

1-[6-(4-Chlorophenyl)-1-[(6-chloropyridin-3-yl)-methyl]-2-[(6-chloropyridin-3-yl)methylsulfanyl]-4-methyl-1,6-dihydropyrimidin-5-yl]ethanone

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Key indicators

Single-crystal X-ray study
 $T = 298\text{ K}$
 Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$
 R factor = 0.050
 wR factor = 0.133
 Data-to-parameter ratio = 17.0

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

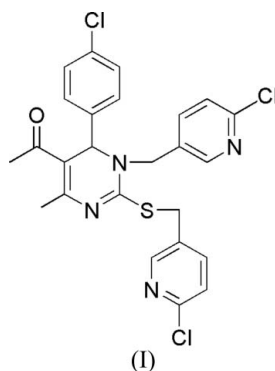
In the title compound, $\text{C}_{25}\text{H}_{21}\text{Cl}_3\text{N}_4\text{OS}$, molecules are linked into centrosymmetric pairs by $\text{C}-\text{H}\cdots\text{O}$ interactions. $\text{C}-\text{H}\cdots\text{Cl}$ interactions link these pairs into a three-dimensional network.

Received 24 March 2007

Accepted 9 April 2007

Comment

Biginelli dihydropyrimidines and their derivatives have attracted interest owing to their wide range of therapeutical and pharmacological properties, such as antiviral, antitumor, antibacterial and anti-inflammatory properties (Kappe, 1993).



The title compound, (I) (Fig. 1), was synthesized by introducing chloropyridine rings into a Biginelli dihydropyrimidine molecular framework. In the crystal structure, intermolecular $\text{C5}-\text{H5}\cdots\text{O1}^i$ and $\text{C25}-\text{H25}\cdots\text{O1}^i$ [symmetry code: (i) $-x, -y, -z$] hydrogen bonds link molecules into centrosymmetric pairs (Fig. 2 and Table 1). These pairs are linked into a three-dimensional network by $\text{C17}-\text{H17}\cdots\text{Cl3}^{ii}$ interactions [symmetry code: (ii) $-x + 1, -y, -z$] (Fig. 2 and Table 1).

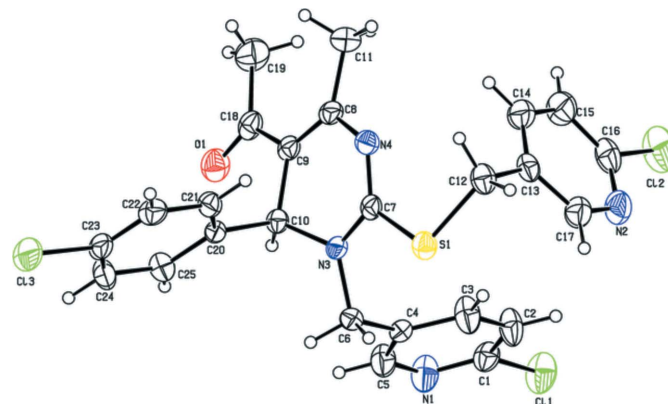


Figure 1

The molecular structure of (I), showing displacement ellipsoids at the 50% probability level for non-H atoms.

Experimental

A solution of 1-[4-(4-chlorophenyl)-6-methyl-2-thioxo-1,2,3,4-tetrahydropyrimidin-5-yl]ethanone (2 mmol), 2-chloro-5-chloromethylpyridine (4 mmol) and K_2CO_3 (4 mmol) in anhydrous dimethylformamide (10 ml) was stirred vigorously at room temperature until the reaction was complete (as monitored by thin-layer chromatography). The solid residue was filtered off and the filtrate was concentrated under vacuum then purified by column chromatography on silica gel using (2:1 v/v) petroleum ether/ethyl acetate as the eluant. Evaporation of the solvent gave a green solid (yield 90%, m.p. 407–408 K). Light-yellow crystals used for X-ray analysis were grown from dichloromethane/hexane (1:1 v/v).

Crystal data

$C_{25}H_{21}Cl_3N_4OS$	$\gamma = 116.332 (2)^\circ$
$M_r = 531.87$	$V = 1218.1 (2) \text{ \AA}^3$
Triclinic, $P\bar{1}$	$Z = 2$
$a = 10.2887 (11) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 11.1487 (12) \text{ \AA}$	$\mu = 0.49 \text{ mm}^{-1}$
$c = 12.6386 (13) \text{ \AA}$	$T = 298 (2) \text{ K}$
$\alpha = 104.740 (2)^\circ$	$0.20 \times 0.15 \times 0.10 \text{ mm}$
$\beta = 95.725 (2)^\circ$	

Data collection

Bruker SMART APEX CCD diffractometer	12693 measured reflections
Absorption correction: multi-scan (SADABS; Bruker, 2000)	5262 independent reflections
$T_{\min} = 0.909$, $T_{\max} = 0.953$	3900 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.052$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.050$	309 parameters
$wR(F^2) = 0.133$	H-atom parameters constrained
$S = 1.03$	$\Delta\rho_{\text{max}} = 0.53 \text{ e \AA}^{-3}$
5262 reflections	$\Delta\rho_{\text{min}} = -0.38 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C5-H5\cdots O1^i$	0.93	2.42	3.326 (3)	165
$C25-H25\cdots O1^i$	0.93	2.55	3.348 (3)	144
$C17-H17\cdots Cl3^{ii}$	0.93	2.80	3.564 (3)	140

Symmetry codes: (i) $-x, -y, -z$; (ii) $-x+1, -y, -z$.

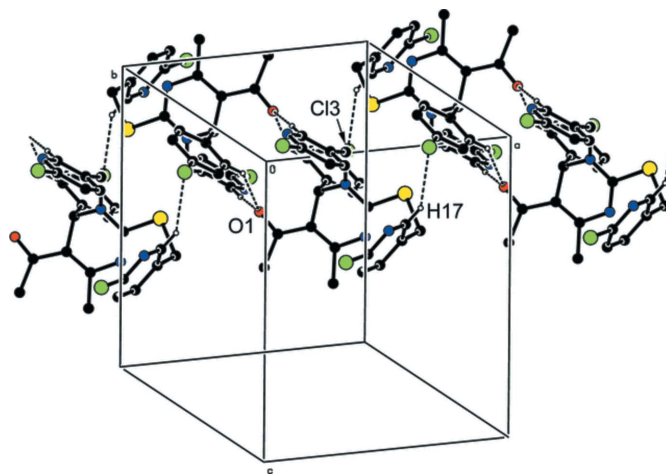


Figure 2

Part of the crystal packing of (I), showing molecules linked into pairs by C—H \cdots O interactions (dashed lines). The pairs are linked further by C—H \cdots Cl interactions (dashed lines). H atoms not involved in these interactions have been omitted.

H atoms were placed in calculated positions with C—H = 0.93–0.98 \AA and refined using a riding-model with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$, or $1.5U_{\text{eq}}(\text{C})$ for the methyl groups. The methyl groups were allowed to rotate about their local threefold axes.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINTE* (Bruker, 2000); data reduction: *SAINTE*; 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*.

The authors are grateful to the Natural Science Foundation of China (grant No. 20302002) for financial support.

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