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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=293 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.007 \AA$
$R$ factor $=0.088$
$w R$ factor $=0.307$
Data-to-parameter ratio $=18.4$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 1,2-Bis(pyrimidin-2-ylsulfanyl)ethane

The title dithioether compound, $\mathrm{C}_{10} \mathrm{H}_{10} \mathrm{~N}_{4} \mathrm{~S}_{2}$, adopts an anti conformation with an intramolecular $\mathrm{S} \cdots \mathrm{S}$ non-bonding distance of 4.419 (2) $\AA$. The dihedral angle between the two pyrimidine rings is $6.8(2)^{\circ}$.

## Comment

A large number of complexes of dithioether ligands containing $N$-heterocyclic groups have been synthesized and investigated, because of their diverse coordination capabilities and the important properties of their metal complexes (Zheng et al., 2003; Hong et al., 2000). However, crystallographic studies of only a few ligands have been reported. In the present paper, we report the crystal structure of the title compound, (I).

(I)

As shown in Fig. 1, the molecule adopts an anti conformation (Goodgame et al., 1999) with a pseudo-torsion angle $\mathrm{C} 4-\mathrm{S} 1 \cdots \mathrm{~S} 2-\mathrm{C} 7$ of $-174.9(2)^{\circ}$. The pyrimidine rings ( $\mathrm{N} 1 /$ $\mathrm{C} 1-\mathrm{C} 3 / \mathrm{N} 2 / \mathrm{C} 4$ and $\mathrm{N} 3 / \mathrm{C} 7 / \mathrm{N} 4 / \mathrm{C} 8-\mathrm{C} 10$ ), with a dihedral angle of $6.8(2)^{\circ}$ to each other, incline to the spacer unit plane $(\mathrm{S} 1-$ C5-C6-S2) at angles of 81.8 (4) and 86.9 (4) ${ }^{\circ}$, respectively. The S1 $\cdot \mathrm{S} 2$ non-bonding distance is 4.419 (2) $\AA$. The bond dimensions are within the range reported in a similar compound, 2,4,6-trimethyl-1,3,5-tris(2-pyrimidinylthiomethyl)benzene (Zheng et al., 2002). Both the $\mathrm{S}-\mathrm{Csp}^{2}$ and the $\mathrm{S}-\mathrm{Csp}{ }^{3}$ bond distances of (I) show little deviation in comparison with those of the analogous compound 1,2-bis(phenylthio)ethane (Hou et al., 2005), despite different substituents. The molecule of (I) does not possess any crystallographic symmetry, in contrast with the inversion symmetry of several reported alkyl dithioether compounds (Chen et al., 2005; Hou et al., 2005).

In the crystal structure of the binuclear silver(I) nitrate complex with (I) as a chelating and bridging ligand (Zheng et al., 2003), the thioether adopts a gauche conformation with an S. . S non-bonding distance of 3.44 (3) Å.

## Experimental

Compound (I) was prepared according to the reported procedure (Zheng et al., 2003). Colourless single crystals of (I) suitable for X-ray diffraction were obtained by slow evaporation of a chloroform solution at room temperature.

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## Crystal data

$\mathrm{C}_{10} \mathrm{H}_{10} \mathrm{~N}_{4} \mathrm{~S}_{2}$
$M_{r}=250.34$
Monoclinic, $P 2_{1} / c$
$a=8.0524(16) \AA$
$b=19.884(4) \AA$
$c=8.1541(16) \AA$
$\beta=116.57(3)^{\circ}$
$V=1167.7(4) \AA^{3}$
$Z=4$
$D_{x}=1.424 \mathrm{Mg} \mathrm{m}^{-3}$
$M_{r}=250.34$
Monoclinic, $P 2_{1} / c$
$b=19.884(4) \AA$
$c=8.1541$ (16) $\AA$
116.57 (3)
$Z=4$
Mo $K \alpha$ radiation
Cell parameters from 11145
reflections
$\theta=3.0-27.5^{\circ}$
$\mu=0.43 \mathrm{~mm}^{-1}$
$T=293$ (2) K
Needle, colourless
$0.79 \times 0.24 \times 0.16 \mathrm{~mm}$
Data collection
Rigaku X-AXIS RAPID IP areadetector diffractometer
$\omega$ scans
Absorption correction: multi-scan (ABSCOR ; Higashi, 1995)
$T_{\text {min }}=0.725, T_{\text {max }}=0.936$
11145 measured reflections
2663 independent reflections
1706 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.080$
$\theta_{\text {max }}=27.5^{\circ}$
$h=-10 \rightarrow 10$
$k=-25 \rightarrow 25$
$l=-9 \rightarrow 10$

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.088$
$w R\left(F^{2}\right)=0.307$
$S=1.02$
2663 reflections
145 parameters
H -atom parameters constrained


Figure 1
ORTEPII (Johnson, 1976) view of (I), showing atomic displacement ellipsoids at the $30 \%$ probability level.

Data collection: RAPID-AUTO (Rigaku, 2004); cell refinement: RAPID-AUTO; data reduction: RAPID-AUTO ; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976); software used to prepare material for publication: CrystalStructure (Rigaku, 2004).

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