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2,4,6-Trimethylpyridinium dihydrogen phosphate

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Key indicators: single-crystal X-ray study; T = 298 K; mean σ (C–C) = 0.005 Å; R factor = 0.047; wR factor = 0.144; data-to-parameter ratio = 14.3.

In the title compound, $C_8H_9N^+\cdot H_2PO_4^-$, both the cation and anion have crystallographically imposed mirror symmetry (all atoms apart from one O atom lie on the mirror plane). In the crystal, anions and cations are linked by $O-H\cdots O$ and $\pi-\pi$ stacking interactions [centroid–centroid distance = 3.4574 (6) Å], forming chains parallel to the *b* axis. Adjacent chains are further connected by $N-H\cdots O$ hydrogen bonds into a two-dimensional network.

Related literature

For background to the properties of pyridine salts as phase-transition dielectric materials, see: Fu *et al.* (2007, 2008, 2009); Fu & Xiong (2008).

$$NH^{+} \cdot H_{2}PO_{4}^{-}$$

Experimental

Crystal data C₈H₉N⁺·H₂O₄P[−]

 $M_r = 216.15$

Monoclinic, $P2_1/m$ Z=2a=8.6323 (17) Å Mo Kα radiation b=6.7133 (13) Å $\mu=0.27 \text{ mm}^{-1}$ C=8.6841 (17) Å T=298 K G=100.99 (3)° $C=10.30 \times 0.05 \times 0.05 \text{ mm}$ $C=10.30 \times 0.05 \times 0.05 \text{ mm}$

Data collection

Rigaku Mercury2 diffractometer Absorption correction: multi-scan (CrystalClear; Rigaku, 2005) $T_{\min} = 0.910, T_{\max} = 1.000$ 5154 measured reflections 1229 independent reflections 1082 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.033$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.047$ $wR(F^2) = 0.144$ S = 1.181229 reflections 86 parameters 1 restraint

H atoms treated by a mixture of independent and constrained refinement

 $\Delta \rho_{\text{max}} = 0.45 \text{ e Å}^{-3}$ $\Delta \rho_{\text{min}} = -0.29 \text{ e Å}^{-3}$

Table 1 Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
$ \begin{array}{c} O2-H2\cdotsO3^{i}\\ N1-H1A\cdotsO1 \end{array} $	0.85 (2)	1.76 (2)	2.6054 (19)	169 (2)
	0.86	1.75	2.602 (3)	173

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

Data collection: *CrystalClear* (Rigaku, 2005); cell refinement: *CrystalClear*; data reduction: *CrystalClear*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *SHELXTL*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: RZ2528).

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supplementary m	aterials	

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