

3,6-Dibromo-9-(4-chlorobenzyl)-9*H*-carbazoleJian-Lan Cui,^{a*} Peng-Mian Huang^b and Wen-Long Guo^a^aDepartment of Chemical Engineering, North University of China, Taiyuan 030051, People's Republic of China, and ^bCollege of Pharmaceuticals & Biotechnology, Tianjin University, Tianjin 300072, People's Republic of ChinaCorrespondence e-mail:
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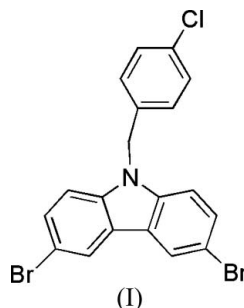
Key indicators

Single-crystal X-ray study
T = 294 K
Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$
R factor = 0.035
wR factor = 0.098
Data-to-parameter ratio = 15.9For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The title compound, $\text{C}_{19}\text{H}_{12}\text{Br}_2\text{ClN}$, was synthesized by *N*-alkylation of 1-chloro-4-(chloromethyl)benzene with 3,6-dibromo-9*H*-carbazole. The carbazole ring system is essentially planar, with a mean deviation of 0.026 Å, and makes a dihedral angle of 75.16 (7)° with the plane of the benzene ring.

Comment

Carbazole derivatives substituted by *N*-alkylation show useful pharmaceutical properties (Buu-Hoi & Royer, 1950; Harfenist & Joyner, 1983; Caulfield *et al.*, 2002; Harper *et al.*, 2002). In this paper, the structure of 3,6-dibromo-9-(4-chlorobenzyl)-9*H*-carbazole, (I), is reported; this was synthesized by *N*-alkylation of 1-chloro-4-(chloromethyl)benzene with 3,6-dibromo-9*H*-carbazole.



The carbazole ring system in (I) is essentially planar, with a mean deviation of 0.026 Å. The dihedral angle formed between the carbazole ring system and the plane of the benzene ring is 75.16 (7)°. The C–Cl distance is 1.738 (4) Å and the C–Br distances are 1.906 (4) and 1.909 (3) Å.

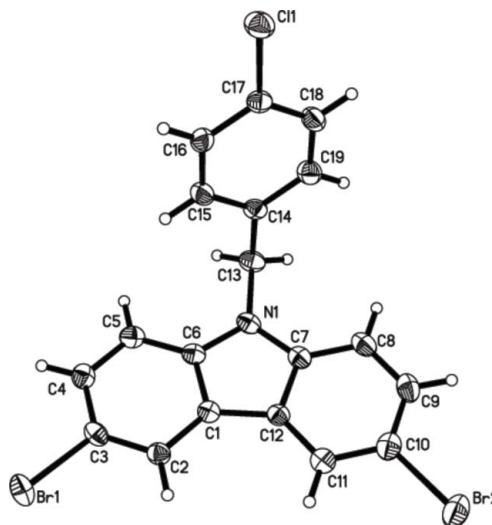


Figure 1
A view of the molecular structure of (I). Displacement ellipsoids are drawn at the 30% probability level.

Experimental

The title compound was prepared according to the procedure of Duan *et al.* (2005). A solution of potassium hydroxide (7.0 g) in dimethylformamide (50 ml) was stirred at room temperature for 20 min. 3,6-Dibromo-9*H*-carbazole (6.50 g, 20 mmol) (Smith *et al.*, 1992) was added and the mixture stirred for a further 40 min. A solution of 1-chloro-4-(chloromethyl)benzene (4.83 g, 30 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 EtOH, giving crystals of (I) (yield: 7.88 g, 87.5%; m.p. 443–444 K). Compound (I) (40 mg) was dissolved in a mixture of chloroform (5 ml) and ethanol (5 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

C ₁₉ H ₁₂ Br ₂ ClN	Mo K α radiation
$M_r = 449.57$	Cell parameters from 4904 reflections
Orthorhombic, <i>Pbca</i>	$\theta = 2.6\text{--}24.9^\circ$
$a = 8.968$ (2) Å	$\mu = 5.08$ mm ⁻¹
$b = 16.690$ (3) Å	$T = 294$ (2) K
$c = 22.019$ (4) Å	Block, colourless
$V = 3295.7$ (11) Å ³	$0.28 \times 0.26 \times 0.22$ mm
$Z = 8$	
$D_x = 1.812$ Mg m ⁻³	

Data collection

Bruker SMART CCD area-detector diffractometer	3315 independent reflections
φ and ω scans	2366 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 1997)	$R_{\text{int}} = 0.053$
$T_{\text{min}} = 0.269$, $T_{\text{max}} = 0.327$	$\theta_{\text{max}} = 26.2^\circ$
17184 measured reflections	$h = -10 \rightarrow 11$
	$k = -8 \rightarrow 20$
	$l = -27 \rightarrow 27$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0503P)^2 + 0.6556P]$
$R[F^2 > 2\sigma(F^2)] = 0.035$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.099$	$(\Delta/\sigma)_{\text{max}} = 0.002$
$S = 1.07$	$\Delta\rho_{\text{max}} = 0.54$ e Å ⁻³
3315 reflections	$\Delta\rho_{\text{min}} = -0.56$ e Å ⁻³
208 parameters	
H-atom parameters constrained	

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

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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