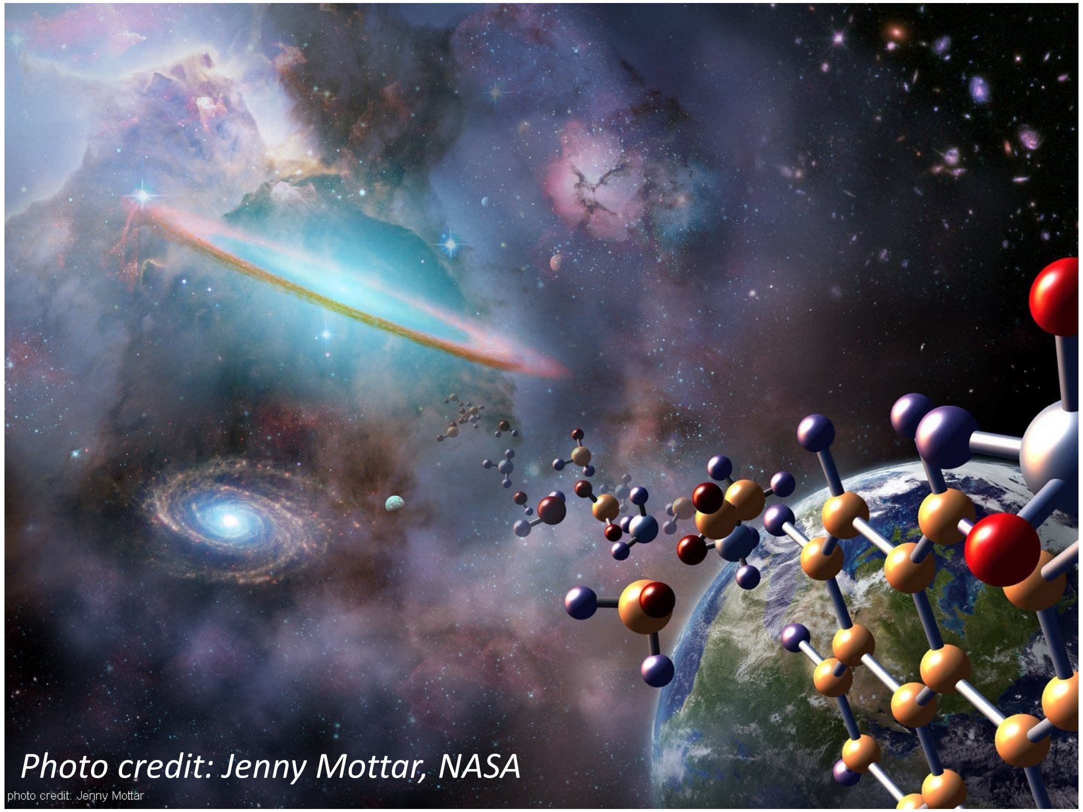
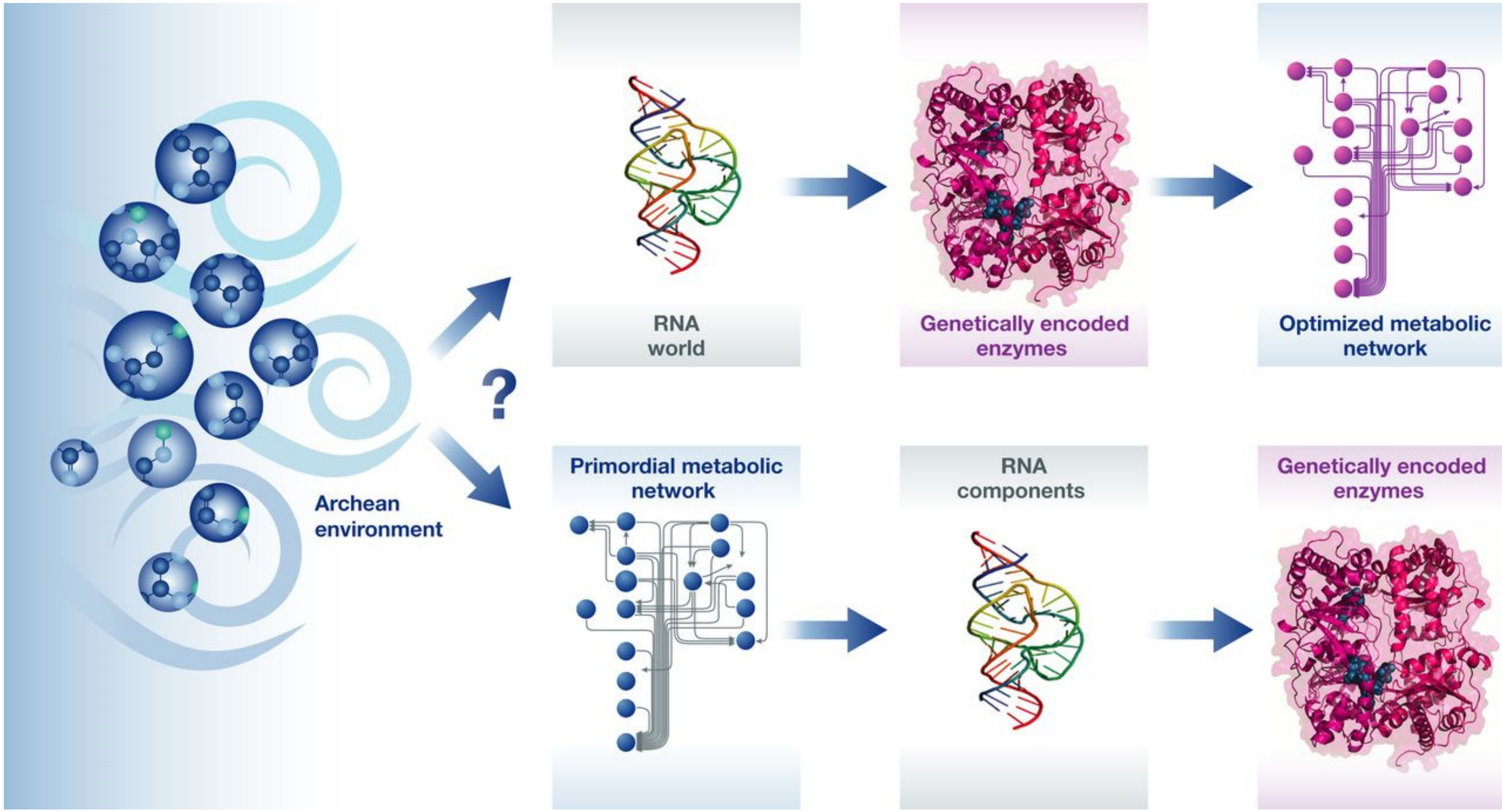
The molecular origins of life



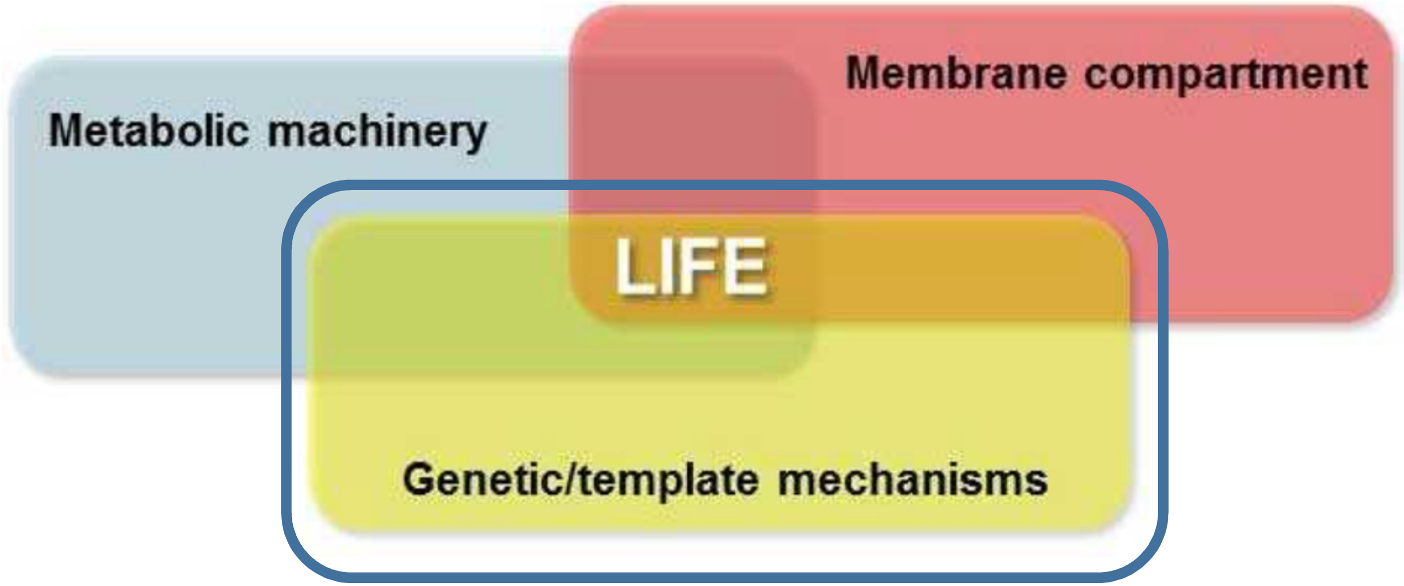
L7 SoSe 2020

Zbigniew Pianowski

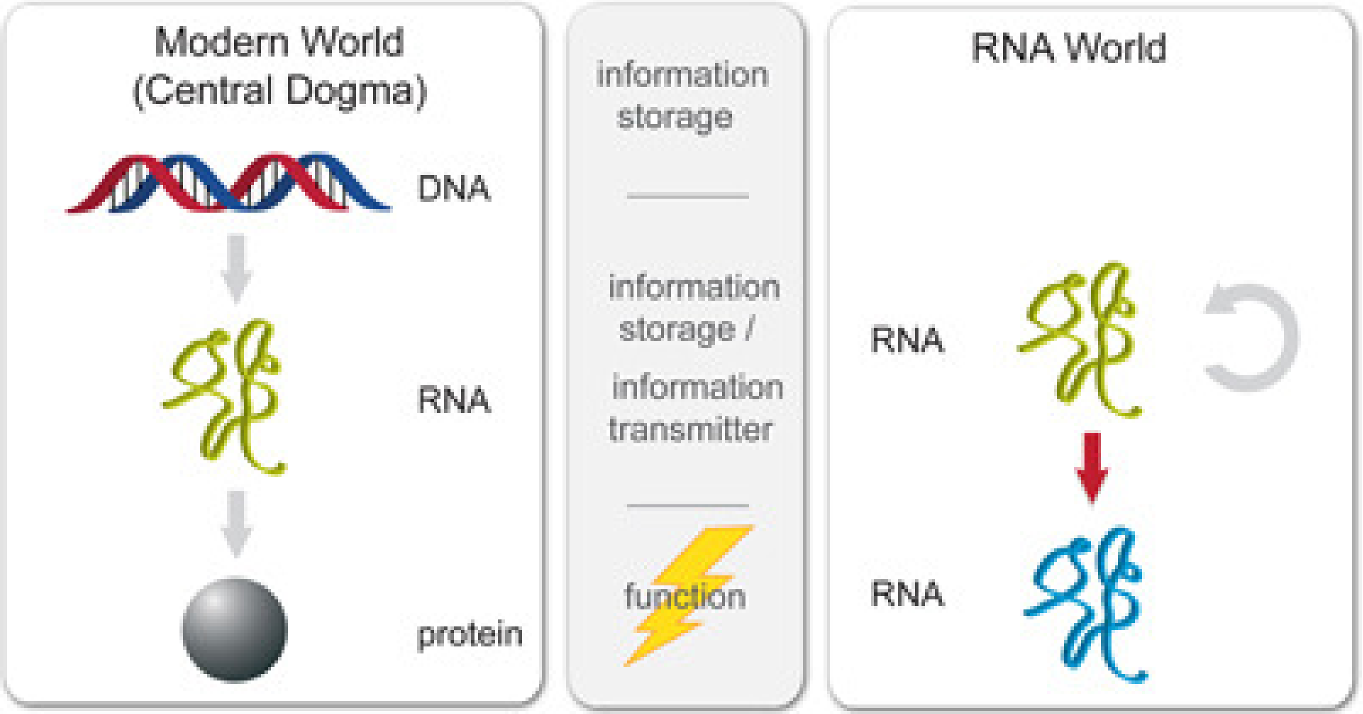
Route to life by chemical networks



P. L. Luisi *Mol Syst Biol.* **2014,** *10*, 729

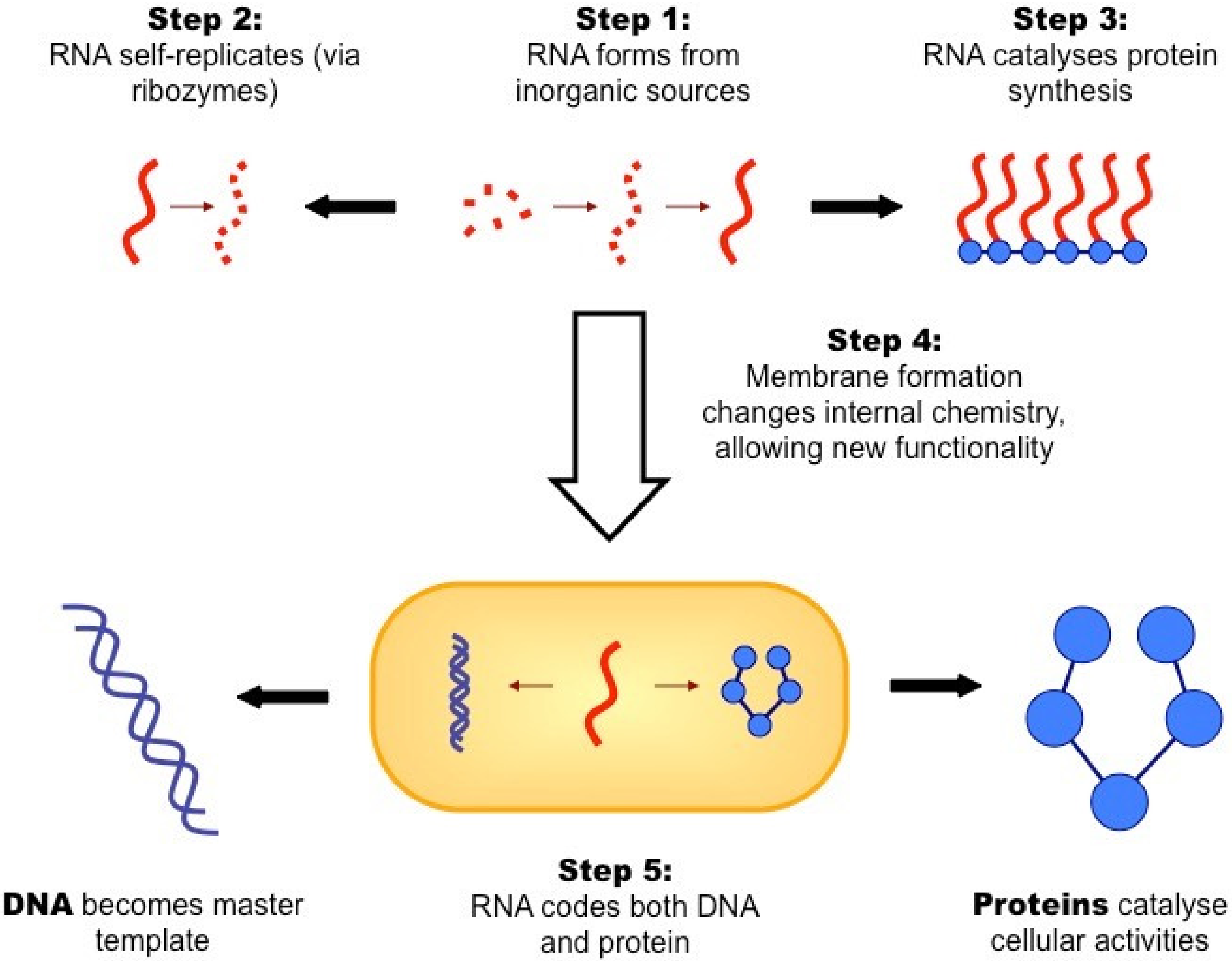

Membrane compartment
Metabolic machinery
LIFE
Genetic/template mechanisms

The RNA world



Conceptual idea that there was a period in the early history of life on Earth when RNA (or its structurally simplified analogue) carried out most of the information processing and metabolic transformations needed for biology to emerge from chemistry

The RNA world



The RNA world

RNA as catalyst

Currently known co-enzymes
Ribozymes, Riboswitches
Ribosome

Evolvability of RNA

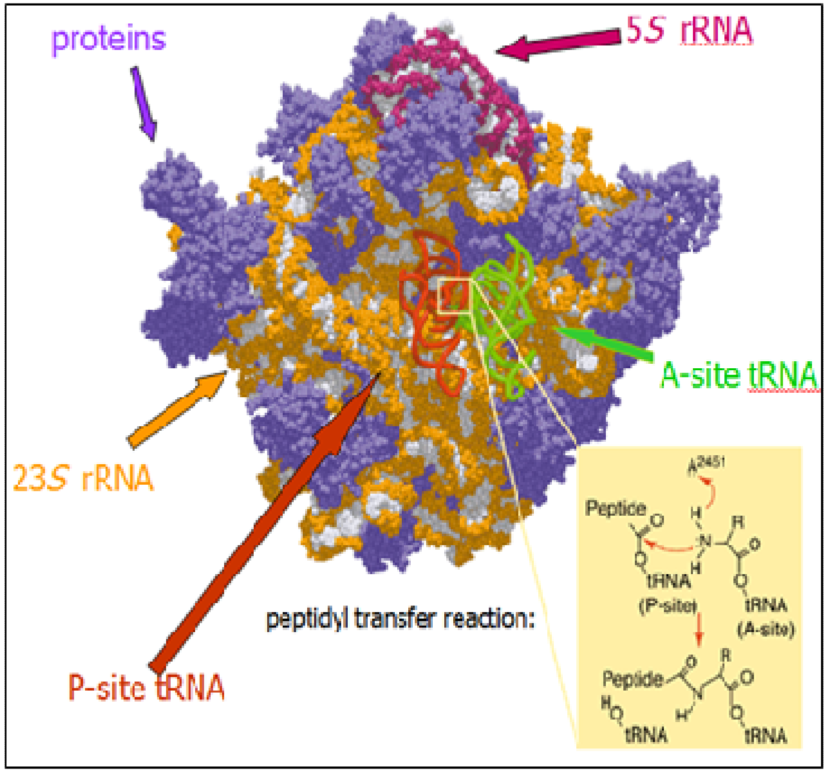
Spiegelman's Monster
Aptamers

RNA (self)-replication

Replicase ribozymes – no self-replication yet, but replicate sequences longer that themselves
Replicating RNA networks

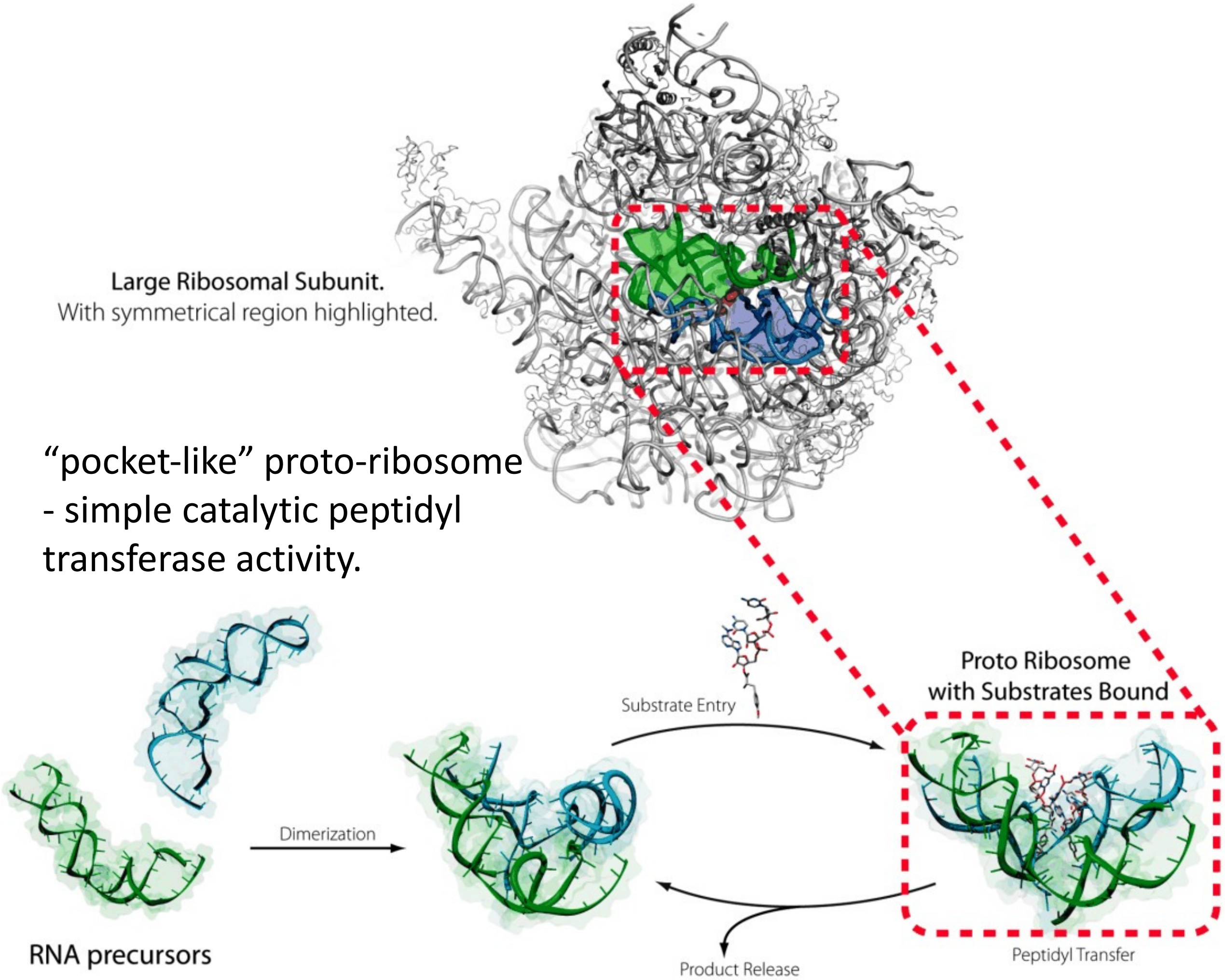
Ribosome – the ‚smoking gun'

Ribosome is a ribozyme!



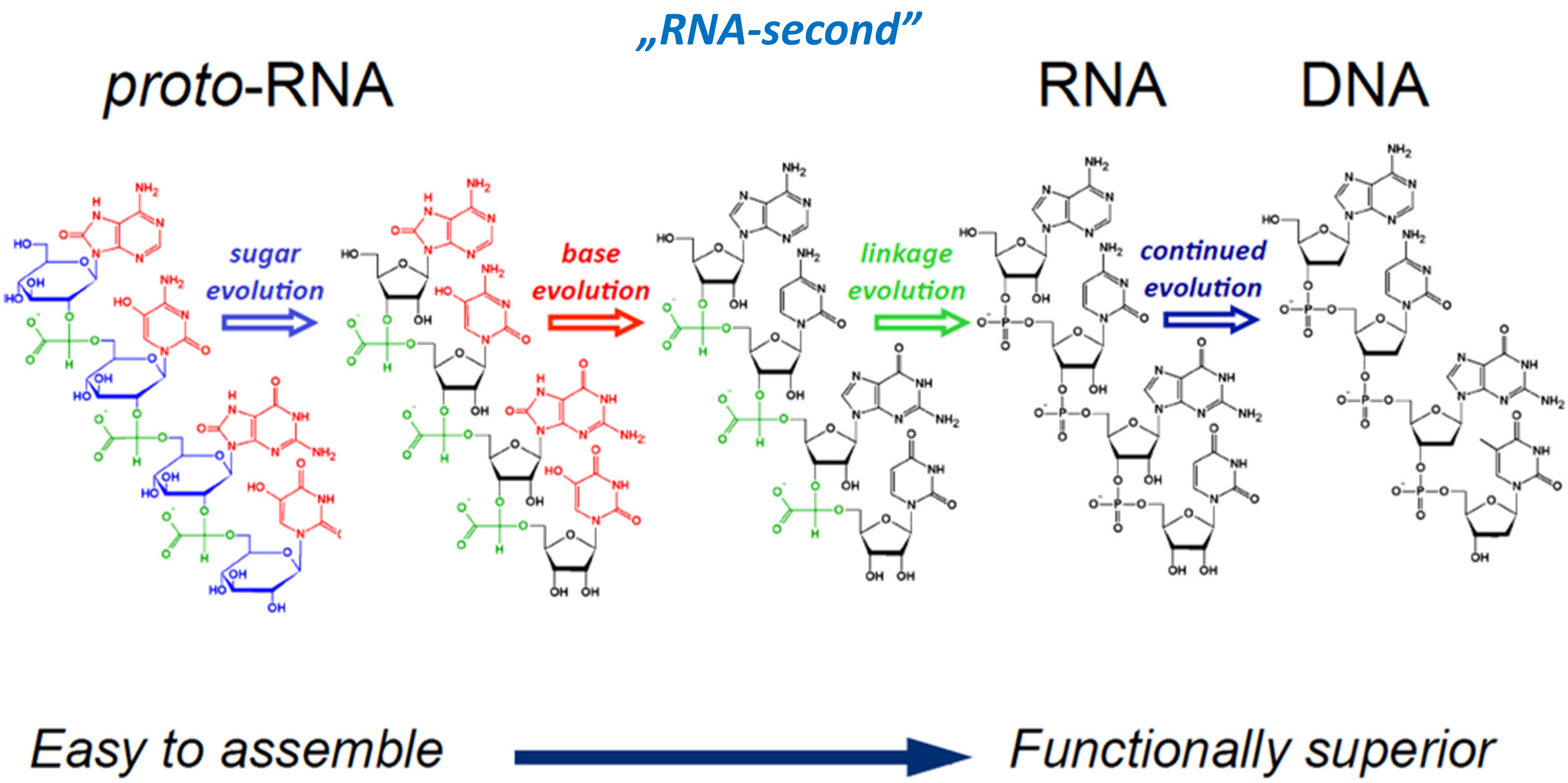
No protein is present within 18 Angstroms from the active site → proteins play a structural role, but DO NOT CATALYZE THE ACYL TRANSFER PROCESS

T. Cech *Science*. **2000**, *289*, 878-879



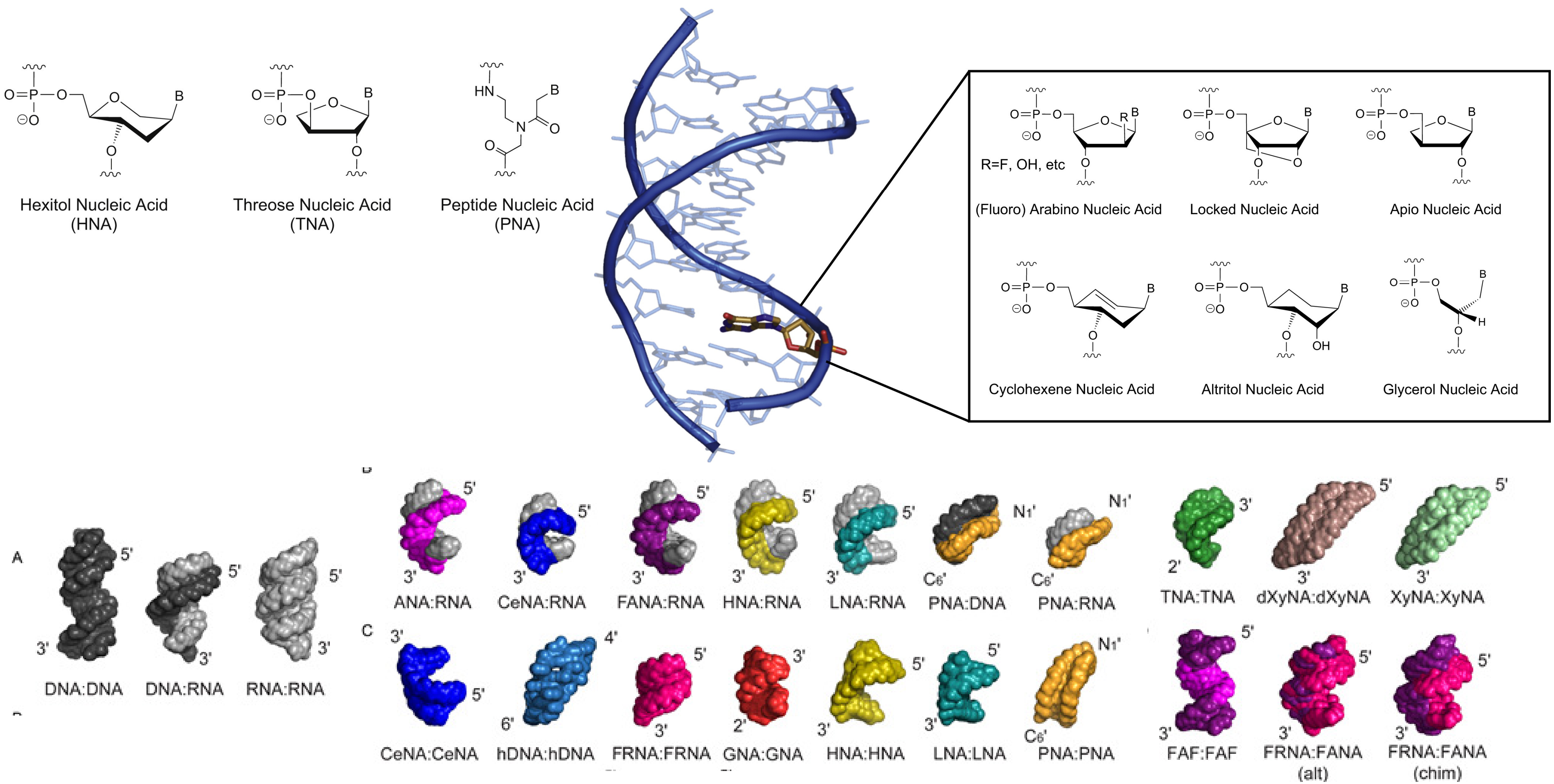
"pocket-like" proto-ribosome
- simple catalytic peptidyl transferase activity.

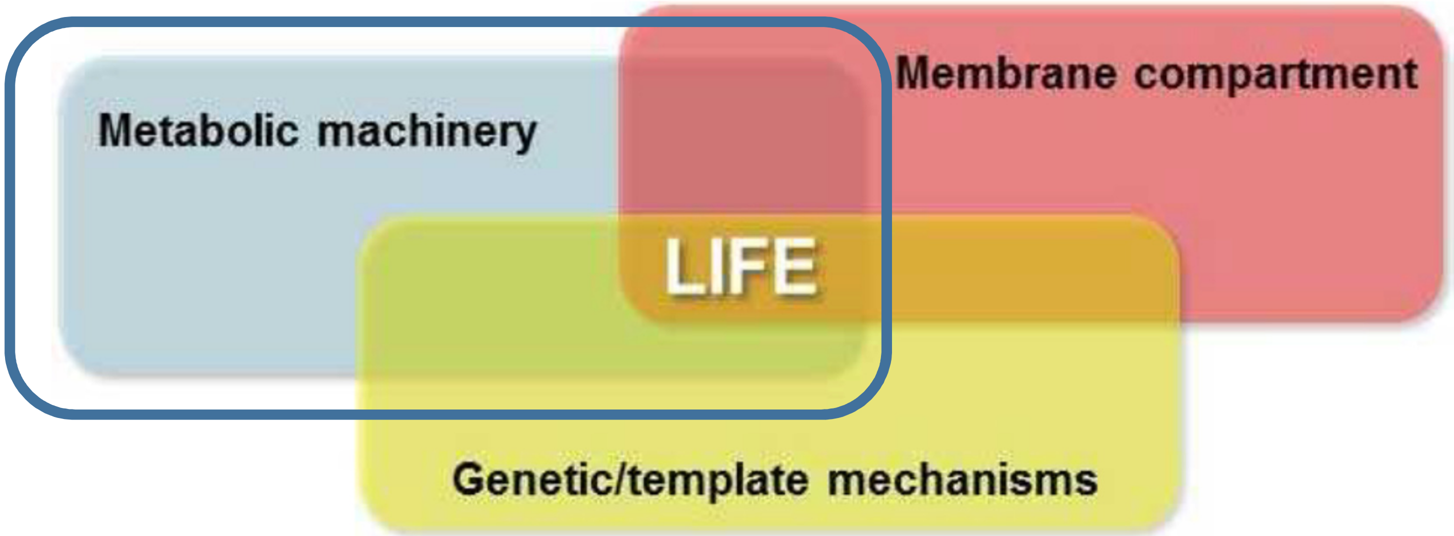
A. Yonath *et al. Israel Journal of Chemistry*, **2010**, *50*, 29-35



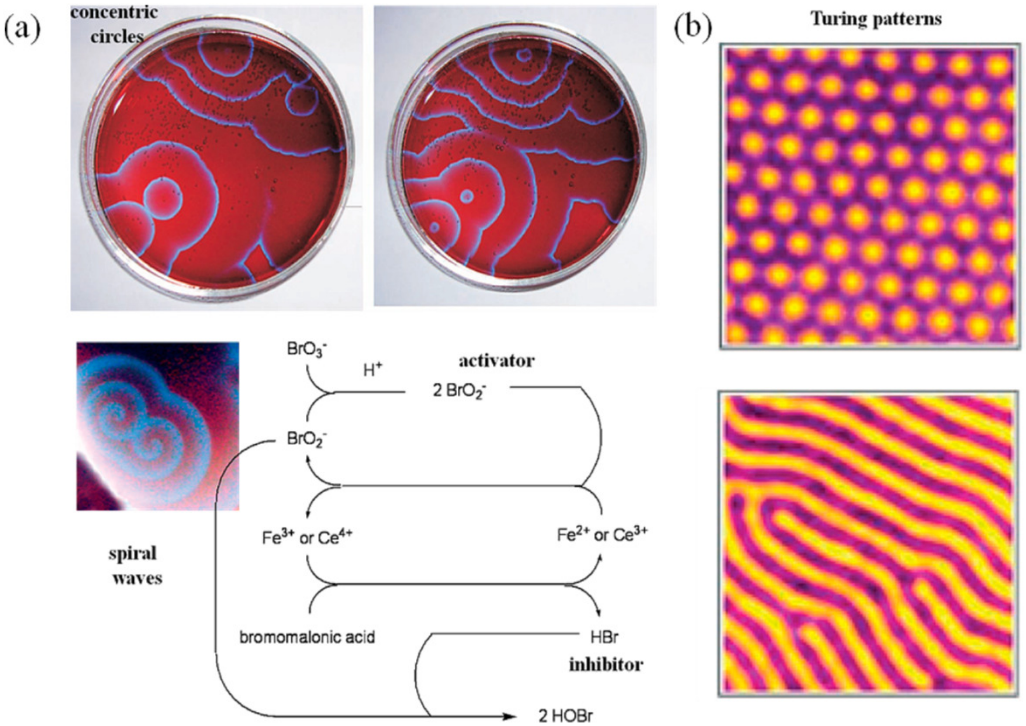
Proto-RNA evolution: *According to the protoRNA theory, each of the components of RNA — sugar, base and phosphate backbone — may have originally taken different forms.*

XNA – Xeno Nucleic Acids




Membrane compartment
Metabolic machinery
LIFE
Genetic/template mechanisms

BZ and CIMA reactions – chemical models for metabolism

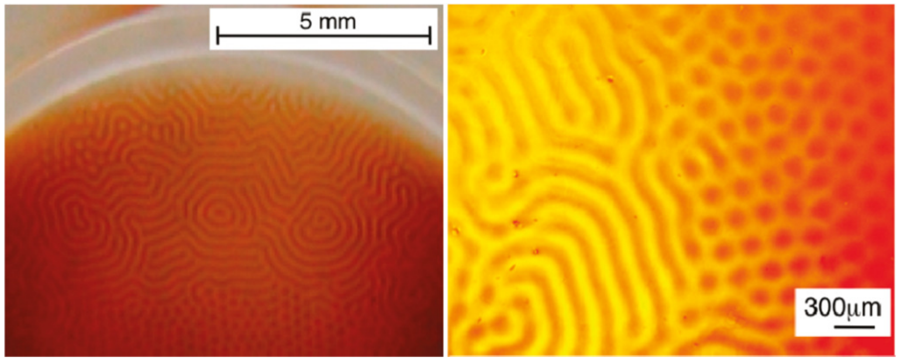


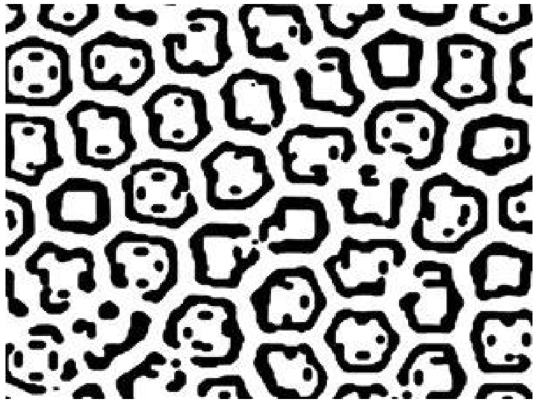
Turing patterns – BZ and CIMA, but also formation of zebra stripes or arrangement of leafs in plants

J. Phys. Chem. B 115(14):3959-63

Turing patterns also observed in metabolic reactions (glycolysis)

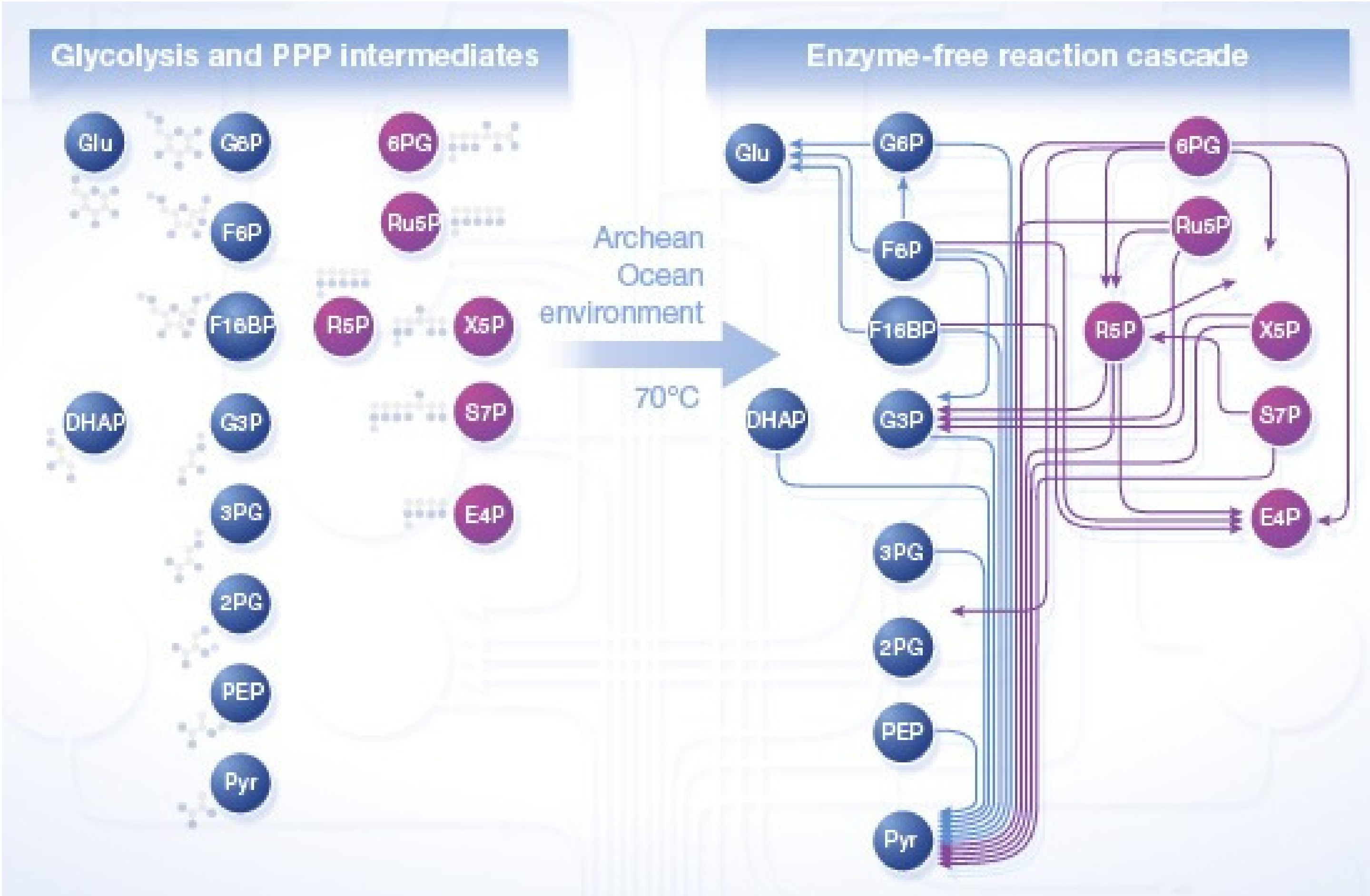
PLoS ONE 2007, 2(10):e1053





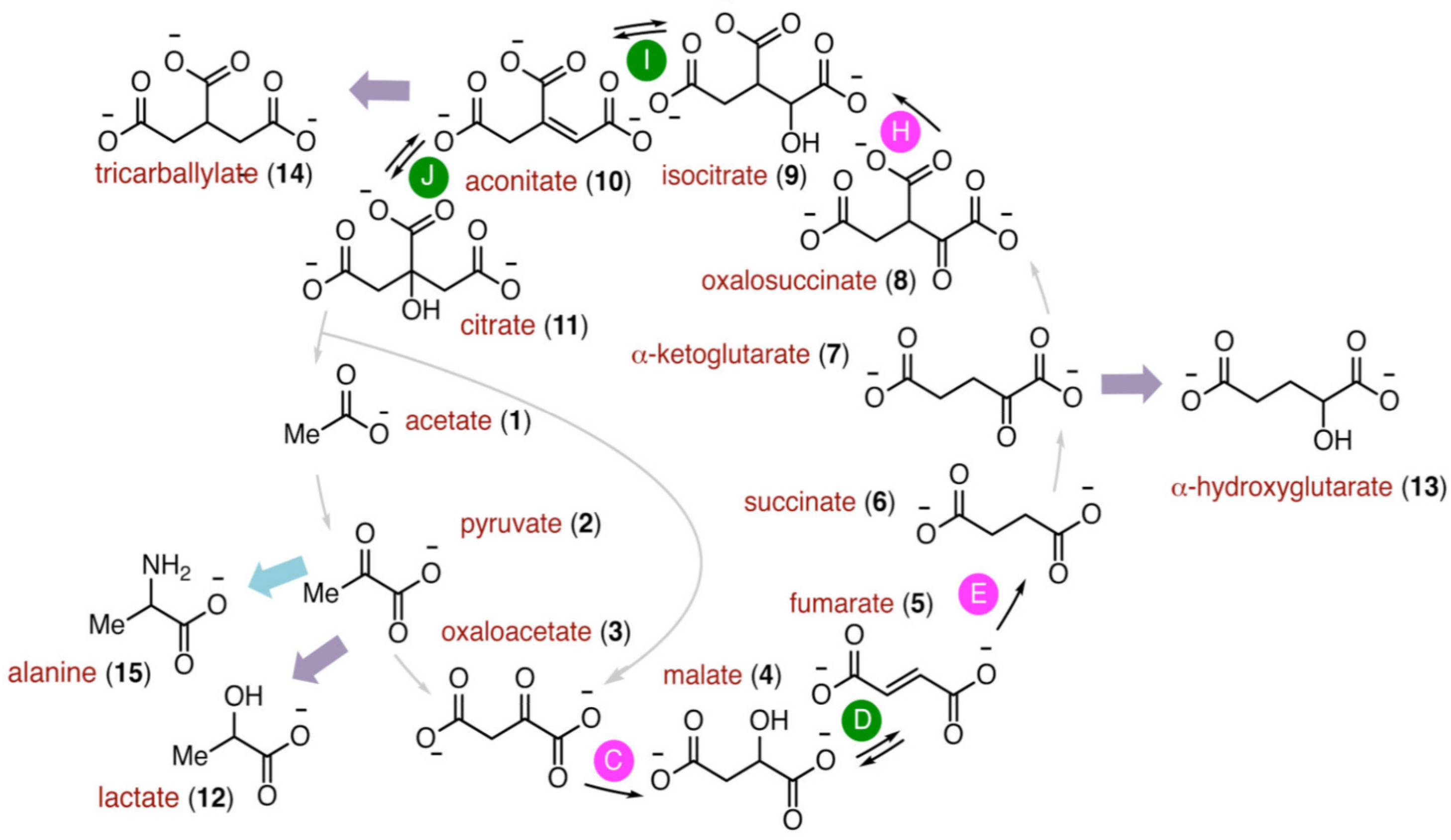
„Rosette" spots of a jaguar can be reproduced by two coupled activator/inhibitor processes

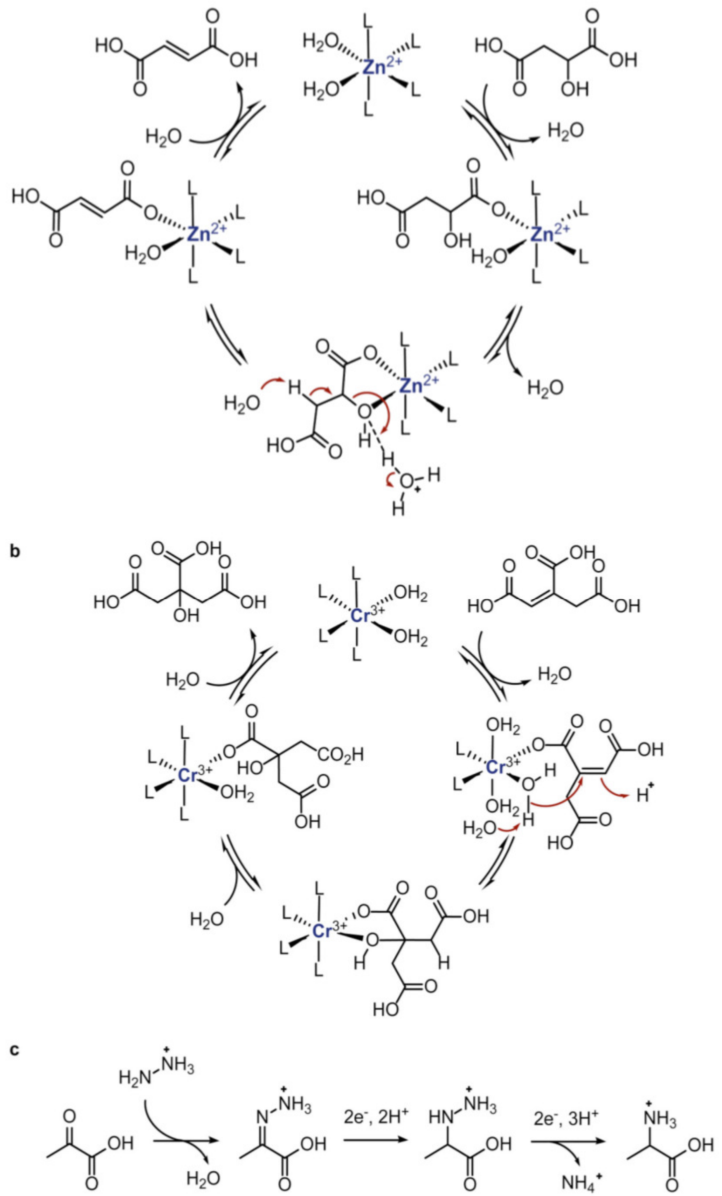
Nonenzymatic sugar phosphate interconversion in a plausible Archean ocean environment



M. Keller *et. al. Molecular Systems Biology* **2014**, *10,* 725-737

Metals promote sequences of the reverse Krebs cycle

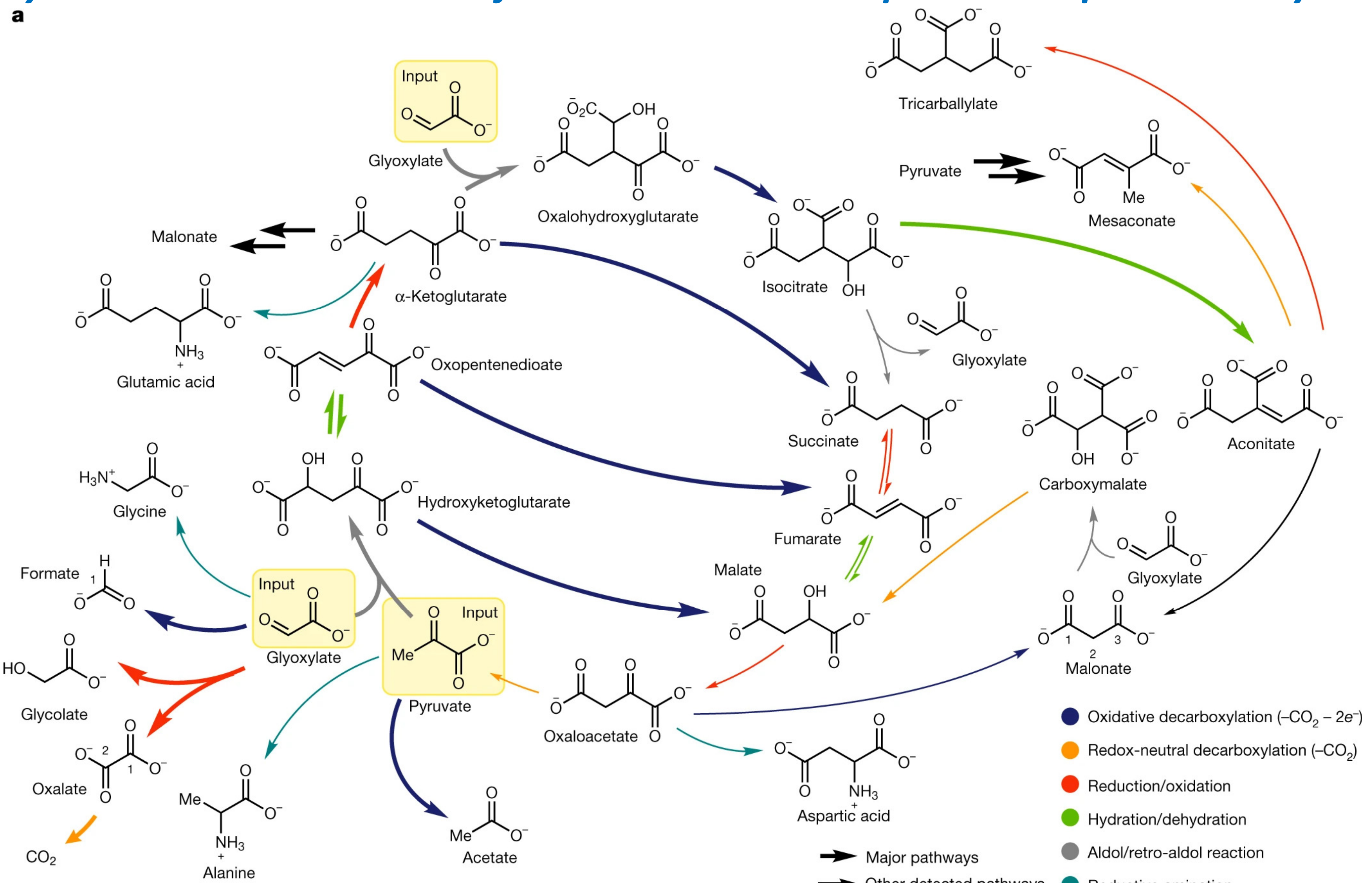




Prebiotic reaction network showing the rTCA cycle, reductive amination (light blue arrow) and potential off-cycle reductions (mauve arrows).

J. Moran *et al. Nat Ecol Evol.* **2017**, *1(11)*, 1716–1721

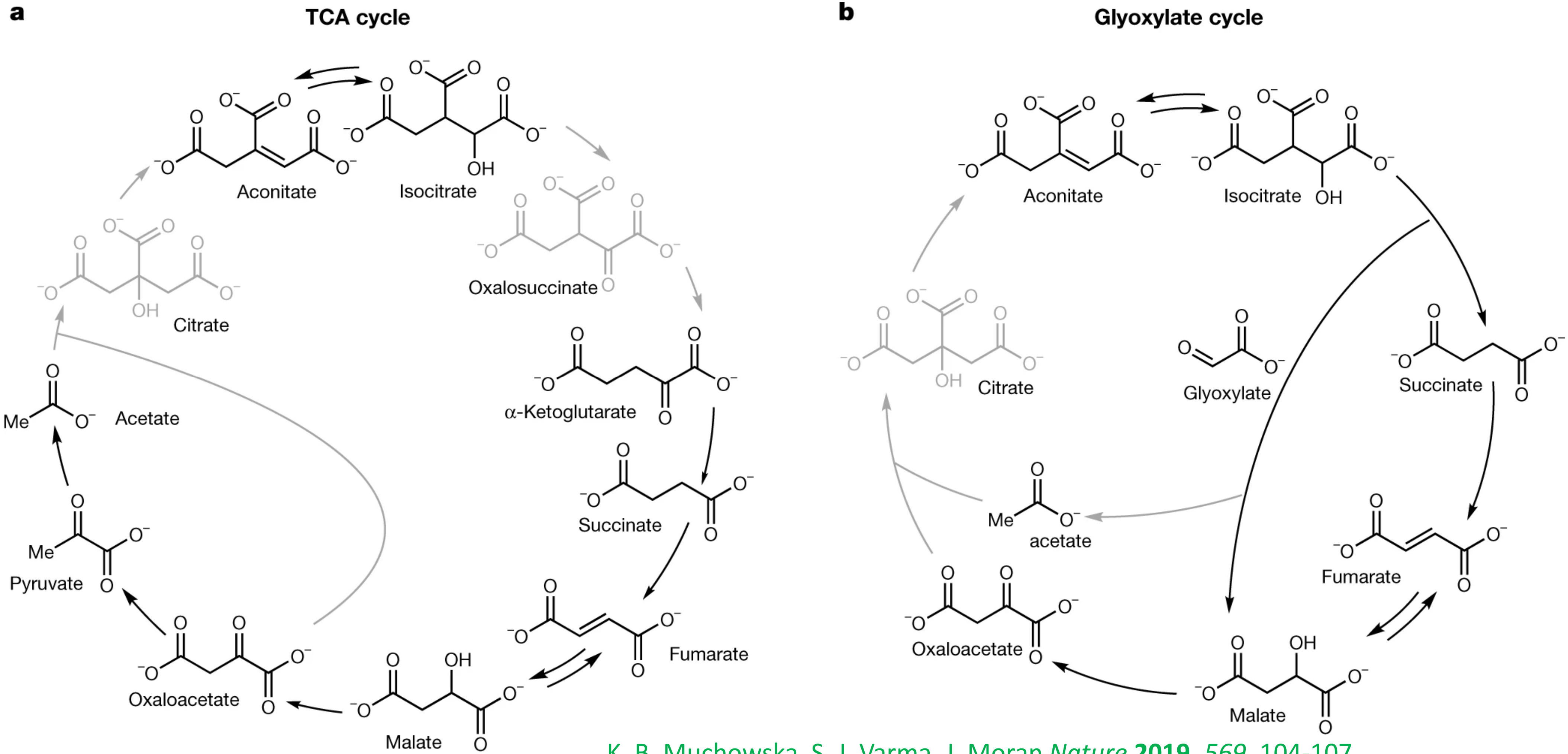
Synthesis and breakdown of universal metabolic precursors promoted by iron



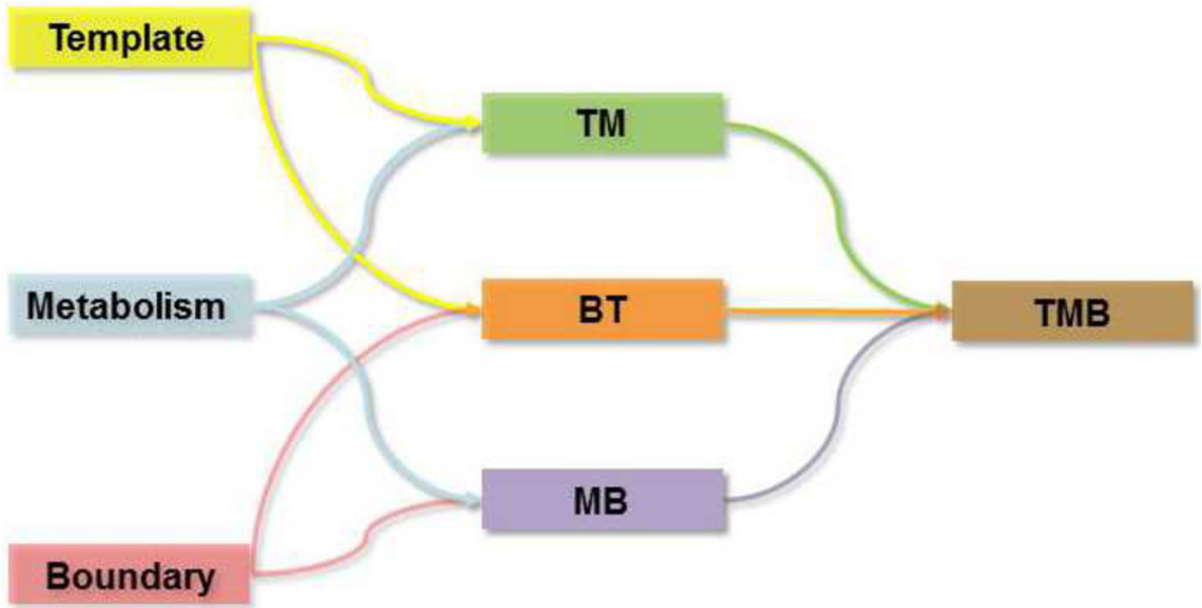
K. B. Muchowska, S. J. Varma, J. Moran *Nature* **2019**, *569*, 104-107

Synthesis and breakdown of universal metabolic precursors promoted by iron

Comparison of the observed reaction network with the TCA and glyoxylate cycles. Intermediates and reactions found in both the biological cycle and the synthetic reaction network shown in black. Those found only in the biological cycle - in grey.



K. B. Muchowska, S. J. Varma, J. Moran *Nature* **2019**, *569*, 104-107

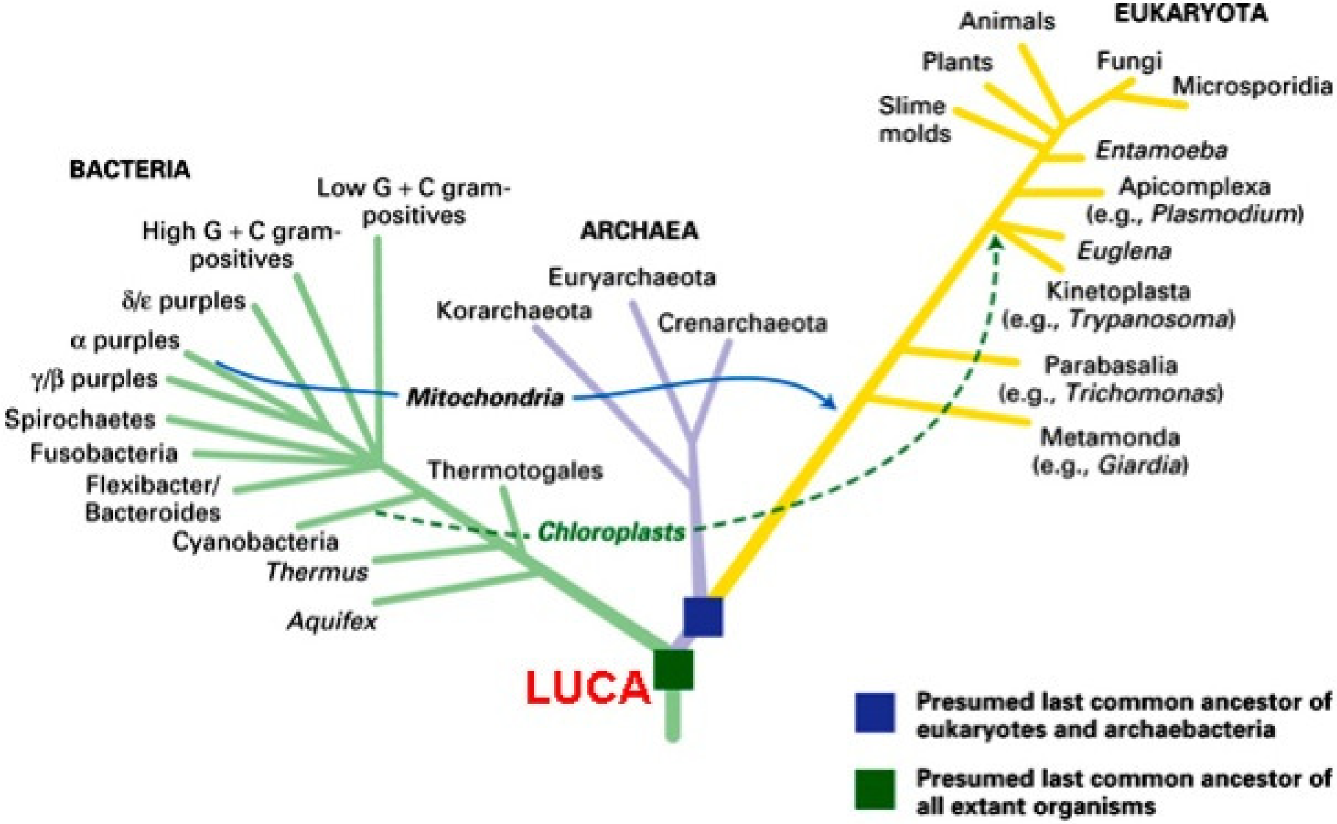

Template
Metabolism
Boundary
TM
BT
MB
TMB

Origin of the Universe – stars, planets, elements

Origin of biorelevant monomers – primordial soup

Complex chemical processes on the way to living systems

Protocells and LUCA



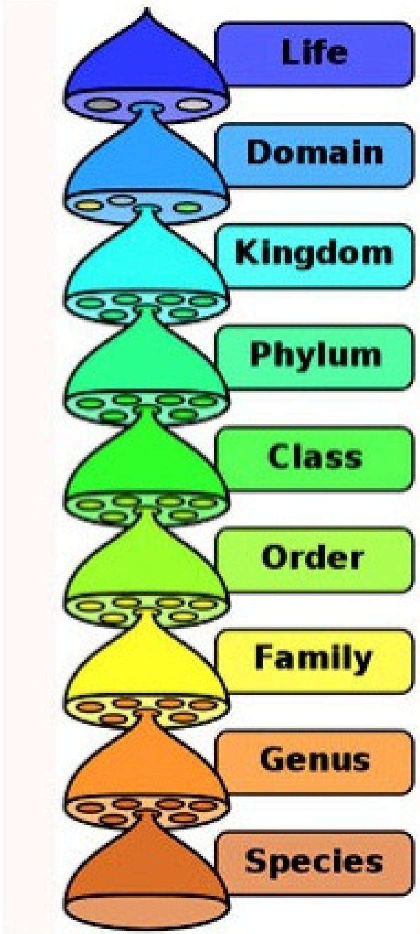
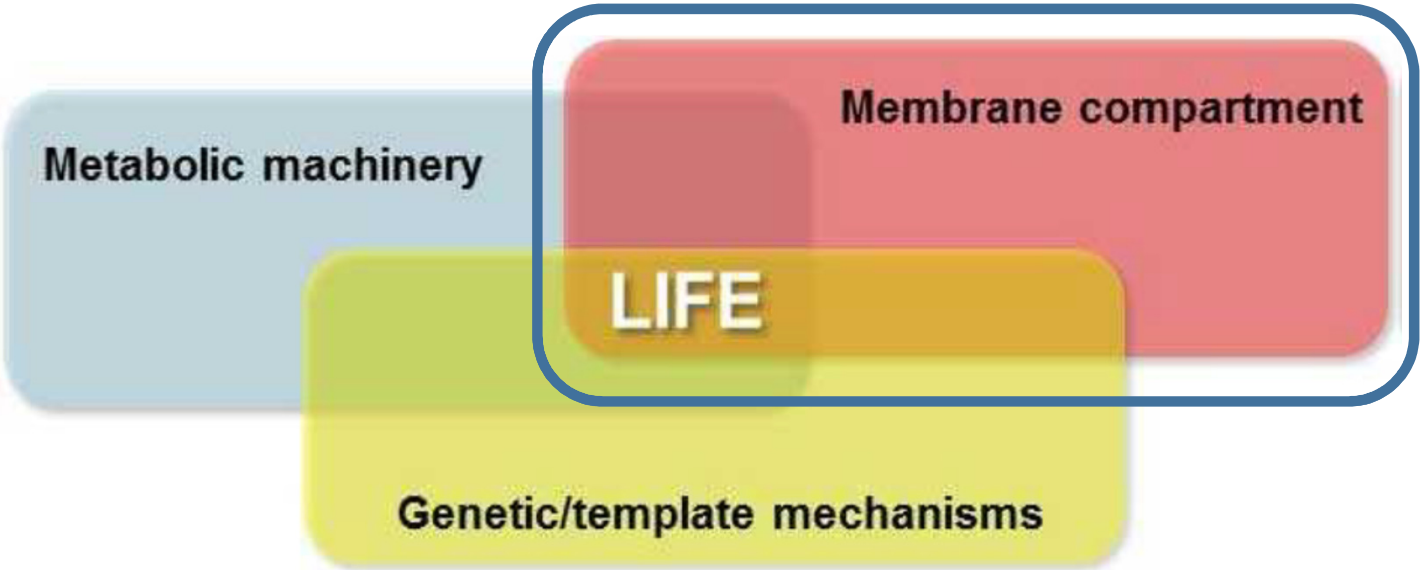
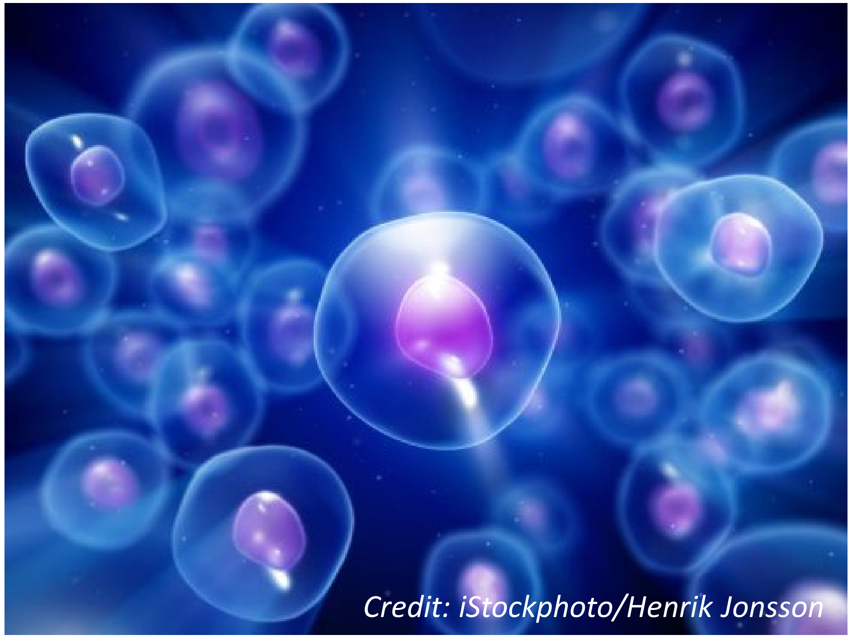


Figure 1.1a
Molecular Cell Biology, Seventh Edition

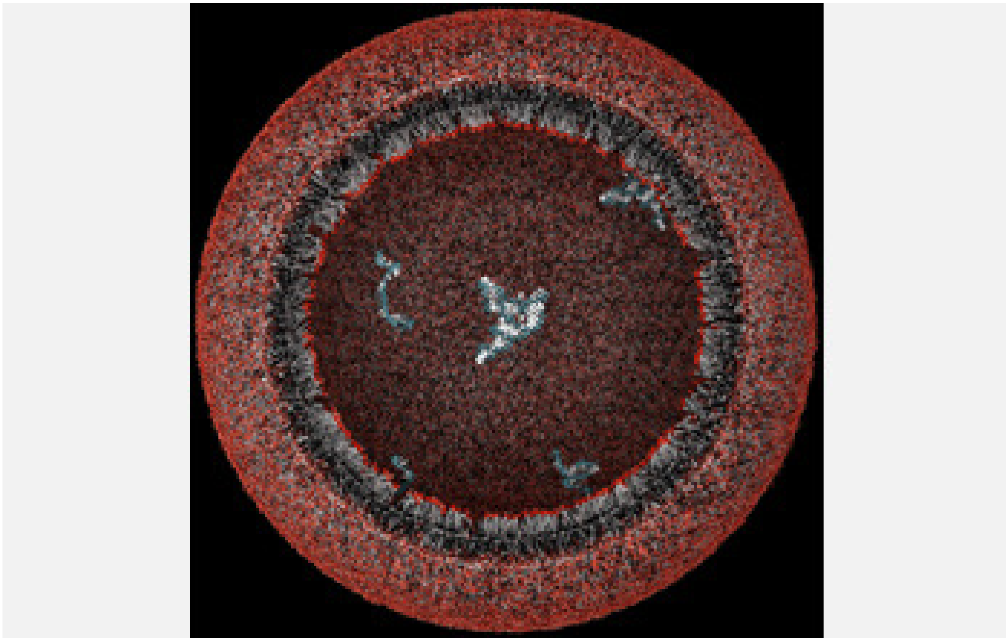

Membrane compartment
Metabolic machinery
LIFE
Genetic/template mechanisms

Encapsulation – essential for life



Membrane compartments

Assembly of amphiphilic monomers into protocellular compartments

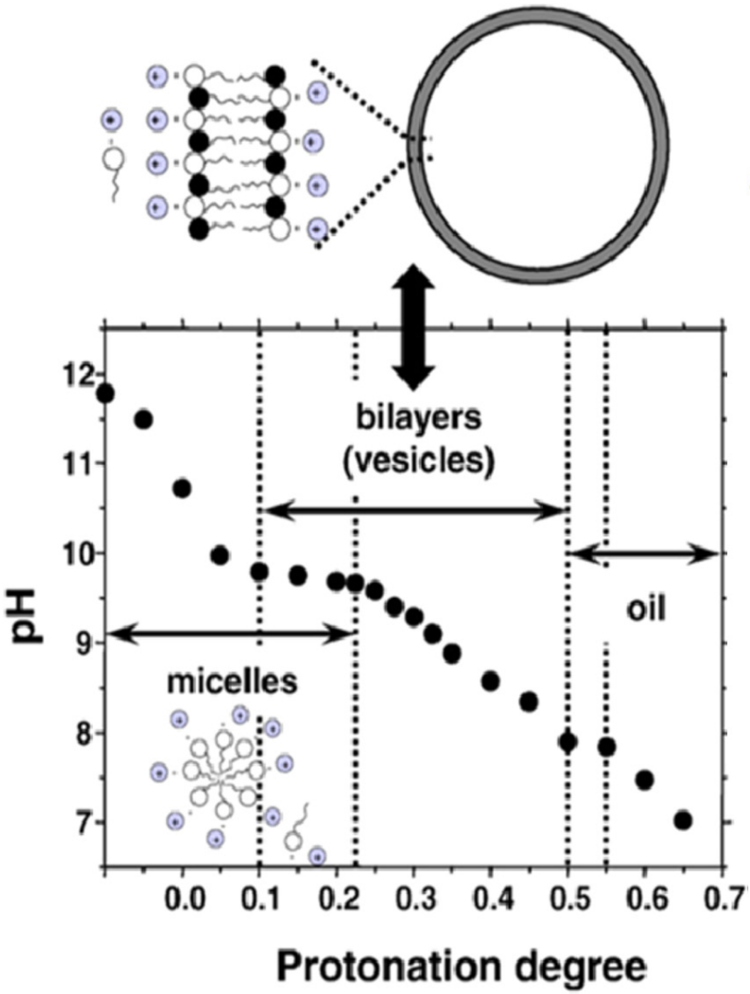


Credit: *Janet Iwasa*

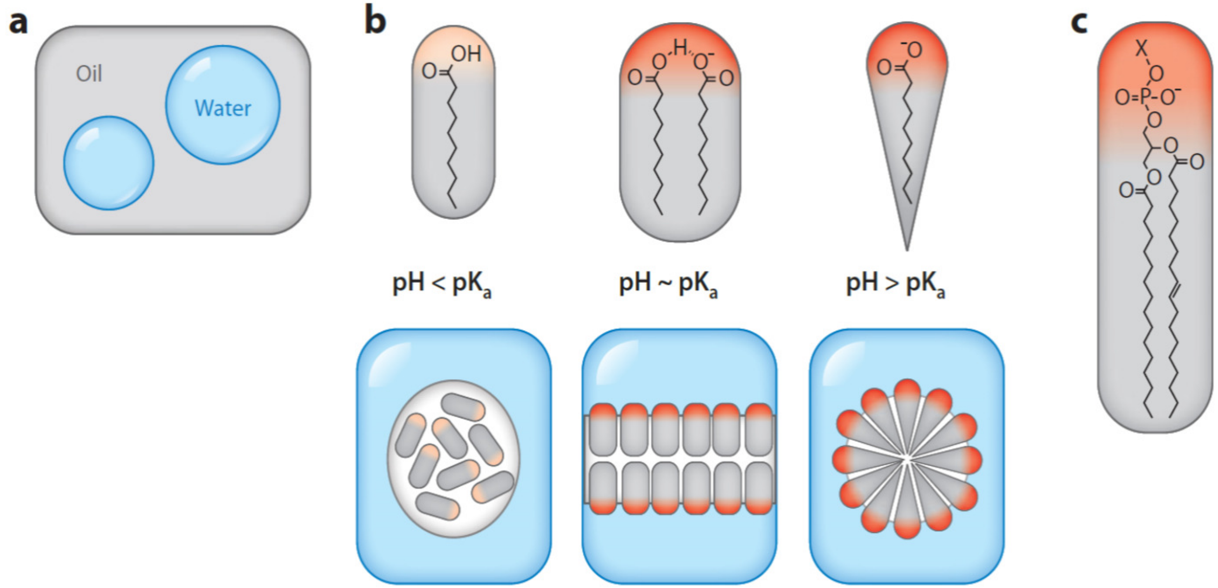
A three-dimensional view of a model protocell (a primitive cell) approximately 100 nanometers in diameter.

The protocell's fatty acid membrane allows nutrients and DNA building blocks to enter the cell and participate in non-enzymatic copying of the cell's DNA. The newly formed strands of DNA remain in the protocell

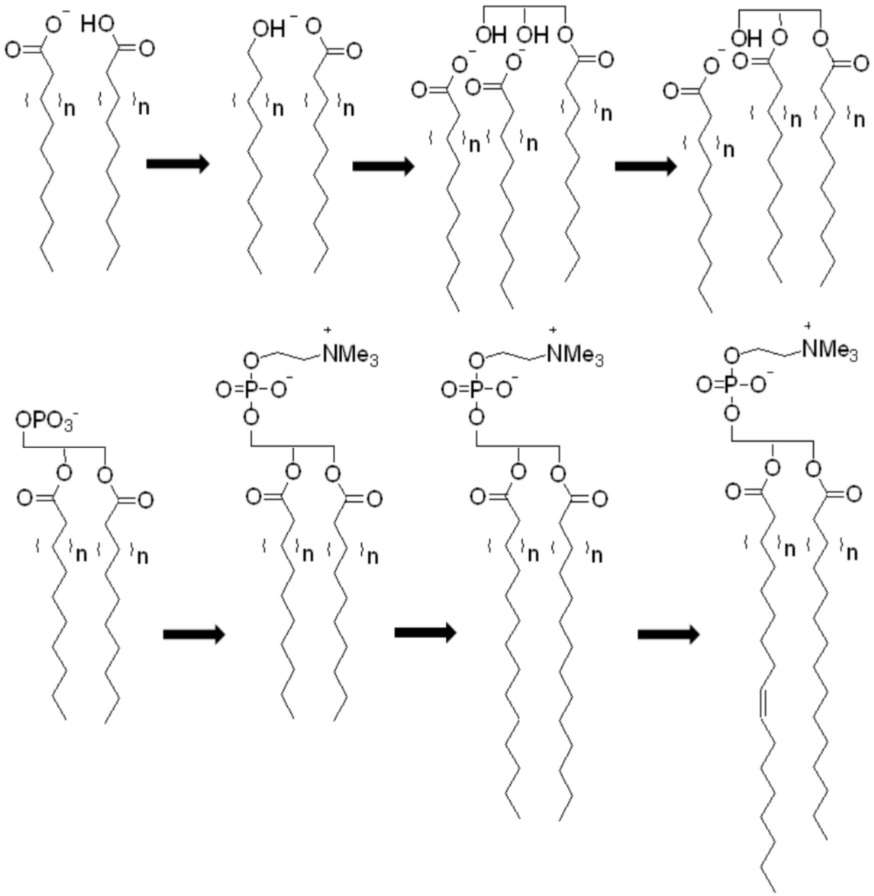
pH-dependent phase behavior of fatty acids in water

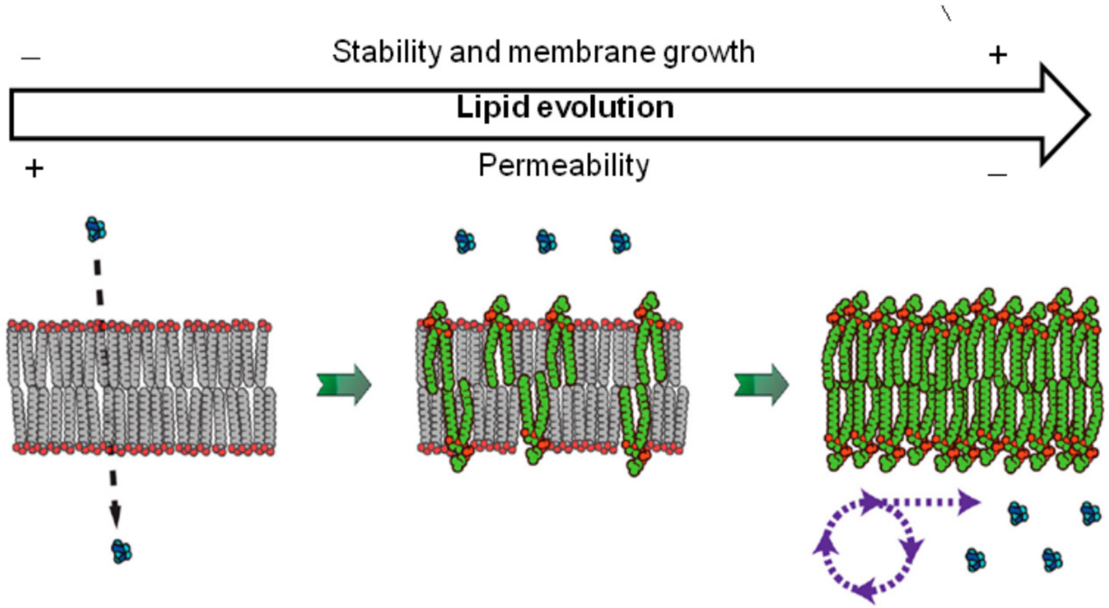


80 mM oleic acid/ sodium oleate in water



Scheme of the membrane evolution

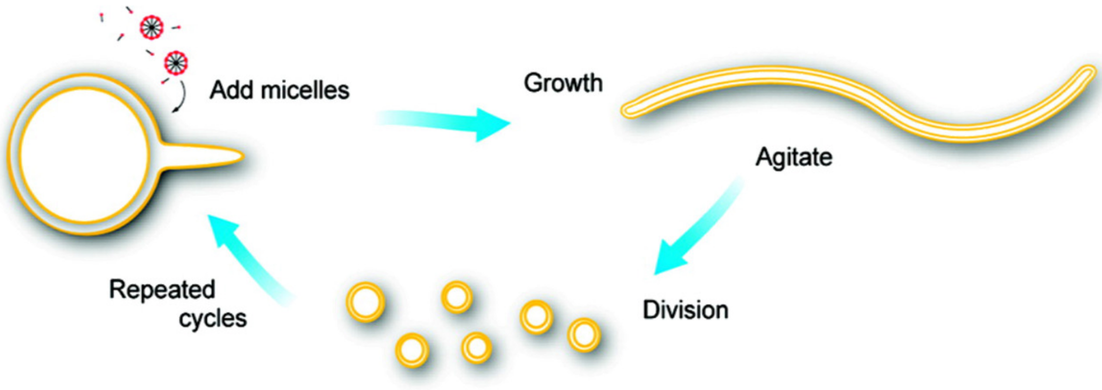


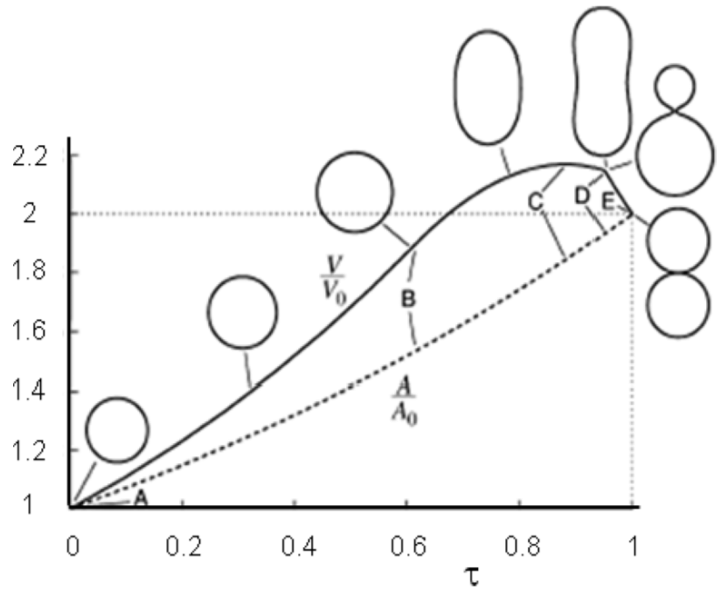


More complex components lead to slower amphiphile desorption and thus faster growth of the protocell. Decreasing permeability is a selective pressure for the emergence of internalized metabolic and transport machinery in the system

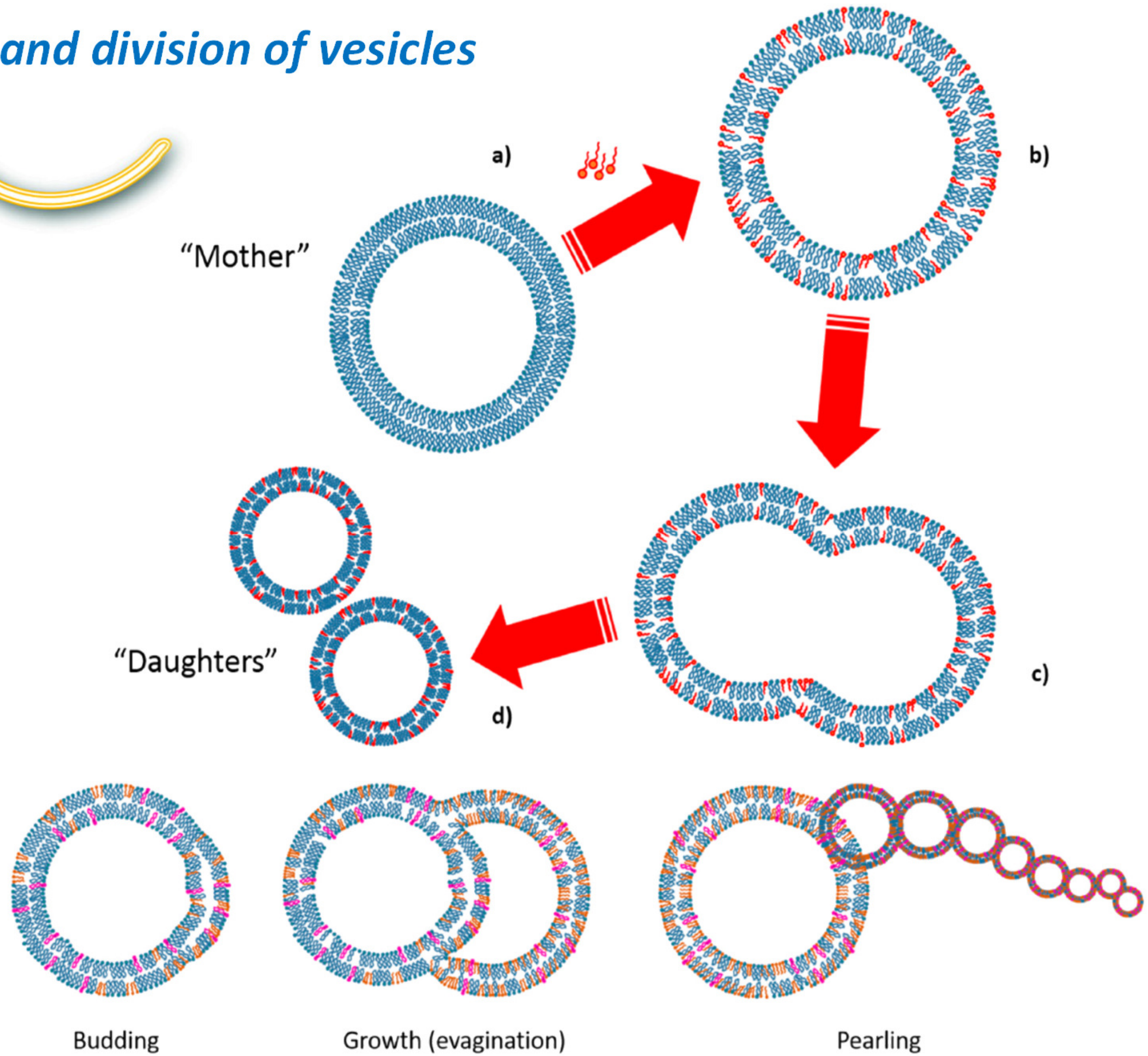
Chemical evolution of membrane components

Growth and division of vesicles



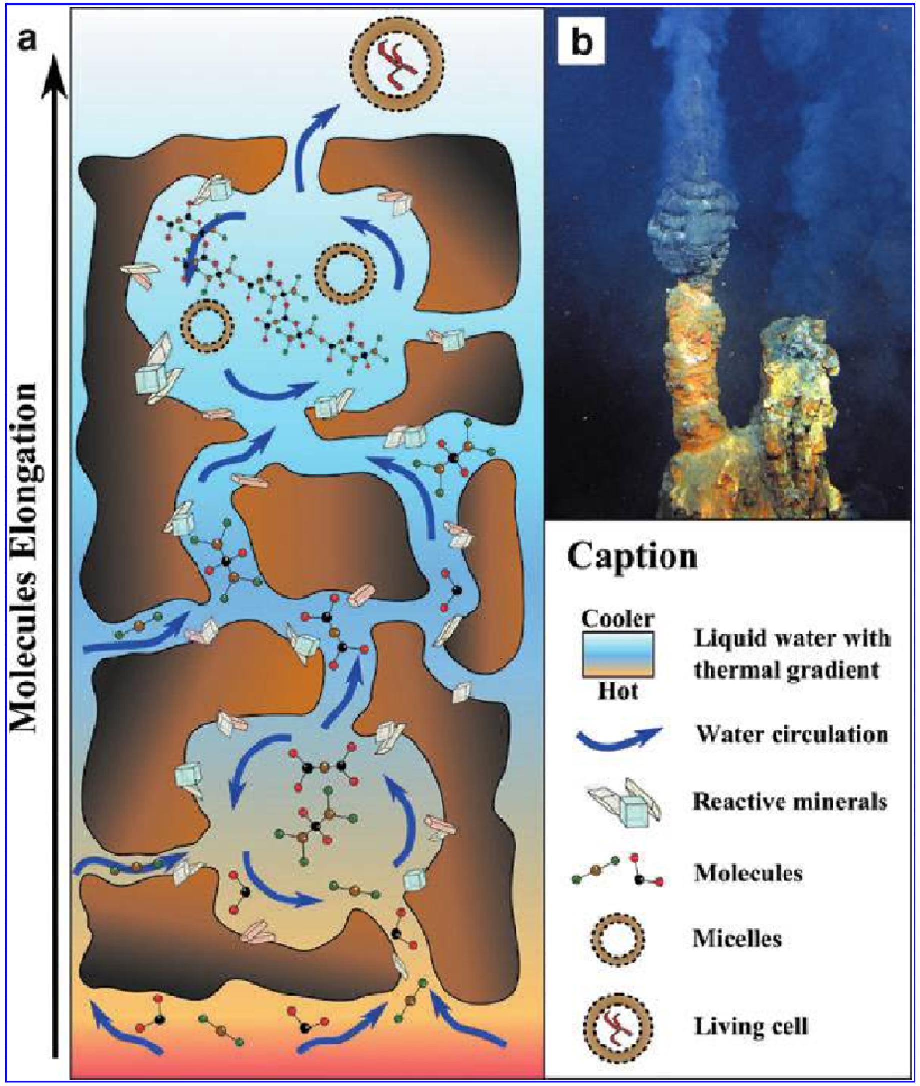


Ting F. Zhu, and Jack W. Szostak
J. Am. Chem. Soc., **2009**, 131 (15), 5705-5713



A. Lopez, M. Fiore *Life* **2019**, 9(49), doi:10.3390/life9020049

Deep sea vent origin of life



Possible origin of life in porous hydrothermal vents.

(a) Sketch showing a porous beehive structure where hydrothermal fluids and seawater can circulate, leading to the accumulation of organic molecules. The reduced mineral surfaces within the vent pores could be favorable locations for the structural organization of macromolecules. We hypothesize the formation of lipid micelles in these environments and the incorporation of information-transferring molecules within the micelles, perhaps due to moderate agitation of the hydrothermal effluent.

(b) Image of a modern black smoker

(image credit: National Oceanographic and Atmospheric Administration). Color images available online at www.liebertonline.com/ast

F. Westall et al., *Astrobiology* **2013**, *13(9)*, 887-897

Transition from the RNA world to LUCA

Ribozymes – self-acting → metabolic

Evolution of ribosome

Incorporation of aminoacids and peptides

The genetic code and archival storage

Enzyme-driven metabolism and membranes

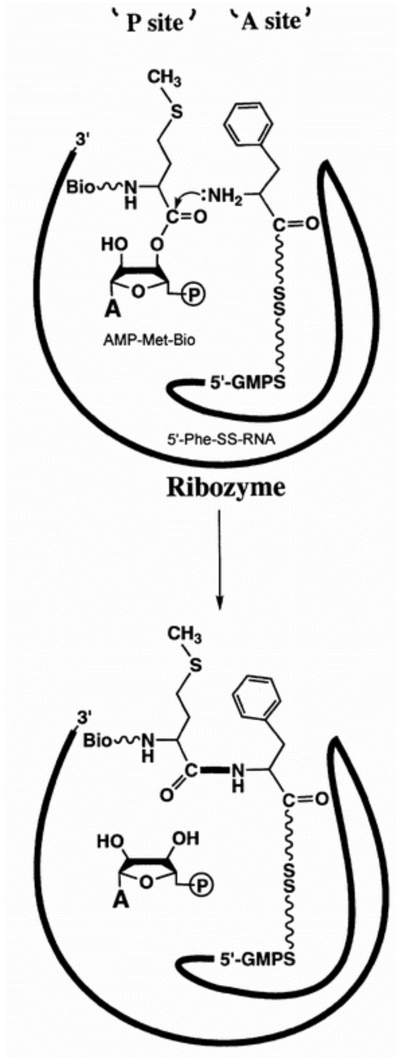
Ribozymes

Initially only self-processing ribozymes (introns, RNAses) discovered.

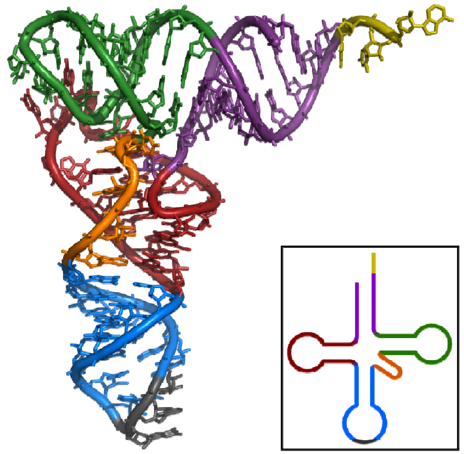
1992 – first ribozyme isolated capable to cleave the bond of methionine with its tRNA (also the reverse reaction – transacylation – is catalysed)

1995 (Yarus) – a random RNA sequence found capable of attaching an activated aminoacid to itself

1997 (Szostak) – an RNA sequence that transfers one aminoacid to another one, forming a dipeptide → analogue of the peptidetransferase center of the ribosome



Ribozymes



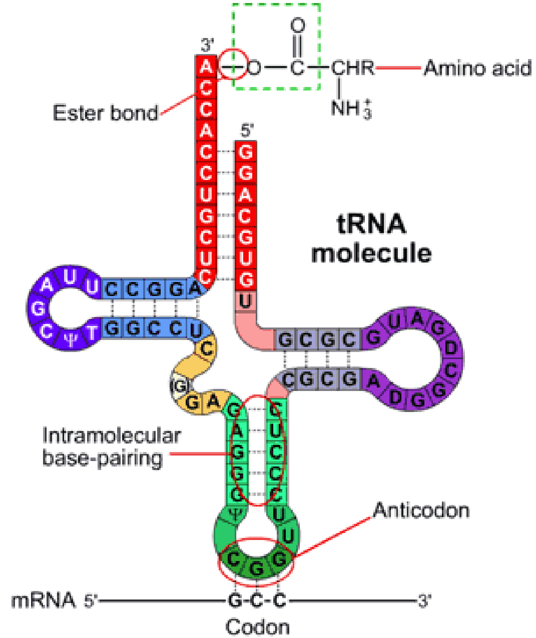
Ribozymes incorporate aminoacids to enhance their catalytic abilities

It opens ways to improved metabolism and provides evolutionary advantage in receiving energy from outside

Initially incorporation of aminoacids may have improved synthesis of nucleotides to produce more RNA

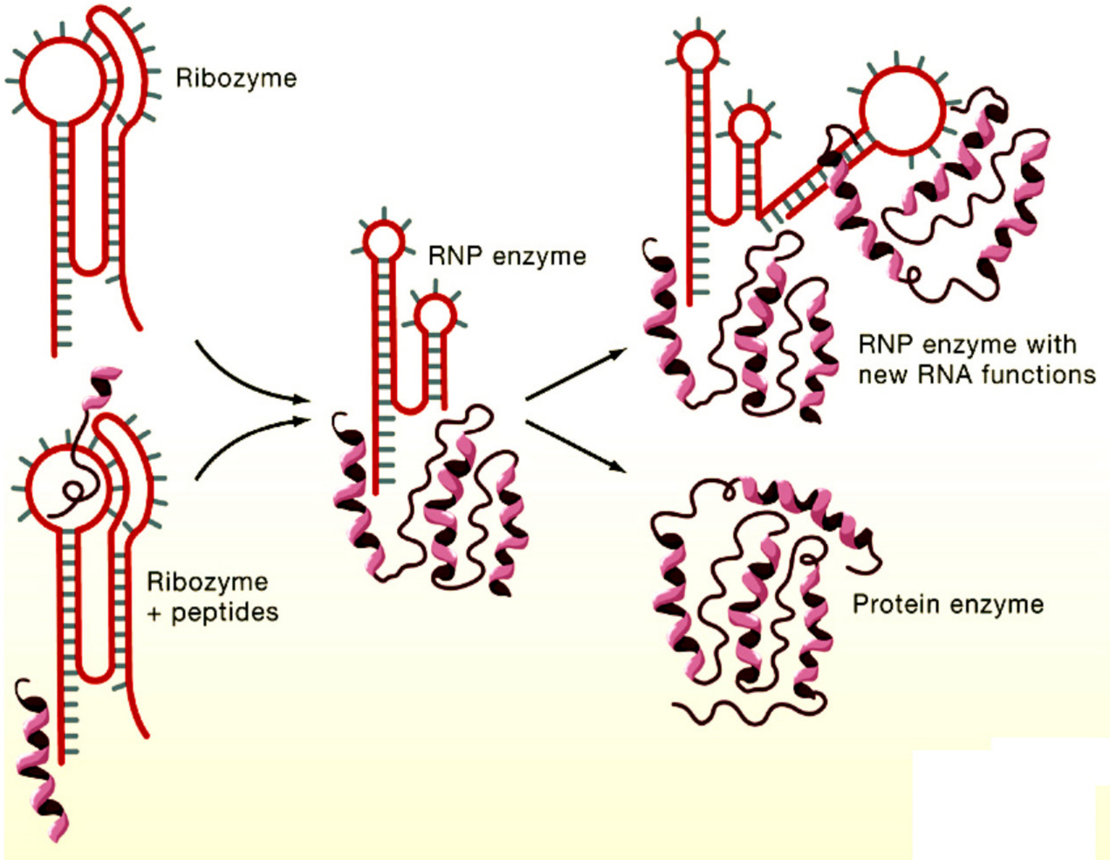
Primordial tRNAs were most likely self-charging, today special enzymes do it (tRNA synthethases)

Peptide chains increase in size, the RNA part decrease → non-covalent binding of nucleoside cofactors to contemporary enzymes



aminoacyl-tRNA

Evolution of biocatalysis



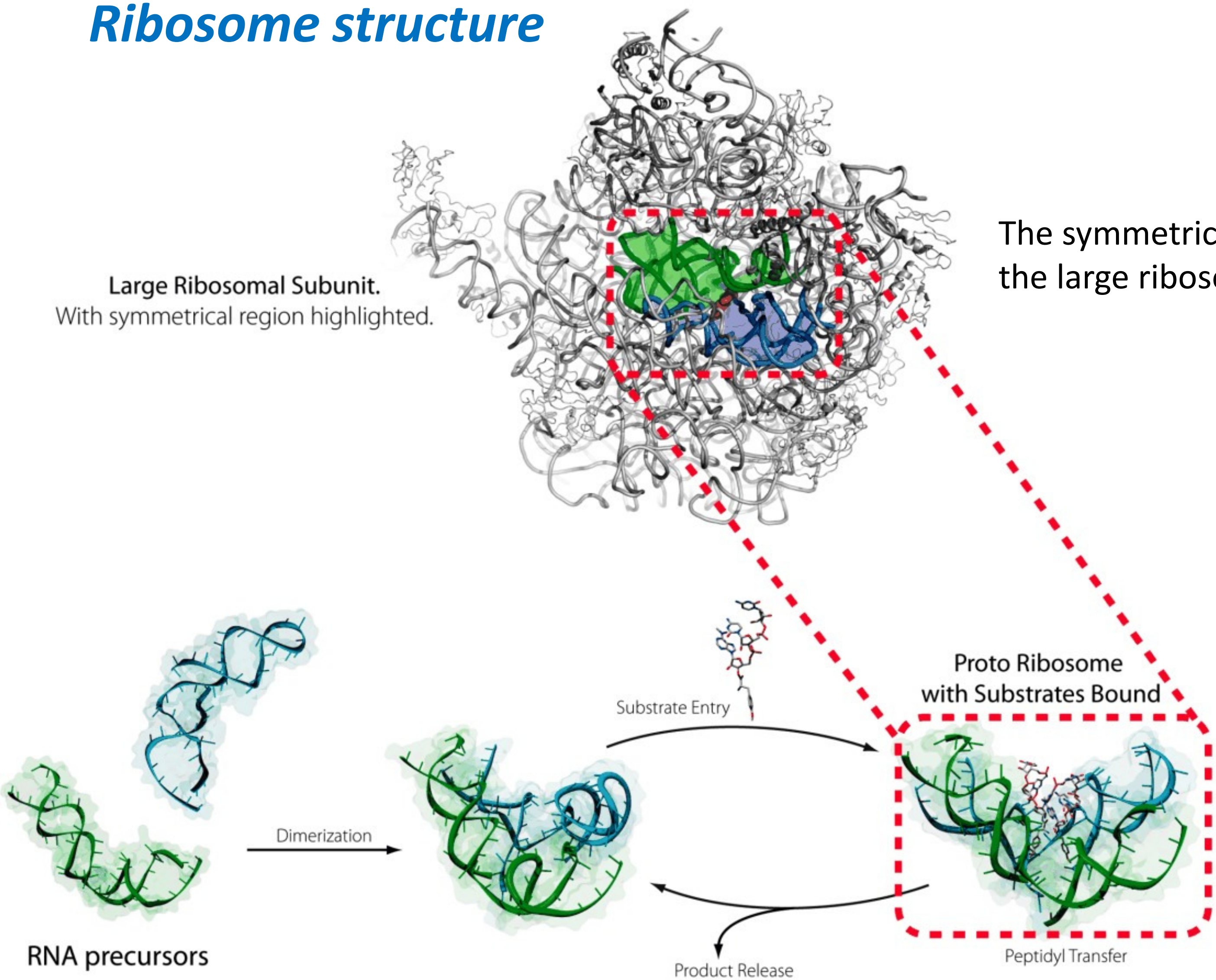
Primordial **RNA-only ribozymes** as well as **complexes of ribozymes and random peptides** could have acted as catalysts during the first steps of the RNA world.

In a more advanced stage, upon the advent of *peptidyltransferase ribozymes*, the availability of RNA-coded proteins allowed the assembly of **ribonucleoprotein (RNP) complexes**.

Some of the RNPs could have shown novel or improved catalytic activities, ultimately including the *translation of mRNA on protoribosomes*. Later, some **RNP enzymes** (upper right) evolved by adding or discarding some RNA subunits and fine-tuning their catalytic activity. In parallel, most RNP complexes (lower right) evolved to **protein-only enzymes**.

Cech, T. R. Cell **2009**, *136*, 599.

Ribosome structure

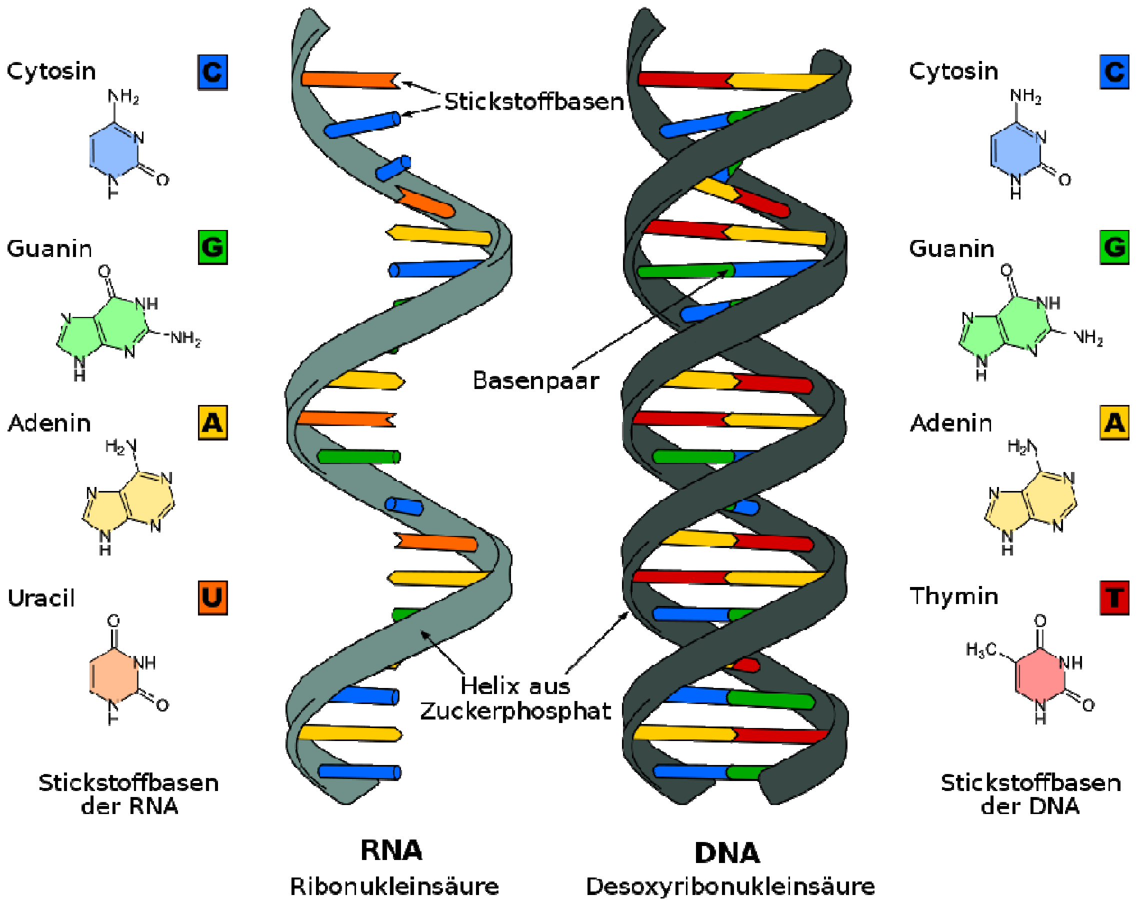


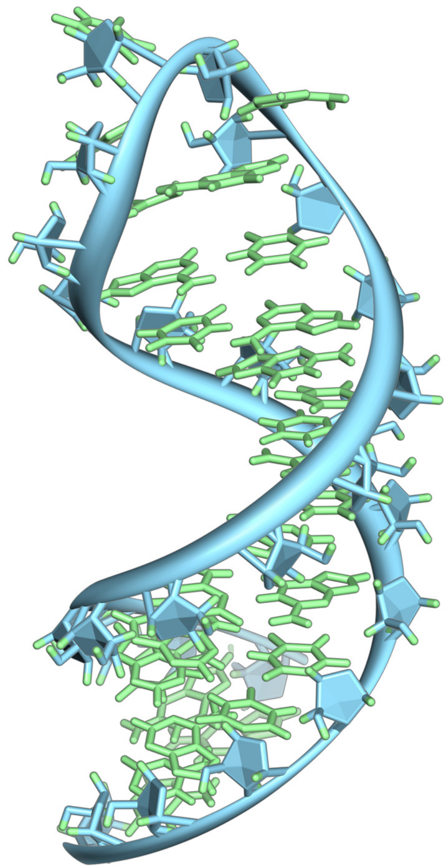
The symmetrical region within the large ribosomal subunit.

Schematic representation of "pocket-like" proto-ribosome formation from a RNA precursor, showing simple catalytic peptidyl transferase activity.

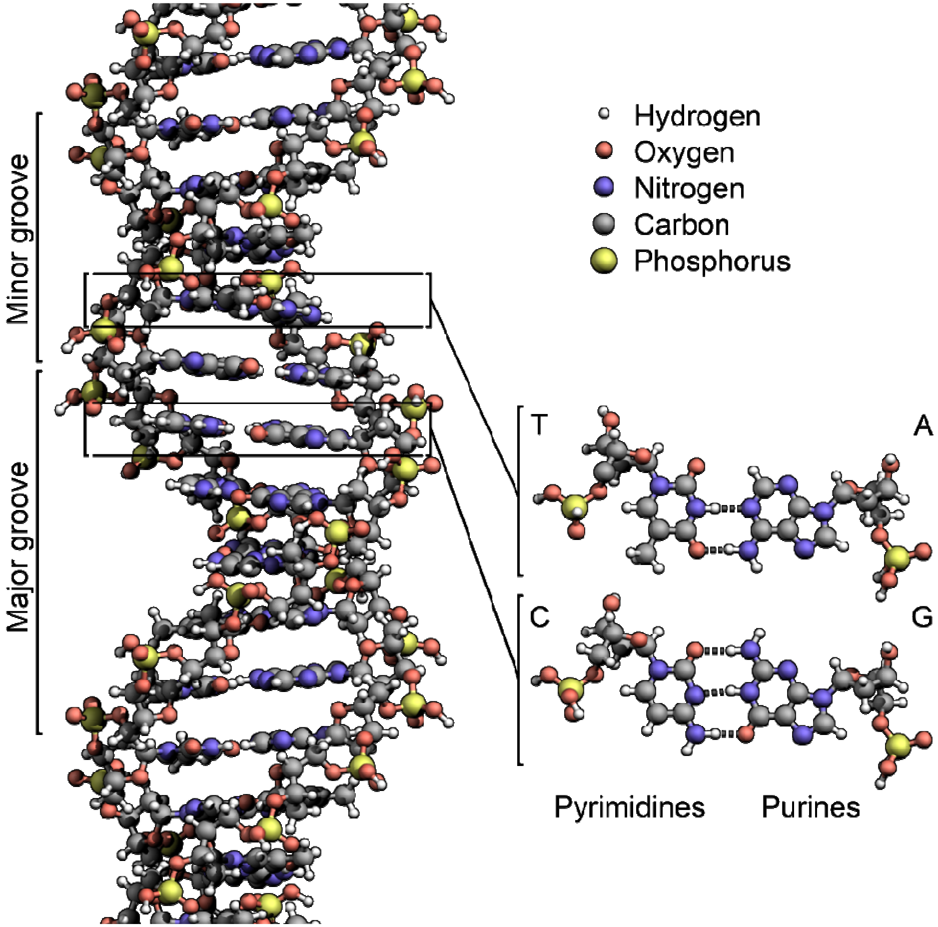
A. Yonath *et al. Israel Journal of Chemistry*, **2010**, *50*, 29-35

The origin of DNA





The origin of DNA



Maximal size of RNA-based genome: 3000-5000 bases (HIV, West Nile virus)

Reason: above that, statistically certain to generate at least one self-cleaving RNA sequence (ribozyme)

Maximal DNA size – unlimited
- no self-cleaving DNAzymes,
- tight storage as dsDNA,
- methylated uracil (thymine) → no accidental C-to-U mutations

The genetic code

1st base	2nd base: U	2nd base: C	2nd base: A	2nd base: G	3rd base in each row
U	UUU (Phe/F) Phenylalanine	UCU (Ser/S) Serine	UAU (Tyr/Y) Tyrosine	UGU (Cys/C) Cysteine	U
U	UUC (Phe/F) Phenylalanine	UCC (Ser/S) Serine	UAC (Tyr/Y) Tyrosine	UGC (Cys/C) Cysteine	C
U	UUA (Leu/L) Leucine	UCA (Ser/S) Serine	UAA Ochre (Stop)	UGA Opal (Stop)	A
U	UUG (Leu/L) Leucine	UCG (Ser/S) Serine	UAG Amber (Stop)	UGG (Trp/W) Tryptophan	G
C	CUU (Leu/L) Leucine	CCU (Pro/P) Proline	CAU (His/H) Histidine	CGU (Arg/R) Arginine	U
C	CUC (Leu/L) Leucine	CCC (Pro/P) Proline	CAC (His/H) Histidine	CGC (Arg/R) Arginine	C
C	CUA (Leu/L) Leucine	CCA (Pro/P) Proline	CAA (Gln/Q) Glutamine	CGA (Arg/R) Arginine	A
C	CUG (Leu/L) Leucine	CCG (Pro/P) Proline	CAG (Gln/Q) Glutamine	CGG (Arg/R) Arginine	G
A	AUU (Ile/I) Isoleucine	ACU (Thr/T) Threonine	AAU (Asn/N) Asparagine	AGU (Ser/S) Serine	U
A	AUC (Ile/I) Isoleucine	ACC (Thr/T) Threonine	AAC (Asn/N) Asparagine	AGC (Ser/S) Serine	C
A	AUA (Ile/I) Isoleucine	ACA (Thr/T) Threonine	AAA (Lys/K) Lysine	AGA (Arg/R) Arginine	A
A	AUG (Met/M) Methionine	ACG (Thr/T) Threonine	AAG (Lys/K) Lysine	AGG (Arg/R) Arginine	G
G	GUU (Val/V) Valine	GCU (Ala/A) Alanine	GAU (Asp/D) Aspartic acid	GGU (Gly/G) Glycine	U
G	GUC (Val/V) Valine	GCC (Ala/A) Alanine	GAC (Asp/D) Aspartic acid	GGC (Gly/G) Glycine	C
G	GUA (Val/V) Valine	GCA (Ala/A) Alanine	GAA (Glu/E) Glutamic acid	GGA (Gly/G) Glycine	A
G	GUG (Val/V) Valine	GCG (Ala/A) Alanine	GAG (Glu/E) Glutamic acid	GGG (Gly/G) Glycine	G

ΔF-508 deletion in cystic fibrosis

- Myotonic dystrophy
- SCA 8

β-Thalassemia

McArdle's disease

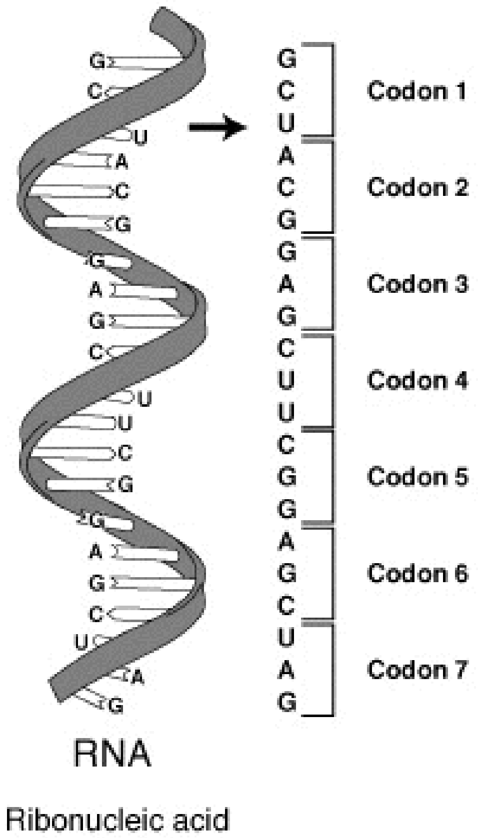
β-Thalassem

Prostate cancer

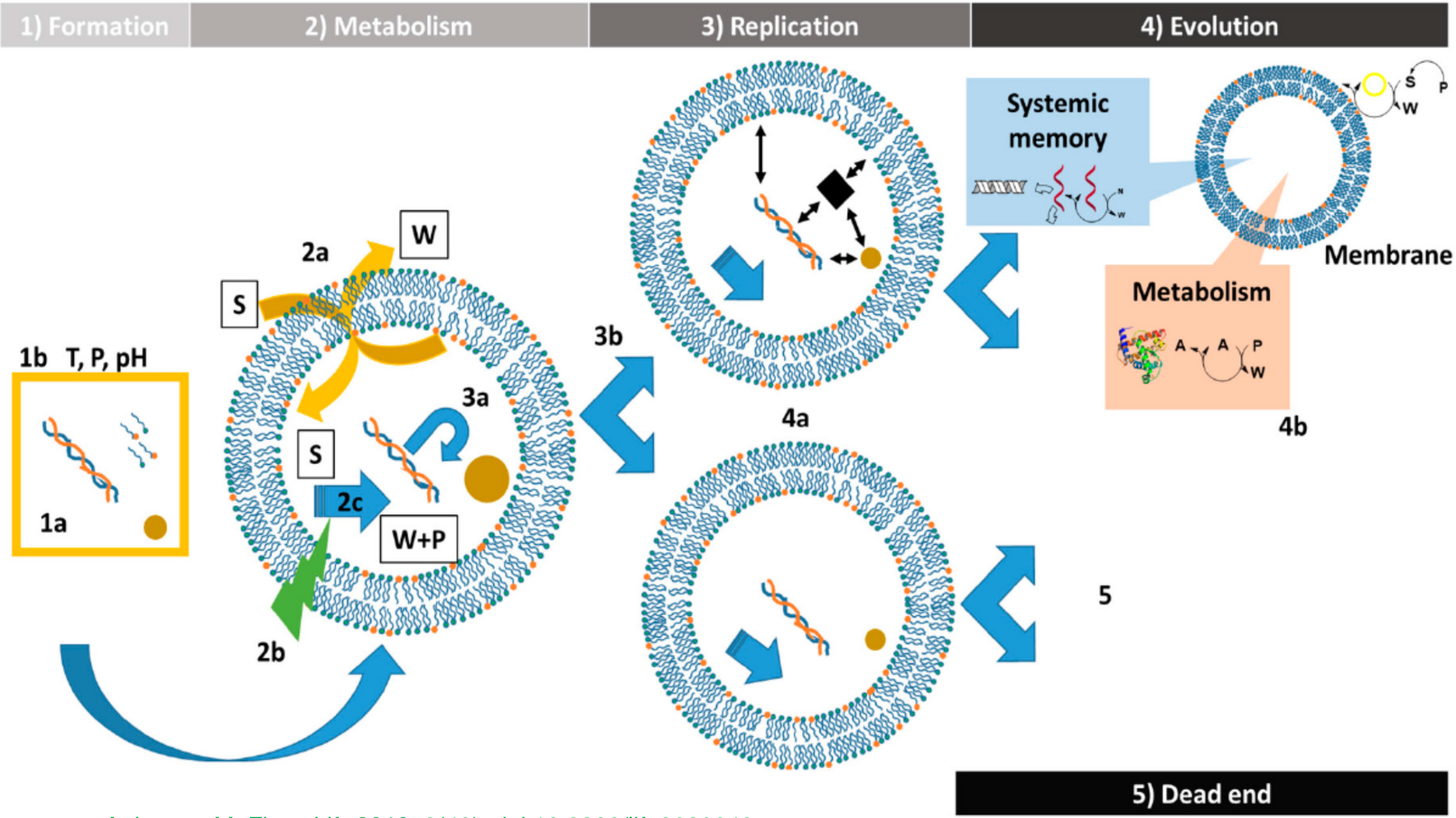
Colorectal cancer

Sickle-cell disease

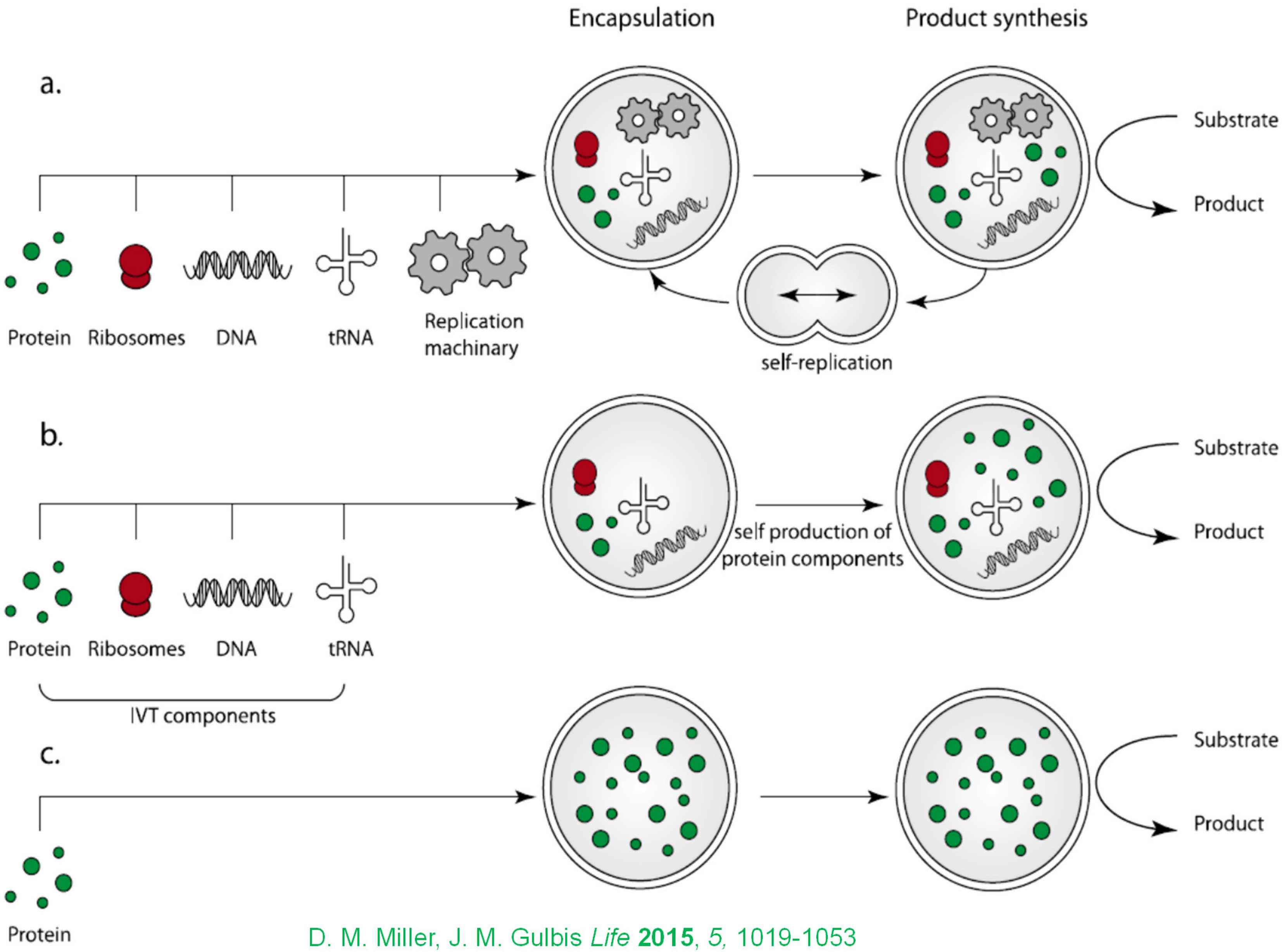
Friedreich's ataxia



Increasing complexity of the protocells

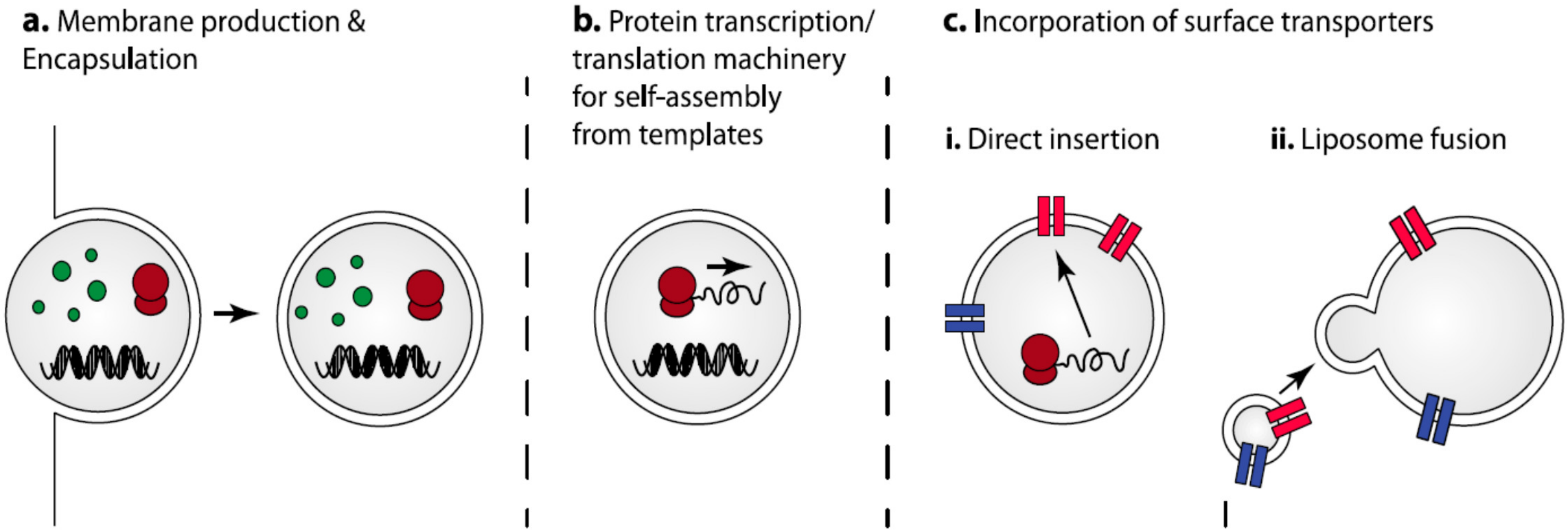


A. Lopez, M. Fiore *Life* **2019**, 9(49), doi:10.3390/life9020049

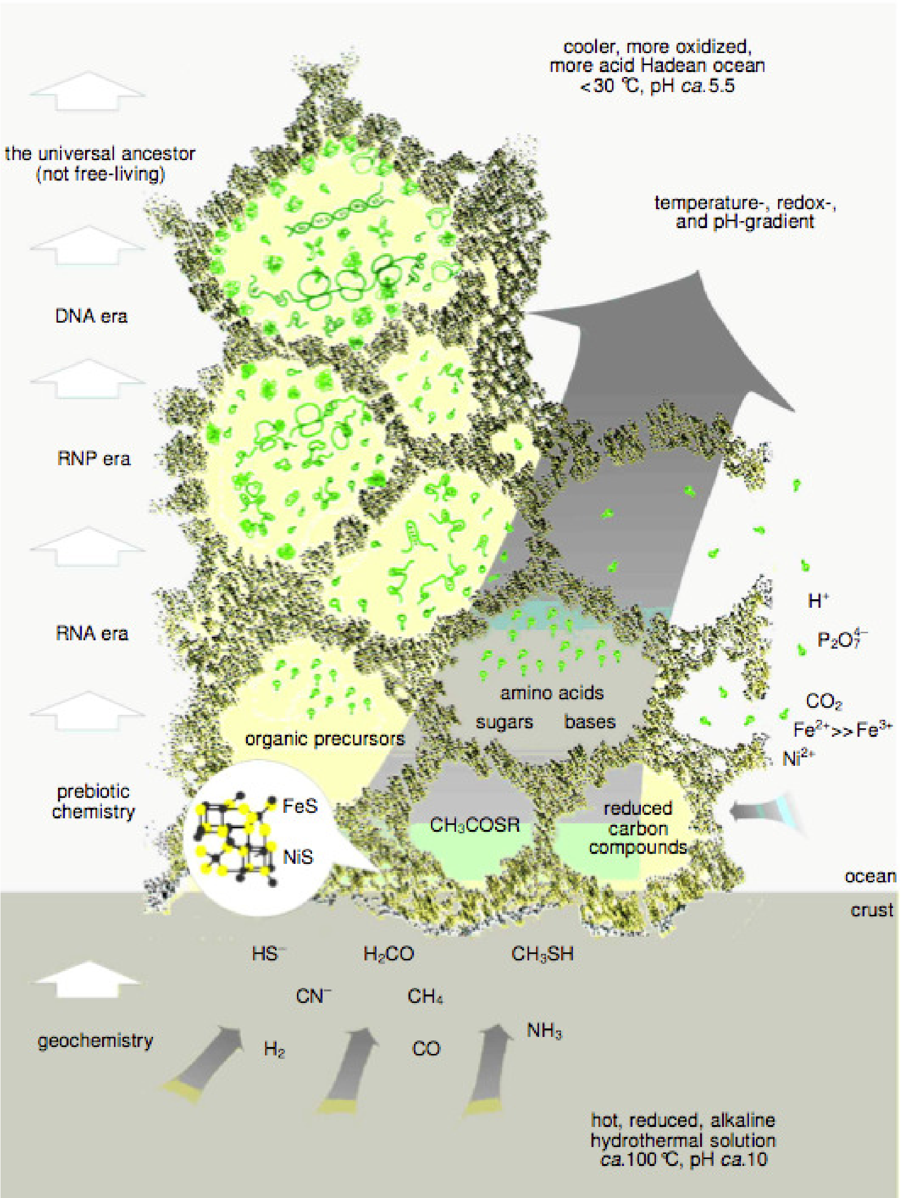


D. M. Miller, J. M. Gulbis *Life* **2015**, *5,* 1019-1053

Increasing complexity of the protocells

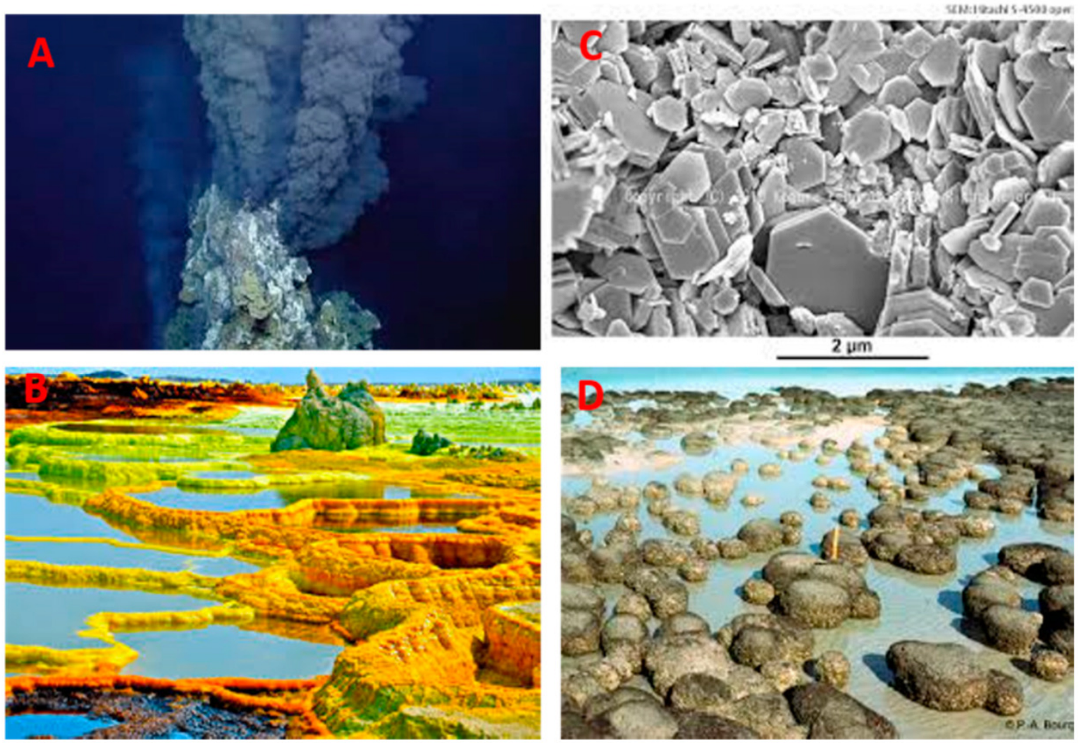


D. M. Miller, J. M. Gulbis *Life* **2015**, *5,* 1019-1053



Compartments in hydrothermal vents?

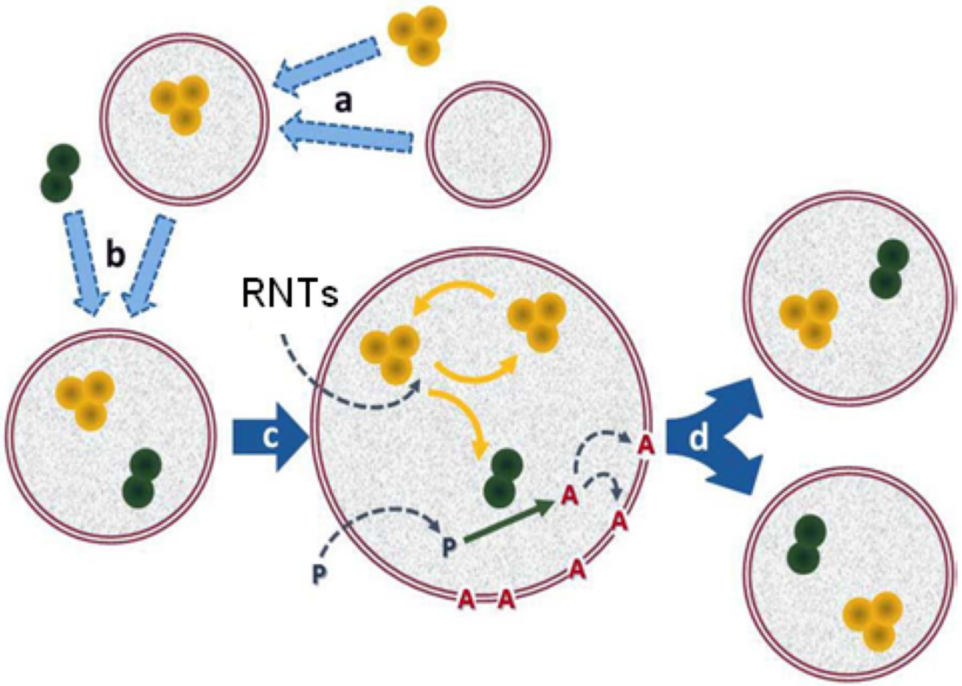
Complex metabolic machinery closed in the same compartment that genetic polymers (RNA) which generated it.



A. Lopez, M. Fiore *Life* **2019**, 9(49), doi:10.3390/life9020049

We don't see ribozyme-based metabolism today anymore, because protein catalysts (enzymes) for the same reactions are orders of magnitude faster than the ribozymes

Primordial synthesis of an RNA-based protocell



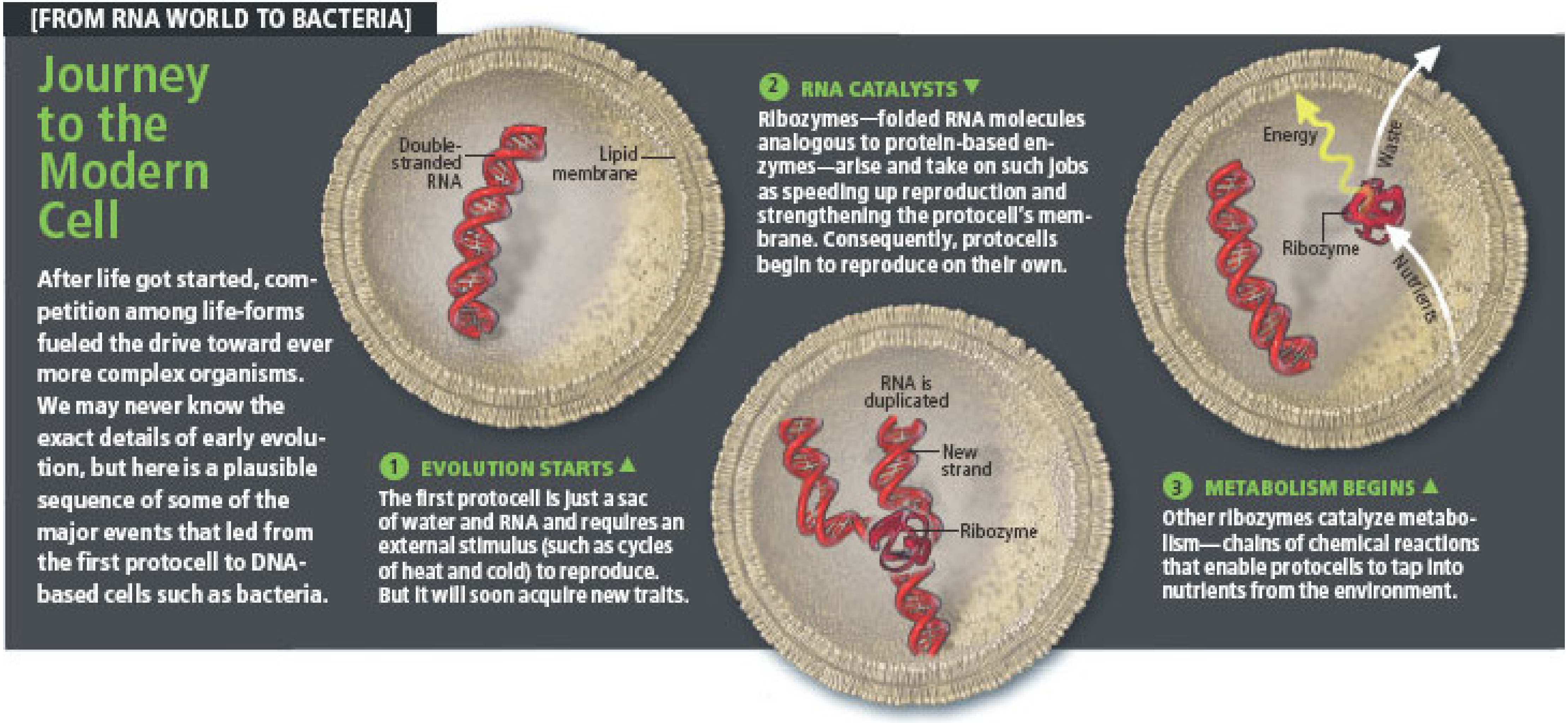
(a) A self-reproducing vesicle is combined with an RNA replicase (yellow).

(b) This system is further combined with a second ribozyme (green) that is able to synthesize amphiphilic molecules (A) from precursor substrates (P), thus leading to an RNA protocell containing two ribozymes.

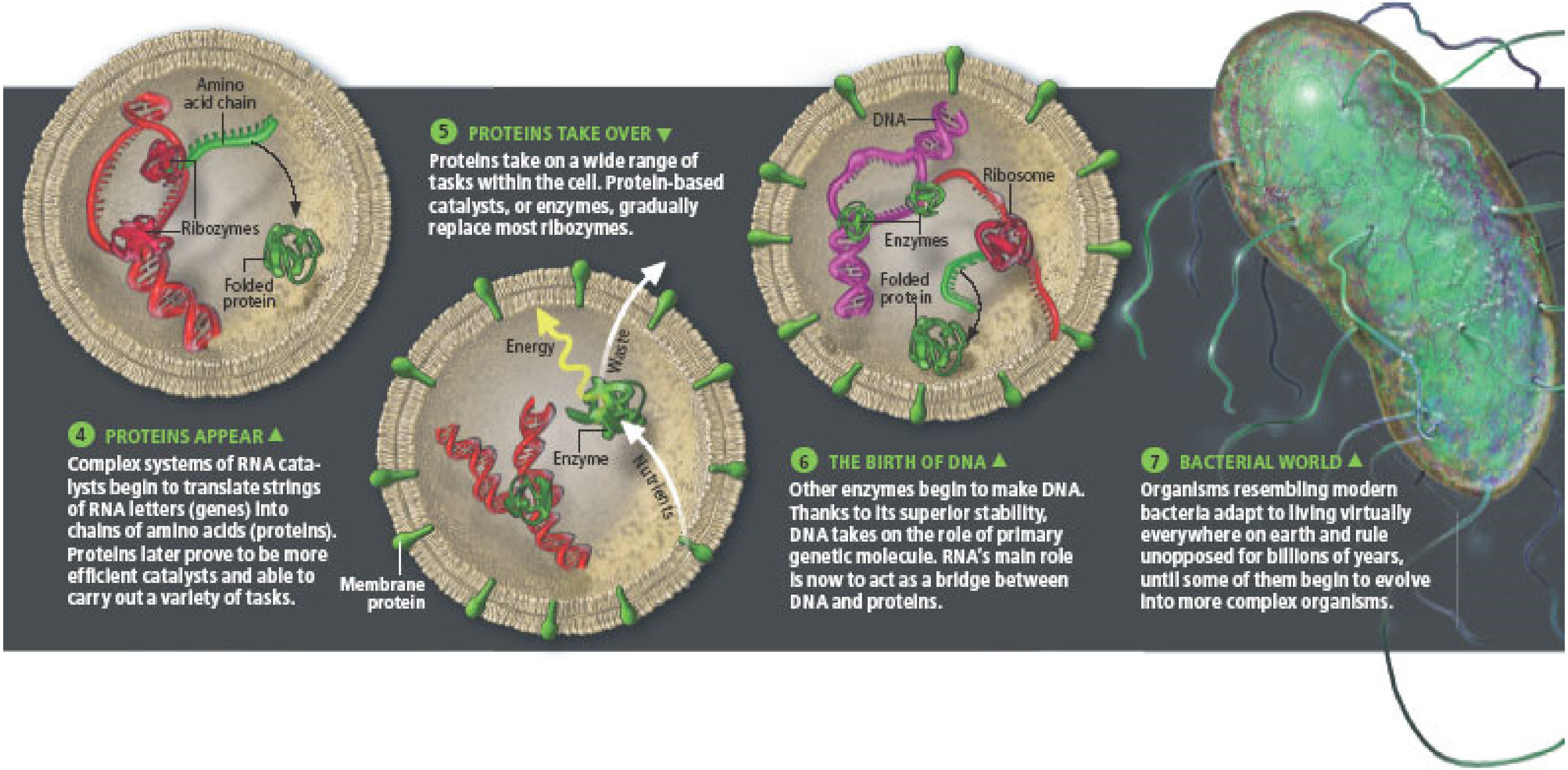
(c) In such a "ribocyte", the RNA replicase is capable of replicating itself and also making copies of the membrane-forming ribozyme, provided that ribonucleotides (RNTs) are available in the surrounding medium and can permeate the vesicle membrane.

(d) Activity of the second ribozyme converts the previously internalized precursors into amphiphiles, which are further incorporated into the membrane; this leads to a progressive increase of the vesicle size and its subsequent division into two daughter vesicles, thus triggering Darwinian evolution of the whole (membrane–genome coupled) system

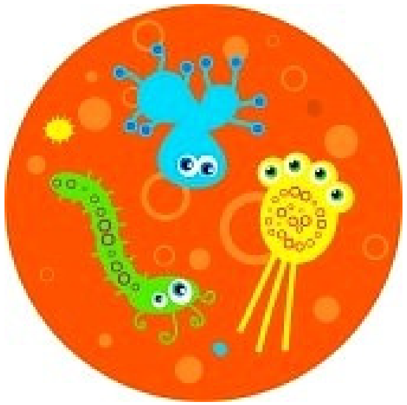
From RNA world to bacteria

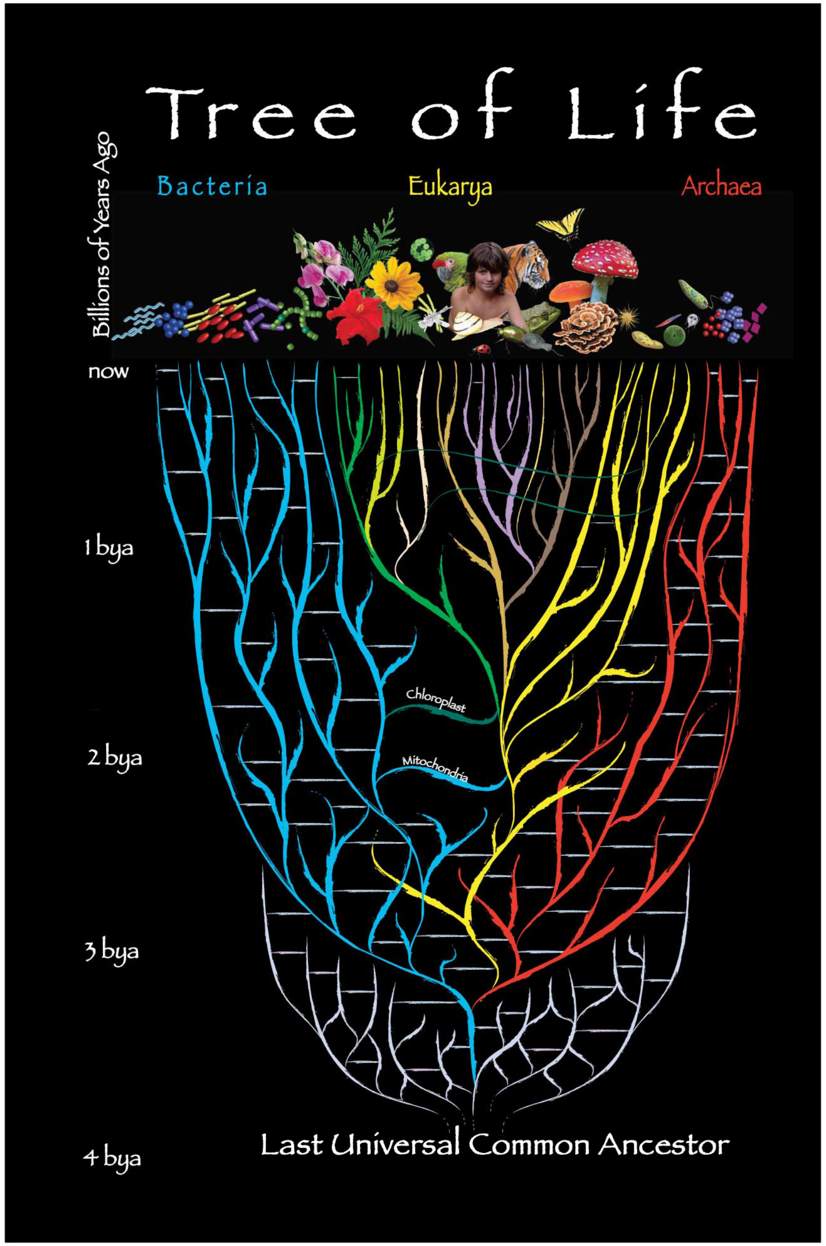


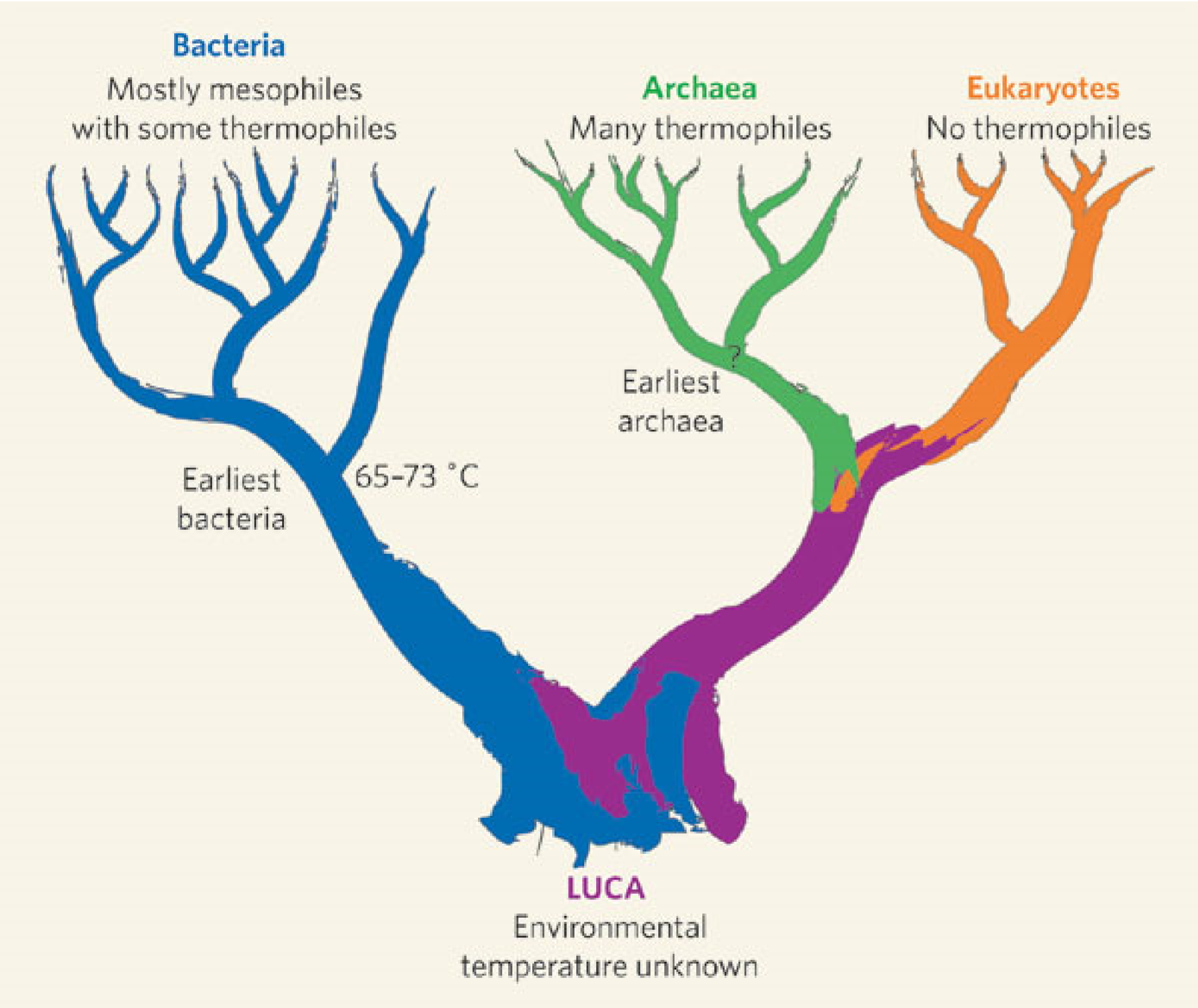
From RNA world to bacteria




LUCA
Last Universal Common Ancestor




Tree of Life
Billions of Years Ago
Bacteria
Eukarya
Archaea
now
1 bya
2 bya
3 bya
4 bya
Chloroplast
Mitochondria
Last Universal Common Ancestor



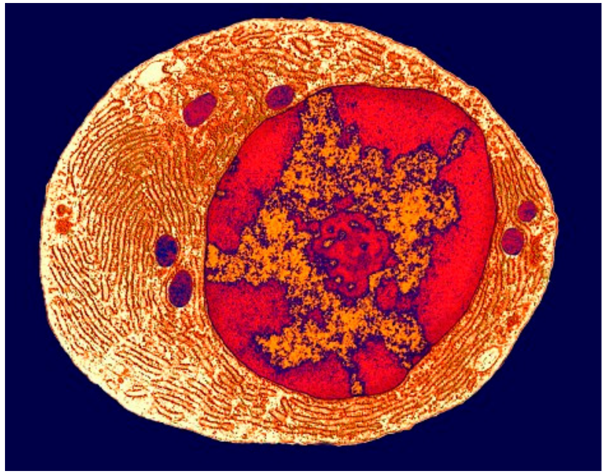
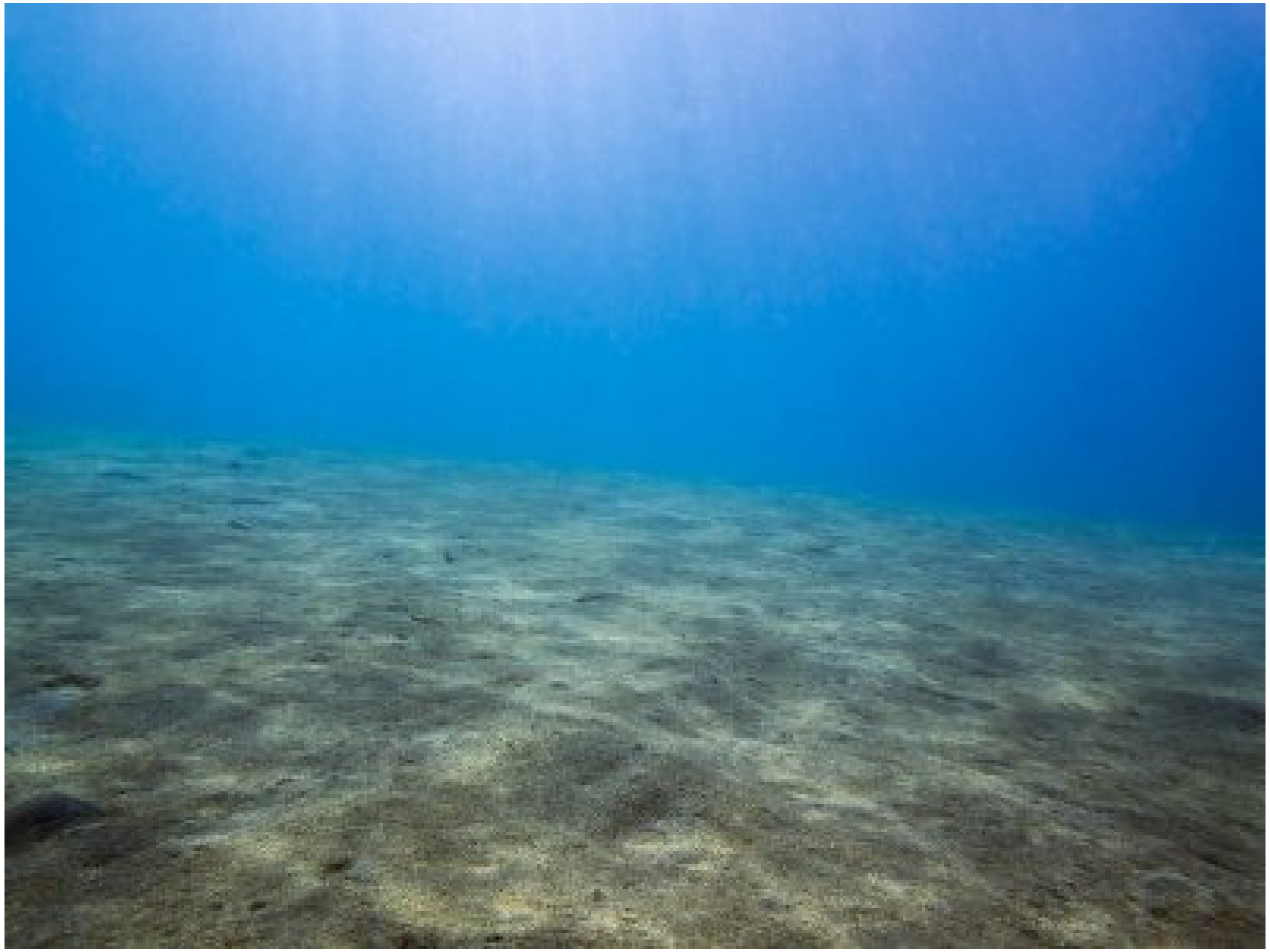


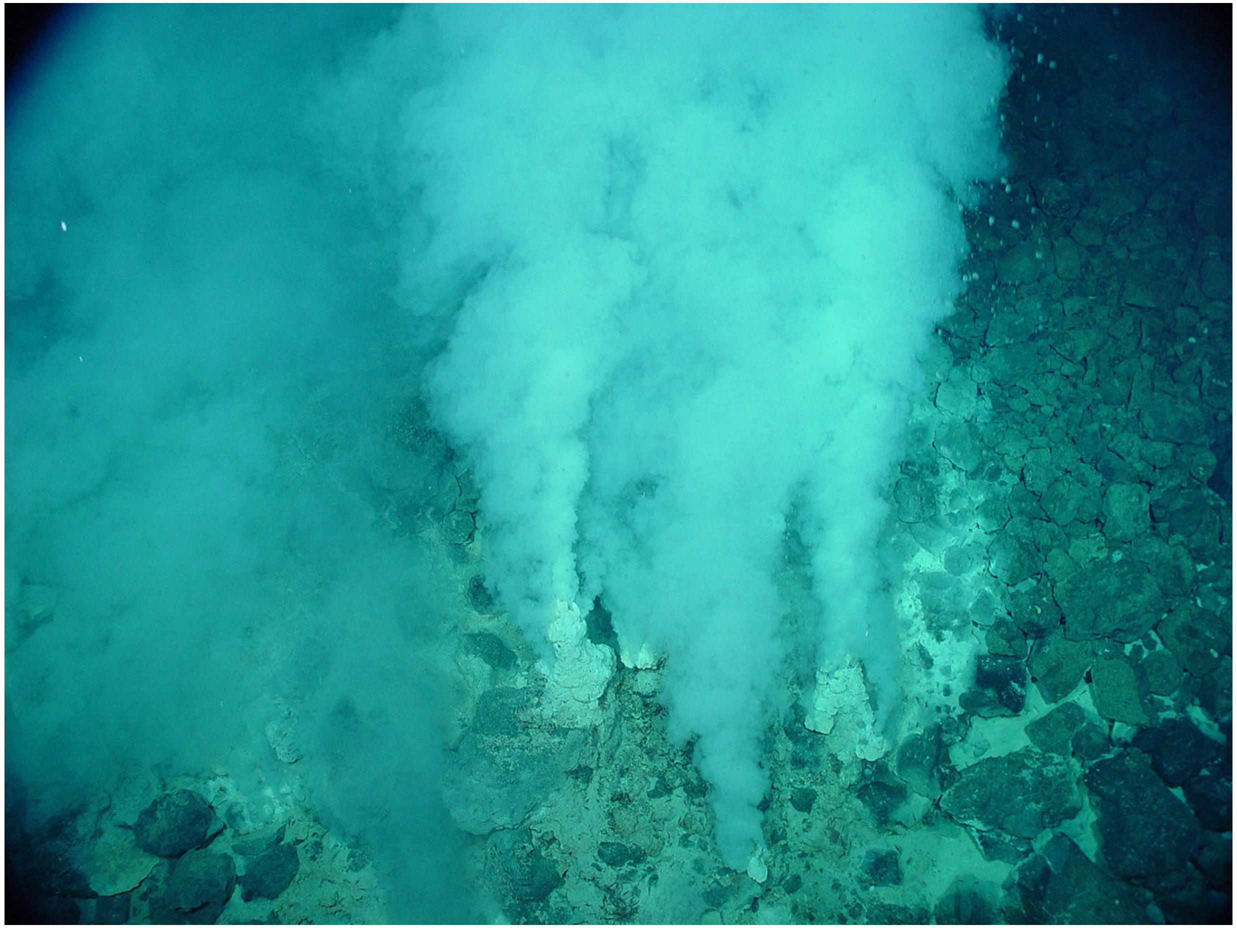
Image of a eukaryotic cell contains numerous organelles, which are now thought to be present in the last universal common ancestor

A colony of the archaea, which form one of the three lines of the tree of life in evolutionary history

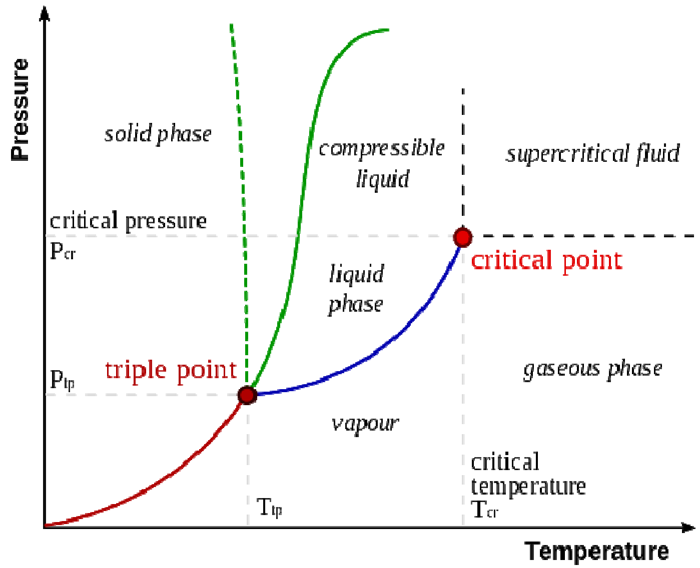
The Origin of Life near Deep Sea Hydrothermal vents?



Hydrothermal vents

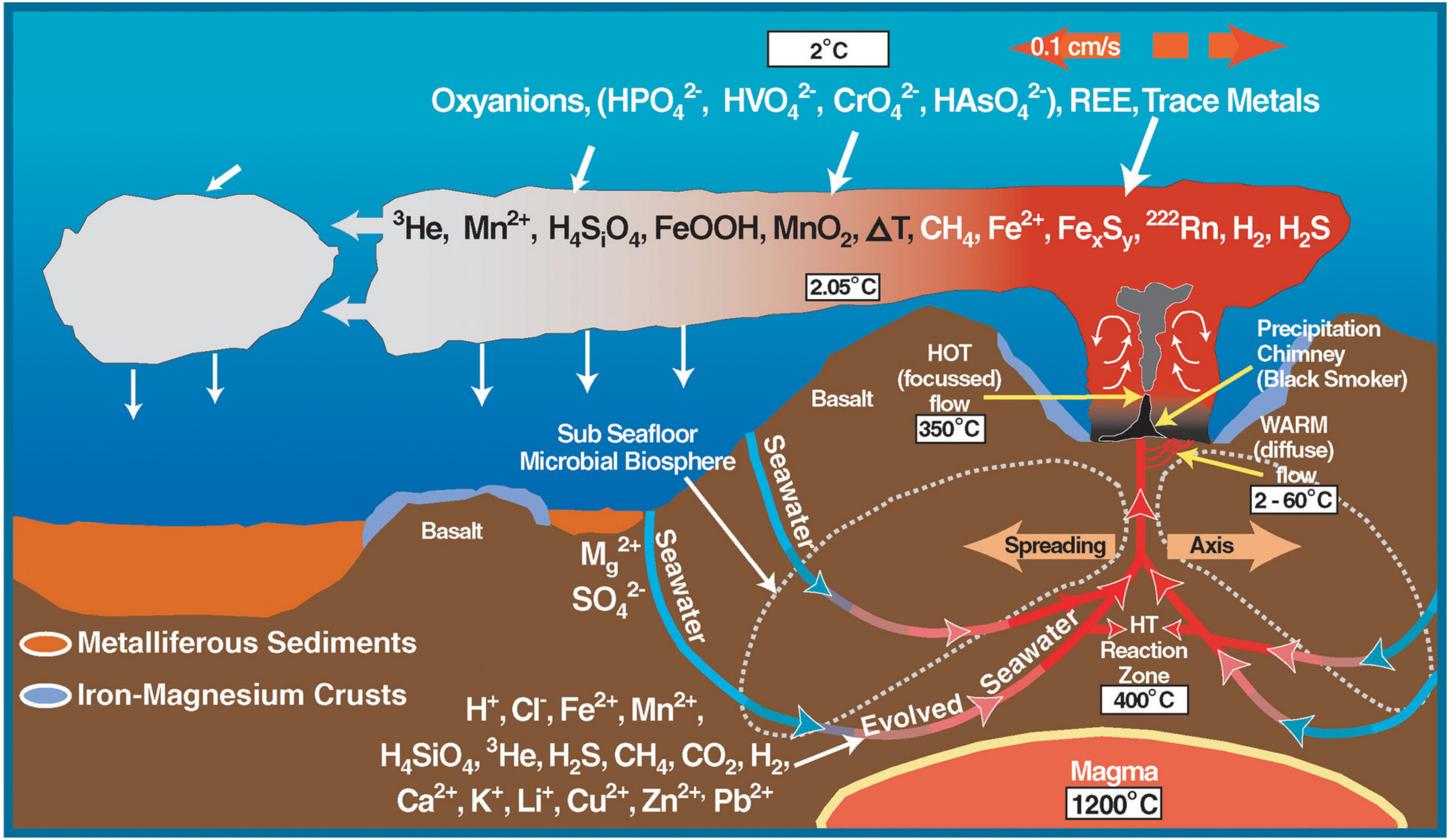


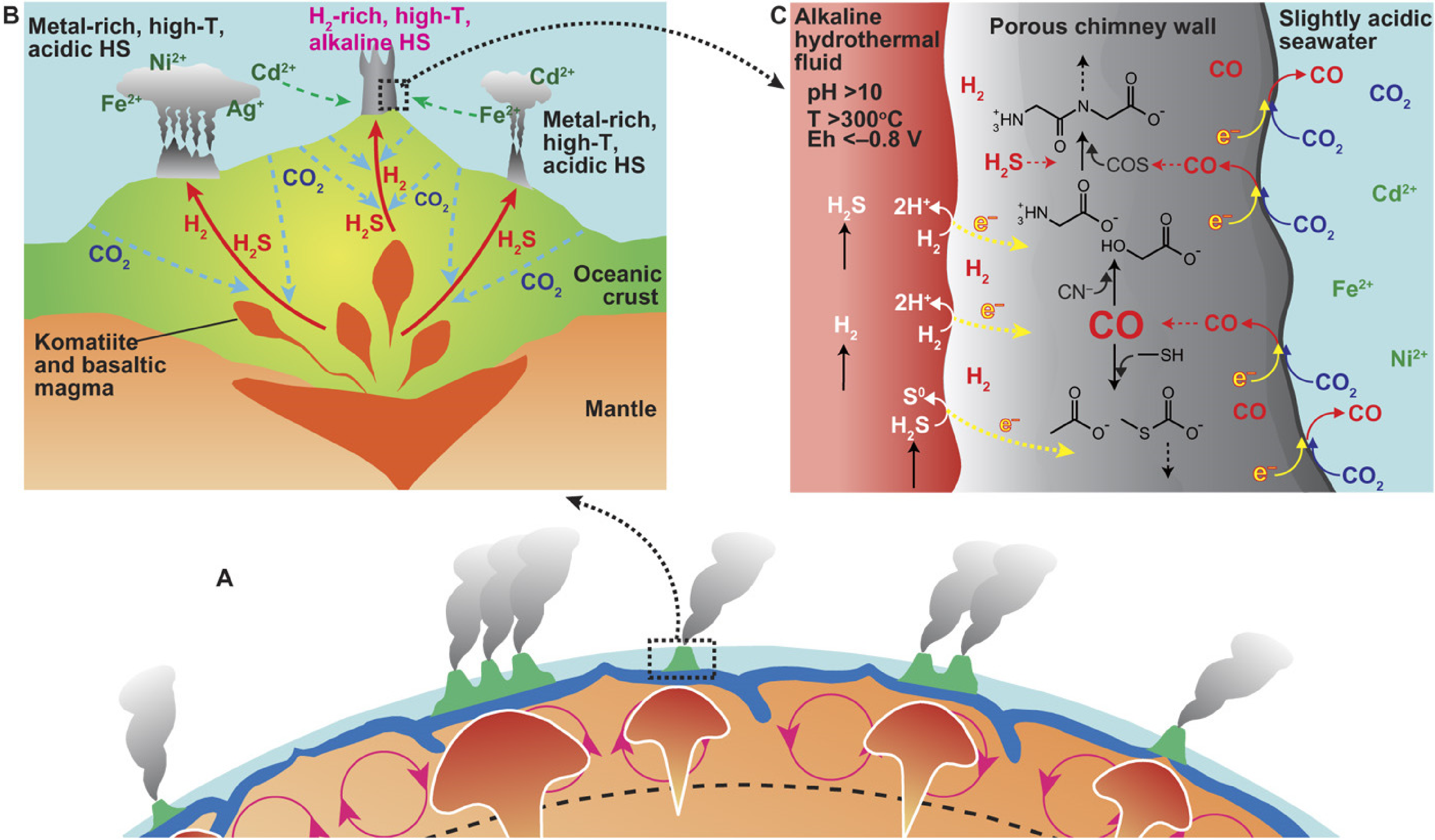
White flocculent mats in and around the extremely gassy, high-temperature (>100°C, 212°F) white smokers at Champagne Vent.



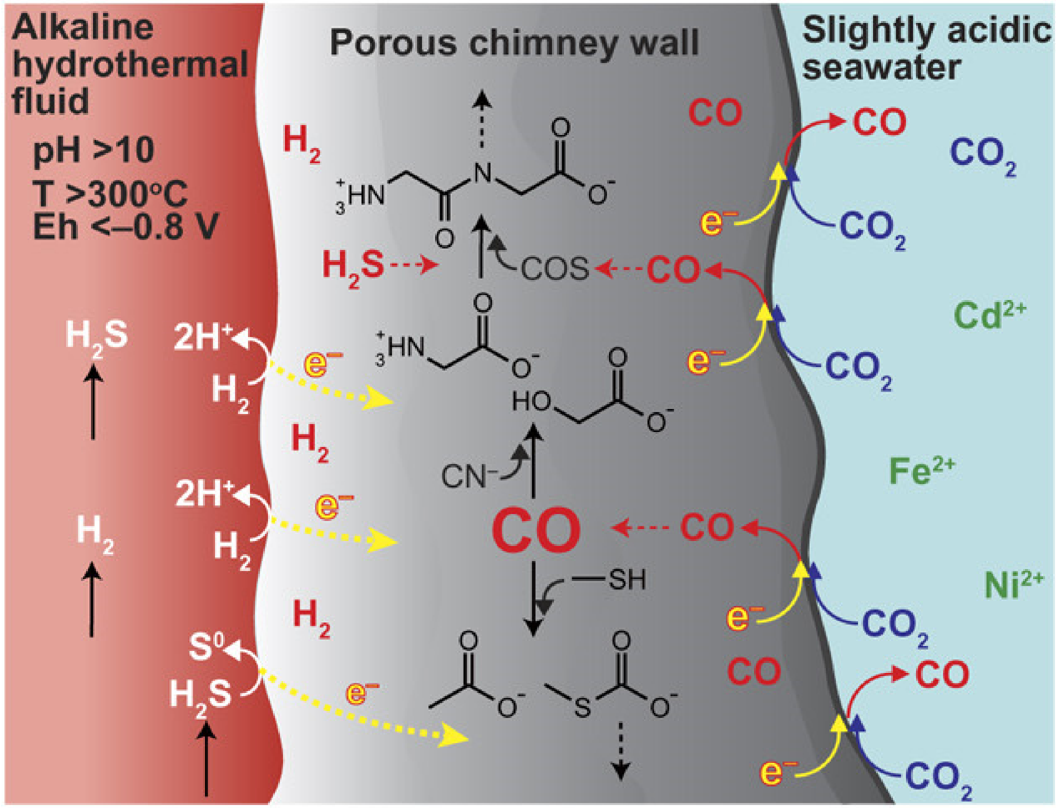
Alkaline hydrothermal vents consist of microscale caverns coated by thin membraneous metal sulfide walls → ‚Iron-sulfur world'

Deep sea vent biogeochemical cycle diagram




B
Metal-rich, high-T, acidic HS
H_2-rich, high-T, alkaline HS
Metal-rich, high-T, acidic HS
Ni^{2+}
Fe^{2+}
Ag^{+}
Cd^{2+}
Cd^{2+}
Fe^{2+}
CO_2
H_2
H_2S
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
H_2S
$2H^+$
S^0
e^-
CO
CO_2
COS
CN^-
SH
Cd^{2+}
Fe^{2+}
Ni^{2+}
A

Deep sea vent origin of life

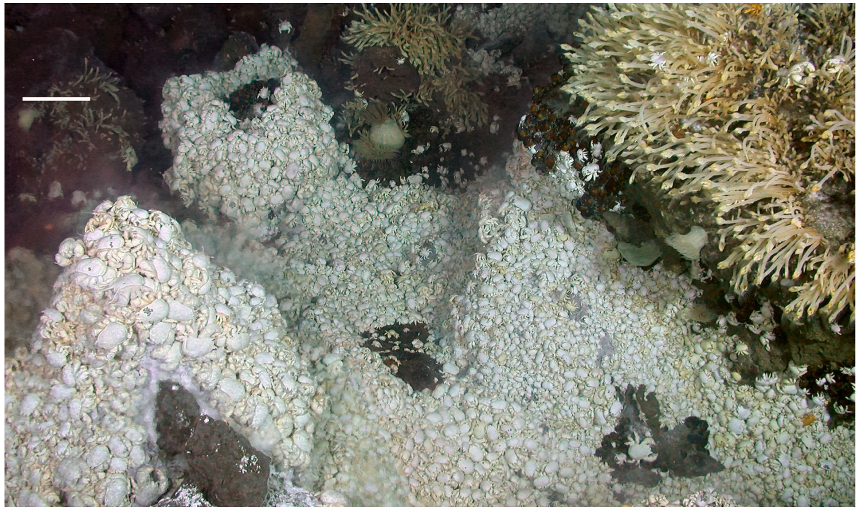


Abiotic carbon fixation in the primitive hydrothermal system.

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

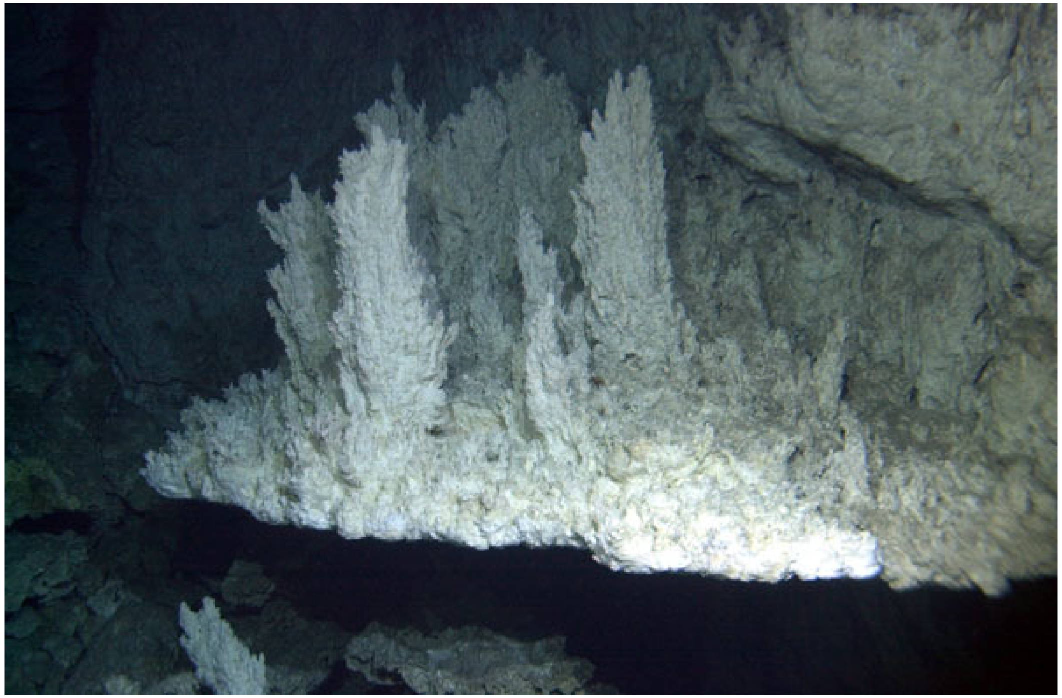
Deep sea vent fauna



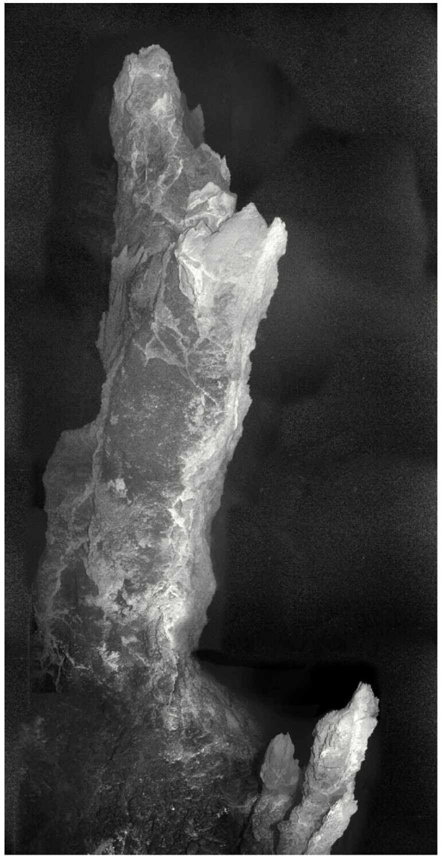
A dense fauna (*Kiwa* anomurans and *Vulcanolepas* like stalked barnacles) near East Scotia Ridge vents

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

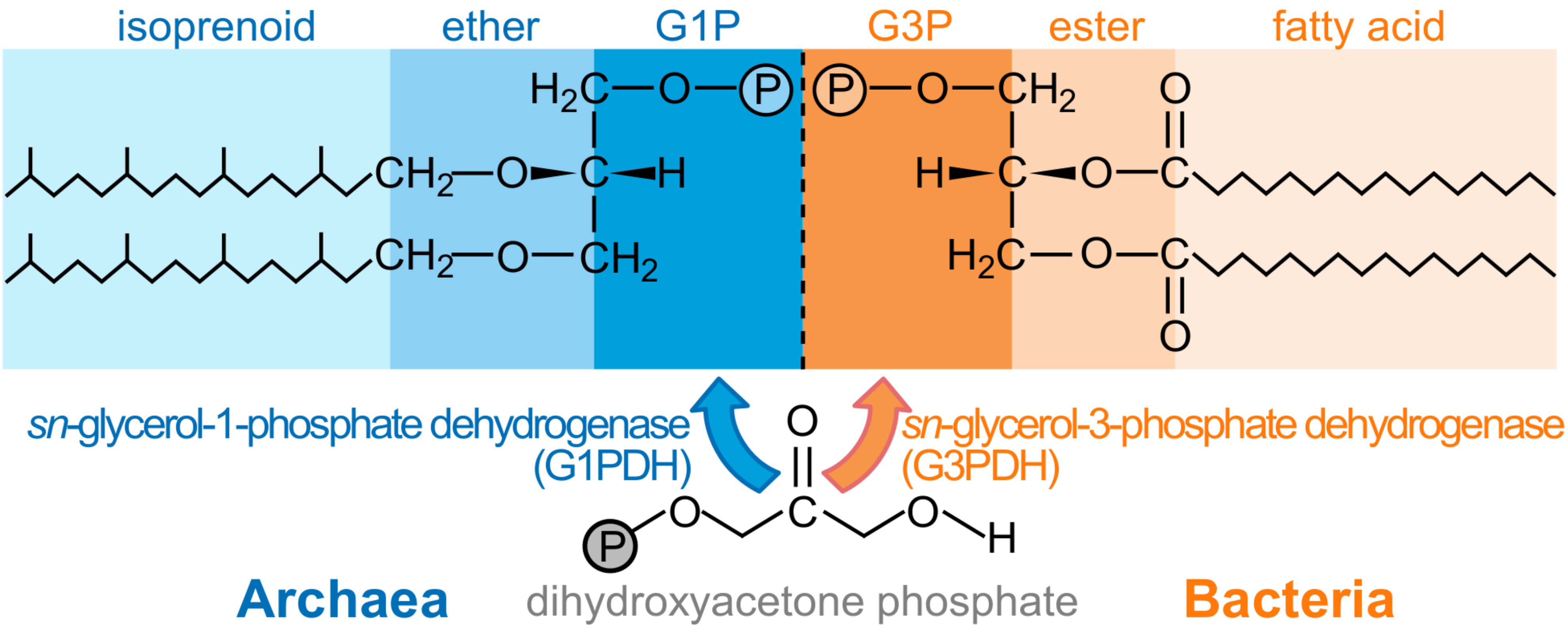
„Lost city" – white smokers: alkaline hydrothermal vents



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.



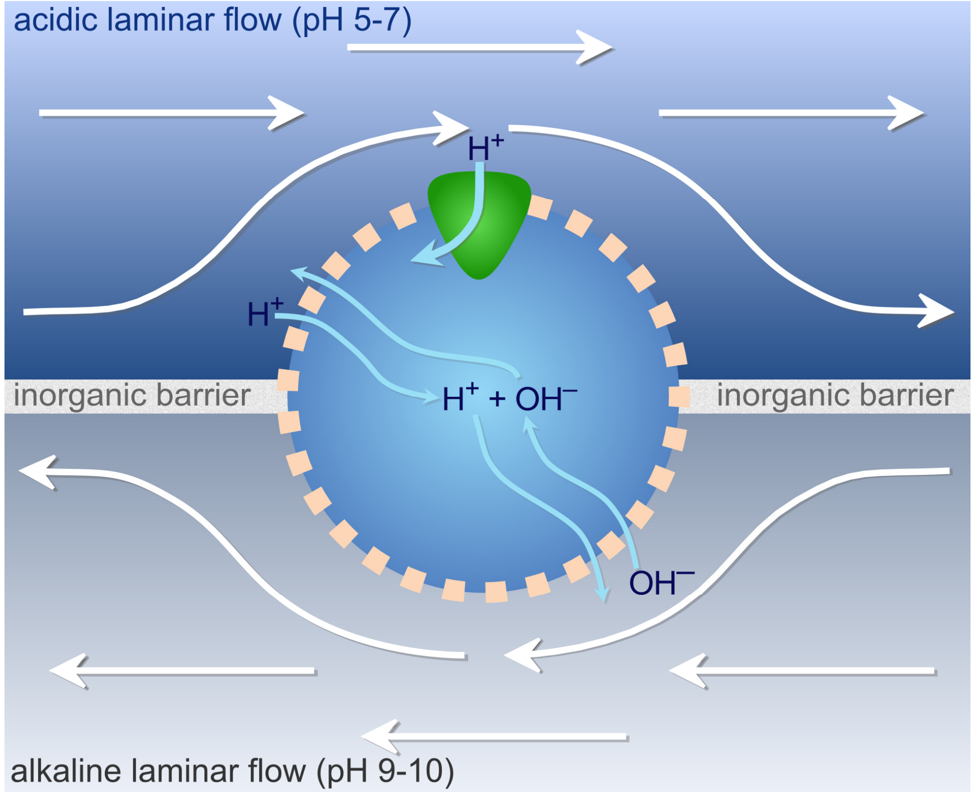
A carbonate chimney more than 9 meters (30 feet) in height. The white, sinuous spine is freshly deposited carbonate material. The top shows evidence of collapse and re-growth, as indicated by the small newly developed cone on its top



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)

V. Sojo, A. Pomiankowski, N. Lane *PLOS Biology,* **2014**, *12(8),* e1001926

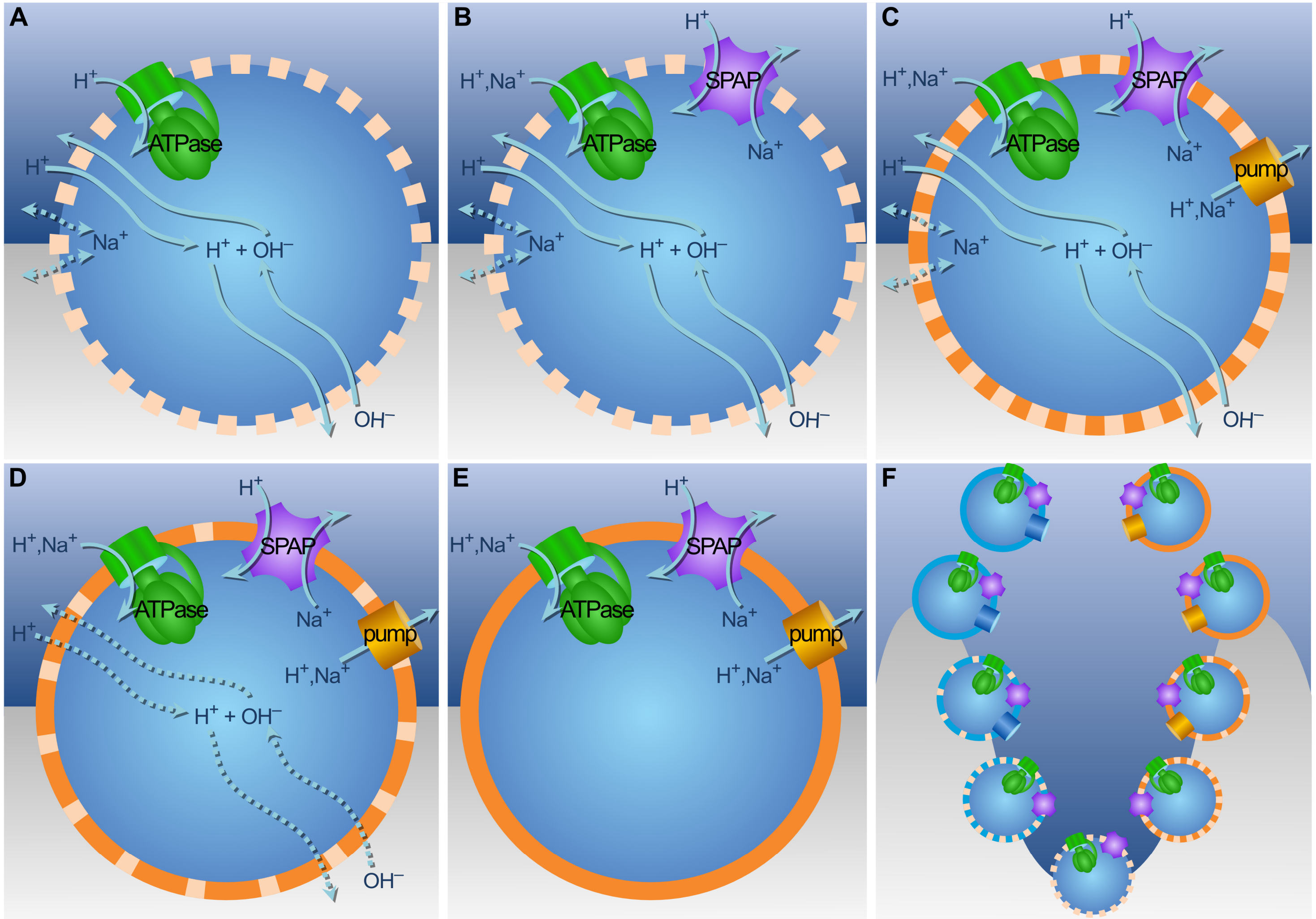


A cell with a semi-permeable membrane at the interface between an alkaline and an acidic fluid (separated elsewhere with an inorganic bareer. H^+, OH^-, Na^+, K^+, Cl^- and other ions flow according to their natural gradients.
Inside the protocell, H^+ and OH^- can neutralize into water, or leave towards 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.

V. Sojo, A. Pomiankowski, N. Lane *PLOS Biology,* **2014**, *12(8),* e1001926

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

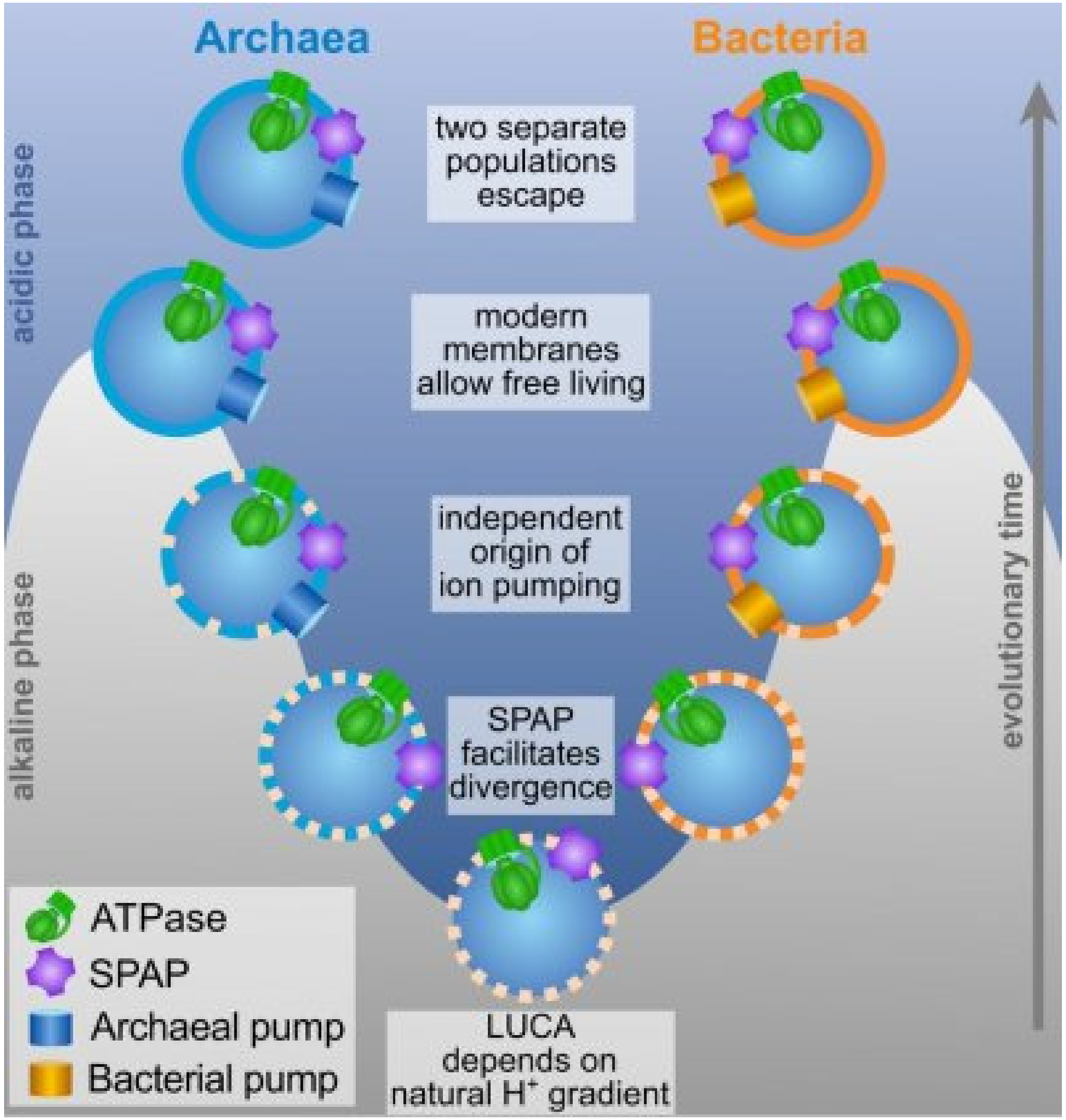
C) Membrane pumps secret H^+ and Na^+

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

V. Sojo, A. Pomiankowski, N. Lane
PLOS Biology, **2014**, *12(8)*, e1001926



Origin of autotrophy and development of cell membrane

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

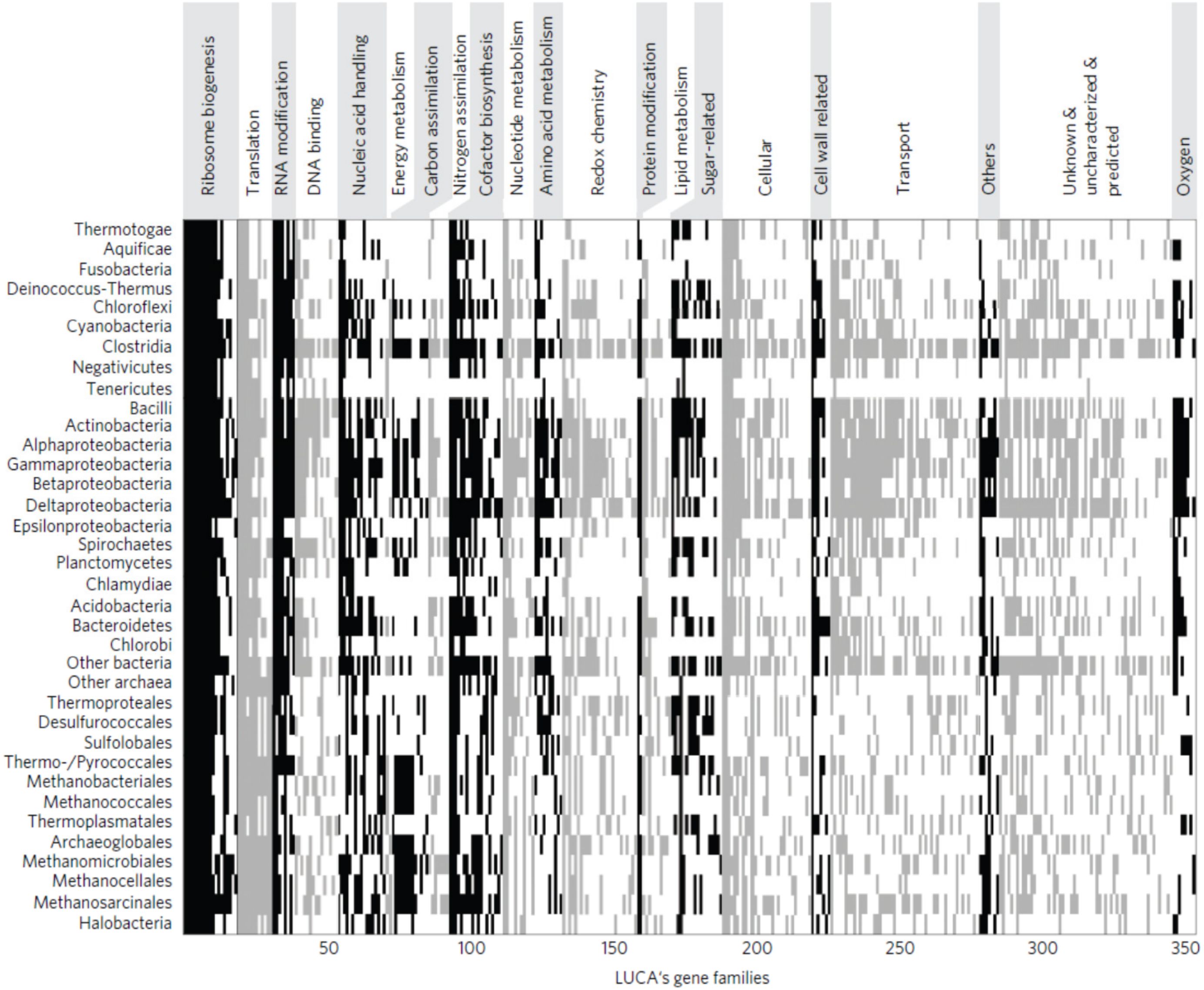
Energy could have been delivered by the natural proton gradient in alkaline hydrothermal vents, if the membrane was much more leaky than contemporary ones.

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

sodium-proton antiporter (SPAP)

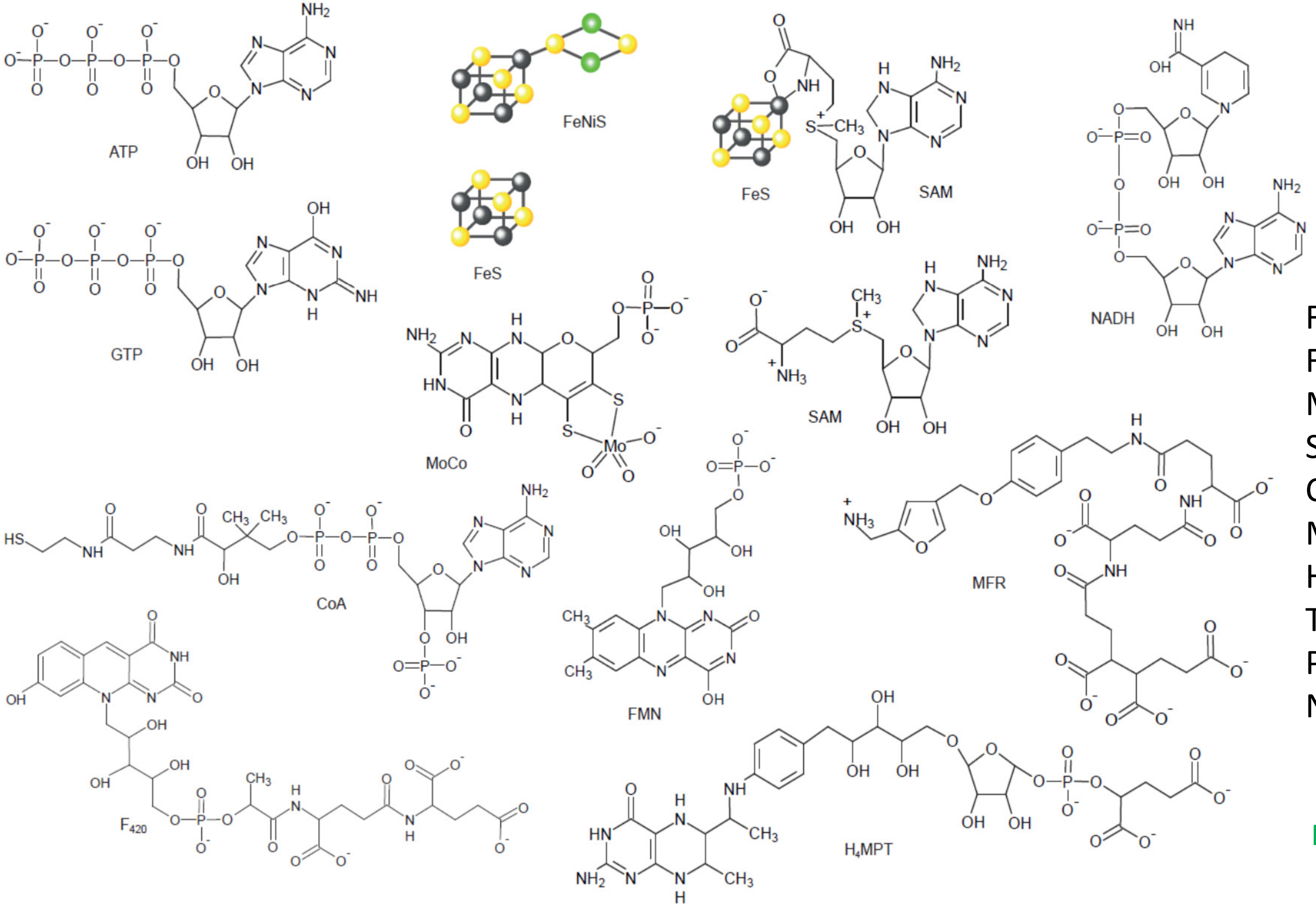
V. Sojo, A. Pomiankowski, N. Lane
PLOS Biology, **2014**, *12(8)*, e1001926

Taxonomic distribution of LUCA's genes grouped by functional categories



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

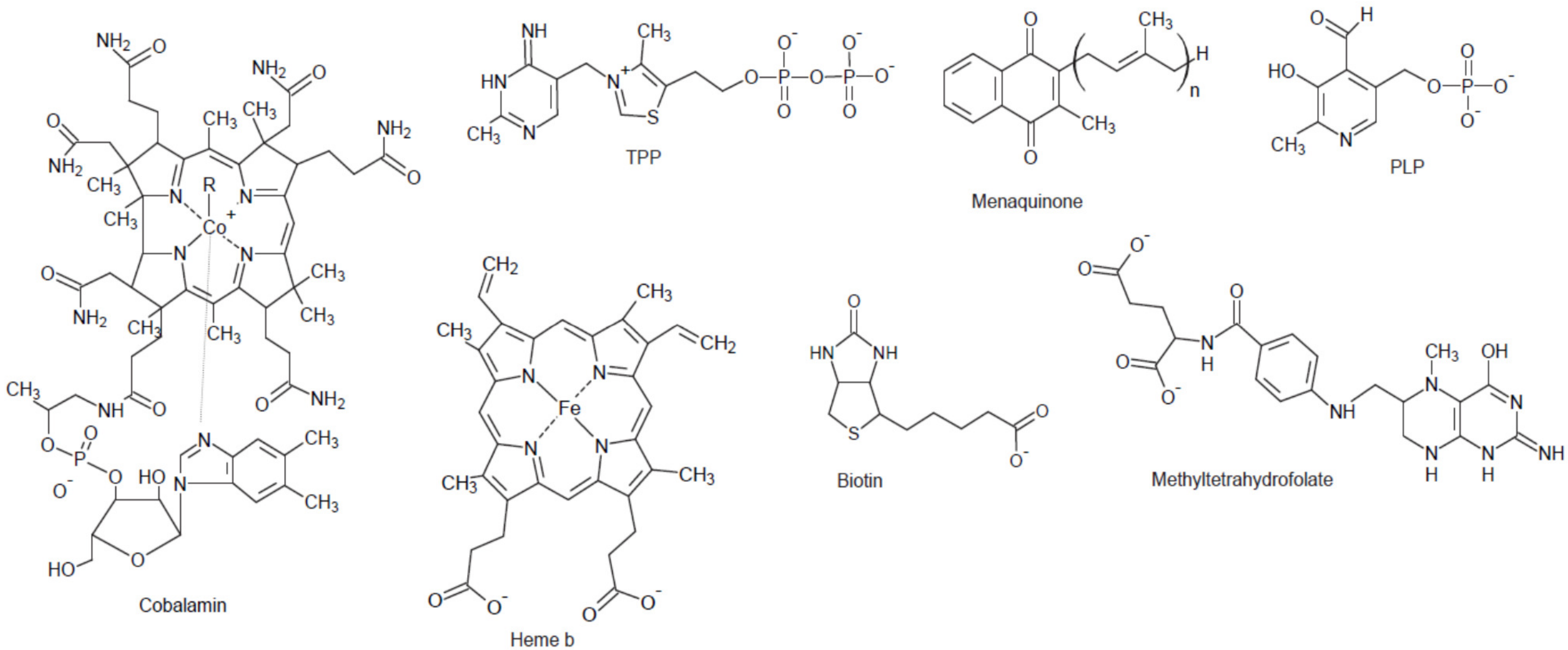
Structures of the cofactors found in LUCA's protein set.



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.

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

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



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

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

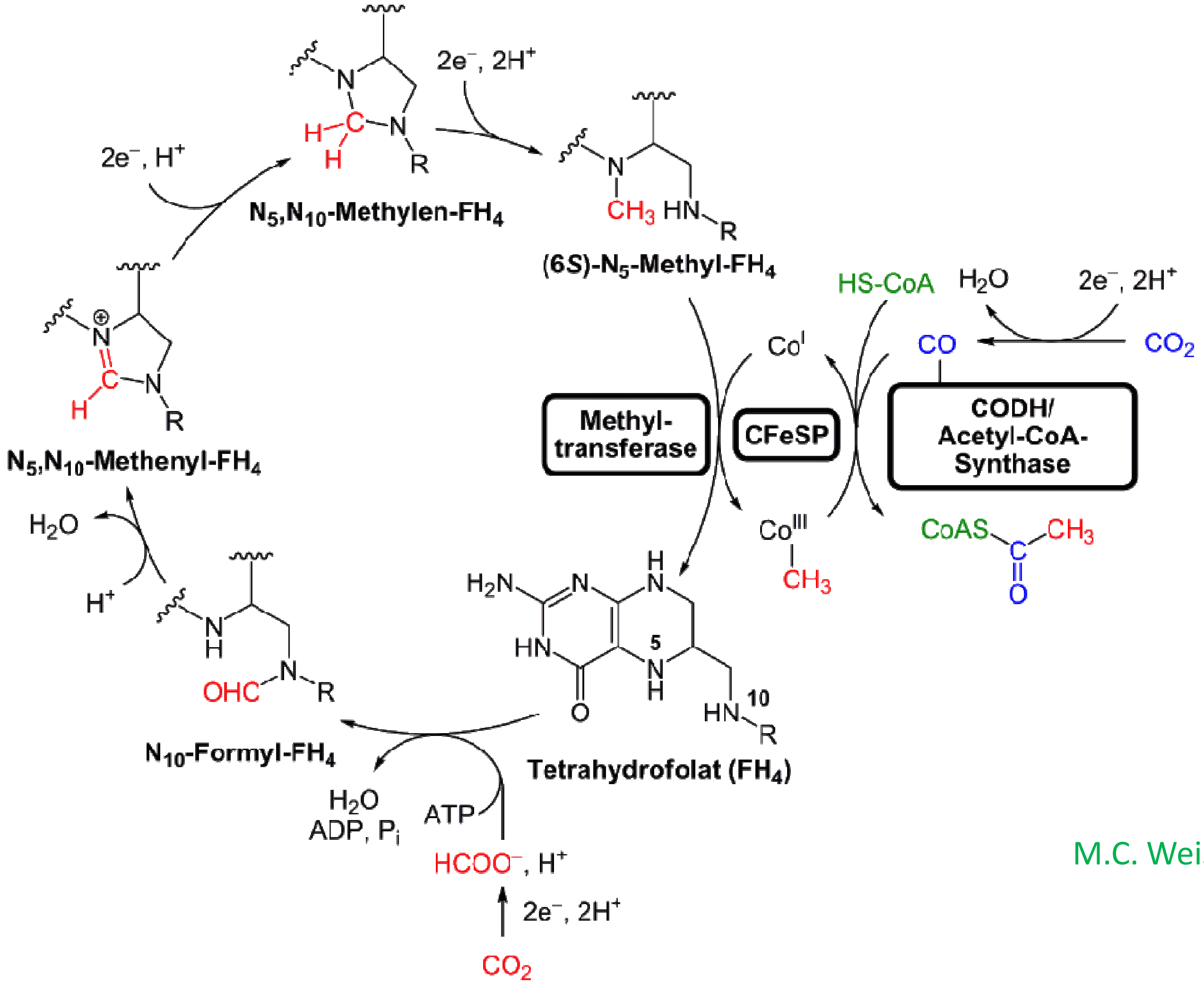
Phylogenetic identification of LUCA’s proteome

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

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

Wood-Ljungdahl (WL) anaerobic pathway of carbon fixation



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

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.

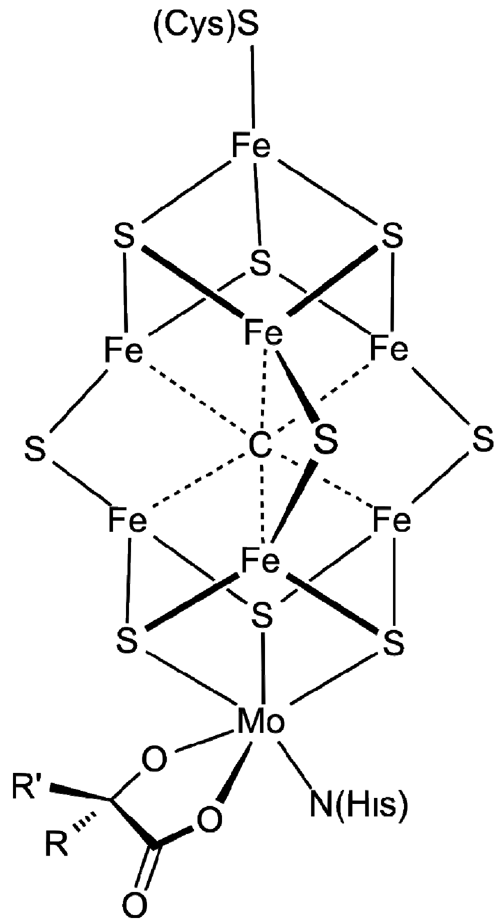
M.C. Weiss et al. *Nature Microbiology,* **2016**, *Article 16116*

Metabolism of LUCA

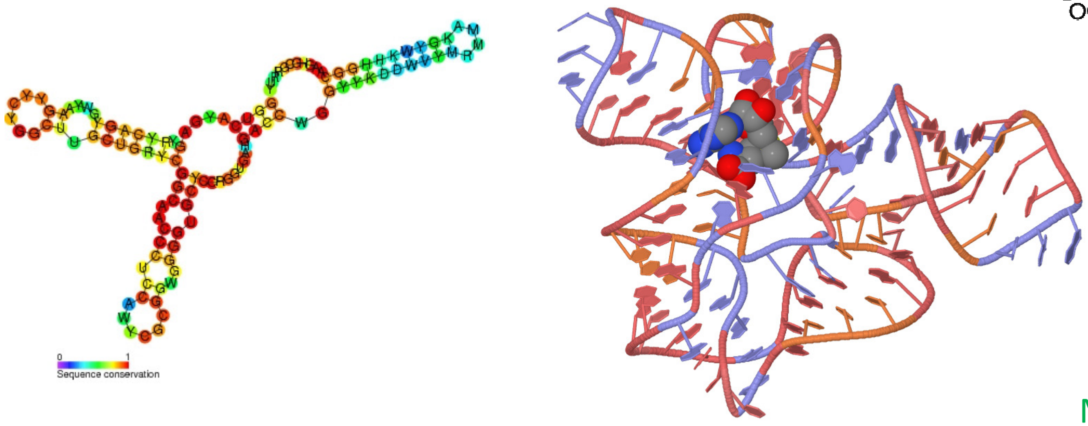
Enzymes for cofactor biosynthesis, including pterins, MoCo, cobalamin, siroheme, TPP, CoM and F_{420}, are also conserved.

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

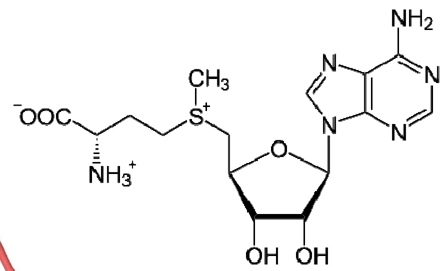
SAM chemistry is based on oxygen-sensitive FeS-containing proteins that initiate radical-dependent methylations.



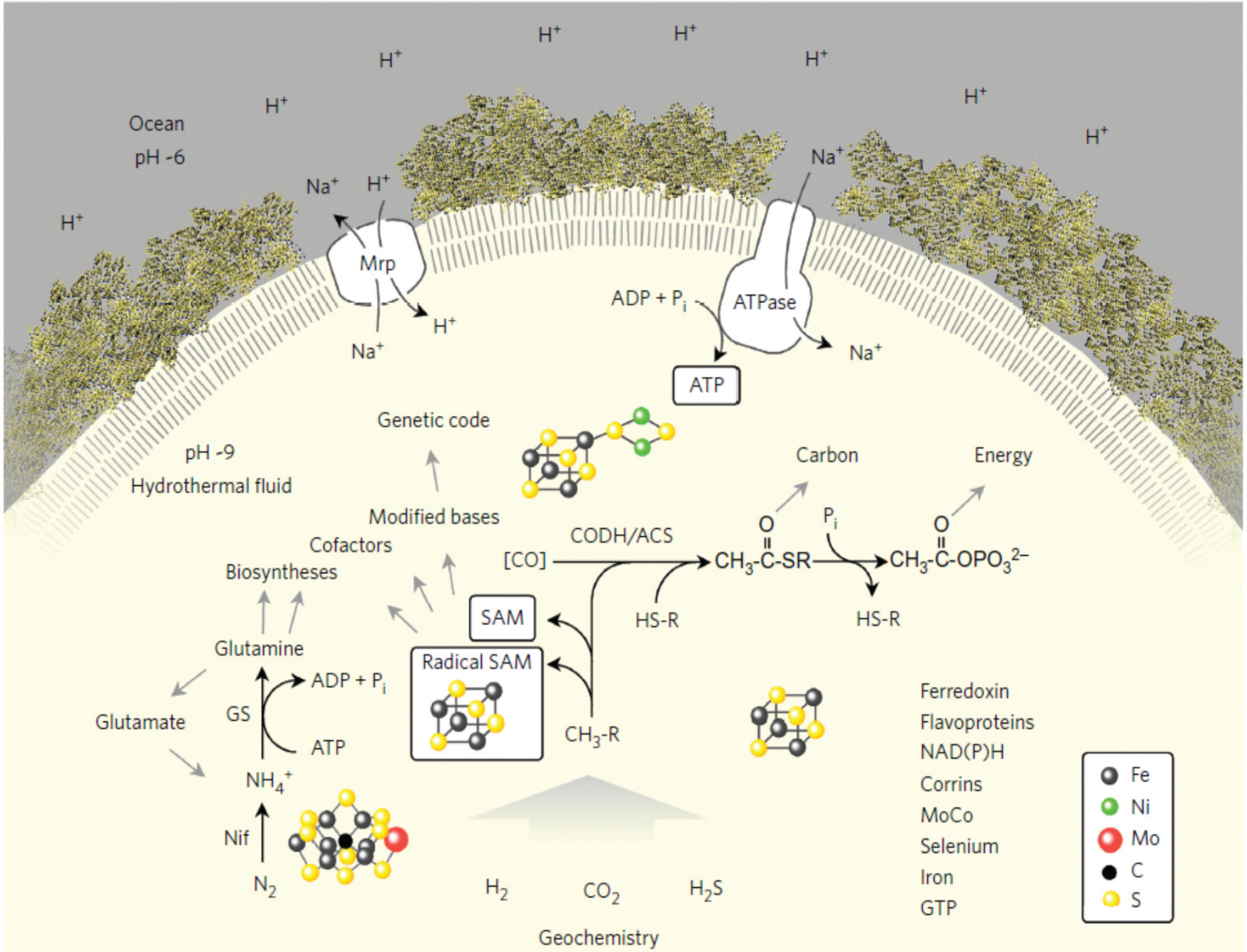
FeMo cofactor of nitrogenase



SAM-binding riboswitches



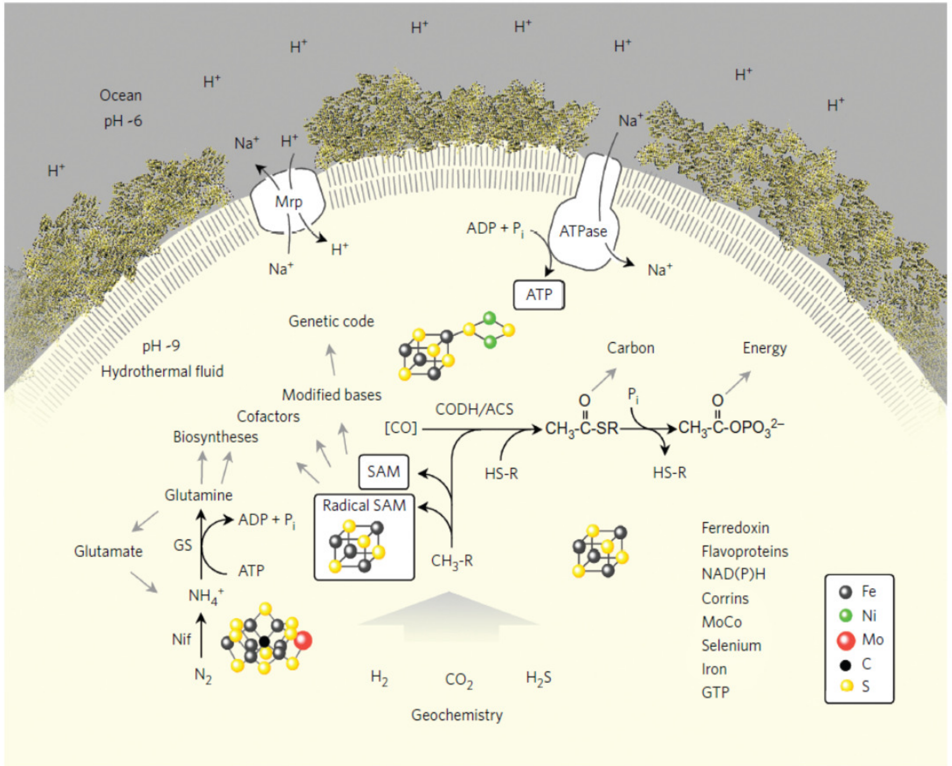
M.C. Weiss et al. *Nature Microbiology,* **2016**, *Article 16116*



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.

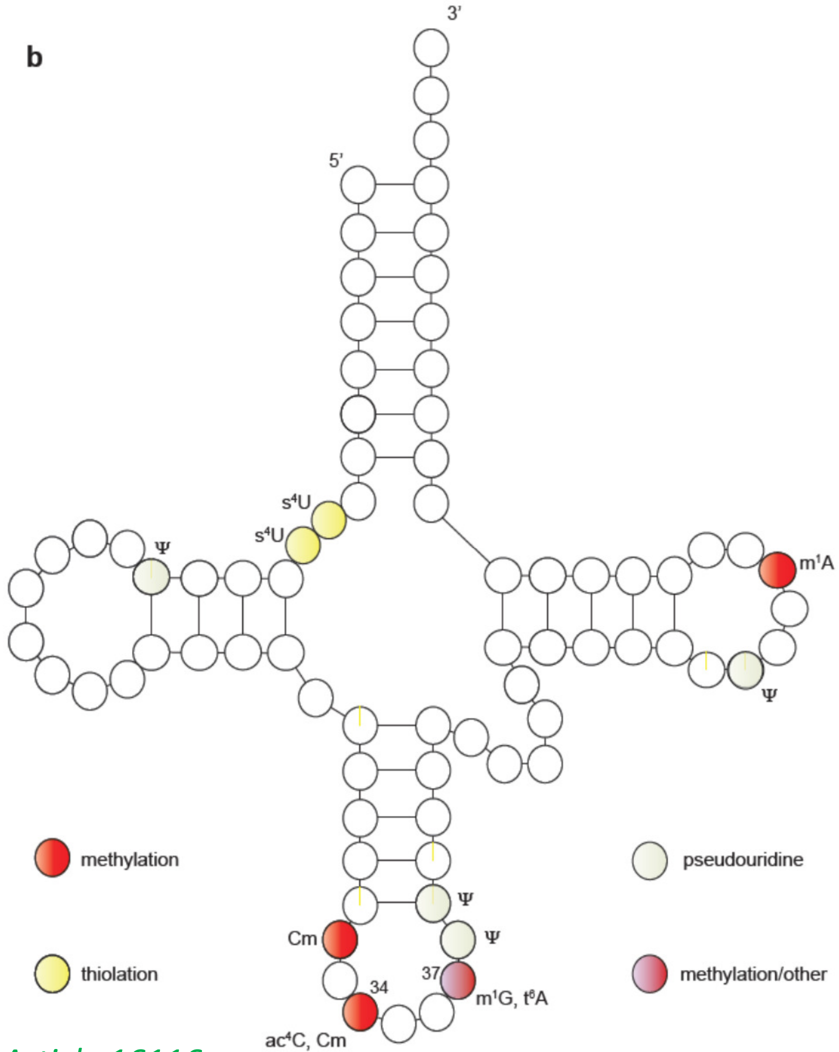


CO source unknown: In modern CODH/ACS complexes, CO is generated from CO_2 and reduced ferredoxin. In primordial metabolism, CO can appear uncatalysed *via* the gas water shift reaction or catalysed *via* transition metals.

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

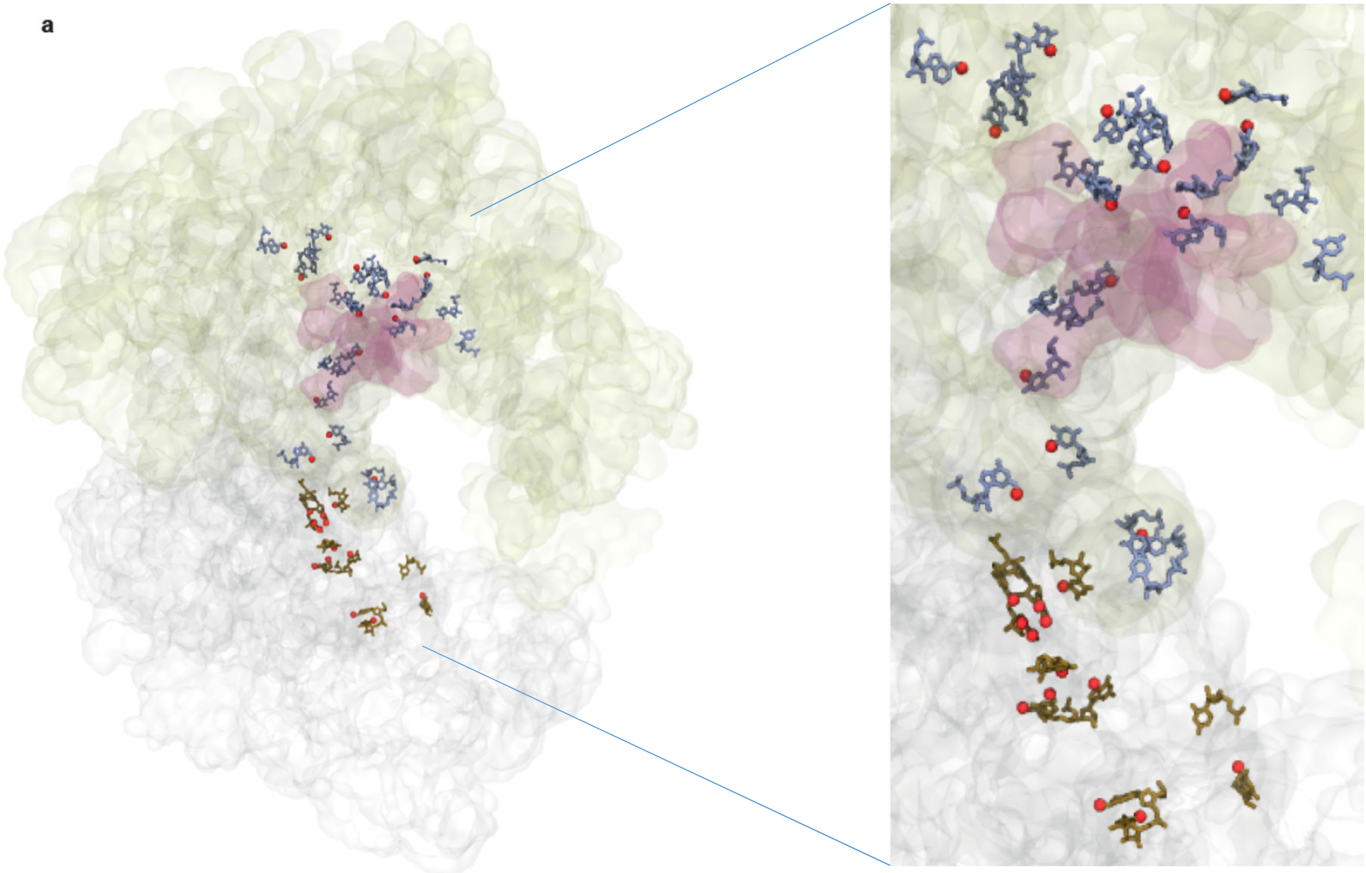
LUCA had also genes involved in RNA nucleoside modifications (mainly methylations and thiomethylations) still required today e.g. for the anticodon recognition process.



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*

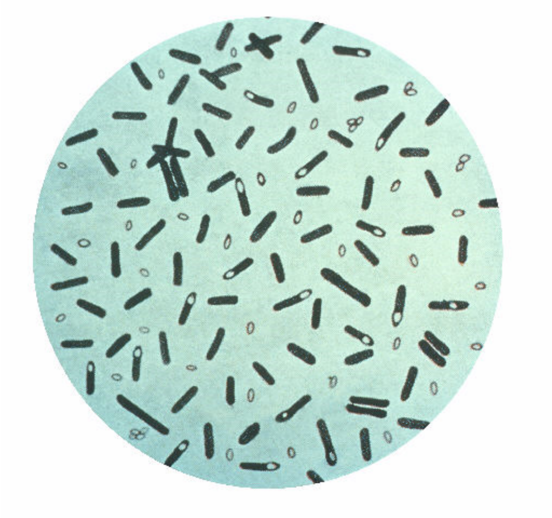
Modified nucleosides and the genetic code



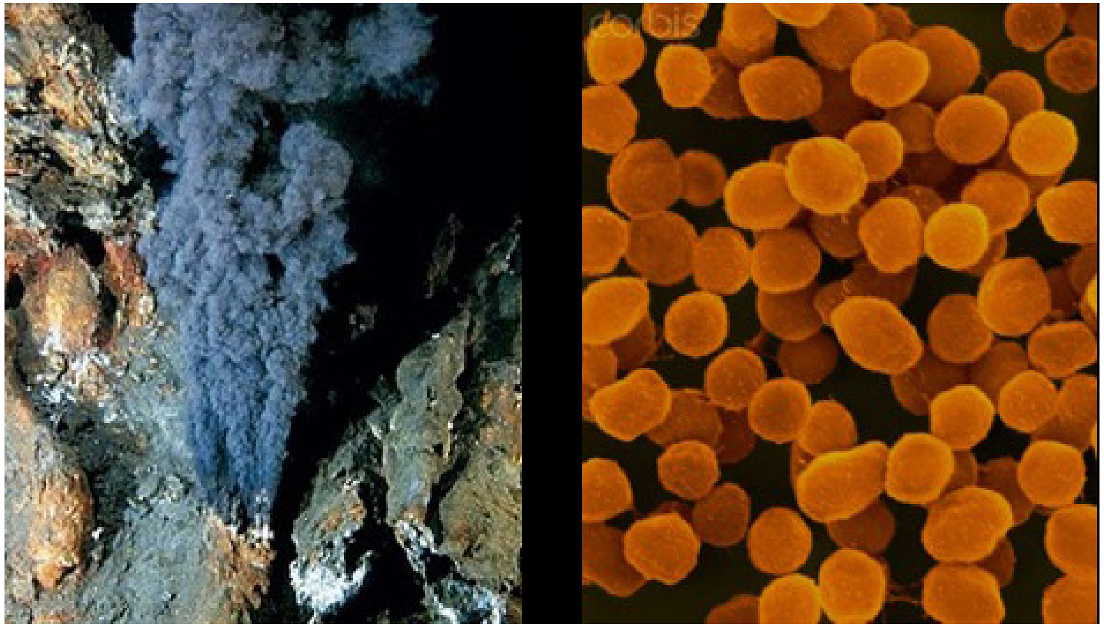
M.C. Weiss et al. *Nature Microbiology,* **2016**, *Article 16116*

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)

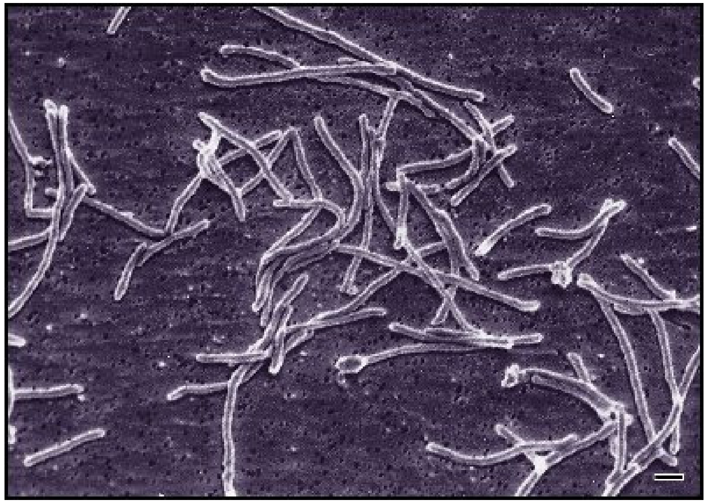


Deep ocean vent - home to the extremophilic archeon
Methanococcus jannaschii

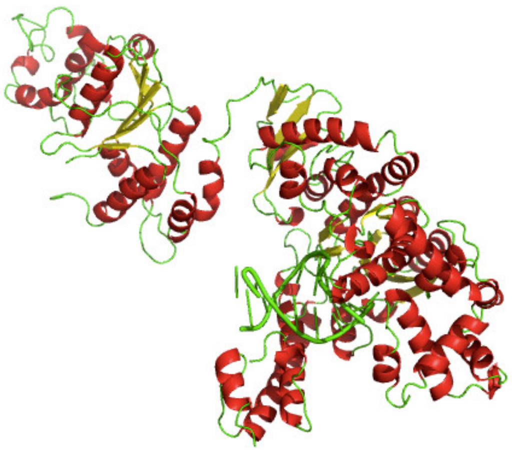
They use the WL pathway, abundant also today, some species can live from methyl groups (methane gas on marshes andwetlands), and they depend on H_2 (from geology or H_2-producing fermentation)

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

Thermophiles



Thermus aquaticus

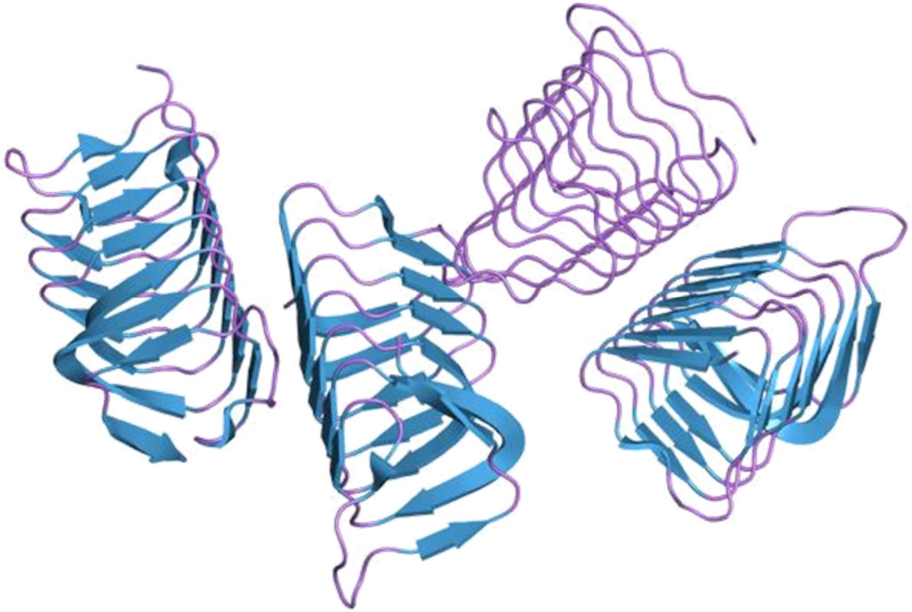


3D structure of Taq Polymerase.

Hot springs with algae and bacteria in Yellowstone National Park

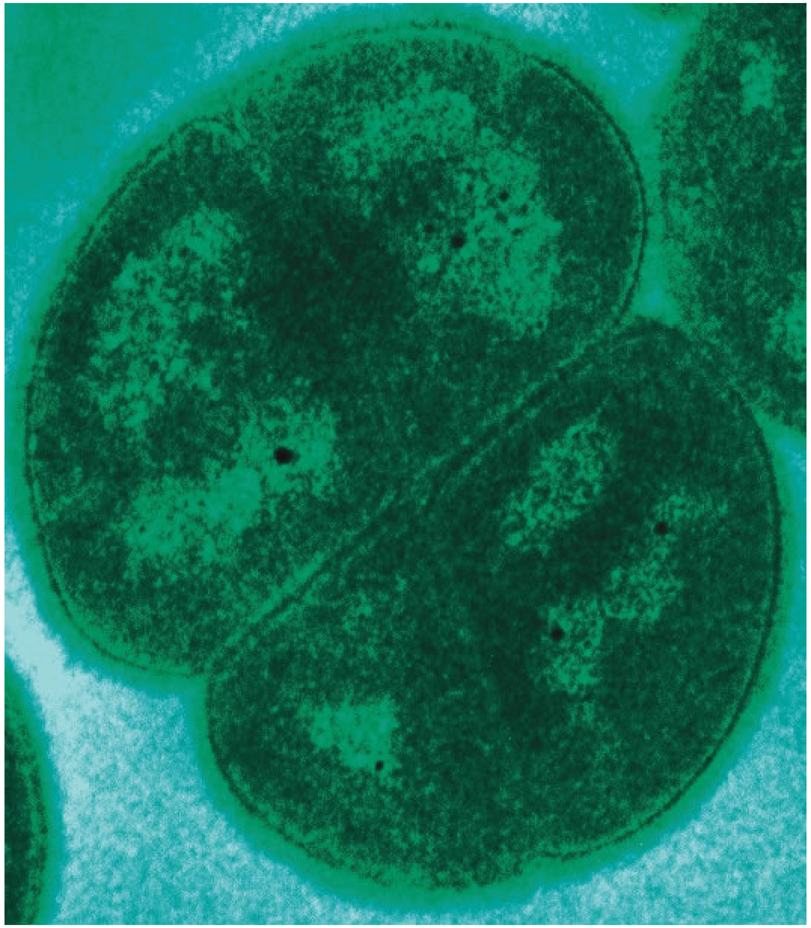
Cold adaptation

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



Structure of *Choristoneura fumiferana* (spruce budworm) beta-helical antifreeze protein

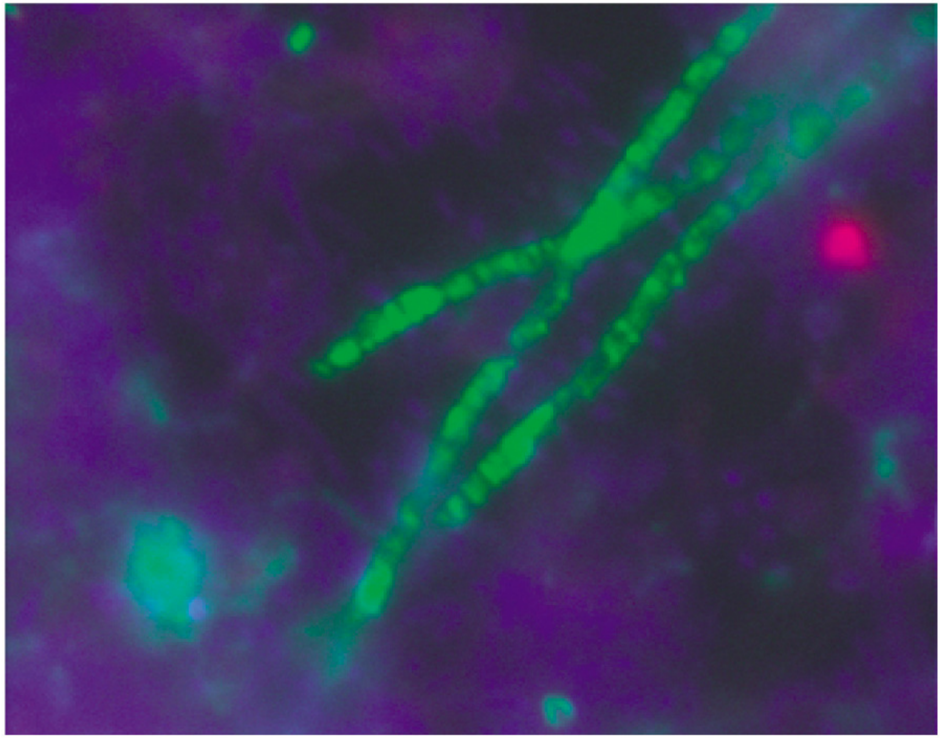
Drought, salinity, radiation



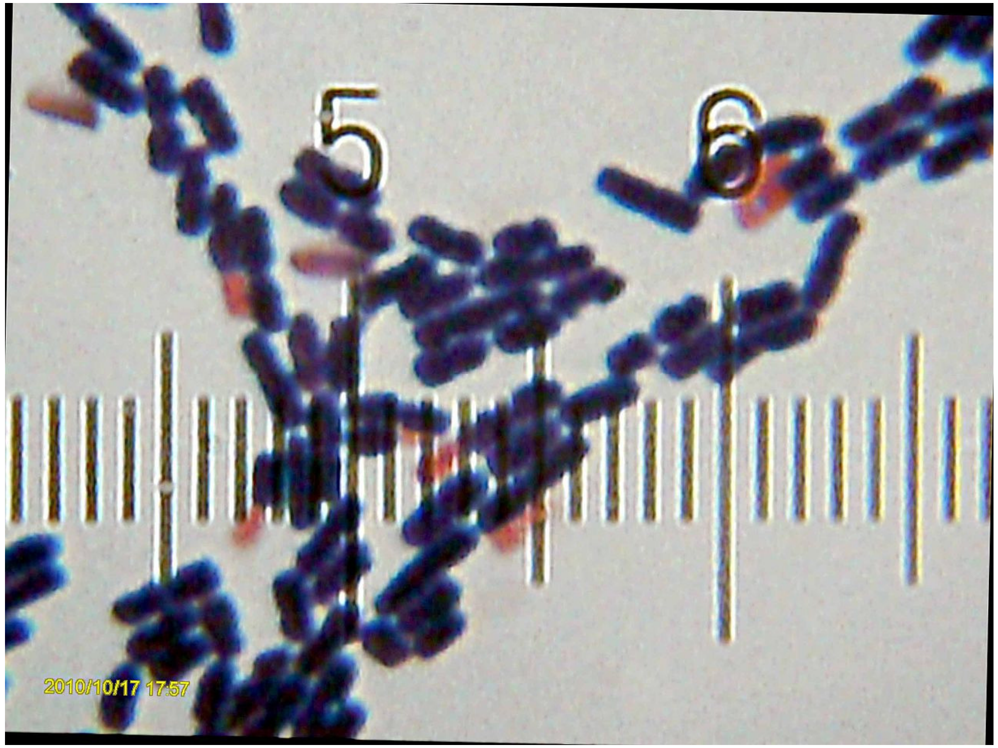
A tetrad of D. *radiodurans*

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

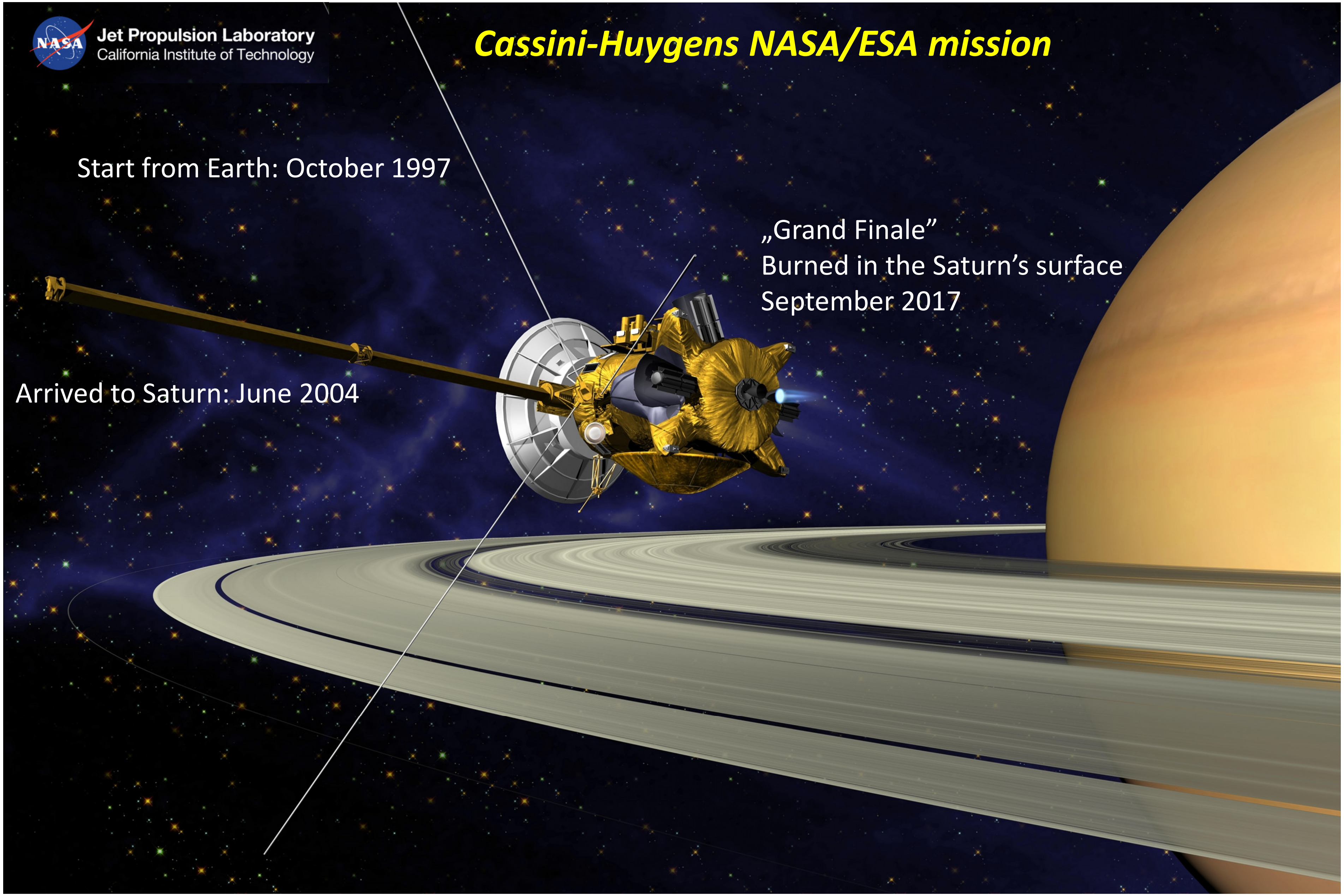
Acid, base

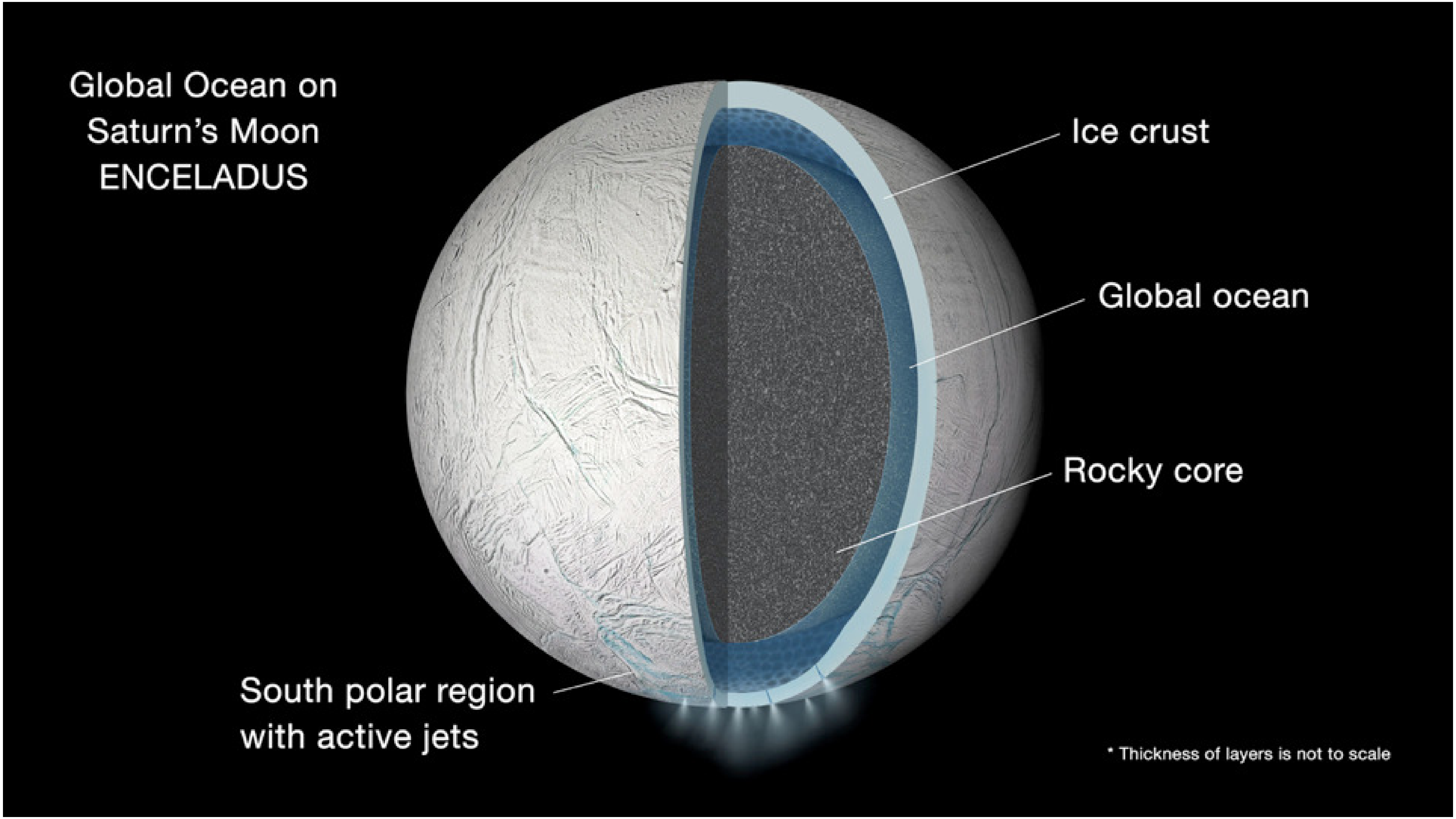


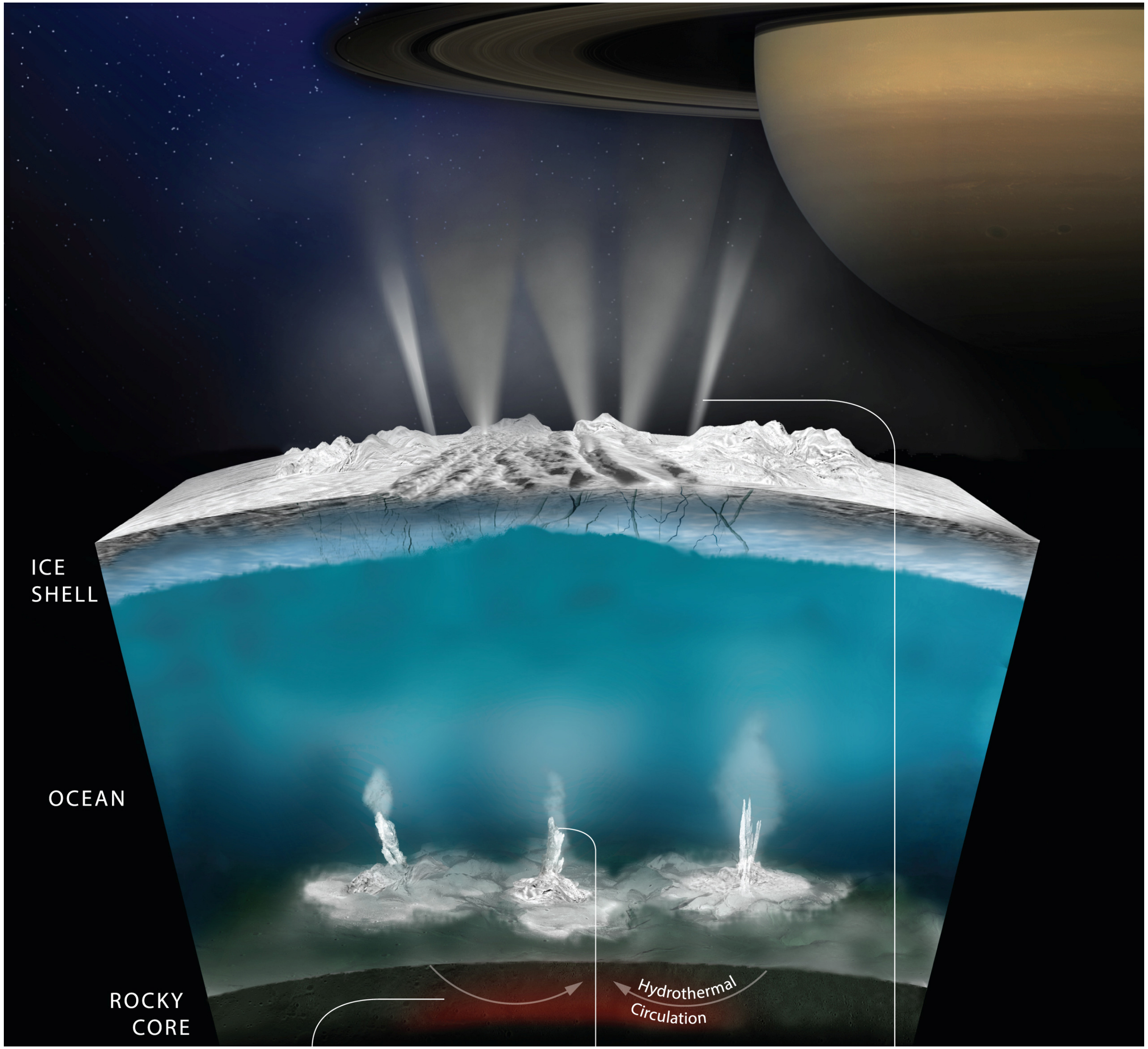
Acidobacterium

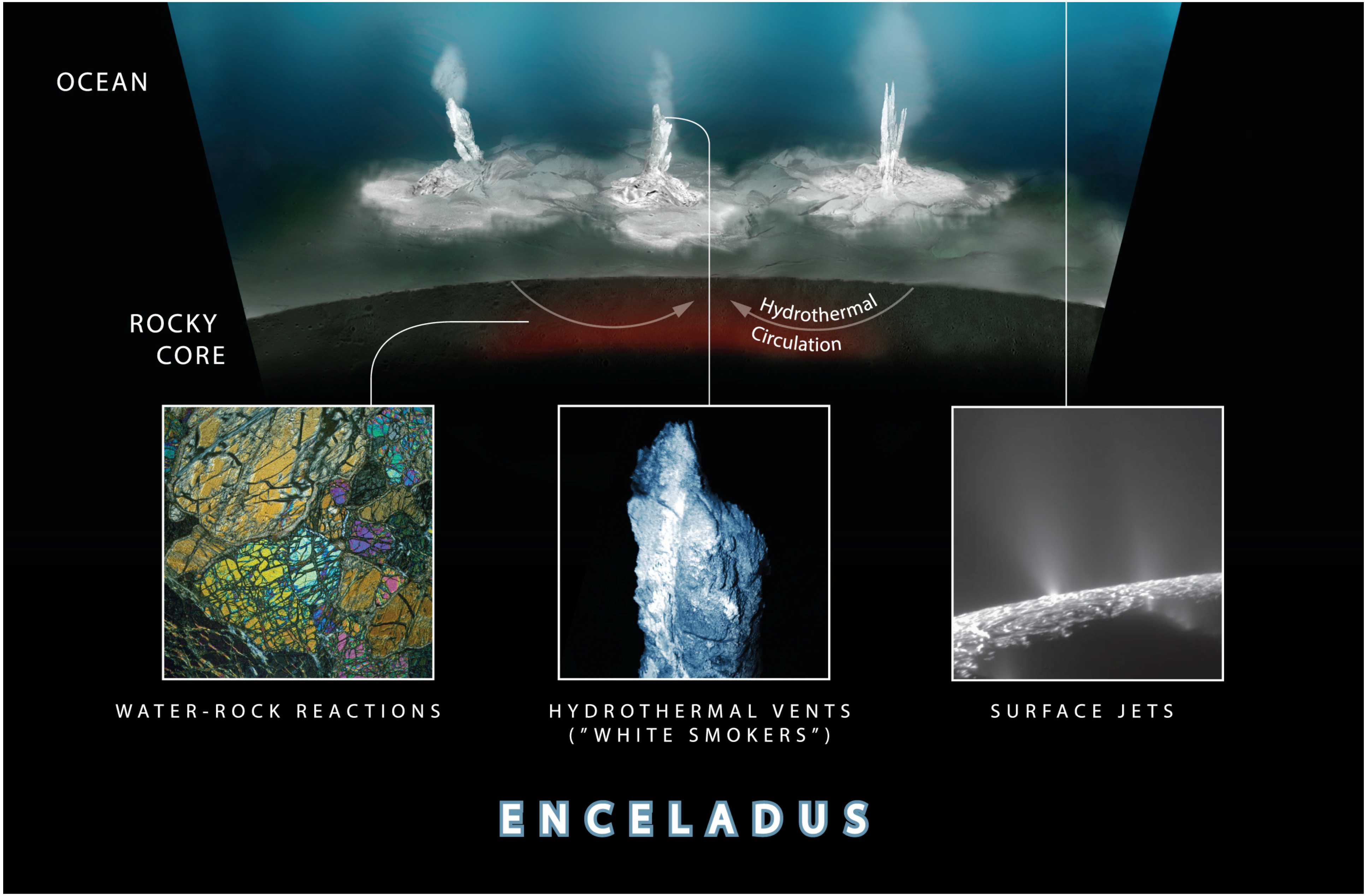


A typical *bacillus* culture. Many alkaliphiles possess a *bacillus* morphology

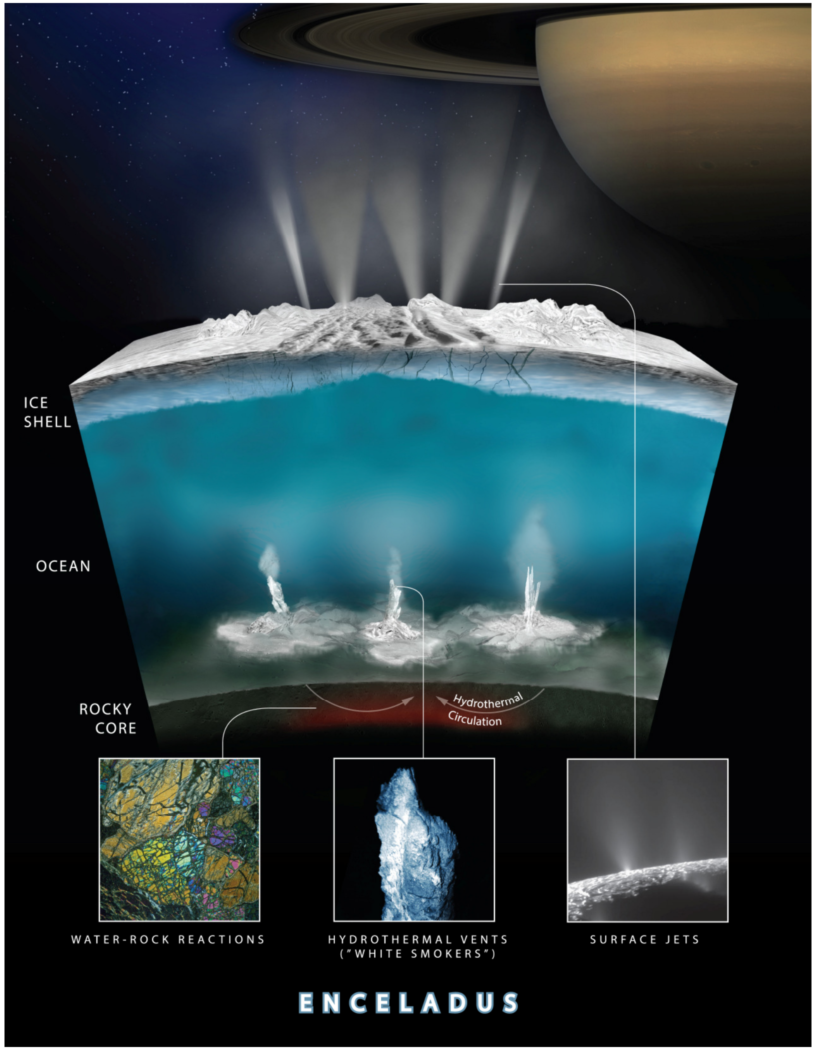

Jet Propulsion Laboratory
California Institute of Technology
Cassini-Huygens NASA/ESA mission
Start from Earth: October 1997
„Grand Finale"
Burned in the Saturn's surface
September 2017
Arrived to Saturn: June 2004

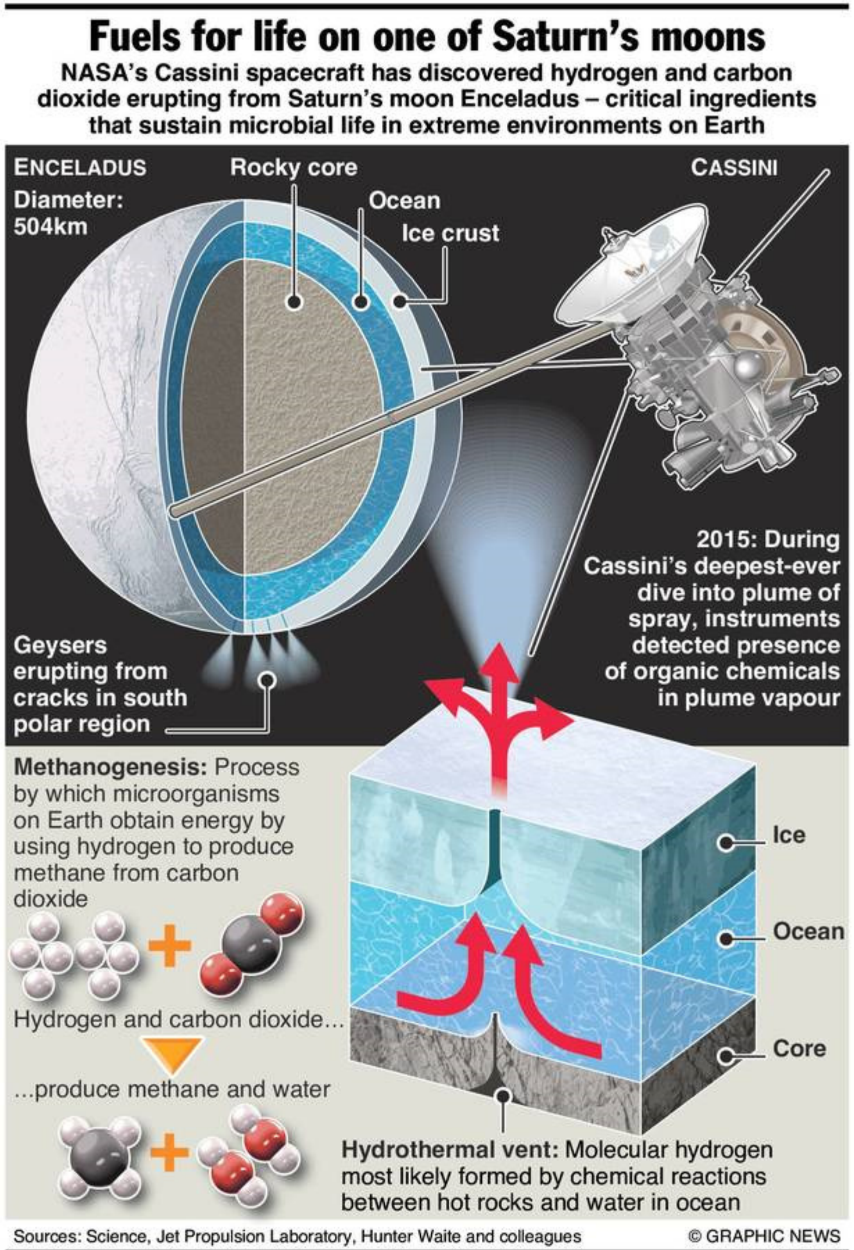

Global Ocean on Saturn's Moon ENCELADUS
Ice crust
Global ocean
Rocky core
South polar region with active jets
* Thickness of layers is not to scale


ICE
SHELL
OCEAN
ROCKY
CORE
Hydrothermal
Circulation


OCEAN
ROCKY CORE
Hydrothermal Circulation
WATER-ROCK REACTIONS
HYDROTHERMAL VENTS ("WHITE SMOKERS")
SURFACE JETS
ENCELADUS

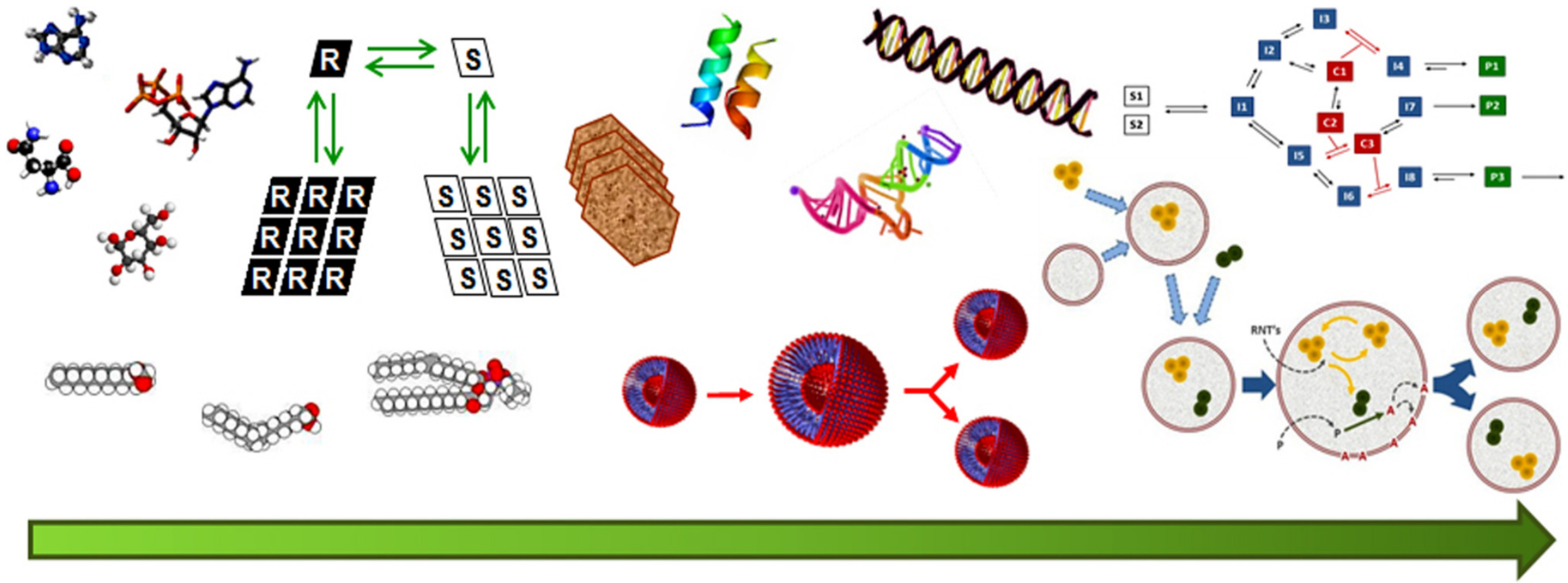
Can (and does?) Enceladus host (microbial) life?





The molecular origins of life – important stages

biomolecules – biopolymers – self-replication – metabolism - compartmentalization



Increasing complexity from molecules to systems