

Hapipah M. Ali, Siti Nadiah  
 Abdul Halim and Seik Weng Ng\*

Department of Chemistry, University of Malaya,  
 50603 Kuala Lumpur, Malaysia

Correspondence e-mail: seikweng@um.edu.my

Key indicators

Single-crystal X-ray study  
 T = 295 K  
 Mean  $\sigma(C-C)$  = 0.004 Å  
 R factor = 0.038  
 wR factor = 0.111  
 Data-to-parameter ratio = 17.7

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

Bis[5-bromo-1H-indole-3-carbaldehyde (2-nitro-  
 benzoyl)hydrazonato- $\kappa^2N,O$ ]bis(pyridine- $\kappa N$ )-  
 nickel(II) pyridine disolvate

The Ni atom in the crystal structure of the title compound,  
 $[Ni(C_5H_5N)_2(C_{16}H_{10}BrN_4O_3)_2] \cdot 2C_5H_5N$ , lies on a special  
 position of site symmetry 2 in an all-*cis* octahedral geometry.

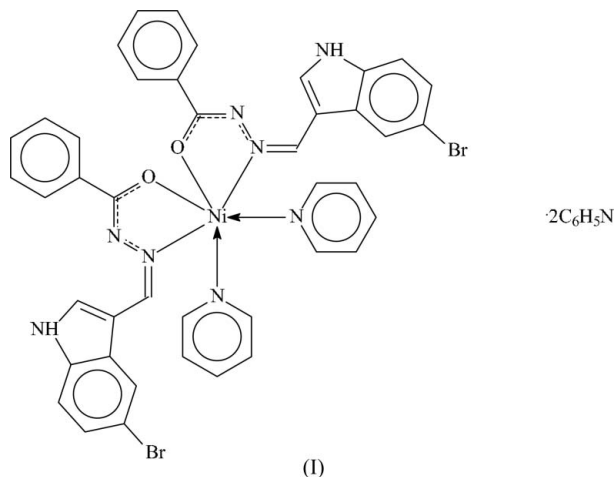
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Comment

A large number of transition metal derivatives of aromatic  
 aldehyde-aryylhydrazones have been crystallographically  
 authenticated; these have a hydroxy substituent in the  
 aromatic aldehyde portion of the ligand that is able to bind  
 covalently to the metal atom, *i.e.* these ligands function as  
 monobasic *O,N,O*-terdentate chelates. Without the hydroxy  
 substituent, the hydrazone can bind as a monobasic bidentate  
 ligand through the deprotonation of the nitrogen-bound H  
 atom. However, there does not appear to be much interest in  
 such metal complexes, as noted from the absence of such an  
 entry in the Cambridge Structural Database (Version 5.26;  
 Allen, 2002).



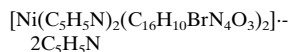
The Schiff base derived from 5-bromoindole-3-carbaldehyde and 2-nitrobenzhydrazine, whose structure is described in a previous study (Ali *et al.*, 2005), has been used to bind to nickel in the present study. Two deprotonated ligands chelate through their N and O atoms to the Ni<sup>II</sup> atom; the compound crystallizes from pyridine as a bispyridine-coordinated complex along with two other uncoordinated pyridine molecules, (I) (Fig. 1). The NH group of the deprotonated ligand interacts with the unique uncoordinated pyridine molecule through a linear hydrogen bond [2.909 (3) Å].

Experimental

5-Bromoindole-3-carbaldehyde was reacted with 2-nitrobenzhydrazide to give the Schiff base (Ali *et al.*, 2005). Aqueous

sodium hydroxide was added to an ethanol solution of the Schiff base (0.50 g, 1.30 mmol) to give a pH of 8.5. Nickel(II) acetate (0.16 g, 0.65 mmol) was added to the solution (approximately 25 ml) and the mixture was heated for 5 h. The solvent was removed to give the crude product, which was then purified by recrystallization from pyridine.

#### Crystal data



$M_r = 1147.49$

Monoclinic,  $C2/c$

$a = 19.369$  (3) Å

$b = 15.515$  (2) Å

$c = 17.246$  (3) Å

$\beta = 93.72$  (1)°

$V = 5171.7$  (14) Å<sup>3</sup>

$Z = 4$

$D_x = 1.474$  Mg m<sup>-3</sup>

Mo  $K\alpha$  radiation

Cell parameters from 16510

reflections

$\theta = 3.1$ – $27.5^\circ$

$\mu = 1.98$  mm<sup>-1</sup>

$T = 295$  (2) K

Block, red

$0.37 \times 0.25 \times 0.17$  mm

#### Data collection

Rigaku R-AXIS RAPID  
diffractometer

$\omega$  scans

Absorption correction: multi-scan  
(*ABSCOR*; Higashi, 1995)

$T_{\min} = 0.334$ ,  $T_{\max} = 0.729$

24781 measured reflections

5907 independent reflections

4302 reflections with  $I > 2\sigma(I)$

$R_{\text{int}} = 0.030$

$\theta_{\text{max}} = 27.5^\circ$

$h = -25 \rightarrow 25$

$k = -20 \rightarrow 20$

$l = -22 \rightarrow 22$

#### Refinement

Refinement on  $F^2$

$R[F^2 > 2\sigma(F^2)] = 0.038$

$wR(F^2) = 0.111$

$S = 1.05$

5907 reflections

334 parameters

H atoms treated by a mixture of  
independent and constrained  
refinement

$w = 1/[\sigma^2(F_o^2) + (0.06P)^2 + 1.7544P]$

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

$(\Delta/\sigma)_{\text{max}} = 0.001$

$\Delta\rho_{\text{max}} = 0.51$  e Å<sup>-3</sup>

$\Delta\rho_{\text{min}} = -0.54$  e Å<sup>-3</sup>

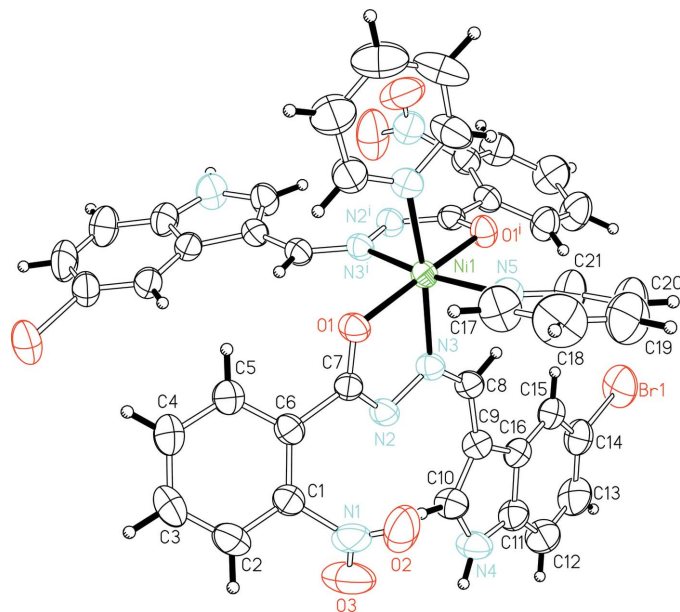
**Table 1**

Selected geometric parameters (Å, °).

Ni1—O1	2.042 (1)	Ni1—N5	2.113 (2)
Ni1—N3	2.061 (2)		
O1—Ni1—O1 <sup>i</sup>	170.7 (1)	N3—Ni1—N3 <sup>i</sup>	90.6 (1)
O1—Ni1—N3	77.9 (1)	N3—Ni1—N5	91.8 (1)
O1—Ni1—N3 <sup>i</sup>	95.4 (1)	N3—Ni1—N5 <sup>i</sup>	170.3 (1)
O1—Ni1—N5	94.3 (1)	N5—Ni1—N5 <sup>i</sup>	87.42 (6)
O1—Ni1—N5 <sup>i</sup>	92.5 (1)		

Symmetry code: (i)  $-x + 1, y, -z + \frac{3}{2}$ .

The carbon-bound H atoms were positioned geometrically ( $C-H = 0.93$  Å) and they were included in the refinement in the riding-model approximation, with  $U_{\text{iso}}(\text{H})$  values set at 1.2 times  $U_{\text{eq}}$  of the parent atoms. The amino H atom was located in a difference Fourier map, and was refined with a distance restraint of  $N-H = 0.85$  (1) Å.



**Figure 1**

ORTEP plot (Johnson, 1976) of (I). Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as spheres of arbitrary radii [symmetry code: (i)  $1 - x, y, \frac{3}{2} - z$ ]. The uncoordinated solvent molecules are not shown.

Data collection: *RAPID-AUTO* (Rigaku, 1998); cell refinement: *RAPID-AUTO*; data reduction: *CrystalStructure* (Rigaku/MS, 2002); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

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