# organic compounds

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# 4,4'-(Azinodimethylene)dipyridinium bis(tetrafluoroborate) and 4-[(4-pyridylmethylene)hydrazonomethyl]pyridinium perchlorate: two different hydrogen-bonding motifs

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In the crystal structures of the title compounds,  $C_{12}H_{12}N_4^{2^+}$ . 2BF<sub>4</sub><sup>-</sup>, (I), and  $C_{12}H_{11}N_4^+$ ·ClO<sub>4</sub><sup>-</sup>, (II), respectively, infinite two- and one-dimensional architectures are built up *via* N– H···F [in (I)] and conventional N–H···N [in (II)] hydrogen bonding. The N–N single bond in (I) lies on a crystallographic centre of symmetry; as a result, the two pyridinium rings are parallel. In (II), the pyridinium and pyridyl ring planes are inclined with a dihedral angle of 14.45 (3)°.

# Comment

Neutral 1,2-bis(4-pyridylmethylene)hydrazine has been known as an antitumour precursor (Hirayama *et al.*, 1980) as well as an analytical reagent for the determination of Fe<sup>2+</sup> concentration in solution (Luque de Castro & Valcarcel, 1978). Recent interest in this and related molecules stems from their use as linear organic mono- or bidentate bridging ligands in the crystal engineering of multidimensional coordination polymers (Ciurtin *et al.*, 2001; Patra & Goldberg, 2003; Kennedy *et al.*, 2005; Granifo *et al.*, 2006). The characterization of 1,2-bis(4-pyridylmethylene)hydrazine (El-Rayyes & Katrib, 1983) and its crystal structure (Shanmuga

$$\begin{bmatrix} H_{-N} & H_{-N} & H_{-N} \end{bmatrix}^{2+} \cdot 2BF_4^- \begin{bmatrix} N & H_{-N} & H_{-N} \end{bmatrix}^+ \cdot CIO_4^-$$

Sundara Raj *et al.*, 2000; Ciurtin *et al.*, 2001), as well as the crystal structure of 4,4'-(azinodimethylene)dipyridinium bis(perchlorate) (Chen *et al.*, 1997), have been reported. The geometric features of the non-isostructural compounds 4,4'-azinodimethylene)dipyridinium bis(tetrafluoroborate), (I), and 4-[(4-pyridylmethylene)hydrazonomethyl]pyridinium perchlorate, (II), are discussed here.

The N1-N1<sup>i</sup> [symmetry code: (i) -x, -y + 2, -z + 2] and N1=C1 bond distances in (I), and N1A-N1B, N1A=C1A and N1B=C1B in (II), are longer than those of the diperchlorate salt [1.400 (4) and 1.260 (4) Å; Chen *et al.*, 1997] but agree well with those reported for the 4,4'-(azinodimethylene)dipyridinium chloranilate dichloromethane disolvate [1.411 (6) and 1.278 (5) Å; Kennedy & Waterson, 2003] (Table 1). Perspective drawings of compounds (I) and (II), together with the atomic numbering schemes, are shown in Figs. 1 and 2, respectively.

The two pyridine rings in (I) are parallel, with an interplanar distance of 0.104 (2) Å, and form a dihedral angle of 1.21 (9)° with the mean plane of the -CH=N-N=CHzigzag-like spacer, which exhibits an ideal antiperiplanar conformation with a torsion angle of 180° and the N–N bond lying on a crystallographic centre of symmetry. In (II), the molecule has no crystallographic centre of symmetry, the two ring planes are inclined by an angle of 14.45 (3)° and the antiperiplanar -CH=N-N= CH– spacer exhibits a torsion angle of -170.34 (2)°.

The parallel molecular stacks in (I) are arranged along the *b* axis (Fig. 3), maintained *via*  $\pi$ - $\pi$  stacking at an interplanar distance of 3.335 (3) Å and supported by a bifurcated N-H···F hydrogen bond building up an extended two-dimensional architecture along the (100) plane and S-like molecular





A perspective drawing of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. [Symmetry code (i) and symmetry code used to generate unlabelled atoms: -x, -y + 2, -z + 2.]



Figure 2

A perspective drawing of (II), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

sheets along the *c* axis. On the first-level graph set, as defined by Bernstein *et al.* (1995) and Grell *et al.* (1999), D(2) and  $D_2^2(16)$  finite patterns are formed *via* hydrogen bonds *a* and *b*, respectively (see Table 2 and Fig. 5). On the second-level



**Figure 3** The packing pattern of (I), projected along the *b* axis.



**Figure 4** The packing pattern of (II), projected along the *a* axis.





The hydrogen-bonding pattern of (I) along the a and c axes, with hydrogen bonds shown as dashed lines. For notation, see Table 2.



Figure 6

The hydrogen-bonding chains of (II) along the b axis, with hydrogen bonds shown as dashed lines. For symmetry code, see Table 3.

graph set,  $C_2^1(4)$  and  $C_2^2(17)$  chains and an  $R_6^6(43)$  ring can be recognized.

In (II), no profound  $\pi-\pi$  stacking exists. However, the zigzag-like molecular stacks built up along the *a*-axis direction (Fig. 4) are cemented by a conventional  $N-H\cdots N^{iv}$  hydrogen bond (Table 3 and Fig. 6), giving rise to an infinite one-dimensional C(13) chain along the vector [011]. Assignments and graph-set analyses were performed using *PLUTO* (Motherwell *et al.*, 1999).

# Experimental

For the preparation of compound (I),  $Fe(BF_4)_2 \cdot 6H_2O$  (1 mmol; Aldrich),  $NH_2NH_2 \cdot H_2O$  (1 mmol; Aldrich) and pyridine-4-carboxaldehyde (2 mmol; Aldrich) were stirred under an N<sub>2</sub> flow in EtOH (95%) at 350–355 K for 2 h. The resulting solution was allowed to cool, and was then filtered and the filtrate evaporated at room temperature for a few days. Yellow crystals were collected by filtration, washed with MeOH and dried *in vacuo*.

For the preparation of compound (II), 1,2-bis(4-pyridylmethylene)hydrazine (1 mmol), prepared as described by El-Rayyes & Katrib (1983), was added to an ethanolic solution of  $Fe(ClO_4)_2 \cdot H_2O$  (1 mmol; Aldrich). The solution was stirred at 350–355 K for 1 h. The resulting solution was cooled, filtered and the filtrate evaporated at room temperature for a few days. Red crystals were collected by filtration, washed with MeOH and dried *in vacuo*.

# Compound (I)

#### Crystal data

 $\begin{array}{l} C_{12}H_{12}N_4^{2+}\cdot 2BF_4^{-}\\ M_r = 385.88\\ \text{Monoclinic, } P2_1/c\\ a = 5.1056 \ (3) \ \text{\AA}\\ b = 16.5856 \ (10) \ \text{\AA}\\ c = 9.6587 \ (6) \ \text{\AA}\\ \beta = 99.962 \ (1)^\circ \end{array}$ 

#### Data collection

Siemens SMART CCD areadetector diffractometer Absorption correction: multi-scan (*SADABS*; Sheldrick, 2003)  $T_{\rm min} = 0.588, T_{\rm max} = 0.981$ 

### Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.040$  $wR(F^2) = 0.119$ S = 1.002925 reflections

## Compound (II)

Crystal data

 $\begin{array}{l} C_{12}H_{11}N_{4}^{+}\cdot CIO_{4}^{-} \\ M_{r} = 310.70 \\ \text{Orthorhombic, } Pca2_{1} \\ a = 15.0896 \ (6) \\ \text{\AA} \\ b = 11.5525 \ (5) \\ \text{\AA} \\ c = 7.8694 \ (3) \\ \text{\AA} \end{array}$ 

#### Data collection

Siemens SMART CCD areadetector diffractometer Absorption correction: multi-scan (SADABS; Sheldrick, 2003)  $T_{min} = 0.795, T_{max} = 0.976$ 

### Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.032$   $wR(F^2) = 0.082$  S = 1.003440 reflections 190 parameters 1 restraint  $V = 805.56 \text{ (8) } \text{Å}^{3}$  Z = 2Mo K\alpha radiation  $\mu = 0.16 \text{ mm}^{-1}$  T = 153 (2) K $0.46 \times 0.26 \times 0.12 \text{ mm}$ 

14300 measured reflections 2925 independent reflections 2154 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.026$ 

 $\begin{array}{l} 118 \text{ parameters} \\ \text{H-atom parameters constrained} \\ \Delta \rho_{\text{max}} = 0.48 \text{ e } \text{\AA}^{-3} \\ \Delta \rho_{\text{min}} = -0.19 \text{ e } \text{\AA}^{-3} \end{array}$ 

 $V = 1371.81 (10) Å^{3}$ Z = 4 Mo K\alpha radiation  $\mu = 0.30 \text{ mm}^{-1}$ T = 153 (2) K 0.18 \times 0.12 \times 0.08 mm

18851 measured reflections 3440 independent reflections 2994 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.040$ 

H-atom parameters constrained  $\Delta \rho_{max} = 0.24 \text{ e} \text{ Å}^{-3}$   $\Delta \rho_{min} = -0.21 \text{ e} \text{ Å}^{-3}$ Absolute structure: Flack (1983), with 1594 Friedel pairs Flack parameter: -0.02 (5)

H atoms were allowed for isotropically and were constrained to ideal geometry using an appropriate riding model, with C-H = 0.95 Å and N-H = 0.88 Å, and with  $U_{iso}(H) = 1.2U_{eq}(C,N)$ .

For both compounds, data collection: *SMART* (Bruker, 2003); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT* and *SADABS* (Sheldrick, 2003); program(s) used to solve structure: *SHELXTL* (Bruker, 2003); program(s) used to refine structure: *SHELXTL*; molecular graphics: *DIAMOND* (Brandenburg, 2006); software used to prepare material for publication: *SHELXTL*.

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# Table 1

Comparison of selected bond distances (Å) for (I) and (II).

Bond	Bond distance	Compound	
$N1 - N1^{i}$ $N1 = C1$ $N1A - N1B$	1.409 (2) 1.276 (1) 1.410 (2)	(I) (I) (II)	
N1A = C1A N1B = C1B	1.275 (2) 1.273 (2)	(II) (II)	

Symmetry code: (i) -x, -y + 2, -z + 2.

#### Table 2

#### Hydrogen-bonding geometry (Å, °) for (I).

Label	$D - \mathbf{H} \cdot \cdot \cdot A$	$D-{\rm H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
a b	$N5-H5\cdots F4^{iii}$ $N5-H5\cdots F2^{ii}$	0.88 0.88	2.01 2.50	2.8183 (12) 3.0320 (12)	152 119
			2	1	

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

#### Table 3

Hydrogen-bond geometry (Å, °) for (II).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$N5A - H5A \cdots N5B^{iv}$	0.88	1.84	2.715 (2)	174
Symmetry code: (iv) x, y	-1, z + 1.			

Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK3115). Services for accessing these data are described at the back of the journal.

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