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Key indicators

Single-crystal X-ray study T = 288 KMean $\sigma(\text{C-C}) = 0.004 \text{ Å}$ R factor = 0.039 wR factor = 0.104 Data-to-parameter ratio = 14.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The title compound, $C_{10}H_{14}N_4S_2$, obtained from the alkylation of methimazole with ethylene dibromide, is centrosymmetric and the two imidazole-2-thione ring moieties are anti-parallel to one another.

1,1'-(1,2-Ethanediyl)bis(2,3-dihydro-3-

methyl-1*H*-imidazole-2-thione)

Comment

Acyclic crown ethers with nitrogen heterocycles as the end groups, which can coordinate and transport metals, continue to receive attention (Vögtle & Weber, 1979; Meth-Cohn & Smith, 1982; Liu & Shi, 1992; Liu *et al.*, 1992, 2001; Matthews *et al.*, 1996). We have reported the syntheses, characterization and coordination properties of non-cyclic crown ethers with methimazole end groups (Liu & Shi, 1992; Liu *et al.*, 1992). We report here the X-ray crystal structure of the title compound, (I).



The whole molecule possesses a centre of symmetry (Fig. 1). The two imidazole-2-thione ring moieties are anti-parallel to one another. The perpendicular distance between the two rings is 1.504 (2) Å. The bridging chain moiety, $-CH_2CH_2-$, adopts an antiperiplanar conformation. The bond lengths and angles in (I) have normal values (Table 1). There is no intermolecular S···S short contact in the crystal packing (Fig. 2).



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Figure 1

The molecular structure of (I), showing 50% probability displacement ellipsoids, and the numbering scheme for non-H atoms.

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This paper is dedicated to Professor Mingli Shi on the occasion of his 70 th birthday.

Experimental

The title compound, (I), was prepared *via* alkylation of methimazole with ethylene dibromide under phase-transfer catalytic conditions (m.p. 467–468.5 K). Single crystals of (I) suitable for X-ray diffraction analysis were obtained by slow evaporation of an ethanol solution.

 $D_x = 1.365 \text{ Mg m}^{-3}$

Cell parameters from 27

Mo $K\alpha$ radiation

reflections

 $\mu = 0.41 \text{ mm}^{-1}$

T = 288 (2) K

 $R_{\rm int} = 0.029$ $\theta_{\rm max} = 25.0^{\circ}$

 $h = 0 \rightarrow 5$

 $\begin{array}{l} k=0\rightarrow 23\\ l=-8\rightarrow 8 \end{array}$

3 standard reflections

every 97 reflections intensity decay: 2.9%

Block, colourless $0.40 \times 0.28 \times 0.20$ mm

 $\theta = 4.8\text{--}13.6^\circ$

Crystal data

 $\begin{array}{l} {\rm C_{10}H_{14}N_4S_2}\\ {M_r} = 254.37\\ {\rm Monoclinic,}\ P2_1/c\\ a = 4.667\ (1)\ {\rm \AA}\\ b = 19.720\ (3)\ {\rm \AA}\\ c = 7.037\ (1)\ {\rm \AA}\\ \beta = 107.08\ (1)^\circ\\ V = 619.0\ (2)\ {\rm \AA}^3\\ Z = 2 \end{array}$

Data collection

Siemens P4 diffractometer ω scans Absorption correction: refined from ΔF (SHELXA; Sheldrick, 1997) $T_{min} = 0.860, T_{max} = 0.921$ 1339 measured reflections 1097 independent reflections 804 reflections with $I > 2\sigma(I)$

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.039$	$w = 1/[\sigma^2(F_o^2) + (0.0578P)^2]$
$wR(F^2) = 0.104$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.01	$(\Delta/\sigma)_{\rm max} < 0.001$
1097 reflections	$\Delta \rho_{\rm max} = 0.22 \ {\rm e} \ {\rm \AA}^{-3}$
74 parameters	$\Delta \rho_{\rm min} = -0.21 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

S-C1	1.679 (2)	N2-C3	1.381 (3)
N1-C1	1.358 (3)	N2-C4	1.451 (3)
N1-C2	1.374 (3)	C2-C3	1.329 (4)
N2-C1	1.364 (3)		
C1-N1-C5	124.6 (2)	N1-C1-S	127.63 (19)
C1-N2-C4	124.4 (2)	N2-C1-S	127.16 (18)
C3-N2-C4	125.9 (2)		
C5-N1-C1-N2	177.4 (2)	C3-N2-C1-S	-178.99 (19)
C2-N1-C1-S	179.3 (2)	C4-N2-C1-S	-1.1(3)
C5-N1-C1-S	-3.6(3)	C1-N1-C2-C3	-0.4(3)
C4-N2-C1-N1	177.93 (19)	C4-N2-C3-C2	-178.2 (2)

All H atoms were positioned geometrically and treated as riding atoms, with C–H distances of 0.93 or 0.97 Å.



Figure 2 The molecular packing diagram of (I); H atoms are omitted.

Data collection: *XSCANS* (Siemens, 1994); cell refinement: *XSCANS*; data reduction: *SHELXTL* (Sheldrick, 1997); program(s) used to solve structure: *SHELXTL*; program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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