

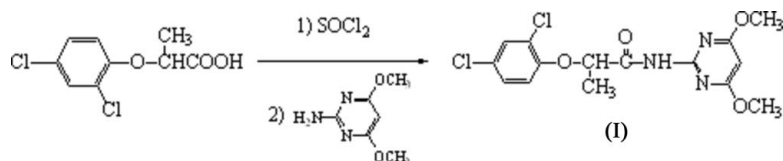
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## Key indicators

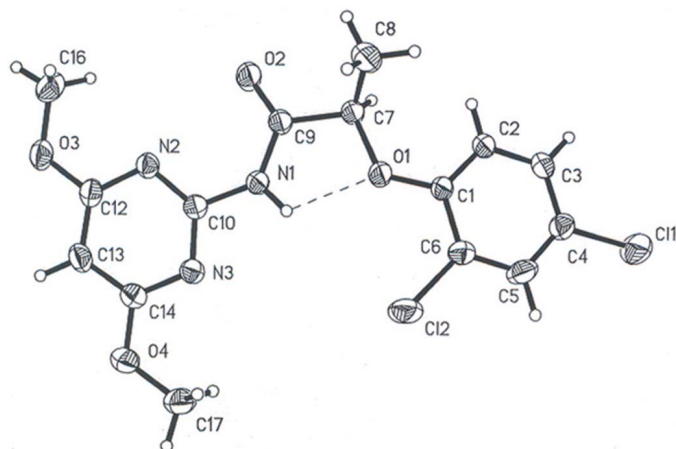
Single-crystal X-ray study  
 $T = 298\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$   
 $R$  factor = 0.057  
 $wR$  factor = 0.173  
Data-to-parameter ratio = 13.6For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.2-(2,4-Dichlorophenoxy)-*N*-(4,6-dimethoxy-  
pyrimidin-2-yl)propionamideThe title compound,  $\text{C}_{15}\text{H}_{15}\text{Cl}_2\text{N}_3\text{O}_4$ , is an amide herbicide  
with a pyrimidine ring attached to the N atom of the CONH  
group. The crystal structure determination reveals that there is  
an intramolecular hydrogen bond, forming a five-membered  
ring.

## Comment

Some amide compounds show high biological herbicidal  
activities with low toxicity (Katsushi *et al.*, 1996; Kenji *et al.*,  
1992; Nobuyuki *et al.*, 1990; Michaely & Knudsen, 1986).  
Investigations using amides as herbicides have become the  
subject of intensive research and many novel structural  
phenoxyalkanoic acid amide herbicides have appeared in the  
literature (Whang *et al.*, 2002, 2003; Yuji *et al.*, 2000; Keiji *et al.*,  
1990; Foerster *et al.*, 1985). Although some of the phenoxy-  
alkanoic acid amides have been described, so far, relatively  
few reports on the crystal structures of amides with a pyri-  
midine ring are available (Tetsuo *et al.*, 1987). We report here  
the synthesis and crystal structure of 2-(2,4-dichlorophenoxy)-  
*N*-(4,6-dimethoxypyrimidin-2-yl)propionamide, (I). The key  
feature of this amide herbicide is that the 2,4-dichloro-  
phenoxypropionyl group is connected to a pyrimidine ring,  
substituted in both *meta* positions, by an amide link, which  
might provide an opportunity for the study of cooperative  
effects between the two types of biologically active groups.The molecular structure of the title compound is shown in  
Fig. 1. An intramolecular hydrogen bond ( $\text{N1}-\text{H1}\cdots\text{O1}$ )  
forms a five membered ring (Table 2).

## Experimental

Under a nitrogen atmosphere, a stirred solution of 2,4-dichloro-  
phenoxypropionic acid (0.50 g, 2.14 mmol) in  $\text{SOCl}_2$  (5 ml) was  
refluxed for 4 h. After removing the  $\text{SOCl}_2$ , to the resulting acid  
chloride was added a solution of 4,6-dimethoxy-2-aminopyrimidine  
(0.33 g, 2.14 mmol) and triethylamine (0.22 g, 2.14 mmol) in dry  
 $\text{CH}_2\text{Cl}_2$  (5 ml) at 273 K over 20 min. The mixture was refluxed and  
stirred for another 2 h. After evaporation of most of the solvent,  
the residue was cooled to room temperature and water (5 ml) was  
added to quench the reaction. The residue was repeatedly extracted  
with 50 ml of diethyl ether. The combined organic layer was washed  
with water and brine, and then dried over  $\text{Na}_2\text{SO}_4$ . After evaporation ofReceived 20 December 2005  
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**Figure 1**

The structure of the title compound, showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. The dashed line represents the hydrogen bond.

solvent, the residue was further purified by column chromatography on silica gel (hexane–ethyl acetate 2:1) to give a white crystalline solid in 65% isolated yield. Crystals suitable for single-crystal X-ray diffraction were obtained by cooling the hot mixture solution of ethyl acetate–hexane (1:1 *v/v*) (yield: 65%; m.p. 371–373 K). <sup>1</sup>H NMR (DMSO-*d*<sub>6</sub>, 400 MHz): δ 10.71 (*s*, 1H, NH), 7.61–6.96 (*m*, 3H, Ph–H), 5.97 (*s*, 1H, py–H), 5.39–5.38 (*q*, 1H, CHCH<sub>3</sub>), 3.87 (*s*, 6H, OCH<sub>3</sub>), 1.59–1.58 (*d*, 3H, CHCH<sub>3</sub>); IR (KBr): 811, 1196, 1719, 3391 cm<sup>-1</sup>; MS(EI) (70 eV) *m/z* (%): 373 (3.29) [*M*+2]<sup>+</sup>, 371 (3.11) [*M*]<sup>+</sup>, 210 (100), 155 (39.33); Analysis calculated for C<sub>15</sub>H<sub>15</sub>Cl<sub>2</sub>N<sub>3</sub>O<sub>4</sub>: C 48.40, H 4.06, N 11.29%; found: C 48.51, H 4.08, N 11.28%.

#### Crystal data

C<sub>15</sub>H<sub>15</sub>Cl<sub>2</sub>N<sub>3</sub>O<sub>4</sub>  
*M<sub>r</sub>* = 372.20  
 Triclinic, *P* $\bar{1}$   
*a* = 8.345 (2) Å  
*b* = 9.944 (4) Å  
*c* = 11.779 (3) Å  
 $\alpha$  = 84.580 (7)°  
 $\beta$  = 71.698 (5)°  
 $\gamma$  = 70.013 (4)°  
*V* = 872.0 (5) Å<sup>3</sup>

*Z* = 2  
*D<sub>x</sub>* = 1.421 Mg m<sup>-3</sup>  
 Mo *K*α radiation  
 Cell parameters from 3006 reflections  
 $\theta$  = 2.0–25.0°  
 $\mu$  = 0.40 mm<sup>-1</sup>  
*T* = 298 (2) K  
 Block, colorless  
 0.35 × 0.10 × 0.10 mm

#### Data collection

Bruker SMART CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Bruker, 1998)  
*T<sub>min</sub>* = 0.874, *T<sub>max</sub>* = 0.962  
 3645 measured reflections

3006 independent reflections  
 2150 reflections with *I* > 2σ(*I*)  
*R<sub>int</sub>* = 0.021  
 $\theta_{\max}$  = 25.0°  
*h* = -7 → 9  
*k* = -11 → 11  
*l* = -13 → 13

#### Refinement

Refinement on *F*<sup>2</sup>  
*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.057  
*wR* (*F*<sup>2</sup>) = 0.173  
*S* = 0.98  
 3006 reflections  
 221 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0917P)^2 + 0.5362P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} < 0.001$   
 $\Delta\rho_{\max} = 0.48 \text{ e \AA}^{-3}$   
 $\Delta\rho_{\min} = -0.48 \text{ e \AA}^{-3}$   
 Extinction correction: SHELXL97  
 Extinction coefficient: 0.009 (1)

**Table 1**

Selected geometric parameters (Å, °).

C1–C4	1.740 (3)	O1–C7	1.439 (3)
C2–C6	1.735 (3)	O2–C9	1.206 (4)
N1–C9	1.353 (4)	O3–C16	1.425 (5)
N1–C10	1.395 (4)	O4–C17	1.432 (4)
C9–N1–C10	129.8 (3)	O2–C9–N1	126.0 (3)
C1–O1–C7	119.2 (2)	O2–C9–C7	118.6 (3)
O1–C7–C9	107.8 (2)	N1–C9–C7	115.4 (3)

**Table 2**

Hydrogen-bond geometry (Å, °).

<i>D</i> –H··· <i>A</i>	<i>D</i> –H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> –H··· <i>A</i>
N1–H1···O1	0.86	2.07	2.551 (3)	115

The H atoms were positioned geometrically (C–H = 0.93, 0.96 or 0.97 Å and N–H = 0.86 Å) and refined using the riding-model approximation, with *U*<sub>iso</sub>(H) = 1.2*U*<sub>eq</sub>(C,N).

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); 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, 1998); software used to prepare material for publication: SHELXTL.

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