BIO1140 StudyFest
Answer Key
April 24th, 2010

1. **Bonding with another Carbon**
   - **Linear, branched or cyclic C backbone chains**
   - **Result in almost unlimited diversity of molecules**

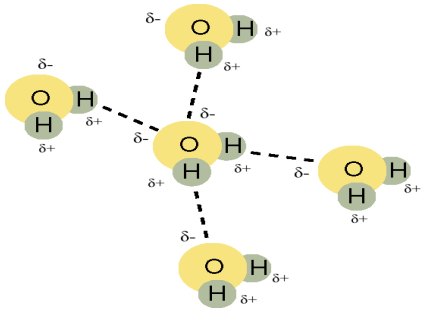
- **Covalent bonding with elements other than carbon**

i. Hydroxyls; found in alcohols, sugars
ii. Carboxyls; found in amino acids, fatty acids
iii. Aminos; found in amino acids, proteins
iv. Sulfhydryls; found in the amino acid cysteine, proteins
v. Phosphates; found in ATP and nucleic acids

2. Hydrogen bond: Strong polarity ->Hydrogen bonds (~5 kcal/mole)

- $\sigma+$ and σ^- dipoles attracted
- Aqueous phase: average ~3 hydrogen bonds per molecule
- Forms interconnected water lattice, less ordered
- Solid phase (ice): 4 hydrogen bond/molecule, rigid bonding and ordered
- Intermolecular spacing increased (volume expansion) -> lower density-> floating
- Water as Solvent: for polar molecules and molecules with ionic bonds salts (hydrophilic)
  - Non-polar moleculs (hydrophobic) are not soluable or poorly soluble in water
- Dipole-dipole interactions form a hydration shell around hydrophilic molecules
- Dispersion of ions and molecules in water=dissolving
- Water=Solvent; dissolved molecules=solute
- Biological importance:
  - Water bridge in macromolecules stabilizes structure
  - All biochemical reactions require aqueous environment
- Cohesion: hydrogen bonding btw water molecules hold them together; this is Cohesion

- Adhesion: hydrogen bonding with other molecules makes water stick to other objects
  - Cohesion and adhesion cause water rise in xyleme fibrils in plants; resist gravity -> continuous flow
- High heat capacity: 1 cal/g raises temp 1˚C, almost twice as others
  - As a result water has high boiling temperature (100˚C)
  - Water resists fast evaporation and cells can resist drying in a wide temperature span



3. Macromolecules: proteins, carbs, lipids, nucleic acids
Role in cell:

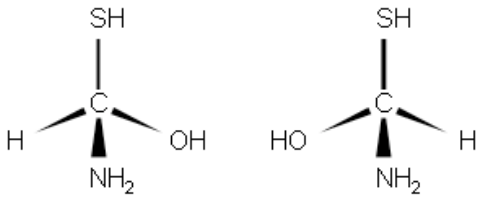
– Informational: order of monomeric units is not random and required for proper function ie. proteins and nucleic acids
– Structural/storage: a single repeating subunit or alternating subunits; order of subunits does not carry information e.g. polysaccharides (cellulose, starch, glycogen)

Recycling of macromolecules:
• Are synthesized from monomers by dehydration reactions
• condensation of monomers by losing a water molecule)
• Degraded by hydrolysis reactions (addition of a water molecule)

4.Monosaccharides
– $(CH_2O)_n$; n = 3 to 7, with n = 5 (pentose) or 6 (hexose) most common
– Aldose sugars (functional group is aldehyde -CHO)
– Ketose sugars (ketone C=O as functional group)

• Isomers: same formula but structurally different eg. glucose, galactose (aldohexoses) and fructose (Ketohexose) all are $C_6H_{12}O_6$ but are structurally different

5. Enantiomers: optical isomers, same folmula, same groups bonding with carbon skeleton, but groups on *asymmetric carbon*
are mirror images of each other, eg in glyceraldehyde
– **D**-form (**D**exter=right) the –OH is facing to the right of backbone
– **L**-form (**L**aevus=left) the –OH is facing to the left



HO H
D-glyceraldehyde L-glyceraldehyde
of backbone; D and L are mirror images and cannot be superimposed

6. Formation of a glycosidic bond:
• Dehydration reaction joins two simple sugars by glycosidic bond
• α 1→4 bond or β1→4 (C1 and C4) is common
• Main polysaccharide backbone
• α 1→6 (C1 and C6) causes branches in the chain
Glycogen and Starch: composed entirely of glucose molecules in the *α* configuration
• **Cellulose** is the most abundant polysaccharide; plant cell wall
• Unbranched glucose polymer with β1→4 glycosidic bond
• H-bonding between many parallel polymers forms strong fibers

7. • **Lipids** have three main roles:
– Energy storage
–Major components of cell membranes
– Important in cell signaling: as steroid hormones and messenger molecules
Fats and oils contain two subunits
– Glycerol is a polyalcohol with three polar –OH groups
– Fatty acids long hydrocarbon chains (16 or 18 carbons) with a carboxyl group (COO–) at one end

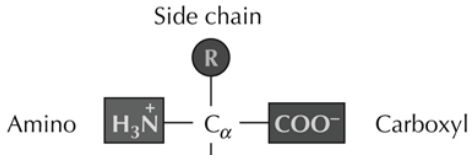
• **Triglyceride:** dehydration reaction adds fatty acids to the –OH groups of glycerol and broken down by hydrolysis reactions

8. **Phospholipids:** principal components of cell membranes
• **Glycerol phospholipids**: 2 fatty acids are bound to carbon in glycerol. The third carbon of glycerol is bound to a phosphate group
• Molecule is hydrophilic at phosphate end and hydrophobic at fatty acid tails
• This is called ***amphipathic*** property; important for formation of bilayer biological membranes

9. – Ethanolamine (phosphatidyl ethanolamine)
– Choline (phosphatidyl choline)
– Serine (phosphatidyl serine)
– Inositol (phosphatidyl inositol)

10. Consist of 2 FA, serine instead of glycerol and one or more sugar instead of phosphate

11. 3 classes of amino acids :
-polar
-nonpolar
-charged



12. Primary structure:
• Sequence of amino acids in a protein is determined by the order of nucleotide bases in a gene

Secondary structure:
3-D structure is a result of interactions between the amino acids regular arrangement of amino acids within localized regions
• There are 2 types of secondary structure:
- The polypeptide can coil in a spiral helix shape
- The polypeptide can fold to form a β pleated sheet (parallel or antiparallel)
• Both are held together by hydrogen bonds between the CO and NH groups of peptide bonds

Tertiary structure:
folding of secondary structural elements to form a 3-D arrangement
• 2° elements connected by loops and less ordered aa's
• interactions btw the side chains of amino acids in different regions of protein stabilizes the structure
- Covalent bonds (S-S bridge)
- Hydrophobic and hydrophilic interactions
• In most proteins this results in **domains**, the basic units of tertiary structure

Quaternary structure:
consists of interactions between different polypeptide chains
• In multi-subunit enzymes
• Hemoglobin, for example, is composed of four polypeptide chains

13. Limiting factor: Surface to volume ratio (S/V)
– Surface is the portal of supply for the volume of cell
– S/V vs X in nonlinear
– S/V exponentially reduced as X increases
• Surface (size of cell) reaches a limit that cannot support the cell's need (volume)
• Eukaryotes: have increased the S/V by extending internal membrane surfaces

14. • **Nuclear envelope** separates nuclear content from the cytoplasm
• selective traffic of proteins and RNAs

• critical in regulating eukaryotic gene
expression
• Consists: two membranes,
underlying nuclear lamina, and nuclear pore complexes
• outer membrane- continuous with the endoplasmic reticulum, has membrane proteins that bind the cytoskeleton
• inner membrane has proteins that bind the nuclear lamina
• Each nuclear membrane is a phospholipid bilayer permeable only to small nonpolar molecules.

15. Nuclear pore- sole channels for small polar molecules, ions, proteins, and RNA to pass through the nuclear envelope
• **Nuclear pore complexes** composed of ~30 different pore proteins (nucleoporins).
• Two mechanisms:
– Passive transport- small molecules pass freely in either direction
– Active transport-
Macromolecules (proteins
and RNAs), energy dependent
• pore complex consists of eight spokes connected to
rings at the nuclear and cytoplasmic surfaces.
• The spoke-ring assembly surrounds a central channel.
• Protein filaments extend from the rings, forming a
basketlike structure on the nuclear side.
• Proteins that must enter the nucleus have amino acid sequences called **nuclear localization signals**.
• These are recognized by **nuclear transport receptors (importins)**

16. **Nuclear Importation:**
• importin binds to the NLS of cargo protein
• complex binds to the cytoplasmic filaments of the pore complex
• Transport proceeds through pore complex by binding to nucleoporins
• cargo/importin complex is disrupted by binding of Ran/GTP.
• conformation change in the importin, releases the cargo into the nucleus
• importin-Ran/GTP complex exported back to the cytoplasm where the GTP is hydrolyzed to GDP
• The importin is released and can participate in another round of transport.
• Ran/GDP is transported back to the nucleus by its own import receptor (NTF2), where Ran/GTP is regenerated.

Ran/GTP Gradient
• Activity of importins regulated by **Ran**, a GTPbinding protein.
• Ran GAP: a GTP hydrolysis to GDP are on the cytoplasmic side of the nuclear envelope
• enzymes for exchange of GDP for GTP are on the nuclear side.
• This leads to higher concentration of Ran/GTP in the nucleus, and determines the

directionality of transport.

Nuclear Exportation

• Proteins are targeted for export from the nucleus by specific amino acid sequences, called **nuclear export signals**.
• These signals are recognized by receptors in the nucleus (**exportins**), which direct protein transport to the cytoplasm.
• Ran is required for nuclear export as well as import.
• Ran/GTP *promotes* binding of exportins and their cargo proteins, but *dissociates* complexes between importins and their cargos.

17. Lysosomes
• Golgi derived membrane-bound vesicles (0.1-1.5 um)
• found in most eucaryotes
• involved in intracellular digestion and recycling of macromolecules
• contain about 40 acid hydrolases
– proteases, nucleases, and phopholipases, amaylases

• maintain an acidic environment by pumping protons into their interior (pH,5.0)
• Digest worn out cellular molecules, engulfed bacteria and viruses
– Fuse with phagosomes (eg engulfed bacteria) to form phagolysosomes
• Lysosomes also participate in apoptosis, or programmed cell death
• Tay-Sachs disease: lysosomal disfunction, autosomal recessive
– Defective Hexosamidase A, a hydrolase involved in breakdown of phospholipids
– Accumulation of lipids in neurons, infantile death

Peroxisomes
• single-membrane-enclosed microbodies
• Originate form ER, cytosolic proteins are imported to peroxisomes (no golgi origin)
• contain enzymes involved in variety of oxidative reactions
• peroxisomal proteins (**peroxins**) are metabolic enzymes
• lipids broken down by oxidative reactions H2O2
• Peroxisomes also contain **catalase**
• Involved in synthesis of amino acids
• Synthesis of cholesterol, bile acids
• Detoxification rxn, eg alcohol

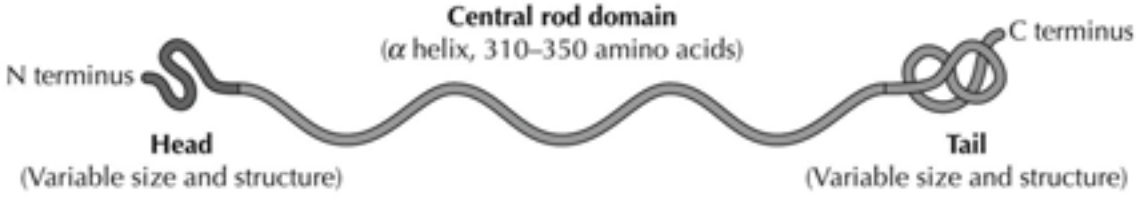
18. Tertiary structures of Actin:
-globular (**G-actin**), 375 aa (43 kD), barbed and pointed ends, binds head-tail to nucleate a trimer
- Filamentous (**F-actin**): monomers added to both end

Actin is “polar” because:
• Polymerization is reversible
• The rate at which monomers are added to filaments is proportional to their concentration
• ATP bound actin binds to barbed end with high affinity
• ADP-actin has low affinity to the pointed ends
• when ATP hydrolyses to ADP
• ADP-actin dissociates from filaments more readily than ATP-actin
• Therefore, the critical concentration of actin monomers is higher for addition to the pointed end than to the barbed end of actin filaments

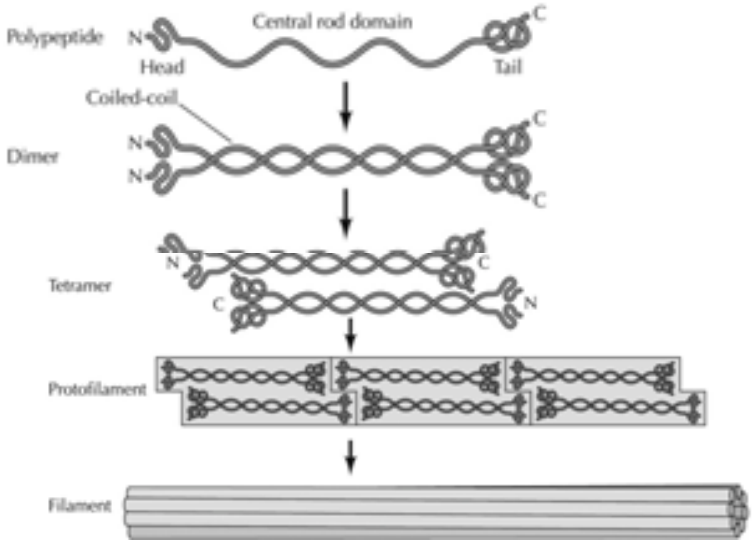
Treadmilling:
• At cellular actin concentrations
• Barbed end of a filament grows 5–10 times faster than the pointed end
• ADP-actin dissociates from pointed end
• Exchange of ATP for ADP[illegible] added to barbed-end
• Process is called **Treadmilling**
• Dynamic growth
• Direction?
Pointed to Barbed

19. Nucleation is the rate-limiting step
• **Formin** and the **Arp2/3 complex** determine where filaments are formed by facilitating nucleation
• Formins nucleate long unbranched actin filaments
• actin filaments actively turn over and branch extensively
• These filaments are nucleated by the Arp2/3 (Actin Related Protein) complex, which binds actin/ATP near the barbed ends

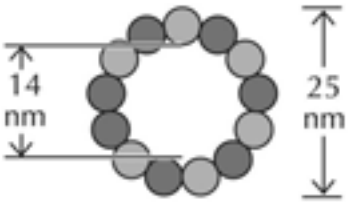
ADF:
• The **ADF/cofilin** (Actin Depolymerizing Factor) family modifies existing filaments
• enhance the rate of dissociation of actin/ADP monomers from the pointed end, and remain bound to the monomers, preventing their reincorporation

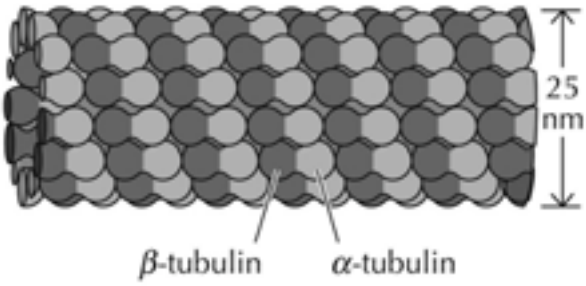


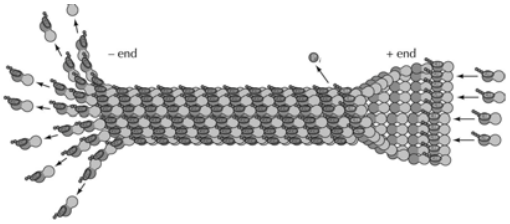
Assembly
• Dimer: central rod form coiled coil
• Tetramer: staggered antiparallel
• Protofilament: tetramers assemble end to end
• Filament: 8 interwound protofilaments



21. • **Microtubules** are rigid hollow rods (25 nm)
• Dynamic structures, undergo continual assembly and disassembly
• Function: cell movements and determining cell shape, organelle transport, mitosis
• Tubulin, globular protein is the monomer
• *α*-tubulin and *β*-tubulin dimers make up microtubules
• *γ*-tubulin in the centrosome plays a critical role in initiating microtubule assembly







• Tubulin dimers polymerize to form microtubules
• consisting of 13 protofilaments assembled around a hollow core
• Protofilaments composed of head-to-tail arrays of tubulin dimers arranged in parallel

• two distinct ends: a fastgrowing + end and a slowgrowing minus end

Treadmilling:

• Microtubules can undergo **treadmilling**
• Tubulin dimers with GTP bound to *β*-tubulin associate with the growing end
• GTP is hydrolyzed , tubulin gets less stable, minus end dimers disassociate

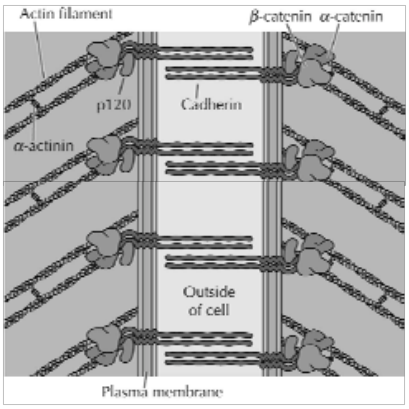
22. **Basal laminae**: thin layer on which epithelial cells rest. Also surrounds muscle cells, adipose cells, and peripheral nerves.
• most abundant in connective tissues

Other components:
• **Fibrous proteins**
• **Polysaccharides**- gel like environment
• **Adhesion proteins**- link components of the matrix to one another and to cells
• Different matrices have different amounts of each component
– Tendons, rich in fibrous proteins
– Cartilage, high in polysaccharides
– Bone, calcium phosphate crystal deposition

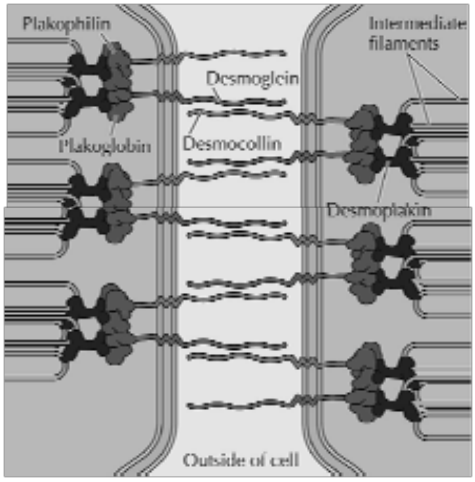
23. Extracellular matrix gels are polysaccharides called **glycosaminoglycans** (**GAGs**).
• GAGs are repeating units of disaccharides: One sugar is either *N*-acetylglucosamine or *N*-acetylgalactosamine, the second is usually acidic (glucuronic acid or iduronic acid).

• sulfate groups make GAGs negatively charged
• bind positively charged ions and trap water molecules to form hydrated gel
• GAGs are linked to proteins to form **proteoglycans**

24. i. Adherens Junctions:
• **Cadherin** form stable cell-cell connections involving actin filaments
• Also include *β*-catenin, p120, and *α*-catenin,
• *β*-catenin and p120 bind to **cadherin** and help maintain stability
• *β*-catenin binds *α*-catenin that interacts with actin filament of cytoskeleton

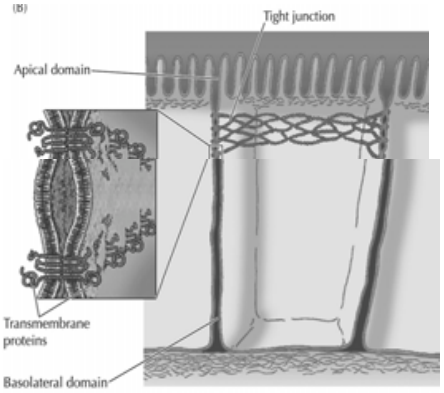


ii. Desmosomes:
• link the intermediate filament of adjacent cells
• **Desmoglein** and **desmocollin**
(transmembrane cadherins) bind by heterophilic

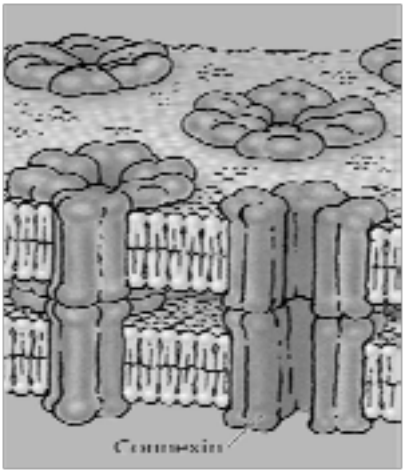


interactions across the junction
• Plakoglobin and plakophilin bind to the cadherins and link to the intermediate
filament binding protein, desmoplakin

iii. Tight Junctions:
Tight junctions provide minimal adhesive strength between the cells, usually associated with adherens junctions and desmosomes in a **junctional complex**
• **Tight junctions** in epithelial cell form a seal that prevents free passage of molecules and ions between cells
• separate apical and basolateral domains of the plasma membrane
• prevent free diffusion of lipids and membrane proteins
• transmembrane proteins, occludin, claudin, and junctional adhesion molecule (JAM), anchored on F-actin
• Bind similar proteins on the adjacent cell
• Sealing the space between cells

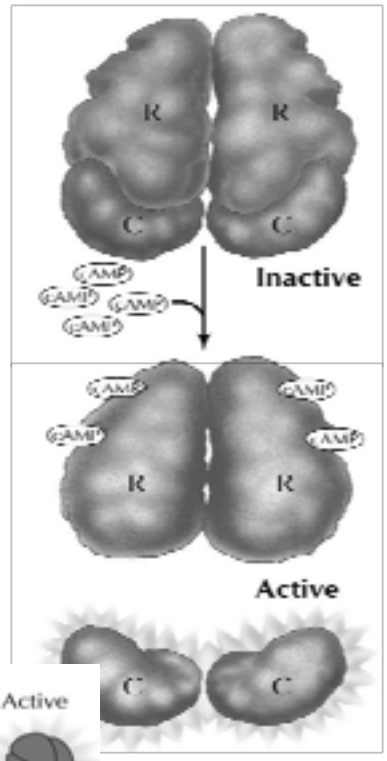


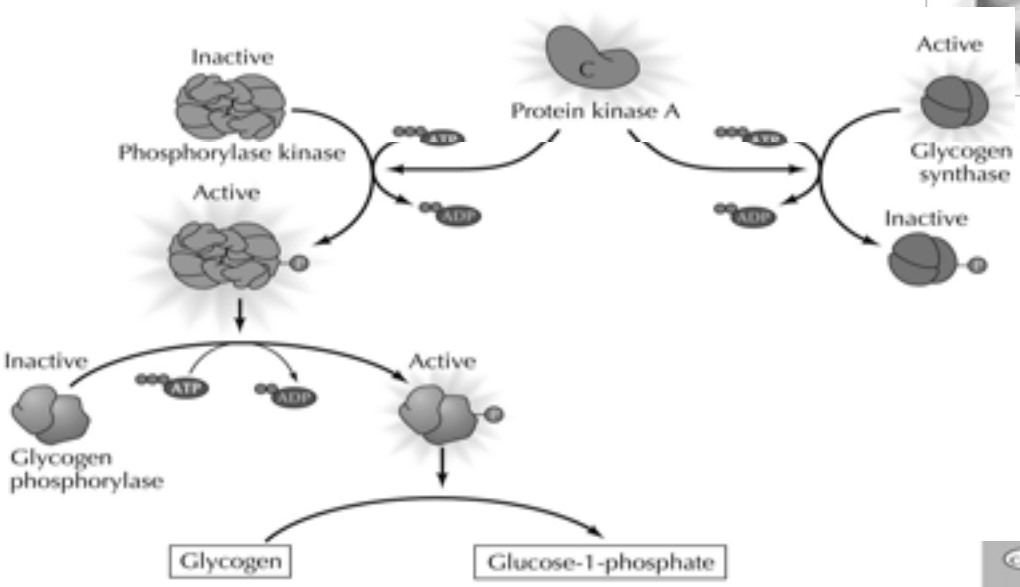
iv. Gap Junctions:
• open channels through the plasma membrane
• allowing ions and small molecules to diffuse freely
• Proteins and nucleic acids can not pass through
• heart muscle cells, passage of ions through gap junctions synchronizes the contractions of neighboring cells
• allow passage of some signaling molecules, such as cAMP and Ca2+, coordinating responses of cells in tissues
• Gap junctions are made of transmembrane proteins in the **connexin** family.
• 6 connexins form a cylinder with an open aqueous pore in its center, called a **connexon**
• Connexons in the plasma membrane adjacent cells align
• form open channels between the two cytoplasms
• Specialized gap junctions occur on specific nerve cells and form an **electrical synapse**
• Individual connexons can be opened or closed. When open, they allow rapid passage of ions between the two nerve cells



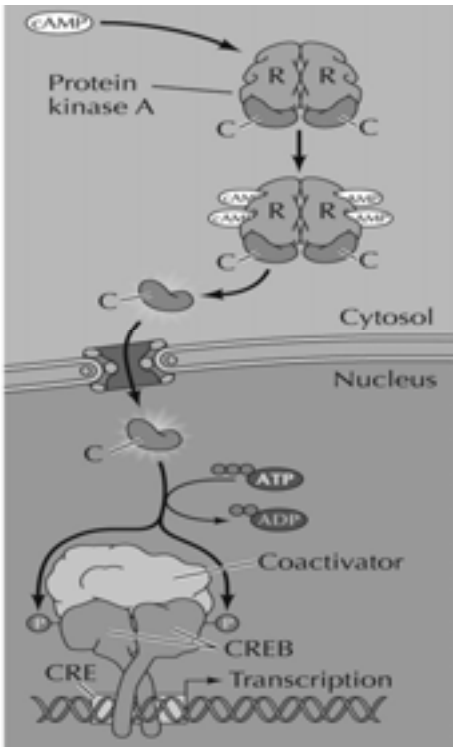
25. **cAMP signaling & cell responses**
1. Metabolic regulation
• Cytosolic Protein Kinase A activation (PKA)
• tetramer of regulatory and catalytic subunits, ie R2C2 (inactive)
• cAMP binding of "R" dissociation of

catalytic subunits (active)
• A serine/threonine kinase Activation or inactivation of substrate proteins
Phosphorylation of two downstream enzymes:
• Glycogen synthase inactivated glycogen synthesis↓
• Phosphorylase kinase activated phosphorylates Glycogen phosphorylase (active)---> Glu-1P↑



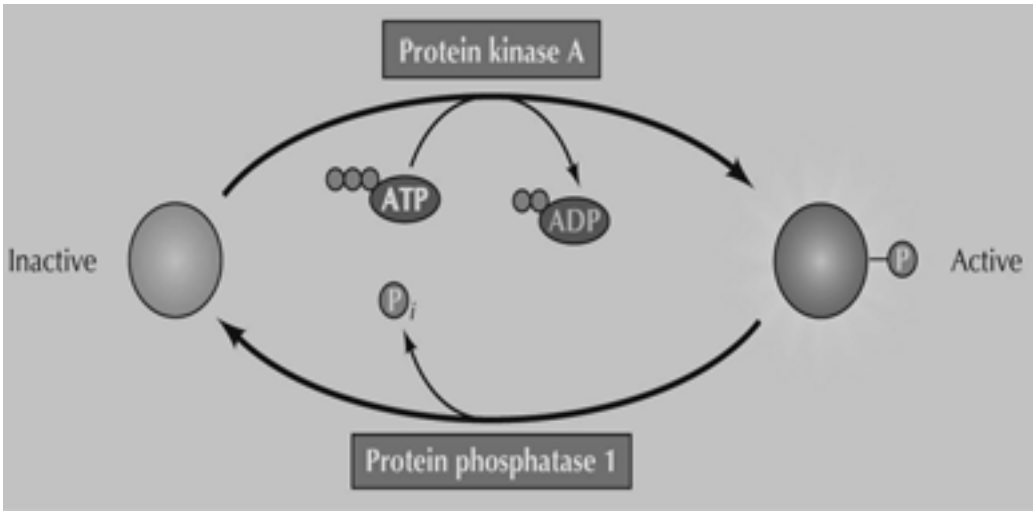


2. Gene regulation
• Increased cAMP activate transcription
• Free PKA C-subunit translocated to the nucleus
• binds Genes containing a regulatory sequence—the **cAMP response element**, or **CRE**
• phosphorylates the transcription factor **CREB** (CRE-binding protein).
• Recruits RNA polymerase
• expression of cAMP-inducible genes

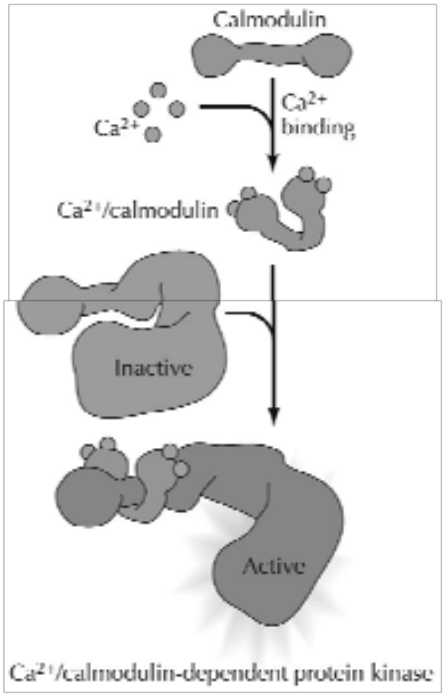


• Proliferation, differentiation, memory, cognition

• Protein phosphorylation is reversed by protein phosphatases
• terminates responses initiated by receptor activation or protein kinase

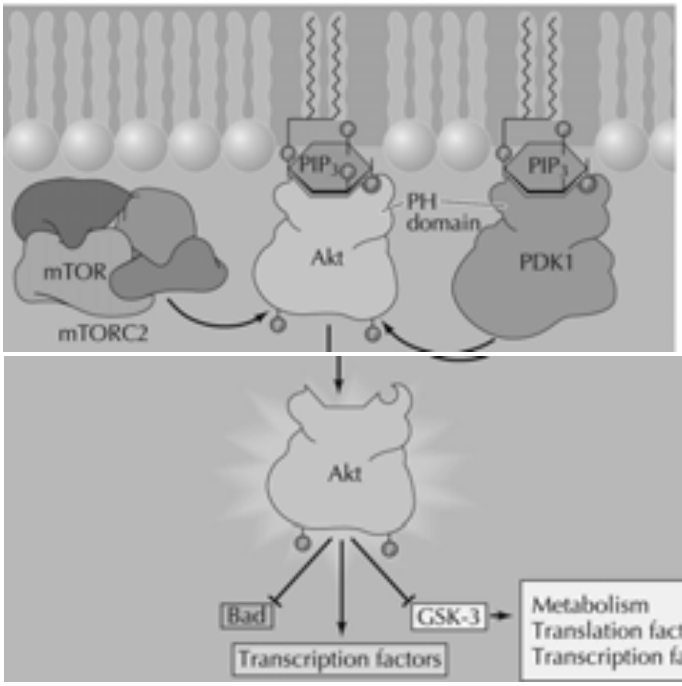


26. • **Calmodulin** is activated when Ca2+ concentration increases
• **CaM kinase** family are activated by Ca2+/ calmodulin



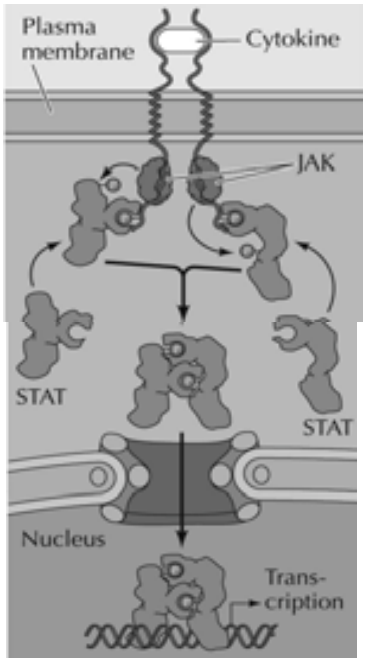
• they phosphorylate and activate other proteins such as,
• protein kinases, phosphatases, metabolic enzymes, ion channels, and transcription factors (eg CREB)
• Also regulates synthesis and release of neurotransmitters

27.PIP2 is also the start of another signaling pathway
• PIP2 is phosphorylated by **phosphatidylinositide (PI) 3 kinase**



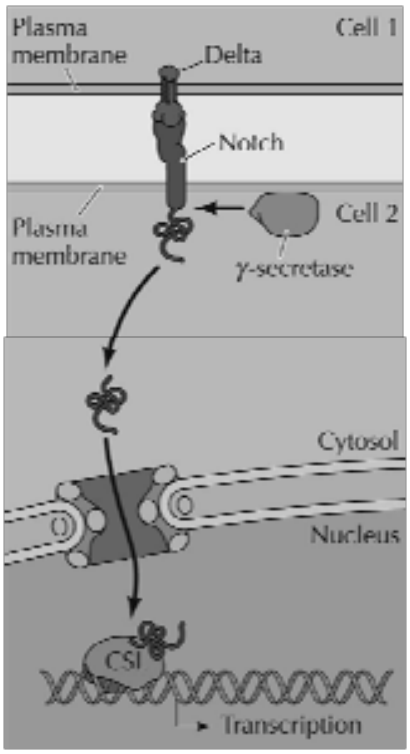
• This yields a second messenger, **phosphatidylinositol 3,4,5-trisphosphate (PIP3)**
PIP3 targets a proteinserine/threonine kinase called **Akt** and also binds protein kinase PDK1

• Activation of Akt also requires protein kinase mTOR (in a complex called mTORC2) which is also stimulated by growth factor
• Akt phosphorylates several target proteins, transcription factors, and other protein kinases
• Transcription factors include members of the Forkhead or FOXO family
• If growth factors are not present, Akt is not active
• FOXO travels to the nucleus, stimulates transcription of genes that inhibit cell proliferation, or induce cell death
• When growth factors attached to receptor/tyrosine kinases
• Akt is phosphorylated (active)
• Akt phosphorylation of FOXO sequesters it in inactive form
• Akt inhibits GSK 3 the general GSK-3, inhibitor of translation
• Inhibition of GSK-3 relieves translation
• Cells are prepared to proliferate



28. JAK/STAT pathway
• Direct signaling from receptor to nucleus
• Ligand: cytokines
• Receptors: Janus Kinases (JAK), nonreceptor protein-tyrosine kinase
• STAT Signal Tansducer & Activators of Transcription
• Transcription factors, contain SH2 domains that mediate binding to phosphotyrosine sequences
• STATs activated, dimerized, translocate to nucleus
• Activate transcription

29. Notch pathway
• **direct cell-cell interactions during development**
• **Notch a receptor for signaling by transmembrane proteins (e.g., Delta) on adjacent cells**
• **Ligand binding ---> proteolytic cleavage of cytosolic domain of Notch**
• **translocated into the nucleus**
• **converts a transcription factor (CSL in mammals) from a repressor to an activator**



• **Downstream genes code for other transcriptional factors**
• **Cell developmental differentiation**

30. Chromatin
-Distributed between:
-Euchromatin (loosely packed region, genes active in RNA
transcription)
-Heterochromatin (densely packed masses, genes are inactive)
-Folds and packs to form thick, rodlike chromosomes during
nuclear division

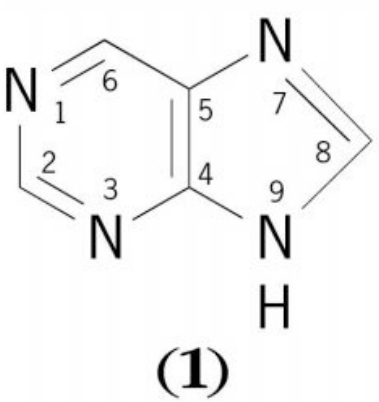
Euchromatin
•Higher histone acetylation
•Lower histone methlylation
•Lower DNA methylation
•Active genes

Heterochromatin
•Lower histone acetylation
•Higher histone methlylation
•Higher DNA methylation
•Inactive genes

HETEROCHROMATIN
•Highly condensed
•Inactive
•DNA is highly methylated.
•15% of genome **
•centromeric and telomeric
regions
•constitutive or facultative
•highly enriched in DNA repeats
EUCHROMATIN
•Dispersed
•Active
•Less methlyated

31. -There are 4 nitrogenous bases (4 types, A, C,G, T)
(adenine, cytosine, guanine, thymine)
-A base is a purine or pyrimidine
(adenine, cytosine, guanine, thymine)
-A base + a pentose sugar = nucleoside.

if the sugar is a deoxyribose,it is a deoxyribonucleoside
(deoxyadenosine, deoxycytidine, deoxyguanosine, deoxythymidine)
-A nucleoside + phosphate = deoxynucleotide
(deoxyadenosine 5'-monophosphate, deoxycytidine 5'-diphosphate, etc.)
-There are 5'-monophosphates, 5'-diphosphates, 5'-triphosphates
(deoxyadenosine 5'-monophosphate (dAMP), deoxadenosine 5'-diphosphate dADP), deoxadenosine 5'-triphosphate dATP).
32. Purine Pyridimine



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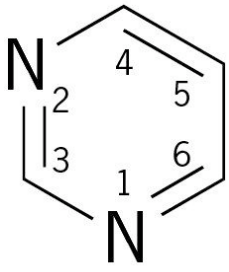


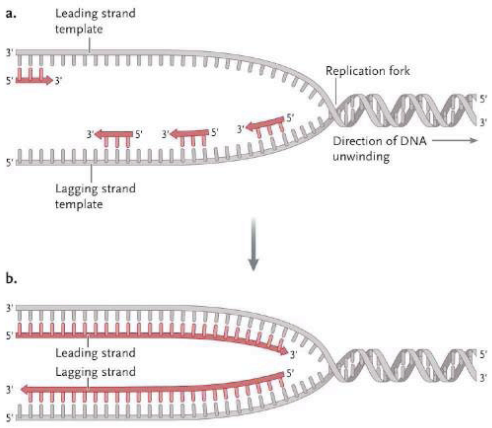
(1)

33. i. The DNA structure is antiparallel. DNA strands go from 5’ to 3’.
ii. Synthesis follows the base-pairing rules, A-T, G-C.
iii. One new DNA strand is synthesized continuously; the other, discontinuously
iv. DNA polymerases are the primary enzymes of DNA replication.
v. DNA replication begins at replication origins
vi.RNA primers provide the starting point for DNA polymerase to begin synthesizing a new DNA chain

34. -Helicase unwinds the DNA
- Primase synthesizes RNA primer (starting point fornucleotide assembly by DNA polymerases)
- DNA polymerases assemble nucleotides into a chain, remove primers, and fill resulting gaps
- DNA ligase closes remaining single-chain nicks

35. Leading strand=continuous
Lagging strand=discontinous

-As DNA helix unwinds, one template strand runs in a
direction allowing new DNA strand to be made continuously in the direction of unwinding



- Other template strand is copied in short lengths that run in the direction opposite to unwinding
- Discontinuous replication produces short lengths, then linked into a continuous strand

36. Mechanisms That Correct Errors

- Errors inevitably occur, during replication or caused by DNA damage
- Proofreading depends on the ability of DNA polymerases to reverse
and remove mismatched bases
- DNA repair corrects errors that escape proofreading or caused by DNA damaging agents

Proofreading by DNA Polymerase:
-If a replication error causes a base to be mispaired, DNA polymerase reverses and removes the most recently added bases.
-The enzyme then resumes DNA synthesis in the forward direction

DNA polymerase enzymes
- Recognize distorted regions caused by mispaired base pairs
- Remove DNA section with mispaired base from the newly synthesized nucleotide chain
- Resynthesize the section correctly, using original template chain as a guide

37. Promoter: Control sequence initiates transcription
- Transcription unit: Portion of gene that is copied into RNA
- Terminator: Signals the end of transcription of a gene

38. Overview of transcription:
- Begins as RNA polymerase binds to DNA
- DNA double helix begins to unwind
- RNA polymerase adds RNA nucleotides sequentially according to DNA template
- Enzyme and completed RNA transcript release from DNA template

RNA polymerase:
- catalyses the polymerization of ribonucleoside 5'-triphosphates(rNTP or NTP)
- does not require a primer, transcription is initiated de novo.
- initiates synthesis at 'promoter' sequences on DNA, upstream (5') to the transcription start site. Other sequences such as enhancers can affect transcription.

- adds NTPs at 3' end of new polynucleotide until it encounters a termination signal at defined sequence and/or structure on the DNA template.

- the “pre-RNA” is “processed” into the mature RNA. In eucaryotes mRNA is transported to the cytoplasm.

39. i. tRNAs are small RNAs of a highly distinctive structure that bring amino acids to the ribosome.
ii. Ribosomes are rRNA-protein complexes that work as automated protein assembly machines
iii. Translation initiation brings the ribosomal subunits, an mRNA, and the first aminoacyl-tRNA together
iv. Newly synthesized polypeptides are processed and folded into finished form
v. Finished proteins contain sorting signals that direct them to cellular locations

40. DNA, three-letter code: Triplet
RNA, three-letter code: Codon

the codon in DNA is written the same as the codon in RNA, except that T becomes U. 5’GAC3’ in DNA is 5’GAC3’ in RNA.
But 5’GTC3 in DNA is 5’GUC3’ in RNA (molecular types often mess this up and use T when writing RNA).

41. **Start codon or initiator codon**
- First amino acid recognized during translation
Specifies amino acid “methionine”
Sense Codons
- Establishes the reading frame
- Sense codons
- 61 codons specify amino acids
- Most amino acids specified by several codons (degeneracy or redundancy)
Ex: CCU, CCC, CCA, CCG all specify proline

Stop codons or termination codons (sometimes “nonsense”)
- End of a polypeptide-encoding mRNA sequence
UAA, UAG, UGA (sometimes referred to as “ochre”, “amber” and “opal”; the names relate to their discovery in mutations)

42. Initiation
- Ribosome assembled with mRNA molecule and initiator methioninetRNA
Elongation
- Amino acids linked to tRNAs added one at a time to growing polypeptide chain
Termination
- New polypeptide released from ribosome
- Ribosomal subunits separate from mRNA

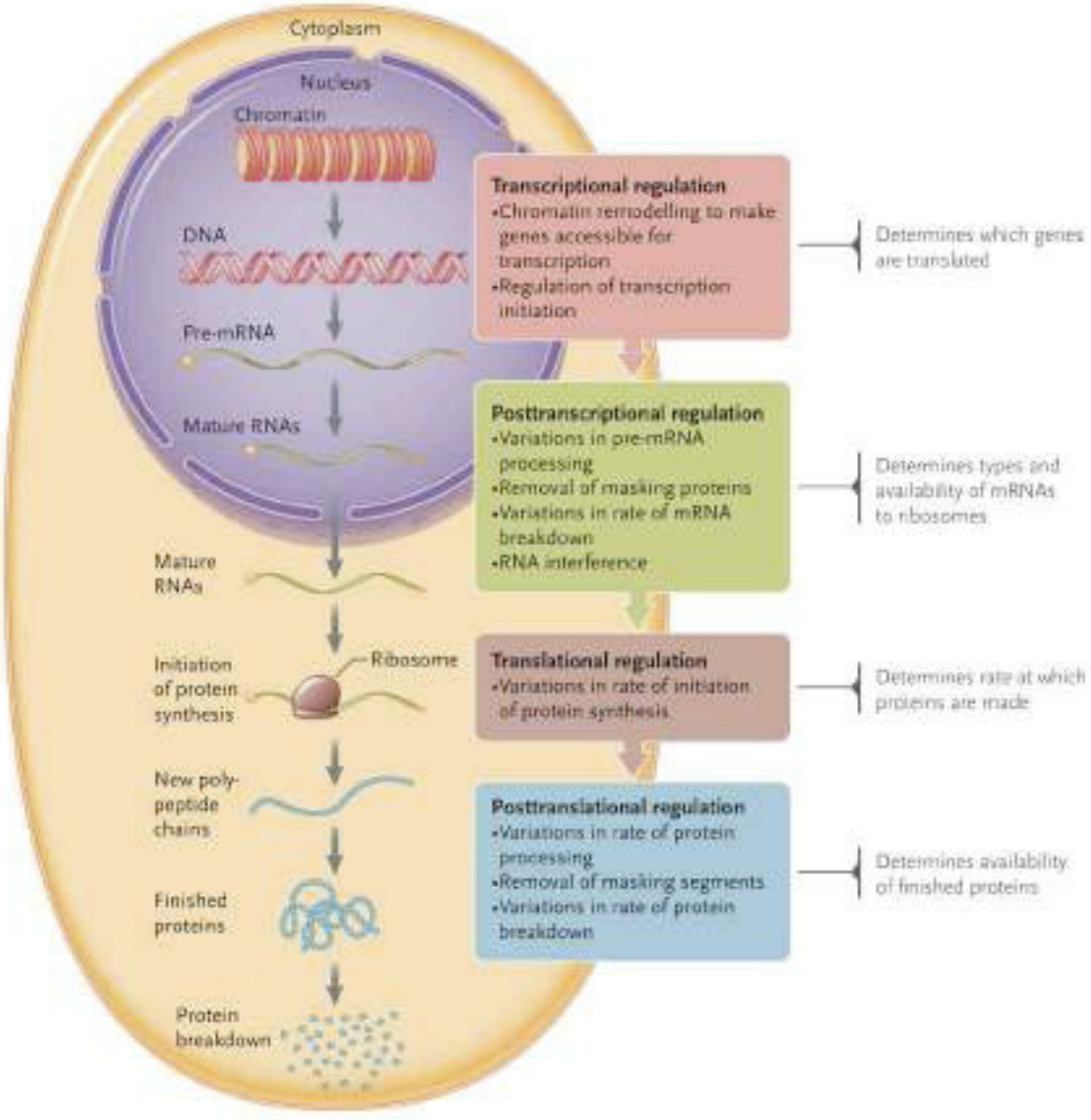
INITIATION
- Initiator tRNA (Met-tRNA) binds to small subunit

- Complex binds to 5´ cap of mRNA, scans along mRNA to find AUG start codon
- Large ribosomal subunit binds to complete initiation

ELONGATION
- Aminoacyl-tRNA matching the next codon enters A site
- Peptidyl transferase catalyzes formation of first peptide bond and cleaves tRNA in P site
- Ribosome moves along mRNA to next codon
- Empty tRNA moves from P site to E site, then released
- Newly formed peptidyl-tRNA moves from A site to P site
- A site empty again

TERMINATION
Begins when A site reaches stop codon
- Release factor (RF) or termination factor binds to A site
- Polypeptide chain released from P site
- Remaining parts of complex separated

43.



44. i. Activators bind to promoter proximal elements and increase transcription rate
ii. Coactivators bridge enhancer and promoter
- Interactions between coactivator, proteins at promoter, and RNA polymerase increase transcription
iii. Repressors oppose effect of activators
- Transcription rate depends on activation and repression signals
- In a multicellular organism these signals may be external (heat, light etc.) or internal (hormones etc.)
- May bind to sites of activator or coactivator or increase association with histones

45. Translation
2. Interaction with receptor & unfolding
-signals on protein
-proteins aid unfolding (chaperones)
3. Translocation
4. Refolding/processing
-proteases may remove signals
-proteins aid unfolding (chaperones)

46. Transport across the membrane into the ER (the lumen) is the first step for targeting to many locations-ER, Golgi, several vesicles and outside of the cell. A signal peptide is required, as is a receptor.
In the absence of further information the protein is exported.
This is referred to as the "default pathway".
What is the nature of the signal peptide?
What is the fate of the signal peptide?
The signal peptide for ER transport is an length of 20-50 aa's with an hydrophobic core. These are recognized by the signal recognition particle and the complex binds to the SRP receptor.
When translation resumes the signal peptide is cleaved by the signal peptidase. We refer to the original protein as the preprotein.
An example: prelysozyme becomes lysozyme when the SP is removed.