

2-Phenylethylammonium bromide

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Key indicators

Single-crystal X-ray study
 $T = 295$ K
Mean $\sigma(\text{C}-\text{C}) = 0.005$ Å
 R factor = 0.032
 wR factor = 0.059
Data-to-parameter ratio = 32.5

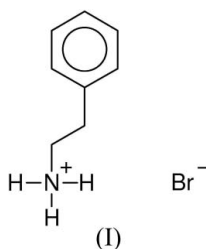
For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

2-Phenylethylammonium bromide, $\text{C}_8\text{H}_{12}\text{N}^+\cdot\text{Br}^-$, adopts a layered structure consisting of alternating hydrophilic and hydrophobic regions. The ammonium groups and bromide anions interact through $\text{N}^+-\text{H}\cdots\text{Br}^-$ hydrogen bonds, forming *transoid* one-dimensional ladders, which are further linked by electrostatic $\text{N}^+\cdots\text{Br}^-$ interactions into two-dimensional sheets.

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Comment

The crystal structure of 2-phenylethylammonium bromide, (I) (Fig. 1), was determined as part of an ongoing study of the structural characteristics and hydrogen-bonding interactions of organic salts consisting of arylammonium cations and halide anions. The unit-cell parameters of (I) have been reported previously by Tsoucaris (1961), but fractional coordinates were not given in that report. The crystal structure of the analogous chloride salt has also been described previously (Tsoucaris, 1961; Horn *et al.*, 1990), and (I) is isostructural to it. Compared to the unit-cell parameters of the chloride salt [$a = 4.603$ (1) Å, $b = 5.906$ (1) Å, $c = 32.360$ (1) Å; Horn *et al.*, 1990], the b parameter in (I) is slightly elongated and the c parameter is slightly shortened. As expected, the unit-cell volume of (I) is larger than that of the chloride salt [880 (1) Å³].



The crystal structure of (I) consists of layers lying parallel to the ab plane, with alternating hydrophobic regions (containing the ammonium groups and bromide anions) and hydrophilic regions (containing the rest of the organic cations) (Fig. 2). In the organic cation, the ethylammonium chain is close to a fully extended all-*trans* conformation, with the $\text{N1}-\text{C1}-\text{C2}-\text{C3}$ torsion angle equal to 173.6 (2)°. The benzene rings pack in a non-interdigitated fashion, with the ring plane forming a dihedral angle of 55.68 (7)° to the ab plane. In this region, the shortest centroid-to-centroid distance between benzene rings is 5.590 (2) Å.

In the hydrophilic regions, ammonium groups and bromide anions interact *via* $\text{N}^+-\text{H}\cdots\text{Br}^-$ hydrogen bonds (Table 1). Each H atom of the ammonium group forms three short,

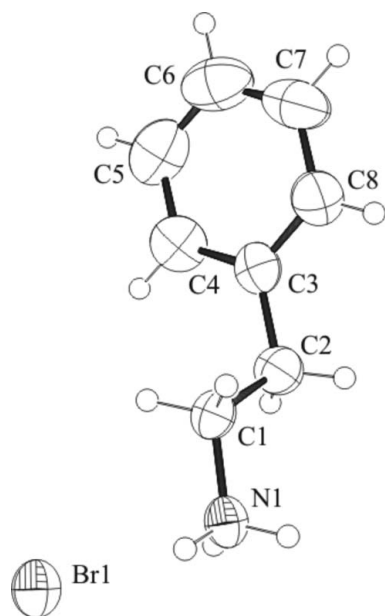


Figure 1
The molecular structure of (I), showing displacement ellipsoids at the 50% probability level for non-H atoms.

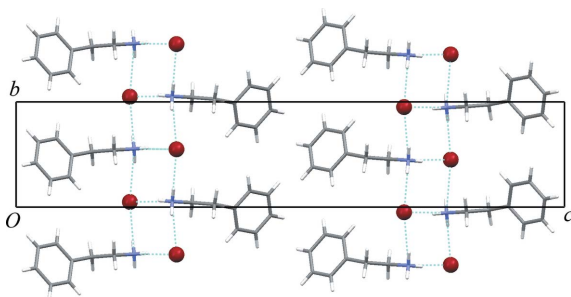


Figure 2
View of (I) down the *a* axis, showing layers lying parallel to the *ab* plane and $N^+ - H \cdots Br^-$ hydrogen bonds (blue dotted lines) forming extended one-dimensional ladders.

charge-assisted hydrogen bonds to three different bromide anions, with $N^+ \cdots Br^-$ distances ranging from 3.3186 (19) Å to 3.370 (2) Å. These interactions define a *transoid* one-dimensional hydrogen-bonded ladder (Fig. 2). A fourth, longer $N^+ \cdots Br^-$ contact [$N1 \cdots Br1^i = 3.459$ (2) Å; symmetry code: (i) $-1 + x, y, z$] links these hydrogen-bonded ladders into corrugated two-dimensional sheets (Fig. 3). A similar sheet structure has been reported for ethylammonium bromide (Jellinek, 1958; Bond, 2005). In both that structure and (I), adjacent sheets are stacked in a parallel offset fashion, with $Br^- \cdots N^+ \cdots Br^-$ angles close to 90° .

Experimental

2-Phenylethylammonium bromide was synthesized by dropwise addition of HBr (8.2 ml, 72.9 mmol, 48%, Fluka) to a solution of 2-phenylethylamine (5.3 ml, 42.2 mmol, Aldrich, 99%) in chloroform (30 ml). The resulting precipitate was filtered off. The crystal used for this structure determination was crystallized from an aqueous solution of 2-phenylethylammonium bromide (0.500 g, 2.47 mmol) and

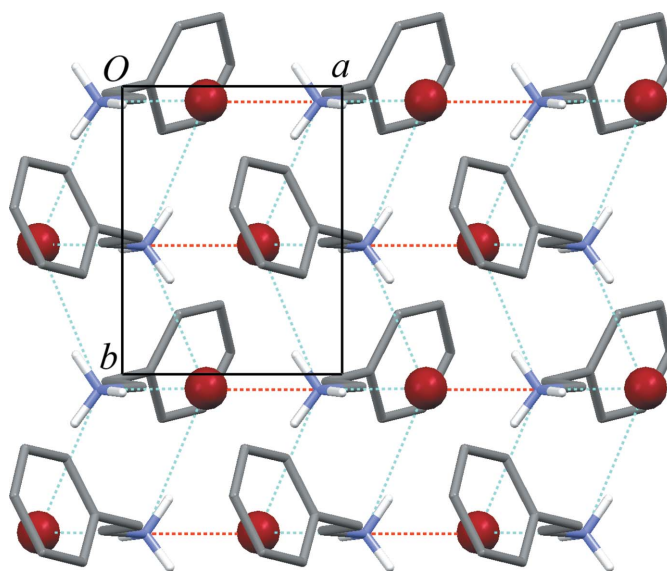


Figure 3
View of (I) down the *c* axis, showing a single two-dimensional sheet in the *ab* plane. $N^+ - H \cdots Br^-$ hydrogen bonds are shown as blue dotted lines, and the longer $N^+ \cdots Br^-$ contacts between ladders are shown as red dotted lines. H atoms bound to C atoms are omitted.

$CoBr_2$ (Aldrich, 99%, 0.271 g, 1.24 mmol) (2:1 molar ratio), open to the atmosphere, at room temperature over a period of eight weeks.

Crystal data

$C_8H_{12}N^+ \cdot Br^-$	$Z = 4$
$M_r = 202.10$	$D_x = 1.455 \text{ Mg m}^{-3}$
Orthorhombic, $P2_12_12_1$	Mo $K\alpha$ radiation
$a = 4.6871$ (4) Å	$\mu = 4.39 \text{ mm}^{-1}$
$b = 6.1419$ (4) Å	$T = 295$ (2) K
$c = 32.047$ (2) Å	Block, colourless
$V = 922.56$ (12) Å ³	$0.30 \times 0.20 \times 0.20 \text{ mm}$

Data collection

Oxford Diffraction Excalibur2 CCD diffractometer	9448 measured reflections
ω scans	2958 independent reflections
Absorption correction: multi-scan (Blessing, 1995)	2063 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.340$, $T_{\max} = 0.419$	$R_{\text{int}} = 0.027$
	$\theta_{\max} = 32.0^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0257P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.032$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.059$	$(\Delta/\sigma)_{\max} = 0.003$
$S = 1.06$	$\Delta\rho_{\max} = 0.46 \text{ e \AA}^{-3}$
2958 reflections	$\Delta\rho_{\min} = -0.86 \text{ e \AA}^{-3}$
91 parameters	Absolute structure: Flack (1983),
H-atom parameters constrained	1047 Friedel pairs
	Flack parameter: 0.029 (15)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N1-H1A \cdots Br1$	0.89	2.49	3.360 (2)	166
$N1-H1B \cdots Br1^i$	0.89	2.46	3.3186 (19)	162
$N1-H1C \cdots Br1^{ii}$	0.89	2.51	3.370 (2)	163

Symmetry codes: (i) $-x + 1, y - \frac{1}{2}, -z + \frac{3}{2}$; (ii) $-x + 1, y + \frac{1}{2}, -z + \frac{3}{2}$.

H atoms were placed in calculated positions, with methylene C–H = 0.97 Å, aromatic C–H = 0.93 Å, and N–H = 0.89 Å, and were refined using a riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{N})$.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2006); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2006); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *Mercury* (Bruno *et al.*, 2002); software used to prepare material for publication: *PLATON* (Spek, 2003) and *WinGX* (Farrugia, 1999).

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