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Key indicators

Single-crystal X-ray study
 $T = 292$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.049
 wR factor = 0.152
Data-to-parameter ratio = 14.9For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

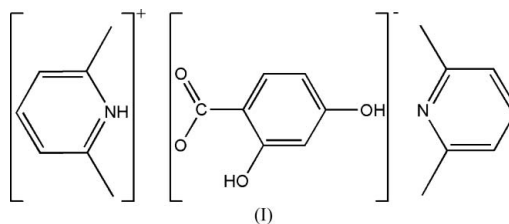
2,6-Dimethylpyridinium 2,4-dihydroxybenzoate 2,6-dimethylpyridine solvate

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The asymmetric unit of the title salt, $\text{C}_7\text{H}_{10}\text{N}^+\cdot\text{C}_7\text{H}_5\text{O}_4^-\cdot\text{C}_7\text{H}_9\text{N}$, consists of one 2,6-dimethylpyridinium cation, one 2,4-dihydroxybenzoate anion and one 2,6-dimethylpyridine solvent molecule, which form 1:1:1 associations by way of $\text{N}-\text{H}\cdots\text{O}$ and $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds. These entities then interact by way of $\text{C}-\text{H}\cdots\pi$ and $\pi-\pi$ interactions.

Comment

This work continues our previous synthetic and structural studies of supramolecular interactions in aromatic molecular salts and adducts (Wang & Wei, 2006).



The asymmetric unit of the title compound, (I), contains one 2,6-dimethylpyridinium cation, one 2,4-dihydroxybenzoate anion and one 2,6-dimethylpyridine solvent molecule (Fig. 1). The three components are linked together by a cation-to-anion $\text{N}-\text{H}\cdots\text{O}$ and an anion-to-solvent $\text{O}-\text{H}\cdots\text{N}$ hydrogen bond (Table 1). An intramolecular $\text{O}-\text{H}\cdots\text{O}$ interaction is also present in the anion.

The N2/C15–C19 ring makes weak $\pi-\pi$ interactions with its symmetry-related neighbours at $(x, \frac{1}{2} - y, -\frac{1}{2} + z)$ and $(x, \frac{1}{2} - y, \frac{1}{2} + z)$ positions with o-centroid distances of 3.9060 (12) Å in both cases. Similar weak $\pi-\pi$ interactions are observed between the N1/C8–C12 ring of the solvent molecule and its symmetry-related rings at $(x, \frac{3}{2} - y, -\frac{1}{2} + z)$ and $(x, \frac{3}{2} - y, \frac{1}{2} + z)$ with centroid separations of 3.9480 (13) Å.

Finally, $\text{C}-\text{H}\cdots\pi$ interactions occur in the crystal structure of (I). The 2,6-dimethylpyridine solvent molecule interacts with the C1–C6 ring (centroid C_g) of a 2,4-dihydroxybenzoate anion at the symmetry position $(1 - x, 1 - y, 2 - z)$ [$\text{H}\cdots C_g = 2.64$ Å]. In addition, a 2,6-dimethylpyridinium cation interacts with another C1–C6 ring at the symmetry position $(-x, -\frac{1}{2} + y, \frac{3}{2} - z)$ with $\text{H}\cdots C_g = 2.84$ Å. Together, these interactions result in a three-dimensional supramolecular network (Fig. 2).

Experimental

2,4-Dihydroxybenzoic acid (2.0 mmol, 0.31 g) was dissolved in 15 ml 2,6-dimethylpyridine. The mixture was stirred for 20 minutes at

343 K. The solution was filtered, and the filtrate was kept at room temperature. Colorless crystals of (I) were obtained from the filtrate after six days.

Crystal data

$C_7H_{10}N^+ \cdot C_7H_5O_4^- \cdot C_7H_9N$
 $M_r = 368.42$
 Monoclinic, $P2_1/c$
 $a = 16.0942$ (14) Å
 $b = 15.7871$ (14) Å
 $c = 7.7950$ (7) Å
 $\beta = 97.217$ (1)°
 $V = 1964.9$ (3) Å³

$Z = 4$
 $D_x = 1.245$ Mg m⁻³
 Mo $K\alpha$ radiation
 $\mu = 0.09$ mm⁻¹
 $T = 292$ (2) K
 Block, colorless
 $0.35 \times 0.30 \times 0.30$ mm

Data collection

Bruker SMART APEX CCD
 diffractometer
 ω scans
 Absorption correction: none
 14075 measured reflections

3846 independent reflections
 2658 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.033$
 $\theta_{max} = 26.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.049$
 $wR(F^2) = 0.152$
 $S = 1.06$
 3846 reflections
 258 parameters
 H atoms treated by a mixture of
 independent and constrained
 refinement

$w = 1/[\sigma^2(F_o^2) + (0.0889P)^2 + 0.0787P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{max} < 0.001$
 $\Delta\rho_{max} = 0.16$ e Å⁻³
 $\Delta\rho_{min} = -0.18$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
O3—H3 \cdots O2	0.847 (10)	1.747 (15)	2.538 (2)	154 (3)
O4—H4 \cdots N1	0.832 (10)	1.910 (12)	2.723 (2)	165 (3)
N2—H22 \cdots O1	0.886 (10)	1.699 (11)	2.581 (2)	173 (3)

The N- and O-bound H atom was located in a difference map and refined with bond-distance restraints of 0.89 (1) and 0.85 (1) Å, respectively. The C-bound H atoms were positioned geometrically ($C-H = 0.93-0.96$ Å) and refined as riding, with $U_{iso}(H) = 1.2U_{eq}(\text{aromatic C})$ or $1.5U_{eq}(\text{methyl C,O})$.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *PLATON*.

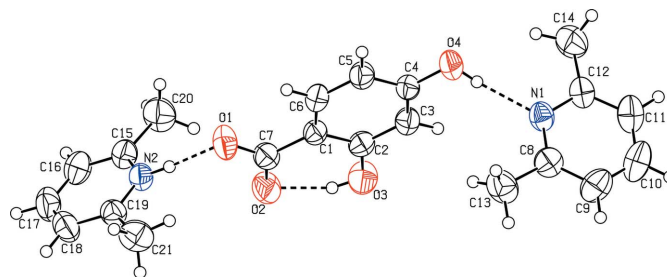


Figure 1

The asymmetric unit of (I), showing 50% probability displacement ellipsoids (arbitrary spheres for the H atoms). Hydrogen bonds are indicated by dashed lines.

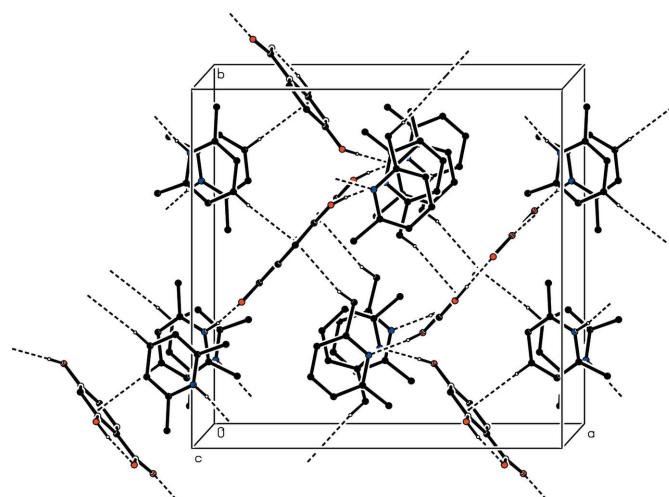


Figure 2

The packing diagram of (I). Hydrogen bonds are shown as dashed lines. For clarity, H atoms not involved in hydrogen bonds are omitted.

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References

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