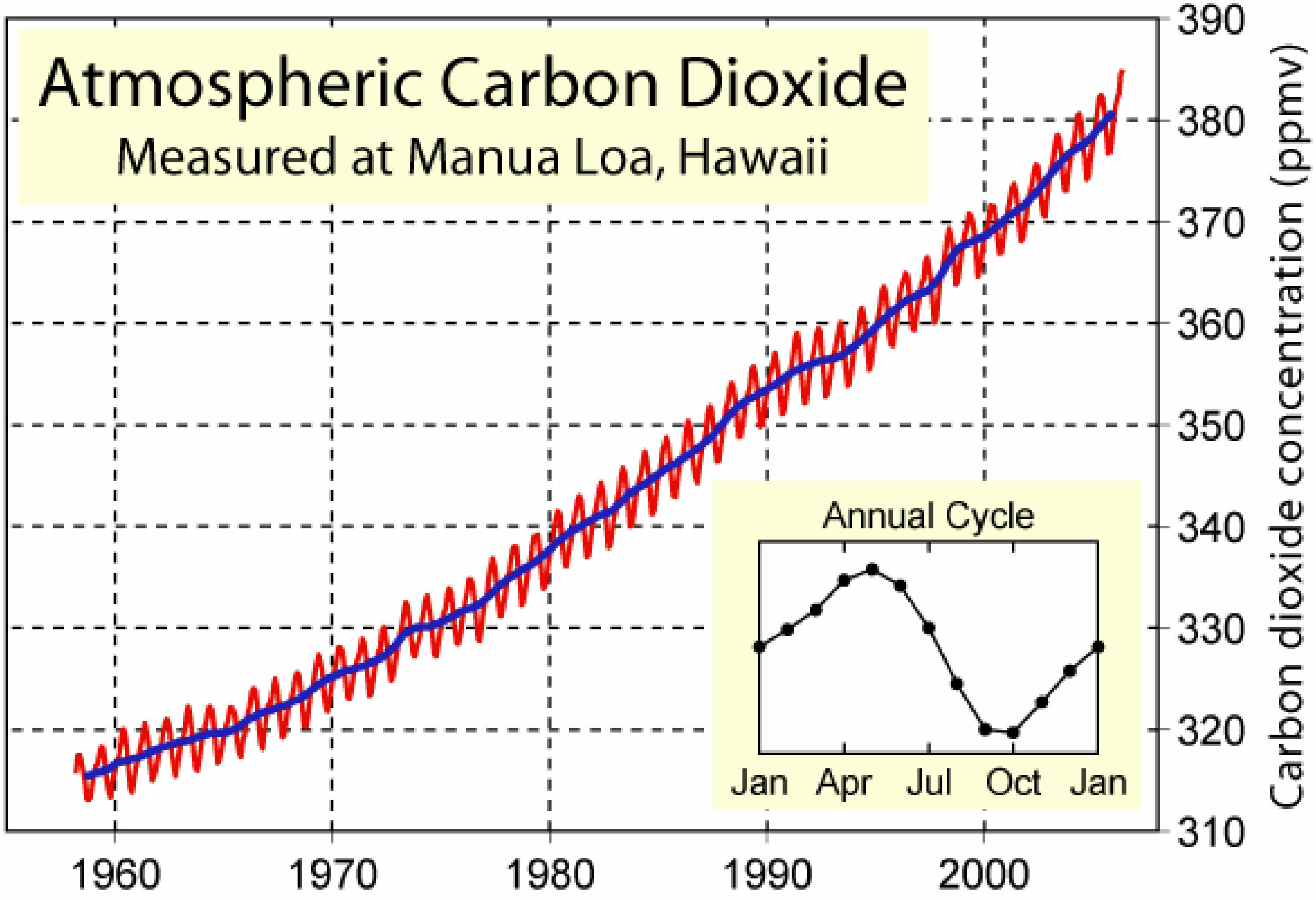
Microbes and Mineral Cycling

Biogeochemical cycles on a global scale


Atmospheric Carbon Dioxide
Measured at Manua Loa, Hawaii
Annual Cycle
Jan
Apr
Jul
Oct
Jan
390
380
370
360
350
340
330
320
310
Carbon dioxide concentration (ppmv)
1960
1970
1980
1990
2000

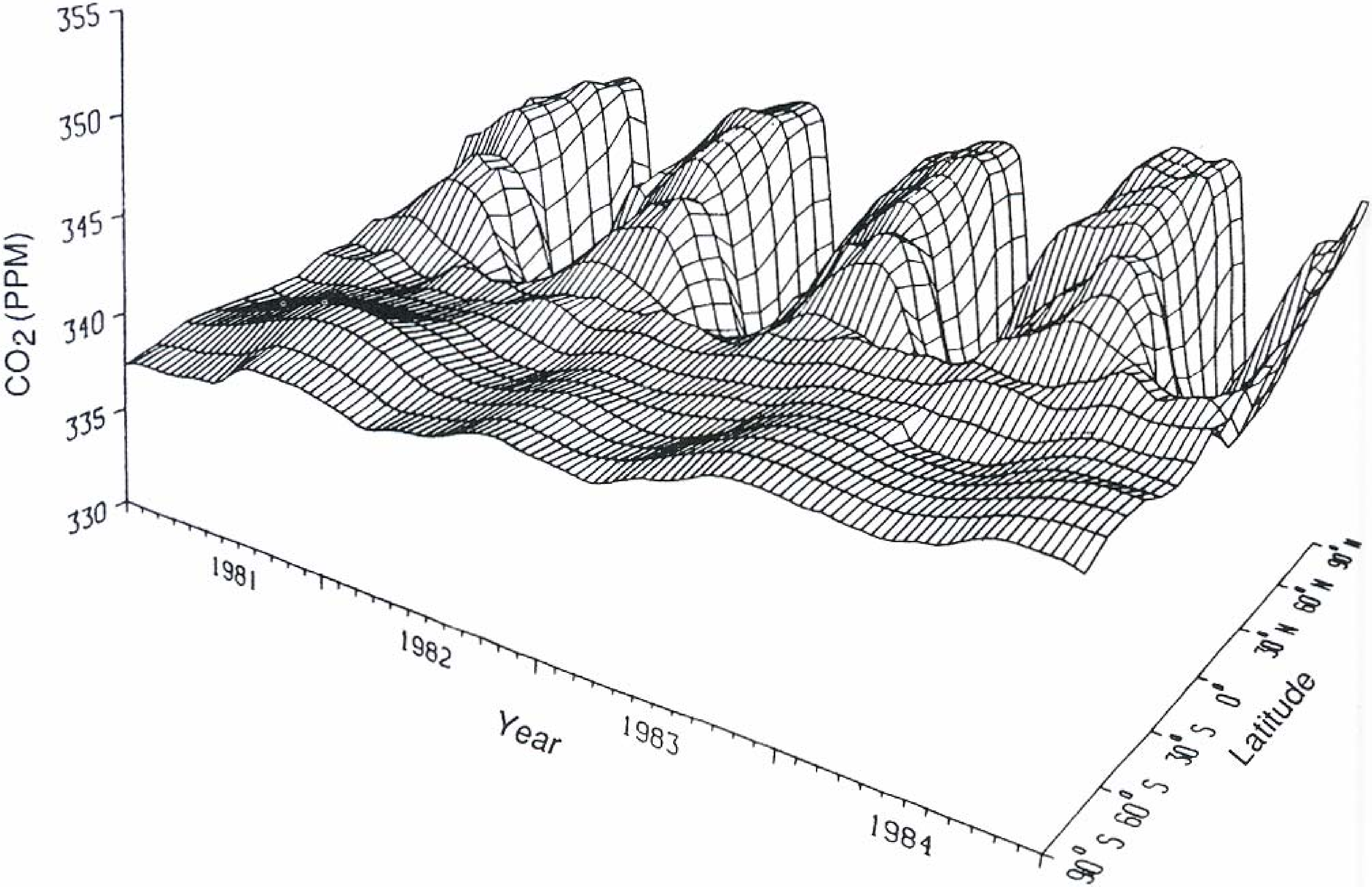
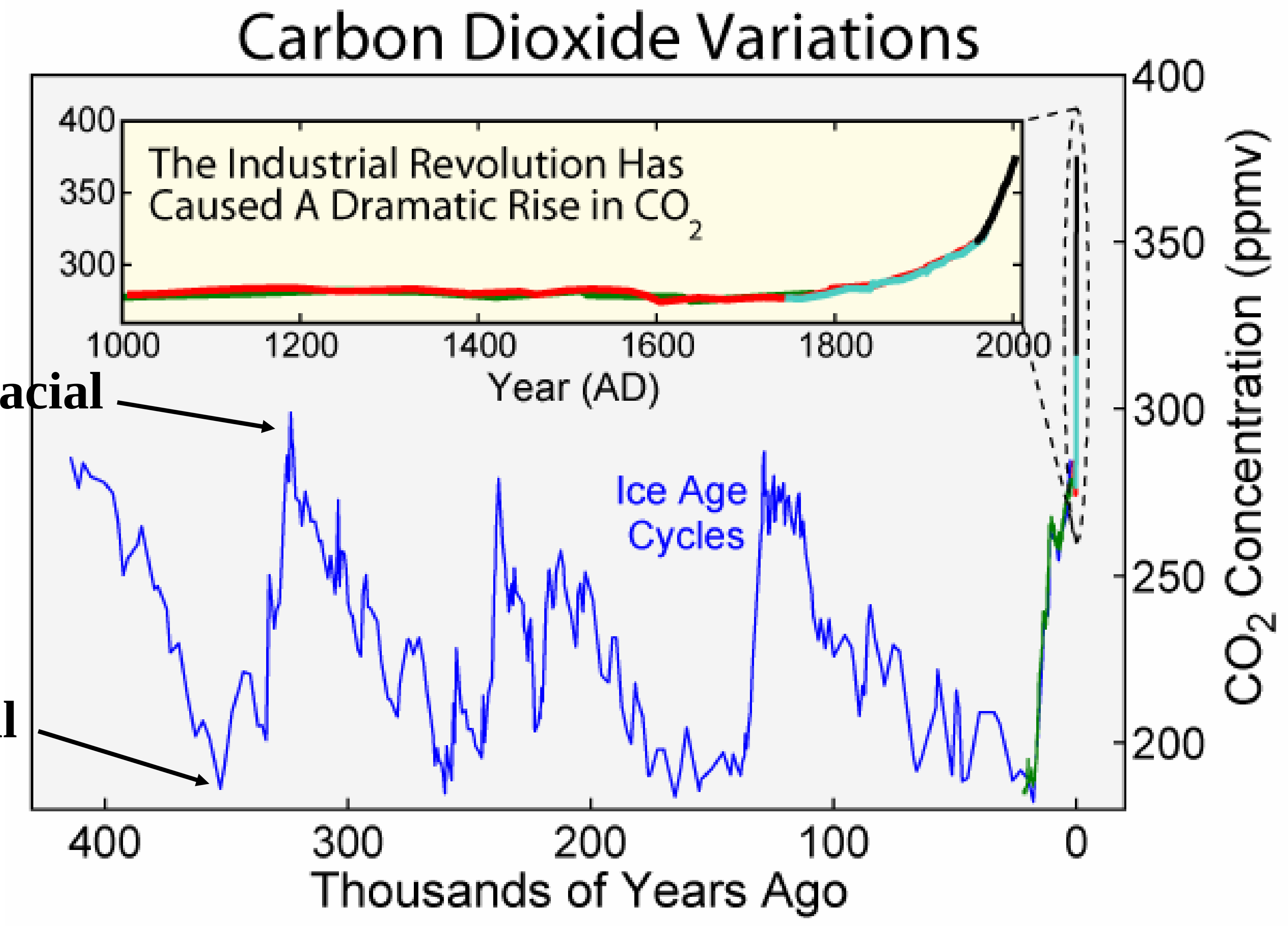


Figure 3.6 Seasonal fluctuations in the concentration of atmospheric CO_2 (1981–1984), shown as a function of 10° latitudinal belts (Conway et al. 1988). Note the smaller amplitude of the fluctuations in the southern hemisphere, reaching peak concentrations during northern hemisphere minima.



Interglacial

Glacial

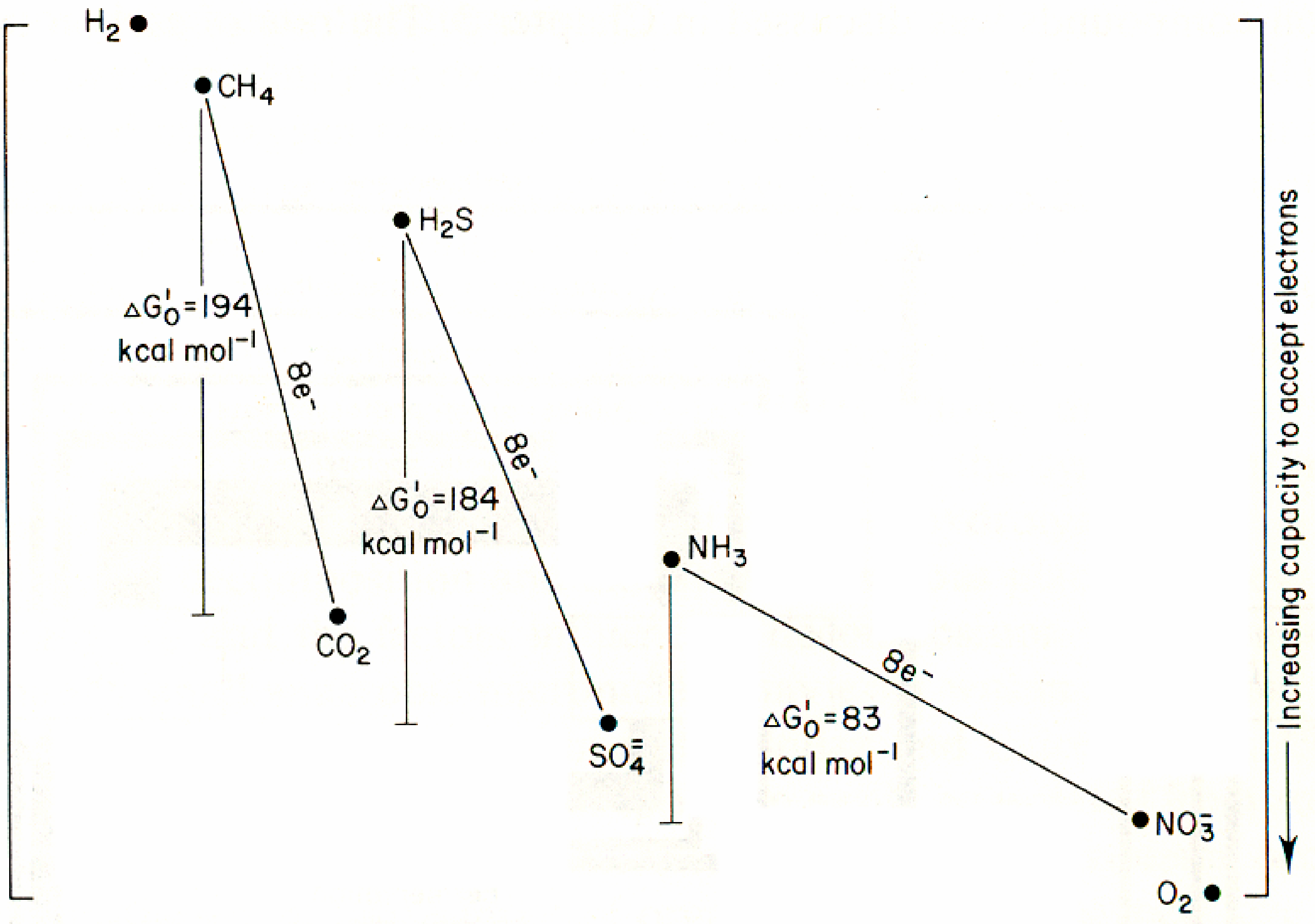


Fig. 22. A comparison between C, S and N oxidation/reductions. The most reduced and the most oxidized compounds of the C, S and N cycles are arranged in pairs, separated by a distance which represents an 8 e^- difference between the extremes. Given vertically are the G'_o for the oxidation, by O_2, of the reduced form. There is a decreasing energy yield through the series C, S to N which is represented by the vertical distance between the oxidized and the reduced forms. The location of the lines relative to each other is only approximately correct and is designed to illustrate the decrease in reducing potential through the series H_2, CH_4, H_2S to NH_3 and the increase in oxidizing potential through the series CO_2, SO_4^{2-}, NO_3^- to O_2.

Microbial Metabolic Menu

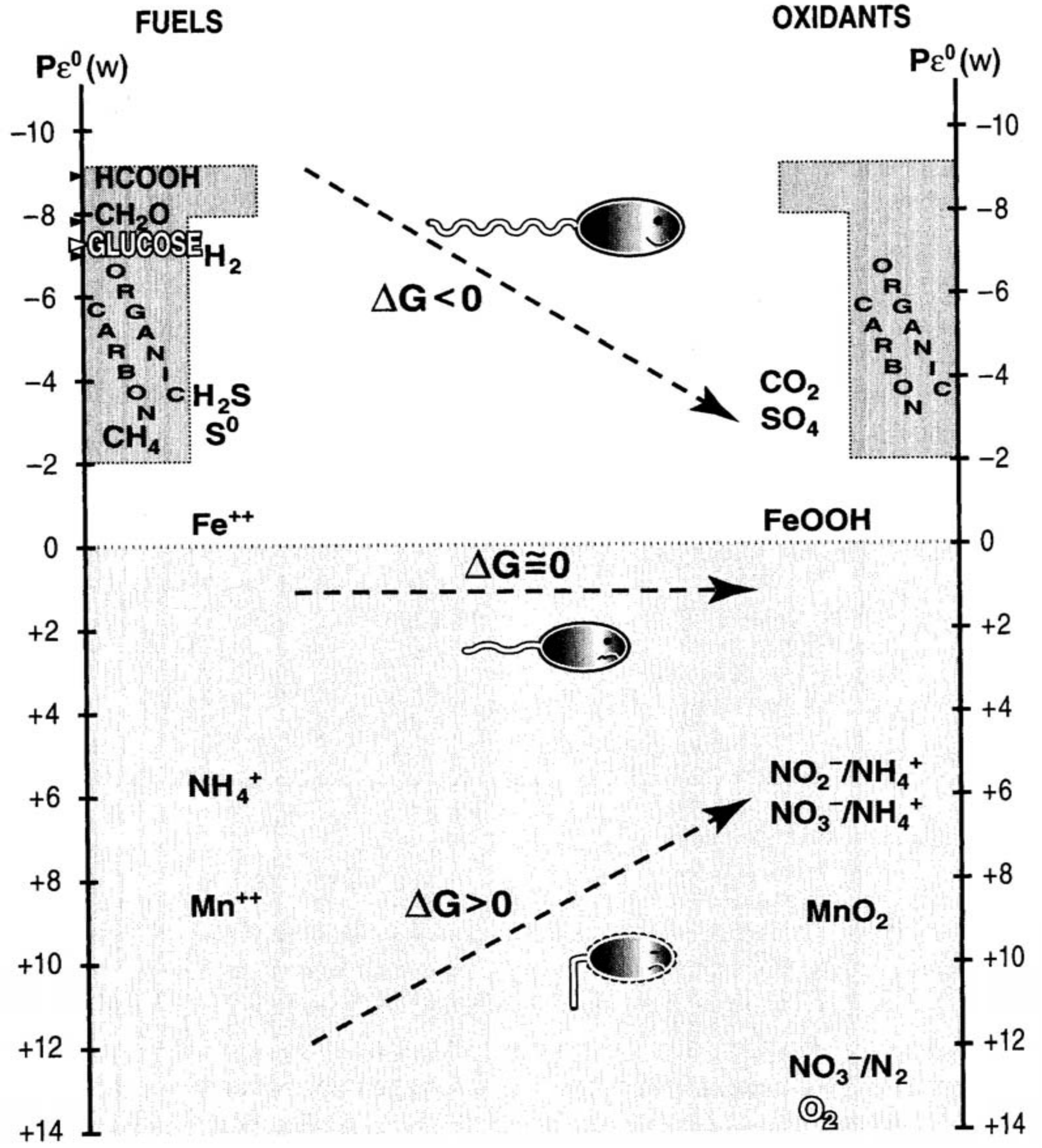
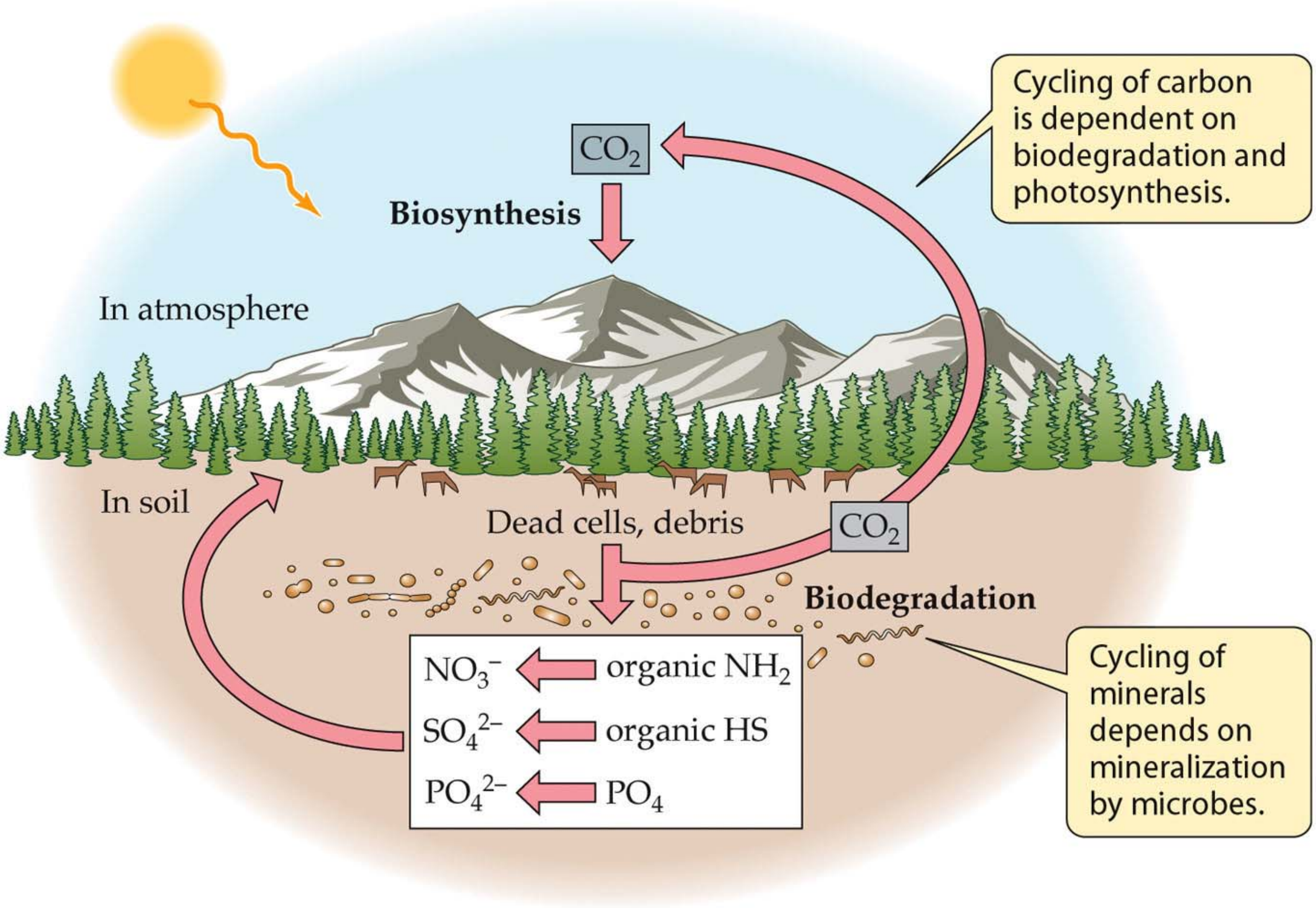


Figure courtesy of Ken Nealson

Balance between biosynthesis and biodegradation



Cycling of carbon is dependent on biodegradation and photosynthesis.

Cycling of minerals depends on mineralization by microbes.

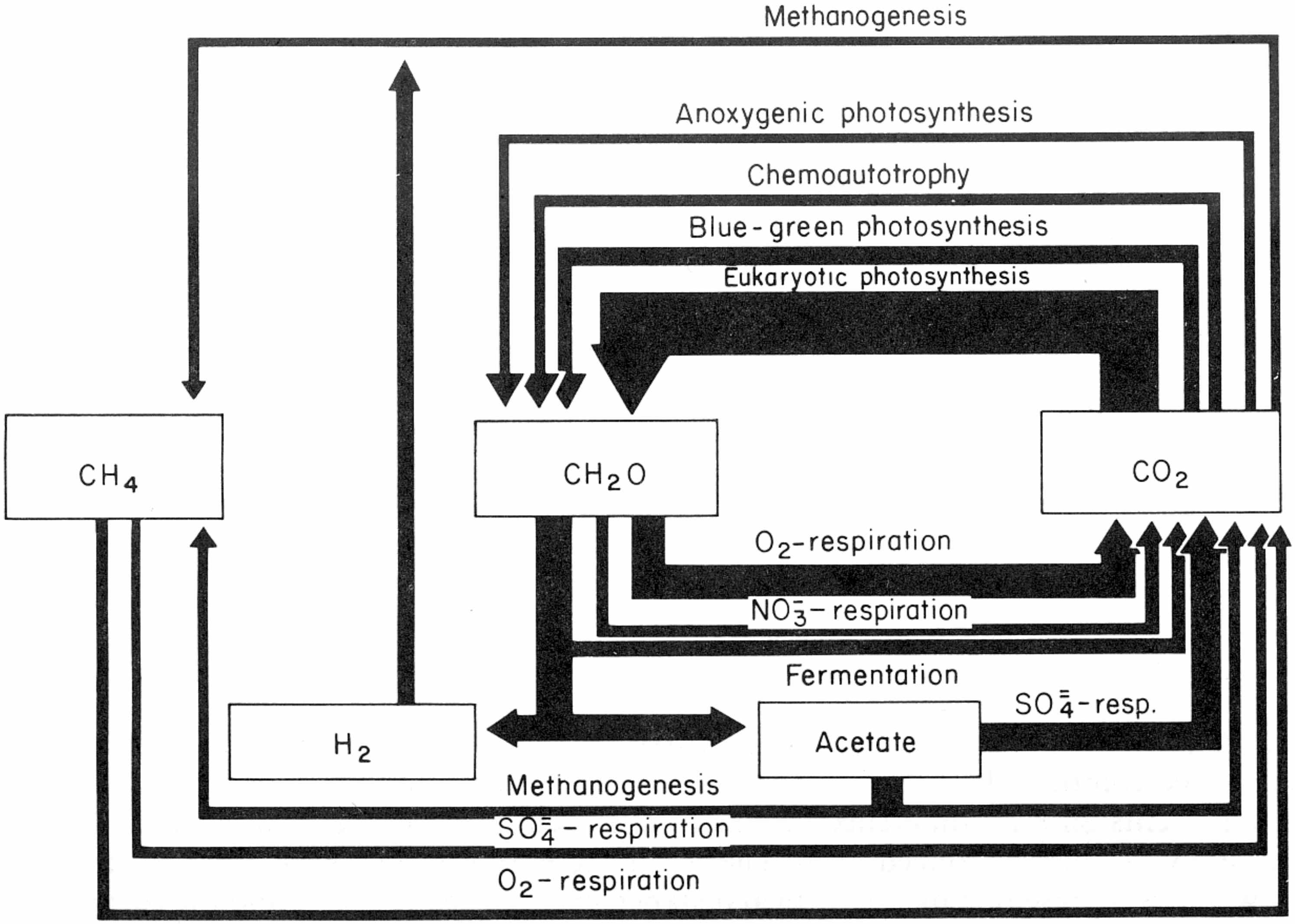
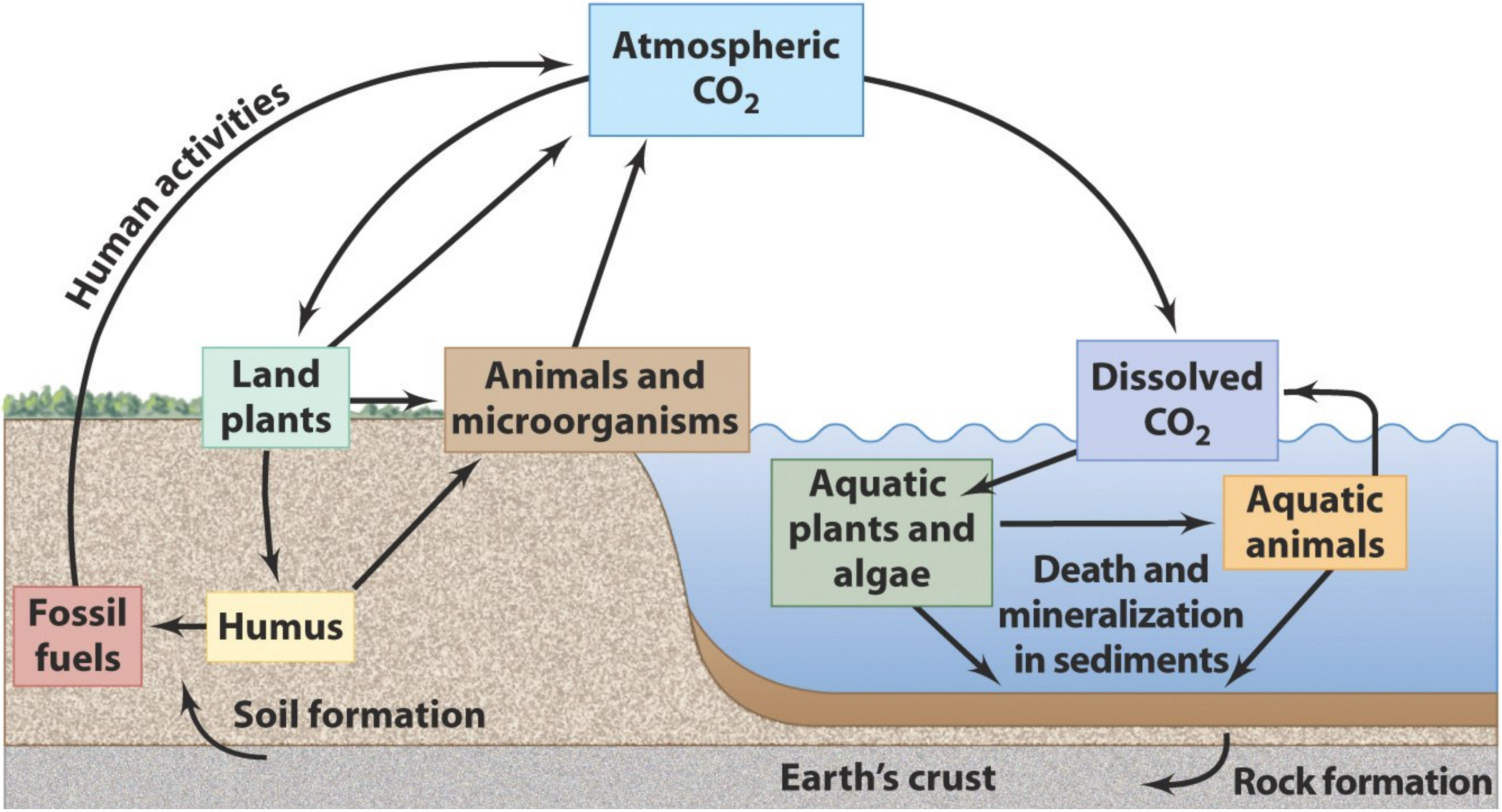


Fig. 23. The microbial carbon cycle. The role of sulfate in the oxidation of methane is largely hypothetical.

The carbon cycle, closely connected with oxygen cycle



Most carbon in carbonate rocks & sediments

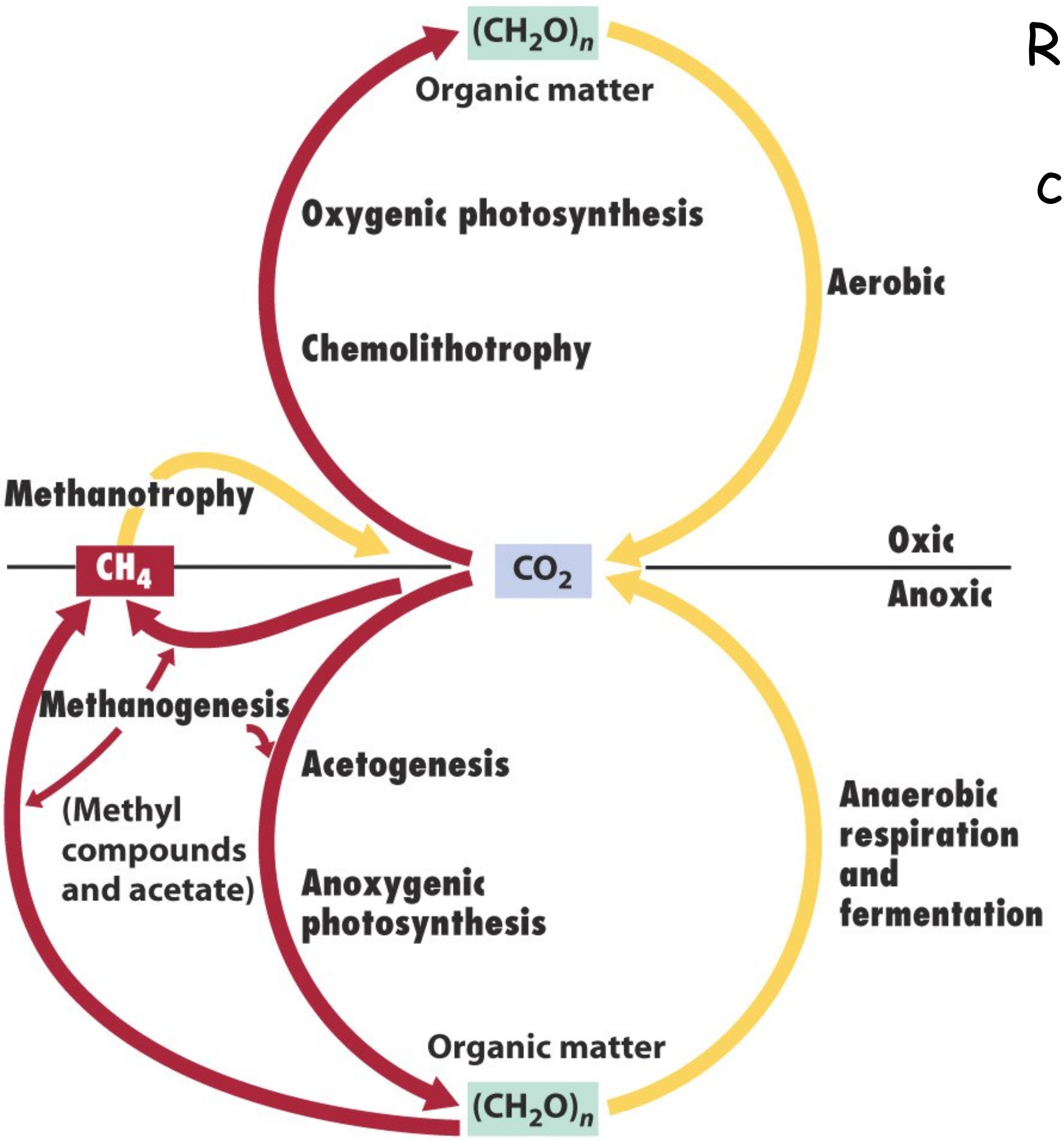
Table 19.3 Major carbon reservoirs on Earth

Reservoir	Carbon (gigatons)[a]	Percent of total carbon on Earth
Oceans	38×10^3 (>95% is inorganic C)	0.05
Rocks and sediments	75×10^6 (>80% is inorganic C)	>99.5[b]
Terrestrial biosphere	2×10^3	0.003
Aquatic biosphere	1–2	0.000002
Fossil fuels	4.2×10^3	0.006
Methane hydrates	10^4	0.014
Atmosphere	**720**	**0.005**

[a] One gigaton is 10^9 tons. Data adapted from *Science 290*:291–295 (2000).

[b] Much of the organic carbon is in prokaryotic cells.

Redox states for the carbon cycle



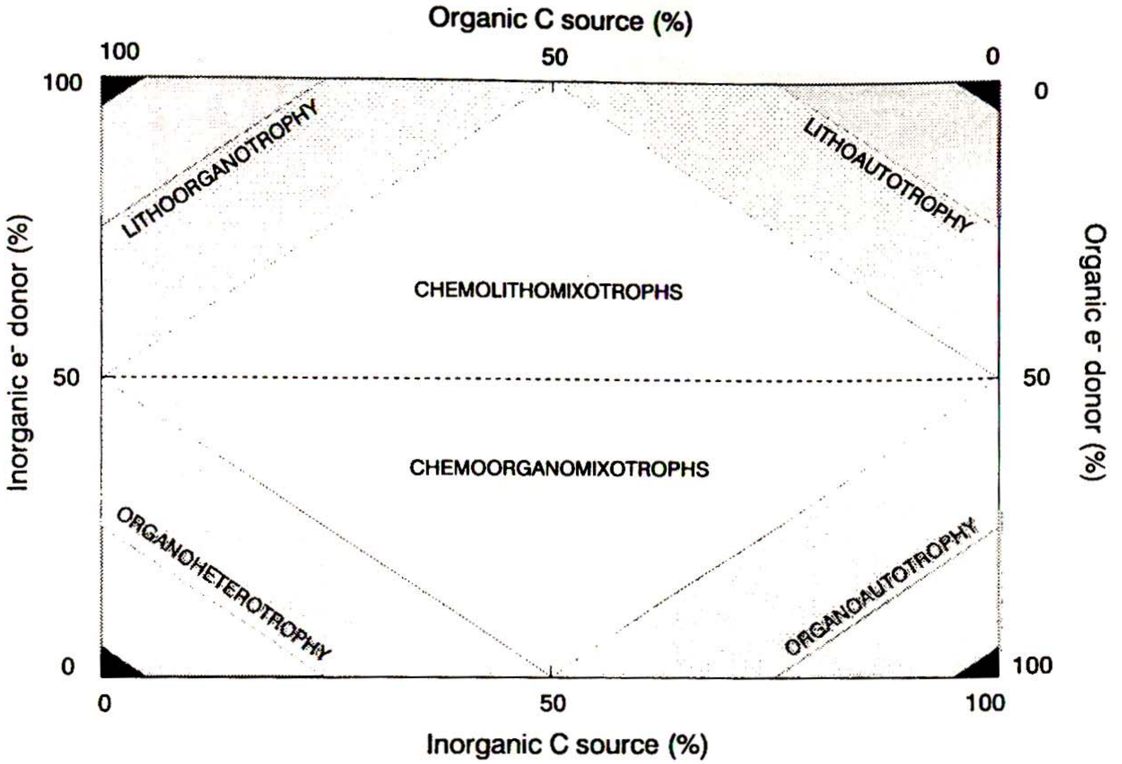
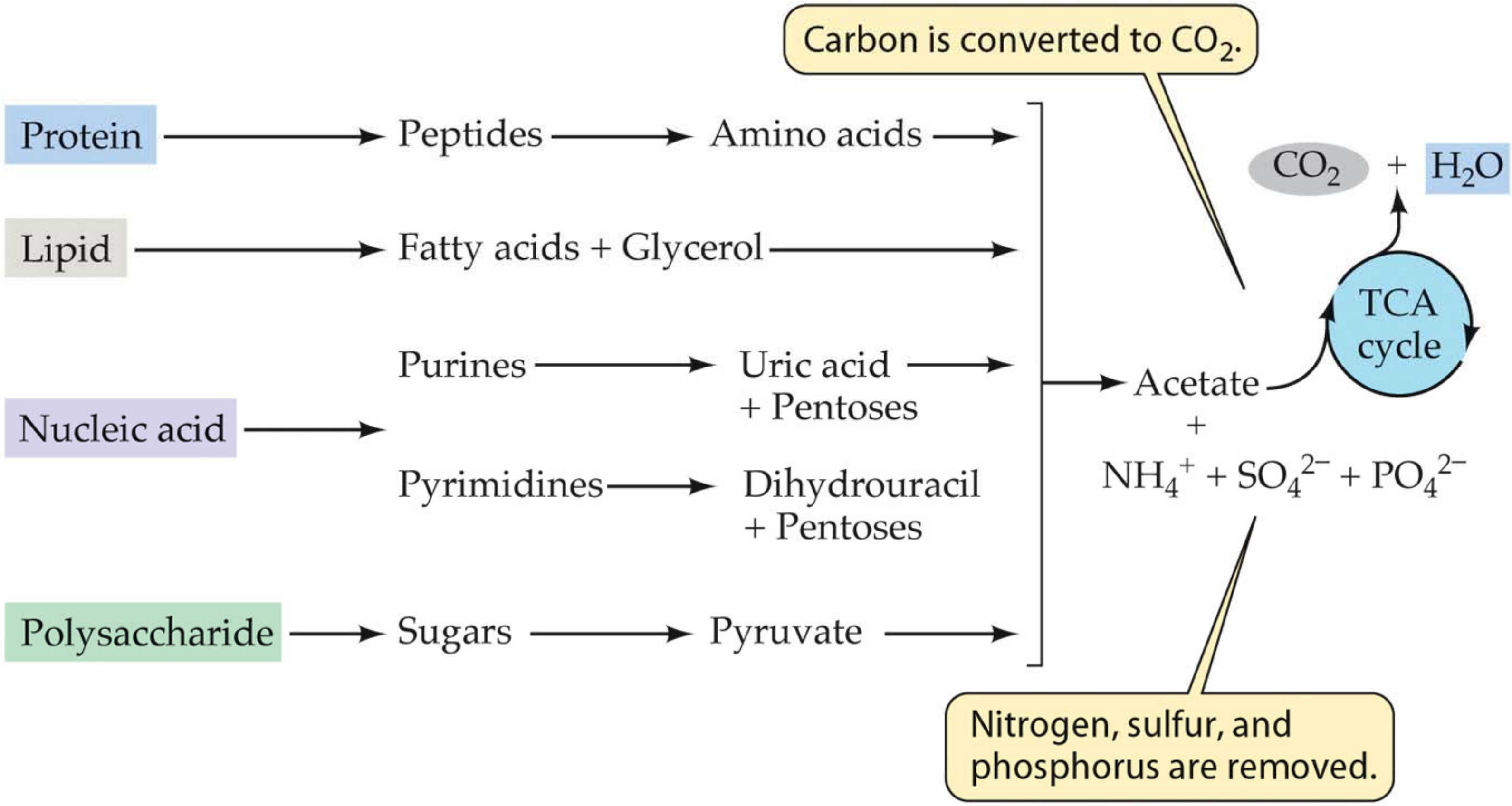
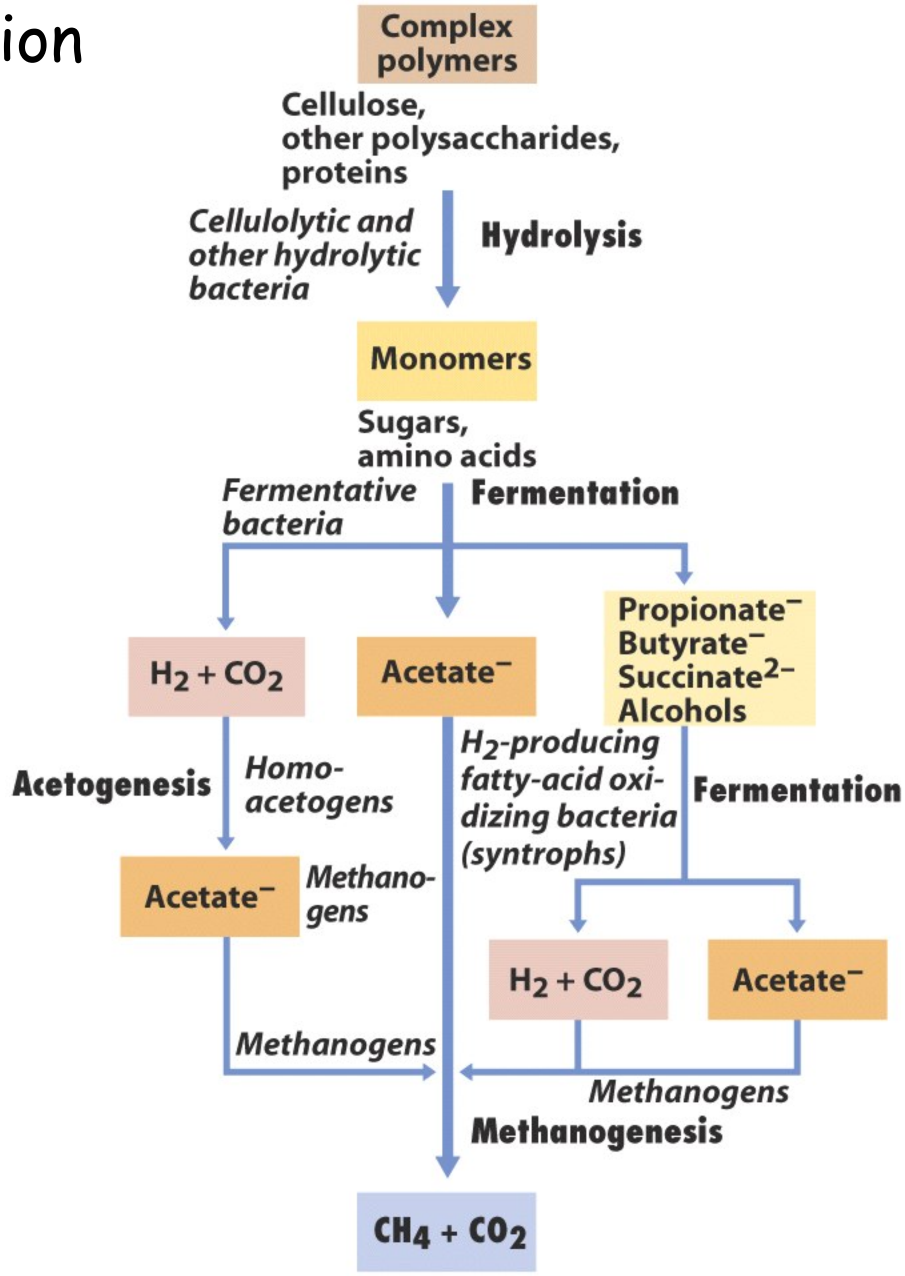


FIGURE 1 Chemotrophic metabolic versatility that is potentially present in deep-sea vent habitats. Growth of microorganisms at the expense of either inorganic or organic electron (e^-) donors and inorganic or organic carbon (C) sources is expressed as variable percentages of total energy and C requirements. The darkened corners depict the characteristics of the obligate end-member metabolic pathways. The infinite gradations from obligatory metabolism through facultative and eventually to the mixotrophic metabolism are also depicted. The dashed line arbitrarily separates the lithomixotrophs from the organomixotrophs at the 50% boundary. Not shown in this figure is the additional potential for phototrophic metabolism at deep-sea hydrothermal vents. (See text for more details on metabolic versatility.)

Fate of major biomolecules



Anoxic decomposition



Complex polymers

Cellulose, other polysaccharides, proteins

Cellulolytic and other hydrolytic bacteria

Hydrolysis

Monomers

Sugars, amino acids

Fermentative bacteria

Fermentation

$H_2 + CO_2$

Acetate$^-$

Propionate$^-$
Butyrate$^-$
Succinate^{2-}
Alcohols

Acetogenesis

Homo-acetogens

H_2-producing fatty-acid oxidizing bacteria (syntrophs)

Fermentation

Acetate$^-$

Methanogens

$H_2 + CO_2$

Acetate$^-$

Methanogens

Methanogens

Methanogenesis

$CH_4 + CO_2$

Take Home Message

- The oxygen and carbon cycles are interconnected through the complementary activities of autotrophic and heterotrophic organisms.

- Microbial decomposition is the single largest source of CO_2 released to the atmosphere.

Schematic pathways for Carbon fixation in chemolithotrophs

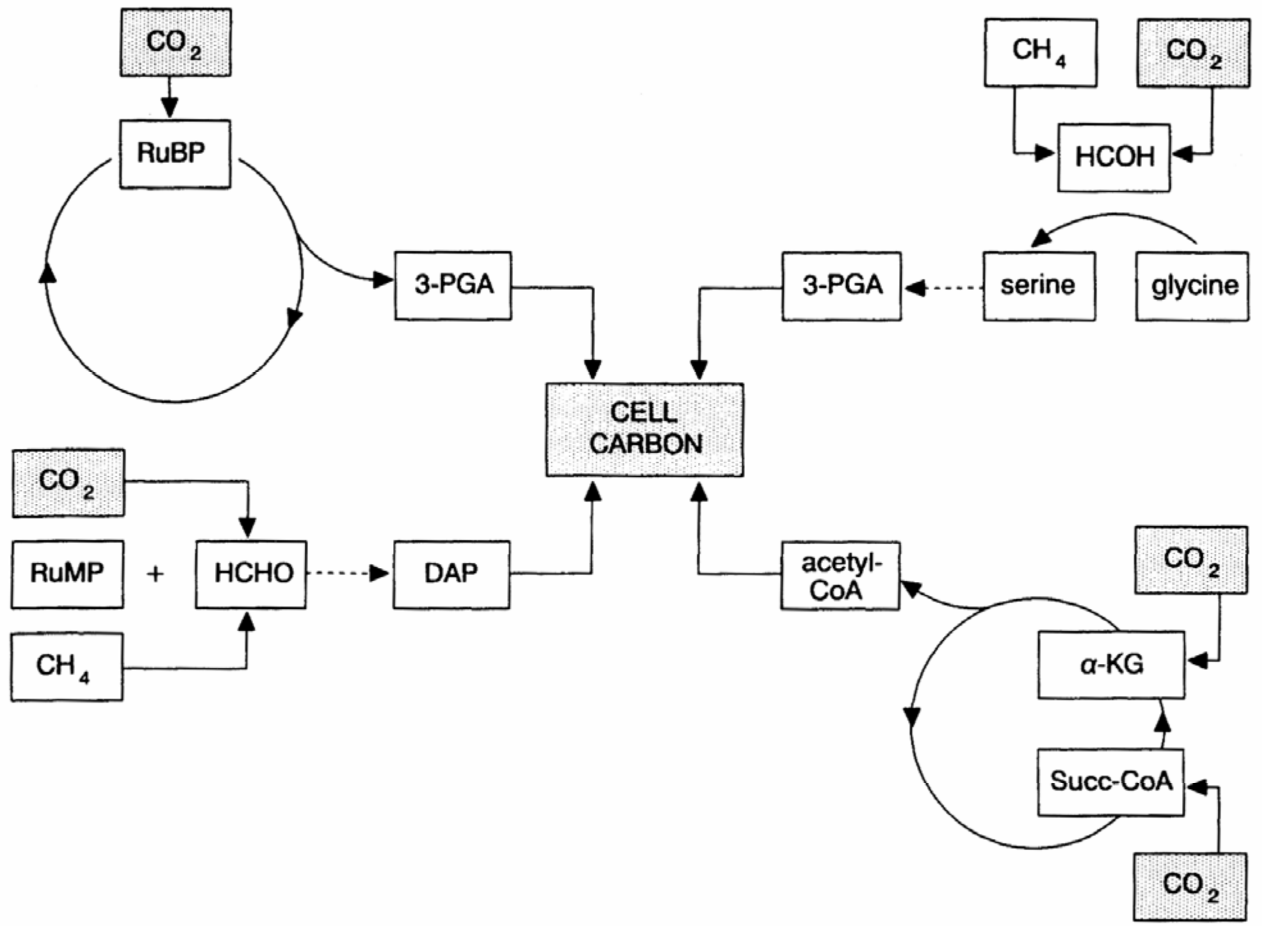
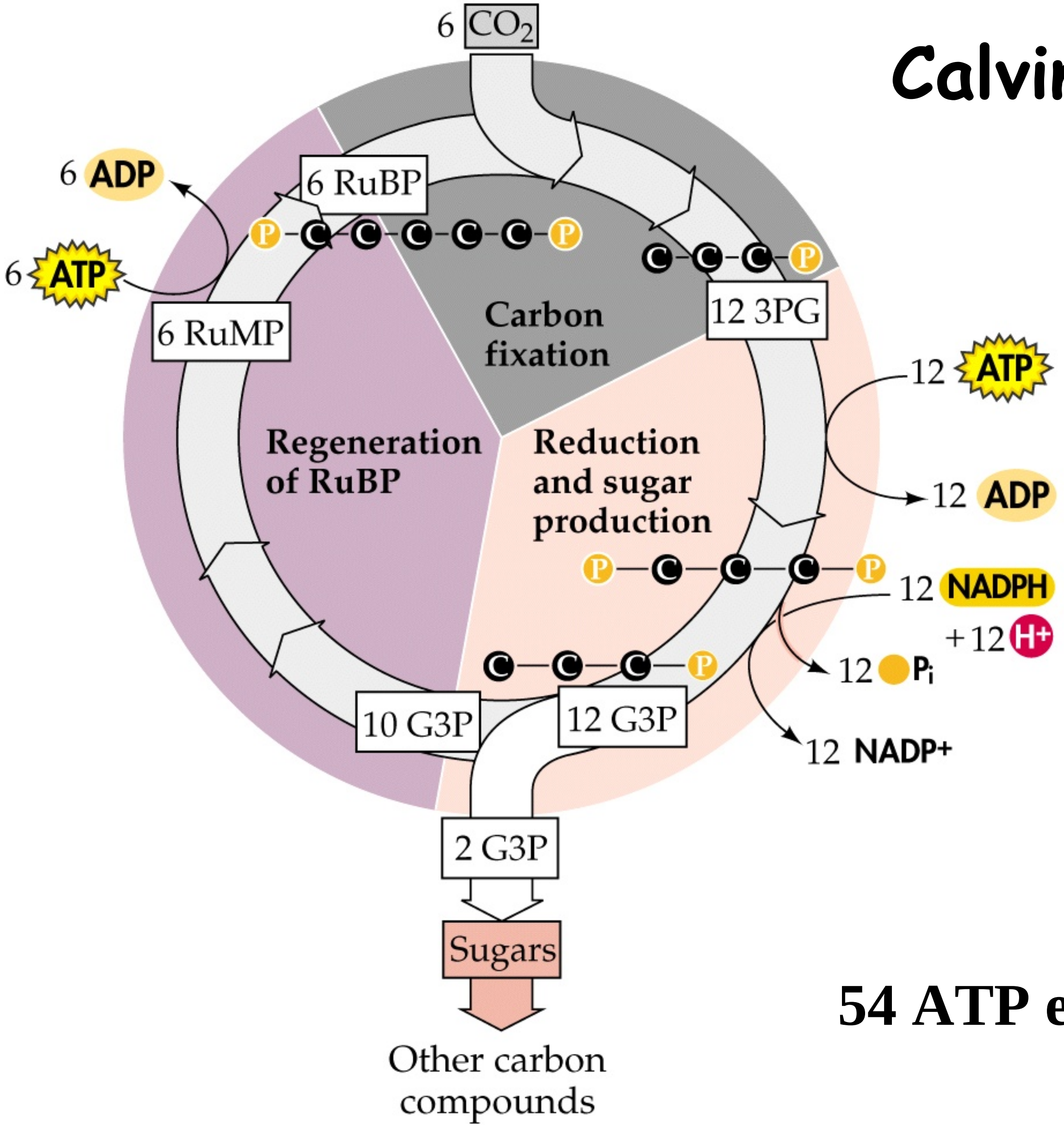


FIGURE 2 Four selected pathways for CO_2 assimilation in chemolithotrophic bacteria. Not shown in this diagram are the noncyclic acetyl-CoA pathway, the reduction of CO_2 to methane, and CO_2 assimilation via anaplerotic reactions (see text for more details). Clockwise from upper left: Calvin cycle, serine pathway, reductive tricarboxylic acid cycle and ribulose monophosphate pathway. Abbreviations include: RuBP=ribulose bisphosphate, 3-PGA=3-phosphoglyceric acid, Succ-CoA=succinyl-CoA, αKG=α-ketoglutarate, RuMP=ribulose monophosphate, and DAP = dihydroxacetone phosphate.

Calvin Cycle



54 ATP equivalents!!!

Calvin Cycle

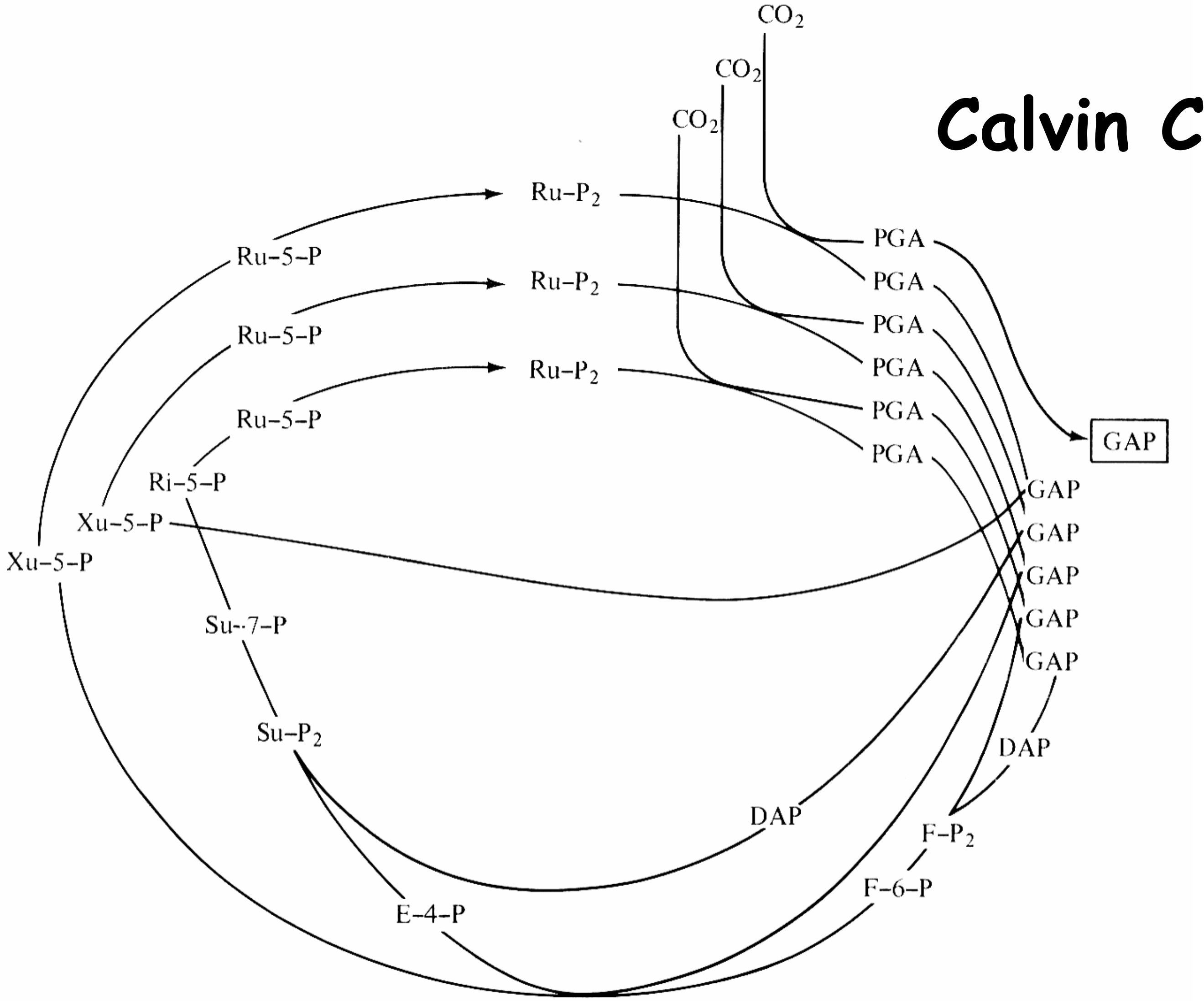
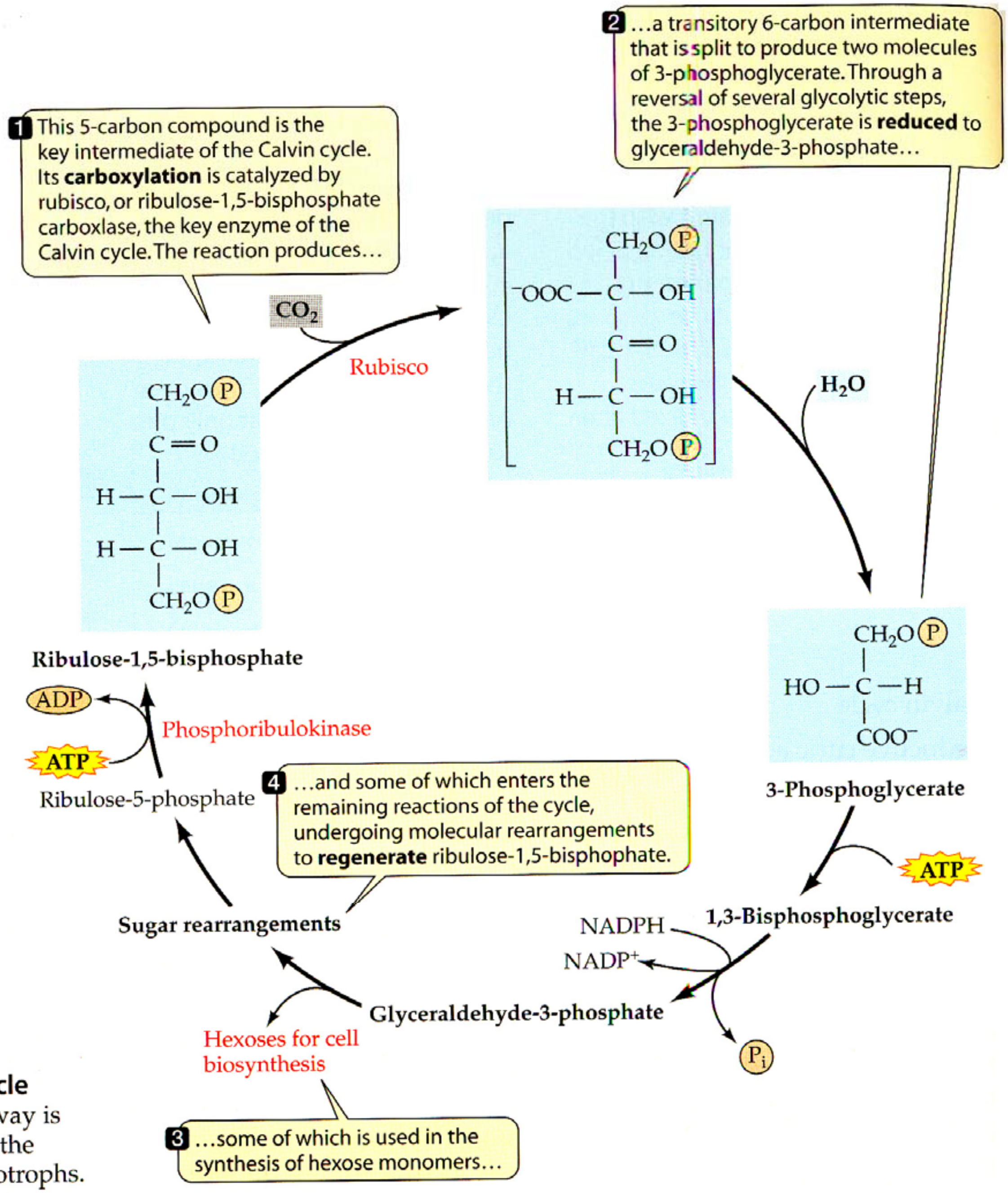


Figure 9.10. The Calvin cycle. Ru-P$_2$, Ribulose-1,5-bisphosphate; PGA, 3-phosphoglycerate; GAP, glyceraldehyde-3-phosphate; DAP, dihydroxyacetone phosphate; F-P$_2$, fructose-1,6-bisphosphate; F-6-P, fructose-6-phosphate; E-4-P, erythrose-4-phosphate; Su-P$_2$, sedoheptulose-1,7-bisphosphate; Su-7-P, sedoheptulose-7-phosphate; Xu-5-P, xylulose-5-phosphate; Ri-5-P, ribose-5-phosphate; Ru-5-P, ribulose-5-phosphate.

Calvin Cycle



1 This 5-carbon compound is the key intermediate of the Calvin cycle. Its **carboxylation** is catalyzed by rubisco, or ribulose-1,5-bisphosphate carboxlase, the key enzyme of the Calvin cycle. The reaction produces…

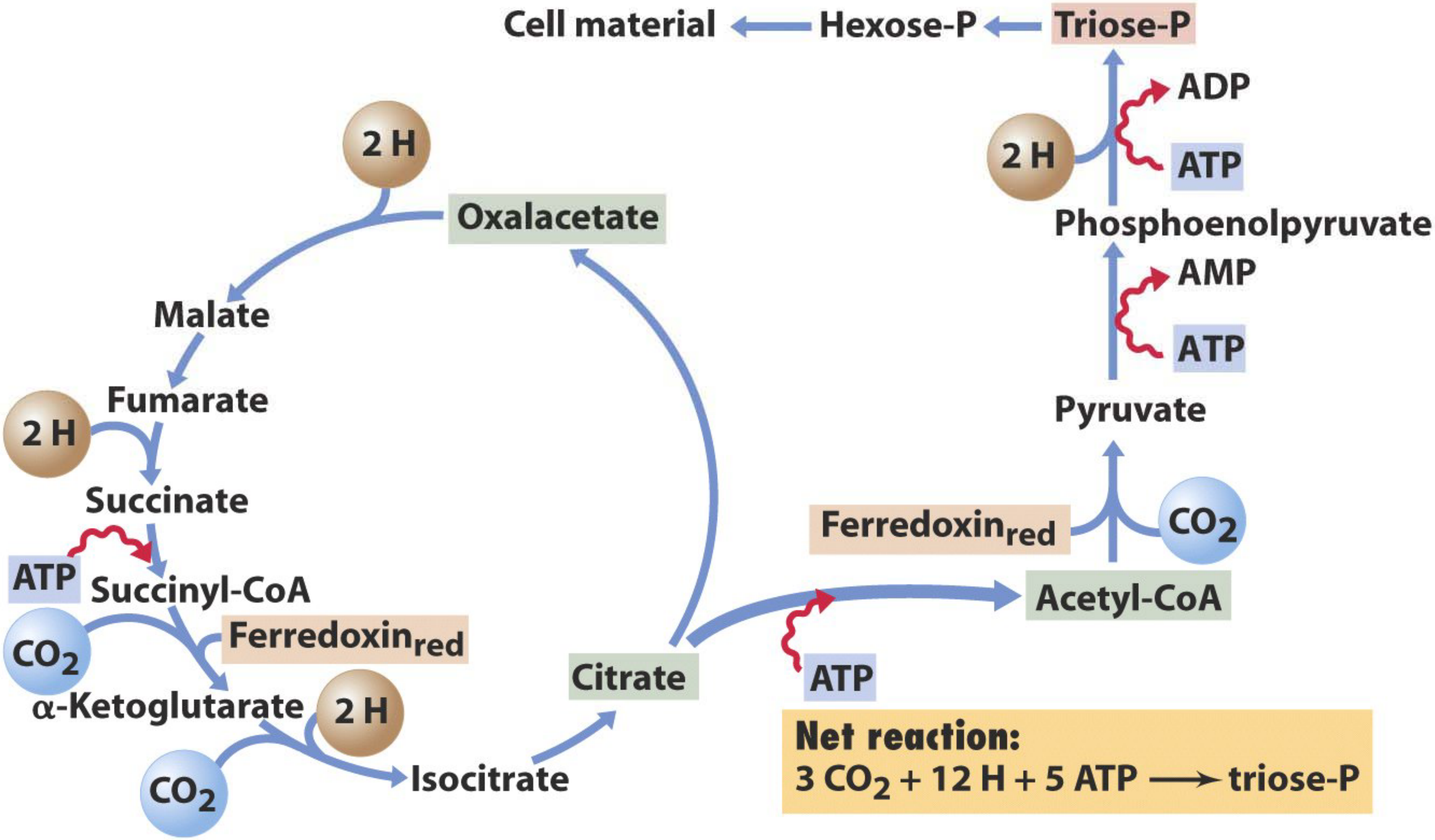
2 …a transitory 6-carbon intermediate that is split to produce two molecules of 3-phosphoglycerate. Through a reversal of several glycolytic steps, the 3-phosphoglycerate is **reduced** to glyceraldehyde-3-phosphate…

3 …some of which is used in the synthesis of hexose monomers…

4 …and some of which enters the remaining reactions of the cycle, undergoing molecular rearrangements to **regenerate** ribulose-1,5-bisphophate.

Figure 10.1 Calvin cycle This CO_2-fixation pathway is predominant in plants, the cyanobacteria, and most other autotrophs.

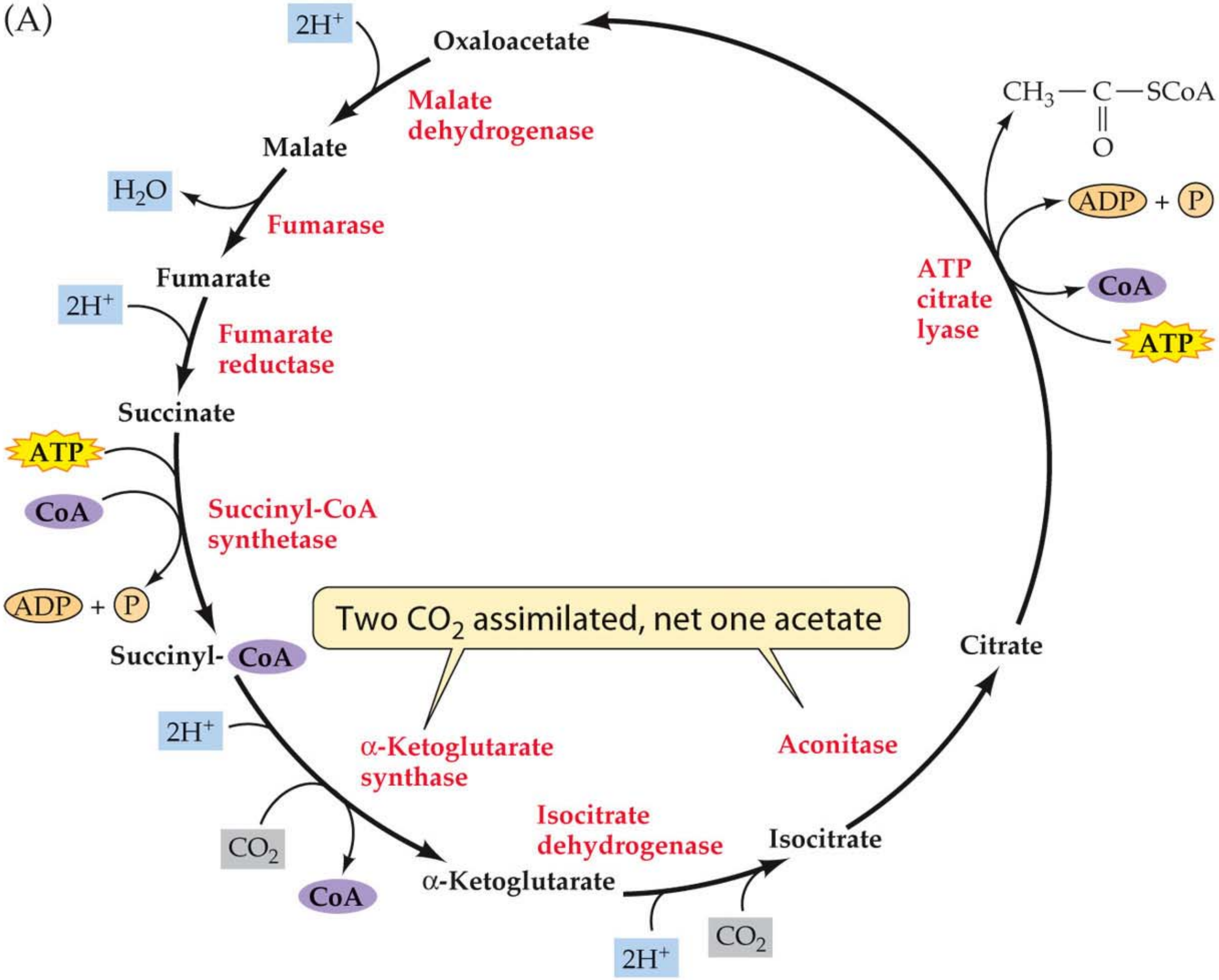
Reverse TCA in GSBs (e.g., Chlorobium), H_2-oxers & some SRBs



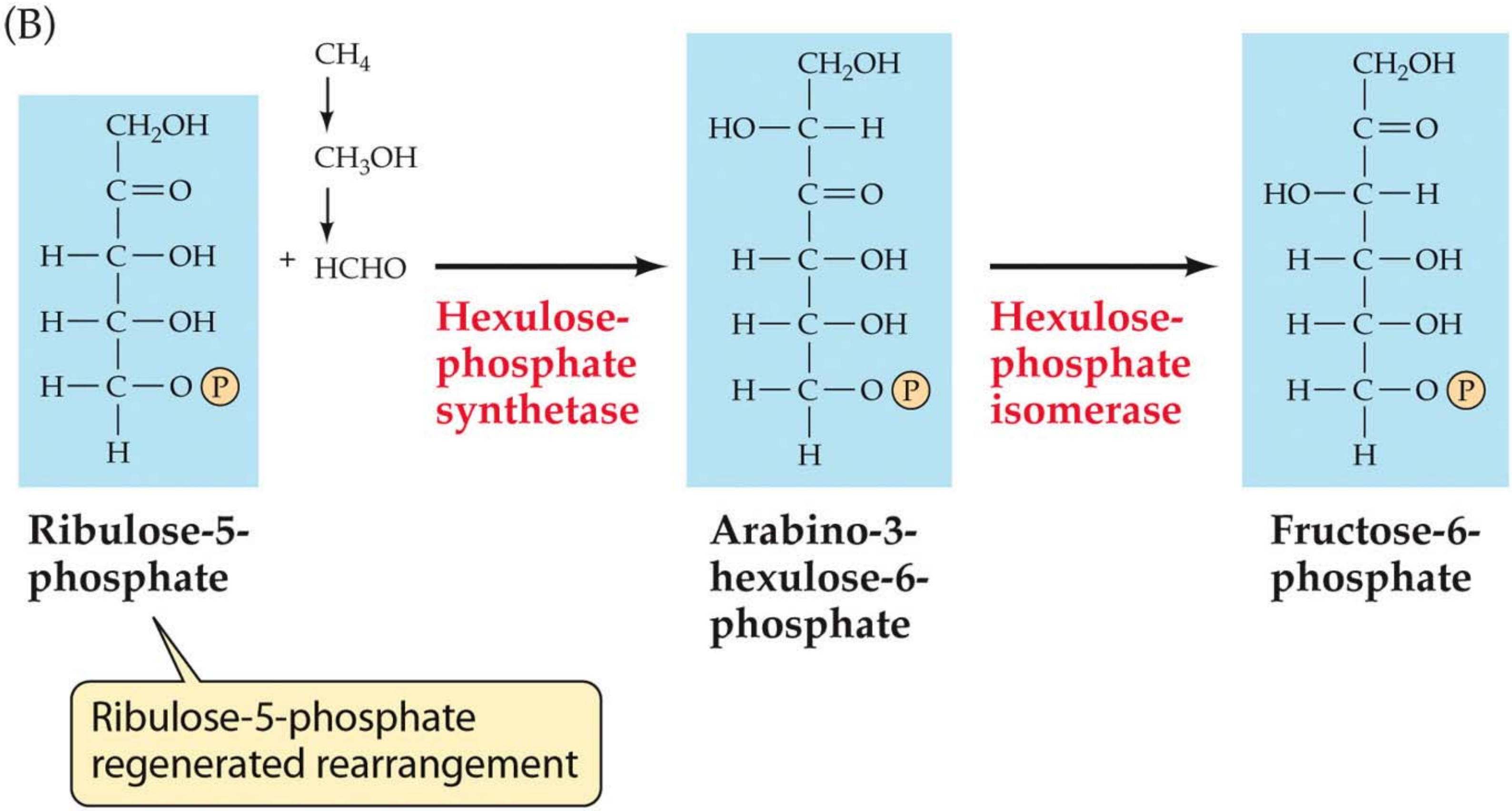
Net reaction:

$3\ CO_2 + 12\ H + 5\ ATP \longrightarrow$ triose-P

Reductive (aka reverse) TCA cycle

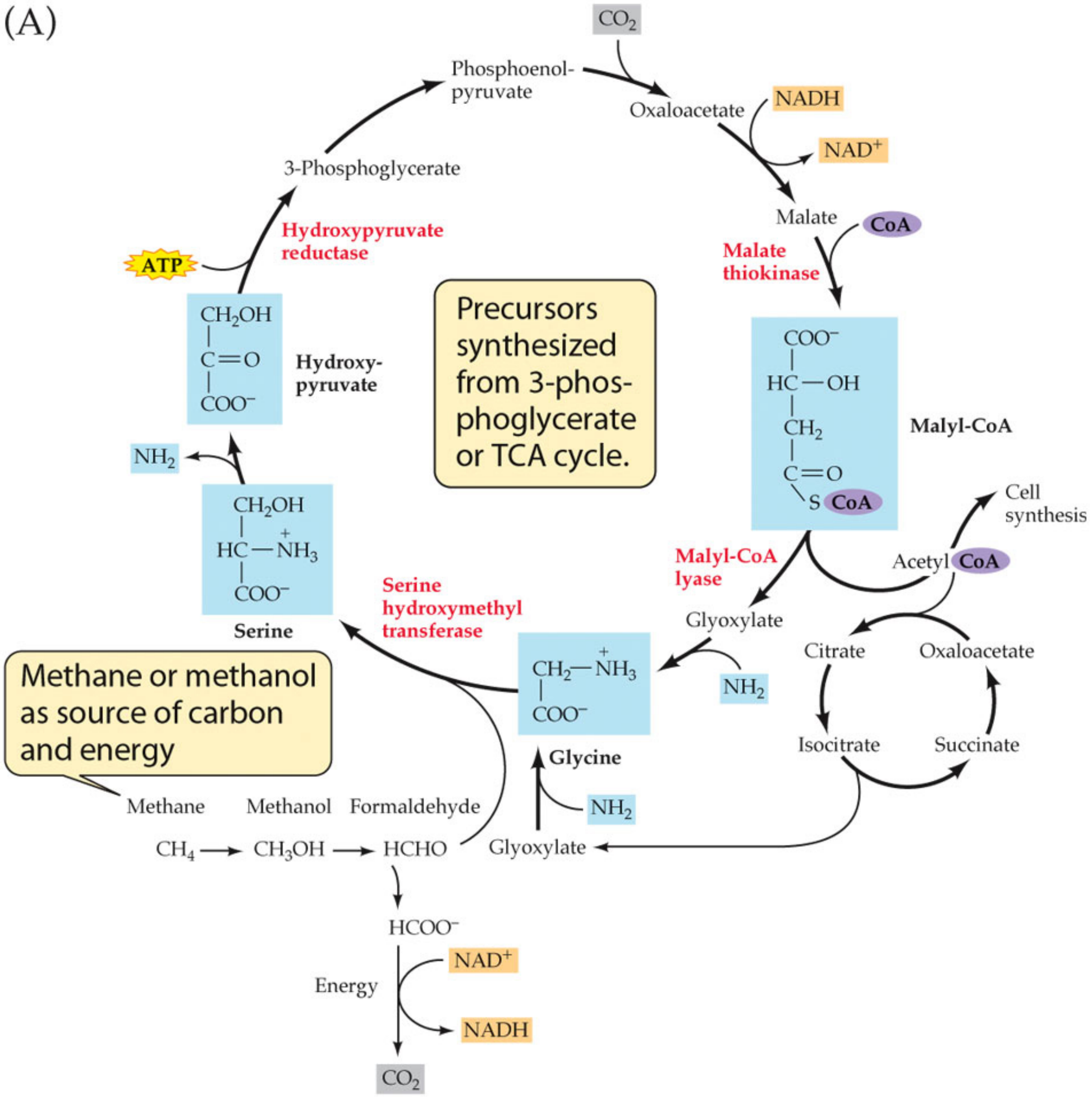


RuMP Pathway: Type I Methylotrophs

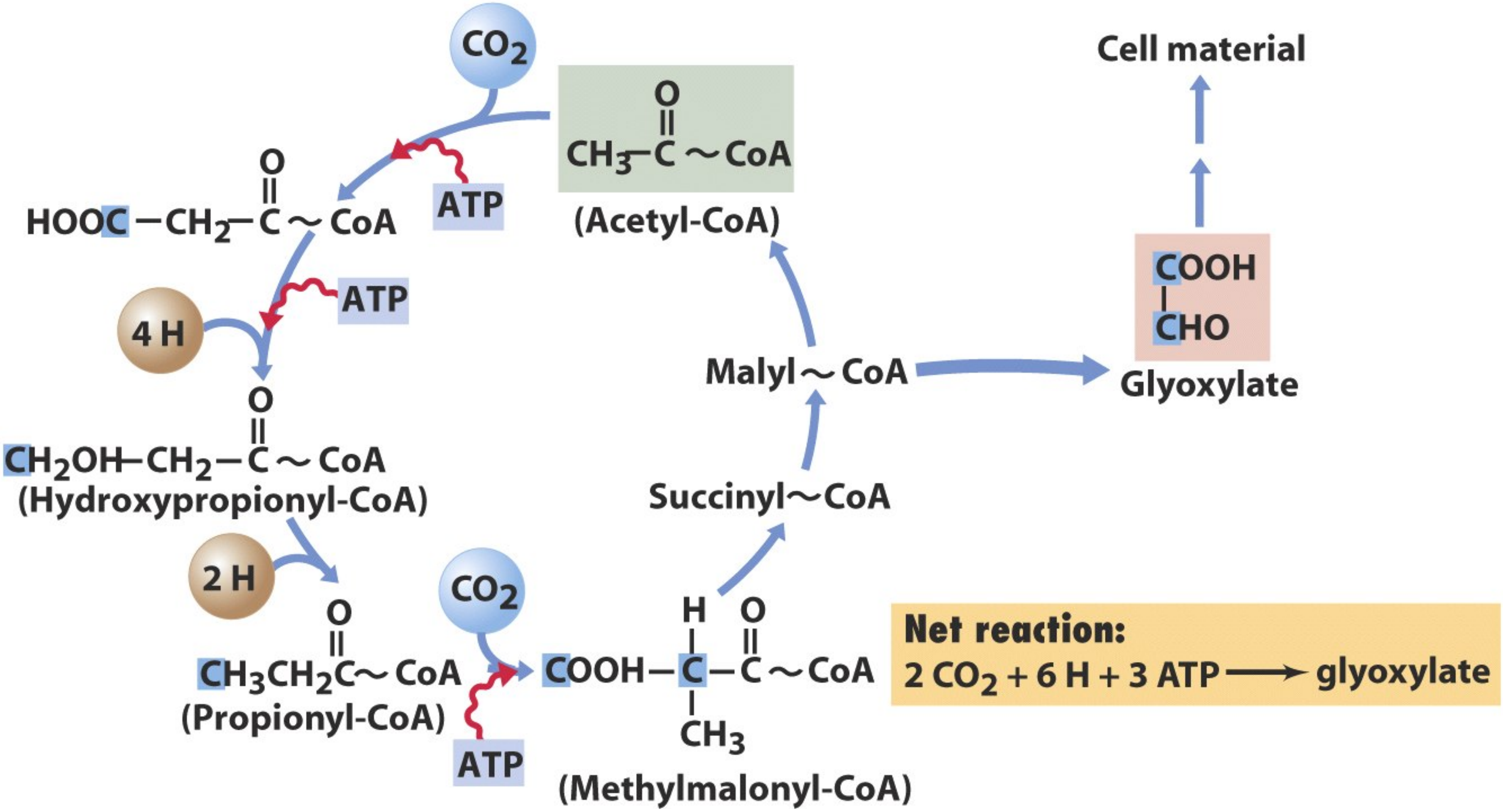


Ribulose-5-phosphate regenerated rearrangement

Serine Pathway: Type II Methylotrophs

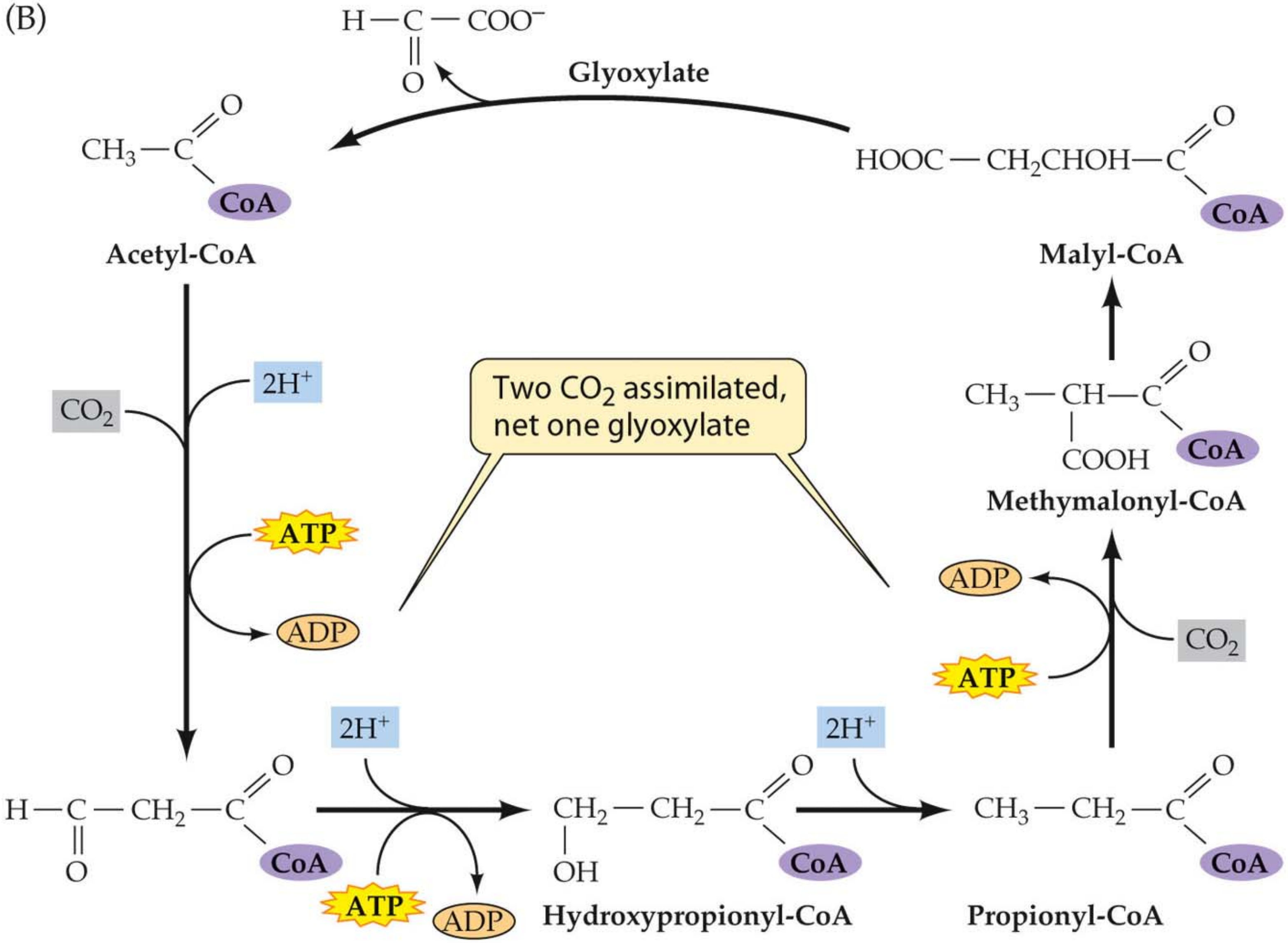


Hydroxyproprionate in GNBs (e.g., Chloroflexus)



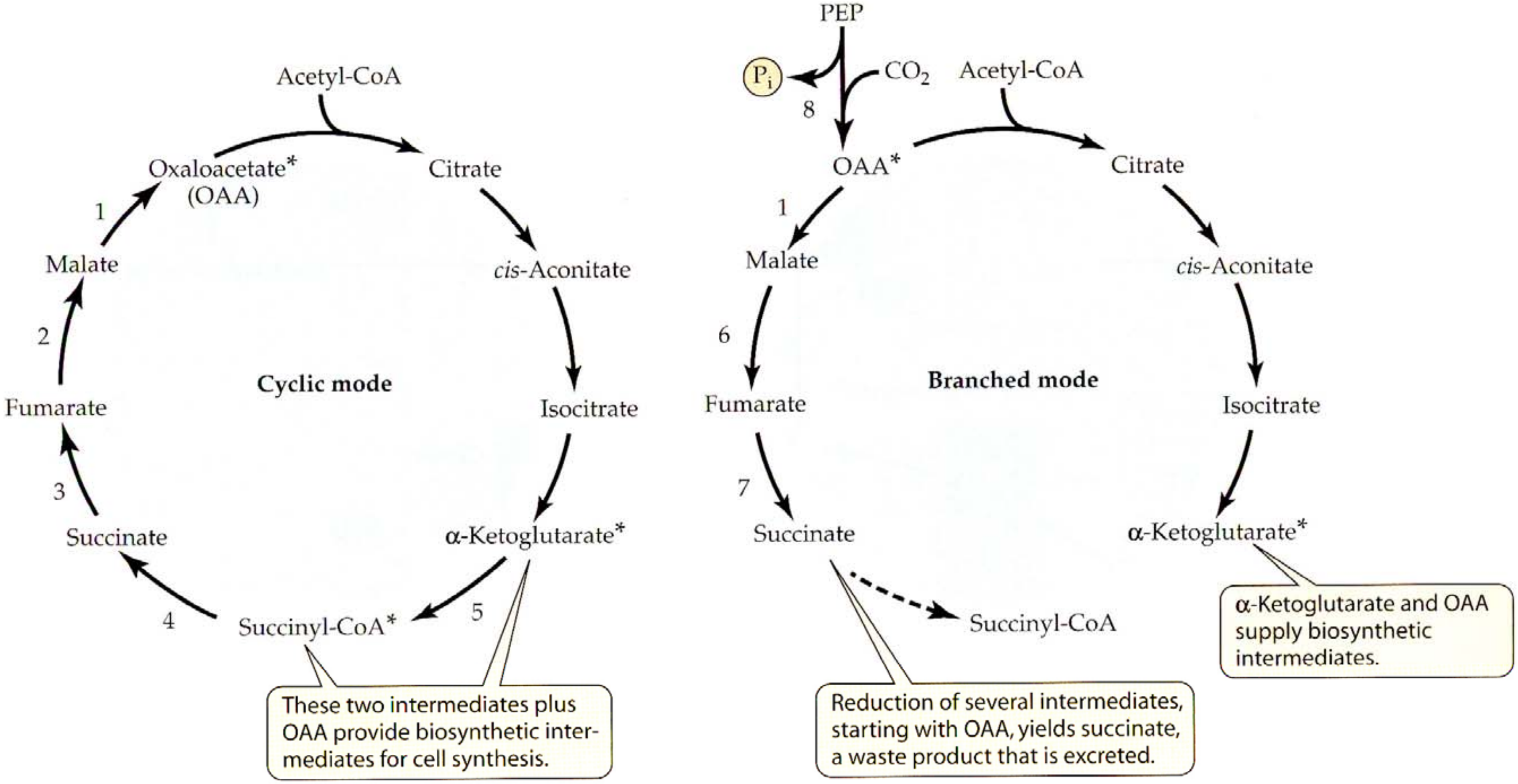
Net reaction:

$2\,CO_2 + 6\,H + 3\,ATP \longrightarrow$ glyoxylate



Two CO_2 assimilated, net one glyoxylate

Anaplerotic reactions regenerate intermediates for TCA



These two intermediates plus OAA provide biosynthetic intermediates for cell synthesis.

Reduction of several intermediates, starting with OAA, yields succinate, a waste product that is excreted.

α-Ketoglutarate and OAA supply biosynthetic intermediates.

Figure 10.9 Branched TCA cycle
During anaerobic conditions in some organisms, the TCA cycle operates in a branched mode (right) to provide for the biosynthetic intermediates needed by the cell (oxaloacetate, α-ketoglutarate). The waste product, succinate is generated from malate by the malate dehydrogenase (1) operating in the reverse direction, plus a distinct fumarase enzyme (6) and fumarate reductase (7). Synthesis of three of the TCA cycle enzymes—succinate dehydrogenase (3), α-ketoglutarate dehydrogenase (4), and succinyl-CoA synthetase (5)—is suppressed. OAA is formed from PEP and CO_2 by PEP carboxylase (8).

The “Adjacent Possible” Concept

- Microbial evolution exhibits signs of increased biocomplexity over time. Might this be an emergent property of evolution?

- The TCA is an example of two less complex (simple) pathways running anaerobically. Once oxygen was present these preadapations only needed to be tweeked ever so slightly (e.g., the α-KG DH bridge) to make aerobic respiration possible.