

## Paz Vaqueiro

 Department of Chemistry, Heriot-Watt  
 University, Edinburgh EH14 4AS, Scotland

Correspondence e-mail: chepv@hw.ac.uk

## Key indicators

 Single-crystal X-ray study  
 $T = 293\text{ K}$   
 Mean  $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$   
 $R$  factor = 0.029  
 $wR$  factor = 0.033  
 Data-to-parameter ratio = 10.7

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

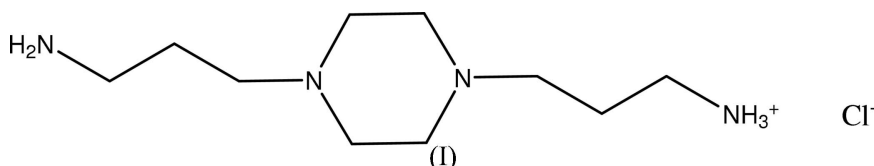
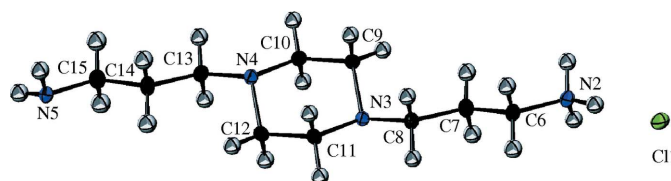
 3-[4-(3-Aminopropyl)piperazin-1-yl]propan-  
 1-aminium chloride

 The title compound,  $\text{C}_{10}\text{H}_{25}\text{N}_4^+\cdot\text{Cl}^-$ , contains monoprotonated amine cations and chloride anions. The cations form chains along the [101] direction *via*  $\text{N}-\text{H}\cdots\text{N}$  bonds, while  $\text{N}-\text{H}\cdots\text{Cl}$  hydrogen bonds link the anions and cations into a three-dimensional structure.

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## Comment

 In solvothermal synthesis, organic amines are generally used as structure-directing agents, and it is known that sometimes salts of the amines appear as unwanted side products. However, recent work on the solvothermal synthesis of phosphates (Rao *et al.*, 2000) and sulfates (Behera *et al.*, 2004) suggests that these amine salts might play a role in the formation of open-framework phases. It has also been found that the use of amine salts as sources of structure-directing agents may result in the formation of new open-framework structures.

 In the title compound,  $\text{C}_{10}\text{H}_{25}\text{N}_4^+\cdot\text{Cl}^-$ , (I), which was the unexpected product of a solvothermal reaction, the amine 1,4-bis(3-aminopropyl)piperazine (bapp) crystallizes as a monoprotonated cation,  $\text{H}^+\text{bapp}$ , accompanied by a charge-balancing chloride anion (Fig. 1). As well as electrostatic forces, the anions and cations in (I) interact by means of hydrogen bonds (Table 1). The  $\text{H}^+\text{bapp}$  cations are connected by strong  $\text{N}-\text{H}\cdots\text{N}$  hydrogen bonds, forming infinite chains that run along the [101] direction. The chains are cross-linked by  $\text{N}-\text{H}\cdots\text{Cl}$  bonds arising from the terminal  $-\text{NH}_2$  and  $-\text{NH}_3^+$  groups to form layers parallel to the *ac* plane (Fig. 2). Further  $\text{N}-\text{H}\cdots\text{Cl}$  hydrogen bonds link the layers into a three-dimensional structure (Fig. 3).


**Figure 1**  
View of (I), showing 50% probability displacement ellipsoids (arbitrary spheres for the H atoms).

## Experimental

A mixture of CuCl (2 mmol), Te (1 mmol) and 1,4-bis(3-amino-propyl)piperazine (4.2 ml) was loaded into a 23 ml Teflon-lined steel autoclave, heated for 13 days at 473 K and then cooled to room temperature over a period of 12 h. The product, consisting of hygroscopic colourless needles of (I) and a black powder, was filtered and washed with methanol and acetone.

### Crystal data

$C_{10}H_{25}N_4^+ \cdot Cl^-$	$Z = 4$
$M_r = 236.79$	$D_x = 1.155 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 10.9035 (9) \text{ \AA}$	$\mu = 0.26 \text{ mm}^{-1}$
$b = 15.9679 (13) \text{ \AA}$	$T = 293 \text{ K}$
$c = 7.8750 (6) \text{ \AA}$	Needle, colourless
$\beta = 96.693 (4)^\circ$	$0.50 \times 0.10 \times 0.10 \text{ mm}$
$V = 1361.74 (19) \text{ \AA}^3$	

### Data collection

Bruker-Nonius APEX2 CCD area-detector diffractometer	18638 measured reflections
$\omega/2\theta$ scans	3967 independent reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	2257 reflections with $I > 3.00\sigma(I)$
$T_{\min} = 0.811$ , $T_{\max} = 0.974$	$R_{\text{int}} = 0.023$
	$\theta_{\text{max}} = 30.1^\circ$

### Refinement

Refinement on $F$	$W = [1 - (\delta F/6\sigma F)^2]/[0.491T_0(x) + 0.340T_1(x) + 0.263T_2(x)]$
$R[F^2 > 2\sigma(F^2)] = 0.029$	where $T_i$ are Chebyshev polynomials and $x = F/F_{\text{max}}$ (Watkin, 1994; Prince, 1982)
$wR(F^2) = 0.033$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.11$	$\Delta\rho_{\text{max}} = 0.32 \text{ e \AA}^{-3}$
2257 reflections	$\Delta\rho_{\text{min}} = -0.18 \text{ e \AA}^{-3}$
211 parameters	
Only H-atom coordinates refined	

**Table 1**

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

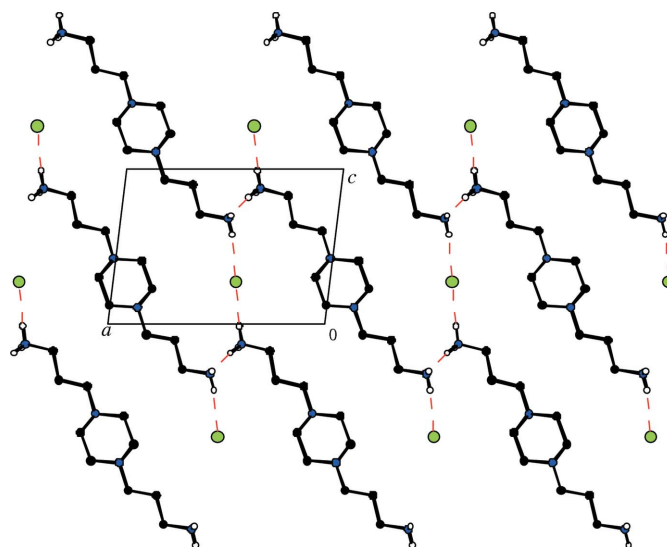
$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N2-H23 \cdots N5^I$	0.93 (2)	1.83 (2)	2.7574 (18)	175 (2)
$N2-H21 \cdots CH1^I$	0.91 (2)	2.27 (2)	3.1761 (12)	176 (2)
$N2-H22 \cdots CH1^{II}$	0.88 (2)	2.30 (2)	3.1853 (13)	178 (1)
$N5-H52 \cdots CH1^{III}$	0.89 (2)	2.58 (2)	3.4104 (13)	156 (2)
$N5-H53 \cdots CH1^{IV}$	0.85 (2)	2.61 (2)	3.4344 (13)	164 (2)

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

H atoms were located in difference maps and their positions were freely refined;  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{carrier})$ .

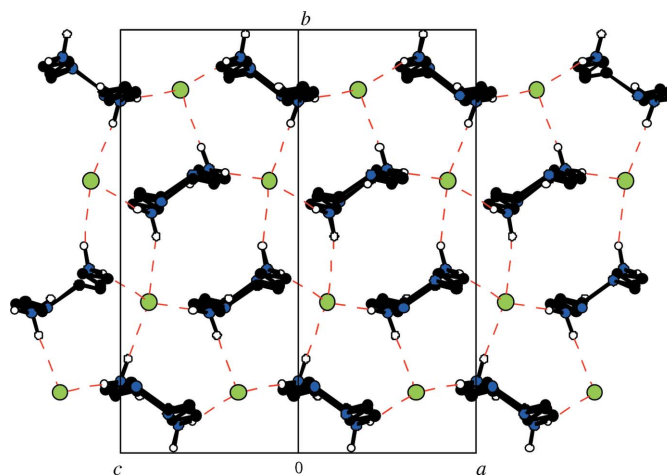
Data collection: APEX2 (Bruker, 2005); cell refinement: APEX2; data reduction: APEX2; program(s) used to solve structure: SIR92 (Altomare *et al.*, 1994); program(s) used to refine structure: CRYSTALS (Betteridge *et al.*, 2003); molecular graphics: ATOMS (Dowty, 2000); software used to prepare material for publication: CRYSTALS.

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**Figure 2**

View of a layer parallel to the (010) plane, showing the network of hydrogen bonds (dashed lines). Hydrogen atoms not participating in hydrogen bonding have been omitted for clarity.



**Figure 3**

View of the packing in (I). Drawing conventions as in Fig. 2.

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