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Key indicators

Single-crystal X-ray study T = 295 KMean σ (C–C) = 0.008 Å Disorder in main residue R factor = 0.064 wR factor = 0.211 Data-to-parameter ratio = 12.2

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

© 2001 International Union of Crystallography Printed in Great Britain – all rights reserved The structure of the title complex, $C_{14}H_{10}O_4$. $C_{13}H_9N$, which was cocrystallized from an ethanol solution containing a 1:1 mixture of diphenic acid and acridine, has been determined. Hydrogen bonding exists between acid–acid and acid–base as well as acridine π – π interactions. Proton transfer occurs in one of the two carboxylic acid–aromatic nitrogen interactions.

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Comment

Diphenic acid (biphenyl-2,2'-dicarboxylic acid) forms infinite zigzag acid chains *via* $R_2^2(8)$ carboxylic acid pairs (Fronczek *et al.*, 1987). It is of interest since it is potentially a good building block in crystal engineering with organic bases. To date, no organic co-crystal structure involving diphenic acid exists in the Cambridge Structural Database (*ConQuest*; CCDC 2001). We report here the first diphenic acid cocrystal structure with acridine as the base, (I).



The asymmetric unit of complex (I) comprises two acid and two base molecules (Fig. 1). The biphenyl units of the two acid molecules adopt twisted conformations, with the least-squares planes through the two phenyl units forming angles of 72 and 89°. A two-acid-two-base unit exists (Fig. 2), involving an O1-H01···O4 intramolecular hydrogen bond, an O7-H03...O3 acid-acid interaction and several acid-base intermolecular interactions (Table 2). In one of the two pairs of acid-base contacts, proton transfer occurs from the carboxylic acid group O3-C14-O4 to aromatic N2, evidenced by the O3-C14 and O4-C14 bond distances (Table 1). H02, the proton involved in the other acid-base contact (located from a difference map) remains within the carboxylic group attached to O5. The O6 site was refined with disorder over two distinct positions (O6A and O6B) with equal occupancy; possible weak hydrogen bonds C40-H40...O6A and C40-H40...O6B are noted. An infinite supramolecular unit is formed along the *a* axis by packing the two-acid-two-base units via $\pi - \pi$ interactions between acridine molecules. Acridine molecular planes are approximately perpendicular to the a axis, with a distance of approximately 3.5 Å between adjacent planes (Fig. 2). The infinite supramolecular units assemble via close packing (Fig. 3).



Figure 1

The asymmetric unit of (I) showing displacement ellipsoids at the 30% probability level. H atoms bonded to carbon have been omitted for clarity (Sheldrick, 1993).

Experimental

Diphenic acid and acridine were obtained from Aldrich. 28 mg of the acid and 18 mg of the base were dissolved in 15 ml of ethanol. Crystals were obtained by slow evaporation of the ethanol solution at room temperature.

Crystal data

$C_{14}H_{10}O_4{\cdot}C_{14}H_9O_4^{-}{\cdot}C_{13}H_9N{\cdot}C_{13}.$
$\mathrm{H_{10}N^+}$
$M_r = 842.86$
Monoclinic, $P2_1/c$
a = 14.461 (3) Å
b = 15.863 (3) Å
c = 19.166 (3) Å
$\beta = 108.98 \ (2)^{\circ}$
$V = 4157.5 (13) \text{ Å}^3$
Z = 4

Data collection

Enraf–Nonius CAD-4 diffractometer $\omega/2\theta$ scans Absorption correction: none 7509 measured reflections 7275 independent reflections 3160 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.045$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.064$ $wR(F^2) = 0.211$ S = 1.017275 reflections 598 parameters $D_x = 1.347 \text{ Mg m}^{-3}$ Mo K α radiation Cell parameters from 25 reflections $\theta = 8.0-15.0^{\circ}$ $\mu = 0.09 \text{ mm}^{-1}$ T = 295 (2) KBlock, yellow $0.30 \times 0.30 \times 0.20 \text{ mm}$

 $\theta_{\max} = 25.0^{\circ}$ $h = -17 \rightarrow 16$ $k = 0 \rightarrow 18$ $l = 0 \rightarrow 22$ 3 standard reflections every 200 reflections intensity decay: none

H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0914P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} = 0.002$ $\Delta\rho_{max} = 0.23 \text{ e} \text{ Å}^{-3}$ $\Delta\rho_{min} = -0.25 \text{ e} \text{ Å}^{-3}$



Figure 2

Projection of the molecular packing of (I) on to the (010) plane, showing the acridine molecules stacked along the *a* axis. (Watkin *et al.*, 1996).

Table 1

Selected geometric parameters (Å, °).

O1-C13	1.325 (6)	O5-C27	1.287 (6)
O2-C13	1.205 (6)	O6A-C27	1.297 (12)
O3-C14	1.265 (5)	O6B-C27	1.223 (11)
O4-C14	1.246 (5)	C28-O8	1.199 (6)
O7-C28	1.308 (6)		

Table 2

Hydrogen-bonding geometry (Å, $^\circ).$

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
O1-H01···O4	0.84	1.74	2.578 (6)	178
O7-H03···O3	0.85	1.75	2.596 (5)	173
$O5-H02\cdots N1^{i}$	0.84	1.86	2.675 (5)	162
C40−H40···O6A ⁱⁱ	0.93	2.39	3.258 (14)	155
$C40-H40\cdots O6B^{ii}$	0.93	2.57	3.282 (12)	133
$N2-H2\cdots O3^{iii}$	0.86	1.88	2.734 (5)	177
	1 1		1.1	1.1

Symmetry codes: (i) $2 - x, \frac{1}{2} + y, \frac{1}{2} - z$; (ii) $2 - x, y - \frac{1}{2}, \frac{1}{2} - z$; (iii) $1 - x, y - \frac{1}{2}, \frac{1}{2} - z$.



Figure 3

Projection on to (100), showing the packing of the infinite supramolecular unit. (Watkin *et al.*, 1996).

Owing to large anisotropic displacement parameters, atom O6 was refined over two distinct positions with equal fixed occupation factors (from refinement). All H atoms bonded to C atoms were placed geometrically and refined using a riding model with the $U_{\rm iso}$ values for each H atom taken as 1.2 $U_{\rm eq}$ of the carrier atom. The O-bound H01, H02 and H03 were located from difference Fourier maps and were included in the model with the O-H distance restrained to 0.82 ± 0.02 Å. Atom H2 was located from the difference Fourier map and was refined using a riding model with the $U_{\rm iso}$ value taken as $1.2U_{\rm eq}$ of N2.

Data collection: *CAD-4 Software* (Enraf–Nonius, 1988); cell refinement: *CAD-4 Software* (*SETANG*); data reduction: *TEXSAN* (Molecular Structure Corporation, 1995); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *XP* (Sheldrick, 1993); software used to prepare material for publication: *SHELXL*97).

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