organic papers

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Key indicators

Powder X-ray study T = 295 KMean σ (C–C) = 0.008 Å R factor = 0.027 wR factor = 0.036

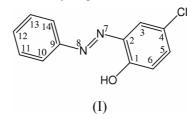
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

4-Chloro-2-(phenyldiazenyl)phenol from powder data: a form stable at room temperature

The low-temperature form of the title compound, C12H9-ClN₂O, (I), was obtained from an ethanol solution of (I) at room temperature. The molecule of (I) is almost planar; the dihedral angle formed by the planes of the phenyl rings is 5.0 (4)°. Translationally related molecules form stacks with an interplanar separation of 3.32 (1) Å.

Comment

The hydroxy group of the title compound, (I), forms an intramolecular hydrogen bond with the azo linkage $[O1 \cdots N8 = 2.622 (12) \text{ Å}]$, thus precluding the formation of strong intermolecular hydrogen bonds.



The molecules form stacks along [010]; the angle between the normal to the molecular plane and the stack axis is 44.0 (1) $^{\circ}$. Neighbouring molecules within the stack overlap each other in essentially the same manner as in the hightemperature form prepared from the melt (Yatsenko et al., 2001), but the two polymorphs differ in the way in which adjacent stacks are arranged with respect to each other. In the room-temperature form, neighbouring molecules belonging to different stacks are crossed (Fig. 1), whereas in the hightemperature form they are arranged side-by-side. Two relatively short intermolecular contacts are present in this structure: the side-by-side contact $H5 \cdots H5(1-x, -1-y, -z)$ (2.12 Å), and the 3.03 (1) Å contact between the phenolic-O atoms. However, this contact is not a hydrogen bond since the $O1 - H1 \cdots O1(\frac{1}{2} - x, y - \frac{1}{2}, -\frac{1}{2} - z)$ angle is 110°.

Experimental

Compound (I) was prepared by the reaction of phenyldiazonium chloride with *p*-chlorophenol according to the established procedure of Socha & Vecera (1969) and recrystallized from ethanol.

Crystal data

C ₁₂ H ₉ ClN ₂ O	Cu $K\alpha$ radiation
$M_r = 232.66$	Cell parameters from 26
Monoclinic, $P2_1/n$	reflections
a = 19.706 (6) Å	$\theta = 3.8 15.6^{\circ}$
b = 4.614 (2) Å	$\mu = 2.95 \text{ mm}^{-1}$
c = 12.308 (4) Å	T = 295 (2) K
$\beta = 104.70 \ (3)^{\circ}$	Yellow
V = 1082.5 (7) Å ³	Specimen shape: flat sheet
Z = 4	$25 \times 25 \times 2.0$ mm
$D_x = 1.428 \text{ Mg m}^{-3}$	Particle morphology: needle

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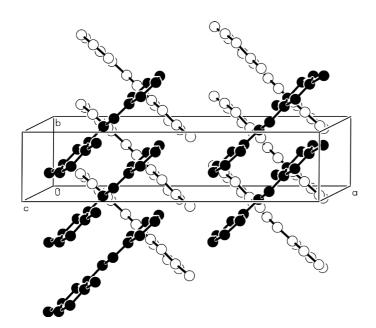


Figure 1 Stacking arrangement adopted by (I).

Data collection

Refinement

-	
$R_p = 0.027$	Profile function: split-type pseudo-
$R_{wp} = 0.036$	Voigt
$R_{\rm exp} = 0.033$	115 parameters
S = 1.09	H-atom parameters not refined
$2\theta_{\min} = 7.0, 2\theta_{\max} = 70.0^{\circ}$	$(\Delta/\sigma)_{\rm max} = 0.034$
Wavelength of incident radiation:	Preferred orientation correction:
1.5418 Å	Spherical harmonics (Ahtee et al.,
Excluded region(s): 5.00-6.98°	1989)

The monoclinic cell dimensions were determined with *TREOR*90 (Werner *et al.*, 1985) and refined to $M_{20} = 20$ and F = 46 (0.0072,71) using the first 26 peak positions. The initial molecular model was built with *MOPAC*7.0 (Stewart, 1993) on the *PM3* level (Stewart, 1989). The position and orientation of the molecule were determined using the grid-search procedure (Chernyshev & Schenk, 1998). The X-ray diffraction profile and the difference between the measured and calculated profiles after Rietveld refinement are shown in Fig. 2, final $R_B = 0.062$. The Cl atom was refined anisotropically; C, N and O atoms were refined isotropically and were gathered together into groups with a common U_{iso} parameter for each group. H atoms were

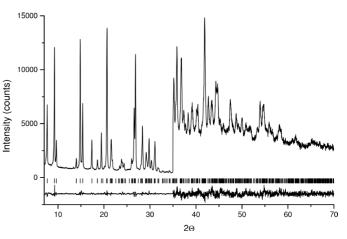


Figure 2

The Rietveld plot showing the observed and difference profiles. The reflection positions are shown above the difference profile. The high-angle area is magnified by a factor of ten.

placed in geometrically calculated positions and their isotropic displacement parameters were fixed at B = 6.0 Å². The planarity of the phenyl groups was restrained. The anisotropy of diffraction-line broadening was approximated by a quartic form in *hkl* (Popa, 1998). The standard uncertainties obtained from the Rietveld refinement were corrected for the serial correlation effects (Bérar & Lelann, 1991).

Data collection: local program; cell refinement: *LSPAID* (Visser, 1986); program(s) used to solve structure: *MRIA* (Zlokazov & Chernyshev, 1992); program(s) used to refine structure: *MRIA*; molecular graphics: *PLUTON* (Spek, 1992); software used to prepare material for publication: *PARST* (Nardelli, 1983).

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