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A low-temperature determination of butyramide

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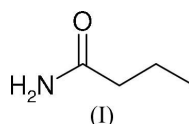
Key indicators

Single-crystal X-ray study
 $T = 150$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.041
 wR factor = 0.111
Data-to-parameter ratio = 13.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

The low-temperature structure determination of butyramide, $\text{C}_4\text{H}_9\text{NO}$, obtained as part of an experimental polymorph screen on adenine, is reported here. Each molecule takes part in four hydrogen bonds to form a three-dimensional ribbon structure.

Comment

The title compound, (I), is one of the *n*-aliphatic amides and has recently been studied as a possible agent for growth inhibition of human neuroblastoma cell lines (Rocchi *et al.*, 1998) and inhibitory effects on DNA synthesis on hepatoma cells (Lea *et al.*, 1993).



The powder diffractogram data for (I) were reported in 1950 (Matthews *et al.*, 1950), as part of a study on derivatives of fatty acids, and the unit cell was determined five years later (Turner & Lingafelter, 1955) using Weissenberg photographs, to give $a = 9.94$ Å, $b = 5.79$ Å, $c = 10.02$ Å and $\beta = 100.9^\circ$. Examination of the systematic absences showed the space group to be $P2_1/a$; however, no atomic coordinates were published. We have solved and refined the crystal structure of butyramide at 150 K, to give a final R value of 0.041. There is a 12° difference in the β angle between the two determinations. In (I), the bond lengths and angles are within expected values (Allen *et al.*, 1987), with the C–C bond lengths in the range 1.5057 (18)–1.515 (2) Å and with N1–C1 and O2–C1 bond lengths of 1.3257 (15) and 1.2395 (13) Å, respectively. There is a relative twist of the carbon chain from planarity, with torsion angles C1–C2–C3–C4 and N1–C1–C2–C3 of 177.41 (21) and 151.62 (12) $^\circ$, respectively. The packing consists of

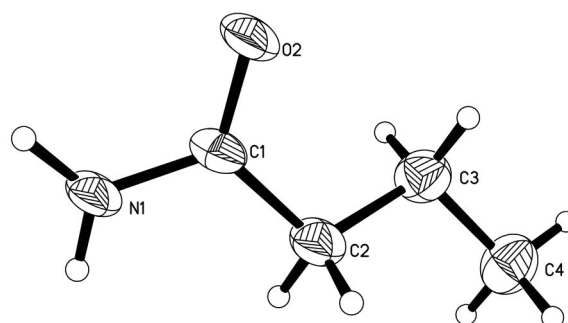


Figure 1
View of (I), showing the atom labelling scheme. Displacement ellipsoids are drawn at the 50% probability level.

centrosymmetric dimers, linked through a pair of N—H...O hydrogen bonds [2.9470 (15) Å]. The other amine H atom is used to hydrogen bond to an adjacent dimer unit which is approximately perpendicular (73°), through an N—H...O hydrogen bond [2.8496 (14) Å], resulting in the formation of a three-dimensional criss-crossed ribbon structure (Fig. 2).

Experimental

As part of an experimental polymorph screen on adenine, (I) was obtained from a 0.3 M aqueous solution of (I), to which approximately 0.15 g of adenine was added, and which was stirred on a hotplate at 303 K for 3 d. This solution was filtered, then evaporated at room temperature (10 ml solution, in 75 × 25 mm vessels) in an attempt to crystallize adenine, as it has been found that the solubility of purine and pyrimidine bases increases in aqueous amide solutions (Herskovits & Bowen, 1974). Colourless block-like crystals of (I) were formed after a number of days.

Crystal data

C ₄ H ₉ NO	$D_x = 1.107 \text{ Mg m}^{-3}$
$M_r = 87.12$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 1237 reflections
$a = 9.814 (3) \text{ \AA}$	$\theta = 2.2\text{--}25.4^\circ$
$b = 5.9232 (17) \text{ \AA}$	$\mu = 0.08 \text{ mm}^{-1}$
$c = 9.701 (3) \text{ \AA}$	$T = 150 (2) \text{ K}$
$\beta = 112.070 (4)^\circ$	Block, colourless
$V = 522.6 (3) \text{ \AA}^3$	$0.38 \times 0.20 \times 0.16 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART APEX diffractometer	1244 independent reflections
ω scans	993 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.021$
$T_{\text{min}} = 0.971$, $T_{\text{max}} = 0.987$	$\theta_{\text{max}} = 28.3^\circ$
4321 measured reflections	$h = -13 \rightarrow 12$
	$k = -7 \rightarrow 7$
	$l = -12 \rightarrow 12$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.064P)^2 + 0.0651P]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.111$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.01$	$\Delta\rho_{\text{max}} = 0.19 \text{ e \AA}^{-3}$
1244 reflections	$\Delta\rho_{\text{min}} = -0.12 \text{ e \AA}^{-3}$
91 parameters	
All H-atom parameters refined	

Table 1

Hydrogen-bond geometry (Å, °).

$D\text{—}H\cdots A$	$D\text{—}H$	$H\cdots A$	$D\cdots A$	$D\text{—}H\cdots A$
N1—H1...O2 ⁱ	0.92 (2)	2.03 (2)	2.9470 (15)	176 (1)
N1—H2...O2 ⁱⁱ	0.89 (2)	1.98 (2)	2.8496 (14)	168 (1)

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

H atoms were refined independently with an isotropic model.

Data collection: SMART (Bruker, 2000); cell refinement: SAINT; data reduction: SAINT (Bruker, 2000); program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 2000) and MERCURY (Bruno *et al.*, 2002); software used to prepare material for publication: SHELXL97.

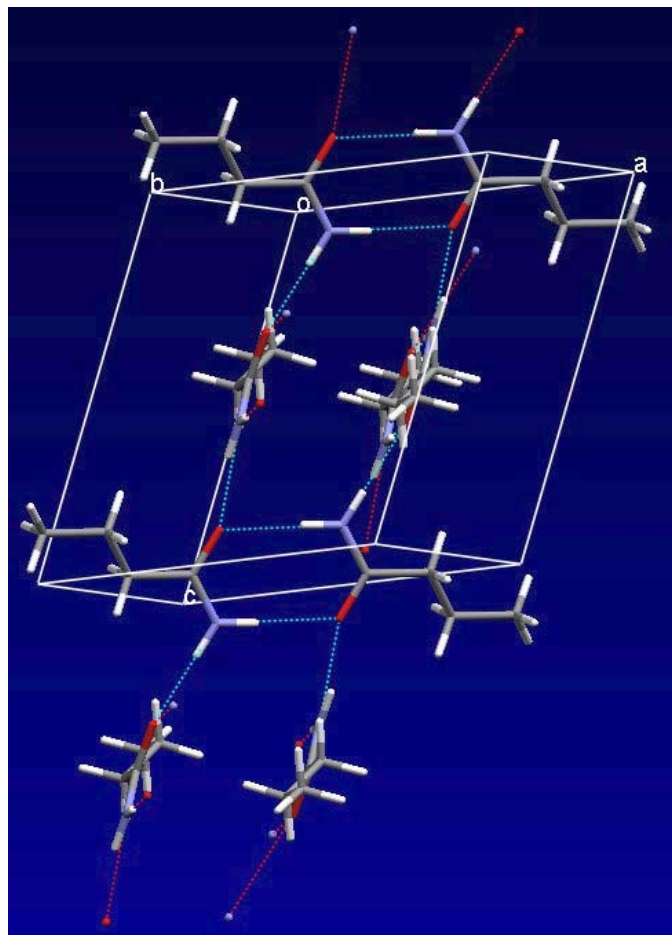


Figure 2

The packing in (I), showing the butyramide dimer unit which forms a hydrogen-bonded (dashed lines) criss-cross ribbon motif.

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