

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\max} < 0.001$
$R(F) = 0.057$	$\Delta\rho_{\max} = 0.81 \text{ e } \text{\AA}^{-3}$
$wR(F^2) = 0.123$	$\Delta\rho_{\min} = -0.62 \text{ e } \text{\AA}^{-3}$
$S = 1.454$	Extinction correction: none
3848 reflections	Scattering factors from
241 parameters	<i>International Tables for</i>
H atoms constrained	<i>Crystallography</i> (Vol. C)
$w = 1/[\sigma^2(F_o^2) + (0.0076P)^2 + 21.4166P]$	
where $P = (F_o^2 + 2F_c^2)/3$	

Table 1. Selected geometric parameters (\AA , $^\circ$)

Rh1—O1	2.051 (4)	O1—C16	1.325 (6)
Rh1—N1	1.900 (4)	N2—C6	1.288 (7)
Rh1—N2	2.089 (4)	N3—C10	1.291 (8)
Rh1—N3	2.102 (5)		
O1—Rh1—N1	178.02 (16)	N2—Rh1—N3	157.99 (19)
O1—Rh1—N2	100.41 (17)	Rh1—O1—C16	127.6 (3)
O1—Rh1—N3	101.52 (17)	C6—N2—C7	119.2 (4)
N1—Rh1—N2	78.87 (19)	C10—N3—C12	118.4 (5)
N1—Rh1—N3	79.15 (18)		

The structure contains a solvent-accessible void, located on a 4_2 axis, with its centre at $(\frac{1}{4}, \frac{3}{4}, -0.024)$. Integration of the electron density in this area resulted in a total of zero electrons.

Data collection: *COLLECT* (Nonius, 1998). Cell refinement: *DirAx* (Duisenberg, 1992). Data reduction: *EVAL14* (Duisenberg, 1998). Program(s) used to solve structure: *SHELXS86* (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997). Molecular graphics: *PLATON* (Spek, 1990). Software used to prepare material for publication: *PLATON*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: BM1325). Services for accessing these data are described at the back of the journal.

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A hydrated diclofenac salt of the hexaaquamagnesium ion

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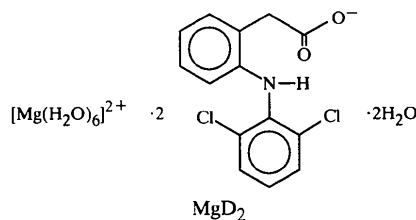
(Received 21 December 1998; accepted 15 March 1999)

Abstract

In the title compound, hexaaquamagnesium bis{[2-(2,6-dichloroanilino)phenyl]acetate} dihydrate, $[\text{Mg}(\text{H}_2\text{O})_6] \cdot (\text{C}_{14}\text{H}_{10}\text{Cl}_2\text{NO}_2)_2 \cdot 2\text{H}_2\text{O}$, the two centrosymmetric hexaaquamagnesium ions, the two [2-(2,6-dichloroanilino)phenyl]acetate anions and the two water molecules are tied into an elaborate network of hydrogen bonds.

Comment

In previous work, we investigated the structures of several diclofenac salts (Castellari & Sabatino, 1994, 1996; Castellari & Ottani, 1995, 1996, 1997). We report here the crystal structure of the dihydrated 1:2 salt of $[\text{Mg}(\text{OH}_2)_6]^{2+}$ with [2-(2,6-dichloroanilino)phenyl]acetate, hereinafter abbreviated as MgD_2 .



Diclofenac sodium salt (NaD) is an effective drug used in rheumatology and magnesium is an essential cofactor in biology. The asymmetric unit of the MgD_2 salt consists of two anions in general positions, two cations located at the inversion centers $\frac{1}{2}, 0, 0$ and $0, \frac{1}{2}, 0$, and two crystallization water molecules. Each cation is coordinated by six water molecules. The hexahydrated magnesium complex, the carboxylate ions and the water molecules are linked by a network of hydrogen bonds in which, as expected, $[\text{Mg}(\text{OH}_2)_6]^{2+}$ cations act as proton donors, carboxylate O atoms as proton acceptors and the two water molecules both

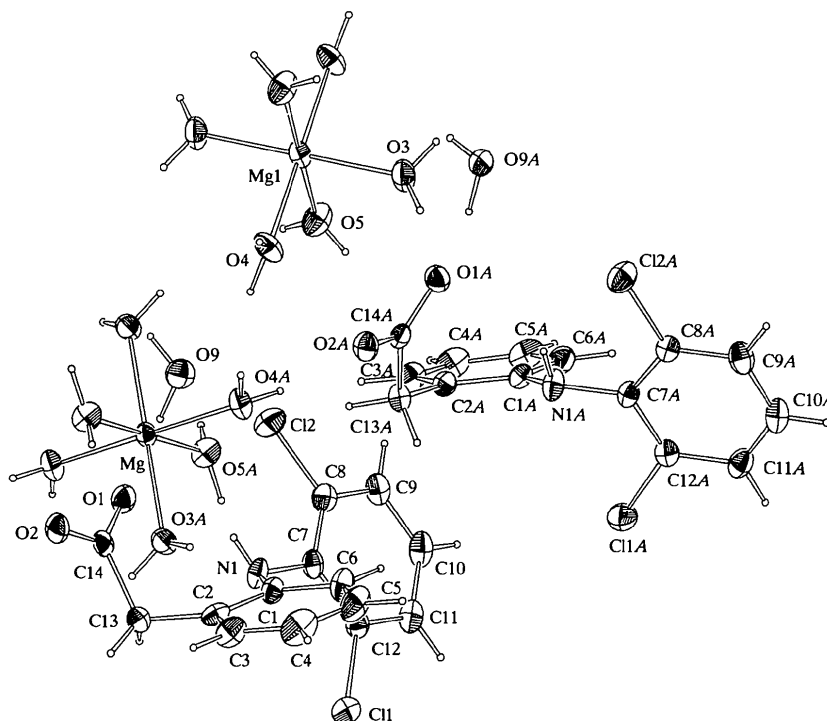


Fig. 1. ORTEP diagram (Johnson, 1976) of MgD_2 . Non-H atoms are represented by displacement ellipsoids of 50% probability and H atoms are of arbitrary size.

as proton donors and acceptors (Table 2). The $\text{O}\cdots\text{O}$ packing contacts around the two hexaaquamagnesium complexes range from 2.673 (4) to 2.902 (4) Å. The crystal engineering leads to an almost complete system of hydrogen bonds; however, the two groups Mg1—O5—H16 and Mg—O5A—H16A point towards the O3 and O3A atoms [$\text{O}\cdots\text{O}$ distances of 2.940 (4) and 2.906 (4) Å, respectively], but with unfavorable $\text{O—H}\cdots\text{O}$ angles [82 (4) and 82 (3)°, respectively]. As a consequence of this rather uniform force field, the two independent MgO_6 moieties exhibit only slight deviations (Table 1) from an idealized O_h symmetry, even though only the inversion center is retained in the crystal. Moreover, both the octahedrons appear more regular than in the analogous structure determined by Julian *et al.* (1973).

The molecular conformation of D^- is of special interest since it is related to the competitive binding of the drug to the arachidonic acid substrate which is responsible of the anti-inflammatory power of diclofenac. In MgD_2 , such structural details of D^- are normal. In fact, both the C—O distances (Table 1) and the dihedral angles between the planes of the two aromatic rings [70.6 (1) and 64.3 (1)° for the two independent D^- anions] fall in the range found by us in other diclofenac salts (Castellari & Sabatino, 1994, 1996; Castellari & Ottani, 1995, 1996, 1997), *i.e.* the C—O bond lengths are in the range 1.237 (3)–1.263 (3) Å and the dihedral angles are in the range 59.3 (1)–73.6 (1)°.

Experimental

Crystalline MgD_2 was prepared from an aqueous solution containing nearly 2 equivalents of NaD and one of MgCl_2 . The precipitate which formed was dried and recrystallized from an ethyl acetate solution.

Crystal data

$[\text{Mg}(\text{H}_2\text{O})_6](\text{C}_{14}\text{H}_{10}\text{Cl}_2\text{-NO}_2)_2 \cdot 2\text{H}_2\text{O}$

$M_r = 758.70$

Monoclinic

$P2_1/c$

$a = 11.670 (3) \text{ \AA}$

$b = 8.538 (2) \text{ \AA}$

$c = 34.208 (10) \text{ \AA}$

$\beta = 92.58 (2)^\circ$

$V = 3405.0 (15) \text{ \AA}^3$

$Z = 4$

$D_x = 1.480 \text{ Mg m}^{-3}$

D_m not measured

Mo $K\alpha$ radiation

$\lambda = 0.71069 \text{ \AA}$

Cell parameters from 25 reflections

$\theta = 6\text{--}14^\circ$

$\mu = 0.429 \text{ mm}^{-1}$

$T = 293 (2) \text{ K}$

Block

$0.20 \times 0.15 \times 0.13 \text{ mm}$

Colorless

Data collection

Enraf–Nonius CAD-4 diffractometer

Profile data from ω scans

Absorption correction: none

8316 measured reflections

8191 independent reflections

3063 reflections with

$I > 2\sigma(I)$

$R_{\text{int}} = 0.091$

$\theta_{\text{max}} = 27.99^\circ$

$h = -15 \rightarrow 15$

$k = 0 \rightarrow 11$

$l = 0 \rightarrow 45$

3 standard reflections

frequency: 160 min

intensity decay: none

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.047$ $wR(F^2) = 0.158$ $S = 0.931$

8182 reflections

489 parameters

H atoms treated by a

mixture of independent
and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0722P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\max} = 0.004$ $\Delta\rho_{\max} = 0.353 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{\min} = -0.355 \text{ e } \text{\AA}^{-3}$

Extinction correction: none

Scattering factors from

*International Tables for
Crystallography* (Vol. C)Table 1. Selected geometric parameters (\AA , $^\circ$)

Mg1—O4	2.048 (3)	Mg—O4A	2.064 (3)
Mg1—O3	2.050 (3)	C14A—O1A	1.257 (4)
Mg1—O5	2.076 (3)	C14A—O2A	1.262 (4)
Mg—O3A	2.048 (3)	C14—O1	1.255 (4)
Mg—O5A	2.056 (3)	C14—O2	1.260 (4)
O4—Mg1—O3	87.23 (12)	O5A—Mg—O4A	89.34 (12)
O4—Mg1—O5	89.59 (13)	C7A—N1A—C1A	123.3 (3)
O3—Mg1—O5	90.91 (13)	O1A—C14A—O2A	123.5 (4)
O3A—Mg—O5A	90.14 (12)	C7—N1—C1	122.4 (3)
O3A—Mg—O4A	88.91 (12)	O1—C14—O2	124.3 (4)
C1A—N1A—C7A—C12A	−59.1 (6)		
C1—N1—C7—C12	65.2 (5)		

Table 2. Hydrogen-bonding geometry (\AA , $^\circ$)

D—H...A	H...A	D...A	D—H...A
N1—H1...Cl2	2.54 (4)	2.990 (4)	119 (4)
N1—H1...O1	2.24 (4)	2.898 (4)	143 (5)
N1A—H1A...Cl2A	2.40 (4)	2.969 (4)	130 (4)
N1A—H1A...O1A	2.36 (4)	2.940 (4)	131 (4)
O3—H11...O1A	2.11 (5)	2.902 (4)	160 (5)
O3A—H11A...O1 ⁱ	1.99 (5)	2.831 (4)	157 (5)
O3—H12...O2 ⁱⁱ	1.87 (4)	2.730 (4)	173 (5)
O3A—H12A...O9A ⁱⁱⁱ	1.95 (5)	2.769 (4)	159 (5)
O4—H13...O9A ^{iv}	1.89 (5)	2.713 (4)	167 (5)
O4A—H13A...O2 ^v	1.92 (4)	2.852 (4)	166 (4)
O4—H14...O9	1.99 (4)	2.879 (4)	159 (4)
O4A—H14A...O2A	1.96 (4)	2.793 (4)	171 (5)
O5—H15...O2A ^{vi}	1.87 (5)	2.758 (4)	167 (4)
O5A—H15A...O9	1.94 (5)	2.734 (4)	169 (5)
O9—H23...O1	1.78 (4)	2.834 (4)	172 (4)
O9A—H23A...O1A	1.64 (4)	2.673 (4)	170 (4)
O9—H24...O2 ^{vii}	1.90 (4)	2.776 (4)	170 (4)
O9A—H24A...O2A ^{iv}	2.08 (4)	2.804 (4)	163 (5)

Symmetry codes: (i) $x, 1 + y, z$; (ii) $1 + x, y, z$; (iii) $x - 1, y, z$; (iv) $1 - x, 1 - y, -z$; (v) $-x, 1 - y, -z$; (vi) $x, y - 1, z$; (vii) $-x, -y, -z$.

The N—H and water H atoms were located from a difference synthesis and were refined isotropically. The remaining H atoms were placed in calculated positions and refined riding on their parent atoms.

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989). Cell refinement: *CAD-4 Software*. Data reduction: *MolEN* (Fair, 1990). Program(s) used to solve structure: *SHELXS86* (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997). Molecular graphics: *ORTEPII* (Johnson, 1976).

We thank Servizio Italiano di Diffusione Dati Cristallografici del CNR (Parma) for access to the Cambridge Structural Database (Allen & Kennard, 1993).

Supplementary data for this paper are available from the IUCr electronic archives (Reference: NA1405). Services for accessing these data are described at the back of the journal.

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trans-Bis(acetato-*O*)bis(2-amino-6-methylpyridine-*N*)copper(II)

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Abstract

In the title compound, [Cu(C₂H₃O₂)₂(C₆H₈N₂)₂], the Cu atom is surrounded by two O atoms from the two monodentate acetate ligands and by two pyridine N atoms from the two 2-amino-6-methylpyridine ligands in a *trans* square-planar arrangement. The Cu—O and Cu—N distances are 1.952 (2) and 2.046 (2) Å, respectively. The complex has an inversion centre. The remaining carboxylate O atoms are located at 2.764 (3) Å from the Cu atom, above and below this plane. The coordination around the Cu atom can therefore be described as (4+2). The pyridine ring is twisted 73.2 (1)° with respect to the plane formed by the Cu, the N and the more strongly bonded O atoms.

Comment

As part of a continuing study of copper(II) carboxylates, we report here the structure of *trans*-bis(acetato-*O*)bis(2-amino-6-methylpyridine-*N*)copper(II), [Cu(C₂H₃O₂)₂(C₆H₈N₂)₂], (I), which is the first copper complex with 2-amino-6-methylpyridine as a ligand [survey of