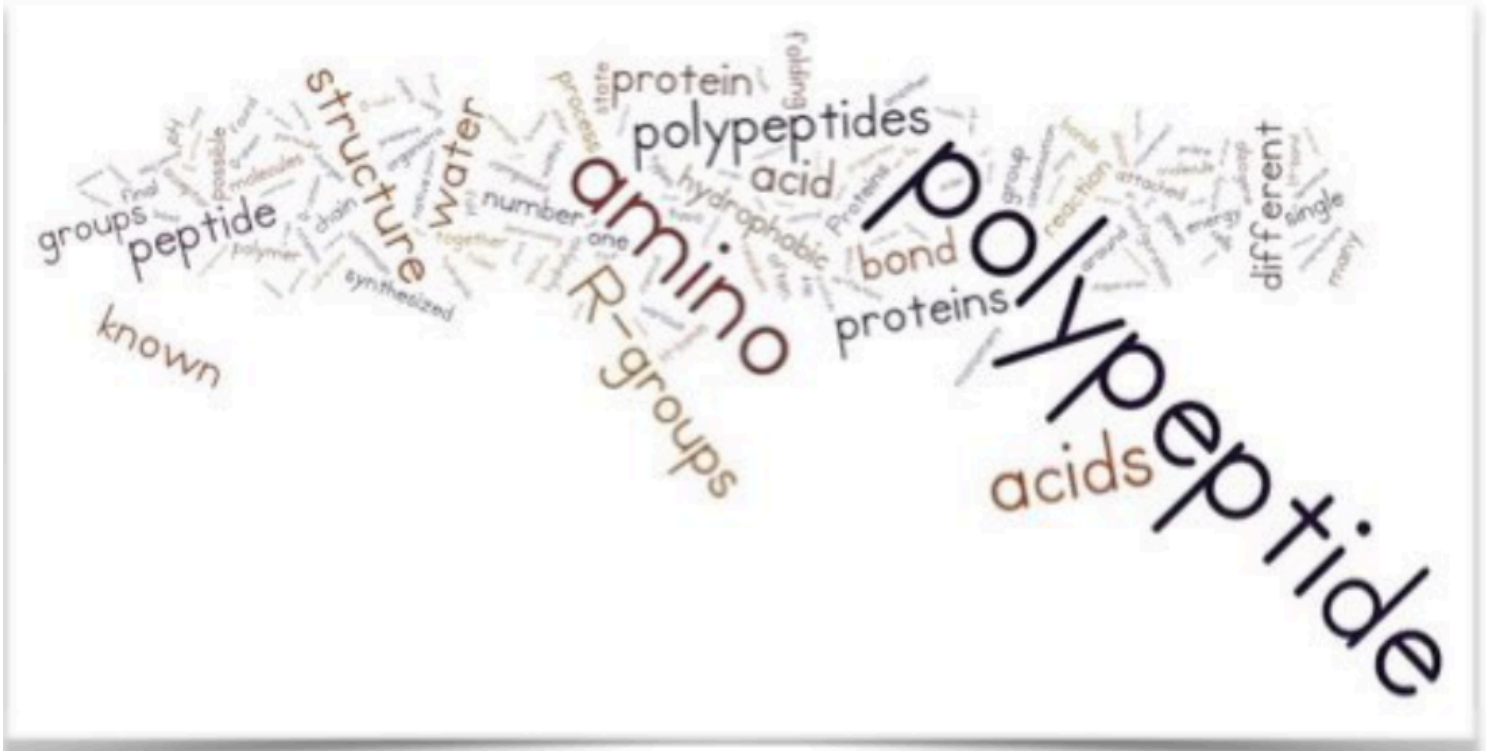
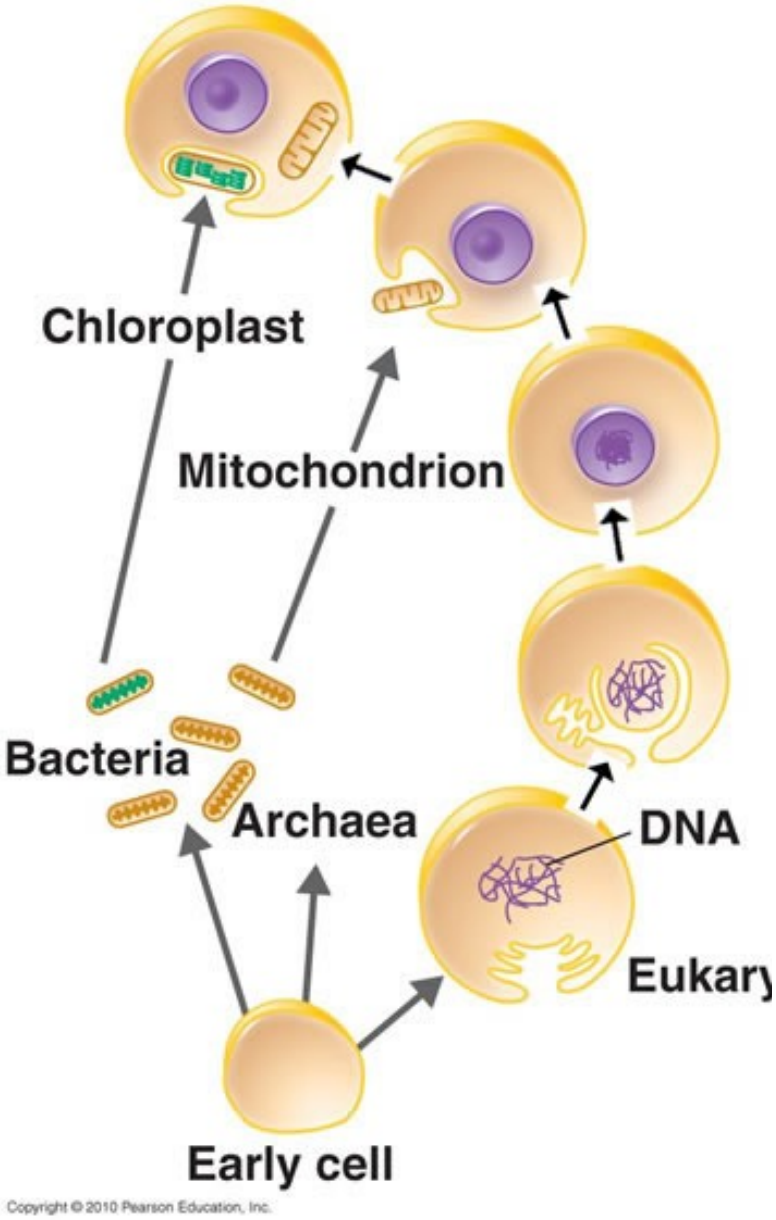


Today and Friday, complete chapter 9
pages 189-196



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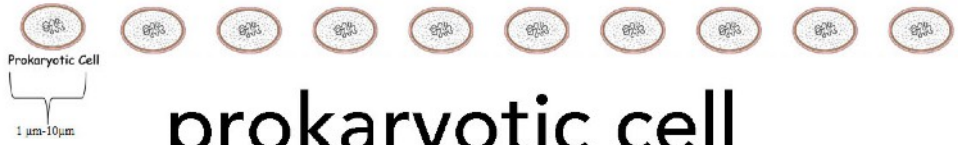


prokaryotic cell

typically 1 to 10um

8.4 read p. 189-196

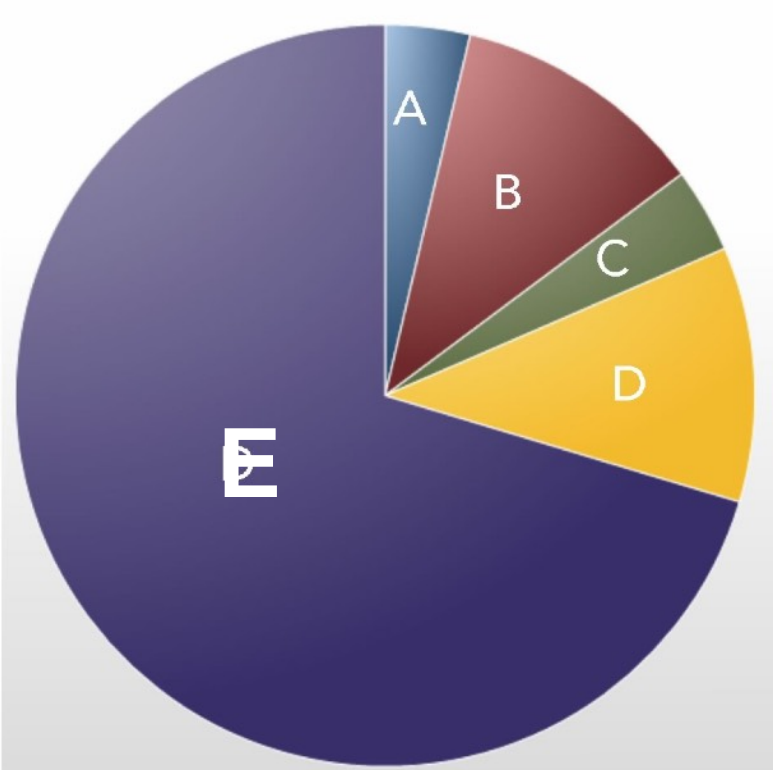
Eukaryotes differ from prokaryotes (eubacteria and archaea) by the presence of a nucleus. Within the nucleus, newly synthesized RNA molelcules are modified before they are transported to the cytoplasm.

Given this fact, where do you think functional ribosomes are located.

- the nucleus
- the cytoplasmic face of the plasma membrane
- the extracellular face of the plasma membrane
- throughout the cell
- throughout the cytoplasmic, but not within the nucleus
- no idea

How does the ab
cytoplasmic influ
prokaryotes?

In prokaryotes the
directly with DNA,
molecules do not n
interact with riboso



GROUP: What are the impacts of the presence of introns in eukaryotes on gene expression, evolution, or other processes?

How might the removal of introns be recognized?

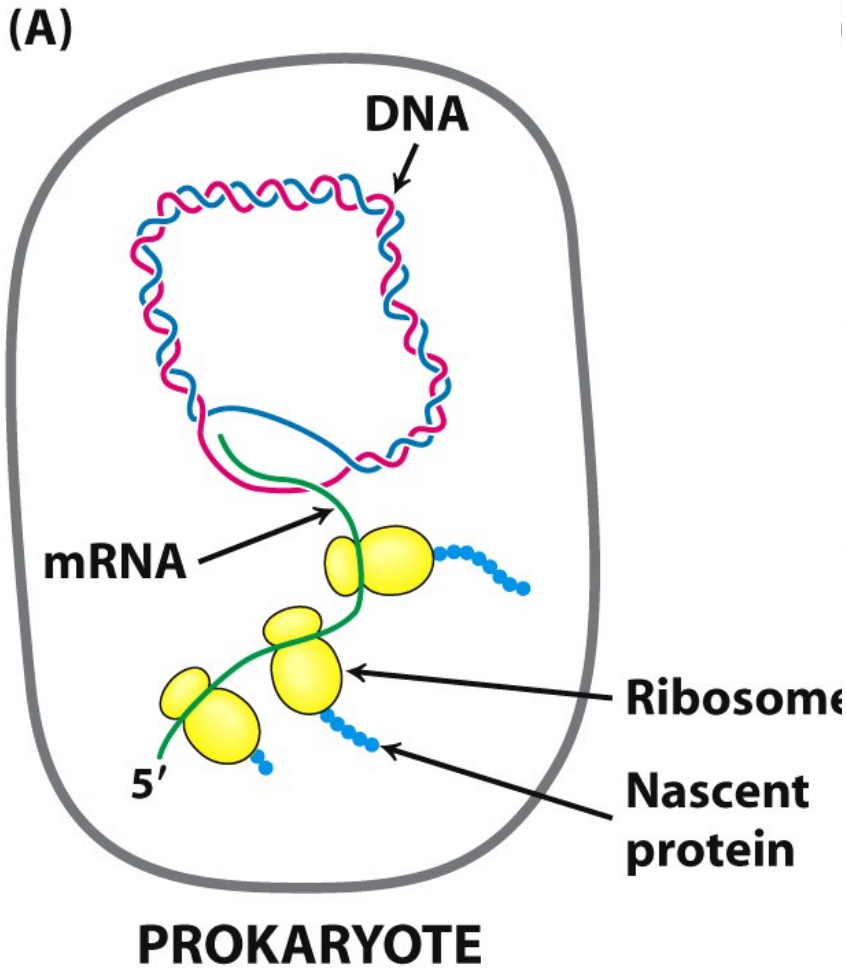


Figure 29.21
***Biochemistry*, Seventh Edition**
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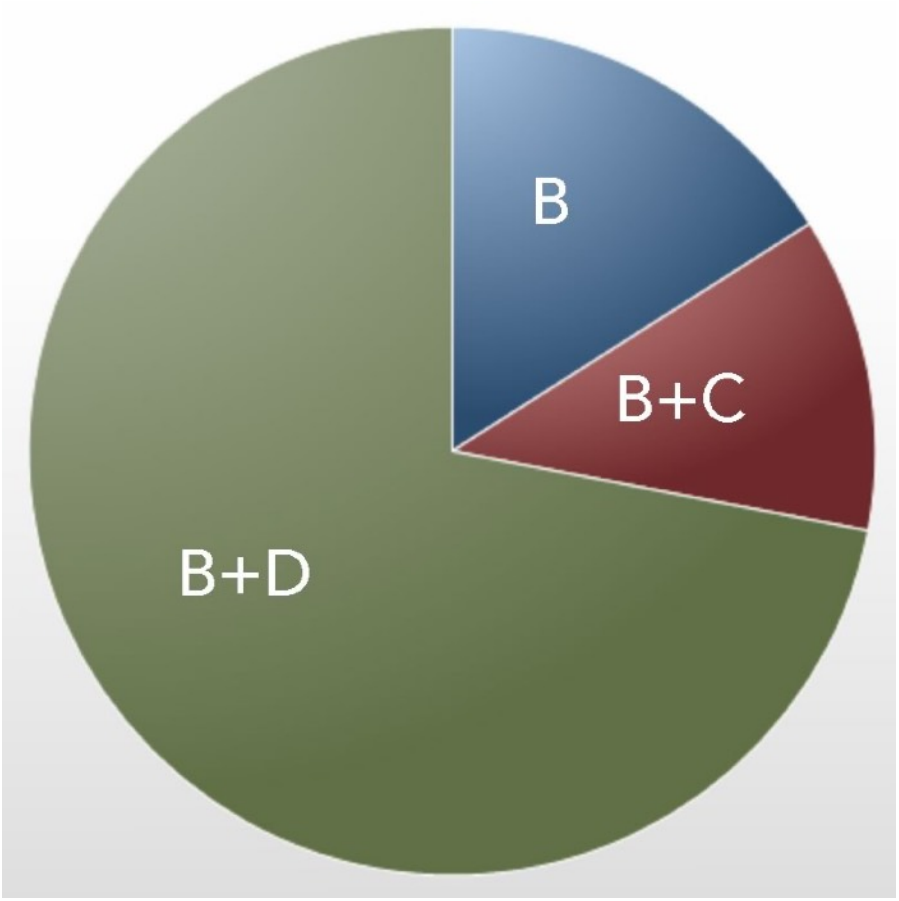
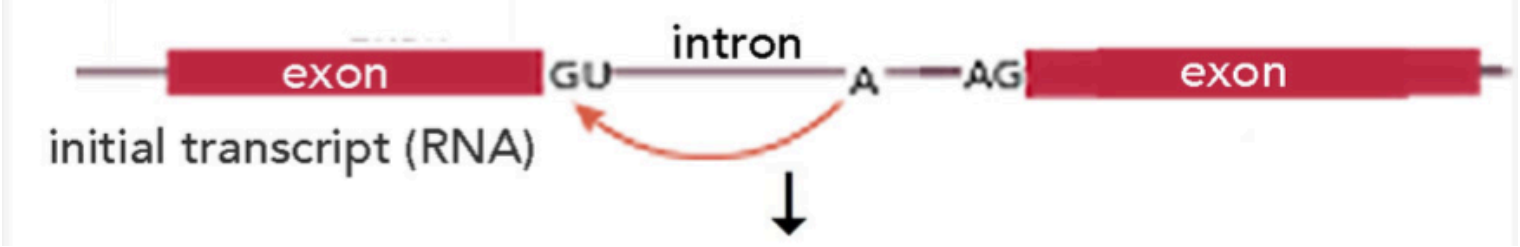
What would be the effects if an intron within the coding region of an to an RNA molecule were not correctly removed?

- A. nothing, the ribosome would skip the intron
- B. it would disrupt the reading frame and introduce new coding sequences
- C. it would introduce new start codons
- D. in would introduce stop codons into the mRNA
- B and C
- B and D

Explain your thinking and consider: A gene has many introns - provide a model for how it might encode functionally distinct polypeptides.



How might the removal of introns be recognized?



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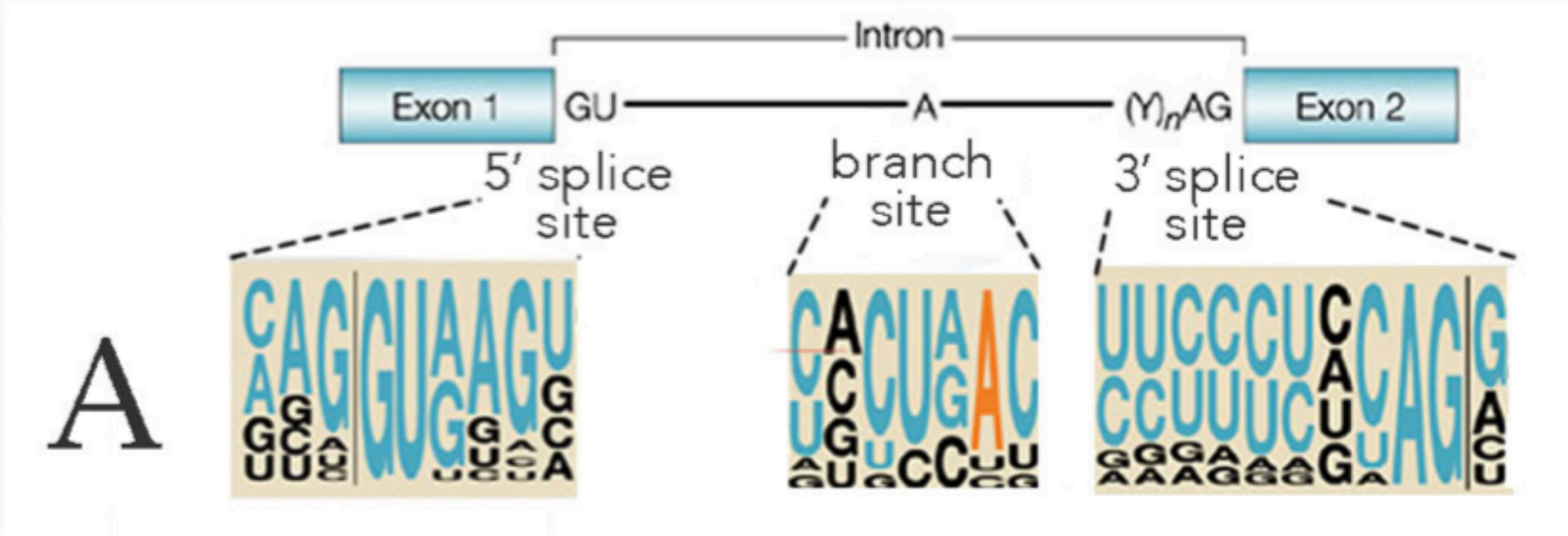
Group to answer

- How do you interpret such a diagram? how can you use it to predict the effect of a mutation

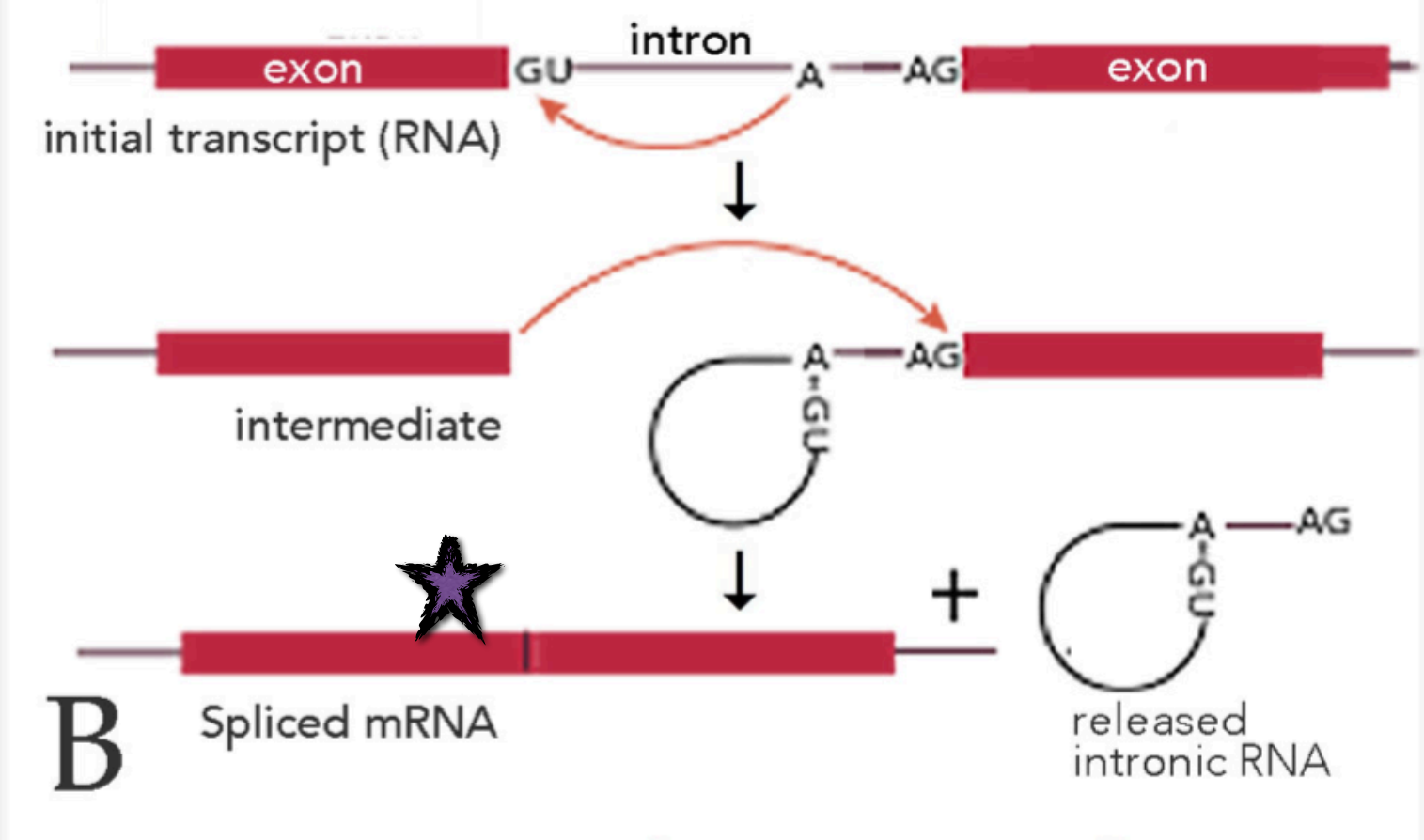


Group

- How does NMD protect against potentially deleterious mutations (alleles)?

How might NMD to work?

nascent RNA splicing



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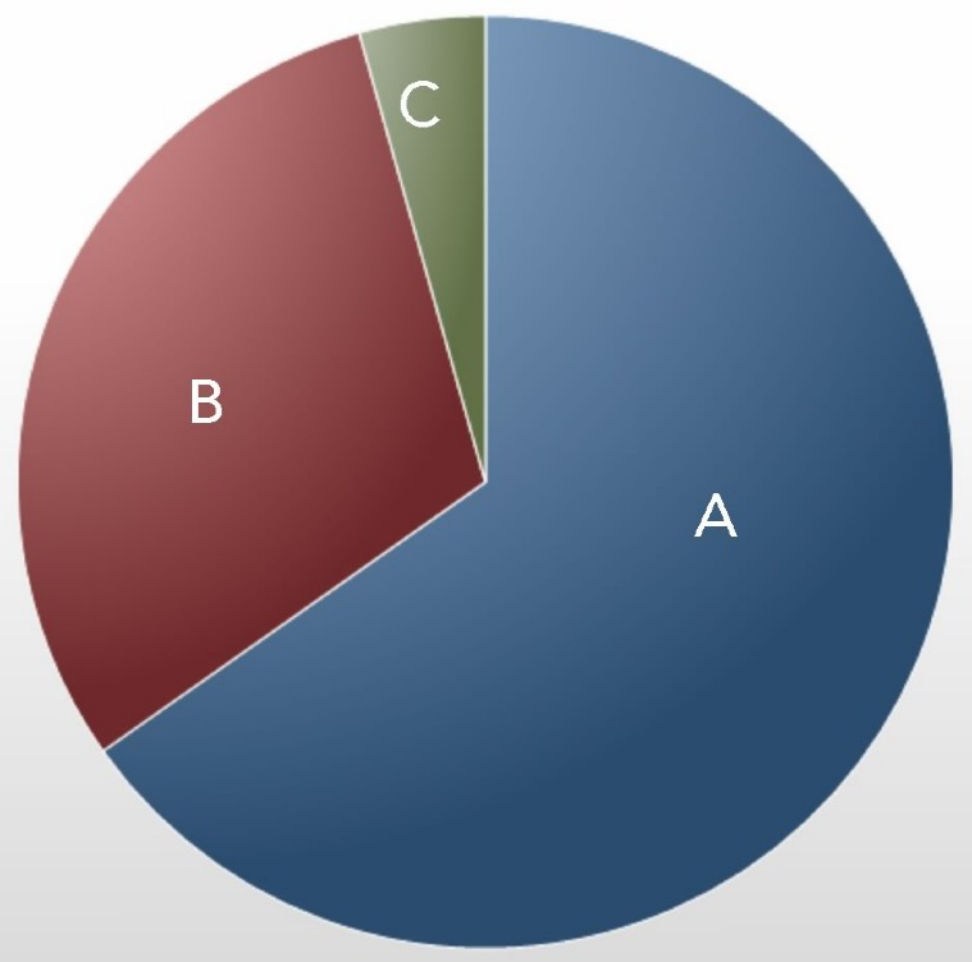
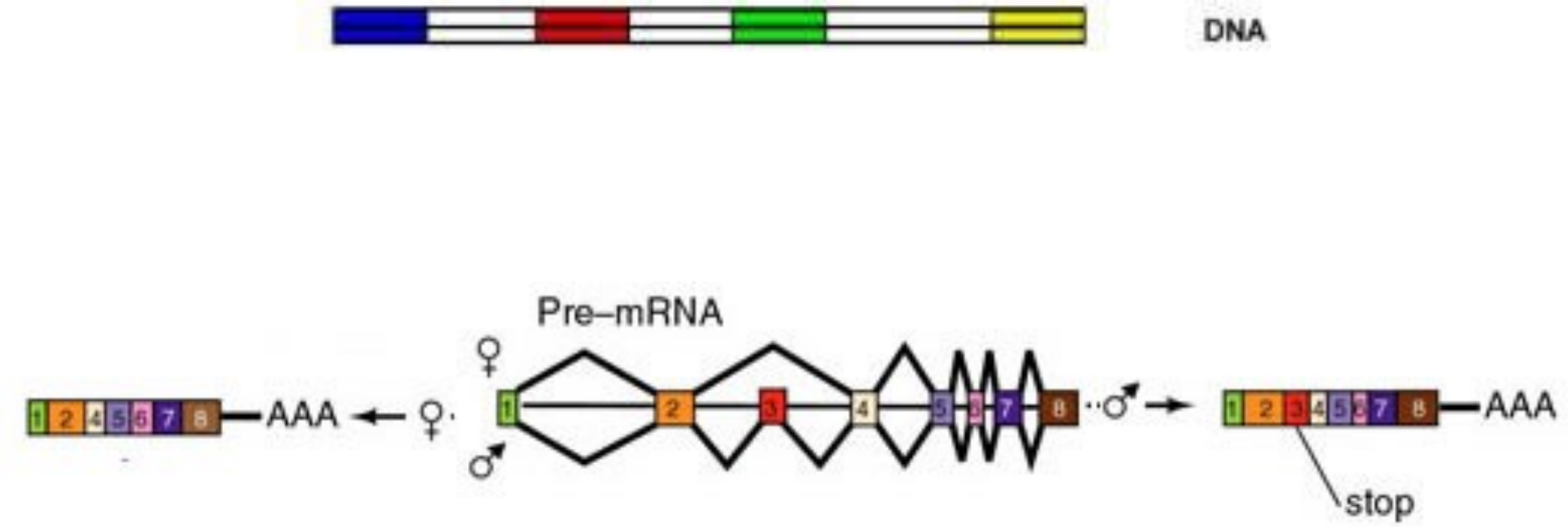
Non-sense mediated decay is involved in destabilizing mRNAs (and so minimizing the effects of mutation that ....

- generate an upstream stop codon
- generate a negatively acting missesne mutation
- any mutation that occurs within the coding region
- mutations that occur in the gene's regulatory regions



Questions to answer (p. 192):

- A gene has many introns - provide a model for how it might encode functionally distinct polypeptides.

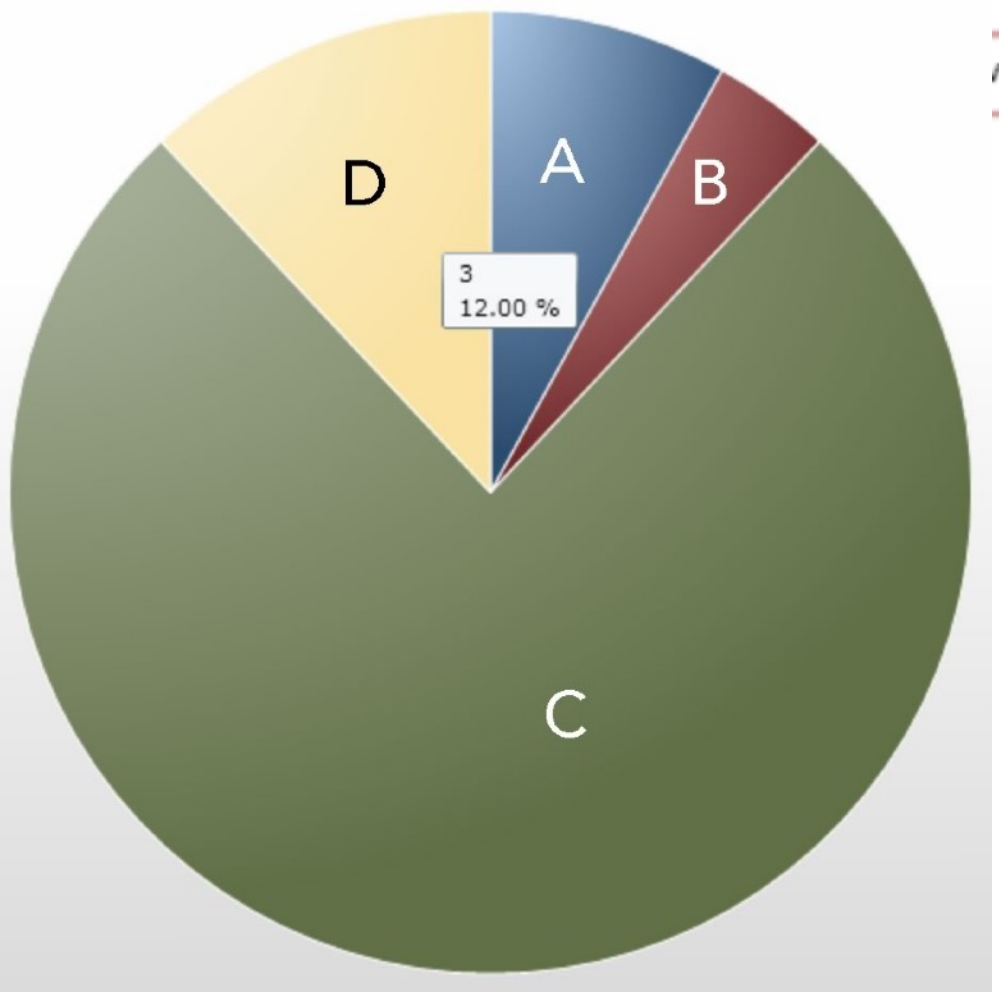


Questions to answer (p. 192):

- Why would a cell want to stop (rather than continue) polypeptide synthesis when it is starving?

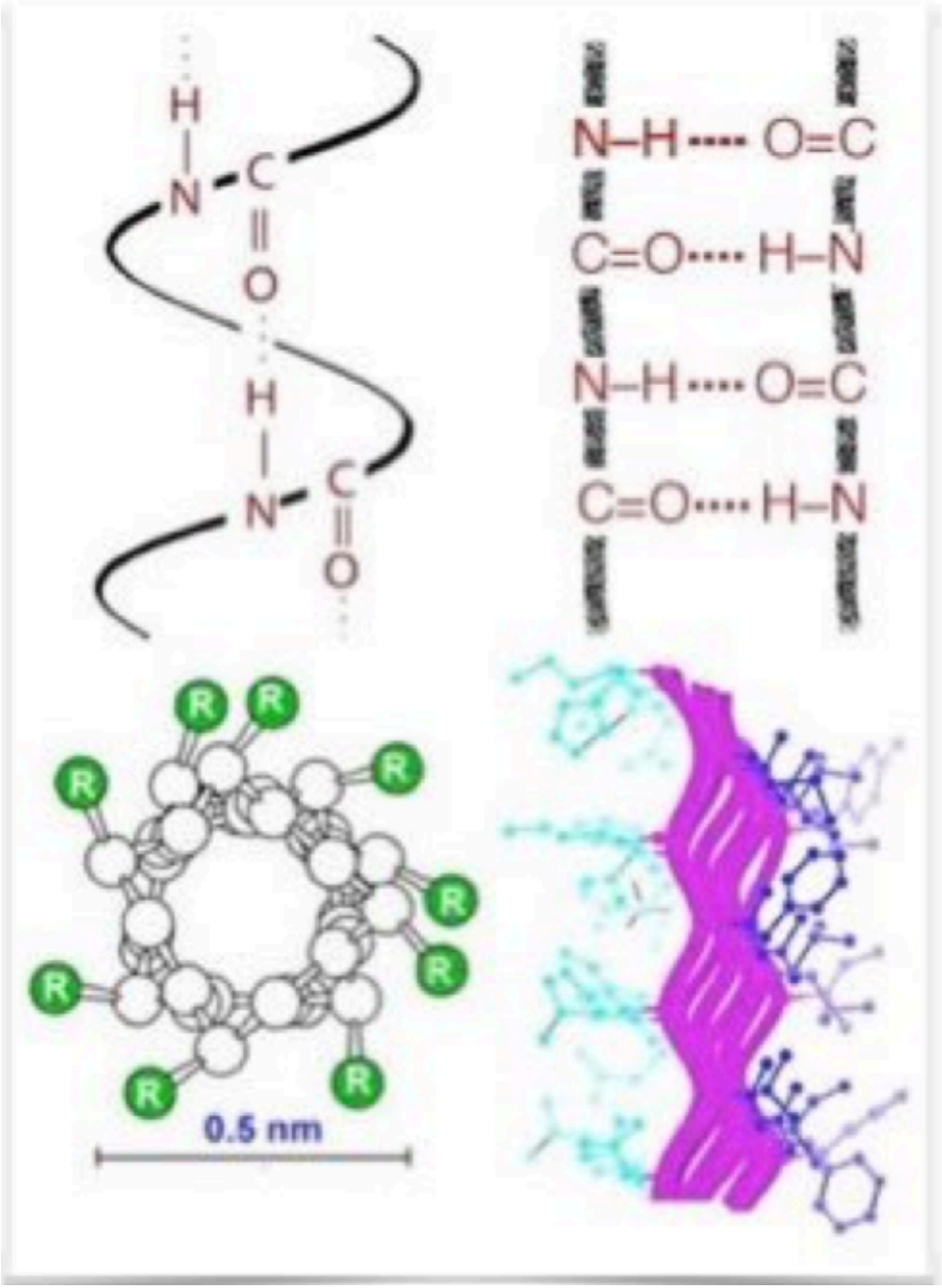
What leads to the activation of an "alarm" response...

- too much mRNA
- too much tRNA
- too much uncharged tRNA
- too few ribosomes

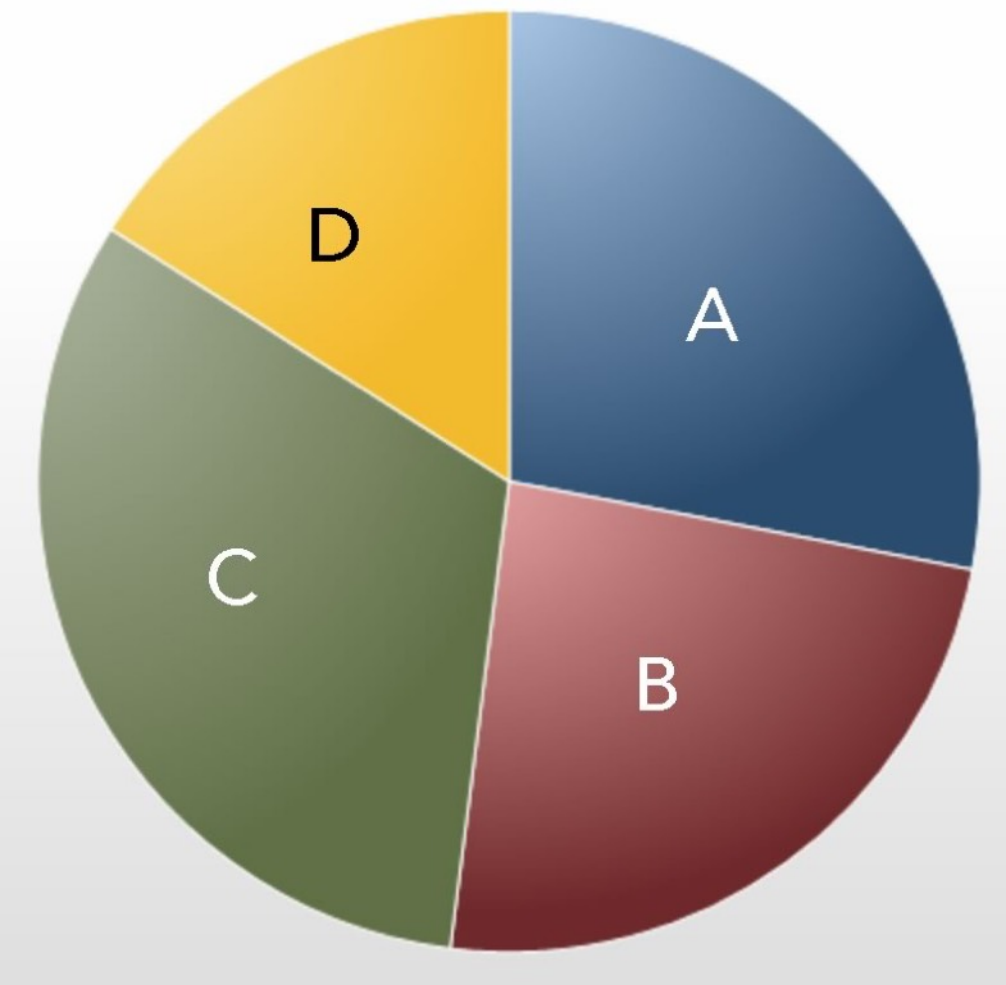


value) of the alarm state

Why are α-helices and β-sheets ubiquitous features of polypeptide structures

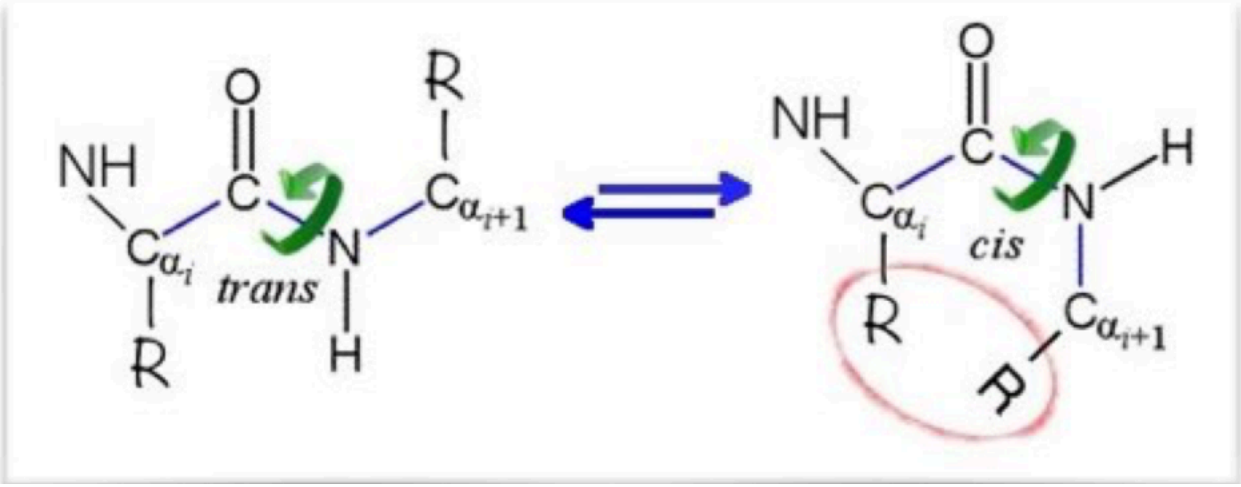


Normally, the groups on the two sides of a single bond can freely rotate around the bond; why is a peptide bond different.



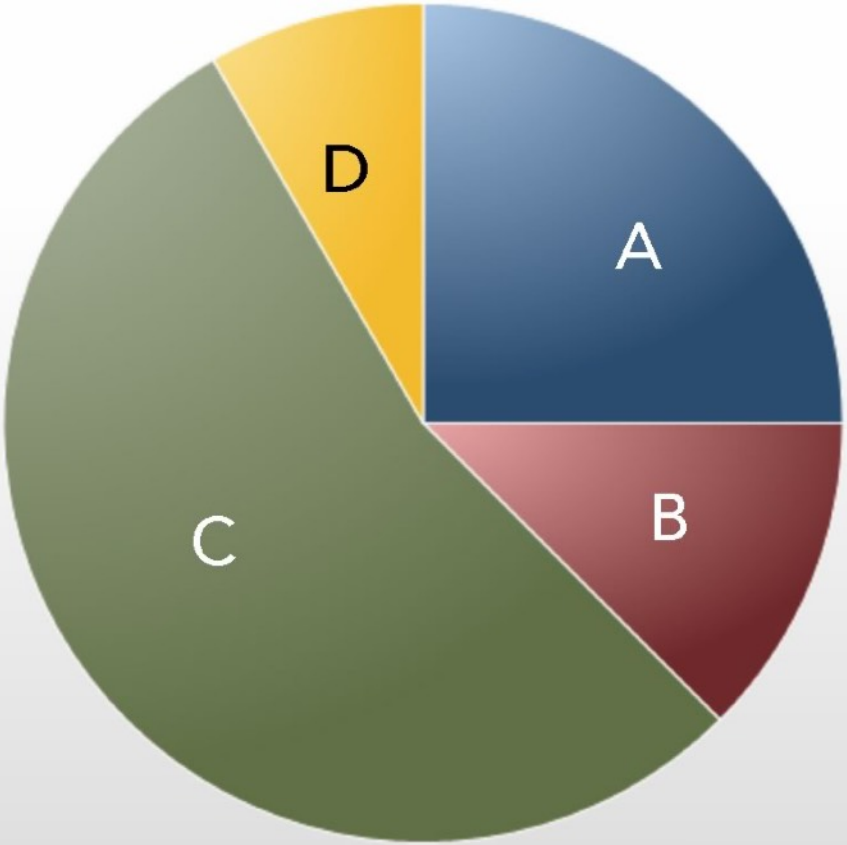
- the R group collide, blocking rotation
- the R groups of adjacent amino acid residue make H-bonds with one another
- it is more like a bond and a half than a single bond
- no idea

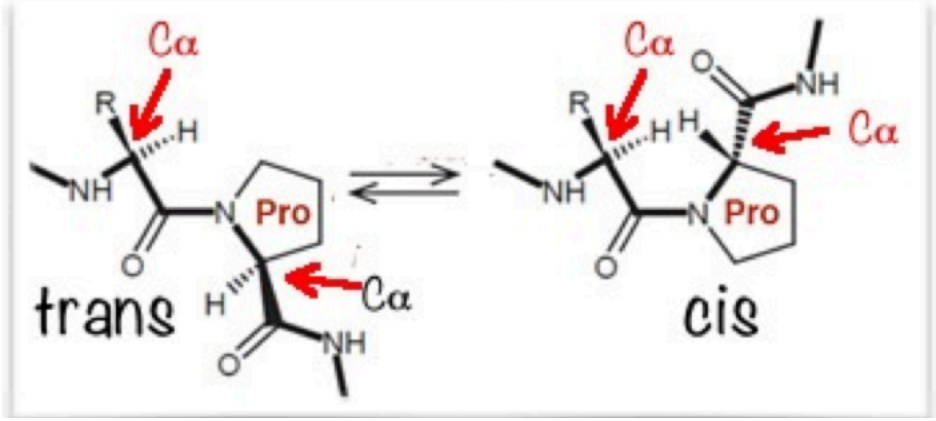
How does the size of an R group influence the cis-trans orientation of amino acid (residues) across peptide bond?



How does the presence of a proline influence the structures of a polypeptide chain?

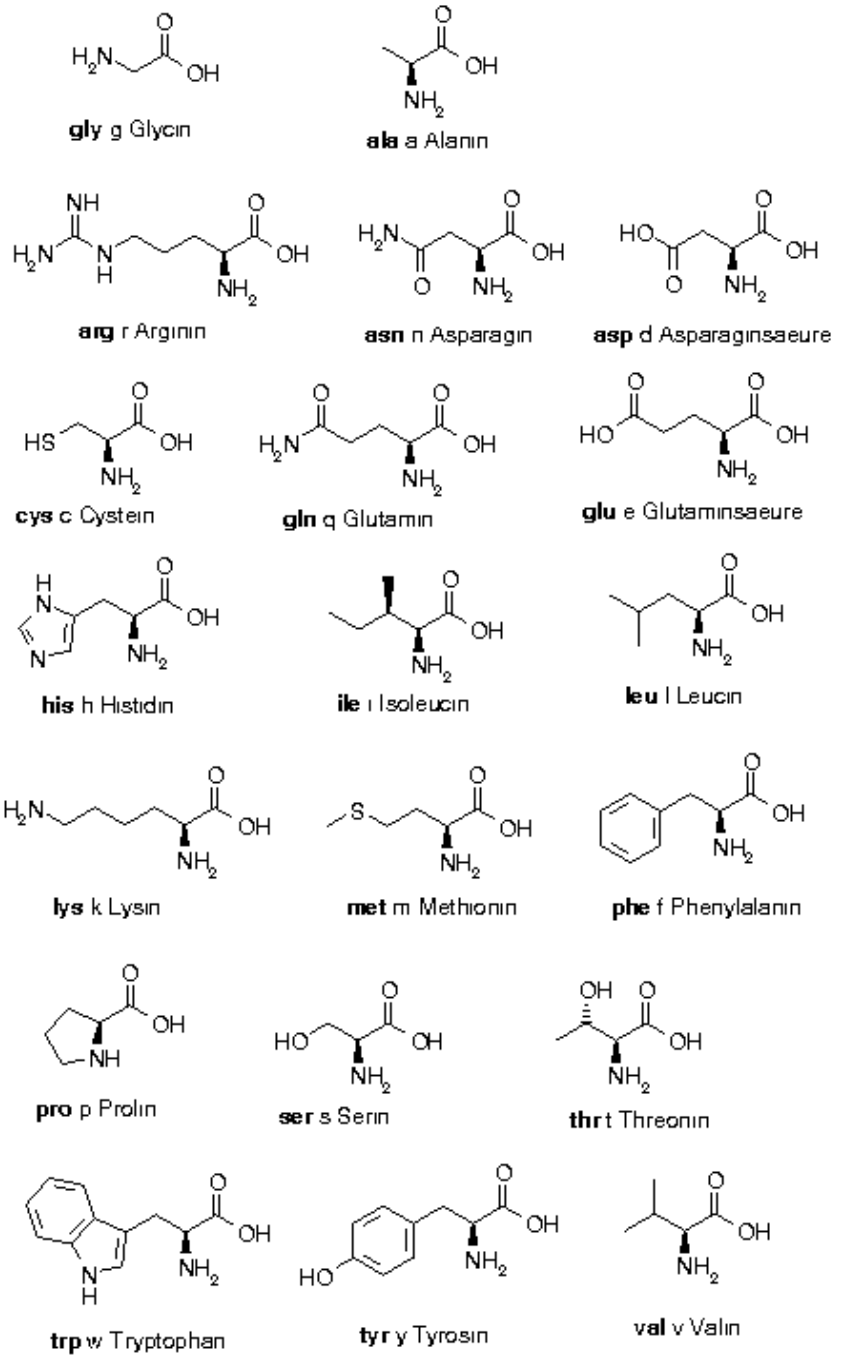
- It is not able to form a peptide bond with another amino acid
- favors the formation of an alpha helix
- tends to produce a kink in the chain (a break in helical or sheet organization
- impossible to know





What is a weak acid / base group; how is it effected by pH?

Why do changes in pH influence polypeptide/protein structure?



Questions to answer (p. 192):

- Why does it matter that rotation around a peptide bond is constrained?
- How can changing the pH of a solution alter a protein's structure and activity?
- Make a model of the structure of a polypeptide if all of its R-groups were hydrophilic or hydrophobic?