



Figure 1
A view of the title complex, showing the atom-labelling scheme and with displacement ellipsoids at the 50% probability level.

The geometric environment around the central metal atom of the title complex is a distorted octahedron, with O—Mn—O 'bite' angles of 86.19 (5) and 83.37 (5)° (Table 1, Fig. 1) for the acac groups. In contrast, the dmaeH ligand, which forms a five-membered chelate ring, has a smaller O—Mn—O bite angle of only 74.67 (5)°. The Mn—O bond lengths for the acac ligands range from 2.118 (12) to 2.156 (12) Å (Table 1). These are in good agreement with the values reported for another manganese(II) bis(acetylacetonate) complex, [Mn(acac)₂(H₂O)₂] (2.123 and 2.142 Å; Montgomery & Lingafelter, 1968), but slightly longer than the values reported for the manganese(III) complex Mn(acac)₃ (1.894–1.959 Å; Morosin *et al.*, 1964). The Mn—N bond length observed here is 2.342 (14) Å, while those for the complex [Mn(bipy)₂(H₂O)₂][Me₂NCH₂CO₃][ClO₃]₂·2H₂O, also octahedral, are 2.245 and 2.257 Å (Chen *et al.*, 1995).

In the crystal structure, an intermolecular O—H...O hydrogen bond (Table 2) links the molecules into centrosymmetric dimers.

Experimental

N,N-Dimethylaminoethanol (0.1 ml, 1.0 mmol) was added to a stirred solution of Mn(acac)₂ (0.254 g, 1.0 mmol) in toluene (20 ml). Continuous stirring at room temperature for 4 h, followed by removal of all volatiles *in vacuo*, gave a dry powder of (I). Yellowish plate-like crystals suitable for single-crystal X-ray analysis were grown from a concentrated solution in toluene at room temperature after one week.

Crystal data

[Mn(C₅H₇O₂)₂(C₄H₁₁N)]
M_r = 342.29
 Triclinic, *P* $\bar{1}$
a = 7.6392 (14) Å
b = 10.5533 (19) Å
c = 11.766 (2) Å
 α = 105.235 (3)°
 β = 103.187 (3)°
 γ = 98.154 (3)°
V = 870.3 (3) Å³

Z = 2
D_x = 1.306 Mg m⁻³
 Mo *K*α radiation
 Cell parameters from 5563 reflections
 θ = 2.3–30.5°
 μ = 0.78 mm⁻¹
T = 110 (2) K
 Plate, yellowish
 0.37 × 0.27 × 0.02 mm

Data collection

Bruker SMART APEX CCD area-detector diffractometer
 ω scans
 Absorption correction: multi-scan (SADABS in SAINT-Plus; Bruker, 2003)
T_{min} = 0.772, *T_{max}* = 0.99
 8862 measured reflections

4296 independent reflections
 3711 reflections with *I* > 2σ(*I*)
R_{int} = 0.026
 θ_{\max} = 28.3°
h = -10 → 10
k = -14 → 14
l = -15 → 15

Refinement

Refinement on *F*²
R[*F*² > 2σ(*F*²)] = 0.037
wR(*F*²) = 0.096
S = 1.05
 4296 reflections
 200 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.054P)^2 + 0.2295P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.63 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\min} = -0.24 \text{ e } \text{Å}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Mn1—O3	2.1183 (12)	Mn1—O2	2.1565 (11)
Mn1—O4	2.1226 (12)	Mn1—O1	2.2354 (12)
Mn1—O5	2.1262 (12)	Mn1—N2	2.3427 (14)
O3—Mn1—O4	102.65 (5)	O5—Mn1—O1	91.31 (5)
O3—Mn1—O5	94.01 (5)	O2—Mn1—O1	91.47 (5)
O4—Mn1—O5	86.19 (5)	O3—Mn1—N2	94.92 (5)
O3—Mn1—O2	83.37 (5)	O4—Mn1—N2	162.14 (5)
O4—Mn1—O2	93.26 (5)	O5—Mn1—N2	89.40 (5)
O5—Mn1—O2	177.15 (4)	O2—Mn1—N2	91.96 (5)
O3—Mn1—O1	168.27 (5)	O1—Mn1—N2	74.67 (5)
O4—Mn1—O1	88.12 (5)		

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O1—H1...O2 ⁱ	0.847 (16)	1.865 (18)	2.6777 (17)	160 (3)

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

The hydroxyl H atom was located in a difference Fourier map and was refined isotropically, with the O—H bond distance restrained to 0.90 (2) Å. All other H atoms were placed in calculated positions, with C—H = 0.95 and 0.98 Å, and were refined with *U_{iso}*(H) = 1.5 (methyl) or 1.2 (methylene) times *U_{eq}*(C). Methyl H atoms were allowed to rotate to best fit the experimental electron density. The s.u. values of the cell parameters are taken from the software, recognizing that the values are unreasonably small (Herbstein, 2000). The highest

residual peak is located 0.81 Å from atom Mn1, and the deepest hole is found 1.22 Å from atom H4C, close to the NMe₂ group.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINTE-Plus* (Bruker, 2003); data reduction: *SAINTE-Plus*; program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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