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**Key indicators**

Single-crystal X-ray study  
 T = 273 K  
 Mean  $\sigma(\text{C}-\text{C}) = 0.007 \text{ \AA}$   
 R factor = 0.046  
 wR factor = 0.122  
 Data-to-parameter ratio = 14.2

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

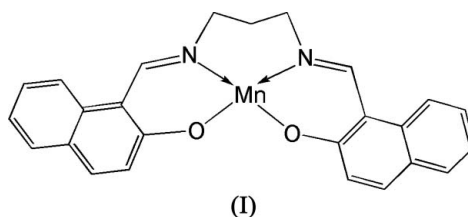
**[N,N'-Bis(2-oxido-1-naphthylmethylidene)-propane-1,3-diamine]manganese(II)**

In the title mononuclear manganese(II) complex,  $[\text{Mn}(\text{C}_{25}\text{H}_{20}\text{N}_2\text{O}_2)]$ , the Mn atom and the central methylene group of the propanediamine fragment of the ligand lie on a mirror plane. The four-coordinate Mn atom binds to two N and two O atoms of the ligand, forming a square-planar geometry.

Received 14 March 2006  
 Accepted 15 March 2006

**Comment**

Manganese(II) compounds are very important in bioinorganic chemistry (Ciringhi *et al.*, 1997; Chen *et al.*, 2003). The structure of a mononuclear manganese(II) complex, (I), is described here.



Atom Mn1 lies on a mirror plane, as does the methylene C13 and its substituent H atoms. Mn1 is four-coordinate, binding to two N and two O atoms of the ligand in a slightly distorted square-planar geometry (Fig. 1). The Mn–N and Mn–O bond lengths (Table 1) are comparable with the corresponding values observed in other manganese(II) complexes (Gallo, Solari, Re *et al.*, 1997; Gallo, Solari, Floriani *et al.*, 1997). The bond angles subtended by *cis* substituents on Mn1 range from 82.17 (19) to 94.3 (2)° (Table 1).

**Experimental**

Compound (I) was obtained by stirring propane-1,3-diamine (1.0 mmol, 79.2 mg), 2-hydroxy-1-naphthaldehyde (2.0 mmol, 343.5 mg) and manganese(II) acetate tetrahydrate (1.0 mmol, 245.1 mg) in EtOH solution (80 ml). The residue was recrystallized from an EtOH solution, giving brown block-like crystals.

*Crystal data*

$[\text{Mn}(\text{C}_{25}\text{H}_{20}\text{N}_2\text{O}_2)]$   
 $M_r = 435.37$   
 Orthorhombic,  $Cmc2_1$   
 $a = 30.650 (1) \text{ \AA}$   
 $b = 8.464 (3) \text{ \AA}$   
 $c = 7.769 (1) \text{ \AA}$   
 $V = 2015.5 (8) \text{ \AA}^3$   
 $Z = 4$   
 $D_x = 1.435 \text{ Mg m}^{-3}$

Mo  $K\alpha$  radiation  
 Cell parameters from 1718 reflections  
 $\theta = 2.5\text{--}22.6^\circ$   
 $\mu = 0.68 \text{ mm}^{-1}$   
 $T = 273 (2) \text{ K}$   
 Block, brown  
 $0.32 \times 0.28 \times 0.22 \text{ mm}$

*Data collection*

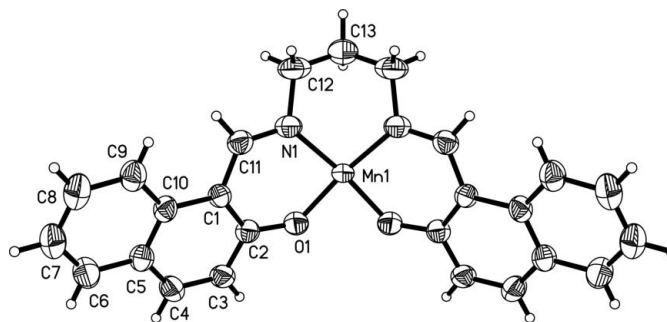
Bruker SMART 1000 CCD area-detector diffractometer  
 $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
 $T_{\min} = 0.812$ ,  $T_{\max} = 0.865$   
 5125 measured reflections

1977 independent reflections  
 1541 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.044$   
 $\theta_{\max} = 26.5^\circ$   
 $h = -29 \rightarrow 38$   
 $k = -10 \rightarrow 10$   
 $l = -9 \rightarrow 9$

*Refinement*

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.046$   
 $wR(F^2) = 0.122$   
 $S = 0.97$   
 1977 reflections  
 139 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0679P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} < 0.001$   
 $\Delta\rho_{\max} = 0.27 \text{ e } \text{\AA}^{-3}$   
 $\Delta\rho_{\min} = -0.35 \text{ e } \text{\AA}^{-3}$   
 Absolute structure: Flack (1983),  
 with 849 Friedel pairs  
 Flack parameter:  $-0.08(4)$

**Figure 1**

The structure of (I), showing the atom-numbering scheme, with displacement ellipsoids drawn at the 30% probability level. Unlabelled atoms are related to labelled atoms by the symmetry operator  $(-x, y, z)$ .

This work was mainly supported by Doctor Research Grants of the East China University of Science and Technology (ECUST) (No. YJ0142119).

**Table 1**

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

Mn1—O1	1.842 (3)	Mn1—N1	1.867 (4)
O1 <sup>i</sup> —Mn1—O1	82.17 (19)	O1—Mn1—N1	91.75 (15)
O1 <sup>i</sup> —Mn1—N1	173.75 (14)	N1—Mn1—N1 <sup>i</sup>	94.3 (2)

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

All H atoms were constrained to their ideal geometries, with C—H = 0.93–0.97  $\text{\AA}$  and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ .

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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