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Key indicators

Single-crystal X-ray study T = 143 KMean $\sigma(\text{N}-\text{C}) = 0.002 \text{ Å}$ R factor = 0.025 wR factor = 0.064 Data-to-parameter ratio = 20.2

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

Tetramethylguanidinium chloride

In the title compound, $C_5H_{14}N_3^+ \cdot Cl^-$, the central C atom displays almost ideal trigonal planar geometry. Classical hydrogen bonds of the form $N^+ - H \cdot \cdot \cdot Cl^-$ link the formula units into discrete centrosymmetric dimers.

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Comment

The title compound was formed as an unexpected hydrolysis product during a study of guanidinophosphine derivatives (Münchenberg, 1996). Its structure is nevertheless of interest because few salts of this cation have been structurally investigated (CCDC refcodes: BEQQOD, KOYWEA, MATKAT and XERHEH; Version Oct. 2002; Allen & Kennard, 1993), and because of its hydrogen-bonding pattern.



The formula unit displays no imposed crystallographic symmetry. The geometry at the central atom C1 is almost ideal trigonal planar; the r.m.s. deviation from the least-squares plane of C1, N1, N2 and N3 is 0.006 Å. The methyl groups are rotated out of this plane (torsion angles are in Table 1).

The classical hydrogen bonds of the form $N^+-H\cdots Cl^-$ (Table 2) link the formula units into discrete centrosymmetric dimers (Fig. 1). Further contacts of the form $C-H\cdots Cl^-$, the shortest of which (C4-H4C···Cl) has a normalized (Steiner, 1998) H···Cl distance of only 2.70 Å, may also be interpreted as hydrogen bonds.

Experimental

Crystal aata	
$C_5H_{14}N_3^+ \cdot Cl^-$	$D_x = 1.222 \text{ Mg m}^{-3}$
$M_r = 151.64$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 50
a = 6.979 (4) Å	reflections
b = 13.153 (7) Å	$\theta = 10-11.5^{\circ}$
c = 9.283 (4) Å	$\mu = 0.39 \text{ mm}^{-1}$
$\beta = 104.73 \ (4)^{\circ}$	T = 143 (2) K
$V = 824.1 (7) \text{ Å}^3$	Block, colourless
Z = 4	$0.7 \times 0.6 \times 0.6 \text{ mm}$

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Data collection

Stoe Stadi-4 diffractometer ω/θ scans Absorption correction: none 3151 measured reflections 1900 independent reflections 1763 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.026$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.025$ $wR(F^2) = 0.065$ S = 1.081900 reflections 94 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

N1-C1 N2-C1	1.3304 (15) 1.3417 (15)	N3-C1	1.3370 (14)
N1-C1-N3 N1-C1-N2	120.91 (10) 119.70 (10)	N3-C1-N2	119.36 (10)
C4-N3-C1-N1 C5-N3-C1-N1	-23.93 (16) 151.32 (11)	C2-N2-C1-N1 C3-N2-C1-N1	-21.74 (16) 145.76 (11)

 $\theta_{\rm max} = 27.6^{\circ}$

 $h = -9 \rightarrow 9$

 $k = -17 \rightarrow 0$ $l = -12 \rightarrow 6$

3 standard reflections

frequency: 60 min

intensity decay: none

 $w = 1/[\sigma^2(F_o^2) + (0.0265P)^2]$

where $P = (F_o^2 + 2F_c^2)/3$

+ 0.1898P]

 $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.16 \text{ e } \text{\AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.19 \text{ e} \text{ \AA}^{-3}$

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - H \cdot \cdot \cdot A$
$N1-H1A\cdots Cl$	0.918 (17)	2.415 (17)	3.2863 (17)	158.4 (13)
$N1-H1B\cdots Cl^{i}$	0.866 (17)	2.373 (17)	3.2268 (17)	168.9 (14)
$C3-H3B\cdots Cl^{ii}$	0.98	2.89	3.773 (2)	150
$C4-H4A\cdots Cl^{iii}$	0.98	3.00	3.776 (2)	137
$C4-H4C\cdots Cl$	0.98	2.77	3.574 (2)	139
$C5-H5A\cdots Cl^{iv}$	0.98	2.96	3.922 (2)	167
$C5-H5B\cdots Cl^{iii}$	0.98	2.81	3.6492 (19)	144

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



Figure 1

Dimeric unit of the title compound. Hydrogen bonds (Table 2) are indicated as thick dashed lines. Ellipsoids are at the 50% probability level.

H atom positions were obtained from difference syntheses. Methyl groups were refined as idealized rigid groups allowed to rotate about the C–N bonds. H atoms of the NH_2 group were refined freely.

Data collection: *DIF*4 (Stoe & Cie, 1992); cell refinement: *DIF*4; data reduction: *REDU*4 (Stoe & Cie, 1992); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *XP* (Siemens, 1994); software used to prepare material for publication: *SHELXL*97.

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