metal-organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

Bin Xu, Yan-Yan Zhang, Wen-Long Liu* and Xiao-Ya Hu

College of Chemistry and Chemical Engineering, Yangzhou Universitry, Yangzhou, 225002, People's Republic of China

Correspondence e-mail: wlliu@yzu.edu.cn

Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.006 \text{ Å}$ R factor = 0.045 wR factor = 0.103 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.

© 2006 International Union of Crystallography

All rights reserved

Hexaaquanickel(II) bis{[N-(2-hydroxybenzylidene)alanylglycinato]cuprate(II)} dodecahydrate

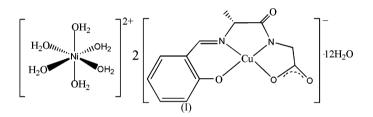
Received 16 May 2006

Accepted 3 June 2006

The crystal structure of the title compound, $[Ni(H_2O)_6]$ - $[Cu(C_{12}H_{11}N_2O_4)]_2 \cdot 12H_2O$, consists of Cu^{II} complex anions, Ni^{II} complex cations and solvent water molecules. The Cu^{II} ion is located on a general position and coordinated by a Schiff base ligand with a square-planar CuN₂O₂ geometry. The Ni^{II} ion is located on an inversion center and coordinated by six water molecules in an octahedral geometry.

Comment

As part of our ongoing investigation on metal complexes with Schiff bases, we present here the structure of the title compound, (I).



The crystal structure of (I) consists of Cu^{II} complex anions, Ni^{II} complex cations and solvent water molecules (Fig. 1). The Cu^{II} ion is located on a general position and coordinated by a trivalent Schiff base anion, *N*-(hydroxybenzylidene)alanyl-glycinate, with a square-planar CuN_2O_2 geometry (Table 1). The Ni^{II} ion is located on an inversion center and coordinated by six water molecules in an octahedral geometry.

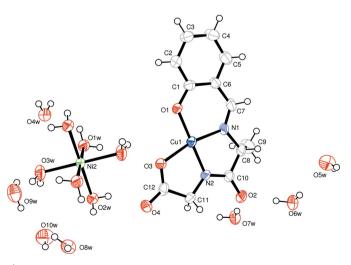


Figure 1

The asymmetric unit of (I), together with additional aqua ligands to complete the coordination of Ni2, with 50% probability displacement ellipsoids (arbitrary spheres for H atoms). Unlabeled atoms are related to labeled atoms by x + 1, -y + 1, -z + 1.

The extensive hydrogen-bonding network (Table 2) helps to stabilize the crystal structure.

Experimental

A methanol/water solution (30 ml, v/v 1:1) containing alanylglycine (5 mmol), salicylaldehyde (5 mmol) and LiOH (10 mmol) was refluxed for 30 min. CuCl₂·2H₂O (5 mmol) in water (15 ml) was added and the resulting solution was adjusted to pH 10 with NaOH solution. After stirring at room temperature for 4 h, Ni(ClO₄)₂.6H₂O (5 mmol) in water (5 ml) was added to the solution with stirring. A violet precipitate appeared immediately. After stirring for 30 min, the precipitate was filtered off and recrystallized from water. Single crystals of (I) were obtained after one week.

Crystal data

 $[Ni(H_2O)_6][Cu(C_{12}H_{11}N_2O_4)]_2$ --V = 4279 (3) Å³ $12H_2O$ Z = 4 $M_r = 1004.53$ $D_r = 1.559 \text{ Mg m}^{-3}$ Monoclinic, C2/c Mo Ka radiation a = 28.314 (9) Å $\mu = 1.51 \text{ mm}^{-1}$ b = 11.792 (4) Å T = 298 (2) Kc = 14.407 (5) Å Block, violet $\beta = 117.17 (1)^{\circ}$ $0.30 \times 0.20 \times 0.15 \text{ mm}$

Data collection

Bruker SMART APEX CCD 10637 measured reflections diffractometer φ and φ scans Absorption correction: multi-scan (SADABS; Sheldrick, 2002) $T_{\rm min} = 0.70, \ T_{\rm max} = 0.79$

Refinement

Refinement on F^2
$$\begin{split} R[F^2 > 2\sigma(F^2)] &= 0.045 \\ wR(F^2) &= 0.103 \end{split}$$
S = 0.933879 reflections 261 parameters

3879 independent reflections 2660 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.078$ $\theta_{\rm max} = 25.2$

H-atom parameters constrained $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0438P)^{2}]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3$ $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.64 \ {\rm e} \ {\rm \AA}^{-3}$ $\Delta \rho_{\rm min} = -0.41 \text{ e} \text{ Å}^{-3}$

Table 1

Selected bond lengths (Å).

Cu1-O1	1.870 (2)	Ni2-O1W	2.063 (3)
Cu1-O3	1.989 (2)	Ni2 - O2W	2.059 (2)
Cu1-N1	1.926 (3)	Ni2-O3W	2.033 (2)
Cu1-N2	1.873 (3)		× /

Table 2

Hydrogen-bond	geometry ([A, °]).
---------------	------------	--------	----

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O1W-H1A\cdots O7W^{i}$	0.82	1.96	2.732 (4)	156
$O1W-H1B\cdots O4W$	0.83	1.97	2.781 (3)	168
$O2W-H2A\cdots O8W$	0.85	2.09	2.754 (4)	135
$O2W-H2B\cdots O4$	0.84	1.98	2.735 (4)	149
$O3W-H3A\cdots O9W$	0.92	1.85	2.733 (4)	159
O3W−H3B···O3 ⁱⁱ	0.90	1.86	2.722 (4)	159
$O4W-H4A\cdots O6W^{iii}$	0.79	2.04	2.808 (3)	167
$O5W-H5A\cdots O8W^{iv}$	0.85	1.99	2.759 (5)	150
$O5W - H5B \cdots O8W^{v}$	0.83	2.03	2.814 (5)	156
$O6W-H6A\cdots O2$	0.84	1.81	2.648 (4)	178
$O6W - H6B \cdots O5W$	0.82	2.07	2.714 (4)	135
$O7W-H7A\cdots O2$	0.85	1.85	2.697 (4)	179
$O7W - H7B \cdot \cdot \cdot O1^{vi}$	0.86	1.91	2.750 (4)	166
$O8W-H8B\cdots O7W^{vii}$	0.86	2.23	2.748 (5)	119
$O9W - H9D \cdots O1W^{viii}$	0.85	2.36	3.114 (4)	149
O9W−H9E···O10W	0.85	2.04	2.877 (5)	165
$O10W - H10A \cdots O5W^{ix}$	0.85	2.03	2.813 (5)	153

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

Water H atoms were located in a difference Fourier map and refined as riding in their as-found relative positions, $U_{iso}(H) =$ $1.5U_{eq}(O)$. Methyl H atoms were placed in calculated positions with C-H = 0.96 Å and the torsion angle was refined to fit the electron density; $U_{iso}(H) = 1.5U_{eq}(C)$. Other H atoms were placed in calculated positions with C-H = 0.93-98 Å, and refined in riding mode; $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C}).$

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.

This work was supported by the National Natural Science Foundation of China.

References

Bruker (2000). SHELXTL. Version 6.10. Bruker AXS Inc., Madison, Wisconsin, USA.

Bruker (2002). SMART. Version 5.630. Bruker AXS Inc., Madison, Wisconsin, USA.

Bruker (2003). SAINT-Plus. Version 6.45. Bruker AXS Inc., Madison, Wisconsin, USA.

Sheldrick, G. M. (2002). SADABS. Version 2.03. University of Göttingen, Germany.