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Key indicators

Single-crystal X-ray study T = 292 K Mean σ (C–C) = 0.004 Å R factor = 0.048 wR factor = 0.161 Data-to-parameter ratio = 14.7

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

5,5-Dimethyl-4-(3-nitrophenyl)-2-oxo-2-(2-pyridyl-amino)-1,3,2-dioxaphosphorinane

In the crystal structure of the title compound, $C_{16}H_{18}N_3O_5P$, molecules are linked by two $N-H\cdots O$ hydrogen bonds, forming rings with an $R_2^2(8)$ motif.

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Comment

The development of intumescent flame-retardant systems (IFR) has become an active research field due to their low smoke and low toxicity characteristics (Leman & Robertson, 1978; Halpen & Mott, 1984; Wolter & Hans, 1985). A number of phosphorus and nitrogen heterocyclic compounds have been shown to have good IFR properties (Jacobson *et al.*, 1991; Rui *et al.*, 1997; Yang *et al.*, 1991) and we report here the molecular structure of one such compound, 5,5-dimethyl-4-(3-nitrophenyl)-2-oxo-2-(2-pyridylamino)-1,3,2-dioxaphosphorinane, (I).



The structure of (I) is shown in Fig.1. The P atom of the oxodioxaphosphorinane ring carries a pyridylamine substituent, with a 3-nitrophenyl substituent at C7 and two methyl groups on C8. The oxaphosphorinane ring adopts a chair conformation. In the crystal structure, molecules form hydrogen bonded dimers linked by $N-H\cdots O$ hydrogenbonded dimers about an inversion centre in an $R_2^2(8)$ motif (Fig. 2).

Experimental

The title compound, (I), was prepared according to the procedure of Maier (1976). Suitable crystals were obtained by vapor diffusion of dioxane into a dimethylformamide solution at room temperature (m.p. 521 K). IR (KBr, $\nu \text{ cm}^{-1}$): 3134, 1596, 1469, 1220, 1045, 1006, 976. ¹H NMR (DMSO-*d*₆): δ 8.35–6.90 (*m*, 8H), 9.21 (*s*, 1H), 5.25–3.95 (*dd*, 3H), 1.15 (*s*, 3H), 0.82 (*s*, 3H). Analysis calculated for C₁₆H₁₈N₃O₅P: C 52.90, H 4.99, P 8.53%; found: C 52.81, H 5.11, P 8.40%.

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Crystal data

 $\begin{array}{l} C_{16}H_{18}N_{3}O_{5}P\\ M_{r}=363.30\\ \text{Triclinic, }P\overline{1}\\ a=8.5644\ (14)\ \text{\AA}\\ b=9.4816\ (16)\ \text{\AA}\\ c=11.7155\ (19)\ \text{\AA}\\ \alpha=79.093\ (3)^{\circ}\\ \beta=73.925\ (3)^{\circ}\\ \gamma=75.318\ (3)^{\circ}\\ V=877.0\ (3)\ \text{\AA}^{3} \end{array}$

Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2000) $T_{\min} = 0.946, T_{\max} = 0.981$ 6266 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.048$ $wR(F^2) = 0.161$ S = 1.093401 reflections 232 parameters

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N2-H2\cdots O5^{i}$	0.86 (1)	1.91 (1)	2.766 (2)	179 (2)
Symmetry code: (i)	$-x \pm 1 - y \pm 2$	_ 7 ⊥ 1		

Z = 2

 $D_x = 1.376 \text{ Mg m}^{-3}$

Cell parameters from 2765

3401 independent reflections

2822 reflections with $I > 2\sigma(I)$

H atoms treated by a mixture of

 $w = 1/[\sigma^2(F_o^2) + (0.1005P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$

independent and constrained

Mo $K\alpha$ radiation

reflections

 $\begin{array}{l} \theta = 2.2 {-} 28.1^{\circ} \\ \mu = 0.19 \ \mathrm{mm}^{-1} \end{array}$

T = 292 (2) K

 $\begin{aligned} R_{\rm int} &= 0.048\\ \theta_{\rm max} &= 26.0^\circ \end{aligned}$

 $h = -9 \rightarrow 10$

 $k = -11 \rightarrow 11$

 $l = -12 \rightarrow 14$

refinement

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

 $\Delta \rho_{\rm max} = 0.24 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\rm min} = -0.48 \text{ e } \text{\AA}^{-3}$

Block, colorless $0.30 \times 0.20 \times 0.10 \text{ mm}$

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

The methyl H atoms were constrained to an ideal geometry, with C-H = 0.96 Å and $U_{iso}(H) = 1.5U_{eq}(C)$, but each group was allowed to rotate freely about its C-C bond. All aromatic H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C-H distances in the range 0.93–0.98 Å and N-H = 0.86 Å, $U_{iso}(H) = 1.2U_{eq}(C,N)$.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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View of (I), showing the labelling of the non-H atoms and 50% probability ellipsoids.



Figure 2

A view of the crystal packing down the *a* axis. Hydrogen bonds are shown as dashed lines. [Symmetry code: (a) 1 - x, 2 - y, 1 - z.]

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