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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.050 wR factor = 0.131 Data-to-parameter ratio = 18.3

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

1,3-Bis(1-phenyl-1*H*-tetrazole-5-ylsulfanyl)propane

In the title compound, $C_{17}H_{16}N_8S_2$, the terminal ring systems extend in opposite directions to minimize steric hindrance.

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Comment

To date, a large number of flexible or rigid chain-linked dithioether ligands containing *N*-heterocyclic units have been synthesized and investigated due to their diverse coordination capabilities and the important properties of their metal complexes (Heuvel *et al.*, 1983; Bu *et al.*, 2002). 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 derivaties have been reported (Lyakhov *et al.*, 2003). We have reported some tetrazole derivatives using rigid chains as linkers, such as 1,2-phenylene, 1,4-phenylene (Luo *et al.*, 2005; Wang *et al.*, 2005). We have now synthesized a new tetrazole derivative, namely 1,3-bis(1-phenyl-1*H*-tetrazole-5-ylsulfanyl)propane, (I), using flexible 1,3-dipropyl as linker. We present its crystal structure here.



In the molecule of (I), the two terminal phenyl rings make a dihedral angle of 50.0 (1)°. The dihedral angles between the phenyl ring C1–C6 and the corresponding tetrazole ring (C7,N1–N4) is 68.8 (1) [54.8 (1)° between C12–C17 and C11,N5–N8]. The pseudo-torsion angle of the two C–S bonds (C7–S1···S2–C11) is 124.4 (3)°, showing that the terminal ring systems extend in opposite directions to minimize steric hindrance.

The π - π conjugation of atom S1 with the tetrazole ring affects the C7–S1 bond distance [1.737 (2) Å] which is shorter than C8–S1 [1.814 (2) Å]. This effect is also observed for S2 and in other tetrazole-thio derivatives reported in the literature (Wang *et al.*, 2004, 2005).

Experimental

A solution of 1,3-dibromopropane (1.01 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

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precipitate was filtered off, washed with water and recrystallized from ethanol (yield 70%). Crystals of (I) suitable for single-crystal X-ray analysis were grown by slow evaporation of a solution in chloroform.

Z = 4

 $D_{\rm v} = 1.396 {\rm Mg m}^{-3}$

Mo $K\alpha$ radiation

Block, colourless

 $0.14 \times 0.12 \times 0.10 \text{ mm}$

14105 measured reflections

4478 independent reflections

 $w = 1/[\sigma^2(F_0^2) + (0.0652P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

Extinction correction: SHELXL97

Extinction coefficient: 0.0165 (19)

3342 reflections with $I > 2\sigma(I)$

 $\mu = 0.30 \text{ mm}^{-1}$

T = 293 (2) K

 $R_{\rm int} = 0.048$

 $\theta_{\rm max} = 27.9^\circ$

 $(\Delta/\sigma)_{\text{max}} = 0.002$ $\Delta\rho_{\text{max}} = 0.24 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.30 \text{ e } \text{\AA}^{-3}$

Crystal data

 $C_{17}H_{16}N_8S_2$ $M_r = 396.5$ Monoclinic, $P2_1/n$ a = 16.774 (3) Å b = 6.5029 (13) Å c = 18.691 (4) Å $\beta = 112.24$ (3)° V = 1887.1 (8) Å³

Data collection

Rigaku Saturn 70 diffractometer ω scans Absorption correction: multi-scan (*REQAB*; Jacobson, 1998) $T_{min} = 0.959, T_{max} = 0.970$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.050$ $wR(F^2) = 0.131$ S = 1.104478 reflections 245 parameters H-atom parameters constrained

 Table 1

 Selected geometric parameters (Å, $^{\circ}$).

S1-C7	1.737 (2)	\$2-C11	1.731 (2)
S1-C8	1.814 (2)	S2-C10	1.8094 (19)
N4-C7-N1	108.23 (17)	N5-C11-N8	108.76 (18)
N4-C7-S1	128.68 (15)	N5-C11-S2	129.12 (15)

All H atoms were positioned geometrically and refined as riding (C-H = 0.93-0.97 Å), with $U_{iso}(H) = 1.2U_{eq}(\text{parent})$.

Data collection: *CrystalClear* (Molecular Structure Corporation & Rigaku, 1999); cell refinement: *CrystalClear*; data reduction: *CrystalStructure* (Rigaku/MSC, 2005); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL*



Figure 1

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

(Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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