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Key indicators

Single-crystal X-ray study T = 293 K Mean $\sigma(C-C) = 0.006 \text{ Å}$ R factor = 0.059 wR factor = 0.179 Data-to-parameter ratio = 14.5

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

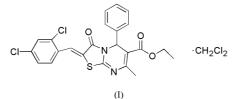
Ethyl 2-(2,4-dichlorobenzylidene)-7methyl-3-oxo-5-phenyl-2,3-dihydro-5Hthiazolo[3,2-a]pyrimidine-6-carboxylate dichloromethane solvate

The title compound, C23H18Cl2N2O3S·CH2Cl2, was synthesized by heating ethyl 2-mercapto-4-methyl-6-phenyl-1,6dihydropyrimidine-5-carboxylate, ethyl chloroacetate and 2,4-dichlorobenzaldehyde in ethanol. In the molecule, the nearly planar thiazole ring is fused with a dihydropyrimidine ring in a boat conformation.

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Comment

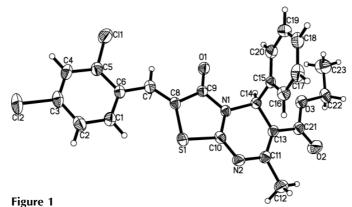
1,4-Dihydropyrimidines show a very similar pharmacological profile to classical dihydropyridine calcium channel modulators (Lu et al., 2002). We report here the synthesis and structure of the product of a dihydropyrimidine fused catalysis, namely ethyl 2-(2,4-dichlorobenzylidene)-7-methyl-3-oxo-5phenyl-2,3-dihydro-5*H*-thiazolo[3,2-*a*]pyrimidine-6-carboxylate dichloromethane solvate, (I). The molecular structure of (I) is illustrated in Fig. 1.



In the molecule, the thiazole ring is fused with a dihydropyrimidine ring in a boat conformation. The thiazoline ring (C8/C9/C10/N1/S1) is essentially planar, with a mean deviation of 0.006 (2) Å. The dihedral angle between the C8/C9/ C10/N1/S1 plane and the C1–C6 benzene ring is $5.3 (2)^{\circ}$, and that between the C8/C9/C10/N1/S1 plane and the C15-C20 phenyl ring is $84.9(3)^{\circ}$.

Experimental

A mixture of 2-mercapto-4-methyl-6-phenyl-1,6-dihydropyrimidine-5-carboxylic acid ethyl ester (0.02 mol), ethyl chloroacetate



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The molecular structure of (I), drawn with 30% probability ellipsoids.

(0.02 mol) and pyridine (0.02 mol) was stirred under reflux in ethanol (40 ml) for 4 h. 2,4-Dichlorobenzaldehyde (0.02 mol) and piperidine (0.02 mol) were added and the mixture was refluxed for 4 h. After cooling and filtration, the title compound was recrystallized from acetic acid. ¹H NMR (p.p.m.): 1.19 (m, 3H, CH₃), 2.52 (s, 3H, CH₃), 4.12 (m, 2H, CH₂), 6.20 (s, 1H, CH), 7.27–7.47 (m, 8H, ArH), 7.74 (s, 1H,CH). M.p. 455–456 K. A portion (20 mg) of (I) was dissolved in dichloromethane (15 ml); the solution was kept at room temperature for 8 d and natural evaporation gave colorless single crystals of (I), suitable for X-ray analysis.

Crystal data

 $\begin{array}{l} C_{23}H_{18}Cl_2N_2O_3S\cdot CH_2Cl_2\\ M_r = 558.28\\ Triclinic, \ \Bar{PI}\\ a = 9.747\ (4)\ \Bar{A}\\ b = 11.291\ (4)\ \Bar{A}\\ c = 12.297\ (5)\ \Bar{A}\\ \alpha = 84.546\ (7)^\circ\\ \beta = 74.655\ (6)^\circ\\ \gamma = 78.378\ (6)^\circ\\ V = 127.1\ (9)\ \Bar{A}^3 \end{array}$

Z = 2 $D_x = 1.452 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 1016 reflections $\theta = 2.2-26.1^{\circ}$ $\mu = 0.58 \text{ mm}^{-1}$ T = 293 (2) KBlock, colorless $0.22 \times 0.16 \times 0.12 \text{ mm}$

4478 independent reflections 2711 reflections with $I > 2\sigma(I)$

 $R_{\rm int}=0.032$

 $\theta_{\rm max} = 25.0^{\circ}$

 $h = -11 \rightarrow 11$

 $k = -13 \rightarrow 8$

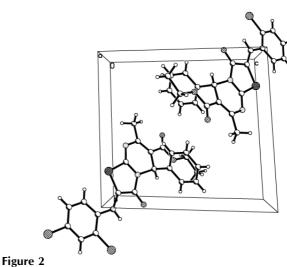
Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 1997) $T_{min} = 0.777, T_{max} = 0.933$ 6583 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.059$ $wR(F^2) = 0.180$ S = 1.054478 reflections 309 parameters H-atom parameters constrained
$$\begin{split} l &= -14 \rightarrow 14 \\ w &= 1/[\sigma^2(F_o^2) + (0.0864P)^2 \\ &+ 0.2487P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &< 0.001 \\ \Delta\rho_{\text{max}} &= 0.50 \text{ e } \text{\AA}_{-3}^{-3} \end{split}$$

 $\Delta \rho_{\rm min} = -0.46 \ {\rm e} \ {\rm \AA}^{-3}$



The crystal structure of (I), viewed along the a axis.

H atoms were positioned geometrically (C-H = 0.93–0.98 Å) and treated as riding [U_{iso} (H) = 1.2 U_{eq} (C)].

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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