

A. G. Pinkus,* Kevin K. Klausmeyer, Rodney P. Feazell, Sundaram Logaraj and Phillip W. Hurd

Department of Chemistry and Biochemistry,
Baylor University, Waco, TX 76798, USA

Correspondence e-mail:
a_g_pinkus@baylor.edu

Key indicators

Single-crystal X-ray study
T = 273 K
Mean $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$
R factor = 0.042
wR factor = 0.108
Data-to-parameter ratio = 16.4

For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

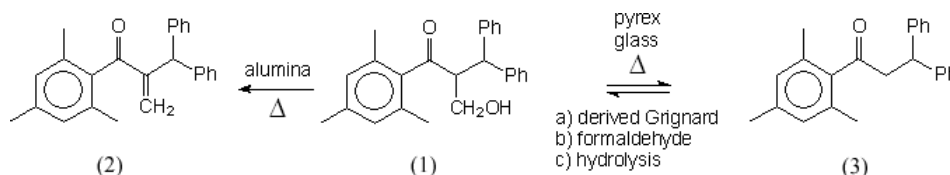
1-Hydroxymethyl-2,2-diphenylethyl 2,4,6-trimethylphenyl ketone

The title compound, $\text{C}_{25}\text{H}_{26}\text{O}_2$, was isolated and characterized as a stable intermediate in the conversion of 2,2-diphenylethyl 2,4,6-trimethylphenyl ketone to its formaldehyde-derived enone.

Received 5 November 2004
Accepted 18 November 2004
Online 27 November 2004

Comment

The title compound, (1) (Fig. 1), was obtained as an intermediate from which the enone (2) could be obtained by loss of water. Since loss of formaldehyde by a pyrolytic retro-aldol condensation to produce the ketone (3) was an undesirable competing reaction, a study of the behavior of (1) on heating under various conditions was carried out in order to maximize formation of the enone (2). A maximum yield of of 97% of (2) could be obtained by heating (1) in contact with alumina particles. Heating (1) in contact with Pyrex glass particles gave a 66% yield of (3). The synthesis of (1) was carried out by reaction of formaldehyde with the derived Grignard product from compound (3) (see scheme).



The torsion angle $\text{C}22-\text{C}17-\text{C}1-\text{O}1$ is $-68.0 (2)^\circ$ (Table 1), which compares with the analogous angle of 65.6° for 2,2-diphenylethyl mesityl ketone (Pinkus *et al.*, 1984). For compounds with *tert*-butylmesityl keto groupings, such as 2,4,6-trimethyl-3-pivaloylbenzoic acid (X-ray study; Bear *et al.*, 1973) and *tert*-butylmesityl and *tert*-butylduryl ketones (dipole moment studies; Pinkus & Custard, 1970, 1975), the corresponding angles are 90° or close to it. An H atom on the carbon attached to the carbonyl group causes a decrease in the angle compared with a *tert*-butyl group attached to the carbonyl in the ketones cited in the references. The hydroxyl group is found to hydrogen bond to its symmetry equivalent, holding two molecules together in the crystal structure (Table 2). All of the bond lengths and angles of compound (1) are within expected ranges.

Experimental

Formaldehyde was generated by heating paraformaldehyde (3.1 g, 0.10 mol) in a stream of dry nitrogen and added to approximately 0.075 mol of the vigorously stirred derived bromomagnesium compound of benzalacetomesitylene [(3); 2,2-diphenylethyl 2,4,6-trimethylphenyl ketone]. After all the paraformaldehyde had been

decomposed to formaldehyde by heating, the reaction mixture was stirred vigorously for 6 h and then hydrolyzed in 2 l of cracked ice and approximately 150 ml of a saturated solution of ammonium chloride. The separated aqueous layer was extracted twice with diethyl ether (150 ml \times 2). The combined organic layers were extracted twice with distilled water and the organic layer was dried over anhydrous magnesium sulfate, followed by removal of the drying agent by filtration. The solvent was removed by rotary evaporation to obtain a crystalline solid which was recrystallized from cyclohexane (m.p. 426–427 K; yield, 50.9%); analysis calculated for $C_{25}H_{26}O_2$: C 83.76, H 7.31%; found: C 84.01, H 7.49% (Galbraith Labs., Knoxville, TN 39721). IR (cm^{-1} ; nujol): 3630, 3590 (O–H stretching); 2940, 2870 (C–H stretching); 1690 (C=O stretching); 1615 (Ar C=C stretching); 1H NMR (60 MHz, hexadeuteroacetone, TMS, p.p.m.): 2.07 (s, *o*-Me), 2.15 (s, *p*-Me), 3.70 (d, CH_2), 4.08 (dt), 4.63 (d, $CHPh_2$), 5.64 (s, OH), 6.64 (s, *m*-H), 7.04, 7.30 (*m*, Ph_2); ^{13}C (22.50 MHz, hexadeuteroacetone, TMS, p.p.m.): 50.998 [$CH(C=O)$], 57.48 [$CH(Ph_2)$], 61.43 [$CH_2(OH)$], 208.842 (C=O).

Crystal data

$C_{25}H_{26}O_2$	$D_x = 1.199 \text{ Mg m}^{-3}$
$M_r = 358.46$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 4193 reflections
$a = 11.7361$ (7) Å	$\theta = 2.5\text{--}26.3^\circ$
$b = 10.5700$ (7) Å	$\mu = 0.07 \text{ mm}^{-1}$
$c = 16.0857$ (10) Å	$T = 273$ (2) K
$\beta = 95.574$ (3)°	Needle, colorless
$V = 1986.0$ (2) Å ³	$0.31 \times 0.11 \times 0.08 \text{ mm}$
$Z = 4$	

Data collection

Bruker X8 APEX CCD area-detector diffractometer	4054 independent reflections
φ and ω scans	3118 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{int} = 0.040$
$T_{min} = 0.991$, $T_{max} = 0.994$	$\theta_{max} = 26.4^\circ$
21 735 measured reflections	$h = -14 \rightarrow 14$
	$k = -13 \rightarrow 13$
	$l = -20 \rightarrow 20$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0451P)^2 + 0.8613P]$
$R[F^2 > 2\sigma(F^2)] = 0.042$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.108$	$(\Delta/\sigma)_{max} < 0.001$
$S = 1.05$	$\Delta\rho_{max} = 0.27 \text{ e \AA}^{-3}$
4054 reflections	$\Delta\rho_{min} = -0.28 \text{ e \AA}^{-3}$
247 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Selected geometric parameters (Å, °).

O1–C1	1.2153 (18)	C4–C11	1.528 (2)
O2–C3	1.413 (2)	C4–C5	1.531 (2)
C1–C17	1.512 (2)	C18–C23	1.513 (2)
C1–C2	1.529 (2)	C20–C24	1.508 (2)
C2–C4	1.550 (2)	C22–C25	1.518 (2)
C2–C3	1.556 (2)		
O1–C1–C17	119.98 (13)	C17–C1–C2	118.35 (12)
O1–C1–C2	121.54 (13)		
C22–C17–C1–O1	–68.0 (2)		

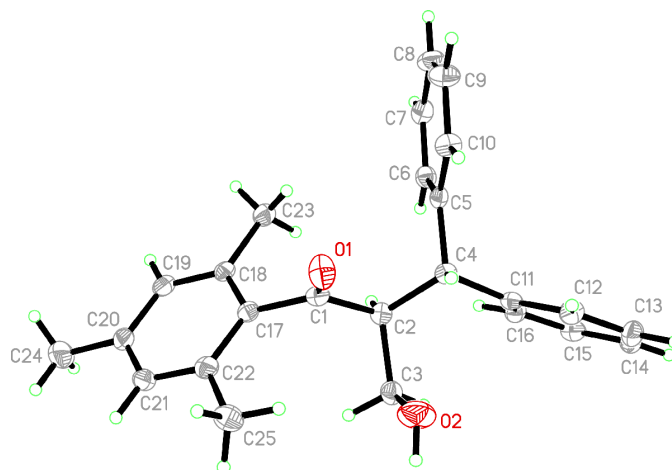


Figure 1

A view of the molecular structure of (1). Displacement ellipsoids are drawn at the 50% probability level

Table 2

Hydrogen-bonding geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O2-H1\cdots O2^i$	0.83	2.45	2.862 (2)	111

Symmetry code: (i) $1 - x, 2 - y, -z$.

Atom H1 was located in a difference map and refined. All other H atoms were included in calculated positions ($C-H = 0.93$ Å) and refined as riding; their isotropic displacement parameters were fixed [$U_{iso}(H) = 1.2U_{iso}(C)$].

Data collection: *APEX2* (Bruker, 2003); cell refinement: *APEX2*; data reduction: *SAINT-Plus* (Bruker, 2003); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 2000); software used to prepare material for publication: *SHELXTL*.

The Bruker X8 APEX diffractometer was purchased with funds received from the National Science Foundation Major Research Instrumentation Program grant CHE-0321214. KK thanks the Robert A. Welch Foundation for support (AA-1508). AGP thanks the Public Health Service, National Institute of Health, for support *via* a research grant.

References

- Bear, C. A., Macdonald, A. L. & Trotter, J. (1973). *Acta Cryst.* **B29**, 2617–2619.
- Bruker (2003). *APEX2* (Version 1.0–5) and *SAINT-Plus* (Version 6.25). Bruker AXS Inc., Madison, Wisconsin, USA.
- Pinkus, A. G. & Custard, H. C. Jr (1970). *J. Phys. Chem.* **74**, 1042–1049.
- Pinkus, A. G. & Custard, H. C. Jr (1975). *Can. J. Chem.* **53**, 2024–2030.
- Pinkus, A. G., Mullica, D. F., Milligan, W. O., Grosse, D. A. & Hurd, P. W. (1984). *Tetrahedron*, **40**, 4829–4835.
- Sheldrick, G. M. (1996). *SADABS*. University of Göttingen, Germany.
- Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
- Sheldrick, G. M. (2000). *SHELXTL*. Version 6.10. Bruker AXS, Inc., Madison, Wisconsin, USA.