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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=294 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.005 \AA$
$R$ factor $=0.038$
$w R$ factor $=0.114$
Data-to-parameter ratio $=16.0$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

[^0]
## 3,6-Dibromo-9-(4-pyridylmethyl)-9H-carbazole

The title compound, $\mathrm{C}_{18} \mathrm{H}_{12} \mathrm{Br}_{2} \mathrm{~N}_{2}$, was synthesized by N alkylation of 4-chloromethylpyridine with 3,6-dibromo-9Hcarbazole. The carbazole ring system is essentially planar, with a mean deviation of $0.012 \AA$, and makes a dihedral angle of $83.2(8)^{\circ}$ with the plane of the pyridine ring. In the crystal structure, weak $\mathrm{C}-\mathrm{H} \cdots \mathrm{Br}$ interactions are observed.

## Comment

Carbazole derivatives substituted by $N$-alkylation have useful pharmaceutical properties (Buu-Hoї \& Royer, 1950; Harfenist \& Joyner, 1983; Caulfield et al., 2002; Harper et al., 2002). In this paper we report the structure of 3,6-dibromo-9-(4-pyridylmethyl)-9 H -carbazole, (I), which was synthesized by N alkylation of 4-chloromethylpyridine with 3,6-dibromo-9Hcarbazole.


The carbazole ring system in (I) is essentially planar, with a mean deviation of $0.012 \AA$, consistent with recent determinations of similar structures (Huang et al., 2005; Duan, Huang et al., 2005). The dihedral angle formed between the carbazole ring system and the plane of the pyridine ring is $83.2(8)^{\circ}$. The $\mathrm{C}-\mathrm{Br}$ distances are in the range 1.903 (3) -1.901 (4)\%A, consistent with the literature (Allen et al., 1987).

## Experimental

The title compound was prepared according to the procedure of Duan, Han et al. (2005). A solution of potassium hydroxide (7.0 g) in dimethylformamide ( 50 ml ) was stirred at room temperature for $20 \mathrm{~min} .3,6$-Dibromo- 9 H -carbazole ( $6.50 \mathrm{~g}, 20 \mathrm{mmol}$ ) (Smith et al., 1992) was added and the mixture stirred for a further 40 min . A solution of 4-chloromethylpyridine ( $3.83 \mathrm{~g}, 30 \mathrm{mmol}$ ) in dimethylformamide ( 50 ml ) was added dropwise with stirring. The resulting mixture was then stirred at room temperature for 12 h and poured into water ( 500 ml ), yielding a white precipitate. The solid product was filtered off, washed with cold water and recrystallized from dichlormethane and EtOH ( $1: 1 \mathrm{v} / \mathrm{v}$ ), giving crystals of (I). Yield: $7.29 \mathrm{~g}(87.6 \%)$; m.p. $510-511 \mathrm{~K}$. Compound (I) ( 40 mg ) was dissolved in a mixture of chloroform ( 5 ml ) and ethanol ( 3 ml ) and the solution

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Figure 1
The molecular structure of (I), with displacement ellopsoids drawn at the $30 \%$ probability level.


Figure 2
Packing of the title compound, viewed along [010]. Dashed lines indicate hydrogen bonds.
was kept at room temperature for 16 d . Natural evaporation of the solution gave colourless crystals suitable for X-ray analysis.

## Crystal data

$$
\begin{aligned}
& \mathrm{C}_{18} \mathrm{H}_{12} \mathrm{Br}_{2} \mathrm{~N}_{2} \\
& M_{r}=416.12 \\
& \text { Monoclinic, } P 2_{1} / n \\
& a=11.266(4) \AA \\
& b=9.729(4) \AA \\
& c=14.367(5) \AA \\
& \beta=98.341(6)^{\circ} \\
& V=1558.1(10) \AA^{3} \\
& Z=4
\end{aligned}
$$

## Data collection

Bruker SMART CCD area-detector diffractometer
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan
(SADABS; Bruker, 1997)
$T_{\text {min }}=0.240, T_{\text {max }}=0.353$
8543 measured reflections
3207 independent reflections 2376 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.068$
$\theta_{\text {max }}=26.5^{\circ}$
$h=-14 \rightarrow 9$
$k=-12 \rightarrow 10$
$l=-17 \rightarrow 18$

## Refinement

Refinement on $F^{2}$

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}^{2}\right)+(0.0619 P)^{2}\right. \\
& \quad \quad+0.1399 P] \\
& \quad \text { where } P=\left(F_{\mathrm{o}}^{2}+2 F_{\mathrm{c}}^{2}\right) / 3 \\
& (\Delta / \sigma)_{\max }=0.001 \\
& \Delta \rho_{\max }=0.70 \mathrm{e}^{2} \AA^{-3} \\
& \Delta \rho_{\min }=-0.80 \mathrm{e}^{-3} \\
& \text { Extinction correction: } S H E L X L 97 \\
& \text { Extinction coefficient: } 0.0067(7)
\end{aligned}
$$

Table 1
Hydrogen-bond geometry $\left(\AA,{ }^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{C} 2-\mathrm{H} 2 \cdots \mathrm{Br}^{\mathrm{i}}$ | 0.93 | 2.87 | $3.653(4)$ | 142 |

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

All H atoms were included using the riding model approximation, with $\mathrm{C}-\mathrm{H}=0.93$ (aromatic) and 0.97 (methylene) $\AA$, and with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C})$.

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

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