Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.002 Å R factor = 0.045 wR factor = 0.124 Data-to-parameter ratio = 15.2

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

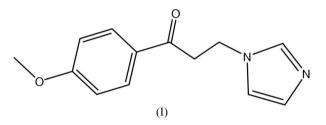
3-(1*H*-Imidazol-1-yl)-1-(4-methoxyphenyl)propan-1-one

In the title compound, $C_{13}H_{14}N_2O_2$, molecules are linked into zigzag layers by intermolecular $C-H\cdots O$ and $C-H\cdots N$ hydrogen bonds. The packing is further stabilized by weak $C-H\cdots \pi$ interactions, forming a three-dimensional framework.

Received 20 June 2005 Accepted 12 July 2005 Online 16 July 2005

Comment

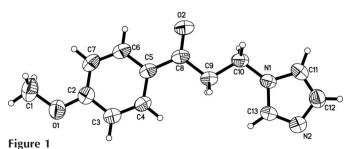
In the title compound, (I) (Fig. 1), the bond lengths and angles are within normal ranges (Allen *et al.*, 1987) and compare well with those reported in a related compound (Wan *et al.*, 2005). The whole molecule is nearly planar, the largest deviation being 0.074 (1) Å for C11. However, the two aromatic rings are slightly twisted with respect to each other by a dihedral angle of 5.25 (9)°.



In the crystal structure, molecules are linked into zigzag layers by intermolecular $C-H\cdots O$ and $C-H\cdots N$ hydrogen bonds (Fig. 2 and Table 1). The packing is further stabilized by weak $C-H\cdots \pi$ interactions (Table 1), leading to a three-dimensional network.

Experimental

To a solution of 3-(dimethylamino)-1-(4-methoxyphenyl)propan-1one (10.3 g, 0.05 mol) in water (25 ml) was added imidazole (4.4 g, 0.06 mol). The mixture was heated under reflux for 4 h, yielding a copious precipitate. Colorless single crystals suitable for X-ray diffraction study were obtained by slow evaporation of an ethyl acetate-petroleum ether (1:1 ν/ν) solution over a period of two weeks.



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organic papers

Crystal data

 $\begin{array}{l} C_{13}H_{14}N_2O_2\\ M_r = 230.26\\ Monoclinic, \ C2/c\\ a = 21.349\ (6)\ Å\\ b = 5.2657\ (14)\ Å\\ c = 21.303\ (6)\ Å\\ \beta = 97.600\ (4)^\circ\\ V = 2373.8\ (11)\ Å^3\\ Z = 8 \end{array}$

Data collection

Siemens SMART 1000 CCD areadetector diffractometer ω scans Absorption correction: multi-scan (using intensity measurements) (*SADABS*; Sheldrick, 1996) $T_{min} = 0.958, T_{max} = 0.990$ 6335 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.045$ $wR(F^2) = 0.124$ S = 1.022343 reflections 154 parameters H-atom parameters constrained

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$C11-H11A\cdots O2^{i}$	0.93	2.45	3.328 (2)	158
$C13-H13A\cdots N2^{ii}$	0.93	2.50	3.418 (2)	170
$C1 - H1A \cdots Cg1^{iii}$	0.96	2.75	3.782	151
$C1 - H1B \cdots Cg2^{iv}$	0.97	2.78	3.622	146
$C9-H9A\cdots Cg1^{iv}$	0.97	2.85	3.709	142
$C9-H9B\cdots Cg2^{v}$	0.97	2.81	3.629	142
Symmetry codes: $-x + \frac{1}{2}, y + \frac{3}{2}, -z - \frac{1}{2}$; (iv	(i) $-x, y - z$ (i) $x, y + 1, z$; (v)		i) $-x + \frac{1}{2}, y + \frac{1}{2}$	$, -z + \frac{1}{2};$ (iii)

 $D_x = 1.289 \text{ Mg m}^{-3}$

Cell parameters from 1951

Mo $K\alpha$ radiation

reflections

 $\theta = 2.5 - 24.7^{\circ}$ $\mu = 0.09 \text{ mm}^{-1}$

T = 293 (2) K

 $R_{\rm int} = 0.021$ $\theta_{\rm max} = 26.1^{\circ}$

 $h = -25 \rightarrow 26$

 $k = -6 \rightarrow 6$

 $l = -19 \rightarrow 25$

Needle, colorless

 $0.49 \times 0.21 \times 0.11 \ \mathrm{mm}$

2343 independent reflections 1855 reflections with $I > 2\sigma(I)$

 $w = 1/[\sigma^2(F_o^2) + (0.0662P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

+ 0.6137P]

 $\Delta \rho_{\rm max} = 0.14 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.21 \text{ e } \text{\AA}^{-3}$

 $(\Delta/\sigma)_{\rm max} < 0.001$

All H atoms were located in difference Fourier maps and constrained to ride on their parent atoms, with C-H distances in the range 0.93–0.97 Å and with $U_{iso}(H) = 1.2-1.5U_{eq}(C)$.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve

Figure 2

A view down the *b* axis. $C-H\cdots O$ and $C-H\cdots N$ hydrogen bonds are indicated by dashed lines.

structure: *SHELXTL* (Sheldrick, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*, *PARST* (Nardelli, 1995) and *PLATON* (Spek, 2003).

This project was supported by the Program for New Century Excellent Talents in University (No. NCET-04–0649), the Project of Educational Administration of Shandong Province (No. J04B12).

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