

2-[(4-*tert*-Butylphenoxy)dichloromethyl]-
phenyl dichlorophosphonateA. G. Pinkus,^{a*}
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Key indicators

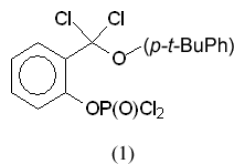
Single-crystal X-ray study
 $T = 273$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.025
 wR factor = 0.069
Data-to-parameter ratio = 26.1For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

The reaction of phosphorus pentachloride with *p-tert*-butylphenyl salicylate yielded the title compound, $\text{C}_{17}\text{H}_{17}\text{Cl}_4\text{O}_3\text{P}$, which was originally thought to contain a P—O—C heterocycle. The true molecular structure has now been established by the determination of its crystal structure.

Comment

It was demonstrated in a previous report (Pinkus *et al.*, 2004) that the reaction product of phosphorus pentachloride with phenyl salicylate is a non-cyclized structure containing a CCl_2 group and a terminal phosphorus oxide rather than a heterocyclic P—O—C structure, as previously believed.

The reaction of phosphorus pentachloride with *p-tert*-butylphenyl salicylate yields a related product, (1), in a similar reaction. The structure of (1) is nearly identical to that of its phenyl-substituted counterpart, with slight differences in its packing due to the increased bulk of the *tert*-butyl substituent.



The molecular structure of (1) (Fig. 1) displays bond lengths and angles that are comparable to other dichlorophosphinic acids and α -dichloroethers.

Experimental

Compound (1) was prepared by dropwise addition of *p-tert*-butylphenyl salicylate (5.41 g, 20 mmol) in dry benzene (20 ml) to a stirred solution of phosphorus pentachloride (4.17 g, 20 mmol) in benzene (25 ml). Removal of the solvent *in vacuo* after 3.5 h of stirring left a yellow oil (9.3 g), which solidified on standing. This solid was then dissolved in hot *n*-hexane and filtered through a sintered glass funnel. On standing, (1) (2.61 g, 29.6%) crystallized out of the solution (m.p. 350.0–350.6 K). Analysis calculated for $\text{C}_{17}\text{H}_{17}\text{Cl}_4\text{O}_3\text{P}$: C 46.19, H 3.88, Cl 32.08%; found: C 45.72, H 3.81, Cl 31.86% (Cl determined by AgNO_3 titration of the hydrolysis product). Diffraction quality crystals of (1) were obtained by dissolving it in hot *n*-hexane, which was allowed to cool slowly.

Crystal data

 $\text{C}_{17}\text{H}_{17}\text{Cl}_4\text{O}_3\text{P}$
 $M_r = 442.08$
Monoclinic, $C2/c$
 $a = 27.166$ (2) Å
 $b = 5.9811$ (5) Å
 $c = 24.158$ (2) Å
 $\beta = 90.944$ (8)°
 $V = 3924.7$ (6) Å³
 $Z = 8$ $D_x = 1.496$ Mg m⁻³
Mo $K\alpha$ radiation
Cell parameters from 8132
reflections
 $\theta = 2.2$ – 30.5 °
 $\mu = 0.70$ mm⁻¹
 $T = 273$ (2) K
Block, colorless
 $0.30 \times 0.29 \times 0.23$ mm

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Data collection

Bruker X8 APEX CCD area
detector diffractometer
 φ and ω scans
Absorption correction: multi-scan
(*SADABS*; Bruker, 1996)
 $T_{\min} = 0.818$, $T_{\max} = 0.859$
60 962 measured reflections

5988 independent reflections
5358 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.031$
 $\theta_{\text{max}} = 30.5^\circ$
 $h = -38 \rightarrow 38$
 $k = -8 \rightarrow 8$
 $l = -34 \rightarrow 34$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.025$
 $wR(F^2) = 0.069$
 $S = 1.07$
5988 reflections
229 parameters
H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0327P)^2 + 3.2995P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.56 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.42 \text{ e } \text{\AA}^{-3}$

Table 1

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

C12–P1	1.9784 (4)	P1–O1	1.5768 (8)
C11–P1	1.9880 (4)	O3–C1	1.376 (1)
P1–O2	1.4577 (9)	O3–C8	1.416 (1)
C1–O3–C8		120.05 (8)	

H atoms were included in calculated positions ($\text{C–H} = 0.93 \text{ \AA}$) and refined as riding; isotropic displacement parameters were fixed [$U_{\text{iso}}(\text{H}) = 1.2U_{\text{iso}}(\text{C})$].

Data collection: *APEX2* (Bruker, 2003); cell refinement: *APEX2*; data reduction: *SAINT-Plus* (Bruker, 2003); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 2000); software used to prepare material for publication: *SHELXTL*.

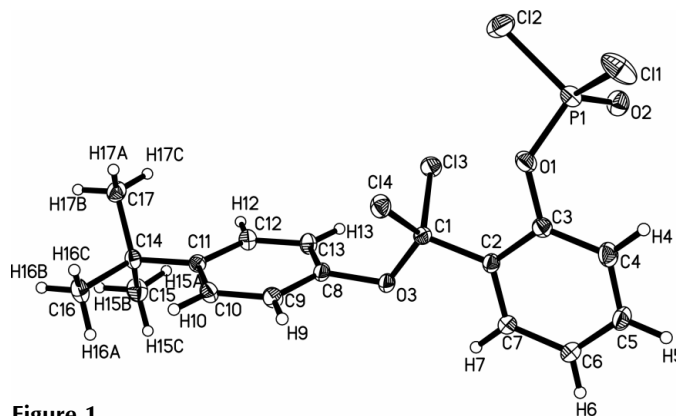


Figure 1

Molecular structure of (1), with displacement ellipsoids drawn at the 50% probability level.

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