Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 296 KMean $\sigma(C-C) = 0.003 \text{ Å}$ Disorder in main residue R factor = 0.051 wR factor = 0.104 Data-to-parameter ratio = 16.5

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

4-[4-(Dimethylamino)phenyl]-1-(phenylsulfonyl)but-3-en-2-one

An *E* configuration is found about the C=C double bond in the title molecule, $C_{18}H_{19}NO_3S$. Evidence is found for significant conjugation in the C_6H_4 -NMe₂ residue.

Received 26 September 2005 Accepted 24 October 2005 Online 27 October 2005

Comment

1-Phenylsulfonyl-3-alken-2-ones attract the attention of organic chemists owing to their utility as asymmetric synthetic reagents (Wada *et al.*, 1996), and as electron-deficient dienophiles, finding applications in asymmetric Diels–Alder chemistry (Pei, 1998). The title compound, (I), has been prepared and studied in order to obtain a better understanding of its stereochemistry. The molecular structure (Fig. 1 and Table 1) shows that an *E* configuration is found about the C3=C4 double bond. The torsion angles listed in Table 1 indicate that the dimethylamine group and its attached benzene ring are essentially coplanar. The N1–C8 bond distance of 1.359 (3) Å is considerably shorter than the normal single N–C bond of 1.43 Å (Allen *et al.*, 1987), indicating conjugation is this region of the molecule.



Experimental

The title compound was prepared according to the procedure of Wada *et al.* (1996). Diffraction quality crystals were obtained by slow evaporation of an ethanol solution of (I) at room temperature.

Crystal data

 $C_{18}H_{19}NO_3S$ $M_r = 329.41$ Monoclinic, $P2_1/n$ a = 7.224 (2) Å b = 19.712 (6) Å c = 12.177 (5) Å $\beta = 105.272$ (14)° V = 1672.7 (10) Å³ Z = 4 $D_x = 1.308 \text{ Mg m}^{-3}$ Mo K α radiation Cell parameters from 11803 reflections $\theta = 3.1-27.5^{\circ}$ $\mu = 0.21 \text{ mm}^{-1}$ T = 296 (1) KBlock, yellow $0.35 \times 0.18 \times 0.16 \text{ mm}$

Acta Cryst. (2005). E61, o3883-o3884

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organic papers

Data collection

Rigaku R-AXIS RAPID diffractometer ω scans Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995) $T_{min} = 0.960, T_{max} = 0.967$ 15968 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.051$ $wR(F^2) = 0.104$ S = 1.013834 reflections 233 parameters H atoms treated by a mixture of independent and constrained refinement 3834 independent reflections 2183 reflections with $F^2 > 2\sigma(F^2)$ $R_{int} = 0.034$ $\theta_{max} = 27.5^{\circ}$ $h = -9 \rightarrow 9$ $k = -25 \rightarrow 25$

 $l = -15 \rightarrow 15$

$$\begin{split} & w = 1/[0.0001F_{o}^{2} + 3\sigma(F_{o}^{2}) + 0.5]/\\ & (4F_{o}^{2})\\ & (\Delta/\sigma)_{max} = 0.002\\ & \Delta\rho_{max} = 0.39 \text{ e } \text{ } \text{A}^{-3}\\ & \Delta\rho_{min} = -0.48 \text{ e } \text{ } \text{A}^{-3}\\ & \text{Extinction correction:}\\ & (\text{Larson, 1970})\\ & \text{Extinction coefficient: } 2.8 (3) \times 10^{2} \end{split}$$

Table 1

Selected geometric parameters (Å, °).

S1-O1	1.4301 (13)	N1-C8	1.359 (3)
S1-O2	1.4339 (16)	N1-C11	1.435 (4)
S1-C1	1.768 (2)	N1-C12	1.453 (3)
S1-C13	1.757 (2)	C31-C41	1.393 (7)
O3-C2	1.186 (4)	C32-C42	1.393 (7)
C8-N1-C11	121.3 (2)	C2-C31-C41	114.5 (4)
C8-N1-C12	121.5 (2)	C5-C41-C31	118.1 (4)
C11-N1-C12	117.1 (2)		
C11-N1-C8-C7	1.2 (3)	C12-N1-C8-C7	-175.2 (2)
C11-N1-C8-C9	-177.8 (2)	C12-N1-C8-C9	5.7 (3)

Atoms C3 and C4 were found to be disordered over two positions, *viz.* C31 and C41, and C32 and C42, and were refined anisotropically with 50% site occupancy factors and equal C–C bond distances of 1.393 (7) Å. The H atoms associated with this group were located in a difference Fourier map and were refined freely [C-H = 0.82 (2)-1.02 (2) Å]. The remaining H atoms were included in the riding-





View of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 40% probability level. Both disorder components are shown.

model approximation, with C-H(aromatic) = 0.98 Å, C-H(methylene) = 0.97 Å and C-H(methyl) = 0.96 Å, and with $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: *PROCESS-AUTO* (Rigaku Corporation, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/MSC, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *CRYS-TALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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