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A 1:2 co-crystal of isonicotinamide and propionic acid

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Key indicators

Single-crystal X-ray study

T = 150 K

Mean σ(C–C) = 0.005 Å

R factor = 0.088

wR factor = 0.198

Data-to-parameter ratio = 17.1

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

Isonicotinamide has been shown to form many 1:1 co-crystals with monofunctional carboxylic acids, but with propionic acid it forms a co-crystal containing two acid molecules and one isonicotinamide molecule per formula unit, C₆H₆N₂O·2C₃H₆O₂. The crystal structure consists of ‘supermolecules’ made up of one isonicotinamide molecule and two acid molecules, and the asymmetric unit contains two of these supermolecules. One of the acid molecules is hydrogen bonded to the pyridine function, and the other to the amide function of the isonicotinamide. Further N—H···O hydrogen bonds connect these supermolecules into chains which run along the [100] direction. The chains are linked into layers perpendicular to (010) by C—H···O and π-stacking interactions. The layers are then linked together by further C—H···O interactions.

Comment

Isonicotinamide has been shown to crystallize with carboxylic acids in a 1:1 stoichiometry to form a robust building block or ‘supermolecule’ consisting of two amide and two acid molecules, (I) (Aakeröy et al., 2002). When a saturated solution of isonicotinamide in warm propionic acid was allowed to cool, colourless crystalline laths were obtained. Single-crystal X-ray diffraction revealed these to be a co-crystal consisting of isonicotinamide and propionic acid in a 1:2 ratio, viz. (II).

Similar preparative routes with formic and acetic acids both yielded 1:1 co-crystals (Oswald, 2004). Attempts to prepare a 1:1 co-crystal with propionic acid failed. For example, a 1:1 mixture of propionic acid and isonicotinamide in ethanol yielded only crystals of (II); even in the presence of excess isonicotinamide, the only crystals obtained were isonicotinamide itself and (II).
The crystal structure of (II) consists of supermolecules comprising two acid and one isonicotinamide molecule. One acid forms an \( R_2^2(8) \) motif with the amide moiety (Bernstein et al., 1995). Another acid molecule forms a hydrogen bond to the pyridine N atom, supported by a weaker C—H—O hydrogen bond (shown as open dashes) are quite weak for this type of interaction (2.73 and 2.72 Å).

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based on molecule $B$ occur at $z = 0, 1, \ldots$ etc. Within the stacks, pairs of pyridine moieties are $\pi$-stacked across inversion centres (Fig. 7). The stacking distances are 3.34 and 3.33 Å for the $A$ and $B$ pyridine rings, respectively.

Thus, layers are formed in the $ac$-plane by chains of hydrogen-bonded supermolecules linked by weak $C-H-O$ hydrogen interactions. The layers are connected via $C-H-O$ hydrogen bonds involving pairs of $C4T-H4T1-O2T$ and $C4V-H4V1-O2S$ interactions disposed about inversion centres (Fig. 8).

**Experimental**

All materials were obtained from Aldrich and used as received. Isonicotinamide (0.50 g, 4.10 mmol) was dissolved in an excess of propionic acid (2.40 g, 32.43 mmol) and warmed until all the solid dissolved. The solution was cooled to room temperature, producing colourless laths.

**Crystal data**

\[
\begin{align*}
C_6H_6N_2O_2C_3H_6O_2 & \\
M_r &= 270.28 \\
Triclinic, \text{ $P\overline{1}$} & \\
a &= 10.038 (3) \text{ Å} \\
b &= 11.559 (4) \text{ Å} \\
c &= 12.740 (4) \text{ Å} \\
\alpha &= 103.243 (6)^\circ \\
\beta &= 90.140 (6)^\circ \\
\gamma &= 102.247 (6)^\circ \\
V &= 1404.5 (8) \text{ Å}^3 \\
Z &= 4 \\
D_x &= 1.278 \text{ Mg m}^{-3} \\
\text{Mo Kα radiation} & \\
\text{Cell parameters from 1107 reflections} & \\
\theta &= 2.6-22.2^\circ \\
\mu &= 0.10 \text{ mm}^{-1} \\
T &= 150 (2) \text{ K} \\
\text{Lath, colourless} & \\
& 0.75 \times 0.20 \times 0.08 \text{ mm}
\end{align*}
\]
Data collection

Bruker SMART CCD area-detector diffractometer with an Oxford Cryosystems low-temperature device (Cosier & Glazer, 1986)

Absorption correction: multi-scan (SADABS; Sheldrick, 2004)

\[ T_{\text{max}} = 0.783, \quad T_{\text{min}} = 1.000 \]

Refinement

Refinement on \( F^2 \)

\[ R(F^2 > 2\sigma(F^2)) = 0.088 \]

\[ wR(F^2) = 0.198 \]

\[ S = 1.04 \]

6498 reflections

379 parameters

H atoms treated by a mixture of independent and constrained refinement

| D – H – A | D – H | H – A | D – A | D – H – A |
|-----------|-------|-------|-------|-----------|
| O3S – H3S – O8A | 0.79 (4) | 1.86 (4) | 2.639 (4) | 170 (4) |
| O3T – H3T – O8B | 0.76 (5) | 1.89 (5) | 2.639 (4) | 169 (5) |
| O3U – H3U – O11B | 0.87 (4) | 1.78 (4) | 2.649 (4) | 177 (5) |
| O3V – H3V – O14A | 0.87 (5) | 1.79 (5) | 2.657 (4) | 174 (5) |
| N9A – H9A – O2S | 0.96 (5) | 1.92 (4) | 2.868 (4) | 170 (5) |
| N9B – H9B1 – O2T1 | 0.93 (4) | 1.94 (4) | 2.880 (4) | 168 (3) |
| N9A – H9A2 – O2T2 | 0.92 (3) | 2.02 (3) | 2.901 (4) | 161 (3) |
| N9B – H9B2 – O2V | 0.93 (3) | 2.01 (3) | 2.900 (4) | 160 (3) |
| C2A – H2A – O3T | 0.95 | 2.50 | 3.267 (5) | 138 |
| C2B – H2B – O3S | 0.95 | 2.51 | 3.281 (5) | 138 |
| C5A – H5A – O2T1 | 0.95 | 2.40 | 3.328 (4) | 167 |
| C5B – H5B – O1V | 0.95 | 2.39 | 3.322 (4) | 168 |
| C6A – H6A – O2V | 0.95 | 2.73 | 3.346 (4) | 123 |
| C6B – H6B – O2T1 | 0.95 | 2.72 | 3.333 (4) | 123 |
| C4T – H4T1 – O2T2 | 0.99 | 2.58 | 3.515 (5) | 157 |
| C4V – H4V1 – O2S | 0.99 | 2.57 | 3.551 (4) | 170 |

Symmetry codes: (i) \( x, 2 – y, z \); (ii) \( x, 1 + y, z \); (iii) \( –x, 1 – y, 1 – z \); (iv) \( x, 1 – y, 1 – z \); (v) \( x, 1 + y, z \); (vi) \( x, 1 + y, 1 + z \); (vii) \( 2 – x, y, 1 – z \); (viii) \( x, y, z \).

H atoms were placed on C atoms in calculated positions \([U_{\text{eq}}(\text{H})] = 1.2U_{\text{eq}}(\text{C})\) and allowed to ride on their parent atoms [C(phenyl) — H = 0.95, C(methylene) — H = 0.99 and C(methyl) — H = 0.98 Å]. Amide and hydroxyl H atoms were located in difference maps and refined freely, the former subject to the restraint N–H = 0.95 (3) A. The ranges of N–H and O–H bond lengths were 0.91 (2)–0.96 (1) and 0.75 (5)–0.87 (4) Å, respectively.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2003); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 2001); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL, MERCURY (Taylor & Macrae, 2001) and DIAMOND (Crystal Impact, 2004); software used to prepare material for publication: SHELXTL, EnCiFer (Allen et al., 2004) and PLATON (Spek, 2003), as incorporated in WinGX (Farrugia, 1999).

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