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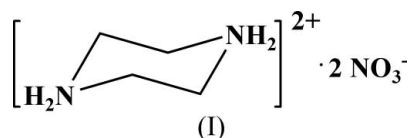
## Key indicators

Single-crystal X-ray study  
 $T = 273$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å  
 $R$  factor = 0.034  
 $wR$  factor = 0.090  
Data-to-parameter ratio = 17.2For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

## Piperazinium dinitrate

In the title compound,  $\text{C}_4\text{H}_8\text{N}_2^{2+} \cdot 2\text{NO}_3^-$ , the piperazinium dication has a centre of symmetry. The ions are linked by  $\text{N}-\text{H} \cdots \text{O}$  hydrogen bonds into a chain.Received 3 December 2006  
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## Comment

Considerable progress has recently been made on the crystal engineering of supramolecular architectures organized and sustained by means of non-covalent supramolecular contacts (such as hydrogen bonds and  $\pi-\pi$  interactions), aurophilicity, and similar interactions (Colacio *et al.*, 2002; Roesky & Andruh, 2003; Guilera & Steed, 1999). Here, we report the crystal structure of piperazinium dinitrate, (I).

The asymmetric unit of (I) consists of one half of the piperazinium cation and one nitrate anion. As shown in Fig. 1, inversion symmetry generates the complete piperazinium cation, and the piperazinium ring in the crystal structure of (I) adopts a chair conformation.

As shown in Fig. 2, two O atoms of the nitrate anion act as hydrogen-bond acceptors and link two piperazinium cations *via*  $\text{N}-\text{H} \cdots \text{O}$  hydrogen bonds (Table 1). The ions are thus linked into a double chain along the  $b$  axis.

## Experimental

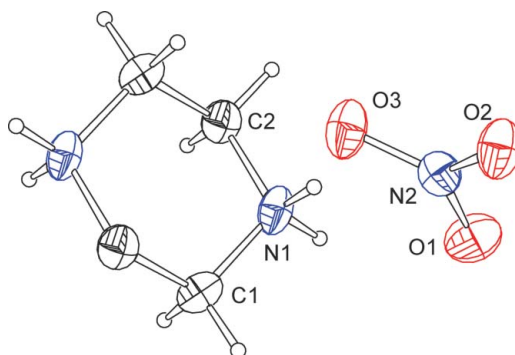
A mixture of  $\text{Zn}(\text{NO}_3)_2 \cdot 6\text{H}_2\text{O}$  (0.30 g, 1 mmol), piperazine (0.087 g, 1 mmol), succinic acid (0.18 g, 1 mmol) and water (18 ml) was sealed

Figure 1

The cation and anion of the title compound, showing 30% probability displacement ellipsoids. [Symmetry code for unlabelled atoms:  $\frac{1}{2} - x, \frac{1}{2} - y, -z$ .]

in a 25 ml Teflon-lined stainless steel reactor and heated at 433 K for 3 d. On completion of the reaction, the reactor was cooled slowly to room temperature and the mixture was filtered, giving colourless single crystals of (I) suitable for X-ray analysis.

#### Crystal data

$C_4H_{12}N_2^{2+} \cdot 2NO_3^-$   
 $M_r = 212.18$   
 Monoclinic,  $C2/c$   
 $a = 14.6895$  (3) Å  
 $b = 5.9301$  (1) Å  
 $c = 12.4018$  (4) Å  
 $\beta = 120.956$  (1)°  
 $V = 926.44$  (4) Å<sup>3</sup>

$Z = 4$   
 $D_x = 1.521$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 $\mu = 0.14$  mm<sup>-1</sup>  
 $T = 273$  (2) K  
 Prism, colourless  
 $0.30 \times 0.20 \times 0.06$  mm

#### Data collection

Siemens SMART 1K CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
 $T_{\min} = 0.88$ ,  $T_{\max} = 1.00$

3535 measured reflections  
 1104 independent reflections  
 535 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.053$   
 $\theta_{\text{max}} = 28.0^\circ$

#### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.034$   
 $wR(F^2) = 0.090$   
 $S = 0.77$   
 1104 reflections  
 64 parameters

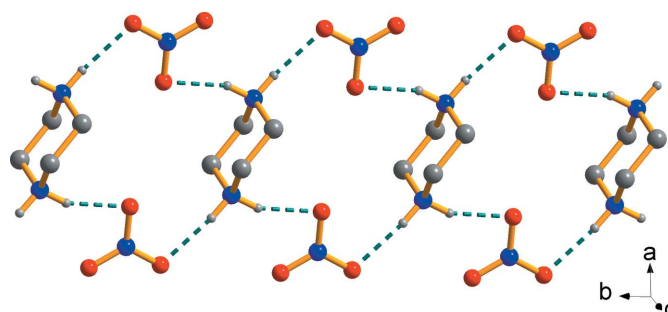
H-atom parameters constrained  
 $w = 1/[\sigma^2(F_o^2) + (0.0417P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.15$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.17$  e Å<sup>-3</sup>

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N1-H1A \cdots O3$	0.90	2.05	2.9025 (17)	158
$N1-H1D \cdots O2^i$	0.90	2.01	2.8694 (17)	160

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



**Figure 2**

The double chain in the title compound. Hydrogen bonds are shown as dashed lines. C-bound H atoms have been omitted.

H atoms were placed at calculated positions and refined using a riding model, with C–H = 0.97 Å and N–H = 0.90 Å, and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$ .

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: DIAMOND (Bergerhoff *et al.*, 1996); software used to prepare material for publication: SHELXL97.

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