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Key indicators

Single-crystal X-ray study T = 173 K Mean σ (C–C) = 0.002 Å R factor = 0.037 wR factor = 0.135 Data-to-parameter ratio = 18.2

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

Ethyl (*E*)-4-(2-hydroxy-1-naphthyl)-2-methyl-2butenoate

The structure determination of the title compound, $C_{17}H_{18}O_3$, shows an *E* conformation about the C=C bond. Molecules associate *via* O-H···O interactions leading to the formation of chains.

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Comment

The title compound, (I), was one of the isomers prepared from the reaction between the ylide Ph₃P=C(Me)C(O)OEt and 2-(2-naphthyl)acetaldehyde (Haselgrove *et al.*, 1999). The structure analysis shows (I) to be the uncyclized (E)butenoate (Fig. 1). The side chain, while not coplanar with the aromatic portion of the molecule, is effectively planar as seen in the sequence of torsion angles of -178.6 (1), 0.8 (1), 179.97 (8) and 179.10 (8)° for C4-C3-C2-C1, C3-C2-C1-O12, C2-C1-O12-C13 and C1-O12-C13-C14, respectively. The only two torsion angles in the molecule with 'non-trivial' values are those describing the overall conformation of the ethylbutenoate group relative to the naphthalene moiety, namely C2'-C1'-C4-C3 and C1'-C4-C3-C2, which are 94.6 (1) and 130.4 (1)°, respectively.



The major intermolecular interaction in the lattice occurs between the O-H2' and translationally related carbonyl O11 atoms, such that O-H2' is 0.92 Å, H2'···O11ⁱ is 1.84 Å, O2'···O11ⁱ is 2.751 (2) Å and the angle at H2' is 174°; symmetry code: (i) 1 + x, y, z. This association leads to the formation of chains along the *a* axis.

Experimental

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The title compound was prepared according to the literature procedure of Haselgrove *et al.* (1999). Crystals were obtained from the slow



Figure 1

The molecular structure and crystallographic numbering scheme for (I). Displacement ellipsoids are shown at the 50% probability level (Johnson, 1976).

evaporation of a dichloromethane solution of the compound (m.p. 369-370 K).

Crystal data

C17H18O3 $M_r = 270.33$ Monoclinic, P21/n a = 9.273 (2) Å b = 4.877(2) A c = 31.976(5) Å $\beta = 92.76 \ (2)^{\circ}$ $V = 1444.5 (7) \text{ Å}^3$ Z = 4

 $D_x = 1.243 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 25 reflections $\theta = 12.2 - 14.9^{\circ}$ $\mu=0.08~\mathrm{mm}^{-1}$ T = 173 KBlock, pale yellow $0.40 \times 0.31 \times 0.16 \text{ mm}$

Data collection

H-atom parameters constrained

Rigaku AFC-7R diffractometer	$h = 0 \rightarrow 12$
ω scans	$k = 0 \rightarrow 6$
3930 measured reflections	$l = -41 \rightarrow 41$
3318 independent reflections	3 standard reflections
2254 reflections with $I > 2\sigma(I)$	every 400 reflections
$R_{\rm int} = 0.041$	intensity decay: 0.3%
$\theta_{\rm max} = 27.5^{\circ}$	
Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0918P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.037$	+ 0.5393P]
$wR(F^2) = 0.135$	where $P = (F_o^2 + 2F_c^2)/3$
S = 0.82	$(\Delta/\sigma)_{\rm max} < 0.001$
3318 reflections	$\Delta \rho_{\rm max} = 0.21 \ {\rm e} \ {\rm \AA}^{-3}$
182 parameters	$\Delta \rho_{\rm min} = -0.17 \text{ e} \text{ Å}^{-3}$

The C-bound H atoms were placed in their geometrically calculated positions and included in the final refinement in the riding model approximation with an overall displacement parameter. The O-H atom was located from a difference map but was not refined.

Data collection: MSC/AFC Diffractometer Control Software (Molecular Structure Corporation, 1996); cell refinement: MSC/AFC Diffractometer Control Software; data reduction: TEXSAN (Molecular Structure Corporation, 1997); program(s) used to solve structure: SIR97 (Altomare et al., 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); software used to prepare material for publication: SHELXL97.

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