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Key indicators

Single-crystal X-ray study T = 150 KMean σ (C–C) = 0.003 Å R factor = 0.045 wR factor = 0.120 Data-to-parameter ratio = 17.8

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

(*N*,*N*-Diethyldithiocarbamato- $\kappa^2 S, S'$)bis-(1,10-phenanthroline)sodium(I)

In the title molecule, $[Na(C_5H_{10}NS_2)(C_{12}H_8N_2)_2]$, which has crystallographic twofold symmetry, the coordination geometry of the Na atom is intermediate between octahedral and trigonal prismatic, coordinated by two S atoms of an *N*,*N*diethyldithiocarbamate ligand and four chelating N atoms of two 1,10-phenanthroline ligands. In the crystal structure, weak $C-H \cdots S$ and $\pi-\pi$ stacking interactions form chains of rings.

Comment

Dithiocarbamate ligands have an ability to complex with a wide variety of transition metals while demonstrating flexibility in coordination mode. An example of the versatility of the thiolate ligand is the dinuclear gold complex $[Au_2(C_{14}H_{14}P)(C_5H_{10}NS_2)]$ in which diethyldithiocarbamate acts as a bridge between transition metal centres (Bardaji *et al.*, 1994). On the other hand, the monodentate bonding mode of the dithiocarbamate ligand is observed in $[Au(C_{18}H_{33}P)-(C_5H_{10}NS_2)]$ (Ho & Tiekink, 2001), as well as in the sodium complex Na[S₂CN(CH₃)₂]·2H₂O (Oskarsson & Ymén, 1983).



The molecular structure of the title compound, (I), is shown in Fig. 1 and selected bond lengths are given in Table 1. The molecule lies on a crystallographic twofold axis which runs through atom Na1 and C13–N3 of the dithiocarbamate ligand. The chelating phenanthroline ligands are bonded in a bidentate fashion through two N atoms, with Na–N distances comparable to those in related complexes (Marek *et al.*, 2003).

In the crystal structure, molecules are connected into dimeric units (Fig. 2) *via* weak C-H···S interactions (Table 2), forming $R_2^2(14)$ rings (Bernstein *et al.*, 1995) which are, in turn, reinforced by π - π stacking interactions, with a perpendicular distance of 3.368 Å [Cg··· $Cg^{iii} = 3.5584$ (12) Å, where Cg is the centroid of atoms C7–C11/N2; symmetry code: (iii) $\frac{3}{2} - x$, $\frac{1}{2} - y$, 1 - z]. The dimeric units propagate along [101], forming one-dimensional chains of rings.

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Experimental

The dropwise addition of a sodium diethyldithiocarbamate trihydrate [Na(Ddtc)·3H₂O] solution (6 mmol in 10 ml of anhydrous methanol) to a solution of 1,10-phenanthroline monohydrate [Phen \cdot H₂O] (2 mmol in 10 ml of anhydrous methanol) resulted in a white precipitate. Upon recrystallization of the product from anhydrous methanol, colourless crystals of (I) suitable for X-ray analysis were obtained.

> $D_x = 1.336 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation

> > reflections

T = 150 (1) KBlock, colourless 0.14 \times 0.12 \times 0.10 mm

 $R_{\rm int} = 0.047$ $\theta_{\rm max} = 27.5^{\circ}$

 $h = -22 \rightarrow 21$

 $k = -13 \rightarrow 13$ $l = -20 \rightarrow 20$

 $\theta = 2.6-27.5^{\circ}$ $\mu = 0.25 \text{ mm}^{-1}$

Cell parameters from 9340

3026 independent reflections

2116 reflections with $I > 2\sigma(I)$

Crystal data

[Na(C5H10NS2)(C12H8N2)2]
$M_r = 531.66$
Monoclinic, $C2/c$
a = 17.7050 (7) Å
b = 10.5385 (4) Å
c = 15.7010 (4) Å
$\beta = 115.5570 \ (19)^{\circ}$
V = 2642.92 (16) Å ³
Z = 4

Data collection

Bruker-Nonius KappaCCD diffractometer φ scans and ω scans with κ offsets Absorption correction: multi-scan (SORTAV; Blessing, 1995) $T_{\rm min} = 0.870, \ T_{\rm max} = 0.978$ 9340 measured reflections

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_0^2) + (0.0556P)^2]$ $R[F^2 > 2\sigma(F^2)] = 0.045$ + 1.4314P] $wR(F^2) = 0.120$ where $P = (F_0^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} = 0.001$ S = 1.04 $\Delta \rho_{\text{max}} = 0.32 \text{ e} \text{ Å}^{-3}$ 3026 reflections $\Delta \rho_{\rm min} = -0.31 \text{ e } \text{\AA}^{-3}$ 170 parameters H-atom parameters constrained

Table 1

Selected geometric parameters (Å, °).

S1-Na1	2.9158 (11)	Na1-N1	2.5451 (17)
Na1-N2	2.4628 (18)		
C13-S1-Na1	88.99 (8)	N1-Na1-S1 ⁱ	112.16 (4)
N2 ⁱ -Na1-N2	107.22 (9)	N2-Na1-S1	149.93 (5)
N2-Na1-N1	66.67 (5)	N1-Na1-S1	98.21 (4)
N2-Na1-N1 ⁱ	92.12 (6)	S1 ⁱ -Na1-S1	61.58 (3)
N1-Na1-N1 ⁱ	144.76 (9)	S1-C13-S1 ⁱ	120.45 (16)
N2-Na1-S1 ⁱ	98.85 (4)		

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

Table 2

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$C8-H8A\cdots$ S1 ⁱⁱ	0.95	2.84	3.720 (3)	155
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Symmetry code: (ii) $x + \frac{1}{2}, -y + \frac{1}{2}, z + \frac{1}{2}$.

H atoms were placed in calculated positions, with C-H distances of 0.95, 0.99 or 0.98 Å (for methyl groups). They were included in the refinement in the riding-model approximation, with $U_{iso}(H) =$ $1.2U_{eq}(C)$ or $1.5U_{eq}(C)$ for methyl H atoms.



Figure 1

The molecular structure of (I), showing 30% probability displacement ellipsoids. The suffix A corresponds to symmetry code (i) in Table 1. H atoms have been omitted.



Figure 2

A partial packing plot (Spek, 2003) of (I), showing hydrogen bonds as dashed lines. H atoms not involved in hydrogen bonding have been omitted.

Data collection: COLLECT (Nonius, 2002); cell refinement: DENZO-SMN (Otwinowski & Minor, 1997); data reduction: DENZO-SMN; program(s) used to solve structure: SIR92 (Altomare et al., 1994); program(s) used to refine structure: SHELXTL (Sheldrick, 2001); molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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