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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=173 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.003 \AA$
$R$ factor $=0.032$
$w R$ factor $=0.091$
Data-to-parameter ratio $=10.4$

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 2-Phenylisophosphindoline-1,3-dione

The title compound, $\mathrm{C}_{14} \mathrm{H}_{9} \mathrm{O}_{2} \mathrm{P}$, displays a near-planar iso-phosphindoline-1,3-dione skeleton with slightly displaced P and O atoms. Weak $\mathrm{C}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonding in the crystal structure results in a three-dimensional network.

## Comment

The title compound, (I), is a rare example of a crystallographically characterized dicarbonylphosphine. The only related compound whose crystal structure has been reported is bis(2,2-dimethylpropionyl)phenylphosphine, $\left.{ }^{t} \mathrm{BuC}(\mathrm{O})\right]_{2} \mathrm{P}-\mathrm{Ph}$, (II) (Becker et al., 1985).

(I)

The isophosphindoline-1,3-dione skeleton in (I) is almost planar, in contrast to compound (II), where rotation around the $\mathrm{P}-\mathrm{C}$ bonds results in an almost orthogonal orientation of the two carbonyl groups with an $\mathrm{O}-\mathrm{C} \cdots \mathrm{C}-\mathrm{O}$ angle of $73.49^{\circ}$ [no standard uncertainty available (Becker et al., 1985)]. In compound (I), the P and O atoms deviate by -0.388 (2), 0.209 (3) and 0.204 (2) $\AA$ from the C1/C3/C3A/C7A plane, most likely because of the steric demand of the phenyl group. In the absence of the phenyl group, as is the case in the isophosphindolyl-1,3-dione anion (Liotta et al., 1984), planarity of the same molecular fragment is observed. The geometry at the P atom is trigonal-pyramidal in compound (I), indicating a stereochemically active electron pair. This is in contrast to the nitrogen analogue of (I) (Magomedova et al., 1981), where the N atom is in a trigonal-planar environment. In the crystal lattice, 2-phenylisophosphindoline-1,3-dione


Figure 1
A view of the title compound, with displacement ellipsoids drawn at the $30 \%$ probability level.

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employs both carbonyl O atoms for $\mathrm{C}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonding (see Table 1), resulting in a three-dimensional network.

## Experimental

The title compound was prepared according to a published procedure (Fenske et al., 1976).

## Crystal data

$\mathrm{C}_{14} \mathrm{H}_{9} \mathrm{O}_{2} \mathrm{P}$
$M_{r}=240.18$
Monoclinic, $P 2_{1} / n$
$a=9.4273(15) \AA$
$b=14.479(2) \AA$
$c=9.4762(15) \AA$
$\beta=117.662(2)^{\circ}$
$V=1145.7(3) \AA^{3}$
$Z=4$
$D_{x}=1.393 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
Cell parameters from 3469 reflections
$\theta=2.5-25.9^{\circ}$
$\mu=0.22 \mathrm{~mm}^{-1}$
$T=173$ (2) K
Plate, yellow
$0.40 \times 0.30 \times 0.05 \mathrm{~mm}$

## Data collection

Bruker SMART 1000/P4
diffractometer
$\omega$ and $\varphi$ scans
Absorption correction: none
5722 measured reflections
1970 independent reflections

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.032$
$w R\left(F^{2}\right)=0.091$
$S=1.07$
1970 reflections
190 parameters
All H -atom parameters refined

Table 1
Hydrogen-bonding geometry $\left(\AA^{\circ},^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :---: | :---: | :---: | :---: | :---: |
| $\mathrm{C} 4-\mathrm{H} 4 \cdots \mathrm{O} 2^{\text {i }}$ | 0.96 (2) | 2.59 (2) | 3.517 (2) | 163.5 (14) |
| $\mathrm{C} 7-\mathrm{H} 7 \cdots \mathrm{O}^{\text {ii }}$ | 0.91 (2) | 2.37 (2) | 3.201 (2) | 150.5 (17) |
| $\mathrm{C} 10-\mathrm{H} 10 \cdots \mathrm{O} 1^{\text {iii }}$ | 0.90 (2) | 2.53 (2) | 3.368 (2) | 155.5 (16) |

Symmetry codes: (i) $1-x,-y,-z$; (ii) $\frac{3}{2}-x, \frac{1}{2}+y, \frac{1}{2}-z$; (iii) $\frac{5}{2}-x, y-\frac{1}{2}, \frac{1}{2}-z$.
H atoms were found in difference Fourier maps and refined with isotropic displacement parameters. The final $\mathrm{C}-\mathrm{H}$ distances are in the range 0.91 (2)-0.96 (2) Å.

Data collection: SMART (Bruker, 1997-1999); cell refinement: SMART; data reduction: SAINT (Bruker, 1997-1999); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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