

Tetraaquabis(isothiocyanato)manganese(II)
bis(2-methylpyrazine-1,4-dioxide)Xu Wen,^a Jing Min Shi^{b*} and
Zhang Xia^b^aSchool of Environment and Engineering,
Shandong Institute of Architecture and Engi-
neering, Jinan 250101, People's Republic of
China, and ^bDepartment of Chemistry,
Shandong Normal University, Jinan 250014,
People's Republic of ChinaCorrespondence e-mail:
shijingmin@beelink.com

Key indicators

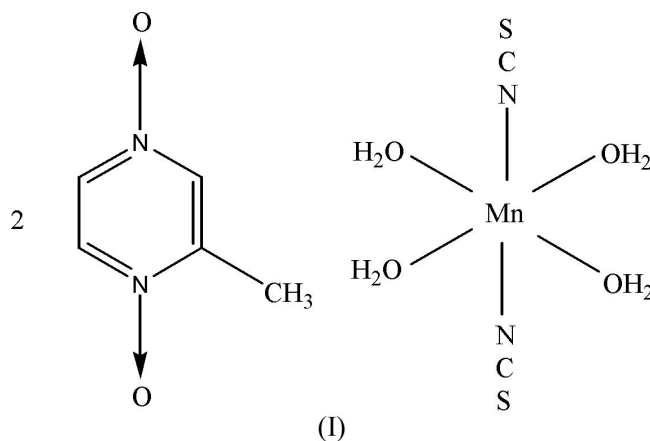
Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
 R factor = 0.035
 wR factor = 0.097
Data-to-parameter ratio = 11.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the title molecular complex, $[\text{Mn}(\text{NCS})_2(\text{H}_2\text{O})_4] \cdot 2\text{C}_5\text{H}_6\text{N}_2\text{O}_2$, the manganese(II) atom has a slightly distorted octahedral coordination, formed by four O atoms from the water molecules and two N atoms from the thiocyanate anions. The Mn complex lies on a special position of site symmetry 2 and $\bar{1}$, and the 2-methylpyrazine-1,4-dioxide molecule is located on a mirror plane. The crystal packing is stabilized by intermolecular $\text{OH}(\text{water}) \cdots \text{O} \leftarrow \text{N}$ hydrogen bonds.

Received 21 March 2005
Accepted 6 April 2005
Online 16 April 2005

Comment

In the title molecular complex, (I), the manganese(II) atom is coordinated by four O atoms from the water molecules and two N atoms from the thiocyanate anions. Atom Mn1 lies on a twofold axis and an inversion centre. The Mn1–O3 and Mn1–N3 bond lengths are 2.1918 (14) Å and 2.188 (3) Å, respectively; the manganese(II) atom has a slightly distorted octahedral coordination. The non-H atoms of the 2-methylpyrazine-1,4-dioxide molecules lie on mirror planes. In the crystal structure, the 2-methylpyrazine-1,4-dioxide molecules are packed as columns along the b axis, with the manganese(II) complexes positioned between the columns. The crystal packing (Fig. 2) is stabilized by intermolecular $\text{OH}(\text{water}) \cdots \text{O} \leftarrow \text{N}$ hydrogen bonds (Table 1).



Experimental

To 15 ml of an aqueous solution of $\text{Mn}(\text{ClO}_4)_2 \cdot 6\text{H}_2\text{O}$ (0.1425 g, 0.394 mmol) and sodium thiocyanate (0.0652 g, 0.804 mmol), 2-methylpyrazine-1,4-dioxide (0.0511 g, 0.405 mmol) was added. The resulting solution was stirred for a few minutes. Colorless single crystals were obtained after the solution was allowed to stand at room temperature for three weeks.

Crystal data

[Mn(NCS)₂(H₂O)₄]·2C₅H₆N₂O₂
M_r = 495.40
 Monoclinic, *C*2/*m*
a = 17.027 (6) Å
b = 6.828 (3) Å
c = 10.126 (4) Å
 β = 111.844 (4)°
V = 1092.7 (8) Å³
Z = 2

D_x = 1.506 Mg m⁻³
 Mo *K*α radiation
 Cell parameters from 2372 reflections
 θ = 2.6–26.9°
 μ = 0.84 mm⁻¹
T = 293 (2) K
 Prism, colorless
 0.20 × 0.15 × 0.11 mm

Data collection

Bruker SMART CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)
T_{min} = 0.848, *T_{max}* = 0.911
 2787 measured reflections

1103 independent reflections
 1026 reflections with *I* > 2σ(*I*)
R_{int} = 0.028
 θ_{\max} = 25.5°
h = -20 → 14
k = -8 → 8
l = -10 → 12

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.035
wR (*F*²) = 0.097
S = 1.09
 1103 reflections
 93 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0634P)^2 + 0.3225P]$,
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.47 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.47 \text{ e \AA}^{-3}$

Table 1

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>
O3–H7A···O2 ⁱ	0.89	1.84	2.716 (2)	170
O3–H6B···O1 ⁱⁱ	0.82	1.96	2.748 (2)	162

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

The methyl H atoms (H4A and H5B) and atom H7A from the coordinated water molecule were found in a difference Fourier map. The rest of the H atoms were positioned geometrically. All H atoms were included in the final cycles of the refinement using a riding model (*C*–H = 0.93–0.97 Å, O–H = 0.82–0.89 Å, *U_{iso}*(H) = 1.2–1.5 *U_{eq}* of the carrier atom).

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 2001); software used to prepare material for publication: *SHELXTL*.

The authors thank the Natural Science Foundation of China (No. 20271043) and the Natural Science Foundation of Shandong Province of China (No. Y2002B10) for financial support.

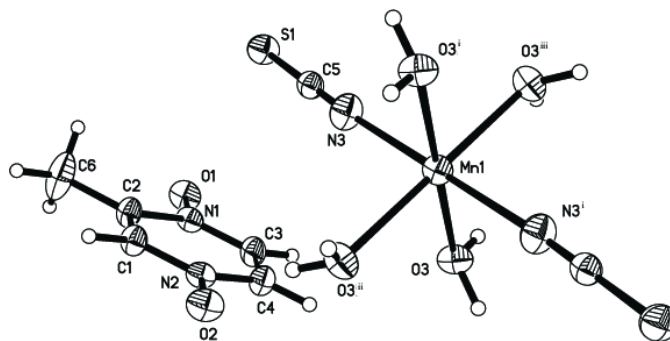


Figure 1 View of (I), showing 30% probability displacement ellipsoids. [Symmetry codes: (i) $-x, -y, -z$; (ii) $x, -y, z$; (iii) $-x, y, -z$].

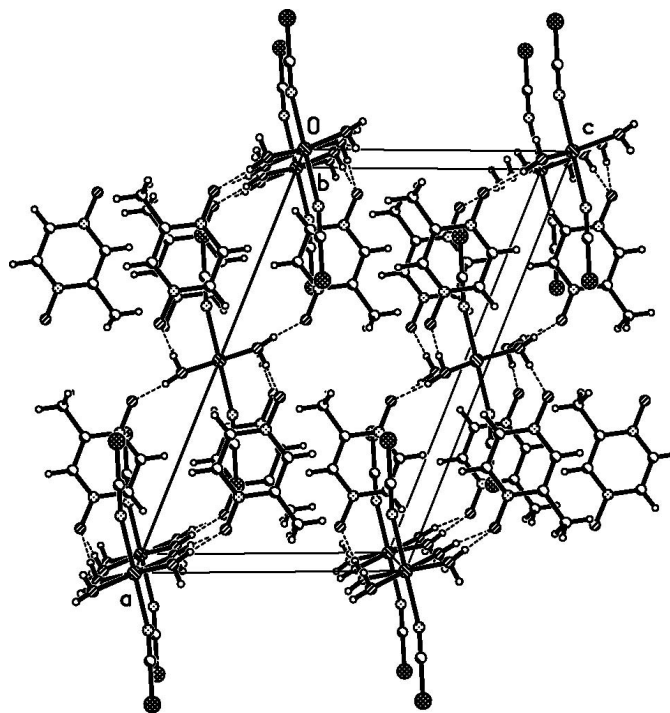


Figure 2 The packing of (I). The intermolecular O–H···O hydrogen bonds are indicated by dashed lines.

References

- Bruker (1997). *SMART* (Version 5.6) and *SAINT* (Version 5.06A). Bruker AXS Inc., Madison, Wisconsin, USA.
 Sheldrick, G. M. (1996). *SADABS*. University of Göttingen, Germany.
 Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
 Sheldrick, G. M. (2001). *SHELXTL*. Version 6.12. Bruker AXS Inc., Madison, Wisconsin, USA.