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#### **Key indicators**

Single-crystal X-ray study T = 296 KMean  $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$  R factor = 0.030 wR factor = 0.077 Data-to-parameter ratio = 20.5

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

# The components of the title compound, $C_9H_9N_2Se^+\cdot Br^-\cdot H_2O$ , are linked to each other *via* N-H···O, N-H···Br and O-H···Br hydrogen bonds.

2-Amino-4-phenylselenazolium bromide

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#### Comment

monohydrate

Selenazoles have attracted considerable interest because they are small building blocks of complex natural products and biologically active compounds (Back, 1999).



In the structure of (I), the selenazole ring is planar, forming a dihedral angle of  $23.93 (13)^{\circ}$  with the benzene ring. All components are involved in a hydrogen-bond network (Table 2), the Br<sup>-</sup> ions and the water molecules bridging the 2amino-4-phenylselenazolium cations into a centrosymmetric dimer (Fig. 2). The dimers are further linked into a layer by an O1-H102····Br<sup>ii</sup> hydrogen bond (see Table 2 for symmetry code).

#### **Experimental**

To a solution of 2-bromo-1-phenylethanone (1.99 g, 10 mmol) in EtOH (30 ml) was added selenourea (1.23 g, 10 mmol). The mixture was refluxed for 3 h. After cooling, the mixture was extracted with  $Et_2O$  and water, dried with anhydrous MgSO<sub>4</sub>, acidified with dry HBr and recrystallized from ethanol to give the salt 4-phenyl-2-amino-1,3-selenazole bromide (yield: 2.4 g, 79%) (Geisler *et al.*, 2004). This was recrystallized from ethanol (95%), giving colourless crystals of (I) suitable for X-ray diffraction.

Crystal data  $C_9H_9N_2Se^+\cdot Br^-\cdot H_2O$   $M_r = 322.06$ Monoclinic,  $P2_1/c$  a = 11.493 (7) Å b = 9.591 (5) Å c = 10.456 (4) Å  $\beta = 94.211$  (19)° V = 1149.6 (10) Å<sup>3</sup> Z = 4

 $D_x = 1.861 \text{ Mg m}^{-3}$ Mo K\alpha radiation Cell parameters from 8209 reflections  $\theta = 3.3-27.5^{\circ}$  $\mu = 6.72 \text{ mm}^{-1}$ T = 296 (1) KPlatelet, colourless  $0.24 \times 0.18 \times 0.08 \text{ mm}$ 

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## organic papers

Data collection

Rigaku R-AXIS RAPID	2622 independent reflections
diffractometer	1834 reflections with $F^2 > 2\sigma(F^2)$
$\omega$ scans	$R_{\rm int} = 0.054$
Absorption correction: multi-scan	$\theta_{\rm max} = 27.5^{\circ}$
(ABSCOR; Higashi, 1995)	$h = -14 \rightarrow 14$
$T_{\min} = 0.263, T_{\max} = 0.584$	$k = -12 \rightarrow 12$
10800 measured reflections	$l = -12 \rightarrow 13$

#### Refinement

Refinement on $F^2$	$w = 1/[0.77\sigma(F_0^2)]/(4F_0^2)$
$R[F^2 > 2\sigma(F^2)] = 0.030$	$(\Delta/\sigma)_{\rm max} < 0.001$
$wR(F^2) = 0.077$	$\Delta \rho_{\rm max} = 0.51 \ {\rm e} \ {\rm \AA}^{-3}$
S = 1.00	$\Delta \rho_{\rm min} = -0.60 \text{ e } \text{\AA}^{-3}$
2622 reflections	Extinction correction: Larson
128 parameters	(1970)
H-atom parameters constrained	Extinction coefficient: 42 (7)

#### Table 1

Selected geometric parameters (Å, °).

Se1-C1	1.874 (2)	N12-C1	1.338 (3)
Se1-C2	1.875 (3)	N12-C3	1.403 (3)
N11-C1	1.309 (3)	C2-C3	1.339 (4)
C1-Se1-C2	85.34 (13)	C1-N12-C3	117.0 (2)

#### Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots$
N12-H121···O1	0.86	1.97	2.805 (3)	165
N11-H111Br1	0.86	2.50	3.330 (3)	162
$N11-H112\cdots Br1^{i}$	0.86	2.76	3.521 (3)	148
$O1-H101\cdots Br1^{i}$	0.85	2.52	3.342 (2)	164
$O1 - H102 \cdots Br1^{ii}$	0.84	2.56	3.388 (3)	167

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

H atoms attached to O and N atoms were located in a difference Fourier map and included in the refinement based on the as-found O-H and N-H bond lengths; their isotropic displacement paramenters were initially refined, then fixed in the final stage. All other H atoms were placed in calculated positions, with C-H = 0.93 Å, and included in the refinement in the riding-model approximation, with  $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C}).$ 

Data collection: PROCESS-AUTO (Rigaku, 1998); cell refinement: PROCESS-AUTO; data reduction: CrystalStructure (Rigaku/ MSC, 2004); program(s) used to solve structure: SIR97 (Altomare et al., 1999); program(s) used to refine structure: CRYSTALS (Betteridge et al., 2003); molecular graphics: ORTEP3 for Windows (Farrugia, 1997); software used to prepare material for publication: CrystalStructure.



#### Figure 1

A view of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 40% probability level.



#### Figure 2

A hydrogen-bonded dimer of (I) [symmetry code: (i) 1 - x, 1 - y, -z].

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