Theoret. chim. Acta (Berl.) 14, 429—431 (1969)

Extended Hückel Calculations on Polypeptide Chains

I. The α Helix*

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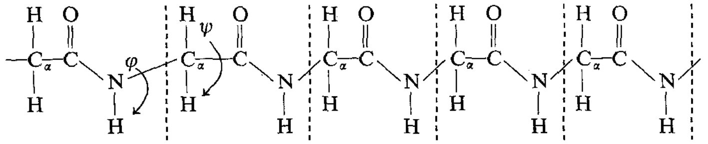
Received June 19, 1969

Extended Hückel molecular orbital calculations on four and five peptide units of polyglycine demonstrate for the first time that the α helix conformation yields a minimum for the total ground state orbital molecular energy ε_T. There is an increased stabilization energy per peptide unit particularly at the α helix conformation as we increase the number of peptide units from four to five which partly reflects the formation of the additional hydrogen bond.

We wish to report some results of extended Hückel molecular orbital calculations on a polyglycine chain of four and five peptide units. The chain is sufficiently long for the first time to incorporate the effects of two intramolecular hydrogen bonds.



The method of calculation has been widely used on organic and inorganic molecules [1–6] as well as more recently on biopolymers [7].

The off-diagonal matrix elements were computed according to the formula:

$$H_{ij} = 0.5\, K(H_{ii} + H_{jj})\, S_{ij} \qquad (1)$$

where K was set equal to $2 - |S_{ij}|$ [8]. The Coulomb integrals and Slater exponents employed in the calculation are given in Table 1. The fixed bond distances and bond angles were those used by Leach, Némethy, and Scheraga [9]. For the C–H distance, however, we have used a value of 1.09 Å rather than 1.0 Å. This slightly larger distance seems to be more representative of the C–H distance observed in a wide variety of organic molecules [10]. We considered various conformations given by the dihedral angles ϕ and ψ as defined by the standard convention [11]. A subroutine

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* This work is being supported by Grant No. GB-6852 of the National Science Foundation. The computational part of this work was carried out in the computer center of the University of Connecticut which is supported in part by Grant No. GP-1819 of the National Science Foundation. We wish to especially thank Professor John L. C. Löf for expediting the calculations.

to generate the cartesian coordinates of the atoms in the chain as a function of ϕ and ψ was written using the matrix equations of Némethy and Scheraga [12] and was incorporated into Hoffmann's program [13].

The results for the total one-electron orbital energy ε_T at the minimum of the right-handed α helix conformation ($\Delta\phi \approx \pm 5°, \Delta\psi \approx \pm 5°$) and at the fully extended chain conformation are given in Table 2.

Table 1. *Extended Hückel theory parameters*

Coulomb integrals	
Electron	**Value (eV)**
H(1*s*)	−13.6
C(2*s*)	−21.4
C(2*p*)	−11.4
N(2*s*)	−26.0
N(2*p*)	−13.4
O(2*s*)	−32.3
O(2*p*)	−14.8
Slater exponents	
Atom	**Value**
H	1.000
C	1.625
N	1.950
O	2.275

Table 2. *Total one-electron orbital energies* ε_T

Number of peptide units	Rotation ϕ	Angles (degrees) ψ	Ground state total one-electron orbital energies ε_T (eV)
4	0	0	−1627.13
5	0	0	−2034.25
4	137	128	−1632.52
5	137	128	−2042.29

From Table 2 and calculations performed on neighbouring points of $\phi = 137°$, $\psi = 128°$ we conclude:

1) the calculations predict the minimum for the α helix conformation ($\phi = 132°$, $\psi = 123°$) within an acceptable range [14],

2) the four peptide unit α helix conformation is predicted to be more stable than the four peptide unit isolated extended chain conformation ($\phi = 0°$, $\psi = 0°$) by approximately 5.4 eV and,

3) the five peptide unit α helix conformation is predicted to be more stable than the five peptide unit extended chain conformation by approximately 8 eV. The greater stabilization energy of the α helix conformation relative to the extended chain conformation in going from four to five peptide units is partly due to the

formation of the additional intramolecular hydrogen bond. The predicted energy difference between the fully extended conformation and the α helix conformation for four and five peptide units are approximately 31 kcal per mole/peptide unit and 37 kcal per mole/peptide unit.

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