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## ***cis*-Dibromobis(1,10-phenanthroline)manganese(II)**

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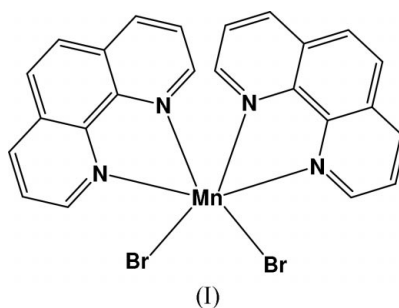
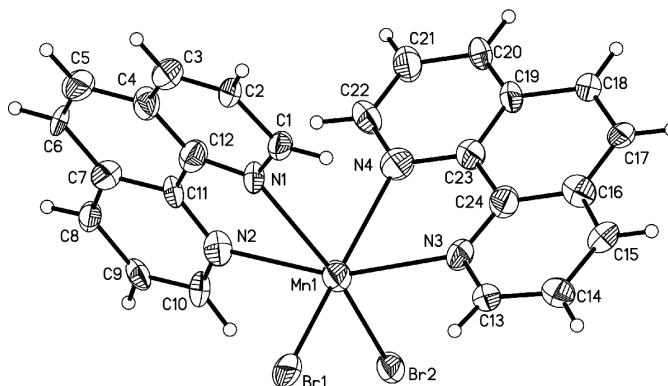
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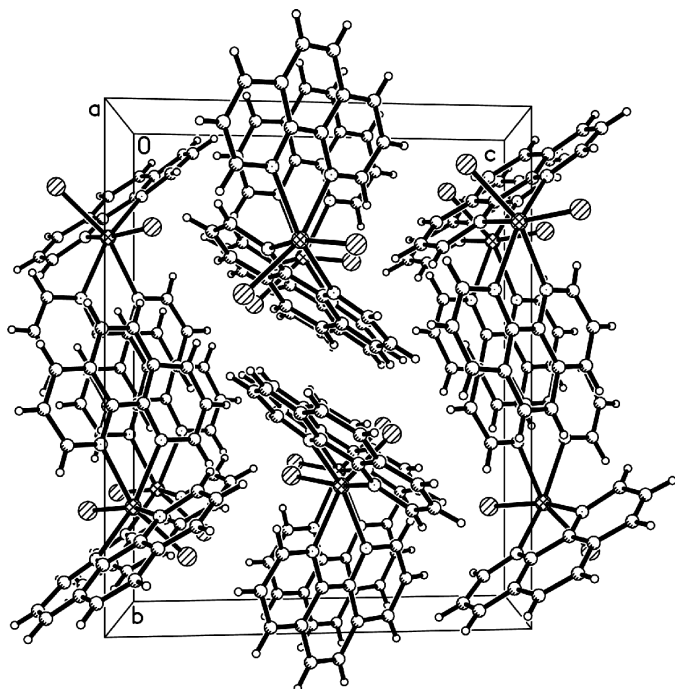
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## Key indicators

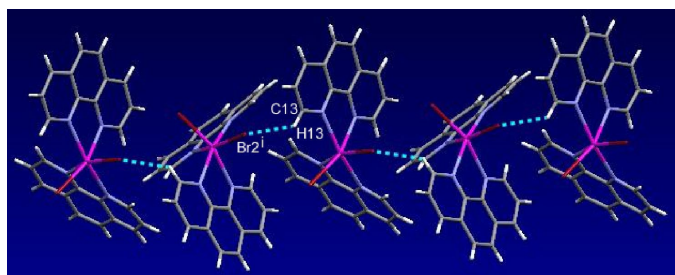
Single-crystal X-ray study  
 $T = 293$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.007$  Å  
 $R$  factor = 0.048  
 $wR$  factor = 0.099  
Data-to-parameter ratio = 15.5For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.*cis*-Dibromobis(1,10-phenanthroline)manganese(II)In the title complex,  $[\text{MnBr}_2(\text{C}_{24}\text{H}_{16}\text{N}_4)]$ , there is a weak C—  
H···Br intermolecular interaction in the crystal structure,  
giving rise to molecular chains along the  $a$  axis.Received 7 June 2004  
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## Comment

In recent years, simple metal complexes of phenanthroline and  
its derivatives have attracted great interest because they can  
be used to study the hydrolysis of biologically important  
phosphate diesters with poor leaving groups, *e.g.* DNA (Wall  
*et al.*, 1999). These complexes can also be used to develop new  
diagnostic and therapeutic agents in DNA binding and  
cleavage (Barton, 1986; Naing *et al.*, 1995). We report here the  
title complex, (I), a new metal complex of phenanthroline. A  
search of the January 2004 Cambridge Structural Database  
(Allen, 2002; Bruno *et al.*, 2002) found no report of (I).Compound (I) has expected values for bond lengths and  
angles. The dihedral angle between the two phenanthroline  
planes is  $84.74(6)^\circ$  and the average Mn—Br bond length is  
 $2.535(2)$  Å, within the range of previously reported values  
 $[2.496(2)$  (Kienitz *et al.*, 2000) and  $2.677(2)$  Å (Goodgame *et al.*,  
1999)]. There is a weak intermolecular interaction, C13—**Figure 1**  
The molecular structure of (I), shown with 30% probability displacement  
ellipsoids.



**Figure 2**  
The packing of (I), viewed down the *a* axis.



**Figure 3**  
The molecular chains formed by the weak intermolecular interaction (dashed lines) of C13–H13...Br2<sup>i</sup> [symmetry code: (i)  $x, \frac{3}{2} - y, \frac{1}{2} + z$ ].

H13...Br2<sup>i</sup> [symmetry code: (i)  $x, \frac{3}{2} - y, \frac{1}{2} + z$ ], in the structure, giving one-dimensional molecular chains arranged along the *a* axis, as shown in Figs. 2 and 3.

## Experimental

To a warm solution of 1,10-phenanthroline (0.344 g, 2 mmol) in CH<sub>3</sub>OH (20 ml) was added MnBr<sub>2</sub>·4H<sub>2</sub>O (0.265 g, 1 mmol) with slow heating and stirring. The mixture was refluxed for 2 h, then cooled to room temperature. After about two weeks, yellow single crystals suitable for X-ray crystallographic analysis were obtained. Analysis calculated for C<sub>24</sub>H<sub>16</sub>Br<sub>2</sub>MnN<sub>4</sub>: C 50.11, H 2.80, N 9.74%; found: C 50.05, H 2.76, N 9.69%.

### Crystal data

[MnBr<sub>2</sub>(C<sub>24</sub>H<sub>16</sub>N<sub>4</sub>)]  
*M<sub>r</sub>* = 575.17  
 Monoclinic, *P*2<sub>1</sub>/*c*  
*a* = 10.423 (3) Å  
*b* = 16.223 (3) Å  
*c* = 13.244 (3) Å  
 $\beta$  = 99.62 (2)°  
*V* = 2208.0 (9) Å<sup>3</sup>  
*Z* = 4

*D<sub>x</sub>* = 1.730 Mg m<sup>-3</sup>  
 Mo *K*α radiation  
 Cell parameters from 1225 reflections  
 $\theta$  = 2.5–20.4°  
 $\mu$  = 4.24 mm<sup>-1</sup>  
*T* = 293 (2) K  
 Block, yellow  
 0.20 × 0.10 × 0.10 mm

### Data collection

Bruker SMART APEX CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Bruker, 2000)  
*T*<sub>min</sub> = 0.61, *T*<sub>max</sub> = 0.66  
 9269 measured reflections

4334 independent reflections  
 3284 reflections with *I* > 2σ(*I*)  
*R*<sub>int</sub> = 0.042  
 $\theta$ <sub>max</sub> = 26.0°  
*h* = −12 → 12  
*k* = −20 → 20  
*l* = −16 → 9

### Refinement

Refinement on *F*<sup>2</sup>  
*R*[*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.048  
*wR*(*F*<sup>2</sup>) = 0.099  
*S* = 1.02  
 4334 reflections  
 280 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.05P)^2 + 1.55P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 ( $\Delta/\sigma$ )<sub>max</sub> < 0.001  
 $\Delta\rho$ <sub>max</sub> = 0.96 e Å<sup>-3</sup>  
 $\Delta\rho$ <sub>min</sub> = −0.73 e Å<sup>-3</sup>

**Table 1**

Selected geometric parameters (Å, °).

Br1–Mn1	2.5313 (10)	Mn1–N3	2.429 (4)
Br2–Mn1	2.5268 (11)	Mn1–N2	2.445 (4)
Mn1–N4	2.391 (4)	Mn1–N1	2.448 (4)
N4–Mn1–N3	67.06 (13)	N2–Mn1–Br2	99.86 (9)
N4–Mn1–N2	95.51 (13)	N1–Mn1–Br2	160.63 (9)
N3–Mn1–N2	161.56 (12)	N4–Mn1–Br1	161.29 (11)
N4–Mn1–N1	80.27 (13)	N3–Mn1–Br1	99.77 (9)
N3–Mn1–N1	107.97 (12)	N2–Mn1–Br1	95.62 (10)
N2–Mn1–N1	61.13 (12)	N1–Mn1–Br1	92.04 (9)
N4–Mn1–Br2	99.19 (11)	Br2–Mn1–Br1	93.66 (3)
N3–Mn1–Br2	89.27 (9)		

**Table 2**

Hydrogen-bonding 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>
C13–H13...Br2 <sup>i</sup>	0.93	2.78	3.466 (5)	131

Symmetry code: (i)  $x, \frac{3}{2} - y, \frac{1}{2} + z$ .

All H atoms were positioned geometrically (C–H = 0.93 Å) and treated as riding, with *U*<sub>iso</sub>(H) = 1.2*U*<sub>eq</sub>(C).

Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINTE* (Bruker, 2000); program(s) used to solve and refine structure: *SHELXTL* (Bruker, 2000); molecular graphics: *SHELXTL* and *MERCURY* (Version 1.2.1; Bruno *et al.*, 2002).

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