

Constructor graph description of hydrogen bonding in a supramolecular assembly of (3,5-dimethyl-1*H*-pyrazol-4-ylmethyl)isopropylammonium chloride monohydrate

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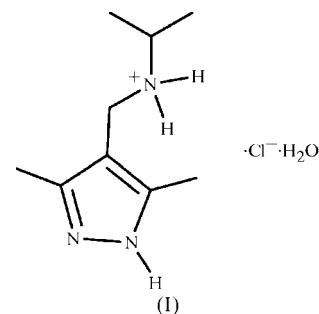
Five distinct strong hydrogen-bonding interactions of four kinds (N–H···Cl, N–H···O, O–H···N, and O–H···Cl) connect molecules of the title compound, C₉H₁₈N₃⁺·Cl[−]·H₂O, in the crystal structure into corrugated sheets stacked along the *a* axis. The intermolecular interactions are efficiently described in terms of the first- through fifth-level graph sets. A two-dimensional constructor graph helps visualize the supramolecular assembly.

Comment

Substituted pyrazoles constitute an important family of heterocyclic compounds that have found use in drug development and catalysis (Elguero, 1996; Brown & Kee, 1993). An important attribute of potential drug chemicals is their solubility in water, which is frequently achieved by derivatization. During our studies towards water-soluble palladium and platinum complexes with potential anticancer properties, we set out to prepare 4-(alkylamino)pyrazoles through the direct reaction of 3,5-dimethylpyrazole with formaldehyde and alkylamines according to Esquiú *et al.* (2000). However, in the reaction with isopropylamine, a two-week long recrystallization of CHCl₃ extracts of the final product yielded the title compound, (I), in 87% yield, and we now report the solid-state structure of this water-soluble ammonium salt.

A molecular drawing of (I) is shown in Fig. 1. The bond distances and angles within the cation are typical, as confirmed by the *Mogul* structural check (Bruno *et al.*, 2004). There are five strong hydrogen-bonding interactions, denoted *a–e* (Table 1), of four types (N–H···Cl, N–H···O, O–H···N, and O–H···Cl). These hydrogen bonds link the ions and water molecules into two-dimensional corrugated sheets (Fig. 2) stacked along the *a* axis, with weak intermolecular

contacts between them (Fig. 3), which will be discussed below. These hydrogen bonds feature relatively short *D*···*A* distances and *D*–H···*A* angles spanning the range 167.9 (18)–173 (2)°, and are comparable in length to other similar hydrogen bonds in the Cambridge Structural Database (CSD; Version 5.28, January 2007 release; Allen, 2002) (Table 1).



The hydrogen-bonding interaction network in (I) generated by the *n*-glide plane normal to the *a* axis can be readily visualized with the help of the constructor graph (Grell *et al.*, 1999; Motherwell *et al.*, 2000). We recently used this approach for an analysis of the intermolecular interactions in *N,N'*-bis(2-hydroxy-1-methylethyl)phthalamide (Guzei *et al.*, 2007).

A constructor graph projection of the hydrogen-bonding interactions in (I) on to the *bc* plane is shown in Fig. 4. The two main ring patterns are immediately identifiable, namely a ring formed by four hydrogen bonds $\vec{a} \leftarrow \vec{c} \vec{b} \vec{d}$ motif $R_4^3(9)$, giving a quaternary system N_4 , and a ring formed by six hydrogen bonds $\vec{a} \leftarrow \vec{e} \vec{d} \vec{b} \vec{e} \leftarrow \vec{c}$ motif $R_6^4(20)$, giving a pentary system N_5 (Bernstein *et al.*, 1995). Arrows denote the direction of the hydrogen bond: \rightarrow designates a donor-to-acceptor *D*–H···*A* interaction, while \leftarrow represents an acceptor-to-donor *A*···H–*D* orientation.

The quaternary ring system links the molecules in a head-to-tail fashion, forming rows of molecules in the [011] direction. The pentary ring system (hydrogen bonds *e*) then links these rows of molecules together to form sheets in the *bc*

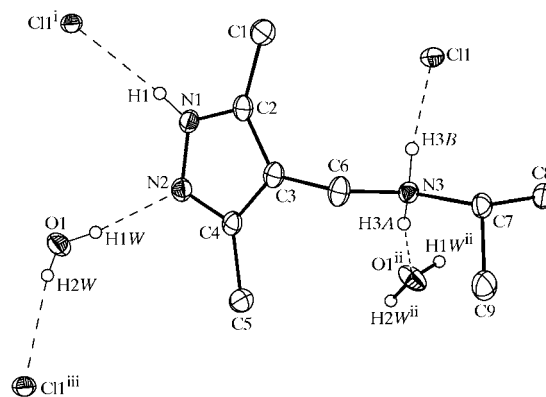


Figure 1

A molecular drawing of (I), shown with 50% probability displacement ellipsoids. All H atoms bonded to C atoms have been omitted for clarity. Hydrogen bonds are shown as dashed lines. [Symmetry codes: (i) $-x + \frac{1}{2}$, $y + \frac{1}{2}$, $z + \frac{1}{2}$; (ii) $-x + \frac{1}{2}$, $y - \frac{1}{2}$, $z - \frac{1}{2}$; (iii) x , y , $z + 1$.]

plane. Several chain motifs propagate in four directions, namely a tertiary $C_3^2(10)$ motif $\overrightarrow{a} \overrightarrow{e} \overrightarrow{b}$ along [010]; a tertiary $C_3^2(10)$ motif $\overrightarrow{d} \overrightarrow{e} \overrightarrow{c}$ along [001]; a binary $C_2^1(8)$ motif $\overrightarrow{a} \overrightarrow{c}$, a binary $C_2^2(8)$ motif $\overrightarrow{b} \overrightarrow{d}$ and their quaternary combination $\overrightarrow{a} \overrightarrow{c} \overrightarrow{d} \overrightarrow{b}$ with the additive representation $C_4^3(16)$ along [011]; and a tertiary $C_3^2(7)$ motif $\overrightarrow{a} \overrightarrow{d} \overrightarrow{e}$, a tertiary $C_3^2(6)$ motif $\overrightarrow{b} \overrightarrow{e} \overrightarrow{c}$ and their pentary combination $C_5^4(13)$ $\overrightarrow{a} \overrightarrow{d} \overrightarrow{e} \overrightarrow{c} \overrightarrow{b} \overrightarrow{e}$ along [011]. Note that in all interactions involving the chloride, the number of acceptors is fewer than the number of donors, since each acidic H atom serves as a donor in exactly one hydrogen-bonding interaction, whereas each chloride serves as the acceptor in three different interactions, viz. *a*, *c*, and *e*.

There are three types of possible weaker intermolecular contacts between the hydrogen-bonded sheets, viz. C8—

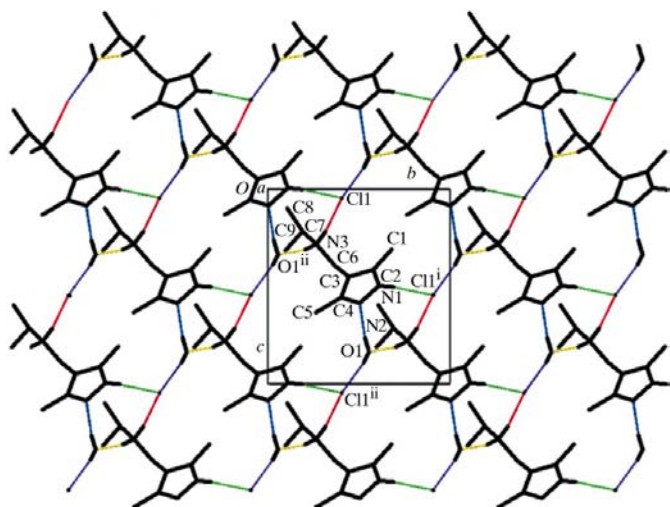


Figure 2
A packing diagram for (I), shown along the *a* axis. All H atoms bonded to C atoms have been omitted for clarity. [Symmetry codes: (i) $-x + \frac{1}{2}, y + \frac{1}{2}, z + \frac{1}{2}$; (ii) $-x + \frac{1}{2}, y - \frac{1}{2}, z - \frac{1}{2}$]

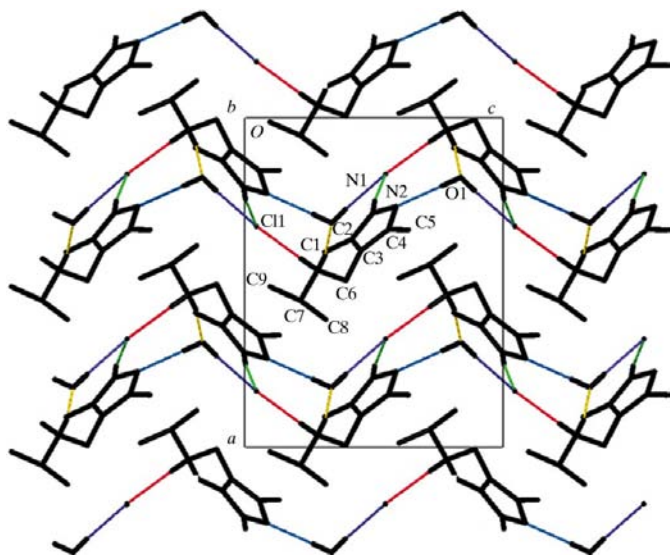


Figure 3
A packing diagram for (I), shown along the *b* axis. All H atoms bonded to C atoms have been omitted for clarity.

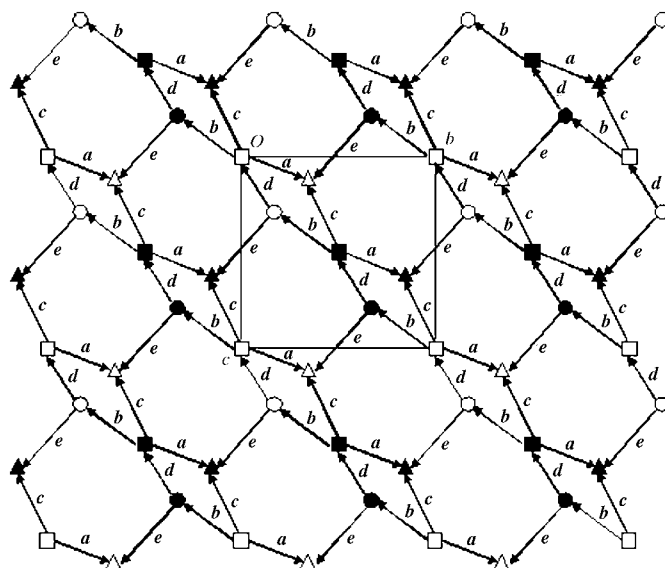


Figure 4
Constructor graph of compound (I), viewed along the *a* axis. The arrows denote the five types of hydrogen bonds, labeled according to Table 1. Arrows originate at the donor molecules and point to acceptor molecules. Squares represent cations, triangles Cl^- anions and circles water molecules. Solid symbols are translated mirror images of the open symbols.

$\text{H8A} \cdots \text{Cl1}$ [$\text{H} \cdots \text{A} = 2.928(19) \text{ \AA}$ and $D-\text{H} \cdots \text{A} = 140.4(16)^\circ$], $\text{C6}-\text{H6A} \cdots \text{Cl1}(1-x, 1-y, z + \frac{1}{2})$ [$2.925(19) \text{ \AA}$ and $115.9(13)^\circ$] and a non-classical $\text{C7}-\text{H7} \cdots \text{N1}(1-x, 1-y, z - \frac{1}{2})$ contact [$2.64(2) \text{ \AA}$ and $151.2(15)^\circ$], which connect the sheets into a three-dimensional framework.

The current work is another illustration of the convenience of the hydrogen-bonding interaction analysis in two-dimensional networks using the constructor graph methodology.

Experimental

A mixture of 3,5-dimethylpyrazole (1.0 g, 10.4 mmol), paraformaldehyde (0.5 g, 16 mmol), KOH (0.9 g, 16 mmol) and isopropylamine (1.3 g, 20 mmol) was dissolved in water (50 ml) and refluxed for 48 h. The product was extracted from the aqueous solution using CHCl_3 (180 ml) and dried over anhydrous MgSO_4 . The solution was concentrated *in vacuo* to ca 50 ml. The concentrated extract was left to stand at room temperature for ca two weeks, whereupon slow evaporation of the solvent yielded X-ray quality crystals (yield 1.53 g, 87%). $^1\text{H NMR}$ (CDCl_3): δ 4.80 (*br*, 1H, NH^iPr), 3.53 (*br s*, 2H, $\text{CH}_2\text{NH}^i\text{Pr}$), 2.81 [*m*, 1H, $\text{NCH}(\text{CH}_3)_2$], 2.23 (*s*, 6H, CH_3), 1.06 [*d*, $^3J_{\text{HH}} = 5.8 \text{ Hz}$, 6H, $\text{NCH}(\text{CH}_3)_2$]; $^{13}\text{C}\{^1\text{H}\}$ NMR (CDCl_3): δ 144.8 [$\text{C}(3,5\text{-pz})$], 113.2 [$\text{C}(4\text{-pz})$], 48.3 [$\text{C}(\text{CH}_3, ^i\text{Pr})$], 39.2 [$\text{C}(\text{CH}_2\text{NH}^i\text{Pr})$], 20.2 [$\text{CH}(\text{CH}_3, ^i\text{Pr})$], 11.1 [$\text{C}(\text{CH}_3, 3,5\text{-pz})$]; IR (Nujol, ν , cm^{-1}): 3272 (N—H), 2962 (N—H + C—H), 1571 (C=N).

Crystal data

$\text{C}_9\text{H}_{18}\text{N}_3^+ \cdot \text{Cl}^- \cdot \text{H}_2\text{O}$
 $M_r = 221.73$
Orthorhombic, $\text{Pna}2_1$
 $a = 12.7944(9) \text{ \AA}$
 $b = 9.3494(7) \text{ \AA}$
 $c = 10.0269(7) \text{ \AA}$

$V = 1199.42(15) \text{ \AA}^3$
 $Z = 4$
Mo $K\alpha$ radiation
 $\mu = 0.30 \text{ mm}^{-1}$
 $T = 100(2) \text{ K}$
 $0.49 \times 0.37 \times 0.25 \text{ mm}$

Data collection

Bruker SMART CCD-1000 area-detector diffractometer	9296 measured reflections
Absorption correction: multi-scan (SADABS; Bruker, 2003)	2446 independent reflections
$T_{\min} = 0.869$, $T_{\max} = 0.930$	2305 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.023$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.023$	All H-atom parameters refined
$wR(F^2) = 0.059$	$\Delta\rho_{\text{max}} = 0.26 \text{ e } \text{\AA}^{-3}$
$S = 1.04$	$\Delta\rho_{\text{min}} = -0.13 \text{ e } \text{\AA}^{-3}$
2446 reflections	Absolute structure: Flack (1983),
208 parameters	with 1150 Friedel pairs
1 restraint	Flack parameter: -0.05 (4)

Table 1

The interionic hydrogen-bonding interactions in (I) (\AA , $^\circ$).

Interaction	$D-H$	$H \cdots A$	$D-H \cdots A$	$D-H \cdots A$
<i>a</i> N1–H1 \cdots Cl1 ⁱ	0.860 (18)	2.344 (18)	3.1980 (14)	171.9 (15)
<i>b</i> N3–H3A \cdots O1 ⁱⁱ	0.868 (18)	1.887 (18)	2.7421 (17)	167.9 (18)
<i>c</i> N3–H3B \cdots Cl1	0.92 (2)	2.30 (2)	3.2064 (13)	170.0 (16)
<i>d</i> O1–H1W \cdots N2	0.82 (2)	1.99 (2)	2.8016 (17)	173 (2)
<i>e</i> O1–H2W \cdots Cl1 ⁱⁱⁱ	0.80 (3)	2.37 (3)	3.1583 (13)	170 (2)

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

Compound (I) crystallizes in the space group $Pna2_1$; the correctness of the chosen molecular arrangement was confirmed by the Flack (1983) parameter value of -0.05 (4) refined with the TWIN/BASF card combination in *SHELXTL* (Bruker, 2003). All H atoms were located in a difference map and refined independently with isotropic displacement parameters.

Data collection: *SMART* (Bruker, 2003); cell refinement: *SAINTE* (Bruker, 2003); data reduction: *SAINTE*; program(s) used to solve

structure: *SHELXTL* (Bruker, 2003); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL* and *Mercury* (Macrae *et al.*, 2006); software used to prepare material for publication: *SHELXTL*.

The manuscript was prepared with the beta test version 1.0.2 of the program *publCIF*, released by the IUCr, and IAG's program *modiCIFer*.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: SF3043). Services for accessing these data are described at the back of the journal.

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