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## Key indicators

Single-crystal X-ray study
$T=295 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.002 \AA$
$R$ factor $=0.025$
$w R$ factor $=0.063$
Data-to-parameter ratio $=16.6$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## Structure Reports

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## (2,2'-Diamino-4, $\mathbf{4}^{\prime}$-bi-1,3-thiazole- $\kappa^{2} N, N^{\prime}$ )-bis(glycinato- $\kappa^{2} N, O$ )nickel(II) dihydrate

In the crystal structure of the title compound, $\left[\mathrm{Ni}\left(\mathrm{C}_{2} \mathrm{H}_{4} \mathrm{NO}_{2}\right)_{2}-\right.$ $\left.\left(\mathrm{C}_{6} \mathrm{H}_{6} \mathrm{~N}_{4} \mathrm{~S}_{2}\right)\right] \cdot 2 \mathrm{H}_{2} \mathrm{O}$, the $\mathrm{Ni}^{\text {II }}$ atom is located on a twofold axis and is coordinated by a diaminobithiazole ligand and two glycinate anions in a distorted octahedral geometry. The glycinate anions chelate to the $\mathrm{Ni}^{\mathrm{II}}$ atom through the amino N and carboxyl O atoms, and display an envelope conformation. Hydrogen bonding consolidates the crystal structure.

## Comment

As metal complexes containing the diaminobithiazole (DABT) ligand have shown interesting magnetic properties (Sun et al., 1997), a series of transition metal complexes incorporating DABT has been prepared in our laboratory (Liu $\& \mathrm{Xu}, 2004)$. As part of the ongoing investigation into the structures of the DABT complexes, we present here the structure of the title $\mathrm{Ni}^{\mathrm{II}}$ complex, (I).


The molecular structure of (I) is shown in Fig. 1. The complex has a distorted octahedral coordination geometry, formed by one DABT and two glycinate ligands. The Ni atom and the mid-point of the $\mathrm{C}-\mathrm{C}$ bond linking the two thiazole rings are located on a twofold axis. The $\mathrm{Ni}^{\mathrm{II}}$ complex is isomorphous with the $\mathrm{Co}^{\text {II }}$ complex (Yu et al., 2005). The $\mathrm{Ni}-$ O and $\mathrm{Ni}-\mathrm{N}$ bond distances in (I) (Table 1) are about $0.04 \AA$ shorter than the corresponding $\mathrm{Co}-\mathrm{O}$ and $\mathrm{Co}-\mathrm{N}$ bond distances found in the $\mathrm{Co}^{\mathrm{II}}$ analogue.

A hydrogen-bonding network (Table 2) consolidates the crystal structure of (I).

## Experimental

An aqueous solution ( 20 ml ) containing DABT $(0.20 \mathrm{~g}, 1 \mathrm{mmol})$ and $\mathrm{NiCl}_{2}(0.13 \mathrm{~g}, 1 \mathrm{mmol})$ was mixed with an aqueous solution $(10 \mathrm{ml})$ of glycine ( $0.15 \mathrm{~g}, 2 \mathrm{mmol})$ and $\mathrm{NaOH}(0.08 \mathrm{~g}, 2 \mathrm{mmol})$. The mixture was refluxed for 6 h . The solution was filtered after cooling to room temperature. Green single crystals of (I) were obtained from the filtrate after three days.

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## Crystal data

$\left[\mathrm{Ni}\left(\mathrm{C}_{2} \mathrm{H}_{4} \mathrm{NO}_{2}\right)_{2}\left(\mathrm{C}_{6} \mathrm{H}_{6} \mathrm{~N}_{4} \mathrm{~S}_{2}\right)\right] \cdot 2 \mathrm{H}_{2} \mathrm{O}$
$M_{r}=441.13$
Monoclinic, $C 2 / c$
$a=13.0342$ (12) $\AA$
$b=8.9631$ (11) A
$c=14.0836$ (12) $\AA$
$\beta=92.811$ (8) ${ }^{\circ}$
$V=1643.4(3) \AA^{3}$
$Z=4$

## Data collection

Rigaku R-AXIS RAPID
diffractometer
$\omega$ scans
Absorption correction: multi-scan
(ABSCOR; Higashi, 1995)
$T_{\text {min }}=0.678, T_{\text {max }}=0.795$
8498 measured reflections

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.025$
$w R\left(F^{2}\right)=0.063$
$S=1.05$
1888 reflections
114 parameters
H -atom parameters constrained

## $D_{x}=1.783 \mathrm{Mg} \mathrm{m}^{-3}$

Mo $K \alpha$ radiation
Cell parameters from 1802
reflections
$\theta=2.8-26.0^{\circ}$
$\mu=1.48 \mathrm{~mm}^{-1}$
$T=295$ (2) K
Prism, green
$0.25 \times 0.22 \times 0.15 \mathrm{~mm}$

1888 independent reflections
1749 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.024$
$\theta_{\text {max }}=27.5^{\circ}$
$h=-16 \rightarrow 16$
$k=-11 \rightarrow 11$
$l=-18 \rightarrow 18$

$$
\begin{aligned}
w= & 1 /\left[\sigma^{2}\left(F_{\mathrm{o}}^{2}\right)+(0.031 P)^{2}\right. \\
& +1.8149 P]
\end{aligned}
$$

where $P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}{ }^{2}\right) / 3$
$(\Delta / \sigma)_{\text {max }}=0.001$
$\Delta \rho_{\text {max }}=0.37 \mathrm{e}^{-3}$
$\Delta \rho_{\min }=-0.34 \mathrm{e}^{-3}$

Table 1
Selected bond lengths ( $\AA$ ).

| $\mathrm{Ni}-\mathrm{O} 1$ | $2.0958(11)$ | $\mathrm{Ni}-\mathrm{N} 3$ | $2.0918(13)$ |
| :--- | :--- | :--- | :--- |
| $\mathrm{Ni}-\mathrm{N} 1$ | $2.1177(13)$ |  |  |

Table 2
Hydrogen-bond geometry ( $\mathrm{A},{ }^{\circ}$ ).

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{O} 1 w-\mathrm{H} 1 A \cdots \mathrm{O} 1^{\text {iii }}$ | 0.91 | 2.12 | $2.947(2)$ | 150 |
| $\mathrm{O}^{2} w-\mathrm{H} 1 B \cdots \mathrm{O} 2$ | 0.89 | 2.02 | $2.884(2)$ | 164 |
| $\mathrm{~N} 2-\mathrm{H} 2 A \cdots \mathrm{O}^{2 i}$ | 0.89 | 2.09 | $2.923(2)$ | 157 |
| $\mathrm{~N} 2-\mathrm{H} 2 B \cdots \mathrm{O} 1^{\mathrm{i}}$ | 0.82 | 2.42 | $3.068(2)$ | 136 |
| $\mathrm{~N} 3-\mathrm{H} 3 A \cdots \mathrm{O} 1 w^{\text {iv }}$ | 0.90 | 2.28 | $3.098(2)$ | 151 |
| $\mathrm{~N} 3-\mathrm{H} 3 B \cdots \mathrm{O}^{\mathrm{v}}$ | 0.87 | 2.45 | $3.2814(19)$ | 160 |
| Symmetry codes: | (i) $-x+1, y,-z+\frac{1}{2} ;$ | (ii) $x-\frac{1}{2},-y+\frac{3}{2}, z-\frac{1}{2} ;$ | (iii) |  |
| $-x+1,-y+2,-z+1 ;$ (iv) $x,-y+2, z-\frac{1}{2} ;(\mathrm{v})-x+\frac{3}{2}, y-\frac{1}{2},-z+\frac{1}{2}$. |  |  |  |  |

The C -bound H atoms were placed in calculated positions with $\mathrm{C}-\mathrm{H}$ distances of $0.93 \AA$ (aromatic) or $0.97 \AA$ (methylene), and included in the final cycles of refinement in riding mode with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C})$. Other H atoms were located in a difference


Figure 1
The molecular structure of (I), with $30 \%$ probability displacement ellipsoids (arbitrary spheres for H atoms); dashed lines indicate the hydrogen bonding [symmetry code: (i) $-x+1, y,-z+\frac{1}{2}$ ].

Fourier map and refined as riding in their as-found relative positions (Table 2) with $U_{\text {iso }}(\mathrm{H})=1.5 U_{\text {eq }}($ carrier atom).

Data collection: PROCESS-AUTO (Rigaku, 1998); cell refinement: PROCESS-AUTO; data reduction: CrystalStructure (Rigaku/ MSC, 2002); program(s) used to solve structure: SIR92 (Altomare et al., 1993); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

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