Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 292 K Mean σ (C–C) = 0.004 Å Disorder in main residue R factor = 0.064 wR factor = 0.179 Data-to-parameter ratio = 12.1

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

(E)-3-(3-Phenylpropoxy)but-2-enoic acid

In the title compound, $C_{13}H_{16}O_3$, molecules related by a centre of symmetry are linked by $O-H\cdots O$ hydrogen bonds between the carboxyl groups to form a dimer. The propoxy chain is disordered, with an occupancy ratio of 0.69 (1):0.31 (1) between two components with roughly enantiomorphic configurations.

Comment

 γ -Alkylation of 1,3-dicarbonyl compounds is a classic reaction in organic synthesis. Removal of a proton from the α -carbon using a base gives the corresponding enolate anion, and this active site can then form a C–C single bond (Carruthers, 1986). The title compound, (I), is obtained by hydrolyzing ethyl 3-(3-phenylpropoxy)but-2-enoate, which is a by-product of the γ -alkylation reaction (Niewöhner *et al.*, 2003).



In the molecule of (I), the propoxy chain, O1-C9-C8-C7-C6, is disordered over two sites (Fig. 1), with group occupancies of 0.69 (1) and 0.31 (1) for the major and minor components, respectively. The configuration of the major and minor components are roughly enantiomorphic.

Intramolecular C–H···O and intermolecular O–H···O hydrogen bonds, and a C–H··· π interaction, play a role in stabilizing the molecular and crystal structures of (I) (Table 1, Fig. 2).

Experimental

Ethyl 3-(3-phenylpropoxy)but-2-enoate (0.1 g, 0.4 mmol) was dissolved in dioxane (2 ml), and then 3.75 *M* sodium hydroxide (2 ml) was added. After stirring for 48 h at room temperature, the mixture was concentrated, treated with water (3 ml) and extracted with diethyl ether. The aqueous phase was cooled to 273 K and treated with 3 *N* hydrochloric acid until pH 1 was reached. It was then extracted with diethyl ether. The ether phase was dried and concentrated, yielding compound (I) (yield 18%). Single crystals of (I) suitable for X-ray diffraction were grown from a diethyl ether solution at 296 K.

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Accepted 17 April 2006



Figure 1

A view of the molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level. The minor disorder component is indicated by dashed lines.



Figure 2

A packing view of (I), showing hydrogen-bonds and $C-H\cdots\pi$ interactions (dashed lines). The suffixes a and b correspond to symmetry codes (-x - 1, -y + 2, -z + 2) and $(\frac{1}{2} - x, 1/2 + y, 3/2 - z)$, respectively.

Crystal data

 $\begin{array}{l} C_{13}H_{16}O_3\\ M_r = 220.26\\ Monoclinic, \ P2_1/n\\ a = 8.8008 \ (9) \ \text{\AA}\\ b = 9.0837 \ (9) \ \text{\AA}\\ c = 15.7827 \ (17) \ \text{\AA}\\ \beta = 101.470 \ (2)^\circ\\ V = 1236.5 \ (2) \ \text{\AA}^3 \end{array}$

Data collection

Bruker SMART 4K CCD areadetector diffractometer φ and ω scans Absorption correction: none 7552 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.064$ $wR(F^2) = 0.179$ S = 1.082159 reflections 178 parameters H atoms treated by a mixture of independent and constrained refinement Z = 4 $D_x = 1.183 \text{ Mg m}^{-3}$ Mo K\alpha radiation $\mu = 0.08 \text{ mm}^{-1}$ T = 292 (2) KBlock, colourless $0.30 \times 0.20 \times 0.10 \text{ mm}$

2159 independent reflections 1586 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.026$ $\theta_{\text{max}} = 25.0^{\circ}$

 $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0769P)^{2} + 0.4223P]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3$ $(\Delta/\sigma)_{max} = 0.002$ $\Delta\rho_{max} = 0.33 \text{ e} \text{ Å}^{-3}$ $\Delta\rho_{min} = -0.23 \text{ e} \text{ Å}^{-3}$

Table 1

Hydrogen-bond geometry (Å, $^{\circ}$).

Cg1 is the centroid of the phenyl ring.

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
C11-H11A···O2	0.96	2.16	2.893 (4)	132
$O3-H3A\cdots O2^{1}$	0.82 (3)	1.83 (3)	2.651 (3)	178 (2)
$C9-H9B\cdots Cg1^{ii}$	0.97	2.93	3.659 (6)	133

Symmetry codes: (i) -x - 1, -y + 2, -z + 2; (ii) $-x + \frac{1}{2}$, $y + \frac{1}{2}$, $-z + \frac{3}{2}$.

All H atoms were initially located in a difference Fourier map. The coordinates of the O-bound H atom were refined freely, with $U_{\rm iso}({\rm H}) = 1.5U_{\rm eq}({\rm O})$. The methyl H atoms were constrained to an ideal geometry, with C–H distances of 0.96 Å and $U_{\rm iso}({\rm H}) = 1.5U_{\rm eq}({\rm C})$, but the methyl group was allowed to rotate freely about its C–C bond. All other H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C–H distances in the range 0.93–0.97 Å and with $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$. The atoms of the O1–C9–C8–C7–C6 linkage are disordered over two positions. The site-occupancy factors were refined to 0.69 (1) and 0.31 (1) and then fixed in the final refinement.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

The authors acknowledge financial support from the National Key Project for Basic Research (grant No. 2002CCA00500), the National Natural Science Foundation of China (grant Nos. 20432010, 20476036 and 20172017), the Programme for New Century Excellent Talents in Universities of China and the Programme for Excellent Research Groups of Hubei Province (grant No. 2004ABC002).

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