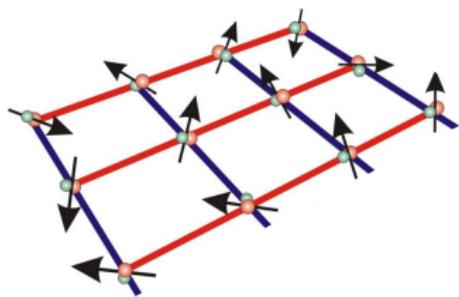


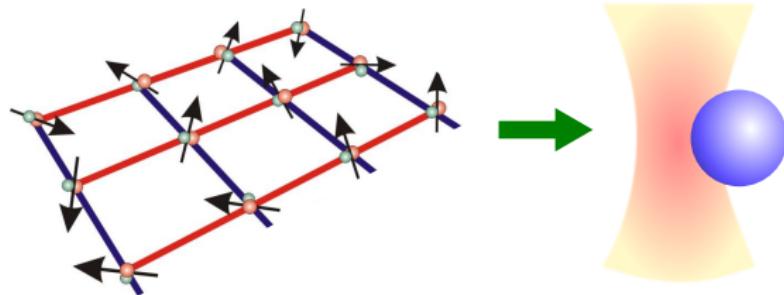
Shortcuts to adiabaticity



adiabatic quantum computing:
maintaining ground state while
driving a quantum system

Demirplak, Rice, JPCA (2003)
Berry, J. Phys. A (2009)

Shortcuts to adiabaticity



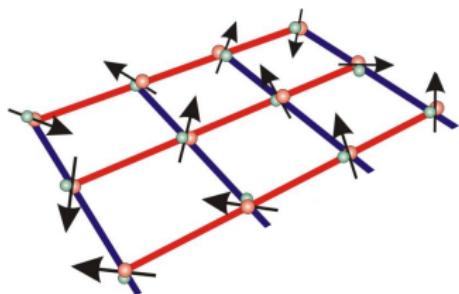
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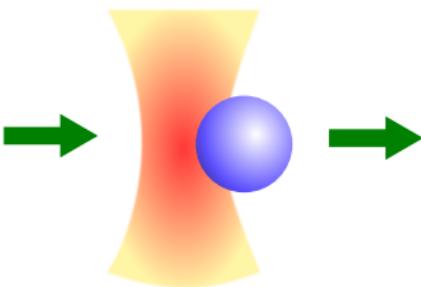
Martinez *et al* Nature Physics (2016)
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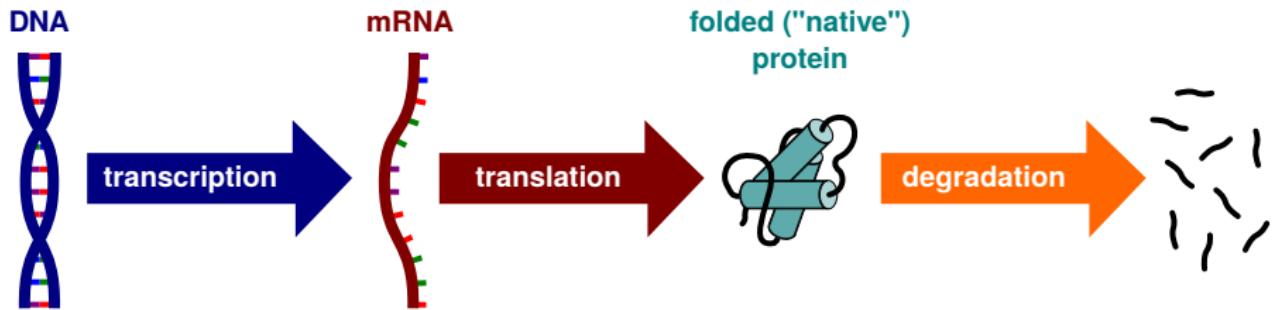
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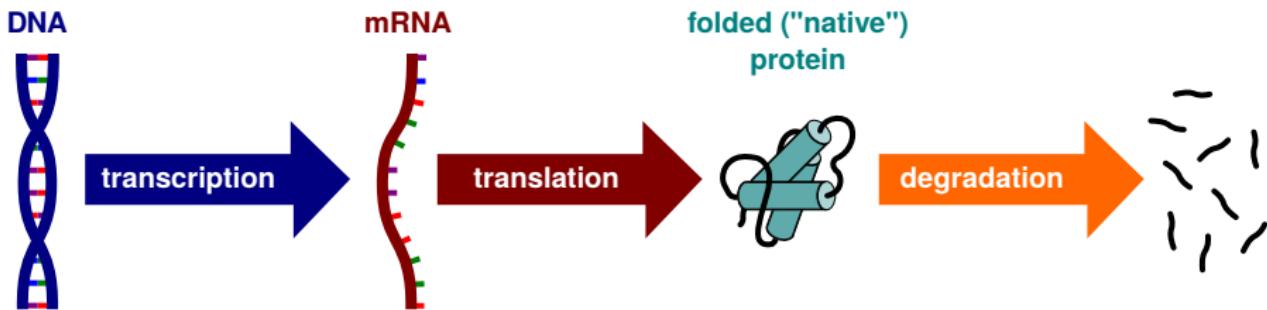


**Possible biological
applications:**
population genetics
molecular chaperones
force spectroscopy

Traditional view of protein production



Traditional view of protein production



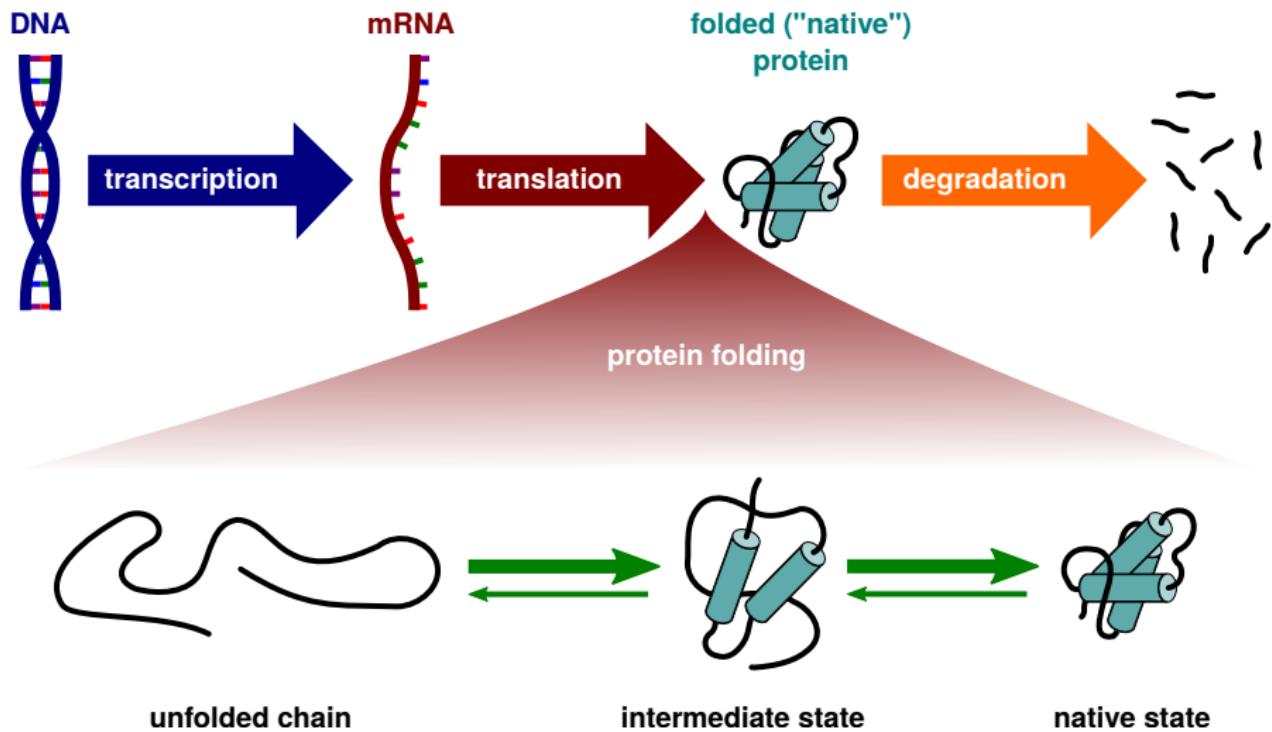
All these processes involve nonequilibrium reaction networks driven by ATP hydrolysis.

The resulting costs of expressing even a single extra protein can be evolutionarily significant for single-celled organisms.

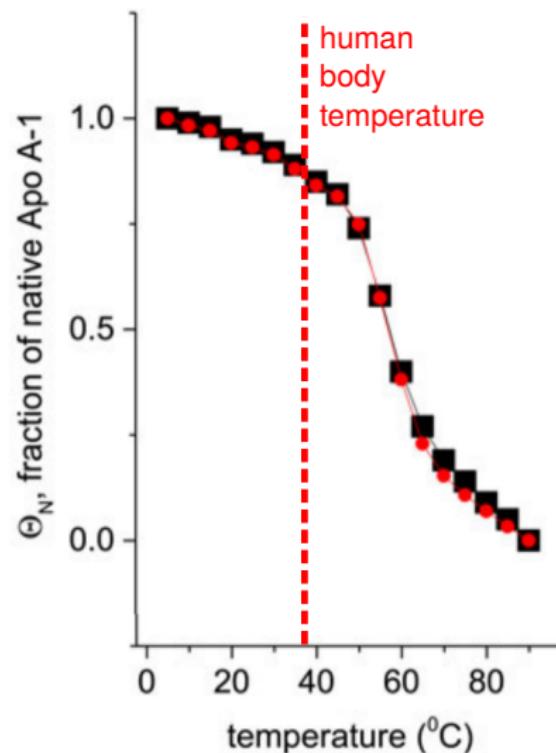
Ilker & Hinczewski, Phys. Rev. Lett. (2019)

Lynch & Marinov, Proc. Natl. Acad. Sci. (2015)

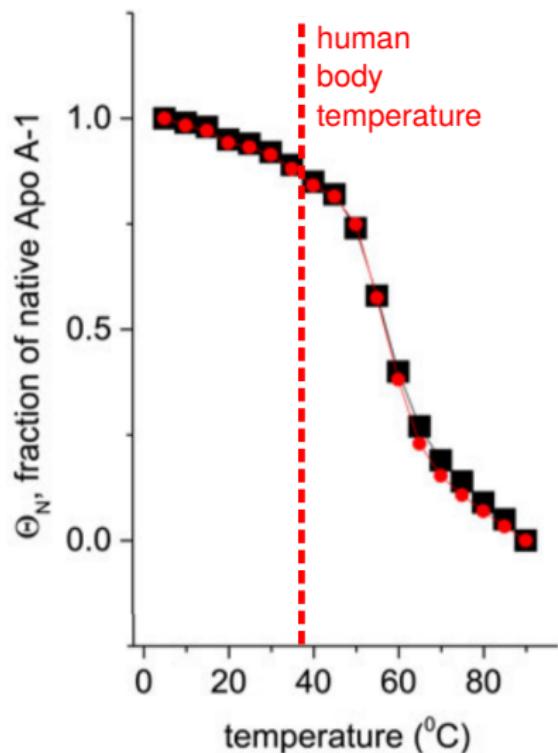
Traditional view of protein production



Proteins function at the cliff edge of unfolding

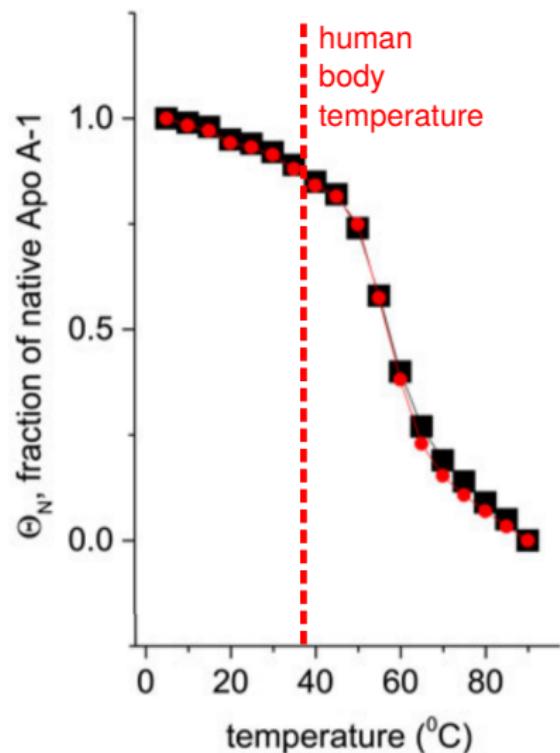


Proteins function at the cliff edge of unfolding



Being on the verge of melting gives proteins the **dynamical flexibility** essential for their diverse roles as enzymes.

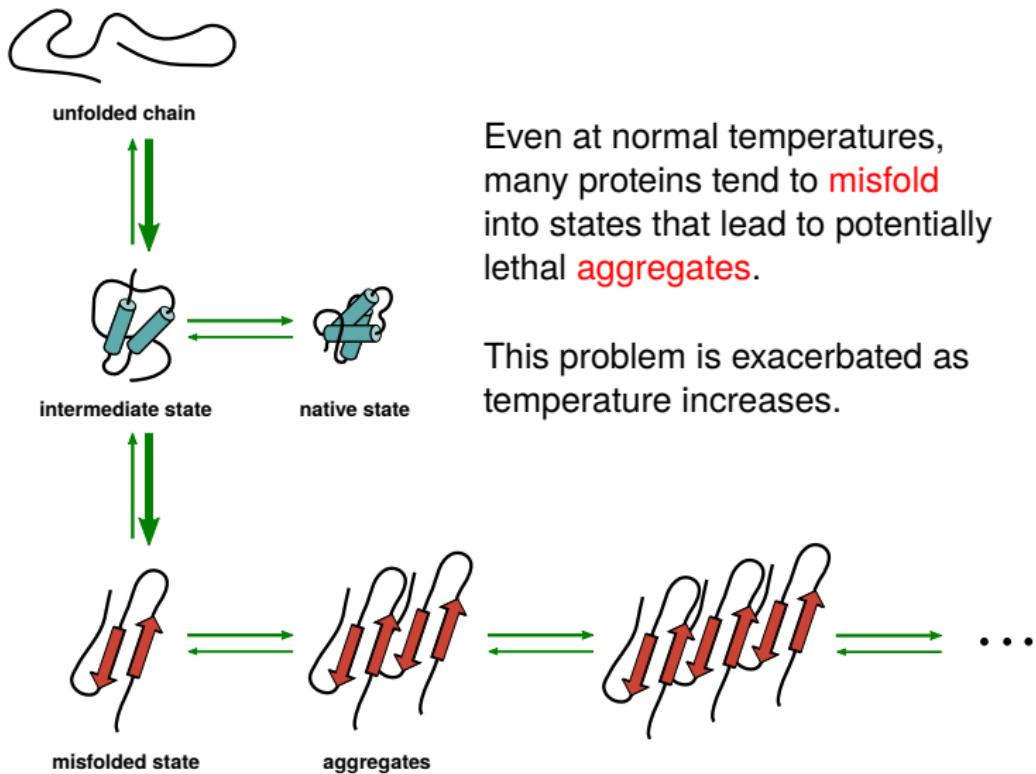
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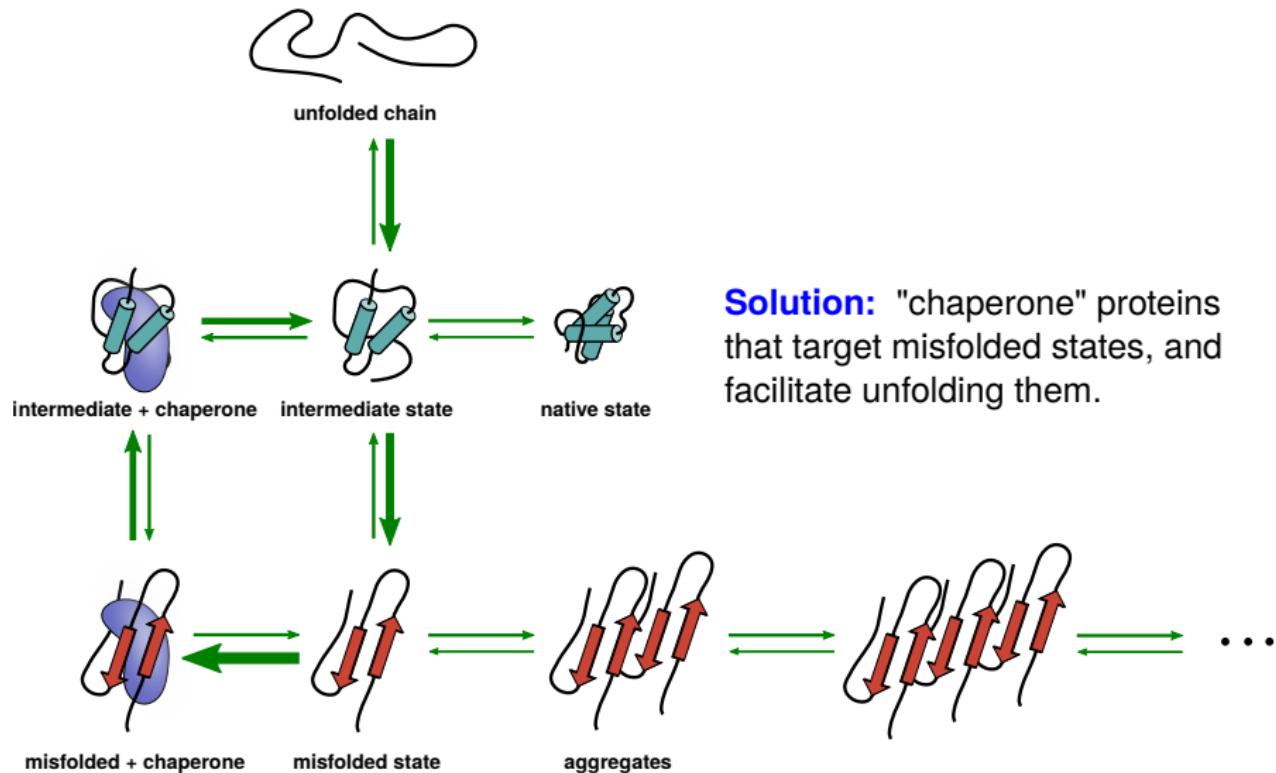
Being on the verge of melting gives proteins the **dynamical flexibility** essential for their diverse roles as enzymes.

But it also makes them highly vulnerable to changes in temperature (even of a few degrees): **heat shock**.

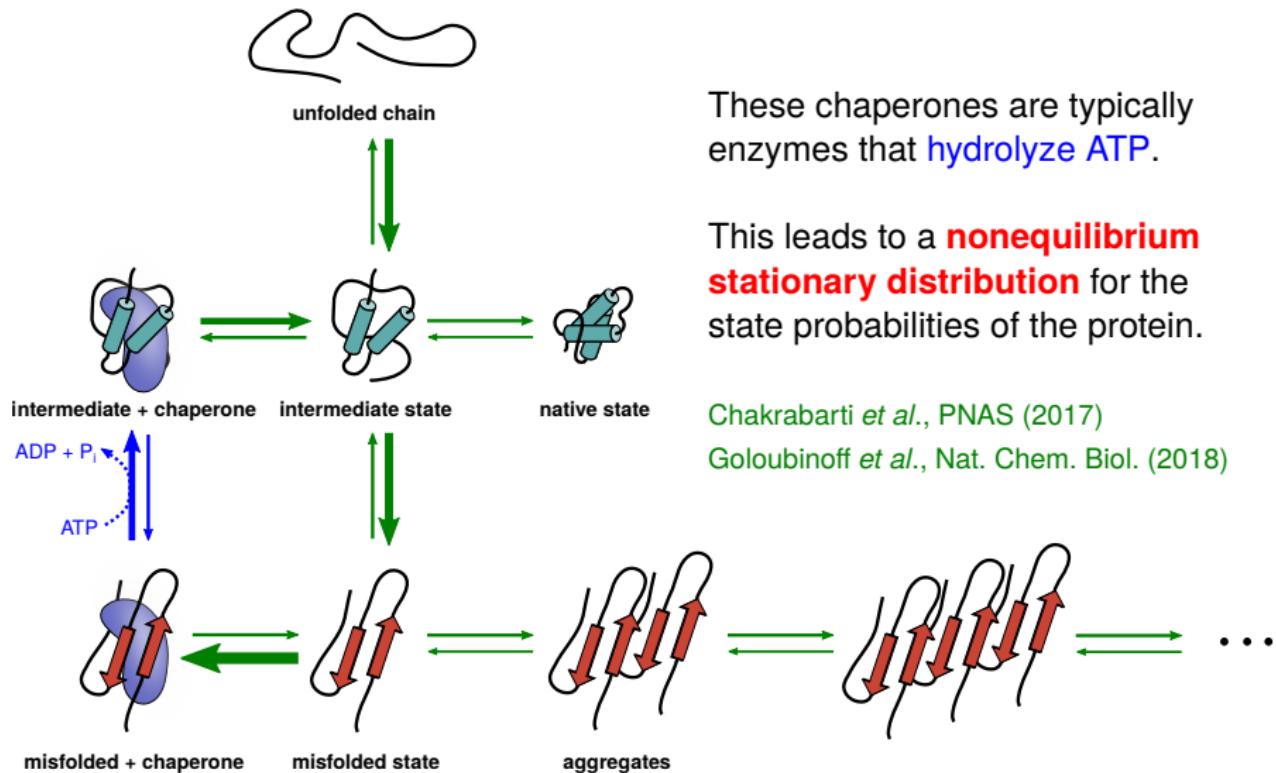
Constant threats: misfolding and aggregation



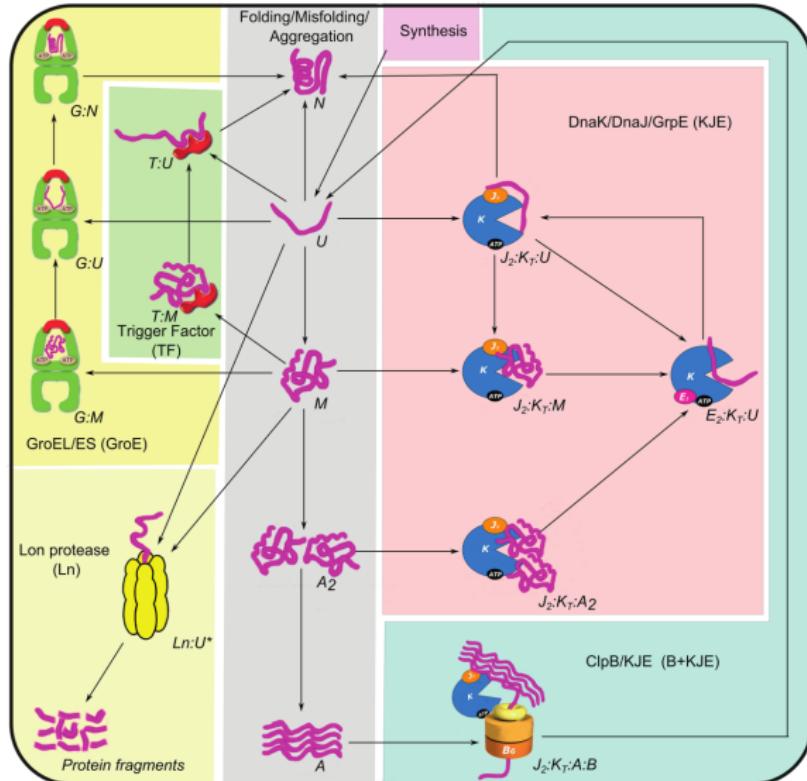
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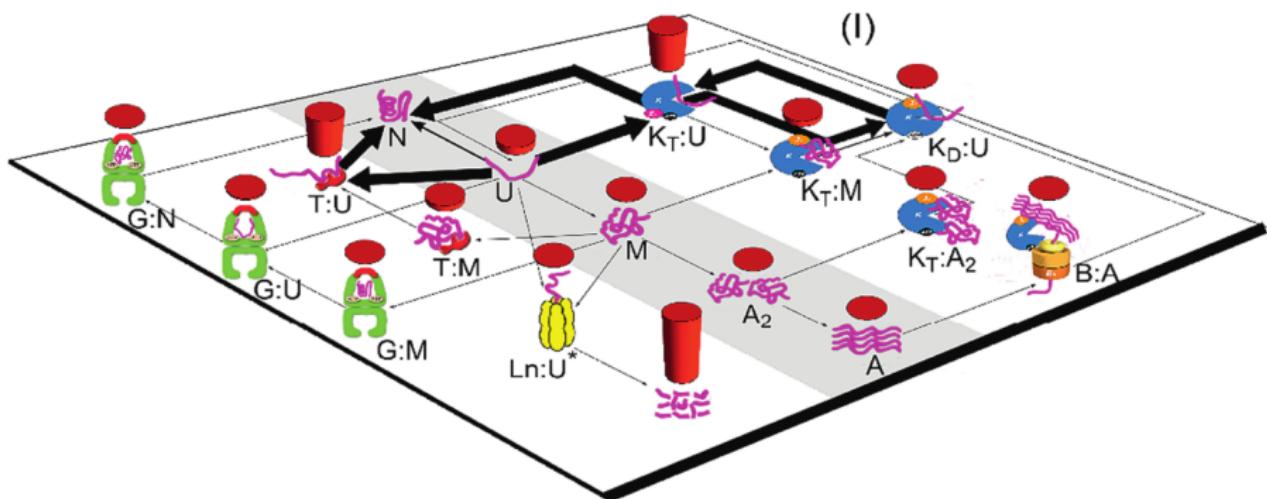
The protein “hospital”: possible chaperone pathways



E. coli chaperone network: Santra *et al.*, PNAS (2017)

The protein “hospital”: possible chaperone pathways

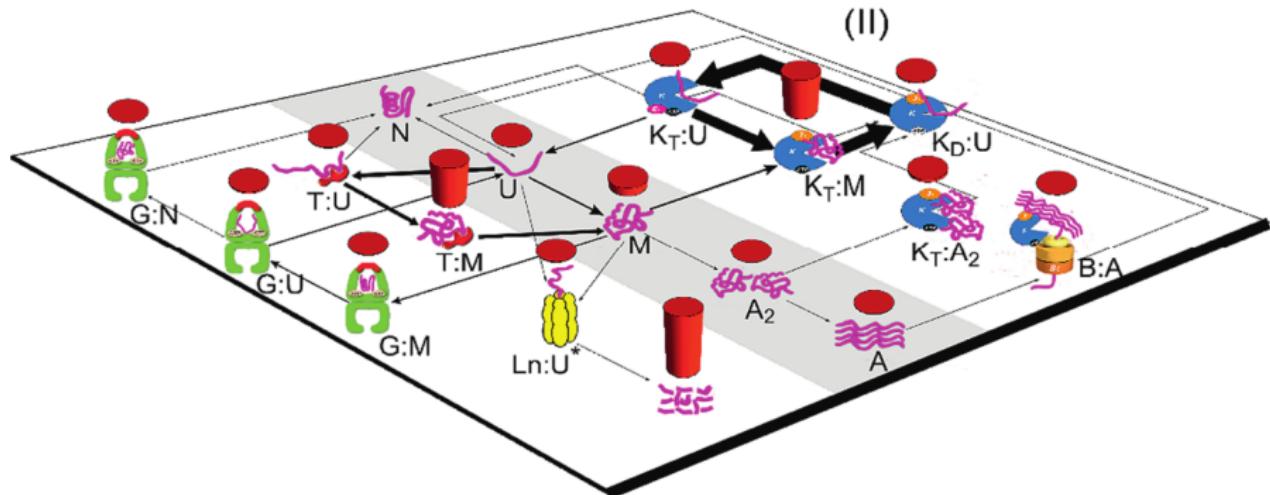
Different classes of proteins interact primarily with different chaperone sub-systems:



Santra *et al.*, PNAS (2017)

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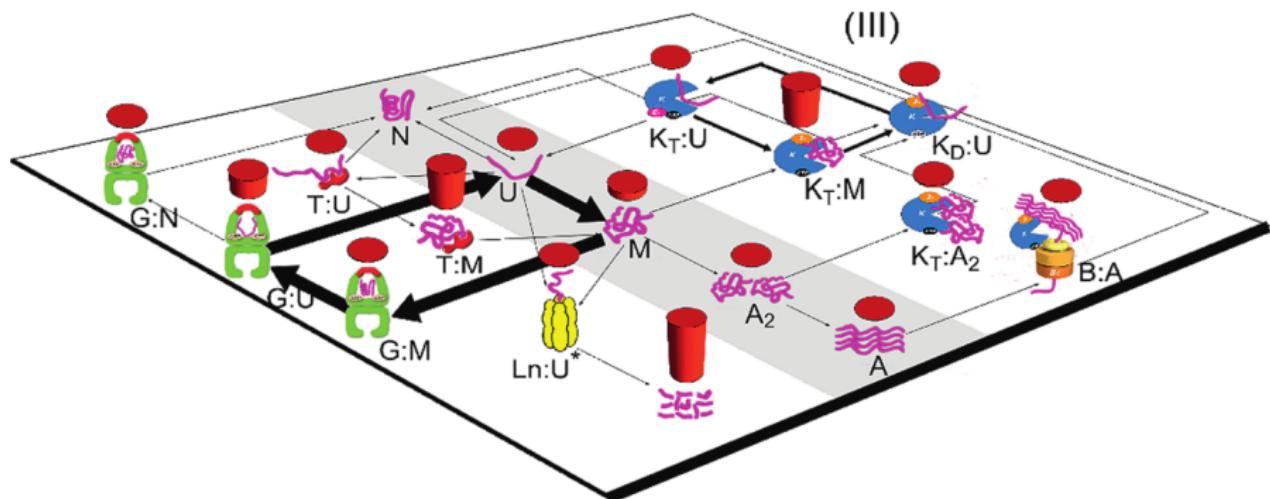
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The protein “hospital”: possible chaperone pathways

Different classes of proteins interact primarily with different chaperone sub-systems:



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Under optimal growth conditions, chaperones are nearly fully occupied by “patient” proteins: spare capacity is too energetically costly.

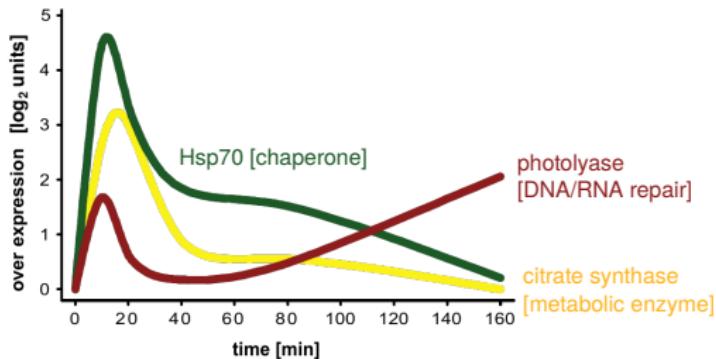
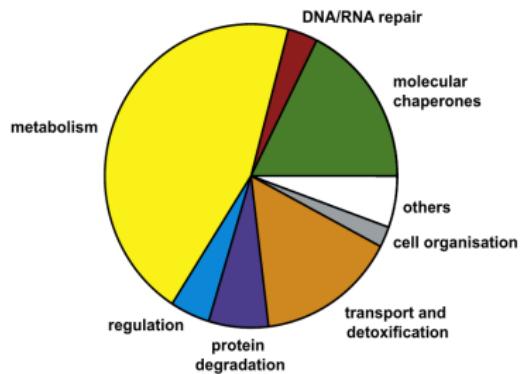
Heat shock

What happens when the cell enters a higher temperature environment?

Heat shock

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Functional classes of upregulated genes in yeast after a heat shock from 25°C to 35°C over 10 min (out of total of 91 genes upregulated by more than 2.8x):

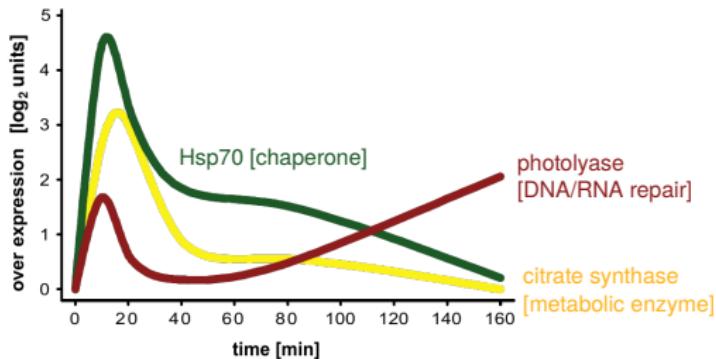
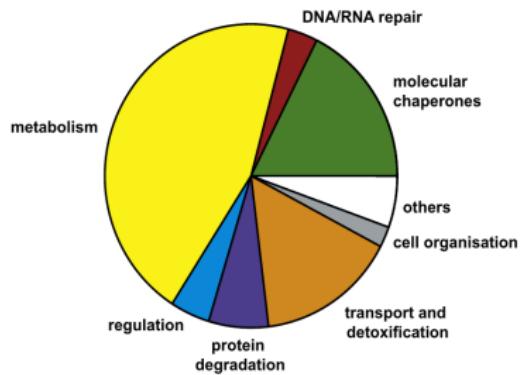


[Richter *et al.*, Molec. Cell (2010)]

Heat shock

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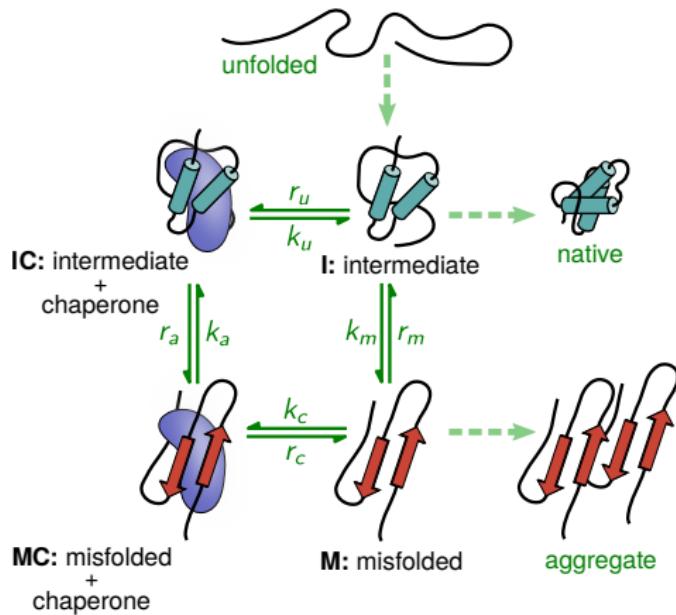
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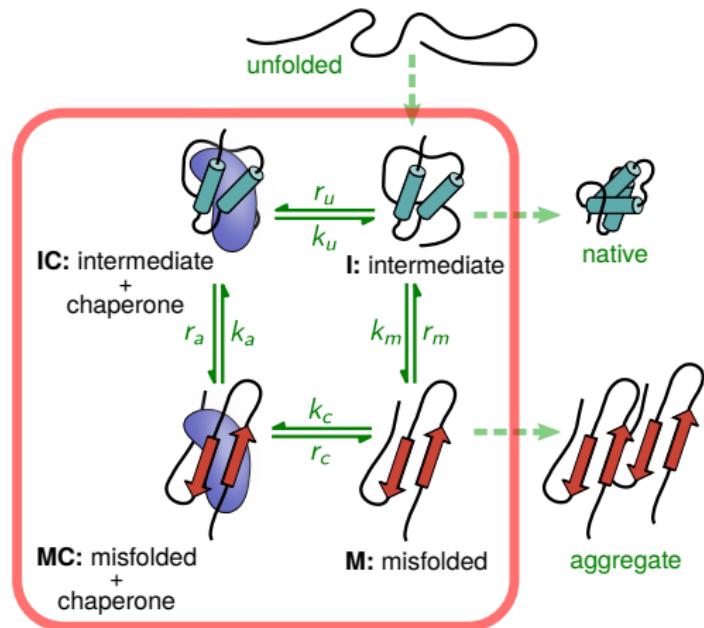
Can we understand this upregulation of chaperones using ideas from thermodynamic control?

Markov model for chaperone-protein interaction



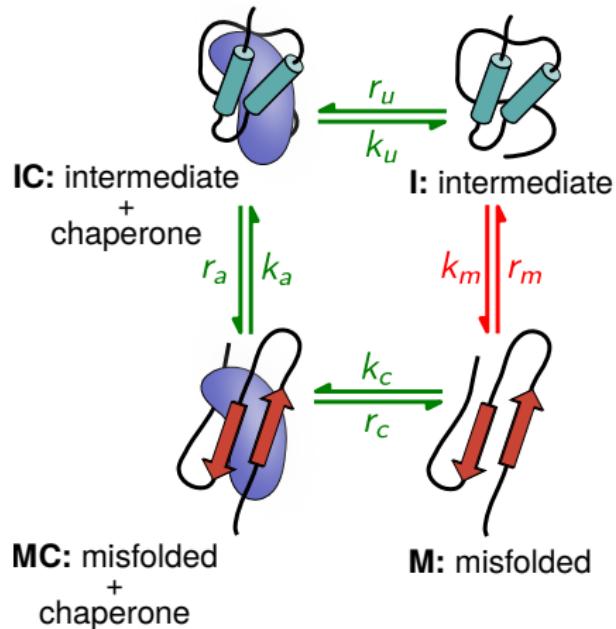
Using separation of timescales we can construct a simplified **Markov model** for a protein that tends to misfold under heat shock, focusing on four key states.

Markov model for chaperone-protein interaction



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Markov model for chaperone-protein interaction



We assume the system is undergoing heat shock, where conditions favor the misfolded over the intermediate state:

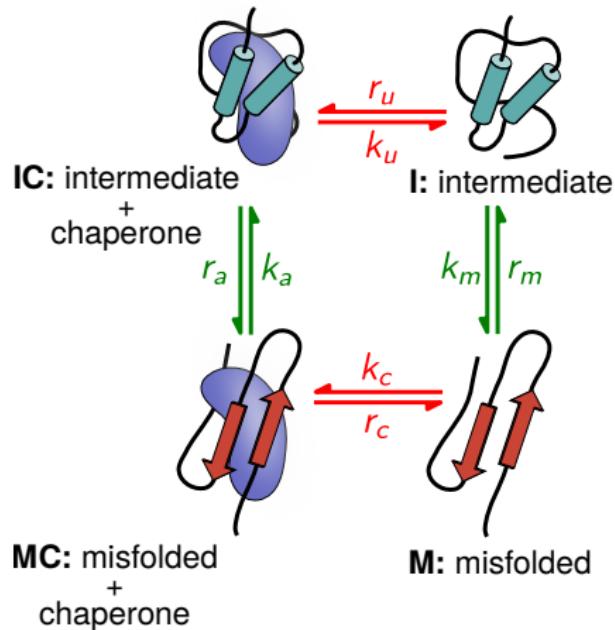
$$\frac{k_m}{r_m} = e^{\beta\epsilon} \gg 1$$

where $\epsilon > 0$ is the free energy difference between the I and M states.

Typical parameter values:

$$k_m = 10 \text{ s}^{-1}, \epsilon = 10 k_B T$$

Markov model for chaperone-protein interaction



Binding rates depend on chaperone concentration C :

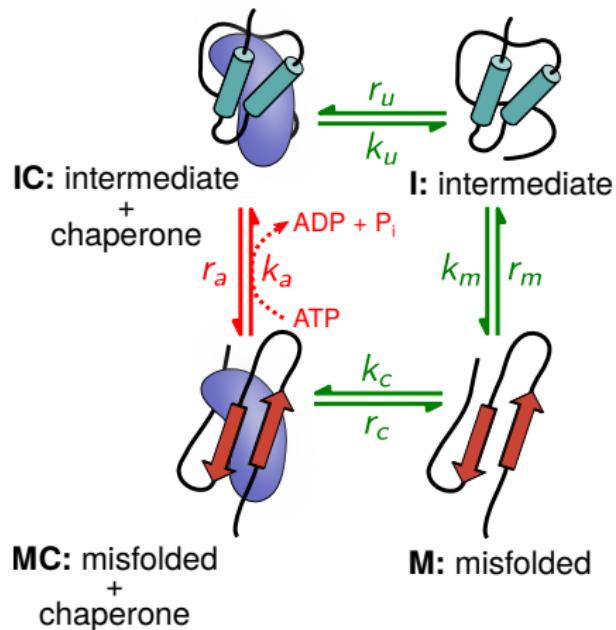
$$k_c = \gamma_c C, \quad r_u = \gamma_u C$$

where usually $\gamma_c \gg \gamma_u$ (chaperone favors binding to misfolded states).

Typical parameter values:

$$\gamma_c = 10^6 \text{ M}^{-1}\text{s}^{-1}, \gamma_u = 10^4 \text{ M}^{-1}\text{s}^{-1},$$
$$r_c = 5 \times 10^{-3} \text{ s}^{-1}, k_u = 0.2 \text{ s}^{-1}$$

Markov model for chaperone-protein interaction



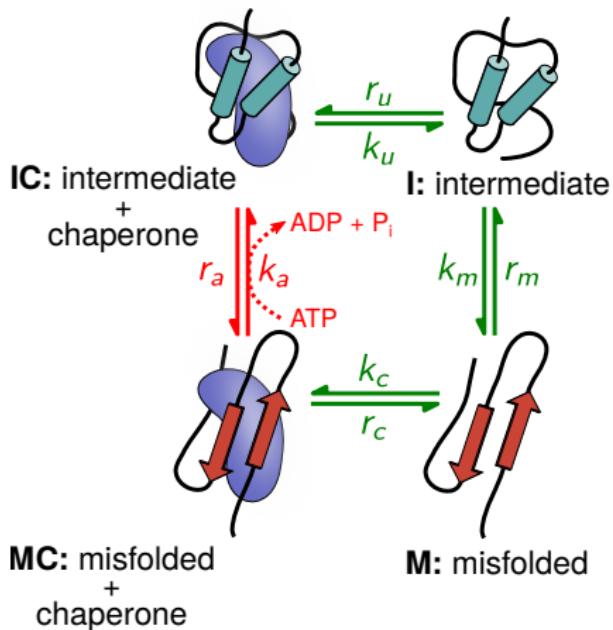
Chaperone-catalyzed reactions follow Michaelis-Menten kinetics that depend on **ATP concentration A** and **ADP concentration B** :

$$k_a = \frac{k_{f,cat}A}{K_{f,M} + A}, \quad r_a = \frac{k_{r,cat}B}{K_{r,M} + B}$$

Typical parameter values:

$$k_{f,cat} = 10^{-2} \text{ s}^{-1}, K_{f,M} = 400 \mu\text{M},$$
$$A = 1 \text{ mM}, B = 0.1 \text{ mM}, \Delta\mu = 22 k_B T$$

Markov model for chaperone-protein interaction



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Local detailed balance leads to two constraints: the “Haldane relation”,

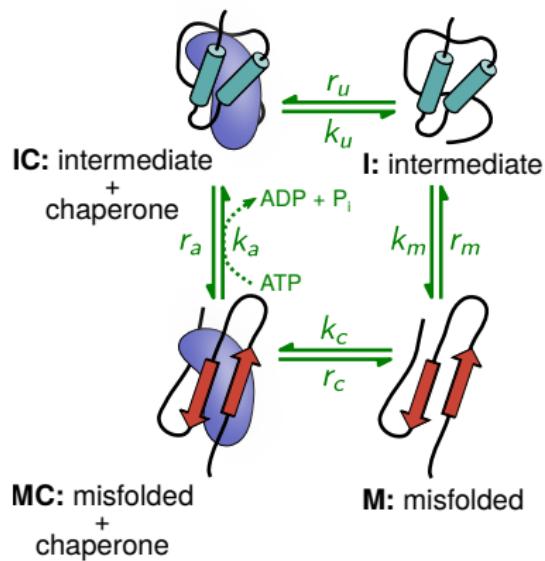
$$\frac{k_{f,cat}K_{r,M}\gamma_c k_u}{k_{r,cat}K_{f,M}\gamma_u r_c} = e^{-\beta\epsilon}$$

and

$$\frac{k_m\gamma_c k_a k_u}{r_m r_c r_a \gamma_u} = e^{\beta\Delta\mu}$$

where $\Delta\mu = \Delta\mu_0 + k_B T \ln(A/B)$ is the ATP hydrolysis chemical potential.

Markov model: dynamics



The state probabilities

$$\mathbf{p}(t) = (p_M(t), p_{MC}(t), p_{IC}(t), p_I(t))$$

obey the master equation

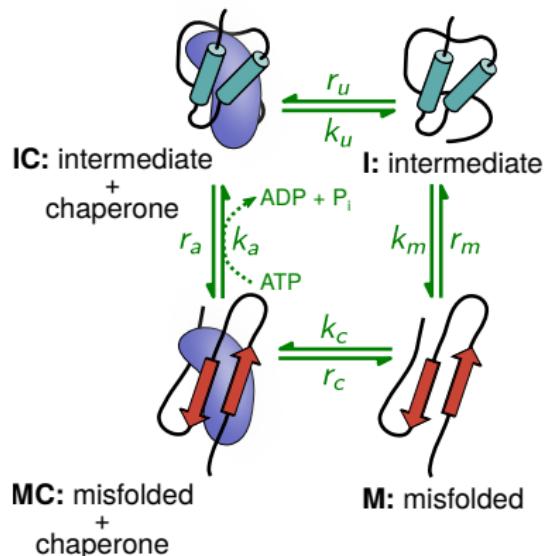
$$\dot{\mathbf{p}}(t) = \Omega \mathbf{p}(t)$$

with transition matrix

$$\Omega =$$

$$\begin{pmatrix} -k_c(C)-r_m & r_c & 0 & k_m \\ k_c(C) & -r_c-k_a(A) & r_a(B) & 0 \\ 0 & k_a(A) & -r_a(B)-k_u & r_u(C) \\ r_m & 0 & k_u & -k_m-r_u(C) \end{pmatrix}$$

Markov model: dynamics



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For given A, B, C , the **stationary distribution** ρ satisfies: $\Omega\rho = 0$.