approaches planarity, the N atom lying 0.16 Å out of the plane of its three bonded neighbors.

The sugar and piperidine rings are rotated about 30° with respect to each other. This mutual orientation is best illustrated by considering the angles between perpendiculars to the 'best' plane through the sugar ring and the glycosidic link plane and between the 'best' plane through the piperidine ring and glycosidic plane; these values are 92 and 60°, respectively. The glycosidic linkage is confirmed to be $\alpha$.

As shown in Fig. 2, the molecules are held together by a strong intermolecular three-dimensional hydrogen-bond network in which all hydroxyl H atoms are involved as donors. Acting as acceptors are the sugar ring O(1) atom, the *N*-oxide O(4) atom and hydroxyl O(9) and O(10) atoms. The hydrogen-bonding details are given in Table 2.

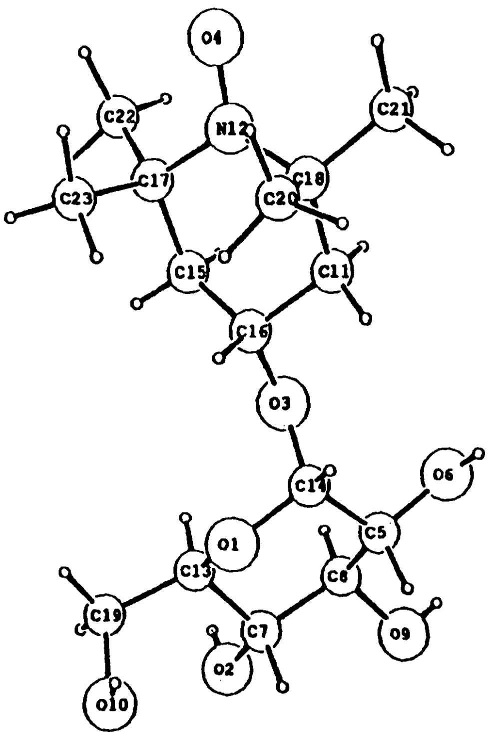

Fig. 1. *ORTEP* (Johnson, 1976) drawing of the molecule showing the atomic numbering scheme.

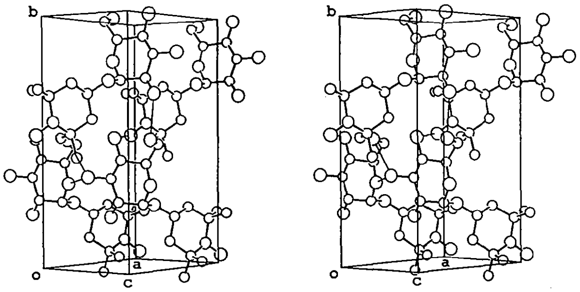

Fig. 2. *ORTEP* stereoscopic projection of the crystal packing.

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# Structure of Debrisoquinium Sulfate

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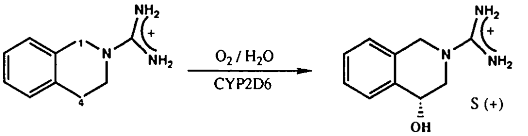
**Abstract.** 3,4-Dihydro-2(1*H*)-isoquinolinecarboxamidinium sulfate, $2C_{10}H_{14}N_3^+.SO_4^{2-}$, $M_r = 448.5$, monoclinic, $C2/c$, $a = 27.214\ (10)$, $b = 6.552\ (1)$, $c = 13.241\ (1)$ Å, $\beta = 113.35\ (2)°$, $V = 2168\ (1)$ Å$^3$, $Z = 4$, $D_x = 1.375$ g cm$^{-3}$, $\lambda$(Mo $K\alpha$) = 0.7107 Å, $\mu = 1.81$ cm$^{-1}$, $F(000) = 952$, room temperature, final $R$

$= 0.042$ for 2446 unique reflections [1661 observed with $I > 3\sigma(I)$]. The crystal structure consists of a hydrogen-bonded network of debrisoquinium cations and sulfate anions. The relative orientations of the two H atoms on C(4) of debrisoquin, one of which is enzymatically replaced by a hydroxyl group, is discussed.

**Introduction.** Debrisoquin, 1,2,3,4-tetrahydroisoquinoline-2-carboxamidine, is an antihypertensive drug (Budavari, O'Neil, Smith & Heckelman, 1989). It is bioactivated, hydroxylated at the C(4) position, by a cytochrome P450 enzyme, CYP2D6 (Lennard, 1990). The activation is stereospecific to give (+)-(*S*)-4-hydroxydebrisoquin as the major product (Eichelbaum, Bertilsson, Kupfer, Steiner & Meese, 1988):



The cytochrome P450 family of enzymes activate many drugs to their active form and many procarcinogens into their ultimate mutagenic form (Lennard, 1990; Wolf, 1986). Knowledge of the exact stereochemistry of debrisoquin will help in the refinement of a three-dimensional molecular template for the substrates to CYP2D6 (Islam, Wolf, Lennard & Sternberg, 1991) and hence certain classes of compounds that are possible carcinogens or potential drugs may be identified.

**Experimental.** Microcrystalline debrisoquinium sulfate (30 mg), manufactured by Roche Products Ltd, was kindly provided for us by Dr M. S. Lennard of the Department of Medicine and Pharmacology, Royal Hallamshire Hospital, Sheffield. The material was dissolved in distilled water (soluble in 40 parts of water). Several crystallization experiments were tried. Eventually well formed colourless crystals were obtained by the slow evaporation of the solvent (approximately two months) from a 5 ml conical flask. A crystal of dimensions 0.23 × 0.24 × 0.30 mm was selected for data collection. Data were collected on an Enraf–Nonius FAST TV area detector diffractometer. With detector-to-crystal distance (det) of 40 mm and a scanning angle ($= 2\theta_D$) of 18°, reflections were found in two 5° $\omega$ rotation regions separated by 90°. The orientation matrix and unit-cell dimensions were determined *via* the *INDEX* and *REFINE* procedures of the *SADONL* software [the 'small molecule' on-line version of *MADNES* (Pflugrath & Messerschmidt, 1989)], using 250 reflections taken from both regions. Accurate values of det and $2\theta_D$ were also determined by refinement (40.55 mm and 17.95°, respectively). Intensity data corresponding to slightly more than one hemisphere of reciprocal space were recorded using two $\omega$ rotations of 100° with 90° $\varphi$ shift, at $\chi = 0°$, and two further $\omega$ rotations of 70°, again with a $\varphi$ shift of 90° at $\chi = 90°$ to record the cusp data. Throughout the data collection the $\omega$ step was 0.15° and the frame measuring time was 20 s. The crystal was moisture and air stable, and since the total data-collection time was relatively short (approximately 8 h), it was not monitored for decomposition.

4308 reflections were collected (*hkl* range: $h$ −35 to 35, $k$ −2 to 8 and $l$ −16 to 16). With the averaging of equivalent reflections, $R_{\rm int} = 0.054$, the total number of unique reflections was 2446. Of these, 1661 reflections were considered to be observed with $I > 3\sigma(I)$. The reflections were corrected for Lorentz and polarization but not absorption or crystal decomposition effects. The structure was solved by direct methods using the program *SHELX76* (Sheldrick, 1976) and refined by full-matrix least squares with $F$'s. The function minimized was $\sum w(|F_o| - |F_c|)^2$, where $w = 1/\sigma^2(F_o)$. The S, N, C and O atoms were refined with anisotropic thermal parameters; the H atoms, located by difference Fourier techniques, were refined with isotropic thermal parameters. Refinement converged at $R = 0.042$ and $wR = 0.045$, max. shift/e.s.d. = 0.08, for 199 refined parameters; $S = 1.31$. The maximum peak in the final Fourier map was 0.11 e Å$^{-3}$ and was located near the S atom; the minimum was −0.13 e Å$^{-3}$. The scattering factors were taken from *International Tables for X-ray Crystallography* (1974, Vol. IV).

Positional parameters and $U_{\rm eq}$ thermal parameters for the non-H atoms are listed in Table 1.* Bond lengths and angles are listed in Table 2. The molecular structure and atomic labelling scheme for the debrisoquin cation are shown in Fig. 1.

**Discussion.** Fig. 2 shows a packing diagram which illustrates the hydrogen-bonding network between debrisoquin cations and sulfate anions. The S atom of each sulfate group lies on a crystallographic twofold axis. Each debrisoquin cation makes hydrogen-bonding contacts to three sulfate anions. An O atom from one sulfate symmetrically bridges the guanidinium group; N—H···O hydrogen-bond distances are

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* Lists of structure factors, anisotropic thermal parameters, H-atom parameters, bond lengths and angles involving H atoms and selected intermolecular and intramolecular non-bonded distances have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 55652 (12 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England. [CIF reference: LI1020]

Table 1. *Coordinates* ($\times 10^4$) *and equivalent isotropic thermal parameters* (Å$^2 \times 10^3$) *for non-*H *atoms with e.s.d.'s in parentheses*

$$U_{eq} = (1/3)\Sigma_i\Sigma_j U_{ij}a_i^*a_j^*\mathbf{a}_i.\mathbf{a}_j.$$

| | $x$ | $y$ | $z$ | $U_{eq}$ |
|---|---|---|---|---|
| S | 5000 | 838 (1) | 2500 | 25.5 (3) |
| O(1) | 5100 (1) | −441 (2) | 1691 (2) | 46 (1) |
| O(2) | 4532 (1) | 2135 (3) | 1918 (2) | 43 (1) |
| N(1) | 4405 (1) | 4319 (3) | −1876 (2) | 34 (1) |
| N(2) | 4075 (1) | 5891 (3) | −711 (2) | 29 (1) |
| N(3) | 4513 (1) | 2761 (3) | −265 (2) | 35 (1) |
| C(1) | 3870 (1) | 7562 (4) | −1510 (2) | 40 (1) |
| C(2) | 4332 (1) | 4337 (3) | −944 (2) | 26 (1) |
| C(3) | 4052 (1) | 6196 (4) | 364 (2) | 42 (1) |
| C(4) | 3486 (1) | 6624 (4) | 224 (2) | 45 (1) |
| C(4*A*) | 3267 (1) | 8443 (3) | −523 (2) | 34 (1) |
| C(5) | 2875 (1) | 9710 (4) | −423 (3) | 48 (1) |
| C(6) | 2680 (1) | 11357 (4) | −1114 (3) | 54 (1) |
| C(7) | 2878 (1) | 11791 (4) | −1895 (3) | 51 (1) |
| C(8) | 3267 (1) | 10566 (4) | −1999 (3) | 43 (1) |
| C(8*A*) | 3461 (1) | 8868 (3) | −1316 (2) | 30 (1) |

Table 2. *Bond lengths* (Å) *and angles* (°) *for non-*H *atoms with e.s.d.'s in parentheses*

| | | | |
|---|---|---|---|
| O(1)—S | 1.469 (3) | O(2)—S | 1.470 (3) |
| C(2)—N(1) | 1.326 (4) | C(1)—N(2) | 1.470 (4) |
| C(2)—N(2) | 1.337 (4) | C(3)—N(2) | 1.463 (4) |
| C(2)—N(3) | 1.329 (4) | C(8*A*)—C(1) | 1.505 (5) |
| C(4)—C(3) | 1.505 (5) | C(4*A*)—C(4) | 1.512 (5) |
| C(5)—C(4*A*) | 1.399 (4) | C(8*A*)—C(4*A*) | 1.378 (4) |
| C(6)—C(5) | 1.377 (5) | C(7)—C(6) | 1.372 (5) |
| C(8)—C(7) | 1.379 (5) | C(8*A*)—C(8) | 1.398 (4) |

| | | | |
|---|---|---|---|
| O(2)—S—O(1) | 108.7 (2) | O(1)—S—O(1$^{i}$) | 110.4 (2) |
| O(2)—S—O(2$^{i}$) | 109.4 (2) | O(1)—S—O(2$^{i}$) | 109.9 (2) |
| C(2)—N(2)—C(1) | 119.0 (3) | C(3)—N(2)—C(1) | 116.6 (3) |
| C(3)—N(2)—C(2) | 123.8 (3) | C(8*A*)—C(1)—N(2) | 113.4 (3) |
| N(2)—C(2)—N(1) | 120.4 (3) | N(3)—C(2)—N(1) | 118.1 (3) |
| N(3)—C(2)—N(2) | 121.5 (3) | C(4)—C(3)—N(2) | 110.0 (3) |
| C(4*A*)—C(4)—C(3) | 110.2 (3) | C(5)—C(4*A*)—C(4) | 121.6 (3) |
| C(8*A*)—C(4*A*)—C(4) | 119.2 (3) | C(8*A*)—C(4*A*)—C(5) | 119.2 (3) |
| C(6)—C(5)—C(4*A*) | 120.7 (4) | C(7)—C(6)—C(5) | 120.0 (3) |
| C(8)—C(7)—C(6) | 120.1 (4) | C(8*A*)—C(8)—C(7) | 120.3 (4) |
| C(4*A*)—C(8*A*)—C(1) | 123.2 (3) | C(8)—C(8*A*)—C(1) | 117.1 (3) |
| C(8)—C(8*A*)—C(4*A*) | 119.7 (3) | | |

Symmetry code: (i) $1 - x, y, 0.5 - z$.

2.00 (2) and 2.11 (3) Å. One O atom from each of the other two sulfates interacts with the outer H atoms of each guanidinium group; N—H···O hydrogen-bond distances are 1.99 (2) and 2.09 (2) Å.

The ring pucker of the saturated ring can be measured by a least-squares plane through the complete ring system; N(2), C(1), C(3), C(4), C(4*A*), C(5), C(6), C(7), C(8) and C(8*A*). The maximum deviation of any ring atom from this plane is, for C(3), 0.487 (3) Å. The angle between this plane and a plane through the guanidinium group is 18.41 (8)°. The extent of ring pucker and the angle the guanidinium group makes with the ring system determines the relative orientation of the two H atoms on C(4) to the guanidinium group. Fig. 3 shows that the C—H bond vector for one of these H atoms, H(41), lies essentially parallel to the N(1)···N(3) interatomic vector of the guanidinium group. The other C—H bond vector, for H(42), lies at right angles to the guanidinium group. Molecular modelling suggests that it is the H(41) atom that is attacked in the enzymatic hydroxylation process (Islam, Wolf, Lennard & Sternberg, 1991).

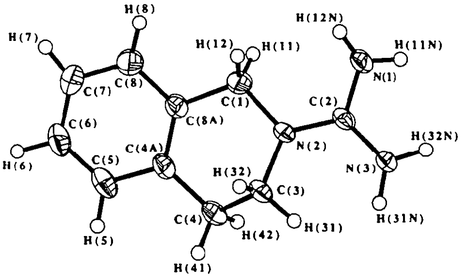

Fig. 1. The molecular structure of the debrisoquin cation. Atomic labelling follows IUPAC convention for fused-ring systems. Thermal ellipsoids are drawn at the 50% probability level.

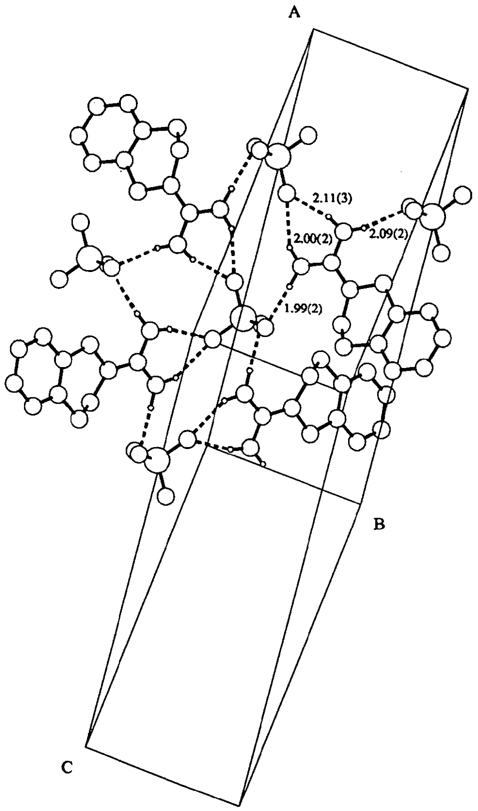

Fig. 2. Packing diagram showing the network of hydrogen-bonding contacts between debrisoquin cations and sulfate anions. The four unique NH···O hydrogen-bonding contacts are displayed in the figure: H(31N)···O(2) 1.99 (2), H(11N)···O(1$^{i}$) 2.00 (2), H(32N)···O(1$^{i}$) 2.11 (3) and H(12N)···O(2$^{ii}$) 2.09 (2) Å [symmetry code: (i) $1 - x, -y, -z$; (ii) $x, 1 - y, -0.5 + z$].

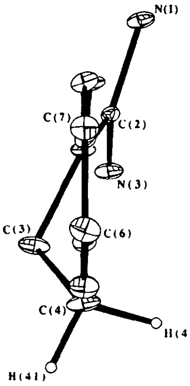

Fig. 3. View of the debrisoquin cation looking edge on to the ring system with the delocalized ring in the foreground. For clarity, thermal ellipsoids are drawn at the 10% probability level and only a few of the atoms are labelled. Only the H atoms on C(4) are shown.

We are grateful to Dr M. S. Lennard (Sheffield, England) for supplying debrisoquinium sulfate and to Professor M. B. Hursthouse (Cardiff, Wales) for the use of his data-collection facilities.

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# Structures of Derivatives of the Diels–Alder Adduct 1,4,4a,5,8,8a,9a,10a-Octahydro-1,4:5,8-dimethano-9,10-anthraquinone

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**Abstract.** 1,4,4a,5,8,8a,9,9a,10,10a-Decahydro-10-oxo-1,4:5,8-dimethanoanthracen-9-yl acetate (*A*), $C_{18}H_{20}O_3$, $M_r = 284.37$, orthorhombic, *Pbca*, $a = 12.036\,(3)$, $b = 28.753\,(3)$, $c = 8.451\,(3)$ Å, $V = 2924.96$ Å$^3$, $Z = 8$, $D_m = 1.28\,(4)$, $D_x = 1.296$ Mg m$^{-3}$, $\lambda(\text{Mo } K\alpha) = 0.71069$ Å, $\mu = 0.081$ mm$^{-1}$, $F(000) = 1216$, $T = 293$ K, $R = 0.054$, $wR = 0.057$ for 1207 reflections. (1a$\alpha$,2$\beta$,2a$\beta$,3$\alpha$,3a$\alpha$,4$\alpha$,4a$\beta$,5a$\beta$,6$\alpha$,6a$\alpha$,7$\alpha$,7a$\beta$,8$\beta$,8a$\alpha$)-Tetradecahydro-7-hydroxy-2,8:4,6-dimethanoanthra[2,3-*b*:6,7-*b*′]bisoxiren-3-yl acetate (*B*), $C_{18}H_{22}O_5$, $M_r = 318.37$, monoclinic, $P2_1/c$, $a = 8.741\,(1)$, $b = 20.477\,(2)$, $c = 9.890\,(1)$ Å, $\beta = 92.17\,(1)°$, $V = 1768.93$ Å$^3$, $Z = 4$, $D_m = 1.18\,(3)$, $D_x = 1.195$ Mg m$^{-3}$, $\lambda(\text{Cu } K\alpha) = 1.54178$ Å, $\mu = 0.677$ mm$^{-1}$, $F(000) = 680$, $T = 293$ K, $R = 0.023$, $wR = 0.029$ for 2141 reflections. The central ring and the two terminal six-membered rings of the polycycle adopt distorted boat conformations in both derivatives. The stereochemistry of the polycycle is *endo*, *cis*, *anti*, *cis*, *endo*. The packing of the molecules in (*B*) is in the form of parallel chains with the weak interchain linkage being consistent with the poor shear strength of its crystals.

**Introduction.** Polycyclic polyfunctional compounds are known to be useful as curing agents for polyurethanes containing —NCO as terminal groups. These polyurethanes are extensively employed in space applications (Robbins, 1970). Bakthavatchalam (1987) synthesized a number of polyfunctional compounds using the Diels–Alder adduct 1,4,4a,5,8,8a,9a,10a-octahydro-1,4:5,8-dimethano-9,10-anthraquinone as starting material. The two compounds

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