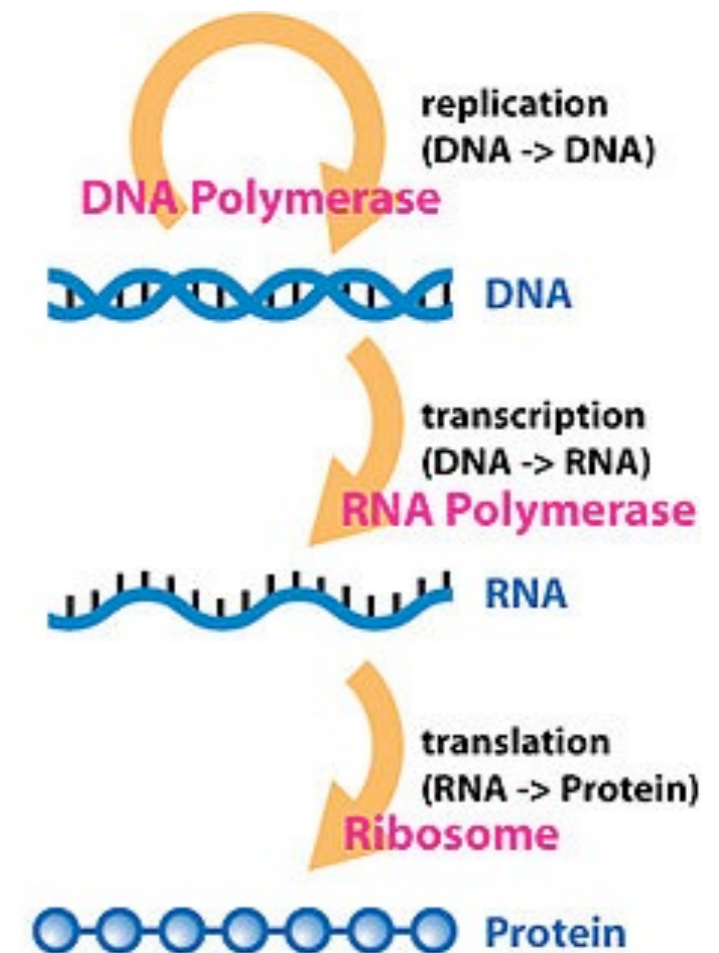


# Proteins

Molecular Machinery

# Proteins & the Central *Dogma* (of Biology)

- Proteins are a **diverse** and **abundant** class of biomolecules, constituting more than 50% of the dry weight of cells.
- The pattern by which each is tailored resides within the genetic information of cells, encoded in a specific sequence of nucleotide bases in DNA.

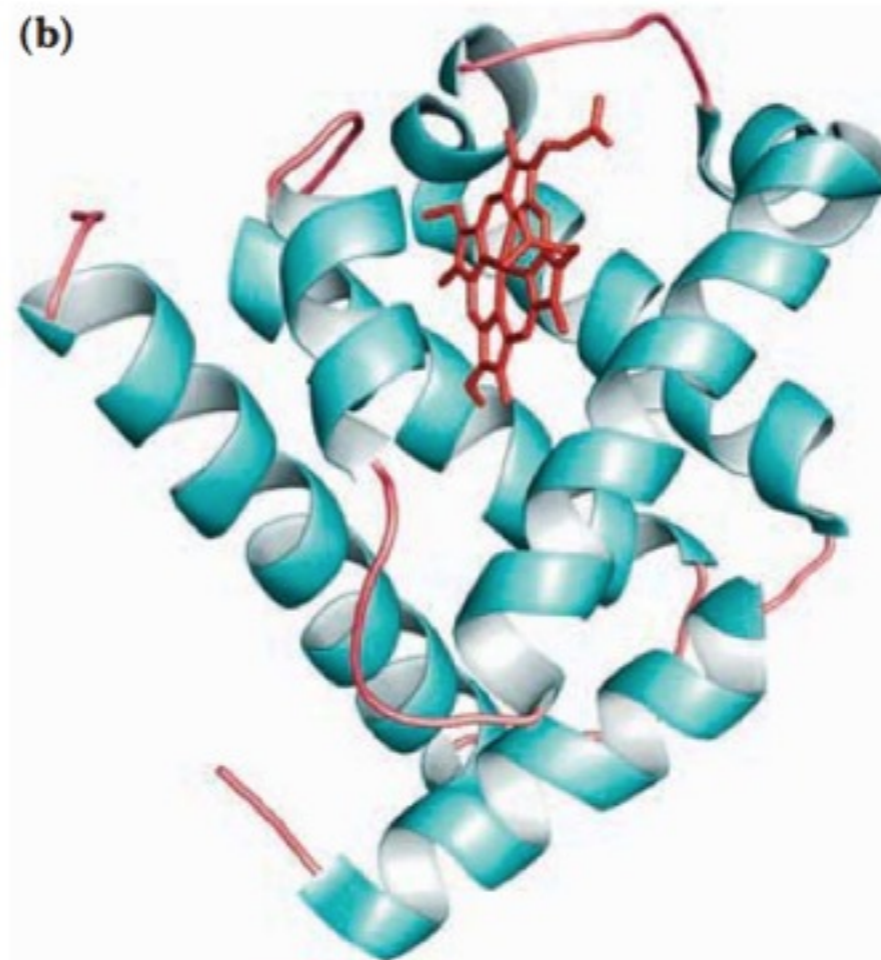


# Protein Classes

- Classification based on shape & solubility



Bacteriorhodopsin, a membrane protein



Myoglobin, a globular protein

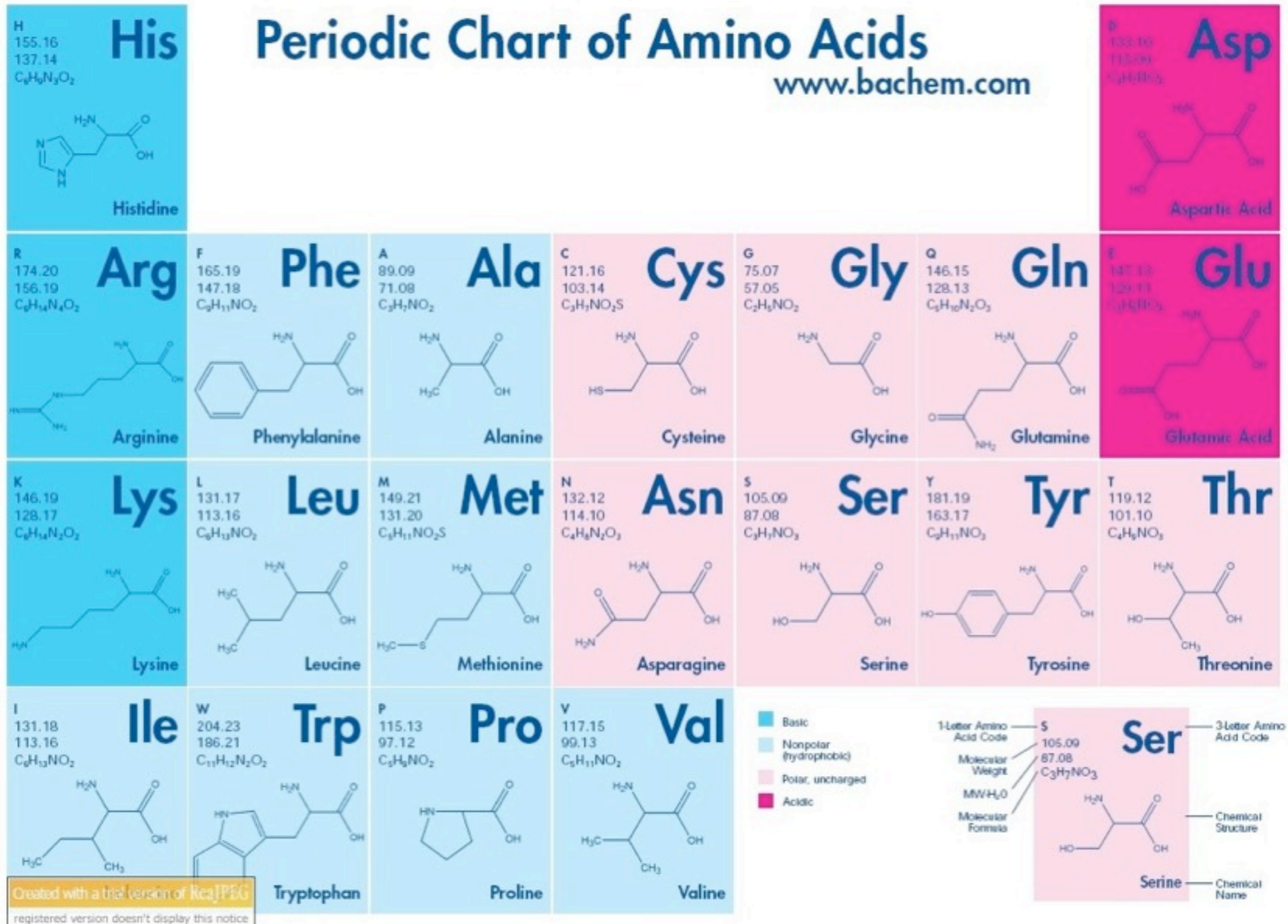


Collagen, a fibrous protein

# Amino Acids

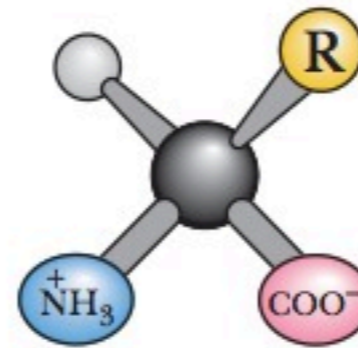
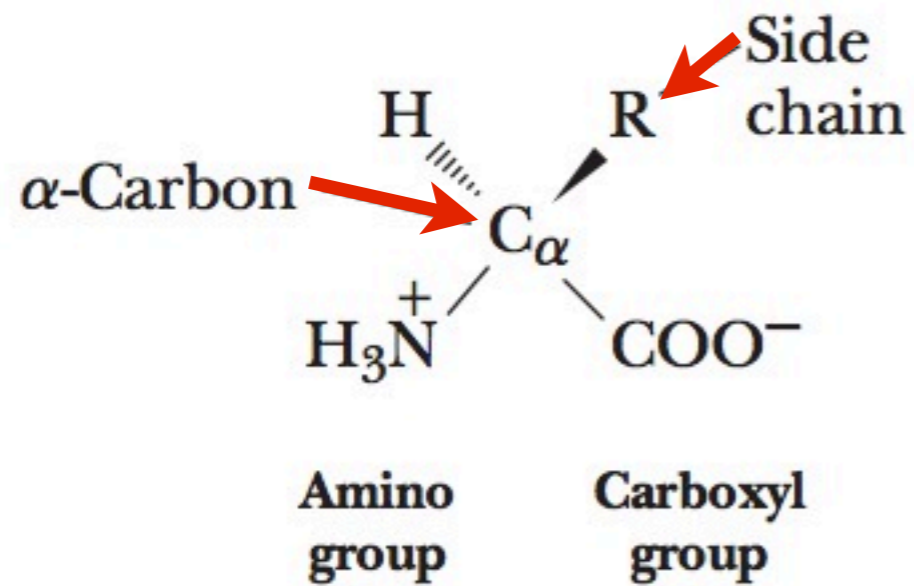
## Periodic Chart of Amino Acids

www.bachem.com

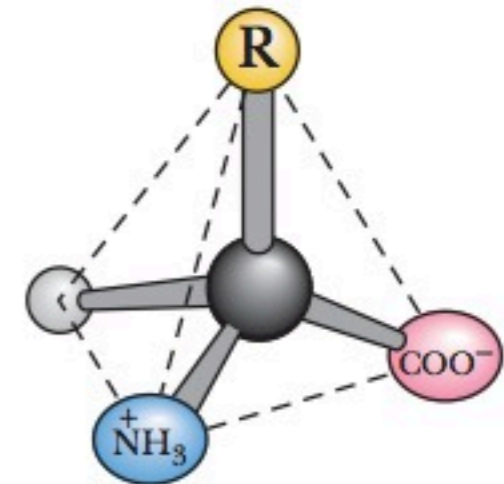


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registered version doesn't display this notice

# Anatomy of Amino Acids

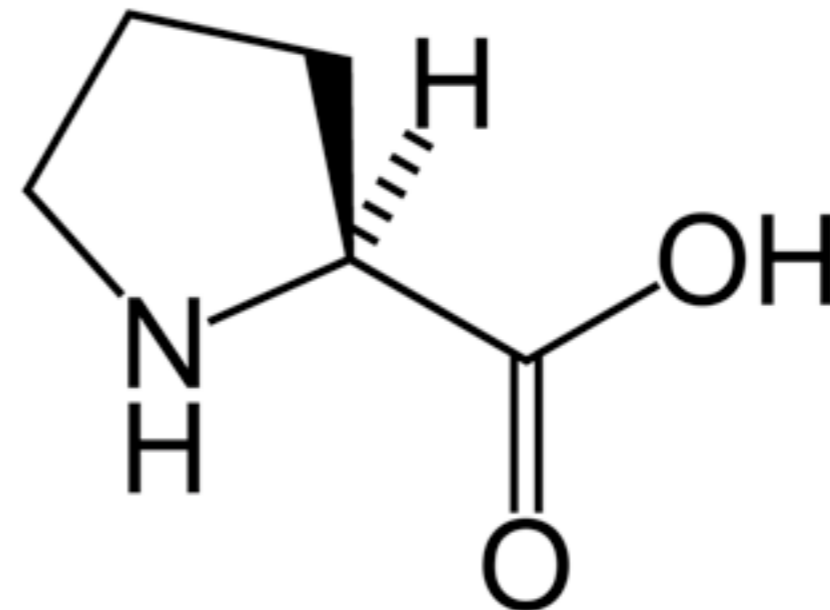


Ball-and-stick model

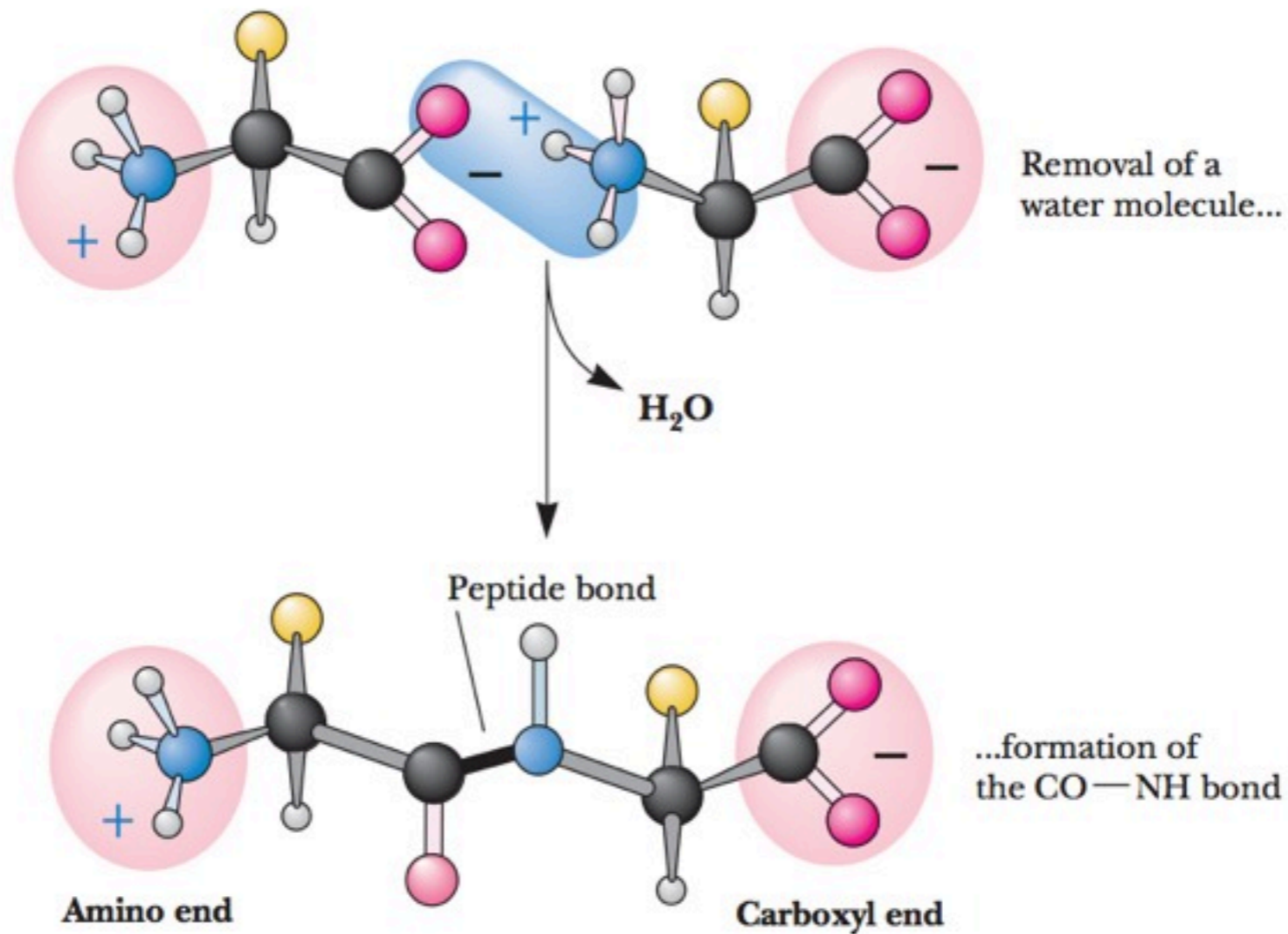
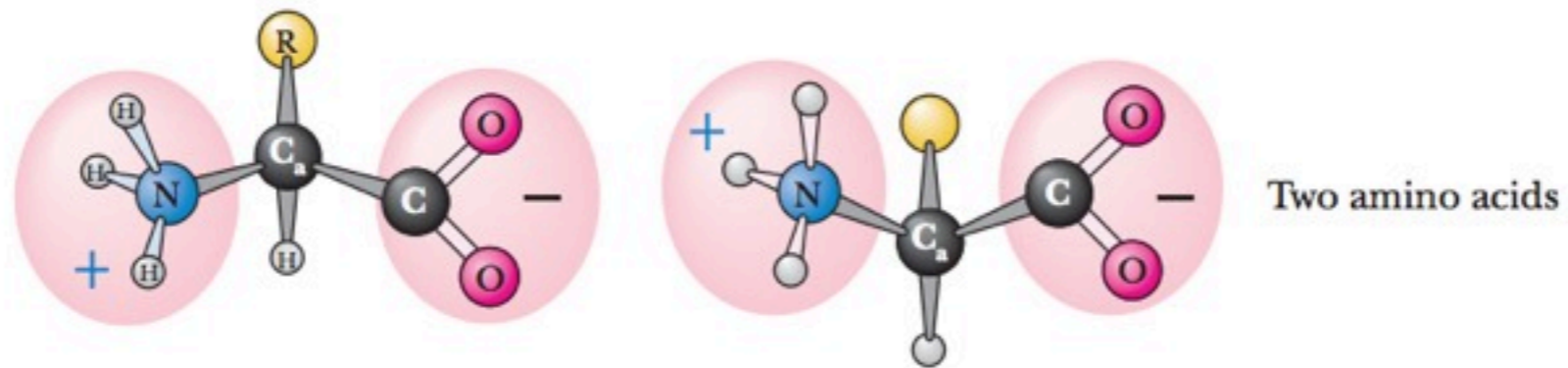


Amino acids are tetrahedral structures

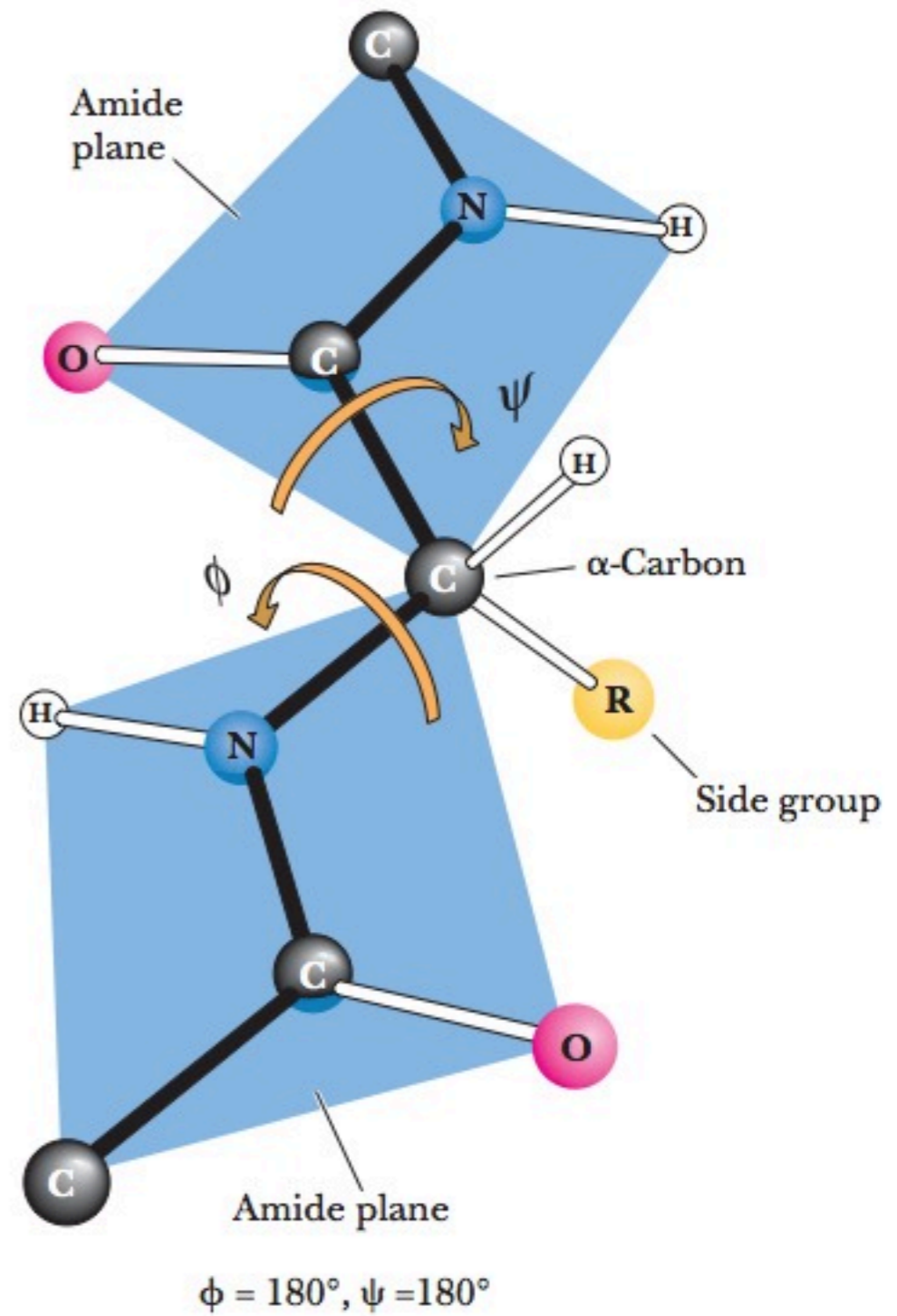
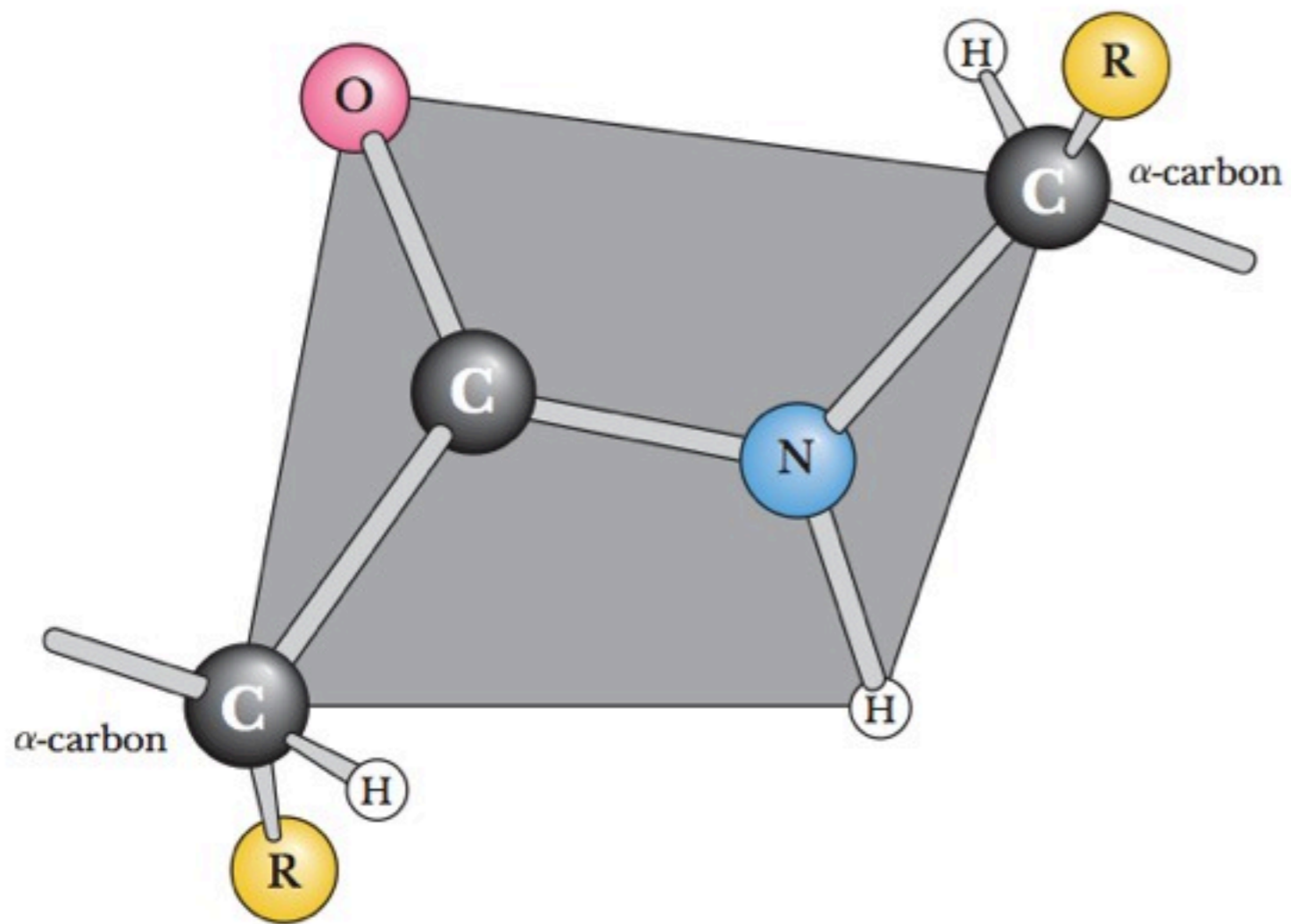
- The only exception is proline (PRO)



# Peptide Bonds

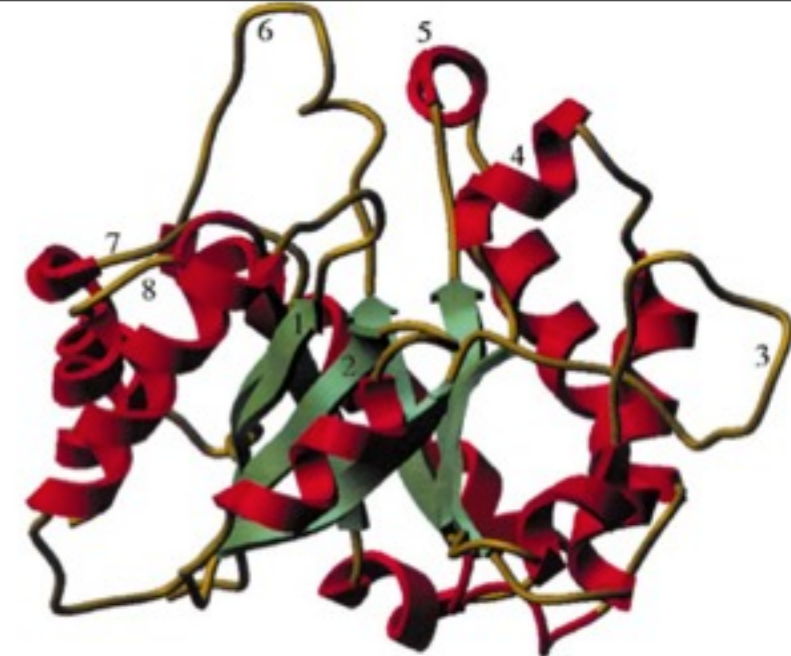


# Dihedral Angles

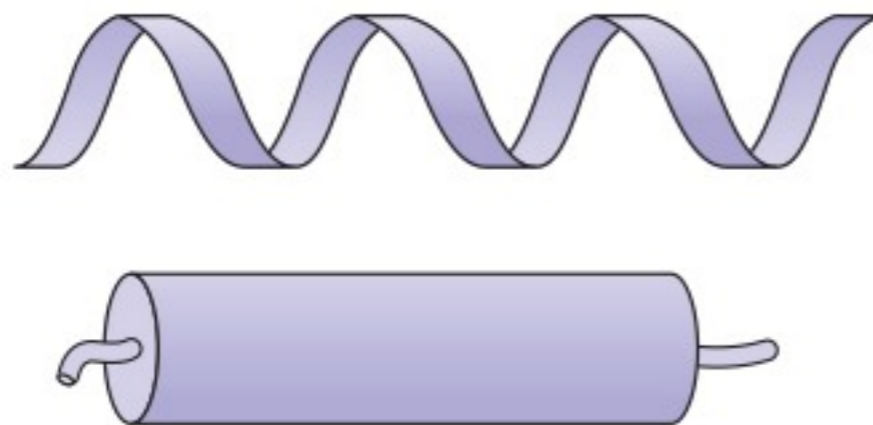


# Structure Levels

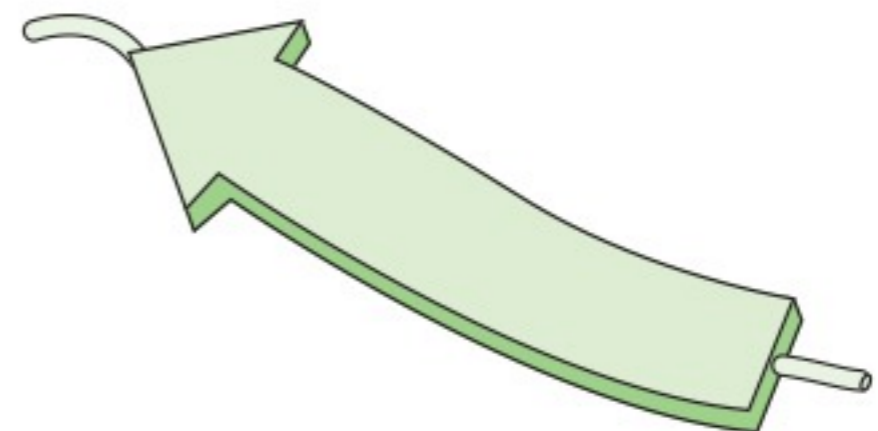
- **Modeling:** coarse-grained VS all-atom
- Primary structure: the amino acid sequence (covalent bonds)
- Secondary structure: through **hydrogen-bonding** interactions between adjacent amino acid residues (“short-range” hydrogen-bond interactions) [alpha-helix; **beta-sheet**]
- Tertiary structure: when the polypeptide chains of protein molecules bend and fold in order to assume (“long-range” non-covalent interactions)
- Quaternary structure: two or more interacting poly-peptide chains of characteristic tertiary structure



“Shorthand”  $\alpha$ -helix



“Shorthand”  $\beta$ -strand

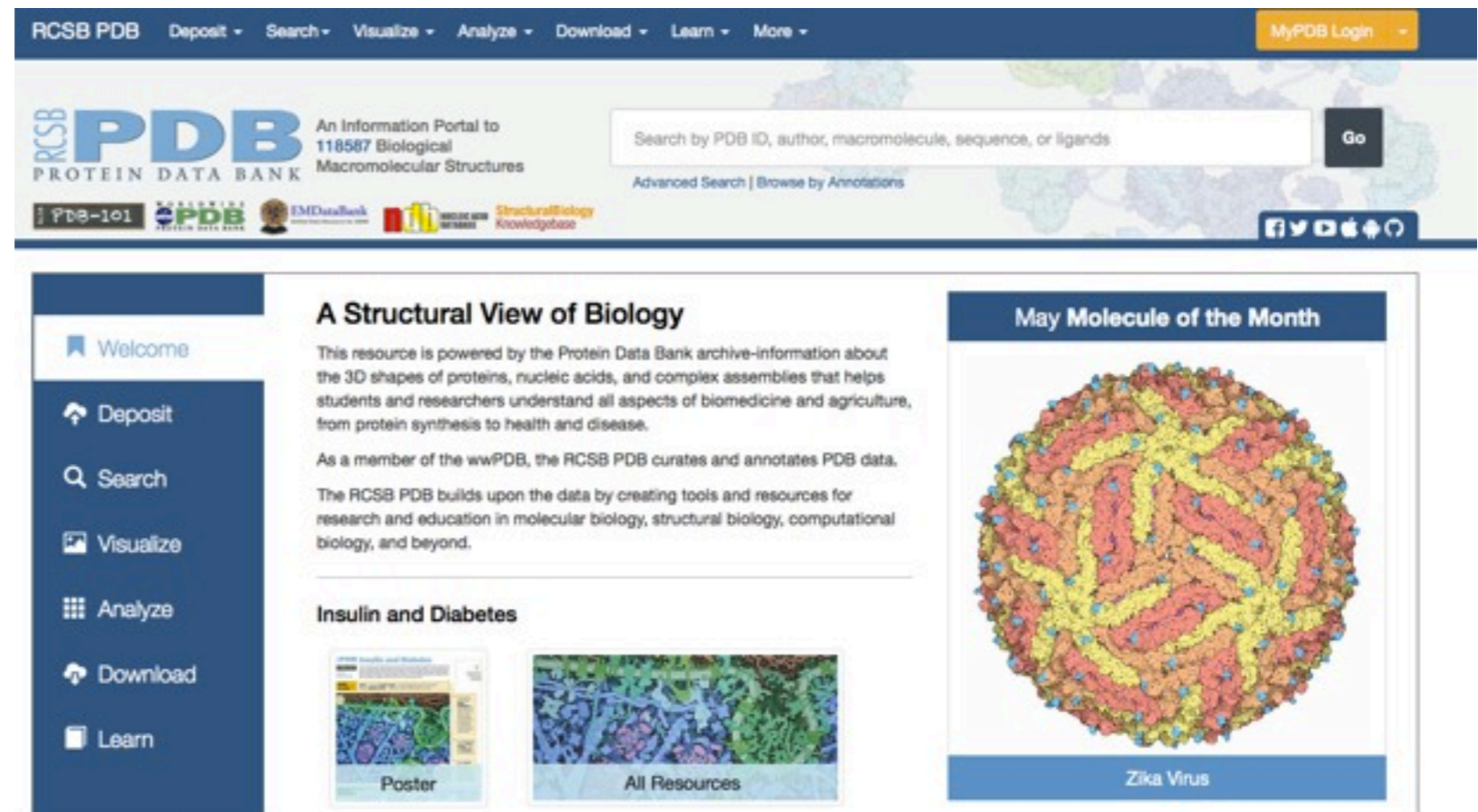


It is important to emphasize that **“all”** the information necessary for a protein molecule to achieve its intricate architecture is contained within its primary structure!



# Homology: Sequence VS Structure

- In the context of proteomics, homology is the existence of shared ancestry between a pair of molecules
- Homologous proteins from different organisms have homologous amino acid sequences
- Computer programs can align sequences and discover homology between proteins
- **Structural similarity**: structure is more evolutionarily conserved than sequence!
- Experimental methods for structure determination: X-ray diffraction (solid state) & NMR (solution)
- Protein Data Bank



The image shows the homepage of the RCSB Protein Data Bank (PDB). The header includes navigation links: Deposit, Search, Visualize, Analyze, Download, Learn, and More, along with a MyPDB Login button. The main content area features the PDB logo, a search bar with the text "Search by PDB ID, author, macromolecule, sequence, or ligands", and a "Go" button. Below the search bar are links for "Advanced Search" and "Browse by Annotations". The page is divided into several sections: a left sidebar with navigation options (Welcome, Deposit, Search, Visualize, Analyze, Download, Learn), a central section titled "A Structural View of Biology" with text about the PDB's mission and a link to "Insulin and Diabetes" resources, and a right section titled "May Molecule of the Month" featuring a 3D model of the Zika Virus and a link to "Zika Virus" resources.