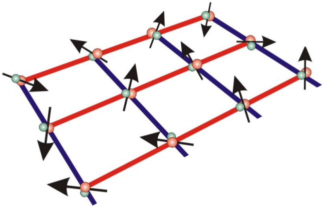
Shortcuts to adiabaticity



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

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

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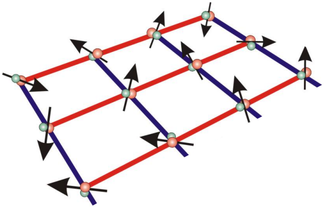

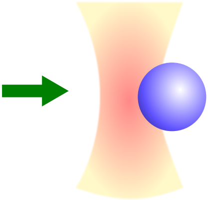

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Brownian motion of bead in optical trap:
maintaining instantaneous
equilibrium as trap changes

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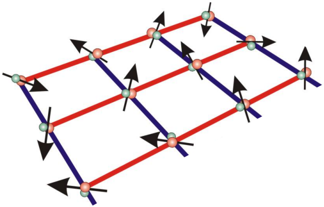

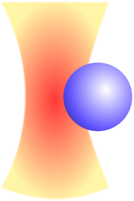

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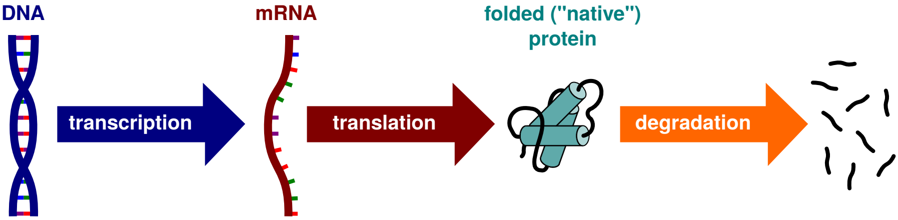
Possible biological applications:
population genetics
molecular chaperones
force spectroscopy

Traditional view of protein production



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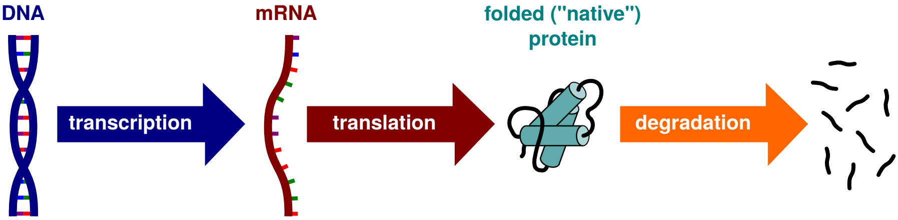
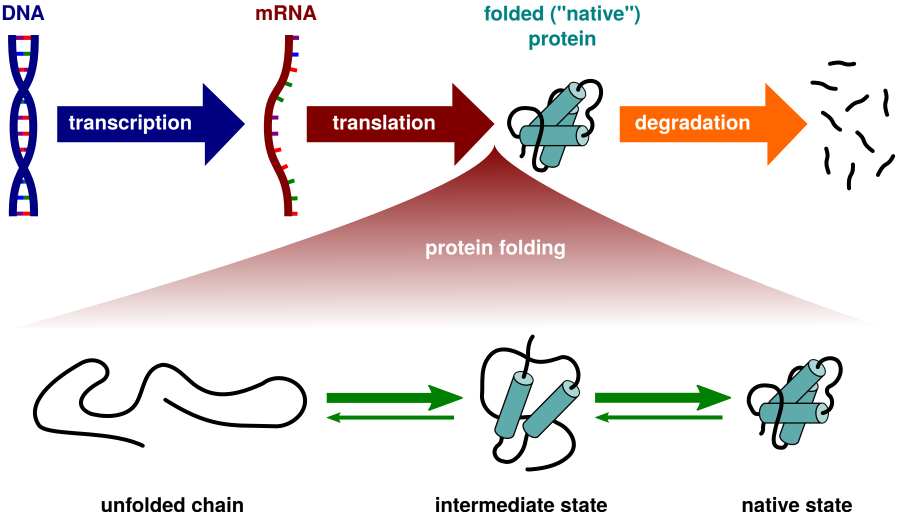


All these processes involve nonequilibrium reaction networks driven by ATP hydrolysis.

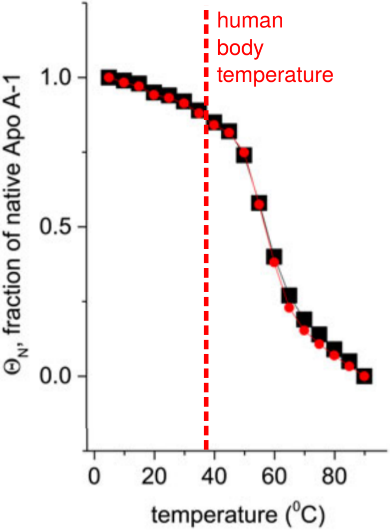
The resulting costs of expressing even a single extra protein can be evolutionarily significant for single-celled organisms.

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



Seelig & Schönfeld, Q. Rev. Biophys. (2016)

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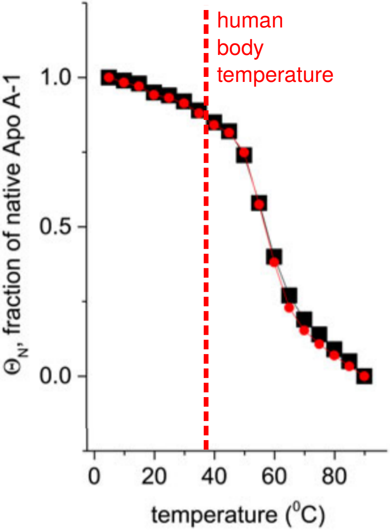

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Being on the verge of melting gives proteins the dynamical flexibility essential for their diverse roles as enzymes.

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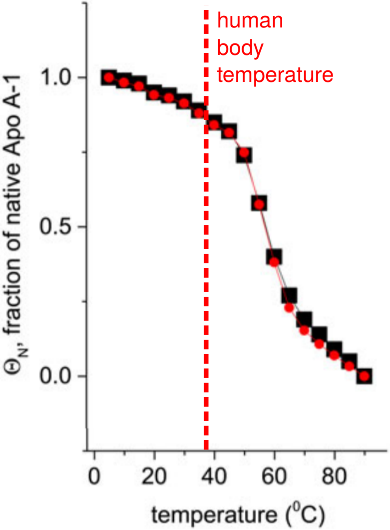

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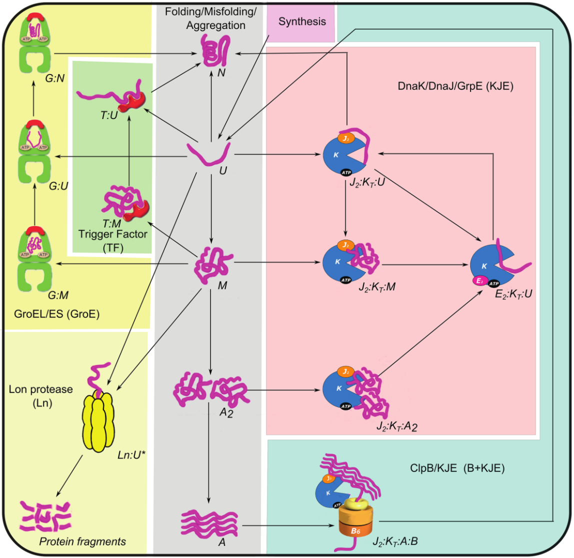
Being on the verge of melting gives proteins the dynamical flexibility essential for their diverse roles as enzymes.

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

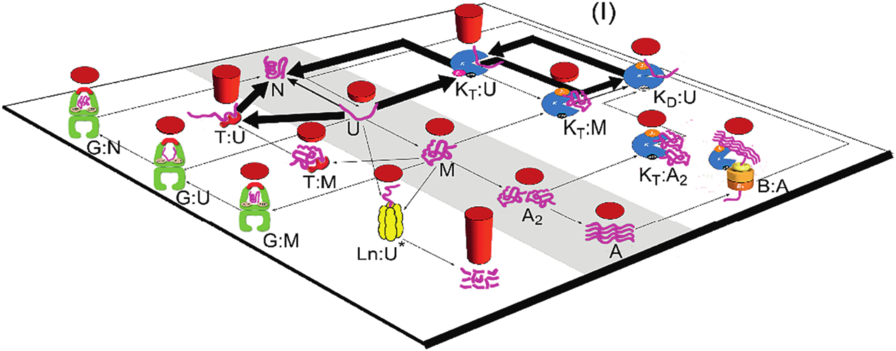
The protein “hospital”: possible chaperone pathways



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:



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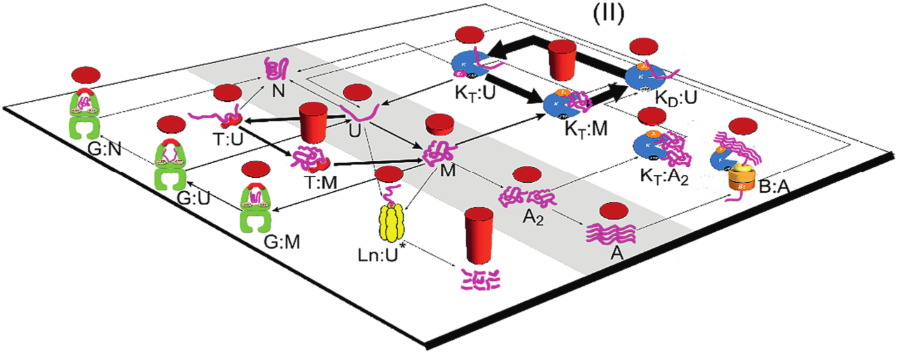

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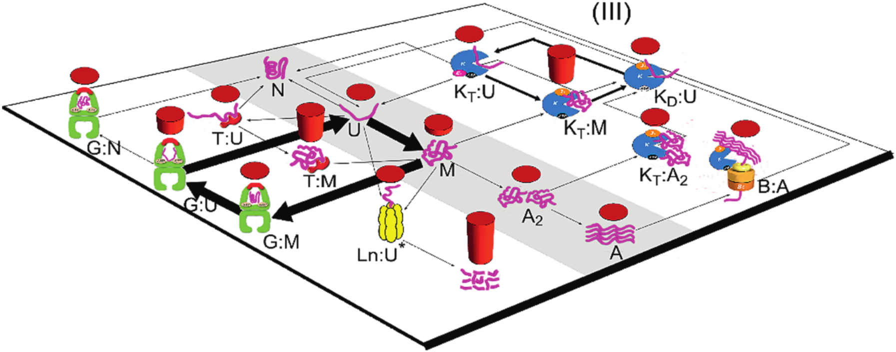
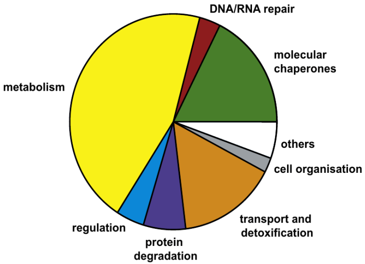


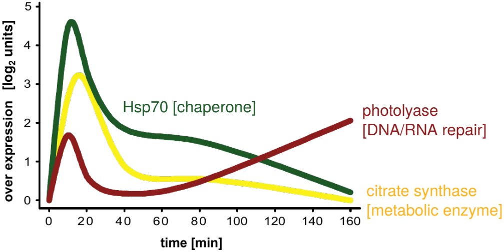
Santra *et al.*, PNAS (2017)

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

Example: heat shock response in yeast

Functional classes of upregulated genes in yeast
after a heat shock from 25°C to 35°C over 10 min:





[Total: 91 genes upregulated by more than 2.8x]

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