

Xin-Gang Liu,^a Ya-Qing Feng,^{a*}
Xiang-Qi Meng,^a Zu-Pei Liang^b
and Guang Yang^a^aSchool of Chemical Engineering and
Technology, Tianjin University, Tianjin 300072,
People's Republic of China, and ^bSchool of
Chemistry and Molecular Engineering, Qingdao
University of Science and Technology, Qingdao
266042, People's Republic of ChinaCorrespondence e-mail:
xingangl2002@yahoo.com.cn

Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.046
 wR factor = 0.129
Data-to-parameter ratio = 14.0For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**(E)-4-[(4-Hydroxyphenyl)diazenyl]benzaldehyde**

The title compound, $\text{C}_{13}\text{H}_{10}\text{N}_2\text{O}_2$, is approximately planar in the solid state and displays a *trans* configuration with respect to the azo double bond. Molecules form infinite chains linked by $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds along the a axis.

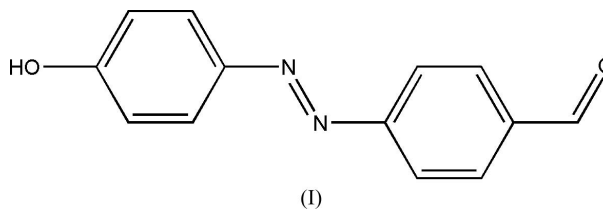
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Comment

Azo compounds are widely utilized as dyes and indicators in chemistry and as stains in the biological field (Kumar & Neckers, 1989). Moreover, azobenzene and some azobenzene derivatives can undergo *cis-trans* isomerization under photochemical stimulation and may be involved in energy-transfer processes (Murakami *et al.*, 1997). We report here the synthesis and structure of the title compound, (I) (Fig. 1).



The molecule is approximately planar, with a mean deviation 0.026 (2) Å from the molecular plane. The dihedral angle between the planes of the two aromatic rings is 1.5 (3)°. Moreover, the title compound displays the expected *trans* configuration with respect to the azo double bond. $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds involving O atoms at either end of the molecule result in the formation of polymeric chains of molecules along the a axis (Figs. 2 and 3, and Table 1).

Experimental

Sodium nitrite (5 mmol) in water (10 ml) was added dropwise to 4-aminobenzaldehyde (4 mmol) dispersed in concentrated HCl (2 ml) at 273–278 K and the mixture stirred for 30 m. The resulting solution was added dropwise to Na_2CO_3 (10 mmol) and phenol (5 mmol) in water (40 ml) and stirred for 30 min. The red–orange



Figure 1

The molecular structure of (I), with atom labels and 30% probability ellipsoids. H atoms are shown as spheres of arbitrary radii.

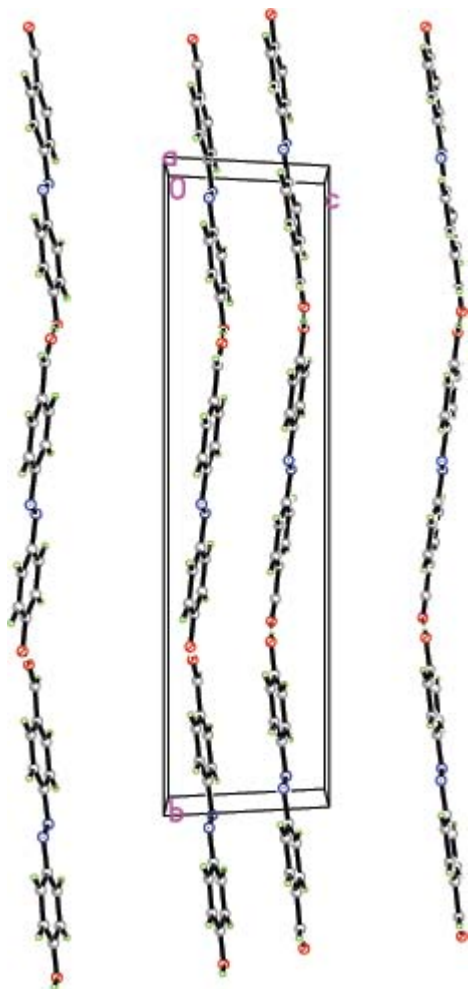


Figure 2
The crystal packing, viewed along the *a* axis, showing the polymeric chains.

precipitate of (I) was filtered and washed with water. ^1H NMR (CDCl_3): δ 5.21 (s, 1H), 6.97–6.99 (d, 2H), 7.92–8.05 (m, 6H), 10.10 (s, 1H). Recrystallization from acetone over 10 d at ambient temperature gave colourless single crystals of (I).

Crystal data

$\text{C}_{13}\text{H}_{10}\text{N}_2\text{O}_2$	$D_x = 1.383 \text{ Mg m}^{-3}$
$M_r = 226.23$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 1178 reflections
$a = 6.405$ (2) Å	$\theta = 3.2$ – 23.6°
$b = 25.820$ (9) Å	$\mu = 0.10 \text{ mm}^{-1}$
$c = 7.197$ (2) Å	$T = 293$ (2) K
$\beta = 114.140$ (6) $^\circ$	Block, colourless
$V = 1086.2$ (6) Å 3	$0.20 \times 0.14 \times 0.08 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART CCD area-detector diffractometer	2206 independent reflections
φ and ω scans	1083 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Bruker, 1997)	$R_{\text{int}} = 0.046$
$T_{\text{min}} = 0.972$, $T_{\text{max}} = 0.991$	$\theta_{\text{max}} = 26.4^\circ$
6049 measured reflections	$h = -7 \rightarrow 7$
	$k = -32 \rightarrow 31$
	$l = -8 \rightarrow 5$

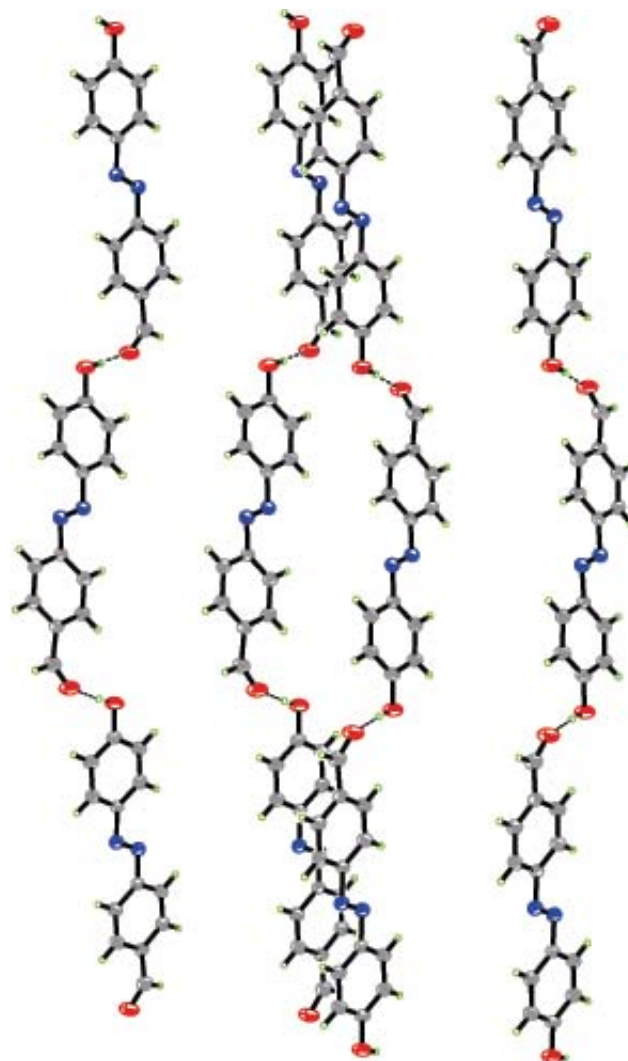


Figure 3
O—H...O hydrogen bonds (dashed lines), forming polymeric chains.

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.046$
 $wR(F^2) = 0.129$
 $S = 1.00$
 2206 reflections
 158 parameters
 H atoms treated by a mixture of independent and constrained refinement

$$w = 1/[\sigma^2(F_o^2) + (0.0555P)^2 + 0.0666P]$$

where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.14 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\text{min}} = -0.18 \text{ e } \text{Å}^{-3}$

Table 1

Hydrogen-bonding geometry (Å, $^\circ$).

$D\text{—H}\cdots A$	$D\text{—H}$	$\text{H}\cdots A$	$D\cdots A$	$D\text{—H}\cdots A$
$\text{O1—H1A}\cdots\text{O2}^i$	0.91 (3)	1.80 (3)	2.711 (3)	176 (3)

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

The hydroxy H atom was located in a difference map and its coordinates and isotropic displacement parameter were freely refined. Other H atoms were positioned geometrically ($\text{C—H} = 0.93 \text{ Å}$) and refined with a riding model, $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{carrier})$.

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

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