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Dibromotetrakis(4-methylimidazole)copper(II)

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Key indicators

Single-crystal X-ray study T = 293 KMean $\sigma(\text{C-C}) = 0.005 \text{ Å}$ Disorder in main residue R factor = 0.038 wR factor = 0.104 Data-to-parameter ratio = 25.8

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

In the structure of the title compound, [CuBr₂(C₄H₆N₂)₄], the copper(II) cations are coordinated by four 4-methylimidazole ligands and two bromide anions within a distorted octahedron. The Cu—Br distances are elongated due to Jahn–Teller distortion. The two crystallographically independent 4-methylimidazole ligands and the single independent Br are located in general positions, whereas the copper(II) cation is located on a centre of inversion. There are short $N-H\cdots$ Br contacts to the bromide ligands, indicating hydrogen bonding.

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Comment

The title compound, (I), is isotypic with dichlorotetrakis(4methylimidazole)copper(II) (Näther et al., 2002). In its crystal structure, the copper(II) cations are coordinated by four N atoms of the 4-methylimidazole ligands within a slightly distorted square-planar arrangement. The Cu-N distances of 2.014 (3) and 2.017 (2) A are comparable to those in dichlorotetrakis(4-methylimidazole)copper(II) (Näther et al., 2002) and to those in known 4-methylimidazole-copper(II) complexes such as tetrakis(4-methylimidazolyl)bis-(perchlorato-O)copper(II) (Su et al., 1992) and tetrakis(4methylimidazol-1-yl)bis(cyanamidonitrate)copper(II) (Kohout et al., 1999). The coordination sphere of the copper(II) cation is completed by two long contacts to two symmetryequivalent bromide anions [3.2371 (5) Å]; these contacts are strongly elongated due to Jahn-Teller distortion. The coordination polyhedron around the copper(II) cation can be described as a strongly distorted octahedron.

The asymmetric unit of the title compound contains one copper(II) cation which is located on a centre of inversion, one Br anion and two crystallographically independent 4-methylimidazole ligands, which are located in general positions.

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There are short $Br \cdot \cdot \cdot H$ distances between the bromide anions and the N-H H atoms of both ligands, of 2.45 and 2.46 Å. The $Br \cdot \cdot \cdot N$ distances of 3.309 (3) and 3.284 (3) Å, and the Br···H−N angles of 177 and 161°, indicate hydrogen bonding.

Experimental

The title compound was prepared by the reaction of 167.6 mg (2 mmol) 4-methylimidazole and 111.7 mg (0.5 mmol) copper(II) bromide in 5 ml acetonitrile. The reaction mixture was stirred over 2 d, and the solid product was filtered off and washed with dimethyl ether. The precipitate is phase pure, as proved by X-ray powder diffraction. It consists of a blue crystalline powder and a few blue single crystals which are suitable for X-ray structure determination.

Crystal data

[CuBr2(C4H6N2)4]	$D_x = 1.626 \text{ Mg m}^{-3}$	
$M_r = 551.79$	Mo $K\alpha$ radiation	
Monoclinic, $P2_1/c$	Cell parameters from 78	
a = 8.2657 (9) Å	reflections	
b = 12.053 (1) Å	$\theta = 10.0 – 17.5^{\circ}$	
c = 11.338 (1) Å	$\mu = 4.53 \text{ mm}^{-1}$	
$\beta = 94.06 (1)^{\circ}$	T = 293 (2) K	
$V = 1126.73 (18) \text{ Å}^3$	Block, blue	
Z = 2	$0.10 \times 0.10 \times 0.08 \text{ mm}$	
D : II ::		

Data collection

Enraf-Nonius CAD-4	$R_{\rm int} = 0.039$
diffractometer	$\theta_{\rm max} = 30.1^{\circ}$
ω scans	$h = 0 \rightarrow 11$
Absorption correction: numerical	$k = -16 \rightarrow 6$
(X-SHAPE; Stoe & Cie, 1998)	$l = -15 \rightarrow 15$
$T_{\min} = 0.687, T_{\max} = 0.881$	3 standard reflections
5129 measured reflections	frequency: 240 min
3300 independent reflections	intensity decay: none
2136 reflections with $I > 2\sigma(I)$	

refinement

Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0461P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.038$	+ 0.9319 <i>P</i>]
$wR(F^2) = 0.104$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.00	$(\Delta/\sigma)_{\text{max}} = 0.001$
3300 reflections	$\Delta \rho_{\text{max}} = 1.23 \text{ e Å}^{-3}$
128 parameters	$\Delta \rho_{\min} = -0.95 \text{ e Å}^{-3}$
H atoms treated by a mixture of	
independent and constrained	

Table 1 Selected geometric parameters (Å, °).

Cu1-N1	2.014 (3)	Cu1-N3	2.017 (2)
N1 ⁱ -Cu1-N1	180.0	N1-Cu1-N3	90.30 (10)
N1 ⁱ -Cu1-N3	89.70 (10)	N3-Cu1-N3 ⁱ	180.0

Symmetry code: (i) 1 - x, 1 - y, 1 - z.

The aromatic H atoms were positioned with idealized geometry and refined using a riding model. The methyl H atoms were disordered and were refined as idealized disordered methyl groups with two positions rotated from each other by 60° and occupation factors

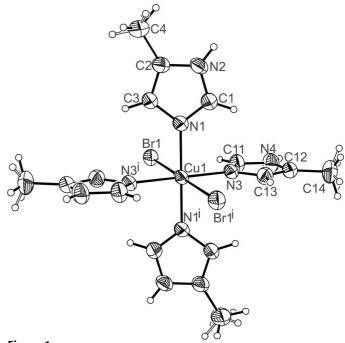


Figure 1 The crystal structure of the title compound with labelling, and with displacement ellipsoids drawn at the 50% probability level. [Symmetry code: (i) -x+1, -y+1, -z+1.]

which refined to 0.30 (6) and 0.70 (6) for the H atoms attached to C4 and to 0.57 (6) and 0.43 (6) for the H atoms attached to C14. All H atoms were refined with fixed isotropic displacement parameters; $U_{\text{iso}}(H) = 1.5U_{\text{eq}}[C(\text{methyl})] \text{ or } 1.2U_{\text{eq}}[C(\text{methylene})].$

Data collection: SDP (Enraf-Nonius, 1985); cell refinement: SDP; data reduction: XCAD4 in SDP; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: XP in SHELXTL (Bruker, 1998); software used to prepare material for publication: CIFTAB in SHELXL97.

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