

4-Carboxypiperidinium 1-carboxy-  
cyclobutane-1-carboxylateLusbely M. Belandria,<sup>a</sup> Asiloé J. Mora,<sup>a\*</sup> Gerzon E.  
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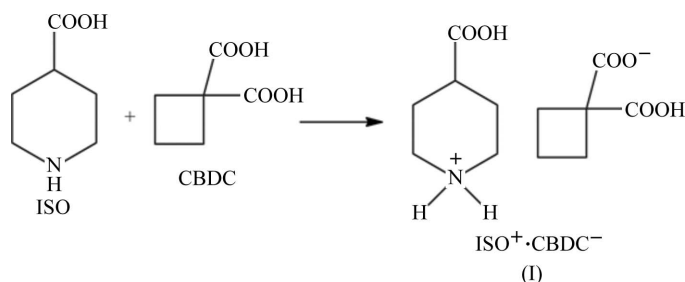
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The title salt,  $C_6H_{12}NO_2^+ \cdot C_6H_7O_4^-$  or  $ISO^+ \cdot CBDC^-$ , is an ionic ensemble assisted by hydrogen bonds. The amino acid moiety (ISO or piperidine-4-carboxylic acid) has a protonated ring N atom ( $ISO^+$  or 4-carboxypiperidinium), while the semiprotonated acid ( $CBDC^-$  or 1-carboxycyclobutane-1-carboxylate) has the negative charge residing on one carboxylate group, leaving the other as a neutral  $-COOH$  group. The  $-^+NH_2-$  state of protonation allows the formation of a two-dimensional crystal packing consisting of zigzag layers stacked along  $a$  separated by van der Waals distances. The layers extend in the  $bc$  plane connected by a complex network of  $N-H \cdots O$  and  $O-H \cdots O$  hydrogen bonds. Wave-like ribbons, constructed from  $ISO^+$  and  $CBDC^-$  units and described by the graph-set symbols  $C_3^3(10)$  and  $R_3^3(14)$ , run alternately in opposite directions along  $c$ . Intercalated between the ribbons are  $ISO^+$  cations linked by hydrogen bonds, forming rings described by the graph-set symbols  $R_6^6(30)$  and  $R_4^4(18)$ . A detailed analysis of the structures of the individual components and the intricate hydrogen-bond network of the crystal structure is given.

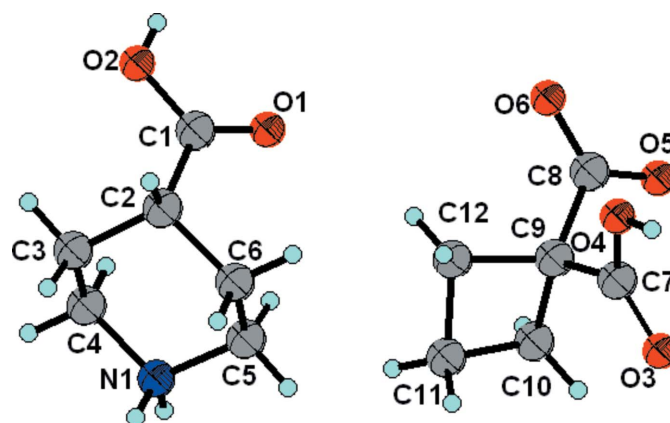
## Comment

Cocrystallization of organic compounds is serendipitous because the resulting multicomponent crystal could be a cocrystal, in which the different components are neutral species, or a salt, in which the components are charged species (Morissette *et al.*, 2004). Many factors appear to influence the formation of either one or the other. Some strategies for the preparation of these materials are described by Tiekink & Vittal (2006) comprising the following aspects: a preparation method such as recrystallization, growth from the melt, grinding *etc.* (Blagden *et al.*, 2007); solvent choice and solubility (Jones & Davey, 2005); and the chemistry of functional groups and  $pK_a$  (Trask *et al.*, 2005). In addition, some authors consider necessary the identification of hierarchical best

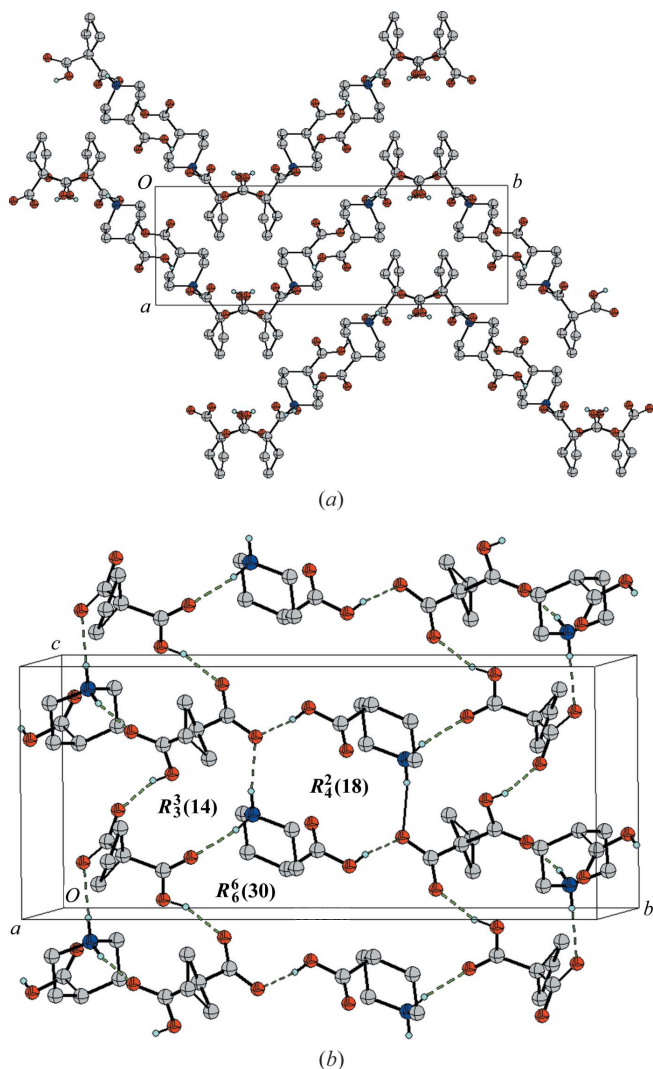
donor/best acceptor synthons (Aakeröy *et al.*, 2001), or scrutinize the tendency to maximize noncovalent interactions among components (Aakeröy *et al.*, 2006) and the charge-assisted ensemble of hydrogen bonds around the charged species in salts (Adams *et al.*, 2006). Hence, predictability has been difficult up to now. However, some homomeric or heteromeric synthons such as amide/amide (Aakeröy *et al.*, 2001), carboxylic acid/aminopyrimidine (Shan & Zaworotko, 2008) and amide/pyridine (Lemmerer *et al.*, 2008) have been used to prepare multicomponent crystals. The Cambridge Structural Database (Version 5.32, November 2011; CSD; Allen, 2002) shows 220 cocrystals and salts having at least one amino acid component. This makes them reliable supramolecular reagents (Aakeröy *et al.*, 2006; Rogowska *et al.*, 2006) with the bonus of having the amino group in different states of protonation, *viz.*  $^+NH_3$ ,  $^+NH_2$  and  $^+NH$ , which provides a way of building three-, two- or one-dimensional supramolecular motifs. In this study, we used isonipecotic acid (piperidine-4-carboxylic acid, ISO), an amino acid that, alone or as a hydrate, shows extended head-to-tail motifs based on  $N-H \cdots O$  hydrogen bonds (Delgado *et al.*, 2001; Mora *et al.*, 2005), mixed with cyclobutane-1,1-dicarboxylic acid (CBDC) (Santarsiero, 1990), in order to prepare the 1:1 multicomponent crystal structure  $ISO^+ \cdot CBDC^-$ , (I).



Salt (I) is an ionic ensemble assisted by hydrogen bonds. The asymmetric unit (Fig. 1) consists of one  $ISO^+$  cation with a positive charge residing on atom N1 and a  $CBDC^-$  anion acting as a semicarboxylate ion, *i.e.* 1-carboxycyclobutane-1-carboxylate [for the carboxyl group, the  $C7-O3$  and  $C7-O4$  bond lengths are 1.218 (2) and 1.306 (2) Å, respectively; for



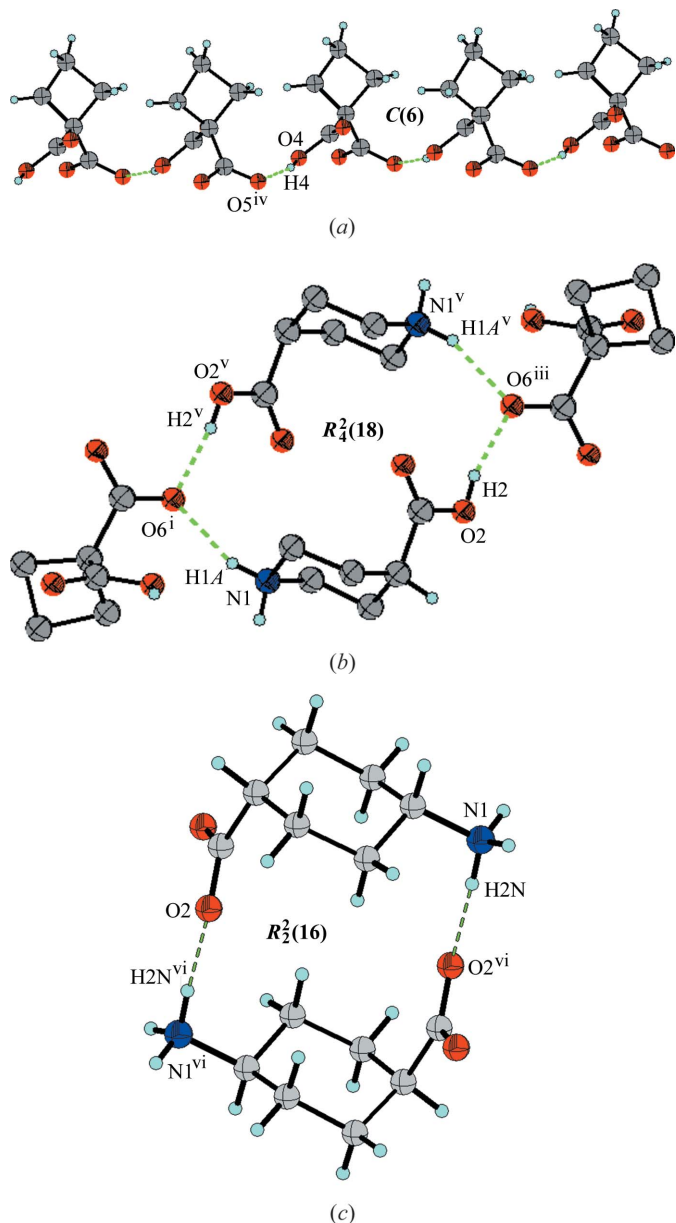
**Figure 1**  
The asymmetric unit of  $ISO^+ \cdot CBDC^-$ , showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level.

**Figure 2**

The crystal packing of  $\text{ISO}^+\cdot\text{CBDC}^-$ , showing (a) a view in the  $ab$  plane of the zigzag layers stacking along  $a$ , and (b) one layer in the  $bc$  plane described by the combination of graph-set symbols  $R_3^3(14)$ ,  $R_6^6(30)$  and  $R_4^4(18)$ .

the carboxylate group, the C8—O5 and C8—O6 bond lengths are both 1.257 (2) Å. A restricted search of the CSD ( $R$  factor less than 0.05) showed five multicomponent crystal structures displaying  $\text{CBDC}^-$  as a semicarboxylate ion [*viz.* with imidazolium (CSD refcode EQUXOD; Ballabh *et al.*, 2003), benzimidazolium (EQUXUJ; Ballabh *et al.*, 2003), dibenzylammonium (MEFRAR; Trivedi *et al.*, 2006), 2-phenylimidazolium (VARHIG; Trivedi *et al.*, 2003) and 1-butanaminium (TOKSUI; Ballabh *et al.*, 2008)]. On the other hand, for  $\text{ISO}^+$ , the C1—O2 and C1—O1 bond lengths are 1.301 (2) and 1.201 (3) Å, respectively. This finding shows that the amino acid is not a zwitterion but a positive ion.

The piperidinium ring in the  $\text{ISO}^+$  cation of (I) adopts the most stable chair conformation (Cremer & Pople, 1975). The orientation of the  $-\text{COOH}$  group in  $\text{ISO}^+$  is axial (Luger & Bülow, 1983), contrasting with the 11  $\text{ISO}$  structures found in a restricted search of the CSD ( $R$  factor less than 0.05), in which the orientation is equatorial. The torsion angles O1—C1—C2—

**Figure 3**

(a) A homomeric  $\text{CBDC}^-$  chain, linked by  $\text{O4}-\text{H4}\cdots\text{O5}^{\text{iv}}$  hydrogen bonds, with the graph-set symbol  $C(6)$ , displaying the cyclobutane rings oriented towards the same side of the chain. (b) The double head-to-tail structure, graph-set symbol  $R_4^4(18)$ , formed by two  $\text{ISO}^+$  cations and two  $\text{CBDC}^-$  anions. It is similar to that observed in (c) *cis*-4-ammoniocyclohexanecarboxylate hemihydrate (Ávila *et al.*, 2004). Owing to the flexibility of the pendant  $^+\text{NH}_2$  group, direct interaction of the amino acid molecules is allowed, while in  $\text{ISO}^+\cdot\text{CBDC}^-$ , the amino acid requires two bridging  $\text{CBDC}^-$  anions to form the  $R_4^4(18)$  ring. [Symmetry codes: (i)  $x+1, y, z$ ; (iii)  $-x, -y+1, -z+1$ ; (iv)  $x, -y+\frac{1}{2}, z-\frac{1}{2}$ ; (v)  $-x+1, -y+1, -z+1$ ; (vi)  $-x+\frac{1}{2}, -y+\frac{1}{2}, -z+2$ .]

C6 and O2—C1—C2—C3 are 3.6 (3) and 60.7 (2)°, respectively. These torsion angles vary significantly in all the reported structures. Mora *et al.* (2005) attributed this effect to the required rotation of this group to optimize the formation of hydrogen bonds with neighbouring molecules. The cyclobutane ring of the  $\text{CBDC}^-$  anion of (I) is slightly puckered, with an internal torsion angle C12—C9—C10—C11 of 17.1 (2)°.

Table 1 gives the geometry of all the relevant hydrogen bonds observed in (I). Fig. 2(a) shows how the crystal structure packs along *a* in the form of zigzag layers, as viewed in the *ab* plane, also seen in the structure of the diacidic form of CBDC (CBUTCA01; Santarsiero, 1990). Fig. 2(b) shows one of the layers viewed in the *bc* plane, which can be described by a combination of graph-set symbols (Bernstein *et al.*, 1995). (i) Wave-like ribbons described by the second-order graph-set symbol  $R_3^3(14)$  are related by *c*-glide planes and run alternately in opposite directions along *c*; these ribbons are formed by double chains of molecules, one of intercalated  $\cdots\text{ISO}-\text{CBDC}-\text{CBDC}-\text{ISO}\cdots$  chains described by the graph-set symbol  $C_3^3(10)$  and one consisting of only CBDC chains described by the graph-set symbol  $C(6)$ . (ii) These ribbons are linked through  $\text{ISO}^+$  cations related to each other by inversion centres, forming two rings with second-order graph-set symbols  $R_6^6(30)$  and  $R_4^2(18)$ . Fig. 3(a) shows how, in the homomeric CBDC chains, graph-set symbol  $C(6)$ , the cyclobutane ring is oriented towards the same side; this contrasts with the previously reported CBDC multicomponent crystals, which all have an alternating orientation of the cyclobutane ring in these chains [EQUXOD (Ballabh *et al.*, 2003), VARHIG (Trivedi *et al.*, 2003) and MEFRAR (Trivedi *et al.*, 2006)]. The ring described by graph-set symbol  $R_4^2(18)$  forms a double head-to-tail structure (Fig. 3b), which has been observed in other amino acids (Ávila *et al.*, 2004); for *cis*-4-aminocyclohexanecarboxylic acid, the terminal amino group hangs outside the cyclohexane ring, providing additional flexibility to this group and allowing its linking through hydrogen bonds to another amino acid unit to form the double head-to-tail structure shown in Fig. 3(c). In contrast, the amino group in (I) does not have such flexibility because the N atom is incorporated in the piperidinium ring, thus requiring the help of two  $\text{CBDC}^-$  anions to form the  $R_4^2(18)$  ring.

## Experimental

The multicomponent title crystal was prepared by mixing piperidine-2-carboxylic acid (0.0809 g, Aldrich, 98%) and cyclobutane-1,1-dicarboxylic acid (0.0702 g, Aldrich, 99.8%) in a 1:1 molar ratio. The reagents were ground separately with an agate pestle and mortar, and dissolved in ethanol (5 ml). The two solutions were mixed and placed in a reflux system for a period of 3 h at a constant temperature of 343 K. Colourless lamellar crystals of (I) of approximately 0.9 × 1.2 mm were obtained by slow evaporation of the reflux solution.

Thermal analysis of (I) was performed using a Perkin–Elmer TGA7 coupled with a DSC console. Samples were heated from 298 to 673 K at a rate of 10 K min<sup>-1</sup> under a nitrogen flux of 100 ml min<sup>-1</sup>.

**Table 1**  
Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N1—H1A...O6 <sup>i</sup>	0.90	1.96	2.816 (2)	158
N1—H1B...O3 <sup>ii</sup>	0.90	2.01	2.899 (2)	169
O2—H2...O6 <sup>iii</sup>	0.82	1.82	2.627 (2)	170
O4—H4...O5 <sup>iv</sup>	0.82	1.74	2.522 (2)	159

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

The sample consisted of a mixture of pure CBDC (m.p. 467.5 K) and the multicomponent  $\text{ISO}^+\cdot\text{CBDC}^-$  crystal (m.p. 555.3 K); no trace of pure ISO (m.p. 570.5 K) was found.

### Crystal data

$\text{C}_6\text{H}_{12}\text{NO}_2^+\cdot\text{C}_6\text{H}_7\text{O}_4^-$	$V = 1306.2 (6) \text{ \AA}^3$
$M_r = 273.28$	$Z = 4$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 7.027 (2) \text{ \AA}$	$\mu = 0.11 \text{ mm}^{-1}$
$b = 20.776 (5) \text{ \AA}$	$T = 293 \text{ K}$
$c = 8.949 (2) \text{ \AA}$	$0.3 \times 0.2 \times 0.1 \text{ mm}$
$\beta = 91.06 (1)^\circ$	

### Data collection

Rigaku AFC-7S Mercury diffractometer	14962 measured reflections
Absorption correction: multi-scan (REQAB; Jacobson, 1998)	2561 independent reflections
$T_{\min} = 0.970, T_{\max} = 0.986$	2026 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.037$

### Refinement

$R[F^2 > 2\sigma(F^2)] = 0.050$	173 parameters
$wR(F^2) = 0.139$	H-atom parameters constrained
$S = 1.04$	$\Delta\rho_{\max} = 0.41 \text{ e \AA}^{-3}$
2561 reflections	$\Delta\rho_{\min} = -0.30 \text{ e \AA}^{-3}$

All H atoms were placed in calculated positions and refined using a riding model, with C—H = 0.97 Å, N—H = 0.90 Å and O—H = 0.82 Å, and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$  or  $1.2U_{\text{eq}}(\text{O})$ . Each hydroxy H atom was placed in the position that was coplanar with the other carboxylic acid atoms and had the nearest potential hydrogen bond acceptor N or O atom (AFIX 83 instruction; Sheldrick, 2008). The low completeness ratio is due to the experimental set-up, whereby the equipment has a  $\chi$  circle and an added area detector (four-circle diffractometer modified with a CCD detector). This precludes the collection of some regions of reciprocal-lattice space and lowers the completeness. In order to compensate, additional redundant data were measured.

Data collection: *CrystalClear* (Rigaku, 2000); cell refinement: *CrystalStructure* (Rigaku/MSO, 2004); data reduction: *CrystalStructure*; program(s) used to solve structure: *SIR2008* (Burla *et al.*, 2007); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *DIAMOND* (Brandenburg, 1998); software used to prepare material for publication: *SHELXL97*, *PLATON* (Spek, 2009) and *pubCIF* (Westrip, 2010).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: SF3160). Services for accessing these data are described at the back of the journal.

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