Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

Anders Madsen, Kent A. Nielsen, Andrew D. Bond* and Jan O. Jeppesen

University of Southern Denmark, Department of Chemistry, Campusvej 55, 5230 Odense M, Denmark

Correspondence e-mail: adb@chem.sdu.dk

Key indicators

Single-crystal X-ray study T = 180 K Mean σ (C–C) = 0.003 Å R factor = 0.026 wR factor = 0.061 Data-to-parameter ratio = 17.7

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

5-(2-Cyanoethylsulfanyl)-4-methylsulfanyl-1,3-dithiole-2-thione

The crystal structure of the title compound, $C_7H_7NS_5$, at 180 K, reveals intermolecular $N \cdots \sigma^*(S-C)$ and $S \cdots \sigma^*(S-C)$ interactions.

Received 27 March 2006 Accepted 28 March 2006

Comment

The crystal structure of the title compound, (I) (Fig. 1), was solved using data recorded at 180 K.



The C atom of the methyl group is coplanar with the 1,3dithiole-2-thione plane [torsion angle C4-S4-C2-C3 = $-179.89 (16)^{\circ}$]. However, in the analogous bis(methylsulfanyl) compound (Simonsen *et al.*, 1990), both methyl groups lie out of the molecular plane [C-S-C-C torsion angles are -121.6 (3) and 156.2 (2)°]. The C6-C7=N1 group of the 2cyanoethylsulfanyl substituent lies above the 1,3-dithiole-2thione plane, pointing approximately parallel to the S3-C3 bond (Fig. 1). A similar conformation is observed in one molecule of the asymmetric unit of the related bis(2-cyanoethylsulfanyl) compound (Yu *et al.*, 2003). The C6-C7=N1 group points towards S4 of an adjacent molecule, forming an N1...S4ⁱ contact of 3.326 (2)Å [symmetry code: (i) -x, 1 - y,



Figure 1

The molecular structure of (I), showing displacement ellipsoids drawn at the 50% probability level for non-H atoms. H atoms are shown as spheres of arbitrary radius.

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organic papers

1 - z]. This arrangement is typical of a nucleophile approaching a C-S-C unit and has been interpreted as an interaction between a electron lone pair on N and the σ^* orbital of the S-C bond (Rosenfield *et al.*, 1977). Similar interactions involve S1...S2ⁱⁱ = 3.5354 (7)Å and S1...S5ⁱⁱⁱ = 3.5816 (7)Å [symmetry codes: (ii) 2 - x, 1 - y, 2 - z; (iii) 1 + x, $\frac{1}{2} - y$, $\frac{1}{2} + z$], with geometry indicative of interactions from lone pairs in sp^2 -hybridized atomic orbitals on S1 (Fig. 2).

Experimental

The compound was prepared according to the literature (Simonsen *et al.*, 1996). Recrystallization from methanol afforded yellow needle-shaped crystals.

 $D_x = 1.592 \text{ Mg m}^{-3}$

Cell parameters from 3035

Mo $K\alpha$ radiation

reflections

T = 180 (2) K

Needle, yellow

 $0.30 \times 0.10 \times 0.10$ mm

 $\begin{array}{l} \theta = 2.9 \mbox{--} 25.5^{\circ} \\ \mu = 1.00 \ \mbox{mm}^{-1} \end{array}$

Crystal data

 $\begin{array}{l} C_{7}H_{7}NS_{5} \\ M_{r} = 265.44 \\ \text{Monoclinic, } P2_{1}/c \\ a = 5.0793 \ (3) \ \text{\AA} \\ b = 15.7214 \ (12) \ \text{\AA} \\ c = 13.9016 \ (11) \ \text{\AA} \\ \beta = 94.186 \ (3)^{\circ} \\ V = 1107.13 \ (14) \ \text{\AA}^{3} \\ Z = 4 \end{array}$

Data collection

Bruker-Nonius X8 APEX-II CCD	2108 independent reflections
diffractometer	1645 reflections with $I > 2\sigma(I)$
thin–slice ω and φ scans	$R_{\rm int} = 0.048$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.9^{\circ}$
(SADABS; Sheldrick, 2003)	$h = -4 \rightarrow 6$
$T_{\min} = 0.803, \ T_{\max} = 0.907$	$k = -19 \rightarrow 19$
14011 measured reflections	$l = -16 \rightarrow 16$

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.026$	$w = 1/[\sigma^2(F_o^2) + (0.0261P)^2]$
$wR(F^2) = 0.061$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.08	$(\Delta/\sigma)_{\rm max} = 0.001$
2108 reflections	$\Delta \rho_{\rm max} = 0.28 \text{ e} \text{ \AA}^{-3}$
119 parameters	$\Delta \rho_{\rm min} = -0.26 \ {\rm e} \ {\rm \AA}^{-3}$

H atoms bound to C atoms were positioned geometrically and allowed to ride during subsequent refinement, with C-H = 0.99Å and $U_{iso}(H) = 1.2U_{eq}(C)$ for the methylene groups, and C-H = 0.98Å and $U_{iso}(H) = 1.5U_{eq}(C)$ for the methyl group. The methyl group was allowed to rotate around its local threefold axis.

Data collection: *APEX2* (Bruker–Nonius, 2004); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.





We are grateful to the Danish Natural Science Research Council (SNF) for funding *via* STENO stipends, Nos. 21-03-0164 (ADB) and 21-03-0317 (JOJ). We also gratefully acknowledge financial support provided by SNF through the SONS programme of the European Commission, Sixth Framework Programme, and the Strategic Research Council of Denmark through the Young Researcher's Programme (JOJ, No. 2117-05-0115).

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