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Key indicators

Single-crystal X-ray study T = 295 K Mean σ (C–C) = 0.004 Å R factor = 0.037 wR factor = 0.107 Data-to-parameter ratio = 7.9

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

(S)-Methyl 6,7,8,9,10,11-hexahydro-1,6dimethyl-10,11-dioxophenanthro[1,2-*b*]furan-6-carboxylate (methyl tashinonate)

The approximately planar molecules of methyl tanshinonate, $C_{20}H_{18}O_5$, are stacked over each other along the *b* axis of the monoclinic unit cell. There are two independent molecules in the asymmetric unit.

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Comment

A recent report on the tanshinone isolated from the root of *Salvia miltiorrhiza* details the structure of 8,9-dihydro-1,6-dimethylphenanthro[1,2-*b*]furan-10,11-dione. The red compound exists as a nearly planar molecule that has no chiral C atoms (Qin *et al.*, 2005). The present compound, (I), was also isolated from the same source. As the C atoms at the 6- and 7-positions in (I) are saturated, the compound can be regarded as being the product of the addition of methy formate across the 6,7 C=C double bond of 8,9-dihydro-1,6-dimethylphenanthro[1,2-*b*]furan-10,11-dione. The structure of methyl tanshinonate was first elucidated by spectroscopic means by Kakisawa *et al.* (1968) who assigned an *S* configuration to the chiral carbon.



The compound crystallizes as two independent molecules (Fig. 1) having similar bond dimensions. In the unit cell, the molecules are stacked over each other (Fig. 2), the distance between the nearly planar molecules being about 3.5 Å. The distances between nearly planar molecules of two kinds of independent molecules are similar.

Experimental

The root of *Salvia miltiorrhiza* Bunge was dried and then crushed into powder. The powdered root was extracted with ethanol; evaporation of the solvent gave a residue that was subjected to silica-gel coloumn chromatography. The compound was eluted with petroleum ether/ ethyl acetate (92:8 ν/ν). Recrystallization from this solvent system yielded red crystals. The formula was established from the FAB–MS m/z peak of 339 for the $[M + 1]^+$ ion, and it was further confirmed by solution NMR measurements.

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Figure 1

The asymmetric unit of (I). Displacement ellipsoids are drawn at the 50% probablity level and H atoms are drawn as spheres of arbitrary radii.

Crystal data

$$C_{20}H_{18}O_5$$

$$M_r = 338.34$$
Monoclinic, P_{2_1}

$$a = 9.184 (1) Å$$

$$b = 13.384 (2) Å$$

$$c = 13.638 (2) Å$$

$$\beta = 105.720 (2)^{\circ}$$

$$V = 1613.7 (4) Å^3$$

$$Z = 4$$

Data collection

Bruker SMART area-detector diffractometer $R_{\rm int} = 0.021$ $\theta_{\max} = 27.1^{\circ}$ $h = -11 \rightarrow 8$ ω and ω scans Absorption correction: none 8266 measured reflections $k = -16 \rightarrow 17$ $l = -14 \rightarrow 17$ 3603 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$ wR(F²) = 0.107 S = 1.023603 reflections 458 parameters H-atom parameters constrained

 $\mu = 0.10 \text{ mm}^{-1}$ T = 295 (2) K Block, red $0.48 \times 0.41 \times 0.34~\text{mm}$ 3071 reflections with $I > 2\sigma(I)$

Cell parameters from 853 reflections

 $D_x = 1.393 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

 $\theta = 2.2 - 27.1^{\circ}$

$w = 1/[\sigma^2(F_o^2) + (0.0661P)^2]$
+ 0.2301P]
where $P = (F_0^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.001$
$\Delta \rho_{\rm max} = 0.20 \ {\rm e} \ {\rm \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.22 \text{ e } \text{\AA}^{-3}$
Extinction correction: SHELXL97
Extinction coefficient: 0.023 (2)

In the absence of significant anomalous dispersion effects, Friedel pairs were merged. H atoms were positioned geometrically (C-H =





ORTEPII (Johnson, 1976) plot illustrating the stacking of the molecules of (I).

0.93 Å for the aromatic atoms, 0.97 Å for the methylene atoms and 0.96 Å for the methyl atoms) and were included in the refinement in the riding-model approximation, with $U_{iso}(H)$ values set at $1.2U_{eq}(C)$ for the aromatic and methylene atoms, and to $1.5U_{eq}(C)$ for the methyl atoms. The methyl groups were rotated to fit the electron density.

Data collection: SMART (Bruker, 2001); cell refinement: SMART (Bruker, 2001); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976); software used to prepare material for publication: SHELXL97.

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