

Carbamazepine *N,N*-dimethylformamide solvateAndrea Johnston,^a Alastair J. Florence^{a*} and Alan R. Kennedy^b^aDepartment of Pharmaceutical Sciences, University of Strathclyde, 27 Taylor Street, Glasgow G4 0NR, Scotland, and ^bDepartment of Pure and Applied Chemistry, University of Strathclyde, 295 Cathedral Street, Glasgow G1 1XL, ScotlandCorrespondence e-mail:
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Key indicators

Single-crystal X-ray study
T = 123 K
Mean $\sigma(\text{C}-\text{C})$ = 0.002 Å
R factor = 0.048
wR factor = 0.117
Data-to-parameter ratio = 15.1For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

In the title compound, $\text{C}_{15}\text{H}_{12}\text{N}_2\text{O}\cdot\text{C}_3\text{H}_7\text{NO}$, carbamazepine molecules form the $R_2^2(8)$ $\text{N}-\text{H}\cdots\text{O}$ hydrogen-bonded dimer arrangement observed in the crystal structures of each of the four known anhydrous polymorphs. The molecules of *N,N*-dimethylformamide are located between adjacent carbamazepine dimers and form an $\text{N}-\text{H}\cdots\text{O}$ hydrogen bond to the *anti*-oriented NH group of the carboxamide moiety of carbamazepine.

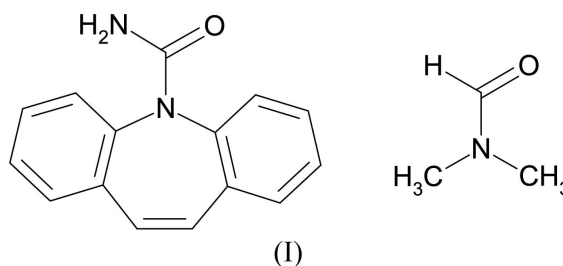
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Comment

The antiepileptic compound carbamazepine (CBZ) is known to crystallize in at least four anhydrous polymorphic forms (Grzesiak *et al.*, 2003) and the crystal structures of several solvates and co-crystals have also been reported (Fleischman *et al.*, 2003). The title solvate, (I), was produced during an automated parallel crystallization polymorph screen on CBZ. The sample was identified as a new form using multi-sample X-ray powder diffraction analysis of all recrystallized samples (Florence *et al.*, 2003). Subsequent manual recrystallization from a saturated *N,N*-dimethylformamide (DMF) solution by slow evaporation at 278 K yielded samples suitable for single-crystal X-ray analysis (Fig. 1).



In the crystal structure of (I), CBZ molecules form the centrosymmetric hydrogen-bonded $R_2^2(8)$ dimer motif observed in all of the known polymorphs and the majority of CBZ solvate crystal structures (Fleischman *et al.*, 2003) (Fig. 2). CBZ also forms a second $\text{N}-\text{H}\cdots\text{O}$ contact to atom O2 of the solvent molecule. Two $\text{C}-\text{H}\cdots\text{O}$ contacts exist between the DMF methyl H atoms (H17C and H18B) and atom O1 of CBZ. Atom O2 of DMF is further involved in a third $\text{C}-\text{H}\cdots\text{O}$ contact with an adjacent DMF molecule, forming a centrosymmetric $R_2^2(10)$ motif (Fig. 2). The CBZ dimers pack back-to-back, forming offset face-to-face hydrophobic interactions between adjacent azepine ring systems (Fig. 3).

Experimental

A single-crystal sample of the title compound was recrystallized from DMF solution by slow evaporation at 278 K.

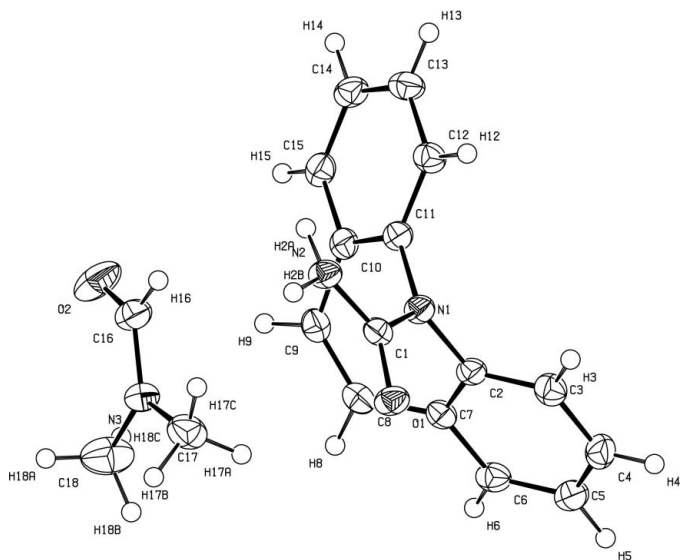


Figure 1
The molecular structure of (1), shown with 50% probability displacement ellipsoids.

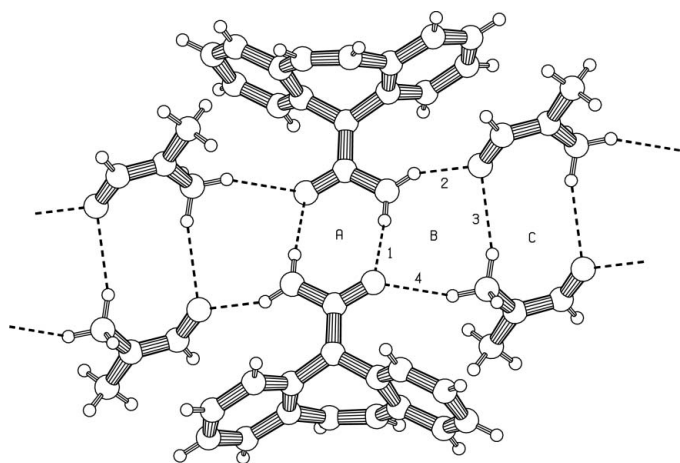


Figure 2
Packing diagram illustrating the non-covalent intermolecular network formed by (1) N2–H2B...O1 [N2...O1 = 2.9719 (19) Å O1 in the molecule at 2–x, –y, 1–z]; (2) N2–H2A...O2 [N2...O2 = 2.822 (2) Å; O2 in the molecule at 2–x, 1–y, 1–z]; (3) C18–H18C...O2 [C18...O = 3.435 (3) Å; C18 in the molecule at 1+x, y, z]; (4) C18–H18B...O1 [C18...O1 = 3.259 (2) Å; O1 in the molecule at 2–x, –y, 1–z] [calculated and illustrated using *PLATON* (Spek, 2003), program version 280604]. These interactions combine to produce three ring motifs: (A) the $R_2^2(8)$ CBZ dimer; (B) an $R_4^2(8)$ motif between CBZ dimers and molecules of DMF and (C) an $R_2^2(10)$ motif connecting DMF molecules in a centrosymmetric dimer configuration.

Crystal data

$C_{15}H_{12}N_2O \cdot C_3H_7NO$
 $M_r = 309.36$
 Triclinic, $P\bar{1}$
 $a = 7.7118$ (4) Å
 $b = 9.1503$ (4) Å
 $c = 11.6969$ (6) Å
 $\alpha = 100.192$ (3)°
 $\beta = 95.379$ (2)°
 $\gamma = 101.908$ (3)°
 $V = 787.58$ (7) Å³

$Z = 2$
 $D_x = 1.305$ Mg m^{–3}
 Mo $K\alpha$ radiation
 Cell parameters from 3432 reflections
 $\theta = 2.9$ – 27.0 °
 $\mu = 0.09$ mm^{–1}
 $T = 123$ (2) K
 Fragment, colourless
 0.20 × 0.20 × 0.05 mm

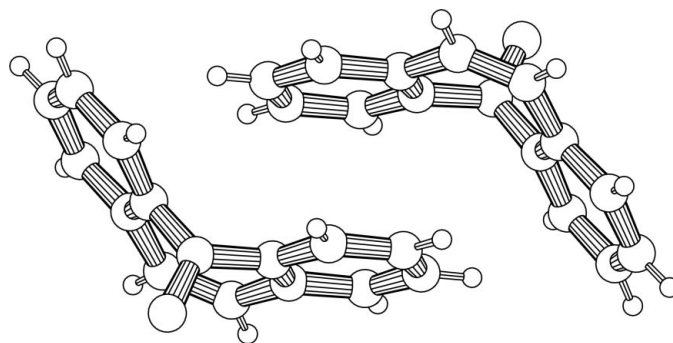


Figure 3
Hydrophobic packing interactions between nearest neighbour CBZ molecules with a centroid–centroid distance of 3.801 (1) Å (the carboxamide groups have been omitted for clarity).

Data collection

Nonius KappaCCD diffractometer
 ω and φ scans
 Absorption correction: none
 15107 measured reflections
 3476 independent reflections
 2475 reflections with $I > 2\sigma(I)$

$R_{int} = 0.054$
 $\theta_{max} = 27.2$ °
 $h = -9 \rightarrow 9$
 $k = -11 \rightarrow 11$
 $l = -14 \rightarrow 14$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.048$
 $wR(F^2) = 0.117$
 $S = 1.03$
 3476 reflections
 230 parameters

$w = 1/[\sigma^2(F_o^2) + (0.0505P)^2 + 0.208P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{max} = 0.002$
 $\Delta\rho_{max} = 0.23$ e Å^{–3}
 $\Delta\rho_{min} = -0.21$ e Å^{–3}

H atoms treated by a mixture of independent and constrained refinement

Table 1

Hydrogen-bonding geometry (Å, °).

D–H...A	D–H	H...A	D...A	D–H...A
N2–H2A...O2 ⁱ	0.921 (18)	1.963 (19)	2.822 (2)	154.5 (18)
N2–H2B...O1 ⁱⁱ	0.884 (19)	2.103 (19)	2.9719 (19)	167.4 (15)
C17–H17C...O1 ⁱⁱ	0.98	2.51	3.373 (3)	147
C18–H18B...O1 ⁱⁱⁱ	0.98	2.43	3.259 (2)	142
C18–H18C...O2 ^{iv}	0.98	2.49	3.435 (3)	163

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

Five H atoms (H2A, H2B, H8, H9 and H16) were located in difference maps and refined isotropically, but all other H atoms were constrained to idealized geometry using a riding model; for CH₃ groups, $U_{iso}(H) = 1.5U_{eq}(C)$ and C–H = 0.98 Å, while for CH groups, $U_{iso}(H) = 1.2U_{eq}(C)$ and C–H = 0.95 Å.

Data collection: *COLLECT* (Hooft, 1988) and *DENZO* (Otwinowski & Minor, 1997); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97*.

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