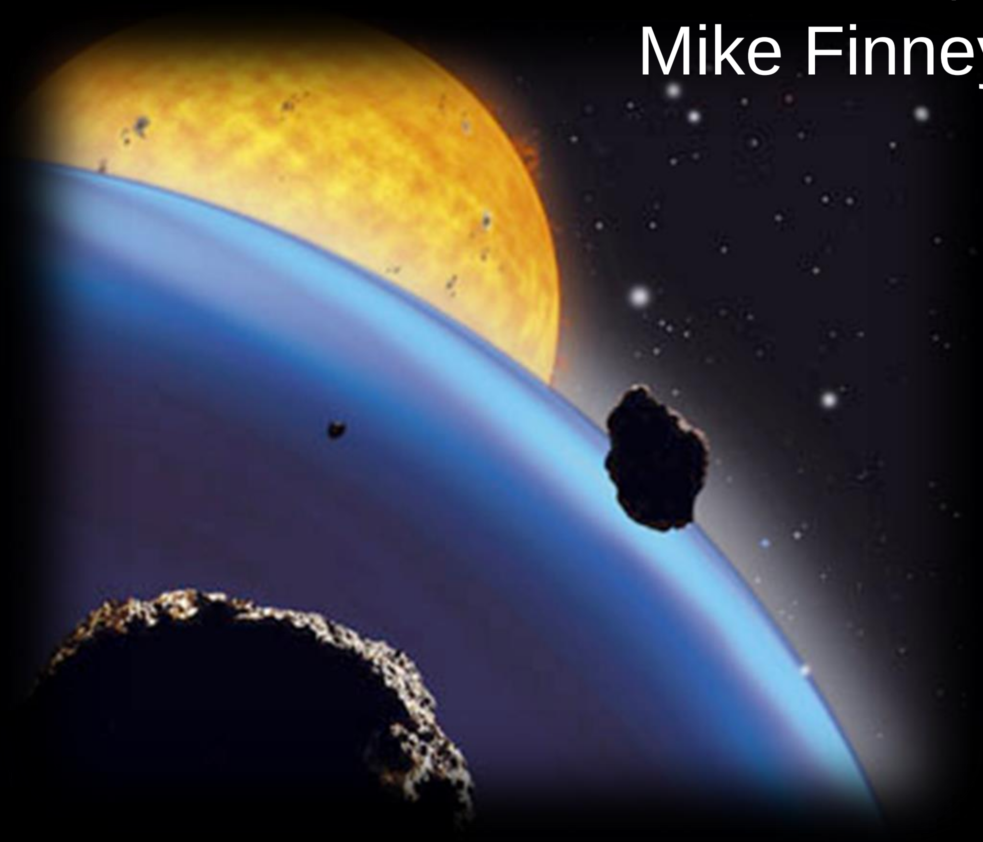
Looking for life as we know it on other planets

Chris Carr, Angel Mojarro, Julie Hachey, Mike Finney, Maria Zuber, Gary Ruvkun



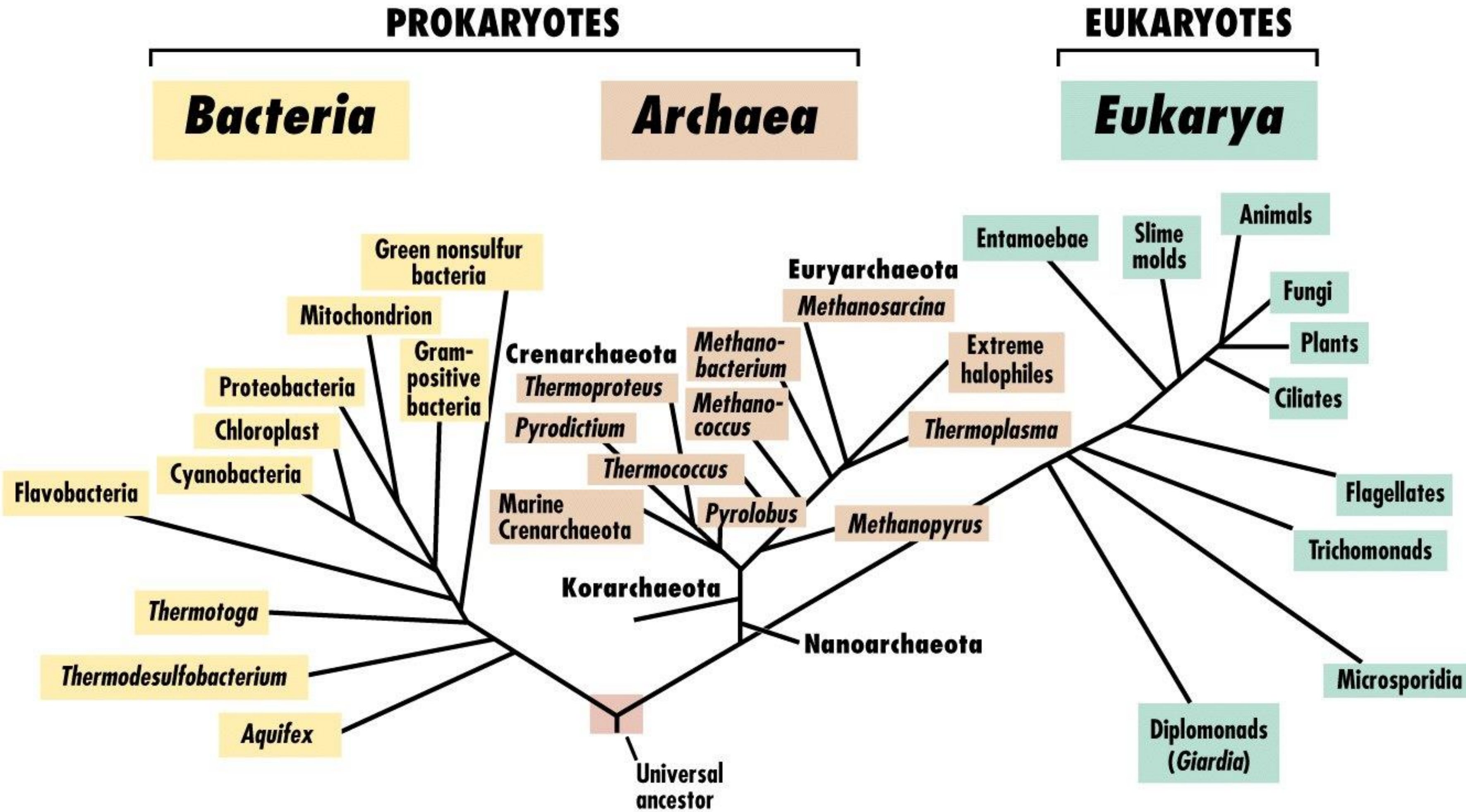


Figure 11-16 Brock Biology of Microorganisms 11/e

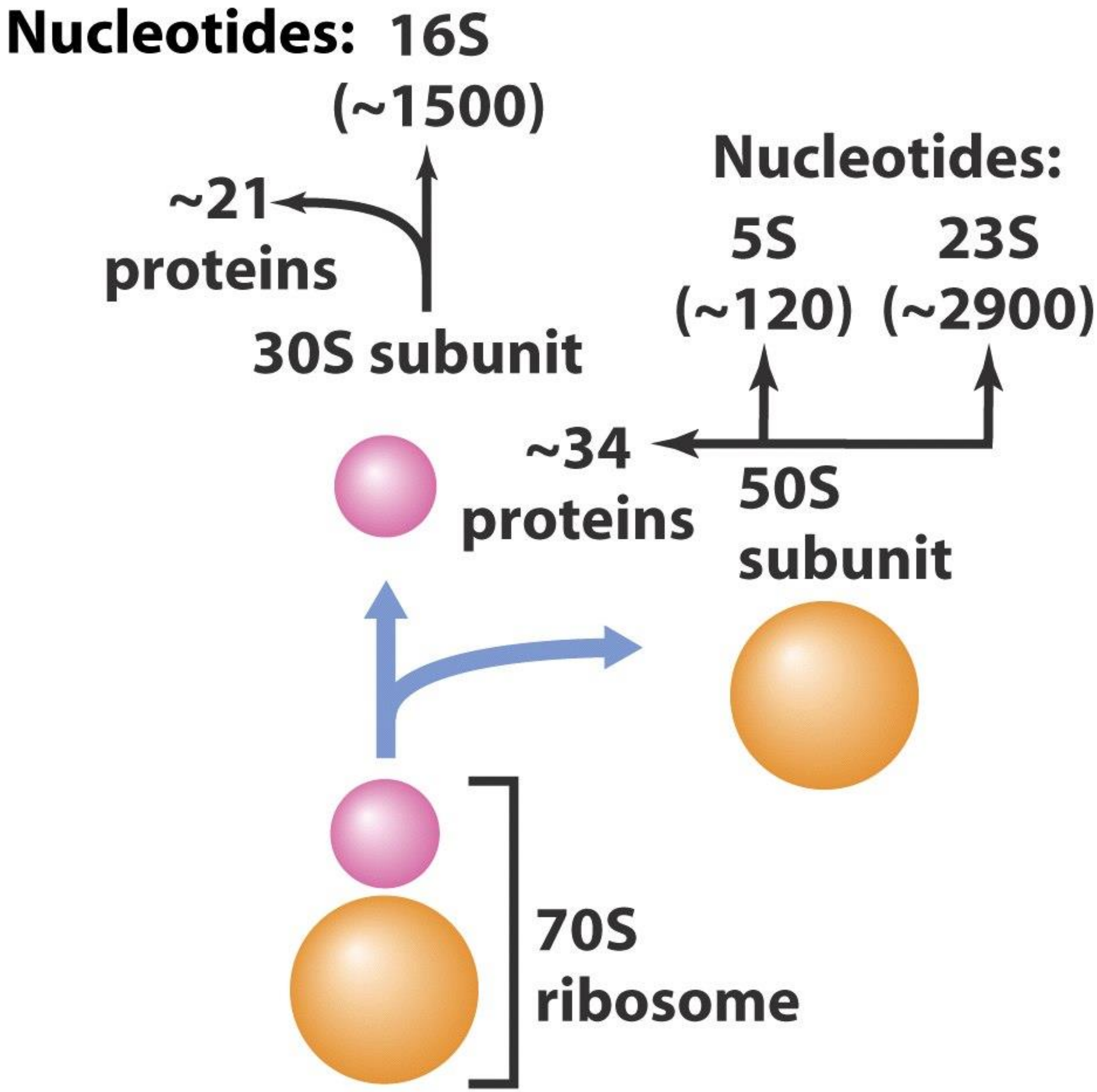


Figure 11-11b Brock Biology of Microorganisms 11/e

Query Human 18S rRNA to worm rDNA , both are animals

Score	Expect	Identities	Gaps	Strand
861 bits(954)	0.0	745/916(81%)	22/916(2%)	Plus/Plus

```
Query  798   GTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCCGAGCCGCCTGGATACCGCAGCT  857
             |||||| ||||| |||| |||||| ||||  || || |  ||    || ||| | || | 
Sbjct  1649  GTTTACCTTGAATAAATCAGAGTGCTCAATACAAGCGCTTGCT---TGAATAGCTCATCA  1705

Query  858   AGGAATAATGGAATAGGACCGCGGTTCTATTTTGTTGGTTTTCGGAACTGAGGCCATGAT  917
              ||||||||| || |||||  ||||||| |||||||||||| | | ||||||    ||| |
Sbjct  1706  TGGAATAATGAAACAGGACTTCGGTTCT-TTTTGTTGGTTCTAG-AACTGATTTAATGGT  1763

Query  918   TAAGAGGACGG-CCGGGGGCATTCGTATTGCGCCGCTAGAGGTGAAATTCTTGGACCGG  976
             |||||||||   ||||||||||||||||     ||| ||||||||||||| ||||||| 
Sbjct  1764  TAAGAGGACAAACCGGGGGCATTCGTATCATTACGCGAGAGGTGAAATTCGTGGACCGT  1823

Query  977   CGCAAGACGGACCAGAGCGAAAGCATTTGCCAAGAATGTTTTCATTAATCAAGAACGAAA  1036
              |  |||||  | | |||||||||||||||||||||| ||||||||||||||||||||
Sbjct  1824  AGTGAGACGCCCAACAGCGAAAGCATTTGCCAAGAATGTCTTCATTAATCAAGAACGAAA  1883

Query  1037  GTCGGAGGTTCGAAGACGATCAGATACCGTCGTAGTTCCGACCATAAACGATGCCGACCG  1096
             ||| ||||||||||| |||| |||||||| | |||||| |||| ||||||||||||  |  
Sbjct  1884  GTCAGAGGTTCGAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTC  1943

Query  1097  GCGATGCGGCGGCGTTATTCCCATGACCCGCCGGGCAGCTTCCGGAAACCAAAGTCTTT  1156
             ||||| ||| || ||| || || ||     ||| | ||||  | |||||| |||||||||
Sbjct  1944  GCGATTCGGAGG-GTTTTTGCCCTG-----CCGAGGAGCTATCCGGAAACGAAAGTCTTT  1997

Query  1157  GGGTTCCGGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACC  1216
              ||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  1998  CGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACC  2057

Query  1217  ACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCCGGCCCGGA  1276
             || ||| ||||||| ||||||||||||||||||||||||||||| ||||||||| |||||
Sbjct  2058  ACAAGGCGTGGAGCTTGCGGCTTAATTTGACTCAACACGGGAAAACTCACCCGGTCCGGA  2117

Query  1277  CACGGACAGGATTGACAGATTGATAGCTCTTTCTCGATTCCGTGGGTGGTGGTGCATGGC  1336
             |||    |||| |||||||||| |||||||||||||  |||| ||||||||||||||
```

Human 18S rRNA query to Archaea Pyrococcus furiosus16S ribosomal RNA gene

```
Score                 Expect     Identities    Gaps        Strand
104 bits(114)     3e-22      86/105(82%)     0/105(0%)   Plus/Plus
Query  1166  GGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGT
1225
             ||||||| ||  |||| |||||||||||||||||||| |||  | |||| || ||| ||
Sbjct  844   GGGGAGTACGGCCGCAAGGCTGAAACTTAAAGGAATTGGCGGGGAGCACTACAAGGGGT  903

Query  1226  GGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCCGG  1270
             ||||| ||||| |||||| || ||||| | || ||||||||| ||
Sbjct  904   GGAGCGTGCGGTTTAATTGGATTCAACGCCGGGAACCTCACCGGG  948
```

```
Score      Expect     Identities    Gaps Strand
59.0 bits(64)     1e-0882/115(71%)     0/115(0%)  Plus/Plus
Query  1605  GGATCGGGGATTGCAATTATTCCCCATGAACGAGGAATTCCCAGTAAGTGCGGGTCATAA  1664
             |||||| ||  ||||| |   || | ||||   ||||| || ||||   ||| ||||| |
Sbjct  1266  GGATCGCGGGCTGCAACTCGCCCGCGTGAAGCTGGAATCCCTAGTACCCGCGTGTCATCA  1325

Query  1665  GCTTGCGTTGATTAAGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGA  1719
              |  |||  || || |||||||| | ||| |||||||||||||| || |  ||||
Sbjct  1326  TCGCGCGGCGAATACGTCCCTGCTCCTTGCACACACCGCCCGTCACTCCACCCGA  1380
```

```
Score      Expect     Identities    Gaps Strand
46.4 bits(50)     8e-0536/43(84%)     0/43(0%)    Plus/Plus
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             |||||||||||||||  ||||||| |||||| |||   |||||
Sbjct  1449  AAGTCGTAACAAGGTAGCCGTAGGGGAACCTACGGCTCGATCA  1491
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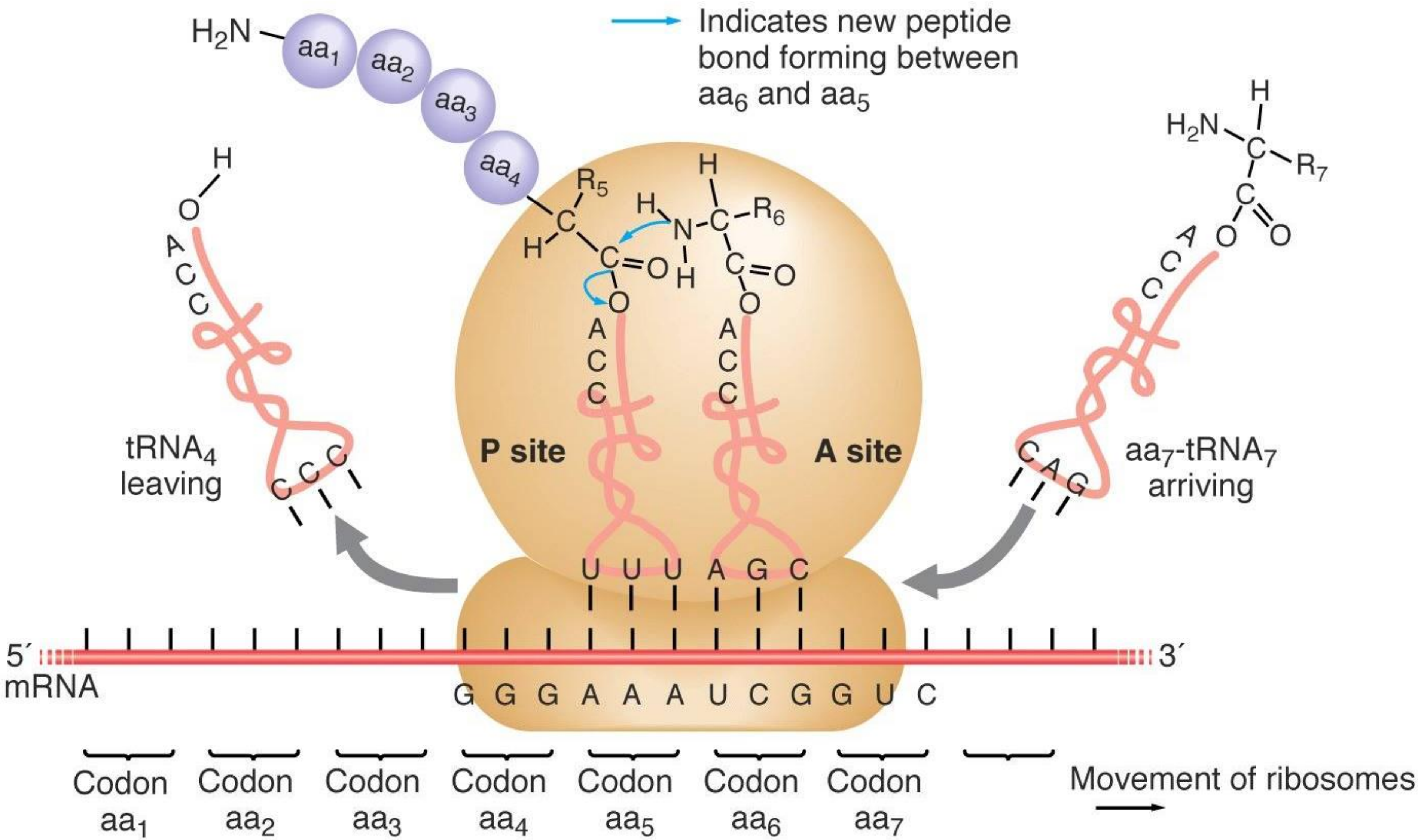
```
Score      Expect     Identities    Gaps Strand
41.0 bits(44)     0.00331/37(84%)     0/37(0%)    Plus/Plus
Query  600  GGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGC  636
            ||||||| | |||| |||| ||||||||||| || ||
```

Ribosomal RNA is the catalytic center of translation by the ribosome



Early genomics:

Early 70s: abundant, easy to purify ribosomal RNAs sequenced
1973 Recombinant DNA allows genes to be purified
1976 Gene sequencing invented (a paper might include 3000 base pairs of DNA sequences
1997 First full animal genome (nematode 10^8 bp)
2001 Human genome (3 x 10^9 bp)

Today

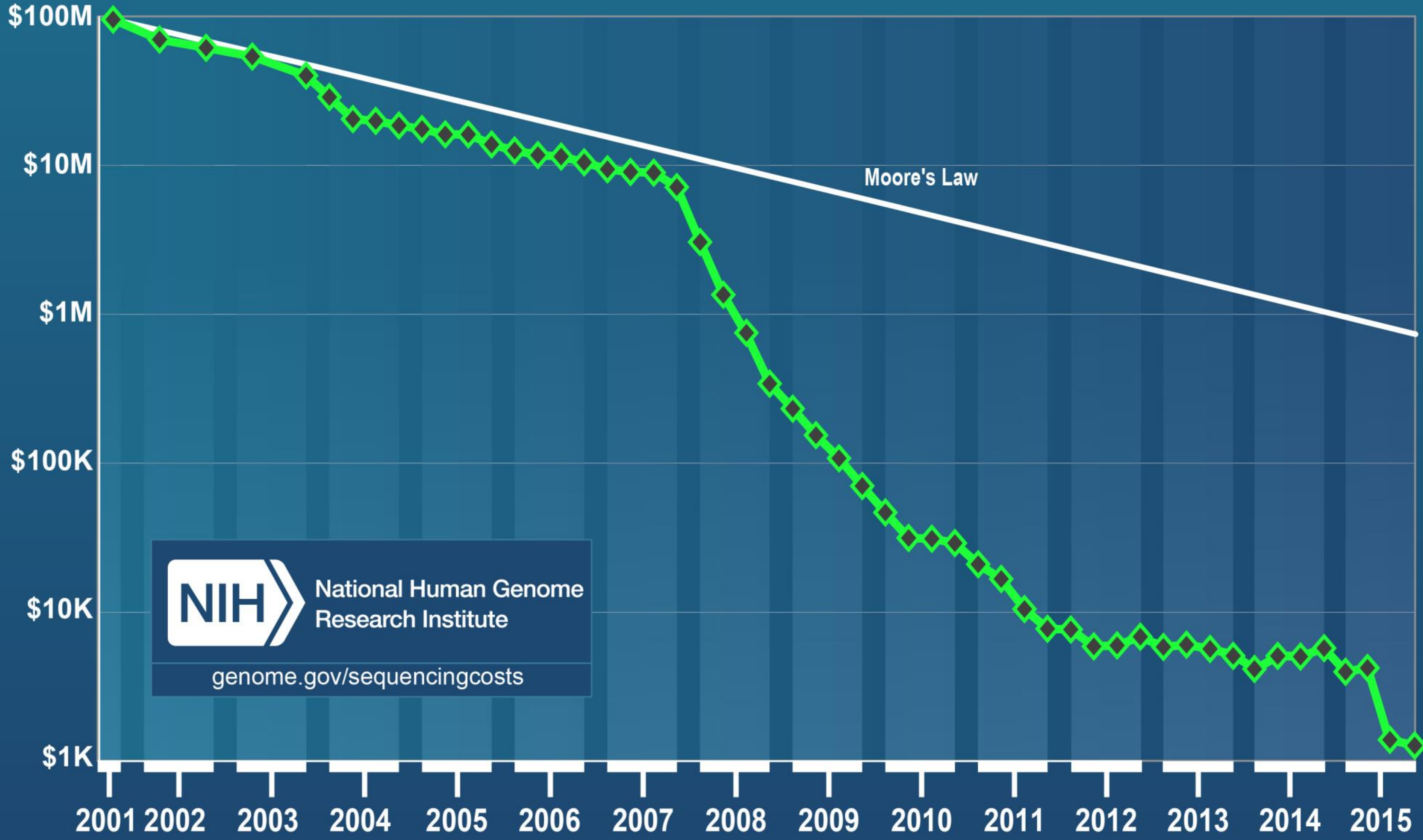
Genome sequences Nov 30 2016

Eukaryotes [3457 assembled genomes, ranging from $5x10^6$ bp to 10^{10} bp, from ameoba to mushrooms to redwood trees to humans]

Bacteria and Archaea [12364 bacterial assembled genomes, each about $4x10^6$ base pairs; 675 archaeal]

Ruvkun lab (a rather typical genomics lab) routinely does hundreds of full animal genome sequences per year (10^{11} bp/year) to find new mutations after genetic analysis, for about $100 per genome). On an Illumina machine installed in the department.

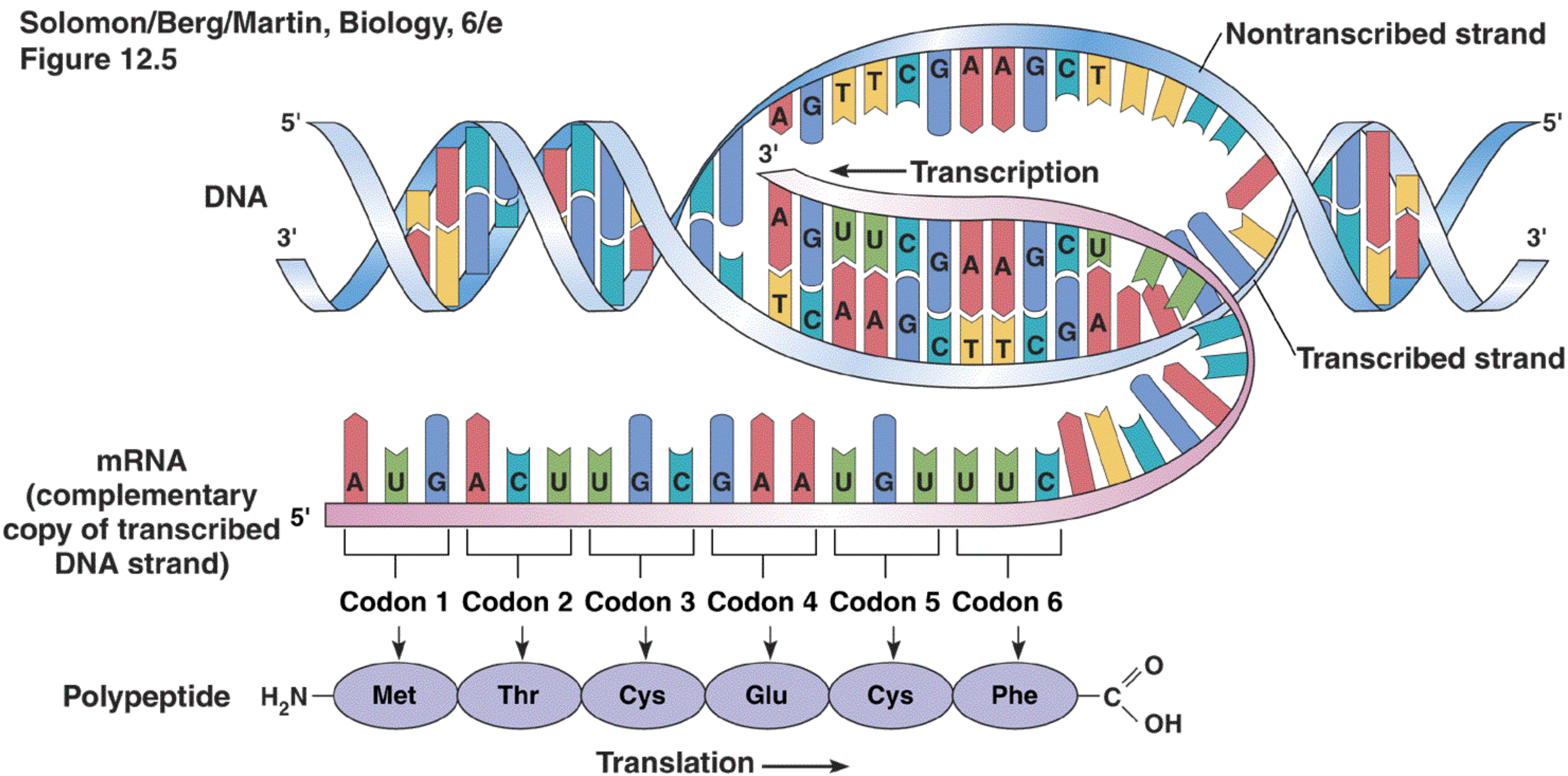
Cost per Genome



- Illumina machines are the largest share of genomics production. 7500 machines in the world (5000 in the US).
- e.g., HiSeq 4000, 498 pounds, 1500W, 400 Gigabases per day.
- ILMN market cap = $24 billion, 4600 employees

- Oxford Nanopore
- MinIon introduced in 2015. Over 1000 users so far.
- Up to 40 Gigabases per day from an 87 gram instrument.
- 260 employees.

From 4 DNA letters to 20 amino acid letters



- **The typical animal genome 10^8 to 10^9 bp and has about 25,000 genes. Closely related animals have nearly identical sets of genes, but from worms to mammals, for example, about 10,000 genes are homologous.**

- **Average bacterial genome is 4×10^6 bp and about 4000 genes**

- **A few hundred of the 4000 genes in each bacteria are universal to all life: bacterial plant animal fungal protist archaea.**

Query is 435 amino acid RPT-1 protein from the animal C. elegans
Subject is from Hadesarchaea archaeon 403 amino acids

Score	Expect	Identities	Positives	Gaps
350 bits(899)	1e-116	168/320(53%)	226/320(70%)	0/320(0%)

```
Query  100  CTKIITSDKHDPRYLINVKQFAKFVVDLADSVAPTDIEEGMRVGVDRNKYQIHLPLPAKI  159
             T ++    D R ++      +FVV ++   +   D++ G+RV +++  + +   LP+K
Sbjct  70   ITAVLLETLEDGRAIVRSSAGPQFVVGVSKFIKEDDLKPGVRVALNQRTFTLVEILPSKK  129

Query  160  DPTVTMMQVEEKPDVTYSDVGGCKDQIEKLREVVETPLLHPERYVNLGIEPPKGVLLYGP  219
            DP V  M+VEE P+VTYSDVGG  +QI +++E VE PLL PE +  +GIEPPKGVLLYGP
Sbjct  130  DPLVLGMEVEEAPEVTYSDVGGLDEQIREIKEAVELPLLKPELFKKVGIEPPKGVLLYGP  189

Query  220  PGTGKTLCARAVANRTDACFIRVIGSELVQKYVGEGARMVRELFEMARTKKACLIFFDEI  279
            PGTGKTL ARAVA+ T A FIRVIGSELVQKY+GEGAR+VRE+FE AR K   ++F DEI
Sbjct  190  PGTGKTLLARAVAHETHASFIRVIGSELVQKYIGEGARLVREMFEFAREKAPSIVFIDEI  249

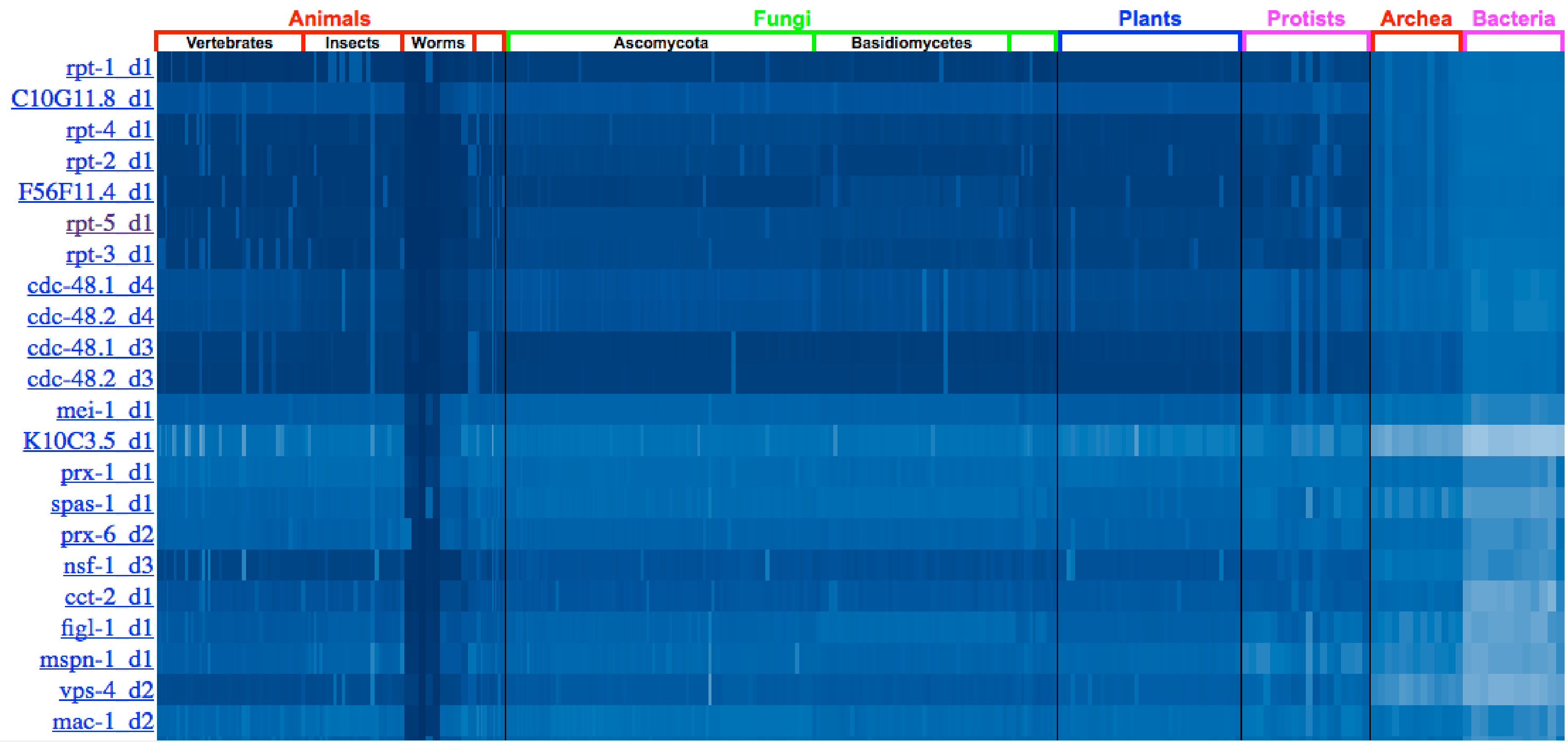
Query  280  DAVGGARFDDGQGGDNEVQRTMLELINQLDGFDPRGNIKVLMATNRPDTLDPALMRPGRL  339
            DA+G  R D    GD EV RT+++L+ ++DGF+PRG +++L ATNRPD LDPAL+RPGR
Sbjct  250  DAIGARRMDTSTSGDREVHRTLMQLLAEIDGFNPRGEVRILAATNRPDILDPALLRPGRF  309

Query  340  DRKVEFALPDLAGRAHILKIHAKQMSVERDIRYDLLARLCPNSTGAEIRSVCTEAGMFAI  399
            DR + F +PD   RA I KIH K+M++  D++ + LA    N+TGA+I+++CTEAGMFAI
Sbjct  310  DRLINFPMPDQKARAAIFKIHTKRMNLAEDVKIEELAAKTVNATGADIKAICTEAGMFAI  369

Query  400  RARRKVATEKDFLEAINKVV  419
            R  R+     DF  AI KV+
Sbjct  370  RGGREKVEVADFEMAIAKVL  389
```

Here is one of about 500 protein domains that are conserved across all of life.
How blue is a measure of the degree of conservation

Organism: Caenorhabditis Elegans, **Domain:** rpt-1_d1 , **Number of Genes:** 200



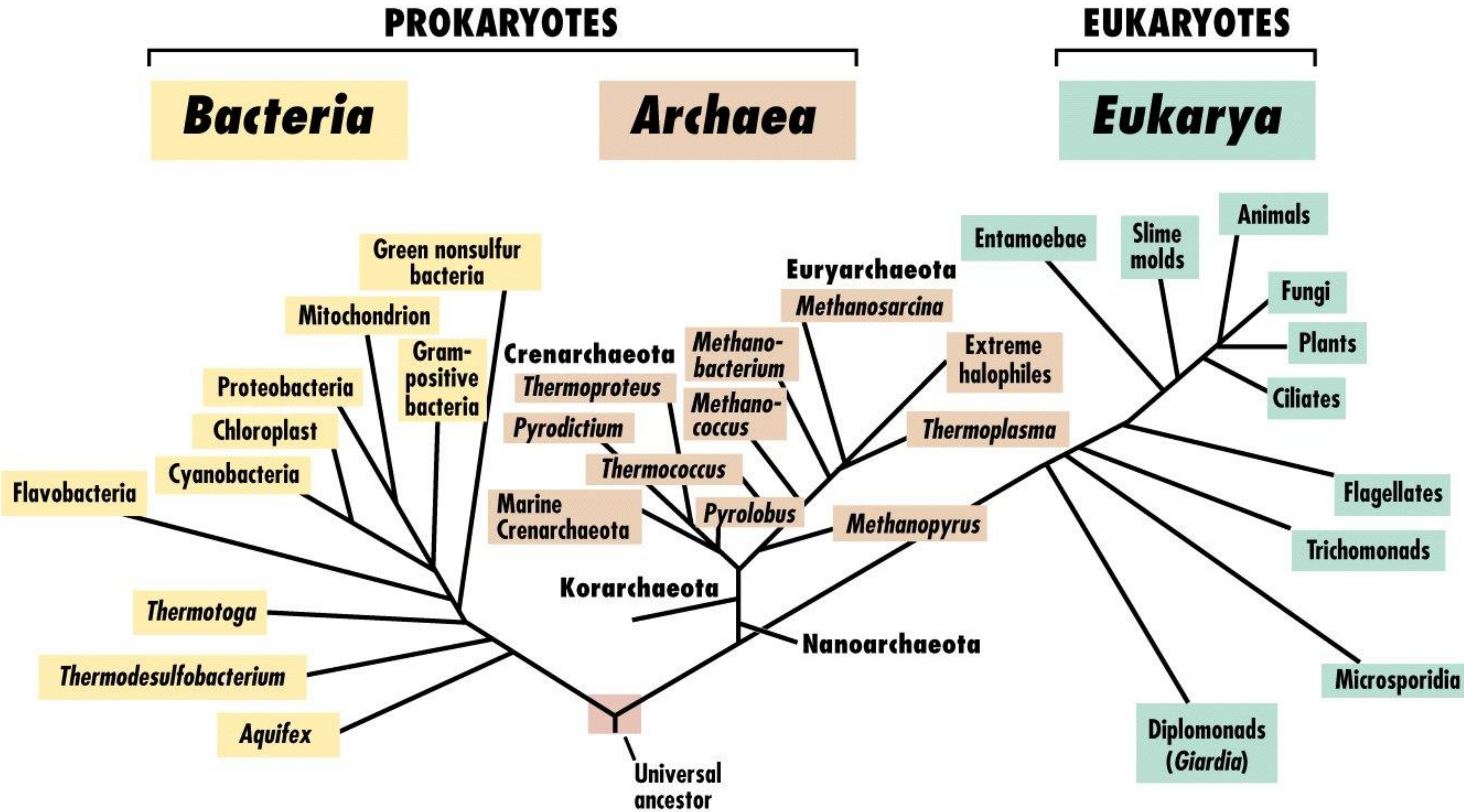


Figure 11-16 Brock Biology of Microorganisms 11/e

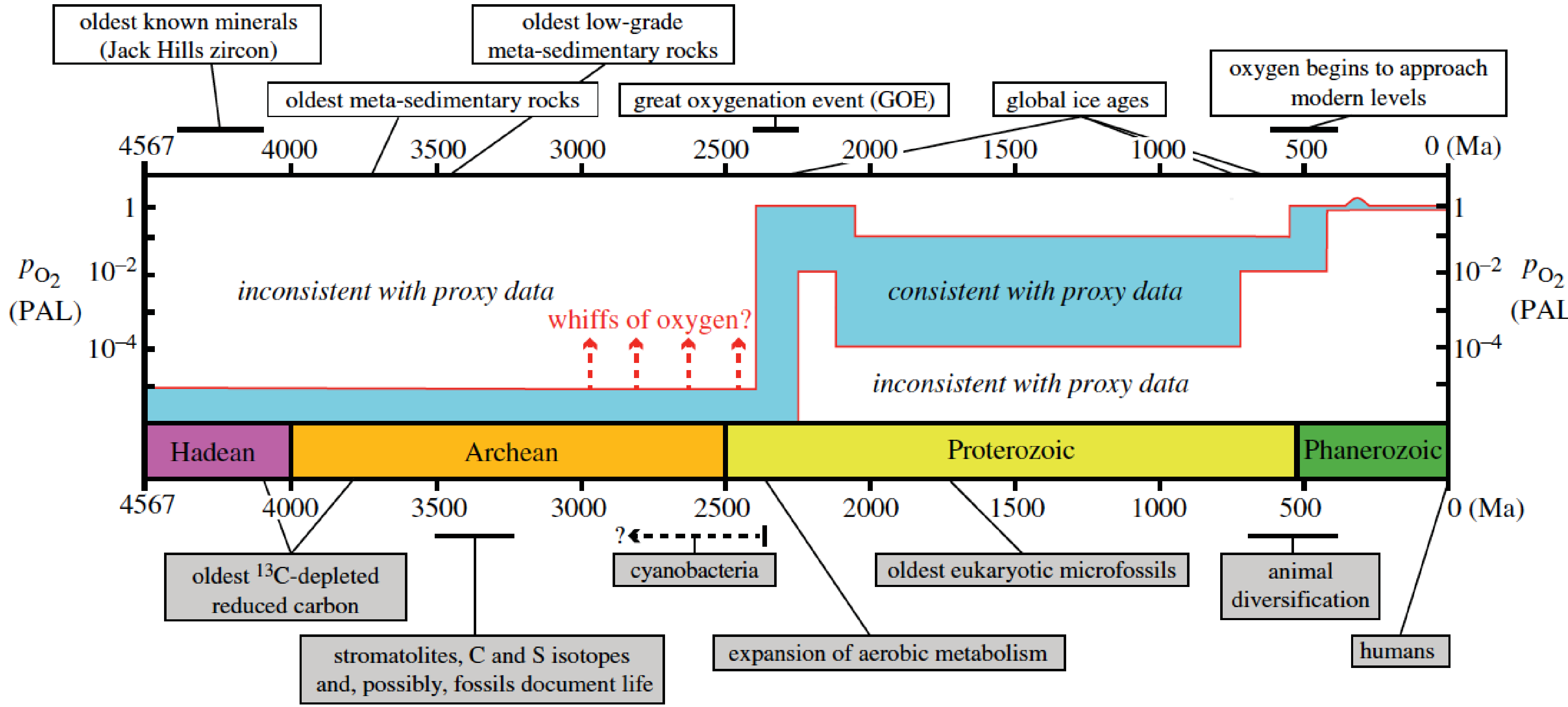


Figure 1. A time table for Earth's early history, showing the major eons (Hadean, Archean, Proterozoic and Phanerozoic), an estimate of atmospheric oxygen his
constructed from geochemical proxy data [1–3] and key environmental (above) and biological (below) events discussed in the text. Oxygen partial pressure in
cent of PAL. (Online version in colour.)

Another slide stolen off the Web,
from an Andy Knoll review (he is a buddy)

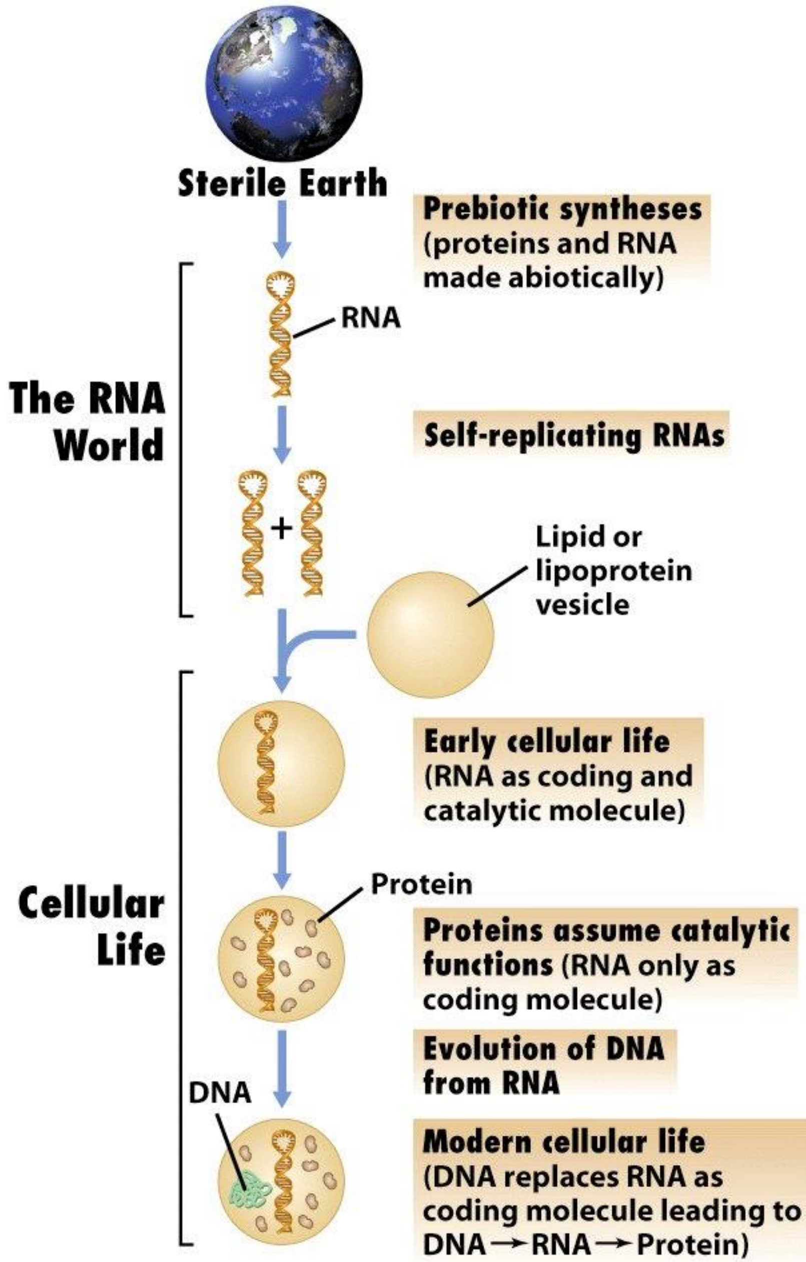
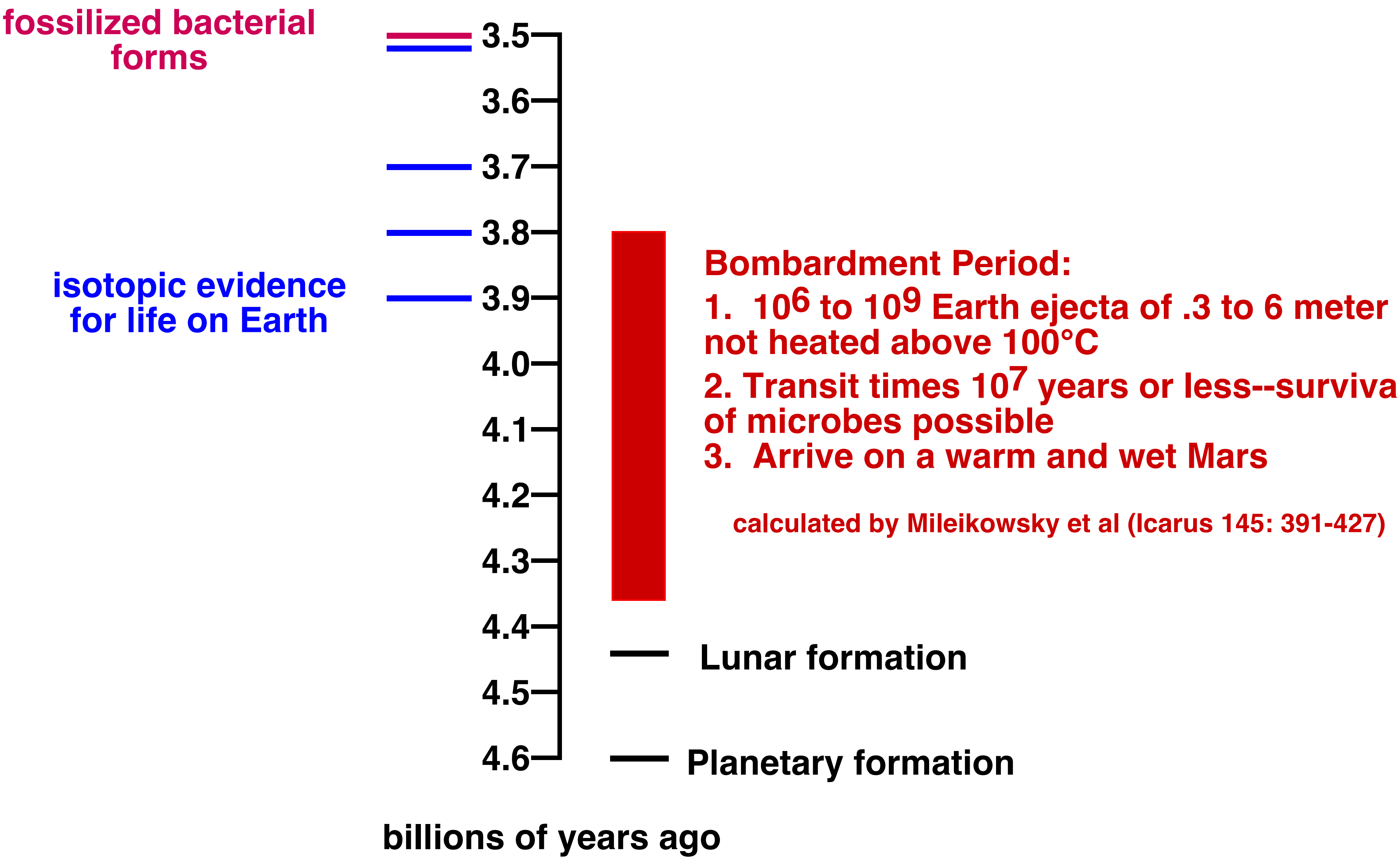
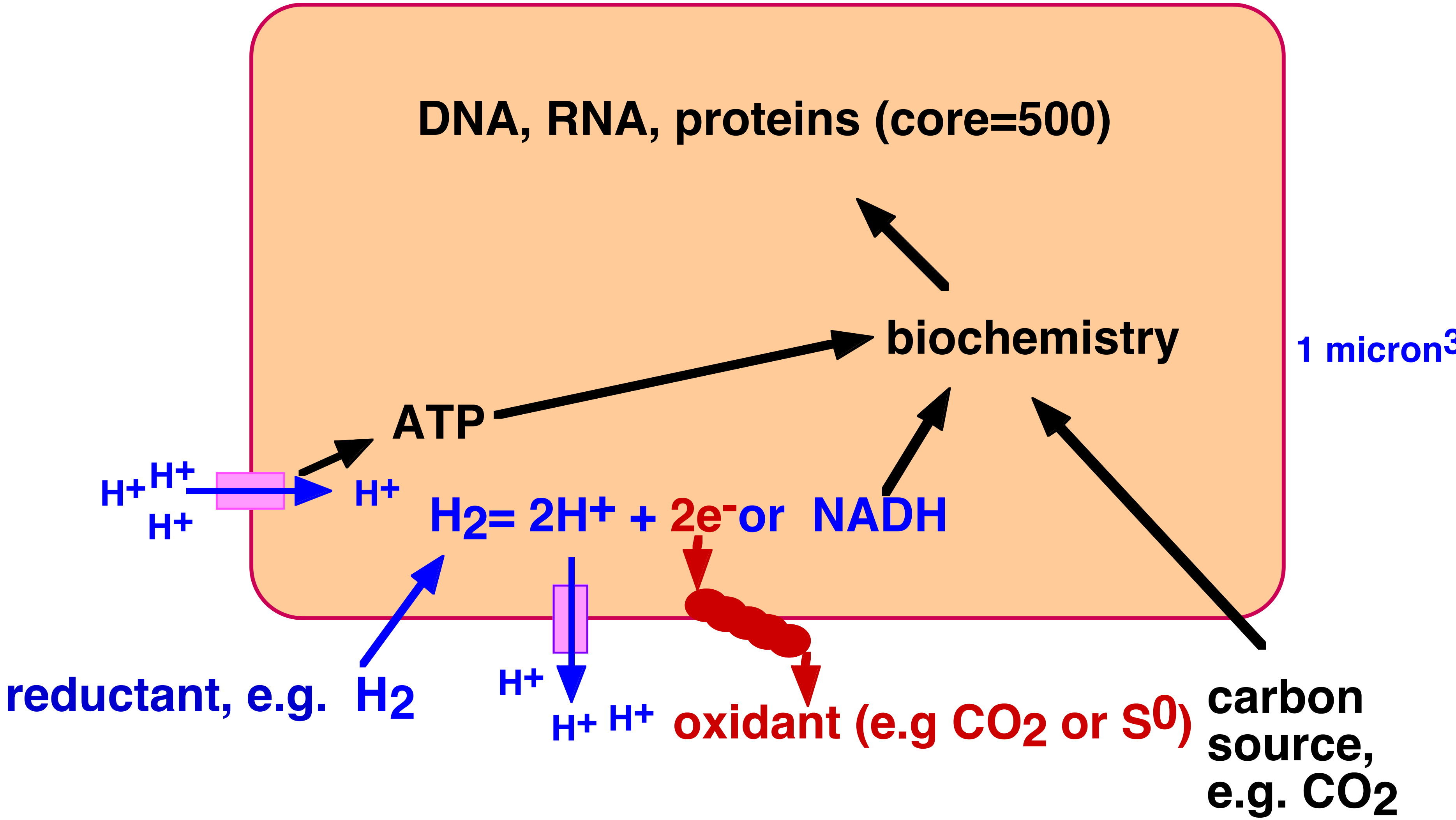


Figure 11-5 Brock Biology of Microorganisms 11/e

There was already life on Earth during the period of intense exchange with a warmer and wetter Mars



Some common features of life on Earth



Why look for life on Mars that is exactly like life on Earth? Have you no imagination?

But Earth is totally infected with bacterial life. They transformed our atmosphere and insinuated themselves into every possible ecosystem.

Is it so idiotic to ask whether life has moved from one utterly contaminated sphere to the next body?

Advantage: the tools of the trillion dollar investment in genomics.

Earth to Mars

Transfer times $<3 \cdot 10^4$ years…

0.001% of ejecta arrives

Gladman et al. (2005); Astrobiology 5:483-496

Earth to Mars

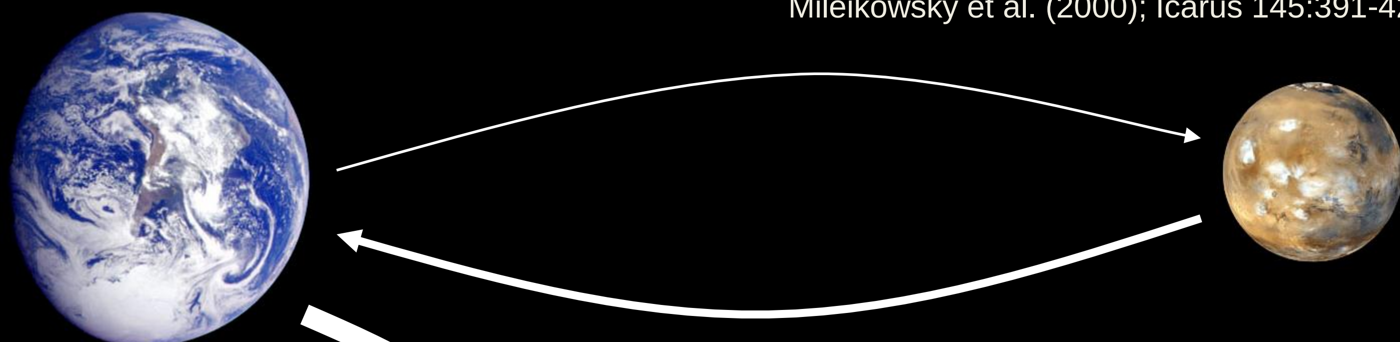
For t $<10^7$ years, T<100ºC

…10^6-10^8 ejecta of 0.01-1 m

Arrival on Warm + Wet Mars

t_{crit} ~ 0.3-1 My ($N/N_0=10^{-6}$)

Mileikowsky et al. (2000); Icarus 145:391-427



Mars to Earth

For t $<10^7$ years, T<100ºC

…10^6-10^9 ejecta of 0.3-6 m

Arrival on Warm + Wet Earth

t_{crit} ~ 0.3 to >10 My ($N/N_0=10^{-6}$)

Mileikowsky et al. (2000); Icarus 145:391-427

Earth to Earth

For t $<3 \cdot 10^4$ years…

1% of ejecta recovered

Gladman et al. (2005); Astrobiology 5:483-496

Launch and reentry of rocks bearing possible living organisms:

Possible acceleration to escape velocity and deceleration from escape velocity without major heating: for a 1 to 20 Km impactor, 10^8 low temperature ejecta

Orbiting ejecta, at slightly less than escape velocity are refugia to microbes (but not dinosaurs) during bombardment period

Black body temperature between Mars and Earth 130- 200 deg K.

Atmospheric entry at 10s Km/sec takes a few seconds.

Transit:

Transit time between Mars and Earth less than 10,000,000 years for 5% but as little as decades to centuries

6 meters of rock can protect vs cosmic and solar radiation for hundreds of millions of years

Hypothesis: That life on Mars (and exoplanets) will be related to life on Earth

Why?

1. At the point of massive meteoritic exchange between Mars and Earth, life had already evolved to modern cellular forms and metabolism. And Mars was probably wetter and warmer.
2. By 3.5 billion years ago, life was already highly evolved protein-based.

How does this help us look for life on Mars?

1. all life on Earth is related to a common ancestor
2. about 500 genes, e.g. the ribosomal RNA genes, are highly conserved over the past 3.5 billion years.
3. amplification and sequencing of random DNA is now used to prospect for diverse life on Earth.
4. if life on Mars shares that common ancestor, we can detect it with DNA sequencing.

The instrument: a 5 kg soil analysis package that amplifies and sequences DNA (or RNA) in situ on Mars

The life signature: a DNA sequence with predictable features that cannot be generated abiotically

Genome sequencing of raw samples of mud, water, feces, ice, snow, etc. is already the standard method for discovery of life in any ecosystem on Earth.

Metagenomics is the study of the sum of genomes in a sample.

6367 papers Nov 30 2016, using search term: Metagenomic

3559 papers using metagenomic and environmental

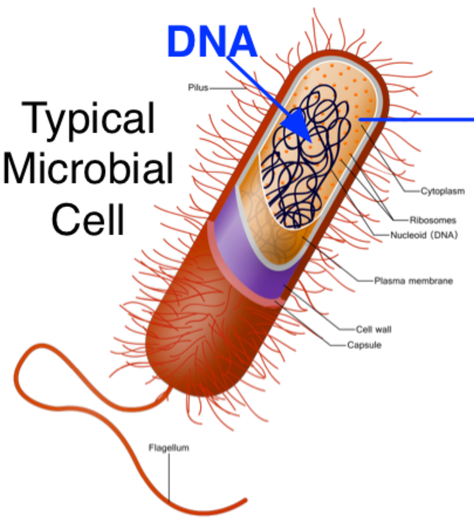
502 papers using the term 16s and Antarctica

An emerging view: 99% cannot be grown in culture---DNA surveys are superior to any other survey.

Overview of SETG

DNA

Typical Microbial Cell



Extract → **Condition** → **Sequence**

Extract

Break Cell Membrane

Separate DNA from Proteins, Lipids, etc.

Concentrate DNA

Condition

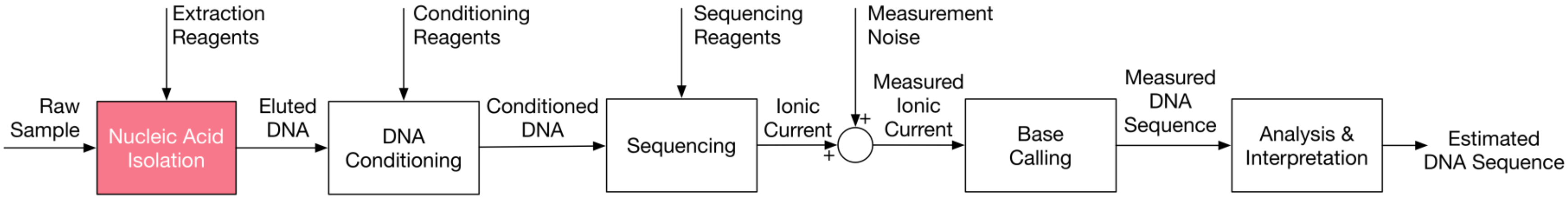
Convert DNA to readable "Library" (technology dependent)

Can involve "cleaning", adding known ends, selecting certain gene regions, amplifying, etc.

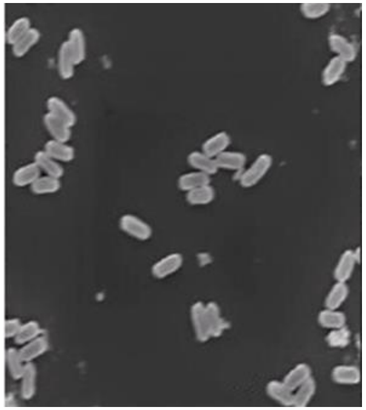
Sequence

Read out sequence of bases (A, C, G, T)

Nucleic Acid Isolation

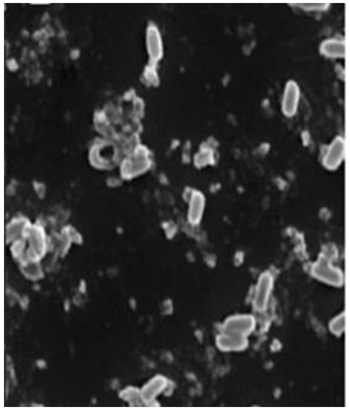


Claremont BioSolutions



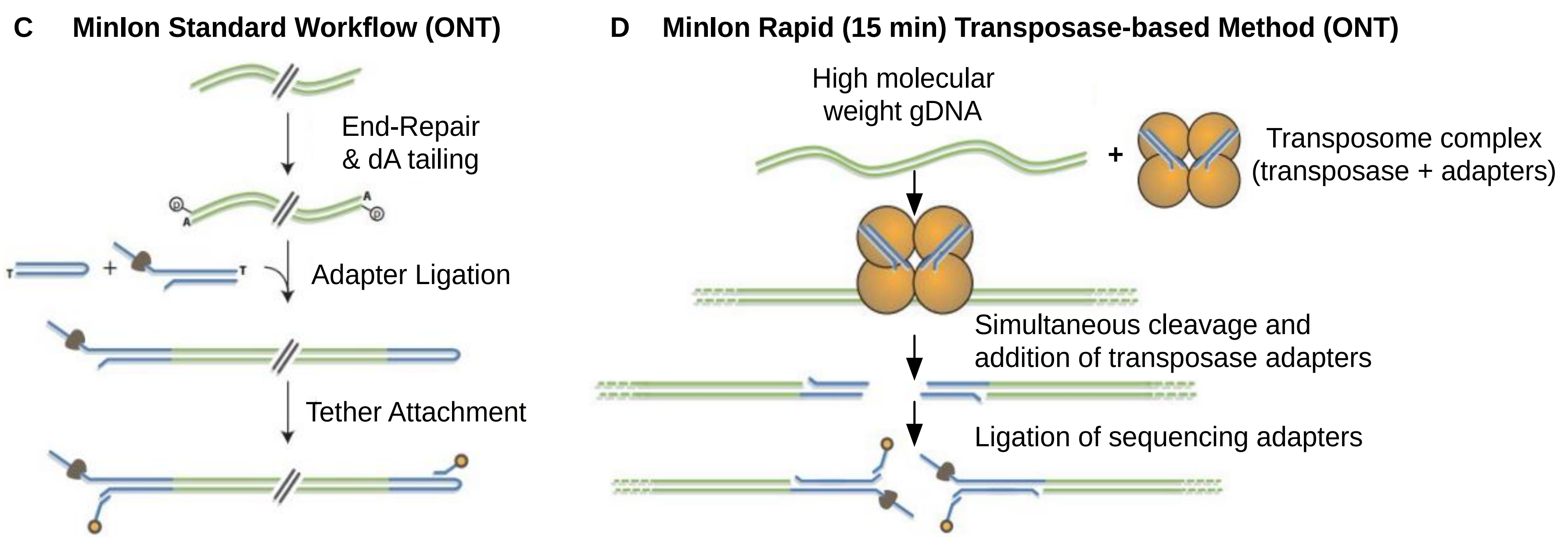
Bacillus subtilis spores

DNA binds to beads



Lysed cells to waste

DNA Conditioning
(Library Preparation)



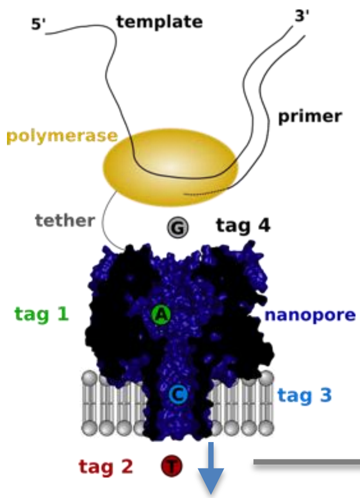
Requirements: Low volume input (ul), preferably concentrated DNA. No carryover that inhibits polymerase.

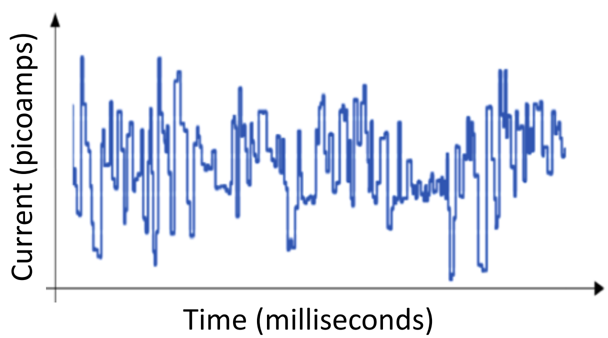
Current specification for ONT MinIon Mark 1B: 10pg - 1µg input DNA

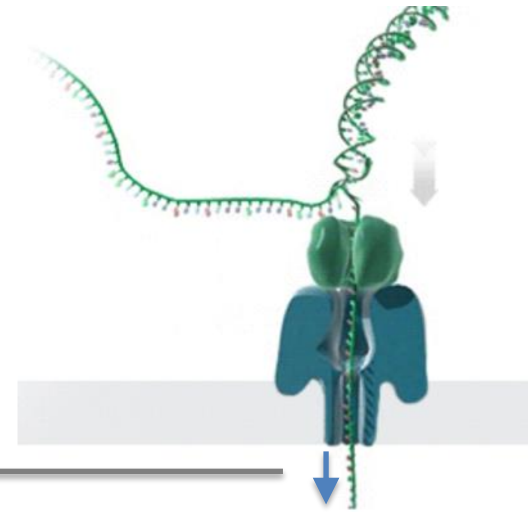
We have tested both these library prep methods (beta test of transposase method). Limitation is currently requires storage at -80˚C. Not easy for the field.

SETG Sequencing

- Sequencing from single molecules using biological nanopores
  - Sensitivity: base read (A, C, G, T) = 2 bits from mass of 650 Daltons
  - Specificity: long (>5 kb) reads can give sub-species ID from single read







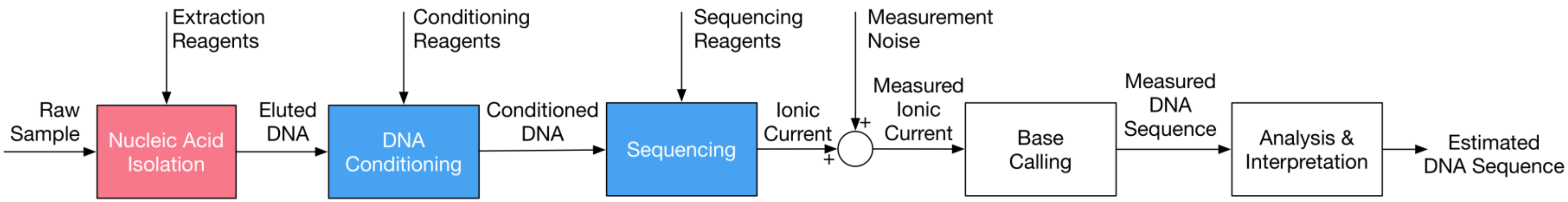
Monitor Ionic Current Through Nanopore(s)

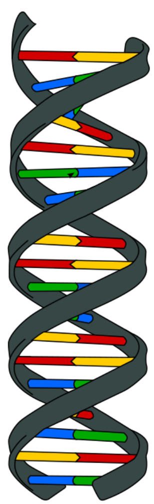
Estimate DNA bases using statistical models

Sequencing By Synthesis
Genia Technologies Inc.

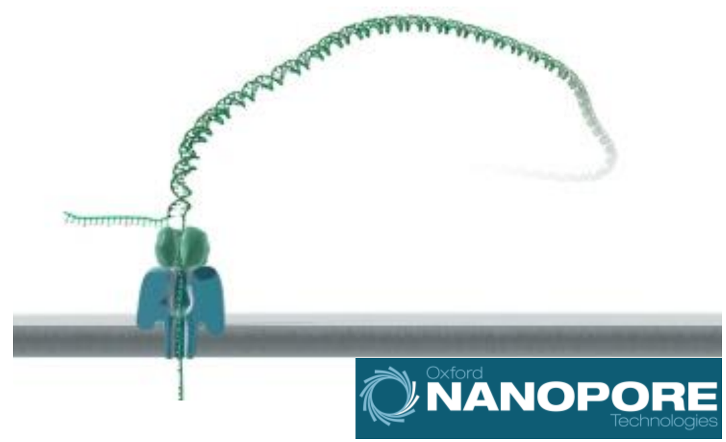
Strand Sequencing
Oxford Nanopore Technologies, Inc.

Nanopore Sequencing

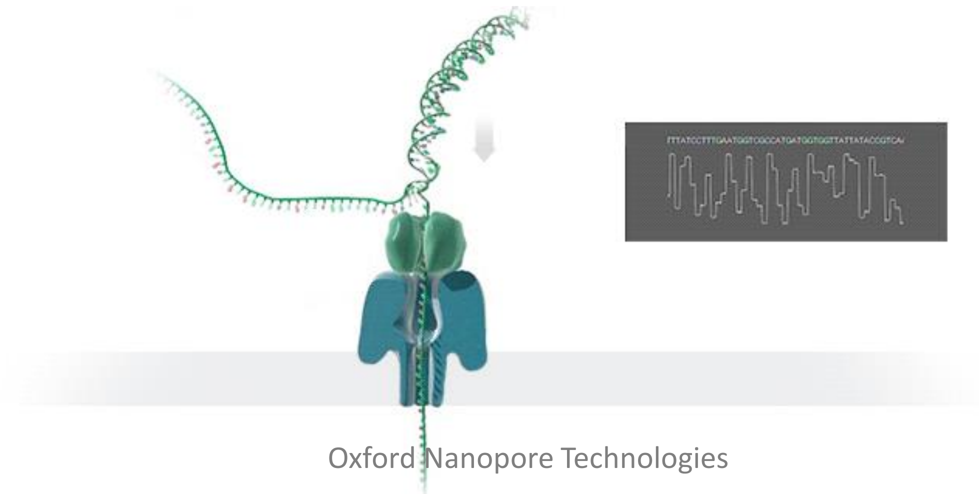


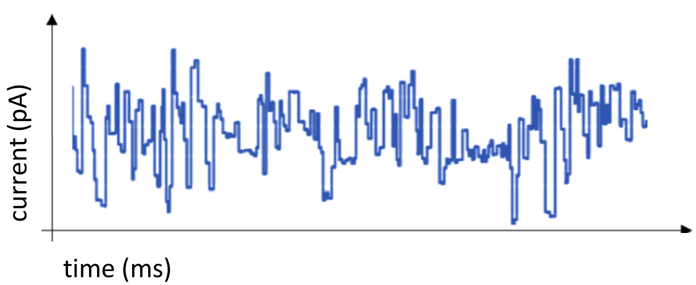


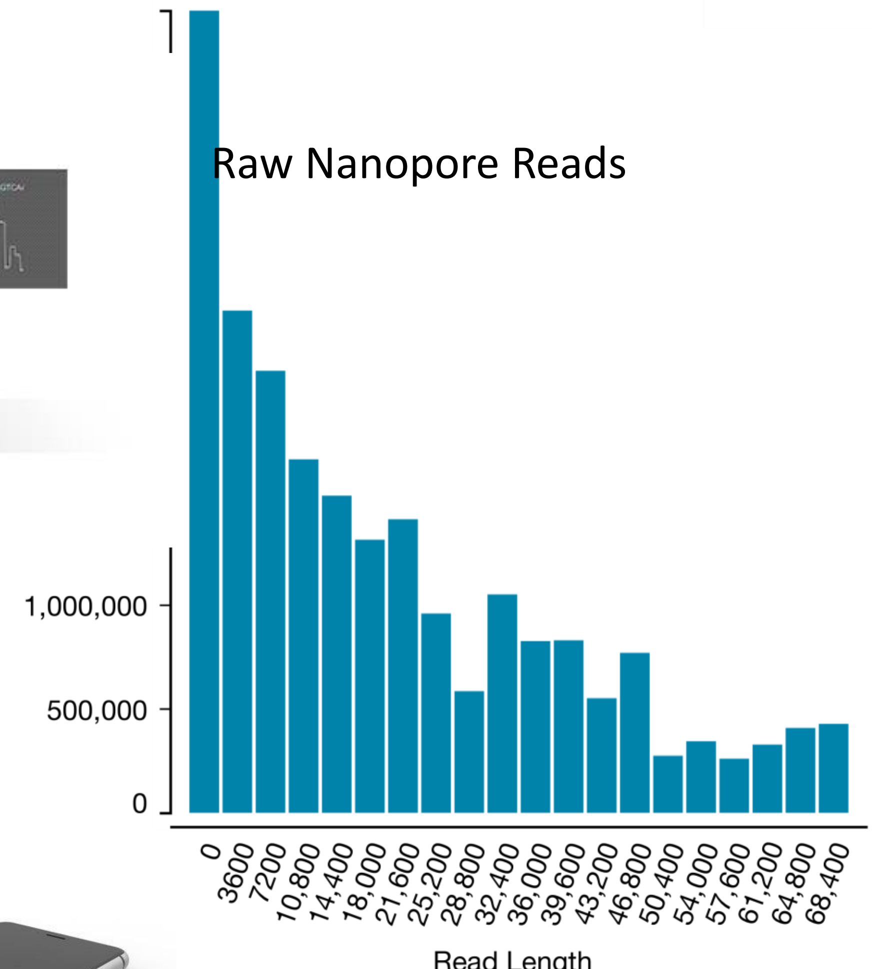
DNA
Deoxyribonucleic acid



Sequencing

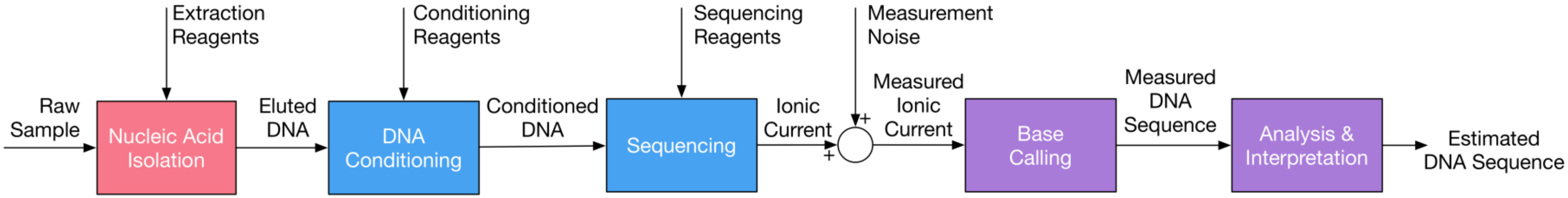

Oxford Nanopore Technologies

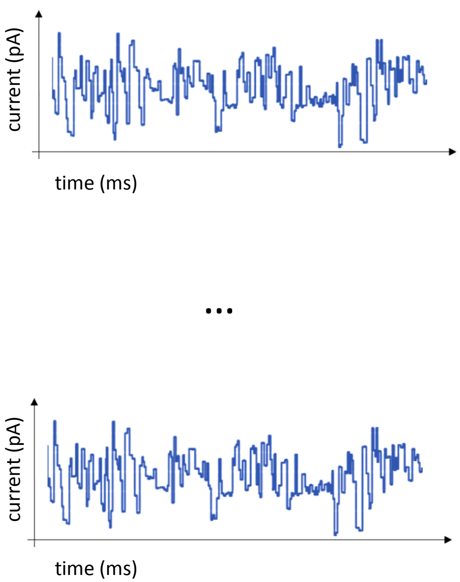

current (pA)
time (ms)

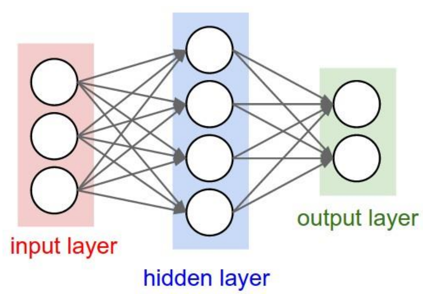

Raw Nanopore Reads
1,000,000
500,000
0
0
3600
7200
10,800
14,400
18,000
21,600
25,200
28,800
32,400
36,000
39,600
43,200
46,800
50,400
54,000
57,600
61,200
64,800
68,400
Read Length


SmidgION

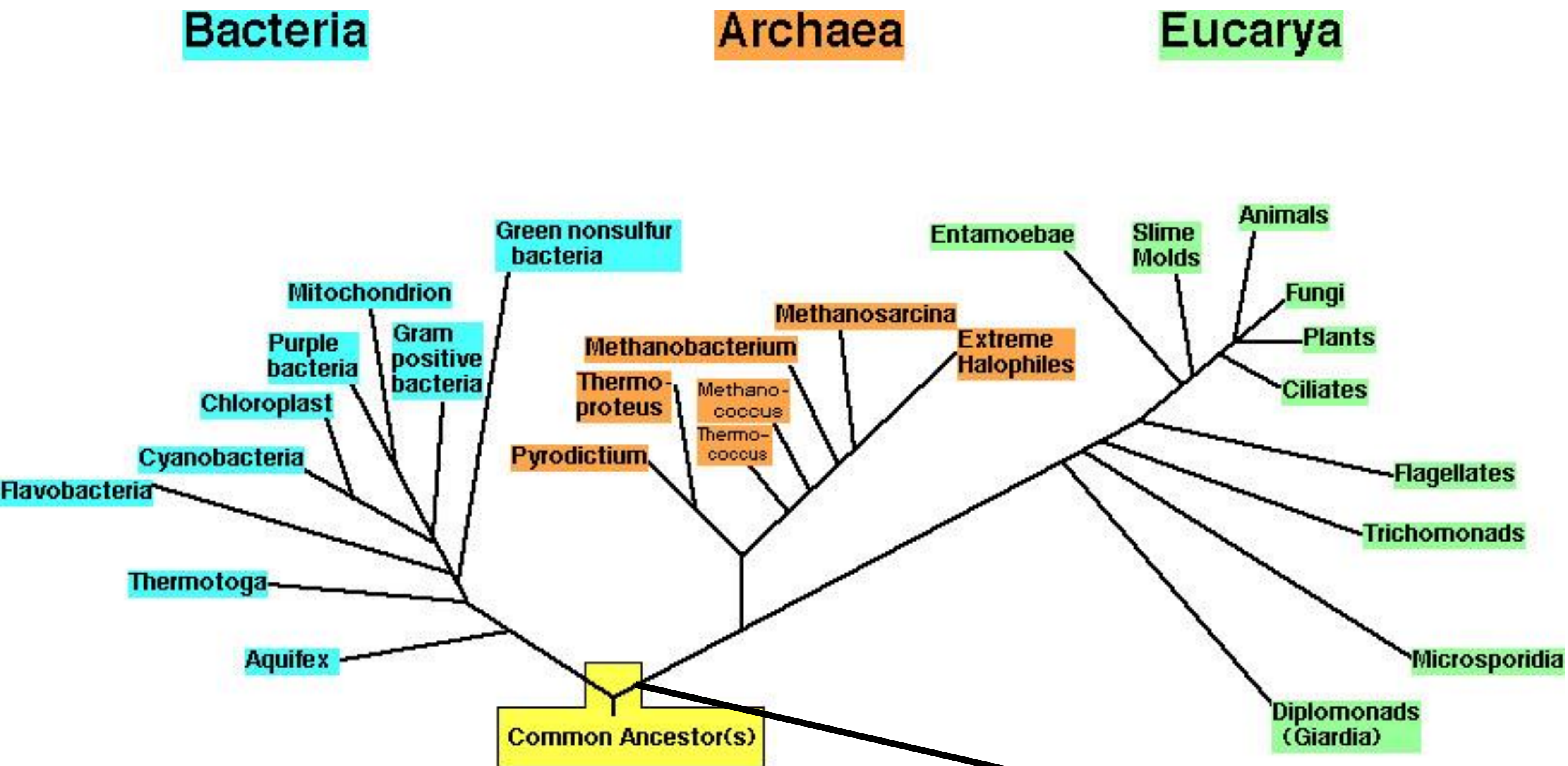
Data Analysis, Basecalling





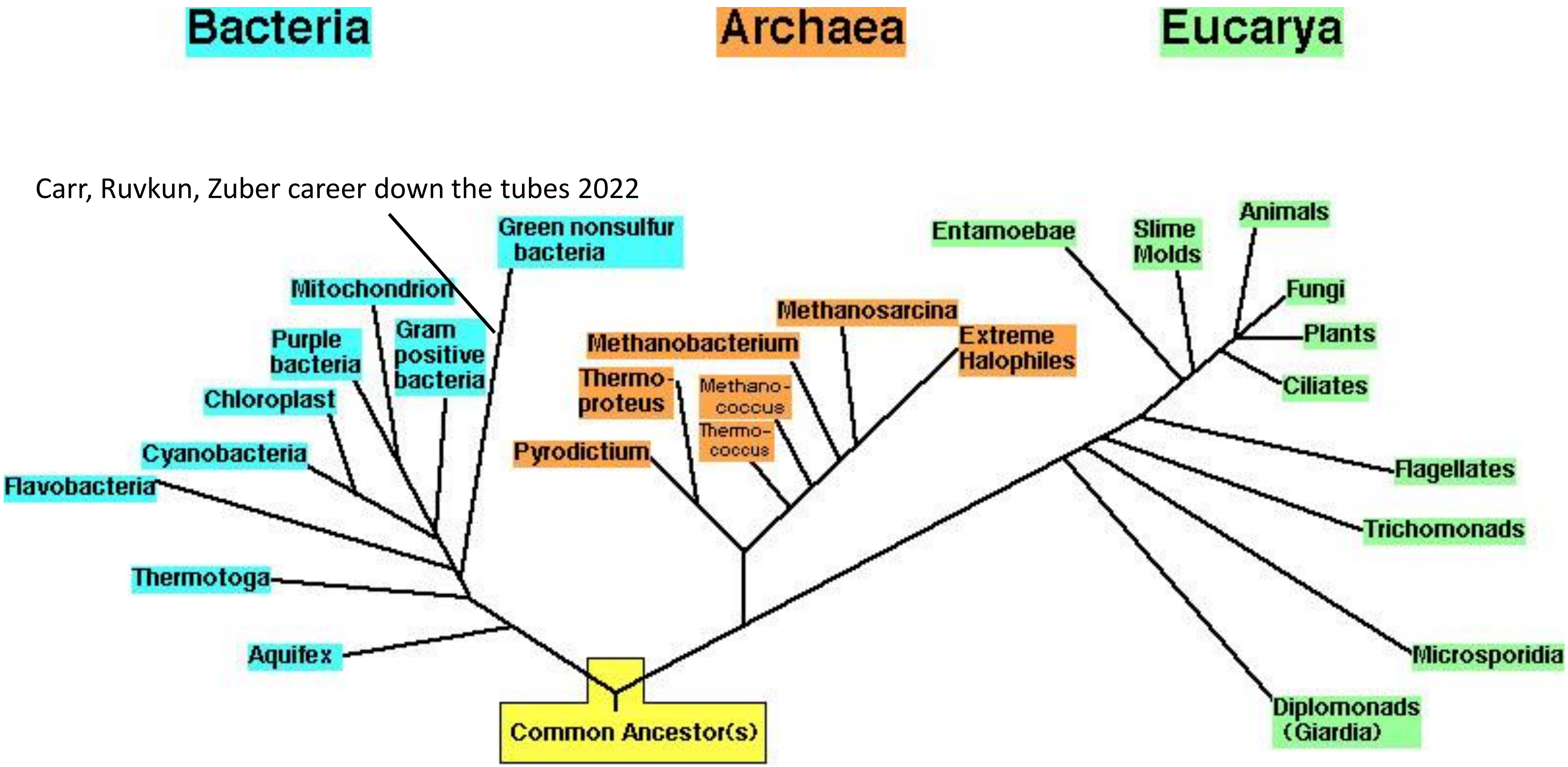


ATCGAATTTTTCATGC
ATGCATGCATCGCGC
GCATCGACTAGCATC
GTACTAGCATGCGCA
TCACATCGAGCATCG



Mars SETG 2022

Carr, Ruvkun, Zuber career down the tubes 2022



Potential problems common to all life detection experiments

1. Life is extinct on Mars.

Some evidence that PCR amplification can detect extinct life. But Martian biota may have adapted to the gradual drying and cooling of Mars. PCR can detect spores which may survive for as long as 10^8 years.

2. No life at the particular landing site or in the particular soil sample analysed.

But PCR amplification can detect one DNA molecule in a sample, i.e. a microbial cell that blows in from an oasis.

3. Life exists much deeper in the soil, ie away from the UV and high oxidation potential on the surface.

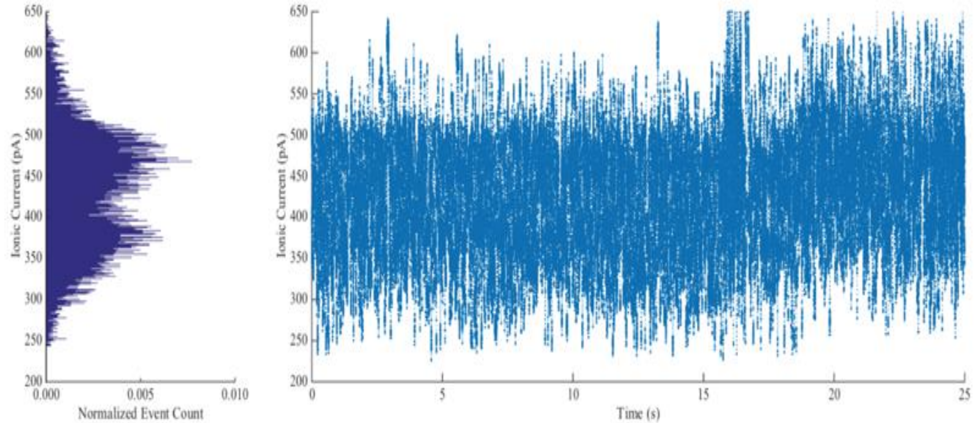
PCR is sensitive enough to detect the detritus (DNA) or spores of such deep life. And we know that life thrives on redox gradients.

4. No life on Mars, never was.

There are LOTS of other planets to try. Same instrument, just change “Mars” to 51 Pegasi b or Mu Arae c

The nanopore can detect non-standard nucleic acids

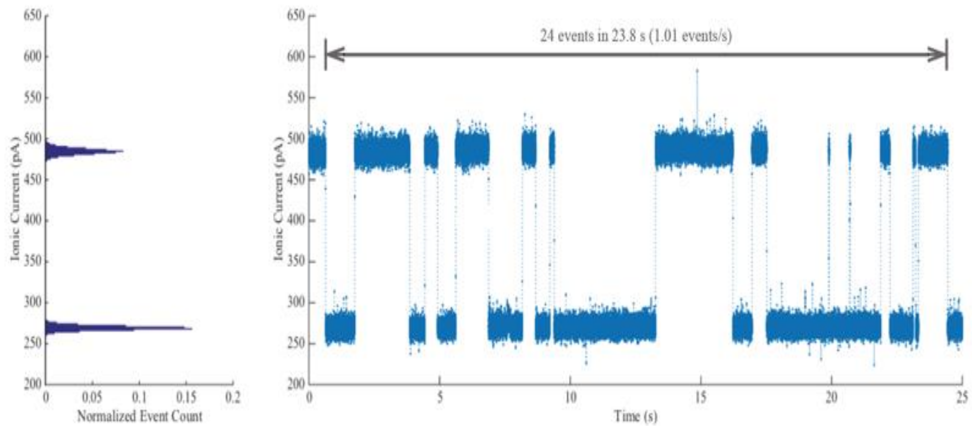
Lambda 50 kb DNA virus



(64) 3-mers composed of A,T,C,G

Poly(deoxyinosinic-deoxycytidylic) acid “Poly(dI-dC)”

…CICICICICICICICICICI…



(2) 3-mers ICI, CIC

Inosine nucleobase (hypoxanthine) found in meteorites

Carr *et al. 2017*
Accepted

The case for lateral transfer

Most conservative lateral transfer model: Earth Mars, about 1 AU

Time frame: 10 to 10,000,000 years.

Mode of transport: Shock accelerated rocks, moving at 10s Km/sec planetary/meteoritic velocities

From Solar System to nearby stars/planetary systems. A few light years.

Time frame: 10^4 years at planetary velocities of 20 Km/sec

Advantage: velocity almost zero at capture by next star, making capture more likely, depends on relative motion of stars.

1000x as much radiation exposure.

Mode of transport: ejected rocky planets? More common for hot Jupiter systems?

planet capture is low probability after system is stable.

Interstellar transfer of life?

- Exposure to radiation, desiccation, limits survival (on Earth, oldest revived bacteria ~ 500kYa)
- A million-fold greater distance (~8 light years vs. ~0.5 AU) for transfer events
- Mechanisms to achieve higher relative velocities may reduce transfer time?
  - Gravitational slingshot (limited to km/sec)
  - Stellar relative motion (~30-100 km/sec)
- Best-case transfer time to another star system? 50 light years / 30 km/sec = 500,000 years
- Transfer feasible given appropriate shielding (meters)
- Ejection probability may be low, but…
- **Life can likely be transported between star systems**

Are we extinct if our genomes are data in a binary string?

Our genome sequence is already transmitted. (Photon Transmission of Human Genomes)

Soon all organisms DNA on Earth will be in photons escaping from our doomed Solar System

Acknowledgments

- SETG Team: Maria Zuber, Chris Carr, Angel Mojarro, Julie Hachey, Alex Pontefract, Jacopo Tani, Mike Finney
- Maturation of Instruments for Solar System Exploration (MatISSE) Award #NNX15AF85G
- Claremont BioSolutions
- Oxford Nanosystems

Extinction with honor-
Trilobites died proud arthropods.
We celebrate their past abundance.
We do not judge them by their extinction.

Life-sustaining planet(oid)s

- Stevenson (1999): Possibility of ejected Earth-mass planets with water oceans
- Debes & Sigurdsson (2007): Earth-sized planets with moons can survive ejection and be habitable (tidal heating); ejection of Earth occurred in ~8% of simulations.
- Laughlin & Adams (2000): 10^{-5} cumulative chance of Earth ejection in future; 10^{-6} for capture around another star.
- Probability of capture given ejection seems high
- Minimum size for life sustaining planetoids may be set by required transfer time and cooling time
- Would allow very long transfer times; up to 1Gy for Earth-sized or larger planets
- **Life likely can be transported between stellar systems**

Our Galaxy: Transfer across our Galaxy: 100,000 light years= 50,000 steps of a few light years each between adjacent stars

10^4 steps x 10^7 years per step or 10^{11} years. Big Bang is 10^{10} years ago. Need to accelerate but only 10x. Each step would involve an amplification of life within a solar system. And more life makes the probability of spread higher. A chain reaction.

Local group=10 million light years, 100x the distance across a galaxy. Another factor of 100. Only 100. A million times the volume. But gets you 3x the galaxies. Not worth the effort.

Virgo supercluster=100 million light years. Another factor of 10. 2500x the number of galaxies.

Ribosomal RNA is the most conserved molecule of life on Earth

Query = Fruit fly 18S ribosomal RNA gene

Subject = Bacillus subtilis 16S ribosomal RNA gene, Length=1522

Identities = 20/20 (100%), Gaps = 0/20 (0%)

```
Query  569  GTGCCAGCAGCCGCGGTAAT  588
            ||||||||||||||||||||
Sbjct  518  GTGCCAGCAGCCGCGGTAAT  537
```

Identities = 61/76 (80%), Gaps = 3/76 (3%)

```
Query  1190  CCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCAC-CACCA
              || ||||||||| ||| ||||  |||||||| ||||||||||||||  |||| | ||| |
Sbjct  890   CCTGGGGAAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGG--GGGCCCGCACAA  9
```

```
Query  1249  GGAGTGGAGCCTGCGG  1264
              |  ||||||| || ||
Sbjct  948   GCGGTGGAGCATGTGG  963
```

Query is 435 amino acid RPT-1 protein from the animal C. elegans
Subject is ATP-dependent metalloprotease, [Escherichia coli]
Length of E. coli protein: 434

Score	Expect	Identities	Positives	Gaps
218 bits(556)	8e-65	111/261(43%)	168/261(64%)	1/261(0%)

```
Query  166  MQVEEKPDVTYSDVGGCKDQIEKLREVVETPLLHPERYVNLGIEPPKGVLLYGPPGTGKT  225
            M  E++   T++DV GC +  E++ E+VE  L  P R+  LG + PKGVL+ GPPGTGKT
Sbjct  141  MLTEDQIKTTFADVAGCDEAKEEVAELVEY-LREPSRFQKLGGKIPKGVLMVGPPGTGKT  199

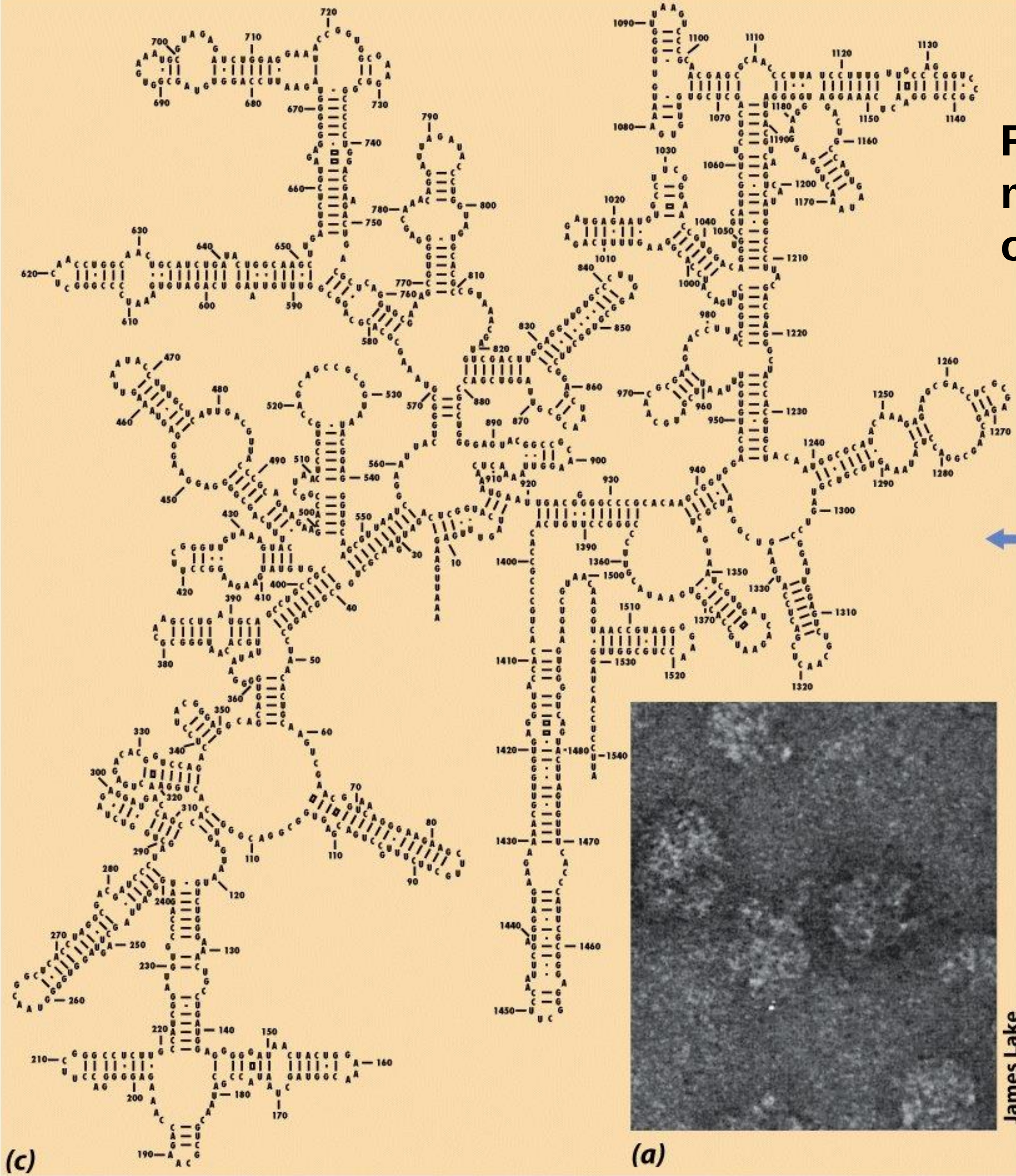
Query  226  LCARAVANRTDACFIRVIGSELVQKYVGEGARMVRELFEMARTKKACLIFFDEIDAVGGA  285
            L A+A+A      F  + GS+ V+ +VG GA  VR++FE A+    C+IF DEIDAVG
Sbjct  200  LLAKAIAGEAKVPFFTISGSDFVEMFVGVGASRVRDMFEQAKKAAPCIIFIDEIDAVGRQ  259

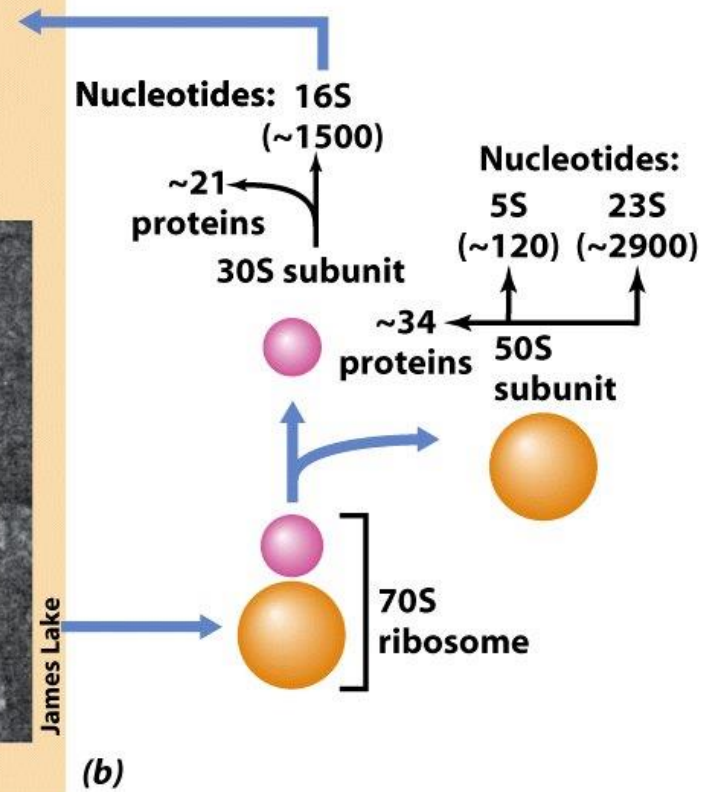
Query  286  RFDDGQGGDNEVQRTMLELINQLDGFDPRGNIKVLMATNRPDTLDPALMRPGRLDRKVEF  345
            R     GG +E ++T+ +++ ++DGF+    I V+ ATNRPD LDPAL+RPGR DR+V
Sbjct  260  RGAGLGGGHDEREQTLNQMLVEMDGFEGNEGIIVIAATNRPDVLDPALLRPGRFDRQVVV  319

Query  346  ALPDLAGRAHILKIHAKQMSVERDIRYDLLARLCPNSTGAEIRSVCTEAGMFAIRARRKV  405
             LPD+ GR  ILK+H +++ +  DI   ++AR  P  +GA++ ++  EA +FA R  ++V
Sbjct  320  GLPDVRGREQILKVHMRRVPLAPDIDAAIIARGTPGFSGADLANLVNEAALFAARGNKRV  379

Query  406  ATEKDFLEAINKVVKGYAKFS  426
             +  +F +A +K++ G  + S
Sbjct  380  VSMVEFEKAKDKIMMGAERRS  400
```

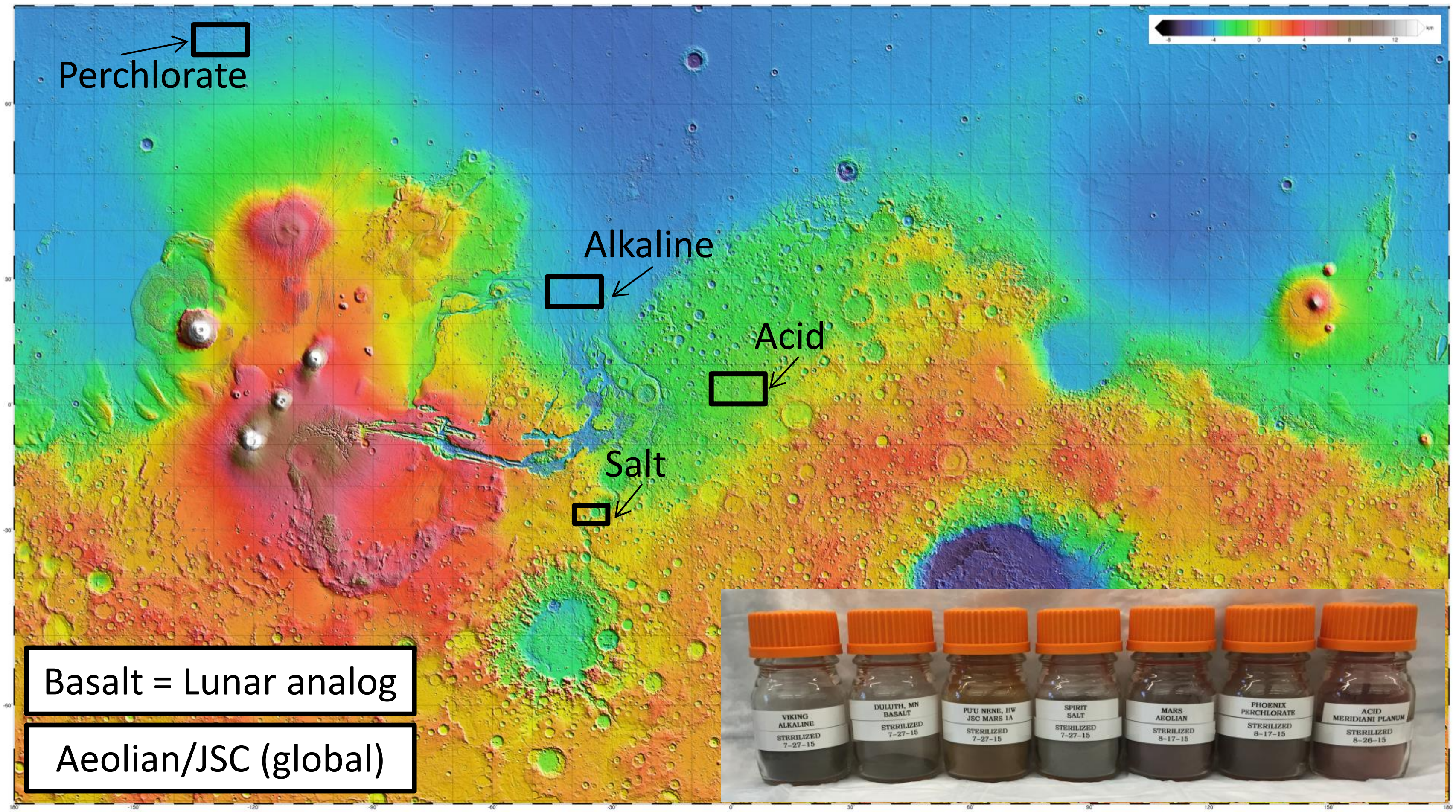
Ribosomal RNA is the most conserved molecule of life on Earth





Synthetic Samples

MOLA Science Team



Schuerger *et al.* 2012

Synthetic samples enable controlled experiments

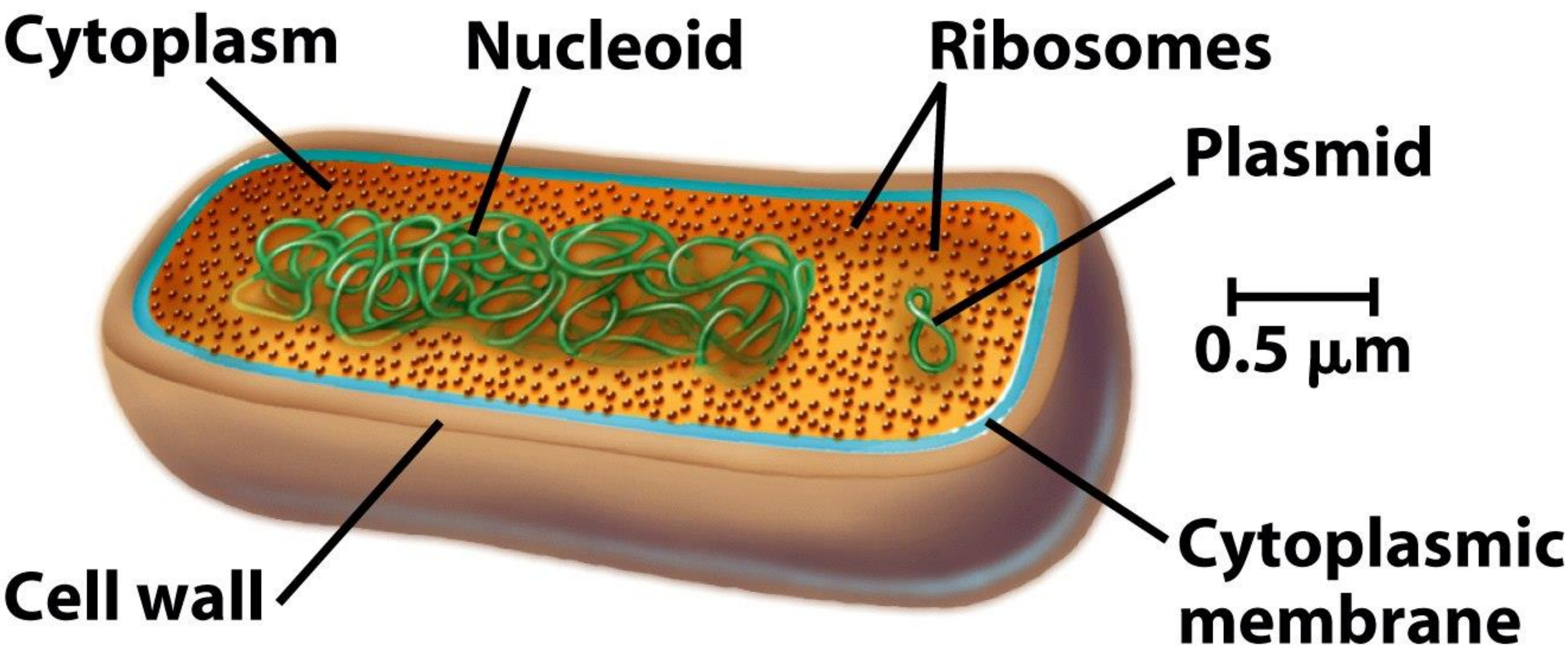


Figure 2-1a Brock Biology of Microorganisms 11/e

And if you send up your hypersophisticated probe to look for positron magneto quantum life, find nothing, and end up 100 years later in desperation, finding DNA based life, who was the fool?

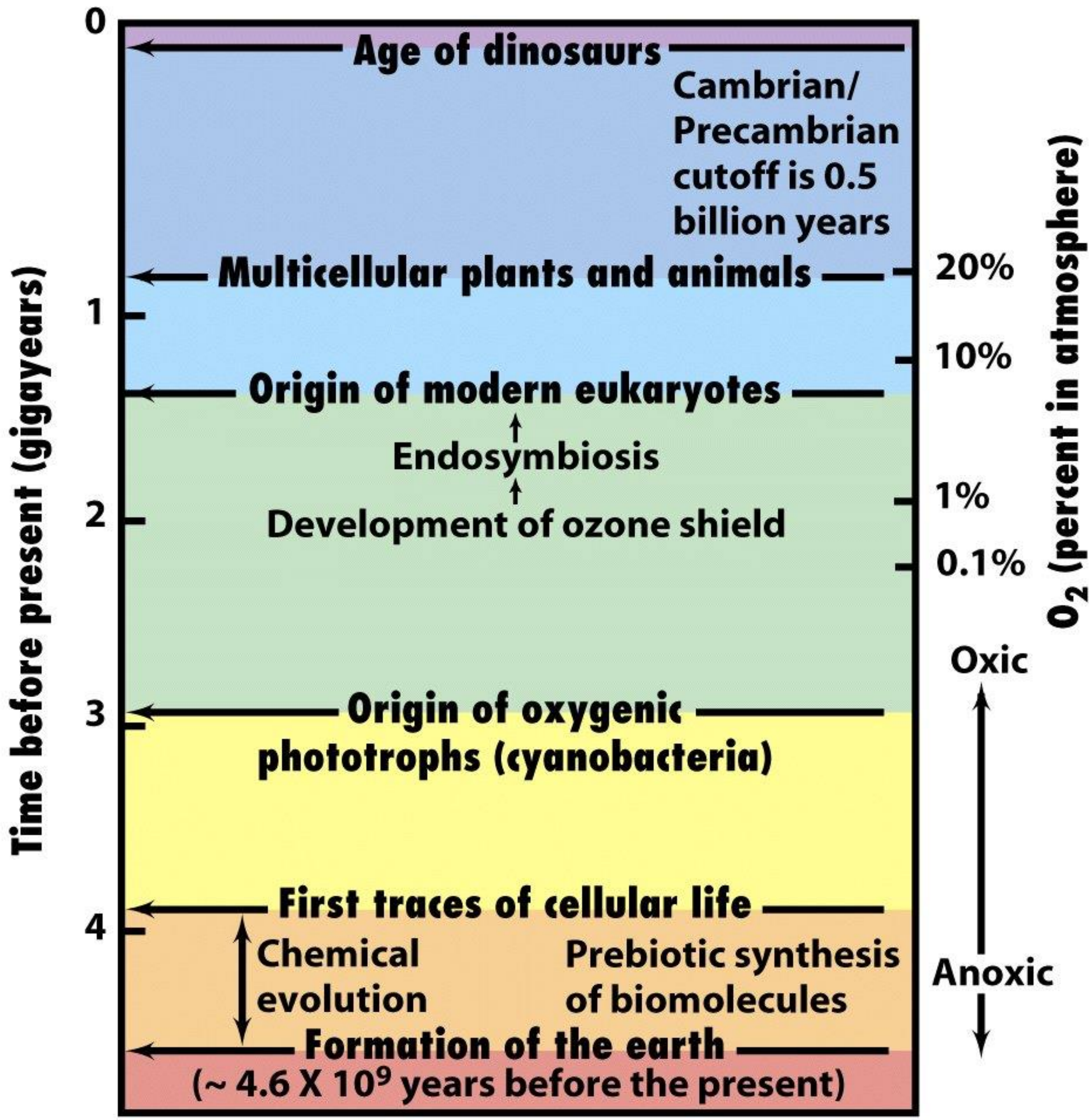
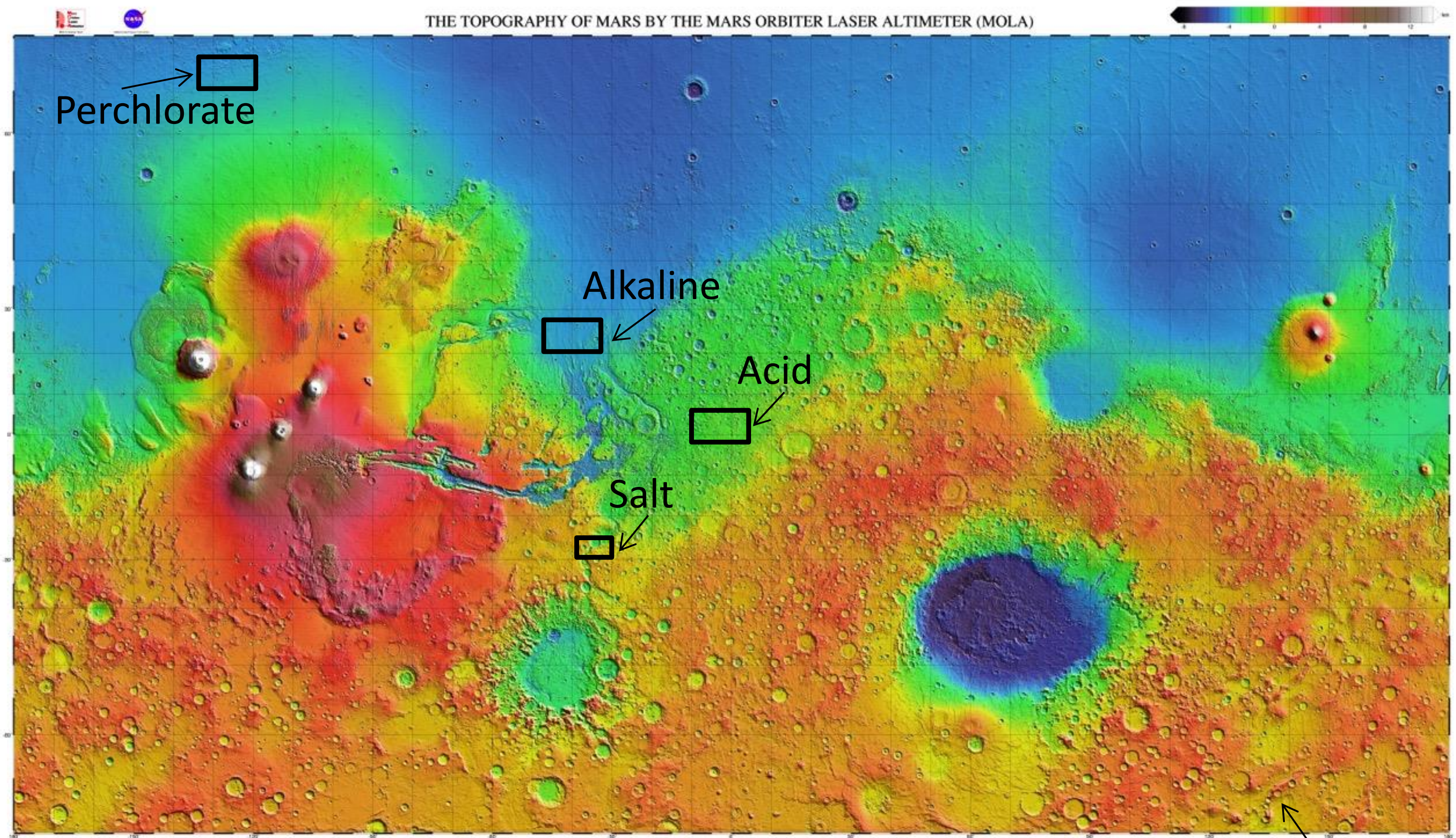


Figure 11-8 Brock Biology of Microorganisms 11/e

Synthetic Mars Analogs

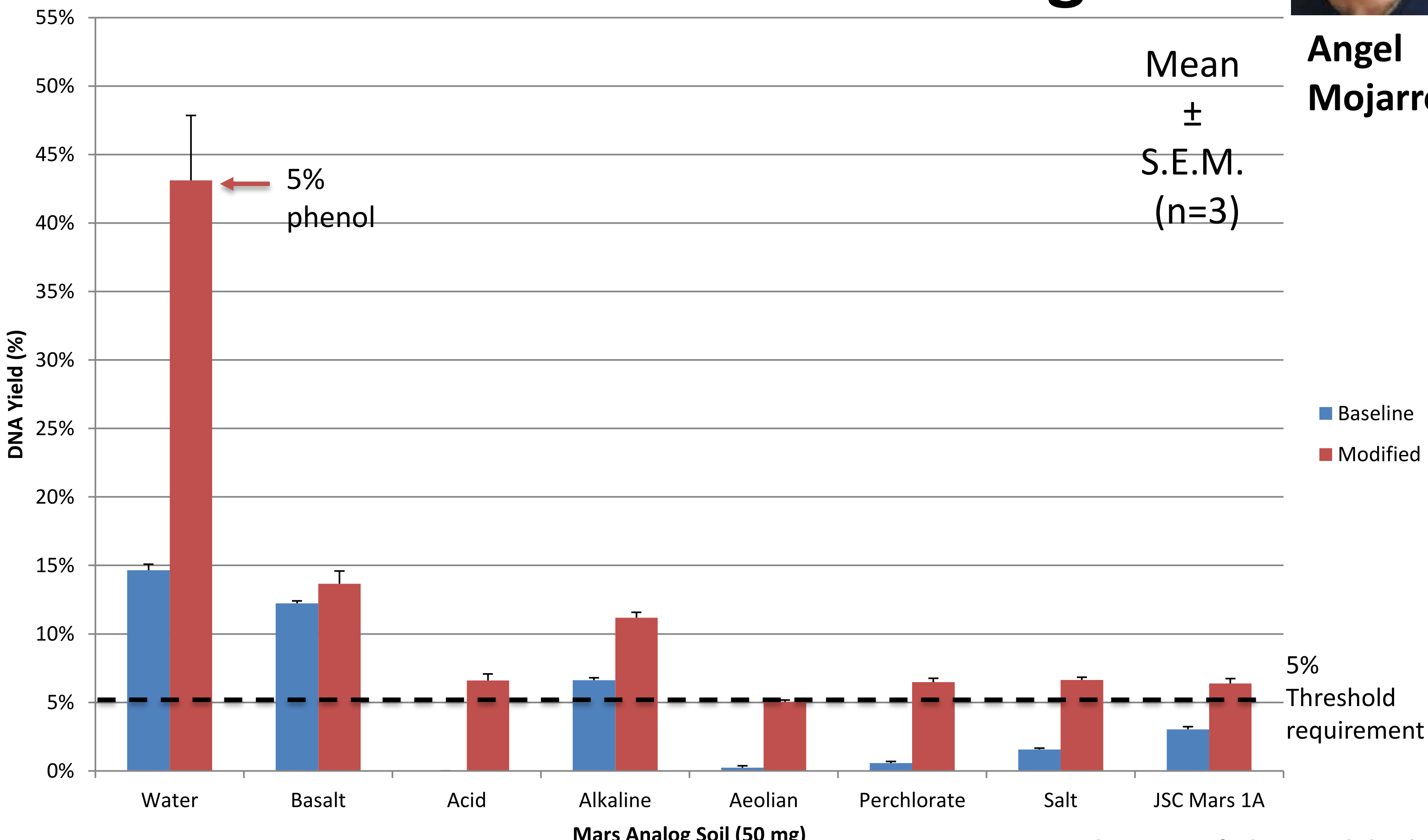


Basalt = Lunar analog

Aeolian/JSC (global)

Modified Extraction Procedure Meets 5% Target

Angel Mojarro



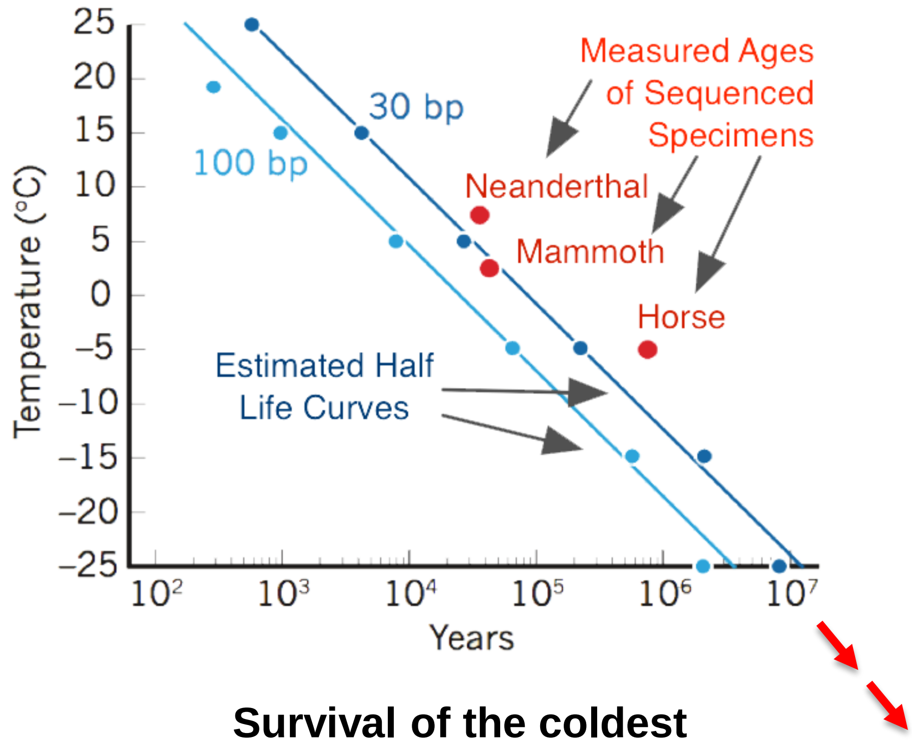
Mojarro et al. (In Revision)

Preserved Life on Mars

Residence time of DNA

- Hydrolysis: $\sim 10^6$ y (Earth), $\sim 10^9$ y (Mars)
- Self radiation: $\sim 10^7$ y (Earth or Mars)
- Space Radiation: Below 2 m
- **Example:** $7 * 10^5$ y old bacteria DNA in permafrost
  Johnson *et al.* 2007

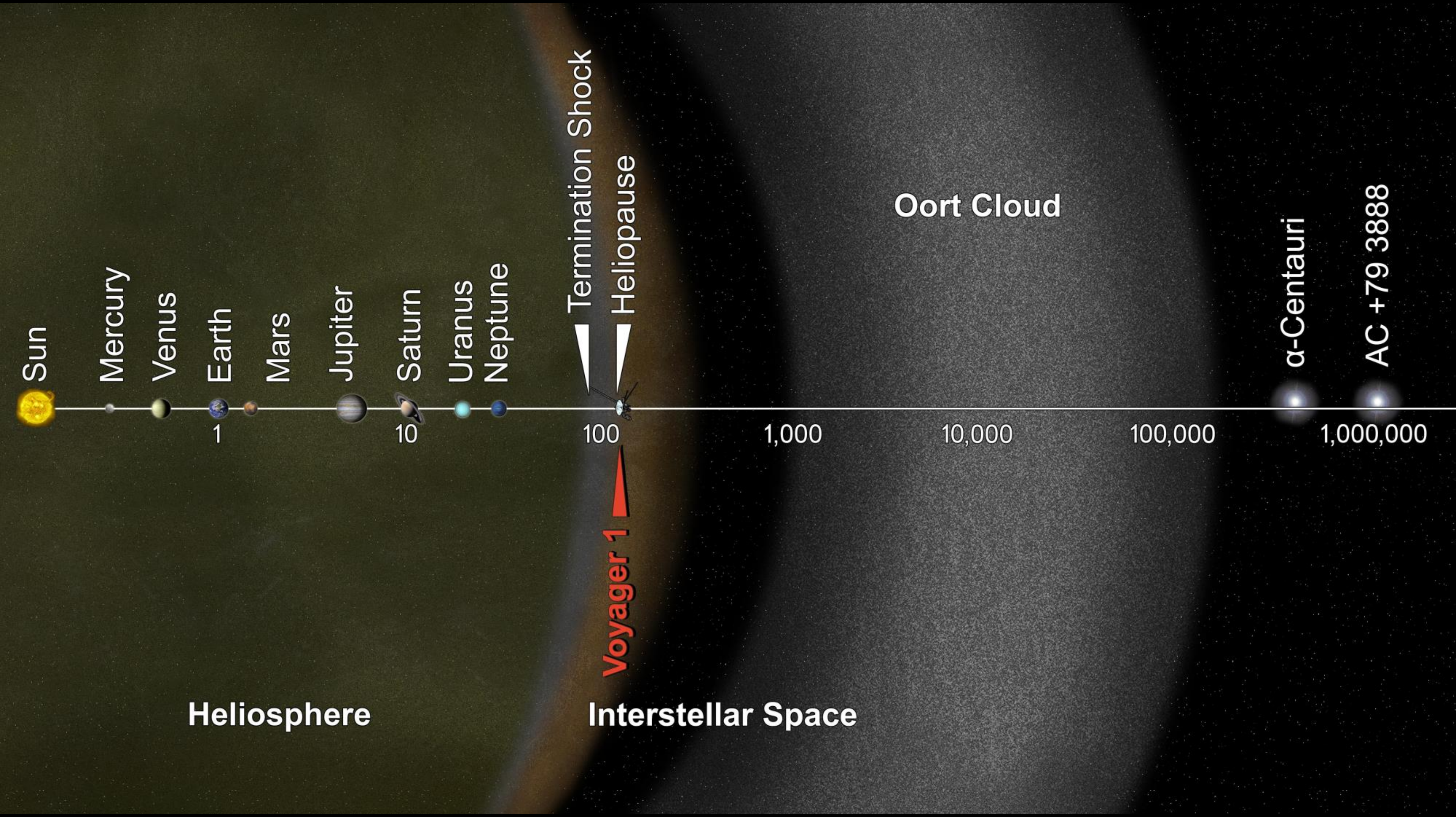
Model of DNA Hydrolysis



Survival of the coldest
adapted from Millar & Lambert, 2013

Mars temperature preserves DNA on longer timescales versus Earth

Oort cloud comets and migrating planets exchange, rarely, between solar systems



Bacteria may not go extinct, given horizontal gene transfer between them. It is a super species in a way.

Perhaps the best way to ensure the survival of our genomes is encoded in bacteria that we launch to other planets.