12 recent discoveries that have changed the debate about design in the universe

Part II

Review of Part I

1. The universe (space-time, matter, energy) had a beginning and will have an end.

2. The laws of physics, the fundamental constants, and the initial conditions of our universe are fine-tuned to allow for the possibility of life.

3. Protein sequence space is far too large to be searched, and highly functional sequences (i.e. enzymes) are incredibly rare.

4. The number of genes in the simplest free-living organism is about 450.

These discoveries are not controversial – but conclusions differ!

Alan Sandage

observational astronomer
> 500 publications

"Here is evidence of what can only be described as a super natural event. There is no way that this could have been predicted within the realm of physics as we know it. …

I now have to go from a stance as a complete materialistic rational scientist and say this super natural event, to me, gives at least some credence to my belief that there is some design put in the universe."

Alan Sandage, *quoted in Return of the God Hypothesis*, 2021, p 108

These discoveries are not controversial – but conclusions differ!

NASA scientist, astronomer

"For the scientist who has lived by his faith in the power of reason, the story ends like a bad dream. He has scaled the mountains of ignorance; he is about to conquer the highest peak; as he pulls himself over the final rock, he is greeted by a band of theologians who have been sitting there for centuries."

R. Jastrow, *God and the Astronomers*,1992, pg 107.

“But I can’t accept it”

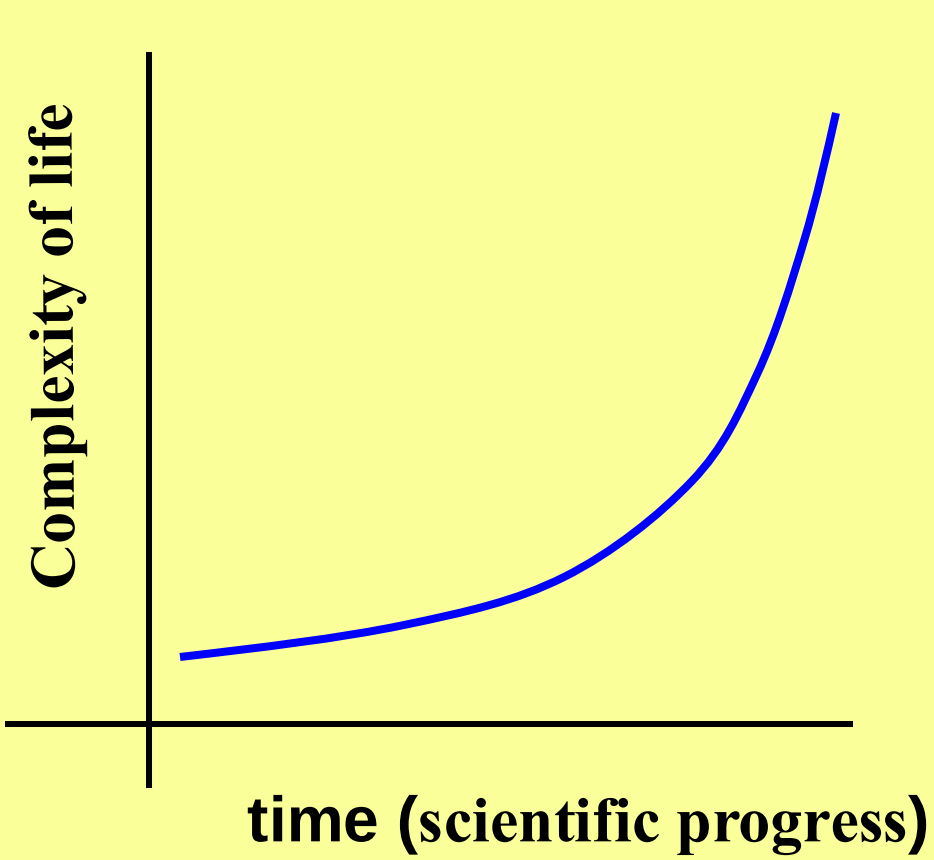
Part II

5. **Life is based on a digital information processing system**

6. **Molecular machines and sophisticated software algorithms are essential to all life-forms**

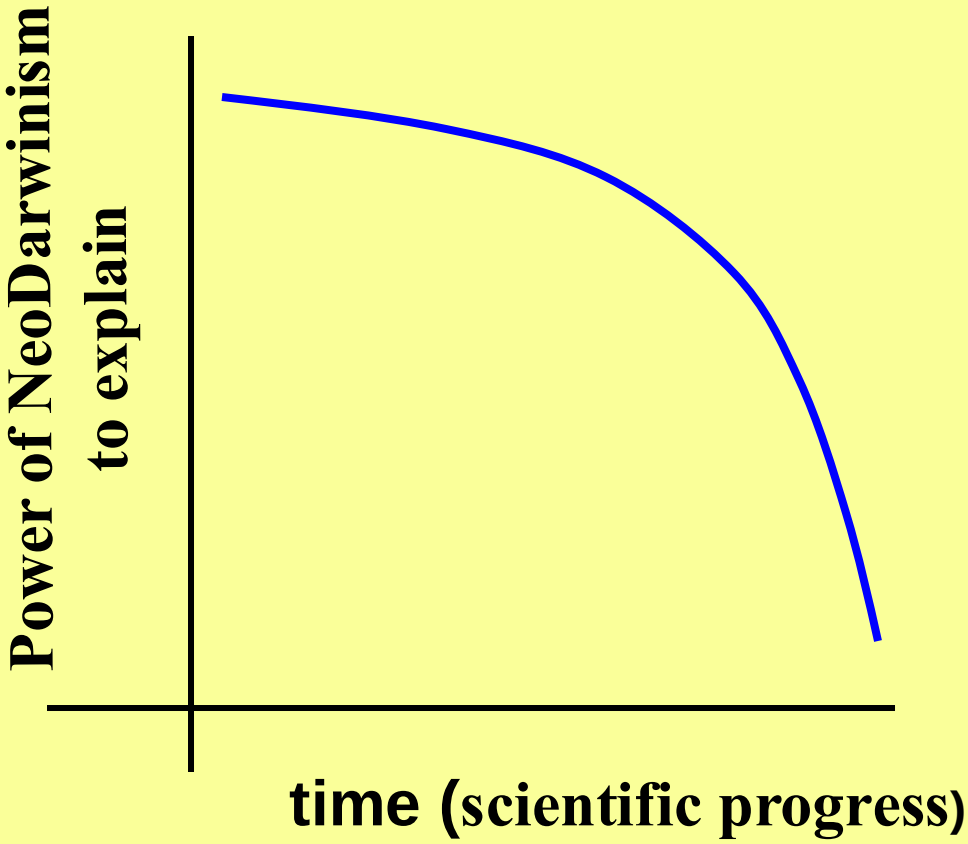
7. **Random mutation + natural selection has severe limitations**

Trend with scientific progress



discoveries #5, #6

Trend with scientific progress

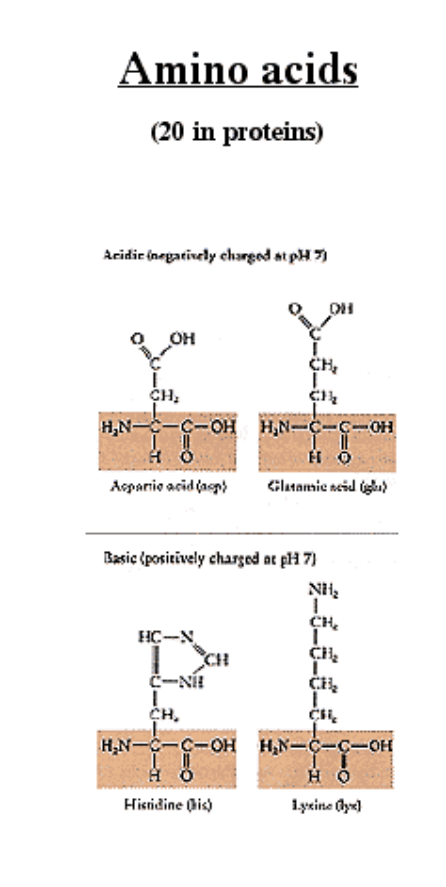


discovery #7

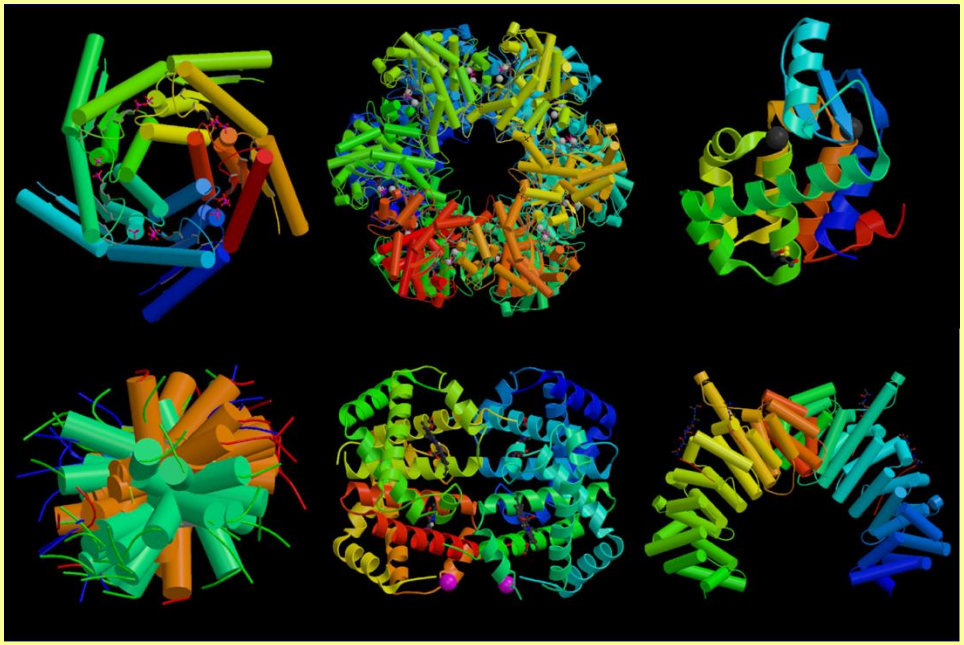
10 recent discoveries that have changed the debate about origins

5. Life is based on a digital information processing system

Proteins



chains of 20 amino acids fold into 3D structures

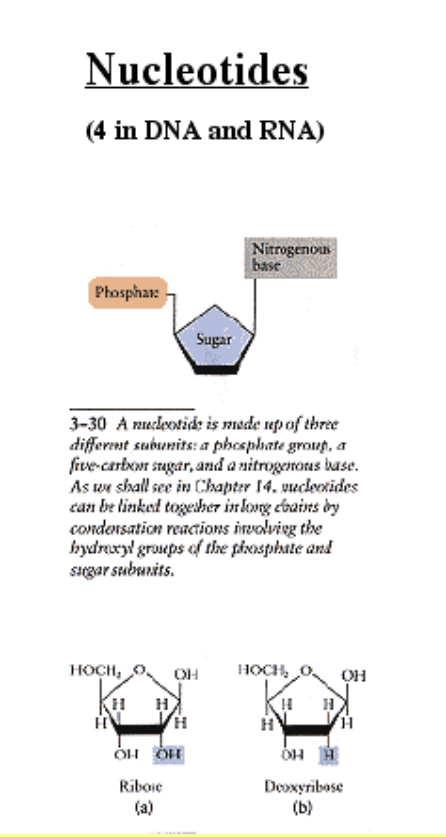


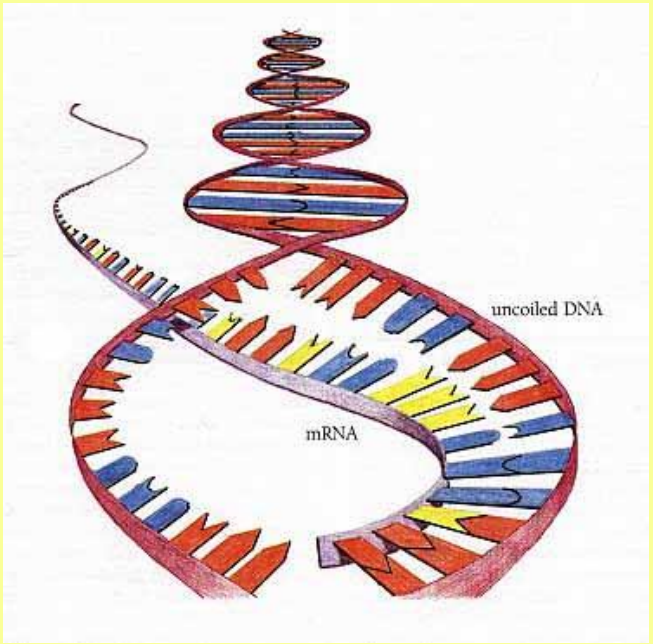
A chain of amino acids:

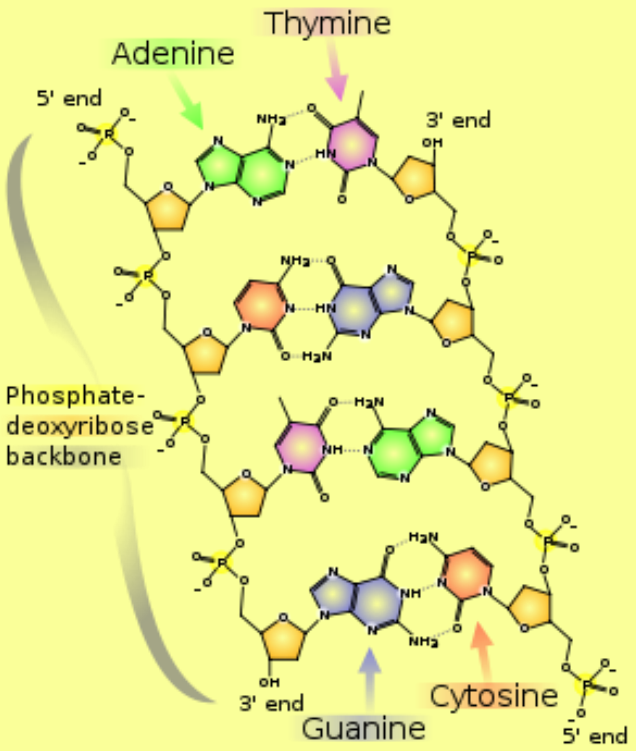
QYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPPNENVVVTNPSRPWWERYQPVSYKLCTRSGNENEFR
DMVTRCNNVGVRIYVDAVINHMCGSGAAAGTGTTCGSYCNPGSREFPAVPYSAWDFNDGKCKTASGGIESYNDPYQVRDC
QLVGLLDLALEKDYVRSMIADYLNKLIDIGVAGFRIDASKHMWPGDIKAVLDKLHNLNTNWFPAGSRPFIFQEVIDLGGE
AIKSSEYFGNGRVTEFKYGAKLGTVVRKWSGEKMSYLKNWGEGWGFMPSDRALVFVDNHDNQRGHGAGGSSILTFWDARL
YKVAVGFMLAHPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNNGVIKEVTINADTTCGNDWVCEHRWREIRNMVWFRNV
VDGEPFANWWDNGSNQVAFGRGNRGFIVFNNDDWQLSSTLQTGLPGGTYCDVISGDKVGNSCTGIKVYVSSDGTAQFSIS
NSAEDPFIAIHAESKL

DNA

chains of 4 nucleotides

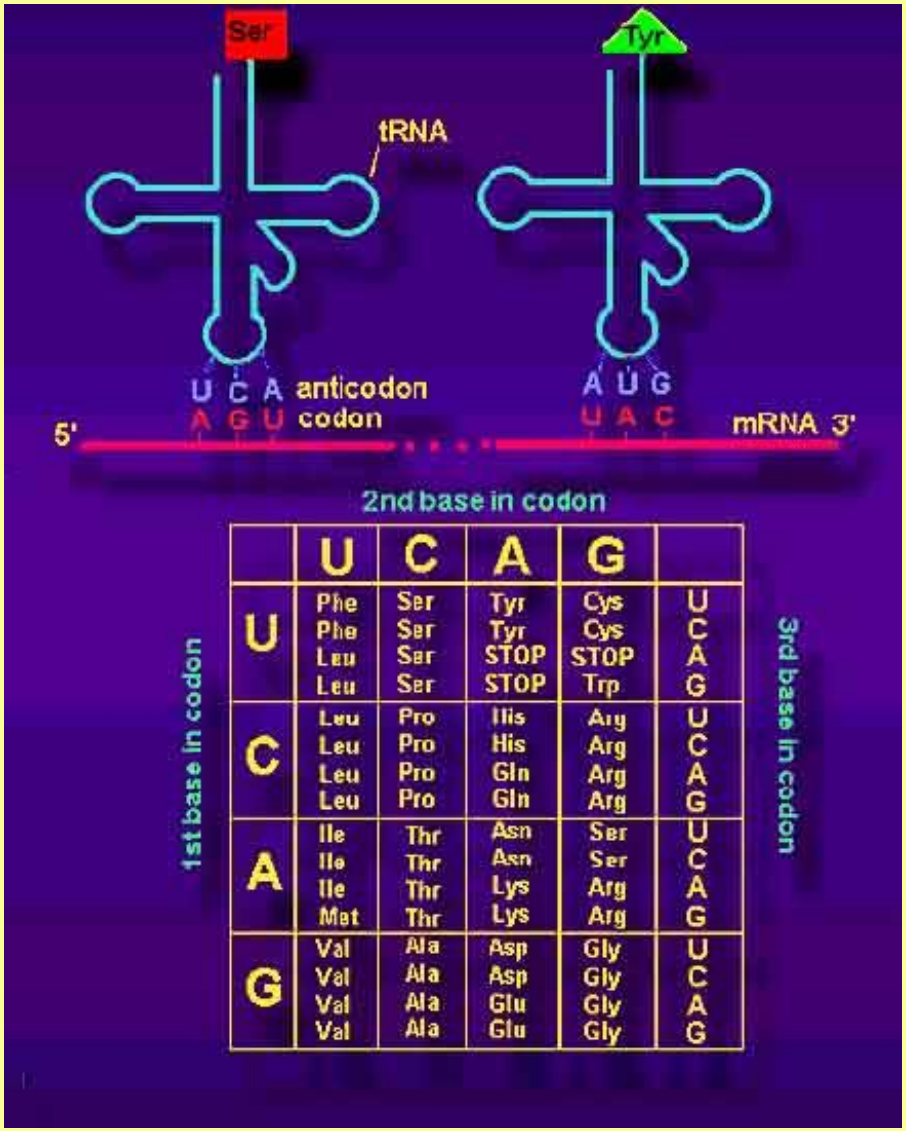






A chain of nucleotides:

ATCGCCTATATAGCGTACAATGGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGC
GCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTAC
ATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGC
CTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGCCTATAT
AGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGAT
GCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAG
CTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGC
TAGC



	U	C	A	G	
U	Phe Phe Leu Leu	Ser Ser Ser Ser	Tyr Tyr STOP STOP	Cys Cys STOP Trp	U C A G
C	Leu Leu Leu Leu	Pro Pro Pro Pro	His His Gln Gln	Arg Arg Arg Arg	U C A G
A	Ile Ile Ile Met	Thr Thr Thr Thr	Asn Asn Lys Lys	Ser Ser Arg Arg	U C A G
G	Val Val Val Val	Ala Ala Ala Ala	Asp Asp Glu Glu	Gly Gly Gly Gly	U C A G

the genetic code

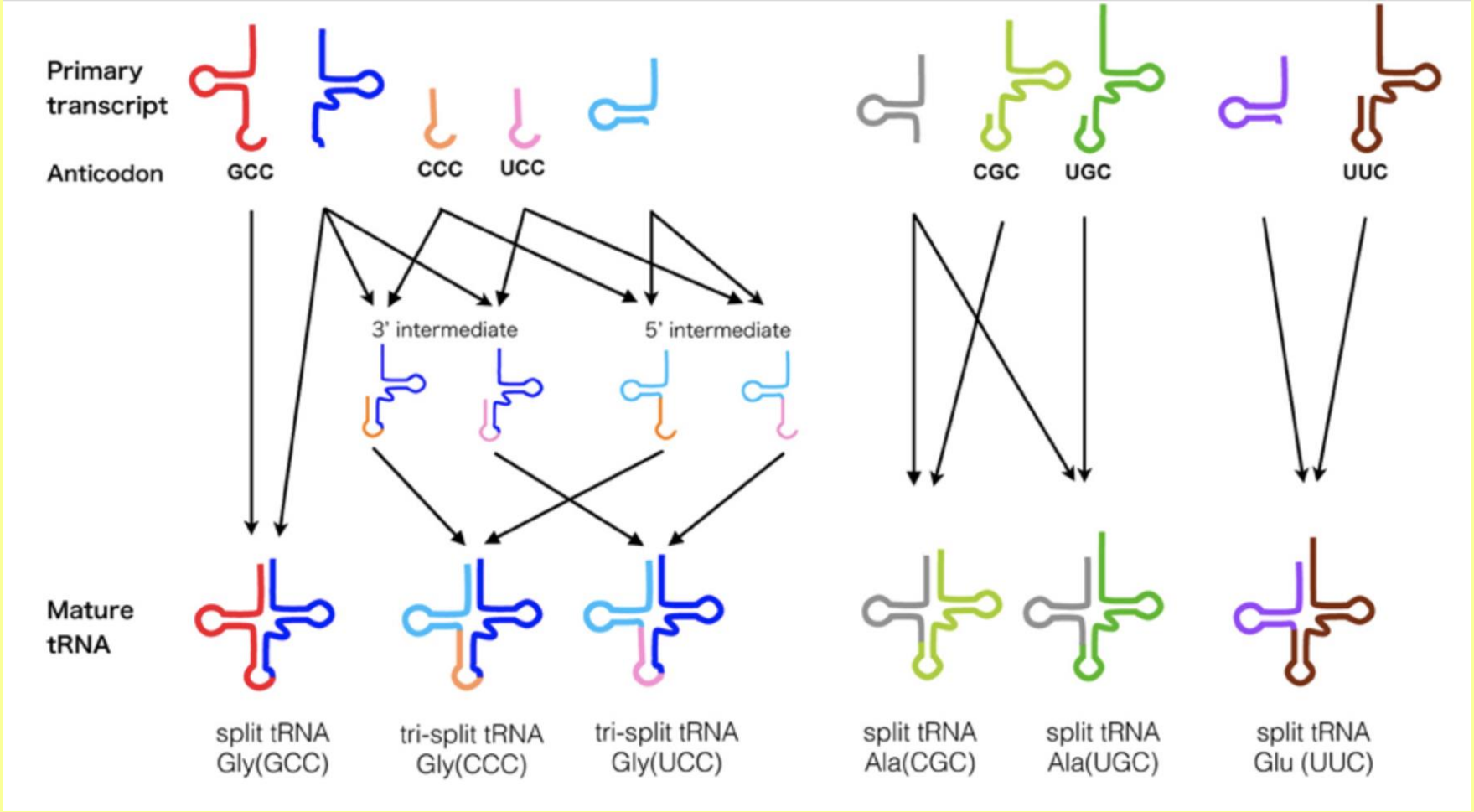
DNA: C, A, T, G

RNA: C, A, U, G

an information processing system!

tRNAs contain the code to translate between the two languages. Where do they come from?

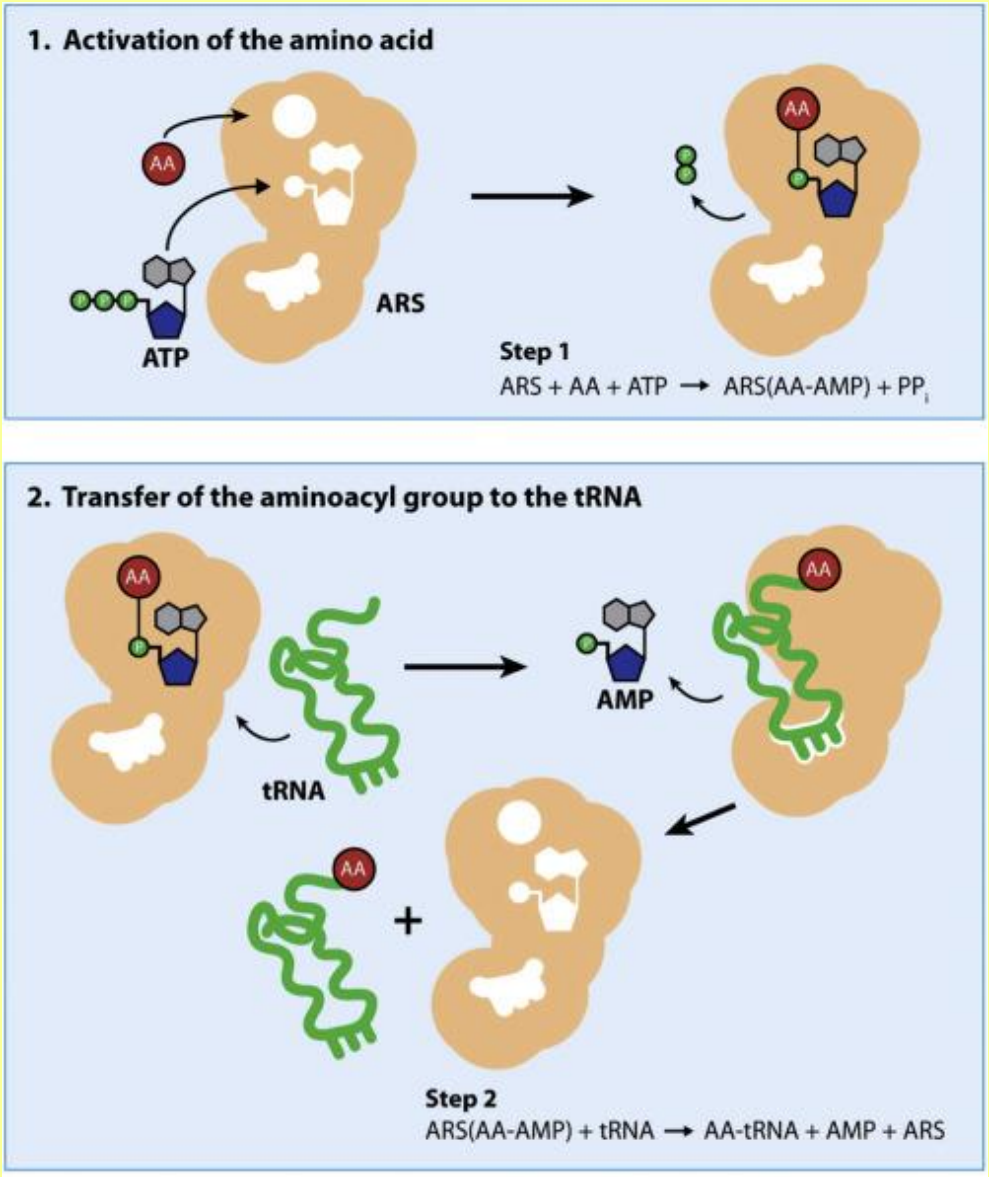
How are tRNAs made?
(Part 1)



How are tRNAs made?
(Part 2)

20 amino acids

20 of these special enzymes!



Enzymes called **tRNA synthetases** construct the tRNAs. They attach the proper amino acid to the tRNA with the corresponding RNA codon. The code is written into these enzymes.

No one knows where these enzymes come from.

Craig Venter: "life is a DNA software system" containing "digital information" or "digital code," and the cell is a "biological machine" full of "protein robots".

Richard Dawkins: "[t]he machine code of the genes is uncannily computer-like."

Carl Sagan: "information content of a simple cell" is "around 10^{12} bits, comparable to about a hundred million pages of the *Encyclopedia Britannica*.

Francis Collins: DNA is something like the hard drive on your computer," containing "programming".

Summary:

Life is based on a digital information processing system. The code is built into a series of enzymes. No one knows where the code came from or how this system could come about.

Infinite universes and chance?

Biology Direct

BioMed Central

Hypothesis

Open Access

The cosmological model of eternal inflation and the transition from chance to biological evolution in the history of life

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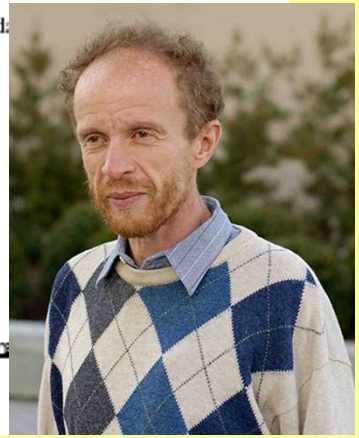


Eugene Koonin
Senior Investigator
NIH

Infinite universes and chance?

Abstract

Background: Recent developments in cosmology radically change the conception of the universe as well as the very notions of "probable" and "possible". The model of eternal inflation implies that all macroscopic histories permitted by laws of physics are repeated an infinite number of times in the infinite multiverse. In contrast to the traditional cosmological models of a single, finite universe, this worldview provides for the origin of an infinite number of complex systems by chance, even as the probability of complexity emerging in any given region of the multiverse is extremely low. This change in perspective has profound implications for the history of any phenomenon, and life on earth cannot be an exception.

Hypothesis: Origin of life is a chicken and egg problem: for biological evolution that is governed, primarily, by natural selection, to take off, efficient systems for replication and translation are required, but even barebones cores of these systems appear to be products of extensive selection. The currently favored (partial) solution is an RNA world without proteins in which replication is catalyzed by ribozymes and which serves as the cradle for the translation system. However, the RNA world faces its own hard problems as ribozyme-catalyzed RNA replication remains a hypothesis and the selective pressures behind the origin of translation remain mysterious. Eternal inflation offers a viable alternative that is untenable in a finite universe, i.e., that a coupled system of translation and replication emerged by chance, and became the breakthrough stage from which biological evolution, centered around Darwinian selection, took off. A corollary of this hypothesis is that an RNA world, as a diverse population of replicating RNA molecules, might have never existed. In this model, the stage for Darwinian selection is set by anthropic selection of complex systems that rarely but inevitably emerge by chance in the infinite universe (multiverse).

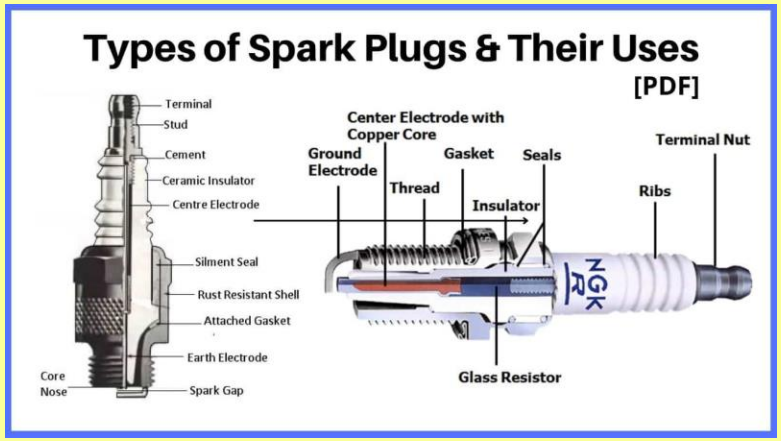
12 discoveries that have changed the debate about origins

6. Molecular machines and sophisticated software algorithms are essential to all life-forms

Two important concepts:

Irreducible complexity

(Darwin's Black Box, Michael Behe)



Several components must be present for function

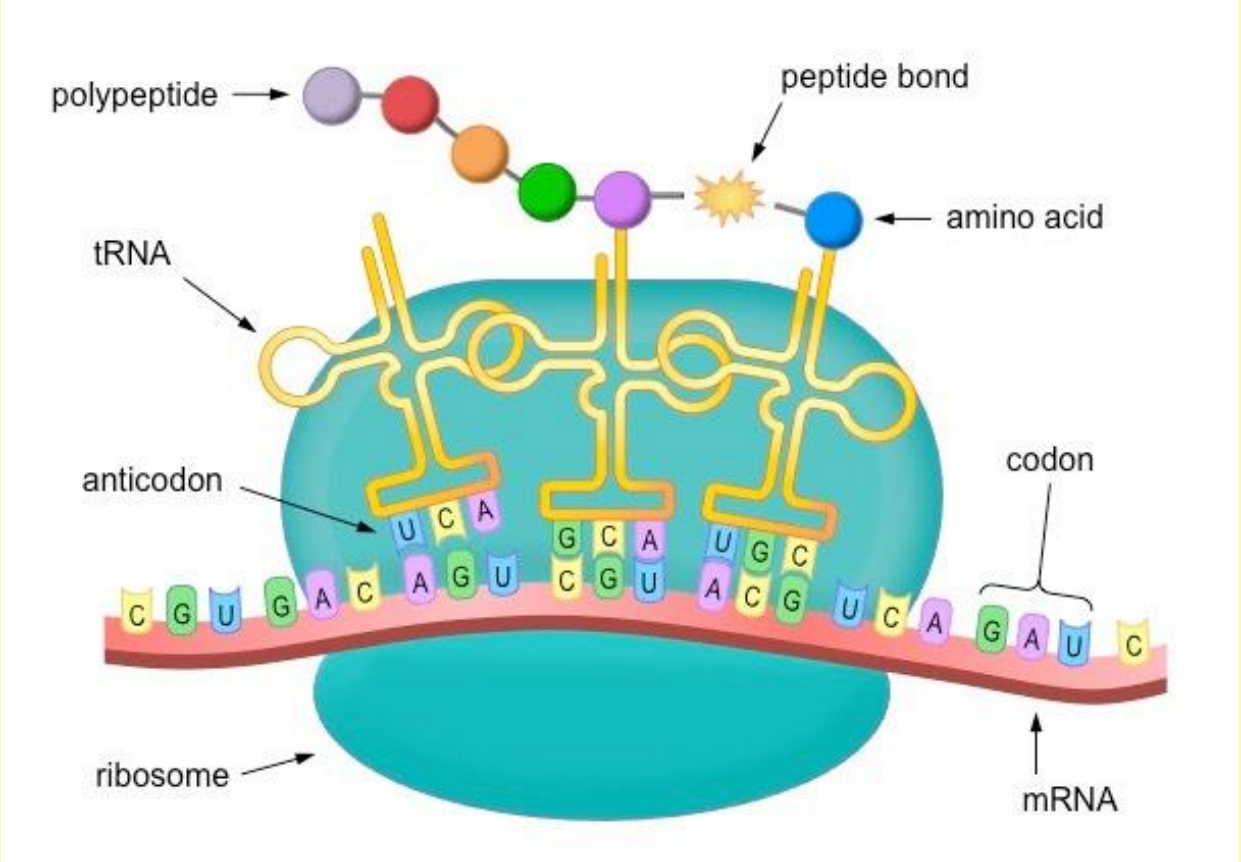
Hierarchical coherence

(Undeniable, Douglas Axe)

Spark plug must fit into a larger system

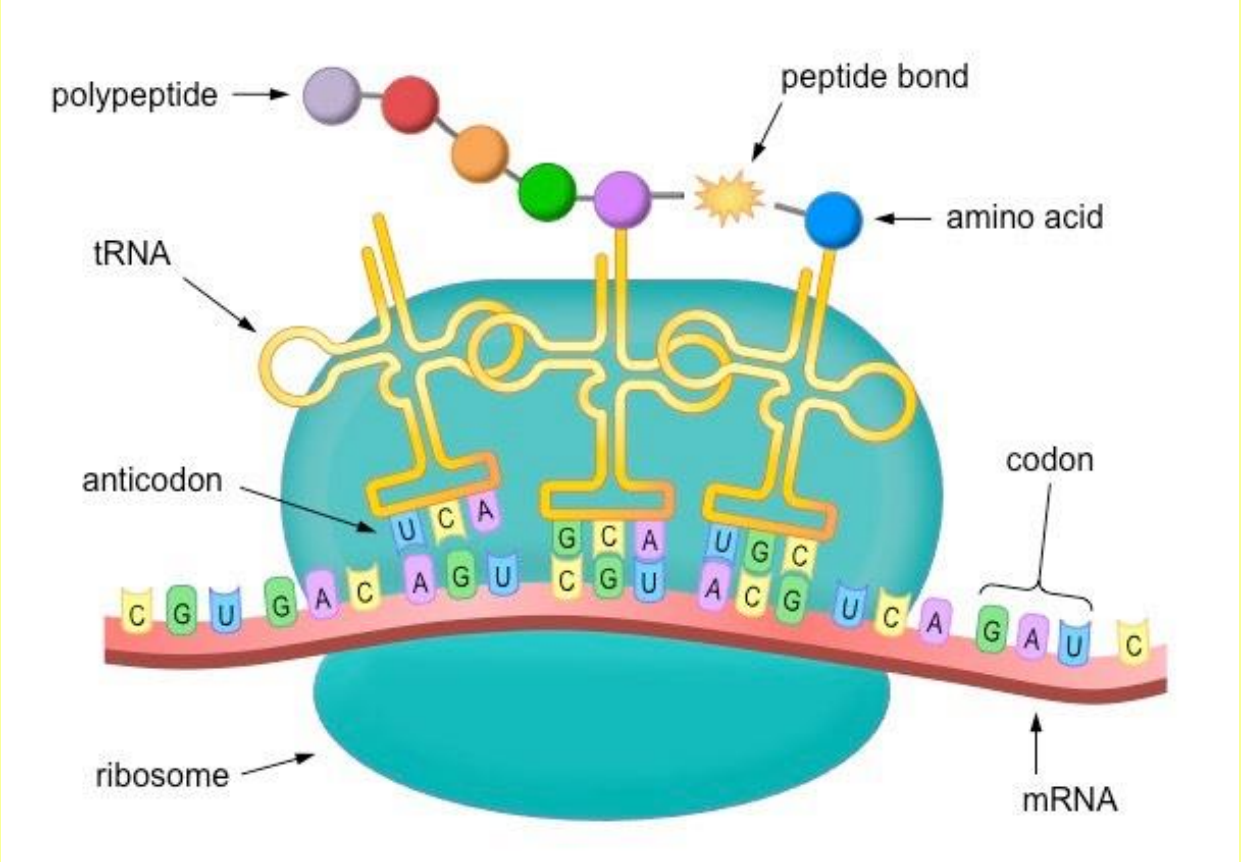
The entire system must be coherent

ribosome



https://www.youtube.com/watch?v=TfYf_rPWUdY

ribosome



Ribosomes must fit into a larger system

The entire system must be coherent

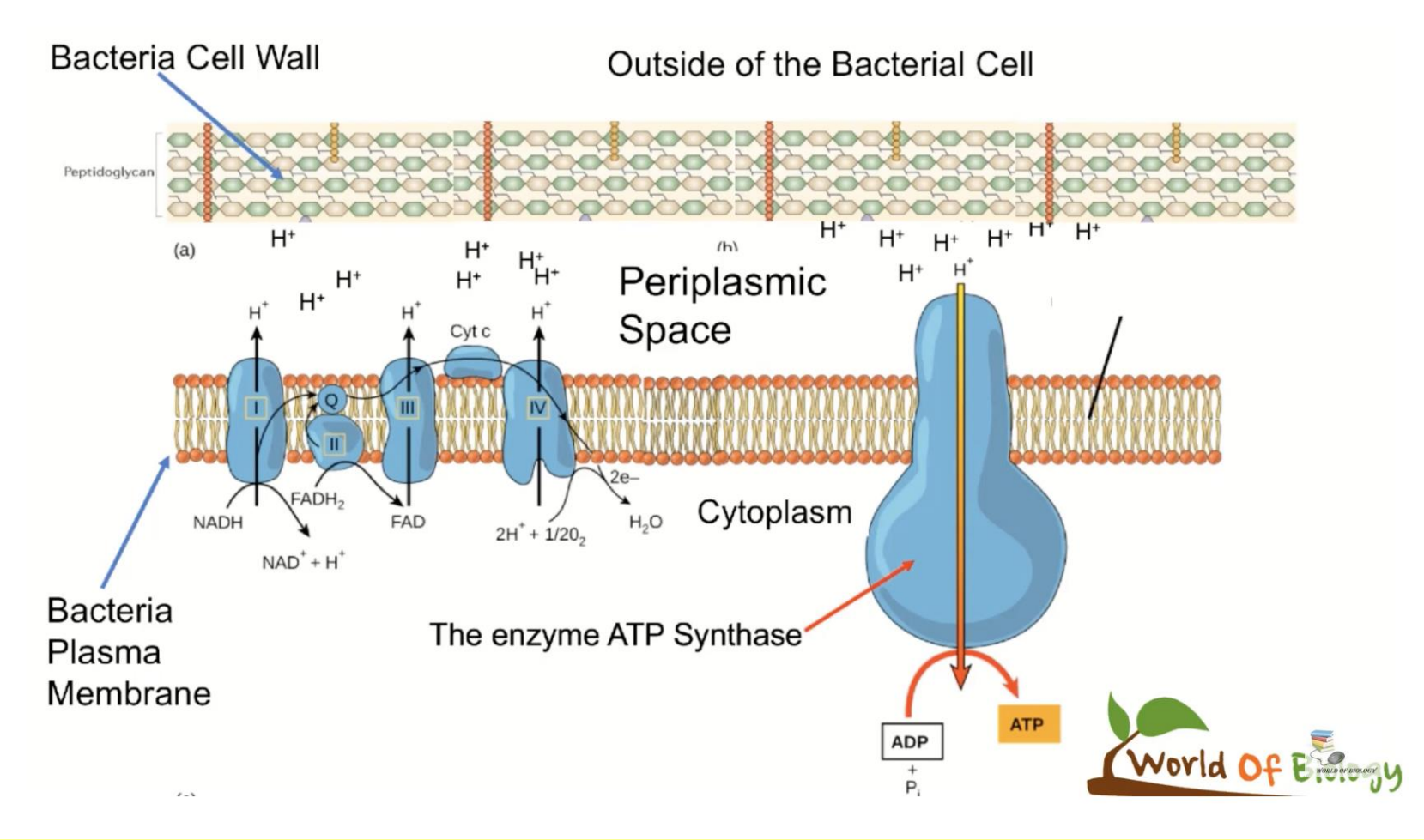
ATP synthase

ATP synthase is a machine that converts a proton gradient to mechanical energy which is converted to chemical energy

ATP synthase

https://www.youtube.com/watch?v=XI8m6o0gXDY

Bacteria



ATP synthases must fit into a larger system

The entire system must be coherent

-NADH and FADH2 require Citric Acid Cycle

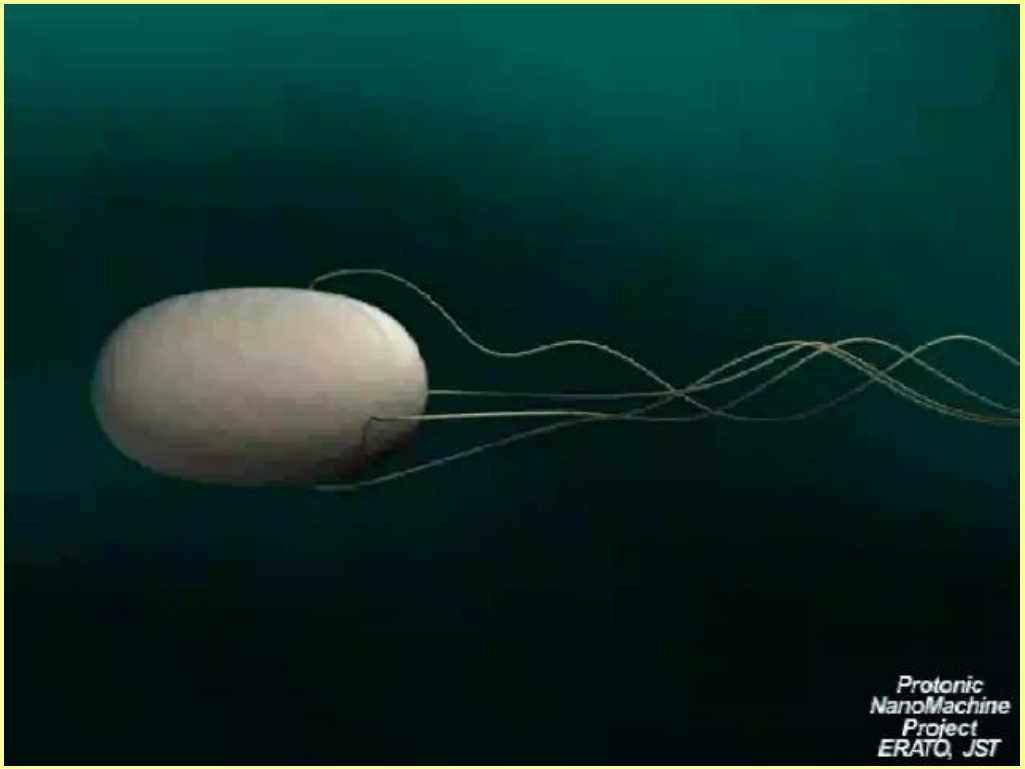
-Citric Acid Cycle requires Pyruvate Oxidation

-Pyruvate Oxidation requires Glycolysis

ATP synthases must fit into a larger system

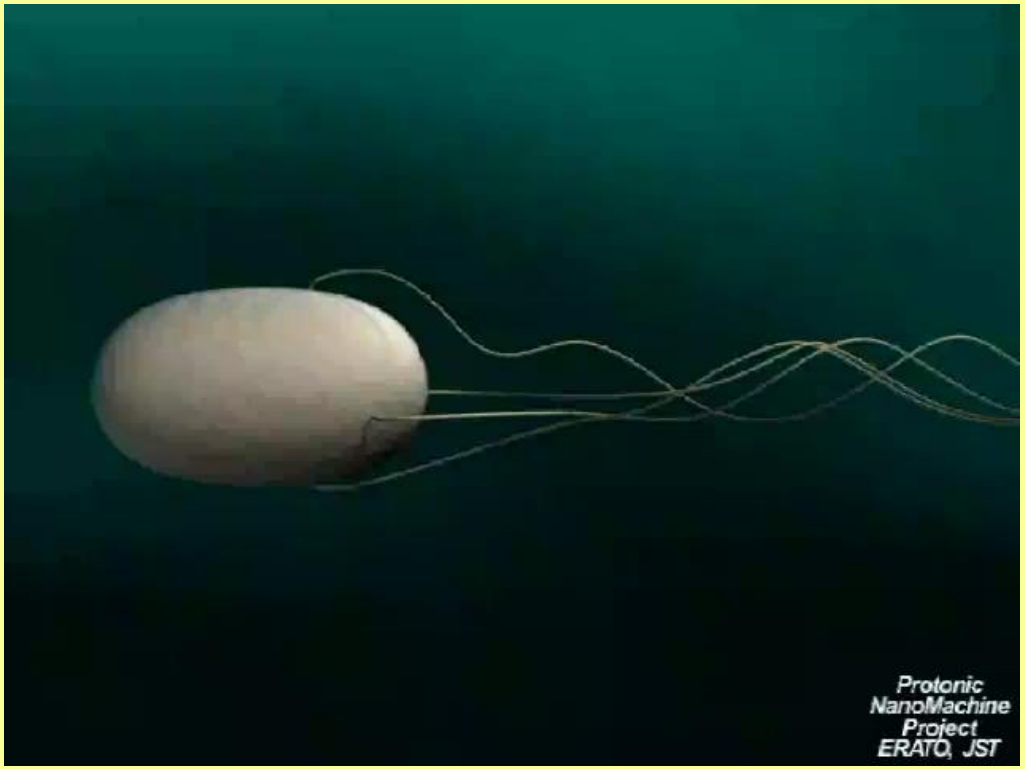
The entire system must be coherent

Bacterial Flagellum



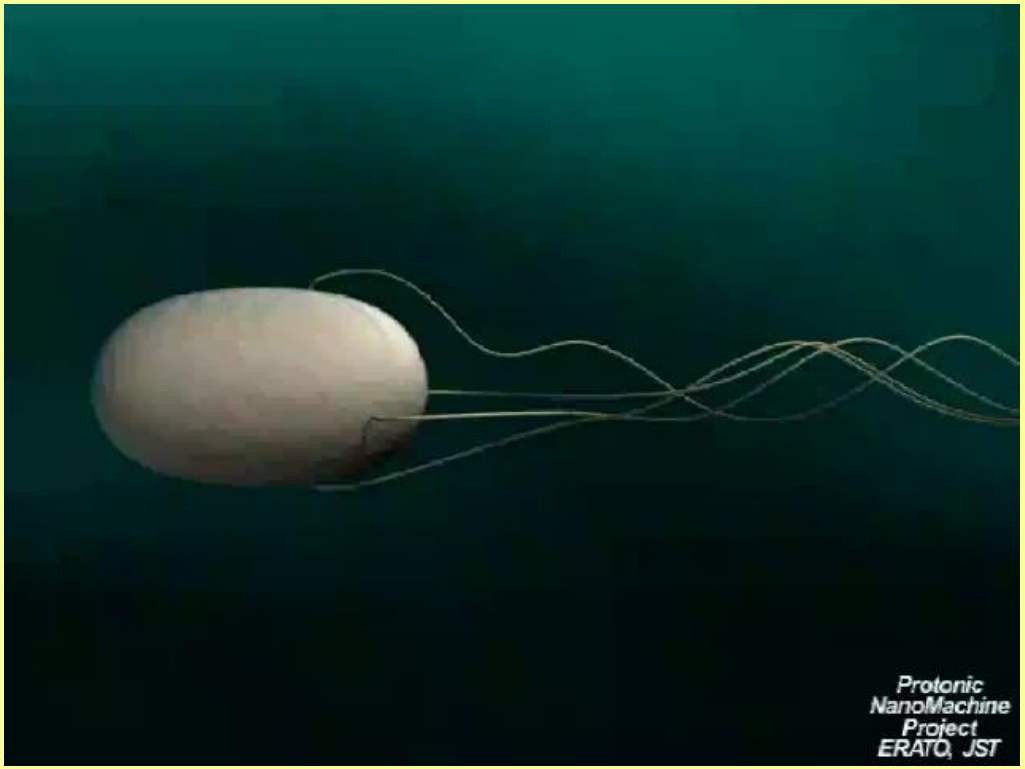
The bacterial flagellum is a machine that converts a proton gradient into mechanical motion

Bacterial Flagellum

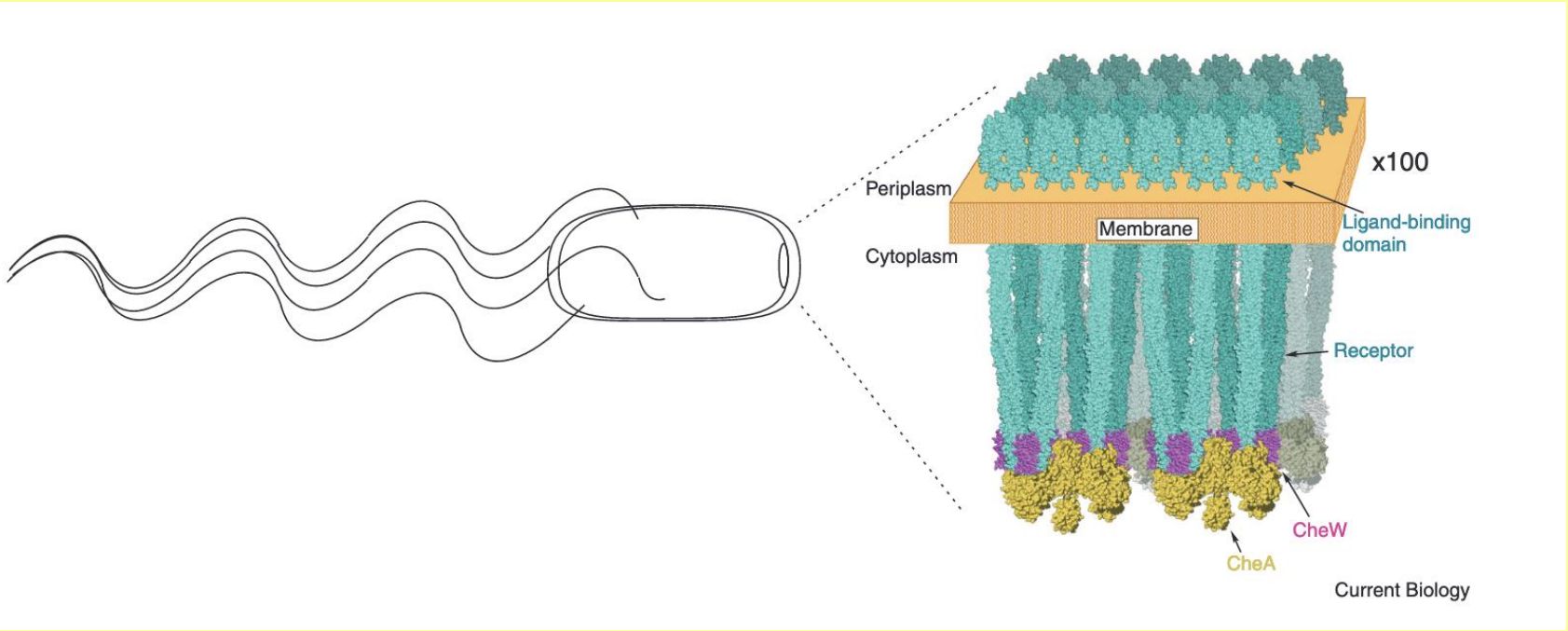


https://www.youtube.com/watch?v=fFq_MGf3sbk&t=44s

Bacterial Flagellum

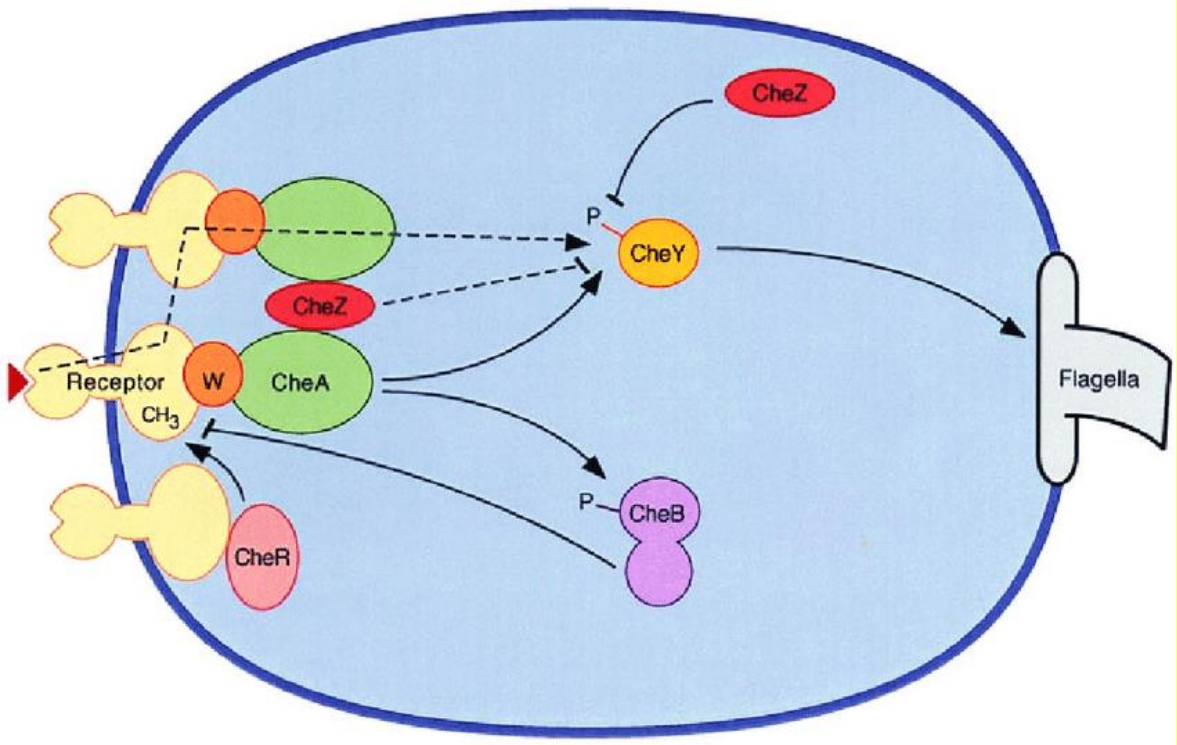


https://www.google.com/search?q=bacterial+flagellum+video&oq=bacterial+flagellum+video&gs_lcrp=EgZjaHJvbWUyBggAEEUYOTIICAEQABgWGB4yCAgCEAAYFhgeMg0IAxAAGIYDGIAEGIoFMg0IBBAAGIYDGIAEGIoFMg0IBRAAGIYDGIAEGIoFMg0IBhAAGIYDGIAEGIoFMgoIBxAAGIAEGKIEMgoICBAAGIAEGKIEMgoICRAAGIAEGKIE0gEIODE4NWowajmoAgiwAgE&sourceid=chrome&ie=UTF-8#fpstate=ive&vld=cid:81311310,vid:MNR48hUd-Hw,st:0



To move toward a food molecule (glucose):

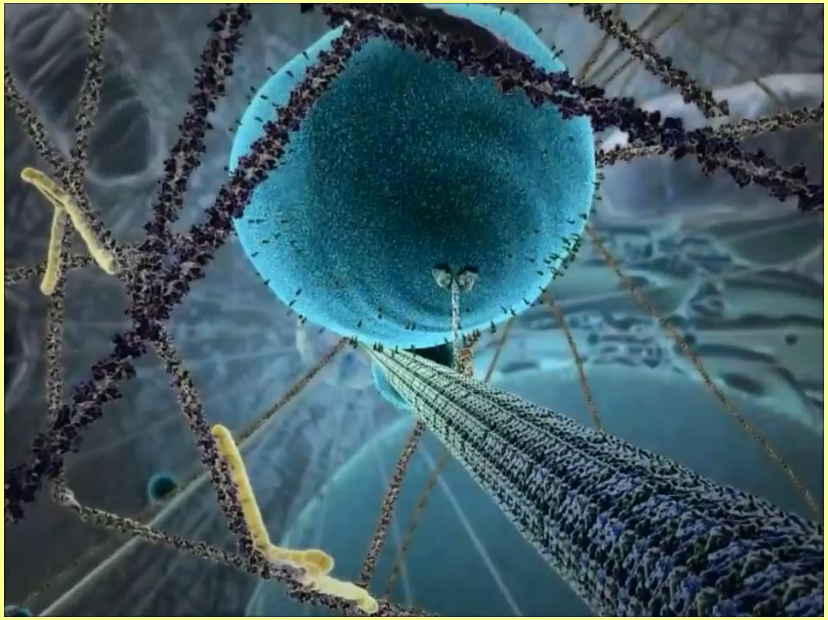
- The flagellar motion must be controlled
- The control mechanism must be connected to a sensor
- The sensor must distinguish between molecules



The flagellum must fit into a larger system

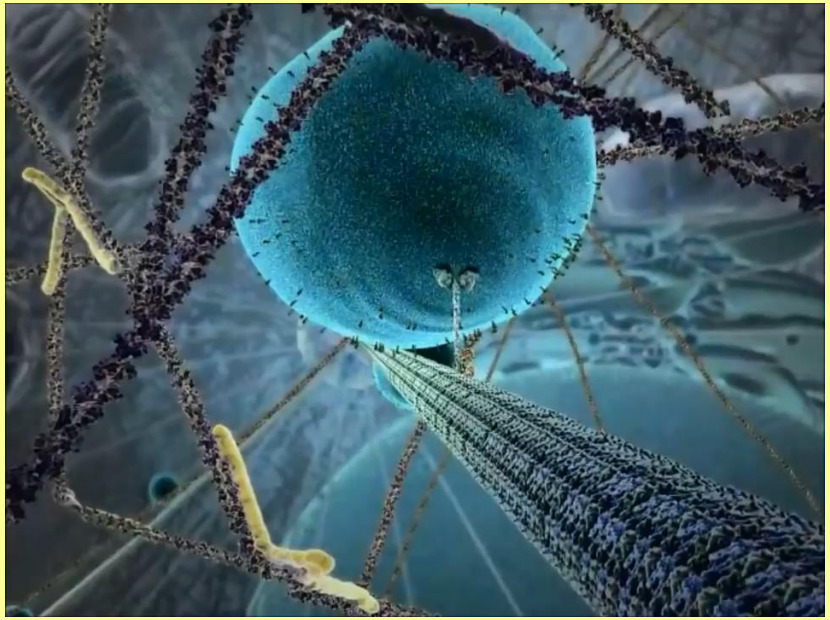
The entire system must be coherent

Kinesin



https://www.youtube.com/watch?v=mBo_o0iO68U

Kinesin

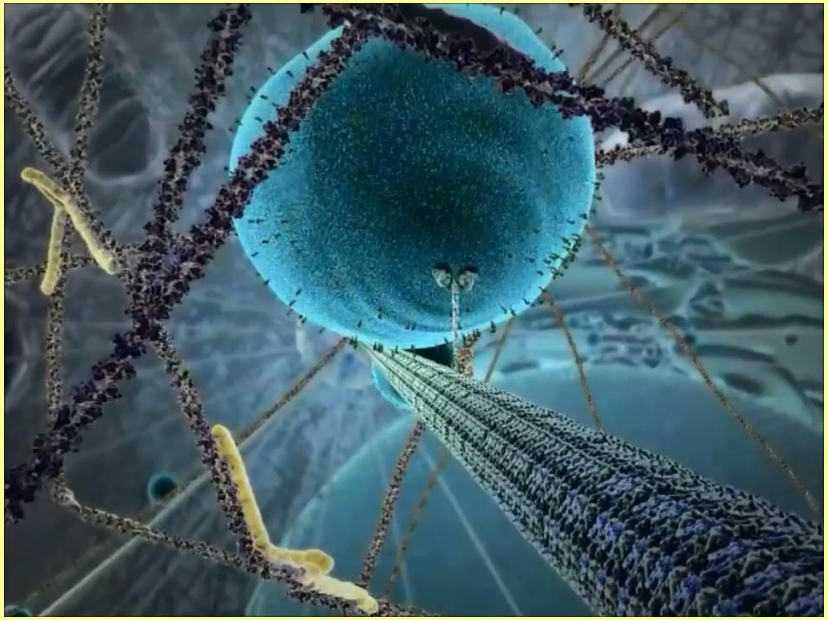


Kinesin must:

- Convert chemical energy to mechanical motion
- Bind to microtubules in correct orientation
- Bind to the cargo
- Release from microtubules and release cargo

- Microtubules must be located between source and destination

Kinesin



Kinesin motor proteins must fit into a larger system

The entire system must be coherent

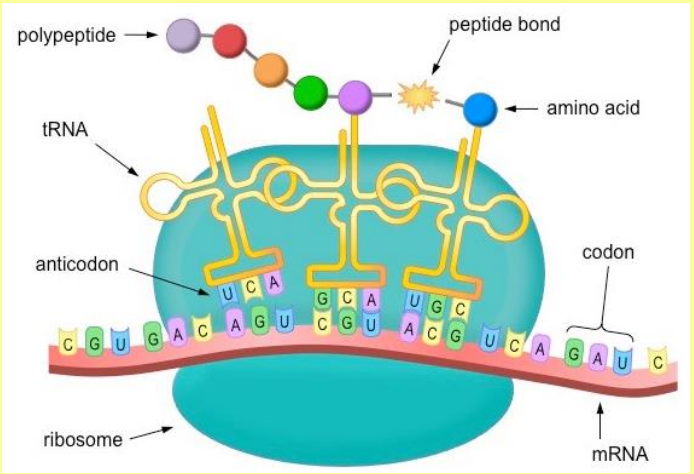
How does it function? **(physics and chemistry)**

Where did it come from? **(a mind)**

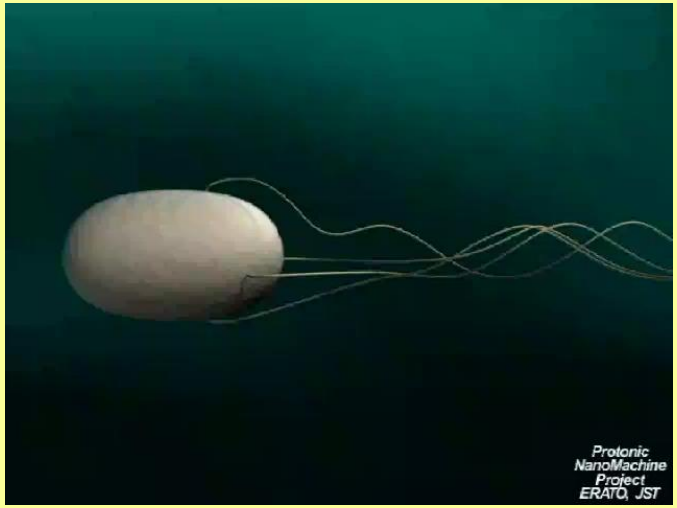
An informational discontinuity

ATP Synthase

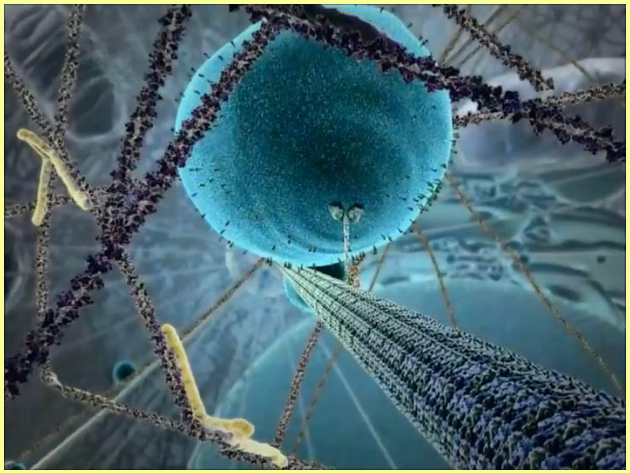
Ribosome



Bacterial Flagellum



Kinesin

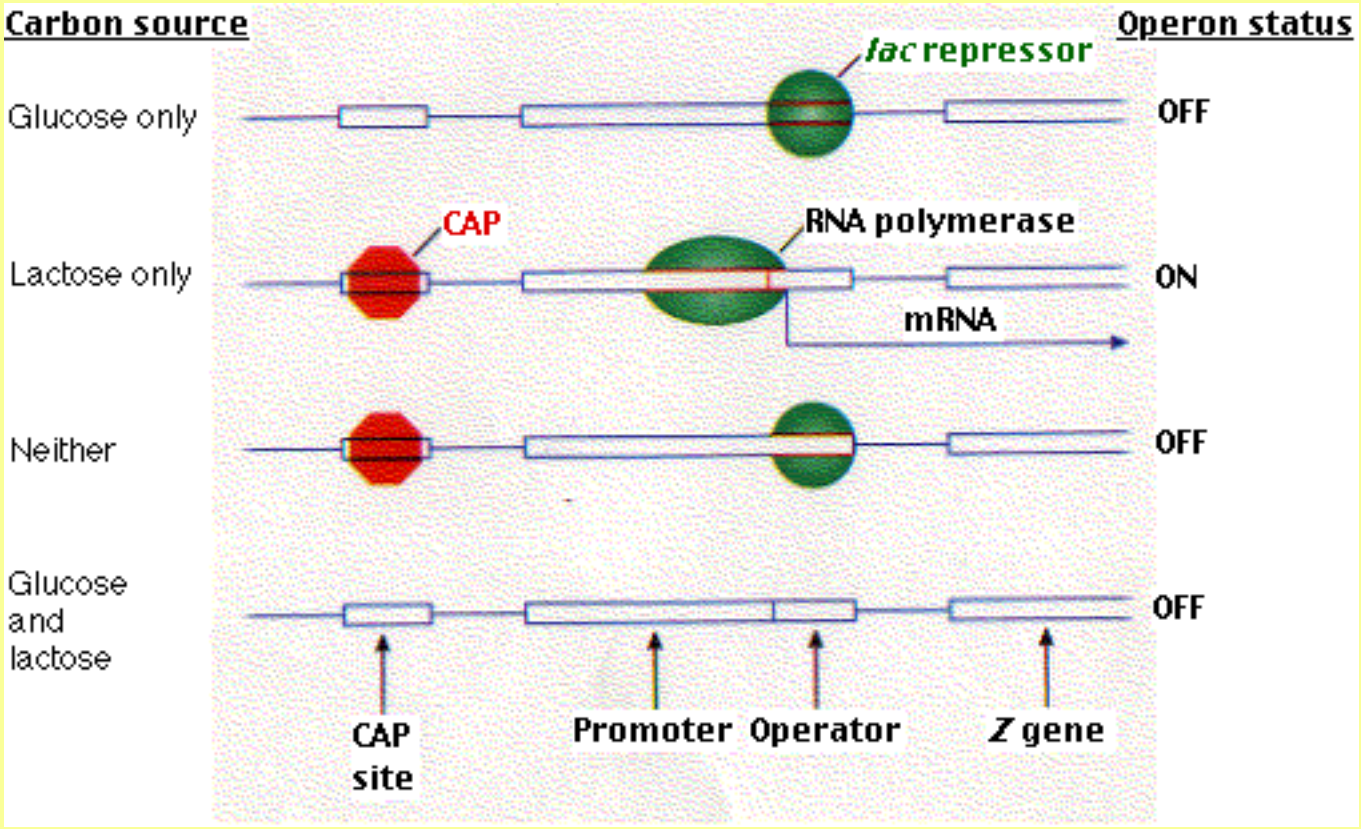


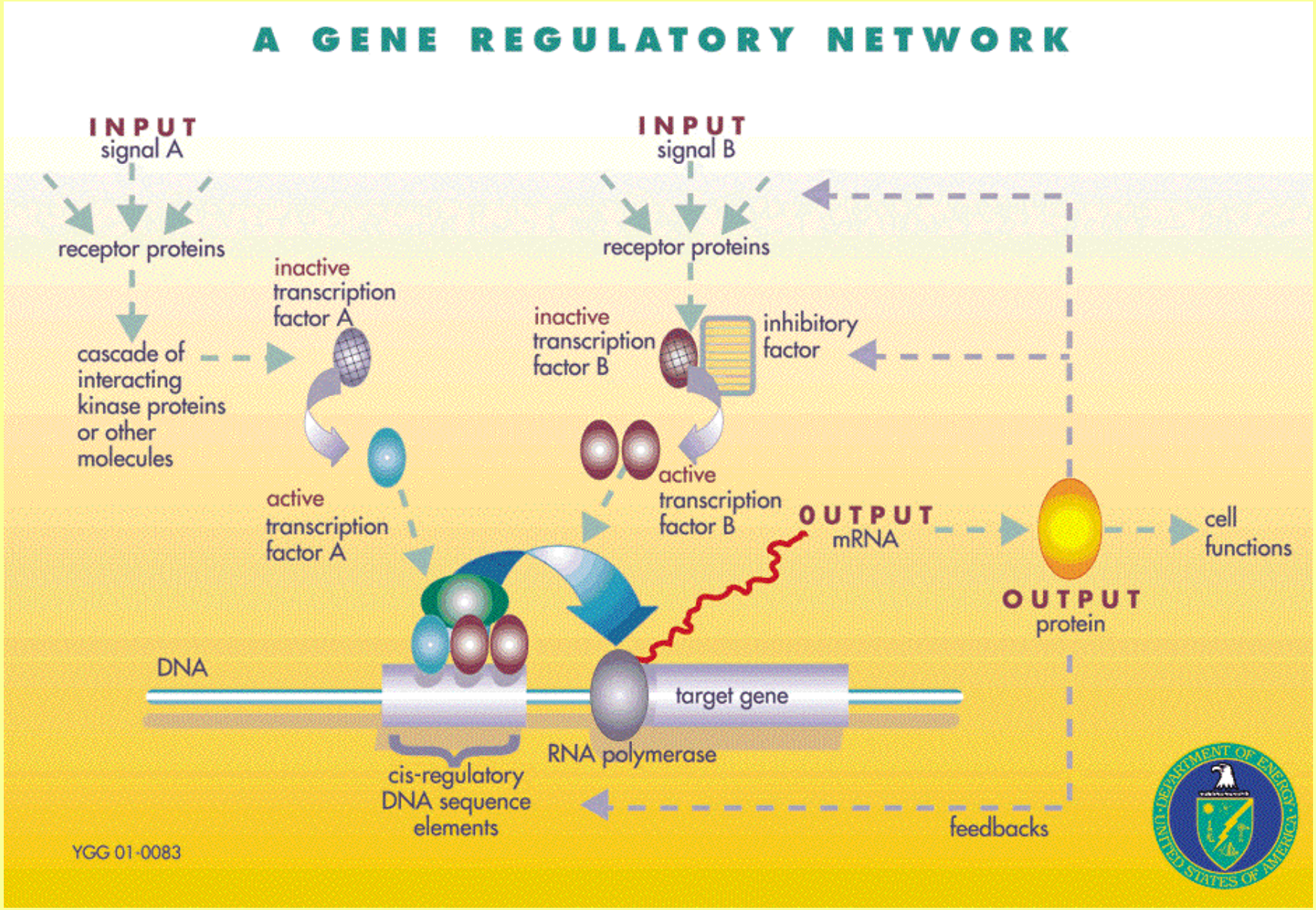
Informational discontinuities?

All Cells Have Sophisticated Software Algorithms

Example of a simple algorithm: (lac operon)

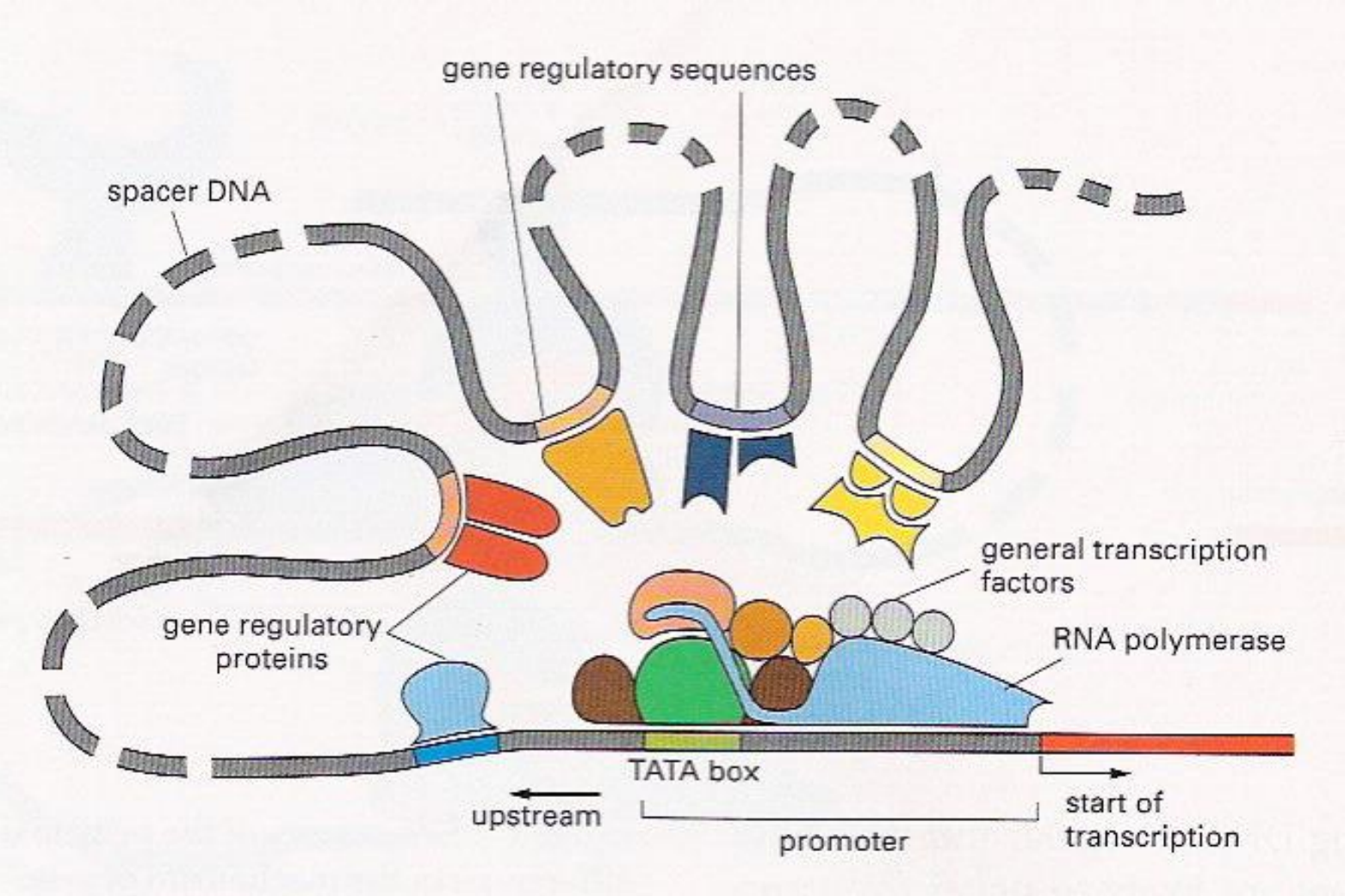
Utilizes both positive (CAP) and negative (repressor) control



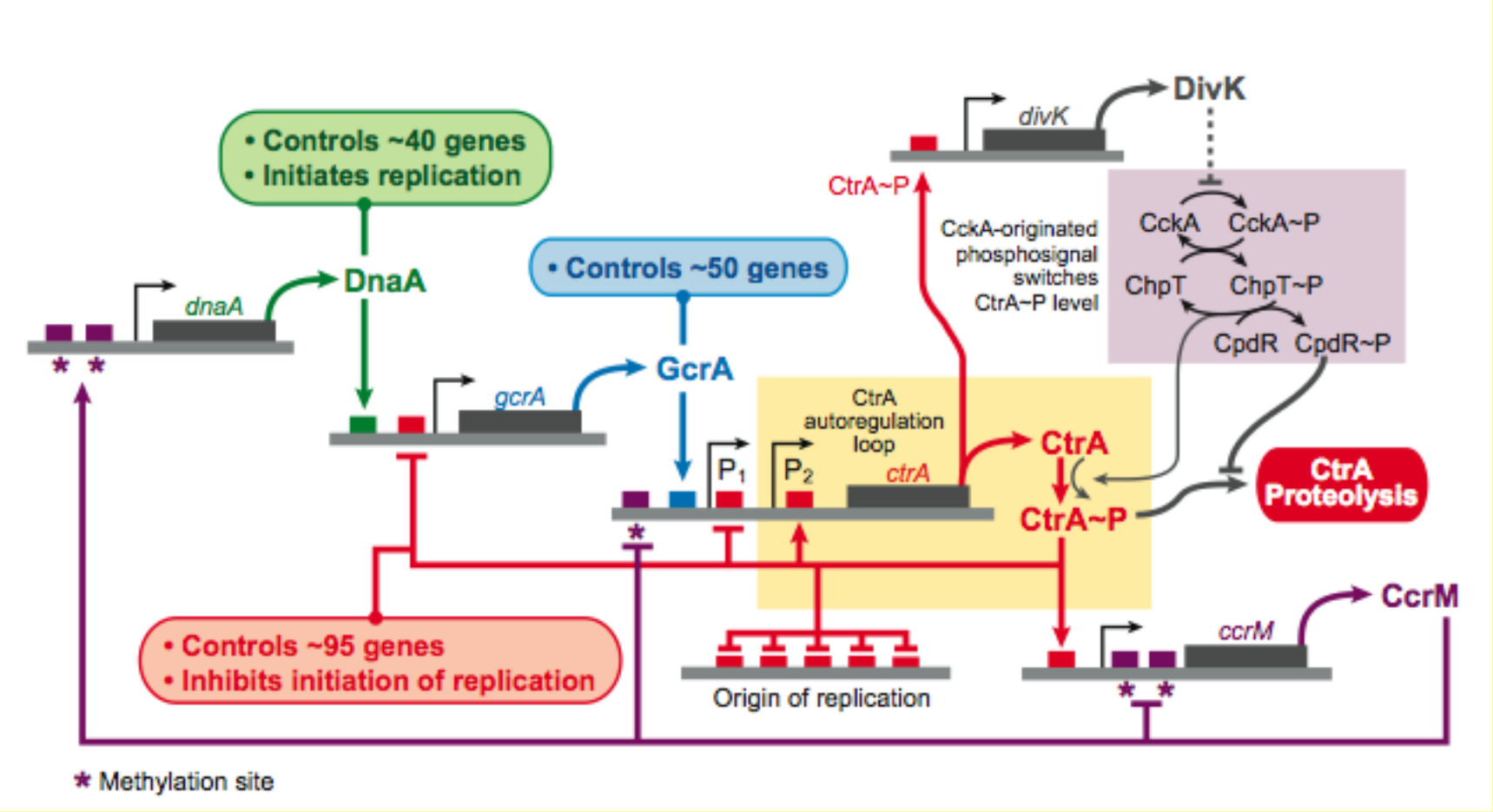

A GENE REGULATORY NETWORK
INPUT
signal A
INPUT
signal B
receptor proteins
receptor proteins
inactive
transcription
factor A
inactive
transcription
factor B
inhibitory
factor
cascade of
interacting
kinase proteins
or other
molecules
active
transcription
factor A
active
transcription
factor B
OUTPUT
mRNA
cell
functions
OUTPUT
protein
DNA
target gene
RNA polymerase
cis-regulatory
DNA sequence
elements
feedbacks
YGG 01-0083

"In animals and plants, it is not unusual to find the regulatory sequences of a gene dotted over distances of 50,000 nucleotide pairs…"

from
"Essential Cell Biology"
Alberts et al



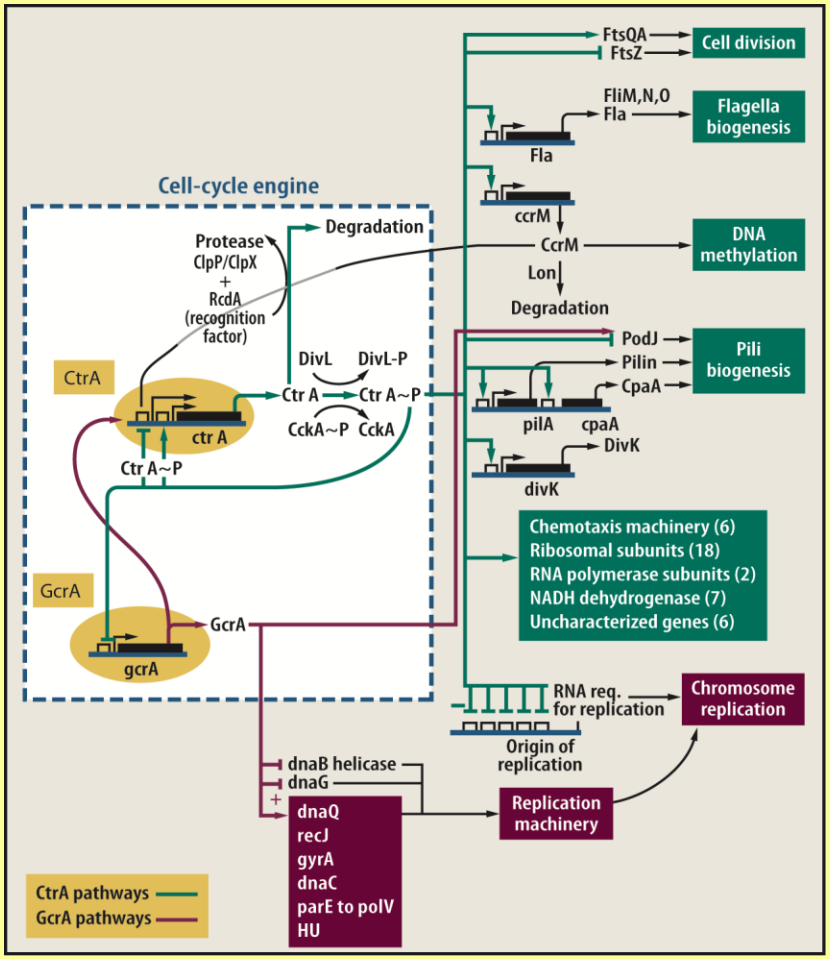
Genetic regulatory network of cell cycle in Caulobacter



Michael T. Laub, Lucy Shapiro, Harlan H. McAdams Annu. Rev. Genet. 2007. 41:429–41

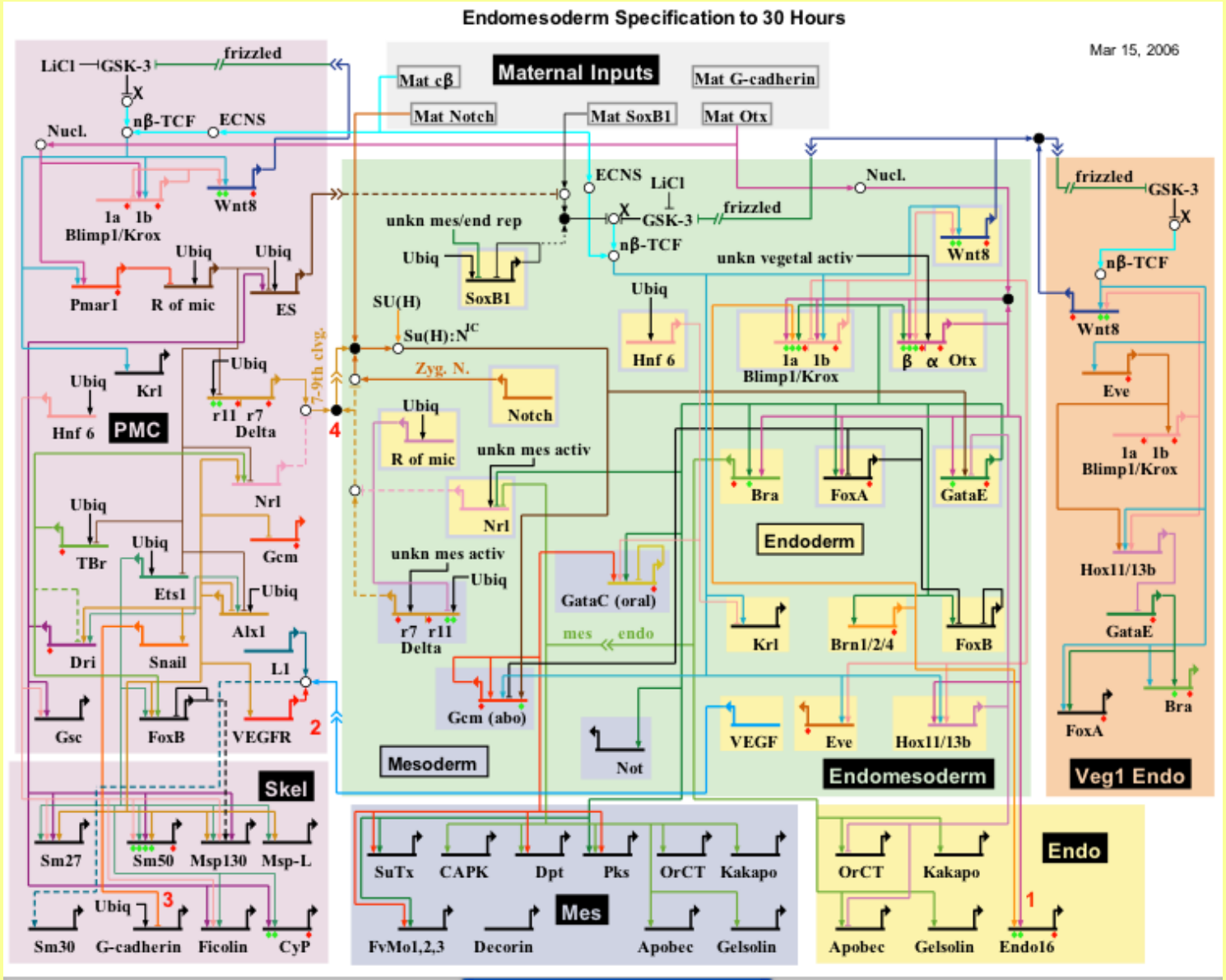
Genetic regulatory network of cell cycle in Caulobacter

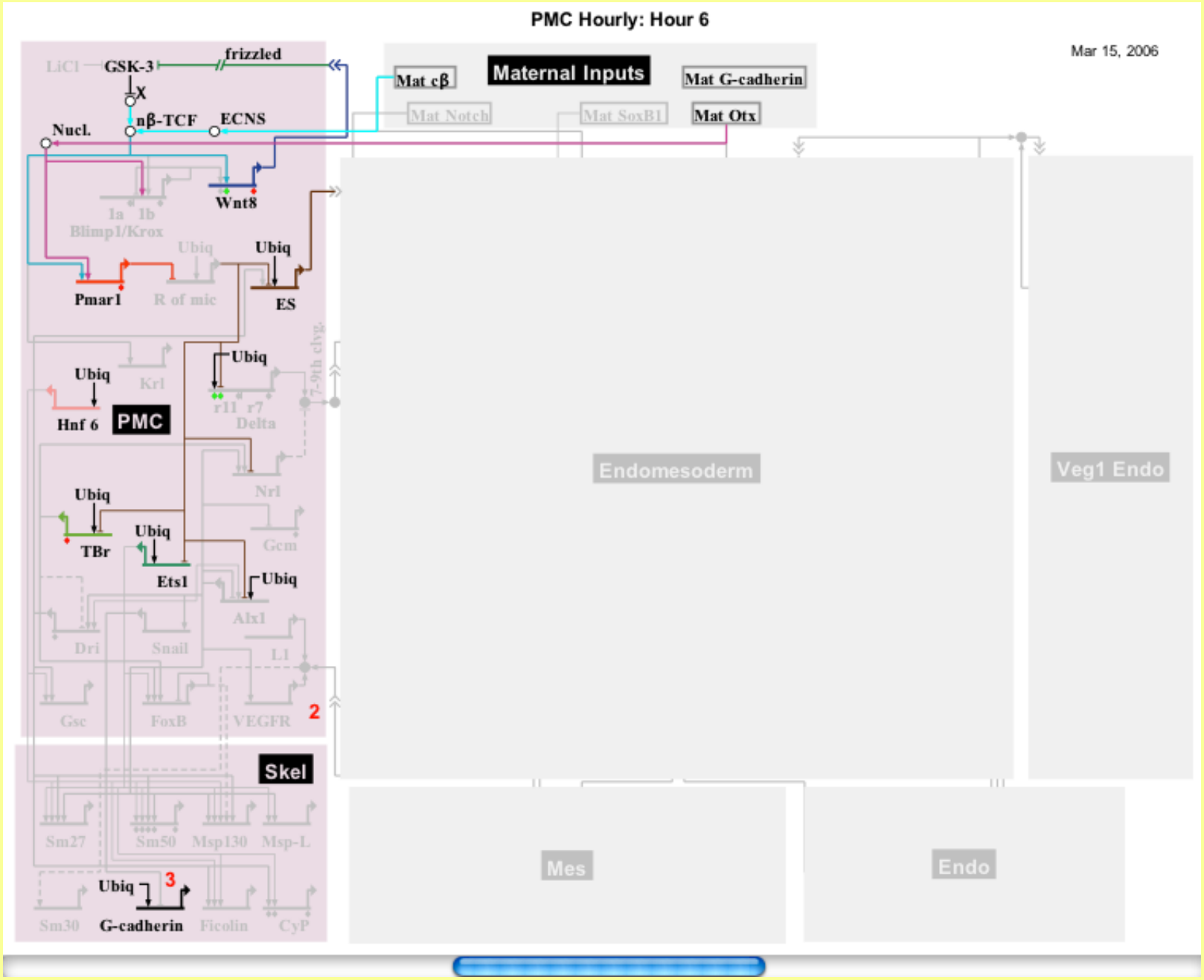
- **550 regulated cell cycle genes, 586 noncoding and antisense RNAs**
- **Hardwired system to turn genes on and off**
- **Chromosome replication is a clock, controls timing**
- **DNA methylation plays a critical role (epigenetic information)**
- **Robust system – many regulation modes**



Genetic regulatory network controlling endomesoderm development in sea urchin embryos:

E. Davidson, et al
http://labs.systemsbiology.net/bolouri/software/BioTapestry/




PMC Hourly: Hour 6
Mar 15, 2006
Maternal Inputs
Mat cβ
Mat G-cadherin
Mat Notch
Mat SoxB1
Mat Otx
LiCl
GSK-3
frizzled
X
Nucl.
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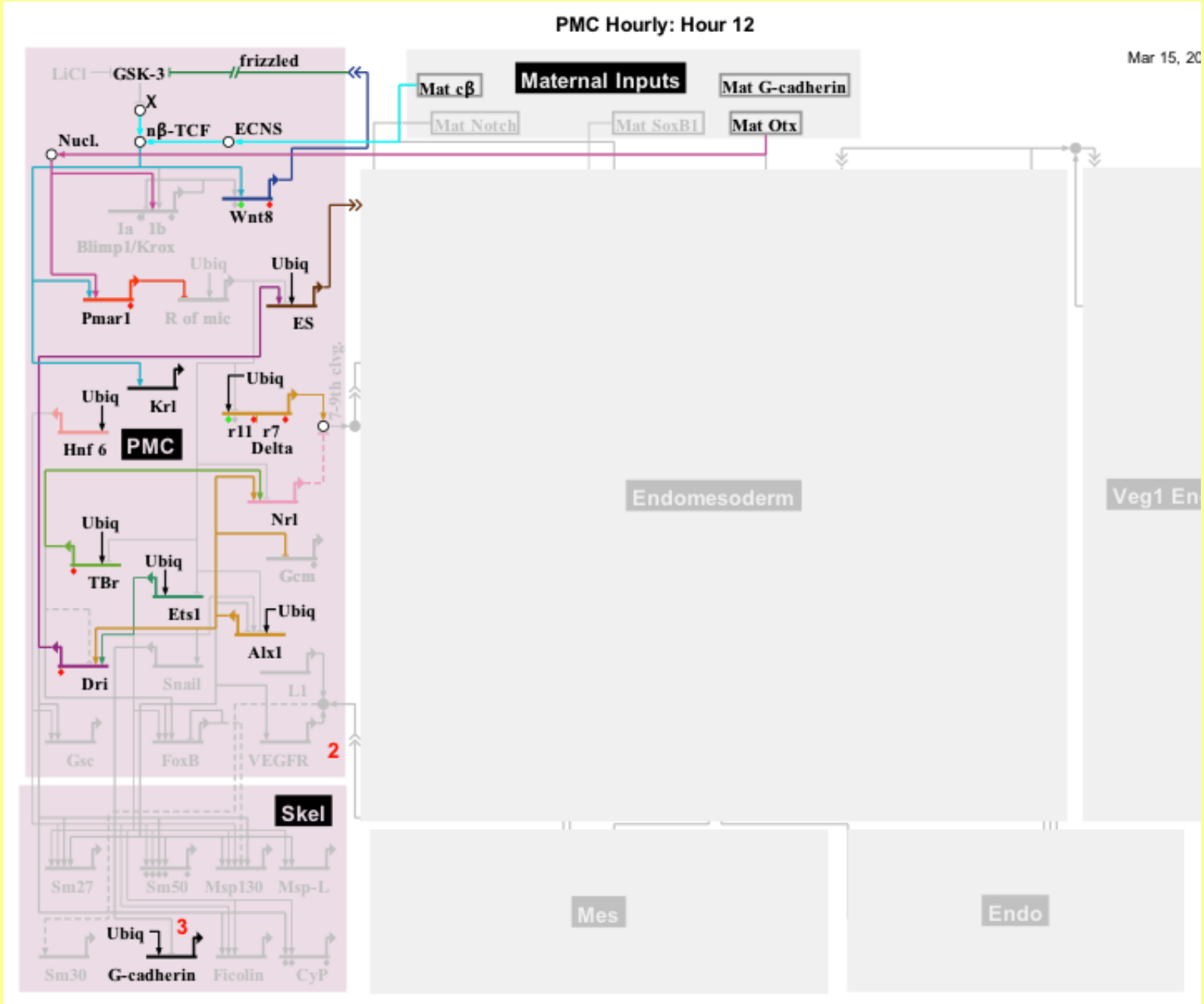
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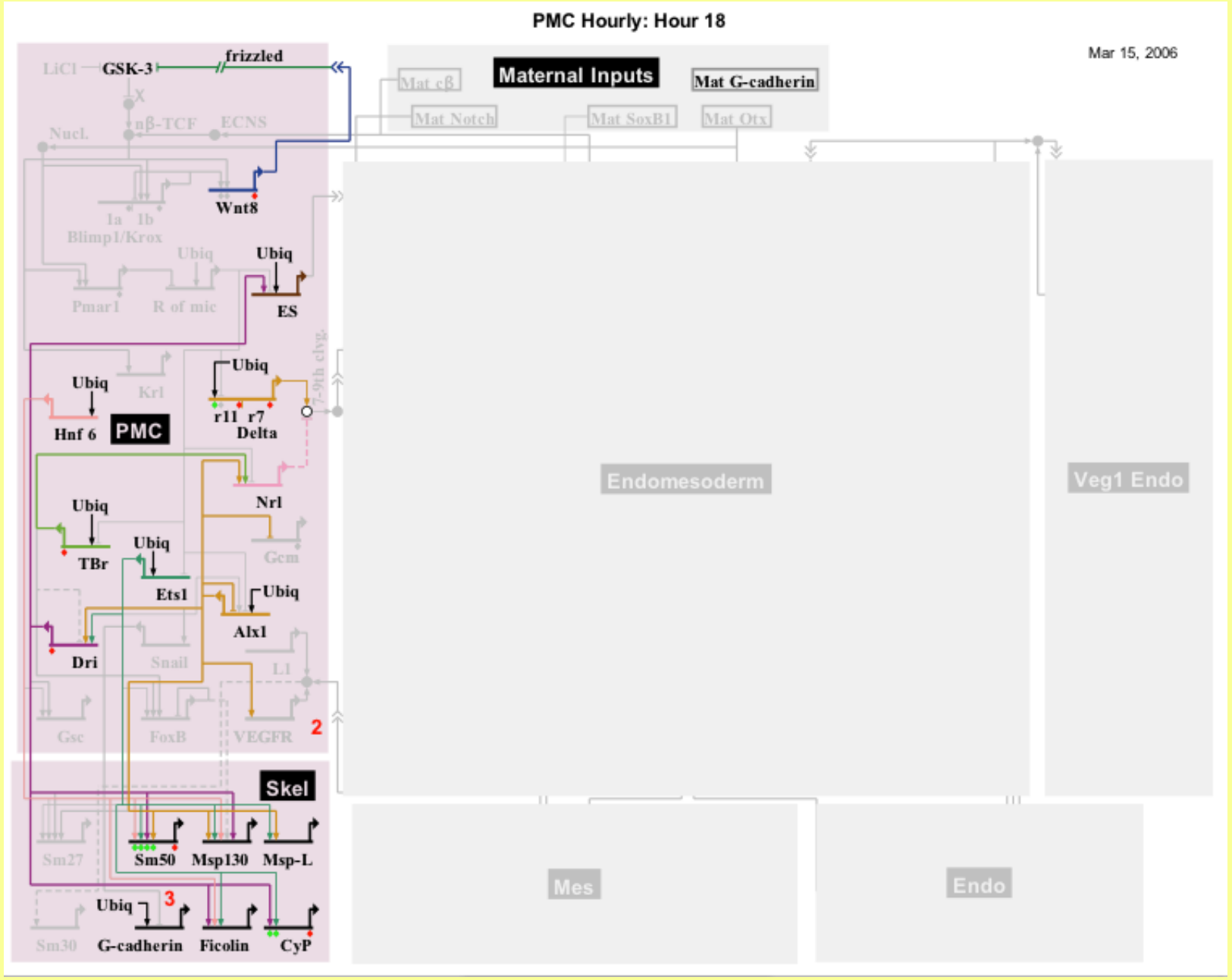
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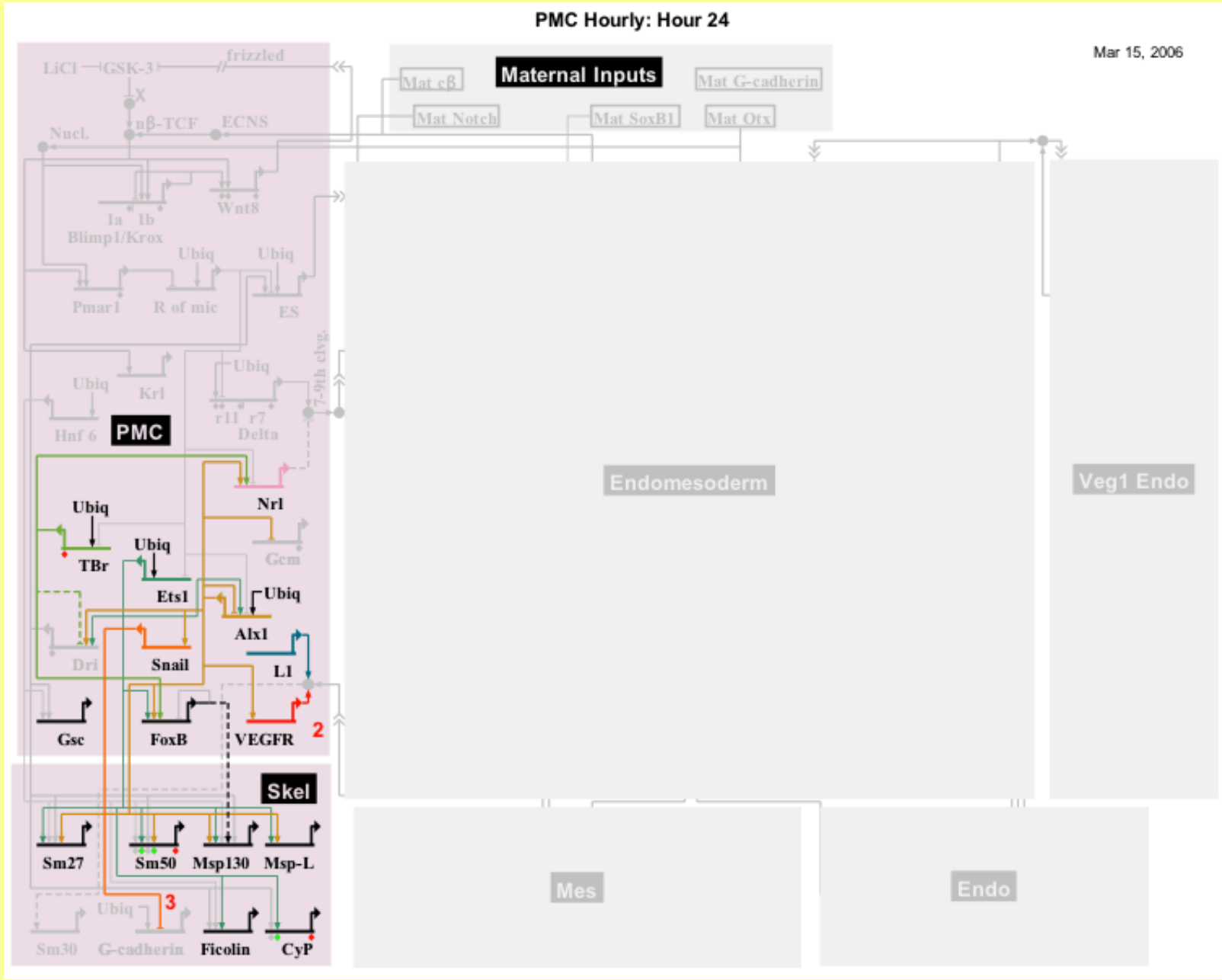
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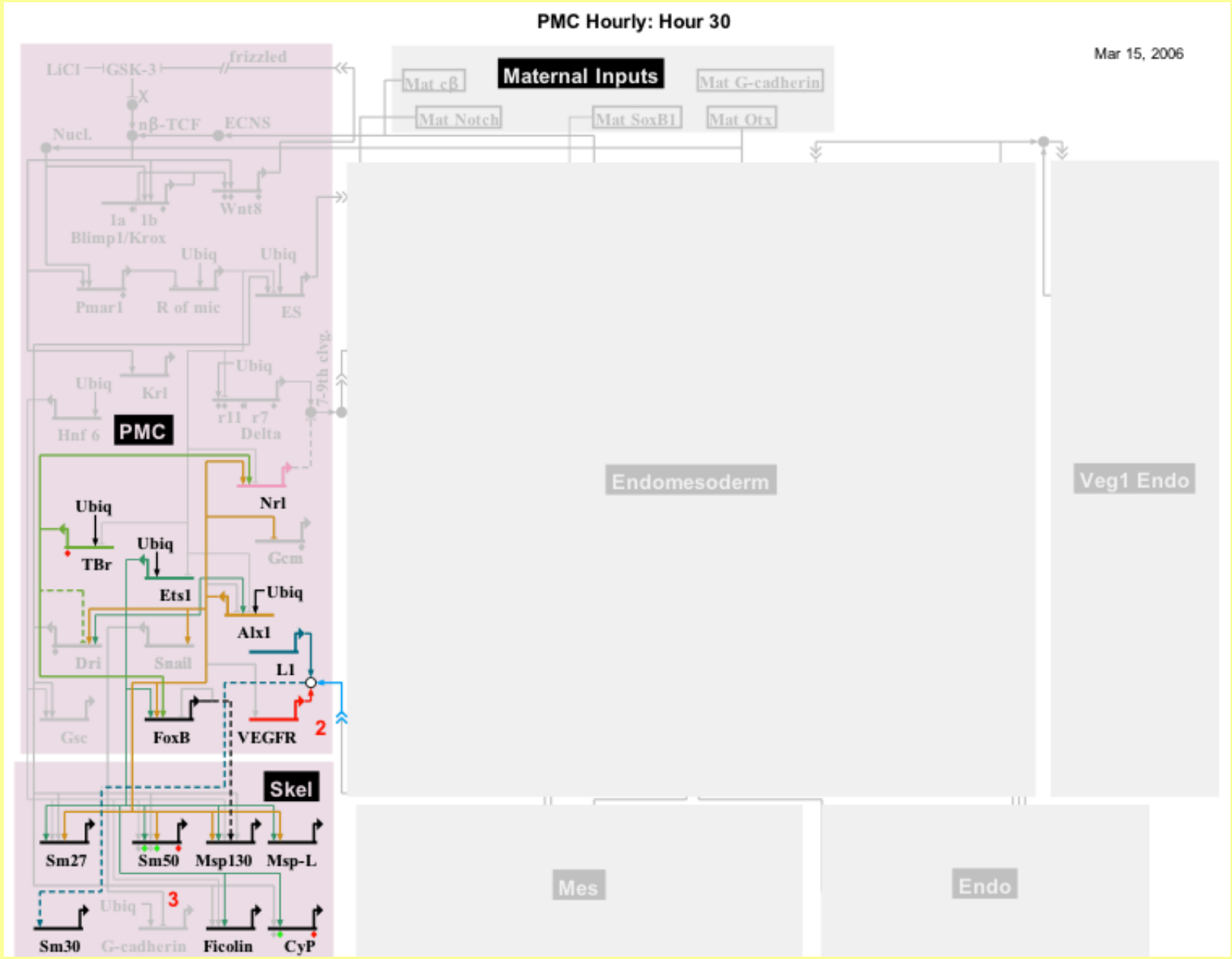
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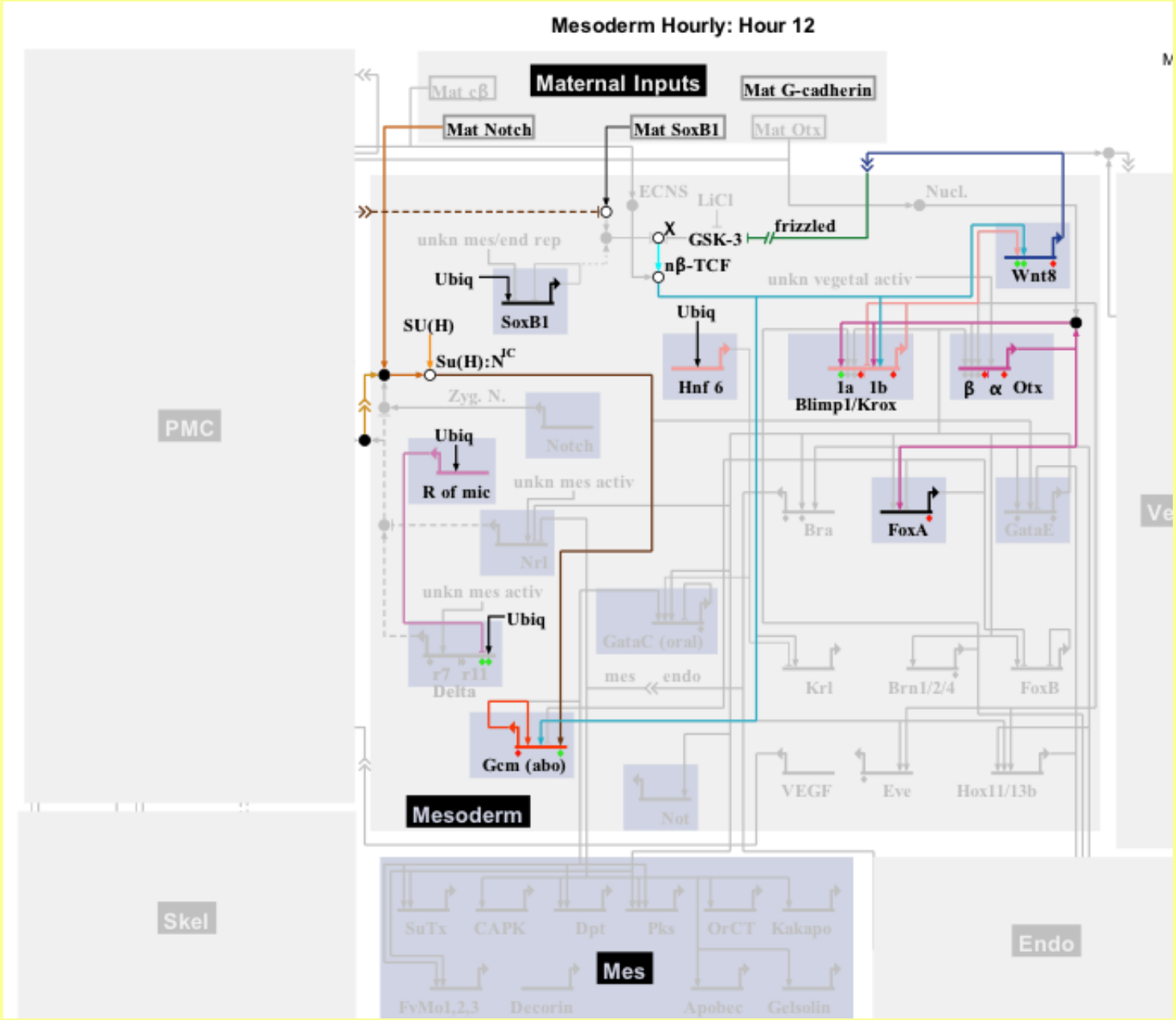
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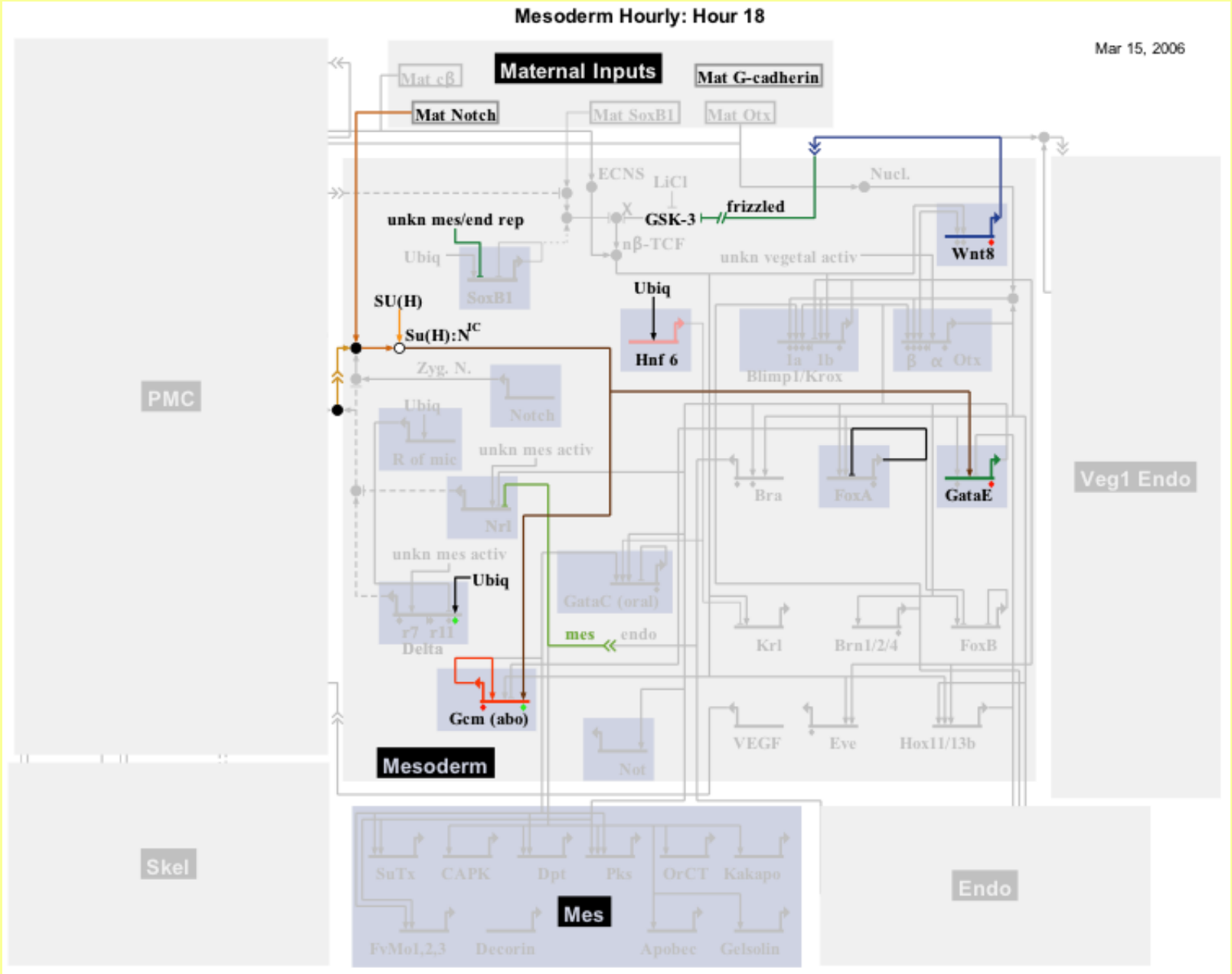
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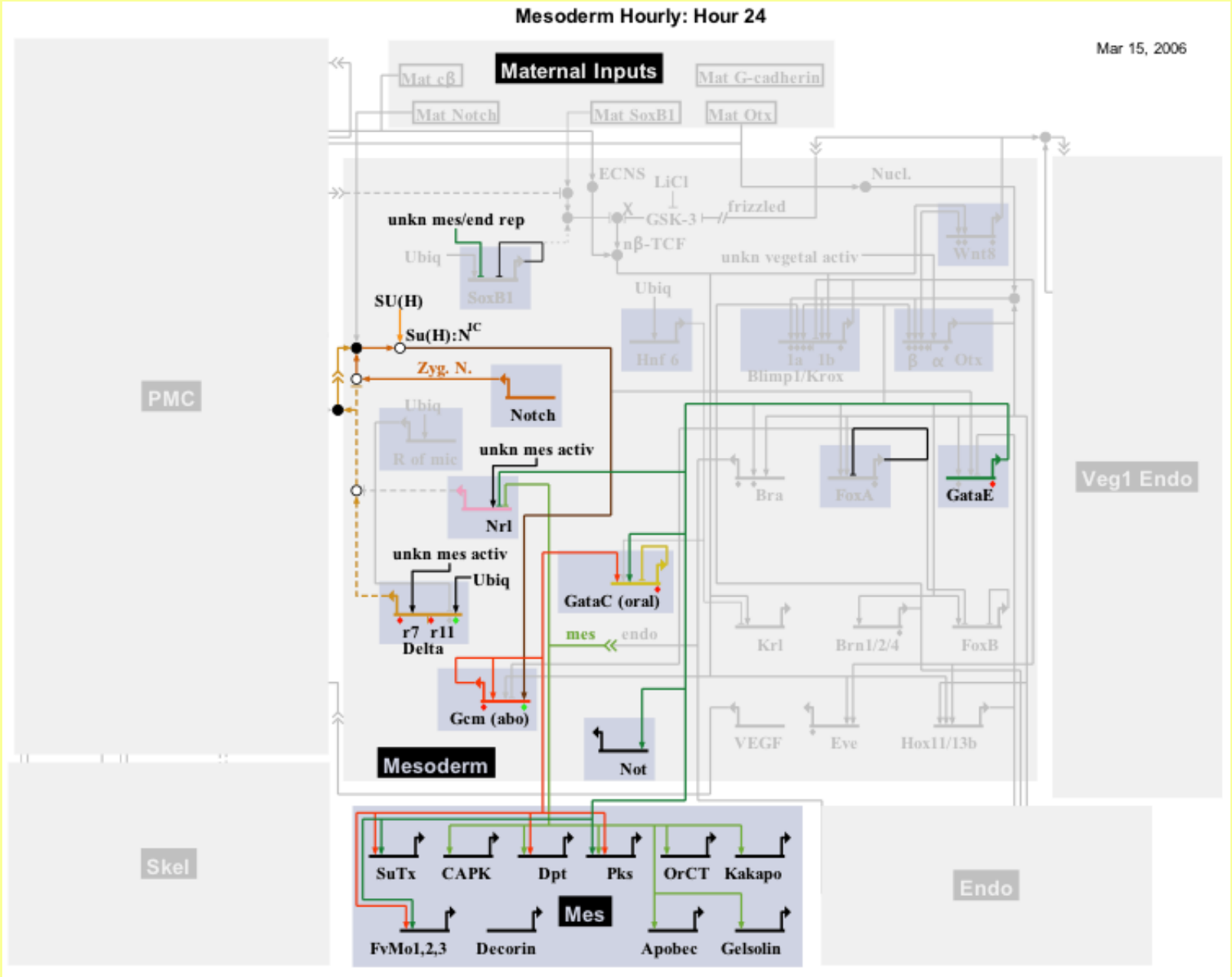
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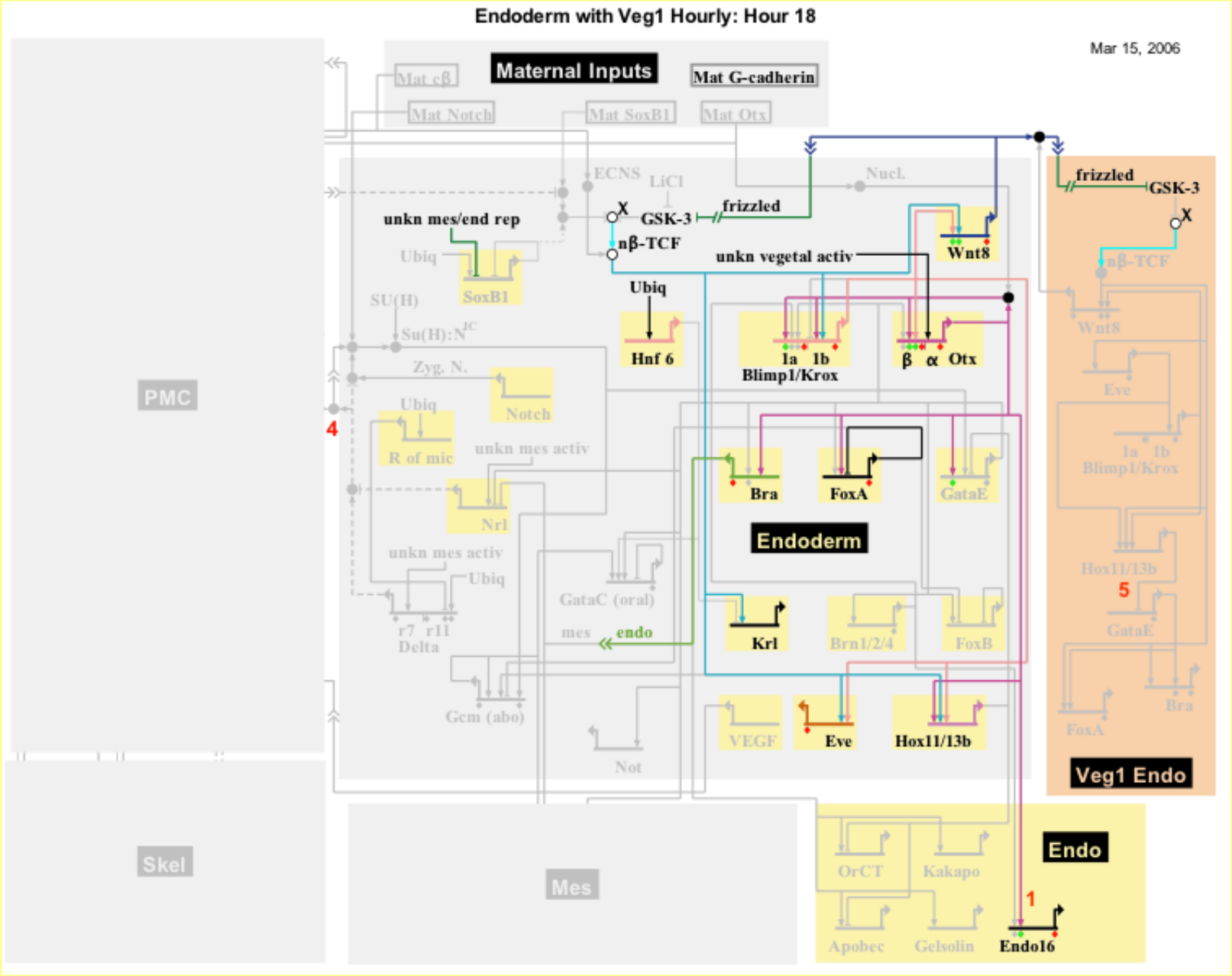
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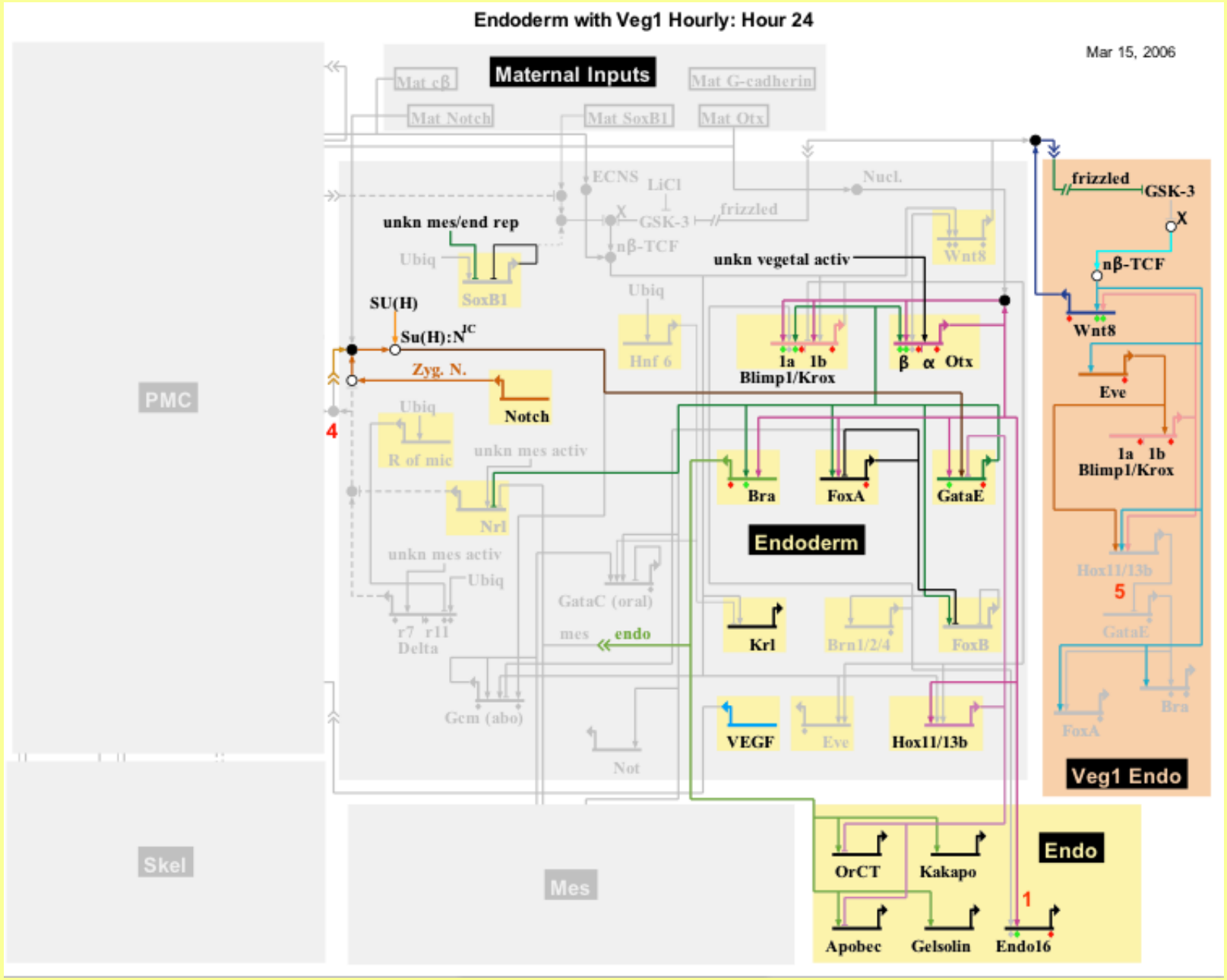
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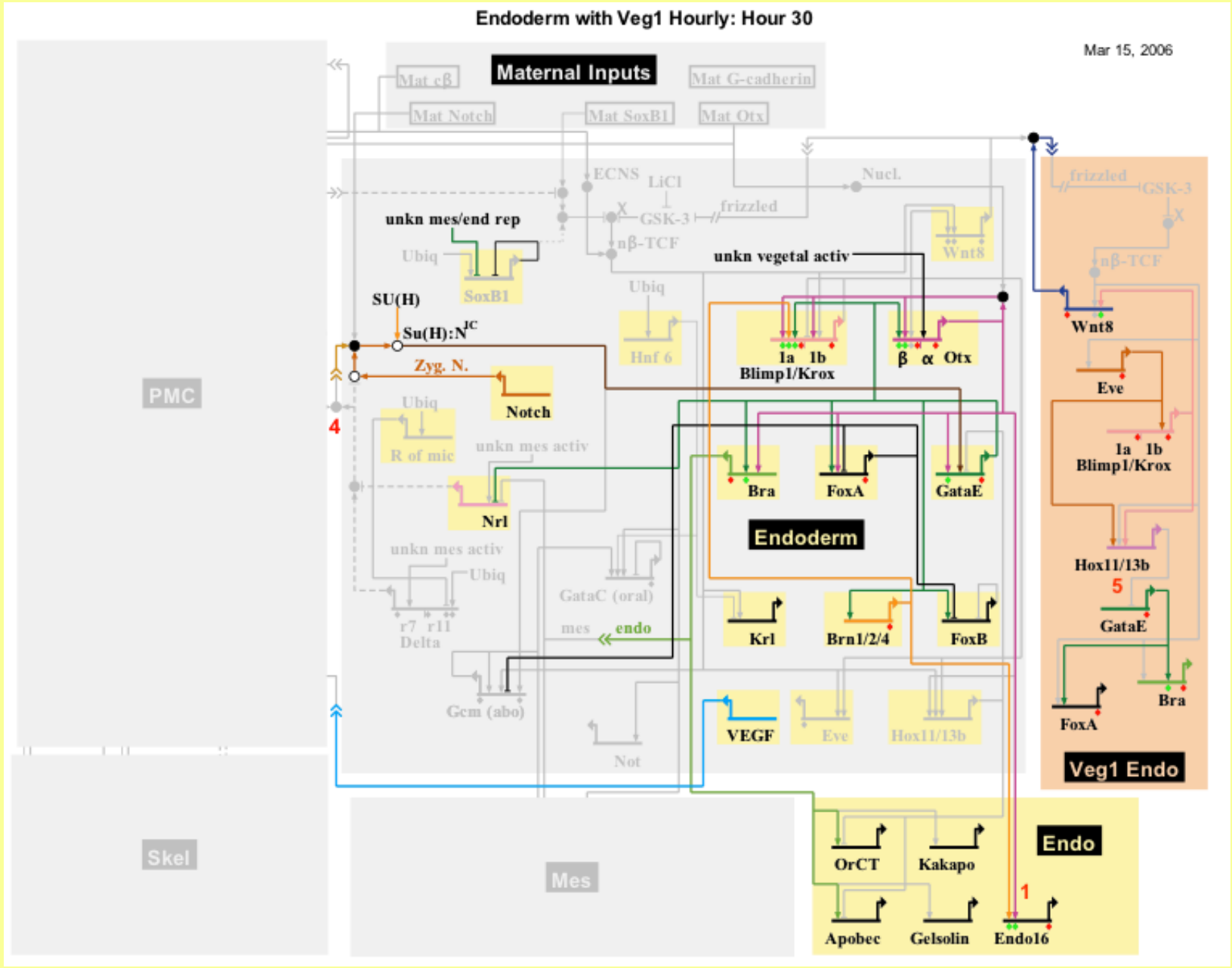
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Mar 15, 2006
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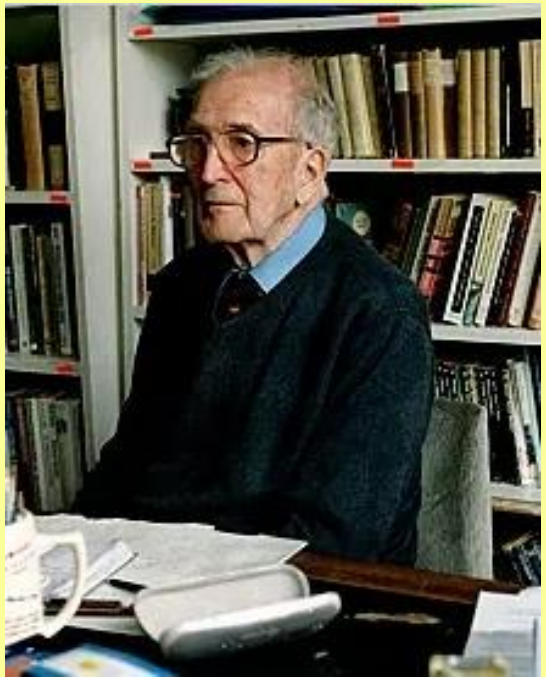
Based on this evidence, some conclude design

The New York Times Magazine

The Turning of an Atheist



By Mark Oppenheimer

Nov. 4, 2007

Antony Flew

David Gelernter

Prof. of computer science
Yale University

Essay by David Gelernter

GIVING UP DARWIN

2019

Based on this evidence, some conclude design

Biochemist
Lehigh University

Michael Behe

Curator fossil insects
State Museum of Natural History
Stuttgart, Germany

Günter Bechley

… but some do not

Thomas Nagel, NYU

"I confess to an ungrounded assumption of my own, in not finding it possible to regard the design alternative as a real option"
Mind and Cosmos, pg 12

"I can't accept it. I am a materialist"

Video interview, Privilidged Planet

Richard Lewontin

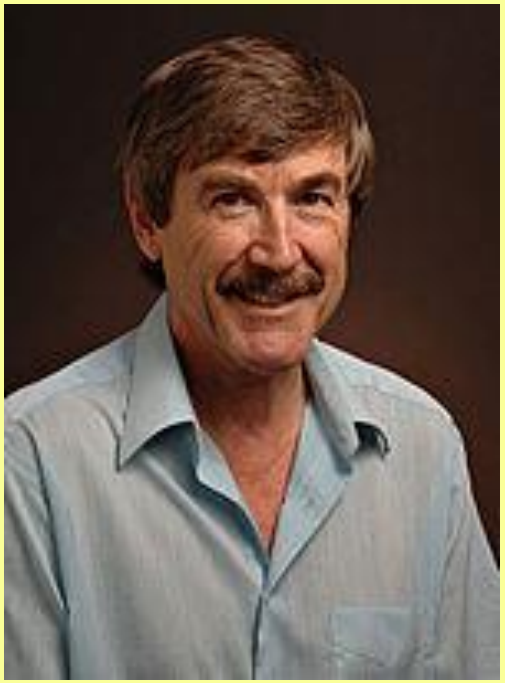
"…materialism is absolute, for we cannot allow a Divine Foot in the door."

New York Review of Books Jan 9, 1997.

… but some do not

"I would go along with you, Denis, except that what you are arguing **would let God back in**."

Dance to the Tune of Life



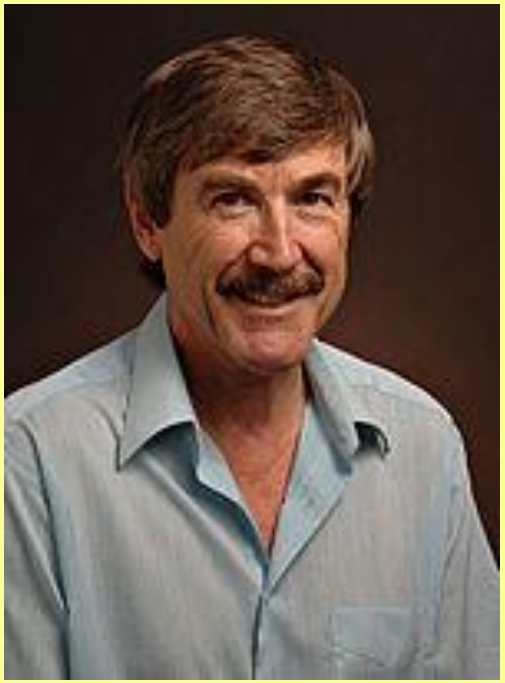
"… **the dreaded T word**: *teleology*. … Teleology, or final causation, is **taboo** in orthodox science."

The Goldilock Enigma

… but some do not

"... is for me evidence that there is something going on behind it all. **The impression of design is overwhelming**."

P. Davies, *Cosmic Blueprint: New Discoveries in Nature's Creative Ability to order the Universe*, 1988, 203



"… **the dreaded T word**: *teleology*. … Teleology, or final causation, is **taboo** in orthodox science."

The Goldilock Enigma

How bad can it get before cause(s) outside nature can be considered?

"Even if all the data point to an intelligent designer, such an hypothesis is excluded from science because it is not naturalistic."

S. C. Todd, Nature, 410:(6752): 423, 1999.

For some people no amount of data could ever be enough!

Summary:

Molecular machines and sophisticated software algorithms are essential to all life forms. Many systems are irreducibly complex. Molecular machines and sophisticated software algorithms must be integrated such that each entire system is coherent.

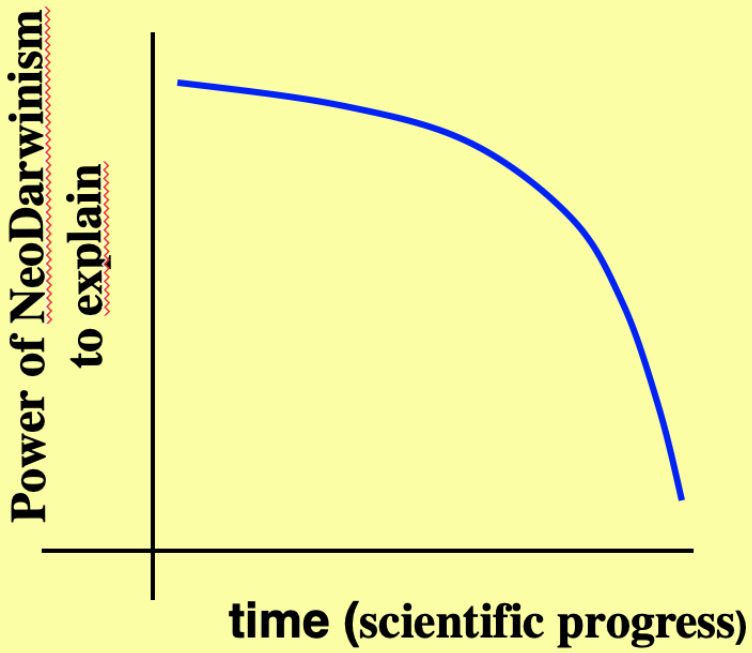
Summary:

Molecular machines and sophisticated software algorithms are essential to all life forms. Many systems are irreducibly complex. Molecular machines and sophisticated software algorithms must be integrated such that each entire system is coherent.

Informational discontinuities?

10 recent discoveries that have changed the debate about origins

7. Random mutation and natural selection has severe limitations



7. Random mutation and natural selection has severe limitations

7a. Experimental evolution shows very limited change.

7b. Sequencing genomes has shown that diversification (microevolution) often occurs by breaking genes.

7c. Mutations that act early in the development of animals are lethal. Mutations that act late in development are tolerated but do not lead to fundamental change.

7d. The "waiting time problem" for two coordinated mutations is now known to be prohibitively long for animals.

7e. Evidence for natural genetic engineering mechanisms for microevolution operating within a constrained design is growing.

7f. Much of the information of any living organism (one estimate is about half for animals) is not encoded in the genome.

7. Random mutation and natural selection has severe limitations

7a. Experimental evolution shows very limited change.

E coli Long Term Experimental Evolution

http://myxo.css.msu.edu/ecoli/

Currently over 65,000 generations

(equiv. to > 1 million yrs for humans, but far more organisms)

Each day: transfer small sample to new culture with 25 mg/L glucose

At 50,000 generations, they sequenced **264** complete genomes

Changes observed:

- Faster growth rates – but improvements diminish over time
- Hyper mutators: 100 times more mutations, due to broken DNA repair genes, these had 97% of the mutations
- Larger average cell sizes
- At 50,000 generations, average genome size declined by 63,000 base pairs (1.4%)

Based on differences in human/chimpanzee genomes, and an inferred split from a common ancestor 6 million yrs ago, we should expect **~100 new genes and ~ 3 new protein families** in the time of Lenski's experiment

How many new genes / proteins have occurred in the long-term evolution experiment?

0

Rapidly evolving groups – variation limited to species and genera

18 SEPTEMBER 2014 | VOL 513 | NATURE | 375

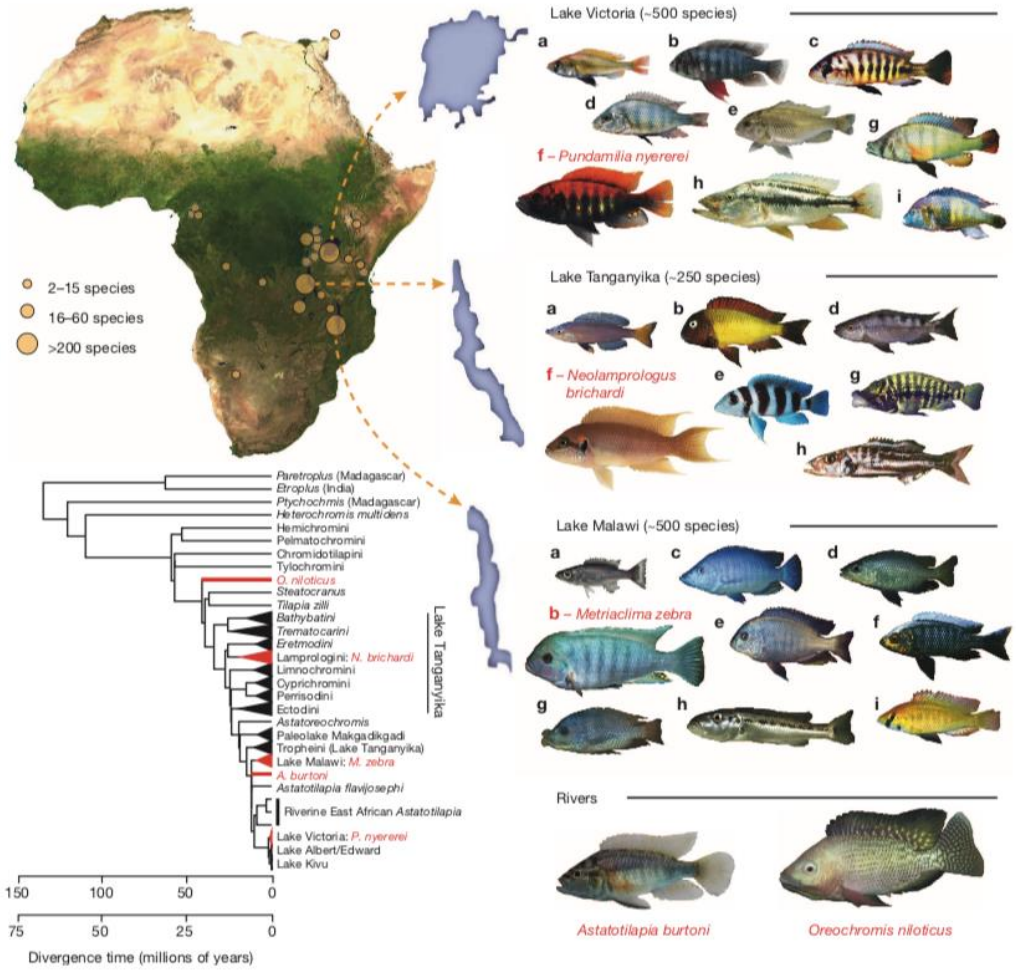


Figure 1 | The adaptive radiation of African cichlid fish. Top left, map of Africa showing lakes in which cichlid fish have radiated. Right, the five sequenced species: *Pundamilia nyererei* (endemic of Lake Victoria); *Neolamprologus brichardi* (endemic of Lake Tanganyika); *Metriaclima zebra* (endemic of Lake Malawi); *Oreochromis niloticus* (from rivers across northern Africa); *Astatotilapia burtoni* (from rivers connected to Lake Tanganyika). Major ecotypes are shown from each lake: **a**, pelagic zooplanktivore; **b**, rock-dwelling algae scraper; **c**, paedophage (absent from Lake Tanganyika); **d**, scale eater; **e**, snail crusher; **f**, reef-dwelling planktivore; **g**, lobe-lipped insect eater; **h**, pelagic piscivore; **i**, ancestral river-dweller also found in lakes (absent from Lake Tanganyika). Bottom left, phylogenetic tree illustrating relationships between the five sequenced species (red), major adaptive radiations and major river lineages. The tree is from ref. 4, pruned to the major lineages. Upper timescale (4), lower timescale (32). Photos by Ad Konings (Tanganyika **a**, **b**, **d**, **e**, **g**, **h**; Malawi **a**, **c**, **d**, **e**, **f**, **g**, **h**, **i**), O.S. (Victoria **a**–**g**, **i**; Malawi **b**), Frans Witte (Victoria **h**), W.S. (Tanganyika **f**), Oliver Selz (Victoria **f**, *A. burtoni*), Marcel Haesler (*O. niloticus*).

Rapidly evolving groups – variation limited to species and genera

Darwin Devolves, pg 167

Table 6.3. New Classifications Produced by Luxuriantly Evolving Groups

	Species	Genera	Families	Higher Classifications
Finches	14	4	0	0
Cichlids	~1500	~75	0	0
Anoles	~300	3	0	0
Honeycreepers	55	24	0	0
Fruit flies	~1000	2	0	0
Beetles	239	1	0	0
Silverswords	50	3	0	0
Lobelias	126	6	0	0

The Family Line

"Minor random variations around a designed blueprint are possible, and can be helpful, but are severely limited in scope. For new basic designs such as those at the biological level of family and above, additional information is necessary, information that is beyond the ability of mindless processes to provide,"

Darwin Devolves, pg 166

7. Random mutation and natural selection has severe limitations

7b. Sequencing genomes has shown that diversification (microevolution) often occurs by breaking genes.

Dog Breeds

- Increased muscle mass due to degradation of a myostatin gene.
- Yellow coat color due to loss-of-fct of melanocortin 1 receptor.
- Black coat due to deletion of a glycine residue from β-defensin.

- Damage to three genes affects fur characteristics (long or curly).
- Variation in size due to 6 genes: half involve degrading changes in protein-coding region, half in the control regions. All mutants decrease size.
- Muzzle size (short) associated with decreased activity of THBS2 and SMOC2, and damaging point mutation to BMP3.
- Short tails due to loss-of-fct mutation of T gene.

dog breeds

Richard Dawkins – dog breeds are premier example of the power of selection (by humans, not by nature) to shape animals.

New York Times July 1 2007

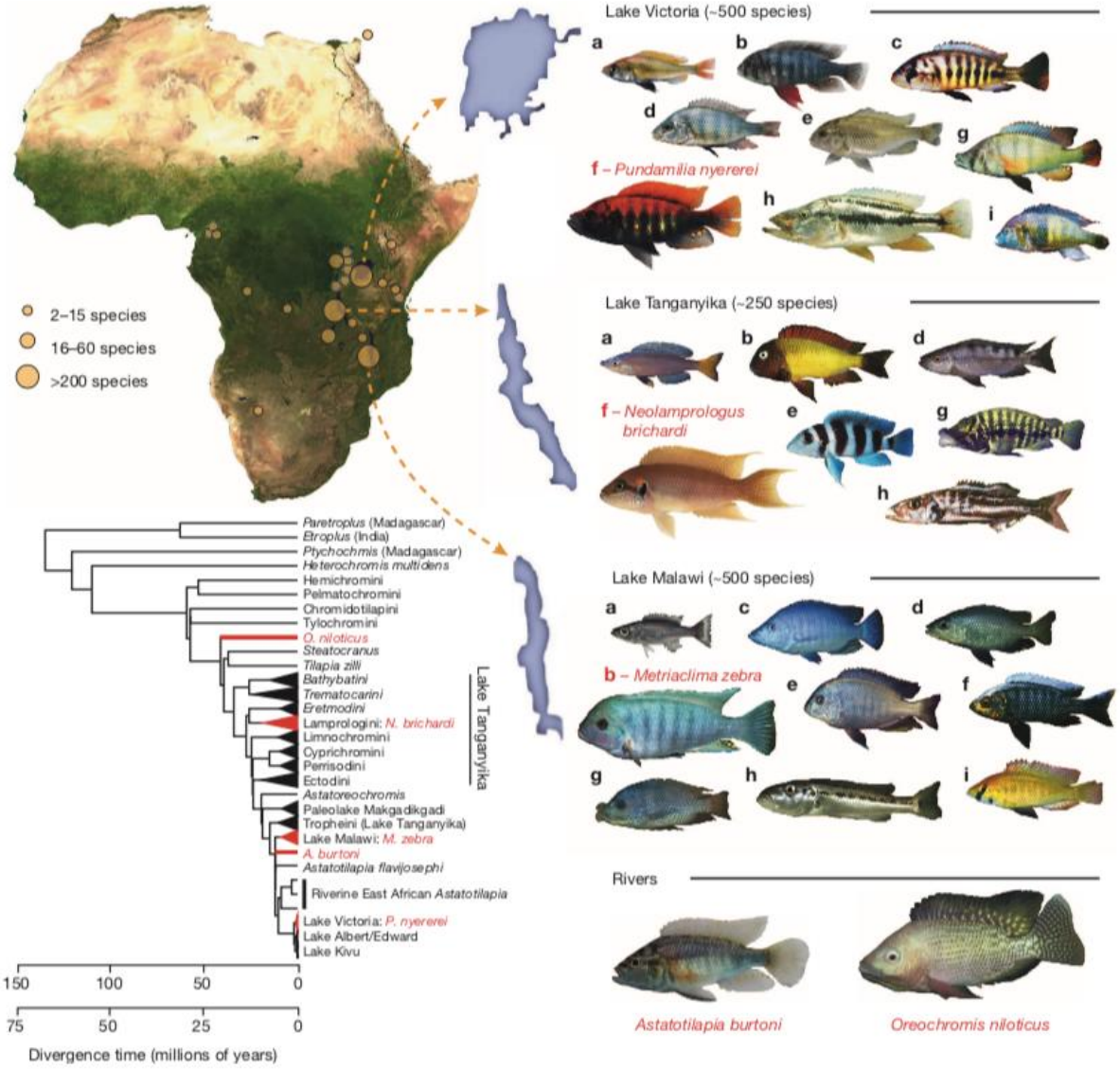
Dawkins is exactly right - dog breeding is a wonderful example of the power of selection acting on hidden random mutations. **But now that we can investigate the molecular level of life, we see that the great majority of dog mutations unwittingly selected by us humans are very likely to be damaging, degrading, or outright loss-of-FCT.**

Darwin Devolves pg 195

cichlids

cichlid variation in Lake Victoria occurred within last 15K yrs

most spectacular example of evolution in modern times



very different in appearance and behavior

Nature 2014, 513, 375

Figure 1 | The adaptive radiation of African cichlid fish. Top left, map of Africa showing lakes in which cichlid fish have radiated. Right, the five sequenced species: *Pundamilia nyererei* (endemic of Lake Victoria); *Neolamprologus brichardi* (endemic of Lake Tanganyika); *Metriaclima zebra* (endemic of Lake Malawi); *Oreochromis niloticus* (from rivers across northern Africa); *Astatotilapia burtoni* (from rivers connected to Lake Tanganyika). Major ecotypes are shown from each lake: **a**, pelagic zooplanktivore; **b**, rock-dwelling algae scraper; **c**, paedophage (absent from Lake Tanganyika); **d**, scale eater; **e**, snail crusher; **f**, reef-dwelling planktivore; **g**, lobe-lipped insect eater; **h**, pelagic piscivore; **i**, ancestral river-dweller also found in lakes (absent from Lake Tanganyika). Bottom left, phylogenetic tree illustrating relationships between the five sequenced species (red), major adaptive radiations and major river lineages. The tree is from ref. 4, pruned to the major lineages. Upper timescale (4), lower timescale (32). Photos by Ad Konings (Tanganyika **a**, **b**, **d**, **e**, **g**, **h**; Malawi **a**, **c**, **d**, **e**, **f**, **g**, **h**, **i**), O.S. (Victoria **a**–**g**, **i**; Malawi **b**), Frans Witte (Victoria **h**), W.S. (Tanganyika **f**), Oliver Selz (Victoria **f**, *A. burtoni*), Marcel Haesler (*O. niloticus*).

What genetic changes produced these variations in cichlids?

- **New genes?**
- **Changes in gene expression levels?**
- **Rearrangements or mutations of existing genes?**

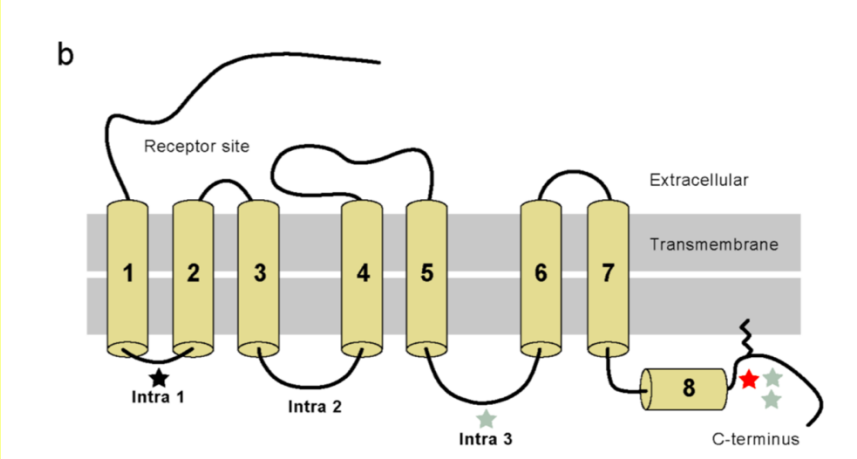
Sequenced the genomes of:

5 species from different (older) lineages

6 closely-related species from recent lineage

The genes underlying adaption in African Great Lake cichloids were present in their ancestral taxa. (no new genes)

One mutated gene involved in production of the fish body has mutations that appear to disable two functions:



Nature 2014, 513, 375

Developmental gene – affects color patterning and jaw development

First rule of Adaptive Evolution (supported by DNA sequencing):

Break or blunt any functional gene whose loss would increase the number of a species's offspring

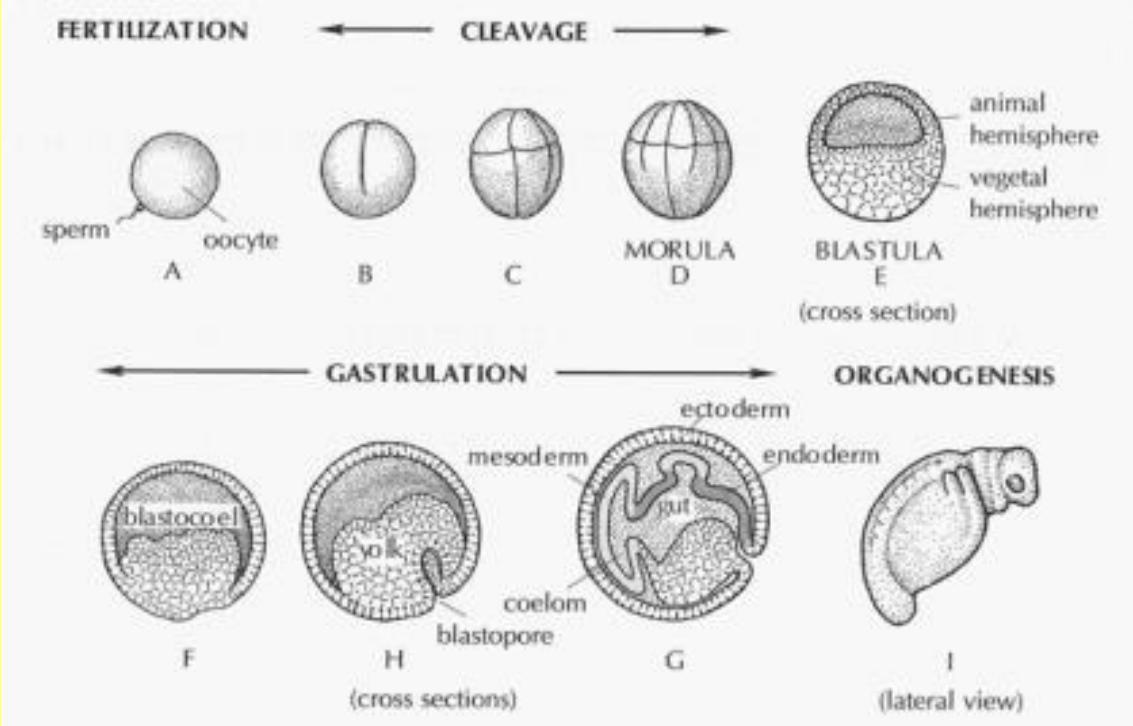
"Minor random variations around a designed blueprint are possible and can be helpful, but are severely limited in scope. For **new basic designs such as those at the biological level of family and above, additional information is necessary, information that is beyond the ability of mindless processes to provide**,"

Darwin Devolves, pg 166

7. Random mutation and natural selection has severe limitations

7c. Mutations that act early in the development of animals are lethal. Mutations that act late in development are tolerated but do not lead to fundamental change.

Embryos don't evolve



"Patterns and Processes of Vertebrate Evolution"
R. L. Carroll, Fig. 10.1

To change body plans, mutations must occur at the point in development where body plans are put into place. But this often occurs right at the beginning. Changes in body plan cannot be accomplished through the accumulation of late-acting mutations.

Embryos don’t evolve

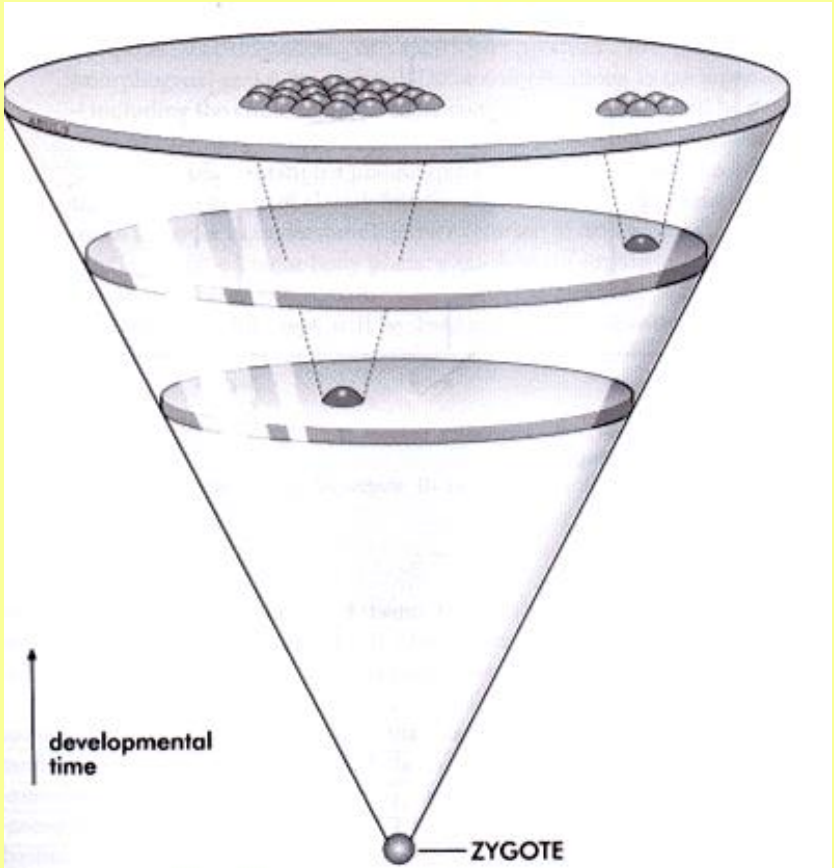
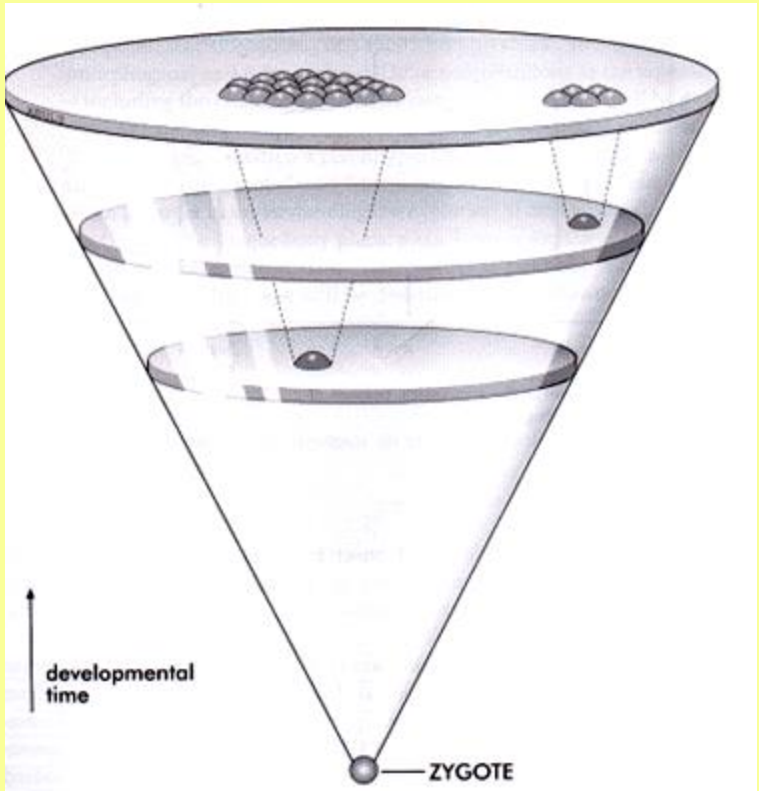


Figure 1–7 The ‘inverted cone’ model
A hypothetical organism develops from zygote to a disc-shaped arrangement of cells which grows in size through cell proliferation. The size of a morphological change in the adult is determined by how early in development the mutant gene controlling the change is switched on: early onset of activity gives rise to a more extensive change.

"This approach has important consequences for the neo-Darwinian view that major morphological differences between organisms from different higher taxa have been produced through the gradual accumulation of very small changes. Specifically, while in a non-developmental approach it seems plausible that many small changes can indeed accumulate to give a larger one, in a developmentally explicit approach **it is clear that many late changes can not accumulate to give an early one**. Thus, if taxonomically distant organisms differ right back to their early embryogenesis, as is often the case, **the mutations involved in their evolutionary divergence did not involve the same genes as those involved in the typical speciation event**, where usually the early embryogeneses of the daughter species concerned are virtually identical."

Wallace Arthur, The Origin of Animal Body Plans, pg 22

Embryos don’t evolve



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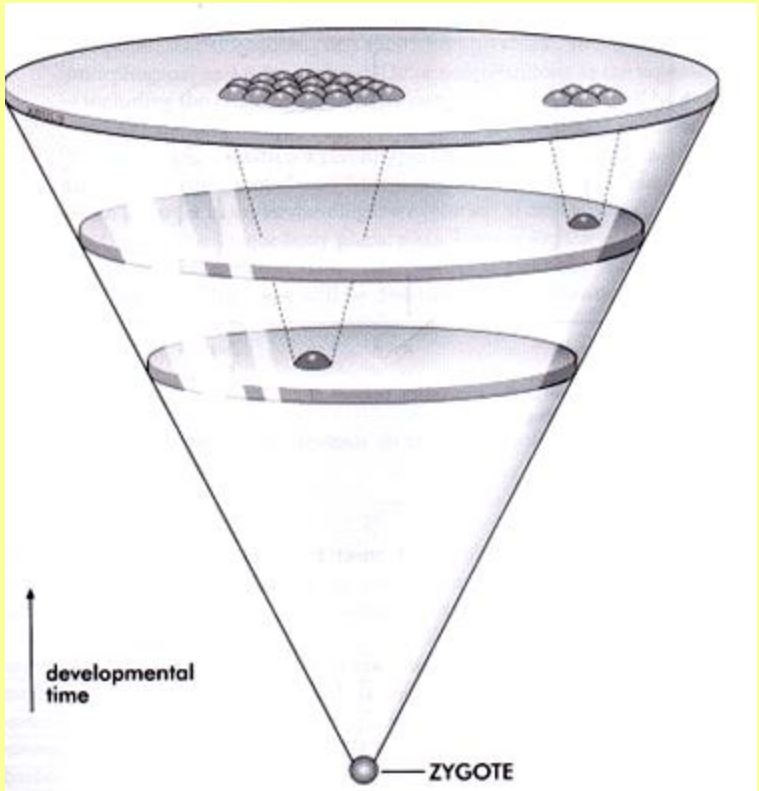
There are significant differences between the nature of the majority of genetic differences studied by evolutionary biologists and of those that contribute to understanding the embryological patterns and processes of interest to developmental biologists. … **It is only late in development**, when their anatomical patterns are nearly fully formed and the young are close to hatching or birth, that the traits commonly studied in classical genetics become evident.

R. L. Carroll, “Patterns and Processes of Vertebrate Evolution”, p 212-213.

Embryos don’t evolve



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A hypothetical organism develops from zygote to a disc-shaped arrangement of cells which grows in size through cell proliferation. The size of a morphological change in the adult is determined by how early in development the mutant gene controlling the change is switched on: early onset of activity gives rise to a more extensive change.

Miklos and Johns argue that macroevolutionary change requires changes in **“very early embryogenesis.”**

B. Johns and G. Miklos, The Eukaryote Genome in Development and Evolution, 1988, pg 309.

From
"The Origin of Animal Body Plans"
by **Wallace Arthur**

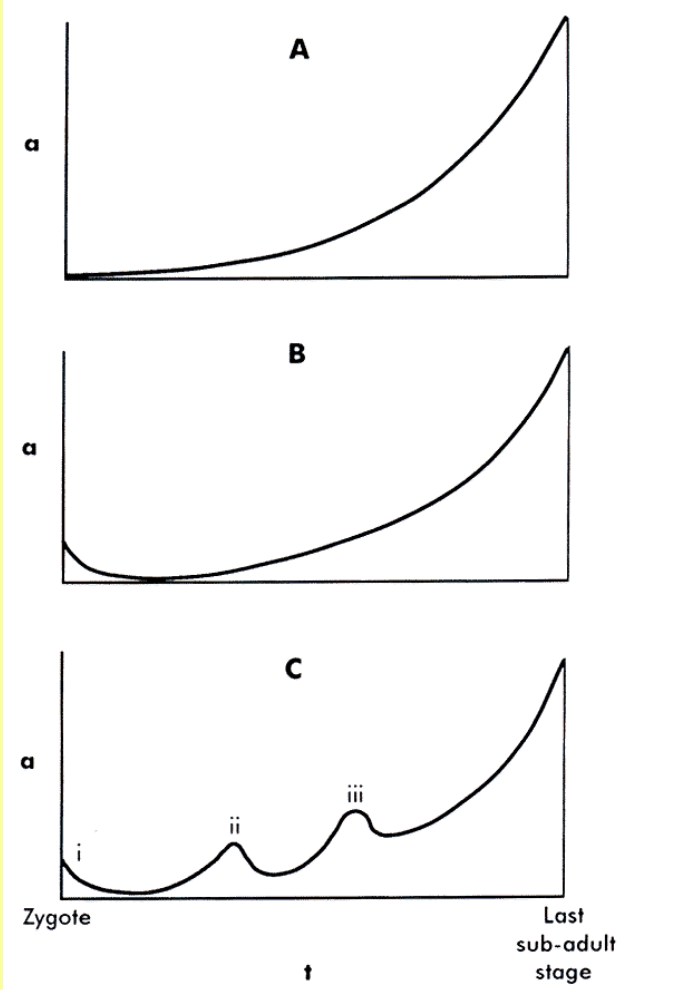


Figure 8–6 Possible relationships between a gene's time of onset of activity (*t*) and the probability of a mutation in it being selectively advantageous (*a*)
(A), (B), (C) Different assumptions: see text. In (B) and (C), the subsidiary peak(s) are all much smaller than the main (right) one – much more so than shown, assuming a linear probability scale. In (C), the relative sizes of i, ii and iii shown are arbitrary.

Embryos don't evolve

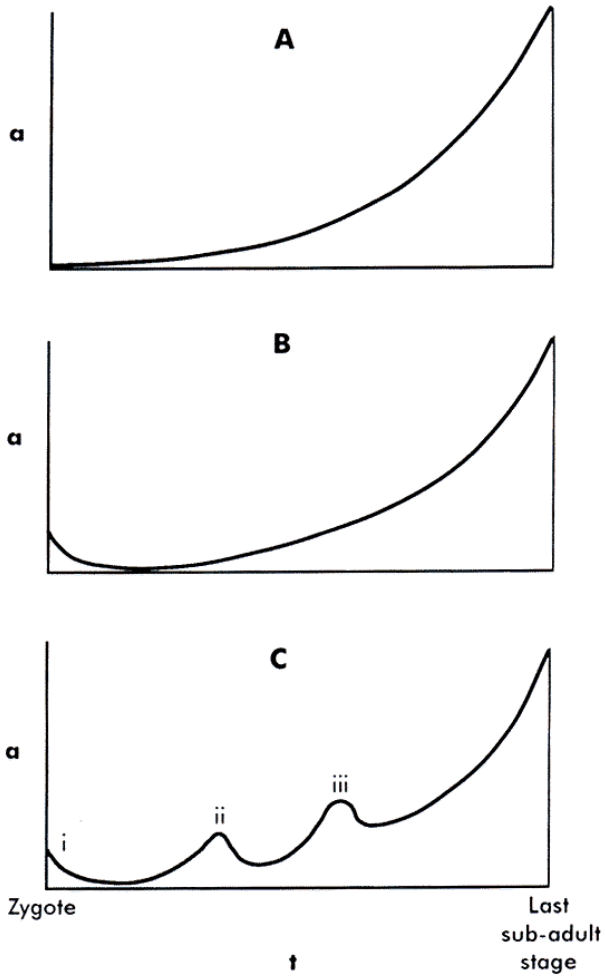
In general, the earlier a gene is expressed, the greater influence it can have on subsequent events during development and the **more likely that its disruption will result in malformation and death**. …

Most mutations known to cause changes in developmental processes are **too damaging** to provide a model for the manner in which evolutionary advances may have occurred.

R. L. Carroll, "Patterns and Processes of Vertebrate Evolution", p 213-214.

From
"The Origin of Animal Body Plans"
by **Wallace Arthur**

Embryos don't evolve



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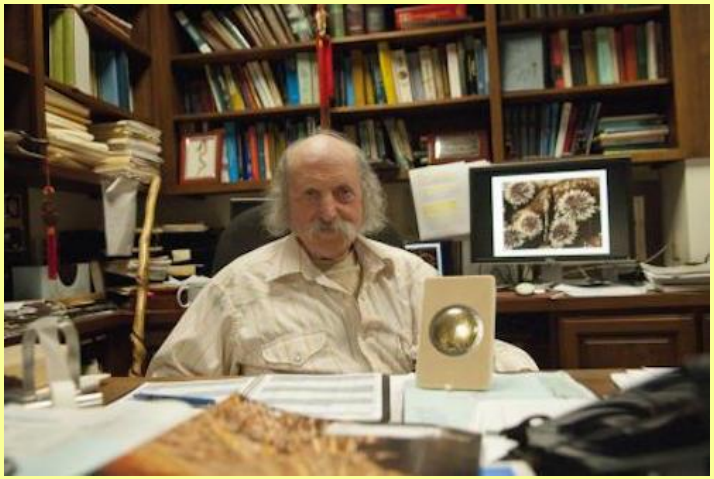
Those genes "that are obviously variable within natural populations do not seem to lie at the base of the many major adaptive changes", while those that "seemingly do constitute the foundation of many, if not most, major adaptive changes **apparently are not variable within natural populations.**"

John F. McDonald, "The Molecular Basis of Adaptation: A Critical Review of Relevant Ideas and Observations," Annual Review of Ecology and Systematics 14 (1983): 77-102; pp. 92-93.

Embryos don’t evolve

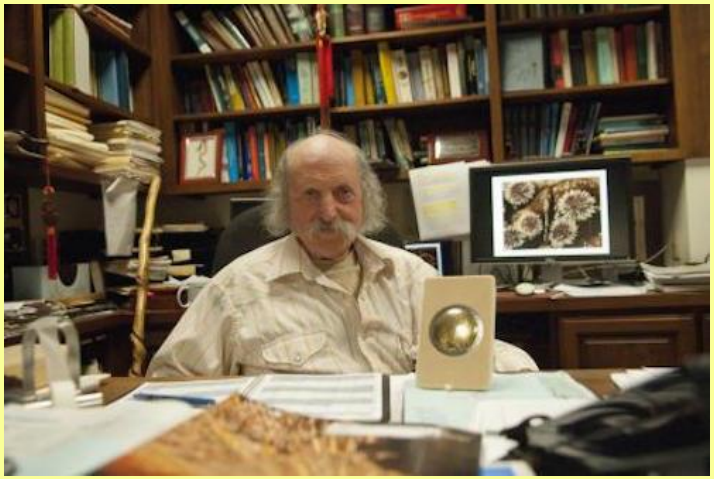


Eric Davidson, CalTech

There is always an observable consequence if a dGRN subcircuit is interrupted. Since these consequences **are always catastrophically bad**, flexibility is minimal, and since the subcircuits are all interconnected, the whole network partakes of the quality that there is only one way for things to work. And indeed the embryos of each species develop in only one way.

Eric H. Davidson and Douglas Erwin. "An Integrated View of Precambrian Eumetazoan Evolution." *Cold Spring Harbor Symposia on Quantitative Biology*, 74: 1-16 (2010)

Embryos don't evolve



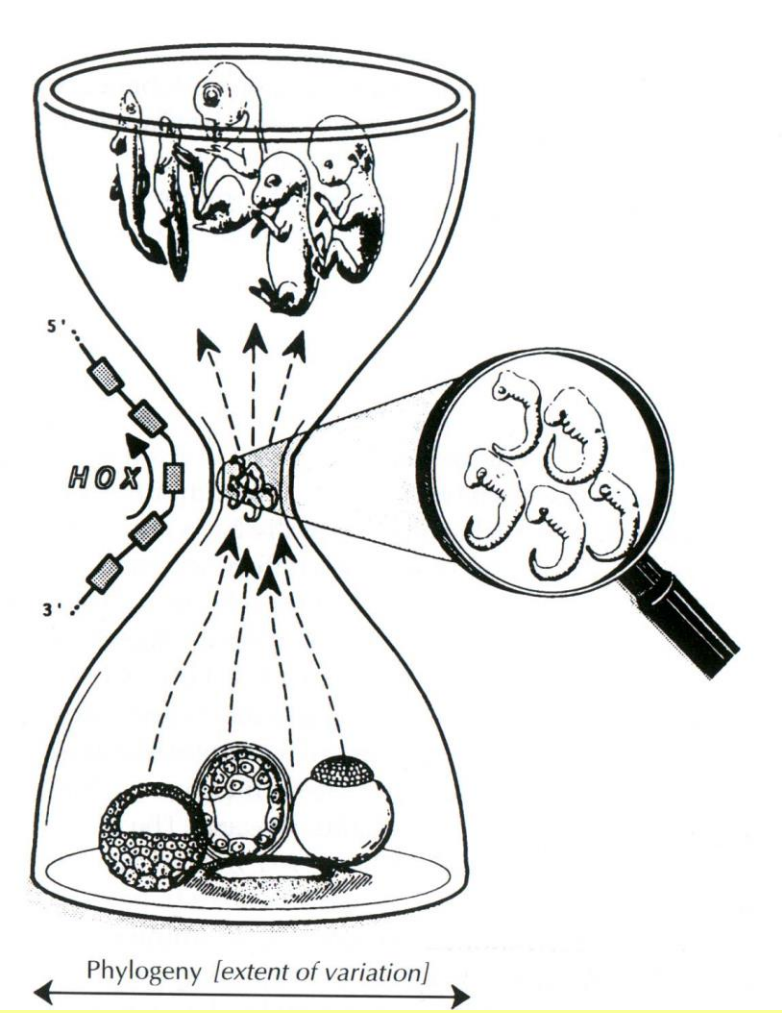
Eric Davidson, CalTech

Neo-Darwinian evolution ... assumes that all processes work the same way, so that evolution of enzymes or flower colors can be used as current proxies for study of evolution of the body plan. It erroneously assumes that change in protein-coding sequence is the basic cause of change in developmental program; and it erroneously assumes that evolutionary change in body-plan morphology occurs by a continuous process. **All of these assumptions are basically counterfactual**. … the neo-Darwinian synthesis from which these ideas stem was a premolecular biology concoction focused on population genetics and . . . natural history, neither of which have any direct mechanistic import for the **genomic regulatory systems that drive embryonic development of the body plan**.

Developmental Biology, 357:35-40 (2011)

Embryos don’t evolve

Hox genes, regulatory genes, and developmental plasticity



"The plain fact is that despite all the talk of "master-control" genes, biologists still have no causal account of morphogenesis".

Evelyn Fox Keller, Biology and Philosophy, 14: 325, 1999.

“Patterns and Processes of Vertebrate Evolution”, R. L. Carroll, Fig. 10.6

7d. The "waiting time problem" for two coordinated mutations is now known to be prohibitively long for animals.

Journal of Theoretical Biology

Volume 220, Issue 2, 21 January 2003, Pages 241–247

ELSEVIER

Regular Article

A Minimum on the Mean Number of Steps Taken in Adaptive Walks

H.ALLEN ORR[1]

Received 15 January 2002, Accepted 11 September 2002, Available online 3 December 2002

Given realistically low mutation rates, double mutants will be so rare that adaptation is essentially constrained to surveying -- and substituting -- one-mutational step neighbors. Thus if a double-mutant sequence is favorable but all single amino acid mutants are deleterious, adaptation will generally not proceed.

H. Orr J. Theor. Biol. 2003, 220, 241

DOI: 10.1534/genetics.107.082610

Waiting for Two Mutations: With Applications to Regulatory Sequence Evolution and the Limits of Darwinian Evolution

Rick Durrett*,[1] and Deena Schmidt†

**Department of Mathematics and †Center for Applied Mathematics, Cornell University, Ithaca, New York 14853*

Manuscript received September 30, 2007
Accepted for publication August 19, 2008

"We now show that two coordinated changes that turn off one regulatory sequence and turn on another one without either mutant becoming fixed **are unlikely to occur in the human population**."

Genetics 2008, 180, 1507

DOI: 10.1534/genetics.107.082610

Waiting for Two Mutations: With Applications to Regulatory Sequence Evolution and the Limits of Darwinian Evolution

Rick Durrett*,[1] and Deena Schmidt†

**Department of Mathematics and †Center for Applied Mathematics, Cornell University, Ithaca, New York 14853*

Manuscript received September 30, 2007
Accepted for publication August 19, 2008

Est. waiting time for two coordinated mutations in humans:

162 million yrs

"…as our new results show, a coordinated pair of mutations that first inactivates a binding site and then creates a new one is very unlikely to occur on a reasonable timescale."

Genetics 2008, 180, 1501

Progressing one mutation at a time is a severe limitation

What can mutation+selection do?

improve a protein

make a new protein complex (protein-protein binding)

make a new protein

make a new regulatory circuit

make a new machine

…

Progressing one mutation at a time is a severe limitation

What can mutation+selection do?

improve a protein **(yes)**

make a new protein complex (protein-protein binding)
(maybe, depends on complexity)

make a new protein **(maybe, depends on complexity)**

make a new regulatory circuit **(no)**

make a new machine **(no)**

…

7. Random mutation and natural selection has severe limitations

7f. Much of the information of any living organism (one estimate is about half for animals) is not encoded in the genome.

"The simplest and also the only strictly correct view of the function of genes is that they supply cells, and ultimately organisms, with chemical materials."

H. F. Nijhout

BioEssays (1990)

"Now that the entire genomes are mapped out and the **genomic approach is seen to be unable to explain biological complexity**, this problem will be a central concern of future research. Recognizing that the **origination of biological form cannot be understood solely from genetic analysis** will necessarily stimulate investigation of the processes that actually construct the phenotype from materials provided, in part, by the genotype."

G. Muller and S. Newman, Origination of Organismal form, 2003, pg 5-6.

"… much work in this area (evolutionary developmental biology) proceeds under the assumption that the only important link between the two processes lies in genetics - **as if the individual generation of form were merely a reading out of evolved genetic programs**. However development does not appear to behave like any program known to computer science - phenotypic outcomes persist despite extensive derangement in lines of "program code" (gene expression levels and interactions) …. Moreover that genetic circuitry involved in development can undergo evolutionary "rewiring" without overt changes in the phenotype suggests that **phenotypes have autonomy that can trump that of the programs they supposedly express**."

G. Muller and S. Newman, Origination of Organismal form, 2003, pg 6.

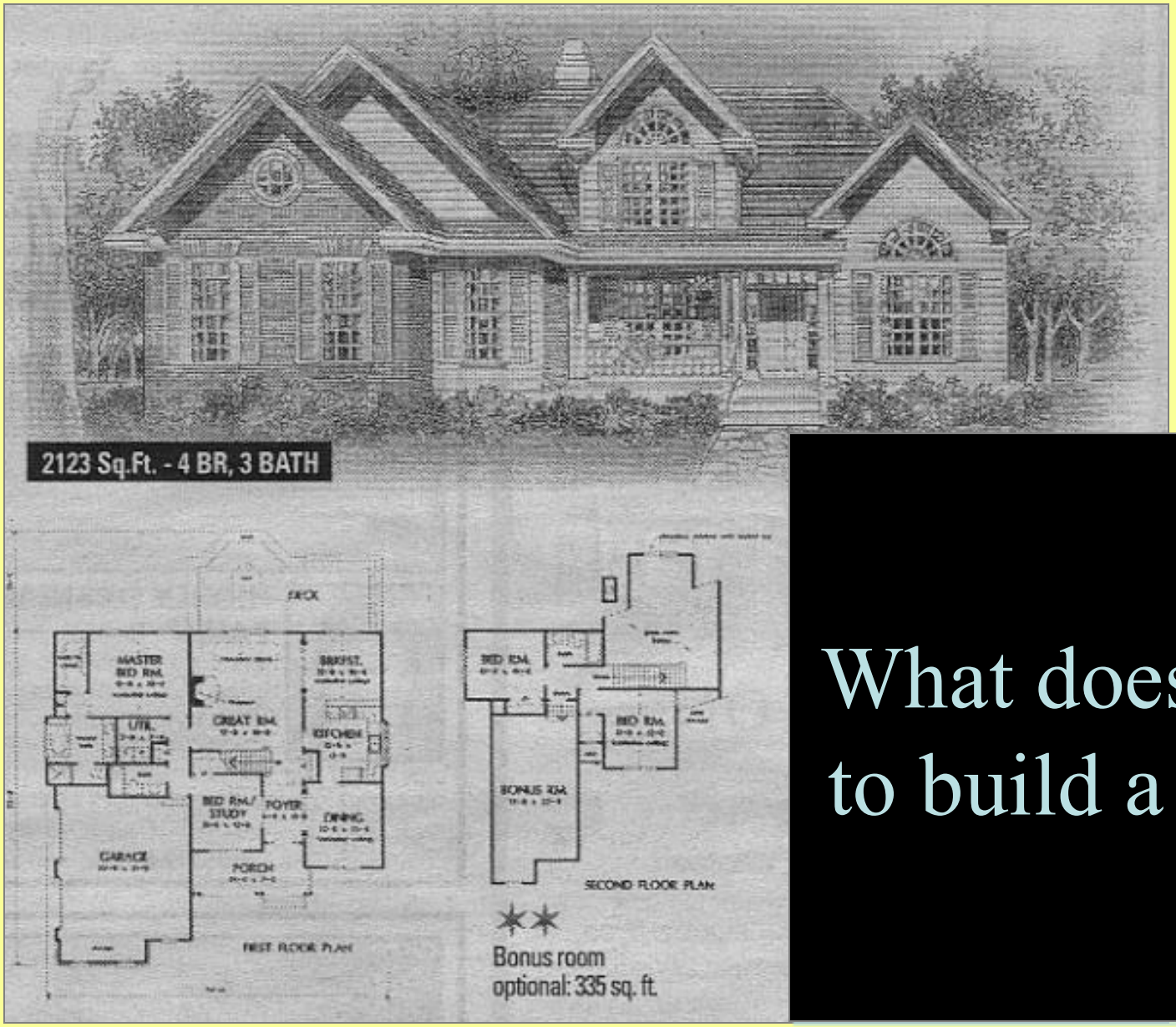
"If, as we suggest, the failure of the current theory of evolution to deal with the problem of origination is the major obstacle to a scientific understanding of organismal form, it is incumbent upon us to provide at least a sketch of an alternative view. In fact, it is our contention that a synthetic, causal understanding of both the development and evolution of morphology can be achieved only by **relinquishing a gene-centered view of these processes**. …

Again, **detailed information at the level of the gene does not serve to explain form**. …

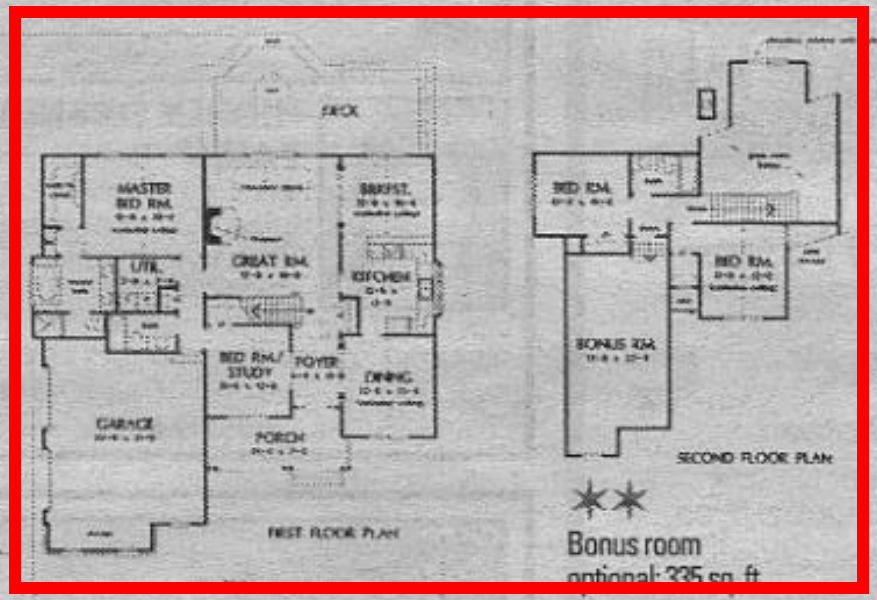
Epigenetic processes … replace gene sequence variation and gene expression as the primary causal agents in morphological origination.

G. Muller and S. Newman, Origination of Organismal form, 2003, pg 6.

If we compare building a body to building a house…



What does it take to build a house?



1. Building materials

2. Assembly instructions

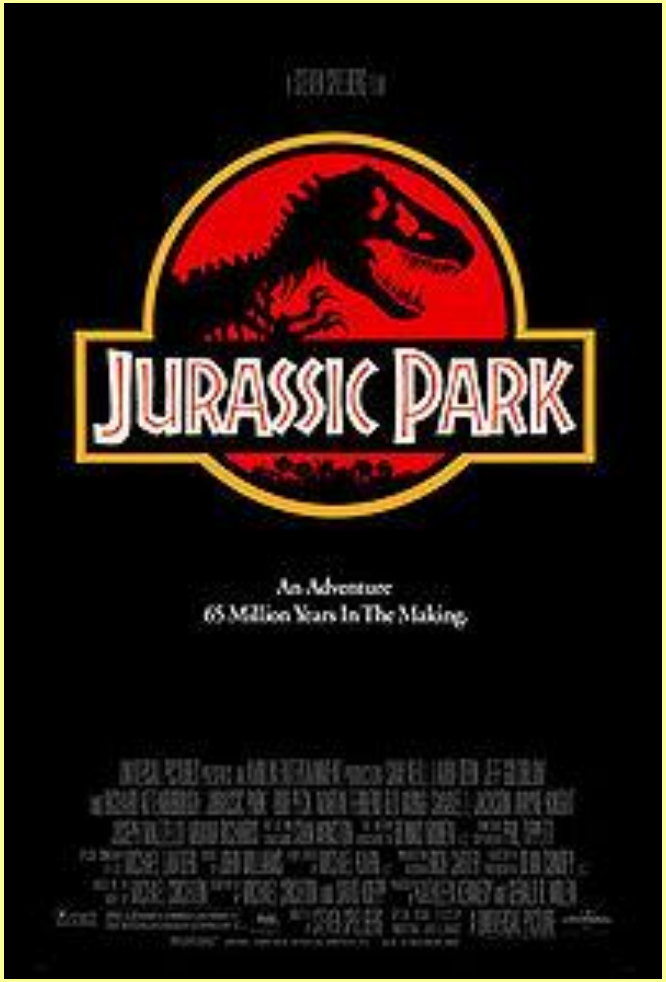
3. Floor plan

The floor plan is not in the DNA!

"The simplest and also the only strictly correct view of the function of genes is that they supply cells, and ultimately organisms, with chemical materials."

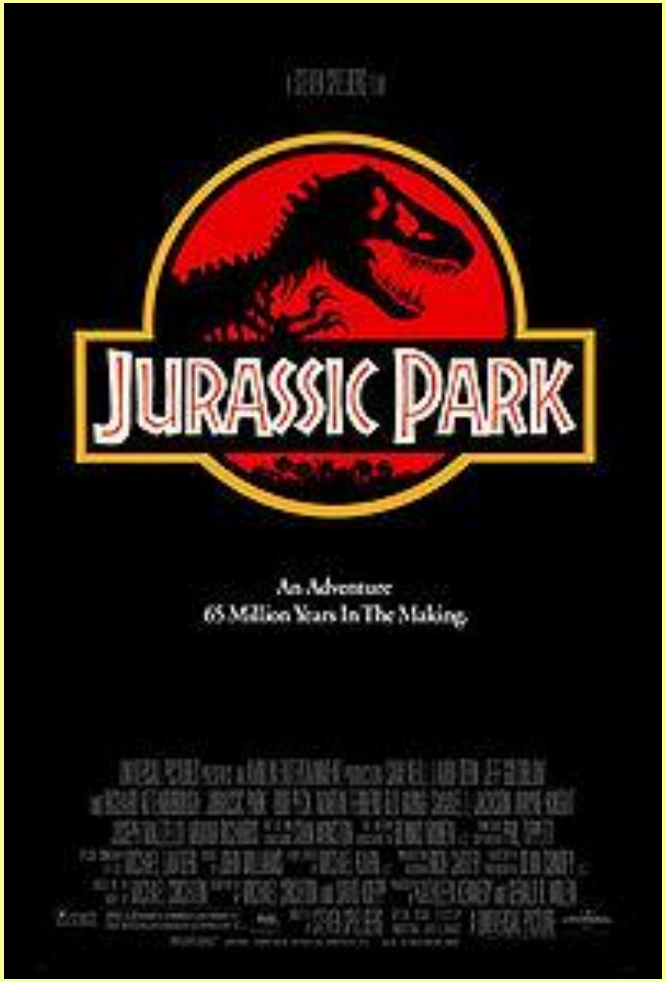
H. F. Nijhout

BioEssays (1990)



In “Jurassic Park,” fragments of dinosaur DNA are extracted from amber and inserted into frog chromosomes. These are injected into live ostrich eggs from which the ostrich DNA has been removed. Baby dinosaurs then hatch from the injected eggs.

Source: Wikipedia



In reality the eggs would die, and nothing would hatch.

Source: Wikipedia

7. Random mutation and natural selection has severe limitations

7a. Experimental evolution shows very limited change.

7b. Sequencing genomes has shown that diversification (microevolution) often occurs by breaking genes.

7c. Mutations that act early in the development of animals are lethal. Mutations that act late in development are tolerated but do not lead to fundamental change.

7d. The "waiting time problem" for two coordinated mutations is now known to be prohibitively long for animals.

7e. Evidence for natural genetic engineering mechanisms for microevolution operating within a constrained design is growing.

7f. Much of the information of any living organism (one estimate is about half for animals) is not encoded in the genome.

The severe limitations of neoDarwinism are becoming a topic for discussion within evolutionary biology

The Third Way

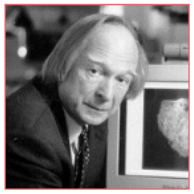
https://www.thethirdwayofevolution.com

James A. Shapiro
Department of Biochemistry and Molecular Biology; University of Chicago

Shapiro has worked as professor of microbiology at the University of Chicago since 1973. An expert in bacterial genetics, he proposes the concept of Natural Genetic Engineering, a process described to account for novelty created in the process of biological evolution. Shapiro is an advocate of non-Darwinian evolution and is a critic of the modern synthesis.

Read profile

Book: "Evolution: A View from the 21st Century"



Denis Noble
Department of Physiology, Anatomy and Genetics; University of Oxford

Professor Emeritus and co-Director of Computational Physiology at Oxford University. One of the pioneers of Systems Biology and developed the first viable mathematical model of the working heart in 1960. Over 500 articles in academic journals, including Nature, Science, PNAS, Journal of Physiology.

Read profile

Book: "The Music of Life: Biology beyond the Genome"

Eugene Koonin
Evolutionary Genomics Research Group; NCBI, Bethesda, MD, USA

Dr. Koonin is a Senior Investigator and the leader of the Evolutionary Genomics Group in the Computational Biology Branch of the National Center for Biotechnology Information. He received his Ph.D. in 1983 from Department of Biology, Moscow State University in Molecular Biology. Dr. Koonin and his research group employ existing and new methods of computational biology to perform research in several major areas in order to gain a better understanding of the evolution of life. He is the author of *The Logic of Chance: The Nature and Origin of Biological Evolution* (2011) and has authored and co-authored over 600 papers. Dr. Koonin was elected Member of the American Academy of Microbiology, Fellow of the American College of Medical Informatics, Fellow of the American Academy of Arts and Sciences, Foreign Associate of the European Molecular Biology Organization, and Doctor Honoris Causa of Universite Aix-Marseille (France).

Read profile

Eva Jablonka
The Cohn Institute for the History and Philosophy of Science and Ideas; Tel Aviv University

Jablonka is a geneticist renowned for her work in epigenetic inheritance and support for Lamarckian principles of evolution. She has published numerous books and papers on epigenetics, including *Evolution in Four Dimensions* along with Marion J. Lamb.

Book: "Evolution in Four Dimensions: Genetic, Epigenetic, Behavioral, and Symbolic Variation in the History of Life"

Read profile

Evelyn Fox Keller
Professor of the History and Philosophy of Science, Emerita (STS); Massachusetts Institute of Technology

Keller is a physicist and author with interest in physics, molecular biology, history and philosophy of modern biology, gender and science. She received her Ph.D in physics from Harvard (1963).

Book: "The Century of the Gene (2002)"

Read profile

Gerd B. Müller
Department of Theoretical Biology; University of Vienna

Müller is a theoretical biologist who concentrates on the role of developmental processes in evolutionary innovation. He advocates an expanded framework of evolution and has published numerous papers and books on the ongoing change in evolutionary theory.

Book: "Evolution - the extended synthesis"

Read profile

The severe limitations of neoDarwinism are becoming a topic for discussion within evolutionary biology

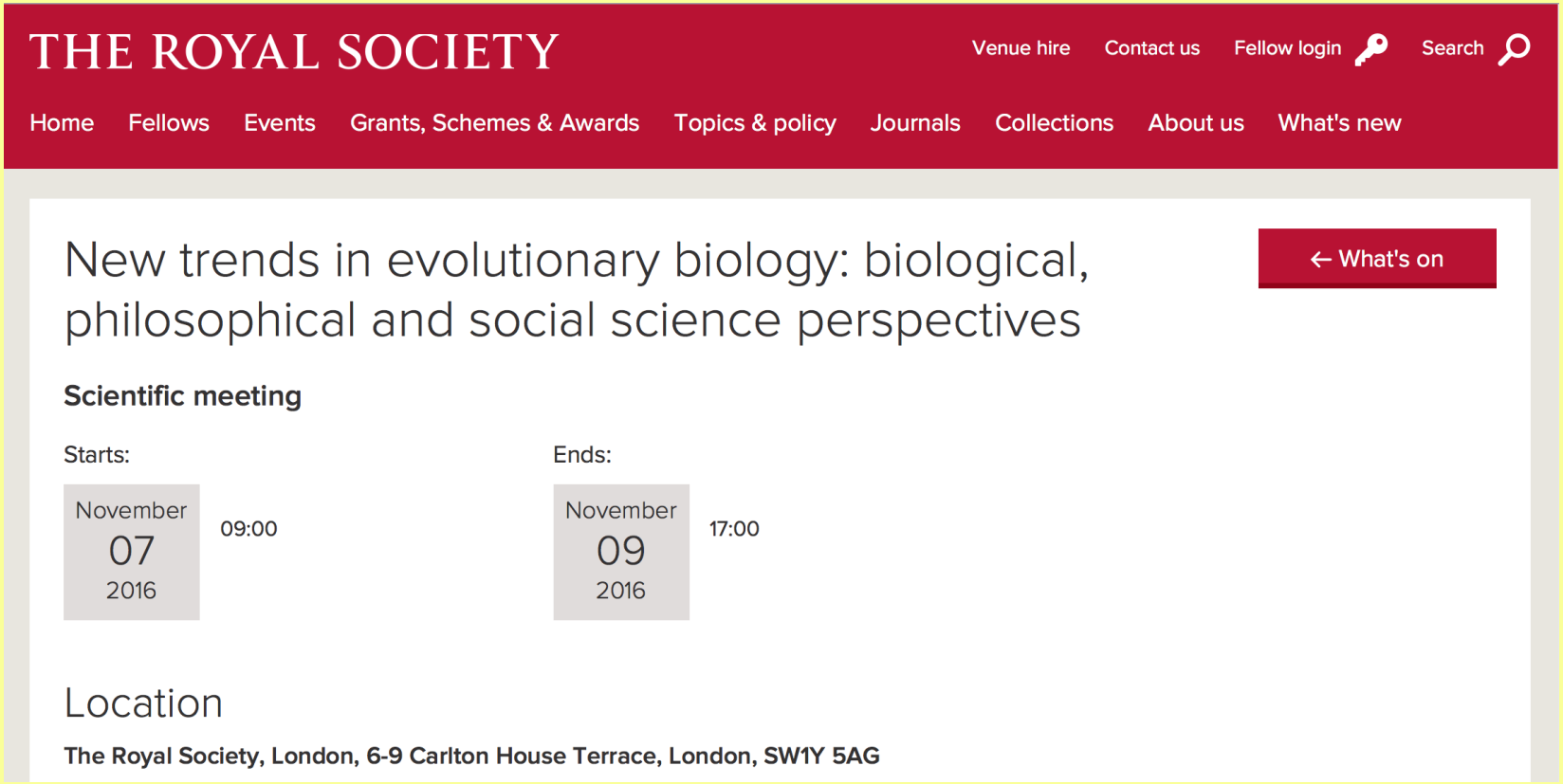
The Third Way

https://www.thethirdwayofevolution.com

The neo-Darwinian paradigm still represents the central explanatory framework of evolution, as exemplified by recent textbooks. … Although this theory can account for the phenomena it concentrates on, namely variation of traits in populations, it leaves aside a number of other aspects of evolution …. Most important, **it completely avoids the origination of phenotypic traits and of organismal form**. In other words, **neo-Darwinism has no theory of the generative**. As a consequence, current evolutionary theory can predict what will be maintained, but not what will appear.

G. Muller and S. Newman, Origination of Organismal form, 2003, pg 7.

2016: Royal Society Mtg: New Trends in Evol. Biology



The severe limitations of neoDarwinism are becoming a topic for discussion within evolutionary biology

2022: Israel Conference: Potential and Limitations of Evolutionary processes

The severe limitations of neoDarwinism are becoming a topic for discussion within evolutionary biology

2022: Israel Conference: Potential and Limitations of Evolutionary processes

Speakers included some who openly advocate Intelligent Design, and some who are open to considering Intelligent Design:

David Snoke, USA
Paul Nelson, USA
Brian Miller, USA
Siegfried Scherer, Germany
Ola Hössjer, Sweden
Michael Behe, USA

The severe limitations of neoDarwinism are becoming a topic for discussion within evolutionary biology

Recent Article in The Guardian

A new wave of scientists argues that mainstream evolutionary theory needs an urgent overhaul. Their opponents have dismissed them as misguided careerists – and the conflict may determine the future of biology

by Stephen Buranyi

June 28, 2022,
The Guardian

https://www.theguardian.com/science/2022/jun/28/do-we-need-a-new-theory-of-evolution

Summary

5. **Life is based on a digital information processing system**

6. **Molecular machines and sophisticated software algorithms are essential to all life-forms**

7. **Random mutation and natural selection has severe limitations**

Extra slides

For more information, see articles and books by the following eminent scholars:

Seigfried Scherer

Prof. of Microbiology, Technical Univ. of Munich

specializes in microbiology and food science

>120 publications

James Tour

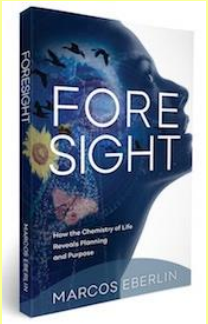
synthetic organic chemist at Rice University

"Scientist of the Year" in 2013, R&D Magazine

Marcos Eberlin

Prof. of chemistry at Univ of Pampinas, Brazil

893 publications



Granville Sewell

Professor of mathematics UTEP

>50 scientific publications

4 books

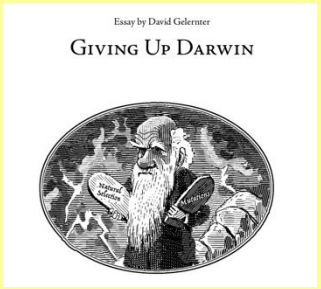
Matti Leisola

Finnish biotechnologist

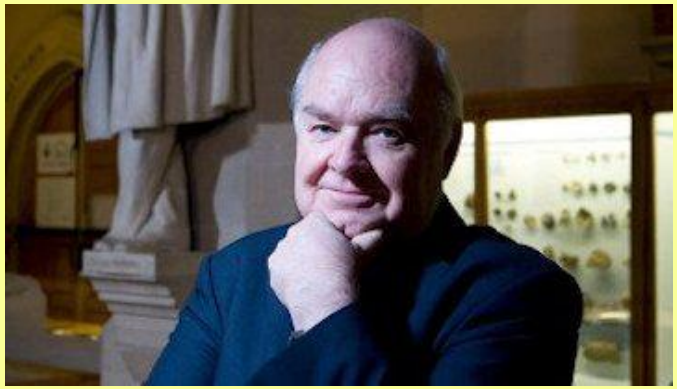
140 scientific publications

David Gelernter

Prof. of computer science at Yale University



John Lennox



Professor Emeritus of
Mathematics

University of Oxford

Günter Bechly

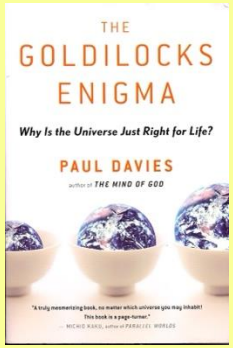
Paleoentomologist,
former curator of the
Museum of Natural History,
Stuttgart Germany

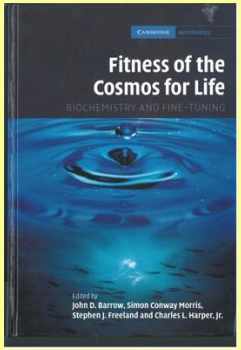
10 recent discoveries that have changed the debate about origins

1. The universe had a beginning and will have an end
2. The universe is fine-tuned to allow for life
3. Only a miniscule fraction of proteins are functional
4. About 450 genes in the simplest free-living organism
5. Life is based on a digital information processing system
6. Life is based on molecular machines and algorithms
7. Random mutation + natural selection has severe limitations
8. The earth is fine-tuned to allow for life
9. In the fossil record new body plans appear without precursors
10. The junk-DNA paradigm has been shown to be false

Physical Sciences

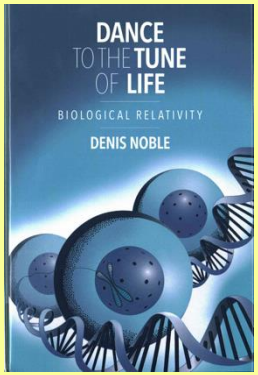
fine-tuning
anthropic coincidences
habitability
discoverability
intelligibility
physical laws
etc





Life Sciences

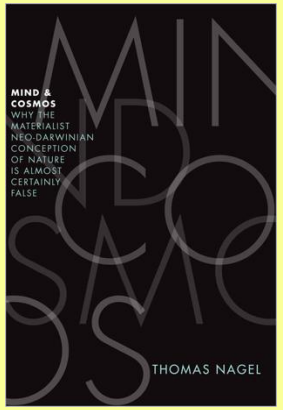
origin of life
molecular machines
hardware and software of cells
micro and macro evolution
basic charact. of fossil record
etc



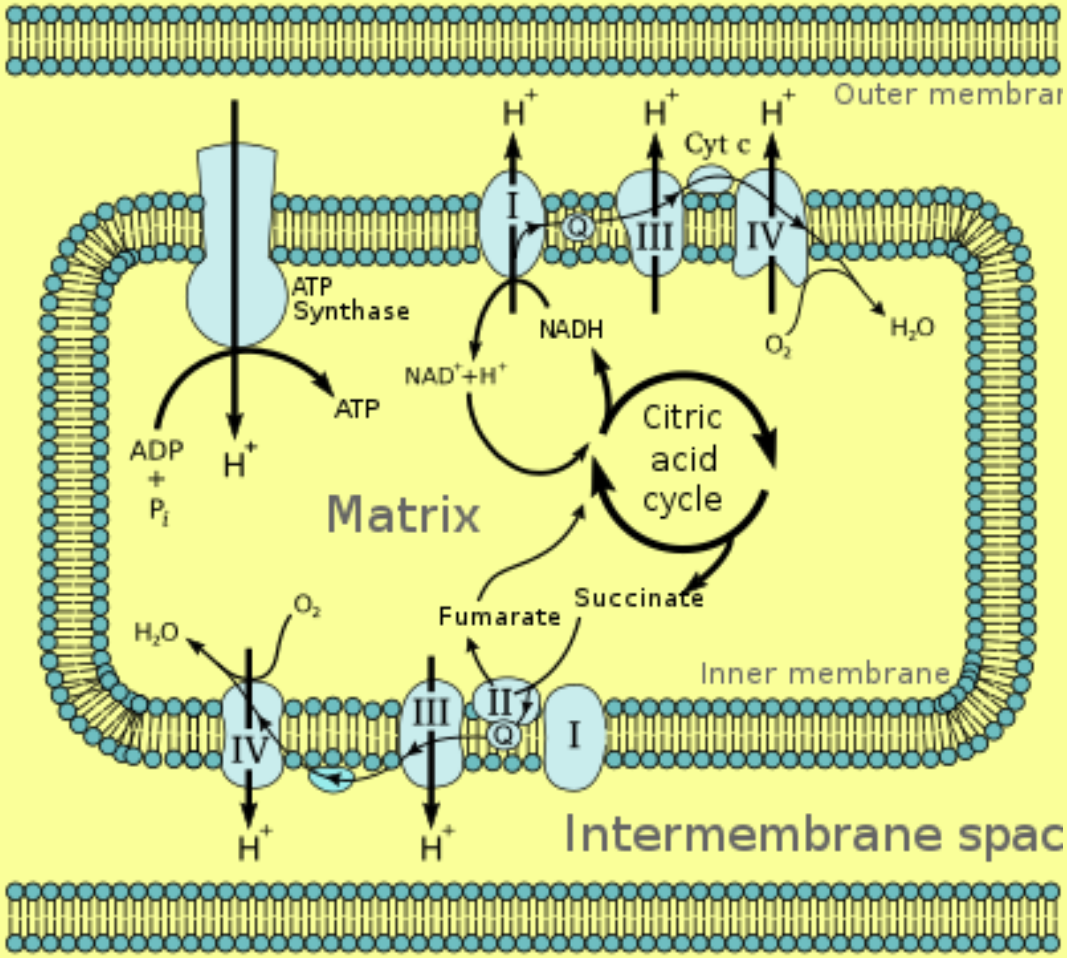
Cognitive Sciences

mind/brain
consciousness
personhood
abstract thought
reasoning
free will
etc

Thomas Nagel
NYU

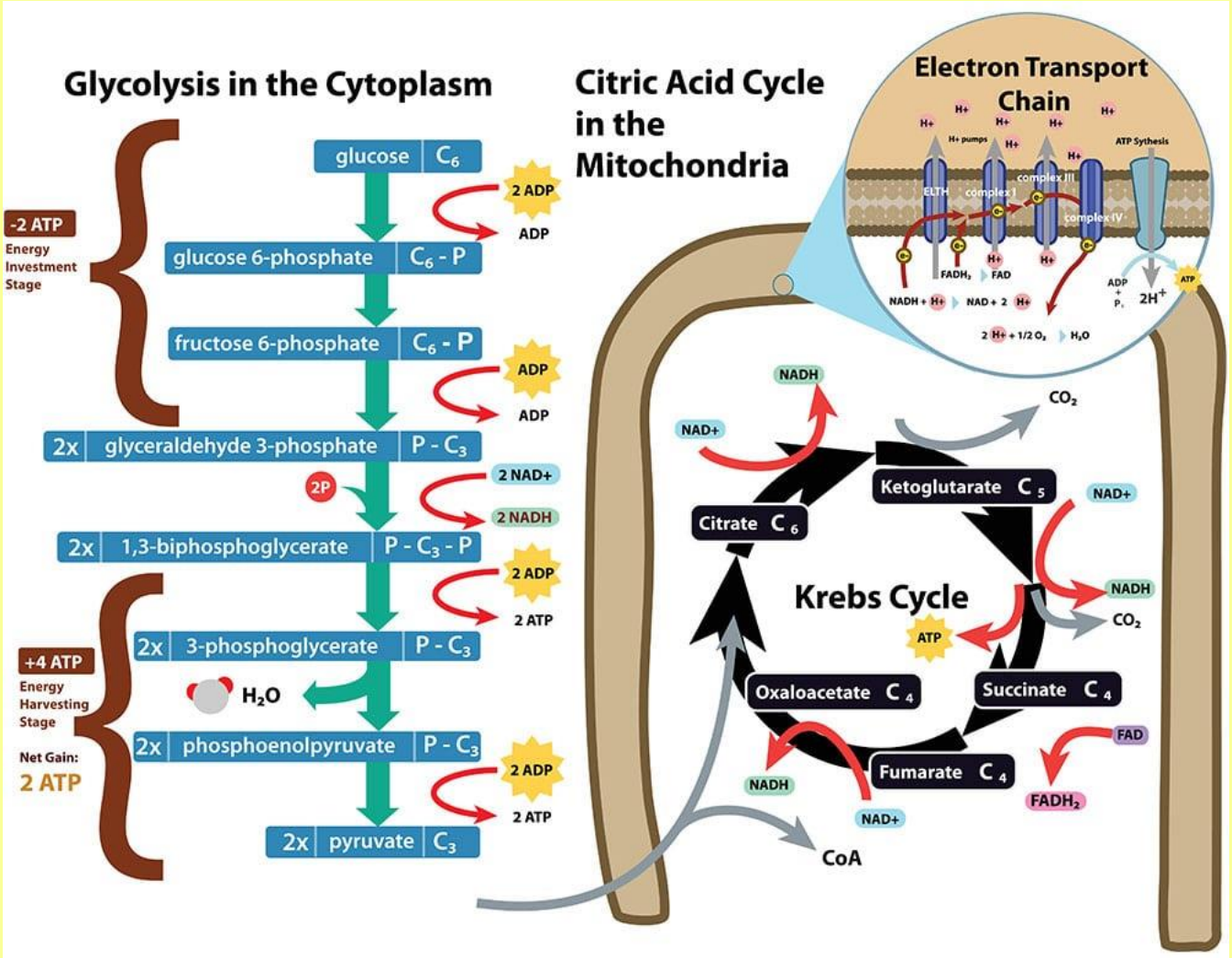


Mitochondria



ATP synthase must fit into a larger system

the entire system must be coherent



ATP synthase must fit into a larger system

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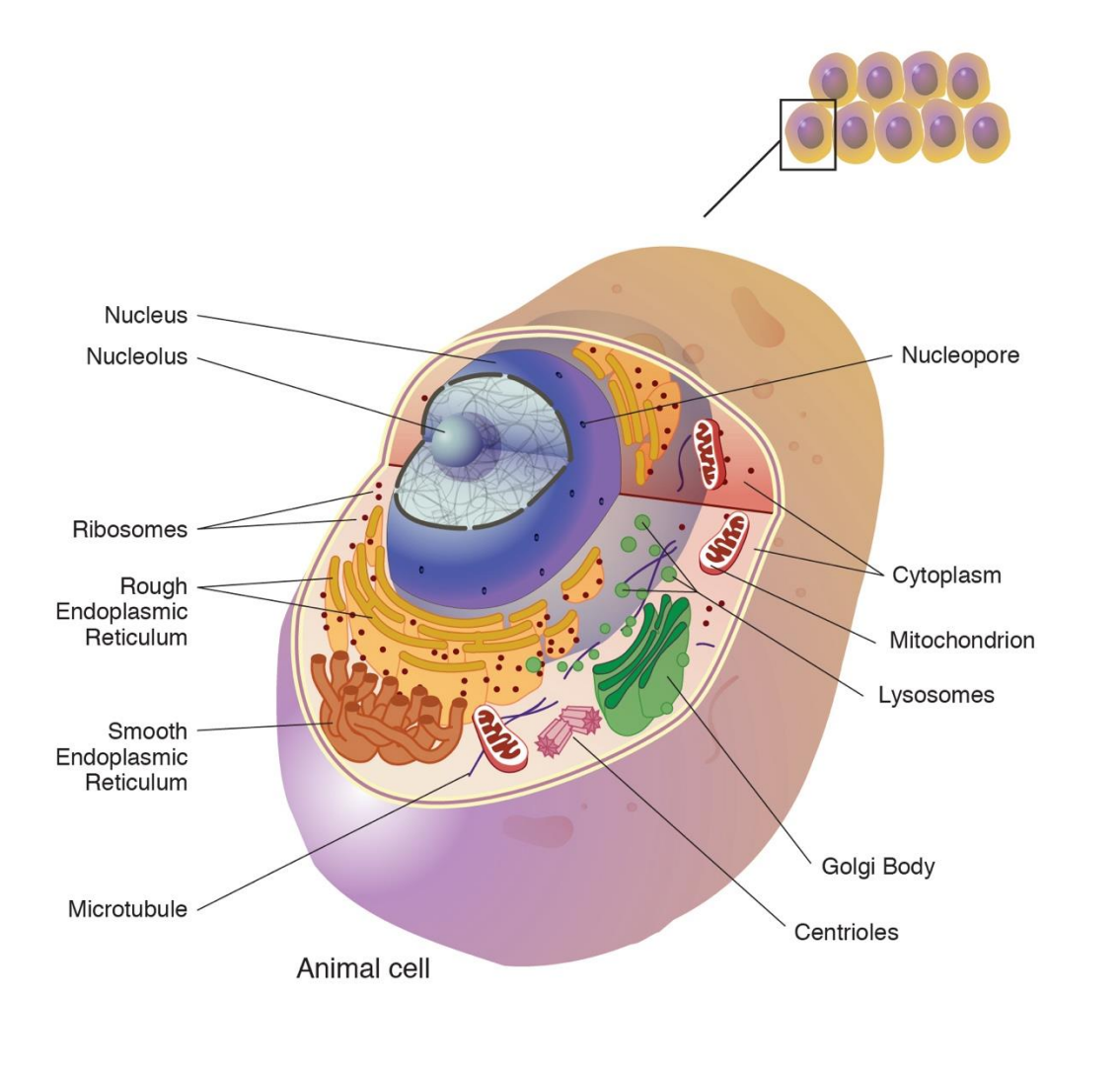
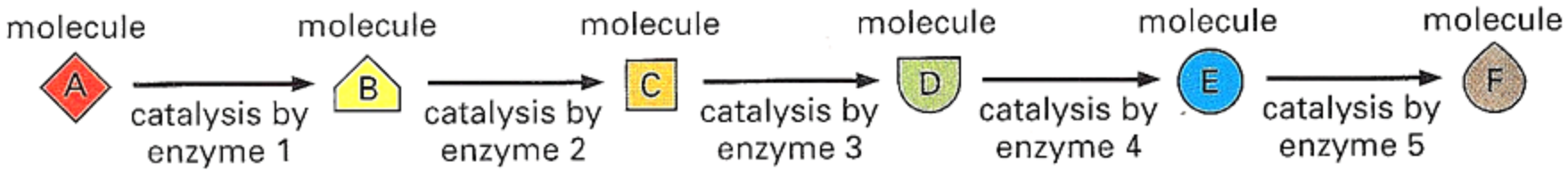


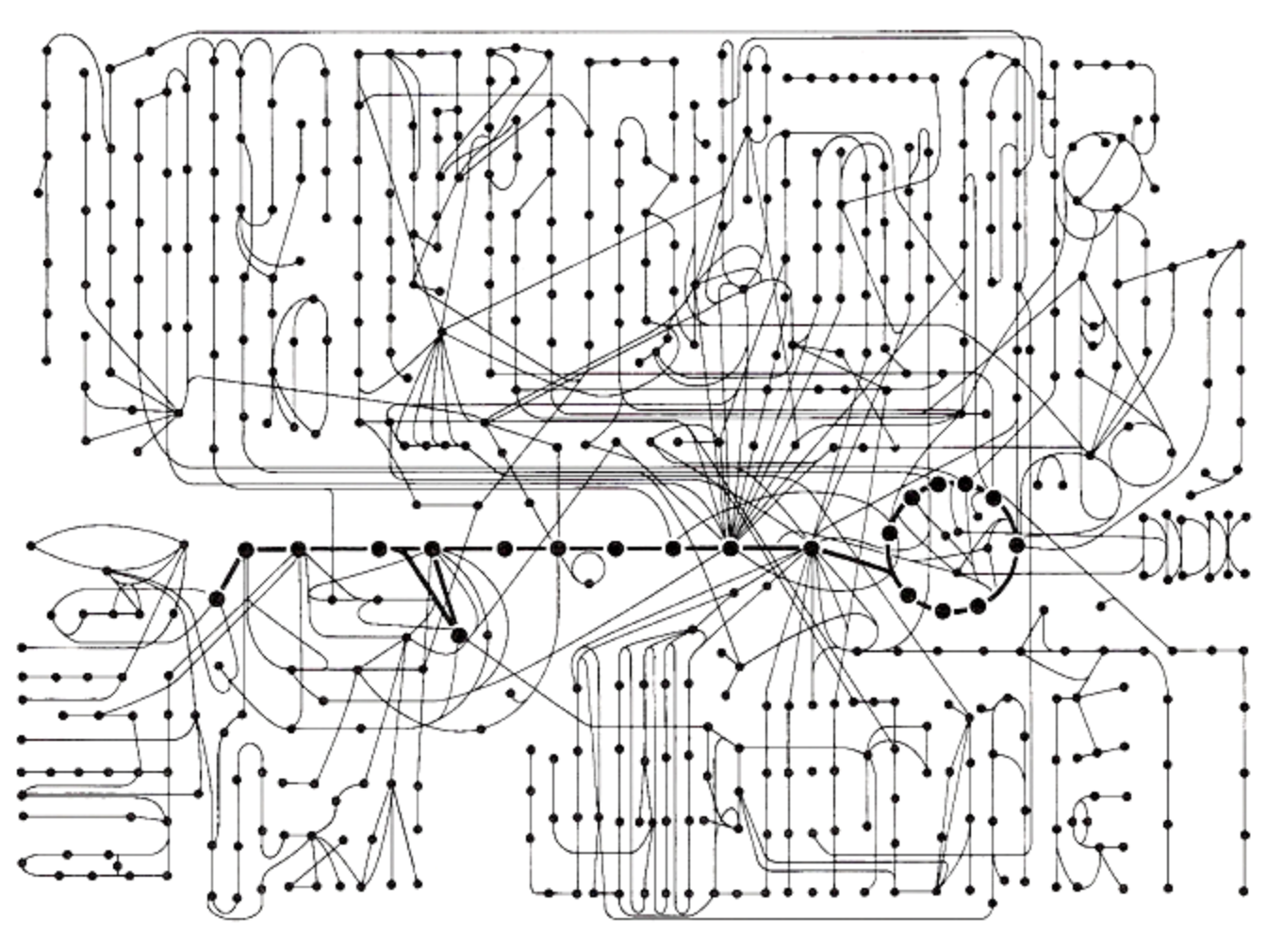
ATP synthase must fit into a larger system

the entire system must be coherent

enzyme pathways



abbreviated as



Some of the metabolic pathways and their interconnections in a typical cell.

from:
Essential Cell Biology