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## Key indicators

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (N–C) = 0.007 Å R factor = 0.032 wR factor = 0.090 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.

# Hexakis( $\mu_2$ -4-amino-4*H*-1,2,4-triazole)hexachlorotricadmium(II)

The molecule of the title trinuclear cadmium(II) complex,  $[Cd_3Cl_6(atrz)_6]$  (atrz = 4-amino-1,2,4-triazole,  $C_2H_4N_4$ ), has a threefold axis of symmetry with three Cd atoms located on the threefold axis. The atrz ligands bridge neighbouring Cd atoms to form the trinuclear complex.

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# Comment

A large number of metal complexes with 1,2,4-triazole derivatives have been prepared and characterized, as a result of their interesting magnetic properties and novel topologies. We present here the structure of the title trinuclear  $Cd^{II}$  complex incorporating the triazole ligand,  $[Cd_3(atrz)_6Cl_6]$  (atrz = 4-amino-1,2,4-triazole), (I).



The molecular structure of (I) is shown in Fig. 1. The trinuclear molecule has a threefold axis of symmetry with three Cd atoms located on the threefold axis. The central Cd2 atom is also located on an inversion centre and coordinated by six N atoms from six atrz ligands, while the terminal Cd1 atom is coordinated by three Cl atoms and three N atoms from three atrz ligands. Each Cd atom has a distorted octahedral coordination geometry (Table 1). The atrz ligands bridge neighbouring Cd atoms to form the trinuclear complex.

Neighbouring trinuclear complexes are linked by N-H···Cl hydrogen bonds (Fig. 2 and Table 2).

## **Experimental**

The atrz ligand was synthesized according to the literature method of Herbst & Garrison (1953). An aqueous solution (10 ml) of  $CdCl_2$  (0.2 mmol, 36.6 mg) and atrz (0.6 mmol, 50.4 mg) was stirred for 5 h at room temperature and filtered. Colourless crystals of (I) were obtained from the filtrate.

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### Figure 1

The molecular structure of (I), with 30% probability displacement ellipsoids and the atom-numbering scheme. H atoms have been omitted. [Symmetry codes: (A) -y + 1, x - y + 2, z; (B) -x + y - 1, -x + 1, z; (C) -x, -y + 2, -z.]



#### Figure 2

A unit-cell packing diagram for (I), showing the hydrogen bonding (dashed lines).

Crystal data

$[Cd_3Cl_6(C_2H_4N_4)_6]$	Mo $K\alpha$ radiation
$M_r = 1054.48$	Cell parameters from 908
Trigonal, R3	reflections
a = 13.032 (4)  Å	$\theta = 2.2-25.0^{\circ}$
c = 17.558 (7)  Å	$\mu = 2.35 \text{ mm}^{-1}$
$V = 2582.4 (15) \text{ Å}^3$	T = 293 (2) K
Z = 3	Block, colourless
$D_x = 2.034 \text{ Mg m}^{-3}$	$0.24 \times 0.20 \times 0.14 \text{ mm}$

#### Data collection

Bruker SMART CCD area-detector	1015 independent reflections
diffractometer	886 reflections with $I > 2\sigma(I)$
$\varphi$ and $\omega$ scans	$R_{int} = 0.048$
Absorption correction: multi-scan	$\theta_{max} = 25.0^{\circ}$
( <i>SADABS</i> ; Sheldrick, 1996)	$h = -15 \rightarrow 13$
$T_{min} = 0.568, T_{max} = 0.720$	$k = -8 \rightarrow 15$
4399 measured reflections	$l = -20 \rightarrow 20$
Refinement	
Refinement on $F^2$	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.032$	$w = 1/[\sigma^2(F_o^2) + (0.0302P)^2]$
$\nu R(F^2) = 0.090$	where $P = (F_o^2 + 2F_o^2)/3$

#### Table 1

S = 1.10

1015 reflections

69 parameters

Selected geometric parameters (Å, °).

Cd1-N1 <sup>i</sup>	2.469 (4)	Cd2-N2 <sup>i</sup>	2.294 (4)
Cd1-Cl1	2.6148 (14)		
N1 <sup>i</sup> -Cd1-N1 <sup>ii</sup>	84.33 (15)	N1 <sup>ii</sup> -Cd1-Cl1 <sup>i</sup>	91.40 (11)
N1 <sup>i</sup> -Cd1-N1	84.32 (15)	Cl1-Cd1-Cl1 <sup>i</sup>	97.32 (4)
N1 <sup>i</sup> -Cd1-Cl1	91.40 (11)	N2 <sup>i</sup> -Cd2-N2	90.65 (15)
N1 <sup>ii</sup> -Cd1-Cl1	86.29 (11)	N2 <sup>i</sup> -Cd2-N2	89.35 (15)
N1-Cd1-Cl1	170.03 (11)	N2-Cd2-N2	179.999 (1)
Cl1-Cd1-Cl1 <sup>ii</sup>	97.32 (4)		

 $(\Delta/\sigma)_{\rm max} < 0.001$ 

 $\Delta \rho_{\text{max}} = 0.68 \text{ e } \text{\AA}^{-3}$  $\Delta \rho_{\text{min}} = -2.08 \text{ e } \text{\AA}^{-3}$ 

Symmetry codes:	(i) $-x + y - $	1, -x + 1, z; (ii)	-y+1, x-y+2, z.
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Table 2Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
N4–H4 $A$ ···Cl1 <sup>iii</sup>	0.89	2.76	3.546 (7)	147
<b>0</b> ()	4 . 2	. 1		

Symmetry code: (iii)  $y - \frac{4}{3}, -x + y - \frac{2}{3}, -z + \frac{1}{3}$ .

H atoms on C atoms were placed in calculated positions and allowed to ride on their parent atoms, with C-H = 0.93 Å and  $U_{iso}(H) = 1.2U_{eq}(C)$ . Amino H atoms were located in a difference Fourier map and refined as riding in their as-found positions relative to the parent N atom, with N-H = 0.89 Å and  $U_{iso}(H) = 1.2U_{eq}(N)$ . The deepest hole in the electron-density map is 0.53 Å away from atom Cl1.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1998); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1998); software used to prepare material for publication: *SHELXTL*.

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