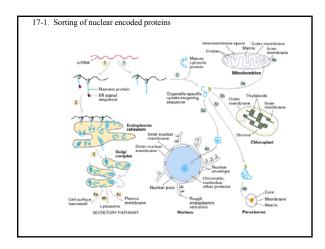
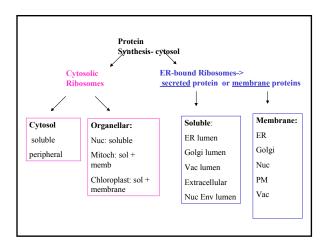
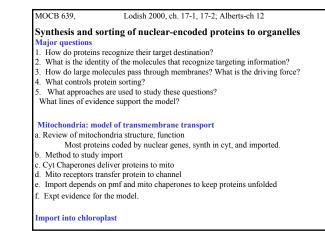
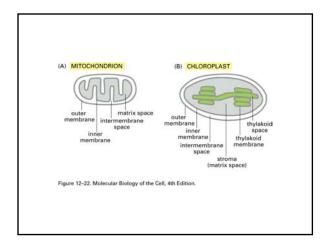


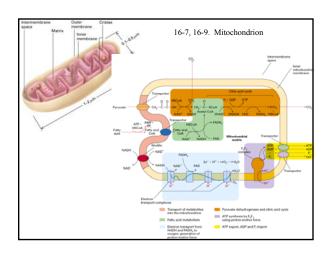
Target Organelle	Usual Signal Location within Protein	Signal Removal*	Nature of Signal
Endoplasmic reticulum	N-terminal	(+)	"Core" of 6-12 mostly hydrophobic amino acids, often preceded by one or more basic amino acids
Mitochondrion <sup>†</sup>	N-terminal	(+)	3-5 nonconsecutive Arg or Lys residues, often with Ser and Thr; no Glu or Asp residues
Chloroplast <sup>†</sup>	N-terminal	(+)	No common sequence motifs; generally rich in Ser, Thr, and small hydrophobic amino acid residues and poor in Glu and Asp residues
Peroxisome	C-terminal	()	Usually Ser-Lys-Leu at extreme C-terminus
Nucleus	Internal	(-)	One cluster of 5 basic amino acids, or two smaller clusters of basic residues separated by ≈10 amino acids
	gnals discussed in the text		oace of the mitochondrion or the corresponding stroma ns into other subcompartments of these organelles.

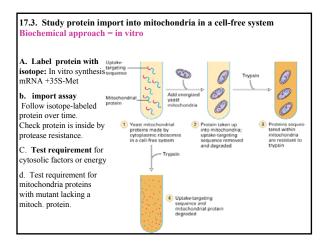


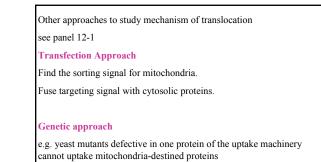


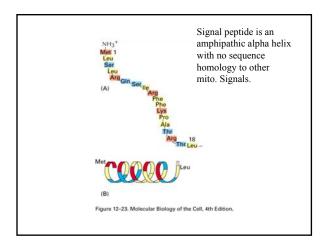


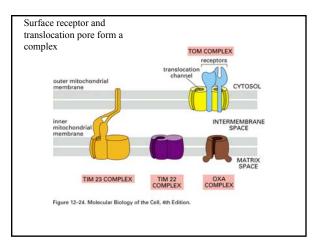


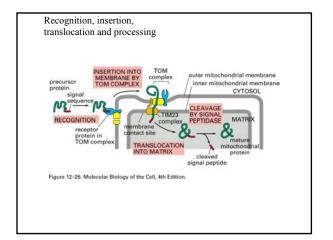


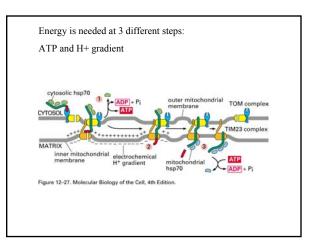


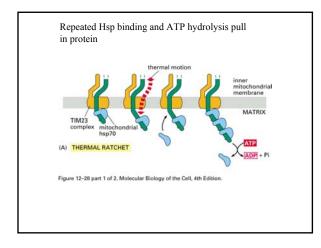


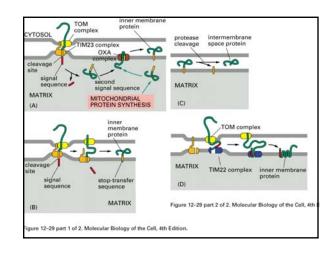


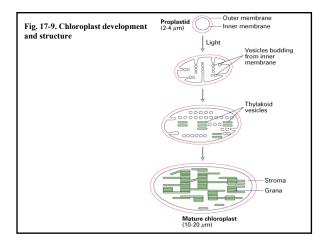


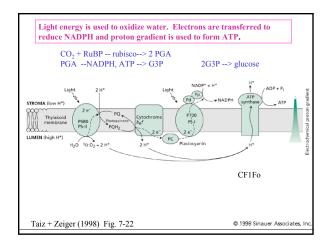


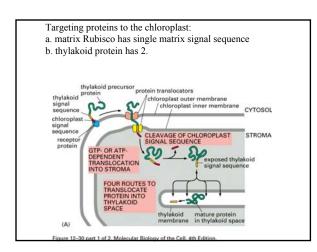


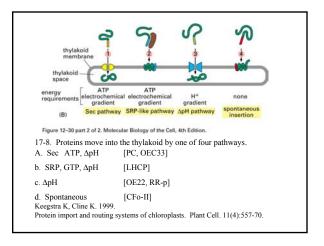






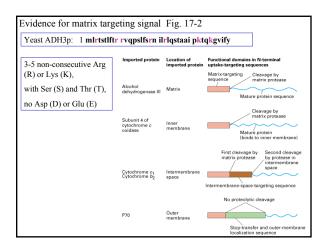






## Summary and a problem

## **Problem**: Do mito and chloroplast-destined proteins have distinct matrix targeting sequences? Design an experiment to test your hypothesis.



## **Protein Import into mitochondrial matrix** Evidence:

- 1. Import depends on cytosolic factors
- 2. ATP is needed to keep protein unfolded
- 3. Mitochondrial receptors are needed
- 4. Import depends on pmf and matrix chaperones

pmf: provides a driving force

