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Key indicators

Single-crystal X-ray study T = 295 K Mean σ (C–C) = 0.003 Å Disorder in main residue R factor = 0.042 wR factor = 0.118 Data-to-parameter ratio = 11.8

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

2-Ethyl-4-hydroxy-3a,4,9,9a-tetrahydro-4,9-[1',2']benzeno-1*H*-benz[*f*]isoindole-1,3(2*H*)-dione

Two molecules of the title compound, $C_{20}H_{17}NO_3$, are linked by a pair of hydroxy–amide interactions over a center of inversion, giving a hydrogen-bonded dimeric structure. Received 3 January 2007 Accepted 4 January 2007

Comment

Anthrone and its derivatives undergo a Diels–Alder reaction with dienophiles, and if the reaction is catalysed by a chiral catalyst, the product is an optically active cyclic compound (Shen *et al.*, 2006). For example, anthrone itself reacts with *N*methylmaleimide to give the cycloadduct in high yield if a chiral β -aminoalcohol is used (Riant & Kagan, 1989); the corresponding cycloadduct is obtained for *N*-phenylmaleimide with a chiral pyrrolidone catalyst (Uemae *et al.*, 2001). In the present study, the use of triethylamine has yielded the racemic title cycloadduct, (I). The compound features a hydroxy group that interacts with one of the two amido O atoms, giving rise to a hydrogen-bonded dimer.



Experimental

Triethylamine (10 mg, 1 mmol) was added to a solution of anthrone (10 mg, 0.5 mmol) and *N*-ethylmaleimide (6.5 mg, 0.5 mmol) in



Figure 1

The molecular structure of (I), with displacement ellipsoids drawn at the 50% probability level and H atoms as spheres of arbitrary radius. The minor disordered OH component is not shown.

© 2007 International Union of Crystallography All rights reserved chloroform (5 ml). After the mixture was stirred to give a clear solution, 1 M HCl (5 ml) was added. The organic phase was separated and washed with saturated sodium chloride solution. The chloform solution was dried over magnesium sulfate. The solvent was removed and the residue purified by column chromatography on silica gel. Colorless crystals were obtained by recrystallization from ethanol.

V = 772.3 (4) Å³

 $D_x = 1.373 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

 $\mu = 0.09 \text{ mm}^{-1}$

T = 295 (2) K

Block, colorless

 $0.27 \times 0.25 \times 0.22$ mm

Z = 2

Crystal data

 $\begin{array}{l} C_{20}H_{17}NO_{3}\\ M_{r}=319.35\\ \text{Triclinic, }P\overline{1}\\ a=7.743\ (2) \ \text{\AA}\\ b=8.133\ (2) \ \text{\AA}\\ c=13.718\ (4) \ \text{\AA}\\ \alpha=74.57\ (2)^{\circ}\\ \beta=85.06\ (2)^{\circ}\\ \gamma=68.06\ (2)^{\circ} \end{array}$

Data collection

1756 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.007$
$\theta_{\rm max} = 25.0^{\circ}$
3 standard reflections
every 300 reflections
intensity decay: <1%

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.042$	$w = 1/[\sigma^2(F_o^2) + (0.0656P)^2]$
$wR(F^2) = 0.118$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.05	$(\Delta/\sigma)_{\rm max} = 0.001$
2707 reflections	$\Delta \rho_{\rm max} = 0.22 \ {\rm e} \ {\rm \AA}^{-3}$
229 parameters	$\Delta \rho_{\rm min} = -0.17 \text{ e} \text{ Å}^{-3}$

Table 1

Hydrogen-bond geometry (A, °)			•	
	Hydrogen-bond	geometry	(A,	°)

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	D-H
$O1-H1o\cdots O2^i$	0.82	1.97	2.778 (2)	169
Symmetry code: (i) -	-x + 1, -y + 1,	-z + 1.		

The hydroxy group is disordered over two positions (at C1 and C8) with site-occupation factors of 0.847 (4) and 0.153 (4). The C–O distances of the two components were restrained to be equal. C-bound H atoms were placed at calculated positions (C–H = 0.93– 0.98 Å) and were included in the refinement in the riding-model approximation, with U_{iso} (H) set at 1.2 U_{eq} (C) or 1.5 times U_{eq} (methyl C). The hydroxy H atoms were also placed at calculated positions (O–H = 0.82 Å) and U_{iso} (H) set at $1.5U_{eq}$ (O). The torsion angles about the C–O bonds were also refined. Although the occupancy of the minor component is only 0.153 (4), its omission gave a large peak (1.13 e Å⁻³) in the final difference Fourier map.

Data collection: *DIFRAC* (Gabe *et al.*, 1993); cell refinement: *DIFRAC*; data reduction: *NRCVAX* (Gabe *et al.*, 1989); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *publCIF* (Westrip, 2006).

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