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## Key indicators

Single-crystal X-ray study  
*T* = 297 K  
Mean  $\sigma(\text{C}-\text{C})$  = 0.003 Å  
*R* factor = 0.052  
*wR* factor = 0.149  
Data-to-parameter ratio = 28.5For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

## Redetermination of piperazine dihydrochloride monohydrate

In the title compound,  $\text{C}_4\text{H}_{12}\text{N}_2^{2+} \cdot 2\text{Cl}^- \cdot \text{H}_2\text{O}$ , the piperazinium dication has a center of symmetry, while the water molecule is on the twofold axis. The structure exhibits chains of piperazinium dications linked together by  $\text{N}-\text{H} \cdots \text{Cl}$  hydrogen bonds with chloride ions. Between the chains, there are weak hydrogen bonds of the  $\text{O}-\text{H} \cdots \text{Cl}$  and  $\text{C}-\text{H} \cdots \text{Cl}$  types.

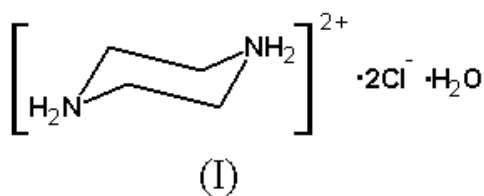
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## Comment

Hydrogen bonding plays an important role in the crystal engineering of organic solids (Desiraju, 1989; Melendez & Hamilton, 1998). There are many examples of one-, two- and three-dimensional motifs formed by hydrogen bonds. The crystal structure of the title compound, (I), has already been reported by R erat (1960), where a photographic method was used for the intensity measurement and an isotropic refinement of non-H atoms was applied. The refinement of low resolution (0.95 Å) and low quality of data resulted in a poor *R* value of 0.28 and no H atoms were located. We present here a redetermination of this structure using data from a Siemens SMART CCD diffractometer.



The atomic numbering for (I) is presented in Fig. 1. The structure exhibits hydrogen bonds of the type  $\text{N}-\text{H} \cdots \text{Cl}$ ,

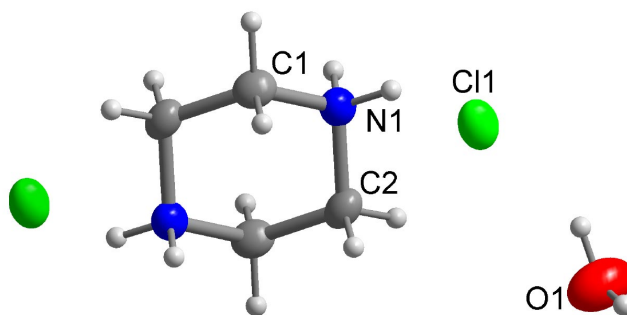
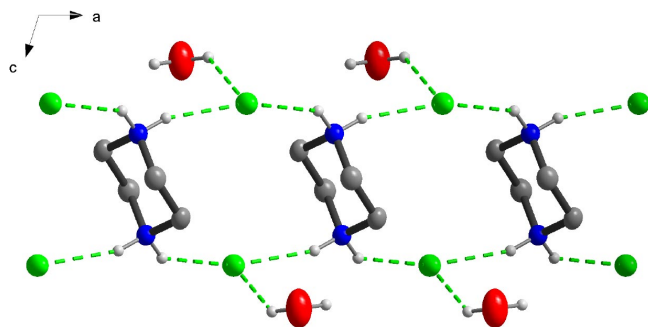
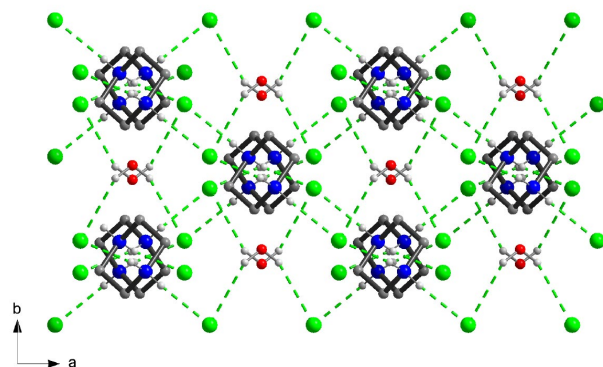


Figure 1

The molecular structure of (I). Displacement ellipsoids are shown at the 50% probability level.



**Figure 2**  
Representation of a hydrogen-bonded chain in the structure of (I). Each chain is involved in hydrogen bonding with water molecules.



**Figure 3**  
A view along the *c* axis showing how chains are crossed with respect to each other. Water molecules are in the channels and are weakly bonded to the chains.

forming chains of hydrogen-bonded ions along the  $[110]$  and  $[\bar{1}10]$  directions (Fig. 2). The water molecules are on twofold axes and are located in the channels formed by crossed chains and they are involved in weak hydrogen bonds of the  $O-H \cdots Cl$  type with the nearest chains (Fig. 3). Thus, the water molecule shows high mobility which is reflected by high anisotropic displacement parameters of the O atom.

## Experimental

The title compound was prepared by the reaction of an ethanolic solution of piperazine and HCl (37% in water) in the molar ratio 1:2.5 at room temperature. Crystals of (I) were obtained by slow evaporation of the solution.

### Crystal data

$C_4H_{12}N_2^{2+} \cdot 2Cl^- \cdot H_2O$   
 $M_r = 177.07$   
 Monoclinic,  $C2/c$   
 $a = 10.2233$  (3) Å  
 $b = 6.3323$  (3) Å  
 $c = 13.5389$  (6) Å  
 $\beta = 107.587$  (2)°  
 $V = 835.50$  (6) Å<sup>3</sup>  
 $Z = 4$

$D_x = 1.408$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 Cell parameters from 1781 reflections  
 $\theta = 1-32^\circ$   
 $\mu = 0.71$  mm<sup>-1</sup>  
 $T = 297$  (2) K  
 Thin plate, colorless  
 $0.40 \times 0.20 \times 0.04$  mm

### Data collection

Siemens SMART CCD diffractometer  
 $\omega$  scans  
 Absorption correction: multi-scan (Sheldrick, 1996)  
 $T_{\min} = 0.764$ ,  $T_{\max} = 0.972$   
 3545 measured reflections

1453 independent reflections  
 974 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.043$   
 $\theta_{\max} = 32.9^\circ$   
 $h = -8 \rightarrow 15$   
 $k = -8 \rightarrow 9$   
 $l = -20 \rightarrow 20$

### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.052$   
 $wR(F^2) = 0.149$   
 $S = 1.02$   
 1453 reflections  
 51 parameters

H atoms treated by a mixture of independent and constrained refinement  
 $w = 1/[\sigma^2(F_o^2) + (0.0792P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} = 0.001$   
 $\Delta\rho_{\max} = 0.48$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.35$  e Å<sup>-3</sup>

**Table 1**

Selected geometric parameters (Å, °).

N1—C2	1.487 (3)	C1—C2 <sup>i</sup>	1.510 (3)
N1—C1	1.491 (3)		
C2—N1—C1	110.92 (16)	N1—C2—C1 <sup>i</sup>	110.23 (17)
N1—C1—C2 <sup>i</sup>	111.01 (17)		

Symmetry code: (i)  $1 - x, 1 - y, 1 - z$ .

**Table 2**

Hydrogen-bonding geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N1—H1B <sup>i</sup> $\cdots$ Cl1	0.90	2.39	3.1412 (19)	141
N1—H1A <sup>i</sup> $\cdots$ Cl1 <sup>i</sup>	0.90	2.29	3.1541 (18)	162
O1—H1 <sup>i</sup> $\cdots$ Cl1 <sup>ii</sup>	0.86 (2)	2.82 (4)	3.492 (3)	137 (5)
C2—H2B <sup>i</sup> $\cdots$ Cl1 <sup>iii</sup>	0.97	2.80	3.475 (2)	128

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

The unique H atom of the water molecule was located from a difference Fourier map and was refined with a fixed isotropic displacement parameter and a restrained bond distance of 0.85 Å, whereas the other H atoms were constrained to idealized geometries using the appropriate riding model.

Data collection: *SMART* (Siemens, 1995); cell refinement: *SAINT* (Siemens, 1995); data reduction: *SAINT* and *SADABS* (Sheldrick, 1996); program(s) used to solve structure: *SHELXTL* (Bruker, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *DIAMOND* (Brandenburg, 2000).

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