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Andrzej Gzella,^a* Maria Chrzanowska,^b Agnieszka Dreas,^b Michał S. Kaczmarek^c and Zenon Woźniak^c

^aDepartment of Organic Chemistry, Poznań University of Medical Sciences, ul. Grunwaldzka 6, 60-780 Poznań, Poland, ^bFaculty of Chemistry, A. Mickiewicz University, ul. Grunwaldzka 6, 60-780 Poznań, Poland, and ^cOptics Division, Faculty of Physics, A. Mickiewicz University, ul. Umultowska 85, 61-614 Poznań, Poland

Correspondence e-mail: akgzella@amp.edu.pl

Key indicators

Single-crystal X-ray study T = 293 KMean $\sigma(C-C) = 0.002 \text{ Å}$ R factor = 0.029 wR factor = 0.087 Data-to-parameter ratio = 13.9

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(3*R*,4*R*)-(–)-3-Hydroxymethyl-4-phenyl-2-o-toluoyl-1,2,3,4-tetrahydroisoquinoline

The absolute configuration of the title compound, $C_{24}H_{23}NO_2$, has been confirmed as 3R,4R. The hydroxymethyl group and phenyl ring at the asymmetric C atoms exhibit α and β orientations, respectively, and the non-planar heterocyclic ring of the tetrahydroisoquinoline system adopts an envelope conformation. The crystal structure is stabilized through hydrogen bonds.

Comment

The title compound, (I), was obtained from the reaction of (3R,4R)-3-hydroxymethyl-4-phenyl-1,2,3,4-tetrahydroisoquinoline (Brózda *et al.*, 2000) and *o*-toluoyl chloride, according to the literature procedure of Chrzanowska *et al.* (2004). We have undertaken an X-ray crystallographic study in order to confirm the correctness of the absolute configuration of (I) which was proposed earlier on the basis of spectroscopic data by Chrzanowska *et al.* (2004), and present the results here.

The results obtained for (I) (Fig. 1) confirm the absolute configuration 3R,4R of the compound. The hydroxymethyl group at the asymmetric atom C3 exhibits an α -orientation, whereas the phenyl group at the asymmetric atom C4 is β -oriented. The substituents at C3 and C4 have a mutually *trans* configuration and occupy pseudo-axial positions with respect to the partially saturated pyridine ring, as seen in the angles of the C3–C20 and C4–C22 bond vectors to the C1/N2/C3/C4/C9/C10 ring-plane normal of 4.15 (8) and 14.40 (8)°, respectively [Cremer & Pople (1975); *PLATON* (Spek, 2003)]. The C20–C3–C4–C22 torsion angle of –168.54 (11)° reveals a mutual orientation between anticlinal and antiperiplanar of atom C20 in the hydroxymethyl group with respect to atom C22 of the phenyl group.

The non-planar partially hydrogenated pyridine ring has an envelope conformation, with puckering parameters (Cremer & Pople, 1975) of Q = 0.508 (1) Å, $\theta = 55.0 (1)^{\circ}$ and $\varphi = 297.07 (19)^{\circ}$. The deviation of atom C3 from the almost planar system of the other five atoms of the heterocyclic ring is 0.6963 (16) Å. The C=O group of the amide group is anti-

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Figure 1

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



Figure 2

The hydrogen bonding (dashed and dotted lines) in the crystal structure of (I). H atoms not involved in hydrogen bonds have been omitted for clarity. [Symmetry codes: (i) $-\frac{1}{2} + x, \frac{3}{2} - y, -z$; (ii) $\frac{1}{2} + x, \frac{5}{2} - y, -z$; (iii) $-\frac{1}{2} + x, \frac{5}{2} - y, -z.$]

periplanar with respect to the N2-C3 bond [torsion angle $178.18 (13)^{\circ}$]. The tertiary amide group (C1/N2/C3/C11/O12) and the benzene ring (C13-C18) are not conjugated, the dihedral angle between their mean planes being 84.88 (5)°. A lack of conjugation between these two groups is frequently observed in amides having aromatic rings at their carbon end (Gdaniec et al., 1979; Pływaczyk et al., 1984; Sugiura et al.,

Atom O21 of the hydroxyl group is synclinal with respect to the N2-C3 bond of the heterocyclic ring in the tetrahydroisoquinoline system [torsion angle N2-C3-C20-O21 = $67.55 (14)^{\circ}$]. We assume that this arrangement of atom O21 is stabilized by the intermolecular O21-H21...O12ⁱ hydrogen bond (Table 1), which links molecules into chains parallel to the *a* axis. An intermolecular $C23-H23\cdots O21^{ii}$ contact (Table 1) links neighbouring chains into a two-dimensional hydrogen-bond network parallel to the *ab* plane (Fig. 2).

Experimental

Compound (I) was synthesized according to the literature procedure of Chrzanowska *et al.* (2004) (m.p. 458–462 K). $[\alpha]_{\rm D} = -57.99$ (c 0.925, MeOH). A crystal suitable for single-crystal X-ray diffraction analysis was selected directly from the analytical sample.

Crystal data

C ₂₄ H ₂₃ NO ₂	Z = 4
$M_r = 357.43$	$D_x = 1.249 \text{ Mg m}^{-3}$
Orthorhombic, $P2_12_12_1$	Cu $K\alpha$ radiation
$a = 9.0424 (10) \text{ Å}_{a}$	$\mu = 0.62 \text{ mm}^{-1}$
b = 10.4114 (11) Å	T = 293 (2) K
c = 20.191 (2) Å	Block, colourless
V = 1900.9 (3) Å ³	$0.40 \times 0.20 \times 0.15 \text{ mm}$

 $R_{\rm int} = 0.013$

 $\theta_{\rm max} = 70.1^{\circ}$

2 standard reflections

every 100 reflections

intensity decay: <2%

Data collection

Kuma KM-4 diffractometer $\omega/2\theta$ scans Absorption correction: none 3740 measured reflections 3480 independent reflections 3297 reflections with $I > 2\sigma(I)$

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\rm max} = 0.001$
$R[F^2 > 2\sigma(F^2)] = 0.029$	$\Delta \rho_{\rm max} = 0.13 \ {\rm e} \ {\rm \AA}^{-3}$
$wR(F^2) = 0.087$	$\Delta \rho_{\rm min} = -0.09 \ {\rm e} \ {\rm \AA}^{-3}$
S = 1.07	Extinction correction: SHELXL97
3480 reflections	(Sheldrick, 1997)
250 parameters	Extinction coefficient: 0.0036 (4)
H atoms treated by a mixture of independent and constrained	Absolute structure: Flack (1983), 1403 Friedel pairs
refinement $w = 1/[\sigma^2(F_o^2) + (0.0537P)^2 + 0.1426P]$ where $P = (F_o^2 + 2F^2)/2$	Flack parameter: 0.0 (2)
where $r = (r_o + 2r_c)/3$	

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\begin{array}{c} 021 - H21 \cdots O12^{i} \\ C19 - H19C \cdots O21 \end{array}$	0.90 (2) 0.96	1.91 (2) 2.54	2.7907 (16) 3.290 (2)	165.0 (19) 135
$C23 - H23 \cdots O21^{n}$	0.93	2.52	3.2774 (19)	139
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Symmetry codes: (i) $x - \frac{1}{2}, -y + \frac{3}{2}, -z$; (ii) $x + \frac{1}{2}, -y + \frac{5}{2}, -z$.

The position of the hydroxyl H atom was obtained from a difference Fourier map and was refined freely. The remaining H atoms were positioned geometrically and were refined with a riding model, with C-H = 0.93–0.98 Å and with $U_{iso}(H) = 1.2U_{eq}(C)$, or $1.5U_{eq}(C)$

for methyl H. The methyl H atoms were refined as a rigid group, which was allowed to rotate. The absolute configuration of (I) was established by refinement of the Flack parameter (Flack, 1983). The rather large s.u. of the Flack parameter is due to the small contribution of atoms with significant anomalous dispersion effects.

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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