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## Key indicators

Single-crystal X-ray study
$T=180 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.004 \AA$
$R$ factor $=0.071$
$w R$ factor $=0.193$
Data-to-parameter ratio $=15.8$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

## 2,4,6-Collidine

The crystal structure of 2,4,6-collidine (2,4,6-trimethylpyridine, $\mathrm{C}_{8} \mathrm{H}_{11} \mathrm{~N}$ ) has been determined at 180 (2) K following in situ crystal growth from the liquid. In space group $P 2_{1} / c$, there are two molecules in the asymmetric unit. Molecules are linked into one-dimensional chains via $\mathrm{C}-\mathrm{H} \cdots \mathrm{N}$ interactions.

## Comment

This work forms part of a study devoted to improving the techniques for determining the crystal structures of substances that are liquids at room temperature. We have reported recently the crystal structures of 3-methylpyridine (3-picoline) and 2-methylpyridine (2-picoline) (Bond \& Davies, 2001a,b), and report here the structure of the trisubstituted molecule 2,4,6-trimethylpyridine (2,4,6-collidine), (I).

(I)

In space group $P 2_{1} / c$, there are two molecules in the asymmetric unit (Fig. 1). The two independent molecules form an interplanar angle of $c a 68^{\circ}$ and the $\mathrm{C} 3 A-\mathrm{H} 3 A \cdots \mathrm{~N} 1 B$ angle of $154^{\circ}$ is indicative of a directional hydrogen-bond interaction ( $\mathrm{H} 3 A \cdots \mathrm{~N} 1 B=2.75 \AA$ ). These interactions, together with a second $\mathrm{C}-\mathrm{H} \cdots \mathrm{N}$ contact $\left[\mathrm{H} 5 B \cdots \mathrm{~N} 1 A^{\mathrm{i}}=2.56 \AA\right.$, $\mathrm{C} 5 B-\mathrm{H} 5 B \cdots \mathrm{~N} 1 A^{\mathrm{i}}=171^{\circ}$; symmetry code (i): $-1+x, y$, $-1+z]$ link the molecules into one-dimensional chains running along the vector [101] (Fig. 2). Between adjacent chains, pyridyl rings adopt both face-to-face offset (with interplanar separation $c a 3.6 \AA$ ), and edge-to-face arrangements (Fig. 3).

## Experimental

The sample ( $99 \%$ ) was obtained from the Aldrich Company and was used without further purification. The crystal was grown in a 0.3 mm glass capillary tube using a technique described previously (Davies \& Bond, 2001). In this case, however, the sample remained liquid at the low-temperature limit of the cooling device ( ca 110 K ), and the initial solid material could only be obtained by immersing the sealed capillary tube directly in liquid nitrogen. The capillary was then transferred to the diffractometer and warmed, and the crystal was grown at ca 212 K (a temperature only slightly less than the melting point of the solid in the capillary tube). Once formed, the crystal was

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Figure 1
Molecular structure and atom-labelling scheme for (I) showing displacement ellipsoids at the $50 \%$ probability level for non-H atoms. The two molecules in the asymmetric unit are denoted by the suffixes $A$ and $B$, and disorder of the H atoms in the methyl group $\mathrm{C} 8 B$ has been omitted for clarity.
cooled to 180 (2) K for data collection. Although the diffraction pattern contained contributions from more than one crystal, the pattern associated with the major crystal component was indexed successfully, and only reflections associated with this component were included in the integration. The length of the cylindrical crystal could not be estimated accurately, but it exceeded the diameter of the collimator ( 0.35 mm ).

## Crystal data

$$
\begin{aligned}
& \mathrm{C}_{8} \mathrm{H}_{11} \mathrm{~N} \\
& M_{r}=121.18 \\
& \text { Monoclinic, } P 2_{1} / c \\
& a=8.7773(5) \AA \\
& b=20.3849(11) \AA \\
& c=8.9935(4) \AA \\
& \beta=107.427(3)^{\circ} \\
& V=1535.29(14) \AA^{3} \\
& Z=8
\end{aligned}
$$

$D_{x}=1.049 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
Cell parameters from 16950
$\quad$ reflections
$\theta=1.0-25.0^{\circ}$
$\mu=0.06 \mathrm{~mm}^{-1}$
$T=180(2) \mathrm{K}$
Cylinder, colourless
0.15 mm (radius)

## Data collection

Nonius KappaCCD diffractometer

## Thin-slice $\omega$ and $\varphi$ scans

Absorption correction: multi-scan
(SORTAV; Blessing, 1997)

$$
\theta_{\max }=25.1^{\circ}
$$

$$
\begin{aligned}
& \theta_{\max }=29.1 \\
& h=10 \rightarrow 10
\end{aligned}
$$

$T_{\text {min }}=0.796, T_{\text {max }}=0.955$

$$
k=-24 \rightarrow 24
$$

11768 measured reflections
2056 reflections with $I>2 \sigma(I)$

$$
l=-10 \rightarrow 10
$$ 2701 independent reflections

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.071$
$w R\left(F^{2}\right)=0.193$
$S=1.13$
2701 reflections

$$
R_{\mathrm{int}}=0.069
$$

171 parameters
H -atom parameters constrained


Figure 2
Molecules of (I) linked into one-dimensional chains via $\mathrm{C}-\mathrm{H} \cdots \mathrm{N}$ interactions.


Figure 3
Projection on to (101) showing chains of (I) running perpendicular to the plane of the page.

The methyl-H atoms associated with atom $\mathrm{C} 8 B$ are disordered and were modelled as two sets of idealized positions. All H atoms were placed geometrically and allowed to refine with isotropic displacement parameters (one common parameter for all methyl-H atoms and one common displacement parameter for the other H atoms). Each methyl group was allowed to rotate about its local threefold axis.

Data collection: COLLECT (Nonius, 1998); cell refinement: $H K L$ SCALEPACK (Otwinowski \& Minor, 1997); data reduction: HKL DENZO (Otwinowski \& Minor, 1997) and SCALEPACK; program(s) used to solve structure: SIR92 (Altomare et al., 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: $X P$ (Sheldrick, 1993) and CAMERON (Watkin et al., 1996); software used to prepare material for publication: SHELXL97.

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