Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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#### **Key indicators**

Single-crystal X-ray study T = 293 KMean  $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$  R factor = 0.041 wR factor = 0.126 Data-to-parameter ratio = 15.4

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The title compound,  $C_{16}H_{20}N_2S_4$ , was synthesized by the reaction of 1,4-dibromomethylbenzene and 1,3-thiazine-2-thione. The molecule is located on a crystallographic centre of inversion. The thiazine ring has an envelope conformation.

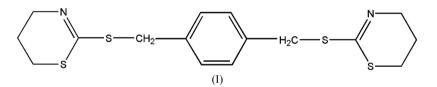
2,2'-(p-Phenylenedimethylenedithio)bis(4,5-dihydro-

Received 13 August 2006 Accepted 15 August 2006

# Comment

1,3-thiazine)

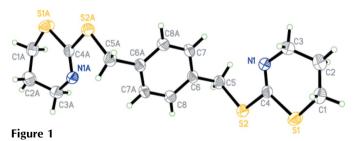
As a type of ditopic ligand, dithioethers can be used as bridging ligands in the construction of coordination polymers with soft metal ions. *N*-Heterocylic units have been synthesized and investigated (Sharma *et al.*, 1999; Constable *et al.*, 2002; Bu *et al.*, 2003; Hong *et al.*, 2000). Thiazine derivatives possess acaricide properties. In order to study the properties of these compounds, we have synthesized several new thiazine derivatives, and we present here the crystal structure of 2,2'-(*p*phenylenedimethylenedithio)bis(4,5-dihydro-1,3-thiazine), (I).



Molecules of (I) have crystallographic inversion symmetry. The thiazine ring has an envelope conformation. Atom C2 deviates by 0.641 (3) Å from the plane of the remaining five ring atoms. Although the sum of the bond angles around C4 is  $360^{\circ}$ , two bond angles deviate significantly from the ideal value of  $120^{\circ}$  (Table 1).

### **Experimental**

A solution of 1,4-dibromomethylbenzene (1.32 g, 5 mmol) in ethanol (5 ml) was added dropwise to a mixture of 1,3-thiazine-2-thione (1.46 g, 11 mmol), KOH (0.615 g, 11 mmol) and ethanol (5 ml). The



View of the molecular structure of (I) showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level. Atoms with the suffix A are generated by the symmetry operation (-x, 1 - y, -z).

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reaction mixture was then stirred for 24 h at room temperature. The mixture was added dropwise to water (30 ml) and a white precipitate appeared. This precipitate was filtered off, washed with water and recrystallized from ethanol and water (yield 65%, m.p. 350–351 K). Analysis calculated for  $C_{16}H_{20}N_2S_4$ : C 52.17, H 5.43, N 7.61%; found: C 52.09, H 5.41, N 7.65%. Crystals of (I) suitable for single-crystal X-ray analysis were grown by slow evaporation of a dichloromethane solution.

#### Crystal data

$C_{16}H_{20}N_2S_4$
$M_r = 368.58$
Monoclinic, $P2_1/c$
a = 14.280(3) Å
$b = 5.1581 (13) \text{\AA}$
c = 12.250 (3) Å
$\beta = 103.782 \ (4)^{\circ}$
$V = 876.3 (4) \text{ Å}^3$

#### Data collection

Bruker SMART CCD area-detector diffractometer  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)  $T_{\rm min} = 0.837, T_{\rm max} = 1.000$ (expected range = 0.793–0.948)

### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.041$   $wR(F^2) = 0.126$  S = 1.061540 reflections 100 parameters H-atom parameters constrained Z = 2  $D_x = 1.397 \text{ Mg m}^{-3}$ Mo K $\alpha$  radiation  $\mu = 0.54 \text{ mm}^{-1}$ T = 293 (2) K Block, colourless  $0.20 \times 0.14 \times 0.10 \text{ mm}$ 

4193 measured reflections 1540 independent reflections 1168 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.029$  $\theta_{\text{max}} = 25.0^{\circ}$ 

$$\begin{split} w &= 1/[\sigma^2(F_{\rm o}^2) + (0.0586P)^2 \\ &+ 0.568P] \\ \text{where } P &= (F_{\rm o}^2 + 2F_{\rm c}^2)/3 \\ (\Delta/\sigma)_{\rm max} &< 0.001 \\ \Delta\rho_{\rm max} &= 0.40 \text{ e } \text{ Å}^{-3} \\ \Delta\rho_{\rm min} &= -0.36 \text{ e } \text{ Å}^{-3} \end{split}$$

# Table 1

Selected bond angles (°).

N1-C4-S1	130.4 (2)	S1-C4-S2	106.73 (15)
N1-C4-S2	122.9 (2)		

All H atoms were positioned geometrically and refined as riding (C-H = 0.93 or 0.97 Å for aromatic and methylene H atoms, respectively).  $U_{\rm iso}({\rm H})$  values were set equal to  $1.2U_{\rm eq}({\rm C})$ .

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

We gratefully acknowledge the 05 L003 project supported by the Education Department of Liao Ning Province in China.

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