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Key indicators

Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.044
 wR factor = 0.118
Data-to-parameter ratio = 14.4For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

2,2'-(1,4-Phenylenedivinylene)diquinolin-8-ol

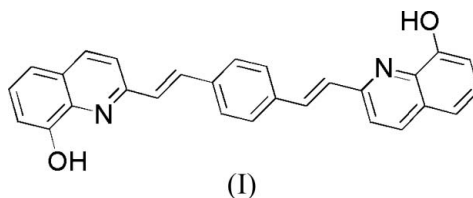
The title compound, $\text{C}_{28}\text{H}_{20}\text{N}_2\text{O}_2$, has a crystallographic
inversion centre, and an intramolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen
bond may have an effect on some bond lengths and angles.

Received 13 June 2005

Accepted 29 June 2005

Online 6 July 2005

Comment

The electroluminescent properties of the title compound, (I),
together with its Al^{III} and Zn^{II} complexes, were reported
previously (Kim *et al.*, 2002; Cui & Kim, 2004).The molecular structure of (I) is illustrated in Fig. 1. The
asymmetric unit contains one half-molecule; the other half is
generated by a centre of inversion, which lies at the centre of
the benzene ring. The intramolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen
bond (Table 2) may have an effect on some bond lengths and
angles. A view of the molecular packing is shown in Fig. 2.

Experimental

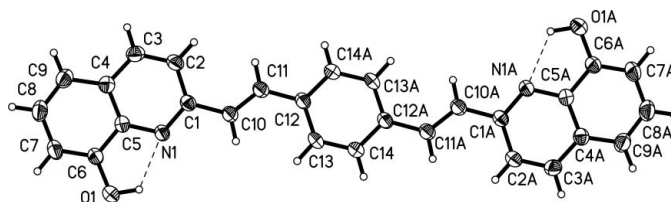
The title compound was synthesized according to the method of
Diakoumakos & Mikroyannidis (1993). Single crystals of (I) suitable
for an X-ray diffraction study were obtained by recrystallization from
a dimethylformamide solution.

Figure 1

A drawing of the molecule of (I), with the atom-numbering scheme.
Displacement ellipsoids are drawn at the 35% probability level. The
broken lines indicate hydrogen bonds. Atoms labelled with the suffix 'A'
are at the symmetry position $(-x, -y, -z)$.

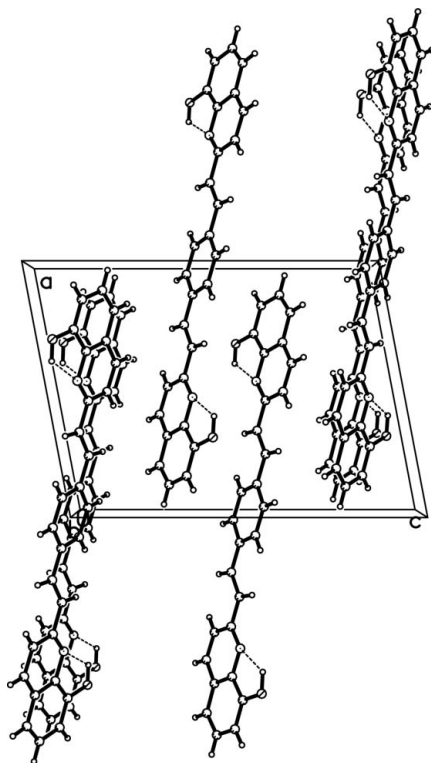


Figure 2
A packing diagram for (I). Dashed lines indicate hydrogen bonds.

Crystal data

$C_{28}H_{20}N_2O_2$	$D_x = 1.320 \text{ Mg m}^{-3}$
$M_r = 416.46$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 1827 reflections
$a = 11.648 (6) \text{ \AA}$	$\theta = 2.6\text{--}26.4^\circ$
$b = 5.777 (3) \text{ \AA}$	$\mu = 0.08 \text{ mm}^{-1}$
$c = 15.852 (8) \text{ \AA}$	$T = 294 (2) \text{ K}$
$\beta = 100.740 (9)^\circ$	Prism, yellow
$V = 1047.9 (10) \text{ \AA}^3$	$0.22 \times 0.20 \times 0.10 \text{ mm}$
$Z = 2$	

Data collection

Bruker SMART CCD area-detector diffractometer	2142 independent reflections
φ and ω scans	1323 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 2002)	$R_{\text{int}} = 0.023$
$T_{\text{min}} = 0.980$, $T_{\text{max}} = 0.992$	$\theta_{\text{max}} = 26.4^\circ$
5549 measured reflections	$h = -14 \rightarrow 10$
	$k = -7 \rightarrow 6$
	$l = -16 \rightarrow 19$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0519P)^2 + 0.0516P]$
$R[F^2 > 2\sigma(F^2)] = 0.044$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.118$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.02$	$\Delta\rho_{\text{max}} = 0.15 \text{ e \AA}^{-3}$
2142 reflections	$\Delta\rho_{\text{min}} = -0.16 \text{ e \AA}^{-3}$
149 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Selected geometric parameters (\AA , $^\circ$).

N1—C1	1.330 (2)	C4—C5	1.417 (2)
N1—C5	1.370 (2)	C5—C6	1.413 (2)
O1—C6	1.368 (2)	C6—C7	1.369 (2)
C1—N1—C5	118.34 (15)	C6—C5—C4	118.88 (15)
N1—C1—C2	121.21 (16)	O1—C6—C7	121.09 (17)
N1—C5—C6	117.15 (16)	O1—C6—C5	118.62 (15)
N1—C5—C4	123.96 (16)		

Table 2

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

$D\text{---}H\cdots A$	$D\text{---}H$	$H\cdots A$	$D\cdots A$	$D\text{---}H\cdots A$
O1—H1 \cdots N1	0.96 (2)	2.06 (2)	2.694 (2)	122 (2)

Atom H1 was located in a difference synthesis and refined freely [$O\text{---}H = 0.96 (2) \text{ \AA}$]. The remaining H atoms were positioned geometrically at distances of 0.93 \AA from their parent C atoms, and a riding model was used during the refinement process, with the $U_{\text{iso}}(\text{H})$ values constrained to 1.2 times U_{eq} of the carrier atom.

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

This work was supported by the Scientific Research Foundation for Returned Overseas Chinese Scholars, Ministry of Education, China.

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