# organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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#### Key indicators

Single-crystal X-ray study T = 168 KMean  $\sigma$ (C–C) = 0.002 Å R factor = 0.039 wR factor = 0.100 Data-to-parameter ratio = 12.9

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the title compound,  $C_{10}H_7NO_3$ , the malamute ring is rotated by 52.75 (5)° with respect to the phenyl ring. There is a weak  $O-H\cdots O$  intermolecular hydrogen bond between the hydroxyl group and one of the malamute O atoms, with an

N-(4-Hydroxyphenyl)maleimide

Received 23 May 2002 Accepted 31 May 2002 Online 14 June 2002

#### Comment

 $O \cdots O$  distance of 2.820 (2) Å.

The title compound, (I), is an important building block in the formation of novel polymer materials (Park & Jang, 1992; Caulfield & Solomon, 1999). As shown in Fig. 1, the dihedral angle between the phenyl ring and the malamute ring is  $52.75(5)^{\circ}$ . The rotation of the malamute ring with respect to the phenyl ring can be attributed to the steric repulsion from adjacent carbonyl moieties. An example of a similar structure without carbonyls, 1-phenyl-3-carbethoxy-4-hydroxypyrroline, does not show this rotation of the five-membered ring relative to the phenyl group (Paulus & Rivo, 1988). The torsion angles C2-C1-N1-C10 and C6-C1-N1-C7 are 51.07 (14)° and 54.67 (14)°, respectively. The reason for two different torsion angles is that the malamute ring is tilted slightly away from the central axis of the molecule defined by the atoms O1, C4, C1, and N1. A packing diagram (Fig. 2) indicates that molecules stack along the *a* axis with identical orientation, aligning the phenyl and malamute rings.



The elongation of the N1–C1 bond relative to the other N–C bonds is consistent with single-bond nature of N attached to a phenyl ring (Table 1). The bond angles show a distorted trigonal planar coordination for N1. The C7–N1–C10 bond angle of 109.22 (14)° is consistent with a typical tetrahedral coordination. The C1–N1–C10 and C1–N1–C7 bond angles [125.55 (13) and 125.12 (13)°, respectively] reveal the distortion of the bonds away from a regular trigonal planar coordination.

Comparison of C–O bond lengths reveals the double-bond character of C7–O2 and C10–O3, compared to the single bond C4–O1. The slightly longer C7–O2 bond, relative to C10–O3, is attributed to the intermolecular hydrogen bond (Fig. 3 and Table 2), whereas the O3 atom has no hydrogen interaction (nearest H atom is H2 at 2.570 Å). The O1–

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Figure 1

Molecular structure of (I). Displacement ellipsoids are shown at the 50% probability level.

H1···O2 hydrogen bonds form a ribbon structure along the b axis.

## **Experimental**

The title compound, (I), was prepared in two steps. In the first step, 1 mole of maleic anhydride was reacted with 1 mole of 4-aminophenol in excess acetone. The product, *cis*-4-[(4-hydroxyphenyl)amino]-4-oxo-2-butenoic acid, was obtained in nearly quantitative yield as an insoluble yellow precipitate which was isolated by filtration and washed with excess acetone. 4-Hydroxyphenyl maleimide was then obtained in the second step by cyclodehydration. One mole of *cis*-4-[(4-hydroxyphenyl)amino]-4-oxo-2-butenoic acid, 0.26 mole of sulfuric acid, and 0.2 mole of phosphorus pentoxide were dissolved in excess dimethylformamide and reacted at 343 K for a minimum of 4 h. The solution was poured over ice to obtain crude product, (I), as a solid orange precipitate. The precipitate was isolated by filtration and washed with excess water and dried. The crystals of (I) were grown from an isopropyl alcohol solution; yield *ca* 60%. The melting point of the crystals is 455–457 K.

#### Crystal data

$C_{10}H_7NO_3$	$D_x = 1.489 \text{ Mg m}^{-3}$
$M_r = 189.17$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 753
$a = 3.864 (1) \text{ Å}_{2}$	reflections
b = 10.691 (3)  Å	$\theta = 2.0-23.3^{\circ}$
c = 20.461 (5)  Å	$\mu = 0.11 \text{ mm}^{-1}$
$\beta = 93.036 (5)^{\circ}$	T = 168 (2)  K
$V = 844.0 (4) \text{ Å}^3$	Needle, orange
Z = 4	$0.18 \times 0.08 \times 0.08 \text{ mm}$



Figure 2

Packing diagram for (I), viewed down the a axis.



#### Figure 3

Packing diagram showing the intermolecular hydrogen bond. Several molecules in the packing diagram were removed for clarity.

#### Data collection

Bruker AXS CCD diffractometer  $\omega$  and  $\varphi$  scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1999)

 $T_{min} = 0.94, T_{max} = 0.99$ 4735 measured reflections 1685 independent reflections

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.039$   $wR(F^2) = 0.100$  S = 1.031685 reflections 131 parameters 1252 reflections with  $I > 2\sigma(I)$   $R_{int} = 0.035$   $\theta_{max} = 26.2^{\circ}$   $h = -4 \rightarrow 3$   $k = -13 \rightarrow 13$  $l = -20 \rightarrow 25$ 

H atoms treated by a mixture of independent and constrained refinement  $w = 1/[\sigma^2(F_o^2) + (0.0506P)^2]$ where  $P = (F_o^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{max} = 0.002$  $\Delta\rho_{max} = 0.17 \text{ e } \text{\AA}^{-3}$  $\Delta\rho_{min} = -0.20 \text{ e } \text{\AA}^{-3}$ 

# Table 1

Selected geometric parameters (Å, °).

N1-C7	1.390 (2)	O3-C10	1.208 (2)
N1-C10	1.408 (2)	C7-C8	1.483 (2)
N1-C1	1.434 (2)	C8-C9	1.318 (2)
O1-C4	1.371 (2)	C9-C10	1.486 (2)
O2-C7	1.215 (2)		
C7-N1-C10	109.22 (14)	N1-C7-C8	106.66 (14)
C7-N1-C1	125.12 (13)	O3-C10-N1	124.72 (16)
C10-N1-C1	125.55 (13)	O3-C10-C9	128.99 (15)
O2-C7-N1	125.29 (16)	N1-C10-C9	106.29 (14)
O2-C7-C8	128.05 (16)		

Table 2		
Hydrogen-bonding geometry	(Å,	°).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O1-H1\cdots O2^i$	0.87 (2)	1.95 (2)	2.820 (2)	175.17 (15)
Symmetry code: (i)	$\frac{5}{2} - x, \frac{1}{2} + y, \frac{3}{2} - z$			

H-atom positions were idealized, with H atoms riding on the atoms to which they were attached. These idealized H atoms had their isotropic displacement parameters fixed at 1.2 or 1.5 times the  $U_{eq}$  of the C atoms to which they were bonded. The H1 hydrogen was the exception, in that it was located from a difference Fourier map; its atomic positional parameters and isotropic displacement parameter were refined.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SMART*; data reduction: *SAINT-Plus* (Bruker, 2001); program(s) used to solve structure: *SHELXTL* (Bruker, 1998); program(s) used to refine structure: *XSHELL* (Bruker, 2000); molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

Sandia is a multiprogram laboratory operated by Sandia Corporation, a Lockheed Martin Company, for the United States Department of Energy under contract DE-AC04-94AL85000. One of the authors (MAR) thanks Brian Scott of Los Alamos National Laboratory and Scott Bunge (Sandia) for useful discussions and aid in the preparation of this manuscript.

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