

## Supporting Information

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#### SI Text

#### Derivation of Energy, Entropy, and Free Energy Functions.

The partition function at a fixed  $(x, y)$  is obtained by

$$Z(x, y) = \nu^{N-x-y} \sum_{\text{conf} \in \{(x, y)\}} \exp(-\beta H), \quad [1]$$

where  $\sum_{\text{conf} \in \{(x, y)\}}$  is summation of conformations under the constraint of  $(x, y)$ ,  $H$  is

Hamiltonian,  $\beta = 1/k_B T$  is the inverse of temperature  $T$ ,  $N$  is the total number of residues, and  $\nu$  is the number of nonnative configurations each residue can take. The order parameters of the native-likeness,  $x$  and  $y$ , are numbers of residues which take the native-like configuration in domain I and domain II, respectively.  $Z(x, y)$  can be rewritten as

$$\begin{aligned} Z(x, y) &= \nu^{N-x-y} \sum_{\text{conf} \in \{(x, y)\}} 1 \bigg/ \left( \nu^{N-x-y} \sum_{\text{conf} \in \{(x, y)\}} 1 \bigg/ Z(x, y) \right) \\ &= \frac{1}{\langle \exp(\beta H) \rangle_{x, y}} \cdot \nu^{N-x-y} \sum_{\text{conf} \in \{(x, y)\}} 1, \end{aligned} \quad [2]$$

where  $\langle \dots \rangle_{x, y}$  is the average taken by using  $Z(x, y)$ .

The free energy at a fixed  $(x, y)$  is

$$\begin{aligned} F(x, y) &= -k_B T \ln Z(x, y) \\ &= k_B T \ln \langle \exp(\beta H) \rangle_{x, y} - T k_B \ln \left[ \nu^{N-x-y} \sum_{\text{conf} \in \{(x, y)\}} 1 \right] \\ &= \langle H \rangle_{x, y} + T k_B \ln \langle \exp[\beta(H - \langle H \rangle_{x, y})] \rangle_{x, y} - T k_B \ln \left[ \nu^{N-x-y} \binom{n_I}{x} \binom{n_{II}}{y} \right]. \end{aligned} \quad [3]$$

Here,  $\sum_{\text{conf} \in \{(x,y)\}} 1 = \sum_{\mu_I(x)} 1 \sum_{\mu_{II}(y)} 1$  with  $\mu_I(x) = \{m_k \mid \sum_{k=1}^{n_I} m_k = x \ (1 \leq k \leq n_I)\}$  and

$\mu_{II}(y) = \{m_k \mid \sum_{k=n_I+1}^N m_k = y \ (n_I+1 \leq k \leq N)\}$  ( $m_k = 0,1$ ), and thus  $\sum_{\mu_I(x)} 1 = \binom{n_I}{x}$  and

$\sum_{\mu_{II}(y)} 1 = \binom{n_{II}}{y}$ , where  $n_I$  and  $n_{II}$  are numbers of residues in the N-terminal domain (domain

I) and the C-terminal domain (domain II), respectively,  $n_I + n_{II} = N$ .

The free energy function can be decomposed into energy and three entropy terms as

$$F(x, y) = E(x, y) - T[S_e(x, y) + S_c(x; n_I) + S_c(y; n_{II})]. \quad [4]$$

$E(x, y)$  is energy at a fixed  $(x, y)$ ,

$$E(x, y) = \langle H \rangle_{x,y} \quad [5]$$

$S_e(x, y)$  is the energy dependent entropy at a fixed  $(x, y)$ ,

$$S_e(x, y) = -k_B \ln \langle \exp[\beta(H - E(x, y))] \rangle_{x,y}. \quad [6]$$

From the inequality  $\langle e^{\beta H} \rangle_{x,y} \geq e^{\beta E(x,y)}$ , we find  $S_e(x, y) \leq 0$ .  $-TS_e(x, y)$  can be expanded as

$$-TS_e(x, y) = \sum_{n=2}^{\infty} \frac{\beta^{n-1}}{n!} \langle H^n \rangle_{x,y}^c, \quad [7]$$

where  $\langle H^n \rangle_{x,y}^c$  is the  $n$ th order cumulant of  $H$  under the constraint of  $(x, y)$ .  $-TS_e(x, y)$

decreases as temperature increases and  $-TS_e(x, y) \approx \frac{1}{2k_B T} (\langle H^2 \rangle_{x,y} - \langle H \rangle_{x,y}^2)$  at high temperature.

$S_c(x; n_I)$  and  $S_c(y; n_{II})$  express chain entropies of domain I and domain II, respectively, which arise from the total number of conformations that each domain can take under the

constraint of  $(x, y)$ , where

$$S_c(x; n) = k_B \ln \left\{ \nu^{n-x} \binom{n}{x} \right\}. \quad [8]$$

Notice that  $S_c(x; n_I)$  and  $S_c(y; n_{II})$  do not depend on the form of Hamiltonian, so that the effects of the domain-domain interactions on entropy are solely expressed in  $S_e(x, y)$ .

We decompose the Hamiltonian into the intra-domain parts,  $H_I$  and  $H_{II}$ , and the inter-domain part  $V$  as  $H = H_I + H_{II} + V$ , where  $H_I$  is a sum of terms belonging to domain I,  $H_{II}$  is a sum of terms belonging to domain II, and  $V$  is a sum of terms of interactions between a residue in domain I and a residue in domain II.

$$\begin{aligned} k_B T \ln \langle \exp(\beta H) \rangle_{x,y} &= k_B T \ln \left[ \frac{\nu^{N-x-y} \sum_{\text{conf} \in \{(x,y)\}} 1}{Z_0(x, y)} \cdot \frac{Z_0(x, y)}{Z(x, y)} \right] \\ &= k_B T \ln \langle \exp[\beta(H_I + H_{II})] \rangle_{0,x,y} + U(x, y), \end{aligned} \quad [9]$$

with  $Z_0(x, y) = \nu^{N-x-y} \sum_{\text{conf} \in \{(x,y)\}} \exp\{-\beta(H_I + H_{II})\}$ , where  $\langle \dots \rangle_{0,x,y}$  is the average taken by using  $Z_0(x, y)$ .

$$U(x, y) \equiv F(x, y) - F_0(x, y) = k_B T \ln \langle \exp(\beta V) \rangle_{x,y}, \quad [10]$$

is difference in free energy between the connected two-domain protein and the separated two non-interacting domains, where  $F_0(x, y) = -k_B T \ln Z_0(x, y)$  is the free energy function of separated domains.  $U(x, y)$  can be described as

$$\begin{aligned} U(x, y) &= \langle V \rangle_{x,y} + T k_B \ln \langle \exp[\beta(V - \langle V \rangle_{x,y})] \rangle_{x,y} \\ &= [E(x, y) - E_0(x, y)] - T[S_e(x, y) - S_{e0}(x, y)]. \end{aligned} \quad [11]$$

**The Constrained Partition Function of Wako-Saito-Muñoz-Eaton (WSME) Hamiltonian.**

The partition function at the constraint  $(x, y) = (n, m)$  is calculated from the generating function:

$$Q(\lambda, \mu) \equiv \sum_{x,y} Z(x, y) \lambda^x \mu^y, \quad [12]$$

as

$$Z(n, m) = \frac{1}{n!m!} \frac{\partial^n}{\partial \lambda^n} \frac{\partial^m}{\partial \mu^m} Q(\lambda, \mu) \Big|_{\lambda=\mu=0}. \quad [13]$$

$Q(\lambda, \mu)$  of the WSME Hamiltonian,

$$H = - \sum_{i < j} \varepsilon_{i,j} \Delta_{i,j} \prod_{k=i}^j m_k.$$

can be obtained by means of the transfer matrix method without introducing any further approximation (1,2).  $Q(\lambda, \mu)$  is expressed as

$$Q(\lambda, \mu) = P_{N-1}(1; \lambda, \mu) e^{-S_0/k_B}, \quad [14]$$

and  $P_{N-1}(1; \lambda, \mu)$  is obtained by calculating the following the recurrence equations:

$$\begin{aligned} P_0(1; \lambda, \mu) &= 1, \\ P_0(l; \lambda, \mu) &= w_{N, N-l+2}(\lambda, \mu), \quad l \neq 1, \\ P_k(1; \lambda, \mu) &= P_{k-1}(1; \lambda, \mu) + P_{k-1}(2; \lambda, \mu), \\ P_k(l; \lambda, \mu) &= w_{N-k, N-k-l+2}(\lambda, \mu) P_{k-1}(l; \lambda, \mu) + P_{k-1}(l+1; \lambda, \mu), \\ l &= 1, 2 \cdots N-k-1, \quad k = 1, 2 \cdots N-1, \end{aligned} \quad [15]$$

with

$$w_{j,i}(\lambda, \mu) = \exp \left[ \sum_{r=i}^{j-1} \sum_{s=r+1}^j \alpha_{r,s} \Delta_{r,s} + \sum_{r=i}^j \sigma_r / k_B \right] \lambda^{X(j,i)} \mu^{Y(j,i)}. \quad [16]$$

Here,  $\alpha_{r,s} = -\varepsilon_{r,s}/k_B T$ , with  $\varepsilon_{r,s}$  being the energy gain by a native contact,  $\sigma_r$  is the entropic cost for a residue to take the native configuration, and  $S_0 = \sum_r \sigma_r$ , where we give the expression for the generic case that  $\varepsilon_{r,s}$  and  $\sigma_r$  are dependent on residue types and positions, respectively, and in this paper we discuss the case of  $\varepsilon_{r,s} = \varepsilon$  and  $\sigma_r = \sigma$ .  $X(j,i)$  and  $Y(j,i)$  are defined as

$$X(j,i) = \sum_{k=i}^j \eta_{\text{I}}(k) \text{ with } \eta_{\text{I}}(k) = \begin{cases} 1 & \text{for } 1 \leq k \leq n_{\text{I}} \\ 0 & \text{otherwise} \end{cases},$$

and

$$Y(j,i) = \sum_{k=i}^j \eta_{\text{II}}(k) \text{ with } \eta_{\text{II}}(k) = \begin{cases} 1 & \text{for } n_{\text{I}} + 1 \leq k \leq N \\ 0 & \text{otherwise} \end{cases}.$$

## References

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2. Bruscolini P, Pelizzola A (2002) Exact solution of the Muñoz-Eaton model for protein folding. *Phys Rev Lett* 88:258101.