Cu^I is coordinated tetrahedrally by cyano and selenocyanato groups which are present as bridging groups. The skeleton cavities are formed by six Cu^I atoms bonded together by CN and SeCN groups (Fig. 1). The Cu^I–NC distances are somewhat longer than the Cu^I–CN (Table 3). This difference is one of the factors which allows distinction between the N and C atoms in the cyano groups.

As a consequence of their bridging function, the selenocyanato groups lose their linearity. Deviations from linearity average 5°. This can be explained from steric factors. Cu^I–Se–C angles are near 100°, unlike the Cu^I–C–N and Cu^I–N–C angles which are near 180° (Table 3). This means that the latter bonds lie along the line connecting the Cu^I atoms.

Our results show that the crystallochemical generalizations of Garaj (1975) are valid also for this complex.

In cuprous–cupric compounds the (Cu^I):(X) ratio (where X represents an anionic ligand) may be classified into five groups. For each group the type of coordination of Cu^I, the function of the anionic ligands and the structure type of the skeleton are characteristic. In this classification Cu$_3$en$_2$(SeCN)$_2$(CN)$_2$.H$_2$O belongs to group II, with the ratio (Cu^I):(X) = 2:4.

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Conformational Polymorphism.
III. The Crystal and Molecular Structures of Form II and Form III of Iminodiacetic Acid

BY J. BERNSTEIN*

School of Chemical Sciences, University of Illinois, Urbana, Illinois 61801, USA

Abstract

The crystal structures of the second and third polymorphic forms of iminodiacetic acid [form I: Boman, Herbertsson & Oskarsson (1974), *Acta Cryst.* B30, 378–382] have been determined by X-ray single-crystal structure analysis. Form II crystallizes in space group *Pbc*2$_1$ with eight molecules in the unit cell a = 5·267 (2), b = 14·140 (4), c = 14·933 (5) Å; form III crystallizes in space group *P*2$_1$/*n* with four molecules in the unit cell a = 5·258 (1), b = 12·206 (2), c = 8·709 (1) Å, β = 100·14 (1)°. Both structures were solved by direct methods and refined anisotropically to R factors of 0·052 and 0·042 respectively. Bond lengths and angles agree well among the four independent molecules in the three structures. However, molecular conformations, as measured by comparison of torsion angles, differ significantly among the three forms, and these differences are related to the packing scheme as determined predominantly by the hydrogen-bonding network.

Introduction

In two recent papers (Bernstein & Hagler, 1978; Hagler & Bernstein, 1978) we demonstrated the utility of studying conformational polymorphs to gain insight into the influence of crystal forces on molecular conformation. A pair of structures was analyzed in which the packing was dominated by van der Waals

* Permanent address: Chemistry Department, Ben-Gurion University of the Negev, Beersheva, Israel.

forces. As part of a program to extend this technique to structures containing hydrogen bonding, we undertook the structure determination of two forms of imino-diacetic acid, $NH(CH_2COOH)_2$, reported here. The structure of one form has been reported earlier (Boman, Herbertsson & Oskarsson, 1974).

Iminodiacetic acid has been shown to crystallize in three polymorphic forms by Tomita, Ando & Ueno (1965) who noted the difference in infrared spectra among the three forms. The spectrum of one form was so different from those of the other two that a significant difference in molecular conformation with respect to the four principal torsional parameters (about the C—C and C—N bonds) was expected. The conformation of iminodiacetic acid has also been shown to vary widely in different crystal environments, such as when it acts as a tridentate or monodentate ligand in coordination compounds (Albertsson & Oskarsson, 1968) or as a donor of hydrogen bonds to halide ions (Oskarsson, 1973). We shall refer to the two forms reported here as IMDA2 and IMDA3, while the earlier reported structure will be denoted by IMDA1. IMDA2 corresponds to the α form listed by Tomita, Ando & Ueno (1965), while IMDA3 corresponds to the γ form.

Experimental

Commercial iminodiacetic acid (Eastman Chemical Co.) was crystallized from water as described by Tomita, Ando & Ueno (1965) and Boman, Herbertsson & Oskarsson (1974). Both IMDA1 (monoclinic, short prismatic) and IMDA2 (orthorhombic, thin plates) are obtained by recrystallization from water. Needle-like crystals of IMDA3 obtained by evaporation of an ethanol:water mixture of approximately 70:30 composition were cut with a razor blade for diffraction experiments. The cell constants reported are based on a least-squares fit of 15 reflections with $13° < 2\theta < 62°$. The crystal data are summarized in Table 1.

Intensity data were collected on a Syntex $P2_1$ automatic diffractometer, employing an ω–2θ scan with scan rate varying from $2°$ min^{-1} to $24°$ min^{-1} as determined by a rapid prescan of the peak intensities. One unique octant of intensities for $2\theta < 141°$ was recorded. No deterioration of the intensity of three monitor reflections was noted during data collection. Data were corrected for Lorentz and polarization factors; no absorption corrections were applied. Estimated standard deviations are based on counting statistics.

Structure solution and refinement

IMDA2

The systematic absences indicated either space group $Pbcm$ or $Pbc2_1$. Intensity statistics were inconclusive in

Table 1. Crystal data

Iminodiacetic acid, $C_4H_7NO_4$, FW 133·1

	IMDA2*	IMDA3
a (Å)	5·267 (2)	5·258 (1)
b (Å)	14·140 (4)	12·206 (2)
c (Å)	14·933 (5)	8·709 (1)
β (°)	–	100·14 (1)
V (Å^3)	1112·2	550·2
D_x (Mg m^{-3})	1·590	1·607
D_m (Mg m^{-3})	1·60	1·60
Space group	$Pbc2_1$ (No. 29)*	$P2_1/n$ (No. 14)
Z	8	4
μ(Cu $K\alpha$) (mm^{-1})	1·30	1·30
Dimensions of data crystal (mm)	0·04 × 0·05 × 0·5	0·1 × 0·25 × 0·35
Total number of intensities measured	1209	1207
Total independent intensities	1124	1028
'Unobserveds' $I < 1·96\sigma(I)$	21	114
R_1 (including unobserveds)	0·052 (0·53)	0·042 (0·047)
R_2 (including unobserveds)	0·064 (0·67)	0·048 (0·048)
Goodness of fit	7·07	4·51

* The four equivalent positions for this non-standard setting (equivalent to $Pca2_1$) are: x,y,z; $-x, \frac{1}{2} + y, z$; $x, \frac{1}{2} - y, \frac{1}{2} + z$; $-x, -y, \frac{1}{2} + z$.

distinguishing between the two, yielding observed values which were between the theoretical quantities for acentric and centric distributions.

The structure was solved with *MULTAN* (Germain, Main & Woolfson, 1971) in space group $Pbc2_1$. Eighteen non-hydrogen atoms appeared among the 19 highest peaks on the E map corresponding to the set of signs with the highest FOM (1·331) and lowest residual (19·74). Initial refinement was carried out *via* the block-diagonal method (one atom per block) with anisotropic temperature factors on all atoms to $R = 0·10$. A difference map revealed ten peaks in positions expected for hydrogen atoms which were included in the refinement with isotropic temperature factors. At this point ($R = 0·09$) six reflections (004, 006, 024, 104, 120, 200) showed strong signs of extinction and they were removed from the refinement, yielding an R of 0·067. The remaining four hydrogens were then located on a difference map, and were also refined with variable isotropic temperature factors. Three of the temperature factors were not well behaved and were fixed at 3·0 Å^2. Three final cycles of full-matrix least squares yielded the agreement factors given in Table 1. For non-hydrogen atoms shifts did not exceed 0·01σ and the final difference map shows no peak higher than 0·23 e Å^{-3}. Final positional parameters are given in Table 2.

The final coordinates of chemically equivalent atoms in the two molecules bear a relationship which approximates a center of symmetry at fractional coordinates 0·74, 0·37, 0·38, suggesting that the centrosymmetric space group $Pbcm$ might in fact be a more suitable choice for the structure. A refinement based on the

Table 2. *Atomic coordinates* ($\times 10^4$ *for non-hydrogen and* $\times 10^3$ *for hydrogen atoms*)

IMDA2

Molecule 1

	$x(\sigma)$	$y(\sigma)$	$z(\sigma)$
N	9356 (6)	4220 (2)	4744 (3)
C(1)	9881 (9)	3677 (4)	5566 (5)
C(2)	8816 (8)	2679 (3)	5543 (4)
C(3)	10487 (7)	5188 (3)	4764 (5)
C(4)	13329 (7)	5160 (2)	4601 (4)
O(1)	7131 (6)	2543 (2)	4913 (4)
O(2)	9474 (9)	2099 (3)	6083 (4)
O(3)	14557 (5)	5905 (2)	4697 (4)
O(4)	14259 (5)	4381 (2)	4370 (4)
H(1)	650 (12)	187 (5)	493 (5)
H(2)	989 (14)	367 (5)	426 (5)
H(3)	789 (10)	420 (4)	474 (4)
H(4)	955 (10)	396 (4)	602 (4)
H(5)	1206 (13)	366 (4)	575 (5)
H(6)	971 (11)	556 (4)	434 (5)
H(7)	1012 (12)	550 (5)	525 (5)

Molecule 2

N'	5313 (6)	3272 (2)	2830
C(1')	4558 (9)	3882 (3)	2058 (5)
C(2')	5783 (8)	4841 (3)	2066 (4)
C(3')	4270 (7)	2300 (3)	2778 (5)
C(4')	1426 (7)	2282 (2)	2967 (4)
O(1')	7648 (6)	4936 (2)	2639 (4)
O(2')	5062 (7)	5442 (3)	1559 (4)
O(3')	300 (5)	1496 (2)	2855 (4)
O(4')	399 (5)	3032 (2)	3218 (4)
H(1')	854 (11)	575 (4)	234 (4)
H(2')	508 (12)	359 (4)	337 (5)
H(3')	694 (10)	321 (3)	285 (4)
H(4')	465 (12)	364 (5)	136 (5)
H(5')	279 (10)	400 (3)	211 (3)
H(6')	476 (11)	204 (4)	207 (4)
H(7')	541 (18)	169 (5)	323 (7)

IMDA3

N	2357 (4)	2470 (2)	10456 (2)
C(1)	2989 (5)	1345 (2)	10005 (3)
C(2)	867 (4)	900 (2)	8762 (2)
C(3)	3086 (4)	3332 (2)	9408 (3)
C(4)	6001 (4)	3475 (2)	9676 (3)
O(1)	1397 (4)	−73 (1)	8320 (2)
O(2)	−1091 (3)	1418 (1)	8294 (2)
O(3)	6876 (3)	4094 (2)	8716 (2)
O(4)	7340 (3)	3000 (1)	10791 (2)
H(1)	−8 (7)	−33 (3)	740 (4)
H(2)	54 (7)	260 (3)	1050 (4)
H(3)	310 (6)	266 (2)	1150 (4)
H(4)	322 (5)	84 (2)	99 (3)
H(5)	463 (6)	137 (2)	960 (3)
H(6)	222 (6)	401 (2)	965 (3)
H(7)	250 (6)	307 (2)	828 (3)

coordinates of molecule 1 which had been shifted to the proper location about the center of symmetry at the origin in space group *Pbcm* was not successful, and a calculation of intermolecular distances based on the starting coordinates for this model yielded a very short intermolecular $O(2)\cdots O(2)$ contact of 0·36 Å across the mirror plane. Furthermore, there is no evidence for disorder in the refinement in $Pbc2_1$. Hence, the original choice of space group $Pbc2_1$ was correct.

IMDA3

Systematic absences were consistent with space group $P2_1/n$. The structure was solved with *MULTAN* (Germain, Main & Woolfson, 1971). The nine highest peaks in the E map for the set of signs with the highest FOM (1·143) and lowest residual (14·39) corresponded to the nine heavy atoms in the structure.

Refinement was carried out by block-diagonal least-squares calculations (one atom per block), and for all non-hydrogen atoms with anisotropic temperature factors it converged at $R = 0·073$. All seven hydrogen atoms appeared on the difference map and were included in a full-matrix refinement with isotropic temperature factors. Final agreement factors are given in Table 1. All shifts were less than 0·01 of the respective standard deviation and the final difference map exhibited no peak higher than 0·26 e Å^{-3}.

Final positional parameters are given in Table 2. Temperature factors and structure factors have been deposited.* Atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1968). All programs used, except *ORTEP* (Johnson, 1965), are part of the Syntex *EXTL* library (Syntex Inc., 1973).

Results and discussion

The atom numbering is shown in Fig. 1. We chose the carboxyl group as the chemical point of reference. On the carboxyl side O(1) is always the hydroxyl oxygen and O(2) the carbonyl oxygen. O(3) is chosen as '*anti*' to N, while O(4) is '*syn*' to N. H(3), H(4) and H(6) are chosen so that the absolute values of their dihedral angles with C(2), O(1) and O(3), respectively, are larger than those made by H(2), H(5) and H(7) with C(2), O(1) and O(3).

Torsion angles

Significant conformational differences due to differences in torsion angles about single bonds are depicted in Newman projections in Fig. 2. The two molecules in IMDA2 have very similar conformations, with C(4) *gauche* to C(1) and C(3) *trans* to C(2), but they are not strictly superimposable. In IMDA1 the torsion angle around N—C(3) is larger (−135°), while C(3) is *gauche* to C(2) and in IMDA3 C(4) and C(3) are essentially *gauche* to C(1) and C(2) respectively.

The other major conformational difference relates the carboxyl group to the nitrogen atom. [By definition of atom labels there is consistency for the relationship between O(3) and O(4) with N.] In IMDA1 and
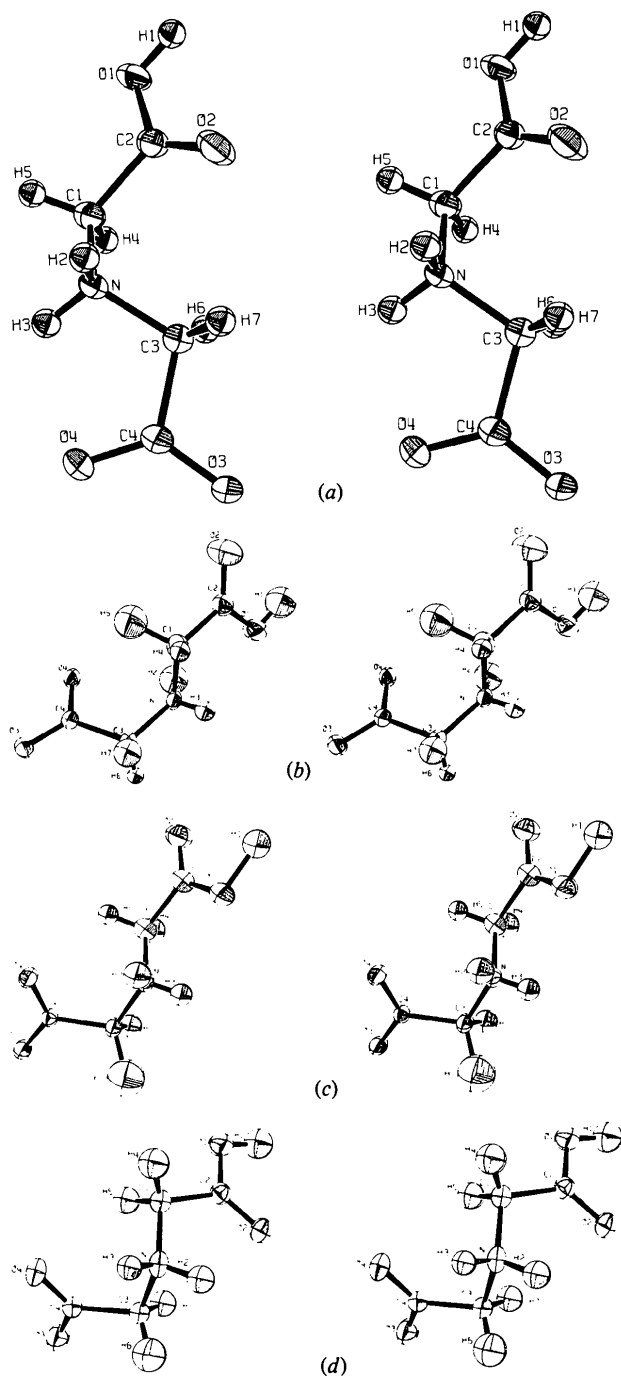
Fig. 1. ORTEP plots of the four molecules of IMDA. Each molecule is plotted on the best plane of all the non-hydrogen atoms. (a) IMDA1, (b) IMDA2, molecule 1, (c) IMDA2, molecule 2, (d) IMDA3.
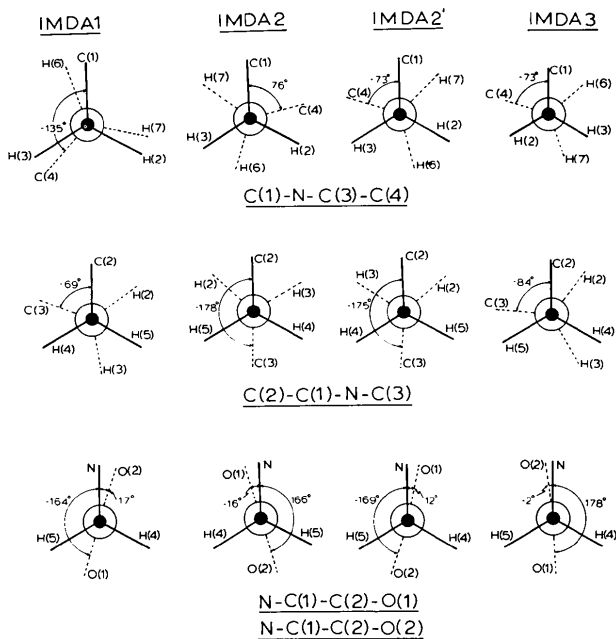

Fig. 2. Comparison of torsional parameters about N—C(3), C(1)—N, C(1)—C(2) in the four molecules of IMDA.

Table 3. The standard deviations for the two IMDA2 molecules are larger than for IMDA1 and IMDA3, due to the relatively lower ratio of observables to parameters. However, there are no inconsistencies within groups of equivalent bond lengths and angles. The values obtained for C=O and C—OH lengths in the neutral carboxyl group agree well with those tabulated by Leiserowitz (1976). The C—O lengths for the ionized carboxylate group are equivalent within experimental significance only for molecule 1 of IMDA2. The inequivalence might be attributed to participation in hydrogen bonding since the oxygen with the longer bond length [O(3) in IMDA1 and O(4) in molecule 1 of IMDA2] is hydrogen bonded to two hydrogen atoms while its mate is bonded to only one. However, this trend breaks down in IMDA3 where both O(3) and O(4) participate in only one hydrogen bond but the lengths are significantly different, and in IMDA2 O(4) of molecule 1 participates in two hydrogen bonds, but has the same bond length with C(4) as O(3). The O—C—O angles are somewhat larger than the average value quoted by Leiserowitz (1976) but do fall within the range of values given in his Table 1.

IMDA3 the hydroxyl oxygen O(1) is *trans* to N while it is nearly eclipsed in both molecules of IMDA2.

Bond lengths and angles

Bond lengths and bond angles for the four independent molecules (including IMDA1) are compared in

Packing and hydrogen bonding

The geometric features of the hydrogen bonding are summarized for all three forms in Table 4, and are shown in Fig. 3. Packing diagrams for the two structures reported here are given in Fig. 4. In all four molecules, each of the three hydrogens available for hydrogen bonding participates in a single hydrogen bond. However, the role of the oxygens differs signifi-

Table 3. *Geometric features of iminodiacetic acids*

(a) Bond lengths (Å)

	IMDA1	IMDA2 Molecule 1	IMDA2 Molecule 2	IMDA3
N—C(1)	1·487 (2)	1·474 (8)	1·494 (6)	1·481 (3)
N—C(3)	1·491 (2)	1·492 (5)	1·482 (5)	1·487 (3)
C(1)—C(2)	1·517 (2)	1·519 (7)	1·502 (6)	1·513 (3)
C(3)—C(4)	1·517 (2)	1·517 (5)	1·524 (5)	1·519 (3)
C(2)—O(1)	1·306 (2)	1·308 (7)	1·310 (7)	1·294 (3)
C(2)—O(2)	1·202 (2)	1·202 (8)	1·199 (7)	1·216 (3)
C(4)—O(3)	1·267 (2)	1·244 (5)	1·270 (5)	1·271 (3)
C(4)—O(4)	1·229 (2)	1·255 (5)	1·248 (5)	1·238 (3)

(b) Bond angles (°)

	IMDA1	IMDA2 Molecule 1	IMDA2 Molecule 2	IMDA3
C(1)—N—C(3)	115·4 (1)	112·7 (4)	113·4 (3)	113·5 (2)
N—C(1)—C(2)	110·4 (1)	113·3 (4)	113·7 (4)	110·6 (2)
N—C(3)—C(4)	110·5 (1)	111·6 (4)	111·7 (4)	110·5 (2)
C(1)—C(2)—O(1)	111·6 (2)	113·8 (4)	114·8 (4)	111·9 (2)
C(1)—C(2)—O(2)	122·6 (2)	120·8 (5)	119·9 (5)	121·8 (3)
O(1)—C(2)—O(2)	125·8 (2)	125·3 (5)	125·3 (5)	126·3 (2)
C(3)—C(4)—O(3)	114·2 (2)	118·2 (4)	116·7 (4)	116·1 (2)
C(3)—C(4)—O(4)	119·9 (2)	116·9 (4)	117·8 (4)	119·0 (2)
O(3)—C(4)—O(4)	125·9 (2)	124·9 (4)	125·5 (4)	124·9 (2)

cantly among the three forms. In IMDA1 O(2) does not participate in any hydrogen bond while O(3) participates in two hydrogen bonds. The two molecules of IMDA2 exhibit similar patterns. Once again O(2) does not participate in hydrogen bonding, but in this case it is O(4) which acts as an acceptor in two hydrogen bonds. Finally, in IMDA3 O(2), O(3) and O(4) participate as acceptors for one hydrogen bond each.

There are also differences in the crystallographic symmetry elements relating hydrogen-bonded molecules. The presence of the 5·3 Å axis in IMDA2 and IMDA3 suggested the presence of hydrogen bonding *via* simple translation along this axis

(Leiserowitz, 1976) and indeed this is found for all three molecules in these two forms (Fig. 4). It is absent in IMDA1, which is unique by virtue of the hydrogen bonding across the inversion center. In all three cases there is an O(1)—H(1)···O(3) hydrogen bond *via* a glide but the second glide-related hydrogen bond, present in IMDA1 [N—H(2)···O(3)] and IMDA3 [N—H(3)···O(2)] is clearly different for these two, being to different ends of the molecule.

Boman, Herbertsson & Oskarsson (1974) cited the presence of two rings containing hydrogen bonds as the 'most striking feature' of the structure of IMDA1. Both are shown in Fig. 3(a). The first, containing ten atoms, is about an inversion center at $\frac{1}{2},0,\frac{1}{2}$ and contains H(3)—N—C(3)—C(4)—O(4) and the atoms related to it through the center. The second contains fourteen atoms related to each other through a center at the origin: H(1)—O(1)—C(2)—C(1)—N—H(2)···O(3)[1 − x, −$\frac{1}{2}$ + y, $\frac{1}{2}$ − z]. IMDA2 and IMDA3 are also characterized by cyclic systems containing hydrogen bonds but with rings of different sizes than in IMDA1. In IMDA2, the smallest ring formed [Fig. 3(b)] has eight members: N—H(2)[1,0,0]···O(4')···H(3')—N'—H(2') [1,0,0]···O(4)[2,0,0]···H(3)[1,0,0]. The next largest ring system contains ten members: N—H(2)··· O(4')—C(4')—C(3')—N'—H(2')[1,0,0]···O(4)—C(4)— C(3). These are pseudocentrosymmetric ring systems which link the two layers, each of which is composed exclusively of molecules 1 or 2. There are also two larger 22-atom cyclic systems of similar composition within each layer as shown in Figs. 3(b) and 4(a):
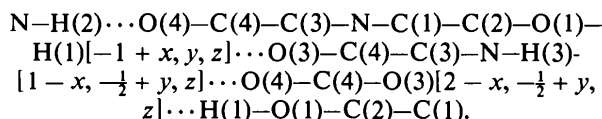
N—H(2)···O(4)—C(4)—C(3)—N—C(1)—C(2)—O(1)—
H(1)[−1 + x, y, z]···O(3)—C(4)—C(3)—N—H(3)-
[1 − x, −$\frac{1}{2}$ + y, z]···O(4)—C(4)—O(3)[2 − x, −$\frac{1}{2}$ + y,
z]···H(1)—O(1)—C(2)—C(1).

Table 4. *Geometrical features of hydrogen bonds in IMDA*

D—H···A*	D···A	H···A	∠D—H···A	Symmetry, translation (a,b,c) for acceptor
IMDA1				
N—H(2)···O(3)	2·81 Å	2·0 Å	149°	c-glide, 1,1,0[1 − x, −$\frac{1}{2}$ + y, $\frac{1}{2}$ − z]
O(1)—H(1)···O(3)	2·54	1·6	180	c-glide, 1,0,1[1 + x, $\frac{1}{2}$ − y, −$\frac{1}{2}$ + z]
N—H(3)···O(4)	2·68	2·0	134	Inversion center at ($\frac{1}{2}$,0,$\frac{1}{2}$)[1 − x, −y, 1 − z]
IMDA2				
O(1)—H(1)···O(3)	2·50	1·5	165	b-glide, 2,1,0[2 − x, −$\frac{1}{2}$ + y, z]
O(1')—H(1')···O(3')	2·48	1·4	128	b-glide, 1,0,0[1 − x, $\frac{1}{2}$ + y, z]
N—H(3)···O(4)	2·75	2·0	161	Translation, 1,00[x − 1, y, z]
N'—H(3')···O(4')	2·76	1·9	165	Translation, 1,0,0[x + 1, y, z]
N—H(2)···O(4')	2·88	1·8	163	Translation, 1,0,0†[x + 1, y, z]
N'—H(2')···O(4)	2·84	1·9	180	Translation, 1,0,0†[x − 1, y, z]
IMDA3				
N—H(2)···O(4)	2·67	1·8	145	Translation, 1,0,0[x − 1, y, z]
N—H(3)···O(2)	2·70	1·9	138	n-glide[$\frac{1}{2}$ + x, $\frac{1}{2}$ − y, $\frac{1}{2}$ + .z]
O(1)—H(1)···O(3)	2·46	1·4	170	n-glide, 0,1,1[$\frac{1}{2}$ − x, −$\frac{1}{2}$ + y, $\frac{3}{2}$ − z]

* The donor atoms in all cases are at x,y,z as given in Table 2.
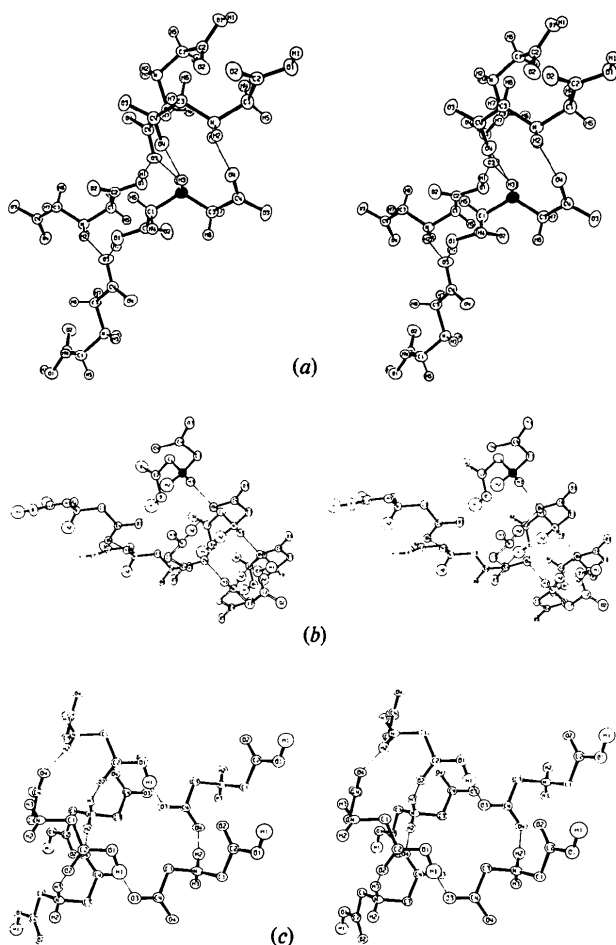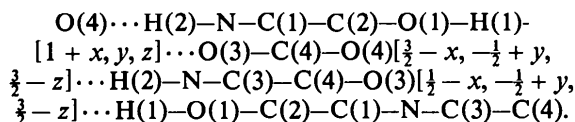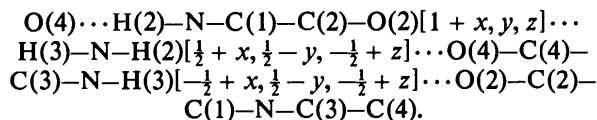† Between two independent molecules in the asymmetric unit.

Fig. 3. Hydrogen-bonding schemes showing the cyclic systems for the three forms of IMDA. The reference molecule is the one with a solid nitrogen atom. Hydrogen bonds are indicated by single lines. H(4), H(5), H(6) and H(7) have been deleted for clarity in a number of cases. (a) IMDA1. (b) IMDA2: molecule 1 is indicated by solid bonds, molecule 2 by open bonds. (c) IMDA3.
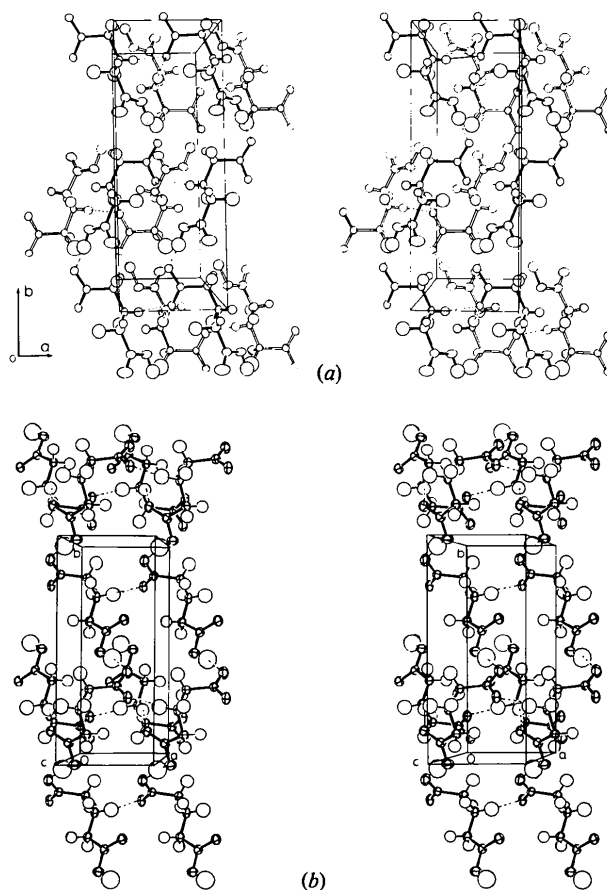

Fig. 4. Packing diagrams for forms II and III of IMDA. Hydrogen bonds are indicated by broken lines. (a) IMDA2: molecule 1 is shown with solid bonds, molecule 2 with open bonds. For clarity only the molecules at equivalent positions x,y,z and $1 - x, \frac{1}{2} + y$, z, and those related to them by translations in a and b are shown. The 10- and 22-membered cyclic systems (see text) are visible here. The 8-membered system is not shown here. (b) IMDA3: for clarity only the molecules at equivalent positions x,y,z; $\frac{1}{2} - x$, $\frac{1}{2} + y, \frac{1}{2} - z$; $\frac{1}{2} + x, \frac{1}{2} - y, \frac{1}{2} + z$ and those related to them by translations in a and b are shown. The 20- and 22-membered hydrogen-bonded cyclic systems may be seen here as well as in Fig. 3.

In IMDA3 there are two large hydrogen-bonded rings. The first comprises 22 atoms as follows [Fig. 3(c)]:

$$O(4)\cdots H(2)-N-C(1)-C(2)-O(1)-H(1)-$$
$$[1 + x, y, z]\cdots O(3)-C(4)-O(4)[\tfrac{3}{2} - x, -\tfrac{1}{2} + y,$$
$$\tfrac{3}{2} - z]\cdots H(2)-N-C(3)-C(4)-O(3)[\tfrac{1}{2} - x, -\tfrac{1}{2} + y,$$
$$\tfrac{3}{2} - z]\cdots H(1)-O(1)-C(2)-C(1)-N-C(3)-C(4).$$

The second contains 20 atoms:

$$O(4)\cdots H(2)-N-C(1)-C(2)-O(2)[1 + x, y, z]\cdots$$
$$H(3)-N-H(2)[\tfrac{1}{2} + x, \tfrac{1}{2} - y, -\tfrac{1}{2} + z]\cdots O(4)-C(4)-$$
$$C(3)-N-H(3)[-\tfrac{1}{2} + x, \tfrac{1}{2} - y, -\tfrac{1}{2} + z]\cdots O(2)-C(2)-$$
$$C(1)-N-C(3)-C(4).$$

The energetic ramifications of the observed differences in conformation and packing are not obvious from the qualitative geometric observations. In terms of the differences in lattice energies, differential thermal

analysis (Tomita, Ando & Ueno, 1965) has shown that IMDA2 is the most stable of the three crystal forms and that both IMDA1 and IMDA3 can be converted to IMDA2 in the temperature range 453–457 K with an accompanying broad weak peak in the DTA spectrum. These data indicate that the transition energy to IMDA2 is quite low and that the energy differences among the three forms are small. For a molecule such as IMDA, where conformational changes are due to rotation about single bonds, populations of different conformers exist in fluid phases. Conformers observed in the various crystal polymorphs may be energetically equivalent or not, depending on the ability of the crystal forces (i.e. the mode of packing) to stabilize an otherwise unfavorable conformation. Since the energies of

rotations about single bonds are generally small, the energetic differences in the molecular conformations observed in polymorphic IMDA are also expected to be small. The system thus provides a fairly sensitive test of the applicability of our earlier computational approach to the relationship between crystal forces and molecular conformations (Bernstein & Hagler, 1978), and calculations on this system are currently under way.

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6β,17β-Dihydroxy-6α-pentyl-4-nor-3,5-secoandrostan-3-oic Acid. A Synthetic Prostaglandin Analog

By D. A. LANGS AND G. T. DeTITTA

Medical Foundation of Buffalo, Inc., 73 High Street, Buffalo, New York 14203, USA

Abstract

The title compound ($C_{23}H_{40}O_4$, $M_r = 380.57$) is a prostaglandin analog synthetically prepared from a simple androstane derivative. Its crystals are orthorhombic, space group $P2_12_12_1$, with $a = 12.0342$ (7), $b = 18.761$ (1), $c = 9.998$ (1) Å, $V = 2257.3$ Å^3, $Z = 4$, $D_{obs} = 1.10$, $D_{calc} = 1.121$ Mg m^{-3}. Intensity measurements were made with Cu $K\alpha$ radiation on a κ-geometry diffractometer employing a crystal of dimensions $0.16 \times 0.30 \times 0.65$ mm; of 2592 independent reflections measured, 1889 were considered observed ($I > 2\sigma_I$) and employed in the refinement. Final residuals are $R = 0.045$, $R_w = 0.060$; S, the goodness of fit parameter, is 1.45. Embedded within the compound are all the atoms normally present in the prostaglandin skeleton, with steroid-derived bridges between atoms C(5) and C(13), and C(4) and C(15) of the prostaglandin. Little conformational homology between the compound and any of the known prostaglandins can be found. A gauche twist at the end of the pentyl chain and a folding back of the carboxylic acid group over the remainder of the steroid A ring characterize the conformation.

Introduction

The configurational similarities of the prostaglandin (PG) and steroid (ST) skeletal structures (Fig. 1), coupled with the repeated observation of PG conformations characterized by the alignment of side chains (DeTitta, Langs, Edmonds & Duax, 1979), has led a number of groups working on steroid synthesis to modify steroids into prostaglandin analogs (Venton, Counsell, Sanner & Sierra, 1974; Baumgarth & Irmscher, 1975a,b). These hybrid steroid/prostaglandins (STPG's) have absolute configurations opposite to those found for PG's but in view of the biological potencies of various epimeric and enantiomeric PG analogs (Andersen & Ramwell, 1974) it is not obvious that STPG's would be inactive compounds on configurational grounds alone. Starting with the androstane skeleton a variety of PG analogs can be synthesized by specifying which of the A, B, or C rings of the ST nucleus will remain intact and which are opened up to form the α and ω chains of the PG. In the case of the title compound (STPG-1), synthesized by Baumgarth & Irmscher (1975a,b), the A ring has been cleaved, and a pentyl chain, corresponding to C(16)