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Key indicators

Single-crystal X-ray study
 $T = 298$ K
Mean $\sigma(\text{C}-\text{C}) = 0.008$ Å
 R factor = 0.064
 wR factor = 0.200
Data-to-parameter ratio = 15.0For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.*O,O*-Diethyl phthalimidophosphonothioate
(Ditalimphos)

The crystal structure of *O,O*-diethyl phthalimidophosphonothioate (also known as Ditalimphos, Laptran[®] and Plondrel[®]), $\text{C}_{12}\text{H}_{14}\text{NO}_4\text{PS}$, contains two molecules per asymmetric unit. The ring systems of the two molecules are at a van der Waals distance from each other, are nearly parallel, and are twisted by $\sim 21^\circ$ with respect to each other.

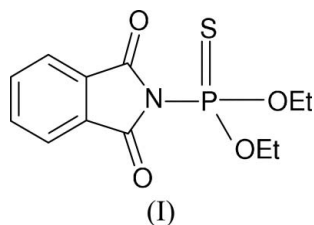
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Comment

As part of an ongoing study of organophosphorus (OP) pesticides (Baughman & Allen, 1995; Baker & Baughman, 1995; Baughman, 1997, and references therein), a determination of the structure of the title antifungal compound (Ditalimphos), (I), was undertaken and the results are presented here. Accurate three-dimensional structure determinations of a series of OP compounds should shed light on any structure–activity relationships.



The π systems of the two molecules present in the asymmetric unit of (I) are in close contact, as the least-squares planes of the approximately parallel ring skeletons (C1/N1/C2–C8) are separated by a distance of about 3.5 Å. As seen in Fig. 1, the thiophosphate groups point in opposite directions, leaving the more electron-deficient N-containing rings stacked with respect to the benzene rings. The distances and angles noted in Table 1 show structural similarities between the two molecules. The $\text{P}=\text{S}$, $\text{P}-\text{OR}$ and $\text{C}=\text{O}$ bond lengths are in general agreement with corresponding bond lengths observed in similar compounds (Baughman & Allen, 1995; Baker & Baughman, 1995; Baughman, 1997). Only one weak intermolecular hydrogen bond involving atoms H4*b* and O2*b* (via an inversion) is noted (Table 2).

The C1/N1/C2–C8 skeletons of the phthalimide rings are planar (r.m.s. deviations of 0.017 Å for both *a* and *b* rings). The planes are at a dihedral angle of 4.8 (2) $^\circ$ and are slightly twisted with respect to each other [$\text{C8a}-\text{C3a}\cdots\text{C3b}-\text{C8b} = 20.9$ (4) $^\circ$]. While the four S1–P1–O–C–C groups are nearly planar (see Table 3), the dihedral angles of the S1–P1–N1 planes to the ring skeletons are similar, but are

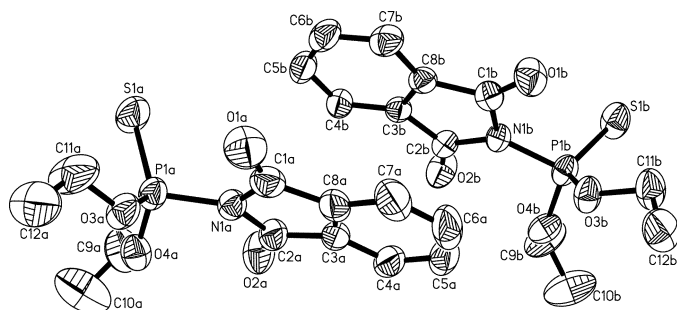


Figure 1
The asymmetric unit of (I), showing the labeling of the non-H atoms. Displacement ellipsoids are drawn at the 30% probability level in order to minimize atom overlap, and H atoms have been omitted.

significantly ($\sim 14\sigma$) different [82.9 (1) and 81.45 (9) $^\circ$ for molecules *a* and *b*, respectively].

Experimental

Crystals of (I) were purchased from Chem Service and were grown by slow evaporation of a solution in ethanol at 298 K. In order to rule out the possibility that the slight disorder in molecule *a* was a result of crystallization conditions, an attempt to minimize the effect was conducted by slow recrystallization from MeOH at 253 K. Of the three crystals analyzed by this procedure, none produced results as good as those reported here (the best of the three crystals obtained from EtOH at 298 K).

Crystal data

$C_{12}H_{14}NO_4PS$	$Z = 4$
$M_r = 299.27$	$D_x = 1.349 \text{ Mg m}^{-3}$
Triclinic, $P\bar{1}$	Mo $K\alpha$ radiation
$a = 8.1696$ (6) \AA	Cell parameters from 100 reflections
$b = 12.4578$ (8) \AA	$\theta = 10.4\text{--}18.3^\circ$
$c = 14.8541$ (9) \AA	$\mu = 0.34 \text{ mm}^{-1}$
$\alpha = 101.277$ (4) $^\circ$	$T = 298$ (2) K
$\beta = 90.134$ (5) $^\circ$	Parallelepiped, colorless
$\gamma = 96.332$ (5) $^\circ$	$0.48 \times 0.48 \times 0.29 \text{ mm}$
$V = 1473.10$ (17) \AA^3	

Data collection

Bruker P4 diffractometer	$R_{\text{int}} = 0.020$
$\omega/2\theta$ scans	$\theta_{\text{max}} = 25.0^\circ$
Absorption correction: integration (XSHELL; Bruker, 1999)	$h = -9 \rightarrow 1$
$T_{\text{min}} = 0.851$, $T_{\text{max}} = 0.916$	$k = -14 \rightarrow 14$
6338 measured reflections	$l = -17 \rightarrow 17$
5158 independent reflections	3 standard reflections
3394 reflections with $I > 2\sigma(I)$	every 100 reflections
	intensity decay: 1.2%

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.1005P)^2 + 0.8864P]$
$R[F^2 > 2\sigma(F^2)] = 0.064$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.200$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.02$	$\Delta\rho_{\text{max}} = 0.37 \text{ e \AA}^{-3}$
5158 reflections	$\Delta\rho_{\text{min}} = -0.32 \text{ e \AA}^{-3}$
343 parameters	
H-atom parameters constrained	

Table 1
Selected geometric parameters (\AA , $^\circ$).

$S1a-P1a$	1.9135 (17)	$S1b-P1b$	1.9116 (16)
$P1a-O3a$	1.559 (3)	$P1b-O3b$	1.557 (3)
$P1a-O4a$	1.545 (4)	$P1b-O4b$	1.553 (3)
$P1a-N1a$	1.707 (3)	$P1b-N1b$	1.705 (3)
$O1a-C1a$	1.194 (6)	$O1b-C1b$	1.199 (5)
$O2a-C2a$	1.189 (6)	$O2b-C2b$	1.193 (5)
$S1a-P1a-O3a$	118.19 (14)	$S1b-P1b-O3b$	118.71 (13)
$S1a-P1a-O4a$	118.08 (14)	$S1b-P1b-O4b$	117.75 (13)
$S1a-P1a-N1a$	114.73 (13)	$S1b-P1b-N1b$	114.52 (12)
$O3a-P1a-O4a$	100.82 (18)	$O3b-P1b-O4b$	100.51 (18)
$O3a-P1a-N1a$	99.79 (17)	$O3b-P1b-N1b$	99.70 (15)
$O4a-P1a-N1a$	102.35 (18)	$O4b-P1b-N1b$	102.80 (16)

Table 2
Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C4b-H4b\cdots O2b^i$	0.93	2.48	3.408 (6)	176

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

Table 3
R.m.s. deviations (\AA) for (I).

Plane	Molecule <i>a</i>	Molecule <i>b</i>
$S1/P1/O3/C11/C12$	0.091	0.054
$S1/P1/O4/C9/C10$	0.213	0.268

Although a number of H atoms were observed in a difference map, methyl H atoms (on C10 and C12) and methylene H atoms (on C9 and C11) were placed in ideal positions and refined as riding. Bond lengths were constrained to 0.93 \AA for aromatic C—H, 0.96 \AA for methyl C—H and 0.97 \AA for methylene C—H, and $U_{\text{iso}}(\text{H})$ were fixed at $1.5U_{\text{eq}}(\text{parent})$ for methyl H atoms and $1.2U_{\text{eq}}(\text{parent})$ for all other H atoms. In the final stages of refinement, nine very small or negative F_o values were deemed to be in severe disagreement with their F_c values and were eliminated from the final refinement.

Data collection: XSCANS (Bruker, 1996); cell refinement: XSCANS; data reduction: XSCANS; program(s) used to solve structure: SHELXS86 (Sheldrick, 1990a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL/PC (Sheldrick, 1990b); software used to prepare material for publication: SHELXTL/PC and SHELXL97.

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