**Metabolism and Bioenergetics**

**12.1: Food and Fuel**

* Summarize the pathways for digesting and mobilizing metabolic fuels.
  + Distinguish autotrophs and heterotrophs.
  + List the monomer and polymer form for each major type of metabolic fuel.
  + For each fuel, summarize the process of digestion, absorption, storage, and mobilization.

**autotrophs vs. heterotrophs**

Chemoautotrophs

Photoautotrophs

Heterotrophs

Consumption of fuels as macromolecular polymers

Digestion breaks down polymers into monomers

**fuel: macromolecules**

starch, protein, fat

**digestion: polymers to monomers**

starch: glucose

protein: amino acids

fat: fatty acids

**digestive enzymes**

starch: amylase

protein: protease

fat: lipase

**fatty acid transport/storage**

transport: cholesteryl esters

storage: TAGs in adipocytes

**glucose storage/mobilization**

storage: glycogen (glycogen synthase)

mobilization: glucose (glycogen phosphorylase)

**lysosomal protein degradation**

Lysosome contains hydrolytic enzymes

Membrane and extracellular proteins taken up by endocytosis; also intracellular vesicular proteins

**proteasomal degradation**

Multiprotein complex with multiple active sites

Peptide bond hydrolysis

Requires substrate tagging with ubiquitin (C-term) to Lys side chain; polyubiquitination (4) is required for degradation

Entry to proteasome is regulated by barrel cap

ATP hydrolysis drives protein unfolding (non-spontaneous), which allows for efficient hydrolysis

Ubiquitin is recycled; proteasome releases ~8 residue polypeptides for further hydrolysis and catabolism/recycling

**12.2: Metabolic Pathways**

* Recognize the common chemical features of metabolic pathways.
  + Recognize common metabolites.
  + Identify oxidized and reduced partners in chemical reactions.
  + Explain why metabolic pathways are connected, regulated, and cell specific.
  + List some vitamins and their biological roles.

**shared metabolic intermediates**

G-3-P: glycolysis, CO2 reduction, TAG synthesis

Pyruvate: glycolysis, CAC (acetyl-CoA), a.a. degradation/biosynthesis

Acetyl-CoA: complete oxidation to CO2, TAG synthesis (f.a. building block)

**anabolic vs. catabolic processes**

catabolism = oxidation of carbon atoms

anabolism = reduction of carbon atoms

Reactions occur in pairs between donors and acceptors.

Reduction of carbons stores free energy harvested from sunlight in carbohydrates.

Free energy is released during (stepwise) breakdown of carbohydrates to CO2.

**redox reactions**

Fe 3+ + e- > Fe2+

Bonds represent pairs of electrons

H atoms carry and electron (e- travels with H+/pair of e- travels with H-)

NAD(P)+ = electron acceptor/NAD(P)H = electron donor

NAD+: catabolic/NADP+: anabolic

Lipid soluble electron carrier

Stepwise uptake of electrons

Q > QH > QH2

Diffusion to membrane bound enzymes

**oxidative phosphorylation**

cofactor recycling to replenish oxidized cofactors

oxygen = final electron acceptor

**vitamins**

Beriberi: B1 deficiency

Pyruvate dehydrogenase requires TPP (pyruvate to acetyl CoA)

Pellagra: niacin deficiency

Relieved by increased Trp intake

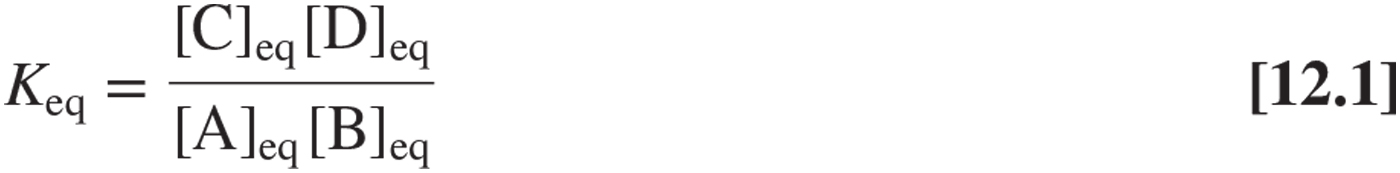
Trp >> Niacin

Vitamin-deficiency more prevalent in impoverished (nutrition-poor) regions

NADP+, NAD+

**12.3: Free Energy Changes in Metabolic Reactions**

* Analyze the free energy changes that occur during metabolic reactions.
  + Distinguish the actual and standard free energy change for a reaction. (calc. 12.1)
  + Relate the free energy change to the concentrations of reactants. (calc. 12.2)
  + Explain what occurs when reactions are coupled.
  + Identify molecules that function as energy currency.
  + Explain how certain reactions can control flux through a pathway.



Reactant concentrations determine free energy change

Concentrations of the reaction species at equilibrium define the *K*eq.

The standard free energy change is the driving force that the reactants undergo to reach their equilibrium values.

@ Eq, forward and reverse rates are equal, but [reactants] and [products] are not!



Biochemical Standard State: 25C, 1 M, pH 7, [H2O] = 55.5 M



In vivo, reaction species are not present at standard state concentrations

ACTUAL free energy change = , which is a function of the actual concentrations and temperature

Spontaneity depends on mass action ratio

**coupled reactions and ATP hydrolysis**

AMP transfer releases Ppi, subsequent cleavage releases same energy

Transfer of phosphoryl groups has a large negative free energy change

Reaction products have less free energy than the reactants

Products of ATP hydrolysis are more stable than the reactants (anionic groups repel each other; charge separation relieves electrostatic repulsion)

Resonance stabilization is increased in hydrolysis products vs. phosphoanhydride compound

Resonance stabilization is higher in free Pi and ADP vs. ATP

**sources of cellular energy**

phosphocreatine, thioester

**regulation of metabolic pathways**

Near-equilibrium reactions: flux depends concentrations of reactants and products

“Far-equilibrium” reactions: large driving force to proceed, rate limited by enzyme activity

Control of pathway can be modulated by increasing enzyme concentration or activity