Acta Cryst. (1975). B31, 49

The Crystal and Molecular Structure of *N*-(t-Butyloxycarbonyl)-L-azetidine-2-carboxylic Acid and Conformational Analysis of Poly-(L-Azetidinecarboxylic Acid)

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(*Received* 22 *April* 1974; *accepted* 8 *July* 1974)

N-(t-Butyloxycarbonyl)-L-azetidine-2-carboxylic acid ($C_9H_{15}NO_4$, BACA) was chosen as a model compound to determine the geometry of the monomeric unit of poly-(L-azetidinecarboxylic acid), hereafter referred to as PACA. BACA is orthorhombic, space group $P2_12_12_1$, with $a=8{\cdot}249$ (8), $b=10{\cdot}904$ (9), $c=12{\cdot}327$ (11) Å, $Z=4$. The structure was determined from 748 X-ray intensities measured on a Siemens automated diffractometer with Mo $K\alpha$ radiation by the $\theta/2\theta$ scan technique. The structure was solved by direct methods with *MULTAN* and refined by least-squares calculations to a final R of 0·050. The azetidine ring and the oxycarbonyl group linked to the nitrogen atom are in the same plane, the greatest atomic deviation being 0·05 Å. The molecular packing is characterized by hydrogen bonds along **c** and by van der Waals interactions, the strongest of which are between methyl and methylene groups. The bond distances and angles of BACA were employed to perform the conformational analysis of PACA as a function of two angles of rotation. The potential-energy calculations show the presence of two minima, markedly deeper than the others, in agreement with spectroscopic results.

Introduction

L-Azetidine-2-carboxylic acid (ACA) is an amino acid containing one methylene group less than L-proline. ACA has toxic effects if it replaces L-proline in collagens and plant proteins (Fowden, 1967; Reusser, 1967; Takeuchi & Prockop, 1969; Takeuchi, Rosenbloom & Prockop, 1969).

The difference in the behaviour of these two amino acids has been attributed to the more flexible pyrrolidine ring of proline compared with the four-membered one of ACA (McGandy, Berman, Burgner & Van Etten, 1969). To elucidate this point the crystal and molecular structure of ACA has been solved (Berman, McGandy, Burgner & Van Etten, 1969). However, ACA has a zwitterionic structure: it is therefore reasonable to suppose that the geometry of the amino acid residue, as found in the polypeptide chains, could be different.

As part of a research programme to provide physicochemical and conformational information about PACA (Boni & Verdini, 1973; Boni, Di Blasi & Verdini, 1973) the structure of BACA (Fig. 1) has been determined. The atoms of the carbonyl group and azetidine ring together with C(12) coincide with those of the monomeric unit of PACA, synthesized by Boni & Verdini (1973) who suggest the existence of more conformations in solution, as for poly-L-proline, on the basis of ultraviolet and c.d. spectroscopic results. To verify the correctness of their hypothesis we decided to calculate the intramolecular potential energy of PACA from the bond lengths and angles determined for BACA.

Experimental

Crystals of BACA were grown from a mixture of ethyl acetate and n-hexane as colourless prisms, m.p. 105°C. The systematic absences ($h00$, $h=2n$; $0k0$, $k=2n$; $00l$, $l=2n$) were consistent with the space group $P2_12_12_1$. The cell dimensions, measured on a Siemens diffractometer with Mo $K\alpha$ radiation ($\lambda=0{\cdot}7107$ Å) at room temperature are: $a=8{\cdot}249$ (8), $b=10{\cdot}904$ (9), $c=12{\cdot}327$ (11) Å. A density of $1{\cdot}21_5$ g cm^{-3}, calculated for $Z=4$, agrees with the value of $1{\cdot}21 \pm 0{\cdot}01$ g cm^{-3} measured by flotation in a mixture of n-hexane and carbon tetrachloride.

Intensities were recorded at room temperature on a Siemens automatic single-crystal AED diffractometer

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equipped with a scintillation detector and pulse-height analyser, with Zr-filtered Mo $K\alpha$ radiation. The scan range varied from 1 to 1·5°. The scanning rate was 2° min^{-1} and the background counts were taken for a time equal to that of the scan. The five-value measurement and the moving-crystal moving-counter method were adopted to collect, up to $2\theta = 54°$, the intensities of 748 independent reflexions greater than $3\sigma(I)$ out of a total of about 1300 possible reflexions from a crystal $0{\cdot}23 \times 0{\cdot}36 \times 0{\cdot}36$ mm ($\mu = 1{\cdot}13$ cm^{-1}). Each reflexion was scanned twice and a check reflexion was monitored every 15 reflexions. The setting angles χ, φ and θ were accurately measured for 14 reflexions by means of a very narrow counter aperture. These observations formed the basis for the least-squares refinement of orientation.

The intensities were corrected for counting losses, background and Lorentz and polarization factors. Standard deviations were assigned according to the formula

$$\sigma(I) = [P + B + (pI)^2]^{1/2}$$

where P is the total integrated peak count obtained in the two scans, B is the total background count, $I = P - B$ and p is the 'ignorance factor' (Corfield, Doedens & Ibers, 1967) fixed as 0·06.

Determination of the structure

The structure factors were scaled by Wilson's (1942) method and converted to normalized structure factors. The structure was solved by *MULTAN* (Germain, Main & Woolfson, 1971). The phases of one enantiomorph- and three origin-defining reflexions together with two symbolic phases and one phase derived from $\sum_1$ relations (Table 1) were used to calculate phases for all 150 reflexions with $|E| \geq 1{\cdot}34$. From an E map computed from one of the two 'best' sets of phases all the non-hydrogen atoms except a carbon atom of one methyl group could be recognized. This atom was generated at the expected position and a set of programs by Domenicano, Spagna & Vaciago (1969) employed to refine the structure and for geometrical calculations. Scattering factors for C, N and O were taken from Cromer & Mann (1968), and for H from Hanson, Herman, Lea & Skillman (1964). Refinement was carried out with isotropic and anisotropic block-diagonal least-squares calculations with the 748 observed reflexions. The function minimized was $\sum w(||F_o| - |F_c||)^2$, w being equal to $(a + |F_o| + b|F_o|^2)^{-1}$. Although a difference synthesis showed all the hydrogen atoms at reasonable positions they were generated at the expected positions. The coordinates of the hydrogen atoms of the methyl and hydroxyl groups were obtained by searching the smallest sum of the distances (Gavuzzo, Pagliuca, Pavel & Quagliata, 1972) between the peaks of the difference synthesis and the hydrogen atoms generated and rotated around the respective carbon–carbon and carbon–oxygen bonds. The hydrogen atoms were included in the last three cycles with an isotropic B of 4 Å^2 but their parameters were not refined. The shifts calculated for the param-

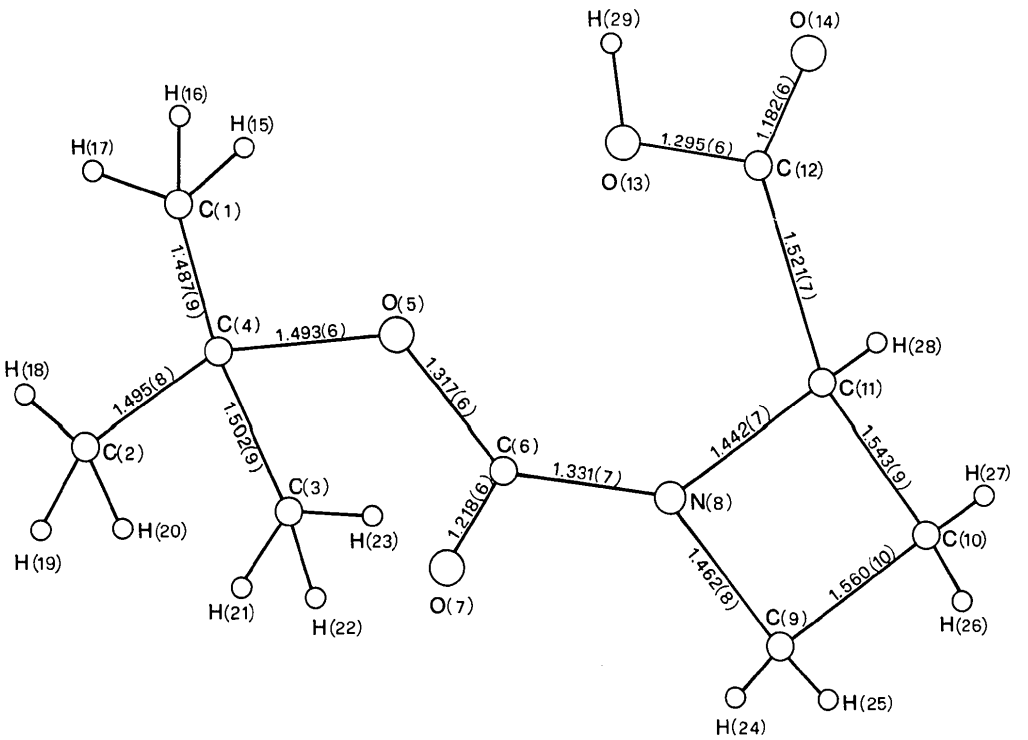

Fig. 1. Atomic numbering and bond distances of BACA.

eters in the final cycle were all less than the corresponding standard deviations. The final R and weighted R were 0·050 and 0·071 respectively. The atomic coordinates and anisotropic thermal parameters are reported in Tables 2 and 3 with their standard deviations. The bond lengths and angles are given in Figs. 1 and 2 with the standard deviations in parentheses.*

Table 1. *Phases assumed during structure determination*

h	k	l	$\|E\|$	Phase	
3	4	0	3·04	$\pi/2$	Origin-defining
0	1	4	2·77	$\pi/2$	Origin-defining
5	0	9	2·26	$\pi/2$	Origin-defining
3	9	1	2·56	$\pi/4$	Enantiomorph-defining
0	2	0	1·45	0	Assumed from $\sum_1$ relations
0	1	2	2·16	$\pm\pi/2$	Symbolic phases
5	1	9	2·07	$\pm\pi/4$, $\pm 3\pi/4$	Symbolic phases

Table 2. *Fractional atomic coordinates of BACA with standard deviations in parentheses* ($\times 10^4$)

	x	y	z
C(1)	6270 (9)	3750 (6)	2017 (6)
C(2)	5418 (8)	2731 (7)	320 (5)
C(3)	4279 (8)	2053 (6)	2074 (7)
C(4)	4927 (6)	3120 (5)	1436 (4)
O(5)	3489 (4)	3946 (3)	1360 (3)
C(6)	3515 (6)	5003 (5)	843 (4)
O(7)	4653 (4)	5461 (3)	362 (3)
N(8)	2052 (5)	5514 (4)	906 (4)
C(9)	1430 (9)	6683 (6)	501 (5)
C(10)	−187 (8)	6369 (6)	1096 (6)
C(11)	625 (6)	5186 (5)	1517 (4)
C(12)	915 (5)	5166 (4)	2735 (4)
O(13)	−168 (5)	4525 (4)	3242 (3)
O(14)	1990 (5)	5691 (5)	3168 (4)
H(15)	7244	3160	2195
H(16)	5837	4227	2715
H(17)	6753	4485	1442
H(18)	4296	2361	−100
H(19)	6250	1943	348
H(20)	5895	3433	−157
H(21)	3723	2418	2833
H(22)	5245	1446	2313
H(23)	3380	1592	1625
H(24)	2029	7424	865
H(25)	1263	6572	−396
H(26)	−354	7023	1710
H(27)	−1088	6126	471
H(28)	52	4411	1152
H(29)	147	4413	4018

Discussion of the structure

The group of atoms O(5), C(6), O(7), N(8) is planar (Table 4) and rigid because of the three short bonds formed by C(6). The double-bond character for C(6)–N(8) appears to be retained. The values of 1·44 and 1·46 Å for the N(8)–C(11) and N(8)–C(9) single bonds, which are adjacent to a double bond, agree with the previous statement. The four heavy atoms of the azetidine ring deviate from a least-squares plane (Table 4) through the ring by amounts ranging up to 0·02 Å. This nearly planar ring shows a different geometry from that found for ACA (Berman, McGandy, Burgner & Van Etten, 1969), in which the four-membered ring is slightly buckled. Furthermore the N(8)–C(9) and N(8)–C(11) lengths are somewhat shorter than the corresponding ones (1·52 and 1·51 Å) of ACA and the C(9)–N(8)–C(11) angle is 96·2°, about 7° greater than that observed in ACA, as a consequence of the trigonal hybridization of the nitrogen atom of BACA. O(5), C(6), O(7), N(8), C(9), C(10), C(11) define a plane (Table 4) with no deviations in excess of 0·05 Å. The carboxyl group and C_α also lie in a plane, with the coefficients reported in Table 4, the atomic deviations being smaller than 0·01 Å.

The torsion angles clarify the conformational features of the molecule. A torsion angle *A–B–C–D* is taken as positive if, starting from the *cis* conformation which corresponds to 0°, the atom *D* is moved in a clockwise direction looking along the bond *C–B*. The peptide group O(7), C(6), N(8) and C(9), with

* A list of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 30566 (8 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 3. *Thermal parameters of BACA with standard deviations in parentheses* ($\times 10^4$)

The form of the anisotropic temperature factor is: $\exp[-(b_{11}h^2+b_{12}hk+b_{13}hl+b_{22}k^2+b_{23}kl+b_{33}l^2)]$.

	b_{11}	b_{12}	b_{13}	b_{22}	b_{23}	b_{33}
C(1)	249 (12)	24 (15)	−108 (16)	122 (7)	−22 (11)	117 (6)
C(2)	262 (14)	203 (19)	−21 (16)	156 (8)	−37 (10)	88 (5)
C(3)	196 (11)	76 (14)	1 (17)	108 (6)	66 (13)	164 (8)
C(4)	116 (7)	57 (10)	−2 (9)	88 (5)	−19 (7)	74 (4)
O(5)	141 (5)	51 (8)	36 (7)	90 (3)	14 (6)	84 (3)
C(6)	173 (8)	21 (11)	22 (9)	82 (4)	−8 (7)	45 (3)
O(7)	167 (6)	−17 (8)	26 (7)	109 (4)	1 (5)	65 (2)
N(8)	197 (8)	94 (11)	79 (10)	97 (4)	52 (7)	84 (4)
C(9)	251 (11)	86 (15)	8 (14)	111 (6)	41 (9)	84 (5)
C(10)	209 (11)	110 (16)	10 (15)	137 (8)	46 (11)	120 (6)
C(11)	153 (8)	46 (11)	9 (10)	89 (5)	5 (7)	67 (4)
C(12)	109 (6)	−26 (9)	11 (8)	70 (4)	−17 (7)	68 (3)
O(13)	223 (7)	−180 (11)	−52 (8)	154 (5)	16 (6)	65 (3)
O(14)	240 (9)	−271 (13)	7 (9)	218 (7)	−46 (8)	92 (3)

Table 4. *Equations of the least-squares planes passing through groups of atoms and atomic deviations* (Å) *from the planes*

The equations are referred to the crystal axes and x, y and z are fractional coordinates.

O(5), C(6), O(7), N(8): $2{\cdot}2704x+5{\cdot}0775y+10{\cdot}3680z-4{\cdot}2068=0$

O(5) 0·002; C(6) −0·005; O(7) 0·002; N(8) 0·002

N(8), C(9), C(10), C(11): $2{\cdot}8325x+5{\cdot}2320y+9{\cdot}9526z-4{\cdot}3846=0$

N(8) 0·017; C(9) −0·015; C(10) 0·014; C(11) −0·016

O(5), C(6), O(7), N(8), C(9), C(10), C(11): $2{\cdot}5640x+5{\cdot}1272y+10{\cdot}1822z-4{\cdot}3236=0$

O(5) 0·022; C(6) −0·001; O(7) −0·038; N(8) 0·048; C(9) 0·021; C(10) −0·010; C(11) −0·040

C(11), C(12), O(13), O(14): $-4{\cdot}7411x+8{\cdot}8579y+1{\cdot}2169z-4{\cdot}4807=0$

C(11) −0·002; C(12) 0·006; O(13) −0·002; O(14) −0·002

C(9) instead of a hydrogen atom, has a *cis* conformation.

The torsion angle of N(8), C(11), C(12), O(14) is 21°, so that O(13) is approximately *cis* with respect to the hydrogen linked to C_α. Furthermore C(1), C(2) and C(3) form with C(4), O(5) and C(6) torsion angles around the bond C(4)–O(5) of 62, −61 and −179° respectively. Therefore C(1) and C(2) give rise to *gauche* conformations while C(3) is *trans*.

The molecular packing is governed by van der Waals forces and hydrogen bonds along **c** (Fig. 3). The hydrogen atoms of the methyl and methylene groups are engaged in good interactions among themselves, and with the oxygen atoms. However there are no intermolecular contacts less than the sum of the van der Waals radii usually assumed for the atom pairs involved.

The hydroxyl group O(13)–H(29) and the carbonyl group C(6)–O(7) of the molecule at (x,y,z) form hydrogen bonds with C(6′)–O(7′) at $(\frac{1}{2}-x,1-y,\frac{1}{2}+z)$ and O(13″)–H(29″) at $(\frac{1}{2}-x,1-y,z-\frac{1}{2})$ respectively. It should be noticed that in the following calculations the coordinates of H(29) were assumed to be 0·0045, 0·4544, 0·4040. They are slightly different from those of Table 2 and were generated after the refinement in the plane of the carboxyl group by putting O(13)–H(29) = 1 Å and the angle C(12)–O(13)–H(29) = 110°, H(29), O(13), C(12) and O(14) being in the *cis* conformation. The distances H(29)···O(7′) and O(13)···O(7′) are 1·65 and 2·65 Å. The more significant angles and dihedral angles are: O(13)–H(29)···O(7′) 178; H(29)···O(7′)–C(6′) 127; C(12)–O(13)···O(7′) 111; O(13)···O(7′)–C(6′) 127; O(13)–H(29)···O(7′)–C(6′) 167; C(12)–O(13)···O(7′)–C(6′) −5; O(14)–C(12)–O(13)–H(29) 0; N(8′)–C(6′)–O(7′)···H(29) −78°. From the above distances and angles it is inferred that all the parameters but one are favourable to the formation of a strong hydrogen bond. However, the last torsion angle indicates that the hydrogen atom is far from the plane of the peptide group and, therefore, neither lies on the line of the C(6′)–O(7′) bond nor on the symmetry axes of the non-bonding

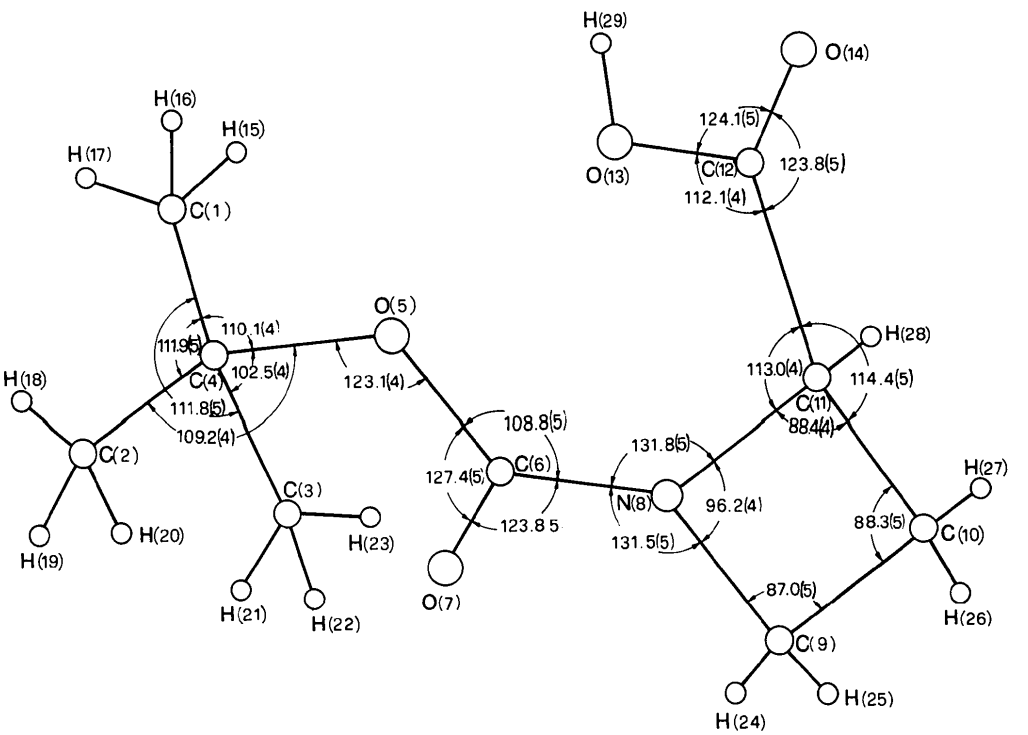

Fig. 2. Bond angles of BACA.

orbitals of O(7'). Since the deviation of H(29) from these lines is large it is reasonable to suppose that the hydrogen bonds of the structure are not strong.

Conformational analysis of PACA

The geometric data of the monomeric unit of PACA were fixed upon completion of the crystal structure determination of BACA and are listed in Table 5 (see Fig. 4 for atomic nomenclature). The azetidine ring was taken as planar and rigid. The potential energy was computed as a function of two internal rotation angles, ψ and ω, which represent the torsion angles N–C_α–C′–N and C_α–C′–N–C_α. The same convention, described above, is assumed. The angle φ (C′–N–C_α–C′) in this case is constant and equal to 64·6°. All the interactions between the atoms of one monomeric unit and those of the seven monomers which follow were taken into account. Atom–atom potentials in the generalized form:

$$V(r) = a \exp(-br)/r^d - cr^{-6}$$

previously verified in known and unknown crystal structures (Coiro, Giglio, Lucano & Puliti, 1973, and references cited therein) and in the conformational analysis of synthetic polymers (De Santis, Giglio, Liquori & Ripamonti, 1963; D'Ilario & Giglio, 1974) and biopolymers (De Santis, Giglio, Liquori & Ripamonti, 1965) were used (Table 6). In addition we introduced for the rotation around the double bond C′=N the torsion potential:

$$V(\omega) = \frac{V_0(\omega)}{2}(1 - \cos 2\omega),$$

putting $V_0(\omega) = 20$ kcal mole^{-1} as is generally accepted. Angular increments of 10° were taken in the first run and, subsequently, the regions of minimum energy were explored by reducing the increments to 5°. Two nearly equal minima, much lower than the others, were found (Fig. 5). They correspond to helices (Figs. 6 and 7) which are characterized by parameters reported in Table 7. Here d represents the helical axial translation per peptide unit and K the number of monomeric units per turn. The values of the energy have no quantitative meaning, and are listed merely to allow a qualitative comparison.

ω was varied since a non-planar distortion of the peptide group has been observed in some linear and cyclic polypeptides and in some small molecules such as *N,N′*-dicyclohexylurea (Coiro, Giglio & Giaco-

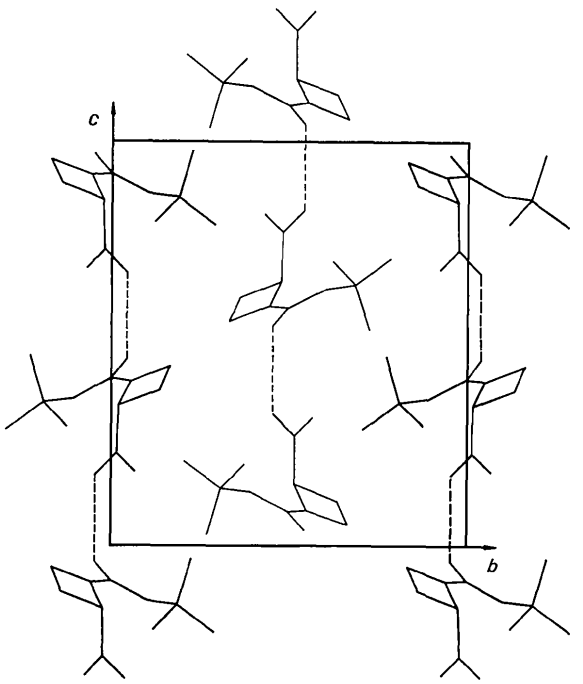

Fig. 3. Molecular packing of BACA projected down the *a* axis. The dashed lines represent hydrogen bonds.

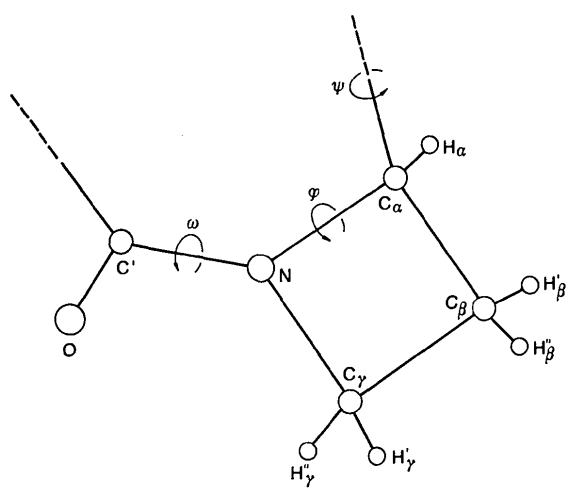

Fig. 4. Atomic nomenclature of the monomeric unit of PACA.

Table 5. *Bond distances* (Å) *and angles* (°) *employed in the conformational analysis of PACA*

N–C_α	1·44	C′—N–C_γ	131·8
C_α–C_β	1·54	C_α–N–C_γ	96·4
C_β–C_γ	1·55	N—C_α–C_β	87·4
N–C_γ	1·46	C_α–C_β–C_γ	88·6
N–C′	1·33	C_β–C_γ–N	87·6
C′–O	1·22	H_α–C_α–N	109·5
C_α–C′	1·52	H_α–C_α–C_β	109·5
C_α–H_α	1·08	C′—C_α–N	113·0
C_β–H'_β	1·08	C′—C_α–C_β	114·3
C_β–H''_β	1·08	H'_β–C_β–C_α	109·5
C_γ–H'_γ	1·08	H'_β–C_β–C_γ	109·5
C_γ–H''_γ	1·08	H''_β–C_β–C_α	109·5
		H''_β–C_β–C_γ	109·5
N–C′–O	123·8	H'_γ–C_γ–C_β	109·5
N–C′–C_α	112·4	H'_γ–C_γ–N	109·5
C_α–C′–O	123·8	H''_γ–C_γ–C_β	109·5
C′–N–C_α	131·8	H''_γ–C_γ–N	109·5

Table 6. *The coefficients of the van der Waals potentials used in the conformational analysis of PACA*

The energy is in kcal per atom pair if the interatomic distance is in Å.

Interaction	$a \times 10^{-3}$	b	c	d
H–H	6·6	4·080	49·2	0
H–C	44·8	2·040	125·0	6
H–N	52·1	2·040	132·0	6
H–O	42·0	2·040	132·7	6
C–C	301·2	0·000	327·2	12
C–N	340·0	0·000	340·0	12
C–O	278·7	0·000	342·3	12
N–N	387·0	0·000	354·0	12
N–O	316·2	0·000	356·0	12
O–O	259·0	0·000	358·5	12

Table 7. *Helical parameters and energies corresponding to the two minima found in the conformational analysis of PACA*

	φ(°)	ψ(°)	ω(°)	d(Å)	K	V(kcal)
PACA I (*cis*)	64·6	190	10	2·16	3·16	−1·55
PACA II (*trans*)	64·6	180	180	3·08	4·58	−1·54

mello, 1971, and references quoted therein). The results obtained for PACA I indicate that a small torsion of 10° around the C′=N double bond gives rise to a gain of about 0·9 kcal. Thus it seems justified to take into account this parameter in working out the conformation of the polypeptides.

The helices of PACA I and II have one hydrophilic spiral of oxygen atoms and a hydrophobic one formed by the azetidine rings. The *trans* form is more elongated and its oxygen atoms may be more easily bound to solvent molecules capable of forming hydrogen bonds. These findings agree with the optical properties of PACA in solution studied by Boni & Verdini (1973), who pointed out the existence of conformers similar to those of poly-(L-proline) I and II. PACA II is expected to be stabilized in solvents forming hydrogen bonds, while PACA I is found in solvents or mixtures of solvents, such as ethanol–water, with both polar and non-polar groups. The ability of PACA I to interact to a lesser extent with hydrogen-bonding solvent molecules, and thus to give an intramolecular stable conformation, could explain the high circular dichroism of the conformer observed in ethanol–water by Boni & Verdini (1973) similar to that of poly-(L-proline) I.

It must be stressed that for poly-(L-proline) I and II (De Santis, Giglio, Liquori & Ripamonti, 1965) as well as for poly-(*S*-thiazolidine-4-carboxylic acid) and poly-(*S*-oxazolidine-4-carboxylic acid) (Goodman, Chen, Benedetti, Pedone & Corradini, 1973) the energy differences between the *cis* and *trans* forms may be changed by varying the ω angle. Moreover, these differences can hardly be related to the existence of mutarotation (Goodman, Chen, Benedetti, Pedone & Corradini, 1973). In fact it is of doubtful validity to put on the same scale the numerical values of different energy terms to obtain a quantitative estimate of the potential energy, which has been evaluated by means of crude potentials. The conversion from one to the other conformer is mainly dependent on the height of the energy barrier rather than on the difference between their energy values. For these reasons we do not feel able to account for the mutarotation of PACA merely on the basis of the conformational analysis, although the energy values of the *cis* and *trans* forms are equal.

We thank Dr R. Boni who supplied us with the compound and Mr G. Conte for skilled technical assistance.

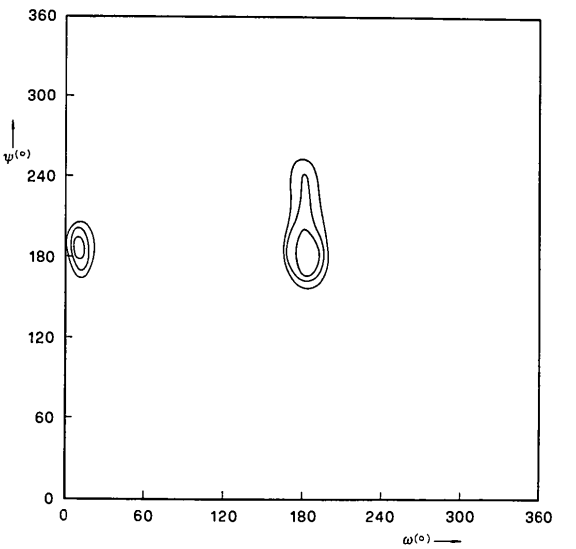

Fig. 5. Potential energy map of PACA. The contour lines are drawn at −1·0, −0·5 and 0·0 kcal.

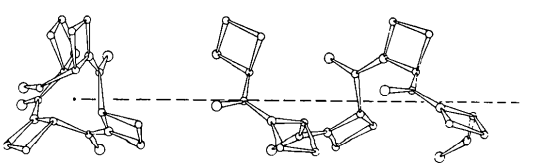

Fig. 6. Helical model of the *cis* conformation of PACA.

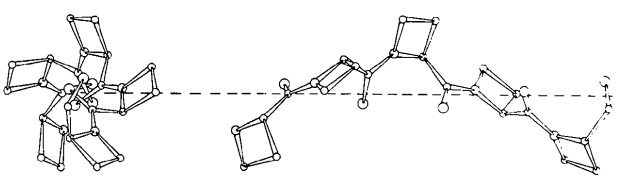

Fig. 7. Helical model of the *trans* conformation of PACA.

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The Crystal and Molecular Structure of Sulphatobis(thiocarbonohydrazide-*N*,*S*)-copper(II) Tetrahydrate

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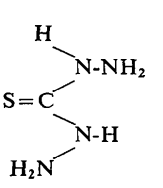
(*Received* 29 *July* 1974; *accepted* 31 *July* 1974)

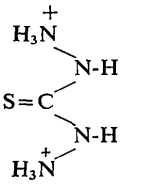
Crystals of the title compound are monoclinic with $a=13{\cdot}430\ (5)$, $b=8{\cdot}340\ (3)$, $c=17{\cdot}070\ (9)$ Å, $\beta=122{\cdot}8\ (1)°$, $Z=4$, space group $P2_1/c$. The structure was solved from diffractometric data by Patterson and Fourier methods and refined by block-diagonal least-squares calculations to $R=0{\cdot}044$ for 2185 observed reflexions. The structure consists of $Cu[SC(NHNH_2)_2]_2SO_4$ complexes and water molecules, linked by hydrogen bonds. The coordination polyhedron around copper is a square pyramid whose base is formed by two sulphur (Cu–S = 2·260, 2·263 Å) and two nitrogen (Cu–N = 2·011, 2·015 Å) atoms of two chelating thiocarbonohydrazide molecules. The apex of the pyramid is occupied by an oxygen (Cu–O = 2·794 Å) atom from the sulphate group. A long Cu···S contact (3·476 Å), in the direction of the d_{z^2} orbitals of the metal, completes the distorted octahedral coordination, joining the complexes to form dimers.

Introduction

Thiocarbonohydrazide (tcaz), $SC(NH–NH_2)_2$, can assume a *cis,trans*-conformation, *i.e.* with the $–NH–NH_2$ groups rotated differently with respect to the S–C bond, or a *cis,cis*-conformation, *i.e.* with both $–NH–NH_2$ groups bent towards the S–C bond. The *cis,trans*-conformation (I) has been found when tcaz is neutral (Braibanti, Tiripicchio & Tiripicchio Camellini, 1969) or monoprotonated (Braibanti, Tiripicchio & Tiripicchio Camellini, 1972). The *cis,cis*-conformation (II) is assumed when tcaz is diprotonated (Braibanti, Pellinghelli, Tiripicchio & Tiripicchio Camellini, 1971; Bigoli, Braibanti, Manotti Lanfredi & Tiripicchio, 1972).



(I)



(II)