We introduce a quantity, the entropic susceptibility, that measures the thermodynamic importance—for the folding transition—of the contacts between amino acids in model proteins. Using this quantity, we find that only one equilibrium run of a computer simulation of a model protein is sufficient to select a subset of contacts that give rise to the peak in the specific heat observed at the folding transition. To illustrate the method, we identify thermodynamically important contacts in a model 46-mer. We show that only about 50% of all contacts present in the protein native state are responsible for the sharp peak in the specific heat at the folding transition temperature, while the remaining 50% of contacts do not affect the specific heat.

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Proteins are heteropolymers, composed of 20 types of amino acids, that perform specific functions. The amino acid composition of proteins determines their unique structure, function, and folding kinetics. Understanding the relevance of the interactions between amino acids to protein folding is a complex task that has been the subject of a number of theoretical and experimental studies [1–13]. The transition from the unfolded to the folded state of a protein is accompanied by a drastic reduction of the entropy. In one popular scenario, the folding transition for short proteins is analogous to a separation of all contacts in two distinct sets with large and small values of $e_{ij}$, which indicates that there is a separation of all contacts in two distinct sets with large and small values of $e_{ij}$. The two minima are separated by a free-energy barrier corresponding to the transition states.

At the folding transition temperature $T_f$, there is an abrupt change in the energy of the system resulting in a pronounced peak in the specific heat. At $T_f$, a small increase in interaction energy $e_{ij}$ between amino acids $i$ and $j$ “contact strength” results in rapid transition to the folding state, while a small decrease in contact strength results in transition to the unfolded state. Temperature is measured in units of $k_B T$ [10]. However, different amino acids have a different contribution to the folding transition. Small variation in $e_{ij}$ for different pairs $i$ and $j$ has a different effect on the folding transition. Here, we study the thermodynamic importance of each interaction during folding by computing the entropic susceptibility—the response function to a small perturbation of $e_{ij}$.

We assume that the protein potential energy is additive in the pair potentials (contacts)

$$ U = \frac{1}{2} \sum_{i,j} U_{ij} = \frac{1}{2} \sum_{i,j} e_{ij} \phi(\vec{r}_i, \vec{r}_j), $$

(1)

where $U_{ij}$ is the energy of a single pair, $\phi(\vec{r}_i, \vec{r}_j)$ models the shape of the potential and protein at positions $\vec{r}_i$ and $\vec{r}_j$. We define the entropic susceptibility $\chi_{ij}$ of a contact between amino acids $i$ and $j$ as

$$ \chi_{ij} = \frac{\delta S}{\delta e_{ij}} = \beta^2 \left( \langle U \rangle_{ij} - \langle U \rangle \right) = \beta^2 \langle \delta U \delta U_{ij} \rangle, $$

(2)

where $\delta U = U - \langle U \rangle$, $\delta U_{ij} = U_{ij} - \langle U_{ij} \rangle$, and $\langle \ldots \rangle$ is the Boltzmann average, $\beta = 1/T$ [14].

The entropic susceptibility measures the effect of a contact strength perturbation on the folding transition of the protein, thus identifying the thermodynamic relevance of such contact for the folding transition. Next, we demonstrate how this measure can be used to study contributions of the various contacts between amino acids in the protein for the folding transition. We simulate the “beads on a string” protein model [12], where the amino acids are hard spheres of unit mass, with the centers at the positions of the corresponding $\alpha$ carbons. The potentials of interaction between amino acids are square wells of depth $e_{ij}$. We study the 46-mer (the folding transition temperature is at $T_f \approx 1.44$) that has been examined in [12]. We use Go model for the contact potential, $U_{ij}$: $U_{ij}$ is attractive ($e_{ij} = -1$) if the contact exists in the native (ground) state, otherwise the contact potential is repulsive ($e_{ij} = +1$) [15,16]. Our simulations employ the discrete molecular dynamics (MD) algorithm and are performed using methods described in [10,12,17]. The matrix of native contacts of the 46-mer is shown in Fig. 1. This particular 46-mer is known to have a stable native state and to undergo first-order-like folding = unfolding transitions without stable intermediates [12].

We calculate $\chi_{ij}$ at different temperatures below and above $T_f$. A histogram of the values of $\chi_{ij}$ for various $T$ is shown in Fig. 2. For $T \approx T_f$ the distribution has a pronounced peak at large values of $\chi_{ij}$, which indicates that there is a separation of all contacts in two distinct sets with large and small values of $\chi_{ij}$. The set of contacts with large values of $\chi_{ij}$ are “thermodynamically important contacts,” since for these contacts a small variation in their strength is correlated with a drastic change in the entropy of the model protein. To select the thermodynamically important contacts, we define a...
In the upper part of Fig. 3, we show only the values of threshold, the filtered map of Fig. 3 shows that they are our definition, corresponds to the thermodynamically important contacts. Although 50% of the contacts are above clustered together and are among well-defined regions of the model protein. Further, we find that the regions of temperature-dependent threshold \( x_{th}(T) \) corresponding to the value of \( \chi_{ij} \) where the distribution has a maximum in the space of all contacts.

Interestingly, thermodynamically important contacts are not randomly distributed in 3d space but are rather concentrated within well-defined structural regions in a model protein. Figure 3 represents the intensity map of the values not randomly distributed in 3d space but are rather concentrated within well-defined structural regions in a model protein. Further, we find that the regions of thermodynamically important interactions \([\chi_{ij}(T) > \chi_{th}(T)]\) in the filtered map remain qualitatively the same as the ones shown in Fig. 3 for temperatures in the range \( T = T_f \pm 5\% \).

To verify that the thermodynamically important contacts are indeed thermodynamically the most relevant to the folding of our 46-mer, we measure the contribution of thermodynamically important contacts to the specific heat

\[
C_V = \frac{1}{2} \sum_{ij} \chi_{ij}.
\]

Thus, we can interpret \( \chi_{ij} \) as the contribution to \( C_V \) of a single contact. It is then possible to partition \( C_V \) as

\[
C_V = C_V^{\text{TIC}} + C_V^{\text{others}},
\]

where \( C_V^{\text{TIC}} \) arises from the thermodynamically important contacts, and \( C_V^{\text{others}} \) from contacts below the threshold \( \chi_{th}(T) \). Figure 4 shows that the thermodynamically important contacts give a sharp contribution to the specific heat around \( T_f \). We find the number of contacts above threshold \( \chi_{th}(T_f) \) is about 50% of the number of contacts in the native state, in agreement with Flory-type arguments [10].

It is natural to inquire whether the thermodynamically important contacts could be determined by analyzing the average contact energies \( \langle U_{ij} \rangle \), which are related to the contact frequency map [11]. For square well potentials, \( \langle U_{ij} \rangle = \epsilon_{ij} f_{ij} \) where \( f_{ij} \) is the contact frequency for amino acids \( i \) and \( j \). We find that the contacts with the largest values of \( f_{ij} \).
Thus, the information about the thermodynamically important contacts can be inferred from the temperature with frequency above 0.5 at most stable elements of the protein three-dimensional structure that remains intact at folding transition temperature. Specifically, they were defined as contacts that are present in the unfolded state at 0.5 of model proteins. The computational effort can be directed to aid experimental studies of real proteins. We thank F. Sciortino, E. I. Shakhnovich, and M. Vendruscolo for very useful discussions. N.V.D. is supported by NIH. The Center for Polymer Studies acknowledges the support of the NSF.

[14] In general, the potential energy can take the form
\[ U = \sum_{i} \sum_{i_1, \ldots, i_n} U^{(n)}_{i_1, \ldots, i_n} \]
where \( U^{(n)}_{i_1, \ldots, i_n} \) is the \( n \)-body interaction between amino acids \( i_1, \ldots, i_n \). The resulting expression for the entropic susceptibility is defined then as
\[ \chi^{(n)}_{i_1, \ldots, i_n} = \beta^2 \langle \delta U / \delta U^{(n)}_{i_1, \ldots, i_n} \rangle. \]
[15] The repulsive potential is necessary to ensure the existence of a nondegenerate ground (folded) state.