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#### **Key indicators**

Single-crystal X-ray study T = 173 K Mean  $\sigma$ (C–C) = 0.001 Å Disorder in main residue R factor = 0.032 wR factor = 0.093 Data-to-parameter ratio = 14.2

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

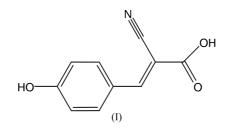
# The title compound, $C_{10}H_7NO_3$ , has an almost planar molecule, forming hydrogen-bonded dimers *via* the carboxyl groups. These dimers are further connected by hydrogen bonds between the hydroxy groups of the benzene rings and the cyano N atoms into ribbons, which are arranged in layers. The H atom of the carboxyl group is disordered over two sites.

2-Cyano-3-(4-hydroxyphenyl)acrylic acid

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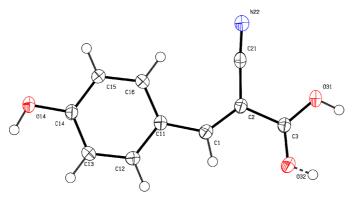
## Comment

The title compound (Fig. 1) has an almost planar molecule (the r.m.s. deviation for all non-H atoms is 0.053 Å). Two molecules form centrosymmetric hydrogen-bonded dimers *via* the carboxyl groups. These dimers are further connected into ribbons (Fig. 2) *via* hydrogen bonds between the hydroxy groups on the benzene rings and the cyano N atoms. These ribbons are arranged into layers perpendicular to [103] so that a two-dimensional structure is formed (Fig. 3). The interplanar distance is 3.12 Å.



## Experimental

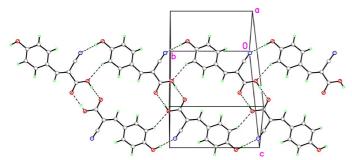
The title compound was prepared according to the procedure described by Karchgaudhuri *et al.* (2002).



## Figure 1

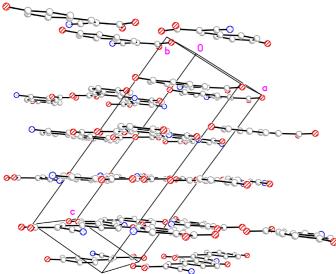
Perspective view of the title compound, with the atom numbering; displacement ellipsoids are shown at the 50% probability level. The bond of the disordered H atom with the minor site occupation factor is drawn with a broken line.

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## Figure 2

Packing diagram. View along [103]; only the major occupied site of the disordered hydroxy H atom is shown. Hydrogen bonding is indicated by broken lines.



#### Figure 3

Packing diagram. View approximately on to the ac plane. H atoms have been omitted.

#### Crystal data

	2
$C_{10}H_7NO_3$	$D_x = 1.473 \text{ Mg m}^{-3}$
$M_r = 189.17$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 508 reflections
a = 5.8182 (5)  Å	$\theta = 3.4-20.9^{\circ}$
b = 9.5061 (7) Å	$\mu = 0.11 \text{ mm}^{-1}$
c = 15.461 (1) Å	T = 173 (2) K
$\beta = 93.890 \ (6)^{\circ}$	Block, yellow
V = 853.15 (11) Å <sup>3</sup>	$0.52 \times 0.48 \times 0.32 \text{ mm}$
Z = 4	
Data collection	
Siemens SMART CCD	1798 reflections with $I > 2\sigma(I)$
diffractometer	$R_{\rm int} = 0.021$
$\omega$ scans	$\theta_{\rm max} = 28.7^{\circ}$
Absorption correction: none	$h = -7 \rightarrow 7$

Absorption correction: none 12 012 measured reflections 1986 independent reflections

 $k = -12 \rightarrow 11$  $l = -20 \rightarrow 20$ 

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + ($
$R[F^2 > 2\sigma(F^2)] = 0.033$	+ 0.1987P]
$wR(F^2) = 0.093$	where $P = (F_o^2)^2$
S = 1.05	$(\Delta/\sigma)_{\rm max} = 0.001$
1986 reflections	$\Delta \rho_{\text{max}} = 0.33 \text{ e Å}$
140 parameters	$\Delta \rho_{\rm min} = -0.20 \ {\rm e}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

### Table 1 Selected bond lengths (Å).

C1-C2	1.3551 (14)	C21-N22	1.1503 (14)
C2-C21	1.4309 (13)	C3-O32	1.2510 (12)
C2-C3	1.4831 (12)	C3-O31	1.2842 (13)

 $+ (0.0546P)^2$ 

-3

еÅ

 $+ 2F_{c}^{2})/3$ 

## Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\begin{array}{c} O14 - H14 \cdots N22^{i} \\ O31 - H31 \cdots O32^{ii} \\ O32 - H32 \cdots O31^{ii} \end{array}$	0.910 (17)	1.934 (17)	2.8435 (12)	177.2 (15)
	0.81 (3)	1.79 (3)	2.5967 (10)	176 (2)
	0.83 (6)	1.77 (6)	2.5967 (10)	173 (4)

Symmetry codes: (i) x, y + 1, z; (ii) -x, -y, -z + 1.

All H atoms were found in a difference map. Those bonded to C atoms were refined with fixed individual displacement parameters  $[U_{iso}(H) = 1.2U_{eq}(C)]$  using a riding model with  $C_{aromatic} - H = 0.95$  Å, H atoms bonded to O atoms were refined freely. The H atom of the carboxyl group is disordered over two sites. The ratio of the site occupation factors of the disordered H atoms refined to 0.63 (5)/ 0.37 (5).

Data collection: SMART (Siemens, 1995); cell refinement: SMART; data reduction: SAINT (Siemens, 1995); program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: PLATON (Spek, 2003) and XP in SHELXTL (Sheldrick, 1991); software used to prepare material for publication: SHELXL97 and PLATON.

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