

Daniel R. Vega,^{a*} Jorge D. Mufato,^b Jose M. Aguirre,^b Elba N. Alesso^c and B. Lantano^c

^aUnidad Actividad Física, Centro Atómico Constituyentes, Comisión Nacional de Energía Atómica, Av. Gral. Paz 1499, (1650) San Martín - Buenos Aires, Argentina, ^bDepartamento de Ciencias Básicas, Universidad Nacional de Luján, Luján (6700), Argentina, and ^cDepartamento de Química Orgánica, Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires, Argentina

Correspondence e-mail: vega@cnea.gov.ar

Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.005$ Å
 R factor = 0.048
 wR factor = 0.101
Data-to-parameter ratio = 14.5

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

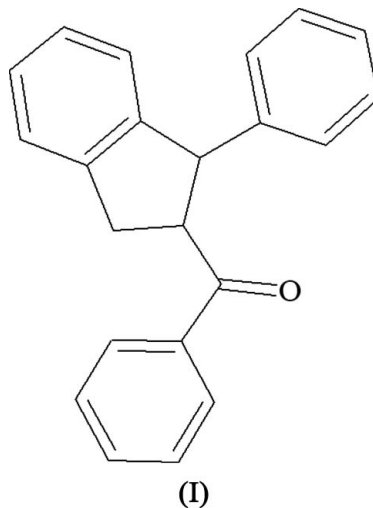
trans-2-Benzoyl-1-phenylindan

The title compound, $\text{C}_{22}\text{H}_{18}\text{O}$, was obtained as a single product from a stereoselective reaction. The five-membered ring adopts an envelope conformation. Two intramolecular $\text{C}-\text{H}\cdots\text{O}$ interactions stabilize the molecular conformation. An intermolecular $\text{C}-\text{H}\cdots\text{O}$ interaction generates chains of molecules running along the b axis.

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Comment

We have been performing extensive research on the synthesis and configurational effects of substitution in the five-membered ring of indan derivatives (Aguirre *et al.*, 1998; Aguirre *et al.*, 1999; Alesso *et al.*, 2002; Alesso *et al.*, 2003). In particular, we have been seeking alternative routes through stereoselective synthesis for indan and tetranilic derivatives *via* condensation of aryl ketones. As part of these results, the compound 2-benzoyl-1-phenylindan, (I), could be synthesized in acid solution and isolated as a single product. The *trans* configuration was assigned by NMR studies in CDCl_3 solution (Mufato *et al.*, 2002).



More recently, Rendy *et al.* (2004) indicated that this compound was obtained as a product from a reaction catalysed by superacids, but no configuration was assigned. The aim of this work is to provide experimental information about the configuration and conformation of (I) by X-ray crystallography and thus to confirm the *trans* configuration previously assigned by NMR studies.

Selected bond distances and angles are given in Table 1. The molecule (Fig. 1) has three planar benzene rings. The five-membered ring can be described as an envelope with C8 as the flap atom, which is displaced 0.488 (5) Å from the C1/C6/C7/

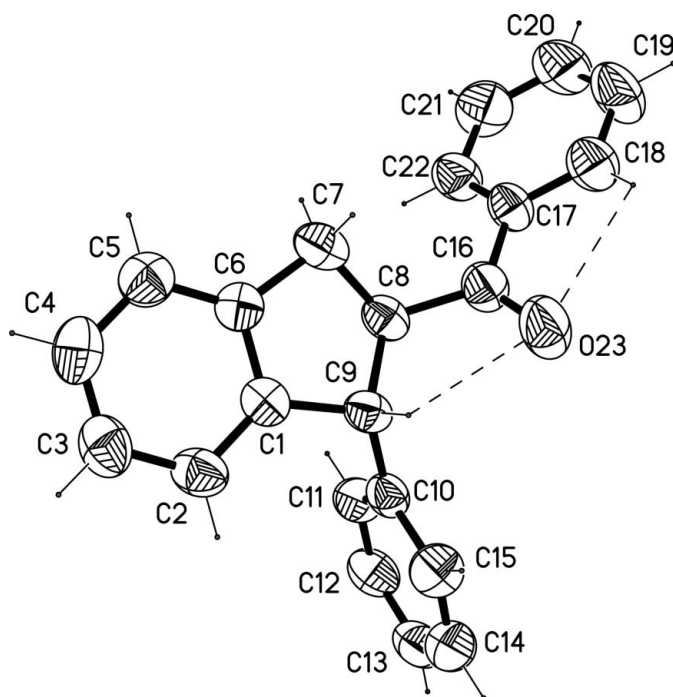


Figure 1
View of (I), showing the numbering scheme and displacement ellipsoids drawn at the 50% probability level. Intramolecular hydrogen bonds are shown as dashed lines.

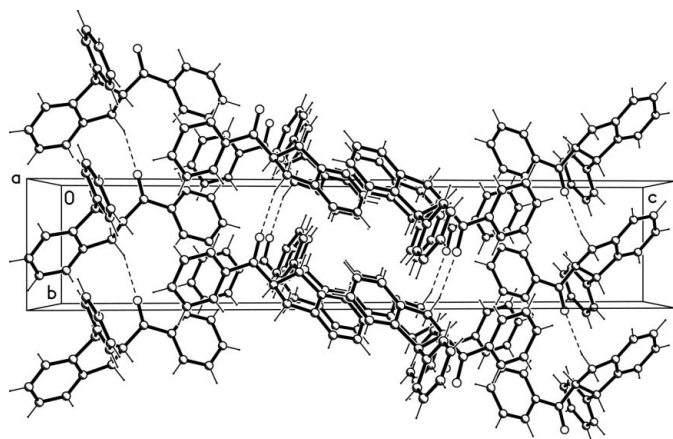


Figure 2
Packing diagram, showing the intermolecular hydrogen-bonding scheme (dashed lines).

C9 mean plane. The ring puckering parameters are $q_2 = 0.312$ (4) Å and $\varphi_2 = 108.0$ (7)° (Cremer & Pople, 1975). The proposed *trans* configuration in solution is also observed in this crystal structure, where the C10–C9–C8–C16 torsion angle has a value of -82.8 (4)°. Moreover, one conformation had been proposed as most probable, with a low value of the C9–C8–C16–O23 torsion angle; this torsion angle in the present crystal structure has a value of -7.9 (5)°.

A search was made for indane derivatives substituted at C8 and C9 in the CSD (Version 5.27; Allen, 2002), the C9–C10 and C8–C16 bonds being excluded from ring formation. Five were found, all of them having an envelope conformation with C8 as the flap atom, and the *trans* configuration was observed,

with the C10–C9–C8–C16 torsion angle spanning a wide range of values: -38.6° in FEVHIX (Troutman *et al.*, 1999), 85.9° in QICXAB (Dandekar *et al.*, 1999), 148.9° in YUPSEH (Yang *et al.*, 1995) and 101.4° and -146.6° in YUPSIL (Yang *et al.*, 1995).

Electrostatic interactions determine the way that the molecule is folded *via* two very weak intramolecular C–H···O interactions (Fig. 1 and Table 2). O23 is also involved in an intermolecular C–H···O interaction (Fig. 2 and Table 2), generating chains of molecules running along the *b* axis. Molecules also display π – π interactions between the C1–C6 ring and its inversion-related partner (symmetry code $1 - x, 1 - y, -z$), with a centroid–centroid distance of 3.969 (2) Å and a slip angle of 28.9° , providing further cohesion to the crystal packing.

Experimental

The compound was synthesized by the method of Mufato *et al.* (2002). Crystals suitable for X-ray diffraction were obtained by slow evaporation of a methanol solution at room temperature.

Crystal data

C₂₂H₁₈O
 $M_r = 298.36$
 Monoclinic, $P2_1/n$
 $a = 9.085$ (1) Å
 $b = 5.981$ (1) Å
 $c = 30.091$ (6) Å
 $\beta = 95.66$ (3)°
 $V = 1627.1$ (6) Å³
 $Z = 4$

$D_x = 1.218$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 20 reflections
 $\theta = 14$ – 25°
 $\mu = 0.07$ mm⁻¹
 $T = 293$ (2) K
 Needle, colourless
 $0.5 \times 0.2 \times 0.1$ mm

Data collection

Rigaku AFC6 diffractometer
 ω scans
 Absorption correction: none
 6911 measured reflections
 3022 independent reflections
 817 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.240$

$\theta_{max} = 25.5^\circ$
 $h = -1 \rightarrow 11$
 $k = -7 \rightarrow 7$
 $l = -36 \rightarrow 36$
 3 standard reflections
 every 147 reflections
 intensity decay: none

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.048$
 $wR(F^2) = 0.101$
 $S = 0.85$
 3022 reflections
 209 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0253P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta\sigma)_{max} < 0.001$
 $\Delta\rho_{max} = 0.16$ e Å⁻³
 $\Delta\rho_{min} = -0.15$ e Å⁻³
 Extinction correction: *SHELXL*
 Extinction coefficient: 0.0036 (5)

Table 1

Selected geometric parameters (Å, °).

C1–C6	1.387 (4)	C8–C16	1.518 (4)
C1–C9	1.521 (4)	C8–C9	1.547 (4)
C6–C7	1.506 (4)	C16–O23	1.218 (3)
C7–C8	1.552 (4)	C16–C17	1.491 (4)
C6–C1–C9	110.5 (3)	C16–C8–C9	113.9 (3)
C1–C6–C7	110.8 (3)	C9–C8–C7	104.8 (2)
C6–C7–C8	102.2 (3)	C1–C9–C8	101.9 (3)

Table 2
Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
C9—H9A...O23	0.98	2.45	2.800 (4)	101
C18—H18A...O23	0.93	2.47	2.769 (4)	99
C7—H7B...O23 ⁱ	0.97	2.40	3.220 (4)	142

Symmetry code: (i) *x*, *y* + 1, *z*.

The crystals were very weakly diffracting, particularly at high θ values, resulting in a high R_{int} value and a low proportion of 'observed' reflections. H atoms were positioned geometrically (C—H = 0.93–0.98 Å) and refined using a riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: *AFC6S Diffractometer Control Software* (Molecular Structure Corporation, 1993); cell refinement: *AFC6S Diffractometer Control Software*; data reduction: *AFC6S Diffractometer Control Software*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL-PC* (Sheldrick, 1994); software used to prepare material for publication: *SHELXTL-PC*.

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