Protein Physics 2016

Lecture 5, February 2

Statistical mechanics, the partition function, and first-order phase transitions

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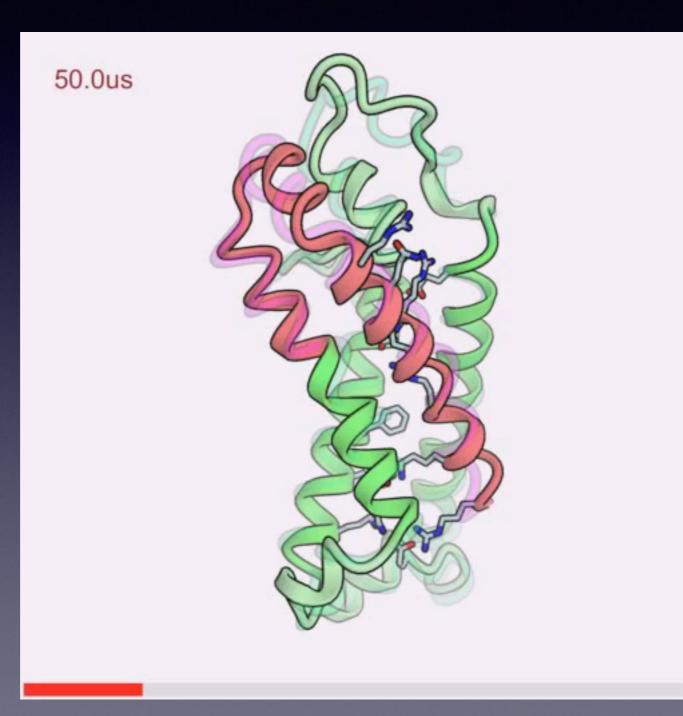




Recap

- Secondary structure & turns
 - Properties, simple stability concepts
 - Geometry/topology
- Amino acid properties, titration
- Natural selection of residues in proteins
- Free energy of hydrogen bond formation in proteins when in vacuo or aqueous solvent

titratable amino acids

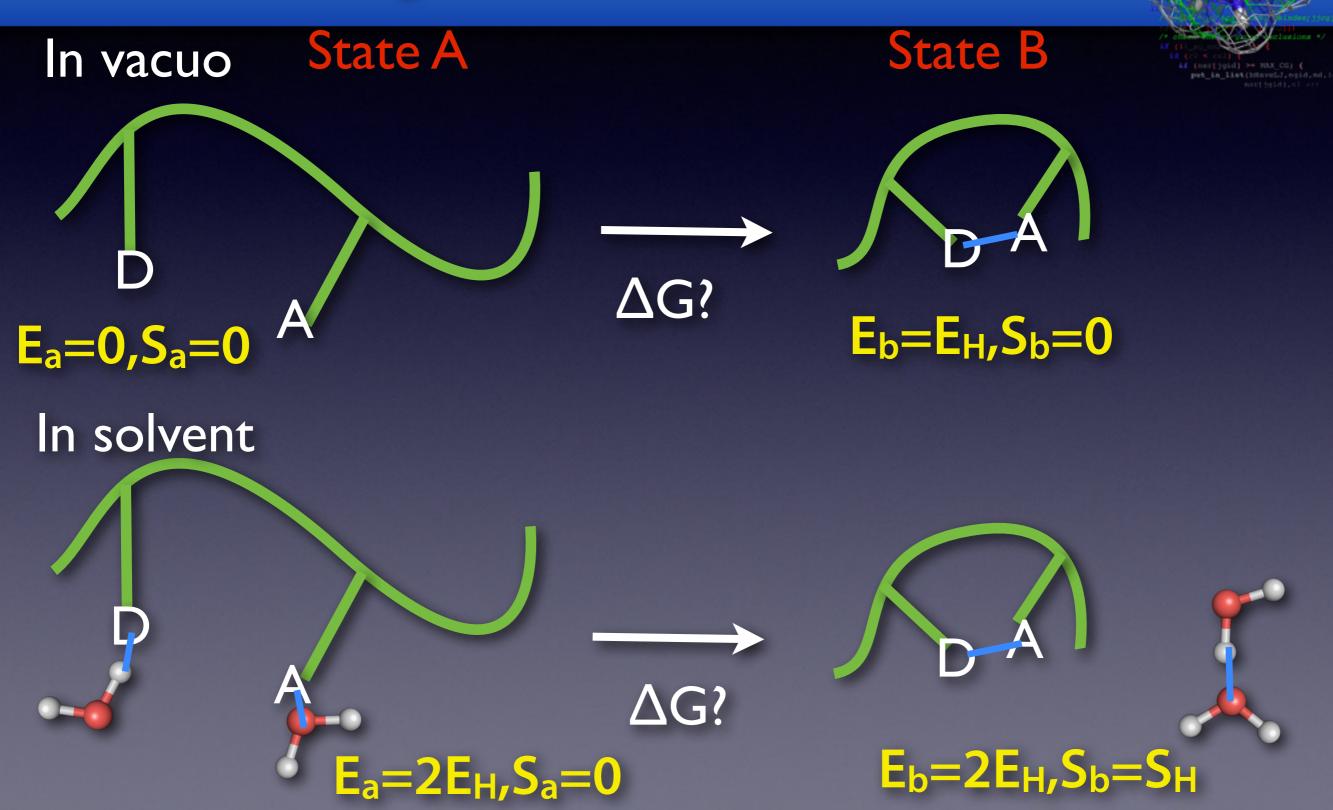


F = E-TS F = E-T(k lnV) i.e. number of accessible states probability ~ exp(-F/kT)



S_{water}>0: Entropy of freely rotating body or complex (1 or 2 waters!)

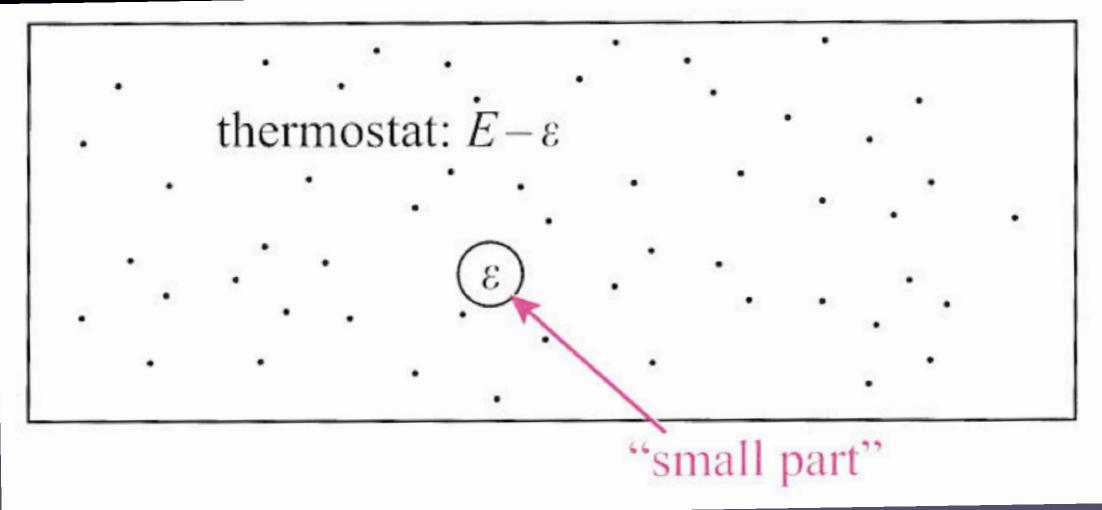






- Statistical mechanics
- The partition function
- Free energy & stable states
- Gradual changes & phase transitions
- Activation barriers & transition kinetics

Fluctuations in a closed system - E conserved



Consider all microstates of this system with energy E # thermostat microstates M_{therm} with the energy (E- ϵ) Define: S = k*ln M_{therm}

Entropy

$$S_{\text{therm}}(E - \epsilon) = \kappa \ln \left[M_{\text{therm}}(E - \epsilon) \right]$$

Now do series expansion; only 1st order matters - why?
$$S_{\text{therm}}(E - \epsilon) = S_{\text{therm}}(E) - \epsilon \left(\frac{dS_{\text{therm}}}{dE} \right) \Big|_{E}$$

Solve for M
$$M(E - \epsilon) = \exp \left[\frac{S_{\text{therm}}(E - \epsilon)}{\kappa} \right]$$
$$= \exp \left[\frac{S_{\text{therm}}(E)}{\kappa} \right] \times \exp \left\{ -\epsilon \left[\frac{(dS_{\text{therm}}/dE)|_{E}}{\kappa} \right] \right\}$$

Observation of microstates

 The probability of observing the small part in this state is proportional to the number of microstates corresponding to it

 $p \propto M(E - \epsilon) \propto \exp\left\{-\epsilon \left[(dS/dE)|_E/\kappa \right] \right\}$

 $\kappa = k$

 $(dS/dE)|_E = \frac{1}{T}$

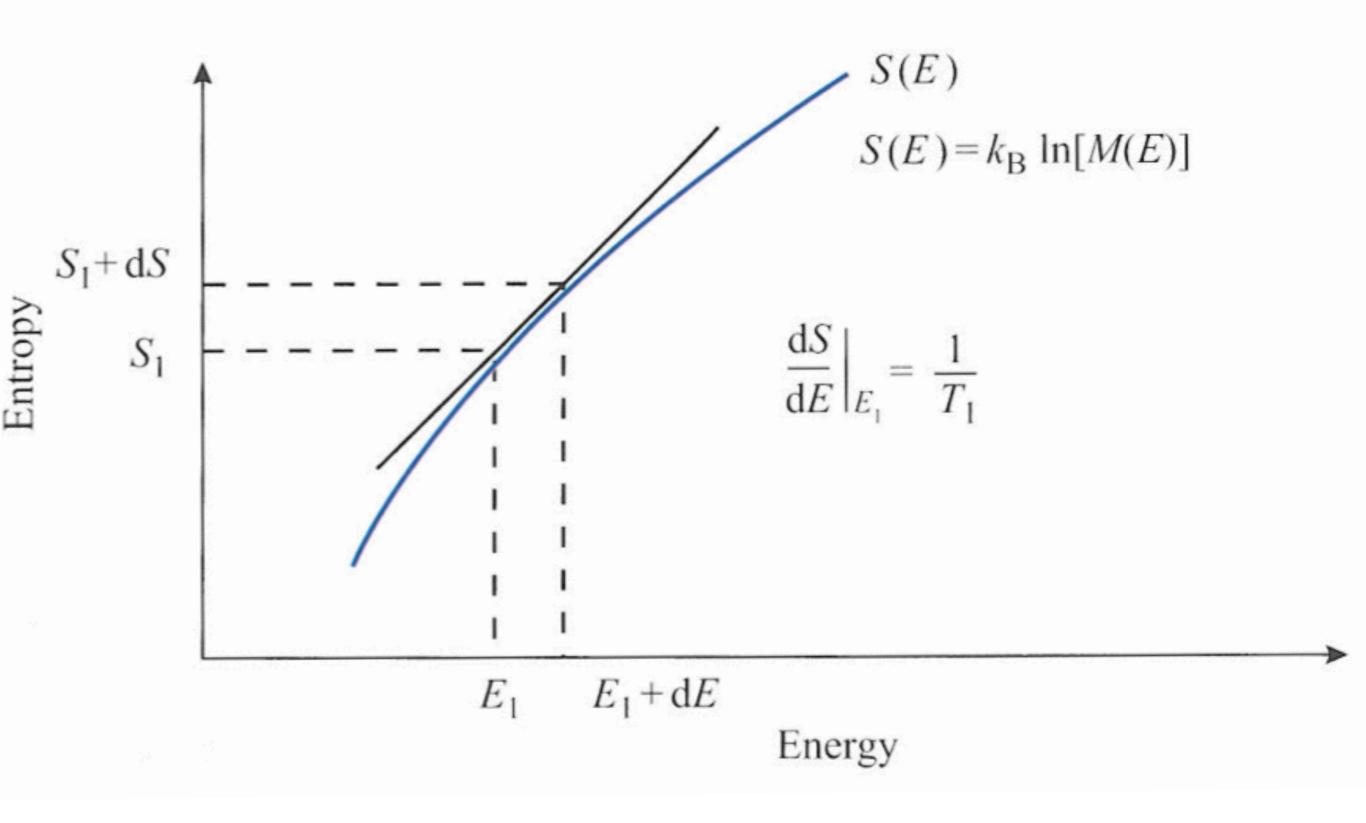
Energy increases

What happens when energy increases by kT?

 $\ln\left[M(E+k_BT)\right] = S(E+k_BT)/k_B =$

 $= \left[S(E) + k_B (1/T) \right] / k_B = \ln \left[M(E) \right] + 1$

e (2.72) times more microstates, regardless of system properties and size!



Probabilities of states

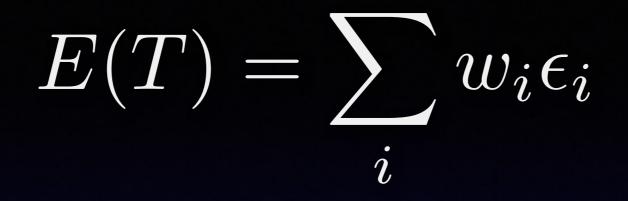
probability of being in a state i

$$w_i(T) = \frac{\exp\left(-\epsilon_i/k_B T\right)}{Z(T)}$$

Normalization factor

$$Z(T) = \sum_{i} \exp\left(-\epsilon_i/k_B T\right)$$

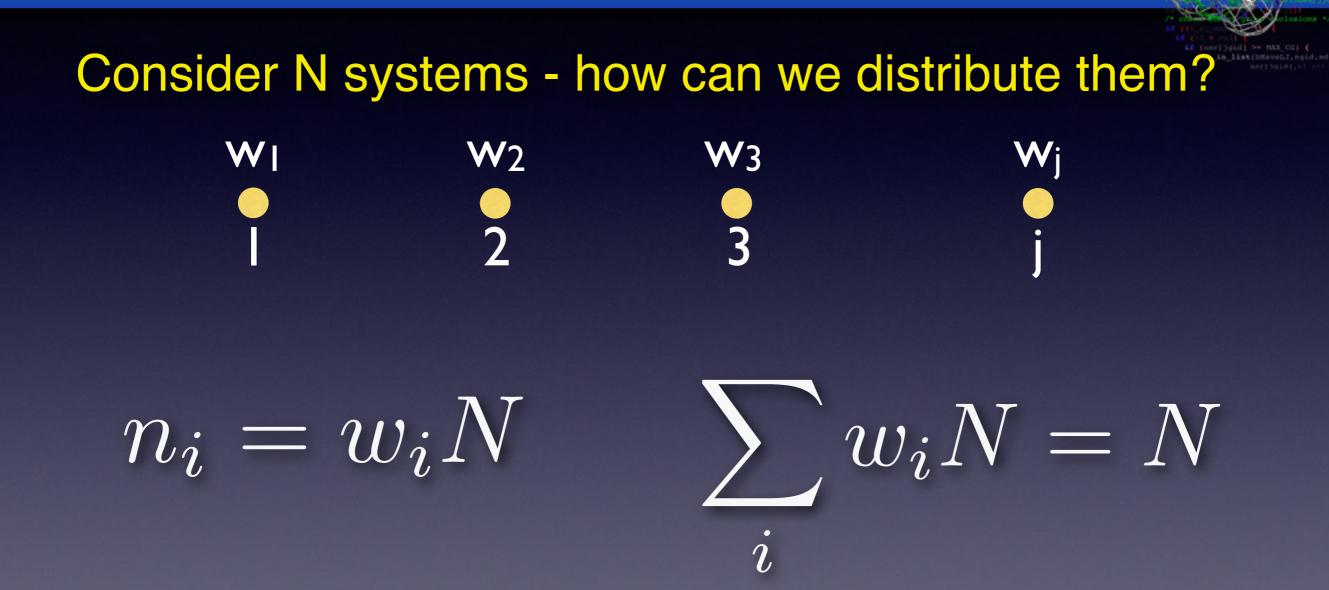
'The partition function'



 $S(T) = \sum_{i} w_i S_i$

How do we calculate S_i?

System distribution over states



Question: how many ways can these systems be distributed over the j states?

Permutations

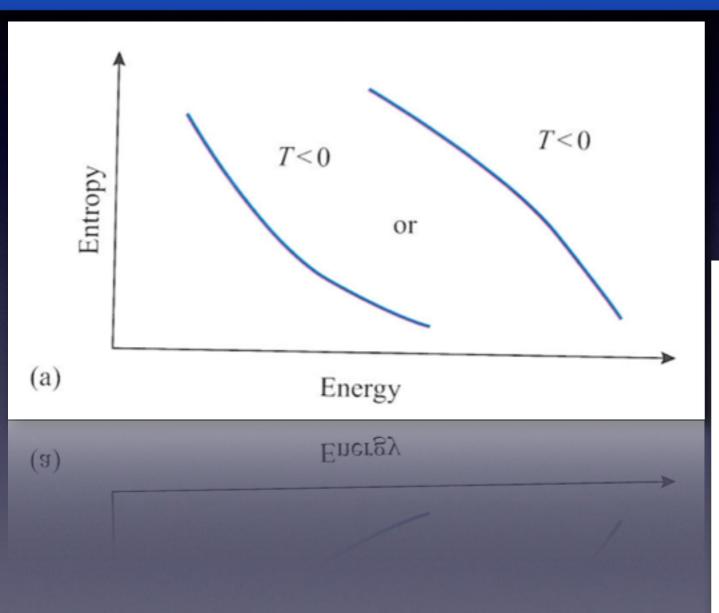
 $\begin{array}{ll} \hline n_1!n_2!...n_j! &= & \text{Stirling: n!}\approx(n/e)^n \\ = (N/n_1)^{n_1}...(N/n_j)^{n_j} = (1/w_1)^{Nw_1}...(1/w_j)^{Nw_j} \\ = \left[1/(w_1^{w_1}...w_j^{w_j}) \right]^N & \text{for N systems} \\ = 1/(w_1^{w_1}...w_j^{w_j}) & \text{for 1 system} \end{array}$

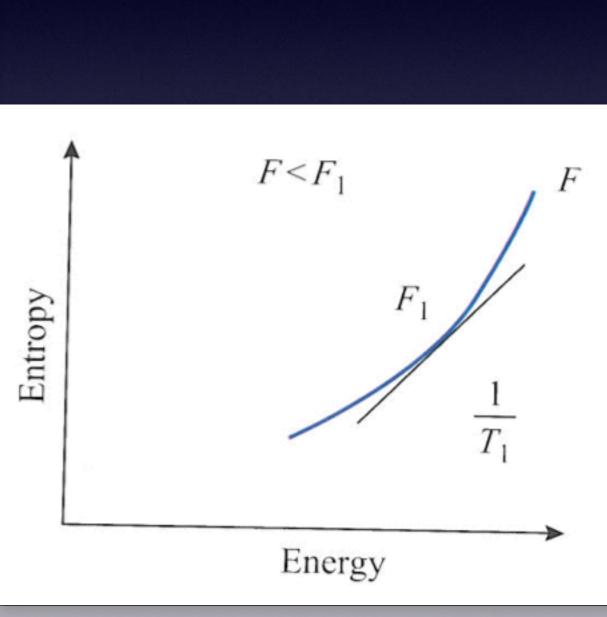
...and the entropy becomes: $S = k_B \ln M = k_B \sum w_i \ln(1/w_i)$ Free energy

 $E(T) = \sum w_i \epsilon_i$ $S = k_B \ln M = k_B \sum w_i \ln(1/w_i)$

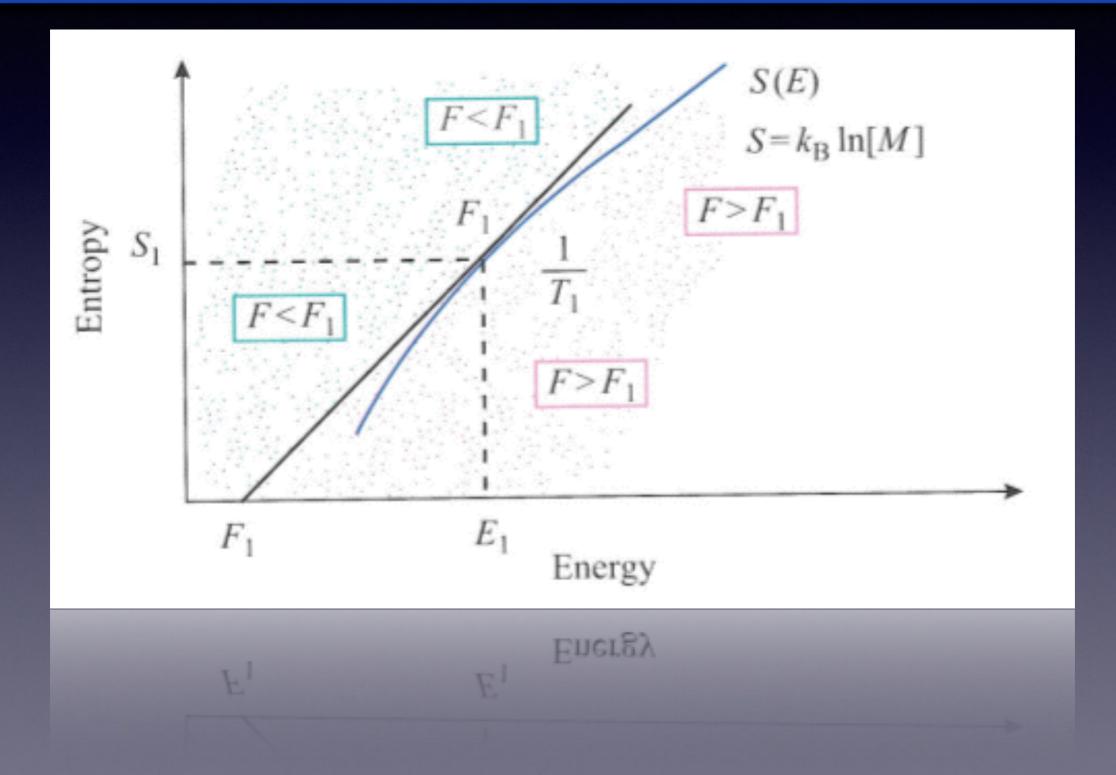
F = E - TSF = -kBT ln [Z(T)]

System instability

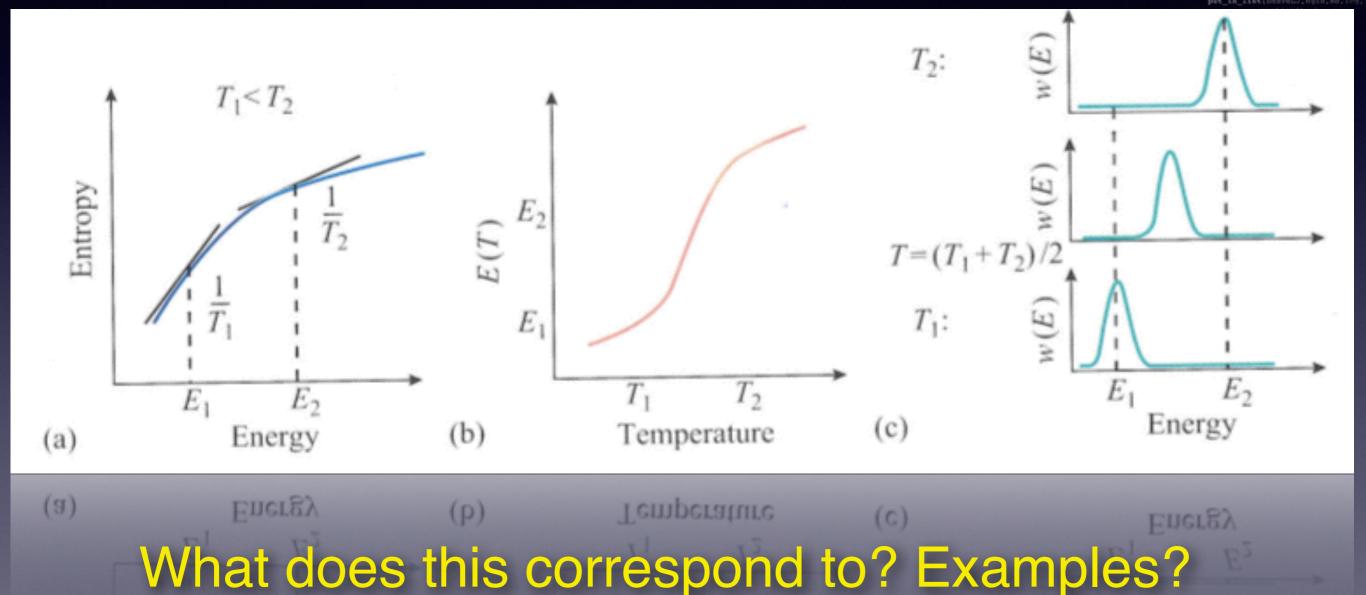




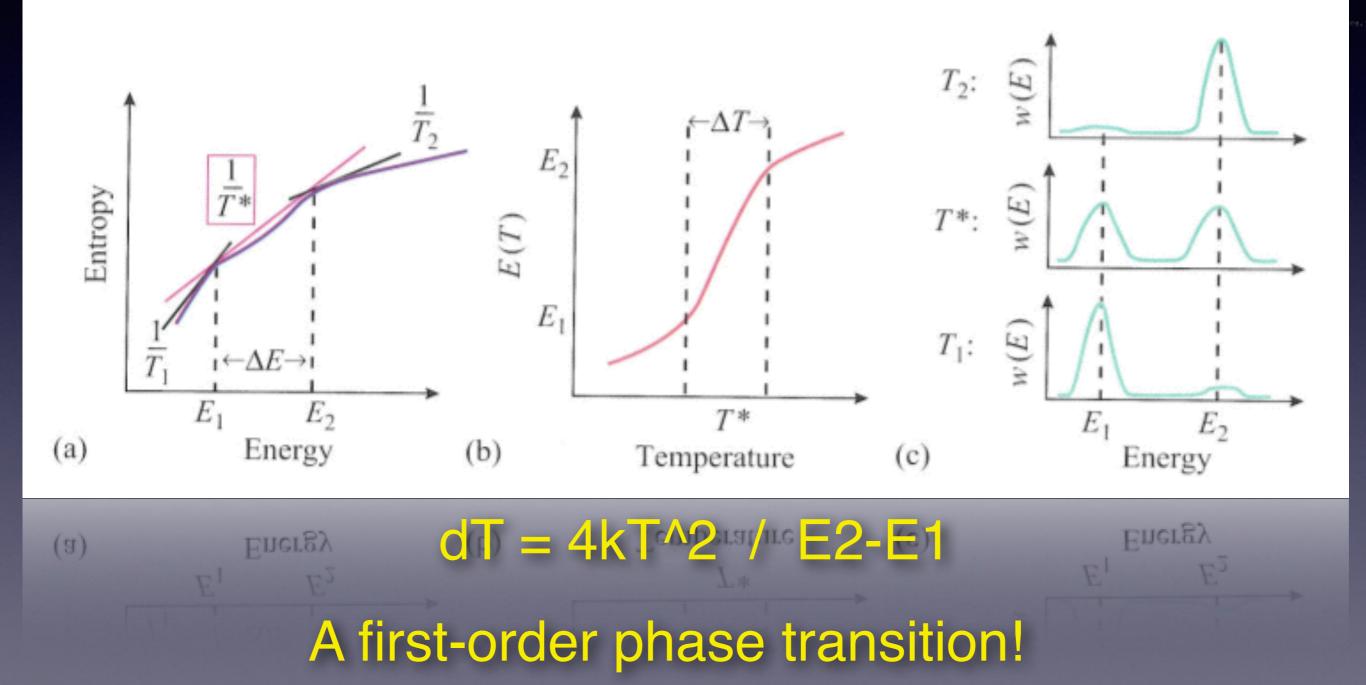
System stability



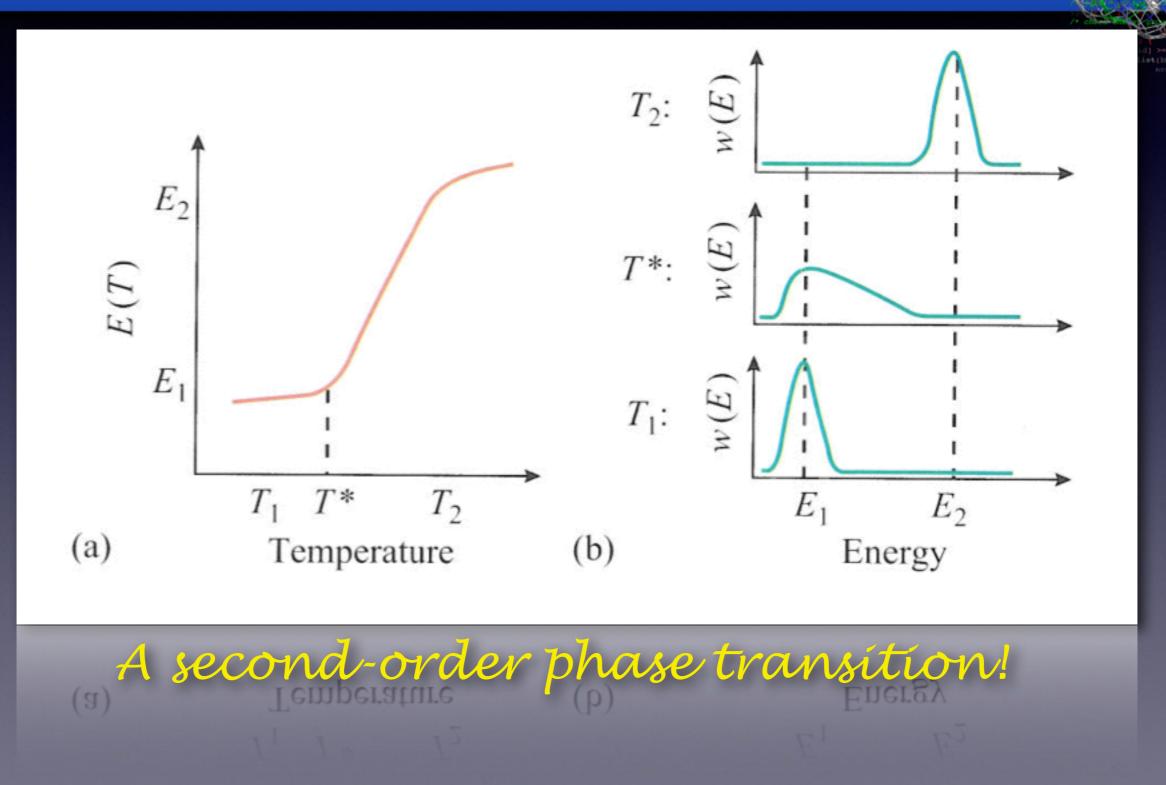
Gradual changes



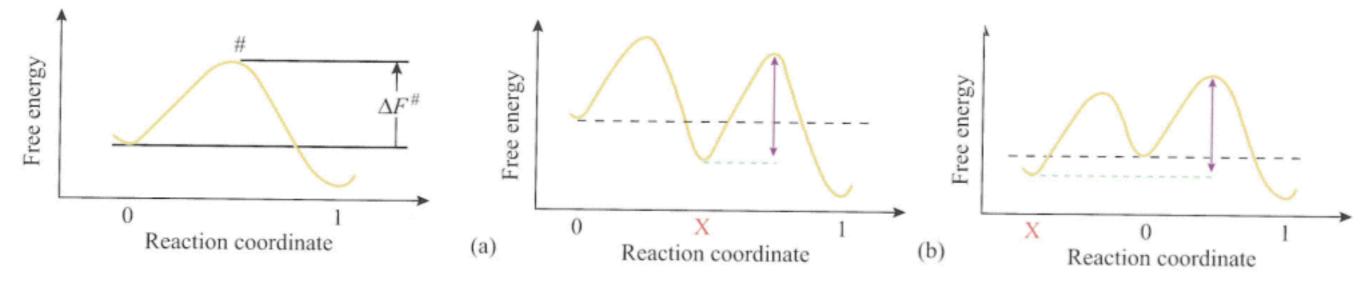
Abrupt changes



A different change.



Free energy barriers



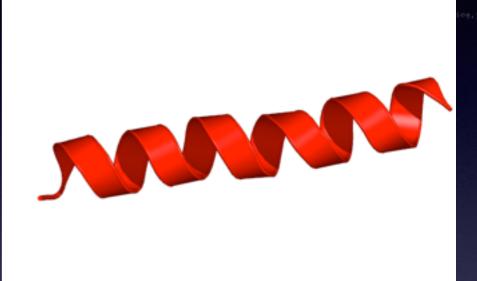
n[#] ~ n exp(- $\Delta F^{\#}/k_{B}T$) T(n/n[#]) ~ T exp($\Delta F^{\#}/k_{B}T$) $t_{0\rightarrow 1} \approx \tau \exp\left(+\Delta F^{\#}/k_{B}T\right)$ Transition rate: $k_{0\rightarrow 1} = 1/t_{0\rightarrow 1}$

Secondary structure

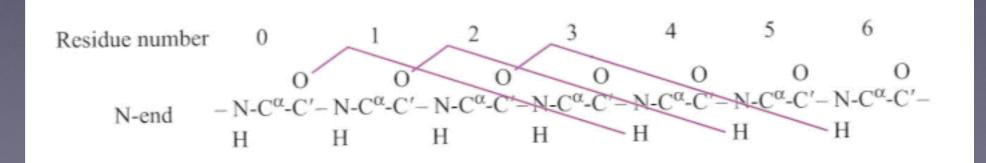
- Alpha helix formation
- Equilibrium between helix & coil
- Beta sheet formation
- Properties of the "random" coil, or the denatured state what is it?

Alpha helix formation

- Hydrogen bonds: i to i+4
 - 0-4, 1-5, 2-6
- First hydrogen bond "locks" residues 1,2,3 in place

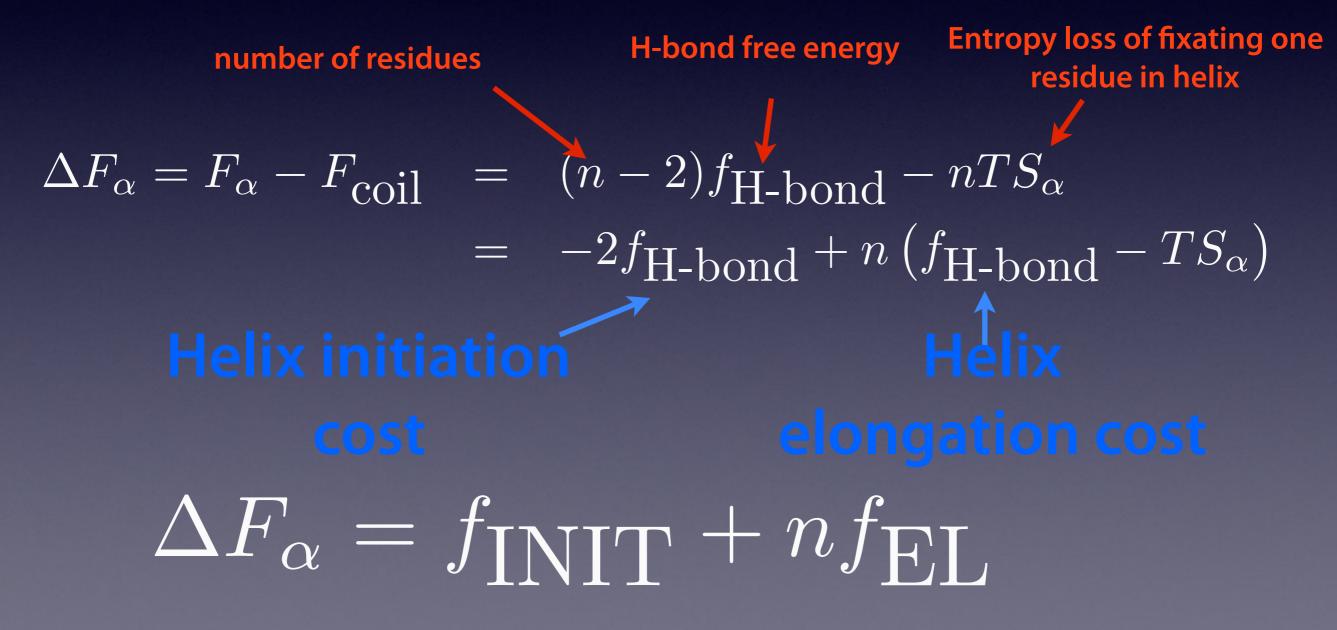


- Second stabilizes 2,3,4 (etc.)
- N residues stabilized by N-2 hydrogen bonds!



Alpha helix free energy

• Free energy of helix vs. "coil" states:



Alpha helix free energy

 $\exp\left(-\Delta F_{\alpha}/k_{B}T\right) = \exp\left(-f_{\text{INIT}}/k_{B}T\right)\exp\left(-nf_{\text{EL}}/k_{B}T\right)$ $= \exp\left(-f_{\text{INIT}}/k_{B}T\right)\left[\exp\left(-f_{\text{EL}}/k_{B}T\right)\right]^{n}$ $= \sigma s^{n}$

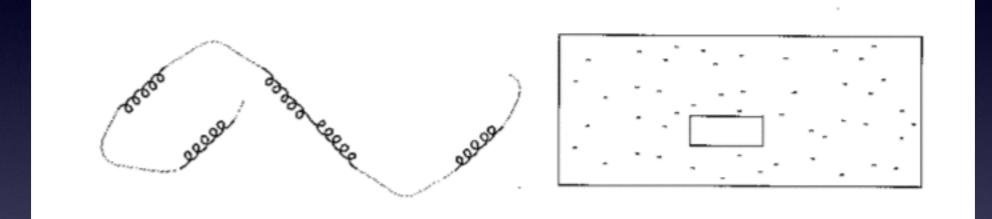
$$s = \exp\left(-f_{\rm EL}/k_BT\right)$$

$$\sigma = \exp\left(-f_{\rm INIT}/k_BT\right)$$

$$\sigma = \exp\left(-f_{\rm INIT}/k_BT\right) = \exp\left(+2f_{\rm H}/k_BT\right) <<1$$

Equilibrium constant for helix of length n

How does a helix form?



• First, consider ice in water $n \propto V \propto r^3$ $A \propto r^2 \propto n^{2/3}$ Surface tension costly! • S = k ln(N)

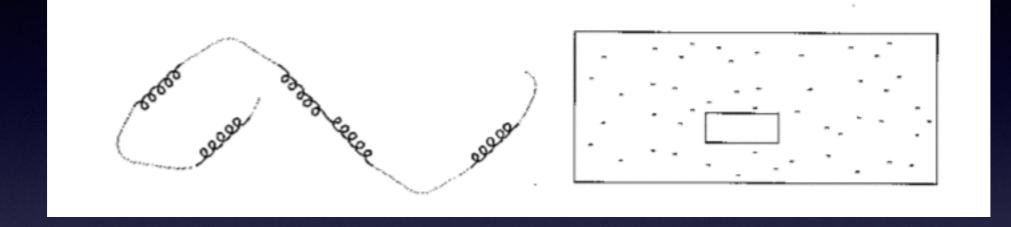
How does a helix form?

- Landau: Phases cannot co-exist in 3D
- First order phase transitions means either state can be stable, but not the mixture
- Think ice/water either freezing or melting $n \propto V \propto r^3$

 $A \propto r^2 \propto n^{2/3}$ Surface tension costly!

- But a helix-coil transition in a chain is 1D!
- Interface helix/coil does not depend on n

How does a helix form?



ice/water: n molecules in ice, N in water energy cost * n^2/3 & entropy: k ln N helix/coil: n residues in helix out of N in total f_{INIT} - kT ln (N-n) i.e. opposite to water/ice!

Helix/coil mixing

- Or: What helix length corresponds to the transition mid-point? $f_{\rm EL} = f_{\rm H} TS_{\alpha} = 0$
- Assuming helix can start/end anywhere, there are N^2/2 positions

 $S = k \ln V \approx k \ln N^2 = 2k \ln N$

 $\Delta F_{\text{helix}} \approx f_{\text{INIT}} - 2kT \ln N$

• At transition midpoint we have $\Delta F=0$ & N=n₀

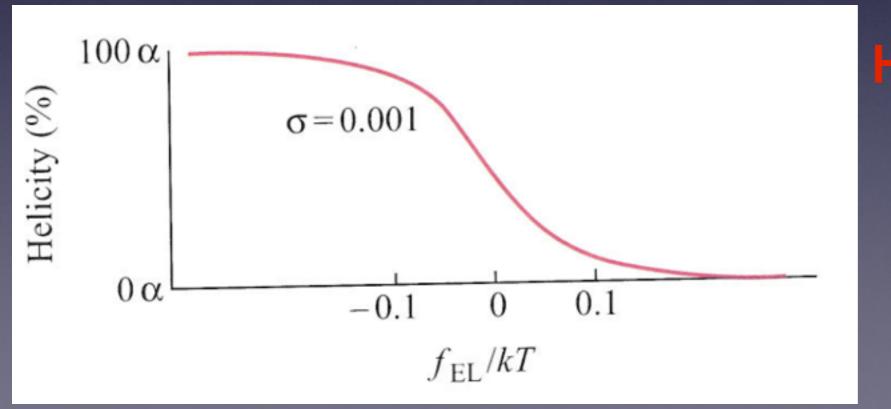
 $n_0 = \exp\left(f_{\rm INIT}/2kT\right) = 1/\sqrt{\sigma}$

Helix parameters

- We can measure n₀ from CD-spectra
- Calculate σ from last equation
- Typical values for common amino acids: $n_0 \approx 30$ $f_{INIT} \approx 4$ kcal/mol $\sigma \approx 0.001$
- $f_H = -f_{INIT}/2 = -2 \text{ kcal/mol}$
- $TS_{\alpha} = f_{H} f_{EL} \approx -2 \text{ kcal/mol}$ (Conformational entropy loss of helix res.)

Helix stability

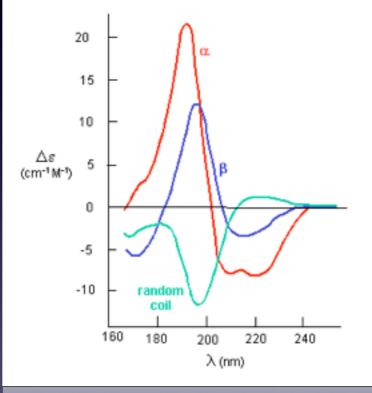
- Temperature dependence
- Elongation term dominant for large n₀
- $dF(alpha) = f_{INIT} + n_0 * f_{EL}$



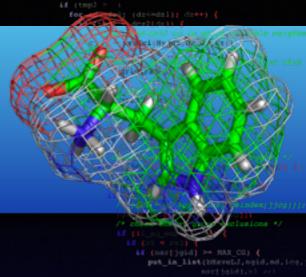
lighly cooperative, but NOT a formal phase transition! (width does not go to zero)

Helix studies

- CD spectra
- Determine s & σ
- Alanine: $s \approx 2$, $f_{EL} \approx -0.4$ kcal/mol
- Glycine: $s \approx 0.2$, $f_{EL} \approx +1$ kcal/mol
- Proline: s≈0.01-0.001 , f_{EL}≈+3-5kcal/mol
- Bioinformatics much more efficient for prediction, though!

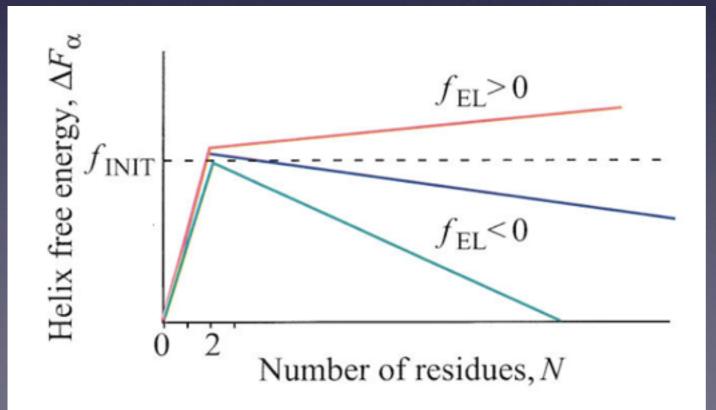


 Δ (nm)



Rate of Formation

- Experimentally: Helices form in ~0.1µs! (20-30 residue segments)
- One residue < 5 ns...



What is the limiting step?

Formation...

T: -residue Rate of formation at position 1: $t_{\text{INIT0}} = \tau \exp \left(f_{\text{INIT}} / kT \right) = \tau / \sigma$ Rate of formation anywhere $(n0\approx 1/\sqrt{\sigma})$: $t_{\rm INIT} = \tau / \sqrt{\sigma}$ **Propagation to all residues:** $tn_0 = \tau/\sqrt{\sigma}$ • Half time spent on initiation, half elongation!

Helix summary

- Very fast formation
- Both initiation & elongation matters
- Quantitative values derived from CD-spectra
- Low free energy barriers, ~1kcal/mol
- Characteristic lengths 20-30 residues