

1,10-Phenanthroline pyridinium perchlorate

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Key indicators

Single-crystal X-ray study

T = 294 K

Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$

R factor = 0.053

wR factor = 0.139

Data-to-parameter ratio = 12.4

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

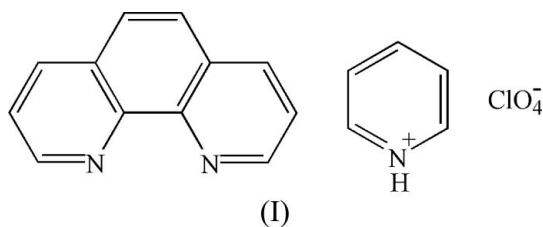
In 1,10-phenanthroline pyridinium perchlorate, $\text{C}_{12}\text{H}_8\text{N}_2 \cdot \text{C}_5\text{H}_6\text{N}^+ \cdot \text{ClO}_4^-$, intra- and intermolecular hydrogen bonding interactions dominate the crystal packing. The phenanthroline molecule, the cation and anion lie on crystallographic twofold rotation axes.

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Comment

Phenanthroline and its derivative ligands and their complexes with metal ions have received considerable attention over the past three decades (Summers, 1978; Weijnen *et al.*, 1991; Guo *et al.*, 2004). In the title compound, (I), the bond lengths and angles are within normal ranges.



The phenanthroline molecule, the cation and anion all lie on crystallographic twofold rotation axes. The dihedral angles formed by plane N1/C1–C5 with N1A/C1A–C5A and C7/C8/C9/C8A/C7A/N2 are 0.9° and 5.4°, respectively, indicating that the three planes in the molecule are approximately coplanar, probably as a result of the hydrogen-bonding requirement. The perchlorate anion plays an important role in forming this structure, *viz.* it forms a chain structure *via* hydrogen bonding. In the crystal structure, strong intra- and intermolecular hydrogen bonds result in a two-dimensional structure (Fig. 2).

Experimental

All commercially available reagents were used as supplied. Magnesium perchlorate (5 mmol) was added to a solution of 1,10-phenanthroline (10 mmol) in pyridine (10 ml). The mixture was stirred continuously for 3 h under reflux and then filtered. Single crystals suitable for X-ray analysis were obtained, after two weeks, by evaporation of the filtrate.

Crystal data

 $\text{C}_{12}\text{H}_8\text{N}_2 \cdot \text{C}_5\text{H}_6\text{N}^+ \cdot \text{ClO}_4^-$ $M_r = 359.76$ Monoclinic, $C2/c$ $a = 10.534 (3) \text{ \AA}$ $b = 22.884 (8) \text{ \AA}$ $c = 6.811 (2) \text{ \AA}$ $\beta = 95.403 (6)^\circ$ $V = 1634.5 (9) \text{ \AA}^3$

Z = 4

 $D_x = 1.462 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation $\mu = 0.26 \text{ mm}^{-1}$

T = 294 (2) K

Block, colourless

 $0.26 \times 0.22 \times 0.18 \text{ mm}$

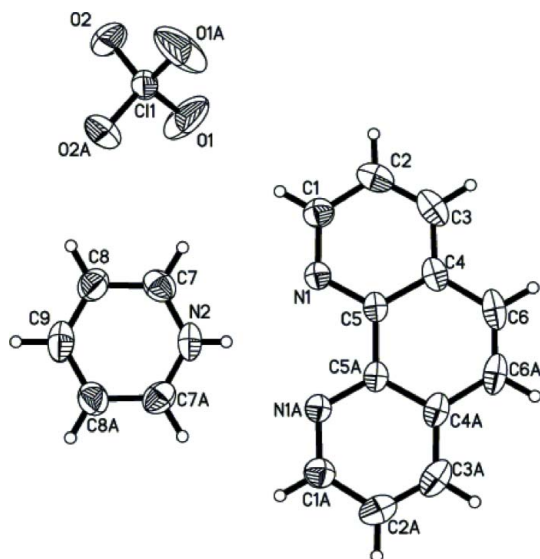


Figure 1
The structure of the components of (I) with 30% probability displacement ellipsoids. In the cation and the organic molecule, symmetry code: (A) $2 - x, y, \frac{1}{2} - z$. In the anion, symmetry code: (A) $1 - x, y, \frac{1}{2} - z$.

Data collection

Bruker SMART CCD area-detector diffractometer	4107 measured reflections
φ and ω scans	1445 independent reflections
Absorption correction: multi-scan (SADABS; Bruker, 2000)	835 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.935, T_{\max} = 0.954$	$R_{\text{int}} = 0.053$
	$\theta_{\max} = 25.0^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.056P)^2 + 0.9324P]$
$R[F^2 > 2\sigma(F^2)] = 0.053$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.139$	$(\Delta/\sigma)_{\max} = 0.001$
$S = 1.03$	$\Delta\rho_{\max} = 0.28 \text{ e } \text{\AA}^{-3}$
1445 reflections	$\Delta\rho_{\min} = -0.24 \text{ e } \text{\AA}^{-3}$
117 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Hydrogen-bond geometry ($\text{\AA}, ^\circ$).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N2-H2A \cdots N1^i$	0.75 (5)	2.34 (4)	2.984 (5)	144.0 (8)
$N2-H2A \cdots N1$	0.75 (5)	2.34 (4)	2.984 (5)	144.0 (7)

Symmetry code: (i) $-x + 2, y, -z + \frac{1}{2}$.

All H atoms were positioned geometrically. Atom H2A on N2 was refined freely.

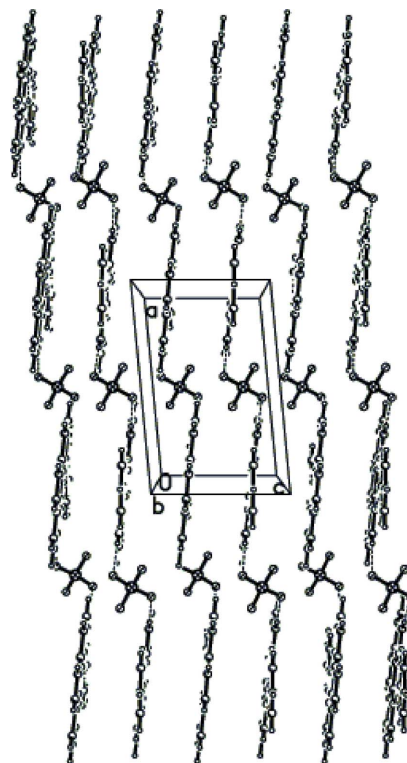


Figure 2
The packing of (I). Hydrogen bonds are indicated by dashed lines.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 2000); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997a); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997a); molecular graphics: *SHELXTL* (Sheldrick, 1997b); software used to prepare material for publication: *SHELXTL*.

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