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Key indicators

Single-crystal X-ray study

T = 288 K

Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$

R factor = 0.053

wR factor = 0.152

Data-to-parameter ratio = 15.4

For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.2-Methyl-2-(trimethylsilyloxy)-3,4-dihydro-2H,5H-
pyrano[3,2-c][1]benzopyran-5-oneIn the title compound, $\text{C}_{16}\text{H}_{20}\text{O}_4\text{Si}$, the coumarin moiety is essentially planar and the pyran ring adopts a half-chair conformation.

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Comment

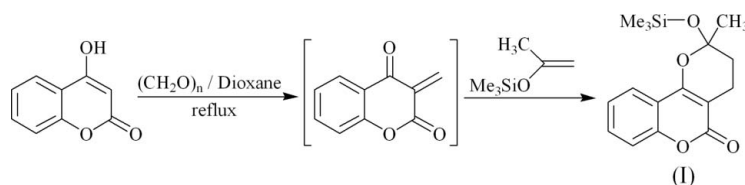
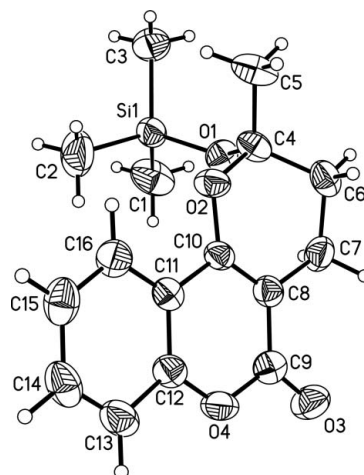
o-Quinone methides constitute a class of highly reactive intermediates and their cycloaddition chemistry has attracted considerable interest (Nair *et al.*, 2001). In our studies of the cycloaddition reactions of *o*-quinone methides derived from 4-hydroxycoumarin, we have found that the cycloaddition reaction between coumarin quinone methide and an excess amount of trimethyl[(1-methylethenyl)oxy]silane afforded the title compound, (I), as one of the products. As part of this study, we have undertaken the X-ray crystallographic analysis of (I) in order to elucidate the conformation and configuration of this cycloadduct product.The bond lengths and angles in (I) (Fig. 1 and Table 1) are in good agreement with those found in related compounds (Savell *et al.*, 1989). The coumarin moiety is essentially planar, with atom O3 deviating from the mean plane by 0.152 (4) Å. The dihedral angle between the heterocyclic plane (C8/C9/O4/

Figure 1

The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

C12/C11/C10) and the fused benzene ring is 3.2 (3)°. The pyran ring (C4/C6–C8/C10/O2) adopts a half-chair conformation, with atoms C4 and C6 deviating from the C7/C8/C10/O2 plane by 0.237 (4) and –0.487 (4) Å, respectively.

In the crystal structure, the molecular packing is stabilized by intermolecular C–H···O interactions, as detailed in Table 2.

Experimental

Under argon, a mixture of 4-hydroxycoumarin, 3 equivalents of trimethyl[(1-methylethenyl)oxy]silane and an excess amount of paraformaldehyde was suspended in dry dioxane and refluxed for about 14 h. Compound (I) was isolated by column chromatography of the reaction mixture on silica gel after evaporation of the solvent, in 76% yield. Single crystals of (I) were obtained by slow evaporation of a petroleum ether–ethyl acetate (3:1 v/v) solution of (I).

Crystal data

C₁₆H₂₀O₄Si
M_r = 304.41
Monoclinic, P2₁/c
a = 11.960 (2) Å
b = 10.456 (2) Å
c = 13.039 (3) Å
β = 105.09 (3)°
V = 1574.4 (6) Å³
Z = 4

D_x = 1.284 Mg m^{–3}
Mo Kα radiation
Cell parameters from 25 reflections
θ = 10–13°
μ = 0.16 mm^{–1}
T = 288 (2) K
Block, colourless
0.40 × 0.31 × 0.28 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
ω/2θ scans
Absorption correction: ψ scan (XCAD4; Harms & Wocadlo, 1995)
T_{min} = 0.922, T_{max} = 0.956
3075 measured reflections
2930 independent reflections

1878 reflections with I > 2σ(I)
R_{int} = 0.028
θ_{max} = 25.5°
h = 0 → 14
k = 0 → 12
l = –15 → 15
3 standard reflections every 200 reflections
intensity decay: none

Refinement

Refinement on F²
R[F² > 2σ(F²)] = 0.053
wR(F²) = 0.152
S = 1.00
2930 reflections
190 parameters
H-atom parameters constrained

w = 1/[σ²(F_o²) + (0.055P)² + 1.48P]
where P = (F_o² + 2F_c²)/3
(Δ/σ)_{max} < 0.001
Δρ_{max} = 0.29 e Å^{–3}
Δρ_{min} = –0.25 e Å^{–3}

Table 1

Selected geometric parameters (Å, °).

O1–C4	1.391 (4)	C4–C6	1.507 (5)
O2–C4	1.464 (4)	C6–C7	1.519 (5)
O3–C9	1.215 (4)		
C4–O1–Si1	134.8 (2)	O1–C4–C5	113.0 (3)

Table 2

Hydrogen-bond geometry (Å, °).

D–H···A	D–H	H···A	D···A	D–H···A
C5–H5C···O3 ⁱ	0.96	2.47	3.426 (5)	171
C13–H13···O3 ⁱⁱ	0.93	2.56	3.492 (4)	175

Symmetry codes: (i) x, –y + ½, z + ½; (ii) –x + 3, y – ½, –z + ½.

H atoms were included in the riding-model approximation, with C–H distances of 0.93, 0.96 and 0.97 Å for aromatic, methyl and methylene H atoms, respectively, and with U_{iso}(H) = 1.2U_{eq}(aromatic and methylene C) or 1.5U_{eq}(methyl C).

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *XCAD4* (Harms & Wocadlo, 1995); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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