



Uncooking the Egg

Modeling protein folding and denaturation



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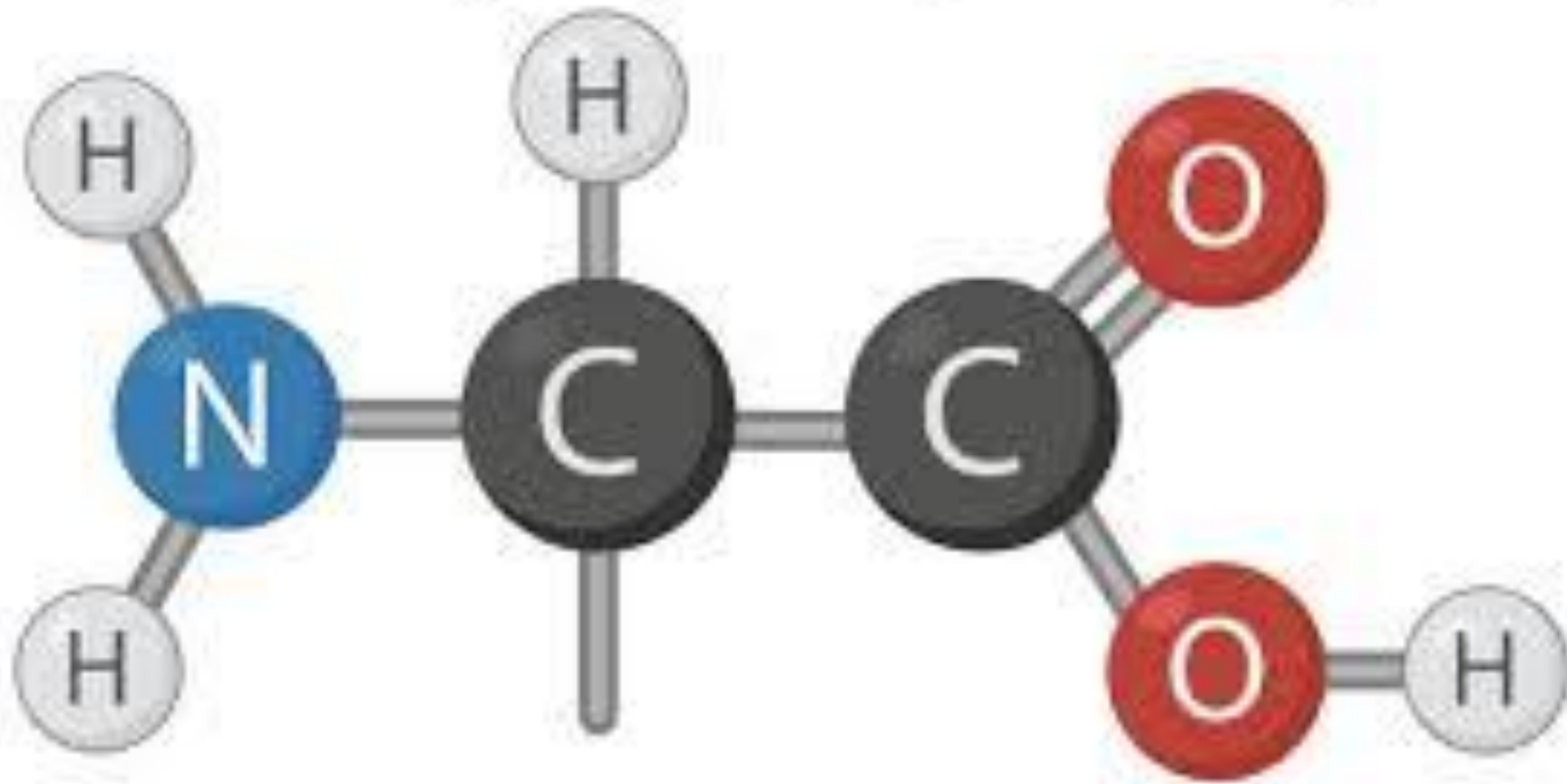
Uncooking the Egg



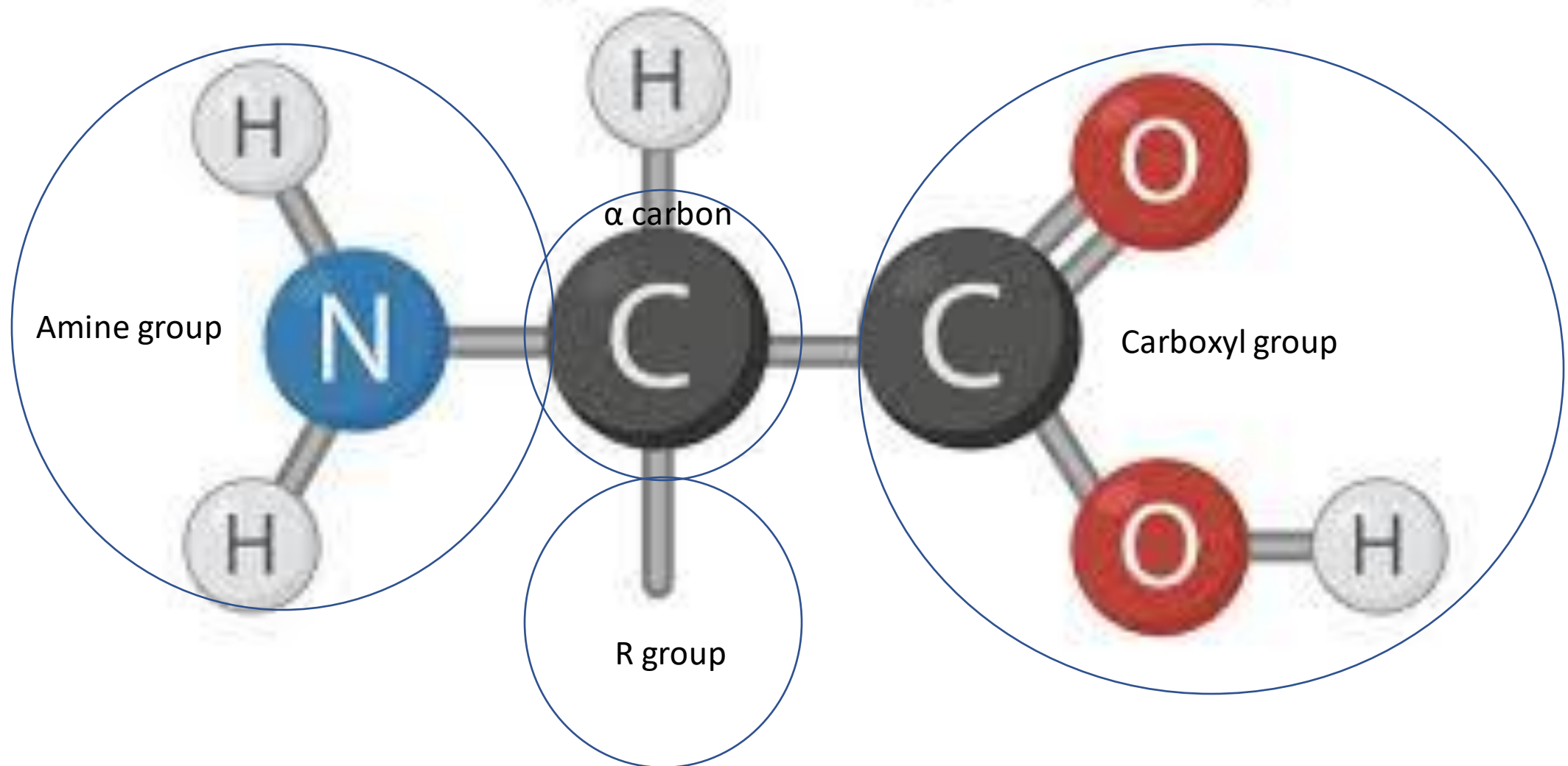
Protein folding and denaturation



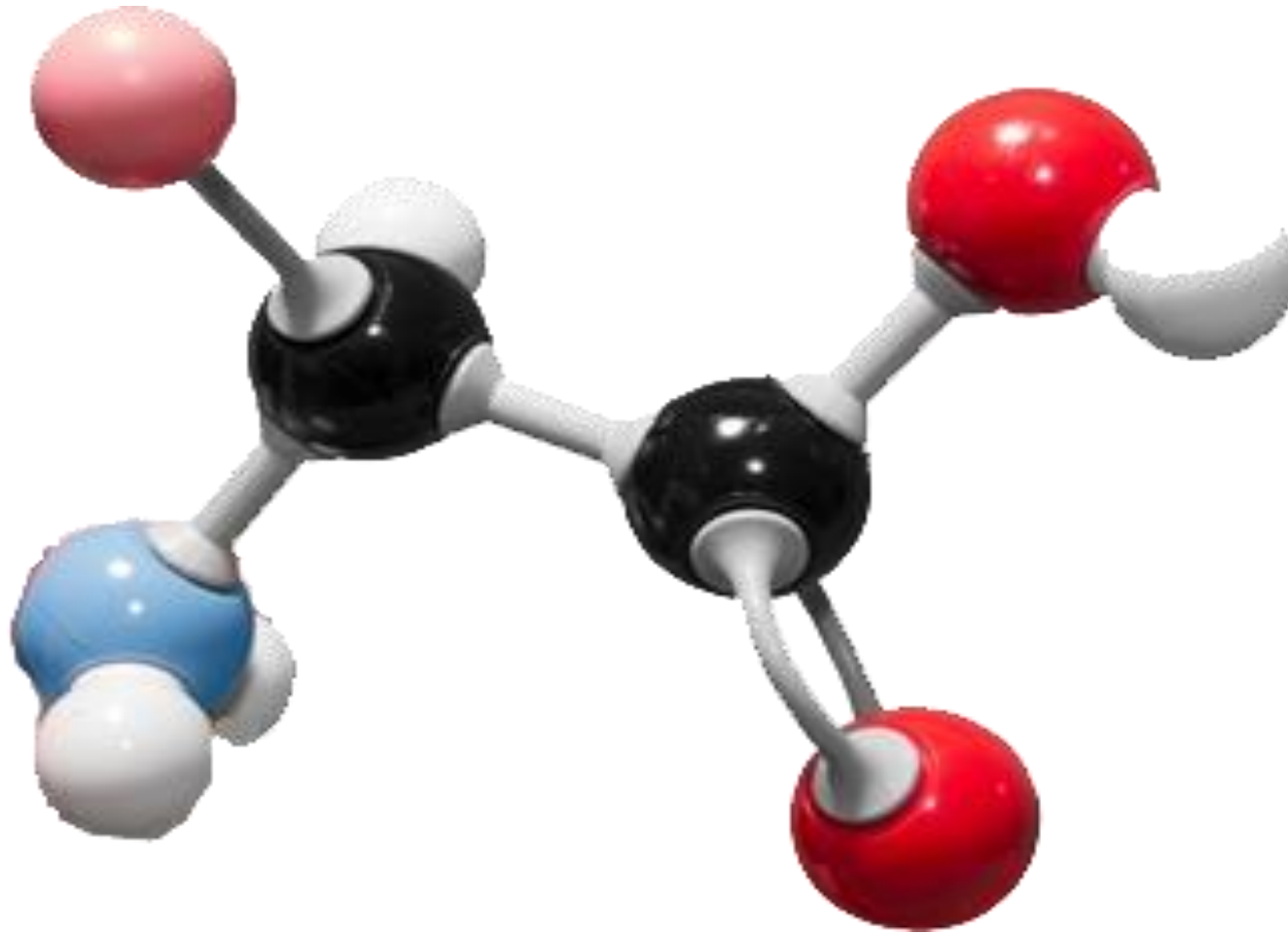
Amino Acids- Properties, Structure, Classification, Functions



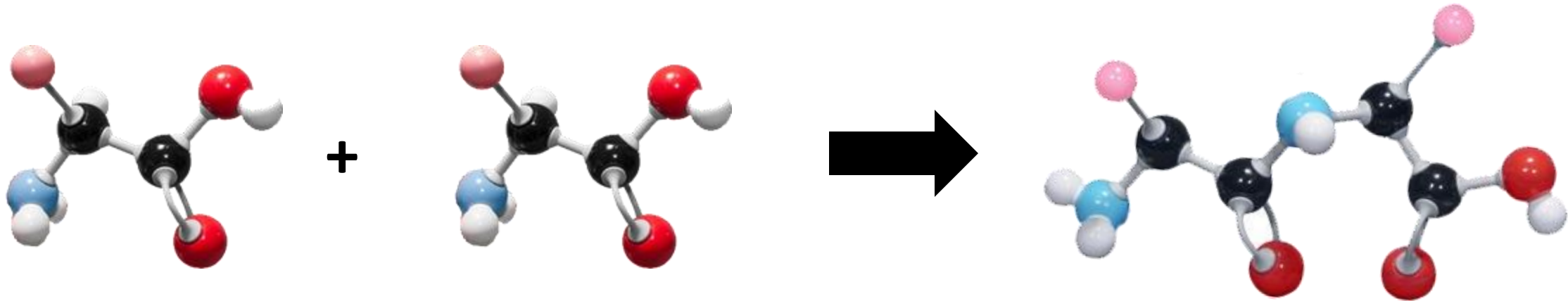
Amino Acids- Properties, Structure, Classification, Functions

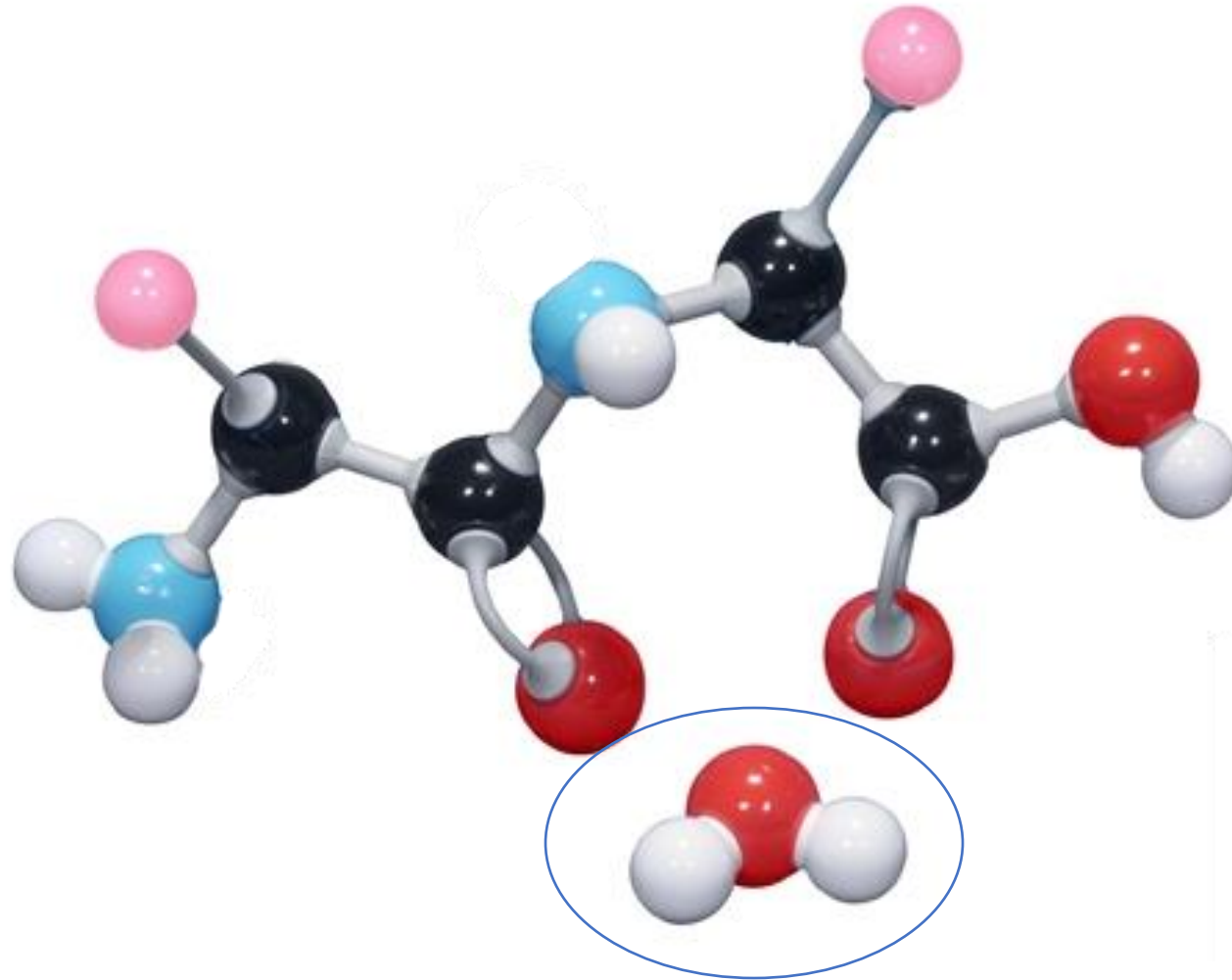


Moly Mods – Amino Acid



How do amino acids form proteins?
(or in this case, a dipeptide?)

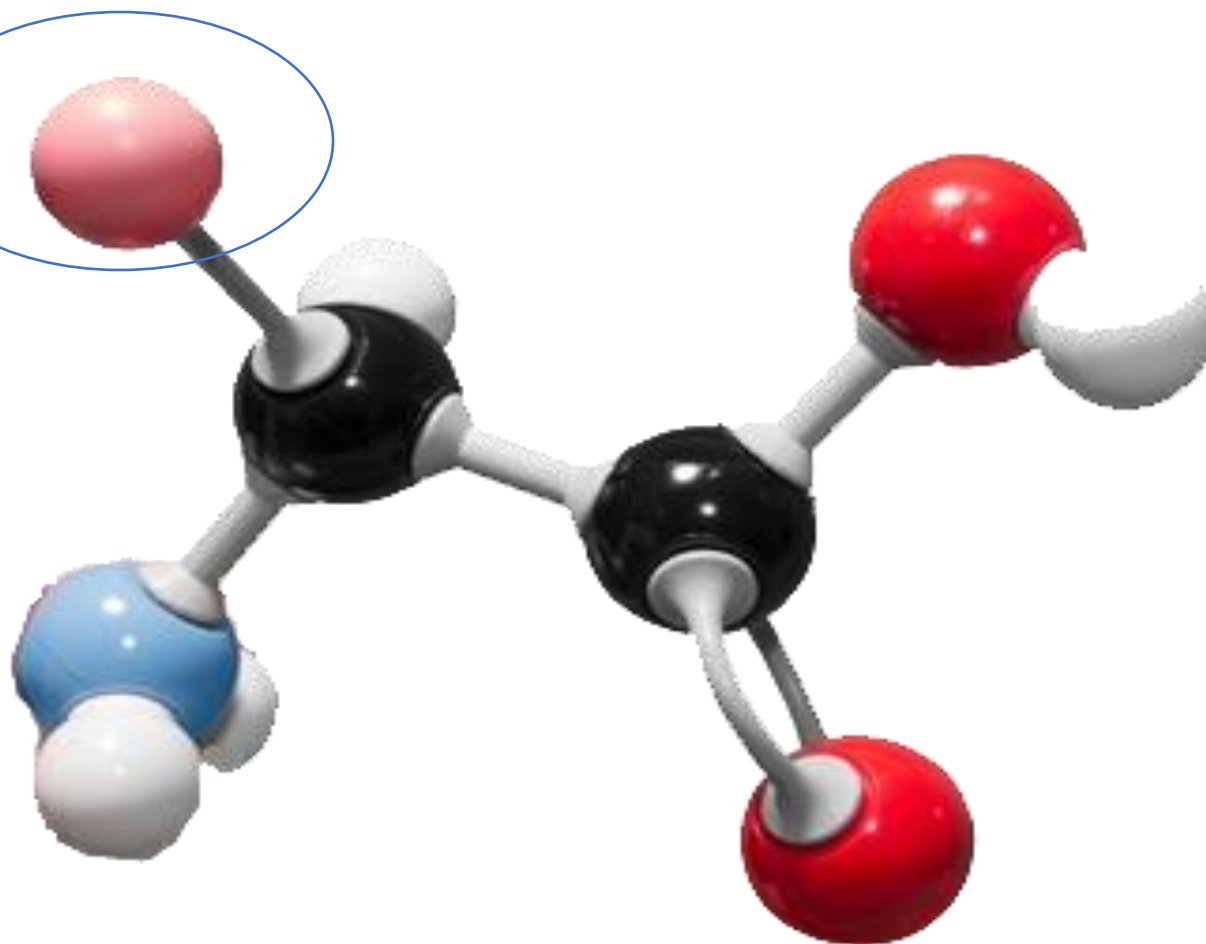




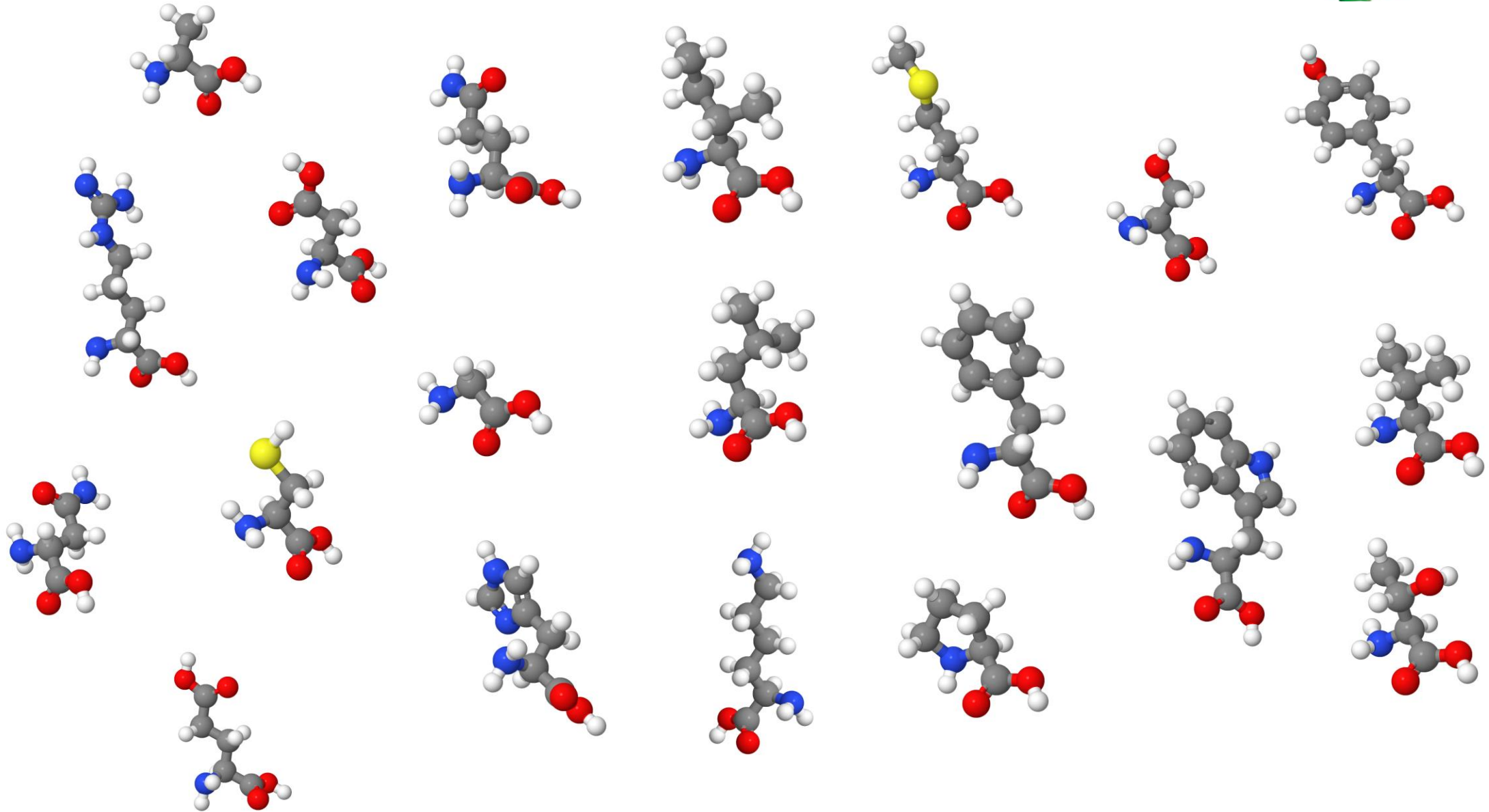
Dehydration Synthesis!



What is this?



Here are all 20 common Amino Acids with their unique R-groups



Amino Acid Side Chain Chart®

Name	Amino Acid	Side Chain	Name	Amino Acid	Side Chain	Name	Amino Acid	Side Chain	Name	Amino Acid	Side Chain
Alanine	Ala	A	Glutamine	Gln	Q	Leucine	Leu	L	Serine	Ser	S
Arginine	Arg	R	Glutamic Acid	Glu	E	Lysine	Lys	K	Threonine	Thr	T
Asparagine	Asn	N	Glycine	Gly	G	Methionine	Met	M	Tryptophan	Trp	W
Aspartic Acid	Asp	D	Histidine	His	H	Phenylalanine	Phe	F	Tyrosine	Tyr	Y
Cysteine	Cys	C	Isoleucine	Ile	I	Proline	Pro	P	Valine	Val	V

Atom Color Key



Amino Acid Property Key

Amino acid clip color and name color indicate property



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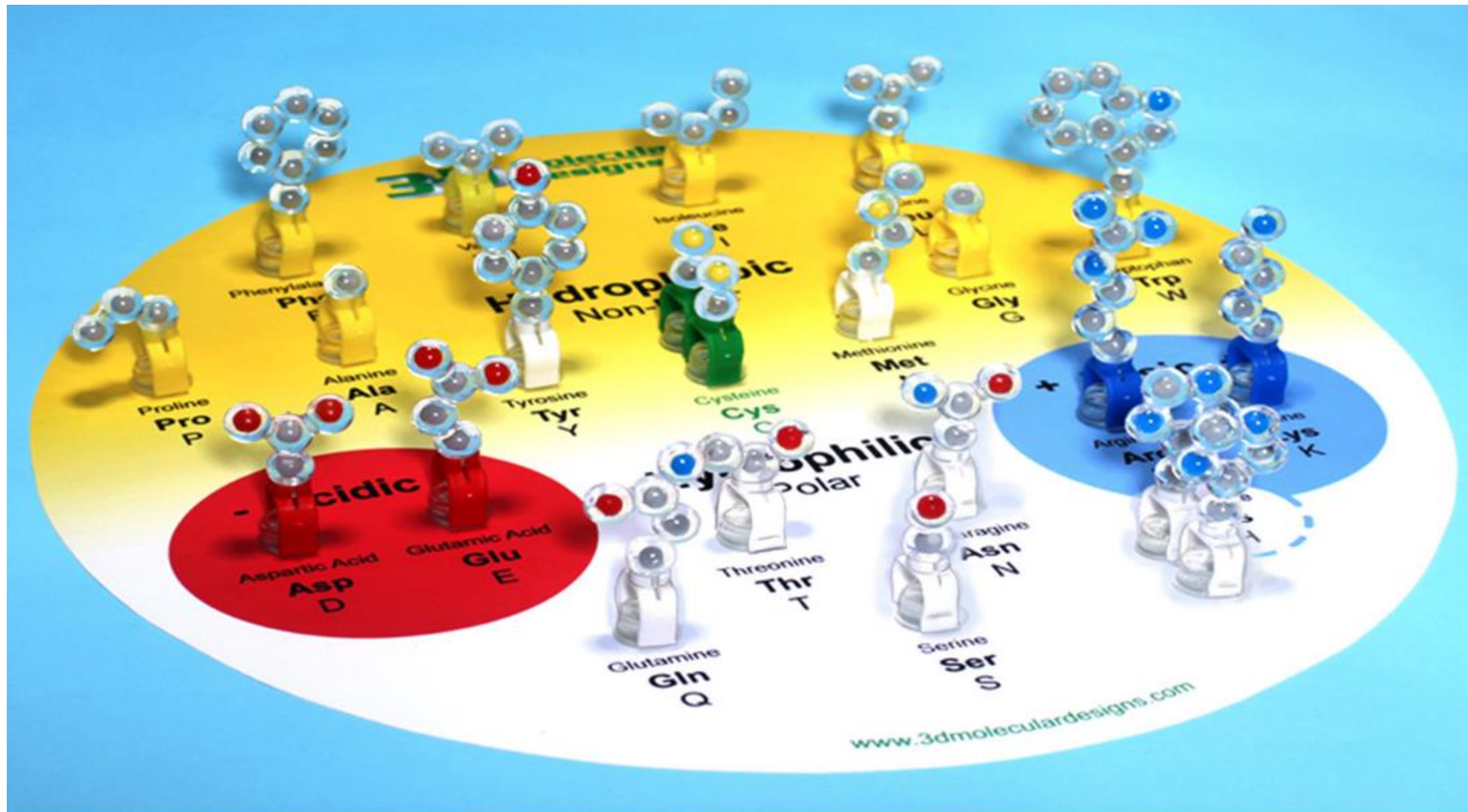


Open your bag and sort your amino acids on the property circle



4:00





Look closer

- What trends do you see?
- What elements are associated with different properties?
- Turn and talk!
- Be prepared to share!

Let's build a random protein!

Begin by choosing your favorite Amino Acids

6 Hydrophobic sidechains

2 Acidic sidechains

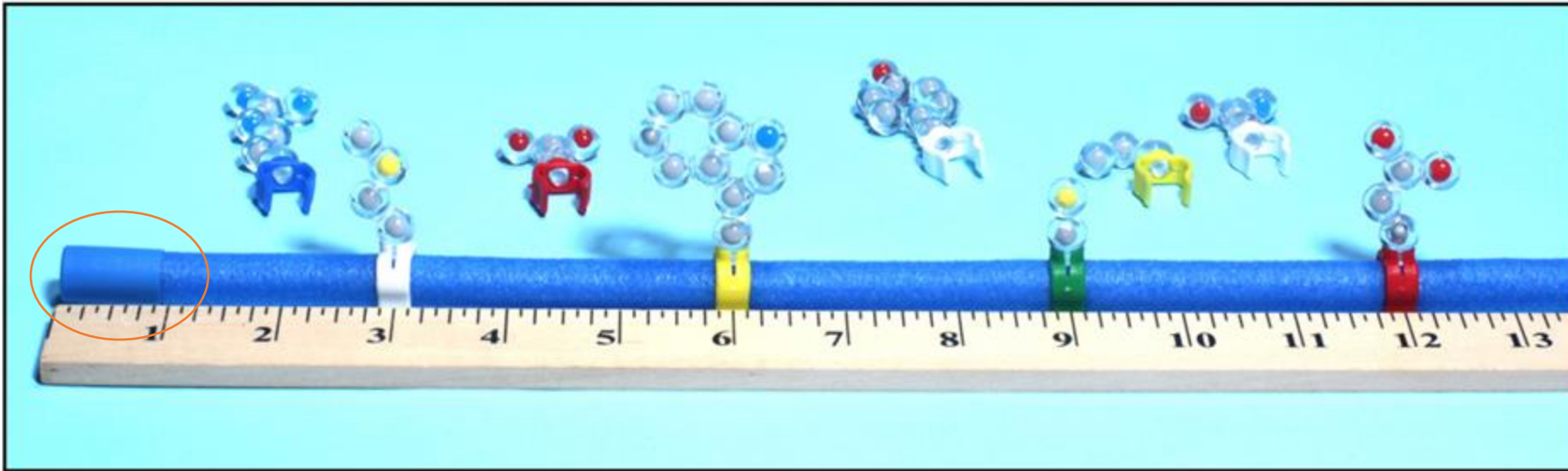
2 Basic sidechains

2 Cysteine sidechains

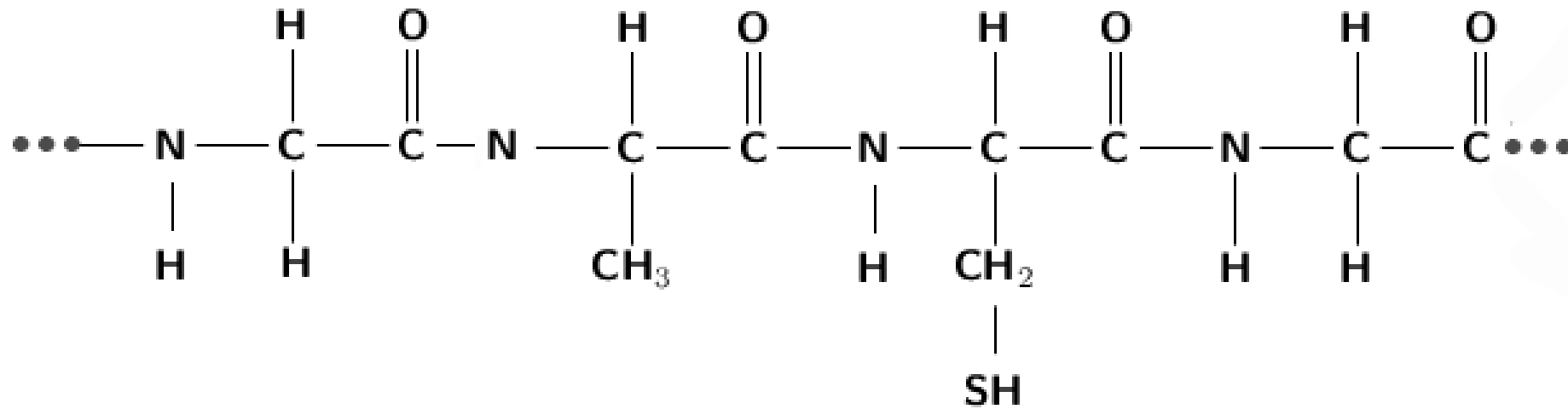
3 Polar sidechains (white)



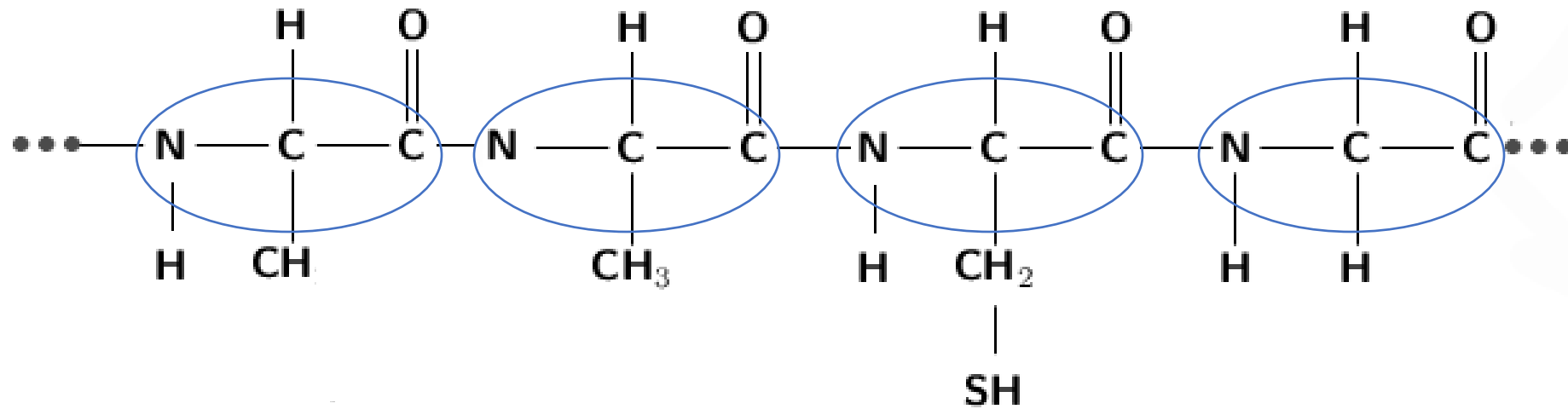
Step 2: Starting at the blue end of your tuber, use the clips to add your selected amino acids to get your primary structure.



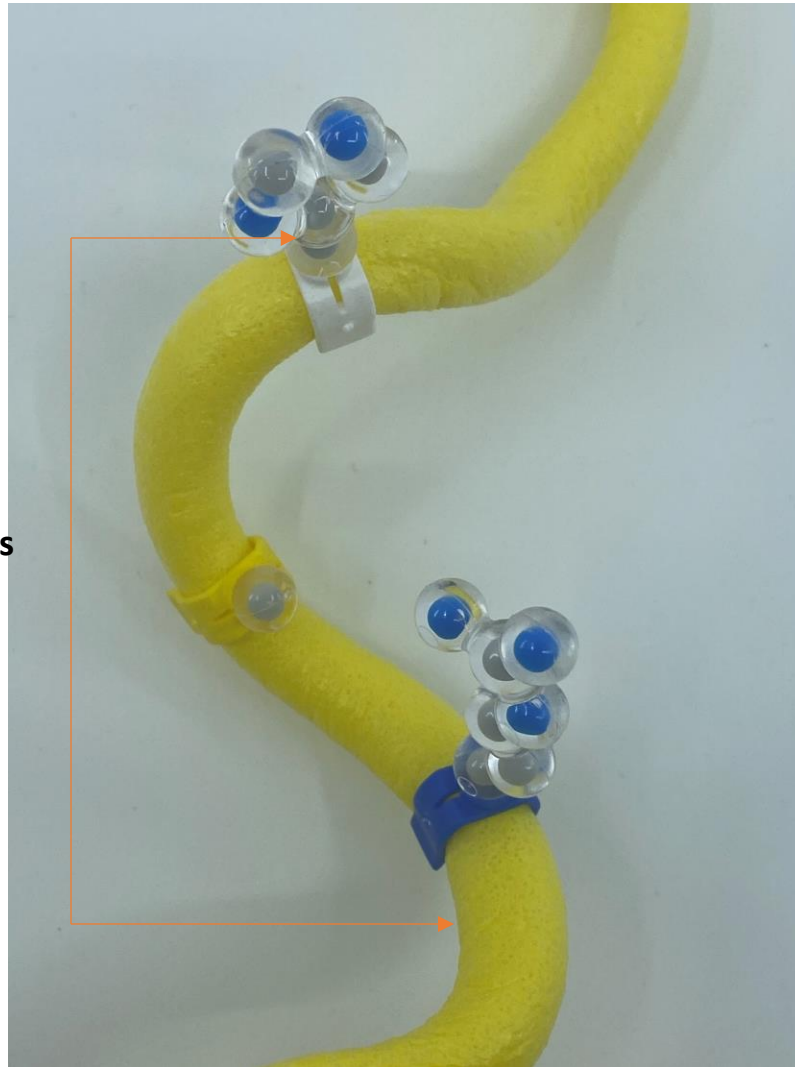
Why did we start at the blue end? What pattern do you notice?



N-C-C-N-C-C-N-C-C-N-C-C ... This is our protein backbone- and the PRIMARY structure of a protein



3.6 Amino Acids
per turn



Secondary Structures –

- 1) Alpha Helixes form because of hydrogen bonding between components of the protein backbone. The helix is usually right-handed.

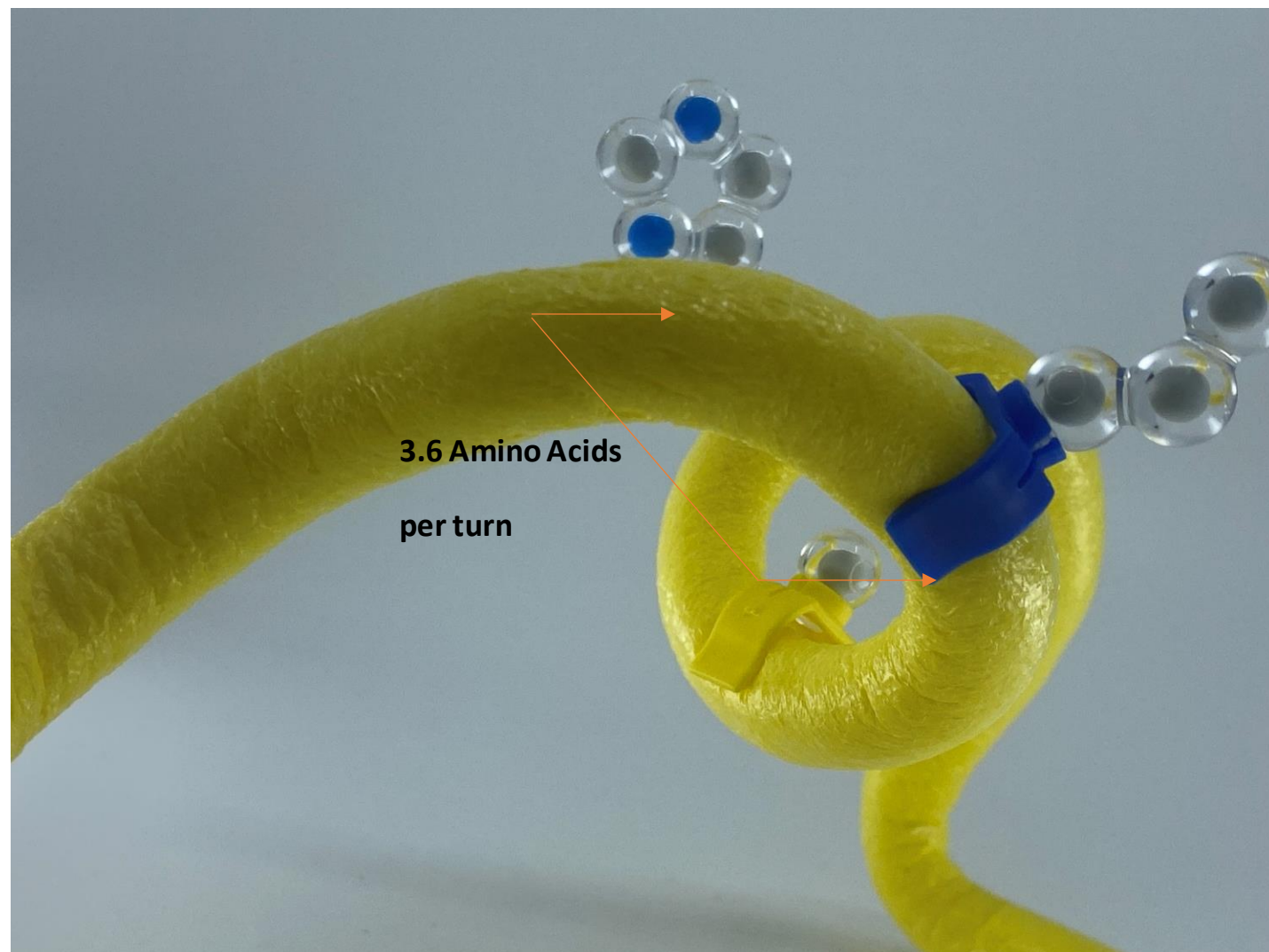
***Add a helix to your toober**

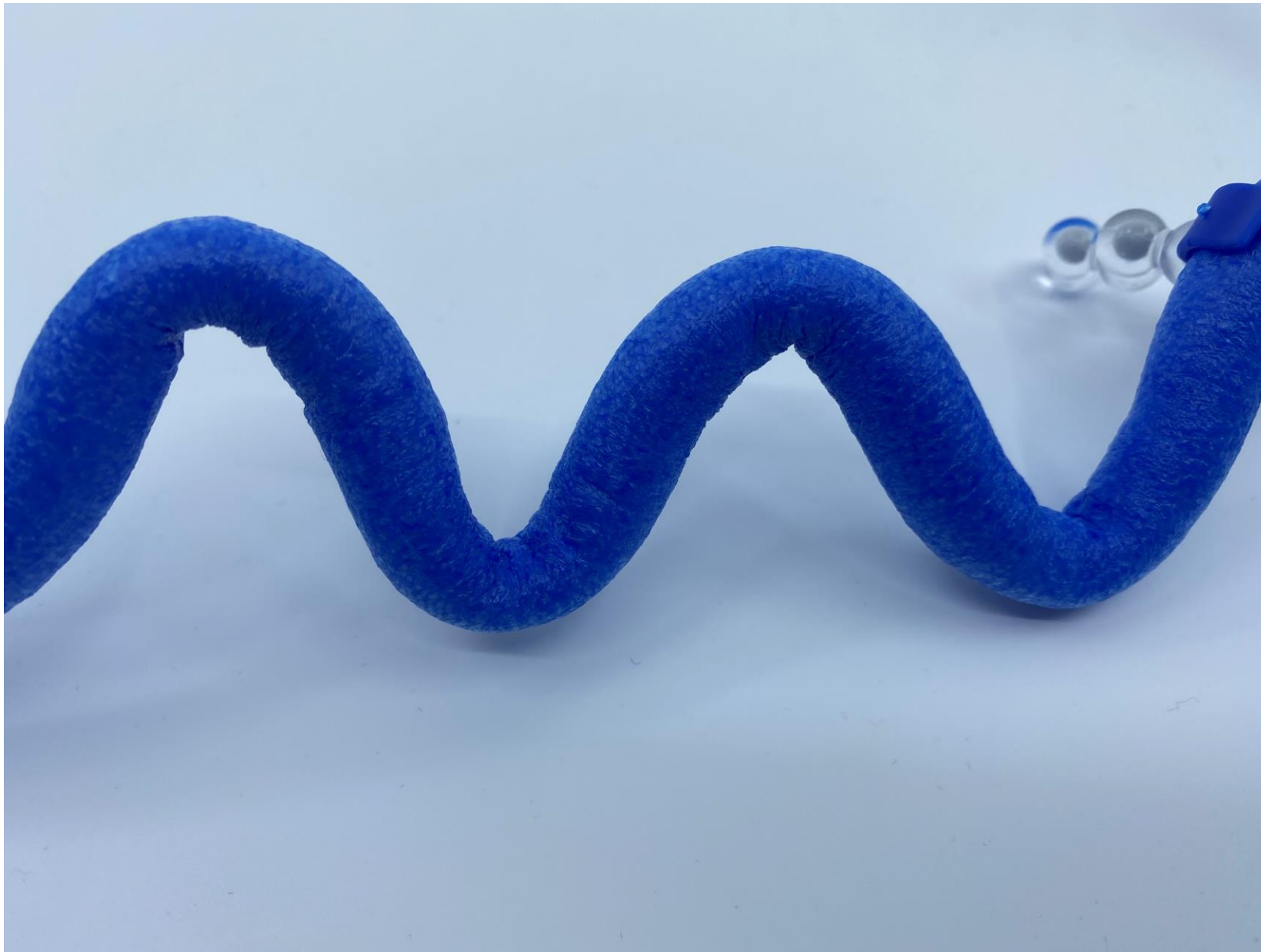


Secondary Structures –

- 1) **Alpha Helixes** form as a result of hydrogen bonding between components of the protein backbone. The helix is usually right-handed.

***Add a helix to your toober**





Secondary Structure

2) Beta Sheets are also formed as a result of hydrogen bonding in the backbone of a protein

* Add 1 sheet to your toober

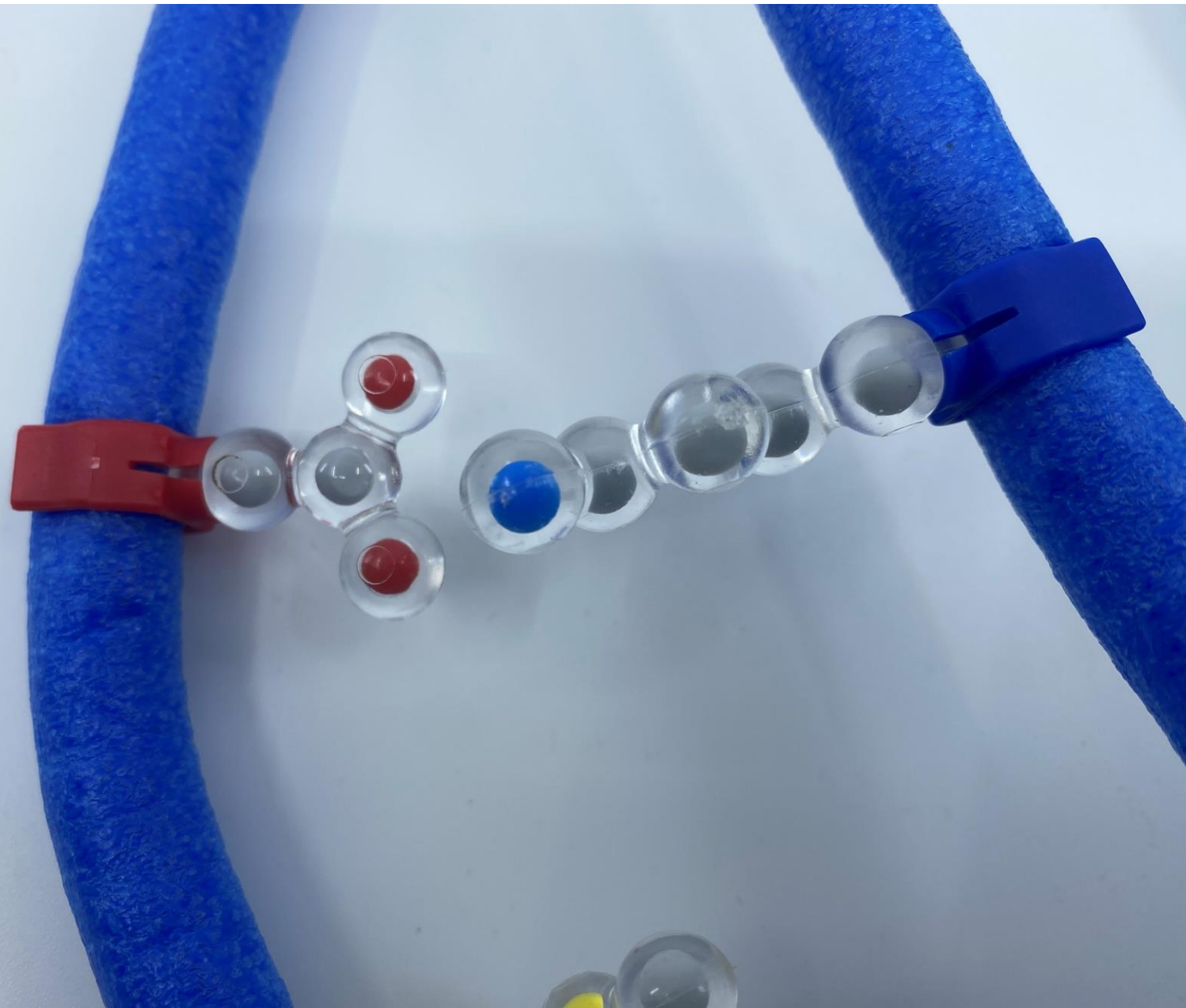


Tertiary structure

1) Cysteines will form a disulfide bond, adding stability to the protein structure-

*Fold your toober so that the Cys – Cys can interact.

Note* - The more disulfide bonds a protein has, the more stable it becomes



Tertiary Structure

2) Acids and bases will form a salt bridge between them

* Fold your toober to create 2 salt bridges

Tertiary Structure

3) Since most of your cells are made of water, the hydrophobic Amino Acids will try to “dive” to the center

* Fold your toober so that the hydrophobic amino acids can interact with each other in the “middle”



Tertiary Structure

4) Hydrophilic Amino Acids will want to interact with the water inside the cell.

*** Spin the hydrophilic amino acids toward the “outside” of your protein so that it can interact with the environment around it.**





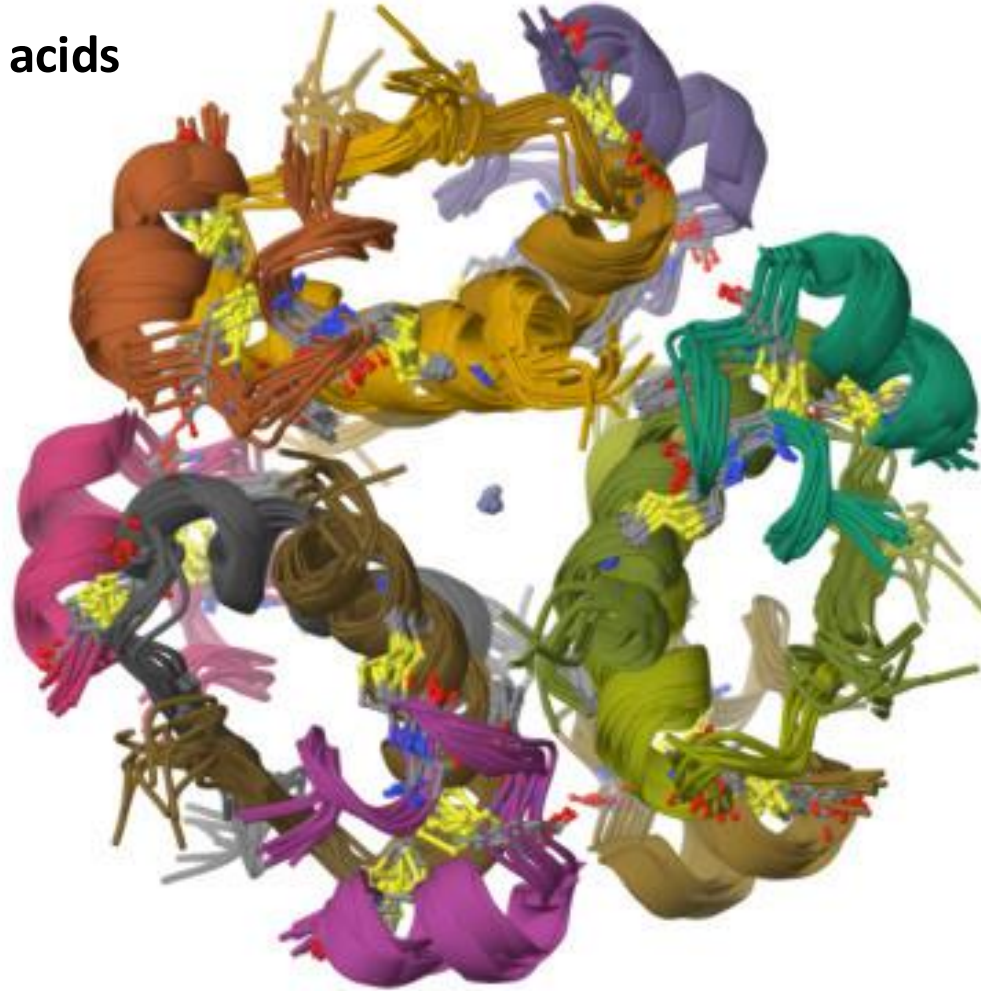
Hold up your protein!

Why is it different from the other groups?

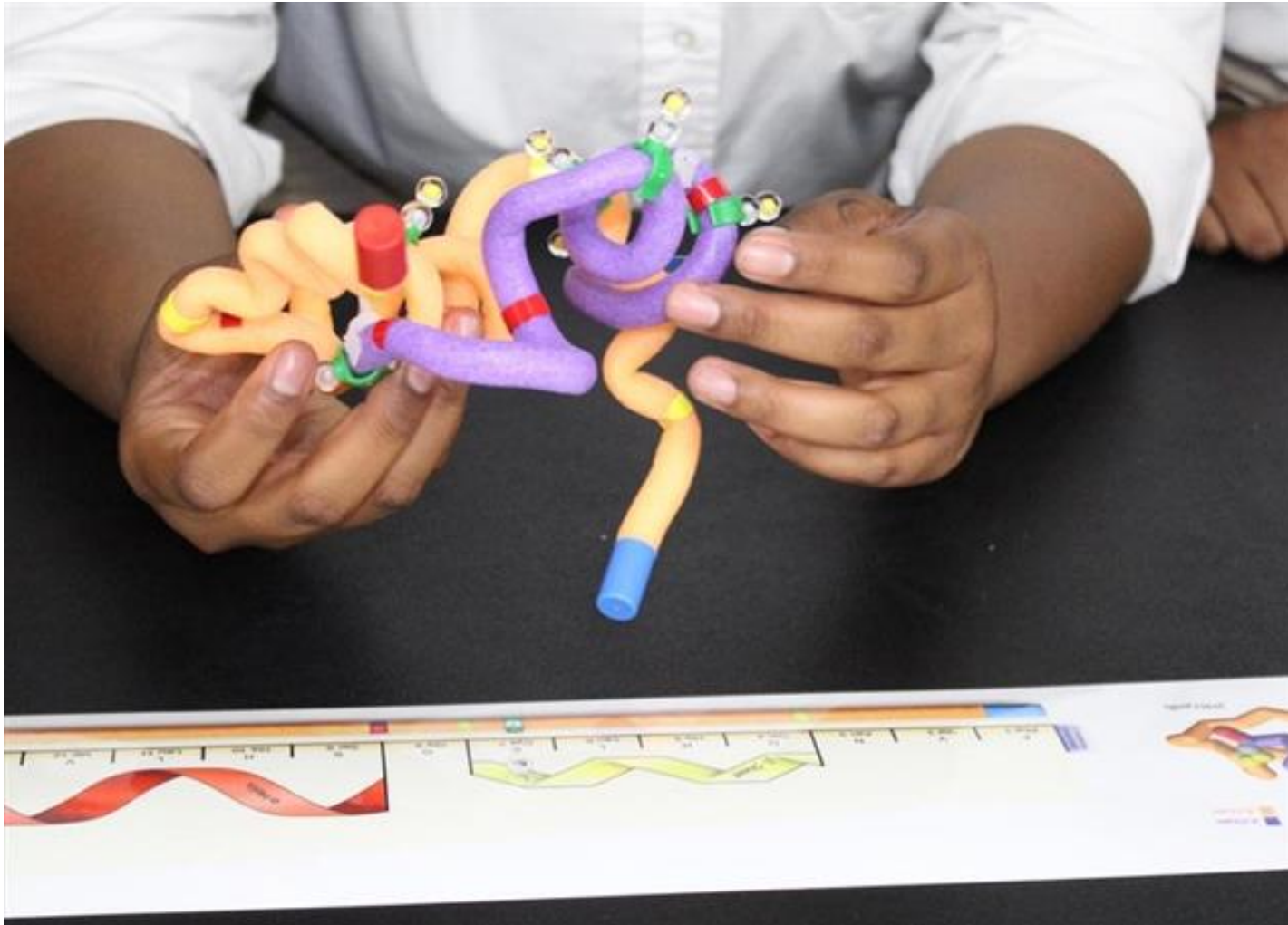


Quaternary Structure

Different proteins interact with each other. Ex. Insulin is comprised of 2 chains of amino acids



How could you model this with students?



Back to the Egg...



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What's actually happening?

Boiling the egg	Urea – 8M	Centrifuge and dilution
Proteins denature, random movement causes primary structure entanglement, new tertiary bonds form	Newly formed tertiary structures denatured, “lubricates” protein strands	Centrifuge causes sheer forces that separate the strands, Dilution causes spontaneous refolding into natural shapes



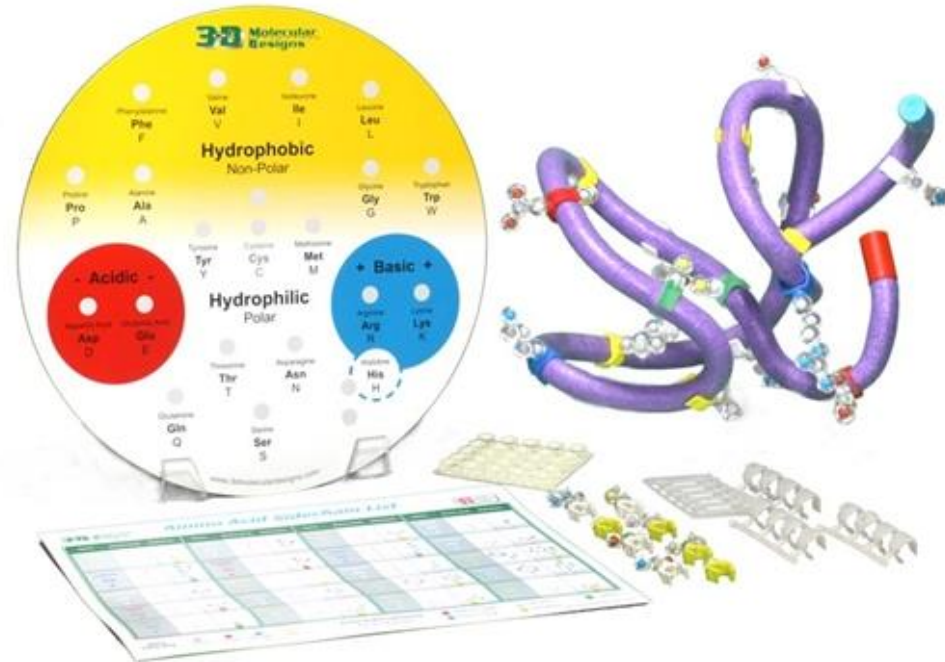
The Principle of Microscopic Reversibility...

“Corresponding to every individual process there is a reverse process, and in a state of equilibrium the average rate of every process is equal to the average rate of its reverse process.”

Lewis, G. N. (1925-03-01). ["A New Principle of Equilibrium"](#)

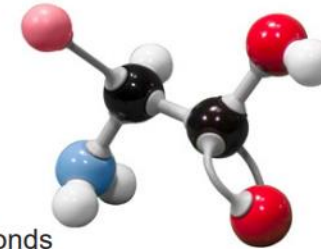


Kit used in this presentation: Amino Acid Starter Kit Amino Acid Building Block Models



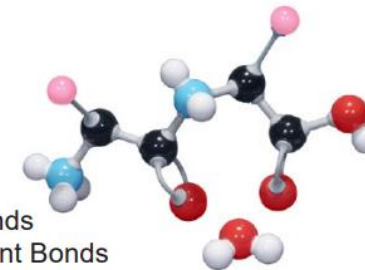
Amino Acid

- 2 Carbon
- 2 Oxygen
- 1 Nitrogen
- 1 R-Groups
- 4 Hydrogen
- 4 Hydrogen Bonds
- 3 Single Covalent Bonds
- 2 Double Covalent Bonds

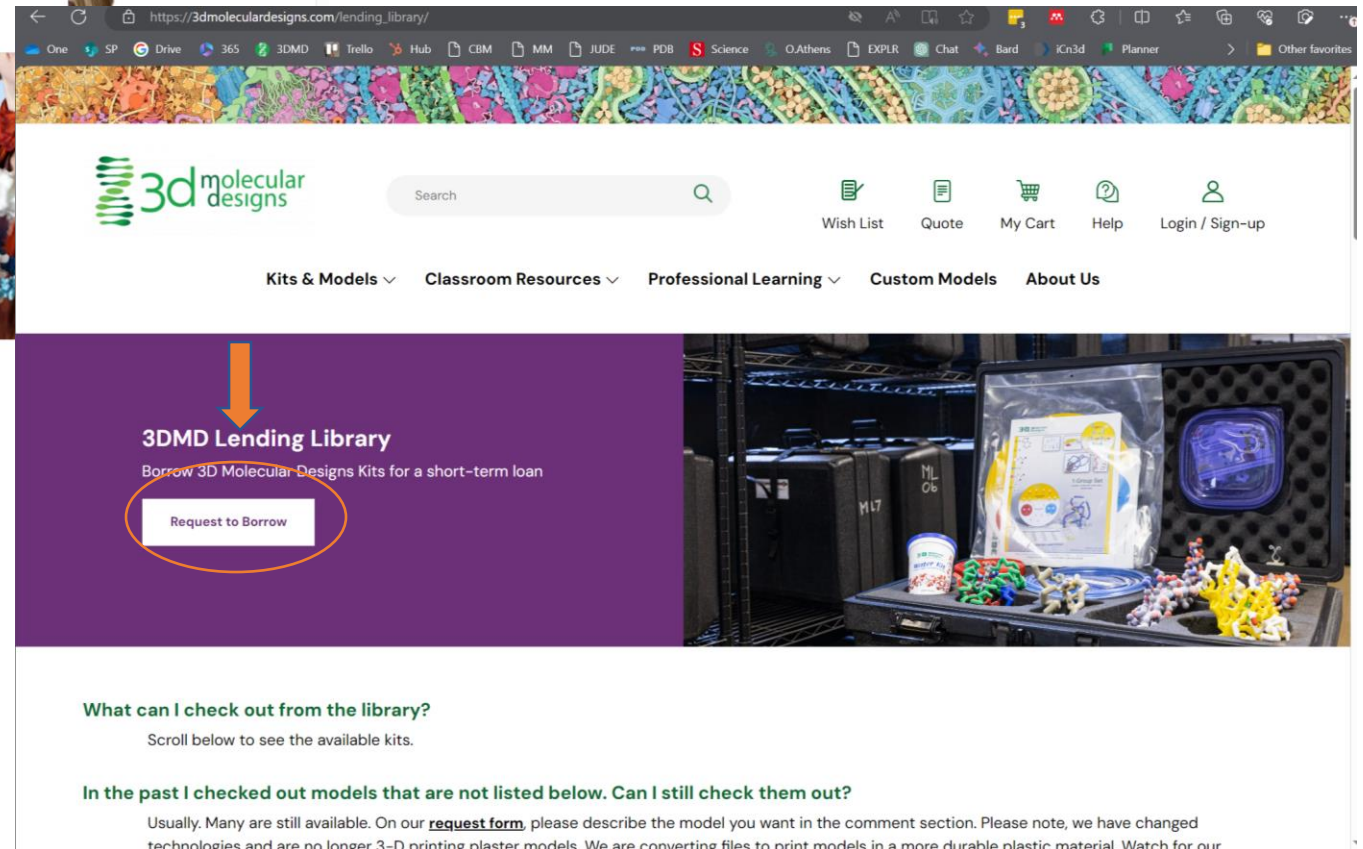
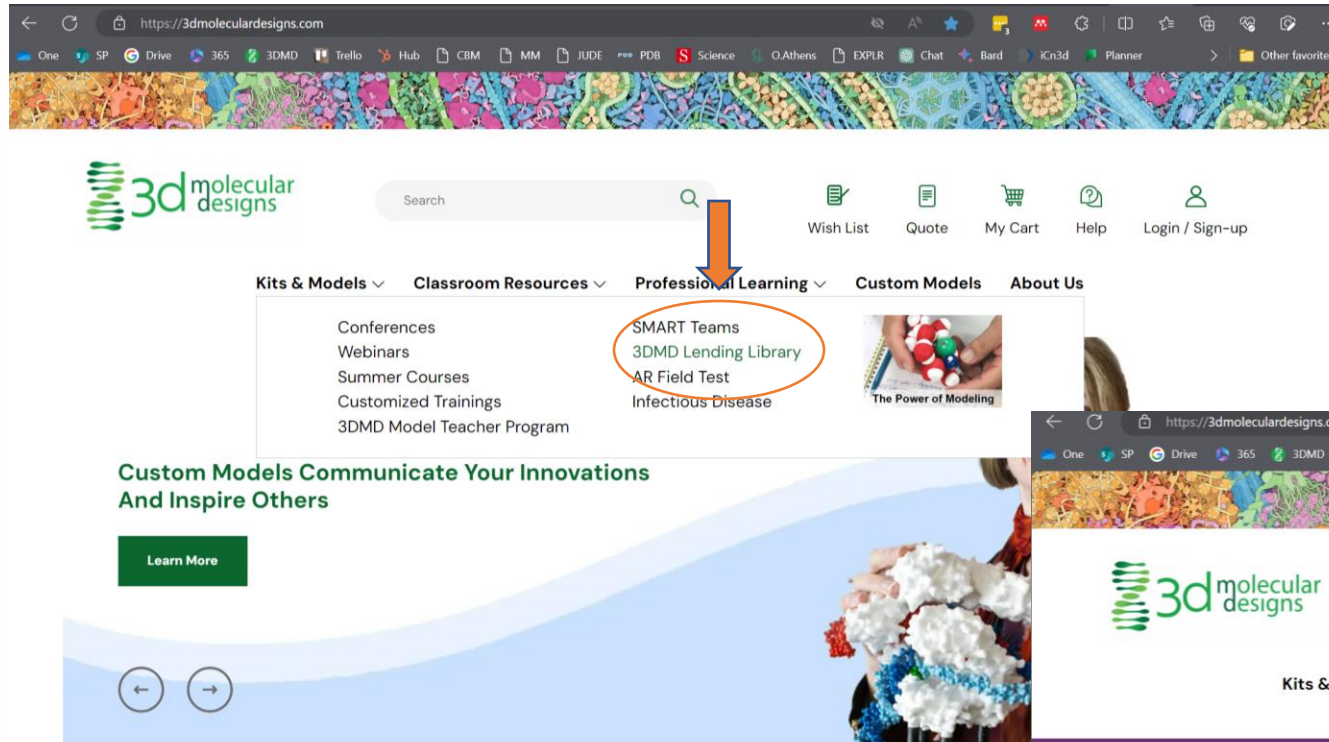


Dipeptide

- 4 Carbon
- 4 Oxygen
- 2 Nitrogen
- 2 R-Groups
- 8 Hydrogen
- 8 Hydrogen Bonds
- 6 Single Covalent Bonds
- 6 Double Covalent Bonds



Lending Library



Scan this QR code and fill out our survey!



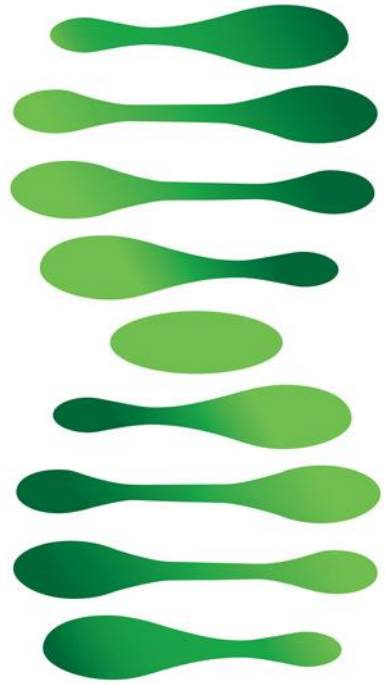
Show me your DNA molecule image
and I'll give you a model with AR
enhancement as a thank-you gift!



Workshop NGSS Connections

SEPs	CCCs	DCIs
Developing and using models	Structure and Function	HS-LS 1-3: Structure and function
Constructing Explanations and Designing Solutions	Patterns	
	Stability and change	
	Systems and models	
	Cause and Effect	





Transforming Science Learning

