Table 3. *Triphenylphosphine oxide and its* H*X adducts* (*X* = F, Cl, Br)

	P—O (Å)	O—H (Å)	H—*X* (Å)	O—*X* (Å)
Ph_3PO	1.491 (2)[a]	—	—	—
	1.494 (4)[b]			
$Ph_3PO.HBr$	1.550 (6)	0.98 (9)	2.0 (1)	2.930 (6)
$Ph_3PO.HCl$	1.517 (2)	1.116 (40)	—	2.747 (2)
$Ph_3PO.HF$	1.495 (4)	1.423	0.998	2.384 (5)
$(Ph_3PO)_2.H_2O.HBr$	1.492 (6)[c]	—	—	—

Notes: (*a*) orthorhombic form, (*b*) monoclinic form, (*c*) mean value.

by the short O—H bond [0.98 (9) Å] and long H—Br distance [2.0 (1) Å]. Following on from this work, a comparison can be made between the structures of $Ph_3PO.HX$, where X = F, Cl, Br (Table 3). The structure of $Ph_3PO.HF$ comprises molecular triphenylphosphine oxide, hydrogen bonded to hydrogen fluoride. The P—O bond length [1.495 (4) Å] is comparable to that of free triphenylphosphine oxide [1.491 (2) Å, orthorhombic form; 1.494 (4) Å, monoclinic form] (Brock, Dunitz & Schweizer, 1985). On the other hand, the structure of the hydrogen chloride adduct has been shown to be that of the ionic $Ph_3P^+OH\cdots Cl^-$, having a much longer P—O distance (1.517 Å) and a short O—H bond (1.116 Å). The lengthening of the P—O bond is more pronounced in the hydrogen bromide adduct now reported, showing the increasing trend to ionicity with the heavier halogens.

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Structure of *N*-(2-Dimethylaminoethyl)phenothiazine-1-carboxamide Hydrochloride

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Abstract. $C_{17}H_{20}N_3OS^+.Cl^-$, $M_r = 349.88$, orthorhombic, $Pna2_1$, $a = 7.983$ (3), $b = 18.028$ (2), $c = 11.668$ (1) Å, $V = 1679.1$ (9) Å^3, $Z = 4$, $D_m = 1.39$ (1), $D_x = 1.419$ g cm^{-3}, Mo $K\alpha$, $\lambda = 0.71069$ Å, $\mu = 4.3$ cm^{-1}, $F(000) = 736$, $T = 293$ (1) K, $R = 0.044$ for 741 [$I > 2.5\sigma(I)$] reflections. The phenothiazine cation adopts a butterfly shape by bending approximately along the S(9)–N(10) direction. The dihedral angle between the individually planar aromatic rings is 160.4°. The amide group is oriented to form an intramolecular hydrogen bond between N(10) and the amide O atom. There are 12 close intermolecular contact distances (non-H) shorter than 3.49 Å. The non-planar structure of this compound is consistent with its observed lack of intercalative binding to DNA.

Introduction. Tricyclic carboxamides of general structure (1) with a coplanar chromophore intercalate DNA and show *in vivo* antitumour activity, whereas analogues with non-planar chromophores do not bind in this manner, and show no activity (Palmer, Rewcastle, Atwell, Baguley & Denny, 1988). The only apparent exception to this was the phenothiazine-1-carboxamide (2), which did not appear to unwind closed circular supercoiled DNA [a typical indicator of intercalation (Atwell, Cain, Baguley, Finlay & Denny, 1984)] but did show significant *in*

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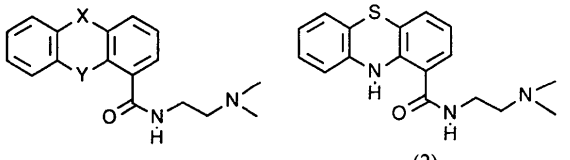
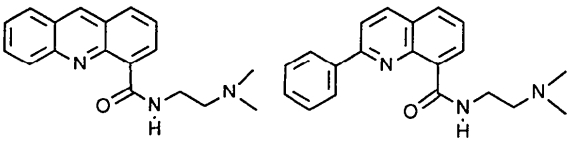
vivo antileukemic activity. In the previous work, the non-planarity of the chromophore of (2) was assumed from that of phenothiazine itself, where the dihedral angle between the *A* and *C* rings is 158.5° in the orthorhombic form (McDowell, 1976) and 153.3° in the monoclinic polymorph (Bell, Blount, Briscoe & Freeman, 1968). The well known antipsychotic drug chlorpromazine [(3) 2-chloro-10-(3-dimethylaminopropyl)phenothiazine] has a similar dihedral angle of 139.4° (McDowell, 1969). However, in view of the above results, the influence of the 4-carboxamide group on the geometry of (2) is of interest, and we have therefore determined its crystal structure.



Experimental. The crystal density was measured by flotation in *n*-hexane/carbon tetrachloride. A diffractometer crystal of 0.22 × 0.18 × 0.15 mm (yellow tablet) was mounted on a Nonius CAD-4 diffractometer. Zr-filtered Mo $K\alpha$ radiation was used. Unit-cell dimensions were determined from 25 reflections with $7.4 < \theta < 8.7°$. Systematic absences $0kl$, $h + k = 2n + 1$; $h0l$, $h = 2n + 1$; $00l$, $l = 2n + 1$ defined the space group as $Pna2_1$. 2810 unique reflections were measured using $\omega/2\theta$ scans, for $1.5 \le \theta \le 30°$ [maximum $(\sin\theta)/\lambda = 0.7035$ Å^{-1}], of which 741 had $I > 2.5\sigma(I)$; $0 \le h \le 9$, $0 \le k \le 25$, $0 \le l \le 14$. Three intensity standards checked every 100 reflections showed no non-statistical variation during data collection. Lorentz and polarization corrections were applied, but absorption corrections were not required. The structure was solved by direct methods using *SHELXS*86 (Sheldrick, 1986) with the best *E* map revealing positions for all non-H atoms. In the F_o refinement of atomic positions, non-H atoms were assigned anisotropic thermal parameters; H atoms were placed in calculated positions (C—H, N—H, 0.95 Å) with fixed isotropic temperature factors of $U = 0.06$ Å^2. Final weight $w = 1.7811/\sigma^2(F) + 5.6 \times 10^{-5}F^2$], $R = 0.044$, $wR = 0.033$, $S = 1.92$; maximum $\Delta/\sigma = 0.238$ for positions; maximum and minimum $\Delta\rho$ excursions in the final difference map 0.29 and -0.24 e Å^{-3}, respectively. Atomic scattering factors were obtained from *International Tables for X-ray Crystallography* (1974, Vol. IV, pp. 99, 149). Calculations were performed with the Enraf–Nonius (1981) *Structure Determination Package* on a PDP-11 computer for initial data reduction, and with *SHELX*76 (Sheldrick, 1976) on the University of Auckland IBM 4341 computer for refinement. Diagrams were produced using *ORTEP* (Johnson, 1965).

Discussion. Atomic coordinates for non-H atoms are listed in Table 1.* Bond distances and angles are given in Table 2. The atomic numbering and molecular geometry are shown in Fig. 1. The molecule is bent into the familiar 'butterfly' shape (Fig. 2) so that the dihedral angle between the best planes of the aromatic rings is 160.4° (Table 3). This extent of folding compares with values of 158.5, 153.3 and 139.4° in the similar compounds described in the *Introduction*. All bond lengths in the entire molecule are normal, and are indistinguishable from those in the related compounds despite their being neutral species whereas the present molecule is a protonated salt. We note a very large number of close intermolecular contact distances in the present compound (there are 12 such non-H-atom contacts between 3.30 and 3.49 Å). The unit-cell packing diagram is given in Fig. 3. A further question to be considered was the disposition of the side chain. Previous crystallographic studies (Hudson, Kuroda, Denny & Neidle, 1987) of the free base of the related acridine-4-carboxamide (4) showed that the amide lies coplanar to the chromophore, owing to a bridging hydrogen bond between the amide NH and the acridine N(10) forming a six-membered ring structure. However,



energy calculations showed the lowest-energy form for the protonated species to be the alternative conformation, with a hydrogen bond between the acridine N(10) proton and the carbonyl O atom of the amide, and a very low barrier to interconversion between the different amide conformations. A crystal-structure determination of the protonated form of the related 2-phenyquinoline-8-carboxamide (5) confirmed these calculations, showing a similar structure with the amide virtually coplanar and a

* 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 55306 (8 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England. [CIF reference: HU1001]

Table 1. *Positional parameters and equivalent isotropic thermal parameters* (Å^2)

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

	x	y	z	B_{eq}
Cl	0.5731 (3)	0.31729 (13)	0.50960 †	4.78 (10)
S(9)	0.1367 (4)	0.24142 (14)	−0.1180 (3)	4.02 (15)
O(1′)	0.4068 (10)	0.0818 (3)	0.2352 (6)	3.4 (4)
N(10)	0.2466 (10)	0.1226 (4)	0.0499 (7)	3.2 (6)
N(1′)	0.4969 (9)	0.1658 (4)	0.3624 (7)	3.3 (5)
N(2′)	0.3837 (11)	0.0991 (4)	0.5889 (7)	3.1 (4)
C(1)	0.2315 (11)	0.3268 (5)	0.0599 (9)	3.2 (7)
C(2)	0.3122 (12)	0.3405 (5)	0.1633 (9)	3.3 (6)
C(3)	0.3685 (12)	0.2838 (5)	0.2295 (9)	3.1 (6)
C(4)	0.3463 (11)	0.2103 (5)	0.1935 (9)	2.3 (5)
C(4a)	0.2699 (12)	0.1955 (5)	0.0884 (9)	2.7 (5)
C(5a)	0.1290 (12)	0.1021 (5)	−0.0305 (8)	2.6 (6)
C(5)	0.0763 (13)	0.0268 (5)	−0.0326 (8)	3.6 (5)
C(6)	−0.0374 (13)	0.0030 (6)	−0.1138 (10)	4.0 (6)
C(7)	−0.1036 (13)	0.0526 (5)	−0.1922 (9)	3.7 (8)
C(8)	−0.0536 (12)	0.1263 (5)	−0.1911 (8)	3.2 (6)
C(8a)	0.0634 (12)	0.1499 (5)	−0.1127 (10)	3.1 (5)
C(9a)	0.2153 (10)	0.2549 (5)	0.0217 (8)	2.6 (4)
C(1′)	0.4165 (13)	0.1476 (6)	0.2660 (9)	3.2 (5)
C(2′)	0.5937 (13)	0.1133 (5)	0.4283 (8)	3.3 (5)
C(3′)	0.4852 (13)	0.0615 (5)	0.5003 (11)	4.3 (5)
C(4′)	0.2876 (14)	0.0416 (6)	0.6521 (10)	4.9 (7)
C(5′)	0.4745 (17)	0.1470 (7)	0.6681 (11)	6.4 (9)

† Coordinate fixed to define origin in c direction.

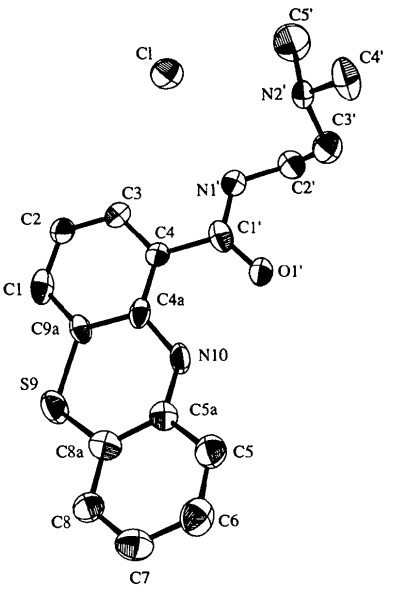


Fig. 1. Molecular geometry and atomic numbering scheme. Atoms are represented as 50% probability surfaces. H atoms are numbered according to the atoms to which they are attached.

Table 2. *Bond distances* (Å) *and angles* (°)

C(8a)—S(9)	1.752 (9)	C(3)—C(2)	1.357 (12)
C(9a)—S(9)	1.763 (9)	C(4)—C(3)	1.402 (11)
C(1′)—O(1′)	1.242 (10)	C(4a)—C(4)	1.395 (12)
C(4a)—N(10)	1.401 (10)	C(1′)—C(4)	1.519 (13)
C(5a)—N(10)	1.378 (10)	C(9a)—C(4a)	1.394 (10)
C(1′)—N(1′)	1.336 (11)	C(5)—C(5a)	1.421 (12)
C(2′)—N(1′)	1.444 (10)	C(8a)—C(5a)	1.391 (11)
C(3′)—N(2′)	1.478 (11)	C(6)—C(5)	1.381 (12)
C(4′)—N(2′)	1.486 (11)	C(7)—C(6)	1.384 (13)
C(5′)—N(2′)	1.459 (11)	C(8)—C(7)	1.387 (11)
C(2)—C(1)	1.389 (12)	C(8a)—C(8)	1.375 (12)
C(9a)—C(1)	1.378 (12)	C(3′)—C(2′)	1.525 (12)

C(9a)—S(9)—C(8a)	102.5 (5)	C(8a)—C(5a)—C(5)	117.9 (9)
C(5a)—N(10)—C(4a)	124.1 (7)	C(6)—C(5)—C(5a)	120.2 (9)
C(2′)—N(1′)—C(1′)	122.9 (8)	C(7)—C(6)—C(5)	120.3 (9)
C(4′)—N(2′)—C(3′)	108.1 (7)	C(8)—C(7)—C(6)	120.1 (10)
C(5′)—N(2′)—C(3′)	116.3 (9)	C(8a)—C(8)—C(7)	119.9 (10)
C(5′)—N(2′)—C(4′)	110.8 (8)	C(5a)—C(8a)—S(9)	118.8 (8)
C(9a)—C(1)—C(2)	119.5 (9)	C(8)—C(8a)—S(9)	119.7 (8)
C(3)—C(2)—C(1)	120.9 (9)	C(8)—C(8a)—C(5a)	121.5 (8)
C(4)—C(3)—C(2)	120.0 (10)	C(1)—C(9a)—S(9)	117.5 (7)
C(4a)—C(4)—C(3)	119.9 (9)	C(4a)—C(9a)—S(9)	121.4 (7)
C(1′)—C(4)—C(3)	119.4 (9)	C(4a)—C(9a)—C(1)	120.9 (8)
C(1′)—C(4)—C(4a)	120.5 (8)	N(1′)—C(1′)—O(1′)	120.6 (9)
C(4)—C(4a)—N(10)	121.3 (8)	C(4)—C(1′)—O(1′)	121.8 (9)
C(9a)—C(4a)—N(10)	120.0 (8)	C(4)—C(1′)—N(1′)	117.5 (9)
C(9a)—C(4a)—C(4)	118.7 (8)	C(3′)—C(2′)—N(1′)	113.0 (8)
C(5)—C(5a)—N(10)	118.0 (8)	C(2′)—C(3′)—N(2′)	114.5 (8)
C(8a)—C(5a)—N(10)	124.1 (8)		

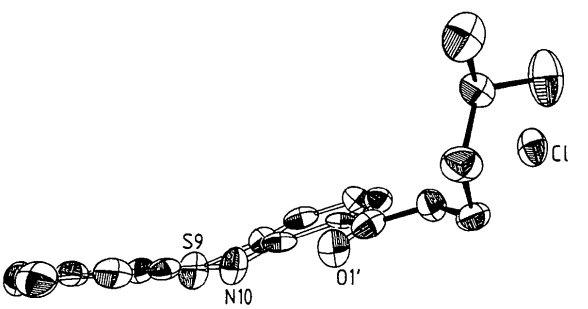


Fig. 2. View showing the buckle in the molecule about the S(9)–N(10) direction.

Table 3. *Mean-plane parameters and deviations* (Å) *of atoms from the planes*

Plane 1				Plane 2			
C(1), C(2), C(3), C(4), C(4a), C(9a)				C(8a), C(8), C(7), C(6), C(5), C(5a)			
$0.8917x + 0.0414y - 0.4507z - 1.5546 = 0$				$0.7529x - 0.2183y - 0.62092z - 0.5829 = 0$			
C(1)	−0.02	C(4)	0.00	C(8a)	0.02	C(5)	−0.01
C(2)	0.01	C(9a)	0.02	C(8)	−0.01	C(5a)	−0.01
C(3)	0.01	S(9)	0.19	C(7)	0.00	S(9)	0.12
C(4)	−0.01	N(10)	−0.01	C(6)	0.01	N(10)	0.02

Dihedral angle between planes is 160.4°.

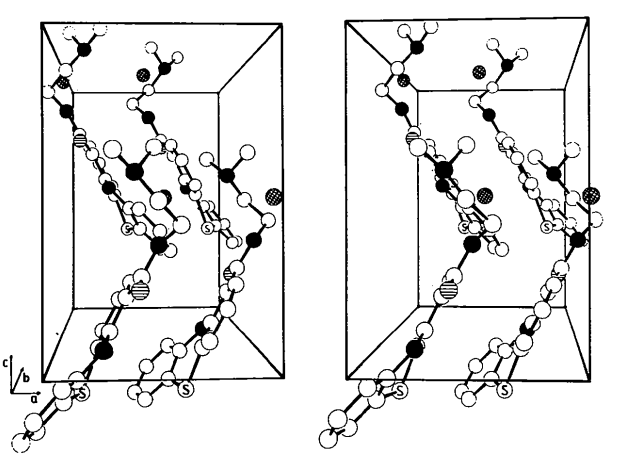


Fig. 3. Stereopair diagrams of the unit-cell packing.

hydrogen bond between the quinoline N(1) proton and the carbonyl O atom of the amide (McKenna, Beveridge, Jenkins, Neidle & Denny, 1989). In the present case the carboxamide side chain is again oriented so as to form a strong intramolecular hydrogen bond between N(10) and the carbonyl O atom [H(N10)···O(1′) 1.94, N(10)···O(1′) 2.62 Å, N(10)—H(N10)···O(1′) 126.7°]. The amide is essentially coplanar with the C(1)→C(4), C(4a), C(9a) aromatic ring.

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Structure of the 1:2 Adduct of *meso*-2,3-Dimercaptosuccinic Acid and *N,N*-Dimethylformamide

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Abstract. $C_4H_6O_4S_2.2C_3H_7NO$, $M_r = 328.20$, monoclinic, $P2_1/c$, $a = 6.408$ (1), $b = 10.433$ (1), $c = 12.388$ (1) Å, $\beta = 98.60$ (1)°, $V = 818.9$ (2) Å^3, $Z = 2$, $D_x = 1.33$ g cm^{-3}, λ(Mo $K\alpha$) = 0.71073 Å, $\mu = 3.3$ cm^{-1}, $F(000) = 348$, $T = 297$ (1) K, $R = 0.041$ for 1006 independent reflections. The C—S bond distance is 1.839 Å. The *meso*-2,3-dimercaptosuccinic acid molecule crystallizes in a staggered configuration with one dimethylformamide molecule hydrogen bonded to each of the carboxylic acid groups.

Introduction. In the 1940's, the dithiol 2,3-dimercapto-1-propanol (British Anti-Lewisite, BAL), was used successfully as an antidote for arsenic poisoning (Peters, Stocken & Thompson, 1945). The effectiveness of BAL in treating poisoning by other heavy metals was tempered by undesirable side effects. The water soluble dithiol 2,3-dimercaptopropanesulfonic acid (DMPS) was synthesized by Petrunkin in the 1950's, and is still the drug of choice for heavy-metal poisoning in the CSR (Petrunkin, 1956). Subsequently, other dithiols have been investigated, *e.g.* *meso*-2,3-dimercaptosuccinic acid (DMSA) (Liang, Chu, Tsen & Ting, 1957) and *N*-(2,3-dimercaptopropyl)phthalamidic acid (Yonaga & Morita, 1981). The dithiol DMSA has been recently approved by the US Food and Drug Administration for the treatment of heavy-metal poisoning.

No structural data are available for any of the dithiols; however, the structure of the monothiol detoxifying agent, 2-amino-3-mercapto-3-methylbutanoic acid (penicillamine) (Rao, Parthasarathy & Cole, 1973), and the structures of several mercury and methylmercury complexes have been determined (Wong, Chieh & Carty, 1973). We report below the structure of the detoxifying agent DMSA, which has been determined as its DMF adduct.

Experimental. Single crystals of the dimercaptosuccinic acid (DMSA)–dimethylformamide (DMF) adduct were produced by cooling a solution of dimercaptosuccinic acid in dimethylformamide. A colorless prism with approximate dimensions 0.27 × 0.33 × 0.50 mm was mounted on a Nicolet/Syntex $P2_1$ diffractometer. The cell constants were determined from 23 reflections in the range $20 < 2\theta < 30°$. The space group was determined to be $P2_1/c$ on the basis of the systematic absences. The $2\theta/\theta$-scan method with a variable scan rate from 2 to 8° min^{-1} (2θ) ($h = 0$ to 7, $k = 0$ to 12, $l = -14$ to 13) was used to collect the data. Three standard reflections, collected after every 96 reflections, decayed by

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