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Key indicators

Single-crystal X-ray study
 T = 295 K
 Mean $\sigma(C-C)$ = 0.004 Å
 R factor = 0.031
 wR factor = 0.078
 Data-to-parameter ratio = 11.5

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

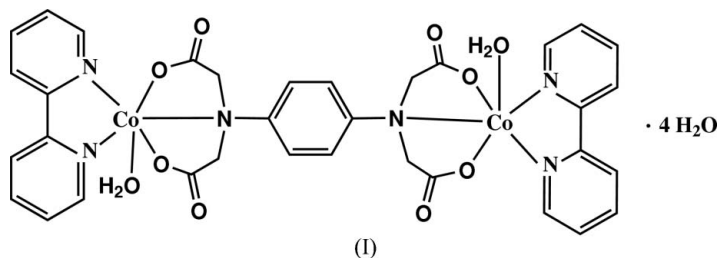
(μ -*p*-Phenylenediaminetetraacetato)bis[2,2'-bipyridine)cobalt(II)] tetrahydrate

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In the crystal structure of the title compound, $[Co_2(C_{14}H_{12}N_2O_8)(C_{10}H_8N_2)_2(H_2O)_2] \cdot 4H_2O$, *p*-phenylenediaminetetraacetate (PhDTA) is located across an inversion center and bridges two Co^{II} atoms to form the dinuclear molecule. The Co^{II} atom has a distorted octahedral coordination geometry. Extensive intermolecular hydrogen bonding helps to stabilize the crystal structure.

Comment

p-Phenylenediaminetetraacetic acid (H_4PhDTA) is structurally similar to edta and plays a multidentate ligand role in metal complexes. In contrast to the flexible edta, there is a rigid aromatic ring in the PhDTA molecule. Thus, it may show different behavior in complex formation. We report here the structure of the title complex, (I).



The molecular structure of (I) is shown in Fig. 1. PhDTA is located across an inversion center and bridges two Co^{II} atoms to form a dinuclear complex. The Co^{II} atom has a distorted octahedral coordination geometry. The $Co1-N1$ bond distance is much longer than $Co1-N2$ and $Co1-N3$ distances (Table 1).

Extensive intermolecular hydrogen bonding occurs (Table 2), which helps to stabilize the crystal structure.

Experimental

H_4PhDTA was prepared according to the literature procedure (Gonzalez *et al.*, 1997). H_4PhDTA (0.3 mmol) and 2,2'-bipyridine (0.3 mmol) were dissolved in an aqueous solution (20 ml) of $Co(NO_3)_2$ (0.3 mmol). The solution was adjusted with an aqueous solution of NaOH to pH 5 and then refluxed for 1 h and filtered. Single crystals of (I) were obtained from the filtrate after 5 d.

Crystal data

$[Co_2(C_{14}H_{12}N_2O_8)(C_{10}H_8N_2)_2 \cdot (H_2O)_2] \cdot 4H_2O$	$\gamma = 86.508 (2)^\circ$
$M_r = 874.58$	$V = 935.59 (15) \text{ \AA}^3$
Triclinic, $P\bar{1}$	$Z = 1$
$a = 9.8813 (9) \text{ \AA}$	$D_x = 1.552 \text{ Mg m}^{-3}$
$b = 9.9042 (9) \text{ \AA}$	Mo $K\alpha$ radiation
$c = 10.824 (1) \text{ \AA}$	$\mu = 0.96 \text{ mm}^{-1}$
$\alpha = 66.108 (2)^\circ$	$T = 295 (2) \text{ K}$
$\beta = 75.257 (2)^\circ$	Block, red
	$0.26 \times 0.22 \times 0.20 \text{ mm}$

Data collection

Bruker APEX area-detector
 diffractometer
 φ and ω scans
 Absorption correction: multi-scan
 (SADABS; Bruker, 2002)
 $T_{\min} = 0.737$, $T_{\max} = 0.820$

6768 measured reflections
 3278 independent reflections
 2976 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.016$
 $\theta_{\text{max}} = 25.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.031$
 $wR(F^2) = 0.078$
 $S = 1.06$
 3278 reflections
 285 parameters
 H atoms treated by a mixture of
 independent and constrained
 refinement

$w = 1/[\sigma^2(F_o^2) + (0.0423P)^2 + 0.2519P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.29 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.21 \text{ e } \text{\AA}^{-3}$

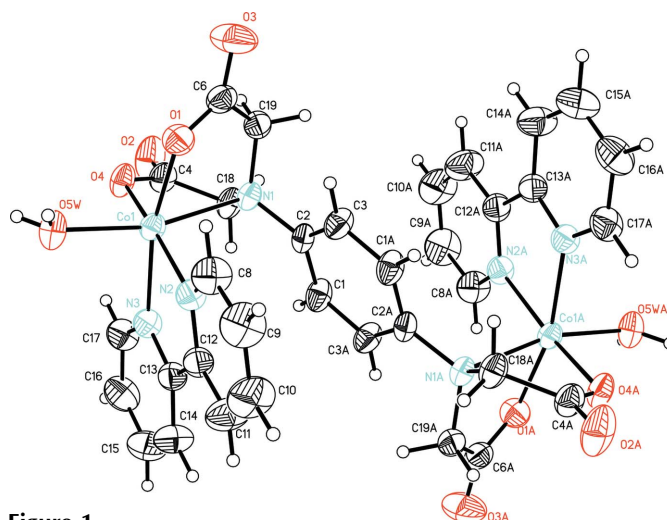


Figure 1

The molecular structure of (I), shown with 50% probability displacement ellipsoids (arbitrary spheres for H atoms) [symmetry code: (A) $1 - x$, $1 - y$, $2 - z$]. The uncoordinated water molecules have been omitted.

Table 1

 Selected geometric parameters (\AA , $^\circ$).

Co1—N1	2.2828 (17)	Co1—O1	2.0366 (15)
Co1—N2	2.1345 (17)	Co1—O4	2.0642 (14)
Co1—N3	2.1268 (17)	Co1—O5W	2.0752 (16)
O1—Co1—O4	97.82 (6)	O5W—Co1—N2	89.20 (7)
O1—Co1—O5W	91.47 (6)	N3—Co1—N2	76.44 (7)
O4—Co1—O5W	95.18 (6)	O1—Co1—N1	78.75 (6)
O1—Co1—N3	165.84 (6)	O4—Co1—N1	75.90 (6)
O4—Co1—N3	93.84 (6)	O5W—Co1—N1	165.56 (6)
O5W—Co1—N3	95.47 (7)	N3—Co1—N1	96.44 (6)
O1—Co1—N2	91.37 (6)	N2—Co1—N1	101.52 (6)
O4—Co1—N2	169.70 (6)		

Table 2

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O5W—H5WA \cdots O6 ⁱ	0.84 (3)	2.06 (3)	2.879 (4)	166 (3)
O5W—H5WB \cdots O4 ⁱⁱ	0.85 (2)	1.87 (2)	2.699 (2)	165 (3)
O6—H6WA \cdots O7 ⁱⁱⁱ	0.84 (2)	1.88 (3)	2.701 (3)	165 (3)
O6—H6WB \cdots O2 ^{iv}	0.85 (2)	2.07 (2)	2.862 (3)	155 (3)
O7—H7WA \cdots O1 ^v	0.84 (2)	2.06 (2)	2.871 (3)	161 (3)
O7—H7WB \cdots O3 ^{vi}	0.83 (3)	1.93 (3)	2.757 (3)	172 (3)

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

H atoms of water molecules were located in a difference Fourier map and refined isotropically. Other H atoms were placed in calculated positions, with C—H = 0.93 (aromatic) or 0.97 \AA (methylene), and refined in riding mode, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997); software used to prepare material for publication: SHELXL97.

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