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Jing-Hua Li* and Chui-Pan Lin

College of Pharmaceutical Sciences, Zhejiang University of Technology, Hangzhou 310032, People's Republic of China

Correspondence e-mail: lijh@zjut.edu.cn

Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(C-C) = 0.003 \text{ Å}$ R factor = 0.049 wR factor = 0.166 Data-to-parameter ratio = 17.7

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

(*E*)-1-Ethoxycarbonyl-2-[(2-hydroxy-1-naphthyl)-(phenyl)methyliminio]propan-1-ide

In the title compound, $C_{23}H_{23}NO_3$, the amino, hydroxy and carbonyl groups are involved in hydrogen bonding, forming a dimer. The crystal packing is further stabilized by intermolecular π - π stacking.

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Comment

As early as the mid-20th century, Mario Betti reported the synthesis of the so-called Betti base by the reaction of benzaldehyde with 2-naphthol and ammonia followed by hydrolysis with hydrochloric acid (Betti, 1941). However, only in recent decades has its usefulness in asymmetric synthesis been recognized (Istvan *et al.*, 2004). As cheap resolving agents, chiral catalysts and optically active ligands, the Betti base and its derivatives are now widely used in organic synthesis (Istvan *et al.*, 2004). Chiral aminoalcohols are of importance in catalytic asymmetric synthesis (Pu *et al.*, 2001). Compound (I), prepared readily from the Betti base by treatment with ethyl acetoacetate, is one of the auxiliary-induced prochiral imino compounds which yields the corresponding chiral aminoalcohol after asymmetric hydrogenation.



In the structure of (I), atoms N2, C18, C19 and C20 are coplanar; this is illustrated clearly by the torsion angle N2–C18-C19-C20 of -2.20 (2)° (Fig. 1). Moreover, the mean plane through these four atoms is perpendicular to the phenyl ring plane, forming a dihedral angle of 89.89 (9)°. The dihedral angle between the naphthalene ring system and phenyl ring plane is 78.71 (6)°.

In the crystal structure, the amino, hydroxy and carbonyl groups are involved in hydrogen bonding. Amino atom N2 acts as hydrogen-bond donor, *via* atom H201, to atom O31 and O32, forming intramolecular hydrogen bonds. A centrosymmetric hydrogen-bond dimer centred at $(0, \frac{1}{2}, \frac{1}{2})$ is formed by the intermolecular hydrogen bond O31–H301…O32ⁱ [symmetry code: (i) -x, 1 - y, 1 - z] (Table 2 and Fig. 2). The crystal packing is further stabilized by intermolecular $\pi - \pi$ stacking. The naphthalene ring system and its symmetry-related partner at (1 - x, 1 - y, 1 - z) are parallel to one

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Figure 1

The molecular configuration and atom-numbering scheme for (I). Displacement ellipsoids are drawn at the 40% probability level. H atoms are drawn as spheres of arbitrary radius.

another, the distance between the centroids of the rings being 3.898 Å.

Experimental

To Betti base {or 1-[amino(phenyl)methyl]naphthalen-2-ol} (1.0 g, 2.8 mmol), methanol (20 ml) and ethyl acetoacetate (1.5 ml) were added with stirring at room temperature. Stirring was continued for 3 h at the same temperature to complete the reaction. The resulting mixture was concentrated *in vacuo* to about 3 ml, and the precipitated crystals were collected by filtration and washed with methanol twice (2 \times 0.8 ml) to give colourless crystals (1.41 g, yield 97%; m.p. 431–432 K), which were recrystallized from methanol.

Crystal data

C23H23NO3	Z = 2
$M_r = 361.44$	$D_x = 1.257$ M
Triclinic, $P\overline{1}$	Mo Kα radi
a = 9.602 (4) Å	Cell parame
b = 9.962 (5) Å	reflection
c = 10.899 (5) Å	$\theta = 3.1 - 27.6^{\circ}$
$\alpha = 100.775 \ (19)^{\circ}$	$\mu = 0.08 \text{ mm}$
$\beta = 109.714 \ (14)^{\circ}$	T = 298 (1)
$\gamma = 93.722 \ (18)^{\circ}$	Chunk, colo
V = 954.9 (7) Å ³	0.30×0.24

Data collection

Rigaku R-AXIS RAPID diffractometer ω scans Absorption correction: none 9527 measured reflections 4346 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.050$ $wR(F^2) = 0.166$ S = 1.004346 reflections 245 parameters H-atom parameters constrained $D_x = 1.257 \text{ Mg m}^{-3}$ Mo K α radiation Cell parameters from 7862 reflections $\theta = 3.1-27.6^{\circ}$ $\mu = 0.08 \text{ mm}^{-1}$ T = 298 (1) KChunk, colorless $0.30 \times 0.24 \times 0.18 \text{ mm}$

3124 reflections with $F^2 > 2\sigma(F^2)$ $R_{\text{int}} = 0.023$ $\theta_{\text{max}} = 27.5^{\circ}$ $h = -12 \rightarrow 11$ $k = -12 \rightarrow 12$ $l = -14 \rightarrow 14$

$$\begin{split} & w = 1/[0.0031 F_{\rm o}^{2} + \sigma(F_{\rm o}^{2})]/(4F_{\rm o}^{2}) \\ & (\Delta/\sigma)_{\rm max} < 0.001 \\ \Delta\rho_{\rm max} = 0.29 \ {\rm e} \ {\rm \AA}^{-3} \\ \Delta\rho_{\rm min} = -0.23 \ {\rm e} \ {\rm \AA}^{-3} \\ & {\rm Extinction \ correction: \ Larson} \\ & (1970) \\ & {\rm Extinction \ coefficient: \ 1.2 \ (4) \ \times \ 10^{2}} \end{split}$$



Figure 2

Partial packing digram for (I), showing the hydrogen-bonded (dashed line) dimer. [Symmetry code: (i) -x, 1 - y, 1 - z.]

Table 1

Selected bond lengths (Å).

O31-C11	1.3624 (17)	O33-C21	1.429 (2)
O32-C20	1.235 (2)	N2-C1	1.4675 (16)
O33-C20	1.350 (2)	N2-C18	1.333 (2)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O31 - H301 \cdots O32^{i}$	0.93	1.80	2.7182 (15)	170
N2-H201···O31	0.89	2.25	2.8182 (17)	122
N2-H201···O32	0.89	2.11	2.7634 (13)	129

Symmetry code: (i) -x, -y + 1, -z + 1.

The H atoms of the amino group and hydroxy groups were located in difference Fourier maps and included in the refinement based on the as-found N–H and O–H bond lengths, but their isotropic displacement parameters were initially refined, then fixed in the final stage. All other H atoms were placed in calculated positions, with C–H = 0.93–0.97 Å, and included in the refinement in the riding model, with $U_{iso}(H) = 1.2U_{eq}(carrier atom)$.

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/ MSC, 2004); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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