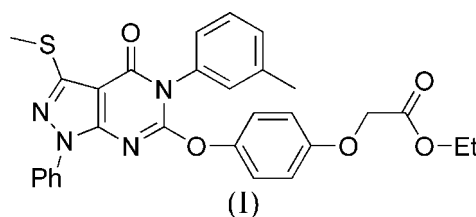


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Key indicators

Single-crystal X-ray study
T = 292 K
Mean $\sigma(\text{C}-\text{C}) = 0.008 \text{ \AA}$
R factor = 0.063
wR factor = 0.185
Data-to-parameter ratio = 15.2For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.Ethyl {4-[5-(3-methylphenyl)-3-methylsulfanyl-4-oxo-1-phenylpyrazolo[3,4-*d*]pyrimidin-6-yloxy]-phenoxy}acetateThe title compound, $\text{C}_{29}\text{H}_{26}\text{N}_4\text{O}_5\text{S}$, is based on an almost planar pyrazolo[3,4-*d*]pyrimidin-4-one core. Molecules are packed through weak intermolecular $\text{C}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\text{N}$ interactions.Received 13 October 2006
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Comment

Pyrazolo[3,4-*d*]pyrimidin-4-one derivatives exhibit a wide spectrum of biological activity, including antibacterial, anti-phlogistic and antitumour properties (Ali *et al.*, 2001; Armstrong *et al.*, 2000; EI-Bendary & Badria, 2000; Tetsuya *et al.*, 1996). The title compound, (I), may then be used as a precursor for obtaining new bioactive molecules. In this paper we present the X-ray crystallographic analysis of this compound.

As shown in Fig. 1, ring atoms in the pyrazolo[3,4-*d*]pyrimidin-4-one group form an essentially planar system. The $\text{C}7=\text{N}2$, $\text{C}8=\text{C}9$ and $\text{C}12=\text{N}4$ bond lengths of 1.313 (5), 1.374 (5) and 1.284 (5) Å, respectively, are longer than those of typical $\text{C}=\text{N}$ (1.28 Å; Sasada, 1984; Chen & Jin, 2002) and $\text{C}=\text{C}$ bonds (1.34 Å). In contrast, the single bond lengths $\text{C}9-\text{N}1$, $\text{C}7-\text{C}8$, $\text{C}8-\text{C}11$, $\text{C}12-\text{N}3$, and $\text{C}9-\text{N}4$, in the range 1.345 (5)–1.433 (5) Å, are significantly shorter than typical $\text{C}sp^2-\text{N}$ (1.426 Å) and $\text{C}-\text{C}$ (1.53 Å) bond lengths, reflecting a degree of delocalization in the pyrazolo[3,4-*d*]pyrimidin-4-one system.

Weak intermolecular $\text{C}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\text{N}$ hydrogen bonds are present in the crystal packing (Table 1 and Fig. 2), as well as $\pi-\pi$ and $\text{C}-\text{H}\cdots\pi$ interactions. Thus, the dihedral angle between five-membered rings defined by atoms $\text{N}1/\text{N}2/\text{C}7/\text{C}8/\text{C}9$ and the neighbouring symmetry-related pyrazole ring (symmetry code: $1 - y, x, \frac{1}{4} + z$) is 4.77 (1)°, and the distance between the corresponding ring centroids is 3.775 (2) Å.

Experimental

To a solution of 4-(ethoxycarbonyl)-3-(methylsulfanyl)-1-phenyl-1*H*-pyrazolo-5-yl iminophosphorane (2 mmol), prepared according to the reported procedure (Molina *et al.*, 1998), in dry dichloromethane

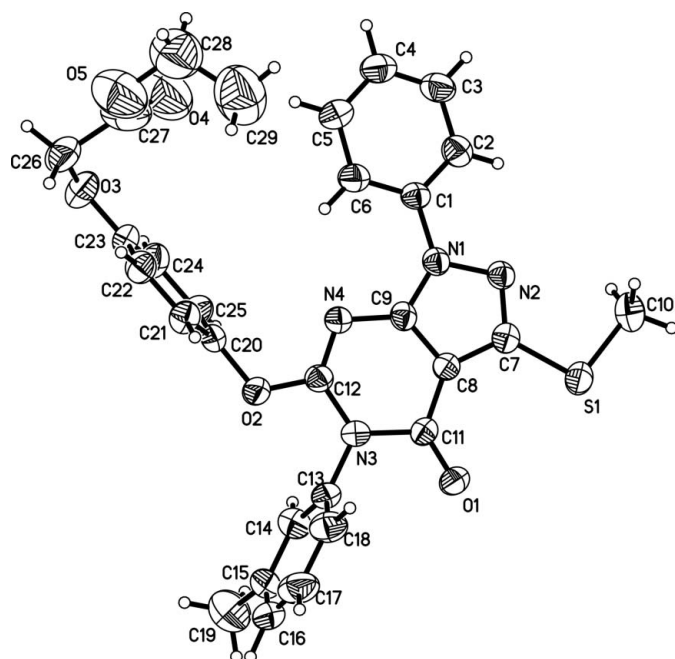


Figure 1
The molecular structure of (I), showing the atom-labelling scheme, and with displacement ellipsoids at the 30% probability level.

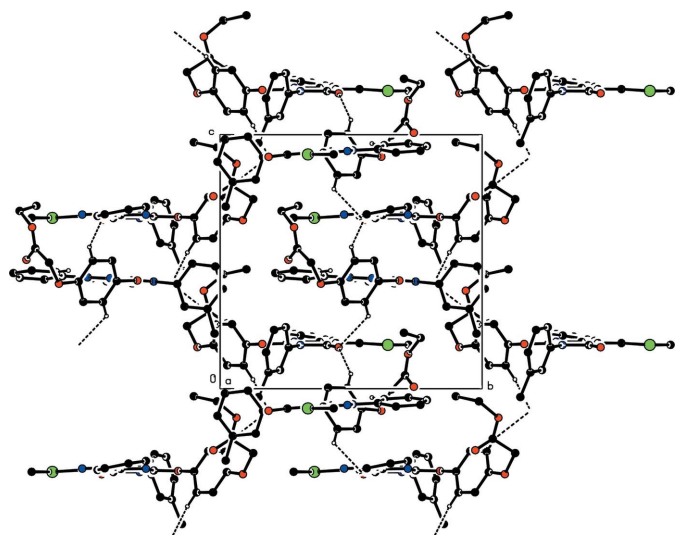


Figure 2
The packing of (I), viewed along [100]. Weak hydrogen bonds are indicated by dashed lines.

(25 ml) was added 3-methylphenyl isocyanate (2 mmol) under N_2 at room temperature. After the reaction mixture had been stirred for 2–5 h, the solvent was removed under reduced pressure, and then anhydrous acetonitrile (25 ml), 2-(4-hydroxyphenoxy)carboxylate (2.0 mmol) (Liu *et al.*, 2005) and anhydrous potassium carbonate (0.05 g) were added to the mixture. After refluxing for 5 h, the mixture was filtered and concentrated under reduced pressure. The resulting residue was recrystallized from ethanol to give (I) in 82% yield. Crystals suitable for X-ray diffraction were grown from $CHCl_3$ at 293 K.

Crystal data

$C_{29}H_{26}N_4O_5S$
 $M_r = 542.60$
 Tetragonal, $P4_1$
 $a = 14.1908$ (16) Å
 $c = 13.760$ (3) Å
 $V = 2771.0$ (8) Å³
 $Z = 4$

$D_x = 1.301$ Mg m⁻³
 Mo $K\alpha$ radiation
 $\mu = 0.16$ mm⁻¹
 $T = 292$ (2) K
 Plate, colourless
 $0.30 \times 0.20 \times 0.04$ mm

Data collection

Bruker SMART APEX CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 2002)
 $T_{min} = 0.953$, $T_{max} = 0.987$

27946 measured reflections
 5408 independent reflections
 3258 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.131$
 $\theta_{max} = 26.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.063$
 $wR(F^2) = 0.185$
 $S = 0.95$
 5408 reflections
 356 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.12P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{max} < 0.001$
 $\Delta\rho_{max} = 0.58$ e Å⁻³
 $\Delta\rho_{min} = -0.31$ e Å⁻³
 Absolute structure: Flack (1983),
 2572 Friedel pairs
 Flack parameter: -0.11 (13)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$C22-H22 \cdots O1^i$	0.93	2.45	3.275 (6)	148
$C25-H25 \cdots O1^{ii}$	0.93	2.49	3.141 (5)	127
$C6-H6 \cdots N4$	0.93	2.32	2.969 (6)	126

Symmetry codes: (i) $-y + 1, x - 1, z + \frac{1}{4}$; (ii) $y, -x + 1, z - \frac{1}{4}$.

H atoms were included in calculated positions, with C–H distances constrained to 0.93 (aromatic CH), 0.96 (methyl CH_3) and 0.97 Å (methylene CH_2). Methyl groups were considered as rigid groups but were allowed to rotate freely about their C–C bonds. Isotropic displacement parameters for H atoms were fixed at $1.5U_{eq}$ (carrier atom) for methyl H atoms and $1.2U_{eq}$ (carrier atom) for other H atoms. Owing to unresolved disorder in the ethyl ester region, atoms C27, C28, C29, O4 and O5 were restrained so that their U^{ij} components approximated to isotropic behaviour.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2001); 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, 2001); software used to prepare material for publication: SHELXTL.

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