

PROTEIN FOLDING 10/14/19

- FOLDING IS COOPERATIVE AND OFTEN TWO-STATE.
 - PROTEINS ARE MARGINALLY STABLE, WITH STABILITIES FROM 5-100 kJ/mol
 - DRIVING FORCE COMES FROM HYDROPHOBIC EFFECT*
 - STRUCTURE COMES FROM HUGE PENALTIES FOR PULLING HYDROGEN BONDS FROM WATER INTO UNFULFILLED STATES
- HOW DO PROTEINS EVEN FIND NATIVE STRUCTURE OUT OF HUGE # OF POSSIBILITIES?
- FOLDING IS MODULAR AND HIERARCHICAL
 - PROTEINS FOLLOW (RELATIVELY) WELL-DEFINED FOLDING PATHWAYS

COOPERATIVE:

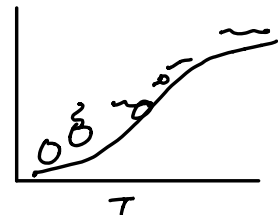
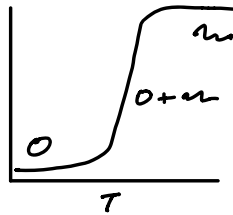
TO A GOOD APPROXIMATION, PROTEINS ARE EITHER FOLDED OR UNFOLDED.

HOW DO WE KNOW?

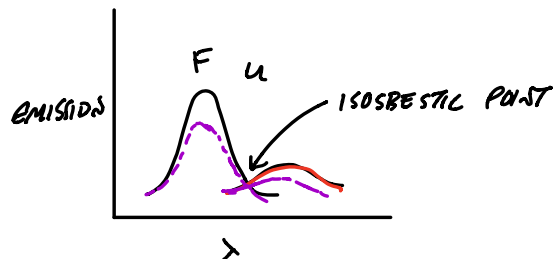
1. UNFOLDING TRANSITION IS SIGMOIDAL

2. $\frac{k_f}{k_u} = \Delta G_{\text{FOLD}}$

S



3. SPECTROSCOPY → LINEAR MIXTURE OF TWO STATES



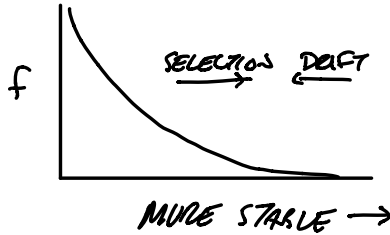
MARGINAL STABILITY:

- BALANCE BETWEEN LARGE # OF TERMS FAVORING FOLDING, LARGE # DISFAVORING FOLDING
- SUMS TO ~ 0 kJ/mol.

WHY?

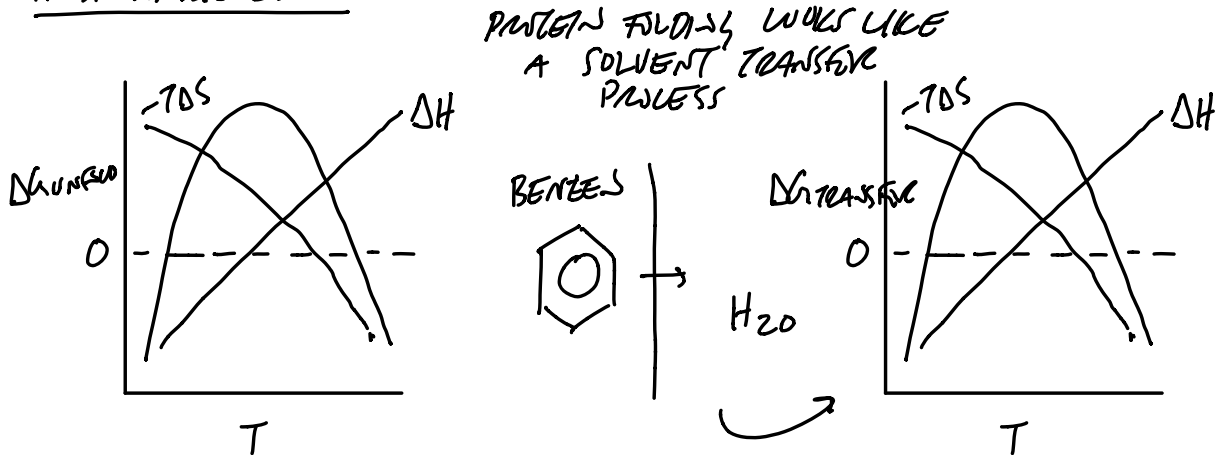
- FUNCTION (E.G. DYNAMICS)
- REGULATION (PROTEOLYTIC TURNOVER)
- EVOLUTION (MUTATION-SELECTION BALANCE)

STABILITY
OF SEQ
ENCODING
FOLD



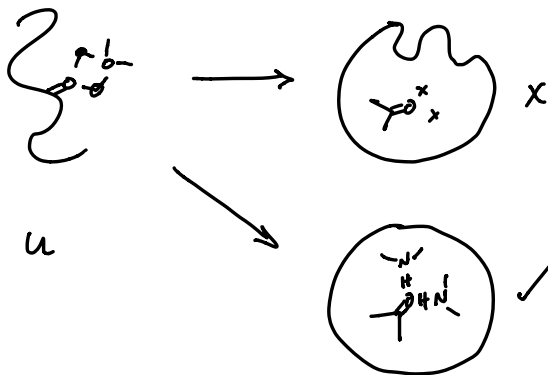
WAY MORE WAYS TO BE UNSTABLE THAN STABLE

HYDROPHOBIC EFFECT



CAN BE QUANTIFIED USING SOLVENT ACCESSIBLE SURFACE AREAS.
(WILL DISCUSS IN ~A WEEK)

STRUCTURE ARISES TO SATISFY ALL NON-COVALENT BONDS



IT COSTS $\sim 20 \text{ kJ/mol}$ TO ENTIRELY
LOSE AN H-BOND WITH WATER.

IF YOU GO THROUGH MANY PROTEIN
STRUCTURES AND CAREFULLY COUNT
UNFULFILLED H-BONDS, ONLY $\sim 1:5,000$
HAVE NO PARTNER. "STATISTICAL POTENTIAL"
IS

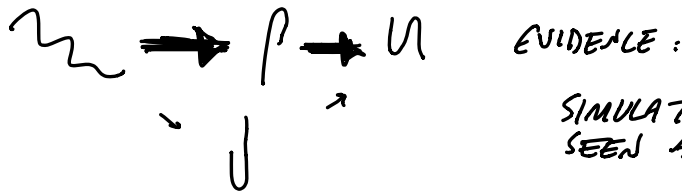
$$-RT \ln(5000/1) = -21 \text{ kJ/mol}$$

HOW DO PROTEINS FIND THEIR FOLDED STATE OUT OF ALL POSSIBILITIES?

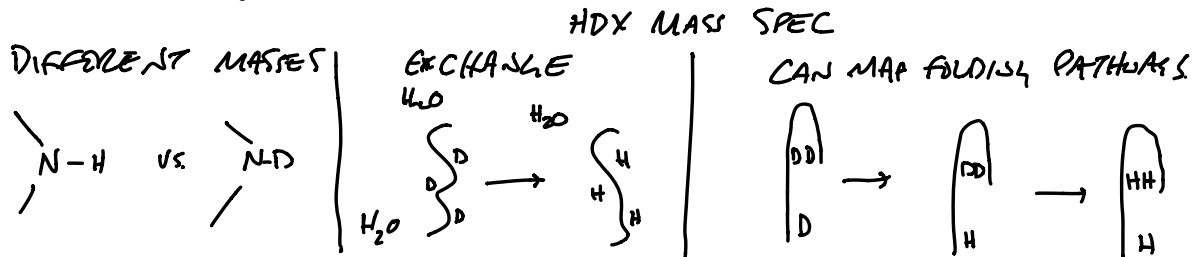
FOLDING IS MODULAR AND HIERARCHICAL

- SECONDARY STRUCTURE \rightarrow DOMAINS \rightarrow ASSEMBLIES
- BIAS TO STRUCTURE: BITS OF IT FORM TRANSIENTLY EVEN IN THE UNFOLDED STATE. MOST STRUCTURES ARE NOT POSSIBLE.

MOSTLY WELL-DEFINED FOLDING PATHWAYS.



SIMULATIONS \rightarrow SAME PATH
SEEN AGAIN AND AGAIN



COOL BIT: CAN SEE NON-LOCAL FOLDING EARLY.

