

2-Aminoquinolin-8-yl 3,5-difluorobenzenesulfonate

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Key indicators

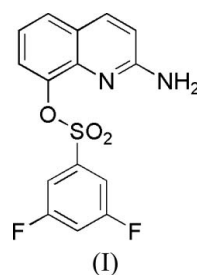
Single-crystal X-ray study
 $T = 299$ K
Mean $\sigma(\text{C—C}) = 0.005$ Å
 R factor = 0.062
 wR factor = 0.186
Data-to-parameter ratio = 11.6For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The molecular packing of the title compound, $\text{C}_{15}\text{H}_{10}\text{F}_2\text{N}_2\text{O}_3\text{S}$, is stabilized by a hydrogen-bonded network. Both H atoms of the amino group form intermolecular hydrogen bonds of types $\text{N—H}\cdots\text{N}$ [2.26 (5) Å] and $\text{N—H}\cdots\text{O}$ [2.30 (5) Å]. The nearly planar quinoline system and the aromatic ring of the toluenesulfonate group form a dihedral angle of 31.1 (6)°; the torsion angle about the central C—O—S—C bridge is -120.4 (2)°.

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Comment

As part of our ongoing search for new lead compounds based on the quinoline system as a potential fluorophore for Alzheimer's disease (da Silva, Joussef *et al.*, 2007*a,b*; da Silva *et al.*, 2007), we have performed an investigation of the crystal structure of the title compound, (I).



The C1—O3—S1—C10 torsion angle of -120.4 (2)° illustrates the non-planarity of the molecule formed by the quinoline system with the benzene ring. The quinoline ring system, with the amino group, is nearly planar with maximum

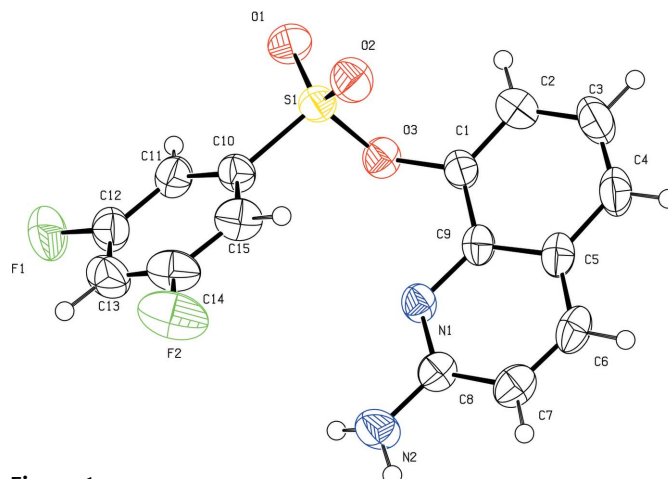


Figure 1
Molecular structure of (I), showing the atom labeling and displacement ellipsoids drawn at the 50% probability level.

deviations from the mean plane of -0.033 (3) Å for atom N1 and 0.043 (3) Å for atom C7; the plane of the aromatic ring of the toluenesulfonate group forms a dihedral angle of 31.1 (6)° with the aminoquinoline plane. The molecular packing of (I) is stabilized by hydrogen bonds (Table 1).

Experimental

The title compound was prepared according to the literature procedure of da Silva, Joussef *et al.* (2007a). Single crystals of (I) suitable for X-ray data collection were obtained by recrystallization of the crude product from a methanol–dichloromethane (1:1) solution of (I) (m.p. 440–441 K).

Crystal data

$C_{15}H_{10}F_2N_2O_3S$	$V = 700.61$ (12) Å ³
$M_r = 336.31$	$Z = 2$
Triclinic, $P\bar{1}$	$D_x = 1.594$ Mg m ⁻³
$a = 7.7926$ (7) Å	Cu $K\alpha$ radiation
$b = 9.253$ (1) Å	$\mu = 2.45$ mm ⁻¹
$c = 9.795$ (1) Å	$T = 299$ (2) K
$\alpha = 90.233$ (9)°	Plate, light brown
$\beta = 96.787$ (8)°	$0.40 \times 0.25 \times 0.08$ mm
$\gamma = 92.516$ (8)°	

Data collection

Nonius CAD-4 diffractometer	2491 independent reflections
$\omega/2\theta$ scans	2028 reflections with $I > 2\sigma(I)$
Absorption correction: ψ scan (North <i>et al.</i> , 1968)	$R_{int} = 0.104$
$T_{min} = 0.403$, $T_{max} = 0.711$ (expected range = 0.466–0.822)	$\theta_{max} = 66.9^\circ$
2699 measured reflections	3 standard reflections
	frequency: 120 min
	intensity decay: 1.5%

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.1277P)^2 + 0.1408P]$
$R[F^2 > 2\sigma(F^2)] = 0.062$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.187$	$(\Delta/\sigma)_{max} < 0.001$
$S = 1.08$	$\Delta\rho_{max} = 0.65$ e Å ⁻³
2491 reflections	$\Delta\rho_{min} = -0.65$ e Å ⁻³
215 parameters	Extinction correction: <i>SHELXL97</i>
H atoms treated by a mixture of independent and constrained refinement	Extinction coefficient: 0.0070 (19)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N2-H21N\cdots N1^i$	0.92 (5)	2.26 (5)	3.144 (4)	162 (4)
$N2-H22N\cdots O1^{ii}$	0.82 (5)	2.30 (5)	3.062 (4)	156 (4)

Symmetry codes: (i) $-x, -y + 1, -z$; (ii) $x, y, z - 1$.

The carbon-bound H atoms were positioned with idealized geometry using a riding model ($C-H = 0.93$ Å). The amino H atoms were located in a difference map and refined freely. All H atoms were refined with isotropic displacement parameters set to $1.2U_{eq}$ of the parent atom.

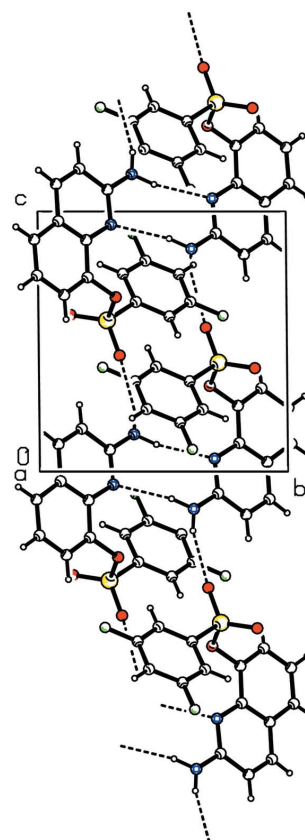


Figure 2

Molecular packing of (I) with hydrogen bonding shown as dashed lines.

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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