FOLDING IN TWO-DIMENSIONAL OFF-LATTICE MODELS OF PROTEINS

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Model off-lattice sequences in two dimensions are constructed so that their native states are close to an on-lattice target. The Hamiltonian involves the Lennard-Jones and harmonic interactions. The native states of these sequences are determined with a high degree of certainty through Monte Carlo processes. The sequences are characterized thermodynamically and kinetically. It is shown that the rank-ordering-based scheme of the assignment of contact energies typically fails in off-lattice models even though it generates high stability of on-lattice sequences. Similar to the on-lattice case, Go-like modeling, in which the interaction potentials are restricted to the native contacts in a target shape, gives rise to good folding properties. Involving other contacts deteriorates these properties.

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I. INTRODUCTION

Understanding of the folding process of proteins is one of the current challenges in molecular biophysics. Many insights into the nature of folding have been provided by studying lattice models in which a protein is represented by a chain of beads on a hypercubic lattice (see for instance ref. [1]). A more realistic modeling of proteins, however, requires considering off-lattice systems. Simple off-lattice systems have been discussed recently by Irback et al. [2] and Klimov and Thirumalai [3]. The former authors have studied a model with two kinds of residues and they have found that very few such sequences give rise to a rapid folding.

In this paper we focus on ways to design off-lattice sequences that form good folders. Specifically, we consider a two-dimensional (2D) target shape and assign two models of interaction energies between the beads. The first model is a generalization of the Go-like approach [4] to off-lattice situations. The second model, on the other hand, is a generalization of the rank-ordering-based assignment of the couplings [5,6]. When the beads are constrained to be located on sites of a lattice, both models provide sequences which are good folders. Here, we demonstrate that this may not be true for off-lattice models. Namely, an extended character of the interactions, that is necessarily present in off-lattice Hamiltonians, gives rise to differing levels of frustration in the two models and leaves only the Go-like sequences as good folders. This is compatible with the principle of minimum frustration proposed by Bryngelson and Wolynes [7].

We formulate our models in the context of the Hamiltonian used by Iori, Marinari, and Parisi [8] (IMP) in which monomers interact via the Lennard-Jones potential. The amplitudes of the attractive part between beads $i$ and $j$ of this potential, $A_{ij}$, representing a residue-dependent interaction, are quenched random variables. Additionally, the monomers are tethered sequentially along the chain by means of harmonic interactions. IMP and Struglia [9] have demonstrated the existence of a compact phase in a 3D version of the model. In these studies the dynamics have been defined in terms of a Monte Carlo process. The true ground state - the native state - however, typically is not known (as in IMP) or there is a substantial degree of uncertainty whether the state assumed to be native is indeed the ground state (as in the paper by Struglia [9]).

Studies of the dynamics of folding require knowing the precise shape of the native state conformation without which the folding time cannot be defined. For small scale lattice models, the ground state may be obtained by an exact enumeration of conformations. This method, however, does not apply to off-lattice models. Here we present 2D Lennard-Jones sequences of 16 monomers in which the ground state is known accurately and with a high degree of certainty. We then provide some basic characterization of these sequences, obtained through the Monte Carlo procedure.

The construction of the model sequences is presented in Sec. II. We consider the lattice target shown in Fig. 1(a). In order to generate a Go-like sequence, $G$, we assign the $A_{ij}$ of the Lennard-Jones potential to be uniform in the native contacts
and zero in the non-native contacts, i.e., all pairs of monomers that do not form contacts in the native state interact only through a short-range repulsion. The second model sequence, $R'$, is constructed by generating Gaussian $A_{ij}$ and adopting the rank-ordering scheme introduced recently in the context of lattice models. Sequence $R'$ is an off-lattice analog of the sequence $R$ discussed in Refs. [5,6]. The principle here is to allocate the most strongly attractive $A_{ij}$ to those pairs of monomers which form contacts in the target compact lattice conformation. The true ground state of the sequence will necessarily be off-lattice but its shape will be close to the lattice target – it can be viewed as a somewhat distorted lattice target conformation.

In Sec. III we describe the procedure adopted to determine the ground state. Basically, we form self-avoiding walks (SAW) in continuum space around all of the 69 maximally compact lattice conformations as the starting configuration of the sequence. We shall denote such starting SAW as CSAW to emphasize closeness to compact structures. We then perform Monte Carlo quenches to reach local energy minima. The rank-ordered allocation of the couplings ensures that the lowest energy minima will be compact. For sequence $R'$ we have shown that the lowest energy state is obtained from CSAW's which are near the target structure. We demonstrate that the use of arbitrary SAW's, i.e., which are not CSAW's, leads to local minima of higher energies. For sequence $G$ both the SAW's and CSAW's starting configurations easily lead to the native state which has the target compact shape. Our conclusion is that it is easier to find the native state for a good folder ($G$) compared to a bad folder ($R'$). We have found also that only sufficiently large values of the spring constant $k$ may guarantee the self-avoidance properties of the chain.

We characterize geometries of conformations in terms of a certain distance away from a reference conformation. In Sec. IV we determine the probability to stay in the basin and the folding temperature. Both quantities are calculated by adopting a well defined characteristic basin size as obtained by the shape distortion approach [10]. In Sec. V we present results on the specific heat and structural susceptibility for $R'$ and $G$ and demonstrate that $G$ is a good folder whereas $R'$ is a bad folder. The bad folding properties of $R'$ are in sharp contrast to what was found for the lattice sequence $R$ [3,4] and are due to the presence of many long-ranged couplings which impose conflicting constraints. Sequence $G$ is a good folder because there are many fewer constraints to satisfy.

II. MODELS OF INTERACTIONS

Following IMP [8], we consider a self-interacting heteropolymer in 2D described by the Hamiltonian given by

$$H = \sum_{i \neq j} \left( k(d_{i,j} - d_0)^2 \delta_{i,j} + 4\left( \frac{C}{d_{i,j}^2} - \frac{A_{ij}}{d_{i,j}^2} \right) \right),$$

where $i$ and $j$ range from 1 to the number of beads, $N$, which in our model is equal to 16. The distance between the beads, $d_{i,j}$, is defined as $|\vec{r}_i - \vec{r}_j|$, where $\vec{r}_i$ denotes the position of bead $i$. The harmonic term in the Hamiltonian with the spring constant $k$, couples the adjacent beads along the chain. The remaining terms represent the Lennard-Jones potential. In [8] $A_{ij}$ is chosen as $A_{ij} = A_0 + \sqrt{C} \eta_{ij}$, where $A_0$ is constant and $\eta_{ij}$'s are Gaussian variables with zero mean and unit variance; $\epsilon$ controls the strength of the quenched disorder. The case of $\eta_{ij} = 0$ and $A_0 = C$ would correspond to a homopolymer with the standard Lennard-Jones interaction used in simulations of liquids. We adopt the units in which $C=1$ and consider $k$ to be either equal to 1 or to 25. We have found that the first choice, which has been used by IMP [8], may lead to local energy minima in which the polymer is self-intersecting.

For $N=16$, there are 120 Lennard-Jones possible couplings between the monomers. The basic choice for the values of $A_{ij}$ that we shall use here is shown in the diagrams.

FIG. 1. (a) Assignment of nine strongest couplings $A_{ij}$ to native contacts for sequence $R'$. The numbers indicate the relative strengths of the contacts. (b) The native conformation of sequence $R'$.

![Diagram](image-url)
in Table I. Here, all of the $A_{ij}$’s are positive, which corresponds to attraction. Table 1 also indicates a rank of a given attractive coupling if these are ranked ordered from the strongest to the weakest attraction. In nine of the couplings, the attraction is enhanced by making the corresponding $A_{ij}$ bigger than one. These were chosen to coincide with the contacts present in the lattice target $R'$ shown in Fig. 1(a). The strongest attraction was assigned to be between beads 1 and 12 and the relative strengths of other native attractions are indicated in the figure. The remaining 111 couplings are assigned $A_{ij}$ with values which are smaller than 1. Overall the mean value $A_0$ is equal to 0.784 and the dispersion to 0.205.

The parameter $d_0$ corresponding to the equilibrium distance in the harmonic potential is chosen to be equal to 1.16, which is close to the equilibrium position of the average Lennard-Jones potential, $(2C/A_0)^{1/6}$. The target lattice shapes are built on a lattice with this lattice constant. For the Go-like sequence (G) we set $A_{ij} = 1$ for native contact and 0 for non-native ones. For this sequence we choose $d_0 = 2^{1/6}$. The qualitative results do not depend, however, on the choice of $d_0$.

### III. LOCAL MINIMA AND NATIVE STATES

In order to find spectra of the local energy minima we use the Monte Carlo procedure with local updating moves. Monomers are moved randomly within a circle (the radius of circle varies from 0.0025$d_0$ to 0.01$d_0$) away from their previous positions. Random quenching by starting from a SAW or a CSAW typically yields a local energy minimum within order 2$^{18}$ steps. In the minimum, the force acting on any of the monomers is at most of order $10^{-7}$ in units of the characteristic coupling (of order 1) divided by $(2C/A_0)^{1/6}$. Simulated annealing runs of comparable number of steps yielded similar results. The results reported on in this paper are based on the quenching procedure.

The starting conformations were obtained by placing monomers within a circle of radius 0.3$d_0$ away from a SAW generated on the lattice or away from a maximally compact conformation on the lattice – CSAW. For each of the 69 maximally conformations, 50 CSAW’s were generated and the results were compared with those obtained based on 500 SAW’s.

We observe that there is a substantial gap, of order 4, between the minima obtained from CSAW’s around the target and those obtained from all other starting configurations.

As to the choice of the elastic constant $k$ we have found that $k=1$ is not very physical because the distances between consecutive monomers are not kept sufficiently rigid. Furthermore, we have observed that in states which are not local energy minima, the polymer conformations may become self-intersecting. This phenomenon was also observed in Ref. [11] for shorter chains. Thus a stronger $k$ is needed and we focus on $k=25$.

The energy histograms for the $R'$ and $G$ sequences for $k=25$ are shown in Figs. 2 and 3, respectively. In the case of $R'$, the SAW configurations happen to yield results comparable to the CSAW configurations, but the statistical frequency of success in finding a low energy state favors the CSAW-based approach. The maximal distance between monomers does not exceed $d_0$ by more than 4% in any local energy minimum, which demonstrates very good self-avoiding properties.

In the case of sequence $G$, about 25% of CSAW’s trajectories and 12% of SAW’s trajectories lead to the native conformation. Thus it is easier to find the native state for $G$ than for $R'$.
The native state conformation of sequence $R'$ is shown in Fig 1(b). The $x-y$ coordinates of the beads of this conformation are listed in Table II. They are used in the studies of kinetics and thermodynamics properties. The native state of sequence $G$ has exactly the lattice shape as shown in Fig. 1(a) because it is only the native contact energies here that one needs to minimize.

As we shall show later, several tasks, like the determination of the folding temperature, are facilitated by introducing a notion of a geometrical distance between two conformations. A convenient definition of the distance $\delta_{ab}$ between two conformations $a$ and $b$ is provided by

$$\delta_{ab}^2 = \min \frac{1}{N} \sum_{i=1}^{N} |\mathbf{r}_i^a - \mathbf{r}_i^b|^2,$$

where $\mathbf{r}_i^{a,b}$ denotes the position of monomer $i$ in conformation $a(b)$. The minimization is performed over translations, rotations and reflections. In practice, we put chain $a$ over chain $b$ by overlapping the two centers of mass, and then we find the optimal rotation of $b$ which minimizes $\delta_{ab}$. We pick the optimal angle from 1000 discrete values into which the $360^\circ$ angle may be divided.

The distances between the native conformations and their lattice counter parts, as in Fig. 1, are found to be equal to 0.296 and $\approx 0$ for sequence $R'$ and $G$ respectively.

**IV. THE FOLDING TEMPERATURE**

We now proceed to the equilibrium characterization of the sequences introduced in this paper. The parameter that plays a primary role in determining the folding characteristics is the folding temperature $T_f$. In the case of lattice models, $T_f$ may be defined [8] as the temperature at which the probability of occupying the native state becomes equal to $\frac{1}{2}$. For the off-lattice model, however, the native state has, strictly speaking, zero measure and one should deal with the probability of occupying the native valley.

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One may define the folding temperature $T_f$ through the following procedure. Suppose that $\delta$ is the distance to the native state and $P(\delta)$ is the probability for a conformation to be in this distance away from the native state. Thus the probability to find the system in the immediate vicinity of the native state is given by

$$P_0 = \int_0^{\delta_c} P(\delta) \, d\delta,$$
where $\delta_c$ is a cutoff distance. The folding temperature $T_f$ is then defined as the temperature at which $P_0 = 1/2$.

The size of the native basin $\delta_c$ was estimated by the shape distortion approach [10]. In this approach one starts from the native state and performs random displacements of individual beads in the chain, through a Monte Carlo routine. The distance to the native state is calculated by using Eq. (2) and the results are averaged over many Monte Carlo trajectories. Below some critical temperature which may be interpreted as a folding temperature $T_f$, the distance to the native state gets saturated at sufficiently long time scales. The saturation value of this distance at the critical temperature can serve as the size of the native basin $\delta_c$. It is found that $\delta_c \approx 0.2$ and $\delta_c \approx 0.09$ for $G$ and $R'$, respectively [10]. The corresponding values of the folding temperatures obtained in this way are equal to $T_f \approx 0.19$ and $T_f \approx 0.09$ for $G$ and $R'$ [10].

![FIG. 5. The probability distribution function $P(\delta)$ to find a state which is in distance $\delta$ away from the native state for sequence $R'$. The values of $T$ are indicated next to the curves.](image)

Figure 5 shows the distribution $P(\delta)$ at different temperatures for sequence $R'$. As the temperature increases the maximum becomes wider and moves toward larger distances to the native state $\delta$.

We now turn to the temperature dependence of the folding time, $t_{fold}$. At high temperatures, reaching the native state takes long due to entropic effects. At low temperatures, on the other hand, glassy phenomena may set in and make the folding process extremely slow. Thus $t_{fold}$ plotted against $T$ typically shows a minimum at a certain temperature $T_{min}$. The idea of the existence of the glassy phase in proteins has originated in the Bryngelson and Wolynes studies of the random energy model [7,12] and was subsequently tested in numerical simulations of lattice models by Socci and Onuchic [13]. Notice that $T_f$ is a characteristic temperature that relates to equilibrium whereas $T_{min}$ is a characteristic temperature that relates to dynamical properties. Even though at $T = T_{min}$ folding is the fastest this temperature also marks the onset of the glassy effects because they become stronger and stronger on departing from $T_{min}$ towards lower temperatures. Thus if $T_f$ is significantly less than $T_{min}$ a sequences is bad folder. If $T_f$ is comparable to $T_{min}$, or preferably larger than $T_{min}$, then the sequence is a good folder [13]. It should be noted that as a characteristic temperature that relates to dynamics one often uses the glass transition temperature $T_g$ [13]. $T_g$ is, however, depends on a cutoff value of the time used in calculations. Our preference here is to use $T_{min}$, instead of $T_g$, not only because its definition is unique and independent of the value of the cutoff but also because the two quantities contain the same the physics: good folders are sequences in which glassy effect are not important around the folding temperature.

In order to obtain $t_{fold}$ we start from random configurations and evolve them through the Monte Carlo process until the native state is reached. $t_{fold}$ is defined as the median number of MC steps after which the system reaches the basin of the native state for the first time. The cutoff value of MC steps is taken to be 20 millions. The number of starting configurations varies from 20 to 40 depending on $T$. Our results are presented in Fig. 6 for sequence $R'$ and $G$. We have $T_{min} = 0.4 \pm 0.1$ and $T_{min} = 0.15 \pm 0.05$ for $R'$ and $G$ respectively. Since $T_f = 0.12$ and $T_f = 0.23$ for these sequences one can see that $R'$ is bad folder whereas $G$ is a good one.
We emphasize that on-lattice Go and rank-ordering schemes lead to comparable ratios of $T_f/T_{\text{min}}$.

We now proceed to a further characterization of the sequences by considering the thermodynamic quantities such as the specific heat, $C$, and the structural susceptibility, $\chi$. It has been suggested that a small temperature difference between the maximum in $C$ and the maximum in $\chi$ when plotted against $T$ indicates good folding properties. Thus studies of these two quantities may serve as a substitute for the information about the kinetics of folding.

In the case of an off-lattice model the departures of the sequence geometry from its native conformation may be described through the structural overlap function as:

$$
\chi_s = 1 - \frac{1}{N^2 - 3N + 1} \sum_{i \neq j, j \neq 1} \Theta(\delta_c - |r_{ij} - r_{ij}^N|),
$$

where $r_{ij}$ is the distance between the beads $i$ and $j$ for a given conformation, $r_{ij}^N$ is the corresponding distance in the native conformation, and $\Theta(x)$ is the Heavyside function. Here $\delta_c$ denotes the size of basin as defined above in the previous Section. If $|r_{ij} - r_{ij}^N| \leq \delta_c$ the beads $i$ and $j$ are assumed to form a contact within the native valley. The susceptibility-like parameter $\chi$ is defined as the thermal fluctuation of $\chi_s$:

$$
\chi(T) = \langle \chi_s^2(T) \rangle - \langle \chi_s(T) \rangle^2,
$$

where the angular brackets indicate a thermodynamic average.

The specific heat is defined in the usual way, i.e. by the energy fluctuations:

$$
C = \frac{\langle E^2 \rangle - \langle E \rangle^2}{T^2}.
$$

A peak in $C$ may be interpreted as corresponding to the onset of slow kinetics and the peak in $\chi$ as corresponding to the folding temperature.
We calculate the thermodynamic quantities using the native state as the starting configurations. The results are averaged over many MC trajectories. The equilibration is checked by monitoring the stability of the data against at least three-times longer runs. We have used $5 \times 10^6$ MC steps as in the studies of $\mathcal{P}_0$ (the first $2.5 \times 10^6$ steps are not taken into account when averaging). This number of MCS appears to be enough to equilibrate the system in the temperature interval we use. We have also found that it is harder to reach the equilibrium using SA W's as starting configurations.

The temperature dependence of $\chi$ and $C$ for sequence $G$ and $R'$ is shown in Fig. 7. The peak in $\chi$ almost coincides with $T_f$. For $G$ maxima of $\chi$ and $C$ are located at the same position suggesting that sequence $G$ is a good folder [14]. This results agrees with that obtained in the previous section by studying kinetics of folding.

For sequence $R'$, the peak in $C$ is found to be broad and it is located at a substantially higher $T$ than the peak in $\chi$ confirming bad folding properties of $R'$. So studies of thermodynamics properties and folding kinetics lead to the same conclusion about folding in our model.

VI. CONCLUSIONS

In this work, we have constructed and studied two off-lattice Lennard-Jones models in two dimensions. The long-range nature of interactions between amino-acids in off-lattice models may lead to too much frustration, as in the case of sequence $R'$, and thus to bad foldicities. Restricting the number of interactions only to the native contacts, as in sequence $G$, may reduce the frustration and bring about good folding properties. We have demonstrated this by studying both thermodynamic and dynamical properties of the two sequences. The values of the folding temperature found from the probability to get out from the native state roughly agree with those obtained by the shape distortion approach. We have studied the kinetic of folding with a simplified MC dynamics whereas previous works have been focused on equilibrium aspects. Similar to the on-lattice models, both approaches give the same information about folding properties.

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| i  | j  | $A_{ij}$ | rank | i  | j  | $A_{ij}$ | rank | i  | j  | $A_{ij}$ | rank | i  | j  | $A_{ij}$ | rank |
|----|----|---------|------|----|----|---------|------|----|----|---------|------|----|----|---------|------|
| 1  | 2  | 0.945354 | 19   | 3  | 5  | 0.581629 | 117  | 1  | 12 | 0.667698 | 79   | 5  | 15 | 0.758490 | 57   |
| 1  | 3  | 0.858677 | 37   | 3  | 6  | 0.598687 | 101  | 5  | 13 | 0.740622 | 62   | 8  | 16 | 0.718888 | 69   |
| 1  | 4  | 0.810776 | 47   | 3  | 7  | 0.513536 | 118  | 5  | 14 | 0.661444 | 83   | 9  | 10 | 0.913366 | 28   |
| 1  | 5  | 0.949365 | 17   | 3  | 8  | 0.781319 | 50   | 5  | 15 | 0.861819 | 36   | 9  | 11 | 0.741376 | 61   |
| 1  | 6  | 0.514208 | 117  | 3  | 9  | 0.746676 | 59   | 5  | 16 | 0.744776 | 60   | 9  | 12 | 0.664109 | 82   |
| 1  | 7  | 0.644279 | 91   | 3  | 10 | 0.666580 | 80   | 6  | 7  | 0.767029 | 54   | 9  | 13 | 0.968419 | 11   |
| 1  | 8  | 1.337928 | 5    | 3  | 11 | 0.835338 | 41   | 6  | 8  | 0.638391 | 93   | 9  | 14 | 0.822724 | 45   |
| 1  | 9  | 0.725085 | 65   | 3  | 12 | 0.729243 | 67   | 6  | 9  | 1.375767 | 4    | 9  | 15 | 0.969623 | 10   |
| 1  | 10 | 0.802427 | 48   | 3  | 13 | 0.518711 | 116  | 6  | 10 | 0.676479 | 76   | 9  | 16 | 0.850939 | 39   |
| 1  | 11 | 0.763514 | 55   | 3  | 14 | 0.660732 | 85   | 6  | 11 | 0.567934 | 109  | 10 | 11 | 0.935812 | 22   |
| 1  | 12 | 1.498411 | 1    | 3  | 15 | 0.852925 | 38   | 6  | 12 | 0.571524 | 108  | 10 | 12 | 0.951547 | 16   |
| 1  | 13 | 0.899355 | 30   | 3  | 16 | 1.050544 | 9    | 6  | 13 | 0.658820 | 86   | 10 | 13 | 0.521468 | 114  |
| 1  | 14 | 1.396376 | 3    | 4  | 5  | 0.878341 | 33   | 6  | 14 | 0.512926 | 119  | 10 | 14 | 0.930277 | 25   |
| 1  | 15 | 0.723510 | 66   | 4  | 6  | 0.763190 | 56   | 6  | 15 | 0.612393 | 99   | 10 | 15 | 0.889378 | 31   |
| 1  | 16 | 0.655780 | 87   | 4  | 7  | 1.269149 | 8    | 6  | 16 | 0.628334 | 95   | 10 | 16 | 0.590144 | 104  |
| 2  | 3  | 0.720592 | 68   | 4  | 8  | 0.577229 | 106  | 7  | 8  | 0.670401 | 78   | 11 | 12 | 0.932459 | 23   |
| 2  | 4  | 0.541154 | 112  | 4  | 9  | 0.614099 | 96   | 7  | 9  | 0.647826 | 89   | 11 | 13 | 0.528390 | 113  |
| 2  | 5  | 0.770339 | 53   | 4  | 10 | 0.918839 | 27   | 7  | 10 | 0.642560 | 92   | 11 | 14 | 0.921718 | 26   |
| 2  | 6  | 0.938498 | 21   | 4  | 11 | 0.597736 | 102  | 7  | 11 | 0.965115 | 12   | 11 | 15 | 0.770826 | 52   |
| 2  | 7  | 1.291634 | 7    | 4  | 12 | 0.571611 | 107  | 7  | 12 | 0.834125 | 42   | 11 | 16 | 0.955652 | 14   |
| 2  | 8  | 0.696944 | 72   | 4  | 13 | 0.561490 | 110  | 7  | 13 | 0.753585 | 58   | 12 | 13 | 0.629158 | 94   |
| 2  | 9  | 0.603317 | 100  | 4  | 14 | 0.725428 | 64   | 7  | 14 | 0.561397 | 111  | 12 | 14 | 0.884585 | 32   |
| 2  | 10 | 0.832387 | 43   | 4  | 15 | 0.954825 | 15   | 7  | 15 | 0.712665 | 70   | 12 | 15 | 0.949139 | 18   |
| 2  | 11 | 0.672241 | 77   | 4  | 16 | 0.514903 | 120  | 7  | 16 | 0.864981 | 35   | 12 | 16 | 0.932023 | 24   |
| 2  | 12 | 0.821738 | 46   | 5  | 6  | 0.687186 | 74   | 8  | 9  | 0.943903 | 20   | 13 | 14 | 0.848886 | 40   |
| 2  | 13 | 0.644946 | 90   | 5  | 7  | 0.660546 | 81   | 8  | 10 | 0.660797 | 84   | 13 | 15 | 0.613872 | 97   |
| 2  | 14 | 0.689698 | 73   | 5  | 8  | 0.686304 | 75   | 8  | 11 | 1.301709 | 6    | 13 | 16 | 0.734204 | 63   |
| 2  | 15 | 1.409250 | 2    | 5  | 9  | 0.771102 | 51   | 8  | 12 | 0.903389 | 29   | 14 | 15 | 0.519439 | 115  |
| 2  | 16 | 0.655129 | 88   | 5  | 10 | 0.595747 | 103  | 8  | 13 | 0.612414 | 98   | 14 | 16 | 0.963250 | 13   |
| 3  | 4  | 0.781090 | 49   | 5  | 11 | 0.707574 | 71   | 8  | 14 | 0.825123 | 44   | 15 | 16 | 0.866528 | 34   |

**TABLE I.** Values of the $A_{ij}$ for sequence $R'$. The rank of a coupling is indicated to the right of its value.
| monomer | $x_N$  | $y_N$  | monomer | $x_N$  | $y_N$  |
|---------|--------|--------|---------|--------|--------|
| 1       | 0.0000 | 0.0000 | 9       | -0.037572 | 2.225111 |
| 2       | 1.005509 | 0.573347 | 10      | -1.073118 | 2.718455 |
| 3       | 2.091357 | 0.126744 | 11      | -0.992672 | 1.573907 |
| 4       | 2.009697 | 1.279681 | 12      | -0.956188 | 0.436143 |
| 5       | 1.946778 | 2.424499 | 13      | -0.972265 | -0.723659 |
| 6       | 0.845883 | 2.806329 | 14      | 0.116648 | -1.062284 |
| 7       | 0.997773 | 1.647486 | 15      | 1.123476 | -0.470181 |
| 8       | -0.035144 | 1.079819 | 16      | 2.154153 | -0.984088 |

TABLE II. The $x - y$ coordinates of the native conformation for $R'$ and $k = 25.$