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The Conformation of Non-Aromatic Ring Compounds. LXV.* The Crystal and Molecular Structure of 3β -*p*-Bromobenzoyloxy- 13α -androst-5-en-17-one

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The steroid 3β -*p*-bromobenzoyloxy- 13α -androst-5-en-17-one crystallizes in the orthorhombic system with four molecules per unit cell. The space group is $P2_12_12_1$ and the lattice constants are $a = 16.216 \pm 0.006$, $b = 19.873 \pm 0.009$ and $c = 6.853 \pm 0.003$ Å. The photographic data were collected at -180°C ($\text{Cu } K\alpha$ radiation) and estimated visually. The structure was determined by application of a minimum function and by Fourier techniques. Refinement by least-squares procedures resulted in an R value of 0.117. The results of separate refinements of a - and c -axis data are discussed. The molecule has a *cis* junction between rings *C* and *D* which causes flattening of ring *C*. Ring *D* has an approximate 'envelope' conformation with the atom C(14) as flap. The *A* and *C* rings have the usual chair conformation while *B* is a 'half chair'.

Introduction

This publication is a continuation of earlier reports on the molecular geometry of steroids with various configurations at the asymmetric carbon atoms (Hesper, Geise & Romers, 1969, and papers cited therein). The title compound 3β -*p*-bromobenzoyloxy- 13α -androst-5-en-17-one (hereafter APBA) has a *trans* junction between rings *B* and *C* and a *cis* junction between rings *C* and *D* (see Fig. 1). Accordingly, its configuration is 8β , 9α , 10β , 13α , 14α . The corresponding compound 3β -*p*-bromobenzoyloxy-androst-5-en-17-one with *trans* *C/D* coupling and belonging to the normal 8β , 9α , 10β , 13β , 14α -series will be discussed in a separate paper (Portheine, Romers & Rutten, 1970). This study was undertaken in order to investigate the conformational differences between the molecule under consideration and its 13β -isomer.

Experimental

Irradiation of the normal steroid 3β -hydroxy-androst-5-en-17-one (13β -configuration) with ultraviolet light in methanol solution induces partial conversion of the

configuration at C(13) (Bots, 1958). From the isolated 13α -isomer the heavy-atom derivative APBA was prepared in benzene/pyridine solution with *p*-bromobenzoylchloride as reagent (Pot, 1964). Colourless orthorhombic needle-shaped crystals were obtained from a solution in acetone.

The unit-cell dimensions were determined from zero-layer Weissenberg photographs about [100] and the needle-axis [001]. The films were calibrated with superposed Al powder lines [$a(\text{Al}) = 4.0492$ Å at 20°C ; $\lambda(\text{Cu } K\alpha_1) = 1.54051$ and $\lambda(\text{Cu } K\alpha_2) = 1.54433$ Å]. The observed density (flotation method) at 20°C corresponds to four molecules per unit cell (see Table 1). Absence of the odd reflexions $h00$, $0k0$ and $00l$ indicates the space group $P2_12_12_1$.

Table 1. Crystallographic data of APBA

3β - <i>p</i> -Bromobenzoyloxy- 13α -androst-5-en-17-one	
Molecular composition	$C_{26}H_{31}BrO_3$, $M = 471.4$ g.mole $^{-1}$
Melting point	162–164 °C
Space group	$P2_12_12_1$
a	16.216 (0.006) Å*
b	19.873 (0.009)
c	6.853 (0.003)
d_{obs}	1.35 (20°C)
d_{calc}	1.417 g.cm $^{-3}$ (-180°C)
V	2208.5 Å 3

* Part LXIV: de Hoog & Havinga (1970).

Table 1 (cont.)

$F(000)$	984 electrons
Z	4 molecules.cell ⁻¹
μ (Cu $K\alpha$)	29.9 cm ⁻¹

* Quoted errors are twice the calculated standard deviations.

Non-integrated intensity data were collected with the equi-inclination Weissenberg multiple-film technique, using Ni-filtered Cu $K\alpha$ radiation at -180°C (Altona, 1964). Data were recorded from a crystal mounted about [001] (layers $l=0-6$) and from a cut crystal about [100] (layers $h=0-9$). The dimensions of the crystals were $0.15 \times 0.10 \times 1.12$ and $0.20 \times 0.20 \times 0.40$ mm respectively. In both cases the longest dimension coincided with the axis of rotation.

Altogether 2523 independent reflexions (including 337 non-observed ones) were obtained from the first crystal and 1744 (including 131 non-observed ones) from the second. The total number of possible independent reflexions in the Cu sphere is 2890.

The reduction of intensities to structure factor moduli, F_{obs} , was performed in the usual way by multiplication with the Lorentz-polarization and Phillips (1956) factors, $(Lp)^{-1}$ and P respectively. No correction for absorption was applied.

Attempts were made to correlate the data from the c - and a -axis crystals by means of the scaling program of Rae (1965). The correlation can be expressed in the 'measure of agreement',

$$\sum 200 |F_{\text{obs}}(a) - F_{\text{obs}}(c)| / [\sum |F_{\text{obs}}(a) + F_{\text{obs}}(c)|],$$

which in this case amounted to 20.0%. The result is rather unsatisfactory and appears to be caused by systematic differences. This is also indicated by the overall temperature factors, which were $\exp(-1.56 \sin^2 \theta/\lambda^2)$ for the a -axis data and $\exp(-2.58 \sin^2 \theta/\lambda^2)$ for the c -axis data. Introduction of an 'extra' temperature factor, $\exp(-1.0 \sin^2 \theta/\lambda^2)$, into the a -axis data gave only a slight improvement in the correlation and was omitted afterwards. For reasons explained in the next section it was decided to keep separate data sets. During the final stages of this investigation the results of separate and simultaneous refinements of these sets were judged by statistical and chemical criteria.

Refinement

The structure was determined by the usual heavy-atom method, *i.e.* scanning of a Patterson function (based upon c -axis data) for the positions of the bromine atoms and application of a Buerger minimum function at these positions. Nine atoms were not located but found in a subsequent Fourier synthesis.

The two data sets were used separately for isotropic refinement of the structure by the least-squares procedure in the block-diagonal approximation. The blocks were 3×3 for positional parameters and 1×1 for the isotropic individual B values. The ten a -axis scaling

factors were combined with an overall temperature factor in an 11×11 block. The same combination was applied to the seven c -axis scaling factors. The number of parameters in the respective refinements was 131 and 128.

The scattering factor used for bromine was the function evaluated by Cromer & Waber (1965); for oxygen and carbon the values were taken from *International Tables for X-ray Crystallography* (1962). For hydrogen the scattering factor values of Stewart, Davidson & Simpson (1965) were employed.

The structure amplitudes F_{obs} were weighted with a factor $w(F_{\text{obs}}) = 1/[a + F_{\text{obs}} + b(F_{\text{obs}})^2]$ if $F_{\text{obs}} > F_{\text{min}}$ and with $w(F_{\text{obs}}) = w(F_{\text{min}})$ if $F_{\text{obs}} \leq F_{\text{min}}$. Values for the parameters $a = 2.00$, $b = 0.20$, and $F_{\text{min}} = 1.30$ in the two refinements were chosen in such a way that $\sum w(F_{\text{obs}}) \times [F_{\text{obs}} - F_{\text{calc}}/S(F_{\text{obs}})]^2$ is independent of the range of F_{obs} values. F_{calc} is the modulus of the calculated structure factors on the absolute scale and $1/S(F_{\text{obs}})$ the scaling factor which reduces F_{calc} to the scale of F_{obs} .

The function $\sum w(F_{\text{obs}}) \times [F_{\text{obs}} - F_{\text{calc}}/S(F_{\text{obs}})]^2$ was minimized in the refinement.

The smallest estimated intensity value (before reduction) was in this case 1.00. The non-observed reflexions were given intensities of 0.25 resulting in slightly varying values of $F' = [0.25 \times (Lp)^{-1} \times P]^{1/2}$ after reduction. Only if $F_{\text{calc}}/S(F') > F'$ were these reflexions included in the refinement with constant weights 0.035 (a -axis data) and 0.070 (c -axis data).

During the final cycles hydrogen atoms were introduced at calculated positions and were not refined; their B values were fixed at 1.56 and 2.58 Å² respectively. Convergence was reached after nine cycles for the a -axis data and ten cycles for the c -axis data. Corresponding final values for the conventional agreement index $R = \sum |F_{\text{obs}} - F_{\text{calc}}|/S(F_{\text{obs}}) / \sum F_{\text{obs}}$ were $R_a = 12.4\%$ and $R_c = 10.8\%$.

The positional parameters resulting from these refinements were virtually the same (see next section) and suggested a simultaneous anisotropic refinement in which the reciprocal layers of each set were utilized with separate scaling factors. The dimensions of the blocks were now 3×3 for positional parameters, 6×6

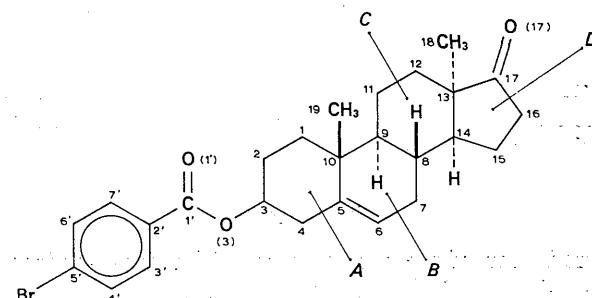


Fig. 1. Numbering of the atoms and nomenclature of 3β -*p*-bromobenzoyloxy-13*α*-androst-5-en-17-one (IUPAC-IUB, 1969).

for vibrational parameters and 18×18 for one overall isotropic temperature factor, ten *a*-axis scaling factors and seven *c*-axis factors.

The hydrogen atoms were treated as indicated before, with a *B* value of 2.07 \AA^2 . The same weighting function

was used, the parameters now being $a=0.00$, $b=0.30$ and $F_{\min}=2.00$. The weight for the non-observed reflexions was 0.11. After seven cycles the shifts were smaller than one sixth of the standard deviations and the refinement was terminated. The *R* value was 11.7 %.

Table 2. Fractional coordinates $\times 10^4$ (r_i) of APBA after isotropic refinement using *a*- and *c*-axis data, their differences Δ (10^{-3} \AA), standard deviations $\sigma(\Delta)$ (10^{-3} \AA), final fractional coordinates $\times 10^4$ after simultaneous anisotropic refinement and standard deviations σ in the latter (10^{-3} \AA)

	r_i	<i>a</i> -Axis	<i>c</i> -Axis	Δ	$\sigma(\Delta)$	Simultaneous	σ
C(1)	<i>x</i>	-1303	-1300	-7	25	-1299	9
	<i>y</i>	1208	1209	-2	18	1208	8
	<i>z</i>	3193	3193	-0	20	3191	8
C(2)	<i>x</i>	-529	-547	28	24	-540	9
	<i>y</i>	976	969	15	17	972	7
	<i>z</i>	2011	2040	-20	21	2019	9
C(3)	<i>x</i>	-803	-807	7	26	-805	9
	<i>y</i>	400	408	-16	17	403	7
	<i>z</i>	680	692	-8	21	697	8
C(4)	<i>x</i>	-1505	-1484	-34	25	-1489	10
	<i>y</i>	640	628	25	17	634	8
	<i>z</i>	-682	-672	-7	22	-683	9
C(5)	<i>x</i>	-2206	-2214	13	22	-2215	9
	<i>y</i>	915	910	10	16	911	7
	<i>z</i>	430	448	-12	22	433	8
C(6)	<i>x</i>	-2972	-2969	-6	25	-2966	9
	<i>y</i>	711	707	7	17	705	7
	<i>z</i>	-6	35	-28	19	2	9
C(7)	<i>x</i>	-3750	-3757	11	27	-3750	9
	<i>y</i>	957	965	-16	19	967	8
	<i>z</i>	930	930	1	22	938	9
C(8)	<i>x</i>	-3621	-3614	-10	25	-3614	9
	<i>y</i>	1605	1592	27	17	1600	8
	<i>z</i>	2200	2213	-9	20	2209	9
C(9)	<i>x</i>	-2807	-2792	-24	24	-2797	9
	<i>y</i>	1517	1530	-26	17	1521	8
	<i>z</i>	3341	3337	3	21	3344	8
C(10)	<i>x</i>	-2053	-2038	-24	25	-2038	9
	<i>y</i>	1450	1441	17	17	1445	7
	<i>z</i>	1955	1935	14	20	1953	9
C(11)	<i>x</i>	-2709	-2698	-17	24	-2700	9
	<i>y</i>	2133	2129	7	16	2128	7
	<i>z</i>	4767	4773	-4	21	4769	8
C(12)	<i>x</i>	-3393	-3396	5	24	-3396	10
	<i>y</i>	2141	2149	-17	18	2142	8
	<i>z</i>	6221	6223	-1	22	6225	9
C(13)	<i>x</i>	-4231	-4249	29	25	-4246	10
	<i>y</i>	2198	2198	-1	17	2197	7
	<i>z</i>	5232	5233	-5	21	5217	8
C(14)	<i>x</i>	-4376	-4353	-37	25	-4366	10
	<i>y</i>	1688	1686	5	17	1686	7
	<i>z</i>	3514	3552	-26	20	3533	9
C(15)	<i>x</i>	-5091	-5098	10	27	-5093	10
	<i>y</i>	1994	1999	-9	18	2000	8
	<i>z</i>	2371	2392	-15	23	2374	9
C(16)	<i>x</i>	-4930	-4926	-7	27	-4926	11
	<i>y</i>	2752	2755	-5	19	2753	9
	<i>z</i>	2460	2456	3	24	2444	10
C(17)	<i>x</i>	-4393	-4383	-17	25	-4390	9
	<i>y</i>	2875	2870	11	16	2867	7
	<i>z</i>	4209	4242	-23	20	4211	8
C(18)	<i>x</i>	-4965	-4933	-51	26	-4940	10
	<i>y</i>	2132	2134	-5	19	2132	9
	<i>z</i>	6717	6751	-23	23	6735	9
C(19)	<i>x</i>	-1829	-1817	-19	27	-1816	10
	<i>y</i>	2118	2113	11	17	2114	8
	<i>z</i>	883	883	0	20	897	9
C(1')	<i>x</i>	464	450	23	24	447	9
	<i>y</i>	-212	-203	-19	17	-207	7
	<i>z</i>	223	233	-7	21	227	9

Table 2 (cont.)

	r_i	<i>a</i> -axis	<i>c</i> -axis	Δ	$\sigma(\Delta)$	Simultaneous	σ
C(2')	<i>x</i>	1091	1075	27	25	1080	9
	<i>y</i>	-425	-440	29	18	-434	7
	<i>z</i>	-1173	-1145	19	21	-1165	9
C(3')	<i>x</i>	1035	1041	-10	25	1035	9
	<i>y</i>	-289	-275	-27	18	-280	8
	<i>z</i>	-3190	-3130	-41	22	-3167	9
C(4')	<i>x</i>	1622	1633	-18	27	1631	11
	<i>y</i>	-504	-508	8	19	-501	8
	<i>z</i>	-4424	-4388	-25	25	-4402	10
C(5')	<i>x</i>	2267	2282	-25	23	2277	9
	<i>y</i>	-894	-884	-19	17	-890	7
	<i>z</i>	-3689	-3705	11	21	-3702	9
C(6')	<i>x</i>	2371	2354	28	27	2361	10
	<i>y</i>	-1024	-1033	18	19	-1028	8
	<i>z</i>	-1702	-1699	-2	24	-1729	10
C(7')	<i>x</i>	1737	1748	-19	28	1748	10
	<i>y</i>	-807	-810	7	20	-810	8
	<i>z</i>	-447	-425	-15	27	-464	11
O(3)	<i>x</i>	-114	-126	20	16	-125	6
	<i>y</i>	198	197	2	12	198	5
	<i>z</i>	-552	-547	-3	15	-557	6
O(17)	<i>x</i>	-4109	-4113	7	17	-4114	7
	<i>y</i>	3411	3398	26	13	3404	6
	<i>z</i>	4742	4734	5	16	4744	7
O(1')	<i>x</i>	424	404	31	17	406	7
	<i>y</i>	-385	-386	3	13	-388	6
	<i>z</i>	1954	1954	-0	16	1950	7
Br	<i>x</i>	3097	3094	6	3	3095	1
	<i>y</i>	-1206	-1205	-2	2	-1206	1
	<i>z</i>	-5439	-5434	-4	2	-5437	1

Discussion of the refinement

The positional and thermal parameters, r_i ($i=x, y, z$ if 1, 2, 3) and B , of the separate refinements are given in Tables 2 and 3 respectively. The atom numbering is shown in Fig. 1. Table 2 indicates that for an arbitrary coordinate the absolute difference in its values resulting from the two refinements, $\Delta = [r_i(a) - r_i(c)]a_i$ (a_i = the corresponding lattice constant), is nowhere larger than twice its standard deviation, $\sigma(\Delta) = (\sigma_a^2 + \sigma_c^2)^{1/2}$.

Table 3. *B* values of APBA after refinement of *a*- and *c*-axis data (B_a and B_c), the difference ($B_a - B_c$) and the standard deviation of this difference $\sigma(B_a - B_c)$

	B_a	B_c	$B_a - B_c$	$\sigma(B_a - B_c)$
C(1)	1.15 Å ²	2.17 Å ²	-1.02 Å ²	0.30 Å ²
C(2)	0.89	2.07	-1.18	0.30
C(3)	1.28	1.88	-0.60	0.31
C(4)	1.17	2.21	-1.04	0.32
C(5)	0.80	1.98	-1.18	0.27
C(6)	1.03	2.14	-1.12	0.31
C(7)	1.58	2.02	-0.44	0.34
C(8)	1.01	1.93	-0.92	0.31
C(9)	1.05	2.08	-1.03	0.31
C(10)	1.06	2.00	-0.95	0.30
C(11)	0.95	2.13	-1.18	0.30
C(12)	0.92	2.59	-1.67	0.32
C(13)	0.88	2.40	-1.52	0.30
C(14)	1.04	1.98	-0.94	0.30
C(15)	1.38	2.15	-0.78	0.33
C(16)	1.21	2.67	-1.46	0.33
C(17)	0.94	1.90	-0.96	0.30
C(18)	1.18	2.69	-1.51	0.34
C(19)	1.30	2.08	-0.78	0.31

Table 3 (cont.)

	B_a	B_c	$B_a - B_c$	$\sigma(B_a - B_c)$
C(1')	1.20	2.11	-0.91	0.30
C(2')	1.16	1.92	-0.76	0.31
C(3')	1.31	2.29	-0.98	0.33
C(4')	1.62	2.78	-1.17	0.35
C(5')	0.83	1.98	-1.15	0.29
C(6')	1.48	2.80	-1.32	0.36
C(7')	2.15	2.94	-0.79	0.37
O(3)	1.17	2.03	-0.85	0.22
O(17)	1.43	2.81	-1.38	0.25
O(1')	1.39	2.58	-1.19	0.25
Br	2.00	3.06	-1.07	0.03

It may be concluded that the positional parameter values of the two refinements are not statistically different. On the other hand, Table 3 reveals a systematic discrepancy between the *B* values:

$$(B_a - B_c) \approx -3\sigma(B_a - B_c).$$

The positional parameters of the two refinements were compared by means of Hamilton's (1964) *R*-ratio test. This test indicates whether, at a certain significance level, the geometric model (positional parameters) of the *a*-axis refinement should be rejected, under the assumption that the *c*-axis model is correct. Using *c*-axis data, refinement of isotropic thermal parameters and scaling factors was carried out with fixed positional *a*-axis parameters. An *R* value $R'_c = 11.3\%$ was obtained.

Consider the function $\mathcal{R}(v, N, \alpha)$ where v is the number of fixed parameters ($v=90$), N is the number of degrees of freedom (in this case the number of observed *c*-axis reflexions, 2186 minus the number of param-

eters, 128) and α is the significance level. If the ratio R'_c/R_c is smaller than $\mathcal{R}(90, 2058, 0.005)=1.03$ the *a*-axis model cannot be rejected. The observed ratio is $11.3/10.8=1.05$ which indicates rejection of the *a*-axis model. However, the hypothesis that the *c*-axis model is the correct one cannot be verified. The *a*-model was not therefore rejected in favour of the *c*-model. The *R*-ratio test is, strictly speaking, only valid for the generalized agreement factor (Hamilton, 1965) but may be applied to the conventional *R* index.

The bond lengths in the two geometric models and the corresponding standard errors are listed in Table 4. The differences in bond lengths do not exceed twice the standard deviations. Moreover, no serious deviations with respect to literature values are observed.

We assumed that the geometric models were equivalent. This equivalence is not valid for the dynamical models (vibrational parameter sets). The observed discrepancies are brought about by an accumulation of systematic errors, *i.e.* spot-shape and extinction effects and neglect of absorption in the *B* values. The physical meaning of these values is therefore doubtful at best.

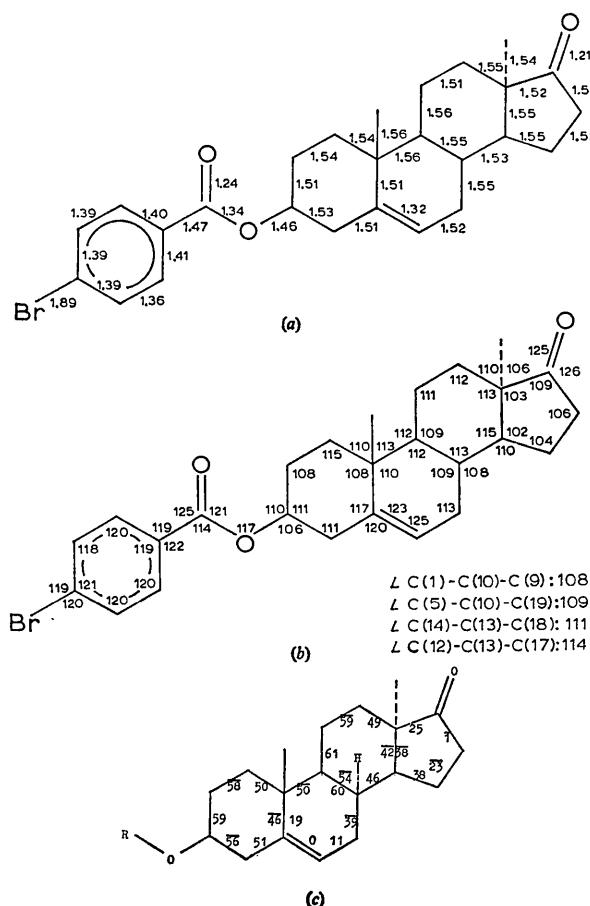


Fig. 2. (a) Bond lengths of APBA in Ångström units, (b) vacency, and (c) torsional angles in the steroid skeleton in degrees.

Table 4. Bond lengths (Å) of APBA and calculated standard errors (10^{-3} Å) after separate and simultaneous refinements

	<i>a</i> -axis	<i>c</i> -axis	simultaneous
C(1)—C(2)	1.563 (27)	1.530 (18)	1.543 (12)
C(1)—C(10)	1.558 (28)	1.547 (18)	1.542 (12)
C(2)—C(3)	1.529 (21)	1.507 (18)	1.511 (11)
C(3)—C(4)	1.547 (28)	1.506 (18)	1.529 (13)
C(4)—C(5)	1.474 (27)	1.519 (18)	1.508 (12)
C(5)—C(6)	1.341 (29)	1.319 (15)	1.318 (12)
C(5)—C(10)	1.511 (20)	1.495 (19)	1.514 (11)
C(6)—C(7)	1.498 (30)	1.507 (17)	1.518 (12)
C(7)—C(8)	1.569 (21)	1.542 (18)	1.545 (11)
C(8)—C(9)	1.544 (29)	1.545 (17)	1.545 (12)
C(8)—C(14)	1.529 (28)	1.521 (18)	1.529 (13)
C(9)—C(10)	1.554 (28)	1.566 (18)	1.564 (13)
C(9)—C(11)	1.574 (20)	1.552 (18)	1.560 (11)
C(10)—C(19)	1.561 (21)	1.559 (17)	1.556 (11)
C(11)—C(12)	1.492 (26)	1.507 (20)	1.506 (13)
C(12)—C(13)	1.522 (29)	1.543 (19)	1.546 (14)
C(13)—C(14)	1.571 (19)	1.547 (20)	1.549 (12)
C(13)—C(17)	1.540 (19)	1.513 (17)	1.519 (10)
C(13)—C(18)	1.572 (28)	1.527 (21)	1.538 (13)
C(14)—C(15)	1.526 (29)	1.572 (18)	1.553 (13)
C(15)—C(16)	1.530 (22)	1.529 (17)	1.522 (12)
C(16)—C(17)	1.501 (25)	1.525 (21)	1.508 (13)
C'(1)—C(2')	1.458 (26)	1.462 (19)	1.471 (13)
C(2')—C(3')	1.411 (21)	1.400 (22)	1.408 (13)
C(2')—C(7')	1.386 (29)	1.407 (17)	1.401 (13)
C(3')—C(4')	1.344 (29)	1.371 (20)	1.357 (14)
C(4')—C(5')	1.395 (27)	1.374 (17)	1.388 (13)
C(5')—C(6')	1.396 (21)	1.410 (23)	1.386 (14)
C(6')—C(7')	1.409 (30)	1.387 (21)	1.389 (14)
C(3)—O(3)	1.456 (24)	1.454 (15)	1.456 (10)
C(17)—O(17)	1.216 (19)	1.185 (13)	1.214 (10)
C(1')—O(3)	1.352 (22)	1.339 (14)	1.340 (10)
C(1')—O(1')	1.237 (18)	1.237 (20)	1.236 (11)
C(5')—Br	1.907 (18)	1.882 (13)	1.889 (9)

After six cycles of *c*-axis refinement a difference map was calculated. Outstanding anisotropy was observed for the bromine atom, the direction of greatest vibration being, in the plane of the benzene ring, perpendicular to the bond Br-C(5'). The thermal effects of the other atoms could not be distinguished. Nor could the hydrogen atoms be located.

Consideration of these facts prompted us to carry out the third refinement procedure mentioned in the previous section. The final positional parameters from this simultaneous refinement are listed in Table 2. The determinants of the U_{ij} tensors are positive definite for all atoms. However, due to the procedure applied, the U_{ij} values cannot have a physical meaning and are not tabulated here.* Table 5 is the final list of observed and calculated structure factors corresponding to an *R* value of 11.7 %. The very strong reflexions 011 and 111 from the *c*-axis data and 170 and 401 from the *a*-axis data were omitted in the last cycles of the refinement.

The geometric model of the simultaneous refinement was tested according to Hamilton using the *a*- and *c*-axis data separately. The resulting *R* values were $R'_a=12.6\%$ and $R'_c=10.9\%$. The ratios $R''_a/R_a=1.02$ and $R''_c/R_c=1.01$ proved to be smaller than the critical

* A list of U_{ij} values is available upon request.

Table 5. Observed and calculated structure factors (FO and FC) of APBA on four times absolute scale

c-axis data are given first; for the non-observed reflexions (minus sign) $\text{FO} \times 0.7$ is on four times absolute scale.

values $\mathcal{R}(90, 1482, 0.005) = 1.04$ and $\mathcal{R}(90, 2058, 0.005) = 1.03$ respectively. Consequently, the 'simultaneous' model cannot be rejected in comparison with the *a*- and *c*-axis models at the significance level 0.005. The geometric calculations of the molecule are therefore based on the 'simultaneous' geometric model. Moreover, it can be seen (Table 4) that for chemical reasons the 'simultaneous' model is the best.

The molecular geometry

The bond lengths and calculated standard errors are tabulated in Table 4 [see also Fig. 2(a)]. Systematic errors were not taken into account and, consequently, the standard errors are too small. The values of the valency and torsional angles are shown in Figs. 2(b) and (c). The average standard deviations are 0.8 and 1.2 degrees respectively.

In view of the size of the standard deviations the observed bond lengths do not differ from the expected values. This is certainly not true for the valency angles; for example C(2)-C(1)-C(10), C(8)-C(14)-C(13) and C(3)-O(3)-C(1'). The observed values are 115, 115 and 117° while the expected values are respectively 111, 110 and 110°.

The ether valency angle C(3)-O(3)-C(1') is quite large but in agreement with recent values found in solid monochloroacetic anhydride (121°; de Kok & Romers, 1969) and in gaseous acetic anhydride (116°; Vledder, Mijlhoff, Leyte & Romers, 1970).

The distribution of torsional-angle values indicates that rings *A* and *C* are 'chairs' and ring *B* is a 'half chair'. Fig. 3 shows the Newman projections along the bond C(13)-C(14) of the compounds APBA and digitoxigenine. The latter is a recently reported steroid which also possesses a *cis* junction of the rings *C* and

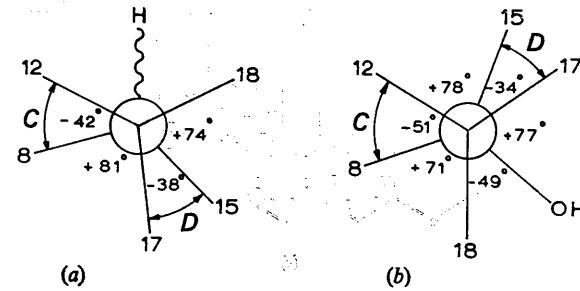


Fig. 3. Newman projections of (a) APBA and (b) digitoxigenine along the bond C(13)-C(14). Coupling of the rings C and D is indicated.

Table 5 (*cont.*)

D (Karle & Karle, 1969). The projections demonstrate the *cis* coupling of *C* and *D*. The atom C(18) has an α -configuration in APBA and a β -configuration in digitoxigenine.

It has been shown (Altona, Geise & Romers, 1968) that a cyclopentane-like ring in any state of its pseudo-rotational circuit can be characterized by its values of the parameters φ_m , the measure of puckering and δ , the phase designating the actual conformation. The conformation of a steroid D-ring can be described as a fixed state in that circuit, with δ confined to the range -36° [C(14)-'envelope' conformation] to $+36^\circ$ [C(13)-'envelope'] for different molecules. The value of $\delta = -34^\circ$ in APBA corresponds to a nearly ideal 'envelope' conformation with C(14) as flap.

In steroids with *D* rings *trans*-fused to *C* rings without keto groups at C(17), φ_m is found in the range 46–50°; steroids with *trans* fusion and possessing such a keto group have somewhat flatter *D* rings with $\varphi_m \approx 44^\circ$ [average of four observations taken from: Braun, Hornstra & Leenhouwers (1969) and from Altona, Geise & Romers (1968)]. For APBA (*cis* *C/D*) φ_m is somewhat smaller (41°).

The puckering of ring D in digitoxigenine ($\varphi_m = 36^\circ$) is still smaller. However, the comparison with this steroid is hardly warranted since it contains a β -hydroxyl group at C(14) and a lactone group at C(17).

The torsional angles $\phi(17-13-14-15)$ and $\phi(12-13-14-8)$ are governed by the 'equality rule' introduced by Bucourt (1964) and later discussed by Geise, Altona & Romers (1967). The observations for this molecule – 38 and – 42°, are in agreement with this rule. A 'normal' C ring in the 'chair' conformation demands a torsional angle $\phi(12-13-14-8) \approx 55^\circ$. Consequently its conformation in APBA is strongly distorted. Since the angle $\phi(14-8-9-11)$ changes only slightly under distortion (Bucourt & Hainaut, 1965) there is no transmission of the distortion towards ring B. The 1,4-interactions C(11)–C(17) and C(8)–C(17) correspond to distances 3.13 and 3.13 Å. These distances would assume the extremely small values of 3.00 and 3.09 Å respectively if $\phi(12-13-14-8)$ retained the value 55°.

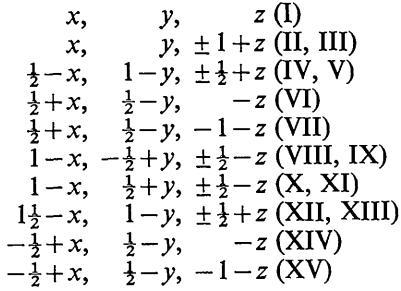
The double bond C(5)-C(6) dictates small values for $\phi(9-10-5-6)$ and $\phi(1-10-5-4)$. This effects the same deformation of ring A as observed for ring C.

The overall-shape of the molecule (Fig. 4) is rather elongated, notwithstanding the *cis* junction of rings C and D.

The packing

A projection of the structure along [001] is shown in Fig. 5. The reference molecule I (x , y , z) is surrounded at a distance less than 4.20 Å by fourteen molecules (II–XIV) having the following coordinates:

Table 5 (cont.)



In the end 106 intermolecular distances proved to be smaller than 4.20 Å. The small stones occur between the carbonyl oxygen atom and other atoms: O(1')-C(4'), (II-I, I-III) 3.20, O(17)-C(6'), (XI-I, I-IX) 3.35, O(17)-C(2), (VII-I, I-XV) 3.44, O(17)-Br, (X-I, I-VIII) 3.47, O(1')-C(3'), (II-I, I-III) 3.51 and O(1')-C(18), (I-IV, V-I) 3.55 Å. The next smallest distance (3.56 Å) is between Br and C(2') (I-XII, XIII-I). The intermolecular interactions of the type I-XIV and I-VI are rather large (smallest value 3.84 Å). No mutual interactions occur between the Br atoms (see Fig. 4).

All calculations were performed on the IBM 360/50 computer of the Central Computing Laboratory of the University of Leiden. We acknowledge the contributions of Mrs E. W. M. Rutten who wrote the least-

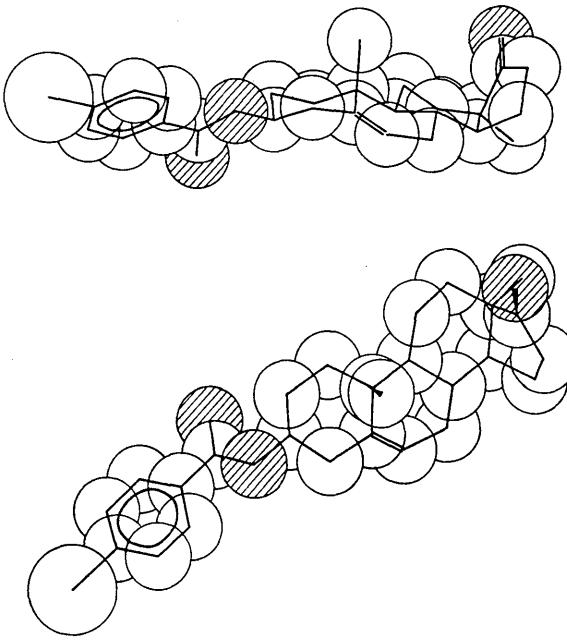


Fig. 4. Side and top view of the molecule of APBA. Atoms are indicated with valence radii by overlapping circles. The 'bond-frame' is superposed for reasons of clarity.

Table 5 (cont.)

squares and Fourier programs and of R. A. G. de Graaff for developing the geometry programs. We wish to express our thanks to Mrs L. Willemse, who produced the photographs and to F. C. Mijlhoff for discussions on the *R*-ratio test.

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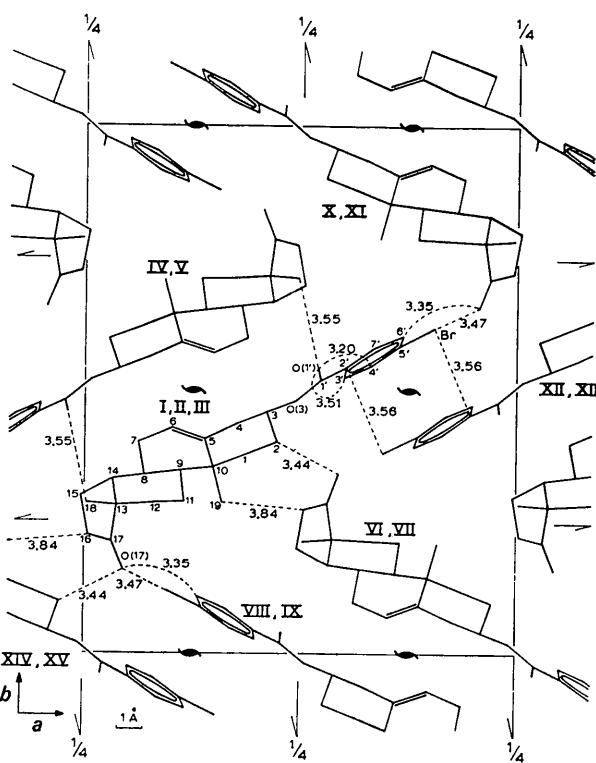


Fig. 5. Projection of APBA along [001]. The Roman numbers are explained in the text. Dotted lines indicate intermolecular distances. The reference molecule I is obtained by application of the transformation $\frac{1}{2} + x, \frac{1}{2} - y, \bar{z}$ to the coordinates of Table 2 (column 'simultaneous').