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Key indicators

Single-crystal X-ray study T = 295 K Mean σ (C–C) = 0.007 Å R factor = 0.054 wR factor = 0.153 Data-to-parameter ratio = 12.6

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

Bis(µ-3-sulfonatobenzoato)bis[bis(2,2'-bipyridine)manganese(II)] dihydrate

The title centrosymmetric dimer, $[Mn_2(C_7H_4O_5S)_2(C_{10}H_8-N_2)_4]\cdot 2H_2O$, was obtained by hydrothermal synthesis. The coordination geometry of the Mn^{II} atom is distorted octahedral, defined by four N atoms from two 2,2'-bipyridine ligands and two O atoms from two carboxylate groups of two μ -3-sulfonatobenzoate ligands. In the crystal structure, Mn^{II} complex molecules are linked, through water molecules, by intermolecular O-H···O hydrogen bonds, forming extended one-dimensional chains along [11].

Comment

Recently, sulfobenzoate–metal complexes have received much attention due to their interesting coordination modes and structural topologies (Ying & Mao, 2004; Miao & Zhu, 2006; Zhang, Zhu & Xiao, 2005; Zhang, Wang et al., 2005). The 4-sulfobenzoate(4-sb)/Mn^{II}/2,2'-bipyridine system produces a monomer, [Mn(4-sb)(2,2'-bipy)(H₂O)₃]·H₂O, (II) (Zhang & Zhu, 2005), in which the carboxylate group acts in a chelating mode. Here, we present the dimeric manganese(II) complex with 3-sulfobenzoate (3-sb) as a ligand, (I).



In (I), the unique Mn^{II} atom in the centrosymmetric dimer has a distorted octahedral geometry defined by two O donors from two carboxylate groups of two μ -3-sulfonatobenzoate ligands and four N atoms from two 2,2'-bipyridine ligands (Fig. 1 and Table 1). The coordination geometry of (I) is different from that of (II), in which the Mn^{II} atom adopts a seven-coordinate geometry. The Mn-O(carboxylate) and Mn-N distances in (I) (Table 1) are slightly shorter than those in (II). In the title compound, the carboxylate groups

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bridge two Mn^{II} atoms and the sulfonyl group is uncoordinated. The carboxylate group forms a dihedral angle of 11.2 (3)° with the benzene ring to which it is attached. The dihedral angles between the two pyridine rings of the 2,2′-bipyridine ligands are 7.1 (2) and 9.7 (3)° for the ligands containing N1/N2 and N3/N4, respectively. In the crystal structure, dimeric complex molecules are linked, through water molecules, by intermolecular O–H···O hydrogen bonds, forming extended one-dimensional chains along [11] (Fig. 2 and Table 2).

Experimental

A mixture of $Mn(CH_3COO)_2$ ·4H₂O (0.122 g, 0.5 mmol), sodium hydrogen 3-sulfobenzoate (0.112 g, 0.5 mmol), 2,2'-bipyridine (0.079 g, 0.5 mmol), and water (30 ml) was stirred and filtered; pale-yellow block crystals were obtained from the filtrate after one day.

V = 1280.2 (3) Å³

 $D_x = 1.519 \text{ Mg m}^{-3}$

0.17 \times 0.10 \times 0.10 mm

9370 measured reflections 4515 independent reflections

3553 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.65 \text{ mm}^{-1}$

T = 295 (2) K Block, pale yellow

 $R_{\rm int} = 0.034$ $\theta_{\rm max} = 25.1^{\circ}$

Z = 1

Crystal data

$$\begin{split} & [\mathrm{Mn}_2(\mathrm{C_7H_4O_5S})_2(\mathrm{C_{10}H_8N_2})_4]\cdot 2\mathrm{H_2O} \\ & M_r = 1170.97 \\ & \mathrm{Triclinic}, \ P\overline{1} \\ & a = 10.1223 \ (15) \ \ \mathring{A} \\ & b = 12.0573 \ (17) \ \ \mathring{A} \\ & c = 12.3757 \ (18) \ \ \mathring{A} \\ & \alpha = 62.927 \ (2)^{\circ} \\ & \beta = 79.505 \ (2)^{\circ} \\ & \gamma = 72.400 \ (2)^{\circ} \end{split}$$

Data collection

Bruker APEX area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2002) $T_{\min} = 0.898, T_{\max} = 0.938$

Refinement

| Refinement on F^2 | $w = 1/[\sigma^2(F_0^2) + (0.0869P)^2]$ |
|---------------------------------|--|
| $R[F^2 > 2\sigma(F^2)] = 0.054$ | + 0.9109P] |
| $wR(F^2) = 0.153$ | where $P = (F_0^2 + 2F_c^2)/3$ |
| S = 0.96 | $(\Delta/\sigma)_{\rm max} = 0.001$ |
| 4515 reflections | $\Delta \rho_{\rm max} = 0.97 \ {\rm e} \ {\rm \AA}^{-3}$ |
| 358 parameters | $\Delta \rho_{\rm min} = -0.26 \text{ e } \text{\AA}^{-3}$ |
| H-atom parameters constrained | |

Table 1

Selected geometric parameters (Å, °).

| Mn1-O1 | 2.104 (2) | Mn1-N4 | 2.262 (3) |
|-------------------------|-------------|-------------------------|-------------|
| Mn1-O2 ⁱ | 2.126 (2) | S1-O3 | 1.422 (4) |
| Mn1-N1 | 2.268 (3) | S1-O4 | 1.451 (4) |
| Mn1-N2 | 2.259 (3) | S1-O5 | 1.428 (3) |
| Mn1-N3 | 2.304 (3) | | |
| O1-Mn1-O2 ⁱ | 101.61 (10) | N4-Mn1-N1 | 99.59 (11) |
| O1-Mn1-N2 | 101.14 (11) | O1-Mn1-N3 | 161.48 (11) |
| $O2^i - Mn1 - N2$ | 96.64 (11) | O2 ⁱ -Mn1-N3 | 86.74 (10) |
| O1-Mn1-N4 | 91.86 (11) | N2-Mn1-N3 | 94.18 (11) |
| O2 ⁱ -Mn1-N4 | 88.72 (11) | N4-Mn1-N3 | 71.64 (12) |
| N2-Mn1-N4 | 164.60 (11) | N1-Mn1-N3 | 84.25 (11) |
| O1-Mn1-N1 | 90.50 (10) | O3-S1-O5 | 115.0 (3) |
| O2 ⁱ -Mn1-N1 | 165.13 (11) | O3-S1-O4 | 112.9 (3) |
| N2-Mn1-N1 | 72.31 (11) | O5-S1-O4 | 110.1 (2) |

Symmetry code: (i) -x + 1, -y + 1, -z.



Figure 1

The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms are omitted. [Symmetry code: (i) 1 - x, 1 - y, -z.]



Figure 2

Part of the one-dimensional hydrogen-bonded chain of (I), propagating in the $[1\overline{1}1]$ direction. Hydrogen bonds are shown as dashed lines.

Table 2

Hydrogen-bond geometry (Å, °).

| $D - H \cdots A$ | D-H | $H \cdot \cdot \cdot A$ | $D \cdot \cdot \cdot A$ | $D - \mathbf{H} \cdot \cdot \cdot A$ |
|-------------------------|---------|-------------------------|-------------------------|--------------------------------------|
| $O1W-H1A\cdots O4$ | 0.85(4) | 2.13 (4) | 2.956 (6) | 165(4) |
| $O1W-H1B\cdots O5^{ii}$ | 0.85(5) | 1.98 (2) | 2.793 (5) | 161(5) |

Symmetry code: (ii) -x + 2, -y, -z + 1.

All C-bound H atoms were placed in calculated positions (C-H = 0.93 Å) and included in the riding-model approximation, and $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$. The water H atoms were located in a difference Fourier map and refined with restraints for O-H distances [0.85 (1) Å] and with $U_{\rm iso}({\rm H}) = 0.08$ Å².

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: *WinGX* (Farrugia, 1999).

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