

1,2-Dihydro-1,6-dimethylphenanthro[1,2-*b*]-  
furan-10,11-dione hemihydrateZhi-Yun Du,<sup>a</sup> Jiang-Ke Qin,<sup>a</sup>  
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## Key indicators

Single-crystal X-ray study  
*T* = 293 K  
Mean  $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$   
*R* factor = 0.036  
*wR* factor = 0.104  
Data-to-parameter ratio = 7.1For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

In the title compound,  $\text{C}_{18}\text{H}_{14}\text{O}_3 \cdot 0.5\text{H}_2\text{O}$ , also known as dihydrotanshinone hemihydrate, the molecular skeleton is a nearly planar. The two molecules in the asymmetric unit are linked by  $\text{O}-\text{H} \cdots \text{O}$  hydrogen bonds involving the carbonyl groups and the solvent water molecule, forming moieties which are, in turn, linked *via* intermolecular  $\pi-\pi$  stacking interactions into a two-dimensional sheet.

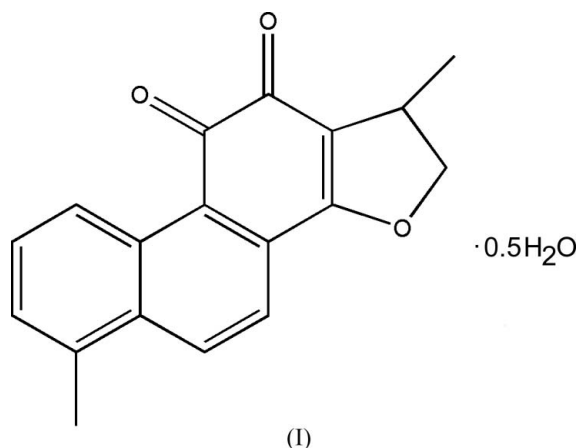
## Comment

Dihydrotanshinone is one of the tanshinones isolated from the root of the Chinese traditional herb *Salvia miltiorrhiza* and it has broad pharmacological activities, such as antibacterial (Fang *et al.*, 1976), antitumor (Ryu *et al.*, 1997) and antiplatelet aggregation (Onitsuka *et al.*, 1983). Tanshinones have been used to treat coronary heart disease (Chang *et al.*, 1991), cerebrovascular and neurasthenic insomnia (Yagi *et al.*, 1989). The structure of dihydrotanshinone was elucidated on the basis of spectroscopic analysis (Yang *et al.*, 1981). We have previously reported the crystal structure of 1,2-dihydro-tanshinquinone, another tanshinone isolated from the root of *Salvia miltiorrhiza* (Qin *et al.*, 2005). We report here the crystal structure of dihydrotanshinone hemihydrate, (I).

Received 1 August 2005

Accepted 9 August 2005

Online 17 August 2005



The X-ray crystallographic study of (I) confirms the molecular structure previously proposed on the basis of spectroscopic data. The asymmetric unit of (I) consists of two independent molecules and one water molecule (Fig. 1). In the crystal structure, the carbonyl group O atoms of two adjacent molecules are linked to one water molecule *via* two  $\text{O}-\text{H} \cdots \text{O}$  hydrogen bonds [ $\text{O} \cdots \text{O} = 3.070(4)$  and  $2.991(4) \text{ \AA}$ ]. Additionally,  $\pi-\pi$  stacking interactions in the crystal structure result in the formation of infinite two-dimensional sheets (Fig. 2).

Experimental

Dried powder, obtained from the root of *Salvia miltiorrhiza*, was extracted with EtOH and the extract concentrated *in vacuo*. The residue was subjected to silical-gel column chromatography, eluting with petroleum ether–ethyl acetate (90:10 (v/v), to yield the title compound. The identity of (I) was confirmed by <sup>1</sup>H NMR and FAB mass spectra. Crystals of (I) were obtain by evaporation of a petroleum ether–ethyl acetate solution. <sup>1</sup>H NMR in CDCl<sub>3</sub> (500 MHz): δ 9.28 (d, 9 Hz, 1H), 8.30 (d, 9 Hz, 1H), 7.76 (d, 9 Hz, 1H), 7.57 (m, 1H), 7.40 (d, 7 Hz, 1H), 4.97 (t, 9.5 Hz, 1H), 4.43 (q, 1H), 3.66 (m, 1H), 2.70 (s, 3H), 1.41 (d, 6.5 Hz, 3H). The FAB mass spectrum showed M<sup>+</sup> ions at 279.

Crystal data

C<sub>18</sub>H<sub>14</sub>O<sub>3</sub>·0.5H<sub>2</sub>O  
M<sub>r</sub> = 287.30  
Monoclinic, P2<sub>1</sub>  
a = 7.287 (2) Å  
b = 26.569 (9) Å  
c = 7.294 (3) Å  
β = 95.590 (7)°  
V = 1405.6 (8) Å<sup>3</sup>  
Z = 4

D<sub>x</sub> = 1.358 Mg m<sup>-3</sup>  
Mo Kα radiation  
Cell parameters from 984 reflections  
θ = 2.9–26.2°  
μ = 0.09 mm<sup>-1</sup>  
T = 293 (2) K  
Plate, red  
0.48 × 0.42 × 0.17 mm

Data collection

Bruker SMART 1000 CCD diffractometer  
φ and ω scans  
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
T<sub>min</sub> = 0.956, T<sub>max</sub> = 0.984  
7831 measured reflections

2782 independent reflections  
1958 reflections with I > 2σ(I)  
R<sub>int</sub> = 0.024  
θ<sub>max</sub> = 26.0°  
h = -4 → 8  
k = -32 → 32  
l = -8 → 8

Refinement

Refinement on F<sup>2</sup>  
R[F<sup>2</sup> > 2σ(F<sup>2</sup>)] = 0.037  
wR(F<sup>2</sup>) = 0.104  
S = 1.03  
2782 reflections  
392 parameters  
H-atom parameters constrained

w = 1/[σ<sup>2</sup>(F<sub>o</sub><sup>2</sup>) + (0.0558P)<sup>2</sup> + 0.1165P]  
where P = (F<sub>o</sub><sup>2</sup> + 2F<sub>c</sub><sup>2</sup>)/3  
(Δ/σ)<sub>max</sub> = 0.001  
Δρ<sub>max</sub> = 0.16 e Å<sup>-3</sup>  
Δρ<sub>min</sub> = -0.15 e Å<sup>-3</sup>

Table 1

Hydrogen-bond geometry (Å, °).

D—H...A	D—H	H...A	D...A	D—H...A
O7—H7A...O5	0.89	2.12	2.991 (4)	164
O7—H7B...O2	0.88	2.26	3.070 (4)	152

In the absence of any significant anomalous scattering, Friedel equivalents were merged prior to the final refinement and the absolute configuration could not be determined. The H atoms were positioned geometrically and treated as riding on their parent C atoms, with C—H distances in the range 0.93–0.98 Å. H atoms

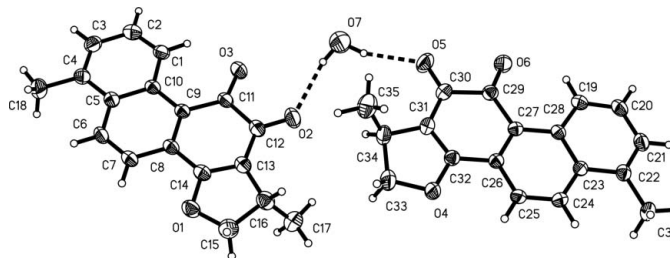


Figure 1 View of the molecules in the asymmetric unit of (I), with displacement ellipsoids drawn at the 30% probability level.

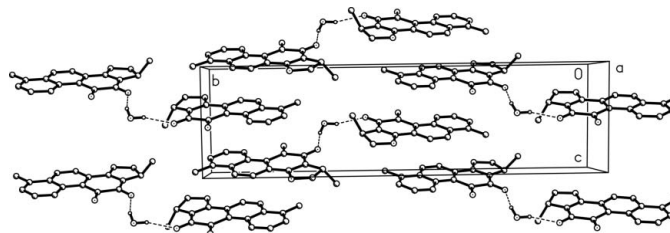


Figure 2 The molecular packing of (I), viewed down the a axis; hydrogen bonds are shown as dashed lines. H atoms not involved in hydrogen bonding have been omitted.

attached to water O atoms were located in difference Fourier maps and constrained to ride on their carrier atoms, with O—H distances in the range 0.88–0.89 Å, and with U<sub>iso</sub>(H) = 1.5U<sub>eq</sub>(O).

Data collection: SMART (Bruker, 1999); cell refinement: SAINT-Plus (Bruker, 1999); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXTL (Bruker, 1999); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

This work was supported by Guanggong Provincial Science Foundation.

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