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Hydrochlorothiazide dimethyl sulfoxide solvate

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Key indicators

Single-crystal X-ray study
T = 123 K
Mean σ(C–C) = 0.003 Å
R factor = 0.040
wR factor = 0.110
Data-to-parameter ratio = 15.7

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

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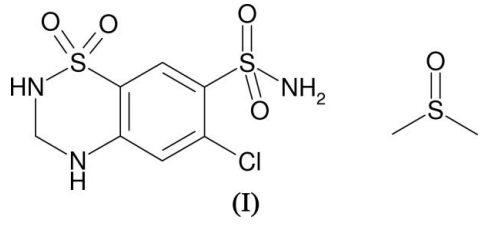
Hydrochlorothiazide forms a 1:1 solvate with dimethyl sulfoxide, $C_7H_8ClN_3O_4S_2\cdot C_2H_6OS$. The crystal structure contains a hydrogen-bonding network comprising three N—H···O contacts.

Comment

Hydrochlorothiazide (HCT) is a thiazide diuretic which is known to crystallize in at least two non-solvated forms; form I (Dupont & Dideberg, 1972) and form II (Florence *et al.*, 2005). The dimethyl sulfoxide (DMSO) solvate, (I), was produced during an automated parallel crystallization polymorph search on HCT. 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 by slow evaporation of a saturated DMSO solution at 278 K yielded samples of (I) suitable for single-crystal X-ray analysis (Fig. 1).



(I)

In (I), the six-membered ring N1—S1—C3—C2—N2—C1 in HCT displays a puckered conformation, atom N1 having a

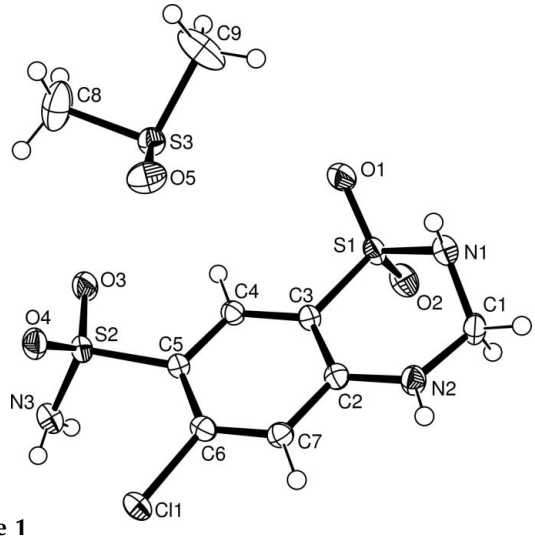


Figure 1
Plot of the asymmetric-unit contents with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

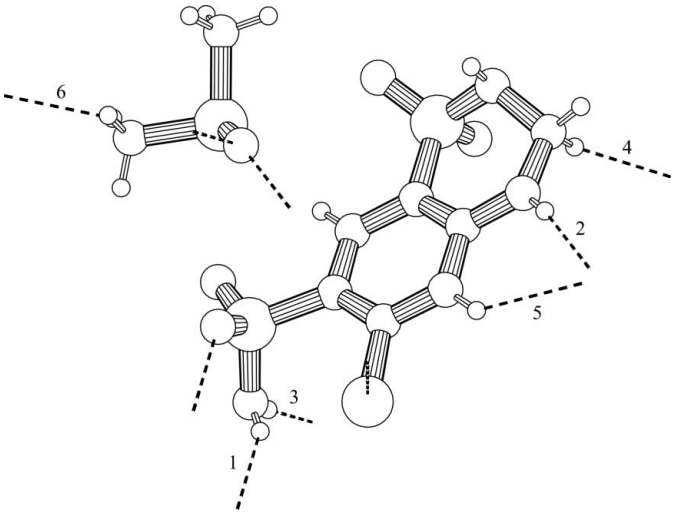


Figure 2
Intermolecular interactions in (I). Dashed lines indicate hydrogen bonds and unique contacts are labelled as follows: 1 = N3···O4, 3.004 (3)Å, O4 in the molecule at $(-x, 2-y, 2-z)$; 2 = N2···O5, 2.806 (3)Å, O5 in the molecule at $(1-x, 1-y, 2-z)$; 3 = N3···O5, 2.776 (3)Å; O5 in the molecule at $(-1+x, y, z)$; 4 = C1···O4, 3.347 (3)Å, O4 in the molecule at $(x, -1+y, z)$; 5 = C7···O5, 3.289 (3)Å, O5 in the molecule at $(1-x, 1-y, 2-z)$; 6 = C8···O3, 3.228 (4)Å, O3 in the molecule at $(1-x, 2-y, 1-z)$. Contacts calculated and illustrated using *PLATON* (Spek, 2003; program version 150306)

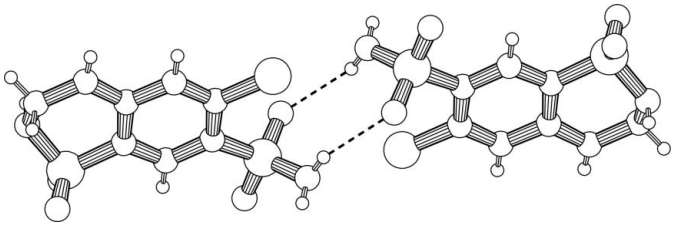


Figure 3
The $R_2^2(8)$ hydrogen-bonded motif in the crystal structure of (I).

deviation of 0.622 (2) Å from the least-squares plane through atoms C2–C7. The sulfonamide side chain adopts an N3—S2—C5—C6 torsion angle of −62.0 (2)°, such that O3 eclipses H4, and atoms O4 and N3 are staggered with respect to Cl1.

The crystal structure is stabilized by three N—H···O hydrogen bonds interconnecting (*a*) HCT molecules (Fig. 2, contact 1) and forming an $R_2^2(8)$ (Etter, 1990) centrosymmetric dimer (Fig. 3), and (*b*) HCT and two DMSO molecules (Fig. 2, contacts 2 and 3).

The aromatic ring formed by atoms C2–C7 is involved in two offset face-to-face π–π interactions between nearest-neighbour HCT molecules with centroid–centroid distances/perpendicular distances between the corresponding planes equal to 4.354 (2)/3.58 Å (centroid at $-x, 1-y, 2-z$) and 4.466 (2)/3.57 Å (centroid at $1-x, 1-y, 2-z$). The HCT aromatic rings form a stacked arrangement in the direction of the *a* axis. The structure also contains three C—H···O contacts between HCT and HCT (Fig.2, contact 4) and between HCT and DMSO (contacts 5 and 6).

Experimental

A single-crystal sample of the title compound was recrystallized by slow evaporation of a dimethyl sulfoxide solution at 278 K.

Crystal data

$C_7H_8ClN_3O_4S_2\cdot C_2H_6OS$
M_r = 375.86
Triclinic, $P\overline{1}$
a = 7.5068 (4) Å
b = 9.8272 (5) Å
c = 10.7311 (6) Å
α = 85.639 (3)°
β = 73.896 (3)°
γ = 80.246 (3)°
V = 749.23 (7) Å^3
Z = 2
D_x = 1.666 Mg m^{-3}
Mo $K\alpha$ radiation
μ = 0.70 mm^{-1}
T = 123 (2) K
Cut fragment, colourless
0.28 × 0.28 × 0.10 mm

Data collection

Nonius KappaCCD diffractometer
φ and ω scans
Absorption correction: none
10594 measured reflections
3267 independent reflections
2669 reflections with $I > 2\sigma(I)$
R_{int} = 0.055
θ_{max} = 27.2°

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.040
$wR(F^2)$ = 0.110
S = 1.03
3267 reflections
208 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0592P)^2 + 0.534P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.001
$\Delta\rho_{max}$ = 0.47 e Å^{-3}
$\Delta\rho_{min}$ = −0.48 e Å^{-3}

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

D—H···A	D—H	H···A	D···A	D—H···A
N3—H4N···O4^{i}	0.80 (3)	2.27 (3)	3.004 (3)	153 (3)
N2—H2N···O5^{ii}	0.81 (3)	2.02 (3)	2.806 (3)	164 (3)
N3—H3N···O5^{iii}	0.83 (3)	1.95 (3)	2.776 (3)	172 (3)
C1—H1A···O4^{iv}	0.99	2.46	3.347 (3)	149
C7—H7···O5^{ii}	0.95	2.56	3.289 (3)	134
C8—H8B···O3^{v}	0.98	2.53	3.228 (4)	128

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

H atoms bonded to N atoms were found in difference maps and refined isotropically, but all other H atoms were constrained to idealized geometry using a riding model; U_{iso}(H) = 1.2U_{eq}(C) and C—H = 0.95 (CH group) or 0.99 Å (CH_2 groups).

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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Control and Prediction of the Organic Solid State (URL: www.cposs.org.uk).

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