and the occurrence of isomers may indicate that the products are artifacts caused by the isolation of the compounds and that the true precursors still have to be found.

The two molecules form a molecular pair through two intermolecular hydrogen bonds (Fig. 2), O(4)···H(O5′)—O(5′) (2.739 Å, 159°) and O(4′)···H(O5)—O(5) (2.644 Å, 164°). The pair remains intact during purification. The molecular pairs form chains along the crystallographic *b* axis *via* a third intermolecular hydrogen bond, O(5)···H(O2′)—O(2′)(x, $y-1$, z) (2.775 Å, 174°).

No unusual bond distances and bond angles were observed (Table 2).

The eight-membered ring in $C_{18}H_{17}NO_2$ (I) assumes a twisted tub-shaped boat conformation, which can be compared to the ideal D_{2d} conformation in 1,3,5,7-cyclooctatetraene (Claus & Krüger, 1988). The D_{2d} symmetry in (I) is disturbed by the sp^3 hybridization of the C(5) and C(6) atoms (Table 3). The amide ring in $C_{18}H_{19}NO_3$ (II) is six-membered and can be described equally well as a (3′)-sofa or a (3′–4′)-half-chair. The asymmetry parameters are: $\Delta C_s(3') = 7.94°$ and $\Delta C_2(3'–4') = 7.82°$. For an ideal sofa conformation, $\Delta C_s = 0.0°$, and for an ideal half-chair, $\Delta C_2 = 0.0°$ (Duax & Norton, 1975).

The planarity of amide groups can be described with three parameters (Winkler & Dunitz, 1971): χ_C, describing the planarity of the three bonds around the carbonyl C atom, χ_N the planarity of the three bonds around the amide N atom and τ the rotation around the C—N bond. All three parameters are 0° for the planar amide group. For a non-planar amide group χ_C is often still close to 0°. It can be seen that the amide groups in both (I) and (II) are distinctly non-planar, but much more so in compound (II) which has a six-membered amide ring.

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Structure of 4′-(9-Acridinylamino)-2′-methoxymethanesulfonanilide (*o*-AMSA) Methanol Solvate, an Inactive Isomer of the Anti-Cancer Drug Amsacrine (*m*-AMSA)

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Abstract. $C_{21}H_{19}N_3O_3S.CH_4O$, $M_r = 425.51$, triclinic, $P\bar{1}$, $a = 9.545$ (2), $b = 14.338$ (1), $c = 8.3748$ (7) Å, $\alpha = 106.032$ (6), $\beta = 103.230$ (9), $\gamma = 70.96$ (1)°, $V = 1029.0$ (3) Å^3, $Z = 2$, $D_x = 1.373$ g cm^{-3}, Mo $K\alpha$, $\lambda = 0.71069$ Å, $\mu = 1.94$ cm^{-1}, $F(000) = 448$, $T = 293$ (1) K, $R = 0.039$ for 2169 observed reflections ($I > 2.5\sigma$). The crystal packing is enhanced by intermolecular hydrogen bonds, by hydrogen bonds with the methanol solvate molecule, and by stacking interactions between the acridine rings. There are no obvious structural features which explain the lack of anti-tumour activity.

Introduction. The anti-cancer drug amsacrine (1) (*m*-AMSA) and a wide range of related compounds have been extensively studied in an attempt to understand the complex relationships between cytotoxicity, anti-tumour activity and DNA intercalating ability

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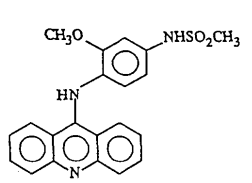
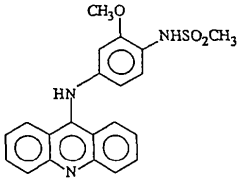
(Wilson, Baguley, Wakelin & Waring, 1981). The largest unresolved anomaly concerns the positional isomer *o*-AMSA (2), which is biologically inactive despite binding strongly to DNA. We have determined the crystal structure of *o*-AMSA (free base) for comparison with the structure of *m*-AMSA (free base and acid salt) (Buckleton & Waters, 1984; Karle, Cysyk & Karle, 1980).



(1)
Amsacrine
(*m*-AMSA)



(2)
o-AMSA

Experimental. The compound was generously provided by Professor W. Denny of the University of Auckland School of Medicine Cancer Research Laboratory. Crystals for the diffraction study were grown as orange rhomboids on cooling a warm ethyl acetate/methanol solution. Diffractometer crystal measured $0.44 \times 0.20 \times 0.24$ mm. Nonius CAD-4 diffractometer; Zr-filtered Mo $K\alpha$ radiation; unit-cell dimensions from 25 reflections with $11.5 < \theta < 14.0°$; no systematic absences, space group assigned as $P\bar{1}$ on the basis of intensity statistics and the satisfactory solution and refinement of the structure. 4602 unique reflections; $\omega/2\theta$ scans, $1 \le \theta \le 30°$, $[(\sin\theta)/\lambda]_{max}$ 0.7035 Å^{-1}, 2169 with $I > 2.5\sigma(I)$; $-13 \le h \le 13$, $-19 \le k \le 19$, $0 \le l \le 11$; three intensity standards checked every 100 reflections showed no non-statistical variation during data collection; Lorentz and polarization corrections applied, no absorption corrections required. The structure proved extremely difficult to solve, with a whole range of programs and approaches failing to give the correct solution. The structure was eventually solved using *SHELXS*86 (Sheldrick, 1986) but only with TREF = 2000, with the best *E* map then revealing positions for all non-hydrogen atoms. F_{obs} refinement of atomic positions, non-H atoms assigned anisotropic thermal parameters, H atoms located in difference maps and individually refined with isotropic temperature factors. Final weight $w = 1/[\sigma^2(F) + 2.49 \times 10^{-4}F^2]$, $R = 0.039$, $wR = 0.037$, $S = 2.1$; $\Delta_{max}/\sigma = 0.17$ for positions, max. and min. $\Delta\rho$ excursions in final difference map 0.22 and -0.28 e Å^{-3}, respectively; atomic scattering factors from *International Tables for X-ray Crystallography* (1974, Vol. IV, pp. 99, 149). Calculations performed with the Enraf–Nonius (1981) *Structure Determination Package* on a PDP-11 computer for initial data reduction, *SHELXS*86 (Sheldrick, 1986) for structure solution, and *SHELX*76 (Sheldrick, 1976) on the University of Auckland IBM 4341 computer for refinement. Diagrams were produced using *ORTEP* (Johnson, 1965).

Table 1. *Positional* ($\times 10^4$) *and thermal parameters, with e.s.d.'s in parentheses*

$B_{eq} = (8/3)\pi^2(a^{*2}U_{11}^2 + b^{*2}U_{22}^2 + c^{*2}U_{33}^2 + 2a^*b^*\cos\gamma^*U_{12} + 2a^*c^*\cos\beta^*U_{13} + 2b^*c^*\cos\alpha^*U_{23})$.

	x	*y*	*z*	B_{eq} (Å^2)
S(1′)	2378 (1)	53 (1)	1159 (1)	3.56 (4)
O(1′*a*)	999 (2)	496 (2)	1829 (3)	4.95 (14)
O(1′*b*)	3744 (2)	−158 (2)	2286 (3)	5.04 (14)
O(2′)	2297 (2)	−955 (1)	−3311 (2)	4.02 (12)
O(*s*)	3257 (2)	2716 (2)	6471 (2)	4.20 (12)
N(9)	6916 (2)	−3626 (2)	−3596 (3)	3.35 (13)
N(10)	10957 (3)	−5709 (2)	−2003 (3)	3.12 (13)
N(1′)	2230 (2)	−1007 (2)	−120 (3)	3.01 (13)
C(1)	6875 (3)	−5414 (2)	−2585 (4)	3.84 (18)
C(1a)	8206 (3)	−5155 (2)	−2513 (3)	2.81 (15)
C(2)	6923 (4)	−6245 (3)	−2088 (4)	4.67 (20)
C(3)	8297 (4)	−6881 (2)	−1494 (4)	4.68 (20)
C(4)	9599 (4)	−6686 (2)	−1452 (4)	3.91 (18)
C(4a)	9611 (3)	−5831 (2)	−1985 (3)	2.90 (16)
C(5)	12365 (3)	−4749 (2)	−2511 (4)	3.83 (17)
C(5a)	10961 (3)	−4892 (2)	−2492 (3)	2.76 (16)
C(6)	12440 (3)	−3940 (3)	−2957 (4)	4.29 (19)
C(7)	11125 (4)	−3198 (2)	−3405 (4)	4.42 (20)
C(8)	9768 (3)	−3296 (2)	−3397 (4)	3.56 (18)
C(8a)	9623 (3)	−4147 (2)	−2973 (3)	2.65 (14)
C(9)	8240 (3)	−4304 (2)	−2993 (3)	2.63 (14)
C(1′)	3465 (3)	−1656 (2)	−972 (3)	2.56 (13)
C(2′)	3481 (3)	1639 (2)	−2625 (3)	2.77 (14)
C(3′)	4626 (3)	−2306 (2)	−3469 (3)	2.72 (14)
C(4′)	5796 (3)	−2981 (2)	−2659 (3)	2.51 (14)
C(5′)	5810 (3)	−2977 (2)	−996 (3)	2.70 (14)
C(6′)	4631 (3)	−2319 (2)	−185 (3)	2.70 (14)
C(1″)	2522 (5)	835 (3)	−41 (5)	6.40 (26)
C(2″)	2323 (4)	−839 (3)	−4933 (4)	6.49 (24)
C(*s*)	3015 (4)	1742 (3)	6141 (5)	5.77 (24)

Discussion. Atomic coordinates for non-H atoms are listed in Table 1.* Bond distances, bond angles and torsion angles are given in Table 2. The atomic numbering and molecular geometry are shown in Fig. 1. The unit cell contains discrete *o*-AMSA molecules, together with methanol molecules of solvation occupying general positions. Each *o*-AMSA molecule forms four hydrogen bonds, two with an adjacent molecule [N(1′)···O(1′*a*) 3.03 Å] and two with the methanol [N(10)···O(solvent) 2.83 Å, N(9)···O(solvent) 2.99 Å].

No other intermolecular contacts are shorter than 3.4 Å. The stereopair diagram, Fig. 2, shows that the hydrogen-bonding pattern creates infinite chains of linked molecules. In addition, the acridine nuclei stack parallel to the *c* axis, the perpendicular distance between centrosymmetrically related pairs

* Lists of structure factors, anisotropic thermal parameters and H-atom positions have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 54853 (10 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 2. *Bond lengths* (Å), *bond angles* (°) *and torsion angles* (°)

S(1′)—O(1′*a*)	1.431 (2)	C(3)—C(4)	1.350 (6)
S(1′)—O(1′*b*)	1.421 (2)	C(4)—C(4a)	1.420 (5)
S(1′)—N(1′)	1.628 (2)	C(5)—C(5a)	1.425 (5)
S(1′)—C(1″)	1.753 (5)	C(5)—C(6)	1.340 (6)
O(2′)—C(2′)	1.364 (3)	C(5a)—C(8a)	1.431 (3)
O(2′)—C(2″)	1.420 (5)	C(6)—C(7)	1.408 (4)
N(9)—C(9)	1.405 (3)	C(7)—C(8)	1.349 (5)
N(9)—C(4′)	1.397 (3)	C(8)—C(8a)	1.417 (5)
N(10)—C(4a)	1.356 (4)	C(8a)—C(9)	1.405 (4)
N(10)—C(5a)	1.344 (4)	C(1′)—C(2′)	1.395 (4)
N(1′)—C(1′)	1.438 (3)	C(1′)—C(6′)	1.377 (3)
C(1)—C(2)	1.350 (6)	C(2′)—C(3′)	1.381 (4)
C(1)—C(1a)	1.419 (5)	C(3′)—C(4′)	1.398 (3)
C(1a)—C(4a)	1.431 (3)	C(4′)—C(5′)	1.388 (4)
C(1a)—C(9)	1.398 (5)	C(5′)—C(6′)	1.385 (3)
C(2)—C(3)	1.404 (4)	O(s)—C(s)	1.431 (5)

O(1′)—S(1′)—O(1′*b*)	118.9 (1)	C(5)—C(5a)—C(8a)	118.0 (3)
O(1′*a*)—S(1′)—N(1′)	105.9 (1)	C(5)—C(6)—C(7)	120.7 (3)
O(1′*a*)—S(1′)—C(1″)	108.7 (2)	C(6)—C(7)—C(8)	120.2 (4)
O(1′*b*)—S(1′)—N(1′)	107.9 (1)	C(7)—C(8)—C(8a)	121.4 (3)
O(1′*b*)—S(1′)—C(1″)	107.5 (4)	C(5a)—C(8a)—C(8)	118.2 (3)
N(1′)—S(1′)—C(1″)	107.4 (2)	C(5a)—C(8a)—C(9)	117.9 (3)
C(2′)—O(2′)—C(2″)	118.0 (2)	C(8)—C(8a)—C(9)	123.9 (2)
C(9)—N(9)—C(4′)	126.0 (2)	N(9)—C(9)—C(1a)	121.3 (3)
C(4a)—N(10)—C(5a)	117.8 (2)	N(9)—C(9)—C(8a)	118.7 (3)
S(1′)—N(1′)—C(1′)	119.7 (2)	C(1a)—C(9)—C(8a)	119.9 (2)
C(1a)—C(1)—C(2)	121.1 (3)	N(1′)—C(1′)—C(2′)	120.3 (2)
C(1)—C(1a)—C(4a)	118.1 (3)	N(1′)—C(1′)—C(6′)	120.7 (3)
C(1)—C(1a)—C(9)	124.2 (2)	C(2′)—C(1′)—C(6′)	119.0 (2)
C(4a)—C(1a)—C(9)	117.7 (3)	O(2′)—C(2′)—C(1′)	115.6 (2)
C(1)—C(2)—C(3)	120.7 (4)	O(2′)—C(2′)—C(3′)	124.4 (3)
C(2)—C(3)—C(4)	120.4 (4)	C(1′)—C(2′)—C(3′)	120.0 (2)
C(3)—C(4)—C(4a)	121.0 (3)	C(2′)—C(3′)—C(4′)	120.3 (3)
N(10)—C(4a)—C(1a)	123.4 (3)	N(9)—C(4′)—C(3′)	116.8 (3)
N(10)—C(4a)—C(4)	118.1 (2)	N(9)—C(4′)—C(5′)	123.4 (2)
C(1a)—C(4a)—C(4)	118.5 (3)	C(3′)—C(4′)—C(5′)	119.8 (2)
C(5a)—C(5)—C(6)	121.4 (3)	C(4′)—C(5′)—C(6′)	119.0 (2)
N(10)—C(5a)—C(5)	118.7 (2)	C(1′)—C(6′)—C(5′)	121.8 (3)
N(10)—C(5a)—C(8a)	123.3 (3)		

O(1′*a*)—S(1′)—N(1′)—C(1′)	−178.2 (2)
O(1′*b*)—S(1′)—N(1′)—C(1′)	−50.0 (2)
C(1″)—S(1′)—N(1′)—C(1′)	65.8 (2)
C(2″)—O(2′)—C(2′)—C(1′)	174.3 (2)
C(2″)—O(2′)—C(2′)—C(3′)	−7.4 (3)
C(4′)—N(9)—C(9)—C(1a)	68.2 (3)
C(4′)—N(9)—C(9)—C(8a)	−115.6 (3)
C(9)—N(9)—C(4′)—C(3′)	174.9 (2)
C(9)—N(9)—C(4′)—C(5′)	−4.3 (3)
S(1′)—N(1′)—C(1′)—C(2′)	−98.5 (2)
S(1′)—N(1′)—C(1′)—C(6′)	83.0 (2)

ranging from 3.49 to 3.63 Å. These are typical distances for stacking interactions. The anilino ring is planar, and inclined at 62.6° to the acridine. The OMe group projects away from the acridine as it does in *m*-AMSA free base. The acridine ring system itself is only approximately planar, being twisted about a line through its length such that C(1) lies 0.11 Å above and C(8) lies 0.06 Å below the plane best fitting the six atoms of the central ring. The acridine ring in *m*-AMSA free base is also not perfectly planar, but there the molecule bends about the C(9)—N(10) direction [max. displacements C(7) 0.06, C(2) 0.17 Å] to give a quasi-butterfly configuration.

The observed intramolecular bonding agrees well with that of *m*-AMSA free base (Buckleton & Waters, 1984). For example, the consistency of bond lengths [*m*-AMSA values in square brackets] {C(9)—N(9) 1.405 (3) [1.395 (4)], N(9)—C(4′) 1.397 (3) [1.406 (4) Å]} and bond angles {C(1a)—C(9)—N(9) 121.3 (3) [120.8 (4)], C(9)—N(9)—C(4′) 126.0 (2) [125.5 (3)], N(9)—C(4′)—C(5′) 123.4 (2) [123.3 (3)°]} shows that the two compounds are electronically equivalent in the region of the acridine moiety. However, the methanesulfonate group is rotated differently, presumably to allow the formation of the hydrogen-bonding network, but this alone is unlikely to be responsible for the lack of biological activity. It has been found that protonation at N(10) in *m*-AMSA.HCl (Karle, Cysyk & Karle, 1980) considerably alters the relative orientation between acridine and anilino ring systems, and we are attempting to produce crystals of an *o*-AMSA acid salt for comparison with *m*-AMSA.HCl and with *o*-AMSA free base.

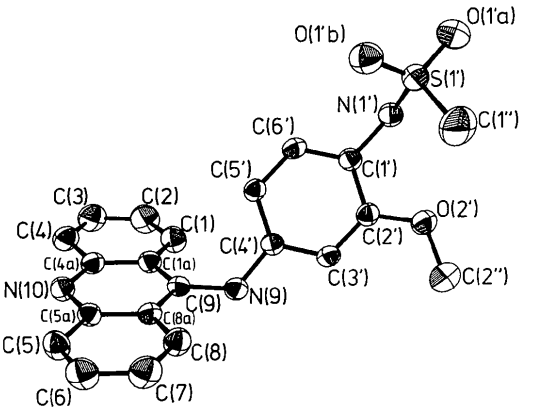


Fig. 1. Molecular geometry and atomic numbering scheme. Atoms are represented as 50% probability ellipsoids.

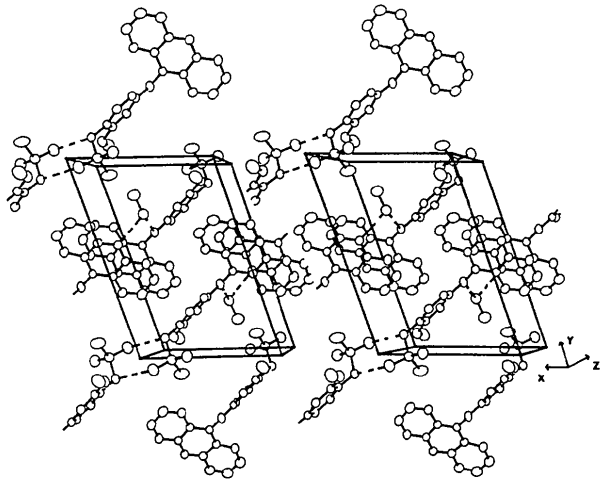


Fig. 2. Stereopair diagrams showing the molecular stacking and hydrogen-bonding interactions.

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Structure of 1,2,4-Triazolidine-3,5-dione (Urazole) at 105 K

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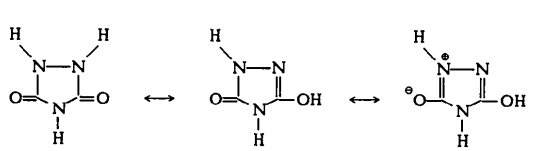
Abstract. $C_2H_3N_3O_2$, $M_r = 101.06$, monoclinic, $P2_1/n$, $a = 3.462$ (1), $b = 9.513$ (1), $c = 10.995$ (2), $\beta = 95.06$ (2)°, $V = 360.7$ (1) Å^3, $Z = 4$, $D_x = 1.861$ g cm^{-3}, λ(Mo $K\alpha$) = 0.71069 Å, $\mu = 1.52$ cm^{-1}, $F(000) = 208$, $T = 105$ K, $R = 0.0458$, $wR = 0.0359$ for 1326 unique observed reflections and 81 parameters. In the crystal the molecules exist in the diketo form. The two adjacent H atoms are in *trans* position; the N atom between the two carbonyl groups has a nearly planar geometry. The H atoms form one bifurcated and two almost linear hydrogen bonds resulting in a three-dimensional hydrogen-bonding network.

Introduction. 1,2,4-Triazolidine-3,5-dione (1) is a long-known parent compound of a large number of derivatives. Whereas the crystal structures of 11 non-fused and 95 fused 1,2,4-triazolidine-3,5-diones have already been reported in the literature, the structure of (1) is unknown, possibly because of its poor crystallization. Recently, the crystal structure of the new compound [1,2,4]triazolo[1,2-*a*][1,2,4]triazole-1,3,5,7(2*H*,6*H*)-tetrone (urazourazole) (2) was determined (Nachbaur, Faleschini, Belaj & Janoschek, 1988). The determination of the structure of the parent compound (1), for which three tautomers (1*a*–*c*) are discussed in the literature (Bourdais, Cugniet, Prin & Chabrier, 1964), was therefore desirable.



(1*a*) (1*b*) (1*c*)

Experimental. A colourless single crystal (0.16 × 0.24 × 0.44 mm), obtained by repeated recrystallization in H_2O, was used to collect data at 105 K on a modified Stoe four-circle diffractometer using graphite-monochromated Mo $K\alpha$ radiation with Nonius low-temperature equipment. Cell parameters were determined from a least-squares fit of 40 well-refined reflections (θ range 9–15°). 2611 reflections were measured using ω scans (scan range 1.6°) for 2θ from 3 to 80° (h 0 to 6, k 0 to 17, l −19 to 19), 1589 reflections had $I > 2.5\sigma(I)$, 1334 were unique. Three standard reflections measured every 100 reflections showed ± 1.3% variation in intensity. Data were corrected for Lp effects, an empirical absorption correction (maximum/minimum transmission factors 1.05/0.89) was applied with *DIFABS* (Walker & Stuart, 1983), and eight low-order reflections were omitted, probably suffering from extinction. The structure solution was by direct methods using *SHELXS*86 (Sheldrick, 1986). Refinement (on F) with anisotropic thermal parameters for all non-H atoms, with individual isotropic temperature factors for the H atoms, N—H bond lengths constrained to 1.02 Å [the mean value obtained from neutron data (Olovsson & Jönsson, 1976)], and refinement of five interlayer scale factors, defined by the index h, until no parameter shifts occurred (maximum $\Delta/\sigma = 0.003$), gave $R = 0.046$, $wR = 0.036$ [$w = 1/\sigma^2(F)$, 1326 reflections, 81 parameters]. The final difference Fourier map maximum and minimum peaks were 0.47 and −0.38 e Å^{-3}, respectively. Scattering factors and anomalous-dispersion corrections from *International Tables for X-ray Crystallography* (Ibers & Hamilton, 1974). VAX 6000 computer, *SHELX*76 (Sheldrick, 1976), *PLATON* (Spek, 1982) and *ORTEP* (Johnson, 1965) programs.

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