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Hua-Li Liu,^a Kui Cheng^a* and Zhi-Bin Li^b

^aDepartment of Chemistry, Wuhan University of Science and Engineering, Wuhan 430073, People's Republic of China, and ^bDepartment of Environment and Urban Construction, Wuhan University of Science and Engineering, Wuhan 430073, People's Republic of China

Correspondence e-mail: kui_cheng@126.com

Key indicators

Single-crystal X-ray study T = 293 KMean σ (C–C) = 0.004 Å R factor = 0.040 wR factor = 0.105 Data-to-parameter ratio = 14.7

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

Diazidodipyridinenickel(II)

The title compound, $[Ni(N_3)_2(C_5H_5N)_2]$, has two half-molecules in the asymmetric unit. One complete molecule is generated by twofold symmetry, the other by inversion. In this mononuclear compound, each Ni^{II} atom is coordinated by four N atoms from two pyridine molecules and two azide anions, thereby forming a slightly distorted square planar configuration.

Comment

In recent years, there has been considerable interest in the development of rational synthetic routes to coordination polymers by self-assembly (Munakata *et al.*, 1999). The prime strategy for designing these materials is to use a suitable bridging ligand (Koner *et al.*, 2003). Much attention has been paid to the azide anion and several azide-bridged complexes have been reported (Zhu *et al.*, 1999; You, 2005). Now, a new mononuclear azide-containing nickel complex, (I), is reported. There are two half-molecules in the asymmetric unit: the complete molecules are generated by twofold symmetry (Ni1, the rotation axis passing also through the pyridine N and *para*-C atoms) and by inversion (Ni2) (Fig. 1).



Both the Ni^{II} atoms are in a square-planar geometry, being coordinated by four N atoms from two *trans* pyridine molecules and two azide ions. The Ni-N bond lengths are normal (Table 1) and the *cis* and *trans* N-Ni-N angles show little deviation from ideal values. The dihedral angle between the N1- and N2-pyridine rings in the Ni1 molecule is 40.2 (3)°. The pyridine rings in the other molecule are exactly parallel by symmetry.

In the crystal structure of (I), the molecules interact with each other *via* weak $C-H\cdots N$ interactions, forming an extended network along the *a* axis (Fig. 2 and Table 2).

Experimental

Benzoic acid (1 mmol, 122 mg) and Ni(NO₃)₂·6H₂O (1 mmol, 290 mg) were suspended in a mixed solvent of pyridine and methanol

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Figure 1

The structure of (I), showing 30% probability displacement ellipsoids (arbitrary spheres for the H atoms). [Symmetry codes: (A) 1 - x, y, $\frac{3}{2} - z$ for the upper molecule; $\frac{1}{2} - x$, $\frac{1}{2} - y$, 1 - z for the lower molecule.]

(1:1 ν/ν , 10 ml). To this solution was added an aqueous solution (2 ml) of NaN₃ (1 mmol, 65 mg). The resulting solution was stirred for 20 min and then filtered. After keeping the filtrate in air for 15 d, large blue block-shaped crystals of (I) formed at the bottom of the vessel. The crystals were isolated, washed three times with water and dried in a vacuum desiccator over CaCl₂ (yield 84.6%). Analysis found: C 39.55, H 3.25, N 37.80%; calculated for C₁₀H₁₀NiN₈: C 39.91, H 3.35, N 37.24%.

Crystal data

Data collection

Bruker SMART CCD area-detector
diffractometer6765 measured reflections
2593 independent reflections
2061 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.070$
 $\theta_{max} = 26.5^{\circ}$
 $T_{min} = 0.589, T_{max} = 0.735$

Refinement

$w = 1/[\sigma^2(F_o^2) + (0.0471P)^2]$
+ 0.0859P]
where $P = (F_0^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} < 0.001$
$\Delta \rho_{\rm max} = 0.29 \ {\rm e} \ {\rm \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.48 \text{ e} \text{ Å}^{-3}$

Table 1

Selected bond lengths (Å).

Ni1-N3	2.000 (2)	Ni2-N7	2.003 (2)
Ni1-N1	2.057 (3)	Ni2-N6	2.017 (2)
Ni1-N2	2.073 (3)		



Figure 2

The crystal packing of (I), viewed along the *a* axis, with $C-H \cdots N$ interactions shown as dashed lines.

Table 2

Hydrogen-bond geometry (Å, $^{\circ}$).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$C1 - H1 \cdots N9^i$	0.93	2.49	3.182 (5)	131
Symmetry code: (i)	$-r + \frac{1}{2} - v + \frac{1}{2}$	-7+1		

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

H atoms were positioned geometrically (C-H = 0.93 Å) and refined as riding, with $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*.

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