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Key indicators

Single-crystal X-ray study
 T = 292 K
 Mean $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$
 R factor = 0.052
 wR factor = 0.120
 Data-to-parameter ratio = 17.0

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

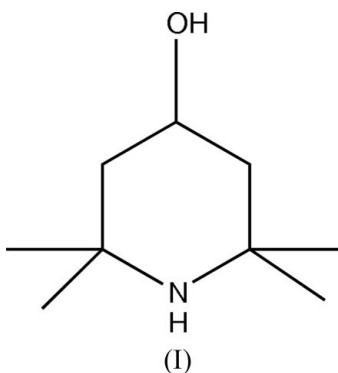
2,2,6,6-Tetramethylpiperidin-4-ol

The molecule of the title compound, $\text{C}_9\text{H}_{19}\text{NO}$, lies on a mirror plane. Intermolecular $\text{N}-\text{H}\cdots\text{O}$ and $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds are observed in the crystal structure.

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Comment

2,2,6,6-Tetramethyl-piperidin-4-ol, (I), is an important compound, since it represents a key intermediate in the preparation of stable nitroxyl radicals, such as 4-hydroxy-2,2,6,6-tetramethylpiperidine-1-oxyl and 4-amino-2,2,6,6-tetramethylpiperidine-1-oxyl, which are used in spin-labeling medicinal studies (Sinha *et al.*, 1979) and as efficient photo-stabilizing agents for plastic products (Bellus *et al.*, 1972).



We present the X-ray crystallographic analysis of (I) (Fig. 1). The molecule lies on a mirror plane, with atoms N1,

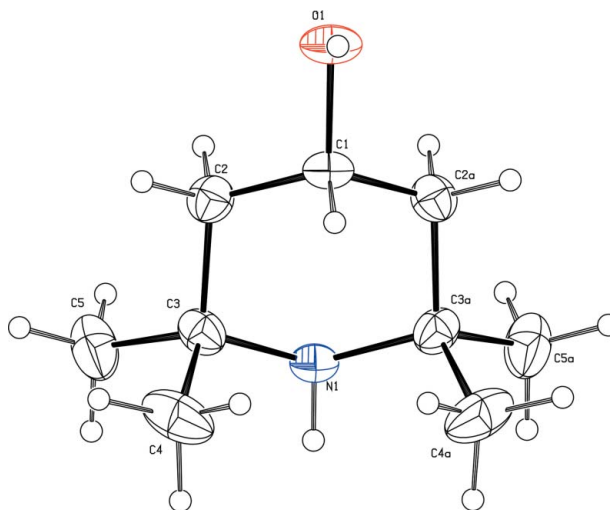


Figure 1
 A drawing of the molecule of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. [Symmetry code: (a) $-x, y, z$.]

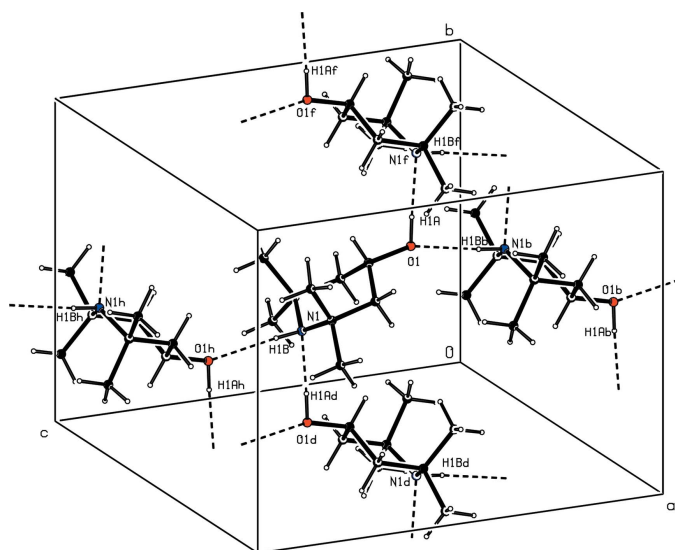


Figure 2
The crystal packing of (I). Dashed lines indicate hydrogen bonds. [Symmetry codes: (b) $-x, \frac{1}{2} - y, -\frac{1}{2} + z$; (d) $x, -\frac{1}{2} + y, \frac{3}{2} + z$; (f) $x, y - \frac{1}{2}, -z + \frac{3}{2}$; (h) $-x, -y + \frac{1}{2}, z + \frac{1}{2}$.]

H1B, C1, H1, O1 and H1A on special positions (0,y,z). The bond lengths and angles are unexceptional. As shown in Fig. 2 and Table 1, N—H···O and O—H···N intermolecular hydrogen bonds link the molecules.

Experimental

The title compound was synthesized according to the procedure of Lutz *et al.* (1962). Crystals suitable for data collection were obtained by slow evaporation of a chloroform solution at 283 K.

Crystal data

$C_9H_{19}NO$	Mo $K\alpha$ radiation
$M_r = 157.25$	Cell parameters from 635 reflections
Orthorhombic, <i>Cmca</i>	$\theta = 2.9\text{--}21.6^\circ$
$a = 14.149$ (2) Å	$\mu = 0.07$ mm $^{-1}$
$b = 10.1346$ (15) Å	$T = 292$ (2) K
$c = 13.3806$ (18) Å	Block, colorless
$V = 1918.7$ (5) Å 3	0.20 × 0.10 × 0.10 mm
$Z = 8$	
$D_x = 1.089$ Mg m $^{-3}$	

Data collection

Bruker SMART 4K CCD area-detector diffractometer	627 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\text{int}} = 0.093$
Absorption correction: none	$\theta_{\text{max}} = 27.0^\circ$
4310 measured reflections	$h = -15 \rightarrow 18$
1091 independent reflections	$k = -12 \rightarrow 11$
	$l = -14 \rightarrow 16$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0544P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.053$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.120$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 0.88$	$\Delta\rho_{\text{max}} = 0.18$ e Å $^{-3}$
1091 reflections	$\Delta\rho_{\text{min}} = -0.18$ e Å $^{-3}$
64 parameters	Extinction correction: <i>SHELXL97</i>
H-atom parameters constrained	Extinction coefficient: 0.0144 (15)

Table 1
Hydrogen-bond geometry (Å, °).

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
N1—H1B···O1 ⁱ	0.85 (2)	2.28 (2)	3.132 (3)	177 (2)
O1—H1A···N1	0.91 (3)	1.99 (3)	2.904 (2)	178 (3)

Symmetry code: (i) $-x, -y + \frac{1}{2}, z + \frac{1}{2}$.

H atoms bonded to N and O atoms were located in a difference map and refined with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$ and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{O})$. Bond lengths were constrained to N—H = 0.85 Å and O—H = 0.91 Å. H atoms bonded to C atoms were placed in calculated positions and treated as riding on their parent atoms, with displacement parameters fixed at $U_{\text{iso}} = 1.5U_{\text{eq}}(\text{carrier atom})$ for methine and methyl groups, and $U_{\text{iso}} = 1.2U_{\text{eq}}(\text{carrier atom})$ for methylene groups. Bond lengths were constrained to 0.96 (methyl CH $_3$), 0.97 (methylene CH $_2$) or 0.98 Å (methine CH).

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINTE* (Bruker, 1999); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

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