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**Key indicators**

Single-crystal X-ray study  
*T* = 100 K  
 Mean  $\sigma(C-C)$  = 0.010 Å  
*R* factor = 0.034  
*wR* factor = 0.069  
 Data-to-parameter ratio = 15.6

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

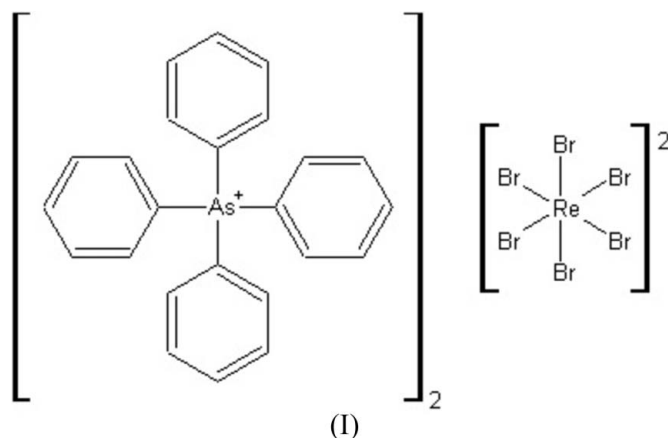
**Bis(tetraphenylarsonium) hexabromorhenate(IV)**

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The title compound,  $(C_{24}H_{20}As)_2[ReBr_6]$ , consists of tetraphenylarsonium cations and  $[ReBr_6]^{2-}$  dianions, the latter lying on inversion centres. A possible  $C-H \cdots Br$  interaction stabilizes the crystal packing.

**Comment**

The title complex, (I) (Fig. 1), is the first reported arsonium salt of the hexabromorhenate(IV) dianion. The Re atom occupies an inversion centre and is octahedrally coordinated by bromide anions. The Re—Br bond lengths in (I) (Table 1) are similar to those found in other hexabromorhenate(IV) dianions (Grundy & Brown, 1970). The cation and anion are linked by a weak  $C-H \cdots Br$  bond (Table 2).



In the crystal packing of (I), each  $[ReBr_6]^{2-}$  anion is surrounded by large organic cations, so there are no short metal–metal contacts: the shortest intermetallic distances in (I) are  $Re \cdots Re^{ii} = 10.4085$  (9),  $Re \cdots Re^{iii} = 10.4157$  (9) and  $Re \cdots Re^{iv} = 10.8892$  (9) Å [symmetry codes: (ii)  $x - 1, y, z$ ; (iii)  $x, y - 1, z$ ; (iv)  $x - 1, y - 1, z$ ].

**Experimental**

$(NH_4)_2ReBr_6$  was obtained in a reaction of  $(NH_4)ReO_4$  with  $H_3PO_2$  in 7 M HBr (Watt & Thompson, 1963). A mixture of  $(NH_4)_2ReBr_6$  (0.46 g), tetraphenylarsonium bromide monohydrate (0.40 g) and a solution of 1 ml of HBr in 50 ml of water was stirred for 5 h at 333 K. The color of the reaction mixture changed from dark violet–red to yellow–brown. After reaction, the mixture was cooled and the first crystalline product was obtained. X-ray quality crystals of (I) were obtained by recrystallization of the crude product from water at room temperature.

## Crystal data

 $(C_{24}H_{20}As)_2[ReBr_6]$  $M_r = 1432.25$ Triclinic,  $P\bar{1}$  $a = 10.4085$  (9) Å $b = 10.4157$  (9) Å $c = 12.1694$  (9) Å $\alpha = 92.565$  (7)° $\beta = 99.915$  (7)° $\gamma = 116.880$  (9)° $V = 1147.85$  (16) Å<sup>3</sup> $Z = 1$  $D_x = 2.072$  Mg m<sup>-3</sup>Mo  $K\alpha$  radiation $\mu = 9.33$  mm<sup>-1</sup> $T = 100$  (2) K

Prism, orange

 $0.13 \times 0.10 \times 0.07$  mm

## Data collection

Kuma KM-4-CCD diffractometer

 $\omega$  scans

Absorption correction: numerical

(CrysAlis RED; Oxford

Diffraction, 2004)

 $T_{\min} = 0.318$ ,  $T_{\max} = 0.598$ 

9761 measured reflections

4040 independent reflections

2979 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.060$  $\theta_{\max} = 25.0^\circ$ 

## Refinement

Refinement on  $F^2$  $R[F^2 > 2\sigma(F^2)] = 0.034$  $wR(F^2) = 0.069$  $S = 0.93$ 

4040 reflections

259 parameters

H-atom parameters constrained

 $w = 1/[\sigma^2(F_o^2) + (0.0254P)^2]$ where  $P = (F_o^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\max} < 0.001$  $\Delta\rho_{\max} = 0.98$  e Å<sup>-3</sup> $\Delta\rho_{\min} = -1.16$  e Å<sup>-3</sup>

Table 1

Selected bond lengths (Å).

Re1—Br1	2.5023 (7)	Re1—Br2	2.5264 (7)
Re1—Br3	2.5197 (7)		

Table 2

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C20—H20 $\cdots$ Br1	0.93	2.86	3.671 (6)	147

The H atoms were positioned geometrically ( $C-H = 0.95$  Å) and refined as riding, with  $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(\text{carrier})$ . The highest differ-

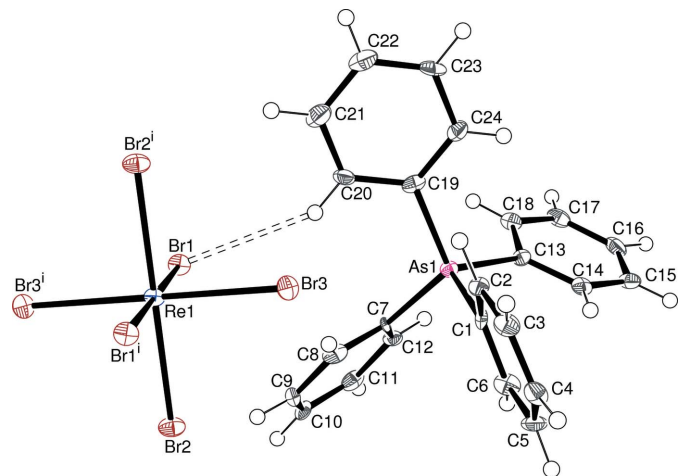


Figure 1

The structure of the ions of (I) showing 50% displacement ellipsoids for the non-H atoms. The  $C-H\cdots Br$  interaction is indicated by a double-dashed line. [Symmetry code: (i)  $1 - x, -y, 1 - z$ .]

ence peak is  $0.98$  Å from atom Re1 and the deepest difference hole is  $1.16$  Å from Re1.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2004); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2004); 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* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

## References

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