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## Structure Reports

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## Qing Yuan, Shan-Zhong Jian and Yan-Guang Wang*

Department of Chemistry, Zhejiang University, 310027 Hangzhou, People's Republic of China

Correspondence e-mail: orgwyg@zju.edu.cn

## Key indicators

Single-crystal X-ray study
$T=293 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.004 \AA$
$R$ factor $=0.044$
$w R$ factor $=0.120$
Data-to-parameter ratio $=9.3$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 4-(9-Acridin-9-ylamino)-2,2,6,6-tetramethylpiperidine $N$-oxide

The title compound, $\mathrm{C}_{22} \mathrm{H}_{26} \mathrm{~N}_{3} \mathrm{O}$, crystallizes in space group $P 2_{1}$ with two molecules in the asymmetric unit. Intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds play an important role in the formation of polymeric chains running along the crystallographic $a$ axis.

## Comment

The title compound is a potential fluorescnet probe to detect the antioxidant capability (Aliga et al., 2003). The asymmetric unit of the title compound, (I), is shown in Fig. 1. The compound crystallizes in space group $P 2_{1}$ with two molecules in the asymmetric unit. There are no significant differences between the bonds lengths and angles of the two molecules; however, there are significant differences in the magnitudes of some of the equivalent torsion angles involving the atoms N1 and N4, N2 and N5 (Tables 1).

(I)

The intermolecular $\mathrm{N} 2-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds play an important role in the formation of polymeric chains running along the crystallographic $a$ axis (Fig. 2). Hydrogen-bond parameters are listed in Table 2.

## Experimental

To a vigorously stirred solution of 9-chloroacridine ( $214 \mathrm{mg}, 1 \mathrm{mmol}$ ) in methanol ( 5 ml ) was added dropwise a solution of 4 -aminoTEMPOL (TEMPOL is 2,2,6,6-tetramethylpiperidine-1-oxyl) ( $171 \mathrm{mg}, 1 \mathrm{mmol}$ ) in methanol ( 2 ml ). This solution was then stirred under reflux for 2 h . The resulting mixture was diluted with $\mathrm{CH}_{2} \mathrm{Cl}_{2}$ ( 10 ml ), washed with saturated $\mathrm{Na}_{2} \mathrm{CO}_{3}$ and water, then dried over anhydrous $\mathrm{Na}_{2} \mathrm{SO}_{4}$, and concentrated. The residue was chromatographed on silica gel (hexane/ethyl acetate $=2: 1$ ) to give the title compound as an orange solid. Orange crystals ( 320 mg , yield $92 \%$ ) were obtained from a $\mathrm{CH}_{2} \mathrm{Cl}_{2} /$ hexane solution after it was left to stand for 4 d . HRMS (ESI) $m / z$ found for $[M+\mathrm{H}]^{+}=349.2115$, calculated for $\mathrm{C}_{22} \mathrm{H}_{27} \mathrm{~N}_{3} \mathrm{O}^{+}=349.2149$.

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## Crystal data

## $\mathrm{C}_{22} \mathrm{H}_{26} \mathrm{~N}_{3} \mathrm{O}$

$M_{r}=348.46$
Monoclinic, $P 2_{1}$
$a=11.1168$ (3) $\AA$
$b=14.2464$ (3) $\AA$
$c=11.8709$ (3) $\AA$
$\beta=92.113$ (1) ${ }^{\circ}$
$V=1878.77(8) \AA^{3}$
$Z=4$
$D_{x}=1.232 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
Cell parameters from 12213
reflections
$\theta=2.2-27.4^{\circ}$
$\mu=0.08 \mathrm{~mm}^{-1}$
$T=293$ (2) K
Block, orange
$0.40 \times 0.30 \times 0.18 \mathrm{~mm}$

## Data collection

Rigaku R-AXIS RAPID
diffractometer
$\omega$ scans
Absorption correction: multi-scan
(ABSCOR; Higashi, 1995)
$T_{\text {min }}=0.954, T_{\text {max }}=0.986$
17974 measured reflections

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.044$
$w R\left(F^{2}\right)=0.120$
$S=1.01$
4441 reflections
480 parameters
H -atom parameters constrained

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{o}{ }^{2}\right)+(0.0776 P)^{2}\right. \\
& +0.0762 P] \\
& \text { where } P=\left(F_{o}{ }^{2}+2 F_{c}^{2}\right) / 3 \\
& (\Delta / \sigma)_{\text {max }}<0.001 \\
& \Delta \rho_{\text {max }}=0.17 \mathrm{e} \AA^{-3} \\
& \Delta \rho_{\text {min }}=-0.17 \mathrm{e}^{-3} \\
& \text { Extinction correction: SHELXL97 } \\
& \text { Extinction coefficient: } 0.0046 \text { (13) }
\end{aligned}
$$

Table 1
Selected geometric parameters ( $\left(\AA^{\circ}{ }^{\circ}\right.$ ).

| C1-N2 | $1.479(3)$ | C25-N4 | $1.485(4)$ |
| :--- | :---: | :--- | ---: |
| C3-N1 | $1.493(3)$ | C28-N4 | $1.490(4)$ |
| C6-N1 | $1.479(4)$ | C32-N5 | $1.387(3)$ |
| C10-N2 | $1.395(3)$ | N1-O1 | $1.281(3)$ |
| C23-N5 | $1.472(3)$ | N4-O2 | $1.284(3)$ |
|  |  |  |  |
| O1-N1-C6 | $116.1(2)$ | O2-N4-C25 | $116.3(2)$ |
| O1-N1-C3 | $115.8(2)$ | O2-N4-C28 | $116.0(2)$ |
| C6-N1-C3 | $124.97(18)$ | C25-N4-C28 | $124.20(19)$ |
| C10-N2-C1 | $121.7(2)$ | C32-N5-C23 | $126.5(2)$ |
|  |  |  |  |
| C5-C3-N1-O1 | $50.5(3)$ | C30-C28-N4-O2 | $69.0(3)$ |
| C4-C3-N1-O1 | $-67.7(3)$ | C29-C28-N4-O2 | $-49.1(3)$ |
| C11-C10-N2-C1 | $121.6(3)$ | C44-C32-N5-C23 | $-123.9(3)$ |
| C22-C10-N2-C1 | $-62.1(4)$ | C33-C32-N5-C23 | $61.8(4)$ |
| C2-C1-N2-C10 | $-98.5(3)$ | C24-C23-N5-C32 | $-133.0(3)$ |
| C9-C1-N2-C10 | $143.0(3)$ | C31-C23-N5-C32 | $109.1(3)$ |

Table 2
Hydrogen-bonding geometry $\left(\AA{ }^{\circ},{ }^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| N5-H555 $\cdots$ O1 | 0.87 | 2.19 | $3.031(3)$ | 162 |
| N2-H222 $\mathrm{O}^{\mathrm{i}}$ |  | 0.89 | 2.27 | $3.109(3)$ |

Symmetry code: (i) $x-1, y, z$.
Atoms H222 and H555 were found in a difference Fourier map and fixed in position. The methyl H atoms were constrained to an ideal geometry $\left[\mathrm{C}-\mathrm{H}=0.96 \AA\right.$ and $\left.U_{\text {iso }}(\mathrm{H})=1.5 U_{\text {eq }}(\mathrm{C})\right]$ and were allowed to rotate freely about the $\mathrm{C}-\mathrm{C}$ bonds. The other H atoms were placed in calculated positions, with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}$ of the carrier



Figure 1
View of the asymmetric unit of (I). Displacement ellipsoids are drawn at the $30 \%$ probability level.


A view of the structure of (I), viewed along the $b$ axis, showing hydrogenbonded chains (dashed lines) running along the $a$ axis. H atoms not involved in the hydrogen bonding have been omitted.
atoms and included in the final cycles of refinement in the riding model approximation.

Data collection: PROCESS-AUTO (Version 1.06; Rigaku, 1998); cell refinement: PROCESS-AUTO; data reduction: CrystalStructure (Version 3.60; Rigaku/MSC, 2004); 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 publication routines (Farrugia, 1999).

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