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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=295 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.006 \AA$
$R$ factor $=0.035$
$w R$ factor $=0.095$
Data-to-parameter ratio $=11.4$

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

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## catena-Poly[[[bis( $1 H$-benzimidazole- $\kappa N^{3}$ )-cobalt(II)]-di- $\mu$-azido] dihydrate]

The crystal structure of the title compound, $\left\{\left[\mathrm{Co}\left(\mathrm{N}_{3}\right)_{2}\left(\mathrm{C}_{7} \mathrm{H}_{6}-\right.\right.\right.$ $\left.\left.\left.\mathrm{N}_{2}\right)_{2}\right] \cdot 2 \mathrm{H}_{2} \mathrm{O}\right\}_{n}$, consists of a di- $\mu$-azido-bridged $\left[\mathrm{Co}\left(\mathrm{N}_{3}\right)_{2}\right]_{n}$ chain that propagates along the $c$ axis of the orthorhombic unit cell, together with uncoordinated water molecules. Adjacent $\mathrm{Co}-\mathrm{N}-\mathrm{Co}-\mathrm{N}$ rhombi are coplanar; the metal atom lies on a special position of $2 / m$ site symmetry and the azide groups on special positions of site symmetry 2 . The heterocycle lies on a mirror plane. The heterocycles are positioned above and below the rhombi so that the geometry of Co is an all-trans octahedral. The chain motif is consolidated by hydrogen bonding with the uncoordinated water molecules, which lie on mirror planes.

## Comment

The azide ( $-\mathrm{N}=\mathrm{N}=\mathrm{N}$ ) anion bridges two Co atoms through only one terminal N atom in a number of cobalt(II) azide adducts, e.g. the adducts with 1-methyl-2-(p-tolylazo)imidazole (Ray et al., 2003), 2,2'-bithiazolinyl, 2,9-dimethyl-1,10phenanthroline (Liu et al., 2003) and 2,2'-bipyrimidine (de Munno et al., 1996). The covalent $\mathrm{Co}-\mathrm{N}$ bond distance is not statistically much different from that of the dative $\mathrm{Co} \leftarrow \mathrm{N}$ bond in these examples; this feature is also noted in the adduct with benzimidazole, (I), which exists as a dihydrate (Fig. 1).


Two azide units, both functioning in a $\mu$-bridging mode, link adjacent Co atoms into a linear chain; the chain is decorated with the donor heterocycle. The chains are consolidated into a three-dimensional network motif by hydrogen bonds (Table 2).

## Experimental

Cobalt(II) nitrate hexahydrate ( $29 \mathrm{mg}, 0.1 \mathrm{mmol}$ ), benzimidazole ( $24 \mathrm{mg}, 0.2 \mathrm{mmol}$ ), sodium azide ( $13 \mathrm{mg}, 0.2 \mathrm{mmol}$ ) and water ( 10 ml ) were placed in a Teflon-lined stainless-steel Parr bomb. The bomb

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was heated at 403 K for 24 h and then allowed to cool to room temperature; pink needle-shaped crystals were isolated in about $15 \%$ yield.

## Crystal data

| $\left[\mathrm{Co}\left(\mathrm{N}_{3}\right)_{2}\left(\mathrm{C}_{7} \mathrm{H}_{6} \mathrm{~N}_{2}\right)_{2}\right] \cdot 2 \mathrm{H}_{2} \mathrm{O}$ | $Z=4$ |
| :--- | :--- |
| $M_{r}=415.30$ | $D_{x}=1.557 \mathrm{Mg} \mathrm{m}^{-3}$ |
| Orthorhombic, Ibam | Mo $K \alpha$ radiation |
| $a=17.112(2) \AA$ | $\mu=1.00 \mathrm{~mm}^{-1}$ |
| $b=15.361(2) \AA$ | $T=295(2) \mathrm{K}$ |
| $c=6.738(1) \AA$ | Needle, pink |
| $V=1771.1(4) \AA^{3}$ | $0.16 \times 0.12 \times 0.08 \mathrm{~mm}$ |
|  |  |
| Data collection |  |
| Bruker SMART area-detector | 4780 measured reflections |
| $\quad$ diffractometer | 993 independent reflections |
| $\varphi$ and $\omega$ scans | 702 reflections with $I>2 \sigma(I)$ |
| Absorption correction: multi-scan | $R_{\text {int }}=0.058$ |
| $\quad(S A D A B S ;$ Sheldrick, 1996$)$ | $\theta_{\max }=26.4^{\circ}$ |
| $\quad T_{\min }=0.856, T_{\text {max }}=0.924$ |  |

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.035$
$w R\left(F^{2}\right)=0.095$
$S=1.03$
993 reflections
87 parameters
H atoms treated by a mixture of independent and constrained refinement


Figure 1
Part of a polymeric chain of the title compound. Displacement ellipsoids are drawn at the $50 \%$ probablity level and H atoms are drawn as spheres of arbitrary radii. Uncoordinated water molecules have been omitted for clarity. Symmetry codes are as given in Table 1.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: XSEED (Barbour, 2001); software used to prepare material for publication: SHELXL97.

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