Biochemistry Essentials Cheatsheet

A concise reference for key biochemical concepts, pathways, and reactions. This cheat sheet covers essential topics for students and professionals in biochemistry and related fields, providing a quick guide to metabolic processes, enzyme kinetics, and biomolecule structures.

Macromolecule Building Blocks

Amino Acids

General Structure:	Amino acids consist of a central carbon atom bonded to an amino group (-NH2), a carboxyl group (-COOH), a hydrogen atom (-H), and a unique side chain (R).
Classification:	Amino acids are classified based on their R-group properties: nonpolar, polar uncharged, positively charged (basic), and negatively charged (acidic).
Peptide Bond:	Amino acids are linked by peptide bonds, formed through dehydration synthesis between the carboxyl group of one amino acid and the amino group of another.
Essential Amino Acids:	These cannot be synthesized by the body and must be obtained from the diet. Examples include leucine, isoleucine, valine, lysine, threonine, tryptophan, phenylalanine, and methionine.
Chirality:	All amino acids, except glycine, are chiral. Only L-amino acids are found in proteins.
pKa Values:	Each amino acid has at least two pKa values, corresponding to the protonation states of the amino and carboxyl groups. Some also have a pKa for their side chain.

Nucleotides

Structure:	Composed of a nitrogenous base (adenine, guanine, cytosine, thymine, or uracil), a pentose sugar (ribose or deoxyribose), and one or more phosphate groups.
Nitrogenous Bases:	Purines (adenine and guanine) have a double-ring structure, while pyrimidines (cytosine, thymine, and uracil) have a single-ring structure.
DNA vs. RNA:	DNA contains deoxyribose and thymine, while RNA contains ribose and uracil.
Phosphodiester Bond:	Nucleotides are linked by phosphodiester bonds between the 3'-hydroxyl group of one nucleotide and the 5'-phosphate group of another.
Base Pairing:	Adenine pairs with thymine (or uracil) via two hydrogen bonds, while guanine pairs with cytosine via three hydrogen bonds.
Nucleosides:	A nucleoside consists of a nitrogenous base and a pentose sugar, but without any phosphate groups.

Carbohydrates

Monosaccharides:	Simple sugars such as glucose, fructose, and galactose. They are the building blocks of complex carbohydrates.
Disaccharides:	Composed of two monosaccharides linked by a glycosidic bond. Examples include sucrose (glucose + fructose), lactose (glucose + galactose), and maltose (glucose + glucose).
Polysaccharides:	Complex carbohydrates made up of many monosaccharides. Examples include starch, glycogen, and cellulose.
Glycosidic Bond:	The covalent bond that joins two monosaccharides. It is formed through dehydration synthesis.
Isomers:	Carbohydrates can exist as different isomers, such as D-glucose and L-glucose, which are mirror images of each other.
Functions:	Carbohydrates serve as energy sources, structural components (e.g., cellulose in plants), and signaling molecules.

Enzyme Kinetics and Mechanisms

Michaelis-Menten Kinetics

Equation:	$v = \frac{V_{max}[S]}{K_M + [S]}$ where: • v = reaction rate • V_{max} = maximum reaction rate • [S] = substrate concentration • K_M = Michaelis constant
K_M:	The substrate concentration at which the reaction rate is half of V_{max}. It is a measure of the affinity of the enzyme for its substrate. A lower K_M indicates higher affinity.
V_{max}:	The maximum rate of reaction when the enzyme is saturated with substrate. It is directly proportional to the enzyme concentration.
Lineweaver-Burk Plot:	A double reciprocal plot of the Michaelis-Menten equation: $\frac{1}{v} = \frac{K_M}{V_{max}} \frac{1}{[S]} + \frac{1}{V_{max}}$ • x-intercept = $-\frac{1}{K_M}$ • y-intercept = $\frac{1}{V_{max}}$
Catalytic Efficiency:	A measure of how efficiently an enzyme converts substrate to product. Given by k_{cat}/K_M, where k_{cat} is the turnover number.
Turnover Number (k_{cat}):	The number of substrate molecules converted to product per enzyme molecule per unit of time when the enzyme is saturated with substrate. $k_{cat} = V_{max}/[E]_T$, where $[E]_T$ is the total enzyme concentration.

Enzyme Inhibition

Competitive Inhibition:	Inhibitor binds to the active site, preventing substrate binding. K_M increases, V_{max} remains unchanged. Can be overcome by increasing substrate concentration.
Uncompetitive Inhibition:	Inhibitor binds only to the enzyme-substrate complex. Both K_M and V_{max} decrease. Cannot be overcome by increasing substrate concentration.
Noncompetitive Inhibition:	Inhibitor binds to a site distinct from the active site, affecting enzyme conformation. V_{max} decreases, K_M remains unchanged. Cannot be overcome by increasing substrate concentration.
Mixed Inhibition:	Inhibitor can bind to either the enzyme or the enzyme-substrate complex. V_{max} decreases, and K_M may increase or decrease. Cannot be overcome by increasing substrate concentration.
Irreversible Inhibition:	Inhibitor binds covalently to the enzyme, permanently inactivating it. Examples include nerve gases and some drugs.
Allosteric Regulation:	Regulation of an enzyme by binding an effector molecule at a site other than the enzyme's active site. Can be activating or inhibitory.

Enzyme Mechanisms

Acid-Base Catalysis:	Enzyme uses acidic or basic amino acid side chains to transfer protons, stabilizing transition states.
Covalent Catalysis:	Enzyme forms a transient covalent bond with the substrate, creating a reactive intermediate.
Metal Ion Catalysis:	Metal ions participate in catalysis by stabilizing charged intermediates, mediating redox reactions, or acting as Lewis acids.
Proximity and Orientation Effects:	Enzymes bring substrates together in the correct orientation, increasing the frequency of collisions and facilitating the reaction.
Transition State Stabilization:	Enzymes bind and stabilize the transition state of the reaction, lowering the activation energy and accelerating the reaction.
Serine Proteases:	A family of enzymes that use a serine residue in their active site to cleave peptide bonds. Examples include chymotrypsin, trypsin, and elastase.

Metabolic Pathways

Glycolysis

Overview:	The breakdown of glucose into pyruvate, producing ATP and NADH. Occurs in the cytoplasm.
Key Enzymes:	Hexokinase/Glucokinase, Phosphofructokinase-1 (PFK-1), Pyruvate Kinase.
Regulation:	PFK-1 is the major regulatory point. Activated by AMP and fructose-2,6-bisphosphate; inhibited by ATP and citrate.
Net Products:	2 ATP, 2 NADH, 2 Pyruvate per glucose molecule.
Anaerobic Fate of Pyruvate:	In the absence of oxygen, pyruvate is converted to lactate by lactate dehydrogenase, regenerating NAD+.
Aerobic Fate of Pyruvate:	In the presence of oxygen, pyruvate is converted to acetyl-CoA, which enters the citric acid cycle.

Citric Acid Cycle (Krebs Cycle)

Overview:	A series of reactions that oxidize acetyl-CoA to carbon dioxide, producing ATP, NADH, and FADH2. Occurs in the mitochondrial matrix.
Key Enzymes:	Citrate Synthase, Isocitrate Dehydrogenase, α-Ketoglutarate Dehydrogenase Complex.
Regulation:	Isocitrate Dehydrogenase is activated by ADP and inhibited by ATP and NADH. α-Ketoglutarate Dehydrogenase is inhibited by ATP, NADH, and succinyl-CoA.
Net Products:	1 ATP, 3 NADH, 1 FADH2, 2 CO2 per acetyl-CoA molecule.
Entry Point:	Acetyl-CoA, derived from pyruvate, fatty acids, and amino acids.
Intermediates:	Citrate, Isocitrate, α-Ketoglutarate, Succinyl-CoA, Succinate, Fumarate, Malate, Oxaloacetate.

Oxidative Phosphorylation

Overview:	The process by which ATP is synthesized using the energy released from the electron transport chain. Occurs in the inner mitochondrial membrane.
Electron Transport Chain (ETC):	A series of protein complexes (Complex I-IV) that transfer electrons from NADH and FADH2 to oxygen, creating a proton gradient.
ATP Synthase:	An enzyme that uses the proton gradient to drive the synthesis of ATP from ADP and inorganic phosphate.
Uncouplers:	Molecules that disrupt the proton gradient, uncoupling electron transport from ATP synthesis. Examples include DNP.
Inhibitors:	Substances that block the electron transport chain at various points. Examples include cyanide (Complex IV) and rotenone (Complex I).
Net ATP Yield:	Approximately 32 ATP per glucose molecule, depending on the efficiency of the proton gradient and ATP synthase.

Lipid Metabolism

Fatty Acid Synthesis

Location:	Cytosol
Precursor:	Acetyl-CoA (transported from mitochondria via citrate shuttle)
Key Enzyme:	Acetyl-CoA Carboxylase (ACC)
Regulation:	ACC is activated by citrate and insulin, inhibited by palmitoyl-CoA and glucagon/epinephrine
Process:	Repeated addition of two-carbon units from malonyl-CoA to a growing fatty acid chain
Product:	Palmitate (C16:0), which can be further elongated and desaturated

Fatty Acid Oxidation (Beta-Oxidation)

Location:	Mitochondrial matrix
Process:	Sequential removal of two-carbon units (acetyl-CoA) from the fatty acid chain
Activation:	Fatty acids are activated by attachment to CoA, forming fatty acyl-CoA
Carnitine Shuttle:	Transports fatty acyl-CoA from the cytosol into the mitochondrial matrix
Products:	Acetyl-CoA, FADH2, NADH
Regulation:	Inhibited by malonyl-CoA (ensures that fatty acid synthesis and oxidation do not occur simultaneously)

Ketone Body Metabolism

Ketone Bodies:	Acetoacetate, 3-hydroxybutyrate, and acetone
Synthesis:	Occurs in the liver mitochondria during prolonged fasting or starvation
Precursor:	Acetyl-CoA (derived from fatty acid oxidation)
Utilization:	Used as an alternative fuel source by the brain, heart, and muscle during glucose deprivation
Ketogenesis:	The process of ketone body synthesis
Ketoacidosis:	Excessive production of ketone bodies, leading to a decrease in blood pH (occurs in uncontrolled diabetes)