Lecture 9: Super-secondary Structure & Domains

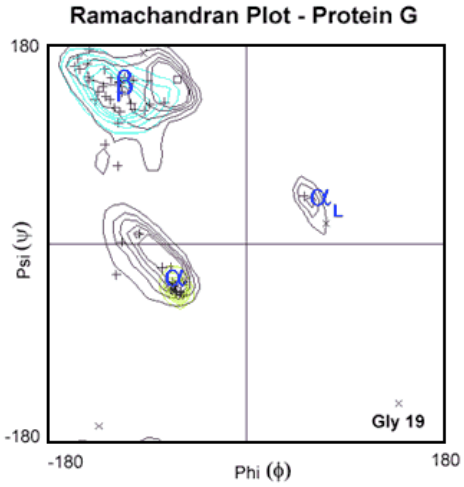
Assigned reading in Campbell: Chapter 4.3

Key Terms:

- Preferred ∏ and ∏ angles in secondary structures (Ramachandran Plot)
- Preferred side chains in ∏-helices, ∏-strands and ∏-turns
- Super-secondary structures or motifs (eg, ∏-∏-∏, ∏-meander, Greek key)
- Domains (eg, ∏-sandwich, ∏-barrel)

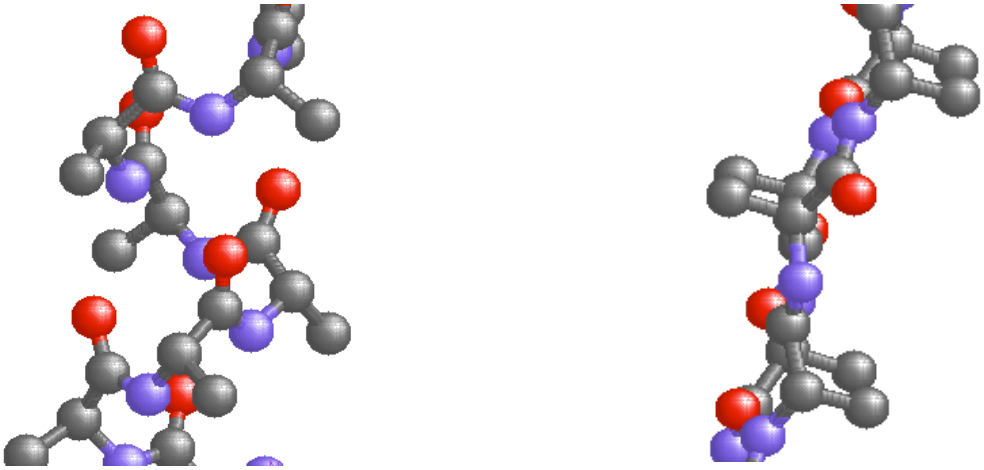
Ramachandran plot:

The entire path of the *peptide backbone* in a protein is known if the ∏ and ∏ angles are specified (note: this is not the entire 3-D structure). Many combinations of ∏ and ∏ angles are not allowed due to steric clash. Those combinations that *are* sterically allowed represent the subclasses of common secondary structure found in most proteins.



The existence of favorable combinations of∏ and ∏ angles in proteins is exemplified by the Ramachandran plot. Note the clustering of ∏ and ∏ values in a few regions of the plot. Sparsely populated regions of the plot represent unfavorable combinations of∏ and ∏ values.

Side-chain packing in an ∏-helix versus a ∏-sheet:



Conformational Preferences of the Amino Acids (adapted from Biochim. Biophys. Acta, 1987, 916:200-204).

Amino acid	∏-helix	∏-strand	Reverse turn
Glu	1.59	0.52	1.01
Ala	1.41	0.72	0.82
Leu	1.34	1.22	0.57
Met	1.30	1.14	0.52
Gln	1.27	0.98	0.84
Lys	1.23	0.69	1.07
Arg	1.21	0.84	0.90
His	1.05	0.80	0.81

Val	0.90	1.87	0.41
Ile	1.09	1.67	0.47
Tyr	0.74	1.45	0.76
Cys	0.66	1.40	0.54
Trp	1.02	1.35	0.65
Phe	1.16	1.33	0.59
Thr	0.76	1.17	0.90
Gly	0.43	0.58	1.77
Asn	0.76	0.48	1.34
Pro	0.34	0.31	1.32
Ser	0.57	0.96	1.22
Asp	0.99	0.39	1.24

Super-secondary Structures: Small structural motifs that contain elements of secondary structure.

□□□	
□□	
□-hairpin	Helix-loop-Helix
□-meander	Coiled-coil
Greek key	Helix bundle

Domains: Discrete, independently folded, compact units consisting of various elements of supersecondary structure. Domains range from ~30 to ~300 amino acids, with an average of ~100 amino acids.

Most proteins are built up in a modular fashion from two or more domains fused together. It appears that the number of protein folds, or domains, in nature is limited. They are used repeatedly in different combinations to create the diversity of proteins found in living organisms.

Some common domains:

- **β-barrel**:
  - Often formed from either a β-meander or a Greek key
  - Provides a mechanism for completing all H-bonds in a β-sheet; otherwise the β-strands at the edge of the sheet must H-bond with water.
  - β-strands are often joined by α-helices around the outside of the barrel.
- **β-sandwich:**
  - Two separate β-sheets pack together face to face.
  - Two sheets are often at right angles to one another.
  - End strands are not H-bonded to one another.
- **α/β barrel:**
  - β-α-β-α motif is repeated four or more times.
  - The strand order is consecutive.
  - Forms a closed barrel.
  - This is the most common domain fold, occurring in 10% of all enzyme structures.