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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.032 wR factor = 0.078 Data-to-parameter ratio = 13.4

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

4-{[(1*E*)-(3,5-Dibromo-2-hydroxyphenyl)methylene]amino}-1,5-dimethyl-2-phenyl-1,2-dihydro-3*H*pyrazol-3-one

The crystal structure of the title compound, $C_{18}H_{15}Br_2N_3O_2$, shows a strong intramolecular $O-H\cdots N$ hydrogen bond $[N\cdots O = 2.609 (4) \text{ Å}, O-H = 0.90 \text{ Å}, H\cdots N = 1.80 \text{ Å}$ and $O-H\cdots N = 148^{\circ}]$, which leads to the existence of a phenolimine tautomer. Received 27 October 2005 Accepted 11 November 2005 Online 19 November 2005

Comment

The Schiff bases derived from salicylaldehyde have been much studied because of their properties, such as tautomeric (Salman *et al.*, 1991), fluorescent (Morishige *et al.*, 1980), and thermo- and photochromic properties (Barbara *et al.*, 1980; Cohen *et al.*, 1964). In a search for new analytical reagents, we have synthesized some compounds of substituted salicylaldehyde with 4-aminoantipyrine. We report here the synthesis and crystal structure of the title compound, (I).



All bond distances and angles are normal and agree with the corresponding values found in a similar compound 4-[(2-hydroxy-3-methoxybenzylidene)amino]-1,5-dimethyl-2phenyl-1,2-dihydro-3*H*-pyrazol-3-one (Diao *et al.*, 2005). There is an intramolecular $O-H\cdots N$ hydrogen bond (Table 2); the compound is, therefore, in the phenol–imine form, as in 4-{[(1*Z*)-2-hydroxyphenyl)methylene]amino}-1,5dimethyl-2-phenyl-1,2-dihydro-3*H*-pyrazol-3-one [N1 \cdots O1 = 2.607 (3) Å, O1-H1 = 0.97 (3) Å, H1 \cdots N1 = 1.71 (3) Å and O1-H1 \cdots N1 = 153 (2)°; Hökelek *et al.*, 2001].

Experimental

3,5-Dibromosalicylaldehyde was synthesized according to the published method (Brewsler, 1924). Ethanol solutions of 3,5dibromosalicylaldehyde (10 mmol, 2.80 g) and 4-aminoantipyrine (10 mmol, 2.03 g) were mixed and refluxed on a water bath for 5 h. The precipitate was filtered off and recrystallized from methanol (yield 81%, m.p. 501–502 K). IR (KBr, cm⁻¹): ν_{max} 3410.5, 1659.6, 1591.2, 1446.5, 1363.6, 1290.3, 1135.0, 765.7. ¹H NMR (200 MHz, CDCl₃): δ 14.42 (1H), 9.71 (1H), 7.22–7.72 (7H), 3.21 (3H), 2.42 (3H).

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organic papers

Crystal data

 $\begin{array}{l} C_{18}H_{15}Br_2N_3O_2\\ M_r = 465.15\\ \text{Monoclinic, } P_{2_1}/n\\ a = 7.092 \ (5) \ \text{\AA}\\ b = 8.231 \ (5) \ \text{\AA}\\ c = 30.487 \ (2) \ \text{\AA}\\ \beta = 91.725 \ (12)^\circ\\ V = 1779 \ (2) \ \text{\AA}^3\\ Z = 4 \end{array}$

Data collection

Siemens SMART CCD area detector diffractometer ω and φ scans Absorption correction: multi-scan (*SADABS*; Bruker 2002) $T_{min} = 0.367, T_{max} = 0.578$ 9143 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.035P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.032$	+ 0.3014P]
$wR(F^2) = 0.078$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.03	$(\Delta/\sigma)_{\rm max} = 0.001$
3224 reflections	$\Delta \rho_{\rm max} = 0.41 \ {\rm e} \ {\rm A}^{-3}$
239 parameters	$\Delta \rho_{\rm min} = -0.34 \text{ e} \text{\AA}^{-3}$
H atoms treated by a mixture of	Extinction correction: SHELXL97
independent and constrained	Extinction coefficient: 0.0018 (4)
refinement	

 $D_x = 1.737 \text{ Mg m}^{-3}$

Cell parameters from 3452

 $0.24 \times 0.19 \times 0.12 \text{ mm}$

3224 independent reflections 2631 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

reflections

 $\theta = 2.6-25.3^{\circ}$ $\mu = 4.57 \text{ mm}^{-1}$

T = 293 (2) K

Block, orange

 $\begin{aligned} R_{\rm int} &= 0.034\\ \theta_{\rm max} &= 25.3^\circ \end{aligned}$

 $h = -8 \rightarrow 8$

 $k = -9 \rightarrow 9$

 $l = -33 \rightarrow 36$

Table 1

Selected geometric parameters (Å, °).

Br1-C3	1.900 (3)	N1-C7	1.292 (4)
Br2-C5	1.889 (3)	N1-C8	1.393 (4)
O1-C6	1.344 (3)	N2-N3	1.414 (3)
O2-C10	1.228 (3)	N3-C10	1.409 (3)
C7-N1-C8	120.4 (3)	O1-C6-C5	120.3 (3)
C2-C1-C7	118.9 (3)	O1-C6-C1	121.9 (2)

Table 2

Hydrogen-bond geometry (Å, °).

$\overline{D-\mathrm{H}\cdots A}$	$D-\mathrm{H}$	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$O1-H1A\cdots N1$	0.90	1.80	2.609 (4)	148
$\begin{array}{c} \text{C7}-\text{H7}A\cdots\text{O2}\\ \text{C18}-\text{H18}A\cdots\text{O2} \end{array}$	0.93 0.93	2.26 2.46	2.958 (4) 2.882 (4)	131 108

The hydroxy H atom (H1A) was positioned from a difference map, refined for several cycles and then fixed at a distance of 0.90 Å; the methyl H atoms on C11 were located in a Fourier synthesis and refined freely. The remaining H atoms were positioned geometrically and treated as riding, at distances of 0.93 (CH) and 0.96 Å (CH₃) $[U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C}) \text{ or } 1.5U_{\rm eq}({\rm C}_{\rm methyl},{\rm O})].$

Data collection: *SMART* (Bruker 2002); cell refinement: *SAINT* (Bruker 2002); data reduction: *SAINT* and *SHELXTL* (Bruker



Figure 1

The structure of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.



Figure 2

The packing of (I), viewed down the a axis. Dashed lines indicate hydrogen bonds.

2002); 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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