

Cinnamoyl shikonin¹Sanjay Sarkhel,^a Shefali,^b Vijayvitthal T. Mathad,^b Kanwal Raj,^b Amiya P. Bhaduri,^b Prakas R. Maulik,^{a*} Charlotte K. Broder^c and Judith A. K. Howard^c

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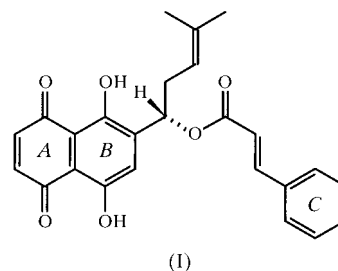
The title compound, 1-(5,8-dihydro-1,4-dihydroxy-5,8-dioxo-2-naphthyl)-4-methylpent-3-en-1-yl cinnamate, C₂₅H₂₂O₆, crystallizes in space group *P*2₁. The phenyl ring of the cinnamate is *anti* to the carbonyl group of the same moiety [C—C—C—C = −175.6 (2)°] and is nearly parallel to the naphthyl ring system. Two six-membered rings formed by intramolecular hydrogen bonds, with O—H···O distances of 2.587 (2) and 2.589 (2) Å, occur on either side of the fused ring system, creating a tetracyclic pyrene-shaped system. The phenyl ring forms an intermolecular stack with the benzoquinone ring, as a result of aromatic π – π interactions.

Comment

Arnebin-1 (β,β -dimethyl acryloyl shikonin), a naturally occurring naphthoquinone from the root of the plant *Arnebia nobilis*, belongs to the alkanin/shikonin family (Shukla *et al.*, 1969). The toxic effects of this compound restricted its further development as a clinically useful therapeutic agent, in spite of its wound healing, anti-inflammatory, antithrombotic, antimicrobial and anticancer activities (Papageorgiou *et al.*, 1999). This necessitated the development of numerous analogues of shikonin with greatly reduced toxicity. One such analogue is the title compound, (I), which shows a growth-inhibitory effect on prostate cancer cells (Gaddipati *et al.*, 2000). This prompted us to undertake the present diffraction study in order to confirm the overall three-dimensional structure of (I).

The conformation of (I) and the atom-numbering scheme are shown in Fig. 1. The molecule contains one naphthaquinone ring (*A/B* fused ring system), to which a phenyl ring (*C*) is attached *via* an ester bond, and one chiral centre (C11). Although the present study does not establish the absolute configuration of the molecule [Flack (1983) parameter 0.3 (9)], the parent shikonin has the *R* configuration, as determined by the chemical degradation method (Arakawa & Nakazaki, 1961). The phenyl ring *C* is almost parallel to the

A/B ring system; the interplanar angle between the two rings is 1.7 (1)°. Moreover, the phenyl ring at C19 is *anti* to the carbonyl group at C17 [C17—C18—C19—C20 = −175.6 (2)°].



The molecule of (I) contains two potential hydrogen-bond donors (–OH groups O5–H5 and O8–H8), which are involved in intramolecular hydrogen-bonding interactions with carbonyl groups C4=O4 and C1=O1 (Table 2) through the formation of six-membered rings (Fig. 1). The formation of such rings is preferred to intermolecular hydrogen bonding (Bilton *et al.*, 2000). The strong intramolecular O···O distances observed in (I) are in the same range as those found in the parent naphthazarin C at 60 K (Herbstein *et al.*, 1985).

The hydroxyl H atoms, H5 and H8, were located in a difference Fourier map, in view of the ambiguity with regard to their positions in related naphthazarin systems (Herbstein *et al.*, 1985). A comparison of bond lengths in (I) with those of naphthazarin C (neutron diffraction at 60 K) and other related systems (Herbstein *et al.*, 1985, and references therein) shows that, on average, C=O is *ca* 0.05 Å longer in (I), while C–OH is *ca* 0.03 Å shorter. This suggests that, in close analogy with the crystal structure of naphthazarin C, the hydroxyl H atoms are not completely localized in (I) at 100 K and ordering will be favoured at lower temperatures, since a complete localization is only possible at 0 K.

In addition, weak hydrogen-bonding interactions of the type C–H···O are also observed (Table 2). The crystal packing (Fig. 2) further shows that the phenyl ring *C* stacks

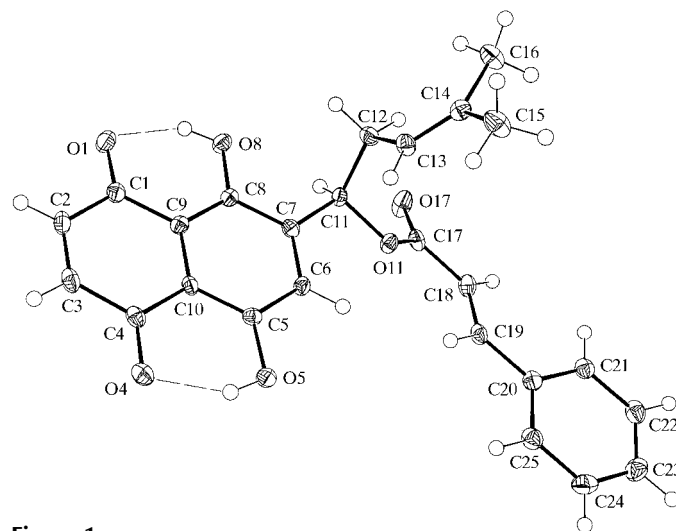


Figure 1
The molecular structure of (I) with the atom-numbering scheme, showing displacement ellipsoids at the 50% probability level. H atoms are drawn as small spheres of arbitrary radii and intramolecular O—H···O bonds are shown by dotted lines.

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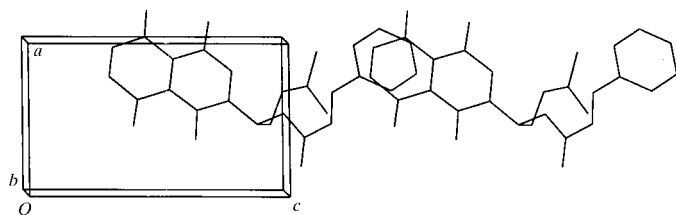


Figure 2
The packing in (I), showing the intermolecular stacking of rings C and A as a result of aromatic π - π interactions.

with the benzoquinone ring A, as a result of aromatic π - π interactions. The average intermolecular stacking distance and the angle between the rings, which overlap substantially in a 'face-to-face' orientation as per the model proposed by Hunter & Sanders (1990), are 3.3 Å and 1.1 (1)°, respectively. Since the benzoquinone ring is electron deficient, it can allow a substantial face-to-face overlap with the relatively neutral phenyl ring without much π - π repulsion.

Experimental

The synthesis of (I) was carried out by hydrolysing β,β -dimethyl acryloyl shikonin with sodium hydroxide, followed by esterification with cinnamic anhydride and 1,3-dicyclohexylcarbodiimide. Crystals of (I) of diffraction quality were grown from a hexane-methylene chloride solution at room temperature.

Crystal data

$C_{25}H_{22}O_6$	$D_x = 1.361 \text{ Mg m}^{-3}$
$M_r = 418.43$	Mo $K\alpha$ radiation
Monoclinic, $P2_1$	Cell parameters from 510 reflections
$a = 6.16770 (10) \text{ \AA}$	$\theta = 4.1\text{--}27.4^\circ$
$b = 15.7416 (3) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$c = 10.5141 (2) \text{ \AA}$	$T = 100 (2) \text{ K}$
$\beta = 90.7630 (10)^\circ$	Block, red
$V = 1020.72 (3) \text{ \AA}^3$	$0.5 \times 0.1 \times 0.1 \text{ mm}$
$Z = 2$	

Data collection

Bruker SMART CCD area-detector diffractometer	4357 independent reflections
ω scans	4011 reflections with $I > 2\sigma(I)$
Absorption correction: ψ scan (XPREP; Sheldrick, 1994)	$R_{\text{int}} = 0.028$
$T_{\text{min}} = 0.885$, $T_{\text{max}} = 1.000$	$\theta_{\text{max}} = 27.5^\circ$
7463 measured reflections	$h = -8 \rightarrow 7$
	$k = -20 \rightarrow 20$
	$l = -13 \rightarrow 11$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0219P)^2 + 0.7688P]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.096$	$(\Delta/\sigma)_{\text{max}} = 0.002$
$S = 1.09$	$\Delta\rho_{\text{max}} = 0.25 \text{ e \AA}^{-3}$
4357 reflections	$\Delta\rho_{\text{min}} = -0.25 \text{ e \AA}^{-3}$
290 parameters	
H atoms treated by a mixture of independent and constrained refinement	

The hydroxyl H atoms, H5 and H8, were located from the difference Fourier map and refined freely. The remaining H atoms were placed in geometrically idealized positions and allowed to ride on their parent atoms, with C-H = 0.93–0.98 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. Three reflections [largest deviation $\Delta(F^2)/\sigma > 6.4$] were suppressed during the final cycles of refinement.

Data collection: SMART (Bruker, 1998); cell refinement: SMART; data reduction: SAINT (Bruker, 1998); program(s) used to solve

Table 1
Selected torsion angles (°).

C9–C1–C2–C3	–0.3 (3)	C3–C4–C10–C9	–1.3 (3)
C1–C2–C3–C4	–1.7 (3)	C7–C11–O11–C17	148.35 (17)
C2–C3–C4–C10	2.4 (3)	C11–O11–C17–C18	176.89 (18)
C10–C5–C6–C7	–0.9 (3)	O11–C17–C18–C19	12.0 (3)
C5–C6–C7–C8	0.3 (3)	C17–C18–C19–C20	–175.6 (2)
C6–C7–C8–C9	0.3 (3)	C25–C20–C21–C22	–0.8 (3)
C7–C8–C9–C10	–0.2 (3)	C20–C21–C22–C23	0.6 (3)
C2–C1–C9–C10	1.4 (3)	C21–C22–C23–C24	0.3 (4)
C6–C5–C10–C9	1.0 (3)	C22–C23–C24–C25	–0.9 (4)
C8–C9–C10–C5	–0.4 (3)	C21–C20–C25–C24	0.1 (3)
C1–C9–C10–C4	–0.6 (3)	C23–C24–C25–C20	0.7 (4)

Table 2
Hydrogen-bonding geometry (Å, °).

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
O5–H5 \cdots O4	0.87 (3)	1.81 (3)	2.587 (2)	148 (3)
O8–H8 \cdots O1	0.88 (4)	1.79 (3)	2.589 (2)	150 (3)
C3–H3 \cdots O17 ⁱ	0.93	2.47	3.356 (3)	160
C11–H11 \cdots O5 ⁱⁱ	0.98	2.56	3.359 (3)	138
C16–H16A \cdots O1 ⁱⁱⁱ	0.96	2.72	3.631 (3)	159
C21–H21 \cdots O4 ^{iv}	0.93	2.62	3.538 (3)	170

Symmetry codes: (i) $1+x, y, z-1$; (ii) $x-1, y, z$; (iii) $x, y, 1+z$; (iv) $x-1, y, 1+z$.

structure: SHELXS86 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: NRCVAX (Gabe *et al.*, 1989), ORTEP (Johnson, 1965) and PLUTO (Motherwell & Clegg, 1978).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: DE1171). Services for accessing these data are described at the back of the journal.

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