

***N*-Benzylquinoline-8-sulfonamide**

Carla Regina Andrighetti-Fröhner,^{a,b} Luiz Everson da Silva,^a Ricardo José Nunes,^{a,b} Cláudia Maria Oliveira Simões^c and Sabine Foro^{b*}

^aDepartamento de Química–UFSC, 88040-900 Florianópolis, SC, Brazil, ^bClemens Schöpf-Institut für Organische Chemie und Biochemie, Technische Universität Darmstadt, Petersenstrasse 22, D-64287 Darmstadt, Germany, and ^cDepartamento de Ciências Farmacêuticas–UFSC, 88040-900 Florianópolis, SC, Brazil

Correspondence e-mail: foro@tu-darmstadt.de

Key indicators

Single-crystal X-ray study

$T = 299\text{ K}$

Mean $\sigma(\text{C}–\text{C}) = 0.007\text{ \AA}$

R factor = 0.078

wR factor = 0.236

Data-to-parameter ratio = 13.2

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

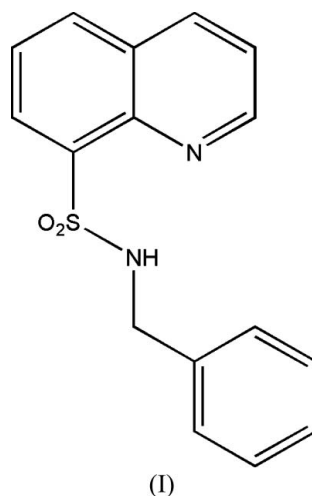
In the title compound, $\text{C}_{16}\text{H}_{14}\text{N}_2\text{O}_2\text{S}$, the $\text{C}–\text{N}–\text{S}–\text{C}$ torsion angle is $-63.1(4)^\circ$. One intramolecular $\text{N}–\text{H}\cdots\text{N}$ hydrogen bond is observed in the structure.

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Comment

Quinoline and its derivatives comprise an important class of heterocyclic compounds present in many biologically active molecules such as multi-drug-resistant cancer cells (Gao *et al.*, 1999) and have demonstrated antibacterial activity (Patel & Patel, 1999). In addition, quinoline derivatives have been reported to show broad-spectrum efficacy against multiple herpes viruses and they may have a potential role in the treatment of a variety of infections, such as those caused by herpes simplex virus type 1 (Hartline *et al.*, 2005; Oliveira *et al.*, 2004), human cytomegalovirus and varicella zoster virus (Oien *et al.*, 2002; Knechtel *et al.*, 2002). As part of a project to investigate the structure–function relationships and develop more effective antiviral drugs (Andrighetti-Fröhner *et al.*, 2003), we report here the crystal structure of the title compound, (I).



The key feature of the molecular structure of (I) (Fig. 1) is the $\text{C}10–\text{N}1–\text{S}1–\text{C}1$ torsion angle of $-63.1(4)^\circ$, which illustrates the non-planarity of the molecule. The H atom of the NH group has an intramolecular contact with the N atom of the quinoline ring system (Table 1).

Experimental

The title compound was prepared by the reaction of 1 equivalent of 8-quinolinesulfonyl chloride (1 mmol) and benzylamine (2 mmol) in the presence of methanol (5 ml) for 2 h, at room temperature,

according to the literature procedure of Buchmann & Schalinatus (1962). Single crystals of (I) suitable for X-ray data collection were obtained by recrystallization from a methanol/dichloromethane solution (1:1).

Crystal data

$C_{16}H_{14}N_2O_2S$ $Z = 4$
 $M_r = 298.35$ $D_x = 1.379 \text{ Mg m}^{-3}$
 Monoclinic, $P2_1/n$ $Cu \text{ K}\alpha$ radiation
 $a = 10.142 (2) \text{ \AA}$ $\mu = 2.05 \text{ mm}^{-1}$
 $b = 9.980 (2) \text{ \AA}$ $T = 299 (2) \text{ K}$
 $c = 14.428 (2) \text{ \AA}$ Block, yellow
 $\beta = 100.25 (2)^\circ$ $0.55 \times 0.40 \times 0.30 \text{ mm}$
 $V = 1437.1 (5) \text{ \AA}^3$

Data collection

Enraf–Nonius CAD-4 diffractometer 2546 independent reflections
 2203 reflections with $I > 2\sigma(I)$
 $\omega/2\theta$ scans $R_{int} = 0.066$
 Absorption correction: ψ scan (North *et al.*, 1968) $\theta_{max} = 66.8^\circ$
 $T_{min} = 0.532$, $T_{max} = 0.611$ 3 standard reflections
 (expected range = 0.470–0.540) frequency: 120 min
 intensity decay: 1.3%
 2649 measured reflections

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.1508P)^2 + 0.7674P]$
 $R[F^2 > 2\sigma(F^2)] = 0.078$ where $P = (F_o^2 + 2F_c^2)/3$
 $wR(F^2) = 0.236$ $(\Delta/\sigma)_{max} = 0.002$
 $S = 1.10$ $\Delta\rho_{max} = 0.80 \text{ e \AA}^{-3}$
 2546 reflections $\Delta\rho_{min} = -0.40 \text{ e \AA}^{-3}$
 193 parameters
 H atoms treated by a mixture of independent and constrained refinement

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1N\cdots N2$	0.84 (5)	2.32 (5)	2.929 (5)	130 (4)

The H atom of the NH group was located in a difference map and its position refined. The carbon-bound H atoms were positioned with idealized geometry, with C–H distances in the range 0.93–0.97 \AA and refined using a riding model. Isotropic displacement parameters for all H atoms were set equal to $1.2U_{eq}(\text{parent atom})$.

Data collection: *CAD-4-PC* (Enraf–Nonius, 1996); cell refinement: *CAD-4-PC*; 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

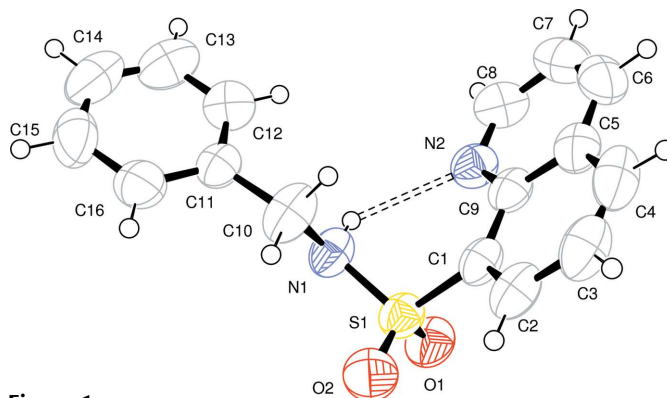


Figure 1

The molecular structure of (I), showing the atom labeling and displacement ellipsoids drawn at the 50% probability level. The intramolecular hydrogen bond is shown dashed.

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

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