organic papers

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Key indicators

Single-crystal X-ray study T = 292 KMean $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$ R factor = 0.056 wR factor = 0.166 Data-to-parameter ratio = 15.6

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

1-Propyl 5-nitrosalicylate

In the title compound, $C_{10}H_{11}NO_5$, all bond lengths and angles show normal values. Weak intermolecular $O-H\cdots O$ hydrogen bonds form centrosymmetric dimers, which are further linked by $\pi-\pi$ interactions into ladders extending along the *a* axis. Received 18 October 2005 Accepted 28 October 2005 Online 5 November 2005

Comment

Many compounds in the salicylate series exhibit a broad range of biological activities (Yuan & Tsao, 1994) and other useful properties (Liu *et al.*, 1996). These derivatives may serve as ligands, coordinating to metal ions through the ester group. As a part of our study of biologically active esters and their complexes (Jin *et al.*, 2004; Jin & Xiao, 2005), we present the crystal structure of the title compound, (I) (Fig. 1).



The bond lengths and angles in (I) show normal values (Table 1). An intramolecular hydrogen bond is observed between the hydroxyl group and the O atom of the carbonyl group (Table 2). In the crystal structure, weak intermolecular $O-H\cdots O$ hydrogen bonds (Table 2) form centrosymmetric



The molecular structure of (I), showing 30% probability displacement

ellipsoids and the intramolecular hydrogen bond (dashed line).

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dimers (Fig. 2). Within the dimer, an $O2 \cdots O2(-x, -y, 1-z)$ short contact of 2.763 (3) Å is observed. The dimers are stacked with π - π interactions, as shown by the short $O1 \cdots C7^{ii}$ contact of 3.182 (3) Å [symmetry code (ii): 1 - x, -y, 1 - z], thus forming ladders extending along the *a* axis.

Experimental

Compound (I) was synthesized according to the literature procedure of Bartlett & Trachtenberg (1958). A crystal suitable for X-ray analysis was grown from a solution in ethanol at room temperature by slow evaporation.

Crystal data

C ₁₀ H ₁₁ NO ₅	$D_x = 1.393 \text{ Mg m}^{-3}$
$M_r = 225.20$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 626
a = 5.1084 (8) Å	reflections
b = 11.5966 (18) Å	$\theta = 2.9 - 19.6^{\circ}$
c = 18.166 (3) Å	$\mu = 0.11 \text{ mm}^{-1}$
$\beta = 94.018 \ (3)^{\circ}$	T = 292 (2) K
V = 1073.5 (3) Å ³	Block, colourless
Z = 4	$0.20 \times 0.16 \times 0.10 \ \mathrm{mm}$
Data collection	
Bruker SMART APEX CCD area-	2346 independent reflections
detector diffractometer	1086 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.046$
Absorption correction: multi-scan	$\theta_{\rm max} = 27.0^{\circ}$

 $h = -6 \rightarrow 6$

 $k = -14 \rightarrow 14$

 $l = -21 \rightarrow 23$

refinement

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

 $\Delta \rho_{\rm max} = 0.15 \text{ e } \text{\AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.15 \text{ e } \text{\AA}^{-3}$

H atoms treated by a mixture of

 $w = \frac{1}{[\sigma^2(F_o^2) + (0.0695P)^2]}$

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

independent and constrained

Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{min} = 0.978, T_{max} = 0.989$ 6263 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.056$ $wR(F^2) = 0.166$ S = 0.972346 reflections 150 parameters

Table 1

Selected geometric parameters (Å, °).

0			
C1-C7	1.467 (3)	C7-O3	1.325 (3)
C2-O1	1.343 (3)	C8-O3	1.459 (3)
C5-N1	1.468 (4)	N1-O4	1.208 (3)
C7-O2	1.214 (3)	N1-O5	1.213 (3)
O1-C2-C1	123.1 (2)	C10-C9-C8	114.6 (3)
O2-C7-O3	122.9 (2)	O4-N1-O5	122.9 (3)
O2-C7-C1	122.9 (2)	C2-O1-H1	105 (2)
O3-C8-C9	108.0 (2)	C7-O3-C8	115.9 (2)
C6-C1-C2-O1	-179.2 (2)	C6-C5-N1-O5	-176.4 (3)
C7-C1-C2-O1	0.9 (4)	02-C7-O3-C8	-2.0(4)
C4-C5-N1-O4	-176.0 (3)	C1-C7-O3-C8	178.1 (2)



Figure 2

A packing diagram for (I). Hydrogen bonds are indicated by dashed lines.

Table 2	
Hydrogen-bond geometry (Å, °).	

$D - \Pi \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$01-H1\cdots O2$	0.94 (4)	1.77 (4)	2.619 (3)	149 (3)
$01-H1\cdots O2^{i}$	0.94 (4)	2.37 (4)	3.045 (3)	129 (3)

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

The hydroxyl H atom was located in a difference Fourier map and refined isotropically, with O–H = 0.94 (4) Å. All other H atoms were positioned geometrically and refined as riding, with C–H distances of 0.93 (aromatic H), 0.96 (methyl H) and 0.97 Å (methylene H), and with $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$ for aromatic and methylene H, or $1.5 U_{\rm eq}({\rm C})$ for methyl H.

Data collection: *SMART APEX* (Bruker, 2001); cell refinement: *SMART APEX*; data reduction: *SAINT-Plus* (Bruker, 2001); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL-NT* (Bruker, 2001); software used to prepare material for publication: *SHELXTL-NT*.

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