We gratefully acknowledge financial support from the Fonds der Chemischen Industrie.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: JZ1280). Services for accessing these data are described at the back of the journal.

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*Acta Cryst.* (1998). C**54**, 1501–1503

# (Z)-5-(2-Naphthylmethylene)-4-oxo-2-thioxo-1,3-thiazolidine-3-acetic Acid Dimethyl Sulfoxide Solvate

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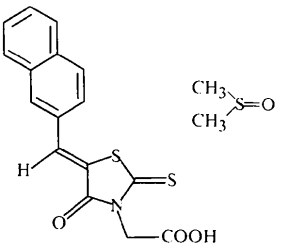
*(Received 21 July 1997; accepted 25 March 1998)*

## Abstract

The title acid (1-H-NOTA), as well as its methoxy derivative (1-$OCH_3$-NOTA), exhibit aldose reductase (AR) inhibitor activity and co-crystallize with dimethyl sulfoxide (DMSO), *i.e.* $C_{16}H_{11}NO_3S_2.C_2H_6OS$. The skeleton of 1-H-NOTA is highly planar, except for the acetic acid group. This conformation confers on the molecule a geometry that complements that of the AR active pocket. 1-H-NOTA molecules are held together by van der Waals and ring-to-ring interactions. The stability of the crystal is enhanced by an O—H···O hydrogen bond [O···O 2.554 (5) Å] which links the DMSO to 1-H-NOTA through its carboxy group.

## Comment

Complications of non-insulin-dependent diabetes mellitus (NIDDM) are caused by glucidic metabolism disorders characterized by enhanced activity of aldose reductase (Cogan *et al.*, 1984; Kador *et al.*, 1985; Benfield, 1986; Raskin & Rosenstock, 1987; Kinoshita & Nishimura, 1984). Consequently, AR inhibition is an appropriate approach to prevent NIDDM complications. In the search for new AR inhibitors, over 30 new compounds have been synthesized (Fresneau, 1996). Two of them, 1-H-NOTA and its derivative 1-$OCH_3$-NOTA, exhibit activities comparable to those of well known AR inhibitors (Kinoshita & Nishimura, 1984; Kador *et al.*, 1985, 1987; Benfield, 1986; Raskin & Rosenstock, 1987; Sarges & Oates, 1993; Tomlinson *et al.*, 1994). 1-$OCH_3$-NOTA has AR inhibition activity one order of magnitude greater than that of 1-H-NOTA. Molecular modelling suggests that a stable NOTA-AR complex may be formed by numerous hydrophobic and hydrogen-bond interactions between the host and guest molecules. In order to determine the structural features required for potential AR inhibitor molecules, and in particular those for NOTA, we have investigated the crystal structure of 1-$OCH_3$-NOTA.DMSO (TranQui *et al.*, 1998) and here we report the structure of 1-H-NOTA.DMSO




1-H-NOTA

The molecular geometry and atom-numbering scheme are shown in Fig. 1. As expected, the heavy-atom skeleton, apart from the carboxy group, is planar. DMSO, used as solvent, is also present in the crystal. The displacement parameters of its atoms (S3, C17, C18 and O4) are similar to those of the other atoms in the structure, indicating that DMSO can be considered as co-crystallized with the inhibitor molecule. It helps to stabilize the crystal by forming a strong hydrogen bond (O2···O4) which links the two molecular species through the carboxylic acid group of 1-H-NOTA.

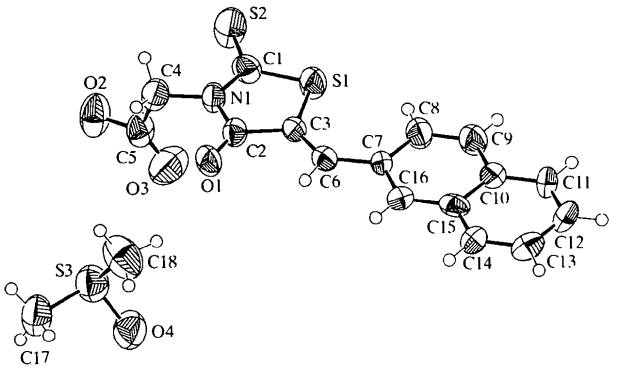



Fig. 1. View of 1-H-NOTA.$C_2H_6OS$ showing the labelling of the non-H atoms. Displacement ellipsoids are shown at the 50% probability level and H atoms are drawn as small circles of arbitrary radii.

## Experimental

The title compound was synthesized according to a procedure described by Fresneau (1996). Single crystals were obtained from DMSO solution by very slow evaporation at room temperature over a period of a month.

*Crystal data*

$C_{16}H_{11}NO_3S_2.C_2H_6OS$
$M_r$ = 407.51
Triclinic
$P\bar{1}$
$a$ = 7.320 (5) Å
$b$ = 8.307 (5) Å
$c$ = 16.399 (5) Å
$\alpha$ = 81.23 (5)°
$\beta$ = 98.52 (5)°
$\gamma$ = 104.46 (5)°
$V$ = 947.9 (9) Å$^3$
$Z$ = 2
$D_x$ = 1.428 Mg m$^{-3}$
$D_m$ not measured

Mo $K\alpha$ radiation
$\lambda$ = 0.71073 Å
Cell parameters from 24 reflections
$\theta$ = 8.4–20.2°
$\mu$ = 0.414 mm$^{-1}$
$T$ = 293 (2) K
Prismatic
0.12 × 0.10 × 0.06 mm
Transparent

*Data collection*

Enraf–Nonius CAD-4 diffractometer
$2\theta/\omega$ scan
Absorption correction: none
5099 measured reflections
2549 independent reflections
2122 reflections with $I > 2\sigma(I)$

$R_{int}$ = 0.047
$\theta_{max}$ = 23.0°
$h = -8 \rightarrow 7$
$k = -8 \rightarrow 9$
$l = 0 \rightarrow 17$
3 standard reflections every 100 reflections
intensity decay: <2%

*Refinement*

Refinement on $F^2$
$R[F^2 > 2\sigma(F^2)]$ = 0.044
$wR(F^2)$ = 0.137
$S$ = 0.974
2481 reflections
241 parameters
H atoms: see below
$w = 1/[\sigma^2(F_o^2) + (0.0570P)^2 + 1.0892P]$ where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.25 e Å$^{-3}$
$\Delta\rho_{min}$ = −0.22 e Å$^{-3}$
Extinction correction: none
Scattering factors from *International Tables for Crystallography* (Vol. C)

Table 1. *Selected geometric parameters (Å, °)*

| | | | |
|---|---|---|---|
| S1—C1 | 1.751 (3) | C7—C8 | 1.407 (4) |
| S1—C3 | 1.755 (3) | C8—C9 | 1.379 (4) |
| S2—C1 | 1.609 (3) | C9—C10 | 1.403 (4) |
| O1—C2 | 1.217 (3) | C10—C11 | 1.399 (4) |
| O2—C5 | 1.315 (4) | C10—C15 | 1.426 (4) |
| O3—C5 | 1.200 (4) | C11—C12 | 1.383 (4) |
| N1—C1 | 1.368 (3) | C12—C13 | 1.409 (4) |
| N1—C2 | 1.382 (3) | C13—C14 | 1.394 (4) |
| N1—C4 | 1.480 (3) | C14—C15 | 1.400 (4) |
| C2—C3 | 1.494 (4) | C15—C16 | 1.387 (4) |
| C3—C6 | 1.332 (4) | S3—O4 | 1.538 (3) |
| C4—C5 | 1.496 (5) | S3—C17 | 1.782 (4) |
| C6—C7 | 1.433 (4) | S3—C18 | 1.775 (5) |
| C7—C16 | 1.388 (4) | O4···O2' | 2.554 (5) |
| C1—S1—C3 | 94.03 (14) | C6—C3—S1 | 130.1 (2) |
| C1—N1—C2 | 119.5 (2) | C2—C3—S1 | 108.5 (2) |
| C1—N1—C4 | 119.2 (2) | N1—C4—C5 | 109.9 (3) |
| C2—N1—C4 | 121.1 (2) | O3—C5—O2 | 122.7 (4) |
| N1—C1—S2 | 127.2 (2) | O3—C5—C4 | 124.1 (3) |
| N1—C1—S1 | 108.4 (2) | O2—C5—C4 | 113.1 (3) |
| S2—C1—S1 | 124.4 (2) | C3—C6—C7 | 132.8 (3) |
| O1—C2—N1 | 124.3 (3) | O4—S3—C17 | 105.0 (2) |
| O1—C2—C3 | 126.2 (3) | O4—S3—C18 | 103.1 (2) |
| N1—C2—C3 | 109.6 (2) | C17—S3—C18 | 98.6 (2) |
| C6—C3—C2 | 121.4 (2) | | |

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

Data collection was terminated at $\theta$ = 23° because of the increasing proportion of reflections with $I < 2\sigma(I)$. To help ensure an acceptable observed data/parameter ratio, each intensity was measured twice. Most H atoms were geometrically placed, except for H5, which was unambiguously located from a difference Fourier synthesis. H atoms were allowed to ride on the parent atoms, but the $U_{iso}$ values and methyl-group orientations were refined.

Data collection: *SDP* (B. A. Frenz & Associates Inc., 1979). Cell refinement: *SDP*. Data reduction: *SDP*. Program(s) used to solve structure: *SHELXS86* (Sheldrick, 1985). Program(s) used to refine structure: *SHELXL93* (Sheldrick, 1993). Molecular graphics: *Xtal_GX* (Hall & du Boulay, 1995).

Supplementary data for this paper are available from the IUCr electronic archives (Reference: MU1359). Services for accessing these data are described at the back of the journal.

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*Acta Cryst.* (1998). C**54**, 1503–1505

# 5-Aminoisophthalic Acid Hemihydrate

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*(Received 2 February 1998; accepted 21 April 1998)*

## Abstract

The title acid, $C_8H_7NO_4.0.5H_2O$, crystallized in the centrosymmetric space group *C2/c* in a zwitterionic form (5-ammonioisophthalate), with the water molecule on a twofold axis. The three ammonio H atoms and the H atom on the remaining carboxyl group, which are involved in hydrogen bonding, are ordered. Three intermolecular N—H···O hydrogen bonds have N···O distances ranging from 2.762 (2) to 2.905 (2) Å and N—H···O angles ranging from 155 (2) to 163 (2)°. Two intermolecular O—H···O hydrogen bonds have O···O distances of 2.536 (2) and 2.746 (2) Å, and O—H···O angles of 178 (2) and 176 (2)°. A three-dimensional network of hydrogen bonds is present. Through basic second-level graphs involving acid-to-acid hydrogen bonds, chains are more numerous than rings.

## Comment

This report on 5-aminoisophthalic acid hemihydrate is one of a series on hydrogen bonding in amino-substituted carboxylic acids, and follows reports on a novel tetragonal phase of γ-aminobutyric acid, on 8-aminocaprylic acid and on 3-aminoisobutyric acid monohydrate (Dobson & Gerkin, 1996, 1998*a*,*b*). The title acid crystallized in the centrosymmetric space group *C2/c* as a zwitterion, (I), one of the carboxyl protons having been transferred to the N atom. The refined molecule and the associated water molecule given in the atom list are shown in Fig. 1, together with the numbering scheme. Geometric details of five hydrogen bonds are given in Table 2. Each acid molecule is directly linked to five acid molecules and to two water molecules by a total of eight hydrogen bonds, as shown in Fig. 2. Each water molecule is directly linked to four acid molecules by four hydrogen bonds. The results of hydrogen-bond graph-set analysis (Bernstein *et al.*, 1995) involving three acid-to-acid hydrogen bonds, which are labeled *a*–*c* in the order given in Table 2, are given in Table 3 for the first-

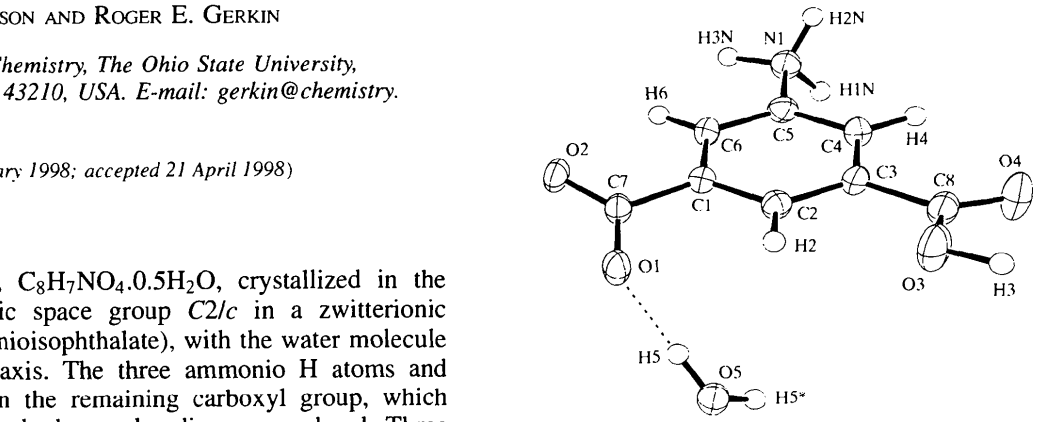



Fig. 1. *ORTEP*II (Johnson, 1976) drawing of 5-aminoisophthalic acid hemihydrate showing the atomic numbering scheme. Displacement ellipsoids are drawn at 50% probability for all atoms except H, for which they have been set artificially small.

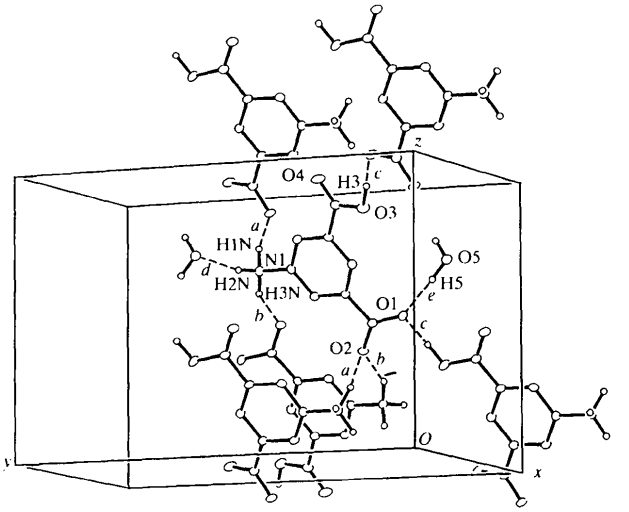
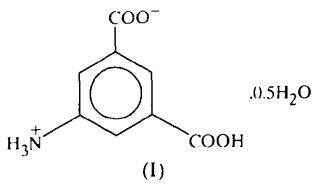



Fig. 2. *ORTEP*II (Johnson, 1976) diagram of a central 5-amino-isophthalic acid molecule and the five acid molecules and two water molecules to which it is directly hydrogen bonded. For clarity, displacement ellipsoids are drawn artificially small for all atoms, and H atoms not involved in hydrogen bonding have been omitted. Intermolecular hydrogen bonds are shown as dashed lines labeled *a*–*e* in the order given in Table 2.




(I)