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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.004 Å R factor = 0.023 wR factor = 0.057 Data-to-parameter ratio = 9.9

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

Triaqua(2,2'-bipyridine)(2-sulfonatobenzoato)cobalt(II)

In the title compound, $[Co(C_7H_4O_5S)(C_{10}H_8N_2)(H_2O)_3]$, the Co^{II} atom has a distorted octahedral geometry formed by three aqua O atoms, one carboxylate O atom from a 2-sulfonatobenzoate dianion and two N atoms of a 2,2'-bipyridine ligand. Intermolecular $O-H\cdots O$ hydrogen bonds link the mononuclear units into a two-dimensional network structure.

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Comment

Like other sulfobenzoic acids, such as 4-sulfobenzoic acid (Zhang *et al.*, 2005) and 5-sulfoisophthalic acid (Li *et al.*, 2005; Xiao & Morsali, 2005; Yuan *et al.*, 2004), which show diverse coordination modes, 2-sulfobenzoic acid (o-H₂sb) is also a versatile ligand and can function variously as a monodentate, bidentate or tridentate ligand; it can also bridge or chelate (Li & Yang, 2004; Su *et al.*, 2005; Xiao *et al.*, 2005). Here, we present the title compound [Co(2,2'-bipy)(o-sb)(H₂O)₃] (2,2'-bipy is 2,2'-bipyridine), (I), in which the o-sb²⁻ dianion functions in a monodentate coordination mode.



In (I), the Co^{II} atom is in a distorted octahedral environment formed by three aqua O atoms, one carboxylate O atom from an *o*-sb²⁻ dianion and two N atoms of a 2,2'-bipyridine ligand (Fig. 1 and Table 1). The *o*-sb²⁻ ligand coordinates to the Co^{II} centre in a monodentate mode, as is the same as observed in the previously reported compound [Mn(phen)₂-(*o*-sb)(H₂O)]·3H₂O (phen is 1,10-phenanthroline; Xiao, 2005). The dihedral angle between the planes of the *o*-sb²⁻ ring and its carboxylate group is 59.7 (1)°, which is comparable with that in [Mn(phen)₂(*o*-sb)(H₂O)]·3H₂O and much larger than that in [Ni(*o*-sb)(bpe)(H₂O)]·0.25H₂O (Xiao *et al.*, 2005). The dihedral angle between the *o*-sb²⁻ ring and the mean plane of the 2,2'-bipyridine rings is 50.6 (2)°.

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Figure 1

The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

The stability of the crystal structure of (I) is enhanced significantly by hydrogen-bonding interactions (Table 2). There are three intramolecular hydrogen bonds between the coordinated water molecule and the uncoordinated carboxylate O atom (O8–H8B···O2), and between the coordinated water molecule and the uncoordinated sulfonate group (O7–H7A···O3 and O6–H6A···O4). Additional O6–H6B···O2, O8–H8A···O3 and O7–H7B···O5 intermolecular hydrogen bonds link neighbouring mononuclear units into a two-dimensional network structure (Fig. 2).

Experimental

An aqueous solution (10 ml) of $CoCl_2 \cdot 6H_2O$ (0.20 mmol, 0.047 g) was added slowly to a solution (10 ml) of *N*,*N*-dimethylformamide containing 2,2'-bipyridine (0.20 mmol, 0.031 g) and 2-sulfobenzoic acid (0.20 mmol, 0.037 g). Red crystals of (I) suitable for X-ray diffraction analysis were obtained on allowing the solution to stand at room temperature for about two months.

Crystal data

$\begin{bmatrix} \text{Co}(\text{C}_{7}\text{H}_{4}\text{O}_{5}\text{S})(\text{C}_{10}\text{H}_{8}\text{N}_{2})(\text{H}_{2}\text{O})_{3} \end{bmatrix}$ $M_{r} = 469.32$ Monoclinic, Pc a = 7.4546 (7) Å b = 12.3272 (11) Å c = 10.5333 (9) Å $\beta = 90.142$ (11)° V = 967.95 (15) Å ³ Z = 2	$D_x = 1.610 \text{ Mg m}^{-3}$ Mo K α radiation Cell parameters from 1079 reflections $\theta = 2.5-25.2^{\circ}$ $\mu = 1.04 \text{ mm}^{-1}$ T = 298 (2) K Block, red $0.32 \times 0.25 \times 0.17 \text{ mm}$
Data collection	
Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 2002) $T_{\min} = 0.731, T_{\max} = 0.843$ 5336 measured reflections	2602 independent reflections 2565 reflections with $I > 2\sigma(I)$ $R_{int} = 0.021$ $\theta_{max} = 26.0^{\circ}$ $h = -8 \rightarrow 9$ $k = -15 \rightarrow 15$ $l = -12 \rightarrow 10$
Refinement	
Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.023$ $wR(F^2) = 0.057$ S = 1.07 2602 reflections 262 parameters H-atom parameters constrained	$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0228P)^2 \\ &+ 0.0468P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &= 0.001 \\ \Delta\rho_{\text{max}} &= 0.21 \text{ e } \text{\AA}^{-3} \\ \Delta\rho_{\text{min}} &= -0.24 \text{ e } \text{\AA}^{-3} \\ \text{Absolute structure: Flack (1983),} \\ \text{with 1897 Friedel pairs} \end{split}$



Figure 2

A view of the two-dimensional network structure formed by hydrogen bonding interactions (shown as dashed lines). For clarity, the 2,2'bipyridine ligands have been omitted.

Table 1

Selected geometric parameters (Å, °).

Co1-07	2.085 (2)	Co1-O8	2.112 (2)
Co1-O1	2.092 (2)	Co1-N1	2.115 (2)
Co1-O6	2.094 (2)	Co1-N2	2.118 (2)
O7-Co1-O1	90.00 (8)	O6-Co1-N1	94.57 (8)
O7-Co1-O6	88.49 (8)	O8-Co1-N1	95.25 (8)
O1-Co1-O6	80.58 (7)	O7-Co1-N2	171.44 (9)
O7-Co1-O8	90.41 (8)	O1-Co1-N2	98.51 (8)
O1-Co1-O8	89.66 (7)	O6-Co1-N2	92.05 (8)
O6-Co1-O8	170.18 (8)	O8-Co1-N2	90.49 (8)
O7-Co1-N1	94.23 (8)	N1-Co1-N2	77.21 (8)
O1-Co1-N1	173.49 (7)		

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

$\overline{D - H \cdots A}$	<i>D</i> _H	HA	$D \cdots A$	D_H4	
	D-II	11	$D \sim 11$	$D = \Pi^{*} \oplus \Pi^{*}$	
O8−H8 <i>B</i> ···O2	0.82	2.02	2.780 (3)	155	
$O8-H8A\cdots O3^{i}$	0.82	2.08	2.873 (3)	164	
$O7 - H7B \cdot \cdot \cdot O5^{i}$	0.82	1.90	2.717 (3)	178	
$O7 - H7A \cdots O3$	0.82	1.89	2.692 (3)	167	
$O6-H6B\cdots O2^{ii}$	0.82	1.93	2.741 (3)	173	
$O6-H6A\cdots O4$	0.82	2.03	2.842 (3)	172	

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

Water H atoms were located in a difference map and refined with the distance restraint O-H = 0.82 (1) Å and with $U_{\rm iso}({\rm H})$ = $1.5U_{\rm eq}({\rm O})$. Other H atoms were positioned geometrically and allowed to ride on their parent atoms, with C-H = 0.93 Å and $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$.

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

Flack parameter: 0.015 (10)

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