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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=294 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.012 \AA$
$R$ factor $=0.045$
$w R$ factor $=0.095$
Data-to-parameter ratio $=14.4$

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 9-Benzyl-3,6-dibromo-9H-carbazole

Two independent molecules comprise the asymmetric unit of the title compound, $\mathrm{C}_{19} \mathrm{H}_{13} \mathrm{Br}_{2} \mathrm{~N}$, which was synthesized by N alkylation of benzyl bromide with 3,6-dibromo- 9 H -carbazole. The carbazole ring system is essentially planar and forms a dihedral angle with the pendant phenyl ring of $66.0(2)^{\circ}$ [70.6 (2) ${ }^{\circ}$ for the second molecule]. In the crystal structure, $\pi-$ $\pi$ interactions and weak $\mathrm{C}-\mathrm{H} \cdots \mathrm{Br}$ interactions are observed.

## Comment

Carbazole derivatives substituted by $N$-alkylation possess valuable pharmaceutical properties (Buu-Hoї \& Royer, 1950; Harfenist \& Joyner, 1983; Caulfield et al., 2002; Harper et al., 2002). In this paper, the structure of 9-benzyl-3,6-dibromo-9 H carbazole, (I), is reported; the compound was synthesized by N -alkylation of benzyl bromide with 3,6-dibromo-9H-carbazole.

(I)

The asymmetric unit of (I) comprises two independent but similar molecules (Fig. 1). The carbazole ring in each is essentially planar, with mean deviations of 0.030 and $0.016 \AA$, respectively, for the two molecules. The dihedral angles formed between the carbazole ring and the plane through the pendant phenyl ring is $66.0(2)^{\circ}$ [70.6 (2) ${ }^{\circ}$ for the second molecule]. The $\mathrm{C}-\mathrm{Br}$ distances fall in the range 1.903 (7)1.925 (8) A , which is consistent with the literature (Allen et al., 1987). In the crystal structure, there are $\pi-\pi$ interactions; the closest, $3.66 \AA$, is formed between the $\mathrm{N} 1 / \mathrm{C} 1 / \mathrm{C} 2 / \mathrm{C} 7 / \mathrm{C} 8$ and $\mathrm{C} 7-\mathrm{C} 12$ rings of translationally related molecules $(x,-1+y$, $z$ ). In addition, there are $\mathrm{C}-\mathrm{H} \cdots \mathrm{Br}$ interactions, as shown in Fig. 2 and as detailed in Table 1.

## Experimental

The title compound was prepared according to the procedure of Duan et al. (2005). A solution of potassium hydroxide ( 7.0 g ) in

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Figure 1
A view of the two independent molecules of (I); displacement ellipsoids are drawn at the $30 \%$ probability level.
dimethylformamide ( 50 ml ) was stirred at room temperature for 20 min . 3,6-Dibromocarbazole ( $6.5 \mathrm{~g}, 20 \mathrm{mmol}$ ), prepared according to Smith et al. (1992), was added and the mixture stirred for a further 40 min . A solution of benzyl bromide ( $5.1 \mathrm{~g}, 30 \mathrm{mmol}$ ) in dimethylformamide ( 50 ml ) was added dropwise with stirring. The resulting mixture was then stirred at room temperature for 10 h and poured into water ( 500 ml ), yielding a white precipitate. The solid product was filtered off, washed with cold water and recrystallized from EtOH, giving crystals of (I) (yield: $7.51 \mathrm{~g}, 90.5 \%$; m.p. $430-432 \mathrm{~K}$ ). ${ }^{1} \mathrm{H}$ NMR (DMSO- $d_{6}$ ): $\delta 5.6(s, 2 \mathrm{H}), 7.2-7.6(m, 9 \mathrm{H}), 8.5(m, 2 \mathrm{H}) ;{ }^{13} \mathrm{C}$ NMR (DMSO- $d_{6}$ ): $\delta 46.8,112.4,112.9,124.1,124.5,127.4,128.3$, $129.6,129.9,138.2,140.2$. Compound (I) ( 40 mg ) was dissolved in a mixture of chloroform $(5 \mathrm{ml})$ and ethanol $(5 \mathrm{ml})$ and the solution was kept at room temperature for 16 d . Natural evaporation of the solution gave colourless crystals suitable for X-ray analysis.

## Crystal data

$\mathrm{C}_{19} \mathrm{H}_{13} \mathrm{Br}_{2} \mathrm{~N}$
$M_{r}=415.12$
Monoclinic, $C c$
$a=39.113(6) \AA$
$b=4.5063(7) \AA$
$c=20.469(3) \AA$
$\beta=116.449(2)^{\circ}$
$V=3230.1(9) \AA^{3}$
$Z=8$

$$
D_{x}=1.707 \mathrm{Mg} \mathrm{~m}^{-3}
$$

Mo $K \alpha$ radiation
Cell parameters from 1791 reflections
$\theta=2.3-21.4^{\circ}$
$\mu=5.01 \mathrm{~mm}^{-1}$
$T=294$ (2) K
Rod, colourless
$0.24 \times 0.18 \times 0.14 \mathrm{~mm}$


Figure 2
A portion of the crystal packing in (I), viewed down the $b$-axis direction. Dashed lines indicate $\mathrm{C}-\mathrm{H} \cdots \mathrm{Br}$ interactions.

## Data collection

Bruker SMART CCD area-detector diffractometer
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan (SADABS; Bruker, 1997)
$T_{\text {min }}=0.310, T_{\text {max }}=0.496$
8574 measured reflections
5698 independent reflections
3115 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.043$
$\theta_{\text {max }}=26.4^{\circ}$
$h=-48 \rightarrow 44$
$k=-3 \rightarrow 5$

## Refinement

Refinement on $F^{2}$
$w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}{ }^{2}\right)+(0.0127 P)^{2}\right]$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.045$
$w R\left(F^{2}\right)=0.095$
$S=0.94$
5698 reflections
397 parameters
H -atom parameters constrained
where $P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}{ }^{2}\right) / 3$
$(\Delta / \sigma)_{\max }=0.001$ 。
$\Delta \rho_{\text {max }}=0.34 \mathrm{e}^{-3}$
$\Delta \rho_{\text {min }}=-0.40 \mathrm{e}^{-3}$
Absolute structure: Flack (1983),
2371 Friedel pairs.
Flack parameter: 0.010 (11)

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

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| C5-H5 $\cdots \mathrm{Br}^{\mathrm{i}}$ | 0.93 | 3.00 | $3.800(4)$ | 146 |
| C12-H12 $^{\mathrm{H}} \mathrm{Br}^{\mathrm{ii}}$ | 0.93 | 3.01 | $3.724(4)$ | 135 |
| C25-H25 $\cdots \mathrm{Br}^{\mathrm{iii}}$ | 0.93 | 2.97 | $3.852(4)$ | 158 |

Symmetry codes: (i) $x, y-1, z$; (ii) $x,-y+1, z-\frac{1}{2}$; (iii) $x,-y+2, z-\frac{1}{2}$.

All H atoms were included in the riding-model approximation, with $\mathrm{C}-\mathrm{H}=0.93$ (aromatic) and $0.97 \AA$ (methylene), 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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