

## **3,5-Dimethyl-4-(2,4,6-trimethylphenyldiazenyl)phenol**

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## 3,5-Dimethyl-4-(2,4,6-trimethylphenyldiazenyl)phenol

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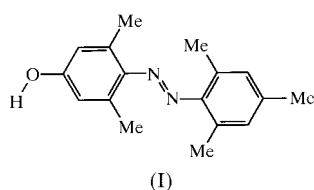
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In the title compound, C<sub>17</sub>H<sub>20</sub>N<sub>2</sub>O, (I), the dihedral angle between the two phenyl rings is 15.69 (6)°. An intermolecular hydrogen-bonding association exists between the hydroxy group and one of the azo N atoms.



### Experimental

Crystals of the title compound were grown from ethyl acetate solution.

#### Crystal data

C<sub>17</sub>H<sub>20</sub>N<sub>2</sub>O  
M<sub>r</sub> = 268.35  
Monoclinic, *P*2<sub>1</sub>/*n*  
*a* = 12.369 (2) Å  
*b* = 7.6809 (3) Å  
*c* = 15.332 (3) Å  
 $\beta$  = 101.842 (9)°  
*V* = 1425.6 (4) Å<sup>3</sup>  
*Z* = 4

*D*<sub>x</sub> = 1.250 Mg m<sup>-3</sup>  
Mo *K*α radiation  
Cell parameters from 25 reflections  
 $\theta$  = 6–14°  
 $\mu$  = 0.078 mm<sup>-1</sup>  
*T* = 298 (2) K  
Block, red  
0.47 × 0.47 × 0.47 mm

#### Data collection

Enraf–Nonius CAD-4 diffractometer  
2θ/ω scans  
2679 measured reflections  
2512 independent reflections  
1717 reflections with *I* > 2σ(*I*)  
*R*<sub>int</sub> = 0.019

$\theta_{\max}$  = 24.97°  
*h* = −5 → 14  
*k* = −4 → 9  
*l* = −18 → 17  
3 standard reflections every 200 reflections  
intensity decay: none

#### Refinement

Refinement on *F*<sup>2</sup>  
*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.042  
*wR*(*F*<sup>2</sup>) = 0.127  
*S* = 1.034  
2512 reflections  
209 parameters  
H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0632P)^2 + 0.3065P]$   
where  $P = (F_o^2 + 2F_c^2)/3$   
(Δ/σ)<sub>max</sub> = 0.005  
Δρ<sub>max</sub> = 0.19 e Å<sup>-3</sup>  
Δρ<sub>min</sub> = −0.16 e Å<sup>-3</sup>

**Table 1**

Hydrogen-bonding 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>
O1–H1...N2 <sup>i</sup>	0.87 (3)	2.16 (3)	2.985 (2)	157 (2)

Symmetry codes: (i)  $\frac{3}{2} - x, y - \frac{1}{2}, \frac{1}{2} - z$ .

All H atoms were included in the refinement at calculated positions as riding models (C–H = 0.96 Å), except for the hydroxy H atom, which was located in difference syntheses and whose positional and displacement parameters were refined.

Data collection: *MolEN* (Fair, 1990); cell refinement: *MolEN*; data reduction: *Xtal3.2* (Hall *et al.*, 1992); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); software used to prepare material for publication: *SHELXL97*.

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