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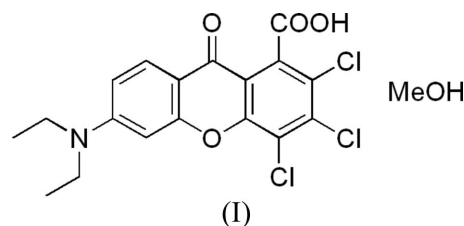
## Key indicators

Single-crystal X-ray study  
 $T = 294\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$   
 $R$  factor = 0.040  
 $wR$  factor = 0.093  
Data-to-parameter ratio = 17.7For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

## 2,3,4-Trichloro-6-(diethylamino)-9-oxo-9H-xanthene-1-carboxylic acid methanol solvate

The crystal structure of the title compound,  $\text{C}_{18}\text{H}_{14}\text{Cl}_3\text{NO}_4 \cdot \text{CH}_3\text{OH}$ , is characterized by  $\text{O}-\text{H} \cdots \text{O}$  hydrogen bonds between the xanthene molecule and the methanol solvent molecule.Received 25 December 2006  
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## Comment

In the present paper, we report the crystal structure of the title compound, (I) (Fig. 1). An extensive hydrogen-bond network is built up by  $\text{O}-\text{H} \cdots \text{O}$  hydrogen-bonding interactions between the xanthene molecule and the methanol solvent molecule (Table 1 and Fig. 2).

## Experimental

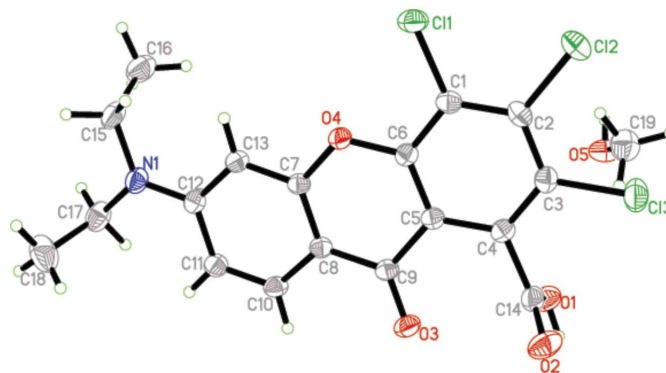
Compound (I) was prepared according to the method described by Lee *et al.* (2002). A solution of 3-diethylaminophenol (0.36 g, 22 mmol) and tetrachlorophthalic anhydride (0.48 g, 22 mmol) was refluxed in toluene (15 ml) for 8 h. The solution was cooled to room temperature and the precipitate collected to yield 2,3,4-trichloro-6-(diethylamino)-9-oxo-9H-xanthene-1-carboxylic acid (0.59 g, 70%). The crude product, (I), was purified by silica-gel flash chromatography (methanol-dichloromethane, 1:10 *v/v*). Crystals of (I) (m.p. 550–551 K) suitable for X-ray diffraction were obtained by slow

Figure 1

The molecular structure of (I). Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radius.

evaporation of a solution in ethyl acetate and acetone (1:3 v/v). <sup>1</sup>H NMR (CDCl<sub>3</sub>, δ, p.p.m.): 1.12 (t, 6H, J = 6.9 Hz), 3.35 (dd, 4H, J = 6.9 and 14.1 Hz), 6.40 (d, 1H, J = 2.1 Hz), 6.61 (dd, 1H, J = 2.4 and 9.3 Hz), 7.83 (d, 1H, J = 9.0 Hz).

Crystal data

C<sub>18</sub>H<sub>14</sub>Cl<sub>3</sub>NO<sub>4</sub>·CH<sub>4</sub>O  
*M<sub>r</sub>* = 446.69  
 Triclinic, *P* $\bar{1}$   
*a* = 8.5125 (12) Å  
*b* = 10.0649 (14) Å  
*c* = 12.4028 (17) Å  
 α = 105.305 (5)°  
 β = 95.552 (9)°  
 γ = 101.563 (6)°  
*V* = 991.5 (2) Å<sup>3</sup>  
*Z* = 2  
*D<sub>x</sub>* = 1.496 Mg m<sup>-3</sup>  
 Mo *K*α radiation  
 μ = 0.49 mm<sup>-1</sup>  
*T* = 294 (2) K  
 Block, yellow  
 0.14 × 0.12 × 0.08 mm

Data collection

Rigaku Saturn diffractometer  
 ω scans  
 Absorption correction: multi-scan (Jacobson, 1998)  
*T<sub>min</sub>* = 0.934, *T<sub>max</sub>* = 0.962  
 12536 measured reflections  
 4699 independent reflections  
 1969 reflections with *I* > 2σ(*I*)  
*R<sub>int</sub>* = 0.063  
*θ<sub>max</sub>* = 27.9°

Refinement

Refinement on *F*<sup>2</sup>  
*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.040  
*wR* (*F*<sup>2</sup>) = 0.093  
*S* = 0.82  
 4699 reflections  
 265 parameters  
 H atoms treated by a mixture of independent and constrained refinement  
*w* = 1/[σ<sup>2</sup>(*F<sub>o</sub>*<sup>2</sup>) + (0.0388*P*)<sup>2</sup>]  
 where *P* = (*F<sub>o</sub>*<sup>2</sup> + 2*F<sub>c</sub>*<sup>2</sup>)/3  
 (Δ/σ)<sub>max</sub> < 0.001  
 Δρ<sub>max</sub> = 0.25 e Å<sup>-3</sup>  
 Δρ<sub>min</sub> = -0.27 e Å<sup>-3</sup>

Table 1  
 Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O1—H1...O5 <sup>i</sup>	0.84 (3)	1.78 (3)	2.589 (2)	163 (3)
O5—H2...O3 <sup>ii</sup>	0.80 (3)	2.03 (3)	2.807 (2)	163 (3)

Symmetry codes: (i) -*x* + 1, -*y* + 1, -*z* + 2; (ii) *x* + 1, *y*, *z*.

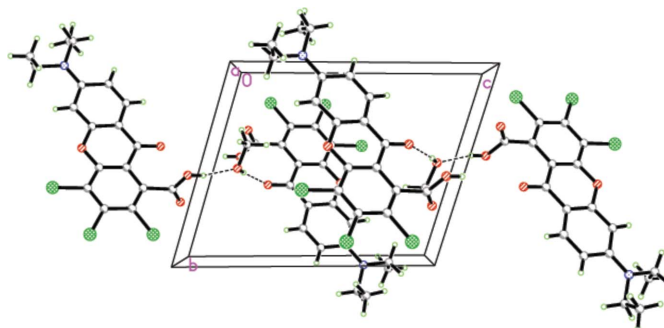


Figure 2  
 The crystal structure of (I), viewed along the *a* axis. Dashed lines indicate the hydrogen-bond interactions.

All O-bound H atoms were located in a difference map and then refined freely. The remaining H atoms were positioned geometrically and refined using a riding model, with C—H = 0.93–0.97 Å and *U<sub>iso</sub>*(H) = 1.2*U<sub>eq</sub>*(C) or 1.5*U<sub>eq</sub>*(methyl C).

Data collection: *CrystalClear* (Rigaku/MSK, 2005); cell refinement: *CrystalClear*; data reduction: *CrystalClear*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXL97*; software used to prepare material for publication: *CrystalStructure* (Rigaku/MSK, 2005).

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