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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.046 wR factor = 0.112 Data-to-parameter ratio = 17.6

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The title compound, $C_{14}H_{17}N_3OS$, exists in the *E,E* configuration with respect to the C=N bonds of the thiadiazole ring. In the crystal packing, molecules are linked into centrosymmetric dimers through N-H···N hydrogen bonds.

2-[5-(Cyclohexylamino)-1,3,4-thiadiazol-2-yl]phenol

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Comment

Thiadiazoles and their derivatives represent a group of compounds possessing a wide spectrum of biological activities, such as hypoglycemic, antitubercular, antifungal and antibacterial properties (Bhat *et al.*, 1967). One route to obtain thiadiazolines is the heterocyclization of thiosemicarbazones (Somogyi, 1991; Kubota *et al.*, 1980). Thiosemicarbazones were subjected to ring closure by means of acetylating agents, to obtain the corresponding 1,3,4-thiadiazolines (Tarbell & Price, 1957). Some thiosemicarbazones and thiadiazolines showed interesting biological activity against *Bacillus subtilis, Candida albicans, Micrococcus luteus, Trichophyton mentagrophites* and *Aspergillus niger* (Turk *et al.*, 1986).



The molecular structure of (I) is shown in Fig. 1, and selected geometric parameters are listed in Table 1. The compound exists in an *E*,*E* configuration with respect to the double bonds C1=N2 and C2=N3. This is confirmed by the torsion angles C3-C2=N3-N2 = 179.73 (16)° and N1-C1=N2-N3 = 178.19 (18)° (Nagao *et al.*, 1998). Bond lengths for C-S, C=N and N-N functionalities are similar to those found in other thiadiazoline derivatives (*e.g.* Hu & Ying, 2005). As an example, the C-S bond lengths are consistent with C-S single bonds rather than with C=S bonds (Suni *et al.*, 2006). Ring puckering analysis (Cremer & Pople, 1975) and least-squares calculations show that the cyclohexyl substituent has a chair conformation ($Q_T = 0.562$ Å) with equatorial substitution at C9 for N1.

When viewed along [100], the molecules form a herringbone arrangement (Fig. 2), similar to that reported in the structural arrangement of *trans*-[N,N'-bis(salicylidene)cyclohexane-1,2-diaminato]nickel(II) (de Castro *et al.*, 2001). The crystal packing involves one intra- and one intermolecular hydrogen-bonding interactions (Table 2). Intramolecular

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hydrogen bonding leads to the formation of an S(6) ring, while intermolecular N-H···N hydrogen bonds form centrosymmetric dimers in the crystal structure.

Experimental

Salicylaldehyde-*N*-cyclohexylthiosemicarbazone (1 mmol, 0.277 g) was refluxed with $Mn(OAc)_2 \cdot 4H_2O$ (1 mmol, 0.291 g) in methanol (25 ml) for 3 h, followed by evaporation to dryness under reduced pressure, resulting in the unexpected formation of (I). Intense gold block crystals suitable for single-crystal X-ray diffraction studies were obtained from a solution of (I) in a mixture of CH_3CN and DMF (1:1).

Z = 4

 $D_r = 1.324 \text{ Mg m}^{-3}$

Block, intense gold

 $0.33 \times 0.26 \times 0.21$ mm

16447 measured reflections

3173 independent reflections

 $w = 1/[\sigma^2(F_0^2) + (0.0601P)^2]$

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

+ 0.2525P]

 $(\Delta/\sigma)_{\rm max} < 0.001$

 $\Delta \rho_{\rm max} = 0.24 \text{ e} \text{ Å}^2$

 $\Delta \rho_{\rm min} = -0.19 \text{ e} \text{ Å}^{-3}$

2483 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.23 \text{ mm}^{-1}$

T = 293 (2) K

 $R_{\rm int} = 0.029$

 $\theta_{\rm max} = 27.5^{\circ}$

Crystal data

 $C_{14}H_{17}N_3OS$ $M_r = 275.37$ Monoclinic, $P2_1/c$ a = 7.9402 (16) Å b = 10.5702 (10) Å c = 16.545 (6) Å $\beta = 95.65 (2)^{\circ}$ $V = 1381.9 (6) Å^{3}$

Data collection

Oxford Diffraction Xcalibur-S diffractometer ω scans Absorption correction: multi-scan (*CrysAlis RED*; Oxford Diffraction, 2006) $T_{min} = 0.928, T_{max} = 0.962$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.046$ $wR(F^2) = 0.112$ S = 1.013173 reflections 180 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

C1-N2	1.313 (2)	C4-O1	1.354 (2)
C1-N1	1.334 (2)	N1-H1N	0.85 (2)
C1-S1	1.7432 (18)	N2-N3	1.376 (2)
C2-N3	1.297 (2)	O1-H101	0.86 (3)
N2-C1-N1	122.95 (16)	C3-C2-S1	123.33 (13)
N2-C1-S1	113.91 (13)	N1-C9-C14	108.84 (16)
N1-C1-S1	123.13 (14)	N1-C9-C10	112.56 (16)
N3-C2-C3	123.56 (16)	C4-O1-H101	107 (2)
N3-C2-S1	113.12 (13)	C2-S1-C1	86.98 (9)

Tal	ble	2
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Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O1-H101\cdots N3$	0.86 (3)	1.84 (3)	2.621 (2)	151 (3)
$N1-H1N\cdots N2^{i}$	0.85 (2)	2.13 (2)	2.968 (2)	175 (2)

Symmetry code: (i) -x + 1, -y + 1, -z + 2.



Figure 1

The molecular structure and labelling scheme for (I), with displacement ellipsoids drawn at the 50% probability level.



Figure 2

A packing diagram for (I), viewed approximately along the [100] axis. Dashed lines indicate intra- and intermolecular hydrogen-bonding interactions.

C-bound H atoms were placed in calculated positions and refined with C–H bond lengths constrained to 0.93 (aromatic CH), 0.97 (methylene CH₂) or 0.98 Å (methine CH), and $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm carrier C atom})$. Heteroatom-bonded H atoms H1N and H101 were found in a difference map and refined with free coordinates and isotropic displacement parameters.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2006); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2006); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997) and *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97*.

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