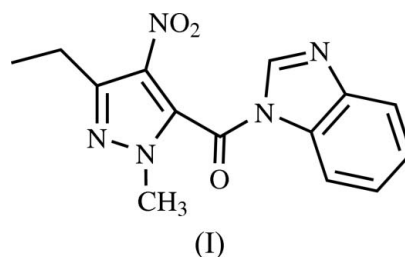
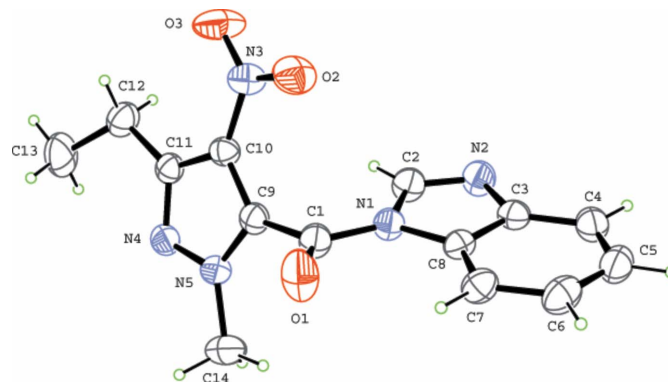


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## Key indicators

Single-crystal X-ray study  
 $T = 298\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$   
 $R$  factor = 0.041  
 $wR$  factor = 0.136  
Data-to-parameter ratio = 16.0For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.3-[(3-Ethyl-1-methyl-4-nitro-1*H*-pyrazol-5-yl)-  
carbonyl]-1*H*-benzimidazoleIn the title compound,  $\text{C}_{14}\text{H}_{13}\text{N}_5\text{O}_3$ , the dihedral angle formed  
between the five-membered pyrazole and the benzimidazole  
ring system is  $68.2(2)^\circ$ .Received 9 May 2006  
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## Comment

Derivatives of pyrazole have high potential for biological  
activity, and some of these have been widely used as pesticides  
and fungicides (Grenda *et al.*, 1965). As a continuation of our  
work on the structure–activity relationship of pyrazole deri-  
vatives, we have obtained a crystalline compound, (I), that was  
the product of the condensation reaction of 3-ethyl-1-methyl-  
4-nitropyrazole-5-carboxylic acid chloride and benzimidazole.An inspection of the geometric parameters (Table 1) indi-  
cates that there is considerable delocalization of  $\pi$ -electron  
density over the pyrazole ring. However, this delocalization  
does not extend over the entire molecule; a dihedral angle of  
 $68.7(2)^\circ$  is formed between the pyrazole and the central C9/  
C1/O1/N1 plane; this latter plane and the benzimidazole ring  
system are essentially coplanar, the dihedral angle between  
them being  $4.2(2)^\circ$ .**Figure 1**  
The structure of (I) with 40% probability displacement ellipsoids.

Experimental

3-Ethyl 1-methyl-4-nitropyrazole-5-carboxylic acid chloride (2.17 g, 10 mmol; Okada *et al.*, 1989) was added dropwise to a chloroform solution (30 ml) containing benzimidazole (1.18 g, 10 mmol), prepared according to the procedure of Wagner & Millett (1939), and triethylamine (1.2 g, 12 mmol). The mixture was stirred for 15 h, poured into ice-water and extracted with chloroform. The chloroform layer was washed with an aqueous solution of sodium carbonate, water and a saturated aqueous solution of sodium chloride. After drying over anhydrous sodium sulfate, the solution was concentrated under reduced pressure. The residue was then recrystallized from ethyl acetate to give colorless blocks (m.p. 414–416 K).

Crystal data

$C_{14}H_{13}N_5O_3$   $Z = 4$   
 $M_r = 299.29$   $D_x = 1.420 \text{ Mg m}^{-3}$   
 Monoclinic,  $P2_1/n$  Mo  $K\alpha$  radiation  
 $a = 10.442 (4) \text{ \AA}$   $\mu = 0.10 \text{ mm}^{-1}$   
 $b = 7.873 (4) \text{ \AA}$   $T = 298 (1) \text{ K}$   
 $c = 17.380 (5) \text{ \AA}$  Block, colorless  
 $\beta = 101.595 (15)^\circ$   $0.42 \times 0.38 \times 0.30 \text{ mm}$   
 $V = 1399.7 (10) \text{ \AA}^3$

Data collection

Rigaku R-AXIS RAPID 3220 measured reflections  
 diffractometer 3200 independent reflections  
 $\omega$  scans 2413 reflections with  $F^2 > 2\sigma(F^2)$   
 Absorption correction: multi-scan  $R_{int} = 0.025$   
 (ABSCOR; Higashi, 1995)  $\theta_{max} = 27.5^\circ$   
 $T_{min} = 0.959, T_{max} = 0.969$

Refinement

Refinement on  $F^2$  H-atom parameters constrained  
 $R[F^2 > 2\sigma(F^2)] = 0.041$   $w = 1/[0.0021F_o^2 + \sigma(F_o^2)]/(4F_o^2)$   
 $wR(F^2) = 0.136$   $(\Delta/\sigma)_{max} < 0.001$   
 $S = 1.01$   $\Delta\rho_{max} = 0.18 \text{ e \AA}^{-3}$   
 3200 reflections  $\Delta\rho_{min} = -0.14 \text{ e \AA}^{-3}$   
 200 parameters

Table 1

Selected bond lengths ( $\text{\AA}$ ).

O1—C1	1.1986 (15)	N2—C3	1.4028 (16)
O2—N3	1.2219 (17)	N3—C10	1.4264 (18)
O3—N3	1.2236 (17)	N4—N5	1.3570 (16)
N1—C1	1.3771 (16)	N4—C11	1.3232 (17)
N1—C2	1.3963 (15)	N5—C9	1.3386 (17)
N1—C8	1.4055 (17)	N5—C14	1.454 (2)
N2—C2	1.2851 (17)		

The H atoms were included in the final cycles of refinement in the riding model approximation, with C—H = 0.93, 0.96 and 0.97  $\text{\AA}$  for aromatic, methyl and methylene H atoms, respectively, and  $U_{iso}(H) = 1.2U_{eq}(C)$ .

Data collection: *PROCESS-AUTO* (Rigaku/MSC, 2004); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/MSC, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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