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#### Key indicators

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.019 Å R factor = 0.101 wR factor = 0.302 Data-to-parameter ratio = 10.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

# Tetra-*n*-butylammonium 7-phenylethynyl-8-phenyl-7,8-*nido*-dicarbadecahydroundecaborate(1-)

The  $[NBu_4]^+$  salt of 7-phenylethynyl-8-phenyl-7,8-*nido*dicarbadecahydroundecaborate(1-),  $C_{16}H_{36}N^+ \cdot C_{16}H_{20}B_9^-$ , has been prepared and studied crystallographically. The carborane cage is ordered, unlike that which crystallizes as the  $[PPh_4]^+$  salt. Received 5 October 2001 Accepted 6 November 2001 Online 17 November 2001

## Comment

In the preceding article (Rosair *et al.*, 2001), we describe the structure of the anion [7-PhC<sub>2</sub>-8-Ph-7,8-*nido*-C<sub>2</sub>B<sub>9</sub>H<sub>10</sub>]<sup>-</sup> as its [PPh<sub>4</sub>]<sup>+</sup> salt. Whilst the Ph group directly bound to C8 of the cage subtends a relatively low  $\theta$  value of 15.8{15.1}° (two crystallographically independent cages), that of the PhCC substituent bound to C7 has a relatively high  $\theta$  value, 57.6{52.2}°. The parameter  $\theta$  is defined as the modulus of the average C<sub>cage</sub>-C<sub>cage</sub>-C<sub>Ph</sub>-C<sub>Ph</sub> torsion angle (Cowie *et al.*, 1994).



In the  $[NBu_4]^+$  salt described herein, there is only one crystallographically independent cage, with  $\theta$  values of 24.3 and 67.4°, respectively. Moreover, the present cage is ordered, unlike those of the  $[PPh_4]^+$  salt; this may reflect the relatively discoidal shape of the  $[NBu_4]^+$  cation compared with the more spherical  $[PPh_4]^+$  cation.

# Experimental

A 5 ml solution of 46.22 mg NBu<sub>4</sub>Br (143.38 mmol) in water was added slowly to 50 mg K[7-CCPh-8-Ph-7,8-C<sub>2</sub>B<sub>9</sub>H<sub>10</sub>] (143.38 mmol) dissolved in 10 ml water, producing a white precipitate. After filtration and washing with water, the white solid was dissolved in CH<sub>2</sub>Cl<sub>2</sub> and dried over MgSO<sub>4</sub>. Recrystallization from 333–353 K light petroleum/CH<sub>2</sub>Cl<sub>2</sub> gave 56.0 mg (73.5%) of the product as white microcrystals. <sup>11</sup>B {<sup>1</sup>H} FT–NMR data: (128.4 MHz, BF<sub>3</sub>·Et<sub>2</sub>O in *d*<sub>6</sub> acetone):  $\delta$ /p.p.m. = -32.0 (1*B*), -29.6 (1*B*), -17.1 (1*B*), -15.9 (1*B*), -13.9 (1*B*), -12.8 (1*B*), -8.2 (1B), -4.2 (2*B*). NMR spectra were recorded on a Bruker DPX400 spectrometer at 293 K.

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## Figure 1

The molecular structure of the title anion showing 40% probability displacement ellipsoids.

#### Crystal data

 $C_{16}H_{36}N^+ \cdot C_{16}H_{20}B_9^ M_r = 552.07$ Orthorhombic,  $Pna2_1$  a = 20.626 (4) Å b = 10.099 (2) Å c = 17.183 (3) Å V = 3579.3 (12) Å<sup>3</sup> Z = 4 $D_x = 1.024$  Mg m<sup>-3</sup>

#### Data collection

Bruker P4 diffractometer  $\omega$  scans Absorption correction: none 3381 measured reflections 2457 independent reflections 1104 reflections with  $I > 2\sigma(I)$  $R_{int} = 0.061$ 

## Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.102$   $wR(F^2) = 0.302$  S = 1.022457 reflections 228 parameters H atoms treated by a mixture of independent and constrained refinement Mo  $K\alpha$  radiation Cell parameters from 59 reflections  $\theta = 3.9-22.2^{\circ}$  $\mu = 0.05 \text{ mm}^{-1}$ T = 293 (2) K Plate, colourless  $0.74 \times 0.42 \times 0.26 \text{ mm}$ 

 $\begin{array}{l} \theta_{\max} = 24.9^{\circ} \\ h = -1 \rightarrow 23 \\ k = -1 \rightarrow 10 \\ l = -20 \rightarrow 1 \\ 3 \text{ standard reflections} \\ \text{every 97 reflections} \\ \text{intensity decay: none} \end{array}$ 

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.1216P)^2 \\ &+ 6.0328P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &< 0.001 \\ \Delta\rho_{\text{max}} &= 0.41 \text{ e } \text{\AA}^{-3} \\ \Delta\rho_{\text{min}} &= -0.27 \text{ e } \text{\AA}^{-3} \end{split}$$

| Table 1  |             |           |      |
|----------|-------------|-----------|------|
| Selected | interatomic | distances | (Å). |

| B1-B2  | 1.77 (2) | B5-B10  | 1.69 (3)   |
|--------|----------|---------|------------|
| B1-B3  | 1.81 (2) | B5-B11  | 1.72 (3)   |
| B1-B4  | 1.80 (2) | B6-B11  | 1.78 (2)   |
| B1-B5  | 1.79 (3) | C7-C8   | 1.608 (15) |
| B1-B6  | 1.77 (2) | C7-B2   | 1.75 (2)   |
| B2-B3  | 1.77 (2) | C7-B6   | 1.71 (2)   |
| B2-B6  | 1.71 (2) | C7-B11  | 1.62 (2)   |
| B3-B4  | 1.80 (2) | C8-B2   | 1.737 (18) |
| B3-B9  | 1.79 (2) | C8-B3   | 1.676 (18) |
| B4-B5  | 1.82 (2) | C8-B9   | 1.605 (17) |
| B4-B9  | 1.78 (2) | B9-B10  | 1.83 (2)   |
| B4-B10 | 1.74 (3) | B10-B11 | 1.80 (3)   |
| B5-B6  | 1.75 (3) |         |            |
|        |          |         |            |

Friedel pairs have been merged and the absolute configuration could not be determined from the experiment because of the lack of any significant anomalous scattering. Beyond  $45^{\circ}$  in  $2\theta$  very little diffraction was observed and, with a sequential detector, it was thought that little would be gained by collecting data at a higher angle. This was the biggest single crystal present in the sample. The study is of limited precision because the crystal was relatively weakly diffracting and data were collected at room temperature. Data collection at low temperature and with a more sensitive detector would have improved the result.

The *exo*-cage-H atoms were constrained to idealized positions (B-H 1.10 Å), as were the phenyl-H atoms (C-H 0.98 Å), methylene (C-H 0.97 Å) and methyl-H atoms (C-H 0.96 Å). The *endo*-cage-H atom was restrained to B-H = 1.10 (2) Å. The isotropic displacement parameters of the cage-H atoms were defined as  $1.2U_{iso}$  of the attached cage atom. The  $U_{iso}$  parameters of the phenyl, methylene and methyl H atoms were defined as 1.2, 1.2 and  $1.5U_{iso}$  of the attached C atom, respectively. The phenyl rings were constrained to idealized hexagons. Only the cage-C and phenyl-C atoms were refined anisotropically.

Data collection: XSCANS (Siemens, 1996); cell refinement: XSCANS; data reduction: XSCANS; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1998); software used to prepare material for publication: SHELXTL.

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