Lecture #5 September 4th

Protein Structure and Function

1. Functional classes of proteins
    a. Structural (actin) – support the cell
    b. Scaffold (axin) – support of other proteins
    c. Enzymes (polymerase) – catalyze reactions
    d. Membrane transport (H pumps) – Move molecules
    e. Regulatory (Hormone receptors) – Activate transcription
    f. Motors (Myosin) – move molecules inside the cell
2. Structure of Protein
    a. Primary structure – Sequence of proteins
    b. Secondary structure – local folding
    c. Tertiary structure – long range folding with other molecules
    d. Quaternary structure – multi protein structure
    e. Super molecular structure – large scale assembly (protein complexes)
3. Proteins are made of amino acids
    a. Building units: 20 amino acids
    b. Center is the alpha carbon atom
        i. Off that is the amino group
        ii. Carboxyl group
        iii. A hydrogen atom
        iv. And a variable side chain or residue group
    c. Amino acids are found in the levo (L) isomer form
4. General groupings of amino acids based on side chains
    a. Hydrophobic (water hating)
    b. Hydrophilic (water loving)
        i. Polar charged – Basic amino acids and acidic amino acids
        ii. Polar uncharged
    c. Special amino acids
        i. Glycine
        ii. Cysteine
        iii. Proline
5. Hydrophobic amino acids
    a. Alanine
    b. Valine
    c. Isoleucine
    d. Leucine
    e. Methionine
    f. Phenylalanine
    g. Tyrosine
    h. Tryptophan
6. Hydrophilic charged
    a. Basic amino acids: Lysine, Arginine, Histidine

    b. Acidic amino acids: Aspartate, Glutamate
    c. Found bound to DNA + charge interacts with – DNA
7. Hydrophilic uncharged
    a. Serine, Threonine - target for phosphorylation
    b. Asparagine, Glutamine
8. Special Amino acids
    a. Glycine – non-chiral, small (can fit where others can't), the side chain is H
    b. Cysteine – Sulfhydryl group (-SH) of 2 cysteines can oxidize to form a disulfide bond (-S-S-). Forms a covalent bond instead of a hydrogen bond which makes it much stronger
    c. Proline – Side chain is covantely linked to amine, so this prevents rotation of the alpha carbon and the amino group. Also this prevents proline from fitting in many secondary structures
9. Primary structure (polypeptide bonds)
    a. Formed with the removal of water
    b. Amino acid side chain and polypeptide backbone
    c. Bond is between carboxyl group and nitrogen group
10. Secondary structure (hydrogen bonds)
    a. Stable spatial arrangements of polypeptide bonds
    b. Held together by hydrogen bonds between (N-H) and (C=O) of peptide bonds
    c. Beta sheets and alpha helix are formed
    d. Amino acid side chains protrude from the structure

SIMILARITIES/DIFFERENCES	α	B
Structure	Helix	Sheet
Location of amino acids	Contiguous (4 apart)	Not contiguous
Residues	Outward	Altering above and below
Bond	Hydrogen	Hydrogen

    e. Proline does not like to be in these structures
11. Two configurations of beta sheet – parallel and antiparallel
12. Tertiary structure (non-covalent bonds and hydrophobic forces)
    a. Hydrophobic core region contains nonpolar side chains
    b. Hydrogen bonds can be formed to the polar side chains on the outside of the molecule
    c. Form electrostatic attractions and hydrogen bonds
    d. Shape of the protein is specified by amino acid sequence
        i. Denatured proteins don't work
        ii. Information that allows proteins to fold is found in amino acids
    e. Chapetonines help fold proteins
13. Tertiary structure (protein domains)
    a. Function – ex. Zinc finger motif (interpret DNA)
    b. Structure – Globular domain or fibrous domain
    c. Topology – based on where its located compared to the cytoplasmic domain
    d. Domains are stable on their own even though they are often found together
14. Quaternary structure (multimeric protein assemblies)
    a. Number and relative position of subunits
    b. Macromolecule complexes – multiple proteins together aka molecular machines

c. Have one subunit and bind to form homodimer (2 of the same proteins) or heterodimer (2 different subunits)
d. Homotetrameter or heterotetremeter (4 of the same or different proteins)

15. Protein binding is highly selective
    a. Folded proteins create specific binding sites
    b. Form non-covalent bonds when they bind

Lecture #6 September 4th 6:25PM lecture – this is only a small section of the lecture because the rest o it is irrelevant to the test on Tuesday and those notes will be put in a separate file

1. Enzymes encourage catalysis in several ways
    a. Precise orientation of molecules – bond certain shapes
    b. Rearrange electrons that favor reaction
    c. Strains substrate towards transition state
2. Some common functional classes of enzymes
    a. Hydrolase
    b. Kinase – enzyme catalyzes phosphate group to a protein (phosphorylation)
    c. Phosphatase – opposite of kinase (removes phosphate)
    d. Nuclease – breaks nucleic acids by hydrolysis
    e. ATPase
    f. Protease
3. Some proteins require ions, co-factors
    a. Small molecules expand versatility of proteins
    b. Vitamins, heme, zinc, magnesium
4. Protein regulation
    a. Allosteric sites
        i. Binding sites in a protein other than substrate site
        ii. Interaction between sites cause structural changes to the protein, affecting its performance
        iii. Sites are common target of inhibitors
        iv. Binds and turns an active enzyme to an inactive enzyme
    b. Phosphorylation – the phosphate group can turn an enzyme on or off
    c. GTP binding – turns off the enzyme through hydrolysis

That's all for the test!