

1,10-Phenanthroline-6-carboxypyridine-2-carboxylate-1,10-phenanthroline-pyridine-2,6-dicarboxylic acid-ethanol-water (1/1/1/1/1)

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Key indicators

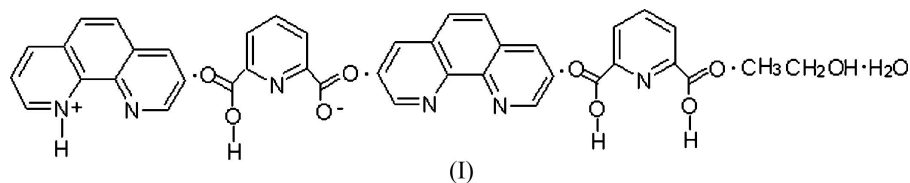
Single-crystal X-ray study
T = 293 K
 Mean σ (C–C) = 0.007 Å
R factor = 0.060
wR factor = 0.141
 Data-to-parameter ratio = 12.3

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

In the title compound, $C_{12}H_9N_2^+ \cdot C_7H_5O_4N^- \cdot C_{12}H_8N_2 \cdot C_7H_4O_4N \cdot C_2H_6O \cdot H_2O$, the cations are stacked along the *b* axis to form a column-like structure. The anions, ethanol molecules and water molecules are linked *via* O–H···O and O–H···N hydrogen bonds to form a zigzag sheet-like structure. The cationic columns and anionic sheets are alternately arranged along the *c* axis.

Comment

The asymmetric unit of (I), contains a $(C_{12}H_8N_2 \cdot C_{12}H_9N_2)^+$ cation, a $(C_7H_5O_4N \cdot C_7H_4O_4N)^-$ anion, a solvent ethanol molecule and a water molecule (Fig. 1). The N3–H3A···N5ⁱ hydrogen-bonded (see Table 2 for symmetry code) 1,10-phenanthroline and 1,10-phenanthroline molecules form a cation, and the O4–H4···O5ⁱⁱⁱ hydrogen-bonded pyridine-2,6-dicarboxylic acid and 6-carboxypyridine-2-carboxylate molecules form an anion. The C–O bond lengths of the carboxylate group [C14–O5 = 1.289 (4) Å and C14–O6 = 1.222 (5) Å] are not equal as the O4–H4···O5ⁱⁱⁱ [O···O = 2.440 (4) Å] hydrogen bond is stronger than the O9–H9···O6^v [O···O = 2.768 (5) Å] hydrogen bond. The other bond lengths and angles in the cation are comparable to corresponding values found in its complexes (Fu, Sun *et al.*, 2004; Fu, Wang & Shen, 2004; Fu, Wang, Shen & Zhang, 2004; Fu, Fu & Yu, 2005), and those in the anion of (I) are consistent with the values found in its complexes (Fu, Wang & Liu, 2004; Fu, Wang & Sun, 2005).



In the crystal structure of (I), the cations are stacked along the *b* axis to form a column-like structure. The anions and ethanol and water molecules are linked *via* O–H···O and O–H···N hydrogen bonds (Table 2) to form a zigzag sheet-like structure. The cationic columns and anionic sheets are alternately arranged along the *c* axis (Fig. 2).

Experimental

Phenanthroline (1 mmol) and dipicolinic acid (1 mmol) were dissolved in a 1:1 alcohol and distilled water solution (20 ml), which was allowed to stand in air. After 14 d, colourless prism-shaped crystals separated. These were collected, washed with water and dried in a vacuum over $CaCl_2$ (yield 41%). Elemental analysis found: C

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63.17, H 4.44, N 10.98%; calculated for C₄₀H₃₄N₆O₁₀: C 63.32, H 4.51, N 11.08%.

Crystal data

C₁₂H₉N₂⁺·C₇H₄NO₄⁻·C₁₂H₈N₂·
C₇H₅NO₄·C₂H₆O·H₂O
M_r = 758.73
Monoclinic, P2₁/c
a = 20.802 (7) Å
b = 7.861 (3) Å
c = 24.488 (6) Å
β = 116.72 (2)°
V = 3577 (2) Å³
Z = 4

D_x = 1.409 Mg m⁻³
Mo Kα radiation
Cell parameters from 1469 reflections
θ = 2.6–20.2°
μ = 0.10 mm⁻¹
T = 293 (2) K
Prism, colourless
0.39 × 0.13 × 0.11 mm

Data collection

Bruker SMART CCD area-detector diffractometer
φ and ω scans
Absorption correction: multi-scan (SADABS; Bruker, 1997)
T_{min} = 0.961, T_{max} = 0.989
18072 measured reflections

6314 independent reflections
2335 reflections with I > 2σ(I)
R_{int} = 0.111
θ_{max} = 25.0°
h = -24 → 20
k = -8 → 9
l = -29 → 29

Refinement

Refinement on F²
R[F² > 2σ(F²)] = 0.060
wR(F²) = 0.141
S = 1.00
6314 reflections
512 parameters

H atoms treated by a mixture of independent and constrained refinement
w = 1/[σ²(F_o²) + (0.0316P)²]
where P = (F_o² + 2F_c²)/3
(Δ/σ)_{max} = 0.001
Δρ_{max} = 0.32 e Å⁻³
Δρ_{min} = -0.28 e Å⁻³

Table 1

Selected geometric parameters (Å, °).

O1—C1	1.196 (5)	O4—C7	1.281 (4)
O2—C1	1.309 (5)	O7—C8	1.321 (5)
O3—C7	1.213 (5)	O8—C8	1.206 (5)
O1—C1—O2	124.2 (4)	O8—C8—O7	120.9 (5)
O1—C1—C2	122.7 (4)	O8—C8—C9	123.1 (5)
O2—C1—C2	113.1 (4)	O7—C8—C9	116.0 (5)
O3—C7—O4	126.5 (5)	O6—C14—O5	125.0 (4)
O3—C7—C6	121.0 (4)	O6—C14—C13	120.7 (4)
O4—C7—C6	112.5 (4)	O5—C14—C13	114.3 (4)

Table 2

Hydrogen-bond geometry (Å, °).

D—H...A	D—H	H...A	D...A	D—H...A
N3—H3A...N5 ⁱ	0.86	2.08	2.863 (5)	152
O2—H2...O10 ⁱⁱ	0.82	1.74	2.549 (4)	170
O4—H4...O5 ⁱⁱⁱ	0.82	1.64	2.440 (4)	164
O7—H7...O9 ^{iv}	0.82	1.93	2.686 (5)	154
O7—H7...N2	0.82	2.17	2.662 (4)	118
O9—H9...O6 ^v	0.82	1.96	2.768 (5)	169
O9—H9...N2 ^v	0.82	2.41	2.850 (5)	114
O10—H1...O1	0.87 (2)	2.02 (2)	2.869 (5)	167 (4)
O10—H6...O3 ^{vi}	0.84 (2)	2.23 (4)	2.876 (4)	134 (4)
O10—H6...N1 ^{vi}	0.84 (2)	2.35 (3)	3.041 (5)	140 (4)

Symmetry codes: (i) -x + 1, y - 1/2, -z + 1/2; (ii) -x + 1, -y + 1, -z + 1; (iii) x, y + 1, z; (iv) -x, y - 1/2, -z + 1/2; (v) -x, y + 1/2, -z + 1/2; (vi) x, y - 1, z.

The water H atoms were located in difference Fourier maps, and were refined with O—H and H...H distance restraints of 0.85 (2) and 1.35 (2) Å, respectively, and with fixed U_{iso} value of 0.08 Å². All other

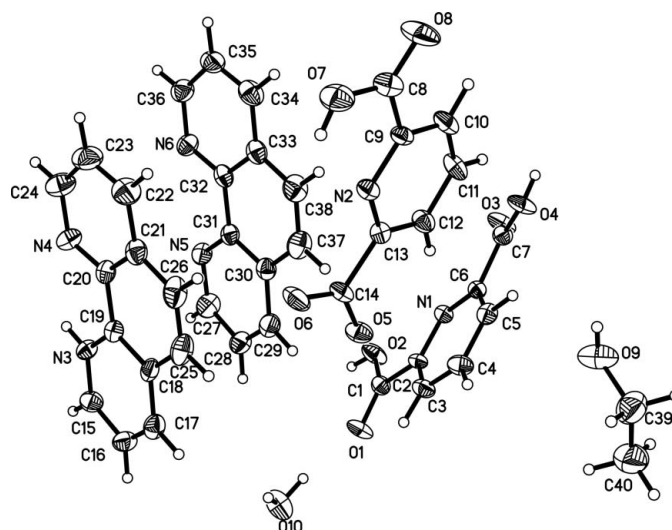


Figure 1
The asymmetric unit of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

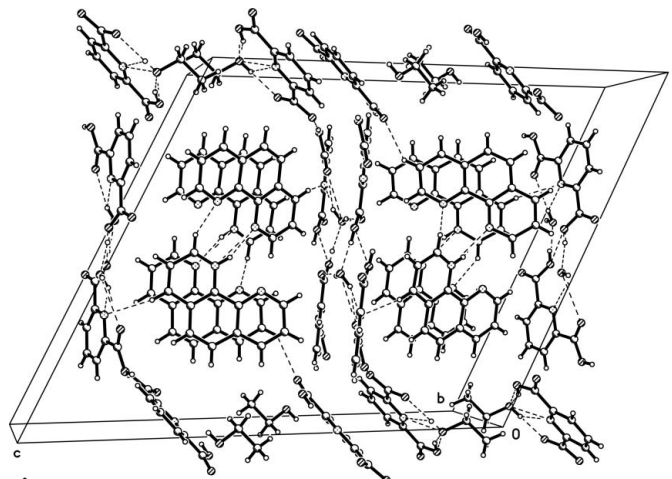


Figure 2
Crystal packing of (I), showing the hydrogen-bonded interactions as dashed lines.

H atoms were placed in idealized positions and constrained to ride on their parent atoms, with O—H = 0.82 Å, N—H = 0.86 Å, C—H = 0.93–0.97 Å, and U_{iso}(H) = 1.5U_{eq}(C,O) for methyl and hydroxy H atoms, and 1.2U_{eq}(C,N) for other H atoms.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPIII (Burnett & Johnson, 1996) and PLATON (Spek, 2003); software used to prepare material for publication: SHELXL97.

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