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Key indicators

Single-crystal X-ray study T = 293 KMean $\sigma(C-C) = 0.004 \text{ Å}$ R factor = 0.041 wR factor = 0.097 Data-to-parameter ratio = 15.8

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

trans-5,5'-[(2-Butene-1,4-diyl)dithio]bis(1-phenyl-1,2,3,4-tetrazole)

The title compound, $C_{18}H_{16}N_8S_2$, crystallizes in the monoclinic space group $P2_1/c$. The two 1-phenyl-1*H*-tetrazole-5-thiol moieties are located on the same side of the butene-1,4-diyl plane but point in opposite directions. Intermolecular N···S interactions link the molecules to form one-dimensional polymeric chains along the *a* axis.

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Comment

To date, a large number of flexible or rigid chain-linked dithioether ligands containing *N*-heterocyclic moieties have been synthesized and investigated, due to their diverse coordination capabilities and the important properties of their metal complexes (Zheng *et al.*, 2003; Bu *et al.*, 2002; Hong *et al.*, 2000). Earlier studies reported that several tetrazole derivatives possess diverse pharmacological properties (Juby *et al.*, 1968, 1982). However, crystallographic studies of only a few complexes of monosubstituted tetrazole derivatives have been reported (van den Heuvel *et al.*, 1983; Lyakhov *et al.*, 2003). Here, we report the synthesis and structure of the title novel tetrazole thioether, (I). Further work on the reaction of this compound with transition metal ions is still in progress.



In (I), the two 1-phenyl-1*H*-tetrazole-5-thiol moieties are located on the same side of the butene-1,4-diyl chain, but they point in opposite directions to reduce the steric repulsion between them (Fig. 1). The two tetrazole rings are close to antiparallel, with a dihedral angle of 7.4 (1)° between them, while that between the benzene rings is $38.6 (1)^\circ$. The two 1-phenyl-1*H*-tetrazole groups are in different conformations; the dihedral angle between the tetrazole and benzene rings within one group is $46.3 (1)^\circ$ and that in the other is $51.8 (1)^\circ$.

The C=C bond distance of 1.297 (3) Å within the butene-1,4-diyl group is shorter than the value of 1.34 Å for a normal C=C bond (Lide, 1992–1993) and equal to the value of 1.299 (5) Å in *trans-S,S'*-(but-2-ene-1,4-diyl)bis(L-cysteine) (Shi *et al.*, 2002). The C8–C9–C10–C11 torsion angle of

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A view of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.

 $-179.6 (2)^{\circ}$ indicates that the butenediyl group is planar. Because of π - π conjugation, the Csp²-S bonds (C7-S1 and C12-S2) are significantly shorter than the Csp^3 -S bonds (C8-S1 and C11-S2), similar to the effect observed in 2,2'-[1,4-phenylenebis(methylenethio)]dithiazole (Zhang et al., 2003).

As shown in Fig. 2, intermolecular $N \cdots S$ interactions $[N2 \cdot \cdot \cdot S2(1 - x, -y, -z) \ 3.304(2) \text{ and } N6 \cdot \cdot \cdot S1(2 - x, -y, -y)]$ -z 3.282 (2) Å] link the molecules of (I) to form onedimensional polymeric chains along the *a* axis. In addition, the crystal structure is stabilized by $C-H\cdots S$ and $C-H\cdots N$ interactions (Table 1).

Experimental

The title compound was synthesized as follows. A solution of trans-1,4-dibromo-2-butene (1.07 g, 5 mmol) in ethanol (10 ml) was added dropwise to a mixture of 1-phenyl-5-thio-1,2,3,4-tetrazole (1.96 g, 11 mmol), KOH (0.615 g, 11 mmol) and ethanol (10 ml). The reaction mixture was then stirred for 24 h at room temperature. The precipitate was filtered off, washed with water and recrystallized from ethanol (yield 67%, m.p. 401-402 K). Spectroscopic analysis: IR $(KBr, v, cm^{-1}): 3073 (w), 3024 (w), 2979 (w), 2935 (w), 1596 (m), 1499$ (s), 1406 (w), 1381 (s), 1316 (m), 1282 (m), 1236 (s), 1094 (m), 992 (s),763 (s), 693 (s); ¹H NMR (CDCl₃, δ, p.p.m.): 3.96 (m, 4H), 5.99 (m, 2H), 7.53 (*m*, 5H); ¹³C NMR (CDCl₃, δ, p.p.m.): 34.42, 123.93, 129.03, 129.80, 130.19. Analysis calculated for C₁₈H₁₆N₈S₂: C 52.87, H 3.92, N 27.42%; found: C 52.90, H 4.05, N 27.50%. Crystals of (I) suitable for single-crystal X-ray analysis were grown by slow evaporation of a solution in acetonitrile.

Crystal data

C.H.N.S.	$D_{\rm c} = 1.392 {\rm Mg}{\rm m}^{-3}$		
$M_r = 408.51$	$D_x = 1.552$ Mg m Mo K α radiation		
Monoclinic, $P2_1/c$	Cell parameters from 893		
a = 9.727 (3) Å	reflections		
b = 12.770 (4) Å	$\theta = 3.1-23.4^{\circ}$		
c = 15.947 (6) Å	$\mu = 0.30 \text{ mm}^{-1}$		
$\beta = 100.332 \ (6)^{\circ}$	T = 293 (2) K		
$V = 1948.7 (11) \text{ Å}^3$	Prism, colourless		
$Z = 4 \qquad \qquad 0.24 \times 0.20 \times 0$			



Figure 2

A packing diagram for (I), viewed down the c axis. The dashed lines show N···S short contacts between neighbouring molecules.

Data collection

Bruker SMART CCD area-detector	3987 independent reflections 2561 reflections with $L > 2\pi(I)$
diffractometer	2501 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.038$
Absorption correction: multi-scan	$\theta_{\rm max} = 26.4^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -12 \rightarrow 9$
$T_{\min} = 0.928, \ T_{\max} = 0.954$	$k = -12 \rightarrow 15$
11 016 measured reflections	$l = -17 \rightarrow 19$
Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0429P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	+ 0.1948P]
$vR(F^2) = 0.097$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.01	$(\Delta/\sigma)_{\rm max} = 0.002$
3987 reflections	$\Delta \rho_{\rm max} = 0.22 \ {\rm e} \ {\rm \AA}^{-3}$
253 parameters	$\Delta \rho_{\rm min} = -0.24 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	$D-{\rm H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
C2-H2···S1	0.93	2.84	3.226 (3)	106
C8-H8A···N7 ⁱ	0.97	2.61	3.471 (3)	148
$C11 - H11B \cdot \cdot \cdot N6$	0.97	2.58	3.030 (3)	108

Symmetry code: (i) 2 - x, -y, -z.

H atoms were placed in calculated positions (C–H = 0.93-0.97 Å) and allowed to ride on their parent atoms, with $U_{iso}(H) =$ $1.2U_{eq}(parent).$

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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