organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 180 KMean σ (C–C) = 0.004 Å Disorder in main residue R factor = 0.036 wR factor = 0.082 Data-to-parameter ratio = 17.7

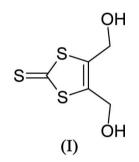
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

4,5-Bis(hydroxymethyl)-1,3-dithiole-2-thione

At 180 K, the title compound, $C_5H_6O_2S_3$, forms a threedimensional hydrogen-bonded network in which the H atoms of the hydroxyl groups are disordered. Received 27 March 2006 Accepted 19 April 2006

Comment

At 180 K, the crystal structure of the title compound, (I) (Fig. 1), contains planar 1,3-dithiole-2-thione units, with the O atom of one hydroxyl group (O1) lying approximately within this plane [torsion angle C3-C2-C4-O1 = 169.8 (2)°]. The O atom of the other hydroxyl group (O2) lies out of the plane, forming a C2-C3-C5-O2 torsion angle of -139.3 (2)°.



Adjacent molecules adopt centrosymmetric face-to-face arrangements, with a perpendicular interplanar separation of 3.56 (1) Å and no lateral offset (*i.e.* the vector joining the two centroids lies normal to the ring planes; Fig. 2).

Both O1 and O2 lie in environments where two neighouring hydroxyl groups offer potential hydrogen-bond acceptors (Table 1). The H atoms of the hydroxyl groups (located in difference Fourier maps) are disordered over two positions, in accordance with the two possibilities for hydrogen-bond formation. The resulting hydrogen-bond network (Fig. 3) is three-dimensional.

Experimental

The title compound was prepared according to the literature procedure of Jeppesen *et al.* (1999). Recrystallization from CH_2Cl_2 -ethyl acetate (1:1) afforded yellow blocks of (I).

Crystal data $C_5H_6O_2S_3$ $M_r = 194.28$ Monoclinic, C2/c a = 13.7118 (7) Å b = 8.9540 (5) Å c = 12.8244 (6) Å $\beta = 101.558$ (2)° V = 1542.59 (14) Å³

Z = 8 D_x = 1.673 Mg m⁻³ Mo K α radiation μ = 0.89 mm⁻¹ T = 180 (2) K Block, yellow 0.40 × 0.40 × 0.25 mm

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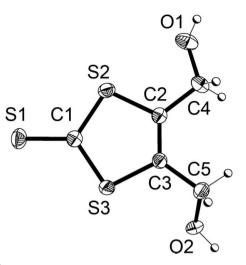


Figure 1

The molecular unit of (I), showing displacement ellipsoids at the 50% probability level. H atoms are shown as spheres of arbitrary radii. Only one H-atom position is shown on each O atom.

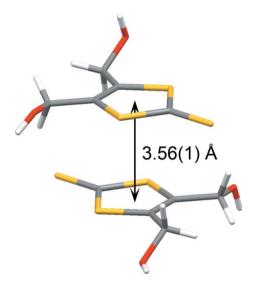


Figure 2

Pairs of molecules forming centrosymmetric face-to-face arrangements. Only one H-atom position is shown on each O atom.

Data collection

Bruker Nonius X8 APEX-II CCD area-detector diffractometer thin–slice ω and φ scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 2003) $T_{\min} = 0.713, T_{\max} = 0.808$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.036$ $wR(F^2) = 0.082$ S = 1.361894 reflections 107 parameters 9611 measured reflections 1894 independent reflections 1770 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.022$ $\theta_{\text{max}} = 28.3^{\circ}$

H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + 4.478P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.37 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{min} = -0.36 \text{ e } \text{\AA}^{-3}$

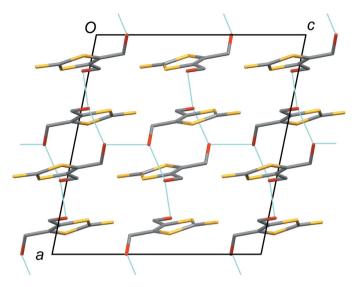


Figure 3

A view of the structure of (I), along b, showing the hydrogen-bonding network (thin green lines). H atoms have been omitted.

Table 1Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$01 - H1B \cdots O1^{i}$	0.84(1)	1.80 (1)	2.641 (4)	172 (6)
$01 - H1A \cdots O2^{ii}$	0.84(1)	1.86 (1)	2.692 (3)	171 (5)
$O2-H2A\cdots O1^{ii}$	0.84(1)	1.86 (1)	2.692 (3)	171 (5)
$O2-H2B\cdots O2^{iii}$	0.84(1)	1.93 (3)	2.722 (3)	154 (6)

Symmetry codes: (i) $-x + \frac{1}{2}, -y - \frac{1}{2}, -z + 1$; (ii) -x, -y, -z + 1; (iii) $-x, y, -z + \frac{3}{2}$.

H atoms bound to C atoms were positioned geometrically and allowed to ride during subsequent refinement, with C–H = 0.99 Å and $U_{iso}(H) = 1.2U_{eq}(C)$. The H atoms of the hydroxyl groups were visible in difference Fourier maps. They were modelled as disordered over two sites, each with 50% occupancy, and their positions and isotropic displacement parameters were refined, with all O–H distances restrained to 0.84 (1) Å.

Data collection: *APEX2* (Bruker Nonius, 2004); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

We are grateful to the Danish Natural Science Research Council (SNF) and Carlsbergfondet for provision of the X-ray equipment, and to the SNF for funding *via* STENO stipends [Nos. 21-03-0164 (ADB) and 21-03-0317 (JOJ)]. We also gratefully acknowledge financial support provided by the SNF through the SONS programme of the European Commission Sixth Framework Programme, by the Strategic Research Council of Denmark through the Young Researchers' Programme (JOJ, No. 2117-05-0115), and by the Danish Technical Research Council (No. 2058-03-0036).

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