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Key indicators

 Single-crystal X-ray study
 T = 293 K
 Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$
 R factor = 0.041
 wR factor = 0.110
 Data-to-parameter ratio = 9.5

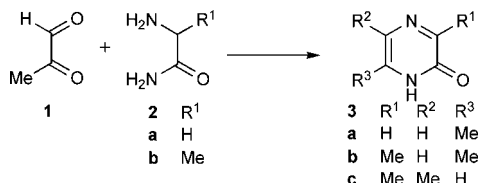
 For details of how these key indicators were
 automatically derived from the article, see
<http://journals.iucr.org/e>.

 Surprising orientation in ring synthesis of
 3,5-dimethylpyrazin-2(1H)-one

 The reaction of pyruvaldehyde with alaninamide gave the title
 compound, $\text{C}_6\text{H}_8\text{N}_2\text{O}$, and not the anticipated 3,6-dimethyl-
 pyrazin-2-one.

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Comment

 One of the standard methods to prepare pyrazin-2-ones is by
 the condensation of a 1,2-dicarbonyl compound with an α -
 amino acid amide (Garg *et al.*, 2002; Jones, 1949; Karmas &
 Spoerri, 1952). For example, pyruvaldehyde (1) (see scheme)
 reacts with glycineamide (2a) to give 6-methylpyrazin-2-one
 (3a) (Yates *et al.*, 1995). The orientation in this ring synthesis
 represents the combination of the amide N atom with the
 ketone carbonyl and of the amine group with the aldehyde
 carbonyl group. In the course of our studies on the dipolar
 cycloaddition reactions of 3-oxidopyraziniums (Kiss *et al.*,
 1987; Allway *et al.*, 1990; Yates *et al.*, 1995), we required 3,6-
 dimethylpyrazin-2-one (3b) and assumed that, by analogy, it
 would result from a reaction of pyruvaldehyde with alana-
 inamide (2b).

 Reaction of pyruvaldehyde with alaninamide produced a
 pyrazinone, as anticipated, but standard spectroscopic analysis
 could not unambiguously confirm the structure of the product.
 For example, ^1H NMR spectroscopy revealed two three-
 hydrogen singlet signals corresponding to the two methyl
 groups at δ 2.22 and 2.41 and a one-hydrogen singlet signal for
 the ring C-hydrogen at δ 6.88, but these data are consistent
 both with the anticipated structure (3b) and also with its
 isomer, 3,5-dimethylpyrazin-2-one (3c).

 Suitable crystals were grown from ethyl acetate and an
 X-ray analysis carried out. This showed the product to be 3,5-
 dimethylpyrazin-2(1H)-one (3c) (Fig. 1). Currently, we have
 no explanation for this unexpected regioselectivity; however,
 the moral from this result is that, for each pyrazinone
 synthesized by this method, unambiguous proof of structure
 must be sought.

Experimental

 A solution of L-alaninamide hydrochloride (95%, 0.26 g, 2 mmol) in
 methanol (1.0 ml) was cooled to 243 K and to it was added a solution

of pyruvaldehyde (40%, 0.36 g, 2 mmol) in methanol (0.5 ml) also precooled to 243 K. Next, with stirring, aqueous sodium hydroxide solution (12.5 M, 0.50 ml, 2.5 mmol) was added dropwise while the temperature was maintained below 263 K. The mixture was allowed to stand at 268 K for 2 h, then at r.t. for 3 h. To the mixture was added hydrochloric acid (12 M, 0.5 ml) followed by solid NaHCO₃ (0.25 g) to neutralize excess acid, and the whole was evaporated to dryness in a vacuum at 363 K. The residue was extracted with three portions (2 ml) of boiling chloroform. Evaporation of the extract left a yellow solid (205 mg, 83%). This was recrystallized from ethyl acetate (2 ml) to give colourless crystals (58 mg, 24%; m.p. 417–419 K).

Crystal data

C ₆ H ₈ N ₂ O	$D_x = 1.261 \text{ Mg m}^{-3}$
$M_r = 124.14$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 12419 reflections
$a = 4.009 (10) \text{ \AA}$	$\theta = 2.3\text{--}24.9^\circ$
$b = 14.59 (3) \text{ \AA}$	$\mu = 0.09 \text{ mm}^{-1}$
$c = 11.59 (3) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\beta = 105.25 (10)^\circ$	Needle, colourless
$V = 654 (3) \text{ \AA}^3$	$0.6 \times 0.1 \times 0.1 \text{ mm}$
$Z = 4$	

Data collection

Rigaku R-Axis diffractometer	$R_{\text{int}} = 0.045$
φ scans	$\theta_{\text{max}} = 24.9^\circ$
Absorption correction: none	$h = 0 \rightarrow 4$
12419 measured reflections	$k = 0 \rightarrow 17$
839 independent reflections	$l = -13 \rightarrow 13$
724 reflections with $I > 2\sigma(I)$	

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0505P)^2 + 0.2114P]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.110$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.10$	$\Delta\rho_{\text{max}} = 0.18 \text{ e \AA}^{-3}$
839 reflections	$\Delta\rho_{\text{min}} = -0.15 \text{ e \AA}^{-3}$
88 parameters	
H atoms treated by a mixture of independent and constrained refinement	

H atoms bonded to C were included in calculated positions using the riding model, with C–H distances of 0.93 and 0.96 Å and with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for methyl H atoms and $1.2U_{\text{eq}}(\text{C})$ for the other H atoms; atom H1, attached to N1, was found by difference Fourier methods and refined isotropically.

Data collection: *MSC Diffractometer Control Software* (Molecular Structure Corporation, 1992); cell refinement: *DENZO* (Otwinowski & Minor, 1987); data reduction: *DENZO*; program(s) used to solve

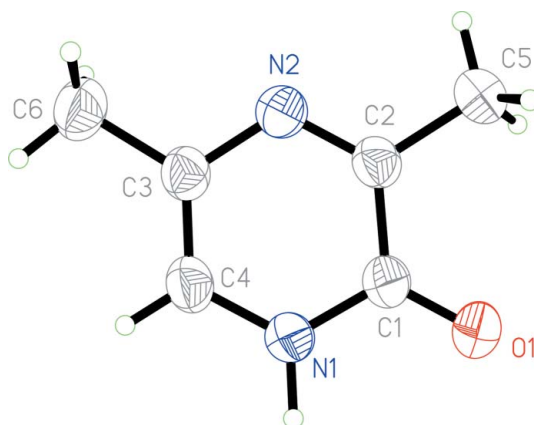


Figure 1 The molecular structure of (3c), with displacement ellipsoids drawn at the 50% probability level.

structure: *SHELXS86* (Sheldrick, 1985); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *TEXSAN* (Molecular Structure Corporation, 1995).

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