

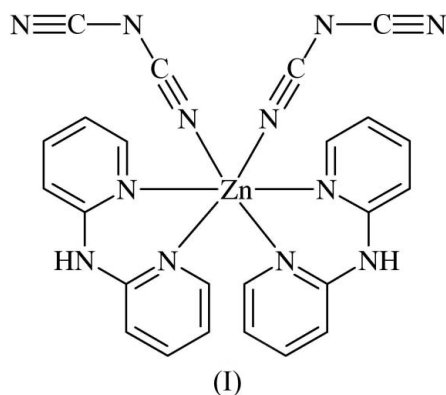
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Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$
 R factor = 0.044
 wR factor = 0.108
Data-to-parameter ratio = 16.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Bis(dicyanamido- κN)(di-2-pyridylamine- $\kappa^2\text{N},\text{N}'$)-
zinc(II)The title mononuclear Zn^{II} complex, $[\text{Zn}(\text{C}_2\text{N}_3)_2(\text{C}_{10}\text{H}_9\text{N}_3)_2]$, is isostructural with its Mn^{II} , Co^{II} and Ni^{II} analogues. The Zn^{II} atom lies on a crystallographic twofold rotation axis and is coordinated by two bidentate di-2-pyridylamine ligands and by two dicyanamide ligands in a *cis* orientation.Received 30 November 2006
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Comment

The title Zn^{II} complex, (I), is isostructural with its Mn^{II} , Co^{II} and Ni^{II} analogues (Xu *et al.*, 2003; Huang *et al.*, 2006). The Zn^{II} atom lies on a crystallographic twofold rotation axis and is coordinated in a distorted octahedral geometry by two bidentate di-2-pyridylamine (dpaH) ligands and by two dicyanamide ligands (Fig. 1 and Table 1). The dihedral angle between the pyridine rings of the dpaH ligands lying *trans* to each other [coordinated through $\text{N}3$ and $\text{N}3^i$; symmetry code: (i) $-x, y, \frac{1}{2} - z$] is $25.5(3)^\circ$. The two dicyanamide ligands adopt a *cis* orientation, and each possesses approximate local C_{2v} symmetry, the $\text{N}4-\text{C}11$ and $\text{N}5-\text{C}11$ bond distances being comparable to $\text{N}5-\text{C}12$ and $\text{N}6-\text{C}12$, and with a $\text{C}11-\text{N}5-\text{C}12$ angle of $123.9(3)^\circ$.

The complexes lie in layers parallel to (001) (Fig. 2), forming hydrogen bonds between the alkylamino NH groups of the dpaH ligand and the non-coordinated terminal N atoms of the dicyanamide ligands (Table 2).

Experimental

A methanol solution (5 ml) of sodium dicyanamide (0.32 g) and di-2-pyridylamine (0.16 g) was added to 10 ml of water. $\text{Zn}(\text{NO}_3)_2 \cdot 6\text{H}_2\text{O}$ (0.25 g) dissolved in methanol (10 ml) was layered on the top and colourless block-shaped crystals were obtained after standing at room temperature for several days.

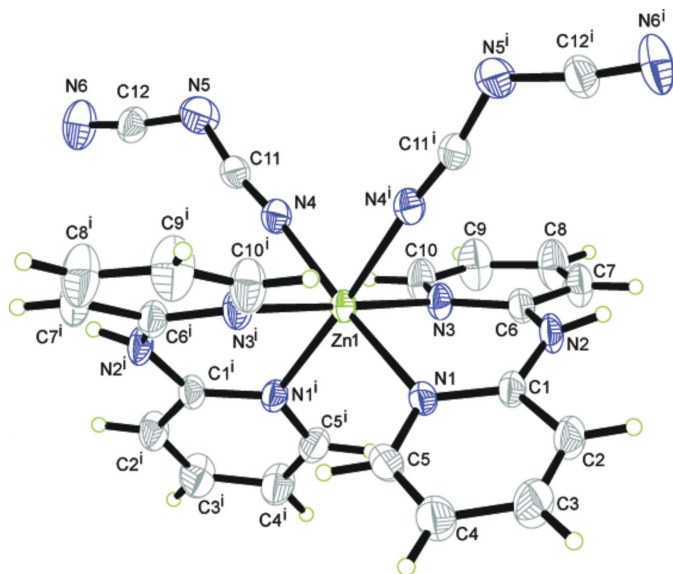


Figure 1

The molecular structure of (I), showing displacement ellipsoids at the 30% probability level for non-H atoms. [Symmetry code: (i) $-x, y, -z + \frac{1}{2}$.]

Crystal data

[Zn(C₂N₃)₂(C₁₀H₉N₃)₂]
M_r = 539.89
 Monoclinic, *C*2/*c*
a = 8.6474 (11) Å
b = 13.5964 (18) Å
c = 21.632 (3) Å
 β = 94.549 (2)°
V = 2535.3 (6) Å³

Z = 4
D_x = 1.414 Mg m⁻³
 Mo *K*α radiation
 μ = 1.01 mm⁻¹
T = 293 (2) K
 Block, colourless
 0.30 × 0.30 × 0.10 mm

Data collection

Bruker APEX2 CCD
 diffractometer
 ω scans
 Absorption correction: multi-scan
 (SADABS; Sheldrick, 2003)
T_{min} = 0.752, *T_{max}* = 0.906

7391 measured reflections
 2836 independent reflections
 1840 reflections with *I* > 2σ(*I*)
R_{int} = 0.045
 θ_{\max} = 27.3°

Refinement

Refinement on *F*²
R[*F*² > 2σ(*F*²)] = 0.044
wR(*F*²) = 0.108
S = 1.00
 2836 reflections
 168 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0478P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.31 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.26 \text{ e \AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Zn1—N1	2.141 (2)	Zn1—N3	2.178 (2)
Zn1—N4	2.157 (3)		
N1 ⁱ —Zn1—N1	95.27 (12)	N1—Zn1—N3	83.07 (9)
N1—Zn1—N4 ⁱ	87.30 (9)	N4 ⁱ —Zn1—N3	89.72 (9)
N1—Zn1—N4	173.16 (9)	N4—Zn1—N3	90.33 (9)
N4 ⁱ —Zn1—N4	90.88 (13)	N3—Zn1—N3 ⁱ	179.93 (13)
N1 ⁱ —Zn1—N3	96.89 (9)		

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

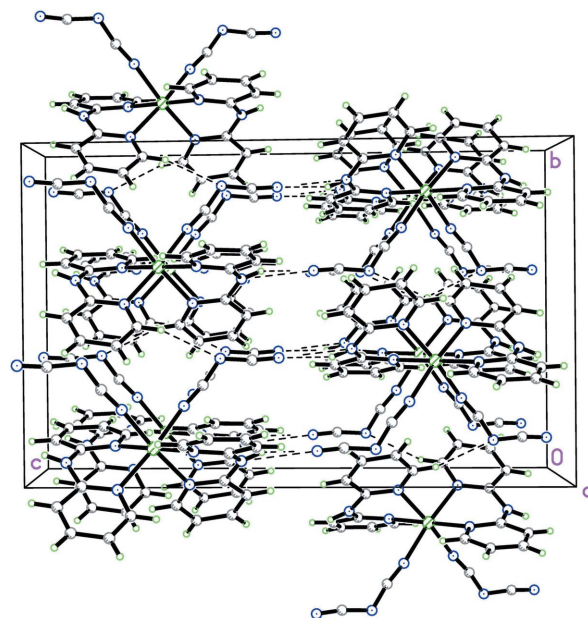


Figure 2

Packing diagram of (I). Dashed lines indicate hydrogen bonds.

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N2—H2B...N6 ⁱⁱ	0.86	2.09	2.904 (4)	157

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

H atoms were placed in calculated positions and allowed to ride during subsequent refinement, with C—H = 0.93 Å or N—H = 0.86 Å, and with *U*_{iso}(H) = 1.2*U*_{eq}(C,N).

Data collection: APEX2 (Bruker, 2005); cell refinement: SAINT (Bruker, 2005); 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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