F1190 Úvod do biofyziky

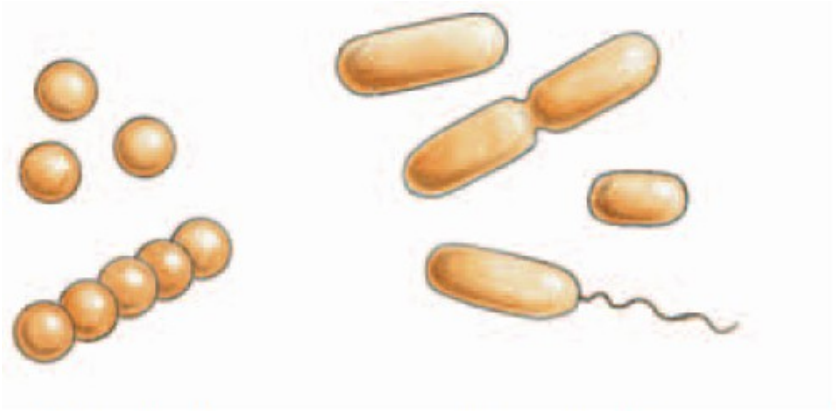
Podzimní semestr 2024

Doc. Mgr. Karel Kubíček, Ph.D., Ústav fyziky kondenzovaných látek, CEITEC MU, karelk@mail.muni.cz, +420 549 49 3253

Buňky

1) Rozdělení
2) Uchování informace a její čtení buňkou
3) Zobrazování buněk
4) Cytoskeleton
5) Ribozom
6) Nukleozom
7) Spliceosom
8) Buněčný cyklus
9) Apoptóza
10) Rakovina

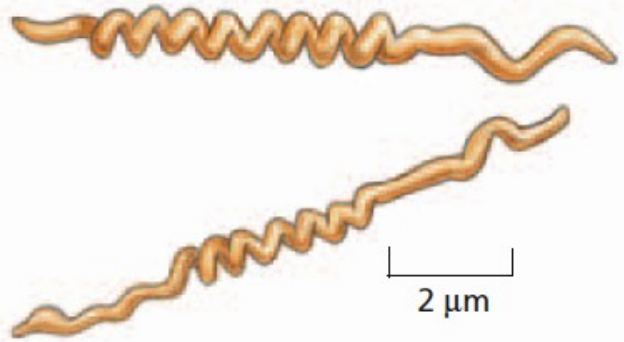
Tvary a velikosti vybraných bakterií



spherical cells
e.g., *Streptococcus*

rod-shaped cells
e.g., *Escherichia coli,*
Vibrio cholerae

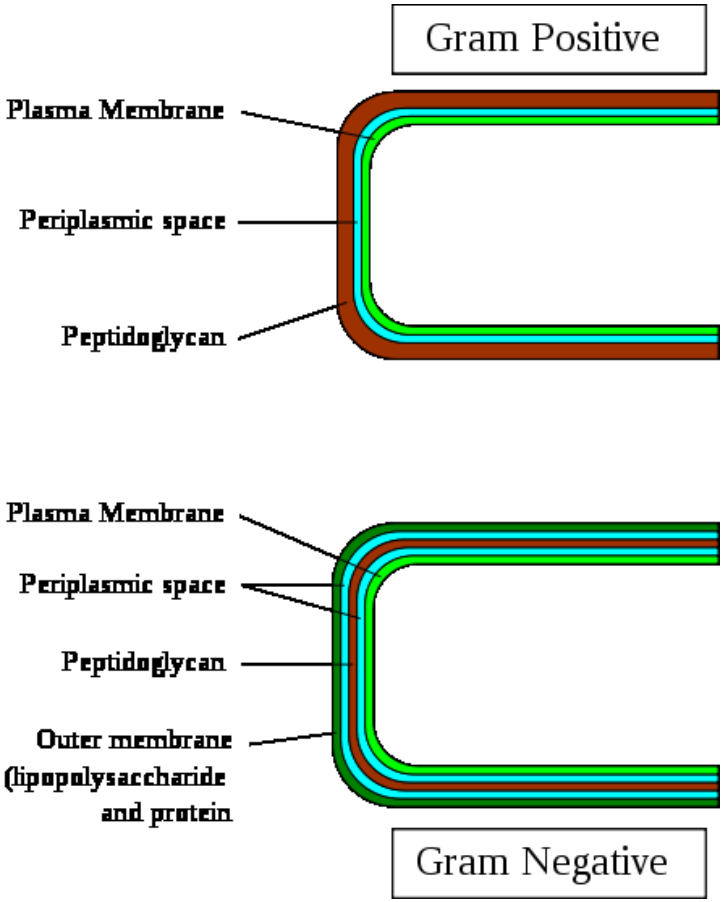
the smallest cells
e.g., *Mycoplasma,*
Spiroplasma

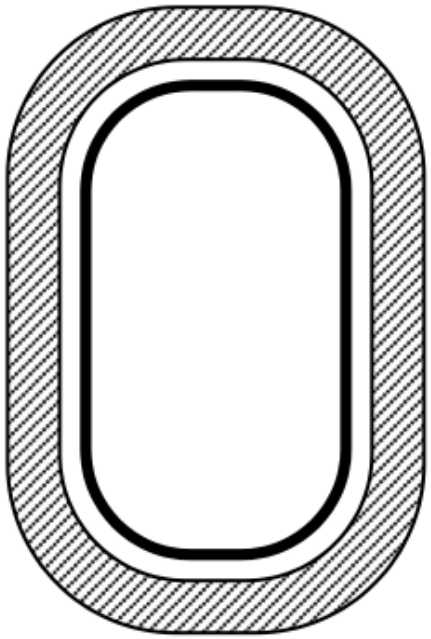


spiral cells
e.g., *Treponema pallidum*

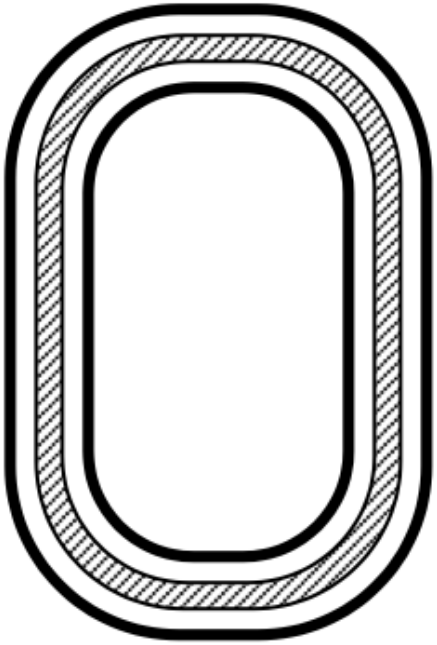
Gram-**negativní** - bakterie NEREAGUJÍ s krystalovou violetí v Gramově protokolu
Gram-**pozitivní** – bakterie, které ZŮSTANOU tmavě modré/fialové po reakci s krystalovou violetí

1) Smíchání krystalové violeti s bakteriální kulturou za horka
2) Přidání iodidu
3) Odbarvení alkoholem nebo acetonem
4) Přidání safraninu/fuchsinu





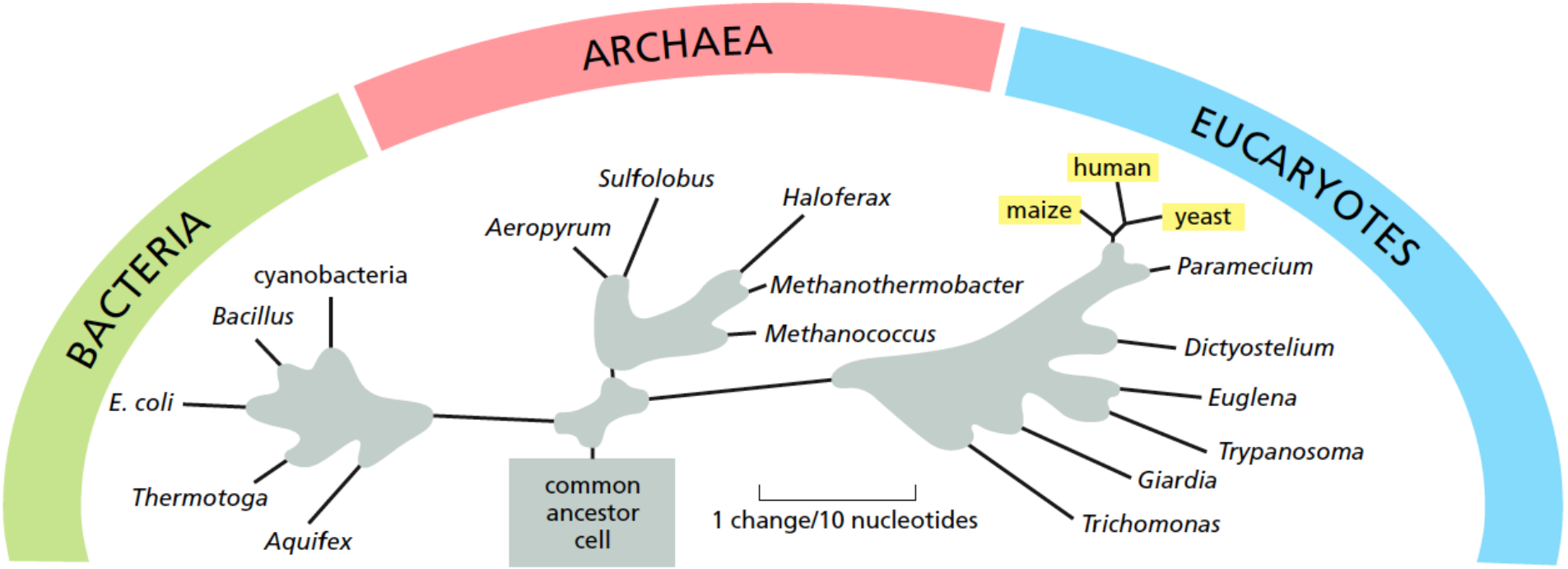
Gram - positive

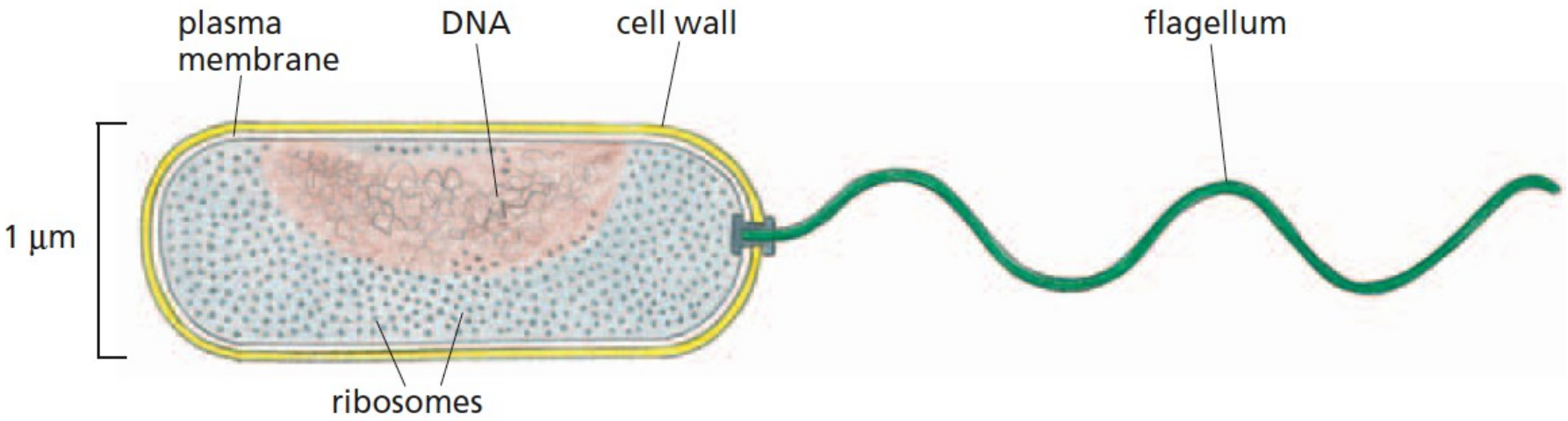


Gram - negative

Základní rozdělení živého světa

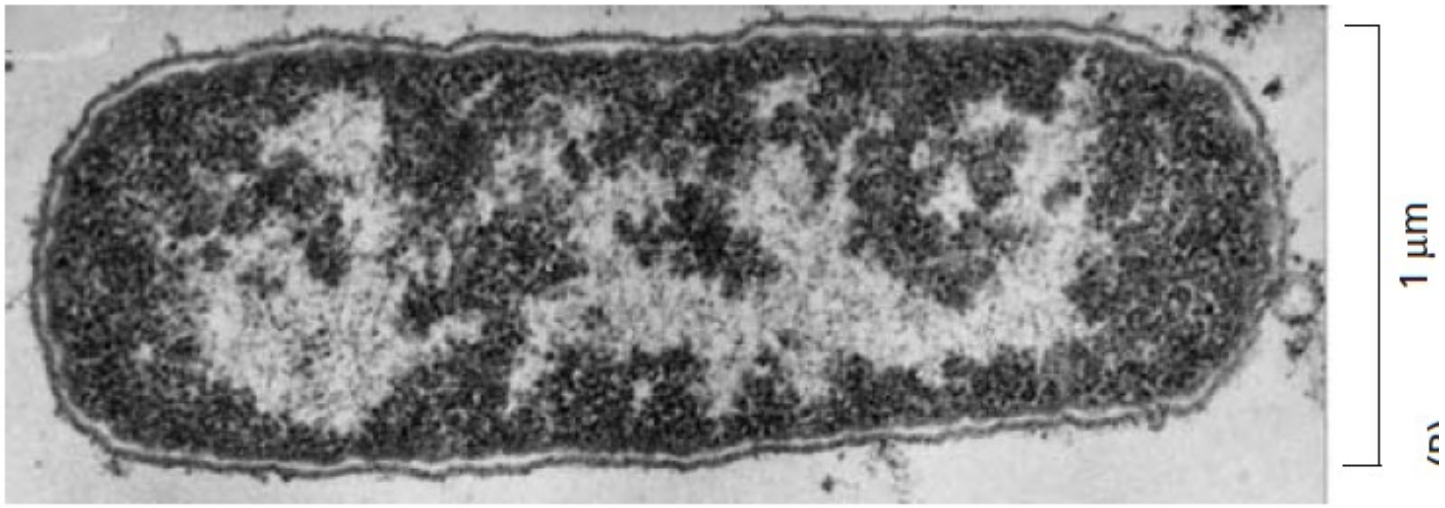
1) Prokaryoty
2) Eukaryoty



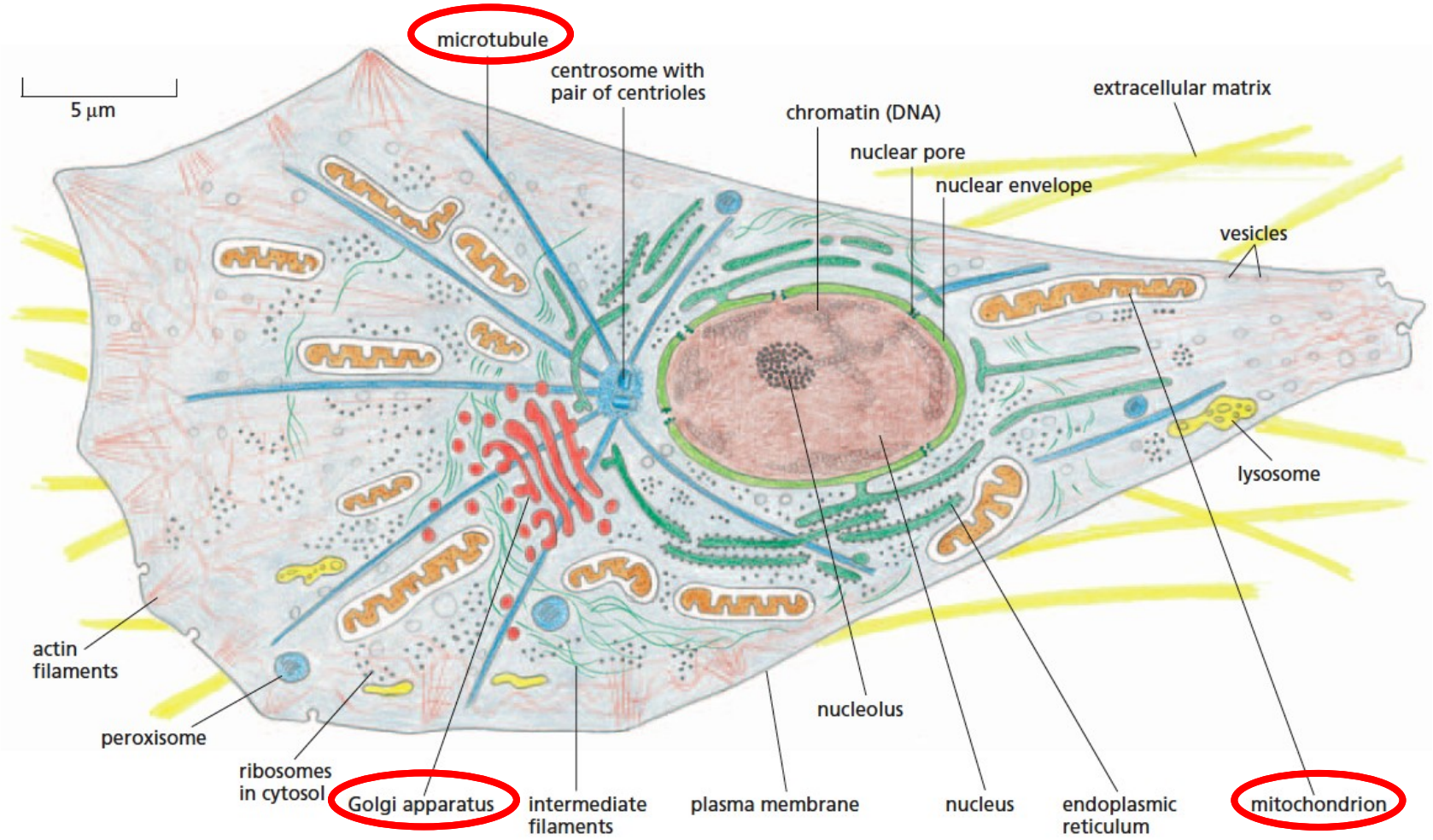


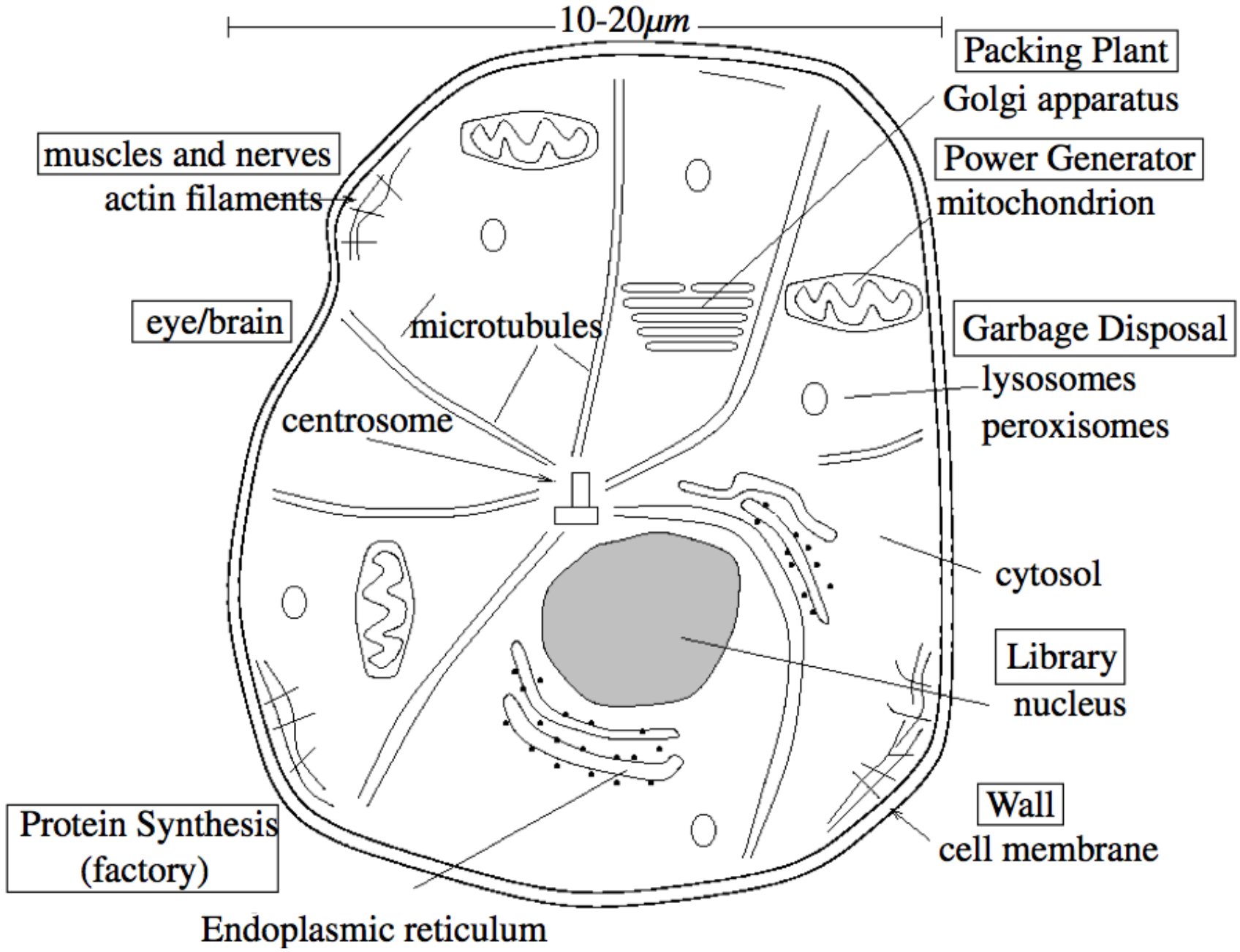
Vibrio cholerae

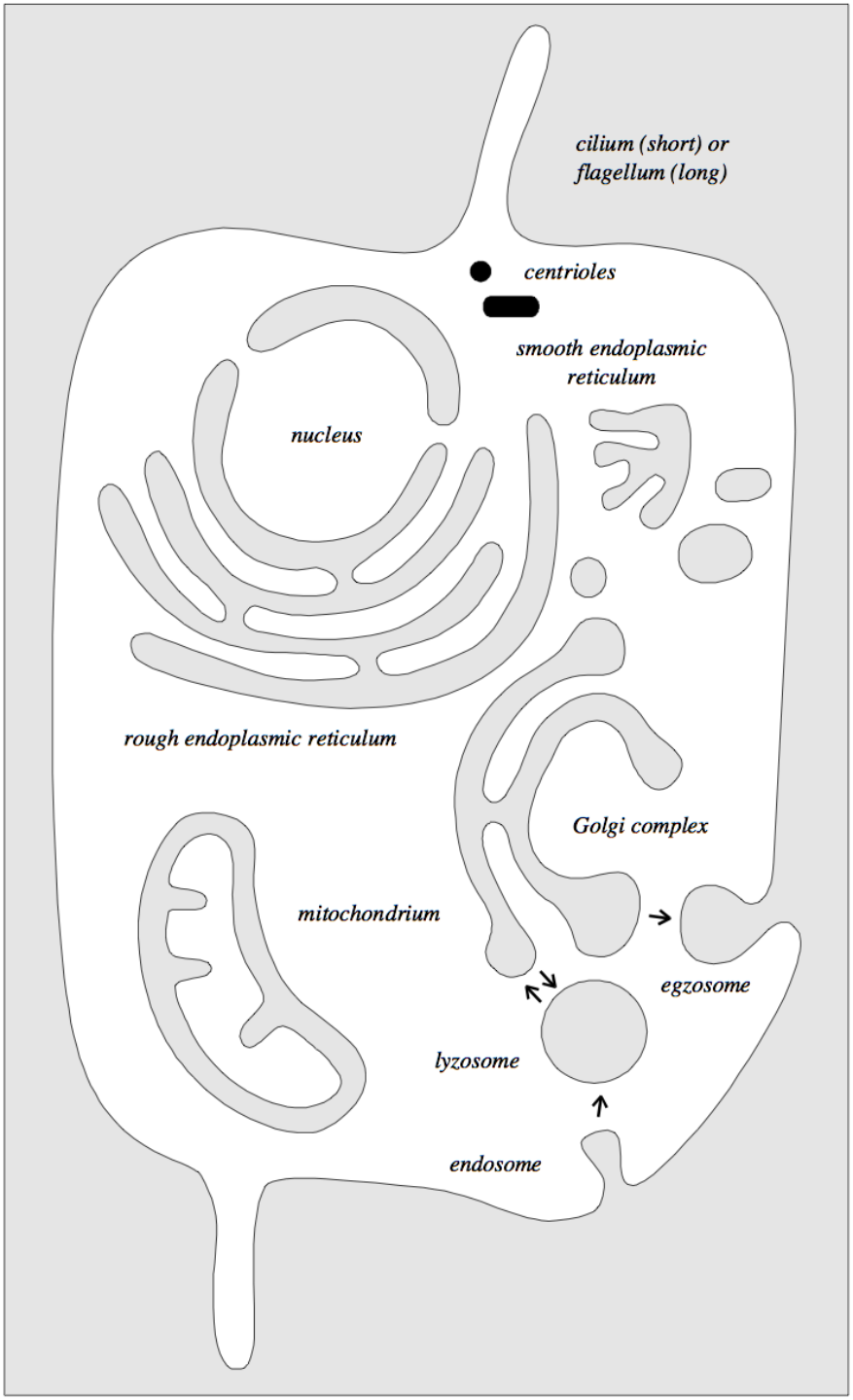
Escherischia coli (E.coli)

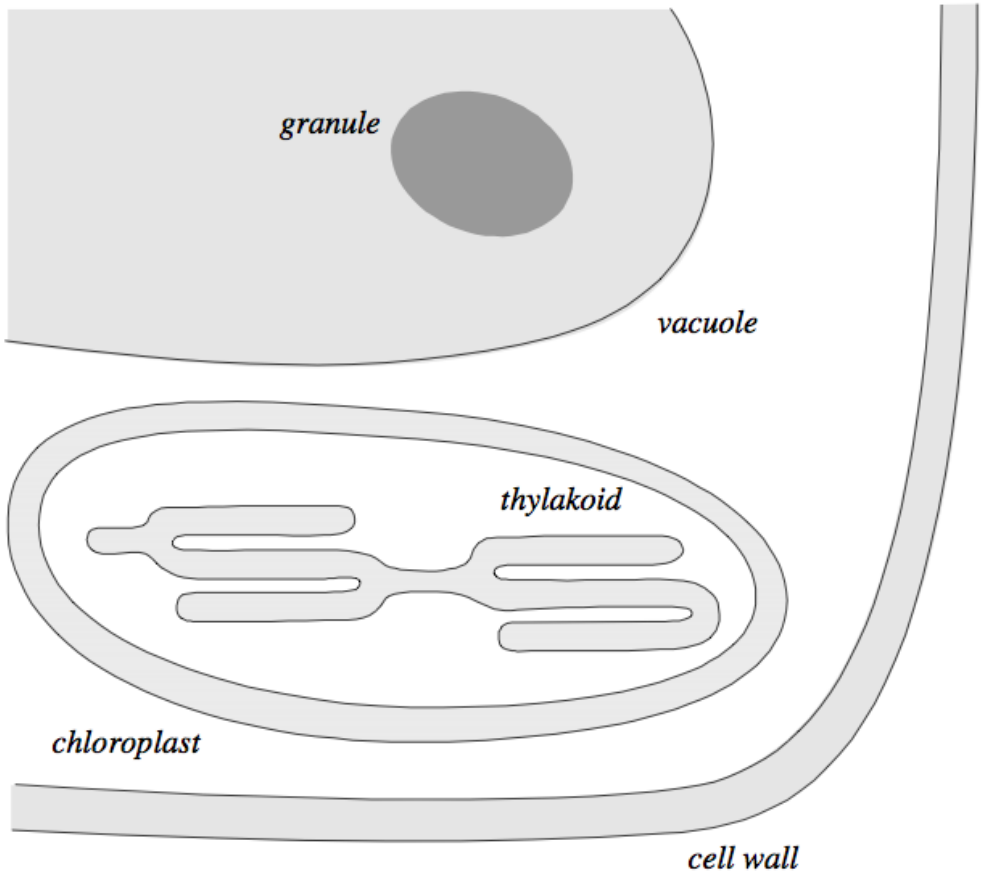


Eukaryotická buňka

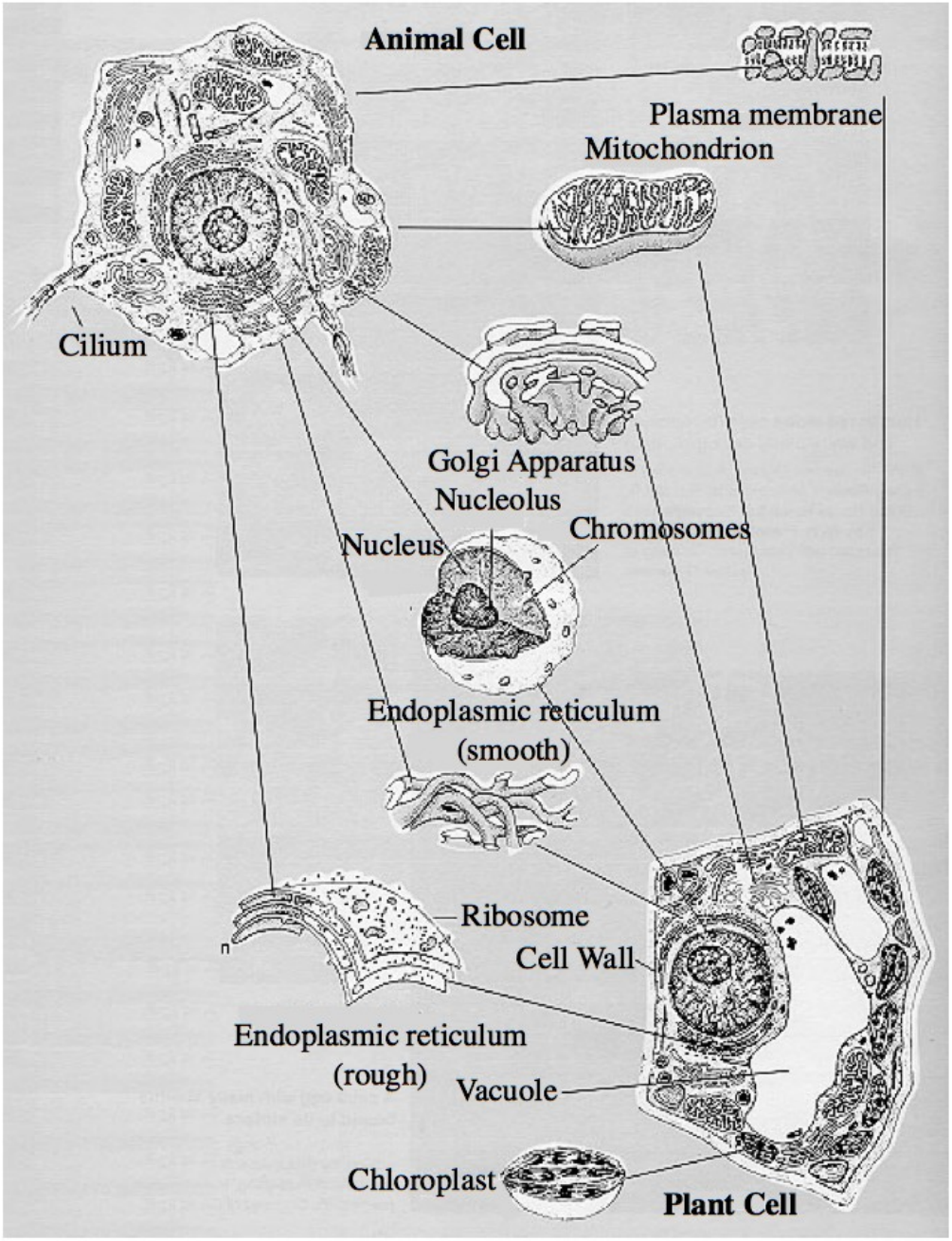



10-20μm
Packing Plant
Golgi apparatus
muscles and nerves
actin filaments
Power Generator
mitochondrion
eye/brain
microtubules
Garbage Disposal
lysosomes
peroxisomes
centrosome
cytosol
Library
nucleus
Wall
cell membrane
Protein Synthesis
(factory)
Endoplasmic reticulum





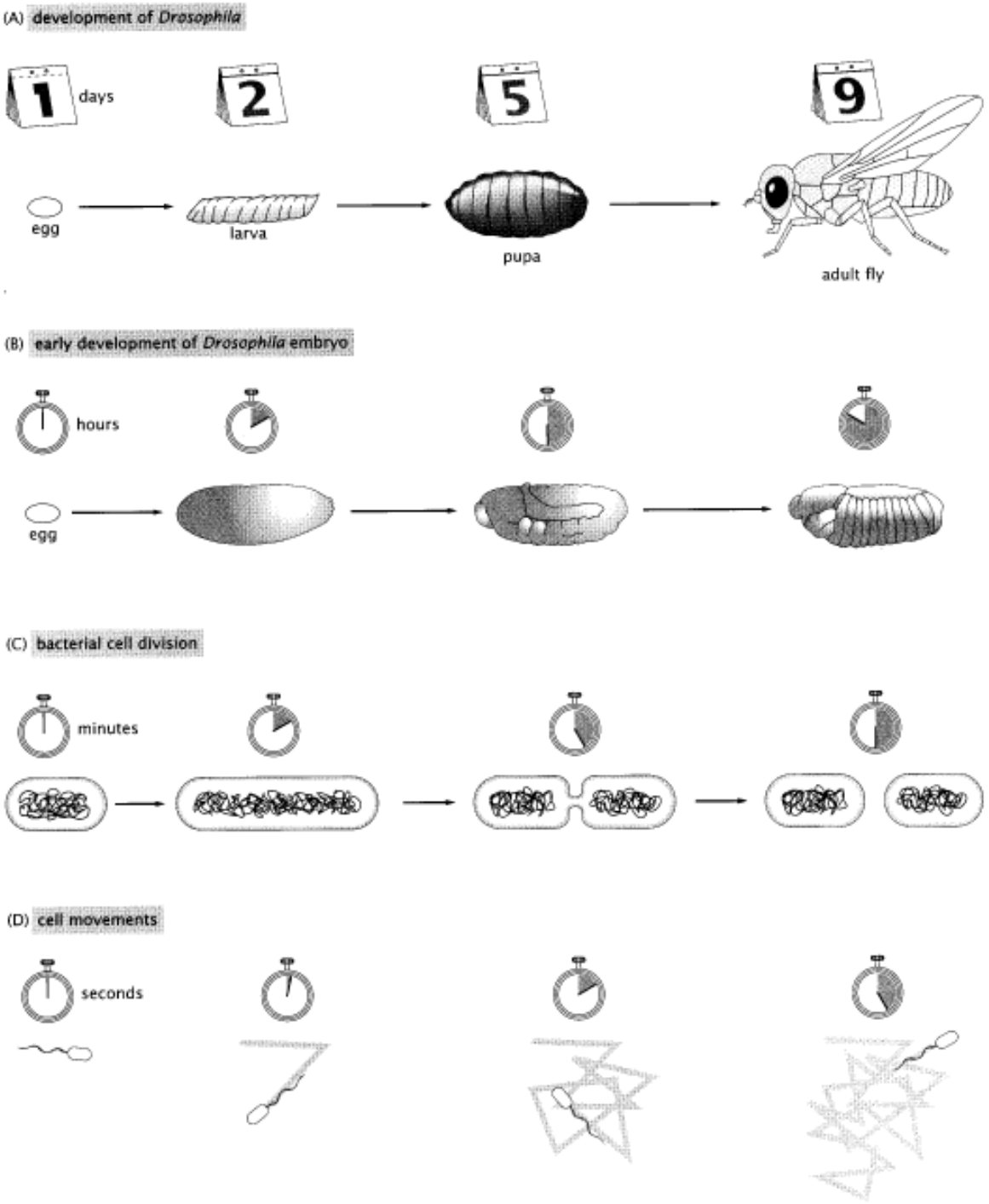
Další organely v rostlinné buňce


Animal Cell
Plasma membrane
Mitochondrion
Cilium
Golgi Apparatus
Nucleolus
Chromosomes
Nucleus
Endoplasmic reticulum
(smooth)
Ribosome
Cell Wall
Endoplasmic reticulum
(rough)
Vacuole
Chloroplast
Plant Cell

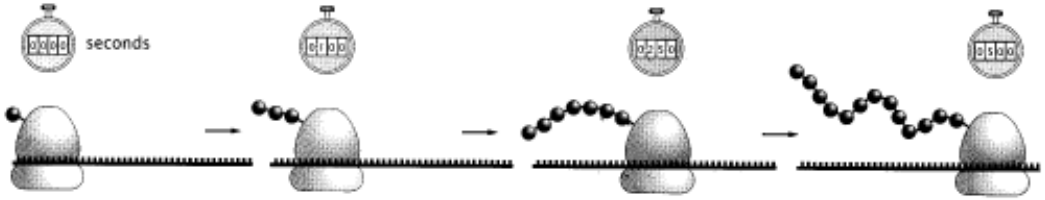
Makromolekulární konsenzus v buňce ***E. coli***

Substance	% of total dry weight	Number of molecules
Macromolecule		
Protein	55.0	2.4×10^6
RNA	20.4	
23S RNA	10.6	19,000
16S RNA	5.5	19,000
5S RNA	0.4	19,000
Transfer RNA (4S)	2.9	200,000
Messenger RNA	0.8	1,400
Phospholipid	9.1	22×10^6
Lipopolysaccharide	3.4	1.2×10^6
DNA	3.1	2
Murein	2.5	1
Glycogen	2.5	4,360
Total macromolecules	**96.1**	
Small molecules		
Metabolites, building blocks, etc.	2.9	
Inorganic ions	1.0	
Total small molecules	**3.9**	

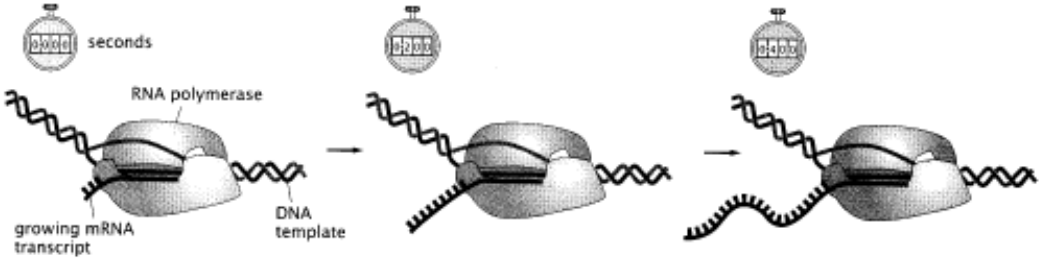
E. coli	Cell volume	$V_{E.\ coli}$	$\approx 1\,\mu m^3$
	Cell mass	$m_{E.\ coli}$	≈ 1 pg
	Cell cycle time	$t_{E.\ coli}$	≈ 3000 s
	Cell surface area	$A_{E.\ coli}$	$\approx 6\,\mu m^2$
	Genome length	$N_{bp}^{E.\ coli}$	$\approx 5 \times 10^6$ bp
	Swimming speed	$v_{E.\ coli}$	$\approx 20\,\mu m/s$
Yeast	Volume of cell	V_{yeast}	$\approx 60\,\mu m^3$
	Mass of cell	m_{yeast}	≈ 60 pg
	Diameter of cell	d_{yeast}	$\approx 5\,\mu m$
	Cell cycle time	t_{yeast}	≈ 200 min
	Genome length	N_{bp}^{yeast}	$\approx 10^7$ bp
Organelles	Diameter of nucleus	$d_{nucleus}$	$\approx 5\,\mu m$
	Length of mitochondrion	l_{mito}	$\approx 2\,\mu m$
	Diameter of transport vesicles	$d_{vesicle}$	≈ 50 nm
Water	Volume of molecule	V_{H_2O}	$\approx 10^{-2}$ nm^3
	Density of water	ρ	1 g/cm^3
	Viscosity of water	η	≈ 1 centipoise (10^{-2} g/(cm s))
	Hydrophobic embedding energy	$\approx E_{hydr}$	25 cal/(mol Å^2)
DNA	Length per base pair	l_{bp}	$\approx 1/3$ nm
	Volume per base pair	V_{bp}	≈ 1 nm^3
	Charge density	λ_{DNA}	2 e/0.34 nm
	Persistence length	ξ_P	50 nm
Amino acids and proteins	Radius of "average" protein	$r_{protein}$	≈ 2 nm
	Volume of "average" protein	$V_{protein}$	≈ 25 nm^3
	Mass of "average" amino acid	M_{aa}	≈ 100 Da
	Mass of "average" protein	$M_{protein}$	$\approx 30{,}000$ Da
	Protein concentration in cytoplasm	$c_{protein}$	≈ 300 mg/mL
	Characteristic force of protein motor	F_{motor}	≈ 5 pN
	Characteristic speed of protein motor	v_{motor}	≈ 200 nm/s
	Diffusion constant of "average" protein	$D_{protein}$	$\approx 100\,\mu m^2/s$
Lipid bilayers	Thickness of lipid bilayer	d	≈ 5 nm
	Area per molecule	A_{lipid}	$\approx \frac{1}{2}$ nm^2
	Mass of lipid molecule	m_{lipid}	≈ 800 Da


(A) development of *Drosophila*
1 days
2
5
9
egg
larva
pupa
adult fly
(B) early development of *Drosophila* embryo
hours
egg
(C) bacterial cell division
minutes
(D) cell movements
seconds

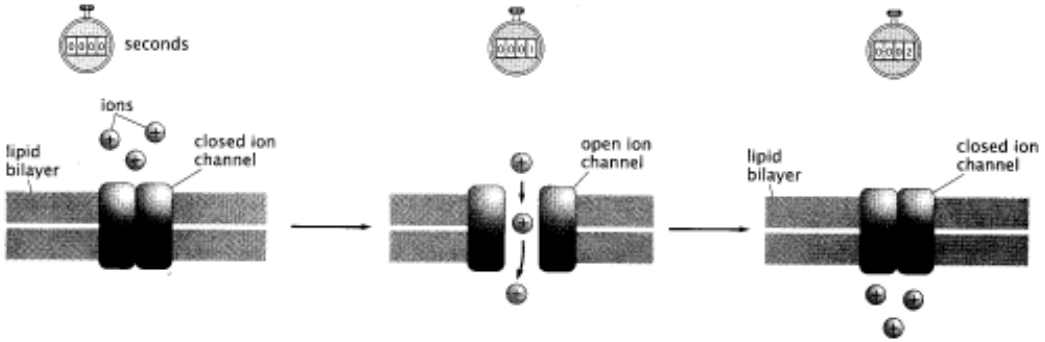
(E) protein synthesis



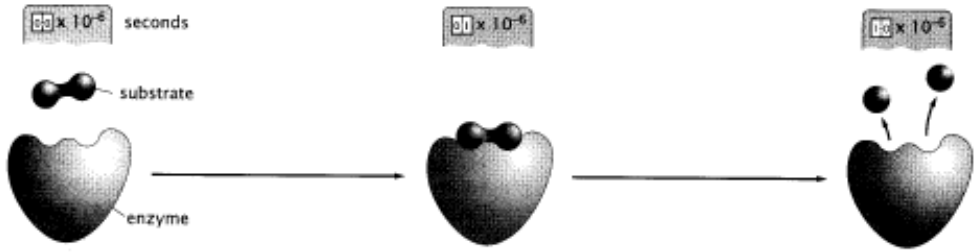
(F) transcription

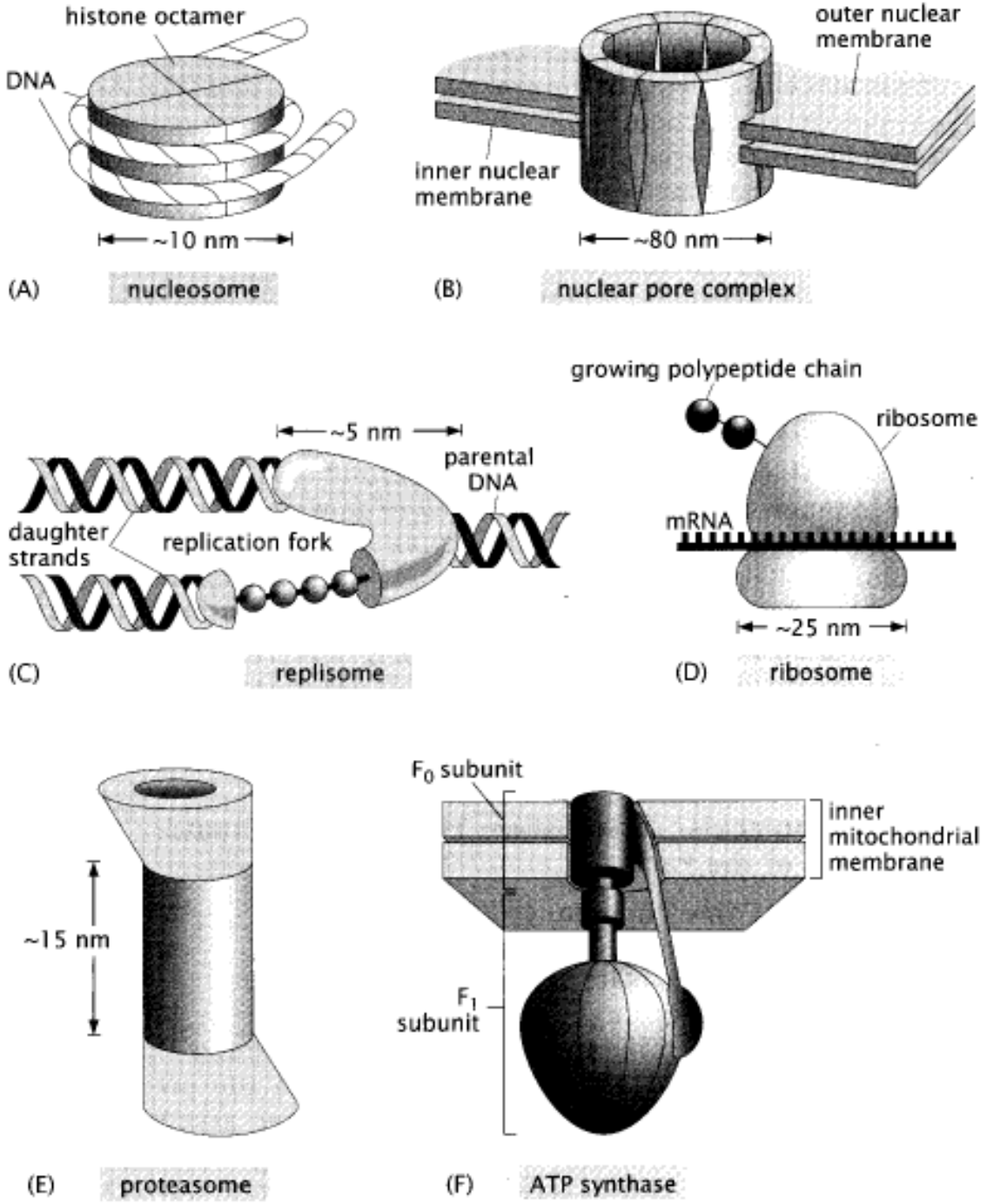


(G) gating of ion channels



(H) enzyme catalysis




histone octamer
DNA
~10 nm
(A) nucleosome
outer nuclear membrane
inner nuclear membrane
~80 nm
(B) nuclear pore complex
~5 nm
parental DNA
daughter strands
replication fork
(C) replisome
growing polypeptide chain
ribosome
mRNA
~25 nm
(D) ribosome
~15 nm
(E) proteasome
F_0 subunit
inner mitochondrial membrane
F_1 subunit
(F) ATP synthase

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View by Month

*The Clinical Trials and Epidemiology subject categories are now closed to new submissions following the completion of bioRxiv's clinical research pilot project and launch of the dedicated health sciences server medRxiv (submit.medrxiv.org). New papers that report results of Clinical Trials must now be submitted to medRxiv. Most new Epidemiology papers also should be submitted to medRxiv, but if a paper contains no health-related information, authors may choose to submit it to another bioRxiv subject category (e.g., Genetics or Microbiology).

Supported by Chan Zuckerberg Initiative

https://www.biorxiv.org/

Mosalaganti, Obarska-Kosinska, Siggel et al

Title: Artificial intelligence reveals nuclear pore complexity

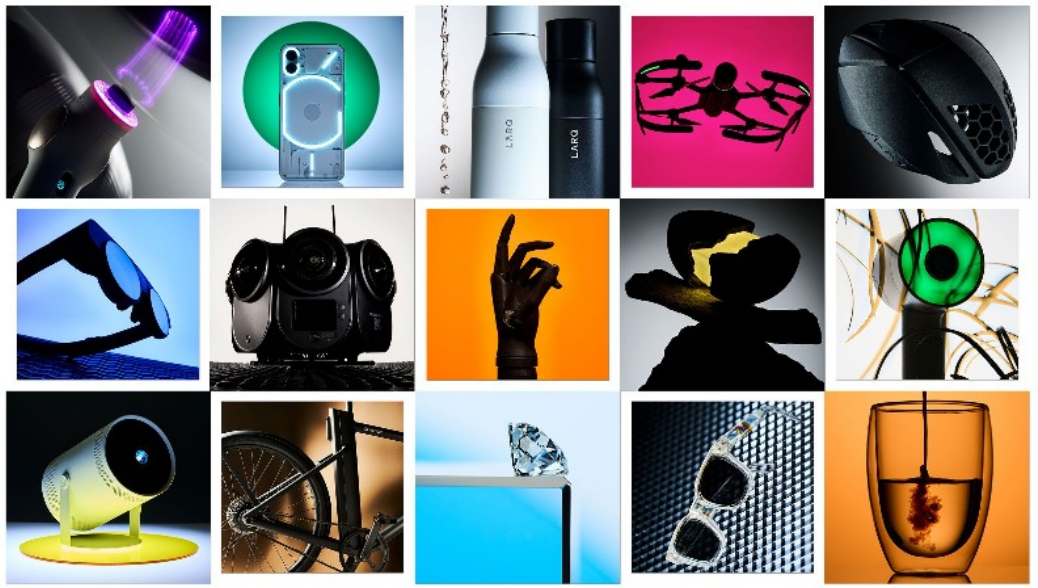
Authors:

Shyamal Mosalaganti[1,2,3†], Agnieszka Obarska-Kosinska[1,4†], Marc Siggel[4,5,6†], Beata Turonova[1,2], Christian E. Zimmerli[1,2], Katarzyna Buczak[2‡] , Florian H. Schmidt[2§], Erica Margiotta[1,2], Marie-Therese Mackmull[2¶], Wim Hagen[2], Gerhard Hummer[5,7*], Martin Beck[1,2*], Jan Kosinski[2,4,6*]

THE BEST INVENTIONS OF 2022

200 innovations changing how we live

How We Chose the List



Sergiy Barchuk for TIME

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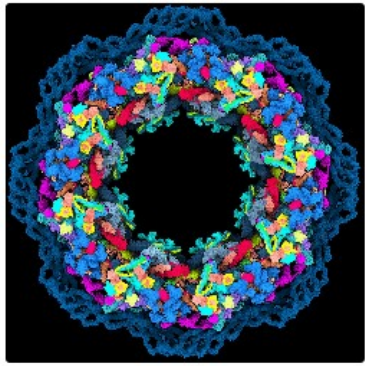
https://time.com/collection/best-inventions-2022/6229912/deepmind-alphafold/

AI



MAPPING LIFE'S BUILDING BLOCKS

DEEPMIND ALPHAFOLD

DETECTING DESTRUCTION OF WAR

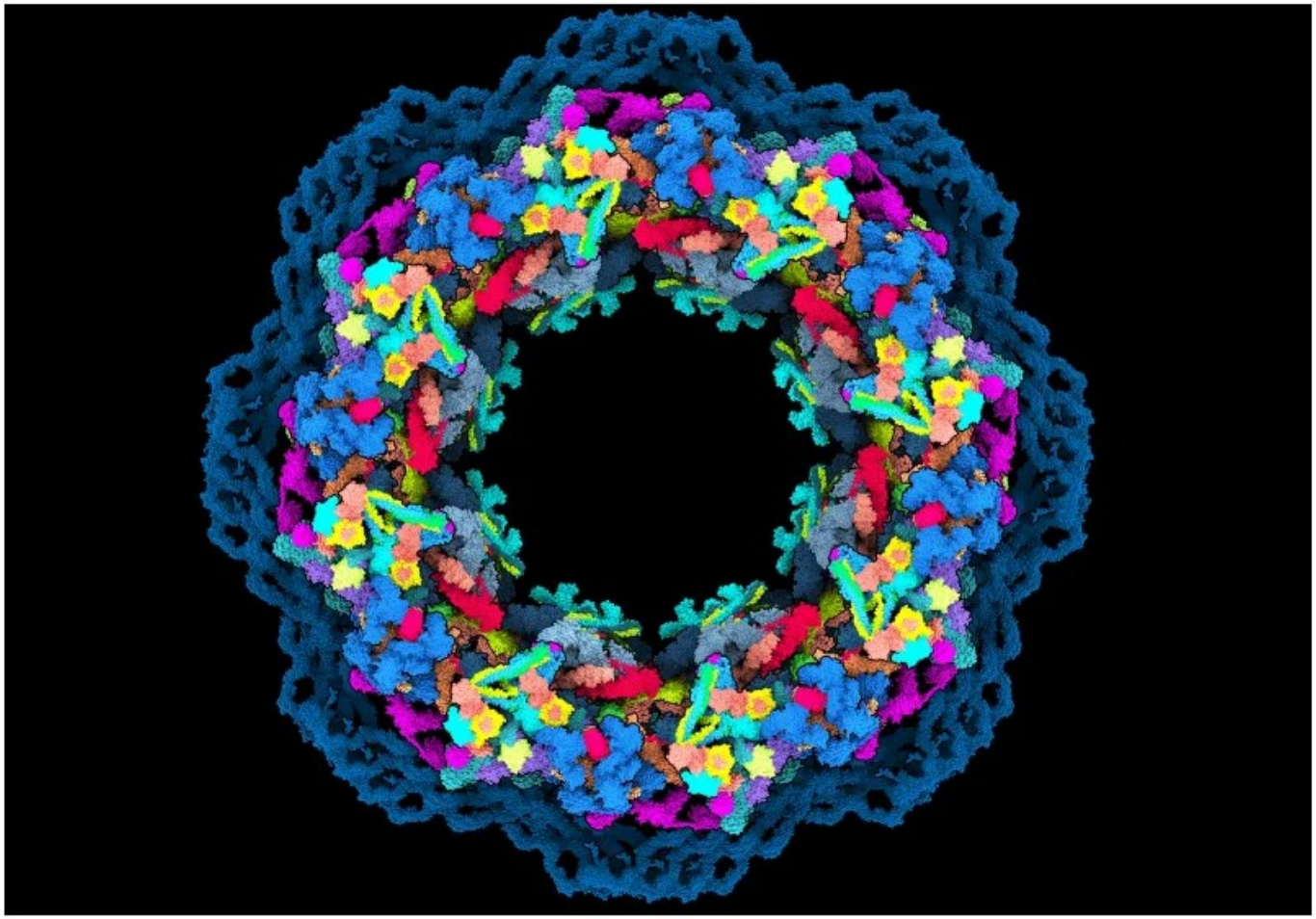
SCALE AI AUTOMATED DAMAGE IDENTIFICATION

ARTIFICIAL IMAGINATION

OPENAI DALL-E 2

Mapping Life

DeepMind AlphaFold

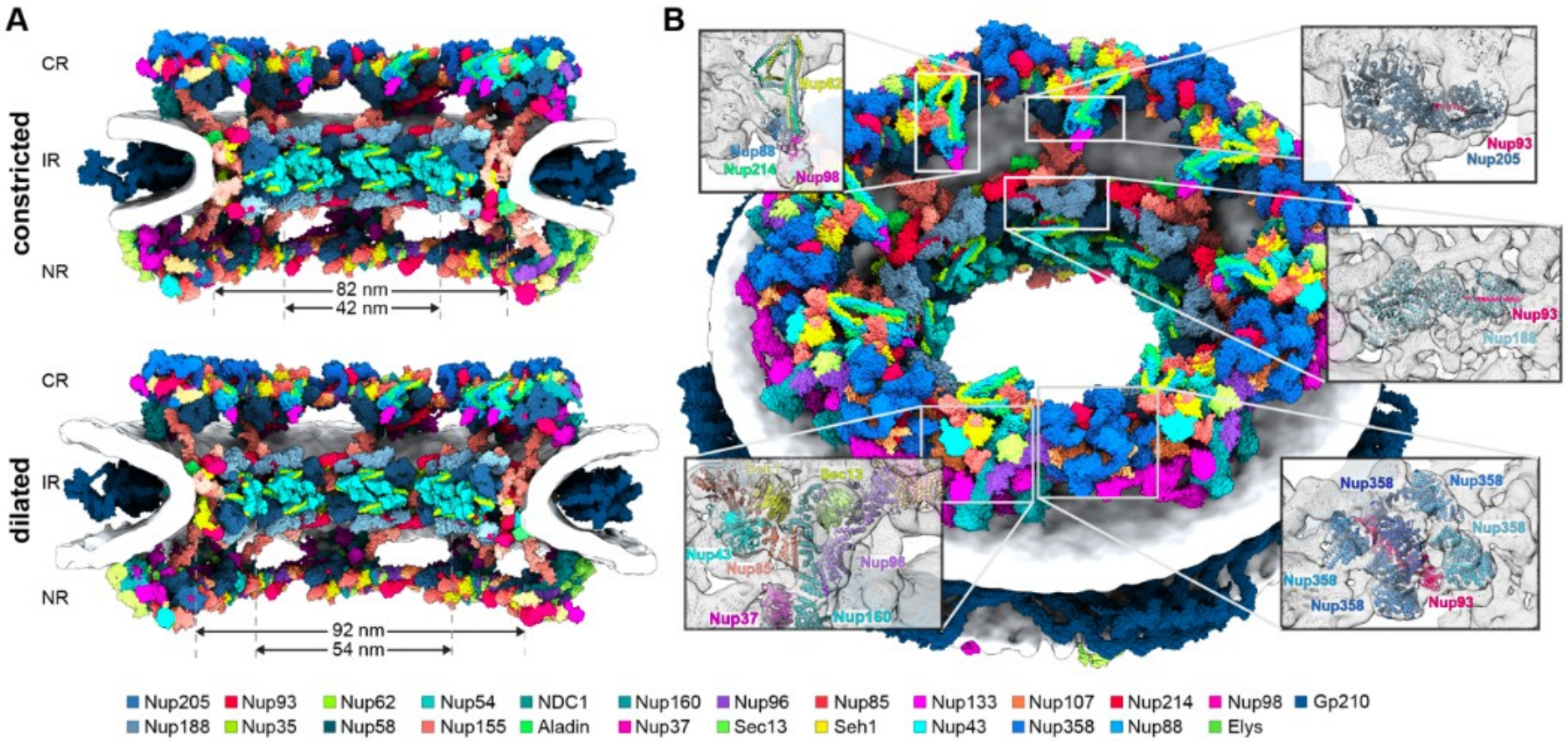


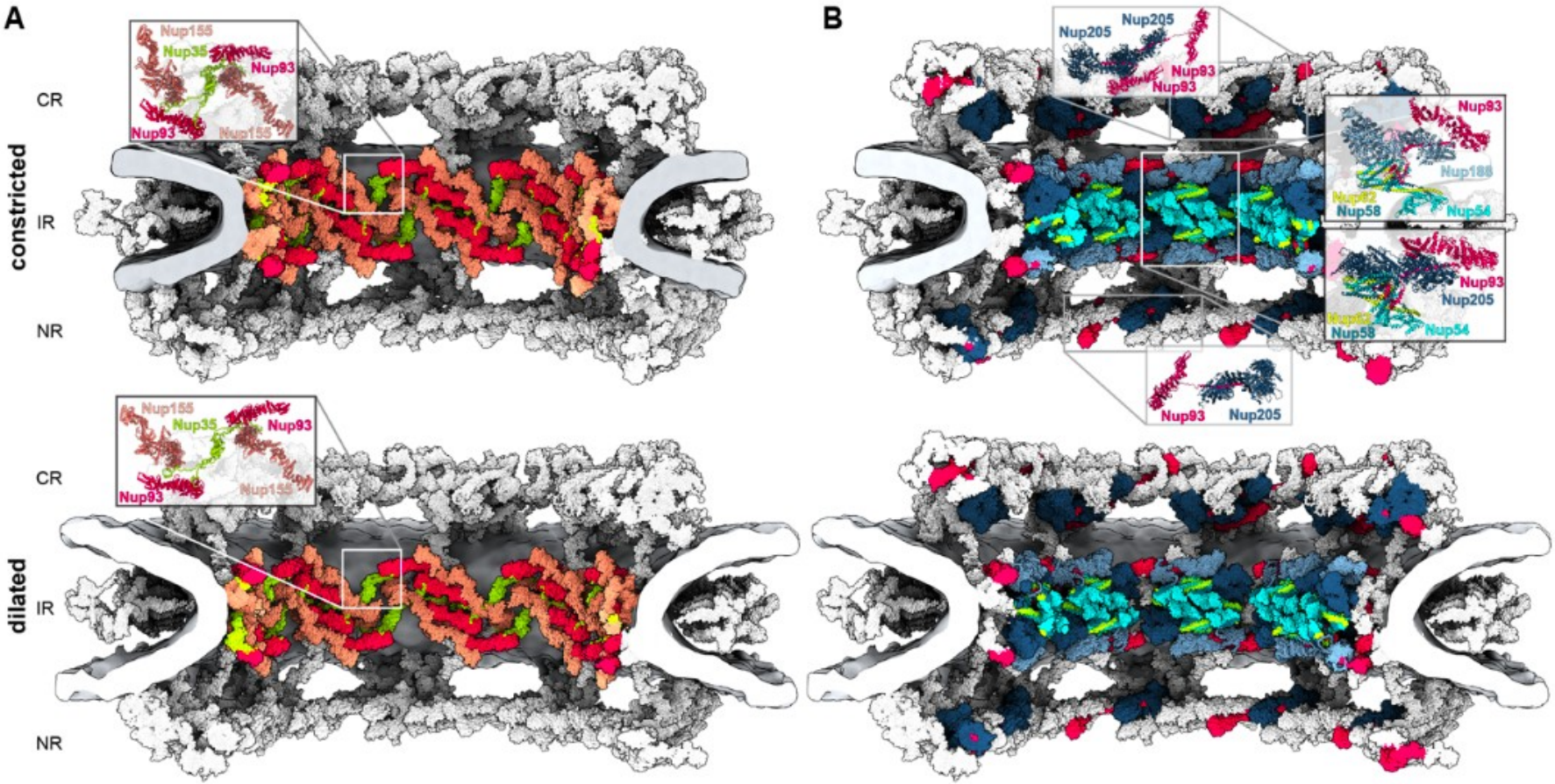
BY BILLY PERRIGO

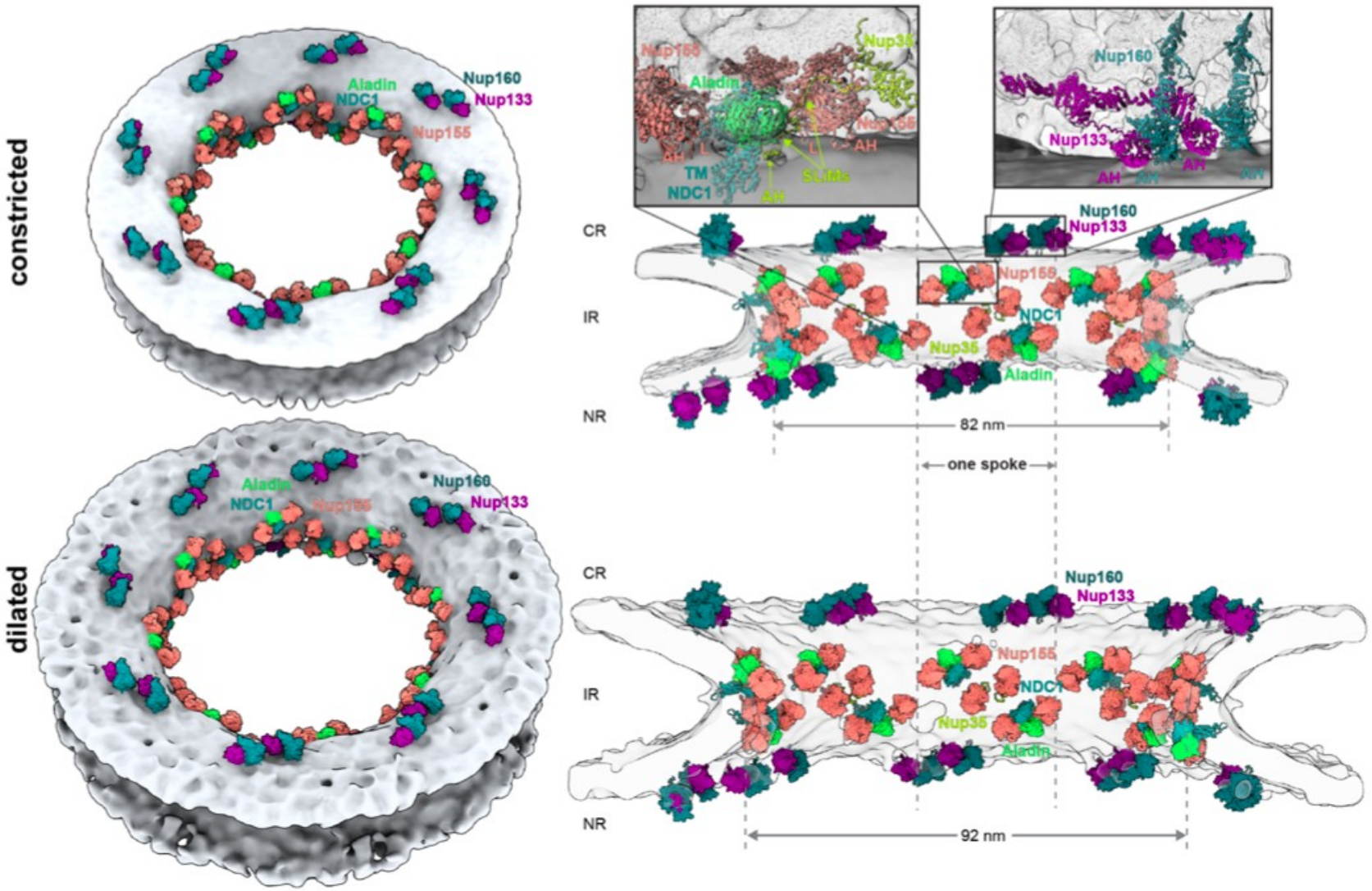
BY **BILLY PERRIGO**

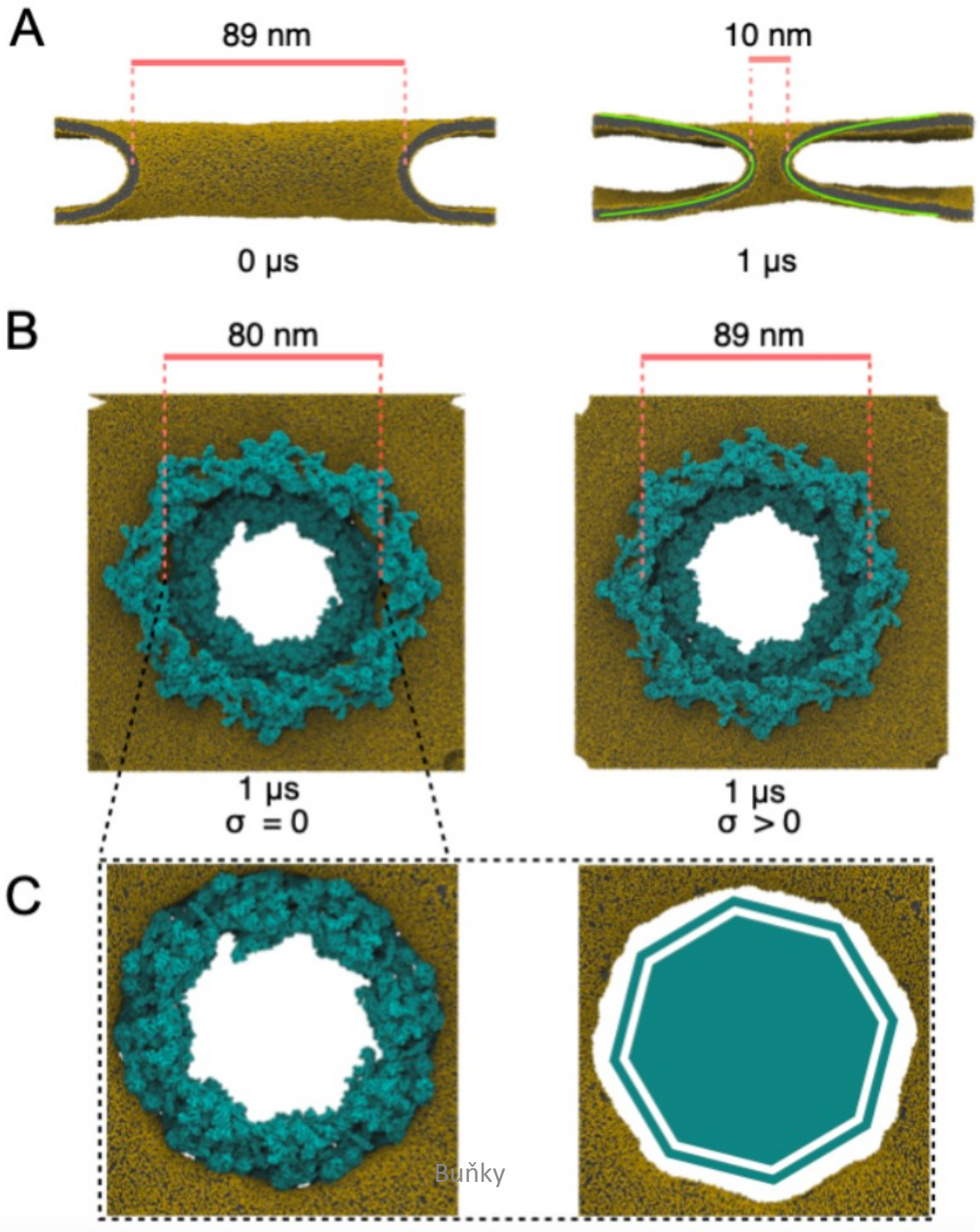
NOVEMBER 10, 2022 6:20 AM EST

In the recent past, discerning the exact 3D structure of a single protein took around five years. Today the same task is possible in seconds thanks to the machine learning program AlphaFold, developed by Alphabet subsidiary DeepMind. In July, the company announced that AlphaFold had predicted the structures of 200 million proteins—nearly all known to humankind. And in what CEO Demis Hassabis described as a "gift to humanity," DeepMind made the structures, along with AlphaFold's underlying code, freely available to all. That will likely accelerate the work of scientists around the world trying to solve humanity's toughest problems. The company says AlphaFold is now being used in efforts as diverse as fighting antibiotic resistance and Parkinson's disease, and tackling plastic pollution.


A
constricted
CR
IR
NR
82 nm
42 nm
dilated
CR
IR
NR
92 nm
54 nm
B
Nup42
Nup88
Nup214
Nup98
Nup93
Nup205
Nup93
Nup188
Sec13
Nup43
Nup85
Nup98
Nup37
Nup160
Nup358
Nup358
Nup358
Nup358
Nup358
Nup93
Nup205 Nup93 Nup62 Nup54 NDC1 Nup160 Nup96 Nup85 Nup133 Nup107 Nup214 Nup98 Gp210
Nup188 Nup35 Nup58 Nup155 Aladin Nup37 Sec13 Seh1 Nup43 Nup358 Nup88 Elys


A
B
constricted
dilated
CR
IR
NR
Nup155
Nup35
Nup93
Nup205
Nup188
Nup82
Nup58
Nup54


constricted
dilated
Aladin
NDC1
Nup160
Nup133
Nup155
Nup35
TM
SLiMs
AH
CR
IR
NR
82 nm
one spoke
92 nm


A
89 nm
10 nm
0 μs
1 μs
B
80 nm
89 nm
1 μs
σ = 0
1 μs
σ > 0
C

Karolin Luger:

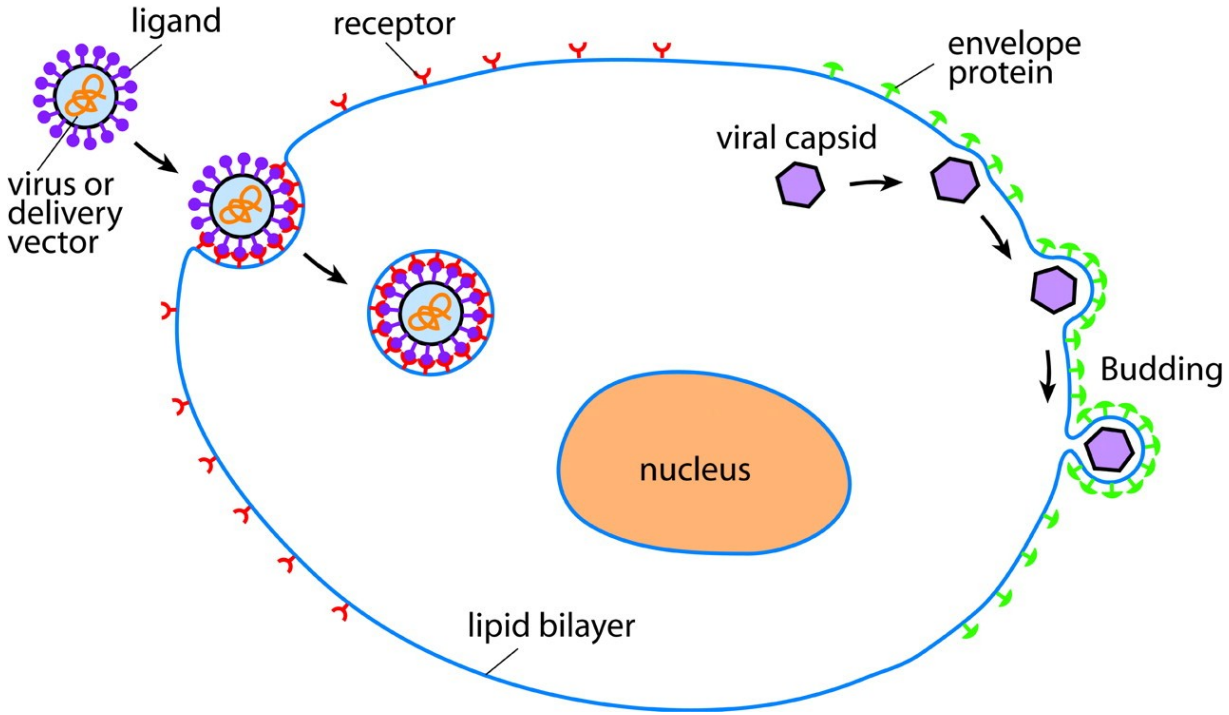
How it all began – Genome organition in humans, ancient bacteria, and giant viruses

https://www.youtube.com/watch?v=RSB9Lm3LscU

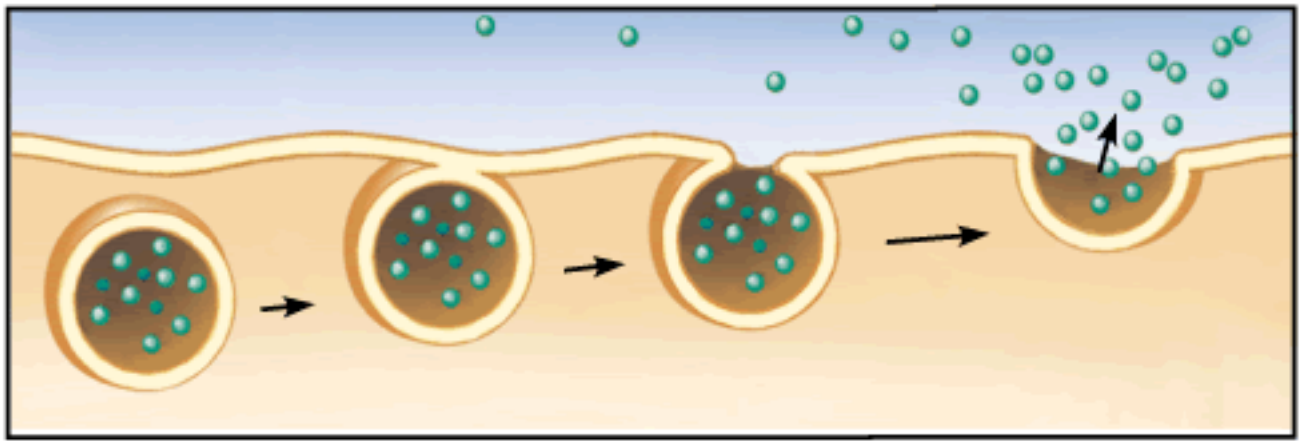
Od cca 18. minuty

ENDO-

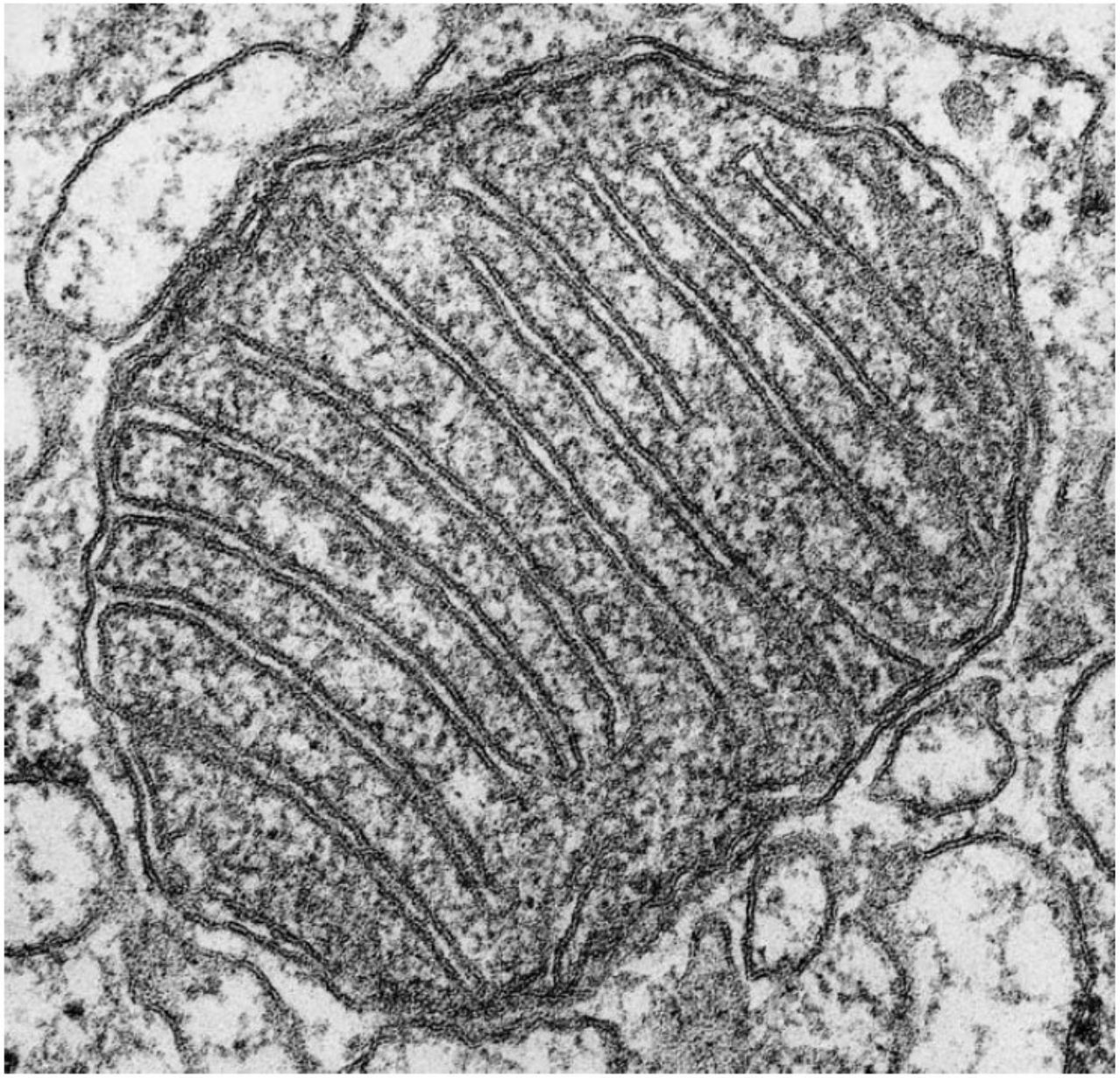
-CYTOSIS

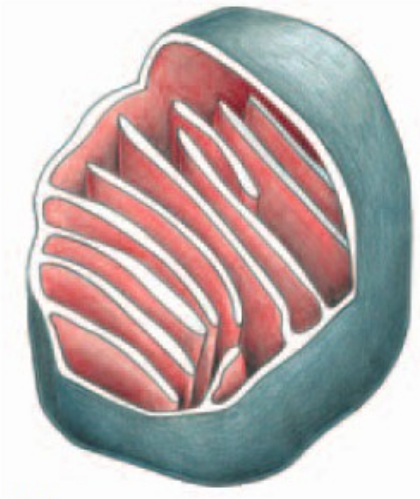


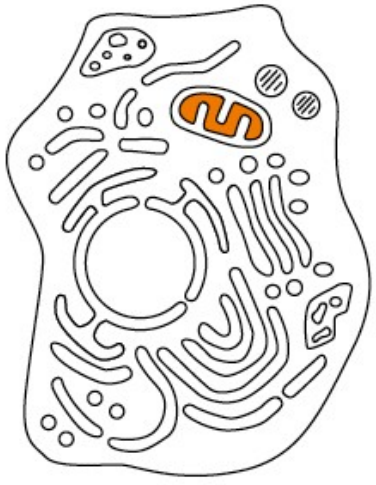
EXO-



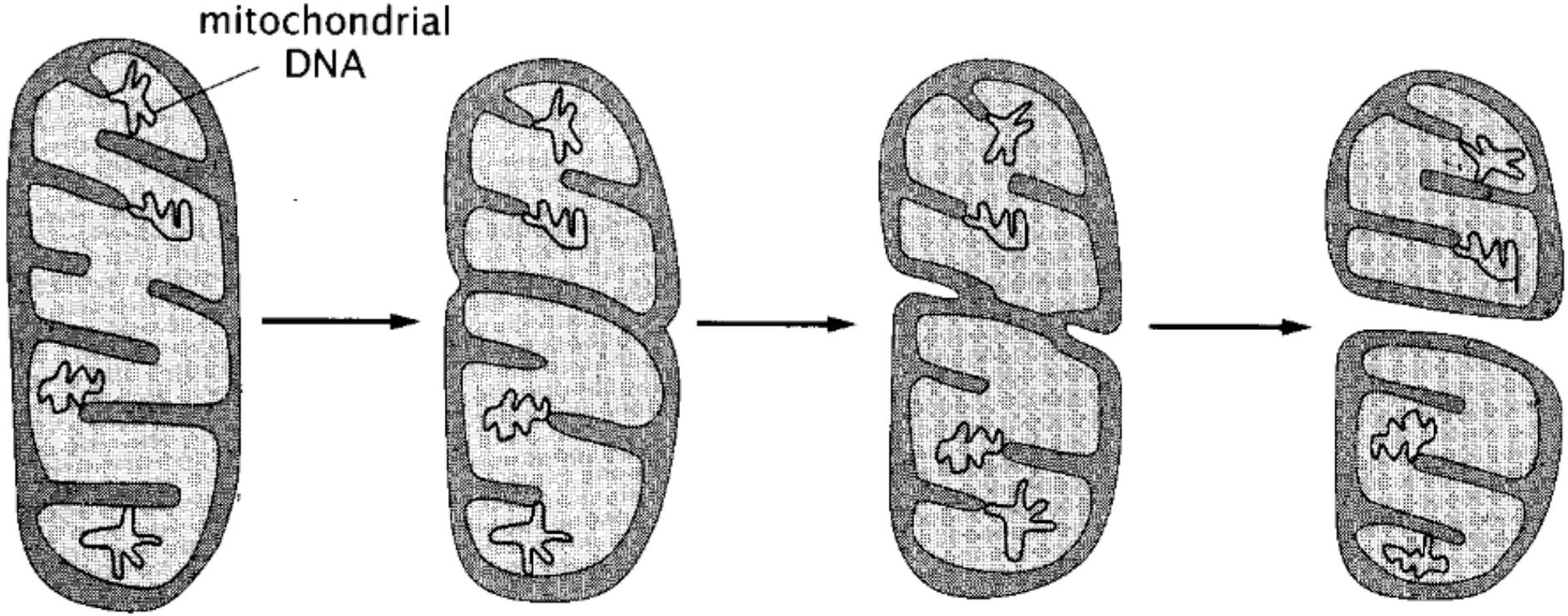
Mitochondrie







Fission – dělení mitochondrie



Vznik mitochondrie