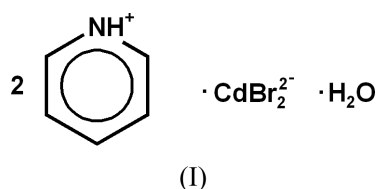


Bis(pyridinium) tetrabromocadmate(II)  
monohydrateHui Zhang<sup>a,b</sup> and Liang Fang<sup>a,b</sup><sup>a</sup>State Key Laboratory of Advanced Technology, for Materials Synthesis and Processing, Wuhan University of Technology, Wuhan 430070, People's Republic of China, and <sup>b</sup>Institut für Anorganische Chemie, RWTH Aachen, Professor-Pirlet-Straße 1, 52056 Aachen, Germany

The title compound, (C<sub>5</sub>H<sub>6</sub>N)<sub>2</sub>[CdBr<sub>4</sub>]·H<sub>2</sub>O, consists of discrete anions, cations and solvent water molecules. Both pyridinium cations and the tetrabromocadmate anion possess a crystallographically imposed mirror symmetry. The solvent water molecule and one pyridinium cation form intermolecular N—H···O and O—H···Br hydrogen bonds, giving a three-dimensional hydrogen-bonded structure.

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## Key indicators

Single-crystal X-ray study  
*T* = 223 K  
Mean  $\sigma$ (C—C) = 0.007 Å  
*R* factor = 0.030  
*wR* factor = 0.077  
Data-to-parameter ratio = 23.0For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

## Experimental

Pyridine (0.010 mol, 0.791 g) and CdBr<sub>2</sub> (0.005 mol, 1.3601 g) were dissolved in dilute HBr (10 ml, 1 M) and the resultant solution was evaporated slowly at *ca* 323 K. The title compound was obtained as prismatic colourless crystals after several days.

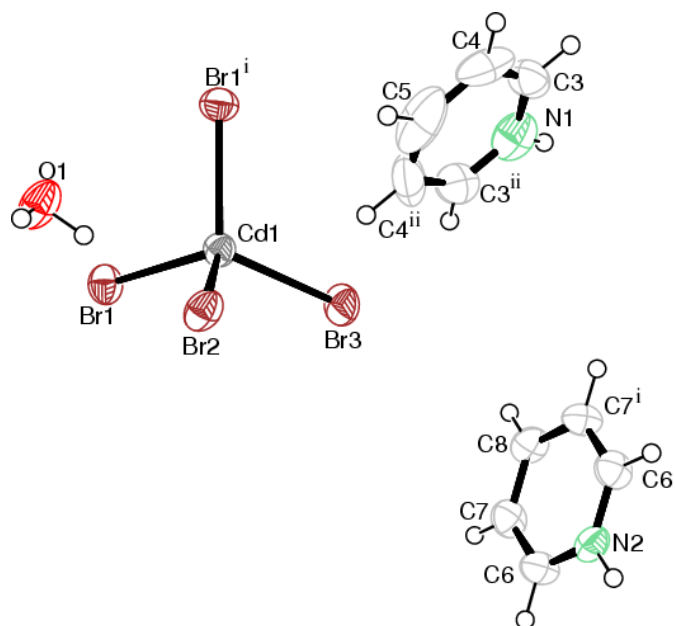


Figure 1

ORTEP-3 drawing (Farrugia, 1997) of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms have been assigned arbitrary radii. [Symmetry codes: (i)  $x, \frac{1}{2} - y, z$ ; (ii)  $x, \frac{3}{2} - y, z$ .]

Crystal data

(C<sub>5</sub>H<sub>6</sub>N)<sub>2</sub>[CdBr<sub>4</sub>]·H<sub>2</sub>O  
*M<sub>r</sub>* = 610.27  
 Orthorhombic, *Pnma*  
*a* = 14.951 (2) Å  
*b* = 9.1564 (15) Å  
*c* = 12.815 (2) Å  
*V* = 1754.3 (5) Å<sup>3</sup>  
*Z* = 4  
*D<sub>x</sub>* = 2.311 Mg m<sup>-3</sup>

Mo *K*α radiation  
 Cell parameters from 2299 reflections  
 $\theta$  = 2.1–28.3°  
 $\mu$  = 10.35 mm<sup>-1</sup>  
*T* = 223 (2) K  
 Prism, colourless  
 0.15 × 0.12 × 0.10 mm

Data collection

Bruker SMART APEX CCD diffractometer  
 $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
*T<sub>min</sub>* = 0.234, *T<sub>max</sub>* = 0.355  
 22963 measured reflections

2299 independent reflections  
 1776 reflections with *I* > 2σ(*I*)  
*R<sub>int</sub>* = 0.060  
 $\theta_{\text{max}}$  = 28.3°  
*h* = -19 → 19  
*k* = -12 → 12  
*l* = -17 → 17

Refinement

Refinement on *F*<sup>2</sup>  
*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.030  
*wR* [*F*<sup>2</sup>] = 0.077  
*S* = 1.10  
 2299 reflections  
 100 parameters  
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0272P)^2 + 2.3887P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.66 \text{ e \AA}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.66 \text{ e \AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Cd1—Br1	2.5736 (6)	Cd1—Br2	2.5983 (9)
Cd1—Br3	2.5838 (9)		
Br1 <sup>i</sup> —Cd1—Br1	106.84 (3)	Br1—Cd1—Br2	108.188 (18)
Br1—Cd1—Br3	114.474 (19)	Br3—Cd1—Br2	104.38 (3)

Symmetry code: (i) *x*,  $\frac{1}{2}$  - *y*, *z*.

Table 2

Hydrogen-bonding geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N2—H2...O1 <sup>ii</sup>	0.87	1.80	2.669 (7)	176
O1—H9...Br3 <sup>iii</sup>	0.86 (8)	2.50 (8)	3.365 (6)	175 (7)
O1—H10...Br2	0.90 (9)	2.36 (9)	3.263 (6)	174 (8)

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

H atoms attached to C and N were constrained to an ideal geometry, with C—H and N—H distances of 0.94 and 0.87 Å,

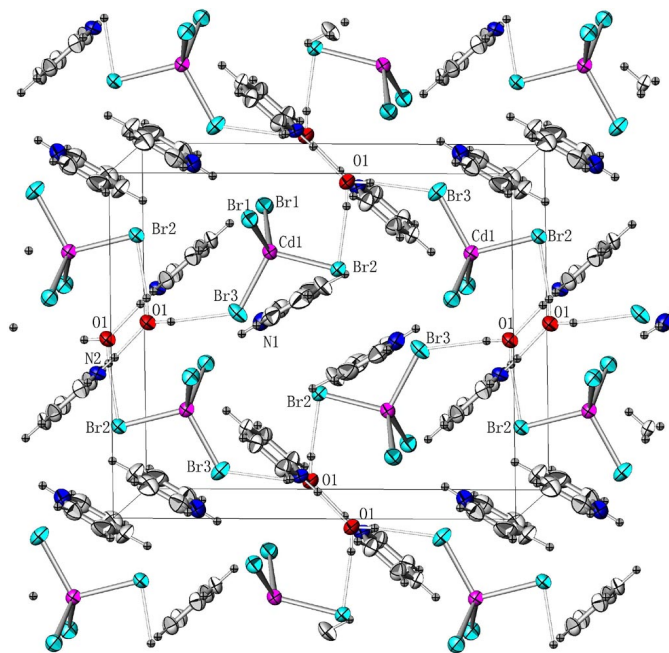


Figure 2

The crystal packing, viewed approximately down the *b* axis, showing the hydrogen-bonded network (dashed lines) formed by atom O1 associated with N2, Br2 and Br3.

respectively, and refined as riding, with *U<sub>iso</sub>*(H) = 1.2*U<sub>eq</sub>*(C). Water H atoms were initially located in a difference Fourier map and their positions were refined freely along with an isotropic displacement parameter.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: ORTEP-3 (Farrugia, 1997); software used to prepare material for publication: SHELXTL.

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