

# *N*-(6-Methoxy-2-methyl-8-quinolyl)-4-*n*-propylbenzenesulfonamide

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## Key indicators

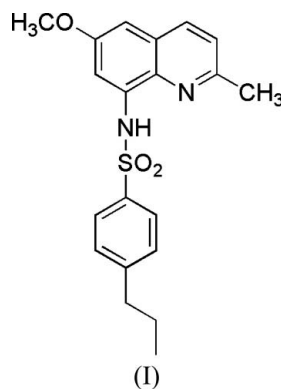
Single-crystal X-ray study  
*T* = 299 K  
Mean  $\sigma(\text{C—C}) = 0.004 \text{ \AA}$   
*R* factor = 0.046  
*wR* factor = 0.131  
Data-to-parameter ratio = 12.5

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

In the title compound,  $\text{C}_{20}\text{H}_{22}\text{N}_2\text{O}_3\text{S}$ , the torsion angle about the N—S bond between the quinoline system and the benzene ring is  $-48.7(2)^\circ$ . An intramolecular N—H $\cdots$ N and an intermolecular C—H $\cdots$ O hydrogen bond are observed in the crystal structure.

## Comment

Various fluorescence-based zinc probes have been developed. Some of these are fluorescent adducts of Zn-chelating peptides and proteins, while others are dye adducts of Zn-chelating macrocyclic compounds. Zinc chelators based on a quinoline core, such as 6-methoxy-(8-*p*-toluenesulfonamide)quinoline (TSQ), are currently the most widely used zinc-activated fluorophores (Fahrni & O'Halloran, 1999). As part of our continuing study of 8-aminoquinolinesulfonamide derivatives capable of binding  $\text{Zn}^{2+}$  (da Silva *et al.*, 2005*a,b,c,d,e*, 2006), the structure of the title compound (I), was determined.



The C1—N1—S1—C10 torsion angle is  $-48.7(2)^\circ$ . The NH group forms an intramolecular hydrogen bond to the quinoline N atom. In addition, there is an intermolecular C—H $\cdots$ O hydrogen bond. The three-dimensional network is shown in the packing diagram (Fig. 2) and details are given in Table 1.

## Experimental

Compound (I) was prepared according to the literature procedure of Kimber *et al.* (2003). Single crystals of (I) suitable for X-ray data collection were obtained by recrystallization from methanol-dichloromethane (1:1 *v/v*).

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## Crystal data

$C_{20}H_{22}N_2O_3S$   
 $M_r = 370.46$   
 Triclinic,  $P\bar{1}$   
 $a = 8.4437$  (8) Å  
 $b = 9.7548$  (8) Å  
 $c = 12.1870$  (8) Å  
 $\alpha = 95.254$  (6)°  
 $\beta = 94.757$  (7)°  
 $\gamma = 103.426$  (8)°  
 $V = 966.62$  (14) Å<sup>3</sup>

$Z = 2$   
 $D_x = 1.273$  Mg m<sup>-3</sup>  
 Cu  $K\alpha$  radiation  
 Cell parameters from 25 reflections  
 $\theta = 4.7$ – $22.8$ °  
 $\mu = 1.66$  mm<sup>-1</sup>  
 $T = 299$  (2) K  
 Plate, light brown  
 $0.30 \times 0.28 \times 0.10$  mm

## Data collection

Enraf–Nonius CAD-4 diffractometer  
 $\omega/2\theta$  scans  
 Absorption correction:  $\psi$  scan (North *et al.*, 1968)  
 $T_{\min} = 0.697$ ,  $T_{\max} = 0.847$   
 4198 measured reflections  
 3438 independent reflections  
 2585 reflections with  $I > 2\sigma(I)$

$R_{\text{int}} = 0.036$   
 $\theta_{\text{max}} = 66.9$ °  
 $h = -10 \rightarrow 1$   
 $k = -11 \rightarrow 11$   
 $l = -14 \rightarrow 14$   
 3 standard reflections  
 frequency: 120 min  
 intensity decay: 1.0%

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.046$   
 $wR(F^2) = 0.131$   
 $S = 1.04$   
 3438 reflections  
 274 parameters  
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0666P)^2 + 0.1977P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} = 0.006$   
 $\Delta\rho_{\text{max}} = 0.18$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.29$  e Å<sup>-3</sup>

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H20\cdots N2$	0.86 (3)	2.12 (3)	2.639 (3)	119 (2)
$C6-H6\cdots O1^i$	0.95 (3)	2.51 (3)	3.356 (3)	149 (2)

Symmetry code: (i)  $x, y - 1, z$ .

The H atoms of the CH<sub>3</sub> groups were positioned with idealized geometry and refined using a riding model, with  $C-H = 0.96$  Å and  $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(C)$ . All other H atoms were located in a difference map. Their coordinates were refined, but their isotropic displacement parameters were set at 1.2 times  $U_{\text{eq}}$  of the parent atom.

Data collection: *CAD-4-PC Software* (Nonius, 1996); cell refinement: *CAD-4-PC Software*; data reduction: *REDU4* (Stoe & Cie, 1987); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97*.

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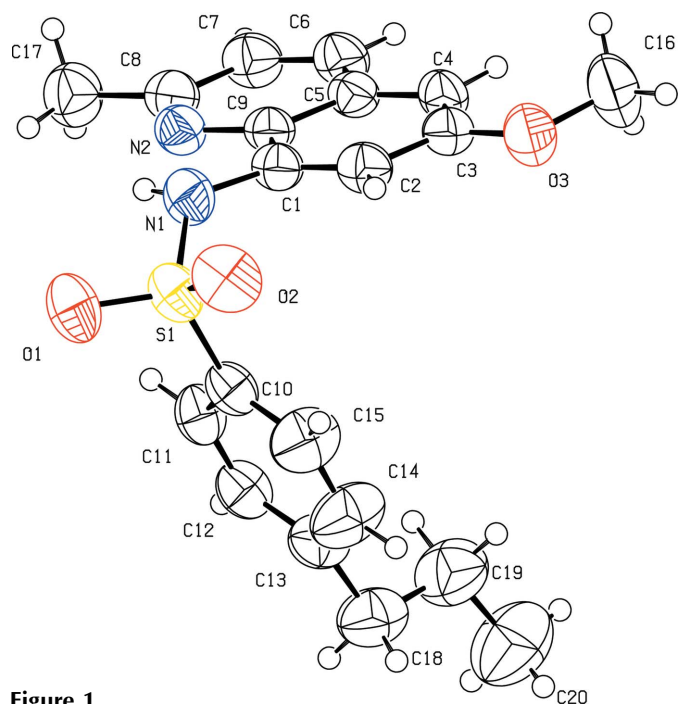


Figure 1

The molecular structure of (I), showing the atom labelling. Displacement ellipsoids are drawn at the 50% probability level.

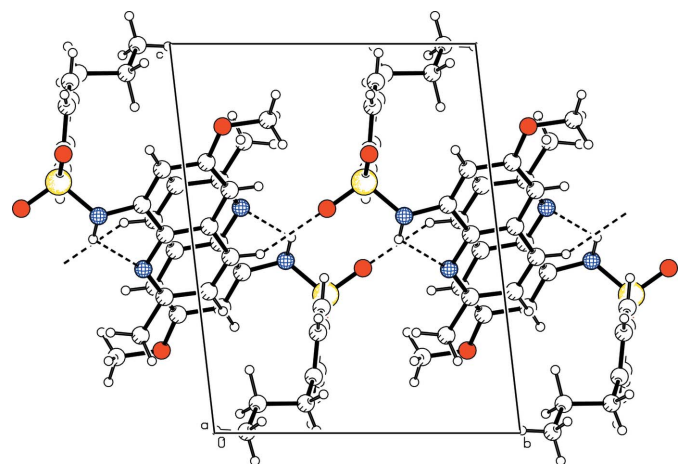


Figure 2

The molecular packing of (I) with hydrogen bonds shown as dashed lines.

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