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Carbamazepine–2,2,2-trifluoroethanol (1/1)

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Key indicators

Single-crystal X-ray study
T = 173 K
Mean σ(C–C) = 0.003 Å
R factor = 0.046
wR factor = 0.140
Data-to-parameter ratio = 13.0

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

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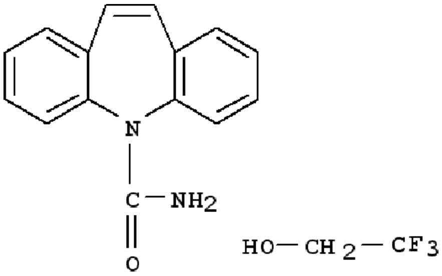
The crystal structure of the title compound, $C_{15}H_{14}N_2O\cdot CF_3CH_2OH$, which is the 2,2,2-trifluoroethanol (TFE) solvate of 5*H*-dibenzo[*b*,*f*]azepine-5-carboxamide (carbamazepine, CBZ), is reported. The asymmetric unit consists of two independent molecules of each component, CBZ and TFE.

Comment

5*H*-Dibenzo[*b*,*f*]azepine-5-carboxamide ($C_{15}H_{14}N_2O$, carbamazepine, CBZ) is the pharmacologically active component of the title compound, $C_{15}H_{14}N_2O\cdot CF_3CH_2OH$, (I) (Fig. 1). CBZ is used for the treatment of epilepsy and trigeminal neuralgia (Brodie & Ditcher, 1996). CBZ is known to exist as at least four polymorphs (Grzesiak *et al.*, 2003; Lang *et al.*, 2001). Furthermore, at least 13 cocrystal phases of CBZ have been reported (Fleischman *et al.*, 2003). In the course of solvatochromic analysis performed on CBZ, four new solvates were discovered. The crystal structure of the 2,2,2-trifluoroethanol (TFE) solvate of CBZ is reported here. The title compound, (I), crystallizes in the triclinic space group $P\overline{1}$ with two molecules of CBZ and two of TFE in the asymmetric unit, shown in Fig. 1.



(I)

In the crystal structure of (I), the two independent molecules of CBZ form a cyclic dimer that involves hydrogen bonding between each of the >C=O groups with the *syn*-oriented H atoms of the –NH$_2$ groups of the other independent molecule (Table 1). The remaining *anti*-oriented H atom on the –NH$_2$ group of molecule *A* is involved in a weak hydrogen-bonding interaction (Table 1) with an F atom of one TFE molecule. The two CBZ dimers are linked through a hydrogen-bonded bridge (Table 1) formed by the –OH group of the TFE molecules to give a closed ring consisting of four TFE and four CBZ molecules, as shown in Fig. 2. These closed ring units stack along the crystallographic *a* axis, as shown in Fig. 3.

The –OH group in TFE is a stronger hydrogen-bond donor (*i.e.* more acidic) and a weaker hydrogen-bond acceptor than

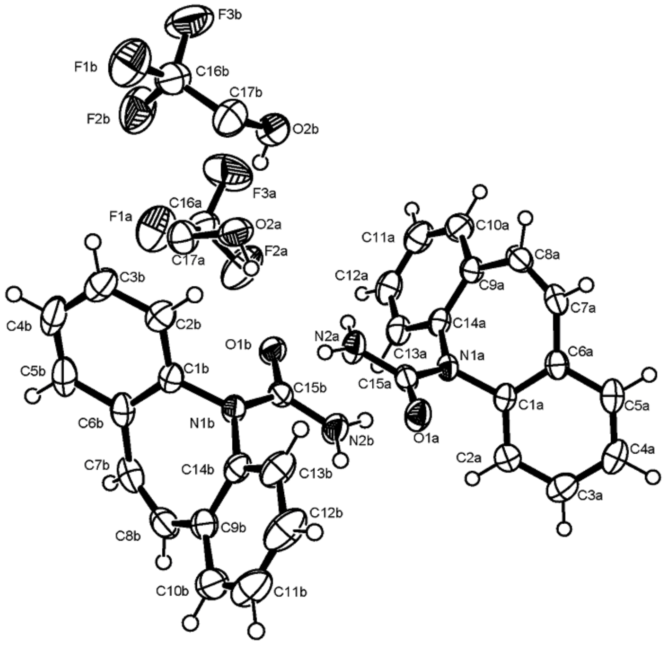


Figure 1
ORTEP-3 (Farrugia, 1997) plot showing the asymmetric unit of the title compound. Non-H atoms are shown with displacement ellipsoids at the 50% probability level.

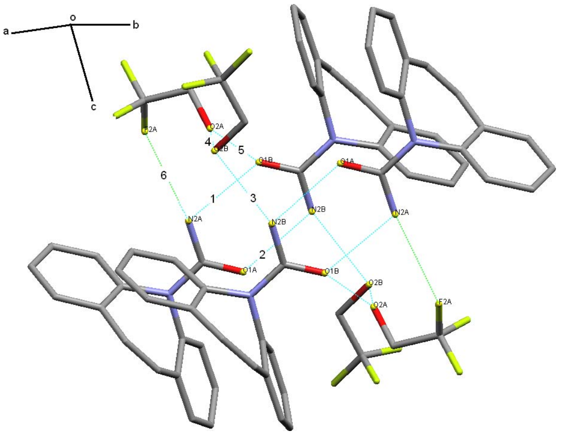


Figure 2
Hydrogen-bond unit containing two CBZ dimers and four TFE molecules forming a closed ring. H atoms have been omitted for clarity. Hydrogen bonds are labeled according to the order given in Table 1.

the –OH group in ethanol because of the electron-withdrawing nature of the F atoms (Dutt & Ghanty, 2003). Therefore, the –OH group of TFE forms a strong hydrogen bond with the >C═O group of CBZ, but a weak hydrogen bond (Table 1) with the $-NH_2$ group of CBZ. Weaker acidity of the –OH group in ethanol than in TFE may be one of the reasons why we did not obtain an ethanol solvate of CBZ under ambient conditions. The F atoms of the TFE molecules cluster together to form columns that run parallel to the crystallographic *a* axis, as shown in Fig. 3.

CBZ exists as dimers in many of its crystalline phases, such as its four polymorphs (Grzesiak *et al.*, 2003; Lang *et al.*, 2001) and its cocrystals with acetone, saccharin and nicotinamide (Fleischman *et al.*, 2003). As in the case of (I), the CBZ dimer involves hydrogen bonding between the >C═O group and the *syn*-oriented H atom of the $-NH_2$ group. The remaining *anti*-oriented H atom is free in all four CBZ polymorphs, while it participates in hydrogen bonding to some extent in the cocrystals of CBZ.

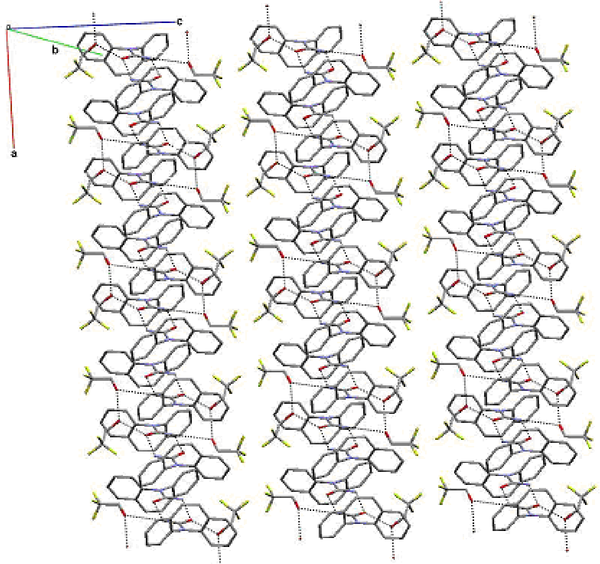


Figure 3
Stacking of hydrogen-bonded rings along the crystal *a* axis. TFE columns run parallel to the *a* axis.

Experimental

CBZ was obtained from Sigma–Aldrich Chemical Company, St Louis, MO, USA. Crystals of (I) were prepared by dissolving CBZ in TFE, followed by slow evaporation of the solvent. The crystals obtained were stored in contact with the mother liquor.

Crystal data

$C_{15}H_{12}N_2O \cdot C_2H_3F_3O$
$M_r = 336.31$
Triclinic, $P\overline{1}$
$a = 10.236$ (2) Å
$b = 12.937$ (2) Å
$c = 13.614$ (2) Å
$\alpha = 62.419$ (2)°
$\beta = 88.218$ (2)°
$\gamma = 84.286$ (2)°
$V = 1589.8$ (5) Å^3
$Z = 4$
$D_x = 1.405$ Mg m^{-3}
Mo *K*α radiation
Cell parameters from 2681 reflections
$\theta = 1.7$–25.1°
$\mu = 0.12$ mm^{-1}
$T = 173$ (2) K
Prism, colorless
0.5 × 0.5 × 0.25 mm

Data collection

Siemens SMART Platform CCD diffractometer
ω scans
Absorption correction: multi-scan (*SADABS*; Bruker 2000)
$T_{min} = 0.940$, $T_{max} = 0.973$
15 796 measured reflections
5632 independent reflections
4132 reflections with $I > 2\sigma(I)$
$R_{int} = 0.033$
$\theta_{max} = 25.1°$
$h = -12 \rightarrow 12$
$k = -15 \rightarrow 15$
$l = -16 \rightarrow 16$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.046$
$wR(F^2) = 0.140$
$S = 1.05$
5632 reflections
433 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0726P)^2 + 0.4499P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.35$ e Å^{-3}
$\Delta\rho_{min} = -0.27$ e Å^{-3}

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

D—H$\cdots A$	D—H	H$\cdots A$	$D\cdots A$	D—H$\cdots A$
N2A—H2$AC\cdots$O1B	0.88	2.05	2.905 (2)	164
N2B—H2$BC\cdots$O1A	0.88	1.96	2.820 (2)	167
N2B—H2$BD\cdots$O2$B^{\rm i}$	0.88	2.44	3.035 (2)	125
O2A—H2$AB\cdots$O1B	0.84	1.80	2.6342 (19)	169
O2B—H2$BB\cdots$O2A	0.84	1.86	2.698 (2)	178
N2A—H2$AD\cdots$F2A	0.88	2.65	3.081 (2)	111

Symmetry code: (i) $-x+2, -y+1, -z+1$.

H atoms were placed in calculated positions (C—H = 0.95 Å and N—H = 0.88 Å), except those of TFE, which were located in a difference Fourier map and refined as a rigid rotor (C—H = 0.99 Å and O—H = 0.84 Å); $U_{\rm iso}$(H) values were set at $1.2U_{\rm eq}$ of the parent atom.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT-Plus* (Bruker, 2003); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*, *ORTEP-3 for Windows* (Farrugia, 1997) and *MERCURY* (Bruno *et al.*, 2002).

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