

There are no unusual carbon-carbon or carbon-oxygen bond distances or angles in the molecule. The mean C-H distance is 1.02 Å, which is as expected in X-ray measurements.

More detailed analyses of the geometry of the BNE molecule are given by Hanson (1969) and by Duax & Norton (1975).

The authors are indebted to Mrs Yuan-Yuan Hsiu for preliminary crystallographic work and to Dr Jesse W. Schilling for helpful discussions and advice on computing. The research was supported in part by Research Grant GM15259 from the National Institutes of Health, U.S. Public Health Service.

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The Crystal and Molecular Structure of (±)-2,3-Dimethoxy-18-nor-8,13-diaza-1,3,5(10)-estratrien-17-one

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The synthetic steroid, (±)-2,3-dimethoxy-18-nor-8,13-diaza-1,3,5(10)-estratrien-17-one, crystallizes in space group $P2_1/n$ with $a = 7.531$ (4), $b = 29.82$ (1), $c = 7.637$ (4) Å, $\beta = 116.92$ (3)° and $Z = 4$. The structure was solved by the Patterson search procedure and was refined by block-diagonal least-squares calculations to a final R value of 0.06. The molecular conformation is very similar to that found in the natural estrogens with the largest deviation in the D ring, which contains a nearly planar amide group. The thermal motion is best described in terms of two rigid groups, one composed mainly of rings A and B , the other of ring D . The largest amplitude of libration is in the latter group.

Introduction

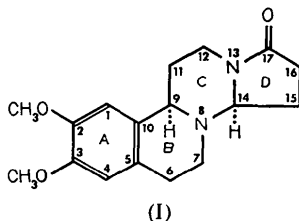
Modification of estrogens to their aza analogs has been suggested as a way to enhance their desirable medicinal properties while reducing unwanted side effects (Martin-Smith & Sugrue, 1964). As described in a preliminary report (Burckhalter, Abramson, MacConnell,

Thill, Olson, Hanson & Nordman, 1968), the azaestrogen (±)-2,3-dimethoxy-18-nor-8,13-diaza-1,3,5(10)-estratrien-17-one (I) has a structure which is very similar to that of 4-bromoestrone (Norton, Kartha & Lu, 1963). The lack of pharmacological evaluation precludes any discussion of these properties in relation to the structure at the present time. However, there are two related azaestrogens whose crystal structures are known; both show low estrogenic activity. The compounds 8-azaestrone hydrobromide (Majeste & Trefonas, 1969) and 8-azaestradiol (Brown & Trefonas, 1972) also have structures which are similar to the cor-

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responding natural estrogens. Their lack of appreciable estrogenic activity has been rationalized (Brown & Trefonas, 1972) in terms of potential protonation of the nitrogen at the 8 position during the initial glucuronidation. The detailed structure of (I) is presented here to aid in the further understanding of azaestrogens.



Experimental

Crystals of (\pm)-2,3-dimethoxy-18-nor-8,13-diaza-1,3,5(10)-estratrien-17-one were given to us by Dr J. H. Burckhalter of the University of Michigan. The cell parameters were calculated by a least-squares procedure (Burnham, 1964) from the measurements of 2 θ values of resolved Cu $K\alpha_{1-2}$ reflections on back-reflection Weissenberg photographs of the $hk0$ and $h0l$ layers.

Crystal data

(\pm)-2,3-Dimethoxy-18-nor-8,13-diaza-1,3,5(10)-estratrien-17-one, $C_{17}H_{22}N_2O_3$, M.W. 302.4. Monoclinic, space group $P2_1/n$; $a=7.531$ (4), $b=29.82$ (1),* $c=7.637$ (4) Å, $\beta=116.92$ (3)°; $V=1534.2$ Å³, $Z=4$; $D_x=1.309$ g cm⁻³; $F(000)=648$; μ for Cu $K\alpha$ ($\lambda=1.5418$ Å) = 7.8 cm⁻¹. $\lambda(\text{Cu } K\alpha_1)=1.54050$; $\lambda(\text{Cu } K\alpha_2)=1.54434$ Å.

Intensity data were collected on a Supper-Datex punched-tape controlled diffractometer of Weissen-

* In the preliminary communication (Burckhalter *et al.*, 1968) the b cell dimension was erroneously given as 29.917 Å.

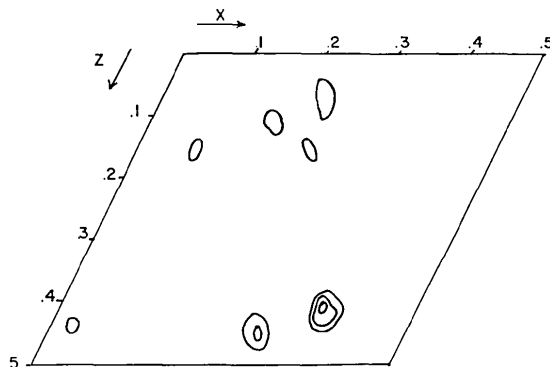


Fig. 1. Two-dimensional Patterson search with vectors between the oriented search group and its 2_1 screw-axis related mate. The contour levels are on an arbitrary scale and are proportional to the value of $\min(5)$.

berg geometry using Cu $K\alpha$ radiation monochromatized by means of Ni-Co balanced filters and pulse-height analysis. A fixed-counter, moving-crystal technique with variable step scans was used (Hanson & Nordman, 1975). In this technique a scan range whose width depended on the expected peak width was calculated for each reflection. Furthermore, each scan range was divided into ten equal parts, whose accumulated counts were individually recorded on the output tape. With crystal scan ranges from 2.5 to 6.0°, several of the partial scans represented readings of the background on each side of the peak. The assignment of 'peak' and 'background' scan steps, and evaluation of the integral under the peak was done by a data reduction program (Hanson, 1969). Data, about the a axis, were collected for 2620 reflections, of which 2191 were judged to be of measurable intensity. Of these reflections, 36 were rejected when it was discovered, during the early stages of the refinement, that some reflections included contributions from neighboring peaks. For many of these reflections the doubling could be seen in the step scan data; for others the doubling might have been masked. Thus, a uniform rejection criterion was applied by means of a computer program which identified all possible overlaps for the detector aperture and reciprocal lattice orientation in question.

Determination and refinement of the structure

Because the molecular geometry of the A ring and the four adjoining atoms was known, the orientation and location of this ten-atom group was determined by a Patterson search procedure (Nordman, 1966). Descriptions of this technique have been given by Schilling (1968, 1970a) and by Nordman & Schilling (1970).

A 'point atom' Patterson function with the origin peak removed was used in all searches. A Wilson treatment was used to obtain an overall isotropic thermal parameter and scale factor, which were used to calculate the above Patterson.

The orientation of the molecule relative to a crystal-fixed Cartesian system was determined in terms of the Euler angles A , B and C which, when used to rotate the intramolecular vectors, gave the best fit to the Patterson function. A set of 21 out of the 45 intramolecular vectors was selected by rejecting redundant, overlapped vectors and vectors between nearest neighbor atoms. The 'weighted minimum average' $\min(5)$ was used as the image seeking function (Schilling, 1968). The peak at $A=27^\circ$, $B=140^\circ$, $C=40^\circ$ had a $\min(5)$ value of 1.6, on a relative scale, as compared to the next highest peaks whose heights were 1.0 and 0.8. The orientation of the group, as subsequently established in the final, refined structure, agrees within 3° with the above values.

The location of the properly oriented group was determined by superposition of vectors between the group and its symmetry-related mates in the Patterson function. The y coordinate of the group was determined with a one-dimensional translation search, where

the search vectors were those between the group and its n glide-related mate. The value of $\min(5)$ at the correct location was more than twice as large as the next highest value. The x and z coordinates of the group were determined by a two-dimensional translation search using vectors between the group and its 2_1 screw axis-related mate. The results of this search are illustrated in Fig. 1, where the highest peak falls at the position subsequently verified as correct.

The above two searches correctly and unambiguously established the location of the oriented search group in the unit cell. However, as an independent check the x , y and z coordinates of the group were also determined by a three-dimensional translation search using vectors between groups related by a center of symmetry. For the sake of computational economy only the nine vectors of highest weight were used. This search presented a somewhat confusing picture because six locations with barely distinguishable image-seeking function values were found. A feature of the peak locations was that they came in pairs related by an approximate center of symmetry. This arises from the fact that the search group itself is almost centrosymmetric. Only one of the pairs of locations was chemically reasonable, and contained the correct solution, consistent with the one- and two-dimensional translation searches. All other locations caused the search group to overlap with its centrosymmetrically related counterpart. The five pairs of false peaks were identified as fits of intergroup vectors to intramolecular vectors between different rings of the nearly planar molecule. The effect of intramolecular vectors can be reduced by removing all the intragroup vectors from the Patterson function before doing the translation searches.

Based on the coordinates of the ten-atom fragment determined above, a weighted difference electron density map was calculated, and five more atom positions were found. The remaining seven atom positions were found in a subsequent map.

The coordinates and isotropic thermal parameters were first refined by diagonal least-squares calculations. The hydrogen atoms were found in two successive difference electron density maps. Additional refinement was done with isotropic thermal parameters for the hydrogen atoms and anisotropic thermal parameters for carbon and oxygen atoms using the block-diagonal mode of the *CLS* least-squares program (Schilling, 1970*b*). During the refinement, 20 reflections which were expected to be most affected by secondary extinction were rejected (Zachariasen, 1967). For most of these reflections F_o was found to be consistently less than F_c in the later stages of refinement. The quantity $\sum w(F_o - kF_c)^2$ was minimized with $w = (1/F_o)^2$ if $F_o > F_{\min}$, and $w = (1/F_{\min})^2$ otherwise, where $F_{\min} = 8$. The final R value is 0.06 for 2135 observed reflections.

The atomic scattering factors of Berghuis, Haanappel, Potters, Loopstra, MacGillavry & Veenendaal (1955) were used for carbon, oxygen and nitrogen and those of Stewart, Davidson & Simpson (1965) for hydrogen. The final parameter values are given in Tables 1 and 2.*

* A table of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 30697 (15 pp., 1 microfiche). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 1. Fractional atomic coordinates and anisotropic thermal parameters ($\times 10^3$) of the non-hydrogen atoms

The estimated standard deviation, given in parentheses, refers to the last significant place. The thermal parameters U_{ij} (\AA^2) are those of the temperature factor $\exp[-2\pi^2(U_{11}a^*^2h^2 + \dots + 2U_{12}a^*b^*hk + \dots)]$.

	x	y	z	U_{11}	U_{22}	U_{33}	U_{12}	U_{13}	U_{23}
C(1)	0.4462 (4)	0.1178 (1)	0.4352 (4)	38 (1)	30 (1)	39 (1)	-4 (1)	20 (1)	-3 (1)
C(2)	0.4796 (4)	0.0866 (1)	0.3194 (3)	35 (1)	36 (1)	34 (1)	2 (1)	17 (1)	2 (1)
C(3)	0.3850 (4)	0.0444 (1)	0.2859 (3)	40 (1)	31 (1)	35 (1)	6 (1)	17 (1)	0 (1)
C(4)	0.2665 (4)	0.0350 (1)	0.3761 (4)	43 (1)	27 (1)	43 (1)	-2 (1)	23 (1)	-1 (1)
C(5)	0.2376 (4)	0.0660 (1)	0.4979 (4)	38 (1)	28 (1)	38 (1)	1 (1)	18 (1)	2 (1)
C(6)	0.1210 (4)	0.0526 (1)	0.6062 (4)	45 (1)	27 (1)	52 (1)	-3 (1)	28 (1)	1 (1)
C(7)	0.1694 (4)	0.0831 (1)	0.7805 (4)	50 (1)	29 (1)	49 (1)	4 (1)	32 (1)	7 (1)
N(8)	0.1440 (3)	0.1299 (1)	0.7137 (3)	40 (1)	24 (1)	39 (1)	0 (1)	24 (1)	1 (1)
C(9)	0.3001 (3)	0.1428 (1)	0.6580 (3)	35 (1)	30 (1)	38 (1)	-4 (1)	20 (1)	-4 (1)
C(10)	0.3243 (3)	0.1081 (1)	0.5242 (3)	36 (1)	29 (1)	36 (1)	-1 (1)	18 (1)	-1 (1)
C(11)	0.2518 (4)	0.1895 (1)	0.5663 (4)	66 (2)	29 (1)	61 (2)	-5 (1)	44 (1)	-1 (1)
C(12)	0.2398 (5)	0.2231 (1)	0.7078 (5)	70 (2)	33 (1)	75 (2)	-6 (1)	48 (2)	-4 (1)
N(13)	0.1139 (4)	0.2058 (1)	0.7895 (3)	57 (1)	28 (1)	58 (1)	-1 (1)	40 (1)	-2 (1)
C(14)	0.1445 (4)	0.1604 (1)	0.8634 (3)	45 (1)	33 (1)	37 (1)	2 (1)	21 (1)	1 (1)
C(15)	-0.0262 (5)	0.1530 (1)	0.9150 (4)	63 (2)	40 (1)	63 (2)	0 (1)	44 (2)	-2 (1)
C(16)	-0.0957 (6)	0.2001 (1)	0.9319 (6)	88 (2)	50 (2)	100 (3)	12 (2)	71 (2)	3 (2)
C(17)	-0.0167 (5)	0.2295 (1)	0.8228 (5)	74 (2)	39 (1)	71 (2)	8 (1)	49 (2)	-2 (1)
O(2)	0.5986 (3)	0.0928 (1)	0.2297 (3)	48 (1)	50 (1)	55 (1)	-10 (1)	36 (1)	-11 (1)
O(3)	0.4244 (3)	0.0158 (1)	0.1686 (3)	59 (1)	34 (1)	53 (1)	2 (1)	36 (1)	-5 (1)
O(17)	-0.0597 (5)	0.2692 (1)	0.7758 (5)	136 (2)	43 (1)	130 (2)	33 (1)	98 (2)	16 (1)
C(O2)	0.7068 (4)	0.1337 (1)	0.2664 (4)	45 (1)	57 (2)	53 (2)	-10 (1)	28 (1)	4 (1)
C(O3)	0.3140 (4)	-0.0249 (1)	0.1120 (4)	55 (2)	39 (1)	60 (2)	3 (1)	30 (1)	-12 (1)

Table 2. *Fractional coordinates and isotropic thermal parameters of the hydrogen atoms*

The numbering follows that of the carbon atoms to which the hydrogens are attached

	<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i> (Å ²)
H(1)	0.507 (4)	0.147 (1)	0.450 (4)	3.6 (6)
H(2)	0.790 (5)	0.131 (1)	0.190 (5)	4.5 (7)
H'(2)	0.799 (5)	0.139 (1)	0.406 (5)	4.8 (7)
H''(2)	0.609 (5)	0.158 (1)	0.209 (5)	4.4 (7)
H(3)	0.172 (5)	-0.017 (1)	0.045 (5)	5.6 (8)
H'(3)	0.352 (5)	-0.041 (1)	0.011 (5)	5.4 (8)
H''(3)	0.360 (6)	-0.044 (1)	0.234 (6)	7.4 (10)
H(4)	0.198 (4)	0.005 (1)	0.353 (4)	3.7 (6)
H(6)	-0.005 (4)	0.055 (1)	0.527 (4)	2.7 (5)
H'(6)	0.155 (4)	0.021 (1)	0.653 (4)	3.8 (6)
H(7)	0.074 (4)	0.076 (1)	0.836 (4)	3.1 (5)
H'(7)	0.306 (4)	0.079 (1)	0.874 (4)	3.9 (6)
H(9)	0.428 (4)	0.145 (1)	0.777 (4)	3.0 (5)
H(11)	0.124 (4)	0.187 (1)	0.460 (4)	3.3 (6)
H'(11)	0.330 (4)	0.201 (1)	0.509 (4)	3.9 (6)
H(12)	0.354 (4)	0.226 (1)	0.806 (3)	2.3 (5)
H'(12)	0.178 (5)	0.253 (1)	0.642 (5)	5.4 (8)
H(14)	0.263 (4)	0.160 (1)	0.974 (4)	2.4 (5)
H(15)	0.022 (5)	0.134 (1)	1.048 (5)	6.1 (9)
H'(15)	-0.125 (5)	0.143 (1)	0.818 (5)	4.9 (7)
H(16)	-0.228 (7)	0.207 (2)	0.866 (7)	9.0 (11)
H'(16)	-0.026 (5)	0.209 (1)	1.081 (4)	5.7 (8)

Analysis of thermal motion

The thermal motion was analyzed in terms of the **T**, **L** and **S** rigid-body motion tensors (Schomaker & Trueblood, 1968). Initially, the entire steroid nucleus was assumed to be rigid. The standard error of fit between the least-squares U_{ij} values and those calculated from this rigid-body model was found to be 0.0045 Å²,

which is large when compared with the average standard deviation of the observed U_{ij} of 0.0012 Å². A considerable improvement was obtained by analyzing two separate parts of the molecule for rigid-body thermal motion. Part I was taken to include rings *A* and *B* and the atoms O(2), O(3) and C(11). Part II consisted of ring *D* and O(17). For the rigid-body parameters listed in Table 3, we obtained standard errors of fit which were 0.0025 Å² and 0.0022 Å² for parts I and II, respectively. For part I the largest r.m.s. libration amplitude (4.8°) is about an axis approximately parallel to the long dimension of the molecule. The origin which symmetrizes **S** lies near the midpoint of the C(5)–C(10) bond. The libration amplitudes of part II are larger than those of part I. The largest amplitude (9.7°) is about an axis nearly parallel to the C(17)–O(17) bond, and the origin which symmetrizes **S** is near the *C/D* ring junction. In both parts the axes of smallest libration are roughly perpendicular to the plane of the fragment. These observations are consistent with a 'flapping' motion of ring *D* superposed on the overall rigid-body motion of the molecule as a whole. This interpretation presupposes a relatively low force constant for out-of-plane bending of the atoms attached to N(13). A low value of this force constant has indeed been postulated by Winkler & Dunitz (1971) in their discussion of distortions of the amide bond.

These thermal motion results must be interpreted with the reservation that the molecular fragments are only approximately rigid. For example, McDermott & Strauss (1972) have shown from far-infrared studies

Table 3. *Rigid-body thermal motion parameters*

Estimated standard deviations are given in units of the last decimal place.

(a) Libration tensors **L**(deg²) in an orthogonal system defined by **a**, **b** and **c***

	Part I			Part II		
	12.7 (11)	-3.9 (7)	-9.2 (8)	34.2 (28)	-12.8 (31)	-19.2 (21)
		7.7 (7)	4.4 (7)		91.4 (81)	-11.4 (39)
			10.2 (9)			24.3 (25)

(b) Eigenvalues and eigenvectors of the libration tensors

	R.m.s. amplitude	Part I			R.m.s. amplitude	Part II		
		<i>a</i>	Direction cosines <i>b</i>	<i>c</i> *		<i>a</i>	Direction cosines <i>b</i>	<i>c</i> *
L (1)	4.8°	0.695	-0.357	-0.624	9.7°	0.171	-0.979	0.111
L (2)	2.4	0.393	0.916	-0.087	7.0	0.772	0.064	-0.632
L (3)	1.4	0.603	-0.184	0.776	2.5	0.612	0.194	0.767

(c) Eigenvalues and eigenvectors of the reduced translation tensors

	R.m.s. amplitude	Part I			R.m.s. amplitude	Part II		
		<i>a</i>	Direction cosines <i>b</i>	<i>c</i> *		<i>a</i>	Direction cosines <i>b</i>	<i>c</i> *
T (1)	0.18 Å	0.324	-0.329	-0.887	0.20 Å	0.945	0.049	0.325
T (2)	0.17	0.946	0.119	0.301	0.17	-0.167	-0.780	0.604
T (3)	0.16	0.006	-0.937	0.350	0.16	0.283	-0.629	-0.728

(d) Displacement of libration axes from intersecting

	Part I	Part II
² Q_1 - ³ Q_1	-1.37 Å	1.15 Å
³ Q_2 - ¹ Q_2	-0.73	-1.68
¹ Q_3 - ² Q_3	0.65	-0.05

that there are two low-energy ring deformation modes in *N*-methylpyrrolidone, a molecule similar to ring *D*. Thus our assumption that part II of the diaza steroid is rigid may not be entirely valid.

Discussion

The results of the determination as illustrated in Fig. 2 confirm the predicted structure (I). The conformation is similar to that of the natural estrogens (Cooper, Norton & Hauptman, 1969) with the largest difference arising from the nearly planar amide group involving atoms C(14), N(13), C(17), C(16) and O(17). Consequently, the *D* ring has a β envelope conformation with C(15) 0.32 Å above the plane defined by the other *D* ring atoms. This is in contrast to 4-bromoestrone (Norton *et al.*, 1963) where the *D* ring has an envelope conformation with C(14) below the *D* ring plane. The effect of the other nitrogen substitution, in the 8-position, is much smaller, as has been observed by Brown & Trefonas (1972) in 8-azaestradiol. The *C* ring is a slightly distorted chair with C(9) 0.72 Å below and N(13) 0.53 Å above a least-squares plane through C(14), N(8), C(12) and C(11). The *B* ring approaches the half-chair conformation found in the structure of estrone (Busetta, Courseille & Hospital, 1973). Duax & Norton (1975) give more detailed data on the conformation of this diaza steroid relative to other steroids.

According to Cooper, Norton & Hauptman (1969) a critical distance in evaluating estrogenic activity is the O(3)–O(17) intramolecular distance. They cite distances from 10.8 to 11.1 Å in three natural estrogens; a low value of 10.31 Å has been reported as compatible with estrogenic activity (Weber & Galantay, 1972). In the diaza steroid the O(3)–O(17) distance is 10.35 Å. This suggests that the compound could have estrogenic activity, provided the system contains an enzyme capable of converting the 17-substituent to a β -hydroxyl. On the other hand, the compound lacks a methyl group on C(13); such a methyl seems to be instrumental for estrogenic activity (Weber & Galantay, 1972).

The bond distances and angles are listed in Fig. 2. Distances corrected for rigid-body thermal motion have been listed for bonds where the model was applicable. There are no unusual bond distances or angles.

The amide group is incorporated into the steroid nucleus in an environment which commonly has a geometry quite different from the ideal planar amide group. Nonetheless, the displacements from the least-squares plane through C(12), N(13), C(14), C(17) and O(17) are all less than 0.06 Å. The dihedral angle ω [C(16)–C(17)–N(13)–C(12)] is 172.3°, only slightly distorted from the 180° assumed for the *trans* peptide bond. Winkler & Dunitz (1971) have studied the deformation of the (transoid) amide group in medium-ring lactams. Their findings indicate that out-of-plane bending occurs more easily at the nitrogen atom than at the carbon atom. In terms of the three

angles τ , χ_C and χ_N employed by Winkler & Dunitz the geometry at N(13) and C(17) is $\chi_N = -7.3^\circ$ and $\chi_C = 2.3^\circ$; the twist angle τ being 5.8° . The relative

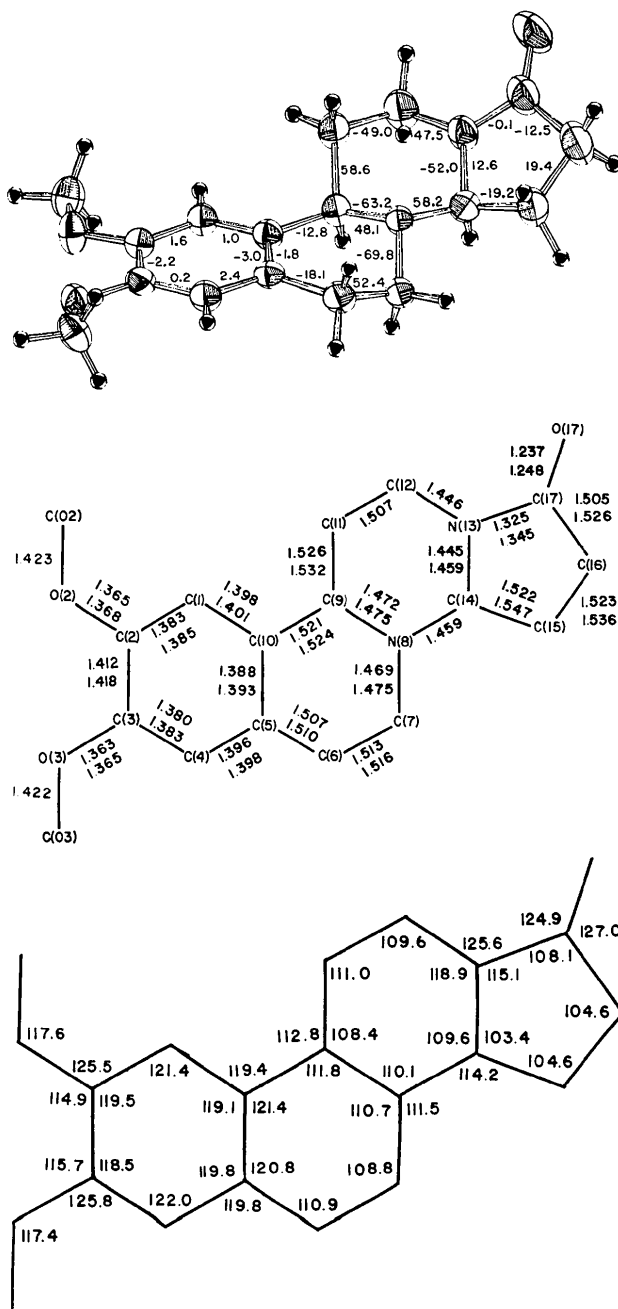


Fig. 2. Top: Projection view of 2,3-dimethoxy-18-nor-8,13-diaza-1,3,5(10)-estratrien-17-one showing ring torsion angles ($^\circ$). The 50% equiprobability ellipsoids represent the thermal motion of all atoms except the hydrogens, which are represented by spheres of radius 0.1 Å. Center and bottom: Non-hydrogen bond lengths (Å) and angles ($^\circ$). The estimated standard deviations for the bond lengths are 0.003 to 0.004 Å. Distances corrected for rigid-body thermal motion have been given below the uncorrected distances. The estimated standard deviation for the bond angles is 0.2° .

magnitudes of χ_N and χ_C indicate easier deformability at the nitrogen atom, in agreement with the observation of Winkler & Dunitz.

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The Crystal Structure and Absolute Configuration of the Antibiotic Actinobolin

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The structure of a solvated derivative of the title compound ($C_{13}H_{21}N_2O_6^+I^- \cdot H_2O \cdot \frac{1}{4}C_2H_5N$) has been determined from diffractometer data and refined to an R_1 of 0.089. The crystals are monoclinic, $P2_1$, $a = 19.340$ (2), $b = 24.202$ (3), $c = 7.968$ (3) Å and $\beta = 102.32$ (2)°, with four molecules of actinobolin. HI, four water molecules and one acetonitrile per asymmetric unit. The absolute configuration was determined from the anomalous scattering of the iodides. The four independent molecules of actinobolin have similar molecular conformations and are involved with the iodides and solvate molecules in a complex network of intermolecular, intramolecular and bifurcated hydrogen bonds.

Introduction

The antibiotic actinobolin was first isolated in 1959 as a sulfate salt from submerged aerated broth cultures of *Streptomyces griseoviridis* var. *atrofaciens* (Pitillo, Fischer, McAlpine, Thompson & Ehrlich, 1959; Haskell & Bartz, 1959). Initial investigations of its biological activity showed actinobolin to be a broad-spectrum antibiotic exhibiting low toxicity (Haskell & Bartz,

1959) and mild anticarcinogenic activity (Sugiura & Reilly, 1959; Burchenal, Holmberg, Reilly, Hemphill & Reppert, 1959; Teller, Wolff & Wagshul, 1964; Cappuccino, Oettgen, Murphy, Reilly & Burchenal, 1960; Merker, Bowie & Ando, 1962).

In 1968 the structure of actinobolin free base was shown by Munk, Nelson, Antosz, Herald & Haskell (1968) to be 4-(2-aminopropionamido)-3,4,4 α ,5,6,7-hexahydro-5,6,8-trihydroxy-3-methyl isocoumarin.