

**10 recent discoveries that have
changed the debate about design in
the universe**

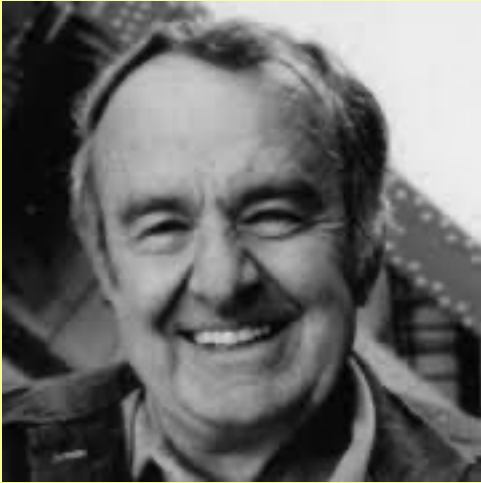
Part II

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. Functional sequences of proteins 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

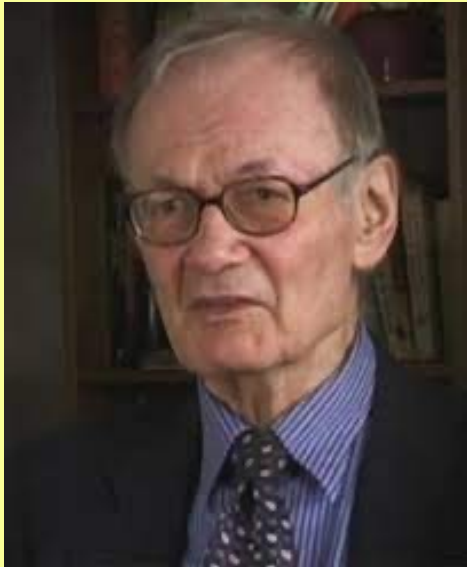
> 500 publications

“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."

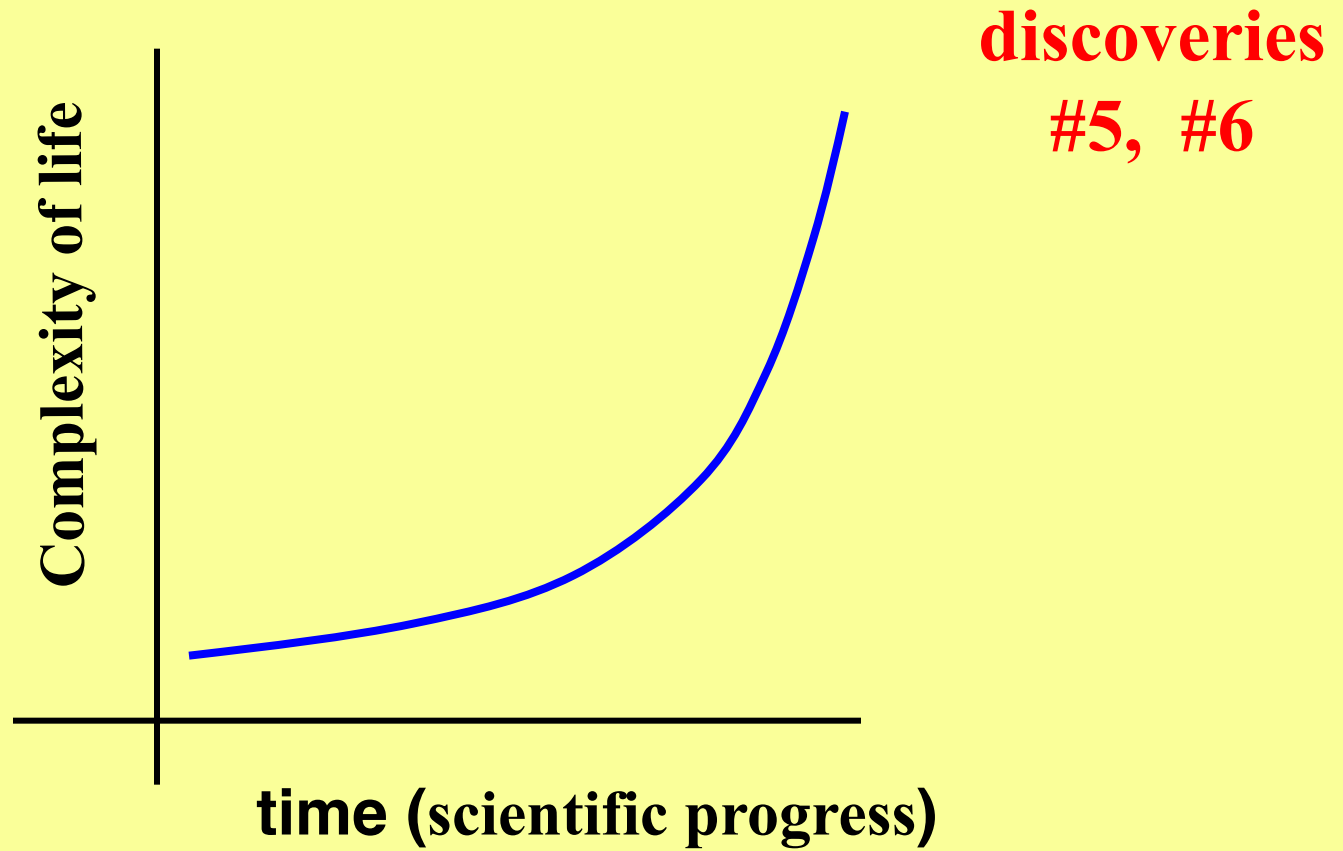
R. Jastrow, *God and the Astronomers*, 1992,
pg 107.

“But I can’t accept it”

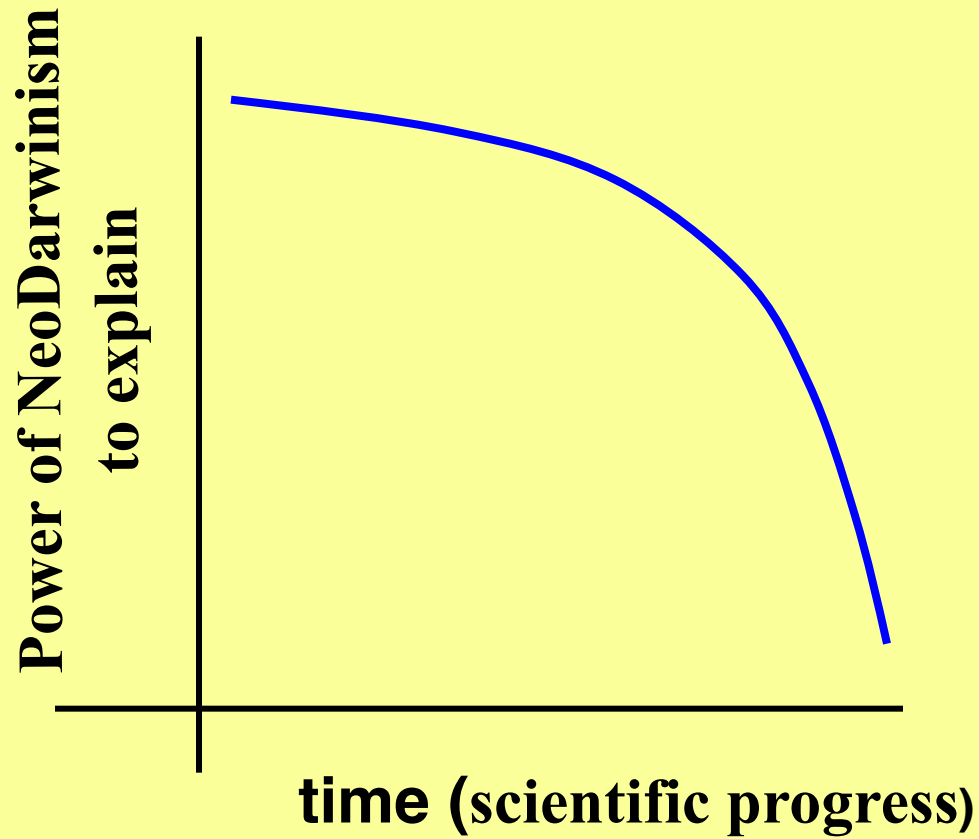
Part II

- 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



Trend with scientific progress



discovery
#7

10 recent discoveries that have changed the debate about origins

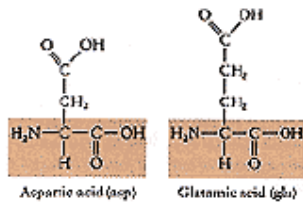
**5. Life is based on a digital information
processing system**

Proteins

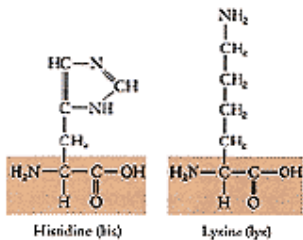
Amino acids

(20 in proteins)

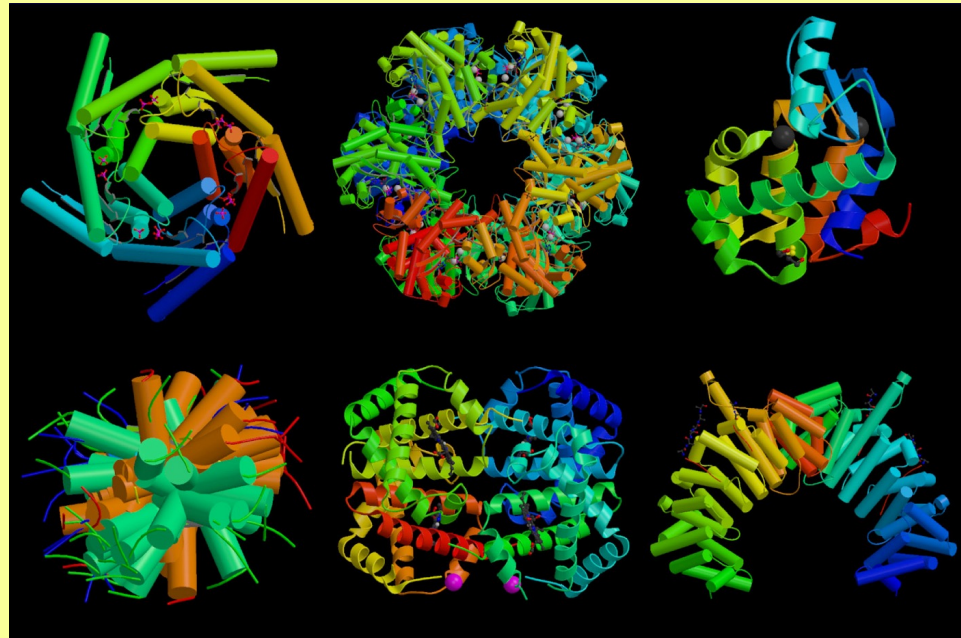
Acidic (negatively charged at pH 7)



Basic (positively charged at pH 7)



chains of **20** amino acids fold into 3D structures



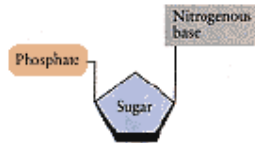
A chain of amino acids:

QYAPQTQSGRTSIVHLFEWRWVDIALECYRLGPKGFGGVQVSPNENVVVTNPSRPWWERYQPVSYKLCTRSGNENEFR
DMVTRCNNVGVRIYVDAVINHMCGSGAAAGTGTTCSYCNPGSREFPAVPYSAWDFNDGKCKTASGGIESYNDPYQVRDC
QLVGLLDLALEKDYVRSMIADYLNKLIDIGVAGFRIDASKHMWPGDIKAVLDKLNHLNTNWFPAWSRPFIFQEVIDLGGE
AIKSSEYFGNGRVTEFKYGAKLGTVVRKWSGEKMSYLNWGEWGFMPDRALVFDNHDNQRGHGAGGSSILTFWDARL
YKVAVGFMLAHPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNGVIKEVTINADTTCGNDWVCEHRWREIRNMVWFRNV
VDGEPFANWWDNGSNQVAFGRGRNGFIVFNDDWQLSSTLQTGLPGGTCDVISGDKVGNSTGVIKVVSSDGTAFQFIS
NSAEDPFIAIHAESKL

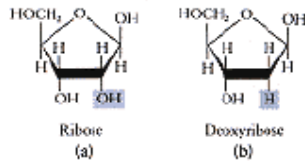
DNA

Nucleotides

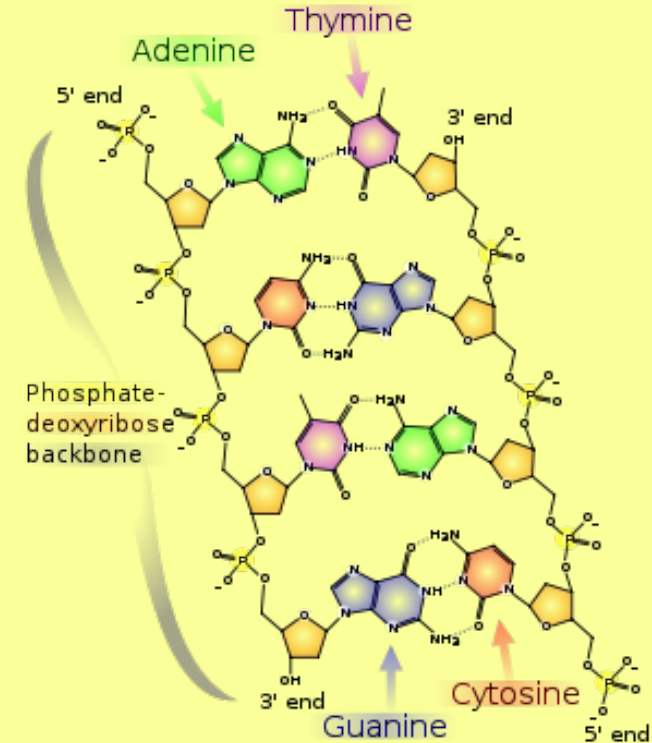
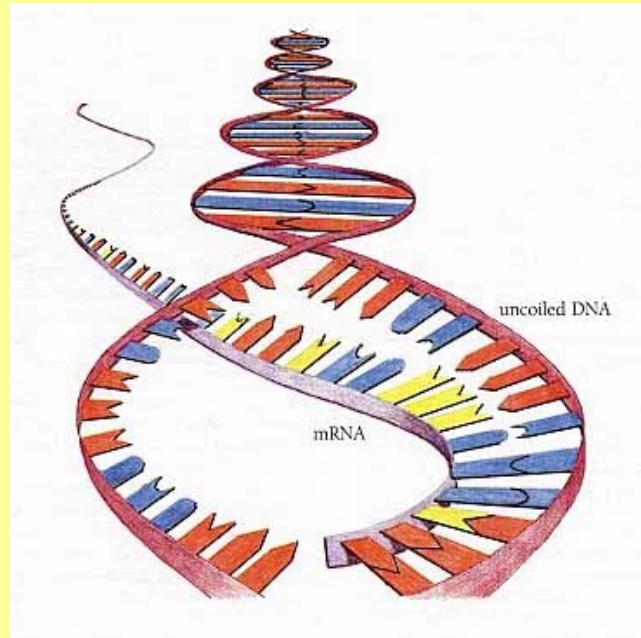
(4 in DNA and RNA)



3-30 A nucleotide is made up of three different subunits: a phosphate group, a five-carbon sugar, and a nitrogenous base. As we shall see in Chapter 14, nucleotides can be linked together in long chains by condensation reactions involving the hydroxyl groups of the phosphate and sugar subunits.

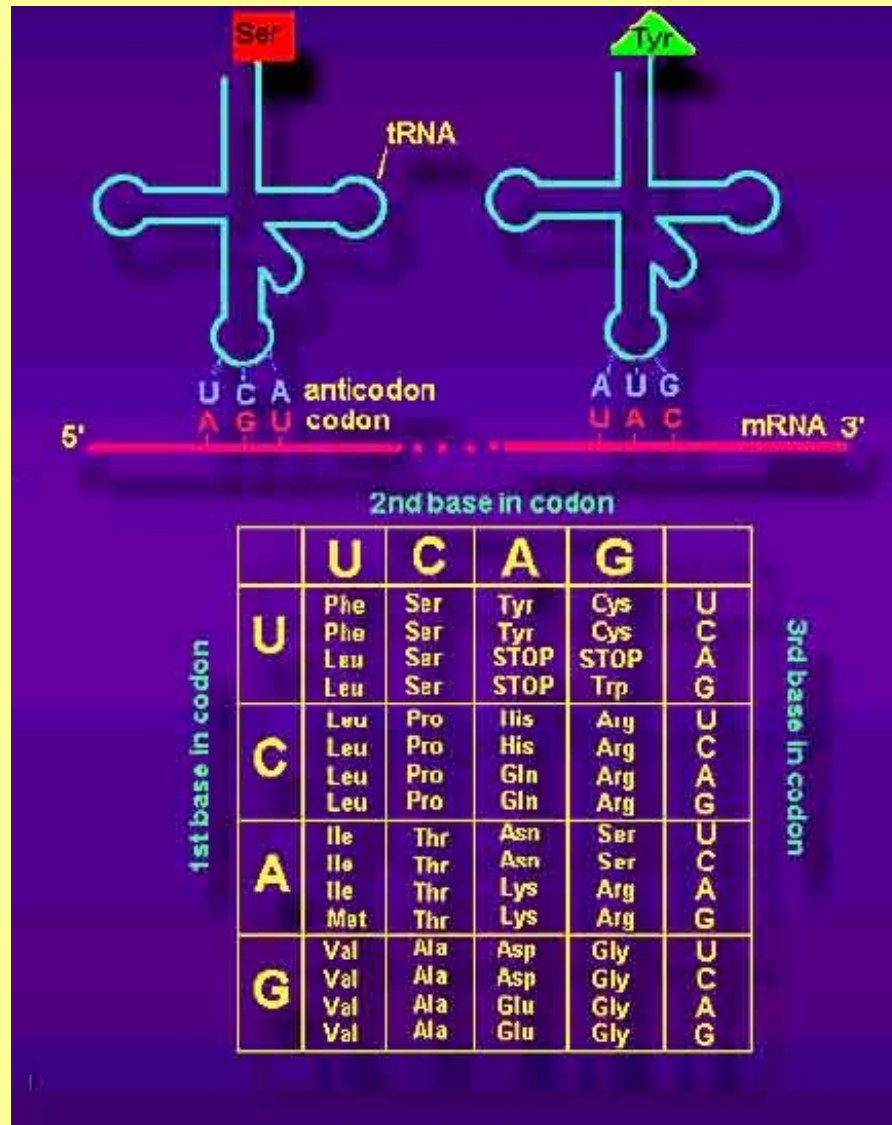


chains of 4 nucleotides



A chain of nucleotides:

ATCGCCTATATAGCGTACAATGGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGC
 GCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTAC
 ATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGC
 CTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGCCTATAT
 AGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGCTAGCGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGAT
 GCTAGCTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAG
 CTAGCTAGCATCGCCTATATAGCGTACAATGGCTACATCGCCTATATAGCGTACAATGGCTACGTAGCTACGATGCTAGCTAGC
 TAGC



the genetic code

DNA: C, A, T, G

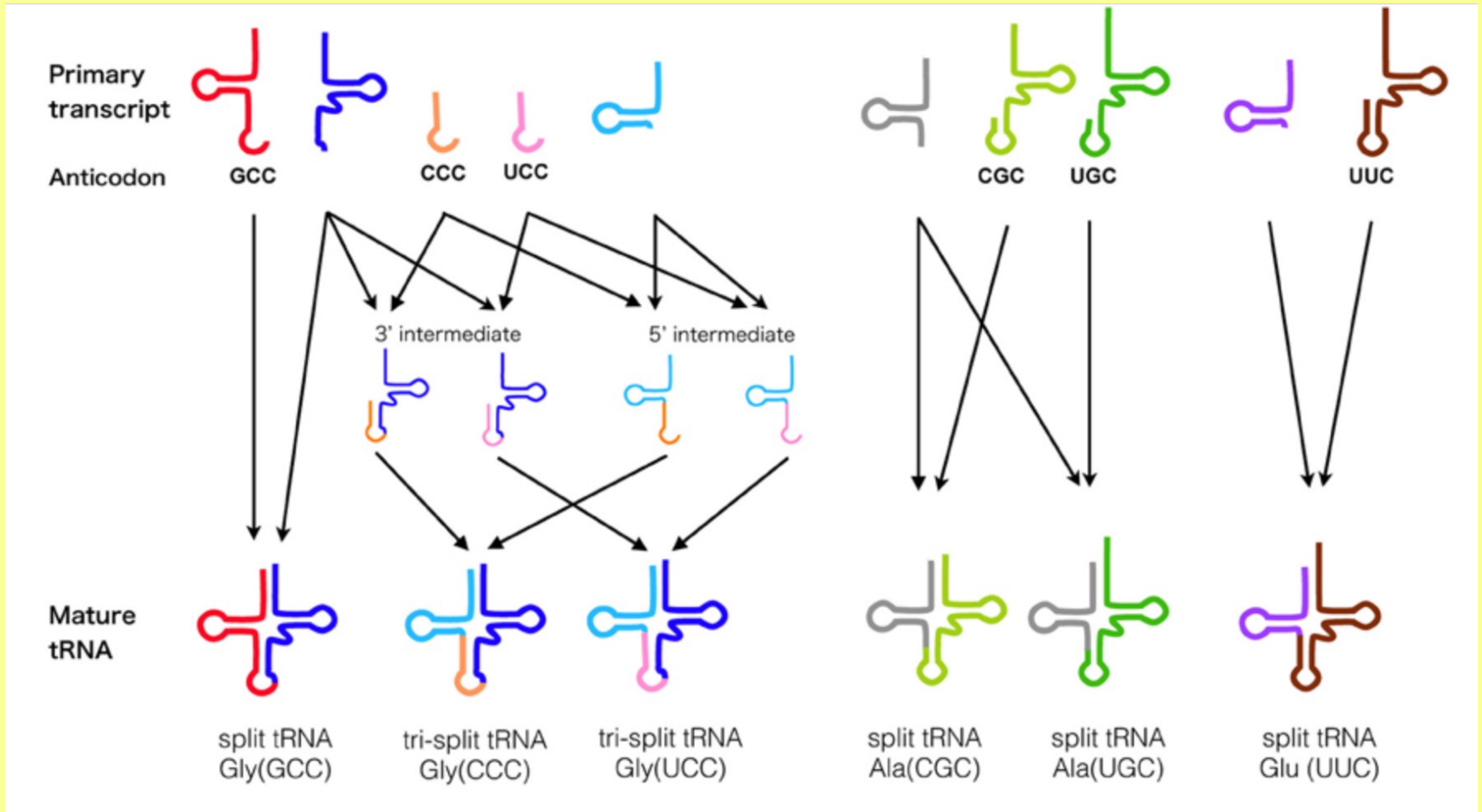
RNA: C, A, U, G

an information processing system!

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

How are tRNAs made?

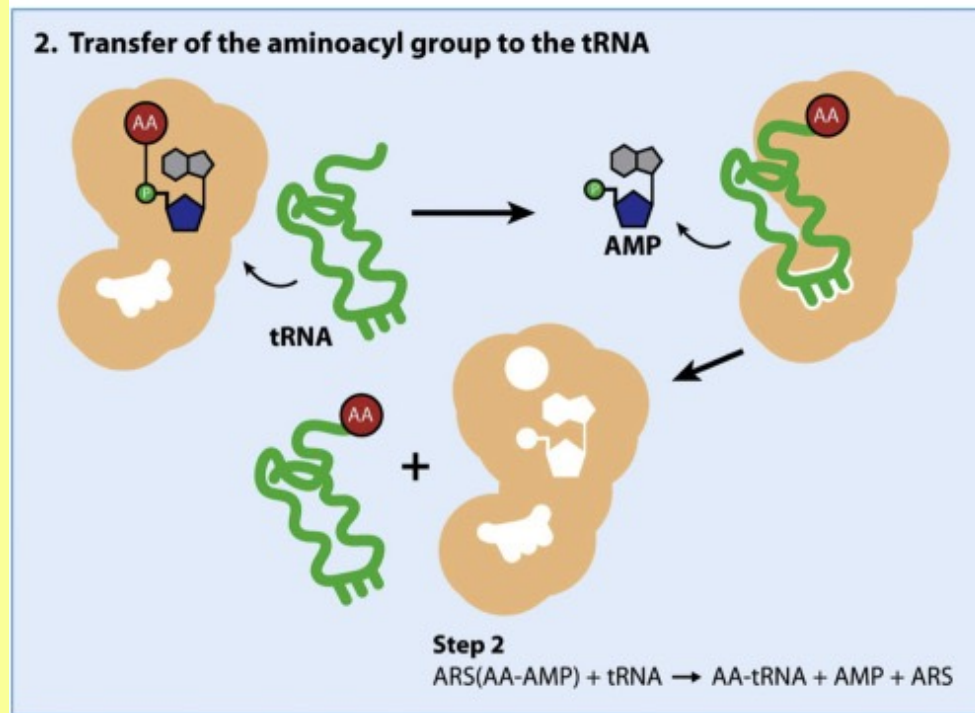
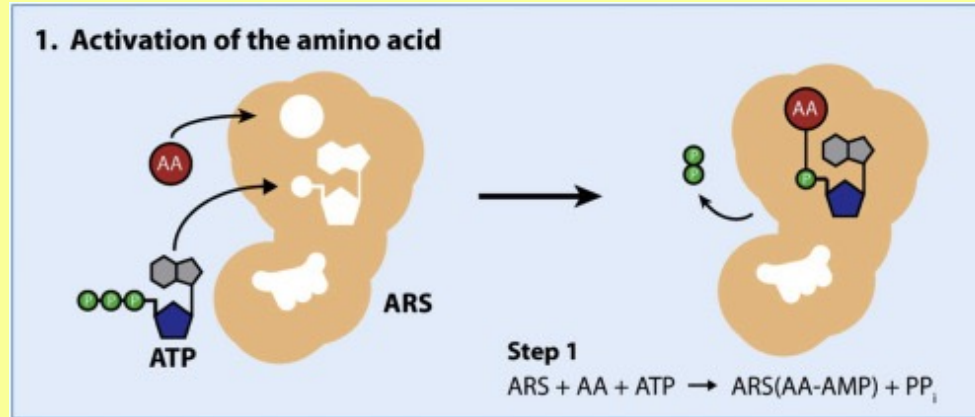
(Part 1)



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.

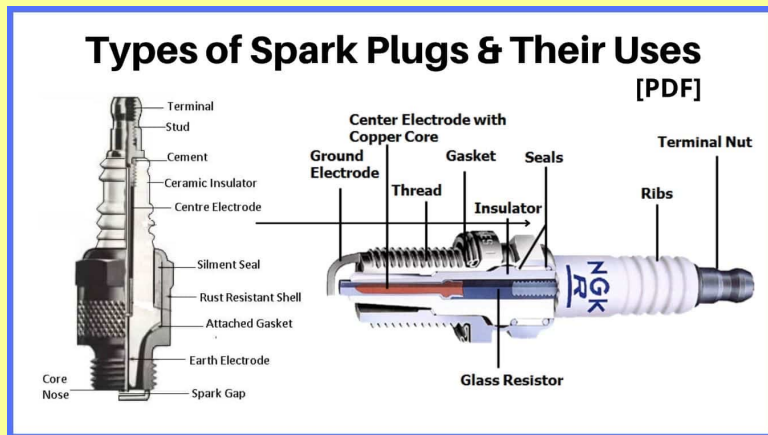
12 discoveries that have changed the debate about origins

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

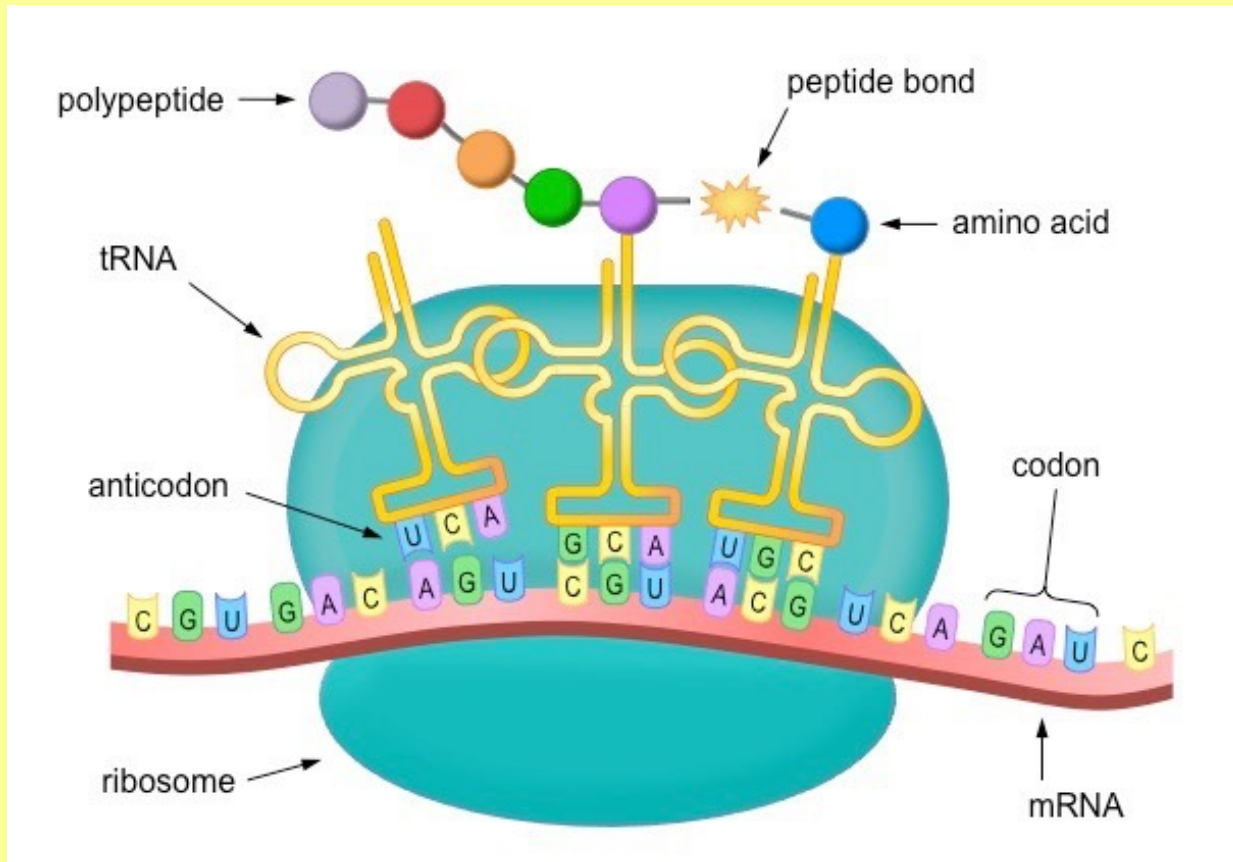
(Undeniable, Douglas Axe)



spark plug must fit into a larger system

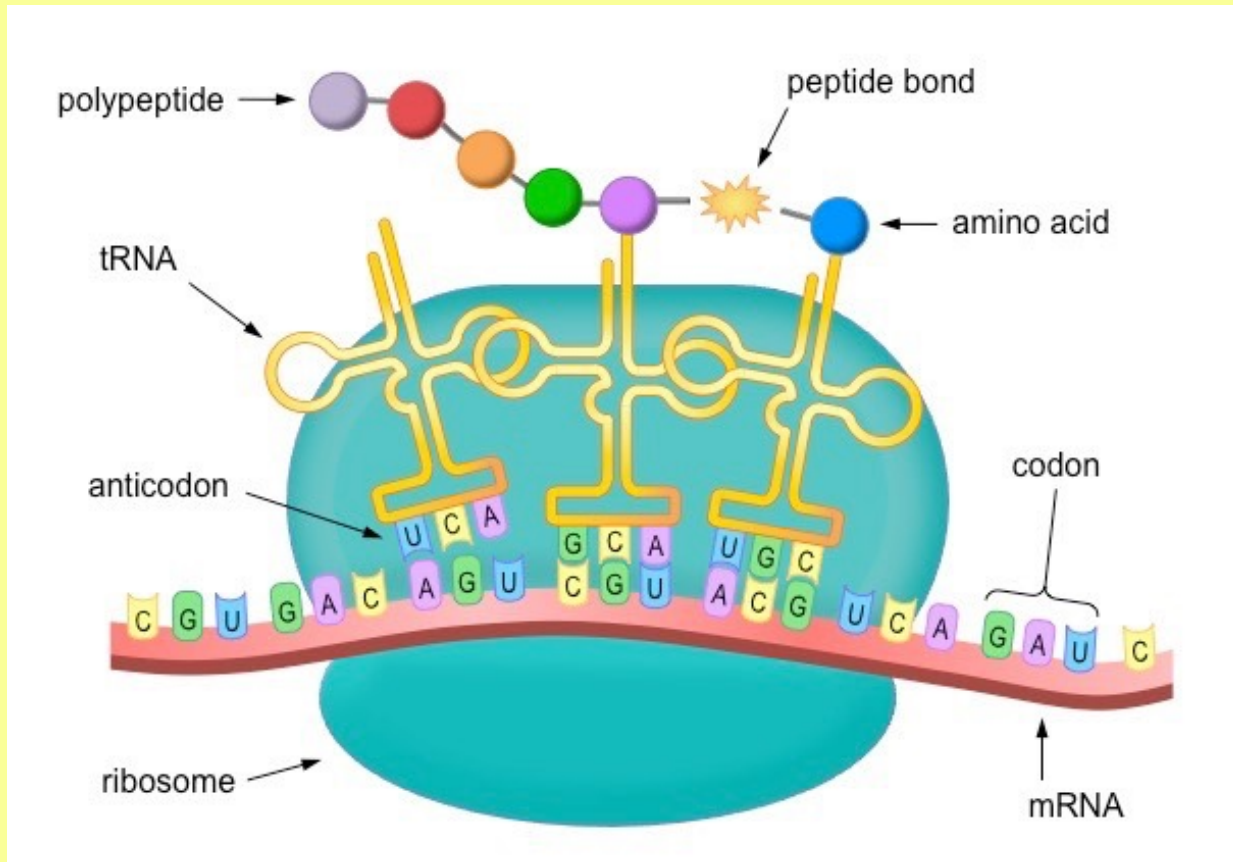
the entire system must be coherent

ribosome



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

ribosome



ribosome must fit into a larger system

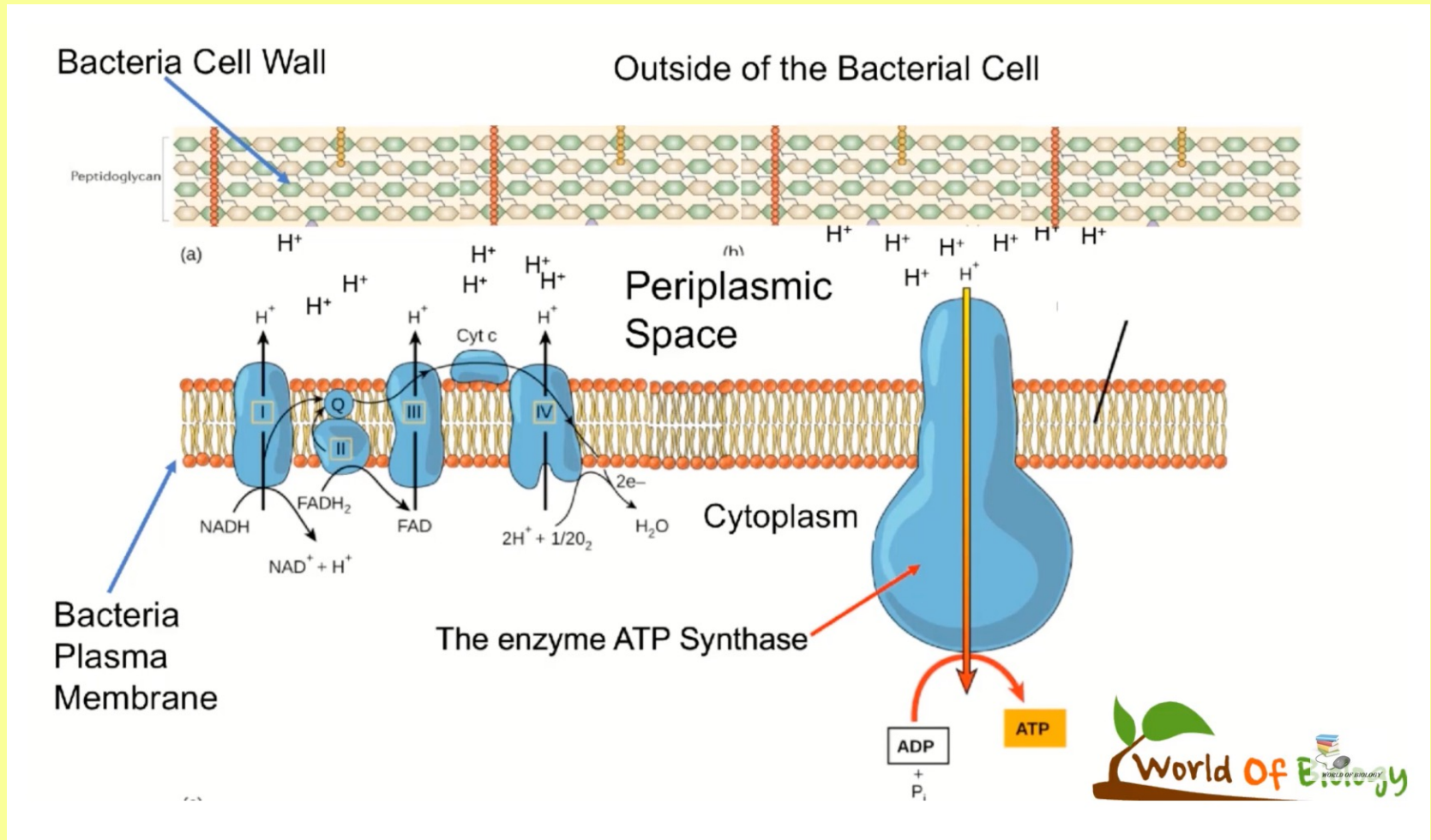
the entire system must be coherent



ATP synthase

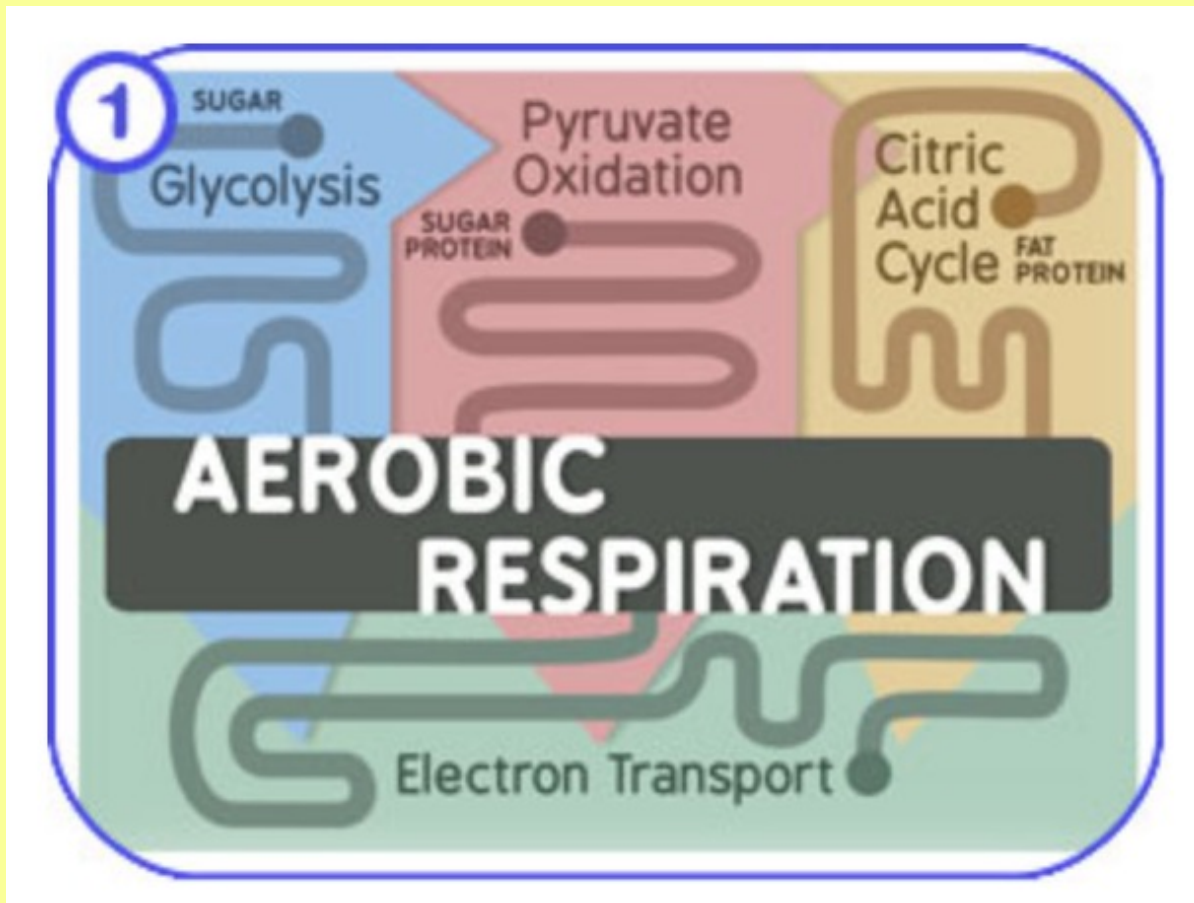
ATP synthase is a machine that converts a proton gradient to mechanical energy which is converted to chemical energy

Bacteria

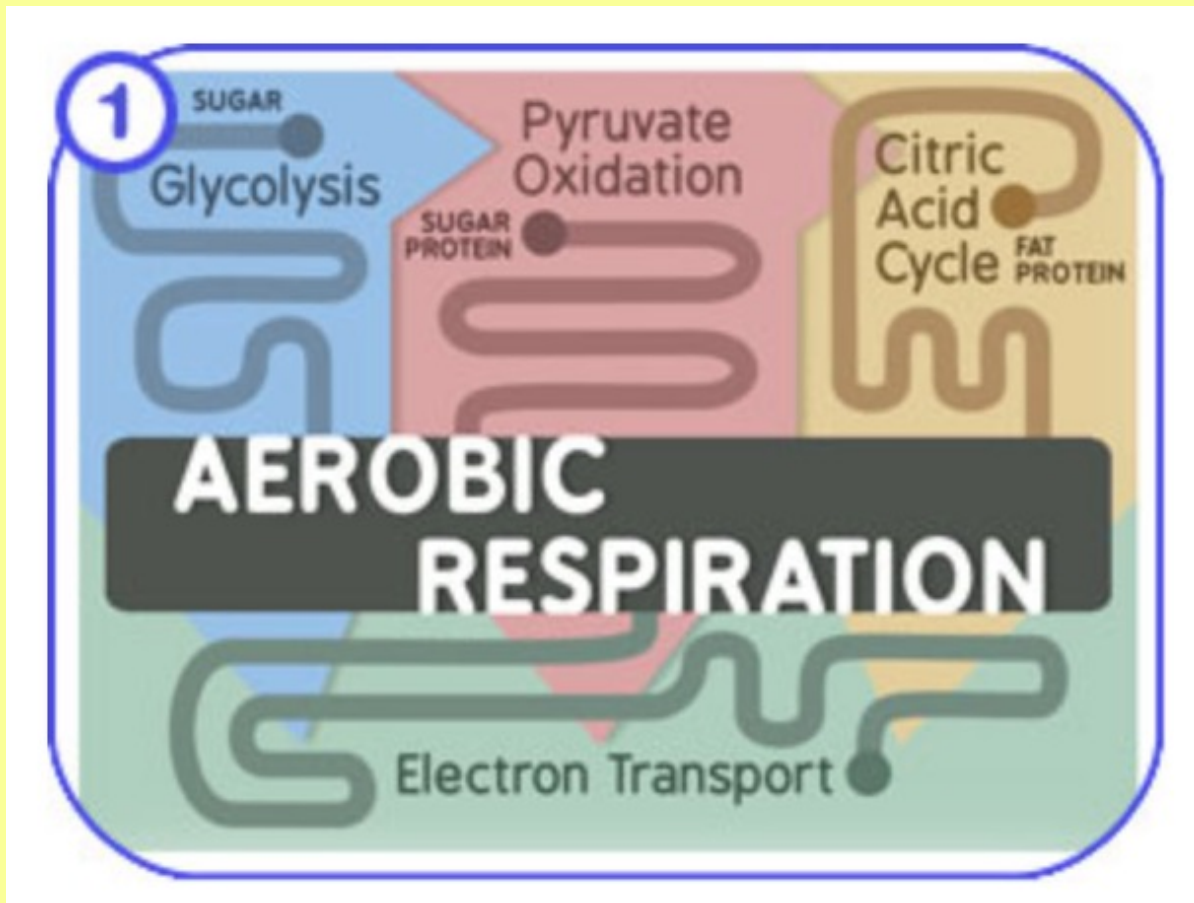


ATP synthase must fit into a larger system

the entire system must be coherent

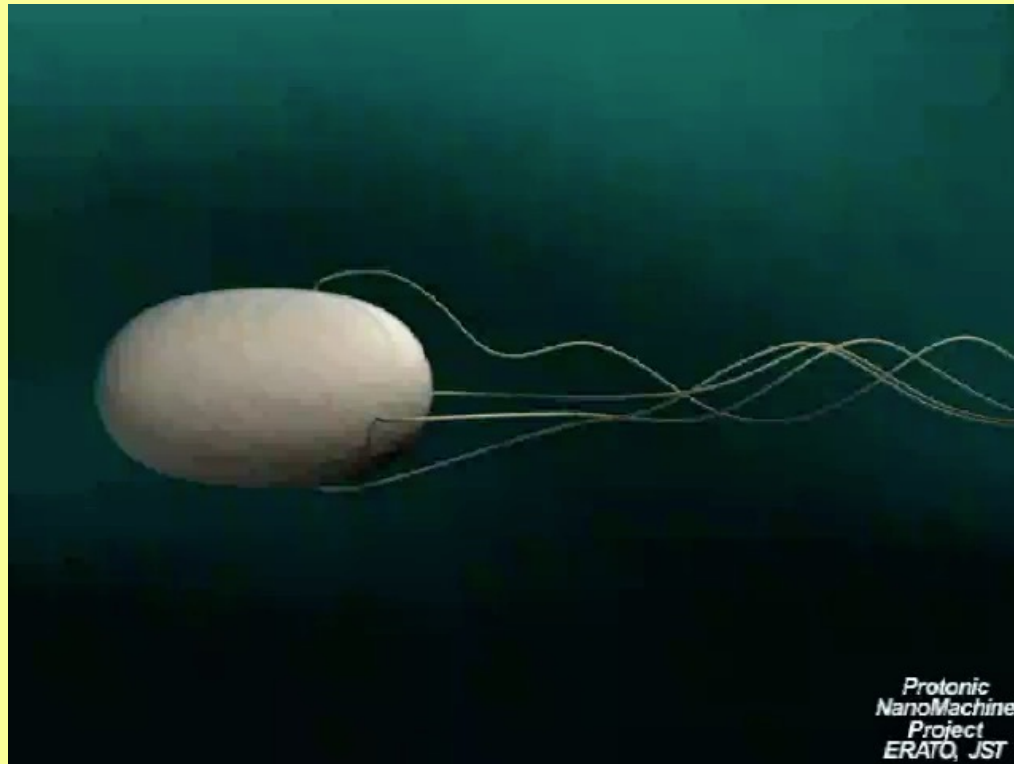


- NADH and FADH₂ require Citric Acid Cycle
- Citric Acid Cycle requires Pyruvate Oxidation
- Pyruvate Oxidation requires Glycolysis

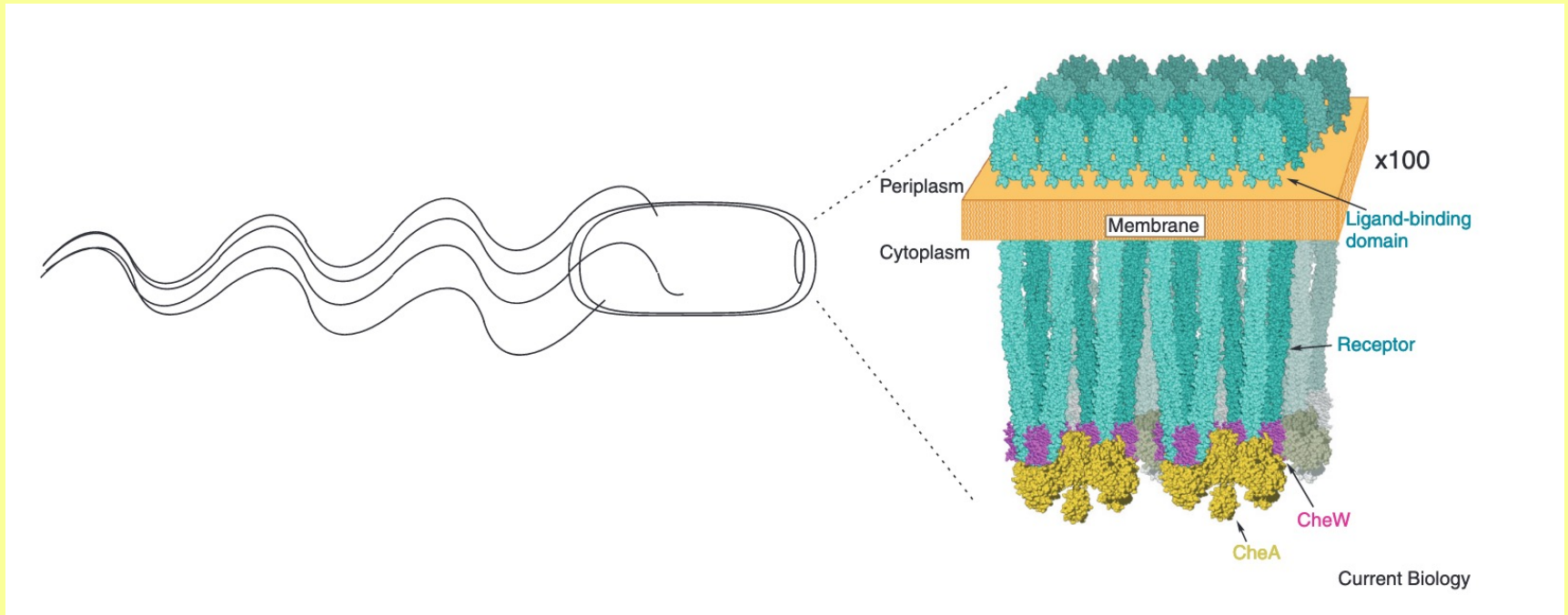


ATP synthase must fit into a larger system

the entire system must be coherent

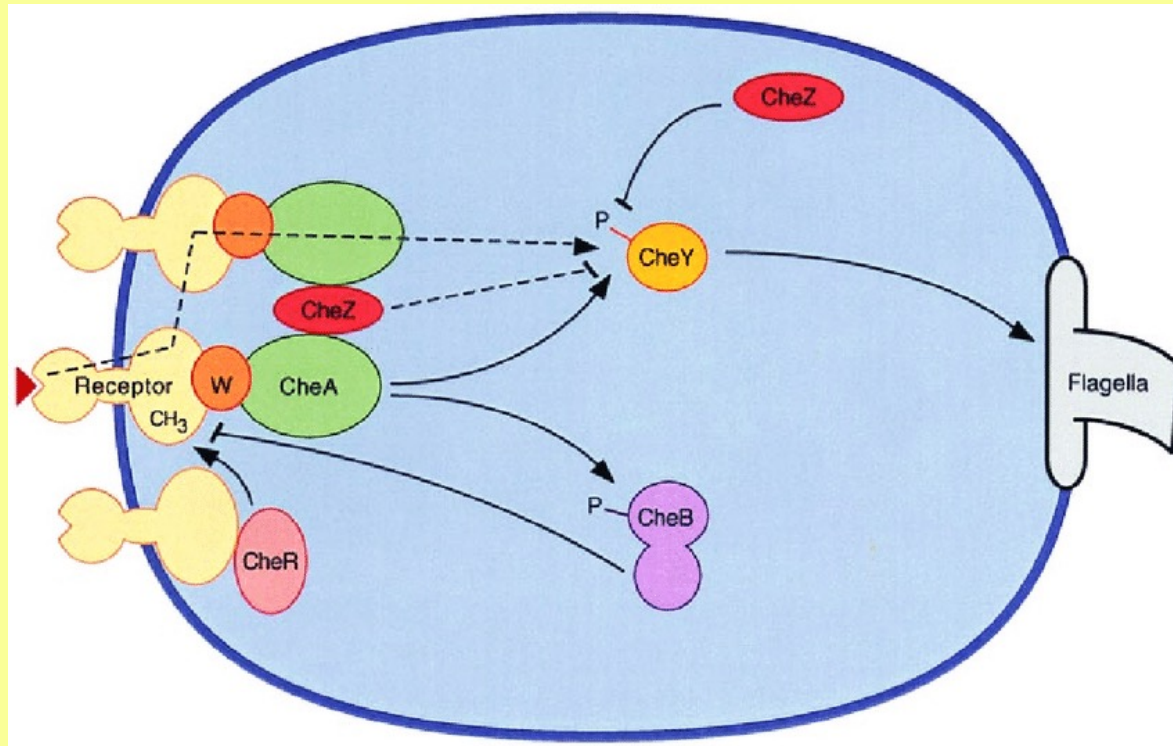


the bacterial flagellum is a machine that converts a proton gradient to mechanical motion



to move toward a food molecule (glucose):

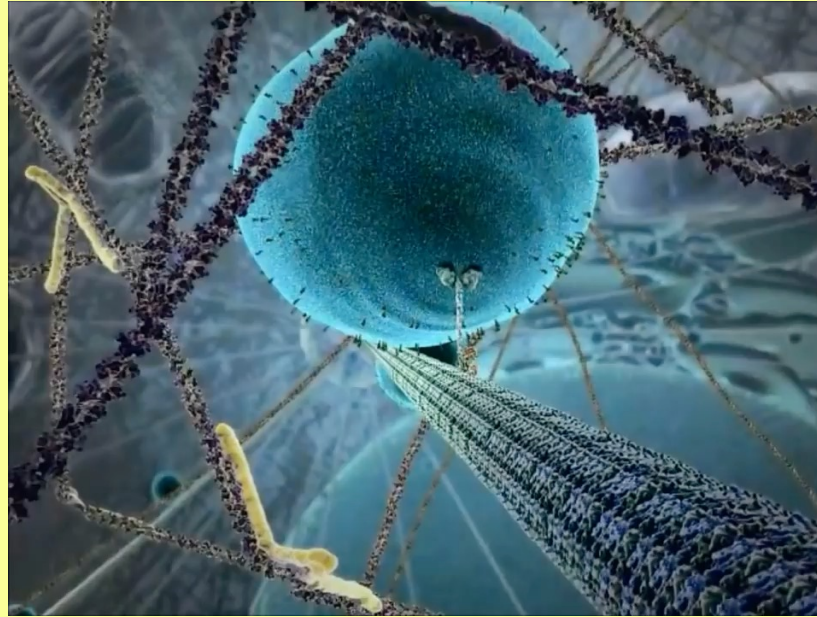
- the flagellar motion must be controlled
- the control mechanism must be connected to a sensor
- the sensor must distinguish between molecules



The flagellum must fit into a larger system

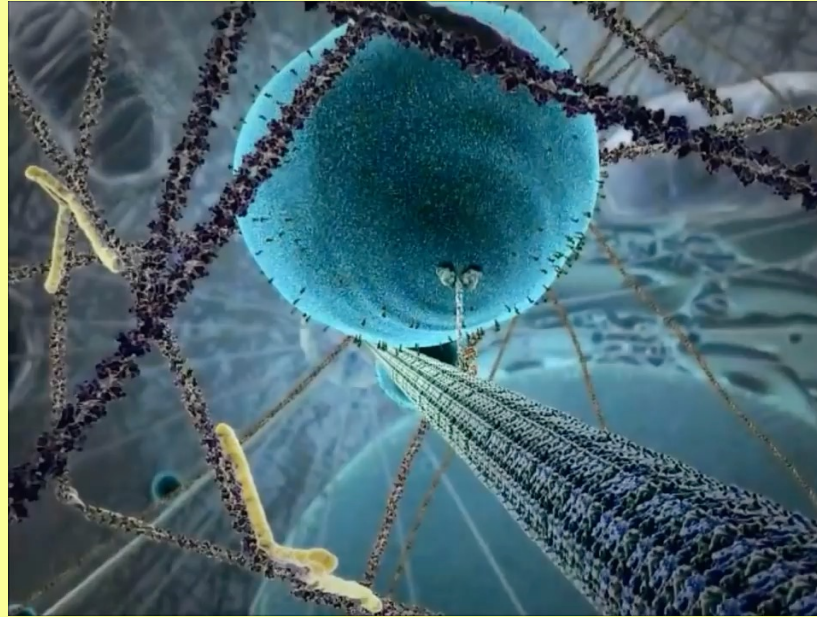
the entire system must be coherent

kinesin



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

kinesin

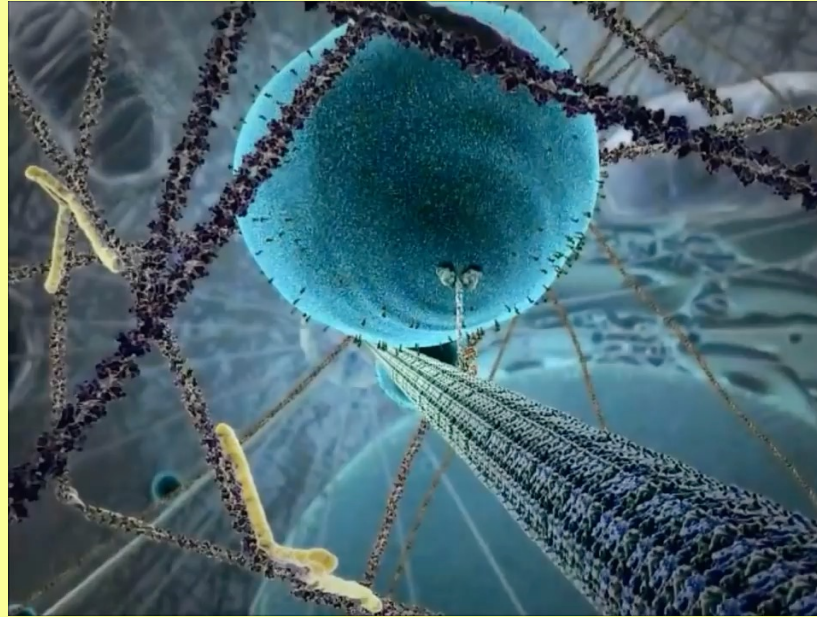


kinesin must:

- 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

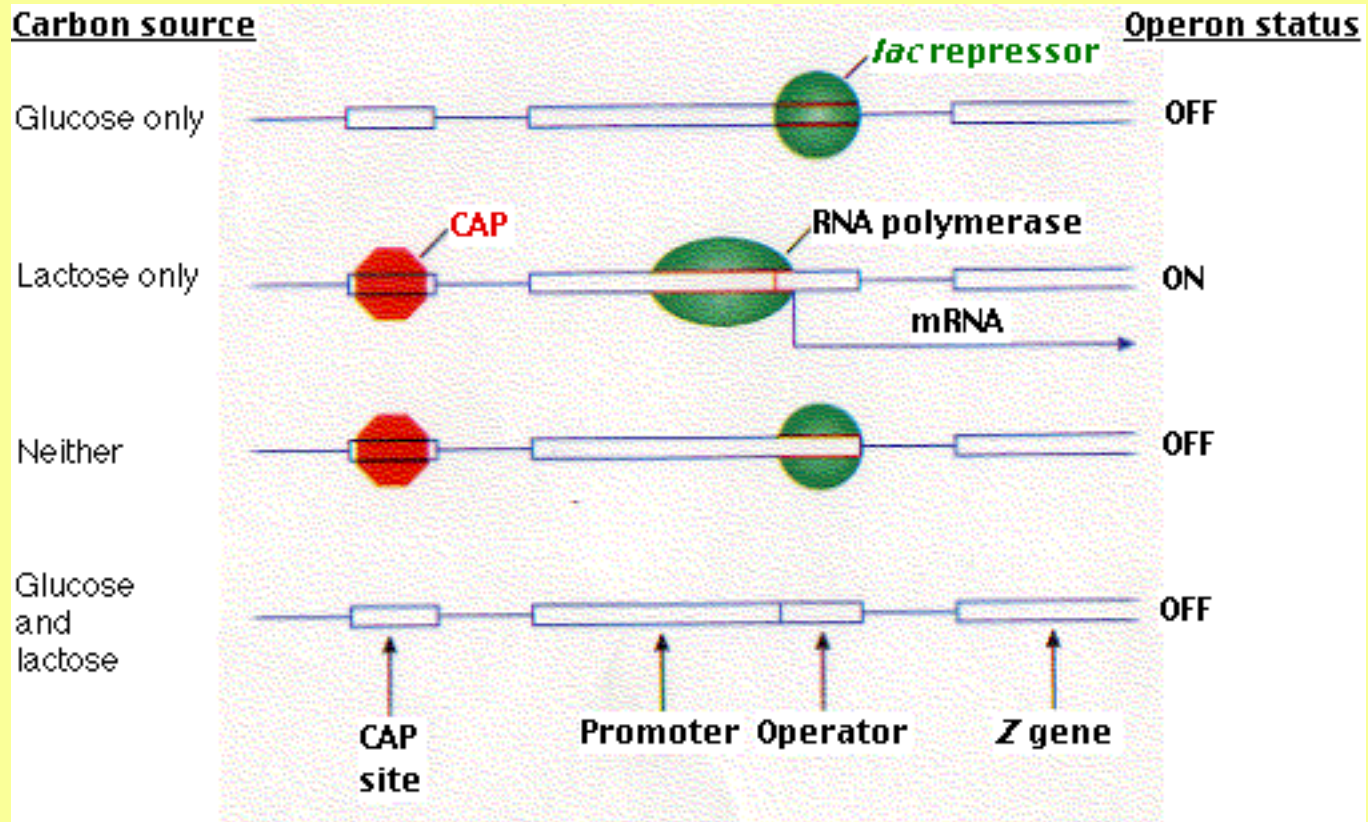
How does it function? (physics and chemistry)
Where did it come from? (a mind)



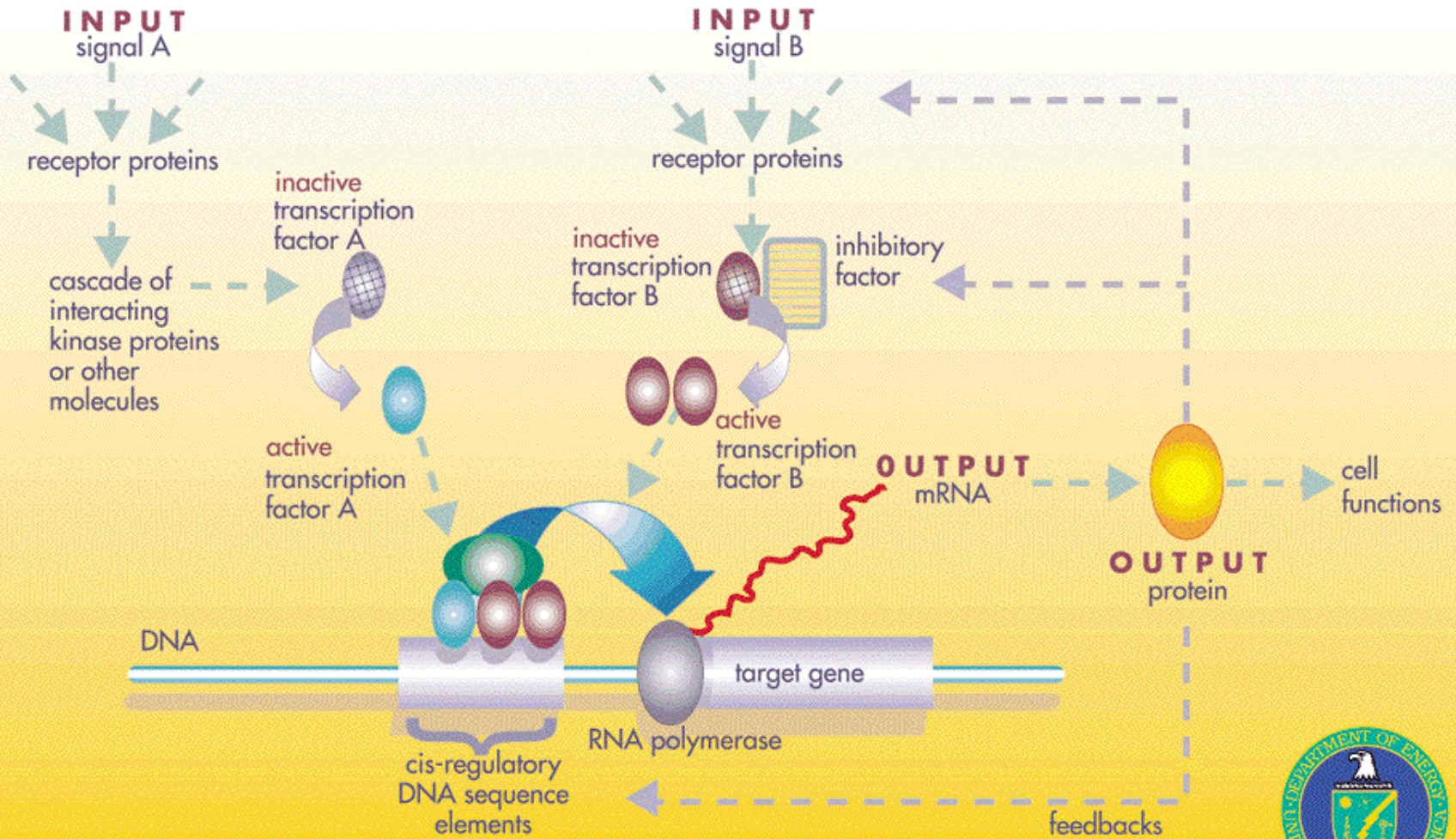
**All Cells Have Sophisticated
Software Algorithms**

Example of a simple algorithm: (lac operon)

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

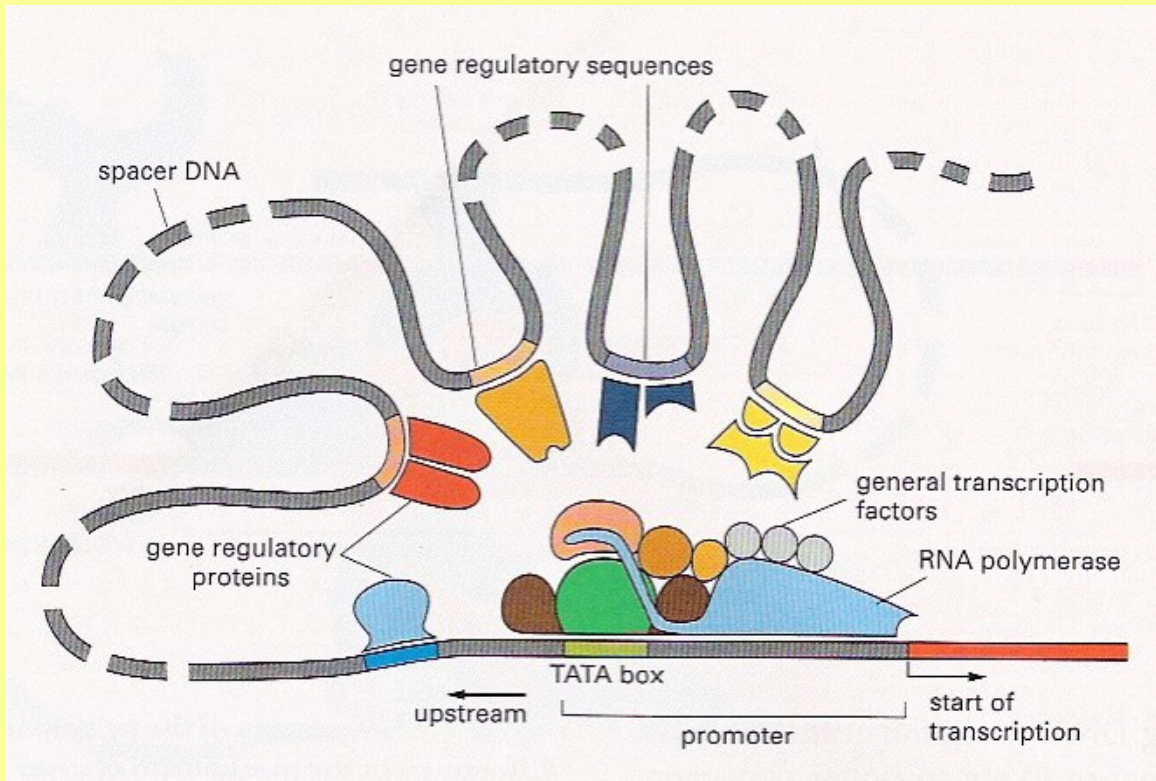


A GENE REGULATORY NETWORK



YGG 01-0083

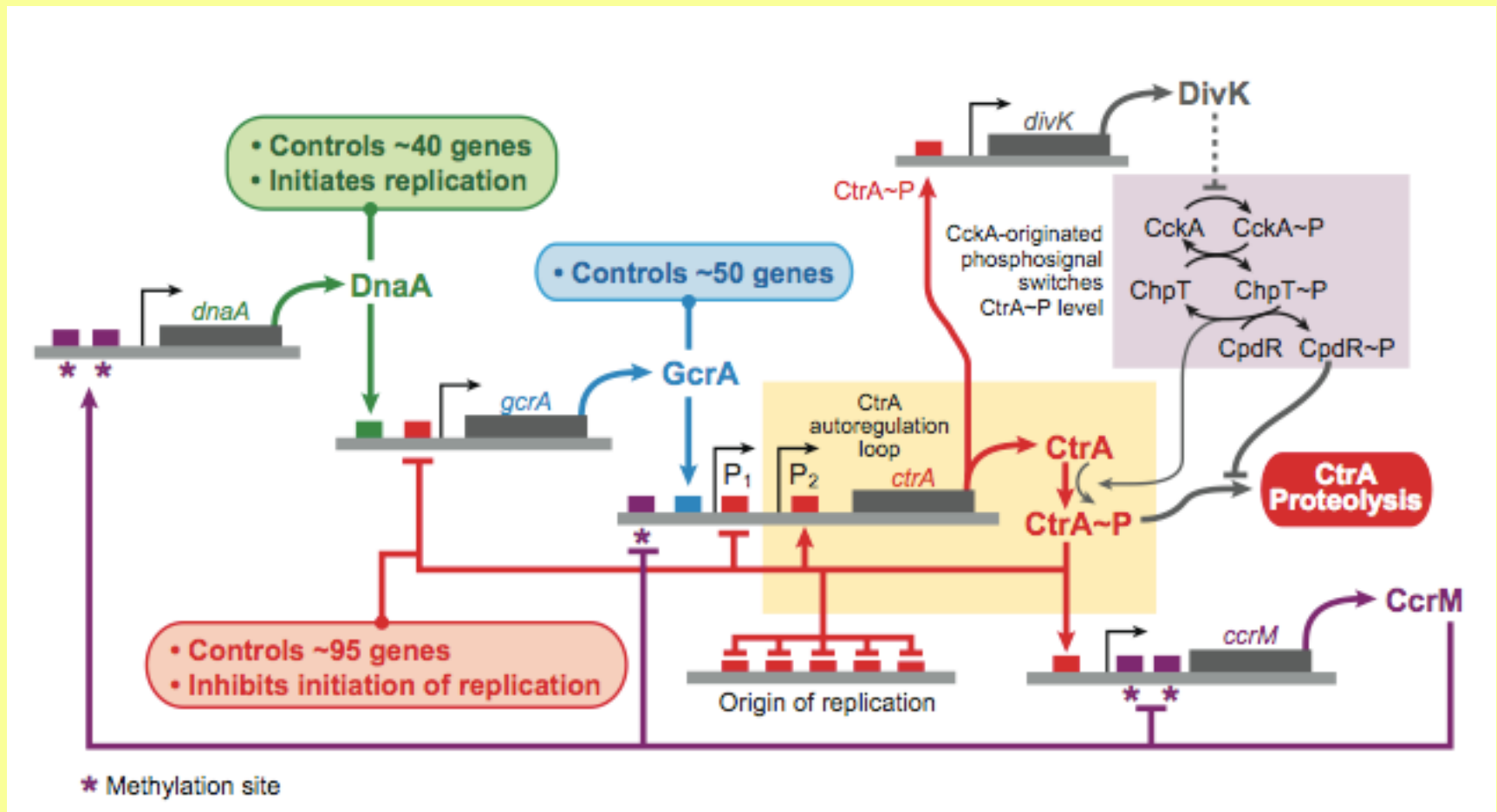




“In animals and plants, it is not unusual to find the regulatory sequences of a gene dotted over distances of 50,000 nucleotide pairs...”

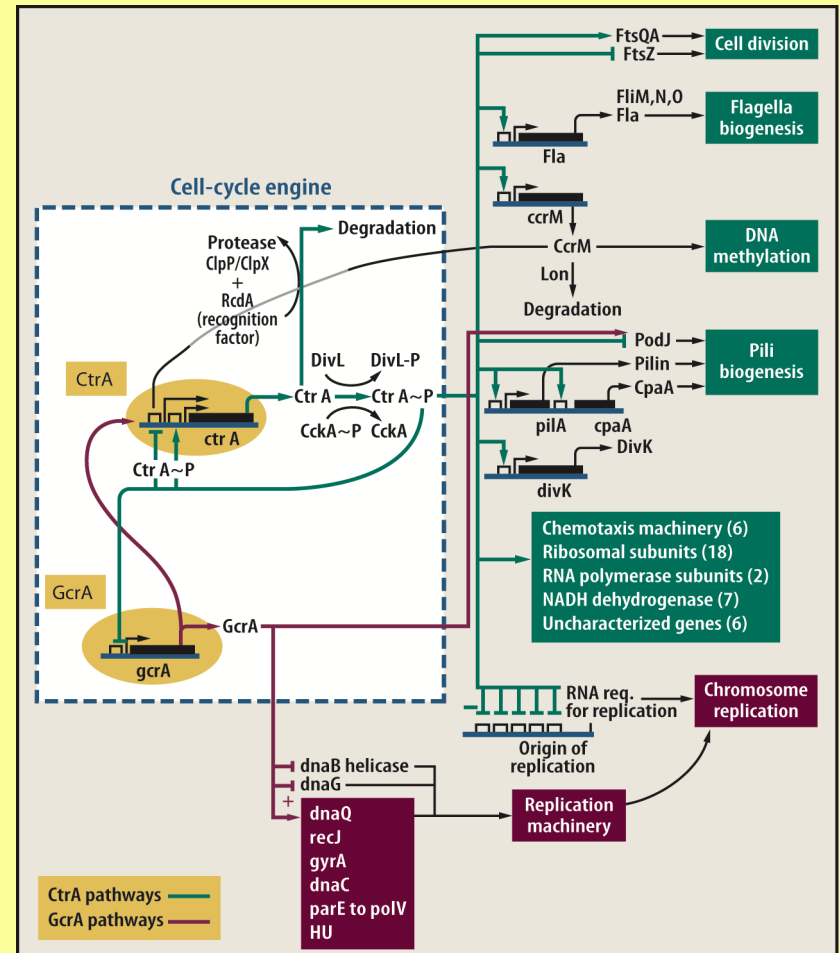
from
“Essential
Cell Biology”
Alberts et al

Genetic regulatory network of cell cycle in *Caulobacter*

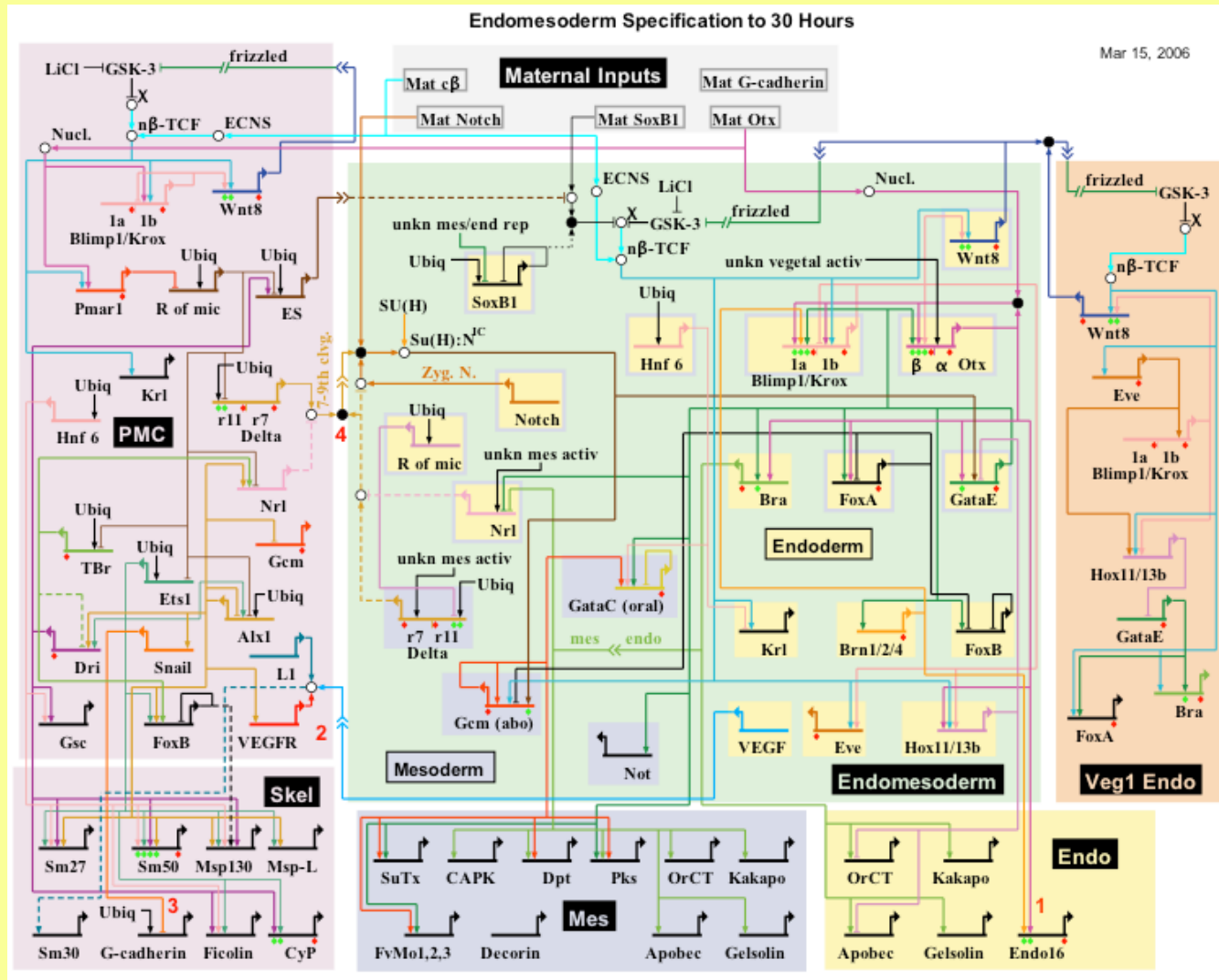


Genetic regulatory network of cell cycle in *Caulobacter*

- 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

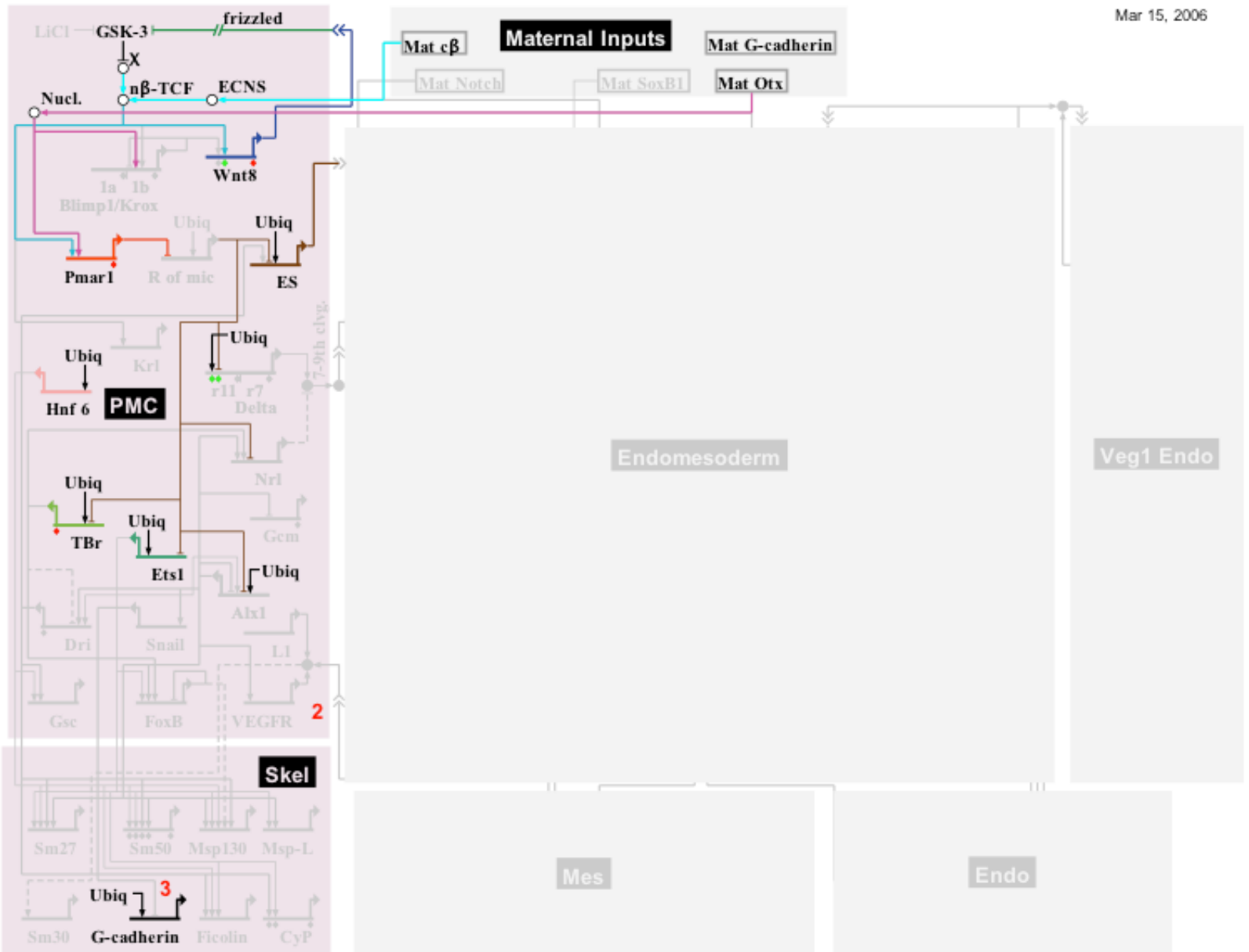


Genetic regulatory network controlling endomesoderm development in sea urchin embryos:



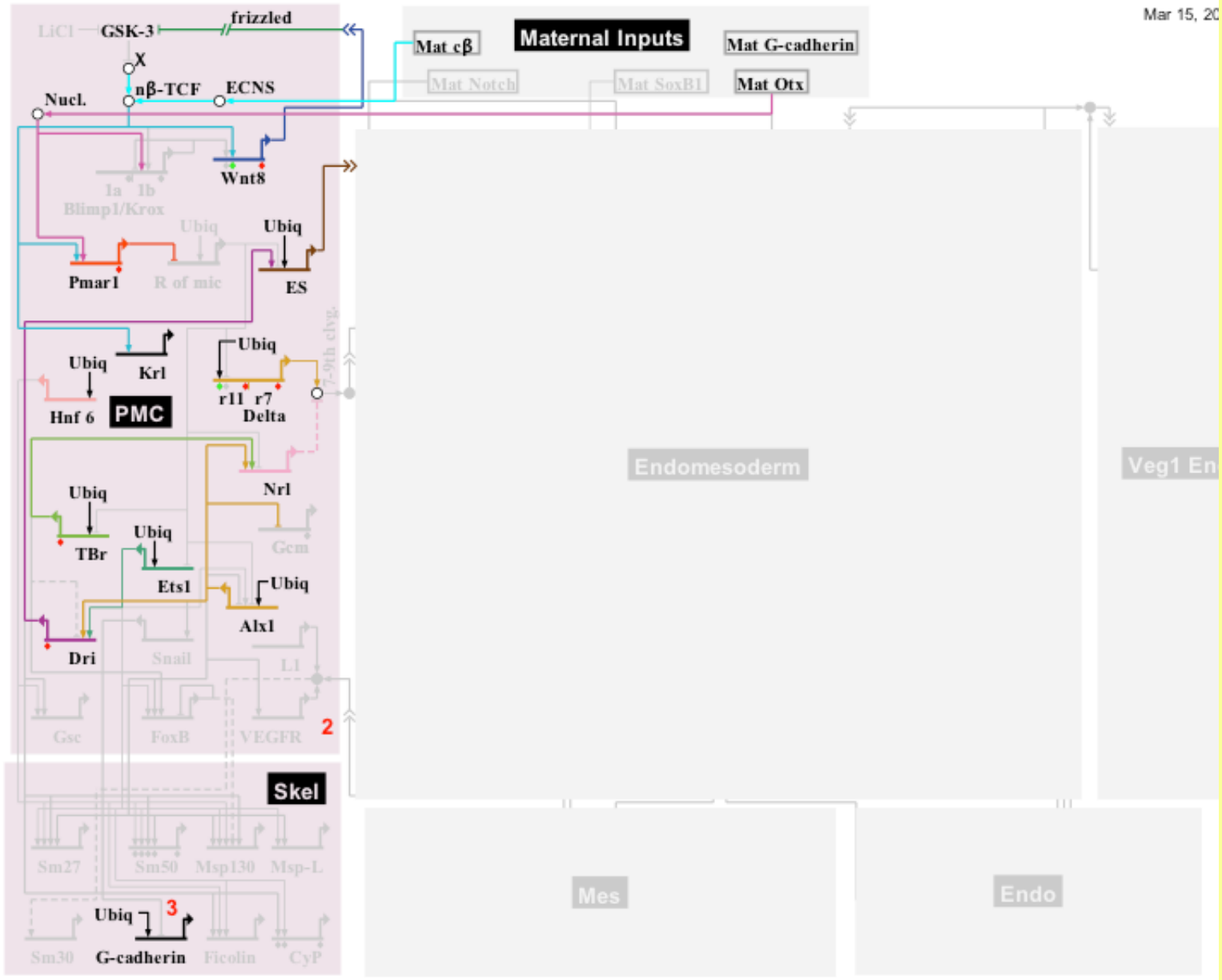
PMC Hourly: Hour 6

Mar 15, 2006



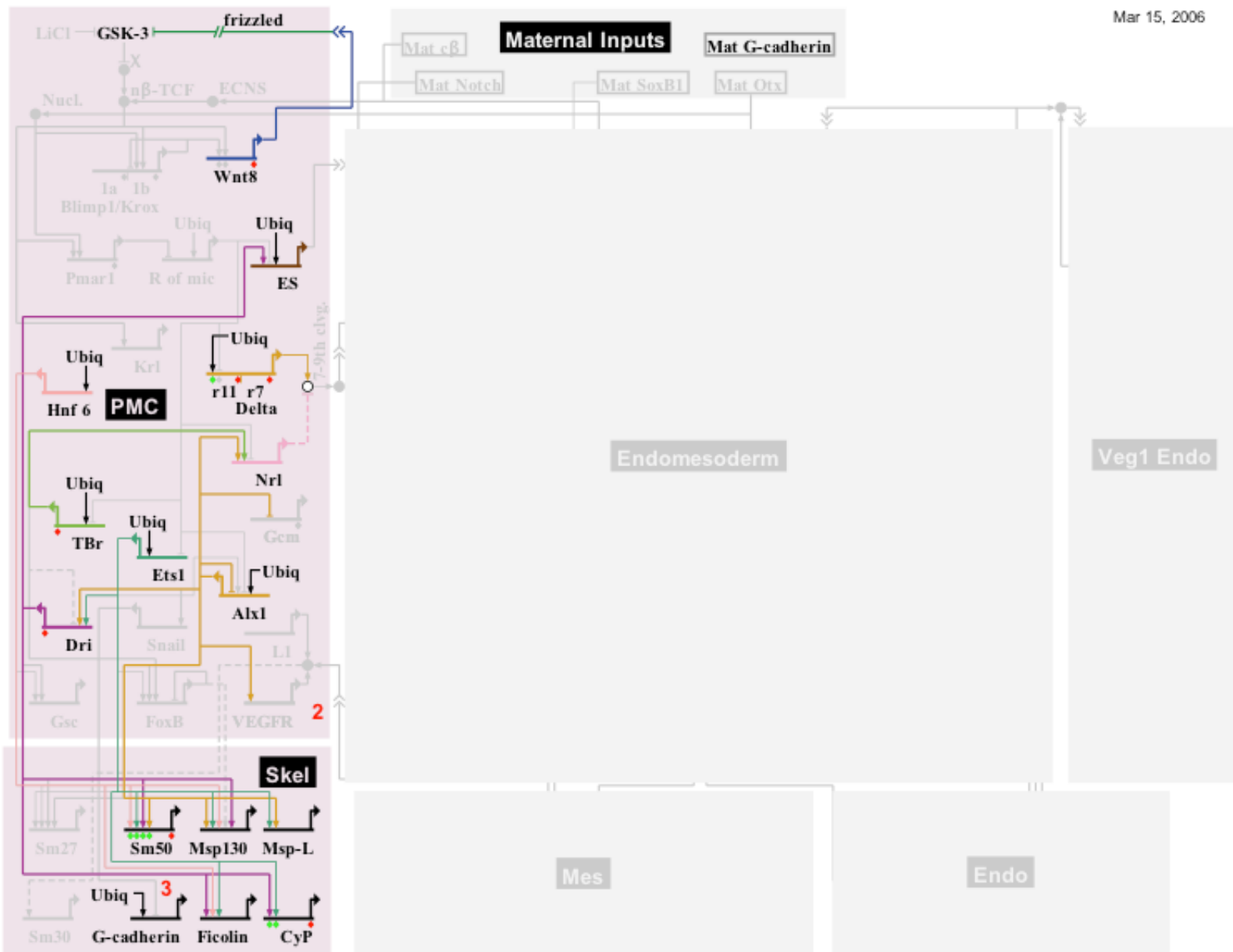
PMC Hourly: Hour 12

Mar 15, 20



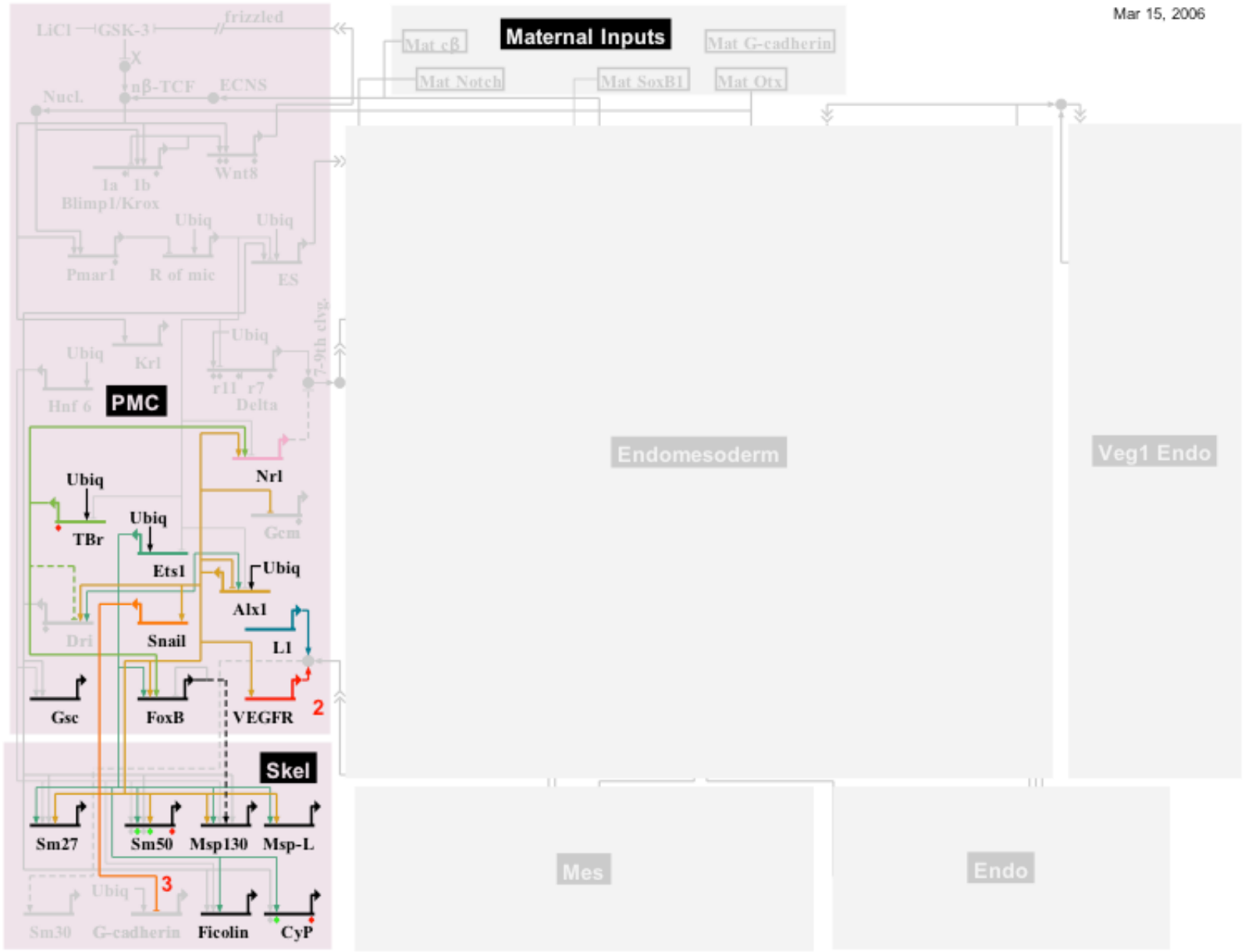
PMC Hourly: Hour 18

Mar 15, 2006



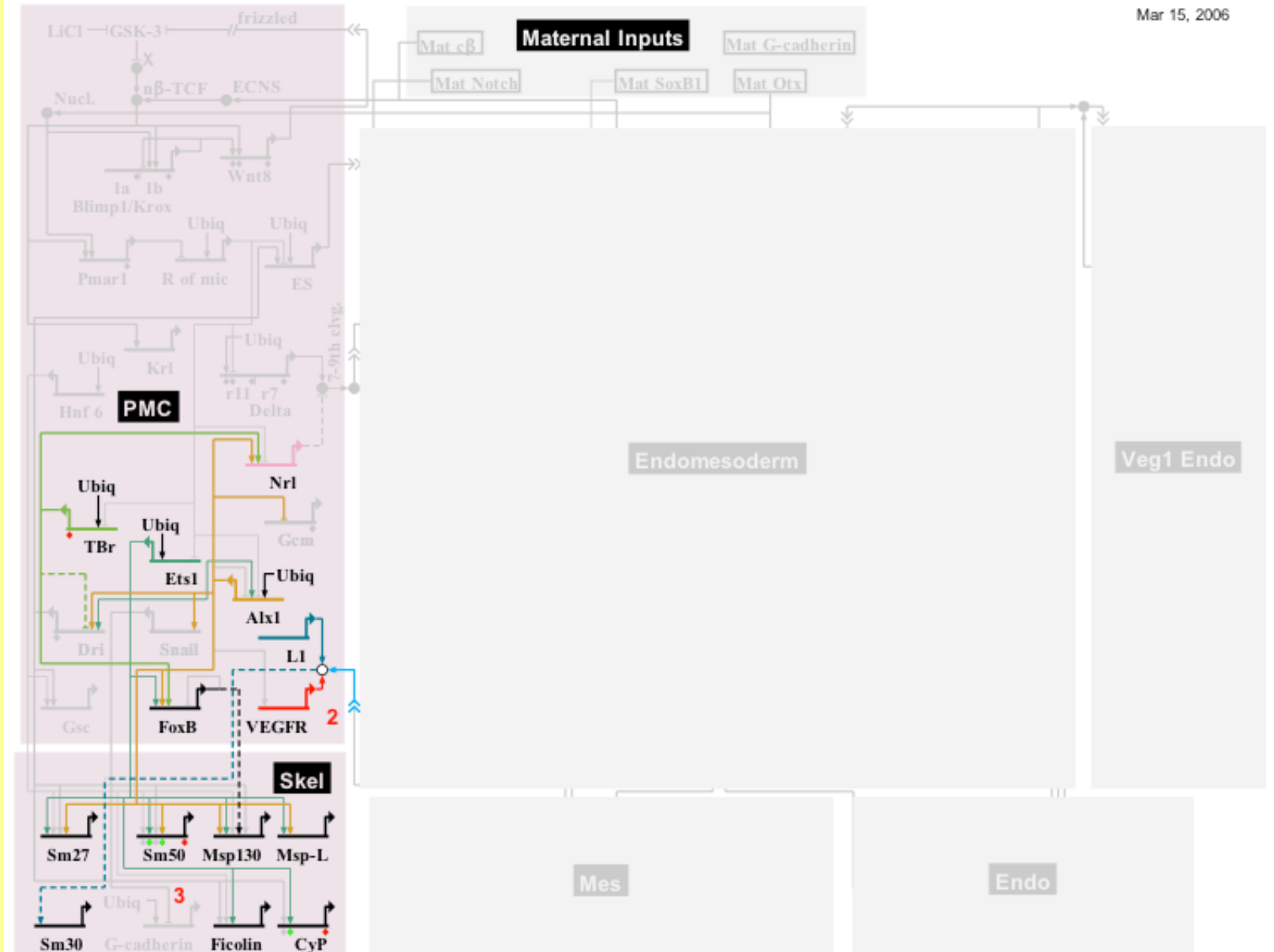
PMC Hourly: Hour 24

Mar 15, 2006

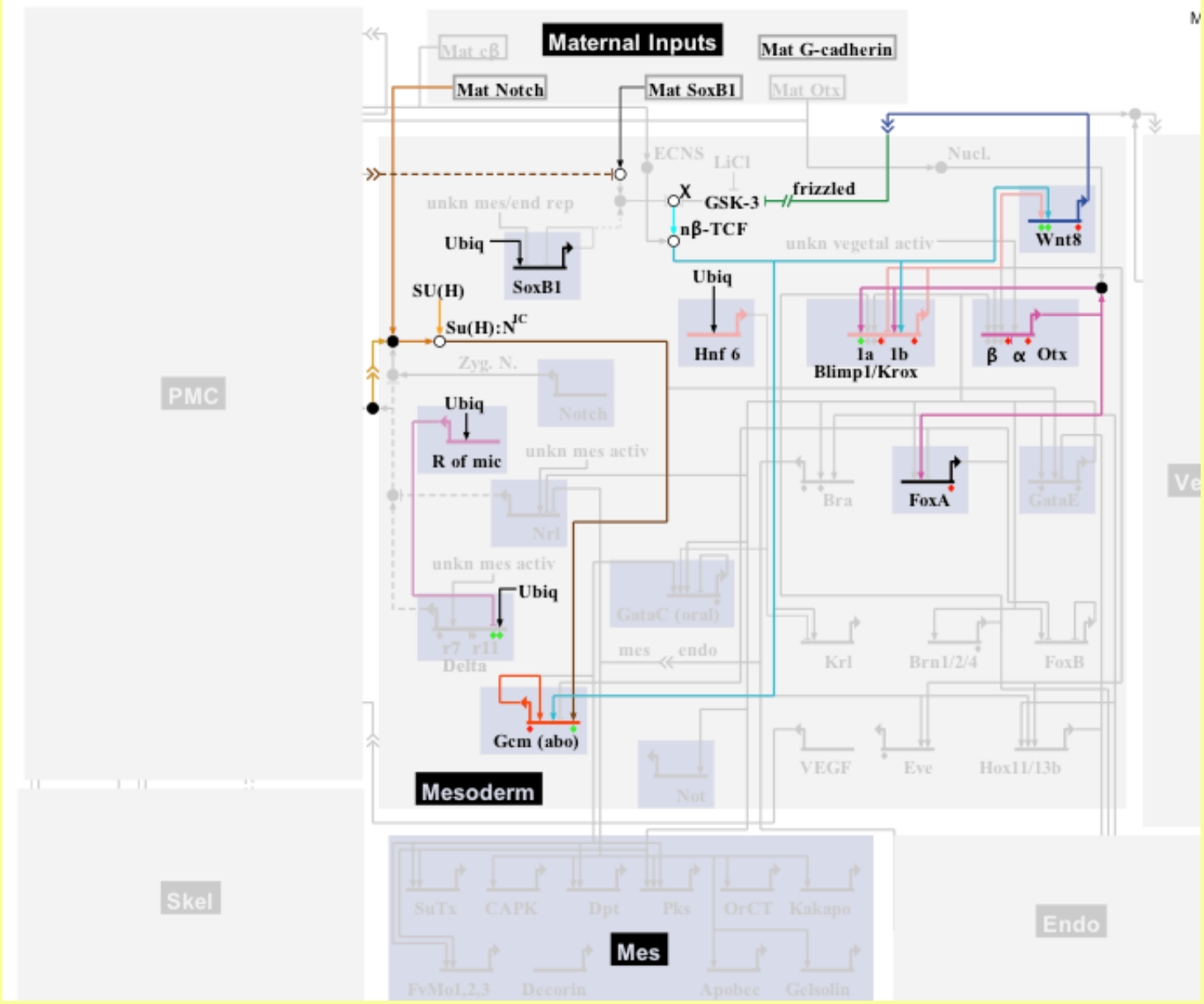


PMC Hourly: Hour 30

Mar 15, 2006

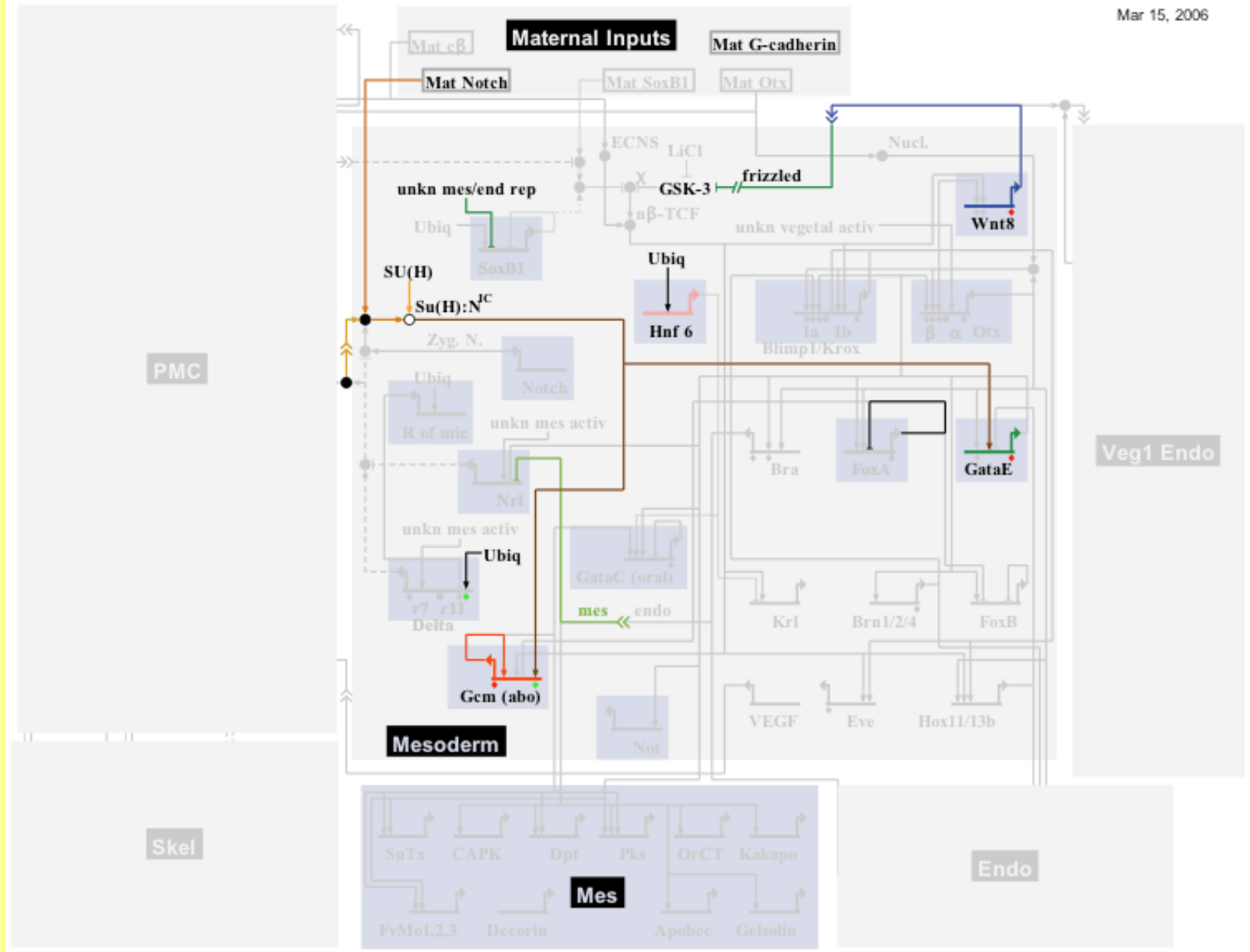


Mesoderm Hourly: Hour 12



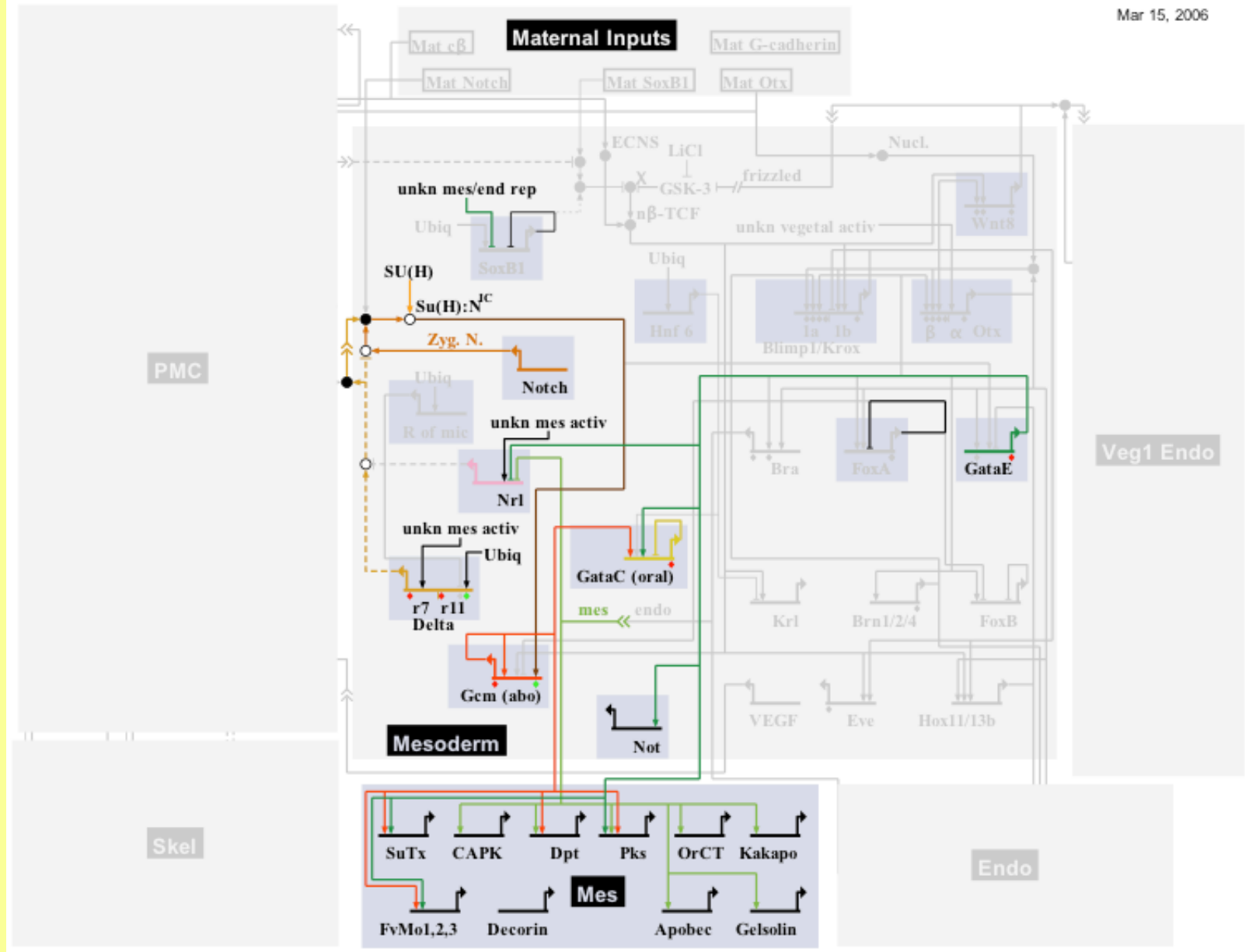
Mesoderm Hourly: Hour 18

Mar 15, 2006



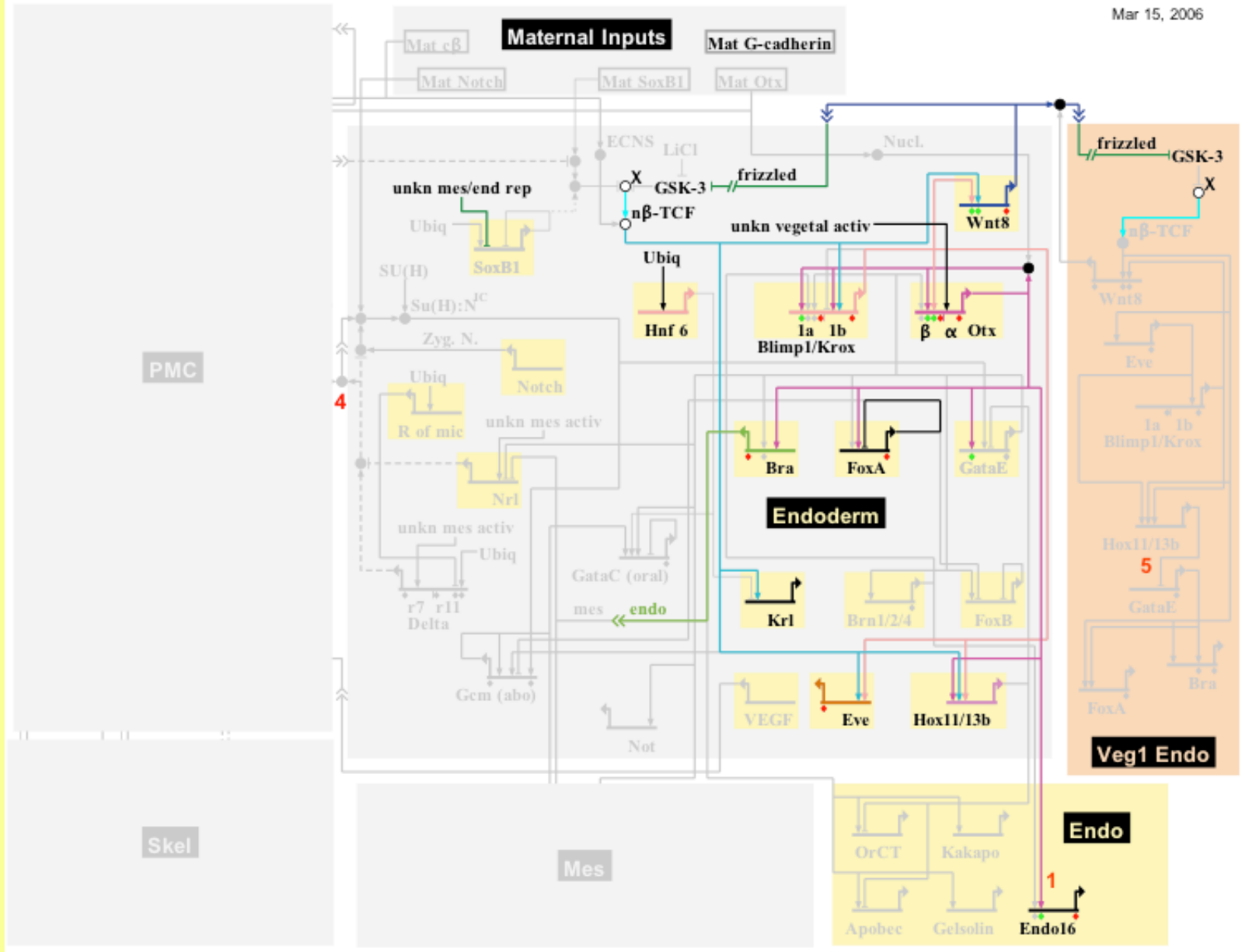
Mesoderm Hourly: Hour 24

Mar 15, 2006



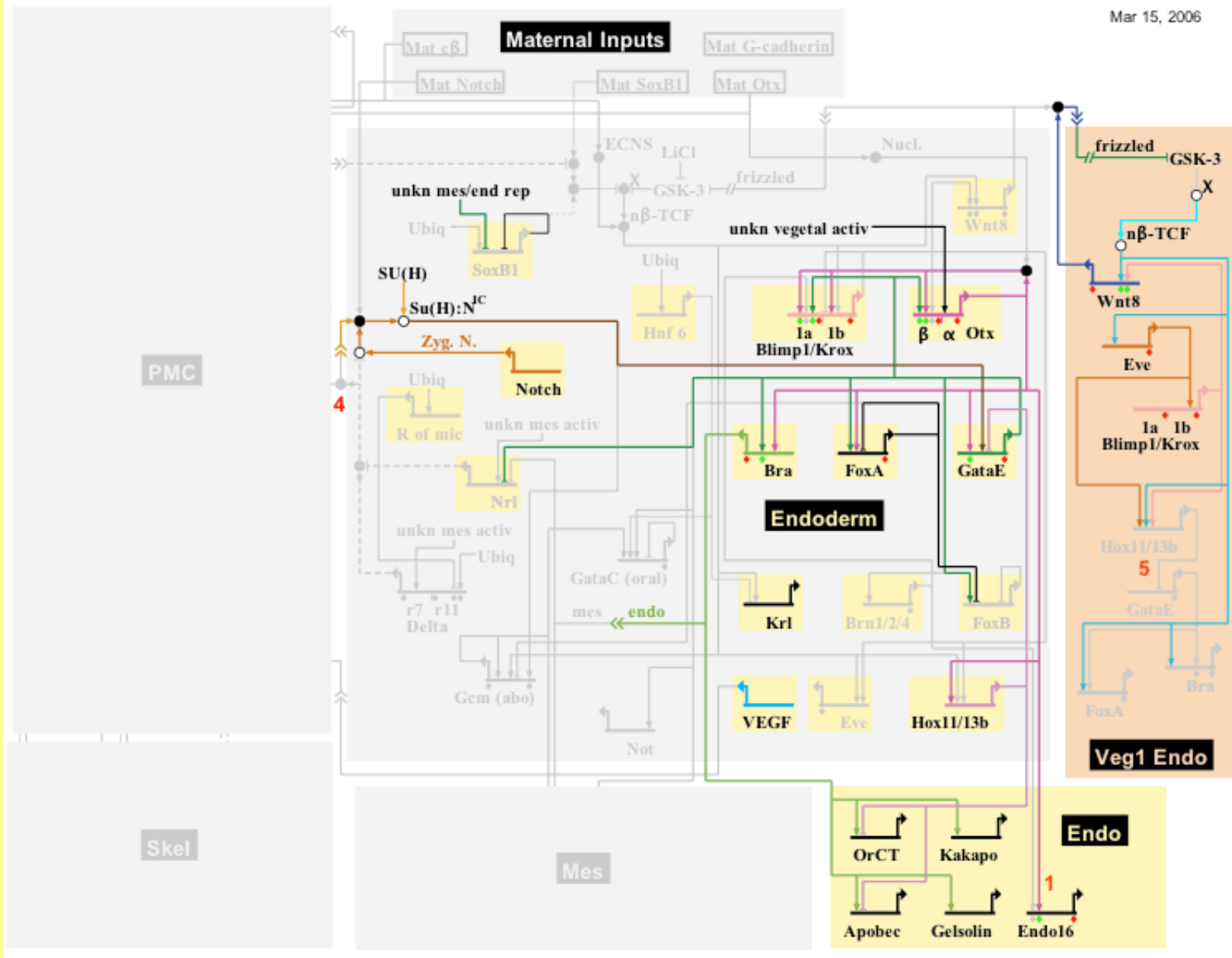
Endoderm with Veg1 Hourly: Hour 18

Mar 15, 2006



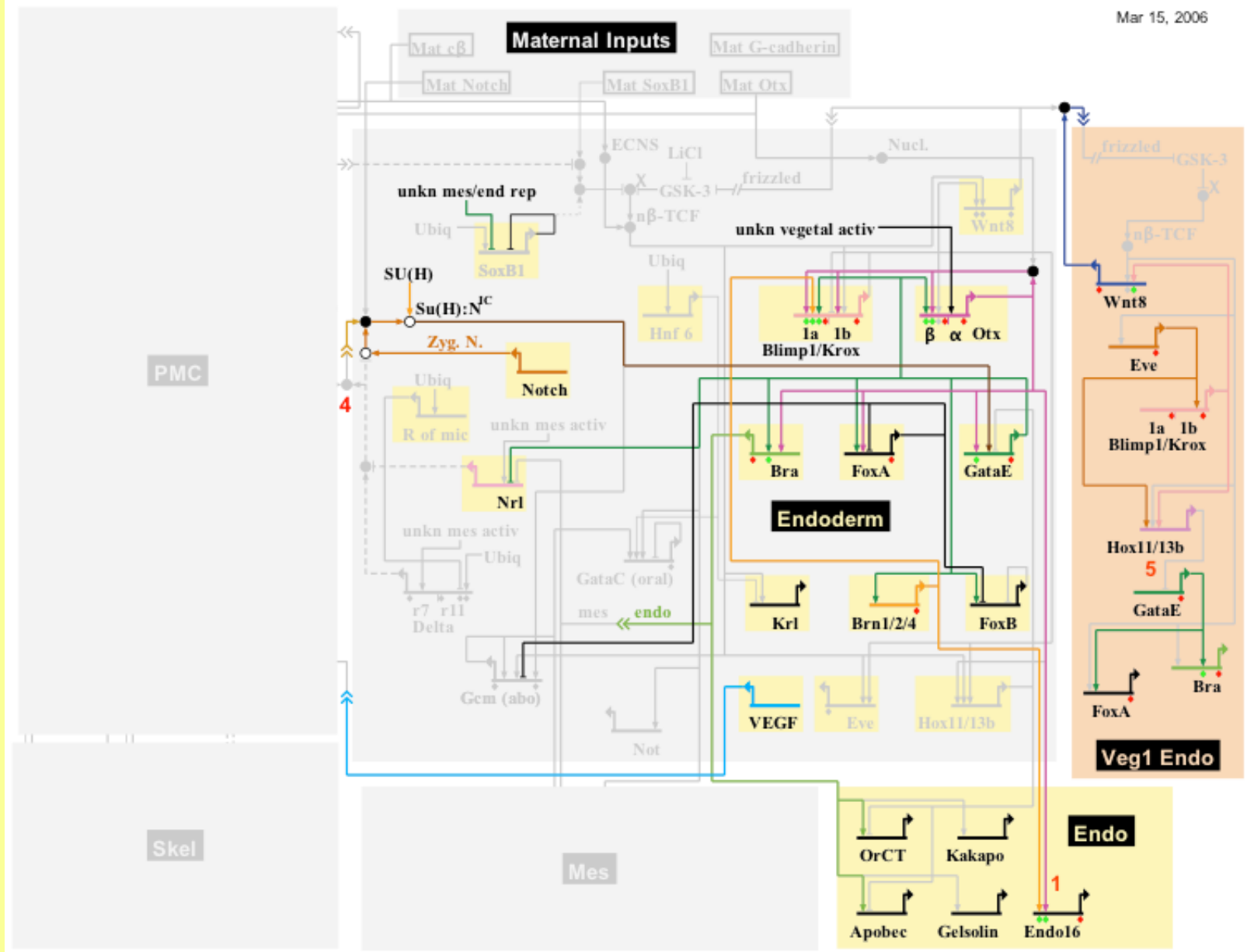
Endoderm with Veg1 Hourly: Hour 24

Mar 15, 2006



Endoderm with Veg1 Hourly: Hour 30

Mar 15, 2006



Based on this evidence, some conclude design

The New York Times Magazine

The Turning of an Atheist



By Mark Oppenheimer

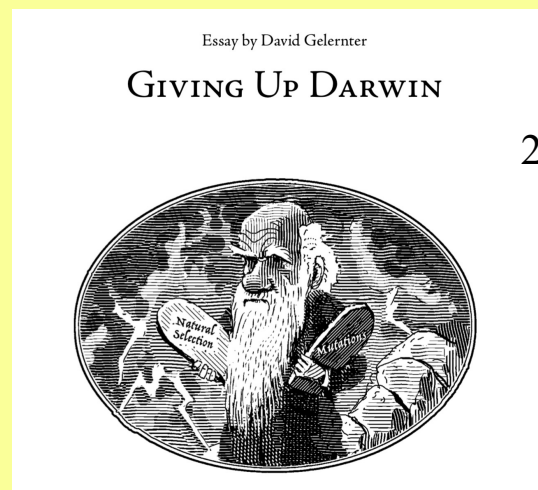
Nov. 4, 2007

Antony Flew

David Gelernter



Prof. of computer science
Yale University



Based on this evidence, some conclude design



Biochemist
Lehigh University

Michael Behe



Curator fossil insects
State Museum of Natural History
Stuttgart, Germany

Günter Bechley

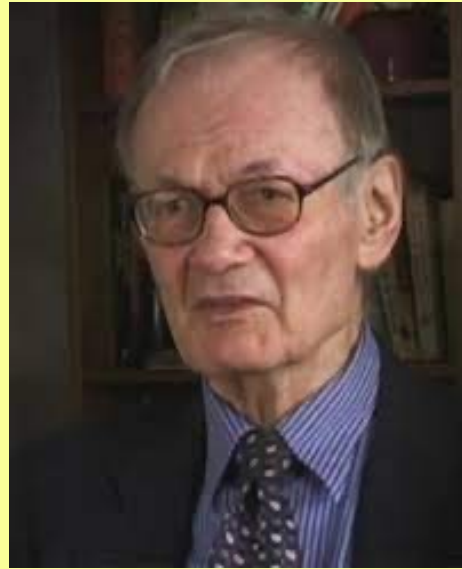
... but some do not



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,
Privileged Planet



Richard Lewontin

“...materialism is absolute, for we cannot allow a Divine Foot in the door.”

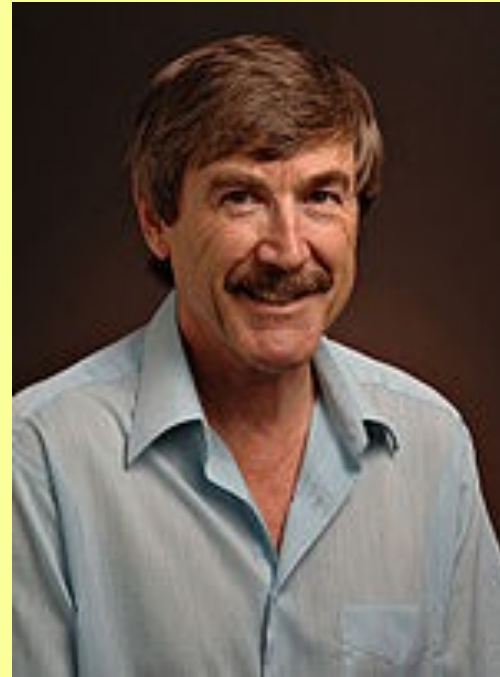
New York Review of Books
Jan 9, 1997.

... 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



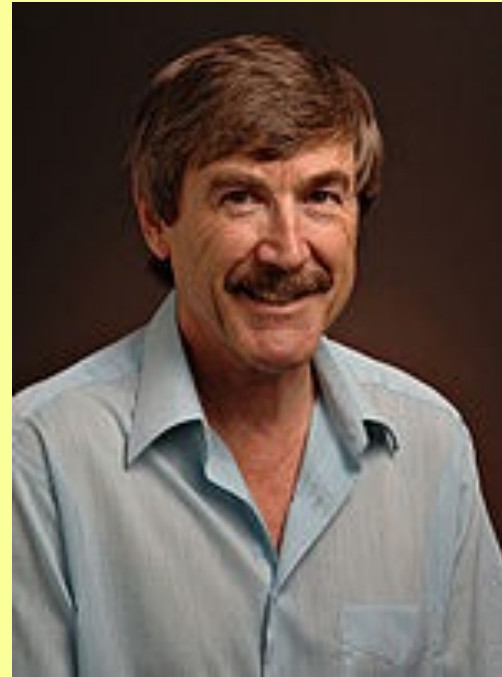
“... **the dreaded T word:** *teleology*. ... Teleology, or final causation, is **taboo** in orthodox science.”

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.

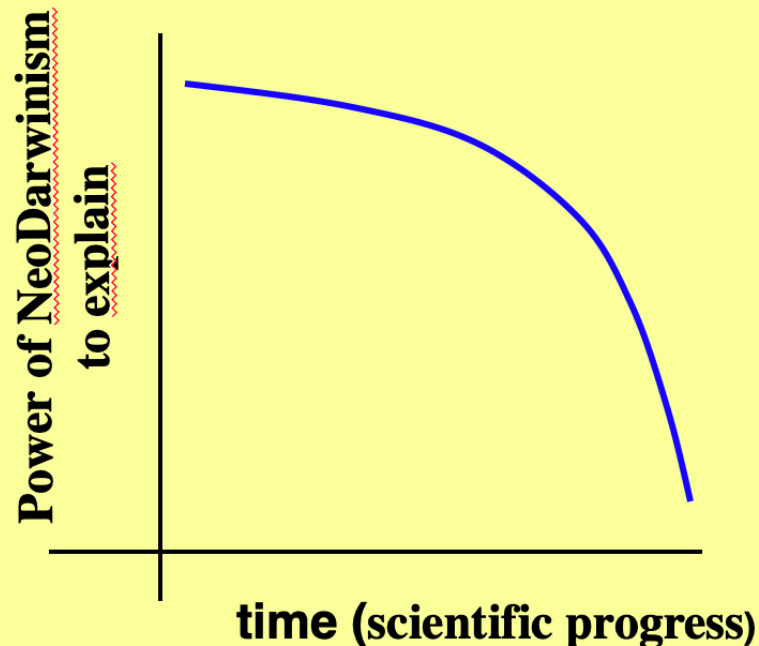
For some people no amount of data could ever be enough!

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.

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.

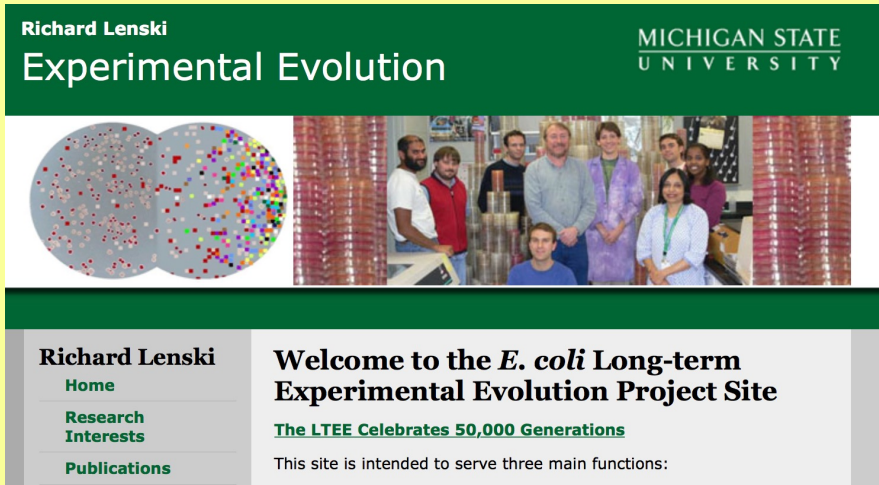
7e. Evidence for natural genetic engineering mechanisms for microevolution operating within a constrained design is growing.

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



Richard Lenski
Experimental Evolution

MICHIGAN STATE UNIVERSITY

Richard Lenski
Home
Research Interests
Publications

Welcome to the *E. coli* Long-term Experimental Evolution Project Site

[The LTEE Celebrates 50,000 Generations](#)

This site is intended to serve three main functions:



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

Currently over 65,000 generations

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



Each day transfers small sample to new culture w 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

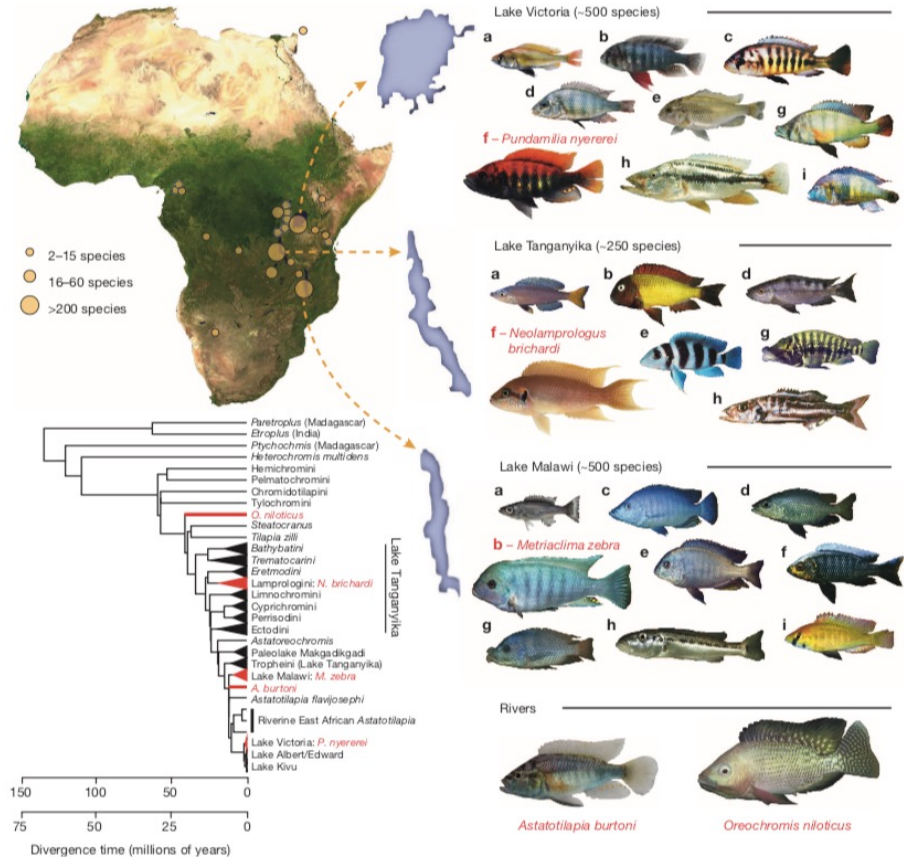


Figure 1 | The adaptive radiation of African cichlid fish. Top left, map of Africa showing lakes in which cichlid fish have radiated. Right, the five sequenced species: *Pundamilia nyererei* (endemic of Lake Victoria); *Neolamprologus brichardi* (endemic of Lake Tanganyika); *Metriaclima zebra* (endemic 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), 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

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

Darwin
Devolves,
pg 167

“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

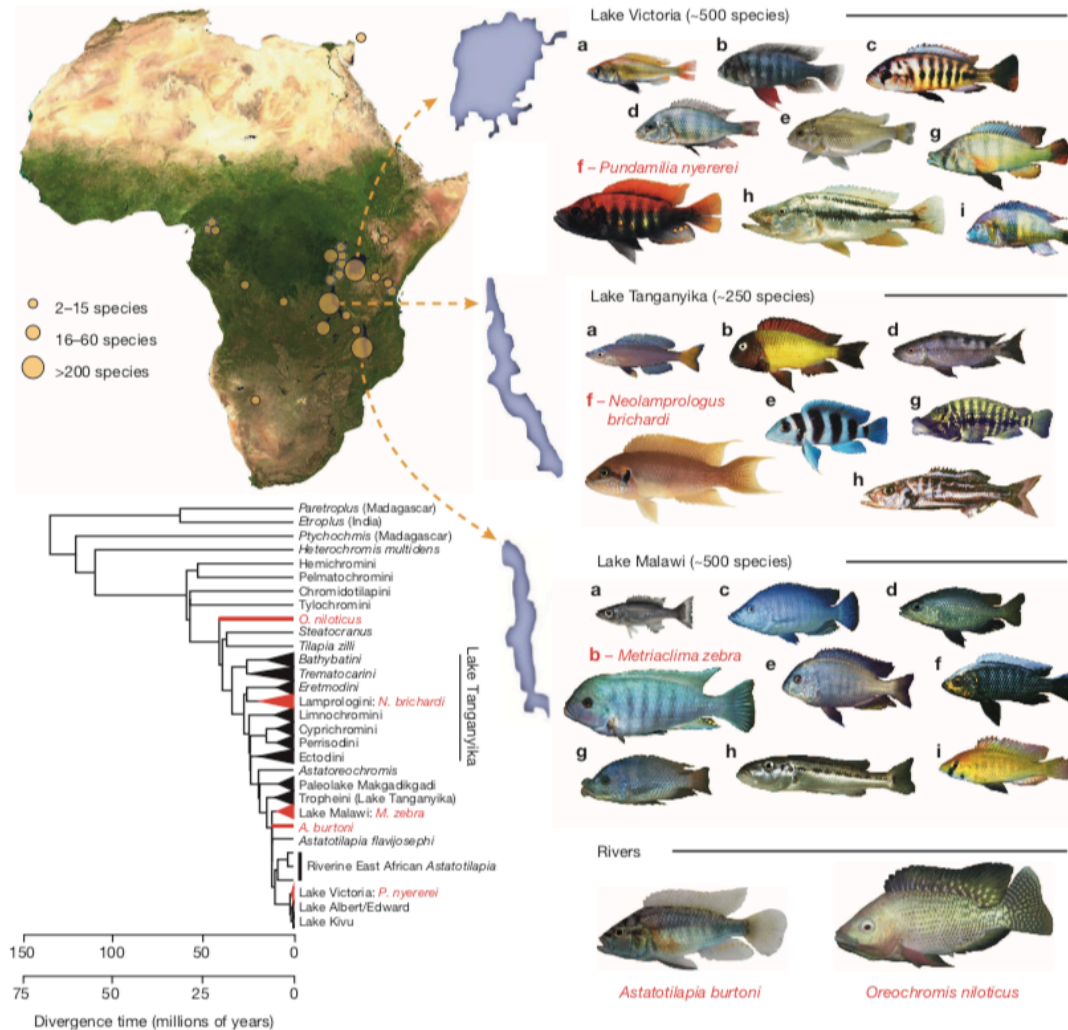
Dawkins is exactly right - dog breeding is a wonderful example of the power of selection acting on hidden random mutations. **But now that we can investigate the molecular level of life, we see that the great majority of dog mutations unwittingly selected by us humans are very likely to be damaging,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

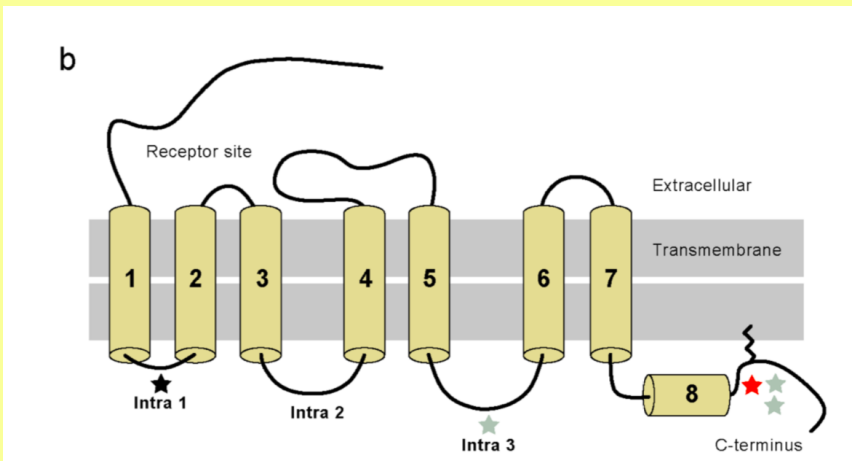
Sequenced the genomes of:

5 species from different (older) lineages

6 closely-related species from recent lineage

The genes underlying adaption in African Great Lake cichlids 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

a

1	HS	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIASLALGDL	LHIVIDIPIN	VYKLLAEDWP	
	DAR	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIASLALGDL	LHIVIDIPIN	VYKLLAEDWP	
	ORL	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIGSLALGDL	LHIIIGIPIN	VYKLLAEDWP	
	ON	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIGSLALGDL	LHIIIAIPIN	VYKLLAEDWP	
	NB	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIGSLALGDL	LHIIIAIPIN	VYKLLAEDWP	
	AB	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIGSLALGDL	LHIIIAIPIN	VYKLLAEDWP	
	PN	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIGSLALGDL	LHIIIAIPIN	VYKLLAEDWP	
	MZ	TFKYINTVVS	CLVFLVGIIG	NSTLLRIIYK	NKCMRNGPNI	LIGSLALGDL	LHIIIAIPIN	VYKLLAEDWP	
7	1	HS	FGAEMCKLVP	FIQKASVGIT	VLSLCAISID	RYRAVASWSR	IKGIGVPKWT	AVEIVLIWVV	SVVLAVPEAI
		DAR	FGVGLCKLVP	FIQKTSVGIT	IISLCAISID	RFRAVSSWNR	IKGIGVPKWT	AEIILIWVWL	SIILAVPEAI
		ORL	FGVNLCKLVP	FVQKASVGIT	VLSLCAISID	RYRAVASWNR	IKGIGVPKWM	AEIETALWVL	SIILAVPEAI
		ON	FGVTLCKLVP	FVQKSSVGIT	VLSLCAISID	RYRAVASWSR	IKGIGVPKWM	AEIETALWVL	SIILAVPEAI
		NB	FGVTLCKLVP	FVQKSSVGIT	VLSLCAISID	RYRAVASWSR	IKGIGVPKWM	AEIETALWVL	SIILAVPEAI
		AB	FGVTLCKLVP	FVQKSSVGIT	VLSLCAISID	RYRAVASWSR	IKGIGVPKWM	AEIETALWVL	SIILAVPEAI
		PN	FGVTLCKLVP	FVQKSSVGIT	VLSLCAISID	RYRAVASWSR	IKGIGVPKWM	AEIETALWVL	SIILAVPEAI
		MZ	FGVTLCKLVP	FVQKSSVGIT	VLSLCAISID	RYRAVASWSR	IKGIGVPKWM	AEIETALWVL	SIILAVPEAI
1	41	HS	GFDIITMDYK	GSYLRIICLLH	PVQKTAEMQF	YKTAQDWWLF	SFYFCLPLAI	TAFFYTLMTC	EMLRKKSGMO
		DAR	AFDMITMDYK	GEHLRICLLH	PKQRIKFMQF	YKKAQDWWLF	SFYFCMLPTC	TAIFYTLMTC	EMLRKKNGVQ
		ORL	AFDMITMYK	GEHLRICLLH	PKQKTEFMRF	YKSAKDWWLF	GAYFCLPLAC	TAIFYTLMTC	EMLRKKNGVQ
		ON	AFDMITMNYK	GEHLRICLLH	PVQKTEFMRF	YKSAKDWWLF	SAYFCLPLAC	TAIFYTLMTC	EMLRKKNGVQ
		NB	AFDMITMNYK	GEHLRICLLH	PVQKTEFMRF	YKSAKEDWWLF	SVYFCLPLAC	TAIFYTLMTC	EMLRKKNGVQ
		AB	AFDMITMNYK	GEHLRICLLH	PVQKTEFMRF	YKSAKEDWWLF	SVYFCLPLAC	TAIFYTLMTC	EMLRKKNGVQ
		PN	AFDMITMNYK	GEHLRICLLH	PVQKTEFMRF	YKSAKDWWLF	SVYFCLPLAC	TAIFYTLMTC	EMLRKKNGVQ
		MZ	AFDMITMNYK	GEHLRICLLH	PVQKTEFMRF	YKSAKDWWLF	SVYFCLPLAC	TAIFYTLMTC	EMLRKKNGVQ
2	11	HS	IALNDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	LYNQDNPNC	ELLSFLLVLD	YIGINMASLN
		DAR	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYDERDPNC	ELLSFLLVLD	YIGINMASLN
		ORL	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYNEEDPNC	ELLSFLLVLD	YIGINMASLN
		ON	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYDEKDPNC	ELLSFLLVLD	YIGINMASLN
		NB	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYDEKDPNC	ELLSFLLVLD	YIGINMASLN
		AB	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYDEKDPNC	ELLSFLLVLD	YIGINMASLN
		PN	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYDEKDPNC	ELLSFLLVLD	YIGINMASLN
		MZ	IALSDHLKQR	REVAKTVEFL	VLVFLCWLPL	LHLSRIKLT	IYDEKDPNC	ELLSFLLVLD	YIGINMASLN
2	81	HS	SCINPIALYL	VSKRFKNCFR	SCLCWCQSF	EELQSLLEEQ	SCLKFK		
		DAR	SCINPIALYM	VSKRFKCSFR	SCLCWCWLP	PEILAMDDKQ	SCIKLK		
		ORL	SCINPIALYM	VSKRFKTCFR	SCLCWCWLP	PEML-MDEKQ	SCMKLK		
		ON	SCINPIALYM	VSKRFKNCFR	SCLCWCWLP	AEML-MDEKQ	SCMKLK		
		NB	SCINPIALYM	VSKRFKNCFR	SCLCWCVT	TEML-MDEKQ	SCMKLK		
		AB	SCINPIALYM	VSKRFKNCFR	SCLCWCVT	TEML-MDEKQ	SCIKLK		
		PN	SCINPIALYM	VSKRFKNCFR	SCLCWCVT	TEML-MDEKQ	SCMKLK		
		MZ	SCINPIALYM	VSKRFKNCFR	SCLCWCVT	TEML-MDEKQ	SCMKLK		

★ Putative site required for SRF activation

★ Putative palmitoylation site

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

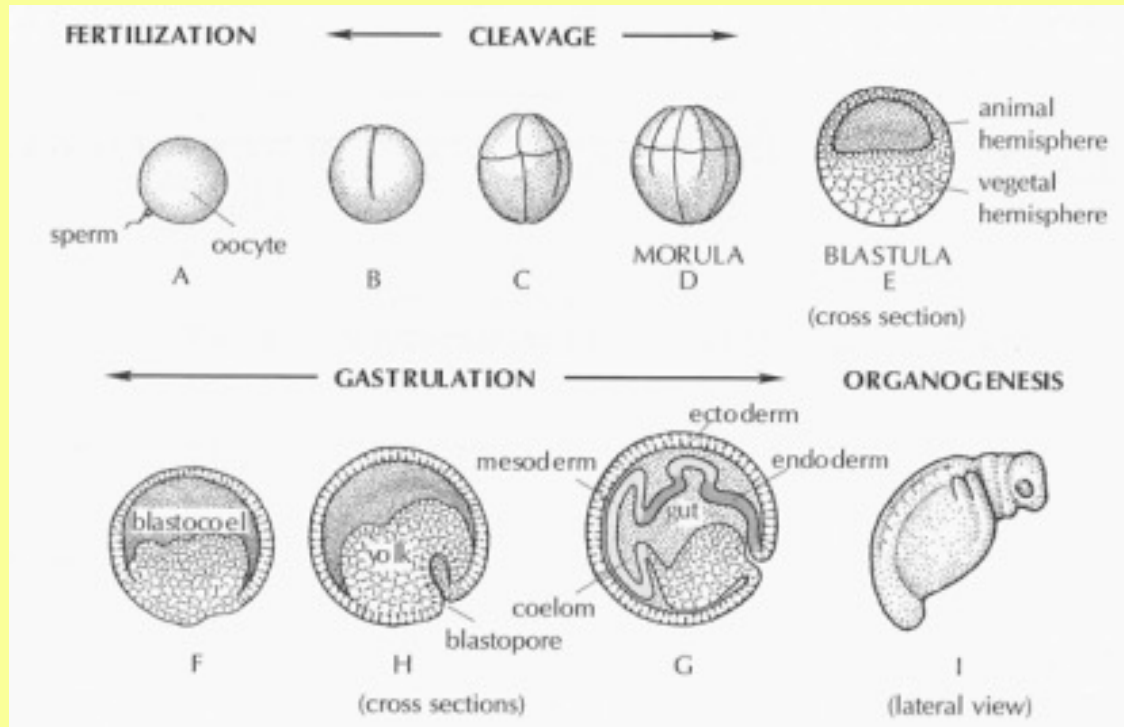
“Minor random variations around a designed blueprint are possible and can be helpful, but are severely limited in scope. For **new basic designs such as those at the biological level of family and above, additional information is necessary, information that is beyond the ability of mindless processes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

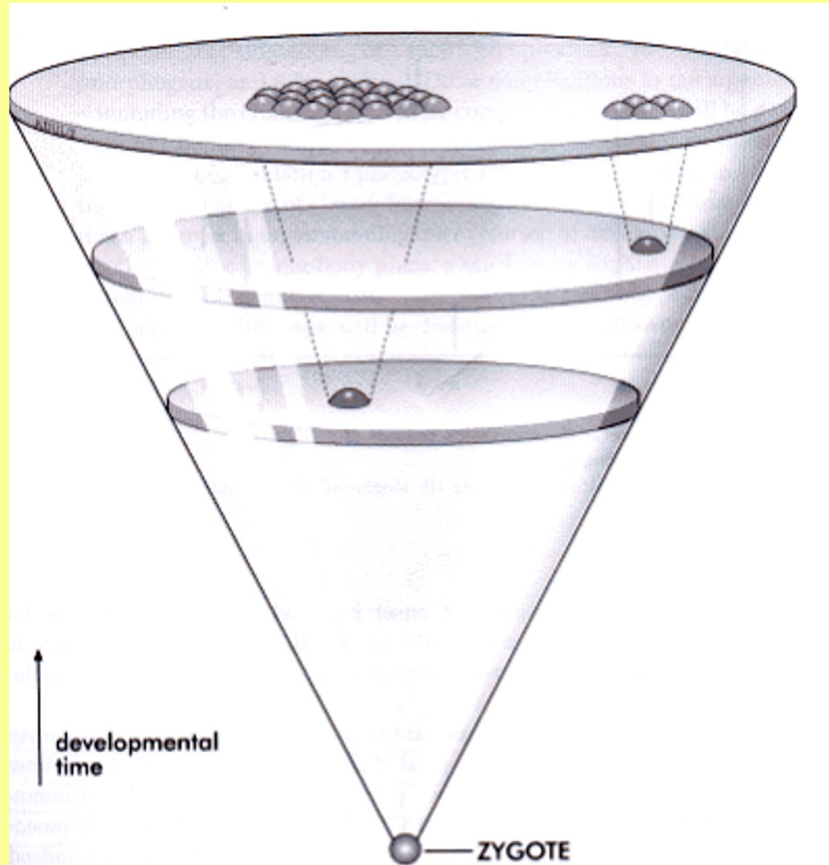


Figure 1-7 The 'inverted cone' model

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

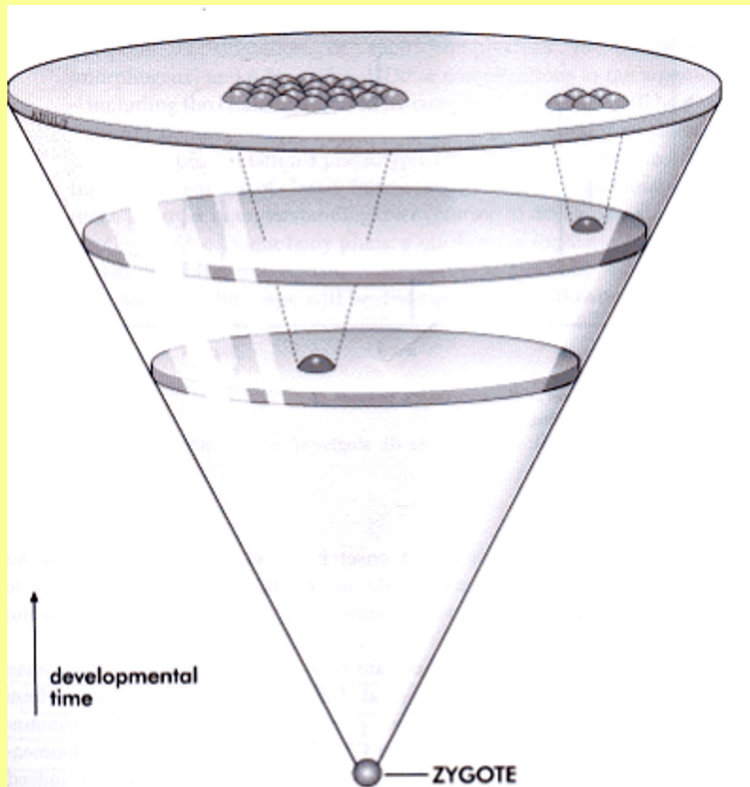


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A hypothetical organism develops from zygote to a disc-shaped arrangement of cells which grows in size through cell proliferation. The size of a morphological change in the adult is determined by how early in development the mutant gene controlling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

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

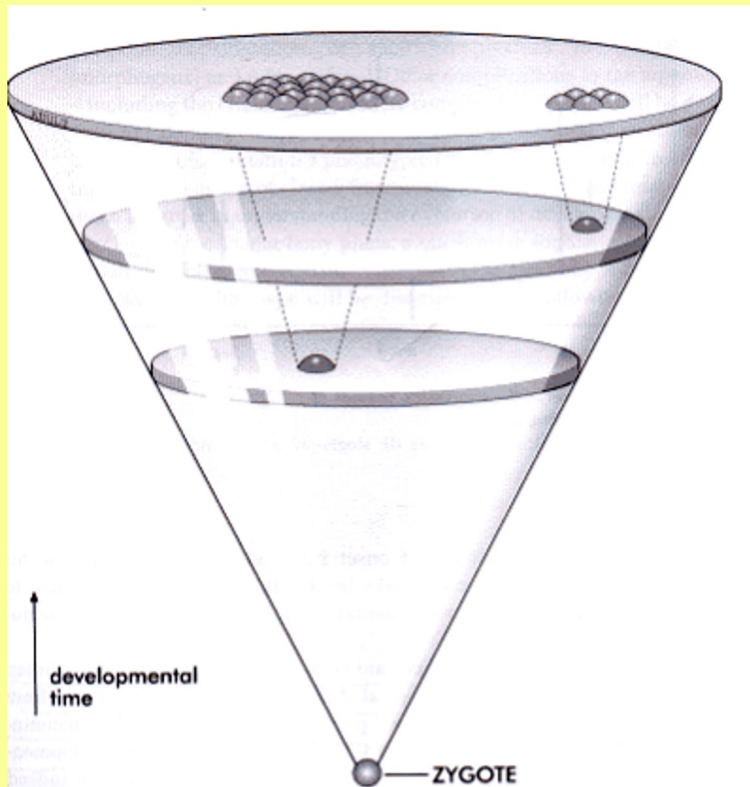


Figure 1-7 The 'inverted cone' model

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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.

Embryos don't evolve

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

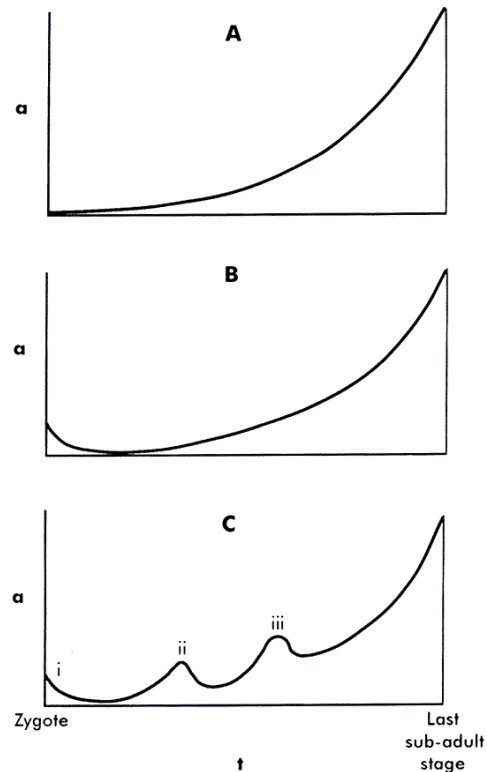


Figure 8-6 Possible relationships between a gene's time of onset of activity (t) and the probability of a mutation in it being selectively advantageous (α)

(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.

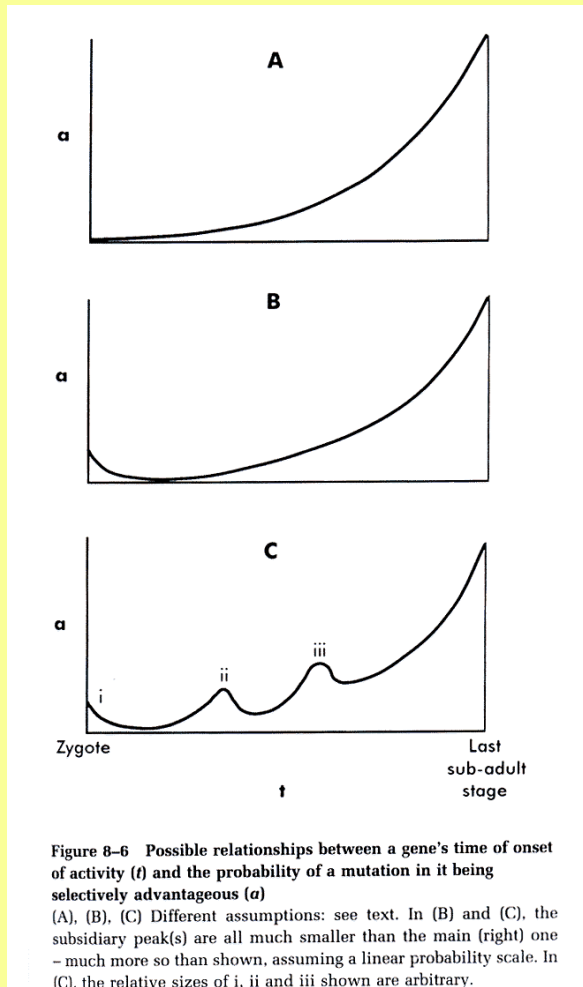
In general, the earlier a gene is expressed, the greater influence it can have on subsequent events during development and the **more likely that its disruption will result in malformation and death.** ...

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.

Embryos don't evolve

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



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

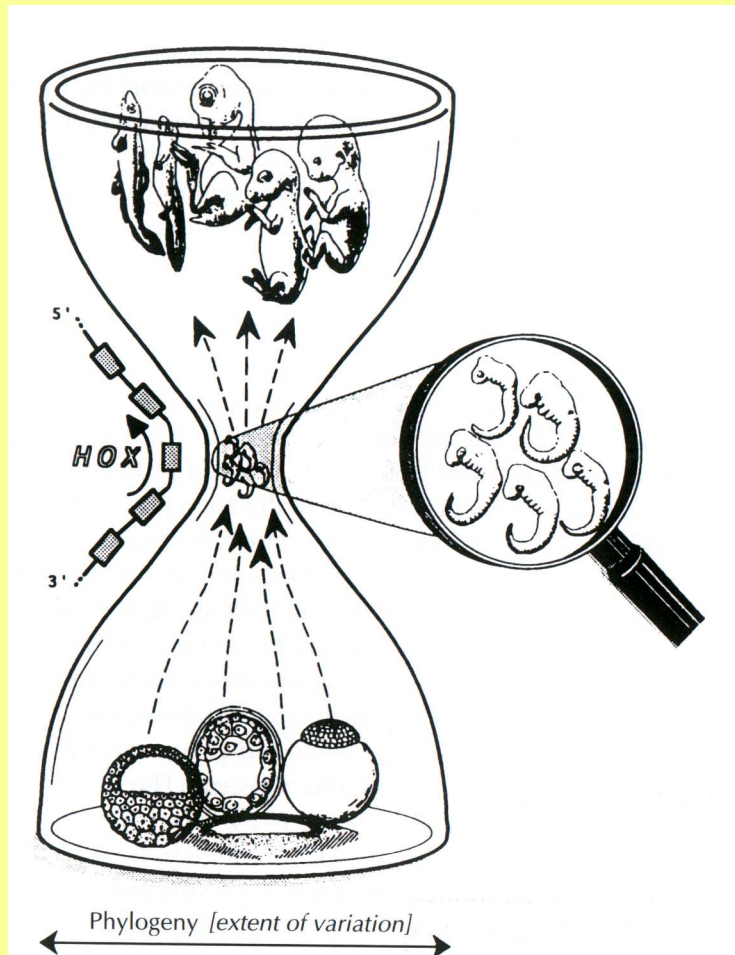


Eric Davidson, CalTech

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 pre-molecular 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.**

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.





Regular Article

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

H.ALLEN ORR¹

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

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

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 (yes)

make a new protein complex (protein-protein binding)

make a new protein

make a new regulatory circuit

make a new machine

...

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**. ...

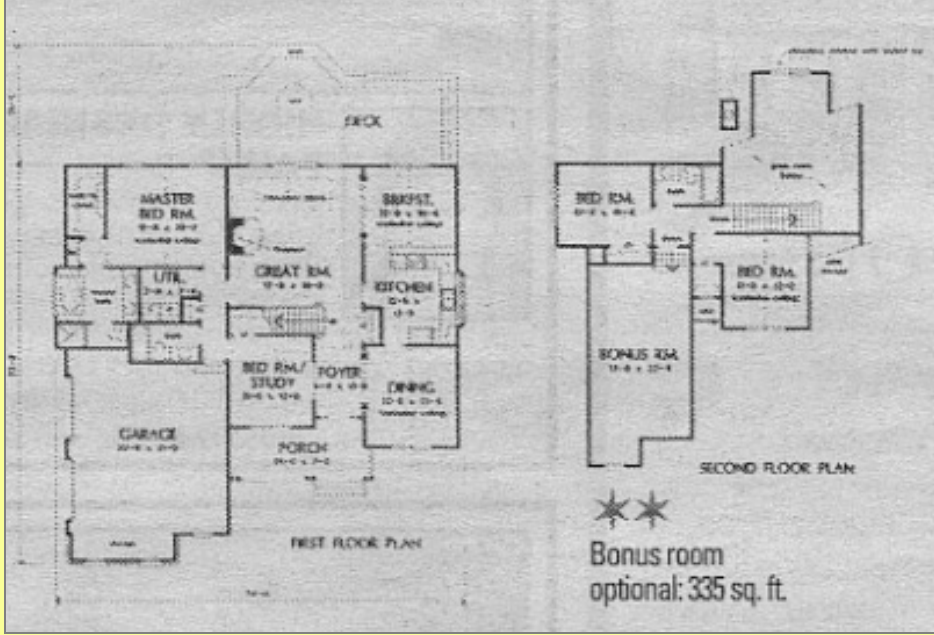
Epigenetic processes ... replace gene sequence variation and gene expression as the primary causal agents in morphological origination.

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

If we compare building
a body to building a
house...



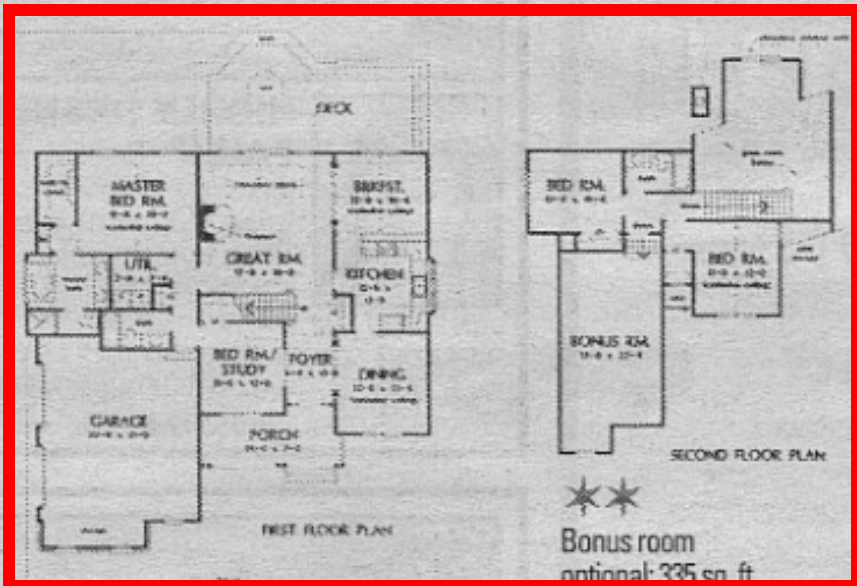
2123 Sq.Ft. - 4 BR, 3 BATH



What does it take to build a house?



2123 Sq.Ft. - 4 BR, 3 BATH



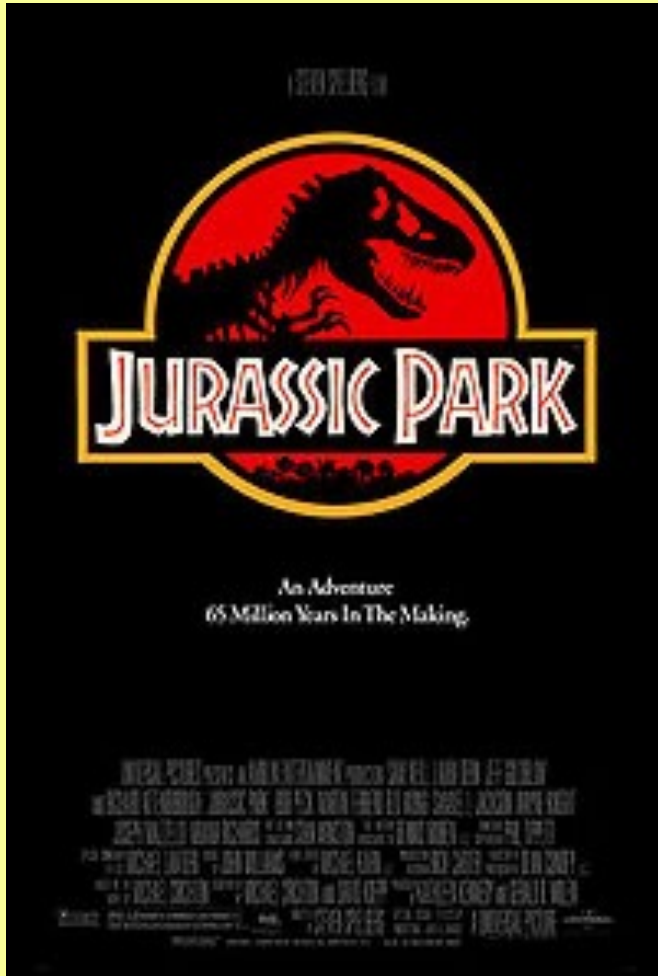
1. Building materials
2. Assembly instructions
3. Floor plan

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

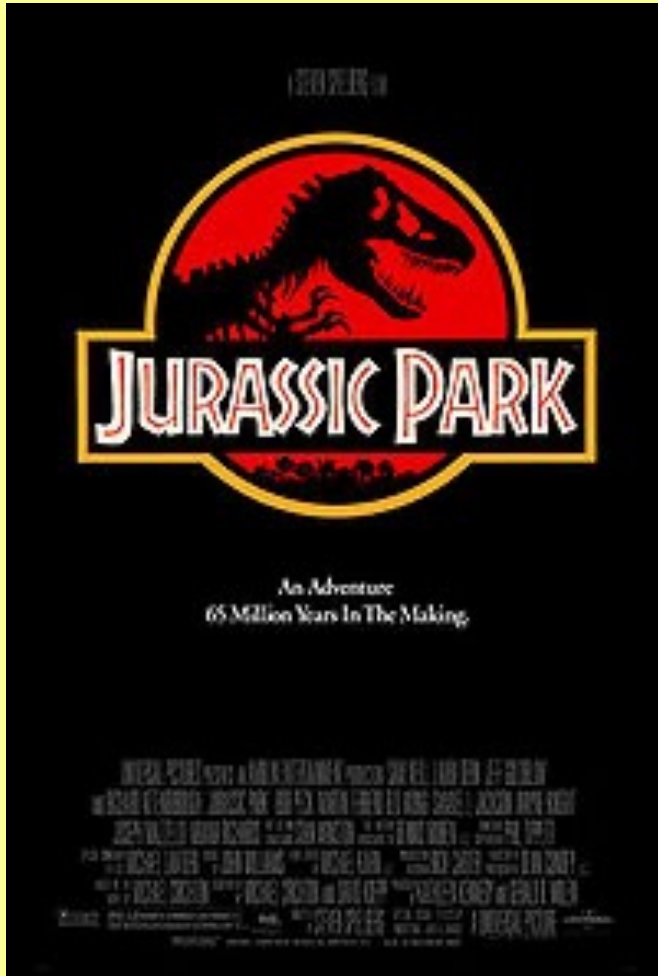
BioEssays (1990)



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

© 1993 Universal Studios



In reality the eggs would die,
nothing would hatch

Source: Wikipedia

© 1993 Universal Studios

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>



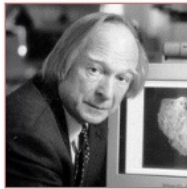
James A. Shapiro

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"

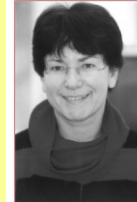


Eugene Koonin

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).

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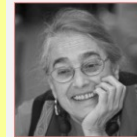
Eva Jablonka

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"

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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)"

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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"

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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

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New trends in evolutionary biology: biological, philosophical and social science perspectives

[← What's on](#)

Scientific meeting

Starts: November 07 2016 09:00

Ends: November 09 2016 17:00

Location
The Royal Society, London, 6-9 Carlton House Terrace, London, SW1Y 5AG

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

2022: Israel Conference: Potential and Limitations of Evolutionary processes

POTENTIAL & LIMITATIONS
OF EVOLUTIONARY PROCESSES

8-12 May, 2022 ISRAEL

[Home](#) [Conference Information](#) [Application](#) [Program](#) [Poster Instructions](#) [Registration and Tours](#) [Contact Us](#)

Potential & Limitations of Evolutionary Processes Conference

8-12 May 2022 | Israel

The main goal of this unique interdisciplinary, international conference is to bring together scientists and scholars who hold a range of views on the potential and possible limitations of chemical and biological processes in evolution, and to explore and discuss new experimental strategies to enhance our understanding of such mechanisms and pathways.

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

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

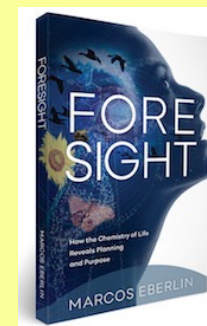
“Scientist of the
Year” in 2013,
R&D Magazine

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

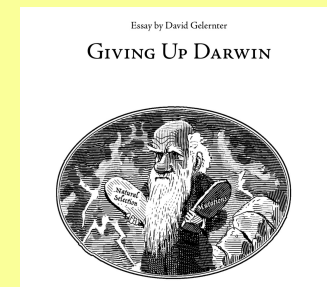
140 scientific
publications



David Gelernter



Prof. of computer
science at Yale
University



John Lennox



Professor Emeritus of
Mathematics

University of Oxford

Günter Bechly



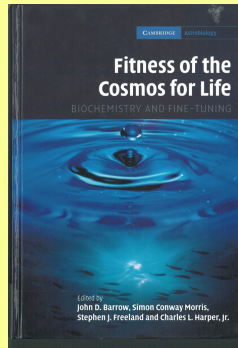
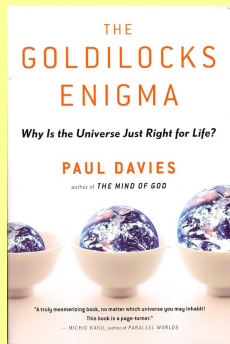
Paleoentomologist,
former curator of the
Museum of Natural History,
Stuttgart Germany

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

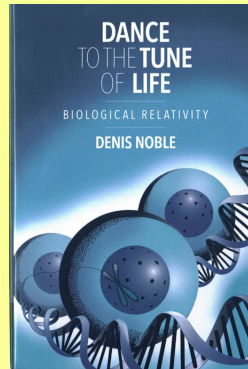
Physical Sciences

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

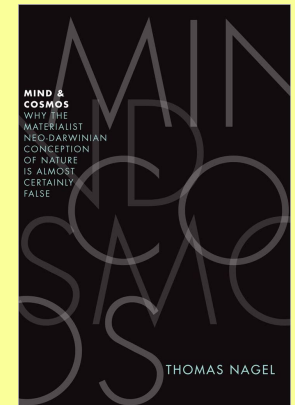


Cognitive Sciences

mind/brain
consciousness
personhood
abstract thought
reasoning
free will
etc



Thomas Nagel
NYU



Resources (Discovery Institute):

<https://www.discovery.org/video-series/long-story-short/>

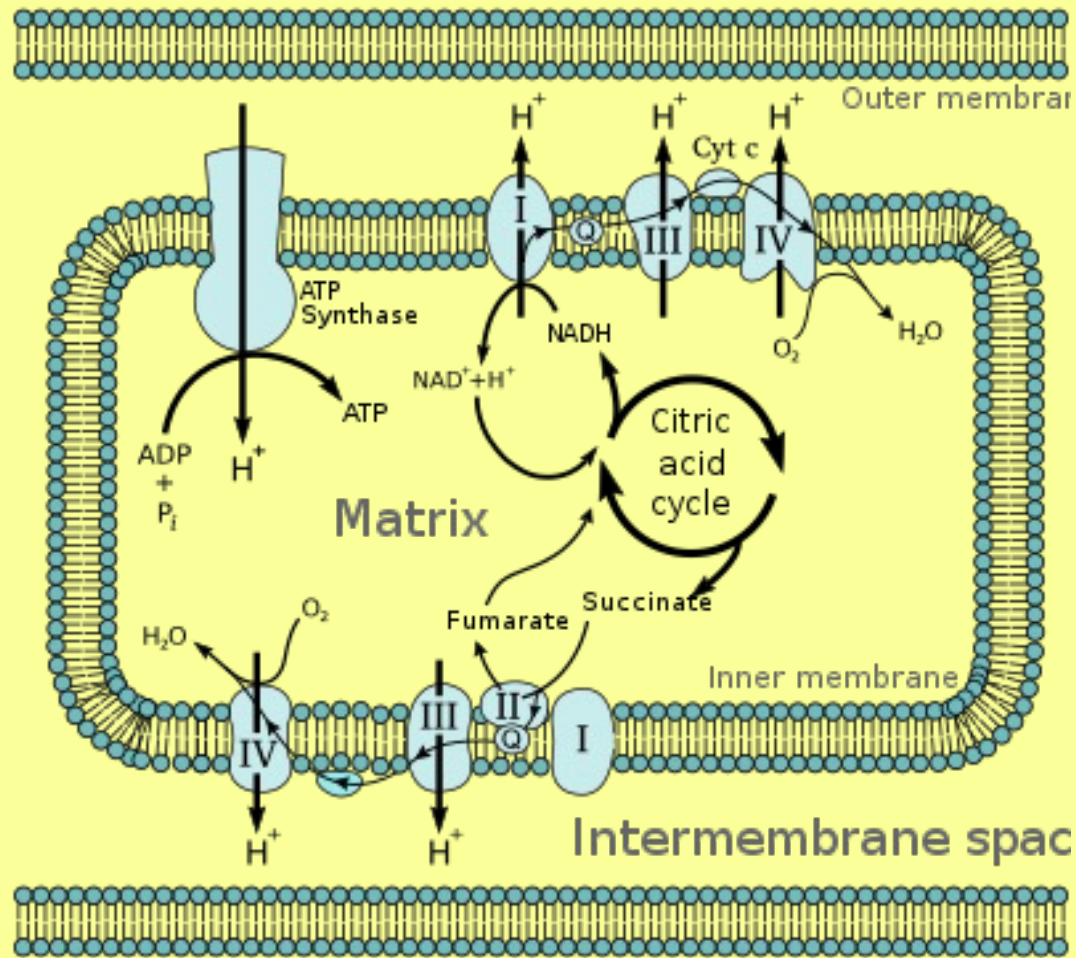
<https://scienceuprising.com/>

<https://michaelbehe.com/videos/secrets-of-the-cell/>

<https://www.youtube.com/user/DiscoveryScienceNews>

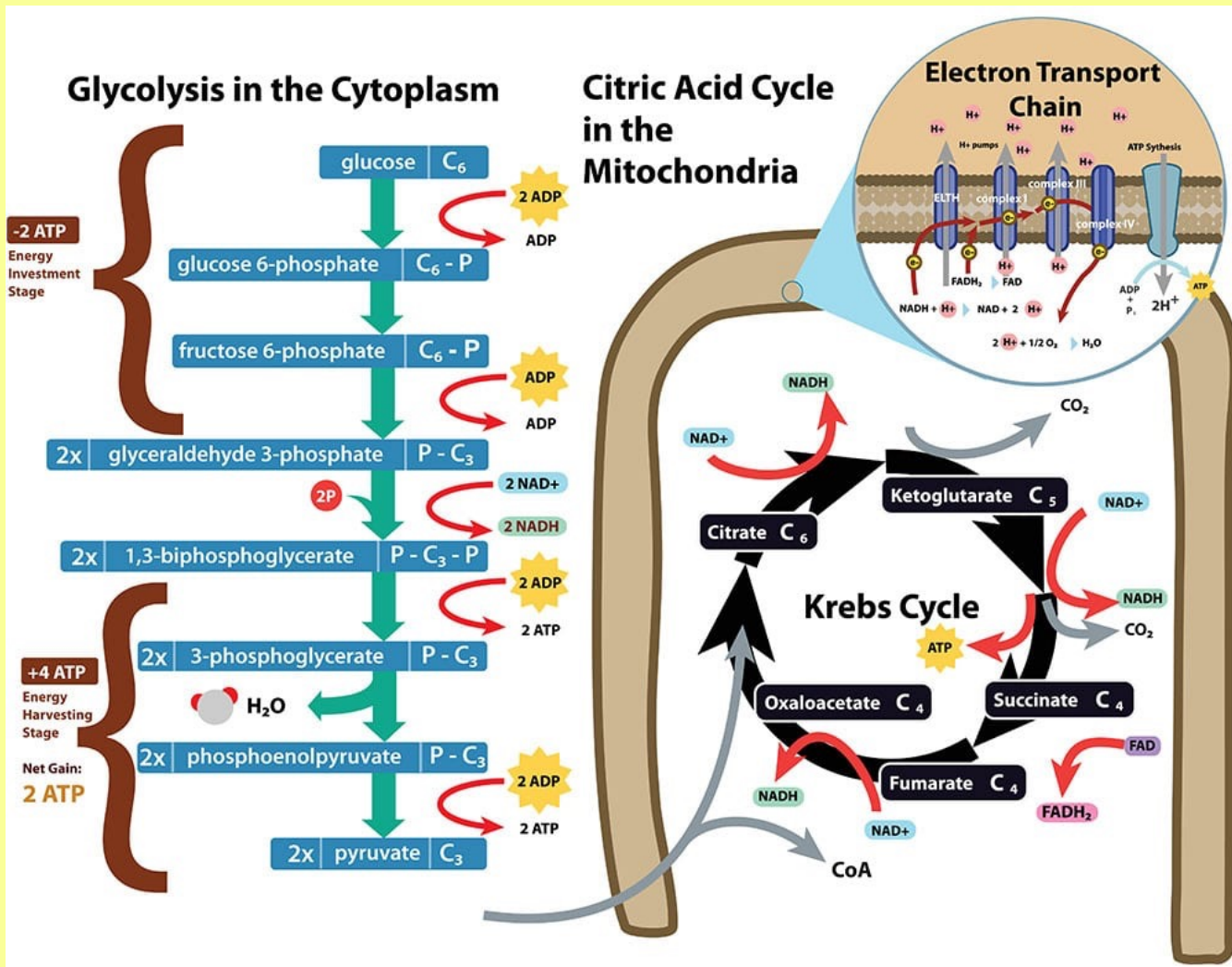
<https://intelligentdesign.org/>

Mitochondria



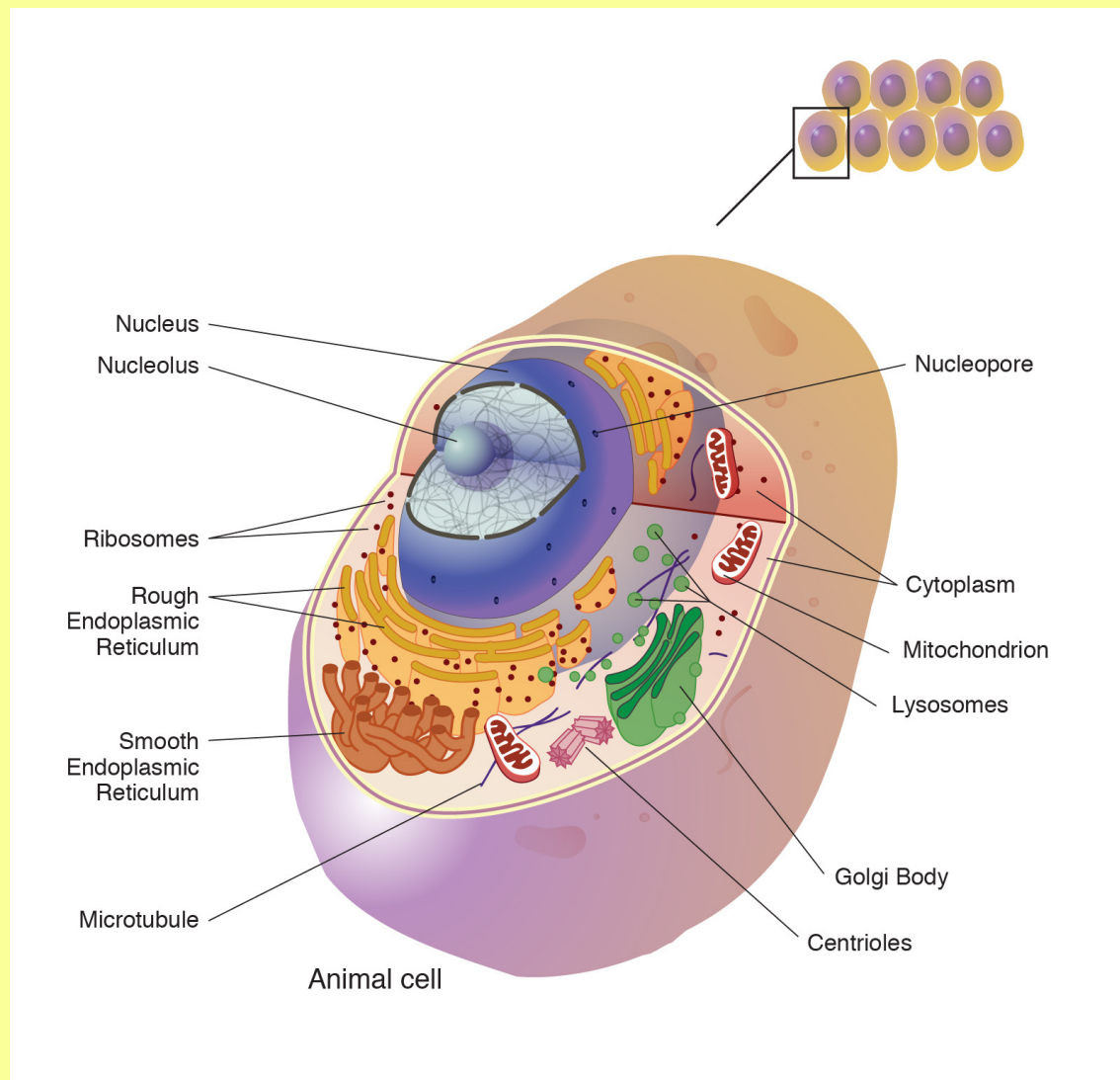
ATP synthase must fit into a larger system

the entire system must be coherent



ATP synthase must fit into a larger system

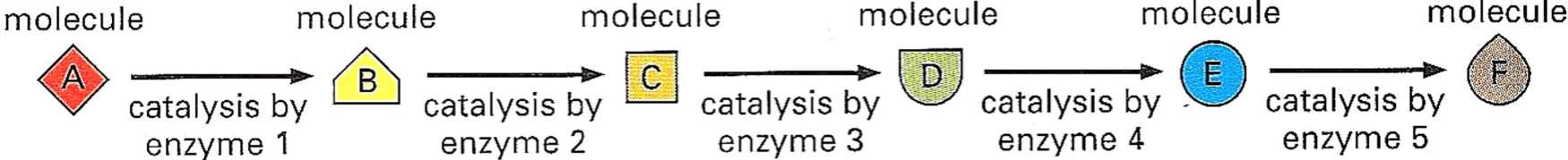
the entire system must be coherent



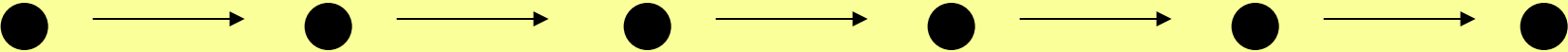
ATP synthase must fit into a larger system

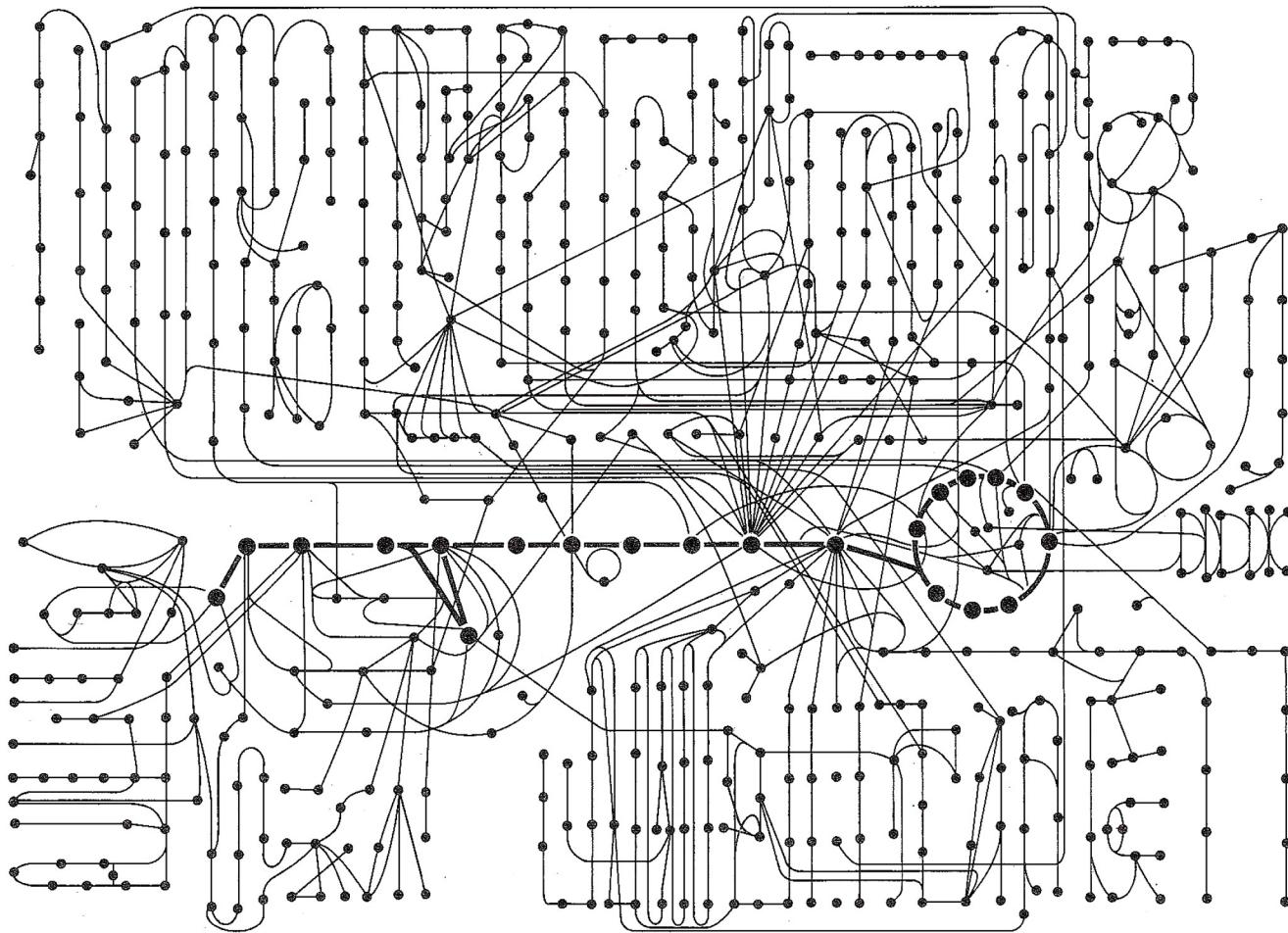
the entire system must be coherent

enzyme pathways



abbreviated as





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

from:
Essential Cell
Biology