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#### Key indicators

Single-crystal X-ray study  
T = 100 K  
Mean  $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$   
R factor = 0.049  
wR factor = 0.117  
Data-to-parameter ratio = 21.2

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

## 2,2'-[1,2-Phenylenebis(nitrilomethylidyne)]-bis(5-methylphenol)

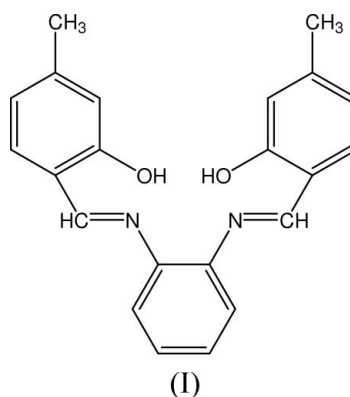
The crystal structure of the title compound,  $\text{C}_{22}\text{H}_{20}\text{N}_2\text{O}_2$ , is stabilized by  $\text{C}-\text{H}\cdots\text{O}$ ,  $\text{C}-\text{H}\cdots\pi$  and  $\pi-\pi$  interactions. The central benzene ring forms dihedral angles of  $58.55(6)$  and  $4.02(6)^\circ$  with the terminal benzene rings.

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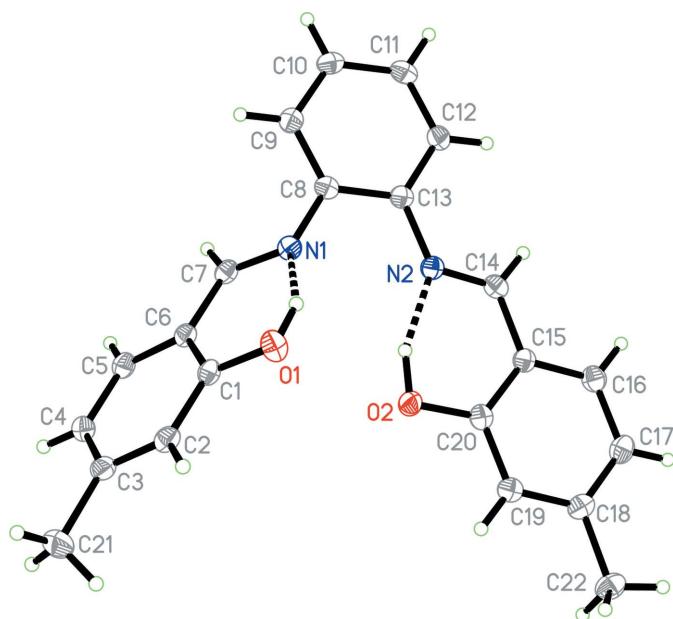
#### Comment

Some Schiff base compounds exhibit various pharmacological activities, *e.g.* anticancer (Dao *et al.*, 2000), anti-HIV (Sriram *et al.*, 2006), antibacterial and antifungal (Karthikeyan *et al.*, 2006). In addition, some of them may be used as analytical reagents for the determination of trace elements (Eltayeb & Ahmed, 2005*a,b*). Recently we have reported the crystal structures of 1-[2-[2-hydroxy-1-naphthyl)methyleneamino]-phenyliminiomethyl]-2-naphtholate methanol hemisolvate (Eltayeb *et al.*, 2007*a*) and 6,6'-dimethyl-2,2'-[1,2-phenylenebis(nitrilomethylidyne)]diphenol (Eltayeb *et al.*, 2007*b*). In this paper, we report the crystal structure of the title compound, (I), obtained by the reaction of *o*-phenylenediamine and 4-methylsalicylaldehyde.



Bond lengths and angles in (I) have normal values (Allen *et al.*, 1987). The dihedral angles between the planes defined by *A* (C1–C6), *B* (C8–C13) and *C* (C15–C20) are  $58.55(6)$  (*A/B*),  $61.04(6)$  (*A/C*) and  $4.02(6)^\circ$  (*B/C*). Intramolecular  $\text{O}-\text{H}\cdots\text{N}$  hydrogen bonds generate *S*(6) ring motifs (Table 1 and Fig. 1) (Bernstein *et al.*, 1995).

The crystal structure is stabilized by intermolecular  $\text{C}-\text{H}\cdots\text{O}$  hydrogen bonds and  $\text{C}-\text{H}\cdots\pi$  interactions involving the C1–C6 benzene ring (centroid *Cg*1). In addition, the crystal packing is stabilized by  $\pi-\pi$  interactions between the C8–C13 (centroid *Cg*2) and C15–C20 (centroid *Cg*3) benzene rings with a  $\text{Cg}2\cdots\text{Cg}3^i$  distance of  $3.6914(8) \text{ \AA}$  [symmetry code (i) is given in Table 1]. The molecules are stacked into columns along the *a* axis (Fig. 2).



**Figure 1**  
The molecular structure of (I), showing 50% probability displacement ellipsoids and the atomic numbering. Hydrogen bonds are shown as dashed lines.

## Experimental

To a solution of *o*-phenylenediamine (0.172 g, 1.6 mmol) in ethanol (20 ml) was added 4-methylsalicylaldehyde (0.444 g, 3.2 mmol). The mixture was refluxed with stirring for 30 min. The resultant orange solution was filtered and orange crystals suitable for X-ray diffraction analysis formed after one week on slow evaporation of the solvent at room temperature (yield 0.35 g, 63.63%; m.p. 410–412 K).

### Crystal data

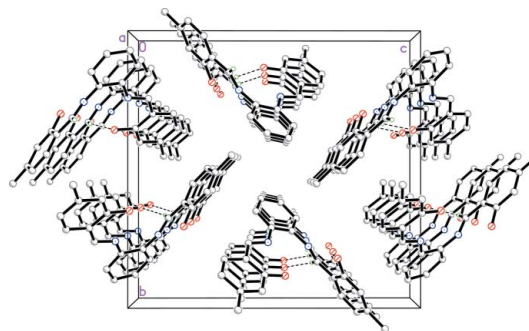
$C_{22}H_{20}N_2O_2$	$Z = 4$
$M_r = 344.40$	$D_x = 1.299 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 6.0782 (2) \text{ \AA}$	$\mu = 0.08 \text{ mm}^{-1}$
$b = 16.5573 (6) \text{ \AA}$	$T = 100.0 (1) \text{ K}$
$c = 17.4989 (6) \text{ \AA}$	Needle, orange
$\beta = 90.348 (2)^\circ$	$0.46 \times 0.11 \times 0.09 \text{ mm}$
$V = 1761.03 (11) \text{ \AA}^3$	

### Data collection

Bruker SMART APEX2 CCD diffractometer	22113 measured reflections
$\omega$ scans	5201 independent reflections
Absorption correction: multi-scan (SADABS; Bruker, 2005)	3751 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.855$ , $T_{\max} = 0.992$	$R_{\text{int}} = 0.034$
	$\theta_{\text{max}} = 30.2^\circ$

### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0447P)^2 + 0.5205P]$
$R[F^2 > 2\sigma(F^2)] = 0.049$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.117$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.05$	$\Delta\rho_{\text{max}} = 0.29 \text{ e \AA}^{-3}$
5201 reflections	$\Delta\rho_{\text{min}} = -0.23 \text{ e \AA}^{-3}$
245 parameters	
H atoms treated by a mixture of independent and constrained refinement	



**Figure 2**  
The crystal packing of (I), viewed down the  $a$  axis. H atoms not involved in intermolecular hydrogen bonding (dashed lines) have been omitted.

**Table 1**

Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O1-H1A\cdots N1$	0.96 (2)	1.73 (2)	2.599 (1)	149 (2)
$O2-H2B\cdots N2$	0.95 (2)	1.67 (2)	2.558 (1)	155 (2)
$C7-H7A\cdots O2^i$	0.93	2.40	3.250 (2)	152
$C12-H12A\cdots Cg1^{ii}$	0.93	2.78	3.643 (2)	156
$C22-H22B\cdots Cg1^{iii}$	0.96	2.92	3.446 (1)	116

Symmetry codes: (i)  $x + 1, y, z$ ; (ii)  $x, -y + \frac{1}{2}, z + \frac{1}{2}$ ; (iii)  $-x, -y, -z + 1$ .

O-bound H atoms were located in difference maps and refined isotropically. The remaining H atoms were positioned geometrically and treated as riding, with  $C-H = 0.93$  or  $0.96 \text{ \AA}$  and  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$  or  $1.5U_{\text{eq}}(\text{methyl C})$ .

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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