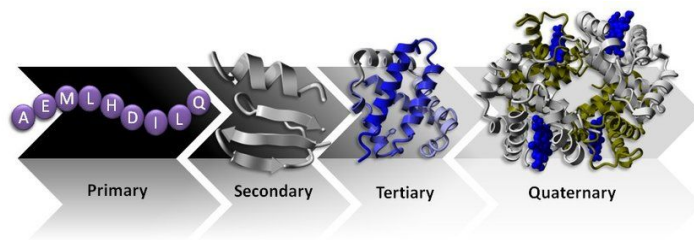


Protein Folding Virtual Activity



Learning Objective:

Explain how a change in the subunits of a polymer may lead to changes in structure or function of the macromolecule.

Visit <https://learn.concord.org/resources/787/protein-folding> and click “Preview”

Follow these instructions to set up Simulation #1:

Make sure *3-letter codes* are checked.

Click on the *hydrophobicity* section and click on *Charge and Hydrophobicity*.

Click on solvent type as *Water*.

Generate a *random protein*

Push play (at bottom). What do you observe?

(You can hit *generate a random protein* several times and compare the effects)

Use the amino acid chart at the end of this handout and your observations from the simulation to describe the properties of the different colored amino acids:

Brown amino acids:	Purple amino acids:
Green amino acids:	Pink amino acids:

Where do most of the brown amino acids congregate? Why?	Where do the green amino acids tend to be found? Why?	Why do purple and pink amino acids move toward one another?

Simulation #2:

Click on *Generate random protein, All hydrophobic*. Push *Play*.
Describe what happened. Why do you think this occurred?

Simulation #3:

Change the solvent from *water* to *oil*.
Describe what happened. Why do you think this occurred?

Simulation #4:

Click *Generate Random Protein, All Hydrophilic, Water*. Push *Play*.
What happened. Why do you think this occurred? Why do some still cluster?

Analysis questions:

1. What type of bond occurs between the amino acids in the primary structure?

2. What could happen to the shape of a protein if you changed ONE amino acid in the primary chain? How would this affect its function?

3. What types of bonds occur between neighboring amino acids in a secondary structure to create alpha helices and beta pleats?

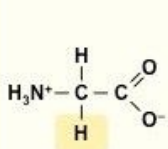
4. What types of bonds occur in tertiary and quaternary structures to cause a “globular” structure?

5. What type of bond occurs between two cysteines?

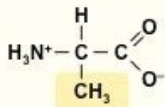
6. What external conditions influence the shape of a polypeptide? How?

7. What is the highest level of protein structure illustrated in this simulation?

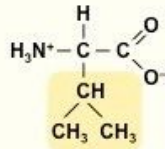
NON-POLAR



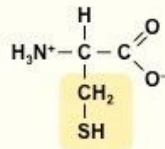
Glycine
(Gly / G)



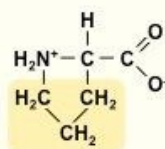
Alanine
(Ala / A)



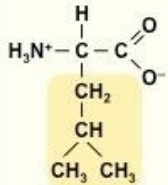
Valine
(Val / V)



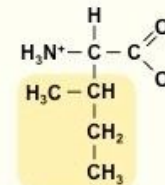
Cysteine
(Cys / C)



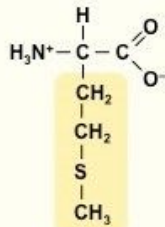
Proline
(Pro / P)



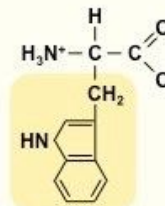
Leucine
(Leu / L)



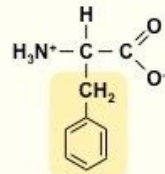
Isoleucine
(Ile / I)



Methionine
(Met / M)

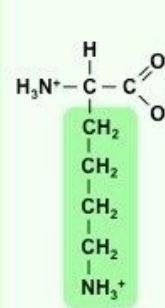


Tryptophan
(Trp / W)

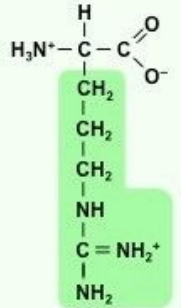


Phenylalanine
(Phe / F)

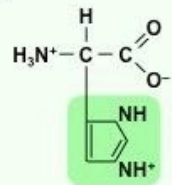
+ CHARGE



Lysine
(Lys / K)

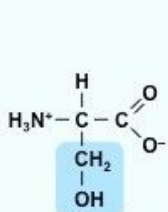


Arginine
(Arg / R)

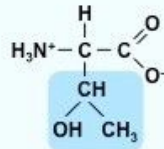


Histidine
(His / H)

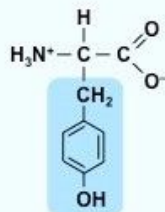
POLAR



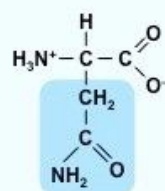
Serine
(Ser / S)



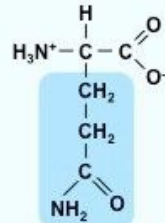
Threonine
(Thr / T)



Tyrosine
(Tyr / Y)

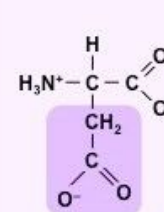


Asparagine
(Asn / N)

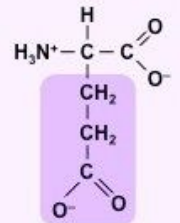


Glutamine
(Gln / Q)

- CHARGE



Aspartic Acid
(Asp / D)



Glutamic Acid
(Glu / E)