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De-Suo Yang

Department of Chemistry and Chemical Engineering, Baoji College of Arts and Sciences, Baoji 721007, People's Republic of China

Correspondence e-mail: desuoyang@yahoo.com.cn

Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.003 \text{ Å}$ R factor = 0.066 wR factor = 0.198 Data-to-parameter ratio = 13.8

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

Bis(pyridinium-4-olate) succinic acid

In the title compound, $2C_5H_5NO \cdot C_4H_6O_4$, a phenolic proton is transferred to the pyridine N atom, yielding a zwitterionic pyridinium-4-olate. The succinic acid molecule lies about a centre of symmetry which also generates the second pyridinium-4-olate molecule. The crystal structure is stabilized by intermolecular $O-H \cdots O$ and $C-H \cdots O$ hydrogen bonds, forming a network structure.

Comment

Proton transfer in molecular associations confers considerable stability in the structure-forming process (Smith *et al.*, 2004, 2004*a,b*; Moghimi *et al.*, 2004). In order to study the role of proton-exchange compounds in the construction of net-like structures, we have prepared the title compound, (I), and its structure is reported here.



In the reaction with succinic acid a phenolic proton is transferred to the pyridine N atom, forming a zwitterionic pyridinium-4-olate. The structure of (I) thus has half of a neutral succinic acid residue and one pyridinium-4-olate molecule in the asymmetric unit, as the succinic acid molecule lies on a centre of symmetry located at the mid-point of the



Figure 1

The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. Unlabelled atoms are related to the equivalent labelled atoms by the symmetry operation (1 - x, 2 - y, 2 - z).

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0352 De-Suo Yang $\cdot 2C_5H_5NO\cdot C_4H_6O_4$

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 $C7-C7^{i}$ bond (see Fig. 1 for symmetry code). All bond lengths in the molecules are within normal ranges (Allen *et al.*, 1987).

In the crystal structure, intermolecular $O-H\cdots O$ hydrogen bonds link succinic acid molecules to two adjacent pyridinium-4-olate residues along the *a* axis. The structure is further stabilized by a number of $C-H\cdots O$ hydrogen bonds (Table 1), forming a network parallel to the *ac* plane (Fig. 2).

Experimental

Pyridin-4-ol (0.2 mmol, 19.1 mg) and succinic acid (0.1 mmol, 11.8 mg) were dissolved in distilled water (10 ml). The mixture was heated under reflux to form a clear colourless solution. Crystals of the title compound were grown by gradual evaporation of water over a period of one week at room temperature.

 $D_x = 1.423 \text{ Mg m}^{-3}$

Cell parameters from 1725

Mo $K\alpha$ radiation

reflections

 $\theta = 2.5 - 26.6^{\circ}$ $\mu = 0.11 \text{ mm}^{-1}$

T = 298 (2) K

 $R_{\rm int} = 0.022$

 $\theta_{\rm max} = 26.5^{\circ}$

 $h = -10 \rightarrow 10$

 $k = -6 \rightarrow 6$

 $l = -20 \rightarrow 20$

 $(\Delta/\sigma)_{\rm max} < 0.001$

 $\Delta \rho_{\rm max} = 0.53 \text{ e} \text{ } \text{\AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.43 \text{ e} \text{ Å}^{-3}$

Plate, colourless

 $0.34 \times 0.20 \times 0.07 \text{ mm}$

1464 independent reflections

 $w = 1/[\sigma^2(F_o^2) + (0.1263P)^2 + 0.2431P]$

where $P = (F_0^2 + 2F_c^2)/3$

1146 reflections with $I > 2\sigma(I)$

Crystal data

 $\begin{array}{l} 2\mathrm{C}_{5}\mathrm{H}_{5}\mathrm{NO}\cdot\mathrm{C}_{4}\mathrm{H}_{6}\mathrm{O}_{4}\\ M_{r}=308.29\\ \mathrm{Monoclinic},\ P2_{1}/n\\ a=8.559\ (2)\ \mathrm{\AA}\\ b=5.178\ (1)\ \mathrm{\AA}\\ c=16.387\ (3)\ \mathrm{\AA}\\ \beta=97.891\ (2)^{\circ}\\ V=719.4\ (3)\ \mathrm{\AA}^{3}\\ Z=2 \end{array}$

Data collection

Bruker SMART APEX areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2002) $T_{min} = 0.963, T_{max} = 0.992$ 5307 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.066$ $wR(F^2) = 0.198$ S = 1.051464 reflections 106 parameters H atoms treated by a mixture of independent and constrained refinement

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

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$ \begin{array}{c} \hline \hline O2 - H2 \cdots O1^{i} \\ C2 - H2A \cdots O1^{ii} \\ C3 - H3 \cdots O3^{iii} \\ C4 - H4 \cdots O2^{i\nu} \end{array} $	0.84 (3)	1.796 (16)	2.611 (2)	163 (4)
	0.93	1.86	2.792 (2)	178 (3)
	0.93	2.48	3.340 (2)	154 (3)
	0.93	2.52	3.360 (2)	150 (3)

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





Atoms H1 and H2, attached to N1 and O2, respectively, were located in a difference Fourier map and refined isotropically, with the N-H distance restrained to 0.97 (1) Å and the O-H distance restrained to 0.84 (1) Å. The other H atoms were placed in idealized positions and constrained to ride on their parent atoms, with C-H distances in the range 0.93–0.97 Å, and with $U_{\rm iso}(\rm H) = 1.2U_{eq}(\rm C)$.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXL97*.

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