LUCA Last Universal Common Ancestor

Tree of Life

Bacteria   Eukarya   Archaea

Billions of Years Ago

now

1 bya

2 bya

3 bya

4 bya

Chloroplast

Mitochondria

Last Universal Common Ancestor

Bacteria
Mostly mesophiles with some thermophiles

Archaea
Many thermophiles

Eukaryotes
No thermophiles

Earliest archaea

Earliest bacteria

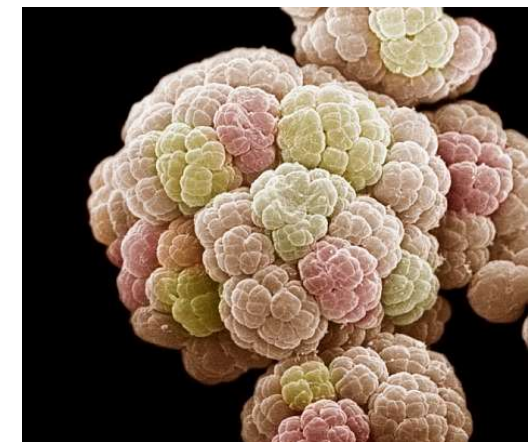65–73 °C

LUCA
Environmental temperature unknown

Image of a eukaryotic cell contains numerous organelles, which are now thought to be present in the last universal common ancestor
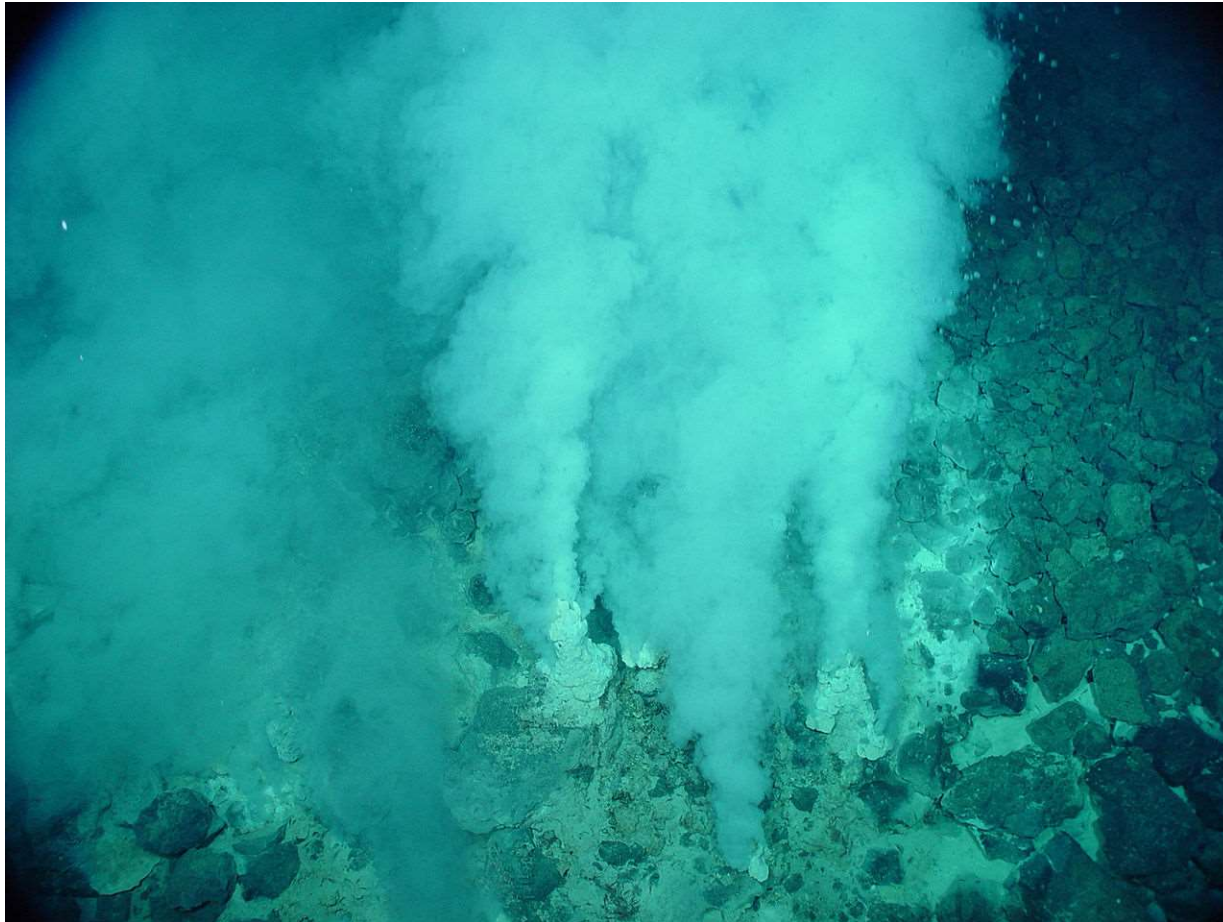

A colony of the archaea, which form one of the three lines of the tree of life in evolutionary history
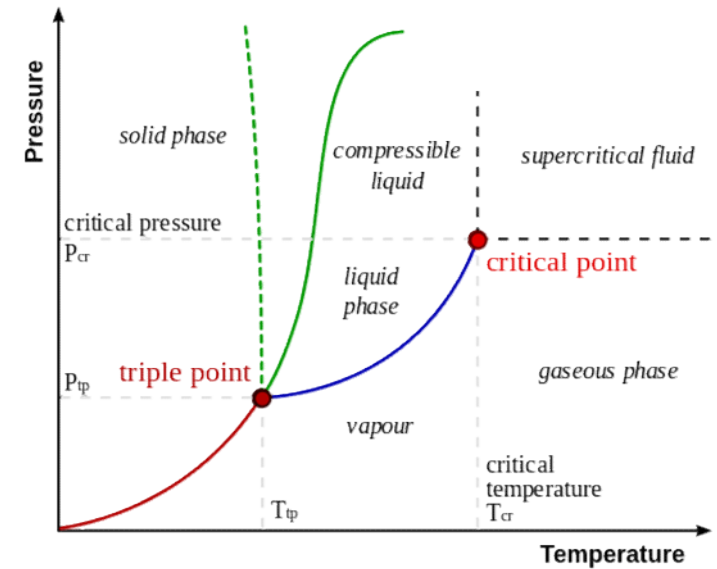
The Origin of Life near Deep Sea Hydrothermal vents?
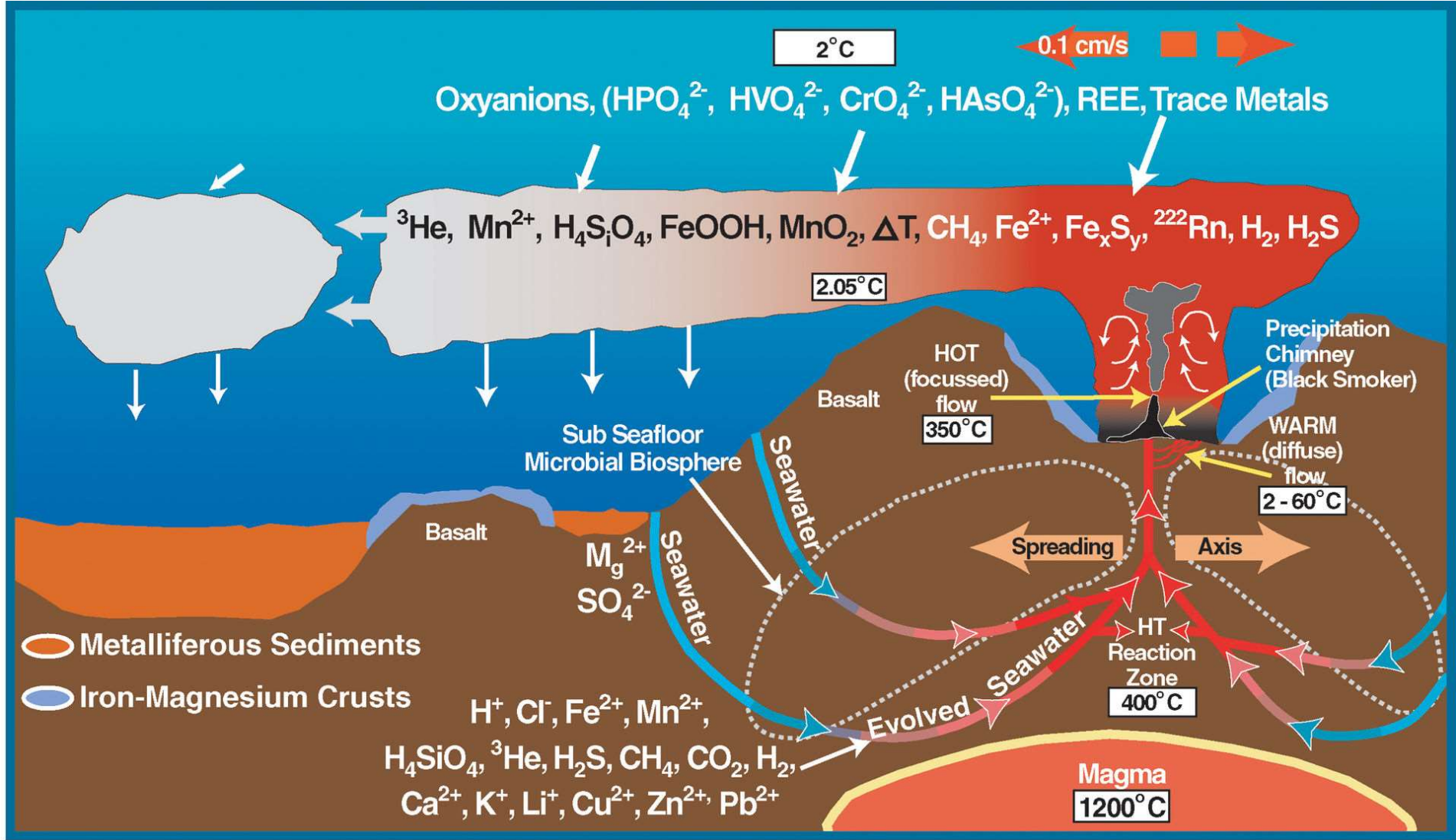
Hydrothermal vents
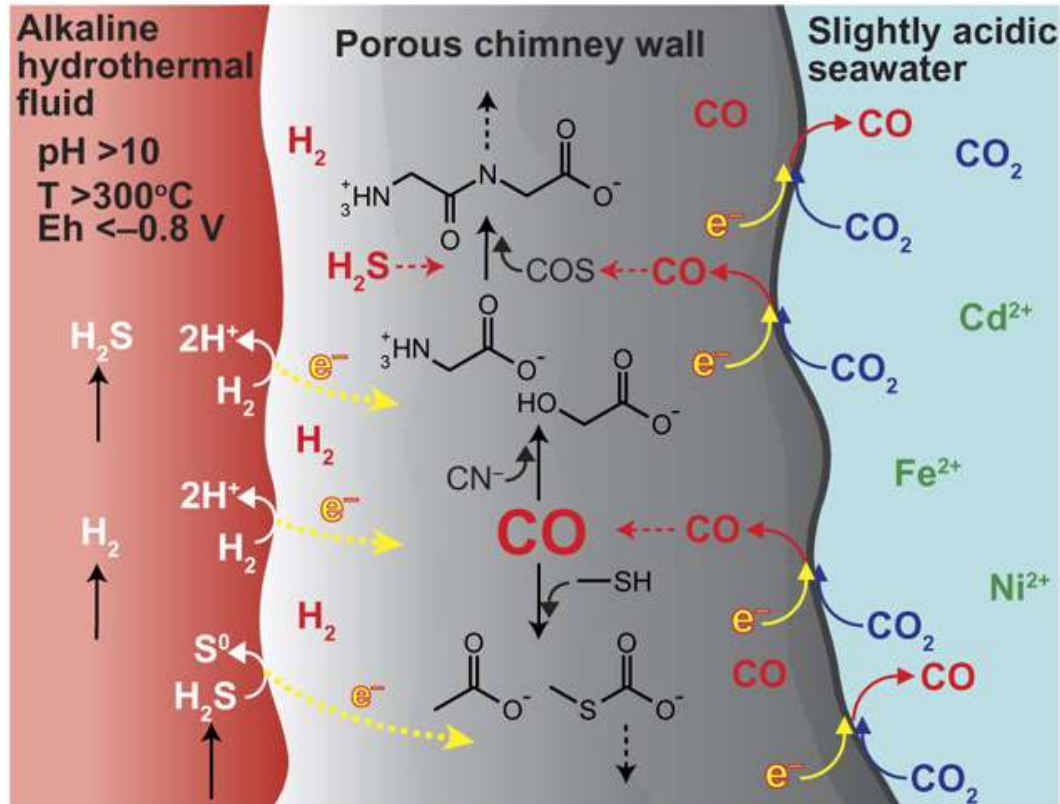

Alkaline hydrothermal vents consist of microscale caverns coated by thin membraneous metal sulfide walls → ‚Iron-sulfur world'

White flocculent mats in and around the extremely gassy, high-temperature (>100°C, 212°F) white smokers at Champagne Vent.

Deep sea vent biogeochemical cycle diagram

B

Metal-rich, high-T, acidic HS

H$_2$-rich, high-T, alkaline HS

Ni^{2+}
Fe^{2+}
Cd^{2+}
Ag$^+$
Cd^{2+}
Fe^{2+}

Metal-rich, high-T, acidic HS

CO$_2$
H$_2$
CO$_2$
H$_2$S

CO$_2$
H$_2$
H$_2$S
H$_2$S

CO$_2$
Oceanic crust

Komatiite and basaltic magma

Mantle

C

Alkaline hydrothermal fluid

pH >10
T >300°C
Eh <−0.8 V

Porous chimney wall

Slightly acidic seawater

H$_2$
$^+_3$HN

CO
CO
CO$_2$
CO$_2$

H$_2$S
COS
CO
e$^-$

H$_2$S
$^+_3$HN
e$^-$
CO$_2$
Cd^{2+}

2H$^+$
H$_2$
e$^-$
HO
e$^-$
CO$_2$
Fe^{2+}

CN$^-$

2H$^+$
H$_2$
e$^-$
CO
CO
Ni^{2+}

H$_2$
SH
e$^-$
CO
CO

S^0
H$_2$S
e$^-$
CO$_2$
CO$_2$

H$_2$
H$_2$S

A

Deep sea vent origin of life

Abiotic carbon fixation in the primitive hydrothermal system.

On the ocean floor, mixing of the hydrothermal fluids and seawater generated sulfide-rich chimneys, and the potential gradient across the chimney drove a continuous electron flow. The electric potential at the chimney-seawater interface could reach less than −1 V (versus SHE) in alkaline hydrothermal vent environments. The low potential, in the presence of sulfides rich in Cd^{2+} and Ag^+, allowed the electrochemical CO_2 reduction to CO with the FE as high as dozens of percent, together with H_2 evolution. The produced CO served as a driving force for the subsequent abiotic organic synthesis that preceded the origin of life as schematically indicated in the figure

Kitadai et al., *Sci. Adv.* **2018**; 4: eaao7265

Deep sea vent fauna
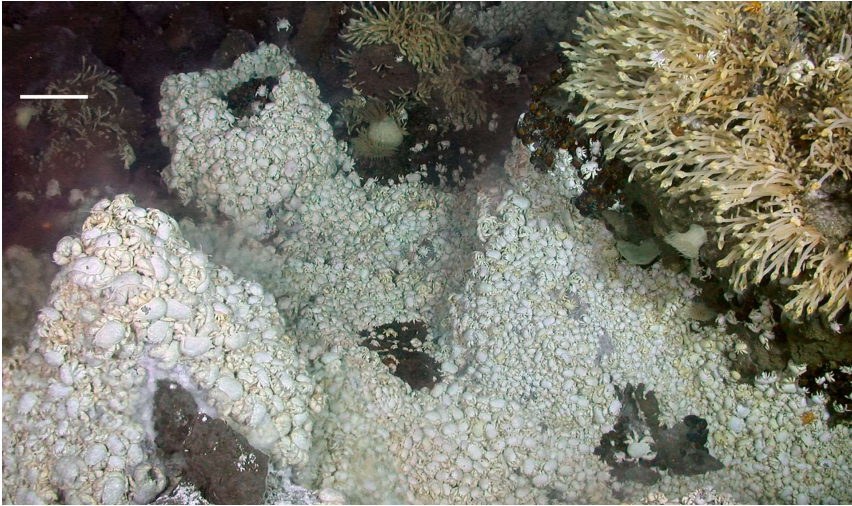
A dense fauna (*Kiwa* anomurans and *Vulcanolepas* like stalked barnacles) near East Scotia Ridge vents

Giant tube worms (*Riftia pachyptila*) cluster around vents in the Galapagos Rift

„Lost city" – white smokers: alkaline hydrothermal vents

A 1.5-meter-wide ledge on the side of a chimney is topped with dendritic carbonate growths that form when mineral-rich vent fluids seep through the flange and come into contact with the cold seawater.

A carbonate chimney more than 9 meters (30 feet) in height. The white, sinuous spine is freshly deposited carbonate material. The top shows evidence of collapse and re-growth, as indicated by the small newly developed cone on its top
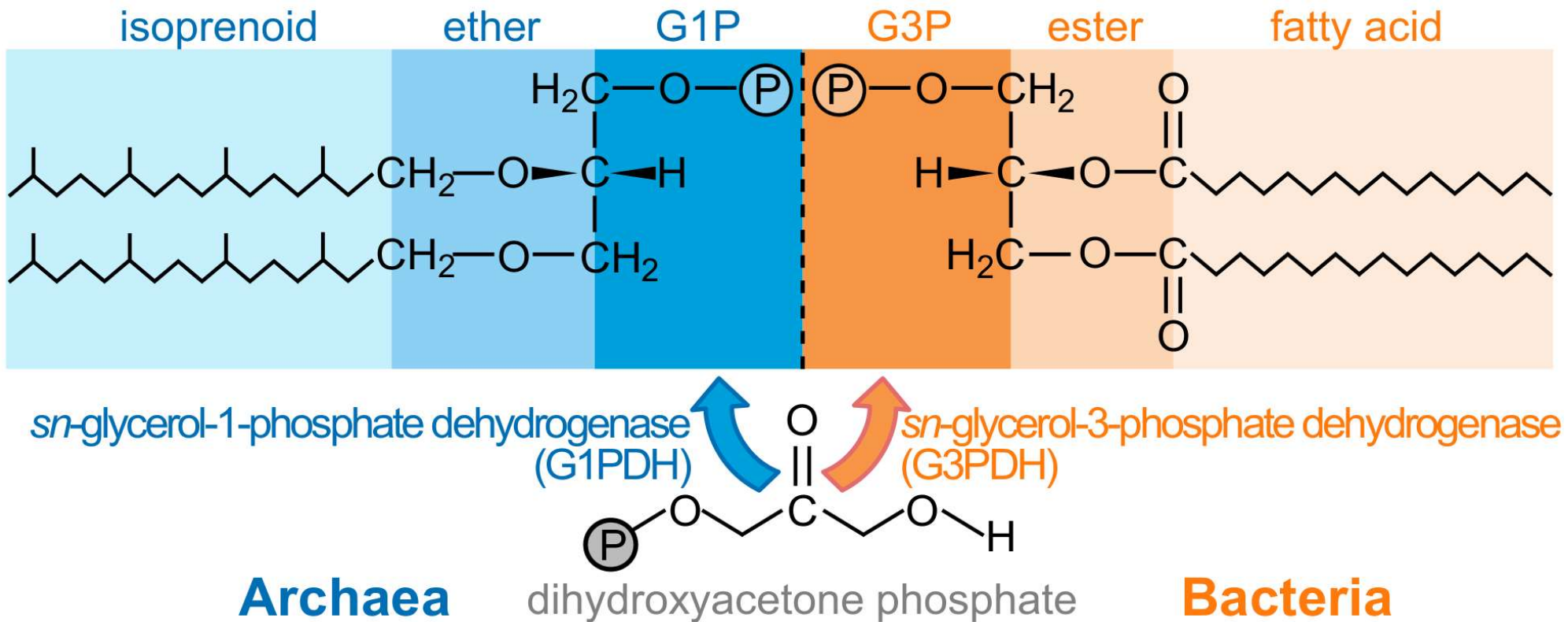
Archaeal lipids: isoprenoid chains + ether bonds + *sn*-glycerol-1-phosphate (G1P) backbone.
Bacterial lipids: fatty acids + ester linkage + *sn*-glycerol-3-phosphate (G3P) skeleton.

Despite widespread horizontal gene transfer, no bacterium has been observed with the archaeal enantiomer, or vice versa.
(ether linkages have been observed in bacterial membranes and isoprenoids are common to all three domains)
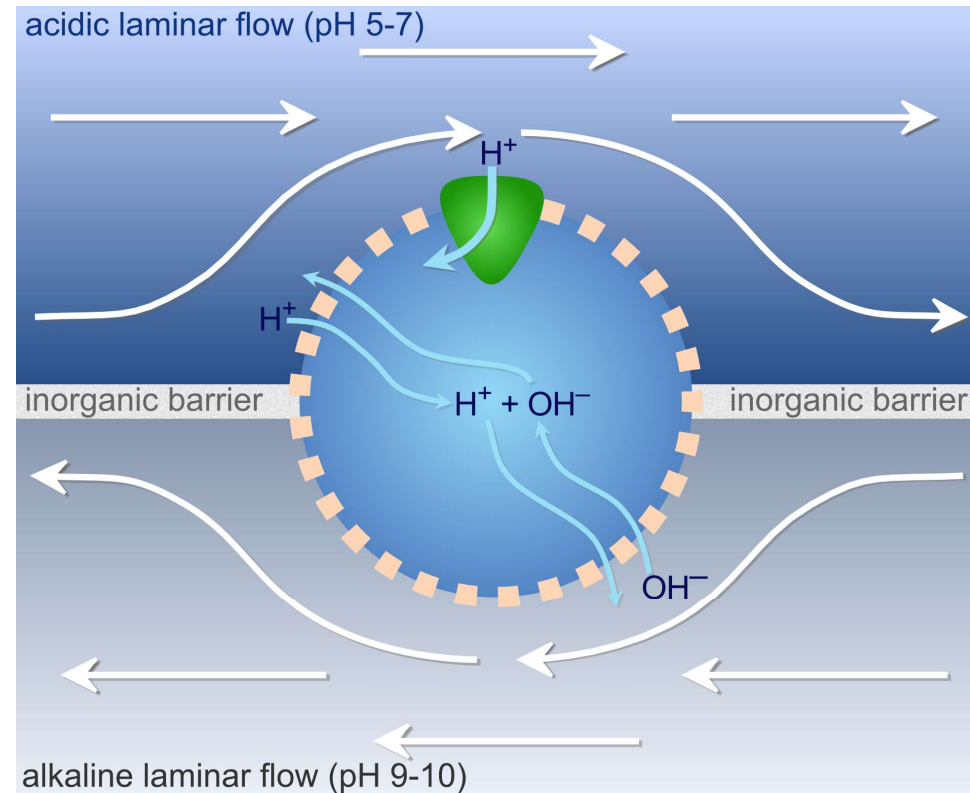
A cell with a semi-permeable membrane at the interface between an alkaline and an acidic fluid (separated elsewhere with an inorganic bareer. H^+, OH^-, Na^+, K^+, Cl^- and other ions flow according to their natural gradients.
Inside the protocell, H^+ and OH^- can neutralize into water, or leave towards either side.

A protein capable of exploiting the natural proton gradient sits on the acidic side, allowing energy assimilation via ATP production, or carbon assimilation via CO_2 fixation.

The role of sodium-proton antiporter (SPAP)
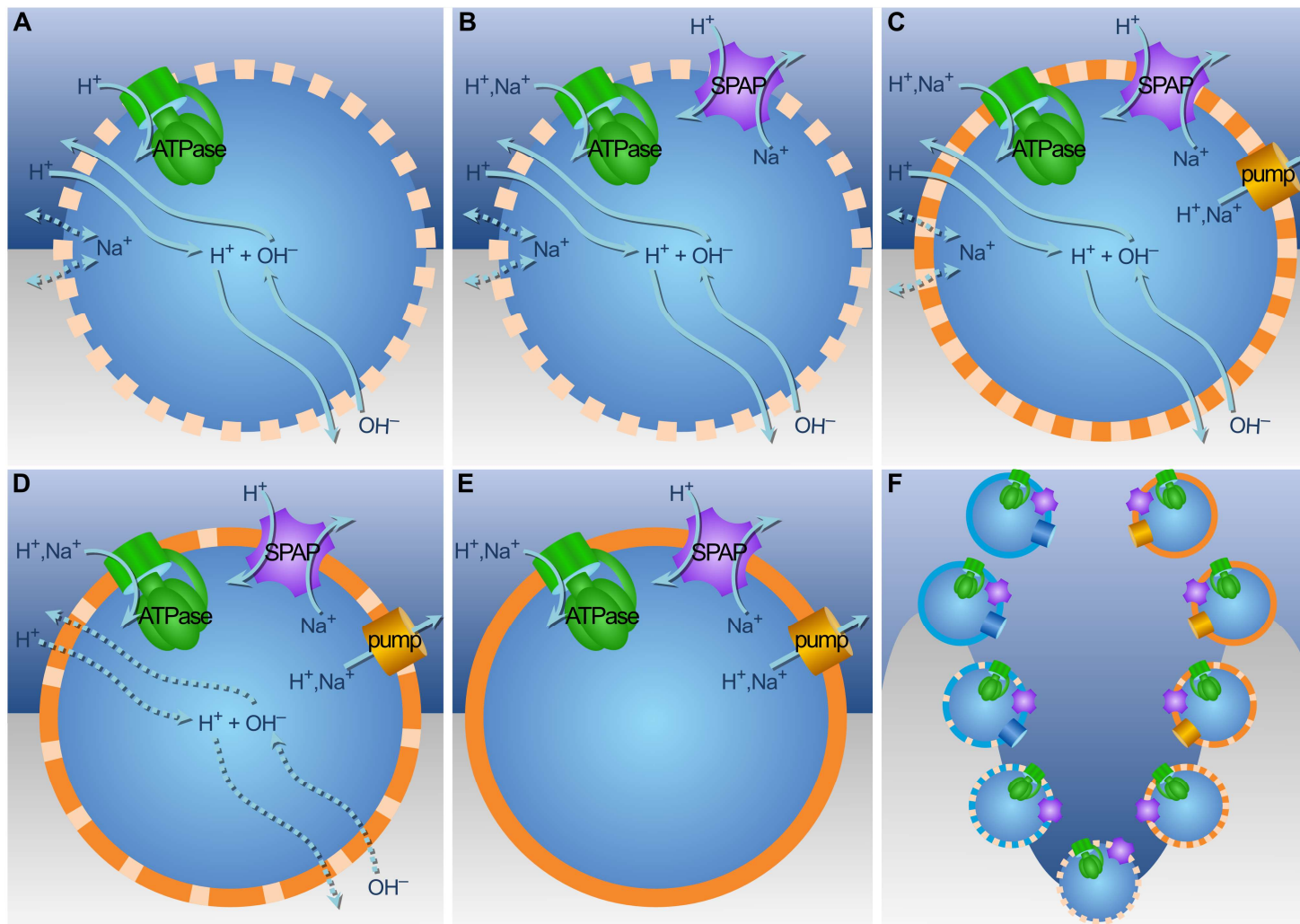
A) H^+ gradient drives energy metabolism (ATPase) or carbon metabolism (Ech)

B) SPAP generates Na^+ from H^+ gradient

C) Membrane pumps secret H^+ and Na^+

D) Tighter membranes are now produced, to colonize less alkaline environments

E) Impermeable membranes → gradients created by proteins, independently from the natural environmental gradients

F) SPAP favors divergence, selection for active pumping and tighter membranes; independent evolution of archea and bacteria
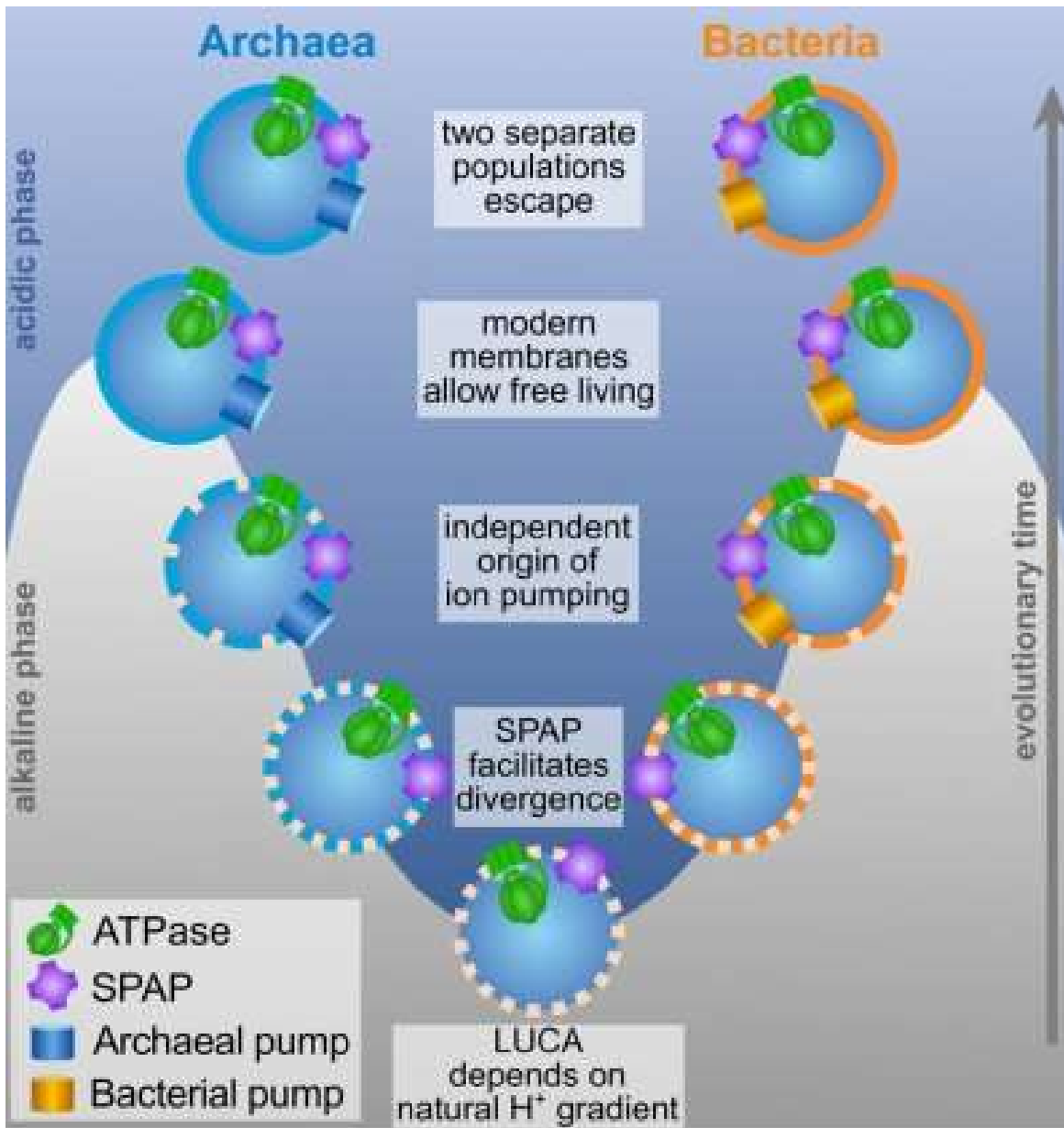
Origin of autotrophy and development of cell membrane

Ion pumping and phospholipid membranes evolved independently in bacteria and archea.

Energy could have been delivered by the natural proton gradient in alkaline hydrothermal vents, if the membrane was much more leaky than contemporary ones.

Development of proton pumping allowed for escape from the vent environment.

sodium-proton antiporter (SPAP)

Taxonomic distribution of LUCA's genes grouped by functional categories
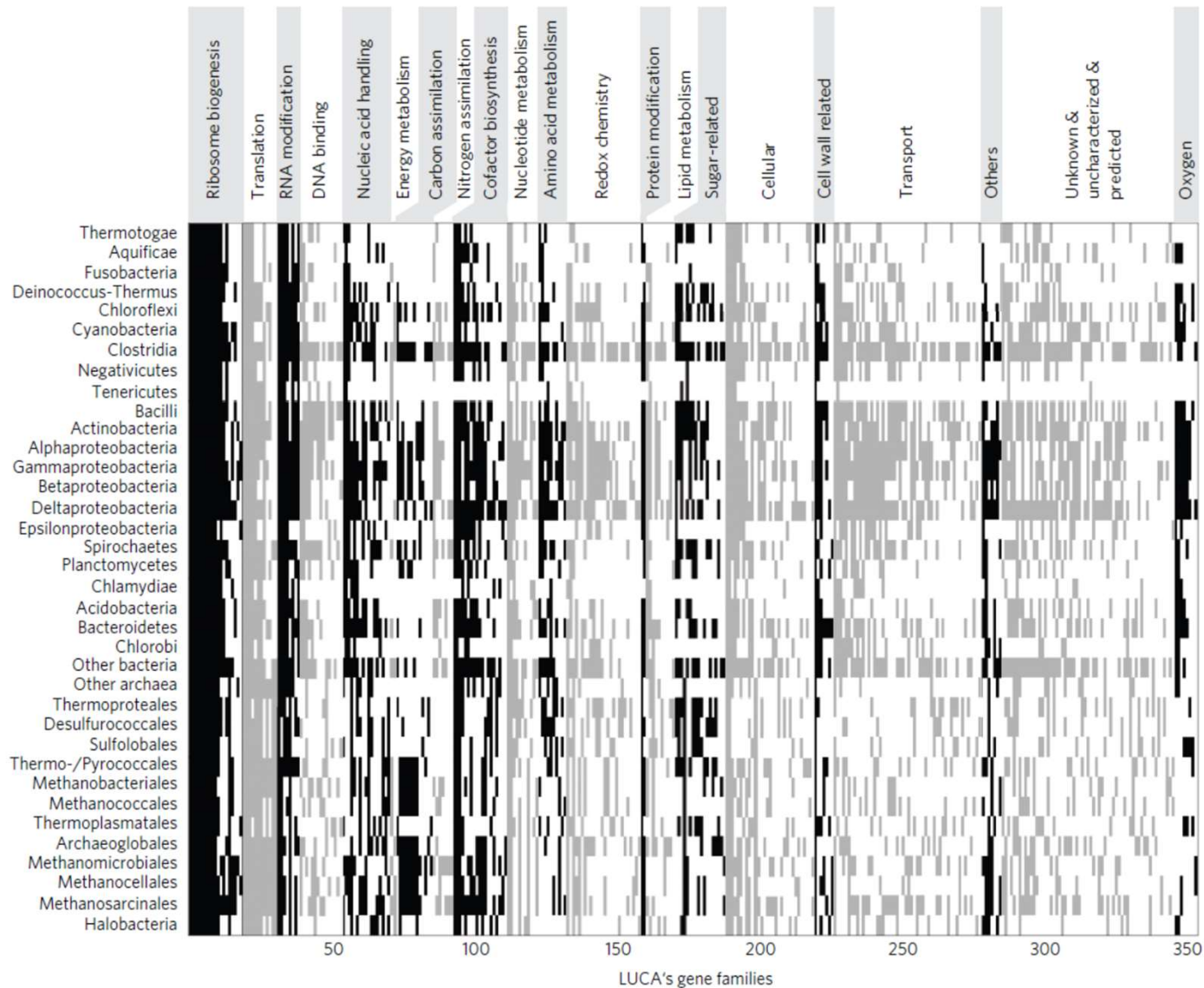
M.C. Weiss et al. *Nature Microbiology,*
2016, *Article 16116*

Structures of the cofactors found in LUCA's protein set.
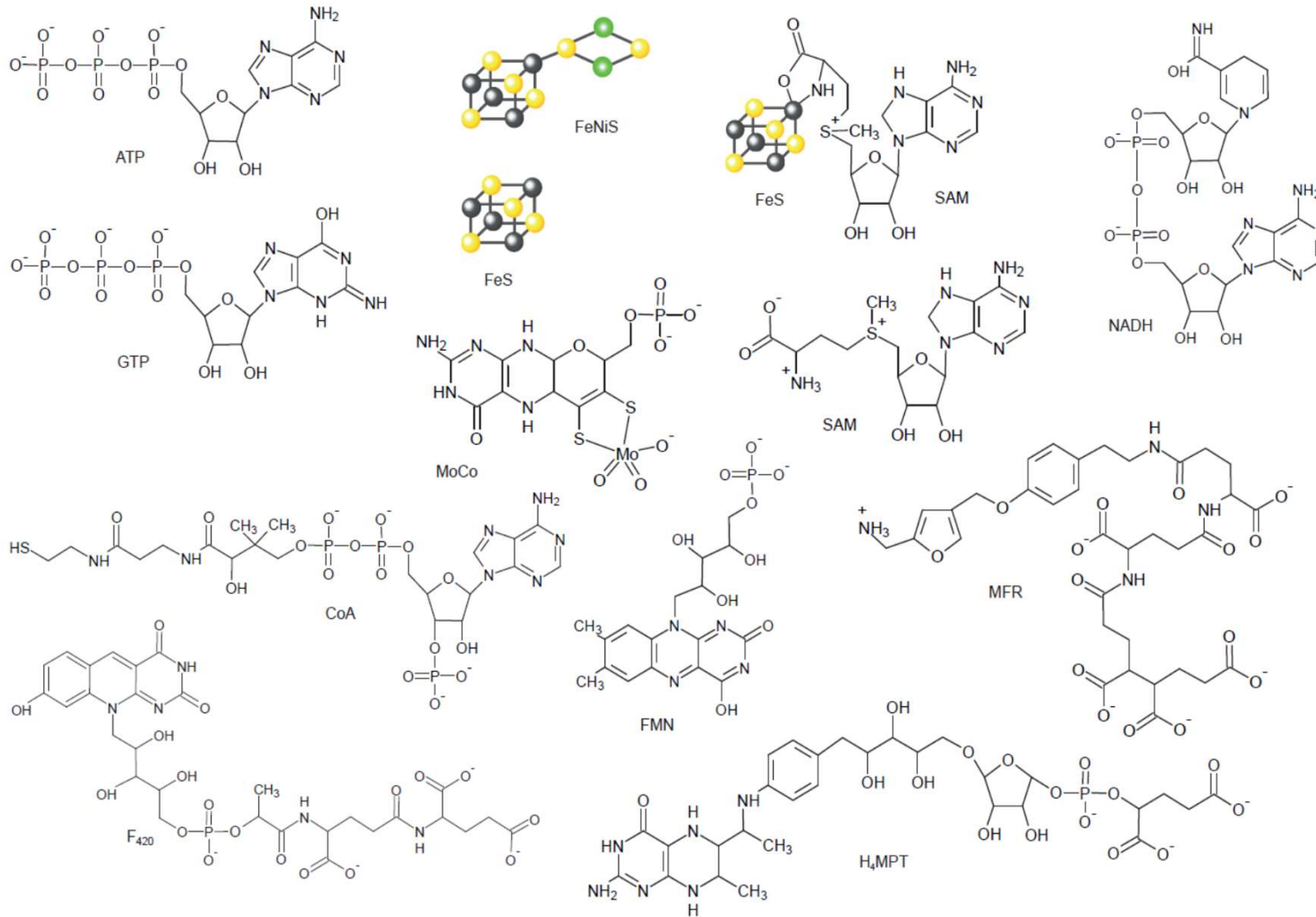
FeNiS – nickel-iron-sulfur cluster
FeS – iron-sulfur cluster
MoCo – molybdenum cofactor
SAM – S-adenosylmethionine
CoA – coenzyme A
MFR – methanofuran
H4MPT – tetrahydromethanopterin
TPP - thiamine pyrophosphate
PLP - pyridoxal phosphate
NTP – nucleoside triphosphate.

Structures of the cofactors found in LUCA's protein set.

Cobalamin

TPP

Menaquinone

PLP

Heme b

Biotin

Methyltetrahydrofolate
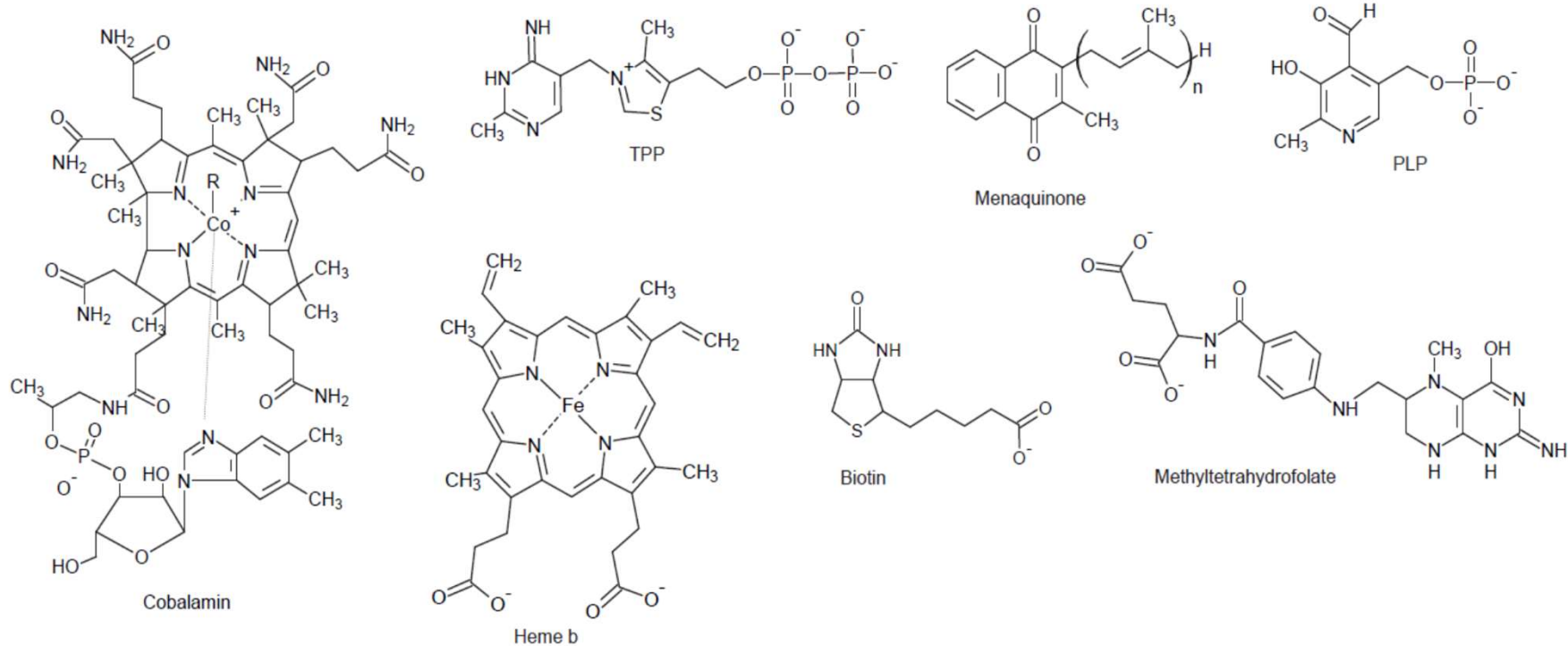
Mononuclear metal centers (Fe and Cu) and the non-standard amino acid selenocysteine are not shown, nor are small protein electron carriers such as ferredoxin or rubredoxin. NTP is also listed as a cofactor, but not shown here as it stands for any of the nucleoside triphosphates in those cases when it's not known which one is bound by the enzyme, or when more than one nucleoside triphosphate can be used

Phylogenetic identification of LUCA's proteome

355 protein families shared among contemporary *archaea* and *bacteria*, including:

- 19 proteins involved in ribosome biogenesis

- 8 aminoacyl tRNA synthethases

- proteins for carbon, energy, and nitrogen metabolism

- rotor-stator ATP synthase subunit (ion gradients were likely supplied geochemically)

- substrate-level phosphorylation (acetylphosphate from acetyl-CoA)

- reverse gyrase – specific for currently living hyperthermophilic organisms

- chemolitoautotrophy enzymes present (WL pathway), chemoorganoautotrophy enzymes absent

Wood-Ljungdahl (WL) anaerobic pathway of carbon fixation
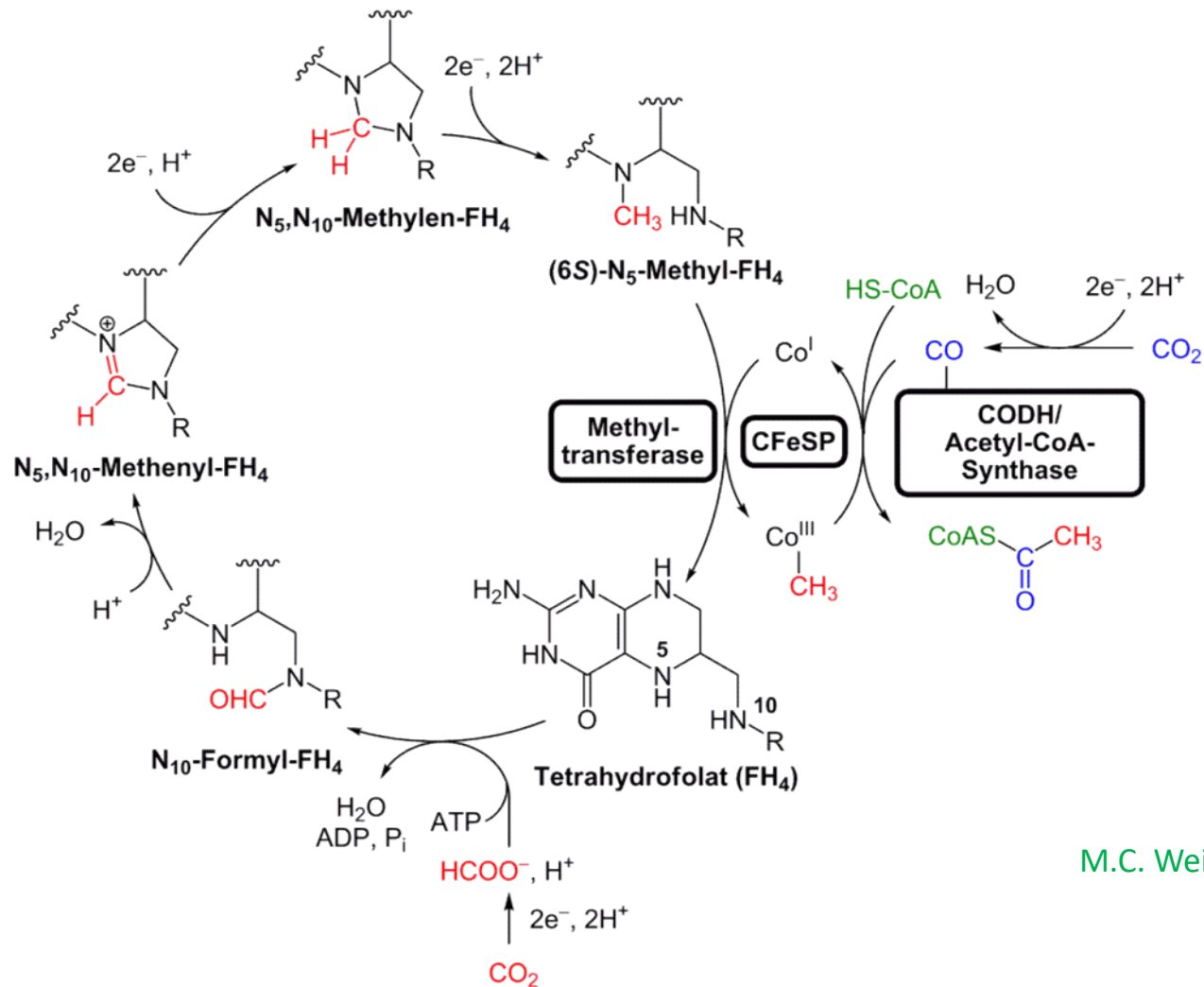
A primitive metabolic pathway for carbon fixation, still used by some contemporary chemoautotrophic organisms

Metabolism of LUCA

Among six currently known pathways of CO_2 fixation, only WL pathway was present in LUCA:

The relevant enzymes are packed with FeS and FeNiS centres

They require cofactors: flavin, F_{420}, methanofuran, two pterins and corrins

Hydrogenases also present in LUCA's genome → electrons likely obtained from hydrogen, as in modern microbes using the WL pathway

Nitrogenase and glutamine synthethase serve for nitrogen fixation

WL pathway, nitrogenase and hydrogenases are very oxygen-sensitive
→ LUCA was an anaerobic autotroph that could live from gases H_2, CO_2, and N_2.

Metabolism of LUCA

Enzymes for cofactor biosynthesis, including pterins, MoCo, cobalamin, siroheme, TPP, CoM and F_{420}, are also conserved.

Many of them are S-adenosyl methionine(SAM)-dependent

SAM chemistry is based on oxygen-sensitive FeS-containing proteins that initiate radical-dependent methylations.
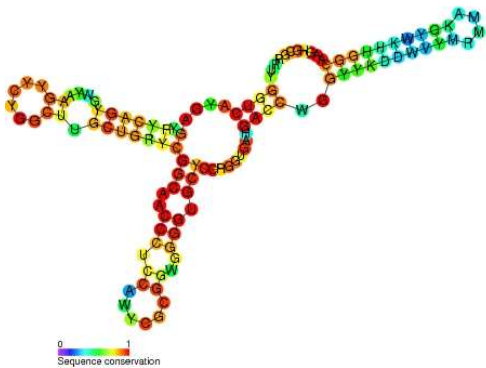
SAM-binding riboswitches
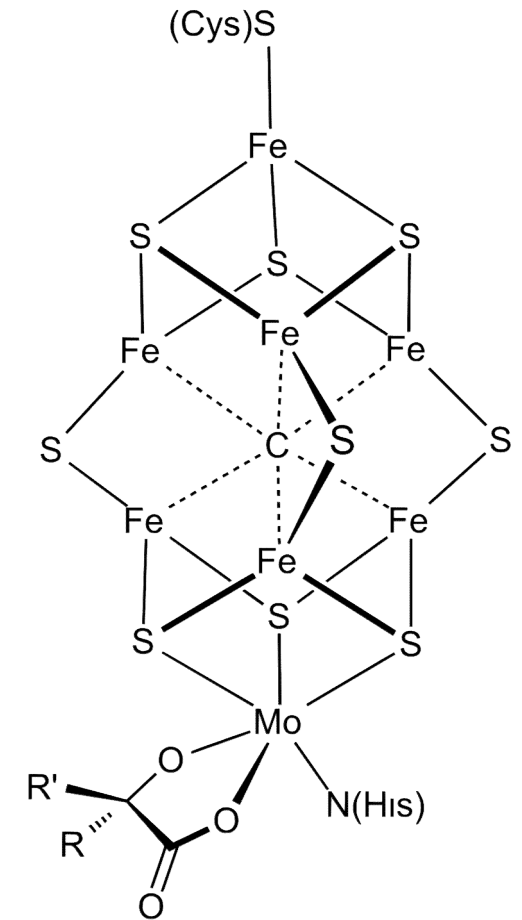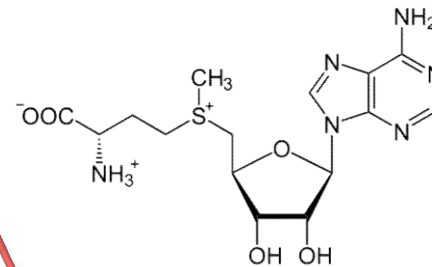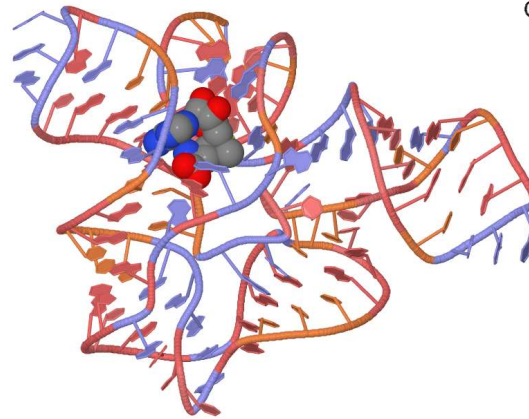
FeMo cofactor of nitrogenase

M.C. Weiss et al. *Nature Microbiology,* **2016**, *Article 16116*

Prebiotic Wood-Ljungdahl (WL) pathway analogue

native transition metals (Fe⁰, Ni⁰ and Co⁰) selectively reduce CO_2 to acetate and pyruvate—the intermediates and end-products of the AcCoA pathway—in near millimolar concentrations in water over hours to days using 1–40 bar CO_2 and at temperatures from 30 to 100 °C.
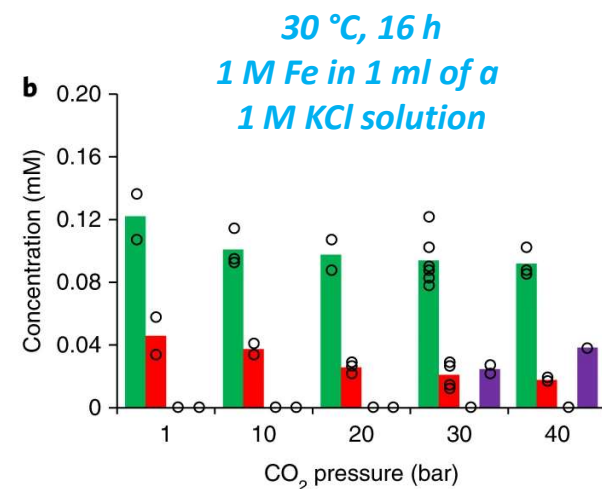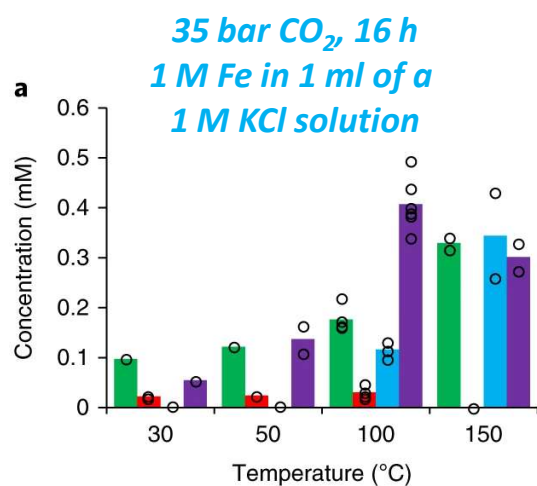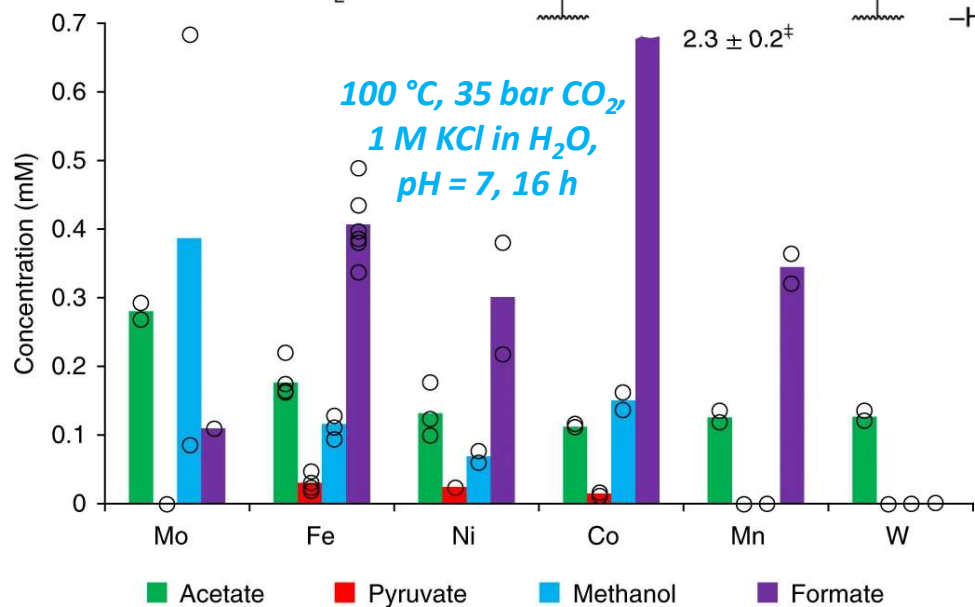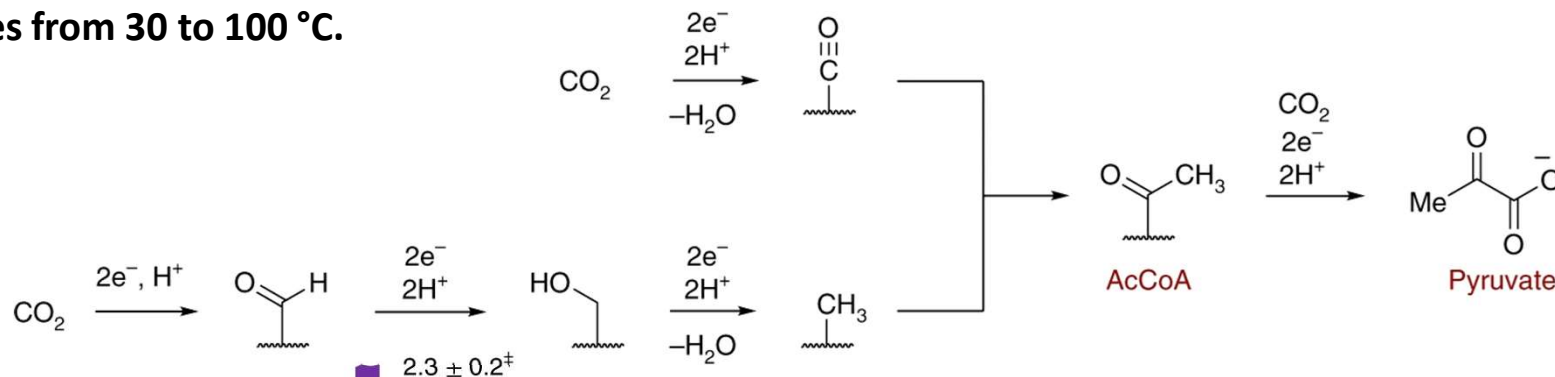
S.I. Varma, K.B. Muchowska, P. Chatelain, J. Moran *Nature Ecology and Evolution,* **2019**, *2,* 1019-1024
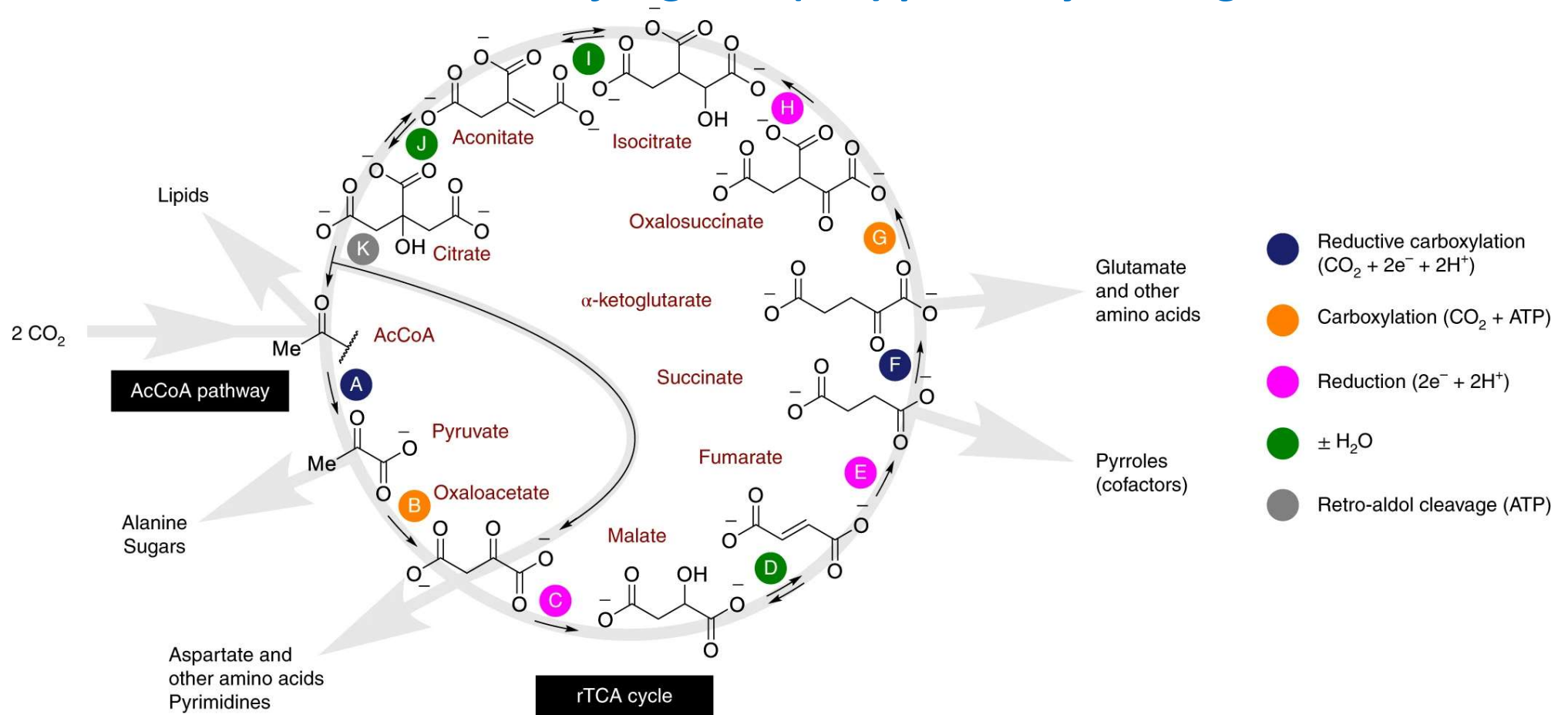
Prebiotic Wood-Ljungdahl (WL) pathway analogue
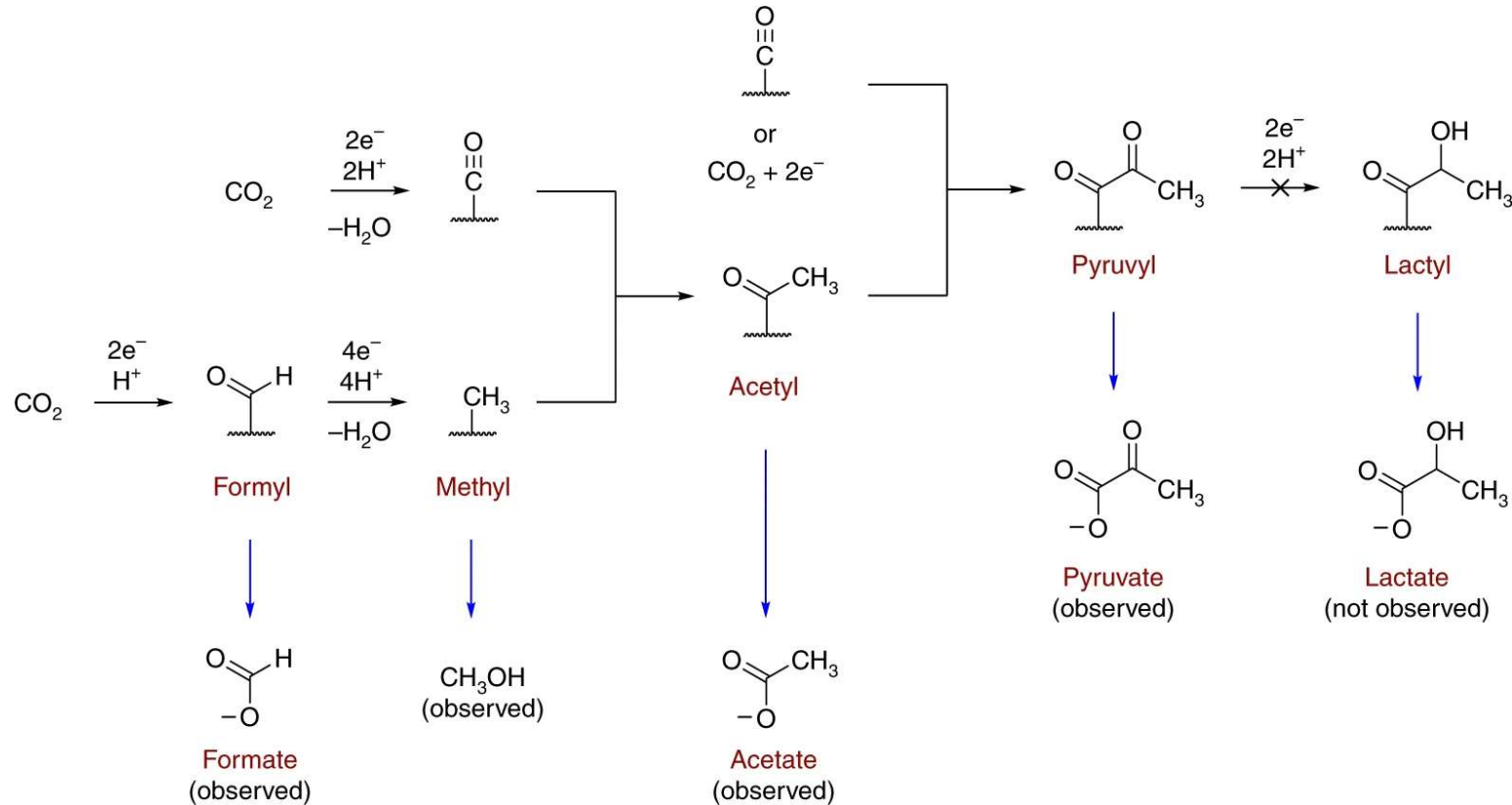
Plausible mechanism for carbon fixation on the surface of Fe⁰ accounting for the detection of formate, methanol, acetate and pyruvate in aqueous solution upon hydrolysis with KOH
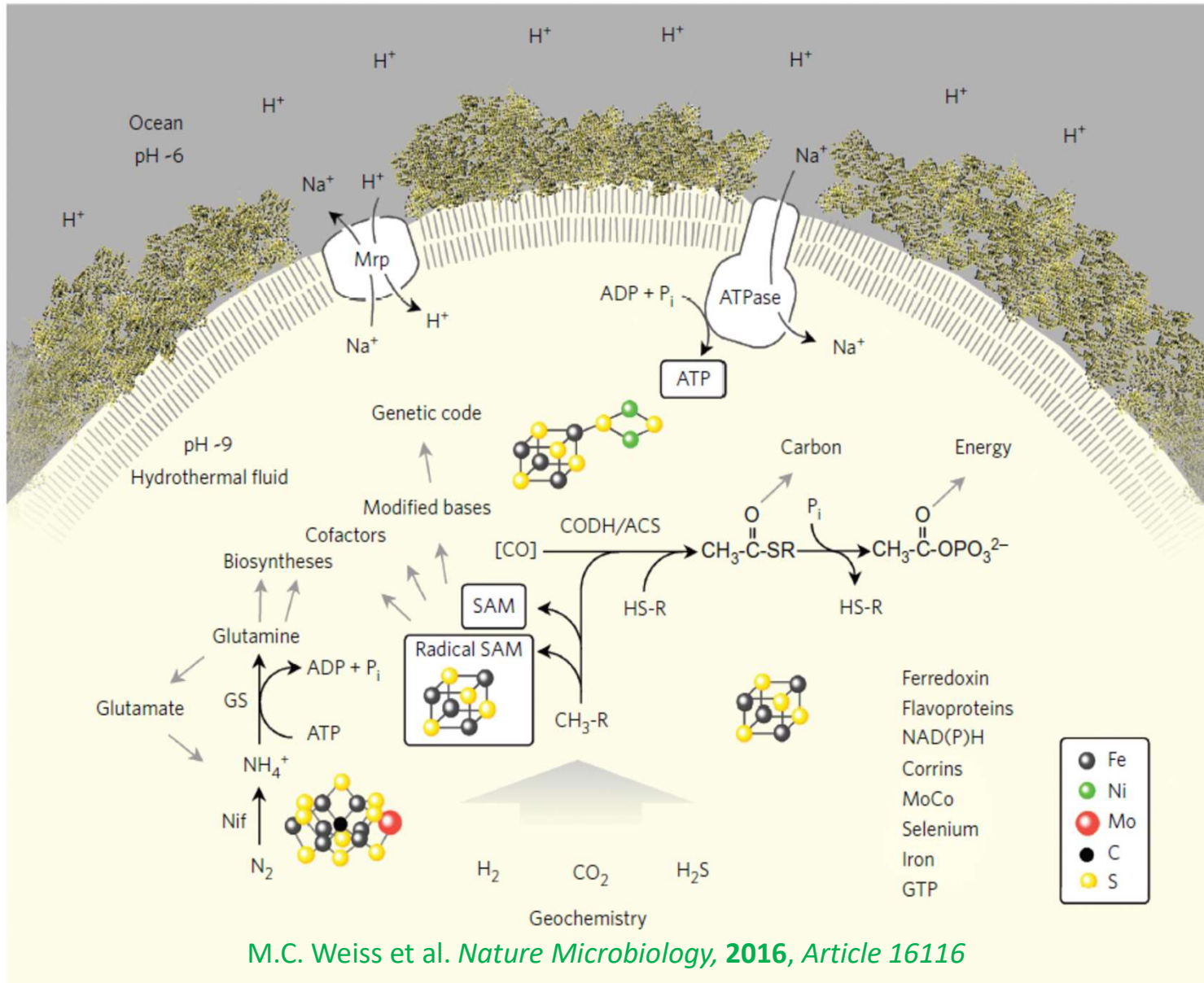
Prebiotic Wood-Ljungdahl (WL) pathway analogue

Hypothetical ancestral proto-anabolic network consisting of a hybrid of the AcCoA pathway and the rTCA cycle, showing the role of its intermediates as universal biosynthetic precursors
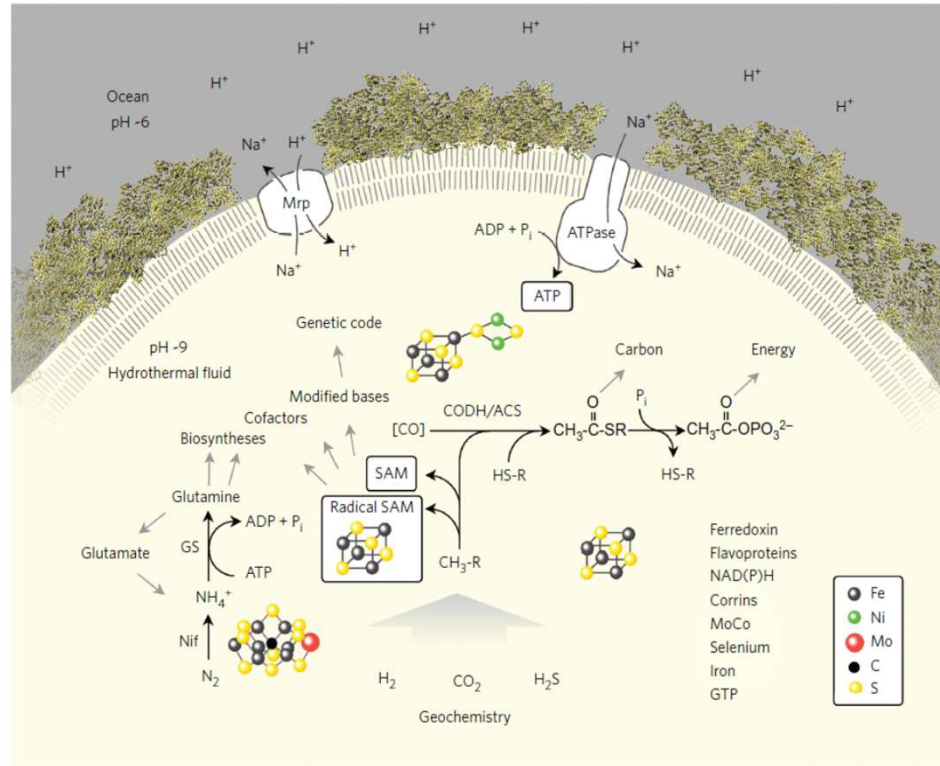
S.I. Varma, K.B. Muchowska, P. Chatelain, J. Moran *Nature Ecology and Evolution,* **2019**, *2,* 1019-1024

M.C. Weiss et al. *Nature Microbiology,* **2016**, *Article 16116*

LUCA reconstructed from the genome data

Summary of the main interactions of LUCA with its environment, a vent-like geochemical setting as inferred from genome data.


In modern CODH/ACS complexes, CO is generated from CO_2 and reduced ferredoxin.
A Na^+/H^+ antiporter could transduce a geochemical pH gradient (indicated on the left) inherent in alkaline hydrothermal vents into a more stable Na^+ gradient to feed a primordial Na-dependent ATP synthase.

# Modified nucleosides and the genetic code

LUCA had also genes involved in RNA nucleoside modifications (mainly methylations and thiomethylations) still required today e.g. for the anticodon recognition process.

Cloverleaf secondary structure representation of tRNA showing only those posttranscriptional nucleoside modifications that are conserved among bacteria and archaea in both identity and position. (5-methoxyuridine at position 34 in archaea has been disputed).
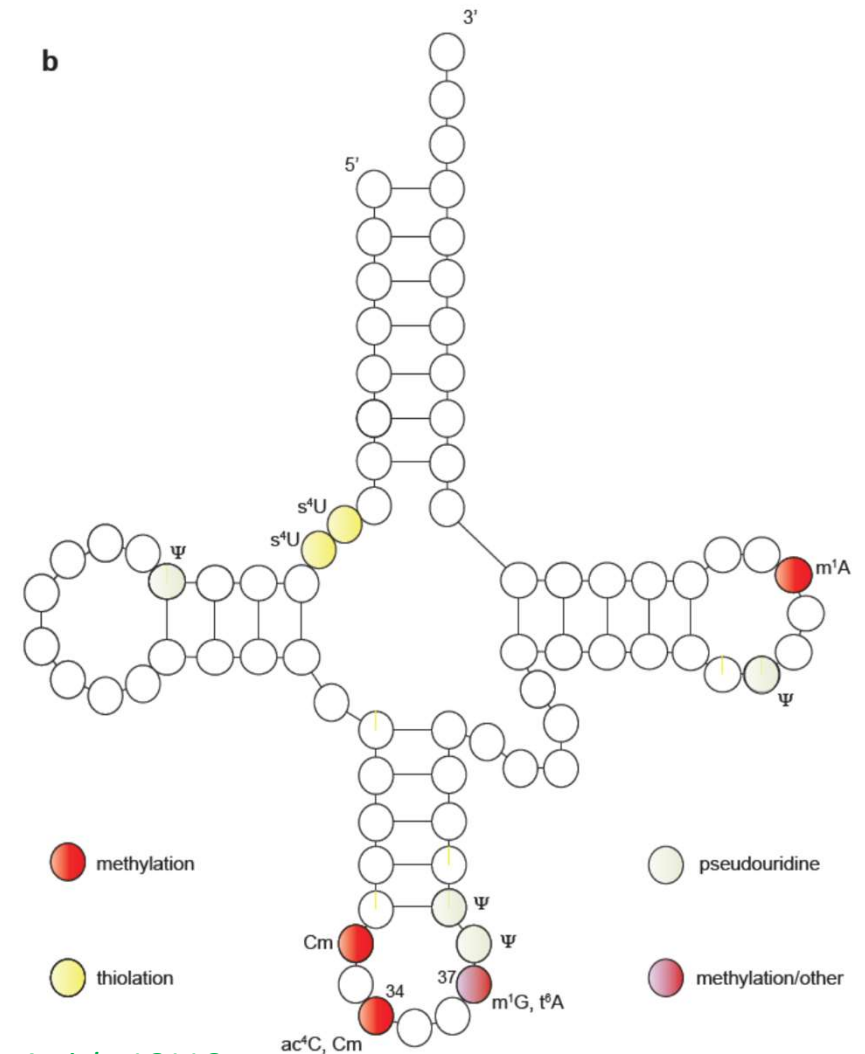
M.C. Weiss et al. *Nature Microbiology,* **2016**, *Article 16116*

Modified nucleosides and the genetic code
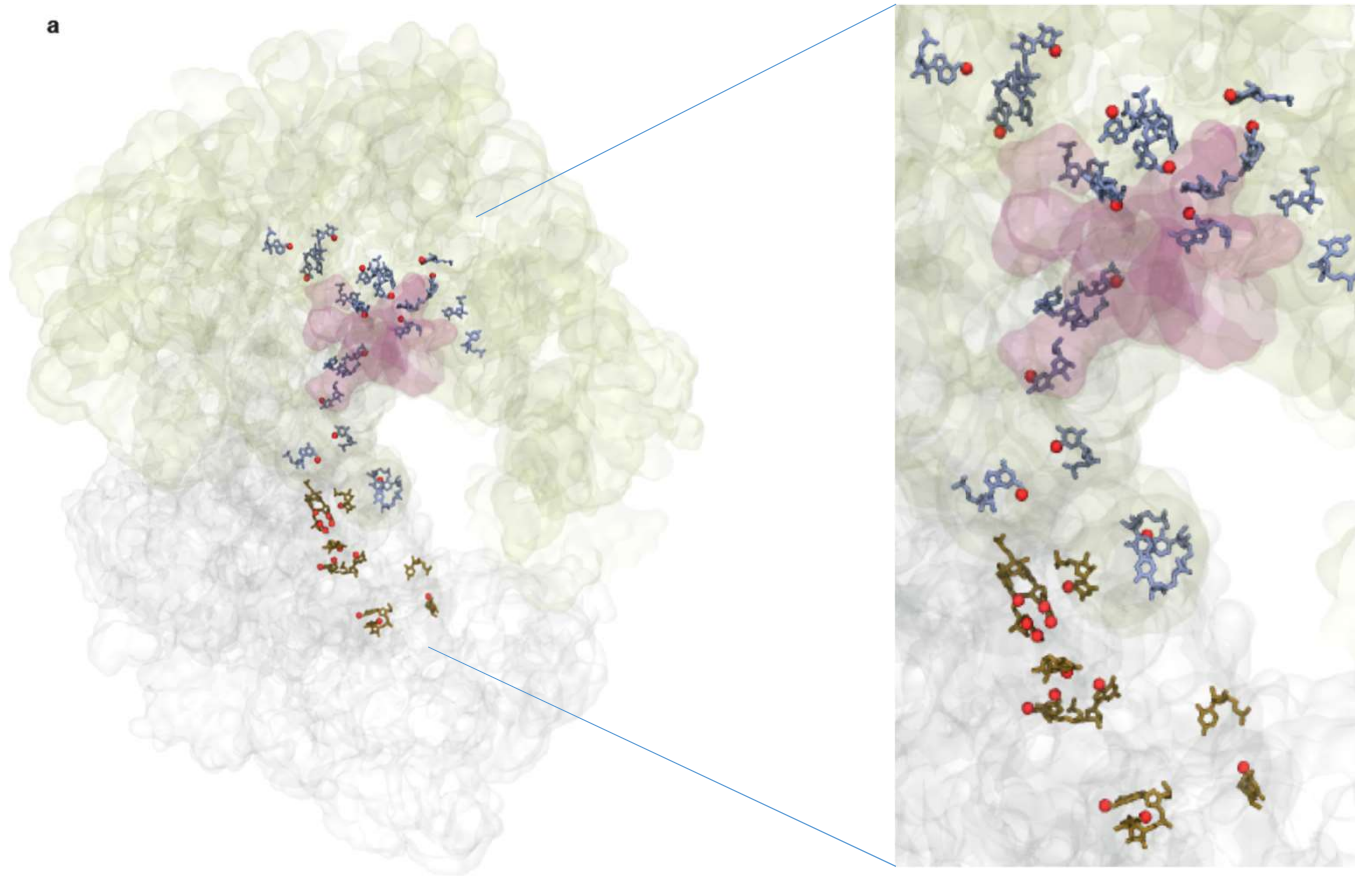
Structure of the E. coli ribosome (PDB ID: 4YBB), with the large and small subunits shown in green and silver, respectively. The peptidyl-transferase site is shaded pink. The modified nucleosides of 23S rRNA are depicted in icy blue, while in 16S rRNA they are ochre. Modification of C2501 to 5-hydroxycytidine is not present in the structure. Methyl group carbons are shown as red balls.

Closest living relatives of LUCA

clostridia
anaerobic bacteria
(botulin, gangrene, tetanus)
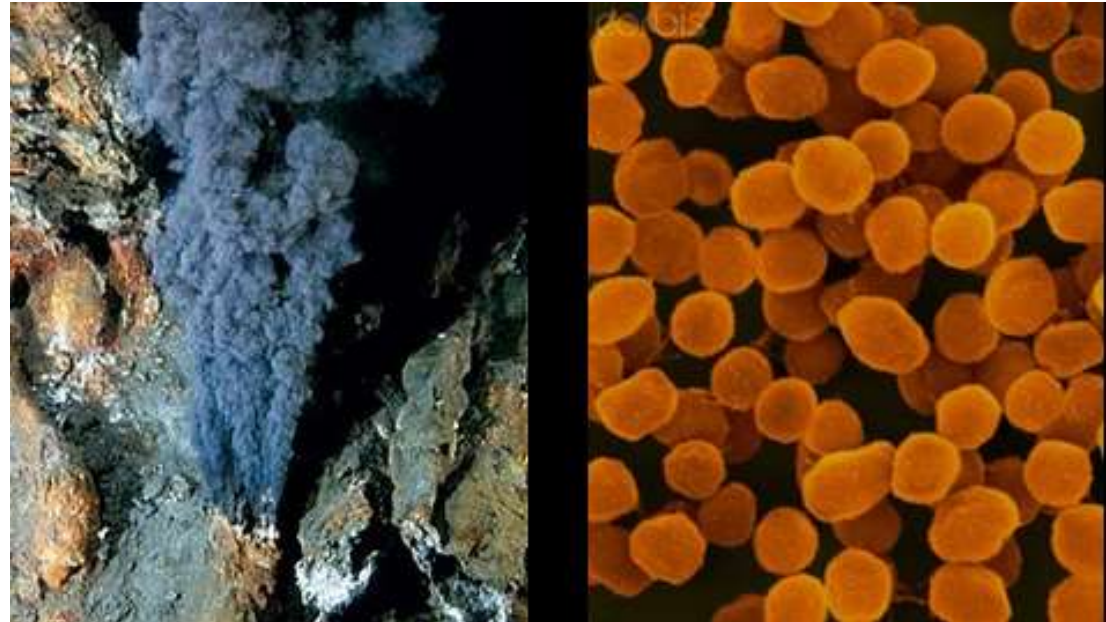
Deep ocean vent - home to the extremophilic archeon
Methanococcus jannaschii

They use the WL pathway, abundant also today, some species can live from methyl groups
(methane gas on marshes andwetlands), and they depend on H_2 (from geology or H_2-producing fermentation)

Geological source of hydrogen: serpentinization (iron + hot water, anoxic) $Fe^{2+} + H_2O \rightarrow Fe_3O_4 + H_2$

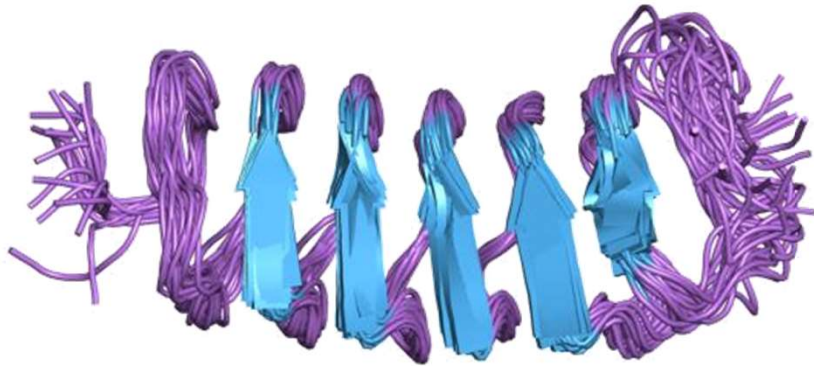# Thermophiles
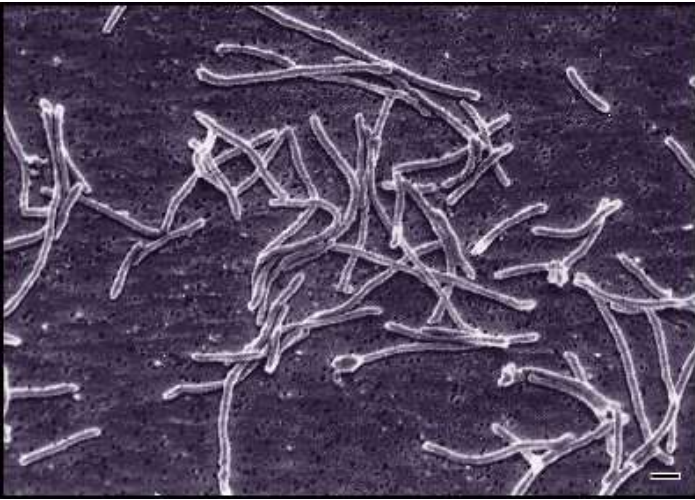
Thermus aquaticus
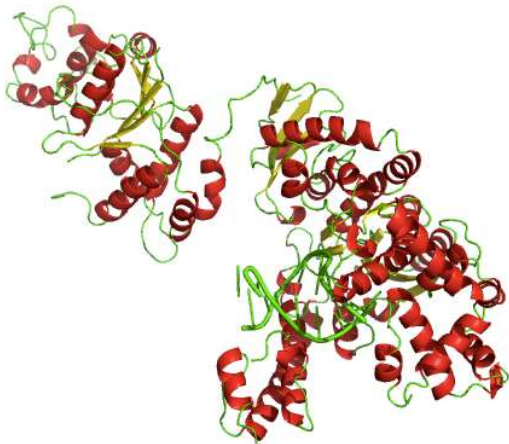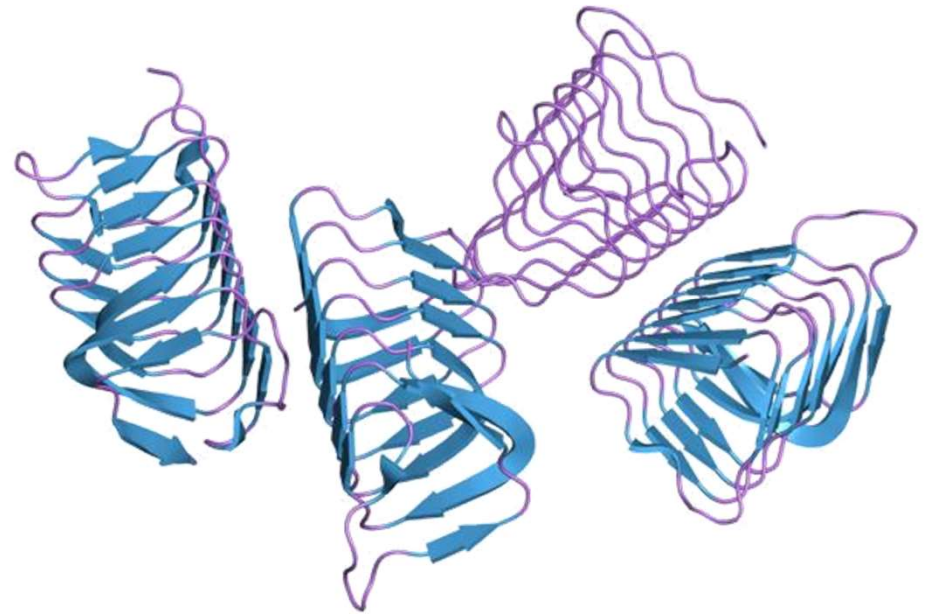

3D structure of Taq Polymerase.

Hot springs with algae and bacteria in Yellowstone National Park
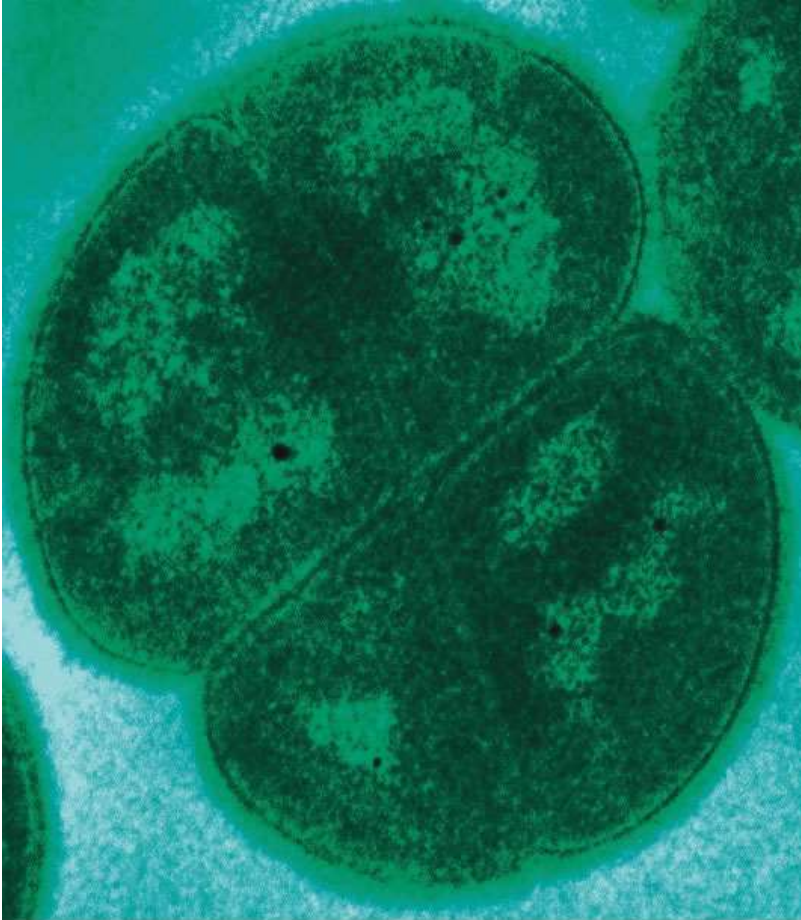
Cold adaptation

Structure of the *Tenebrio molitor* beta-helical antifreeze protein

Structure of *Choristoneura fumiferana* (spruce budworm) beta-helical antifreeze protein
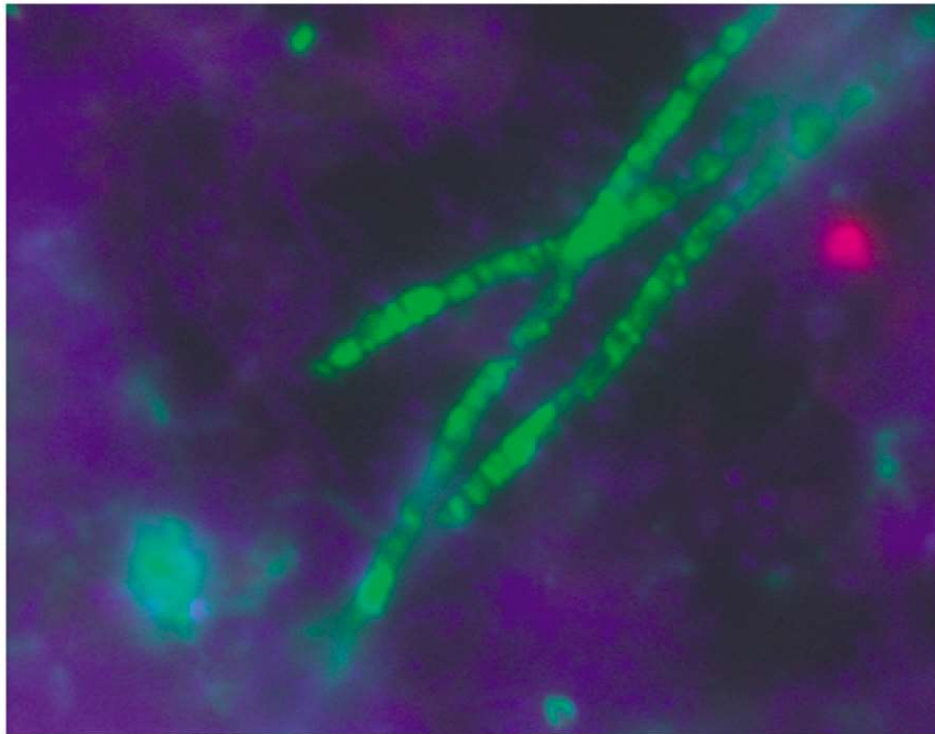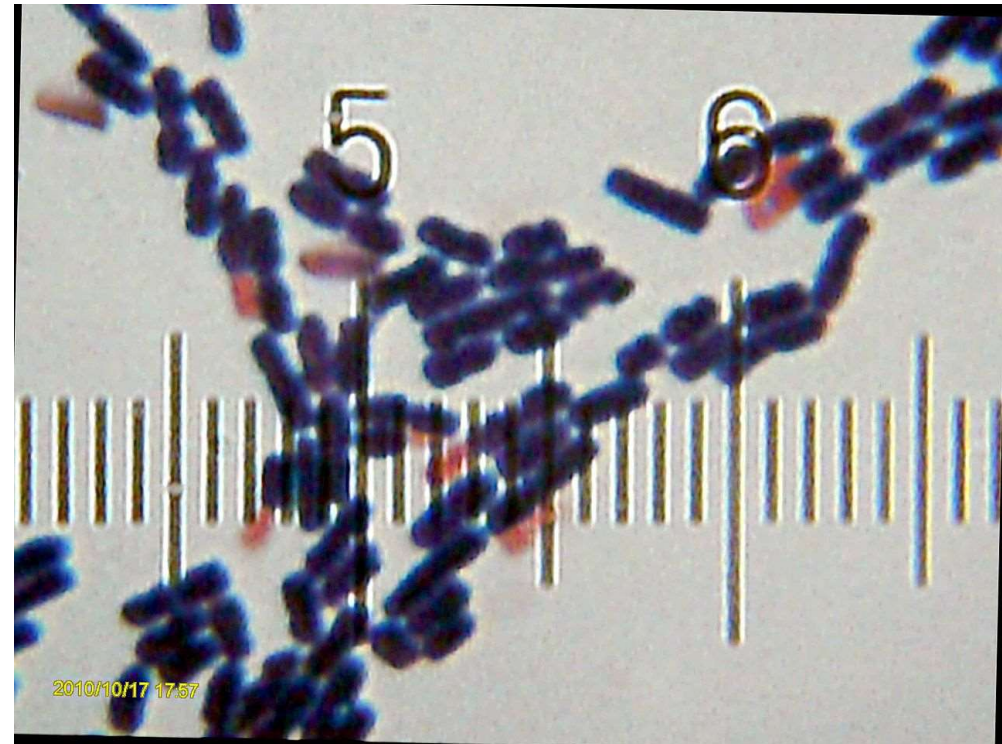
Drought, salinity, radiation

A tetrad of D. *radiodurans*

Efficient DNA damage repair,
Trehalose as the main sugar – glass solid, no crystallization

Acid, base

Acidobacterium

A typical *bacillus* culture. Many alkaliphiles possess a *bacillus* morphology