

Wu-Yan Wang and Zhen-Ming Yin*

College of Chemistry and Life Sciences, Tianjin Normal University, Tianjin 300074, People's Republic of China

Correspondence e-mail:
hsxyzm@mail.tjnu.edu.cn

Key indicators

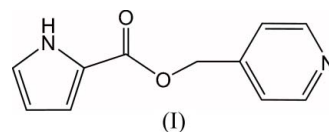
Single-crystal X-ray study
 $T = 294\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.040
 wR factor = 0.121
Data-to-parameter ratio = 15.3For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.4-Pyridylmethyl 1*H*-pyrrole-2-carboxylate

The title compound, $\text{C}_{11}\text{H}_{10}\text{N}_2\text{O}_2$, has been synthesized by the reaction of 2-(trichloroacetyl)pyrrole with 4-(hydroxymethyl)pyridine. In the solid state, the molecules form a one-dimensional infinite ladder structure through intermolecular $\text{N}-\text{H}\cdots\text{N}$ and $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds.

Received 13 March 2007
Accepted 26 March 2007

Comment

Hydrogen-bond-mediated self-assembly represents an area of considerable current interest (Burrows, 2004). Recently, it was found that pyrrole-based entities are also capable of undergoing self-assembly through hydrogen bonds, especially in the solid state (Sessler *et al.*, 2003; Wang & Yin, 2006; Yin & Li, 2006). We report here the self-assembly of the title compound, (I), *via* conventional $\text{N}-\text{H}\cdots\text{N}$ and non-classical $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds.



The molecular structure of (I) is shown in Fig. 1. In the solid state, the carbonyl group is arranged *anti* to its adjacent pyrrole NH group; this is quite different from the previous observation (Yin & Li, 2006). The dihedral angle between the pyrrole ring and the pyridine ring is $75.55(14)^\circ$. Two molecules of (I) are held together by a pair of $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds. The dimers are further connected by a pair of non-classical $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds (Table 1), forming a one-dimensional ladder-type structure (Fig. 2).

Experimental

4-(Hydroxymethyl)pyridine (109 mg, 1 mmol), 2-(trichloroacetyl)pyrrole (316 mg, 1.5 mmol) and triethylamine (0.5 ml) were added to acetonitrile (20 ml), and the mixture was refluxed for 20 h. The

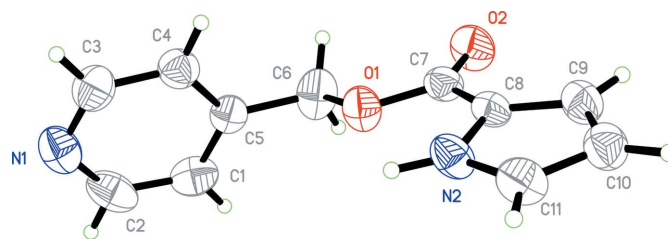


Figure 1
The molecular structure of (I), with the numbering scheme and 30% probability displacement ellipsoids.

solution was evaporated under reduced pressure and the residue was purified by column chromatography on silica gel with ethyl acetate–petroleum ether (1:2 v/v), affording the title compound (white powder, 164 mg, 81%). Analysis calculated for C₁₁H₁₀N₂O₂: C 65.34, H 4.98, N 13.85%; found: C 65.25, H 5.07, N 13.76%.

Crystal data

C₁₁H₁₀N₂O₂ V = 1053.2 (7) Å³
 M_r = 202.21 Z = 4
 Monoclinic, P2₁/c Mo Kα radiation
 a = 7.698 (3) Å μ = 0.09 mm⁻¹
 b = 15.796 (6) Å T = 294 (2) K
 c = 8.789 (3) Å 0.26 × 0.24 × 0.20 mm
 β = 99.771 (7)°

Data collection

Bruker SMART CCD area-detector 5812 measured reflections
 diffractometer 2147 independent reflections
 Absorption correction: multi-scan 884 reflections with I > 2σ(I)
 (SADABS; Bruker, 1997) R_{int} = 0.055
 T_{min} = 0.977, T_{max} = 0.982

Refinement

R[F² > 2σ(F²)] = 0.040 H atoms treated by a mixture of
 wR(F²) = 0.121 independent and constrained
 S = 0.91 refinement
 2147 reflections Δρ_{max} = 0.14 e Å⁻³
 140 parameters Δρ_{min} = -0.15 e Å⁻³
 1 restraint

Table 1

Hydrogen-bond geometry (Å, °).

D–H...A	D–H	H...A	D...A	D–H...A
N2–H2A...N1 ⁱ	0.90 (2)	2.01 (2)	2.902 (3)	169 (3)
C11–H11...O2 ⁱⁱ	0.93	2.47	3.331 (3)	155

Symmetry codes: (i) -x, -y + 1, -z + 2; (ii) x - 1, y, z.

The N-bound H atom was located in a difference map and refined freely. Other H atoms were positioned geometrically (C–H = 0.93 or 0.97 Å) and refined using a riding model, with U_{iso}(H) = 1.2U_{cq}(C).

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

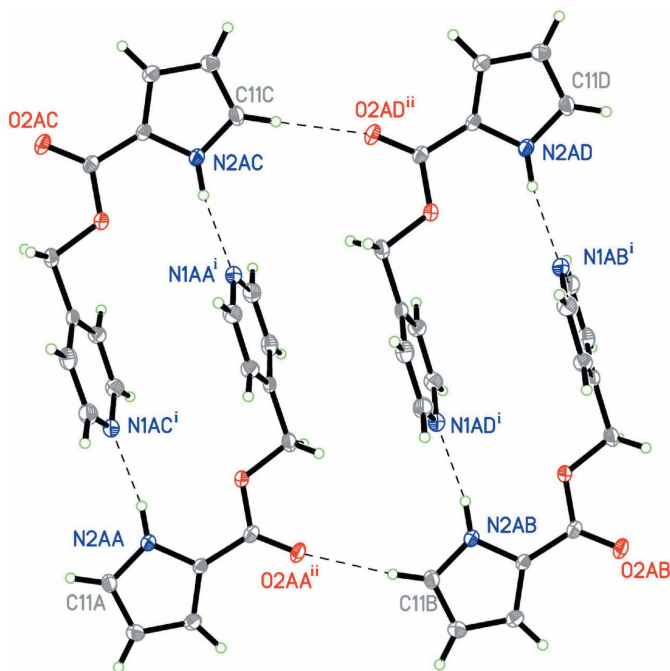


Figure 2

Part of the ladder structure of (I), with molecules connected by N–H...N(-x, 1 - y, 2 - z) and C–H...O(x - 1, y, z) hydrogen bonds (dashed lines).

YZM acknowledges financial support from the University Science Foundation of Tianjin Educational Committee (No. 20050609).

References

Bruker (1997). SADABS (Version 2.10), SMART (Version 5.63), SAINT (Version 6.45) and SHELXTL (Version 6.12). Bruker AXS Inc., Madison, Wisconsin, USA.
 Burrows, A. D. (2004). *Struct. Bond.*, **108**, 55–96.
 Sessler, J. L., Berthon-Gelloz, G., Gale, P. A., Camiolo, S., Anslyn, E. V., Anzenbacher, P. Jr, Furuta, H., Kirkovits, G. J., Lynch, V. M., Maeda, H., Morosini, P., Scherer, M., Shriver, J. & Zimmerman, R. S. (2003). *Polyhedron*, **22**, 2963–2983.
 Sheldrick, G. M. (1997). SHELXS97 and SHELXL97. University of Göttingen, Germany.
 Wang, J.-Y. & Yin, Z.-M. (2006). *Acta Cryst.* **E62**, o230–o232.
 Yin, Z. & Li, Z. (2006). *Tetrahedron Lett.* **47**, 7875–7879.