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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.041 wR factor = 0.078 Data-to-parameter ratio = 11.6

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

trans-Bis(3-aminopyridine)diaquabis-(4-cyanobenzoato)cobalt(II) dihydrate

The reaction of cobalt(II) acetate with 4-cyanobenzoic acid and 3-aminopyridine gave the title centrosymmetric complex, $[Co(C_8H_4NO_2)_2(C_5H_6N_2)_2(H_2O)_2]\cdot 2H_2O$. The coordination geometry around the Co^{II} ion is distorted octahedral, and the 4-cyanobenzoate and 3-aminopyridine ligands act in a monodentate fashion. The hydrogen bonds among the water molecules and cyano and amino groups ensure a twodimensional hydrogen-bonding architecture. Received 14 November 2003 Accepted 20 November 2003 Online 29 November 2003

Comment

The amino group of 3-aminopyridine (apy), in general, is difficult to coordinate to metal atoms (Akyuz, 1998; Kamaluddin, 2000); nevertheless, the amine group could provide a donor site for the formation of hydrogen bonds. In the present paper, we report the crystal structure of the title compound, (I), which contains apy and 4-cyanobenzoate (cba) ligands, both of which are building blocks for hydrogen bonds.



Complex (I) is monomeric and has a center of symmetry (Fig. 1). The geometry of the cobalt ion is distorted octahedral (Table 1). The carboxy group of the cba ligand coordinates in a monodentate mode, similar to those in $[Cu(4,4'-bipy)(cba)_2]_n$ (He & Zhu, 2003), $[Co(4,4'-bipy)(cba)_2(H_2O)_2]_n$ (He *et al.*, 2003) and $[Cu(phen)(H_2O)Cl(cba)] \cdot H_2O$ (Zhou *et al.*, 2003). The Co-O1(cba) distance [2.0777 (14) Å] is similar to that reported for $[Co(4,4'-bipy)(cba)_2(H_2O)_2]_2$ [2.0792 (12) Å].

The cyano group of the cba ligand forms a hydrogen bond with atom O4 (Table 2). Furthermore, there is a hydrogen bond between atoms O4 and O2 (the uncoordinated O atom of the carboxy group). Thus the { $[Co(cba)_2](H_2O)_2$ } units form a one-dimensional chain *via* hydrogen bonds, in which a hydrogen-bonding [$(cba)_2(H_2O)_2$] loop is formed (Fig. 2). The amine group forms a hydrogen bond with atom O3 (of the coordinated water molecule). The combination of [$Co(apy)_2$ - $(H_2O)_2$]²⁺ and { $[Co(cba)_2](H_2O)_2$ } units creates a two-dimensional hydrogen-bonded architecture (Fig. 2).

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Figure 1

ORTEP-3 diagram (Farrugia, 1997) of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level. The labeled part of the molecule is related to the unlabeled part by the symmetry operation (-x, 1 - y, 2 - z).



Figure 2

View of the two-dimensional hydrogen-bonding network. H atoms have been omitted for clarity.

Experimental

A methanol solution (20 ml) of $Co(CH_3COO)_2 \cdot 4H_2O$ (0.0624 g, 0.25 mmol) was added to an aqueous solution (10 ml) of 4-cyanobenzoic acid (0.0757 g, 0.5 mmol) and 3-aminopyridine (0.0481 g, 0.5 mmol). After the mixture had been allowed to stand for three weeks at room temperature, purple crystals of (I) were obtained and dried at room temperature. Analysis calculated for $C_{26}H_{28}CON_6O_8$: C 51.07, H 4.62, N 13.74%; found: C 51.13, H 4.67, N 13.82%.

Crystal data

Z = 1
$D_{\rm r} = 1.487 {\rm Mg} {\rm m}^{-3}$
Mo $K\alpha$ radiation
Cell parameters from 1267
reflections
$\theta = 5.5 - 52.1^{\circ}$
$\mu = 0.69 \text{ mm}^{-1}$
T = 293 (2) K
Plate, purple
$0.30 \times 0.15 \times 0.07 \text{ mm}$

Data collection

Bruker SMART CCD area-detector	2824 independent reflections
diffractometer	2360 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{int} = 0.036$
Absorption correction: multi-scan	$\theta_{max} = 26.8^{\circ}$
(<i>SADABS</i> ; Sheldrick, 1997)	$h = -9 \rightarrow 9$
$T_{min} = 0.805, T_{max} = 0.960$	$k = -9 \rightarrow 9$
3999 measured reflections	$l = -16 \rightarrow 8$
Refinement	
Refinement on F^2	All H-atom parameters refined
$R[F^2 > 2\sigma(F^2)] = 0.041$	$w = 1/[\sigma^2(F_o^2) + (0.0241P)^2]$
$wR(F^2) = 0.078$	where $P = (F_o^2 + 2F_c^2)/3$
S = 0.94	$(\Delta/\sigma)_{max} < 0.001$
2824 reflections	$\Delta\rho_{max} = 0.46 \text{ e } \text{\AA}^{-3}$
243 parameters	$\Delta\rho_{min} = -0.28 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Co-O1	2.0777 (14)	Co-N1	2.1646 (17)
Co-O3	2.1202 (16)		
O1-Co-O3	89.44 (7)	O3-Co-N1	89.01 (7)
O1-Co-N1	87.02 (6)		

Table 2Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\begin{array}{c} 03 - H11 \cdots 02^{i} \\ 03 - H12 \cdots N2^{ii} \\ 04 - H13 \cdots N3^{iii} \\ 04 - H14 \cdots 02^{iv} \end{array}$	0.88 (3) 0.81 (3) 0.81 (3) 0.79 (4)	1.81 (3) 2.07 (3) 2.22 (4) 2.15 (4)	2.672 (2) 2.871 (3) 3.021 (4) 2.931 (3)	165 (3) 169 (2) 172 (3) 168 (4)

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

All H atoms were located from difference Fourier maps and refined isotropically. The C–H, N–H and O–H bond lengths are 0.91 (2)–0.97 (2), 0.85 (2)–0.86 (3) and 0.79 (4)–0.88 (3) Å, respectively.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* and *SHELXTL* (Bruker, 1997); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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