

Complete chapter 8

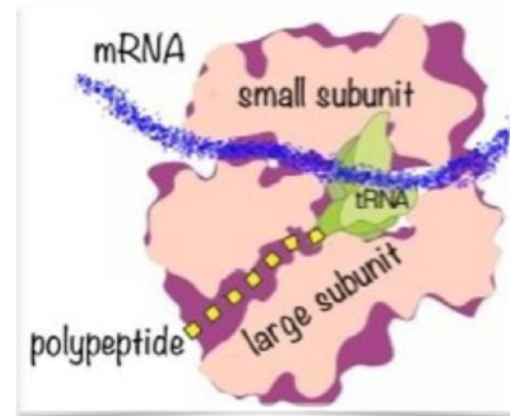


Review -
signals associated
with RNA
splicing
and Non-sense
mediated
decay

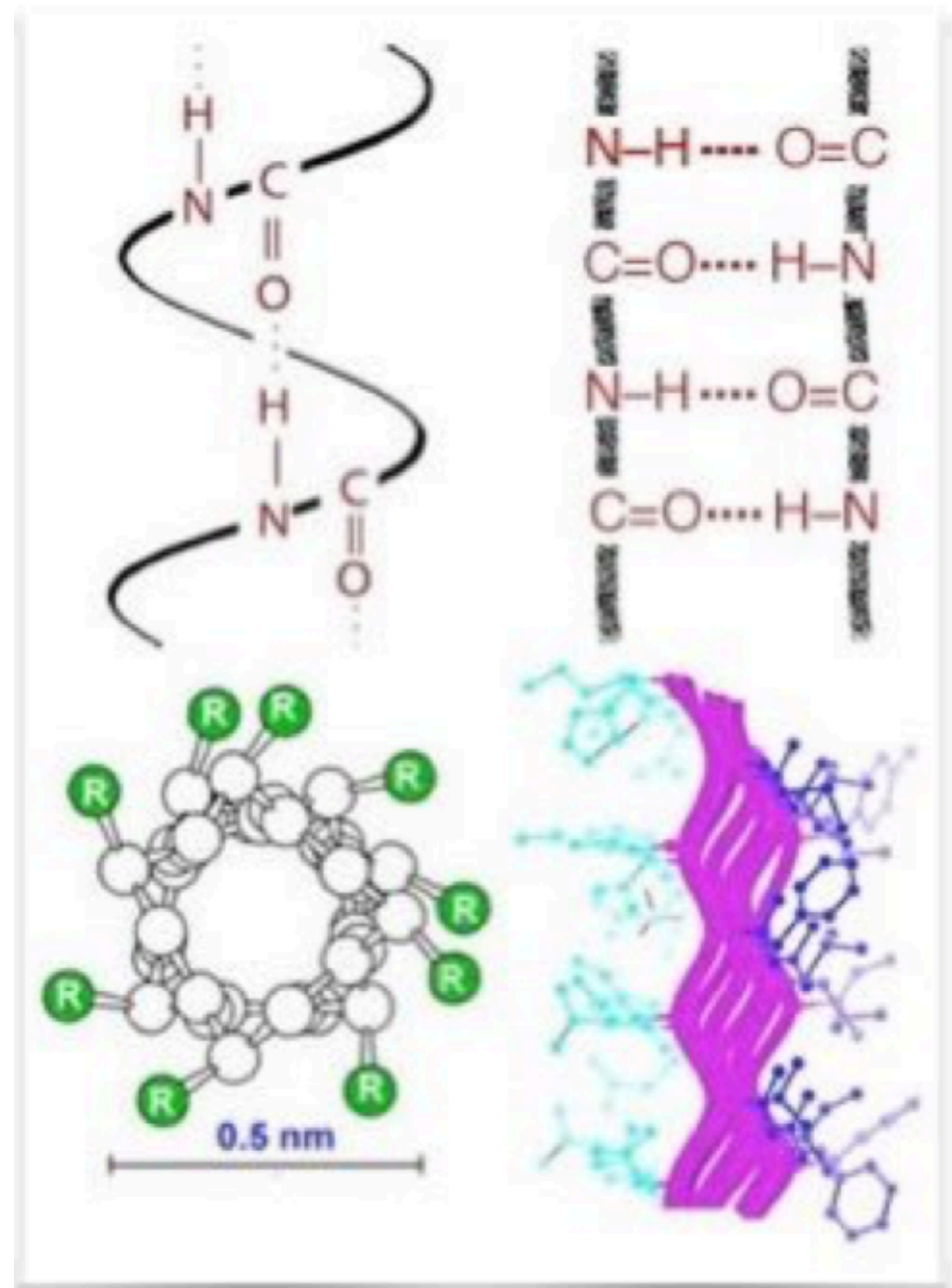
A protein is a functional entity.

- A gene encodes a polypeptide (mRNA) or a functional, non-coding RNA
- Proteins is the function unit; proteins are composed of one or more polypeptides
- A protein may also contain non-polypeptide components, such as metal atoms (such as Fe in hemoglobin) of “prothetic groups” or “co-enzymes”, many derived from vitamins.
- Assembly of a multi-subunit proteins may require accessory proteins, known as chaperones.

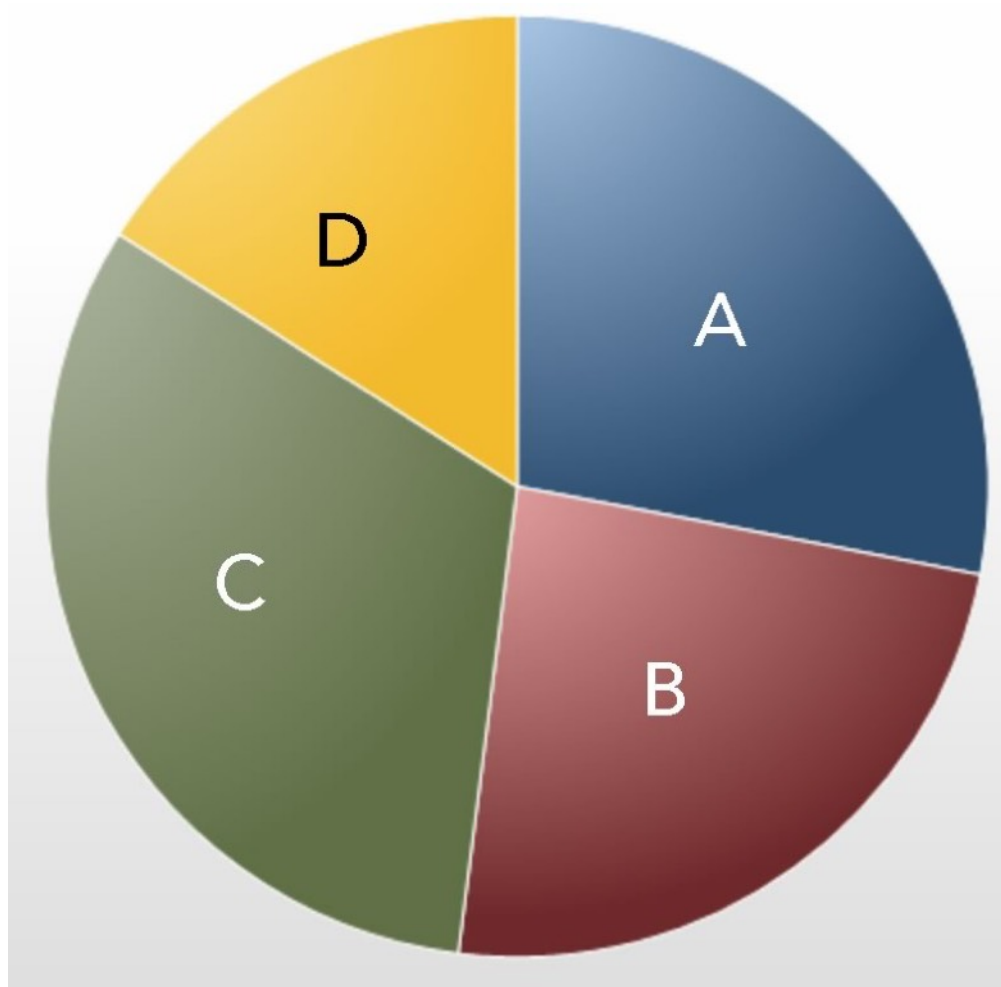
Why is predicting the final, function form of a polypeptide / protein a computationally difficult problem?



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

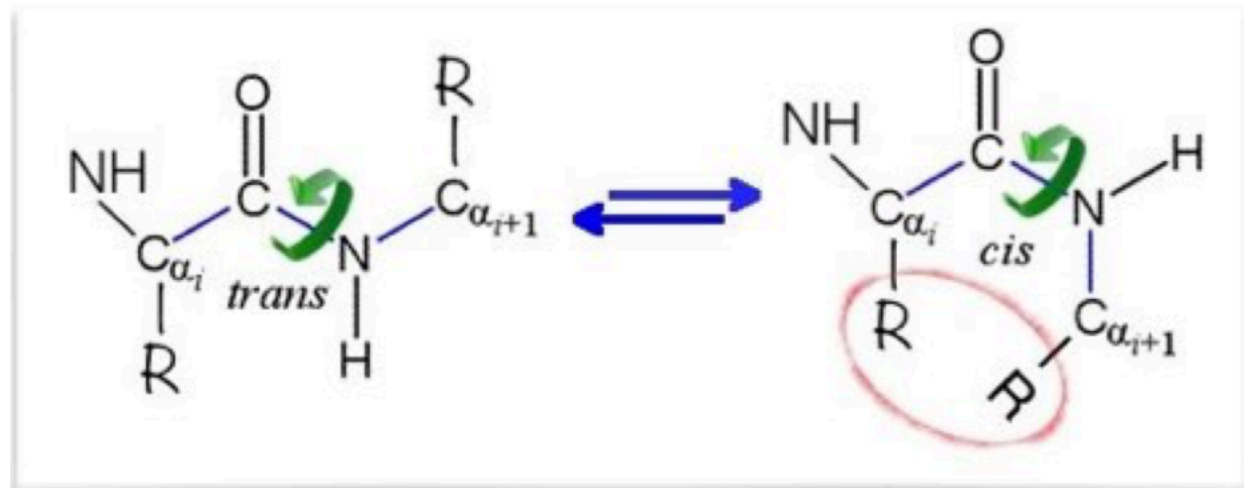


Normally, the groups on the two sides of a single bond can freely rotate around the bond; why is a peptide bond different.



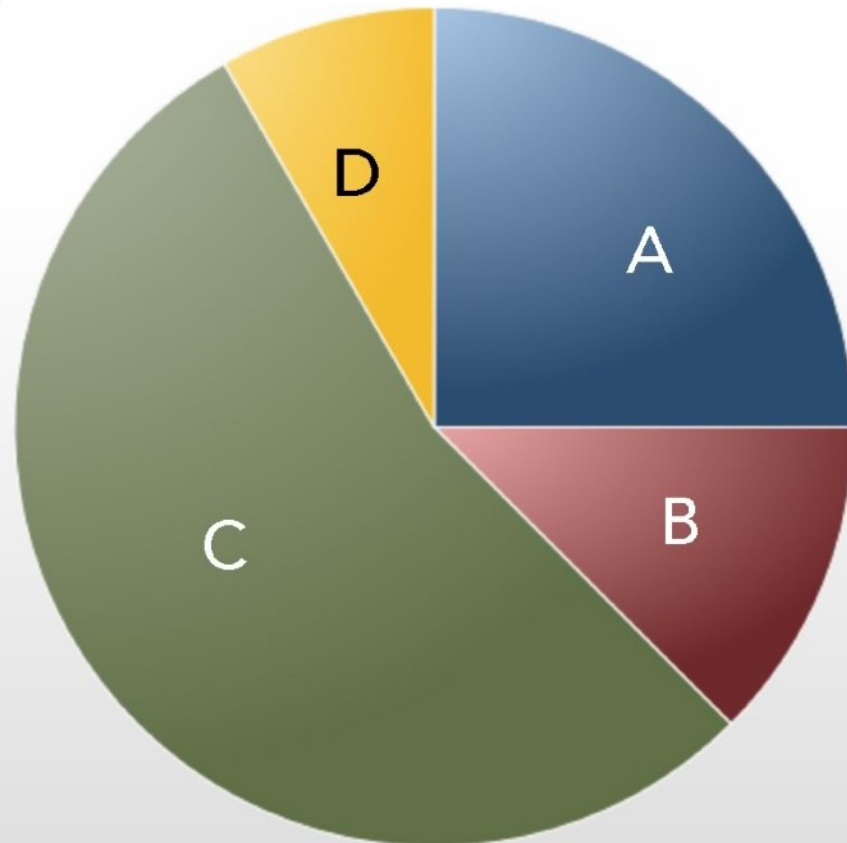
- ☐ the R group collide, blocking rotation
- ☐ the R groups of adjacent amino acid residue make H-bonds with one another
- ☐ it is more like a bond and a half than a single bond
- ☐ no idea

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

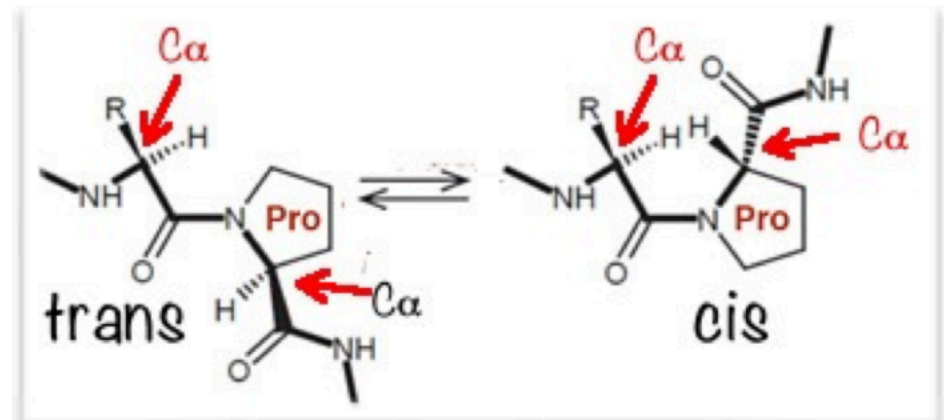


How does the presence of a proline influence the structures of a polypeptide chain?

- ☐ 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

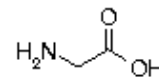


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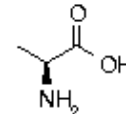


What is a weak acid / base group; how is it effected by pH?

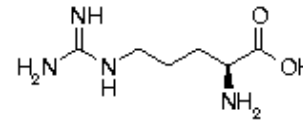
Why do changes in pH influence polypeptide/protein structure?



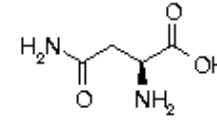
gly g Glycin



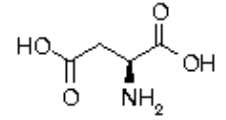
ala a Alanin



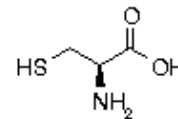
arg r Arginin



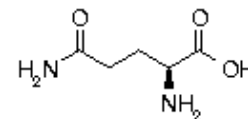
asn n Asparagin



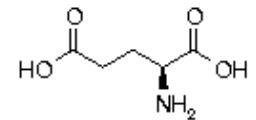
asp d Asparaginsäure



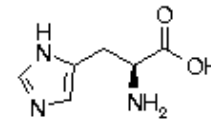
cys c Cystein



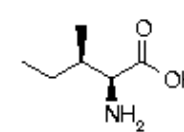
gln q Glutamin



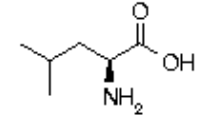
glu e Glutaminsäure



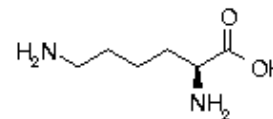
his h Histidin



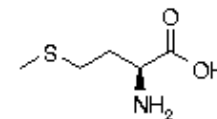
ile i Isoleucin



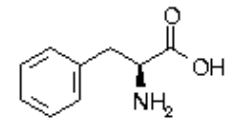
leu l Leucin



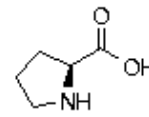
lys k Lysin



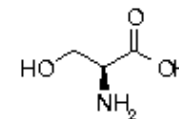
met m Methionin



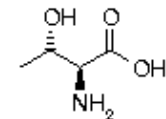
phe f Phenylalanin



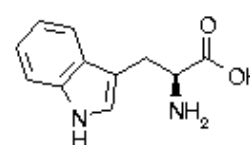
pro p Prolin



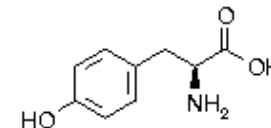
ser s Serin



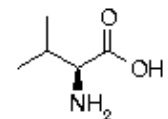
thr t Threonin



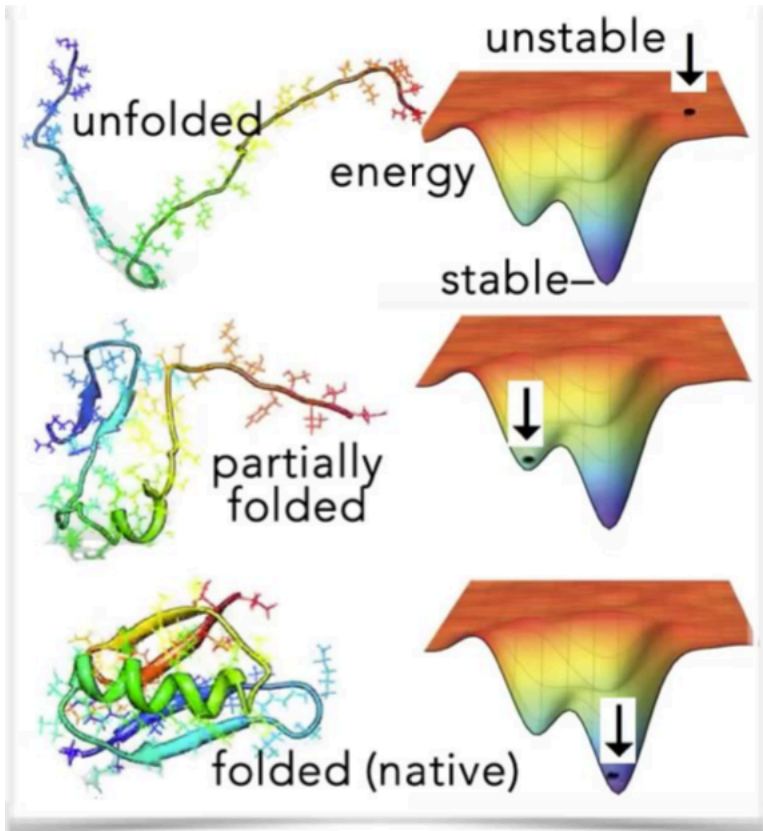
trp w Tryptophan



tyr y Tyrosin



val v Valin



Molecular simulation
of protein folding

Questions to answer (p. 198):

- Make a model of the structure of a polypeptide if all of its R-groups were hydrophilic?

How does an allosteric effector or a post-translational modification influence protein activity?

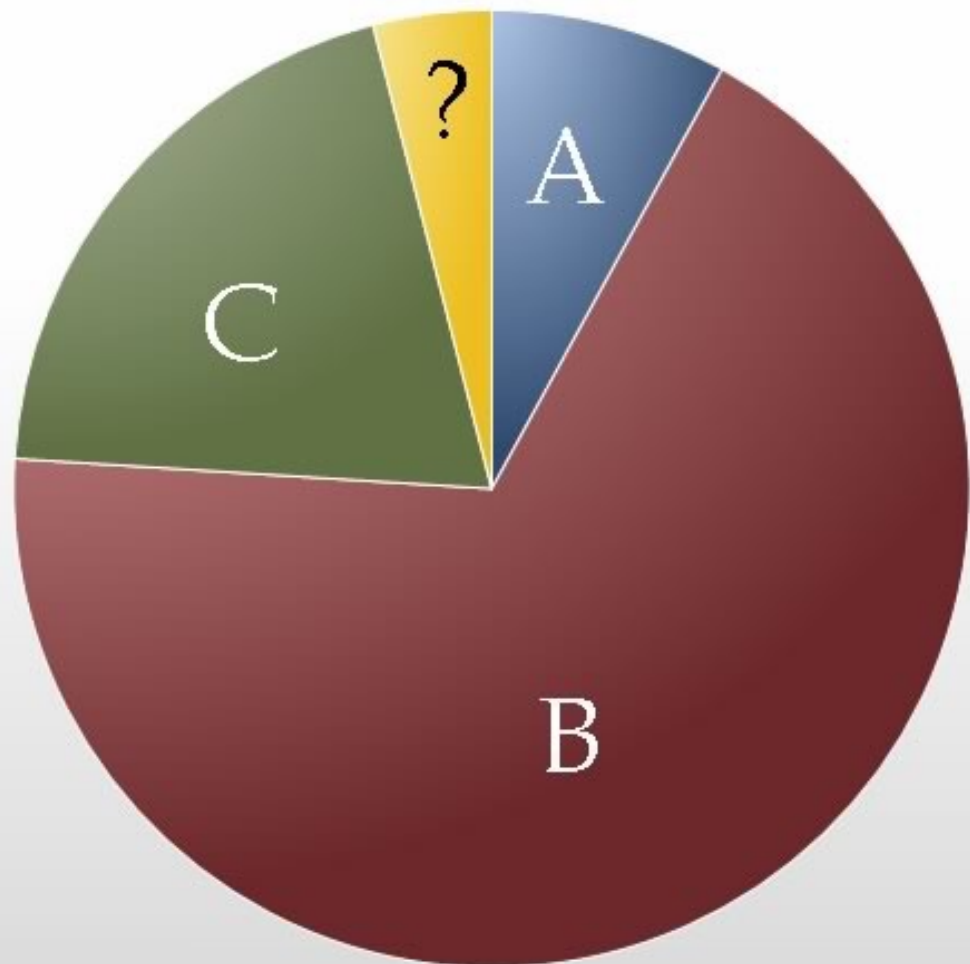
How proteolytic processing of a protein/polypeptide different from the effects of an allosteric effector or a post-translational modification?

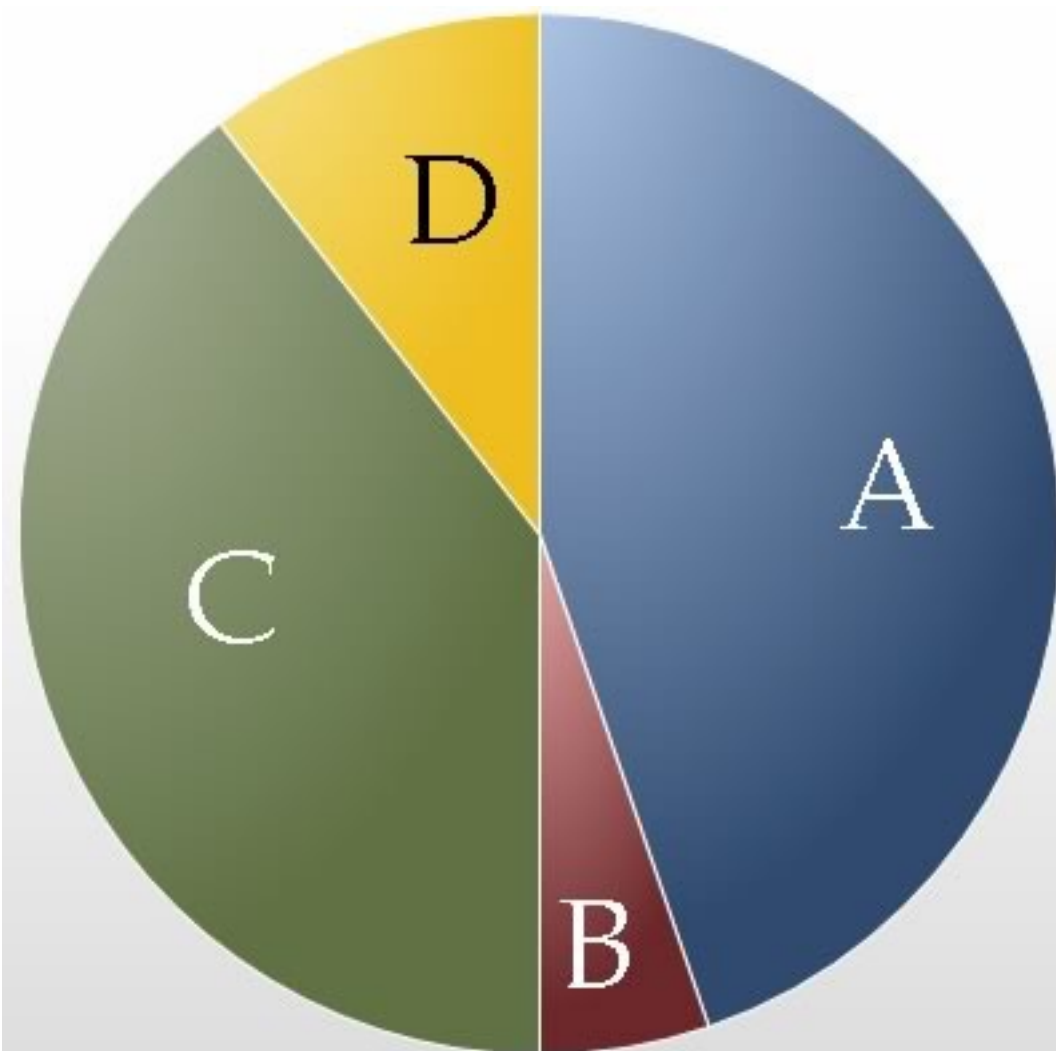
How can proteolytic processing (or allosteric effectors) influence the activity of “signals” within a polypeptide, such as those used to localize or exclude a protein from the nucleus?

8.4 read p. 196-203

Q: Pick ALL statements that are **NOT** true of chaperones...

- ☒ A. they are required for polypeptide synthesis
- ☐ B. some can unfold incorrectly folded polypeptides
- ☒ C. they determine the final structure of a polypeptide (protein)
- ☐ D. They are encoded by genes and can require other chaperones to fold correctly
- ☐ no idea

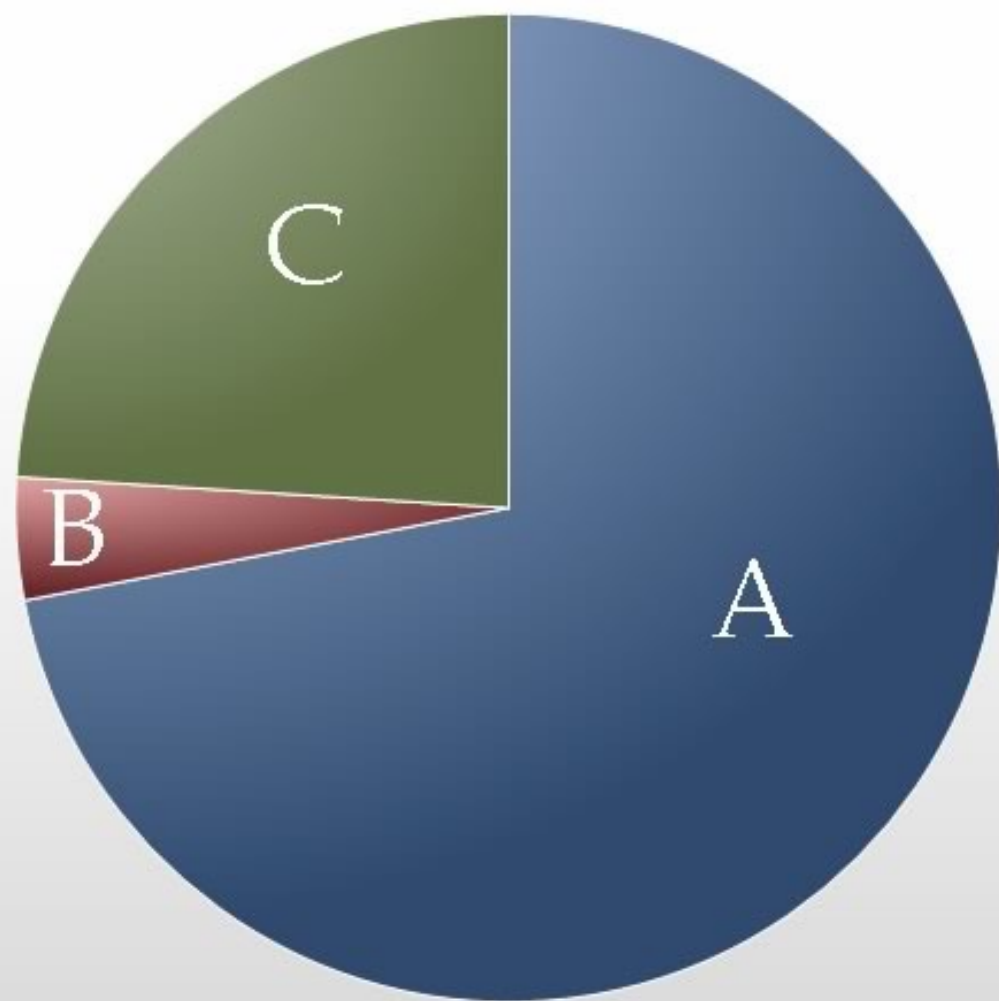




How does activating the expression of a gene expressing a "heat-shock" chaperone help a cell adapt to a changing environment?

- ☐ by increasing the number of mutations that occur
- ☒ by helping unfolded proteins refold
- ☐ by degrading unfolded proteins
- ☐ by increasing the rate of translation
- ☐ no idea

For a chaperone to be active, do you think it have to be coupled to a thermodynamically favorable reaction?



- ☐ yes
- ☐ no
- ☐ depends upon the chaperone
- ☐ no idea

Here is a cartoon of a eukaryotic cell, indicate where a protein would be located if there were a mutation that destroyed its "signal sequence".

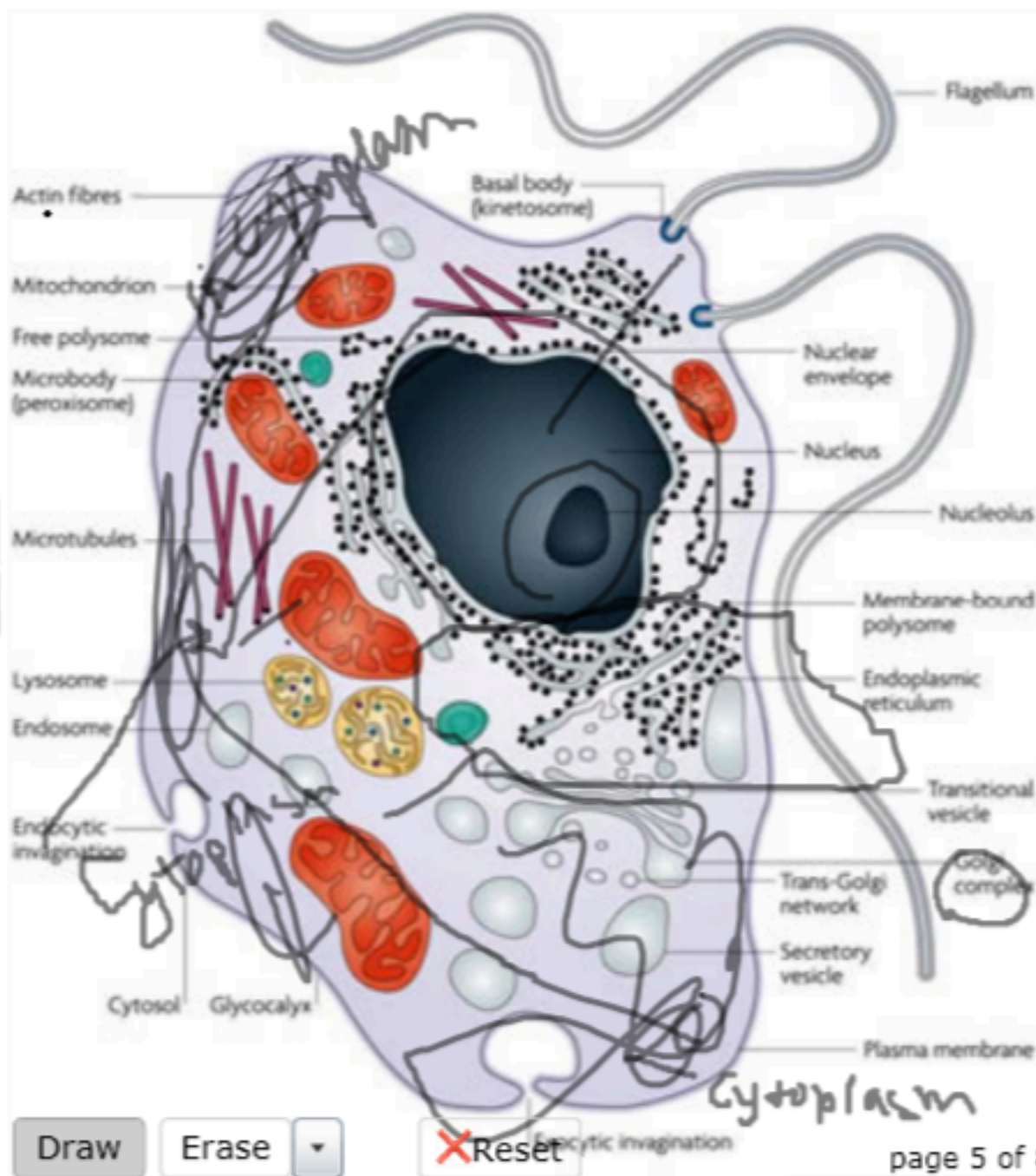
Fill in the blank: The mutated protein would most likely be found in the ...

☒ Check

Would it be the same or different in a prokaryotic cell?

- ☐ same
- ☐ different

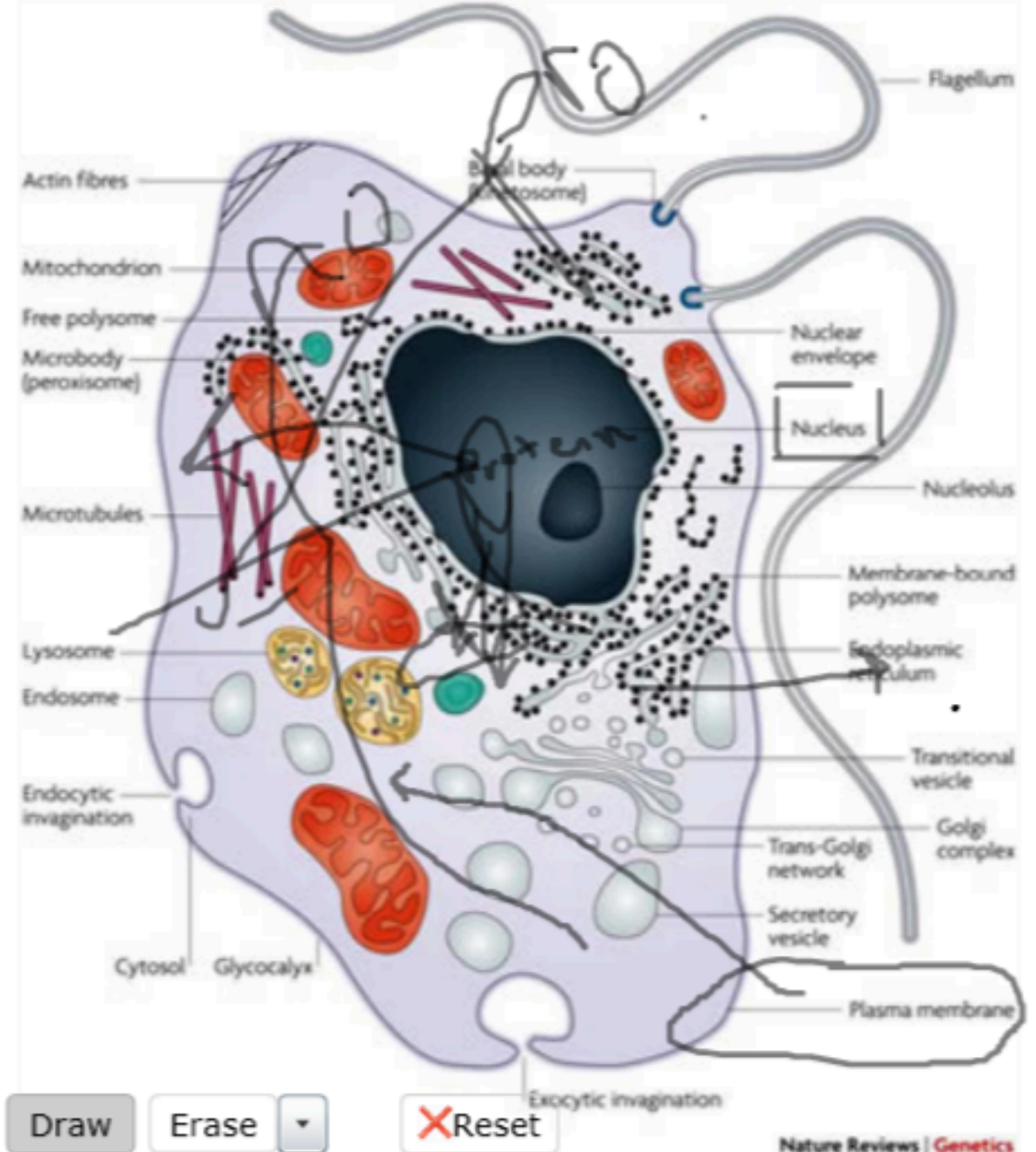
☐ question does not make sense, prokaryotic and eukaryotic cells are completely different



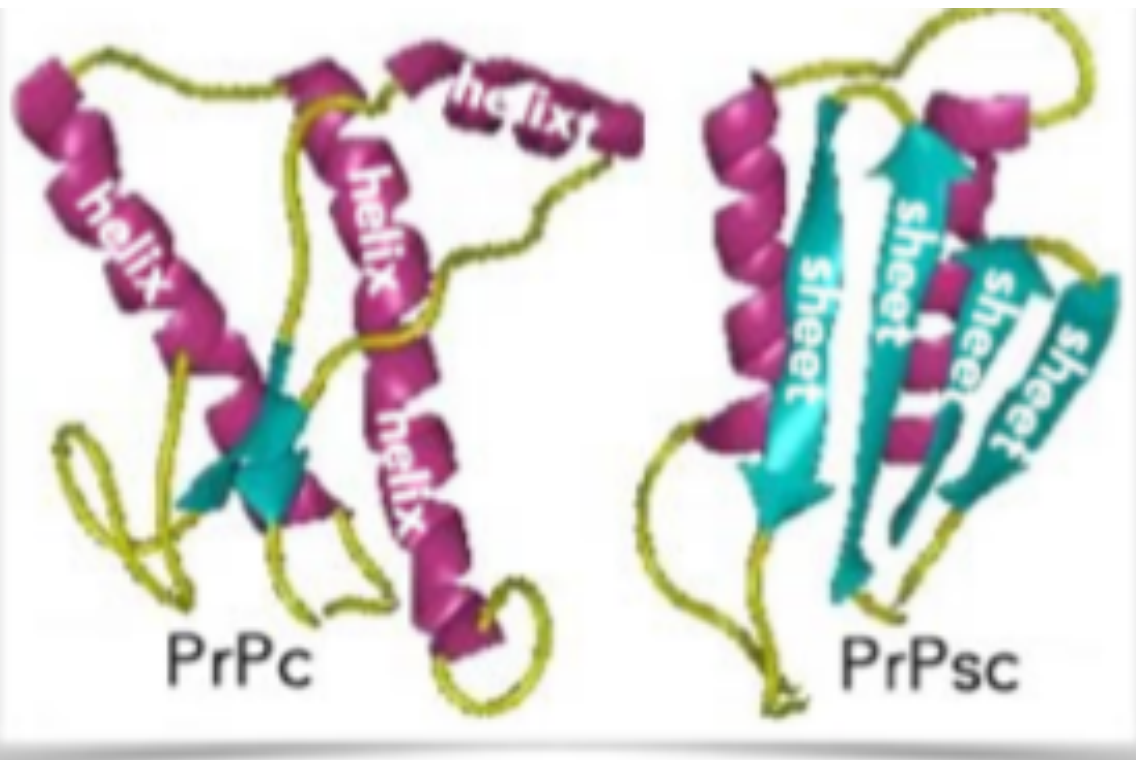
Now indicate the effect (on the drawing) of a mutation that destroys a protein's nuclear localization sequence.

Where would the protein most likely end up?

- ☐ secreted out of the cell
- ☐ in the cytoplasm
- ☐ in the nucleus
- ☐ in the plasma membrane
- ☐ in impossible to predict
- ☐ no idea



How could a “mis-folded” protein influence the correctly folded protein?



A protein in motion with water molecules

prion appregation

Have a thankful (and safe) thanksgiving!



crispr video

Molecular simulation of protein folding

A protein in motion with water molecules

ligand release from protein