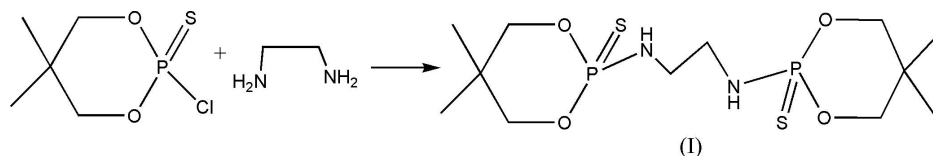


Hai-Bing Li,* Ya Li, De-Jun Xiong
and De-Mei TianKey Laboratory of Pesticides and Chemical
Biology, Ministry of Education, College of
Chemistry, Central China Normal University,
Wuhan 430079, People's Republic of ChinaCorrespondence e-mail:
lhbing@mail.ccnu.edu.cn

Key indicators

Single-crystal X-ray study
 $T = 298\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$
 R factor = 0.056
 wR factor = 0.149
Data-to-parameter ratio = 20.6For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.*N,N'*-Bis(5,5-dimethyl-2-thioxo-1,3,2-dioxaphosphinan-2-yl)ethane-1,2-diamineIn the title compound, $\text{C}_{12}\text{H}_{26}\text{N}_2\text{O}_4\text{P}_2\text{S}_2$, the molecules are
linked into a three-dimensional structure by one $\text{C}-\text{H}\cdots\text{O}$
and two $\text{N}-\text{H}\cdots\text{S}$ hydrogen bonds.Received 4 December 2006
Accepted 7 January 2007

Comment

Organic phosphorus compounds are widely used in pesticide
science because of their significant biological properties. The
title compound, (I), has been used as a precursor of organic
phosphorus pesticides. The crystal structure is illustrated in
Fig. 1. The $\text{P1}-\text{S1}$ and $\text{P2}-\text{S2}$ bond distances [1.9141 (11) and
1.9299 (12) \AA , respectively] indicate $\text{P}=\text{S}$ double-bond char-
acter, as observed previously in a similar compound (Zheng *et al.*,
2006). Molecules are linked into a three-dimensional
structure by a combination of one $\text{C}-\text{H}\cdots\text{O}$ and two $\text{N}-\text{H}\cdots\text{S}$
hydrogen bonds (Table 1 and Fig. 2).

Experimental

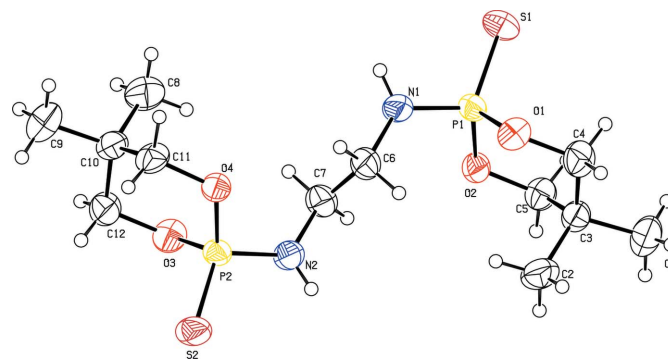
A mixture of 2-chloro-5,5-dimethyl-1,3,2-dioxaphosphinane 2-sulfide
(10 mmol) and ethylenediamine (5 mmol) in THF (30 ml) was stirred
for 4 h and the solvent was removed under reduced pressure. After
filtration, crystals suitable for X-ray investigation were obtained by
recrystallization from methanol and chloroform (1:1 v/v).

Figure 1
The molecular structure of (I), showing the atom-labelling scheme.
Displacement ellipsoids are drawn at the 50% probability level.

Crystal data

$C_{12}H_{26}N_2O_4P_2S_2$
 $M_r = 388.41$
 Monoclinic, $P2_1/c$
 $a = 14.545 (2) \text{ \AA}$
 $b = 11.2714 (16) \text{ \AA}$
 $c = 12.1561 (18) \text{ \AA}$
 $\beta = 98.560 (3)^\circ$
 $V = 1970.8 (5) \text{ \AA}^3$

$Z = 4$
 $D_x = 1.309 \text{ Mg m}^{-3}$
 Mo $K\alpha$ radiation
 $\mu = 0.45 \text{ mm}^{-1}$
 $T = 298 (2) \text{ K}$
 Needle, colourless
 $0.40 \times 0.12 \times 0.06 \text{ mm}$

Data collection

Bruker SMART APEX CCD
 diffractometer
 φ and ω scans
 Absorption correction: none
 14414 measured reflections

4296 independent reflections
 2741 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.058$
 $\theta_{\text{max}} = 27.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.056$
 $wR(F^2) = 0.149$
 $S = 1.01$
 4296 reflections
 209 parameters

H atoms treated by a mixture of
 independent and constrained
 refinement
 $w = 1/[\sigma^2(F_o^2) + (0.0697P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.007$
 $\Delta\rho_{\text{max}} = 0.29 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.31 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1\cdots S2^i$	0.856 (10)	2.692 (19)	3.465 (3)	151 (3)
$N2-H2\cdots S2^{ii}$	0.849 (10)	2.665 (17)	3.450 (3)	154 (3)
$C11-H11A\cdots O3^{iii}$	0.97	2.55	3.264 (4)	131

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

Carbon-bound H atoms were positioned geometrically and refined using a riding model, with $C-H = 0.96 \text{ \AA}$ (methyl) and 0.97 \AA (methylene); $U_{\text{iso}}(\text{H}) = xU_{\text{eq}}(\text{carrier atom})$, where $x = 1.5$ for methyl and 1.2 for methylene. The two H atoms attached to N were located in a difference map and refined freely, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics:

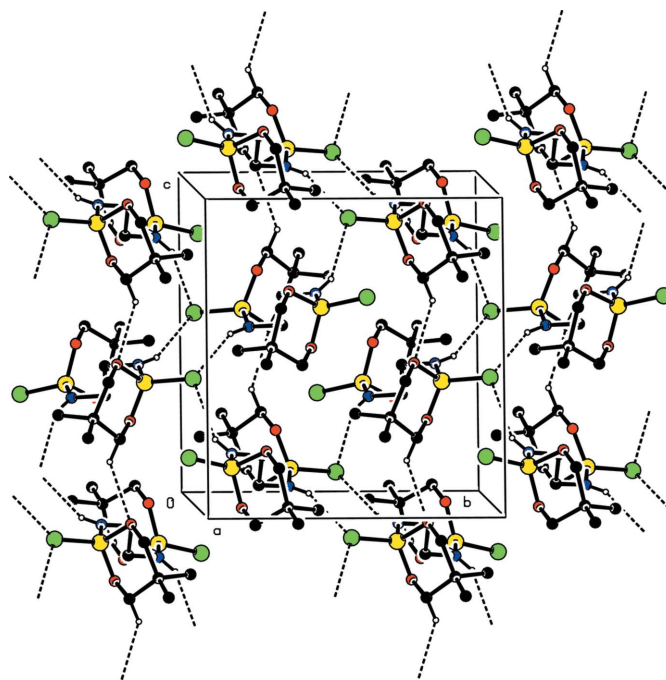


Figure 2

A view of the packing of molecules in the crystal structure. Dashed lines indicate hydrogen bonds. H atoms not involved in hydrogen bonding have been omitted. (colour code: red, yellow, green and black indicate oxygen, phosphorus sulfur and carbon, respectively; open circles represent H atoms).

SHELXTL (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

References

- Bruker (1997). *SMART*. Version 5.054. Bruker AXS Inc., Madison, Wisconsin, USA.
 Bruker (1999). *SAINT*. Version 6.01. Bruker AXS Inc., Madison, Wisconsin, USA.
 Bruker (2001). *SHELXTL*. Version 6.12. Bruker AXS Inc., Madison, Wisconsin, USA.
 Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
 Zheng, H., Liu, Y.-K., Xu, D.-Q. & Xu, Z.-Y. (2006). *Acta Cryst. E62*, o3101–o3102.