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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.035 wR factor = 0.094 Data-to-parameter ratio = 12.5

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

© 2006 International Union of Crystallography All rights reserved N-(2-Hydroxyphenyl)-N'-phenethyl succinamide

Molecules of the title compound, $C_{18}H_{20}N_2O_3$, adopt a rodlike shape, probably influenced by $N-H\cdots O$ and $O-H\cdots O$ intermolecular hydrogen bonds, which also determine the formation of polymeric chains along the glide direction. Received 20 September 2006 Accepted 1 November 2006

Comment

 β -Phenylethylamide 2-hydroxisuccinanilic acid (phensuccinal) is a novel prospective pharmacological agent which possesses antidiabetogenic effects due to the stimulation of pancreatic β -cell regeneration and to its antioxidant effect in animals with heterogeneous insulin insufficiency (Poltorack *et al.*, 1995). Knowledge of its molecular and crystal structure might be important in order to design other pharmaceutically acceptable forms.

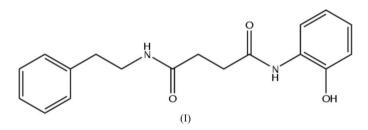
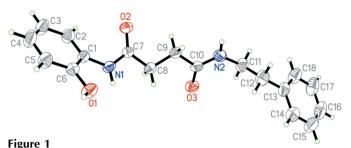


Fig. 1 shows a perspective view of the title molecule, (I). The central amide fragment and the C11 atom are coplanar within 0.01 Å, in spite of the short intramolecular contact $H9B \cdot \cdot \cdot H2N$ [2.30 Å; sum of van der Waals radii is 2.34 Å (Zefirov & Zorky, 1995)]. The methylenephenyl substituent at atom C11 is oriented almost orthogonal to the C10-N2 bond [the C10-N2-C11-C12 torsion angle is $-106.4 (2)^{\circ}$]. The phenyl substituent adopts an ap conformation relative to the C11-N2 bond [the N2-C11-C12-C13 torsion angle is $175.5 (2)^{\circ}$ and is twisted with respect to the C11-C12 bond [the C11-C12-C13-C18 torsion angle is $46.4 (2)^{\circ}$]. Such an orientation of the phenyl ring is caused by the repulsion between the C11 and C12 methylene groups and the atoms of the aromatic ring, as suggested by the short intramolecular contacts C11···H18 (2.76 Å; sum of van der Waals radii 2.87 Å), H11A···C18 (2.80 Å), H12A···H14 (2.31 Å; sum of van der Waals radii 2.34 Å), H11A···H18 (2.32 Å). The carbonyl groups of the two amide fragments are oriented in opposite directions and are twisted slightly with respect to the C8-C9 bond [the O2-C7-C8-C9 and O3-C10-C9-C8 torsion angles are -176.0(1) and $13.4(2)^{\circ}$, respectively]. The hydroxyphenyl substituent has an ap orientation relative to the C8–C7 bond and is essentially non-coplanar with respect to the carbamide fragment [the C1-N1-C7-C8 and C7-



The molecular structure of the title compound. The non-H atoms are shown with displacement ellipsoids drawn at the 50% probability level.

N1-C1-C2 torsion angles are -174.8(1) and $36.6(2)^{\circ}$, respectively]. This is probably caused by the short intramolecular contacts C7···H2 (2.85 Å; sum of van der Waals radii), O2···C2 (2.94 Å; sum of van der Waals radii 3.00 Å), H1N···O1 (2.38 Å; sum of van der Waals radii 2.45 Å).

The molecules of the title compound form polymeric chains along the *c*- axis direction (Fig. 2) due to the formation of N– $H \cdots O$ and $O-H \cdots O$ intermolecular hydrogen bonds (Table 2). This, probably, results in an elongation of the N1– C7 and O3–C10 bonds (Table 1) compared with their mean values of 1.334 and 1.210 Å (Bürgi & Dunitz, 1994), respectively, and the shortening of the N2–C10 and N2–C11 bonds (mean values are 1.334 and 1.469 Å, respectively). Finally, there is a short intramolecular contact H1 $N \cdots$ H8B (2.21 Å; sum of van der Waals radii 2.34 Å). The formation of intermolecular hydrogen bonds is probably a stabilizing factor for the elongated rod-like shape of the molecules.

Experimental

The title compound was prepared according to Patent 36464 A Ukraine (2001). Crystals suitable for X-ray analysis were obtained by crystallization from isopropanol.

Crystal data

 $\begin{array}{l} C_{18}H_{20}N_2O_3\\ M_r = 312.36\\ \text{Monoclinic, } P2_1/c\\ a = 19.630 \ (4) \ \text{\AA}\\ b = 5.1128 \ (8) \ \text{\AA}\\ c = 17.326 \ (4) \ \text{\AA}\\ \beta = 114.17 \ (2)^\circ\\ V = 1586.5 \ (6) \ \text{\AA}^3 \end{array}$

Data collection

Oxford Diffraction Xcalibur-3 diffractometer ω scans Absorption correction: none 9600 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.035$ $wR(F^2) = 0.094$ S = 0.982755 reflections 220 parameters Z = 4 $D_x = 1.308 \text{ Mg m}^{-3}$ Mo K\alpha radiation $\mu = 0.09 \text{ mm}^{-1}$ T = 293 (2) KPlate, colourless $0.30 \times 0.20 \times 0.05 \text{ mm}$

2755 independent reflections 1954 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.019$ $\theta_{\text{max}} = 25.0^{\circ}$

H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0589P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.18 \text{ e } \text{Å}^{-3}$ $\Delta\rho_{min} = -0.14 \text{ e } \text{Å}^{-3}$

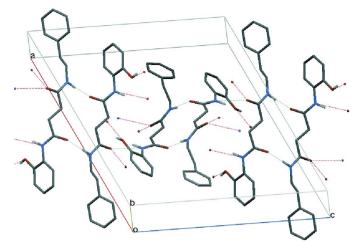


Figure 2

Partial packing view of the structure, showing the hydrogen-bonded (dashed lines) polymeric chains.

Table 1Selected bond lengths (Å).

N1-C7	1.3435 (18)	O1-C6	1.3551 (17)
N1-C1	1.4148 (18)	O2-C7	1.2246 (15)
N2-C10	1.3224 (19)	O3-C10	1.2428 (16)
N2-C11	1.4495 (19)	C7-C8	1.498 (2)

Table 2

Hydrogen-bond geometry (Å, °).

$\overline{D-\mathrm{H}\cdots A}$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$N1-H1N\cdotsO3^{i}$ $O1-H1O\cdotsO3^{ii}$ $N2-H2N\cdotsO2^{iii}$	0.816 (15) 0.84 (2) 0.836 (16)	2.224 (15) 1.88 (2) 2.094 (17)	2.9615 (17) 2.6648 (15) 2.9254 (18)	150.6 (13) 156 (2) 173.0 (15)
Symmetry codes: -x + 1, -y + 1, -z + 1		$-\frac{1}{2}, -z + \frac{3}{2};$ (ii)	$-x+1, y-\frac{3}{2},$	$-z + \frac{3}{2};$ (iii)

H atoms involved in hydrogen bonding were located in difference maps and refined with isotropic displacement factors [final N–H = 0.816 (15) and 0.836 (16) Å, and O–H = 0.84 (2) Å]; those attached to carbon were positioned geometrically (C–H = 0.93 or 0.97 Å) and allowed to ride, with $U_{\rm iso}(\rm H) = 1.2U_{eq}(\rm C)$.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2006); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2006); data reduction: *CrysAlis RED*; program(s) used to solve and refine structure: *SHELXTL* (Sheldrick, 1998); molecular graphics: *XP* (Siemens, 1998); software used to prepare material for publication: *SHELXTL*.

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