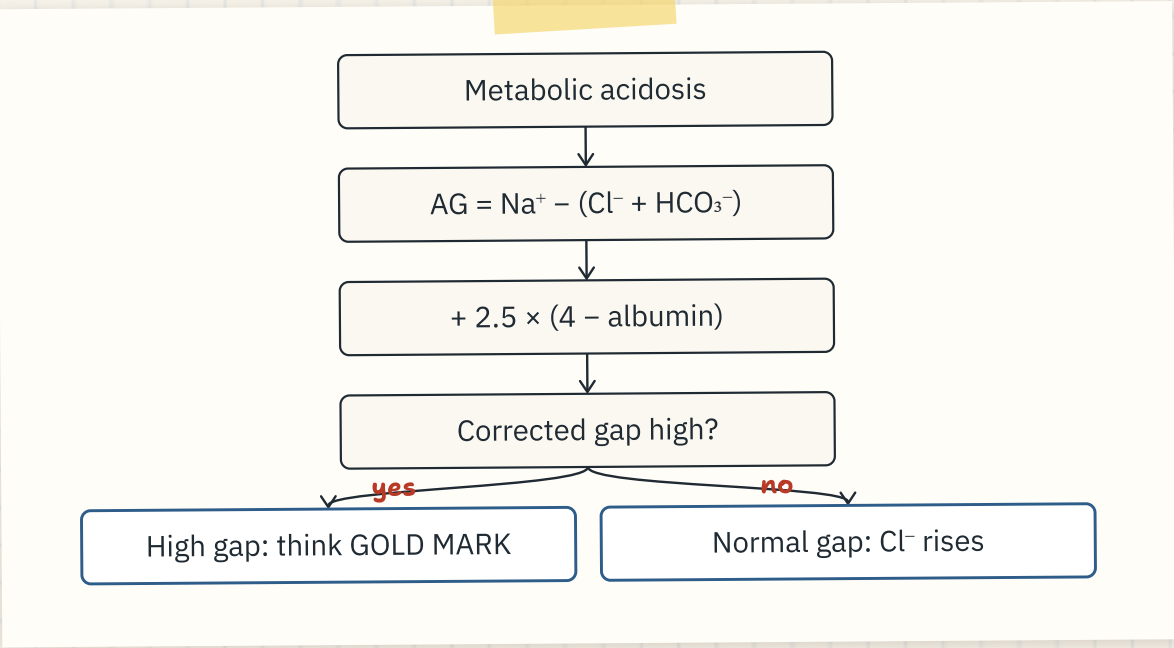
Anion gap in 3 steps

Calculate, correct for albumin, classify



Step by step

1. Calculate: $Na^+ - (Cl^- + HCO_3^-)$.
2. Correct: add 2.5 for every g/dL of albumin below 4.
3. Classify: high gap = added unmeasured anion; normal gap = HCO_3^- lost or not regenerated, Cl^- gained.

ANION GAP AND ALBUMIN CORRECTION

$$AG = Na^+ - (Cl^- + HCO_3^-); \quad \text{corrected AG} = AG + 2.5 \times (4 - \text{albumin})$$

Normal ≈ 8–12 mEq/L without K^+ (≈ 12–16 with K^+); use your lab's range. Albumin in g/dL.

	High gap	Normal gap (hyperchloremic)
Mechanism	Acid added; its anion is unmeasured	HCO_3^- lost or not regenerated (or Cl^- added)
Chloride	Stays put	Rises to replace HCO_3^-
Causes	GOLD MARK	Gut losses (diarrhea, fistulas), RTA, acetazolamide, urinary diversion, rapid saline

High gap vs normal gap metabolic acidosis

GOLD MARK (high gap)

Glycols · 5-Oxoproline · L-lactate · D-lactate

Methanol · Aspirin · Renal failure · Ketoacidosis

Exam traps

- Low albumin lowers the gap and can hide a high-gap acidosis: 12 → 17 with albumin 2 g/dL.
- Normal ranges differ (8–12, 12–16 with K^+, 3–9 or 3–11 on many modern analysers): trust your lab.
- Kidney disease can produce either a high-gap or a normal-gap pattern.

Anion gap explained: high vs normal gap metabolic acidosis

Video, written lesson, practice question and sources: medservatory.com/usmle-step-1/renal-acid-base/anion-gap

For exam study only, not medical advice. Follow local guidelines and your lab's ranges.
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