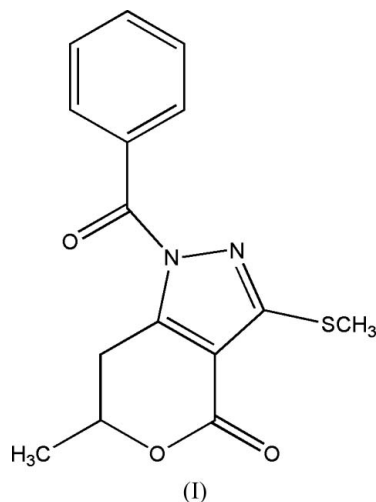


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haojjchem@yahoo.com.cn**Key indicators**Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.005$ Å
 R factor = 0.033
 wR factor = 0.083
Data-to-parameter ratio = 10.4For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.**1-Benzoyl-6-methyl-3-methylsulfanyl-6,7-dihydro-1H-pyrano[4,3-c]pyrazol-4-one**

The title compound, $\text{C}_{15}\text{H}_{14}\text{N}_2\text{O}_3\text{S}$, a potent new bioactive molecule which contains pyrazole and pyrone ring systems, was synthesized by the reaction of benzohydrazide and 3-[bis(methylsulfanyl)methylene]dihydro-6-methyl-3H-pyran-2,4-dione in ethanol.

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In recent years, there have been a few reports of pyrone derivatives. Some patents reported pyrandione derivatives inhibiting activity for HIV proteinase (Ellsworth & Lunney, 1995; Thaisrivongs & Yang, 1994). Some bioactivities, such as antitobacco viral activity, plant-growth regulation activity, fungicidal and herbicidal bioactivities, have also been reported (Wang *et al.*, 2000; Li *et al.*, 2004). Significant activities against *Biomphalaria glabrata* egg masses have been reported (de Souza *et al.*, 2004). In view of these facts and in continuation of our interest in the chemistry of heterocycles, we have attempted to synthesize a series of pyranopyrazole derivatives, one of which, (I), is reported here.



The molecular structure of (I) is shown in Fig. 1. The X-ray analysis reveals that there are two independent molecules which have different orientations in the asymmetric unit.

Experimental

The title compound was synthesized by adding benzohydrazide (0.136 g, 1 mmol) to an absolute ethanol solution (30 ml) containing 3-[bis(methylsulfanyl)methylene]dihydro-6-methyl-3H-pyran-2,4-dione (0.232 g, 1 mmol). The mixture was stirred for 5.5 h at room temperature. The product was obtained by silica-gel column chromatography using a 1:5 mixture of ethyl acetate and petroleum ether as eluant. Colourless single crystals suitable for X-ray diffraction

analysis were obtained by diffusion of *n*-hexane into a solution of the crude product in dichloromethane. $^1\text{H NMR}$ (CDCl_3): δ 7.49–8.16 (*m*, 5H), 4.73–4.80 (*m*, 1H), 3.15–3.69 (*m*, 2H), 2.53 (*s*, 3H), 1.58 (*d*, 3H, $J = 6.3$ Hz); $^{13}\text{C NMR}$ (CDCl_3): δ 166.72, 161.28, 153.22, 151.45, 133.52, 131.63, 130.97, 127.98, 110.90, 75.36, 31.25, 30.88, 20.54, 13.28; elemental analysis calculated for $\text{C}_{15}\text{H}_{16}\text{N}_2\text{O}_2\text{S}$: C 59.59, H 4.67, N 9.27%; found: C 59.56, H 4.61, N 9.26%.

Crystal data

$\text{C}_{15}\text{H}_{14}\text{N}_2\text{O}_3\text{S}$
 $M_r = 302.35$
 Monoclinic, *Cc*
 $a = 24.083$ (3) Å
 $b = 7.393$ (1) Å
 $c = 18.820$ (3) Å
 $\beta = 117.765$ (2)°
 $V = 2965.2$ (7) Å³
 $Z = 8$

$D_x = 1.354$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 2146 reflections
 $\theta = 2.3$ – 23.6 °
 $\mu = 0.23$ mm⁻¹
 $T = 293$ (2) K
 Block, colourless
 $0.38 \times 0.20 \times 0.10$ mm

Data collection

Bruker APEX-II CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
 $T_{\min} = 0.725$, $T_{\max} = 1.000$
 7700 measured reflections

3972 independent reflections
 3298 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.020$
 $\theta_{\text{max}} = 25.0$ °
 $h = -28 \rightarrow 28$
 $k = -8 \rightarrow 8$
 $l = -22 \rightarrow 20$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.033$
 $wR(F^2) = 0.083$
 $S = 1.04$
 3972 reflections
 383 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0203P)^2 + 0.9288P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.16$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.15$ e Å⁻³
 Absolute structure: Flack (1983),
 436 Friedel pairs
 Flack parameter: -0.01 (7)

All H atoms were placed in calculated positions [$\text{C}-\text{H} = 0.93, 0.96, 0.97$ or 0.98 Å for phenyl, methyl, methylene and methine H atoms, respectively] and included in the refinement using a riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{methyl C})$.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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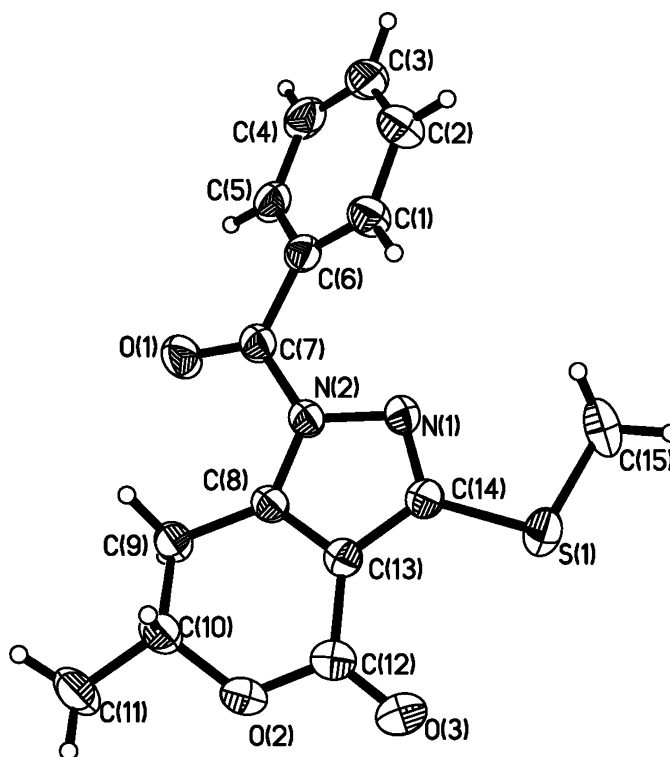


Figure 1
 A view of (I), with displacement ellipsoids drawn at the 30% probability level.

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