

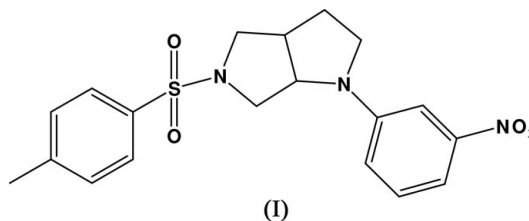
1-(3-Nitrophenyl)-5-tosylperhydropyrrolo-  
[3,4-*b*]pyrroleD. Gayathri,<sup>a</sup> D. Sujatha,<sup>b</sup> D. Velmurugan,<sup>a\*</sup> K. Ravikumar<sup>c</sup> and M. Poornachandran<sup>d</sup><sup>a</sup>Department of Crystallography and Biophysics, University of Madras, Guindy Campus, Chennai 600 025, India, <sup>b</sup>Department of Biochemistry, University of Madras, Guindy Campus, Chennai 600 025, India, <sup>c</sup>Laboratory of X-ray Crystallography, Indian Institute of Chemical Technology, Hyderabad 500 007, India, and <sup>d</sup>Department of Organic Chemistry, University of Madras, Guindy Campus, Chennai 600 025, India

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## Key indicators

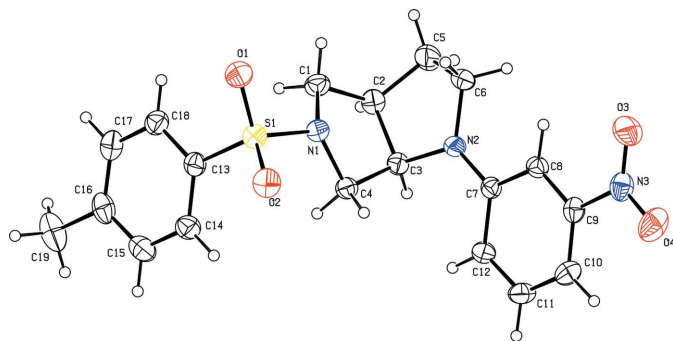
Single-crystal X-ray study  
 $T = 273$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å  
 $R$  factor = 0.046  
 $wR$  factor = 0.116  
Data-to-parameter ratio = 13.1For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.In the title compound,  $\text{C}_{19}\text{H}_{21}\text{N}_3\text{O}_4\text{S}$ , one of the pyrrolidine rings adopt a half-chair conformation, while the other is in an envelope conformation. The molecules are linked into  $C(9)$  chains by  $\text{C}-\text{H}\cdots\text{O}$  hydrogen bonds.Received 7 April 2006  
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## Comment

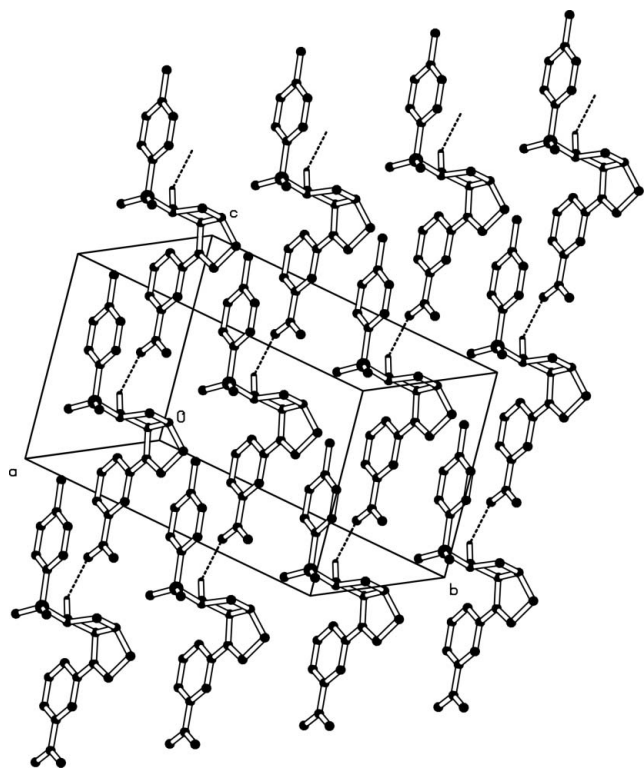
The pyrrolidine motif occurs in many families of biologically important compounds. Owing to the ease of substitution and modifications at several positions, many derivatives of pyrrolidine have been synthesized with varying properties (Baldwin *et al.*, 1994). The derivatives of pyrrolidine have been found to exhibit antifungal and antimicrobial activities (Amal Raj *et al.*, 2003). It has been shown that *N*-substituted pyrrole derivatives inhibit human immunodeficiency virus type-I (HIV-I) (Jiang *et al.*, 2004). We report here the crystal structure of the title compound, (I).The bond lengths in (I) (Fig. 1) show normal values (Allen *et al.*, 1987). The  $\text{O}-\text{S}-\text{O}$  angle deviates significantly from the ideal tetrahedral value compared to  $\text{N}-\text{S}-\text{C}$ ,  $\text{N}-\text{S}-\text{O}$  and  $\text{C}-\text{S}-\text{O}$  angles (Table 1). The sums of the bond angles around N1 ( $343.6^\circ$ ) and N2 ( $359.4^\circ$ ) indicate that N1 is  $sp^3$ -hybridized and N2 is  $sp^2$ -hybridized. The N1/C1-C4 pyrrolidine ring adopts a half-chair conformation with an asymmetry parameter (Nardelli, 1983)  $\Delta C_2(\text{C}2)$  of  $4.1$  ( $2^\circ$ ), and puckering parameters (Cremer & Pople, 1975)  $q_2$  of  $0.342$  ( $2^\circ$ ) Å and  $\varphi$  of  $-23.1$  ( $3^\circ$ ). The other pyrrolidine ring (N2/C3/C2/C5/C6) is in an envelope conformation, with  $\Delta C_s(\text{C}5)$ ,  $q_2$  and  $\varphi$  values of  $7.8$  ( $2^\circ$ ),  $0.343$  ( $3^\circ$ ) Å and  $116.4$  ( $4^\circ$ ), respectively. The deviation of atom C5 from the mean plane defined by atoms N2, C3, C2 and C6 is  $0.522$  ( $4^\circ$ ) Å. The dihedral angle between the N2/C3/C2/C6 and C7-C12 planes is  $8.25$  ( $6^\circ$ ). $\text{C}-\text{H}\cdots\text{O}$  hydrogen bonds (Table 2) link the molecules into chains; atom C4 in the molecule at  $(x, y, z)$  acts as a hydrogen-bond donor to atom O4 in the molecule at  $(x, y, 1+z)$ , forming a  $C(9)$  chain running along the  $c$  axis (Fig. 2).

## Experimental

A solution of *N*-allyl-*N*-(2-oxoethyl)-4-methylbenzene sulfonamide (1 mmol) and *m*-nitrophenylglycine (1.2 mmol) in dry toluene (20 ml) was refluxed for 3 h. After completion of the reaction, the solvent was



**Figure 1**  
The structure of (I), showing 30% probability displacement ellipsoids.



**Figure 2**  
The crystal packing of (I). For the sake of clarity, H atoms not involved in hydrogen bonds (dashed lines) have been omitted.

evaporated under vacuum and the residue was chromatographed using a hexane and ethyl acetate (9:1) mixture to yield the title compound. The compound was recrystallized from ethyl acetate by slow evaporation.

**Crystal data**

$C_{19}H_{21}N_3O_4S$   
 $M_r = 387.45$   
 Monoclinic,  $P2_1/c$   
 $a = 7.4456$  (4) Å  
 $b = 25.2680$  (15) Å  
 $c = 10.0594$  (6) Å  
 $\beta = 104.286$  (1)°  
 $V = 1834.00$  (18) Å<sup>3</sup>

$Z = 4$   
 $D_x = 1.403$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 $\mu = 0.21$  mm<sup>-1</sup>  
 $T = 273$  (2) K  
 Block, colourless  
 $0.25 \times 0.22 \times 0.21$  mm

**Data collection**

Bruker SMART APEX CCD area-detector diffractometer  
 $\omega$  scans  
 Absorption correction: none  
 17515 measured reflections

3217 independent reflections  
 2942 reflections with  $I > 2\sigma(I)$   
 $R_{int} = 0.025$   
 $\theta_{max} = 25.0^\circ$

**Refinement**

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.046$   
 $wR(F^2) = 0.116$   
 $S = 1.14$   
 3217 reflections  
 245 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0504P)^2 + 0.7696P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{max} = 0.001$   
 $\Delta\rho_{max} = 0.41$  e Å<sup>-3</sup>  
 $\Delta\rho_{min} = -0.22$  e Å<sup>-3</sup>

**Table 1**

Selected geometric parameters (Å, °).

C1–N1	1.475 (3)	C13–S1	1.767 (2)
C3–N2	1.463 (2)	N1–S1	1.631 (2)
C4–N1	1.474 (2)	N3–O3	1.212 (3)
C6–N2	1.447 (3)	N3–O4	1.221 (2)
C7–N2	1.367 (2)	O1–S1	1.428 (2)
C9–N3	1.468 (3)	O2–S1	1.425 (2)
C4–N1–C1	107.7 (2)	O4–N3–C9	118.2 (2)
C4–N1–S1	118.3 (1)	O2–S1–O1	120.2 (1)
C1–N1–S1	117.6 (1)	O2–S1–N1	106.6 (1)
C7–N2–C6	123.6 (2)	O1–S1–N1	106.2 (1)
C7–N2–C3	123.7 (2)	O2–S1–C13	108.0 (1)
C6–N2–C3	112.1 (2)	O1–S1–C13	107.9 (1)
O3–N3–O4	122.9 (2)	N1–S1–C13	107.3 (1)
O3–N3–C9	118.9 (2)		

**Table 2**

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
C4–H4A $\cdots$ O4 <sup>i</sup>	0.97	2.56	3.431 (3)	150

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

H atoms were positioned geometrically and allowed to ride on their parent C atoms, with C–H distances in the range 0.93–0.98 Å and with  $U_{iso}(H) = 1.2-1.5U_{eq}(\text{parent C})$ .

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; 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* and *PARST* (Nardelli, 1995).

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**References**

Allen, F. H., Kennard, O., Watson, D., Brammer, L., Orpen, A. G. & Taylor, R. (1987). *J. Chem. Soc. Perkin Trans. 2*, pp. S1–19.

- Amal Raj, A., Raghunathan, R., Sridevi Kumari, M. R. & Raman, N. (2003). *Bioorg. Med. Chem.* **11**, 407–409.
- Baldwin, J. E., Mackenzie Turner, S. C. & Molony, M. G. (1994). *Tetrahedron*, **35**, 9411–9424.
- Bruker (2001). *SMART* (Version 5.625) and *SAINT* (Version 6.28a). Bruker AXS Inc., Madison, Wisconsin, USA.
- Cremer, D. & Pople, J. A. (1975). *J. Am. Chem. Soc.* **97**, 1354–1358.
- Jiang, S., Lu, H., Liu, S., Zhao, Q., He, Y. & Debnath, A. K. (2004). *Antimicrob. Agents Chemother.* **48**, 4349–4359.
- Nardelli, M. (1983). *Acta Cryst.* **C39**, 1141–1142.
- Nardelli, M. (1995). *J. Appl. Cryst.* **28**, 659.
- Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
- Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.