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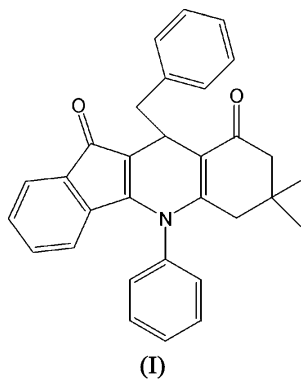
Key indicators

Single-crystal X-ray study
 $T = 173$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.056
 wR factor = 0.110
Data-to-parameter ratio = 13.4For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.10-Benzyl-7,8-dihydro-7,7-dimethyl-5-phenyl-5H-
indeno[1,2-*b*]quinoline-9,11(6*H*,10*H*)-dioneIn the molecule of the title compound, $\text{C}_{31}\text{H}_{27}\text{NO}_2$, the dihydropyridine and cyclohexene rings adopt flattened-boat and envelope conformations, respectively. The molecules are linked by intermolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds, forming a chain structure.

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Comment

Multicomponent reactions (MCRs) occupy an outstanding position in organic and medicinal chemistry for their high degree of atom economy, application in combinatorial chemistry and diversity-oriented synthesis (Ramón & Yus, 2005; Burke & Schreiber, 2004; Andreana *et al.*, 2004). It is well known that indenoquinoline derivatives show a diverse range of biological properties, such as antitumour agents, acetylcholinesterase inhibitors and potent new cytotoxic agents (Deady *et al.*, 1999, 2000; Rampa *et al.*, 2000; Yamato *et al.*, 1989). In this paper, we report the crystal structure of the title compound, (I).In the molecule of compound (I) (Fig. 1), the bond lengths and angles are in normal ranges (Allen *et al.*, 1987).An examination of the deviations from the least-squares planes through the individual rings shows that rings *A* (C7–C12), *B* (C19–C24), *C* (C26–C31) and *D* (C1/C2/C6/C7/C12) are planar. Rings *E* (N1/C1–C5) and *F* (C4/C5/C13–C16) are, of course, not planar. Ring *E* adopts a flattened-boat conformation, with puckering parameters (Cremer & Pople, 1975) $\varphi_2 = 121.56$ (2)°, $\theta_2 = 73.81$ (2)° and $Q_T = 0.154$ (2) Å, while the conformation of ring *F* is an envelope [$\varphi_2 = -110.34$ (2)°, $\theta_2 = 24.25$ (2)° and $Q_T = 0.468$ (2) Å] with atom C15 at the flap position, 0.625 (3) Å from the mean plane through the other five atoms.The crystal structure of (I) is stabilized by intermolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds (Table 1), resulting in the formation of a chain structure (Fig. 2).

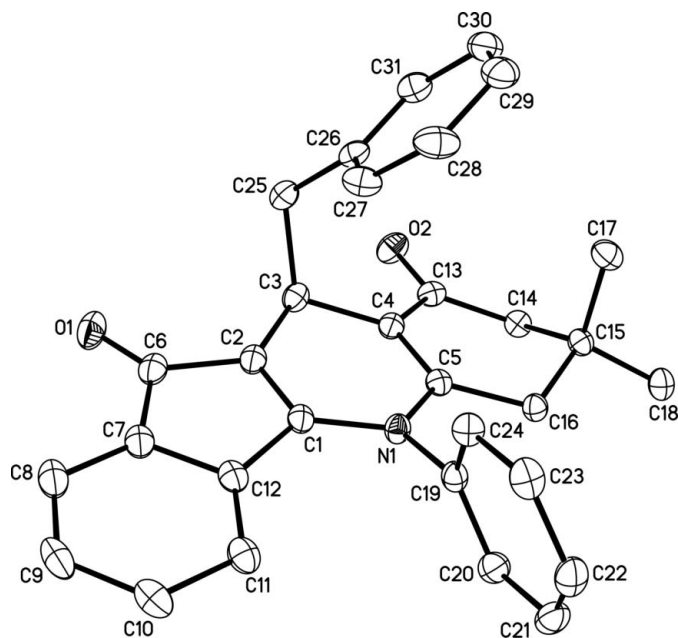


Figure 1
A drawing of the title molecular structure, with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms have been omitted for clarity.

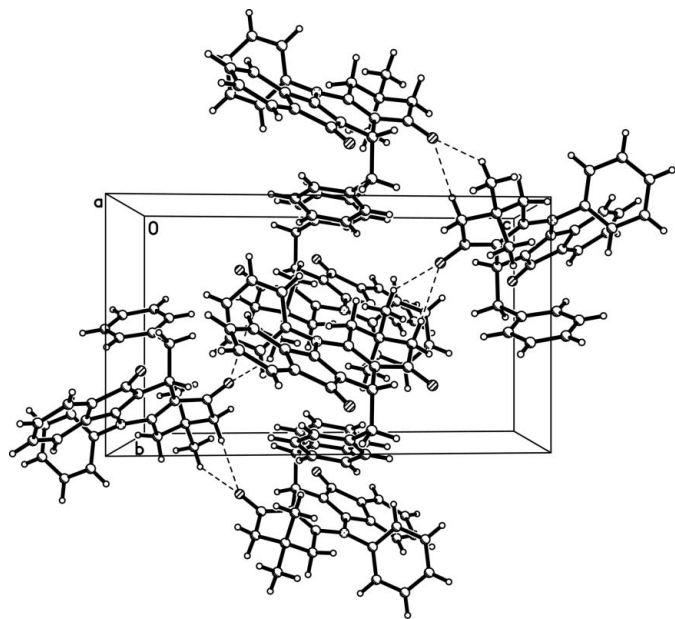


Figure 2
A packing diagram of (I). Hydrogen bonds are shown as dashed lines.

Experimental

The title compound was prepared by the reaction of 2-phenylacetaldehyde (120 mg, 1.0 mmol), 3-(phenylamino)-5,5-dimethylcyclohex-2-enone (220 mg, 1.0 mmol) and 1,3-indanedione (150 mg, 1.0 mmol) in a mixed solvent of glycol (0.5 ml) and acetic acid (1.0 ml) under microwave irradiation. Single crystals of (I) suitable for X-ray diffraction were obtained by slow evaporation of a 95% aqueous ethanol solution (yield 380 mg, 85%; m.p. 480–482 K). Spectroscopic analysis: IR (KBr, cm^{-1}): 1686 (CO), 1637 (CO).

Crystal data

$\text{C}_{31}\text{H}_{27}\text{NO}_2$
 $M_r = 445.54$
Monoclinic, $P2_1/n$
 $a = 14.783 (2) \text{ \AA}$
 $b = 9.4408 (12) \text{ \AA}$
 $c = 16.345 (2) \text{ \AA}$
 $\beta = 96.878 (3)^\circ$
 $V = 2264.6 (5) \text{ \AA}^3$

$Z = 4$
 $D_x = 1.307 \text{ Mg m}^{-3}$
Mo $K\alpha$ radiation
 $\mu = 0.08 \text{ mm}^{-1}$
 $T = 173 (2) \text{ K}$
Block, red
 $0.79 \times 0.32 \times 0.14 \text{ mm}$

Data collection

Rigaku Mercury diffractometer
 ω scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
 $T_{\min} = 0.939$, $T_{\max} = 0.989$

21579 measured reflections
4144 independent reflections
3611 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.040$
 $\theta_{\max} = 25.4^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.056$
 $wR(F^2) = 0.110$
 $S = 1.18$
4144 reflections
310 parameters
H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0325P)^2 + 0.9725P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.20 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.18 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$\text{C14-H14B} \cdots \text{O2}^i$	0.99	2.40	3.337 (2)	157
$\text{C18-H18A} \cdots \text{O2}^i$	0.98	2.58	3.429 (2)	145

Symmetry code: (i) $-x + \frac{3}{2}, y - \frac{1}{2}, -z + \frac{3}{2}$.

H atoms were positioned geometrically, with $C-H = 0.95, 0.98, 0.99$ and 1.00 \AA for aromatic, methyl, methylene and methine H, respectively, and were constrained to ride on their parent atoms, with $U_{\text{iso}}(\text{H}) = xU_{\text{eq}}(\text{C})$, where $x = 1.5$ for methyl H and $x = 1.2$ for all other H.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1999); software used to prepare material for publication: SHELXTL.

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