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Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$
 R factor = 0.025
 wR factor = 0.069
Data-to-parameter ratio = 13.8For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

Diaquabis[5-(pyrazin-2-yl)tetrazolato]manganese(II)

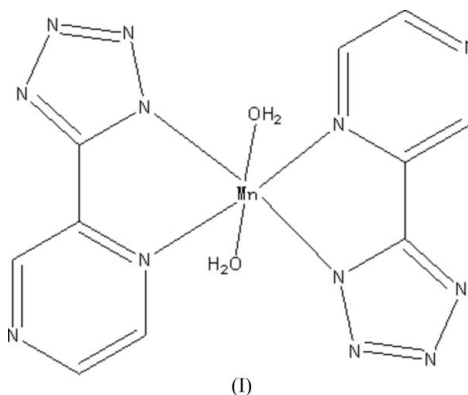
In the title complex, $[\text{Mn}(\text{C}_5\text{H}_3\text{N}_3)_2(\text{H}_2\text{O})_2]$, the Mn^{II} atom, located on an inversion center, is coordinated by four N atoms from two 5-(2-pyrazinyl)tetrazolate ligands and two water molecules in a distorted octahedral geometry. The packing is governed by intermolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds.

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Comment

The design, synthesis, characterization, and properties of supramolecular networks formed by using functionalized organic molecules as bridges between metal centers are of great interest (Rizk *et al.*, 2005; Eddaoudi *et al.*, 2001). Reports on tetrazoles are increasing rapidly, since tetrazoles play an important role as a ligand in coordination chemistry (Song & Xi, 2006). Recently, 5-substituted 1*H*-tetrazoles have been synthesized by a facile approach (Demko & Sharpless, 2001*a,b*). In the general reaction, the tetrazoles are prepared by the addition of an azide to a nitrile in water with the aid of a Lewis acid such as Zn^{2+} . In this paper, we selected 2-cyanopyrazine, NaN_3 and a Lewis acid MnCl_2 as reagents to yield, in one-step, the title mononuclear complex, (I), under hydrothermal conditions.



In (I), the Mn^{II} atom, located on an inversion center, is coordinated by four N atoms from two 5-(2-pyrazinyl)tetrazolate ligands and two water molecules in a distorted octahedral geometry. In each ligand, the pyrazinyl and tetrazolyl rings are almost coplanar, making a dihedral angle of $2.51(5)^\circ$. Intermolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds (Table 2) stabilize the crystal packing.

Experimental

Hydrothermal treatment of $\text{MnCl}_2\cdot 4\text{H}_2\text{O}$ (1.0 mmol, 0.197 g), 2-cyanopyrazine (1 mmol, 0.105 g), NaN_3 (1 mmol, 0.065 g), and water

(3 ml) over 50 h at 422 K yielded red block-shaped crystals (yield: 60%).

Crystal data

[Mn(C₅H₃N₃)₂(H₂O)₂] Z = 2
M_r = 385.24 *D_x* = 1.733 Mg m⁻³
 Monoclinic, *P*2₁/*n* Mo *K*α radiation
a = 5.9840 (3) Å μ = 0.93 mm⁻¹
b = 11.7421 (5) Å *T* = 293 (2) K
c = 10.8646 (5) Å Block, yellow
 β = 104.731 (2)° 0.25 × 0.20 × 0.17 mm
V = 738.31 (6) Å³

Data collection

Bruker APEX-II area-detector 9055 measured reflections
 diffractometer 1700 independent reflections
 φ and ω scans 1576 reflections with *I* > 2σ(*I*)
 Absorption correction: multi-scan *R*_{int} = 0.022
 (SADABS; Sheldrick, 1996) θ_{max} = 27.5°
*T*_{min} = 0.800, *T*_{max} = 0.858

Refinement

Refinement on *F*² $w = 1/[\sigma^2(F_o^2) + (0.0389P)^2 + 0.1934P]$
R[*F*² > 2σ(*F*²)] = 0.025 where *P* = (*F_o*² + 2*F_c*²)/3
wR(*F*²) = 0.069 (Δ/σ)_{max} < 0.001
S = 1.05 Δρ_{max} = 0.17 e Å⁻³
 1700 reflections Δρ_{min} = -0.28 e Å⁻³
 123 parameters
 H atoms treated by a mixture of independent and constrained refinement

Table 1

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>
O1W—H1W...N6 ⁱ	0.83 (2)	1.92 (2)	2.7425 (16)	169 (2)
O1W—H2W...N4 ⁱⁱ	0.77 (3)	2.04 (3)	2.7939 (18)	167 (2)

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

H atoms of the water molecule were located in a difference Fourier map and were refined isotropically. Other H atoms were placed in calculated positions and treated as riding on their parent atoms, with C—H = 0.93 Å and *U*_{iso}(H) = 1.2*U*_{eq}(C).

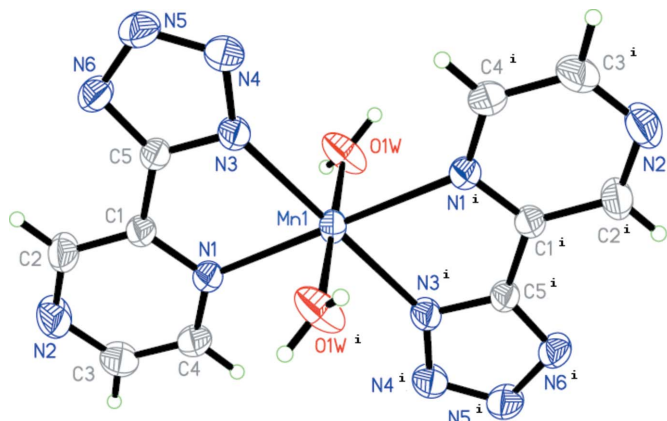


Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Non-H atoms are shown as 50% probability displacement ellipsoids. H atoms are represented as small spheres of arbitrary radii. [Symmetry code: (i) $2 - x, 2 - y, 1 - z$.]

Data collection: *SMART* (Bruker,1998); cell refinement: *SAINTE* (Bruker, 1999); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1998); software used to prepare material for publication: *SHELXTL*.

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