

A monoclinic modification of 2-[(1,3-benzothiazol-2-yl)iminomethyl]phenol

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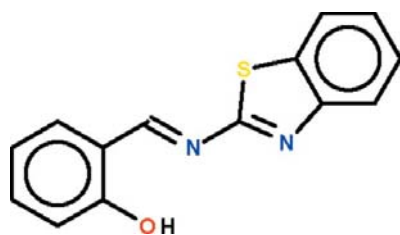
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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; R factor = 0.040; wR factor = 0.110; data-to-parameter ratio = 15.8.

In the title Schiff base, $\text{C}_{14}\text{H}_{10}\text{N}_2\text{OS}$, the azomethine double bond is in an *E* configuration; the benzothiazolyl ring (r.m.s. deviation = 0.007 Å) is coplanar with the phenylene ring (r.m.s. deviation = 0.007 Å), the two rings being slightly bent at $2.6(1)^\circ$. The hydroxy H atom forms an intramolecular hydrogen bond to the imino group. The bond dimensions of the monoclinic modification are similar to those of the orthorhombic modification [Liu *et al.* (2009). *Acta Cryst. E* **65**, o738].

Related literature

For an orthorhombic modification of this structure, see: Liu *et al.* (2009).



Experimental

Crystal data

$\text{C}_{14}\text{H}_{10}\text{N}_2\text{OS}$

$M_r = 254.30$

Monoclinic, Pn
 $a = 8.6391(4)$ Å
 $b = 6.2313(4)$ Å
 $c = 11.4459(8)$ Å
 $\beta = 108.893(1)^\circ$
 $V = 582.97(6)$ Å³

$Z = 2$
Mo $K\alpha$ radiation
 $\mu = 0.26$ mm⁻¹
 $T = 100$ K
 $0.14 \times 0.13 \times 0.08$ mm

Data collection

Bruker SMART APEX diffractometer
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
 $T_{\min} = 0.964$, $T_{\max} = 0.979$

5307 measured reflections
2599 independent reflections
2512 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.029$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.040$
 $wR(F^2) = 0.110$
 $S = 1.05$
2599 reflections
164 parameters
2 restraints

H-atom parameters constrained
 $\Delta\rho_{\max} = 0.40$ e Å⁻³
 $\Delta\rho_{\min} = -0.25$ e Å⁻³
Absolute structure: Flack (1983), 1242 Friedel pairs
Flack parameter: 0.27 (8)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$\text{O1}-\text{H1} \cdots \text{N1}$	0.87	1.73	2.550 (2)	156

Data collection: APEX2 (Bruker, 2009); cell refinement: SAINT (Bruker, 2009); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: X-SEED (Barbour, 2001); software used to prepare material for publication: publCIF (Westrip, 2010).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: NK2043).

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