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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.002 Å R factor = 0.038 wR factor = 0.117 Data-to-parameter ratio = 13.1

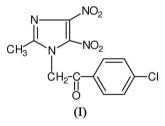
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

1-(4-Chlorophenacyl)-2-methyl-4,5-dinitro-1*H*-imidazole

In the title compound, $C_{12}H_9ClN_4O_5$, both nitro groups are rotated significantly from the imidazole plane. The C-4–NO₂ bond length is only slightly shorter than the value for a normal single Csp^2 –NO₂ bond and the C-5–NO₂ bond length is significantly shorter than C-4–NO₂. In consequence, the C-4nitro group is easily replaced by morpholine, while the C-5nitro group shows an extraordinary stability on treatment with the amine. In the crystal structure, the molecules are linked through C–H···O hydrogen bonds.

Comment

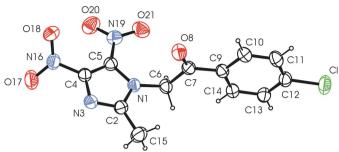
1-(4-Chlorophenacyl)-2-methyl-4,5-dinitroimidazole, (I), has been used as a substrate in nucleophilic substitution with morpholine. The only product isolated from the reaction mixture was 1-(4-chlorophenacyl)-2-methyl-4-morpholino-5nitroimidazole, even when the amine was used in sixfold excess at elevated reaction temperature (Zaprutko *et al.*, 1989). In order to explain the behaviour of the nitro groups in the reaction with morpholine, compound (I) was subjected to an X-ray crystallographic study.



Results of the X-ray analysis show that the C4- and C5-nitro groups subtend different interplanar angles of 46.16 (10) and 14.9 (3) $^{\circ}$, respectively, to the imidazole ring. Some differences are also noted in the exocyclic $C-NO_2$ bond distances. The C4–N16 distance of 1.445 (2) Å is longer than the C5–N19 bond of 1.424 (2) Å by about 7σ . The former is only slightly shortened with respect to the normal length of the $Csp^2 - NO_2$ bond of 1.468 (1) Å (Allen et al., 1987). This observation indicates weak conjugation between the C5-nitro group and the imidazole ring, despite the rotation of this substituent from the five-membered heterocyclic ring plane by about 15°. The dihedral angles between the nitro groups and the imidazole ring observed in compound (I) have also been noted in 3chloro-1-(4,5-dinitroimidazol-1-yl)propan-2-ol (Gzella et al., 1999) $[C4-NO_2 = 20.3 (2)^\circ \text{ and } C5-NO_2 = 42.8 (1)^\circ]$. In spite of that, the lengths of the bonds $C-NO_2$ in the two nitro groups are comparable $[C4-NO_2 = 1.442 (3) \text{ Å} and C5 NO_2 = 1.448 (4) \text{ Å}$ and are similar to the C4–N16 bond distance of (I). It should be emphasized that in 3-chloro-1Received 28 April 2006 Accepted 2 May 2006

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The molecular structure of (I), showing the atomic labelling scheme. Non-H atoms are drawn as 30% probability displacement ellipsoids.

(4,5-dinitroimidazol-1-yl)propan-2-ol, both nitro groups are exchanged for a morpholine residue. As follows from the above discussion, the inability of the C5-nitro group in compound (I) to undergo nucleophilic substitution is mainly a result of the shortening of the C $-NO_2$ bond and, to a lower degree, its orientation.

The C6/C7/O8/C9 fragment of the chlorophenacyl substituent is flat and approximately perpendicular to the imidazole ring [dihedral angle = 84.83 (6)°]. The phenyl ring is twisted by 5.69 (13)° from the C6/C7/O8/C9 plane and makes a dihedral angle of 83.44 (5)° with the imidazole ring. This mutual arrangement of these systems is frequently observed in other phenacyl derivatives of imidazole (Borowiak *et al.*, 1989; Wolska *et al.*, 1991, 1993, 1994; Zaprutko *et al.*, 2003). The group C7=O8 belonging to the phenacyl system assumes a synperiplanar conformation with respect to the N1–C6 bond [N1–C6–C7–O8 = 5.5 (2)°].

In the crystal structure of (I), the molecules are connected by $C-H\cdots O$ hydrogen bonds, forming a two-dimensional hydrogen-bond network parallel to the *bc* plane (Table 1 and Fig. 2).

Experimental

Compound (I) was synthesized according to the literature procedure of Zaprutko *et al.*, (1989). Crystals suitable for single-crystal X-ray diffraction analysis were grown by slow evaporation of a methanol solution.

Z = 8

 $D_r = 1.572 \text{ Mg m}^{-3}$

Cu Ka radiation

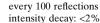
 $\mu = 2.78 \text{ mm}^{-1}$ T = 293 (2) K

Crystal data

C12H9ClN4O5
$M_r = 324.68$
Monoclinic, C2/c
a = 20.094 (3) Å
b = 9.4907 (14) Å
c = 15.0418 (17) Å
$\beta = 106.953 \ (12)^{\circ}$
$V = 2743.9 (7) \text{ Å}^3$

Data collection

Kuma KM-4 diffractometer ω -2 θ scans Absorption correction: ψ scan (North *et al.*, 1968) $T_{min} = 0.203$, $T_{max} = 0.459$ 5181 measured reflections 2615 independent reflections Prism, yellow $0.60 \times 0.30 \times 0.28 \text{ mm}$ 2316 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.024$ $\theta_{\text{max}} = 70.1^{\circ}$ 2 standard reflections



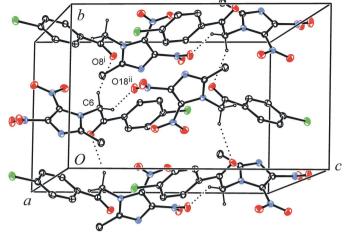


Figure 2

The hydrogen bonding (dotted lines) in (I) [symmetry codes: (i) $\frac{3}{2} - x$, $\frac{1}{2} + y$, $\frac{1}{2} - z$; (ii) x, 1 - y, $\frac{1}{2} - z$]. H atoms not involved in hydrogen bonds have been omitted for clarity.

Refinement

 $\begin{array}{ll} \mbox{Refinement on } F^2 & w = 1/[\sigma^2(F_o^2) + (0.0681P)^2 \\ R[F^2 > 2\sigma(F^2)] = 0.038 & w = 0.8575P] \\ wR(F^2) = 0.117 & where $P = (F_o^2 + 2F_c^2)/3$ \\ S = 1.03 & (\Delta/\sigma)_{max} = 0.001 \\ 2615 \mbox{ reflections } & \Delta\rho_{max} = 0.31 \mbox{ e } {\rm \AA}^{-3} \\ 200 \mbox{ parameters constrained } & \Delta\rho_{min} = -0.21 \mbox{ e } {\rm \AA}^{-3} \\ \end{array}$

 Table 1

 Hydrogen-bond geometry (Å, °).

$D - \mathbf{H} \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
C6-H6B···O21	0.97	2.34	2.803 (2)	108
$C6-H6B\cdotsO8^{i}$	0.97	2.54	3.427 (2)	152
$C6-H6A\cdots O18^{ii}$	0.97	2.37	3.178 (2)	140

Symmetry codes: (i) $-x + \frac{3}{2}$, $y + \frac{1}{2}$, $-z + \frac{1}{2}$; (ii) x, -y + 1, $z + \frac{1}{2}$.

All H atoms were placed in geometrically calculated positions and were refined using a riding model, with C–H = 0.93–0.97 Å and $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$ or $1.5U_{\rm eq}({\rm C})$ for methyl H atoms. The methyl group was refined as a rigid group, which was allowed to rotate.

Data collection: *KM-4 Software* (Kuma, 1996); cell refinement: *KM-4 Software*; data reduction: *KM-4 Software*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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