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{2,6-Bis[bis(2-pyridylmethyl)aminomethyl]pyridine}manganese(II) bis(perchlorate) 0.435-hydrate

Alan Hazella and Hans Toftlundb*

^aDepartment of Chemistry, Aarhus University, Langelandsgade 140, 8000 Århus C, Denmark, and bDepartment of Physics and Chemistry, University of Southern Denmark, Campusvej 55, 5230 Odense M. Denmark

Correspondence e-mail: ach@chem.au.dk

Key indicators

Single-crystal X-ray study T = 100 KMean $\sigma(C-C) = 0.002 \text{ Å}$ Disorder in solvent or counterion R factor = 0.035wR factor = 0.037 Data-to-parameter ratio = 17.5

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

The title compound, $[Mn(C_{31}H_{31}N_7)](ClO_4)_2.0.435H_2O$, contains a high-spin Mn^{II} atom which is coordinated by seven N atoms at the corners of a distorted pentagonal bipyramid.

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Comment

The title compound, $[Mn(BPATPA)](ClO_4)_2.0.435H_2O$, (I), is isostructural with [Co(BPATPA)](ClO₄)₂.0.365H₂O, described in our preceding report (Hazell & Toftlund, 2007). In (I), the Mn^{II} atom is coordinated by seven N atoms which form a distorted pentagonal bipyramid (Fig. 1 and Table 1), with atoms N21 and N31 in the axial positions. The axial Mn $-Nsp^2$ bonds are longer than the equatorial $Mn - Nsp^2$ bonds and are similar in length to the Mn-Nsp³ bonds (atoms N1 and N9). The mean Mn-N bond length of 2.351 Å compares with the mean Fe-N bond length of 2.313 Å in [Fe(BPATPA)]-(ClO₄)₂·H₂O (Lonnon et al., 2002) and the mean Co-N bond length of 2.274 Å in [Co(BPATPA)](ClO₄)₂.0.365H₂O (Hazell & Toftlund, 2007). Thus, the mean M-N bond length decreases regularly with increasing number of unpaired d electrons on M in these high-spin complexes.

As is the case for the Co^{II} complex, the water molecule is included with fractional site occupancy and is hydrogen bonded to two O atoms of two perchlorate anions (Table 2).

(I)

Experimental

The BPATPA ligand (0.25 g, 0.5 mmol) was dissolved in methanol (10 ml) and the solution was flushed with dinitrogen for 5 min. Mn(ClO₄)₂·6H₂O (0.18 g, 0.5 mmol) was added and the solution was stirred with continuous bubbling of dinitrogen for another 15 min. The solution was then left to stand in a closed vessel and crystals of (I) formed overnight.

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Crystal data

[Mn(C₃₁H₃₁N₇)](ClO₄)₂·0.435H₂O Z=4 $D_x=1.556 \text{ Mg m}^{-3}$ Monoclinic, $P2_1/c$ Mo $K\alpha$ radiation $\mu=0.63 \text{ mm}^{-1}$ $E=0.63 \text{ mm}^{-1}$ Mo $E=0.63 \text{ mm}^{-1}$ Mo E=0.63 mm

Data collection

Siemens SMART CCD areadetector diffractometer 35942 measured reflections 9357 independent reflections

Refinement

Table 1 Selected bond lengths (Å).

Mn1-N1	2.397 (1)	Mn1-N21	2.431 (1)
Mn1-N9	2.409 (1)	Mn1-N31	2.350(1)
Mn1-N10	2.290 (1)	Mn1-N41	2.279 (1)
Mn1-N11	2.306 (1)		

Table 2 Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathbf{H}\cdot\cdot\cdot A$
O9−H9 <i>A</i> ···O5	0.85	1.92	2.768 (4)	180
O9−H9 <i>B</i> ···O4	0.85	2.31	3.165 (4)	180

H atoms bound to C atoms were placed in calculated positions, with C-H = 0.95 Å, and refined using a riding model, with $U_{iso}(H)$ =

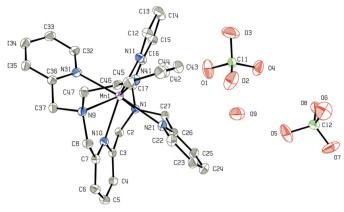


Figure 1

The molecular structure of (I), showing displacement ellipsoids at the 50% probability level. H atoms have been omitted.

 $1.2U_{\rm eq}(C)$. The H atoms of the water molecule were placed along the vector from O9 to the nearest hydrogen-bond acceptor O atom, with O9-H = 0.85 Å. They were allowed to ride during subsequent refinement, with $U_{\rm iso}({\rm H})=1.2U_{\rm eq}({\rm O})$. The refined site occupancy factor of atom O9 is 0.435 (5).

Data collection: *SMART* (Siemens, 1995); cell refinement: *SAINT* (Siemens, 1995); data reduction: *SAINT*; program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1997); program(s) used to refine structure: *KRYSTAL* (Hazell, 1995); molecular graphics: *ORTEPIII* (Burnett & Johnson, 1996); software used to prepare material for publication: *KRYSTAL*.

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