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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.008 Å R factor = 0.062 wR factor = 0.164 Data-to-parameter ratio = 15.6

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

Bis(3,5-dimethyl-1,2,4-triazolato- κN^4)bis(pivalic acid- κO)copper(II) dihydrate

The molecule of the title complex, $[Cu(C_4H_6N_3)_2(C_5H_{10}O_2)_2]$ -2H₂O, is situated about a site of symmetry 2/m and shows a *trans*-N₂O₂ square-planar coordination geometry for the Cu^{II} centre. The crystal structure exhibits a two-dimensional layer arrangement mediated by intermolecular hydrogen bonds.

Comment

Molecular materials exhibiting interesting magnetic and luminescent properties have received increasing attention in recent years (Kahn *et al.*, 1992; Kahn, 1993; Haasnoot, 2000; Thompson, 2002). 1,2,4-Triazole and its derivatives are able to provide several bridging coordination modes to link metal(II) ions, an important consideration for molecular materials. Indeed, many structures of coordination complexes have been reported, showing a variety of coordination modes (Haasnoot, 2000). Rare examples of structures containing the bridging 3,5-dimethyl-1,2,4-triazole ligand include N^1,N^2 bridging (Yi *et al.*, 2004) and N^1,N^2,N^4 bridging (Drew *et al.*, 1985; Zhang *et al.*, 2004). Here, we report the title copper(II) complex, (I), with the 3,5-dimethyl-1,2,4-triazole ligand exhibiting a monodentate N^4 coordination mode.



The molecule of (I) is disposed about a site of symmetry 2/m (Fig. 1 and Table 1). The Cu^{II} atom is coordinated by two N^4 atoms from two 3,5-dimethyl-1,2,4-triazole anions in a *trans* configuration. The Cu $-N^4$ bond distances [mean 1.994 (5) Å] are in the range of those reported for *catena*-[[μ_3 -3,5-dimethyl-1,2,4-triazolato- $\kappa^3 N, N', N''$]copper(I)] [1.963 (1)–2.016 (1) Å; Zhang *et al.*, 2004]. The two remaining coordination sites in the square-planar geometry are occupied by O atoms from two pivalic acid molecules.

The crystal structure of (I) features intermolecular hydrogen bonds, as shown in Fig. 2; geometric details are given in Table 2. The hydroxyl group of (I) forms a hydrogen bond with the O atom of the solvent water molecule (O1-H1B···O3). The water molecule, in turn, links two N2 atoms, so that a two-dimensional layer structure results.

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The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level and H atoms have been omitted for clarity.



The two-dimensional layer structure of (I) [symmetry code: (i) $\frac{1}{2} - x$, $\frac{1}{2} - y$, 2 - z]. Dashed lines indicate hydrogen bonds.

Experimental

3,5-Dimethyl-1,2,4-triazole (0.068 g, 0.7 mmol) was added to an ethanol solution (10 ml) of $[Cu(Me_3CCOO)_2]_2$ (0.15 g, 0.28 mmol) with stirring. The resulting solution was stirred at 276 K for 24 h and then filtered. Uncharacterized blue compounds, which formed on slow evaporation of the mother liquor, were filtered off several times, before red crystals of (I) suitable for X-ray diffraction analysis were obtained from the mother liquor (18% yield). Analysis calculated for $C_{18}H_{36}Cu_1N_6O_6$: C 43.58, H 7.32, N 16.94%; found: C 43.83, H 7.61, N 16.74%; IR (KBr, v, cm⁻¹): 3375 (*br*), 3053 (*w*), 2966 (*m*), 2935 (*w*), 2720 (*w*), 1596 (*m*), 1553 (*vs*), 1484 (*m*), 1439 (*w*), 1418 (*s*), 1378 (*m*),

1364 (*m*), 1322 (*w*), 1225 (*m*), 1146 (*w*), 1087 (*w*), 1051 (*w*), 902 (*w*), 754 (*w*), 619 (*m*).

 $D_x = 1.222 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation

reflections

 $\mu = 0.85 \text{ mm}^{-1}$

T = 293 (2) K

Block, red

 $R_{\rm int}=0.053$

 $\theta_{\rm max} = 25.5^{\circ}$ $h = -16 \rightarrow 15$

 $\begin{array}{l} k = -15 \rightarrow 15 \\ l = -10 \rightarrow 9 \end{array}$

+ 1.95P]

 $(\Delta/\sigma)_{\rm max} < 0.001$

 $\Delta \rho_{\rm max} = 0.38 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.50 \ {\rm e} \ {\rm \AA}^{-3}$

 $\theta = 2.9 - 22.9^{\circ}$

Cell parameters from 709

 $0.33 \times 0.28 \times 0.23 \text{ mm}$

1311 independent reflections

 $w = 1/[\sigma^2(F_o^2) + (0.09P)^2]$

where $P = (F_o^2 + 2F_c^2)/3$

1141 reflections with $I > 2\sigma(I)$

Crystal data

 $\begin{bmatrix} Cu(C_4H_6N_3)_2(C_5H_{10}O_2)_2 \end{bmatrix} \cdot 2H_2O \\ M_r = 496.07 \\ Monoclinic, C2/m \\ a = 13.270 (3) Å \\ b = 12.861 (3) Å \\ c = 8.770 (2) Å \\ \beta = 115.791 (4)^{\circ} \\ V = 1347.6 (5) Å^3 \\ Z = 2 \end{bmatrix}$

Data collection

Bruker SMART APEX CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2000) $T_{\min} = 0.767, T_{\max} = 0.829$ 3525 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.062$ $wR(F^2) = 0.164$ S = 1.091311 reflections 84 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

Cu1-O2	1.974 (4)	C3-O2	1.253 (8)
Cu1-N1	1.994 (5)	C3-C4	1.480 (7)
C1-C2	1.488 (6)	C4-C5	1.501 (7)
C2-N2	1.306 (6)	C4-C6	1.503 (10)
C2-N1	1.337 (5)	N2-N2 ⁱ	1.399 (8)
C3-O1	1.251 (7)		
01-C3-O2	120.7 (5)	Cu1-N1-C2	127.6 (3)
O1-C3-C4	120.8 (6)	Cu1-O2-C3	103.3 (3)
O1-C3-C4-C6	180	C1-C2-N1-Cu1	1.1 (6)
O2-C3-C4-C6	0	O2-Cu1-N1-C2	120.2 (3)
N2-C2-N1-Cu1	179.6 (3)	O2 ⁱⁱ -Cu1-N1-C2	-59.8 (3)

Symmetry codes: (i) 1 - x, y, 2 - z; (ii) 1 - x, -y, 2 - z.

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$O1 - H1B \cdots O3$	0.85	1.86	2.637 (6)	151
$O3-H3A\cdots N2^{i}$	0.85	2.07	2.748 (5)	137

Symmetry code: (i) $\frac{1}{2} - x, \frac{1}{2} - y, 2 - z$.

Atoms H1*B* and H3*A* were found in a difference Fourier map and not refined. All other H atoms were positioned geometrically and refined in the riding-model approximation, with C-H = 0.96 Å and $U_{iso}(H) = 1.2$ (1.5 for methyl H) times U_{eq} (parent atom).

Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 2000); 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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