

Gang Yu, Yi-Zhi Li, Li-Ya Cao,
Xiao-Mo Zhang, Kai Wang and
Hong-Wen Hu*Coordination Chemistry Institute, State Key
Laboratory of Coordination Chemistry, Nanjing
University, Nanjing 210093, People's Republic
of China

Correspondence e-mail: llyyz@nju.edu.cn

Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$
Disorder in solvent or counterion
 R factor = 0.052
 wR factor = 0.147
Data-to-parameter ratio = 12.0For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.1-Ethyl-2-oxo-5-phenyl-1,6-dihydro-2H-
oxazolo[4',5':5,6]pyrido[3,4-b]indole
methanol hemisolvateThe title compound, $\text{C}_{20}\text{H}_{15}\text{N}_3\text{O}_2 \cdot 0.5\text{CH}_3\text{OH}$, has been
synthesized from the ene-lactam with $\text{P}(\text{OEt})_3$ under an N_2
atmosphere. The title indole molecules are linked *via* $\text{N}-\text{H} \cdots \text{O}$
hydrogen bonds, forming one-dimensional chains.

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Comment

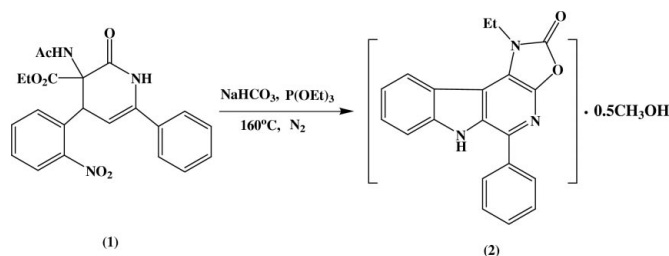
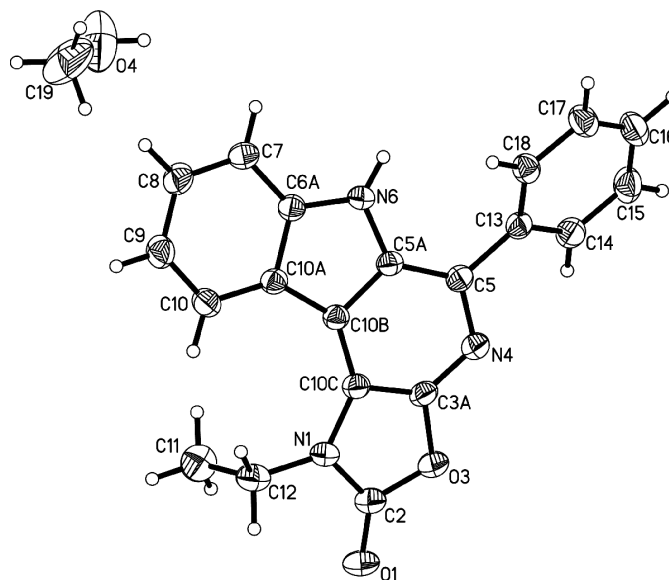
Azaelliptitoxin (azatoxin) as a potent inhibitor of DNA
topoisomerase II and tubulin polymerization have attracted
much attention (Tepe *et al.*, 1996). However, the crystal
structures of azaelliptitoxin and its analogues have rarely been
reported (Abu-Safieh *et al.*, 2002). Conveniently, we have
synthesized the title compound, (2), similar to azaelliptitoxin
in one pot from the ene-lactam (1) with $\text{P}(\text{OEt})_3$ under an N_2
atmosphere (Yu *et al.*, 2004).The asymmetric unit of (2) comprises one title indole
molecule and one-half of a methanol molecule of crystal-

Figure 1

The molecular structure of (2) with 30% probability displacement
ellipsoids. The methanol atom O4 shows positional disorder and one of
two possible positions has been omitted for clarity.

lization (Fig. 1). The title indole molecules are linked by N—H···O hydrogen bonds (Table 1), forming one-dimensional chains (Fig. 2). Neighbouring molecular chains are parallel to one another, forming layers (Fig. 3); neighboring layers are cross-linked to each other through solvent methanol molecules, leading to the three-dimensional supermolecular framework.

Experimental

The ene-lactam (1) (1.06 g, 2.5 mmol) and NaHCO₃ (0.21 g, 2.5 mmol) in P(OEt)₃ (25 ml) were heated at 393 K under nitrogen. After 3 h, all ene-lactam (1) had disappeared (monitored by thin-layer chromatography). The solvent was removed *in vacuo*, then the title compound was collected by chromatography on silica gel with CH₂Cl₂–EtOAc–petroleum ether (1:10:10). Crystals of (2) suitable for X-ray analysis were obtained by recrystallization from MeOH.

Crystal data

C₂₀H₁₅N₃O₂·0.5CH₄O
M_r = 345.37
 Monoclinic, *C2/c*
a = 17.728 (4) Å
b = 8.5045 (19) Å
c = 22.575 (5) Å
 β = 105.925 (4)°
V = 3273.0 (12) Å³
Z = 8

D_x = 1.402 Mg m⁻³
 Mo Kα radiation
 Cell parameters from 883 reflections
 θ = 2.4–22.7°
 μ = 0.09 mm⁻¹
T = 293 (2) K
 Block, colourless
 0.3 × 0.2 × 0.2 mm

Data collection

Bruker SMART APEX CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.97, *T_{max}* = 0.98
 7860 measured reflections

2884 independent reflections
 2232 reflections with *I* > 2σ(*I*)
R_{int} = 0.071
 θ_{max} = 25.0°
h = -17 → 20
k = -10 → 9
l = -26 → 18

Refinement

Refinement on *F*²
R[*F*² > 2σ(*F*²)] = 0.052
wR(*F*²) = 0.147
S = 1.06
 2884 reflections
 241 parameters
 H-atom parameters constrained

w = 1/[σ²(*F_o*²) + (0.081*P*)² + 0.3023*P*]
 where *P* = (*F_o*² + 2*F_c*²)/3
 (Δ/*σ*)_{max} = 0.011
 Δρ_{max} = 0.28 e Å⁻³
 Δρ_{min} = -0.23 e Å⁻³

Table 1

Hydrogen-bonding geometry (Å, °).

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
N6—H6···O1 ⁱ	0.86	2.16	2.938 (2)	150

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

Methanol atom C19 lies on a twofold axis parallel to *b*, and atom O4 shows positional disorder over two sites. All H atoms were positioned geometrically, with C—H = 0.93–0.97 Å, O—H = 0.85 Å

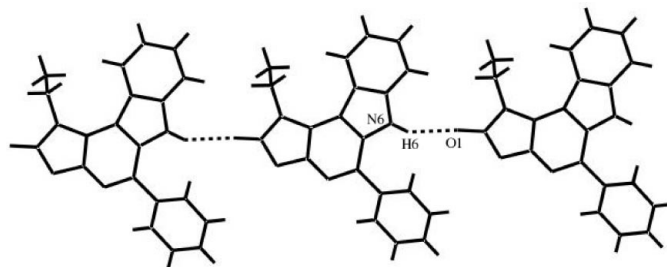


Figure 2

The one-dimensional chain of molecules linked by hydrogen bonds (dashed lines). Symmetry code of atom O1: $\frac{1}{2} + x, \frac{1}{2} + y, z$.

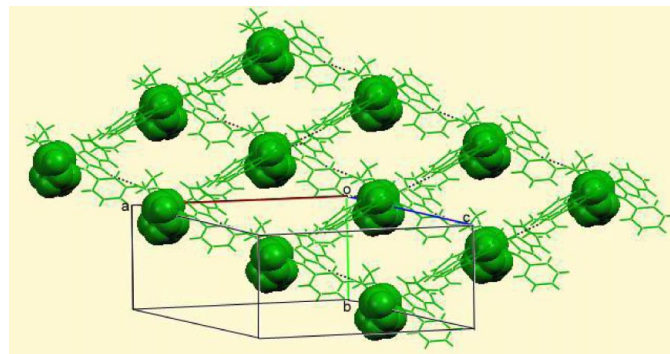


Figure 3

The crystal structure of (2).

and N—H = 0.86 Å, and were refined as riding, with *U*_{iso}(H) set at 1.2 or 1.5 times *U*_{eq} of the parent atom.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 2000); program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL* and *Mercury* (Version 1.2.1; Bruno *et al.*, 2002); software used to prepare material for publication: *SHELXTL*.

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