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## Key indicators

Single-crystal X-ray study  
 $T = 273\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$   
 $R$  factor = 0.059  
 $wR$  factor = 0.138  
Data-to-parameter ratio = 14.8For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

## 1-(2-Hydroxyphenyl)ethanone benzoylhydrazone

In the title compound, the planes of the phenyl and 2-(1-iminoethyl)phenol fragments form dihedral angles of  $28.18(11)$  and  $28.51(11)^\circ$ , respectively, with the central  $-\text{N}-\text{C}(=\text{O})-$  fragment. The molecule is stabilized by intermolecular  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds, which form a one-dimensional chain parallel to the  $a$  axis.

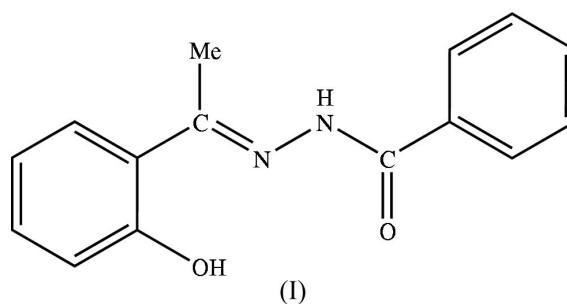
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## Comment

The title compound, (I), is the product of the condensation reaction of benzhydrazide with 2-hydroxyacetophenone. Like many benzoylhydrazone derivatives, the molecule exists in the keto tautomeric form (Fig. 1).



The phenyl (C1–C6), 2-(1-imino-ethyl)phenol (C10–C15/O2/C8/C9/N2) and N1/C7/O1 fragments are each planar, with maximum deviations of  $0.011(2)\text{ \AA}$  for atoms C3 and C6. The geometric parameters of the molecule are in normal ranges (Allen *et al.*, 1987) and in agreement with other benzoylhydrazone compounds, such as 1-(4-fluoro-2-hydroxyphenyl)ethanone 4-nitrobenzoylhydrazone (Ali *et al.*, 2004).

The molecule of (I) resembles an asymmetric wing. The planes of the phenyl and 2-(1-imino-ethyl)phenol fragments form dihedral angles of  $28.18(11)$  and  $28.51(11)^\circ$ , respectively, with the central N1/C7/O1 fragment. The dihedral angle

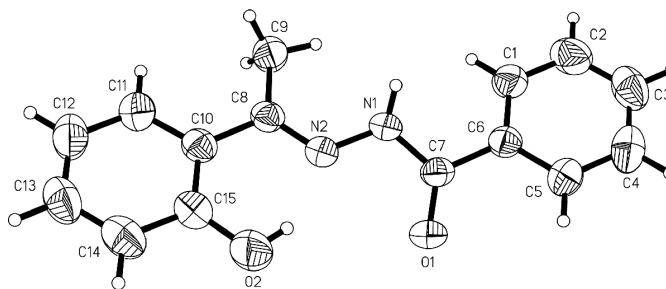


Figure 1

The molecular structure of (I), with the atom-numbering scheme and 50% probability displacement ellipsoids.

between the phenyl and 2-(1-imino-ethyl)phenol groups is 11.15 (10)°.

There are two intramolecular O2—H2A···N2 and C9—H9A···N1 hydrogen bonds. In the crystal structure, the molecules are stabilized by intermolecular N1—H1B···O1<sup>i</sup> hydrogen bonds (symmetry code given in Table 2) to form a one-dimensional chain parallel to the *a* axis (Fig. 2).

### Experimental

An equimolar mixture of benzhydrazide (10 mmol) and 2-hydroxyphenylacetophenone (10 mmol) in ethanol was refluxed in a two-necked round-bottomed flask for 2 h. The solution was then filtered to remove some undissolved solids. Colourless crystals of (I) were obtained in the filtrate after 1 h of evaporation at room temperature (yield 90%; m.p. 446–447 K). Analysis, calculated: C 70.84, H 5.55, N 11.02, O 12.59%; found: C 69.92, H 5.60, N 11.00, O 12.38%.

#### Crystal data

C <sub>15</sub> H <sub>14</sub> N <sub>2</sub> O <sub>2</sub>	<i>D</i> <sub>x</sub> = 1.313 Mg m <sup>-3</sup>
<i>M</i> <sub>r</sub> = 254.28	Mo Kα radiation
Monoclinic, <i>P</i> 2 <sub>1</sub> / <i>n</i>	Cell parameters from 1000 reflections
<i>a</i> = 4.9110 (18) Å	<i>θ</i> = 1.9–26.5°
<i>b</i> = 12.466 (4) Å	<i>μ</i> = 0.09 mm <sup>-1</sup>
<i>c</i> = 21.018 (7) Å	<i>T</i> = 273 (2) K
<i>β</i> = 91.299 (6)°	Block, colourless
<i>V</i> = 1286.4 (8) Å <sup>3</sup>	0.43 × 0.22 × 0.19 mm
<i>Z</i> = 4	

#### Data collection

Bruker SMART APEX CCD area-detector diffractometer	2662 independent reflections
<i>ω</i> scans	2342 reflections with <i>I</i> > 2σ( <i>I</i> )
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	<i>R</i> <sub>int</sub> = 0.030
<i>T</i> <sub>min</sub> = 0.964, <i>T</i> <sub>max</sub> = 0.985	<i>θ</i> <sub>max</sub> = 26.5°
13 472 measured reflections	<i>h</i> = -6 → 6
	<i>k</i> = -15 → 15
	<i>l</i> = -26 → 26

#### Refinement

Refinement on <i>F</i> <sup>2</sup>	<i>w</i> = 1/[σ <sup>2</sup> ( <i>F</i> <sub>o</sub> <sup>2</sup> ) + (0.0477 <i>P</i> ) <sup>2</sup> + 0.3287 <i>P</i> ]
<i>R</i> [ <i>F</i> <sup>2</sup> > 2σ( <i>F</i> <sup>2</sup> )] = 0.059	where <i>P</i> = ( <i>F</i> <sub>o</sub> <sup>2</sup> + 2 <i>F</i> <sub>c</sub> <sup>2</sup> )/3
<i>wR</i> ( <i>F</i> <sup>2</sup> ) = 0.138	(Δ/ <i>σ</i> ) <sub>max</sub> < 0.001
<i>S</i> = 1.24	Δ <i>ρ</i> <sub>max</sub> = 0.15 e Å <sup>-3</sup>
2662 reflections	Δ <i>ρ</i> <sub>min</sub> = -0.13 e Å <sup>-3</sup>
180 parameters	Extinction correction: none
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Selected geometric parameters (Å, °).

O1—C7	1.227 (2)	N2—N1	1.387 (2)
N2—C8	1.285 (2)	C7—N1	1.350 (2)
C1—C6—C7—O1	150.85 (18)	C8—N2—N1—C7	-158.92 (16)
O1—C7—N1—N2	10.0 (3)		

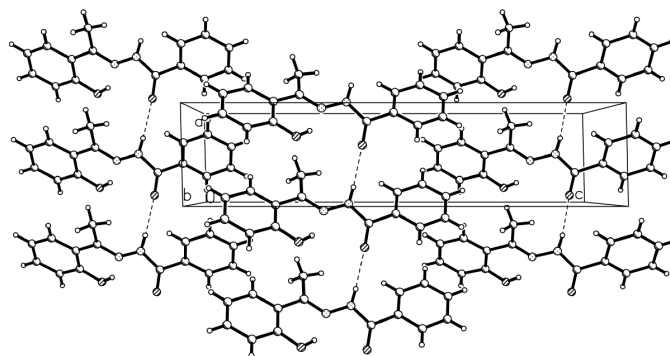


Figure 2

A packing diagram for (I), viewed down the *b* axis. Dashed lines denote N1—H1B···O1 hydrogen bonds.

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
O2—H2A···N2	0.82 (3)	1.81 (3)	2.545 (2)	148 (3)
C9—H9A···N1	0.96	2.36	2.792 (3)	107
N1—H1B···O1 <sup>i</sup>	0.83 (2)	2.10 (2)	2.919 (2)	165 (2)

Symmetry code: (i) *x* - 1, *y*, *z*.

All H atoms were located in a difference map. Atoms H1B and H2A were refined isotropically. All other H atoms were positioned geometrically and allowed to ride on their parent C atoms, with C—H distances in the range 0.93–0.96 Å, and with *U*<sub>iso</sub>(H) = 1.2*U*<sub>eq</sub>(C) for CH and 1.5*U*<sub>eq</sub>(C) for CH<sub>3</sub>.

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL, PARST (Nardelli, 1995) and PLATON (Spek, 2003).

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