

Zhong-Zhen Zhou, Wei Huang,
Pei-Liang Zhao, Qiong Chen and
Guang-Fu Yang*Key Laboratory of Pesticide and Chemical
Biology of Ministry of Education, College of
Chemistry, Central China Normal University,
Wuhan 430079, People's Republic of ChinaCorrespondence e-mail:
gfyang@mail.ccnu.edu.cn

Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$
 R factor = 0.044
 wR factor = 0.134
Data-to-parameter ratio = 16.5For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.3-[3-(4-Chlorophenyl)-4-oxothiazolidin-2-yl]-
6-methyl-4*H*-benzopyran-4-oneThe molecular structure of the title compound,
 $\text{C}_{19}\text{H}_{14}\text{ClNO}_3\text{S}$, contains a 4-oxothiazolidine ring in a near
planar geometry.

Received 22 March 2005

Accepted 17 June 2005

Online 24 June 2005

Comment

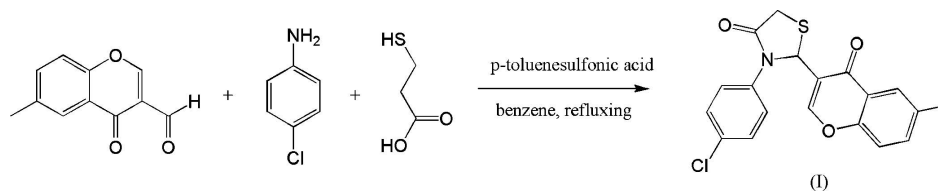
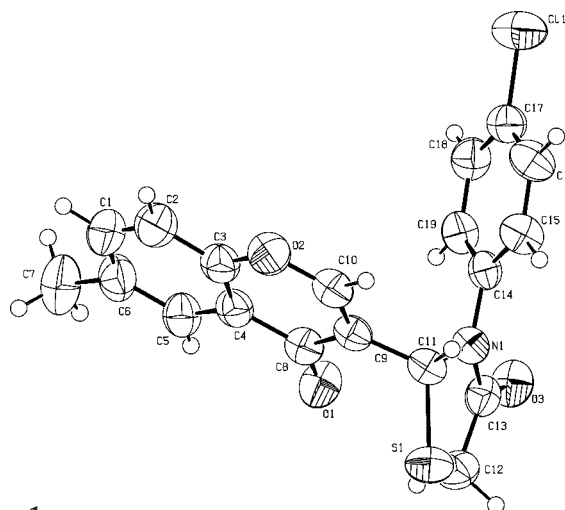
3-Substituted chromones are important because of their
widespread occurrence in nature and their interesting biologi-
cal activities. Meanwhile, thiazolidinones have been
reported to possess a wide range of biological activities,
including antifungal, antibacterial, antihistaminic, anti-
microbial and anti-inflammatory activities. We are interested
in heterocyclic compounds with a combination of thia-
zolidinonyl and chromonyl groups, in the hope of discovering
novel lead structures for the development of antifungal and
antimicrobial agents. The title compound, (I), is readily
synthesized by condensing 6-methyl-4-oxo-4*H*-chromene-3-
carbaldehyde with *p*-chloroaniline and mercaptoacetic acid
(Fitton *et al.*, 1984).The crystal structure (Fig. 1) shows that the benzene ring of
the 4-chlorophenyl substituent is not coplanar with the thia-
zolidine ring, and the thiazolidine ring is also not coplanar

Figure 1
View of the molecule of (I), showing the atom-labeling scheme and 50%
probability displacement ellipsoids.

with the pyran ring [the dihedral angles between the thiazolidine ring and pyran ring is 85.69 (4)^o] so they cannot form a conjugated system in the solid state (Table 1).

Experimental

A mixture of 6-methyl-4-oxo-4*H*-chromene-3-carbaldehyde (5 mmol), 4-chlorobenzenamine (5 mmol) and *p*-toluenesulfonic acid (10 mg, 0.058 mmol) was refluxed and stirred in benzene (40 ml) for 1 h, and then mercaptoacetic acid (25 mmol) was added. The reactant was refluxed for another 8 h. The solvent was removed *in vacuo*. The resulting residue was washed with ethanol to afford the crude product, which was then recrystallized from ethanol to give colorless crystals. ¹H NMR (400 MHz, CDCl₃): δ 2.45 (*s*, 3H), 3.77 (*d*, *J* = 15.6 Hz, 1H), 4.11 (*dd*, *J* = 15.6 Hz, *J* = 1.4 Hz, 1H), 6.08 (*s*, 1H), 7.25–7.32 (*m*, 5H), 7.47 (*dd*, *J* = 8.6 Hz, *J* = 1.8 Hz, 1H), 7.74 (*s*, 1H), 7.99 (*s*, 1H); MS (EI, *m/z*): 373 (*M*⁺ + 1), 372 (*M*⁺); elemental analysis calculated for C₁₉H₁₄ClNO₃S: C 61.37, H 3.79, N 3.77%; found: C 61.46, H 3.78, N 3.71%.

Crystal data

C ₁₉ H ₁₄ ClNO ₃ S	<i>D</i> _x = 1.429 Mg m ⁻³
<i>M</i> _r = 371.82	Mo <i>K</i> α radiation
Monoclinic, <i>P</i> 2 ₁ / <i>n</i>	Cell parameters from 3801 reflections
<i>a</i> = 11.1830 (9) Å	<i>θ</i> = 2.4–27.7°
<i>b</i> = 13.9851 (10) Å	<i>μ</i> = 0.36 mm ⁻¹
<i>c</i> = 12.3419 (9) Å	<i>T</i> = 293 (2) K
<i>β</i> = 116.445 (1)°	Block, colorless
<i>V</i> = 1728.2 (2) Å ³	0.40 × 0.38 × 0.34 mm
<i>Z</i> = 4	

Data collection

Bruker SMART CCD area-detector diffractometer	3747 independent reflections
<i>φ</i> and <i>ω</i> scans	2974 reflections with <i>I</i> > 2σ(<i>I</i>)
Absorption correction: multi-scan (SADABS; Sheldrick, 1997)	<i>R</i> _{int} = 0.018
<i>T</i> _{min} = 0.870, <i>T</i> _{max} = 0.888	<i>θ</i> _{max} = 27.0°
9946 measured reflections	<i>h</i> = -13 → 14
	<i>k</i> = -17 → 13
	<i>l</i> = -14 → 15

Refinement

Refinement on <i>F</i> ²	$w = 1/[\sigma^2(F_o^2) + (0.0722P)^2 + 0.3678P]$
$R[F^2 > 2\sigma(F^2)] = 0.044$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.134$	(<i>Δ</i> /σ) _{max} = 0.001
<i>S</i> = 1.05	<i>Δρ</i> _{max} = 0.31 e Å ⁻³
3747 reflections	<i>Δρ</i> _{min} = -0.20 e Å ⁻³
227 parameters	
H-atom parameters constrained	

Table 1

Selected geometric parameters (Å, °).

C3–O2	1.382 (3)	C11–N1	1.473 (2)
C8–O1	1.225 (2)	C11–S1	1.8197 (18)
C8–C9	1.463 (3)	C12–S1	1.803 (2)
C9–C10	1.336 (3)	C13–O3	1.219 (2)
C9–C11	1.505 (3)	C13–N1	1.354 (2)
C10–O2	1.344 (3)	C14–N1	1.425 (2)
N1–C11–C9	111.39 (14)	C13–N1–C14	124.09 (15)
N1–C11–S1	104.79 (12)	C13–N1–C11	118.00 (15)
C9–C11–S1	115.60 (13)	C14–N1–C11	116.83 (13)
C13–C12–S1	107.61 (13)	C10–O2–C3	117.83 (15)
N1–C13–C12	112.55 (17)	C12–S1–C11	93.10 (9)

All H atoms were initially located in a difference Fourier map. The methyl H atoms were then constrained to an ideal geometry, with C–H distances of 0.96 Å and *U*_{iso}(H) = 1.5*U*_{eq}(C), but each group was allowed to rotate freely about its C–C bond. All other H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C–H distances in the range 0.93–0.98 Å and with *U*_{iso}(H) = 1.2*U*_{eq}(C).

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

The present work was supported by the National Key Project for Basic Research (Nos. 2003CB114400 and 2002CCA00500), the National Natural Science Foundation of China (Nos. 20172017 and 20203009), and the Program for New Century Excellent Talents in University of China.

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