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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.005 Å R factor = 0.039 wR factor = 0.089 Data-to-parameter ratio = 6.7

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. 7-(4-Fluorophenyl)-8*H*-benzo[*h*]indeno-[1,2-*b*]quinolin-8-one

The title compound, $C_{26}H_{14}FNO$, was synthesized by the reaction of 4-fluorobenzaldehyde, 1-naphthylamine and 1,3indanedione in glycol under microwave irradiation. The fused ring system is approximately planar and the attached fluorophenyl ring forms a dihedral angle of 65.21 (8)°. The molecules are linked by intermolecular $C-H\cdots O$ hydrogen bonds and $\pi-\pi$ interactions, forming a chain structure

Comment

Indenoquinoline derivatives show a wide range of biological properties, such as 5-HT-receptor binding activity and antiinflammatory activity (Lu *et al.*, 2003). They also act as antitumor agents, inhibitors for steroid reductase (Deady *et al.*, 2000), acetylcholinesterase inhibitors and anti-malarial agents (Rampa *et al.*, 2000). We report here the crystal structure of the title compound, (I).



The fused ring system containing the naphthalene, pyridine and indenone rings is approximately planar with an r.m.s. deviation of 0.045 Å (Fig. 1). The dihedral angle between the N1/O1/C1–C20 and C21–C26 planes is 65.21 (8)°.

The crystal structure of (I) is stabilized by intermolecular C-H···O hydrogen bonds (Table 1), and π - π stacking interactions involving the C1/C2/C7-C9 (centroid Cg1) and C11-C14/C19/C20 (centroid Cg2) rings, with a Cg1···Cg2^{iv} distance of 3.542 (3) Å [symmetry code: (iv) x, 1 + y, z], resulting in the formation of a chain structure along the b axis. In addition, a C-H··· π interaction involving the C14-C19 benzene ring (centroid Cg3) is observed.

Experimental

Compound (I) was prepared by the reaction of 4-fluorobenzaldehyde (1 mmol), 1-naphthylamine (1 mmol) and 1,3-indanedione (1 mmol) in glycol (2 ml) under microwave irradiation for 3 min. Single crystals of (I) suitable for X-ray diffraction were obtained by slow evaporation of a 95% aqueous ethanol solution (yield 93%; m.p. 573 K).

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Crystal data

 $\begin{array}{l} C_{26}H_{14}\text{FNO} \\ M_r = 375.38 \\ \text{Monoclinic, } P2_1 \\ a = 10.971 \ (4) \ \text{\AA} \\ b = 6.274 \ (2) \ \text{\AA} \\ c = 13.540 \ (4) \ \text{\AA} \\ \beta = 103.115 \ (5)^{\circ} \\ V = 907.7 \ (5) \ \text{\AA}^3 \end{array}$

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\min} = 0.956, T_{\max} = 0.989$

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.039$	$w = 1/[\sigma^2(F_o^2) + (0.039P)^2]$
$wR(F^2) = 0.089$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.00	$(\Delta/\sigma)_{\rm max} = 0.001$
1751 reflections	$\Delta \rho_{\rm max} = 0.15 \ {\rm e} \ {\rm \AA}^{-3}$
262 parameters	$\Delta \rho_{\rm min} = -0.12 \text{ e} \text{ Å}^{-3}$

Z = 2

 $D_x = 1.373 \text{ Mg m}^{-3}$

 $0.50 \times 0.23 \times 0.12 \text{ mm}$

4768 measured reflections

1751 independent reflections

1130 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.09 \text{ mm}^{-1}$ T = 298 (2) K

Block, yellow

 $R_{\rm int} = 0.044$

 $\theta_{\rm max} = 25.0^{\circ}$

Table 1

Hydrogen-bond geometry (Å, °).

D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
0.93	2.44	3.365 (5)	173
0.93	2.34	3.237 (5)	163
0.93	2.88	3.685 (4)	146
	<i>D</i> -H 0.93 0.93 0.93	D−H H···A 0.93 2.44 0.93 2.34 0.93 2.88	$D-H$ $H\cdots A$ $D\cdots A$ 0.93 2.44 3.365 (5) 0.93 2.34 3.237 (5) 0.93 2.88 3.685 (4)

Symmetry codes: (i) $-x, y + \frac{1}{2}, -z + 1$; (ii) x, y - 1, z; (iii) $-x + 1, y - \frac{1}{2}, -z + 2$. Cg3 is the centroid of the C14–C19 benzene ring.

H atoms were positioned geometrically and treated as riding, with C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$. In the absence of significant anomalous dispersion effects, Friedel pairs were merged before the final refinement.

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*.



The structure of (I), showing 30% probability displacement ellipsoids.

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