organic papers

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Key indicators

Single-crystal X-ray study T = 296 KMean $\sigma(C-C) = 0.004 \text{ Å}$ R factor = 0.042 wR factor = 0.134 Data-to-parameter ratio = 19.6

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

(Z)-4-(tert-Butylamino)-4-oxo-2-butenoic acid

The title compound, $C_8H_{13}NO_3$, is an amidated maleic acid derivative. There are intramolecular $O-H \cdots O$ and intermolecular step-like $N-H \cdots O$ hydrogen bonds, forming zigzag chains along the *c* axis.

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Comment

On deprotonation, a carboxylic acid having a neighboring amide group may form an intramolecular $N-H\cdots O$ hydrogen bond between the carboxylate O atom and the neighboring amide NH group. Previously, we have synthesized various aliphatic carboxylic acids having the neighboring amide group and reported the crystal structures (Takahashi *et al.*, 2003, 2004). In these carboxylic acids, however, only intermolecular hydrogen bonds are observed. In the present study, we synthesized a novel amidated carboxylic acid derivative, (I), from maleic anhydride and *tert*-butylamine.



In (I), there is an $O3-H2\cdots O1=C4$ intramolecular hydrogen bond (Fig. 1, Tables 1 and 2). This intramolecular $O-H\cdots O=C$ hydrogen bond is also observed in a chloroform[D₁] solution using ¹H NMR and NOESY spectroscopy (10 m*M*). There is also an intermolecular N1-H1 $\cdots O2^{i}=C1^{i}$ [symmetry code: (i) $x, -\frac{1}{2} - y, \frac{1}{2} + z$] hydrogen bond, forming zigzag chains along the *c* axis (Fig. 2). This zigzag-chain hydrogen-bonded network results from the bulky *tert*-butyl group and is very rare in comparison with similar halfamidated maleic acid derivatives, as discussed in previous reports (*e.g.* Allen & Kennard, 1973; Prasad *et al.*, 2002; Lynch & McClenaghan, 2002). There is a hydrophobic layer containing *tert*-butyl groups sandwiched between layers of the hydrogen-bonded chains.

Experimental

To maleic anhydride (10 g, 0.10 mol), *tert*-butylamine (10 ml, 0.095 mol) was added dropwise over an ice–water bath, without direct sunlight, and the mixed solution was stirred at room temperature. After 12 h, 3.5% aqueous HCl solution was added, yielding a precipitate, which was collected by filtration and washed with water. The product was recrystallized from ethyl acetate to give colorless crystals of (I) suitable for X-ray analysis (yield 71%; m.p. 431–434 K). ¹H NMR ([*D*₆]DMSO at 303 K): δ 15.1 (1H, *br*), 8.73 (1H, *s*), 6.31 [1H, ³*J*(H,H) = 12.9 Hz, *d*], 6.10 [1H, ³*J*(H,H) = 12.9 Hz, *d*], 1.23 (9H, *s*). Elemental analysis calculated for C₈H₁₃NO₃: C 56.13, H 7.65, N 8.18%; found: C 55.98, H 7.65, N 8.20%.

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Crystal data

 $C_8H_{13}NO_3$ $M_r = 171.19$ Monoclinic, $P2_1/c$ a = 9.283 (4) Å b = 8.416 (3) Å c = 12.680 (5) Å $\beta = 105.42$ (3)° V = 955.0 (7) Å³ Z = 4

Data collection

Rigaku AFC-5*R* diffractometer ω -2 θ scans Absorption correction: ψ scan (North *et al.*, 1968) $T_{min} = 0.900, T_{max} = 0.962$ 2325 measured reflections 2195 independent reflections 994 reflections with $I > 2\sigma(I)$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.057P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.042$	+ 0.0332P]
$wR(F^2) = 0.134$	where $P = (F_o^2 + 2F_c^2)/3$
S = 0.98	$(\Delta/\sigma)_{\rm max} < 0.001$
2195 reflections	$\Delta \rho_{\rm max} = 0.14 \text{ e } \text{\AA}^{-3}$
112 parameters	$\Delta \rho_{\rm min} = -0.19 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

Table 1

Selected geometric parameters (Å, $^{\circ}$).

O1-C4	1.248 (2)	N1-C4	1.319 (2)
O2-C1	1.216 (3)	N1-C5	1.486 (3)
O3-C1	1.305 (3)	C2-C3	1.329 (3)
C3-C2-C1	131.6 (2)	C2-C3-C4	128.58 (19)
O2-C1-C2-C3	-167.3 (2)	C1-C2-C3-C4	-2.5 (4)
O3-C1-C2-C3	13.6 (4)	C5-N1-C4-C3	-178.40 (18)

 $D_x = 1.191 \text{ Mg m}^{-3}$

Cell parameters from 25

 $0.50 \times 0.20 \times 0.20$ mm

Mo $K\alpha$ radiation

reflections

Prism. colorless

 $\theta = 14.3 - 15.0^{\circ}$ $\mu = 0.09 \text{ mm}^{-1}$

T = 296 K

 $\begin{aligned} R_{\rm int} &= 0.037\\ \theta_{\rm max} &= 27.5^\circ\\ h &= 0 \rightarrow 12 \end{aligned}$

 $k=0\rightarrow 10$

 $l = -16 \rightarrow 15$

3 standard reflections

every 150 reflections

intensity decay: 0.4%

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$\begin{array}{c} N1 - H1 \cdots O2^{i} \\ O3 - H2 \cdots O1 \end{array}$	0.86 1.01 (3)	2.05 1.46 (3)	2.897 (3) 2.458 (2)	168 172 (2)
	1 1.			

Symmetry code: (i) $x, -\frac{1}{2} - y, \frac{1}{2} + z$.

Atom H2 of the carboxylic group was located in a difference map and refined freely. Other H atoms were positioned geometrically and were treated as riding on their parent atoms, with methyl and methylene C-H distances and an amide N-H distance of 0.96 Å, 0.93 Å and 0.86 Å, respectively. Rotating-group refinement was used for the methyl groups and carboxylic acid group. $U_{\rm iso}({\rm H})$ values were set to $1.2U_{\rm eq}$ (carrier atom).

Data collection: MSC/AFC Diffractometer Control Software (Molecular Structure Corporation, 1991); cell refinement: MSC/AFC



Figure 1





Figure 2

A packing diagram of (I). Dashed lines indicate hydrogen bonds, and the grey molecules are affiliated with other hydrogen-bonded networks.

Diffractometer Control Software; data reduction: TEXSAN (Molecular Structure Corporation, 2000); program(s) used to solve structure: SIR92 (Altomare et al., 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: TEXSAN and MERCURY (Bruno et al., 2002); software used to prepare material for publication: TEXSAN and MERCURY.

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