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Methyl (*E*)-3-acetamido-2-pentenoate

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Key indicators

Single-crystal X-ray study T = 294 KMean $\sigma(\text{C-C}) = 0.004 \text{ Å}$ R factor = 0.059 wR factor = 0.155Data-to-parameter ratio = 19.3

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

The title compound, $C_8H_{13}NO_3$, is an E isomer and there are two molecules in the asymmetric unit. The molecules are assembled into chains, along the a axis, via intermolecular interactions.

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Comment

The title compound, (I), is one of the products obtained from reaction of methyl 3-amine-2-pentenoate with acetic anhydride under reflux for 24 h. This prochiral olefin is a model substrate studied in the asymmetric hydrogenation reaction (Hackler & Wickiser, 1985; Lubell *et al.*, 1991).

The structure determination of (I) was conducted in order to obtain more stereochemical information about the behaviour of these kinds of substrates in hydrogenation reactions. The crystal structure of (I) contains two independent molecules in the asymmetric unit (Fig. 1). A pairwise comparison between these two molecules shows no significant differences in their bond lengths or angles, although the conformations of the two molecules are different. The C1–C2 bond distance of 1.338 (3) Å is indicative of double-bond character. The angles C1–C2–C3 [125.1 (2)°] and C2–C1–C5 [124.8 (2)°] are larger, and N1–C1–C5 [112.0 (2)°] smaller than 120°. This results in a close mutual repulsion between the ethyl group on C1 and carbonyl group on C3.

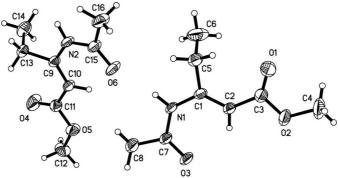


Figure 1
The molecular structure of (I), showing ellipsoids at the 50% probability level (Siemens, 1995).

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The molecules are interconnected by $N-H\cdots O$ hydrogen bonding in the crystal (Table 2). As illustrated in Fig. 2, the hydrogen bonding links the molecules along the a axis.

Experimental

The title compound was synthesized according to the literature (Zhu *et al.*, 1999). A crystal suitable for X-ray analysis was slowly grown in a mixed solvent of ethyl acetate and hexane at room temperature. ¹H NMR (400 MHz, acetone- d_6 , Bruker): δ 1.09–1.12 (t, J = 7.5 Hz, 3H), 2.06 (s, 3H), 2.71–2.77 (q, J = 7.5 Hz, 2H), 3.59 (s, 3H), 6.87 (s, 1H), 8.75 (br, 1H).

Crystal data

$D_x = 1.220 \text{ Mg m}^{-3}$
Mo $K\alpha$ radiation
Cell parameters from 2920
reflections
$\theta = 1-27.5^{\circ}$
$\mu = 0.09 \text{ mm}^{-1}$
T = 294 (2) K
Needle, colorless
$0.38\times0.12\times0.10~\text{mm}$

Data collection

Siemens SMART CCD area-	4308 independent reflections
detector diffractometer	1544 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.057$
Absorption correction: multi-scan	$\theta_{\rm max} = 27.6^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -12 \rightarrow 12$
$T_{\min} = 0.965, T_{\max} = 0.991$	$k = -15 \rightarrow 16$
12544 measured reflections	$l = -16 \rightarrow 20$

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.059$	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.05P)^{2}]$
$wR(F^2) = 0.156$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.06	$(\Delta/\sigma)_{\rm max} < 0.001$
4308 reflections	$\Delta \rho_{\text{max}} = 0.17 \text{ e Å}^{-3}$
223 parameters	$\Delta \rho_{\min} = -0.19 \text{ e Å}^{-3}$

Table 1 Selected geometric parameters (Å, °).

O1-C3	1.190(3)	O4-C11	1.198 (3)
O3-C7	1.219(3)	O6-C15	1.222 (3)
N1-C7	1.355 (3)	N2-C15	1.356 (3)
N1-C1	1.391(3)	N2-C9	1.388 (3)
C1-C2	1.338 (3)	C9-C10	1.334 (3)
C2-C3	1.445 (4)	C10-C11	1.443 (3)
C2-C1-C5	124.8 (2)	O1-C3-C2	129.4 (3)
N1-C1-C5	112.0(2)	O2 - C3 - C2	109.7 (2)
C1-C2-C3	125.1 (2)	O3-C7-N1	123.0(2)
O1-C3-O2	120.9(3)	O3 - C7 - C8	121.7 (2)
N1-C1-C2-C3	-176.8(3)	C4-O2-C3-C2	-179.4(2)
C5-C1-C2-C3	2.6 (4)	C1-N1-C7-O3	-4.0(5)
C4-O2-C3-O1	0.3 (4)	C1-N1-C7-C8	175.5 (3)

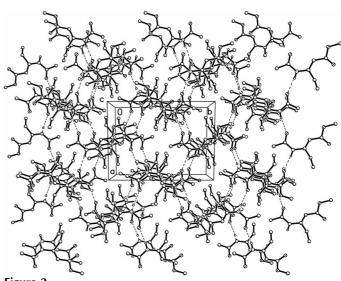


Figure 2
Packing diagram for (I). Hydrogen bonds are indicated by dashed lines.

 Table 2

 Hydrogen-bonding geometry (Å, °).

D $ H$ $\cdot \cdot \cdot A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
$ \begin{array}{c} N1 - H1A \cdots O6 \\ N2 - H2A \cdots O3^{i} \end{array} $	0.86	2.11	2.967 (3)	173
	0.86	2.08	2.936 (3)	174

Symmetry code: (i) x - 1, y, z.

H atoms were included in the riding-model approximation, with $U_{\rm iso}$ values equal to $U_{\rm eq}$ of the atom to which they are bound.

Data collection: *SMART* (Siemens, 1995); cell refinement: *SMART*; data reduction: *SAINT* (Siemens, 1995) and *SHELXTL* (Siemens, 1995); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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