

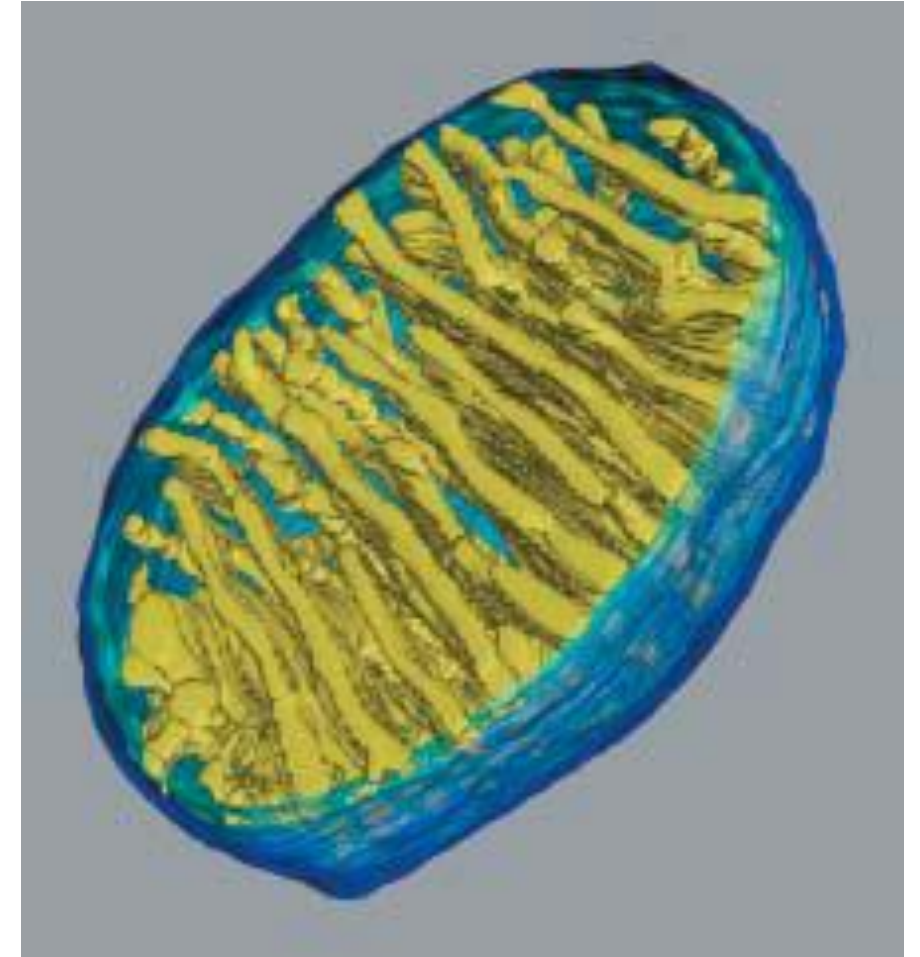
Lecture 12

Mitochondria

The opposite of ATP hydrolysis –ATP generation

Aerobic oxidation occurs in nearly all cells

In aerobic oxidation, fatty acids and sugars, principally glucose, are metabolized to carbon dioxide (CO_2) and water (H_2O), and the released energy is converted to the chemical energy of phosphoanhydride bonds in ATP



Computer-generated model of a section of a mitochondrion from chicken brain, based on a three-dimensionalelectron tomogram.

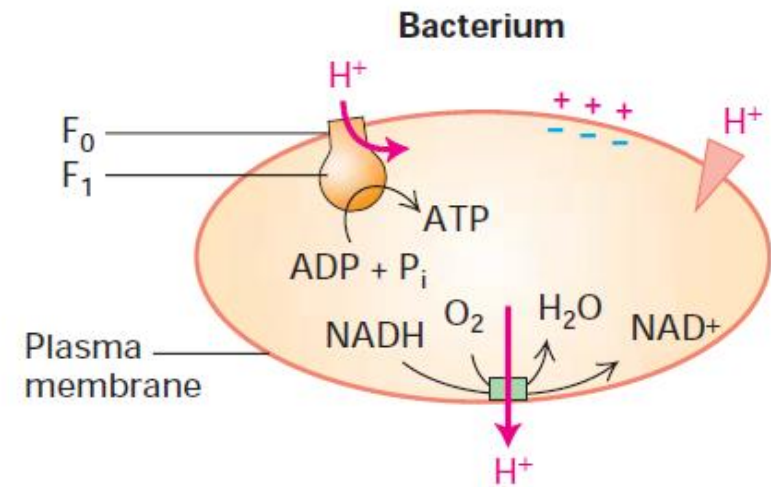
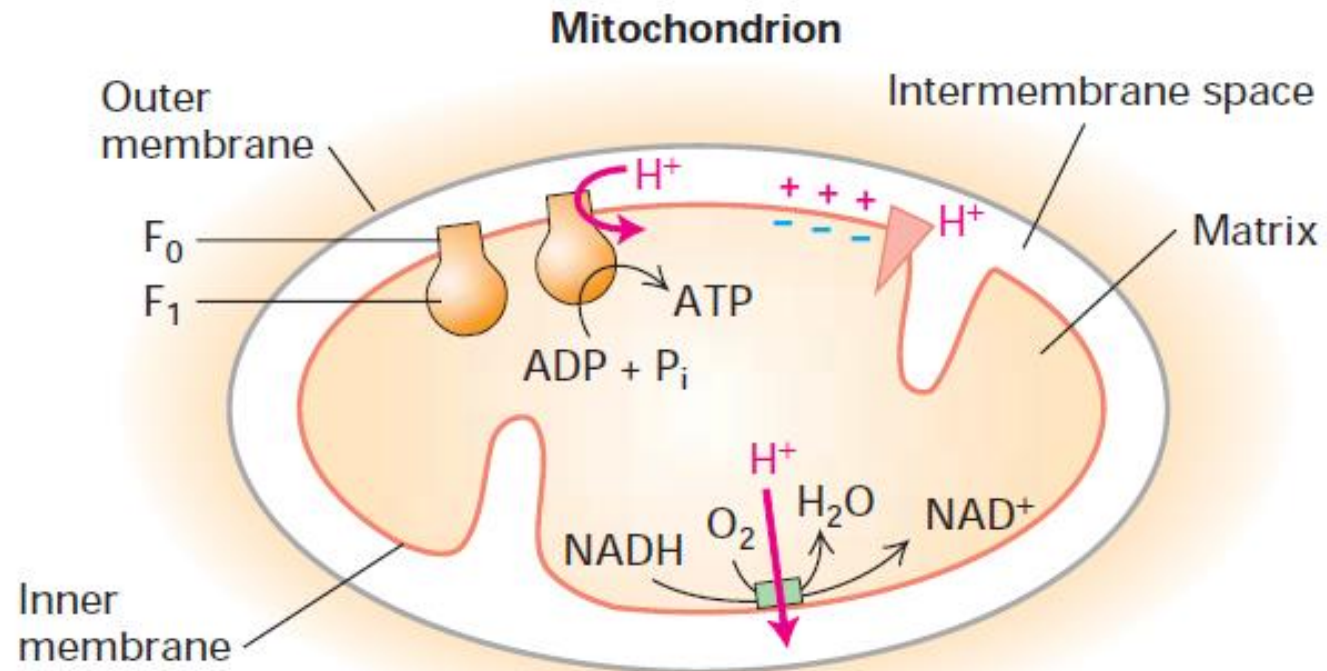
The initial steps in the oxidation of glucose, called **glycolysis**, occur in the cytosol in both eukaryotes and prokaryotes and do not require oxygen (O_2).

The final steps, which require oxygen, generate most of the ATP.

In eukaryotes, these later stages of aerobic oxidation occur in **mitochondria**

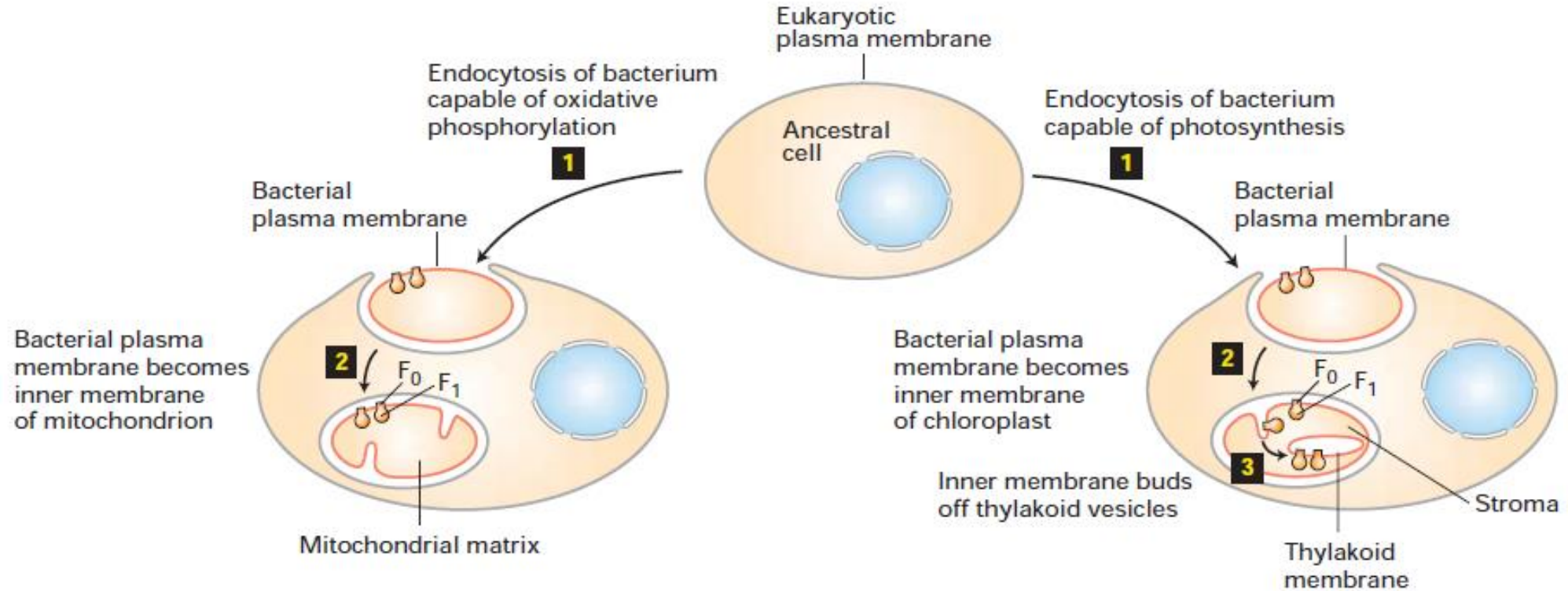
In **prokaryotes**, which contain only a plasma membrane and lack internal organelles, many of the final steps occur on the **plasma membrane**.

The final stages of fatty acid metabolism sometimes occur in mitochondria and generate ATP; in most eukaryotic cells, however, fatty acids are metabolized to CO_2 and H_2O in **peroxisomes** without production of ATP.



Evolutionary origin of mitochondria and chloroplasts according to endosymbiont hypothesis.

endosymbiosis



Mitochondria Possess Two Structurally and Functionally Distinct Membranes

Mitochondria are among the larger organelles in the cell, each one being about the size of an *E. coli* bacterium.

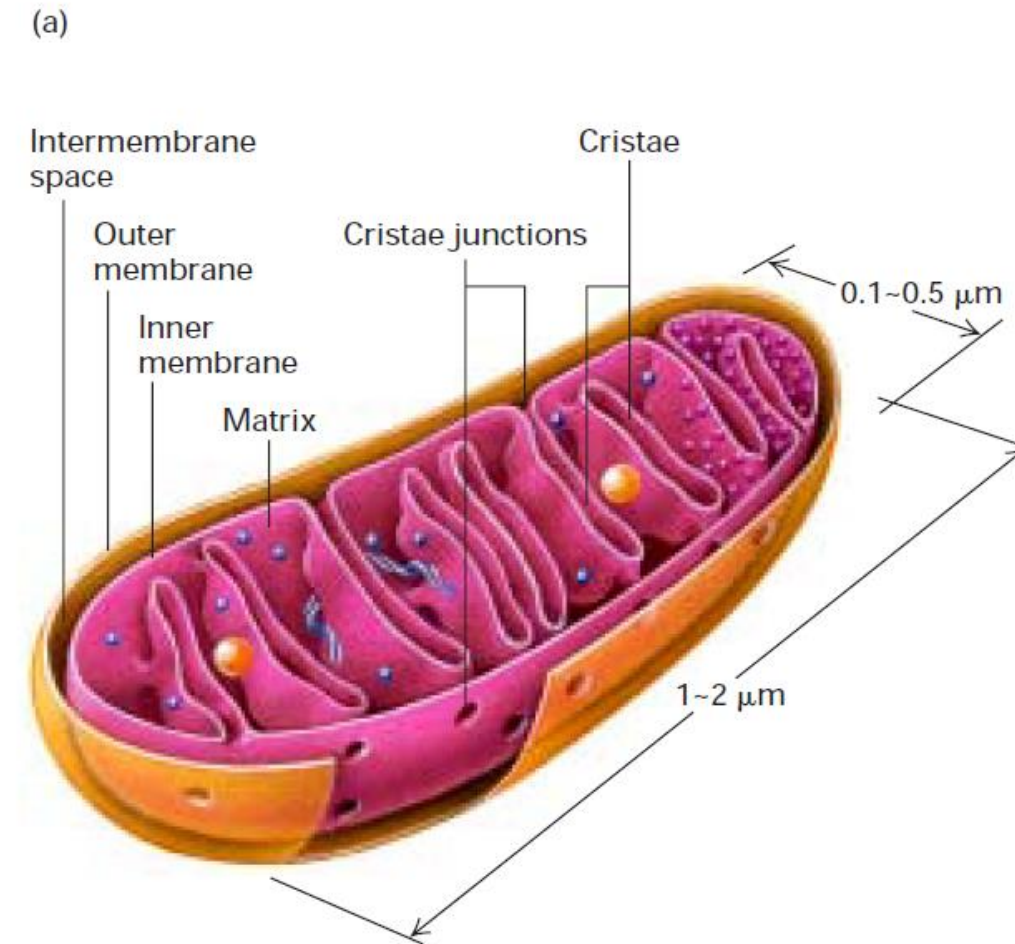
Most eukaryotic cells contain many mitochondria, which collectively can occupy as much as 25 percent of the volume of the cytoplasm.

The outer membrane defines the smooth outer perimeter of the mitochondrion.

In contrast, the inner membrane has numerous invaginations called **cristae**.

These membranes define two submitochondrial compartments: the **intermembrane space** between the outer membrane and the inner membrane with its cristae, and the **matrix**, or central compartment

The cristae greatly expand the surface area of the inner mitochondrial membrane, enhancing its ability to generate ATP



The outer membrane contains mitochondrial ***porin***, a transmembrane channel protein similar in structure to bacterial porins

Ions and most small molecules (up to about 5000 Da) can readily pass through these channel proteins.

Inner membrane, is the site of electron transport and ATP synthesis

Various transport proteins located in the inner membrane and cristae allow otherwise impermeable molecules, such as ADP and P_i , to pass from the cytosol to the matrix, and other molecules, such as ATP, to move from the matrix into the cytosol.

Protein constitutes 76 percent of the total weight of the inner membrane—a higher fraction than in any other cellular membrane.

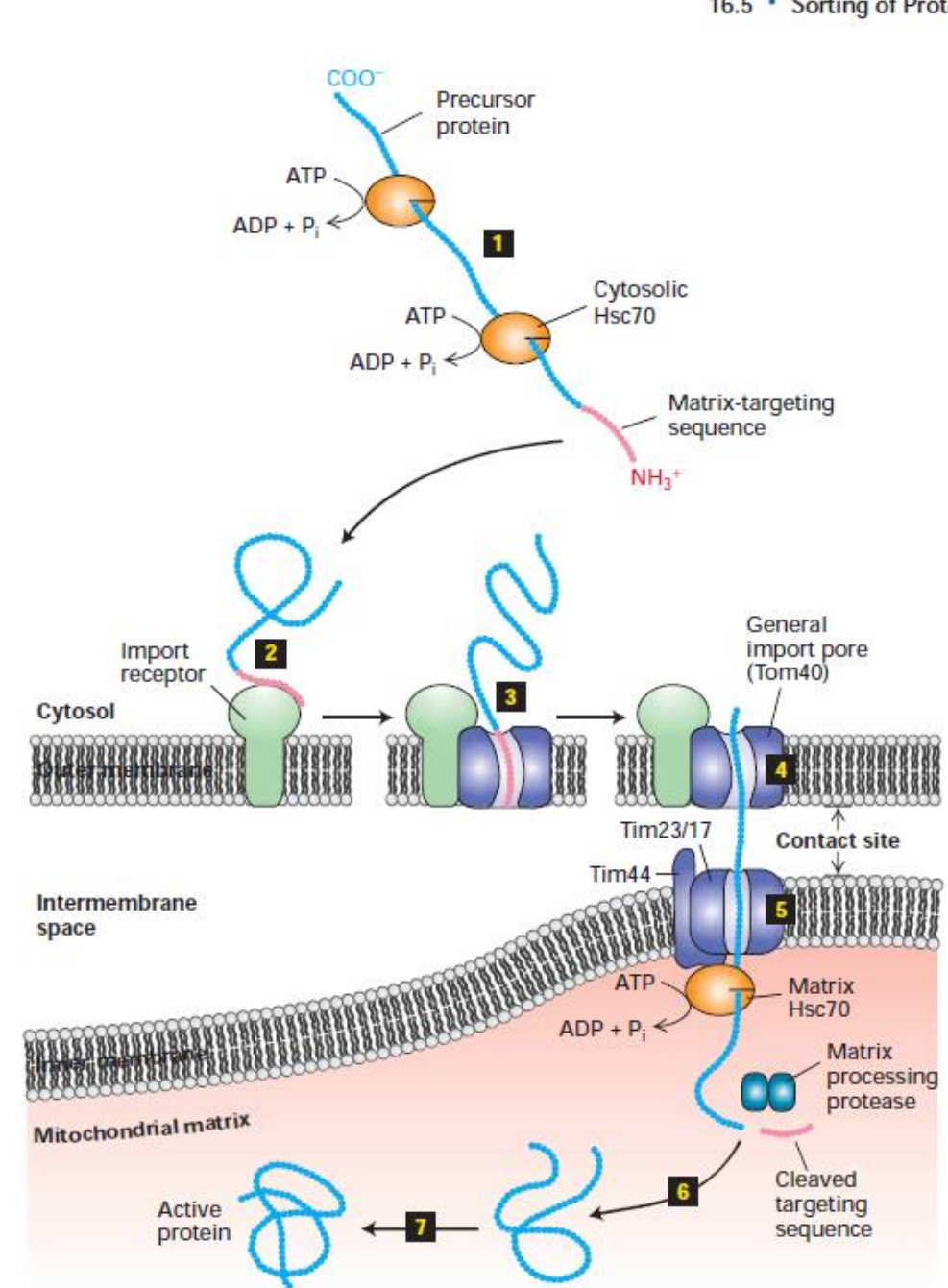
Cardiolipin (diphosphatidyl glycerol), a lipid concentrated in the inner membrane, sufficiently reduces the membrane's permeability to protons that a proton-motive force can be established across it.

In typical liver mitochondria, for example, the area of the inner membrane including cristae is about five times that of the outer membrane.

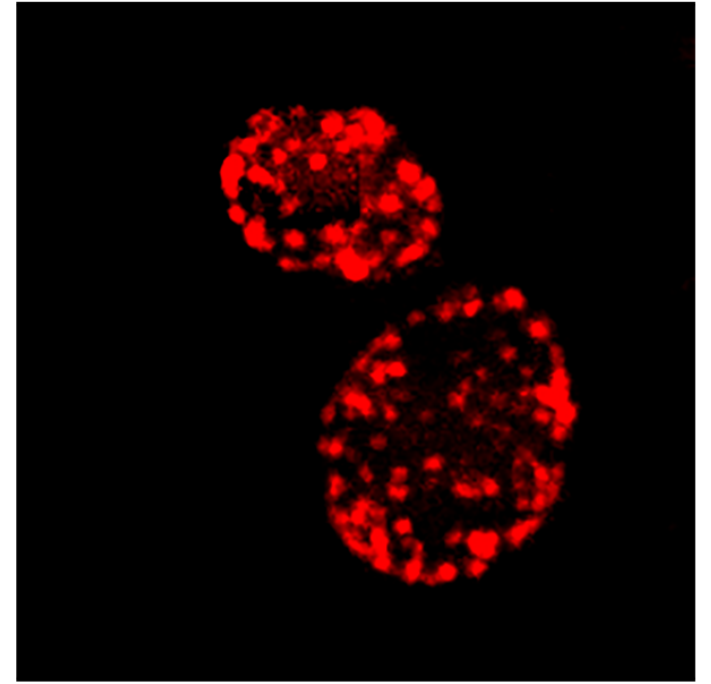
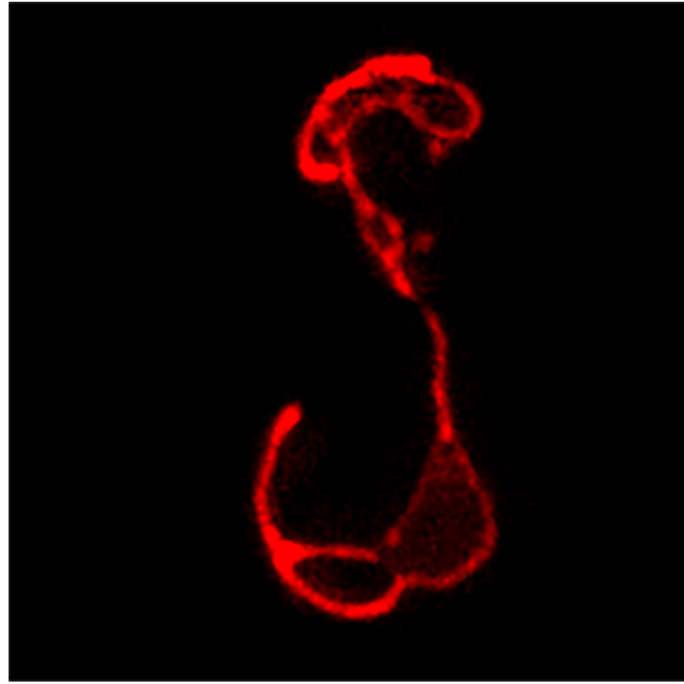
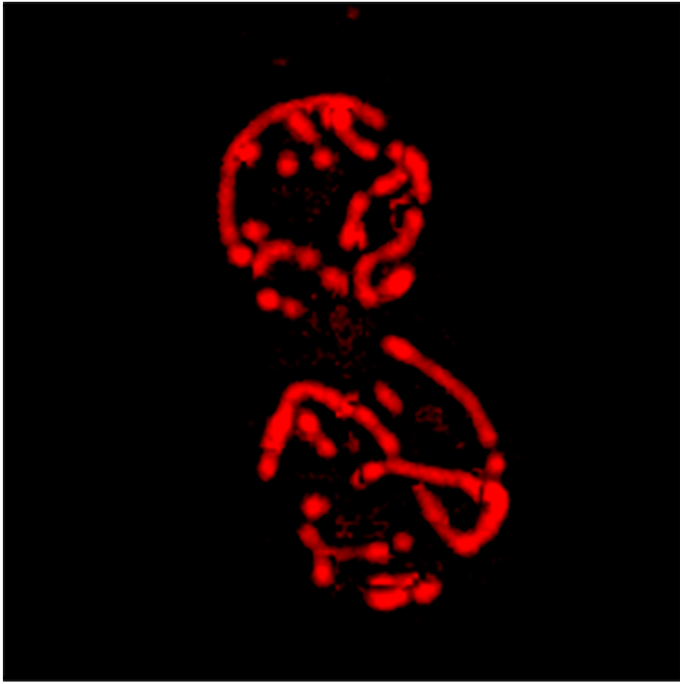
In fact, the total area of all inner mitochondrial membranes in liver cells is about 17 times that of the plasma membrane.

The mitochondria in heart and skeletal muscles contain three times as many cristae as are found in typical liver mitochondria—presumably reflecting the greater demand for ATP by muscle cells.

Protein import into the mitochondrial matrix.



Mitochondria are dynamic organelles



mtDNA

The size of the mtDNA, the number and nature of the proteins it encodes, and even the mitochondrial genetic code itself vary greatly between different organisms.

Human mtDNA, a circular molecule that has been completely sequenced, is among the smallest known mtDNAs, containing 16,569 base pairs.

It encodes the two rRNAs found in mitochondrial ribosomes and the 22 tRNAs used to translate mitochondrial mRNAs.

Human mtDNA has 13 sequences that begin with an ATG (methionine) codon, end with a stop codon, and are long enough to encode a polypeptide of more than 50 amino acids; all the possible proteins encoded by these open reading frames have been identified.

As far as is known, all RNA transcripts of mtDNA and their translation products remain in the mitochondrion, and all mtDNA-encoded proteins are synthesized on mitochondrial ribosomes.

UGA, for example, is normally a stop codon, but is read as tryptophan by human and fungal mitochondrial translation systems; however, in plant mitochondria, UGA is still recognized as a stop codon.

AGA and AGG, the standard nuclear codons for arginine, also code for arginine in fungal and plant mtDNA, but they are stop codons in mammalian mtDNA and serine codons in *Drosophila* mtDNA.

