

Cocrystal of 2,5-di-4-pyridyl-1,3,4-oxadiazole and malonic acid (1/1)

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Key indicators

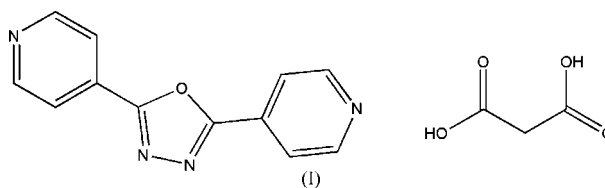
Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.058
 wR factor = 0.186
Data-to-parameter ratio = 10.2For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the title compound, $\text{C}_{12}\text{H}_8\text{N}_4\text{O}\cdot\text{C}_3\text{H}_4\text{O}_4$, a single $\text{O}-\text{H}\cdots\text{N}$ hydrogen bond links the two molecules. In addition, $\text{C}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\text{N}$ hydrogen bonds link these units into a two-dimensional framework.

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Comment

Hydrogen bonding is important in the areas of crystal engineering, supramolecular chemistry, materials science and biological recognition (Desiraju, 1989; Jeffrey & Saenger, 1991; Holman *et al.*, 2001). Recently, angular dipyridyl-donor basic compounds, such as 2,5-bis(4-pyridyl)-1,3,4-oxadiazole (bpo), have been used to produce a series of infinite/discrete coordination polymers/supramolecules with interesting structures and properties (Wang, Tang & Qin, 2005; Dong *et al.*, 2003; Du *et al.*, 2005, and references therein). In our effort to characterize the properties of cocrystals of fatty diacids with linear/angular base components and to further understand the role of synthons in crystal engineering, we have prepared and determined the crystal structure of the acid–base cocrystal (I), consisting of bpo and the most typical fatty carboxylic acid, malonic acid.



The asymmetric unit consists of one bpo molecule and a molecule of malonic acid (Fig. 1). The geometry of the bpo

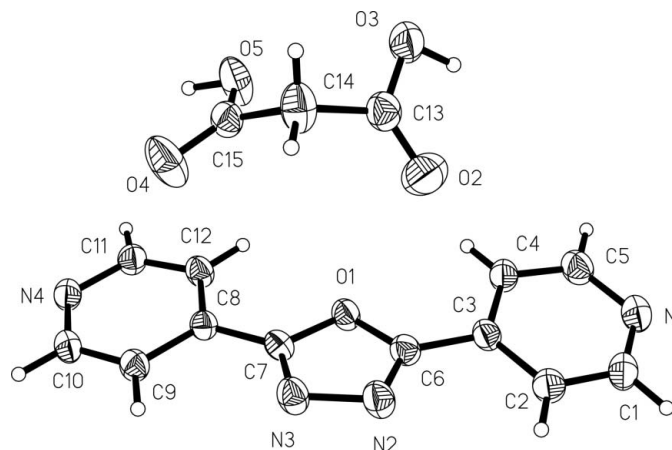


Figure 1
View of (I), showing displacement ellipsoids at the 30% probability level. H atoms are represented by circles of arbitrary size.

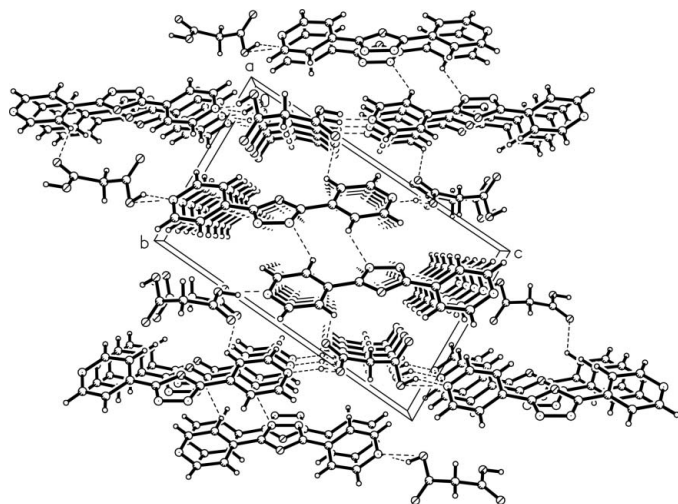


Figure 2
A packing diagram, showing hydrogen bonds as dashed lines.

molecule is very similar to that of the parent structure (Stockhause *et al.*, 2001); likewise, the malonic acid geometry is close to that of free malonic acid (Vishweshwar *et al.*, 2003). In the crystal structure, a two-dimensional framework is formed *via* O—H···N, C—H···N and C—H···O hydrogen bonds (Table 1 and Fig. 2).

Experimental

A mixture of 2,5-bis(4-pyridyl)-1,3,4-oxadiazole (112 mg, 0.5 mmol) (Wang, Tang, Qin & Duan, 2005) and malonic acid (52 mg, 0.5 mmol) was recrystallized from methanol and water in about 77% yield (126 mg); from this, a colourless block suitable for X-ray diffraction was selected. Analysis found: C 54.78, H 3.65, N 17.17%; calculated: C 54.88, H 3.68, N 17.07%; IR (KBr, cm^{-1}): ν 2452, 1708, 1602, 1570, 1534, 1418, 1271, 1211, 1018, 835, 743, 723.

Crystal data

$\text{C}_{12}\text{H}_8\text{N}_4\text{O}\cdot\text{C}_3\text{H}_4\text{O}_4$	$Z = 2$
$M_r = 328.29$	$D_x = 1.462 \text{ Mg m}^{-3}$
Triclinic, $P\bar{1}$	Mo $K\alpha$ radiation
$a = 5.1232 (8) \text{ \AA}$	Cell parameters from 100 reflections
$b = 9.5108 (15) \text{ \AA}$	$\theta = 17\text{--}23^\circ$
$c = 15.566 (3) \text{ \AA}$	$\mu = 0.11 \text{ mm}^{-1}$
$\alpha = 85.297 (3)^\circ$	$T = 293 (2) \text{ K}$
$\beta = 81.159 (3)^\circ$	Block, colourless
$\gamma = 86.289 (3)^\circ$	$0.26 \times 0.15 \times 0.13 \text{ mm}$
$V = 745.9 (2) \text{ \AA}^3$	

Data collection

Bruker SMART CCD area-detector diffractometer	2692 independent reflections
φ and ω scans	1843 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.014$
$T_{\text{min}} = 0.971$, $T_{\text{max}} = 0.986$	$\theta_{\text{max}} = 25.5^\circ$
3788 measured reflections	$h = -6 \rightarrow 4$
	$k = -11 \rightarrow 11$
	$l = -17 \rightarrow 18$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.058$
 $wR(F^2) = 0.186$
 $S = 1.00$
 2692 reflections
 265 parameters

All H-atom parameters refined
 $w = 1/[\sigma^2(F_o^2) + (0.1148P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.35 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.21 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D\text{---}H\cdots A$	$D\text{---}H$	$H\cdots A$	$D\cdots A$	$D\text{---}H\cdots A$
O3—H3A···N1 ⁱ	0.99 (7)	1.77 (7)	2.666 (4)	149 (5)
O5—H5A···N4 ⁱⁱ	0.97 (3)	1.66 (3)	2.611 (3)	166 (3)
C9—H9···N3	0.95 (3)	2.61 (3)	2.938 (3)	101 (2)
C9—H9···N3 ⁱⁱⁱ	0.95 (3)	2.55 (3)	3.327 (3)	139 (2)
C11—H11···O4 ⁱⁱ	0.92 (3)	2.59 (3)	3.298 (4)	134 (2)
C12—H12···O4 ^{iv}	0.94 (3)	2.48 (3)	3.146 (4)	128 (2)

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

All H atoms were refined independently with isotropic displacement parameters [O—H = 0.97 (4) and 0.99 (7) \AA , C—H = 0.89 (4)–0.97 (3) \AA].

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: SHELXTL (Sheldrick, 1999) and PLATON (Spek, 2003); software used to prepare material for publication: SHELXTL.

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