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Key indicators

Single-crystal X-ray study T = 294 KMean $\sigma(\text{C}-\text{C}) = 0.002 \text{ Å}$ R factor = 0.030 wR factor = 0.087 Data-to-parameter ratio = 20.2

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

Hexakis(1-methyl-1*H*-imidazole- κN^3)manganese(II) dichloride dihydrate

In the title compound, $[Mn(C_4H_6N_2)_6]Cl_2 \cdot 2H_2O$, the Mn^{II} ion is located on an inversion center and is coordinated by six 1-methylimidazole molecules in a distorted octahedral geometry.

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Comment

As part of an investigation on Mn complexes with nitrogen donor ligands, we present here the crystal structure of the title compound, (I). The crystal structure of (I) consists of Mn^{II} complex cations, Cl⁻ anions and solvent water molecules. The Mn^{II} ion is located on an inversion center and is coordinated by six 1-methylimidazole molecules in a distorted octahedral geometry (Table 1).



The Cl⁻ anions and water molecules are linked together by $O-H\cdots Cl$ hydrogen bonds (Table 2), forming a planar quadrilateral. This quadrilateral links with 1-methylimidazole ligands *via* weak $C-H\cdots O$ and $C-H\cdots Cl$ interactions.

A packing diagram of (I) is presented in Fig. 2. The Mn^{II} complex cations form a three-dimensional network with a hollow mesh along the *a* axis, in which lie the quadrilaterals formed by Cl⁻ anions and solvent molecules.

Experimental

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 $MnCl_2 \cdot 4H_2O$ (80 mg, 0.40 mmol) was added to 1-methylimidazole (1.000 g, 12.18 mmol) in 2.0 ml acetonitrile. The resulting white

metal-organic papers



Figure 1

The molecular structure of (I) with 50% probability displacement ellipsoids (arbitrary spheres for H atoms). Dashed lines indicate hydrogen bonds. [Symmetry codes: (i) -x, -y, 2 - z; (ii) -x, 1 - y, 2 - z.]



Figure 2

The packing of (I), viewed along the a axis. Dashed lines indicate hydrogen bonds.

precipitate was dissolved in a suitable quantity of hot acetonitrile and then filtered. Single crystals of (I) were obtained from the filtrate.

Crystal data

$$\begin{split} & [\mathrm{Mn}(\mathrm{C}_4\mathrm{H}_6\mathrm{N}_2)_6]\mathrm{Cl}_2\cdot\mathrm{2H}_2\mathrm{O}\\ & M_r = 654.52\\ & \mathrm{Monoclinic}, P_{2_1}/n\\ & a = 8.1645 \ (2) \ \mathrm{\AA}\\ & b = 13.4135 \ (4) \ \mathrm{\AA}\\ & c = 15.1186 \ (4) \ \mathrm{\AA}\\ & \beta = 97.994 \ (11)^\circ\\ & V = 1639.62 \ (9) \ \mathrm{\AA}^3 \end{split}$$

Z = 2 D_x = 1.326 Mg m⁻³ Mo Kα radiation μ = 0.61 mm⁻¹ T = 294 (2) K Block, colorless 0.32 × 0.25 × 0.24 mm

Data collection

Bruker SMART APEX CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 2005) $T_{min} = 0.768, T_{max} = 0.864$

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_0^2) + (0.044P)^2]$ $R[F^2 > 2\sigma(F^2)] = 0.030$ wR(F²) = 0.087 + 0.3715P] where $P = (F_0^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} = 0.001$ S = 1.06 $\Delta \rho_{\rm max} = 0.24 \ {\rm e} \ {\rm \AA}^{-3}$ 4028 reflections $\Delta \rho_{\rm min} = -0.23 \text{ e } \text{\AA}^{-3}$ 199 parameters H atoms treated by a mixture of Extinction correction: SHELXL97 independent and constrained Extinction coefficient: 0.0058 (11) refinement

Table 1

Selected bond lengths (Å).

Mn1-N2	2.2755 (11)	Mn1-N6	2.2585 (11)
Mn1-N4	2.3197 (11)		

11514 measured reflections

 $R_{\rm int}=0.014$

 $\theta_{\rm max} = 28.3^{\circ}$

4028 independent reflections

3529 reflections with $I > 2\sigma(I)$

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
O1−H13···Cl1	0.78 (3)	2.42 (3)	3.1972 (18)	172 (3)
$O1-H14\cdots Cl1^{i}$	0.80 (3)	2.42 (3)	3.2059 (19)	167 (3)
$C4-H4C\cdots O1$	0.96	2.42	3.342 (3)	161
C5−H5···Cl1 ⁱⁱ	0.93	2.83	3.6714 (15)	150
C9−H9···Cl1	0.93	2.71	3.4920 (14)	142
$C10-H10\cdots Cl1^{iii}$	0.93	2.76	3.6318 (16)	156
Symmetry codes: $-x + \frac{1}{2}, y - \frac{1}{2}, -z + \frac{3}{2}.$	(i) $-x, -x$	y+1, -z+2;	(ii) $-x, -y, -y$	-z + 2; (iii)

The methyl H atoms were constrained to an ideal geometry, with C-H = 0.96 Å and $U_{iso}(H) = 1.5U_{eq}(C)$; each methyl group was allowed to rotate freely about its N-C bond. The water H atoms were located in a difference Fourier map and refined isotropically. Other H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: *SMART* (Bruker, 2005); cell refinement: *SAINT* (Bruker, 2005); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *SHELXTL* (Bruker, 2000).

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