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Helix—Coil Transition under External Forces

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ABSTRACT: The helix—coil transition of a polypeptide is investigated for the case in which a tensile force is applied at the chain ends. The free energy is calculated by the use of a Green's function which was first introduced by de Gennes. The helix content, the mean end-to-end vector, and the mean length of the helical sequences are calculated as functions of the external force. It is found that in the coil region, the helical sequences continue to break as the external force increases. However, in the helix region, the external force first winds the polypeptide and produces longer helical sequences, but when the force becomes strong enough, the helical sequences break abruptly, and finally the polypeptide is brought to the random coil state.

KEY WORDS Helix—Coil Transition / Polypeptide / Tensile Force / Helix Content / Expansion / Green's Function /

The statistical mechanical theory of the helix—coil transition of polypeptides has been investigated by a number of authors.[1] Many characteristic features of the transition have been clarified, such as the change in helix content and the expansion of the polypeptide chain as functions of the PH or the temperature.

In this paper, we shall focus our attention on the effect produced by an external force applied at the chain ends. This problem was first considered by Birshtein[2] using a one-dimensional model. She assumed that peptide units in the helical state are aligned in the direction of the applied force and those in the coil state arrange themselves, with different probabilities, either parallel or antiparallel to that direction. Similar calculations have been reported by other workers[3,4] who were concerned with tension—length isotherms in keratins. A more realistic three-dimensional model was treated by Saito and Go,[5] who expanded the partition function of a polypeptide subjected to a tension in powers of the applied force. Following their treatment, the problem is reduced to the calculation of the moments of the end-to-end vector $\langle \boldsymbol{R}^2 \rangle$, $\langle \boldsymbol{R}^4 \rangle$, $\cdots$, the quantities which were discussed by many authors.[1,6,7] However, the calculation is very cumbersome even for the fourth moment, and for this reason their results are restricted to the case where the external force is very small.

In the present paper, we solve the problem without recourse to such an expansion method. The model considered here is the same as that used by previous authors in the computation of the moments.[1,7] The random coil part of the chain is regarded as a Gaussian chain and the helical part is assumed to be a rigid rod. The essential point is that we consider the partition function of these parts as functions of their end-to-end vectors. Such treatment was first introduced by de Gennes,[8] who applied the method to the helex—coil transition of polynucleotides forming a hair-pin-type helix. In comparison with the conventional treatment, the method seems to be more advantageous because of the simplicity of the calculation.

We shall calculate the exact partition function of a polypeptide with tensions in the limit of large degree of polymerization, and discuss the change in the helix content and the mean end-to-end distance with the tensile forces. In particular, the effect of large external forces is discussed. It will be shown that an interesting feature, which could not be predicted by the expansion method, appears in the presence of large external forces.

PARTITION FUNCTION

Let us consider the partition function $Z(\boldsymbol{R})$

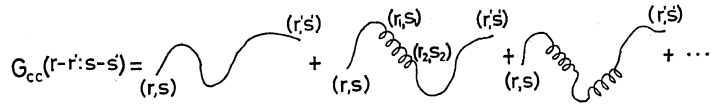

Figure 1. Illustration of eq 4. The partition function is obtained by summing up all the statistical weights of various interupted helix states.

of a polypeptide chain with a given end-to-end vector $\boldsymbol{R}$. Since the polypeptide can be in any of the interrupted helix states shown in Figure 1, we must sum up all the statistical weights of these conformations. The statistical weight of a portion of the chain may be calculated as follows.

For a random coil part of s peptide units starting at point $\boldsymbol{r}'$, and ending at point $\boldsymbol{r}$, the statistical weight is given by

$$G_c^{(0)}(\boldsymbol{r}-\boldsymbol{r}', s) = \left(\frac{3}{2\pi b^2 s}\right)^{3/2} e^{-us} \exp\left(-\frac{3(\boldsymbol{r}-\boldsymbol{r}')^2}{2b^2 s}\right)\Theta(s) \quad (1)$$

with

$$\Theta(s)=\begin{cases}1 & s\geq 0\\ 0 & s<0\end{cases}$$

where b is the effective bond length of the chain in the random coil state and u is the free energy (divided by k_BT) of a peptide unit. On the other hand, for a helical sequence of s peptide units starting at $\boldsymbol{r}'$ and ending at $\boldsymbol{r}$, the statistical weight is expressed as

$$G_h^{(0)}(\boldsymbol{r}-\boldsymbol{r}', s)=[4\pi(as)^2]^{-1}\delta(|\boldsymbol{r}-\boldsymbol{r}'|-as)\Theta(s) \quad (2)$$

where a is the length of a bond projected onto the helical axis.

The above statistical weights are subject to the normalization conditions:

$$\int G_h^{(0)}(\boldsymbol{r}, s)d^3\boldsymbol{r}=1$$
$$\int G_c^{(0)}(\boldsymbol{r}, s)d^3\boldsymbol{r}=e^{-us} \quad (3)$$

if all the free energies are measured from the complete helix state. Thus, in what follows, u is taken as the free energy difference between the coil and the helix states. If $u>0$, the helix state is more stable than the coil state, so that we shall refer to $u>0$ as the "helix region" and to $u<0$ as the "coil region."

Let us consider the part of the peptide chain between the s-th peptide unit and the s'-th one, and let $\boldsymbol{r}$ and $\boldsymbol{r}'$ be the position vectors of its end peptides. When these terminal peptides are in the coil state, the statistical weight of the portion under consideration is given by (see Figure 1)

$$G_{cc}(\boldsymbol{r}-\boldsymbol{r}', s-s') = \sum_{n=0}^{\infty} v^{2n}\int d^3\boldsymbol{r}_1 ds_1 \int d^3\boldsymbol{r}_2 ds_2 \cdots \int d^3\boldsymbol{r}_{2n} ds_{2n} \times[G_c^{(0)}(\boldsymbol{r}-\boldsymbol{r}_1, s-s_1)G_h^{(0)}(\boldsymbol{r}_1-\boldsymbol{r}_2, s_1-s_2) \times G_c^{(0)}(\boldsymbol{r}_2-\boldsymbol{r}_3, s_2-s_3)\cdots G_c^{(0)}(\boldsymbol{r}_{2n}-\boldsymbol{r}', s_{2n}-s')] \quad (4)$$

where v is the statistical weight of the boundary between the helix and the random coil sequences, at which there is a lack of hydrogen bonding. The integral in eq 4 may be extended from minus infinity to plus infinity for both $\boldsymbol{r}$ and s because of the Θ function involved in eq 1 and 2. Similarly, it is possible to define the statistical weights $G_{hh}(\boldsymbol{r}, s)$, $G_{ch}(\boldsymbol{r}, s)$, and $G_{hc}(\boldsymbol{r}, s)$ for the portions of the chain whose terminal peptides are in helix and helix, coil and helix, and helix and coil, respectively. But we shall not discuss them further since only G_{cc} is necessary for the following discussion.

The sum in eq 4 can be evaluated by use of Fourier transforms. Let us consider the functions

$$G_c^{(0)}(\boldsymbol{k}, \omega)=\int d^3\boldsymbol{r} ds e^{i\boldsymbol{k}\cdot\boldsymbol{r}-i\omega s}G_c^{(0)}(\boldsymbol{r}, s) = (i\omega+u+\tfrac{1}{6}b^2k^2)^{-1} \quad (5)$$

$$G_h^{(0)}(\boldsymbol{k}, \omega)=\int d^3\boldsymbol{r} ds e^{i\boldsymbol{k}\cdot\boldsymbol{r}-i\omega s}G_h^{(0)}(\boldsymbol{r}, s) = \frac{1}{2ika}\ln\frac{\omega+ka}{\omega-ka} \quad (6)$$

where

$$k=|k|$$

In these equations, we have used the same symbols $G_c^{(0)}$ and $G_h^{(0)}$ for the original statistical weights and their Fourier transforms. This

will cause no confusion because we shall use the variables $\boldsymbol{k}$, $\boldsymbol{k}'$ and ω, ω', $\cdots$ for the arguments of the Fourier transformed functions. The Fourier transform of eq 4 gives

$$\begin{aligned} G_{cc}(\boldsymbol{k}, \omega) &= \int d^3\boldsymbol{r} ds e^{i\boldsymbol{k}\cdot\boldsymbol{r}-i\omega s} G_{cc}(\boldsymbol{r}, s) \\ &= \sum_{n=0}^{\infty} v^{2n} G_c^{(0)}(\boldsymbol{k}, \omega) \\ &\quad \times [G_h^{(0)}(\boldsymbol{k}, \omega) G_c^{(0)}(\boldsymbol{k}, \omega)]^n \\ &= \frac{G_c^{(0)}(\boldsymbol{k}, \omega)}{1 - v^2 G_c^{(0)}(\boldsymbol{k}, \omega) G_h^{(0)}(\boldsymbol{k}, \omega)} \\ &= \left[i\omega + u + \frac{b^2k^2}{6} - \frac{v^2}{2ika} \ln \frac{\omega + ka}{\omega - ka} \right]^{-1} \end{aligned} \tag{7}$$

Since it has been assumed that the peptides at the chain ends are in the coil state, the partition function of the whole chain $Z(\boldsymbol{R})$ is equal to the statistical weight $G_{cc}(\boldsymbol{R}, N)$, where N is the degree of polymerization. Thus

$$Z(\boldsymbol{R}) = \int \frac{d^3\boldsymbol{k}}{(2\pi)^3} \frac{d\omega}{2\pi} e^{-i\boldsymbol{k}\cdot\boldsymbol{R}+i\omega N} G_{cc}(\boldsymbol{k}, \omega) \tag{8}$$

We now proceed to the case in which a constant force $\boldsymbol{F}$ is applied at the ends of the polypeptide. The partition function for this case is given by

$$Q(\boldsymbol{F}) = \int d^3\boldsymbol{R} Z(\boldsymbol{R}) \exp\left[\frac{\boldsymbol{F}\cdot\boldsymbol{R}}{k_B T} \right] \tag{9}$$

Comparing this with eq 8, we obtain

$$Q(\boldsymbol{F}) = \int \frac{d\omega}{2\pi} e^{i\omega N} G_{cc}\left(\boldsymbol{k} = \frac{-i\boldsymbol{F}}{k_B T}, \omega \right) \tag{10}$$

or by use of eq 7

$$Q(\boldsymbol{F}) = \int \frac{d\omega}{2\pi} e^{i\omega N} \left[i\omega + u - \frac{1}{6}\xi^2 - \frac{v^2}{2\xi\gamma} \ln \frac{\omega - i\xi\gamma}{\omega + i\xi\gamma} \right]^{-1} \tag{11}$$

where

$$\xi = \frac{|\boldsymbol{F}|b}{k_B T} \quad \text{and} \quad \gamma = \frac{a}{b} \tag{12}$$

Analytical properties of the integrand on the right-hand-side of eq 11 in the complex ω-plane are illustrated in Figure 2. There are two poles P and P′, and two branch points A and B on the imaginary axis. The contour of the integral is denoted by C. If we deform the contour C to C′, the integral is evaluated as a sum of

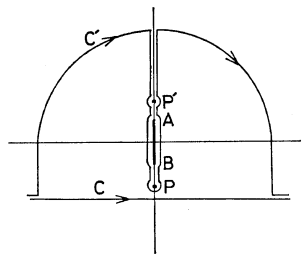

Figure 2. The contour for the integral of eq 11.

three contributions; two contributions from the poles P ($=i\nu$) and P′ ($=i\nu'$) and one contribution from the cut AB (A$=-i\xi\gamma$ and B$=i\xi\gamma$). The order of magnitude of these contributions is $e^{-\nu N}$, $e^{-\nu' N}$, and $e^{\xi\gamma N}$, respectively. Thus for sufficiently large N, the integral is predominated by the contribution from the lower pole $i\nu$. From eq 11, the equation for ν is shown to be

$$\nu - u + \frac{1}{6}\xi^2 = -\frac{v^2}{2\xi\gamma} \ln \frac{\nu - \xi\gamma}{\nu + \xi\gamma} \tag{13}$$

The integral is then evaluated to give

$$Q(\boldsymbol{F}) = \frac{e^{-\nu N}}{1 + v^2/(\nu^2 - (\xi\gamma)^2)} \tag{14}$$

The second term multiplied by v^2 in the denominator of eq 14 is associated with the effect of chain ends, which can be neglected when N is large. Thus we finally obtain

$$Q(\boldsymbol{F}) = e^{-\nu N} \tag{15}$$

This simple relation is the starting point of the following analysis. Equation 15 implies that ν is the free energy (divided by $k_B T$) per peptide unit under the action of the tensile force F.

APPROXIMATE EXPRESSIONS FOR THE EREE ENERGY

Equation 13 is a transcendental equation for ν, but it can be solved numerically. The result is shown in Figure 3, where ν is plotted as a function of the reduced external force ξ. The values chosen for γ and v are $\gamma = 0.066$ and $v^2 = 2 \times 10^{-4}$ (we shall use these throughout this paper). It is seen that in the coil region where $u < 0$, $\nu(\xi)$ is a smooth function (almost parabolic), but that in the helix region where $u > 0$, $\nu(\xi)$ appears to be composed of three parts: a parabolic part for small ξ, a linear part in the

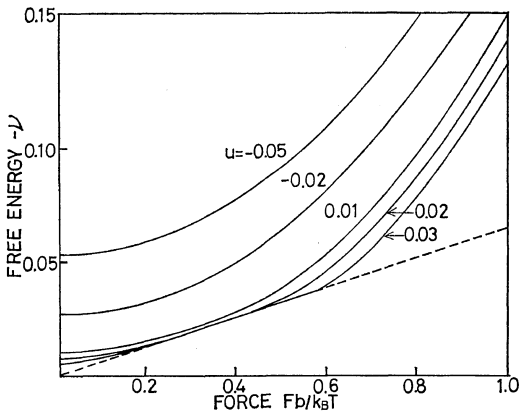

Figure 3. Free energy per peptide unit is plotted against external force.

intermediate region, and again a parabolic part for large ξ. To investigate in some detail this specific behavior of $\nu(\xi)$ in the helix region, we consider the graphical solution of eq 13.

In Figure 4, we have plotted the following two functions of x which appear on both sides of eq 13:

$$y_1=x-u+\tfrac{1}{6}\xi^2$$

$$y_2=-\frac{v^2}{2\xi\gamma}\ln\frac{x+\xi\gamma}{x-\xi\gamma}$$

The two straight lines in Figure 4 represent the graph of y_1 for the helix region ($u>0$) and the coil region ($u<0$). The graph of y_2 is common to these two regions, and the points of intersection give the solution of eq 13. As ξ increases, the graph of y_1 shifts upward and that of y_2 shifts to the left. Since the graph of y_2 rapidly approaches the asymptotes $y=0$ and $x=-\xi\gamma$, the solution of eq 13 is approximately determined as a function of ξ.

(a) *The Case of Small External Forces*

In this case, we can solve eq 13 by expanding $\nu(\xi)$ in powers of ξ

$$\nu(\xi)=\nu_0+A\xi^2 \tag{16}$$

The odd order terms disappear because eq 13 remains unchanged for the transformation $\xi\rightarrow-\xi$. Substituting eq 16 into eq 13 and comparing terms of the same order in ξ, we obtain

$$\nu_0=-\tfrac{1}{2}(\sqrt{u^2+4v^2}-u)$$
$$A=\frac{-\nu_0^3+2\gamma^2v^2}{6\nu_0(\nu_0^2+v^2)} \tag{17}$$

The unperturbed term ν_0 is the free energy per peptide unit in the absence of the external force. Note that for all values of u, v, and γ, ν_0 and A are negative. This should be so since if $A>0$, the system would be unstable.

(b) *The Intermediate Case*

This case is illustrated in Figure 4b, where the point of intersection is close to the asymptote $x=-\xi\gamma$, so that the solution is approximately given by

$$\nu(\xi)=-\xi\gamma \tag{18}$$

(c) *The Case of Strong External Forces*

In this case, the point of intersection is close to the x-axis, as illustrated in Figure 4c. Therefore, the solution is approximately given by the equation $y_1=0$, which leads to

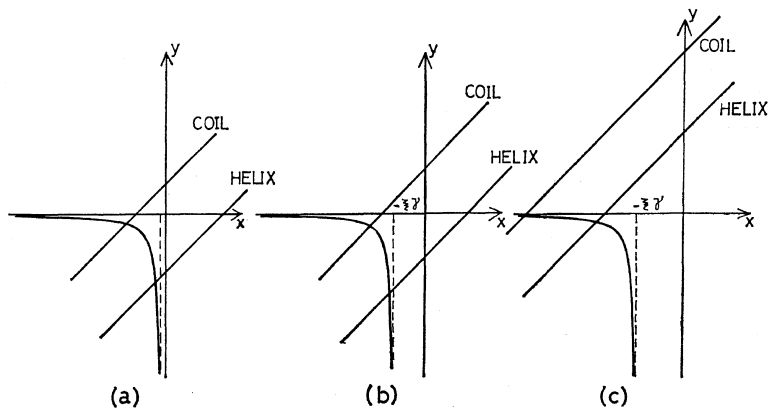

Figure 4. Graphical solution of eq 13.

$$\nu(\xi)=-\tfrac{1}{6}\xi^2+u \tag{19}$$

There is no definite borderline between cases (b) and (c), but we can estimate a critical value ξ_c which may be used to distinguish the two cases. As observed in Figure 4, we may presume that, at the critical state between the cases (b) and (c), the graph of y_1 passes the point $(-\xi\gamma, 0)$, and therefore ξ_c satisfies

$$-\xi_c\gamma-u+\tfrac{1}{6}\xi_c{}^2=0 \tag{20}$$

whence

$$\xi_c=3\gamma+\sqrt{9\gamma^2+6u} \tag{21}$$

It should be again stressed that the above approximate expressions for free energy, eq 16—19, apply only to the helix-rich state. On the other hand, in the coil-rich state, $\nu(\xi)$ is approximately given by eq 19, as is expected from Figure 4. In the following section, we shall make use of these approximate expressions for $\nu(\xi)$.

HELIX CONTENT AND MEAN END-TO-END VECTOR

The mean end-to-end vector $\langle \boldsymbol{R}\rangle$ is immediately obtained from eq 10 as

$$\langle \boldsymbol{R}\rangle=\frac{\int \mathrm{d}^3\boldsymbol{R}\exp\left(\frac{\boldsymbol{F}\cdot\boldsymbol{R}}{k_BT}\right)Z(\boldsymbol{R})\boldsymbol{R}}{\int \mathrm{d}^3\boldsymbol{R}\exp\left(\frac{\boldsymbol{F}\cdot\boldsymbol{R}}{k_BT}\right)Z(\boldsymbol{R})}=k_BT\frac{\partial}{\partial \boldsymbol{F}}\ln Q(\boldsymbol{F}) \tag{22}$$

Since $\langle \boldsymbol{R}\rangle$ is always parallel to the vector $\boldsymbol{F}$, we shall discuss only its magnitude $R=|\boldsymbol{R}|$. Use of eq 12 and 15 gives

$$\langle R\rangle=-Nb\frac{\partial\nu}{\partial\xi} \tag{23}$$

In a similar manner, from eq 4, we can calculate the mean number of peptide units in the coil state

$$\begin{aligned}\langle N_c\rangle=[Q(\boldsymbol{F})]^{-1}\sum_{n=0}^{\infty}&\int \mathrm{d}^3\boldsymbol{R}\exp\left(\frac{\boldsymbol{F}\cdot\boldsymbol{R}}{k_BT}\right)\\ &\times\int \mathrm{d}^3\boldsymbol{r}_1\mathrm{d}s_1\cdots\int \mathrm{d}^3\boldsymbol{r}_{2n}\mathrm{d}s_{2n}\\ &\times(N-s_1+s_2-s_3+\cdots+s_{2N})v^{2n}\\ &\times G_c{}^{(0)}(\boldsymbol{R}-\boldsymbol{r}_1, N-s_1)G_h{}^{(0)}(\boldsymbol{r}_1-\boldsymbol{r}_2, s_1-s_2)\cdots\\ &\times G_c{}^{(0)}(\boldsymbol{r}_{2n}, s_{2n})\\ =-\frac{\partial}{\partial u}&\ln Q(\boldsymbol{F})\end{aligned} \tag{24}$$

Using eq 15, this may be written

$$\langle N_c\rangle=N\frac{\partial\nu}{\partial u} \tag{25}$$

Therefore, the helix content is given by

$$\theta\equiv\frac{N-\langle N_c\rangle}{N}=1-\frac{\partial\nu}{\partial u} \tag{26}$$

The derivatives in eq 23 and 26 can be expressed in terms of ν. Differentiation of eq 13 with respect to u yields

$$\frac{\partial\nu}{\partial u}=\frac{\nu^2-(\xi\gamma)^2}{\nu^2+v^2-(\xi\gamma)^2} \tag{27}$$

Hence eq 26 gives

$$\theta=\frac{v^2}{\nu^2+v^2-(\xi\gamma)^2} \tag{28}$$

In a similar manner, from eq 13 and 23 we have

$$\frac{\langle R\rangle}{Nb}=\frac{\nu^2-(\xi\gamma)^2}{\nu^2+v^2-(\xi\gamma)^2}\left[\frac{\nu-u}{\xi}+\frac{\xi}{2}-\frac{\nu v^2}{\xi(\nu^2-(\xi\gamma)^2)}\right] \tag{29}$$

Thus by using the curves for ν shown in Figure 3, it is possible to calculate the helix content and the mean end-to-end vector. The numerical results are shown in Figures 5 and 6.

Helix Content

As seen from Figure 5, a small external force either increases or decreases the helix content. This fact was first pointed out by Saito and Go.[5] To investigate it in more detail, let us calculate θ by use of eq 16 and 26. The result is

$$\theta=\theta_0\left[1+\frac{\nu_0{}^3+3\nu_0{}^2\gamma^2+\gamma^2v^2}{3(\nu_0{}^2+v^2)^2}\xi^2+\cdots\right] \tag{30}$$

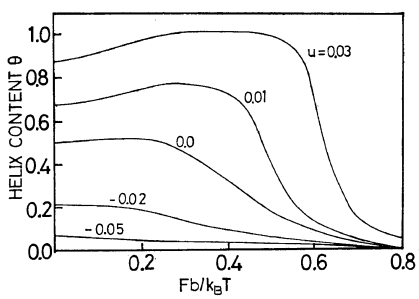

Figure 5. The helix content is plotted against the external force.

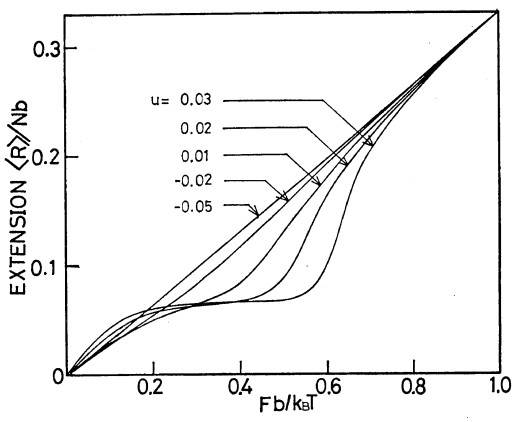

Figure 6. The mean end-to-end distance is plotted against the external force.

where θ_0 is the helix content in the absence of the external force, *i.e.*,

$$\theta_0=\frac{v^2}{\nu_0^2+v^2} \tag{31}$$

Therefore the helix content either increases or decreases depending on

$$\nu_0^3+3\nu_0^2\gamma^2+\gamma^2v^2\gtrless 0 \tag{32}$$

This property is closely related to the well-known fact that there is a minimum in the mean-square end-to-end distance plotted as a function of temperature[6] (or u in the present case). To varify this, we note that

$$\frac{\partial\theta}{\partial\xi}=-\frac{\partial^2\nu}{\partial\xi\partial u}=\frac{1}{Nb}\frac{\partial\langle R\rangle}{\partial u} \tag{33}$$

On the other hand, according to the linear response theory

$$\langle R\rangle=\frac{\langle \boldsymbol{R}^2\rangle_0}{3k_BT}F \tag{34}$$

where the angular brackets with suffix 0 refer to the average in the absence of external force. Hence eq 33 is written

$$\frac{\partial\theta}{\partial\xi}=\frac{F}{3k_BTNb}\frac{\partial\langle \boldsymbol{R}^2\rangle_0}{\partial u} \tag{35}$$

which shows that θ increases or decreases in accordance with the sign of $\partial\langle \boldsymbol{R}^2\rangle_0/\partial u$.

As the external force increases, the helix content continues to decrease in the coil region, whereas, in the helix region, the helix content increases first to a maximum, and then begins to decrease abruptly as the external force becomes large. This behavior may be qualitatively understood by the approximate free energies obtained in the foregoing section. In fact, eq 16—20 and 26 give

$$\begin{aligned}\text{for}\quad &\text{(a)}\quad (\xi\ll 1)\quad \theta=\theta_0-\frac{\partial A}{\partial u}\xi^2\\ &\text{(b)}\quad (\xi\lesssim\xi_c)\quad \theta=1\\ &\text{(c)}\quad (\xi\gtrsim\xi_c)\quad \theta=0\end{aligned} \tag{36}$$

These simple expressions for θ agree closely with the exact numerical results for $u=0.03$.

Mean End-to-End Vector

In the coil region, the mean end-to-end distance is proportional to the external force, and it is well described by the relation

$$\langle R\rangle=\frac{Nb^2}{3k_BT}F \tag{37}$$

However in the helix region, $\langle R\rangle$ shows a somewhat complicated behavior. For small external forces, $\langle R\rangle$ is proportional to F, but as F increases, $\langle R\rangle$ becomes almost constant, and for larger F, $\langle R\rangle$ abruptly approaches the curve given by eq 37. Such behavior of $\langle R\rangle$ is also predictable from eq 16—20 and 23, which give

$$\text{for}\quad \text{(a)}\quad \frac{\langle R\rangle}{Nb}=2A\xi \tag{38}$$

$$\text{(b)}\quad \frac{\langle R\rangle}{Nb}=\gamma \tag{39}$$

$$\text{(c)}\quad \frac{\langle R\rangle}{Nb}=\frac{1}{3}\xi \tag{40}$$

These expressions agree well with the curve for $u=0.03$ in Figure 6.

The constant value of $\langle R\rangle$ given by eq 39 is Na, which is equal to the length of the completely helical polypeptide. This fact suggests that the external force tends to produce a longer helical sequence, and that the increase of the helix content shown in Figure 5 is not a result of the appearance of new short helices but a result of the growth of the existing helices.

To confirm the above picture of the helix—coil transition under tensions, we calculate the probability $P_h(s)$ that a helical sequence consists of s peptide units. This probability is given by the statistical weight that a helical sequence is

followed by interrupted helices. Thus

$$P_h(s) \propto \int d^3\boldsymbol{r} d^3\boldsymbol{r}' G_h^{(0)}(\boldsymbol{r}', s) \times G_{cc}(\boldsymbol{r}-\boldsymbol{r}', N-s) \exp\left(\frac{\boldsymbol{F}\cdot\boldsymbol{r}}{k_BT}\right) = G_h^{(0)}\left(\boldsymbol{k}=\frac{-i\boldsymbol{F}}{k_BT}, s\right) G_{cc}\left(\boldsymbol{k}=\frac{-i\boldsymbol{F}}{k_BT}, N-s\right) \quad (41)$$

Therefore

$$P_h(s) = C \frac{\sinh \xi\gamma s}{\xi\gamma s} e^{\nu s} \quad (42)$$

where C is a normalization constant given by

$$C^{-1} = \int_0^\infty ds \frac{\sinh \xi\gamma s}{\xi\gamma s} e^{\nu s} = \frac{1}{2} \ln \frac{\nu-\xi\gamma}{\nu+\xi\gamma} \quad (43)$$

The mean number of the peptide units in a helical sequence is thus calculated as

$$\langle l_h \rangle = \int_0^\infty ds P_h(s) s = \frac{2\xi\gamma}{\nu^2-(\xi\gamma)^2} \left[\ln\left(\frac{\nu-\xi\gamma}{\nu+\xi\gamma}\right)\right]^{-1} \quad (44)$$

In Figure 7, $\langle l_h \rangle$ is plotted against the external force ξ. It is seen that the curve for $u=0.03$ exhibits a very sharp maximum in the region (b). This clearly confirms the picture mentioned previously. Furthermore, in Figure 8, the mean number $\langle n_h \rangle$ of helical sequences defined by

$$\langle n_h \rangle = N\theta / \langle l_h \rangle \quad (45)$$

is illustrated. In the helix region, the number of helical sequences becomes very small for moderately strong forces. This implies the existence of long helical sequences. As ξ increases the curve of $\langle n_h \rangle$ shows a peak, corresponding to the break of the long helical sequences. The critical force for the break can be estimated roughly be eq 21, yielding $\xi_c=0.67$ ($u=0.03$) and $\xi_c=0.60$ ($u=0.02$), which agree relatively well with the ξ values for the peaks in Figure 8.

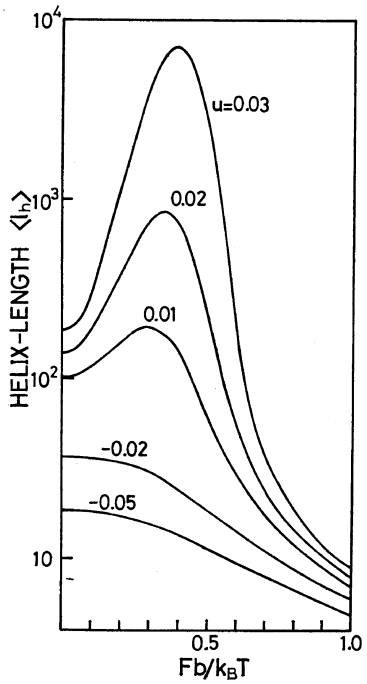

Figure 7. The mean number of the peptide units in a helical sequence is plotted against the tensile force. The length of the polypeptide chain is assumed to be infinite.

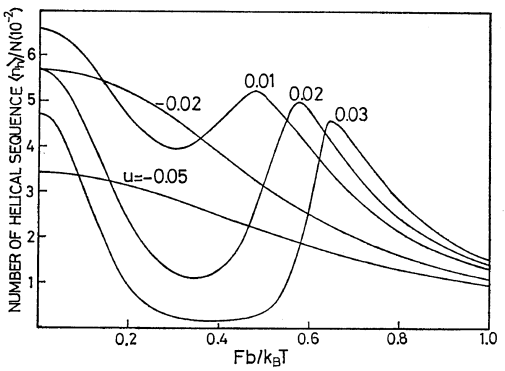

Figure 8. The mean number of helical sequences.

DISCUSSION

In the present paper, we have investigated effects of tensile forces on the helix—coil transition of polypeptides. The results are summarized as follows. (i) In the coil region, the external force breaks the helical sequences, and both the helix content and the number of helical sequences decrease as the external force increases. (ii) In the helix region, the effect is somewhat complicated. The small external force winds the polypeptide and produces long helical sequences. However, when the external force becomes sufficiently strong, the helical sequences break abruptly, and many short helical sequences appear, and at last the polypeptide tends to be completely randomly coiled.

Although the present theory is concerned with a single polypeptide chain, it may apply to polypeptide fibrils in which the intermolecular interactions are unimportant. Since the critical force which breaks the long helical sequence into random coils is as small as 10^{-6} dyn for the parameters used in this paper, there will be a possibility that the theoretically predicted effects of tensions are experimentally observed in such systems.

The present calculation may also find an application in the case where a polypeptide molecule is subjected to a static electric field. Recently a theory for the helix—coil transition in this case has been worked out by Bean and Bennett[9] based on the all-or-none model[1] for the polypeptide. This model is appropriate for short chains, but for sufficiently long chains, the present theory should be more relevant.

Suppose a polypeptide molecule is placed in an electric field $\boldsymbol{E}$. Let μ_h and μ_c be the dipole moments of a peptide unit in the helix and coil states, respectively. We assume that the dipole moment $\boldsymbol{P}_h$ of a helical sequence (and $\boldsymbol{P}_c$ in case of a coiled sequence) is proportional to the end-to-end vector $\boldsymbol{r}$ of the sequence. Therefore we may write

$$\boldsymbol{P}_h=\frac{\boldsymbol{r}}{a}\mu_h, \quad \boldsymbol{P}_c=\frac{\boldsymbol{r}}{b}\mu_c \tag{46}$$

Then the partition function is given by

$$\begin{aligned}\tilde{Q}(\boldsymbol{E})=&\sum_{n=0}^{\infty} v^{2n}\int d^3\boldsymbol{r}\int d^3\boldsymbol{r}_1 ds_1\cdots\int d^3\boldsymbol{r}_{2n} ds_{2n}\\ &\times[G_c^{(0)}(\boldsymbol{r}-\boldsymbol{r}_1, N-s_1)e^{-\xi_E\cdot(r-r_1)}\\ &\times G_h^{(0)}(\boldsymbol{r}_1-\boldsymbol{r}_2, s_1-s_2)e^{-\gamma_E\xi_E\cdot(r_1-r_2)}\cdots\\ &\times G_c^{(0)}(\boldsymbol{r}_{2n}, s_{2n})e^{-\xi_E\cdot r_{2n}}]\\ =&\int\frac{d\omega}{2\pi}e^{i\omega N}\sum_{n=0}^{\infty} v^{2n}G_c^{(0)}(\boldsymbol{k}=-i\hat{\boldsymbol{\xi}}_E, \omega)\\ &\times[G_h^{(0)}(\boldsymbol{k}=-i\hat{\boldsymbol{\xi}}_E\gamma_E, \omega)G_c^{(0)}(\boldsymbol{k}=-i\hat{\boldsymbol{\xi}}_E\omega)]^n\\ =&\int\frac{d\omega}{2\pi}e^{i\omega N}\left[i\omega+u-\frac{1}{6}\xi_E^2\right.\\ &\left.-\frac{v^2}{2\hat{\xi}_E\gamma_E}\ln\frac{\omega-i\hat{\xi}_E\gamma_E}{\omega+i\hat{\xi}_E\gamma_E}\right]^{-1}\end{aligned} \tag{47}$$

where

$$\hat{\xi}_E=\frac{E\mu_c}{ak_BT}, \quad \hat{\xi}_E=|\hat{\boldsymbol{\xi}}_E|, \quad \gamma_E=\frac{a\mu_h}{b\mu_c} \tag{48}$$

Equation 47 agrees with eq 12 if the parameters $\hat{\xi}_E$ and γ_E are replaced by $\hat{\xi}$ and γ. Therefore the present method of calculation can be directly applied to the case under consideration.

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