Protein structure
(and biomolecular structure more generally)

CS/CME/BioE/Biophys/BMI 279
Sept. 28 and Oct. 3, 2017
Ron Dror
• Please interrupt if you have questions, and especially if you’re confused!

• Assignment 1 will be posted shortly
  – Look through it, especially the final problem, to decide whether to attend the tutorial next Wednesday (or, alternatively, ask the TAs for help during office hours)
Outline

• Visualizing proteins
• The Protein Data Bank (PDB)
• Chemical (2D) structure of proteins
• What determines the 3D structure of a protein? Physics underlying biomolecular structure
  – Basic interactions
  – Complex interactions
• Protein structure: a more detailed view
  – Properties of amino acids
  – Secondary structure
  – Tertiary structure, quaternary structure, and domains
• Structures of other biomolecules
Visualizing proteins
Protein surrounded by other molecules (mostly water)

Water (and salt ions)

Cell membrane (lipids)

Protein (adrenaline receptor)
Protein only

Adrenaline receptor
Protein only — simplified representation

Adrenaline receptor
Key take-aways from these visualizations

- Protein is a long chain of amino acids.
- Protein and surrounding atoms fill space (close-packed).
- There are a lot of atoms. Simplified visual representations help you figure out what’s going on.
The Protein Data Bank (PDB)
The Protein Data Bank (PDB)

• Examples of structures from PDB.

https://upload.wikimedia.org/wikipedia/commons/thumb/2/24/Protein_structure_examples.png/1024px-Protein_structure_examples.png
(Axel Griewel)

You’re not responsible for these; they’re just examples.
The Protein Data Bank (PDB)

- [http://www.rcsb.org/pdb/home/home.do](http://www.rcsb.org/pdb/home/home.do)
- A collection of (almost) all published experimental structures of biomacromolecules (e.g., proteins)
- Each identified by 4-character code (e.g., 1rcx)
- Currently ~134,000 structures. 90% of those are determined by x-ray crystallography.
- Browse it and look at some structures. Options:
  - 3D view in applet on PDB web pages
  - PyMol: fetch 1rcx
  - VMD: mol pdbload 1rcx
The Protein Data Bank (PDB)
Chemical (two-dimensional) structure of proteins
Two-dimensional (chemical) structure vs. three-dimensional structure

- Two-dimensional (chemical) structure shows *covalent bonds* between atoms. Essentially a graph.
- Three-dimensional structure shows relative positions of atoms.

Proteins are built from amino acids

- 20 “standard” amino acids
- Each has three-letter and one-letter abbreviations (e.g., Threonine = Thr = T; Tryptophan = Trp = W)

The “side chain” is different in each amino acid.

All amino acids have this part in common.

You don’t need to memorize all the structures

https://en.wikipedia.org/wiki/Proteinogenic_amino_acid
That's right, four eyes! You're nothing without me! While I'm an essential part of any protein, even yours, you're still a so-so professor with no chance of tenure! Haha!

A mean o' acid

Source unknown. American Scientist?
Asparagine

by Robin Betz
Proteins are chains of amino acids

- Amino acids link together through a chemical reaction ("condensation")

\[
\begin{array}{c}
\text{H}_2\text{N}\text{C}^\text{-}\text{COOH} + \text{H}_2\text{N}\text{-}\text{C}^\text{-}\text{COOH} \rightarrow \text{H}_2\text{N}\text{-}\text{C}^\text{-}\text{N}^\text{-}\text{C}^\text{-}\text{COOH} + \text{H}_2\text{O}
\end{array}
\]

http://en.wikipedia.org/wiki/Condensation_reaction

- Elements of the chain are called "amino acid residues" or just "residues" (important term!)
- The bonds linking these residues are "peptide bonds." The chains are also called "polypeptides"
Proteins have uniform backbones with differing side chains


From Protein Structure and Function by Gregory A Petsko and Dagmar Ringe

© 1999-2004 New Science Press
What determines the 3D structure of a protein?
Physics underlying biomolecular structure
Why do proteins have well-defined structure?

• The sequence of amino acids in a protein (usually) suffices to determine its structure.
• A chain of amino acids (usually) “folds” spontaneously into the protein’s preferred structure, known as the “native structure”
• Why?
  – Intuitively: some amino acids prefer to be inside, some prefer to be outside, some pairs prefer to be near one another, etc.
  – To understand this better, examine forces acting between atoms
What determines the 3D structure of a protein? Physics underlying biomolecular structure

Basic interactions
Geometry of an atom

• To a first approximation (which suffices for the purposes of this course), we can think of an atom simply as a sphere.

• It occupies a position in space, specified by the \((x, y, z)\) coordinates of its center, at a given point in time.
Geometry of a molecule

• A molecule is a set of atoms connected in a graph
• \((x, y, z)\) coordinates of each atom specify its geometry
Alternatively, we can specify the geometry of a molecule using bond lengths, bond angles, and torsion angles.
Forces between atoms

• We can approximate the total energy as a sum of individual contributions. Terms are additive.
  – Thus force on each atom is also a sum of individual contributions. Remember: force is the derivative of energy.
  – We will ignore quantum effects. Think of atoms as balls and forces as springs.

• Two types of forces:
  – Bonded forces: act between closely connected sets of atoms in bond graph
  – Non-bonded forces: act between all pairs of atoms
Bond length stretching

• A bonded pair of atoms is effectively connected by a spring with some preferred (natural) length. Stretching or compressing it requires energy.
Bond angle bending

- Likewise, each bond angle has some natural value. Increasing or decreasing it requires energy.
Torsional angle twisting

- Certain values of each torsional angle are preferred over others.
Electrostatic interaction

- Like charges repel. Opposite charges attract.
- Acts between all pairs of atoms, including those in different molecules.
- Each atom carries some "partial charge" (may be a fraction of an elementary charge), which depends on which atoms it’s connected to.
van der Waals interaction

- van der Waals forces act between all pairs of atoms and do not depend on charge.
- When two atoms are too close together, they repel strongly.
- When two atoms are a bit further apart, they attract one another weakly.

Energy is minimal when atoms are “just touching” one another.
What determines the 3D structure of a protein?
Physics underlying biomolecular structure

Complex interactions
Hydrogen bonds

- Favorable interaction between an electronegative atom (e.g., N or O) and a hydrogen bound to another electronegative atom
- Result of multiple electrostatic and van der Waals interactions
- Very sensitive to geometry of the atoms (distance and alignment)
- Strong relative to typical van der Waals or electrostatic forces
- Critical to protein structure
Hydrogen bonds

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Water molecules form hydrogen bonds

- Water molecules form extensive hydrogen bonds with one another and with protein atoms
- The structure of a protein depends on the fact that it is surrounded by water

Hydrophilic vs. hydrophobic

- Hydrophilic molecules are polar and thus form hydrogen bonds with water
  - Polar = contains charged atoms. Molecules containing oxygen or nitrogen are usually polar.
- Hydrophobic molecules are apolar and don’t form hydrogen bonds with water

Hydrophilic (polar)  
\[
\begin{array}{c}
\text{H} \\
\text{H-H-C-O-H-H} \\
\text{H}
\end{array}
\]

Hydrophobic (apolar)  
\[
\begin{array}{c}
\text{H} \\
\text{H-H-C-H-H} \\
\text{H}
\end{array}
\]
Hydrophobic effect

• Hydrophobic molecules cluster in water
  – “Oil and water don’t mix”

• This is critical to protein structure
EXPLAINING HYDROPHOBICITY

- Water molecules next to solute cannot move freely.
- They are ordered and have less entropy. They are unhappy.
- The system changes so that fewer water molecules are in the surface layer.
- The hydrophobic solutes aggregate.

Slide from Michael Levitt
We will discuss entropy next week. If this isn’t clear now, don’t worry.
Protein structure: a more detailed view
“Levels” of protein structure

• Primary structure: sequence of amino acids
• Secondary structure: local structural elements
• Tertiary structure: overall structure of the polypeptide chain
• Quaternary structure: how multiple polypeptide chains come together
Protein structure: a more detailed view

Properties of amino acids
Proteins are built from amino acids

- 20 “standard” amino acids
- Each has three-letter and one-letters abbreviations (e.g., Threonine = Thr = T; Tryptophan = Trp = W)

The “side chain” is different in each amino acid

All amino acids have this part in common.

You don’t need to memorize all the structures

https://en.wikipedia.org/wiki/Proteinogenic_amino_acid
Amino acid properties

• Amino acid side chains have a wide range of properties. These differences bring about the 3D structures of proteins.

• Examples:
  – Large side chains take up more space than small ones
  – Hydrophobic side chains want to be near one another
  – Hydrophilic side chains form hydrogen bonds to one another and to water molecules
  – Negatively charged (acidic) side chains want to be near positively charged (basic) side chains
Amino acid properties

You don’t need to memorize which amino acids have which properties.

There are many properties. They cluster logically.

Slide from Michael Levitt
Protein structure: a more detailed view

Secondary structure
Secondary structure

• “Secondary structure” refers to certain local structural elements found in many proteins
  – These are energetically favorable primarily because of hydrogen bonds between backbone atoms

• Most important secondary structure elements:
  – alpha helix
  – beta sheet

https://upload.wikimedia.org/wikipedia/commons/6/60/Myoglobin.png

http://www.biotek.com/assets/tech_resources/11596/figure2.jpg
http://upload.wikimedia.org/wikipedia/commons/e/e6/Spombe_Pop2p_protein_structure_rainbow.png
The alpha helix

Image from “Protein Structure and Function” by Gregory A Petsko and Dagmar Ringe
The alpha helix

Linus Pauling

https://www.msu.edu/course/lbs/333/fall/images/PAULING.JPG
Reserved for
Nobel Laureate
Nobel Laureate Reserved Space
Parking Permit Required At All Times

Violators will be cited and/or towed
Per UCB violation codes 010-1000-YC 2265m
For Towed Vehicles Call 310.842.3700
The beta sheet

From Michael Levitt
The beta sheet

From Michael Levitt
Other secondary structure

- There are several less common secondary structures
- Regions connecting well-defined secondary structure elements are often referred to as “loops”
The remaining backbone bond (N–C, the “peptide bond”) is rigid.

From Michael Levitt

- The torsion angle rotating about the N–CA bond is called $\phi$.
- The torsion angle rotating about the CA–C bond is called $\psi$.
- Together they are the $(\phi, \psi)$ angles.
Ramachandran diagrams

• A plot showing a distribution in the ($\Phi$, $\Psi$) plane is called a Ramachandran diagram
  – Such a diagram can be a scatterplot, or a two-dimensional histogram visualized as a contour map or heat map
  – For example, one might make a Ramachandran diagram for many residues of the same amino acid type

• Some amino acid types have distinctive Ramachandran diagrams

• Alpha helices and beta sheets have characteristic Ramachandran diagrams
Protein structure: a more detailed view

Tertiary structure, quaternary structure, and domains
Tertiary structure

- Tertiary structure: the overall three-dimensional structure of a polypeptide chain

Myoglobin

Green Fluorescent Protein

Pop2p
Quaternary structure

- Quaternary structure: the arrangement of multiple polypeptide chains in a larger protein
Domains

• Large proteins often consist of multiple compact 3D structures called *domains*
  – Many contacts with a domain. Few contacts between domains.
  – “Domain \(\approx\) blob”

• One polypeptide chain can form multiple domains

http://en.wikipedia.org/wiki/Protein_domain
Disulfide bonds

• One particular amino acid type, cysteine, can form a covalent bond with another cysteine (called a disulfide bond or bridge)
• Apart from the bonds within an amino acid residue and the peptide bonds that connect residues, disulfide bonds are the only common covalent bonds within a protein
• In a typical cellular environment, disulfide bonds can be formed and broken quite easily

http://www.crc.dk/yeast/yeasthome/yeasthome/images/ls_jpgs/fig2.jpg
Structures of other biomolecules
What determines the structure of other biomolecules?

- The physical interactions that determine protein structure also determine the structures of other biomolecules
  - More generally, the great majority of the material covered in this course for proteins applies to other biomolecules as well
DNA

- DNA (deoxyribonucleic acid) stores the genetic code
- DNA, like protein, is a string of units with a uniform backbone
  - The units are nucleotides, instead of amino acid residues
  - Different nucleotides contain different nucleobases (bases) instead of side chains
- Only four common DNA bases
  - Adenine pairs with Thymine
  - Guanine pairs with Cytosine

Khan Academy (https://ka-perseus-images.s3.amazonaws.com/9d1d07df110f35ba532c792c73bceb164679a165.png)
DNA

- DNA forms one dominant 3D structure: a double helix
  - DNA acts more as information storage than as “machinery”
  - Long stretches of double helix can form coarser-scale structures, as we’ll see later on

http://www.nature.com/scitable/content/ne0000/ne0000/ne0000/104944953/73_1_2.jpg
Cambridge, 1953. Shortly before discovering the structure of DNA, Watson and Crick, depressed by their lack of progress, visit the local pub.
RNA

• RNA (ribonucleic acid) is a string of nucleotides, like DNA
• RNA, however, generally occurs as a single string (strand) rather than paired strands
• RNA bases often pair with other bases in the same RNA strand
  – Much work on RNA structure focuses on the “secondary structure”: which bases pair with one another
  – Note that “secondary structure” has different meanings for RNA and protein
• RNA can form machines with well-defined, varied 3D structure
  – Example: RNA in the ribosome

http://www.tbi.univie.ac.at/~pkerp/forgi/_images/1y26_ss.png
Small molecules

- Most drugs and many hormones, neurotransmitters, and other natural signaling molecules are “small molecules” (~100 atoms or fewer)
- Cambridge Structural Database is a repository of small molecule 3D structures, generally from x-ray crystallography
- However, these molecules are usually highly flexible and thus likely to take on a different 3D structure when bound to a protein

Adrenaline (epinephrine)

https://upload.wikimedia.org/wikipedia/commons/thumb/7/76/Epinephrine_ball-and-stick_model.png

LSD on its own (yellow) and receptor-bound (magenta)

Wacker et al., Cell (2017)