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#### **Key indicators**

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.005 Å R factor = 0.032 wR factor = 0.058 Data-to-parameter ratio = 14.8

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

# catena-Poly[[tris(benzimidazole)cadmium(II)]μ-benzene-1,2-dicarboxylato]

In the title compound,  $[Cd(C_8H_4O_4)(C_7H_6N_2)_3]_n$ , the Cd atom is seven-coordinated by four O atoms from two benzene-1,2dicarboxylate (1,2-BDC) ligands and three N atoms from three benzimidazole ligands, resulting in a distorted pentagonal-bipyramid geometry. The 1,2-BDC ligands bridge the Cd atoms to form an extended helical chain structure. Neighbouring chains interact through  $\pi$ - $\pi$  interactions, resulting in a two-dimensional structure.

## Comment

Coordination polymers with a variety of supramolecular structures have been studied extensively because of their novel topologies and potential application as functional materials (Eddaoudi *et al.*, 2002). Benzimidazole-like ligands have been widely used as antiviral compounds, as they have exhibited bioactivity (Katz & Luong, 1999). However, coordination polymers with benzimidazole (bzim) ligands prepared by hydrothermal synthesis have rarely been documented. We selected benzene-1,2-dicarboxylic acid (1,2-H<sub>2</sub>BDC) as a linker and bzim as a secondary ligand, generating a new coordination polymer, [Cd(bzim)<sub>3</sub>(1,2-BDC)], (I).



In compound (I), the Cd atom is coordinated by three N atoms from three bzim ligands and four O atoms from two bridging 1,2-BDC ligands, in a distorted pentagonal-bipyramidal geometry (Fig. 1). Adjacent Cd atoms are connected by a bridging 1,2-BDC ligand, generating a one-dimensional helical chain structure (Fig. 2). Three bzim ligands are bonded to a Cd atom in a T-shaped coordination geometry to minimize the effect of steric hindrance.

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#### Figure 1

Part of the polymeric structure of (I). Displacement ellipsoids are drawn at the 30% probability level. [Symmetry code: (i)  $\frac{1}{2} - x$ ,  $\frac{1}{2} + y$ ,  $\frac{1}{2} - z$ .]



#### Figure 2

The one-dimensional helical chain in (I), viewed down the c axis. H atoms have been omitted for clarity. [Symmetry code: (i)  $\frac{1}{2} - x$ ,  $\frac{1}{2} + y$ ,  $\frac{1}{2} - z$ .]

There are intrachain hydrogen bonds between bzim and 1,2-BDC ligands (Table 2). The average plane-to-plane distance of 3.73 Å between the benzene ring (C9–C14) and its symmetry equivalent at (-x, 1 - y, -z), in an offset fashion, indicates  $\pi$ - $\pi$  interactions between the two neighbouring chains, which result in a two-dimensional supramolecular structure. It is clear that the  $\pi$ - $\pi$  interactions and the intrachain N–H···O hydrogen bonds stabilize the structure of (I) (Che, 2006).

## **Experimental**

Benzimidazole (0.35 g, 3 mmol), 1,2-H<sub>2</sub>BDC (0.67 g, 1 mmol) and cadmium acetate (0.27 g, 1 mmol) in water (16 ml) were stirred for 30 min and the pH value was then adjusted to 7.1. The mixture, with a

total volume of 21 ml, was heated at 413 K for 5 d in a sealed 25 ml Teflon-lined stainless steel vessel under autogenous pressure. After the reaction mixture had been slowly cooled to room temperature at a rate of  $5 \text{ K h}^{-1}$ , pale-yellow crystals of (I) were collected by filtration, washed with distilled water and dried in air (yield 51% based on Cd).

Z = 4

 $D_x = 1.534 \text{ Mg m}^{-3}$ 

Column, pale yellow

 $0.17 \times 0.08 \times 0.07 \text{ mm}$ 

14148 measured reflections

5339 independent reflections 3698 reflections with  $I > 2\sigma(I)$ 

Mo  $K\alpha$  radiation

 $\mu = 0.85 \text{ mm}^{-1}$ 

T = 293 (2) K

 $\begin{aligned} R_{\rm int} &= 0.056\\ \theta_{\rm max} &= 26.0^\circ \end{aligned}$ 

#### Crystal data

 $\begin{bmatrix} Cd(C_8H_4O_4)(C_7H_6N_2)_3 \end{bmatrix} \\ M_r = 630.93 \\ Monoclinic, P_{2_1}/n \\ a = 13.285 (3) Å \\ b = 9.3058 (18) Å \\ c = 22.913 (5) Å \\ \beta = 105.296 (4)^{\circ} \\ V = 2732.3 (10) Å^3 \end{bmatrix}$ 

#### Data collection

Bruker SMART APEXII CCD area-detector diffractometer  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)  $T_{\min} = 0.912, T_{\max} = 0.933$ 

## Refinement

Refinement on  $F^2$ H-atom parameters constrained $R[F^2 > 2\sigma(F^2)] = 0.032$  $w = 1/[\sigma^2(F_o^2) + (0.0051P)^2]$  $wR(F^2) = 0.058$ where  $P = (F_o^2 + 2F_c^2)/3$ S = 0.96 $(\Delta/\sigma)_{max} = 0.001$ 5339 reflections $\Delta\rho_{max} = 0.46 \text{ e } \text{\AA}^{-3}$ 361 parameters $\Delta\rho_{min} = -0.46 \text{ e } \text{\AA}^{-3}$ 

## Table 1

Selected geometric parameters (Å, °).

N1-Cd	2.319 (3)	O2-Cd	2.363 (2)
N3-Cd	2.321 (2)	O3–Cd <sup>i</sup>	2.414 (2)
N5-Cd	2.334 (2)	O4-Cd <sup>i</sup>	2.5500 (19)
O1-Cd	2.733 (3)		
N1-Cd-N3	177.04 (9)	N3-Cd-O4 <sup>ii</sup>	89.89 (8)
N1-Cd-N5	90.13 (9)	N5-Cd-O4 <sup>ii</sup>	142.88 (8)
N3-Cd-N5	89.16 (9)	O2-Cd-O4 <sup>ii</sup>	80.66 (7)
N1-Cd-O2	91.39 (8)	O3 <sup>ii</sup> -Cd-O4 <sup>ii</sup>	52.94 (6)
N3-Cd-O2	91.11 (8)	N1-Cd-O1	98.13 (9)
N5-Cd-O2	136.47 (8)	N3-Cd-O1	84.70 (9)
N1-Cd-O3 <sup>ii</sup>	88.68 (9)	N5-Cd-O1	86.55 (8)
N3-Cd-O3 <sup>ii</sup>	88.44 (9)	O2-Cd-O1	50.20 (6)
N5-Cd-O3 <sup>ii</sup>	89.93 (8)	O3 <sup>ii</sup> -Cd-O1	172.33 (8)
O2-Cd-O3 <sup>ii</sup>	133.59 (7)	O4 <sup>ii</sup> -Cd-O1	130.28 (6)
N1-Cd-O4 <sup>ii</sup>	88.93 (8)		

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

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

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N2 - H2A \cdots O4^{iii}$ $N4 - H4A \cdots O2^{i}$	0.86 0.86	2.13 1.99	2.849 (3) 2.756 (3)	141 148
	. 1 1 .	1 (***)		

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

All H atoms were positioned geometrically and refined as riding atoms, with C-H = 0.93 Å and N-H = 0.86 Å, and with  $U_{iso}(H) = 1.2U_{eq}(C,N)$ .

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

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