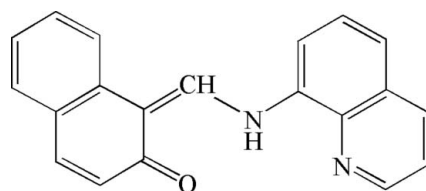
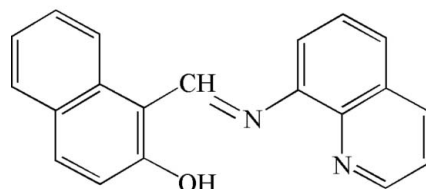


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Key indicatorsSingle-crystal X-ray study
 $T = 93\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.037
 wR factor = 0.107
Data-to-parameter ratio = 7.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**1-(8-Quinolylaminomethylene)naphthalen-2(1H)-one**The title hydroxynaphthalene derivative, $\text{C}_{20}\text{H}_{14}\text{N}_2\text{O}$, crystallizes in the keto form. Intramolecular $\text{N}-\text{H}\cdots\text{O}/\text{N}$ hydrogen bonds stabilize the planar conformation of the molecule.Received 17 May 2006
Accepted 1 June 2006**Comment**The title compound, (I), has been reported as a fluorescent reagent for molybdenum (Jiang *et al.*, 2001) and beryllium (Jiang & He, 2003). The structure of (I) has not been reported, although the structures of the mononuclear complexes of technetium (Tisato *et al.*, 1990) and vanadium (Asgedom *et al.*, 1996) containing (I) as ligand have been determined. The molecule of (I) may show tautomerism, and keto and enol forms are possible. The present study reveals that the molecule adopts the keto form in the crystal structure.

(I), keto form



(I), enol form

In (I), all the atoms are located almost in the same plane (Fig. 1). Selected bond distances and angles are listed in Table 1. The $\text{O1}-\text{C1}$ distance is shorter than the $\text{O}-\text{C}$ bond of phenol (1.372 \AA ; Zavodnik *et al.*, 1987), indicating double-bond character. There exist intramolecular $\text{N1}-\text{H1}\cdots\text{O1}/\text{N2}$ hydrogen bonds (Table 2), forming six- and five-membered rings. The hydrogen bonds and the multiple bond character of $\text{C10}-\text{C11}$, $\text{C11}-\text{N1}$ and $\text{N1}-\text{C12}$ stabilize the planar conformation of the molecule.**Experimental**Compound (I) was synthesized according to the method of Jiang *et al.* (2001). For recrystallization, compound (I) (100 mg) in ethanol (30 ml) was refluxed for 1 h (353 K). The solution was filtered quickly and cooled to ambient temperature to obtain crystals suitable for X-ray analysis.

Crystal data

$C_{20}H_{14}N_2O$
 $M_r = 298.34$
 Monoclinic, Pc
 $a = 11.7365$ (19) Å
 $b = 5.8687$ (5) Å
 $c = 14.251$ (2) Å
 $\beta = 134.496$ (4)°
 $V = 700.15$ (17) Å³

$Z = 2$
 $D_x = 1.415$ Mg m⁻³
 Mo $K\alpha$ radiation
 $\mu = 0.09$ mm⁻¹
 $T = 93.1$ K
 Needle, orange
 $0.55 \times 0.10 \times 0.05$ mm

Data collection

Rigaku Mercury diffractometer
 ω scans
 Absorption correction: multi-scan
 (Jacobson, 1998)
 $T_{\min} = 0.933$, $T_{\max} = 0.996$

6503 measured reflections
 1610 independent reflections
 1521 reflections with $F^2 > 2\sigma(F^2)$
 $R_{\text{int}} = 0.014$
 $\theta_{\max} = 27.5^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.037$
 $wR(F^2) = 0.107$
 $S = 1.08$
 1610 reflections
 209 parameters
 H-atom parameters not refined

$w = 1/[\sigma^2(F_o^2) + (0.0746P)^2 + 0.0816P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.32$ e Å⁻³
 $\Delta\rho_{\min} = -0.22$ e Å⁻³

Table 1

Selected geometric parameters (Å, °).

O1—C1	1.256 (3)	C1—C2	1.453 (3)
N1—C11	1.334 (3)	C1—C10	1.461 (5)
N1—C12	1.407 (2)	C10—C11	1.381 (2)
C11—N1—C12	124.6 (2)	C1—C10—C11	119.8 (2)
O1—C1—C2	120.8 (3)	N1—C11—C10	125.3 (3)
O1—C1—C10	122.1 (2)		
C11—N1—C12—C13	1.3 (2)	C8—C9—C10—C11	5.4 (2)
C12—N1—C11—C10	179.11 (17)	C1—C10—C11—N1	1.4 (2)
O1—C1—C10—C11	-4.1 (2)	N1—C12—C20—N2	-3.9 (2)

Table 2

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N1—H1 \cdots O1	0.92	1.94	2.624 (3)	131
N1—H1 \cdots N2	0.92	2.29	2.698 (3)	107

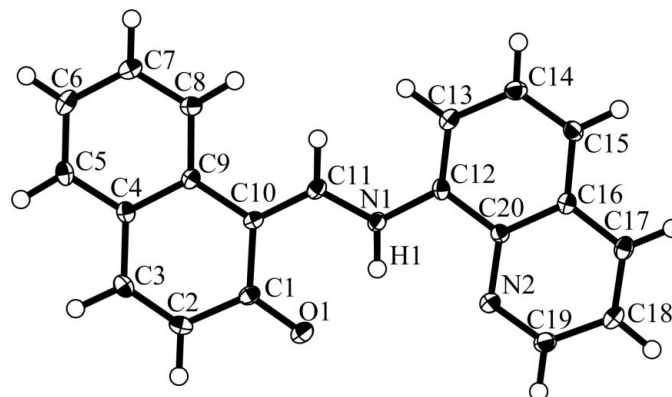


Figure 1

The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

All H atoms were located in difference maps, and their positional parameters were fixed with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$. In the absence of significant anomalous scattering effects, Friedel pairs were averaged.

Data collection: *CrystalClear* (Rigaku, 1999); cell refinement: *CrystalClear*; data reduction: *CrystalStructure* (Rigaku/MS, 2005); program(s) used to solve structure: *SIR2002* (Burla *et al.*, 2003); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *CrystalStructure*; software used to prepare material for publication: *CrystalStructure*.

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