metal-organic papers

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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.007 \text{ Å}$ R factor = 0.041 wR factor = 0.096 Data-to-parameter ratio = 14.9

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

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Hexaaquacadmium(II) bis{[N-(2-oxidobenzylidene)alanylglycinato]cuprate(II)} dodecahydrate

In the title compound, $[Cd(H_2O)_6][Cu(C_{12}H_{11}N_2O_4)]_2 \cdot 12H_2O$, the Cd²⁺ ion lies on an inversion center and the coordination by six aqua ligands is slightly distorted octahedral. The Cu^{II} atom has a square-planar coordination with two N and two O atoms of the tetradentate Schiff base ligand L^{3-} , which was derived from alanylglycine and salicylaldehyde. The $[Cd(H_2O)_6]^{2+}$ cations and $[CuL]^-$ anions each form columns along the *c* axis; these are well segregated from each other.

Comment

We are making a systematic investigation of metal complexes of Schiff bases derived from simple peptides, to which little attention has been given, and have recently reported a series of Cu^{II} complexes of Schiff base ligands resulting from the condensation of glycylglycine with salicylaldehyde (Zou *et al.*, 2003, 2004; Liu *et al.*, 2004). In these complexes, hydrogen bonds and π - π stacking interactions generally exist. Here we report the synthesis and the structure of the title compound, (I).



The asymmetric unit of (I) consists of one [CuL]⁻ anion (H₃L is a Schiff base derived from alanylglycine and salicylaldehvde), one half-cation (Cd/O1W/O2W/O3W), five uncoordinated water molecules (O4W, O6W, O8W, O9W and O10W) in general positions and half each of two uncoordinated water molecules on twofold axes (O5W and O7W). [CuL]⁻ shows approximately square-planar coordination. The deprotonated Schiff base is a triple negatively charged tetradentate ligand, coordinating to the Cu^{II} ion via one phenolate O atom (O1), one imine N atom (N1), one deprotonated amide N atom (N2), and one carboxylate O atom (O3). The benzene ring (C1-C6) and the O1/C1/C6/C7/N1/Cu chelate ring are almost coplanar, with a dihedral angle of $1.0 (1)^{\circ}$. The Cd^{II} atom lies on an inversion center and the coordination by six aqua ligands is slightly distorted octahedral (Table 1). The anions and cations each form columns along the c axis; these are well segregated from each other. O-H···O hydrogen bonds (Table 2) play an important role in the stabilization of the crystal structure.

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Figure 1

The structure of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level. Unlabeled atoms are related to labeled atoms by the symmetry code (1 - x, 1 - y, 1 - z).

Experimental

Alanylglycine (5 mmol), salicylaldehyde (5 mmol) and LiOH (10 mmol) were dissolved and refluxed in MeOH/H₂O (30 ml, 1:1 ν/ν); CuCl₂·2H₂O (5 mmol) was then added to the solution and the resulting solution was adjusted to pH 9–11. Finally, CdCl₂·6H₂O (5 mmol) was added. The precipitate was recrystallized from water. Violet crystals of (I) suitable for X-ray diffraction were obtained after one week (yield 42% based on CuCl₂·2H₂O).

Crystal data

$[Cd(H_2O)_6][Cu(C_{12}H_{11}N_2O_4)]_2$.	$V = 4378.2 (13) \text{ Å}^3$
12H ₂ O	Z = 4
$M_r = 1058.22$	$D_x = 1.605 \text{ Mg m}^{-3}$
Monoclinic, C2/c	Mo $K\alpha$ radiation
a = 28.635 (5) Å	$\mu = 1.53 \text{ mm}^{-1}$
b = 11.815 (2) Å	T = 298 (2) K
c = 14.584 (3) Å	Block, violet
$\beta = 117.458 \ (3)^{\circ}$	$0.30 \times 0.20 \times 0.15 \text{ mm}$

Data collection

Bruker SMART APEX CCD diffractometer φ and ω scans Absorption correction: multi-scan (*SHELXTL*; Bruker, 2000) $T_{\rm min} = 0.70, T_{\rm max} = 0.79$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.041$ $wR(F^2) = 0.096$ S = 1.023893 reflections 261 parameters 10785 measured reflections 3893 independent reflections 2766 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.065$ $\theta_{\text{max}} = 25.1^{\circ}$

H-atom parameters constrained $w = 1/[\sigma^2(F_o^2) + (0.0328P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.79$ e Å⁻³ $\Delta\rho_{min} = -0.56$ e Å⁻³

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Selected geometric parameters (Å, °).

Cu-O1	1.872 (3)	Cd-O1W	2.240 (3)
Cu-N2	1.874 (3)	Cd-O3W	2.270 (3)
Cu-N1	1.926 (3)	Cd-O2W	2.300 (3)
Cu-O3	1.987 (3)		
O1-Cu-N2	179.37 (16)	N1-Cu-O3	166.70 (13)
O1-Cu-N1	95.91 (14)	O1W-Cd-O3W	89.52 (11)
N2-Cu-N1	83.93 (15)	O1W-Cd-O2W	90.25 (12)
O1-Cu-O3	97.30 (12)	O3W-Cd-O2W	84.19 (11)
N2-Cu-O3	82.85 (13)		

Table 2Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O1W-H1A\cdots O3$	0.85	2.19	2.703 (4)	118
$O1W - H1B \cdots O4W$	0.85	1.98	2.692 (5)	140
$O2W - H2A \cdots O5W$	0.85	2.20	2.746 (4)	122
$O2W - H2B \cdots O8W$	0.85	2.32	2.740 (4)	111
$O3W - H3A \cdots O6W^{i}$	0.85	2.10	2.774 (4)	136
$O3W - H3B \cdot \cdot \cdot O4^{i}$	0.85	1.96	2.723 (4)	149
$O4W - H4A \cdots O7W^{i}$	0.85	2.33	2.836 (6)	119
$O4W - H4B \cdot \cdot \cdot O2W^{ii}$	0.85	2.28	3.124 (5)	175
$O5W - H5A \cdots O9W^{i}$	0.85	2.45	2.826 (4)	108
$O6W - H6A \cdots O10W^{iii}$	0.85	2.25	2.750 (5)	118
$O6W - H6B \cdots O8W$	0.85	1.91	2.749 (5)	168
$O7W - H7A \cdots O10W^{iii}$	0.85	2.10	2.813 (5)	142
$O8W - H8A \cdots O2^{iv}$	0.85	1.86	2.689 (5)	163
$O8W - H8B \cdot \cdot \cdot O1^{i}$	0.85	2.02	2.771 (4)	147
$O9W - H9D \cdots O2^{v}$	0.85	2.21	2.643 (4)	111
$O9W - H9E \cdots O4^{i}$	0.85	2.11	2.812 (5)	139
$O10W - H10A \cdot \cdot \cdot O6W^{i}$	0.85	2.00	2.803 (5)	157
O10W−H10B···O9W	0.85	1.92	2.711 (4)	155

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

The water H atoms were located in difference Fourier maps, while other H atoms were positioned geometrically; they were constrained as riding atoms, with O-H = 0.85 Å, C-H = 0.93-0.97 Å, and $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(C,O)$ for the methyl group and water molecules.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT-Plus* (Bruker, 2003); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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