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Key indicators

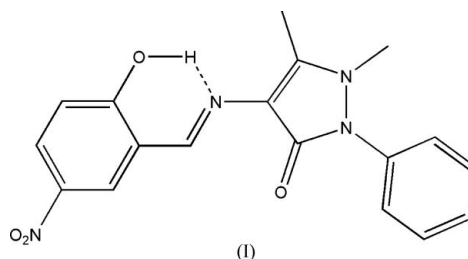
Single-crystal X-ray study
 $T = 298$ K
Mean $\sigma(\text{C}-\text{C}) = 0.006$ Å
 R factor = 0.084
 wR factor = 0.197
Data-to-parameter ratio = 12.3For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.4-[(1*E*)-(2-Hydroxy-5-nitrophenyl)methylene-
amino]-1,5-dimethyl-2-phenyl-1*H*-pyrazol-
3(2*H*)-one

The title compound, $\text{C}_{18}\text{H}_{16}\text{N}_4\text{O}_4$, has been synthesized by condensation of 5-nitrosalicylaldehyde and 4-aminoantipyrine. There are two molecules in the asymmetric unit. The crystal structure shows a strong intramolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen bond, which leads to the existence of a phenol-imine tautomer.

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Comment

Salicylaldehyde and its derivatives have attracted an intense interest because of their properties, such as tautomeric (Salman *et al.*, 1991), fluorescent (Morishige, 1980), and thermo- and photochromic properties (Barbara *et al.*, 1980; Cohen *et al.*, 1964). In a search for new analytical reagents, we report here the synthesis and crystal structure of the title compound, (I).



There are two molecules in the asymmetric unit. All the bond distances and angles are normal and agree with the corresponding values found in a similar compound, *viz.* 4-[(2-hydroxy-3-methoxybenzylidene)amino]-1,5-dimethyl-2-phenyl-1,2-dihydro-3*H*-pyrazol-3-one (Diao *et al.*, 2005). In each unique molecule of the title compound, the pyrazoline and the nitrophenyl ring are approximately coplanar as a

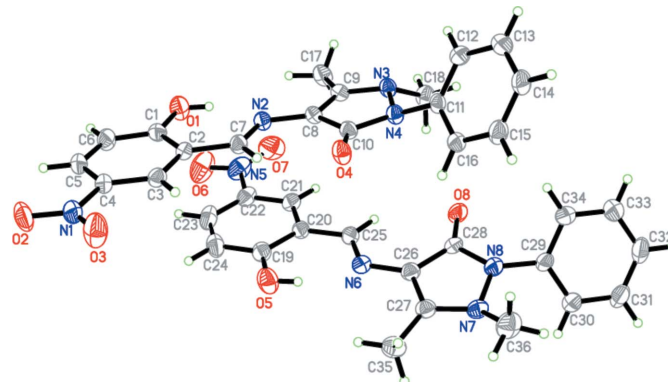


Figure 1

The asymmetric unit of the title compound, showing 30% probability displacement ellipsoids and the atom-numbering scheme.

result of conjugation *via* the imino C=N double bond, with dihedral angles of 3.6 (9) and 13.0 (2)°.

The imino N atoms are linked to the phenol O atoms and act as hydrogen-bond acceptors in O—H...N intramolecular interactions (Table 1), as in 4-[[*(E)*-(2-hydroxyphenyl)methylidene]amino]-1,5-dimethyl-2-phenyl-2,3-dihydro-1*H*-pyrazol-3-one (Hökelek *et al.*, 2001).

Experimental

To 5-nitrosalicylaldehyde (10 mmol, 1.67 g) in MeOH (15 ml) was added 4-aminoantipyrine (10 mmol, 2.03 g) dissolved in MeOH (15 ml). The reaction mixture was refluxed in a water bath for 1 h. After cooling, the separated precipitate was filtered off, washed and recrystallized from methanol (yield 83%, m.p. 472.4–472.8 K).

Crystal data

| | |
|---|---|
| C ₁₈ H ₁₆ N ₄ O ₄ | Z = 8 |
| M _r = 352.35 | D _x = 1.409 Mg m ⁻³ |
| Monoclinic, P2 ₁ /c | Mo Kα radiation |
| a = 8.4387 (13) Å | μ = 0.10 mm ⁻¹ |
| b = 36.870 (5) Å | T = 298 (2) K |
| c = 13.3937 (16) Å | Block, yellow |
| β = 127.155 (7)° | 0.31 × 0.24 × 0.18 mm |
| V = 3321.3 (8) Å ³ | |

Data collection

| | |
|---|---------------------------------|
| Bruker APEX area-detector diffractometer | 17376 measured reflections |
| φ and ω scans | 5837 independent reflections |
| Absorption correction: multi-scan (SADABS; Sheldrick, 2002) | 4596 reflections with I > 2σ(I) |
| T _{min} = 0.969, T _{max} = 0.978 | R _{int} = 0.039 |
| | θ _{max} = 25.0° |

Refinement

| | |
|---|--|
| Refinement on F ² | w = 1/[σ ² (F _o ²) + (0.0805P) ² + 1.0761P] |
| R[F ² > 2σ(F ²)] = 0.084 | where P = (F _o ² + 2F _c ²)/3 |
| wR(F ²) = 0.197 | (Δ/σ) _{max} = 0.001 |
| S = 1.23 | Δρ _{max} = 0.27 e Å ⁻³ |
| 5837 reflections | Δρ _{min} = -0.24 e Å ⁻³ |
| 476 parameters | Extinction correction: SHELXL97 |
| H-atom parameters constrained | Extinction coefficient: 0.0041 (8) |

Table 1

Hydrogen-bond geometry (Å, °).

| D—H...A | D—H | H...A | D...A | D—H...A |
|------------|------|-------|-----------|---------|
| O1—H1...N2 | 0.82 | 1.88 | 2.612 (3) | 147 |
| O5—H5...N6 | 0.82 | 1.86 | 2.586 (4) | 148 |

All H atoms were positioned geometrically and were treated as riding on their parent C and O atoms, with aromatic C—H distances of 0.93 Å [*U*_{iso}(H) = 1.2*U*_{eq}(C)], other C—H distances of 0.96 Å [*U*_{iso}(H) = 1.5*U*_{eq}(C)] and O—H distances of 0.82 Å [*U*_{iso}(H) = 1.5*U*_{eq}(O)].

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Sheldrick, 2000); software used to prepare material for publication: SHELXL97.

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