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#### Key indicators

Single-crystal X-ray study T = 295 KMean  $\sigma(C-C) = 0.004 \text{ Å}$  R factor = 0.037 wR factor = 0.089 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.

# Tris(1*H*-imidazole- $\kappa N^3$ )(DL-malato- $\kappa^3 O, O', O''$ )nickel(II)

In the title complex,  $[Ni(C_4H_4O_5)(C_3H_4N_2)_3]$ , the Ni<sup>II</sup> atom is coordinated by one tridentate malate dianion and three imidazole molecules with a distorted octahedral geometry. The imidazole H atom links with both carboxyl O atoms of the neighboring complex to form a three-centered hydrogen bond, which results in a long centroid–centroid distance of 4.447 (2) Å between neighboring parallel imidazole rings.

# Comment

Recently, we have paid much attention to the nature of  $\pi$ - $\pi$  stacking in metal complexes (Pan & Xu, 2004), as  $\pi$ - $\pi$  stacking between aromatic rings plays an important role in the electron transfer process in some biological system (Deisenhofer & Michel, 1989). The crystal structures of several metal complexes incorporating the imidazole ligand show the existence of  $\pi$ - $\pi$  stacking between imidazole rings (Xu & Xu, 2004; Lin *et al.*, 2005). As part of an ongoing investigation into  $\pi$ - $\pi$  stacking, the title Ni<sup>II</sup> complex, (I), has recently been prepared and its crystal structure is presented here.



The molecular structure of (I) is illustrated in Fig. 1. The Ni<sup>II</sup> atom is coordinated by one tridentate malate dianion and three imidazole molecules with a distorted octahedral geometry (Table 1). The structure is similar to that found in the Co<sup>II</sup> analog (Jin *et al.*, 2003). While the carboxyl groups coordinate to the Ni<sup>II</sup> atom in a monodentate mode, the hydroxy group of the malate coordinates to the Ni<sup>II</sup> atom to form one five-membered and one six-membered chelate ring. The five-membered ring displays an envelope conformation, with the Ni<sup>II</sup> atom in the flap position and deviating from the mean plane formed by the other four atoms by 1.019 (3) Å. In the five-membered chelate ring, the Ni–O<sub>hydroxy</sub> bond distance is identical to the Ni–O<sub>carboxyl</sub> distance. The two carboxyl planes of the malate anion are nearly perpendicular

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#### Figure 1

The molecular structure of (I), with 30% probability displacement ellipsoids.



#### Figure 2

The packing of (I), showing the intermolecular hydrogen bonding (dashed lines) [symmetry code: (iv) 1 - x, 2 - y, 1 - z].

Extensive intermolecular hydrogen bonding occurs in the crystal structure. It is notable that imidazole atom H31 links with both O atoms of the C4-carboxyl group of the neighboring complex molecule to form a three-centered hydrogen bond (Fig. 2 and Table 2); this results in a long centroidcentroid distance of 4.447 (2) Å between the neighboring parallel imidazole rings, suggesting no  $\pi$ - $\pi$  stacking between imidazole rings in the crystal structure of (I).

### **Experimental**

An ethanol solution (5 ml) of imidazole (2 mmol) was mixed with an aqueous solution (5 ml) of NiCl<sub>2</sub>·6H<sub>2</sub>O (1 mmol) and an aqueous solution (5 ml) containing DL-malic acid (1 mmol) and Na<sub>2</sub>CO<sub>3</sub> (1 mmol). The solution was refluxed for 1 h and filtered. Blue single crystals of (I) were obtained after 20 d.

#### Crystal data

[Ni(C <sub>4</sub> H <sub>4</sub> O <sub>5</sub> )(C <sub>3</sub> H <sub>4</sub> N <sub>2</sub> ) <sub>3</sub> ] $M_r = 395.03$ Monoclinic, $P2_1/c$ a = 8.4419 (4) Å b = 8.5266 (2) Å c = 22.3912 (4) Å $\beta = 90.5840$ (11)°	$D_x = 1.628 \text{ Mg m}^{-3}$ Mo K $\alpha$ radiation Cell parameters from 7674 reflections $\theta = 2.5-25.0^{\circ}$ $\mu = 1.24 \text{ mm}^{-1}$ T = 295 (2) K
$\begin{aligned} & \beta = 90.5840 \ (11)^{\circ} \\ & V = 1611.65 \ (9) \ \text{\AA}^3 \\ & Z = 4 \end{aligned}$	$\mu = 1.24 \text{ mm}$ T = 295 (2)  K Prism, blue $0.32 \times 0.25 \times 0.18 \text{ mm}$

### Data collection

Rigaku R-AXIS RAPID	3525 independent reflections
diffractometer	3115 reflections with $I > 2\sigma(I)$
$\omega$ scans	$R_{\rm int} = 0.025$
Absorption correction: multi-scan	$\theta_{\rm max} = 27.5^{\circ}$
(ABSCOR; Higashi, 1995)	$h = -10 \rightarrow 9$
$T_{\min} = 0.692, \ T_{\max} = 0.805$	$k = -11 \rightarrow 10$
12885 measured reflections	$l = -29 \rightarrow 25$
Defin an ant	

## Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0424P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.037$	+ 1.2519 <i>P</i> ]
$vR(F^2) = 0.089$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.06	$(\Delta/\sigma)_{\rm max} = 0.001$
3525 reflections	$\Delta \rho_{\rm max} = 0.53 \text{ e } \text{\AA}^{-3}$
26 parameters	$\Delta \rho_{\rm min} = -0.31 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

#### Table 1

Selected interatomic distances (Å).

Ni-O1	2.0766 (16)	Ni-N13	2.0766 (19)
Ni-O3	2.1193 (15)	Ni-N23	2.0700 (19)
Ni-O5	2.0782 (16)	Ni-N33	2.0540 (18)

# Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$05-H5\cdots 04^{i}$ $N11-H11\cdots 01^{ii}$ $N21-H21\cdots 02^{iii}$ $N31-H31\cdots 03^{iv}$ $N31-H31\cdots 04^{iv}$	0.87 0.86 0.86 0.86 0.86	1.74 1.92 1.99 2.12 2.28	2.586 (3) 2.764 (2) 2.836 (3) 2.899 (3) 3.049 (3)	163 168 165 150 149
			.,	

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

The hydroxy H atom was located in a difference Fourier map and refined as riding in its as-found position relative to atom O5, with a fixed isotropic displacement parameter of 0.05 Å<sup>2</sup>. Other H atoms were placed in calculated positions, with C—H = 0.93–0.98 Å and N—H = 0.86 Å, and included in the final cycles of refinement in a riding model, with  $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm carrier})$ .

Data collection: *PROCESS-AUTO* (Rigaku Corporation, 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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