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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.061 wR factor = 0.177 Data-to-parameter ratio = 16.4

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

Ethyl 2,2"-dioxo-2',3',5',6',7',7a'-hexahydroacenaphthene-1-spiro-3'-1'H-pyrrolizine-2'spiro-1"acenaphthene-1-carboxylate

> In the title compound, $C_{32}H_{25}NO_4$, the mean plane through the pyrrolizidine system is almost perpendicular [dihedral angle 88.9 (1)°] to that through one of the acenaphthene units, and the dihedral angle between the pyrrolizidine and the second acenaphthene system is 81.6 (1)°. In the pyrrolizidine system, one of the rings is in a half-chair conformation while the other is in an envelope conformation. The overall conformation is twisted about the fusion bond. The crystal structure is stabilized by a C–H···O intermolecular hydrogen bond.

Comment

Pyrrolizidine alkaloids represent a group of compounds present in a variety of plants throughout the world. Crogyrodine has been found to exhibit significant neuromuscularblocking activity (Suri *et al.*, 1976). Polycyclic aromatic hydrocarbons are of particular interest because of their high toxicity (Jacob, 1996). Bis(*N*-imino)acenaphthene (Ar-BIAN) has been used as the spectator molecule in reaction sequences, modelling the copolymerization of CO and alkenes (Van Asselt *et al.*, 1994; Markies *et al.*, 1995). The structure of the title pyrrolizidine derivative, (I), is reported here (Fig. 1).



The three N–C distances in (I) differ from each other considerably. Generally, the bond distances and angles of the pyrrolizidine unit are distorted and this can be explained by the spiro character of the compound and the fused-ring system. In the pyrrolizidine unit, the ring-fusion distance [N1–C5 1.480 (3) Å] is in good agreement with values in similar structures (Hay *et al.*, 1982; Sussman & Wedak, 1973; Pérez-Salazar *et al.*, 1978). Bond lengths and angles around the quaternary atom C3 are distorted to some extent from ideal tetrahedral values. For example, the C2–C3 bond is longer than a typical C–C bond of 1.54 (2) Å. The angles around C3 vary from 101.0 (1) to 116.0 (2)°.

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The molecular structure of (I), showing 30% probability displacement ellipsoids.

The bond lengths and angles of the acenaphthene units of (I) are typical of such systems (Repo *et al.*, 1996; Edwards *et al.*, 1980; Selvanayagam *et al.*, 2004). Ketone atom O1 deviates by 0.230 (2) Å from the C2/C9/C10/C15/C16 plane and is observed as the acceptor in a weak intramolecular hydrogen bond from C6–H6A. On the other hand, ketone atom O2 is displaced from the C3/C27/C26/C21/C20 plane by 0.239 (2) Å and acts as an acceptor in a strong intermolecular hydrogen bond from C23–H23 (Table 2).

The dihedral angles between the acenaphthene rings (atoms C2/C9–C19 and C3/C20–C30) and the pyrrolizidine unit (atoms N1/C2–C8) are 88.9 (1) and 82.2 (1)°, respectively. The torsion angles show that the ring containing atoms N1/C2–C5 is in a half-chair conformation, with atom C2 displaced out of the plane of the other four by 0.609 (2) Å, while the ring of atoms N1/C5–C8 is in a near-perfect envelope conformation, with atom C7 displaced out of the plane of the other four of the plane of the other four atoms by 0.441 (4) Å. The overall conformation of the pyrrolizidine unit is folded and twisted about the fusion bond N1–C5, and this observation is consistent with the structure reported by Sawhney *et al.* (1983). The degree of twist about the N1–C5 bond is given by the torsion angles C8–N1–C5–C6 = 17.1 (2)° and C8–N1–C5–H5 = -99.4 (2)°.

The packing of the molecules of (I) in the crystal structure is stabilized by an intermolecular $C-H\cdots O$ -type hydrogen bond.

Experimental

Acenaphthenequinone (1 mmol) and proline (1 mmol) were added to a refluxing solution of $(2 \cdot oxo \cdot 2H \cdot acenapthylen \cdot 1 \cdot ylidene)$ acetic acid ethyl ester (1 mmol) in methanol (10 ml). The mixture was refluxed for 7 h. The solvent was evaporated under reduced pressure and the





The packing of (I), viewed down the a axis. Hydrogen bonds are drawn as dashed lines.

residue was subjected to column chromotography using hexane–ethyl acetate (8:2), to afford (I) in 78% yield. Crystals suitable for X-ray diffraction were obtained by slow evaporation of dichloromethane–hexane mixture (2:1).

Crystal data

$C_{32}H_{25}NO_4$	$D_x = 1.312 \text{ Mg m}^{-3}$
$M_r = 487.53$	Mo- $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 4014
$a = 14.8348 (12) \text{\AA}$	reflections
b = 11.1902 (9) Å	$\theta = 2.3-26^{\circ}$
c = 16.0909 (13) Å	$\mu = 0.09 \text{ mm}^{-1}$
$\beta = 112.479 \ (1)^{\circ}$	T = 293 (2) K
V = 2468.2 (3) Å ³	Block, colourless
Z = 4	$0.23 \times 0.21 \times 0.20 \text{ mm}$

Data collection

Bruker SMART APEX CCD areadetector diffractometer4065 reflections with $I > 2\sigma(I)$ $M_{int} = 0.024$ $R_{int} = 0.024$ ω scans $\theta_{max} = 28.0^{\circ}$ Absorption correction: none $h = -19 \rightarrow 18$ 14755 measured reflections $k = -12 \rightarrow 14$ 5507 independent reflections $l = -20 \rightarrow 19$

Refinement

Selected geometric	parameters (Å,	²).	
01-C9	1.205 (2)	N1-C8	
O2-C20	1.201 (2)	N1-C5	
O3-C31	1.196 (2)	C2-C3	
O4-C31	1.326 (2)	C9-C10	
O4-C32	1.450 (3)	C20-C21	
N1-C2	1.450 (2)	C32-C33	
C2-N1-C8	118.6 (2)	C27-C3-C20	

110.0 (1)

108.8 (2)

100.5(1)

114.9 (1)

17.1 (2)

C4-C3-C20

C27-C3-C2

C4-C3-C2

C20-C3-C2

Table 1		
Selected geometric parameters	(Å	0)

Table 2		

C2-N1-C5

C8-N1-C5

N1-C2-C3

C27 - C3 - C4

C8-N1-C5-C6

Hydrogen-bond geometry (Å, °).

D=II···A	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$
C6-H6A···O1	0.97	2.57	3.214 (3)	124
$C23{-}H23{\cdots}O2^i$	0.93	2.35	3.162 (3)	146

H atoms were positioned geometrically and were treated as riding on their parent C atoms, with aromatic C-H distances of 0.93 Å, methyl C-H distances of 0.96 Å and methylene C-H distances of 0.97 Å, and with $U_{iso}(H) = 1.5U_{eq}(C)$ for methyl H and $1.2U_{eq}(C)$ for other H.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2001); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 (Farrugia, 1997) and PLATON (Spek, 2003); software used to prepare material for publication: SHELXL97 and PARST (Nardelli, 1995).

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References

1.474 (3)

1.480(2)

1.571 (3)

1.473 (3) 1.481 (3)

1.456 (5)

102.2 (2)

116.0 (2)

111.0 (1)

101.0 (1)

112.2 (1)

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