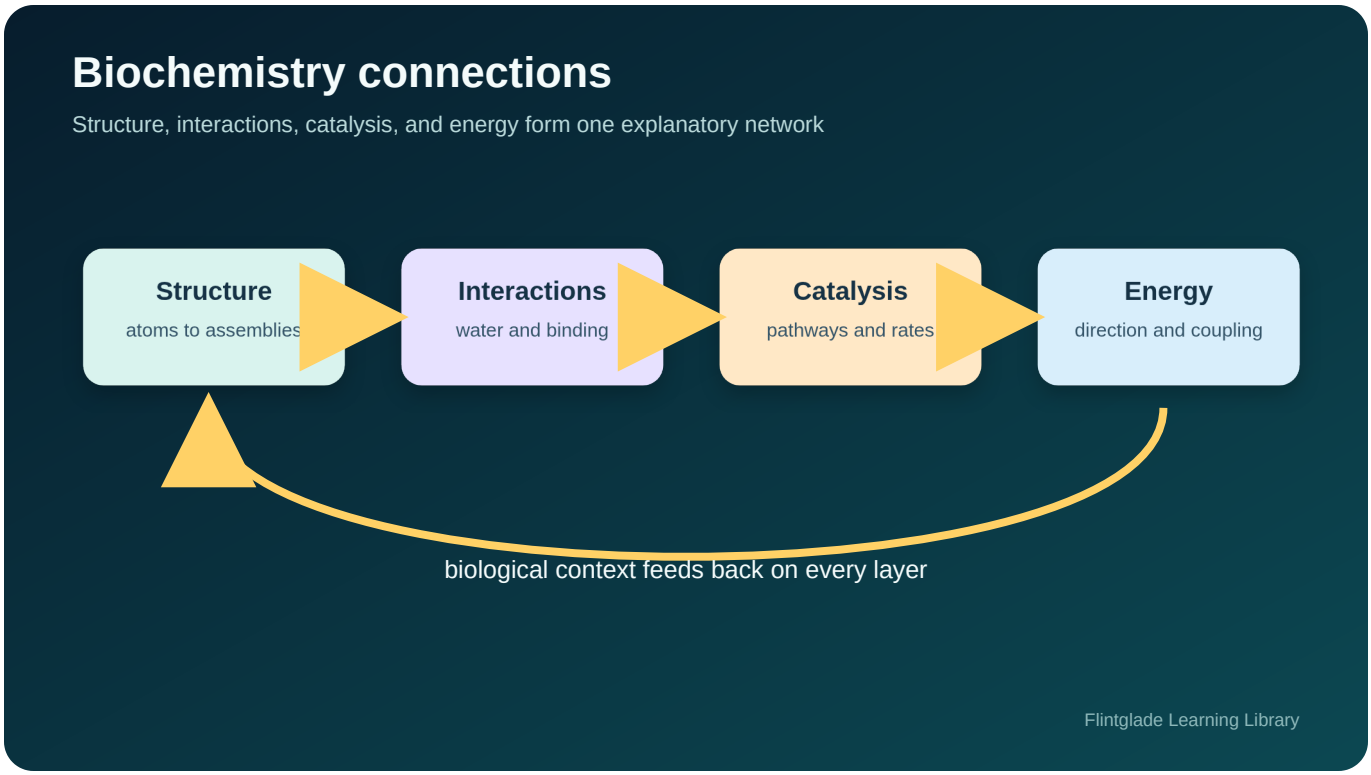
Biochemistry: A High-Density Reference

Flintglade Learning Library · General Biochemistry

Audience: Learners who want formulas, pathway checkpoints, and compact biochemical reference tables.

MCAT connections: This guide can assist study of enzymes and kinetics, energetics and metabolism while keeping general biochemistry as its primary frame.



About this edition: This standalone edition organizes the material for independent reading with clear navigation, reusable reasoning frameworks, and print-ready presentation.

Learning goals

- Connect common equations to the quantities they describe
- Compare carrier roles and pathway control points
- Use compact tables without losing the assumptions behind them

Navigate this guide

The sections below pair each compact table with the reasoning for using it.

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1. Amino Acid pKa Table

Why: These values support net-charge calculations, ionization-state predictions, pKa-shift reasoning, and efficient multi-step work; a self-contained reference should include them.

2. Residue Mass Table (for MS/MS calculations)

Why: Same logic — a self-contained reference includes masses to calculate y-ion or b-ion m/z values. These are pure lookup and not derivable.

3. Key ΔG°' Values for Coupled Reaction Problems

Why: A recurring application uses coupled reaction calculations (1,3-BPG → 3PG + ATP, PEP → Pyruvate + ATP, etc.). Having the standard free energies of hydrolysis for key molecules eliminates an error-prone step:

- PEP: −61.9 kJ/mol
- 1,3-BPG: −49.4 kJ/mol
- ATP: −30.5 kJ/mol
- Acetyl CoA thioester: ~−31.4 kJ/mol

4. The Michaelis-Menten / Lineweaver-Burk / Inhibitor Summary Table

Why: The inhibitor classification table (competitive/uncompetitive/noncompetitive effects on Vmax, KM, and L-B plot patterns) is high-density, high-value information that's easy to confuse under pressure.

Type	Vmax	KM	L-B Pattern
Competitive	same	↑ (αKM)	Intersect y-axis
Uncompetitive	↓	↓	Parallel lines
Pure Noncompetitive	↓ (Vmax/α)	same	Intersect x-axis

Plus: $\alpha = 1 + [I]/KI$, and the formula $v_0 = kcat[S]/(KM + [S])$ for comparing isozymes at physiological [S].

5. PDH Cofactor-Role Matching

Why: This relationship is central to cofactor-function matching. Five cofactors, five roles, and confusing the order between TPP → lipoamide → CoA → FAD → NAD^+ is a common mistake during multi-step reasoning. A compact table:

- TPP (E1): electron sink for decarboxylation
- Lipoamide (E2): reduced by hydroxyethyl-TPP; carries acetyl to CoA
- CoA (E2): accepts acetyl from acetyl-lipoamide (transesterification)
- FAD (E3): catalytic reoxidation of dihydrolipoamide (reduced cysteines)
- NAD^+ (E3): stoichiometric reoxidation of $FADH^-$

6. Glycolysis Enzyme Names + Regulatory Status

Why: A compact enzyme-to-regulatory-significance list complements the structural details elsewhere:

- Hexokinase: irreversible, inhibited by G6P
- PFK-1: COMMITTED STEP, activated by AMP/F2,6-BP, inhibited by ATP/citrate
- Pyruvate kinase: irreversible, activated by F1,6-BP (feed-forward), inhibited by ATP/Ala
- GAPDH: requires NAD^+ + Pi (not ATP)

7. Gluconeogenesis Bypass Enzymes

Why: The three bypass reactions and their enzymes are frequently used, and mixing up which glycolytic step they replace is an easy mistake:

- Pyruvate kinase bypass → Pyruvate carboxylase (biotin, ATP, mito) + PEPCK (GTP, cyto)
- PFK-1 bypass → FBPase-1
- Hexokinase bypass → Glucose-6-phosphatase (liver/kidney ONLY)

8. F2,6-BP Regulatory Logic

Why: This single molecule reciprocally controls glycolysis and gluconeogenesis, and it can be summarized as a compact rule. One line: "F2,6-BP activates PFK-1 (glycolysis ON), inhibits FBPase-1 (gluconeogenesis OFF)."

9. Transport Free Energy Equation

Why: The electrochemical gradient calculation ($\Delta G = RT \ln([C]in/[C]out) + zF\Delta\psi$) is easy to set up wrong with sign errors. Having the formula with clear sign conventions (z = charge of ion, $\Delta\psi$ = inside minus outside, F = 96.5 kJ/mol·V) prevents costly mistakes on transport problems like the H^+/K^+-ATPase calculation in a worked transport example.

10. ETC Summary: Complexes, Electron Carriers, H^+ Pumped

Why: Dense factual content that's hard to reconstruct from first principles:

- Complex I: NADH → Q, pumps 4 H^+
- Complex II: $FADH_2$ → Q, pumps 0 H^+
- Complex III: QH_2 → cyt c, pumps 4 H^+ (Q cycle)
- Complex IV: cyt c → O_2, pumps 2 H^+ (+2 H^+ consumed)
- ATP synthase: ~3-4 H^+ per ATP

11. ATP Yield Summary

Why: The complete glucose → ~30 ATP accounting is a useful calculation. Having the breakdown (which step produces what, NADH vs $FADH_2$ yields, shuttle differences) as a compact reference prevents arithmetic errors.

12. Hill Plot Equations

Why: The Hill plot analysis ($\log(\theta/(1-\theta)) = n \cdot \log(pO_2) - n \cdot \log(p50)$) and how to extract p50 from the linear regression (p50 = 10^(y-intercept/slope)) is used quantitatively. Having the formula avoids rederivation.

13. Key Thermodynamic Relationships (Compact)

Why: These relationships are gathered here for convenience:

- $\Delta G = \Delta H - T\Delta S$
- $\Delta G^{\circ\prime} = -RT \ln Keq$
- $\Delta G = \Delta G^{\circ\prime} + RT \ln Q$
- $\theta = [L]/(Kd + [L])$
- $v_0 = Vmax[S]/(KM + [S])$
- $1/v_0 = (KM/Vmax)(1/[S]) + 1/Vmax$
- $R = 8.314 \times 10^{-3}$ kJ/(mol·K)
- F = 96.5 kJ/(mol·V)

Suggested Reference Order

Core reference: Items 4, 5, 9, 10, 13

Useful extensions: Items 3, 6, 7, 11, 12

Additional lookups: Items 1, 2, 8