3-Nitroso-2-phenylimidazo[1,2-a]pyrimidine

Abderahmane Anaflous,[a]
Nour-Eddine Benchat,[a] **Taibi**
Ben-Hadda,[a] **Brahim El Bali**[b] **and**
Michael Bolte[c]*****

[a]Department of Chemistry, Faculty of Sciences, University Mohamed I, 60000 Oujda, Morocco, [b]Département de Chimie, Faculté des Sciences Dhar Mehraz, Université Sidi Mohamed Ben Abdellah, 30000 Fès, Morocco, and [c]Institut für Anorganische Chemie, J. W. Goethe-Universität Frankfurt, Marie-Curie-Straße 11, 60439 Frankfurt/Main, Germany

Correspondence e-mail:
bolte@chemie.uni-frankfurt.de

Key indicators

Single-crystal X-ray study
T = 173 K
Mean σ(C–C) = 0.004 Å
R factor = 0.054
wR factor = 0.140
Data-to-parameter ratio = 11.9

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

The title compound, $C_{12}H_8N_4O$, is of pharmacological interest. It contains an imidazo[1,2-a]pyrimidine heterocycle, carrying a nitroso group in position 3 and a phenyl group in position 2. Both substituents are almost coplanar with the heterocycle.

Comment

Functionalized imidazo[1,2-a]pyrimidines (IPM) have emerged as potentially interesting drugs, particularly with regard to their antimicrobial activity (Revanker et al., 1975; Rival et al., 1992), but also for their analgesic, antipyretic and anti-inflammatory properties as well as their use against ulcers (Abignente et al., 1987; Vidal et al., 2001). Antimicrobial screening of imidazo[1,2-a]pyrimidine derivatives has been undertaken. The studies showed that compounds bearing a formyl, hydroxy or nitroso side chain in position 3 are highly active (Benchat et al., 2001). From general structure–activity relationship observations, it appears that functionalized side chain(s) characterized by arms such as $[X-(C)_n-Y]$, where X,Y = O, N or S, and n = 2 or 3, are crucial for bioactivity. These atoms or centres that have critical interactions with the bacterial cell receptor constitute the pharmacophore and are vital for antimicrobial activities. These interactions have typically precise geometric requirements that are readily described in terms of the distances between the atoms and their orientation in the pharmacophore. In continuation of this line of investigations, we have synthesized (I), which will be subjected to further pharmacological investigations, especially tests of its antipsychotic activity. Compound (I) is stable at ambient temperature. Its structure has been determined by IR, MS and NMR (^{1}H and ^{13}C) spectroscopy. Since these techniques did not provide sufficient information about the conformation of the reaction product, we carried out the X-ray structure analysis, described in this paper.

(I)
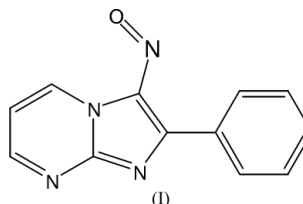
Bond lengths and angles of (I) do not show any unusual values. The phenyl and nitroso groups are almost coplanar with the imidazo[1,2-a]pyrimidine moiety (Table 1). The molecules crystallize in parallel stacks along the *a* axis (Fig. 2). The molecules in a stack are related by centres of inversion. The crystal packing is stabilized by several short C—H···O and C—H···N contacts (see Table 2).
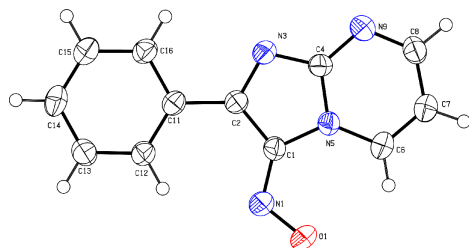
Figure 1
Perspective view of the title compound, with the atom numbering; displacement ellipsoids are drawn at the 50% probability level.
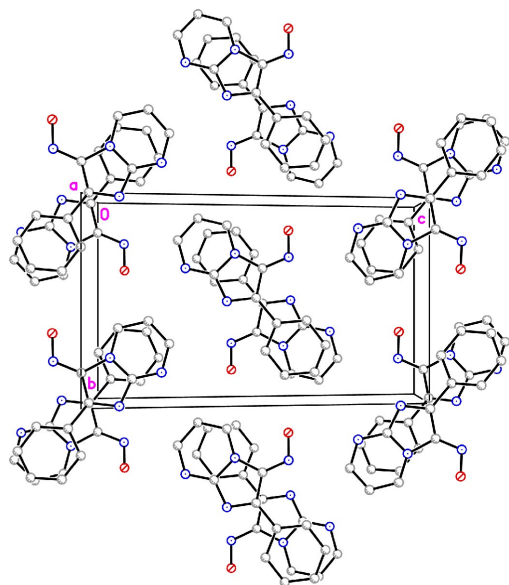

Figure 2
Packing of the title compound, viewed along the *a* axis. H atoms have been omitted.

Experimental

The synthesis of 3-nitroso-2-phenylimidazo[1,2-*a*]pyrimidine, (I), involved the condensation of the unsubstituted 2-aminopyrimidine intermediate with the chlorinated precursor Cl—CH$_2$—CO—C$_6$H$_5$ in boiling ethanol. The reaction gives a good yield of 2-phenyl-imidazo[1,2-*a*]pyrimidine. This derivative was then functionalized with a nitroso group at position 3 by treatment with sodium nitrite in acetic acid (Grassy & Rival, 1985; Rival *et al.*, 1991). Compound (I) was crystallized from CCl$_4$.

Crystal data

C$_{12}$H$_8$N$_4$O	$D_x = 1.485$ Mg m^{-3}
$M_r = 224.22$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 3097
$a = 7.0734$ (16) Å	reflections
$b = 9.2564$ (16) Å	$\theta = 3.5$–25.4°
$c = 15.704$ (4) Å	$\mu = 0.10$ mm^{-1}
$\beta = 102.755$ (18)°	$T = 173$ (2) K
$V = 1002.8$ (4) Å^3	Block, green
$Z = 4$	$0.21 \times 0.17 \times 0.15$ mm

Data collection

Stoe IPDS-II two-circle diffractometer	1051 reflections with $I > 2\sigma(I)$
ω scans	$R_{int} = 0.080$
Absorption correction: none	$\theta_{max} = 25.5°$
4715 measured reflections	$h = -5 \rightarrow 8$
1832 independent reflections	$k = -11 \rightarrow 11$
	$l = -18 \rightarrow 18$

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.054$	$w = 1/[\sigma^2(F_o^2) + (0.0722P)^2]$
$wR(F^2) = 0.140$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 0.88$	$(\Delta/\sigma)_{max} < 0.001$
1832 reflections	$\Delta\rho_{max} = 0.20$ e Å^{-3}
154 parameters	$\Delta\rho_{min} = -0.24$ e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

O1—N1	1.276 (3)	C4—N9	1.329 (4)
N1—C1	1.340 (4)	C4—N5	1.386 (4)
C1—N5	1.411 (4)	N5—C6	1.370 (4)
C2—N3	1.348 (4)	C8—N9	1.334 (4)
N3—C4	1.354 (4)		
O1—N1—C1	115.6 (2)	C6—N5—C1	132.6 (2)
C2—N3—C4	106.5 (2)	C4—N5—C1	106.7 (2)
C6—N5—C4	120.7 (2)	C4—N9—C8	115.8 (3)
O1—N1—C1—N5	−2.8 (5)	C1—C2—C11—C12	−2.0 (5)
O1—N1—C1—C2	177.7 (3)	N3—C2—C11—C16	−2.6 (4)
N3—C2—C11—C12	177.7 (3)	C1—C2—C11—C16	177.7 (3)

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

D—H⋯A	D—H	H⋯A	D⋯A	D—H⋯A
C6—H6⋯O1	0.95	2.36	2.860 (4)	113
C6—H6⋯O1^i	0.95	2.56	3.211 (4)	126
C12—H12⋯N1	0.95	2.36	3.034 (4)	127
C13—H13⋯O1^{ii}	0.95	2.51	3.458 (4)	172
C16—H16⋯N3	0.95	2.49	2.825 (4)	101

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

H atoms were refined with fixed individual displacement parameters [$U(H) = 1.2U_{eq}(C)$], using a riding model with C—H = 0.95 Å.

Data collection: *X-AREA* (Stoe & Cie, 2001); cell refinement: *X-AREA*; data reduction: *X-AREA*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL-Plus* (Sheldrick, 1991) and *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL*97 and *PLATON*.

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