

Bis[O-methyl (4-ethoxyphenyl)dithio-phosphonato- κ^2S,S']nickel(II)

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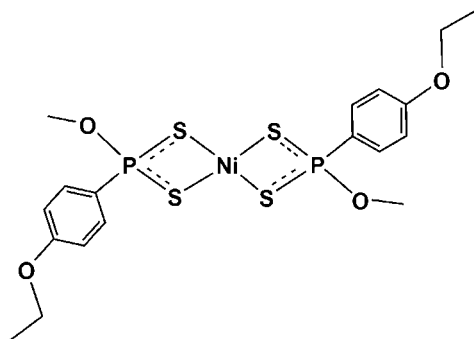
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Key indicators: single-crystal X-ray study; $T = 173$ K; mean $\sigma(C-C) = 0.002$ Å; R factor = 0.023; wR factor = 0.062; data-to-parameter ratio = 21.1.

In the title compound, $[Ni(C_9H_{12}O_2PS_2)_2]$, the Ni^{II} atom resides on an inversion center and is coordinated by four S atoms [$Ni-S = 2.2328(4)$ and $2.2455(3)$ Å] in a distorted square-planar geometry [$S-Ni-S = 88.443(13)$ and $91.557(13)^\circ$]. In the crystal, molecules related by translation in $[110]$ are linked into chains *via* weak $C-H\cdots O$ interactions. The crystal packing exhibits short intermolecular $S\cdots S$ contacts of $3.3366(5)$ Å.

Related literature

For information on dithiophosphonate compounds, see: Van Zyl & Fackler (2000); Van Zyl (2010); Van Zyl & Woollins (2012). For related structures of nickel(II) dithiophosphonate complexes, see: Hartung (1967); Liu *et al.* (2004); Gray *et al.* (2004); Aragoni *et al.* (2007); Arca *et al.* (1997); Özcan *et al.* (2002).



Experimental

Crystal data

$[Ni(C_9H_{12}O_2PS_2)_2]$

$M_r = 553.26$

Monoclinic, $P2_1/c$
 $a = 13.5866(5)$ Å
 $b = 6.4212(2)$ Å
 $c = 14.1047(5)$ Å
 $\beta = 109.389(2)^\circ$
 $V = 1160.74(7)$ Å³

$Z = 2$
Mo $K\alpha$ radiation
 $\mu = 1.36$ mm⁻¹
 $T = 173$ K
 $0.43 \times 0.31 \times 0.24$ mm

Data collection

Bruker SMART APEXII CCD diffractometer
Absorption correction: multi-scan (SADABS; Bruker, 2008)
 $T_{min} = 0.593$, $T_{max} = 0.737$

19824 measured reflections
2850 independent reflections
2609 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.036$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.023$
 $wR(F^2) = 0.062$
 $S = 1.07$
2850 reflections
135 parameters

2 restraints
H-atom parameters constrained
 $\Delta\rho_{max} = 0.56$ e Å⁻³
 $\Delta\rho_{min} = -0.44$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C3-H3\cdots O1^i$	0.95	2.57	3.5123 (18)	171

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

Data collection: APEX2 (Bruker, 2008); cell refinement: SAINT-Plus (Bruker, 2008); data reduction: SAINT-Plus and XPREP (Bruker, 2008); program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: SHELXTL (Sheldrick, 2008); software used to prepare material for publication: SHELXL97.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: CV5358).

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