departure of the N–C* bond from the C–C′O–N plane is allowed; (3) no distances between non-bonded atoms are unreasonably short; and (4) the configuration around each alpha carbon atom is *levo*, with the Fischer convention correct.[6]

These assumptions are insufficient to determine the coördinates uniquely, the values obtained depending on the postulates made with regard to the hydrogen bond length and the minimum permissible distance between the β carbon atom and neighboring oxygen atoms. Nevertheless, the following set of coördinates is presented, with certain other pertinent magnitudes derived from them.

	x, Å.	y, Å.	z, Å.	ρ, Å.	φ, deg.
Axis	0	0		0	
C	0.00	−2.245	0.00	2.245	0.0
C′	1.21	−1.30	0.00	1.78	42.9
O	1.70	−0.90	−1.06	1.92	62.1
N	1.69	−0.95	1.18	1.94	60.7
C*	2.21	0.39	1.47	2.245	100.0
C_β	0.28	−3.48	−0.88	3.51	4.2
H_N	1.18	−1.36	1.96	1.80	41.0

Hydrogen bond distance	2.88Å.
Angle between N–C* and C–C′O–N plane	30°
Angle H–N···O between N–H bond and hydrogen bond axis	5°
Angle C′=O···N between C′=O bond and hydrogen bond axis	140°
Angle between C=O and helical axis	31°
Angle between N–H and helical axis	39°
Angle N–C–C_β	116°
Angle C′–C–C_β	112°

To obtain the coördinates of the hydrogen atom of the NH group, it was assumed that the N–H bond has a length of 1.014Å., that it lies in the C–C′O–N plane, and that it makes equal angles (113°) with the N–C′ and N–C* bonds. In computing the C_β coördinates, this atom was assumed to be 2.97Å. from each of the two neighboring carbonyl oxygen atoms. This leads to the slightly large value given for the N–C–C_β angle.

Reasonable minor changes in the assumptions would lead to some variations from the coördinates given. They would not, however, reduce the angle between the N–C* bond and the C–C′O–N plane significantly, nor would they change greatly the angles of tilt of the C=O and N–H bonds.

The coördinates listed are for a right-handed spiral, since (assuming the Fischer convention correct) a left-handed spiral would lead to much too small a distance between the β carbon atom and a carbonyl oxygen atom in the next turn of the helix. It may be noted that Pauling and Corey's second alternative set of C_β coördinates for the 13-atom ring structure, which are the ones to use (according to the Fischer convention) for *levo* polypeptides in their left-handed spiral, give a $C_\beta \cdots O$ distance of only 2.64Å. I conclude that *levo* polypeptides form right-handed spirals and *dextro* polypeptides left-handed spirals, whichever of these two types of structure is correct.

Some of the conclusions to be drawn from the results of these calculations are discussed briefly in another communication.[1]

(6) A. F. Peerdeman, A. J. Van Bommel and J. M. Bijvoet, *Proc. Acad. Sci. Amsterdam*, **B54**, 3 (1951).

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MAURICE L. HUGGINS

RECEIVED JUNE 23, 1952

THE PLANARITY OF THE AMIDE GROUP IN POLYPEPTIDES

Sir:

Dr. M. L. Huggins has kindly sent us copies of his Letters,[1,2] in which he has proposed a helical configuration of polypeptide chains as an alternative to the α helix described in our earlier publications.[3,4,5] In his configuration the amide group is not planar. The deformation of the amide group from the planar configuration can be described as a rotation of 17.5° of the NHC* plane about the C′–N axis plus a bending of 15° of the N–C* bond and the N–H bond out of the rotated plane, to the same side. The part of the strain energy due to the rotation of the π orbital of the nitrogen atom can be calculated by the formula[6,7] $A \sin^2 \delta$ with $A = 30$ kcal. mole^{-1} and $\delta = 17.5°$; this calculation gives 2.7 kcal. mole^{-1}. The strain energy of deformation of the N–C* bond and the N–H bond can be calculated by the assumption that the bond energy is proportional to the strength of the bond orbital of the nitrogen atom in the bond direction, which is for these bonds 15° from the the direction of maximum strength. With use of the bond energies of the bonds (48.6 and 83.7 kcal. mole^{-1}, respectively), this calculation leads to 3.3 kcal. mole^{-1} for the bending energy of the two bonds. The total strain energy for the distorted amide group is thus found to be 6 kcal. mole^{-1}. This strain energy, which in the structure proposed by Huggins applies to every residue, is so great as to make the structure unacceptable in comparison with the α helix, which is just as satisfactory in every other respect, so far as we are aware, and which involves planar amide groups.

(1) M. L. Huggins, THIS JOURNAL, **74**, 3963 (1952).
(2) M. L. Huggins, *ibid.*, **74**, 3963 (1952).
(3) L. Pauling and R. B. Corey, *ibid.*, **72**, 5349 (1950).
(4) L. Pauling, R. B. Corey and H. R. Branson, *Proc. Nat. Acad. Sci.*, **37**, 205 (1951).
(5) L. Pauling and R. B. Corey, *ibid.*, **37**, 235 (1951).
(6) L. Pauling and R. B. Corey, *ibid.*, **37**, 251 (1951).
(7) R. B. Corey and L. Pauling, *Proc. Roy. Soc. (London)*, to be published; presented at the Discussion Conference of the Royal Society of London, May 1, 1952.

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ROBERT B. COREY

RECEIVED JULY 7, 1952

LIPOTHIAMIDE PYROPHOSPHATE: COENZYME FOR OXIDATIVE DECARBOXYLATION OF α-KETO ACIDS

Sir:

It has been reported[1] recently that lipothiamide (LT), the amide of α-lipoic acid (α-LA) and thiamin, is required for oxidation of pyruvate and α-ketoglutarate by resting cell suspensions of an *Escherichia coli* mutant. The organism lacks the

(1) L. J. Reed and B. G. DeBusk, THIS JOURNAL, **74**, 3457 (1952).

capacity to conjugate α-lipoic acid and the pyrimidine moiety of thiamin.

Soluble enzyme preparations from the mutant catalyze the dismutation of pyruvate only when lipothiamide pyrophosphate (LTPP), the amide of α-La and thiamin pyrophosphate (TPP), is present (Table I). Likewise, LTPP is required for oxidation of α-ketoglutarate by the cell-free extracts, as measured by succinylation of sulfanilamide[3] (Table II).

TABLE I

DISMUTATION OF PYRUVATE

System	μM Products per ml. in 90 min. Carbon dioxide	Acetyl phosphate	Lactate
A[a]	0.3	0.2	0.3
A + boiled extract of yeast[b]	3.1	2.3	2.7
A + LTPP,[c] 14γ	3.4	3.0	3.3
A + LT,[c] 11γ	0.4	0.3	0.3
A + LTP,[c] 12γ	0.6	0.5	0.6
A + TPP, 25γ	0.3	0.2	0.2
A + α-LA, 5γ, + TPP, 25γ	0.3	0.2	0.3

[a] System A contained per ml.: *E. coli* mutant extract, 3.2 mg. protein; potassium phosphate buffer, *p*H 6.0, 50μM; L-cysteine, 20μM; magnesium chloride, 2.4μM; manganese chloride, 1.6μM; coenzyme A (CoA), 5 units; diphosphopyridine nucleotide (DPN), 100γ; pyruvate, 50μM; lactic dehydrogenase, 1600 units; transacetylase, 5 units. Gas phase, nitrogen; temperature, 25°. [b] From 5 mg. dried yeast. [c] Crude synthetic preparations.[1] *E. coli* mutant extract prepared by method of Korkes, *et al.*[2]

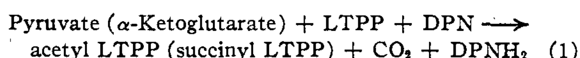
TABLE II

SUCCINYLATION OF SULFANILAMIDE

System	γ Sulfanilamide disappearing
B[a]	0
B + PL,[b] 0.3 ml.	4
B + PL + α-LA[c] + TPP[c]	2
B + PL + LTPP[c]	42
B + LTPP	1
B + boiled extract of yeast[c]	3
B + PL + boiled extract of yeast	36

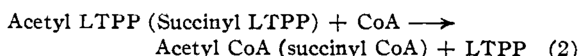
[a] System B contained per ml.: mutant extract, 10.5 mg protein; sulfanilamide, 90γ; L-cysteine, 10μM; catalase, 0.25 units; magnesium chloride, 5μM; CoA, 10 units; sodium bicarbonate, 3μM; α-ketoglutarate, 5μM. Incubated 90 min. at 37°. [b] Pigeon liver acetone powder extract.[4] [c] Same levels as in Table I.

In view of these and other[2,3] results, it is proposed that Reaction 1 represents an initial step in the oxidative decarboxylation of pyruvate and α-ketoglutarate.



Pyruvate (α-Ketoglutarate) + LTPP + DPN ⟶ acetyl LTPP (succinyl LTPP) + CO_2 + $DPNH_2$ (1)

Transfer of the acyl group to CoA (Reaction 2) would provide the acyl CoA required in a number of known enzymatic reactions.



Acetyl LTPP (Succinyl LTPP) + CoA ⟶ Acetyl CoA (succinyl CoA) + LTPP (2)

The authors are indebted to Drs. E. R. Stadtman, A. Kornberg and F. Lipmann, respectively, for preparations of transacetylase, lactic dehydrogenase and CoA.

(2) S. Korkes, *et al.*, *J. Biol. Chem.*, **193**, 721 (1951).

(3) D. R. Sanadi and J. W. Littlefield, *ibid.*, **193**, 683 (1951); *Federation Proc.*, **11**, 280 (1952).

(4) N. O. Kaplan and F. Lipmann, *ibid.*, **174**, 37 (1948).

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RECEIVED JUNE 23, 1952

ON VISCOSITY MEASUREMENT IN THE ULTRACENTRIFUGE[1]

Sir:

During the course of a study on sodium desoxyribonucleate (DNA) attempts were made to measure viscosity by the rate of sedimentation of macromolecules. In view of the striking results with DNA and the interest in the problem of viscosity in connection with ultracentrifugation, a preliminary account of our results seems warranted.

The rate of sedimentation, s_0, of various macromolecules and particles, hereafter called Indicator Particles (IP), through a solvent medium is compared with the sedimentation rate, s, of the same IP through solutions containing an additional viscous component such as DNA. The ratio, s_0/s, gives some measure of the relative viscosity of the solution containing the asymmetric molecules. Several factors aside from viscosity, such as density, backward flow and the effect of covolumes on viscosity, contribute to the ratio s_0/s, and a detailed study of them is now under investigation.

Experiments have been conducted with a variety of IP such as polystyrene latex (PSL), bacteriophage (T3) and bushy stunt virus (BSV), in solutions containing different concentrations of fibrinogen and DNA. Whenever possible, viscosities of the solutions were also determined in a capillary viscometer of shear gradient about 300 sec.$^{-1}$.

Table I shows representative data obtained on a freshly prepared solution of fibrinogen using BSV as IP. The agreement between columns 3 and 4 suggests that the ultracentrifuge method may yield valuable information regarding the viscosity of solutions.[2]

TABLE I

VISCOSITY OF FIBRINOGEN SOLUTIONS

Fibrinogen concn., g./100 cc.	Solvent	η/η_0, capillary	s_0/s BSV
1.0	0.3μ NaCl-cacodylate, *p*H 7	1.23	1.22
2.0	0.3μ NaCl-cacodylate, *p*H 7	1.55	1.64
3.0	0.3μ NaCl-cacodylate, *p*H 7	2.16	2.10

When DNA was used as the viscous component, strikingly different results, shown in Table II, were obtained. The apparent viscosities with PSL are much higher than the capillary values or any viscosities previously reported except those of Katz and Ferry.[3] When particles smaller than PSL were used, however, regardless of the ionic strength or the *p*H employed, the IP sedimented

(1) This work was supported in part by grants from the Rockefeller Foundation and Lederle Laboratories.

(2) In preliminary experiments with tobacco mosaic virus as the viscous component, η/η_0 from capillary measurements was slightly less than s_0/s using PSL as IP.

(3) S. Katz and J. D. Ferry, abstracts, A.C.S. meeting, March, 1952.