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# **Structure Reports Online**

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# Dichlorobis(1,3-dimethylthiourea-κS)zinc(II)

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#### **Key indicators**

Single-crystal X-ray study  $T=150~\mathrm{K}$  Mean  $\sigma(\mathrm{N-C})=0.003~\mathrm{\mathring{A}}$  R factor = 0.028 wR factor = 0.067 Data-to-parameter ratio = 18.6

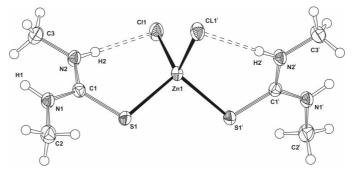
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

Determination of the crystal structure of the title compound,  $[ZnCl_2(C_3H_6N_2S)_2]$ , reveals a distorted tetrahedral geometry around the zinc centre which occupies a twofold axis. Both intra- and intermolecular hydrogen bonding is observed between the 1,3-dimethylthiourea NH groups and the coordinated Cl atoms.

#### Comment

The title compound, (I), was formed as part of our investigations into the formation of bis-thiourea zinc(II) dicarboxylate polymers (Burrows *et al.*, 2000, 2004; Burke *et al.*, 2003).

The asymmetric unit of (I) (Fig. 1) consists of a zinc(II) centre occupying a twofold symmetry axis, to which is coordinated one 1,3-dimethylthiourea ligand, *via* the S atom, and one Cl<sup>-</sup>. The complete molecule is generated by transformation through a twofold rotation axis, inherent in the space group. The geometry around the Zn centre is distorted tetrahedral, with bond angles ranging from 104.35 (3) to



**Figure 1** A view of the molecule of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms represented by small spheres. [Symmetry code: (i) 1 - x, y,  $\frac{1}{2} - z$ .]

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## metal-organic papers

113.300 (19)°. This study confirms previous conclusions on the structure of (I) which emerged on the basis of IR studies (Marcotrigiano, 1975).

The NH groups of the 1,3-dimethylthiourea ligands are arranged such that they facilitate the formation of both intraand intermolecular hydrogen bonds, involving  $Cl^-$  anions as acceptors in both cases; details are given in Table 1. As seen in a number of zinc(II) bis(thiourea) dicarboxylate polymers (Burrows *et al.*, 2000), the intramolecular hydrogen bonds have graph-set notation S(6). The intermolecular hydrogen bonds link the molecules into infinite hydrogen-bonded chains (Fig. 2). These interactions occur pairwise and lead to hydrogen-bonded rings with graph-set notation  $R_2^2(12)$ . There is no inter-chain hydrogen bonding present.

#### **Experimental**

Equimolar aqueous solutions of zinc(II) tetra(1,3-dimethylthiourea) dichloride (Ashcroft, 1970) and sodium salts of succinic, itaconic or mesaconic acids were allowed to evaporate slowly over a period of two weeks, in each case resulting in the formation of colourless crystals. Analysis by single-crystal X-ray diffraction revealed the identity of the products as (I) and confirmed that the dicarboxylate was not incorporated into the structure.

#### Crystal data

· ·	
[ZnCl2(C3H6N2S)2]	$D_x = 1.652 \text{ Mg m}^{-3}$
$M_r = 344.62$	Mo $K\alpha$ radiation
Monoclinic, C2/c	Cell parameters from 1063
a = 13.0230 (4)  Å	reflections
b = 8.9470 (3)  Å	$\theta = 0.2 - 26.3^{\circ}$
c = 12.4350 (3)  Å	$\mu = 2.44 \text{ mm}^{-1}$
$\beta = 106.967 (2)^{\circ}$	T = 150 (2)  K
$V = 1385.82 (7) \text{ Å}^3$	Block, colourless
Z = 4	$0.18 \times 0.15 \times 0.15 \text{ mm}$

#### Data collection

Nonius KappaCCD area-detector diffractometer  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (Blessing, 1995)  $T_{\min} = 0.655, T_{\max} = 0.697$  8273 measured reflections

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.028$   $wR(F^2) = 0.067$  S = 1.141580 reflections 85 parameters H atoms treated by a mixture of independent and constrained refinement 1580 independent reflections 1439 reflections with  $I > 2\sigma(I)$   $R_{\rm int} = 0.034$   $\theta_{\rm max} = 27.5^{\circ}$   $h = -16 \rightarrow 16$   $k = -11 \rightarrow 11$   $l = -16 \rightarrow 16$ 

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0178P)^2 \\ &+ 2.1477P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &< 0.001 \\ \Delta\rho_{\text{max}} &= 0.43 \text{ e Å}^{-3} \\ \Delta\rho_{\text{min}} &= -0.44 \text{ e Å}^{-3} \end{split}$$



Figure 2 A view of the intermolecular hydrogen-bond interactions in (I), leading to chains along the crystallographic [101] direction.

**Table 1** Hydrogen-bonding geometry (Å, °).

$D-H\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
$ \begin{array}{c} N2-H2\cdots Cl1 \\ N1-H1\cdots Cl1^{i} \end{array} $	0.884 (17)	2.337 (18)	3.2110 (19)	170 (3)
	0.887 (17)	2.47 (2)	3.2737 (19)	152 (2)

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

H atoms were included at calculated positions on all carbon centres, being constrained to an ideal geometry with C—H distances of 0.98 Å and  $U_{\rm iso}({\rm H})=1.5U_{\rm eq}({\rm C})$ . Each group was allowed to rotate freely about its C—N bond. The position of the amino H atoms were located from the difference map and refined isotropically subject to a distance constraint of 0.89 Å.

Data collection: *COLLECT* (Hooft, 1998); cell refinement: *HKL DENZO* (Otwinowski & Minor, 1997); data reduction: *DENZO* and *SCALEPACK* (Otwinowski & Minor, 1997); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL* and local programs.

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# supporting information

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Crystal data

[ZnCl<sub>2</sub>(C<sub>3</sub>H<sub>6</sub>N<sub>2</sub>S)<sub>2</sub>]  $M_r = 344.62$  Monoclinic, C2/c Hall symbol: -C2yc a = 13.0230 (4) Å b = 8.9470 (3) Å c = 12.4350 (3) Å  $\beta = 106.967$  (2)° V = 1385.82 (7) Å<sup>3</sup> Z = 4

Data collection

Nonius KappaCCD area-detector diffractometer Radiation source: sealed tube Graphite monochromator  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (Blessing, 1995)  $T_{\min} = 0.655$ ,  $T_{\max} = 0.697$ 

Refinement

Least-squares matrix: full  $R[F^2 > 2\sigma(F^2)] = 0.028$   $wR(F^2) = 0.067$  S = 1.14 1580 reflections 85 parameters 2 restraints

Refinement on  $F^2$ 

Primary atom site location: structure-invariant direct methods

F(000) = 704

 $D_{\rm x} = 1.652 {\rm Mg m}^{-3}$ 

Mo  $K\alpha$  radiation,  $\lambda = 0.71070$  Å Cell parameters from 25 reflections

 $\theta = 0.2 - 26.3^{\circ}$ 

 $\mu = 2.44 \text{ mm}^{-1}$ 

T = 150 K

Block, colourless

 $0.18\times0.15\times0.15~mm$ 

8273 measured reflections 1580 independent reflections 1439 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.034$  $\theta_{\text{max}} = 27.5^{\circ}, \ \theta_{\text{min}} = 4.0^{\circ}$  $h = -16 \rightarrow 16$ 

 $k = -11 \longrightarrow 11$  $l = -16 \longrightarrow 16$ 

Secondary atom site location: difference Fourier man

Hydrogen site location: difference Fourier map H atoms treated by a mixture of independent

and constrained refinement

 $w = 1/[\sigma^2(F_0^2) + (0.0178P)^2 + 2.1477P]$ where  $P = (F_0^2 + 2F_0^2)/3$ 

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

 $\Delta \rho_{\text{max}} = 0.43 \text{ e Å}^{-3}$ 

 $\Delta \rho_{\min} = -0.44 \text{ e Å}^{-3}$ 

#### Special details

**Geometry**. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

**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 F-factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters  $(\mathring{A}^2)$ 

	x	y	Z	$U_{ m iso}$ * $/U_{ m eq}$	
Zn1	0.5000	0.65085 (4)	0.2500	0.02036 (12)	
Cl1	0.39368 (4)	0.80208 (7)	0.32074 (4)	0.03019 (15)	
S1	0.60867 (4)	0.49039 (6)	0.38451 (4)	0.02451 (15)	
N1	0.74153 (14)	0.5551(2)	0.58578 (15)	0.0249 (4)	
H1	0.760(2)	0.611 (3)	0.6472 (19)	0.043 (8)*	
N2	0.59505 (15)	0.7072(2)	0.52832 (15)	0.0248 (4)	
H2	0.5344 (16)	0.730(3)	0.477 (2)	0.034 (7)*	
C1	0.65113 (16)	0.5921 (2)	0.50836 (17)	0.0205 (4)	
C2	0.8128 (2)	0.4339 (3)	0.5763 (2)	0.0334 (5)	
H2A	0.8203	0.4326	0.5001	0.043 (8)*	
H2C	0.7827	0.3385	0.5914	0.052 (9)*	
H2B	0.8834	0.4490	0.6309	0.054 (9)*	
C3	0.62235 (19)	0.7902(3)	0.63317 (19)	0.0302 (5)	
H3A	0.6953	0.8301	0.6488	0.022 (6)*	
Н3В	0.6185	0.7237	0.6945	0.043 (8)*	
Н3С	0.5716	0.8730	0.6270	0.042 (8)*	

Atomic displacement parameters  $(\mathring{A}^2)$ 

	$U^{11}$	$U^{22}$	$U^{33}$	$U^{12}$	$U^{13}$	$U^{23}$
Zn1	0.02062 (19)	0.02289 (19)	0.01535 (18)	0.000	0.00177 (13)	0.000
Cl1	0.0290(3)	0.0365(3)	0.0220(3)	0.0119(2)	0.0026(2)	-0.0025 (2)
S1	0.0288 (3)	0.0223 (3)	0.0178 (3)	0.0039(2)	-0.0006(2)	-0.00186 (19)
N1	0.0237 (9)	0.0275 (9)	0.0198 (9)	0.0034 (7)	0.0005 (7)	-0.0016 (7)
N2	0.0226 (9)	0.0285 (10)	0.0196 (9)	0.0047 (7)	0.0002 (7)	-0.0026 (7)
C1	0.0200 (10)	0.0223 (10)	0.0187 (9)	-0.0023(8)	0.0047 (8)	0.0015 (8)
C2	0.0321 (12)	0.0357 (13)	0.0277 (11)	0.0124 (10)	0.0016 (9)	0.0000 (10)
С3	0.0304 (12)	0.0328 (12)	0.0256 (12)	0.0019 (10)	0.0051 (9)	-0.0072 (9)

#### Geometric parameters (Å, °)

Zn1—Cl1	2.2874 (6)	N2—C1	1.327 (3)
$Zn1$ — $Cl1^i$	2.2874 (6)	N2—C3	1.452 (3)
Zn1—S1	2.3410 (5)	C2—H2A	0.9800
$Zn1$ — $S1^i$	2.3410 (5)	C2—H2C	0.9800
S1—C1	1.734 (2)	C2—H2B	0.9800
N1—H1	0.887 (17)	С3—Н3А	0.9800
N1—C1	1.327 (3)	C3—H3B	0.9800
N1—C2	1.454 (3)	С3—Н3С	0.9800
N2—H2	0.884 (17)		

# supporting information

Cl1—Zn1—Cl1 <sup>i</sup> Cl1—Zn1—S1 Cl1 <sup>i</sup> —Zn1—S1 <sup>i</sup> Cl1—Zn1—S1 <sup>i</sup> Cl1 <sup>i</sup> —Zn1—S1 S1—Zn1—S1 S1—Zn1—S1-Cl H1—N1—Cl H1—N1—C2 C1—N1—C2 H2—N2—C1 H2—N2—C3 S1—C1—N1	107.47 (3) 113.300 (19) 113.300 (19) 109.27 (2) 109.27 (2) 104.35 (3) 106.40 (7) 116.6 (19) 118.0 (19) 125.39 (19) 117.8 (18) 117.8 (18) 124.14 (18) 119.92 (16)	S1—C1—N2 N1—C1—N2 N1—C2—H2A N1—C2—H2C N1—C2—H2B H2A—C2—H2C H2A—C2—H2B H2C—C2—H2B N2—C3—H3A N2—C3—H3B N2—C3—H3C H3A—C3—H3C H3B—C3—H3C	121.53 (15) 118.55 (19) 109.5 109.5 109.5 109.5 109.5 109.5 109.5 109.5 109.5 109.5 109.5
Cl1—Zn1—S1—Cl Cl1 <sup>i</sup> —Zn1—S1—Cl Sl <sup>i</sup> —Zn1—S1—Cl C2—N1—Cl—Sl C2—N1—Cl—N2	-38.29 (8) 81.50 (7) -157.04 (8) 1.1 (3) -179.0 (2)	C3—N2—C1—S1 C3—N2—C1—N1 Zn1—S1—C1—N1 Zn1—S1—C1—N2	175.64 (17) -4.3 (3) -155.05 (15) 25.05 (19)

Symmetry code: (i) -x+1, y, -z+1/2.

### Hydrogen-bond geometry (Å, °)

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	$H\cdots A$	D··· $A$	<i>D</i> —H··· <i>A</i>
N2—H2···Cl1	0.88(2)	2.34(2)	3.2110 (19)	170 (3)
N1—H1···Cl1 <sup>ii</sup>	0.89(2)	2.47 (2)	3.2737 (19)	152 (2)

Symmetry code: (ii) x+1/2, -y+3/2, z+1/2.