



Grossoehme, Nicholas <grossoehmen2@mailbox.winthrop.edu>

Protein Stability

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EDIT RESPONSE

Protein Stability

Every amino acid contributes approximately _____ kJ/mol of energy to help stabilize the protein.

How much energy is needed to break a single H-bond?

What is the major contributor to the stability of proteins?

Remind me, what is the main source of stabilizing energy in the hydrophobic effect?

- LDF created when hydrophobic amino acid side chains interact
- The exothermic energy from breaking H-bonds.
- The entropy gain from water escaping to the solvent.
- Other:

Which amino acid side chain has the greatest hydrophobic tendency?

Isoleucine (highest hydropathy value)

Which amino acid side chain is most likely to be able to interact with hydrophobic and hydrophilic regions of a protein?

glycine (closest hydropathy to 0)

What role does H-bonding play in protein stability?

It helps fine tune the structure. The packing of hydrophobic residues ensures that the protein has most of its stabilizing energy - H-bonds make sure that the protein finds the most stable conformation.

What are salt bridges?

Ionic contacts between an acidic and basic amino acid side chain

Where are salt bridges typically located?

the surface of a protein

What is the only major covalent contributor to protein structure?

disulfide bridge between two cysteine residues

List four ways that you can denature a protein.

heat, chaotropic agent (urea), detergent, changing the pH

Proteins are restricted to a single stable conformation.

- True
 False

What is meant by protein breathing?

The protein structure is not rigid. Instead, proteins are continually sampling different conformations. This makes the structure of proteins quite dynamic and fluid - this is fondly referred to as breathing.

Briefly describe a protein folding pathway.

1. the backbone folds adopts the appropriate secondary structure.
2. 2 structure elements fold into common structural motifs.
3. these domains interact to form the globular core of a protein.
4. The complex domains interact through surface contacts.

What are molecular chaperones and what role do they play in protein stability?

Proteins that have evolved to use ATP energy to ensure that a polypeptide chain folds into the correct structure.

What are two major diseases/disorders caused by the misfolding of proteins?

lots of choices here. How about ALS and Parkinson's Disease

Prion proteins contain mostly hydrophobic residues. What is a consequence of this observation?

When they misfold or are degraded, they aggregate into "clumps" similar to amyloid plaques that play a role in neuronal degeneration.

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