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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(C-C) = 0.008 \text{ Å}$ Disorder in main residue R factor = 0.050 wR factor = 0.155 Data-to-parameter ratio = 17.1

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

Aquapentakis(1*H*-imidazole- κN^3)nickel(II) dibromosuccinate

The title compound, $[Ni(C_3H_4N_2)_5(H_2O)](C_4H_2Br_2O_4)$, consists of Ni^{II} complex cations and dibromosuccinate anions. The Ni atom, water O atom and one imidazole N atom of the complex cation lie on a twofold axis. The anion lies on an inversion centre. The crystal packing is reinforced by O– $H \cdots O$ and $N-H \cdots O$ hydrogen bonds, but there are no $\pi-\pi$ stacking interactions even though the complex contains five aromatic imidazole rings. The compound is isostructural with its cobalt analogue.

Comment

As π - π stacking plays an important role in some biological processes (Deisenhofer & Michel, 1989), the nature of these stacking interactions has attracted our attention. A series of metal complexes incorporating different aromatic ligands has been prepared and their structures determined to compare the effect of the size of the aromatic ring on π - π stacking. The research results show that not all complexes containing aromatic rings display π - π stacking interactions. The title Ni^{II} complex, (I), with imidazole ligands and dibromosuccinate anions, has been prepared, but its crystal structure shows no π - π stacking.



The crystal structure of (I) consists of Ni^{II} complex cations and dibromosuccinate anions (DBrS), as shown in Fig. 1. The compound is isostructural with the corresponding Co^{II} complex (Li *et al.*, 2004). The Ni^{II} atom, located on a twofold axis, is coordinated by five imidazole ligands and one water molecule in an octahedral geometry. The coordinated water O atom and the N5-containing imidazole ligand are also located on the twofold axis. Thus, the N5-imidazole is disordered, with atoms N6 and C10 occupying the same site, each with 0.5 occupancy. The N5-imidazole is linked to the carboxyl group of DBrS *via* a disordered N6–H11···O1ⁱ or C10–H11···O1ⁱ hydrogen bond [Table 2; symmetry code: (i) x, 1 + y, z].

The DBrS anion lies on an inversion centre. Each carboxyl group participates in similar hydrogen-bond linkages with the N2ⁱⁱ-imidazole, the N4ⁱⁱⁱ-imidazole and the O3 water molecule

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Figure 1

The molecular structure of (I), with 30% probability displacement ellipsoids. The atomic label of N6/C10 indicates two different atoms occupying the same site within the N5-imidazole ligand. Hydrogen bonds are shown as dashed lines. [Symmetry codes: (i) 1 - x, y, $\frac{1}{2} - z$; (iv) x, 1 + y, z; (v) 1 - x, 1 + y, $\frac{1}{2} - z$.]



Figure 2

The crystal packing of (I). Dashed lines indicate the hydrogen bonding between imidazole ligands and carboxyl groups. [Symmetry codes: (vi) $\frac{3}{2} - x$, $-\frac{1}{2} + y$, $\frac{1}{2} - z$; (vii) x, 1 + y, $-\frac{1}{2} - z$.]

[symmetry codes: (ii) $\frac{3}{2} - x$, $\frac{1}{2} + y$, $\frac{1}{2} - z$; (iii) $\frac{3}{2} - x$, $\frac{3}{2} - y$, 1 - z], as shown in Fig. 2. No $\pi - \pi$ stacking is observed in (I). The nearest distance between imidazole rings of neighbouring complex cations is 3.284 (6) Å (N4···N4ⁱⁱⁱ; Fig.3).





Experimental

An ethanol–water solution (5 ml, 1:1) of NiCl₂·6H₂O (0.24 g, 1 mmol) was mixed with an aqueous solution (4 ml) containing DBrSH₂ (0.55 g, 2 mmol) and Na₂CO₃ (0.21 g, 2 mmol). The mixture was refluxed for 4 h and filtered. After cooling to room temperature, imidazole (0.20 g, 3 mmol) was added to the filtrate and green single crystals of (I) were obtained after 4 d.

Crystal data

 $[Ni(C_3H_4N_2)_5(H_2O)](C_4H_2Br_2O_4)$ $D_x = 1.702 \text{ Mg m}^{-3}$ $M_r = 690.97$ Mo $K\alpha$ radiation Monoclinic, C2/c Cell parameters from 175 a = 15.8702 (11) Åreflections b = 12.9262 (11) Å $\theta = 2.5 - 24.5^{\circ}$ $\mu = 3.73 \text{ mm}^{-1}$ c = 13.9436 (11) Å T = 298 (2) K $\beta = 109.468 (3)^{\circ}$ V = 2696.9 (4) Å³ Prism, green Z = 4 $0.36 \times 0.24 \times 0.22$ mm

Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 1999) $T_{min} = 0.355$, $T_{max} = 0.440$ 5513 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.050$ $wR(F^2) = 0.156$ S = 1.053000 reflections 175 parameters 3000 independent reflections 2048 reflections with $I > 2\sigma(I)$ $R_{int} = 0.020$ $\theta_{max} = 27.2^{\circ}$ $h = -20 \rightarrow 20$ $k = -16 \rightarrow 16$ $l = -17 \rightarrow 17$

H-atom parameters constrained $w = 1/[\sigma^2(F_o^2) + (0.0964P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.67 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{min} = -0.66 \text{ e } \text{\AA}^{-3}$

Table 1Selected geometric parameters (Å, °).					
Ni-N3	2.147 (3)	Ni-N1	2.185 (3)		
Ni-O3	2.183 (4)	Ni-N5	2.217 (5)		
N3-Ni-N3 ⁱ	176.24 (17)	N1 ⁱ -Ni-N1	172.14 (19)		

88.12 (9)

89.13 (14)

90.61 (14)

86.07 (10)

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

N3-Ni-O3

N3-Ni-N1

N3ⁱ-Ni-N1

O3-Ni-N1

Table 2 Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
O3-H12···O2	0.92	1.85	2.743 (5)	165
$N2-H3\cdots O1^{ii}$	0.86	2.04	2.773 (9)	143
N4-H7···O2 ⁱⁱⁱ	0.86	1.95	2.771 (6)	158
$N6-H11\cdots O1^{iv}$	0.84	2.55	3.372 (8)	167
$C10{-}H11{\cdots}O1^{iv}$	0.84	2.55	3.372 (8)	167
Symmetry codes: (i $x, y + 1, z$.	i) $-x + \frac{3}{2}, y - \frac{3}{2}$	$+\frac{1}{2}, -z + \frac{1}{2};$ (ii)	ii) $-x + \frac{3}{2}, -y + \frac{3}{2}$	$\frac{3}{2}, -z+1;$ (iv)

N3-Ni-N5

O3-Ni-N5

N1ⁱ-Ni-N5

The water H atoms were located in a difference Fourier map and included in the final cycles of refinement with fixed positional and displacement parameters, with O-H = 0.92 Å and $U_{iso}(H) = 0.05 \text{ Å}^2$. Other H atoms were placed in calculated positions, with C-H =0.93 Å (aromatic) or 0.98 Å (methine), and included in the final cycles of refinement in the riding model, with $U_{iso}(H) = 1.2U_{eq}$ or $1.5U_{eq}$ of the carrier atoms.

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

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91.88 (9)

180.000(1)

93.93 (10)

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