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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.003 Å R factor = 0.045 wR factor = 0.124 Data-to-parameter ratio = 15.9

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. 2-Amino-2'-chloro-5-methylbenzophenone

The title compound, $C_{14}H_{12}$ ClNO, was synthesized by the photo-Fries reaction of 2-chloro-*N*-(4-methylphenyl)benzamide in acetonitrile. The crystal structure contains intramolecular N-H···O and intermolecular N-H···O hydrogen bonds. Received 10 October 2005 Accepted 17 October 2005 Online 22 October 2005

Comment

The derivatives of benzophenone have been widely studied because of their extensive application in varied areas, such as medicine (Mahendra *et al.*, 2004; Wiesner *et al.*, 2003), materials (Wang & Lee, 2003) and photochemistry (Koshima *et al.*, 2003; Wrzyszczynshi *et al.*, 2003). They are mainly produced by Fridel–Crafts acylation. Some amine- or hydroxy-substituted derivatives are also prepared by the photo-Fries rearrangement (Mayouf, 2005; Sriraghavan, 2003). Recently, our group has focused on the effect of halogen on the photo-Fries rearrangement of related benzophenone derivatives. We present here the crystal structure of the photo-Fries product of N-(4-methylphenyl)-2-chlorobenzamide, *viz.* the title compound, (I).



The molecular structure of (I) is non-planar (Fig. 1). The dihedral angle between the two benzene rings is 96.2 (2)°, and the dihedral angles of the 2-chlorophenyl and 4-methylphenyl planes with the C7/C8/C9/N1/O1 plane [mean deviation of 0.0028 (2) Å] are 94.7 (3) and 1.8 (2)°, respectively. The C9–C8–C7–O1 and O1–C7–C6–C5 torsion angles are 1.0 (3) and 92.4 (2)°, respectively. The above results indicate that the carbonyl is almost coplanar with the 4-methylphenyl plane and nearly perpendicular to the 2-chlorophenyl plane.

As shown in Fig. 2, the carbonyl O atom acts as a double hydrogen-bond receptor, involved in not only an intramolecular $N-H \cdots O$ hydrogen bond with one amine H atom to form a six-membered ring, but also an intermolecular $N-H \cdots O$ hydrogen bond with another amine H atom of an adjacent molecule (Table 2). The molecules are linked into an infinite chain structure through the intermolecular hydrogen bonds.

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Experimental

The title compound was prepared by the photolysis of *N*-(4-methylphenyl)-2-chlorobenzamide (MPCB) in acetonitrile. A solution of MPCB (245 mg) in acetonitrile (100 ml) was irradiated under a 254 nm low-pressure mercury lamp for 7 h and then concentrated. The product was isolated by column chromatography (cyclohexane/dichloromethane, 7: 1 ν/ν). Single crystals of (I) suitable for X-ray analysis were obtained from a cyclohexane/dichloromethane (1:1) solution.

 $D_x = 1.283 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 2400

reflections

 $\theta = 3.0-25.6^{\circ}$

 $\mu = 0.28~\mathrm{mm}^{-1}$

T = 294 (2) K Block, light yellow $0.28 \times 0.22 \times 0.14$ mm

 $\begin{aligned} R_{\text{int}} &= 0.027\\ \theta_{\text{max}} &= 26.4^{\circ}\\ h &= -12 \rightarrow 12\\ k &= -12 \rightarrow 13\\ l &= -6 \rightarrow 14 \end{aligned}$

2595 independent reflections 1758 reflections with $I > 2\sigma(I)$

Crystal data

$C_{14}H_{12}CINO$
$M_r = 245.70$
Monoclinic, $P2_1/c$
a = 10.3419 (19) Å
b = 10.892 (2) Å
c = 11.592 (2) Å
$\beta = 102.982 \ (3)^{\circ}$
V = 1272.4 (4) Å ³
Z = 4

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\min} = 0.908, T_{\max} = 0.961$
7003 measured reflections

Refinement

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Refinement on F^2
w = 1/[\sigma^2(F_o^2) + (0.056P)^2 + 0.3319P]

R[F^2 > 2\sigma(F^2)] = 0.045
w = 1/[\sigma^2(F_o^2) + (0.056P)^2 + 0.3319P]

wR(F^2) = 0.124
where P = (F_o^2 + 2F_c^2)/3

S = 1.03
(\Delta/\sigma)_{max} = 0.001

2595 reflections
\Delta\rho_{max} = 0.20 \text{ e Å}^{-3}

163 parameters
\Delta\rho_{min} = -0.34 \text{ e Å}^{-3}

H atoms treated by a mixture of independent and constrained refinement
A^{\rho_{max}} = 0.20 \text{ e Å}^{-3}
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Table 1

Selected geometric parameters (Å, °).

Cl1-C1	1.740 (2)	N1-C9	1.346 (3)
O1-C7	1.239 (2)		
C5-C6-C7-O1	-92.4 (2)	O1-C7-C8-C9	-1.0 (3)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1B \cdots O1$	0.89 (3)	2.03 (3)	2.691 (3)	131 (2)
$N1-H1A\cdotsO1^{i}$	0.92 (3)	2.20 (3)	3.121 (3)	172 (2)

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

All H atoms were initially located in a difference Fourier map. The C–H atoms were then constrained to an ideal geometry, with C_{methyl} –H distances of 0.96 Å, $C_{aromatic}$ –H distances of 0.93 Å, and



Figure 1

The structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 35% probability level. The intramolecular hydrogen bond is shown as a dashed line.



Figure 2

Packing view of (I), showing the inter- and intramolecular hydrogen bonds as dashed lines.

 $U_{iso}(H) = 1.2U_{eq}(C_{aromatic})$ or $1.5U_{eq}(C_{methyl})$. The amine H atoms were refined with the restraint N-H = 0.89 (3) Å.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; 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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