

RefinementRefinement on F^2 $R = 0.0286$ $wR = 0.0345$ $S = 3.901$

1073 reflections

67 parameters

All H atoms refined

 $w = 1/[\sigma^2(F_o) + 0.00002|F_o|^2]$ $(\Delta/\sigma)_{\max} = <0.001$ $\Delta\rho_{\max} = 0.26 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{\min} = -0.36 \text{ e } \text{\AA}^{-3}$

Extinction correction: none

Scattering factors from

International Tables for Crystallography (Vol. C)Table 1. Selected geometric parameters (\AA , $^\circ$)

S1—S2	2.0398 (8)	S3—C3	1.731 (2)
S1—C1	1.818 (2)	C1—C1 ¹	1.521 (4)
S2—C2	1.741 (2)	C2—C3	1.316 (3)
S3—C1	1.817 (2)		
S2—S1—C1	99.18 (6)	S1—C1—C1 ¹	113.5 (2)
S1—S2—C2	100.48 (8)	S3—C1—C1 ¹	113.0 (2)
C1—S3—C3	106.75 (9)	S2—C2—C3	125.7 (2)
S1—C1—S3	111.13 (9)	S3—C3—C2	132.5 (2)

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

The weak reflections [$I < 10\sigma(I)$] were rescanned (maximum five times) and the counts were accumulated to assure good counting statistics. The structure was solved by the direct methods *SHELXS86* program (Sheldrick, 1985) and expanded using Fourier techniques (*DIRDIF*; Beurskens *et al.*, 1992). The positions of all H atoms were determined from the difference Fourier synthesis map and refined isotropically. The non-H atoms were refined anisotropically. All calculations were performed using the *TEXSAN* crystallographic software package (Molecular Structure Corporation, 1985, 1992) and *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1988) was used for data collection and cell refinement.

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Lists of atomic coordinates, displacement parameters, structure factors and complete geometry have been deposited with the IUCr (Reference: AB1429). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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2,5-Diaziridinyl-3-phenyl-*p*-benzoquinone

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Abstract

The crystal structure of the title compound, $\text{C}_{16}\text{H}_{14}\text{N}_2\text{O}_2$, a novel anticancer agent, has been determined at 295 (1) K. The aziridine rings form approximately regular triangles, with N—C distances of 1.442 (5)–1.456 (5) \AA , C—C distances of 1.462 (6) and 1.467 (6) \AA , C—N—C angles of 60.5 (3) and 60.7 (3) $^\circ$, and C—C—N angles of 59.7 (3)–60.1 (3) $^\circ$. The aziridine ring planes make dihedral angles of 48.1 (3) and 48.3 (3) $^\circ$ with the quinone ring. The dihedral angle between the quinone ring plane and the phenyl ring is 49.8 (2) $^\circ$. The molecules are linked by C—H \cdots X hydrogen bonding into bilayers which stack along the *c* axis; C \cdots O distances range from 3.355 (4) to 3.631 (5) \AA and the unique C \cdots N distance is 3.427 (5) \AA .

Comment

Mitomycin C (MC) is an important clinical anticancer agent which is effective for the treatment of a wide range of solid tumors (Crooke & Bradner, 1976; Powis, 1987; Verweij & Pinedo, 1990). Its significant biological activity has, in part, been attributed to its selective activation in cancerous tissues by reducing enzymes, such as DT-diaphorase (DTD) (Siegel, Gibson, Preusch & Ross, 1990). Marked elevation in DT-diaphorase activity and mRNA content have been documented in both preneoplastic and established cancers (Malkinson

et al., 1992). With these discoveries, there has been an intense effort to develop cytotoxic agents that are good substrates of DT-diaphorase. Among them, the antitumor quinones, streptonigrin, EO9, MeDZQ and the most recently synthesized analogue PDZQ (Beall *et al.*, 1992) have been shown to be excellent substrates for recombinant and rat DTD (Beall *et al.*, 1992). Although PDZQ is highly cytotoxic against H460 human non-small cell lung cancer cells which are rich in DTD activity, it is also quite cytotoxic against H596 cells which are devoid of DTD activity. The reasons for this apparent lack of biological selectivity of PDZQ are unclear, but may include alternative routes of bioactivation in H596 cells or chemical activation. There is presently a concerted effort to elucidate the biological mechanism of PDZQ and in this communication we report the unambiguous determination of its structure.

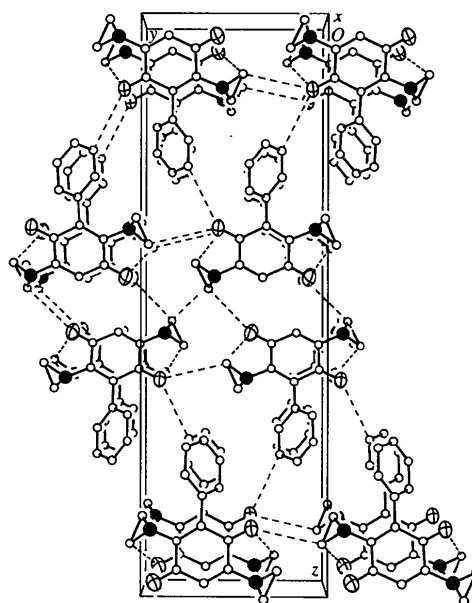
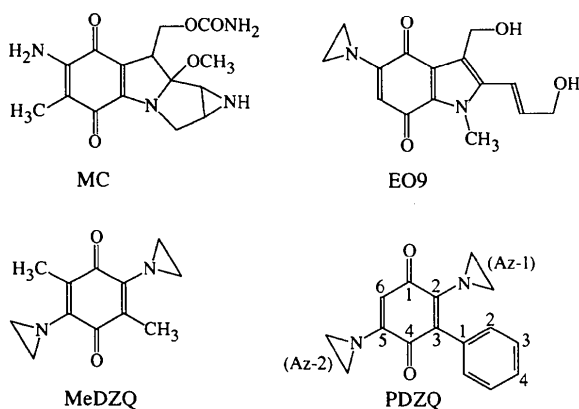


Fig. 2 Packing diagram viewed down the *a* axis.

C...N interaction of 3.427(5) Å. Although some of these contacts fall slightly outside the range reported for similar contacts (Taylor & Kennard, 1982), they possess reasonable geometry for this type of interaction.

Experimental

PDZQ was synthesized as a red solid in 26% yield by the reaction of aziridine with phenyl-1,4-quinone in dry ethanol. X-ray quality crystals were grown by slow evaporation of a solution of the compound in hexane–methylene chloride (10:1). The crystal used for analysis was mounted with epoxy onto the end of a glass fiber. The ¹H and ¹³C NMR spectra of PDZQ were measured at room temperature on a Bruker AM-300 spectrometer in CDCl₃ with TMS as an internal standard (δ 0 p.p.m). The ¹³C NMR [δ 114.9 (C6), 125.9 (Ph-1), 127.7 (Ph-3), 127.9 (Ph-4), 130.8 (Ph-2), 131.3 (C3), 151.3 and 156.4 (C2 and C5), 181.9 and 183.4 (C1 and C4)] and ¹H NMR signals [δ 2.02 (*s*, 4H, Az-1), 2.08 (*s*, 4H, Az-2), 6.05 (*s*, 1H, H6), 7.35–7.5 (*m*, 5H, Ph)] ruled out the possibility of 2,3-diaziridinylated PDZQ, but could not distinguish between the 2,5- and 2,6- isomers.

Crystal data

C₁₆H₁₄N₂O₂
M_r = 266.29
 Orthorhombic
*P*2₁2₁
a = 5.0997(9) Å
b = 9.1740(10) Å
c = 28.375(5) Å
V = 1327.5(4) Å³
Z = 4
D_x = 1.332 Mg m⁻³
D_m not measured

Cu Kα radiation
 λ = 1.54178 Å
 Cell parameters from 48 reflections
 θ = 25.31–49.21°
 μ = 0.724 mm⁻¹
T = 295(1) K
 Plate
 0.28 × 0.11 × 0.10 mm
 Red

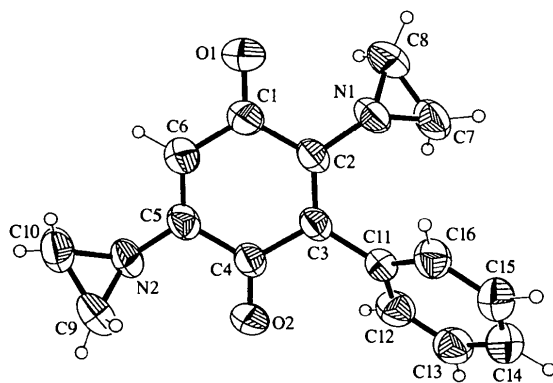


Fig. 1. The molecular structure of PDZQ showing 50% probability displacement ellipsoids.

The molecular geometry in PDZQ compares well with that of related compounds such as 2,5-bis(ethyleneimino)-1,4-benzoquinone (Ito & Sakurai, 1973) and 2-(4-methoxyphenyl)-1,4-benzoquinone (Desiraju, Paul & Curtin, 1977). The packing of PDZQ molecules in the crystal (Fig. 2) is influenced by weak C—H...X hydrogen bonding. Contacts range from 3.355(4) to 3.631(5) Å for C...O interactions and there is a

Data collection

Siemens R3m/V diffractometer
 ω - 2θ scans
 Absorption correction: empirical via ψ scans (Sheldrick, 1990)
 $T_{\min} = 0.82$, $T_{\max} = 0.93$
 1354 measured reflections
 1354 independent reflections

831 reflections with $I > 2\sigma(I)$
 $\theta_{\max} = 65^\circ$
 $h = 0 \rightarrow 6$
 $k = -10 \rightarrow 0$
 $l = 0 \rightarrow 33$
 3 standard reflections every 97 reflections
 intensity decay: 7.0%

Refinement

Refinement on F^2
 $R(F) = 0.0451$
 $wR(F^2) = 0.1094$
 $S = 1.029$
 1354 reflections
 183 parameters
 H atoms riding
 $w = 1/[\sigma^2(F_o^2) + (0.0795P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.159 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.158 \text{ e } \text{\AA}^{-3}$

Extinction correction: SHELXL93
 Extinction coefficient: 0.0023 (7)
 Scattering factors from *International Tables for Crystallography* (Vol. C)
 Absolute configuration: Flack (1983)
 Flack parameter = 1.5 (8)

Table 1. Selected bond lengths (\AA)

O1—C1	1.228 (4)	C1—C2	1.492 (6)
O2—C4	1.223 (4)	C2—C3	1.358 (4)
N1—C2	1.387 (4)	C3—C4	1.479 (5)
N1—C7	1.455 (6)	C3—C11	1.490 (5)
N1—C8	1.456 (5)	C4—C5	1.495 (6)
N2—C5	1.394 (4)	C5—C6	1.332 (5)
N2—C9	1.442 (5)	C8—C7	1.467 (6)
N2—C10	1.454 (6)	C9—C10	1.462 (6)
C1—C6	1.443 (5)		

Table 2. Contact distances (\AA)

C8...O2 ⁱ	3.570 (4)	C10...N2 ^v	3.427 (5)
C8...O1 ⁱⁱ	3.542 (4)	C10...O1 ⁱⁱⁱ	3.376 (4)
C9...O2 ⁱⁱⁱ	3.528 (4)	C15...O2 ^{iv}	3.355 (4)
C9...O1 ^v	3.631 (5)		

Symmetry codes: (i) $x, y-1, z$; (ii) $x-1, y, z$; (iii) $1+x, y, z$; (iv) $x, 1+y, z$; (v) $\frac{1}{2} + x, \frac{3}{2} - y, -z$; (vi) $\frac{1}{2} + x, \frac{3}{2} - y, -z$; (vii) $-x, y - \frac{1}{2}, \frac{1}{2} - z$.

The title structure was solved by direct methods and refined by full-matrix least-squares techniques. All non-H atoms were refined anisotropically and H atoms were generated with ideal geometries (C—H = 0.96 \AA) and refined as riding groups with a single group displacement parameter [$U_{\text{H}} = 0.086 (4) \text{\AA}^2$].

Data collection: P3 Software (Siemens, 1989). Cell refinement: P3 Software. Data reduction: SHELXTL-Plus (Sheldrick, 1990). Program(s) used to solve structure: SHELXTL-Plus. Program(s) used to refine structure: SHELXL93 (Sheldrick, 1993). Molecular graphics: SHELXTL-Plus.

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Lists of atomic coordinates, displacement parameters, structure factors and complete geometry have been deposited with the IUCr (Reference: HA1183). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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Benzyltrimethylammonium Tetramethoxoborate

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Abstract

In the title compound, $\text{C}_{10}\text{H}_{16}\text{N}^+\cdot\text{C}_4\text{H}_{12}\text{BO}_4^-$ or $[\text{PhCH}_2\text{NMe}_3][\text{B}(\text{OMe})_4]$, the anion has essentially $\bar{4}2m$ (D_{2d}) symmetry, with a tetragonal elongation to give two opposite O—B—O angles markedly smaller than the other four. Comparison with the structures of other salts indicates that this is an intrinsic property of the anion rather than the result of specific interionic or intermolecular interactions.

Comment

In the course of our investigations into non-aqueous polyborate chemistry, we have synthesized an organic salt of tetramethoxoborate, $[\text{B}(\text{OMe})_4]^-$, as a soluble building block. The benzyltrimethylammonium salt, (I), is readily prepared from $\text{B}(\text{OMe})_3$ and $[\text{PhCH}_2\text{NMe}_3]^+[\text{OMe}]^-$ in methanol.