Data reduction: *ABSMAD* (Karaulov, 1992). Program(s) used to solve structure: *SHELXS86* (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL93* (Sheldrick, 1993). Molecular graphics: *SNOOP1* (Davies, 1983). Software used to prepare material for publication: *SHELXL93*.

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Lists of structure factors, anisotropic displacement parameters, Hatom coordinates and complete geometry have been deposited with the IUCr (Reference: SZ1047). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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C—C—O torsion angles of -69.8(2) and $-63.0(2)^{\circ}$, cause no distortion of the bond lengths and bond angles of the sugar moiety.

Comment

The title compound, 2,3,4,5-tetra-O-acetyl-1,6-di-O-(triphenylmethyl)-D-mannitol, (I), is one of the acyclic alditol derivatives which have have shown, by crystal structure analyses, to possess some interesting conformational features (Kopf, Morf, Zimmer, Bischoff & Koll 1992). The structure of (I) was determined in order to confirm the identity of the reaction product and to observe to what extent the conformation of its parent compound, D-mannitol, (II) (Kim, Jeffrey & Rosenstein 1968; Kanters, Roelofsen & Smiths 1977), might be affected by the presence of the two bulky triphenylmethyl groups.



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2,3,4,5-Tetra-*O*-acetyl-1,6-di-*O*-(triphenylmethyl)-D-mannitol

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Abstract

The central six-C-atom chain of the title compound, $C_{52}H_{50}O_{10}$, adopts a nearly planar extended conformation free from C//C, C//O and O//O 1,3-parallel interactions. The three torsion angles formed by these atoms have values of 177.4 (2), 174.2 (2) and $-178.0 (2)^{\circ}$. The bulky triphenylmethyl groups, which are oriented *gauche* to their neighboring acetoxy groups with O—

The molecular structure of (I) (Fig. 1) reveals that the molecule does not possess crystallographic twofold symmetry as observed in the parent compound (II). Approximate twofold symmetry is present, however, and the mannitol core has an extended conformation with no 1,3-parallel interactions between the heavy atoms. This conformation is described by the three anti torsion angles given in the Abstract, as well as O1-C1-C2-C3 and C4-C5-C6-O6 [47.7 (2) and 53.9 (2)°, respectively]. The C-C bond distances in the sugar moiety are in the range 1.514(3)-1.526(3) Å while the C—O bonds are in the range 1.411(2)-1.445(2) Å, in good agreement with the corresponding values for (II) and other related carbohydrate structures (Jeffrey & French, 1978; Allen, 1986; Allen, Kennard, Watson, Brammer, Orpen & Taylor, 1987). The orientation of the triphenylmethyl groups at the terminal positions (C1 and C6) are gauche to their neighbouring acetoxy O atoms, as are the primary hydroxy groups in the parent compound (II), the torsion angles O1-C1-C2-O2 and O6-C6-C5-O5 being -69.8 (2) and -63.0 (2)°, respectively. The four acetoxy groups, on C2, C3, C4, and C5, are oriented in the sequence trans, gauche, trans; the torsion angles O2-C2-C3-O3, O3-C3-C4—O4 and O5—C5—C4—O4 are 178.5(2), 49.9(2)

and -177.3 (1)°, respectively. Thus, the presence of the Data collection bulky triphenylmethyl groups on O1 and O6 causes no distortion of the bond lengths and bond angles of the sugar moiety, nor any large effect on the conformation of (I) compared with that of (II).



Fig. 1. ORTEPII (Johnson, 1976) drawing of the title compound with displacement ellipsoids drawn at the 30% probability level.

Experimental

The title compound was prepared in 95% yield by the treatment of D-mannitol, (II), with 2 molar equivalents of triphenylmethyl chloride followed by acetylation of the resultant 1,6-di-O-(triphenylmethyl)-D-mannitol with acetic anhydride in pyridine.

Crystal data

$C_{52}H_{50}O_{10}$	Cu $K\alpha$ radiation
$M_r = 835.0$	$\lambda = 1.54184 \text{ Å}$
Orthorhombic	Cell parameters from 25
$P2_{1}2_{1}2_{1}$	reflections
a = 14.542 (2) Å	$\theta = 24-30^{\circ}$
b = 16.5650(2) Å	$\mu = 0.63 \text{ mm}^{-1}$
c = 19.334(2) Å	T = 293 K
$V = 4658 (2) \text{ Å}^3$	Irregular fragment
Z = 4	$0.42 \times 0.28 \times 0.20$ mm
$D_x = 1.191 \text{ Mg m}^{-3}$	Colorless
D_m not measured	

 $(\Delta/\sigma)_{\rm max} = 0.05$

01 **O**2

> 07 08 09

O10

Cl C2 C3 C4 C5 C6

C7 C8

C9

C10

C11

C12 C13 C14

C15 C16 C17 C18 C19 C20 C21 C22 C23 C24 C25 C26 C27 C28 C29

Enraf–Nonius CAD-4	4672 observed reflections
diffractometer	$[I > 3\sigma(I)]$
$\omega/2\theta$ scans	$\theta_{\rm max} = 75^{\circ}$
Absorption correction:	$h = 0 \rightarrow 17$
ψ scan (North, Phillips	$k = 0 \rightarrow 20$
& Mathews, 1968)	$l = 0 \rightarrow 24$
$T_{\min} = 0.961, T_{\max} =$	3 standard reflections
0.999	frequency: 167 min
5213 measured reflections	intensity decay: 2.4%
5213 independent reflections	
-	
Refinement	
Refinement on F	$\Delta \rho_{\rm max} = 0.13 \ {\rm e} \ {\rm \AA}^{-3}$
R = 0.034	$\Delta \rho_{\rm min} = -0.04 \ {\rm e} \ {\rm \AA}^{-3}$
wR = 0.046	Extinction correction:
S = 2.273	$(I + gI_c)^{-1}$ applied to F_c
4672 reflections	Extinction coefficient:
560 parameters	$g = 5.2(3) \times 10^{-7}$
H-atom parameters not	Atomic scattering factors
refined	from International Tables
$w = 4F_o^2 / [\sigma^2(I) + (0.02F_o^2)^2]$	for X-ray Crystallography
$(\Delta/\sigma)_{\rm max} = 0.05$	(1974, Vol. IV)

Table 1. Fractional atomic coordinates and equivalent isotropic displacement parameters $(Å^2)$

$B_{\rm eq} = (8\pi^2/3) \sum_i \sum_j U_{ij} a_i^* a_i^* \mathbf{a}_i \cdot \mathbf{a}_j.$

~	.,	-	P
A 0.69072 (0)	0 52212 (7)	0 42525 (6)	
0.06972 (9)	0.32213(7)	0.42333 (0)	3.01 (3)
0.00838 (9)	0.04900 (8)	0.52/95 (6)	4.04 (3)
0.58874 (9)	0.00800 (8)	0.35262 (6)	3.75 (3)
0.5560(1)	0.80463 (9)	0.42803 (8)	4.50 (3)
0.78880 (9)	0.78794 (8)	0.36540 (6)	3.76(3)
0.74272 (9)	0.91910(7)	0.45033 (7)	3.81 (3)
0.5493 (1)	0.6423 (1)	0.60095 (9)	6.87 (4)
0.7098(1)	0.6364 (1)	0.28480(7)	5.21 (3)
0.5629(1)	0.8209(1)	0.54322 (9)	6.69 (4)
0.7972 (1)	0.8171 (1)	0.25264 (8)	7.05 (5)
0.6031(1)	0.5451 (1)	0.4536(1)	3.67 (4)
0.6079(1)	0.6343 (1)	0.47037 (9)	3.41 (3)
0.6475 (1)	0.6842 (1)	0.41119 (9)	3.22 (3)
0.6492 (1)	0.7744 (1)	0.42535 (9)	3.40 (3)
0.6978 (1)	0.8225 (1)	0.36877 (9)	3.56 (4)
0.7024 (2)	0.9122 (1)	0.3842 (1)	4.13 (4)
0.6287 (2)	0.6542 (1)	0.5912(1)	5.16 (5)
0.6971 (3)	0.6754 (3)	0.6448 (1)	9.6(1)
0.6282 (1)	0.6406(1)	0.2936 (1)	4.05 (4)
0.5571 (2)	0.6169 (2)	0.2429 (1)	6.74 (7)
0.5205 (2)	0.8248 (1)	0.4907 (1)	5.21 (5)
0.4233 (2)	0.8508 (2)	0.4837 (2)	8.76 (9)
0.8289 (2)	0.7848 (1)	0.3025 (1)	4.51 (4)
0.9148 (2)	0.7369 (2)	0.3045 (1)	5.92 (6)
0.7059(1)	0.4369(1)	0.41611 (9)	3.45 (4)
0.7136(1)	0.3957 (1)	0.48717 (9)	3.51 (4)
0.7437 (1)	0.4402(1)	0.5439(1)	4.17 (4)
0.7540 (2)	0.4047 (2)	0.6077 (1)	5.50 (6)
0.7355 (2)	0.3242 (2)	0.6168 (1)	5.93 (6)
0.7075 (2)	0.2788 (1)	0.5615(1)	5.64 (5)
0.6959 (2)	0.3144 (1)	0.4968 (1)	4.60 (5)
0.6301 (2)	0.4019(1)	0.3702 (1)	4.33 (4)
0.5460 (2)	0.3775 (2)	0.3979(1)	5.21 (5)
0.4761 (2)	0.3513 (2)	0.3554 (2)	7.71 (7)
0.4867 (2)	0.3498 (2)	0.2861 (2)	10.55 (9)
0.5677 (3)	0.3733 (3)	0.2576 (2)	10.9 (1)
0.6406 (2)	0.4005 (2)	0.2989(1)	7.45 (8)
0.8007 (1)	0.4311 (1)	0.3806(1)	3.96 (4)
0.8400 (2)	0.3562 (1)	0.3690(1)	5.09 (5)

C30	0.9249 (2)	0.3499 (2)	0.3365 (1)	6.49 (6)
C31	0.9700 (2)	0.4167 (2)	0.3153 (2)	7.13 (7)
C32	0.9332 (2)	0.4916 (2)	0.3268 (2)	7.26 (7)
C33	0.8473 (2)	0.4987 (1)	0.3587(1)	5.38 (5)
C34	0.7563 (2)	0.9988(1)	0.4792 (1)	3.67 (4)
C35	0.8410(1)	1.0394 (1)	0.4471 (1)	3.95 (4)
C36	0.8992 (2)	0.9988 (2)	0.4037(1)	5.05 (5)
C37	0.9753 (2)	1.0378 (2)	0.3756 (2)	6.29 (6)
C38	0.9934 (2)	1.1166 (2)	0.3907 (2)	6.13 (6)
C39	0.9364 (2)	1.1573 (2)	0.4359(1)	5.62 (6)
C40	0.8614 (2)	1.1191 (1)	0.4642(1)	4.64 (5)
C41	0.6683(1)	1.0481 (1)	0.4686(1)	3.83 (4)
C42	0.6607 (2)	1.1061 (1)	0.4172(1)	4.44 (4)
C43	0.5790 (2)	1.1473 (1)	0.4060(1)	5.56 (5)
C44	0.5031 (2)	1.1298 (2)	0.4455 (2)	6.18 (6)
C45	0.5075 (2)	1.0715 (2)	0.4954 (2)	6.12 (6)
C46	0.5903 (2)	1.0297 (1)	0.5069(1)	5.09 (5)
C47	0.7782(1)	0.9809(1)	0.5555 (1)	3.97 (4)
C48	0.7538 (2)	1.0320(1)	0.6087 (1)	5.39 (5)
C49	0.7758 (2)	1.0135 (2)	0.6764 (1)	6.62 (7)
C50	0.8219 (2)	0.9441 (2)	0.6919 (1)	6.95 (7)
C51	0.8489 (2)	0.8932 (2)	0.6395 (1)	6.71 (6)
C52	0.8266 (2)	0.9114 (2)	0.5719(1)	5.46 (5)

Table 2. Selected geometric parameters (Å, °)

01C1	1.424 (2)	O8—C9	1.201 (3)
01C15	1.443 (2)	O9C 11	1.190 (3)
02C2	1.439 (2)	O10-C13	1.195 (3)
O2C7	1.356 (3)	C1C2	1.514 (3)
03C3	1.444 (2)	C2C3	1.525 (3)
03С9	1.357 (2)	C3C4	1.519 (3)
04—C4	1.445 (2)	C4—C5	1.526 (3)
04—C11	1.359 (3)	C5—C6	1.518 (3)
05C5	1.443 (2)	C7C8	1.479 (4)
O5C13	1.350 (2)	C9-C10	1.477 (3)
O6-C6	1.411 (2)	C11C12	1.484 (4)
07C7	1.185 (3)	C13C14	1.480 (4)
C1-01-C15	117.0(1)	O5-C5-C6	110.9 (2)
C2-02C7	116.7 (2)	C4C6	112.9 (2)
С3—О3—С9	118.2(1)	06-C6-C5	106.0 (1)
C4-04-C11	118.3 (2)	02C707	123.2 (2)
C5-05-C13	116.9 (1)	O2C7C8	111.1 (2)
01C1C2	107.6(1)	07C8	125.7 (2)
02C1C1	111.1 (2)	03—C9—O8	123.8 (2)
O2C2C3	104.9 (1)	O3-C9-C10	110.6 (2)
C1C2C3	112.7 (2)	O8C9C10	125.6 (2)
O3—C3—C2	105.3 (1)	O4—C11—O9	123.4 (2)
O3C3C4	109.5 (1)	O4—C11—C12	110.6 (2)
C2C3C4	113.9 (1)	09-C11-C12	126.0 (3)
O4-C4-C3	109.4 (1)	05—C13—O10	122.9 (2)
04—C4—C5	106.2 (1)	O5-C13-C14	111.2 (2)
C3C4C5	113.0(1)	O10-C13-C14	125.9 (2)
O5C5C4	104.5(1)		
C15-01-C1-C2	170.1 (2)	O3—C3—C4—O4	49.9 (2)
C34-06-C6-C5	179.9 (2)	C2—C3—C4—C5	174.2 (2)
01	-69.8 (2)	04—C4—C5—O5	-177.3 (2)
01C1C2C3	47.7 (2)	C3—C4—C5—C6	-178.0(2)
02	178.5 (2)	O5-C5-C6O6	-63.0 (2)
C1C2C3C4	177.4 (2)	C4-C5-C6O6	53.9 (2)

H atoms were visible in difference maps, but were placed in idealized positions with C—H = 0.95 Å and $B_{iso} = 1.3B_{eq}$ of the bonded C atom, and were not refined.

Data collection: CAD-4 Software (Enraf-Nonius, 1989). Cell refinement: CAD-4 Software. Data reduction: MolEN (Fair, 1990). Structure solution: RANTAN (Yao, 1981). Structure refinement: MolEN. Molecular graphics: ORTEPII (Johnson, 1976). Preparation of material for publication: MolEN.

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Cyclo(L-alanyl-L-seryl).H₂O and Cyclo-(glycyl-L-seryl)

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Abstract

We have determined the crystal structures of two diketopiperazines, cyclo(L-alanyl-L-seryl).H₂O (*cis*-6-hydroxymethyl-3-methyl-2,5-piperazinedione hydrate, $C_6H_{10}N_2O_3.H_2O$) and cyclo(glycyl-L-seryl) (3-hydro-xymethyl-2,5-piperazinedione, $C_5H_8N_2O_3$). The crystal structure of cyclo(L-alanyl-L-seryl).H₂O [cyclo(L-Ala-L-Ser)] consists of a peptide backbone that is hydrogen bonded to two adjacent diketopiperazine rings, forming extended chains through the crystal. The serine hydroxy group of cyclo(L-Ala-L-Ser) is hydrated by two adjacent water molecules in the crystal. In contrast, the crystal structure of cyclo(glycyl-L-seryl) [cyclo(Gly-L-Ser)] is