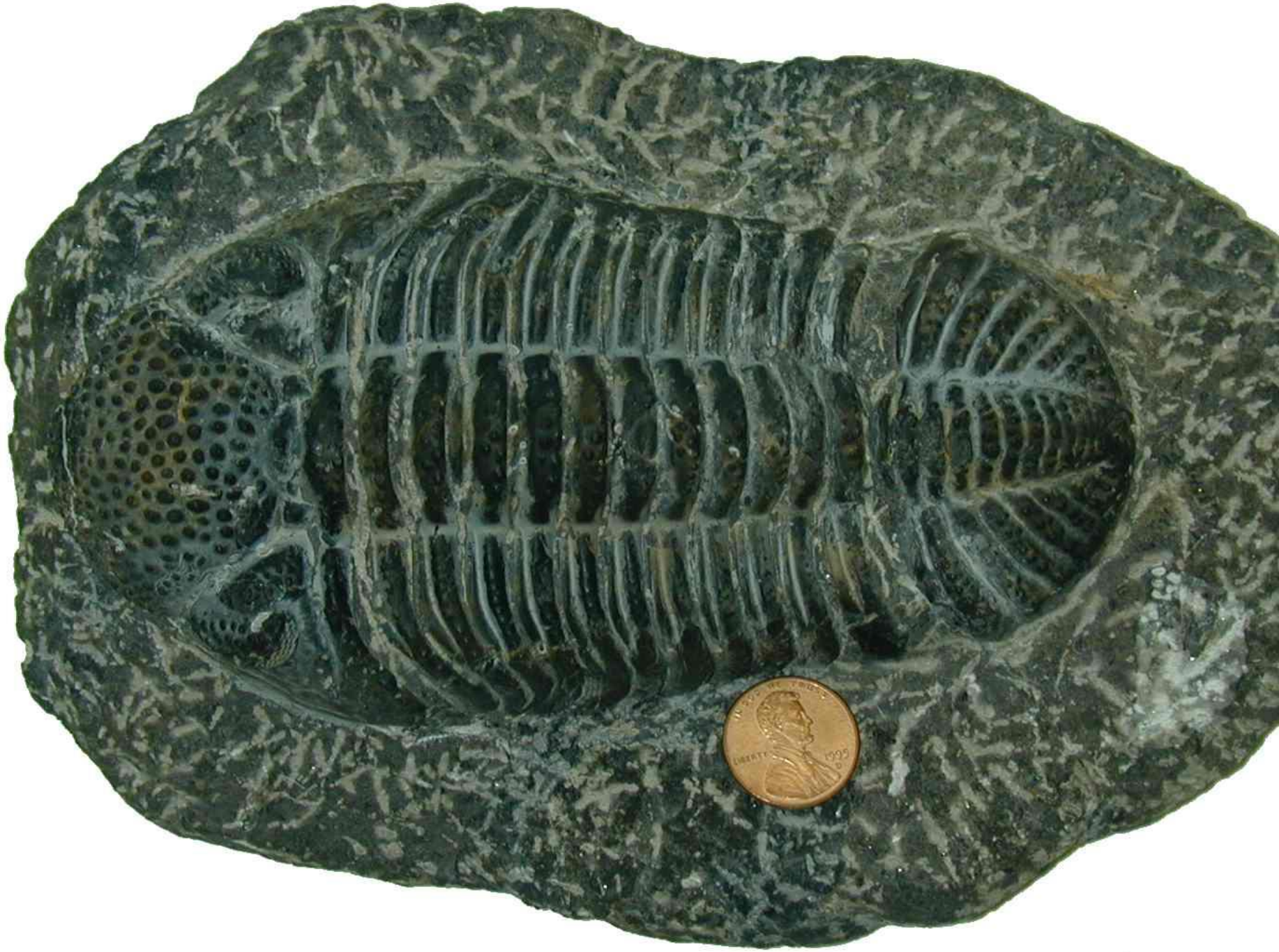
Compelling Evidence for Design in Nature:

Why evolution is not a candidate

Art Chadwick, Ph.D.
Research Professor of Biology and Geology
Southwestern Adventist University



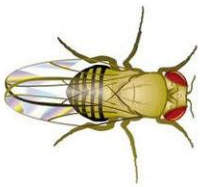
Proterozoic

Phanerozoic

Annelida

Mollusca

Arthropoda



Trilobitomorpha

Echinodermata

Agnatha

Gnathostomata

Plantae

Protostomia

Deuterostomia

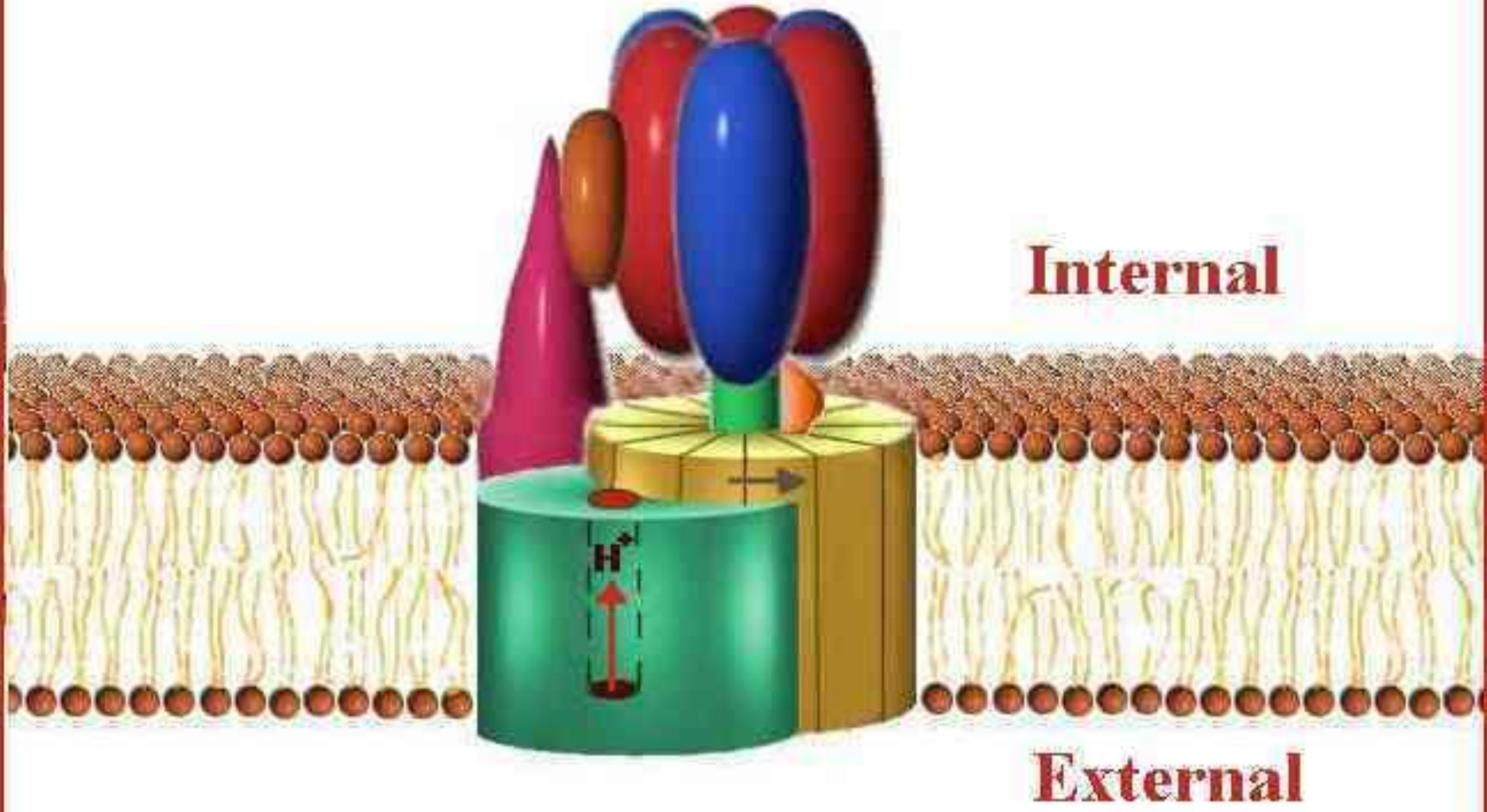
Animalia

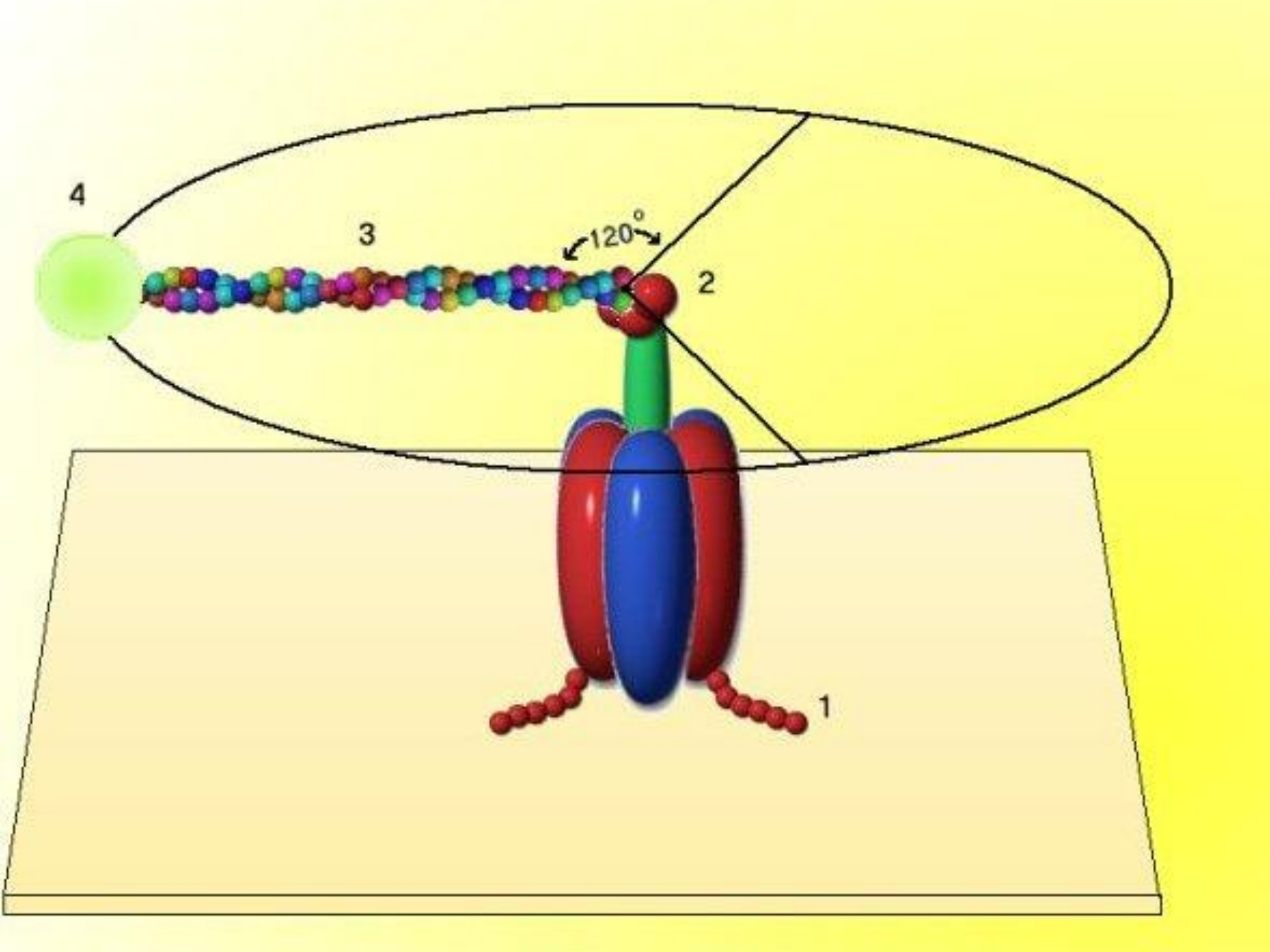
Plantae

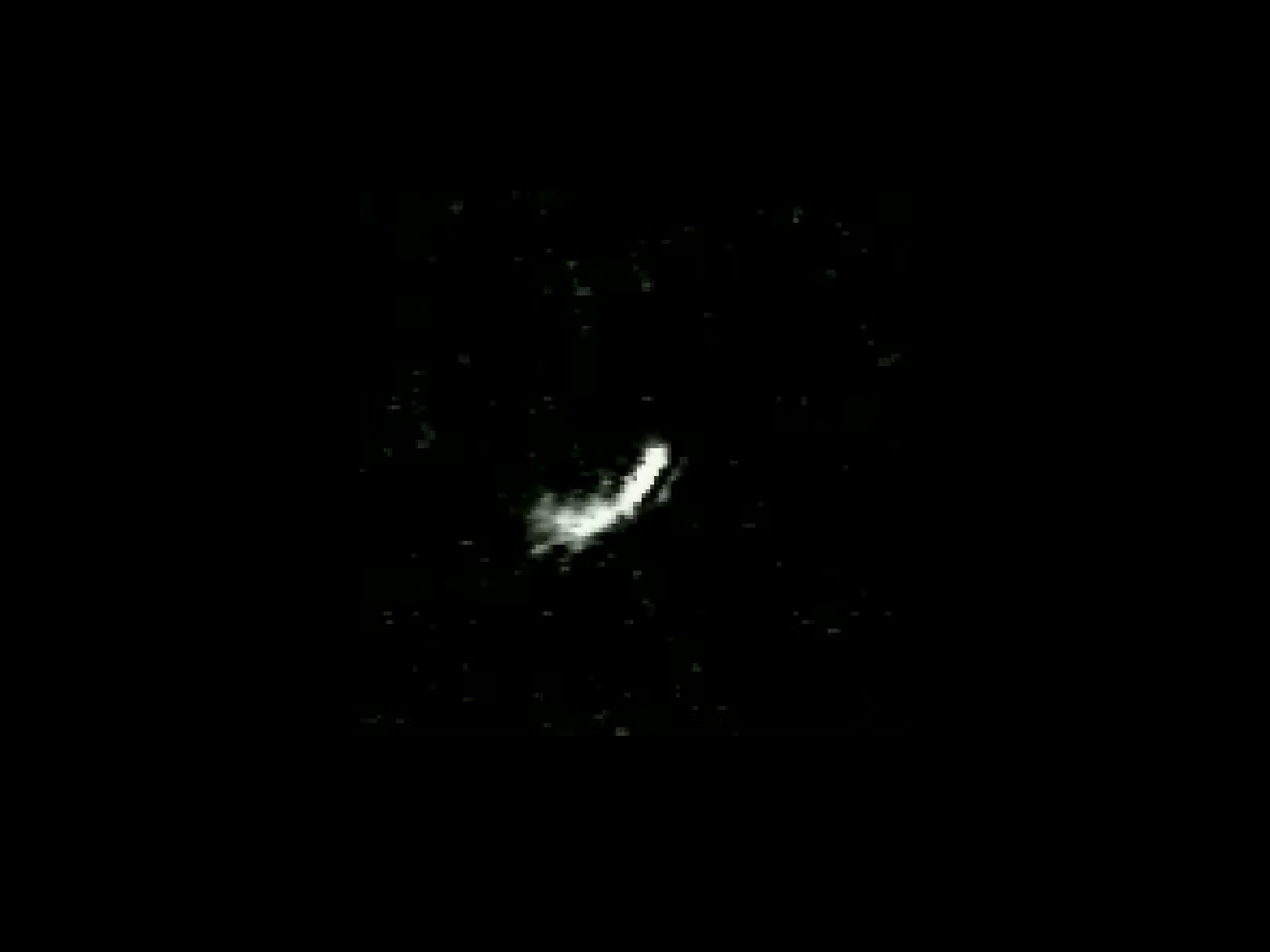
"We have always underestimated cells. … The entire cell can be viewed as a factory that contains an elaborate network of interlocking assembly lines, each of which is composed of a set of large protein machines. … Why do we call the large protein assemblies that underlie cell function protein machines? Precisely because, like machines invented by humans to deal efficiently with the macroscopic world, these protein assemblies contain highly coordinated moving parts."

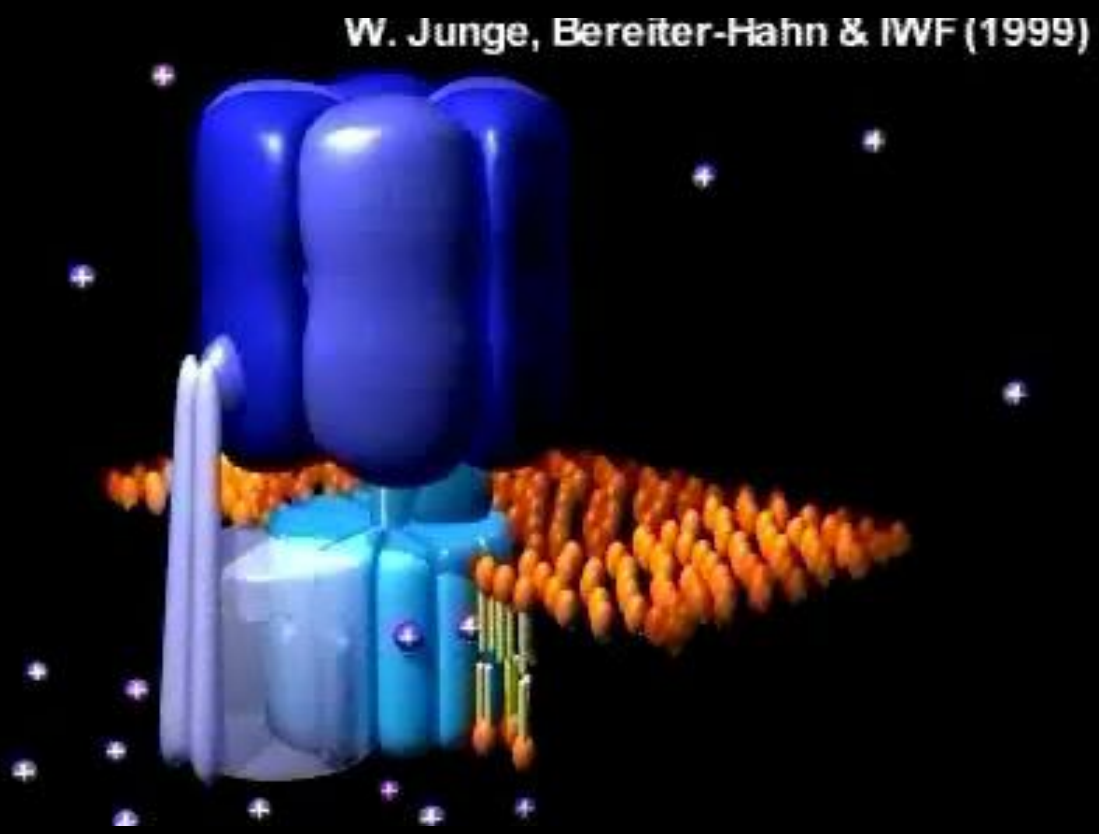
-Bruce Alberts, "The Cell as a Collection of Protein Machines: Preparing the Next Generation of Molecular Biologists," *Cell*, 92 (February 8, 1998)

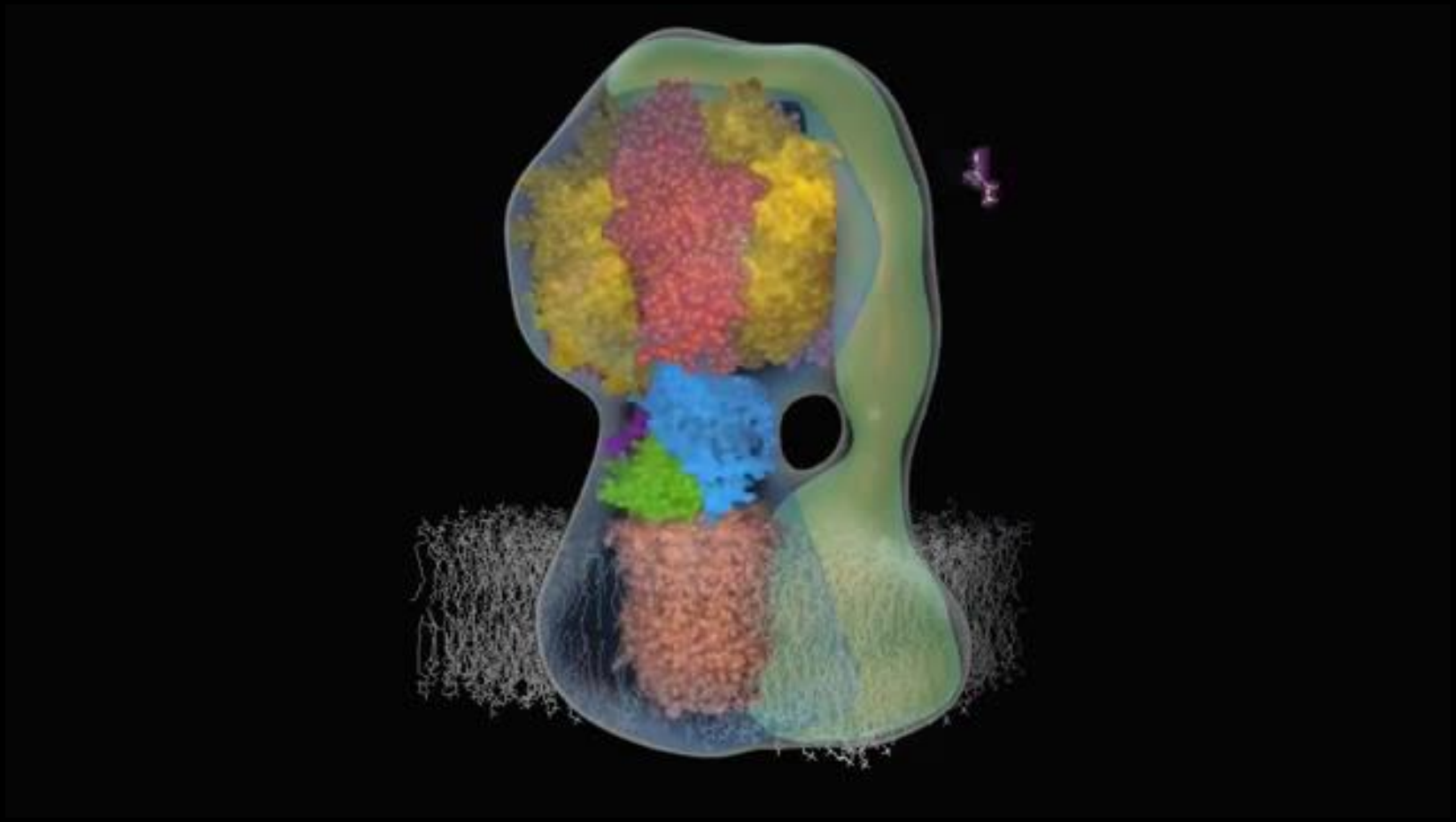
ATP Synthase Complex




4
3
120°
2
1




W. Junge, Bereiter-Hahn & IWF (1999)



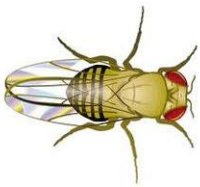
Proterozoic

Phanerozoic

Annelida

Mollusca

Arthropoda



Trilobitomorpha

Echinodermata

Agnatha

Gnathostomata

Plantae

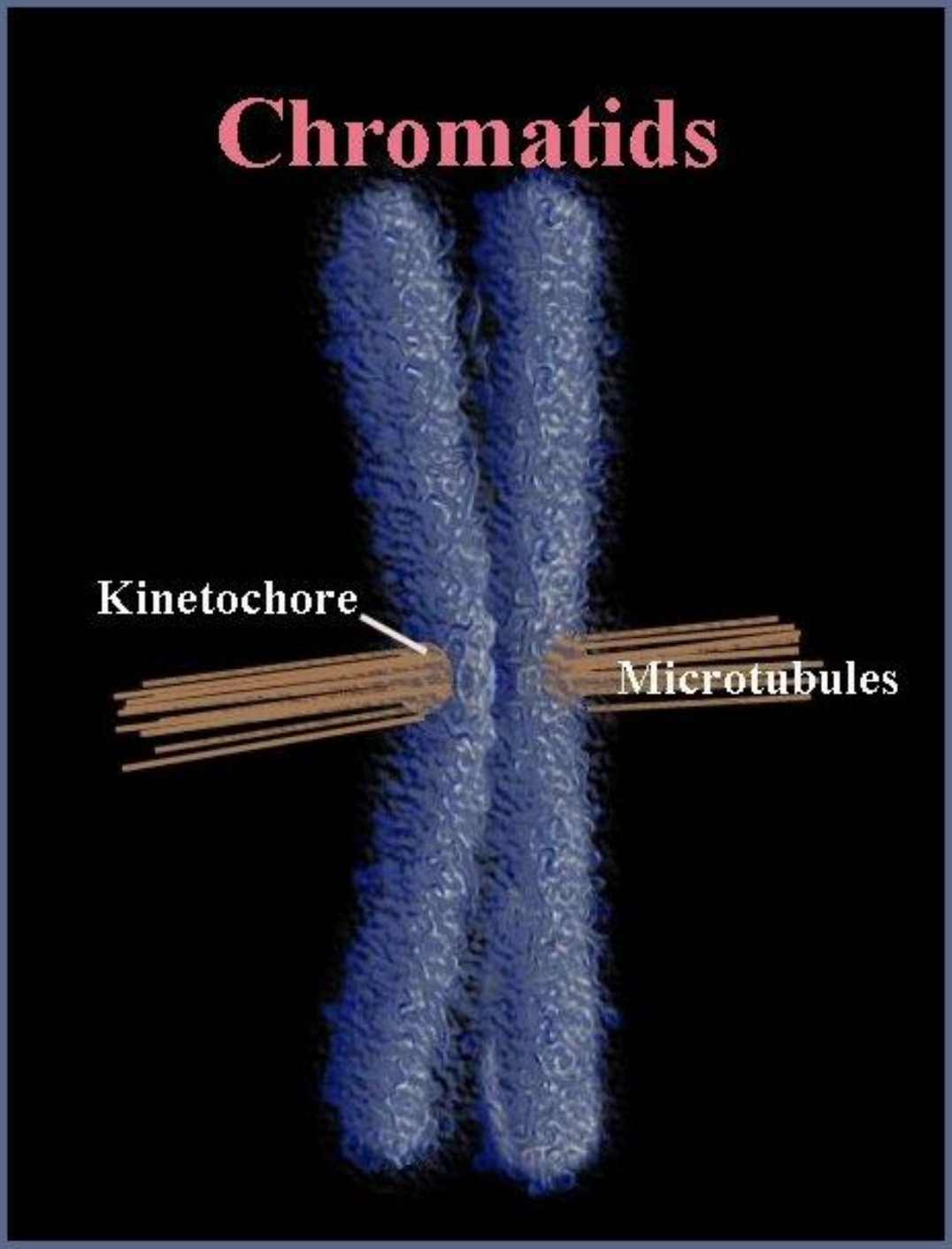
Protostomia

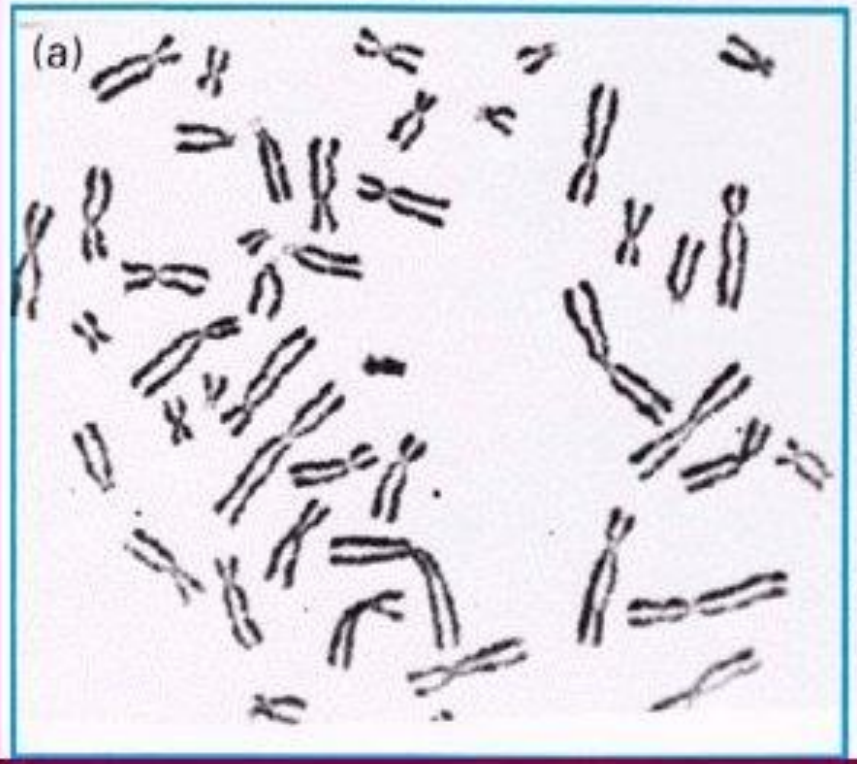
Deuterostomia

Animalia

Plantae

Chromatids





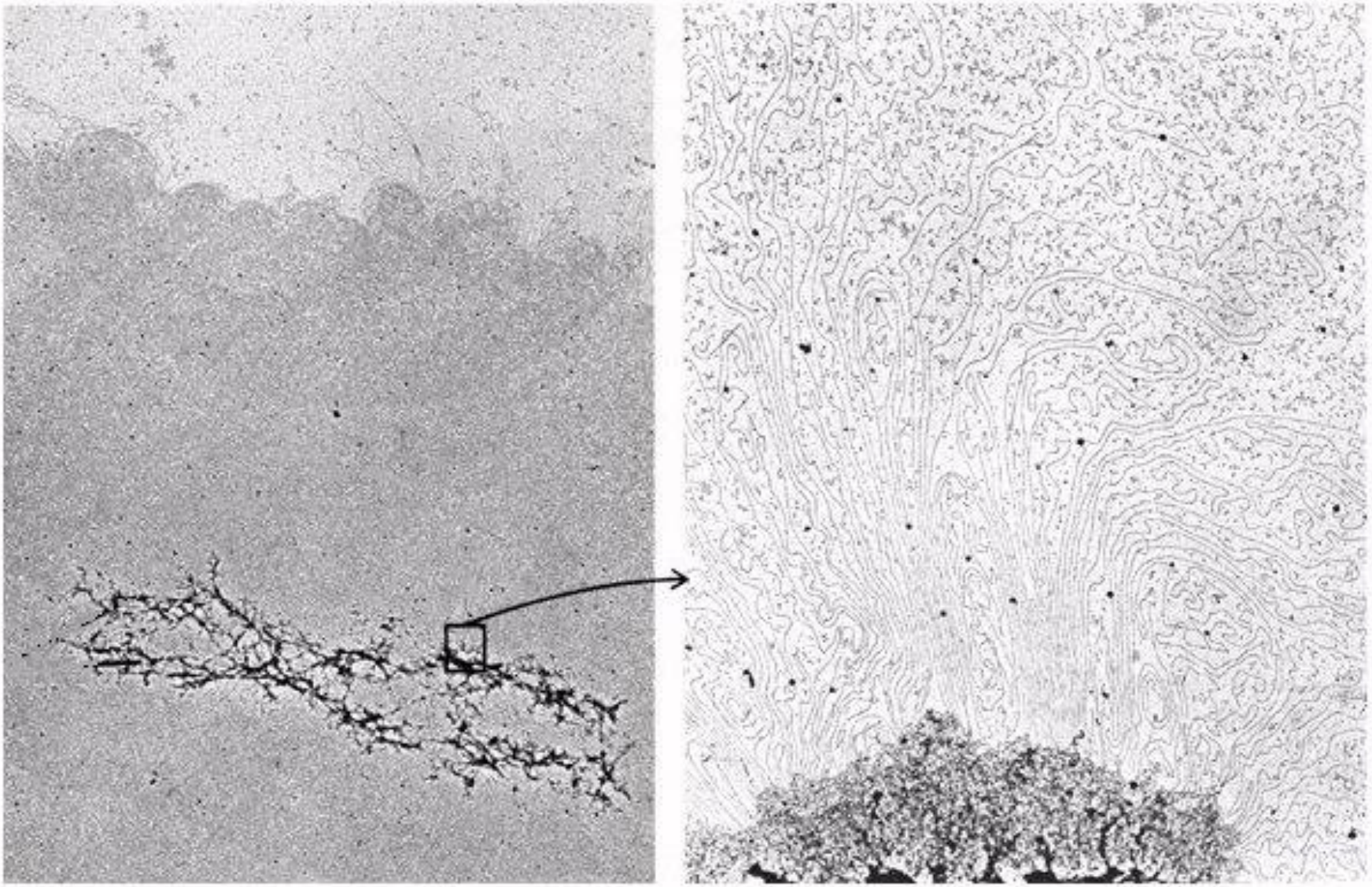
1 2 3 4 5 6 X

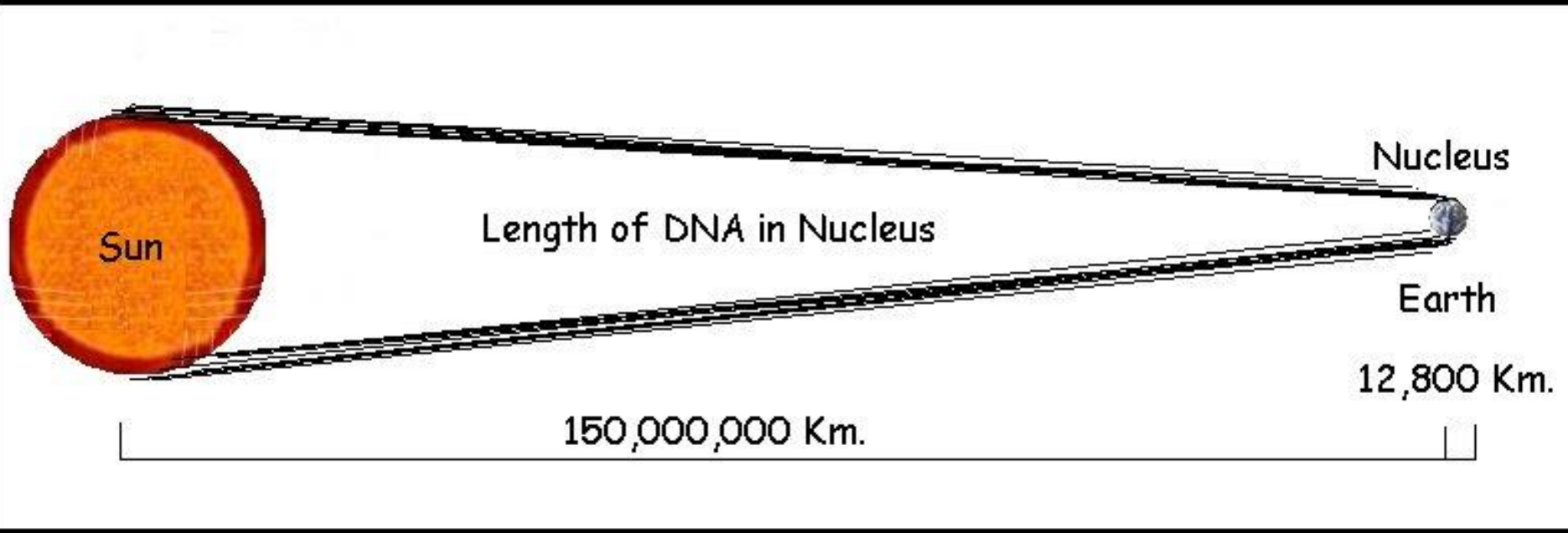
7 8 9 10 11 12

13 14 15

16 17 18

19 20 21 22 Y



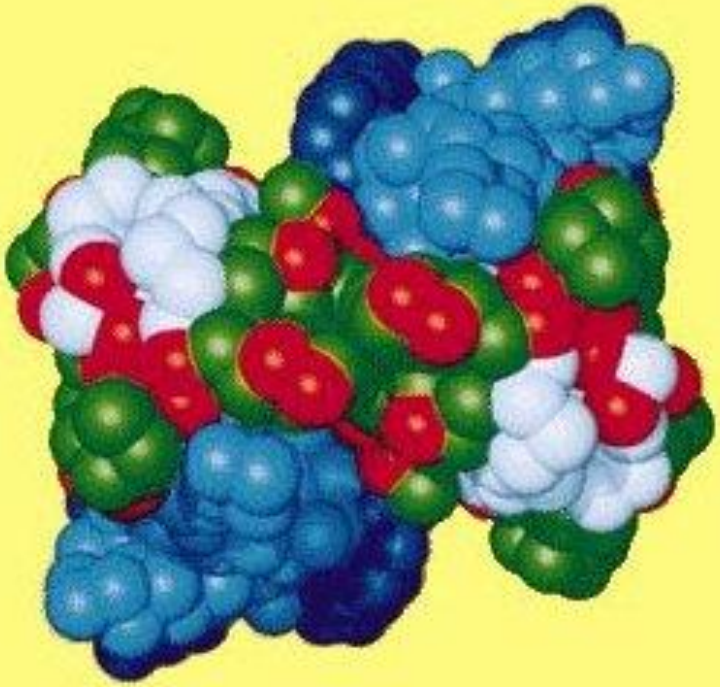

Nucleus
Length of DNA in Nucleus
Sun
Earth
12,800 Km.
150,000,000 Km.

wehi.edu.au

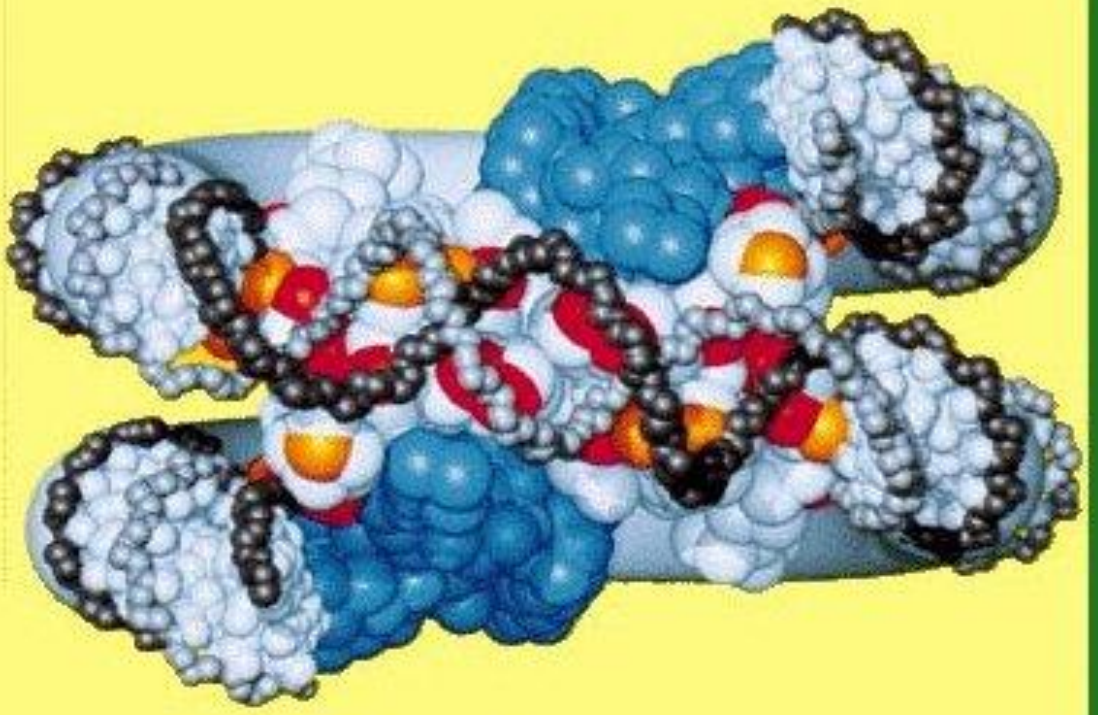
Molecular visualizations of

DNA

2. *DNA Replication*



Histone
Octamer



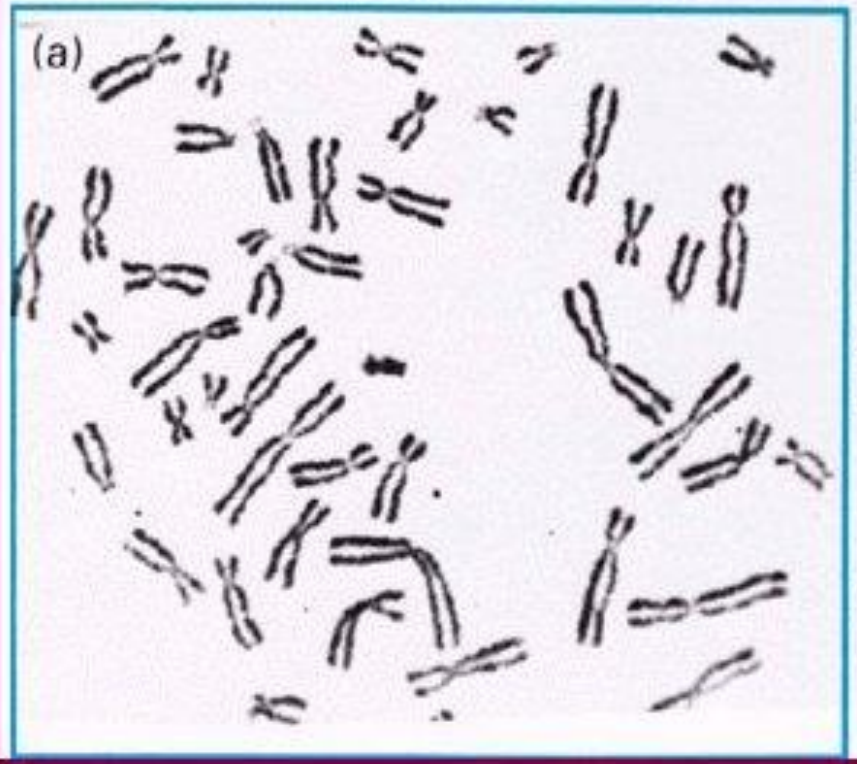
Nucleosome

wehi.edu.au

Molecular visualizations of

DNA

1. DNA Wrapping



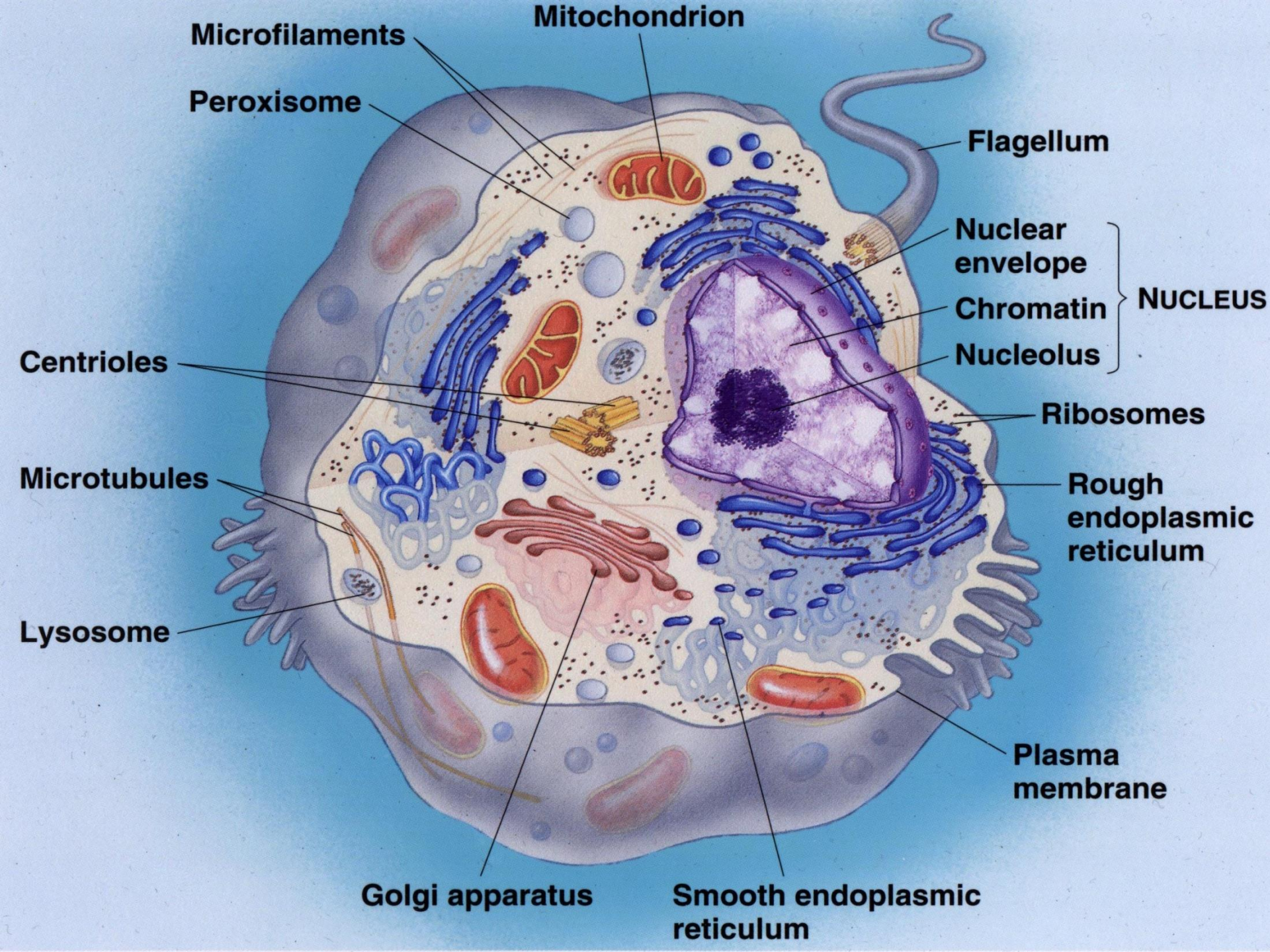
1 2 3 4 5 6 X

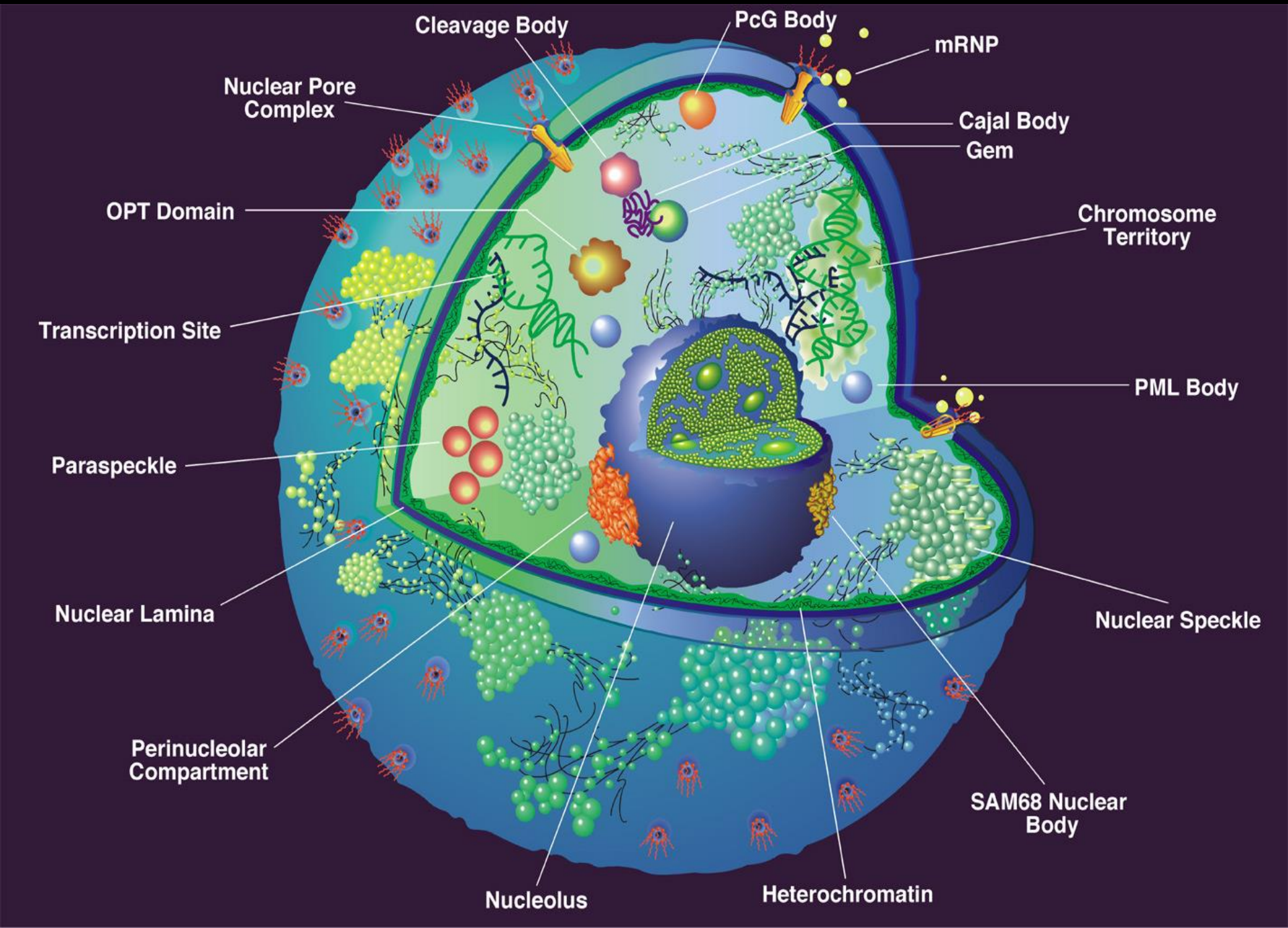
7 8 9 10 11 12

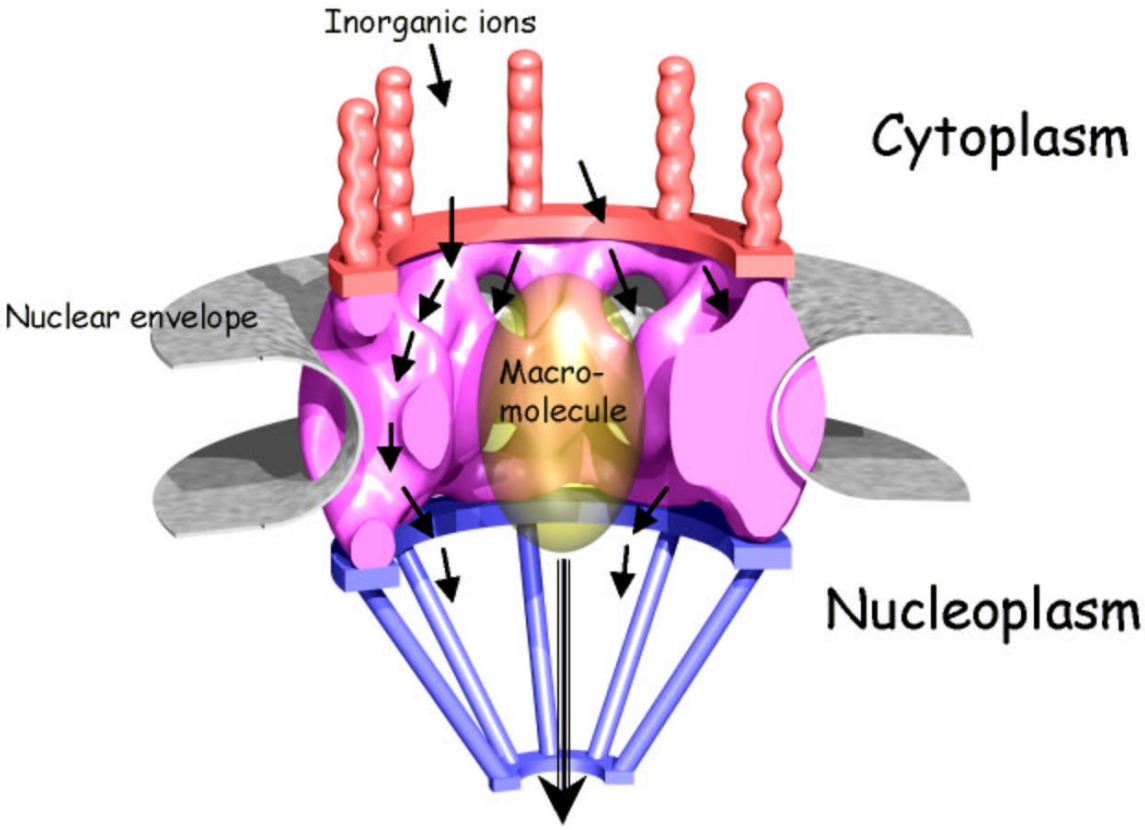
13 14 15

16 17 18

19 20 21 22 Y


Microfilaments
Mitochondrion
Peroxisome
Flagellum
Nuclear envelope
Chromatin
Nucleolus
NUCLEUS
Centrioles
Ribosomes
Microtubules
Rough endoplasmic reticulum
Lysosome
Plasma membrane
Golgi apparatus
Smooth endoplasmic reticulum


Cleavage Body
PcG Body
mRNP
Nuclear Pore Complex
Cajal Body
Gem
OPT Domain
Chromosome Territory
Transcription Site
PML Body
Paraspeckle
Nuclear Lamina
Nuclear Speckle
Perinucleolar Compartment
SAM68 Nuclear Body
Nucleolus
Heterochromatin


Inorganic ions
Cytoplasm
Nuclear envelope
Macro-
molecule
Nucleoplasm

Proterozoic

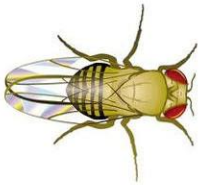
Phanerozoic

Annelida

Mollusca

Protostomia

Arthropoda



Trilobitomorpha

Animalia

Deuterostomia

Echinodermata

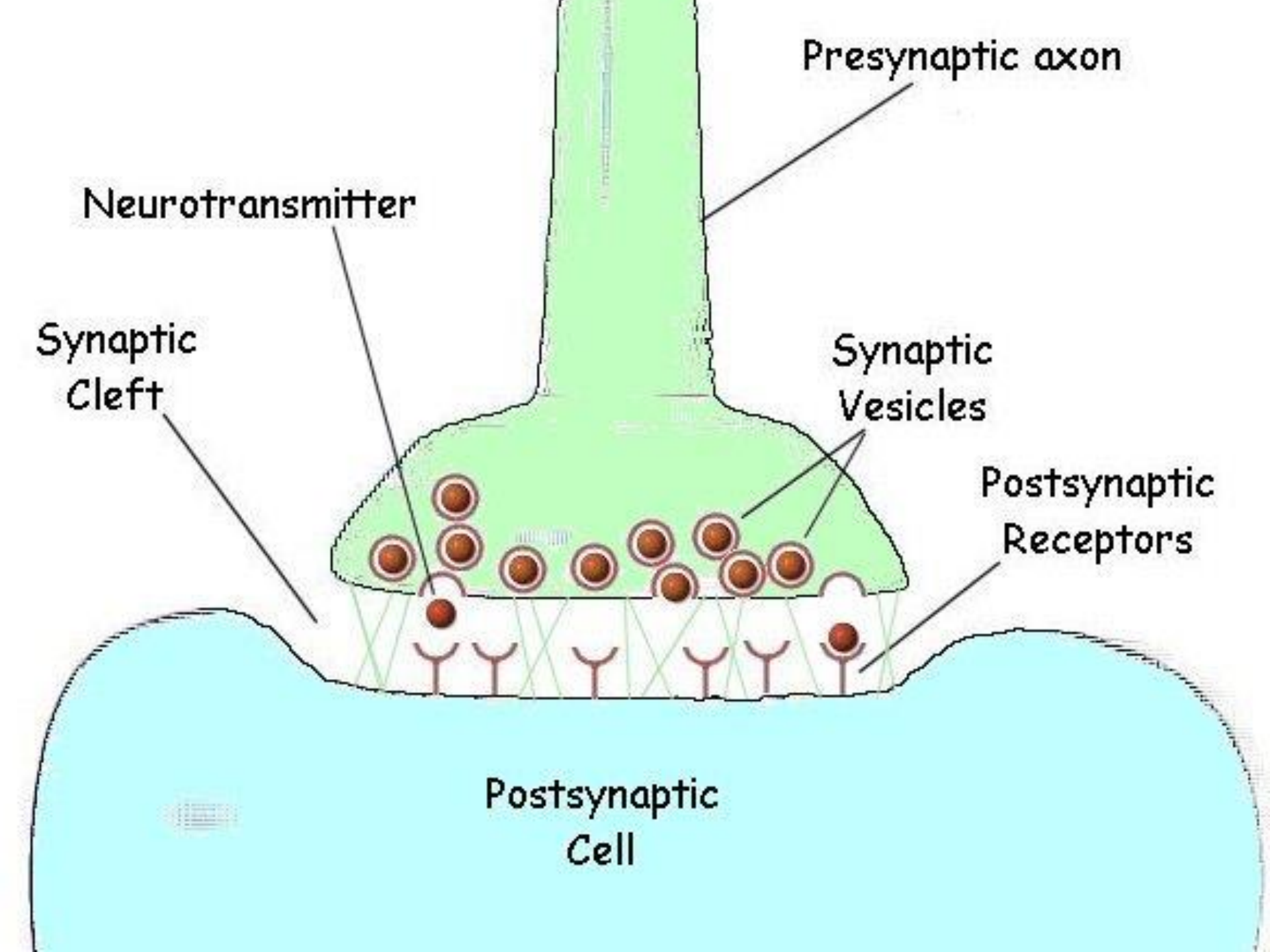
?

Agnatha

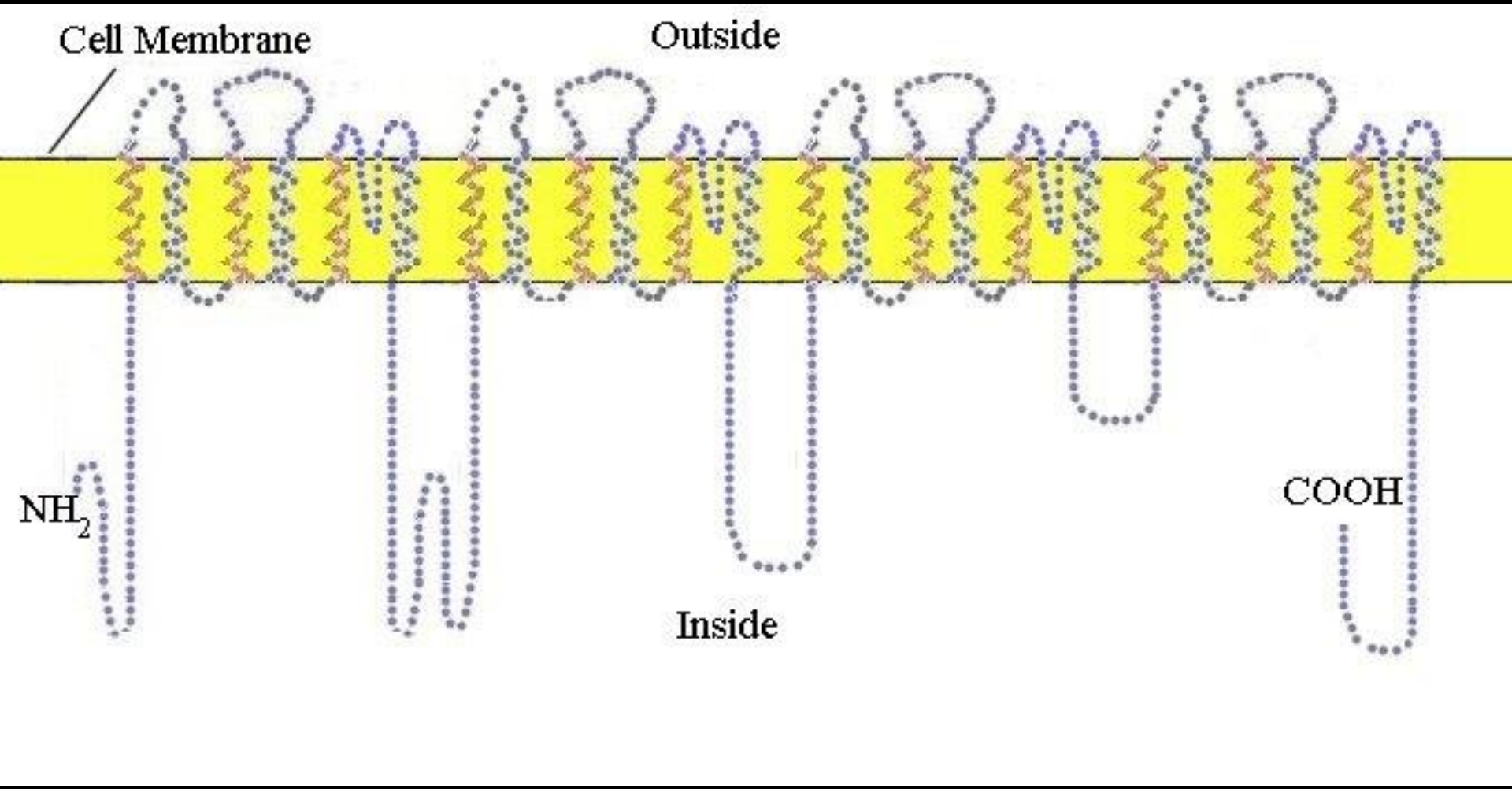
Plantae

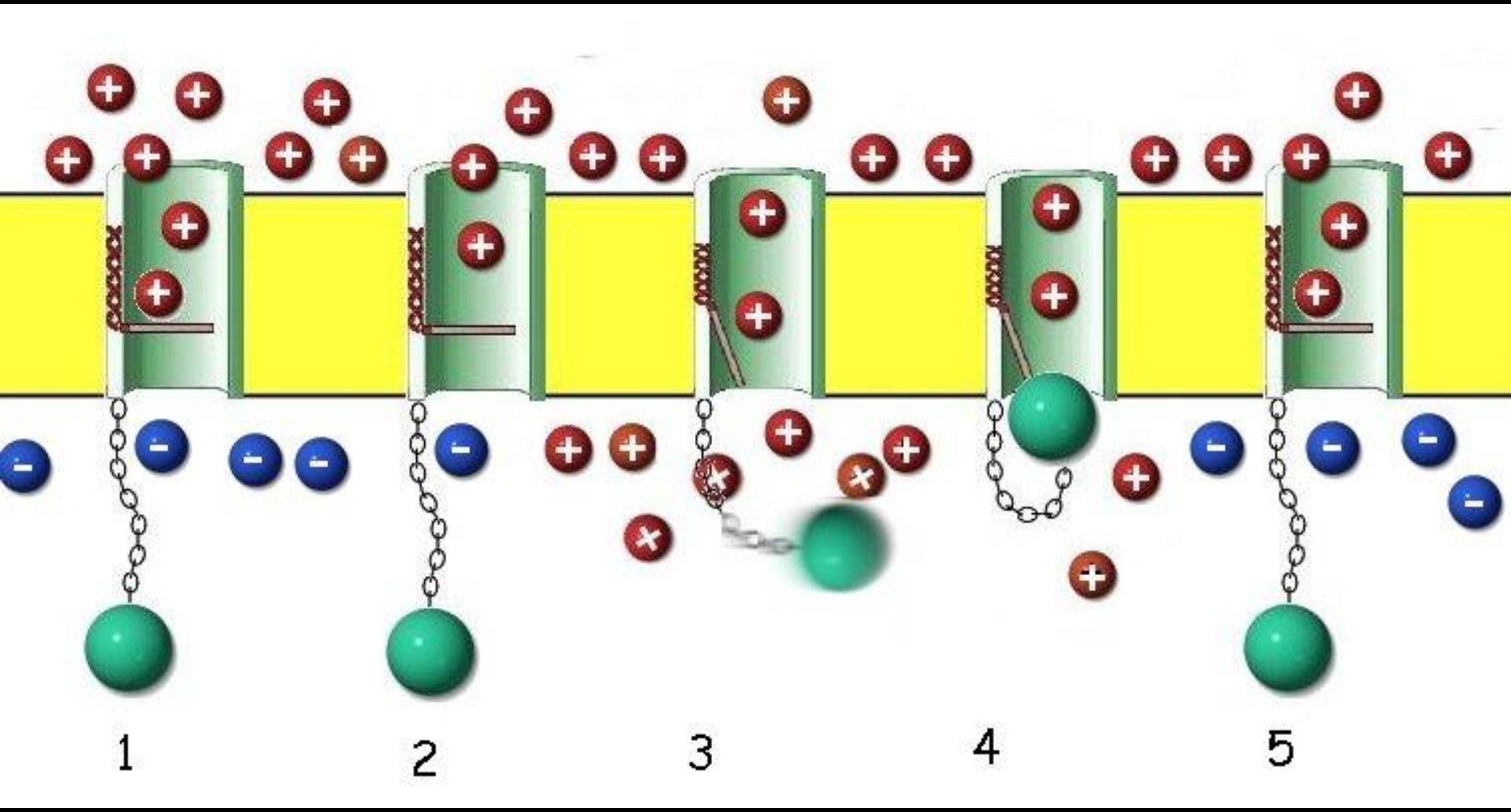
Gnathostomata

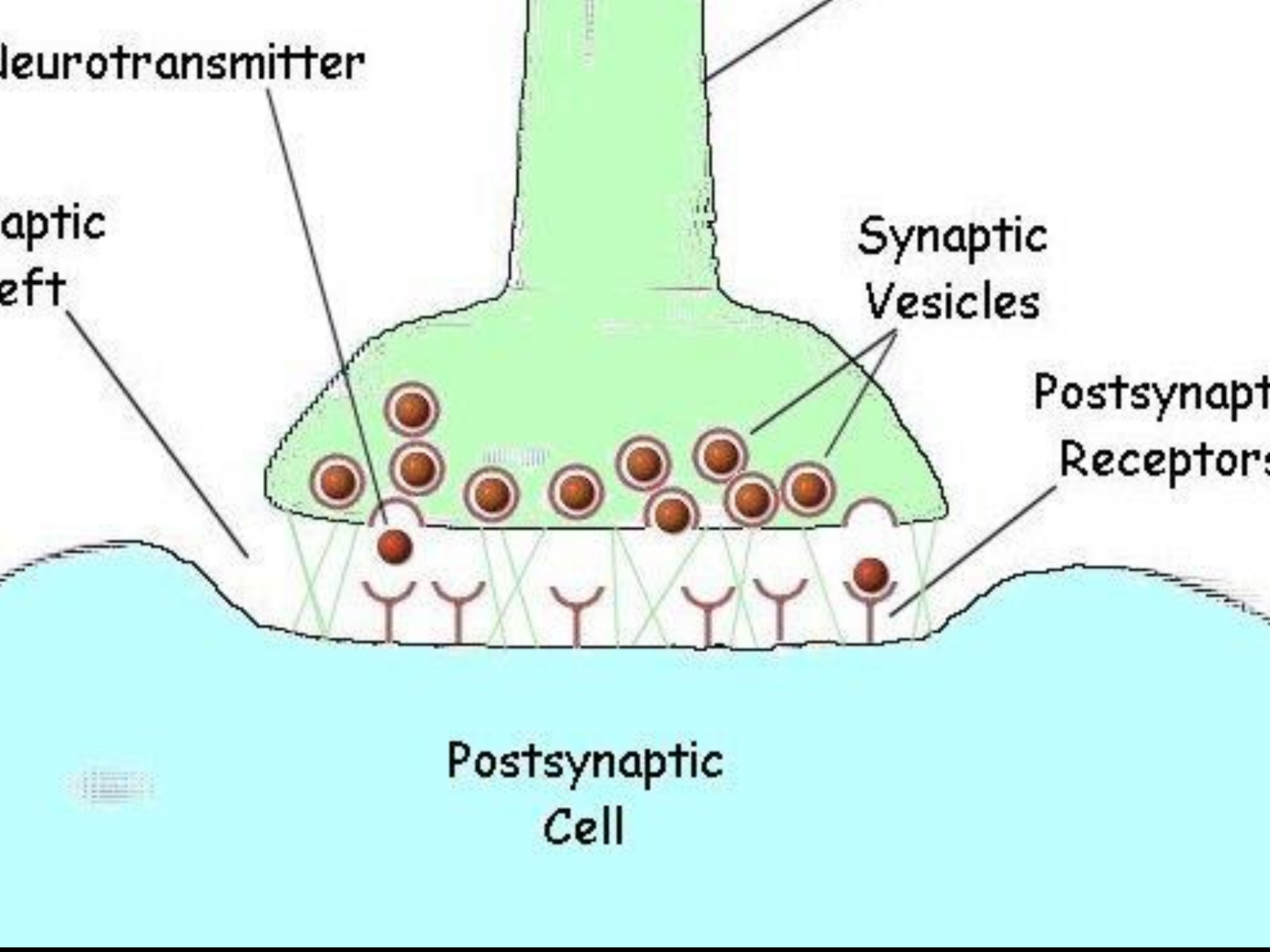
Plantae

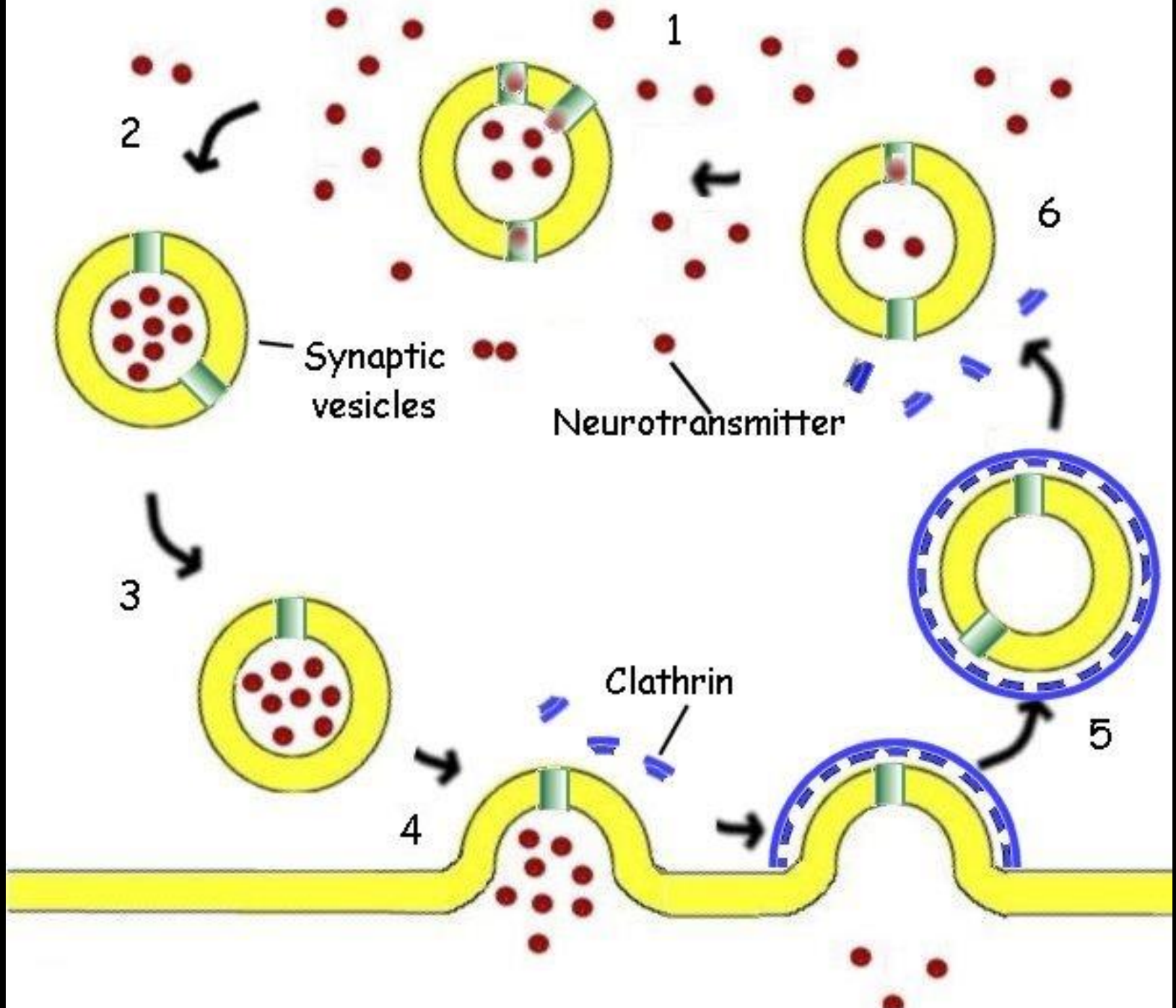

Presynaptic axon
Neurotransmitter
Synaptic Cleft
Synaptic Vesicles
Postsynaptic Receptors
Postsynaptic Cell

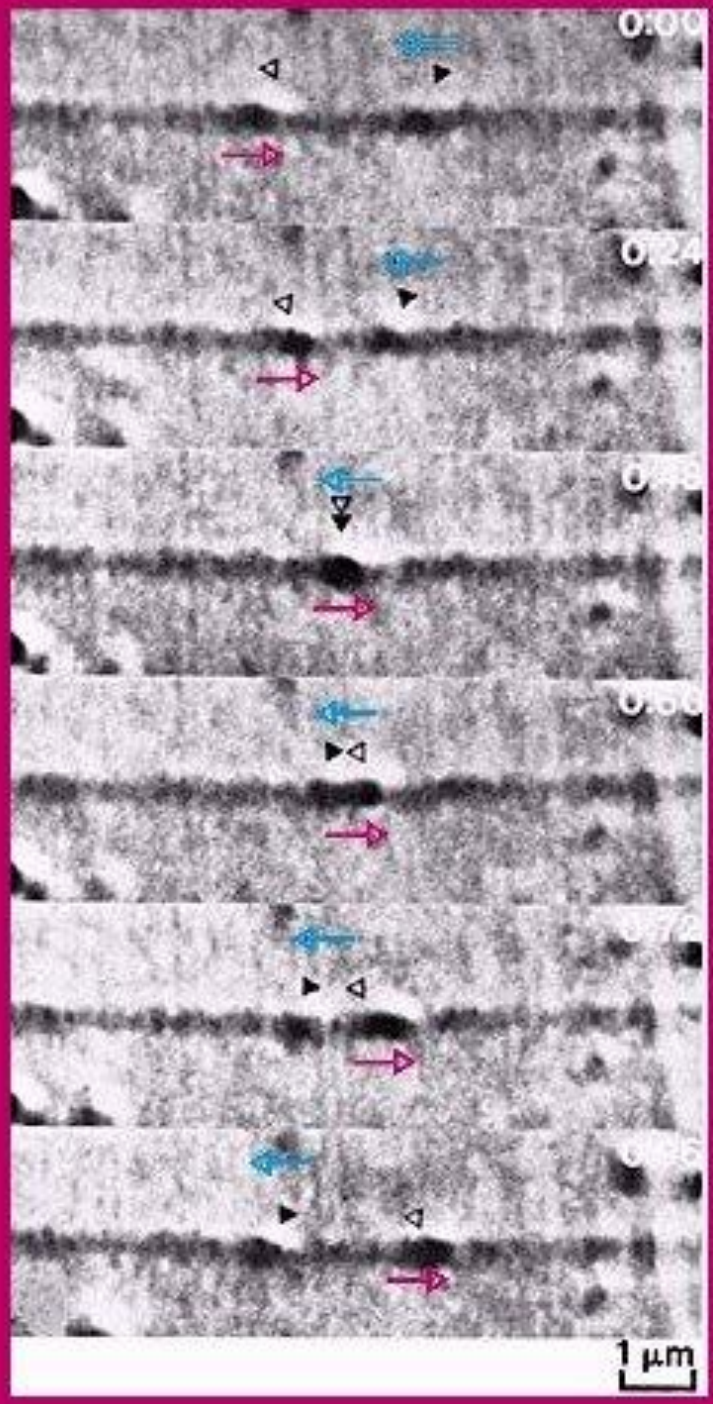
Voltage Gated Sodium Channel Protein

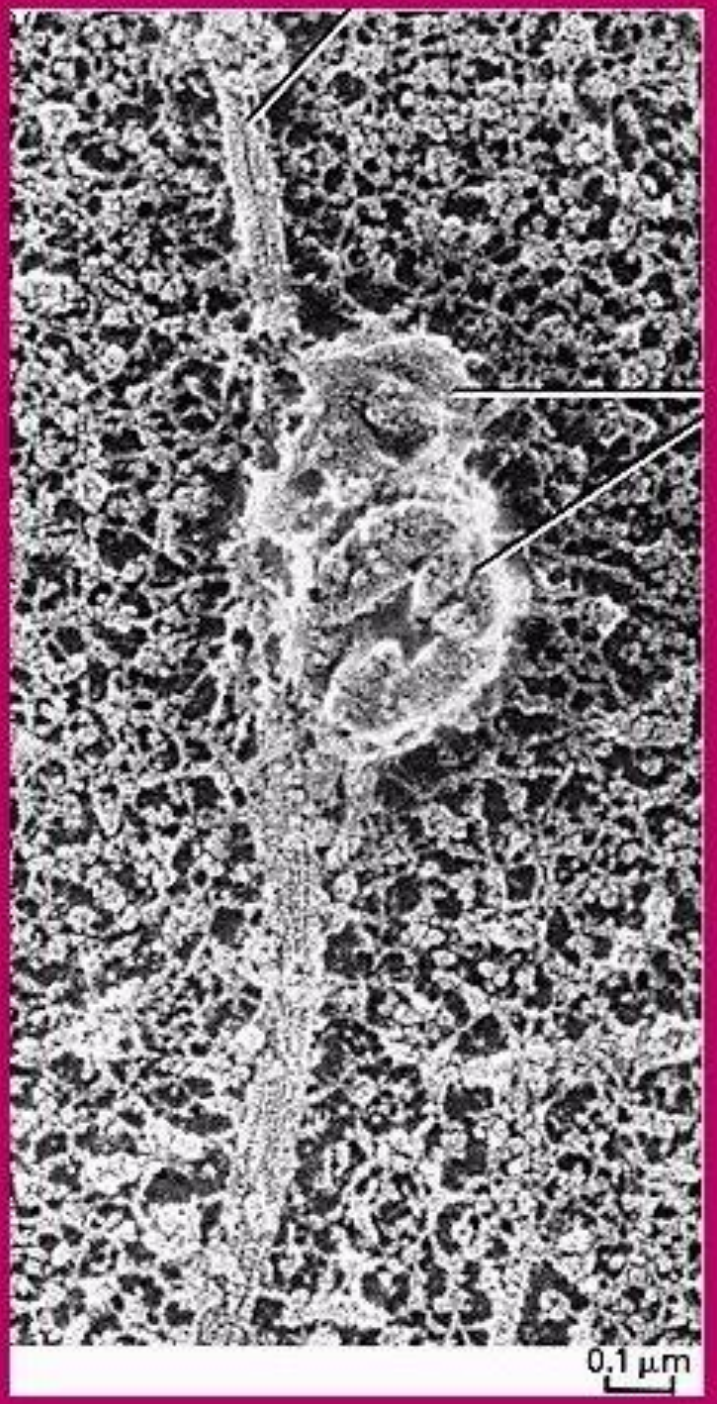


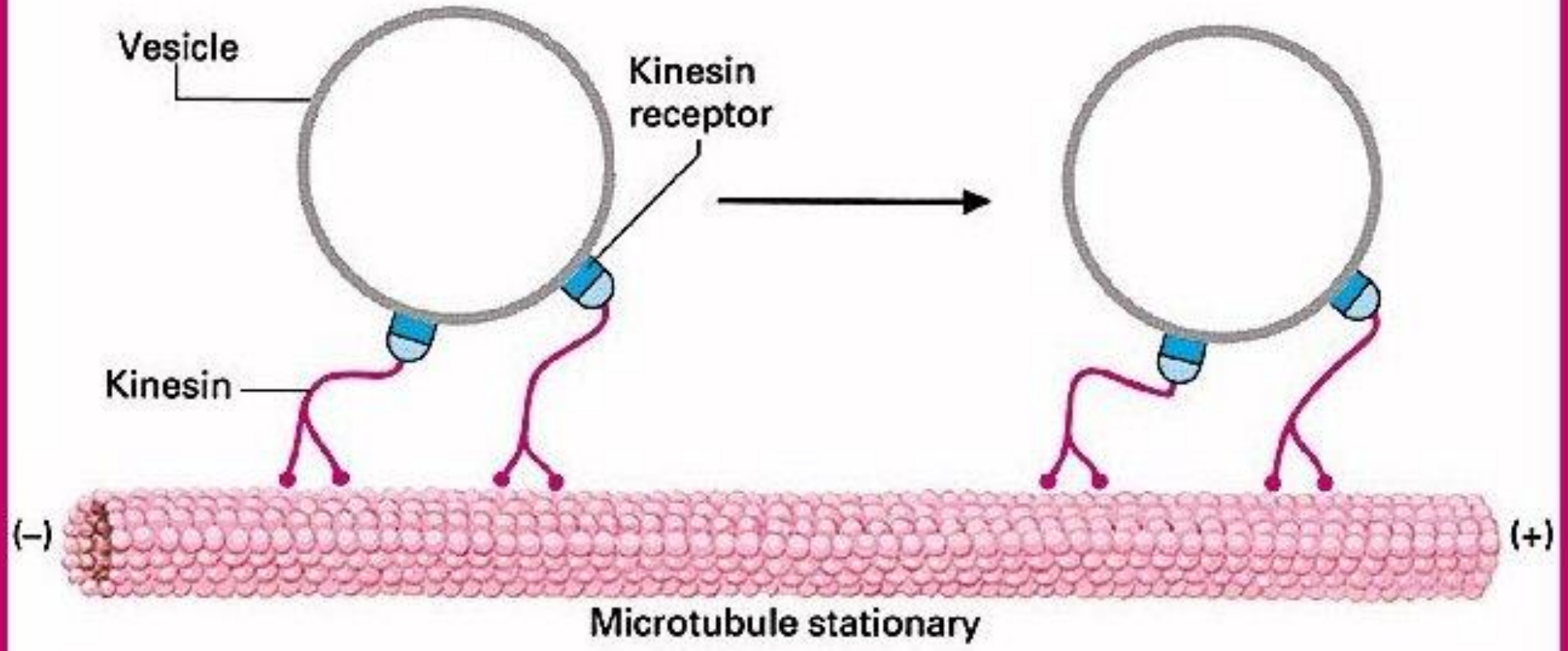

1
2
3
4
5

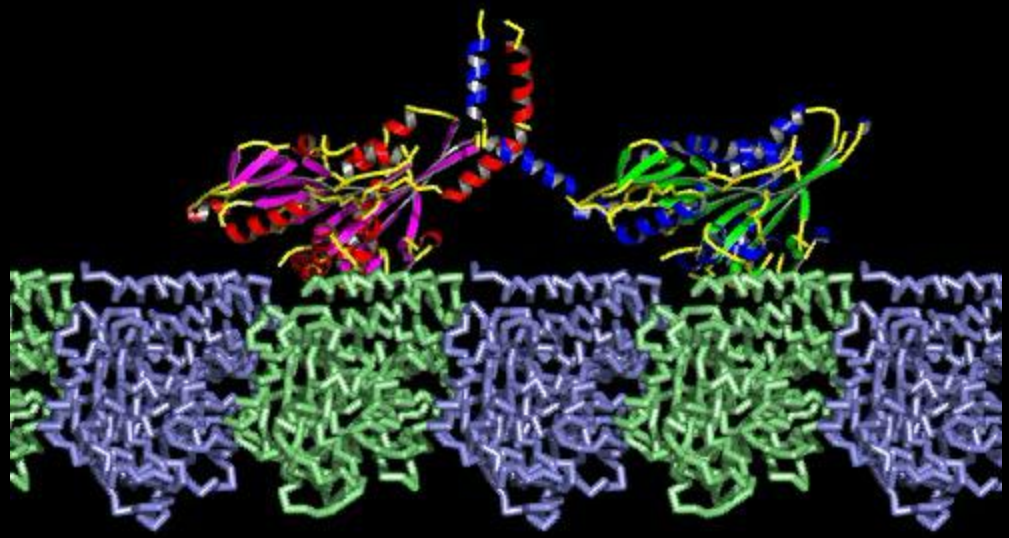

leurotransmitter
aptic
eft
Synaptic
Vesicles
Postsynapt
Receptors
Postsynaptic
Cell

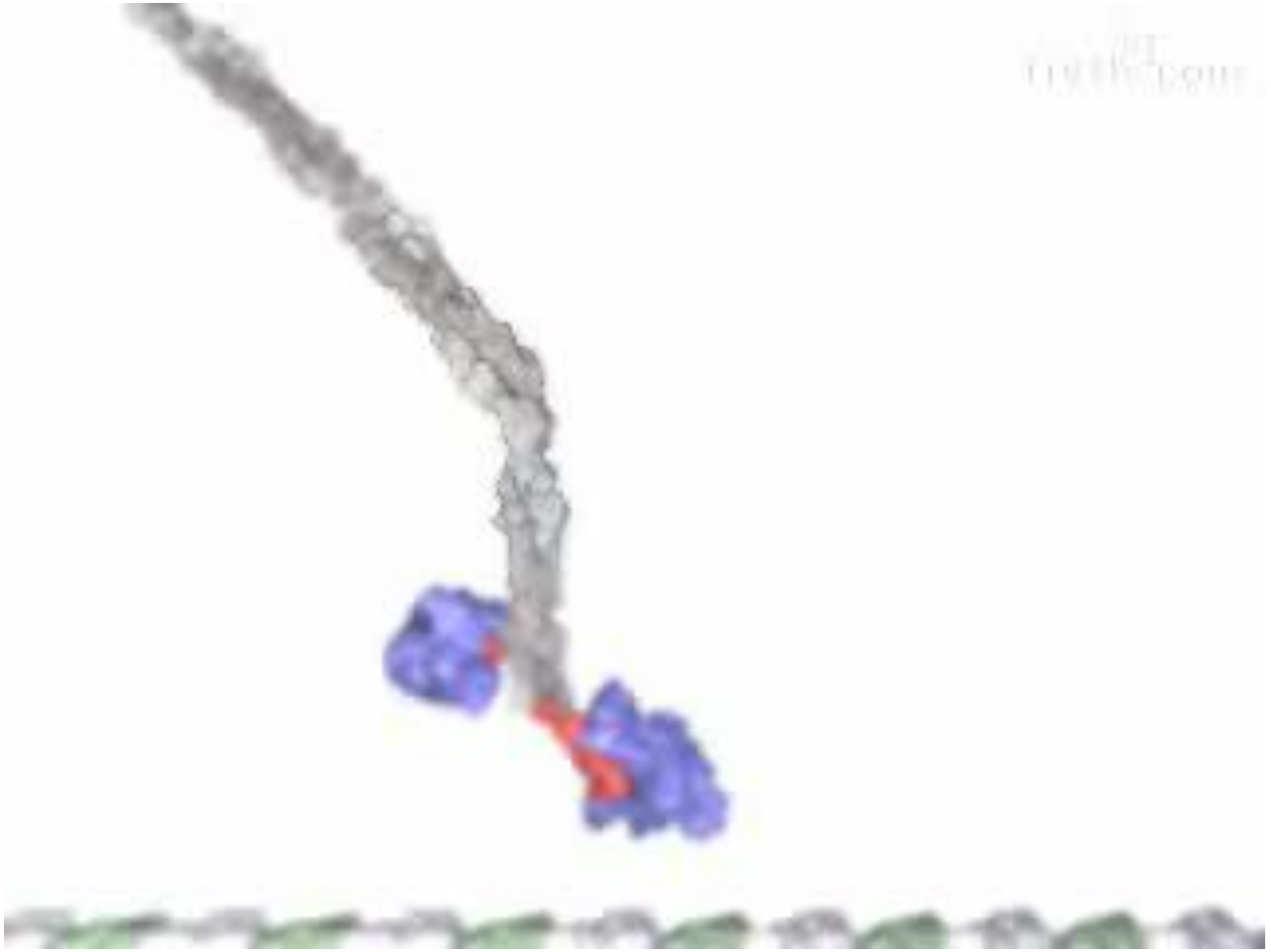

1
2
3
4
5
6
Synaptic vesicles
Neurotransmitter
Clathrin

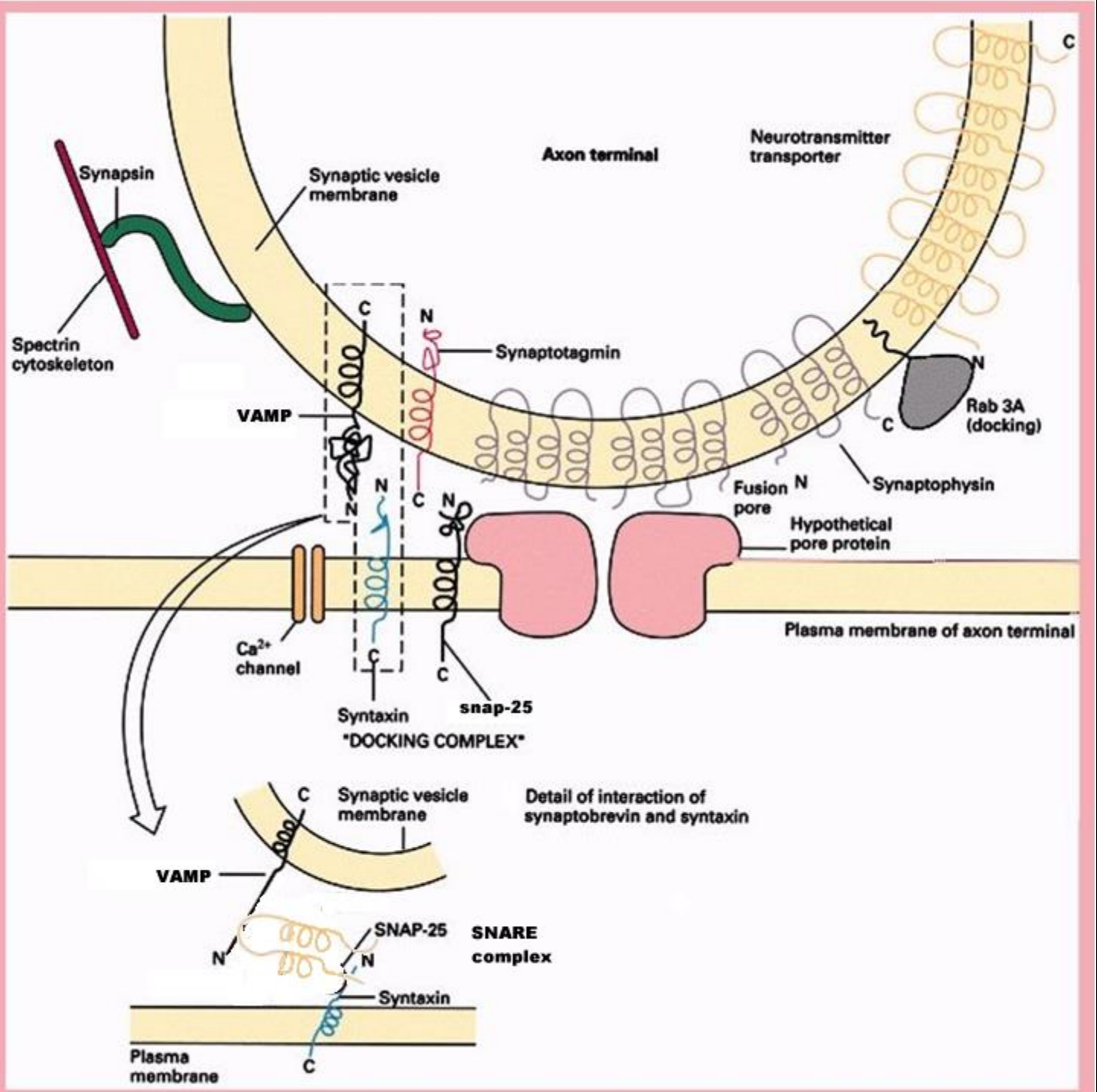

1 µm

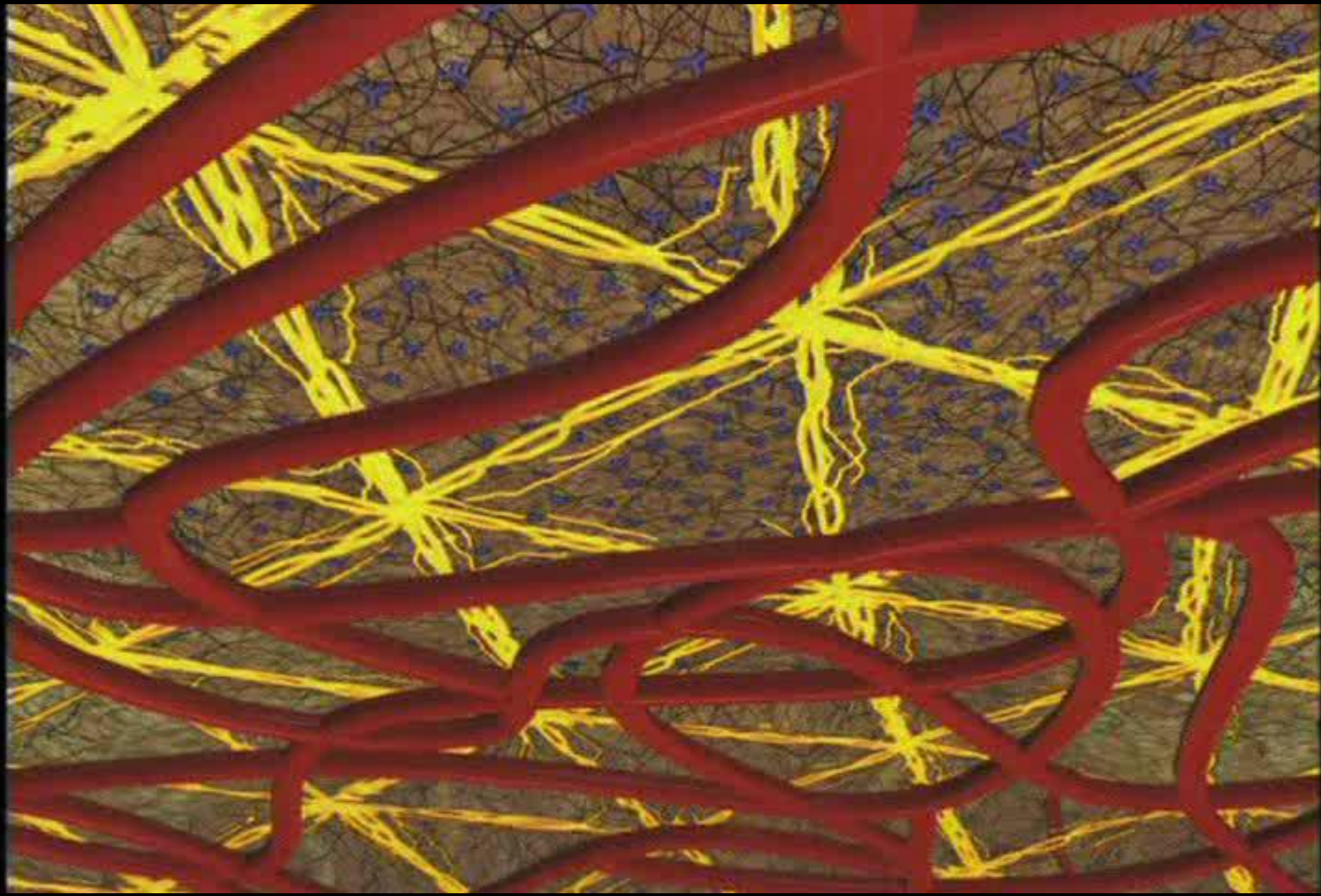

0.1 µm


Vesicle
Kinesin receptor
Kinesin
(–)
(+)
Microtubule stationary






Axon terminal
Neurotransmitter transporter
Synapsin
Synaptic vesicle membrane
Spectrin cytoskeleton
Synaptotagmin
VAMP
Rab 3A (docking)
Synaptophysin
Fusion pore
Hypothetical pore protein
Plasma membrane of axon terminal
Ca2+ channel
Syntaxin
snap-25
"DOCKING COMPLEX"
Detail of interaction of synaptobrevin and syntaxin
Synaptic vesicle membrane
VAMP
SNAP-25
SNARE complex
Syntaxin
Plasma membrane



Proterozoic

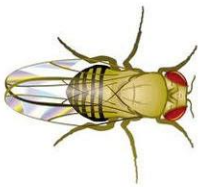
Phanerozoic

Annelida

Mollusca

Protostomia

Arthropoda



?

Trilobitomorpha

Deuterostomia

Animalia

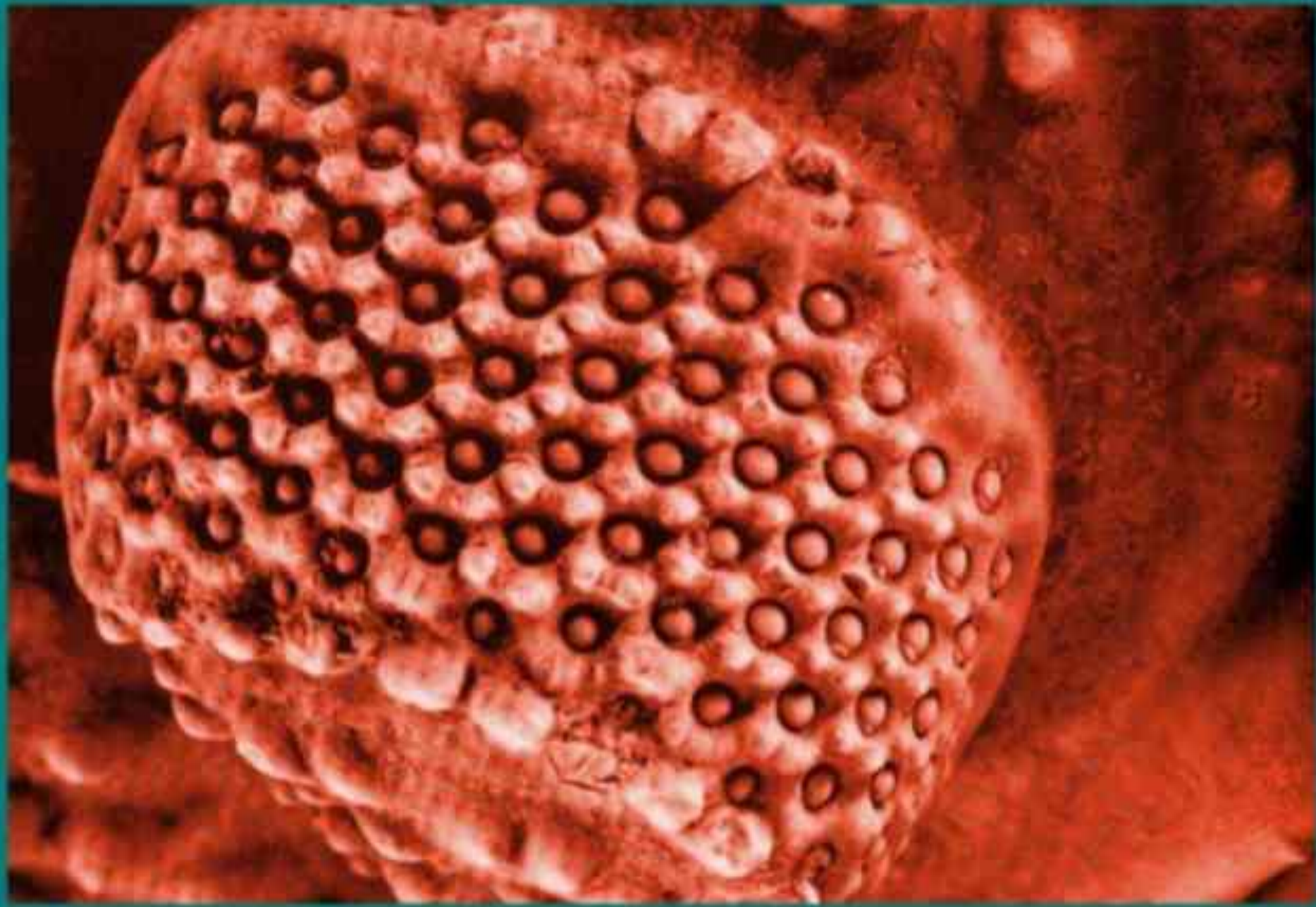
Echinodermata

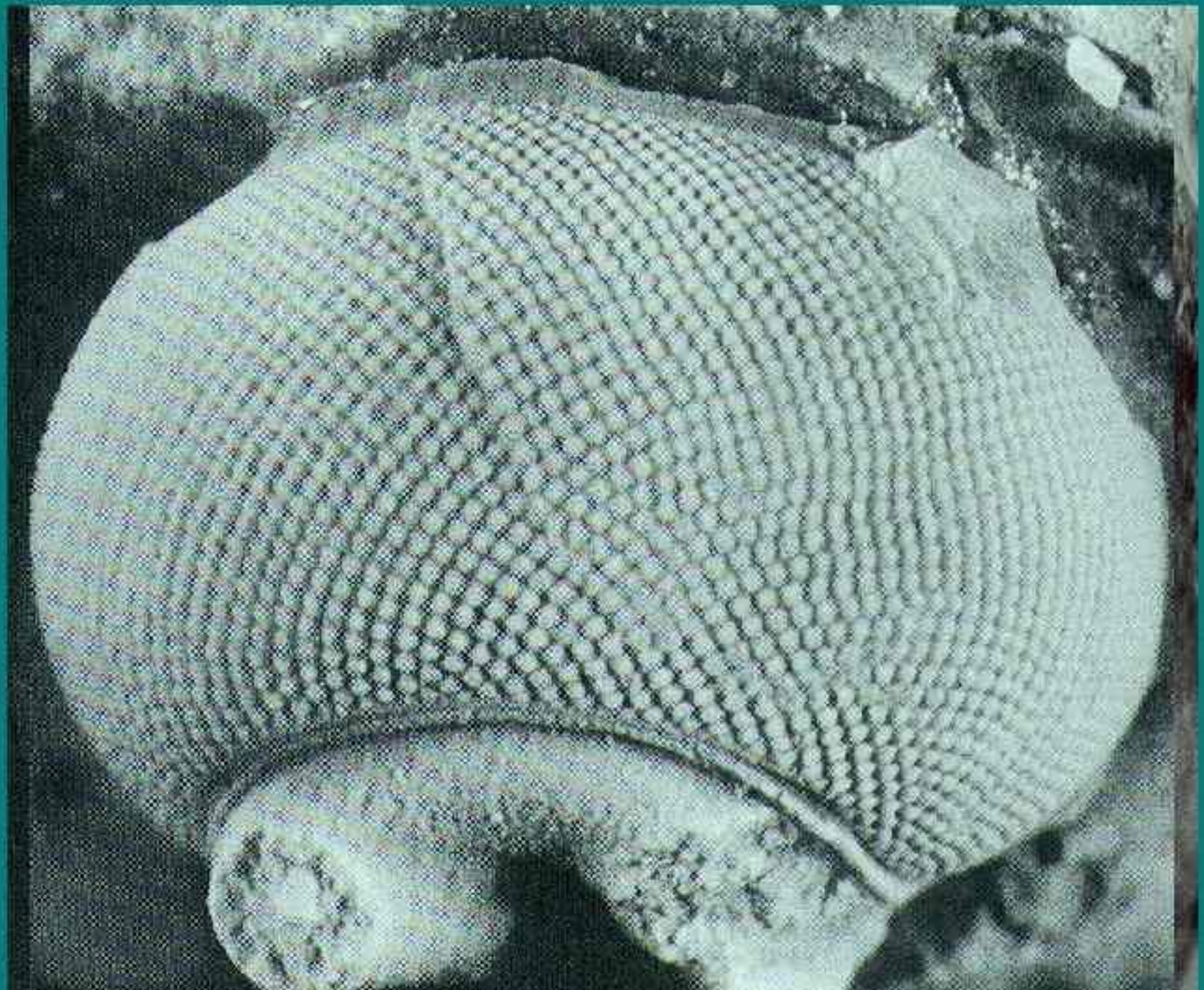
Agnatha

Plantae

Gnathostomata

Plantae





A Sampling of "Evolutionarily Conserved" Functions

	#genes	Systems
1. Axon guidance : The role of Netrins and the netrin receptor Frazzled	3	C,V
2. Axon repulsion: The role of Semaphorins/collapsins and a downstream target	3	C,V
3. Subdivision of the brain - Role of orthodenticle and empty spiracles and other transcription factors and signaling proteins.	14	C,V
4. Cell cycle 1: Replication licensing factor (RLF) and ORC	4	Y,M
5. Cell cycle 2: G1-S transition. Involvement of E2F, Cyclin D, Cyclin E and Retinoblastoma protein	8	Y,M
6. Cell cycle 3: The G2-M transition - Cyclin A, Cyclin B, Cdc2, Wee kinase and Cdc25 phosphatase	4	Y,M
7. Cell survival: EGF and its receptor - the Ras pathway - ETS	7	C,M
8. Chromatin assembly and gene activation	5	Y,M
9. Compartmentalization: The roles of Wingless in adherins junction dynamics and in targeting of LIM domain proteins and Engrailed	12	C,M
10. Dorsal-ventral patterning and the immune response - A common pathway activates Dorsal and NF-kappaB	5	X,M

y = Yeast, C = C. elegans, V = Vertebrates, M = Mammals, X = Xenopus

A Sampling of "Evolutionarily Conserved" Functions

	#genes	Systems
11. Ectoderm/mesoderm interaction - Ectodermal FGF involvement in development of respiratory and muscle systems	3	C,M
12. Determination of endodermal and ectodermal portions of the digestive system - Transcription factors required for development of the gut	3	C,M
13. Extracellular matrix: Functional conservation of extracellular modular proteins and cell surface receptors	6	V
14. Eye morphogenesis control genes - Eyeless (Pax-6) and Sine oculis	Many	All
15. General gene activation machines: NURF and SWI/SNF	5	Y,M
16. Hindbrain and the spinal cord - Conserved role for Antennapedia class homeobox proteins	4	V
17. Lateral inhibition - The Notch pathway	8	C,M
18. The Learning Pathway - cAMP Second Messenger System	9	V
19. Mesoderm determination and the early differentiation of muscle	5	V
20. Muscle induction pathways involved in cardiac and somatic muscle	8	V

y = Yeast, C = C. elegans, V = Vertebrates, M = Mammals, X = Xenopus

A Sampling of "Evolutionarily Conserved" Functions

	#genes	Systems
21. Neural, ectodermal and mesodermal patterning	12	M
22. Neuron differentiation - Involvement of POU domain protein in the terminal differentiation of neurons	4	C,M
23. Photoperiod response: Pas domain proteins and neurons functioning as a central clock apparatus	1	M
24. Programmed cell death - apoptosis	4	M
25. Proneural pathway - Achaete-Scute homologs and interacting proteins	4	C,M
26. Segment polarity: Hedgehog and its targets	9	V
27. Segmentation and segment polarity - conserved role for Engrailed	1	V
28. Septate junctions and MAGUK proteins: Cell-cell interaction and signaling to the interior of cells	6	M
29. Spemann's organizer: Homologous structure in Drosophila?	8	V
30. Subdivision of anterior-posterior axis by Homeobox cluster	8	M

y = Yeast, C = C. elegans, V = Vertebrates, M = Mammals, X = Xenopus

A Sampling of "Evolutionarily Conserved" Functions

	#genes	Systems
31. Stress activated and cell motility feedback pathway: The Jun-N-terminal kinase (JNK) activated MAP kinase cascade links the Rho family of GTP-binding proteins to transcription of Jun	6	M
32. Subdivision of anterior-posterior axis by Homeobox cluster	8	M
33. Invertebrate photoreceptor trp pathway for phototransduction, highly conserved from worms to humans.	1	C,M
34. Evolutionarily conserved QM homolog found in worms, human, plants; human most similar to maize (86% identity for 412 nucleotides)		
35. Cyclin genes (regulatory subunits of cyclin-dependent protein kinases) conserved in plants and animals	Many	All
36. Aquaporins belong to a family of integral membrane proteins with members in animals, plants, yeast, and bacteria	Many	All
37. Peptidyl-prolyl cis-trans isomerases (PPIases) evolutionarily conserved and ubiqitous; folding and trafficking of proteins.	?	Y,M

y = Yeast, C = C. elegans, V = Vertebrates, M = Mammals, X = Xenopus

Notable Quotes

Steven J. Gould, Harvard: "Fast is now a lot faster than we thought, and that's extraordinarily interesting"

Samuel A. Bowring, M.I.T.: "We now know how fast fast is, and what I like to ask my biologist friends is, How fast can evolution get before they start feeling uncomfortable?"

Rudolph Raff, Indiana U.: "There must be limits to change. After all, we've had these same old body plans for half a billion years"

G. M. Narbonne, Queens U.: "What Darwin described in the Origin of Species was the steady background kind of evolution. But there also seems to be a non-Darwinian kind of evolution that functions over extremely short time periods--and that's where all the action is."

All quotes from: "When Life Exploded". Time Magazine, Dec. 4, 1995, Vol 146, No. 23.

Proterozoic

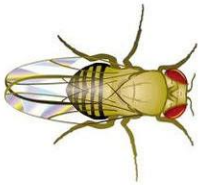
Phanerozoic

Annelida

Mollusca

Protostomia

Arthropoda



Trilobitomorpha

Animalia

Deuterostomia

Echinodermata

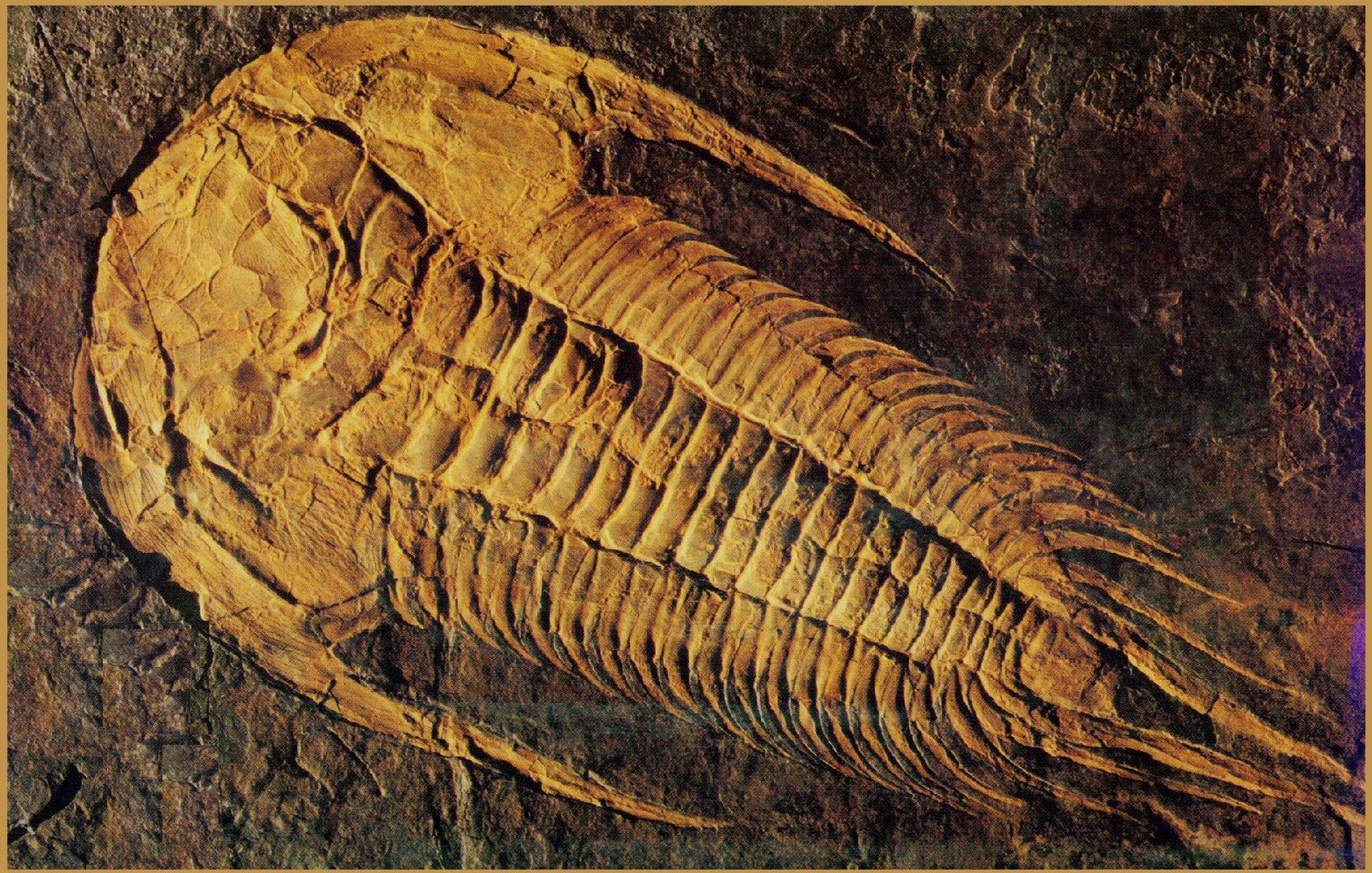
?

Agnatha

Plantae

Gnathostomata

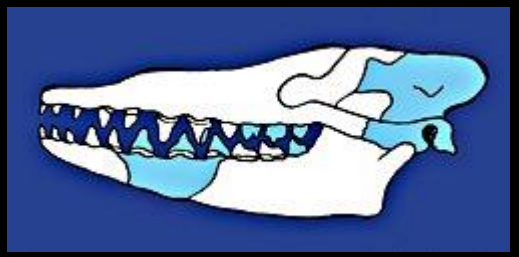
Plantae



ACKNOWLEDGMENTS

- Videos for mitochondria, microtubules, vesicle and DNA are taken from “Voyage Inside the Cell” by Sardet, Larsonneur and Koch (Digital Studio)
- Video for Synthase is from W. Junge, Bereiter-Hahn and IWF
- Video for Clathrin from Allison Bruce
- Video for ribbon Kinase model is from Max-Planck Unit for Structural Molecular Biology, Hamburg
- Video for space-filling Kinesin is from Molecular Biology of the Cell
- Video for dividing cell from Molecular Biology of the Cell
- Some trilobite pictures from Trilobites by Riccardo Levi-Setti
- Several illustrations taken from Molecular Cell Biology
- Drosophila photos from Flybase and Thomas Kaufman and Rudolf Turner, Department of Biology, Indiana University
- Video on cell functions from Howard Hughes Medical Institute via Harvard University

Whale evolution



- Mesonychid: Robert Carroll - "[i]t is not possible to identify a sequence of mesonychids leading directly to whales," This statement understate the problem.[10] It is not even possible to identify a single ancestral species. All known mesonychids are excluded from the actual chain of descent by the paleontologists' own criteria.
- Pachycetus: Gingerich - 'In time and in its morphology, *Pakicetus* is perfectly intermediate, a missing link between earlier land mammals and later, full-fledged whales.'
- de Muizon - 'All the postcranial bones indicate that pakicetids were land mammals, and … indicate that the animals were runners, with only their feet touching the ground.'

- Robert L. Carroll, *Patterns and Processes of Vertebrate Evolution* (Cambridge: University Press, 1997), 329.
- Gingerich, P.D., The whales of Tethys, *Natural History*, p. 86, April 1994.
- de Muizon, C., Walking with whales, *Nature* **413**(6853):259–260, 20 Sep. 2001.

RICHARD DAWKINS ON "DESIGNED"

- "Its terribly terribly tempting to use the word designed, time and again I have to bite my tongue, and stop myself. [...] when talking to other biologists, we none of us bother to bite our tongues, we just use the word designed."

- Richard Dawkins, *Waking up in the Universe,* 1991 Royal Institution Christmas Lecture; 2nd lecture - *Designed and designoid objects*.

RICHARD DAWKINS ON “JUNK DNA”

- Before ENCODE: “Pseudogenes are genes that once did something useful but have now been sidelined and are never transcribed or translated. They might as well not exist, as far as the animal's welfare is concerned. But as far as the scientist is concerned they very much exist, and they are exactly what we need for an evolutionary clock. .. . . What pseudogenes are useful for is embarrassing creationists. It stretches even their creative ingenuity to make up a convincing reason why an intelligent designer should have created a pseudogene --a gene that does absolutely nothing and gives every appearance of being a superannuated version of a gene that used to do something, unless he was deliberately setting out to fool us."
  Dawkins then continues: "Leaving pseudogenes aside, it is a remarkable fact that the greater part (95 percent in the case of humans) of the genome might as well not be there, for all the difference it makes." The Greatest Show on Earth, 2009, pp 332-333.
- After ENCODE: "I know there are some creationists who have jumped on it because they think it is awkward for Darwinism. Quite the contrary, of course. It is exactly what a Darwinist would hope for -- is to find usefulness in the living world."

"PSEUDOGENES ARE NOT PSEUDO ANY MORE

- "The study of functional pseudogenes is just at the beginning. There remain many questions to be addressed, such as the regulatory elements controlling the cell or tissue specific expression of pseudogenes. But, definitely, the so-called pseudogenes **are really functional, not to be considered any more as just "junk" or "fossil" DNA**. Surely, many functional pseudogenes and novel regulatory mechanisms remain to be discovered and explored in diverse organisms."

- Wen et al, RNA Biology 9:27-32. Jan 2012

LEVINTHAL PARADOX OF THE INTERACTOME

- Anyone who has studied the protein folding problem will have met the famous Levinthal paradox, formulated in 1969 by the molecular biologist Cyrus Levinthal. Put simply, the Levinthal paradox states that when one calculates the number of possible topological (rotational) configurations for the amino acids in even a small (say, 100 residue) unfolded protein, random search could never find the final folded conformation of that same protein during the lifetime of the physical universe. Therefore, concluded Levinthal, given that proteins obviously *do* fold, they are doing so, not by random search, but by following favored pathways. The challenge of the protein folding problem is to learn what those pathways are. That's the classical version of the paradox.
- **But now consider the origin of an entire cell.** All cells possess what has been called an "interactome," namely, "a complex network" comprising "a host of cellular constituents" -- proteins, nucleic acids, lipids, metal ion cofactors, and so on. If the Levinthal paradox (old version) arises from the difficulty of searching the space of possible configurations for a single protein, the new version of the paradox, formulated by Tompa and Rose, asks the same question for the possible arrangements of the cell's interactome, an enormously larger collection of objects with a correspondingly greater search space. As Tompa and Rose express the problem,

- Tompa, P. and G.D. Rose. Levinthal paradox of the interactome," *Protein Science* 20 (2011):2074-79

LEVINTHAL PARADOX OF THE INTERACTOME

- “Unlike protein folding, self-assembly of the interactome has not yet prompted such widespread attention, and for understandable reasons. It is a problem of bewildering complexity…Where does one begin? Our goal here is to show that assembly of the interactome in biological real-time is analogous to folding in that the functional state is selected from a staggering number of useless or potentially deleterious alternatives.”

- Tompa and Rose calculate the "total number of possible distinct patterns of interactions," using yeast, a unicellular eukaryote, as their model system; this "total number" is the size of the space that must be searched. With approximately 4,500 proteins in yeast, the interactome search space "is on the order of 10^7200, an unimaginably large number," they write -- but "more realistic" estimates, they continue, are "yet more complicated." Proteins present many possible surfaces for chemical interaction. "In all," argue Tompa and Rose, "an average protein would have approximately 3540 distinguishable interfaces," and if one uses this number for the interactome space calculation, the result is 10 followed by the exponent 7.9 x 10^10.

LEVINTHAL PARADOX OF THE INTERACTOME

- Tompa and Rose draw a number of lessons from their calculations. They argue, first, that any increase in biological realism will only make the Levinthal interactome paradox worse:
- “Of course, there are additional complicating factors such as alternative splicing, post-translational modifications, non-pairwise macromolecular interactions, incorrect complex formation that is adventitiously stable, and so forth. However, even neglecting such complications, the numbers preclude formation of a functional interactome by trial and error complex formation within any meaningful span of time. This numerical exercise…is tantamount to a proof that the cell does not organize by random collisions of its interacting constituents.”
- But secondly, what they call "the most profound conclusion" from their analysis bears directly on widely held assumptions about the origin of life.
- A highly enriched soup of proteins and nucleic acids will never form a functional cell, even if lipid bilayer membranes were provided to help these materials become organized.

LEVINTHAL PARADOX OF THE INTERACTOME

- Indeed, the fully functional contents of a living cell, once the wall or membrane enclosing them has been breached (thus, killing the cell), move irreversibly in the direction of non-living chemistry. It enters what Tompa and Rose call the "zone of chaos," never to return.

- Tompa and Rose have sketched the theoretical basis for *why* this happens:
- "[O]ur calculations of combinatorial complexity [show] that the emergent interactome could not have self-organized spontaneously from its isolated protein components. Rather, it attains its functional state by templating the interactome of a mother cell and maintains that state by a continuous expenditure of energy. In the absence of a prior framework of existing interactions, it is far more likely that combined cellular constituents would end up in a non-functional, aggregated state, one incompatible with life…The spontaneous origination of a *de novo* cell has yet to be observed; all extant cells are generated by the division of pre-existing cells that provide the necessary template for perpetuation of the interactome."

PROTHERO ON STASIS

- The first major discovery was that stasis was much more prevalent in the fossil record than had been previously supposed. Many paleontologists came forward and pointed out that the geological literature was one vast monument to stasis, with relatively few cases where anyone had observed gradual evolution. If species didn't appear suddenly in the fossil record and remain relatively unchanged, then biostratigraphy would never work—and yet almost two centuries of successful biostratigraphic correlations was evidence of just this kind of pattern. As Gould put it, it was the "dirty little secret" hidden in the paleontological closet. Most paleontologists were trained to focus on gradual evolution as the only pattern of interest, and ignored stasis as "not evolutionary change" and therefore uninteresting, to be overlooked or minimized. Once Eldredge and Gould had pointed out that stasis was equally important ("stasis is data[sic]" in Gould's words), paleontologists all over the world saw that stasis was the general pattern, and that gradualism was rare—and that is still the consensus 40 years later.

PROTHERO ON STASIS

- In my dissertation on the incredibly abundant and well preserved fossil mammals of the Big Badlands of the High Plains, I had over 160 well-dated, well-sampled lineages of mammals, so I could evaluate the relative frequency of gradualism versus stasis in an entire regional fauna. I also had a wide geographic spread [...]. I had large fossil samples of many species, with dozens at each level, and excellent stratigraphic data. When I finally plunged in and plotted and analyzed my data carefully, it was clear that nearly every lineage showed stasis, with one minor example of gradual size reduction in the little oreodont *Miniochoerus*. I could point to this data set and make the case for the prevalence of stasis without any criticism of bias in my sampling. More importantly, the fossil mammals showed no sign of responding to the biggest climate change of the past 50 million years [...]. In North America, dense forests gave way to open scrublands, crocodiles and pond turtles were replaced by land tortoises, and the snails changed from those typical of Nicaragua to those of Baja California. Yet out of all the 160 lineages of mammals in this time interval, there was virtually no response.

PROTHERO ON STASIS

- After six years of work and publication, the conclusion is clear: none of the common Ice Age mammals and birds responded to any of the climate changes at La Brea in the last 35,000 years, even though the region went from dry chaparral to snowy piñon-juniper forests during the peak glacial 20,000 years ago, and then back to the modern chaparral again.
- In four of the biggest climatic-vegetational events of the last 50 million years, the mammals and birds show no noticeable change in response to changing climates. No matter how many presentations I give where I show these data, no one (including myself) has a good explanation yet for such widespread stasis despite the obvious selective pressures of changing climate. Rather than answers, we have more questions—and that's a good thing! Science advances when we discover what we don't know, or we discover that simple answers we'd been following for years no longer work.

EVOLUTIONARY RELATIONSHIPS PRIAPULIDS (GROUP OF MARINE WORMS)

- See http://www.sciencedaily.com/releases/2012/10/121009092533.htm. Excerpt: He explained: "The fossils from the Cambrian period can cause a real headache for evolutionary biologists. Instinct tells us to expect simple organisms evolving over time to become increasingly more complex. However during the Cambrian period there was an apparent explosion of different major groups of animals, all appearing simultaneously in the fossil record. We looked at priapulid worms, which were among the first ever predators. What's remarkable is that they had already evolved into a diverse array of forms -- comparable to the morphological variety of their living cousins -- when we first encounter them in the Cambrian fossil record. It's precisely this apparent explosion of anatomical diversity that vexed Darwin and famously attracted the attention of Harvard biologist Stephen Jay Gould."
- Dr Ruta, from the School of Life Sciences at the University of Lincoln, continued: "Our work has shown that despite many new fossil finds, including many from China in the last decade, the picture remains largely unchanged.

NEW FOSSILS SUGGEST ANCIENT ORIGINS OF MODERN-DAY DEEP-SEA ANIMALS

- A collection of fossil animals discovered off the coast of Florida suggests that present day deep-sea fauna like sea urchins, starfish and sea cucumbers may have evolved earlier than previously believed and survived periods of mass extinctions similar to those that wiped out the dinosaurs.
- Previously, researchers believed that these present-day animals evolved in the relatively recent past, following at least two periods of mass extinction caused by changes in their oceanic environment. The new fossil collection described in this study predates the oldest known records of the present-day fauna. "We were amazed to see that a 114 million year old deep-sea assemblage was so strikingly similar to the modern equivalents," says lead author Ben Thuy.
- According to the authors, this evidence shows that the ancestors of modern deep-sea animals have lived in these deep waters for much longer than previously thought. That this collection of fossils appears to have survived several drastic changes in oceanic climates also suggests that deep-sea biodiversity may be more resilient than shallow-water life forms, and more resistant to extinction events than previously thought.
- *Thuy B, Gale AS, Kroh A, Kucera M, Numberger-Thuy LD, et al.. Ancient Origin of the Modern Deep-Sea Fauna. PLoS ONE, 2012 DOI: 10.1371/journal.pone.0046913*