

## 4-n-Propyl-N-(8-quinolyl)benzenesulfonamide

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### Key indicators

Single-crystal X-ray study

$T = 299\text{ K}$

Mean  $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$

Disorder in main residue

$R$  factor = 0.044

$wR$  factor = 0.132

Data-to-parameter ratio = 12.8

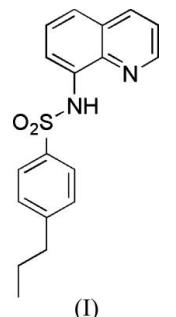
For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

In the title compound,  $\text{C}_{18}\text{H}_{18}\text{N}_2\text{O}_2\text{S}$ , the torsion angle about the N–S bond between the quinoline ring system and the benzene ring is  $-60.9(2)^\circ$ . The NH group forms an intramolecular hydrogen bond to the quinoline N atom.

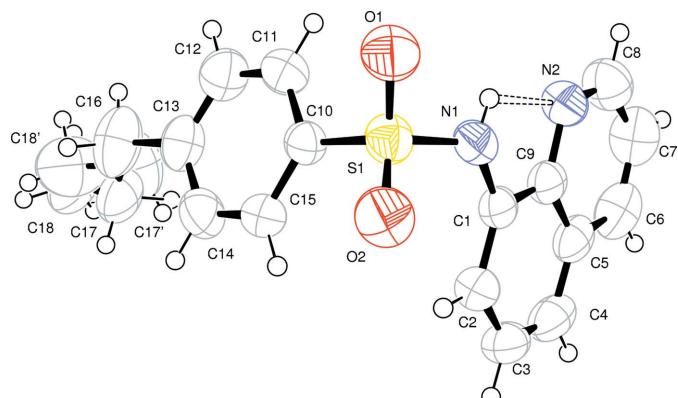
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### Comment

Zinc(II)-specific fluorophores are of substantial importance in the study of intracellular  $\text{Zn}^{2+}$ . Various fluorescence-based quinoline cores are currently the most widely used zinc-activated fluorophores (Frederickson *et al.*, 1987; Savage *et al.*, 1989; Kimber *et al.*, 2000). We report here the structure of the title compound, (I), determined as part of our studies to investigate potential new fluorophores to be used as ligands for coordination to  $\text{Zn}^{\text{II}}$  and  $\text{Cu}^{\text{II}}$  ions (da Silva *et al.*, 2005*a,b,c,d,e*, 2006).



The quinoline ring system forms a C1–N1–S1–C10 torsion angle with the benzene ring of  $-60.9(2)^\circ$ , indicating non-planarity in the molecule. The NH group forms an intramolecular hydrogen bond to the quinoline N atom (Table 1).



**Figure 1**

The molecular structure of (I), showing the atom labelling and displacement ellipsoids drawn at the 50% probability level. Both disorder components are shown. The hydrogen bonding is shown as dashed lines.

## Experimental

Compound (I) was prepared by according to the literature procedure of Xue *et al.* (2000). Suitable crystals were obtained by recrystallization from methanol–dichloromethane (1:1) (m.p. 378 K).

### Crystal data

$C_{18}H_{18}N_2O_2S$	$Z = 4$
$M_r = 326.40$	$D_x = 1.312 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/n$	$\text{Cu } K\alpha \text{ radiation}$
$a = 6.7242 (8) \text{ \AA}$	$\mu = 1.83 \text{ mm}^{-1}$
$b = 14.031 (1) \text{ \AA}$	$T = 299 (2) \text{ K}$
$c = 17.513 (1) \text{ \AA}$	Block, colourless
$\beta = 90.891 (9)^\circ$	$0.50 \times 0.30 \times 0.17 \text{ mm}$
$V = 1652.1 (2) \text{ \AA}^3$	

### Data collection

Nonius CAD-4 diffractometer  
 $\omega/2\theta$  scans  
 Absorption correction:  $\psi$  scan (North *et al.*, 1968)  
 $T_{\min} = 0.546$ ,  $T_{\max} = 0.723$   
 6255 measured reflections  
 2933 independent reflections

### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.044$   
 $wR(F^2) = 0.133$   
 $S = 1.06$   
 2933 reflections  
 230 parameters  
 H atoms treated by a mixture of independent and constrained refinement

2431 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.051$   
 $\theta_{\text{max}} = 66.9^\circ$   
 3 standard reflections  
 frequency: 120 min  
 intensity decay: 1.5%  
 $w = 1/[\sigma^2(F_o^2) + (0.0681P)^2 + 0.3991P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} = 0.002$   
 $\Delta\rho_{\text{max}} = 0.34 \text{ e } \text{\AA}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.31 \text{ e } \text{\AA}^{-3}$   
 Extinction correction: *SHELXL97*  
 Extinction coefficient: 0.0079 (7)

**Table 1**  
 Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
N1—H1N $\cdots$ N2	0.80 (3)	2.19 (3)	2.651 (3)	117 (2)

The H atom of the NH group was located in a difference map and its position refined [ $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$ ]. The carbon-bound H atoms

were positioned with idealized geometry and refined using a riding model, with C—H distances in the range 0.93–0.97  $\text{\AA}$  and isotropic displacement parameters set at 1.2 times  $U_{\text{eq}}$  value of the parent atom. Atoms C17 and C18 of the propyl group are disordered and were refined with a split model. The corresponding site-occupation factors were refined but later fixed at 0.5/0.5.

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: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

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