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Di- μ -chlorido-bis[(2-aminobenzamide- κ^2N^2,O)chloridocopper(II)]

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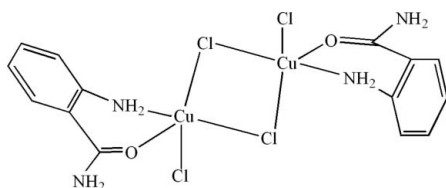
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Key indicators: single-crystal X-ray study; $T = 180$ K; mean $\sigma(C-C) = 0.002$ Å; R factor = 0.022; wR factor = 0.058; data-to-parameter ratio = 17.4.

The title compound, $[Cu_2Cl_4(C_7H_8N_2O)_2]$, crystallizes as discrete $[CuLCl_2]_2$ ($L = 2$ -aminobenzamide) dimers with inversion symmetry. Each Cu^{II} ion is five-coordinated and is bound to two bridging chloride ligands, a terminal chloride ligand and a bidentate 2-aminobenzamide ligand. The crystal structure exhibits alternating layers parallel to (010) along the b -axis direction. In the crystal, the components are linked *via* $N-H\cdots Cl$ hydrogen bonds, forming a three-dimensional network. These interactions link the molecules within the layers and also link the layers together and reinforce the cohesion of the structure.

Related literature

For general background to 2-aminobenzamide derivatives, see: Nagaoka *et al.* (2006); Butsch *et al.* (2011); Kapoor *et al.* (2010). For related structures, see: Yang *et al.* (2012); Lah *et al.* (2006). For standard bond lengths, see: Allen (2002)



Experimental

Crystal data

$[Cu_2Cl_4(C_7H_8N_2O)_2]$
 $M_r = 541.21$
Monoclinic, $P2_1/c$

$a = 8.1888$ (5) Å
 $b = 13.8545$ (6) Å
 $c = 8.1592$ (4) Å

$\beta = 98.771$ (5)°
 $V = 914.85$ (8) Å³
 $Z = 2$
Mo $K\alpha$ radiation

$\mu = 2.93$ mm⁻¹
 $T = 180$ K
 $0.15 \times 0.13 \times 0.12$ mm

Data collection

Agilent Xcalibur (Sapphire1)
diffractometer
Absorption correction: multi-scan
(*CrysAlis PRO*; Agilent, 2011)
 $T_{min} = 0.699$, $T_{max} = 1$

5578 measured reflections
2058 independent reflections
1897 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.022$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.022$
 $wR(F^2) = 0.058$
 $S = 1.04$
2058 reflections

118 parameters
H-atom parameters constrained
 $\Delta\rho_{max} = 0.41$ e Å⁻³
 $\Delta\rho_{min} = -0.41$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1A\cdots Cl2^i$	0.9200	2.4100	3.3113 (16)	166.00
$N2-H2A\cdots Cl1^{ii}$	0.8800	2.7800	3.6439 (16)	169.00
$N2-H2B\cdots Cl2^{iii}$	0.8800	2.5400	3.3493 (17)	153.00

Symmetry codes: (i) $-x + 1, -y, -z + 1$; (ii) $-x, y - \frac{1}{2}, -z + \frac{3}{2}$; (iii) $x, y, z + 1$.

Data collection: *CrysAlis PRO* (Agilent, 2011); cell refinement: *CrysAlis PRO*; data reduction: *CrysAlis PRO*; program(s) used to solve structure: *SIR2002* (Burla *et al.*, 2003); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 2012) and *DIAMOND* (Brandenburg & Berndt, 2001); software used to prepare material for publication: *WinGX* (Farrugia, 2012).

This work was supported by the Unité de Recherche de Chimie de l'Environnement et Moléculaire Structurale, CHEMS, Université Constantine1. 25000 Algeria, and the Laboratoire de Chimie de Coordination, 31077 Toulouse cedex, France. Thanks are due to the Ministère de l'Enseignement Supérieur et de la Recherche Scientifique - Algérie (PNR project) for financial support.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HG5337).

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Di- μ -chlorido-bis[(2-aminobenzamide- κ^2 N²,O)chloridocopper(II)]

Maamar Damous, George Dénès, Sofiane Bouacida, Meriem Hamlaoui, Hocine Merazig and Jean-Claude Daran

S1. Comment

2-aminobenzamide derivatives are well known compounds as anticancer agents (Nagaoka *et al.*, 2006). In addition, it was reported that some 2-aminobenzamide derivatives possessed biological activities, such as Anti-herpes simplex virus activity (Yang *et al.*, 2012). As part of our ongoing studies of complexes based on copper and derivatives we report here synthesis and the crystal structure of the title compound, obtained by the reaction of 2-aminobenzamide ligand with copper(II) chloride. The molecular structure of (I), and the atomic numbering used, is illustrated in Fig. 1. The asymmetric unit of (I) consists of one-half of the molecule, with the other half generated by a crystallographic inversion center. All bond distances and angles are within the ranges of accepted values (CSD, Allen, 2002). The complex contains five-coordinate Cu atoms (Fig. 1) which may be described either as square pyramidal with C11 apically bound to a pseudoplanar Cu1—O1—C12—C11a—N1 (*a*: -*x*, -*y*, 1 - *z*) fragment or as trigonal bipyramidal with N1 and C11a apical (Butsch *et al.*, 2011; Kapoor *et al.*, 2010). The Cu atoms are linked by double Cl atoms bridges, resulting in the formation of a dimer. The two Cu atoms, separated by 3.430 (1) Å, are doubly bridged by two chlorido ligands. The bridge is far from symmetrical with Cu—Cl1 and Cu—Cl1a (*a*: -*x*, -*y*, 1 - *z*) distances of 2.3983 (5) and 2.2990 (6) Å, respectively, and a Cu—Cl1—Cu_a bridging angle of 93.77 (2)°. The 2-aminobenzamide ligand binds to a single Cu metal ion within the dimer in a chelating manner [Cu—N1: 1.9923 (15) Å and Cu—O1: 2.0988 (13) Å]. The fifth coordination site is occupied by a terminal chlorido ligand at a distance of 2.3043 (6) Å (Lah *et al.*, 2006).

The crystal structure exhibits alternating layers parallel to the (010) plane along the *b* axis (Fig. 2). In the crystal, the components of the structure are linked *via* intermolecular N—H...Cl hydrogen bonds to form a three-dimensional network (Table 1 and Fig. 2). These interaction bonds link the molecules within the layers and also link the layers together and reinforce the cohesion of the structure.

S2. Experimental

An aqueous acidic solution of copper(II) chloride was added to an aqueous solution of the 2-aminobenzamide ligand (*L*) (1:1 mol ratio). The mixture was then stirred for several hours during which time darkish green crystals of [CuLCl₂]₂ were deposited. This crystalline product was collected and washed with ether and was carefully isolated under a polarizing microscope for analysis by X-ray diffraction.

S3. Refinement

All non-H atoms were refined with anisotropic atomic displacement parameters. The remaining H atoms were localized on Fourier maps but introduced in calculated positions and treated as riding on their parent atoms (C and N) with C—H = 0.95 Å and N—H = 0.88 or 0.92 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C or N})$.

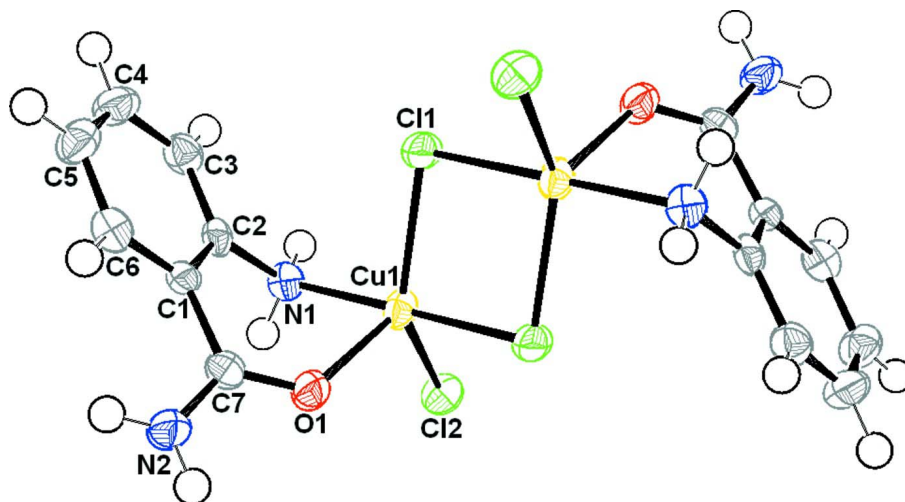


Figure 1

(Farrugia, 2012) The molecule structure of the title dimer with the atomic labelling scheme. Displacement are drawn at the 50% probability level. H atoms are represented as small spheres of arbitrary radius. Only the contents of the asymmetric unit are numbered.

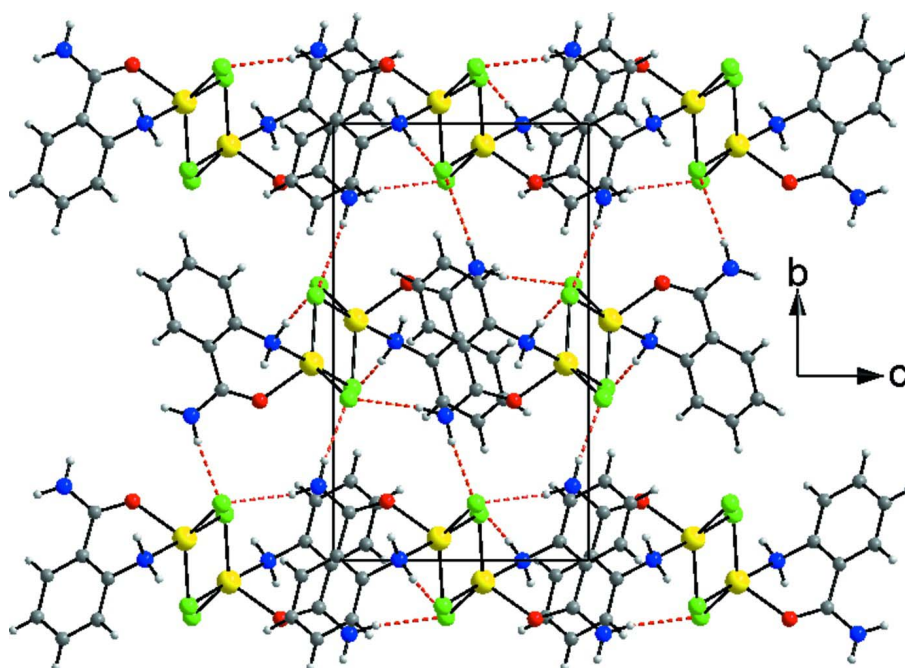


Figure 2

(Brandenburg & Berndt, 2001) A diagram of the layered crystal packing in (I), viewed down the *b* axis, showing layers parallel to (010) and hydrogen bond connections as dashed line.

Di- μ -chlorido-bis[(2-aminobenzamide- κ^2 N²,O)chloridocopper(II)]

Crystal data

[Cu₂Cl₄(C₇H₈N₂O)₂]
M_r = 541.21

Monoclinic, *P*2₁/*c*
 Hall symbol: -P 2ybc

$a = 8.1888$ (5) Å
 $b = 13.8545$ (6) Å
 $c = 8.1592$ (4) Å
 $\beta = 98.771$ (5)°
 $V = 914.85$ (8) Å³
 $Z = 2$
 $F(000) = 540$
 $D_x = 1.965$ Mg m⁻³

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å
 Cell parameters from 3363 reflections
 $\theta = 2.9$ – 28.2 °
 $\mu = 2.93$ mm⁻¹
 $T = 180$ K
 Cube, green
 $0.15 \times 0.13 \times 0.12$ mm

Data collection

Agilent Xcalibur (Sapphire1)
 diffractometer
 Radiation source: fine-focus sealed tube
 Graphite monochromator
 Detector resolution: 8.2632 pixels mm⁻¹
 ω scans
 Absorption correction: multi-scan
 (CrysAlis PRO; Agilent, 2011)
 $T_{\min} = 0.699$, $T_{\max} = 1$

5578 measured reflections
 2058 independent reflections
 1897 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.022$
 $\theta_{\max} = 28.3$ °, $\theta_{\min} = 2.9$ °
 $h = -9 \rightarrow 10$
 $k = -17 \rightarrow 18$
 $l = -10 \rightarrow 10$

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.022$
 $wR(F^2) = 0.058$
 $S = 1.04$
 2058 reflections
 118 parameters
 0 restraints
 Primary atom site location: structure-invariant
 direct methods

Secondary atom site location: difference Fourier
 map
 Hydrogen site location: inferred from
 neighbouring sites
 H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0307P)^2 + 0.3739P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.003$
 $\Delta\rho_{\max} = 0.41$ e Å⁻³
 $\Delta\rho_{\min} = -0.41$ e Å⁻³

Special details

Experimental. Absorption correction: empirical using spherical harmonics, implemented in SCALE3 ABSPACK scaling algorithm CrysAlis PRO (Agilent, 2011).

Geometry. Bond distances, angles *etc.* have been calculated using the rounded fractional coordinates. All su's are estimated from the variances of the (full) variance-covariance matrix. The cell e.s.d.'s are taken into account in the estimation of distances, angles and torsion angles

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) *etc.* and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
Cu1	0.18491 (3)	-0.04957 (2)	0.58700 (3)	0.0126 (1)
Cl1	0.05270 (6)	0.10533 (3)	0.57135 (6)	0.0161 (1)
Cl2	0.36324 (6)	-0.12970 (3)	0.44121 (6)	0.0162 (1)
O1	0.15024 (17)	-0.13480 (9)	0.79155 (16)	0.0156 (4)
N1	0.37924 (19)	-0.00155 (11)	0.74251 (18)	0.0126 (4)
N2	0.1556 (2)	-0.16908 (11)	1.0607 (2)	0.0180 (5)
C1	0.2398 (2)	-0.00937 (12)	0.9884 (2)	0.0107 (5)

C2	0.3341 (2)	0.04226 (12)	0.8882 (2)	0.0111 (5)
C3	0.3819 (2)	0.13689 (13)	0.9288 (2)	0.0147 (5)
C4	0.3337 (3)	0.18053 (13)	1.0665 (2)	0.0181 (5)
C5	0.2408 (3)	0.13070 (13)	1.1664 (2)	0.0171 (5)
C6	0.1958 (2)	0.03556 (13)	1.1275 (2)	0.0140 (5)
C7	0.1801 (2)	-0.10930 (12)	0.9406 (2)	0.0122 (5)
H1A	0.43529	0.04286	0.68835	0.0152*
H1B	0.44964	-0.05231	0.77350	0.0152*
H2A	0.11781	-0.22765	1.03652	0.0216*
H2B	0.17697	-0.15031	1.16476	0.0216*
H3	0.44744	0.17143	0.86209	0.0176*
H4	0.36477	0.24546	1.09246	0.0217*
H5	0.20810	0.16101	1.26070	0.0206*
H6	0.13389	0.00073	1.19728	0.0168*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
Cu1	0.0105 (1)	0.0152 (1)	0.0119 (1)	0.0003 (1)	0.0005 (1)	-0.0027 (1)
Cl1	0.0141 (2)	0.0125 (2)	0.0198 (2)	0.0006 (2)	-0.0036 (2)	-0.0023 (2)
Cl2	0.0160 (2)	0.0175 (2)	0.0162 (2)	0.0013 (2)	0.0059 (2)	-0.0026 (2)
O1	0.0214 (7)	0.0129 (6)	0.0121 (6)	-0.0036 (5)	0.0016 (5)	-0.0002 (5)
N1	0.0118 (7)	0.0148 (7)	0.0119 (7)	-0.0002 (6)	0.0038 (6)	0.0005 (6)
N2	0.0280 (10)	0.0118 (7)	0.0140 (8)	-0.0036 (7)	0.0026 (7)	-0.0001 (6)
C1	0.0100 (8)	0.0100 (8)	0.0113 (8)	0.0013 (7)	-0.0007 (7)	0.0004 (7)
C2	0.0084 (8)	0.0147 (8)	0.0094 (8)	0.0021 (7)	-0.0011 (7)	0.0005 (7)
C3	0.0141 (9)	0.0149 (8)	0.0146 (9)	-0.0020 (7)	0.0009 (7)	0.0026 (7)
C4	0.0193 (10)	0.0124 (8)	0.0217 (10)	-0.0016 (7)	0.0004 (8)	-0.0032 (7)
C5	0.0177 (10)	0.0176 (9)	0.0162 (9)	0.0016 (8)	0.0030 (8)	-0.0049 (7)
C6	0.0118 (9)	0.0167 (9)	0.0135 (9)	0.0006 (7)	0.0022 (7)	0.0026 (7)
C7	0.0103 (9)	0.0127 (8)	0.0135 (9)	0.0016 (7)	0.0018 (7)	0.0014 (7)

Geometric parameters (Å, °)

Cu1—Cl1	2.3983 (5)	C1—C2	1.403 (2)
Cu1—Cl2	2.3043 (6)	C1—C6	1.389 (2)
Cu1—O1	2.0988 (13)	C1—C7	1.500 (2)
Cu1—N1	1.9923 (15)	C2—C3	1.394 (2)
Cu1—Cl1 ⁱ	2.2990 (6)	C3—C4	1.385 (2)
O1—C7	1.254 (2)	C4—C5	1.382 (3)
N1—C2	1.433 (2)	C5—C6	1.392 (3)
N2—C7	1.322 (2)	C3—H3	0.9500
N1—H1A	0.9200	C4—H4	0.9500
N1—H1B	0.9200	C5—H5	0.9500
N2—H2A	0.8800	C6—H6	0.9500
N2—H2B	0.8800		
Cl1—Cu1—Cl2	136.06 (2)	C2—C1—C6	118.81 (15)

Cl1—Cu1—O1	115.54 (4)	C2—C1—C7	120.37 (14)
Cl1—Cu1—N1	92.60 (5)	C6—C1—C7	120.74 (15)
Cl1—Cu1—Cl1 ⁱ	86.23 (2)	N1—C2—C1	120.14 (15)
Cl2—Cu1—O1	108.22 (4)	N1—C2—C3	119.81 (15)
Cl2—Cu1—N1	88.98 (5)	C1—C2—C3	120.04 (15)
Cl1 ⁱ —Cu1—Cl2	95.55 (2)	C2—C3—C4	119.93 (16)
O1—Cu1—N1	82.72 (6)	C3—C4—C5	120.73 (17)
Cl1 ⁱ —Cu1—O1	93.00 (4)	C4—C5—C6	119.28 (16)
Cl1 ⁱ —Cu1—N1	174.57 (5)	C1—C6—C5	121.19 (16)
Cu1—Cl1—Cu1 ⁱ	93.77 (2)	O1—C7—C1	121.32 (15)
Cu1—O1—C7	125.63 (11)	N2—C7—C1	117.78 (15)
Cu1—N1—C2	112.82 (11)	O1—C7—N2	120.88 (16)
C2—N1—H1A	109.00	C2—C3—H3	120.00
C2—N1—H1B	109.00	C4—C3—H3	120.00
H1A—N1—H1B	108.00	C3—C4—H4	120.00
Cu1—N1—H1A	109.00	C5—C4—H4	120.00
Cu1—N1—H1B	109.00	C4—C5—H5	120.00
H2A—N2—H2B	120.00	C6—C5—H5	120.00
C7—N2—H2A	120.00	C1—C6—H6	119.00
C7—N2—H2B	120.00	C5—C6—H6	119.00
Cl2—Cu1—Cl1—Cu1 ⁱ	94.09 (3)	Cu1—N1—C2—C1	55.55 (18)
O1—Cu1—Cl1—Cu1 ⁱ	-91.53 (5)	C6—C1—C2—N1	-179.03 (15)
N1—Cu1—Cl1—Cu1 ⁱ	-174.69 (5)	C7—C1—C6—C5	-175.43 (17)
Cl1 ⁱ —Cu1—Cl1—Cu1 ⁱ	0.00 (4)	C2—C1—C7—O1	-29.6 (2)
Cl1—Cu1—Cl1 ⁱ —Cu1 ⁱ	0.00 (4)	C6—C1—C2—C3	0.0 (2)
Cl2—Cu1—Cl1 ⁱ —Cu1 ⁱ	-135.94 (2)	C6—C1—C7—O1	147.06 (17)
O1—Cu1—Cl1 ⁱ —Cu1 ⁱ	115.41 (4)	C6—C1—C7—N2	-31.2 (2)
Cl1—Cu1—O1—C7	-53.92 (15)	C2—C1—C7—N2	152.19 (16)
Cl2—Cu1—O1—C7	121.99 (14)	C2—C1—C6—C5	1.3 (3)
N1—Cu1—O1—C7	35.49 (15)	C7—C1—C2—C3	176.68 (15)
Cl1 ⁱ —Cu1—O1—C7	-141.17 (14)	C7—C1—C2—N1	-2.3 (2)
Cl1—Cu1—N1—C2	55.31 (11)	C1—C2—C3—C4	-1.2 (3)
Cl2—Cu1—N1—C2	-168.63 (11)	N1—C2—C3—C4	177.83 (17)
O1—Cu1—N1—C2	-60.11 (11)	C2—C3—C4—C5	1.2 (3)
Cu1—O1—C7—C1	2.6 (2)	C3—C4—C5—C6	0.1 (3)
Cu1—O1—C7—N2	-179.23 (12)	C4—C5—C6—C1	-1.3 (3)
Cu1—N1—C2—C3	-123.45 (14)		

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

Hydrogen-bond geometry ($\text{\AA}, ^\circ$)

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N1—H1A \cdots Cl2 ⁱⁱ	0.9200	2.4100	3.3113 (16)	166.00
N2—H2A \cdots Cl1 ⁱⁱⁱ	0.8800	2.7800	3.6439 (16)	169.00
N2—H2B \cdots Cl2 ^{iv}	0.8800	2.5400	3.3493 (17)	153.00

Symmetry codes: (ii) $-x+1, -y, -z+1$; (iii) $-x, y-1/2, -z+3/2$; (iv) $x, y, z+1$.