

Jens K. Bjernemose and
Andrew D. Bond*University of Southern Denmark, Department of
Chemistry, Campusvej 55, 5230 Odense,
Denmark

Correspondence e-mail: adb@chem.sdu.dk

Key indicators

Single-crystal X-ray study
 $T = 180$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
 R factor = 0.059
 wR factor = 0.147
Data-to-parameter ratio = 16.5For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.*meso*-1,2-Bis(pyridin-2-yl)ethane-1,2-diolIn the crystal structure of *meso*-1,2-bis(pyridin-2-yl)ethane-1,2-diol, $\text{C}_{12}\text{H}_{12}\text{N}_2\text{O}_2$, at 180 K, the molecules lie on inversion centres and are linked into ribbons by complementary $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds.

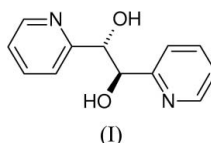
Received 14 February 2005

Accepted 16 February 2005

Online 26 February 2005

Comment

The title compound (I), $\text{C}_{12}\text{H}_{12}\text{N}_2\text{O}_2$ (Fig. 1), was obtained as a byproduct from the synthesis of the tetrapodal N_4 ligand *N,N*-bis[2-(pyridin-2-yl)ethyl]-*N*-[(pyridin-2-yl)methyl]amine (II), $\text{N}(\text{CH}_2\text{C}_5\text{H}_4\text{N})(\text{CH}_2\text{CH}_2\text{C}_5\text{H}_4\text{N})_2$, by reductive alkylation. Its formation appears to be the result of a rare example of a pinacol coupling induced by sodium trihydrocyanoborate (Smith & March, 2001). In the crystal structure of (I) at 180 K, the *meso* molecules are sited on inversion centres. The molecular conformation is such that the $\text{C}6-\text{H}6a$ bond lies close to the plane of the pyridyl ring and the $\text{C}6-\text{O}1$ bond lies approximately perpendicular to this plane. Adjacent molecules are linked by complementary $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds [$\text{H}1\cdots\text{N}1^i = 1.97$ Å, $\text{O}1\cdots\text{N}1^i = 2.797$ (3) Å and $\text{O}-\text{H}\cdots\text{N} = 169^\circ$; symmetry code (i): $1-x, -y, 1-z$] into ribbons running along [100] (Fig. 2).



In the closely comparable bis-methylated analogue of (I), 2,3-bis(pyridin-2-yl)butane-2,3-diol (Brown *et al.*, 1972), the $\text{C}-\text{CH}_3$ bonds lie approximately perpendicular to the planes of the pyridyl rings. In this conformation – apparently driven by the steric influence of the methyl groups – the $\text{C}-\text{O}(\text{H})$ bonds lie approximately in the planes of the pyridyl rings, and intramolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds exist.

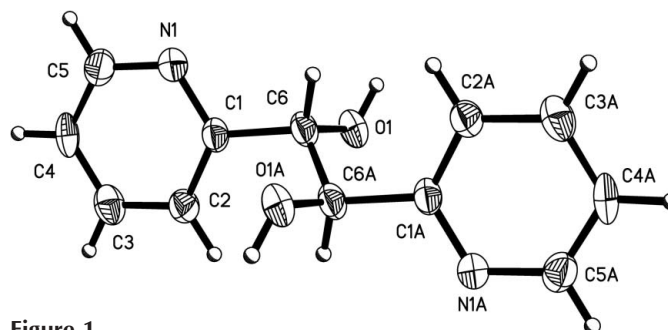


Figure 1

The molecular structure, showing displacement ellipsoids drawn at the 50% probability level. H atoms are shown as spheres of arbitrary radius. Suffix A denotes symmetry operator $-x, -y, 1-z$.

Experimental

For the preparation of the title compound, *N,N*-bis[2-(pyridin-2-yl)ethyl]amine hemihydrate (1.464 g, 6.195 mmol) (Leaver *et al.*, 2003) and pyridine-2-carboxaldehyde (4.36 g, 40.1 mmol) were dissolved in ethanol over 4 Å molecular sieves. The solution was stirred for 30 min at 323 K and excess sodium trihydrocyanoborate was added slowly. Stirring was continued for 1 h and the solution was allowed to cool and then filtered. Excess trihydrocyanoborate was destroyed by the addition of hydrochloric acid (6 M). The solution was made alkaline [2 M NaOH(aq)] and extracted with CH₂Cl₂. The organic phase was dried (MgSO₄) and the solvent was removed by rotary evaporation to give 3.3 g impure *N,N*-bis[2-(pyridin-2-yl)ethyl]-*N*-[(pyridin-2-yl)-methyl]amine, (II). The mass spectrum showed primarily (II)Na⁺ (*m/z* 341.4, 100%). The crude product was left to stand in a freezer (255 K) for several months, during which time crystals of the title compound were formed. At this point, there was still no indication of (I) in the mass spectrum of the bulk product. Careful selection of a few crystals of (I) for ESI-MS showed some contamination with (II), but a main peak due to (I)Na⁺ (*m/z* 239.1). Under more gentle ionization conditions, peaks due to (I)H⁺ (*m/z* 217.2, 20%) were also evident.

Crystal data

C₁₂H₁₂N₂O₂
M_r = 216.24
 Monoclinic, *P*2₁/c
a = 5.3155 (14) Å
b = 8.108 (2) Å
c = 11.737 (3) Å
 β = 90.196 (10)°
V = 505.8 (2) Å³
Z = 2
D_x = 1.420 Mg m⁻³
 Mo Kα radiation
 Cell parameters from 1853 reflections
 θ = 3.8–25.1°
 μ = 0.10 mm⁻¹
T = 180 (2) K
 Needle, pale orange
 0.30 × 0.08 × 0.08 mm

Data collection

Bruker–Nonius X8APEX-II CCD diffractometer
 Thin-slice ω and φ scans
 Absorption correction: multi-scan *SADABS* (Sheldrick, 2003)
T_{min} = 0.588, *T_{max}* = 0.992
 6075 measured reflections
 1236 independent reflections
 1026 reflections with *I* > 2σ(*I*)
R_{int} = 0.043
 θ_{max} = 28.3°
h = -7 → 6
k = -10 → 8
l = -15 → 12

Refinement

Refinement on *F*²
R[*F*² > 2σ(*F*²)] = 0.059
wR(*F*²) = 0.147
S = 1.11
 1236 reflections
 75 parameters
 H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0396P)^2 + 0.2558P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 (Δ/σ)_{max} < 0.001
 Δρ_{max} = 0.32 e Å⁻³
 Δρ_{min} = -0.25 e Å⁻³

Table 1

Hydrogen-bonding geometry (Å, °).

<i>D</i> –H... <i>A</i>	<i>D</i> –H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> –H... <i>A</i>
O1–H1...N1 ⁱ	0.84	1.97	2.797 (3)	169

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

The crystal is monoclinic with β close to 90° and was twinned: twin law (100,0 $\bar{1}$ 0,00 $\bar{1}$), refined twin ratio 0.614:0.386 (3). The wide range

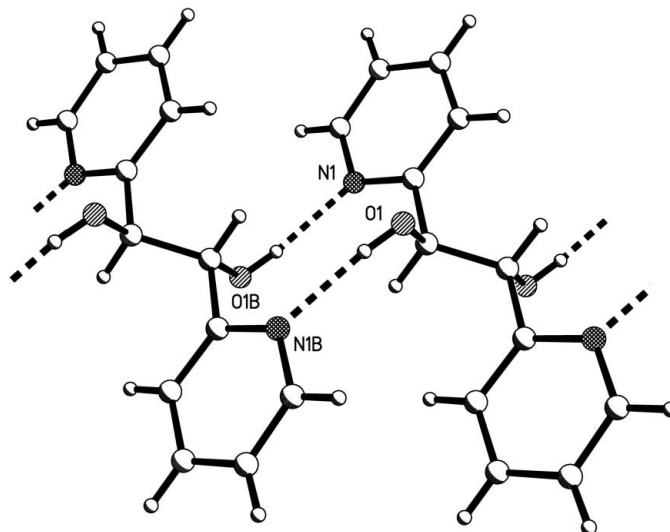


Figure 2
 Complementary O–H...N hydrogen bonds (dashed lines) between adjacent molecules of (I). Suffix B denotes symmetry operator 1 - *x*, -*y*, 1 - *z*.

of transmission factors suggests that the multi-scan correction treats systematic effects other than absorption by the crystal itself. H atoms bound to C atoms were positioned geometrically and allowed to ride during subsequent refinement with C–H = 0.95 Å, *U*_{iso}(H) = 1.2 *U*_{eq}(C) for C(*sp*²) and C–H = 1.00 Å, *U*_{iso}(H) = 1.2 *U*_{eq}(C) for C(*sp*³). The H atom of the hydroxyl group was not evident in a difference Fourier map; it was placed geometrically with O–H = 0.84 Å and allowed to rotate around the C6–O1 bond during subsequent refinement, with *U*_{iso}(H) = 1.5 *U*_{eq}(O).

Data collection: *APEX2* (Bruker–Nonius, 2004); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT* (Bruker, 2003); program(s) used to solve structure: *SHELXTL* (Sheldrick, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

We are grateful to the Danish Natural Science Research Council (SNF) and Carlsbergfondet for provision of the X-ray equipment.

References

Brown, J. N., Jenevein, R. M., Stocker, J. H. & Trefonas, L. M. (1972). *J. Org. Chem.* **37**, 3712–3718.
 Bruker (2003). *SAINT*. Version 7.06a. Bruker AXS Inc., Madison, Wisconsin, USA.
 Bruker–Nonius (2004). *APEX2*. Version 1.0–22. Bruker–Nonius BV, Delft, The Netherlands.
 Leaver, S. A., Palaniandavar, M., Kilner, C. A. & Halcrow, M. A. (2003). *Dalton Trans.* pp. 4224–4225.
 Sheldrick, G. M. (2003). *SADABS*. Version 2.10. Bruker AXS Inc., Madison, Wisconsin, USA.
 Sheldrick, G. M. (2000). *SHELXTL*. Version 6.10. Bruker AXS Inc., Madison, Wisconsin, USA.
 Smith, M. B. & March, J. (2001). *March's Advanced Organic Chemistry*, 5th ed., pp. 1559–1561. New York: John Wiley and Sons.