

**2-Thiocytosinium bromide**

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**Key indicators**

Single-crystal X-ray study

T = 295 K

Mean  $\sigma(C-C) = 0.004 \text{ \AA}$

R factor = 0.032

wR factor = 0.082

Data-to-parameter ratio = 20.3

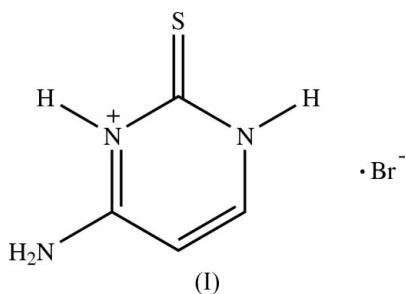
For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The structure of the title compound (systematic name: 6-amino-2-thioxo-2,3-dihydropyrimidin-1-ium bromide),  $C_4H_6N_3S^+\cdot Br^-$ , has two 2-thiocytosinium cations and two  $Br^-$  anions in the asymmetric unit and is isostructural with 2-thiocytosinium chloride. Both six-membered rings are essentially planar. S atoms and  $Br^-$  anions serve as hydrogen-bond acceptors, forming sheets parallel to (101).

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**Comment**

During our electron paramagnetic resonance investigations of the influence of ionizing radiation on DNA, we have used crystals of DNA bases as model systems (Sanković *et al.*, 1988, 1996, 2003; Herak *et al.*, 1994, 1997). It was found that not only spacial distribution and stacking of DNA bases, but also their environment in the crystal structure, plays a significant role in electron/hole long-range migration processes. We are currently investigating the influence of different base arrangements and different environments on the mechanism and range of these transfer processes. Knowledge of the crystal structure is essential for such a study (Matković-Čalogović & Sanković, 1999; Matković-Čalogović *et al.*, 2002; Prugovečki *et al.*, 2005). Here, we report the structure of 2-thiocytosinium bromide, (I), another model system appropriate for the study of long-range charge migration.



Compound (I) is isostructural with 2-thiocytosinium chloride (Prugovečki *et al.*, 2005) (Fig. 1), with two cations and two anions in the asymmetric unit. The replacement of  $Cl^-$  with  $Br^-$  ions does not change the hydrogen-bonding pattern. Both  $Br^-$  ions in (I) serve as hydrogen-bond acceptors. One thiocytosine cation forms hydrogen bonds of the type N—H $\cdots$ Br with three  $Br^-$  anions and the other with four  $Br^-$  ions, interconnecting them in the plane parallel to (101). There is also an intermolecular N42—H $\cdots$ S22 hydrogen bond (Table 2 and Fig. 2).

Parallel layers with closest contacts are shown in Fig. 3. Similar to what is observed in 2-thiocytosinium chloride, there is no stacking of the pyrimidine rings, but  $Br11$  forms contacts



**Table 2**  
Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
N11—H11···Br11 <sup>i</sup>	0.85 (3)	2.37 (3)	3.208 (2)	173 (2)
N12—H12···Br12 <sup>ii</sup>	0.83 (3)	2.62 (3)	3.377 (2)	153 (3)
N31—H31···Br11 <sup>iii</sup>	0.82 (4)	2.42 (4)	3.240 (2)	179 (6)
N32—H32···Br12	0.83 (4)	2.56 (4)	3.345 (2)	158 (3)
N41—H121···Br12 <sup>iv</sup>	0.85 (3)	2.60 (3)	3.427 (3)	166 (4)
N41—H122···S21 <sup>v</sup>	0.78 (4)	2.73 (4)	3.309 (3)	134 (4)
N42—H221···Br12	0.76 (4)	2.80 (4)	3.533 (3)	161 (3)
N42—H222···Br11 <sup>vi</sup>	0.87 (3)	2.58 (3)	3.415 (3)	162 (3)

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

H atoms were found in a difference Fourier map and refined isotropically. The highest peak and the deepest hole are 0.94 and 0.92  $\text{\AA}$  from S21, respectively.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2003); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2003); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97*.

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