,65	0
5	NAG	A	1955	14/15	0.90	0.17	0.89	44,46,47,47	0
6	NAG	A	1962	14/15	0.91	0.12	-0.62	41,44,47,48	0
6	NAG	A	1961	14/15	0.91	0.12	-0.78	42,45,51,51	0
6	MAN	A	1968	11/12	0.94	0.12	-0.81	46,50,52,53	0
6	MAN	A	1969	11/12	0.91	0.10	-2.15	49,51,52,52	0
4	BMA	A	1949	11/12	0.88	0.25	-	50,55,57,59	0
7	NAG	A	1976	14/15	0.91	0.20	-	46,51,55,57	0
6	MAN	A	1964	11/12	0.90	0.11	-	43,44,47,48	0
4	MAN	A	1951	11/12	0.84	0.18	-	57,61,64,69	0
6	MAN	A	1971	11/12	0.89	0.17	-	51,53,54,56	0
6	MAN	A	1970	11/12	0.89	0.15	-	48,55,62,63	0
4	MAN	A	1952	11/12	0.65	0.43	-	63,65,67,68	0
4	NAG	A	1948	14/15	0.81	0.19	-	44,48,53,54	0
5	BMA	A	1957	11/12	0.88	0.21	-	48,51,55,58	0
6	BMA	A	1963	11/12	0.95	0.12	-	43,45,50,50	0
7	NAG	A	1977	14/15	0.85	0.28	-	67,73,78,80	0
6	MAN	A	1965	11/12	0.93	0.18	-	45,48,53,57	0
2	BMA	A	1945	11/12	0.81	0.34	-	54,57,59,62	0
2	NAG	A	1944	14/15	0.92	0.20	-	46,50,51,52	0
5	MAN	A	1960	11/12	0.71	0.24	-	65,66,68,70	0
6	MAN	A	1967	11/12	0.79	0.19	-	47,51,53,53	0
4	MAN	A	1953	11/12	0.86	0.27	-	51,60,62,64	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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	1974	14/15	0.84	0.30	8.30	54,59,68,70	0
10	PE4	A	2000	12/24	0.79	0.17	1.84	57,61,66,66	0
3	NAG	A	1973	14/15	0.79	0.30	1.76	56,60,63,68	0
3	NAG	A	1975	14/15	0.90	0.19	1.18	40,43,46,47	0
3	NAG	A	1946	14/15	0.90	0.14	0.24	39,44,48,48	0
8	CD	A	1990	1/1	0.96	0.10	-2.10	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
8	CD	A	1981	1/1	0.98	0.07	-	50,50,50,50	0
8	CD	A	1992	1/1	0.96	0.17	-	87,87,87,87	1
8	CD	A	1979	1/1	0.98	0.08	-	43,43,43,43	0
9	NA	A	1998	1/1	0.89	0.17	-	40,40,40,40	0
13	CL	A	2003	1/1	0.89	0.15	-	49,49,49,49	0
9	NA	A	1995	1/1	0.70	0.30	-	54,54,54,54	0
9	NA	A	1997	1/1	0.93	0.28	-	30,30,30,30	0
8	CD	A	1983	1/1	0.96	0.08	-	52,52,52,52	0
9	NA	A	1999	1/1	0.95	0.19	-	33,33,33,33	0
8	CD	A	1987	1/1	0.98	0.08	-	81,81,81,81	0
8	CD	A	1978	1/1	0.99	0.10	-	39,39,39,39	0
8	CD	A	1993	1/1	0.91	0.39	-	44,44,44,44	0
8	CD	A	1988	1/1	0.97	0.07	-	74,74,74,74	0
9	NA	A	2004	1/1	0.97	0.33	-	37,37,37,37	0
8	CD	A	1985	1/1	0.98	0.09	-	51,51,51,51	0
8	CD	A	1989	1/1	0.93	0.05	-	80,80,80,80	0
8	CD	A	1984	1/1	0.94	0.08	-	76,76,76,76	0
8	CD	A	1982	1/1	0.91	0.06	-	72,72,72,72	0
9	NA	A	1996	1/1	0.95	0.28	-	48,48,48,48	0
8	CD	A	1986	1/1	0.98	0.05	-	59,59,59,59	0
3	NAG	A	1972	14/15	0.87	0.14	-	54,59,64,67	0
8	CD	A	1980	1/1	0.98	0.10	-	58,58,58,58	0
11	PEG	A	2001	7/7	0.78	0.19	-	58,60,62,64	0
8	CD	A	1994	1/1	0.92	0.61	-	44,44,44,44	0
12	CA	A	2002	1/1	0.95	0.08	-	54,54,54,54	0
8	CD	A	1991	1/1	0.74	0.20	-	125,125,125,125	1

6.5 Other polymers [i](#)

There are no such residues in this entry.